Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				1.00E-30	102.39	1150.38	48.20	226529.8
AHQ-1-2, 2081 - 2102	R.ALEEAMEQK.A	1049.18068	2	2.60E-04	0.90	3.40	-	1012.8
AHQ-1-3, 2030	R.ALEEAMEQK.A	1049.18068	1	8.60E-04	0.60	2.44	-	769.9
AHQ-1-2, 2058 - 2125	R.ALEEAMEQK.A	1049.18068	1	1.65E-04	0.33	2.22	-	626.6
AHQ-1-1, 2201	R.ALEEAMEQK.A	1049.18068	2	4.13E-05	0.92	3.58	-	1020.0
AHQ-1-4, 2020	R.ALEEAMEQK.A	1049.18068	2	5.24E-04	0.74	2.79	-	714.7
AHQ-1-1, 3891	K.ALELDSNLYR.I	1194.31920	2	9.12E-07	0.94	3.54	-	1216.7
AHQ-1-3, 3809	K.ALELDSNLYR.I	1194.31920	1	4.26E-06	0.10	2.26	-	212.2
AHQ-1-4, 3843	K.ALELDSNLYR.I	1194.31920	2	9.53E-07	0.95	4.14	-	1120.9
AHQ-1-3, 3806 - 3813	K.ALELDSNLYR.I	1194.31920	2	5.38E-08	0.94	4.04	-	1107.4
AHQ-1-5, 3721	K.ALELDSNLYR.I	1194.31920	1	7.75E-04	0.13	2.27	-	206.1
AHQ-1-2, 3821	K.ALELDSNLYR.I	1194.31920	2	9.25E-08	0.95	3.64	-	1496.1
AHQ-1-13- , 3863	K.ALELDSNLYR.I	1194.31920	2	8.93E-06	0.85	3.20	-	863.0
AHQ-1-5, 3707 - 3713	K.ALELDSNLYR.I	1194.31920	2	1.35E-07	0.95	4.03	-	1267.7
AHQ-1-2, 3943 - 4013	K.ALELDSNLYR.I	1194.31920	2	6.09E-07	0.95	4.07	-	1145.5
AHQ-1-3, 3905	K.ALELDSNLYR.I	1194.31920	2	9.05E-06	0.86	2.85	-	1006.6
AHQ-1-6, 2782	R.ALEQQVEEMK.T	1205.36380	2	4.06E-05	0.84	3.23	-	835.8
AHQ-1-3, 2873	R.ALEQQVEEMK.T	1205.36380	2	1.20E-04	0.83	3.32	-	974.6
AHQ-1-1, 3000	R.ALEQQVEEMK.T	1205.36380	2	3.10E-05	0.89	3.17	-	1083.9
AHQ-1-2, 2981 - 3059	R.ALEQQVEEMK.T	1205.36380	2	2.20E-05	0.90	3.66	-	1014.8
AHQ-1-2, 2215	R.ALEQQVEEM*K.T	1221.36320	2	5.09E-06	0.80	3.44	-	794.6
AHQ-1-7, 2813	R.ALEQQVEEMK.T	1205.36380	2	5.90E-04	0.77	2.94	-	919.0
AHQ-1-1, 2280	R.ALEQQVEEM*K.T	1221.36320	2	4.05E-06	0.82	2.97	-	928.1
AHQ-1-3, 2138	R.ALEQQVEEM*K.T	1221.36320	2	2.84E-05	0.82	3.40	-	874.5
AHQ-1-4, 2890 - 2891	R.ALEQQVEEMK.T	1205.36380	2	7.47E-05	0.90	3.65	-	1027.1
AHQ-1-5, 2006	R.ALEQQVEEM*K.T	1221.36320	2	4.34E-05	0.67	2.83	-	770.8
AHQ-1-3, 6527 - 6589	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.62E-12	0.97	6.15	-	1761.3
AHQ-1-2, 7349	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	5.26E-07	0.96	6.21	-	1493.5
AHQ-1-2, 6951 - 7026	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	6.37E-09	0.97	5.76	-	1838.1
AHQ-1-1, 6456 - 6471	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	5.16E-14	0.97	5.91	-	1958.4
AHQ-1-2, 6713 - 6777	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.24E-11	0.97	6.07	-	1638.4
AHQ-1-3, 7209	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	3.00E-08	0.96	5.58	-	1405.8
AHQ-1-6, 6470 - 6538	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	3.26E-07	0.96	5.99	-	1293.7
AHQ-1-4, 7386	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	1.41E-05	0.96	6.15	-	1244.7
AHQ-1-5, 6634	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.56E-08	0.95	5.75	-	1044.2
AHQ-1-2, 5537	K.ANLQIDQINTDLNLER.S	1871.04187	2	7.19E-09	0.97	5.83	-	1302.7
AHQ-1-3, 5391	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.03E-08	0.97	5.74	-	1435.3
AHQ-1-3, 5102 - 5175	K.ANLQIDQINTDLNLER.S	1871.04187	2	5.38E-11	0.98	6.06	-	1555.4
AHQ-1-10, 4577	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.65E-06	0.96	5.08	-	1432.6
AHQ-1-8, 5091	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.45E-05	0.97	5.10	-	1538.6
AHQ-1-2, 5093	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.25E-06	0.96	5.22	-	874.6
AHQ-1-4, 4966 - 5034	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.79E-05	0.83	4.17	-	408.8
AHQ-1-2, 5230 - 5301	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.08E-10	0.98	6.18	-	1786.5
AHQ-1-4, 5242	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.46E-06	0.87	3.74	-	643.4
AHQ-1-9, 5011	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.98E-04	0.97	5.19	-	1550.6
AHQ-1-1, 5387	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.74E-04	0.97	4.95	-	1762.1
AHQ-1-1, 5189 - 5251	K.ANLQIDQINTDLNLER.S	1871.04187	2	5.97E-04	0.97	5.35	-	1315.4
AHQ-1-2, 5369 - 5438	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.56E-07	0.98	7.12	-	1738.0
AHQ-1-6, 5094 - 5096	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.78E-07	0.96	4.82	-	1178.2
AHQ-1-1, 4980	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.15E-08	0.94	4.83	-	700.2
AHQ-1-3, 5267	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.73E-10	0.97	5.78	-	1276.1
AHQ-1-5, 2215	K.ASITALEAK.I	904.04321	2	5.19E-06	0.90	3.02	-	954.5
AHQ-1-4, 2367	K.ASITALEAK.I	904.04321	2	2.59E-06	0.89	2.91	-	913.0
AHQ-1-1, 2512	K.ASITALEAK.I	904.04321	2	5.98E-05	0.92	3.01	-	1125.4
AHQ-1-2, 2445	K.ASITALEAK.I	904.04321	2	2.30E-06	0.90	3.14	-	940.9
AHQ-1-3, 2350	K.ASITALEAK.I	904.04321	2	1.40E-04	0.92	2.94	-	1120.5
AHQ-1-1, 2237	R.ASREEILAQAK.E	1216.36955	2	1.84E-05	0.92	3.32	-	1417.8
AHQ-1-3, 2063	R.ASREEILAQAK.E	1216.36955	2	4.00E-06	0.93	3.54	-	1583.8
AHQ-1-2, 2115 - 2174	R.ASREEILAQAK.E	1216.36955	2	9.21E-05	0.91	3.24	-	1360.2
AHQ-1-4, 2044	R.ASREEILAQAK.E	1216.36955	2	1.41E-06	0.91	3.38	-	1467.0
AHQ-1-2, 3317	R.DELADEIANSSGK.G	1349.38323	2	2.19E-07	0.97	4.56	-	1896.4
AHQ-1-1, 3284	R.DELADEIANSSGK.G	1349.38323	2	1.64E-05	0.93	4.06	-	1012.7
AHQ-1-3, 3214	R.DELADEIANSSGK.G	1349.38323	2	3.87E-07	0.97	4.29	-	1792.8
AHQ-1-6, 6895	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	3.22E-05	0.96	5.08	-	1529.2
AHQ-1-4, 7224	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.48E-06	0.91	3.98	-	1459.1
AHQ-1-1, 6839 - 6911	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	2	1.14E-07	0.94	4.79	-	879.4
AHQ-1-1, 6740	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	3.25E-10	0.98	6.38	-	2039.0
AHQ-1-2, 7199 - 7227	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	6.82E-08	0.93	4.17	-	1395.3
AHQ-1-5, 7038	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	3.87E-05	0.95	4.68	-	1770.4
AHQ-1-3, 6898	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	6.85E-05	0.93	4.32	-	1529.8
AHQ-1-3, 6646	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	1.09E-10	0.84	3.85	-	531.1
AHQ-1-1, 6413	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	3.50E-05	0.70	3.27	-	523.2
AHQ-1-2, 6607 - 6681	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	1.24E-10	0.93	5.54	-	590.2
AHQ-1-3, 6441 - 6511	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	1.19E-12	0.95	5.33	-	982.2
AHQ-1-2, 6749 - 6751	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	4.40E-06	0.62	3.11	-	587.6
AHQ-1-9, 7338	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.99E-06	0.96	5.30	-	1869.5
AHQ-1-2, 7437	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.18E-09	0.97	5.12	-	2058.3
AHQ-1-5, 7505	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	2.71E-07	0.97	5.53	-	2113.2
AHQ-1-7, 7528	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	4.46E-06	0.85	3.85	-	950.2
AHQ-1-3, 7154 - 7223	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.67E-15	0.99	7.55	-	3012.9
AHQ-1-6, 7314	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.46E-08	0.95	5.30	-	1573.8
AHQ-1-1, 7039	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	3.89E-09	0.93	4.51	-	1396.7
AHQ-1-3, 7361	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.29E-08	0.95	5.24	-	1638.8
AHQ-1-2, 3151	R.ELEDATETADAMNR.E	1566.63006	2	2.81E-05	0.75	2.61	-	786.1
AHQ-1-3, 2871	R.ELEDATETADAMNR.E	1566.63006	2	4.35E-08	0.87	3.82	-	845.6
AHQ-1-6, 2794 - 2806	R.ELEDATETADAMNR.E	1566.63006	2	1.78E-04	0.88	3.88	-	844.1
AHQ-1-5, 2806	R.ELEDATETADAMNR.E	1566.63006	2	5.54E-07	0.75	2.92	-	809.8
AHQ-1-2, 2333	R.ELEDATETADAM*NR.E	1582.62946	2	4.82E-05	0.68	2.85	-	643.9
AHQ-1-10, 2685	R.ELEDATETADAMNR.E	1566.63006	2	2.26E-04	0.87	3.51	-	863.0
AHQ-1-4, 2895 - 2900	R.ELEDATETADAMNR.E	1566.63006	2	4.49E-05	0.88	3.59	-	1012.1
AHQ-1-2, 2862	R.ELEDATETADAMNR.E	1566.63006	2	1.57E-05	0.52	2.61	-	306.6
AHQ-1-1, 2936 - 2937	R.ELEDATETADAMNR.E	1566.63006	2	3.31E-06	0.95	4.26	-	1321.7
AHQ-1-3, 2222	R.ELEDATETADAM*NR.E	1582.62946	2	1.51E-04	0.84	3.12	-	814.8
AHQ-1-9, 5834	R.ELESQISELQEDLESER.A	2035.10956	2	9.59E-04	0.92	4.32	-	772.7
AHQ-1-3, 5901	R.ELESQISELQEDLESER.A	2035.10956	2	2.23E-08	0.94	4.93	-	904.5
AHQ-1-3, 5835 - 5905	R.ELESQISELQEDLESER.A	2035.10956	2	2.71E-06	0.97	5.93	-	1426.7
AHQ-1-2, 6141	R.ELESQISELQEDLESER.A	2035.10956	2	2.68E-04	0.82	3.83	-	682.9
AHQ-1-3, 5470	R.ELESQISELQEDLESER.A	2035.10956	2	1.10E-06	0.96	4.74	-	1105.6
AHQ-1-4, 5982 - 6051	R.ELESQISELQEDLESER.A	2035.10956	2	2.43E-04	0.85	4.40	-	822.4
AHQ-1-4, 5484	R.ELESQISELQEDLESER.A	2035.10956	2	1.20E-04	0.83	3.39	-	897.4
AHQ-1-7, 5986	R.ELESQISELQEDLESER.A	2035.10956	2	1.30E-07	0.94	4.67	-	888.4
AHQ-1-2, 5999 - 6070	R.ELESQISELQEDLESER.A	2035.10956	2	1.06E-11	0.94	4.90	-	942.7
AHQ-1-2, 6387	R.ELESQISELQEDLESER.A	2035.10956	2	2.37E-07	0.93	3.99	-	1007.0
AHQ-1-2, 5659	R.ELESQISELQEDLESER.A	2035.10956	2	7.85E-06	0.89	3.98	-	669.2

AHQ-1-2, 6091	R.ELESQISELQEDLESER.A	2035.10956	3	2.47E-06	0.98	6.22	-	2334.7
AHQ-1-1, 5843 - 5907	R.ELESQISELQEDLESER.A	2035.10956	2	2.70E-08	0.94	4.74	-	918.8
AHQ-1-3, 2542	R.EMEAELEDER.K	1251.30306	2	6.75E-04	0.58	2.55	-	479.5
AHQ-1-2, 2285	R.EMEAELEDERK.Q	1379.47597	2	6.03E-05	0.93	3.50	-	1365.7
AHQ-1-1, 2347	R.EMEAELEDERK.Q	1379.47597	2	2.94E-04	0.84	2.80	-	1043.7
AHQ-1-4, 2203	R.EMEAELEDERK.Q	1379.47597	2	7.47E-07	0.90	3.21	-	1237.8
AHQ-1-3, 2205	R.EMEAELEDERK.Q	1379.47597	2	9.53E-05	0.86	2.82	-	1191.1
AHQ-1-2, 4747	K.EQADFAIEALAK.A	1306.44632	1	1.74E-05	0.36	2.64	-	272.6
AHQ-1-3, 4490	K.EQADFAIEALAK.A	1306.44632	2	4.53E-04	0.79	2.71	-	684.4
AHQ-1-2, 4939	K.EQADFAIEALAK.A	1306.44632	2	3.46E-05	0.71	2.75	-	500.1
AHQ-1-2, 4651	K.EQADFAIEALAK.A	1306.44632	1	6.54E-05	0.33	2.76	-	249.7
AHQ-1-4, 2406	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	3.85E-07	0.89	4.23	-	669.4
AHQ-1-6, 2324	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	6.33E-08	0.90	4.25	-	726.2
AHQ-1-1, 2552	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	7.99E-07	0.91	4.41	-	790.9
AHQ-1-2, 2350	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	6.78E-06	0.74	3.15	-	615.0
AHQ-1-5, 2301	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.12E-04	0.83	3.81	-	546.4
AHQ-1-3, 2401 - 2409	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.86E-05	0.90	4.13	-	833.0
AHQ-1-2, 3595	R.FLSNGHVTIPGQQDK.D	1641.80946	2	7.36E-06	0.69	3.04	-	464.9
AHQ-1-2, 5329 - 5397	R.FLSNGHVTIPGQQDKDMFQETMEAM*R.I	3028.39040	3	3.93E-06	0.86	5.08	-	946.9
AHQ-1-2, 6131 - 6210	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	1.76E-05	0.91	4.64	-	657.3
AHQ-1-6, 5971	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	3.07E-05	0.91	4.76	-	653.1
AHQ-1-2, 4438	R.GDLPFVVPR.R	1000.17581	2	2.38E-05	0.74	2.73	-	785.5
AHQ-1-1, 3044	K.HEAMITDLEER.L	1344.47646	2	1.71E-08	0.97	3.83	-	1614.0
AHQ-1-2, 2991	K.HEAMITDLEER.L	1344.47646	1	4.00E-05	0.68	2.93	-	652.2
AHQ-1-3, 2430	K.HEAM*ITDLEER.L	1360.47586	2	7.81E-04	0.96	3.79	-	1490.4
AHQ-1-2, 2978	K.HEAMITDLEER.L	1344.47646	2	1.28E-07	0.95	3.69	-	1120.6
AHQ-1-6, 3434	R.HEMPPHIYAITDTAYR.S	1916.14944	3	2.15E-09	0.97	4.37	-	2369.9
AHQ-1-6, 3151	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	3.46E-08	0.96	4.61	-	1785.4
AHQ-1-5, 3163	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	8.71E-04	0.78	2.74	-	650.9
AHQ-1-1, 3459	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	1.80E-04	0.94	3.55	-	1152.4
AHQ-1-3, 3319	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	8.89E-09	0.97	5.01	-	1973.7
AHQ-1-3, 3323	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	7.93E-06	0.85	3.15	-	692.8
AHQ-1-2, 3423	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	3.51E-04	0.82	2.88	-	627.2
AHQ-1-2, 3426 - 3437	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	1.43E-07	0.97	4.70	-	2429.2
AHQ-1-2, 3843 - 3857	R.HEMPPHIYAITDTAYR.S	1916.14944	3	5.03E-07	0.97	4.21	-	2354.5
AHQ-1-2, 3758 - 3829	R.HEMPPHIYAITDTAYR.S	1916.14944	2	7.08E-05	0.95	4.30	-	1002.5
AHQ-1-7, 3178	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	7.44E-04	0.58	2.70	-	464.5
AHQ-1-5, 3178	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	5.42E-06	0.92	4.14	-	1204.9
AHQ-1-2, 3754	R.HEMPPHIYAITDTAYR.S	1916.14944	3	8.42E-10	0.97	4.25	-	2763.0
AHQ-1-3, 3627	R.HEMPPHIYAITDTAYR.S	1916.14944	3	1.97E-09	0.96	4.07	-	2083.3
AHQ-1-1, 3797	R.HEMPPHIYAITDTAYR.S	1916.14944	3	9.90E-07	0.94	3.72	-	1663.5
AHQ-1-10, 3317	R.HEMPPHIYAITDTAYR.S	1916.14944	2	1.65E-06	0.55	2.98	-	320.5
AHQ-1-2, 5023	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.22E-11	0.98	5.77	-	1925.6
AHQ-1-1, 4659	K.HSQAVEELAEQLEQTK.R	1840.96940	3	3.21E-05	0.94	4.38	-	1475.7
AHQ-1-3, 4597	K.HSQAVEELAEQLEQTK.R	1840.96940	2	4.16E-14	0.98	6.28	-	2331.1
AHQ-1-5, 4474 - 4481	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.02E-06	0.99	6.24	-	2646.6
AHQ-1-2, 4766	K.HSQAVEELAEQLEQTK.R	1840.96940	3	4.57E-04	0.97	4.97	-	1984.9
AHQ-1-2, 4758	K.HSQAVEELAEQLEQTK.R	1840.96940	2	6.22E-07	0.98	4.94	-	2202.1
AHQ-1-3, 4533 - 4609	K.HSQAVEELAEQLEQTK.R	1840.96940	2	5.54E-05	0.98	5.67	-	2429.0
AHQ-1-3, 4598 - 4611	K.HSQAVEELAEQLEQTK.R	1840.96940	3	6.86E-07	0.96	5.38	-	1500.0
AHQ-1-3, 4169 - 4237	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.21E-12	0.98	7.60	-	2155.4
AHQ-1-2, 4321 - 4401	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.88E-11	0.98	7.03	-	2331.5
AHQ-1-2, 4322 - 4327	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	4.00E-09	0.98	6.05	-	2421.6
AHQ-1-3, 4183	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	9.11E-11	0.98	6.09	-	2449.5
AHQ-1-3, 4485	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	7.37E-09	0.97	5.92	-	1618.2
AHQ-1-5, 4071	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	3.70E-06	0.98	6.16	-	1986.1
AHQ-1-6, 4023	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.56E-05	0.95	4.98	-	1279.7
AHQ-1-2, 4415	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.04E-11	0.98	5.36	-	2020.9
AHQ-1-1, 4241 - 4315	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	4.79E-09	0.98	5.81	-	2456.8
AHQ-1-4, 4223	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	8.22E-09	0.97	5.42	-	1621.8
AHQ-1-4, 4220 - 4228	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	4.36E-05	0.96	5.10	-	1134.2
AHQ-1-5, 4061	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	5.83E-07	0.97	5.73	-	1383.0
AHQ-1-1, 4311	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	5.30E-09	0.97	5.48	-	1485.1
AHQ-1-2, 4069 - 4147	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.01E-10	0.98	5.04	-	2370.2
AHQ-1-2, 4005 - 4074	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.16E-10	0.95	4.53	-	1554.5
AHQ-1-3, 3783 - 3857	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.67E-05	0.96	4.57	-	1715.3
AHQ-1-4, 4068	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.23E-06	0.97	5.04	-	1940.1
AHQ-1-4, 3958	R.IAEFTTNLTEEEEK.S	1654.75371	2	6.47E-07	0.86	3.26	-	1202.9
AHQ-1-3, 3927 - 3999	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.38E-09	0.96	4.30	-	1696.0
AHQ-1-6, 3608 - 3658	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.02E-04	0.95	3.94	-	1527.3
AHQ-1-1, 4065	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.21E-04	0.83	3.09	-	992.3
AHQ-1-2, 3918 - 3989	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.70E-09	0.97	4.96	-	1684.4
AHQ-1-7, 3752	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.15E-05	0.95	3.86	-	1423.5
AHQ-1-1, 3971 - 3993	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.57E-07	0.89	3.34	-	1312.7
AHQ-1-4, 3806 - 3884	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.24E-06	0.96	4.31	-	1745.8
AHQ-1-5, 3694	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.20E-08	0.95	4.53	-	1224.5
AHQ-1-1, 3843 - 3907	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.07E-10	0.97	4.69	-	1976.4
AHQ-1-2, 4222	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.65E-06	0.97	4.30	-	2616.6
AHQ-1-3, 4013	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.72E-06	0.95	3.81	-	1880.5
AHQ-1-1, 5321	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	5.73E-06	0.78	3.45	-	850.4
AHQ-1-1, 5603	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	8.77E-09	0.85	3.84	-	868.1
AHQ-1-1, 5608	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	3.83E-06	0.92	4.53	-	932.9
AHQ-1-4, 3444 - 3460	K.IAQLEEQLDNETK.E	1531.64695	2	2.70E-05	0.97	4.82	-	1589.5
AHQ-1-10, 3128 - 3143	K.IAQLEEQLDNETK.E	1531.64695	2	4.53E-06	0.96	4.13	-	1501.4
AHQ-1-5, 3325 - 3395	K.IAQLEEQLDNETK.E	1531.64695	2	2.01E-04	0.91	3.14	-	1500.9
AHQ-1-1, 3888	K.IAQLEEQLDNETK.E	1531.64695	2	3.11E-06	0.86	3.39	-	880.7
AHQ-1-2, 3522 - 3594	K.IAQLEEQLDNETK.E	1531.64695	2	8.60E-06	0.96	4.24	-	1491.8
AHQ-1-6, 3294 - 3295	K.IAQLEEQLDNETK.E	1531.64695	2	1.13E-08	0.98	5.33	-	1854.4
AHQ-1-1, 3253	K.IAQLEEQLDNETK.E	1531.64695	2	4.88E-09	0.96	4.45	-	1752.8
AHQ-1-2, 3246	K.IAQLEEQLDNETK.E	1531.64695	2	3.29E-04	0.92	3.30	-	1250.9
AHQ-1-3, 3539 - 3587	K.IAQLEEQLDNETK.E	1531.64695	2	3.45E-04	0.91	3.23	-	1260.3
AHQ-1-3, 3623	K.IAQLEEQLDNETK.E	1531.64695	2	6.83E-10	0.96	4.61	-	1445.8
AHQ-1-8, 3198 - 3204	K.IAQLEEQLDNETK.E	1531.64695	2	2.63E-06	0.89	3.33	-	1175.3
AHQ-1-3, 3130 - 3207	K.IAQLEEQLDNETK.E	1531.64695	2	3.50E-08	0.96	3.99	-	1671.7
AHQ-1-11, 3198 - 3266	K.IAQLEEQLDNETK.E	1531.64695	2	5.91E-06	0.96	4.68	-	1470.3
AHQ-1-2, 3962 - 3997	K.IAQLEEQLDNETK.E	1531.64695	2	5.36E-08	0.84	3.22	-	559.7
AHQ-1-7, 3322	K.IAQLEEQLDNETK.E	1531.64695	2	6.23E-05	0.68	2.54	-	782.2
AHQ-1-1, 3463 - 3465	K.IAQLEEQLDNETK.E	1531.64695	2	3.90E-10	0.97	4.96	-	1899.9
AHQ-1-3, 3401 - 3437	K.IAQLEEQLDNETK.E	1531.64695	2	1.01E-06	0.96	4.47	-	1355.3
AHQ-1-9, 3214	K.IAQLEEQLDNETK.E	1531.64695	2	4.28E-06	0.97	5.12	-	1554.2
AHQ-1-4, 3224	K.IAQLEEQLDNETK.E	1531.64695	2	1.59E-04	0.84	3.10	-	913.3
AHQ-1-2, 3666 - 3746	K.IAQLEEQLDNETK.E	1531.64695	2	1.46E-07	0.97	5.42	-	1505.1
AHQ-1-2, 6781 - 6845	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.09E-05	0.96	4.60	-	1462.8
AHQ-1-2, 6922	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.86E-04	0.95	4.61	-	1281.0
AHQ-1-13- , 6453 - 6455	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.81E-04	0.95	4.98	-	968.3
AHQ-1-11, 5930 - 5931	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.77E-05	0.96	4.97	-	1159.9
AHQ-1-14- , 6220 - 6223	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.06E-06	0.98	5.78	-	1513.9
AHQ-1-6, 6582 - 6610	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.58E-07	0.97	5.91	-	1456.4

AHQ-1-3, 6031	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.14E-05	0.89	4.04	-	822.4
AHQ-1-4, 6776	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.58E-04	0.80	3.75	-	547.5
AHQ-1-10, 5824	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.91E-04	0.86	3.57	-	750.8
AHQ-1-1, 5381	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.00E-04	0.72	3.12	-	487.4
AHQ-1-6, 5791 - 5870	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	4.99E-04	0.87	4.54	-	707.1
AHQ-1-4, 6791	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	3.03E-04	0.96	5.02	-	1533.4
AHQ-1-2, 5917 - 5989	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.61E-05	0.96	5.40	-	945.3
AHQ-1-7, 6769	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	7.36E-06	0.95	4.95	-	1054.4
AHQ-1-5, 6671 - 6737	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.06E-06	0.98	6.47	-	1694.7
AHQ-1-1, 5968	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.12E-04	0.94	4.23	-	1295.4
AHQ-1-2, 4182	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	1.03E-07	0.95	4.36	-	1109.0
AHQ-1-2, 5475 - 5478	R.IMGIPEEEQMGLLR.V	1616.92826	2	2.10E-04	0.88	4.19	-	390.0
AHQ-1-3, 5330 - 5343	R.IMGIPEEEQMGLLR.V	1616.92826	2	2.61E-06	0.84	3.71	-	390.9
AHQ-1-1, 5411	R.IMGIPEEEQMGLLR.V	1616.92826	2	1.44E-05	0.71	2.99	-	347.5
AHQ-1-4, 5439 - 5444	R.IMGIPEEEQMGLLR.V	1616.92826	2	6.28E-06	0.89	4.21	-	440.2
AHQ-1-2, 4933	R.IM*GIPEEEQMGLLR.V	1632.92766	2	6.37E-06	0.94	3.77	-	884.5
AHQ-1-2, 4815 - 4865	R.IMGIPEEEQM*GLLR.V	1632.92766	2	2.42E-09	0.80	3.44	-	436.1
AHQ-1-7, 5313 - 5389	R.IMGIPEEEQMGLLR.V	1616.92826	2	1.06E-06	0.91	4.18	-	590.1
AHQ-1-5, 5353 - 5357	R.IMGIPEEEQMGLLR.V	1616.92826	2	5.08E-07	0.87	3.54	-	430.4
AHQ-1-1, 5928	K.IRELESQISELQEDLESER.A	2304.45416	2	5.84E-07	0.98	6.60	-	1007.9
AHQ-1-6, 5862	K.IRELESQISELQEDLESER.A	2304.45416	3	1.17E-08	0.98	5.52	-	2384.5
AHQ-1-6, 5858	K.IRELESQISELQEDLESER.A	2304.45416	2	9.40E-08	0.98	6.53	-	2199.6
AHQ-1-4, 6027	K.IRELESQISELQEDLESER.A	2304.45416	3	7.14E-08	0.98	6.79	-	2064.2
AHQ-1-4, 6016 - 6019	K.IRELESQISELQEDLESER.A	2304.45416	2	1.73E-12	0.98	6.84	-	1845.6
AHQ-1-3, 5894 - 5915	K.IRELESQISELQEDLESER.A	2304.45416	3	3.14E-11	0.98	7.03	-	1993.0
AHQ-1-5, 5994	K.IRELESQISELQEDLESER.A	2304.45416	2	1.55E-04	0.97	5.36	-	1002.5
AHQ-1-2, 6077 - 6145	K.IRELESQISELQEDLESER.A	2304.45416	2	4.08E-04	0.98	7.46	-	1532.8
AHQ-1-1, 5923	K.IRELESQISELQEDLESER.A	2304.45416	3	3.69E-09	0.97	5.57	-	1916.8
AHQ-1-2, 5867	K.ITDVIIGFQACCR.G	1555.80136	2	1.24E-05	0.91	3.33	-	1083.5
AHQ-1-3, 4807	K.KANLQIDQINTDLNLER.S	1999.21478	2	4.19E-09	0.97	5.48	-	1601.6
AHQ-1-2, 4966 - 4983	K.KANLQIDQINTDLNLER.S	1999.21478	3	1.02E-04	0.75	3.68	-	694.6
AHQ-1-2, 4607 - 4687	K.KANLQIDQINTDLNLER.S	1999.21478	2	9.14E-05	0.86	5.16	-	777.5
AHQ-1-1, 4667	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.62E-06	0.97	5.96	-	1625.9
AHQ-1-5, 4550	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.82E-06	0.97	5.48	-	1732.8
AHQ-1-7, 4500	K.KANLQIDQINTDLNLER.S	1999.21478	2	4.92E-04	0.95	5.25	-	1047.2
AHQ-1-2, 4773	K.KANLQIDQINTDLNLER.S	1999.21478	2	6.78E-07	0.98	6.07	-	1799.4
AHQ-1-3, 4634	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.12E-06	0.97	5.85	-	1232.5
AHQ-1-2, 4774 - 4791	K.KANLQIDQINTDLNLER.S	1999.21478	3	1.62E-05	0.94	5.53	-	951.1
AHQ-1-2, 4627	K.KANLQIDQINTDLNLER.S	1999.21478	3	7.34E-04	0.49	3.48	-	482.2
AHQ-1-9, 4356 - 4360	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.86E-04	0.96	4.96	-	1248.1
AHQ-1-2, 4978	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.10E-10	0.96	5.49	-	1073.4
AHQ-1-3, 4457	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.29E-05	0.95	5.04	-	884.6
AHQ-1-2, 2638	R.KKVEAQLQELQVK.F	1541.81761	2	3.07E-08	0.98	5.42	-	1947.6
AHQ-1-4, 2559 - 2560	R.KKVEAQLQELQVK.F	1541.81761	2	3.38E-09	0.98	5.45	-	1927.3
AHQ-1-3, 2553	R.KKVEAQLQELQVK.F	1541.81761	2	7.64E-06	0.97	4.71	-	1751.3
AHQ-1-6, 2446	R.KKVEAQLQELQVK.F	1541.81761	2	1.64E-08	0.96	4.54	-	1643.8
AHQ-1-5, 2411	R.KKVEAQLQELQVK.F	1541.81761	2	5.22E-08	0.98	5.43	-	2205.7
AHQ-1-1, 2740	R.KKVEAQLQELQVK.F	1541.81761	2	6.85E-09	0.95	4.43	-	1404.9
AHQ-1-2, 2954	R.KKVEAQLQELQVK.F	1541.81761	2	1.29E-07	0.97	5.43	-	1803.4
AHQ-1-2, 3714 - 3781	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.41E-11	0.98	5.65	-	1971.6
AHQ-1-4, 3514	K.KLEEEQIILEDQNCK.L	1891.08992	2	9.32E-04	0.97	5.37	-	1932.4
AHQ-1-2, 3959	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.01E-05	0.98	5.98	-	1639.5
AHQ-1-4, 3539 - 3608	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.49E-10	0.98	6.02	-	1951.8
AHQ-1-3, 3489	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.82E-06	0.98	5.72	-	1986.6
AHQ-1-2, 3725	K.KLEEEQIILEDQNCK.L	1891.08992	3	9.86E-05	0.91	4.41	-	1174.8
AHQ-1-3, 3753	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.56E-04	0.91	3.60	-	694.5
AHQ-1-2, 3617 - 3630	K.KLEEEQIILEDQNCK.L	1891.08992	3	4.61E-04	0.92	4.47	-	1378.0
AHQ-1-3, 3505 - 3583	K.KLEEEQIILEDQNCK.L	1891.08992	2	8.48E-10	0.98	6.94	-	1812.5
AHQ-1-5, 3381	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.06E-10	0.97	5.77	-	1386.7
AHQ-1-1, 3561 - 3587	K.KLEEEQIILEDQNCK.L	1891.08992	2	9.31E-05	0.98	6.04	-	1827.9
AHQ-1-2, 3878	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.31E-05	0.96	4.60	-	1263.8
AHQ-1-1, 3680	K.KLEEEQIILEDQNCK.L	1891.08992	3	1.16E-05	0.87	4.10	-	1253.3
AHQ-1-1, 3675 - 3677	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.27E-12	0.98	5.62	-	2144.5
AHQ-1-2, 3607	K.KLEEEQIILEDQNCK.L	1891.08992	2	4.34E-04	0.96	5.43	-	1164.7
AHQ-1-2, 4091	K.KLEEEQIILEDQNCKLAK.E	2203.49930	3	6.06E-05	0.94	4.77	-	1142.2
AHQ-1-3, 7102 - 7170	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	2.47E-08	0.97	5.60	-	1481.9
AHQ-1-1, 6893	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	4.72E-09	0.97	5.87	-	1379.9
AHQ-1-3, 6255	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.79E-05	0.97	6.05	-	2157.9
AHQ-1-1, 6891	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.97E-04	0.91	4.97	-	746.0
AHQ-1-5, 7277 - 7278	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	8.40E-05	0.88	4.37	-	861.1
AHQ-1-2, 7223 - 7258	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	6.96E-13	0.98	6.75	-	1473.4
AHQ-1-2, 7257 - 7266	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.99E-06	0.94	5.66	-	891.0
AHQ-1-5, 7265 - 7281	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	2.39E-07	0.94	4.54	-	1169.7
AHQ-1-4, 7278 - 7286	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	4.25E-07	0.94	5.54	-	836.8
AHQ-1-3, 7101	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	3.20E-05	0.88	4.28	-	791.1
AHQ-1-7, 7304	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	2.16E-07	0.95	4.42	-	1178.0
AHQ-1-2, 6429 - 6499	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.02E-09	0.96	5.83	-	1490.1
AHQ-1-4, 7280 - 7348	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	4.96E-08	0.97	6.28	-	1193.8
AHQ-1-4, 2782	K.KLVWVPSDK.S	1072.28194	1	4.09E-04	0.50	2.40	-	476.4
AHQ-1-3, 2777	K.KLVWVPSDK.S	1072.28194	2	1.94E-04	0.86	3.48	-	772.5
AHQ-1-10, 2616	K.KLVWVPSDK.S	1072.28194	2	2.63E-04	0.89	3.77	-	750.1
AHQ-1-2, 2870	K.KLVWVPSDK.S	1072.28194	2	8.11E-06	0.74	3.02	-	597.5
AHQ-1-6, 2644	K.KLVWVPSDK.S	1072.28194	2	2.58E-05	0.88	3.25	-	1002.4
AHQ-1-1, 2973 - 2976	K.KLVWVPSDK.S	1072.28194	2	8.82E-04	0.87	3.38	-	833.3
AHQ-1-10, 2615 - 2635	K.KLVWVPSDK.S	1072.28194	1	9.51E-04	0.35	2.16	-	430.1
AHQ-1-2, 2871	K.KLVWVPSDK.S	1072.28194	1	1.50E-04	0.64	2.49	-	555.0
AHQ-1-4, 3682	K.KMEDSVGCLETAEEVK.R	1827.02450	2	1.45E-04	0.93	4.39	-	1199.3
AHQ-1-3, 3650	K.KMEDSVGCLETAEEVK.R	1827.02450	2	2.58E-07	0.92	3.85	-	1125.5
AHQ-1-1, 3317	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	2.18E-04	0.78	3.01	-	648.6
AHQ-1-2, 3029	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	5.60E-06	0.96	5.02	-	1468.1
AHQ-1-1, 3397	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.42E-06	0.91	4.05	-	1246.8
AHQ-1-2, 3414	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	1.10E-10	0.97	4.87	-	1972.9
AHQ-1-5, 3182	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	8.43E-09	0.95	4.54	-	1278.0
AHQ-1-4, 3340	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	6.40E-05	0.91	4.42	-	1212.5
AHQ-1-1, 3051	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	1.19E-04	0.98	6.15	-	1958.8
AHQ-1-3, 3305	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	1.32E-06	0.97	5.14	-	1307.7
AHQ-1-2, 3031 - 3034	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	2.70E-08	0.87	3.72	-	554.0
AHQ-1-4, 2919	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	1.46E-05	0.95	5.04	-	1376.1
AHQ-1-5, 3179	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	7.23E-09	0.95	5.22	-	1019.9
AHQ-1-3, 3302	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	6.24E-08	0.96	5.63	-	1212.4
AHQ-1-4, 4990	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	1.52E-04	0.56	2.63	-	342.8
AHQ-1-1, 4992	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	2.81E-08	0.95	5.04	-	1648.7
AHQ-1-3, 4905	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	1.19E-06	0.90	4.47	-	1183.2
AHQ-1-3, 4907	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	9.12E-08	0.85	3.88	-	514.8
AHQ-1-4, 4196	K.KQELEEICHDLEAR.V	1771.93036	3	5.66E-04	0.95	4.89	-	1535.7
AHQ-1-9, 3964	K.KQELEEICHDLEAR.V	1771.93036	2	4.36E-06	0.94	4.87	-	1165.6
AHQ-1-2, 4298 - 4369	K.KQELEEICHDLEAR.V	1771.93036	2	5.94E-06	0.96	5.07	-	1595.5

AHQ-1-6, 4008	K.KQELEEICHDLEAR.V	1771.93036	2	1.07E-05	0.97	5.33	-	1798.1
AHQ-1-5, 4054	K.KQELEEICHDLEAR.V	1771.93036	2	6.10E-05	0.95	4.95	-	1325.2
AHQ-1-4, 4188	K.KQELEEICHDLEAR.V	1771.93036	2	1.69E-06	0.95	4.65	-	1414.2
AHQ-1-1, 4252	K.KQELEEICHDLEAR.V	1771.93036	3	4.38E-06	0.95	5.10	-	1388.5
AHQ-1-5, 2757	K.KVEAQLQELQVK.F	1413.64470	2	1.42E-05	0.97	5.12	-	1806.0
AHQ-1-3, 2925 - 2998	K.KVEAQLQELQVK.F	1413.64470	2	2.65E-06	0.95	4.76	-	1161.0
AHQ-1-4, 2944	K.KVEAQLQELQVK.F	1413.64470	1	4.32E-04	0.36	2.52	-	394.3
AHQ-1-1, 3091	K.KVEAQLQELQVK.F	1413.64470	2	5.98E-06	0.95	4.15	-	1460.5
AHQ-1-4, 2930	K.KVEAQLQELQVK.F	1413.64470	2	1.67E-06	0.96	4.42	-	1828.8
AHQ-1-2, 3055	K.KVEAQLQELQVK.F	1413.64470	1	2.08E-07	0.53	2.96	-	396.5
AHQ-1-3, 2938	K.KVEAQLQELQVK.F	1413.64470	3	4.05E-07	0.93	4.88	-	1134.2
AHQ-1-2, 3051	K.KVEAQLQELQVK.F	1413.64470	3	1.04E-06	0.91	3.91	-	1390.0
AHQ-1-6, 2810	K.KVEAQLQELQVK.F	1413.64470	2	4.52E-07	0.95	4.19	-	1459.2
AHQ-1-2, 3045	K.KVEAQLQELQVK.F	1413.64470	1	2.31E-04	0.19	2.40	-	314.9
AHQ-1-2, 3977	K.KVIQYLAYVASSHK.S	1607.87775	2	1.48E-05	0.83	2.71	-	1008.2
AHQ-1-1, 3904 - 3984	K.LEEEQIILEDQNCK.L	1762.91700	2	3.46E-09	0.97	5.44	-	1164.2
AHQ-1-2, 4085 - 4109	K.LEEEQIILEDQNCK.L	1762.91700	2	1.88E-09	0.98	5.93	-	1595.9
AHQ-1-4, 4014	K.LEEEQIILEDQNCK.L	1762.91700	2	6.70E-09	0.96	5.02	-	1304.7
AHQ-1-2, 3987	K.LEEEQIILEDQNCK.L	1762.91700	2	1.57E-04	0.80	3.57	-	274.4
AHQ-1-4, 3922	K.LEEEQIILEDQNCK.L	1762.91700	2	1.58E-08	0.95	4.11	-	1279.2
AHQ-1-3, 3953 - 4030	K.LEEEQIILEDQNCK.L	1762.91700	2	5.18E-09	0.96	4.85	-	1247.0
AHQ-1-3, 7181 - 7182	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	3.36E-11	0.96	6.09	-	769.8
AHQ-1-2, 7325	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	2.79E-07	0.96	5.82	-	1372.2
AHQ-1-1, 6944	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	1.59E-05	0.91	4.63	-	941.3
AHQ-1-2, 3662	R.LEVNLQAMK.A	1046.26630	2	7.45E-05	0.91	3.87	-	788.0
AHQ-1-5, 3411	R.LEVNLQAMK.A	1046.26630	2	7.03E-07	0.77	2.72	-	500.0
AHQ-1-1, 3664 - 3715	R.LEVNLQAMK.A	1046.26630	2	3.51E-04	0.76	3.01	-	595.7
AHQ-1-3, 3555 - 3571	R.LEVNLQAMK.A	1046.26630	2	6.87E-05	0.85	3.54	-	581.6
AHQ-1-2, 2677	R.LEVNLQAM*K.A	1062.26570	2	1.55E-05	0.88	3.10	-	771.7
AHQ-1-6, 3402	R.LEVNLQAMK.A	1046.26630	2	1.47E-05	0.79	3.10	-	610.9
AHQ-1-2, 3634	K.LKDVLLQVDDER.R	1443.62767	2	8.21E-11	0.96	4.58	-	1573.2
AHQ-1-3, 3507 - 3579	K.LKDVLLQVDDER.R	1443.62767	2	8.89E-08	0.96	4.00	-	1883.6
AHQ-1-1, 3217	K.LKDVLLQVDDERR.N	1599.81402	2	3.29E-04	0.81	3.29	-	939.3
AHQ-1-2, 3169	K.LKDVLLQVDDERR.N	1599.81402	3	3.68E-04	0.87	3.02	-	1286.6
AHQ-1-5, 2878	K.LKDVLLQVDDERR.N	1599.81402	2	7.16E-05	0.88	3.43	-	1088.0
AHQ-1-3, 3061	K.LKDVLLQVDDERR.N	1599.81402	2	1.39E-05	0.87	3.88	-	909.1
AHQ-1-2, 2966	K.LKNKHEAMITDLEER.L	1828.08363	2	1.20E-07	0.93	3.59	-	1051.6
AHQ-1-2, 2065	K.LKQVEDEKNSFR.E	1493.64677	2	4.50E-05	0.63	2.77	-	532.3
AHQ-1-2, 7415 - 7481	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	3.25E-06	0.86	3.13	-	886.9
AHQ-1-2, 7543	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	2.82E-04	0.84	2.93	-	881.1
AHQ-1-2, 7469 - 7537	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	3	1.19E-05	0.93	4.96	-	1240.8
AHQ-1-5, 6205	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.52E-04	0.87	4.10	-	644.4
AHQ-1-1, 6160 - 6164	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.70E-05	0.92	4.76	-	957.1
AHQ-1-2, 6503	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	4.62E-06	0.74	3.23	-	735.6
AHQ-1-1, 6159	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.37E-06	0.96	4.80	-	1443.5
AHQ-1-5, 6209 - 6210	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.38E-09	0.98	5.89	-	1977.9
AHQ-1-2, 5875	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	4.68E-06	0.92	4.57	-	895.3
AHQ-1-4, 6255	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.90E-08	0.96	5.03	-	1458.8
AHQ-1-7, 6233	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.68E-09	0.96	4.38	-	1608.4
AHQ-1-3, 5031 - 5035	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.74E-12	0.96	4.62	-	1565.9
AHQ-1-6, 6106	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	7.87E-05	0.80	3.51	-	752.8
AHQ-1-4, 6258	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.82E-05	0.76	3.45	-	468.7
AHQ-1-3, 6141	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.33E-11	0.96	4.81	-	1552.6
AHQ-1-2, 5859	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.16E-06	0.90	4.02	-	1061.1
AHQ-1-2, 6495 - 6570	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.92E-09	0.95	4.62	-	1260.3
AHQ-1-2, 6313 - 6385	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.23E-11	0.97	5.61	-	1403.8
AHQ-1-6, 6110 - 6114	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.91E-11	0.97	5.44	-	1616.9
AHQ-1-1, 5728	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.41E-06	0.92	4.58	-	860.5
AHQ-1-3, 6123	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.37E-12	0.97	5.72	-	1297.2
AHQ-1-4, 5624	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.65E-07	0.96	5.22	-	1207.1
AHQ-1-3, 5459 - 5517	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.19E-08	0.94	4.57	-	1046.8
AHQ-1-2, 5671	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.65E-06	0.95	4.65	-	1009.0
AHQ-1-4, 5951 - 5983	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.37E-07	0.97	5.37	-	1394.9
AHQ-1-4, 6099	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.27E-07	0.88	4.00	-	686.1
AHQ-1-3, 5838 - 5909	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.00E-30	0.98	6.57	-	1394.4
AHQ-1-2, 6066 - 6133	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.93E-10	0.98	5.90	-	1541.2
AHQ-1-1, 5532	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.67E-07	0.95	4.35	-	1298.6
AHQ-1-1, 5824 - 5887	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.92E-06	0.98	5.69	-	1878.7
AHQ-1-3, 5945 - 6023	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.95E-08	0.98	6.50	-	1244.5
AHQ-1-2, 6206 - 6246	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.54E-10	0.97	5.92	-	1424.7
AHQ-1-5, 6039	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.14E-05	0.87	3.26	-	949.8
AHQ-1-2, 5983 - 6053	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.16E-07	0.98	6.20	-	1632.1
AHQ-1-5, 5914 - 5967	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.62E-12	0.98	6.29	-	1748.3
AHQ-1-6, 5834	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.58E-05	0.95	4.46	-	1273.6
AHQ-1-3, 6215	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.50E-12	0.97	5.77	-	1421.3
AHQ-1-1, 3651	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	1.38E-04	0.78	3.07	-	881.4
AHQ-1-3, 5201	R.LTEMETLQSQLMAEK.L	1753.03211	2	8.08E-04	0.61	2.85	-	669.5
AHQ-1-6, 5066	R.LTEMETLQSQLMAEK.L	1753.03211	2	2.78E-05	0.69	3.00	-	770.5
AHQ-1-3, 4074	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	3.27E-06	0.97	4.31	-	2310.2
AHQ-1-2, 5322 - 5331	R.LTEMETLQSQLM*AEK.L	1769.03151	2	6.94E-04	0.57	3.43	-	684.7
AHQ-1-2, 4757	R.LTEMETLQSQLM*AEK.L	1769.03151	2	2.02E-06	0.95	4.73	-	1047.4
AHQ-1-3, 3566 - 3637	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	1.20E-06	0.95	4.09	-	1273.8
AHQ-1-2, 5381	R.LTEMETLQSQLMAEK.L	1753.03211	2	6.78E-05	0.97	4.73	-	1639.1
AHQ-1-2, 4225 - 4299	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	2.93E-07	0.98	5.09	-	2313.5
AHQ-1-3, 4617 - 4694	R.LTEMETLQSQLM*AEK.L	1769.03151	2	1.84E-06	0.94	4.14	-	1241.5
AHQ-1-4, 4679	R.LTEMETLQSQLM*AEK.L	1769.03151	2	1.45E-05	0.87	3.72	-	883.8
AHQ-1-5, 5137 - 5143	R.LTEMETLQSQLMAEK.L	1753.03211	2	1.53E-06	0.95	4.51	-	1417.4
AHQ-1-2, 4850 - 4923	R.LTEMETLQSQLM*AEK.L	1769.03151	2	3.08E-06	0.76	3.52	-	651.4
AHQ-1-2, 3693 - 3774	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	7.57E-06	0.96	4.77	-	1179.7
AHQ-1-1, 6796	K.LTKDFSALESQLQDTQELLQEENR.Q	2837.04608	3	3.09E-06	0.82	3.73	-	950.8
AHQ-1-2, 6857	K.LTKDFSALESQLQDTQELLQEENR.Q	2837.04608	3	1.35E-07	0.94	5.12	-	1454.9
AHQ-1-2, 4110	K.MEDSVGCLETAEEVK.R	1698.85159	2	3.07E-06	0.93	3.82	-	919.0
AHQ-1-4, 4026	K.MEDSVGCLETAEEVK.R	1698.85159	2	3.17E-05	0.90	3.79	-	763.5
AHQ-1-3, 3981 - 3985	K.MEDSVGCLETAEEVK.R	1698.85159	2	5.03E-07	0.92	4.65	-	654.8
AHQ-1-2, 3713	K.MEDSVGCLETAEEVKR.K	1855.03794	3	2.05E-05	0.79	3.52	-	818.9
AHQ-1-3, 3595	K.MEDSVGCLETAEEVKR.K	1855.03794	3	6.84E-07	0.77	3.19	-	705.3
AHQ-1-1, 3345	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	4.14E-05	0.81	3.16	-	494.4
AHQ-1-2, 3709	K.MEDSVGCLETAEEVKR.K	1855.03794	2	3.66E-04	0.76	3.43	-	412.5
AHQ-1-4, 3620	K.MEDSVGCLETAEEVKR.K	1855.03794	2	1.85E-06	0.77	3.25	-	511.7
AHQ-1-3, 3529 - 3603	K.MEDSVGCLETAEEVKR.K	1855.03794	2	6.47E-06	0.73	3.12	-	408.8
AHQ-1-2, 5761 - 5829	K.MQQNIQELEEQLEEEESAR.Q	2334.46063	3	9.56E-08	0.82	3.79	-	1022.8
AHQ-1-7, 5328 - 5341	K.NFINNPLAQADWAAK.K	1673.85315	2	2.25E-10	0.95	4.67	-	1142.1
AHQ-1-9, 5187	K.NFINNPLAQADWAAK.K	1673.85315	2	1.28E-06	0.93	4.00	-	1082.4
AHQ-1-2, 6125	K.NFINNPLAQADWAAK.K	1673.85315	2	3.43E-09	0.91	3.89	-	840.2
AHQ-1-14- , 5203 - 5214	K.NFINNPLAQADWAAK.K	1673.85315	2	2.18E-09	0.96	4.86	-	1137.7
AHQ-1-3, 5977	K.NFINNPLAQADWAAK.K	1673.85315	2	1.23E-08	0.92	4.15	-	756.0
AHQ-1-2, 5669	K.NFINNPLAQADWAAK.K	1673.85315	2	2.77E-08	0.88	3.74	-	722.2

AHQ-1-13- , 5279 - 5347	K.NFINNPLAQADWAAK.K	1673.85315	2	8.36E-07	0.97	5.77	-	1091.2
AHQ-1-3, 5362 - 5386	K.NFINNPLAQADWAAK.K	1673.85315	2	8.39E-04	0.45	2.66	-	406.7
AHQ-1-13, 5033	K.NFINNPLAQADWAAK.K	1673.85315	2	1.19E-09	0.96	5.04	-	1152.0
AHQ-1-2, 5463 - 5533	K.NFINNPLAQADWAAK.K	1673.85315	2	4.83E-11	0.96	5.32	-	1227.2
AHQ-1-2, 5899	K.NFINNPLAQADWAAK.K	1673.85315	2	1.50E-04	0.93	3.92	-	1007.9
AHQ-1-1, 5911	K.NFINNPLAQADWAAK.K	1673.85315	2	2.00E-07	0.89	3.25	-	883.2
AHQ-1-1, 5443 - 5452	K.NFINNPLAQADWAAK.K	1673.85315	2	2.24E-11	0.96	4.88	-	1081.3
AHQ-1-6, 5279 - 5283	K.NFINNPLAQADWAAK.K	1673.85315	2	5.99E-06	0.96	5.59	-	975.0
AHQ-1-10, 4725	K.NFINNPLAQADWAAK.K	1673.85315	2	2.49E-07	0.92	4.07	-	960.6
AHQ-1-4, 5470	K.NFINNPLAQADWAAK.K	1673.85315	2	2.65E-05	0.93	4.25	-	965.2
AHQ-1-5, 5373	K.NFINNPLAQADWAAK.K	1673.85315	2	2.69E-06	0.95	4.82	-	1053.1
AHQ-1-11, 4872 - 4882	K.NFINNPLAQADWAAK.K	1673.85315	2	3.54E-07	0.95	4.95	-	867.2
AHQ-1-2, 3155	K.NKHEAMITDLEER.L	1586.75247	2	1.19E-08	0.89	3.61	-	995.1
AHQ-1-3, 2199	K.NKHEAM*ITDLEER.L	1602.75187	3	5.97E-06	0.94	3.79	-	1813.9
AHQ-1-3, 2541	K.NKHEAMITDLEER.L	1586.75247	2	1.10E-08	0.94	3.63	-	1534.3
AHQ-1-2, 2637	K.NKHEAMITDLEER.L	1586.75247	2	9.74E-10	0.93	3.78	-	1211.1
AHQ-1-4, 2554	K.NKHEAMITDLEER.L	1586.75247	2	1.16E-07	0.92	3.50	-	1135.1
AHQ-1-11, 5258	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.09E-04	0.81	3.47	-	402.1
AHQ-1-5, 5823 - 5841	K.NLPIYSEEIVEMYK.G	1728.98720	2	6.53E-04	0.91	3.09	-	867.9
AHQ-1-12, 5453	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.31E-04	0.91	3.90	-	595.7
AHQ-1-3, 5847	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.71E-05	0.84	3.48	-	553.6
AHQ-1-9, 5634 - 5643	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.49E-04	0.76	3.15	-	513.1
AHQ-1-3, 5225	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.49E-04	0.92	3.66	-	882.2
AHQ-1-13, 5341 - 5400	K.NLPIYSEEIVEMYK.G	1728.98720	2	3.54E-04	0.86	3.41	-	623.5
AHQ-1-13- , 5739 - 5741	K.NLPIYSEEIVEMYK.G	1728.98720	2	8.92E-07	0.94	4.12	-	871.4
AHQ-1-6, 5143	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.22E-04	0.93	3.56	-	871.8
AHQ-1-4, 5302	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.62E-07	0.91	4.08	-	619.3
AHQ-1-2, 6009 - 6079	K.NLPIYSEEIVEMYK.G	1728.98720	2	4.68E-06	0.94	4.04	-	912.3
AHQ-1-2, 6211	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.32E-04	0.83	3.02	-	656.1
AHQ-1-2, 5379	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.26E-09	0.94	4.08	-	873.1
AHQ-1-1, 5863	K.NLPIYSEEIVEMYK.G	1728.98720	2	4.87E-05	0.88	3.21	-	702.0
AHQ-1-1, 5299 - 5300	K.NLPIYSEEIVEM*YK.G	1744.98660	2	9.73E-06	0.95	4.34	-	1164.6
AHQ-1-5, 5538	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	7.18E-08	0.93	4.42	-	751.4
AHQ-1-2, 5837	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	6.97E-08	0.91	4.05	-	782.4
AHQ-1-2, 5945 - 6018	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.24E-07	0.94	4.45	-	867.2
AHQ-1-3, 5117	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	3.09E-05	0.87	3.93	-	922.3
AHQ-1-2, 5254	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	2.62E-07	0.66	3.21	-	690.8
AHQ-1-6, 5460	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.19E-04	0.89	4.55	-	617.9
AHQ-1-1, 5653	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	5.79E-05	0.91	3.90	-	895.3
AHQ-1-2, 5746	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	5.97E-05	0.84	3.93	-	534.5
AHQ-1-2, 5261 - 5339	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	1.22E-08	0.94	4.15	-	1207.4
AHQ-1-3, 7286 - 7287	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	5.83E-08	0.98	5.58	-	1765.4
AHQ-1-2, 7425	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	6.06E-07	0.98	6.43	-	2426.5
AHQ-1-2, 2442	K.PLLQVSR.Q	812.98013	1	5.40E-04	0.45	2.16	-	388.9
AHQ-1-1, 3320	R.QAQQERDELADEIANSSGK.G	2090.15168	2	1.29E-05	0.94	4.68	-	718.1
AHQ-1-3, 2826	R.QAQQERDELADEIANSSGK.G	2090.15168	2	9.49E-07	0.87	4.26	-	423.8
AHQ-1-1, 2939	R.QAQQERDELADEIANSSGK.G	2090.15168	2	2.58E-04	0.66	3.43	-	392.9
AHQ-1-3, 3299	R.QAQQERDELADEIANSSGK.G	2090.15168	2	1.06E-04	0.84	3.60	-	565.8
AHQ-1-3, 3213 - 3291	R.QAQQERDELADEIANSSGK.G	2090.15168	3	1.00E-03	0.75	3.56	-	604.4
AHQ-1-2, 3411	R.QAQQERDELADEIANSSGK.G	2090.15168	2	6.67E-06	0.86	4.14	-	396.4
AHQ-1-3, 2287	K.QIATLHAQVADM*K.K	1442.66637	2	4.82E-05	0.78	2.99	-	582.8
AHQ-1-2, 2378	K.QIATLHAQVADM*K.K	1442.66637	2	7.93E-04	0.68	3.09	-	342.4
AHQ-1-3, 2031	R.QLEEAEEEAQR.A	1332.35590	2	8.95E-06	0.81	3.56	-	585.1
AHQ-1-2, 2106	R.QLEEAEEEAQR.A	1332.35590	2	2.86E-04	0.82	3.31	-	692.8
AHQ-1-1, 2180	R.QLEEAEEEAQR.A	1332.35590	2	7.36E-06	0.86	3.36	-	811.6
AHQ-1-5, 1910	R.QLEEAEEEAQR.A	1332.35590	2	2.64E-06	0.76	3.29	-	681.7
AHQ-1-1, 3735	R.RGDLPFVVPR.R	1156.36217	2	6.64E-07	0.96	3.68	-	1524.6
AHQ-1-2, 3715 - 3791	R.RGDLPFVVPR.R	1156.36217	2	8.47E-06	0.95	3.76	-	1351.1
AHQ-1-3, 3602	R.RGDLPFVVPR.R	1156.36217	2	4.08E-05	0.93	3.27	-	1441.9
AHQ-1-4, 3616	R.RGDLPFVVPR.R	1156.36217	2	1.13E-05	0.94	3.43	-	1178.6
AHQ-1-10, 3263	R.RGDLPFVVPR.R	1156.36217	2	2.86E-06	0.93	3.32	-	1364.5
AHQ-1-6, 3415 - 3487	R.RGDLPFVVPR.R	1156.36217	2	1.58E-05	0.91	3.40	-	1056.6
AHQ-1-9, 3276	R.RGDLPFVVPR.R	1156.36217	2	1.42E-05	0.93	3.59	-	1024.8
AHQ-1-11, 3352	R.RGDLPFVVPR.R	1156.36217	2	2.53E-05	0.86	3.11	-	826.9
AHQ-1-3, 6803	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	2.26E-08	0.96	6.03	-	1275.3
AHQ-1-4, 6978	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	2.21E-07	0.95	5.77	-	1127.5
AHQ-1-2, 7126	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.72E-04	0.95	5.43	-	1297.9
AHQ-1-2, 7021	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	3.05E-09	0.97	6.11	-	1974.2
AHQ-1-1, 6744	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.18E-08	0.95	5.70	-	1392.1
AHQ-1-3, 2003	K.RQLEEAEEEAQR.A	1488.54225	2	1.46E-09	0.98	4.79	-	3347.0
AHQ-1-2, 2083	K.RQLEEAEEEAQR.A	1488.54225	2	2.04E-08	0.98	5.05	-	3426.6
AHQ-1-6, 6139	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.30E-08	0.93	4.97	-	1160.1
AHQ-1-2, 6373 - 6450	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.47E-08	0.97	6.26	-	1342.5
AHQ-1-2, 7523	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	3.35E-12	0.92	4.95	-	685.2
AHQ-1-2, 6606	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	7.38E-10	0.93	4.88	-	997.9
AHQ-1-2, 6518	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	4.62E-10	0.96	5.26	-	1458.5
AHQ-1-5, 6302	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.39E-09	0.71	3.28	-	576.8
AHQ-1-3, 6195	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.43E-05	0.88	4.74	-	471.7
AHQ-1-2, 7123	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.42E-05	0.88	4.27	-	697.3
AHQ-1-13, 5779 - 5835	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	6.80E-05	0.63	3.52	-	429.7
AHQ-1-1, 6176 - 6235	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.45E-11	0.94	5.23	-	1017.0
AHQ-1-1, 6328	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	3.06E-10	0.96	5.49	-	1370.6
AHQ-1-5, 6974 - 7045	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	4.12E-06	0.95	3.98	-	1924.5
AHQ-1-3, 4802	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.87E-05	0.93	4.16	-	1003.4
AHQ-1-2, 6002 - 6081	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	2.62E-07	0.95	5.40	-	1495.1
AHQ-1-3, 6877	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	4.29E-08	0.97	5.10	-	2261.0
AHQ-1-2, 4974 - 5038	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.87E-09	0.97	5.29	-	1747.9
AHQ-1-3, 5575 - 5646	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	9.06E-07	0.88	4.46	-	985.2
AHQ-1-1, 4812	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	6.14E-10	0.97	4.97	-	1639.1
AHQ-1-1, 4941	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.17E-06	0.87	3.69	-	846.6
AHQ-1-2, 7013 - 7078	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.05E-06	0.98	6.33	-	1727.3
AHQ-1-2, 7058	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	5.32E-08	0.95	5.02	-	1475.0
AHQ-1-3, 6825 - 6893	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	4.07E-05	0.98	6.17	-	1676.0
AHQ-1-2, 7141 - 7209	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	3.27E-07	0.95	4.79	-	1309.1
AHQ-1-5, 3435	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	6.68E-07	0.97	5.68	-	1394.4
AHQ-1-7, 3486	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	6.67E-04	0.78	3.45	-	795.4
AHQ-1-2, 3673	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	4.95E-07	0.97	5.88	-	1588.2
AHQ-1-7, 3665 - 3674	K.TDLLLEPYNK.Y	1206.36989	2	1.36E-05	0.91	3.76	-	1028.1
AHQ-1-4, 3790 - 3791	K.TDLLLEPYNK.Y	1206.36989	2	4.54E-05	0.93	3.87	-	1133.2
AHQ-1-3, 3757	K.TDLLLEPYNK.Y	1206.36989	2	1.01E-06	0.83	3.32	-	920.1
AHQ-1-6, 3584 - 3595	K.TDLLLEPYNK.Y	1206.36989	2	1.36E-05	0.92	4.01	-	970.1
AHQ-1-5, 3618 - 3641	K.TDLLLEPYNK.Y	1206.36989	2	1.70E-04	0.81	3.10	-	929.4
AHQ-1-2, 3874 - 3897	K.TDLLLEPYNK.Y	1206.36989	2	1.41E-06	0.93	4.13	-	1043.2
AHQ-1-2, 3883	K.TDLLLEPYNK.Y	1206.36989	1	1.59E-04	0.29	2.21	-	350.3
AHQ-1-1, 3839	K.TDLLLEPYNK.Y	1206.36989	2	4.54E-05	0.91	3.89	-	1253.8
AHQ-1-2, 4082	K.TDLLLEPYNKYR.F	1525.73037	2	1.71E-06	0.62	2.84	-	524.1
AHQ-1-1, 4397 - 4419	K.TELEDTLDSTAAQQELR.S	1921.00969	2	3.21E-05	0.90	3.50	-	1154.6

AHQ-1-4, 4478	K.TELEDTLDSTAAQQELR.S	1921.00969	2	4.31E-08	0.97	5.43	-	1958.7
AHQ-1-2, 4583	K.TELEDTLDSTAAQQELR.S	1921.00969	3	1.42E-04	0.97	5.38	-	2131.7
AHQ-1-2, 4559	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.99E-07	0.94	4.30	-	1491.8
AHQ-1-5, 4414	K.TELEDTLDSTAAQQELR.S	1921.00969	2	9.81E-06	0.96	4.60	-	1615.5
AHQ-1-3, 4405 - 4411	K.TELEDTLDSTAAQQELR.S	1921.00969	2	2.23E-07	0.97	5.57	-	1769.5
AHQ-1-3, 3134 - 3135	R.TEMEDLMSSK.D	1171.32449	2	5.52E-04	0.85	2.78	-	742.9
AHQ-1-2, 3245 - 3249	R.TEMEDLMSSK.D	1171.32449	2	2.46E-05	0.88	3.09	-	799.1
AHQ-1-1, 3227	R.TEMEDLMSSK.D	1171.32449	2	2.80E-05	0.77	2.68	-	483.0
AHQ-1-6, 3279	R.TEMEDLMSSKDDVGK.S	1685.85626	2	5.76E-07	0.63	3.01	-	699.4
AHQ-1-2, 3533	R.TEMEDLMSSKDDVGK.S	1685.85626	2	5.63E-06	0.92	4.11	-	1048.5
AHQ-1-4, 3220	R.TEMEDLMSSKDDVGK.S	1685.85626	2	9.12E-05	0.67	3.10	-	597.4
AHQ-1-5, 3291	R.TEMEDLMSSKDDVGK.S	1685.85626	2	2.47E-05	0.85	3.13	-	973.8
AHQ-1-3, 6494	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.54E-06	0.93	4.19	-	1343.7
AHQ-1-4, 6676	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	7.29E-05	0.90	3.94	-	1007.5
AHQ-1-2, 6774	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.13E-07	0.97	5.27	-	1430.0
AHQ-1-2, 6675	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.48E-04	0.96	5.12	-	1550.6
AHQ-1-1, 6599	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	6.01E-08	0.94	4.20	-	1371.9
AHQ-1-2, 6677	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	5.06E-09	0.99	5.72	-	3195.9
AHQ-1-9, 6404	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	7.17E-05	0.97	4.97	-	1787.9
AHQ-1-1, 2121	K.VAAYDKLEK.T	1037.19123	2	1.29E-04	0.80	2.67	-	735.5
AHQ-1-3, 1894	K.VAAYDKLEK.T	1037.19123	2	8.48E-04	0.69	2.55	-	624.5
AHQ-1-2, 1978 - 2029	K.VAAYDKLEK.T	1037.19123	2	8.45E-04	0.83	3.02	-	603.2
AHQ-1-3, 3321	K.VEAQLQELQVK.F	1285.47179	2	6.11E-04	0.86	3.37	-	941.3
AHQ-1-4, 3350 - 3351	K.VEAQLQELQVK.F	1285.47179	1	4.65E-04	0.13	2.46	-	406.0
AHQ-1-5, 3197	K.VEAQLQELQVK.F	1285.47179	2	1.06E-04	0.90	3.64	-	1078.8
AHQ-1-6, 3204	K.VEAQLQELQVK.F	1285.47179	2	7.26E-06	0.80	2.82	-	915.1
AHQ-1-4, 3346	K.VEAQLQELQVK.F	1285.47179	2	2.44E-06	0.93	3.55	-	1393.6
AHQ-1-10, 5277	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.48E-07	0.89	4.45	-	790.2
AHQ-1-5, 6094	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.18E-07	0.91	4.05	-	728.7
AHQ-1-5, 5998 - 6075	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.24E-04	0.89	4.01	-	711.6
AHQ-1-5, 5285 - 5359	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.29E-05	0.83	3.70	-	574.2
AHQ-1-2, 5498 - 5534	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	7.88E-07	0.93	4.33	-	1253.1
AHQ-1-2, 5507 - 5573	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.97E-10	0.88	4.09	-	571.7
AHQ-1-6, 5970 - 5982	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	7.08E-11	0.96	4.99	-	1029.1
AHQ-1-9, 5874	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.70E-06	0.72	3.38	-	590.8
AHQ-1-6, 5272	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.60E-08	0.85	3.65	-	663.6
AHQ-1-9, 5867 - 5936	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	6.05E-05	0.66	3.38	-	309.0
AHQ-1-10, 5244 - 5276	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	3.36E-12	0.92	4.65	-	598.9
AHQ-1-13- , 5316 - 5323	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	2.06E-04	0.63	3.07	-	509.1
AHQ-1-2, 6154 - 6221	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	5.59E-06	0.84	3.82	-	596.9
AHQ-1-2, 6197	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.01E-07	0.69	3.03	-	535.2
AHQ-1-4, 6152	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.15E-08	0.96	4.92	-	931.6
AHQ-1-4, 6143	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	3.08E-06	0.85	3.42	-	855.1
AHQ-1-4, 5455	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	5.33E-04	0.55	2.98	-	481.8
AHQ-1-2, 6399	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.06E-12	0.96	5.16	-	1033.0
AHQ-1-1, 5400 - 5464	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.67E-08	0.90	3.98	-	649.0
AHQ-1-2, 6401	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	5.32E-05	0.81	3.83	-	563.3
AHQ-1-10, 4708	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.76E-12	0.90	3.97	-	686.3
AHQ-1-6, 5986	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.65E-08	0.85	3.65	-	748.6
AHQ-1-8, 5807	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	5.16E-04	0.24	2.58	-	271.7
AHQ-1-1, 6184 - 6197	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.32E-06	0.66	3.14	-	620.9
AHQ-1-3, 6038	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.31E-04	0.82	3.73	-	491.3
AHQ-1-1, 6041	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.18E-07	0.83	3.60	-	771.3
AHQ-1-3, 6035	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	6.87E-11	0.91	4.09	-	703.3
AHQ-1-3, 5354	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	4.66E-06	0.91	4.43	-	665.8
AHQ-1-3, 5350 - 5367	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.29E-04	0.76	3.37	-	711.0
AHQ-1-7, 6061 - 6069	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.46E-07	0.87	4.20	-	469.0
AHQ-1-7, 6074	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.60E-10	0.93	4.55	-	948.7
AHQ-1-13, 4935 - 5015	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.03E-05	0.70	3.36	-	319.2
AHQ-1-1, 2164	R.VEEEEERCQHLQAEK.K	1916.01642	2	7.15E-04	0.85	3.64	-	883.9
AHQ-1-2, 2110	R.VEEEEERCQHLQAEK.K	1916.01642	3	6.55E-09	0.91	4.33	-	906.1
AHQ-1-10, 3585	K.VIQYLAYVASSHK.S	1479.70484	2	1.44E-06	0.95	3.84	-	1309.3
AHQ-1-3, 4015	K.VIQYLAYVASSHK.S	1479.70484	2	9.39E-04	0.93	3.78	-	1114.0
AHQ-1-6, 3796	K.VIQYLAYVASSHK.S	1479.70484	2	3.87E-05	0.95	3.99	-	1441.0
AHQ-1-6, 3795 - 3804	K.VIQYLAYVASSHK.S	1479.70484	3	8.76E-06	0.85	3.78	-	745.2
AHQ-1-7, 3884	K.VIQYLAYVASSHK.S	1479.70484	2	5.79E-08	0.94	4.17	-	1137.8
AHQ-1-1, 4125 - 4127	K.VIQYLAYVASSHK.S	1479.70484	2	3.42E-07	0.94	4.19	-	1084.9
AHQ-1-5, 3857	K.VIQYLAYVASSHK.S	1479.70484	3	1.08E-04	0.73	3.06	-	545.3
AHQ-1-9, 3648	K.VIQYLAYVASSHK.S	1479.70484	2	9.00E-04	0.94	3.35	-	1431.0
AHQ-1-4, 4043	K.VIQYLAYVASSHK.S	1479.70484	2	1.07E-06	0.94	3.83	-	1236.8
AHQ-1-5, 3851	K.VIQYLAYVASSHK.S	1479.70484	2	2.16E-08	0.95	3.95	-	1392.8
AHQ-1-2, 4154 - 4169	K.VIQYLAYVASSHK.S	1479.70484	2	1.57E-04	0.92	3.75	-	1101.6
AHQ-1-2, 4275	K.VIQYLAYVASSHK.S	1479.70484	2	9.57E-05	0.95	4.03	-	1358.6
AHQ-1-6, 6499	R.VISGVLQLGNIVFK.K	1487.81155	2	6.63E-06	0.96	4.01	-	1909.5
AHQ-1-4, 6690 - 6755	R.VISGVLQLGNIVFK.K	1487.81155	2	3.40E-10	0.97	4.79	-	1634.9
AHQ-1-13, 6016	R.VISGVLQLGNIVFK.K	1487.81155	2	4.14E-05	0.95	4.24	-	1155.2
AHQ-1-2, 6609 - 6682	R.VISGVLQLGNIVFK.K	1487.81155	2	6.30E-09	0.96	4.85	-	1324.9
AHQ-1-2, 6694	R.VISGVLQLGNIVFK.K	1487.81155	1	1.05E-04	0.30	2.89	-	330.6
AHQ-1-3, 6521 - 6585	R.VISGVLQLGNIVFK.K	1487.81155	2	4.23E-09	0.97	4.24	-	1979.3
AHQ-1-10, 5756	R.VISGVLQLGNIVFK.K	1487.81155	2	3.68E-04	0.96	4.47	-	1437.3
AHQ-1-5, 6629 - 6702	R.VISGVLQLGNIVFK.K	1487.81155	2	3.70E-05	0.96	4.23	-	1674.7
AHQ-1-2, 6722 - 6785	R.VISGVLQLGNIVFK.K	1487.81155	2	1.85E-07	0.97	4.46	-	2008.6
AHQ-1-2, 6939	R.VISGVLQLGNIVFK.K	1487.81155	2	6.60E-09	0.98	4.60	-	2370.5
AHQ-1-1, 6492 - 6496	R.VISGVLQLGNIVFK.K	1487.81155	2	1.20E-04	0.89	2.86	-	1294.6
AHQ-1-7, 6606	R.VISGVLQLGNIVFK.K	1487.81155	2	9.71E-04	0.97	4.58	-	1941.4
AHQ-1-1, 5971	R.VISGVLQLGNIVFKK.E	1615.98446	2	2.63E-07	0.94	4.41	-	1159.1
AHQ-1-5, 4859 - 4933	K.VSHLLGINVTDFTR.G	1572.79026	2	7.14E-11	0.96	4.53	-	1401.9
AHQ-1-1, 5091	K.VSHLLGINVTDFTR.G	1572.79026	2	1.34E-09	0.95	4.43	-	1340.2
AHQ-1-1, 5095	K.VSHLLGINVTDFTR.G	1572.79026	3	2.39E-05	0.91	3.89	-	1239.2
AHQ-1-2, 5095 - 5145	K.VSHLLGINVTDFTR.G	1572.79026	2	8.08E-11	0.96	4.33	-	1550.5
AHQ-1-2, 5139	K.VSHLLGINVTDFTR.G	1572.79026	3	5.16E-04	0.83	3.30	-	984.8
AHQ-1-4, 5066	K.VSHLLGINVTDFTR.G	1572.79026	2	2.83E-10	0.97	4.84	-	1470.5
AHQ-1-2, 5422	K.VSHLLGINVTDFTR.G	1572.79026	2	1.59E-06	0.95	3.68	-	1289.3
AHQ-1-3, 4985	K.VSHLLGINVTDFTR.G	1572.79026	2	7.94E-12	0.94	3.94	-	1240.0
AHQ-1-7, 4858	K.VSHLLGINVTDFTR.G	1572.79026	2	1.97E-11	0.96	4.15	-	1608.6
AHQ-1-3, 4993	K.VSHLLGINVTDFTR.G	1572.79026	3	1.32E-05	0.89	3.75	-	1080.2
AHQ-1-6, 4806 - 4854	K.VSHLLGINVTDFTR.G	1572.79026	2	3.41E-08	0.94	4.08	-	1293.7
AHQ-1-2, 3290	R.VVFQEFR.Q	925.06580	2	8.76E-04	0.79	2.74	-	467.6
AHQ-1-5, 3019	R.VVFQEFR.Q	925.06580	2	4.83E-05	0.74	2.52	-	493.0
AHQ-1-5, 3983 - 4001	R.YEILTPNSIPK.G	1275.47536	2	8.29E-05	0.91	3.86	-	1011.8
AHQ-1-2, 4265	R.YEILTPNSIPK.G	1275.47536	2	1.38E-05	0.85	3.44	-	901.1
AHQ-1-1, 4185 - 4188	R.YEILTPNSIPK.G	1275.47536	2	1.31E-04	0.92	3.66	-	1137.5
AHQ-1-2, 4178 - 4197	R.YEILTPNSIPK.G	1275.47536	2	7.77E-06	0.91	3.05	-	1145.7
AHQ-1-4, 4107 - 4115	R.YEILTPNSIPK.G	1275.47536	2	4.50E-05	0.93	3.03	-	1466.9
AHQ-1-2, 4429	R.YEILTPNSIPK.G	1275.47536	2	1.69E-04	0.86	2.83	-	1014.7
AHQ-1-2, 4262	R.YEILTPNSIPK.G	1275.47536	1	8.79E-04	0.53	2.54	-	585.9
AHQ-1-2, 4434	R.YEILTPNSIPK.G	1275.47536	1	5.31E-04	0.46	1.92	-	734.4

AHQ-1-3, 4042 - 4113	R.YEILTPNSIPK.G	1275.47536	2	1.16E-05	0.89	3.72	-	949.8
AHQ-1-1, 6147	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	3	1.67E-08	0.96	5.10	-	1370.2
AHQ-1-2, 6363	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	2	3.11E-10	0.93	4.21	-	952.4
AHQ-1-10, 5433	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	2	8.60E-04	0.55	2.58	-	291.9
AHQ-1-2, 6267	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	2	9.78E-04	0.65	2.67	-	560.3
gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]				1.00E-30	29.55	350.31	30.50	129351.8
AHQ-1-2, 4279	K.AGTLDLSLTVQGK.Q	1303.48711	2	4.77E-04	0.94	3.70	-	1381.0
AHQ-1-2, 2842	R.AQLYIDCEK.M	1141.27636	2	6.54E-05	0.89	3.43	-	675.7
AHQ-1-2, 2838	R.AQLYIDCEK.M	1141.27636	1	4.57E-04	0.15	1.93	-	487.9
AHQ-1-2, 6301	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	1.91E-05	0.94	4.86	-	1181.3
AHQ-1-1, 4000	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.36E-06	0.70	3.00	-	425.3
AHQ-1-3, 3873	R.CENTDPGYNCLPCPPR.F	1954.10800	2	3.06E-11	0.89	3.78	-	591.2
AHQ-1-4, 4200	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.79E-05	0.88	3.80	-	458.7
AHQ-1-3, 4134	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.85E-06	0.88	4.00	-	475.9
AHQ-1-5, 4011 - 4014	R.CENTDPGYNCLPCPPR.F	1954.10800	2	9.65E-06	0.93	4.15	-	752.4
AHQ-1-4, 3930	R.CENTDPGYNCLPCPPR.F	1954.10800	2	3.44E-08	0.80	2.79	-	619.4
AHQ-1-2, 4257	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.42E-12	0.90	3.85	-	734.9
AHQ-1-4, 3971	K.CNYLGHYSDPMYR.C	1677.84222	2	1.13E-06	0.93	3.82	-	802.4
AHQ-1-5, 3311	K.CNYLGHYSDPM*YR.C	1693.84162	2	1.59E-04	0.89	3.76	-	737.2
AHQ-1-3, 3933	K.CNYLGHYSDPMYR.C	1677.84222	2	7.69E-09	0.93	3.60	-	938.4
AHQ-1-4, 3423	K.CNYLGHYSDPM*YR.C	1693.84162	2	8.28E-05	0.90	3.41	-	740.1
AHQ-1-4, 3450	K.DCVGDVTENQICNK.Q	1654.75869	2	1.18E-06	0.91	4.08	-	698.4
AHQ-1-2, 3510	K.DCVGDVTENQICNK.Q	1654.75869	2	3.99E-05	0.91	3.45	-	1011.2
AHQ-1-5, 2669	K.DHSGQVFSVVSNGK.A	1461.56164	2	3.31E-07	0.95	3.85	-	1451.4
AHQ-1-13- , 2833	K.DHSGQVFSVVSNGK.A	1461.56164	2	3.11E-06	0.92	3.38	-	1046.2
AHQ-1-2, 2859	K.DHSGQVFSVVSNGK.A	1461.56164	2	3.17E-08	0.95	3.70	-	1277.8
AHQ-1-5, 3087	R.DNCQYVYNVDQR.D	1575.64166	2	7.28E-05	0.91	3.50	-	1101.8
AHQ-1-2, 3418	R.DNCQYVYNVDQR.D	1575.64166	2	2.30E-05	0.84	3.27	-	891.3
AHQ-1-2, 3233 - 3309	R.DNCQYVYNVDQR.D	1575.64166	2	1.17E-04	0.86	3.53	-	694.3
AHQ-1-2, 3087	R.DNCQYVYNVDQR.D	1575.64166	2	4.09E-05	0.93	3.89	-	1222.2
AHQ-1-3, 3122 - 3137	R.DNCQYVYNVDQR.D	1575.64166	2	2.51E-05	0.93	4.30	-	922.3
AHQ-1-4, 3355	R.DNCQYVYNVDQR.D	1575.64166	2	6.60E-07	0.88	3.68	-	939.4
AHQ-1-7, 3102	R.DNCQYVYNVDQR.D	1575.64166	2	6.48E-05	0.95	4.34	-	1373.2
AHQ-1-3, 3297	R.DNCQYVYNVDQR.D	1575.64166	2	6.26E-07	0.91	3.96	-	847.6
AHQ-1-3, 4186 - 4257	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	7.83E-08	0.92	4.59	-	826.7
AHQ-1-6, 3824	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	4.26E-13	0.88	4.00	-	829.7
AHQ-1-4, 4172	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.69E-04	0.90	4.57	-	674.2
AHQ-1-4, 4318	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	6.91E-09	0.93	5.03	-	673.6
AHQ-1-3, 3790 - 3859	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.72E-06	0.90	4.50	-	913.5
AHQ-1-2, 4317 - 4385	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	4.00E-06	0.92	4.71	-	697.0
AHQ-1-1, 3880	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.32E-04	0.87	4.81	-	558.2
AHQ-1-5, 3882	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.64E-13	0.77	3.20	-	904.3
AHQ-1-4, 3908	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.00E-30	0.84	3.97	-	744.3
AHQ-1-2, 3969 - 4042	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.22E-14	0.94	5.17	-	914.4
AHQ-1-5, 3565	K.FQDLVDAVR.A	1063.18877	2	3.71E-04	0.90	3.06	-	1103.5
AHQ-1-10, 3315	K.FQDLVDAVR.A	1063.18877	1	2.48E-04	0.15	1.94	-	365.8
AHQ-1-11, 3423	K.FQDLVDAVR.A	1063.18877	2	4.98E-05	0.89	2.71	-	1042.4
AHQ-1-3, 3695	K.FQDLVDAVR.A	1063.18877	2	5.64E-05	0.89	2.75	-	1231.8
AHQ-1-10, 3320	K.FQDLVDAVR.A	1063.18877	2	2.24E-06	0.82	2.80	-	847.0
AHQ-1-3, 2929	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	7.04E-08	0.73	3.55	-	422.3
AHQ-1-2, 3114	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.59E-11	0.86	3.81	-	474.6
AHQ-1-1, 3025	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	7.29E-11	0.74	3.58	-	274.0
AHQ-1-4, 3084	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.63E-08	0.82	3.50	-	583.5
AHQ-1-2, 3198	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.79E-08	0.81	3.50	-	528.2
AHQ-1-6, 2750	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.20E-04	0.68	3.03	-	499.7
AHQ-1-2, 2969 - 3038	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	8.53E-07	0.92	4.47	-	691.0
AHQ-1-4, 2871 - 2898	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	5.86E-07	0.91	4.31	-	475.5
AHQ-1-4, 2836 - 2908	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	2.13E-05	0.63	3.13	-	489.9
AHQ-1-3, 2867	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	8.54E-06	0.89	4.39	-	627.4
AHQ-1-3, 3034	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.00E-10	0.95	4.71	-	739.3
AHQ-1-3, 2834 - 2905	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.61E-08	0.93	4.43	-	611.7
AHQ-1-1, 5673	R.FVFGTTPEDILR.N	1395.58470	2	5.22E-04	0.72	2.65	-	774.3
AHQ-1-6, 5520 - 5559	R.FVFGTTPEDILR.N	1395.58470	1	5.43E-07	0.03	1.95	-	89.3
AHQ-1-11, 5046 - 5066	R.FVFGTTPEDILR.N	1395.58470	2	8.22E-05	0.75	3.20	-	585.6
AHQ-1-6, 5540	R.FVFGTTPEDILR.N	1395.58470	1	3.24E-05	0.22	2.63	-	103.5
AHQ-1-10, 4889	R.FVFGTTPEDILR.N	1395.58470	2	2.35E-05	0.80	2.86	-	822.3
AHQ-1-4, 5722	R.FVFGTTPEDILR.N	1395.58470	2	1.05E-04	0.87	2.87	-	836.9
AHQ-1-4, 5732	R.FVFGTTPEDILR.N	1395.58470	1	3.27E-05	0.07	1.94	-	145.9
AHQ-1-2, 5789	R.FVFGTTPEDILR.N	1395.58470	2	1.98E-04	0.69	2.65	-	548.0
AHQ-1-3, 5710	K.GFLLLASLR.Q	990.22407	2	4.98E-05	0.97	3.63	-	2394.9
AHQ-1-6, 5608	K.GFLLLASLR.Q	990.22407	2	1.19E-04	0.97	4.34	-	2100.0
AHQ-1-2, 5895	K.GFLLLASLR.Q	990.22407	2	3.04E-04	0.97	3.61	-	2098.4
AHQ-1-7, 4448	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.28E-05	0.91	3.94	-	940.9
AHQ-1-5, 4469	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.75E-05	0.90	4.17	-	901.7
AHQ-1-1, 4595 - 4663	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.66E-05	0.92	4.33	-	1050.8
AHQ-1-10, 4115 - 4180	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.67E-06	0.71	3.35	-	615.4
AHQ-1-4, 4594 - 4607	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.73E-04	0.67	3.42	-	600.9
AHQ-1-2, 4897 - 4913	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.72E-04	0.87	4.18	-	667.5
AHQ-1-2, 4801	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.47E-10	0.91	4.23	-	809.1
AHQ-1-10, 4007 - 4017	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.34E-04	0.91	4.54	-	878.7
AHQ-1-5, 4567 - 4638	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.01E-09	0.93	4.22	-	994.1
AHQ-1-6, 4322 - 4390	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.65E-05	0.90	3.92	-	890.3
AHQ-1-5, 4803	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.28E-05	0.63	2.82	-	545.6
AHQ-1-13, 4273 - 4335	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.34E-07	0.83	4.18	-	482.8
AHQ-1-4, 4826 - 4894	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.92E-07	0.88	4.29	-	694.2
AHQ-1-3, 4378	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.12E-06	0.84	3.41	-	798.0
AHQ-1-6, 4539 - 4582	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.41E-10	0.90	4.07	-	736.6
AHQ-1-3, 4761 - 4826	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.23E-06	0.90	3.95	-	777.6
AHQ-1-2, 4715 - 4797	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.71E-08	0.94	4.67	-	1031.5
AHQ-1-10, 3911 - 3920	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.12E-06	0.92	4.45	-	941.8
AHQ-1-9, 4671	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.14E-04	0.83	3.70	-	665.5
AHQ-1-11, 4134 - 4151	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.13E-05	0.89	4.55	-	748.4
AHQ-1-13- , 4544	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.06E-04	0.75	3.53	-	566.0
AHQ-1-7, 4636	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.14E-07	0.92	4.29	-	839.9
AHQ-1-9, 4326 - 4403	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.52E-05	0.80	3.37	-	603.8
AHQ-1-9, 4531	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.01E-08	0.94	4.07	-	1267.1
AHQ-1-4, 2160 - 2175	K.GPDPSSPAFR.I	1031.10364	2	4.05E-06	0.70	3.02	-	481.3
AHQ-1-6, 2054	K.GPDPSSPAFR.I	1031.10364	2	2.57E-04	0.55	2.53	-	478.8
AHQ-1-5, 2039	K.GPDPSSPAFR.I	1031.10364	2	3.93E-06	0.65	2.63	-	419.2
AHQ-1-3, 2174	K.GPDPSSPAFR.I	1031.10364	2	5.28E-05	0.76	2.74	-	530.0
AHQ-1-2, 2250	K.GPDPSSPAFR.I	1031.10364	2	1.42E-04	0.60	2.78	-	409.2
AHQ-1-11, 2142	K.GPDPSSPAFR.I	1031.10364	2	1.21E-04	0.71	3.17	-	395.8
AHQ-1-10, 2089	K.GPDPSSPAFR.I	1031.10364	2	1.36E-04	0.82	3.18	-	585.3
AHQ-1-4, 3106	R.GTLLALER.K	873.03234	2	8.01E-04	0.91	3.49	-	1053.6
AHQ-1-6, 2950	R.GTLLALER.K	873.03234	2	7.78E-04	0.91	3.09	-	1047.7
AHQ-1-2, 3189	R.GTLLALER.K	873.03234	2	9.92E-04	0.92	3.32	-	1156.1
AHQ-1-12, 3026	R.GTLLALER.K	873.03234	2	1.05E-04	0.84	3.03	-	942.9

AHQ-1-3, 3079 - 3083	R.GTLLALER.K	873.03234	2	8.01E-04	0.90	3.62	-	869.7
AHQ-1-2, 2779	K.GTSQNDPNWVVR.H	1373.45608	2	1.37E-06	0.76	3.29	-	884.4
AHQ-1-7, 2593	K.GTSQNDPNWVVR.H	1373.45608	2	1.43E-04	0.49	2.61	-	709.0
AHQ-1-1, 6531 - 6596	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.00E-05	0.51	2.67	-	253.3
AHQ-1-3, 6613 - 6631	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.73E-06	0.60	3.27	-	274.0
AHQ-1-1, 6516 - 6587	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.64E-10	0.67	3.44	-	344.9
AHQ-1-1, 6648	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.32E-08	0.88	4.31	-	497.6
AHQ-1-3, 6765	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.77E-08	0.60	3.29	-	312.9
AHQ-1-14- , 6344	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.38E-05	0.82	3.64	-	535.6
AHQ-1-10, 5931 - 5939	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.28E-06	0.73	3.42	-	390.7
AHQ-1-10, 5869 - 5932	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	9.01E-07	0.74	3.93	-	365.9
AHQ-1-13, 6027 - 6105	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.30E-05	0.73	3.73	-	365.6
AHQ-1-7, 6749 - 6761	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.07E-06	0.60	3.15	-	354.0
AHQ-1-10, 5800 - 5865	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.22E-05	0.84	3.76	-	347.4
AHQ-1-5, 6713 - 6787	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.71E-08	0.67	3.25	-	400.7
AHQ-1-4, 6774 - 6854	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	9.56E-12	0.64	3.30	-	330.7
AHQ-1-4, 6783 - 6855	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.46E-08	0.65	3.13	-	198.3
AHQ-1-4, 6931 - 6932	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.68E-08	0.72	3.51	-	347.6
AHQ-1-12, 6131 - 6134	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	9.14E-09	0.72	3.36	-	211.7
AHQ-1-7, 6756 - 6770	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.78E-06	0.76	3.34	-	279.9
AHQ-1-6, 6574 - 6640	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.80E-09	0.76	3.95	-	369.6
AHQ-1-2, 6782 - 6849	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.65E-08	0.78	3.48	-	535.1
AHQ-1-11, 5908 - 5974	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	8.46E-09	0.73	3.21	-	355.9
AHQ-1-11, 5914	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.94E-05	0.49	2.63	-	246.9
AHQ-1-2, 2715	K.IMADSGPIYDK.T	1210.38204	2	3.69E-05	0.88	3.30	-	762.3
AHQ-1-14- , 2332 - 2367	K.IM*ADSGPIYDK.T	1226.38144	2	9.80E-04	0.71	2.77	-	521.7
AHQ-1-11, 2550	K.IMADSGPIYDK.T	1210.38204	2	2.06E-06	0.91	3.54	-	688.8
AHQ-1-2, 2461	K.IM*ADSGPIYDK.T	1226.38144	2	4.35E-05	0.75	3.16	-	507.0
AHQ-1-13, 6343 - 6344	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.21E-10	0.97	6.11	-	922.2
AHQ-1-14- , 6543	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	9.45E-12	0.97	5.55	-	1088.1
AHQ-1-4, 7170	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.10E-10	0.95	5.03	-	1009.8
AHQ-1-10, 6117 - 6196	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.47E-08	0.96	5.30	-	1091.8
AHQ-1-2, 7177 - 7245	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.33E-08	0.97	5.33	-	1204.6
AHQ-1-9, 7083	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	6.33E-11	0.95	4.77	-	944.5
AHQ-1-9, 6930	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.54E-08	0.96	5.57	-	1030.5
AHQ-1-13- , 6795	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.75E-09	0.97	5.50	-	1252.1
AHQ-1-1, 6851	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.01E-06	0.97	5.49	-	1239.9
AHQ-1-3, 7006 - 7083	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.04E-09	0.97	5.25	-	1361.8
AHQ-1-7, 7145	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.01E-07	0.93	4.46	-	867.0
AHQ-1-6, 6970 - 6972	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.50E-10	0.96	5.83	-	914.5
AHQ-1-5, 7126 - 7133	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.39E-09	0.97	5.75	-	1338.6
AHQ-1-10, 2211 - 2256	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.90E-06	0.59	2.82	-	498.1
AHQ-1-6, 2198	R.KDHSGQVFSVVSNGK.A	1589.73455	3	3.72E-07	0.91	3.62	-	1405.3
AHQ-1-6, 2203	R.KDHSGQVFSVVSNGK.A	1589.73455	2	4.29E-05	0.90	3.78	-	982.7
AHQ-1-9, 2158 - 2227	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.13E-09	0.73	3.20	-	485.1
AHQ-1-5, 2305	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.27E-07	0.71	2.80	-	831.1
AHQ-1-3, 2357	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.32E-07	0.78	2.85	-	928.5
AHQ-1-4, 2346	R.KDHSGQVFSVVSNGK.A	1589.73455	2	3.58E-07	0.86	3.36	-	839.9
AHQ-1-3, 2462	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.01E-05	0.93	3.50	-	1195.6
AHQ-1-2, 2554	R.KDHSGQVFSVVSNGK.A	1589.73455	2	3.69E-08	0.94	3.71	-	1405.5
AHQ-1-2, 2469	R.KDHSGQVFSVVSNGK.A	1589.73455	2	9.08E-09	0.89	3.96	-	894.5
AHQ-1-4, 2444	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.28E-07	0.88	3.35	-	957.1
AHQ-1-2, 2507	K.KIMADSGPIYDK.T	1338.55496	1	2.61E-04	0.68	2.75	-	582.9
AHQ-1-4, 2395	K.KIMADSGPIYDK.T	1338.55496	2	4.90E-04	0.86	3.56	-	694.0
AHQ-1-2, 2509	K.KIMADSGPIYDK.T	1338.55496	2	1.24E-04	0.84	3.38	-	546.1
AHQ-1-3, 2373	R.KVTEENKELANELR.R	1673.84976	2	2.88E-10	0.93	4.18	-	1538.3
AHQ-1-1, 2531	R.KVTEENKELANELR.R	1673.84976	3	9.43E-04	0.68	3.13	-	625.2
AHQ-1-6, 2359	R.KVTEENKELANELR.R	1673.84976	2	4.85E-09	0.95	4.46	-	1332.2
AHQ-1-5, 2226	R.KVTEENKELANELR.R	1673.84976	3	4.07E-05	0.85	3.92	-	786.2
AHQ-1-3, 2378 - 2451	R.KVTEENKELANELR.R	1673.84976	3	3.82E-06	0.85	4.23	-	683.1
AHQ-1-4, 2360 - 2370	R.KVTEENKELANELR.R	1673.84976	2	3.07E-11	0.95	4.99	-	1204.8
AHQ-1-4, 2375	R.KVTEENKELANELR.R	1673.84976	3	7.23E-06	0.80	3.60	-	794.5
AHQ-1-1, 2476 - 2545	R.KVTEENKELANELR.R	1673.84976	2	7.98E-08	0.95	4.80	-	1386.4
AHQ-1-2, 2474	R.KVTEENKELANELR.R	1673.84976	2	1.38E-07	0.93	4.66	-	1119.1
AHQ-1-3, 2122	R.KVTEENKELANELR.R	1673.84976	2	5.49E-08	0.93	4.55	-	1146.0
AHQ-1-6, 2236	R.KVTEENKELANELR.R	1673.84976	2	6.98E-07	0.94	4.84	-	1215.9
AHQ-1-3, 2531	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	8.81E-07	0.80	3.55	-	357.6
AHQ-1-2, 2262	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	2.64E-04	0.71	3.24	-	422.5
AHQ-1-5, 2478	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.67E-10	0.90	4.04	-	569.8
AHQ-1-2, 2609	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	5.98E-05	0.86	3.52	-	980.4
AHQ-1-2, 2605 - 2610	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	5.85E-09	0.82	3.83	-	502.6
AHQ-1-4, 2206	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	3	1.93E-05	0.84	3.88	-	664.8
AHQ-1-2, 5905 - 5914	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.60E-04	0.92	4.60	-	533.1
AHQ-1-1, 5764	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.21E-04	0.64	3.08	-	267.1
AHQ-1-5, 5489 - 5494	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.86E-04	0.80	3.49	-	635.7
AHQ-1-11, 5146 - 5159	K.MENAELDVPIQSVFTR.D	1850.08607	2	6.34E-07	0.93	4.57	-	595.2
AHQ-1-4, 5844	K.MENAELDVPIQSVFTR.D	1850.08607	2	6.38E-04	0.89	3.72	-	725.8
AHQ-1-3, 5747	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.31E-08	0.89	4.10	-	486.0
AHQ-1-9, 5523 - 5531	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.31E-09	0.93	4.61	-	550.9
AHQ-1-3, 5489	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.33E-07	0.90	3.83	-	645.4
AHQ-1-5, 5710	K.MENAELDVPIQSVFTR.D	1850.08607	2	6.34E-04	0.88	3.53	-	613.0
AHQ-1-7, 5692	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.32E-05	0.78	3.46	-	361.0
AHQ-1-2, 5665	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	7.32E-10	0.93	4.31	-	728.7
AHQ-1-3, 3138	K.QVTQSYWDTNPTR.A	1596.68241	2	5.73E-07	0.71	2.67	-	695.9
AHQ-1-7, 3056	K.QVTQSYWDTNPTR.A	1596.68241	2	1.23E-06	0.87	3.11	-	762.4
AHQ-1-1, 3252	K.QVTQSYWDTNPTR.A	1596.68241	2	8.09E-06	0.76	3.17	-	528.3
AHQ-1-2, 3262	K.QVTQSYWDTNPTR.A	1596.68241	2	7.73E-06	0.92	3.64	-	903.9
AHQ-1-9, 2976	K.QVTQSYWDTNPTR.A	1596.68241	2	2.00E-05	0.71	2.58	-	504.1
AHQ-1-5, 3041	K.QVTQSYWDTNPTR.A	1596.68241	2	1.05E-06	0.90	3.66	-	657.4
AHQ-1-9, 2679	R.RPPLCYHNGVQYR.N	1661.86889	2	1.46E-04	0.89	3.32	-	946.7
AHQ-1-2, 2786	R.RPPLCYHNGVQYR.N	1661.86889	2	1.88E-04	0.86	3.27	-	628.9
AHQ-1-2, 2933	R.RPPLCYHNGVQYR.N	1661.86889	2	1.92E-06	0.88	3.82	-	593.9
AHQ-1-5, 2683 - 2753	R.RPPLCYHNGVQYR.N	1661.86889	2	9.98E-04	0.93	4.05	-	671.9
AHQ-1-4, 3946	K.SITLFVQEDR.A	1208.34588	2	2.21E-06	0.93	3.45	-	1287.3
AHQ-1-13, 3836	K.SITLFVQEDR.A	1208.34588	2	1.36E-05	0.93	3.33	-	1538.7
AHQ-1-2, 4067 - 4086	K.SITLFVQEDR.A	1208.34588	2	2.85E-06	0.95	3.89	-	1391.0
AHQ-1-6, 3704 - 3756	K.SITLFVQEDR.A	1208.34588	2	1.66E-07	0.93	2.93	-	1430.1
AHQ-1-11, 3616	K.SITLFVQEDR.A	1208.34588	2	9.80E-05	0.92	3.46	-	1270.8
AHQ-1-13- , 3975	K.SITLFVQEDR.A	1208.34588	2	2.79E-06	0.93	3.54	-	1242.9
AHQ-1-3, 3922	K.SITLFVQEDR.A	1208.34588	2	8.99E-07	0.91	3.01	-	1159.0
AHQ-1-10, 3516	K.SITLFVQEDR.A	1208.34588	2	7.48E-06	0.94	3.92	-	1195.6
AHQ-1-13, 3747 - 3827	K.SITLFVQEDR.A	1208.34588	2	2.67E-05	0.88	3.00	-	981.8
AHQ-1-12, 3738	K.SITLFVQEDR.A	1208.34588	2	2.17E-06	0.90	2.92	-	1191.1
AHQ-1-5, 3798	K.SITLFVQEDR.A	1208.34588	2	3.60E-06	0.87	2.92	-	1047.1
AHQ-1-1, 4583	R.TIVTTLQDSIR.K	1247.42355	2	5.18E-07	0.97	4.16	-	1850.6
AHQ-1-12, 4266	R.TIVTTLQDSIR.K	1247.42355	2	4.70E-07	0.95	3.45	-	1666.0
AHQ-1-6, 4335 - 4338	R.TIVTTLQDSIR.K	1247.42355	2	7.47E-07	0.97	3.95	-	1872.5

AHQ-1-4, 4620	R.TIVTTLQDSIR.K	1247.42355	2	6.97E-05	0.92	3.20	-	1213.6
AHQ-1-2, 4690	R.TIVTTLQDSIR.K	1247.42355	2	2.83E-07	0.96	4.41	-	1542.7
AHQ-1-4, 4536 - 4548	R.TIVTTLQDSIR.K	1247.42355	2	3.35E-07	0.97	4.06	-	1824.6
AHQ-1-7, 4416	R.TIVTTLQDSIR.K	1247.42355	2	5.35E-07	0.95	3.52	-	1470.3
AHQ-1-9, 4244 - 4314	R.TIVTTLQDSIR.K	1247.42355	2	3.66E-06	0.94	3.24	-	1439.5
AHQ-1-6, 3282	R.TIVTTLQDSIR.K	1247.42355	2	1.55E-05	0.95	3.30	-	1497.0
AHQ-1-3, 3386	R.TIVTTLQDSIR.K	1247.42355	2	3.34E-04	0.95	3.38	-	1748.3
AHQ-1-5, 4419	R.TIVTTLQDSIR.K	1247.42355	2	2.95E-06	0.96	4.09	-	1414.9
AHQ-1-3, 4513 - 4531	R.TIVTTLQDSIR.K	1247.42355	2	5.57E-06	0.97	4.21	-	1900.0
AHQ-1-6, 2475	K.VTEENKELANELR.R	1545.67685	2	4.09E-05	0.89	3.66	-	997.6
AHQ-1-9, 2452 - 2455	K.VTEENKELANELR.R	1545.67685	2	2.61E-06	0.88	3.98	-	791.8
AHQ-1-5, 2454	K.VTEENKELANELR.R	1545.67685	2	4.32E-08	0.79	3.23	-	791.1
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				1.00E-30	27.75	330.36	62.60	75429.7
AHQ-1-9, 3120	K.AGDALWLR.F	902.03223	2	4.22E-04	0.92	3.94	-	1148.3
AHQ-1-14- , 6440	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	8.38E-04	0.92	4.13	-	1168.8
AHQ-1-6, 6740 - 6806	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.63E-04	0.96	4.85	-	896.2
AHQ-1-12, 6377 - 6378	R.ASFSQPLFQAVAAICR.L	1768.02967	2	7.51E-08	0.94	4.39	-	1044.6
AHQ-1-11, 6083 - 6151	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.16E-05	0.84	3.49	-	528.5
AHQ-1-10, 6045	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.95E-04	0.91	4.00	-	823.3
AHQ-1-1, 6785	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.03E-05	0.89	3.97	-	641.3
AHQ-1-9, 6732 - 6786	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.53E-06	0.96	5.13	-	936.7
AHQ-1-4, 7046	R.ASFSQPLFQAVAAICR.L	1768.02967	2	6.96E-07	0.96	4.90	-	1025.2
AHQ-1-6, 6787 - 6855	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.82E-08	0.94	4.41	-	898.5
AHQ-1-2, 7090	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.34E-04	0.90	3.90	-	711.3
AHQ-1-6, 6790	R.ASFSQPLFQAVAAICR.L	1768.02967	3	2.19E-06	0.92	4.46	-	1056.2
AHQ-1-6, 7074	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.13E-09	0.90	4.02	-	731.1
AHQ-1-7, 6986	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.41E-08	0.93	4.20	-	760.5
AHQ-1-5, 6985	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.43E-08	0.93	4.02	-	923.6
AHQ-1-3, 6882	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.03E-06	0.90	3.79	-	718.0
AHQ-1-9, 3443	K.EKEPEEELYDLSK.V	1609.71294	2	4.59E-10	0.82	3.55	-	608.2
AHQ-1-7, 3657	K.EKEPEEELYDLSK.V	1609.71294	2	2.31E-05	0.74	3.30	-	376.8
AHQ-1-3, 3750	K.EKEPEEELYDLSK.V	1609.71294	2	4.08E-04	0.66	2.72	-	374.0
AHQ-1-6, 3484 - 3530	K.EKEPEEELYDLSK.V	1609.71294	2	5.95E-04	0.55	2.93	-	305.4
AHQ-1-6, 7115 - 7194	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	1.11E-09	0.96	5.33	-	757.7
AHQ-1-6, 7068	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	4.32E-05	0.92	4.46	-	578.4
AHQ-1-12, 6493	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	2.59E-04	0.94	4.57	-	653.3
AHQ-1-6, 3206	K.GCEVVPDVNVSGQK.F	1489.63335	1	5.75E-08	0.90	4.01	-	819.5
AHQ-1-9, 3155	K.GCEVVPDVNVSGQK.F	1489.63335	1	4.06E-06	0.86	3.39	-	774.5
AHQ-1-9, 3151	K.GCEVVPDVNVSGQK.F	1489.63335	1	6.25E-04	0.70	2.82	-	673.0
AHQ-1-7, 3257	K.GCEVVPDVNVSGQK.F	1489.63335	2	6.69E-04	0.82	3.09	-	694.7
AHQ-1-6, 7146 - 7147	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	2.72E-08	0.93	4.10	-	1129.8
AHQ-1-14- , 6619	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	1.90E-08	0.86	3.49	-	753.8
AHQ-1-6, 3067	R.GM*PAHFSDSAQTEACYHM*LSR.P	2430.63997	3	2.73E-05	0.91	4.32	-	1220.1
AHQ-1-6, 3990	R.GMPAHFSDSAQTEACYHMLSR.P	2398.64117	3	3.41E-08	0.97	5.97	-	1357.9
AHQ-1-9, 2611	R.HPEELSLLR.A	1094.24601	1	5.87E-05	0.22	1.95	-	282.1
AHQ-1-14- , 3888	R.IDLAVGDVVK.T	1029.21223	1	1.07E-04	0.58	2.35	-	575.3
AHQ-1-6, 3818 - 3886	R.IDLAVGDVVK.T	1029.21223	2	9.58E-05	0.88	3.32	-	899.6
AHQ-1-13- , 3987	R.IDLAVGDVVK.T	1029.21223	1	4.29E-04	0.82	3.13	-	643.6
AHQ-1-6, 3819 - 3887	R.IDLAVGDVVK.T	1029.21223	1	4.02E-05	0.24	2.00	-	414.2
AHQ-1-11, 3672	R.IDLAVGDVVK.T	1029.21223	1	4.24E-04	0.34	2.19	-	424.0
AHQ-1-1, 4061	R.IDLAVGDVVK.T	1029.21223	2	4.39E-04	0.93	3.54	-	1433.9
AHQ-1-6, 4471 - 4542	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.00E-30	0.98	6.56	-	2325.8
AHQ-1-6, 4706	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.80E-13	0.98	7.27	-	1553.9
AHQ-1-6, 4486 - 4562	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	5.48E-05	0.63	3.09	-	1132.1
AHQ-1-11, 4220	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	3.00E-05	0.95	5.92	-	1249.0
AHQ-1-5, 4599	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.07E-04	0.92	4.89	-	1128.4
AHQ-1-11, 4222	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	3.33E-14	0.98	6.82	-	2072.5
AHQ-1-12, 4401	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.00E-08	0.98	5.74	-	2006.8
AHQ-1-13- , 4567 - 4637	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	4.20E-05	0.98	5.54	-	2018.0
AHQ-1-9, 4639 - 4647	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	9.24E-06	0.95	4.67	-	1398.0
AHQ-1-9, 4418 - 4486	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	8.05E-07	0.91	4.84	-	1111.5
AHQ-1-1, 4709 - 4732	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	1.29E-05	0.85	3.82	-	898.8
AHQ-1-13, 4381	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.50E-11	0.98	5.72	-	1787.1
AHQ-1-9, 4383 - 4454	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.31E-06	0.98	5.85	-	2575.6
AHQ-1-6, 4887	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.00E-15	0.97	5.19	-	1430.3
AHQ-1-7, 4522	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	7.43E-08	0.98	6.05	-	2122.6
AHQ-1-3, 4666	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	8.54E-08	0.96	4.90	-	2134.2
AHQ-1-6, 4566	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.95E-13	0.98	7.06	-	2111.0
AHQ-1-9, 2486 - 2487	R.KDEILGIANNR.L	1243.39499	2	9.05E-04	0.88	3.06	-	894.5
AHQ-1-13, 2754 - 2811	R.KDEILGIANNR.L	1243.39499	2	2.11E-07	0.95	4.12	-	1387.2
AHQ-1-13- , 2767 - 2831	R.KDEILGIANNR.L	1243.39499	2	1.44E-07	0.94	3.96	-	1261.6
AHQ-1-6, 2674 - 2751	R.KDEILGIANNR.L	1243.39499	2	3.68E-06	0.79	3.35	-	870.0
AHQ-1-6, 2519 - 2590	R.KDEILGIANNR.L	1243.39499	1	2.83E-05	0.48	2.08	-	344.6
AHQ-1-6, 2515 - 2586	R.KDEILGIANNR.L	1243.39499	2	6.10E-07	0.95	4.28	-	1280.4
AHQ-1-12, 2619	R.KDEILGIANNR.L	1243.39499	2	5.21E-04	0.94	3.40	-	1370.2
AHQ-1-9, 2482 - 2555	R.KDEILGIANNR.L	1243.39499	1	1.52E-05	0.31	2.00	-	279.0
AHQ-1-11, 3863	R.KQDWSDHAIWWEQK.R	1858.00504	2	2.24E-04	0.69	2.96	-	634.7
AHQ-1-7, 3970 - 4048	R.KQDWSDHAIWWEQK.R	1858.00504	2	9.85E-04	0.79	3.44	-	631.0
AHQ-1-6, 3967	R.KQDWSDHAIWWEQK.R	1858.00504	3	1.26E-09	0.94	4.34	-	1363.9
AHQ-1-8, 6886 - 6895	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	4.54E-06	0.81	3.89	-	487.2
AHQ-1-9, 6766	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.95E-07	0.82	3.64	-	380.5
AHQ-1-6, 5770	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.17E-04	0.75	3.60	-	343.4
AHQ-1-7, 6952 - 6954	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.35E-06	0.96	5.31	-	1006.5
AHQ-1-6, 6359	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.32E-04	0.91	4.28	-	640.1
AHQ-1-7, 5826	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.88E-04	0.74	3.35	-	439.2
AHQ-1-10, 6008 - 6071	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	6.66E-04	0.74	3.35	-	455.9
AHQ-1-6, 6542 - 6554	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	4.19E-05	0.93	3.94	-	1056.1
AHQ-1-6, 6658 - 6735	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.15E-05	0.89	3.92	-	741.0
AHQ-1-5, 6961	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.00E-05	0.82	3.66	-	541.8
AHQ-1-6, 6775 - 6842	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.91E-06	0.95	4.66	-	942.2
AHQ-1-4, 7006	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.30E-05	0.48	3.10	-	355.8
AHQ-1-13- , 6669 - 6704	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	9.35E-04	0.63	2.87	-	459.5
AHQ-1-3, 6839 - 6915	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.67E-04	0.83	3.92	-	521.1
AHQ-1-6, 6478	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	3.71E-10	0.79	3.57	-	361.6
AHQ-1-6, 2395	R.LFFGPQHR.P	1002.15349	2	4.94E-05	0.84	2.57	-	892.9
AHQ-1-6, 5972	K.LLVPSPEGMSEIYLR.C	1705.01201	3	1.39E-09	0.98	5.36	-	2534.2
AHQ-1-12, 4687 - 4745	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	1.16E-06	0.55	2.53	-	277.0
AHQ-1-5, 6098 - 6114	K.LLVPSPEGMSEIYLR.C	1705.01201	2	1.27E-05	0.57	3.05	-	182.4
AHQ-1-6, 1871 - 1930	R.LPRPSSLSDK.T	1100.25055	2	7.19E-04	0.88	2.65	-	1390.1
AHQ-1-4, 7207	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.61E-04	0.90	4.44	-	1106.2
AHQ-1-3, 7045	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	9.47E-07	0.86	3.39	-	1216.8
AHQ-1-7, 7176	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.04E-05	0.88	4.29	-	974.3
AHQ-1-6, 6980 - 7050	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	8.59E-10	0.94	5.32	-	1165.9
AHQ-1-2, 7217 - 7221	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.75E-11	0.88	3.98	-	1191.7
AHQ-1-1, 6859 - 6928	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	8.74E-06	0.96	5.19	-	1797.6
AHQ-1-7, 2309	R.LTQLYEQAR.W	1122.25622	2	3.85E-05	0.85	2.99	-	1155.6
AHQ-1-6, 2240 - 2306	R.LTQLYEQAR.W	1122.25622	2	5.55E-06	0.90	3.60	-	861.3

AHQ-1-6, 2294	R.LTQLYEQAR.W	1122.25622	1	1.21E-04	0.30	1.95	-	128.1
AHQ-1-9, 2234	R.LTQLYEQAR.W	1122.25622	2	4.55E-05	0.93	3.35	-	1503.6
AHQ-1-6, 5106	R.QWLLQTHWTLDK.Y	1569.78807	2	1.25E-08	0.44	2.96	-	200.7
AHQ-1-14- , 4080	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	2.05E-06	0.85	3.38	-	486.5
AHQ-1-12, 4009 - 4081	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.68E-08	0.89	4.00	-	502.6
AHQ-1-4, 4290	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	2.41E-06	0.81	3.46	-	469.1
AHQ-1-7, 4152 - 4154	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.44E-08	0.87	3.96	-	433.6
AHQ-1-3, 4249	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	6.26E-04	0.83	3.66	-	424.5
AHQ-1-6, 4326	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.12E-09	0.87	3.67	-	521.5
AHQ-1-6, 4064 - 4146	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	4.35E-06	0.88	4.23	-	522.1
AHQ-1-6, 4214	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.77E-05	0.83	3.63	-	443.2
AHQ-1-14- , 4424 - 4430	K.TASGDYIDSSWELR.V	1600.66783	2	7.17E-07	0.90	3.31	-	957.1
AHQ-1-9, 4342	K.TASGDYIDSSWELR.V	1600.66783	2	2.26E-04	0.92	3.55	-	934.2
AHQ-1-13, 4280	K.TASGDYIDSSWELR.V	1600.66783	2	1.83E-04	0.78	2.91	-	757.4
AHQ-1-6, 4382 - 4450	K.TASGDYIDSSWELR.V	1600.66783	2	7.71E-09	0.96	4.42	-	1145.6
AHQ-1-6, 4519 - 4586	K.TASGDYIDSSWELR.V	1600.66783	2	3.28E-08	0.90	3.23	-	1109.8
AHQ-1-7, 3893	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	7.70E-05	0.79	3.96	-	584.2
AHQ-1-9, 3748	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	4.95E-04	0.94	4.40	-	1003.2
AHQ-1-9, 3759	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.75E-07	0.95	5.10	-	1001.8
AHQ-1-9, 3911	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	3.13E-04	0.90	4.21	-	621.3
AHQ-1-1, 4135 - 4136	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	4.07E-10	0.94	5.13	-	977.8
AHQ-1-3, 4021	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	1.97E-05	0.94	5.46	-	1069.6
AHQ-1-6, 3854 - 3934	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	7.66E-05	0.98	7.05	-	1653.6
AHQ-1-6, 3794 - 3866	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	6.23E-06	0.95	4.79	-	854.7
AHQ-1-5, 3887	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.68E-04	0.84	3.64	-	472.0
AHQ-1-6, 7310 - 7311	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	5.35E-09	0.97	5.88	-	1795.6
AHQ-1-9, 3971 - 3974	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.09E-10	0.96	4.69	-	1449.6
AHQ-1-1, 4192 - 4257	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.22E-10	0.96	4.69	-	1509.7
AHQ-1-14- , 3983 - 4052	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.41E-10	0.96	4.67	-	1494.8
AHQ-1-4, 4192	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.61E-05	0.86	3.48	-	957.2
AHQ-1-10, 3732	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.79E-05	0.95	4.41	-	1231.9
AHQ-1-13- , 4108	R.VFVGEEDPEAESVTLR.V	1777.91007	2	8.97E-10	0.96	4.33	-	1774.3
AHQ-1-5, 4103	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.25E-09	0.94	4.08	-	1183.7
AHQ-1-6, 4032	R.VFVGEEDPEAESVTLR.V	1777.91007	3	4.11E-04	0.97	4.97	-	1993.3
AHQ-1-6, 3963 - 4034	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.49E-09	0.95	4.63	-	1313.7
AHQ-1-12, 3933	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.22E-07	0.92	4.20	-	1035.9
AHQ-1-8, 4047	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.19E-10	0.94	4.40	-	1052.0
AHQ-1-11, 3818	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.08E-05	0.95	4.24	-	1476.3
AHQ-1-6, 4102	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.37E-09	0.91	3.73	-	1108.1
AHQ-1-2, 4287 - 4326	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.95E-06	0.83	3.40	-	877.5
AHQ-1-7, 4100	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.23E-06	0.93	4.35	-	1075.5
AHQ-1-14- , 2788 - 2866	R.VTGESHIGGVLLK.I	1310.52448	2	9.01E-07	0.95	3.98	-	1450.3
AHQ-1-1, 3029	R.VTGESHIGGVLLK.I	1310.52448	2	1.31E-06	0.97	4.48	-	2088.1
AHQ-1-8, 2494	R.VTGESHIGGVLLK.I	1310.52448	2	2.39E-09	0.95	3.93	-	1636.0
AHQ-1-12, 2851	R.VTGESHIGGVLLK.I	1310.52448	2	2.78E-06	0.87	3.38	-	1115.6
AHQ-1-11, 2743	R.VTGESHIGGVLLK.I	1310.52448	2	9.60E-06	0.91	3.83	-	1377.0
AHQ-1-6, 2694	R.VTGESHIGGVLLK.I	1310.52448	1	2.11E-04	0.55	1.97	-	815.8
AHQ-1-10, 2689	R.VTGESHIGGVLLK.I	1310.52448	2	8.11E-05	0.56	2.51	-	808.4
AHQ-1-9, 2627	R.VTGESHIGGVLLK.I	1310.52448	2	8.87E-07	0.94	4.09	-	1433.3
AHQ-1-9, 2644	R.VTGESHIGGVLLK.I	1310.52448	1	1.06E-08	0.88	3.43	-	970.9
AHQ-1-6, 2710	R.VTGESHIGGVLLK.I	1310.52448	1	7.46E-08	0.88	3.21	-	931.6
AHQ-1-6, 2690 - 2760	R.VTGESHIGGVLLK.I	1310.52448	2	8.53E-10	0.97	4.80	-	2091.2
AHQ-1-11, 4550	K.VVLAGGVAPALFR.G	1270.54832	2	4.57E-09	0.94	3.51	-	1410.6
AHQ-1-1, 5096	K.VVLAGGVAPALFR.G	1270.54832	2	1.25E-06	0.97	4.64	-	1641.3
AHQ-1-10, 4412	K.VVLAGGVAPALFR.G	1270.54832	2	5.14E-08	0.97	4.34	-	1874.2
AHQ-1-6, 4818 - 4886	K.VVLAGGVAPALFR.G	1270.54832	2	1.14E-07	0.98	5.60	-	1815.1
AHQ-1-9, 4760 - 4762	K.VVLAGGVAPALFR.G	1270.54832	1	2.09E-04	0.75	3.41	-	244.2
AHQ-1-9, 4756	K.VVLAGGVAPALFR.G	1270.54832	2	9.49E-08	0.97	4.70	-	1832.5
AHQ-1-2, 5161	K.VVLAGGVAPALFR.G	1270.54832	2	5.81E-07	0.96	4.44	-	1535.2
AHQ-1-7, 4904	K.VVLAGGVAPALFR.G	1270.54832	2	6.07E-08	0.97	4.93	-	1703.7
AHQ-1-3, 5019	K.VVLAGGVAPALFR.G	1270.54832	2	6.81E-07	0.97	5.26	-	1678.0
AHQ-1-4, 5106	K.VVLAGGVAPALFR.G	1270.54832	2	4.66E-08	0.96	4.53	-	1443.0
AHQ-1-5, 4949	K.VVLAGGVAPALFR.G	1270.54832	2	5.12E-08	0.96	4.53	-	1409.2
AHQ-1-6, 2470 - 2471	K.YGILADAR.L	878.99544	2	6.11E-05	0.93	3.20	-	1269.8
AHQ-1-9, 5342	K.YYSFFDLDPK.T	1295.42046	2	4.89E-05	0.91	3.79	-	887.6
AHQ-1-6, 5411 - 5478	K.YYSFFDLDPK.T	1295.42046	2	6.79E-06	0.77	3.67	-	586.6
gi|4827056|ref|NP_005103.1| WD repeat-containing protein 1 isoform 2 [Homo sapiens]				1.00E-30	13.04	160.31	49.80	58001.9
AHQ-1-6, 5034	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	1.81E-05	0.91	3.98	-	908.2
AHQ-1-6, 5151	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	1.55E-05	0.93	5.21	-	965.3
AHQ-1-6, 5035	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	1.27E-08	0.97	5.94	-	1683.1
AHQ-1-9, 5702	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.75E-12	0.93	4.65	-	932.2
AHQ-1-6, 5708 - 5790	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.00E-30	0.96	5.62	-	1125.6
AHQ-1-13- , 5643	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.15E-06	0.82	3.64	-	687.6
AHQ-1-10, 5107	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.00E-30	0.96	5.44	-	1001.0
AHQ-1-6, 5855	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.82E-10	0.91	4.19	-	946.2
AHQ-1-7, 5893	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	6.88E-14	0.96	5.14	-	1427.4
AHQ-1-5, 5951	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.50E-08	0.80	3.72	-	592.8
AHQ-1-6, 3968 - 4010	R.FATASADGQIYIYDGK.T	1720.86021	2	1.92E-04	0.61	2.90	-	423.7
AHQ-1-6, 5831	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	2	1.22E-04	0.93	4.23	-	970.1
AHQ-1-6, 5815 - 5832	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	3	7.33E-08	0.79	3.51	-	838.2
AHQ-1-6, 4867	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	9.99E-05	0.71	3.55	-	603.1
AHQ-1-6, 4718 - 4795	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	5.59E-07	0.97	4.86	-	1633.0
AHQ-1-6, 1740	R.IAVVGEGR.E	800.92621	2	7.90E-04	0.73	2.55	-	676.2
AHQ-1-6, 2222	K.IKDIAWTEDSKR.I	1462.63267	2	1.16E-06	0.94	3.88	-	1329.1
AHQ-1-6, 3047	K.KVFASLPQVER.G	1274.49383	2	2.24E-05	0.83	2.91	-	903.3
AHQ-1-6, 5584 - 5654	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	2.01E-09	0.94	4.65	-	883.2
AHQ-1-6, 5663 - 5726	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	3.50E-06	0.89	4.10	-	873.6
AHQ-1-6, 5523 - 5590	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.41E-07	0.84	3.78	-	630.7
AHQ-1-6, 5782 - 5812	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.90E-09	0.91	4.75	-	708.4
AHQ-1-13, 3997 - 4021	R.LYSILGTTLKDEGK.L	1538.76736	2	4.64E-05	0.85	3.44	-	735.2
AHQ-1-6, 3930	R.LYSILGTTLKDEGK.L	1538.76736	3	2.00E-05	0.47	3.34	-	287.6
AHQ-1-7, 4012	R.LYSILGTTLKDEGK.L	1538.76736	2	1.67E-04	0.90	3.41	-	1073.1
AHQ-1-6, 3919 - 3950	R.LYSILGTTLKDEGK.L	1538.76736	2	8.78E-05	0.92	4.00	-	933.8
AHQ-1-6, 4982 - 5059	R.MTVDESGQLISCSMDDTVR.Y	2146.36365	2	6.97E-06	0.72	3.28	-	584.9
AHQ-1-6, 4299	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	1.68E-05	0.69	3.31	-	446.6
AHQ-1-7, 1896	K.SIQCLTVHKNGGK.S	1443.65418	2	8.84E-05	0.80	2.79	-	876.6
AHQ-1-6, 4198	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	7.57E-08	0.98	6.18	-	2306.3
AHQ-1-12, 3879	K.YAPSGFYIASGDVSGK.L	1619.75589	2	2.39E-08	0.87	3.52	-	588.9
AHQ-1-6, 3928 - 3999	K.YAPSGFYIASGDVSGK.L	1619.75589	2	9.64E-06	0.86	3.01	-	706.6
AHQ-1-11, 3775 - 3780	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.85E-08	0.89	3.85	-	608.2
AHQ-1-6, 2772	K.YEYQPFAGK.I	1103.20822	2	6.71E-07	0.78	2.80	-	615.1
gi|7669492|ref|NP_002037.2| glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]				1.00E-30	9.38	110.38	48.40	36053.0
AHQ-1-9, 3866 - 3872	R.GALQNIIPASTGAAK.A	1412.61680	1	1.49E-04	0.73	3.01	-	565.4
AHQ-1-11, 3540	R.GALQNIIPASTGAAK.A	1412.61680	1	2.93E-07	0.78	3.19	-	567.2
AHQ-1-9, 3460 - 3530	R.GALQNIIPASTGAAK.A	1412.61680	1	2.75E-04	0.75	3.05	-	573.0
AHQ-1-9, 3470 - 3539	R.GALQNIIPASTGAAK.A	1412.61680	1	3.42E-08	0.80	3.24	-	647.3
AHQ-1-9, 6095 - 6160	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	1.38E-07	0.97	6.85	-	1387.6

AHQ-1-13, 4115	K.RVIISAPSADAPMFVM*GVNHEK.Y	2386.77962	3	5.36E-07	0.79	3.46	-	990.4
AHQ-1-9, 4042 - 4056	K.RVIISAPSADAPMFVM*GVNHEK.Y	2386.77962	3	2.48E-05	0.92	4.99	-	948.8
AHQ-1-9, 4543	K.RVIISAPSADAPMFVMGVNHEK.Y	2370.78022	3	3.66E-08	0.95	4.80	-	1262.8
AHQ-1-9, 4747 - 4755	K.RVIISAPSADAPMFVMGVNHEK.Y	2370.78022	3	1.73E-08	0.97	5.87	-	1613.1
AHQ-1-9, 7352 - 7354	K.VDIVAINDPFIDLNYMVYM*FQYDSTHGK.F	3326.74330	3	2.45E-05	0.79	4.83	-	485.6
AHQ-1-10, 6293	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	1.00E-30	0.97	7.44	-	2083.7
AHQ-1-11, 6387	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	7.99E-06	0.97	6.00	-	1984.4
AHQ-1-10, 6296	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	2.63E-09	0.96	5.75	-	2225.0
AHQ-1-9, 7162 - 7166	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	4.68E-12	0.99	7.53	-	2465.0
AHQ-1-9, 5159	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	3.93E-07	0.95	4.41	-	914.2
AHQ-1-10, 4724 - 4779	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	2.92E-04	0.56	3.24	-	627.4
AHQ-1-9, 4864 - 4910	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	5.88E-06	0.90	3.78	-	678.9
AHQ-1-9, 4379 - 4380	R.VIISAPSADAPMFVM*GVNHEK.Y	2230.59327	2	7.90E-07	0.49	3.51	-	282.7
AHQ-1-10, 4593	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	1.15E-04	0.55	3.04	-	255.7
AHQ-1-14, 4988	R.VPTANVSVVDLTCR.L	1532.74450	2	1.43E-06	0.90	3.52	-	894.8
AHQ-1-14- , 4098	R.VPTANVSVVDLTCR.L	1532.74450	2	1.27E-10	0.93	3.91	-	916.6
AHQ-1-13, 4029 - 4087	R.VPTANVSVVDLTCR.L	1532.74450	2	2.75E-04	0.95	4.23	-	1094.0
AHQ-1-12, 4003 - 4065	R.VPTANVSVVDLTCR.L	1532.74450	2	4.00E-09	0.93	3.98	-	1066.3
AHQ-1-9, 4340 - 4350	R.VPTANVSVVDLTCR.L	1532.74450	2	3.27E-06	0.94	4.14	-	984.2
AHQ-1-11, 3914	R.VPTANVSVVDLTCR.L	1532.74450	2	6.27E-08	0.95	4.26	-	1085.8
AHQ-1-14- , 4252	R.VPTANVSVVDLTCR.L	1532.74450	2	2.94E-04	0.86	3.08	-	845.0
AHQ-1-9, 4199 - 4270	R.VPTANVSVVDLTCR.L	1532.74450	2	4.58E-09	0.96	4.41	-	1285.9
AHQ-1-9, 4062 - 4122	R.VPTANVSVVDLTCR.L	1532.74450	2	1.42E-07	0.96	4.40	-	1105.3
AHQ-1-9, 3959 - 3976	R.VPTANVSVVDLTCR.L	1532.74450	2	1.92E-10	0.93	3.64	-	943.7
AHQ-1-9, 3874	R.VPTANVSVVDLTCR.L	1532.74450	2	9.76E-08	0.86	3.33	-	811.1
AHQ-1-6, 4184	R.VPTANVSVVDLTCR.L	1532.74450	2	5.33E-09	0.93	3.70	-	997.4
AHQ-1-10, 3805 - 3859	R.VPTANVSVVDLTCR.L	1532.74450	2	1.01E-08	0.96	4.20	-	1273.9
AHQ-1-13- , 4243 - 4307	R.VPTANVSVVDLTCR.L	1532.74450	2	1.59E-09	0.95	4.24	-	1033.1
AHQ-1-4, 4367	R.VPTANVSVVDLTCR.L	1532.74450	2	1.00E-07	0.88	3.41	-	757.4
AHQ-1-9, 7446 - 7462	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	9.12E-07	0.93	4.41	-	804.2
AHQ-1-9, 7304 - 7375	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.31E-08	0.96	5.04	-	1104.9
AHQ-1-9, 7187	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.96E-08	0.95	4.77	-	916.4
AHQ-1-9, 6896 - 6962	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.04E-06	0.92	3.70	-	995.2
AHQ-1-9, 6811	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.69E-10	0.77	3.22	-	598.5
AHQ-1-9, 6736	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	4.40E-04	0.61	3.28	-	343.5
AHQ-1-9, 6712	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.52E-06	0.89	4.03	-	718.7
AHQ-1-9, 6631 - 6648	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	3.16E-04	0.55	2.77	-	382.8
AHQ-1-9, 6628	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.92E-07	0.89	3.88	-	735.9
AHQ-1-9, 6538 - 6615	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	7.93E-10	0.93	4.56	-	730.4
AHQ-1-13- , 5703	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	1.46E-05	0.95	5.09	-	871.8
AHQ-1-13- , 5792	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	1.30E-07	0.94	4.39	-	887.5
AHQ-1-13- , 6285 - 6347	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	4.50E-08	0.95	4.76	-	956.0
AHQ-1-13- , 6384	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.96E-04	0.69	2.99	-	606.0
AHQ-1-9, 6387 - 6451	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	3.47E-08	0.94	4.54	-	838.0
AHQ-1-9, 7031	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	6.83E-04	0.41	3.35	-	162.3
AHQ-1-14- , 6055	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.95E-06	0.94	4.16	-	961.7
gi|16753233|ref|NP_006280.2| talin 1 [Homo sapiens]				5.55E-16	116.92	1320.37	55.40	269665.3
AHQ-1-3, 3193 - 3201	K.AAAFEEQENETVVVK.E	1664.79496	2	3.56E-08	0.95	4.87	-	1305.2
AHQ-1-1, 4007	K.AAAFEEQENETVVVK.E	1664.79496	2	8.60E-04	0.80	3.19	-	817.9
AHQ-1-14- , 3147	K.AAAFEEQENETVVVK.E	1664.79496	2	3.79E-05	0.96	4.74	-	1418.2
AHQ-1-2, 3974	K.AAAFEEQENETVVVK.E	1664.79496	2	7.30E-04	0.84	3.68	-	936.6
AHQ-1-4, 3215 - 3290	K.AAAFEEQENETVVVK.E	1664.79496	2	2.84E-06	0.93	4.58	-	1120.6
AHQ-1-2, 3566	K.AAAFEEQENETVVVK.E	1664.79496	2	1.46E-04	0.94	4.25	-	1394.6
AHQ-1-2, 3322 - 3395	K.AAAFEEQENETVVVK.E	1664.79496	2	7.81E-05	0.93	4.01	-	1220.8
AHQ-1-1, 3288	K.AAAFEEQENETVVVK.E	1664.79496	2	3.39E-05	0.93	4.31	-	1244.8
AHQ-1-12, 3095	K.AAAFEEQENETVVVK.E	1664.79496	2	2.46E-05	0.85	3.96	-	738.8
AHQ-1-5, 2490	R.AAM*EPIVISAK.T	1146.38260	1	8.64E-04	0.43	2.48	-	262.2
AHQ-1-4, 3288	R.AAMEPIVISAK.T	1130.38320	1	3.07E-04	0.75	2.76	-	870.4
AHQ-1-4, 2596 - 2598	R.AAM*EPIVISAK.T	1146.38260	2	1.18E-05	0.79	2.51	-	785.3
AHQ-1-1, 2749	R.AAM*EPIVISAK.T	1146.38260	2	5.12E-07	0.84	3.08	-	773.9
AHQ-1-3, 2597	R.AAM*EPIVISAK.T	1146.38260	2	7.85E-05	0.74	2.84	-	643.4
AHQ-1-3, 2606	R.AAM*EPIVISAK.T	1146.38260	1	6.43E-04	0.38	2.50	-	173.9
AHQ-1-2, 2685	R.AAM*EPIVISAK.T	1146.38260	2	1.61E-06	0.84	2.93	-	777.4
AHQ-1-3, 3266	R.AAMEPIVISAK.T	1130.38320	2	2.68E-07	0.79	2.61	-	607.2
AHQ-1-2, 2683	R.AAM*EPIVISAK.T	1146.38260	1	3.28E-04	0.07	2.01	-	141.8
AHQ-1-6, 3142	R.AAMEPIVISAK.T	1130.38320	1	6.77E-05	0.24	2.17	-	560.3
AHQ-1-3, 1973	K.ADAEGESDLENSR.K	1393.35296	2	2.68E-07	0.88	3.45	-	906.4
AHQ-1-2, 2022	K.ADAEGESDLENSR.K	1393.35296	2	8.74E-08	0.93	3.42	-	1287.9
AHQ-1-1, 2123	K.ADAEGESDLENSR.K	1393.35296	2	4.27E-07	0.93	3.76	-	1066.5
AHQ-1-2, 2021 - 2089	K.ADAEGESDLENSR.K	1393.35296	2	8.40E-07	0.94	3.91	-	1249.2
AHQ-1-5, 1839	K.ADAEGESDLENSR.K	1393.35296	2	1.82E-07	0.83	3.00	-	782.1
AHQ-1-2, 1593 - 1666	K.ADAEGESDLENSRK.L	1521.52588	2	4.60E-06	0.83	2.80	-	1121.3
AHQ-1-3, 2517	K.AGALQCSPSDAYTK.K	1470.58689	2	2.11E-04	0.69	3.12	-	566.1
AHQ-1-1, 2745	K.AGALQCSPSDAYTK.K	1470.58689	2	8.91E-04	0.90	3.67	-	851.7
AHQ-1-6, 2562	K.AGALQCSPSDAYTK.K	1470.58689	2	2.19E-04	0.89	3.26	-	928.5
AHQ-1-4, 2646	K.AGALQCSPSDAYTK.K	1470.58689	2	1.75E-04	0.83	3.42	-	682.6
AHQ-1-2, 2742	K.AGALQCSPSDAYTK.K	1470.58689	1	2.34E-06	0.85	3.72	-	620.6
AHQ-1-8, 6286 - 6303	K.AGFLDLKDFLPK.E	1364.61374	2	4.85E-04	0.96	4.35	-	1938.4
AHQ-1-4, 4090 - 4170	K.AIAVTVQEMVTK.S	1290.55498	2	2.00E-04	0.92	3.73	-	983.6
AHQ-1-1, 3019	K.AIAVTVQEM*VTK.S	1306.55438	2	2.38E-04	0.88	3.05	-	1033.9
AHQ-1-3, 4050 - 4123	K.AIAVTVQEMVTK.S	1290.55498	2	9.21E-09	0.95	3.86	-	1502.0
AHQ-1-2, 4282	K.AIAVTVQEMVTK.S	1290.55498	2	1.92E-09	0.96	4.34	-	1516.1
AHQ-1-4, 2970	K.AIAVTVQEM*VTK.S	1306.55438	2	5.17E-04	0.95	3.94	-	1222.7
AHQ-1-3, 2945 - 2957	K.AIAVTVQEM*VTK.S	1306.55438	2	3.47E-08	0.96	4.18	-	1280.0
AHQ-1-5, 3946 - 3957	K.AIAVTVQEMVTK.S	1290.55498	2	2.49E-07	0.95	4.44	-	1185.9
AHQ-1-2, 3043	K.AIAVTVQEM*VTK.S	1306.55438	2	3.33E-04	0.92	3.77	-	800.9
AHQ-1-2, 4427	K.AIAVTVQEMVTK.S	1290.55498	2	3.11E-05	0.95	3.62	-	1425.0
AHQ-1-2, 2743	K.ALDGAFTEENR.A	1223.27427	2	1.02E-06	0.95	3.45	-	1894.8
AHQ-1-3, 2507	K.ALDGAFTEENR.A	1223.27427	2	3.99E-06	0.87	2.82	-	1006.8
AHQ-1-3, 2641 - 2715	K.ALDGAFTEENR.A	1223.27427	2	7.39E-06	0.94	3.59	-	1453.6
AHQ-1-13- , 2765	K.ALDGAFTEENR.A	1223.27427	2	3.01E-04	0.94	3.31	-	1456.8
AHQ-1-4, 2664	K.ALDGAFTEENR.A	1223.27427	2	1.41E-04	0.95	3.97	-	1499.3
AHQ-1-5, 2505 - 2578	K.ALDGAFTEENR.A	1223.27427	2	2.23E-06	0.92	3.52	-	1301.8
AHQ-1-4, 2503	K.ALDGAFTEENR.A	1223.27427	2	2.21E-07	0.95	3.45	-	1831.4
AHQ-1-2, 2593	K.ALDGAFTEENR.A	1223.27427	2	1.82E-04	0.89	2.88	-	1228.0
AHQ-1-13- , 3440	K.ALDYYM*LR.N	1061.23626	2	2.33E-05	0.91	2.73	-	1072.3
AHQ-1-13, 3923	K.ALDYYMLR.N	1045.23686	2	1.08E-04	0.94	3.48	-	847.1
AHQ-1-13- , 4083 - 4088	K.ALDYYMLR.N	1045.23686	2	1.27E-04	0.94	3.42	-	982.2
AHQ-1-8, 3739	K.ALDYYMLR.N	1045.23686	2	9.04E-06	0.93	3.35	-	796.9
AHQ-1-2, 2033 - 2046	R.ALEATTEHIR.Q	1141.25953	2	3.92E-08	0.82	3.11	-	962.4
AHQ-1-7, 1852	R.ALEATTEHIR.Q	1141.25953	2	2.28E-04	0.74	2.80	-	903.2
AHQ-1-2, 2161	R.ALEATTEHIR.Q	1141.25953	2	3.78E-06	0.86	3.06	-	1018.2
AHQ-1-5, 1786 - 1855	R.ALEATTEHIR.Q	1141.25953	2	3.83E-06	0.73	2.95	-	796.3
AHQ-1-3, 1985	R.ALEATTEHIR.Q	1141.25953	1	1.29E-05	0.11	1.89	-	346.2
AHQ-1-6, 1830 - 1883	R.ALEATTEHIR.Q	1141.25953	2	2.11E-05	0.64	2.61	-	765.6
AHQ-1-3, 1961 - 1993	R.ALEATTEHIR.Q	1141.25953	2	4.15E-04	0.89	2.95	-	1511.7
AHQ-1-4, 1934	R.ALEATTEHIR.Q	1141.25953	2	1.27E-05	0.93	3.61	-	1465.0

AHQ-1-7, 3410	K.ALGDLISATK.A	989.14811	1	8.85E-05	0.15	2.32	-	245.6
AHQ-1-4, 3516	K.ALGDLISATK.A	989.14811	2	2.21E-06	0.92	3.60	-	952.5
AHQ-1-3, 3483	K.ALGDLISATK.A	989.14811	2	2.97E-06	0.89	3.51	-	708.5
AHQ-1-2, 3581	K.ALGDLISATK.A	989.14811	2	2.14E-06	0.93	3.82	-	872.3
AHQ-1-6, 3366	K.ALGDLISATK.A	989.14811	2	5.14E-05	0.87	3.14	-	745.7
AHQ-1-1, 3553	K.ALGDLISATK.A	989.14811	2	5.64E-05	0.93	4.00	-	659.2
AHQ-1-5, 3389	K.ALGDLISATK.A	989.14811	2	3.08E-05	0.82	3.01	-	687.6
AHQ-1-5, 2499 - 2569	K.ALSTDPAAPNLK.S	1198.35099	2	2.38E-05	0.57	2.89	-	399.2
AHQ-1-3, 2635	K.ALSTDPAAPNLK.S	1198.35099	2	1.48E-07	0.78	2.90	-	668.8
AHQ-1-2, 2718 - 2745	K.ALSTDPAAPNLK.S	1198.35099	2	2.96E-06	0.78	3.23	-	621.0
AHQ-1-1, 2768 - 2775	K.ALSTDPAAPNLK.S	1198.35099	2	3.62E-05	0.83	3.33	-	606.8
AHQ-1-7, 2589	K.ALSTDPAAPNLK.S	1198.35099	2	2.79E-06	0.81	3.09	-	713.5
AHQ-1-4, 6647 - 6722	R.ANQAIQMACQSLGEPGCTQAQVLSAATIVAK.H	3220.64522	3	6.21E-04	0.90	4.63	-	686.5
AHQ-1-3, 6323	K.APGQLECETAIAALNSCLR.D	2077.32566	3	5.31E-05	0.86	4.27	-	685.9
AHQ-1-4, 6459 - 6464	K.APGQLECETAIAALNSCLR.D	2077.32566	2	7.67E-08	0.98	6.50	-	1646.0
AHQ-1-3, 5615	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.32E-08	0.97	5.04	-	1337.4
AHQ-1-4, 5727 - 5807	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.68E-06	0.93	4.10	-	1060.1
AHQ-1-2, 6493	K.APGQLECETAIAALNSCLR.D	2077.32566	2	6.99E-08	0.97	5.66	-	1335.6
AHQ-1-3, 6321	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.11E-08	0.97	5.57	-	1492.1
AHQ-1-1, 6264	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.22E-05	0.96	5.06	-	1245.1
AHQ-1-2, 6498	K.APGQLECETAIAALNSCLR.D	2077.32566	3	4.12E-05	0.84	3.92	-	778.3
AHQ-1-2, 6758	K.APGQLECETAIAALNSCLR.D	2077.32566	2	8.75E-11	0.97	4.84	-	1318.7
AHQ-1-3, 6905 - 6909	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	7.46E-10	0.97	5.75	-	1809.9
AHQ-1-1, 6771 - 6784	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	9.40E-06	0.93	4.37	-	1470.2
AHQ-1-6, 6875	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	3.22E-04	0.91	4.51	-	1007.8
AHQ-1-5, 7019 - 7022	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.34E-06	0.97	5.78	-	2159.5
AHQ-1-1, 6767	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	2	6.08E-05	0.87	3.32	-	901.8
AHQ-1-2, 7165	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.72E-05	0.95	4.69	-	1722.7
AHQ-1-2, 7082 - 7083	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	2.15E-08	0.98	5.79	-	2428.1
AHQ-1-4, 3004	K.ASAGPQPLLVQSCK.A	1457.67763	1	6.83E-08	0.27	2.95	-	294.8
AHQ-1-1, 3117	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.51E-04	0.26	2.27	-	346.6
AHQ-1-4, 3243	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.40E-08	0.74	3.18	-	370.6
AHQ-1-4, 2947 - 3018	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.51E-06	0.92	4.24	-	608.0
AHQ-1-5, 2846	K.ASAGPQPLLVQSCK.A	1457.67763	1	3.26E-11	0.68	3.11	-	474.2
AHQ-1-5, 2811	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.18E-05	0.74	2.74	-	491.5
AHQ-1-2, 3030 - 3101	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.05E-09	0.90	3.75	-	535.5
AHQ-1-4, 2994	K.ASAGPQPLLVQSCK.A	1457.67763	1	4.19E-06	0.18	2.05	-	415.7
AHQ-1-7, 2794 - 2873	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.68E-07	0.89	3.86	-	583.8
AHQ-1-6, 2875	K.ASAGPQPLLVQSCK.A	1457.67763	1	2.28E-09	0.76	4.02	-	394.3
AHQ-1-6, 2856	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.28E-06	0.69	3.00	-	328.4
AHQ-1-3, 2983 - 2989	K.ASAGPQPLLVQSCK.A	1457.67763	1	5.11E-07	0.16	2.07	-	333.0
AHQ-1-3, 2954 - 2973	K.ASAGPQPLLVQSCK.A	1457.67763	2	6.35E-06	0.86	3.61	-	468.7
AHQ-1-1, 3096	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.16E-05	0.68	2.93	-	385.7
AHQ-1-1, 4387 - 4400	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	6.53E-05	0.90	4.02	-	638.0
AHQ-1-2, 4065	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.47E-08	0.95	4.76	-	847.2
AHQ-1-2, 4485 - 4553	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.21E-10	0.94	4.66	-	998.7
AHQ-1-5, 3730 - 3731	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	6.22E-07	0.94	4.98	-	667.2
AHQ-1-3, 3937	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.43E-07	0.95	4.87	-	801.4
AHQ-1-5, 3879	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.60E-09	0.87	3.78	-	581.5
AHQ-1-4, 3987 - 3994	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.89E-07	0.91	4.38	-	617.0
AHQ-1-4, 3826	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	6.31E-06	0.54	2.64	-	388.5
AHQ-1-7, 3758	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	9.69E-05	0.86	3.71	-	533.5
AHQ-1-6, 3666 - 3674	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.35E-06	0.90	4.03	-	725.1
AHQ-1-1, 3824 - 3827	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	9.00E-08	0.92	4.28	-	668.3
AHQ-1-3, 4350 - 4426	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	6.79E-07	0.93	4.65	-	660.1
AHQ-1-4, 4414 - 4491	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.36E-09	0.95	5.39	-	660.6
AHQ-1-3, 3785	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.80E-07	0.88	3.80	-	671.3
AHQ-1-1, 4481	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	4.07E-13	0.89	4.29	-	558.8
AHQ-1-1, 3967	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	3.36E-08	0.87	3.89	-	723.6
AHQ-1-2, 4633 - 4674	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	4.26E-10	0.94	4.55	-	795.6
AHQ-1-4, 4583	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	9.44E-15	0.84	3.91	-	453.9
AHQ-1-2, 4975	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.09E-07	0.93	4.22	-	797.1
AHQ-1-6, 4238	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.97E-06	0.86	3.79	-	510.1
AHQ-1-5, 4325 - 4341	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	5.79E-08	0.92	4.22	-	789.6
AHQ-1-5, 4495	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.55E-10	0.92	4.60	-	601.0
AHQ-1-4, 4499	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.18E-05	0.67	2.91	-	399.7
AHQ-1-7, 4320 - 4332	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	5.85E-06	0.88	3.64	-	656.5
AHQ-1-6, 4408	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.91E-05	0.67	3.36	-	352.9
AHQ-1-4, 4402	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	5.94E-07	0.88	4.31	-	467.2
AHQ-1-3, 4519	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	6.78E-10	0.88	3.87	-	524.7
AHQ-1-5, 5042	K.AVAEQIPLLVQGVR.G	1493.77619	1	6.86E-07	0.27	2.94	-	118.0
AHQ-1-2, 5595	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.28E-05	0.90	3.99	-	754.4
AHQ-1-5, 4989 - 5057	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.03E-08	0.95	4.52	-	1074.7
AHQ-1-2, 5477	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.25E-07	0.93	3.08	-	1195.8
AHQ-1-4, 5126 - 5134	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.34E-07	0.89	3.41	-	747.6
AHQ-1-4, 5144	K.AVAEQIPLLVQGVR.G	1493.77619	1	6.50E-07	0.71	3.35	-	252.3
AHQ-1-2, 5225	K.AVAEQIPLLVQGVR.G	1493.77619	1	1.63E-05	0.74	3.61	-	358.0
AHQ-1-2, 5210	K.AVAEQIPLLVQGVR.G	1493.77619	3	4.13E-09	0.97	4.74	-	2583.7
AHQ-1-1, 5173	K.AVAEQIPLLVQGVR.G	1493.77619	3	2.49E-06	0.97	4.31	-	2592.4
AHQ-1-1, 5143	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.73E-04	0.81	3.46	-	579.3
AHQ-1-7, 4985 - 4993	K.AVAEQIPLLVQGVR.G	1493.77619	2	8.97E-05	0.90	4.31	-	621.0
AHQ-1-2, 5187 - 5257	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.78E-07	0.82	3.03	-	629.7
AHQ-1-6, 4943 - 4947	K.AVAEQIPLLVQGVR.G	1493.77619	2	7.80E-07	0.75	2.99	-	500.6
AHQ-1-3, 5057	K.AVAEQIPLLVQGVR.G	1493.77619	3	5.08E-06	0.95	4.45	-	1729.4
AHQ-1-6, 3747	K.AVASAAAALVLK.A	1085.32216	2	8.94E-07	0.96	3.06	-	2088.3
AHQ-1-2, 4161	K.AVASAAAALVLK.A	1085.32216	2	1.09E-04	0.95	3.79	-	1652.8
AHQ-1-2, 4077	K.AVASAAAALVLK.A	1085.32216	2	1.21E-05	0.92	3.69	-	1137.8
AHQ-1-4, 3976 - 4022	K.AVASAAAALVLK.A	1085.32216	2	5.46E-07	0.95	4.16	-	1341.8
AHQ-1-1, 3964 - 4031	K.AVASAAAALVLK.A	1085.32216	2	2.84E-06	0.97	4.05	-	2000.7
AHQ-1-3, 3993	K.AVASAAAALVLK.A	1085.32216	2	1.71E-04	0.96	3.89	-	1714.5
AHQ-1-5, 3793	K.AVASAAAALVLK.A	1085.32216	2	7.78E-08	0.97	4.23	-	2074.1
AHQ-1-1, 3872 - 3892	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.07E-08	0.97	5.58	-	1618.7
AHQ-1-1, 3983	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	8.14E-08	0.86	3.89	-	827.9
AHQ-1-4, 4294 - 4328	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.66E-07	0.92	4.12	-	1127.8
AHQ-1-2, 5937 - 6011	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.24E-04	0.41	2.80	-	507.2
AHQ-1-2, 4858	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.10E-06	0.78	3.73	-	701.5
AHQ-1-2, 4554 - 4631	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.42E-07	0.90	4.10	-	965.0
AHQ-1-1, 4165	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.46E-06	0.97	5.21	-	1719.4
AHQ-1-6, 4048 - 4059	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.69E-04	0.64	2.77	-	575.5
AHQ-1-4, 4151 - 4224	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.50E-06	0.60	3.21	-	446.7
AHQ-1-2, 4405 - 4481	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.92E-06	0.96	5.19	-	1310.5
AHQ-1-1, 4256	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.77E-06	0.80	3.24	-	940.7
AHQ-1-3, 3845 - 3921	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.49E-05	0.92	3.81	-	1238.6
AHQ-1-2, 5515	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.30E-07	0.95	4.73	-	1153.4
AHQ-1-3, 4509	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.08E-07	0.75	3.31	-	785.2
AHQ-1-5, 4261 - 4301	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.43E-04	0.67	3.37	-	690.1
AHQ-1-4, 3907	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.90E-05	0.87	3.65	-	1029.1

AHQ-1-3, 3995	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	9.63E-04	0.65	3.24	-	719.3
AHQ-1-2, 4261 - 4330	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.20E-06	0.87	4.22	-	680.9
AHQ-1-3, 4130 - 4201	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.88E-07	0.96	4.89	-	1456.8
AHQ-1-2, 4153 - 4155	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.66E-06	0.95	4.44	-	1582.1
AHQ-1-4, 3999	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.14E-06	0.91	4.14	-	1235.7
AHQ-1-2, 3961	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.34E-04	0.86	3.59	-	944.2
AHQ-1-5, 4430	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.62E-05	0.71	2.98	-	441.7
AHQ-1-3, 4269 - 4338	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.21E-05	0.83	3.19	-	888.4
AHQ-1-2, 5162	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	7.86E-04	0.90	4.02	-	1111.9
AHQ-1-2, 4043	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	7.96E-09	0.90	3.73	-	1046.0
AHQ-1-5, 7338 - 7346	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	2.75E-05	0.72	3.77	-	730.7
AHQ-1-3, 7085 - 7153	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	4.24E-06	0.97	6.02	-	2039.2
AHQ-1-6, 7170	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	6.03E-04	0.92	4.12	-	1419.9
AHQ-1-2, 7230 - 7294	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	7.74E-12	0.98	6.34	-	2599.8
AHQ-1-2, 5925	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	3	1.20E-04	0.87	4.14	-	663.5
AHQ-1-6, 6090	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	3.50E-05	0.67	2.84	-	473.1
AHQ-1-5, 6233	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	5.43E-07	0.82	3.57	-	372.9
AHQ-1-1, 6059	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	7.91E-07	0.83	3.86	-	408.8
AHQ-1-3, 4833 - 4843	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	2.35E-06	0.86	4.11	-	418.4
AHQ-1-9, 6076	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	7.42E-04	0.59	3.05	-	340.0
AHQ-1-4, 5886	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	7.82E-05	0.65	3.12	-	380.2
AHQ-1-2, 4891 - 4973	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	3.05E-06	0.50	3.21	-	226.8
AHQ-1-3, 6110	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	2.03E-04	0.86	3.77	-	623.4
AHQ-1-2, 6273 - 6281	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.48E-05	0.89	3.92	-	664.1
AHQ-1-1, 5720	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	3.26E-05	0.77	3.60	-	443.9
AHQ-1-1, 5727	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	3	1.14E-04	0.77	3.48	-	494.4
AHQ-1-4, 4912	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	2.17E-06	0.77	3.38	-	525.6
AHQ-1-3, 5875	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.85E-09	0.91	5.01	-	686.7
AHQ-1-6, 6150 - 6222	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	8.45E-08	0.91	4.41	-	973.9
AHQ-1-1, 5864	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	3.82E-07	0.92	4.47	-	1099.9
AHQ-1-4, 6286 - 6354	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	4.71E-11	0.92	4.70	-	888.3
AHQ-1-1, 6135	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.01E-07	0.92	4.81	-	874.2
AHQ-1-2, 6357 - 6426	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	9.44E-15	0.94	5.29	-	1190.7
AHQ-1-2, 5191	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.22E-06	0.79	3.46	-	643.1
AHQ-1-3, 6261 - 6342	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	4.05E-14	0.94	4.82	-	1398.9
AHQ-1-3, 6151 - 6197	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.50E-13	0.95	5.48	-	1113.1
AHQ-1-4, 5988 - 6058	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	3.19E-08	0.90	4.93	-	752.1
AHQ-1-2, 6047 - 6117	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	9.73E-10	0.94	5.57	-	1077.9
AHQ-1-5, 6285 - 6359	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.51E-13	0.95	5.36	-	1289.7
AHQ-1-4, 2431	R.CVSCLPGQR.D	1079.23309	2	1.44E-04	0.85	2.96	-	887.9
AHQ-1-5, 2353	R.CVSCLPGQR.D	1079.23309	2	9.06E-04	0.74	2.85	-	683.2
AHQ-1-4, 2436	R.CVSCLPGQR.D	1079.23309	1	1.25E-04	0.43	2.60	-	147.8
AHQ-1-3, 2427	R.CVSCLPGQR.D	1079.23309	2	1.89E-04	0.91	3.29	-	888.7
AHQ-1-3, 3609	R.DDILNGSHPVSFDK.A	1544.64741	2	3.13E-10	0.83	3.29	-	786.2
AHQ-1-10, 3209 - 3269	R.DDILNGSHPVSFDK.A	1544.64741	2	2.56E-05	0.30	2.52	-	455.0
AHQ-1-9, 3591	R.DDILNGSHPVSFDK.A	1544.64741	2	1.18E-07	0.95	4.11	-	1367.2
AHQ-1-13, 3462	R.DDILNGSHPVSFDK.A	1544.64741	2	1.61E-06	0.90	3.51	-	997.0
AHQ-1-1, 3660	R.DDILNGSHPVSFDK.A	1544.64741	2	5.78E-06	0.86	3.61	-	744.8
AHQ-1-7, 3765	R.DDILNGSHPVSFDK.A	1544.64741	2	6.47E-08	0.91	3.49	-	1080.3
AHQ-1-4, 3631	R.DDILNGSHPVSFDK.A	1544.64741	2	9.54E-08	0.93	3.92	-	1060.5
AHQ-1-7, 3552	R.DDILNGSHPVSFDK.A	1544.64741	2	5.48E-08	0.90	3.48	-	930.1
AHQ-1-8, 3562 - 3634	R.DDILNGSHPVSFDK.A	1544.64741	2	2.24E-09	0.96	4.21	-	1397.5
AHQ-1-10, 3433	R.DDILNGSHPVSFDK.A	1544.64741	2	1.22E-07	0.90	3.68	-	1002.8
AHQ-1-8, 4842	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	2.81E-04	0.95	4.69	-	1072.2
AHQ-1-2, 6289	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	7.54E-05	0.76	3.54	-	767.5
AHQ-1-2, 6290 - 6309	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.93E-08	0.96	5.17	-	1222.7
AHQ-1-3, 5743	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.94E-09	0.89	3.42	-	905.5
AHQ-1-2, 5531	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.80E-11	0.87	3.50	-	802.1
AHQ-1-3, 6105 - 6107	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.95E-08	0.97	5.59	-	1513.3
AHQ-1-2, 5919	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.81E-07	0.94	4.65	-	893.4
AHQ-1-3, 6347	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.71E-10	0.70	3.07	-	579.0
AHQ-1-5, 5405	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.03E-10	0.95	4.71	-	900.3
AHQ-1-3, 6042 - 6109	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	2.96E-05	0.86	4.71	-	809.1
AHQ-1-4, 6239	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.02E-09	0.92	4.47	-	913.4
AHQ-1-6, 6078	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.04E-09	0.95	4.73	-	1075.7
AHQ-1-9, 6060	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.69E-10	0.86	3.56	-	730.2
AHQ-1-3, 6273 - 6346	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	1.38E-10	0.91	3.88	-	1329.9
AHQ-1-4, 6499	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.74E-12	0.94	4.25	-	1101.3
AHQ-1-4, 5452 - 5490	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.01E-07	0.91	4.60	-	725.8
AHQ-1-1, 6091	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.75E-10	0.96	5.04	-	1172.7
AHQ-1-1, 5417	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.33E-13	0.96	4.91	-	1261.6
AHQ-1-3, 5327 - 5373	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.70E-12	0.95	4.28	-	1258.9
AHQ-1-3, 5885	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.99E-04	0.84	3.37	-	742.2
AHQ-1-8, 6154	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.91E-11	0.94	4.56	-	1007.5
AHQ-1-4, 6403	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	8.96E-05	0.89	3.72	-	820.7
AHQ-1-4, 5416 - 5482	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	9.65E-11	0.96	5.61	-	814.0
AHQ-1-4, 5476 - 5492	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	3.25E-05	0.94	4.45	-	1882.0
AHQ-1-1, 5371	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	7.85E-06	0.96	4.37	-	2122.5
AHQ-1-2, 5505	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	4.41E-05	0.95	4.48	-	2202.3
AHQ-1-5, 5421	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	1.27E-08	0.93	4.46	-	1642.0
AHQ-1-14- , 5131	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.73E-04	0.75	3.03	-	720.7
AHQ-1-2, 4875	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.46E-05	0.65	2.57	-	789.0
AHQ-1-2, 5929	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.20E-04	0.56	2.55	-	590.8
AHQ-1-3, 5355 - 5358	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	4.78E-06	0.94	5.00	-	1763.7
AHQ-1-3, 5342 - 5409	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.98E-06	0.86	3.77	-	709.9
AHQ-1-3, 4737	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	7.95E-06	0.93	4.29	-	1052.4
AHQ-1-2, 3766	R.DPPSWSVLAGHSR.T	1409.53156	3	8.21E-05	0.87	3.91	-	757.7
AHQ-1-2, 3759	R.DPPSWSVLAGHSR.T	1409.53156	2	5.60E-07	0.81	2.84	-	378.1
AHQ-1-5, 3479 - 3495	R.DPPSWSVLAGHSR.T	1409.53156	2	1.20E-08	0.90	3.60	-	692.0
AHQ-1-3, 3621 - 3629	R.DPPSWSVLAGHSR.T	1409.53156	2	2.70E-08	0.94	3.98	-	692.9
AHQ-1-6, 3454	R.DPPSWSVLAGHSR.T	1409.53156	2	9.72E-09	0.80	3.26	-	413.8
AHQ-1-4, 3646 - 3648	R.DPPSWSVLAGHSR.T	1409.53156	2	4.04E-10	0.94	3.91	-	743.4
AHQ-1-7, 3520	R.DPPSWSVLAGHSR.T	1409.53156	2	1.13E-07	0.80	2.72	-	514.8
AHQ-1-4, 3656	R.DPPSWSVLAGHSR.T	1409.53156	3	3.02E-07	0.88	4.25	-	594.6
AHQ-1-3, 3625	R.DPPSWSVLAGHSR.T	1409.53156	3	9.40E-07	0.92	4.44	-	678.4
AHQ-1-1, 5360	R.DPVQLNLLYVQAR.D	1529.76539	2	3.86E-07	0.97	4.89	-	1549.1
AHQ-1-9, 5163	R.DPVQLNLLYVQAR.D	1529.76539	2	2.57E-08	0.94	4.24	-	1247.1
AHQ-1-8, 5230 - 5304	R.DPVQLNLLYVQAR.D	1529.76539	2	2.20E-05	0.96	4.73	-	1522.4
AHQ-1-13- , 5216	R.DPVQLNLLYVQAR.D	1529.76539	2	2.01E-06	0.81	3.34	-	737.6
AHQ-1-6, 2379	K.EAAYHPEVAPDVR.L	1454.56910	1	8.05E-04	0.22	1.90	-	370.5
AHQ-1-6, 2366	K.EAAYHPEVAPDVR.L	1454.56910	2	1.87E-06	0.82	3.06	-	651.0
AHQ-1-5, 2350	K.EAAYHPEVAPDVR.L	1454.56910	2	3.90E-04	0.84	2.67	-	1010.5
AHQ-1-2, 2551 - 2559	K.EAAYHPEVAPDVR.L	1454.56910	1	4.58E-05	0.58	2.48	-	430.9
AHQ-1-2, 2549 - 2550	K.EAAYHPEVAPDVR.L	1454.56910	2	1.63E-06	0.88	3.43	-	774.4
AHQ-1-3, 2465	K.EAAYHPEVAPDVR.L	1454.56910	2	2.15E-06	0.67	2.51	-	799.7
AHQ-1-3, 2467	K.EAAYHPEVAPDVR.L	1454.56910	1	5.85E-04	0.81	2.87	-	709.2
AHQ-1-7, 2392	K.EAAYHPEVAPDVR.L	1454.56910	2	6.69E-04	0.67	2.84	-	614.4

AHQ-1-2, 6169 - 6237	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.34E-07	0.97	5.34	-	1564.4
AHQ-1-1, 6265	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.66E-09	0.94	4.64	-	1275.2
AHQ-1-7, 6176	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.27E-07	0.86	3.68	-	978.1
AHQ-1-5, 6246 - 6325	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.25E-06	0.97	5.29	-	1584.9
AHQ-1-5, 6146	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.50E-06	0.89	3.74	-	1078.8
AHQ-1-3, 6062 - 6101	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.34E-08	0.94	4.53	-	1125.5
AHQ-1-6, 6030	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.02E-05	0.94	4.53	-	1044.0
AHQ-1-3, 6159 - 6233	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.23E-05	0.95	4.85	-	1246.2
AHQ-1-2, 6297 - 6371	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.28E-08	0.97	5.49	-	1859.5
AHQ-1-4, 5979	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.08E-10	0.89	4.07	-	711.1
AHQ-1-2, 6443 - 6519	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.72E-09	0.97	5.25	-	1522.7
AHQ-1-4, 6140 - 6210	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.08E-07	0.95	4.65	-	1308.2
AHQ-1-10, 5332	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.97E-04	0.63	3.05	-	726.8
AHQ-1-2, 7551	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.92E-04	0.61	2.70	-	676.1
AHQ-1-9, 5999	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.63E-05	0.94	4.35	-	1366.1
AHQ-1-10, 5440 - 5499	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.00E-04	0.62	3.32	-	788.4
AHQ-1-4, 6283 - 6352	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.40E-08	0.96	4.97	-	1234.7
AHQ-1-4, 6444	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.94E-07	0.91	3.99	-	1183.4
AHQ-1-1, 6027 - 6088	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.67E-07	0.96	5.03	-	1632.7
AHQ-1-1, 7004	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	1.33E-06	0.90	3.93	-	1177.2
AHQ-1-5, 7459 - 7462	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	9.94E-05	0.89	4.38	-	630.1
AHQ-1-3, 7253	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	1.04E-09	0.93	4.56	-	1144.1
AHQ-1-9, 7286 - 7288	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	2.32E-06	0.84	4.01	-	900.3
AHQ-1-9, 7284	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	1.15E-04	0.83	3.77	-	627.4
AHQ-1-6, 7266	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	1.89E-14	0.94	4.86	-	1418.8
AHQ-1-4, 7430	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	3.12E-08	0.95	5.43	-	1210.8
AHQ-1-2, 7389 - 7395	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	2.33E-06	0.96	5.57	-	1516.8
AHQ-1-2, 7385 - 7450	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	7.60E-06	0.88	4.51	-	751.3
AHQ-1-8, 7542 - 7544	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	6.22E-07	0.98	7.11	-	1806.3
AHQ-1-10, 6444 - 6445	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.24E-08	0.97	6.31	-	1637.3
AHQ-1-4, 7400 - 7427	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	4.33E-07	0.78	3.49	-	674.7
AHQ-1-3, 7222 - 7289	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	2.42E-11	0.98	6.95	-	1901.4
AHQ-1-3, 7163	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	5.58E-08	0.95	5.51	-	1009.0
AHQ-1-5, 7445 - 7515	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.35E-10	0.95	5.61	-	1177.4
AHQ-1-11, 6523	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	3.90E-08	0.90	4.40	-	937.1
AHQ-1-1, 6999	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.40E-05	0.69	3.01	-	1030.1
AHQ-1-7, 7532	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	2.43E-06	0.95	5.69	-	1608.0
AHQ-1-2, 7309	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	3.07E-07	0.88	4.18	-	767.9
AHQ-1-6, 7264 - 7318	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	5.45E-09	0.95	5.74	-	1343.3
AHQ-1-2, 7314	R.ELLENPVQPINDMSYFGCLDSVMENSK.V	3132.48874	3	1.25E-07	0.94	4.62	-	1144.8
AHQ-1-4, 7251	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	4.58E-05	0.85	4.46	-	687.0
AHQ-1-2, 6919	R.ELLENPVQPINDMSYFGCLDSVM*ENSK.V	3148.48814	3	4.64E-06	0.62	3.43	-	326.3
AHQ-1-7, 3041 - 3042	R.EQGVEEHETLLLR.R	1553.69898	2	2.16E-04	0.85	3.44	-	515.5
AHQ-1-8, 2812 - 2885	R.EQGVEEHETLLLR.R	1553.69898	2	7.28E-04	0.84	3.14	-	686.3
AHQ-1-8, 5546 - 5548	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	2.22E-15	0.97	6.52	-	1614.0
AHQ-1-13- , 5663	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	2.33E-11	0.98	7.10	-	2149.9
AHQ-1-13, 5340	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	5.55E-16	0.98	6.70	-	1764.0
AHQ-1-1, 5771 - 5833	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	2.93E-08	0.92	5.07	-	1172.2
AHQ-1-14- , 5514	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	5.07E-13	0.97	5.75	-	1777.5
AHQ-1-8, 5116 - 5195	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	2.36E-06	0.98	6.40	-	1880.9
AHQ-1-13- , 5275	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	2.92E-04	0.97	5.17	-	1803.2
AHQ-1-13, 4981	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.15E-08	0.97	5.47	-	1830.2
AHQ-1-14- , 5146	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	9.63E-08	0.97	5.59	-	1808.2
AHQ-1-4, 2364	K.EVANSTANLVK.T	1146.27608	2	4.36E-04	0.74	2.69	-	907.1
AHQ-1-13, 4541 - 4603	K.EVIQEWNLTNIK.R	1487.68214	2	4.32E-06	0.94	4.04	-	1331.7
AHQ-1-1, 4859 - 4935	K.EVIQEWNLTNIK.R	1487.68214	2	3.12E-04	0.81	2.90	-	734.9
AHQ-1-8, 4712	K.EVIQEWNLTNIK.R	1487.68214	1	5.46E-04	0.33	2.73	-	198.8
AHQ-1-8, 4706 - 4720	K.EVIQEWNLTNIK.R	1487.68214	2	4.07E-07	0.93	4.48	-	963.0
AHQ-1-11, 4384 - 4462	K.EVIQEWNLTNIK.R	1487.68214	2	9.62E-05	0.83	3.19	-	655.8
AHQ-1-8, 4075	K.EVIQEWNLTNIKR.W	1643.86849	2	4.05E-05	0.70	3.51	-	577.2
AHQ-1-8, 2936 - 3004	K.FFYSDQNVDSR.D	1378.42795	2	8.68E-06	0.93	3.58	-	1105.4
AHQ-1-9, 2928	K.FFYSDQNVDSR.D	1378.42795	2	1.65E-05	0.91	3.26	-	978.1
AHQ-1-10, 2855	K.FFYSDQNVDSR.D	1378.42795	2	3.26E-05	0.90	3.28	-	1008.5
AHQ-1-7, 3017	K.FFYSDQNVDSR.D	1378.42795	2	3.10E-06	0.83	3.08	-	664.5
AHQ-1-8, 6150 - 6175	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	9.59E-09	0.98	5.59	-	2529.3
AHQ-1-1, 6137	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	2.73E-05	0.82	3.31	-	851.3
AHQ-1-8, 6243	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	5.64E-12	0.96	5.33	-	1756.1
AHQ-1-10, 5428	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	8.15E-07	0.93	4.32	-	1537.5
AHQ-1-8, 6182	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	2	7.63E-04	0.52	2.95	-	232.0
AHQ-1-3, 6394 - 6465	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	3.02E-05	0.93	5.50	-	876.6
AHQ-1-2, 6550 - 6619	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	6.17E-08	0.92	4.81	-	895.0
AHQ-1-4, 6563	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	2.80E-05	0.88	3.36	-	1107.0
AHQ-1-4, 7291	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	1.16E-07	0.82	4.22	-	499.1
AHQ-1-4, 7288 - 7292	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	9.36E-04	0.90	4.13	-	931.1
AHQ-1-3, 7115	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	3.07E-11	0.85	3.95	-	658.2
AHQ-1-1, 6321	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	2.51E-07	0.80	3.41	-	724.4
AHQ-1-1, 6312	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	2.86E-06	0.85	4.24	-	650.7
AHQ-1-2, 6565 - 6637	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	1.91E-07	0.93	4.26	-	1074.7
AHQ-1-2, 7470 - 7538	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	1.06E-05	0.79	4.00	-	718.2
AHQ-1-3, 7422	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	1.05E-07	0.86	4.25	-	596.3
AHQ-1-4, 6559 - 6627	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	3.52E-06	0.88	4.40	-	683.3
AHQ-1-2, 7254	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	3.01E-06	0.87	4.62	-	689.3
AHQ-1-3, 6395 - 6475	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	7.81E-06	0.83	3.12	-	1100.7
AHQ-1-3, 7341	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	1.29E-07	0.85	4.01	-	704.9
AHQ-1-4, 2791 - 2794	K.FLPSELRDEH	1243.35032	2	1.25E-04	0.69	2.79	-	345.2
AHQ-1-2, 5377	K.GLAGAVSELLR.S	1086.26701	2	3.47E-07	0.97	4.67	-	1994.3
AHQ-1-4, 5279	K.GLAGAVSELLR.S	1086.26701	2	1.01E-06	0.98	5.03	-	1956.4
AHQ-1-1, 5323	K.GLAGAVSELLR.S	1086.26701	2	9.24E-06	0.97	4.57	-	2011.7
AHQ-1-3, 5217	K.GLAGAVSELLR.S	1086.26701	2	4.74E-07	0.98	4.36	-	2406.3
AHQ-1-9, 4970	K.GLAGAVSELLR.S	1086.26701	2	1.86E-06	0.98	4.80	-	2185.5
AHQ-1-5, 5158	K.GLAGAVSELLR.S	1086.26701	2	7.71E-07	0.97	4.74	-	1973.3
AHQ-1-6, 5102	K.GLAGAVSELLR.S	1086.26701	2	7.92E-07	0.97	5.14	-	1650.4
AHQ-1-8, 4924	K.GLAGAVSELLR.S	1086.26701	2	7.19E-07	0.98	5.27	-	2207.6
AHQ-1-2, 6618	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	5.90E-08	0.92	4.34	-	1371.5
AHQ-1-2, 6873 - 6938	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.81E-06	0.93	5.14	-	762.5
AHQ-1-2, 6961 - 7025	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.69E-06	0.91	4.70	-	1021.9
AHQ-1-5, 6821 - 6885	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	4.65E-04	0.94	5.24	-	893.2
AHQ-1-2, 7009	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.81E-09	0.86	4.11	-	524.9
AHQ-1-2, 7211	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	5.85E-08	0.86	4.00	-	466.5
AHQ-1-6, 6662 - 6736	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.59E-10	0.93	5.14	-	970.5
AHQ-1-6, 6590 - 6666	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.45E-07	0.94	5.02	-	749.4
AHQ-1-5, 6749 - 6813	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	5.90E-07	0.91	4.61	-	1054.0
AHQ-1-2, 6834 - 6897	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	8.72E-06	0.89	4.29	-	881.4
AHQ-1-3, 6842	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	5.46E-04	0.84	3.98	-	498.9
AHQ-1-4, 6799 - 6866	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.92E-06	0.93	5.39	-	593.7
AHQ-1-1, 6543 - 6603	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	8.64E-04	0.92	4.63	-	1293.4
AHQ-1-1, 6611 - 6680	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	9.99E-05	0.96	5.75	-	1039.0

AHQ-1-1, 6659 - 6721	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	7.04E-05	0.93	4.79	-	1115.5
AHQ-1-1, 6809 - 6881	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	7.22E-09	0.88	3.62	-	1413.7
AHQ-1-5, 7537	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.38E-11	0.98	6.14	-	2252.5
AHQ-1-6, 7342	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	3.06E-11	0.97	6.21	-	1906.4
AHQ-1-7, 7556	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	5.55E-14	0.97	6.39	-	1421.4
AHQ-1-13- , 7019	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.16E-05	0.92	4.56	-	1530.5
AHQ-1-9, 7371	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	3.82E-08	0.96	5.83	-	1526.6
AHQ-1-4, 7378	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	2.25E-05	0.98	7.30	-	2272.0
AHQ-1-4, 7375	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	9.51E-08	0.98	6.72	-	1178.3
AHQ-1-2, 7278 - 7345	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.11E-15	0.98	6.39	-	2786.6
AHQ-1-6, 7211	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	7.26E-10	0.98	6.32	-	1987.8
AHQ-1-8, 7483	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.16E-07	0.94	4.64	-	1080.5
AHQ-1-2, 7529	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	8.30E-04	0.47	2.94	-	452.9
AHQ-1-2, 7398	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.97E-05	0.96	5.56	-	898.9
AHQ-1-2, 7397	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.71E-06	0.95	4.70	-	1181.2
AHQ-1-4, 5980	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.79E-08	0.93	4.56	-	1056.1
AHQ-1-2, 6031 - 6049	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.77E-07	0.93	4.57	-	1209.3
AHQ-1-9, 7290	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.60E-05	0.93	5.06	-	776.4
AHQ-1-7, 7486	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.96E-05	0.85	4.13	-	547.0
AHQ-1-8, 7482	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.45E-05	0.94	4.96	-	885.6
AHQ-1-7, 7484	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.39E-08	0.92	4.00	-	1098.4
AHQ-1-12, 6658	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.78E-09	0.94	4.44	-	1292.9
AHQ-1-13- , 6893 - 6968	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.90E-06	0.93	5.22	-	1011.1
AHQ-1-3, 7261	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.30E-07	0.94	5.08	-	912.2
AHQ-1-5, 7455	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.58E-07	0.95	5.37	-	1051.8
AHQ-1-1, 5912	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.87E-05	0.89	4.43	-	545.9
AHQ-1-14- , 6728	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.89E-05	0.81	4.15	-	560.7
AHQ-1-3, 5862	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	7.36E-06	0.92	4.75	-	557.6
AHQ-1-4, 7438	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.90E-07	0.91	4.16	-	961.8
AHQ-1-6, 7274	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.90E-08	0.91	4.32	-	961.6
AHQ-1-2, 6033	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.93E-05	0.86	4.22	-	521.2
AHQ-1-6, 7275	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.32E-04	0.92	4.71	-	821.4
AHQ-1-1, 7015	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.03E-05	0.94	5.01	-	786.1
AHQ-1-1, 6996	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	7.23E-07	0.88	4.08	-	978.4
AHQ-1-14- , 6726	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.39E-04	0.84	3.16	-	1032.2
AHQ-1-5, 7453	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.29E-09	0.94	4.94	-	1153.4
AHQ-1-7, 3265	R.IGITNHDEYSLVR.E	1517.66833	2	1.66E-10	0.90	3.71	-	1062.6
AHQ-1-10, 3115 - 3185	R.IGITNHDEYSLVR.E	1517.66833	2	1.31E-09	0.93	3.48	-	1374.2
AHQ-1-13, 3657	R.IGITNHDEYSLVR.E	1517.66833	2	6.25E-06	0.85	3.00	-	835.6
AHQ-1-13- , 3439 - 3445	R.IGITNHDEYSLVR.E	1517.66833	2	2.76E-08	0.94	3.57	-	1364.4
AHQ-1-11, 3183	R.IGITNHDEYSLVR.E	1517.66833	2	3.85E-09	0.92	3.79	-	1136.3
AHQ-1-13, 3366	R.IGITNHDEYSLVR.E	1517.66833	3	9.38E-05	0.82	3.55	-	672.3
AHQ-1-13, 3279 - 3357	R.IGITNHDEYSLVR.E	1517.66833	2	1.49E-04	0.94	3.76	-	1465.9
AHQ-1-13- , 3448 - 3461	R.IGITNHDEYSLVR.E	1517.66833	3	1.79E-09	0.93	4.36	-	908.0
AHQ-1-10, 3391	R.IGITNHDEYSLVR.E	1517.66833	2	8.49E-06	0.92	3.51	-	1079.0
AHQ-1-8, 3234 - 3308	R.IGITNHDEYSLVR.E	1517.66833	2	7.59E-09	0.95	4.02	-	1438.8
AHQ-1-12, 3593	R.IGITNHDEYSLVR.E	1517.66833	2	5.07E-04	0.73	2.76	-	600.5
AHQ-1-12, 3271	R.IGITNHDEYSLVR.E	1517.66833	2	1.62E-10	0.95	4.15	-	1353.4
AHQ-1-8, 4886	R.ILAQATSDLVNAIK.A	1457.69748	2	1.21E-07	0.98	5.03	-	1922.5
AHQ-1-2, 5274	R.ILAQATSDLVNAIK.A	1457.69748	2	6.97E-10	0.97	4.80	-	2015.1
AHQ-1-1, 4272	R.ILAQATSDLVNAIK.A	1457.69748	2	9.14E-07	0.98	4.82	-	2239.3
AHQ-1-7, 5064	R.ILAQATSDLVNAIK.A	1457.69748	2	3.72E-08	0.97	5.07	-	1781.2
AHQ-1-4, 5186	R.ILAQATSDLVNAIK.A	1457.69748	2	1.20E-08	0.98	5.66	-	2055.6
AHQ-1-2, 4609	R.ILAQATSDLVNAIK.A	1457.69748	2	1.92E-05	0.86	3.00	-	959.5
AHQ-1-2, 4373	R.ILAQATSDLVNAIK.A	1457.69748	2	5.43E-08	0.97	4.34	-	1994.1
AHQ-1-3, 5127 - 5147	R.ILAQATSDLVNAIK.A	1457.69748	2	8.54E-09	0.98	5.02	-	2106.1
AHQ-1-5, 4162	R.ILAQATSDLVNAIK.A	1457.69748	2	9.01E-08	0.96	3.45	-	1743.2
AHQ-1-2, 5449	R.ILAQATSDLVNAIK.A	1457.69748	2	2.60E-07	0.98	4.85	-	2148.6
AHQ-1-4, 4520	R.ILAQATSDLVNAIK.A	1457.69748	2	3.02E-08	0.89	3.11	-	926.0
AHQ-1-1, 5187 - 5191	R.ILAQATSDLVNAIK.A	1457.69748	2	1.16E-09	0.98	5.53	-	2485.0
AHQ-1-3, 4245	R.ILAQATSDLVNAIK.A	1457.69748	2	1.90E-09	0.97	4.63	-	1490.0
AHQ-1-4, 4282	R.ILAQATSDLVNAIK.A	1457.69748	2	1.11E-06	0.97	4.61	-	2274.2
AHQ-1-5, 5331	R.ILAQATSDLVNAIK.A	1457.69748	2	2.95E-04	0.82	2.95	-	1290.4
AHQ-1-1, 4713	R.ILAQATSDLVNAIK.A	1457.69748	2	1.59E-06	0.96	3.68	-	1957.6
AHQ-1-5, 5103 - 5135	R.ILAQATSDLVNAIK.A	1457.69748	2	4.71E-05	0.96	3.82	-	2063.3
AHQ-1-5, 5125	R.ILAQATSDLVNAIK.A	1457.69748	1	5.98E-04	0.88	3.80	-	821.8
AHQ-1-3, 4483	R.ILAQATSDLVNAIK.A	1457.69748	2	8.10E-07	0.96	3.94	-	1733.0
AHQ-1-6, 4099	R.ILAQATSDLVNAIK.A	1457.69748	2	1.16E-05	0.97	4.61	-	2144.1
AHQ-1-13, 5633	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	3	2.43E-04	0.63	3.28	-	623.7
AHQ-1-9, 6056	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	4.70E-04	0.93	4.57	-	692.9
AHQ-1-13- , 5972 - 5996	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.84E-07	0.97	5.43	-	1107.9
AHQ-1-14- , 5794	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.37E-05	0.93	4.60	-	746.5
AHQ-1-7, 6221	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	7.50E-04	0.93	4.37	-	705.6
AHQ-1-13, 5589 - 5648	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	3.53E-04	0.94	4.58	-	1118.0
AHQ-1-10, 5377 - 5381	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	3.24E-04	0.91	4.37	-	675.0
AHQ-1-1, 6043 - 6099	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	4.26E-05	0.85	4.04	-	721.3
AHQ-1-13, 5219 - 5283	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.76E-05	0.89	3.87	-	1200.0
AHQ-1-10, 4924 - 5001	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.48E-05	0.91	3.96	-	1373.4
AHQ-1-1, 5713	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	4.72E-08	0.95	5.23	-	1183.3
AHQ-1-9, 5399 - 5412	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	8.74E-05	0.90	4.10	-	1243.4
AHQ-1-14- , 5363 - 5446	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.20E-11	0.95	4.58	-	1664.5
AHQ-1-8, 5387 - 5394	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	2	5.58E-08	0.97	5.44	-	1309.8
AHQ-1-11, 5090	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	6.07E-10	0.93	4.25	-	1385.5
AHQ-1-14, 6274 - 6349	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.48E-06	0.94	4.84	-	1288.6
AHQ-1-8, 2461	R.KFFYSDQNVDSR.D	1506.60087	2	9.22E-05	0.83	3.48	-	706.3
AHQ-1-8, 2189	K.KGIWLEAGK.A	1002.19171	1	3.13E-04	0.21	2.22	-	395.8
AHQ-1-4, 2727	K.LAQAAQSSVATITR.L	1417.59344	2	5.56E-09	0.97	4.79	-	2006.5
AHQ-1-4, 2740	K.LAQAAQSSVATITR.L	1417.59344	1	8.20E-04	0.79	3.64	-	241.5
AHQ-1-2, 3050 - 3127	K.LAQAAQSSVATITR.L	1417.59344	2	5.26E-07	0.95	4.47	-	1466.2
AHQ-1-5, 2462 - 2465	K.LAQAAQSSVATITR.L	1417.59344	2	2.87E-08	0.97	4.62	-	1675.2
AHQ-1-2, 2645 - 2669	K.LAQAAQSSVATITR.L	1417.59344	2	4.08E-10	0.94	3.80	-	1419.2
AHQ-1-2, 2819	K.LAQAAQSSVATITR.L	1417.59344	1	1.34E-04	0.37	2.97	-	177.6
AHQ-1-9, 2590	K.LAQAAQSSVATITR.L	1417.59344	2	9.14E-07	0.98	4.44	-	2277.9
AHQ-1-5, 2617 - 2630	K.LAQAAQSSVATITR.L	1417.59344	2	1.78E-08	0.98	5.42	-	1971.7
AHQ-1-14- , 2744	K.LAQAAQSSVATITR.L	1417.59344	2	1.57E-07	0.96	4.03	-	1704.7
AHQ-1-4, 2567	K.LAQAAQSSVATITR.L	1417.59344	2	1.17E-09	0.97	4.92	-	1594.9
AHQ-1-7, 2648 - 2701	K.LAQAAQSSVATITR.L	1417.59344	2	7.85E-07	0.96	4.45	-	1629.7
AHQ-1-3, 2569	K.LAQAAQSSVATITR.L	1417.59344	2	3.35E-07	0.97	4.66	-	1525.6
AHQ-1-2, 2797 - 2833	K.LAQAAQSSVATITR.L	1417.59344	2	1.87E-09	0.97	4.91	-	1350.3
AHQ-1-1, 2843 - 2911	K.LAQAAQSSVATITR.L	1417.59344	2	3.65E-06	0.94	3.69	-	1539.8
AHQ-1-6, 2623 - 2632	K.LAQAAQSSVATITR.L	1417.59344	2	6.31E-08	0.95	4.03	-	1327.3
AHQ-1-3, 2725 - 2763	K.LAQAAQSSVATITR.L	1417.59344	2	1.15E-11	0.96	4.23	-	1614.3
AHQ-1-7, 2505	K.LAQAAQSSVATITR.L	1417.59344	2	2.04E-05	0.70	2.55	-	789.2
AHQ-1-6, 2479	K.LAQAAQSSVATITR.L	1417.59344	2	3.81E-11	0.95	4.08	-	1460.3
AHQ-1-2, 3139	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	6.49E-12	0.95	4.68	-	941.0
AHQ-1-4, 3260 - 3263	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.97E-07	0.96	5.67	-	825.7
AHQ-1-4, 3258 - 3294	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.85E-08	0.96	5.40	-	1422.4

AHQ-1-2, 3366	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.98E-09	0.97	5.73	-	1820.7
AHQ-1-2, 3371	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.65E-09	0.94	4.90	-	920.5
AHQ-1-1, 3377 - 3385	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	8.80E-09	0.95	5.30	-	772.3
AHQ-1-1, 3368	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.49E-08	0.97	5.72	-	2369.2
AHQ-1-3, 3219 - 3262	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.05E-11	0.97	5.96	-	1741.8
AHQ-1-3, 3261	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	3.11E-06	0.91	3.92	-	710.3
AHQ-1-4, 3046	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	4.19E-06	0.94	4.91	-	1319.8
AHQ-1-6, 3112	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	5.68E-07	0.86	4.08	-	463.1
AHQ-1-3, 3565	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	4.37E-12	0.95	5.24	-	1269.9
AHQ-1-6, 3100	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.18E-06	0.97	5.19	-	2159.4
AHQ-1-2, 3137	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	6.59E-07	0.95	5.10	-	1515.0
AHQ-1-1, 3667	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	9.21E-07	0.96	4.86	-	1661.4
AHQ-1-5, 3113 - 3118	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.99E-12	0.97	6.17	-	1848.0
AHQ-1-3, 5774	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.30E-04	0.95	4.76	-	932.5
AHQ-1-3, 5494 - 5569	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.79E-06	0.97	5.25	-	1194.5
AHQ-1-2, 5431 - 5511	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.72E-06	0.96	5.59	-	954.1
AHQ-1-13, 5155	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.26E-05	0.91	3.87	-	998.4
AHQ-1-3, 5538 - 5554	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	2.74E-08	0.92	4.46	-	1225.5
AHQ-1-3, 5279 - 5349	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.27E-07	0.97	5.37	-	1138.7
AHQ-1-6, 5262 - 5286	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.27E-10	0.96	5.13	-	1185.3
AHQ-1-6, 5450	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.01E-06	0.96	5.03	-	1102.8
AHQ-1-3, 5413	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.55E-09	0.92	4.50	-	708.3
AHQ-1-1, 5379	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.71E-07	0.95	4.50	-	1229.2
AHQ-1-5, 5330 - 5385	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.40E-09	0.96	5.20	-	1165.5
AHQ-1-7, 5524 - 5544	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.62E-04	0.97	5.28	-	1430.2
AHQ-1-2, 5673 - 5741	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.01E-06	0.97	5.60	-	1546.0
AHQ-1-7, 5337	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.16E-05	0.87	3.86	-	749.9
AHQ-1-4, 5604 - 5674	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.47E-04	0.96	5.22	-	1098.1
AHQ-1-1, 5581	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	6.83E-09	0.98	6.18	-	2827.9
AHQ-1-4, 5634 - 5648	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	7.24E-09	0.95	3.88	-	2204.4
AHQ-1-2, 5710 - 5718	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.64E-10	0.97	4.82	-	2433.6
AHQ-1-1, 5569 - 5575	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.11E-05	0.97	5.45	-	1071.6
AHQ-1-4, 5864 - 5883	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.65E-12	0.96	5.01	-	1248.6
AHQ-1-2, 5897 - 5941	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.64E-10	0.96	4.98	-	1095.8
AHQ-1-1, 5721	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.25E-05	0.95	4.42	-	989.4
AHQ-1-5, 5713	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.89E-11	0.97	5.52	-	1437.9
AHQ-1-5, 5518 - 5593	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.16E-05	0.97	5.26	-	1268.1
AHQ-1-11, 4831	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.23E-05	0.90	4.34	-	548.5
AHQ-1-14, 6162	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.90E-05	0.91	4.08	-	882.8
AHQ-1-8, 3429	K.LHTDDELNWLDHGR.T	1721.81153	2	3.17E-05	0.97	5.25	-	1865.0
AHQ-1-9, 3572 - 3584	K.LHTDDELNWLDHGR.T	1721.81153	2	1.72E-04	0.94	3.69	-	1332.9
AHQ-1-1, 4024	K.LHTDDELNWLDHGR.T	1721.81153	2	6.97E-06	0.96	3.96	-	1870.2
AHQ-1-9, 3588 - 3652	K.LHTDDELNWLDHGR.T	1721.81153	3	7.66E-04	0.78	3.38	-	748.9
AHQ-1-2, 4587	K.LLAALLEDEGGSGR.P	1401.54764	2	5.94E-05	0.96	3.99	-	1626.3
AHQ-1-3, 4425	K.LLAALLEDEGGSGR.P	1401.54764	2	5.20E-10	0.97	3.95	-	1941.2
AHQ-1-11, 4854 - 4912	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.62E-09	0.97	5.55	-	1450.0
AHQ-1-2, 5373 - 5383	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.44E-06	0.94	5.10	-	611.3
AHQ-1-4, 5410	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.25E-04	0.98	6.23	-	1428.4
AHQ-1-7, 5284	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.66E-12	0.98	6.70	-	1753.9
AHQ-1-11, 4852	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.23E-09	0.95	5.21	-	1267.6
AHQ-1-9, 5119 - 5127	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.90E-09	0.98	6.76	-	1480.2
AHQ-1-4, 5408 - 5420	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.25E-05	0.97	5.91	-	1532.4
AHQ-1-7, 5290	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.47E-10	0.96	5.17	-	1527.0
AHQ-1-9, 5122	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.92E-10	0.97	5.47	-	1859.0
AHQ-1-2, 5371	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.64E-05	0.94	4.66	-	1156.1
AHQ-1-3, 5317	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.00E-06	0.96	5.38	-	1240.6
AHQ-1-3, 5321 - 5322	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	5.59E-12	0.97	5.79	-	1886.3
AHQ-1-10, 4697	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	7.31E-12	0.97	6.44	-	1095.7
AHQ-1-6, 5236	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	6.78E-07	0.98	6.38	-	1415.2
AHQ-1-13- , 5331	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.15E-08	0.93	4.28	-	1202.2
AHQ-1-5, 5309 - 5333	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.64E-10	0.94	4.79	-	1308.5
AHQ-1-1, 5461	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	9.27E-09	0.97	5.44	-	1825.4
AHQ-1-13, 5032	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.28E-05	0.95	5.21	-	758.4
AHQ-1-8, 4987 - 5004	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.19E-08	0.98	5.79	-	1995.0
AHQ-1-3, 5527	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.60E-07	0.95	4.84	-	1055.5
AHQ-1-6, 5235	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.85E-09	0.96	5.52	-	1557.0
AHQ-1-10, 4699	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.97E-07	0.94	5.41	-	1146.0
AHQ-1-13, 5036	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	9.94E-09	0.95	5.05	-	1331.7
AHQ-1-12, 5075	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.16E-09	0.97	5.76	-	1213.8
AHQ-1-5, 5310	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	8.66E-11	0.97	5.78	-	1249.0
AHQ-1-12, 5073	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.27E-05	0.95	4.42	-	1374.3
AHQ-1-1, 5460	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.76E-10	0.96	5.85	-	880.4
AHQ-1-2, 5462	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.97E-04	0.98	6.17	-	1494.2
AHQ-1-2, 5465	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.58E-09	0.96	5.54	-	1307.2
AHQ-1-8, 4988	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.02E-08	0.97	6.45	-	1056.4
AHQ-1-3, 5329	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	1.81E-05	0.84	4.38	-	828.5
AHQ-1-4, 5418	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	1.21E-04	0.75	4.22	-	484.3
AHQ-1-5, 5318	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	4.58E-06	0.82	5.07	-	405.9
AHQ-1-2, 4710 - 4723	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.23E-06	0.66	3.51	-	160.7
AHQ-1-4, 4442 - 4510	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	7.39E-08	0.78	3.78	-	263.4
AHQ-1-4, 4306 - 4374	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.62E-05	0.89	3.98	-	368.9
AHQ-1-7, 4225 - 4304	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.00E-05	0.77	3.83	-	221.0
AHQ-1-1, 4213 - 4279	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	5.54E-08	0.68	2.93	-	347.9
AHQ-1-2, 4557 - 4617	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	7.14E-07	0.94	4.44	-	551.4
AHQ-1-2, 4479 - 4549	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.71E-04	0.81	3.52	-	271.3
AHQ-1-3, 4461 - 4530	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.62E-04	0.78	3.55	-	280.2
AHQ-1-2, 4341 - 4413	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.66E-09	0.89	3.85	-	467.2
AHQ-1-3, 4311 - 4390	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	4.99E-06	0.91	4.56	-	427.4
AHQ-1-5, 4297 - 4366	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.24E-10	0.79	3.78	-	336.2
AHQ-1-1, 4348 - 4415	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	7.91E-12	0.62	2.94	-	247.7
AHQ-1-3, 4253 - 4321	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.24E-11	0.90	4.06	-	395.3
AHQ-1-5, 4153 - 4229	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.39E-14	0.93	4.66	-	418.1
AHQ-1-1, 4544	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	7.70E-04	0.29	2.64	-	233.7
AHQ-1-6, 4122 - 4191	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.29E-06	0.74	3.43	-	281.9
AHQ-1-3, 4233	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	3	5.26E-04	0.95	4.90	-	1328.2
AHQ-1-3, 5757 - 5829	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.26E-13	0.98	5.51	-	2261.6
AHQ-1-2, 6058 - 6129	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.96E-11	0.98	6.05	-	1914.8
AHQ-1-2, 5918 - 5987	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.18E-05	0.95	4.62	-	1050.4
AHQ-1-10, 4939	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.82E-04	0.90	3.69	-	900.2
AHQ-1-4, 5750	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.76E-12	0.98	6.01	-	1663.1
AHQ-1-4, 5758	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.17E-04	0.98	6.45	-	1849.4
AHQ-1-7, 5634	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	3.64E-10	0.98	5.30	-	2562.6
AHQ-1-2, 5375 - 5443	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.67E-05	0.95	4.36	-	1374.8
AHQ-1-3, 5641 - 5642	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	7.67E-11	0.98	6.72	-	2417.5
AHQ-1-6, 5550	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.41E-11	0.97	5.04	-	1688.9
AHQ-1-6, 5566	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.14E-04	0.98	6.30	-	3391.6
AHQ-1-3, 5637 - 5701	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.55E-14	0.98	6.20	-	1794.7

AHQ-1-5, 6021	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.23E-08	0.93	4.12	-	1084.8
AHQ-1-4, 5990 - 6007	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.81E-07	0.96	4.90	-	1406.0
AHQ-1-2, 6198	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.63E-13	0.98	5.92	-	1886.1
AHQ-1-1, 5687 - 5749	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.91E-13	0.98	5.77	-	2126.9
AHQ-1-4, 4566 - 4596	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.57E-05	0.85	3.94	-	601.0
AHQ-1-5, 5883	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.22E-09	0.95	4.97	-	968.6
AHQ-1-1, 5691	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	3.62E-04	0.96	5.16	-	1672.8
AHQ-1-5, 4483	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.06E-08	0.97	5.63	-	1169.4
AHQ-1-11, 5095	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.18E-08	0.97	4.64	-	1574.1
AHQ-1-3, 5543	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.17E-09	0.98	5.89	-	1454.8
AHQ-1-8, 5451	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.64E-07	0.95	4.44	-	1283.8
AHQ-1-2, 5591	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.90E-08	0.89	3.70	-	885.5
AHQ-1-2, 4650	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.67E-09	0.94	4.59	-	1019.2
AHQ-1-3, 5899 - 5978	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.37E-06	0.81	3.08	-	712.7
AHQ-1-2, 6113	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	6.39E-06	0.88	3.67	-	1054.4
AHQ-1-2, 5827 - 5835	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.11E-07	0.98	6.62	-	2391.8
AHQ-1-3, 5411	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.39E-12	0.97	5.34	-	1432.3
AHQ-1-9, 5468	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.37E-09	0.96	4.61	-	1580.6
AHQ-1-2, 5817 - 5847	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.58E-09	0.97	5.42	-	1525.7
AHQ-1-7, 5625	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.11E-11	0.97	5.59	-	1401.5
AHQ-1-3, 4499 - 4574	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.74E-08	0.94	4.80	-	853.7
AHQ-1-5, 5550 - 5625	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.56E-11	0.98	6.03	-	1636.8
AHQ-1-1, 5857 - 5883	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.33E-07	0.92	4.19	-	904.6
AHQ-1-2, 5583 - 5621	R.LNEAAAGLNQAATELVQASRGTPQDLAR.A	2867.12501	3	1.11E-04	0.54	3.07	-	541.6
AHQ-1-2, 2185	R.MATNAAAQNAIK.K	1204.38227	2	3.51E-05	0.87	3.12	-	1040.6
AHQ-1-3, 2046	R.MATNAAAQNAIK.K	1204.38227	2	8.19E-04	0.47	2.72	-	515.3
AHQ-1-6, 1920 - 1996	R.MATNAAAQNAIK.K	1204.38227	2	6.83E-04	0.61	2.82	-	638.5
AHQ-1-4, 1940 - 2006	R.MATNAAAQNAIK.K	1204.38227	2	7.15E-06	0.78	3.15	-	673.8
AHQ-1-2, 2079 - 2105	R.MATNAAAQNAIK.K	1204.38227	2	1.32E-06	0.83	3.63	-	574.4
AHQ-1-4, 4376	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	5.14E-05	0.62	3.26	-	551.0
AHQ-1-1, 4223	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	5.06E-08	0.73	3.68	-	542.8
AHQ-1-3, 4162	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	6.89E-09	0.93	5.07	-	923.6
AHQ-1-3, 4538 - 4563	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	2.65E-05	0.96	4.75	-	1736.3
AHQ-1-2, 4305 - 4306	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.42E-09	0.95	5.26	-	1068.1
AHQ-1-5, 3191	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.75E-06	0.93	4.30	-	1307.1
AHQ-1-5, 4077 - 4079	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.07E-12	0.95	5.79	-	1126.3
AHQ-1-2, 4221	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	6.96E-09	0.90	4.70	-	845.6
AHQ-1-9, 4331	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	9.26E-05	0.79	3.51	-	1013.6
AHQ-1-4, 4210	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	2	2.61E-06	0.68	3.01	-	475.5
AHQ-1-7, 4348 - 4361	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	8.99E-07	0.82	3.43	-	888.9
AHQ-1-2, 4605	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	1.09E-04	0.53	2.74	-	352.2
AHQ-1-6, 4196 - 4275	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	3.57E-07	0.95	4.36	-	1691.1
AHQ-1-5, 4270 - 4345	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	2.18E-05	0.77	4.00	-	752.9
AHQ-1-2, 4493 - 4562	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.79E-04	0.90	4.39	-	1138.2
AHQ-1-1, 6608 - 6627	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	4.18E-04	0.79	3.30	-	765.5
AHQ-1-13- , 6584	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	3.77E-04	0.97	5.07	-	1595.7
AHQ-1-2, 6589	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	2.20E-09	0.97	5.87	-	1483.9
AHQ-1-6, 6671 - 6672	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	2.21E-07	0.98	6.48	-	2230.7
AHQ-1-5, 6778 - 6845	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	5.47E-04	0.96	4.82	-	1531.8
AHQ-1-7, 6844	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.23E-05	0.97	4.95	-	1771.3
AHQ-1-13- , 5853 - 5915	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	3.08E-08	0.96	4.55	-	1658.3
AHQ-1-4, 7156 - 7168	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	3.04E-10	0.98	5.80	-	1968.9
AHQ-1-2, 6911	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	3	3.14E-06	0.98	6.11	-	2408.4
AHQ-1-2, 7191	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	7.61E-08	0.97	5.11	-	1434.4
AHQ-1-14- , 6334	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.48E-04	0.97	5.24	-	1373.1
AHQ-1-4, 7026	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	5.96E-04	0.76	3.78	-	753.3
AHQ-1-3, 6133	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	3.01E-06	0.96	4.70	-	1318.9
AHQ-1-5, 7109	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.10E-11	0.97	5.55	-	1680.6
AHQ-1-4, 6256	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	3.49E-10	0.98	5.51	-	1872.9
AHQ-1-4, 6862 - 6863	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	4.30E-04	0.95	4.92	-	1214.2
AHQ-1-12, 6214	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	8.75E-07	0.96	4.52	-	1286.9
AHQ-1-9, 6640	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	5.68E-10	0.98	5.51	-	1629.4
AHQ-1-6, 6966	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	7.62E-11	0.98	6.13	-	1614.5
AHQ-1-4, 6576	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	4.37E-06	0.95	4.67	-	1289.0
AHQ-1-13, 6141	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	9.94E-05	0.90	3.63	-	887.9
AHQ-1-1, 6131	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	3.07E-07	0.97	5.12	-	1633.3
AHQ-1-9, 6915	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	4.78E-12	0.97	4.92	-	1628.1
AHQ-1-4, 6486	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	6.07E-07	0.93	4.27	-	889.7
AHQ-1-3, 6997 - 7063	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.12E-11	0.97	5.61	-	1413.8
AHQ-1-2, 4573 - 4642	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.03E-05	0.93	3.92	-	791.4
AHQ-1-3, 4371 - 4429	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.25E-06	0.86	3.49	-	527.0
AHQ-1-2, 4714	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.34E-11	0.86	3.75	-	492.9
AHQ-1-3, 4497 - 4566	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.69E-07	0.81	3.08	-	591.6
AHQ-1-1, 4656	K.NGNLPEFGDAISTASK.A	1621.73018	2	7.57E-06	0.78	3.02	-	537.8
AHQ-1-6, 4624	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.58E-08	0.79	3.21	-	462.9
AHQ-1-1, 4559	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.87E-04	0.56	3.07	-	255.0
AHQ-1-4, 4448 - 4518	K.NGNLPEFGDAISTASK.A	1621.73018	2	4.61E-06	0.89	3.99	-	522.3
AHQ-1-1, 4421 - 4495	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.15E-07	0.92	3.85	-	784.1
AHQ-1-9, 4623	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.20E-05	0.51	3.11	-	280.4
AHQ-1-3, 4231	K.NLGTALAELR.T	1058.21367	1	1.78E-04	0.21	2.21	-	113.1
AHQ-1-4, 4244	K.NLGTALAELR.T	1058.21367	2	5.40E-04	0.86	3.25	-	883.6
AHQ-1-2, 4375 - 4381	K.NLGTALAELR.T	1058.21367	2	3.35E-04	0.86	2.96	-	918.0
AHQ-1-1, 4343	K.NLGTALAELR.T	1058.21367	2	9.33E-04	0.86	3.02	-	887.3
AHQ-1-3, 2722	K.PAAVAAENEEIGSHIK.H	1636.78798	3	3.93E-09	0.97	5.33	-	1769.8
AHQ-1-5, 2601	K.PAAVAAENEEIGSHIK.H	1636.78798	3	9.25E-11	0.97	5.55	-	2012.3
AHQ-1-6, 2619	K.PAAVAAENEEIGSHIK.H	1636.78798	2	4.23E-10	0.98	5.72	-	2200.7
AHQ-1-1, 2891	K.PAAVAAENEEIGSHIK.H	1636.78798	2	8.69E-09	0.93	4.04	-	1131.8
AHQ-1-6, 2584	K.PAAVAAENEEIGSHIK.H	1636.78798	3	5.74E-07	0.96	4.97	-	1594.1
AHQ-1-3, 2731	K.PAAVAAENEEIGSHIK.H	1636.78798	2	2.13E-07	0.98	5.20	-	1940.6
AHQ-1-4, 2723	K.PAAVAAENEEIGSHIK.H	1636.78798	3	3.19E-12	0.97	5.51	-	2182.7
AHQ-1-5, 2603	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.74E-13	0.98	5.44	-	2106.7
AHQ-1-2, 2783 - 2837	K.PAAVAAENEEIGSHIK.H	1636.78798	2	9.94E-08	0.97	5.04	-	1707.3
AHQ-1-4, 2722	K.PAAVAAENEEIGSHIK.H	1636.78798	2	4.03E-07	0.98	5.59	-	2177.5
AHQ-1-7, 2637	K.PAAVAAENEEIGSHIK.H	1636.78798	2	2.06E-07	0.96	3.88	-	1683.8
AHQ-1-2, 2802 - 2814	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.51E-09	0.97	5.67	-	1888.0
AHQ-1-1, 2895	K.PAAVAAENEEIGSHIK.H	1636.78798	3	8.56E-07	0.96	4.97	-	1471.1
AHQ-1-6, 3154 - 3176	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	4.96E-06	0.82	3.75	-	1094.5
AHQ-1-3, 3471 - 3478	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	9.37E-10	0.87	4.45	-	466.3
AHQ-1-3, 3315	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	9.90E-04	0.88	3.92	-	723.5
AHQ-1-1, 3577	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.54E-07	0.72	3.51	-	527.5
AHQ-1-1, 3444 - 3460	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	6.21E-06	0.78	3.69	-	425.5
AHQ-1-2, 3258	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.91E-04	0.45	2.78	-	329.2
AHQ-1-1, 3413	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	5.55E-06	0.76	3.22	-	857.1
AHQ-1-5, 3337	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.30E-07	0.87	4.03	-	542.0
AHQ-1-5, 3170	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.46E-04	0.94	5.24	-	750.0
AHQ-1-4, 3498	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	2.26E-04	0.82	3.30	-	971.7
AHQ-1-5, 3167	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	6.02E-04	0.71	3.32	-	570.4

AHQ-1-4, 3500 - 3508	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	4.75E-07	0.93	4.98	-	653.1
AHQ-1-2, 4058	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.27E-08	0.63	3.34	-	362.4
AHQ-1-2, 3605	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.02E-09	0.88	4.45	-	617.8
AHQ-1-2, 3599	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	8.20E-04	0.75	3.15	-	817.8
AHQ-1-6, 3163	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.21E-04	0.85	3.54	-	646.8
AHQ-1-2, 3422	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.23E-07	0.90	3.92	-	624.1
AHQ-1-1, 4075 - 4151	R.QELAVFCSPEPPAK.T	1574.77985	2	9.13E-08	0.83	2.97	-	738.8
AHQ-1-5, 4017 - 4030	R.QELAVFCSPEPPAK.T	1574.77985	2	5.75E-08	0.93	4.07	-	1017.5
AHQ-1-2, 4223 - 4294	R.QELAVFCSPEPPAK.T	1574.77985	2	2.20E-06	0.91	3.52	-	1037.8
AHQ-1-5, 7357 - 7437	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	3.02E-11	0.94	5.14	-	919.2
AHQ-1-6, 7250	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	3.52E-04	0.71	3.28	-	434.3
AHQ-1-2, 7354	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	4.55E-08	0.94	4.94	-	1284.9
AHQ-1-4, 7394 - 7470	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	4.65E-08	0.85	4.26	-	645.6
AHQ-1-3, 7237 - 7238	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	1.68E-09	0.94	5.44	-	968.3
AHQ-1-13- , 3879 - 3881	K.QVAASTAQLLVACK.V	1461.70942	2	3.08E-06	0.92	4.18	-	551.9
AHQ-1-2, 4017 - 4089	K.QVAASTAQLLVACK.V	1461.70942	2	2.76E-06	0.89	3.68	-	539.8
AHQ-1-10, 3464	K.QVAASTAQLLVACK.V	1461.70942	2	9.65E-05	0.76	2.73	-	515.3
AHQ-1-3, 4967	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	2.13E-04	0.91	4.32	-	497.9
AHQ-1-4, 6086	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	9.48E-05	0.98	5.86	-	2350.5
AHQ-1-2, 5129	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	2.93E-05	0.95	4.42	-	817.4
AHQ-1-4, 5051	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	5.70E-05	0.92	3.97	-	644.0
AHQ-1-3, 5985	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	4.15E-05	0.97	5.23	-	1556.6
AHQ-1-2, 6173	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	3.73E-07	0.98	5.73	-	1965.8
AHQ-1-2, 6182	K.RVAGSVTELIQAAEAMK.G	1775.06387	3	3.52E-05	0.89	4.09	-	1025.2
AHQ-1-4, 3695	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	1.12E-05	0.71	3.59	-	341.0
AHQ-1-1, 3389	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	6.97E-05	0.84	3.90	-	809.1
AHQ-1-4, 3927	R.SGASGPENFQVGSMPPAQQQITSGQM*HR.G	2945.19807	3	4.51E-05	0.59	3.52	-	333.8
AHQ-1-9, 2788	K.SIAAATSALVK.A	1032.21612	2	6.77E-04	0.91	3.08	-	1122.6
AHQ-1-4, 3048	K.SIAAATSALVK.A	1032.21612	2	5.04E-05	0.89	3.55	-	955.4
AHQ-1-10, 2797 - 2879	K.SIAAATSALVK.A	1032.21612	2	9.94E-04	0.82	2.99	-	852.0
AHQ-1-1, 3177	K.SIAAATSALVK.A	1032.21612	2	7.13E-06	0.85	2.97	-	828.1
AHQ-1-2, 3150	K.SIAAATSALVK.A	1032.21612	2	9.02E-06	0.91	3.14	-	1187.9
AHQ-1-13- , 3996	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	1.70E-04	0.95	4.96	-	1587.0
AHQ-1-8, 4208	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	2.52E-11	0.96	5.08	-	1112.7
AHQ-1-8, 4209	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	5.91E-06	0.97	5.77	-	1936.1
AHQ-1-9, 4276	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	1.29E-05	0.95	4.17	-	1901.6
AHQ-1-12, 4230 - 4234	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	1.44E-06	0.97	5.70	-	1916.8
AHQ-1-8, 3867	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	1.10E-08	0.96	5.63	-	1489.3
AHQ-1-1, 5493 - 5523	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.83E-07	0.80	3.58	-	389.1
AHQ-1-2, 5001 - 5022	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.72E-06	0.73	3.18	-	438.0
AHQ-1-4, 5695 - 5696	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.28E-05	0.91	4.13	-	708.4
AHQ-1-4, 5539 - 5611	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.29E-09	0.89	4.32	-	428.8
AHQ-1-2, 5251	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.19E-07	0.89	3.95	-	640.7
AHQ-1-4, 5450	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.97E-06	0.84	3.73	-	491.8
AHQ-1-4, 5362 - 5380	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.07E-06	0.74	3.40	-	404.7
AHQ-1-2, 5457 - 5525	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.03E-07	0.89	3.93	-	516.4
AHQ-1-7, 5301 - 5305	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.85E-05	0.85	3.88	-	441.7
AHQ-1-4, 4964	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.74E-08	0.74	3.19	-	456.6
AHQ-1-4, 4750 - 4759	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.84E-08	0.89	4.08	-	493.4
AHQ-1-3, 4695	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.27E-04	0.80	3.62	-	378.3
AHQ-1-8, 5219	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.76E-05	0.88	3.44	-	710.4
AHQ-1-3, 5337 - 5405	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.75E-07	0.78	3.34	-	439.8
AHQ-1-3, 4859	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.57E-04	0.55	3.00	-	322.5
AHQ-1-2, 5587 - 5657	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.32E-04	0.74	3.17	-	422.0
AHQ-1-1, 5355 - 5419	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.88E-05	0.85	3.94	-	433.9
AHQ-1-2, 5699 - 5773	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.37E-07	0.90	4.30	-	475.9
AHQ-1-2, 5869 - 5882	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.86E-05	0.39	3.08	-	405.1
AHQ-1-9, 5171	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.18E-04	0.52	2.83	-	247.7
AHQ-1-3, 5118	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.12E-07	0.83	3.39	-	518.6
AHQ-1-3, 5202 - 5277	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.18E-05	0.63	2.76	-	394.4
AHQ-1-5, 5570	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.78E-09	0.94	4.61	-	717.5
AHQ-1-3, 5593	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.05E-07	0.67	3.17	-	299.5
AHQ-1-5, 5473	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.44E-05	0.88	3.95	-	444.4
AHQ-1-3, 5426 - 5493	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.63E-10	0.87	3.95	-	391.7
AHQ-1-1, 4679	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.96E-06	0.73	3.55	-	264.4
AHQ-1-6, 5464	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.40E-06	0.78	3.35	-	468.0
AHQ-1-6, 4600	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.97E-07	0.69	3.17	-	335.3
AHQ-1-5, 4685	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.00E-08	0.82	3.74	-	392.1
AHQ-1-5, 5295 - 5377	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.95E-07	0.92	4.40	-	611.1
AHQ-1-2, 4831	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.11E-09	0.86	4.16	-	610.0
AHQ-1-6, 5223	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.95E-06	0.91	4.33	-	528.6
AHQ-1-2, 7113 - 7173	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	8.89E-04	0.78	3.65	-	966.9
AHQ-1-2, 7351 - 7427	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	6.50E-07	0.97	5.64	-	1904.4
AHQ-1-4, 7358 - 7367	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.87E-10	0.97	5.50	-	2367.8
AHQ-1-5, 7374	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	8.16E-14	0.97	6.31	-	1872.0
AHQ-1-2, 7446 - 7517	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.07E-07	0.95	4.95	-	1345.0
AHQ-1-6, 7119 - 7186	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	5.85E-13	0.96	5.69	-	1582.2
AHQ-1-7, 7397	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.39E-11	0.98	6.54	-	2083.5
AHQ-1-3, 7429	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	4.75E-08	0.88	4.17	-	871.4
AHQ-1-10, 3976	K.TKEVIQEWNLTNIK.R	1716.95938	2	2.78E-08	0.95	4.24	-	1439.5
AHQ-1-9, 4211	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.17E-06	0.96	4.81	-	1422.8
AHQ-1-12, 4235	K.TKEVIQEWNLTNIK.R	1716.95938	2	2.10E-04	0.96	4.52	-	1582.4
AHQ-1-8, 4151 - 4155	K.TKEVIQEWNLTNIK.R	1716.95938	2	2.01E-04	0.96	4.77	-	1597.4
AHQ-1-8, 4159	K.TKEVIQEWNLTNIK.R	1716.95938	3	1.54E-06	0.93	4.91	-	990.9
AHQ-1-11, 4087	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.22E-04	0.96	4.09	-	1863.2
AHQ-1-8, 3428	K.TKEVIQEWNLTNIKR.W	1873.14573	2	4.39E-06	0.96	4.60	-	1220.9
AHQ-1-9, 6460 - 6466	K.TLAESALQLLYTAK.E	1522.76793	2	5.63E-04	0.95	3.86	-	1386.8
AHQ-1-12, 6069	K.TLAESALQLLYTAK.E	1522.76793	2	1.51E-04	0.95	4.07	-	1070.2
AHQ-1-14- , 6198 - 6204	K.TLAESALQLLYTAK.E	1522.76793	2	7.29E-06	0.97	4.85	-	1448.1
AHQ-1-7, 6616 - 6617	K.TLAESALQLLYTAK.E	1522.76793	2	2.56E-06	0.94	4.00	-	953.6
AHQ-1-3, 6498 - 6561	K.TLAESALQLLYTAK.E	1522.76793	2	6.84E-09	0.97	4.80	-	1422.5
AHQ-1-6, 6487 - 6495	K.TLAESALQLLYTAK.E	1522.76793	2	3.32E-07	0.96	4.55	-	1252.2
AHQ-1-4, 6666 - 6730	K.TLAESALQLLYTAK.E	1522.76793	2	4.69E-08	0.97	5.25	-	1198.4
AHQ-1-2, 6669 - 6745	K.TLAESALQLLYTAK.E	1522.76793	2	1.10E-11	0.97	5.28	-	1326.2
AHQ-1-4, 6886	K.TLAESALQLLYTAK.E	1522.76793	2	1.35E-09	0.95	4.09	-	1070.0
AHQ-1-2, 6914 - 6917	K.TLAESALQLLYTAK.E	1522.76793	2	1.51E-04	0.94	4.01	-	1157.3
AHQ-1-1, 6643 - 6684	K.TLAESALQLLYTAK.E	1522.76793	2	3.16E-07	0.84	3.22	-	752.9
AHQ-1-5, 6605 - 6614	K.TLAESALQLLYTAK.E	1522.76793	2	1.92E-05	0.97	5.01	-	1197.4
AHQ-1-3, 6731 - 6801	K.TLAESALQLLYTAK.E	1522.76793	2	5.29E-06	0.93	3.68	-	1257.5
AHQ-1-1, 6469 - 6475	K.TLAESALQLLYTAK.E	1522.76793	2	1.45E-09	0.97	5.06	-	1163.9
AHQ-1-13, 6000	K.TLAESALQLLYTAK.E	1522.76793	2	1.27E-04	0.82	2.91	-	751.6
AHQ-1-1, 3391	K.TLSHPQQMALLDQTK.T	1711.96464	2	5.03E-05	0.95	4.73	-	841.0
AHQ-1-6, 3114	K.TLSHPQQMALLDQTK.T	1711.96464	2	6.49E-05	0.95	4.58	-	959.9
AHQ-1-2, 3409	K.TLSHPQQMALLDQTK.T	1711.96464	2	7.92E-06	0.92	4.07	-	758.8
AHQ-1-2, 3383 - 3387	K.TLSHPQQMALLDQTK.T	1711.96464	3	2.56E-06	0.93	4.91	-	937.0
AHQ-1-3, 3258	K.TLSHPQQMALLDQTK.T	1711.96464	3	3.25E-08	0.95	5.17	-	1311.9
AHQ-1-4, 3262	K.TLSHPQQMALLDQTK.T	1711.96464	3	3.45E-06	0.95	4.57	-	1442.6

AHQ-1-4, 3254	K.TLSHPQQMALLDQTK.T	1711.96464	2	5.29E-05	0.88	3.49	-	558.7
AHQ-1-5, 3122	K.TLSHPQQMALLDQTK.T	1711.96464	2	7.73E-07	0.95	4.59	-	870.7
AHQ-1-5, 3129	K.TLSHPQQMALLDQTK.T	1711.96464	3	3.87E-05	0.95	4.78	-	1642.5
AHQ-1-8, 3028	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.49E-05	0.90	4.47	-	440.4
AHQ-1-3, 2509 - 2526	K.TLSHPQQM*ALLDQTK.T	1727.96404	2	2.02E-04	0.88	3.75	-	481.8
AHQ-1-5, 2398	K.TLSHPQQM*ALLDQTK.T	1727.96404	2	5.67E-04	0.81	3.16	-	466.0
AHQ-1-5, 4317 - 4322	K.TMLESAGGLIQTAR.A	1448.67095	2	2.63E-07	0.93	4.11	-	1315.5
AHQ-1-3, 4143	K.TMLESAGGLIQTAR.A	1448.67095	2	4.49E-09	0.91	4.02	-	1129.2
AHQ-1-1, 3611	K.TM*LESAGGLIQTAR.A	1464.67035	2	2.05E-06	0.97	5.16	-	2043.6
AHQ-1-3, 4330 - 4397	K.TMLESAGGLIQTAR.A	1448.67095	2	1.83E-07	0.96	4.71	-	1642.1
AHQ-1-5, 3374 - 3443	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.07E-09	0.94	4.37	-	1185.9
AHQ-1-4, 4426 - 4440	K.TMLESAGGLIQTAR.A	1448.67095	2	9.81E-09	0.95	4.31	-	1646.8
AHQ-1-3, 4381	K.TM*LESAGGLIQTAR.A	1464.67035	2	3.62E-04	0.77	2.87	-	898.3
AHQ-1-4, 4447	K.TMLESAGGLIQTAR.A	1448.67095	1	5.23E-04	0.05	2.07	-	171.2
AHQ-1-1, 4371 - 4452	K.TMLESAGGLIQTAR.A	1448.67095	2	2.48E-07	0.93	4.22	-	1282.4
AHQ-1-2, 4482 - 4550	K.TMLESAGGLIQTAR.A	1448.67095	2	9.21E-12	0.95	4.76	-	1491.9
AHQ-1-2, 4302	K.TMLESAGGLIQTAR.A	1448.67095	2	3.86E-09	0.92	3.98	-	1215.4
AHQ-1-4, 3563 - 3592	K.TM*LESAGGLIQTAR.A	1464.67035	2	4.96E-04	0.93	3.84	-	1337.1
AHQ-1-6, 4250 - 4254	K.TMLESAGGLIQTAR.A	1448.67095	2	1.92E-07	0.94	4.51	-	1376.3
AHQ-1-8, 4201	K.TMLESAGGLIQTAR.A	1448.67095	2	1.25E-05	0.90	3.36	-	1520.4
AHQ-1-2, 3658 - 3730	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.14E-05	0.95	4.36	-	1466.1
AHQ-1-10, 4405	K.TMQFEPSTMVYDACR.I	1838.07571	2	2.71E-04	0.88	3.33	-	585.1
AHQ-1-14- , 4826	K.TMQFEPSTMVYDACR.I	1838.07571	2	9.56E-04	0.65	2.96	-	446.4
AHQ-1-13- , 4063 - 4123	K.TMQFEPSTM*VYDACR.I	1854.07511	2	4.21E-05	0.88	3.61	-	437.1
AHQ-1-13- , 4936 - 4937	K.TMQFEPSTMVYDACR.I	1838.07571	2	1.81E-07	0.96	5.27	-	720.5
AHQ-1-8, 3398	K.TM*QFEPSTM*VYDACR.I	1870.07451	2	2.17E-05	0.45	2.65	-	347.7
AHQ-1-8, 4241	K.TM*QFEPSTMVYDACR.I	1854.07511	2	5.84E-05	0.80	3.35	-	558.9
AHQ-1-8, 4819	K.TMQFEPSTMVYDACR.I	1838.07571	2	1.76E-04	0.90	4.24	-	522.4
AHQ-1-13, 4180	K.TM*QFEPSTMVYDACR.I	1854.07511	2	1.53E-05	0.85	3.41	-	549.3
AHQ-1-8, 3683	K.TVTDM*LM*TICAR.I	1445.70887	2	1.29E-04	0.74	3.06	-	403.7
AHQ-1-8, 5114	K.TYGVSFFLVK.E	1161.37395	2	4.66E-06	0.90	3.36	-	693.5
AHQ-1-8, 5215	K.TYGVSFFLVK.E	1161.37395	2	3.42E-05	0.91	3.28	-	774.5
AHQ-1-12, 5129 - 5131	K.TYGVSFFLVK.E	1161.37395	2	5.03E-08	0.93	3.72	-	760.6
AHQ-1-11, 4920	K.TYGVSFFLVK.E	1161.37395	2	7.52E-07	0.91	3.84	-	813.8
AHQ-1-2, 6594	R.VAGSVTELIQAAEAMK.G	1618.87752	2	7.54E-11	0.97	4.54	-	1531.7
AHQ-1-7, 5365	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	6.75E-05	0.92	3.95	-	1054.2
AHQ-1-4, 6586 - 6594	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.71E-06	0.97	4.86	-	1503.1
AHQ-1-5, 6457 - 6526	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.41E-09	0.96	5.02	-	1277.1
AHQ-1-4, 5498 - 5506	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	4.23E-05	0.95	4.34	-	1381.4
AHQ-1-7, 6510	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.64E-06	0.97	5.23	-	1646.5
AHQ-1-3, 5390 - 5458	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.06E-06	0.95	4.79	-	1231.6
AHQ-1-3, 6426	R.VAGSVTELIQAAEAMK.G	1618.87752	2	9.72E-06	0.91	3.96	-	1026.2
AHQ-1-13- , 6340	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.27E-05	0.96	4.95	-	1183.4
AHQ-1-6, 6398 - 6410	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.62E-07	0.98	5.79	-	2176.7
AHQ-1-1, 6415 - 6417	R.VAGSVTELIQAAEAMK.G	1618.87752	2	7.11E-07	0.98	5.11	-	2292.1
AHQ-1-1, 6553	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.06E-07	0.85	2.96	-	877.4
AHQ-1-9, 6346	R.VAGSVTELIQAAEAMK.G	1618.87752	2	9.22E-05	0.96	4.20	-	1692.4
AHQ-1-9, 5232	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	1.14E-05	0.92	4.00	-	971.5
AHQ-1-4, 3708	K.VEHGSVALPAIMR.S	1380.64144	2	7.06E-07	0.89	3.07	-	1020.3
AHQ-1-2, 6285 - 6353	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.89E-04	0.93	4.47	-	912.7
AHQ-1-3, 6025 - 6089	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.14E-08	0.88	4.34	-	477.2
AHQ-1-2, 6109 - 6149	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.24E-11	0.94	4.83	-	661.5
AHQ-1-5, 5894 - 5953	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.36E-09	0.94	4.37	-	1014.4
AHQ-1-3, 6161	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.90E-06	0.80	3.61	-	443.9
AHQ-1-1, 5996 - 6063	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.44E-08	0.90	4.44	-	585.3
AHQ-1-13, 5453 - 5517	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.73E-09	0.90	4.03	-	793.3
AHQ-1-5, 6033 - 6113	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.26E-11	0.96	5.32	-	873.0
AHQ-1-2, 5979 - 6025	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.32E-11	0.97	5.54	-	1051.0
AHQ-1-1, 5939 - 6003	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.41E-10	0.95	4.97	-	816.4
AHQ-1-5, 6239 - 6250	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.09E-06	0.75	3.04	-	420.4
AHQ-1-2, 5911 - 5955	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.57E-07	0.93	4.62	-	755.7
AHQ-1-7, 6021 - 6100	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.69E-08	0.96	5.82	-	822.5
AHQ-1-4, 6272	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.83E-04	0.79	3.22	-	452.1
AHQ-1-4, 6138 - 6215	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.08E-09	0.96	5.21	-	1145.3
AHQ-1-7, 5880	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.63E-06	0.88	4.06	-	584.9
AHQ-1-1, 5837 - 5899	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.24E-09	0.88	4.16	-	393.8
AHQ-1-4, 6043	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.85E-05	0.83	3.51	-	612.6
AHQ-1-9, 5656 - 5683	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.08E-07	0.93	4.95	-	623.4
AHQ-1-11, 5255	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.79E-06	0.49	2.75	-	367.5
AHQ-1-4, 5924 - 5938	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.50E-08	0.96	4.96	-	1186.2
AHQ-1-4, 5800	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.47E-07	0.87	3.81	-	599.5
AHQ-1-9, 5898 - 5935	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.16E-11	0.97	6.04	-	1089.7
AHQ-1-11, 5359 - 5426	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.21E-06	0.96	5.24	-	934.2
AHQ-1-1, 5821	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	4.16E-06	0.77	3.18	-	1005.2
AHQ-1-1, 5761 - 5825	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.86E-04	0.69	3.43	-	352.5
AHQ-1-3, 5941 - 5949	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.15E-11	0.91	4.53	-	440.0
AHQ-1-12, 5619	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.41E-06	0.83	3.96	-	485.7
AHQ-1-9, 6051	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.16E-05	0.51	2.97	-	208.7
AHQ-1-3, 5786 - 5857	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.92E-08	0.96	5.63	-	977.5
AHQ-1-10, 5207 - 5287	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.37E-08	0.95	5.79	-	649.7
AHQ-1-6, 5788 - 5814	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.35E-06	0.95	4.33	-	1125.7
AHQ-1-6, 5894	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.42E-09	0.95	4.75	-	761.5
AHQ-1-6, 5990	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.17E-11	0.94	5.00	-	673.5
AHQ-1-6, 6100	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.10E-11	0.95	5.01	-	767.9
AHQ-1-2, 6114 - 6189	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	3.02E-05	0.95	4.73	-	1627.7
AHQ-1-8, 5962	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.87E-12	0.96	5.36	-	991.2
AHQ-1-4, 3892	K.VGDDPAVWQLK.N	1228.37879	2	7.77E-09	0.92	3.71	-	903.0
AHQ-1-2, 4026	K.VGDDPAVWQLK.N	1228.37879	2	3.52E-08	0.93	3.82	-	884.8
AHQ-1-1, 3959	K.VGDDPAVWQLK.N	1228.37879	2	7.32E-08	0.94	4.16	-	879.7
AHQ-1-3, 3825 - 3893	K.VGDDPAVWQLK.N	1228.37879	2	7.25E-08	0.92	3.68	-	842.6
AHQ-1-7, 3792 - 3840	K.VGDDPAVWQLK.N	1228.37879	2	5.40E-04	0.90	3.27	-	989.9
AHQ-1-2, 3963 - 4037	K.VGDDPAVWQLK.N	1228.37879	2	5.34E-09	0.94	4.32	-	897.7
AHQ-1-6, 3710 - 3754	K.VGDDPAVWQLK.N	1228.37879	2	3.11E-08	0.89	3.30	-	771.0
AHQ-1-3, 3874	K.VGDDPAVWQLK.N	1228.37879	2	3.12E-08	0.93	4.37	-	770.6
AHQ-1-5, 3747	K.VGDDPAVWQLK.N	1228.37879	2	5.23E-09	0.92	3.99	-	825.3
AHQ-1-2, 3417	K.VGDDPAVWQLKNSAK.V	1628.81068	2	9.30E-07	0.81	3.31	-	571.9
AHQ-1-4, 2386 - 2403	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.27E-04	0.94	4.27	-	1209.6
AHQ-1-4, 3362	K.VLGEAMTGISQNAK.N	1419.62961	2	6.13E-12	0.94	3.67	-	1418.1
AHQ-1-7, 3076	K.VLGEAMTGISQNAK.N	1419.62961	2	1.12E-08	0.96	3.81	-	1677.0
AHQ-1-4, 3196 - 3231	K.VLGEAMTGISQNAK.N	1419.62961	1	1.13E-04	0.77	3.13	-	478.2
AHQ-1-3, 3165 - 3166	K.VLGEAMTGISQNAK.N	1419.62961	1	8.90E-04	0.55	2.03	-	538.7
AHQ-1-14- , 2371 - 2451	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.48E-04	0.95	3.83	-	1575.4
AHQ-1-2, 3286	K.VLGEAMTGISQNAK.N	1419.62961	1	6.52E-07	0.70	3.11	-	516.3
AHQ-1-2, 3259 - 3303	K.VLGEAMTGISQNAK.N	1419.62961	2	2.20E-08	0.97	4.99	-	1729.8
AHQ-1-2, 2589	K.VLGEAM*TGISQNAK.N	1435.62901	2	3.30E-06	0.95	3.57	-	1598.2
AHQ-1-3, 2495	K.VLGEAM*TGISQNAK.N	1435.62901	2	9.99E-05	0.93	3.54	-	1099.7
AHQ-1-2, 2478	K.VLGEAM*TGISQNAK.N	1435.62901	2	2.85E-07	0.90	4.07	-	753.2

AHQ-1-4, 3186	K.VLGEAMTGISQNAK.N	1419.62961	2	2.87E-09	0.97	3.62	-	2373.8
AHQ-1-2, 3430 - 3433	K.VLGEAMTGISQNAK.N	1419.62961	2	4.68E-07	0.97	3.94	-	1945.7
AHQ-1-1, 3275 - 3291	K.VLGEAMTGISQNAK.N	1419.62961	2	6.72E-05	0.98	5.41	-	1788.4
AHQ-1-1, 4901	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	3.51E-04	0.85	4.31	-	362.9
AHQ-1-4, 5514 - 5582	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	6.56E-11	0.83	4.11	-	575.9
AHQ-1-3, 5401 - 5465	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	7.35E-10	0.93	5.25	-	935.3
AHQ-1-2, 5018 - 5089	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	5.88E-05	0.87	4.33	-	604.5
AHQ-1-1, 4991	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	1.59E-05	0.91	4.56	-	880.7
AHQ-1-1, 5472	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	8.22E-04	0.90	4.49	-	961.2
AHQ-1-2, 5585 - 5649	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	3.01E-08	0.93	5.28	-	780.3
AHQ-1-3, 1625 - 1657	K.VLVQNAAGSQEK.L	1244.37976	2	8.18E-07	0.93	3.63	-	1079.3
AHQ-1-6, 1791	K.VLVQNAAGSQEK.L	1244.37976	2	1.41E-07	0.92	3.59	-	1064.4
AHQ-1-6, 1596 - 1614	K.VLVQNAAGSQEK.L	1244.37976	2	1.54E-09	0.90	3.51	-	865.7
AHQ-1-1, 1932 - 2012	K.VLVQNAAGSQEK.L	1244.37976	2	6.08E-04	0.83	2.83	-	904.2
AHQ-1-2, 1758 - 1959	K.VLVQNAAGSQEK.L	1244.37976	1	3.67E-05	0.33	2.32	-	454.4
AHQ-1-3, 1717 - 1790	K.VLVQNAAGSQEK.L	1244.37976	2	6.92E-06	0.90	3.53	-	902.9
AHQ-1-2, 1665 - 1730	K.VLVQNAAGSQEK.L	1244.37976	2	1.71E-07	0.94	3.82	-	1074.6
AHQ-1-3, 1850 - 1929	K.VLVQNAAGSQEK.L	1244.37976	2	2.55E-08	0.90	3.30	-	969.5
AHQ-1-5, 1543 - 1606	K.VLVQNAAGSQEK.L	1244.37976	2	2.83E-06	0.92	3.66	-	1009.0
AHQ-1-2, 1989	K.VLVQNAAGSQEK.L	1244.37976	2	6.51E-08	0.94	3.43	-	1360.8
AHQ-1-4, 1611 - 1670	K.VLVQNAAGSQEK.L	1244.37976	2	4.03E-06	0.93	3.62	-	1170.8
AHQ-1-4, 1712 - 1835	K.VLVQNAAGSQEK.L	1244.37976	1	1.22E-05	0.33	2.35	-	293.1
AHQ-1-4, 1730 - 1790	K.VLVQNAAGSQEK.L	1244.37976	2	3.65E-04	0.76	3.00	-	649.9
AHQ-1-4, 1874 - 1952	K.VLVQNAAGSQEK.L	1244.37976	2	2.99E-10	0.87	3.38	-	703.3
AHQ-1-6, 1694	K.VLVQNAAGSQEK.L	1244.37976	2	2.13E-07	0.81	3.08	-	622.0
AHQ-1-2, 1793 - 1857	K.VLVQNAAGSQEK.L	1244.37976	2	1.72E-06	0.92	3.94	-	1002.5
AHQ-1-3, 4413	K.VM*VTNVTSLLK.T	1221.49262	2	4.91E-05	0.80	2.99	-	666.6
AHQ-1-2, 4569	K.VM*VTNVTSLLK.T	1221.49262	2	1.86E-04	0.76	3.04	-	730.3
AHQ-1-5, 4679 - 4689	K.VMVTNVTSLLK.T	1205.49322	2	1.16E-06	0.96	4.55	-	1155.4
AHQ-1-2, 4937	K.VMVTNVTSLLK.T	1205.49322	2	5.72E-06	0.91	3.77	-	839.7
AHQ-1-4, 4828 - 4838	K.VMVTNVTSLLK.T	1205.49322	2	5.29E-07	0.94	4.30	-	917.5
AHQ-1-2, 4958	K.VM*VTNVTSLLK.T	1221.49262	2	5.75E-04	0.63	2.82	-	736.1
AHQ-1-2, 5030	K.VMVTNVTSLLK.T	1205.49322	2	4.18E-05	0.88	3.59	-	728.5
AHQ-1-7, 4629 - 4646	K.VMVTNVTSLLK.T	1205.49322	2	7.24E-05	0.86	3.43	-	681.7
AHQ-1-3, 4785	K.VMVTNVTSLLK.T	1205.49322	2	2.02E-04	0.92	4.03	-	822.3
AHQ-1-4, 4455 - 4471	K.VM*VTNVTSLLK.T	1221.49262	2	5.87E-04	0.89	3.53	-	768.8
AHQ-1-6, 4255 - 4332	K.VM*VTNVTSLLK.T	1221.49262	2	8.27E-06	0.85	3.30	-	726.3
AHQ-1-1, 4489	K.VM*VTNVTSLLK.T	1221.49262	2	3.24E-04	0.62	2.65	-	514.7
AHQ-1-1, 4839 - 4840	K.VMVTNVTSLLK.T	1205.49322	2	1.60E-04	0.93	4.23	-	921.2
AHQ-1-6, 4610	K.VMVTNVTSLLK.T	1205.49322	2	1.37E-05	0.91	3.97	-	765.8
AHQ-1-5, 4314	K.VM*VTNVTSLLK.T	1221.49262	2	6.62E-07	0.81	3.38	-	625.4
AHQ-1-11, 2720	R.VQELGHGCAALVTK.A	1484.70307	2	5.09E-04	0.95	3.75	-	1450.9
AHQ-1-6, 2706	R.VQELGHGCAALVTK.A	1484.70307	2	1.24E-04	0.96	4.42	-	1465.1
AHQ-1-1, 2909 - 2980	R.VQELGHGCAALVTK.A	1484.70307	2	3.93E-04	0.94	4.34	-	1014.7
AHQ-1-4, 2806	R.VQELGHGCAALVTK.A	1484.70307	2	6.62E-05	0.98	5.05	-	1928.1
AHQ-1-3, 2823	R.VQELGHGCAALVTK.A	1484.70307	1	5.48E-06	0.83	3.80	-	497.4
AHQ-1-1, 2967	R.VQELGHGCAALVTK.A	1484.70307	2	2.71E-08	0.97	5.05	-	1626.2
AHQ-1-7, 2726	R.VQELGHGCAALVTK.A	1484.70307	2	9.66E-04	0.94	3.81	-	1298.1
AHQ-1-2, 2935	R.VQELGHGCAALVTK.A	1484.70307	1	3.13E-07	0.84	3.78	-	578.8
AHQ-1-2, 2914	R.VQELGHGCAALVTK.A	1484.70307	2	2.98E-04	0.95	4.38	-	1194.2
AHQ-1-2, 2739 - 2809	K.VSHVLAALQAGNR.G	1336.52525	2	9.66E-09	0.97	4.69	-	1756.2
AHQ-1-2, 2806	K.VSHVLAALQAGNR.G	1336.52525	1	5.54E-06	0.88	3.54	-	509.2
AHQ-1-5, 2554 - 2570	K.VSHVLAALQAGNR.G	1336.52525	2	6.68E-05	0.90	3.17	-	1006.3
AHQ-1-4, 2660 - 2730	K.VSHVLAALQAGNR.G	1336.52525	2	3.65E-11	0.96	4.12	-	1669.6
AHQ-1-4, 2707	K.VSHVLAALQAGNR.G	1336.52525	1	6.94E-06	0.88	3.37	-	553.7
AHQ-1-5, 2562	K.VSHVLAALQAGNR.G	1336.52525	1	1.25E-04	0.34	2.24	-	278.3
AHQ-1-7, 2600	K.VSHVLAALQAGNR.G	1336.52525	1	3.50E-06	0.67	2.62	-	482.3
AHQ-1-6, 2676	K.VSHVLAALQAGNR.G	1336.52525	2	1.57E-04	0.95	3.33	-	1694.5
AHQ-1-7, 2596	K.VSHVLAALQAGNR.G	1336.52525	2	9.46E-07	0.94	3.65	-	1311.9
AHQ-1-3, 2653 - 2727	K.VSHVLAALQAGNR.G	1336.52525	2	3.06E-05	0.96	4.19	-	1591.3
AHQ-1-4, 2714	K.VSHVLAALQAGNR.G	1336.52525	2	8.35E-09	0.98	5.20	-	1828.5
AHQ-1-3, 2706	K.VSHVLAALQAGNR.G	1336.52525	1	1.40E-07	0.80	3.35	-	423.6
AHQ-1-1, 2888	K.VSHVLAALQAGNR.G	1336.52525	1	2.18E-04	0.39	2.03	-	479.9
AHQ-1-1, 2887	K.VSHVLAALQAGNR.G	1336.52525	2	7.00E-07	0.97	4.36	-	2118.4
AHQ-1-6, 2570 - 2574	K.VSHVLAALQAGNR.G	1336.52525	2	2.31E-07	0.96	4.19	-	1713.7
AHQ-1-4, 2716	K.VSHVLAALQAGNR.G	1336.52525	1	1.63E-04	0.78	3.28	-	377.2
AHQ-1-7, 6934 - 6953	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.31E-05	0.95	4.84	-	870.0
AHQ-1-6, 6734 - 6750	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.87E-07	0.95	5.14	-	763.9
AHQ-1-6, 5927	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.02E-07	0.94	4.06	-	1244.8
AHQ-1-3, 5922 - 5989	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.75E-05	0.92	4.62	-	797.0
AHQ-1-12, 6307	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.81E-04	0.76	3.71	-	335.1
AHQ-1-2, 7119	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.52E-11	0.98	6.17	-	1260.1
AHQ-1-2, 6985 - 7055	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.14E-05	0.96	5.51	-	954.8
AHQ-1-10, 5987 - 6032	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.13E-04	0.87	3.82	-	777.2
AHQ-1-2, 6894 - 6973	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	8.03E-07	0.96	5.74	-	853.3
AHQ-1-2, 6886	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.91E-09	0.93	4.51	-	801.0
AHQ-1-11, 6102 - 6107	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	7.42E-05	0.89	4.45	-	493.8
AHQ-1-4, 6100	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.18E-04	0.88	3.54	-	808.5
AHQ-1-4, 6867	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.99E-04	0.87	4.25	-	549.7
AHQ-1-4, 6958	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	2.16E-06	0.82	3.71	-	931.1
AHQ-1-11, 5395	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.24E-06	0.87	4.04	-	651.0
AHQ-1-3, 6854 - 6929	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.82E-06	0.92	5.16	-	487.3
AHQ-1-3, 6797 - 6805	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	2.38E-07	0.97	5.14	-	2147.5
AHQ-1-3, 5973	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.30E-05	0.92	4.36	-	775.3
AHQ-1-4, 7079 - 7142	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.61E-08	0.97	5.34	-	1222.6
AHQ-1-3, 6707 - 6789	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.15E-06	0.96	5.71	-	857.6
AHQ-1-3, 6119	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.51E-05	0.82	3.83	-	527.9
AHQ-1-3, 6010	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.24E-06	0.93	4.78	-	726.4
AHQ-1-5, 7098	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.47E-06	0.76	2.93	-	591.0
AHQ-1-3, 5990 - 5997	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	4.01E-10	0.93	4.44	-	1353.0
AHQ-1-5, 6911 - 6913	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.27E-06	0.97	6.35	-	1006.4
AHQ-1-7, 5950	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.14E-05	0.95	4.80	-	981.5
AHQ-1-1, 6807 - 6833	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.52E-08	0.96	5.55	-	772.8
AHQ-1-1, 6677 - 6735	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.18E-07	0.96	5.31	-	903.5
AHQ-1-5, 6037 - 6038	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.31E-04	0.96	5.09	-	1253.6
AHQ-1-14- , 6418	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.10E-05	0.95	5.26	-	823.6
AHQ-1-1, 5989	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.22E-04	0.95	4.83	-	1028.9
AHQ-1-2, 4745	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.01E-06	0.90	4.23	-	415.6
AHQ-1-5, 4818 - 4897	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.95E-11	0.93	4.74	-	492.3
AHQ-1-5, 4710 - 4715	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.16E-07	0.96	5.05	-	1010.2
AHQ-1-14, 5353 - 5360	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.07E-07	0.92	4.22	-	765.9
AHQ-1-5, 4601	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.54E-07	0.93	4.70	-	537.3
AHQ-1-11, 4307	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.99E-04	0.81	3.86	-	381.3
AHQ-1-9, 4582	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.48E-07	0.95	4.91	-	871.9
AHQ-1-4, 5110 - 5124	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.94E-10	0.85	3.96	-	410.3
AHQ-1-1, 5065	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.11E-12	0.93	4.93	-	478.1
AHQ-1-4, 4979	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.16E-12	0.92	4.15	-	604.5

AHQ-1-2, 5175 - 5178	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.72E-12	0.94	4.82	-	689.3
AHQ-1-4, 4795 - 4870	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.69E-07	0.96	5.34	-	691.0
AHQ-1-1, 4896	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.95E-05	0.52	2.75	-	261.9
AHQ-1-4, 4670	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.49E-08	0.91	4.57	-	408.0
AHQ-1-1, 4723	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.78E-05	0.92	4.21	-	717.2
AHQ-1-6, 4622 - 4623	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.72E-07	0.97	5.87	-	1027.9
AHQ-1-1, 4620	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.70E-07	0.91	4.55	-	415.3
AHQ-1-2, 5035 - 5049	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.54E-13	0.96	5.06	-	904.8
AHQ-1-14- , 4544	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.27E-04	0.55	2.76	-	309.7
AHQ-1-6, 4959	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.10E-04	0.39	2.76	-	235.2
AHQ-1-12, 4467	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.48E-07	0.95	5.06	-	738.4
AHQ-1-2, 4861 - 4930	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.09E-04	0.93	4.47	-	627.1
AHQ-1-3, 5042 - 5110	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.97E-04	0.64	3.52	-	407.3
AHQ-1-3, 4902 - 4971	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.42E-13	0.89	4.02	-	523.0
AHQ-1-3, 4741 - 4750	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	4.98E-10	0.91	4.48	-	968.1
AHQ-1-3, 4733	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.47E-05	0.93	4.49	-	649.0
AHQ-1-10, 4183	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.04E-04	0.84	3.71	-	370.2
AHQ-1-5, 5049	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.38E-05	0.77	3.81	-	364.1
AHQ-1-3, 4607	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.98E-04	0.66	3.78	-	118.0
AHQ-1-8, 4667	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.43E-08	0.91	4.53	-	555.7
gi|4501885|ref|NP_001092.1| beta actin; beta cytoskeletal actin [Homo sapiens]				5.55E-16	13.29	150.37	36.00	41736.5
AHQ-1-14- , 6012	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	3.56E-05	0.91	4.68	-	499.6
AHQ-1-12, 5881 - 5907	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.56E-05	0.65	3.38	-	347.6
AHQ-1-13, 5776 - 5832	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.36E-09	0.94	5.05	-	843.8
AHQ-1-13, 6217 - 6237	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	3.80E-08	0.82	4.64	-	601.1
AHQ-1-10, 6228	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	4.33E-04	0.83	4.04	-	568.3
AHQ-1-10, 6141 - 6207	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.03E-05	0.78	3.51	-	515.4
AHQ-1-10, 5991 - 6063	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	4.08E-06	0.79	4.25	-	576.9
AHQ-1-10, 5553 - 5607	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.82E-04	0.44	3.07	-	327.6
AHQ-1-9, 7036 - 7118	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.09E-07	0.96	5.68	-	1041.7
AHQ-1-9, 6730 - 6795	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	4.70E-04	0.67	4.04	-	330.6
AHQ-1-9, 6636 - 6714	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	5.44E-07	0.64	3.93	-	263.8
AHQ-1-8, 7599	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.44E-09	0.91	4.24	-	781.7
AHQ-1-8, 7311 - 7382	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	4.83E-14	0.96	5.41	-	1181.6
AHQ-1-8, 7222 - 7290	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.20E-12	0.96	5.37	-	1130.1
AHQ-1-8, 7088 - 7159	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.09E-07	0.94	5.12	-	864.8
AHQ-1-8, 7079 - 7146	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	7.52E-05	0.80	4.38	-	529.9
AHQ-1-8, 6846 - 6915	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	9.56E-08	0.80	4.47	-	590.3
AHQ-1-8, 6755 - 6822	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.11E-04	0.72	3.92	-	386.6
AHQ-1-8, 6554	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	5.20E-04	0.73	3.82	-	452.2
AHQ-1-5, 7303	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.28E-05	0.85	3.74	-	542.5
AHQ-1-8, 6402 - 6471	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.46E-06	0.94	4.89	-	938.6
AHQ-1-13- , 6157 - 6239	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	6.61E-04	0.86	4.10	-	524.0
AHQ-1-13- , 6495 - 6560	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.01E-04	0.92	5.21	-	731.5
AHQ-1-13- , 6623 - 6683	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	3.54E-05	0.81	4.45	-	545.3
AHQ-1-13- , 6757	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	2.42E-04	0.66	3.54	-	365.4
AHQ-1-8, 7522 - 7591	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	5.24E-09	0.93	4.46	-	854.5
AHQ-1-8, 7487 - 7559	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	3.09E-05	0.93	5.00	-	1187.0
AHQ-1-8, 7628	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.00E-06	0.89	4.40	-	845.3
AHQ-1-8, 7658 - 7659	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	6.14E-08	0.88	3.86	-	739.3
AHQ-1-9, 7099 - 7171	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.66E-05	0.91	4.03	-	771.0
AHQ-1-8, 7250 - 7318	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	7.71E-08	0.89	4.31	-	552.9
AHQ-1-8, 5583 - 5658	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.88E-05	0.82	4.03	-	599.7
AHQ-1-4, 7310	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	4.32E-04	0.75	3.83	-	788.6
AHQ-1-8, 7528	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.96E-08	0.91	4.71	-	854.7
AHQ-1-8, 7336 - 7414	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	2.74E-05	0.93	4.91	-	1325.8
AHQ-1-10, 6259 - 6260	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.55E-06	0.94	5.21	-	1159.7
AHQ-1-10, 6240	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	3.14E-06	0.56	2.77	-	638.5
AHQ-1-8, 7386 - 7454	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.24E-09	0.89	3.69	-	759.5
AHQ-1-8, 7466 - 7534	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	5.63E-06	0.93	4.86	-	988.4
AHQ-1-8, 6738 - 6851	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	1.63E-08	0.94	5.61	-	1089.3
AHQ-1-8, 7090 - 7155	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	5.57E-11	0.98	7.44	-	1997.5
AHQ-1-13- , 6581 - 6645	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	2.34E-06	0.88	4.42	-	704.2
AHQ-1-10, 5888 - 5959	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	2.74E-05	0.81	4.65	-	746.2
AHQ-1-8, 2395 - 2467	R.GYSFTTTAER.E	1133.19273	2	4.57E-04	0.91	3.02	-	1158.8
AHQ-1-13- , 2624 - 2663	R.GYSFTTTAER.E	1133.19273	2	1.08E-04	0.91	3.45	-	971.2
AHQ-1-10, 2391 - 2463	R.GYSFTTTAER.E	1133.19273	2	4.47E-04	0.91	3.34	-	1015.5
AHQ-1-11, 2480 - 2490	R.GYSFTTTAER.E	1133.19273	2	6.89E-05	0.94	3.09	-	1278.2
AHQ-1-5, 2429	R.GYSFTTTAER.E	1133.19273	2	7.21E-05	0.89	3.13	-	980.5
AHQ-1-6, 2443 - 2494	R.GYSFTTTAER.E	1133.19273	2	3.37E-04	0.82	2.84	-	862.1
AHQ-1-14- , 2523 - 2527	R.GYSFTTTAER.E	1133.19273	2	5.34E-04	0.89	3.26	-	987.1
AHQ-1-3, 2533	R.GYSFTTTAER.E	1133.19273	2	1.10E-04	0.93	3.07	-	1254.2
AHQ-1-9, 2374 - 2446	R.GYSFTTTAER.E	1133.19273	2	7.58E-04	0.91	3.18	-	945.1
AHQ-1-2, 2627	R.GYSFTTTAER.E	1133.19273	2	5.22E-04	0.91	3.02	-	1184.4
AHQ-1-13, 2641 - 2661	R.GYSFTTTAER.E	1133.19273	2	2.52E-05	0.87	2.97	-	797.4
AHQ-1-8, 2281 - 2325	R.GYSFTTTAER.E	1133.19273	2	1.06E-04	0.91	3.15	-	1233.1
AHQ-1-7, 2473	R.GYSFTTTAER.E	1133.19273	2	9.61E-04	0.85	3.08	-	842.4
AHQ-1-13, 4607	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.71E-05	0.91	3.96	-	766.7
AHQ-1-10, 3949 - 3959	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	3.94E-04	0.95	4.51	-	1159.2
AHQ-1-10, 4307	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.68E-06	0.78	2.91	-	636.2
AHQ-1-8, 4730 - 4759	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	9.17E-06	0.96	4.42	-	1395.6
AHQ-1-8, 4324	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	5.50E-05	0.96	4.80	-	1607.7
AHQ-1-14- , 4699 - 4752	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	5.24E-04	0.72	2.93	-	526.1
AHQ-1-13, 4156	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	3.60E-05	0.63	2.65	-	571.3
AHQ-1-13- , 4369	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	4.92E-04	0.82	3.04	-	688.8
AHQ-1-10, 6495 - 6531	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	5.91E-05	0.90	3.50	-	1003.7
AHQ-1-9, 7374 - 7444	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	6.07E-06	0.96	5.55	-	1708.3
AHQ-1-10, 6219 - 6277	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	1.65E-06	0.97	5.14	-	1852.8
AHQ-1-5, 5779	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.18E-06	0.93	4.80	-	1048.3
AHQ-1-5, 6050	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.22E-08	0.97	5.95	-	1854.3
AHQ-1-5, 6147	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.95E-10	0.97	5.23	-	2259.1
AHQ-1-8, 6204 - 6272	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.98E-07	0.97	5.96	-	1838.7
AHQ-1-9, 5390 - 5410	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.05E-09	0.97	6.23	-	1392.1
AHQ-1-9, 5478 - 5550	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.62E-09	0.97	5.72	-	1976.5
AHQ-1-9, 5715 - 5795	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.85E-12	0.96	6.17	-	1189.7
AHQ-1-9, 5851 - 5931	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.00E-11	0.97	6.22	-	1465.4
AHQ-1-9, 5926 - 6004	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	9.24E-05	0.68	3.85	-	788.7
AHQ-1-9, 5998 - 6072	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.01E-09	0.94	5.22	-	1182.4
AHQ-1-4, 5918	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.57E-07	0.93	4.78	-	1111.8
AHQ-1-4, 5819	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.37E-08	0.96	6.09	-	1089.4
AHQ-1-3, 6073	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.10E-07	0.93	4.74	-	1066.2
AHQ-1-5, 5646	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.03E-06	0.92	5.16	-	723.6
AHQ-1-4, 6126	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.93E-06	0.96	5.95	-	1329.5
AHQ-1-8, 5934 - 5998	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.15E-11	0.98	6.82	-	1772.2
AHQ-1-8, 5796 - 5866	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.55E-16	0.96	5.79	-	1562.0
AHQ-1-14, 6444	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.27E-06	0.78	4.13	-	649.3
AHQ-1-8, 5714 - 5782	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.34E-13	0.98	6.78	-	2008.9

AHQ-1-8, 5466 - 5530	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.03E-09	0.96	5.76	-	1264.9
AHQ-1-10, 4857 - 4915	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	9.54E-08	0.95	5.17	-	1493.0
AHQ-1-10, 4975 - 5031	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.32E-10	0.98	6.81	-	1764.1
AHQ-1-10, 5191 - 5247	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.00E-11	0.97	5.98	-	1747.2
AHQ-1-10, 5303 - 5359	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.66E-10	0.97	6.37	-	1552.5
AHQ-1-3, 5733 - 5805	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.60E-06	0.96	5.53	-	1378.2
AHQ-1-8, 5370 - 5398	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.35E-08	0.96	5.93	-	1166.9
AHQ-1-8, 5287 - 5320	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.67E-06	0.61	3.16	-	605.2
AHQ-1-2, 6187 - 6253	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.96E-06	0.94	5.46	-	914.2
AHQ-1-8, 6066 - 6131	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.65E-11	0.96	5.87	-	1544.9
AHQ-1-2, 5913 - 5982	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	9.10E-05	0.96	5.84	-	1468.7
AHQ-1-13- , 5560 - 5636	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.25E-09	0.97	5.83	-	2136.4
AHQ-1-13- , 5823 - 5903	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.78E-15	0.97	5.80	-	1954.5
AHQ-1-14- , 5419 - 5484	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.09E-05	0.95	5.35	-	1037.1
AHQ-1-6, 6034 - 6042	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.51E-12	0.97	5.91	-	1376.6
AHQ-1-14, 6270 - 6324	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.39E-08	0.98	6.88	-	2224.4
AHQ-1-11, 5098	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.96E-13	0.97	6.55	-	1618.1
AHQ-1-11, 5186	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.36E-09	0.95	5.34	-	1283.5
AHQ-1-11, 5308 - 5368	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.24E-07	0.93	4.79	-	1205.6
AHQ-1-11, 5446	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.41E-08	0.96	5.41	-	1600.2
AHQ-1-7, 6130	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.26E-09	0.95	5.35	-	1425.5
AHQ-1-1, 6001 - 6075	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.28E-12	0.95	5.16	-	1499.9
AHQ-1-12, 5321 - 5383	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.76E-08	0.93	4.71	-	1094.3
AHQ-1-12, 5654 - 5714	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.59E-10	0.91	4.98	-	653.5
AHQ-1-1, 5751 - 5820	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.45E-08	0.97	5.95	-	1514.8
AHQ-1-7, 5978 - 6052	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.32E-07	0.74	3.39	-	810.1
AHQ-1-13, 5611	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.09E-10	0.95	5.65	-	992.9
AHQ-1-13, 5472 - 5547	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.18E-11	0.97	5.93	-	1787.5
AHQ-1-7, 5620 - 5689	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.30E-07	0.94	5.26	-	1053.9
AHQ-1-14- , 5678 - 5758	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.75E-12	0.97	5.46	-	1924.4
AHQ-1-13, 5245 - 5308	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.44E-08	0.97	5.77	-	1664.3
AHQ-1-13, 3919	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	1.43E-04	0.52	3.05	-	519.5
AHQ-1-13, 3883 - 3943	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.32E-05	0.94	4.62	-	960.2
AHQ-1-12, 3801 - 3873	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	3.82E-05	0.87	4.87	-	734.8
AHQ-1-12, 3793 - 3861	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.30E-06	0.92	4.64	-	712.4
AHQ-1-14, 4824	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.23E-07	0.90	4.04	-	721.9
AHQ-1-11, 3676	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.14E-06	0.92	4.03	-	905.9
AHQ-1-10, 3587 - 3647	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	8.43E-05	0.84	4.34	-	1046.6
AHQ-1-10, 3584 - 3643	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.52E-09	0.91	4.55	-	757.8
AHQ-1-13- , 4043 - 4100	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	9.63E-04	0.75	3.99	-	880.6
AHQ-1-13- , 4044 - 4113	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.78E-10	0.94	4.55	-	1099.6
AHQ-1-9, 3606 - 3680	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.21E-07	0.93	4.20	-	992.7
AHQ-1-8, 3872 - 3947	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.51E-06	0.94	4.67	-	963.2
AHQ-1-8, 3847 - 3856	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.25E-09	0.93	4.81	-	785.2
AHQ-1-8, 3717 - 3787	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.07E-07	0.94	4.71	-	932.8
AHQ-1-8, 3572 - 3641	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.18E-05	0.94	4.84	-	951.4
AHQ-1-8, 3556 - 3637	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	9.23E-04	0.72	4.03	-	586.1
AHQ-1-8, 3476 - 3548	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.18E-04	0.93	4.56	-	750.2
AHQ-1-7, 3900	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.42E-04	0.88	3.92	-	830.5
AHQ-1-6, 3823	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	1.87E-04	0.75	3.72	-	792.7
AHQ-1-14- , 3944 - 3963	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.26E-05	0.91	4.39	-	928.1
AHQ-1-6, 3822	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.14E-06	0.87	4.00	-	665.1
AHQ-1-5, 3893 - 3894	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.50E-05	0.89	3.94	-	665.0
AHQ-1-9, 3750 - 3818	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.75E-06	0.90	4.21	-	643.1
AHQ-1-1, 4133	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.12E-06	0.89	3.82	-	815.1
gi|4507949|ref|NP_003395.1| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,				5.55E-16	4.54	50.28	30.10	28082.2
AHQ-1-13- , 1960	K.AVTEQGHELSNEER.N	1599.64147	2	1.16E-04	0.75	3.03	-	548.9
AHQ-1-10, 1796 - 1851	K.AVTEQGHELSNEER.N	1599.64147	2	8.66E-06	0.90	3.70	-	830.0
AHQ-1-13- , 4227 - 4237	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	5.38E-07	0.76	4.00	-	385.1
AHQ-1-10, 3815 - 3816	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	4.16E-08	0.92	4.80	-	607.5
AHQ-1-10, 4011 - 4016	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	3.60E-09	0.96	5.58	-	1147.2
AHQ-1-13, 6319	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	1.44E-07	0.93	4.65	-	937.8
AHQ-1-13- , 6771 - 6828	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	5.94E-05	0.97	5.28	-	1334.4
AHQ-1-10, 6135 - 6208	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	8.00E-06	0.93	4.36	-	918.8
AHQ-1-10, 6144	K.TAFDEAIAELDTLNEESYK.D	2160.27705	3	5.64E-04	0.95	4.16	-	1840.7
AHQ-1-10, 6411	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	4.35E-04	0.57	3.16	-	356.8
AHQ-1-14- , 6530	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	3.89E-10	0.96	5.19	-	1145.9
AHQ-1-10, 6464	K.TAFDEAIAELDTLNEESYKDSTLIM*QLLR.D	3347.69249	3	5.55E-16	0.96	5.23	-	1922.7
AHQ-1-13- , 3004 - 3013	K.YLIPNATQPESK.V	1361.52512	2	3.70E-06	0.88	3.83	-	641.6
AHQ-1-10, 2739 - 2805	K.YLIPNATQPESK.V	1361.52512	2	1.71E-05	0.84	3.29	-	573.2
AHQ-1-10, 2737	K.YLIPNATQPESK.V	1361.52512	1	1.84E-05	0.83	3.56	-	642.4
AHQ-1-10, 2821	K.YLIPNATQPESK.V	1361.52512	1	9.71E-05	0.21	1.89	-	443.5
AHQ-1-10, 2913	K.YLIPNATQPESK.V	1361.52512	1	5.25E-08	0.75	2.43	-	835.8
gi|5729770|ref|NP_000382.3| ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky				5.55E-16	0.96	10.25	4.80	61247.6
AHQ-1-8, 7468	R.VPIPWVSGTSASTPVFGGILSLINEHR.I	2836.23725	3	5.55E-16	0.96	4.91	-	1666.3
gi|9507215|ref|NP_061816.1| tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]				1.11E-15	4.32	50.22	13.10	50093.2
AHQ-1-7, 5473 - 5496	R.AVMIDLEPTVVDEVR.A	1686.95185	2	2.90E-04	0.76	3.45	-	643.9
AHQ-1-14- , 4920	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	3.97E-07	0.92	4.33	-	792.7
AHQ-1-7, 3553	K.DVNVAIAAIK.T	1014.20080	2	1.68E-06	0.93	3.38	-	1233.9
AHQ-1-7, 5698 - 5733	R.IHFPLVTYAPIISAEK.A	1800.13312	2	2.77E-07	0.81	3.22	-	461.1
AHQ-1-9, 5554	R.IHFPLVTYAPIISAEK.A	1800.13312	2	9.36E-04	0.85	3.57	-	450.7
AHQ-1-14, 6189	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	3.12E-10	0.94	4.34	-	994.9
AHQ-1-7, 5550 - 5626	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	2.44E-11	0.87	3.86	-	669.1
AHQ-1-14- , 5286	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	1.11E-15	0.91	3.98	-	799.7
AHQ-1-13, 5144	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	1.49E-07	0.67	3.50	-	306.0
gi|4504517|ref|NP_001531.1| heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M				1.11E-15	1.91	20.34	26.30	22782.3
AHQ-1-11, 6356	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	1.11E-15	0.97	6.87	-	1219.1
AHQ-1-13, 4520	R.VSLDVNHFAPDELTVK.T	1784.99058	2	3.18E-04	0.91	3.83	-	1046.6
AHQ-1-10, 4308	R.VSLDVNHFAPDELTVK.T	1784.99058	2	7.27E-08	0.93	4.18	-	985.9
gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act				1.67E-15	103.52	1210.36	56.00	280757.4
AHQ-1-4, 5438 - 5507	R.AEAGVPAEFSIWTR.E	1534.69735	2	2.98E-09	0.88	3.92	-	483.3
AHQ-1-5, 5341 - 5414	R.AEAGVPAEFSIWTR.E	1534.69735	2	4.65E-09	0.93	4.19	-	708.1
AHQ-1-1, 2424	R.AEFTVETR.S	953.03118	2	2.21E-04	0.87	2.78	-	1018.1
AHQ-1-5, 2147	R.AEFTVETR.S	953.03118	2	7.02E-04	0.87	2.72	-	983.7
AHQ-1-6, 2430	K.AEISFEDR.K	967.01472	2	3.74E-04	0.78	2.61	-	961.8
AHQ-1-1, 2664	K.AEISFEDR.K	967.01472	2	5.01E-04	0.88	3.02	-	1032.3
AHQ-1-4, 2642	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.41E-06	0.92	3.30	-	1356.5
AHQ-1-9, 2531	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	5.78E-05	0.88	2.68	-	1446.2
AHQ-1-7, 2584	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.01E-05	0.84	2.81	-	931.4
AHQ-1-1, 2700 - 2771	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.11E-10	0.93	3.37	-	1263.3
AHQ-1-1, 2915 - 2996	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.16E-06	0.93	3.45	-	1302.9
AHQ-1-3, 2625 - 2695	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.11E-06	0.92	3.02	-	1294.6
AHQ-1-5, 2538	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	6.36E-05	0.93	2.73	-	2041.5
AHQ-1-2, 2711 - 2781	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	7.59E-07	0.95	3.71	-	1579.8
AHQ-1-8, 2465	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.93E-05	0.90	3.39	-	1105.6
AHQ-1-6, 2552 - 2580	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.36E-08	0.96	3.38	-	1823.6
AHQ-1-14, 4396	K.AGNNMLLVGVHGPR.T	1435.68033	2	5.16E-07	0.74	2.93	-	572.3

AHQ-1-14, 4173	K.AGNNMLLVGVHGPR.T	1435.68033	3	1.27E-07	0.79	3.12	-	1108.1
AHQ-1-14- , 2908	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.55E-06	0.80	2.82	-	626.8
AHQ-1-14- , 2912 - 2934	K.AGNNM*LLVGVHGPR.T	1451.67973	3	1.29E-06	0.86	3.48	-	1098.5
AHQ-1-14, 4148	K.AGNNMLLVGVHGPR.T	1435.68033	2	2.92E-05	0.84	3.23	-	929.6
AHQ-1-14- , 3458 - 3482	K.AGNNMLLVGVHGPR.T	1435.68033	3	2.25E-08	0.92	4.47	-	1137.6
AHQ-1-14- , 3454 - 3504	K.AGNNMLLVGVHGPR.T	1435.68033	2	5.13E-09	0.85	3.35	-	739.4
AHQ-1-14, 3812	K.AGNNM*LLVGVHGPR.T	1451.67973	3	3.62E-07	0.94	3.58	-	1931.6
AHQ-1-14, 3638 - 3712	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.74E-05	0.78	3.03	-	710.4
AHQ-1-14- , 2782 - 2846	K.AGNNM*LLVGVHGPR.T	1451.67973	3	3.20E-06	0.90	3.90	-	1125.6
AHQ-1-5, 3123	K.AGNNMLLVGVHGPR.T	1435.68033	3	6.10E-06	0.90	3.29	-	1767.3
AHQ-1-14- , 3206 - 3211	K.AGNNMLLVGVHGPR.T	1435.68033	2	7.65E-06	0.76	3.27	-	552.0
AHQ-1-14- , 3227	K.AGNNMLLVGVHGPR.T	1435.68033	1	2.21E-07	0.45	2.29	-	126.1
AHQ-1-14- , 2778 - 2843	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.32E-04	0.88	3.60	-	881.9
AHQ-1-14- , 3207	K.AGNNMLLVGVHGPR.T	1435.68033	3	2.25E-08	0.92	3.79	-	1532.3
AHQ-1-2, 1761 - 1838	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	4.90E-04	0.80	3.53	-	607.1
AHQ-1-4, 1668	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	5.61E-05	0.53	2.92	-	653.5
AHQ-1-5, 2170	K.AGVAPLQVK.V	883.07036	2	1.35E-04	0.63	2.65	-	442.2
AHQ-1-4, 2304	K.AGVAPLQVK.V	883.07036	2	3.27E-04	0.63	2.54	-	529.1
AHQ-1-3, 2379	K.AGVAPLQVK.V	883.07036	1	7.75E-04	0.28	1.95	-	480.4
AHQ-1-1, 2451 - 2485	K.AGVAPLQVK.V	883.07036	2	1.18E-04	0.69	2.51	-	513.1
AHQ-1-3, 2310 - 2311	K.AGVAPLQVK.V	883.07036	2	2.98E-05	0.89	3.16	-	737.1
AHQ-1-2, 7474 - 7534	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	4.69E-05	0.97	6.18	-	1447.3
AHQ-1-2, 6747	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	1.70E-04	0.87	3.79	-	1098.0
AHQ-1-4, 2651 - 2663	K.AHVVPCFDASK.V	1232.39073	2	2.64E-04	0.70	2.61	-	503.7
AHQ-1-3, 2633	K.AHVVPCFDASK.V	1232.39073	2	5.38E-05	0.70	2.58	-	507.4
AHQ-1-1, 2787 - 2805	K.AHVVPCFDASK.V	1232.39073	2	6.17E-08	0.86	2.87	-	851.0
AHQ-1-2, 2726	K.AHVVPCFDASK.V	1232.39073	2	1.73E-04	0.66	2.63	-	549.2
AHQ-1-4, 6498 - 6570	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.67E-15	0.95	5.66	-	958.5
AHQ-1-7, 6437 - 6440	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.24E-06	0.94	5.42	-	811.5
AHQ-1-6, 6227 - 6306	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.56E-12	0.95	5.70	-	885.5
AHQ-1-4, 6362 - 6427	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.31E-05	0.66	3.53	-	408.7
AHQ-1-6, 6318 - 6382	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.42E-11	0.94	5.41	-	784.8
AHQ-1-9, 6366	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.47E-07	0.88	4.43	-	646.8
AHQ-1-1, 6116 - 6183	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.26E-06	0.89	4.70	-	666.0
AHQ-1-3, 6330 - 6397	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.98E-06	0.90	4.64	-	898.5
AHQ-1-1, 6247 - 6307	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.63E-06	0.88	4.59	-	529.4
AHQ-1-1, 6367 - 6431	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.97E-06	0.88	4.88	-	453.0
AHQ-1-2, 6286 - 6337	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.44E-05	0.93	5.27	-	766.3
AHQ-1-3, 6213 - 6257	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.16E-08	0.87	4.52	-	506.6
AHQ-1-5, 6518 - 6534	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.04E-12	0.89	4.67	-	497.6
AHQ-1-10, 5663	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.77E-09	0.60	3.16	-	325.7
AHQ-1-3, 6463 - 6542	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.96E-09	0.87	4.21	-	748.0
AHQ-1-5, 6363 - 6442	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.64E-08	0.95	5.84	-	951.2
AHQ-1-2, 6622 - 6699	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.10E-05	0.92	5.12	-	512.8
AHQ-1-8, 6406 - 6482	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.29E-07	0.87	4.43	-	486.4
AHQ-1-2, 6421 - 6489	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.34E-10	0.95	5.32	-	993.4
AHQ-1-5, 6277	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.53E-06	0.93	5.12	-	817.1
AHQ-1-2, 6529 - 6593	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.44E-11	0.96	6.19	-	937.6
AHQ-1-9, 6282	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.99E-11	0.94	5.89	-	625.5
AHQ-1-2, 1506	R.ALTQTGGPHVK.A	1109.26067	1	5.11E-05	0.05	1.89	-	169.8
AHQ-1-2, 1542 - 1602	R.ALTQTGGPHVK.A	1109.26067	1	6.28E-04	0.02	1.91	-	224.1
AHQ-1-3, 1547	R.ALTQTGGPHVK.A	1109.26067	2	9.04E-04	0.72	2.93	-	531.1
AHQ-1-4, 3375 - 3396	R.ANLPQSFQVDTSK.A	1435.56409	2	3.87E-07	0.70	2.77	-	367.5
AHQ-1-5, 3254 - 3329	R.ANLPQSFQVDTSK.A	1435.56409	2	3.24E-08	0.93	3.89	-	679.9
AHQ-1-2, 3374 - 3449	R.ANLPQSFQVDTSK.A	1435.56409	2	5.69E-09	0.91	3.55	-	658.6
AHQ-1-1, 3592 - 3659	R.ANLPQSFQVDTSK.A	1435.56409	2	9.58E-09	0.89	3.61	-	597.8
AHQ-1-3, 3339 - 3411	R.ANLPQSFQVDTSK.A	1435.56409	2	3.44E-05	0.88	3.43	-	648.2
AHQ-1-9, 3162	R.ANLPQSFQVDTSK.A	1435.56409	2	1.17E-05	0.79	2.93	-	533.2
AHQ-1-9, 3171	R.ANLPQSFQVDTSK.A	1435.56409	1	4.89E-04	0.52	2.64	-	390.5
AHQ-1-2, 3654	R.ANLPQSFQVDTSK.A	1435.56409	1	1.12E-07	0.33	2.62	-	334.0
AHQ-1-7, 3281	R.ANLPQSFQVDTSK.A	1435.56409	1	2.44E-06	0.53	2.66	-	450.5
AHQ-1-2, 3462	R.ANLPQSFQVDTSK.A	1435.56409	1	8.70E-06	0.78	3.30	-	489.6
AHQ-1-3, 3351 - 3353	R.ANLPQSFQVDTSK.A	1435.56409	1	1.51E-04	0.33	2.20	-	368.5
AHQ-1-1, 3552	R.APSVANVGSHCDLSLK.I	1656.84249	2	6.68E-05	0.83	3.69	-	485.7
AHQ-1-4, 3499	R.APSVANVGSHCDLSLK.I	1656.84249	2	1.84E-04	0.92	4.23	-	546.3
AHQ-1-5, 3345 - 3346	R.APSVANVGSHCDLSLK.I	1656.84249	2	1.59E-06	0.94	4.87	-	841.5
AHQ-1-5, 1707	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	1.67E-04	0.94	4.48	-	846.9
AHQ-1-1, 2029 - 2036	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	3.37E-08	0.95	4.16	-	1018.9
AHQ-1-13- , 1951 - 2031	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	2.51E-05	0.92	4.29	-	541.5
AHQ-1-4, 1799	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	1.13E-06	0.84	3.90	-	543.3
AHQ-1-11, 1894 - 1898	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	4.24E-04	0.90	4.27	-	590.6
AHQ-1-3, 1801 - 1862	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	6.10E-05	0.96	4.87	-	982.2
AHQ-1-7, 1725	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	1.26E-05	0.90	4.10	-	632.4
AHQ-1-1, 3783	R.AWGPGLEGGVVGK.S	1227.39403	2	4.95E-04	0.92	3.84	-	834.5
AHQ-1-5, 3570	R.AWGPGLEGGVVGK.S	1227.39403	2	6.90E-05	0.93	3.48	-	1059.2
AHQ-1-2, 3831 - 3901	R.AWGPGLEGGVVGK.S	1227.39403	2	1.92E-05	0.91	4.24	-	730.8
AHQ-1-4, 3743	R.AWGPGLEGGVVGK.S	1227.39403	2	2.80E-06	0.87	3.47	-	781.8
AHQ-1-6, 3546	R.AWGPGLEGGVVGK.S	1227.39403	2	7.29E-04	0.84	3.29	-	573.9
AHQ-1-7, 3636	R.AWGPGLEGGVVGK.S	1227.39403	2	4.51E-05	0.88	2.97	-	994.9
AHQ-1-3, 3703	R.AWGPGLEGGVVGK.S	1227.39403	2	5.26E-05	0.83	3.21	-	617.4
AHQ-1-2, 3283 - 3358	R.AYGPGIEPTGNMVK.K	1434.64274	2	3.59E-04	0.68	2.74	-	639.7
AHQ-1-5, 3075 - 3149	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.72E-04	0.82	3.41	-	605.6
AHQ-1-1, 2872	R.AYGPGIEPTGNM*VK.K	1450.64214	2	6.38E-08	0.92	3.59	-	803.3
AHQ-1-4, 3503 - 3575	R.AYGPGIEPTGNMVK.K	1434.64274	2	6.45E-06	0.73	2.99	-	656.7
AHQ-1-7, 3152 - 3156	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.99E-04	0.85	3.79	-	533.4
AHQ-1-4, 2635 - 2748	R.AYGPGIEPTGNM*VK.K	1450.64214	2	2.20E-04	0.42	2.91	-	261.2
AHQ-1-3, 2617 - 2669	R.AYGPGIEPTGNM*VK.K	1450.64214	2	2.69E-04	0.63	3.26	-	341.3
AHQ-1-2, 6459	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	5.33E-06	0.74	3.12	-	505.8
AHQ-1-2, 6403	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	4.19E-10	0.97	5.50	-	1769.9
AHQ-1-2, 6339 - 6386	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.39E-04	0.96	5.15	-	874.2
AHQ-1-3, 6053	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	7.46E-08	0.90	3.72	-	818.6
AHQ-1-3, 6221 - 6253	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	5.56E-06	0.83	3.53	-	521.1
AHQ-1-3, 6235 - 6242	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.60E-09	0.96	5.62	-	1524.8
AHQ-1-1, 6139 - 6148	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.67E-05	0.82	3.88	-	442.4
AHQ-1-1, 6155	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	2.23E-11	0.96	4.56	-	1663.9
AHQ-1-5, 6337 - 6403	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.03E-06	0.79	3.73	-	394.4
AHQ-1-4, 6380	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.08E-07	0.85	3.84	-	452.1
AHQ-1-2, 6837	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	7.43E-06	0.77	3.59	-	544.0
AHQ-1-3, 6405 - 6469	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	4.23E-04	0.69	3.47	-	329.8
AHQ-1-2, 6599 - 6665	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	6.01E-05	0.54	3.34	-	472.6
AHQ-1-2, 6733 - 6753	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	6.62E-05	0.88	4.36	-	577.1
AHQ-1-3, 2994 - 2995	K.CSGPGLSPGMVR.A	1219.41699	2	7.34E-05	0.80	3.02	-	627.1
AHQ-1-1, 3084	K.CSGPGLSPGMVR.A	1219.41699	2	1.69E-07	0.63	2.79	-	544.7
AHQ-1-5, 5450 - 5451	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	7.81E-12	0.93	4.15	-	881.8
AHQ-1-2, 5149	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	9.21E-11	0.95	4.44	-	877.4
AHQ-1-5, 4953 - 4955	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	3.81E-05	0.77	3.22	-	542.6
AHQ-1-2, 5603 - 5670	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	2.18E-11	0.94	5.30	-	762.5

AHQ-1-1, 5121	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	1.83E-06	0.83	3.30	-	634.0
AHQ-1-4, 5063 - 5067	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	8.01E-06	0.84	3.85	-	692.9
AHQ-1-4, 5554	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	6.85E-08	0.87	3.79	-	804.6
AHQ-1-3, 5451	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	2.48E-09	0.85	3.95	-	859.4
AHQ-1-3, 5466	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	3.20E-07	0.92	3.56	-	1019.1
AHQ-1-6, 4902 - 4908	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	1.04E-04	0.82	4.04	-	239.6
AHQ-1-2, 5641 - 5645	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	1.43E-08	0.96	5.02	-	982.9
AHQ-1-2, 4775	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	2.02E-04	0.94	4.43	-	1186.3
AHQ-1-1, 4097	R.DAEM*PATEKDLAEDAPWK.K	2034.18987	2	2.09E-04	0.88	3.68	-	698.1
AHQ-1-1, 3596 - 3672	R.DAEM*PATEKDLAEDAPWKK.I	2162.36278	3	1.14E-05	0.71	3.11	-	606.7
AHQ-1-2, 4295	R.DAEMPATEKDLAEDAPWKK.I	2146.36338	2	1.48E-05	0.90	3.45	-	1129.0
AHQ-1-1, 4067 - 4131	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	5.48E-06	0.93	4.46	-	1331.1
AHQ-1-8, 4004	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	7.74E-06	0.89	3.86	-	985.8
AHQ-1-13, 3880 - 3949	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	3.87E-05	0.51	2.60	-	821.8
AHQ-1-5, 4025 - 4098	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.13E-08	0.97	5.52	-	1448.1
AHQ-1-10, 3656	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	7.43E-07	0.94	3.91	-	1440.8
AHQ-1-4, 4110 - 4183	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.89E-08	0.96	4.80	-	1347.9
AHQ-1-13- , 4008	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	2.46E-07	0.92	4.03	-	1048.9
AHQ-1-5, 4133	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	4.58E-08	0.92	3.70	-	1177.4
AHQ-1-3, 3978 - 4058	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.64E-05	0.94	4.32	-	1208.2
AHQ-1-1, 4208	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	6.91E-06	0.92	4.27	-	1035.7
AHQ-1-6, 3975	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.82E-06	0.84	3.56	-	756.7
AHQ-1-3, 4979	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	8.07E-06	0.84	2.81	-	1258.8
AHQ-1-2, 5117	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	2.97E-07	0.93	4.15	-	1264.7
AHQ-1-1, 4967	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	4.75E-07	0.92	3.77	-	1387.1
AHQ-1-7, 4372 - 4385	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.50E-08	0.93	4.11	-	1275.1
AHQ-1-2, 4618 - 4637	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	4.50E-12	0.93	4.30	-	1328.5
AHQ-1-10, 3953	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.95E-07	0.88	3.98	-	1006.0
AHQ-1-2, 4851	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.32E-06	0.71	3.22	-	635.8
AHQ-1-1, 4492 - 4560	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	3.70E-04	0.72	3.03	-	805.3
AHQ-1-1, 4491 - 4555	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.31E-10	0.96	4.70	-	1529.9
AHQ-1-8, 4223	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	9.43E-05	0.89	4.15	-	903.3
AHQ-1-9, 4250 - 4264	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.78E-05	0.89	4.09	-	912.5
AHQ-1-5, 4395	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	1.24E-08	0.79	3.03	-	938.1
AHQ-1-11, 4072	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.62E-12	0.94	4.51	-	1105.8
AHQ-1-3, 4454 - 4522	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.36E-06	0.94	4.40	-	1246.9
AHQ-1-2, 4751 - 4827	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.51E-09	0.95	4.36	-	1179.6
AHQ-1-3, 4687	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	7.16E-07	0.78	3.12	-	897.7
AHQ-1-6, 4308 - 4314	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.55E-07	0.94	3.83	-	1515.9
AHQ-1-4, 4483 - 4562	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.36E-05	0.74	2.96	-	859.4
AHQ-1-2, 4613 - 4685	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.51E-06	0.96	4.36	-	1566.6
AHQ-1-1, 4636 - 4717	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.50E-09	0.94	4.27	-	1109.4
AHQ-1-6, 4319	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	2.48E-06	0.80	3.28	-	985.9
AHQ-1-2, 4706	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	2.26E-06	0.90	3.73	-	1489.7
AHQ-1-7, 4620	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	2.01E-04	0.63	3.04	-	420.6
AHQ-1-5, 4611 - 4687	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.83E-11	0.95	4.16	-	1497.6
AHQ-1-1, 4704	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	9.31E-06	0.58	3.17	-	544.0
AHQ-1-5, 4402	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	8.54E-08	0.76	2.58	-	1158.2
AHQ-1-4, 4856	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	6.43E-05	0.61	3.01	-	660.8
AHQ-1-3, 4627	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.57E-13	0.96	4.34	-	1573.1
AHQ-1-1, 4603	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	3.21E-10	0.94	4.34	-	1256.9
AHQ-1-5, 4882	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.67E-07	0.81	3.40	-	757.0
AHQ-1-1, 4361 - 4435	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	2.38E-09	0.96	4.56	-	1457.5
AHQ-1-2, 4759	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.42E-06	0.95	4.38	-	1514.4
AHQ-1-5, 4753	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	2.39E-04	0.75	2.94	-	1012.6
AHQ-1-3, 1883 - 1945	R.DAPQDFHPDR.V	1198.22650	2	6.17E-05	0.59	2.58	-	553.2
AHQ-1-1, 4881 - 4963	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.28E-04	0.78	4.03	-	511.6
AHQ-1-1, 5055	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.22E-05	0.38	3.01	-	305.3
AHQ-1-5, 4958 - 5029	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.52E-04	0.91	4.82	-	616.1
AHQ-1-5, 5255	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.15E-05	0.92	4.49	-	759.3
AHQ-1-4, 4996 - 5003	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.49E-05	0.90	4.55	-	608.2
AHQ-1-3, 4909 - 4910	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	9.49E-05	0.87	4.10	-	604.1
AHQ-1-2, 5046 - 5050	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.61E-05	0.89	4.55	-	587.2
AHQ-1-6, 4927 - 5002	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	6.26E-04	0.78	3.42	-	602.2
AHQ-1-6, 5088	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.22E-06	0.60	3.47	-	395.4
AHQ-1-8, 4942 - 4946	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.29E-04	0.87	4.56	-	650.7
AHQ-1-5, 5099 - 5178	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	9.63E-06	0.88	4.52	-	590.1
AHQ-1-14, 3353	K.DKGEYTLVVK.W	1152.32223	1	7.34E-04	0.37	2.39	-	613.4
AHQ-1-11, 2416	K.DKGEYTLVVK.W	1152.32223	1	2.31E-04	0.34	2.16	-	572.9
AHQ-1-12, 2469	K.DKGEYTLVVK.W	1152.32223	2	9.56E-04	0.74	2.52	-	615.9
AHQ-1-1, 2637 - 2641	K.DKGEYTLVVK.W	1152.32223	1	4.77E-04	0.48	2.76	-	509.1
AHQ-1-14- , 2466 - 2532	K.DKGEYTLVVK.W	1152.32223	2	2.11E-06	0.75	2.79	-	557.6
AHQ-1-1, 3315	K.DNGNGTYSCSYVPR.K	1591.64109	2	8.57E-05	0.81	2.81	-	1063.6
AHQ-1-2, 3427	K.DNGNGTYSCSYVPR.K	1591.64109	2	1.13E-04	0.84	2.72	-	1111.9
AHQ-1-2, 3223	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	1.54E-05	0.71	3.15	-	526.3
AHQ-1-3, 3093 - 3095	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	5.96E-07	0.92	3.94	-	1027.2
AHQ-1-2, 3265	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.55E-07	0.96	4.56	-	1092.4
AHQ-1-3, 3342	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.83E-06	0.79	3.00	-	941.7
AHQ-1-7, 3009	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.28E-05	0.78	2.84	-	812.0
AHQ-1-1, 3123 - 3203	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.76E-04	0.94	3.66	-	1340.2
AHQ-1-2, 3135 - 3205	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	4.65E-05	0.70	3.19	-	413.6
AHQ-1-2, 3381 - 3447	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.27E-07	0.84	3.33	-	617.1
AHQ-1-4, 3034 - 3110	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.60E-06	0.90	3.73	-	961.4
AHQ-1-6, 2984	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	4.28E-04	0.76	2.81	-	852.3
AHQ-1-3, 3185	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.16E-06	0.86	3.58	-	907.2
AHQ-1-1, 3280	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	4.05E-06	0.85	3.39	-	793.2
AHQ-1-9, 2899 - 2904	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.60E-05	0.40	2.70	-	511.1
AHQ-1-6, 3334	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	6.09E-09	0.65	3.60	-	269.7
AHQ-1-4, 3479	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	2.81E-06	0.96	4.50	-	1331.4
AHQ-1-5, 3353	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	2.15E-07	0.73	3.37	-	290.2
AHQ-1-8, 3201 - 3202	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	1.40E-04	0.68	3.63	-	302.2
AHQ-1-5, 3350 - 3373	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	6.13E-08	0.97	4.27	-	1785.9
AHQ-1-1, 3487 - 3556	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	8.95E-08	0.96	4.34	-	1831.9
AHQ-1-3, 3461 - 3474	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	4.31E-06	0.94	4.16	-	1047.8
AHQ-1-6, 3318 - 3319	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.23E-10	0.95	4.17	-	1356.5
AHQ-1-6, 2530 - 2532	R.EATTEFSVDAR.A	1226.27493	2	1.67E-04	0.83	2.94	-	975.1
AHQ-1-2, 2701 - 2774	R.EATTEFSVDAR.A	1226.27493	2	1.09E-05	0.88	3.30	-	830.4
AHQ-1-1, 2731 - 2761	R.EATTEFSVDAR.A	1226.27493	2	7.18E-05	0.86	3.38	-	771.7
AHQ-1-3, 2611	R.EATTEFSVDAR.A	1226.27493	2	8.87E-06	0.86	3.04	-	991.7
AHQ-1-6, 6308 - 6383	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.71E-09	0.95	5.41	-	1068.2
AHQ-1-5, 6461 - 6538	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.83E-08	0.95	5.89	-	699.0
AHQ-1-3, 6473 - 6553	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.84E-07	0.87	4.41	-	508.3
AHQ-1-8, 6510	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.01E-08	0.89	4.73	-	647.7
AHQ-1-3, 6322 - 6401	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.03E-07	0.96	6.83	-	800.4
AHQ-1-9, 6371	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.87E-06	0.67	3.57	-	362.4
AHQ-1-1, 6259 - 6331	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	5.91E-07	0.95	6.00	-	735.8
AHQ-1-1, 6347 - 6405	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	5.13E-10	0.88	4.66	-	522.7

AHQ-1-7, 6461 - 6533	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.00E-04	0.91	4.94	-	527.6
AHQ-1-4, 6488 - 6558	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.00E-08	0.94	5.32	-	755.0
AHQ-1-2, 6470 - 6537	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.39E-09	0.93	5.36	-	705.9
AHQ-1-4, 6606 - 6623	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	7.20E-11	0.92	5.35	-	582.2
AHQ-1-2, 6601 - 6666	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.12E-05	0.91	5.05	-	524.2
AHQ-1-5, 5174 - 5243	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.05E-05	0.74	3.42	-	409.3
AHQ-1-2, 5334	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	3.97E-04	0.95	5.11	-	1463.9
AHQ-1-2, 5266 - 5345	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.94E-09	0.90	3.81	-	1069.6
AHQ-1-3, 5125 - 5206	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.08E-09	0.91	4.02	-	947.6
AHQ-1-10, 4569 - 4583	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.04E-06	0.86	3.69	-	677.9
AHQ-1-2, 5026	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.29E-06	0.86	3.89	-	620.7
AHQ-1-1, 5211	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	1.16E-05	0.95	4.90	-	1523.1
AHQ-1-1, 5153 - 5219	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	6.59E-08	0.92	3.98	-	1140.3
AHQ-1-1, 4872	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.54E-07	0.39	3.18	-	378.6
AHQ-1-9, 5008 - 5027	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	7.70E-06	0.93	4.18	-	983.4
AHQ-1-6, 5099	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.62E-06	0.88	3.78	-	886.7
AHQ-1-7, 5078 - 5153	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	7.59E-06	0.59	2.83	-	484.3
AHQ-1-7, 3913	R.ENGVYLIDVK.F	1150.30633	1	4.66E-04	0.11	1.93	-	252.4
AHQ-1-5, 3898 - 3969	R.ENGVYLIDVK.F	1150.30633	2	5.49E-04	0.67	2.79	-	471.3
AHQ-1-4, 4072	R.ENGVYLIDVK.F	1150.30633	2	2.75E-04	0.86	3.19	-	604.4
AHQ-1-5, 1490	K.ETGEHLVHVK.K	1149.28166	1	7.60E-05	0.30	2.38	-	259.6
AHQ-1-13- , 3539 - 3547	K.FADQHVPGSPFSVK.V	1516.68203	2	4.53E-06	0.80	3.28	-	586.4
AHQ-1-6, 3350	K.FADQHVPGSPFSVK.V	1516.68203	2	1.26E-06	0.87	3.65	-	504.4
AHQ-1-3, 3542	K.FADQHVPGSPFSVK.V	1516.68203	3	1.65E-07	0.91	3.74	-	1105.9
AHQ-1-5, 3378	K.FADQHVPGSPFSVK.V	1516.68203	3	1.60E-07	0.91	4.09	-	957.7
AHQ-1-1, 3617	K.FADQHVPGSPFSVK.V	1516.68203	2	1.86E-05	0.87	3.29	-	614.2
AHQ-1-1, 3619	K.FADQHVPGSPFSVK.V	1516.68203	3	1.60E-05	0.95	3.90	-	1535.5
AHQ-1-7, 3388 - 3390	K.FADQHVPGSPFSVK.V	1516.68203	2	6.99E-07	0.72	3.23	-	399.2
AHQ-1-3, 3525	K.FADQHVPGSPFSVK.V	1516.68203	2	7.03E-05	0.76	3.31	-	524.2
AHQ-1-4, 3551	K.FADQHVPGSPFSVK.V	1516.68203	3	2.04E-08	0.95	4.17	-	1600.1
AHQ-1-6, 3352	K.FADQHVPGSPFSVK.V	1516.68203	3	2.06E-06	0.87	3.84	-	835.4
AHQ-1-4, 3538	K.FADQHVPGSPFSVK.V	1516.68203	2	3.37E-04	0.81	3.53	-	400.1
AHQ-1-5, 5623 - 5627	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.03E-06	0.93	4.31	-	1033.5
AHQ-1-12, 5283	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.74E-06	0.95	5.14	-	1101.8
AHQ-1-13, 5197	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.21E-04	0.87	4.19	-	777.1
AHQ-1-4, 5811 - 5891	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.42E-10	0.94	5.09	-	838.7
AHQ-1-9, 5392 - 5459	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.86E-04	0.84	4.28	-	590.0
AHQ-1-1, 5499 - 5504	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.07E-04	0.89	4.49	-	738.3
AHQ-1-4, 5747 - 5770	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.50E-08	0.95	4.69	-	963.7
AHQ-1-12, 5255	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.52E-05	0.75	3.54	-	441.2
AHQ-1-2, 5926	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.56E-06	0.87	3.42	-	785.7
AHQ-1-10, 4900	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.66E-04	0.73	3.50	-	550.6
AHQ-1-2, 5893 - 5961	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.97E-06	0.91	4.72	-	801.3
AHQ-1-1, 5609 - 5671	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.50E-05	0.91	4.63	-	779.3
AHQ-1-3, 5709 - 5773	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	7.42E-11	0.93	5.72	-	779.5
AHQ-1-2, 5793 - 5861	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	7.60E-10	0.98	6.03	-	1506.3
AHQ-1-1, 5675 - 5680	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.94E-12	0.97	6.01	-	1276.8
AHQ-1-3, 5657 - 5685	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.72E-05	0.97	5.61	-	1228.2
AHQ-1-1, 5735 - 5799	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	7.84E-08	0.85	4.24	-	754.3
AHQ-1-2, 5757 - 5826	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	6.74E-10	0.95	5.75	-	718.9
AHQ-1-13- , 5615	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.95E-04	0.87	4.22	-	657.5
AHQ-1-8, 5415 - 5432	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.95E-07	0.94	5.23	-	1051.1
AHQ-1-3, 5578 - 5645	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.72E-07	0.94	4.94	-	872.2
AHQ-1-2, 5617 - 5691	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.70E-05	0.95	5.64	-	1062.9
AHQ-1-5, 5201 - 5269	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	5.18E-08	0.94	5.26	-	663.2
AHQ-1-8, 5086	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	5.53E-08	0.96	5.17	-	865.4
AHQ-1-5, 5401 - 5438	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	2.87E-07	0.90	4.34	-	533.2
AHQ-1-9, 5034	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	2.00E-04	0.83	3.13	-	777.6
AHQ-1-6, 5146	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	5.79E-04	0.74	2.90	-	549.7
AHQ-1-1, 3937 - 4012	K.FNGTHIPGSPFK.I	1302.46259	2	9.80E-06	0.62	2.69	-	486.8
AHQ-1-3, 3879	K.FNGTHIPGSPFK.I	1302.46259	2	1.58E-05	0.74	3.02	-	580.8
AHQ-1-4, 3894	K.FNGTHIPGSPFK.I	1302.46259	2	1.54E-06	0.44	2.58	-	438.5
AHQ-1-2, 4030	K.FNGTHIPGSPFK.I	1302.46259	2	2.20E-06	0.84	2.77	-	797.0
AHQ-1-1, 3837	K.FNGTHIPGSPFK.I	1302.46259	2	1.27E-07	0.87	3.30	-	761.4
AHQ-1-5, 3729	K.FNGTHIPGSPFK.I	1302.46259	2	1.19E-05	0.86	3.58	-	558.6
AHQ-1-5, 2889	R.FVPAEMGTHTVSVK.Y	1503.74821	2	9.36E-06	0.92	3.75	-	800.1
AHQ-1-1, 3148	R.FVPAEMGTHTVSVK.Y	1503.74821	2	7.75E-08	0.74	2.79	-	622.3
AHQ-1-6, 2914	R.FVPAEMGTHTVSVK.Y	1503.74821	2	9.30E-05	0.75	2.63	-	562.1
AHQ-1-4, 6924 - 6938	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	1.11E-05	0.89	4.14	-	524.5
AHQ-1-3, 6250	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	6.03E-05	0.39	2.64	-	280.2
AHQ-1-2, 6266	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	1.15E-05	0.93	4.59	-	743.4
AHQ-1-6, 3283 - 3298	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.87E-07	0.86	3.10	-	969.9
AHQ-1-8, 3180	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	4.56E-05	0.87	3.24	-	793.1
AHQ-1-1, 3621 - 3649	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.06E-04	0.88	3.41	-	975.4
AHQ-1-3, 3631	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.38E-05	0.21	2.66	-	255.5
AHQ-1-2, 3455 - 3529	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	7.02E-07	0.93	4.57	-	828.5
AHQ-1-3, 3513	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.73E-05	0.51	2.57	-	468.7
AHQ-1-3, 3361 - 3429	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	6.27E-06	0.89	3.59	-	856.0
AHQ-1-1, 3464 - 3535	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	6.68E-07	0.85	3.68	-	648.1
AHQ-1-5, 3306 - 3330	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.07E-06	0.86	3.33	-	833.6
AHQ-1-4, 3442 - 3448	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.82E-04	0.74	3.28	-	616.2
AHQ-1-2, 3674 - 3750	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	7.34E-06	0.88	3.68	-	897.7
AHQ-1-3, 3446 - 3499	K.GKLDVQFSGLTK.G	1293.49392	2	2.81E-05	0.90	3.53	-	848.1
AHQ-1-1, 5067 - 5137	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	3	1.07E-05	0.72	3.27	-	567.0
AHQ-1-3, 5007 - 5081	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	5.52E-09	0.93	4.36	-	1112.6
AHQ-1-1, 5216 - 5279	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.79E-11	0.96	5.09	-	1182.3
AHQ-1-2, 5137 - 5205	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.84E-08	0.93	4.48	-	882.8
AHQ-1-1, 5064 - 5135	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.90E-10	0.96	5.17	-	944.5
AHQ-1-1, 4931 - 4995	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	4.39E-08	0.93	4.37	-	824.2
AHQ-1-4, 5187	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.81E-05	0.79	3.42	-	535.8
AHQ-1-1, 6437	K.GLVEPVDVVDNADGTQTVNYVPSREGPYSISVLYGDEEVPR.S	4437.77937	3	5.47E-08	0.82	3.70	-	541.5
AHQ-1-2, 6735 - 6738	K.GLVEPVDVVDNADGTQTVNYVPSREGPYSISVLYGDEEVPR.S	4437.77937	3	2.26E-13	0.95	5.92	-	882.7
AHQ-1-4, 2228 - 2235	K.GTVEPQLEAR.G	1100.20741	2	1.06E-04	0.80	2.92	-	555.5
AHQ-1-3, 2231	K.GTVEPQLEAR.G	1100.20741	2	3.40E-05	0.73	2.89	-	553.5
AHQ-1-6, 2115 - 2119	K.GTVEPQLEAR.G	1100.20741	2	3.35E-06	0.75	2.95	-	417.1
AHQ-1-2, 2315 - 2385	K.GTVEPQLEAR.G	1100.20741	2	1.73E-04	0.73	3.03	-	493.2
AHQ-1-1, 2367	K.GTVEPQLEAR.G	1100.20741	2	4.08E-04	0.78	2.76	-	566.6
AHQ-1-2, 5399 - 5421	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.06E-10	0.96	5.20	-	1149.1
AHQ-1-3, 5186 - 5255	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	3.60E-05	0.94	4.26	-	1043.4
AHQ-1-2, 5143	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.23E-05	0.94	4.31	-	1040.9
AHQ-1-1, 5681	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	4.69E-04	0.96	5.20	-	1058.9
AHQ-1-4, 5272 - 5283	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	6.43E-06	0.96	4.69	-	1263.8
AHQ-1-4, 5688	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	7.07E-05	0.97	4.93	-	1619.4
AHQ-1-2, 5393	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	4.03E-05	0.87	3.93	-	1148.9
AHQ-1-1, 5333 - 5336	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	8.59E-05	0.84	3.78	-	946.8
AHQ-1-1, 5327	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	3.79E-05	0.95	5.05	-	1009.2
AHQ-1-2, 5781 - 5782	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	4.53E-04	0.96	4.53	-	1244.7

AHQ-1-5, 5185	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.15E-06	0.95	4.65	-	1187.8
AHQ-1-2, 5786 - 5795	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	3	2.52E-05	0.72	3.99	-	432.5
AHQ-1-1, 4063	R.IANLQTDLSDGLR.L	1416.56231	2	2.21E-06	0.94	4.24	-	964.9
AHQ-1-9, 4111	R.IANLQTDLSDGLR.L	1416.56231	2	4.03E-07	0.92	4.14	-	792.1
AHQ-1-2, 4465 - 4541	R.IANLQTDLSDGLR.L	1416.56231	2	8.79E-07	0.92	4.15	-	827.2
AHQ-1-3, 3917	R.IANLQTDLSDGLR.L	1416.56231	2	2.21E-07	0.95	3.93	-	1246.3
AHQ-1-10, 3864	R.IANLQTDLSDGLR.L	1416.56231	2	1.17E-07	0.92	3.36	-	976.4
AHQ-1-2, 4355	R.IANLQTDLSDGLR.L	1416.56231	2	3.39E-06	0.95	4.34	-	1190.9
AHQ-1-1, 4247	R.IANLQTDLSDGLR.L	1416.56231	2	7.47E-06	0.95	4.30	-	1336.2
AHQ-1-5, 4233 - 4234	R.IANLQTDLSDGLR.L	1416.56231	2	5.34E-07	0.94	4.41	-	948.2
AHQ-1-2, 4139	R.IANLQTDLSDGLR.L	1416.56231	2	8.90E-07	0.95	3.86	-	1237.4
AHQ-1-1, 3963	R.IANLQTDLSDGLR.L	1416.56231	2	9.99E-07	0.92	3.66	-	926.2
AHQ-1-1, 4372	R.IANLQTDLSDGLR.L	1416.56231	1	5.66E-04	0.43	2.48	-	304.6
AHQ-1-5, 3843	R.IANLQTDLSDGLR.L	1416.56231	2	4.75E-05	0.92	3.83	-	915.1
AHQ-1-1, 4516	R.IANLQTDLSDGLR.L	1416.56231	2	6.56E-06	0.90	3.57	-	741.6
AHQ-1-13- , 4299 - 4308	R.IANLQTDLSDGLR.L	1416.56231	2	6.30E-07	0.94	4.01	-	994.7
AHQ-1-3, 4214	R.IANLQTDLSDGLR.L	1416.56231	2	2.94E-06	0.94	4.24	-	966.9
AHQ-1-2, 4061	R.IANLQTDLSDGLR.L	1416.56231	1	2.49E-05	0.39	2.63	-	244.5
AHQ-1-2, 4053 - 4066	R.IANLQTDLSDGLR.L	1416.56231	2	3.31E-06	0.94	4.02	-	1140.4
AHQ-1-2, 4614 - 4670	R.IANLQTDLSDGLR.L	1416.56231	2	1.26E-07	0.93	3.37	-	1227.0
AHQ-1-8, 4136	R.IANLQTDLSDGLR.L	1416.56231	2	1.51E-04	0.82	2.81	-	884.0
AHQ-1-13, 4107	R.IANLQTDLSDGLR.L	1416.56231	2	2.57E-08	0.95	4.02	-	1127.1
AHQ-1-6, 4166 - 4186	R.IANLQTDLSDGLR.L	1416.56231	2	8.24E-08	0.92	4.01	-	908.5
AHQ-1-11, 3939	R.IANLQTDLSDGLR.L	1416.56231	2	3.57E-04	0.92	3.82	-	1021.1
AHQ-1-7, 4242 - 4256	R.IANLQTDLSDGLR.L	1416.56231	2	6.48E-07	0.89	3.42	-	849.7
AHQ-1-12, 4073	R.IANLQTDLSDGLR.L	1416.56231	2	1.77E-04	0.92	3.99	-	881.6
AHQ-1-6, 3771	R.IANLQTDLSDGLR.L	1416.56231	2	1.75E-05	0.92	3.30	-	1384.8
AHQ-1-4, 3970	R.IANLQTDLSDGLR.L	1416.56231	2	1.04E-05	0.93	3.71	-	1064.4
AHQ-1-3, 4313 - 4383	R.IANLQTDLSDGLR.L	1416.56231	2	3.77E-06	0.92	4.12	-	823.6
AHQ-1-4, 4371	R.IANLQTDLSDGLR.L	1416.56231	2	2.31E-08	0.94	4.72	-	829.9
AHQ-1-3, 4514	R.IANLQTDLSDGLR.L	1416.56231	2	3.14E-05	0.78	2.73	-	727.0
AHQ-1-1, 5867 - 5875	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.64E-05	0.93	4.66	-	639.4
AHQ-1-4, 4240 - 4270	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.23E-04	0.98	5.58	-	1809.2
AHQ-1-6, 4103 - 4108	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.04E-05	0.98	5.90	-	1880.7
AHQ-1-5, 5946 - 5955	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.29E-13	0.97	5.08	-	1337.7
AHQ-1-1, 5621	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	1.74E-04	0.89	4.26	-	703.6
AHQ-1-1, 5584 - 5643	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	7.90E-08	0.98	5.47	-	1963.8
AHQ-1-5, 5611	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	9.24E-07	0.93	4.57	-	1260.8
AHQ-1-5, 5589 - 5645	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.04E-09	0.98	5.93	-	2116.8
AHQ-1-5, 4154 - 4225	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.17E-05	0.97	4.94	-	1829.4
AHQ-1-3, 5605	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.41E-09	0.98	5.47	-	1859.6
AHQ-1-1, 4193 - 4261	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	3.24E-07	0.98	5.82	-	2145.4
AHQ-1-7, 5582	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.50E-08	0.96	5.09	-	1115.8
AHQ-1-6, 5506	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.95E-08	0.97	5.34	-	1695.0
AHQ-1-5, 5130	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.07E-07	0.78	3.42	-	599.7
AHQ-1-5, 4951	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.57E-07	0.91	3.80	-	1030.1
AHQ-1-8, 5471	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.20E-11	0.97	5.21	-	1696.4
AHQ-1-12, 5249	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.55E-12	0.98	5.75	-	1652.8
AHQ-1-3, 4225	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.31E-04	0.95	4.33	-	1407.1
AHQ-1-3, 2549	K.IVGPSGAAVPCK.V	1157.36530	2	1.34E-05	0.82	2.97	-	601.2
AHQ-1-5, 2466	K.IVGPSGAAVPCK.V	1157.36530	2	3.60E-07	0.91	3.51	-	886.1
AHQ-1-2, 2625	K.IVGPSGAAVPCK.V	1157.36530	2	1.95E-08	0.92	3.43	-	978.9
AHQ-1-4, 2571	K.IVGPSGAAVPCK.V	1157.36530	2	1.92E-06	0.90	3.94	-	716.6
AHQ-1-3, 4243 - 4319	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.05E-07	0.93	4.71	-	1256.9
AHQ-1-3, 4259 - 4277	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.69E-05	0.89	4.41	-	415.5
AHQ-1-4, 4320 - 4322	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	3.97E-05	0.91	4.46	-	416.1
AHQ-1-4, 4314 - 4324	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	4.74E-04	0.94	4.97	-	1463.6
AHQ-1-1, 4424	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.25E-04	0.82	3.94	-	739.6
AHQ-1-5, 4210	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.43E-07	0.81	3.95	-	785.2
AHQ-1-1, 4295 - 4296	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	5.09E-07	0.92	4.84	-	335.3
AHQ-1-1, 4285 - 4360	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	8.39E-08	0.94	5.19	-	1250.6
AHQ-1-2, 4391 - 4462	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.02E-10	0.92	5.08	-	1015.9
AHQ-1-6, 4139	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.23E-04	0.94	4.57	-	1251.2
AHQ-1-2, 4393 - 4463	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.68E-05	0.90	4.30	-	579.7
AHQ-1-2, 4533	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.99E-08	0.84	3.58	-	969.4
AHQ-1-2, 4538	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	9.81E-04	0.88	3.81	-	467.8
AHQ-1-1, 4479 - 4549	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	7.95E-06	0.91	4.38	-	816.5
AHQ-1-1, 4475 - 4547	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	4.67E-06	0.91	4.83	-	991.6
AHQ-1-4, 4467 - 4472	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.93E-06	0.94	5.01	-	727.0
AHQ-1-2, 4610 - 4686	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.30E-05	0.66	3.28	-	822.7
AHQ-1-8, 4148	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	5.95E-05	0.93	4.56	-	732.9
AHQ-1-1, 4523 - 4569	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	8.83E-13	0.97	5.95	-	2059.0
AHQ-1-4, 4462	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	5.09E-09	0.98	5.86	-	2417.4
AHQ-1-3, 4441 - 4445	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	5.75E-09	0.97	5.63	-	1853.1
AHQ-1-1, 4428 - 4497	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.06E-08	0.96	5.51	-	1723.3
AHQ-1-5, 4237	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	3.32E-04	0.57	2.83	-	331.5
AHQ-1-5, 4315 - 4342	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.65E-10	0.95	5.01	-	1601.0
AHQ-1-1, 4500	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.59E-07	0.74	3.37	-	402.7
AHQ-1-3, 3447 - 3451	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	1.03E-05	0.95	4.77	-	923.9
AHQ-1-1, 3543	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	8.24E-05	0.92	4.67	-	638.7
AHQ-1-4, 3622	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.65E-04	0.82	3.46	-	875.6
AHQ-1-1, 3643 - 3709	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.19E-08	0.91	4.24	-	958.3
AHQ-1-2, 3722	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	1.56E-05	0.80	3.41	-	485.7
AHQ-1-3, 3439 - 3457	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.88E-08	0.94	4.62	-	1266.4
AHQ-1-6, 3280	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	3.45E-04	0.86	3.79	-	872.8
AHQ-1-2, 3545 - 3613	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.31E-08	0.95	5.50	-	1029.0
AHQ-1-2, 3690 - 3761	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.15E-04	0.96	4.84	-	1467.5
AHQ-1-1, 3540	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.60E-08	0.95	5.03	-	1110.2
AHQ-1-2, 4137 - 4165	K.LDVQFSGLTK.G	1108.26945	2	5.74E-05	0.92	3.70	-	912.7
AHQ-1-1, 4059	K.LDVQFSGLTK.G	1108.26945	2	8.39E-07	0.93	3.55	-	1088.4
AHQ-1-3, 4006	K.LDVQFSGLTK.G	1108.26945	2	8.22E-07	0.94	3.70	-	1173.4
AHQ-1-3, 4005 - 4081	K.LDVQFSGLTK.G	1108.26945	1	2.59E-04	0.08	2.03	-	222.8
AHQ-1-4, 4042	K.LDVQFSGLTK.G	1108.26945	1	3.12E-05	0.46	2.31	-	329.4
AHQ-1-2, 4151	K.LDVQFSGLTK.G	1108.26945	1	4.57E-05	0.16	2.17	-	213.9
AHQ-1-4, 4044 - 4060	K.LDVQFSGLTK.G	1108.26945	2	2.24E-04	0.83	3.11	-	787.0
AHQ-1-2, 4138	K.LDVQFSGLTK.G	1108.26945	1	3.96E-06	0.09	1.90	-	224.5
AHQ-1-1, 4068	K.LDVQFSGLTK.G	1108.26945	1	4.68E-05	0.16	2.09	-	233.7
AHQ-1-6, 4788 - 4798	K.LPQLPITNFSR.D	1286.50461	2	3.91E-05	0.88	3.45	-	622.1
AHQ-1-3, 4949 - 4959	K.LPQLPITNFSR.D	1286.50461	2	3.59E-05	0.75	2.64	-	604.6
AHQ-1-2, 5085	K.LPQLPITNFSR.D	1286.50461	2	5.57E-04	0.88	3.28	-	735.8
AHQ-1-11, 4502	K.LPQLPITNFSR.D	1286.50461	2	6.87E-05	0.89	2.98	-	851.4
AHQ-1-2, 5302 - 5347	K.LPQLPITNFSR.D	1286.50461	2	8.56E-06	0.85	3.14	-	590.0
AHQ-1-2, 5115	K.LPQLPITNFSR.D	1286.50461	1	6.02E-05	0.44	2.90	-	165.7
AHQ-1-3, 5194	K.LPQLPITNFSR.D	1286.50461	2	6.68E-06	0.83	3.24	-	550.9
AHQ-1-4, 5271	K.LPQLPITNFSR.D	1286.50461	2	1.18E-05	0.89	3.22	-	755.4
AHQ-1-2, 5105	K.LPQLPITNFSR.D	1286.50461	1	6.91E-04	0.40	2.15	-	274.3
AHQ-1-5, 4918	K.LPQLPITNFSR.D	1286.50461	1	3.83E-04	0.25	2.35	-	133.5

AHQ-1-1, 5152 - 5223	K.LPQLPITNFSR.D	1286.50461	2	2.56E-05	0.83	3.43	-	612.5
AHQ-1-5, 4847 - 4917	K.LPQLPITNFSR.D	1286.50461	2	3.95E-04	0.88	3.32	-	625.5
AHQ-1-1, 4989 - 5052	K.LPQLPITNFSR.D	1286.50461	2	3.24E-05	0.91	3.45	-	701.3
AHQ-1-2, 5213	K.LPQLPITNFSR.D	1286.50461	2	1.12E-06	0.84	2.86	-	886.9
AHQ-1-4, 5027 - 5036	K.LPQLPITNFSR.D	1286.50461	2	6.40E-05	0.87	2.98	-	679.3
AHQ-1-3, 5487 - 5553	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.45E-06	0.95	5.42	-	840.3
AHQ-1-6, 5416 - 5494	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.26E-10	0.97	5.61	-	1151.2
AHQ-1-1, 5477 - 5551	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.89E-15	0.98	6.83	-	2337.5
AHQ-1-7, 5562 - 5572	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.65E-08	0.93	4.28	-	858.2
AHQ-1-2, 5634 - 5701	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.18E-07	0.96	5.73	-	692.1
AHQ-1-4, 5606 - 5687	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.88E-08	0.96	5.50	-	1039.3
AHQ-1-2, 5823	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	5.21E-05	0.93	4.85	-	1016.7
AHQ-1-1, 5648	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.41E-10	0.96	5.09	-	1035.6
AHQ-1-5, 5549 - 5617	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.36E-08	0.97	5.43	-	1063.6
AHQ-1-9, 5328 - 5408	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.41E-06	0.90	3.81	-	957.9
AHQ-1-1, 5485 - 5559	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.61E-05	0.85	3.51	-	845.4
AHQ-1-2, 5737 - 5806	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	8.63E-05	0.94	3.95	-	1221.4
AHQ-1-4, 5595 - 5663	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.95E-08	0.98	7.28	-	2288.2
AHQ-1-4, 5788 - 5808	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.60E-08	0.91	4.30	-	718.2
AHQ-1-2, 5633 - 5653	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	6.76E-05	0.95	4.96	-	1250.7
AHQ-1-3, 5654	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.05E-09	0.93	4.72	-	758.4
AHQ-1-3, 5519	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	9.42E-07	0.81	3.58	-	384.8
AHQ-1-6, 3019	R.LRNGHVGISFVPK.E	1424.67564	2	4.70E-04	0.62	2.75	-	496.5
AHQ-1-1, 3325	R.LRNGHVGISFVPK.E	1424.67564	3	5.62E-04	0.94	3.64	-	1778.6
AHQ-1-5, 2835	R.LRNGHVGISFVPK.E	1424.67564	3	1.69E-05	0.91	3.40	-	1498.7
AHQ-1-9, 2903	R.LRNGHVGISFVPK.E	1424.67564	3	1.61E-06	0.91	3.59	-	1734.0
AHQ-1-5, 2986	R.LRNGHVGISFVPK.E	1424.67564	2	5.95E-04	0.68	2.64	-	646.3
AHQ-1-1, 4191	R.LSPFMADIR.D	1050.25664	2	7.21E-04	0.60	2.55	-	344.4
AHQ-1-3, 4093 - 4097	R.LSPFMADIR.D	1050.25664	2	8.30E-06	0.60	2.63	-	450.1
AHQ-1-1, 3491 - 3571	R.LTVSSLQESGLK.V	1262.43499	2	1.06E-04	0.74	2.87	-	521.3
AHQ-1-1, 3588	R.LTVSSLQESGLK.V	1262.43499	2	2.88E-07	0.90	3.35	-	920.2
AHQ-1-5, 3938	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.43E-04	0.87	3.57	-	841.1
AHQ-1-13, 4056	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.70E-04	0.93	4.42	-	840.1
AHQ-1-11, 4118	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.90E-08	0.97	5.55	-	1067.3
AHQ-1-13, 4069	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.03E-04	0.81	3.30	-	879.9
AHQ-1-1, 4587	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.20E-11	0.97	5.25	-	1112.2
AHQ-1-1, 4591	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	3.54E-11	0.97	5.81	-	1377.3
AHQ-1-7, 4093	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.16E-05	0.96	5.51	-	1082.9
AHQ-1-1, 4308	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	5.40E-06	0.96	5.45	-	1143.9
AHQ-1-14- , 4091	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	3.25E-06	0.96	4.71	-	1501.2
AHQ-1-5, 4266	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.68E-07	0.96	5.14	-	1166.0
AHQ-1-6, 4022	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	6.18E-06	0.93	4.81	-	924.3
AHQ-1-1, 4307	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	7.51E-09	0.96	5.09	-	1550.3
AHQ-1-13- , 4241	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.14E-06	0.95	4.98	-	1087.2
AHQ-1-7, 4413	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.84E-05	0.90	4.28	-	545.0
AHQ-1-5, 4073	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.10E-08	0.98	5.80	-	1650.1
AHQ-1-5, 4409 - 4426	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.69E-10	0.96	4.77	-	1582.9
AHQ-1-8, 4027	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.31E-07	0.97	5.18	-	1419.6
AHQ-1-8, 4029	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.98E-07	0.96	4.88	-	1435.8
AHQ-1-5, 4415 - 4497	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.55E-08	0.97	5.23	-	1353.7
AHQ-1-6, 4354	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.60E-08	0.92	3.96	-	1136.2
AHQ-1-6, 4362	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.93E-08	0.94	4.74	-	878.7
AHQ-1-10, 3795	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	4.09E-06	0.92	4.32	-	874.6
AHQ-1-11, 3886	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.72E-06	0.95	5.05	-	811.6
AHQ-1-14- , 4088	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.48E-10	0.96	5.24	-	1092.8
AHQ-1-4, 4231	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.14E-08	0.97	5.66	-	1431.1
AHQ-1-4, 4236	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	7.54E-10	0.97	5.89	-	1743.3
AHQ-1-4, 4576 - 4604	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.38E-10	0.97	5.09	-	1342.2
AHQ-1-4, 2524	K.MDCQECPEGYR.V	1447.55375	2	8.30E-06	0.84	3.26	-	709.8
AHQ-1-1, 2341	K.M*DCQECPEGYR.V	1463.55315	2	1.65E-05	0.93	2.82	-	1789.2
AHQ-1-1, 2600	K.MDCQECPEGYR.V	1447.55375	2	5.45E-05	0.76	3.08	-	640.5
AHQ-1-5, 2433	K.MDCQECPEGYR.V	1447.55375	2	3.47E-06	0.85	3.37	-	696.3
AHQ-1-5, 2995	R.NGHVGISFVPK.E	1155.33104	1	8.06E-07	0.39	2.34	-	408.8
AHQ-1-3, 4837	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	1.69E-07	0.76	3.13	-	1161.0
AHQ-1-4, 4914	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	3.97E-07	0.93	4.44	-	694.2
AHQ-1-1, 4844	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	7.23E-04	0.98	5.48	-	1742.7
AHQ-1-5, 4957	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	3.96E-05	0.73	3.29	-	757.4
AHQ-1-5, 4789	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	3.58E-09	0.96	4.82	-	1240.4
AHQ-1-5, 1833	K.RAEFTVETR.S	1109.21754	2	1.19E-05	0.94	3.53	-	945.5
AHQ-1-1, 2212	K.RAEFTVETR.S	1109.21754	2	3.02E-05	0.90	3.40	-	774.8
AHQ-1-3, 2038 - 2045	K.RAEFTVETR.S	1109.21754	2	4.15E-06	0.94	3.43	-	1136.9
AHQ-1-2, 2101	K.RAEFTVETR.S	1109.21754	2	2.31E-06	0.92	3.53	-	972.4
AHQ-1-4, 3082	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	2.43E-05	0.97	5.13	-	2325.6
AHQ-1-5, 2919	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	1.12E-06	0.97	5.97	-	1931.0
AHQ-1-1, 3201 - 3204	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	5.13E-05	0.98	5.45	-	2108.2
AHQ-1-3, 3049	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	6.55E-06	0.98	5.04	-	2653.5
AHQ-1-1, 3143 - 3220	R.RLTVSSLQESGLK.V	1418.62134	2	3.99E-04	0.97	4.33	-	2196.5
AHQ-1-5, 2810 - 2883	R.RLTVSSLQESGLK.V	1418.62134	2	1.63E-05	0.98	4.87	-	2385.5
AHQ-1-4, 2940 - 3086	R.RLTVSSLQESGLK.V	1418.62134	2	6.88E-05	0.97	4.38	-	1877.4
AHQ-1-5, 3047 - 3095	R.RLTVSSLQESGLK.V	1418.62134	2	1.39E-05	0.96	3.87	-	2025.2
AHQ-1-3, 7345 - 7406	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	4.95E-07	0.96	6.20	-	1546.8
AHQ-1-2, 7561 - 7562	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	4.65E-04	0.88	3.37	-	1063.2
AHQ-1-7, 3886	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.07E-09	0.92	4.05	-	1339.9
AHQ-1-2, 4370	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.22E-07	0.88	4.20	-	469.4
AHQ-1-4, 3947 - 4010	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.57E-06	0.90	4.37	-	568.9
AHQ-1-1, 4177	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.62E-07	0.87	4.09	-	567.5
AHQ-1-3, 4105	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.20E-07	0.87	4.18	-	470.3
AHQ-1-4, 4011	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.63E-10	0.95	4.70	-	1187.9
AHQ-1-1, 4119 - 4199	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.82E-07	0.90	4.19	-	1093.7
AHQ-1-1, 4316	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	9.85E-06	0.60	3.33	-	227.7
AHQ-1-7, 3880 - 3881	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.52E-05	0.90	4.45	-	530.9
AHQ-1-4, 4100	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.77E-05	0.88	4.23	-	564.2
AHQ-1-5, 3869	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	6.35E-06	0.93	5.18	-	605.2
AHQ-1-3, 3969	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	8.31E-09	0.93	4.87	-	635.9
AHQ-1-2, 4253 - 4254	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.02E-07	0.95	5.13	-	843.1
AHQ-1-3, 3973	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	6.57E-06	0.91	3.87	-	999.3
AHQ-1-2, 4417 - 4437	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	4.52E-04	0.92	4.10	-	1319.8
AHQ-1-2, 4105 - 4173	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.65E-08	0.93	4.16	-	1330.3
AHQ-1-2, 4103 - 4174	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.87E-07	0.94	4.97	-	741.8
AHQ-1-2, 4527	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.16E-07	0.92	4.37	-	669.5
AHQ-1-5, 3853 - 3931	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	7.18E-09	0.94	4.60	-	1112.8
AHQ-1-6, 3788	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.63E-07	0.89	3.98	-	1012.9
AHQ-1-1, 3992 - 4055	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	9.62E-10	0.94	4.38	-	1453.3
AHQ-1-1, 4039 - 4103	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.62E-06	0.91	4.13	-	716.0
AHQ-1-8, 3839	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.37E-05	0.92	4.42	-	655.8
AHQ-1-9, 3760 - 3806	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.57E-04	0.78	3.49	-	382.6
AHQ-1-1, 3509	K.SPFEVYVDK.S	1084.20321	1	3.39E-04	0.77	3.18	-	836.4

AHQ-1-4, 3446	K.SPFEVYVDK.S	1084.20321	2	1.65E-05	0.90	3.02	-	1038.9
AHQ-1-1, 3501 - 3504	K.SPFEVYVDK.S	1084.20321	2	4.18E-06	0.94	3.56	-	1163.3
AHQ-1-1, 3500	K.SPFEVYVDK.S	1084.20321	1	2.32E-04	0.74	2.38	-	1005.2
AHQ-1-3, 3413	K.SPFEVYVDK.S	1084.20321	2	2.50E-05	0.93	3.60	-	1098.7
AHQ-1-3, 3431	K.SPFEVYVDK.S	1084.20321	1	6.79E-08	0.77	2.54	-	792.8
AHQ-1-7, 3341	K.SPFEVYVDK.S	1084.20321	2	1.98E-05	0.94	3.29	-	1450.1
AHQ-1-2, 3509 - 3521	K.SPFEVYVDK.S	1084.20321	2	9.69E-06	0.95	3.48	-	1405.3
AHQ-1-2, 3517	K.SPFEVYVDK.S	1084.20321	1	1.61E-05	0.86	3.29	-	869.2
AHQ-1-5, 3322	K.SPFEVYVDK.S	1084.20321	2	1.78E-06	0.90	2.78	-	1247.0
AHQ-1-5, 3341	K.SPFEVYVDK.S	1084.20321	1	2.59E-06	0.84	2.99	-	868.0
AHQ-1-6, 4958 - 4972	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.58E-05	0.77	3.05	-	765.1
AHQ-1-2, 5262	K.SPFSVAVSPSLDLSK.I	1534.73557	2	5.20E-04	0.84	3.42	-	640.9
AHQ-1-3, 5122	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.47E-04	0.88	3.15	-	1039.9
AHQ-1-2, 5146 - 5221	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.27E-04	0.94	4.54	-	1026.3
AHQ-1-3, 5013 - 5082	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.18E-05	0.85	4.24	-	549.7
AHQ-1-1, 5036 - 5093	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.78E-06	0.92	3.80	-	1111.8
AHQ-1-5, 5037 - 5038	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.30E-07	0.95	4.63	-	1048.4
AHQ-1-2, 3787	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.24E-05	0.86	3.90	-	362.1
AHQ-1-1, 3708	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.41E-08	0.90	3.88	-	653.7
AHQ-1-5, 3417	R.SPYTVTVGQACNPSACR.A	1871.04208	2	5.41E-05	0.91	4.22	-	534.3
AHQ-1-6, 3328 - 3399	R.SPYTVTVGQACNPSACR.A	1871.04208	2	7.91E-04	0.88	3.69	-	502.8
AHQ-1-1, 3531 - 3565	R.SPYTVTVGQACNPSACR.A	1871.04208	2	5.12E-04	0.41	2.74	-	318.5
AHQ-1-6, 3379	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.66E-05	0.89	4.07	-	463.5
AHQ-1-3, 3453 - 3521	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.16E-04	0.84	4.05	-	335.1
AHQ-1-2, 2841	K.SQGDASKVTAQGPGLEPSGNIANK.T	2327.49419	2	4.46E-04	0.77	4.10	-	329.1
AHQ-1-14- , 2188	K.SSFTVDCSK.A	1032.10676	1	1.85E-05	0.58	2.65	-	416.5
AHQ-1-14- , 2163 - 2234	K.SSFTVDCSK.A	1032.10676	1	3.01E-04	0.49	1.95	-	505.0
AHQ-1-3, 5066 - 5133	R.TFSVWYVPEVTGTHK.V	1751.96228	2	5.79E-04	0.78	3.20	-	435.4
AHQ-1-6, 4879 - 4955	R.TFSVWYVPEVTGTHK.V	1751.96228	2	9.85E-04	0.32	2.73	-	206.9
AHQ-1-7, 4988 - 5061	R.TFSVWYVPEVTGTHK.V	1751.96228	2	8.22E-04	0.46	2.76	-	298.2
AHQ-1-5, 5002 - 5011	R.TFSVWYVPEVTGTHK.V	1751.96228	3	3.20E-06	0.64	3.46	-	399.2
AHQ-1-3, 5083	R.TFSVWYVPEVTGTHK.V	1751.96228	3	4.18E-06	0.71	3.27	-	466.8
AHQ-1-1, 3337 - 3344	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	4.18E-05	0.88	4.11	-	732.7
AHQ-1-5, 2955	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	7.81E-09	0.93	4.42	-	900.9
AHQ-1-2, 3138 - 3211	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.14E-06	0.87	3.56	-	854.0
AHQ-1-4, 3087 - 3090	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	1.94E-07	0.91	4.13	-	685.0
AHQ-1-4, 3096	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	6.11E-07	0.75	3.06	-	916.6
AHQ-1-6, 2962	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	9.06E-06	0.87	3.70	-	549.1
AHQ-1-3, 3065	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	3.42E-08	0.76	3.12	-	779.2
AHQ-1-1, 3137 - 3209	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.59E-05	0.93	4.14	-	1185.2
AHQ-1-2, 3133 - 3202	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	9.17E-06	0.94	4.42	-	873.1
AHQ-1-2, 3070 - 3142	R.TGVELGKPTHFTVNAK.A	1699.93205	2	1.55E-07	0.88	3.74	-	651.4
AHQ-1-3, 2950 - 3021	R.TGVELGKPTHFTVNAK.A	1699.93205	2	4.09E-04	0.82	3.53	-	568.1
AHQ-1-3, 2851 - 2866	R.TGVELGKPTHFTVNAK.A	1699.93205	3	5.53E-06	0.82	4.12	-	512.0
AHQ-1-1, 3016	R.TGVELGKPTHFTVNAK.A	1699.93205	3	1.43E-04	0.63	3.26	-	538.3
AHQ-1-1, 3147	R.TGVELGKPTHFTVNAK.A	1699.93205	2	7.44E-05	0.89	3.84	-	710.4
AHQ-1-2, 2953	R.TGVELGKPTHFTVNAK.A	1699.93205	2	3.11E-06	0.92	4.43	-	657.2
AHQ-1-5, 2702	R.TGVELGKPTHFTVNAK.A	1699.93205	2	2.59E-06	0.87	3.81	-	539.5
AHQ-1-1, 3200 - 3273	K.THEAEIVEGENHTYCIR.F	2060.19046	3	8.16E-11	0.94	4.73	-	1034.1
AHQ-1-8, 2996	K.THEAEIVEGENHTYCIR.F	2060.19046	2	5.99E-13	0.98	5.01	-	1883.4
AHQ-1-1, 3285	K.THEAEIVEGENHTYCIR.F	2060.19046	2	1.30E-05	0.92	4.84	-	553.5
AHQ-1-2, 3231	K.THEAEIVEGENHTYCIR.F	2060.19046	3	8.67E-08	0.92	4.40	-	896.7
AHQ-1-5, 3091	K.THEAEIVEGENHTYCIR.F	2060.19046	2	7.36E-13	0.98	5.55	-	2102.3
AHQ-1-5, 2890 - 2961	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.16E-06	0.93	4.17	-	1047.0
AHQ-1-5, 2958 - 3013	K.THEAEIVEGENHTYCIR.F	2060.19046	2	3.57E-10	0.99	6.48	-	2472.8
AHQ-1-4, 3239	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.20E-08	0.97	4.79	-	1798.9
AHQ-1-4, 3150	K.THEAEIVEGENHTYCIR.F	2060.19046	2	6.14E-12	0.98	5.27	-	1901.2
AHQ-1-3, 3090	K.THEAEIVEGENHTYCIR.F	2060.19046	3	5.77E-05	0.85	3.62	-	831.2
AHQ-1-7, 2990	K.THEAEIVEGENHTYCIR.F	2060.19046	2	6.34E-04	0.98	5.29	-	1754.1
AHQ-1-4, 3076 - 3146	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.60E-07	0.91	4.16	-	1165.2
AHQ-1-1, 3985	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	2	4.27E-11	0.97	4.63	-	1635.5
AHQ-1-1, 3859 - 3932	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	3	8.77E-04	0.73	3.25	-	381.2
AHQ-1-10, 2920 - 2928	R.TPCEEILVK.H	1090.27249	2	3.25E-04	0.80	2.96	-	783.6
AHQ-1-4, 3190	R.TPCEEILVK.H	1090.27249	2	5.77E-04	0.89	3.34	-	771.5
AHQ-1-4, 3203	R.TPCEEILVK.H	1090.27249	1	1.98E-06	0.52	2.49	-	496.0
AHQ-1-13, 3123 - 3138	R.TPCEEILVK.H	1090.27249	2	3.60E-05	0.87	3.03	-	866.9
AHQ-1-1, 3259	R.TPCEEILVK.H	1090.27249	2	2.08E-06	0.79	2.69	-	630.5
AHQ-1-14- , 3095 - 3158	R.TPCEEILVK.H	1090.27249	2	3.48E-05	0.87	3.30	-	666.1
AHQ-1-7, 3088 - 3097	R.TPCEEILVK.H	1090.27249	2	4.46E-06	0.91	3.17	-	928.3
AHQ-1-3, 3163	R.TPCEEILVK.H	1090.27249	2	2.43E-05	0.68	2.89	-	520.6
AHQ-1-13- , 3169	R.TPCEEILVK.H	1090.27249	2	3.79E-05	0.84	2.66	-	1018.8
AHQ-1-14, 4014 - 4017	R.TPCEEILVK.H	1090.27249	2	9.42E-07	0.75	2.73	-	600.4
AHQ-1-14- , 3107	R.TPCEEILVK.H	1090.27249	1	3.58E-05	0.59	2.82	-	501.6
AHQ-1-11, 3002	R.TPCEEILVK.H	1090.27249	2	8.91E-07	0.81	2.76	-	640.2
AHQ-1-6, 3054	R.TPCEEILVK.H	1090.27249	2	7.28E-05	0.80	3.06	-	622.1
AHQ-1-5, 3069	R.TPCEEILVK.H	1090.27249	2	6.40E-05	0.89	3.19	-	792.0
AHQ-1-2, 3582 - 3653	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.34E-13	0.93	4.17	-	703.8
AHQ-1-1, 3235	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.10E-09	0.94	4.27	-	876.9
AHQ-1-7, 3268	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.70E-04	0.90	3.85	-	870.2
AHQ-1-1, 3615	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.03E-13	0.59	2.50	-	555.2
AHQ-1-4, 3504	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.45E-10	0.89	3.85	-	609.6
AHQ-1-3, 3325	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.73E-13	0.89	4.03	-	484.7
AHQ-1-2, 3726	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.36E-05	0.93	4.06	-	1006.3
AHQ-1-1, 3511 - 3591	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.00E-12	0.96	4.64	-	1089.9
AHQ-1-3, 3462 - 3537	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.95E-10	0.95	4.79	-	908.7
AHQ-1-2, 3415 - 3485	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.62E-11	0.93	4.08	-	857.3
AHQ-1-13- , 3369	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.11E-05	0.86	3.67	-	599.4
AHQ-1-5, 3410	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.72E-08	0.88	3.99	-	756.7
AHQ-1-8, 3154	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.58E-05	0.90	3.51	-	919.3
AHQ-1-5, 3218 - 3278	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.91E-10	0.91	3.82	-	658.4
AHQ-1-3, 3306 - 3377	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.89E-12	0.95	4.14	-	1267.6
AHQ-1-1, 3373 - 3443	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.02E-13	0.94	4.05	-	972.4
AHQ-1-8, 2647	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.49E-06	0.82	3.25	-	613.5
AHQ-1-10, 2495	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.76E-04	0.34	2.67	-	264.2
AHQ-1-4, 2858	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.20E-05	0.89	4.27	-	490.6
AHQ-1-3, 2846	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.16E-04	0.88	3.87	-	613.8
AHQ-1-9, 2690	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.84E-04	0.57	2.90	-	408.2
AHQ-1-5, 2515	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	8.37E-06	0.67	3.14	-	456.7
AHQ-1-1, 2861 - 2927	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	6.11E-07	0.92	4.08	-	795.4
AHQ-1-5, 2739	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.98E-05	0.93	4.17	-	909.0
AHQ-1-1, 2979	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	8.51E-07	0.87	3.70	-	675.8
AHQ-1-4, 2776	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.55E-06	0.82	3.35	-	643.9
AHQ-1-2, 2949	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.21E-05	0.81	3.52	-	489.7
AHQ-1-13- , 2915	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.44E-04	0.81	3.19	-	587.7
AHQ-1-3, 3654	K.VDINTEDLEDGTCR.V	1638.69283	2	2.88E-07	0.81	3.21	-	877.3
AHQ-1-4, 3438	K.VDINTEDLEDGTCR.V	1638.69283	2	1.87E-04	0.89	3.45	-	883.6
AHQ-1-9, 3548	K.VDINTEDLEDGTCR.V	1638.69283	2	9.22E-07	0.89	3.49	-	958.0

AHQ-1-1, 3387	K.VDINTEDLEDGTCR.V	1638.69283	2	7.90E-06	0.88	3.50	-	830.1
AHQ-1-5, 3307 - 3377	K.VDINTEDLEDGTCR.V	1638.69283	2	4.98E-04	0.92	3.54	-	943.1
AHQ-1-6, 3567	K.VDINTEDLEDGTCR.V	1638.69283	2	3.03E-05	0.87	3.35	-	830.3
AHQ-1-1, 3609 - 3669	K.VDINTEDLEDGTCR.V	1638.69283	2	5.28E-06	0.87	3.38	-	852.7
AHQ-1-13, 3505	K.VDINTEDLEDGTCR.V	1638.69283	2	2.69E-04	0.91	3.35	-	1214.7
AHQ-1-8, 3609	K.VDINTEDLEDGTCR.V	1638.69283	2	1.26E-04	0.91	3.96	-	898.8
AHQ-1-5, 3463	K.VDINTEDLEDGTCR.V	1638.69283	2	3.29E-06	0.87	3.27	-	888.8
AHQ-1-5, 3613	K.VDINTEDLEDGTCR.V	1638.69283	2	1.74E-05	0.92	3.80	-	991.3
AHQ-1-1, 3492	K.VDINTEDLEDGTCR.V	1638.69283	2	6.43E-08	0.91	3.53	-	1132.5
AHQ-1-5, 3761	K.VDINTEDLEDGTCR.V	1638.69283	2	7.30E-09	0.89	3.22	-	995.7
AHQ-1-7, 3664 - 3737	K.VDINTEDLEDGTCR.V	1638.69283	2	7.56E-06	0.85	3.19	-	850.3
AHQ-1-2, 3785	K.VDINTEDLEDGTCR.V	1638.69283	2	1.27E-06	0.92	3.93	-	876.5
AHQ-1-3, 3385	K.VDINTEDLEDGTCR.V	1638.69283	2	4.40E-08	0.87	3.68	-	847.7
AHQ-1-6, 2482	K.VDVGKDQEFTVK.S	1365.51377	2	6.94E-09	0.78	3.07	-	609.2
AHQ-1-1, 2703	K.VDVGKDQEFTVK.S	1365.51377	2	4.03E-09	0.86	3.32	-	740.4
AHQ-1-5, 2461	K.VDVGKDQEFTVK.S	1365.51377	2	1.64E-07	0.75	3.41	-	400.2
AHQ-1-3, 2565	K.VDVGKDQEFTVK.S	1365.51377	2	2.02E-06	0.87	3.32	-	655.5
AHQ-1-4, 2566 - 2572	K.VDVGKDQEFTVK.S	1365.51377	2	3.43E-09	0.88	3.62	-	706.6
AHQ-1-3, 2575	K.VDVGKDQEFTVK.S	1365.51377	1	4.73E-06	0.26	2.55	-	281.2
AHQ-1-2, 2647 - 2659	K.VDVGKDQEFTVK.S	1365.51377	2	3.14E-05	0.85	3.18	-	738.1
AHQ-1-3, 2710 - 2789	K.VEPGLGADNSVVR.F	1313.44209	2	9.36E-08	0.74	2.98	-	259.8
AHQ-1-2, 2805 - 2878	K.VEPGLGADNSVVR.F	1313.44209	2	1.02E-07	0.89	3.74	-	438.7
AHQ-1-1, 2840 - 2917	K.VEPGLGADNSVVR.F	1313.44209	2	2.79E-04	0.70	2.70	-	271.3
AHQ-1-3, 6297 - 6369	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.61E-07	0.96	6.38	-	1170.2
AHQ-1-1, 6339	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	3.83E-07	0.82	4.06	-	496.1
AHQ-1-3, 6438 - 6449	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.69E-04	0.86	4.45	-	367.9
AHQ-1-4, 6534	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.19E-05	0.90	5.12	-	457.6
AHQ-1-2, 6465 - 6533	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	6.72E-06	0.94	5.15	-	994.0
AHQ-1-1, 6219 - 6279	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	4.05E-05	0.93	5.11	-	849.3
AHQ-1-5, 6422 - 6502	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	6.34E-05	0.95	5.64	-	713.6
AHQ-1-3, 7214 - 7221	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	3.50E-04	0.89	4.02	-	716.6
AHQ-1-1, 6907 - 6971	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.51E-09	0.94	4.86	-	786.9
AHQ-1-8, 7434 - 7472	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.93E-05	0.93	4.96	-	582.8
AHQ-1-10, 6343 - 6344	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	2.80E-07	0.95	5.17	-	801.1
AHQ-1-5, 7407	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	7.46E-09	0.96	5.74	-	779.1
AHQ-1-8, 7435 - 7440	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	8.29E-04	0.79	3.86	-	598.0
AHQ-1-2, 1507 - 1583	R.VHGPGIQSGTTNKPNK.F	1635.80645	2	2.63E-04	0.90	3.45	-	922.3
AHQ-1-1, 4532	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	4.01E-11	0.96	5.40	-	1146.3
AHQ-1-4, 4523	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.86E-06	0.89	3.75	-	1121.2
AHQ-1-4, 4608	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	4.83E-06	0.94	4.41	-	1162.0
AHQ-1-7, 4393	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	2.81E-04	0.96	4.75	-	1272.4
AHQ-1-3, 4489	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	1.18E-04	0.95	4.87	-	1451.1
AHQ-1-6, 4323	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	6.30E-08	0.97	5.51	-	1241.4
AHQ-1-5, 4389	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.52E-08	0.94	4.84	-	714.7
AHQ-1-9, 4615 - 4624	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	4.80E-13	0.93	4.91	-	897.4
AHQ-1-5, 4801	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.19E-11	0.90	4.57	-	659.3
AHQ-1-5, 4741	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.67E-15	0.94	4.63	-	868.3
AHQ-1-5, 4703 - 4726	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	6.95E-11	0.91	4.65	-	676.2
AHQ-1-3, 4817	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.86E-06	0.69	3.27	-	355.1
AHQ-1-2, 4993	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.11E-14	0.86	3.83	-	705.4
AHQ-1-4, 4882	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.94E-09	0.92	4.83	-	631.3
AHQ-1-4, 4892	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	2.77E-06	0.90	4.62	-	445.1
AHQ-1-6, 4662	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.61E-05	0.92	4.69	-	673.6
AHQ-1-1, 4925	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.04E-09	0.94	4.45	-	1235.0
AHQ-1-7, 4713	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.67E-06	0.92	5.26	-	553.5
AHQ-1-8, 4596	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.48E-08	0.92	4.28	-	794.8
AHQ-1-8, 4587 - 4659	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	6.46E-07	0.84	3.61	-	748.3
AHQ-1-1, 4855 - 4920	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.47E-09	0.95	5.26	-	861.9
AHQ-1-4, 3814	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.86E-08	0.83	3.66	-	511.8
AHQ-1-4, 3926	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.34E-06	0.91	3.69	-	673.9
AHQ-1-8, 3538	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.39E-09	0.91	4.05	-	666.8
AHQ-1-5, 3693 - 3719	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.02E-07	0.82	3.68	-	478.9
AHQ-1-5, 3787 - 3862	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.18E-06	0.91	4.35	-	559.0
AHQ-1-2, 4014	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.15E-05	0.92	4.12	-	620.2
AHQ-1-9, 3575	K.VNQPASFAVSLNGAK.G	1503.68480	2	7.27E-05	0.87	3.49	-	652.1
AHQ-1-1, 3855 - 3919	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.71E-08	0.82	3.41	-	480.5
AHQ-1-3, 3789 - 3870	K.VNQPASFAVSLNGAK.G	1503.68480	2	9.58E-07	0.87	3.85	-	548.7
AHQ-1-6, 3650 - 3728	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.36E-07	0.92	4.36	-	601.2
AHQ-1-2, 3930	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.11E-07	0.94	4.09	-	708.5
AHQ-1-3, 3877	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.16E-08	0.65	2.85	-	481.2
AHQ-1-7, 3809 - 3825	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.64E-06	0.78	3.12	-	477.9
AHQ-1-2, 1589 - 1662	K.VPVHDVTDASK.V	1168.28175	1	5.73E-04	0.62	2.39	-	739.4
AHQ-1-1, 1804 - 1865	K.VPVHDVTDASK.V	1168.28175	2	1.36E-07	0.96	3.71	-	1548.2
AHQ-1-3, 1673	K.VPVHDVTDASK.V	1168.28175	2	6.01E-07	0.88	2.86	-	848.5
AHQ-1-3, 1579	K.VPVHDVTDASK.V	1168.28175	2	5.19E-08	0.92	3.27	-	1181.3
AHQ-1-4, 1596	K.VPVHDVTDASK.V	1168.28175	2	1.35E-08	0.93	3.41	-	1196.2
AHQ-1-2, 1559 - 1617	K.VPVHDVTDASK.V	1168.28175	2	6.95E-08	0.96	3.25	-	1750.4
AHQ-1-4, 4243	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.28E-06	0.94	3.99	-	1367.4
AHQ-1-3, 4310	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.11E-04	0.93	4.10	-	958.9
AHQ-1-3, 4198 - 4218	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.36E-09	0.97	5.41	-	1384.6
AHQ-1-2, 4466	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.75E-10	0.94	4.67	-	1124.5
AHQ-1-2, 4325 - 4397	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.67E-07	0.97	5.32	-	1409.7
AHQ-1-4, 4387	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.12E-10	0.88	3.98	-	693.3
AHQ-1-1, 4239	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.53E-06	0.95	4.45	-	1200.0
AHQ-1-1, 4412	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.18E-06	0.92	4.35	-	1151.9
AHQ-1-5, 4305	R.VQVQDNEGCPVEALVK.D	1786.98493	2	6.62E-07	0.94	4.08	-	1265.8
AHQ-1-1, 5481 - 5497	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.43E-06	0.86	3.92	-	900.9
AHQ-1-2, 5509 - 5582	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	2.22E-15	0.95	5.00	-	1491.6
AHQ-1-2, 5374 - 5441	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	6.24E-06	0.92	4.37	-	1153.5
AHQ-1-3, 5410	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	6.21E-08	0.91	4.12	-	1317.4
AHQ-1-3, 5138 - 5209	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	9.59E-09	0.95	5.30	-	1301.7
AHQ-1-5, 5261 - 5329	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	4.06E-07	0.77	3.59	-	912.6
AHQ-1-1, 5147	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	8.92E-07	0.94	4.69	-	1417.3
AHQ-1-1, 5351 - 5415	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	3.92E-08	0.93	4.84	-	1097.6
AHQ-1-7, 4701	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.63E-06	0.95	4.84	-	1050.8
AHQ-1-1, 4959	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	3.84E-04	0.96	5.16	-	1236.6
AHQ-1-1, 4943 - 5019	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	3.49E-10	0.96	5.83	-	1399.8
AHQ-1-3, 4861	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.79E-09	0.93	4.65	-	941.1
AHQ-1-5, 4862	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	5.17E-11	0.95	5.23	-	1164.3
AHQ-1-5, 4694 - 4765	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.87E-09	0.95	5.45	-	1086.2
AHQ-1-4, 4926 - 5004	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	6.67E-10	0.96	5.52	-	1365.4
AHQ-1-9, 4600	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	2.04E-04	0.89	4.06	-	567.4
AHQ-1-13, 4608	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	5.82E-06	0.72	2.92	-	415.9
AHQ-1-9, 4616	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	7.50E-06	0.94	4.57	-	1145.7
AHQ-1-8, 4432	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	5.01E-08	0.93	4.71	-	1009.8
AHQ-1-13- , 4879	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.67E-06	0.95	5.27	-	1410.0
AHQ-1-2, 5057	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.95E-06	0.95	4.99	-	1122.6

AHQ-1-6, 4675	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	6.51E-04	0.81	3.33	-	622.3
AHQ-1-2, 5065	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	3.74E-05	0.87	3.73	-	647.1
AHQ-1-13, 4543 - 4611	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	8.27E-04	0.89	4.30	-	696.1
AHQ-1-1, 2796 - 2868	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.52E-07	0.91	4.52	-	657.0
AHQ-1-4, 2731	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.22E-04	0.78	3.53	-	422.9
AHQ-1-6, 2724	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.17E-06	0.92	4.20	-	861.3
AHQ-1-6, 2626	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.26E-07	0.70	3.08	-	402.2
AHQ-1-2, 2775 - 2846	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.77E-05	0.92	4.44	-	617.2
AHQ-1-3, 2721 - 2790	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	3.38E-06	0.84	4.03	-	482.8
AHQ-1-3, 2829 - 2901	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.29E-10	0.89	4.41	-	463.0
AHQ-1-5, 2703 - 2713	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	5.76E-05	0.77	3.44	-	409.2
AHQ-1-2, 2917 - 2985	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.23E-07	0.88	4.08	-	480.6
AHQ-1-8, 2489	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	3.37E-04	0.77	3.06	-	639.3
AHQ-1-9, 2586	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	6.27E-04	0.89	3.61	-	615.7
AHQ-1-1, 3369	K.VTVLFAGQHIAK.S	1284.53185	3	5.60E-05	0.80	3.60	-	690.6
AHQ-1-1, 3375	K.VTVLFAGQHIAK.S	1284.53185	1	8.53E-04	0.24	1.84	-	573.1
AHQ-1-3, 3226	K.VTVLFAGQHIAK.S	1284.53185	3	1.89E-05	0.78	3.69	-	585.9
AHQ-1-6, 3076	K.VTVLFAGQHIAK.S	1284.53185	3	7.57E-05	0.87	4.00	-	654.2
AHQ-1-3, 3149 - 3230	K.VTVLFAGQHIAK.S	1284.53185	2	5.06E-08	0.91	3.76	-	831.6
AHQ-1-2, 3334 - 3363	K.VTVLFAGQHIAK.S	1284.53185	2	6.90E-07	0.93	3.85	-	976.5
AHQ-1-5, 3058	K.VTVLFAGQHIAK.S	1284.53185	2	1.47E-07	0.91	3.43	-	1070.0
AHQ-1-5, 3067	K.VTVLFAGQHIAK.S	1284.53185	1	1.62E-04	0.22	1.86	-	493.8
AHQ-1-2, 3349	K.VTVLFAGQHIAK.S	1284.53185	1	5.63E-04	0.66	3.19	-	484.8
AHQ-1-1, 3367	K.VTVLFAGQHIAK.S	1284.53185	2	6.99E-07	0.92	4.14	-	825.6
AHQ-1-6, 3062	K.VTVLFAGQHIAK.S	1284.53185	2	6.30E-05	0.86	3.29	-	788.1
AHQ-1-7, 3080	K.VTVLFAGQHIAK.S	1284.53185	2	8.40E-05	0.82	3.09	-	634.1
AHQ-1-4, 3240	K.VTVLFAGQHIAK.S	1284.53185	2	2.88E-05	0.90	3.74	-	754.5
AHQ-1-5, 5290 - 5321	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.04E-08	0.85	3.67	-	377.6
AHQ-1-1, 5183	R.VTYCPTEPGNYIINIK.F	1884.14221	2	7.67E-08	0.90	3.84	-	463.9
AHQ-1-2, 5293 - 5319	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.26E-05	0.87	3.65	-	412.5
AHQ-1-1, 4828	R.VTYCPTEPGNYIINIK.F	1884.14221	2	7.01E-04	0.57	2.78	-	247.0
AHQ-1-4, 5075	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.99E-09	0.78	3.37	-	332.0
AHQ-1-1, 5199	R.VTYCPTEPGNYIINIK.F	1884.14221	3	1.03E-04	0.86	3.96	-	627.4
AHQ-1-1, 5309	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.88E-06	0.77	3.57	-	304.2
AHQ-1-6, 4923	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.61E-05	0.88	3.57	-	544.1
AHQ-1-5, 5123 - 5193	R.VTYCPTEPGNYIINIK.F	1884.14221	2	5.24E-07	0.92	4.47	-	520.0
AHQ-1-7, 4997	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.86E-04	0.42	2.56	-	267.8
AHQ-1-4, 5212	R.VTYCPTEPGNYIINIK.F	1884.14221	2	5.35E-05	0.68	3.46	-	301.4
AHQ-1-3, 5143	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.56E-05	0.88	3.60	-	451.2
AHQ-1-8, 5351	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.19E-05	0.71	2.79	-	393.0
AHQ-1-6, 4987	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	9.42E-04	0.62	2.69	-	326.9
AHQ-1-13, 5217	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	7.87E-04	0.70	2.83	-	443.8
AHQ-1-13- , 5527	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.45E-04	0.89	3.66	-	748.4
AHQ-1-6, 5490	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	8.04E-04	0.72	2.62	-	614.7
AHQ-1-11, 5027	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.51E-04	0.81	3.07	-	510.2
AHQ-1-4, 5698 - 5763	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	8.16E-04	0.80	3.03	-	712.4
AHQ-1-5, 5515 - 5561	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.45E-04	0.82	3.17	-	600.1
AHQ-1-14- , 4923 - 4943	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	1.89E-04	0.52	2.94	-	311.2
AHQ-1-2, 5785 - 5803	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	5.14E-05	0.46	2.71	-	328.9
AHQ-1-9, 5374 - 5376	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	6.48E-04	0.77	3.42	-	432.8
AHQ-1-14- , 5382	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	6.85E-04	0.84	3.24	-	636.1
AHQ-1-4, 5614 - 5694	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.08E-05	0.80	2.76	-	745.5
AHQ-1-4, 2671	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	3.43E-05	0.84	2.81	-	1005.8
AHQ-1-13- , 3472	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.54E-07	0.88	3.48	-	739.0
AHQ-1-1, 2784	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	4.67E-05	0.82	2.89	-	880.7
AHQ-1-13- , 2748	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	8.39E-04	0.68	2.53	-	692.1
AHQ-1-13, 3382	R.YAPSEAGLHEMDIR.Y	1589.75482	2	9.51E-04	0.74	2.80	-	776.3
AHQ-1-5, 3287	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.17E-04	0.91	3.79	-	993.5
AHQ-1-9, 3188	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.02E-04	0.70	2.76	-	645.5
AHQ-1-6, 3287	R.YAPSEAGLHEMDIR.Y	1589.75482	2	4.62E-06	0.67	2.64	-	621.0
AHQ-1-8, 3161	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.08E-05	0.75	3.01	-	761.0
AHQ-1-1, 4392	K.YGGDEIPFSPYR.V	1401.50466	1	2.22E-04	0.17	2.02	-	356.5
AHQ-1-2, 4497 - 4498	K.YGGDEIPFSPYR.V	1401.50466	1	7.78E-04	0.39	2.75	-	430.9
AHQ-1-12, 4113 - 4114	K.YGGDEIPFSPYR.V	1401.50466	2	6.13E-04	0.76	3.42	-	471.9
AHQ-1-1, 4409	K.YGGDEIPFSPYR.V	1401.50466	1	4.16E-07	0.25	2.26	-	426.8
AHQ-1-1, 4380 - 4443	K.YGGDEIPFSPYR.V	1401.50466	2	2.69E-05	0.72	3.10	-	438.8
AHQ-1-3, 4346	K.YGGDEIPFSPYR.V	1401.50466	1	1.00E-06	0.57	2.78	-	495.5
AHQ-1-4, 4403 - 4404	K.YGGDEIPFSPYR.V	1401.50466	1	5.16E-04	0.27	2.31	-	381.4
AHQ-1-3, 4345	K.YGGDEIPFSPYR.V	1401.50466	1	9.45E-04	0.22	1.85	-	457.6
AHQ-1-10, 3127	K.YGGPYHIGGSPFK.A	1380.53182	2	3.86E-06	0.96	4.42	-	1636.6
AHQ-1-9, 3123	K.YGGPYHIGGSPFK.A	1380.53182	1	6.36E-04	0.88	3.09	-	795.3
AHQ-1-11, 3191 - 3194	K.YGGPYHIGGSPFK.A	1380.53182	2	7.88E-07	0.98	5.10	-	1982.0
AHQ-1-1, 3493	K.YGGPYHIGGSPFK.A	1380.53182	2	7.08E-06	0.93	3.69	-	1179.1
AHQ-1-5, 3213	K.YGGPYHIGGSPFK.A	1380.53182	2	5.98E-07	0.96	4.39	-	1583.6
AHQ-1-6, 3214	K.YGGPYHIGGSPFK.A	1380.53182	2	4.29E-07	0.93	3.86	-	1335.0
AHQ-1-13- , 3488	K.YGGPYHIGGSPFK.A	1380.53182	2	3.31E-05	0.95	3.98	-	1329.5
AHQ-1-3, 3383	K.YGGPYHIGGSPFK.A	1380.53182	2	3.56E-07	0.97	4.13	-	1915.1
AHQ-1-5, 3219	K.YGGPYHIGGSPFK.A	1380.53182	1	3.09E-07	0.87	3.54	-	562.6
AHQ-1-4, 3384	K.YGGPYHIGGSPFK.A	1380.53182	2	3.75E-08	0.97	4.48	-	2163.4
AHQ-1-5, 3222	K.YGGPYHIGGSPFK.A	1380.53182	3	9.62E-05	0.88	4.24	-	687.3
AHQ-1-2, 3499	K.YGGPYHIGGSPFK.A	1380.53182	2	4.10E-07	0.94	3.71	-	1275.9
AHQ-1-8, 3092	K.YGGPYHIGGSPFK.A	1380.53182	2	6.00E-06	0.93	3.24	-	1606.9
AHQ-1-8, 3097	K.YGGPYHIGGSPFK.A	1380.53182	2	1.35E-10	0.95	3.99	-	1370.7
AHQ-1-3, 3195 - 3197	K.YGGQPVPNFPSK.L	1291.43658	2	9.66E-04	0.86	3.15	-	559.7
AHQ-1-1, 3164	K.YGGQPVPNFPSK.L	1291.43658	1	1.21E-04	0.33	2.64	-	289.5
AHQ-1-5, 2966 - 2997	K.YGGQPVPNFPSK.L	1291.43658	2	1.81E-05	0.86	2.96	-	513.0
AHQ-1-1, 3144	K.YGGQPVPNFPSK.L	1291.43658	2	1.30E-04	0.88	3.25	-	587.1
AHQ-1-3, 3062 - 3063	K.YGGQPVPNFPSK.L	1291.43658	1	6.53E-05	0.28	1.87	-	446.7
AHQ-1-3, 3053 - 3054	K.YGGQPVPNFPSK.L	1291.43658	2	2.28E-05	0.93	4.11	-	642.4
AHQ-1-6, 2975 - 2986	K.YGGQPVPNFPSK.L	1291.43658	2	8.19E-06	0.91	3.79	-	564.0
AHQ-1-2, 3147 - 3217	K.YGGQPVPNFPSK.L	1291.43658	2	7.05E-05	0.92	3.62	-	524.0
AHQ-1-1, 6207	K.YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR.E	4038.44995	3	6.40E-09	0.93	4.76	-	1034.7
AHQ-1-4, 4411	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.55E-05	0.86	3.77	-	887.8
AHQ-1-5, 4197	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	5.06E-04	0.87	3.99	-	777.9
AHQ-1-1, 2989	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.82E-07	0.90	3.62	-	630.9
AHQ-1-8, 2498	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.03E-05	0.91	3.77	-	622.2
AHQ-1-4, 2852 - 2863	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.26E-08	0.95	4.54	-	680.4
AHQ-1-4, 3130	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.40E-08	0.84	3.33	-	425.3
AHQ-1-5, 2991	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.62E-06	0.67	2.91	-	460.2
AHQ-1-1, 2999	K.YNEQHVPGSPFTAR.V	1603.71978	3	3.49E-06	0.91	4.52	-	1012.7
AHQ-1-3, 2847	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.58E-04	0.65	2.78	-	404.5
AHQ-1-3, 3127	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.30E-06	0.69	2.63	-	522.9
AHQ-1-2, 2965	K.YNEQHVPGSPFTAR.V	1603.71978	2	4.55E-04	0.77	2.63	-	505.7
AHQ-1-5, 2701	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.02E-05	0.93	3.61	-	907.5
AHQ-1-10, 2661	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.32E-04	0.50	2.55	-	344.7
AHQ-1-5, 2706	K.YNEQHVPGSPFTAR.V	1603.71978	3	2.65E-08	0.92	4.08	-	1138.1
AHQ-1-13- , 2943	K.YNEQHVPGSPFTAR.V	1603.71978	2	3.50E-08	0.80	2.95	-	442.9

AHQ-1-6, 2744	K.YNEQHVPGSPFTAR.V	1603.71978	2	5.77E-04	0.90	3.33	-	770.1
AHQ-1-11, 2731	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.05E-04	0.65	2.73	-	399.8
AHQ-1-3, 4446 - 4455	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.66E-04	0.59	2.64	-	581.3
AHQ-1-2, 4598	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.66E-06	0.84	3.57	-	687.4
AHQ-1-10, 4111	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.54E-04	0.85	4.13	-	390.5
AHQ-1-11, 4226	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.38E-08	0.84	3.22	-	756.5
AHQ-1-3, 4589 - 4657	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.78E-07	0.92	4.37	-	618.8
AHQ-1-1, 4729 - 4803	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.13E-07	0.94	4.77	-	718.4
AHQ-1-2, 4725 - 4805	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.29E-05	0.96	4.80	-	1283.9
AHQ-1-9, 4492	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.27E-05	0.89	3.52	-	736.3
AHQ-1-1, 4588 - 4655	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	8.52E-07	0.95	5.27	-	619.3
AHQ-1-1, 4468	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.41E-05	0.86	3.96	-	454.5
AHQ-1-2, 4909 - 4977	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.92E-08	0.91	4.40	-	537.7
AHQ-1-3, 4757 - 4825	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.12E-07	0.95	5.24	-	697.8
AHQ-1-4, 4846	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.42E-09	0.90	4.02	-	662.3
AHQ-1-4, 4662 - 4730	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.32E-08	0.94	4.49	-	803.7
AHQ-1-5, 4553 - 4625	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.09E-05	0.95	4.73	-	811.8
AHQ-1-6, 4546	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.84E-05	0.93	4.41	-	775.9
AHQ-1-8, 4559	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.33E-04	0.74	3.33	-	381.3
AHQ-1-3, 6733 - 6807	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.44E-05	0.82	3.08	-	700.6
AHQ-1-2, 6566	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.04E-11	0.94	3.90	-	1235.3
AHQ-1-1, 6667	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	2.69E-06	0.86	3.51	-	772.1
AHQ-1-1, 6805	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.23E-07	0.87	3.27	-	749.9
AHQ-1-3, 6726 - 6794	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	2.83E-06	0.67	3.03	-	545.6
AHQ-1-2, 6779	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	2.72E-08	0.92	3.79	-	1141.1
AHQ-1-2, 7033 - 7101	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	7.06E-12	0.82	3.47	-	653.6
AHQ-1-5, 6846	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	4.16E-05	0.75	2.53	-	771.0
AHQ-1-2, 6925 - 6989	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.86E-06	0.95	4.73	-	1017.1
AHQ-1-1, 6355 - 6379	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	2.65E-09	0.93	3.66	-	1000.6
gi|13124879|ref|NP_002465.1| smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]				3.89E-15	7.60	90.35	5.00	227336.7
AHQ-1-1, 4889	R.DLGEELEALK.T	1117.23151	2	1.55E-04	0.86	3.41	-	683.7
AHQ-1-2, 5039	R.DLGEELEALK.T	1117.23151	2	3.32E-06	0.89	3.44	-	855.8
AHQ-1-6, 2702	R.EDQSILCTGESGAGK.T	1553.63107	2	2.87E-04	0.63	2.95	-	386.1
AHQ-1-1, 3027	K.FDQLLAEEK.N	1093.21165	2	3.78E-05	0.90	2.86	-	1225.9
AHQ-1-4, 2883	K.FDQLLAEEK.N	1093.21165	1	4.41E-05	0.56	2.07	-	971.8
AHQ-1-2, 2993	K.FDQLLAEEK.N	1093.21165	2	1.43E-04	0.93	3.29	-	1627.7
AHQ-1-2, 3005	K.FDQLLAEEK.N	1093.21165	1	1.25E-04	0.44	2.41	-	694.5
AHQ-1-3, 2890	K.FDQLLAEEK.N	1093.21165	2	1.79E-05	0.92	3.25	-	1426.5
AHQ-1-1, 3032	K.FDQLLAEEK.N	1093.21165	1	7.50E-04	0.79	2.71	-	949.3
AHQ-1-3, 2481	K.KEEELQAALAR.L	1258.40643	3	8.40E-05	0.93	3.35	-	1812.9
AHQ-1-1, 2647	K.KEEELQAALAR.L	1258.40643	3	5.31E-04	0.91	3.61	-	1526.6
AHQ-1-3, 2469	K.KEEELQAALAR.L	1258.40643	2	4.14E-04	0.89	3.37	-	1049.8
AHQ-1-2, 2565 - 2566	K.KEEELQAALAR.L	1258.40643	2	1.51E-04	0.83	3.20	-	905.0
AHQ-1-2, 2594	K.KEEELQAALAR.L	1258.40643	3	2.36E-06	0.94	3.64	-	1848.0
AHQ-1-6, 2654	R.KFDQLLAEEK.N	1221.38456	2	8.85E-04	0.87	3.05	-	1089.7
AHQ-1-3, 2801	R.KFDQLLAEEK.N	1221.38456	1	1.44E-06	0.31	2.04	-	689.1
AHQ-1-3, 2797 - 2874	R.KFDQLLAEEK.N	1221.38456	2	1.71E-04	0.82	3.36	-	720.0
AHQ-1-1, 5440 - 5509	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	4.61E-14	0.98	6.85	-	2274.9
AHQ-1-2, 5563 - 5630	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	2.39E-14	0.98	6.74	-	1697.4
AHQ-1-3, 5289	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	7.66E-14	0.98	6.62	-	2429.9
AHQ-1-5, 6137 - 6174	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	4.66E-11	0.98	6.00	-	2743.4
AHQ-1-2, 6265 - 6287	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	3.89E-15	0.98	6.96	-	3070.0
AHQ-1-2, 6269	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	4.42E-10	0.96	4.51	-	1574.3
AHQ-1-3, 5230 - 5297	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	2.02E-04	0.66	2.81	-	437.8
AHQ-1-4, 6218	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	4.65E-05	0.95	5.05	-	1478.7
AHQ-1-2, 6481 - 6549	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.44E-13	0.97	5.62	-	2271.4
AHQ-1-6, 6040	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	2.72E-09	0.98	6.25	-	3443.9
AHQ-1-1, 6083 - 6108	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	8.39E-08	0.96	5.46	-	1651.4
AHQ-1-4, 6226	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	4.15E-06	0.97	4.37	-	1840.8
AHQ-1-2, 6610 - 6611	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.45E-11	0.97	5.43	-	1043.5
AHQ-1-2, 6447 - 6513	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.91E-10	0.97	4.54	-	1424.3
AHQ-1-5, 6519	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.72E-04	0.61	2.83	-	561.6
AHQ-1-2, 6338 - 6346	K.QLLQANPILEAFGNAK.T	1727.98540	2	5.07E-06	0.95	4.73	-	1015.8
AHQ-1-6, 6230 - 6240	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.26E-07	0.91	3.93	-	663.7
AHQ-1-5, 6353 - 6378	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.82E-06	0.93	4.03	-	903.8
AHQ-1-9, 6174 - 6183	K.QLLQANPILEAFGNAK.T	1727.98540	2	6.96E-04	0.90	3.84	-	680.1
AHQ-1-3, 6282 - 6329	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.07E-06	0.95	4.72	-	881.6
AHQ-1-3, 6461	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.76E-06	0.93	3.91	-	824.8
AHQ-1-1, 6171 - 6243	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.33E-10	0.96	4.57	-	1213.4
AHQ-1-7, 6356 - 6373	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.84E-05	0.94	4.32	-	922.3
AHQ-1-4, 6612	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.84E-10	0.96	4.62	-	1190.7
AHQ-1-1, 6303 - 6351	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.29E-06	0.92	3.59	-	1042.6
AHQ-1-1, 6407	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.00E-08	0.94	4.72	-	671.3
AHQ-1-4, 6458	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.87E-05	0.71	3.07	-	483.6
AHQ-1-4, 5948	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.11E-07	0.96	5.81	-	1302.9
AHQ-1-5, 5829 - 5830	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.23E-07	0.98	6.40	-	2436.1
AHQ-1-4, 5895 - 5931	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.51E-08	0.98	6.26	-	1863.0
AHQ-1-3, 5797 - 5803	K.TQLEELEDELQATEDAK.L	1963.04334	2	6.78E-07	0.96	4.73	-	1571.0
AHQ-1-1, 5788	K.TQLEELEDELQATEDAK.L	1963.04334	3	9.99E-05	0.92	5.04	-	989.4
AHQ-1-1, 5803	K.TQLEELEDELQATEDAK.L	1963.04334	2	5.33E-04	0.92	3.38	-	1200.2
AHQ-1-1, 4117	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.49E-04	0.93	4.38	-	831.6
AHQ-1-6, 5755	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.37E-07	0.98	6.39	-	2175.4
AHQ-1-2, 5974 - 5990	K.TQLEELEDELQATEDAK.L	1963.04334	3	3.07E-08	0.96	6.06	-	1221.4
AHQ-1-2, 5965 - 6037	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.41E-08	0.98	5.94	-	2037.4
AHQ-1-7, 5832	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.32E-08	0.97	5.39	-	1652.7
AHQ-1-2, 4214 - 4217	K.TQLEELEDELQATEDAK.L	1963.04334	2	6.57E-13	0.97	5.54	-	1181.0
AHQ-1-3, 5809 - 5823	K.TQLEELEDELQATEDAK.L	1963.04334	3	3.99E-06	0.96	5.72	-	1281.6
gi|21956645|ref|NP_665807.1| myotrophin; granule cell differentiation protein [Homo sapiens]				3.89E-15	3.86	40.32	49.20	12894.7
AHQ-1-14- , 4512	K.GADINAPDKHHITPLLSAVYEGHVSCVK.L	3031.39193	3	1.53E-06	0.95	5.74	-	930.5
AHQ-1-14, 5412	K.GADINAPDKHHITPLLSAVYEGHVSCVK.L	3031.39193	3	7.38E-07	0.97	6.16	-	1793.2
AHQ-1-14- , 4028 - 4090	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	5.78E-08	0.96	4.94	-	1190.8
AHQ-1-13, 3908 - 3963	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	5.99E-07	0.97	5.08	-	1638.7
AHQ-1-14, 4902 - 4960	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.69E-07	0.94	4.40	-	971.2
AHQ-1-14, 4920	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.57E-08	0.97	5.59	-	1093.7
AHQ-1-14, 5020 - 5086	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	9.98E-04	0.74	3.56	-	547.5
AHQ-1-14, 4804 - 4864	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	9.43E-04	0.96	4.67	-	1394.2
AHQ-1-13, 4019 - 4088	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.41E-08	0.94	5.04	-	953.6
AHQ-1-14- , 4043	K.GPDGLTAFEATDNQAIK.A	1748.87196	3	1.75E-07	0.88	4.05	-	929.8
AHQ-1-13- , 4107 - 4171	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	4.03E-06	0.97	4.93	-	1753.8
AHQ-1-13- , 4236	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.61E-07	0.85	3.10	-	774.5
AHQ-1-14- , 3938 - 4007	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.89E-15	0.98	5.91	-	1681.1
AHQ-1-14- , 4015	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	4.35E-09	0.98	6.37	-	2520.8
AHQ-1-14- , 3598	K.NGDLDEVKDYVAK.G	1466.57496	2	8.10E-10	0.92	3.10	-	1395.2
AHQ-1-14, 4472	K.NGDLDEVKDYVAK.G	1466.57496	2	3.51E-08	0.95	3.82	-	1689.7
AHQ-1-13- , 3801	K.NGDLDEVKDYVAK.G	1466.57496	2	1.35E-08	0.88	3.70	-	829.1
AHQ-1-14- , 3707 - 3708	K.NGDLDEVKDYVAK.G	1466.57496	2	3.79E-08	0.95	4.02	-	1647.6
AHQ-1-13, 3687 - 3757	K.NGDLDEVKDYVAK.G	1466.57496	2	7.38E-08	0.87	3.02	-	1076.8

gi|4505839|ref|NP_002645.1| pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro				6.11E-15	18.70	210.30	46.00	57913.6
AHQ-1-7, 5013	R.AGKPVICATQMLESM*IK.K	1895.29809	2	4.67E-04	0.91	4.33	-	1024.6
AHQ-1-7, 6546	R.AGKPVICATQMLESMIK.K	1879.29869	3	1.83E-05	0.93	4.76	-	1402.4
AHQ-1-7, 6556 - 6576	R.AGKPVICATQMLESMIK.K	1879.29869	2	1.93E-07	0.97	5.01	-	1096.5
AHQ-1-7, 5588	K.CDENILWLDYK.N	1470.62849	1	3.23E-07	0.75	3.35	-	493.7
AHQ-1-7, 6222 - 6292	R.EAEAAIYHLQLFEELR.R	1933.15326	2	4.38E-08	0.93	4.08	-	838.3
AHQ-1-7, 6110 - 6181	R.EAEAAIYHLQLFEELR.R	1933.15326	2	2.42E-07	0.95	4.30	-	1086.2
AHQ-1-7, 7440 - 7441	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	1.53E-09	0.98	5.72	-	1657.2
AHQ-1-7, 7504 - 7505	K.FGVEQDVDMVFASFIR.K	1861.11055	2	1.43E-10	0.97	5.17	-	1402.5
AHQ-1-7, 5312	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.98E-12	0.95	4.41	-	1428.8
AHQ-1-7, 4876 - 4946	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.94E-07	0.94	4.61	-	1142.1
AHQ-1-7, 4708 - 4742	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.43E-05	0.91	4.16	-	951.5
AHQ-1-7, 5022 - 5060	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.84E-06	0.92	4.42	-	934.6
AHQ-1-7, 6916 - 6984	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	6.11E-15	0.97	5.77	-	1836.9
AHQ-1-10, 6039	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	9.49E-07	0.74	3.40	-	386.4
AHQ-1-14- , 6450	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	2.91E-11	0.96	4.95	-	1835.9
AHQ-1-7, 6957 - 7020	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	9.91E-05	0.96	4.85	-	1099.4
AHQ-1-7, 6969	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	1.24E-10	0.91	3.93	-	623.6
AHQ-1-7, 7049	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.17E-04	0.93	4.28	-	1276.9
AHQ-1-8, 6940	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.33E-04	0.97	5.09	-	2090.6
AHQ-1-13- , 6705 - 6717	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.81E-08	0.97	5.74	-	1635.8
AHQ-1-9, 6814	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	2.66E-04	0.95	3.85	-	1977.7
AHQ-1-3, 4839	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	1.22E-06	0.89	3.53	-	728.6
AHQ-1-7, 4682 - 4753	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	6.66E-08	0.97	6.02	-	971.8
AHQ-1-1, 4845	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	5.48E-04	0.53	2.57	-	451.9
AHQ-1-7, 3126 - 3197	K.ITLDNAYMEK.C	1198.37126	2	4.89E-05	0.58	2.62	-	439.5
AHQ-1-7, 6401 - 6481	K.ITLDNAYMEKCDENILWLDYK.N	2649.97716	2	6.95E-06	0.88	3.89	-	785.5
AHQ-1-7, 6070 - 6121	K.ITLDNAYM*EKCDENILWLDYK.N	2665.97656	3	3.40E-05	0.88	4.30	-	798.4
AHQ-1-8, 4101 - 4107	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	1.36E-05	0.97	5.05	-	1502.7
AHQ-1-7, 4184 - 4208	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	4.09E-05	0.97	5.46	-	1525.9
AHQ-1-7, 4197	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	6.36E-06	0.92	4.17	-	1251.4
AHQ-1-10, 3861	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	2.22E-04	0.96	5.14	-	1187.4
AHQ-1-7, 5426	K.KGVNLPGAAVDLPAVSEKDIQDLK.F	2478.82685	3	9.26E-08	0.98	5.56	-	2544.1
AHQ-1-13, 5492	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.06E-07	0.93	4.50	-	721.6
AHQ-1-11, 5403	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.44E-06	0.94	4.61	-	885.2
AHQ-1-7, 6196 - 6264	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	7.96E-06	0.97	5.63	-	1358.2
AHQ-1-7, 6469 - 6549	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.01E-06	0.96	4.48	-	1422.6
AHQ-1-7, 5629	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.63E-06	0.95	4.29	-	1087.3
AHQ-1-7, 6060 - 6129	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.27E-06	0.98	5.93	-	1630.4
AHQ-1-7, 6625 - 6701	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.02E-04	0.74	3.34	-	424.5
AHQ-1-10, 5283	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.39E-08	0.94	4.48	-	870.3
AHQ-1-3, 6007 - 6087	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	9.94E-04	0.48	3.06	-	472.7
AHQ-1-9, 5890 - 5967	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.37E-06	0.94	4.49	-	846.5
AHQ-1-7, 6332 - 6400	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.37E-04	0.97	5.33	-	1288.8
AHQ-1-1, 5929 - 5969	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.08E-05	0.90	4.10	-	557.0
AHQ-1-14- , 3463	R.LDIDSPPITAR.N	1198.35099	2	7.00E-07	0.95	3.68	-	1475.7
AHQ-1-13, 3443	R.LDIDSPPITAR.N	1198.35099	2	8.17E-04	0.79	3.10	-	628.6
AHQ-1-7, 3438 - 3472	R.LDIDSPPITAR.N	1198.35099	2	2.17E-05	0.93	3.74	-	959.2
AHQ-1-7, 2617	R.LNFSHGTHEYHAETIK.N	1885.02879	2	3.53E-11	0.70	3.23	-	434.4
AHQ-1-9, 2230	R.LNFSHGTHEYHAETIK.N	1885.02879	2	1.05E-07	0.89	4.14	-	503.8
AHQ-1-7, 4080 - 4082	R.NTGIICTIGPASR.S	1361.54994	2	3.17E-06	0.86	3.40	-	897.5
AHQ-1-13, 3455 - 3467	R.NTGIICTIGPASR.S	1361.54994	2	4.18E-05	0.94	3.71	-	1236.7
AHQ-1-3, 3581	R.NTGIICTIGPASR.S	1361.54994	2	1.76E-05	0.87	2.97	-	1139.0
AHQ-1-11, 3304	R.NTGIICTIGPASR.S	1361.54994	2	2.34E-05	0.88	3.45	-	869.5
AHQ-1-7, 3801	R.NTGIICTIGPASR.S	1361.54994	2	9.20E-05	0.91	3.78	-	1072.6
AHQ-1-7, 3424 - 3452	R.NTGIICTIGPASR.S	1361.54994	2	1.86E-05	0.94	3.95	-	1182.1
AHQ-1-14- , 3484	R.NTGIICTIGPASR.S	1361.54994	2	6.45E-04	0.93	3.81	-	1135.9
AHQ-1-13- , 3548 - 3559	R.NTGIICTIGPASR.S	1361.54994	2	2.62E-06	0.93	3.97	-	1045.3
AHQ-1-7, 4922	R.RFDEILEASDGIMVAR.G	1823.06385	2	2.92E-09	0.95	4.48	-	926.6
AHQ-1-7, 5484	R.RFDEILEASDGIMVAR.G	1823.06385	2	1.05E-04	0.91	4.19	-	798.5
AHQ-1-7, 5009	R.RFDEILEASDGIMVAR.G	1823.06385	2	4.00E-04	0.90	4.53	-	482.2
AHQ-1-7, 5241 - 5280	R.RFDEILEASDGIMVAR.G	1823.06385	2	9.59E-13	0.98	5.70	-	1582.4
AHQ-1-7, 5834 - 5904	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	2.87E-04	0.44	2.89	-	147.1
AHQ-1-11, 5372 - 5387	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	9.37E-05	0.76	3.50	-	313.8
AHQ-1-11, 5366	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	7.33E-07	0.66	3.07	-	695.1
AHQ-1-13, 5391 - 5469	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	1.27E-05	0.80	3.32	-	841.4
AHQ-1-14- , 5706 - 5782	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	5.90E-05	0.86	3.78	-	967.3
AHQ-1-7, 2869 - 2880	R.VNFAMNVGK.A	980.16641	2	2.30E-06	0.89	2.94	-	810.9
gi|13562114|ref|NP_110400.1| beta tubulin 1, class VI [Homo sapiens]				1.05E-14	19.74	220.38	61.40	50326.6
AHQ-1-7, 7384	K.AFVHWYTSEGM*DINEFGEAENNIHDLVSEYQQFQDAK.A	4380.62526	3	1.40E-04	0.91	4.76	-	876.4
AHQ-1-1, 6443 - 6445	R.ALSVAELTQQMFDAR.N	1680.90740	2	7.85E-06	0.88	3.82	-	1031.1
AHQ-1-10, 5703	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.15E-04	0.97	5.15	-	1542.8
AHQ-1-9, 6394	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.01E-06	0.94	4.39	-	1289.9
AHQ-1-3, 6477	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.08E-05	0.96	4.76	-	1501.2
AHQ-1-9, 4675	R.ALSVAELTQQM*FDAR.N	1696.90680	2	3.38E-05	0.89	3.98	-	917.0
AHQ-1-13- , 6369 - 6379	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.08E-04	0.92	3.54	-	1322.5
AHQ-1-6, 6452	R.ALSVAELTQQMFDAR.N	1680.90740	2	4.37E-06	0.91	3.78	-	1028.9
AHQ-1-8, 6474 - 6478	R.ALSVAELTQQMFDAR.N	1680.90740	2	3.75E-04	0.96	4.58	-	1767.3
AHQ-1-11, 5807 - 5824	R.ALSVAELTQQMFDAR.N	1680.90740	2	3.59E-04	0.80	3.00	-	846.1
AHQ-1-7, 6544 - 6548	R.ALSVAELTQQMFDAR.N	1680.90740	2	6.19E-04	0.97	5.34	-	1290.0
AHQ-1-7, 4785 - 4792	R.ALSVAELTQQM*FDAR.N	1696.90680	2	3.69E-08	0.97	5.40	-	1650.9
AHQ-1-14- , 4108	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	6.79E-05	0.80	3.53	-	515.3
AHQ-1-7, 4954 - 5025	R.AVLVDLEPGTMDSIR.S	1616.86162	2	4.91E-08	0.93	4.75	-	662.5
AHQ-1-7, 3856	R.EIVHIQIGQCGNQIGAK.F	1867.11965	3	1.04E-04	0.94	4.66	-	1229.6
AHQ-1-7, 4021 - 4094	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	3.36E-05	0.75	3.43	-	436.3
AHQ-1-14- , 3838 - 3842	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	2.48E-04	0.93	4.38	-	865.9
AHQ-1-12, 3123 - 3195	K.EVDQQLLSVQTR.N	1416.56231	2	3.44E-04	0.58	2.65	-	464.1
AHQ-1-3, 3335	K.EVDQQLLSVQTR.N	1416.56231	2	5.53E-04	0.79	3.45	-	600.5
AHQ-1-10, 3059 - 3067	K.EVDQQLLSVQTR.N	1416.56231	2	8.05E-06	0.94	4.39	-	1255.9
AHQ-1-7, 4802 - 4806	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	6.70E-08	0.94	4.53	-	783.2
AHQ-1-11, 4886	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	5.24E-06	0.97	5.63	-	1394.7
AHQ-1-14- , 4691	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	1.34E-07	0.97	4.72	-	1267.5
AHQ-1-7, 5393 - 5428	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	8.40E-09	0.98	7.10	-	1776.3
AHQ-1-7, 5514 - 5585	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	3.40E-05	0.96	4.27	-	1638.3
AHQ-1-7, 5600	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	3.22E-06	0.96	4.85	-	1135.2
AHQ-1-13- , 5345	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	9.79E-12	0.98	5.92	-	2429.0
AHQ-1-12, 5082	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.22E-06	0.98	5.61	-	1921.7
AHQ-1-13- , 5340	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	2.58E-08	0.93	3.95	-	1429.5
AHQ-1-14- , 5196 - 5218	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	2.07E-10	0.95	5.13	-	1082.1
AHQ-1-13, 5052 - 5112	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.46E-06	0.94	3.96	-	1062.8
AHQ-1-8, 5231	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.53E-06	0.98	6.34	-	2062.6
AHQ-1-14- , 5198	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.05E-14	0.98	5.67	-	2123.7
AHQ-1-7, 7153	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.02E-04	0.95	4.75	-	1476.7
AHQ-1-14- , 6563	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	9.25E-06	0.93	4.42	-	1730.6
AHQ-1-13- , 6817	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	8.89E-07	0.98	6.61	-	2393.8
AHQ-1-13- , 6815	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	5.04E-04	0.93	4.35	-	1624.1
AHQ-1-12, 6477 - 6482	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.48E-08	0.99	7.53	-	3093.3

AHQ-1-7, 7069	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.97E-04	0.92	4.41	-	1577.3
AHQ-1-12, 6478	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	2.00E-06	0.86	4.38	-	1103.1
AHQ-1-14- , 6566 - 6567	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.89E-12	0.99	7.21	-	2927.0
AHQ-1-8, 7020	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.01E-09	0.98	6.08	-	2675.0
AHQ-1-8, 7031	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.28E-04	0.92	4.42	-	1708.8
AHQ-1-10, 6165	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.10E-07	0.98	5.99	-	1982.8
AHQ-1-11, 6280	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	3.37E-04	0.90	3.98	-	1604.0
AHQ-1-4, 7196	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.71E-06	0.98	5.68	-	2849.0
AHQ-1-11, 6275 - 6352	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.81E-05	0.98	5.64	-	1982.9
AHQ-1-7, 7068 - 7070	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	8.96E-09	0.99	7.50	-	2438.9
AHQ-1-9, 6922	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.45E-06	0.77	4.14	-	698.1
AHQ-1-9, 6914 - 6992	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.59E-11	0.98	6.24	-	2071.6
AHQ-1-6, 6987 - 7007	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.31E-06	0.93	4.09	-	1435.3
AHQ-1-13, 6359	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.80E-12	0.99	7.28	-	2839.4
AHQ-1-13, 6360	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	2.20E-04	0.96	4.72	-	2500.4
AHQ-1-13- , 6596	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.71E-08	0.89	4.32	-	734.3
AHQ-1-14- , 6284 - 6366	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	9.81E-08	0.95	4.69	-	992.2
AHQ-1-13, 6169	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.22E-06	0.90	4.27	-	711.9
AHQ-1-7, 6882 - 6888	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	9.49E-08	0.93	4.51	-	845.5
AHQ-1-9, 6704	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	4.99E-11	0.93	4.36	-	779.5
AHQ-1-7, 3050	R.IMNSFSVM*PSPK.V	1354.62100	2	4.63E-04	0.83	2.83	-	807.5
AHQ-1-7, 4032	R.IMNSFSVMPSPK.V	1338.62160	2	5.04E-06	0.93	3.56	-	1095.8
AHQ-1-7, 3902 - 3917	R.IMNSFSVMPSPK.V	1338.62160	2	3.25E-05	0.95	3.93	-	1364.4
AHQ-1-13- , 3436	R.ISVYYNEAYGR.K	1335.44622	2	8.34E-06	0.75	2.77	-	571.6
AHQ-1-14, 4068 - 4072	R.ISVYYNEAYGR.K	1335.44622	2	6.32E-07	0.89	3.13	-	968.7
AHQ-1-7, 3172	R.ISVYYNEAYGR.K	1335.44622	2	4.65E-07	0.94	3.24	-	1323.5
AHQ-1-1, 3364 - 3372	R.ISVYYNEAYGR.K	1335.44622	2	5.53E-04	0.64	2.69	-	446.8
AHQ-1-8, 3088	R.ISVYYNEAYGR.K	1335.44622	2	2.99E-08	0.93	3.13	-	1296.9
AHQ-1-14- , 3174	R.ISVYYNEAYGR.K	1335.44622	2	1.25E-08	0.92	3.46	-	1023.4
AHQ-1-7, 3261	R.ISVYYNEAYGR.K	1335.44622	2	4.06E-08	0.92	3.11	-	1158.4
AHQ-1-7, 3190 - 3262	R.ISVYYNEAYGR.K	1335.44622	1	1.93E-04	0.25	2.37	-	190.9
AHQ-1-7, 5252	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	3.55E-08	0.67	2.81	-	547.4
AHQ-1-13- , 5160	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	8.36E-08	0.86	3.73	-	877.0
AHQ-1-7, 5249	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	7.89E-06	0.95	4.72	-	895.2
AHQ-1-10, 5304	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	8.99E-04	0.96	4.85	-	1796.3
AHQ-1-10, 5297	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	9.10E-05	0.92	3.99	-	727.6
AHQ-1-11, 4858	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.18E-06	0.98	5.86	-	1347.3
AHQ-1-14- , 5830	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	2.29E-04	0.72	3.28	-	1102.6
AHQ-1-8, 5659	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	5.51E-06	0.97	5.50	-	957.5
AHQ-1-9, 5790 - 5794	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	1.95E-05	0.95	4.92	-	749.4
AHQ-1-9, 5100 - 5108	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	1.96E-04	0.98	5.95	-	2300.1
AHQ-1-11, 5476	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	3.17E-08	0.96	5.42	-	797.3
AHQ-1-7, 7018 - 7082	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	5.39E-11	0.94	4.43	-	958.4
AHQ-1-1, 6815	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	1.28E-06	0.83	3.74	-	832.2
AHQ-1-9, 6839 - 6908	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	4.16E-04	0.91	4.92	-	910.2
AHQ-1-8, 7447	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	1.25E-08	0.94	5.02	-	1119.5
AHQ-1-9, 6888	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	3.64E-09	0.87	3.87	-	875.6
AHQ-1-9, 7186 - 7255	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	8.57E-08	0.95	5.18	-	786.3
AHQ-1-7, 7445	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.17E-06	0.95	5.25	-	733.8
AHQ-1-7, 7444 - 7446	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	1.49E-05	0.94	5.12	-	1125.7
AHQ-1-7, 7078	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	7.84E-06	0.93	4.76	-	1168.2
AHQ-1-8, 7446	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	2.14E-09	0.95	5.29	-	805.4
AHQ-1-7, 7013 - 7040	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.29E-05	0.91	5.17	-	667.7
AHQ-1-9, 7256	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	3.91E-09	0.93	4.77	-	1219.5
AHQ-1-10, 6100	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	3.93E-04	0.77	3.62	-	434.3
AHQ-1-14- , 6496 - 6534	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	6.96E-06	0.95	5.40	-	1109.9
AHQ-1-4, 7411	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	4.73E-04	0.80	3.38	-	975.4
AHQ-1-9, 5424	R.NSSCFVEWIPNNVK.V	1695.87718	2	1.43E-06	0.89	3.52	-	863.5
AHQ-1-7, 3001	R.VSEHFSAMFK.R	1183.36152	2	9.03E-07	0.87	2.68	-	1041.2
AHQ-1-9, 5266	R.YLTVACIFR.G	1144.36822	2	1.02E-04	0.86	2.79	-	758.9
AHQ-1-11, 4956	R.YLTVACIFR.G	1144.36822	2	5.29E-04	0.88	2.66	-	896.6
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				2.55E-14	20.14	220.35	19.50	191612.6
AHQ-1-4, 7464	K.AFMTADLPNELIELLEK.I	1948.26956	2	4.34E-04	0.23	2.71	-	195.0
AHQ-1-3, 7285	K.AFMTADLPNELIELLEK.I	1948.26956	2	6.10E-05	0.92	4.31	-	610.9
AHQ-1-3, 4527	R.ALEHFTDLYDIK.R	1465.63179	2	5.73E-06	0.90	3.24	-	969.0
AHQ-1-3, 7281	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	2.92E-06	0.89	4.18	-	1016.2
AHQ-1-6, 7300	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	3.94E-04	0.70	3.40	-	543.5
AHQ-1-3, 4913	R.GQFSTDELVAEVEK.R	1552.66462	2	2.35E-07	0.95	4.51	-	1292.4
AHQ-1-1, 4945	R.GQFSTDELVAEVEK.R	1552.66462	2	3.98E-05	0.88	3.22	-	1044.4
AHQ-1-4, 4896	R.GQFSTDELVAEVEKR.N	1708.85097	2	6.14E-10	0.85	3.53	-	784.9
AHQ-1-5, 4738	R.GQFSTDELVAEVEKR.N	1708.85097	2	6.97E-07	0.83	3.40	-	727.3
AHQ-1-3, 4821	R.GQFSTDELVAEVEKR.N	1708.85097	2	3.10E-09	0.88	3.53	-	909.8
AHQ-1-3, 3378	K.HDVVFLITK.Y	1072.28194	2	1.35E-07	0.92	3.06	-	1134.8
AHQ-1-3, 3517	R.HSSLAGCQIINYR.T	1520.69551	2	2.16E-06	0.96	4.21	-	1247.4
AHQ-1-3, 2085	R.IHEGCEEPATHNALAK.I	1778.92458	2	2.06E-05	0.91	3.83	-	831.7
AHQ-1-3, 5357	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	2.55E-14	0.97	5.96	-	1352.0
AHQ-1-3, 7094	R.KFDVNTSAVQVLIEHIGNLDR.A	2369.66218	3	9.35E-13	0.98	6.49	-	2046.6
AHQ-1-6, 4423	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	3	4.15E-05	0.83	3.09	-	1071.3
AHQ-1-3, 4578	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	3	4.47E-04	0.91	4.18	-	1134.0
AHQ-1-3, 4583 - 4585	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	1.90E-11	0.97	5.34	-	1196.9
AHQ-1-3, 4415	K.LHIIEVGTPPTGNQPFPK.K	1946.23831	2	7.60E-09	0.89	4.12	-	506.8
AHQ-1-3, 3795	K.LLYNNVSNFGR.L	1297.44435	2	6.98E-04	0.89	3.13	-	886.6
AHQ-1-3, 6865	R.LPVVIGGLLDVDCSEDVIK.N	2043.36744	2	2.69E-05	0.96	5.29	-	1184.0
AHQ-1-3, 6374	R.NLQNLLILTAIK.A	1354.66353	2	1.26E-06	0.97	5.05	-	1820.7
AHQ-1-3, 4398	R.NNLAGAEELFAR.K	1305.42165	2	4.68E-08	0.90	3.43	-	977.5
AHQ-1-4, 7092	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	5.50E-07	0.93	4.74	-	941.3
AHQ-1-5, 7041	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	3.38E-04	0.95	5.30	-	1354.5
AHQ-1-3, 6918 - 6922	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	1.64E-06	0.98	6.93	-	1643.7
AHQ-1-5, 5105	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	8.84E-08	0.96	4.52	-	1908.5
AHQ-1-3, 7062	K.VGYTPDWIFLLR.N	1480.73443	2	1.55E-08	0.89	3.69	-	572.6
AHQ-1-4, 7228	K.VGYTPDWIFLLR.N	1480.73443	2	1.20E-07	0.83	3.54	-	428.2
AHQ-1-3, 3153	K.VIQCFAETGQVQK.I	1509.70940	2	5.73E-06	0.96	3.88	-	1929.2
AHQ-1-3, 3830	R.VVGAMQLYSVDR.K	1338.55819	2	4.90E-06	0.93	3.50	-	1212.4
AHQ-1-3, 3218	R.VVGAM*QLYSVDR.K	1354.55759	2	3.95E-04	0.64	2.71	-	573.3
gi|4501881|ref|NP_001091.1| alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA				3.05E-14	12.38	180.27	46.40	42050.8
AHQ-1-1, 2093	K.AGFAGDDAPR.A	977.01283	2	4.50E-05	0.85	2.75	-	1047.6
AHQ-1-8, 1551 - 1620	K.AGFAGDDAPR.A	977.01283	2	5.45E-06	0.88	3.66	-	799.2
AHQ-1-8, 1687 - 1768	K.AGFAGDDAPR.A	977.01283	2	7.78E-06	0.89	3.37	-	965.6
AHQ-1-13- , 2027 - 2096	K.AGFAGDDAPR.A	977.01283	2	6.29E-05	0.89	3.28	-	993.5
AHQ-1-13, 2034 - 2090	K.AGFAGDDAPR.A	977.01283	2	5.22E-04	0.88	3.38	-	949.8
AHQ-1-8, 1908 - 1975	K.AGFAGDDAPR.A	977.01283	2	1.61E-05	0.89	3.31	-	989.3
AHQ-1-12, 2013	K.AGFAGDDAPR.A	977.01283	2	2.13E-04	0.87	2.65	-	1203.0
AHQ-1-12, 1890 - 1953	K.AGFAGDDAPR.A	977.01283	2	3.29E-04	0.86	3.33	-	967.7
AHQ-1-10, 1829 - 1849	K.AGFAGDDAPR.A	977.01283	2	3.89E-04	0.84	2.78	-	1003.7
AHQ-1-8, 2040	K.AGFAGDDAPR.A	977.01283	2	3.69E-04	0.86	2.86	-	978.4
AHQ-1-9, 1676 - 1746	K.AGFAGDDAPR.A	977.01283	2	1.22E-06	0.87	3.03	-	937.0
AHQ-1-4, 3276	R.AVFPSIVGRPR.H	1199.43018	2	3.98E-05	0.21	2.50	-	397.8

AHQ-1-8, 4055	R.DLTDYLMK.I	999.16326	1	8.88E-05	0.50	2.49	-	488.1
AHQ-1-8, 3789 - 3860	R.DLTDYLM*K.I	1015.16266	2	2.90E-04	0.88	3.55	-	546.9
AHQ-1-8, 3309	R.DLTDYLMK.I	999.16326	1	5.97E-05	0.23	1.86	-	376.1
AHQ-1-5, 4593	R.DLTDYLMK.I	999.16326	2	5.60E-04	0.62	2.51	-	413.8
AHQ-1-12, 4287	R.DLTDYLMK.I	999.16326	2	3.83E-04	0.78	2.74	-	454.9
AHQ-1-8, 4497 - 4540	R.DLTDYLMK.I	999.16326	2	1.02E-04	0.46	2.55	-	322.2
AHQ-1-9, 3711	R.DLTDYLM*K.I	1015.16266	1	6.02E-05	0.15	2.11	-	109.2
AHQ-1-1, 4573	R.DLTDYLMK.I	999.16326	2	2.78E-04	0.68	2.88	-	399.7
AHQ-1-13- , 3803	R.DLTDYLM*K.I	1015.16266	1	5.64E-04	0.20	2.20	-	140.6
AHQ-1-14- , 4850 - 4911	K.DLYANNVMSGGTTM*YPGIADR.M	2263.49384	2	9.17E-05	0.65	3.74	-	373.7
AHQ-1-8, 1969	K.DSYVGDEAQSK.R	1199.20634	1	1.78E-04	0.23	2.06	-	250.9
AHQ-1-8, 1479 - 1547	K.DSYVGDEAQSK.R	1199.20634	2	2.50E-05	0.69	3.28	-	539.3
AHQ-1-8, 1943 - 2017	K.DSYVGDEAQSK.R	1199.20634	2	4.47E-04	0.67	3.24	-	567.8
AHQ-1-13, 2983 - 3006	K.EITALAPSTMK.I	1162.38206	2	4.75E-05	0.87	3.01	-	734.3
AHQ-1-2, 2529	K.EITALAPSTM*K.I	1178.38146	2	2.35E-06	0.80	3.09	-	617.1
AHQ-1-12, 2935 - 2937	K.EITALAPSTMK.I	1162.38206	1	8.76E-05	0.70	3.00	-	414.2
AHQ-1-12, 2933 - 2934	K.EITALAPSTMK.I	1162.38206	2	5.10E-04	0.84	3.02	-	722.5
AHQ-1-6, 2895 - 2910	K.EITALAPSTMK.I	1162.38206	2	2.33E-04	0.61	2.61	-	441.6
AHQ-1-13- , 2428 - 2503	K.EITALAPSTM*K.I	1178.38146	2	1.09E-04	0.76	3.13	-	512.2
AHQ-1-14- , 2882 - 2956	K.EITALAPSTMK.I	1162.38206	1	3.50E-05	0.57	2.92	-	280.4
AHQ-1-14, 3894	K.EITALAPSTMK.I	1162.38206	1	4.79E-07	0.34	2.68	-	196.8
AHQ-1-10, 2261 - 2275	K.EITALAPSTM*K.I	1178.38146	2	9.01E-04	0.58	2.60	-	451.5
AHQ-1-13- , 2975 - 3027	K.EITALAPSTMK.I	1162.38206	2	1.69E-04	0.78	2.80	-	613.3
AHQ-1-14, 3244 - 3276	K.EITALAPSTM*K.I	1178.38146	2	8.01E-05	0.50	2.79	-	385.1
AHQ-1-14, 3872 - 3928	K.EITALAPSTMK.I	1162.38206	1	5.69E-06	0.61	2.68	-	401.7
AHQ-1-9, 2255 - 2259	K.EITALAPSTM*K.I	1178.38146	2	5.83E-04	0.90	3.17	-	927.2
AHQ-1-3, 3027	K.EITALAPSTMK.I	1162.38206	1	3.89E-06	0.35	2.19	-	319.6
AHQ-1-14- , 2880 - 2954	K.EITALAPSTMK.I	1162.38206	2	1.00E-04	0.74	2.99	-	529.8
AHQ-1-4, 3030	K.EITALAPSTMK.I	1162.38206	1	2.84E-07	0.58	2.38	-	356.8
AHQ-1-10, 2708 - 2767	K.EITALAPSTMK.I	1162.38206	1	4.68E-04	0.65	2.32	-	439.1
AHQ-1-1, 3140	K.EITALAPSTMK.I	1162.38206	1	9.43E-04	0.27	2.41	-	307.0
AHQ-1-4, 2423	K.EITALAPSTM*K.I	1178.38146	2	6.37E-04	0.81	2.81	-	746.1
AHQ-1-14- , 2378 - 2402	K.EITALAPSTM*K.I	1178.38146	2	3.35E-06	0.90	3.68	-	713.1
AHQ-1-8, 2557 - 2626	K.EITALAPSTMK.I	1162.38206	2	3.41E-04	0.83	2.93	-	722.9
AHQ-1-8, 2553 - 2766	K.EITALAPSTMK.I	1162.38206	1	3.20E-04	0.72	3.28	-	341.4
AHQ-1-8, 7310 - 7390	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	2	7.05E-07	0.79	4.03	-	425.6
AHQ-1-8, 7239 - 7320	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	3	9.60E-04	0.57	3.19	-	686.3
AHQ-1-8, 7338 - 7407	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	3	1.44E-04	0.66	3.57	-	579.9
AHQ-1-12, 1878 - 1939	R.HQGVMVGMGQK.D	1172.40691	2	1.32E-06	0.81	3.02	-	620.9
AHQ-1-8, 1525 - 1591	R.HQGVMVGMGQK.D	1172.40691	2	2.71E-05	0.94	3.97	-	773.2
AHQ-1-8, 2485	R.HQGVMVGMGQKDSYVGDEAQSK.R	2352.59065	2	1.71E-04	0.90	3.76	-	652.1
AHQ-1-8, 2487	R.HQGVMVGMGQKDSYVGDEAQSK.R	2352.59065	3	5.90E-05	0.98	4.33	-	3199.5
AHQ-1-5, 2870	K.IWHHTFYNELR.V	1516.68695	3	1.61E-05	0.92	4.39	-	1485.0
AHQ-1-13, 3121	K.IWHHTFYNELR.V	1516.68695	3	1.38E-05	0.93	4.12	-	1258.5
AHQ-1-13, 3117 - 3183	K.IWHHTFYNELR.V	1516.68695	2	1.18E-06	0.80	3.44	-	671.7
AHQ-1-12, 3354	K.IWHHTFYNELR.V	1516.68695	2	1.40E-05	0.59	2.74	-	413.6
AHQ-1-8, 2985 - 3056	K.IWHHTFYNELR.V	1516.68695	2	5.07E-08	0.87	3.74	-	898.9
AHQ-1-8, 2901 - 2965	K.IWHHTFYNELR.V	1516.68695	3	9.34E-08	0.93	3.94	-	1557.1
AHQ-1-8, 2681	K.IWHHTFYNELR.V	1516.68695	3	1.68E-05	0.94	4.55	-	1663.2
AHQ-1-12, 3006 - 3013	K.IWHHTFYNELR.V	1516.68695	3	2.25E-05	0.87	3.80	-	1240.9
AHQ-1-12, 2995 - 3059	K.IWHHTFYNELR.V	1516.68695	2	8.09E-07	0.79	3.19	-	832.0
AHQ-1-8, 2589 - 2657	K.IWHHTFYNELR.V	1516.68695	2	1.02E-05	0.82	3.43	-	872.0
AHQ-1-11, 2954	K.IWHHTFYNELR.V	1516.68695	3	1.28E-04	0.95	4.65	-	1444.0
AHQ-1-11, 2946 - 2960	K.IWHHTFYNELR.V	1516.68695	2	3.76E-05	0.89	3.75	-	1104.4
AHQ-1-6, 2916	K.IWHHTFYNELR.V	1516.68695	3	1.80E-05	0.90	4.12	-	1455.4
AHQ-1-10, 2976	K.IWHHTFYNELR.V	1516.68695	2	3.13E-07	0.90	3.35	-	942.9
AHQ-1-10, 2820	K.IWHHTFYNELR.V	1516.68695	3	5.69E-05	0.92	4.14	-	1127.6
AHQ-1-10, 2757 - 2832	K.IWHHTFYNELR.V	1516.68695	2	1.30E-04	0.73	3.16	-	813.4
AHQ-1-8, 2840 - 2920	K.IWHHTFYNELR.V	1516.68695	2	1.46E-04	0.69	2.74	-	615.6
AHQ-1-8, 2493 - 2561	K.IWHHTFYNELR.V	1516.68695	2	4.46E-06	0.86	3.93	-	803.1
AHQ-1-12, 3135	K.IWHHTFYNELR.V	1516.68695	2	1.67E-09	0.93	3.37	-	1164.1
AHQ-1-5, 2861 - 2931	K.IWHHTFYNELR.V	1516.68695	2	1.64E-05	0.52	2.60	-	602.2
AHQ-1-8, 2517 - 2586	K.IWHHTFYNELR.V	1516.68695	3	1.11E-04	0.96	4.29	-	1747.1
AHQ-1-9, 2734 - 2803	K.IWHHTFYNELR.V	1516.68695	2	3.02E-06	0.79	3.67	-	651.1
AHQ-1-9, 2743	K.IWHHTFYNELR.V	1516.68695	3	9.54E-04	0.92	3.98	-	1694.8
AHQ-1-9, 2982 - 2994	K.IWHHTFYNELR.V	1516.68695	2	5.82E-10	0.92	3.57	-	1101.0
AHQ-1-3, 3002 - 3074	K.IWHHTFYNELR.V	1516.68695	2	4.77E-04	0.38	2.57	-	529.0
AHQ-1-13- , 3155 - 3159	K.IWHHTFYNELR.V	1516.68695	2	3.53E-08	0.72	3.23	-	735.4
AHQ-1-13- , 3156 - 3173	K.IWHHTFYNELR.V	1516.68695	3	2.42E-06	0.94	4.27	-	1374.1
AHQ-1-9, 5316 - 5334	R.LDLAGRDLTDYLMK.I	1624.88375	2	9.77E-04	0.57	2.76	-	560.3
AHQ-1-9, 4468 - 4551	K.SYELPDGQVITIGNER.F	1791.93998	2	9.55E-12	0.95	4.67	-	871.6
AHQ-1-2, 5430	K.SYELPDGQVITIGNER.F	1791.93998	2	2.36E-07	0.91	3.83	-	723.0
AHQ-1-9, 4562 - 4586	K.SYELPDGQVITIGNER.F	1791.93998	2	3.44E-13	0.92	4.02	-	783.9
AHQ-1-9, 4684	K.SYELPDGQVITIGNER.F	1791.93998	2	4.43E-12	0.96	4.30	-	1229.8
AHQ-1-13- , 4596	K.SYELPDGQVITIGNER.F	1791.93998	2	1.57E-11	0.95	4.63	-	992.4
AHQ-1-9, 4838 - 4906	K.SYELPDGQVITIGNER.F	1791.93998	2	9.21E-11	0.94	4.15	-	968.8
AHQ-1-9, 4974 - 5026	K.SYELPDGQVITIGNER.F	1791.93998	2	3.90E-09	0.96	4.92	-	1095.3
AHQ-1-7, 4677	K.SYELPDGQVITIGNER.F	1791.93998	2	1.67E-06	0.88	3.33	-	604.2
AHQ-1-9, 5095 - 5166	K.SYELPDGQVITIGNER.F	1791.93998	2	1.09E-11	0.95	4.00	-	1346.1
AHQ-1-4, 4776	K.SYELPDGQVITIGNER.F	1791.93998	2	4.27E-08	0.89	3.42	-	925.7
AHQ-1-7, 5044 - 5066	K.SYELPDGQVITIGNER.F	1791.93998	2	1.39E-04	0.59	2.68	-	623.9
AHQ-1-2, 5245	K.SYELPDGQVITIGNER.F	1791.93998	2	7.41E-08	0.89	3.82	-	659.3
AHQ-1-6, 5238	K.SYELPDGQVITIGNER.F	1791.93998	2	1.53E-07	0.96	4.79	-	1286.6
AHQ-1-6, 4990 - 5020	K.SYELPDGQVITIGNER.F	1791.93998	2	7.01E-06	0.95	4.12	-	1095.2
AHQ-1-13- , 4696 - 4720	K.SYELPDGQVITIGNER.F	1791.93998	2	5.50E-13	0.94	4.02	-	1056.5
AHQ-1-8, 5234 - 5302	K.SYELPDGQVITIGNER.F	1791.93998	2	1.86E-11	0.97	5.19	-	1489.3
AHQ-1-8, 5127 - 5194	K.SYELPDGQVITIGNER.F	1791.93998	2	4.96E-11	0.96	4.85	-	1030.1
AHQ-1-13- , 4989 - 5071	K.SYELPDGQVITIGNER.F	1791.93998	2	4.94E-10	0.96	4.73	-	1112.3
AHQ-1-10, 4067 - 4141	K.SYELPDGQVITIGNER.F	1791.93998	2	6.57E-07	0.95	4.46	-	942.0
AHQ-1-1, 5131 - 5177	K.SYELPDGQVITIGNER.F	1791.93998	2	9.60E-10	0.93	3.69	-	862.3
AHQ-1-10, 4237 - 4300	K.SYELPDGQVITIGNER.F	1791.93998	2	3.42E-07	0.94	4.62	-	782.2
AHQ-1-10, 4409 - 4471	K.SYELPDGQVITIGNER.F	1791.93998	2	5.27E-11	0.95	4.58	-	1047.8
AHQ-1-10, 4453 - 4527	K.SYELPDGQVITIGNER.F	1791.93998	2	8.87E-13	0.97	5.38	-	1236.4
AHQ-1-10, 4484	K.SYELPDGQVITIGNER.F	1791.93998	3	2.93E-08	0.95	4.66	-	1371.4
AHQ-1-10, 4624 - 4679	K.SYELPDGQVITIGNER.F	1791.93998	2	3.51E-11	0.96	4.77	-	1196.2
AHQ-1-8, 4994 - 5058	K.SYELPDGQVITIGNER.F	1791.93998	2	1.58E-10	0.96	4.66	-	1296.3
AHQ-1-8, 4894 - 4958	K.SYELPDGQVITIGNER.F	1791.93998	2	3.05E-14	0.97	5.20	-	1035.9
AHQ-1-11, 4280	K.SYELPDGQVITIGNER.F	1791.93998	2	1.32E-06	0.76	2.75	-	680.6
AHQ-1-11, 4379	K.SYELPDGQVITIGNER.F	1791.93998	2	9.66E-11	0.91	4.01	-	824.4
AHQ-1-11, 4760 - 4824	K.SYELPDGQVITIGNER.F	1791.93998	2	2.04E-12	0.96	4.62	-	1264.8
AHQ-1-8, 4750 - 4812	K.SYELPDGQVITIGNER.F	1791.93998	2	1.03E-12	0.96	4.63	-	1198.2
AHQ-1-2, 4969	K.SYELPDGQVITIGNER.F	1791.93998	2	9.93E-05	0.91	4.01	-	673.3
AHQ-1-2, 4863 - 4867	K.SYELPDGQVITIGNER.F	1791.93998	2	3.46E-06	0.89	3.90	-	714.9
AHQ-1-5, 5263 - 5337	K.SYELPDGQVITIGNER.F	1791.93998	2	2.78E-07	0.92	4.13	-	968.5
AHQ-1-5, 5089	K.SYELPDGQVITIGNER.F	1791.93998	2	1.05E-06	0.90	3.61	-	953.9
AHQ-1-8, 4623	K.SYELPDGQVITIGNER.F	1791.93998	3	4.54E-09	0.94	4.40	-	1556.9
AHQ-1-8, 4618 - 4682	K.SYELPDGQVITIGNER.F	1791.93998	2	1.97E-10	0.95	4.66	-	1124.1

AHQ-1-13- , 5145 - 5223	K.SYELPDGQVITIGNER.F	1791.93998	2	7.32E-12	0.96	4.76	-	1186.3
AHQ-1-8, 4485	K.SYELPDGQVITIGNER.F	1791.93998	2	1.09E-07	0.82	3.46	-	557.9
AHQ-1-14, 5756	K.SYELPDGQVITIGNER.F	1791.93998	2	2.80E-06	0.85	3.72	-	661.0
AHQ-1-5, 4681	K.SYELPDGQVITIGNER.F	1791.93998	2	3.09E-09	0.86	3.48	-	674.0
AHQ-1-12, 4318	K.SYELPDGQVITIGNER.F	1791.93998	2	3.99E-09	0.88	3.09	-	807.8
AHQ-1-12, 4441 - 4442	K.SYELPDGQVITIGNER.F	1791.93998	2	1.12E-11	0.95	4.47	-	909.1
AHQ-1-12, 4525	K.SYELPDGQVITIGNER.F	1791.93998	2	7.51E-10	0.95	4.27	-	975.6
AHQ-1-12, 4767 - 4830	K.SYELPDGQVITIGNER.F	1791.93998	2	1.73E-10	0.87	3.26	-	772.5
AHQ-1-12, 4963	K.SYELPDGQVITIGNER.F	1791.93998	2	3.61E-04	0.81	3.12	-	773.1
AHQ-1-1, 5297 - 5301	K.SYELPDGQVITIGNER.F	1791.93998	2	2.20E-07	0.96	4.89	-	1166.7
AHQ-1-14- , 4542	K.SYELPDGQVITIGNER.F	1791.93998	2	3.27E-09	0.87	3.42	-	848.1
AHQ-1-3, 4841	K.SYELPDGQVITIGNER.F	1791.93998	2	1.68E-06	0.80	3.06	-	564.8
AHQ-1-3, 5090 - 5091	K.SYELPDGQVITIGNER.F	1791.93998	2	1.67E-10	0.95	4.69	-	786.5
AHQ-1-13, 4292	K.SYELPDGQVITIGNER.F	1791.93998	2	1.42E-07	0.89	3.47	-	829.3
AHQ-1-3, 5251	K.SYELPDGQVITIGNER.F	1791.93998	2	1.19E-04	0.93	3.90	-	795.7
AHQ-1-13, 4391	K.SYELPDGQVITIGNER.F	1791.93998	2	3.95E-08	0.77	3.01	-	612.6
AHQ-1-9, 5214	K.SYELPDGQVITIGNER.F	1791.93998	2	1.10E-11	0.96	4.64	-	1078.2
AHQ-1-13, 4487 - 4488	K.SYELPDGQVITIGNER.F	1791.93998	2	9.86E-07	0.95	4.11	-	1217.8
AHQ-1-13, 4737 - 4795	K.SYELPDGQVITIGNER.F	1791.93998	2	1.18E-08	0.92	4.06	-	817.2
AHQ-1-13, 4876 - 4948	K.SYELPDGQVITIGNER.F	1791.93998	2	3.52E-11	0.96	4.73	-	1171.1
AHQ-1-4, 5148	K.SYELPDGQVITIGNER.F	1791.93998	2	9.78E-09	0.95	4.01	-	1237.3
AHQ-1-10, 3625	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	7.22E-06	0.60	2.82	-	352.5
AHQ-1-12, 3749 - 3815	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	2.44E-04	0.50	2.91	-	371.3
AHQ-1-10, 4088 - 4104	K.YPIEHGIITNWDDMEK.I	1962.17174	3	4.08E-07	0.83	4.12	-	835.8
AHQ-1-13, 4331	K.YPIEHGIITNWDDMEK.I	1962.17174	2	6.85E-04	0.84	3.97	-	676.8
AHQ-1-13, 4485	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.06E-06	0.83	3.80	-	455.9
AHQ-1-9, 5064 - 5143	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.83E-04	0.82	3.54	-	627.4
AHQ-1-9, 4702 - 4724	K.YPIEHGIITNWDDMEK.I	1962.17174	2	9.21E-06	0.86	3.56	-	727.2
AHQ-1-9, 4506	K.YPIEHGIITNWDDMEK.I	1962.17174	2	8.72E-05	0.38	2.58	-	518.4
AHQ-1-9, 4140	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.08E-04	0.90	4.12	-	781.3
AHQ-1-13- , 4069 - 4145	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	5.13E-04	0.90	3.91	-	651.2
AHQ-1-13- , 4543 - 4611	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.73E-04	0.92	4.57	-	823.7
AHQ-1-9, 3962	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	1.45E-04	0.83	3.47	-	729.9
AHQ-1-13- , 4644 - 4724	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.27E-05	0.80	3.81	-	531.1
AHQ-1-4, 4842	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.35E-05	0.78	3.54	-	549.9
AHQ-1-8, 5094 - 5096	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.28E-05	0.88	4.22	-	583.6
AHQ-1-8, 4523 - 4595	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.53E-04	0.87	4.04	-	562.8
AHQ-1-3, 4650	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.09E-05	0.68	3.20	-	554.1
AHQ-1-4, 4694	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.40E-04	0.52	2.82	-	474.4
AHQ-1-6, 4480	K.YPIEHGIITNWDDMEK.I	1962.17174	2	8.39E-04	0.92	4.10	-	1005.0
AHQ-1-9, 4068	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	7.21E-04	0.58	3.00	-	439.9
AHQ-1-8, 5544	K.YPIEHGIITNWDDM*EKIWHHTFYNELR.V	3475.83549	3	1.27E-04	0.92	5.39	-	690.4
gi|29741246|ref|XP_294070.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				3.28E-14	4.99	60.34	17.70	35032.0
AHQ-1-13- , 5417 - 5497	K.AENGKLVINGNPITIFQER.D	2114.39062	2	6.69E-09	0.65	2.74	-	682.2
AHQ-1-9, 5291 - 5359	K.AENGKLVINGNPITIFQER.D	2114.39062	2	7.76E-07	0.74	3.64	-	503.6
AHQ-1-9, 5435 - 5502	K.AENGKLVINGNPITIFQER.D	2114.39062	2	2.71E-06	0.65	3.60	-	316.8
AHQ-1-9, 5570 - 5572	K.AENGKLVINGNPITIFQER.D	2114.39062	2	2.87E-07	0.81	3.44	-	796.9
AHQ-1-13, 5185	K.AENGKLVINGNPITIFQER.D	2114.39062	2	1.53E-07	0.63	3.10	-	432.7
AHQ-1-12, 5238	K.AENGKLVINGNPITIFQER.D	2114.39062	2	7.61E-06	0.23	2.53	-	298.2
AHQ-1-14- , 5036	K.LISWYENEFGYSNR.V	1778.90145	2	1.16E-06	0.89	3.22	-	954.7
AHQ-1-9, 5648 - 5718	K.LVINGNPITIFQER.D	1614.87029	2	2.06E-12	0.94	3.87	-	1164.0
AHQ-1-10, 5260	K.LVINGNPITIFQER.D	1614.87029	2	6.67E-06	0.94	3.87	-	1321.9
AHQ-1-12, 5603 - 5678	K.LVINGNPITIFQER.D	1614.87029	2	9.00E-07	0.80	3.16	-	569.4
AHQ-1-11, 5288 - 5360	K.LVINGNPITIFQER.D	1614.87029	2	3.25E-11	0.95	3.86	-	1199.9
AHQ-1-12, 5473 - 5539	K.LVINGNPITIFQER.D	1614.87029	2	1.67E-10	0.89	3.69	-	852.9
AHQ-1-9, 5854 - 5856	K.LVINGNPITIFQER.D	1614.87029	2	1.33E-08	0.93	4.11	-	918.4
AHQ-1-13- , 5747 - 5811	K.LVINGNPITIFQER.D	1614.87029	2	4.32E-08	0.96	4.33	-	1479.4
AHQ-1-9, 5215 - 5258	K.LVINGNPITIFQERDPSK.I	2042.32440	2	1.41E-05	0.58	3.43	-	477.9
AHQ-1-11, 5934	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	1.48E-12	0.96	5.58	-	2454.8
AHQ-1-10, 5821	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	1.15E-08	0.97	5.61	-	1338.2
AHQ-1-9, 7111 - 7182	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	2	1.78E-04	0.96	5.64	-	1862.9
AHQ-1-9, 6659	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	2.58E-05	0.91	4.72	-	1615.7
AHQ-1-9, 6512 - 6586	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	3.28E-14	0.97	6.86	-	2321.7
AHQ-1-11, 5944	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	2	9.04E-05	0.76	3.71	-	855.4
AHQ-1-11, 6386	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	7.61E-08	0.96	6.90	-	1873.2
gi|4507729|ref|NP_001060.1| tubulin, beta polypeptide [Homo sapiens]				3.39E-14	10.24	120.36	36.60	49906.7
AHQ-1-14, 5760	R.AILVDLEPGTMDSVR.S	1616.86162	2	1.57E-06	0.64	3.46	-	296.3
AHQ-1-13- , 4964 - 4988	R.AILVDLEPGTMDSVR.S	1616.86162	2	4.14E-04	0.87	3.38	-	672.9
AHQ-1-11, 4583	R.AILVDLEPGTMDSVR.S	1616.86162	2	5.02E-04	0.81	3.52	-	449.7
AHQ-1-14- , 4875 - 4890	R.AILVDLEPGTMDSVR.S	1616.86162	2	2.39E-04	0.91	4.47	-	660.8
AHQ-1-12, 2925	R.EIVHIQAGQCGNQIGAK.F	1825.03962	2	8.15E-08	0.89	3.56	-	847.6
AHQ-1-7, 2914	K.EVDEQMLNVQNK.N	1447.59668	2	1.54E-04	0.91	4.28	-	1019.2
AHQ-1-9, 2852	K.EVDEQMLNVQNK.N	1447.59668	2	1.11E-04	0.78	3.27	-	705.8
AHQ-1-7, 2925	K.EVDEQMLNVQNK.N	1447.59668	1	8.96E-07	0.60	3.23	-	328.1
AHQ-1-13- , 6459	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.00E-08	0.99	7.25	-	2436.4
AHQ-1-9, 6459	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	7.45E-05	0.91	4.74	-	1038.4
AHQ-1-10, 5759	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	5.92E-04	0.83	3.75	-	1098.9
AHQ-1-14- , 6218	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.39E-14	0.98	6.73	-	2492.1
AHQ-1-11, 5871	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.93E-07	0.96	4.81	-	1220.0
AHQ-1-13, 6004 - 6015	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	7.18E-06	0.90	4.83	-	863.2
AHQ-1-13- , 6451 - 6452	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	8.28E-06	0.94	5.31	-	1247.0
AHQ-1-7, 4717	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	9.37E-11	0.98	6.52	-	1313.7
AHQ-1-9, 6447 - 6454	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	9.91E-07	0.98	6.45	-	2556.9
AHQ-1-7, 6584 - 6636	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.35E-07	0.98	6.48	-	2627.4
AHQ-1-7, 6585 - 6614	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	1.11E-04	0.88	4.40	-	815.4
AHQ-1-13, 6003	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.43E-08	0.99	6.55	-	3013.5
AHQ-1-12, 6073	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.85E-08	0.98	6.45	-	2253.1
AHQ-1-8, 6535 - 6542	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.49E-12	0.99	6.80	-	2859.3
AHQ-1-10, 5751	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.12E-09	0.98	5.49	-	2087.8
AHQ-1-7, 4653	R.ISEQFTAMFR.R	1230.41818	2	6.53E-06	0.93	3.51	-	1151.5
AHQ-1-7, 3633	R.ISEQFTAM*FR.R	1246.41758	2	5.09E-06	0.90	3.46	-	883.1
AHQ-1-7, 4550 - 4558	R.ISEQFTAMFR.R	1230.41818	2	7.30E-06	0.92	3.86	-	1088.6
AHQ-1-9, 7154 - 7156	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	5.35E-07	0.91	4.41	-	1300.1
AHQ-1-7, 6386 - 6460	K.LTTPTYGDLNHLVSATM*SGVTTCLR.F	2727.06467	3	2.94E-04	0.67	3.10	-	681.3
AHQ-1-7, 7352	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	2.99E-09	0.96	5.95	-	718.5
AHQ-1-9, 7155	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	1.39E-08	0.92	4.60	-	764.7
AHQ-1-7, 7353	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	8.45E-07	0.89	4.12	-	1180.6
AHQ-1-8, 7346	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	1.28E-05	0.88	4.01	-	1062.6
AHQ-1-7, 6488	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	9.88E-06	0.85	3.31	-	716.1
AHQ-1-12, 6150	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	2.42E-06	0.79	3.38	-	981.2
AHQ-1-7, 6800	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	1.84E-08	0.92	4.62	-	1125.2
AHQ-1-14- , 6003	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	1.66E-05	0.66	3.60	-	645.2
AHQ-1-7, 6368 - 6369	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	7.12E-05	0.86	4.29	-	996.1
AHQ-1-9, 6063	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.30E-04	0.47	2.66	-	464.3
AHQ-1-7, 5645 - 5721	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.02E-05	0.91	4.52	-	762.4
AHQ-1-7, 5800	K.NSSYFVEWIPNNVK.T	1697.87148	2	4.11E-09	0.88	3.43	-	873.4
AHQ-1-7, 6212	K.NSSYFVEWIPNNVK.T	1697.87148	2	2.24E-04	0.84	3.59	-	692.6

AHQ-1-7, 6297 - 6310	K.NSSYFVEWIPNNVK.T	1697.87148	2	8.28E-05	0.46	2.88	-	490.3
AHQ-1-7, 6382 - 6456	K.NSSYFVEWIPNNVK.T	1697.87148	2	8.34E-07	0.88	4.04	-	759.3
AHQ-1-7, 5548 - 5624	K.NSSYFVEWIPNNVK.T	1697.87148	2	6.06E-09	0.95	5.14	-	917.1
AHQ-1-12, 5378 - 5446	K.NSSYFVEWIPNNVK.T	1697.87148	2	9.87E-07	0.88	3.87	-	723.1
AHQ-1-8, 6572	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	2.79E-05	0.96	5.87	-	1379.8
AHQ-1-7, 6732 - 6797	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.10E-09	0.98	6.62	-	2545.6
AHQ-1-8, 6576 - 6646	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	3.54E-06	0.95	4.94	-	973.3
AHQ-1-7, 6700 - 6768	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	3.78E-07	0.97	6.12	-	1026.3
AHQ-1-3, 6614	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	2.76E-10	0.97	5.44	-	1885.5
AHQ-1-13, 6045 - 6103	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	2.87E-08	0.95	5.50	-	1490.0
AHQ-1-11, 5867 - 5927	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.87E-11	0.97	6.58	-	1631.9
AHQ-1-9, 6452 - 6532	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	3.76E-04	0.96	5.46	-	1103.7
AHQ-1-10, 5769	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	2.68E-04	0.92	4.49	-	593.3
AHQ-1-9, 6458 - 6527	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.39E-14	0.97	6.68	-	1706.0
AHQ-1-13- , 6500 - 6564	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	2.06E-07	0.93	5.07	-	1112.2
AHQ-1-13, 5963 - 6019	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	8.40E-05	0.94	5.33	-	1227.2
AHQ-1-10, 5757 - 5832	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.80E-04	0.88	4.68	-	730.5
AHQ-1-14- , 6166 - 6227	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	7.95E-10	0.98	6.53	-	2260.6
AHQ-1-14- , 6308	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	5.19E-07	0.98	6.38	-	2408.7
AHQ-1-7, 2361	K.TAVCDIPPR.G	1030.18038	2	1.61E-05	0.90	2.86	-	1072.0
gi|21361657|ref|NP_005304.3| glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom				3.66E-14	13.02	160.36	41.40	56782.0
AHQ-1-7, 2077 - 2110	R.EATNPPVIQEEKPK.K	1580.76433	2	6.38E-07	0.82	3.28	-	605.4
AHQ-1-7, 6022 - 6037	R.ELSDFISYLQR.E	1371.52000	2	2.07E-04	0.96	4.25	-	1246.2
AHQ-1-7, 6298	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	3	1.30E-07	0.88	4.14	-	846.0
AHQ-1-7, 6666	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	2	2.37E-10	0.96	4.95	-	1260.2
AHQ-1-7, 6830	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	2	1.06E-06	0.46	2.60	-	360.8
AHQ-1-7, 6665 - 6676	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	3	2.09E-06	0.94	4.60	-	1603.7
AHQ-1-7, 5702	K.FIQENIFGICPHMTEDNKDLIQGK.D	2850.21952	2	1.96E-04	0.73	3.17	-	573.7
AHQ-1-9, 7140	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	9.59E-10	0.98	5.93	-	2834.3
AHQ-1-7, 7336 - 7344	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	3.66E-14	0.98	7.27	-	2824.5
AHQ-1-7, 7305 - 7338	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	2	2.92E-07	0.83	3.59	-	677.7
AHQ-1-7, 4169 - 4240	R.FLQDYFDGNLKR.Y	1516.68203	2	4.58E-04	0.83	3.41	-	766.3
AHQ-1-7, 2470	K.FVM*QEEFSR.D	1189.32290	2	3.17E-05	0.91	3.23	-	971.4
AHQ-1-7, 4700 - 4704	R.GFPTIYFSPANK.K	1342.52349	2	2.21E-07	0.78	2.84	-	571.8
AHQ-1-7, 6032	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	2	9.69E-06	0.95	4.78	-	1056.2
AHQ-1-7, 6029	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	3	2.79E-05	0.92	4.37	-	1180.4
AHQ-1-7, 2249 - 2260	K.LSKDPNIVIAK.M	1198.43727	2	2.79E-05	0.85	3.11	-	1048.0
AHQ-1-7, 3514 - 3524	K.MDATANDVPSPYEVR.G	1665.80646	2	1.68E-05	0.53	2.78	-	368.4
AHQ-1-7, 3122 - 3148	K.M*DATANDVPSPYEVR.G	1681.80586	2	4.23E-05	0.87	3.71	-	432.6
AHQ-1-7, 2482	K.SEPIPESNDGPVK.V	1369.45928	1	2.83E-04	0.29	2.22	-	368.0
AHQ-1-9, 6370	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	3	3.22E-05	0.78	3.81	-	683.5
AHQ-1-7, 6518	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	2	7.16E-05	0.96	4.62	-	1403.5
AHQ-1-7, 4506 - 4578	K.VVVAENFDEIVNNENK.D	1833.97686	2	1.34E-04	0.89	4.28	-	749.0
AHQ-1-7, 3124	K.YGVSGYPTLK.I	1085.23435	1	2.08E-04	0.57	2.60	-	376.0
AHQ-1-7, 3120 - 3136	K.YGVSGYPTLK.I	1085.23435	2	9.90E-05	0.89	3.37	-	627.0
gi|4501891|ref|NP_001093.1| actinin, alpha 1 [Homo sapiens]				4.22E-14	39.48	440.32	50.60	103056.9
AHQ-1-6, 7299 - 7379	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	1.69E-05	0.94	5.56	-	687.9
AHQ-1-5, 7541 - 7543	R.AAPFNNWMEGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4380.81962	3	8.42E-08	0.94	6.32	-	1396.3
AHQ-1-5, 7489 - 7490	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	4.52E-07	0.92	5.15	-	945.2
AHQ-1-4, 5594	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.90E-05	0.72	4.13	-	612.7
AHQ-1-10, 4825	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.54E-04	0.47	3.36	-	501.7
AHQ-1-5, 5454	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	3.48E-06	0.85	4.37	-	866.3
AHQ-1-12, 5174	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.01E-04	0.85	4.04	-	579.0
AHQ-1-6, 5391 - 5459	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	4.76E-06	0.77	4.16	-	741.8
AHQ-1-11, 4966	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	5.15E-05	0.84	3.79	-	605.1
AHQ-1-6, 5400	K.AGTQIENIEEDFRDGLK.L	1936.06918	3	1.88E-04	0.60	3.37	-	373.6
AHQ-1-4, 6771	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	1.59E-07	0.85	3.90	-	685.4
AHQ-1-5, 5733	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	3	8.48E-07	0.76	3.22	-	872.1
AHQ-1-5, 5667 - 5742	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	2.50E-09	0.87	3.92	-	578.0
AHQ-1-7, 6680	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	9.13E-05	0.75	3.35	-	380.1
AHQ-1-5, 6601 - 6670	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	9.79E-09	0.93	4.44	-	906.3
AHQ-1-5, 6645 - 6653	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	5.02E-05	0.79	3.14	-	708.8
AHQ-1-4, 6766	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	2.10E-07	0.96	5.14	-	1124.4
AHQ-1-6, 5636	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	2.76E-04	0.72	3.23	-	485.3
AHQ-1-5, 3241	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	3.70E-06	0.95	4.52	-	1923.9
AHQ-1-5, 3251	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	1.21E-05	0.94	4.03	-	1198.1
AHQ-1-5, 3467 - 3483	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	3.19E-08	0.79	3.24	-	538.3
AHQ-1-5, 1514 - 1529	K.ATLPDADKER.L	1116.20684	2	7.80E-05	0.66	2.76	-	464.7
AHQ-1-1, 5791	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	4.95E-06	0.90	4.29	-	760.4
AHQ-1-3, 5831	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.70E-07	0.89	3.86	-	762.7
AHQ-1-9, 5724	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	4.05E-05	0.90	4.08	-	758.7
AHQ-1-5, 5969	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	7.01E-06	0.96	4.25	-	1448.4
AHQ-1-5, 5870 - 5937	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.07E-12	0.97	5.71	-	1343.7
AHQ-1-2, 6007	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	4.76E-06	0.88	3.44	-	944.7
AHQ-1-6, 5778 - 5779	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	2.21E-05	0.97	5.50	-	1293.2
AHQ-1-5, 5299	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	4.94E-09	0.92	3.89	-	973.3
AHQ-1-4, 5944 - 5966	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.28E-06	0.97	5.11	-	1704.8
AHQ-1-5, 4981 - 4982	K.DGLGFCALIHR.H	1260.44730	2	1.71E-05	0.92	3.01	-	1304.4
AHQ-1-4, 5112	K.DGLGFCALIHR.H	1260.44730	2	1.03E-04	0.96	3.00	-	2087.2
AHQ-1-5, 5214	K.DGLGFCALIHR.H	1260.44730	2	2.75E-06	0.94	3.17	-	1578.6
AHQ-1-5, 2406 - 2409	R.DHSGTLGPEEFK.A	1317.38606	2	2.11E-06	0.94	3.97	-	951.1
AHQ-1-4, 2540	R.DHSGTLGPEEFK.A	1317.38606	2	7.89E-05	0.91	3.56	-	960.2
AHQ-1-6, 2435	R.DHSGTLGPEEFK.A	1317.38606	2	9.99E-06	0.91	3.27	-	837.0
AHQ-1-6, 3738	K.DYETATLSEIK.A	1270.36761	2	9.23E-07	0.94	3.61	-	1234.9
AHQ-1-5, 3799 - 3803	K.DYETATLSEIK.A	1270.36761	2	2.06E-07	0.94	3.86	-	1302.4
AHQ-1-5, 3393 - 3445	R.ELPPDQAEYCIAR.M	1563.71392	2	2.19E-04	0.40	2.51	-	132.0
AHQ-1-4, 3652 - 3732	R.ELPPDQAEYCIAR.M	1563.71392	2	4.15E-05	0.41	2.56	-	132.6
AHQ-1-6, 3166	R.ETADTDTADQVM*ASFK.I	1746.83148	2	4.23E-05	0.72	2.89	-	709.7
AHQ-1-1, 4592 - 4593	R.ETADTDTADQVMASFK.I	1730.83208	2	2.35E-08	0.92	3.83	-	1028.9
AHQ-1-13, 4285	R.ETADTDTADQVMASFK.I	1730.83208	2	1.59E-07	0.94	3.88	-	1103.5
AHQ-1-10, 4055	R.ETADTDTADQVMASFK.I	1730.83208	2	3.14E-05	0.81	3.52	-	596.3
AHQ-1-7, 3230	R.ETADTDTADQVM*ASFK.I	1746.83148	2	1.15E-04	0.88	4.16	-	544.1
AHQ-1-13- , 3281	R.ETADTDTADQVM*ASFK.I	1746.83148	2	1.18E-05	0.89	3.81	-	663.8
AHQ-1-2, 4733	R.ETADTDTADQVMASFK.I	1730.83208	2	1.29E-07	0.91	3.70	-	1064.5
AHQ-1-13- , 4484	R.ETADTDTADQVMASFK.I	1730.83208	2	4.01E-09	0.95	4.20	-	1415.9
AHQ-1-5, 3205	R.ETADTDTADQVM*ASFK.I	1746.83148	2	1.26E-07	0.94	4.22	-	1053.8
AHQ-1-3, 4575	R.ETADTDTADQVMASFK.I	1730.83208	2	1.67E-05	0.93	4.12	-	968.4
AHQ-1-6, 4454	R.ETADTDTADQVMASFK.I	1730.83208	2	6.25E-06	0.95	3.68	-	1336.5
AHQ-1-5, 4530 - 4607	R.ETADTDTADQVMASFK.I	1730.83208	2	6.24E-05	0.97	5.52	-	1330.7
AHQ-1-4, 4639	R.ETADTDTADQVMASFK.I	1730.83208	2	2.34E-07	0.93	4.18	-	1007.9
AHQ-1-5, 2149	K.GISQEQM*NEFR.A	1355.45931	2	4.92E-04	0.82	2.96	-	831.0
AHQ-1-4, 3024	K.GISQEQMNEFR.A	1339.45991	2	4.77E-05	0.85	3.06	-	889.3
AHQ-1-3, 3026	K.GISQEQMNEFR.A	1339.45991	2	1.26E-07	0.74	2.59	-	773.7
AHQ-1-6, 2894	K.GISQEQMNEFR.A	1339.45991	2	3.40E-05	0.86	3.14	-	879.9
AHQ-1-5, 2851 - 2867	K.GISQEQMNEFR.A	1339.45991	2	1.22E-05	0.89	3.46	-	846.7
AHQ-1-6, 2171	K.GISQEQM*NEFR.A	1355.45931	2	8.25E-06	0.83	3.10	-	777.7
AHQ-1-5, 3094	K.GISQEQMNEFR.A	1339.45991	2	1.14E-06	0.81	2.83	-	721.2

AHQ-1-2, 3146	K.GISQEQMNEFR.A	1339.45991	2	9.63E-05	0.70	2.65	-	687.1
AHQ-1-4, 2280	K.GISQEQM*NEFR.A	1355.45931	2	7.19E-06	0.90	3.20	-	990.2
AHQ-1-5, 1973	R.HRPELIDYGK.L	1228.38202	3	1.23E-04	0.91	3.84	-	937.0
AHQ-1-6, 2027	R.HRPELIDYGK.L	1228.38202	3	2.16E-04	0.94	3.88	-	1369.4
AHQ-1-7, 2012	R.HRPELIDYGK.L	1228.38202	2	3.77E-04	0.88	3.15	-	679.4
AHQ-1-4, 2154	R.HRPELIDYGK.L	1228.38202	2	3.36E-04	0.92	3.75	-	609.7
AHQ-1-9, 1975	R.HRPELIDYGK.L	1228.38202	2	6.89E-05	0.88	3.45	-	606.7
AHQ-1-5, 1965 - 2029	R.HRPELIDYGK.L	1228.38202	2	4.43E-04	0.89	3.66	-	564.5
AHQ-1-7, 5050 - 5082	K.ICDQWDNLGALTQK.R	1663.83349	2	1.96E-05	0.92	3.78	-	1254.5
AHQ-1-4, 5060 - 5132	K.ICDQWDNLGALTQK.R	1663.83349	2	6.11E-08	0.97	4.35	-	2107.8
AHQ-1-3, 5074	K.ICDQWDNLGALTQK.R	1663.83349	2	2.64E-05	0.98	5.17	-	2418.7
AHQ-1-5, 5439	K.ICDQWDNLGALTQK.R	1663.83349	2	3.97E-07	0.94	3.78	-	1401.3
AHQ-1-6, 4974	K.ICDQWDNLGALTQK.R	1663.83349	2	8.77E-06	0.97	4.13	-	2150.6
AHQ-1-5, 4655 - 4730	K.ICDQWDNLGALTQK.R	1663.83349	2	5.39E-12	0.96	5.23	-	1284.3
AHQ-1-5, 5058 - 5066	K.ICDQWDNLGALTQK.R	1663.83349	2	1.58E-10	0.98	5.42	-	2732.9
AHQ-1-10, 4464	K.ICDQWDNLGALTQK.R	1663.83349	2	8.69E-05	0.88	3.54	-	1168.5
AHQ-1-6, 5983 - 6000	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	1.41E-07	0.93	4.90	-	1215.4
AHQ-1-10, 5284 - 5345	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	7.89E-04	0.92	4.04	-	1016.6
AHQ-1-5, 6185	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	8.38E-07	0.96	4.94	-	1828.8
AHQ-1-5, 5950	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	4.78E-08	0.97	5.37	-	2279.0
AHQ-1-5, 3474	K.ILAGDKNYITM*DELR.R	1769.01293	2	4.14E-04	0.87	3.78	-	555.5
AHQ-1-5, 4159 - 4195	K.ILAGDKNYITMDELR.R	1753.01353	2	1.56E-05	0.96	4.80	-	1131.6
AHQ-1-5, 4190	K.ILAGDKNYITMDELR.R	1753.01353	3	5.91E-06	0.90	4.17	-	828.4
AHQ-1-5, 5046 - 5118	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	2	1.39E-04	0.92	4.08	-	956.7
AHQ-1-5, 4411	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	3	1.84E-07	0.95	4.44	-	1829.4
AHQ-1-5, 4413	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	2	1.16E-05	0.85	3.76	-	371.8
AHQ-1-5, 5043	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	3	2.89E-12	0.97	5.23	-	2006.4
AHQ-1-5, 4370	K.IVQTYHVNM*AGTNPYTTITPQEINGK.W	2908.23575	2	9.27E-07	0.91	3.97	-	910.9
AHQ-1-5, 4739	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	1.33E-05	0.66	2.89	-	423.2
AHQ-1-5, 4867	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	4.18E-13	0.93	4.63	-	940.2
AHQ-1-5, 4222	K.IVQTYHVNM*AGTNPYTTITPQEINGK.W	2908.23575	2	1.00E-04	0.78	3.03	-	596.2
AHQ-1-5, 4869 - 4873	R.KAGTQIENIEEDFRDGLK.L	2064.24210	2	1.02E-04	0.88	4.50	-	959.2
AHQ-1-5, 4485 - 4507	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	2.96E-09	0.95	4.70	-	1166.9
AHQ-1-7, 4980	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	6.11E-04	0.97	4.90	-	1927.1
AHQ-1-9, 4840	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	4.99E-07	0.96	5.29	-	1021.5
AHQ-1-6, 4931	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.15E-05	0.95	4.64	-	1014.4
AHQ-1-5, 4975 - 5045	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.54E-07	0.97	5.11	-	1333.8
AHQ-1-5, 5134	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	3.57E-05	0.94	4.39	-	920.6
AHQ-1-4, 5100	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	3.18E-07	0.97	5.44	-	1280.1
AHQ-1-6, 4315	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	9.02E-04	0.93	4.59	-	912.1
AHQ-1-7, 3301 - 3305	R.LAILGIHNEVSK.I	1294.52505	2	1.22E-06	0.92	3.61	-	979.8
AHQ-1-5, 3249	R.LAILGIHNEVSK.I	1294.52505	2	7.40E-09	0.95	4.17	-	1034.9
AHQ-1-4, 6307	K.LASDLLEWIR.R	1216.41115	2	1.16E-07	0.97	4.40	-	2345.4
AHQ-1-7, 6236	K.LASDLLEWIR.R	1216.41115	2	9.05E-07	0.97	4.59	-	2086.7
AHQ-1-4, 6314	K.LASDLLEWIR.R	1216.41115	1	3.97E-04	0.22	2.21	-	397.6
AHQ-1-1, 6203 - 6204	K.LASDLLEWIR.R	1216.41115	2	3.93E-08	0.98	4.99	-	2537.2
AHQ-1-5, 6211 - 6278	K.LASDLLEWIR.R	1216.41115	2	4.55E-07	0.97	4.17	-	1954.2
AHQ-1-3, 6191	K.LASDLLEWIR.R	1216.41115	2	6.28E-08	0.97	4.20	-	1782.3
AHQ-1-6, 6119	K.LASDLLEWIR.R	1216.41115	2	9.41E-08	0.96	3.40	-	1984.6
AHQ-1-14- , 6291	K.LLETIDQLYLEYAK.R	1712.96427	2	1.48E-08	0.94	4.07	-	1159.3
AHQ-1-5, 6742 - 6805	K.LLETIDQLYLEYAK.R	1712.96427	2	2.30E-10	0.98	5.52	-	1480.3
AHQ-1-3, 6675	K.LLETIDQLYLEYAK.R	1712.96427	2	2.31E-09	0.97	5.18	-	1152.2
AHQ-1-10, 5889 - 5897	K.LLETIDQLYLEYAK.R	1712.96427	2	5.78E-05	0.82	3.38	-	601.6
AHQ-1-2, 6853 - 6865	K.LLETIDQLYLEYAK.R	1712.96427	2	2.60E-04	0.92	3.71	-	1053.2
AHQ-1-6, 6630	K.LLETIDQLYLEYAK.R	1712.96427	2	5.79E-08	0.96	4.87	-	1207.5
AHQ-1-7, 6824	K.LLETIDQLYLEYAK.R	1712.96427	2	1.71E-07	0.96	4.79	-	1147.8
AHQ-1-1, 6572	K.LLETIDQLYLEYAK.R	1712.96427	2	1.32E-07	0.95	4.16	-	1329.1
AHQ-1-5, 6874 - 6942	K.LLETIDQLYLEYAK.R	1712.96427	2	1.29E-08	0.98	5.27	-	1439.4
AHQ-1-5, 4678	K.LRKDDPLTNLNTAFDVAEK.Y	2161.40091	3	3.23E-04	0.86	3.81	-	831.3
AHQ-1-6, 2535 - 2551	R.LSNRPAFMPSEGR.M	1462.65941	2	8.33E-05	0.87	3.94	-	694.1
AHQ-1-5, 3427 - 3430	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	5.97E-04	0.63	3.09	-	484.7
AHQ-1-5, 3674	K.MLDAEDIVGTARPDEK.A	1760.94769	2	8.45E-06	0.86	3.63	-	1008.3
AHQ-1-8, 3989	K.MLDAEDIVGTARPDEK.A	1760.94769	2	7.27E-06	0.62	3.20	-	485.4
AHQ-1-6, 3951	K.MLDAEDIVGTARPDEK.A	1760.94769	3	5.28E-07	0.86	4.02	-	596.3
AHQ-1-6, 3946	K.MLDAEDIVGTARPDEK.A	1760.94769	2	3.64E-06	0.89	4.27	-	874.0
AHQ-1-4, 3712	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	5.02E-05	0.83	3.47	-	470.2
AHQ-1-5, 3981	K.MLDAEDIVGTARPDEK.A	1760.94769	2	8.40E-09	0.93	4.34	-	1091.9
AHQ-1-4, 4130 - 4139	K.MLDAEDIVGTARPDEK.A	1760.94769	2	1.74E-06	0.92	3.98	-	1079.6
AHQ-1-5, 3989 - 3990	K.MLDAEDIVGTARPDEK.A	1760.94769	3	1.39E-08	0.80	3.56	-	691.1
AHQ-1-9, 3887	K.MLDAEDIVGTARPDEK.A	1760.94769	2	7.25E-07	0.84	3.79	-	798.9
AHQ-1-9, 3888	K.MLDAEDIVGTARPDEK.A	1760.94769	3	7.48E-08	0.61	3.11	-	416.4
AHQ-1-5, 3547	K.M*LDAEDIVGTARPDEK.A	1776.94709	3	4.18E-04	0.87	3.51	-	955.7
AHQ-1-5, 3545	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	6.20E-05	0.92	3.71	-	1084.0
AHQ-1-7, 5780	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	4.37E-05	0.90	4.11	-	733.0
AHQ-1-5, 5411 - 5485	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	3.69E-10	0.98	5.33	-	1508.3
AHQ-1-4, 5922	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	3.34E-06	0.64	3.02	-	373.6
AHQ-1-4, 5835	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.70E-07	0.92	4.17	-	668.3
AHQ-1-4, 5623	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	5.28E-04	0.88	3.81	-	657.6
AHQ-1-5, 5281 - 5287	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	8.46E-09	0.95	4.47	-	1037.0
AHQ-1-6, 5442	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.33E-07	0.95	4.55	-	1292.3
AHQ-1-3, 5798	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.63E-06	0.73	2.90	-	635.3
AHQ-1-5, 6226	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.03E-11	0.95	4.31	-	1167.0
AHQ-1-5, 5478	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	4.93E-08	0.85	4.03	-	479.8
AHQ-1-9, 5632	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.33E-04	0.45	2.72	-	428.7
AHQ-1-5, 5530 - 5531	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.05E-08	0.97	5.50	-	1167.7
AHQ-1-5, 6045 - 6115	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.35E-07	0.96	4.88	-	1292.0
AHQ-1-5, 5654 - 5699	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.57E-06	0.95	4.80	-	1227.8
AHQ-1-5, 5695 - 5703	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.01E-07	0.95	4.81	-	902.0
AHQ-1-5, 5891	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	3.51E-10	0.94	4.67	-	847.8
AHQ-1-6, 5911	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.26E-07	0.93	4.43	-	940.6
AHQ-1-6, 5188	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.83E-10	0.96	4.66	-	1128.6
AHQ-1-6, 5728	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	3.14E-05	0.95	4.74	-	1138.2
AHQ-1-5, 5785	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.36E-07	0.97	5.31	-	1269.2
AHQ-1-6, 5630	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	8.86E-06	0.92	4.37	-	666.2
AHQ-1-6, 5594	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.49E-09	0.95	4.45	-	1157.6
AHQ-1-9, 4642 - 4710	K.NVNIQNFHISWK.D	1500.68583	2	4.17E-09	0.96	4.63	-	1320.4
AHQ-1-4, 4946	K.NVNIQNFHISWK.D	1500.68583	2	1.86E-07	0.95	4.32	-	1127.6
AHQ-1-5, 4717 - 4734	K.NVNIQNFHISWK.D	1500.68583	2	3.02E-06	0.94	4.04	-	1182.0
AHQ-1-6, 4712	K.NVNIQNFHISWK.D	1500.68583	2	2.08E-05	0.93	3.33	-	1191.3
AHQ-1-4, 5287	K.QFGAQANVIGPWIQTK.M	1759.00118	2	1.34E-05	0.76	3.14	-	635.2
AHQ-1-6, 5130	K.QFGAQANVIGPWIQTK.M	1759.00118	2	5.07E-04	0.82	3.97	-	459.9
AHQ-1-5, 4145	R.TINEVENQILTR.D	1430.58898	1	1.15E-05	0.44	2.38	-	405.6
AHQ-1-3, 4061	R.TINEVENQILTR.D	1430.58898	2	2.40E-05	0.91	3.85	-	997.7
AHQ-1-7, 3992	R.TINEVENQILTR.D	1430.58898	2	7.71E-04	0.78	3.53	-	784.3
AHQ-1-5, 4078 - 4149	R.TINEVENQILTR.D	1430.58898	2	4.81E-08	0.86	3.64	-	670.5
AHQ-1-4, 3658	R.TINEVENQILTR.D	1430.58898	2	6.21E-07	0.77	2.90	-	554.9
AHQ-1-5, 3014 - 3085	R.TINEVENQILTR.D	1430.58898	2	3.04E-07	0.85	3.18	-	886.4

AHQ-1-5, 3954	R.TINEVENQILTR.D	1430.58898	1	7.96E-04	0.14	2.50	-	152.0
AHQ-1-6, 3914	R.TINEVENQILTR.D	1430.58898	2	5.10E-06	0.87	3.49	-	807.1
AHQ-1-8, 3945	R.TINEVENQILTR.D	1430.58898	2	2.78E-05	0.82	3.17	-	869.3
AHQ-1-4, 4082	R.TINEVENQILTR.D	1430.58898	2	7.32E-08	0.91	3.83	-	1125.3
AHQ-1-9, 3863 - 3867	R.TINEVENQILTR.D	1430.58898	2	1.91E-04	0.78	3.09	-	665.8
AHQ-1-2, 7215	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.86E-07	0.95	5.38	-	1190.4
AHQ-1-1, 6855	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.64E-06	0.98	6.46	-	1782.0
AHQ-1-5, 7269 - 7299	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	7.34E-05	0.91	4.04	-	799.2
AHQ-1-3, 7042	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	4.98E-05	0.94	5.04	-	945.8
AHQ-1-1, 6856 - 6860	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	7.28E-08	0.93	4.85	-	887.6
AHQ-1-5, 7137 - 7214	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.58E-05	0.89	4.16	-	1147.3
AHQ-1-11, 6078	R.VGWEQLLTTIAR.T	1387.60894	2	9.82E-08	0.94	3.66	-	1354.6
AHQ-1-9, 6683 - 6703	R.VGWEQLLTTIAR.T	1387.60894	2	2.18E-06	0.95	4.46	-	1173.2
AHQ-1-7, 6889	R.VGWEQLLTTIAR.T	1387.60894	2	1.84E-06	0.93	4.13	-	1234.1
AHQ-1-13- , 6671	R.VGWEQLLTTIAR.T	1387.60894	2	3.01E-07	0.95	3.61	-	1757.2
AHQ-1-6, 6722	R.VGWEQLLTTIAR.T	1387.60894	2	9.49E-06	0.96	4.28	-	1499.4
AHQ-1-14- , 6410	R.VGWEQLLTTIAR.T	1387.60894	2	1.49E-04	0.86	3.30	-	823.7
AHQ-1-8, 6791	R.VGWEQLLTTIAR.T	1387.60894	2	4.40E-07	0.94	3.83	-	1360.7
AHQ-1-2, 6986	R.VGWEQLLTTIAR.T	1387.60894	2	1.28E-06	0.95	3.90	-	1506.7
AHQ-1-13, 6207	R.VGWEQLLTTIAR.T	1387.60894	2	5.87E-06	0.89	3.60	-	1291.0
AHQ-1-3, 6782	R.VGWEQLLTTIAR.T	1387.60894	2	7.76E-08	0.97	4.33	-	1825.9
AHQ-1-10, 5955	R.VGWEQLLTTIAR.T	1387.60894	2	7.26E-07	0.95	3.95	-	1414.4
AHQ-1-4, 6922 - 6926	R.VGWEQLLTTIAR.T	1387.60894	2	2.70E-09	0.96	4.35	-	1436.8
AHQ-1-5, 6801 - 6879	R.VGWEQLLTTIAR.T	1387.60894	2	1.57E-05	0.96	4.19	-	1700.5
AHQ-1-1, 6645 - 6703	R.VGWEQLLTTIAR.T	1387.60894	2	5.50E-07	0.94	3.82	-	1233.5
AHQ-1-9, 4232	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.11E-04	0.92	4.07	-	942.6
AHQ-1-8, 4207	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.09E-06	0.89	4.39	-	605.2
AHQ-1-7, 4346	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.40E-08	0.96	5.31	-	1131.6
AHQ-1-6, 4248	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	6.74E-06	0.94	4.79	-	912.5
AHQ-1-5, 4786 - 4791	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.22E-14	0.97	5.29	-	1605.9
AHQ-1-5, 4642	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.71E-09	0.93	4.46	-	857.8
AHQ-1-5, 4527	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	5.55E-12	0.98	5.99	-	1707.8
AHQ-1-5, 4438	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.50E-10	0.96	5.03	-	1056.1
AHQ-1-5, 4350	K.VLAVNQENEQLMEDYEK.L	2053.23635	3	5.00E-10	0.91	4.39	-	1130.0
AHQ-1-5, 4327	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.53E-07	0.96	5.00	-	1209.8
AHQ-1-5, 3859	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.15E-05	0.93	4.00	-	1093.1
AHQ-1-5, 3775 - 3783	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.20E-08	0.95	4.99	-	887.6
AHQ-1-5, 3591 - 3661	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.27E-07	0.96	4.68	-	1637.1
AHQ-1-5, 3502	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	3.12E-09	0.93	4.36	-	689.1
AHQ-1-4, 3730 - 3734	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	4.11E-06	0.96	5.07	-	1070.0
AHQ-1-3, 4406	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.16E-06	0.96	5.12	-	1364.6
AHQ-1-2, 4575 - 4577	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	6.79E-05	0.95	4.64	-	1273.6
AHQ-1-1, 4451	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.10E-05	0.92	4.24	-	1007.7
AHQ-1-1, 3757	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	3.90E-07	0.82	4.14	-	528.5
gi|4557305|ref|NP_000025.1| aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho				6.05E-14	14.05	160.29	62.40	39419.7
AHQ-1-8, 2111 - 2115	R.ALANSLACQGK.Y	1134.28859	2	1.07E-04	0.80	3.31	-	629.2
AHQ-1-14- , 2308	R.ALANSLACQGK.Y	1134.28859	2	5.80E-05	0.71	2.53	-	805.5
AHQ-1-8, 4475	R.ALANSLACQGKYTPSGQAGAAASESLFVSNHAY	3344.61352	3	7.69E-04	0.60	3.16	-	311.1
AHQ-1-8, 4582 - 4651	R.ALANSLACQGKYTPSGQAGAAASESLFVSNHAY	3344.61352	3	2.32E-06	0.70	3.42	-	342.1
AHQ-1-8, 4156	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	7.07E-09	0.96	5.82	-	1061.4
AHQ-1-9, 4334	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	6.19E-05	0.86	3.54	-	954.1
AHQ-1-8, 6246 - 6259	K.CPLLKPWALTFSYGR.A	1811.13929	2	5.21E-09	0.94	4.58	-	659.3
AHQ-1-9, 6126 - 6190	K.CPLLKPWALTFSYGR.A	1811.13929	2	1.21E-05	0.74	3.36	-	452.4
AHQ-1-9, 4298 - 4310	K.FSHEEIAMATVTALR.R	1676.91875	2	1.50E-09	0.96	4.65	-	1323.8
AHQ-1-9, 3631	K.FSHEEIAM*ATVTALR.R	1692.91815	2	8.87E-04	0.90	4.11	-	830.9
AHQ-1-8, 4233	K.FSHEEIAMATVTALR.R	1676.91875	2	8.87E-09	0.95	4.16	-	1590.7
AHQ-1-11, 2848	K.GILAADESTGSIAK.R	1333.47008	2	1.06E-08	0.96	4.43	-	1266.2
AHQ-1-9, 2815 - 2826	K.GILAADESTGSIAK.R	1333.47008	2	2.39E-09	0.97	5.03	-	1613.9
AHQ-1-12, 2909	K.GILAADESTGSIAK.R	1333.47008	2	1.41E-05	0.94	3.90	-	1164.7
AHQ-1-8, 2770 - 2790	K.GILAADESTGSIAK.R	1333.47008	2	5.74E-08	0.97	4.90	-	1540.7
AHQ-1-8, 2772	K.GILAADESTGSIAK.R	1333.47008	1	6.63E-05	0.75	2.78	-	603.1
AHQ-1-9, 4614 - 4683	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	6.05E-14	0.91	5.64	-	764.3
AHQ-1-8, 4435	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	2.89E-07	0.76	4.62	-	519.5
AHQ-1-9, 4274 - 4302	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	1.45E-08	0.90	4.97	-	1123.7
AHQ-1-1, 4777	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	4.96E-08	0.47	3.41	-	355.9
AHQ-1-9, 4095	K.IGEHTPSALAIM*ENANVLAR.Y	2124.40728	2	5.03E-05	0.96	4.30	-	1206.7
AHQ-1-9, 5039	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.99E-11	0.96	5.09	-	1024.4
AHQ-1-9, 5398 - 5467	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	3.08E-06	0.89	3.81	-	736.9
AHQ-1-8, 5364 - 5367	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.24E-04	0.96	5.42	-	838.3
AHQ-1-9, 7467	R.TVPPAVTGITFLSGGQSEEEASINLNAINK.C	3059.37393	3	6.95E-05	0.79	3.58	-	701.3
AHQ-1-9, 4316	K.VDKGVVPLAGTNGETTTQGLDGLSER.C	2615.83564	3	1.31E-07	0.77	3.92	-	1063.7
AHQ-1-9, 6040 - 6084	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	5.08E-07	0.93	5.01	-	675.3
AHQ-1-9, 5888 - 5964	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	3.13E-06	0.97	5.09	-	1602.5
AHQ-1-9, 6054 - 6124	R.YASICQQNGIVPIVEPEILPDGDHDLK.R	3023.36334	3	4.16E-04	0.83	4.42	-	514.9
AHQ-1-9, 5582 - 5652	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	6.91E-08	0.92	5.16	-	651.6
AHQ-1-8, 4475	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	7.01E-05	0.89	3.98	-	534.9
AHQ-1-8, 4582 - 4651	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	1.99E-07	0.84	3.92	-	411.7
AHQ-1-9, 4487 - 4554	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	4.91E-04	0.82	3.24	-	652.0
gi|4504745|ref|NP_000410.1| integrin alpha 2b precursor [Homo sapiens]				1.12E-13	32.78	370.32	43.40	113374.2
AHQ-1-4, 2030	R.AEAQVELR.G	916.01408	2	6.80E-05	0.91	3.22	-	1289.2
AHQ-1-4, 1774 - 1838	R.AEAQVELR.G	916.01408	2	6.57E-04	0.84	2.86	-	1006.9
AHQ-1-4, 1764 - 2050	R.AEAQVELR.G	916.01408	1	7.87E-04	0.04	1.81	-	174.0
AHQ-1-11, 4892	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.10E-05	0.93	4.33	-	858.6
AHQ-1-1, 5473 - 5480	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.93E-09	0.95	4.39	-	949.3
AHQ-1-10, 4743	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.85E-07	0.83	2.94	-	731.4
AHQ-1-13, 5071 - 5072	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.36E-07	0.96	4.58	-	1073.2
AHQ-1-9, 5231	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.65E-05	0.94	4.42	-	906.7
AHQ-1-4, 5136 - 5215	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.62E-05	0.81	2.92	-	765.8
AHQ-1-7, 5357 - 5376	R.AEGGQCPSLLFDLR.D	1564.74505	2	7.34E-04	0.94	4.17	-	870.2
AHQ-1-13- , 5372	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.20E-05	0.90	3.33	-	1000.8
AHQ-1-4, 5456 - 5522	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.25E-06	0.93	4.15	-	1010.9
AHQ-1-4, 5655	R.AEGGQCPSLLFDLR.D	1564.74505	2	8.37E-10	0.95	4.39	-	1029.6
AHQ-1-5, 5354 - 5389	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.88E-08	0.94	3.36	-	1250.8
AHQ-1-6, 5294 - 5314	R.AEGGQCPSLLFDLR.D	1564.74505	2	8.73E-09	0.93	3.56	-	1151.8
AHQ-1-3, 5313 - 5389	R.AEGGQCPSLLFDLR.D	1564.74505	2	7.22E-07	0.92	3.68	-	986.1
AHQ-1-1, 3008 - 3011	R.ALSNVEGFER.L	1122.21308	2	6.15E-06	0.91	3.58	-	811.9
AHQ-1-4, 2835 - 2884	R.ALSNVEGFER.L	1122.21308	2	4.94E-06	0.88	3.37	-	790.1
AHQ-1-6, 2754	R.ALSNVEGFER.L	1122.21308	2	2.84E-07	0.82	2.69	-	746.1
AHQ-1-5, 2722	R.ALSNVEGFER.L	1122.21308	2	5.94E-05	0.90	3.01	-	1199.6
AHQ-1-3, 2857 - 2859	R.ALSNVEGFER.L	1122.21308	2	4.49E-07	0.90	3.22	-	952.4
AHQ-1-7, 2781	R.ALSNVEGFER.L	1122.21308	2	1.12E-05	0.90	3.10	-	986.3
AHQ-1-6, 2752	R.ALSNVEGFER.L	1122.21308	1	8.74E-04	0.14	2.05	-	68.1
AHQ-1-4, 5210 - 5282	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	3.67E-07	0.88	4.32	-	640.7
AHQ-1-3, 5165 - 5199	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	8.10E-04	0.54	2.69	-	590.6
AHQ-1-5, 5129 - 5133	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	1.28E-05	0.94	4.80	-	926.5
AHQ-1-4, 3108	R.DETRNVGSQTLQTFK.A	1724.85363	2	4.44E-06	0.90	3.84	-	1001.3
AHQ-1-3, 3987	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.03E-04	0.65	3.14	-	408.4

AHQ-1-4, 4180 - 4258	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	3.72E-08	0.94	4.73	-	887.3
AHQ-1-6, 3902	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	7.85E-08	0.90	3.92	-	831.6
AHQ-1-5, 4203	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	4.70E-10	0.89	4.16	-	812.7
AHQ-1-5, 3971	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	8.36E-10	0.91	4.25	-	664.0
AHQ-1-4, 4642 - 4643	R.FGSAIAPLGDLDR.D	1332.48700	1	1.98E-04	0.60	2.60	-	447.7
AHQ-1-4, 5942 - 6023	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.66E-12	0.93	5.04	-	1021.2
AHQ-1-7, 6009 - 6050	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.75E-06	0.85	4.65	-	481.1
AHQ-1-4, 6090 - 6163	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	8.95E-07	0.93	5.61	-	669.2
AHQ-1-5, 6006 - 6077	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.65E-05	0.95	5.84	-	991.6
AHQ-1-6, 5839 - 5907	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.09E-06	0.81	3.66	-	890.2
AHQ-1-1, 6072	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.86E-05	0.82	3.44	-	993.3
AHQ-1-6, 5980	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	6.60E-04	0.85	4.45	-	793.2
AHQ-1-3, 5910 - 5958	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.90E-06	0.87	4.43	-	550.9
AHQ-1-4, 6618 - 6687	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	1.13E-05	0.85	4.15	-	725.4
AHQ-1-4, 6751 - 6818	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.21E-08	0.95	5.10	-	681.9
AHQ-1-4, 6491 - 6562	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	8.16E-06	0.93	4.94	-	613.9
AHQ-1-4, 6890 - 6963	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.64E-08	0.97	5.99	-	863.4
AHQ-1-4, 6484 - 6551	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	6.82E-05	0.69	3.67	-	490.0
AHQ-1-4, 6400 - 6467	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.71E-08	0.96	5.29	-	988.9
AHQ-1-4, 7018 - 7082	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	1.41E-05	0.95	5.31	-	1470.6
AHQ-1-4, 7044 - 7115	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.76E-05	0.95	5.18	-	686.5
AHQ-1-4, 7190 - 7238	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.01E-05	0.94	4.72	-	739.0
AHQ-1-4, 7510 - 7584	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	5.62E-05	0.82	3.91	-	765.4
AHQ-1-4, 6610 - 6684	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	3.90E-13	0.97	5.77	-	845.6
AHQ-1-4, 6891 - 6954	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	8.94E-04	0.86	4.43	-	725.9
AHQ-1-13, 4911 - 4921	R.GEAQVWTQLLR.A	1301.47614	2	5.51E-05	0.93	4.17	-	915.2
AHQ-1-10, 4536 - 4595	R.GEAQVWTQLLR.A	1301.47614	2	9.79E-06	0.93	3.82	-	1169.5
AHQ-1-1, 5312	R.GEAQVWTQLLR.A	1301.47614	2	5.94E-06	0.89	3.31	-	1198.0
AHQ-1-11, 4716	R.GEAQVWTQLLR.A	1301.47614	2	1.06E-06	0.93	3.92	-	1003.4
AHQ-1-10, 4795 - 4797	R.GEAQVWTQLLR.A	1301.47614	1	9.28E-04	0.23	2.25	-	249.0
AHQ-1-11, 4710	R.GEAQVWTQLLR.A	1301.47614	2	3.03E-06	0.94	4.42	-	931.4
AHQ-1-12, 4942	R.GEAQVWTQLLR.A	1301.47614	2	5.28E-06	0.91	3.67	-	935.7
AHQ-1-13- , 5196 - 5204	R.GEAQVWTQLLR.A	1301.47614	2	1.95E-06	0.95	4.20	-	1060.7
AHQ-1-4, 5612 - 5679	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.79E-08	0.95	4.75	-	889.4
AHQ-1-4, 5878 - 5947	R.GNSFPASLVVAAEEGER.E	1733.86053	2	6.34E-12	0.93	4.35	-	897.6
AHQ-1-4, 5746 - 5812	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.12E-13	0.93	4.43	-	937.2
AHQ-1-4, 5535 - 5610	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.94E-06	0.89	3.95	-	658.6
AHQ-1-4, 5407 - 5474	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.15E-07	0.78	3.51	-	483.0
AHQ-1-4, 6074	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.03E-09	0.88	3.81	-	679.0
AHQ-1-4, 6835 - 6902	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	2.62E-04	0.72	3.58	-	504.5
AHQ-1-4, 6611 - 6642	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	2.31E-07	0.73	3.69	-	415.2
AHQ-1-4, 6470 - 6544	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	1.83E-04	0.76	4.27	-	435.4
AHQ-1-4, 6710 - 6767	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	4.15E-09	0.82	4.14	-	486.7
AHQ-1-4, 5182	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.03E-07	0.96	5.05	-	849.2
AHQ-1-6, 5190	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	8.90E-08	0.96	5.49	-	996.0
AHQ-1-2, 5467	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	3.42E-09	0.95	4.98	-	732.5
AHQ-1-7, 5152	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.16E-05	0.95	5.03	-	892.1
AHQ-1-4, 5322 - 5384	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.38E-06	0.98	6.30	-	1244.5
AHQ-1-2, 5474	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	2.33E-04	0.89	3.44	-	1309.1
AHQ-1-5, 5238	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.22E-06	0.95	4.68	-	815.4
AHQ-1-1, 5435	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	3.29E-05	0.86	3.76	-	874.9
AHQ-1-6, 5186 - 5187	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	8.85E-06	0.85	3.44	-	1197.0
AHQ-1-5, 5241 - 5242	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	1.33E-05	0.84	3.98	-	739.9
AHQ-1-4, 5324 - 5400	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	4.51E-05	0.86	3.60	-	929.9
AHQ-1-4, 5435	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	4.87E-07	0.91	4.30	-	609.3
AHQ-1-4, 5436 - 5508	R.GQVLVFLGQSEGLR.S	1503.72793	2	9.90E-10	0.97	4.77	-	1617.3
AHQ-1-4, 5290 - 5359	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.60E-07	0.96	4.28	-	1509.5
AHQ-1-4, 5188 - 5262	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.01E-06	0.97	5.25	-	1471.4
AHQ-1-3, 5154	R.GQVLVFLGQSEGLR.S	1503.72793	2	3.17E-08	0.97	5.04	-	1432.1
AHQ-1-6, 5026	R.GQVLVFLGQSEGLR.S	1503.72793	2	2.22E-05	0.94	4.00	-	1037.9
AHQ-1-5, 5085	R.GQVLVFLGQSEGLR.S	1503.72793	2	4.15E-07	0.97	4.88	-	1681.9
AHQ-1-7, 4410 - 4485	R.HDLLVGAPLYMESR.A	1601.85188	2	3.28E-05	0.93	3.94	-	1102.3
AHQ-1-5, 4417	R.HDLLVGAPLYMESR.A	1601.85188	2	3.51E-07	0.97	4.56	-	1712.6
AHQ-1-4, 3990	R.HDLLVGAPLYM*ESR.A	1617.85128	3	3.55E-04	0.84	3.48	-	959.6
AHQ-1-4, 4532 - 4602	R.HDLLVGAPLYMESR.A	1601.85188	2	2.05E-05	0.96	4.75	-	1253.4
AHQ-1-4, 3819 - 3847	K.HSPICHTTMAFLR.D	1572.83705	2	1.00E-07	0.59	2.61	-	274.8
AHQ-1-11, 4142 - 4143	K.IVLLDVPVR.A	1024.28196	2	8.58E-04	0.88	3.33	-	763.7
AHQ-1-3, 4553	K.IVLLDVPVR.A	1024.28196	2	4.94E-04	0.90	3.35	-	931.2
AHQ-1-12, 4306	K.IVLLDVPVR.A	1024.28196	2	7.50E-04	0.90	3.60	-	758.5
AHQ-1-5, 4450	K.IVLLDVPVR.A	1024.28196	2	9.01E-04	0.94	3.89	-	1168.0
AHQ-1-6, 4363 - 4376	K.IVLLDVPVR.A	1024.28196	2	2.56E-04	0.85	3.37	-	736.4
AHQ-1-4, 4588	R.IYVENDFSWDK.R	1416.51610	1	1.28E-06	0.48	2.35	-	437.8
AHQ-1-6, 3855 - 3923	R.IYVENDFSWDKR.Y	1572.70245	2	2.84E-04	0.62	2.74	-	589.7
AHQ-1-7, 3985	R.IYVENDFSWDKR.Y	1572.70245	2	5.29E-07	0.92	3.47	-	1199.7
AHQ-1-4, 4066 - 4138	R.IYVENDFSWDKR.Y	1572.70245	2	9.38E-07	0.96	4.30	-	1492.5
AHQ-1-13- , 6756	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	3.25E-05	0.69	2.99	-	298.8
AHQ-1-13- , 5875	R.LQDPVLVSCDSAPCTVVQCDLQEM*AR.G	3012.36084	3	2.99E-04	0.92	4.08	-	1290.5
AHQ-1-11, 6228	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	1.17E-06	0.85	3.47	-	513.7
AHQ-1-10, 6052 - 6112	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	7.49E-06	0.93	4.88	-	441.9
AHQ-1-10, 6033 - 6115	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	3	3.40E-06	0.77	3.72	-	500.1
AHQ-1-10, 6247	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	5.30E-06	0.31	2.52	-	180.5
AHQ-1-4, 4626 - 4666	K.LSLNAELQLDR.Q	1272.43310	2	3.13E-08	0.92	3.65	-	958.0
AHQ-1-5, 4547	K.LSLNAELQLDR.Q	1272.43310	2	3.50E-05	0.93	3.64	-	1320.4
AHQ-1-10, 2084	R.NRPPLEEDDEEGE	1529.50164	2	1.04E-10	0.93	3.68	-	1327.5
AHQ-1-11, 2138	R.NRPPLEEDDEEGE	1529.50164	2	1.88E-06	0.86	3.47	-	857.7
AHQ-1-13- , 2215	R.NRPPLEEDDEEGE	1529.50164	2	1.42E-08	0.91	3.22	-	1191.9
AHQ-1-7, 2778	R.NVGSQTLQTFK.A	1223.36055	2	1.46E-05	0.69	2.90	-	354.9
AHQ-1-9, 2691 - 2694	R.NVGSQTLQTFK.A	1223.36055	1	6.78E-04	0.12	1.88	-	194.9
AHQ-1-9, 2700	R.NVGSQTLQTFK.A	1223.36055	2	1.00E-04	0.84	3.13	-	543.3
AHQ-1-4, 3332	R.NVGSQTLQTFK.A	1223.36055	1	7.16E-06	0.50	2.43	-	346.0
AHQ-1-10, 2695	R.NVGSQTLQTFK.A	1223.36055	2	3.63E-07	0.89	3.77	-	568.0
AHQ-1-11, 2779	R.NVGSQTLQTFK.A	1223.36055	2	5.71E-04	0.82	3.10	-	509.9
AHQ-1-4, 3062 - 3127	R.NVGSQTLQTFK.A	1223.36055	2	7.08E-04	0.73	2.89	-	455.9
AHQ-1-4, 3119	R.NVGSQTLQTFK.A	1223.36055	1	5.03E-04	0.10	2.03	-	154.8
AHQ-1-4, 7426	R.QGLGASVVSWSDVIVACAPWQHWNVLEK.T	3139.53208	3	1.43E-07	0.91	5.30	-	531.8
AHQ-1-5, 6286 - 6362	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.91E-08	0.97	6.19	-	1522.6
AHQ-1-4, 6240 - 6306	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.05E-08	0.97	6.15	-	1564.9
AHQ-1-4, 6244 - 6311	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	1.38E-07	0.95	5.53	-	539.0
AHQ-1-6, 6102 - 6147	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.39E-11	0.97	6.00	-	1855.4
AHQ-1-4, 6358 - 6422	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	8.09E-08	0.96	6.20	-	1276.7
AHQ-1-7, 6208 - 6224	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.47E-09	0.97	5.71	-	1886.6
AHQ-1-1, 6173	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	6.37E-09	0.97	5.87	-	1940.2
AHQ-1-3, 6174 - 6186	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.38E-09	0.96	6.26	-	1265.9
AHQ-1-5, 6199 - 6221	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.44E-11	0.96	5.86	-	1083.5
AHQ-1-14- , 5878	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.91E-05	0.85	4.04	-	1001.8
AHQ-1-4, 3980	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.82E-11	0.81	3.62	-	488.5
AHQ-1-6, 3659	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.34E-06	0.90	3.75	-	671.2

AHQ-1-10, 3429	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.35E-09	0.84	3.65	-	494.2
AHQ-1-4, 3759 - 3831	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.24E-07	0.95	4.74	-	716.3
AHQ-1-7, 3734 - 3762	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	5.95E-04	0.82	3.35	-	510.9
AHQ-1-5, 3689	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.74E-08	0.95	4.85	-	699.7
AHQ-1-4, 5856	R.TLGPSQEETGGVFLCPWR.A	2036.25364	3	4.66E-06	0.92	4.47	-	1036.6
AHQ-1-5, 5723 - 5789	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	9.42E-07	0.96	5.34	-	1098.1
AHQ-1-4, 5914 - 5975	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.48E-06	0.97	5.20	-	1269.8
AHQ-1-13, 5319	R.TLGPSQEETGGVFLCPWR.A	2036.25364	3	4.52E-04	0.60	3.06	-	474.9
AHQ-1-11, 5174 - 5240	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.41E-05	0.84	3.78	-	922.1
AHQ-1-6, 5666	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.10E-07	0.92	4.30	-	716.9
AHQ-1-10, 5025 - 5092	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.45E-06	0.92	4.47	-	758.4
AHQ-1-1, 5715 - 5780	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.06E-05	0.88	4.00	-	727.8
AHQ-1-3, 5683 - 5703	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.82E-04	0.59	2.92	-	588.1
AHQ-1-4, 5771 - 5848	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.39E-09	0.95	4.47	-	1108.0
AHQ-1-13- , 5612 - 5644	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.44E-06	0.94	4.85	-	738.8
AHQ-1-7, 5716	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.13E-04	0.95	4.89	-	1110.5
AHQ-1-9, 5566	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.91E-06	0.92	4.13	-	788.3
AHQ-1-12, 5358 - 5431	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.30E-08	0.94	4.30	-	1114.9
AHQ-1-4, 3842 - 3911	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.54E-07	0.94	4.74	-	848.2
AHQ-1-3, 3839	K.TPVGSCFLAQPESGR.R	1607.76993	2	9.50E-05	0.76	3.05	-	719.3
AHQ-1-9, 3622	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.84E-06	0.89	3.48	-	871.4
AHQ-1-7, 3780	K.TPVGSCFLAQPESGR.R	1607.76993	2	6.91E-06	0.91	4.20	-	701.7
AHQ-1-5, 3750	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.87E-07	0.90	3.97	-	597.0
AHQ-1-6, 3694	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.11E-07	0.86	3.29	-	825.3
AHQ-1-4, 4030 - 4032	K.TPVGSCFLAQPESGR.R	1607.76993	2	8.48E-08	0.94	4.21	-	1084.5
AHQ-1-1, 3901	K.TPVGSCFLAQPESGR.R	1607.76993	2	7.41E-08	0.91	4.08	-	647.2
AHQ-1-10, 3448	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.43E-06	0.94	4.30	-	825.4
AHQ-1-11, 3547	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.30E-07	0.90	3.78	-	694.6
AHQ-1-4, 4978	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.94E-05	0.91	4.26	-	988.4
AHQ-1-4, 5214 - 5255	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	8.77E-05	0.95	5.06	-	1373.0
AHQ-1-4, 5440	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	9.42E-06	0.91	4.79	-	957.7
AHQ-1-4, 6383	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.51E-04	0.93	4.71	-	1029.5
AHQ-1-4, 4771	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	1.41E-06	0.91	4.06	-	1230.0
AHQ-1-4, 4680 - 4702	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	8.68E-07	0.96	5.02	-	1555.7
AHQ-1-4, 5776	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	6.52E-08	0.96	4.96	-	1402.9
AHQ-1-5, 4594	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	3.02E-08	0.93	4.57	-	1292.6
AHQ-1-13, 2719	R.VAIVVGAPR.T	882.08560	2	2.75E-04	0.93	3.32	-	1168.1
AHQ-1-7, 2540	R.VAIVVGAPR.T	882.08560	2	5.81E-06	0.93	3.45	-	1427.2
AHQ-1-5, 2494 - 2495	R.VAIVVGAPR.T	882.08560	2	5.76E-06	0.94	3.69	-	1277.6
AHQ-1-13- , 2719	R.VAIVVGAPR.T	882.08560	2	3.54E-05	0.90	2.68	-	1101.2
AHQ-1-12, 2606	R.VAIVVGAPR.T	882.08560	2	2.89E-05	0.92	3.14	-	1179.6
AHQ-1-4, 2602 - 2606	R.VAIVVGAPR.T	882.08560	2	4.43E-04	0.95	3.82	-	1395.4
AHQ-1-6, 2514	R.VAIVVGAPR.T	882.08560	2	3.03E-06	0.92	3.53	-	1238.8
AHQ-1-4, 7526 - 7594	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.75E-08	0.98	5.82	-	1942.3
AHQ-1-4, 6134 - 6207	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.77E-07	0.97	5.67	-	1478.2
AHQ-1-4, 6947 - 6966	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	3.43E-06	0.97	5.52	-	1696.9
AHQ-1-4, 6802 - 6875	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.13E-08	0.96	5.91	-	1163.1
AHQ-1-4, 6707 - 6788	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	3.16E-12	0.96	5.43	-	1437.3
AHQ-1-4, 6620 - 6624	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.40E-04	0.97	5.65	-	1228.4
AHQ-1-5, 5987	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	6.64E-07	0.92	4.26	-	1052.0
AHQ-1-4, 6278 - 6302	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	3.17E-06	0.98	6.38	-	2184.0
AHQ-1-4, 7035 - 7098	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.73E-06	0.95	5.47	-	924.8
AHQ-1-4, 4259 - 4266	R.VVLCELGNPMK.K	1261.53692	2	3.93E-07	0.96	4.46	-	1380.0
AHQ-1-4, 4267	R.VVLCELGNPMK.K	1261.53692	1	1.59E-05	0.78	3.00	-	754.3
AHQ-1-5, 4165 - 4174	R.VVLCELGNPMK.K	1261.53692	2	3.14E-08	0.95	4.00	-	1306.6
AHQ-1-4, 3419 - 3430	R.VVLCELGNPM*K.K	1277.53632	2	4.59E-04	0.94	4.18	-	1226.8
AHQ-1-4, 4303 - 4379	R.VYLFLQPR.G	1036.25129	2	8.11E-06	0.95	3.94	-	1284.0
AHQ-1-6, 4142	R.VYLFLQPR.G	1036.25129	2	2.40E-05	0.95	3.26	-	1329.2
AHQ-1-5, 4189 - 4193	R.VYLFLQPR.G	1036.25129	2	8.87E-06	0.95	3.67	-	1392.3
gi|10835002|ref|NP_001166.1| Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]				1.22E-13	5.51	60.30	47.30	22987.8
AHQ-1-10, 2384 - 2385	K.APEPHVEEDDDDELDSK.L	1940.90995	2	3.01E-11	0.98	6.06	-	1747.4
AHQ-1-10, 2404 - 2440	K.APEPHVEEDDDDELDSK.L	1940.90995	3	2.21E-05	0.89	4.08	-	788.4
AHQ-1-13- , 2561	K.APEPHVEEDDDDELDSK.L	1940.90995	2	1.22E-13	0.97	5.69	-	1484.5
AHQ-1-13, 2581	K.APEPHVEEDDDDELDSK.L	1940.90995	2	6.49E-10	0.97	5.50	-	1320.6
AHQ-1-13, 5372	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	5.51E-05	0.73	3.32	-	543.1
AHQ-1-14- , 5556 - 5579	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	4.95E-04	0.87	4.16	-	771.4
AHQ-1-12, 5433 - 5438	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.26E-09	0.93	4.96	-	833.5
AHQ-1-10, 5289 - 5347	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	2	3.72E-05	0.92	4.56	-	704.3
AHQ-1-14- , 5771	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	8.04E-04	0.71	3.18	-	597.9
AHQ-1-10, 2979	K.ELQEMDKDDESLIK.Y	1693.85489	2	1.32E-07	0.91	4.26	-	837.5
AHQ-1-13- , 6763 - 6764	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	1.43E-08	0.85	3.68	-	758.1
AHQ-1-10, 6095 - 6153	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	1.02E-07	0.83	3.63	-	574.4
AHQ-1-11, 3262 - 3291	K.TLLGDGPVVTDPK.A	1312.49400	2	6.26E-05	0.93	3.31	-	1432.9
AHQ-1-13- , 3423 - 3503	K.TLLGDGPVVTDPK.A	1312.49400	2	8.40E-09	0.94	3.79	-	1379.5
AHQ-1-13, 3418	K.TLLGDGPVVTDPK.A	1312.49400	2	6.11E-04	0.90	3.72	-	986.0
gi|4505879|ref|NP_002655.1| pleckstrin; p47 [Homo sapiens]				1.23E-13	9.34	110.41	41.40	40082.5
AHQ-1-11, 5315 - 5339	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.46E-05	0.97	6.57	-	1032.9
AHQ-1-12, 5469	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	7.76E-07	0.97	6.08	-	2086.8
AHQ-1-10, 5153	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	2.10E-04	0.56	2.63	-	429.3
AHQ-1-8, 5695 - 5754	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	4.07E-09	0.98	6.86	-	1850.0
AHQ-1-8, 5715 - 5790	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	7.24E-05	0.80	3.40	-	481.9
AHQ-1-10, 5125 - 5155	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.10E-05	0.93	5.37	-	800.7
AHQ-1-13- , 5764	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	9.43E-05	0.96	6.22	-	1330.4
AHQ-1-13, 5423 - 5425	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	8.65E-12	0.97	6.44	-	1521.2
AHQ-1-8, 2509 - 2539	K.GSTLTSPCQDFGKR.M	1555.69502	2	1.93E-09	0.32	2.65	-	238.7
AHQ-1-11, 2800	K.GSTLTSPCQDFGKR.M	1555.69502	2	3.32E-05	0.55	2.51	-	451.2
AHQ-1-8, 7298 - 7347	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	9.49E-05	0.97	4.62	-	1632.8
AHQ-1-13, 6555 - 6557	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.23E-13	0.99	7.74	-	3272.0
AHQ-1-10, 6412 - 6413	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	3.89E-08	0.98	7.73	-	2394.2
AHQ-1-12, 6661 - 6734	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	9.36E-09	0.98	7.24	-	2094.8
AHQ-1-8, 7502 - 7503	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	3.30E-10	0.99	8.22	-	3039.0
AHQ-1-11, 6491	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.56E-12	0.98	7.41	-	2707.5
AHQ-1-13- , 6975	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	6.64E-12	0.98	7.07	-	2862.7
AHQ-1-12, 5545	R.LPETIDLGALYLSM*K.D	1680.98719	2	7.04E-05	0.95	4.49	-	1137.1
AHQ-1-8, 5795 - 5871	R.LPETIDLGALYLSM*K.D	1680.98719	2	5.51E-04	0.95	4.29	-	1189.6
AHQ-1-10, 5915	R.LPETIDLGALYLSMK.D	1664.98779	2	5.22E-05	0.95	3.92	-	1394.3
AHQ-1-9, 6670	R.LPETIDLGALYLSMK.D	1664.98779	2	2.05E-05	0.96	4.61	-	1467.8
AHQ-1-8, 6932	R.LPETIDLGALYLSMK.D	1664.98779	2	1.18E-05	0.96	3.55	-	1858.1
AHQ-1-11, 6026 - 6098	R.LPETIDLGALYLSMK.D	1664.98779	2	9.26E-05	0.97	3.86	-	2490.9
AHQ-1-8, 6778 - 6860	R.LPETIDLGALYLSMK.D	1664.98779	2	1.61E-06	0.98	5.02	-	1865.0
AHQ-1-12, 6213 - 6237	R.LPETIDLGALYLSMK.D	1664.98779	2	5.41E-09	0.98	4.86	-	2048.5
AHQ-1-1, 5980	R.LPETIDLGALYLSM*K.D	1680.98719	2	3.55E-05	0.90	3.85	-	759.6
AHQ-1-12, 5137 - 5197	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	3	1.03E-05	0.84	3.90	-	842.9
AHQ-1-8, 6274 - 6298	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	2.14E-04	0.98	6.54	-	1756.6
AHQ-1-8, 6256 - 6278	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	3	8.14E-04	0.89	4.42	-	767.1
AHQ-1-10, 5579	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	7.82E-05	0.90	4.06	-	707.8
AHQ-1-10, 5563 - 5565	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	3	7.48E-06	0.76	3.59	-	630.7

AHQ-1-10, 5321	R.NRQEGLMIASSLLNEGYLQPAGDM*SK.S	2840.18322	2	2.12E-04	0.91	4.35	-	518.8
AHQ-1-11, 4352	K.QQDHFFQAAFLEER.D	1766.89390	2	3.92E-07	0.42	2.54	-	117.3
AHQ-1-8, 4488	K.QQDHFFQAAFLEER.D	1766.89390	2	1.49E-07	0.75	2.98	-	237.7
AHQ-1-8, 7568	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.61E-10	0.93	4.76	-	1080.5
AHQ-1-10, 6465	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	6.32E-06	0.85	4.44	-	400.9
AHQ-1-10, 6467	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	4.07E-09	0.91	4.48	-	969.9
AHQ-1-12, 6701	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	3.34E-08	0.89	4.40	-	705.1
AHQ-1-9, 7366	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.77E-12	0.95	5.18	-	1256.2
AHQ-1-13- , 7016	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	9.52E-09	0.89	4.55	-	773.1
gi|7656991|ref|NP_055140.1| coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;				1.91E-13	6.55	80.31	23.40	53248.7
AHQ-1-6, 5964 - 6031	R.AIFLADGNVFTTGFSR.M	1716.91793	2	1.13E-09	0.96	4.89	-	1349.2
AHQ-1-6, 6112 - 6171	R.AIFLADGNVFTTGFSR.M	1716.91793	2	2.09E-05	0.97	4.86	-	1761.8
AHQ-1-7, 6136	R.AIFLADGNVFTTGFSR.M	1716.91793	2	6.05E-05	0.96	5.00	-	1217.1
AHQ-1-6, 3262	R.KCEPIIMTVPR.K	1345.65706	2	2.16E-05	0.61	2.74	-	512.2
AHQ-1-6, 2614	R.KCEPIIM*TVPR.K	1361.65646	2	2.16E-05	0.71	2.57	-	547.8
AHQ-1-7, 7364 - 7438	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	8.00E-10	0.97	6.15	-	1386.2
AHQ-1-6, 7142	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	9.79E-08	0.90	4.74	-	699.8
AHQ-1-6, 3972	K.NADPILISLK.H	1084.29103	1	1.16E-04	0.06	1.94	-	301.8
AHQ-1-6, 3974	K.NADPILISLK.H	1084.29103	2	1.96E-05	0.87	2.99	-	730.4
AHQ-1-7, 2368	K.SIKDTICNQDER.I	1480.58332	2	3.67E-05	0.93	3.27	-	1496.0
AHQ-1-6, 2330	K.SIKDTICNQDER.I	1480.58332	2	2.57E-05	0.82	2.91	-	937.6
AHQ-1-6, 4410 - 4455	R.VTWDSSFCAVNPR.F	1540.68205	2	1.30E-04	0.67	2.69	-	626.5
AHQ-1-7, 6308	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	9.44E-07	0.96	4.99	-	1011.5
AHQ-1-7, 6312	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	7.81E-08	0.93	4.45	-	857.1
AHQ-1-6, 6190 - 6199	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	1.11E-04	0.83	3.28	-	737.9
AHQ-1-6, 6194	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	1.91E-13	0.93	4.76	-	728.2
AHQ-1-9, 6166	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	6.48E-05	0.74	3.03	-	526.5
AHQ-1-10, 5504	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	8.56E-04	0.77	3.02	-	749.2
AHQ-1-10, 5508	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	7.36E-05	0.74	3.04	-	735.7
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				2.14E-13	1.93	20.31	7.40	32164.8
AHQ-1-1, 4981	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.08E-06	0.91	4.26	-	669.1
AHQ-1-1, 5123 - 5133	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.39E-04	0.93	4.43	-	831.2
AHQ-1-2, 5125	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.08E-09	0.86	3.81	-	585.2
AHQ-1-2, 5275	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.22E-05	0.84	4.34	-	475.6
AHQ-1-2, 5622	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.79E-05	0.78	3.27	-	571.1
AHQ-1-3, 4997	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.06E-13	0.94	4.61	-	820.5
AHQ-1-3, 5126 - 5131	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.84E-06	0.93	4.64	-	838.4
AHQ-1-4, 5082	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.47E-09	0.95	4.68	-	997.6
AHQ-1-4, 5236	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.29E-04	0.92	4.96	-	736.2
AHQ-1-4, 5563	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.46E-08	0.94	4.42	-	1115.5
AHQ-1-5, 5062	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.61E-06	0.97	4.87	-	1381.3
AHQ-1-5, 5182	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.22E-05	0.87	3.97	-	684.5
AHQ-1-5, 5529	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.66E-07	0.93	4.50	-	795.9
AHQ-1-6, 4951	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.77E-08	0.92	4.29	-	850.9
AHQ-1-6, 5086	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.09E-06	0.94	5.01	-	789.4
AHQ-1-6, 5407	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.86E-06	0.97	5.97	-	1485.2
AHQ-1-7, 5674	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.09E-05	0.89	4.17	-	705.9
AHQ-1-8, 5002 - 5066	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.54E-07	0.95	5.13	-	785.2
AHQ-1-8, 5132 - 5198	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.43E-05	0.96	5.33	-	1006.4
AHQ-1-8, 5266 - 5342	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.24E-05	0.95	5.10	-	954.2
AHQ-1-8, 5355 - 5427	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.18E-04	0.94	4.62	-	870.1
AHQ-1-8, 5362 - 5442	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.49E-05	0.90	3.87	-	843.8
AHQ-1-8, 5702 - 5768	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.90E-04	0.95	5.11	-	869.4
AHQ-1-8, 5834 - 5902	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.68E-06	0.96	5.29	-	983.9
AHQ-1-8, 5966 - 6035	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.46E-05	0.96	5.37	-	804.1
AHQ-1-8, 6102 - 6167	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.80E-06	0.96	6.11	-	821.1
AHQ-1-8, 6234 - 6310	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.29E-04	0.95	5.11	-	767.1
AHQ-1-8, 6590 - 6667	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.68E-05	0.95	5.89	-	657.0
AHQ-1-8, 6979 - 7019	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.64E-04	0.94	5.04	-	697.8
AHQ-1-8, 7032 - 7106	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.47E-05	0.90	4.31	-	763.5
AHQ-1-8, 7411	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.45E-04	0.85	3.51	-	780.7
AHQ-1-8, 7642	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.07E-07	0.93	4.73	-	861.4
AHQ-1-9, 4903	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.93E-09	0.92	4.26	-	713.6
AHQ-1-9, 5014 - 5090	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.49E-04	0.92	4.25	-	700.0
AHQ-1-9, 5511 - 5586	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.44E-05	0.96	5.14	-	1245.7
AHQ-1-9, 5791 - 5858	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.16E-04	0.78	3.47	-	674.0
AHQ-1-10, 4408 - 4427	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.14E-13	0.96	5.64	-	782.1
AHQ-1-10, 4507 - 4633	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.78E-04	0.96	4.88	-	1281.0
AHQ-1-10, 4691 - 4701	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.49E-08	0.93	4.85	-	849.0
AHQ-1-10, 4835	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.29E-05	0.93	4.43	-	865.4
AHQ-1-10, 4916 - 4991	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.99E-06	0.96	5.49	-	835.8
AHQ-1-10, 5163 - 5179	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.63E-06	0.96	5.06	-	964.3
AHQ-1-11, 4534	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.50E-07	0.97	5.58	-	1267.6
AHQ-1-11, 4650	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.41E-05	0.92	4.46	-	764.6
AHQ-1-11, 4918	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.56E-05	0.96	5.52	-	1152.6
AHQ-1-12, 4689	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.37E-07	0.93	4.80	-	595.1
AHQ-1-12, 4998	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.19E-04	0.94	4.90	-	962.8
AHQ-1-12, 5090	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.61E-04	0.93	3.90	-	1140.2
AHQ-1-12, 5222 - 5278	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.90E-04	0.91	4.51	-	609.8
AHQ-1-12, 5422	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.18E-06	0.86	3.97	-	676.1
AHQ-1-13, 4639 - 4703	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.80E-09	0.95	5.21	-	970.5
AHQ-1-13, 4763 - 4784	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.11E-04	0.94	4.86	-	858.2
AHQ-1-13, 5011 - 5067	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.70E-05	0.96	4.96	-	1375.0
AHQ-1-13, 5053	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.36E-05	0.85	3.95	-	598.6
AHQ-1-14, 5529 - 5588	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.50E-06	0.76	3.46	-	527.3
AHQ-1-14, 5648 - 5704	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.92E-06	0.96	5.24	-	1140.2
AHQ-1-14, 5764 - 5820	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.34E-07	0.97	5.45	-	1138.1
AHQ-1-14, 5876 - 5936	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.77E-04	0.95	5.31	-	980.8
AHQ-1-14, 5960 - 6016	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.55E-06	0.97	5.70	-	1495.9
AHQ-1-14, 6357 - 6426	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.91E-04	0.76	3.61	-	389.1
AHQ-1-13- , 4811 - 4876	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.75E-10	0.98	5.67	-	1644.5
AHQ-1-13- , 4943 - 5011	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.73E-04	0.95	5.17	-	937.9
AHQ-1-13- , 5059	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.69E-04	0.93	4.46	-	967.4
AHQ-1-13- , 5183 - 5203	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.11E-08	0.96	5.15	-	1032.6
AHQ-1-13- , 5264 - 5327	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.77E-08	0.96	5.56	-	1079.5
AHQ-1-13- , 5305	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.37E-04	0.82	3.62	-	659.3
AHQ-1-13- , 5468 - 5531	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.94E-06	0.97	6.20	-	924.1
AHQ-1-13- , 5595 - 5675	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.38E-04	0.96	5.40	-	1053.0
AHQ-1-13- , 5753	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.47E-08	0.94	4.71	-	920.0
AHQ-1-14- , 4711 - 4782	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.61E-07	0.94	5.01	-	691.8
AHQ-1-14- , 4820 - 4902	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.01E-04	0.97	5.35	-	1180.8
AHQ-1-14- , 4962 - 5035	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.35E-06	0.95	4.98	-	987.3
AHQ-1-14- , 5098 - 5170	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.60E-08	0.95	5.16	-	765.3
AHQ-1-14- , 5130 - 5191	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.85E-12	0.97	5.84	-	1157.8
AHQ-1-14- , 5280 - 5342	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.71E-06	0.95	4.99	-	999.6
AHQ-1-14- , 5402 - 5474	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.78E-05	0.95	5.27	-	863.1
gi|27498332|ref|XP_212565.1| similar to tubulin, beta 5 [Homo sapiens]				2.28E-13	5.03	60.32	11.90	49670.5

AHQ-1-11, 5312	R.ALTVPELTQQVFDAK.N	1660.89259	2	4.02E-05	0.73	2.89	-	348.8
AHQ-1-8, 5640	R.ALTVPELTQQVFDAK.N	1660.89259	2	8.47E-04	0.89	3.70	-	590.8
AHQ-1-7, 5805 - 5876	R.ALTVPELTQQVFDAK.N	1660.89259	2	2.23E-04	0.87	3.47	-	413.9
AHQ-1-11, 5266 - 5323	R.ALTVPELTQQVFDAK.N	1660.89259	2	1.82E-04	0.86	3.84	-	388.5
AHQ-1-7, 4041	R.IMNTFSVVPSPK.V	1320.58277	2	1.67E-06	0.84	3.25	-	690.3
AHQ-1-7, 3372	R.IM*NTFSVVPSPK.V	1336.58217	2	1.49E-04	0.87	3.01	-	931.7
AHQ-1-7, 3530 - 3600	R.IM*NTFSVVPSPK.V	1336.58217	2	1.44E-04	0.64	2.90	-	427.6
AHQ-1-7, 3896 - 3969	R.IMNTFSVVPSPK.V	1320.58277	2	1.71E-05	0.91	3.15	-	1363.0
AHQ-1-7, 7194	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	8.71E-04	0.85	3.59	-	630.5
AHQ-1-7, 7288	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	7.26E-07	0.96	5.06	-	1030.1
AHQ-1-14- , 6411 - 6432	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.15E-07	0.95	4.72	-	1052.0
AHQ-1-7, 7021 - 7084	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.28E-13	0.97	5.04	-	1204.7
AHQ-1-7, 6709 - 6714	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	3.36E-04	0.92	3.94	-	849.6
AHQ-1-1, 6564	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.49E-07	0.98	4.75	-	2063.9
AHQ-1-13, 6213	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.08E-04	0.67	2.99	-	573.5
AHQ-1-13, 6300	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.09E-08	0.95	4.50	-	973.1
AHQ-1-13- , 6448 - 6515	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	7.96E-04	0.91	3.96	-	949.9
AHQ-1-13- , 6700 - 6747	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.22E-11	0.96	4.76	-	1064.6
AHQ-1-14- , 6200 - 6259	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	3.05E-08	0.98	6.45	-	1784.5
AHQ-1-14- , 6499	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	6.52E-08	0.94	4.38	-	785.2
AHQ-1-7, 4481	R.YLTVAAVFR.G	1040.23994	2	2.66E-05	0.90	3.32	-	819.3
gi|11968039|ref|NP_071930.1| hypothetical protein FLJ22405 [Homo sapiens]				2.34E-13	0.95	10.21	4.60	46880.2
AHQ-1-14- , 6544	R.AVAPSPSGAIGGLLEQFAR.G	1842.08850	2	2.34E-13	0.95	4.27	-	837.7
gi|4826898|ref|NP_005013.1| profilin 1; profilin-1 [Homo sapiens]				2.64E-13	18.00	200.29	71.40	15054.2
AHQ-1-13, 4881 - 4892	K.CSVIRDSLLQDGEFSM*DLR.T	2259.50329	3	4.08E-05	0.94	4.84	-	1157.1
AHQ-1-13- , 5044	K.CSVIRDSLLQDGEFSM*DLR.T	2259.50329	3	1.37E-04	0.94	5.00	-	1243.8
AHQ-1-13- , 5155	K.CSVIRDSLLQDGEFSM*DLR.T	2259.50329	3	2.70E-05	0.97	5.57	-	1773.5
AHQ-1-13- , 1805 - 1863	K.CYEM*ASHLR.R	1184.32794	2	2.69E-05	0.87	2.73	-	1302.4
AHQ-1-13- , 1923 - 1983	K.CYEM*ASHLR.R	1184.32794	2	4.98E-05	0.95	3.36	-	1672.4
AHQ-1-13- , 2455 - 2477	K.CYEMASHLR.R	1168.32854	2	6.50E-04	0.95	3.51	-	1649.8
AHQ-1-14- , 2438 - 2450	K.CYEMASHLR.R	1168.32854	2	5.99E-04	0.95	2.96	-	2002.0
AHQ-1-13- , 1700 - 1769	K.CYEM*ASHLR.R	1184.32794	2	4.00E-05	0.77	2.59	-	834.0
AHQ-1-13, 1973 - 2029	K.CYEM*ASHLR.R	1184.32794	2	6.26E-04	0.83	2.72	-	1079.9
AHQ-1-13, 2094	K.CYEM*ASHLR.R	1184.32794	2	3.35E-04	0.88	2.65	-	1253.7
AHQ-1-13, 2557 - 2569	K.CYEMASHLR.R	1168.32854	2	3.60E-04	0.95	3.81	-	1661.9
AHQ-1-13- , 4203	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	7.82E-10	0.97	5.58	-	1333.3
AHQ-1-13, 4023 - 4096	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.66E-06	0.97	5.58	-	1098.8
AHQ-1-13- , 4344	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	7.61E-12	0.97	5.34	-	1150.5
AHQ-1-13, 4153 - 4157	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	2.64E-13	0.95	5.24	-	779.7
AHQ-1-12, 5398	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.93E-07	0.87	2.96	-	1180.1
AHQ-1-13- , 4765	R.DSLLQDGEFSM*DLR.T	1642.76963	3	5.24E-08	0.94	4.42	-	1686.8
AHQ-1-13- , 4707 - 4785	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.39E-08	0.96	3.66	-	2032.6
AHQ-1-12, 5254 - 5317	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.00E-10	0.97	4.55	-	1869.2
AHQ-1-13- , 4472 - 4483	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.05E-05	0.96	4.78	-	1538.8
AHQ-1-12, 5122 - 5193	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.97E-09	0.97	4.97	-	1503.5
AHQ-1-12, 4547 - 4621	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.47E-09	0.95	3.78	-	1843.8
AHQ-1-13- , 4831 - 4912	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.50E-04	0.96	4.03	-	1741.1
AHQ-1-12, 4458 - 4459	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.96E-08	0.95	4.40	-	1133.5
AHQ-1-14- , 5426 - 5438	R.DSLLQDGEFSMDLR.T	1626.77023	2	9.80E-11	0.97	4.85	-	2035.6
AHQ-1-13- , 4979	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.99E-04	0.95	4.19	-	1496.9
AHQ-1-13- , 6977 - 7044	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.29E-06	0.92	3.51	-	1240.3
AHQ-1-13- , 5336 - 5363	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.83E-07	0.92	4.05	-	1138.4
AHQ-1-14- , 5508 - 5586	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.71E-06	0.96	4.32	-	1801.2
AHQ-1-13- , 5371 - 5449	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.29E-05	0.85	3.27	-	1116.0
AHQ-1-13- , 5495 - 5559	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.65E-07	0.97	4.54	-	2033.9
AHQ-1-14- , 5163 - 5242	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.74E-06	0.95	3.94	-	1512.6
AHQ-1-13- , 5563	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.73E-04	0.94	3.62	-	1593.5
AHQ-1-14- , 4680 - 4698	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.39E-06	0.94	3.68	-	1512.5
AHQ-1-13- , 5623 - 5692	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.61E-08	0.97	4.81	-	2074.3
AHQ-1-13- , 4576 - 4643	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.07E-09	0.97	5.65	-	1355.3
AHQ-1-14, 5338 - 5396	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.03E-05	0.78	2.96	-	856.6
AHQ-1-13- , 5759 - 5825	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.56E-08	0.97	4.49	-	2106.2
AHQ-1-13, 5424 - 5487	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.05E-08	0.95	3.44	-	1897.6
AHQ-1-13, 5307 - 5367	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.47E-07	0.98	5.08	-	2163.8
AHQ-1-13, 4287 - 4368	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.14E-09	0.95	4.54	-	1095.1
AHQ-1-14- , 4550	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.46E-05	0.88	3.35	-	912.4
AHQ-1-13, 4373 - 4440	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.54E-06	0.95	4.11	-	1320.8
AHQ-1-13, 5183 - 5248	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.64E-10	0.97	4.83	-	2123.8
AHQ-1-13, 4499 - 4565	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.44E-10	0.97	4.25	-	1979.8
AHQ-1-13, 4623	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.05E-06	0.94	3.98	-	1652.1
AHQ-1-13, 4721 - 4725	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.90E-06	0.96	3.74	-	1762.7
AHQ-1-14, 5544	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.50E-05	0.89	3.11	-	1337.6
AHQ-1-13, 5069 - 5127	R.DSLLQDGEFSMDLR.T	1626.77023	2	9.80E-06	0.96	4.01	-	1873.2
AHQ-1-13, 5100 - 5173	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.12E-06	0.90	3.83	-	956.3
AHQ-1-13- , 3617 - 3683	K.DSPSVWAAVPGK.T	1214.35211	2	2.74E-06	0.88	3.61	-	841.0
AHQ-1-13- , 3435 - 3444	K.DSPSVWAAVPGK.T	1214.35211	2	1.22E-06	0.89	3.12	-	1122.8
AHQ-1-14- , 3632 - 3644	K.DSPSVWAAVPGK.T	1214.35211	2	3.65E-08	0.89	3.09	-	1057.9
AHQ-1-13, 3373 - 3375	K.DSPSVWAAVPGK.T	1214.35211	2	2.41E-06	0.89	3.53	-	1090.9
AHQ-1-13, 3534 - 3599	K.DSPSVWAAVPGK.T	1214.35211	2	2.75E-05	0.93	3.51	-	1248.7
AHQ-1-13- , 3748	K.DSPSVWAAVPGK.T	1214.35211	2	3.56E-06	0.90	3.60	-	896.4
AHQ-1-13, 3648 - 3712	K.DSPSVWAAVPGK.T	1214.35211	2	4.49E-05	0.86	2.65	-	1048.7
AHQ-1-12, 3533 - 3553	K.DSPSVWAAVPGK.T	1214.35211	2	3.09E-06	0.87	3.18	-	881.0
AHQ-1-13, 6252 - 6256	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	1.92E-04	0.94	4.62	-	1532.4
AHQ-1-13- , 6675	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	5.47E-09	0.93	4.50	-	1620.1
AHQ-1-13, 2305	K.KCYEMASHLR.R	1296.50145	2	2.02E-07	0.79	2.77	-	782.3
AHQ-1-14- , 4400	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.25E-09	0.51	2.77	-	391.6
AHQ-1-14, 5272	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.54E-07	0.93	4.22	-	828.4
AHQ-1-14, 5281	R.SSFYVNGLTLGGQK.C	1471.63957	1	5.23E-06	0.44	2.18	-	511.7
AHQ-1-12, 4246	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.78E-06	0.39	2.17	-	345.8
AHQ-1-12, 4383 - 4462	R.SSFYVNGLTLGGQK.C	1471.63957	2	6.37E-05	0.97	4.79	-	1296.1
AHQ-1-13, 4197 - 4237	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.39E-06	0.75	3.06	-	476.7
AHQ-1-13, 4200 - 4561	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.55E-05	0.58	3.22	-	393.4
AHQ-1-13, 4283	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.52E-08	0.92	3.74	-	836.8
AHQ-1-13, 4195 - 4223	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.46E-07	0.95	4.22	-	974.6
AHQ-1-14- , 4390	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.55E-08	0.95	4.17	-	972.4
AHQ-1-14- , 4539 - 4616	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.50E-09	0.53	2.34	-	408.6
AHQ-1-13- , 4940	R.SSFYVNGLTLGGQK.C	1471.63957	2	9.54E-05	0.77	2.58	-	660.9
AHQ-1-12, 4473 - 4543	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.06E-10	0.95	3.86	-	1419.7
AHQ-1-13- , 4767 - 4833	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.43E-08	0.89	3.62	-	795.5
AHQ-1-13- , 4619 - 4699	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.12E-08	0.97	4.63	-	1669.4
AHQ-1-13- , 4471 - 4551	R.SSFYVNGLTLGGQK.C	1471.63957	2	9.58E-08	0.95	4.29	-	952.8
AHQ-1-13- , 4391 - 4792	R.SSFYVNGLTLGGQK.C	1471.63957	1	4.12E-05	0.44	3.02	-	314.1
AHQ-1-13- , 4387 - 4691	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.30E-09	0.79	3.31	-	538.7
AHQ-1-13- , 4385 - 4451	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.44E-07	0.92	4.14	-	733.8
AHQ-1-13, 4364 - 4443	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.84E-09	0.97	4.40	-	1703.2
AHQ-1-13, 4495 - 4575	R.SSFYVNGLTLGGQK.C	1471.63957	2	8.81E-06	0.90	3.92	-	782.8
AHQ-1-12, 4241	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.35E-04	0.94	4.03	-	936.6

AHQ-1-12, 4389 - 4463	R.SSFYVNGLTLGGQK.C	1471.63957	1	4.02E-07	0.73	2.68	-	569.8
AHQ-1-13- , 5125	R.SSFYVNGLTLGGQKCSVIR.D	2088.37322	2	1.53E-07	0.86	3.32	-	760.2
AHQ-1-12, 3014 - 3094	K.STGGAPTFNVTVTK.T	1380.52843	2	1.32E-08	0.89	4.03	-	442.5
AHQ-1-13- , 3323 - 3387	K.STGGAPTFNVTVTK.T	1380.52843	2	1.16E-06	0.90	3.55	-	551.7
AHQ-1-13- , 3239 - 3299	K.STGGAPTFNVTVTK.T	1380.52843	2	4.89E-07	0.81	3.32	-	423.6
AHQ-1-13- , 3001 - 3071	K.STGGAPTFNVTVTK.T	1380.52843	2	6.41E-06	0.80	3.33	-	381.7
AHQ-1-13- , 3100	K.STGGAPTFNVTVTK.T	1380.52843	1	3.63E-04	0.71	3.07	-	435.5
AHQ-1-13, 3015 - 3078	K.STGGAPTFNVTVTK.T	1380.52843	2	3.21E-06	0.94	4.31	-	651.6
AHQ-1-13, 3122 - 3165	K.STGGAPTFNVTVTK.T	1380.52843	2	2.52E-07	0.71	2.65	-	436.6
AHQ-1-13, 3230 - 3289	K.STGGAPTFNVTVTK.T	1380.52843	2	1.29E-05	0.83	3.31	-	511.3
AHQ-1-13- , 3140	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	2.87E-05	0.84	3.55	-	530.9
AHQ-1-13- , 2964	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	2.73E-04	0.73	3.25	-	403.8
AHQ-1-13- , 3621 - 3699	K.TDKTLVLLMGK.E	1219.51989	2	2.42E-07	0.96	4.15	-	1542.1
AHQ-1-12, 3573	K.TDKTLVLLMGK.E	1219.51989	2	1.20E-05	0.94	3.51	-	1171.6
AHQ-1-13- , 2987 - 2991	K.TDKTLVLLM*GK.E	1235.51929	2	5.84E-05	0.91	3.56	-	957.3
AHQ-1-13, 3537 - 3600	K.TDKTLVLLMGK.E	1219.51989	2	3.27E-04	0.77	2.61	-	891.5
AHQ-1-12, 5553 - 5609	K.TFVNITPAEVGVLVGK.D	1644.93630	2	6.03E-04	0.57	2.52	-	406.5
AHQ-1-12, 5670 - 5691	K.TFVNITPAEVGVLVGK.D	1644.93630	3	3.35E-07	0.95	4.73	-	1370.6
AHQ-1-13, 5659 - 5715	K.TFVNITPAEVGVLVGK.D	1644.93630	2	4.33E-06	0.89	3.96	-	712.5
AHQ-1-13, 5552	K.TFVNITPAEVGVLVGK.D	1644.93630	3	2.72E-06	0.96	4.79	-	1523.4
AHQ-1-14- , 5911	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.84E-05	0.83	3.54	-	580.0
AHQ-1-12, 5646 - 5705	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.42E-07	0.94	4.57	-	773.6
AHQ-1-13, 5527	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.68E-05	0.95	4.35	-	1065.7
AHQ-1-13, 5255 - 5335	K.TFVNITPAEVGVLVGK.D	1644.93630	2	4.40E-04	0.62	3.16	-	419.6
AHQ-1-12, 5401	K.TFVNITPAEVGVLVGK.D	1644.93630	2	8.32E-05	0.83	3.36	-	519.8
AHQ-1-14- , 5826	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.54E-06	0.82	3.26	-	799.0
AHQ-1-13- , 5637 - 5653	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.15E-04	0.85	3.38	-	818.9
AHQ-1-13- , 5744 - 5799	K.TFVNITPAEVGVLVGK.D	1644.93630	2	6.02E-04	0.90	4.23	-	667.2
AHQ-1-13, 5515 - 5576	K.TFVNITPAEVGVLVGK.D	1644.93630	2	7.20E-07	0.94	4.42	-	948.5
AHQ-1-13- , 5827 - 5907	K.TFVNITPAEVGVLVGK.D	1644.93630	2	4.65E-08	0.95	4.74	-	970.0
AHQ-1-13- , 5877 - 5939	K.TFVNITPAEVGVLVGK.D	1644.93630	3	2.75E-09	0.97	5.83	-	1436.4
AHQ-1-13- , 6092 - 6159	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.80E-06	0.95	4.79	-	1011.3
AHQ-1-13- , 5543 - 5551	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	6.44E-08	0.94	4.58	-	845.7
AHQ-1-13, 5233	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	7.47E-05	0.65	3.09	-	592.5
AHQ-1-13, 5236 - 5303	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	6.66E-06	0.91	4.11	-	790.5
AHQ-1-13, 5936 - 5980	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	1.84E-04	0.68	3.50	-	591.2
AHQ-1-13- , 2899 - 2919	R.TKSTGGAPTFNVTVTK.T	1609.80568	3	1.74E-05	0.82	3.50	-	897.5
AHQ-1-13, 2771 - 2849	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	1.01E-04	0.89	3.87	-	676.8
AHQ-1-13- , 2821 - 2885	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	7.15E-04	0.95	4.43	-	983.9
AHQ-1-12, 2803	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	1.40E-05	0.92	3.99	-	894.9
AHQ-1-13- , 3776 - 3855	K.TLVLLMGK.E	875.15478	2	1.08E-05	0.71	2.54	-	462.6
AHQ-1-14- , 3023	K.TLVLLM*GK.E	891.15418	2	4.68E-04	0.81	2.71	-	559.1
AHQ-1-13, 3592 - 3780	K.TLVLLMGK.E	875.15478	1	8.58E-04	0.57	2.60	-	625.7
AHQ-1-14- , 3816	K.TLVLLMGK.E	875.15478	2	1.67E-05	0.81	2.96	-	536.1
AHQ-1-12, 3665 - 3666	K.TLVLLMGK.E	875.15478	2	1.05E-05	0.75	2.82	-	502.7
AHQ-1-12, 2955	K.TLVLLM*GK.E	891.15418	2	1.50E-04	0.73	2.70	-	578.9
AHQ-1-13, 3656 - 3731	K.TLVLLMGK.E	875.15478	2	1.46E-05	0.82	2.94	-	465.3
AHQ-1-13- , 3060 - 3127	K.TLVLLM*GK.E	891.15418	2	6.65E-04	0.82	2.65	-	703.9
gi|4502549|ref|NP_001734.1| calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta				2.93E-13	1.92	20.26	22.10	16837.5
AHQ-1-11, 3895 - 3950	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	1.65E-04	0.93	3.74	-	1070.1
AHQ-1-12, 4077 - 4141	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	8.35E-09	0.95	4.28	-	1496.5
AHQ-1-12, 3745 - 3809	R.VFDKDGNGYISAAELR.H	1755.90933	2	2.93E-13	0.97	5.10	-	1457.2
AHQ-1-12, 3874 - 3946	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.51E-04	0.81	3.50	-	712.0
AHQ-1-11, 3730	R.VFDKDGNGYISAAELR.H	1755.90933	2	5.15E-09	0.97	4.79	-	1580.9
AHQ-1-13, 3828	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.92E-10	0.95	4.31	-	1238.9
AHQ-1-14, 4744	R.VFDKDGNGYISAAELR.H	1755.90933	2	8.23E-07	0.60	2.53	-	610.9
AHQ-1-11, 3623 - 3668	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.08E-04	0.84	3.43	-	945.5
gi|21735621|ref|NP_005909.2| mitochondrial malate dehydrogenase precursor [Homo sapiens]				3.05E-13	6.33	70.34	37.00	35503.0
AHQ-1-9, 3100	K.AGAGSATLSMAYAGAR.F	1455.62204	2	6.36E-05	0.84	3.62	-	675.7
AHQ-1-9, 6390 - 6470	K.GYLGPEQLPDCLKGCDVVVIPAGVPR.K	2813.24211	2	6.69E-08	0.87	4.16	-	412.4
AHQ-1-9, 5308	K.IFGVTTLDIVR.A	1234.46961	2	6.43E-07	0.94	3.92	-	1337.4
AHQ-1-9, 5714	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	3	5.48E-09	0.98	6.71	-	2519.9
AHQ-1-9, 5711	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	2	3.59E-04	0.80	3.01	-	617.6
AHQ-1-9, 5608 - 5616	K.SQETECTYFSTPLLLGK.K	1976.19328	2	1.14E-08	0.97	5.49	-	1748.2
AHQ-1-9, 6744	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	3.05E-13	0.97	5.69	-	1343.9
AHQ-1-13, 6244 - 6272	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	6.94E-04	0.94	4.28	-	1172.6
AHQ-1-13- , 6688	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	1.39E-09	0.93	3.89	-	1156.7
AHQ-1-9, 4991 - 5062	K.VDFPQDQLTALTGR.I	1561.72111	2	1.08E-05	0.75	3.05	-	619.6
gi|4502295|ref|NP_001677.1| ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti				3.50E-13	10.58	120.27	28.80	57955.2
AHQ-1-7, 7560	R.DQEGQDVLLFIDNIFR.F	1923.11524	2	3.90E-11	0.96	5.14	-	1147.2
AHQ-1-8, 7570	R.DQEGQDVLLFIDNIFR.F	1923.11524	2	3.50E-13	0.97	5.34	-	1264.0
AHQ-1-7, 4618 - 4669	R.FTQAGSEVSALLGR.I	1436.59522	2	3.43E-06	0.92	3.58	-	1229.7
AHQ-1-8, 4431	R.FTQAGSEVSALLGR.I	1436.59522	2	1.55E-09	0.94	4.24	-	1043.9
AHQ-1-8, 7455	K.GFQQILAGEYDHLPEQAFYMVGPIEEAVAK.A	3352.76051	3	4.52E-08	0.87	4.52	-	541.4
AHQ-1-7, 7456	K.GFQQILAGEYDHLPEQAFYMVGPIEEAVAK.A	3352.76051	3	1.28E-06	0.71	3.38	-	576.3
AHQ-1-7, 7341	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	3.99E-05	0.92	5.26	-	897.1
AHQ-1-8, 3769 - 3799	R.IMNVIGEPIDER.G	1386.59962	2	5.19E-05	0.85	3.54	-	757.6
AHQ-1-7, 4854	R.IPSAVGYQPTLATDMGTMQER.I	2267.56880	2	2.18E-04	0.88	4.03	-	419.0
AHQ-1-7, 4106	R.IPSAVGYQPTLATDM*GTMQER.I	2283.56820	2	9.27E-05	0.74	4.46	-	392.3
AHQ-1-7, 4362	R.IPSAVGYQPTLATDMGTM*QER.I	2283.56820	2	6.09E-04	0.78	4.59	-	531.6
AHQ-1-8, 4772	R.IPSAVGYQPTLATDMGTMQER.I	2267.56880	2	3.10E-05	0.84	3.52	-	474.9
AHQ-1-7, 4280	R.LVLEVAQHLGESTVR.T	1651.88893	2	2.66E-07	0.97	4.38	-	1569.3
AHQ-1-8, 4141	R.LVLEVAQHLGESTVR.T	1651.88893	2	3.81E-07	0.97	4.38	-	1650.0
AHQ-1-7, 5934 - 5936	R.VALTGLTVAEYFR.D	1440.66861	2	1.58E-05	0.98	4.41	-	2119.6
AHQ-1-8, 5675	R.VALTGLTVAEYFR.D	1440.66861	2	2.83E-04	0.89	3.26	-	1106.8
AHQ-1-8, 3301 - 3306	K.VALVYGQMNQPPGAR.A	1601.85511	2	2.29E-05	0.82	3.35	-	719.0
AHQ-1-7, 4825	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	1.81E-07	0.90	4.43	-	397.5
AHQ-1-8, 4740	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	1.18E-04	0.63	3.08	-	320.7
gi|4505981|ref|NP_002695.1| pro-platelet basic protein (includes platelet basic protein, bet; Pro-p				3.68E-13	7.12	80.30	40.60	13894.1
AHQ-1-14, 5392 - 5457	K.EESLDSDLYAELR.C	1540.61070	2	8.36E-08	0.68	2.85	-	586.8
AHQ-1-14, 5709 - 5769	K.EESLDSDLYAELR.C	1540.61070	2	2.00E-04	0.89	3.30	-	1086.0
AHQ-1-14- , 4740 - 4806	K.EESLDSDLYAELR.C	1540.61070	2	4.97E-09	0.97	4.92	-	1381.6
AHQ-1-14, 5604 - 5664	K.EESLDSDLYAELR.C	1540.61070	2	6.29E-09	0.97	4.87	-	1505.5
AHQ-1-14- , 4450 - 4518	K.EESLDSDLYAELR.C	1540.61070	2	2.24E-10	0.88	3.62	-	581.9
AHQ-1-14- , 4683	K.GKEESLDSDLYAELR.C	1725.83517	2	1.89E-11	0.98	6.05	-	2537.1
AHQ-1-13, 4149	K.GKEESLDSDLYAELR.C	1725.83517	3	8.21E-04	0.74	3.71	-	628.6
AHQ-1-14- , 4483	K.GKEESLDSDLYAELR.C	1725.83517	2	3.43E-05	0.87	2.76	-	1155.9
AHQ-1-14- , 4684	K.GKEESLDSDLYAELR.C	1725.83517	3	1.80E-04	0.89	3.39	-	1241.7
AHQ-1-14- , 4398 - 4466	K.GKEESLDSDLYAELR.C	1725.83517	2	5.67E-11	0.98	5.48	-	2721.8
AHQ-1-14- , 4310 - 4370	K.GKEESLDSDLYAELR.C	1725.83517	2	2.06E-11	0.98	5.66	-	2279.2
AHQ-1-14- , 4262 - 4338	K.GKEESLDSDLYAELR.C	1725.83517	3	1.36E-06	0.90	4.34	-	966.8
AHQ-1-14- , 4171 - 4244	K.GKEESLDSDLYAELR.C	1725.83517	2	1.29E-11	0.98	5.12	-	2598.2
AHQ-1-12, 4134 - 4137	K.GKEESLDSDLYAELR.C	1725.83517	2	1.42E-11	0.98	5.41	-	2082.9
AHQ-1-14- , 4087 - 4154	K.GKEESLDSDLYAELR.C	1725.83517	2	1.59E-10	0.98	5.59	-	2617.2
AHQ-1-14- , 4056 - 4060	K.GKEESLDSDLYAELR.C	1725.83517	3	2.06E-05	0.89	4.23	-	823.2
AHQ-1-14- , 3967 - 3975	K.GKEESLDSDLYAELR.C	1725.83517	3	1.38E-05	0.89	4.38	-	1019.0
AHQ-1-14- , 3966 - 4031	K.GKEESLDSDLYAELR.C	1725.83517	2	1.66E-10	0.98	6.03	-	2280.6

AHQ-1-14- , 3827	K.GKEESLDSDLYAELR.C	1725.83517	2	2.08E-06	0.97	4.65	-	1790.6
AHQ-1-13- , 4352	K.GKEESLDSDLYAELR.C	1725.83517	3	3.65E-05	0.91	3.95	-	1192.3
AHQ-1-13- , 4311 - 4345	K.GKEESLDSDLYAELR.C	1725.83517	2	9.97E-10	0.98	5.56	-	2412.7
AHQ-1-14, 5961	K.GKEESLDSDLYAELR.C	1725.83517	2	4.79E-07	0.92	3.99	-	1177.5
AHQ-1-14, 5877 - 5900	K.GKEESLDSDLYAELR.C	1725.83517	2	7.15E-07	0.96	4.27	-	1438.4
AHQ-1-14, 5750 - 5818	K.GKEESLDSDLYAELR.C	1725.83517	2	3.75E-08	0.98	5.39	-	2082.6
AHQ-1-11, 4011	K.GKEESLDSDLYAELR.C	1725.83517	2	9.33E-08	0.97	4.84	-	2247.8
AHQ-1-14, 5606 - 5678	K.GKEESLDSDLYAELR.C	1725.83517	2	3.08E-10	0.98	4.72	-	2173.7
AHQ-1-14- , 4140 - 4219	K.GKEESLDSDLYAELR.C	1725.83517	3	1.42E-05	0.95	4.95	-	1598.1
AHQ-1-14, 4816 - 4872	K.GKEESLDSDLYAELR.C	1725.83517	2	3.24E-10	0.98	5.53	-	1939.8
AHQ-1-14, 5465 - 5536	K.GKEESLDSDLYAELR.C	1725.83517	2	5.99E-08	0.97	4.51	-	2256.3
AHQ-1-14, 4844	K.GKEESLDSDLYAELR.C	1725.83517	3	2.36E-04	0.94	4.52	-	1377.1
AHQ-1-14, 4928 - 5001	K.GKEESLDSDLYAELR.C	1725.83517	2	1.93E-05	0.97	4.76	-	1939.1
AHQ-1-10, 3908	K.GKEESLDSDLYAELR.C	1725.83517	2	7.91E-10	0.95	4.03	-	1560.5
AHQ-1-14, 5045 - 5121	K.GKEESLDSDLYAELR.C	1725.83517	3	2.85E-06	0.93	4.18	-	1314.4
AHQ-1-14, 5060 - 5140	K.GKEESLDSDLYAELR.C	1725.83517	2	5.23E-11	0.98	5.52	-	2351.7
AHQ-1-14, 5317 - 5349	K.GKEESLDSDLYAELR.C	1725.83517	2	3.68E-13	0.98	5.20	-	2604.5
AHQ-1-14, 5200 - 5257	K.GKEESLDSDLYAELR.C	1725.83517	2	2.48E-11	0.98	5.86	-	2787.8
AHQ-1-14, 5174 - 5245	K.GKEESLDSDLYAELR.C	1725.83517	3	4.20E-06	0.83	3.77	-	739.3
AHQ-1-14- , 4970 - 5050	K.GKEESLDSDLYAELR.C	1725.83517	2	6.19E-09	0.91	3.84	-	1085.2
AHQ-1-14, 5229 - 5289	K.GTHCNQVEVIATLK.D	1571.78073	2	1.73E-04	0.89	3.49	-	837.3
AHQ-1-14, 5097 - 5166	K.GTHCNQVEVIATLK.D	1571.78073	2	3.60E-07	0.96	4.50	-	1483.8
AHQ-1-14, 5361 - 5377	K.GTHCNQVEVIATLK.D	1571.78073	2	6.59E-09	0.91	3.69	-	975.7
AHQ-1-14, 4974 - 4998	K.GTHCNQVEVIATLK.D	1571.78073	2	8.70E-06	0.96	4.73	-	1435.0
AHQ-1-14, 4836 - 4917	K.GTHCNQVEVIATLK.D	1571.78073	2	9.91E-08	0.98	4.85	-	2094.3
AHQ-1-14, 5493	K.GTHCNQVEVIATLK.D	1571.78073	2	5.71E-05	0.94	4.03	-	1141.8
AHQ-1-14, 4709 - 4780	K.GTHCNQVEVIATLK.D	1571.78073	2	3.98E-10	0.98	5.42	-	2279.7
AHQ-1-13, 3401 - 3415	K.GTHCNQVEVIATLK.D	1571.78073	2	2.38E-05	0.92	3.68	-	1059.0
AHQ-1-14, 4580 - 4650	K.GTHCNQVEVIATLK.D	1571.78073	2	1.07E-08	0.97	4.73	-	1882.7
AHQ-1-14, 4464 - 4521	K.GTHCNQVEVIATLK.D	1571.78073	2	1.68E-10	0.98	5.23	-	1778.9
AHQ-1-14- , 4288 - 4350	K.GTHCNQVEVIATLK.D	1571.78073	2	3.00E-05	0.97	4.29	-	1866.7
AHQ-1-14, 4368	K.GTHCNQVEVIATLK.D	1571.78073	2	2.94E-05	0.96	4.35	-	1499.4
AHQ-1-14- , 4027 - 4055	K.GTHCNQVEVIATLK.D	1571.78073	2	5.93E-08	0.98	5.23	-	2101.9
AHQ-1-13- , 3484	K.GTHCNQVEVIATLK.D	1571.78073	2	1.33E-07	0.97	4.07	-	2252.3
AHQ-1-14, 4250 - 4312	K.GTHCNQVEVIATLK.D	1571.78073	2	3.25E-05	0.96	4.60	-	1423.3
AHQ-1-14, 4336 - 4408	K.GTHCNQVEVIATLK.D	1571.78073	2	8.13E-05	0.97	4.42	-	1719.4
AHQ-1-14- , 3886 - 3960	K.GTHCNQVEVIATLK.D	1571.78073	2	7.35E-06	0.97	5.11	-	1685.5
AHQ-1-14- , 3762 - 3826	K.GTHCNQVEVIATLK.D	1571.78073	2	2.39E-06	0.96	4.78	-	1291.6
AHQ-1-14- , 3674 - 3746	K.GTHCNQVEVIATLK.D	1571.78073	2	2.95E-06	0.97	4.43	-	1626.3
AHQ-1-14- , 3607 - 3682	K.GTHCNQVEVIATLK.D	1571.78073	2	5.07E-07	0.98	5.59	-	2085.7
AHQ-1-14- , 3478 - 3554	K.GTHCNQVEVIATLK.D	1571.78073	2	2.64E-07	0.98	5.08	-	2109.4
AHQ-1-14- , 3347 - 3426	K.GTHCNQVEVIATLK.D	1571.78073	2	7.81E-08	0.97	4.74	-	1588.5
AHQ-1-14- , 3078 - 3154	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	3.73E-09	0.98	6.09	-	2318.2
AHQ-1-14- , 3223	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	1.93E-07	0.97	4.97	-	1196.2
AHQ-1-14- , 3224 - 3290	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.81E-10	0.97	5.55	-	1241.2
AHQ-1-14, 3977	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	3.44E-07	0.97	4.76	-	1539.2
AHQ-1-14- , 3074 - 3150	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	4.57E-07	0.95	4.89	-	1399.2
AHQ-1-14, 4044 - 4122	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	6.07E-07	0.92	4.04	-	1148.0
AHQ-1-14, 4076 - 4132	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	4.12E-04	0.97	5.19	-	1685.0
AHQ-1-14- , 3511 - 3575	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.24E-09	0.91	4.58	-	732.1
AHQ-1-14, 4346	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.47E-09	0.89	4.30	-	797.4
AHQ-1-14, 4257	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	9.14E-05	0.92	4.19	-	919.5
AHQ-1-14- , 3655	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.37E-04	0.92	4.20	-	1049.7
AHQ-1-14, 3676	K.GTHCNQVEVIATLKDGRK.I	2028.27941	3	4.02E-07	0.81	3.52	-	903.5
AHQ-1-14- , 2808	K.GTHCNQVEVIATLKDGRK.I	2028.27941	2	7.34E-05	0.96	5.85	-	977.3
AHQ-1-14, 3760 - 3820	K.ICLDPDAPR.I	1058.19059	2	1.45E-05	0.84	3.16	-	848.1
AHQ-1-14- , 2562 - 2660	R.KICLDPDAPR.I	1186.36350	1	2.55E-05	0.17	2.54	-	153.9
AHQ-1-14- , 2542 - 2564	R.KICLDPDAPR.I	1186.36350	2	5.52E-05	0.86	3.31	-	846.7
AHQ-1-14- , 2748	R.KICLDPDAPR.I	1186.36350	2	7.11E-05	0.83	3.16	-	733.6
AHQ-1-14, 3516 - 3596	R.KICLDPDAPR.I	1186.36350	2	2.39E-06	0.83	3.21	-	699.1
AHQ-1-14, 3404 - 3460	R.KICLDPDAPR.I	1186.36350	2	3.10E-05	0.89	3.25	-	901.7
AHQ-1-13- , 2699	R.KICLDPDAPR.I	1186.36350	2	8.44E-06	0.92	3.50	-	1064.5
AHQ-1-14, 3802	R.KICLDPDAPR.I	1186.36350	2	7.93E-05	0.72	2.80	-	597.1
AHQ-1-14- , 2626 - 2687	R.KICLDPDAPR.I	1186.36350	2	1.65E-05	0.85	3.02	-	875.8
AHQ-1-13, 2697	R.KICLDPDAPR.I	1186.36350	2	2.07E-05	0.84	3.16	-	682.2
AHQ-1-14- , 3239 - 3302	K.NIQSLEVIGK.G	1101.27845	2	1.35E-06	0.83	3.32	-	673.1
AHQ-1-14- , 4183	K.NIQSLEVIGK.G	1101.27845	2	2.25E-04	0.94	3.35	-	1637.3
AHQ-1-14- , 4186 - 4266	K.NIQSLEVIGK.G	1101.27845	1	4.58E-04	0.82	2.67	-	798.0
AHQ-1-14, 4197 - 4261	K.NIQSLEVIGK.G	1101.27845	2	4.80E-06	0.83	3.19	-	652.1
AHQ-1-14, 4377 - 4436	K.NIQSLEVIGK.G	1101.27845	2	3.40E-04	0.79	2.66	-	778.4
AHQ-1-14- , 3559 - 3623	K.NIQSLEVIGK.G	1101.27845	2	9.58E-05	0.67	2.79	-	600.4
AHQ-1-14, 4288 - 4348	K.NIQSLEVIGK.G	1101.27845	2	1.42E-06	0.87	3.44	-	745.3
AHQ-1-14- , 3752	K.NIQSLEVIGK.G	1101.27845	2	1.97E-04	0.81	2.66	-	1145.3
AHQ-1-14- , 3714 - 3778	K.NIQSLEVIGK.G	1101.27845	1	2.26E-04	0.89	3.16	-	1130.4
AHQ-1-14, 4680 - 4682	K.NIQSLEVIGK.G	1101.27845	2	3.76E-04	0.80	2.76	-	943.0
AHQ-1-14- , 3366 - 3446	K.NIQSLEVIGK.G	1101.27845	2	2.43E-06	0.81	3.18	-	587.0
AHQ-1-12, 3298	K.NIQSLEVIGK.G	1101.27845	2	5.80E-05	0.90	3.75	-	813.6
AHQ-1-14, 5120	K.NIQSLEVIGK.G	1101.27845	1	3.16E-05	0.82	2.88	-	763.2
gi|4759082|ref|NP_004648.1| serum deprivation response protein; serum deprivation response; phospha				3.94E-13	5.33	60.27	25.20	47172.9
AHQ-1-13, 6007	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	4.96E-05	0.95	4.31	-	1111.8
AHQ-1-1, 6520	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.48E-04	0.75	3.27	-	712.3
AHQ-1-12, 6209	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.14E-04	0.70	3.03	-	559.7
AHQ-1-12, 6078 - 6098	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.31E-06	0.97	5.17	-	1726.7
AHQ-1-11, 5910	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	6.72E-04	0.95	4.15	-	1495.2
AHQ-1-13- , 6416	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.53E-04	0.90	3.43	-	906.3
AHQ-1-6, 6575	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	3.55E-05	0.92	3.94	-	934.2
AHQ-1-9, 6526 - 6603	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.12E-05	0.96	4.88	-	1202.5
AHQ-1-7, 6717	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.92E-04	0.90	3.21	-	1122.9
AHQ-1-13- , 3651 - 3669	K.LVNMLDAVQENQHK.M	1639.85851	2	1.19E-04	0.90	3.82	-	857.4
AHQ-1-11, 3386 - 3446	K.LVNMLDAVQENQHK.M	1639.85851	2	7.46E-07	0.90	4.07	-	816.6
AHQ-1-9, 3382	K.LVNMLDAVQENQHK.M	1639.85851	3	1.56E-06	0.62	3.26	-	268.7
AHQ-1-9, 3891	R.QEKPSSPSPM*PSSTPSPSLNLGNTEEAIR.D	3056.30877	3	1.47E-04	0.82	4.39	-	481.3
AHQ-1-6, 3354	R.SDGDPVQPAVLQVHQTS	1778.90130	2	4.50E-07	0.74	2.85	-	607.3
AHQ-1-9, 6354 - 6422	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.99E-07	0.96	5.28	-	968.4
AHQ-1-6, 6316 - 6334	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	7.01E-06	0.95	4.83	-	829.5
AHQ-1-10, 5593	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	5.10E-05	0.91	3.82	-	843.3
AHQ-1-9, 6231 - 6286	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.10E-04	0.96	5.02	-	847.0
AHQ-1-7, 6436 - 6468	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.53E-06	0.94	4.70	-	980.3
AHQ-1-11, 5687 - 5702	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	6.17E-05	0.94	4.15	-	959.6
AHQ-1-5, 6477	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.72E-05	0.96	5.23	-	787.4
AHQ-1-13- , 6228	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.91E-09	0.95	4.62	-	933.6
AHQ-1-12, 5905 - 5926	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	6.92E-05	0.95	5.07	-	741.0
AHQ-1-4, 6547 - 6548	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.27E-06	0.96	5.43	-	897.1
AHQ-1-3, 6382	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	5.05E-05	0.95	4.53	-	1110.9
AHQ-1-13, 5836	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	5.97E-06	0.96	4.91	-	1085.5
AHQ-1-8, 6366	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	9.02E-05	0.94	4.59	-	780.8
AHQ-1-1, 6337 - 6348	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.63E-04	0.90	4.15	-	716.1

AHQ-1-14- , 6030 - 6031	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.03E-05	0.93	4.29	-	899.4
AHQ-1-6, 2823 - 2827	R.YEGSYALTSEEAER.S	1605.64124	2	3.94E-13	0.94	3.98	-	897.5
AHQ-1-12, 2845	R.YEGSYALTSEEAER.S	1605.64124	2	1.64E-10	0.89	3.19	-	832.7
gi|23510338|ref|NP_003325.2| ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity				4.11E-13	5.22	60.24	8.30	117848.1
AHQ-1-4, 4835	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	4.11E-13	0.82	3.20	-	455.8
AHQ-1-4, 4739	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	5.93E-06	0.89	3.81	-	603.9
AHQ-1-4, 2443	R.KPLLESGTLGTK.G	1244.46280	2	2.40E-04	0.82	3.29	-	695.8
AHQ-1-5, 5458	R.LAGTQPLEVLEAVQR.S	1624.86348	2	2.58E-07	0.85	3.48	-	540.2
AHQ-1-4, 5543	R.LAGTQPLEVLEAVQR.S	1624.86348	2	3.10E-05	0.80	3.53	-	399.2
AHQ-1-4, 3810	R.LQTSSVLVSGLR.G	1260.46546	2	4.73E-04	0.88	3.01	-	1046.2
AHQ-1-4, 6108	R.NEEDAAELVALAQAVNAR.A	1885.02541	2	1.90E-05	0.96	4.32	-	1818.2
AHQ-1-4, 4168	R.YDGQVAVFGSDLQEK.L	1656.77453	2	3.18E-06	0.89	3.26	-	940.0
gi|4506025|ref|NP_000936.1| protein phosphatase 3, regulatory subunit B, alpha isoform 1; protein p				4.27E-13	1.83	20.25	16.50	19299.8
AHQ-1-12, 4307	K.EFIEGVSQFSVK.G	1370.53201	2	1.73E-04	0.86	3.26	-	755.3
AHQ-1-12, 5333 - 5343	R.VIDIFDTDGNGEVDFK.E	1784.90107	2	4.27E-13	0.97	5.05	-	1609.8
gi|10835187|ref|NP_000627.1| superoxide dismutase 2, mitochondrial [Homo sapiens]				4.34E-13	4.36	50.24	39.60	24733.0
AHQ-1-11, 5684 - 5758	K.AIWNVINWENVTER.Y	1744.93137	2	5.55E-07	0.86	3.71	-	677.0
AHQ-1-13, 5913	K.AIWNVINWENVTER.Y	1744.93137	2	7.13E-04	0.92	3.86	-	1117.7
AHQ-1-12, 5977	K.AIWNVINWENVTER.Y	1744.93137	2	1.40E-06	0.92	3.45	-	1263.2
AHQ-1-11, 5772	K.AIWNVINWENVTER.Y	1744.93137	3	1.57E-08	0.95	4.88	-	1408.3
AHQ-1-14- , 6104	K.AIWNVINWENVTER.Y	1744.93137	2	2.87E-05	0.84	3.42	-	776.5
AHQ-1-11, 4332	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	3	2.27E-05	0.65	3.10	-	595.3
AHQ-1-11, 4334	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	2	5.47E-08	0.85	3.94	-	466.5
AHQ-1-11, 3694 - 3755	K.GDVTAQIALQPALK.F	1425.65548	2	6.63E-06	0.80	2.57	-	922.8
AHQ-1-11, 2419 - 2486	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	5.79E-06	0.51	2.56	-	162.5
AHQ-1-11, 2546	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	4.31E-07	0.85	3.27	-	733.4
AHQ-1-11, 2282 - 2355	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	4.34E-13	0.97	4.86	-	1414.6
AHQ-1-11, 6555	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	2.05E-07	0.79	3.56	-	501.5
AHQ-1-11, 5778	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	8.32E-04	0.91	4.18	-	777.5
gi|4502027|ref|NP_000468.1| albumin precursor; PRO0883 protein [Homo sapiens]				5.95E-13	26.99	310.33	54.50	69366.4
AHQ-1-6, 2466	K.AAFTECCQAADK.A	1374.47927	2	1.10E-04	0.90	3.00	-	1126.2
AHQ-1-5, 2455 - 2470	K.AAFTECCQAADK.A	1374.47927	2	1.89E-07	0.90	3.33	-	1072.2
AHQ-1-6, 2480	K.AAFTECCQAADK.A	1374.47927	1	4.11E-04	0.56	2.45	-	620.9
AHQ-1-6, 7231 - 7302	K.ALVLIAFAQYLQQCPFEDHVK.L	2492.87697	3	1.32E-09	0.96	5.14	-	1310.3
AHQ-1-5, 7415	K.ALVLIAFAQYLQQCPFEDHVK.L	2492.87697	3	2.24E-11	0.95	4.88	-	1236.4
AHQ-1-6, 4478 - 4548	K.AVM*DDFAAFVEK.C	1359.52946	2	3.05E-08	0.93	3.32	-	1216.7
AHQ-1-13- , 5579	K.AVMDDFAAFVEK.C	1343.53006	2	1.48E-06	0.94	3.70	-	1181.5
AHQ-1-3, 5674	K.AVMDDFAAFVEK.C	1343.53006	2	1.14E-04	0.87	3.56	-	757.3
AHQ-1-5, 4631	K.AVM*DDFAAFVEK.C	1359.52946	2	2.36E-05	0.96	3.97	-	1562.9
AHQ-1-6, 5578	K.AVMDDFAAFVEK.C	1343.53006	2	4.75E-10	0.96	4.04	-	1460.5
AHQ-1-6, 5583 - 5586	K.AVMDDFAAFVEK.C	1343.53006	1	3.61E-04	0.77	2.40	-	1137.4
AHQ-1-5, 5665 - 5666	K.AVMDDFAAFVEK.C	1343.53006	2	2.00E-09	0.95	4.09	-	1314.6
AHQ-1-14- , 5428	K.AVMDDFAAFVEK.C	1343.53006	2	1.90E-07	0.95	4.14	-	1267.4
AHQ-1-6, 2110	K.CCAAADPHECYAK.V	1556.67999	2	2.65E-07	0.90	3.79	-	734.6
AHQ-1-5, 2378	K.CCTESLVNR.R	1141.25805	2	2.62E-04	0.82	2.67	-	972.8
AHQ-1-6, 6932 - 6955	K.DVFLGM*FLYEYAR.R	1640.88331	2	1.74E-06	0.96	4.69	-	970.2
AHQ-1-5, 2573	R.FKDLGEENFK.A	1227.34766	2	2.37E-04	0.83	3.06	-	829.5
AHQ-1-14- , 2699 - 2759	R.FKDLGEENFK.A	1227.34766	2	5.96E-05	0.65	2.70	-	498.7
AHQ-1-5, 2877	K.FQNALLVR.Y	961.14282	2	8.39E-06	0.87	2.74	-	898.2
AHQ-1-6, 2899 - 2930	K.FQNALLVR.Y	961.14282	2	3.80E-04	0.91	2.98	-	1166.2
AHQ-1-6, 6670 - 6686	R.HPYFYAPELLFFAK.R	1744.02658	2	2.27E-05	0.50	2.52	-	266.8
AHQ-1-6, 6682	R.HPYFYAPELLFFAK.R	1744.02658	3	1.91E-07	0.95	4.59	-	1097.1
AHQ-1-5, 6786	R.HPYFYAPELLFFAK.R	1744.02658	3	9.38E-06	0.91	3.90	-	1022.4
AHQ-1-5, 2522	K.KQTALVELVK.H	1129.37494	1	1.17E-04	0.24	2.26	-	347.4
AHQ-1-5, 3211	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.46E-08	0.86	3.17	-	606.4
AHQ-1-5, 3490	K.KVPQVSTPTLVEVSR.N	1640.90605	2	4.36E-08	0.88	3.43	-	616.6
AHQ-1-9, 3339	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.90E-05	0.71	2.67	-	530.3
AHQ-1-10, 3280 - 3344	K.KVPQVSTPTLVEVSR.N	1640.90605	2	9.50E-08	0.62	2.88	-	438.9
AHQ-1-2, 3806	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.76E-07	0.93	3.91	-	832.7
AHQ-1-6, 3450	K.KVPQVSTPTLVEVSR.N	1640.90605	3	2.77E-06	0.95	4.73	-	1524.0
AHQ-1-6, 3448 - 3455	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.70E-08	0.95	4.08	-	1315.0
AHQ-1-6, 3186	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.27E-05	0.74	2.88	-	439.1
AHQ-1-5, 3494	K.KVPQVSTPTLVEVSR.N	1640.90605	3	1.65E-08	0.96	5.18	-	1655.2
AHQ-1-4, 3690	K.KVPQVSTPTLVEVSR.N	1640.90605	2	6.17E-06	0.85	3.23	-	652.8
AHQ-1-5, 2265 - 2293	K.LKECCEKPLLEK.S	1549.83503	2	1.36E-04	0.91	3.76	-	1062.7
AHQ-1-6, 2316 - 2336	K.LKECCEKPLLEK.S	1549.83503	2	2.37E-04	0.93	4.32	-	996.4
AHQ-1-5, 3262 - 3270	K.LVNEVTEFAK.T	1150.30633	2	2.54E-06	0.86	3.23	-	705.3
AHQ-1-3, 3374	K.LVNEVTEFAK.T	1150.30633	2	1.00E-05	0.86	3.28	-	739.4
AHQ-1-1, 3481	K.LVNEVTEFAK.T	1150.30633	2	9.73E-06	0.78	2.72	-	674.1
AHQ-1-6, 3140	K.LVNEVTEFAK.T	1150.30633	1	2.83E-06	0.50	2.27	-	408.6
AHQ-1-13, 3329 - 3335	K.LVNEVTEFAK.T	1150.30633	2	1.54E-05	0.73	3.03	-	412.3
AHQ-1-6, 5871	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	5.30E-04	0.97	5.49	-	1938.1
AHQ-1-6, 5439	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	9.42E-10	0.97	6.27	-	1467.0
AHQ-1-5, 5490 - 5519	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	1.15E-09	0.98	6.53	-	1908.8
AHQ-1-6, 5124	K.QNCELFEQLGEYK.F	1659.79847	2	3.66E-05	0.84	3.36	-	613.2
AHQ-1-6, 3982 - 4011	R.RHPDYSVVLLLR.L	1468.72842	2	3.78E-08	0.93	3.32	-	1315.3
AHQ-1-5, 4038 - 4105	R.RHPDYSVVLLLR.L	1468.72842	2	2.21E-04	0.75	2.88	-	576.4
AHQ-1-3, 4209	R.RHPDYSVVLLLR.L	1468.72842	2	1.47E-04	0.88	3.14	-	905.6
AHQ-1-6, 6098	R.RHPYFYAPELLFFAK.R	1900.21293	2	5.36E-06	0.98	5.14	-	2994.7
AHQ-1-7, 6125	R.RHPYFYAPELLFFAK.R	1900.21293	2	6.78E-05	0.95	4.40	-	1187.8
AHQ-1-5, 6187	R.RHPYFYAPELLFFAK.R	1900.21293	3	1.26E-11	0.97	5.53	-	1900.6
AHQ-1-6, 6095	R.RHPYFYAPELLFFAK.R	1900.21293	3	1.37E-09	0.98	5.54	-	2051.3
AHQ-1-6, 7222 - 7223	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	1.48E-04	0.98	6.68	-	1660.2
AHQ-1-5, 7405 - 7406	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	2.88E-06	0.97	6.08	-	1742.1
AHQ-1-6, 7187 - 7188	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	3.11E-05	0.96	5.65	-	1361.2
AHQ-1-6, 4754 - 4822	R.RPCFSALEVDETYVPK.E	1913.14041	3	1.15E-08	0.89	4.09	-	771.0
AHQ-1-4, 4911 - 4980	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.18E-04	0.70	3.39	-	380.4
AHQ-1-10, 4320 - 4377	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.53E-04	0.90	4.12	-	613.4
AHQ-1-7, 4817	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.79E-05	0.69	3.22	-	380.1
AHQ-1-13- , 4844	R.RPCFSALEVDETYVPK.E	1913.14041	3	7.19E-04	0.87	3.87	-	791.5
AHQ-1-3, 4893	R.RPCFSALEVDETYVPK.E	1913.14041	2	9.69E-04	0.80	3.99	-	519.8
AHQ-1-5, 4827	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.62E-04	0.89	4.32	-	482.8
AHQ-1-6, 4748	R.RPCFSALEVDETYVPK.E	1913.14041	2	7.72E-04	0.89	3.66	-	774.3
AHQ-1-11, 4471	R.RPCFSALEVDETYVPK.E	1913.14041	2	7.10E-06	0.74	3.42	-	359.4
AHQ-1-7, 7140	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	1.39E-04	0.92	4.87	-	774.0
AHQ-1-5, 7115 - 7121	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	1.42E-04	0.95	4.84	-	1172.7
AHQ-1-6, 6906 - 6974	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	1.00E-09	0.95	5.63	-	970.2
AHQ-1-3, 7018 - 7081	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	1.16E-04	0.81	4.47	-	300.8
AHQ-1-5, 7161 - 7177	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	2.43E-04	0.93	5.01	-	958.6
AHQ-1-5, 7075 - 7151	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	9.47E-10	0.95	5.84	-	705.0
AHQ-1-5, 6589	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	2	9.48E-05	0.95	4.62	-	1107.0
AHQ-1-5, 2501	K.SLHTLFGDK.L	1018.14800	1	2.28E-05	0.56	2.08	-	606.7
AHQ-1-5, 5150	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	7.51E-05	0.88	3.30	-	889.2
AHQ-1-5, 6051	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.17E-08	0.92	4.40	-	546.0
AHQ-1-3, 5993	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.97E-05	0.87	3.52	-	607.5
AHQ-1-5, 5857	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.24E-04	0.91	4.51	-	532.3
AHQ-1-2, 6170	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.99E-06	0.90	4.28	-	439.4

AHQ-1-5, 6053	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.80E-06	0.97	5.52	-	1555.5
AHQ-1-6, 5914 - 5915	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	5.38E-06	0.97	5.37	-	1440.5
AHQ-1-1, 5977	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.91E-05	0.86	3.43	-	489.6
AHQ-1-9, 5812	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	7.77E-05	0.80	3.79	-	355.6
AHQ-1-4, 6106	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.66E-04	0.79	3.70	-	349.2
AHQ-1-7, 6004	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.17E-05	0.70	3.44	-	240.3
AHQ-1-7, 6024	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.50E-10	0.96	5.06	-	1568.4
AHQ-1-6, 5878 - 5946	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.95E-13	0.92	4.70	-	467.3
AHQ-1-5, 3017 - 3051	K.VHTECCHGDLLECADDR.A	2091.20307	2	9.21E-07	0.93	4.14	-	878.3
AHQ-1-5, 3762	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	5.56E-06	0.66	2.97	-	474.7
AHQ-1-5, 3745	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	6.24E-05	0.89	4.43	-	602.7
AHQ-1-6, 3910	K.VPQVSTPTLVEVSR.N	1512.73313	2	3.00E-07	0.86	3.15	-	827.7
AHQ-1-5, 3961	K.VPQVSTPTLVEVSR.N	1512.73313	2	2.15E-04	0.88	3.22	-	814.2
AHQ-1-5, 2297 - 2298	K.YICENQDSISSK.L	1445.53420	2	3.81E-09	0.93	3.61	-	947.3
AHQ-1-7, 2341	K.YICENQDSISSK.L	1445.53420	2	8.05E-05	0.82	3.14	-	756.3
AHQ-1-6, 2420	K.YICENQDSISSK.L	1445.53420	2	4.42E-04	0.92	3.89	-	767.2
AHQ-1-6, 2314	K.YICENQDSISSK.L	1445.53420	1	1.42E-07	0.53	2.79	-	283.0
AHQ-1-6, 2307	K.YICENQDSISSK.L	1445.53420	2	4.28E-06	0.92	3.72	-	656.3
AHQ-1-1, 2493	K.YICENQDSISSK.L	1445.53420	2	1.01E-05	0.83	3.02	-	717.6
gi|6912638|ref|NP_036557.1| ras suppressor protein 1 [Homo sapiens]				5.99E-13	6.12	70.34	45.80	31540.1
AHQ-1-10, 6395 - 6396	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	1.16E-06	0.86	3.93	-	610.7
AHQ-1-10, 5735 - 5791	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	1.63E-05	0.93	4.72	-	491.7
AHQ-1-10, 5685 - 5689	R.ALYLSDNDFEILPPDIGK.L	2021.25559	3	7.29E-06	0.88	4.41	-	713.6
AHQ-1-10, 5604 - 5679	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	2.15E-10	0.93	4.65	-	594.0
AHQ-1-13- , 6272 - 6335	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	8.03E-06	0.89	4.32	-	443.3
AHQ-1-10, 6375	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	3	8.46E-09	0.60	3.61	-	361.9
AHQ-1-10, 6376	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	2	1.93E-08	0.86	4.15	-	334.9
AHQ-1-10, 6313 - 6317	R.GISNM*LDVNGLFTLSHITQLVLSHNK.L	2869.28903	3	1.17E-11	0.90	4.80	-	674.5
AHQ-1-11, 5440 - 5511	K.LQILSLRDNDLISLPK.E	1839.16919	2	3.40E-04	0.54	3.18	-	663.9
AHQ-1-10, 5296	K.LQILSLRDNDLISLPK.E	1839.16919	2	7.06E-07	0.94	5.16	-	1362.3
AHQ-1-10, 5379 - 5453	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	9.88E-05	0.96	4.60	-	965.2
AHQ-1-10, 5389	R.LTVLPPELGNLDLTGQK.Q	1809.09672	3	3.72E-07	0.96	5.59	-	1247.1
AHQ-1-10, 5492 - 5561	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	3.10E-07	0.87	3.79	-	453.5
AHQ-1-11, 5514 - 5570	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	2.04E-04	0.84	3.67	-	384.3
AHQ-1-13- , 6012 - 6083	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	2.45E-05	0.93	4.02	-	777.9
AHQ-1-12, 5734 - 5793	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	4.16E-04	0.52	3.00	-	262.0
AHQ-1-12, 5737	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	5.60E-10	0.91	4.04	-	499.8
AHQ-1-10, 6291 - 6361	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	2	9.56E-05	0.87	4.21	-	375.2
AHQ-1-11, 6447	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	3	5.99E-13	0.97	6.85	-	1300.3
gi|4503571|ref|NP_001419.1| enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n				6.19E-13	13.19	160.38	45.20	47168.7
AHQ-1-14- , 5299 - 5300	R.AAVPSGASTGIYEALELR.D	1806.00979	2	4.54E-10	0.87	4.18	-	327.2
AHQ-1-13- , 5441 - 5451	R.AAVPSGASTGIYEALELR.D	1806.00979	2	6.35E-06	0.96	4.99	-	946.0
AHQ-1-12, 5169	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.99E-05	0.88	4.18	-	477.5
AHQ-1-8, 5274 - 5344	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.62E-06	0.92	3.93	-	620.9
AHQ-1-13, 5139	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.59E-10	0.95	5.23	-	526.3
AHQ-1-14, 6216 - 6286	R.AAVPSGASTGIYEALELR.D	1806.00979	2	7.65E-08	0.94	4.21	-	918.0
AHQ-1-11, 4970	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.00E-04	0.83	3.69	-	375.5
AHQ-1-8, 4679 - 4754	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	1.54E-08	0.88	4.18	-	898.7
AHQ-1-8, 6231	K.DATNVGDEGGFAPNILENKEGLELLK.T	2744.99178	2	6.19E-13	0.81	4.72	-	533.0
AHQ-1-11, 6284	K.DYPVVSIEDPFDQDDWGAWQK.F	2511.63977	2	9.94E-06	0.54	2.64	-	429.7
AHQ-1-8, 4782	K.FTASAGIQVVGDDLTVTNPK.R	2034.25590	2	1.52E-07	0.92	4.24	-	948.5
AHQ-1-13- , 4381 - 4384	R.GNPTVEVDLFTSK.G	1407.55065	1	8.59E-04	0.32	2.61	-	439.0
AHQ-1-8, 4196	R.GNPTVEVDLFTSK.G	1407.55065	1	4.86E-04	0.24	1.98	-	564.2
AHQ-1-8, 4203 - 4204	R.GNPTVEVDLFTSK.G	1407.55065	2	1.04E-07	0.82	3.36	-	749.9
AHQ-1-8, 4205	R.GNPTVEVDLFTSK.G	1407.55065	1	9.86E-09	0.52	3.26	-	455.0
AHQ-1-8, 6188	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	1.84E-08	0.96	5.55	-	1277.7
AHQ-1-8, 2140	R.IGAEVYHNLK.N	1144.30502	2	5.24E-05	0.94	3.92	-	1249.4
AHQ-1-8, 5570	K.LAM*QEFM*ILPVGAANFR.E	1941.30692	2	1.30E-06	0.96	4.99	-	961.9
AHQ-1-8, 6491	K.LAMQEFM*ILPVGAANFR.E	1925.30752	2	1.29E-04	0.91	4.63	-	741.1
AHQ-1-9, 6099 - 6167	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	1.12E-04	0.49	3.18	-	412.2
AHQ-1-9, 6963	K.LAMQEFMILPVGAANFR.E	1909.30812	2	1.76E-04	0.82	3.98	-	395.4
AHQ-1-8, 7082	K.LAMQEFMILPVGAANFR.E	1909.30812	2	6.73E-04	0.93	4.76	-	632.0
AHQ-1-8, 3133 - 3220	K.LAQANGWGVMVSHR.S	1526.74832	2	1.70E-04	0.66	2.59	-	964.8
AHQ-1-8, 3038 - 3042	K.LMIEMDGTENK.S	1281.48208	2	4.23E-04	0.90	3.68	-	705.7
AHQ-1-8, 7111	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	3	3.73E-10	0.98	7.57	-	2481.9
AHQ-1-8, 7104	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	2	3.68E-05	0.63	3.30	-	468.3
AHQ-1-8, 4866 - 4882	R.YISPDQLADLYK.S	1426.59557	2	2.63E-09	0.96	4.94	-	871.5
AHQ-1-8, 4876 - 4955	R.YISPDQLADLYK.S	1426.59557	1	8.65E-06	0.67	3.13	-	501.0
AHQ-1-9, 4878	R.YISPDQLADLYK.S	1426.59557	2	3.51E-07	0.87	3.38	-	700.4
gi|4758086|ref|NP_004069.1| cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain				6.68E-13	5.59	60.25	45.60	20567.3
AHQ-1-11, 4030 - 4095	K.GFGFGQGAGALVHSE	1434.53788	2	3.09E-07	0.93	3.41	-	1163.4
AHQ-1-13, 4185	K.GFGFGQGAGALVHSE	1434.53788	2	4.46E-04	0.74	2.98	-	583.3
AHQ-1-13- , 4377	K.GFGFGQGAGALVHSE	1434.53788	2	1.89E-05	0.86	3.28	-	811.3
AHQ-1-12, 3315	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.57E-06	0.97	4.98	-	1473.6
AHQ-1-11, 3230	K.GLESTTLADKDGEIYCK.G	1902.06957	3	8.27E-06	0.92	4.59	-	814.3
AHQ-1-11, 3162 - 3210	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.26E-07	0.96	5.09	-	1263.2
AHQ-1-13- , 2685	K.GYGYGQGAGTLSTDK.G	1475.54194	2	1.67E-04	0.86	3.12	-	839.0
AHQ-1-11, 2522	K.GYGYGQGAGTLSTDK.G	1475.54194	2	3.20E-07	0.95	3.97	-	1337.5
AHQ-1-13- , 3737	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	8.31E-09	0.90	4.40	-	608.2
AHQ-1-12, 3526	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	9.10E-11	0.94	4.59	-	1085.1
AHQ-1-13, 3605	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	5.88E-10	0.78	3.57	-	465.6
AHQ-1-11, 3358 - 3434	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	8.57E-07	0.72	3.04	-	765.3
AHQ-1-13- , 3739	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	4.34E-10	0.76	3.04	-	675.6
AHQ-1-11, 3430 - 3438	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	3.24E-11	0.89	3.83	-	970.7
AHQ-1-11, 3391 - 3392	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	6.68E-13	0.96	4.38	-	1119.3
AHQ-1-12, 3493	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	6.53E-04	0.91	3.91	-	907.8
AHQ-1-11, 3840	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	3.67E-09	0.89	4.08	-	647.3
gi|20535366|ref|XP_053177.4| similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap				7.43E-13	2.73	30.25	9.60	49858.2
AHQ-1-12, 3074	K.DVNAAIATIK.T	1016.17355	2	6.55E-05	0.94	3.41	-	1559.5
AHQ-1-8, 2882	K.DVNAAIATIK.T	1016.17355	1	1.41E-04	0.15	1.88	-	398.8
AHQ-1-7, 3280	K.DVNAAIATIK.T	1016.17355	1	3.24E-04	0.44	2.11	-	491.7
AHQ-1-7, 3114	K.DVNAAIATIK.T	1016.17355	2	8.46E-04	0.87	3.49	-	969.0
AHQ-1-4, 5472	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.57E-06	0.88	3.33	-	975.1
AHQ-1-3, 5363	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	8.97E-06	0.69	2.96	-	607.1
AHQ-1-7, 5130 - 5201	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	9.34E-05	0.76	3.57	-	399.8
AHQ-1-7, 5361 - 5433	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.95E-10	0.95	4.62	-	1108.8
AHQ-1-7, 5468	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.70E-09	0.94	4.65	-	904.4
AHQ-1-7, 5614	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.04E-09	0.93	4.90	-	625.2
AHQ-1-7, 4976	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.65E-06	0.80	3.55	-	374.5
AHQ-1-6, 5303	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.68E-07	0.88	3.69	-	843.0
AHQ-1-9, 5230	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.83E-07	0.86	3.74	-	625.1
AHQ-1-10, 4736 - 4811	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.29E-04	0.28	2.93	-	345.3
AHQ-1-11, 4538	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.31E-05	0.89	3.99	-	476.7
AHQ-1-1, 5425	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.41E-07	0.94	4.80	-	739.1
AHQ-1-12, 5053	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.64E-07	0.91	4.53	-	485.2
AHQ-1-14- , 5148 - 5211	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.43E-13	0.95	5.09	-	791.3
AHQ-1-13, 5020 - 5084	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.49E-05	0.82	3.44	-	681.5

AHQ-1-14, 5981 - 6040	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.51E-04	0.40	2.98	-	281.2
AHQ-1-14, 6100 - 6156	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	8.22E-05	0.64	2.94	-	458.6
AHQ-1-14, 6281	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.30E-08	0.74	3.56	-	457.8
AHQ-1-14- , 5371	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	9.22E-07	0.80	3.24	-	717.4
AHQ-1-12, 5514 - 5573	R.TIQFVDWCPTGFK.V	1600.81899	2	1.42E-05	0.84	3.72	-	647.5
gi|4503631|ref|NP_000120.1| coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,				7.59E-13	24.00	280.29	41.90	83232.8
AHQ-1-5, 5423 - 5545	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	5.45E-05	0.39	3.01	-	133.2
AHQ-1-5, 2235 - 2257	R.CGPASVQAIK.H	1032.19627	2	3.11E-05	0.91	2.96	-	1177.5
AHQ-1-5, 2513	R.CLGIPAR.I	787.95073	1	3.10E-04	0.49	2.17	-	333.7
AHQ-1-5, 2477	K.DGTHVVENVDATHIGK.L	1692.81163	3	4.46E-07	0.90	4.11	-	1012.1
AHQ-1-6, 2499	K.DGTHVVENVDATHIGK.L	1692.81163	3	3.76E-05	0.88	4.03	-	914.8
AHQ-1-6, 2500	K.DGTHVVENVDATHIGK.L	1692.81163	2	1.21E-05	0.83	3.59	-	620.0
AHQ-1-9, 2472	K.DGTHVVENVDATHIGK.L	1692.81163	2	8.64E-13	0.95	4.39	-	1220.3
AHQ-1-5, 2619	K.DGTHVVENVDATHIGK.L	1692.81163	2	4.60E-05	0.94	3.99	-	1272.8
AHQ-1-5, 2473	K.DGTHVVENVDATHIGK.L	1692.81163	2	3.53E-10	0.94	4.13	-	1073.4
AHQ-1-9, 4339	R.EIRPNSTVQWEEVCRPWVSGHR.K	2724.99524	3	2.51E-04	0.75	3.59	-	436.2
AHQ-1-5, 5927 - 6001	K.ETFDVTLEPLSFK.K	1526.71190	2	4.10E-09	0.93	4.05	-	860.9
AHQ-1-9, 5746 - 5748	K.ETFDVTLEPLSFK.K	1526.71190	2	2.75E-06	0.74	2.96	-	642.0
AHQ-1-10, 5187	K.ETFDVTLEPLSFK.K	1526.71190	2	2.42E-06	0.92	3.47	-	1047.0
AHQ-1-11, 5287 - 5334	K.ETFDVTLEPLSFK.K	1526.71190	2	1.32E-07	0.91	3.61	-	948.1
AHQ-1-5, 7194	R.GTQVVGSDMTVTVQFTNPLK.E	2123.41609	2	2.95E-08	0.90	3.78	-	1080.5
AHQ-1-5, 6986	R.GTQVVGSDMTVTVQFTNPLK.E	2123.41609	2	1.05E-05	0.91	4.00	-	720.6
AHQ-1-5, 6803	R.GTQVVGSDMTVTVQFTNPLK.E	2123.41609	2	2.90E-11	0.98	4.79	-	2254.5
AHQ-1-5, 6598 - 6667	R.GTQVVGSDMTVTVQFTNPLK.E	2123.41609	2	7.25E-05	0.92	4.03	-	938.7
AHQ-1-3, 5863	K.GTYIPVPIVSELQSGK.W	1688.94594	2	5.31E-06	0.64	2.60	-	403.6
AHQ-1-5, 5765 - 5833	K.GTYIPVPIVSELQSGK.W	1688.94594	2	3.81E-04	0.83	3.25	-	495.0
AHQ-1-12, 5439	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.73E-05	0.66	2.84	-	352.6
AHQ-1-13- , 5724 - 5729	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.28E-04	0.59	2.90	-	239.0
AHQ-1-6, 5736 - 5739	K.GTYIPVPIVSELQSGK.W	1688.94594	2	1.60E-04	0.73	3.19	-	319.3
AHQ-1-7, 7252 - 7257	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	4.28E-08	0.97	5.12	-	1431.7
AHQ-1-8, 7158	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	6.92E-06	0.95	4.74	-	959.2
AHQ-1-12, 6513	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.90E-07	0.95	4.65	-	1125.5
AHQ-1-14- , 6594 - 6595	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	4.07E-08	0.97	5.84	-	1500.8
AHQ-1-10, 6235	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	5.62E-08	0.95	5.30	-	919.5
AHQ-1-5, 7321	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.32E-08	0.96	4.95	-	1653.1
AHQ-1-11, 6307	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.12E-07	0.96	5.46	-	1103.9
AHQ-1-6, 7086 - 7094	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	4.70E-09	0.95	4.59	-	992.5
AHQ-1-5, 7209 - 7219	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	1.66E-07	0.86	3.81	-	869.6
AHQ-1-13- , 6843	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	4.60E-06	0.89	4.04	-	707.0
AHQ-1-9, 7038 - 7039	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	4.21E-08	0.96	4.90	-	1131.7
AHQ-1-2, 7265	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.63E-06	0.89	3.84	-	980.2
AHQ-1-1, 6908	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	4.08E-07	0.80	3.39	-	692.7
AHQ-1-5, 7186 - 7253	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	4.56E-06	0.96	4.92	-	1314.6
AHQ-1-5, 6863 - 6939	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	1.58E-05	0.94	5.77	-	902.7
AHQ-1-5, 7051 - 7118	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	1.64E-07	0.96	5.46	-	1568.9
AHQ-1-5, 2089 - 2101	K.KDGTHVVENVDATHIGK.L	1820.98455	3	5.38E-04	0.95	4.04	-	1815.0
AHQ-1-5, 2094 - 2095	K.KDGTHVVENVDATHIGK.L	1820.98455	2	2.22E-09	0.97	4.89	-	1576.8
AHQ-1-5, 2221 - 2289	K.KDGTHVVENVDATHIGK.L	1820.98455	2	7.59E-13	0.93	3.85	-	936.0
AHQ-1-5, 2223 - 2295	K.KDGTHVVENVDATHIGK.L	1820.98455	3	5.27E-05	0.97	5.88	-	1547.5
AHQ-1-6, 2132	K.KDGTHVVENVDATHIGK.L	1820.98455	2	5.04E-07	0.94	4.26	-	1012.9
AHQ-1-9, 2107	K.KDGTHVVENVDATHIGK.L	1820.98455	3	1.91E-04	0.79	3.28	-	1193.7
AHQ-1-7, 2124	K.KDGTHVVENVDATHIGK.L	1820.98455	2	1.17E-05	0.92	3.79	-	1048.6
AHQ-1-11, 4786	K.KETFDVTLEPLSFK.K	1654.88482	2	6.08E-04	0.91	3.54	-	1409.9
AHQ-1-5, 5355	K.KETFDVTLEPLSFK.K	1654.88482	2	1.00E-04	0.80	3.26	-	979.5
AHQ-1-5, 5226	K.KETFDVTLEPLSFK.K	1654.88482	2	2.59E-06	0.97	4.61	-	1798.5
AHQ-1-6, 5174	K.KETFDVTLEPLSFK.K	1654.88482	2	1.21E-05	0.94	3.92	-	1342.4
AHQ-1-5, 2599	R.KLIASMSSDSLR.H	1308.53039	2	9.30E-08	0.95	4.18	-	1299.3
AHQ-1-9, 4651	R.LALETALMYGAK.K	1281.54655	2	5.97E-08	0.97	4.05	-	1717.2
AHQ-1-9, 4176	R.LALETALM*YGAK.K	1297.54595	2	7.73E-05	0.71	2.65	-	879.9
AHQ-1-5, 4763 - 4779	R.LALETALMYGAK.K	1281.54655	2	1.43E-04	0.97	4.26	-	1908.6
AHQ-1-14- , 2283	K.LIASM*SSDSLR.H	1196.35688	2	3.10E-05	0.86	3.04	-	717.3
AHQ-1-5, 2929	K.LIASMSSDSLR.H	1180.35748	2	6.67E-06	0.94	3.57	-	1166.2
AHQ-1-5, 2141 - 2150	K.LIASM*SSDSLR.H	1196.35688	2	6.46E-04	0.91	3.30	-	830.6
AHQ-1-5, 5706 - 5709	R.M*YVAVWTPYGVLR.T	1571.86734	2	1.95E-05	0.96	4.37	-	1202.2
AHQ-1-7, 5704	R.M*YVAVWTPYGVLR.T	1571.86734	2	2.62E-08	0.95	3.83	-	1215.0
AHQ-1-11, 5634	R.MYVAVWTPYGVLR.T	1555.86794	2	6.88E-04	0.78	3.10	-	461.2
AHQ-1-6, 6180 - 6246	R.MYVAVWTPYGVLR.T	1555.86794	2	6.37E-05	0.93	3.85	-	1038.5
AHQ-1-6, 5670	R.M*YVAVWTPYGVLR.T	1571.86734	2	1.14E-04	0.92	3.83	-	874.0
AHQ-1-5, 6331	R.MYVAVWTPYGVLR.T	1555.86794	2	1.04E-05	0.91	4.38	-	648.4
AHQ-1-6, 6716	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	2.12E-11	0.88	4.33	-	731.6
AHQ-1-9, 6718	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	3.57E-06	0.94	4.99	-	1001.1
AHQ-1-5, 3586	R.NVWVHLDGPGVTR.P	1450.62682	2	4.46E-06	0.92	3.57	-	1031.6
AHQ-1-5, 3627 - 3647	R.NVWVHLDGPGVTRPMK.K	1807.11248	2	2.07E-06	0.90	3.69	-	668.6
AHQ-1-5, 3209	R.NVWVHLDGPGVTRPM*K.K	1823.11188	2	5.62E-06	0.92	4.24	-	789.6
AHQ-1-5, 4445	K.QIGGDGMMDITDTYK.F	1645.83696	2	1.65E-05	0.71	2.62	-	552.0
AHQ-1-5, 5885 - 5909	R.SNVDMDFEVENAVLGK.D	1767.93869	2	4.45E-08	0.90	4.14	-	1054.6
AHQ-1-5, 4757 - 4758	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.42E-08	0.97	5.35	-	1421.6
AHQ-1-6, 5383 - 5430	R.SNVDMDFEVENAVLGK.D	1767.93869	2	4.75E-05	0.85	3.67	-	972.3
AHQ-1-5, 5479 - 5493	R.SNVDMDFEVENAVLGK.D	1767.93869	2	7.70E-09	0.97	5.27	-	1709.4
AHQ-1-6, 4680	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.28E-06	0.97	4.70	-	2049.0
AHQ-1-11, 5358 - 5362	K.STVLTIPEIIIK.V	1327.63485	2	7.68E-05	0.92	3.96	-	967.8
AHQ-1-13, 5507	K.STVLTIPEIIIK.V	1327.63485	2	2.34E-04	0.91	3.08	-	1409.8
AHQ-1-9, 5694	K.STVLTIPEIIIK.V	1327.63485	2	1.62E-04	0.90	3.28	-	1167.8
AHQ-1-13- , 5851 - 5852	K.STVLTIPEIIIK.V	1327.63485	2	2.64E-05	0.94	3.66	-	1565.8
AHQ-1-3, 5991	K.STVLTIPEIIIK.V	1327.63485	2	4.57E-05	0.77	2.93	-	712.6
AHQ-1-7, 5877	K.STVLTIPEIIIK.V	1327.63485	2	3.73E-05	0.88	3.24	-	1322.4
AHQ-1-10, 5215	K.STVLTIPEIIIK.V	1327.63485	2	6.87E-04	0.88	3.28	-	1180.2
AHQ-1-5, 5578 - 5594	R.YPQENKGTYIPVPIVSELQSGK.W	2448.75607	2	3.27E-04	0.66	2.94	-	455.7
gi|5453595|ref|NP_006358.1| adenylyl cyclase-associated protein [Homo sapiens]				8.62E-13	11.48	140.34	43.40	51672.7
AHQ-1-7, 7508 - 7510	K.AGAAPYVQAFDSLLAGPVAEYLK.I	2352.66999	3	2.04E-07	0.94	5.43	-	956.9
AHQ-1-7, 2890 - 2961	R.ALLVTASQCQQPAENK.L	1759.96271	2	1.14E-06	0.81	3.64	-	566.2
AHQ-1-9, 2704 - 2715	R.ALLVTASQCQQPAENK.L	1759.96271	2	6.73E-07	0.96	4.92	-	1051.1
AHQ-1-7, 2780 - 2784	R.ALLVTASQCQQPAENK.L	1759.96271	2	5.07E-04	0.96	5.02	-	867.0
AHQ-1-7, 7029	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	1.23E-08	0.93	5.16	-	1047.4
AHQ-1-7, 6776 - 6858	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	5.94E-06	0.90	4.78	-	792.6
AHQ-1-7, 2566 - 2636	K.KEPAVLELEGK.K	1213.40557	2	4.64E-07	0.68	2.52	-	468.2
AHQ-1-11, 2642	K.KEPAVLELEGK.K	1213.40557	2	1.73E-05	0.86	3.43	-	525.7
AHQ-1-7, 1566	R.LEAVSHTSDMHR.G	1383.51591	1	9.77E-04	0.36	2.86	-	331.3
AHQ-1-7, 1549	R.LEAVSHTSDMHR.G	1383.51591	2	6.47E-04	0.95	4.21	-	1455.0
AHQ-1-7, 7116	K.LFNHLSAVSESIQALGWVAM*APK.P	2486.87415	3	5.57E-05	0.93	4.52	-	1224.4
AHQ-1-7, 7584 - 7588	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	2.09E-11	0.98	6.85	-	1656.1
AHQ-1-10, 4588	K.LSDLLAPISEQIK.E	1427.66814	1	1.79E-05	0.29	2.29	-	443.4
AHQ-1-13, 4893	K.LSDLLAPISEQIK.E	1427.66814	2	2.34E-06	0.86	3.30	-	837.4
AHQ-1-11, 4732	K.LSDLLAPISEQIK.E	1427.66814	2	1.23E-05	0.82	3.39	-	604.7
AHQ-1-9, 4990	K.LSDLLAPISEQIK.E	1427.66814	2	7.05E-05	0.66	2.89	-	495.2
AHQ-1-7, 5116 - 5134	K.LSDLLAPISEQIK.E	1427.66814	2	1.20E-06	0.94	4.30	-	1059.6
AHQ-1-7, 5121	K.LSDLLAPISEQIK.E	1427.66814	1	7.43E-06	0.72	3.16	-	485.0

AHQ-1-7, 5077 - 5148	K.LSDLLAPISEQIK.E	1427.66814	1	6.96E-05	0.26	2.21	-	333.6
AHQ-1-7, 3389 - 3393	K.NSLDCEIVSAK.S	1237.36245	1	6.38E-06	0.32	2.04	-	517.9
AHQ-1-7, 3085 - 3110	K.NSLDCEIVSAK.S	1237.36245	2	2.24E-04	0.88	3.17	-	848.8
AHQ-1-7, 4721	R.SALFAQINQGESITHALK.H	1929.16615	2	8.10E-09	0.85	3.72	-	501.5
AHQ-1-9, 4720	R.SALFAQINQGESITHALK.H	1929.16615	2	4.03E-08	0.95	4.77	-	947.0
AHQ-1-10, 4375	R.SALFAQINQGESITHALK.H	1929.16615	2	2.08E-07	0.82	4.05	-	486.8
AHQ-1-7, 4936	R.SALFAQINQGESITHALK.H	1929.16615	2	1.26E-07	0.86	4.21	-	455.5
AHQ-1-7, 4829 - 4864	R.SALFAQINQGESITHALK.H	1929.16615	3	1.91E-05	0.74	3.55	-	543.1
AHQ-1-7, 4830 - 4840	R.SALFAQINQGESITHALK.H	1929.16615	2	2.55E-07	0.92	4.33	-	769.1
AHQ-1-7, 5041	R.SALFAQINQGESITHALK.H	1929.16615	2	1.81E-08	0.74	3.64	-	451.2
AHQ-1-7, 2101	R.SGPKPFSAPKPQTSPSPK.R	1839.08461	3	3.80E-04	0.81	3.58	-	781.0
AHQ-1-14- , 6507	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.96E-05	0.44	2.79	-	228.6
AHQ-1-14- , 5994	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	2.26E-04	0.82	4.00	-	271.4
AHQ-1-13- , 6664 - 6676	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	4.51E-05	0.66	2.88	-	348.1
AHQ-1-9, 4780	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.62E-04	0.55	2.69	-	457.4
AHQ-1-10, 4364 - 4368	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.40E-04	0.91	4.43	-	670.1
AHQ-1-8, 4799	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	3.09E-08	0.93	4.98	-	661.4
AHQ-1-7, 5185	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.80E-06	0.95	4.62	-	877.3
AHQ-1-7, 5032 - 5101	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.51E-06	0.94	4.49	-	938.6
AHQ-1-11, 4499	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.44E-04	0.90	4.02	-	835.5
AHQ-1-7, 4901	R.VENQENVSNLVIEDTELK.Q	2074.23206	3	1.83E-06	0.90	4.41	-	817.4
AHQ-1-12, 4665	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	8.62E-13	0.93	4.50	-	793.7
AHQ-1-13, 4649	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.36E-04	0.93	3.85	-	1012.8
AHQ-1-7, 4888 - 4956	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.02E-08	0.95	5.02	-	926.2
AHQ-1-14, 5636	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.65E-06	0.83	3.73	-	539.7
AHQ-1-7, 4689	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.27E-05	0.59	3.17	-	352.5
AHQ-1-14- , 4786	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.82E-04	0.92	4.18	-	832.8
AHQ-1-7, 4366	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.38E-05	0.89	4.18	-	530.7
AHQ-1-5, 4923	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.05E-06	0.68	3.40	-	699.5
gi|7705296|ref|NP_057271.1| bridging integrator 2; bridging integrator-2; breast cancer associated				9.16E-13	4.82	60.31	19.70	61746.8
AHQ-1-13- , 6121 - 6200	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	3.02E-08	0.96	4.69	-	1295.0
AHQ-1-6, 6208	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	7.75E-05	0.75	3.13	-	712.2
AHQ-1-10, 5503 - 5569	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	1.56E-07	0.95	4.95	-	1002.5
AHQ-1-7, 6434	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	9.16E-13	0.96	4.60	-	1414.2
AHQ-1-13, 5764	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	2.73E-05	0.88	3.63	-	995.8
AHQ-1-7, 6337	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	5.70E-06	0.65	3.13	-	388.6
AHQ-1-10, 6397 - 6439	K.AQTVFEDLNQELLEELPILYNSR.I	2736.02649	2	4.45E-05	0.85	3.56	-	642.1
AHQ-1-10, 6447 - 6448	K.AQTVFEDLNQELLEELPILYNSR.I	2736.02649	3	2.73E-04	0.95	6.20	-	716.0
AHQ-1-11, 2776	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	6.69E-06	0.86	4.13	-	500.4
AHQ-1-7, 2789	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	7.78E-05	0.90	4.20	-	680.1
AHQ-1-9, 2687	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	8.76E-08	0.93	4.15	-	928.7
AHQ-1-13- , 2928	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	2.49E-05	0.95	4.85	-	836.8
AHQ-1-10, 2545	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	2.13E-06	0.66	3.15	-	392.7
AHQ-1-10, 2663	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	4.70E-10	0.93	4.63	-	685.8
AHQ-1-13, 2897	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	1.37E-04	0.84	3.53	-	670.8
AHQ-1-9, 6828 - 6895	R.IGCYVTIFQNISNLR.D	1800.07167	2	4.88E-08	0.92	4.87	-	679.0
AHQ-1-9, 6758 - 6830	R.IGCYVTIFQNISNLR.D	1800.07167	2	9.58E-06	0.91	3.70	-	963.3
AHQ-1-6, 6866	R.IGCYVTIFQNISNLR.D	1800.07167	2	6.83E-06	0.93	3.64	-	1109.0
AHQ-1-13, 6257 - 6275	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.36E-04	0.73	3.40	-	723.5
AHQ-1-7, 7000	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.51E-07	0.93	4.06	-	952.3
AHQ-1-7, 4344	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	2.06E-04	0.75	3.58	-	532.9
AHQ-1-6, 4282	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	1.53E-06	0.55	2.74	-	494.3
AHQ-1-9, 4215	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	6.90E-04	0.74	3.38	-	562.1
AHQ-1-10, 4609	R.VSETLQEIYSSEWDGHEELK.A	2380.50595	2	3.38E-04	0.60	2.85	-	341.5
gi|4504165|ref|NP_000168.1| gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]				1.04E-12	23.39	260.33	40.90	85696.9
AHQ-1-5, 3757	K.AGALNSNDAFVLK.T	1320.47622	1	2.90E-08	0.41	2.39	-	412.4
AHQ-1-5, 3837 - 3910	K.AGALNSNDAFVLK.T	1320.47622	2	6.88E-09	0.93	3.83	-	870.7
AHQ-1-5, 3755	K.AGALNSNDAFVLK.T	1320.47622	2	3.23E-08	0.84	3.69	-	574.6
AHQ-1-5, 3655	K.AGALNSNDAFVLK.T	1320.47622	2	1.42E-04	0.63	3.23	-	354.7
AHQ-1-5, 3506 - 3585	K.AGALNSNDAFVLK.T	1320.47622	2	3.97E-06	0.90	3.67	-	968.3
AHQ-1-5, 3874	K.AGALNSNDAFVLK.T	1320.47622	1	1.28E-06	0.50	2.32	-	545.9
AHQ-1-6, 3492 - 3566	K.AGALNSNDAFVLK.T	1320.47622	2	8.74E-07	0.88	3.78	-	669.3
AHQ-1-5, 2951	K.AGKEPGLQIWR.V	1255.45060	3	5.99E-06	0.92	4.35	-	1153.5
AHQ-1-6, 5844	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.95E-05	0.75	3.41	-	375.3
AHQ-1-13, 5443	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.55E-05	0.91	4.10	-	791.9
AHQ-1-7, 5736	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	7.33E-08	0.93	4.88	-	601.8
AHQ-1-7, 5933	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.40E-07	0.93	4.47	-	704.3
AHQ-1-5, 5718 - 5729	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.15E-05	0.97	6.12	-	1079.2
AHQ-1-6, 5642	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.58E-06	0.80	3.76	-	437.2
AHQ-1-11, 5318	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.40E-07	0.93	4.98	-	566.2
AHQ-1-11, 5167	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.17E-05	0.90	4.37	-	539.3
AHQ-1-6, 5944	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.05E-04	0.84	4.09	-	286.5
AHQ-1-9, 5575	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	7.44E-05	0.91	4.57	-	431.1
AHQ-1-5, 5858	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.43E-06	0.96	5.25	-	718.4
AHQ-1-10, 5019 - 5024	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.30E-05	0.95	5.40	-	744.0
AHQ-1-5, 5949 - 6017	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.79E-07	0.97	6.02	-	1040.7
AHQ-1-2, 6106	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.66E-04	0.48	2.64	-	388.0
AHQ-1-5, 6167	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.37E-04	0.84	3.61	-	503.9
AHQ-1-5, 6067 - 6085	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.08E-06	0.97	6.65	-	840.8
AHQ-1-8, 5732 - 5800	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.24E-07	0.94	4.55	-	821.4
AHQ-1-9, 5731	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.81E-04	0.85	3.55	-	534.2
AHQ-1-5, 5825 - 5903	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	3.48E-10	0.95	5.01	-	1208.2
AHQ-1-7, 5814	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.16E-08	0.86	3.53	-	1246.8
AHQ-1-6, 5774	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	4.86E-05	0.96	5.13	-	1374.0
AHQ-1-13, 2329 - 2387	K.DSQEEEKTEALTSAK.R	1666.72289	2	4.95E-07	0.93	3.69	-	1279.5
AHQ-1-8, 2087	K.DSQEEEKTEALTSAK.R	1666.72289	2	9.69E-08	0.90	3.50	-	1132.4
AHQ-1-13, 2333	K.DSQEEEKTEALTSAK.R	1666.72289	3	4.79E-09	0.95	4.30	-	1878.1
AHQ-1-11, 2190	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.85E-05	0.89	3.62	-	983.9
AHQ-1-5, 2187 - 2259	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.94E-07	0.95	4.21	-	1383.9
AHQ-1-7, 2149	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.99E-05	0.85	3.10	-	1186.5
AHQ-1-5, 2106	K.DSQEEEKTEALTSAK.R	1666.72289	3	3.86E-06	0.95	3.74	-	2090.3
AHQ-1-5, 2099 - 2113	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.50E-06	0.92	3.50	-	1346.5
AHQ-1-9, 2118 - 2120	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.50E-07	0.96	4.79	-	1483.6
AHQ-1-13- , 2279	K.DSQEEEKTEALTSAK.R	1666.72289	2	9.98E-09	0.94	3.78	-	1460.1
AHQ-1-10, 2131	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.21E-09	0.94	3.83	-	1457.7
AHQ-1-13- , 2287	K.DSQEEEKTEALTSAK.R	1666.72289	3	4.96E-06	0.97	4.11	-	2794.4
AHQ-1-6, 2135	K.DSQEEEKTEALTSAK.R	1666.72289	3	6.86E-06	0.91	3.36	-	1583.3
AHQ-1-2, 2338	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.38E-08	0.91	3.65	-	1323.2
AHQ-1-1, 2364	K.DSQEEEKTEALTSAK.R	1666.72289	2	9.93E-06	0.93	3.71	-	1563.3
AHQ-1-6, 2120 - 2122	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.89E-09	0.95	3.94	-	1539.3
AHQ-1-5, 6474 - 6549	R.EVQGFESATFLGYFK.S	1723.90570	2	2.12E-11	0.97	5.10	-	1455.1
AHQ-1-13- , 6225 - 6273	R.EVQGFESATFLGYFK.S	1723.90570	2	6.53E-11	0.96	4.59	-	1331.8
AHQ-1-5, 6597 - 6665	R.EVQGFESATFLGYFK.S	1723.90570	2	6.06E-05	0.84	3.53	-	718.8
AHQ-1-13, 5869 - 5891	R.EVQGFESATFLGYFK.S	1723.90570	2	2.23E-07	0.97	4.34	-	1871.9
AHQ-1-12, 5925 - 6006	R.EVQGFESATFLGYFK.S	1723.90570	2	8.21E-07	0.94	4.03	-	990.7
AHQ-1-5, 7606	R.EVQGFESATFLGYFK.S	1723.90570	2	1.13E-06	0.94	3.27	-	1439.1
AHQ-1-5, 6841 - 6870	R.EVQGFESATFLGYFK.S	1723.90570	2	2.43E-06	0.91	3.24	-	1152.8

AHQ-1-5, 6937 - 7017	R.EVQGFESATFLGYFK.S	1723.90570	2	2.19E-07	0.96	4.16	-	1382.9
AHQ-1-14- , 6051	R.EVQGFESATFLGYFK.S	1723.90570	2	4.99E-09	0.90	3.91	-	817.1
AHQ-1-5, 7483 - 7557	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	2	2.50E-04	0.79	3.19	-	448.3
AHQ-1-7, 2212 - 2216	K.HVVPNEVVVQR.L	1276.46981	2	1.08E-08	0.91	3.20	-	730.1
AHQ-1-9, 2174	K.HVVPNEVVVQR.L	1276.46981	2	9.54E-08	0.91	3.29	-	662.4
AHQ-1-5, 2395	K.HVVPNEVVVQR.L	1276.46981	1	1.41E-08	0.46	2.14	-	481.2
AHQ-1-5, 2389 - 2414	K.HVVPNEVVVQR.L	1276.46981	2	6.11E-05	0.87	3.03	-	610.8
AHQ-1-5, 2185 - 2186	K.HVVPNEVVVQR.L	1276.46981	1	3.26E-09	0.47	2.53	-	309.9
AHQ-1-5, 2181 - 2253	K.HVVPNEVVVQR.L	1276.46981	2	2.95E-09	0.90	3.17	-	726.8
AHQ-1-6, 2202	K.HVVPNEVVVQR.L	1276.46981	2	8.77E-10	0.88	3.45	-	567.0
AHQ-1-11, 2266	K.HVVPNEVVVQR.L	1276.46981	2	2.24E-04	0.87	3.02	-	547.8
AHQ-1-5, 6419 - 6493	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	1.58E-11	0.89	4.00	-	1086.0
AHQ-1-5, 6907 - 6919	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	6.28E-05	0.96	5.31	-	1353.3
AHQ-1-5, 6789	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	1.25E-06	0.95	4.93	-	1461.4
AHQ-1-5, 6573 - 6641	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	3.91E-05	0.91	4.24	-	1088.1
AHQ-1-6, 6362 - 6388	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	6.68E-04	0.87	4.05	-	992.8
AHQ-1-5, 5714 - 5715	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	2	8.66E-04	0.75	3.53	-	337.3
AHQ-1-5, 5689 - 5761	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	5.49E-08	0.95	5.49	-	978.2
AHQ-1-5, 6329	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.36E-12	0.93	4.89	-	967.7
AHQ-1-5, 2017	K.PALPAGTEDTAK.E	1171.28241	2	1.86E-07	0.81	2.87	-	458.7
AHQ-1-5, 2415	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	1.09E-06	0.93	4.04	-	778.4
AHQ-1-5, 4833 - 4903	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	1.02E-04	0.77	3.09	-	399.2
AHQ-1-5, 5030 - 5035	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	2.36E-07	0.88	3.80	-	486.4
AHQ-1-5, 2942	K.SEDCFILDHGK.D	1322.42590	3	1.08E-05	0.73	3.04	-	423.8
AHQ-1-7, 2980	K.SEDCFILDHGK.D	1322.42590	2	5.59E-05	0.96	3.71	-	1657.4
AHQ-1-5, 2921	K.SEDCFILDHGK.D	1322.42590	2	1.94E-04	0.95	3.90	-	1405.8
AHQ-1-6, 2967	K.SEDCFILDHGK.D	1322.42590	2	3.87E-06	0.91	3.00	-	1047.7
AHQ-1-8, 2075	K.TGAQELLR.V	888.00387	2	7.43E-05	0.81	2.66	-	907.2
AHQ-1-5, 2054	K.TGAQELLR.V	888.00387	2	1.02E-04	0.85	2.88	-	892.3
AHQ-1-6, 2087	K.TGAQELLR.V	888.00387	2	9.37E-06	0.88	2.93	-	1011.0
AHQ-1-5, 4603 - 4673	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	9.27E-06	0.95	4.59	-	1142.0
AHQ-1-6, 4298	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.28E-04	0.72	3.13	-	580.9
AHQ-1-5, 4491 - 4561	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.30E-05	0.98	5.16	-	2021.2
AHQ-1-10, 3964 - 4032	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	4.69E-04	0.89	3.55	-	1061.7
AHQ-1-5, 4663 - 4742	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.04E-12	0.97	5.62	-	1492.2
AHQ-1-6, 4935	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	3.48E-07	0.97	5.69	-	1064.4
AHQ-1-8, 4815	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	1.59E-04	0.95	4.70	-	754.0
AHQ-1-5, 4927 - 4997	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	2.55E-07	0.97	5.83	-	1268.7
AHQ-1-5, 5314	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	1.64E-08	0.95	6.02	-	688.9
AHQ-1-5, 4385	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	9.87E-05	0.92	4.76	-	765.3
AHQ-1-6, 5234	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	6.76E-09	0.92	4.76	-	674.6
AHQ-1-5, 5098	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAKEDAANR.K	3960.33442	3	4.99E-10	0.97	6.29	-	1184.5
AHQ-1-5, 3549 - 3626	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	1.90E-05	0.92	5.47	-	1120.2
AHQ-1-5, 3141	R.VPFDAATLHTSTAM*AAQHGM*DDDGTGQK.Q	2907.10021	3	6.55E-04	0.80	3.70	-	568.9
AHQ-1-5, 4026	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	2.26E-08	0.97	6.22	-	1231.1
AHQ-1-5, 6978	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	2	2.38E-06	0.74	3.05	-	632.9
AHQ-1-5, 6914	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	3	9.67E-04	0.81	4.49	-	876.5
AHQ-1-5, 6681	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	2	3.16E-07	0.93	4.16	-	901.0
AHQ-1-5, 5537 - 5607	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	2.89E-06	0.93	4.86	-	767.0
AHQ-1-6, 5458 - 5527	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	1.12E-07	0.83	3.15	-	747.8
AHQ-1-5, 1705	R.YIETDPANR.D	1079.14506	2	2.04E-05	0.64	2.67	-	502.5
gi|23308579|ref|NP_006592.3| unactive progesterone receptor, 23 kD; likely ortholog of mouse telome				1.17E-12	0.94	10.24	10.60	18697.3
AHQ-1-11, 4599	K.HLNEIDLFHCIDPNDSK.H	2069.24049	3	1.17E-12	0.94	4.78	-	1090.2
gi|14251209|ref|NP_001279.2| chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo				1.19E-12	9.19	110.26	51.00	26922.5
AHQ-1-13- , 5867	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	2	1.13E-08	0.46	2.57	-	406.3
AHQ-1-12, 5602	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	3	1.26E-10	0.96	5.02	-	1690.9
AHQ-1-13, 5520	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	2	6.39E-07	0.41	2.62	-	370.5
AHQ-1-10, 5313	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	3	1.86E-06	0.91	4.70	-	971.9
AHQ-1-9, 6456	K.FLDGNELTLADCNLLPK.L	1935.18752	2	1.64E-08	0.70	3.56	-	757.9
AHQ-1-10, 5595 - 5669	K.FLDGNELTLADCNLLPK.L	1935.18752	2	4.63E-07	0.92	5.04	-	986.5
AHQ-1-12, 5882	K.FLDGNELTLADCNLLPK.L	1935.18752	2	1.86E-04	0.89	4.29	-	1086.7
AHQ-1-10, 5704	K.FLDGNELTLADCNLLPK.L	1935.18752	2	3.76E-07	0.90	4.38	-	1020.0
AHQ-1-10, 3503	K.FSAYIKNSNPALNDNLEK.G	2039.23424	2	1.19E-12	0.88	4.68	-	795.6
AHQ-1-9, 3280	K.GVTFNVTTVDTK.R	1282.42476	2	5.48E-06	0.92	3.74	-	1038.6
AHQ-1-13- , 3477 - 3543	K.GVTFNVTTVDTK.R	1282.42476	2	2.40E-06	0.93	3.99	-	948.0
AHQ-1-13, 3434	K.GVTFNVTTVDTK.R	1282.42476	2	8.85E-07	0.93	3.72	-	934.6
AHQ-1-10, 3181 - 3245	K.GVTFNVTTVDTK.R	1282.42476	2	3.08E-06	0.91	3.52	-	1029.5
AHQ-1-10, 2337	K.IGNCPFSQR.L	1080.19948	2	8.83E-04	0.82	3.10	-	558.6
AHQ-1-9, 5835	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	1.67E-04	0.75	3.41	-	733.6
AHQ-1-10, 5337	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	4.18E-07	0.88	4.84	-	982.7
AHQ-1-10, 5164 - 5219	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	3.78E-04	0.87	4.52	-	1016.9
AHQ-1-10, 4863	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.90E-06	0.96	5.26	-	917.2
AHQ-1-10, 5135	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.75E-06	0.94	4.68	-	790.4
AHQ-1-10, 5017	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	6.77E-05	0.87	4.12	-	367.2
AHQ-1-9, 5378 - 5400	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.94E-06	0.96	5.22	-	753.5
AHQ-1-13- , 5613	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.64E-07	0.92	4.43	-	624.2
AHQ-1-14, 6266 - 6344	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.54E-04	0.85	4.14	-	385.1
AHQ-1-12, 5262	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.00E-04	0.96	4.47	-	1038.2
AHQ-1-9, 5590 - 5671	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.49E-06	0.90	3.77	-	725.7
AHQ-1-14- , 5359	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.86E-05	0.93	4.60	-	659.0
AHQ-1-13- , 5491	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.92E-06	0.94	4.52	-	791.7
AHQ-1-13, 5300	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.96E-11	0.94	4.92	-	607.2
AHQ-1-13, 5133 - 5191	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.26E-05	0.89	3.73	-	567.1
AHQ-1-14- , 5736	R.LFM*VLWLK.G	1066.38391	2	4.11E-04	0.88	2.70	-	1039.3
AHQ-1-13- , 2923	K.LHIVQVVCK.K	1097.35623	1	3.28E-04	0.74	2.31	-	774.6
AHQ-1-10, 2177	K.NSNPALNDNLEK.G	1329.39838	2	1.79E-07	0.55	3.23	-	370.4
AHQ-1-10, 4683	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	5.21E-04	0.38	2.85	-	215.6
AHQ-1-13- , 5351	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	1.28E-05	0.68	3.60	-	248.9
AHQ-1-12, 5135	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	1.30E-08	0.90	4.77	-	321.3
AHQ-1-12, 5118	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	6.77E-06	0.75	3.48	-	326.4
AHQ-1-10, 4760 - 4824	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	3	5.45E-07	0.94	5.19	-	937.5
AHQ-1-10, 4765 - 4823	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	3.30E-07	0.91	4.59	-	404.7
AHQ-1-10, 4967	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	2.93E-04	0.60	2.75	-	385.7
AHQ-1-13, 5076	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	4.83E-06	0.50	2.81	-	290.7
gi|5453549|ref|NP_006397.1| thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho				1.26E-12	2.65	30.23	10.00	30539.7
AHQ-1-13, 3768	K.DYGVYLEDSGHTLR.G	1625.72052	2	3.60E-07	0.96	4.53	-	1107.2
AHQ-1-10, 3504	K.DYGVYLEDSGHTLR.G	1625.72052	2	1.26E-12	0.97	4.27	-	1802.7
AHQ-1-10, 4629	R.IPLLSDLTHQISK.D	1465.71961	2	2.55E-08	0.96	3.94	-	1366.6
AHQ-1-13- , 3092	R.LVQAFQYTDK.H	1213.36412	2	1.51E-04	0.71	2.63	-	910.5
gi|13994151|ref|NP_066272.1| PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H				1.29E-12	16.63	200.29	60.50	36071.5
AHQ-1-13, 6307	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.99E-08	0.91	4.85	-	526.4
AHQ-1-14- , 6546	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.92E-08	0.86	4.14	-	577.0
AHQ-1-14- , 6462 - 6518	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	4.23E-08	0.91	4.80	-	617.2
AHQ-1-14- , 6047	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	4.28E-10	0.89	4.45	-	505.8
AHQ-1-14- , 5922 - 5987	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	6.14E-05	0.77	3.74	-	673.6
AHQ-1-13- , 6851 - 6853	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.29E-12	0.95	5.75	-	738.4
AHQ-1-13- , 6715 - 6789	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.39E-05	0.92	5.05	-	483.3

AHQ-1-14- , 6606	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	6.67E-08	0.91	4.97	-	643.6
AHQ-1-11, 6198 - 6272	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	7.87E-04	0.81	4.26	-	374.8
AHQ-1-13- , 4579	K.CGTGIVGVFVK.L	1138.36198	2	1.80E-06	0.91	3.30	-	1069.2
AHQ-1-12, 4399	K.CGTGIVGVFVK.L	1138.36198	2	8.70E-04	0.93	3.00	-	1196.4
AHQ-1-14- , 3638 - 3640	K.DFEQPLAISR.V	1176.30388	2	1.24E-06	0.94	4.21	-	981.9
AHQ-1-14, 4562	K.DFEQPLAISR.V	1176.30388	1	3.16E-04	0.37	1.87	-	395.9
AHQ-1-14, 4557 - 4560	K.DFEQPLAISR.V	1176.30388	2	5.97E-05	0.88	3.67	-	723.1
AHQ-1-13, 3613 - 3631	K.DFEQPLAISR.V	1176.30388	2	5.87E-05	0.87	3.15	-	799.8
AHQ-1-12, 3569	K.DFEQPLAISR.V	1176.30388	2	6.79E-07	0.92	3.67	-	973.3
AHQ-1-13- , 3459	K.GCTDNLTLTVAR.S	1322.47058	2	7.44E-04	0.84	3.39	-	724.1
AHQ-1-10, 3756	K.GHFFVEDQIYCEK.H	1673.82684	2	7.33E-06	0.91	3.57	-	862.9
AHQ-1-13- , 4156 - 4228	K.GHFFVEDQIYCEK.H	1673.82684	2	3.71E-05	0.96	4.44	-	1190.2
AHQ-1-12, 3922 - 3945	K.GHFFVEDQIYCEK.H	1673.82684	2	5.25E-05	0.94	4.02	-	1034.4
AHQ-1-12, 3995 - 4018	K.GHFFVEDQIYCEK.H	1673.82684	2	1.71E-06	0.96	4.31	-	1200.2
AHQ-1-13, 3980 - 4044	K.GHFFVEDQIYCEK.H	1673.82684	2	2.17E-05	0.96	4.09	-	1333.5
AHQ-1-14, 4916 - 4996	K.GHFFVEDQIYCEK.H	1673.82684	2	5.26E-04	0.93	3.74	-	1012.8
AHQ-1-14- , 4039	K.GHFFVEDQIYCEK.H	1673.82684	2	7.41E-05	0.93	3.70	-	1067.3
AHQ-1-9, 3970	K.GHFFVEDQIYCEK.H	1673.82684	2	1.66E-05	0.96	4.27	-	1380.2
AHQ-1-12, 2997	R.HPECYVCTDCGTNLK.Q	1858.02023	2	6.07E-04	0.83	3.35	-	500.4
AHQ-1-12, 2669	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	4.93E-10	0.97	4.95	-	1653.7
AHQ-1-14- , 2751	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	1.83E-06	0.97	5.01	-	1917.0
AHQ-1-13- , 2789	R.HRHPECYVCTDCGTNLK.Q	2151.34648	2	2.42E-04	0.89	4.24	-	449.9
AHQ-1-13, 3227	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.59E-07	0.83	3.53	-	703.1
AHQ-1-9, 3052 - 3054	R.IKGCTDNLTLTVAR.S	1563.80174	2	3.47E-08	0.94	4.11	-	1051.2
AHQ-1-14- , 3178	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.71E-09	0.94	4.04	-	1009.7
AHQ-1-11, 3056	R.IKGCTDNLTLTVAR.S	1563.80174	3	3.37E-05	0.82	3.66	-	1136.0
AHQ-1-12, 3122	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.65E-08	0.93	4.06	-	810.3
AHQ-1-14, 4069	R.IKGCTDNLTLTVAR.S	1563.80174	2	8.12E-08	0.91	3.60	-	943.2
AHQ-1-11, 3048	R.IKGCTDNLTLTVAR.S	1563.80174	2	4.60E-07	0.93	4.23	-	1009.4
AHQ-1-13- , 3341	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.39E-08	0.90	3.95	-	703.2
AHQ-1-13- , 3480 - 3531	R.IKGCTDNLTLTVAR.S	1563.80174	2	4.86E-04	0.87	3.58	-	606.5
AHQ-1-13- , 4932	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	2	8.09E-04	0.89	3.50	-	686.5
AHQ-1-13, 4668	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	2	7.87E-04	0.53	2.67	-	385.0
AHQ-1-13- , 5380	K.LPMCDKCGTGIVGVFVK.L	1884.27358	3	2.30E-05	0.78	3.29	-	860.5
AHQ-1-12, 5113	K.LPMCDKCGTGIVGVFVK.L	1884.27358	3	2.31E-07	0.79	3.63	-	699.4
AHQ-1-12, 4682	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	3	1.04E-04	0.56	3.03	-	723.3
AHQ-1-14, 4606 - 4664	R.LVGGKDFEQPLAISR.V	1630.86972	2	2.88E-08	0.96	4.36	-	1501.9
AHQ-1-9, 3586	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.03E-04	0.77	3.29	-	558.3
AHQ-1-14- , 3792	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.23E-08	0.96	4.62	-	1372.3
AHQ-1-9, 3374	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	1.35E-07	0.91	3.96	-	820.6
AHQ-1-13, 3667 - 3699	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	8.74E-04	0.61	3.16	-	590.2
AHQ-1-13- , 3833	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	5.14E-06	0.92	3.95	-	761.1
AHQ-1-13, 3668 - 3683	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	2.76E-05	0.89	3.86	-	566.6
AHQ-1-13, 6308	K.QSTSFLVLQEILESEEK.G	1981.18977	2	4.91E-07	0.91	3.49	-	1203.9
AHQ-1-9, 6859	K.QSTSFLVLQEILESEEK.G	1981.18977	2	2.17E-04	0.94	3.95	-	1144.7
AHQ-1-12, 6410	K.QSTSFLVLQEILESEEK.G	1981.18977	2	1.24E-07	0.90	3.33	-	1261.3
AHQ-1-13- , 6752	K.QSTSFLVLQEILESEEK.G	1981.18977	2	2.96E-11	0.96	4.82	-	1583.3
AHQ-1-9, 2890	R.SAMPFTASPASSTTAR.V	1583.74859	2	9.79E-06	0.55	2.77	-	373.0
AHQ-1-12, 2417 - 2418	R.SAM*PFTASPASSTTAR.V	1599.74799	2	5.94E-07	0.91	3.58	-	1138.3
AHQ-1-11, 2390	R.SAM*PFTASPASSTTAR.V	1599.74799	2	6.09E-07	0.79	2.66	-	968.3
AHQ-1-9, 2308	R.SAM*PFTASPASSTTAR.V	1599.74799	2	3.40E-07	0.85	3.16	-	938.6
AHQ-1-13- , 2511 - 2512	R.SAM*PFTASPASSTTAR.V	1599.74799	2	6.61E-04	0.91	3.67	-	1132.6
AHQ-1-12, 5301	R.VITNQYNNPAGLYSSENISNFNNALESK.T	3103.30221	3	1.07E-04	0.90	4.62	-	687.5
AHQ-1-13- , 4913 - 4980	R.VTPPEGYEVVTVFPK	1662.90695	2	1.99E-04	0.59	2.63	-	198.6
AHQ-1-12, 3551	K.VWSPLVTEEGK.R	1245.40612	1	2.70E-05	0.59	2.01	-	837.6
AHQ-1-13- , 3215	K.VWSPLVTEEGKR.H	1401.59247	2	9.73E-07	0.80	2.85	-	837.6
AHQ-1-11, 3010	K.VWSPLVTEEGKR.H	1401.59247	2	1.83E-06	0.76	2.77	-	670.3
AHQ-1-14- , 3180 - 3188	K.VWSPLVTEEGKR.H	1401.59247	2	1.51E-08	0.77	2.55	-	879.7
gi|27500274|ref|XP_113950.3|	similar to Munc13-4 protein [Homo sapiens]			1.41E-12	12.26	140.31	21.30	123281.1
AHQ-1-4, 7391 - 7536	K.AFGELCPNTAPLPQLVTEALQTGTTEWFHLK.Q	3472.91108	3	1.00E-06	0.71	3.67	-	377.4
AHQ-1-4, 7347	K.ALLGLVQDVIGDLHQCQR.T	2037.32944	3	4.50E-07	0.97	4.56	-	1982.8
AHQ-1-4, 6654	R.ALLYEDALYTVLHR.L	1677.92484	2	3.59E-10	0.97	4.48	-	1993.9
AHQ-1-4, 6047 - 6056	R.AVQMDELVPLGELTK.H	1643.92698	2	5.44E-09	0.80	3.44	-	506.8
AHQ-1-4, 2488	R.DLELQAASSR.E	1090.16939	2	1.03E-05	0.94	3.56	-	1596.2
AHQ-1-4, 4863	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	1.05E-09	0.98	6.13	-	1940.7
AHQ-1-4, 4876	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	2	1.12E-06	0.97	4.81	-	1760.3
AHQ-1-4, 3594 - 3614	R.IQQQAETTSEELGAVTVK.A	1933.10674	2	2.33E-08	0.98	5.72	-	1808.5
AHQ-1-4, 3468	R.LGHPEPNHVTEASELLR.Y	1900.08490	2	4.34E-04	0.57	2.81	-	339.4
AHQ-1-4, 5599 - 5660	K.LPAQLAWEALEQR.V	1525.73360	2	1.41E-12	0.94	4.20	-	1089.7
AHQ-1-4, 7387 - 7402	R.LPLTYPAPNGDPILQLLEGR.K	2178.51621	2	6.30E-06	0.86	3.76	-	635.9
AHQ-1-4, 4238 - 4248	R.SVFPLSVSDSPAR.L	1362.51311	2	1.77E-04	0.82	2.87	-	909.6
AHQ-1-4, 4384	R.TLAEQLEVGIAK.H	1272.47301	2	3.06E-05	0.95	3.44	-	1575.4
AHQ-1-4, 6446 - 6456	R.WFQPAIPSWLQK.T	1501.75533	2	6.30E-05	0.84	3.50	-	459.1
AHQ-1-4, 3531	R.YLQEAFHVEPEEHQQTLQR.V	2383.56113	2	8.34E-04	0.88	3.69	-	686.3
AHQ-1-4, 3451 - 3528	R.YLQEAFHVEPEEHQQTLQR.V	2383.56113	3	5.86E-04	0.93	4.27	-	1455.5
gi|4502303|ref|NP_001688.1|	mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m			1.71E-12	2.68	30.23	23.50	23277.2
AHQ-1-11, 6330	R.FSPLTTNLINLLAENGR.L	1874.13050	2	1.71E-12	0.83	3.78	-	731.3
AHQ-1-14- , 5588	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	2.31E-05	0.93	4.69	-	729.9
AHQ-1-11, 3182	K.VAASVLNPYVK.R	1161.37549	2	2.45E-07	0.92	3.98	-	678.8
gi|4503689|ref|NP_000499.1|	fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M			1.84E-12	15.29	190.26	32.60	94972.5
AHQ-1-7, 6073 - 6092	K.DSDWPFCSDEDWNYK.C	1965.98609	2	2.40E-07	0.92	3.54	-	707.8
AHQ-1-6, 5903	K.DSDWPFCSDEDWNYK.C	1965.98609	2	7.69E-10	0.91	3.70	-	586.4
AHQ-1-8, 6068	K.DSDWPFCSDEDWNYK.C	1965.98609	2	9.00E-04	0.84	3.28	-	476.2
AHQ-1-9, 5922 - 5924	K.DSDWPFCSDEDWNYK.C	1965.98609	2	1.41E-06	0.89	3.96	-	571.0
AHQ-1-6, 5884	K.DSHSLTTNIMEILR.G	1630.84839	2	4.84E-06	0.97	4.41	-	2061.2
AHQ-1-10, 5213	K.DSHSLTTNIMEILR.G	1630.84839	2	2.20E-04	0.95	4.23	-	1146.1
AHQ-1-6, 2186	K.ESSSHHPGIAEFPSR.G	1638.72252	2	1.69E-05	0.81	2.88	-	717.1
AHQ-1-11, 2275	K.ESSSHHPGIAEFPSR.G	1638.72252	2	2.31E-04	0.67	2.66	-	536.3
AHQ-1-9, 2499	R.EVDLKDYEDQQK.Q	1510.58460	2	2.83E-05	0.74	3.15	-	434.9
AHQ-1-13- , 2717	R.EVDLKDYEDQQK.Q	1510.58460	2	4.33E-06	0.88	3.54	-	792.9
AHQ-1-2, 2707	R.EVDLKDYEDQQK.Q	1510.58460	2	3.55E-05	0.80	2.95	-	717.1
AHQ-1-6, 2526	R.EVDLKDYEDQQK.Q	1510.58460	2	4.75E-06	0.81	3.01	-	830.1
AHQ-1-14- , 2666	R.EVDLKDYEDQQK.Q	1510.58460	2	4.81E-08	0.68	2.70	-	597.2
AHQ-1-8, 2459	R.EVDLKDYEDQQK.Q	1510.58460	2	1.29E-06	0.86	3.09	-	769.6
AHQ-1-4, 2631	R.EVDLKDYEDQQK.Q	1510.58460	2	1.38E-05	0.75	3.06	-	550.7
AHQ-1-6, 6622	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	2.18E-05	0.91	4.66	-	838.6
AHQ-1-7, 6804	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	2.64E-05	0.91	4.30	-	1234.3
AHQ-1-6, 6880	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	3.17E-08	0.93	4.73	-	1133.2
AHQ-1-13- , 6432	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	1.52E-06	0.85	3.87	-	966.6
AHQ-1-13- , 6031	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	1.39E-05	0.90	4.56	-	915.6
AHQ-1-13- , 6304	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	1.96E-04	0.92	4.45	-	1154.2
AHQ-1-1, 6376 - 6380	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	6.47E-04	0.91	4.87	-	911.8
AHQ-1-6, 1659	R.GGSTSYGTGSETESPR.N	1573.55765	2	1.71E-05	0.70	2.96	-	525.0
AHQ-1-7, 1640 - 1692	R.GGSTSYGTGSETESPR.N	1573.55765	2	8.03E-05	0.42	2.51	-	253.1
AHQ-1-5, 4881	K.GLIDEVNQDFTNR.I	1521.61384	2	1.47E-06	0.95	4.31	-	1127.1
AHQ-1-10, 4281 - 4311	K.GLIDEVNQDFTNR.I	1521.61384	2	4.89E-07	0.91	3.47	-	933.3
AHQ-1-1, 4852 - 4853	K.GLIDEVNQDFTNR.I	1521.61384	2	1.90E-08	0.95	4.77	-	1134.4

AHQ-1-4, 4950	K.GLIDEVNQDFTNR.I	1521.61384	2	2.97E-06	0.82	2.93	-	776.5
AHQ-1-9, 4754 - 4759	K.GLIDEVNQDFTNR.I	1521.61384	2	8.46E-09	0.93	4.13	-	886.2
AHQ-1-9, 5192	K.GLIDEVNQDFTNR.I	1521.61384	2	1.56E-07	0.93	4.17	-	1047.2
AHQ-1-6, 4155	K.GLIDEVNQDFTNR.I	1521.61384	2	5.26E-07	0.87	3.78	-	646.5
AHQ-1-6, 4723 - 4791	K.GLIDEVNQDFTNR.I	1521.61384	2	1.97E-08	0.93	4.03	-	813.7
AHQ-1-12, 4561	K.GLIDEVNQDFTNR.I	1521.61384	2	9.76E-09	0.93	3.80	-	1027.2
AHQ-1-3, 4865	K.GLIDEVNQDFTNR.I	1521.61384	2	8.14E-06	0.84	3.07	-	796.6
AHQ-1-8, 4807	K.GLIDEVNQDFTNR.I	1521.61384	2	1.72E-09	0.85	3.73	-	691.8
AHQ-1-2, 5019	K.GLIDEVNQDFTNR.I	1521.61384	2	1.79E-06	0.93	4.21	-	979.3
AHQ-1-4, 2258	R.GSESGIFTNTK.E	1141.21317	1	5.55E-04	0.11	1.89	-	219.3
AHQ-1-13- , 2363	R.GSESGIFTNTK.E	1141.21317	1	2.53E-04	0.26	2.06	-	266.1
AHQ-1-3, 2273	R.GSESGIFTNTK.E	1141.21317	2	1.43E-04	0.71	2.56	-	697.7
AHQ-1-6, 2127	R.GSESGIFTNTK.E	1141.21317	1	3.90E-04	0.23	2.07	-	315.8
AHQ-1-6, 2276	R.GSESGIFTNTK.E	1141.21317	1	4.86E-04	0.14	1.85	-	192.5
AHQ-1-6, 2131	R.GSESGIFTNTK.E	1141.21317	2	1.15E-07	0.83	2.93	-	843.5
AHQ-1-12, 2582	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	4.60E-04	0.96	4.57	-	1930.2
AHQ-1-13- , 2739	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	5.16E-06	0.96	4.93	-	1042.5
AHQ-1-10, 2481	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.61E-04	0.94	4.55	-	862.8
AHQ-1-6, 2444	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	5.41E-06	0.97	5.27	-	1280.3
AHQ-1-6, 2372 - 2448	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	8.89E-05	0.96	4.13	-	2161.1
AHQ-1-13- , 2735 - 2808	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	4.43E-06	0.93	4.15	-	1212.3
AHQ-1-11, 2519	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	6.28E-04	0.97	5.03	-	1344.0
AHQ-1-7, 2452	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	6.81E-04	0.94	4.35	-	858.6
AHQ-1-13, 2759	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.93E-05	0.91	3.74	-	822.7
AHQ-1-7, 2746	R.MELERPGGNEITR.G	1502.67870	2	7.60E-05	0.85	3.48	-	667.0
AHQ-1-1, 3457	R.NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPR.P	4123.15285	3	1.22E-04	0.62	3.58	-	335.8
AHQ-1-6, 2100 - 2170	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	2.01E-08	0.96	4.47	-	1129.6
AHQ-1-7, 2120 - 2196	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	1.84E-12	0.95	4.84	-	837.7
AHQ-1-9, 2094	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	5.46E-08	0.92	4.23	-	790.4
AHQ-1-1, 2329	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	3.89E-04	0.84	3.40	-	732.1
AHQ-1-6, 2683	K.NSLFEYQK.N	1029.12765	1	8.15E-06	0.14	2.08	-	165.9
AHQ-1-9, 2106	R.PGSTGTWNPGSSER.G	1433.46515	2	6.20E-04	0.91	3.88	-	693.6
AHQ-1-1, 2384	R.PGSTGTWNPGSSER.G	1433.46515	2	7.13E-07	0.82	3.35	-	523.3
AHQ-1-8, 2080	R.PGSTGTWNPGSSER.G	1433.46515	2	4.82E-06	0.85	3.67	-	505.0
AHQ-1-6, 4779 - 4850	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	2.72E-10	0.96	4.99	-	1133.5
AHQ-1-10, 4292 - 4356	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.32E-04	0.59	3.46	-	403.9
AHQ-1-12, 4585 - 4647	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	3.24E-07	0.90	4.10	-	730.7
AHQ-1-13, 4620	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	2.71E-04	0.82	3.48	-	338.4
AHQ-1-10, 6363 - 6364	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.11E-09	0.88	4.15	-	453.2
AHQ-1-7, 7453	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.47E-05	0.69	3.02	-	291.3
AHQ-1-3, 7233 - 7235	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	8.27E-05	0.89	3.86	-	538.8
AHQ-1-11, 6243 - 6248	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	8.58E-04	0.56	3.33	-	188.6
AHQ-1-11, 6442	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.84E-08	0.81	3.36	-	345.8
AHQ-1-2, 7303 - 7378	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	6.66E-05	0.74	3.17	-	312.3
AHQ-1-6, 7242 - 7322	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.35E-05	0.85	3.54	-	417.2
AHQ-1-5, 7107 - 7145	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	3.08E-04	0.59	2.91	-	177.1
AHQ-1-12, 6455	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	4.97E-04	0.73	3.49	-	200.6
AHQ-1-13- , 6793	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.21E-04	0.52	2.82	-	217.0
AHQ-1-13- , 6941 - 6999	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.13E-09	0.77	3.51	-	310.8
AHQ-1-13, 6333	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	3.95E-04	0.68	3.14	-	187.1
AHQ-1-3, 7038	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	6.86E-07	0.75	3.00	-	340.0
AHQ-1-3, 2419	K.VQHIQLLQK.N	1107.33106	2	4.63E-04	0.81	2.75	-	721.2
AHQ-1-7, 2242	K.VQHIQLLQK.N	1107.33106	1	2.48E-04	0.64	2.68	-	552.3
AHQ-1-3, 2414	K.VQHIQLLQK.N	1107.33106	1	9.00E-04	0.22	2.11	-	482.5
AHQ-1-6, 2235	K.VQHIQLLQK.N	1107.33106	2	5.25E-05	0.83	2.97	-	777.4
AHQ-1-8, 2117 - 2119	K.VQHIQLLQK.N	1107.33106	1	4.51E-04	0.70	2.82	-	678.4
AHQ-1-10, 2236	K.VQHIQLLQK.N	1107.33106	1	4.89E-04	0.74	2.93	-	600.4
AHQ-1-10, 2231	K.VQHIQLLQK.N	1107.33106	1	4.89E-04	0.66	2.84	-	676.4
AHQ-1-9, 2166	K.VQHIQLLQK.N	1107.33106	1	5.72E-04	0.65	2.49	-	711.5
AHQ-1-9, 2172	K.VQHIQLLQK.N	1107.33106	1	3.51E-04	0.72	2.81	-	596.4
gi|29729616|ref|XP_292963.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				1.88E-12	1.87	20.32	16.40	18025.4
AHQ-1-12, 4743 - 4805	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	6.16E-08	0.97	6.44	-	1368.2
AHQ-1-12, 4893	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	3.36E-04	0.58	3.27	-	241.5
AHQ-1-12, 5365 - 5425	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	1.22E-05	0.91	4.75	-	731.9
AHQ-1-12, 5379 - 5437	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	1.88E-12	0.91	4.91	-	1126.3
AHQ-1-12, 5485 - 5486	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	7.51E-05	0.91	4.36	-	686.3
AHQ-1-13, 4747	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	8.85E-04	0.89	4.61	-	900.9
AHQ-1-13, 4755	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	6.39E-04	0.83	3.82	-	466.2
AHQ-1-13, 4861	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	3.33E-04	0.62	3.43	-	514.9
AHQ-1-13- , 5003	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.54E-05	0.90	4.60	-	827.8
AHQ-1-14- , 4883	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.07E-05	0.96	5.56	-	1393.5
gi|4505257|ref|NP_002435.1| moesin [Homo sapiens]				2.12E-12	13.91	150.29	31.90	67819.5
AHQ-1-6, 2114 - 2116	R.ALELEQER.K	988.07707	2	1.52E-04	0.89	2.96	-	1278.8
AHQ-1-6, 2474	K.ALTSELANAR.D	1046.15975	2	2.41E-06	0.90	3.38	-	805.6
AHQ-1-6, 7207	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	2	3.27E-07	0.76	3.94	-	241.4
AHQ-1-6, 7208	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	3	1.99E-09	0.93	5.25	-	902.6
AHQ-1-6, 3167	K.ERQEAEEAKEALLQASR.D	1959.10752	3	1.44E-08	0.84	3.60	-	866.9
AHQ-1-6, 6251 - 6319	R.EVWFFGLQYQDTK.G	1661.83760	2	4.95E-05	0.95	3.91	-	1216.4
AHQ-1-13, 6416	K.FYPEDVSEELIQDITQR.L	2083.24065	2	1.80E-06	0.94	4.32	-	1123.5
AHQ-1-6, 7148 - 7150	K.FYPEDVSEELIQDITQR.L	2083.24065	2	1.28E-09	0.96	5.81	-	915.8
AHQ-1-6, 7151 - 7154	K.FYPEDVSEELIQDITQR.L	2083.24065	3	5.43E-10	0.95	5.01	-	1339.7
AHQ-1-13- , 6875	K.FYPEDVSEELIQDITQR.L	2083.24065	2	7.81E-06	0.92	4.00	-	990.4
AHQ-1-7, 7361	K.FYPEDVSEELIQDITQR.L	2083.24065	2	9.40E-07	0.91	3.89	-	1137.1
AHQ-1-6, 5047	R.GMLREDAVLEYLK.I	1537.80610	2	2.35E-04	0.89	3.91	-	876.1
AHQ-1-6, 6256	K.IAQDLEMYGVNYFSIK.N	1892.16455	2	6.82E-07	0.93	4.51	-	921.9
AHQ-1-6, 6370	K.IAQDLEMYGVNYFSIK.N	1892.16455	2	8.14E-07	0.81	3.17	-	667.2
AHQ-1-6, 5574 - 5650	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	1.05E-07	0.97	4.78	-	1454.0
AHQ-1-6, 6144	K.IAQDLEMYGVNYFSIK.N	1892.16455	2	9.21E-07	0.91	3.95	-	885.9
AHQ-1-6, 1826	R.IQVWHEEHR.G	1234.34835	2	1.32E-04	0.94	3.69	-	1320.1
AHQ-1-6, 2194	R.ISQLEMAR.Q	948.12272	2	1.18E-04	0.86	2.95	-	904.2
AHQ-1-6, 4730 - 4731	K.KTQEQLALEMAELTAR.I	1833.10018	2	2.75E-10	0.97	4.97	-	1519.9
AHQ-1-6, 3070	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	2.99E-11	0.97	5.89	-	1696.9
AHQ-1-6, 3607	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	2.12E-12	0.96	5.35	-	1396.9
AHQ-1-6, 5378 - 5382	K.TQEQLALEMAELTAR.I	1704.92727	2	2.53E-09	0.98	5.53	-	1699.2
gi|4507877|ref|NP_003364.1| vinculin isoform VCL [Homo sapiens]				2.15E-12	49.20	600.29	50.20	116721.6
AHQ-1-14- , 6742	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.83E-07	0.97	5.12	-	1278.3
AHQ-1-4, 7462 - 7535	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.85E-08	0.97	5.44	-	980.3
AHQ-1-13- , 6988	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.64E-11	0.96	5.00	-	1007.2
AHQ-1-4, 7466	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	3	2.97E-05	0.95	4.40	-	1651.3
AHQ-1-12, 6675 - 6677	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.08E-04	0.96	4.97	-	969.0
AHQ-1-11, 6498 - 6566	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.14E-10	0.97	5.31	-	1343.4
AHQ-1-10, 6425 - 6501	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.79E-08	0.97	5.85	-	1185.2
AHQ-1-9, 7326	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.85E-04	0.96	4.91	-	981.2
AHQ-1-8, 7526	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	6.21E-07	0.97	5.32	-	982.4
AHQ-1-1, 7031 - 7104	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.33E-06	0.96	4.34	-	1111.0
AHQ-1-3, 7218 - 7290	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.72E-06	0.93	4.19	-	982.1
AHQ-1-5, 7349	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	8.42E-08	0.95	4.35	-	1032.4

AHQ-1-5, 7493 - 7494	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.65E-10	0.97	5.55	-	1062.8
AHQ-1-6, 7306 - 7370	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	9.29E-11	0.97	5.01	-	1068.9
AHQ-1-7, 7512	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.11E-06	0.97	5.34	-	1039.4
AHQ-1-2, 7429	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.79E-06	0.97	5.31	-	1075.5
AHQ-1-5, 3273 - 3299	R.ALASQLQDSLK.D	1174.32943	2	1.30E-05	0.91	3.69	-	1001.7
AHQ-1-4, 3399 - 3472	R.ALASQLQDSLK.D	1174.32943	2	2.39E-05	0.83	3.33	-	755.4
AHQ-1-3, 3389	R.ALASQLQDSLK.D	1174.32943	2	1.69E-05	0.84	3.23	-	782.7
AHQ-1-8, 3184	R.ALASQLQDSLK.D	1174.32943	2	1.22E-04	0.83	2.68	-	1018.3
AHQ-1-7, 3504 - 3572	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.18E-04	0.89	3.24	-	1066.7
AHQ-1-4, 3607 - 3678	K.AQQVSQGLDVLTAK.V	1458.64233	2	8.46E-11	0.97	5.38	-	1676.5
AHQ-1-5, 3458 - 3530	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.20E-09	0.96	4.20	-	1307.5
AHQ-1-4, 3671	K.AQQVSQGLDVLTAK.V	1458.64233	1	2.17E-04	0.34	2.51	-	406.8
AHQ-1-4, 3675	K.AQQVSQGLDVLTAK.V	1458.64233	1	1.63E-05	0.70	3.56	-	354.5
AHQ-1-5, 3522	K.AQQVSQGLDVLTAK.V	1458.64233	1	2.16E-04	0.75	3.56	-	397.7
AHQ-1-1, 3748	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.75E-04	0.95	3.46	-	1410.5
AHQ-1-8, 3330	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.97E-11	0.96	4.64	-	1363.4
AHQ-1-2, 3809	K.AQQVSQGLDVLTAK.V	1458.64233	2	6.37E-10	0.96	4.64	-	1282.3
AHQ-1-7, 3588	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.74E-05	0.95	3.67	-	1446.1
AHQ-1-4, 2720	K.AVAGNISDPGLQK.S	1270.41721	2	8.58E-05	0.59	2.55	-	533.9
AHQ-1-7, 2440	K.AVAGNISDPGLQK.S	1270.41721	2	3.75E-04	0.70	2.97	-	515.2
AHQ-1-5, 2401 - 2417	K.AVAGNISDPGLQK.S	1270.41721	2	1.19E-04	0.86	3.65	-	640.7
AHQ-1-5, 2530	K.AVAGNISDPGLQK.S	1270.41721	2	2.21E-05	0.76	3.40	-	578.7
AHQ-1-2, 2581 - 2599	K.AVAGNISDPGLQK.S	1270.41721	2	1.02E-05	0.78	3.10	-	609.0
AHQ-1-4, 2490	K.AVAGNISDPGLQK.S	1270.41721	2	9.51E-06	0.69	2.78	-	690.3
AHQ-1-1, 2631	K.AVAGNISDPGLQK.S	1270.41721	2	3.20E-06	0.89	3.47	-	736.6
AHQ-1-3, 2515	K.AVAGNISDPGLQK.S	1270.41721	2	3.72E-05	0.85	3.15	-	819.2
AHQ-1-3, 6050	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	2.90E-04	0.94	3.88	-	1359.3
AHQ-1-6, 6018	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	1.38E-05	0.96	5.12	-	1565.0
AHQ-1-4, 6154	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	6.35E-06	0.94	4.08	-	1252.6
AHQ-1-4, 6160	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	9.76E-05	0.89	4.25	-	1126.9
AHQ-1-4, 6367	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	7.81E-07	0.92	3.77	-	1010.6
AHQ-1-5, 6126 - 6141	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	5.31E-05	0.94	3.50	-	1349.1
AHQ-1-5, 6130 - 6145	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	7.64E-07	0.96	5.59	-	1480.7
AHQ-1-6, 6011 - 6068	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	6.15E-05	0.78	2.99	-	789.3
AHQ-1-3, 6055	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	1.94E-06	0.89	4.13	-	1233.5
AHQ-1-4, 6587	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	2.04E-05	0.69	3.17	-	417.0
AHQ-1-4, 2359	R.DPSASPGDAGEQAIR.Q	1471.51169	1	2.02E-05	0.27	2.07	-	215.4
AHQ-1-4, 2343	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.15E-12	0.87	3.22	-	725.8
AHQ-1-5, 2290	R.DPSASPGDAGEQAIR.Q	1471.51169	1	6.71E-04	0.18	2.02	-	115.3
AHQ-1-4, 2244	R.DPSASPGDAGEQAIR.Q	1471.51169	2	7.52E-06	0.88	3.66	-	706.4
AHQ-1-3, 2293 - 2361	R.DPSASPGDAGEQAIR.Q	1471.51169	2	7.35E-07	0.92	3.93	-	720.7
AHQ-1-7, 2325	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.81E-04	0.91	3.38	-	821.8
AHQ-1-1, 2447	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.17E-07	0.86	3.24	-	692.0
AHQ-1-6, 2284	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.69E-08	0.91	3.78	-	676.4
AHQ-1-5, 2587	R.DYLIDGSR.G	939.00451	1	9.22E-05	0.21	1.95	-	199.0
AHQ-1-5, 2491	R.DYLIDGSR.G	939.00451	1	6.17E-04	0.59	2.59	-	389.6
AHQ-1-3, 4874	K.ELLPVLISAM*K.I	1230.54265	2	6.44E-04	0.64	2.75	-	660.5
AHQ-1-5, 6007	K.ELLPVLISAMK.I	1214.54325	2	6.31E-07	0.86	3.32	-	659.8
AHQ-1-5, 4762	K.ELLPVLISAM*K.I	1230.54265	2	3.02E-06	0.86	3.27	-	806.7
AHQ-1-4, 6148	K.ELLPVLISAMK.I	1214.54325	2	2.15E-06	0.68	2.83	-	541.5
AHQ-1-4, 4915 - 4948	K.ELLPVLISAM*K.I	1230.54265	2	3.75E-05	0.87	3.64	-	733.1
AHQ-1-6, 5966	K.ELLPVLISAMK.I	1214.54325	2	9.32E-05	0.68	3.02	-	414.6
AHQ-1-6, 2634 - 2642	R.ELTPQVVSAAR.I	1171.32878	2	8.65E-04	0.92	3.00	-	1320.1
AHQ-1-5, 2633 - 2646	R.ELTPQVVSAAR.I	1171.32878	2	6.59E-04	0.93	3.40	-	1281.9
AHQ-1-5, 3082	K.ETVQTTEDQILK.R	1405.53306	1	7.87E-06	0.08	2.26	-	113.7
AHQ-1-14- , 3134	K.ETVQTTEDQILK.R	1405.53306	2	4.97E-04	0.76	2.61	-	668.7
AHQ-1-4, 3202	K.ETVQTTEDQILK.R	1405.53306	1	9.92E-10	0.13	2.62	-	156.4
AHQ-1-14- , 3054	K.ETVQTTEDQILKR.D	1561.71942	2	2.85E-06	0.57	2.89	-	405.6
AHQ-1-4, 3043	K.ETVQTTEDQILKR.D	1561.71942	2	1.14E-05	0.90	3.54	-	976.3
AHQ-1-14, 3914	K.ETVQTTEDQILKR.D	1561.71942	2	2.26E-08	0.69	3.07	-	610.3
AHQ-1-5, 2894	K.ETVQTTEDQILKR.D	1561.71942	2	2.28E-07	0.71	2.90	-	707.0
AHQ-1-9, 2848	K.ETVQTTEDQILKR.D	1561.71942	2	6.75E-06	0.80	3.11	-	749.4
AHQ-1-6, 2923 - 2938	K.ETVQTTEDQILKR.D	1561.71942	2	1.78E-05	0.54	2.94	-	543.6
AHQ-1-12, 2943	K.ETVQTTEDQILKR.D	1561.71942	2	5.90E-05	0.74	2.89	-	912.4
AHQ-1-3, 3041	K.ETVQTTEDQILKR.D	1561.71942	2	6.39E-05	0.86	2.96	-	1161.5
AHQ-1-1, 6824 - 6904	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.12E-05	0.79	3.54	-	592.3
AHQ-1-4, 7570	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.59E-04	0.80	3.53	-	558.6
AHQ-1-4, 7227 - 7298	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.26E-05	0.91	3.96	-	822.0
AHQ-1-4, 7100 - 7179	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.11E-05	0.81	3.48	-	622.0
AHQ-1-5, 7273	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.09E-04	0.94	4.61	-	887.8
AHQ-1-11, 6338	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	8.34E-07	0.93	4.63	-	804.3
AHQ-1-4, 6830	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	3	2.43E-09	0.81	3.57	-	715.9
AHQ-1-4, 6822	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	2.78E-08	0.89	3.80	-	1012.5
AHQ-1-12, 2139	K.GNDIIAAAK.R	872.98920	2	1.18E-04	0.87	2.77	-	1150.8
AHQ-1-4, 1531 - 2227	K.GNDIIAAAK.R	872.98920	1	2.84E-04	0.27	2.06	-	315.5
AHQ-1-5, 3509	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	3.40E-04	0.92	4.65	-	666.1
AHQ-1-4, 3662	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	8.42E-07	0.87	4.01	-	609.9
AHQ-1-4, 3668	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	3	6.62E-08	0.88	4.23	-	829.2
AHQ-1-4, 2223	K.IAELCDDPKER.D	1347.47690	3	3.14E-06	0.83	3.48	-	710.0
AHQ-1-4, 2218	K.IAELCDDPKER.D	1347.47690	2	1.92E-06	0.81	3.08	-	571.5
AHQ-1-3, 3157	R.IPTISTQLK.I	1001.20202	2	1.87E-04	0.74	2.52	-	634.5
AHQ-1-12, 3050	R.IPTISTQLK.I	1001.20202	2	5.48E-04	0.77	2.55	-	679.3
AHQ-1-5, 3174	R.KIAELCDDPKERDDILR.S	2088.32839	3	5.30E-06	0.62	3.18	-	508.9
AHQ-1-4, 3323	R.KIAELCDDPKERDDILR.S	2088.32839	3	4.17E-04	0.81	3.29	-	929.7
AHQ-1-5, 3175	R.KIAELCDDPKERDDILR.S	2088.32839	2	1.59E-04	0.65	3.60	-	275.2
AHQ-1-4, 4460 - 4530	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.59E-09	0.87	3.92	-	513.6
AHQ-1-5, 4365 - 4433	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.03E-05	0.74	3.29	-	332.8
AHQ-1-4, 3458	R.LANVMMGPYR.Q	1152.41560	2	2.02E-04	0.90	3.73	-	783.9
AHQ-1-5, 3301 - 3334	R.LANVMMGPYR.Q	1152.41560	2	1.08E-04	0.93	3.79	-	845.9
AHQ-1-6, 2802 - 2816	R.LANVMM*GPYR.Q	1168.41500	2	1.39E-04	0.78	3.16	-	714.8
AHQ-1-4, 2924 - 2928	R.LANVMM*GPYR.Q	1168.41500	2	2.66E-04	0.83	3.69	-	610.8
AHQ-1-2, 4558	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	5.73E-04	0.84	3.74	-	705.6
AHQ-1-4, 4486 - 4487	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	5.46E-10	0.62	3.11	-	603.0
AHQ-1-3, 4401 - 4402	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	3.79E-07	0.66	3.78	-	585.2
AHQ-1-5, 4302 - 4374	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	2.57E-09	0.82	3.81	-	806.9
AHQ-1-4, 4582 - 4590	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	2	5.14E-05	0.89	3.82	-	761.3
AHQ-1-4, 4382 - 4451	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	2	3.89E-04	0.77	3.81	-	268.2
AHQ-1-4, 4458	R.LTDELAPPKPPLPEGEVPPPRPPPPEEK.D	3025.44391	3	6.07E-05	0.68	4.10	-	463.2
AHQ-1-4, 4648 - 4718	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	4.04E-05	0.86	4.08	-	796.5
AHQ-1-6, 3682	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.03E-05	0.94	4.24	-	929.5
AHQ-1-3, 4662 - 4677	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	2.70E-04	0.74	3.02	-	596.5
AHQ-1-6, 4570 - 4571	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	2.85E-05	0.94	5.16	-	675.2
AHQ-1-4, 4726 - 4748	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	6.00E-07	0.95	4.80	-	1418.0
AHQ-1-3, 3835 - 3838	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	4.87E-05	0.89	3.98	-	584.2
AHQ-1-1, 3871	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	2.19E-06	0.73	2.91	-	569.1
AHQ-1-4, 3888	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	3	1.68E-06	0.95	4.81	-	1486.1
AHQ-1-4, 4480	R.MALLMAEMSR.L	1153.46531	2	7.12E-08	0.96	4.42	-	1715.6

AHQ-1-2, 4419	K.MLGQMTDQVADLR.A	1478.72055	2	1.90E-07	0.93	4.01	-	1227.2
AHQ-1-4, 2958 - 2960	K.M*LGQM*TDQVADLR.A	1510.71935	2	6.71E-05	0.95	4.06	-	1570.9
AHQ-1-2, 4009	K.M*LGQMTDQVADLR.A	1494.71995	2	1.20E-05	0.84	3.02	-	709.4
AHQ-1-8, 4116	K.MLGQMTDQVADLR.A	1478.72055	2	3.70E-06	0.93	4.61	-	987.7
AHQ-1-5, 3754 - 3766	K.M*LGQMTDQVADLR.A	1494.71995	2	7.73E-08	0.97	4.08	-	2467.9
AHQ-1-6, 3699	K.M*LGQMTDQVADLR.A	1494.71995	2	5.90E-05	0.95	3.40	-	1720.6
AHQ-1-5, 2849	K.M*LGQM*TDQVADLR.A	1510.71935	2	2.38E-05	0.96	4.07	-	1673.8
AHQ-1-6, 4135 - 4140	K.MLGQMTDQVADLR.A	1478.72055	2	4.72E-07	0.96	4.44	-	1608.7
AHQ-1-3, 4274	K.MLGQMTDQVADLR.A	1478.72055	2	2.44E-05	0.94	3.95	-	1329.1
AHQ-1-7, 4192	K.MLGQMTDQVADLR.A	1478.72055	2	4.41E-07	0.95	3.91	-	1659.9
AHQ-1-4, 3820 - 3878	K.M*LGQMTDQVADLR.A	1494.71995	2	8.24E-06	0.93	3.53	-	1393.3
AHQ-1-4, 4312	K.M*LGQM*TDQVADLR.A	1510.71935	2	8.31E-04	0.86	3.35	-	971.0
AHQ-1-5, 3242 - 3250	K.MLGQM*TDQVADLR.A	1494.71995	2	3.07E-06	0.90	3.62	-	1304.4
AHQ-1-4, 4292	K.MLGQMTDQVADLR.A	1478.72055	2	8.52E-04	0.80	2.92	-	1119.6
AHQ-1-5, 4181 - 4182	K.MLGQMTDQVADLR.A	1478.72055	2	5.18E-07	0.97	5.08	-	1533.3
AHQ-1-4, 3374	K.MLGQM*TDQVADLR.A	1494.71995	2	1.25E-04	0.94	3.59	-	1734.4
AHQ-1-5, 3105	K.M*SAEINEIIR.V	1192.36823	2	5.36E-06	0.91	2.82	-	1231.5
AHQ-1-4, 3235	K.M*SAEINEIIR.V	1192.36823	2	8.61E-04	0.86	3.01	-	863.8
AHQ-1-4, 3988	K.MSAEINEIIR.V	1176.36883	2	7.02E-06	0.96	4.27	-	1920.0
AHQ-1-5, 3753 - 3759	K.MSAEINEIIR.V	1176.36883	2	6.48E-06	0.94	3.80	-	1536.1
AHQ-1-4, 3667	K.MTGLVDEAIDTK.S	1293.46936	2	5.53E-07	0.96	3.72	-	1789.1
AHQ-1-6, 3490	K.MTGLVDEAIDTK.S	1293.46936	2	3.83E-08	0.97	4.13	-	1590.2
AHQ-1-5, 3057	K.M*TGLVDEAIDTK.S	1309.46876	2	6.89E-07	0.94	3.80	-	1260.2
AHQ-1-4, 3123 - 3198	K.M*TGLVDEAIDTK.S	1309.46876	2	2.28E-08	0.91	3.11	-	1190.9
AHQ-1-5, 3525	K.MTGLVDEAIDTK.S	1293.46936	2	1.08E-09	0.97	3.98	-	1703.5
AHQ-1-4, 3212	K.M*TGLVDEAIDTK.S	1309.46876	1	9.18E-04	0.23	2.27	-	205.7
AHQ-1-4, 3176	K.M*TGLVDEAIDTK.S	1309.46876	2	9.15E-07	0.94	3.58	-	1375.6
AHQ-1-5, 2857	R.NPGNQAAYEHFETMK.N	1737.87437	3	6.42E-04	0.78	3.27	-	551.5
AHQ-1-5, 2855	R.NPGNQAAYEHFETMK.N	1737.87437	2	2.03E-05	0.95	4.14	-	1189.4
AHQ-1-4, 3022	R.NPGNQAAYEHFETMK.N	1737.87437	2	1.74E-04	0.96	4.32	-	1268.5
AHQ-1-4, 2495	R.NPGNQAAYEHFETM*K.N	1753.87377	2	4.89E-05	0.90	4.02	-	673.2
AHQ-1-4, 2247	K.NQGIEEALKNR.N	1272.39320	2	9.21E-05	0.83	2.79	-	1199.0
AHQ-1-4, 2991	K.NQWIDNVEK.M	1146.23464	1	2.14E-04	0.38	2.36	-	240.7
AHQ-1-5, 2826	K.NQWIDNVEK.M	1146.23464	1	5.95E-04	0.18	1.83	-	274.3
AHQ-1-4, 3142	K.QVATALQNLQTK.T	1315.50112	2	1.79E-04	0.93	4.07	-	1041.5
AHQ-1-5, 2769 - 2777	K.QVATALQNLQTK.T	1315.50112	2	3.66E-07	0.91	3.83	-	660.8
AHQ-1-4, 2926 - 2927	K.QVATALQNLQTK.T	1315.50112	2	3.72E-09	0.90	3.47	-	778.5
AHQ-1-6, 3374	R.SLGEISALTSK.L	1106.25186	2	9.07E-06	0.92	3.44	-	908.6
AHQ-1-4, 3536	R.SLGEISALTSK.L	1106.25186	2	8.80E-07	0.94	3.96	-	966.0
AHQ-1-4, 3543	R.SLGEISALTSK.L	1106.25186	1	1.20E-06	0.20	2.44	-	188.7
AHQ-1-5, 3386	R.SLGEISALTSK.L	1106.25186	1	2.63E-07	0.20	2.10	-	187.9
AHQ-1-3, 3545	R.SLGEISALTSK.L	1106.25186	2	1.63E-05	0.94	3.74	-	1079.7
AHQ-1-7, 3416	R.SLGEISALTSK.L	1106.25186	1	2.46E-05	0.62	2.82	-	335.3
AHQ-1-1, 3633	R.SLGEISALTSK.L	1106.25186	2	3.18E-07	0.95	3.90	-	1144.7
AHQ-1-5, 3261	K.SLLDASEEAIKK.D	1304.47187	2	7.90E-05	0.80	2.98	-	782.6
AHQ-1-7, 3296 - 3300	K.SLLDASEEAIKK.D	1304.47187	2	7.40E-06	0.79	2.91	-	685.1
AHQ-1-4, 3394 - 3470	K.SLLDASEEAIKK.D	1304.47187	2	2.04E-06	0.89	3.34	-	827.1
AHQ-1-6, 3276	K.SLLDASEEAIKK.D	1304.47187	2	6.95E-06	0.73	2.65	-	568.4
AHQ-1-3, 3409	K.SLLDASEEAIKK.D	1304.47187	2	5.81E-05	0.75	2.73	-	768.9
AHQ-1-3, 2431	K.STVEGIQASVK.T	1119.25064	2	1.90E-06	0.86	3.04	-	745.5
AHQ-1-4, 2404	K.STVEGIQASVK.T	1119.25064	2	3.63E-07	0.92	3.70	-	779.9
AHQ-1-12, 2494 - 2495	R.TDAGFTLR.W	880.96819	2	9.47E-06	0.86	2.65	-	903.2
AHQ-1-4, 2506	R.TDAGFTLR.W	880.96819	2	9.13E-06	0.89	2.79	-	988.6
AHQ-1-9, 7276	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	7.49E-05	0.79	3.60	-	502.4
AHQ-1-11, 6436	R.TIESILEPVAQQISHLVIM*HEEGEVDGK.A	3119.49274	3	6.04E-04	0.79	3.60	-	411.4
AHQ-1-1, 4892	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	6.87E-04	0.80	3.75	-	822.5
AHQ-1-12, 5330 - 5391	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	2.57E-05	0.91	4.43	-	695.0
AHQ-1-12, 5689 - 5746	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	2.85E-04	0.90	4.97	-	736.8
AHQ-1-4, 5367	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	2.71E-04	0.82	4.14	-	496.1
AHQ-1-12, 5697 - 5729	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	4.89E-06	0.86	4.12	-	580.1
AHQ-1-4, 4935	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	4.80E-04	0.59	3.01	-	326.6
AHQ-1-10, 6251	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.35E-06	0.92	4.94	-	602.6
AHQ-1-13, 6391 - 6468	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.15E-08	0.46	3.11	-	415.0
AHQ-1-13- , 6740 - 6792	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	9.95E-09	0.57	3.28	-	363.9
AHQ-1-14- , 5460 - 5463	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	1.37E-04	0.78	3.61	-	496.7
AHQ-1-4, 6338 - 6339	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	5.11E-05	0.82	4.27	-	561.1
AHQ-1-10, 5449	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	7.03E-07	0.83	4.26	-	536.5
AHQ-1-5, 7297 - 7301	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	3.67E-08	0.94	5.28	-	797.7
AHQ-1-9, 7119	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	5.03E-05	0.90	4.57	-	659.9
AHQ-1-1, 6825	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	1.58E-04	0.81	4.02	-	488.6
AHQ-1-8, 7279	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	6.60E-04	0.70	3.14	-	573.4
AHQ-1-4, 7024	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	2.27E-04	0.54	3.41	-	404.6
AHQ-1-12, 3170	R.TNLLQVCER.I	1134.28859	2	7.00E-04	0.87	3.29	-	1021.2
AHQ-1-4, 5626	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	4.64E-05	0.88	4.44	-	567.2
AHQ-1-5, 5505	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	2.60E-05	0.93	4.77	-	1818.0
AHQ-1-5, 5021 - 5095	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	1.08E-05	0.80	3.68	-	534.4
AHQ-1-7, 5385 - 5456	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	1.73E-04	0.89	4.47	-	559.9
AHQ-1-4, 5531 - 5598	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	1.32E-08	0.87	3.93	-	1715.1
AHQ-1-4, 6234	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	3	8.51E-05	0.94	4.89	-	1301.9
AHQ-1-2, 5689	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	2.76E-06	0.88	4.46	-	612.3
AHQ-1-4, 5802	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	3	9.01E-04	0.92	4.65	-	1419.6
AHQ-1-4, 5111	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	8.72E-05	0.94	4.26	-	1982.3
AHQ-1-5, 6197	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	3	8.91E-10	0.96	5.34	-	1628.0
AHQ-1-3, 5643 - 5713	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	2	7.91E-04	0.55	3.45	-	364.4
AHQ-1-5, 6179 - 6193	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	3.13E-06	0.95	5.03	-	799.2
AHQ-1-5, 5690	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	3	7.11E-06	0.90	4.58	-	1330.9
AHQ-1-4, 5335	R.VDQLTAQLADLAAR.G	1485.66778	2	5.36E-06	0.95	3.83	-	1652.9
AHQ-1-4, 5234 - 5235	R.VDQLTAQLADLAAR.G	1485.66778	1	5.57E-04	0.66	2.79	-	338.5
AHQ-1-5, 5149 - 5157	R.VDQLTAQLADLAAR.G	1485.66778	2	1.94E-07	0.98	4.99	-	2421.9
AHQ-1-2, 5726	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.21E-05	0.86	2.57	-	1078.4
AHQ-1-4, 5518 - 5579	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.40E-04	0.78	2.83	-	765.0
AHQ-1-7, 5532 - 5533	R.VLQLTSWDEDAWASK.D	1749.90156	2	3.20E-08	0.98	5.42	-	1625.9
AHQ-1-3, 5533	R.VLQLTSWDEDAWASK.D	1749.90156	2	7.69E-06	0.78	2.54	-	847.4
AHQ-1-1, 5595 - 5596	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.56E-08	0.97	5.31	-	1590.1
AHQ-1-5, 5442 - 5517	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.71E-07	0.95	4.02	-	1301.9
AHQ-1-4, 5836	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.69E-08	0.94	4.22	-	925.0
AHQ-1-5, 5525 - 5587	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.64E-05	0.97	5.20	-	1475.3
AHQ-1-6, 5438 - 5507	R.VLQLTSWDEDAWASK.D	1749.90156	2	4.11E-05	0.79	3.07	-	688.5
AHQ-1-4, 5622 - 5654	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.94E-11	0.97	5.34	-	1427.5
AHQ-1-4, 3343	R.VMLVNSMNTVK.E	1236.53081	1	1.18E-04	0.29	1.97	-	392.0
AHQ-1-4, 3280	R.VMLVNSMNTVK.E	1236.53081	2	2.47E-04	0.89	3.16	-	987.0
AHQ-1-4, 2484	R.VMLVNSM*NTVK.E	1252.53021	2	4.14E-05	0.93	3.34	-	1114.5
AHQ-1-5, 3157	R.VMLVNSMNTVK.E	1236.53081	2	8.78E-04	0.87	3.23	-	899.8
AHQ-1-4, 3647	R.VMLVNSMNTVK.E	1236.53081	2	7.93E-07	0.75	3.06	-	615.2
gi|4504515|ref|NP_002146.1| heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B				2.29E-12	3.92	50.24	6.40	70853.4
AHQ-1-6, 5063 - 5075	R.ARFEELCSDLFR.S	1544.71384	2	5.38E-06	0.95	4.72	-	998.9
AHQ-1-6, 5138	R.FEELCSDLFR.S	1317.44926	2	7.58E-05	0.86	3.53	-	778.3

AHQ-1-6, 4942 - 4956	R.IINEPTAAAIAYGLDR.R	1688.90603	2	2.29E-12	0.95	4.43	-	1117.4
AHQ-1-6, 4504	K.LLQDFFNGK.E	1082.23369	1	4.16E-04	0.39	2.31	-	436.0
AHQ-1-6, 4403 - 4407	K.LLQDFFNGK.E	1082.23369	1	5.97E-06	0.25	2.22	-	340.9
AHQ-1-6, 4488	K.LLQDFFNGKELNK.S	1566.78249	2	1.04E-04	0.93	4.06	-	1174.6
AHQ-1-6, 4343 - 4400	K.LLQDFFNGKELNK.S	1566.78249	2	1.60E-06	0.91	3.84	-	1020.3
gi|5802974|ref|NP_006784.1| peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide				2.34E-12	4.09	60.29	28.90	27692.5
AHQ-1-11, 4359	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	2.40E-06	0.93	4.65	-	1131.4
AHQ-1-11, 3883 - 3884	K.DLSLDDFK.G	953.02795	1	4.32E-05	0.30	2.16	-	451.0
AHQ-1-11, 5110 - 5112	R.DYGVLLEGSGLALR.G	1463.66058	2	2.34E-12	0.98	5.72	-	2746.7
AHQ-1-11, 5336	R.GLFIIDPNGVIK.H	1286.54452	2	1.25E-05	0.87	3.59	-	821.8
AHQ-1-11, 5326	R.GLFIIDPNGVIK.H	1286.54452	1	3.33E-06	0.24	2.01	-	286.4
AHQ-1-11, 5059	R.GLFIIDPNGVIK.H	1286.54452	2	6.53E-06	0.87	3.07	-	1120.1
AHQ-1-11, 5187	R.GLFIIDPNGVIK.H	1286.54452	2	7.45E-04	0.38	2.56	-	389.0
AHQ-1-11, 4894	K.GTAVVNGEFKDLSLDDFK.G	1956.14200	2	1.43E-04	0.86	3.85	-	730.8
AHQ-1-11, 2878 - 2926	K.HLSVNDLPVGR.S	1207.36435	2	1.12E-05	0.78	3.02	-	493.1
gi|29732955|ref|XP_291603.1| similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA				2.50E-12	0.83	10.23	16.80	11173.0
AHQ-1-9, 4471 - 4518	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.55E-08	0.75	3.36	-	689.0
AHQ-1-10, 3671 - 3739	K.NISNASCTTNCIAPLAK.M	1838.05353	2	4.40E-08	0.94	4.54	-	1092.0
AHQ-1-10, 3848 - 3872	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.50E-12	0.83	3.77	-	1229.8
AHQ-1-11, 4082	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.62E-05	0.49	3.14	-	615.6
AHQ-1-12, 3947	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.81E-07	0.66	3.29	-	861.9
AHQ-1-9, 4278 - 4354	K.NISNASCTTNCIAPLAK.M	1838.05353	2	6.13E-07	0.86	4.24	-	1130.3
gi|5453898|ref|NP_006212.1| protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1; dod;				2.75E-12	0.96	10.21	9.20	18243.2
AHQ-1-12, 4050	R.TKEEALELINGYIQK.I	1749.98614	2	2.75E-12	0.96	4.29	-	1689.8
gi|5031987|ref|NP_005720.1| peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]				2.82E-12	5.11	70.28	45.40	22040.1
AHQ-1-12, 3814 - 3890	R.FPDENFTLK.H	1111.22866	2	8.58E-04	0.79	2.90	-	608.0
AHQ-1-12, 3731 - 3778	R.FPDENFTLK.H	1111.22866	2	4.91E-05	0.76	2.75	-	607.4
AHQ-1-12, 3999 - 4030	R.FPDENFTLK.H	1111.22866	2	1.47E-04	0.77	2.67	-	609.1
AHQ-1-12, 5021	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	2	7.68E-06	0.57	2.74	-	296.8
AHQ-1-11, 4819	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	2.82E-12	0.85	3.70	-	804.2
AHQ-1-14- , 5318 - 5319	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	3	1.38E-04	0.94	4.91	-	1186.3
AHQ-1-12, 5721	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	2	1.02E-07	0.67	3.29	-	307.5
AHQ-1-12, 5810 - 5874	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	3	2.40E-05	0.91	4.12	-	1586.4
AHQ-1-12, 5175 - 5233	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	3	1.80E-05	0.96	5.67	-	1324.7
AHQ-1-12, 5677 - 5754	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	3	1.42E-05	0.89	3.87	-	1313.5
AHQ-1-12, 1550 - 1595	K.HVVFGHVK.E	923.09628	1	5.30E-04	0.25	2.15	-	341.9
AHQ-1-12, 4558	R.VIPSFMCQAGDFTNHNGTGGK.S	2240.46178	2	7.62E-06	0.81	3.47	-	718.7
AHQ-1-12, 3955	R.VIPSFM*CQAGDFTNHNGTGGK.S	2256.46118	2	1.72E-05	0.82	3.55	-	384.7
gi|5031635|ref|NP_005498.1| cofilin 1 (non-muscle) [Homo sapiens]				2.90E-12	10.80	120.35	59.60	18502.4
AHQ-1-12, 4115	K.AVLFCLSEDK.K	1183.35638	2	2.31E-04	0.88	3.20	-	764.0
AHQ-1-12, 3485 - 3549	K.AVLFCLSEDKK.N	1311.52930	2	1.79E-05	0.72	2.83	-	639.6
AHQ-1-12, 3362 - 3425	K.AVLFCLSEDKK.N	1311.52930	2	5.41E-09	0.91	3.60	-	910.2
AHQ-1-12, 3395	K.AVLFCLSEDKK.N	1311.52930	1	6.42E-04	0.68	3.00	-	460.9
AHQ-1-12, 5581 - 5598	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.08E-07	0.96	5.13	-	1035.1
AHQ-1-13- , 5548 - 5611	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	9.88E-05	0.53	2.68	-	504.7
AHQ-1-14- , 5634	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	5.91E-07	0.97	5.20	-	1533.6
AHQ-1-12, 5261 - 5314	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.85E-06	0.79	3.29	-	454.6
AHQ-1-13- , 5772	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	2.88E-08	0.97	5.32	-	1314.1
AHQ-1-11, 5275 - 5346	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.71E-08	0.96	5.06	-	1045.6
AHQ-1-12, 5459 - 5534	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	5.85E-10	0.98	6.36	-	1374.0
AHQ-1-13, 5436	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.11E-05	0.96	4.60	-	1339.4
AHQ-1-12, 5351 - 5409	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	2.24E-06	0.97	4.97	-	1606.9
AHQ-1-12, 5887 - 5893	K.ESKKEDLVFIFWAPESAPLK.S	2335.68256	3	5.94E-05	0.78	3.82	-	576.5
AHQ-1-12, 2433 - 2501	K.HELQANCYEEVKDR.C	1792.90812	3	2.05E-09	0.98	6.32	-	2116.3
AHQ-1-12, 2491	K.HELQANCYEEVKDR.C	1792.90812	2	5.59E-04	0.89	3.87	-	481.8
AHQ-1-12, 2571	K.HELQANCYEEVKDR.C	1792.90812	3	1.77E-08	0.97	5.09	-	1973.7
AHQ-1-12, 2573 - 2578	K.HELQANCYEEVKDR.C	1792.90812	2	2.95E-07	0.96	4.21	-	1258.7
AHQ-1-12, 2362 - 2425	K.HELQANCYEEVKDR.C	1792.90812	2	1.44E-06	0.98	4.96	-	2177.4
AHQ-1-12, 2323 - 2385	K.HELQANCYEEVKDR.C	1792.90812	3	3.05E-07	0.98	5.88	-	3112.6
AHQ-1-14- , 2470	K.HELQANCYEEVKDR.C	1792.90812	3	7.47E-06	0.93	3.83	-	1537.0
AHQ-1-12, 2950	K.KAVLFCLSEDKK.N	1439.70221	2	2.99E-04	0.84	3.57	-	652.7
AHQ-1-12, 2957	K.KAVLFCLSEDKK.N	1439.70221	3	2.12E-06	0.95	5.03	-	1217.8
AHQ-1-12, 6221 - 6285	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	2.84E-11	0.95	5.41	-	1111.9
AHQ-1-13- , 6633	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	1.20E-06	0.95	5.32	-	1255.5
AHQ-1-13- , 6639	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.56E-04	0.96	5.15	-	1019.7
AHQ-1-12, 6345	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	1.28E-06	0.95	4.80	-	957.4
AHQ-1-11, 6042 - 6043	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	5.80E-07	0.94	4.34	-	1013.3
AHQ-1-12, 6217 - 6274	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.83E-09	0.97	5.56	-	1326.7
AHQ-1-12, 6254	K.KNIILEEGKEILVGDVGQTVDDPYATFVK.M	3192.60499	3	1.20E-07	0.98	6.67	-	2071.0
AHQ-1-12, 4002	K.LGGSAVISLEGKPL	1341.57848	2	9.14E-07	0.95	4.14	-	1323.1
AHQ-1-14- , 4492 - 4507	K.LGGSAVISLEGKPL	1341.57848	2	5.36E-04	0.89	3.54	-	1116.5
AHQ-1-12, 4374 - 4438	K.LGGSAVISLEGKPL	1341.57848	2	1.43E-07	0.95	4.11	-	1232.7
AHQ-1-13- , 4532	K.LGGSAVISLEGKPL	1341.57848	2	4.16E-04	0.95	4.64	-	985.0
AHQ-1-12, 4231 - 4310	K.LGGSAVISLEGKPL	1341.57848	2	2.18E-04	0.93	3.45	-	1416.1
AHQ-1-12, 4437 - 4497	K.LGGSAVISLEGKPL	1341.57848	2	4.18E-06	0.95	3.87	-	1220.0
AHQ-1-12, 6283 - 6354	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.08E-04	0.90	5.31	-	764.6
AHQ-1-12, 6635 - 6695	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	6.47E-04	0.95	5.30	-	1399.6
AHQ-1-13, 6259 - 6335	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.90E-12	0.97	6.37	-	1977.5
AHQ-1-12, 6409 - 6465	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	9.22E-12	0.97	6.98	-	1522.5
AHQ-1-12, 6690 - 6750	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.47E-09	0.97	6.66	-	1755.6
AHQ-1-12, 3130 - 3251	R.YALYDATYETK.E	1338.44364	1	3.33E-06	0.46	2.60	-	332.7
AHQ-1-12, 3119 - 3189	R.YALYDATYETK.E	1338.44364	2	2.04E-05	0.92	3.49	-	987.5
AHQ-1-12, 3213	R.YALYDATYETK.E	1338.44364	2	2.62E-07	0.95	3.70	-	1219.5
AHQ-1-13, 3294	R.YALYDATYETK.E	1338.44364	1	1.86E-08	0.54	2.61	-	298.8
AHQ-1-13- , 3373	R.YALYDATYETK.E	1338.44364	1	1.58E-06	0.47	2.70	-	375.0
AHQ-1-11, 3096 - 3155	R.YALYDATYETK.E	1338.44364	2	4.21E-06	0.90	3.33	-	938.0
AHQ-1-12, 2866	R.YALYDATYETKESK.K	1682.80875	2	1.05E-05	0.94	3.72	-	1344.6
gi|4757826|ref|NP_004039.1| beta-2-microglobulin [Homo sapiens]				3.36E-12	3.20	40.22	38.70	13714.5
AHQ-1-14- , 6408	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	2	1.24E-05	0.78	3.21	-	476.3
AHQ-1-14- , 6415 - 6479	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	3	1.49E-04	0.65	3.17	-	306.7
AHQ-1-14- , 6555 - 6559	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	3	5.47E-07	0.83	4.32	-	422.5
AHQ-1-14- , 6459 - 6531	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	3.36E-12	0.90	4.11	-	945.7
AHQ-1-14- , 6107 - 6187	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	6.01E-12	0.72	3.56	-	516.5
AHQ-1-14- , 6326 - 6387	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	1.30E-08	0.84	3.82	-	760.6
AHQ-1-14- , 2142 - 2274	K.VEHSDLSFSK.D	1149.23530	1	2.40E-05	0.82	3.21	-	613.3
AHQ-1-14- , 1992 - 2058	R.VNHVTLSQPK.I	1123.28735	2	1.58E-04	0.82	2.70	-	716.5
AHQ-1-14- , 1844 - 1903	R.VNHVTLSQPK.I	1123.28735	1	4.20E-04	0.48	2.51	-	347.4
AHQ-1-14- , 2190 - 2216	R.VNHVTLSQPK.I	1123.28735	1	1.22E-08	0.66	2.93	-	337.7
gi|4557677|ref|NP_000203.1| integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu				3.76E-12	18.94	230.30	37.40	87185.6
AHQ-1-3, 5505	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	3.43E-06	0.89	4.27	-	841.3
AHQ-1-6, 5344	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	6.67E-05	0.79	3.66	-	709.9
AHQ-1-4, 5524 - 5596	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	7.19E-04	0.91	4.79	-	820.5
AHQ-1-9, 5332	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	9.62E-04	0.93	4.37	-	1340.8
AHQ-1-3, 5377 - 5443	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	2	8.62E-06	0.86	3.69	-	682.2
AHQ-1-3, 5374 - 5442	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	1.21E-06	0.90	4.61	-	773.8
AHQ-1-1, 5516	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	7.17E-05	0.92	4.80	-	1114.0
AHQ-1-2, 4586	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	1.05E-04	0.87	4.46	-	409.2

AHQ-1-5, 4441	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	7.98E-07	0.52	3.00	-	481.9
AHQ-1-4, 4492 - 4511	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	9.03E-06	0.72	3.38	-	427.3
AHQ-1-1, 4429	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	3.30E-07	0.86	4.12	-	613.8
AHQ-1-3, 4430 - 4502	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.09E-09	0.87	4.42	-	545.5
AHQ-1-6, 4358	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	1.40E-07	0.82	4.13	-	335.1
AHQ-1-1, 4533 - 4551	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	8.50E-05	0.95	4.32	-	1147.8
AHQ-1-3, 5998 - 6017	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.50E-05	0.96	5.29	-	830.3
AHQ-1-3, 5930 - 5950	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	5.79E-07	0.90	3.69	-	715.7
AHQ-1-1, 5885 - 5925	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.21E-09	0.92	4.16	-	855.0
AHQ-1-3, 4549 - 4619	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	4.82E-05	0.89	3.75	-	653.3
AHQ-1-3, 6098 - 6167	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.09E-06	0.96	5.19	-	692.1
AHQ-1-3, 6030 - 6099	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.04E-05	0.93	4.25	-	944.6
AHQ-1-3, 5009	K.DDLWSIQNLGTK.L	1390.52332	2	5.49E-07	0.93	4.18	-	906.6
AHQ-1-4, 5094	K.DDLWSIQNLGTK.L	1390.52332	2	3.50E-04	0.93	3.92	-	797.4
AHQ-1-1, 5043	K.DDLWSIQNLGTK.L	1390.52332	2	1.50E-04	0.90	3.98	-	702.0
AHQ-1-4, 5104	K.DDLWSIQNLGTK.L	1390.52332	1	2.05E-06	0.55	2.59	-	430.1
AHQ-1-2, 5174	K.DDLWSIQNLGTK.L	1390.52332	2	1.07E-05	0.79	2.94	-	856.7
AHQ-1-5, 4521 - 4523	K.DNCAPESIEFPVSEAR.V	1822.93099	2	7.89E-05	0.90	3.48	-	1048.1
AHQ-1-1, 4508	K.DNCAPESIEFPVSEAR.V	1822.93099	2	4.06E-06	0.54	2.73	-	572.3
AHQ-1-3, 4431 - 4506	K.DNCAPESIEFPVSEAR.V	1822.93099	2	3.22E-04	0.95	3.81	-	1482.0
AHQ-1-9, 4396	K.DNCAPESIEFPVSEAR.V	1822.93099	2	4.77E-04	0.92	3.09	-	1450.1
AHQ-1-6, 4427	K.DNCAPESIEFPVSEAR.V	1822.93099	2	3.76E-06	0.72	3.03	-	667.5
AHQ-1-7, 3232 - 3308	K.EATSTFTNITYR.G	1404.50685	2	1.96E-07	0.42	2.59	-	511.7
AHQ-1-6, 3286	K.EATSTFTNITYR.G	1404.50685	2	3.76E-06	0.51	2.68	-	343.0
AHQ-1-1, 3467	K.EATSTFTNITYR.G	1404.50685	2	3.68E-06	0.83	3.30	-	664.9
AHQ-1-4, 3426	K.EATSTFTNITYR.G	1404.50685	2	2.72E-05	0.84	2.92	-	915.8
AHQ-1-5, 3294	K.EATSTFTNITYR.G	1404.50685	2	2.42E-07	0.64	2.61	-	555.6
AHQ-1-2, 2466 - 2467	R.FQYYEDSSGK.S	1224.25749	1	7.76E-04	0.61	2.30	-	622.1
AHQ-1-4, 2338 - 2344	R.FQYYEDSSGK.S	1224.25749	1	8.36E-05	0.40	1.86	-	534.7
AHQ-1-3, 3662 - 3663	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	1.74E-06	0.83	3.66	-	655.4
AHQ-1-2, 3805	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	8.00E-09	0.87	3.57	-	727.7
AHQ-1-6, 3575	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.31E-05	0.77	3.02	-	875.9
AHQ-1-3, 3655 - 3658	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.03E-06	0.96	4.25	-	1491.4
AHQ-1-4, 3702 - 3735	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.66E-07	0.94	4.14	-	1190.6
AHQ-1-1, 3707 - 3776	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.89E-07	0.92	3.52	-	1260.0
AHQ-1-5, 3609	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	4.37E-09	0.95	4.34	-	1297.5
AHQ-1-3, 4354	R.GKCECGSCVCIQPGSYGDTCEKCPTCPDACTFKK.E	4028.42584	3	2.12E-05	0.90	4.71	-	579.8
AHQ-1-4, 1876 - 1946	K.GSGDSSQVTQVSPQR.I	1533.58302	2	2.87E-04	0.40	2.76	-	456.3
AHQ-1-4, 2012 - 2078	K.GSGDSSQVTQVSPQR.I	1533.58302	2	8.38E-04	0.78	3.37	-	703.6
AHQ-1-3, 2002 - 2067	K.GSGDSSQVTQVSPQR.I	1533.58302	2	4.64E-05	0.58	3.20	-	664.2
AHQ-1-1, 2081	K.GSGDSSQVTQVSPQR.I	1533.58302	2	5.77E-04	0.70	2.69	-	883.6
AHQ-1-7, 1778 - 1840	K.GSGDSSQVTQVSPQR.I	1533.58302	2	2.77E-04	0.81	3.25	-	978.4
AHQ-1-2, 2811	K.HVLTLTDQVTR.F	1283.45912	2	9.83E-08	0.88	3.50	-	533.1
AHQ-1-6, 2592	K.HVLTLTDQVTR.F	1283.45912	2	3.64E-05	0.86	3.48	-	556.2
AHQ-1-4, 2712	K.HVLTLTDQVTR.F	1283.45912	2	1.67E-05	0.82	3.33	-	537.5
AHQ-1-3, 2534	K.HVLTLTDQVTR.F	1283.45912	2	1.10E-05	0.93	3.41	-	901.4
AHQ-1-3, 2703 - 2705	K.HVLTLTDQVTR.F	1283.45912	2	3.39E-07	0.92	3.45	-	768.4
AHQ-1-7, 2606	K.HVLTLTDQVTR.F	1283.45912	2	6.37E-04	0.78	3.14	-	427.6
AHQ-1-5, 2589	K.HVLTLTDQVTR.F	1283.45912	2	3.16E-07	0.94	3.79	-	925.9
AHQ-1-4, 2715	K.HVLTLTDQVTR.F	1283.45912	1	6.40E-04	0.39	2.11	-	400.5
AHQ-1-4, 2719	K.HVLTLTDQVTR.F	1283.45912	1	1.83E-04	0.56	2.75	-	312.5
AHQ-1-8, 2473	K.HVLTLTDQVTR.F	1283.45912	2	1.09E-06	0.90	3.55	-	636.9
AHQ-1-3, 4605	K.IGDTVSFSIEAK.V	1267.41009	2	4.82E-05	0.93	3.66	-	951.0
AHQ-1-3, 4414 - 4482	K.IGDTVSFSIEAK.V	1267.41009	2	1.52E-06	0.79	2.60	-	704.3
AHQ-1-1, 4085	K.IGDTVSFSIEAK.V	1267.41009	2	1.25E-08	0.92	3.34	-	1079.9
AHQ-1-3, 3667	K.IGDTVSFSIEAK.V	1267.41009	2	6.70E-05	0.93	3.03	-	1291.0
AHQ-1-3, 5161	R.LAGIVQPNDGQCHVGSDNHYSASTTM*DYPSLGLMTEK.L	4013.35457	3	7.28E-05	0.83	4.36	-	844.2
AHQ-1-3, 5523 - 5591	R.LAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEK.L	3997.35517	3	5.44E-11	0.96	6.06	-	1014.2
AHQ-1-4, 5584	R.LAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEK.L	3997.35517	3	6.74E-04	0.89	4.44	-	765.4
AHQ-1-3, 5393 - 5457	R.LAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEK.L	3997.35517	3	5.77E-04	0.80	3.56	-	677.3
AHQ-1-2, 4126 - 4141	R.NDASHLLVFTTDAK.T	1532.67977	2	7.74E-06	0.91	3.85	-	883.0
AHQ-1-1, 4501	R.NDASHLLVFTTDAK.T	1532.67977	2	8.68E-06	0.93	3.90	-	986.4
AHQ-1-6, 3768 - 3774	R.NDASHLLVFTTDAK.T	1532.67977	2	6.93E-06	0.96	4.65	-	1404.7
AHQ-1-3, 3950 - 3959	R.NDASHLLVFTTDAK.T	1532.67977	3	4.80E-06	0.97	5.29	-	1823.9
AHQ-1-5, 3805 - 3821	R.NDASHLLVFTTDAK.T	1532.67977	2	5.93E-09	0.97	5.12	-	1626.8
AHQ-1-3, 4299	R.NDASHLLVFTTDAK.T	1532.67977	2	7.28E-06	0.88	3.53	-	822.3
AHQ-1-1, 4049 - 4073	R.NDASHLLVFTTDAK.T	1532.67977	2	9.72E-10	0.97	5.28	-	1366.6
AHQ-1-4, 4484	R.NDASHLLVFTTDAK.T	1532.67977	2	1.12E-04	0.85	3.46	-	753.1
AHQ-1-3, 3942 - 3947	R.NDASHLLVFTTDAK.T	1532.67977	2	8.78E-09	0.97	4.41	-	1728.8
AHQ-1-3, 4449 - 4459	R.NDASHLLVFTTDAK.T	1532.67977	2	3.76E-12	0.96	4.52	-	1223.3
AHQ-1-5, 4405	R.NDASHLLVFTTDAK.T	1532.67977	2	1.02E-08	0.91	3.86	-	870.4
AHQ-1-8, 3462	R.NDASHLLVFTTDAK.T	1532.67977	2	1.39E-09	0.97	5.19	-	1281.2
AHQ-1-4, 4522 - 4528	K.SILYVVEEPECPK.G	1564.78173	2	2.57E-06	0.85	2.90	-	996.3
AHQ-1-1, 4513 - 4515	K.SILYVVEEPECPK.G	1564.78173	2	1.89E-04	0.91	3.93	-	845.9
AHQ-1-3, 2922	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.83E-08	0.93	3.70	-	1340.3
AHQ-1-5, 2815	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.97E-06	0.85	3.08	-	1077.0
AHQ-1-5, 2910	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.14E-06	0.88	3.34	-	969.8
AHQ-1-3, 3007	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	6.96E-09	0.92	3.66	-	1042.6
AHQ-1-4, 3776	R.TDTCMSSNGLLCSGR.G	1661.81786	2	2.26E-07	0.92	3.56	-	1062.9
AHQ-1-7, 3585	R.TDTCMSSNGLLCSGR.G	1661.81786	2	5.73E-04	0.50	2.52	-	621.4
AHQ-1-4, 3602 - 3651	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.86E-09	0.81	3.19	-	731.8
AHQ-1-3, 3635 - 3702	R.TDTCMSSNGLLCSGR.G	1661.81786	2	6.00E-09	0.74	2.78	-	605.3
AHQ-1-4, 3070	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.52E-07	0.66	2.65	-	464.3
AHQ-1-1, 3679	R.TDTCMSSNGLLCSGR.G	1661.81786	2	7.10E-07	0.88	3.50	-	899.7
AHQ-1-4, 2972	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.64E-08	0.96	4.05	-	1661.4
AHQ-1-6, 3479 - 3495	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.01E-07	0.77	2.75	-	750.7
AHQ-1-3, 2830	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.98E-06	0.87	3.29	-	935.3
AHQ-1-4, 2882	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	5.20E-08	0.93	3.77	-	1172.2
AHQ-1-1, 2904	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.97E-06	0.96	4.42	-	1327.7
AHQ-1-1, 2141	R.VLEDRPLSDK.G	1172.31354	2	1.18E-05	0.92	3.72	-	1054.3
AHQ-1-3, 1914 - 1989	R.VLEDRPLSDK.G	1172.31354	2	2.07E-05	0.93	3.73	-	967.5
AHQ-1-7, 1817	R.VLEDRPLSDK.G	1172.31354	2	3.84E-04	0.85	2.76	-	1119.8
AHQ-1-4, 1911	R.VLEDRPLSDK.G	1172.31354	2	8.16E-06	0.85	3.26	-	807.6
AHQ-1-3, 2791	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	6.17E-09	0.93	4.65	-	1472.9
AHQ-1-2, 2891	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	4.49E-09	0.93	4.30	-	1660.8
AHQ-1-3, 3275 - 3346	K.WDTANNPLYK.E	1222.33111	2	9.18E-04	0.81	3.20	-	512.4
AHQ-1-1, 3427	K.WDTANNPLYK.E	1222.33111	2	7.16E-05	0.66	2.86	-	567.6
AHQ-1-4, 3740 - 3766	K.YCECDDFSCVR.Y	1514.59674	2	1.10E-05	0.91	3.24	-	970.1
AHQ-1-3, 3691 - 3761	K.YCECDDFSCVR.Y	1514.59674	2	7.86E-04	0.93	3.63	-	1151.8
AHQ-1-1, 3733	K.YCECDDFSCVR.Y	1514.59674	2	3.68E-05	0.94	3.34	-	1281.4
gi|18104967|ref|NP_000953.2| prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland				4.20E-12	7.08	80.27	23.20	68686.0
AHQ-1-6, 3966	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	3.50E-07	0.76	3.11	-	466.5
AHQ-1-6, 3883	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	3	6.76E-05	0.80	3.42	-	774.8
AHQ-1-6, 3874	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	2	7.05E-04	0.95	4.93	-	1140.0
AHQ-1-6, 5192	R.FGMKPYTSFQELVGEK.E	1862.13845	2	3.68E-08	0.91	3.98	-	579.9
AHQ-1-6, 7014 - 7079	K.GLLGNPICSPEYWKPSTFGGEVGFNIVK.T	3069.47853	3	4.20E-08	0.87	4.49	-	451.3
AHQ-1-6, 7324	K.IVIEEYVQQLSGYFLQLK.F	2171.52045	3	4.20E-12	0.96	5.44	-	1494.5

AHQ-1-6, 3326 - 3396	R.VPDASQDDGPAVERPSTEL	1984.06747	2	2.63E-09	0.95	4.85	-	1069.7
AHQ-1-6, 5454 - 5484	K.YQVLDGEMYPPSVEEAPVLM*HYPR.G	2838.20739	3	4.36E-04	0.89	4.79	-	677.3
AHQ-1-6, 5987 - 6006	K.YQVLDGEMYPPSVEEAPVLMHYPR.G	2822.20799	3	1.46E-10	0.94	5.41	-	799.6
gi|27498267|ref|XP_209737.1| similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,				4.60E-12	3.56	40.39	33.70	11063.6
AHQ-1-11, 5622	R.DICNDVLSLLEK.F	1420.61093	2	6.08E-08	0.91	3.60	-	975.7
AHQ-1-13, 5740	R.DICNDVLSLLEK.F	1420.61093	2	2.38E-05	0.96	3.89	-	1613.0
AHQ-1-13- , 6908	R.DICNDVLSLLEK.F	1420.61093	2	1.95E-06	0.98	5.69	-	2131.2
AHQ-1-13- , 6095 - 6100	R.DICNDVLSLLEK.F	1420.61093	2	1.12E-06	0.95	3.81	-	1551.1
AHQ-1-13, 5749	R.DICNDVLSLLEK.F	1420.61093	1	5.48E-06	0.20	2.16	-	531.4
AHQ-1-10, 5853	R.DICNDVLSLLEK.F	1420.61093	2	5.44E-06	0.86	2.98	-	1020.0
AHQ-1-10, 5515	R.DICNDVLSLLEK.F	1420.61093	1	3.75E-10	0.76	2.75	-	800.0
AHQ-1-10, 4763 - 4821	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.17E-08	0.98	5.57	-	1636.6
AHQ-1-10, 4881 - 4944	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.87E-11	0.98	5.90	-	1891.4
AHQ-1-10, 4980 - 5037	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.76E-07	0.94	4.30	-	1212.1
AHQ-1-10, 5096 - 5151	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.60E-09	0.97	5.13	-	1639.0
AHQ-1-10, 5217 - 5281	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.20E-06	0.97	5.54	-	1394.1
AHQ-1-10, 4720 - 4731	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	7.00E-10	0.99	7.15	-	2797.0
AHQ-1-10, 5617 - 5680	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.91E-05	0.84	3.84	-	657.0
AHQ-1-10, 4659 - 4707	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.86E-08	0.98	5.66	-	1985.6
AHQ-1-10, 5925 - 5985	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.83E-07	0.93	4.14	-	1034.9
AHQ-1-10, 6504	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.19E-09	0.96	5.27	-	1086.8
AHQ-1-10, 4451	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.92E-09	0.95	4.80	-	1078.2
AHQ-1-11, 4842	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.39E-07	0.96	5.50	-	990.3
AHQ-1-11, 4848	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	2.36E-05	0.96	4.93	-	1770.4
AHQ-1-11, 5012 - 5088	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.72E-04	0.69	3.06	-	488.0
AHQ-1-11, 5248	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.67E-07	0.97	5.59	-	1245.7
AHQ-1-1, 5384	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.61E-05	0.94	4.59	-	990.7
AHQ-1-12, 4954 - 5013	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.34E-07	0.97	5.50	-	1662.7
AHQ-1-12, 5010	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	7.55E-09	0.96	5.26	-	1264.2
AHQ-1-12, 5018	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.46E-08	0.97	5.15	-	2241.1
AHQ-1-13, 4632	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.30E-10	0.96	5.00	-	1348.2
AHQ-1-13, 4715	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.01E-09	0.96	4.65	-	1335.6
AHQ-1-13, 4959 - 5028	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.87E-10	0.97	5.35	-	1439.9
AHQ-1-13, 4968 - 4988	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.65E-09	0.98	6.13	-	2126.8
AHQ-1-13, 5088 - 5152	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.20E-05	0.91	4.12	-	799.8
AHQ-1-13, 5345	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.60E-12	0.97	5.27	-	1748.3
AHQ-1-10, 4303 - 4367	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.64E-09	0.96	4.47	-	1442.6
AHQ-1-13- , 5676	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	7.49E-10	0.97	5.48	-	1336.5
AHQ-1-14, 5940	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.02E-07	0.96	5.10	-	1158.2
AHQ-1-13- , 5433 - 5501	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.41E-09	0.97	5.90	-	1381.4
AHQ-1-13- , 4852	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.04E-11	0.95	4.68	-	1376.7
AHQ-1-13- , 4960	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.48E-10	0.96	4.65	-	1223.9
AHQ-1-13- , 5224 - 5267	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.48E-08	0.97	5.98	-	1283.8
AHQ-1-13- , 5235 - 5243	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.43E-08	0.99	7.84	-	3166.3
AHQ-1-14- , 5118	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.08E-07	0.97	5.11	-	1421.8
AHQ-1-10, 4341	K.GIVDQSQQAYQEAFEISKK.E	2170.36467	3	8.81E-04	0.77	3.25	-	785.2
AHQ-1-10, 4335	K.GIVDQSQQAYQEAFEISKK.E	2170.36467	2	9.67E-06	0.85	4.17	-	438.7
AHQ-1-11, 4363 - 4368	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	9.71E-06	0.98	6.42	-	1784.3
AHQ-1-13- , 4727	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	1.08E-06	0.98	5.58	-	1910.6
gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]				4.74E-12	12.01	150.27	66.80	22391.3
AHQ-1-11, 5486 - 5559	R.DDGLFSGDPNWFPK.K	1595.69288	2	7.21E-09	0.97	4.91	-	1630.6
AHQ-1-12, 5669 - 5722	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.90E-05	0.92	3.60	-	1003.1
AHQ-1-12, 5877	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.24E-04	0.94	4.27	-	1153.9
AHQ-1-12, 5731 - 5779	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.99E-06	0.96	4.42	-	1314.8
AHQ-1-11, 5707	R.DDGLFSGDPNWFPK.K	1595.69288	2	4.63E-04	0.94	4.23	-	923.2
AHQ-1-11, 5614 - 5647	R.DDGLFSGDPNWFPK.K	1595.69288	2	8.56E-09	0.96	4.40	-	1472.9
AHQ-1-11, 6046	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.76E-06	0.89	3.87	-	801.0
AHQ-1-13, 5961 - 5972	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	8.67E-06	0.74	3.30	-	493.9
AHQ-1-13- , 6359	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	4.30E-09	0.95	4.85	-	878.5
AHQ-1-11, 5832	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.25E-04	0.83	3.59	-	634.5
AHQ-1-14- , 6732	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	5.51E-06	0.93	4.48	-	765.8
AHQ-1-12, 6029	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	4.61E-04	0.92	4.32	-	809.3
AHQ-1-11, 5398 - 5399	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.04E-05	0.85	3.95	-	552.2
AHQ-1-11, 5406	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.06E-07	0.74	3.16	-	854.9
AHQ-1-12, 6605 - 6611	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.52E-10	0.95	5.43	-	1101.1
AHQ-1-11, 5602	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	4.18E-08	0.83	3.53	-	1042.6
AHQ-1-12, 6613 - 6614	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.22E-07	0.88	4.62	-	504.9
AHQ-1-13, 6488 - 6491	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.34E-06	0.91	4.40	-	1058.1
AHQ-1-11, 6435 - 6443	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.49E-07	0.89	4.20	-	912.5
AHQ-1-12, 5594	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	7.07E-07	0.84	3.70	-	762.8
AHQ-1-13- , 6932	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.56E-08	0.76	3.51	-	565.2
AHQ-1-14- , 6690	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.55E-08	0.92	4.54	-	912.7
AHQ-1-14- , 6694	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	3.55E-06	0.63	2.84	-	521.4
AHQ-1-11, 2663	R.GASQAGMTGYGMPR.Q	1384.56732	2	1.15E-04	0.81	3.25	-	816.4
AHQ-1-12, 1966 - 2025	R.GPAYGLSR.E	820.91599	2	2.89E-04	0.83	3.07	-	793.5
AHQ-1-12, 1991	R.GPAYGLSR.E	820.91599	1	2.25E-04	0.22	2.11	-	205.9
AHQ-1-11, 2502	K.IQASTMAFK.Q	997.19374	1	7.33E-04	0.63	2.76	-	468.1
AHQ-1-12, 2298	K.KIQASTMAFK.Q	1125.36665	2	4.57E-04	0.84	2.91	-	1042.5
AHQ-1-11, 2162 - 2218	R.NFSDNQLQEGK.N	1280.32582	2	9.96E-04	0.90	3.43	-	892.7
AHQ-1-12, 2101 - 2161	R.NFSDNQLQEGK.N	1280.32582	2	1.72E-04	0.88	3.49	-	842.4
AHQ-1-12, 2162 - 2245	R.NFSDNQLQEGK.N	1280.32582	1	3.25E-07	0.17	2.20	-	299.4
AHQ-1-11, 2334 - 2411	R.NFSDNQLQEGK.N	1280.32582	1	6.98E-05	0.41	2.28	-	316.7
AHQ-1-12, 2381	R.NFSDNQLQEGK.N	1280.32582	1	9.82E-06	0.11	2.14	-	181.4
AHQ-1-12, 2586	R.NFSDNQLQEGK.N	1280.32582	1	4.75E-06	0.14	1.93	-	376.9
AHQ-1-14- , 2298	R.NFSDNQLQEGK.N	1280.32582	2	8.38E-04	0.81	2.99	-	778.5
AHQ-1-11, 2410	R.NFSDNQLQEGK.N	1280.32582	2	1.05E-05	0.87	3.37	-	971.2
AHQ-1-11, 2558	R.NFSDNQLQEGK.N	1280.32582	1	1.14E-06	0.20	1.93	-	393.0
AHQ-1-13- , 2325 - 2328	R.NFSDNQLQEGK.N	1280.32582	2	5.37E-05	0.87	3.22	-	849.4
AHQ-1-11, 2959 - 3018	K.NVIGLQMGTNR.G	1203.39751	2	1.57E-07	0.93	3.41	-	1260.1
AHQ-1-11, 2322 - 2330	K.NVIGLQM*GTNR.G	1219.39691	2	1.62E-06	0.93	3.47	-	1146.6
AHQ-1-12, 5318	K.QMEQISQFLQAAER.Y	1679.87950	3	3.29E-10	0.95	4.86	-	1507.2
AHQ-1-12, 5821 - 5845	K.QMEQISQFLQAAER.Y	1679.87950	2	1.48E-05	0.97	4.57	-	2126.1
AHQ-1-11, 5654	K.QMEQISQFLQAAER.Y	1679.87950	2	5.26E-05	0.95	4.01	-	1505.0
AHQ-1-11, 5264 - 5320	K.QMEQISQFLQAAER.Y	1679.87950	2	2.83E-05	0.97	4.97	-	1339.9
AHQ-1-12, 4786	K.QM*EQISQFLQAAER.Y	1695.87890	2	6.76E-07	0.88	3.90	-	645.2
AHQ-1-14- , 5456	K.QMEQISQFLQAAER.Y	1679.87950	2	1.00E-06	0.93	3.59	-	1162.0
AHQ-1-11, 5102	K.QMEQISQFLQAAER.Y	1679.87950	2	5.97E-04	0.94	4.29	-	975.5
AHQ-1-11, 4246 - 4263	R.TLMNLGGLAVAR.D	1216.47932	2	4.85E-05	0.88	3.91	-	936.8
AHQ-1-11, 3466	R.TLM*NLGGLAVAR.D	1232.47872	2	2.03E-05	0.90	3.59	-	990.4
AHQ-1-12, 3953	R.TLM*NLGGLAVAR.D	1232.47872	2	2.32E-05	0.93	3.32	-	1301.1
AHQ-1-12, 4367 - 4447	R.TLMNLGGLAVAR.D	1216.47932	2	3.29E-06	0.93	4.11	-	1056.2
AHQ-1-13- , 4628 - 4631	R.TLMNLGGLAVAR.D	1216.47932	2	6.39E-07	0.91	4.26	-	906.0
AHQ-1-14- , 4600	R.TLMNLGGLAVAR.D	1216.47932	2	1.58E-04	0.92	3.61	-	1167.4
AHQ-1-13- , 6867 - 6868	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.40E-09	0.97	5.30	-	1180.6
AHQ-1-11, 6235	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.71E-06	0.94	4.82	-	728.9
AHQ-1-11, 6226 - 6304	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.23E-05	0.92	4.30	-	804.0
AHQ-1-12, 6371 - 6441	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.07E-11	0.97	4.84	-	1460.7

AHQ-1-11, 5996 - 6076	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.79E-05	0.81	3.58	-	673.0
AHQ-1-13, 6332 - 6411	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.24E-09	0.95	4.91	-	1018.6
AHQ-1-14- , 6620	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	4.74E-12	0.96	4.94	-	1276.1
AHQ-1-11, 6440 - 6514	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	9.17E-07	0.95	4.47	-	1045.8
AHQ-1-12, 6537	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.19E-08	0.96	5.20	-	1089.1
AHQ-1-11, 6596	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.52E-07	0.91	4.05	-	865.0
gi|5453740|ref|NP_006462.1| myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat				4.79E-12	6.33	70.29	32.70	19794.0
AHQ-1-11, 5875 - 5952	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.36E-05	0.80	3.53	-	561.9
AHQ-1-14- , 5664	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	5.43E-08	0.73	3.25	-	447.4
AHQ-1-14- , 5447 - 5448	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.20E-08	0.97	5.38	-	1260.8
AHQ-1-12, 5969 - 5973	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	2.71E-04	0.97	5.00	-	1717.9
AHQ-1-12, 5322	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	3.26E-07	0.96	4.30	-	1495.9
AHQ-1-14- , 6108 - 6110	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	6.44E-09	0.98	4.99	-	2072.9
AHQ-1-11, 5118 - 5188	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.60E-07	0.97	4.66	-	1563.8
AHQ-1-11, 5700 - 5770	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	2.65E-06	0.96	4.55	-	1654.9
AHQ-1-11, 5523	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	9.12E-09	0.90	3.31	-	1732.9
AHQ-1-11, 5626 - 5635	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	4.79E-12	0.97	4.82	-	1885.6
AHQ-1-11, 5627	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	8.19E-10	0.97	5.29	-	1740.8
AHQ-1-11, 5518 - 5574	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.58E-06	0.98	5.82	-	2454.0
AHQ-1-11, 5708	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	6.54E-04	0.89	3.77	-	816.2
AHQ-1-14- , 5879	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	5.25E-12	0.97	4.80	-	1570.9
AHQ-1-11, 4318 - 4320	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	3.86E-05	0.96	5.29	-	1026.5
AHQ-1-12, 4505	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	2.75E-04	0.90	3.93	-	661.6
AHQ-1-12, 5745	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	8.99E-12	0.95	4.93	-	1201.3
AHQ-1-12, 5742	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	2.68E-05	0.80	3.43	-	857.4
AHQ-1-11, 2600	R.ELLTTMGDR.F	1036.18513	2	9.12E-05	0.81	2.73	-	678.8
AHQ-1-12, 4146	K.GNFNYIEFTR.I	1261.36733	2	4.20E-04	0.78	3.31	-	623.5
AHQ-1-13, 4176 - 4179	K.GNFNYIEFTR.I	1261.36733	2	7.57E-06	0.70	2.75	-	677.1
AHQ-1-14, 5122	K.GNFNYIEFTR.I	1261.36733	2	5.02E-05	0.76	2.81	-	686.9
AHQ-1-13- , 4363 - 4371	K.GNFNYIEFTR.I	1261.36733	2	8.67E-04	0.82	3.34	-	700.3
AHQ-1-11, 4139 - 4184	K.GNFNYIEFTR.I	1261.36733	2	8.91E-04	0.84	3.11	-	1035.2
AHQ-1-11, 4362	K.GNFNYIEFTR.I	1261.36733	1	3.79E-04	0.41	2.14	-	359.5
AHQ-1-11, 4355	K.GNFNYIEFTR.I	1261.36733	2	6.02E-04	0.78	2.95	-	882.2
AHQ-1-11, 3436	K.KGNFNYIEFTR.I	1389.54025	2	2.96E-09	0.95	4.19	-	980.1
gi|18860900|ref|NP_002834.2| protein tyrosine phosphatase, receptor type, J precursor; protein tyro				4.82E-12	7.95	90.26	10.60	145926.2
AHQ-1-1, 3468	R.AGSPTAPVHDESLVGPVDPSSGQQSR.D	2576.71806	3	1.08E-04	0.92	4.60	-	1201.2
AHQ-1-1, 4432 - 4444	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	3	2.76E-09	0.96	4.67	-	1601.0
AHQ-1-1, 4431	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	2	2.33E-07	0.98	5.27	-	2074.4
AHQ-1-1, 3079	K.GDPLGTEGGLDASNTER.S	1689.71978	2	1.17E-08	0.94	4.05	-	1051.1
AHQ-1-1, 5263 - 5267	K.GLIDGAESYVSFSR.Y	1501.62253	2	5.52E-09	0.97	4.33	-	2276.2
AHQ-1-1, 4968	K.SFCTDPASM*ASFDCEVVPK.E	2167.37954	2	5.17E-04	0.60	2.93	-	568.0
AHQ-1-1, 5739	K.SFCTDPASMASFDCEVVPK.E	2151.38014	2	6.38E-06	0.87	4.21	-	655.8
AHQ-1-1, 5404	K.SPDGASEYVYHLVIESK.H	1895.05866	2	4.82E-12	0.93	4.21	-	1059.4
AHQ-1-1, 4325	K.VITEPIPVSDLR.V	1339.56259	2	5.41E-04	0.83	3.02	-	565.5
AHQ-1-1, 3899	R.VLLESIGSHEELTQDSR.L	1914.06352	2	3.40E-07	0.86	3.54	-	896.9
AHQ-1-1, 3911	R.VLLESIGSHEELTQDSR.L	1914.06352	3	3.75E-10	0.93	4.63	-	748.4
gi|12408656|ref|NP_005177.2| calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ				5.11E-12	9.84	110.30	15.80	81889.4
AHQ-1-6, 3634	R.DFFLANASR.A	1041.14166	2	7.89E-05	0.87	2.85	-	1163.7
AHQ-1-6, 6416 - 6448	R.DM*ETIGFAVYEVPPELVGQPAVHLK.R	2757.15391	3	5.11E-12	0.93	4.08	-	1191.0
AHQ-1-6, 6760	R.DMETIGFAVYEVPPELVGQPAVHLK.R	2741.15451	3	1.36E-07	0.83	3.73	-	782.8
AHQ-1-6, 6154	R.FRLPPGEYVVVPSTFEPNKEGDFVLR.F	2994.39160	3	1.93E-07	0.96	5.95	-	1363.0
AHQ-1-6, 4391 - 4411	R.KAPSDLYQIILK.A	1389.66474	2	3.01E-06	0.95	4.50	-	1148.9
AHQ-1-6, 3783	R.KWNTTLYEGTWR.R	1555.71826	2	3.51E-09	0.91	3.62	-	921.1
AHQ-1-6, 4875	R.LPPGEYVVVPSTFEPNK.E	1874.12573	2	6.80E-05	0.89	3.87	-	706.1
AHQ-1-6, 5898	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	2	4.21E-04	0.70	3.20	-	258.0
AHQ-1-6, 5886	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	2.65E-07	0.83	4.02	-	451.4
AHQ-1-6, 6584	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	3	2.64E-08	0.90	4.18	-	893.8
AHQ-1-6, 3083	R.SEQFINLR.E	1007.12521	2	8.40E-04	0.85	2.68	-	1032.5
AHQ-1-6, 3302	K.YLGQDYEQLR.V	1285.38720	2	2.37E-07	0.91	3.41	-	979.3
gi|5453555|ref|NP_006316.1| ras-related nuclear protein [Homo sapiens]				5.33E-12	1.56	20.19	12.50	24422.9
AHQ-1-10, 5279	K.SNYNFEKPFLWLAR.K	1786.02509	2	5.33E-12	0.82	3.86	-	524.4
AHQ-1-10, 4085	R.VCENIPIVLCGNK.V	1518.78102	2	1.90E-04	0.73	3.01	-	554.7
gi|21361755|ref|NP_004090.3| stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie				5.41E-12	9.87	110.38	51.00	31708.5
AHQ-1-14- , 4687 - 4688	K.EASMVITESPAALQLR.Y	1716.98119	2	3.81E-08	0.93	4.13	-	1078.9
AHQ-1-1, 4863 - 4875	K.EASMVITESPAALQLR.Y	1716.98119	2	1.50E-05	0.79	3.55	-	774.4
AHQ-1-14- , 4100	K.EASM*VITESPAALQLR.Y	1732.98059	2	1.38E-07	0.93	4.12	-	1006.0
AHQ-1-13- , 4240	K.EASM*VITESPAALQLR.Y	1732.98059	2	5.10E-05	0.94	4.36	-	1261.5
AHQ-1-1, 4320	K.EASM*VITESPAALQLR.Y	1732.98059	2	2.66E-07	0.95	4.10	-	1518.1
AHQ-1-13- , 4751	K.EASMVITESPAALQLR.Y	1716.98119	2	7.89E-08	0.93	4.31	-	927.1
AHQ-1-9, 7250	K.GPGLFFILPCTDSFIK.V	1814.13672	2	4.19E-05	0.94	4.57	-	758.2
AHQ-1-10, 6348 - 6349	K.GPGLFFILPCTDSFIK.V	1814.13672	2	6.83E-05	0.95	5.20	-	770.5
AHQ-1-13- , 6935	K.GPGLFFILPCTDSFIK.V	1814.13672	2	1.71E-06	0.94	4.49	-	833.7
AHQ-1-1, 2547	R.LLAQTTLR.N	916.10035	2	3.09E-05	0.83	2.96	-	621.4
AHQ-1-10, 6271	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	1.20E-09	0.98	7.59	-	2373.6
AHQ-1-10, 6073	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	2.04E-06	0.91	4.28	-	1180.8
AHQ-1-13- , 7023	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	3.68E-04	0.89	3.98	-	456.5
AHQ-1-10, 6383	K.NSTIVFPLPIDM*LQGIIGAK.H	2144.56315	2	4.63E-05	0.90	4.27	-	471.2
AHQ-1-1, 5604 - 5668	R.TISFDIPPQEILTK.D	1602.85305	2	3.39E-04	0.60	2.56	-	283.6
AHQ-1-1, 2400	K.VIAAEGEMNASR.A	1248.39191	2	1.57E-08	0.97	4.67	-	1438.6
AHQ-1-13- , 2319	K.VIAAEGEMNASR.A	1248.39191	2	8.13E-08	0.97	4.66	-	1411.7
AHQ-1-13, 2375	K.VIAAEGEMNASR.A	1248.39191	2	6.35E-06	0.95	4.06	-	1271.1
AHQ-1-10, 2156	K.VIAAEGEMNASR.A	1248.39191	2	6.01E-06	0.96	3.49	-	1692.1
AHQ-1-10, 3695	R.VQNATLAVANITNADSATR.L	1931.09731	2	5.91E-10	0.96	5.48	-	882.1
AHQ-1-10, 3563	R.VQNATLAVANITNADSATR.L	1931.09731	2	2.63E-06	0.93	4.80	-	654.4
AHQ-1-1, 3920	R.VQNATLAVANITNADSATR.L	1931.09731	2	5.41E-12	0.96	4.90	-	1087.8
AHQ-1-1, 4008 - 4032	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.17E-08	0.97	4.96	-	1458.4
AHQ-1-1, 4277	R.VQNATLAVANITNADSATR.L	1931.09731	2	9.26E-10	0.96	4.75	-	1179.6
AHQ-1-2, 4113	R.VQNATLAVANITNADSATR.L	1931.09731	2	3.18E-08	0.92	3.76	-	1110.4
AHQ-1-13- , 4116	R.VQNATLAVANITNADSATR.L	1931.09731	2	7.37E-08	0.93	4.31	-	885.0
AHQ-1-1, 4629	R.VQNATLAVANITNADSATR.L	1931.09731	2	6.42E-08	0.93	4.54	-	757.8
AHQ-1-10, 3779 - 3855	R.VQNATLAVANITNADSATR.L	1931.09731	2	3.88E-11	0.96	5.26	-	1072.1
AHQ-1-13, 3811	R.YLQTLTTIAAEK.N	1352.55813	2	3.58E-04	0.81	2.65	-	1249.5
AHQ-1-10, 3539	R.YLQTLTTIAAEK.N	1352.55813	2	1.32E-04	0.90	3.26	-	1202.1
AHQ-1-1, 4019	R.YLQTLTTIAAEK.N	1352.55813	2	1.14E-07	0.95	3.77	-	1710.8
AHQ-1-14, 4756 - 4758	R.YLQTLTTIAAEK.N	1352.55813	2	5.07E-04	0.85	3.14	-	850.1
gi|4507953|ref|NP_003397.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep				6.33E-12	9.66	110.29	53.10	27744.9
AHQ-1-10, 3233 - 3376	K.FLIPNASQAESK.V	1305.46156	1	3.94E-07	0.35	2.03	-	382.5
AHQ-1-10, 3019 - 3080	K.FLIPNASQAESK.V	1305.46156	2	1.29E-09	0.88	2.78	-	700.5
AHQ-1-11, 3166	K.FLIPNASQAESK.V	1305.46156	2	4.96E-07	0.77	2.79	-	529.4
AHQ-1-13, 3501	K.FLIPNASQAESK.V	1305.46156	1	1.58E-04	0.30	1.93	-	475.7
AHQ-1-13- , 6963	K.IETELRDICNDVLSLLEK.F	2162.44718	3	7.50E-04	0.83	4.21	-	963.1
AHQ-1-10, 6393	K.IETELRDICNDVLSLLEK.F	2162.44718	3	1.21E-07	0.91	5.14	-	1090.6
AHQ-1-10, 5675 - 5731	K.IETELRDICNDVLSLLEK.F	2162.44718	2	4.59E-06	0.93	4.61	-	1077.7
AHQ-1-10, 6405 - 6415	R.LGLALNFSVFYYEILNSPEK.A	2318.65200	2	4.68E-05	0.95	5.15	-	807.6
AHQ-1-10, 6401 - 6404	R.LGLALNFSVFYYEILNSPEK.A	2318.65200	2	1.35E-06	0.81	4.00	-	292.0
AHQ-1-10, 2283 - 2320	K.SVTEQGAELSNEER.N	1549.57922	2	5.73E-09	0.96	5.05	-	958.5
AHQ-1-13- , 2376	K.SVTEQGAELSNEER.N	1549.57922	2	8.41E-10	0.90	3.92	-	1039.4

AHQ-1-10, 2472 - 2539	K.SVTEQGAELSNEER.N	1549.57922	2	1.25E-06	0.96	4.66	-	1571.0
AHQ-1-14- , 2288 - 2346	K.SVTEQGAELSNEER.N	1549.57922	2	9.14E-10	0.95	4.29	-	1554.0
AHQ-1-12, 2329 - 2330	K.SVTEQGAELSNEER.N	1549.57922	2	3.33E-09	0.92	4.32	-	1054.3
AHQ-1-11, 2296 - 2299	K.SVTEQGAELSNEER.N	1549.57922	2	9.98E-06	0.95	4.12	-	1261.7
AHQ-1-14- , 2186 - 2256	K.SVTEQGAELSNEER.N	1549.57922	2	6.52E-07	0.96	4.48	-	1542.9
AHQ-1-13, 2421	K.SVTEQGAELSNEER.N	1549.57922	2	1.46E-06	0.93	4.25	-	1194.4
AHQ-1-10, 2223 - 2264	K.SVTEQGAELSNEER.N	1549.57922	2	1.00E-06	0.93	3.36	-	1587.2
AHQ-1-9, 2239	K.SVTEQGAELSNEER.N	1549.57922	2	7.16E-06	0.92	3.92	-	1134.0
AHQ-1-10, 4571	K.SVTEQGAELSNEERNLLSVAYK.N	2438.63331	2	8.46E-04	0.81	3.34	-	713.9
AHQ-1-10, 4709 - 4712	K.SVTEQGAELSNEERNLLSVAYK.N	2438.63331	2	4.44E-05	0.95	5.17	-	794.5
AHQ-1-10, 5656 - 5729	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.23E-09	0.83	3.44	-	634.1
AHQ-1-13, 6431	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.20E-06	0.97	5.44	-	1400.2
AHQ-1-10, 6299	K.TAFDEAIAELDTLSEESYK.D	2133.25160	3	3.01E-07	0.96	5.78	-	1274.4
AHQ-1-13, 6432 - 6445	K.TAFDEAIAELDTLSEESYK.D	2133.25160	3	4.84E-10	0.96	5.19	-	1490.8
AHQ-1-14- , 6568 - 6640	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	7.62E-09	0.96	5.09	-	1048.3
AHQ-1-13- , 5797	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.02E-06	0.96	4.96	-	1094.8
AHQ-1-13- , 6811 - 6887	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	2.10E-08	0.97	5.36	-	1357.5
AHQ-1-13- , 6891	K.TAFDEAIAELDTLSEESYK.D	2133.25160	3	1.08E-05	0.95	5.39	-	1108.9
AHQ-1-11, 6388	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	6.33E-12	0.97	5.56	-	1188.3
AHQ-1-9, 7200	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	2.57E-05	0.96	5.31	-	976.8
AHQ-1-12, 6566	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	2.87E-09	0.89	3.48	-	1108.6
AHQ-1-10, 6252 - 6295	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.26E-11	0.96	5.17	-	1252.1
AHQ-1-10, 6369 - 6441	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	4.53E-04	0.89	4.56	-	803.1
AHQ-1-10, 6511	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	2.55E-11	0.96	5.73	-	1376.0
AHQ-1-10, 1487 - 1557	R.VVSSIEQK.T	890.01653	2	9.11E-07	0.66	3.14	-	400.2
AHQ-1-13- , 2628	R.YDDMAACMK.S	1106.27579	2	3.48E-06	0.92	3.09	-	1105.5
AHQ-1-10, 2445	R.YDDMAACMK.S	1106.27579	1	6.21E-04	0.26	1.81	-	314.6
AHQ-1-10, 2137 - 2216	R.YLAEVAAGDDK.K	1152.23595	2	4.46E-05	0.92	3.13	-	994.6
AHQ-1-13- , 2388	R.YLAEVAAGDDK.K	1152.23595	1	2.49E-05	0.79	2.53	-	1400.7
AHQ-1-13- , 2391	R.YLAEVAAGDDK.K	1152.23595	2	5.20E-04	0.90	2.95	-	1045.2
AHQ-1-10, 2133 - 2212	R.YLAEVAAGDDK.K	1152.23595	1	2.27E-05	0.77	2.86	-	1031.3
AHQ-1-13, 2435	R.YLAEVAAGDDK.K	1152.23595	1	5.81E-05	0.58	2.20	-	991.5
AHQ-1-10, 2027	R.YLAEVAAGDDKK.G	1280.40887	2	3.35E-05	0.84	3.18	-	873.6
AHQ-1-10, 1940	R.YLAEVAAGDDKK.G	1280.40887	3	1.16E-05	0.78	3.09	-	996.9
AHQ-1-10, 1929 - 1988	R.YLAEVAAGDDKK.G	1280.40887	1	2.45E-04	0.88	3.62	-	865.8
AHQ-1-10, 1912 - 1967	R.YLAEVAAGDDKK.G	1280.40887	2	2.86E-05	0.96	4.30	-	1614.0
AHQ-1-11, 2030 - 2099	R.YLAEVAAGDDKK.G	1280.40887	2	2.62E-04	0.90	3.09	-	1453.5
AHQ-1-13, 2157 - 2229	R.YLAEVAAGDDKK.G	1280.40887	2	5.70E-05	0.86	3.08	-	1024.5
AHQ-1-13- , 2069 - 2135	R.YLAEVAAGDDKK.G	1280.40887	2	5.34E-08	0.95	3.82	-	1553.7
gi|4885063|ref|NP_005156.1| aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase				6.50E-12	0.80	10.26	6.30	39455.6
AHQ-1-9, 4343 - 4382	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	2.67E-07	0.79	4.65	-	615.1
AHQ-1-9, 4786	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.21E-10	0.69	4.01	-	358.4
AHQ-1-10, 4236	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	8.61E-08	0.52	3.86	-	273.4
AHQ-1-12, 4506	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	6.50E-12	0.80	4.18	-	682.9
AHQ-1-8, 4671 - 4742	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	6.01E-10	0.88	5.21	-	740.4
gi|30159830|ref|XP_302246.1| similar to HSPC280 [Homo sapiens]				6.92E-12	1.92	20.24	3.90	45644.4
AHQ-1-14- , 6682 - 6752	K.CANLFEALVGTLK.A	1437.68632	2	4.35E-07	0.97	4.74	-	1522.5
AHQ-1-14- , 6639	R.DDKCANLFEALVGTLK.A	1796.03496	3	2.90E-04	0.93	4.20	-	1710.9
AHQ-1-14- , 6630 - 6707	R.DDKCANLFEALVGTLK.A	1796.03496	2	6.92E-12	0.96	4.30	-	1314.4
gi|17986273|ref|NP_524144.1| fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2				7.42E-12	1.85	20.20	8.20	21145.0
AHQ-1-12, 3429	R.VFDKEGNGTVMGAELR.H	1723.93228	2	1.61E-07	0.52	2.54	-	467.2
AHQ-1-13, 3327	R.VFDKEGNGTVMGAELR.H	1723.93228	2	4.19E-05	0.83	2.90	-	904.0
AHQ-1-14- , 2690 - 2692	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	1.31E-09	0.93	3.92	-	980.0
AHQ-1-14- , 3340	R.VFDKEGNGTVMGAELR.H	1723.93228	2	7.42E-12	0.92	3.98	-	963.6
AHQ-1-12, 2630 - 2694	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	6.28E-06	0.86	3.61	-	840.6
gi|4504523|ref|NP_002148.1| heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (				8.07E-12	1.89	20.28	25.50	10931.6
AHQ-1-14- , 3007	K.VLQATVVAVGSGSK.G	1316.52902	2	4.02E-04	0.89	3.19	-	810.0
AHQ-1-14- , 2834 - 2836	K.VLQATVVAVGSGSK.G	1316.52902	2	6.89E-11	0.98	5.53	-	1807.5
AHQ-1-14, 3728	K.VLQATVVAVGSGSK.G	1316.52902	2	8.07E-12	0.97	4.92	-	1336.6
AHQ-1-14- , 5028 - 5106	K.VVLDDKDYFLFR.D	1530.74861	2	8.30E-10	0.90	3.38	-	1022.7
AHQ-1-14- , 5030	K.VVLDDKDYFLFR.D	1530.74861	3	2.88E-07	0.86	3.41	-	584.0
AHQ-1-14, 5928 - 6001	K.VVLDDKDYFLFR.D	1530.74861	2	2.81E-10	0.92	3.60	-	1023.1
gi|4503327|ref|NP_000389.1| cytochrome b5 reductase membrane-bound isoform; diaphorase (NADH) [Homo				8.19E-12	9.01	110.33	49.50	34234.6
AHQ-1-9, 4532	R.AIMKDPDDHTVCHLLFANQTEK.D	2585.89793	3	8.19E-12	0.88	4.19	-	837.6
AHQ-1-9, 5114	R.APEAWDYGQGFVNEEM*IR.D	2129.29457	2	2.92E-05	0.91	3.79	-	834.8
AHQ-1-9, 4790 - 4791	K.DILLRPELEELR.N	1496.73370	2	2.97E-07	0.84	3.88	-	575.2
AHQ-1-9, 6238 - 6246	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	3	4.51E-10	0.95	5.58	-	1110.1
AHQ-1-9, 6250 - 6254	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	2	1.14E-07	0.95	5.29	-	679.2
AHQ-1-9, 2872	R.GPSGLLVYQGK.G	1119.29547	1	1.15E-05	0.79	3.39	-	464.9
AHQ-1-9, 2866	R.GPSGLLVYQGK.G	1119.29547	2	3.32E-05	0.96	4.27	-	1398.1
AHQ-1-9, 6086	R.IDGNLVVRPYTPISSDDDKGFVDLVIK.V	2977.35765	3	2.51E-05	0.97	6.57	-	1251.8
AHQ-1-9, 3627	R.STPAITLESPDIK.Y	1372.54621	1	2.88E-05	0.64	3.01	-	428.4
AHQ-1-11, 3603	R.STPAITLESPDIK.Y	1372.54621	2	3.15E-04	0.53	2.68	-	559.9
AHQ-1-12, 3719	R.STPAITLESPDIK.Y	1372.54621	2	2.58E-05	0.62	2.70	-	449.6
AHQ-1-9, 4638	R.STPAITLESPDIKYPLR.L	1902.18061	2	1.56E-05	0.88	3.94	-	651.2
AHQ-1-9, 6012	K.SVGMIAGGTGITPMLQVIR.A	1902.31543	2	3.35E-05	0.78	3.66	-	475.2
AHQ-1-9, 5528	K.SVGM*IAGGTGITPMLQVIR.A	1918.31483	2	1.06E-04	0.82	3.83	-	538.9
AHQ-1-9, 5080 - 5104	K.SVGMIAGGTGITPM*LQVIR.A	1918.31483	2	1.71E-04	0.56	3.15	-	371.1
gi|5729877|ref|NP_006588.1| heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD				8.52E-12	14.41	160.27	27.20	70897.6
AHQ-1-7, 4486	R.ARFEELNADLFR.G	1481.63768	2	1.05E-04	0.82	2.90	-	704.3
AHQ-1-6, 4387	R.ARFEELNADLFR.G	1481.63768	3	1.91E-04	0.97	5.37	-	1952.1
AHQ-1-6, 4380 - 4460	R.ARFEELNADLFR.G	1481.63768	2	2.16E-07	0.96	4.50	-	1104.2
AHQ-1-6, 4746	R.FEELNADLFR.G	1254.37310	2	1.10E-06	0.91	3.70	-	977.9
AHQ-1-6, 5362	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	2	4.11E-10	0.95	5.22	-	764.6
AHQ-1-14- , 5166 - 5244	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	5.17E-05	0.86	4.00	-	588.8
AHQ-1-6, 5754 - 5772	K.ILDKCNEIINWLDK.N	1776.04688	2	4.55E-05	0.93	4.46	-	1116.2
AHQ-1-6, 2834 - 2835	K.MKEIAEAYLGK.T	1253.49320	2	3.04E-07	0.92	3.55	-	1146.8
AHQ-1-6, 3378	R.MVNHFIAEFK.R	1236.46756	2	6.64E-08	0.94	3.88	-	1186.6
AHQ-1-6, 2778	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	8.52E-12	0.90	3.45	-	853.1
AHQ-1-13- , 3756	K.NQVAMNPTNTVFDAK.R	1650.83816	2	2.36E-04	0.91	3.74	-	826.3
AHQ-1-6, 3446	K.NQVAMNPTNTVFDAK.R	1650.83816	2	2.54E-11	0.93	4.23	-	772.6
AHQ-1-6, 3427	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	4.73E-06	0.89	3.53	-	817.5
AHQ-1-6, 4098	K.NSLESYAFNMK.A	1304.45393	2	3.83E-06	0.89	3.59	-	832.4
AHQ-1-6, 3304	K.NSLESYAFNM*K.A	1320.45333	2	1.07E-05	0.86	3.34	-	819.3
AHQ-1-6, 2598	R.RFDDAVVQSDMK.H	1411.56603	2	2.46E-06	0.96	4.33	-	1539.9
AHQ-1-12, 5093 - 5107	K.SFYPEEVSSMVLTK.M	1617.84485	2	1.72E-04	0.64	3.04	-	294.1
AHQ-1-6, 5256 - 5323	K.SFYPEEVSSMVLTK.M	1617.84485	2	3.35E-04	0.74	3.20	-	440.8
AHQ-1-6, 4484 - 4555	K.SFYPEEVSSM*VLTK.M	1633.84425	2	1.06E-04	0.87	3.11	-	756.1
AHQ-1-6, 6922 - 6986	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	3.82E-08	0.97	5.38	-	1438.3
AHQ-1-7, 7090	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	8.76E-06	0.94	4.42	-	981.9
AHQ-1-6, 3010	K.SQIHDIVLVGGSTR.I	1482.66712	1	1.05E-11	0.92	4.27	-	719.3
AHQ-1-9, 2916	K.SQIHDIVLVGGSTR.I	1482.66712	2	2.03E-08	0.97	4.02	-	1985.0
AHQ-1-6, 3000 - 3002	K.SQIHDIVLVGGSTR.I	1482.66712	2	2.07E-08	0.97	4.53	-	1844.5
AHQ-1-6, 3003	K.SQIHDIVLVGGSTR.I	1482.66712	1	3.95E-05	0.91	3.69	-	894.5
AHQ-1-7, 3034	K.SQIHDIVLVGGSTR.I	1482.66712	2	1.76E-10	0.98	4.42	-	2585.0
AHQ-1-8, 2802	K.SQIHDIVLVGGSTR.I	1482.66712	1	8.98E-04	0.86	3.45	-	730.1
AHQ-1-6, 4580 - 4650	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	1.14E-04	0.87	4.10	-	442.7

AHQ-1-6, 4722 - 4770	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	7.87E-04	0.77	3.59	-	308.9
AHQ-1-6, 4840 - 4872	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	2.38E-04	0.56	3.26	-	234.2
AHQ-1-6, 4666	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	3	2.00E-04	0.92	4.28	-	1266.3
gi|18201905|ref|NP_000166.2| glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras				8.67E-12	6.87	80.29	24.40	63146.7
AHQ-1-7, 6926	K.ILLANFLAQTEALM*R.G	1721.05778	2	1.38E-04	0.94	3.62	-	1419.9
AHQ-1-7, 7481	K.ILLANFLAQTEALMR.G	1705.05838	2	6.87E-09	0.97	5.74	-	1432.6
AHQ-1-7, 5140 - 5141	K.KIEPELDGSAQVTSHDASTNGLINFIK.Q	2886.16347	3	3.07E-04	0.90	4.73	-	803.6
AHQ-1-7, 3028	K.TFTTQETITNAETAK.E	1656.77283	2	1.08E-05	0.80	3.32	-	692.4
AHQ-1-7, 7301 - 7317	K.TITDVINIGIGGSDLGPLM*VTEALKPYSSGGPR.V	3346.79723	3	6.51E-07	0.84	3.77	-	814.3
AHQ-1-7, 6358 - 6372	K.TLAQLNPESSLFIIASK.T	1833.11828	2	7.10E-05	0.74	3.41	-	417.1
AHQ-1-7, 3289	K.VFEGNRPTNSIVFTK.L	1709.92693	2	3.90E-04	0.79	3.36	-	741.8
AHQ-1-7, 3938 - 3958	R.VWYVSNIDGTHIAK.T	1603.80282	2	8.67E-12	0.88	3.20	-	808.4
gi|10834976|ref|NP_000572.1| glutathione peroxidase 1 [Homo sapiens]				8.73E-12	5.04	60.29	42.80	21909.0
AHQ-1-11, 5126 - 5200	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	8.73E-12	0.86	3.60	-	550.9
AHQ-1-11, 3934	K.FLVGPDGVPLR.R	1170.38561	2	1.29E-04	0.74	2.60	-	682.4
AHQ-1-11, 4758 - 4759	R.GLVVLGFPCNQFGHQENAK.N	2117.37312	2	1.16E-04	0.86	4.02	-	473.6
AHQ-1-11, 3750 - 3754	K.LITWSPVCR.N	1133.34543	2	2.23E-04	0.65	2.59	-	496.7
AHQ-1-14, 4846	R.PLAGGEPVSLGSLR.G	1353.54935	2	3.05E-06	0.96	4.74	-	1124.3
AHQ-1-14- , 3974	R.PLAGGEPVSLGSLR.G	1353.54935	2	1.24E-07	0.96	4.23	-	1063.8
AHQ-1-11, 3735 - 3742	R.PLAGGEPVSLGSLR.G	1353.54935	2	3.76E-09	0.96	5.03	-	1105.5
AHQ-1-11, 5023	K.YVRPGGGFEPNFMLFEK.C	1989.28515	2	3.91E-06	0.97	5.72	-	1624.1
AHQ-1-11, 5031	K.YVRPGGGFEPNFMLFEK.C	1989.28515	3	9.10E-04	0.95	4.82	-	1421.0
gi|16507237|ref|NP_005338.1| heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he				9.14E-12	11.26	130.30	22.50	72332.5
AHQ-1-6, 5023	R.AKFEELNMDLFR.S	1513.74309	2	8.58E-08	0.92	3.89	-	984.1
AHQ-1-6, 4162	R.AKFEELNM*DLFR.S	1529.74249	2	1.37E-06	0.87	2.77	-	1143.0
AHQ-1-6, 5751	K.DNHLLGTFDLTGIPPAPR.G	1935.17239	2	8.98E-09	0.95	4.44	-	1060.6
AHQ-1-6, 5660	K.DNHLLGTFDLTGIPPAPR.G	1935.17239	2	6.20E-09	0.95	4.43	-	1071.3
AHQ-1-6, 6067 - 6142	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	4.60E-08	0.95	4.08	-	1450.1
AHQ-1-6, 7415	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	1.05E-06	0.95	4.34	-	1275.5
AHQ-1-6, 6211 - 6279	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	2.23E-04	0.92	3.98	-	960.1
AHQ-1-6, 6350	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	1.95E-06	0.95	4.61	-	1057.0
AHQ-1-6, 4768 - 4794	K.IEWLESHQDADIEDFK.A	1976.08864	2	9.14E-12	0.98	5.96	-	1904.9
AHQ-1-6, 4446 - 4459	R.IINEPTAAAIAYGLDKR.E	1817.07894	2	1.37E-10	0.76	3.77	-	804.5
AHQ-1-6, 3731	K.KSDIDEIVLVGGSTR.I	1589.77277	2	2.55E-08	0.96	4.30	-	1648.9
AHQ-1-6, 3256	K.KSQIFSTASDNQPTVTIK.V	1966.18156	2	5.63E-05	0.88	4.21	-	734.6
AHQ-1-6, 3442	K.KVTHAVVTVPAYFNDAQR.Q	2017.27663	2	8.99E-08	0.97	5.79	-	1280.7
AHQ-1-6, 4386	K.SDIDEIVLVGGSTR.I	1461.59985	1	2.36E-06	0.35	2.31	-	364.8
AHQ-1-6, 3742	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	5.53E-05	0.81	3.27	-	784.7
AHQ-1-7, 3833 - 3836	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	1.05E-06	0.92	4.23	-	863.4
AHQ-1-6, 2928 - 3008	K.TKPYIQVDIGGGQTK.T	1605.81703	2	1.54E-04	0.79	3.26	-	664.7
AHQ-1-6, 3898	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	2.38E-11	0.95	4.83	-	751.4
AHQ-1-7, 3982	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	4.66E-08	0.88	3.96	-	487.8
AHQ-1-6, 4031	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	1.33E-05	0.80	3.20	-	432.3
gi|4758606|ref|NP_004508.1| integrin-linked kinase [Homo sapiens]				9.81E-12	11.75	140.32	34.30	51418.9
AHQ-1-13, 5019 - 5023	R.EVPFADLSNMEIGM*K.V	1697.95498	2	5.07E-04	0.74	3.10	-	598.7
AHQ-1-10, 5197	R.EVPFADLSNMEIGMK.V	1681.95558	2	9.60E-06	0.55	2.57	-	281.8
AHQ-1-7, 5350 - 5364	R.EVPFADLSNMEIGM*K.V	1697.95498	2	4.18E-05	0.89	3.88	-	561.7
AHQ-1-13- , 5299	R.EVPFADLSNMEIGM*K.V	1697.95498	2	3.51E-06	0.71	3.35	-	366.7
AHQ-1-7, 5797	K.FDMIVPILEK.M	1205.49168	2	4.35E-05	0.91	3.42	-	868.5
AHQ-1-7, 2138	R.GDDTPLHLAASHGHR.D	1584.67809	2	1.31E-10	0.89	3.20	-	1162.6
AHQ-1-9, 1983 - 1984	R.GDDTPLHLAASHGHR.D	1584.67809	2	1.85E-07	0.47	2.79	-	365.6
AHQ-1-10, 2063	R.GDDTPLHLAASHGHR.D	1584.67809	2	2.38E-07	0.78	2.93	-	802.6
AHQ-1-7, 1909 - 2028	R.GDDTPLHLAASHGHR.D	1584.67809	2	1.48E-10	0.94	3.82	-	1203.5
AHQ-1-7, 5205	R.GM*AFLHTLEPLIPR.H	1611.93301	2	2.27E-05	0.86	3.20	-	816.4
AHQ-1-7, 6114 - 6142	R.GMAFLHTLEPLIPR.H	1595.93361	2	8.90E-05	0.94	3.78	-	1298.7
AHQ-1-7, 2233	K.LNENHSGELWK.G	1327.42732	2	3.85E-04	0.76	2.97	-	957.8
AHQ-1-7, 2429	K.LNENHSGELWK.G	1327.42732	2	4.36E-07	0.84	3.68	-	849.9
AHQ-1-7, 2428 - 2433	K.LNENHSGELWK.G	1327.42732	1	2.23E-05	0.42	2.23	-	386.3
AHQ-1-7, 6449	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	1.06E-08	0.93	5.03	-	1028.3
AHQ-1-7, 6301 - 6381	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	6.37E-09	0.97	6.48	-	1343.5
AHQ-1-7, 4321 - 4392	R.M*YAPAWVAPEALQK.K	1591.85542	2	6.03E-05	0.93	3.98	-	864.4
AHQ-1-7, 4822	R.MYAPAWVAPEALQK.K	1575.85602	2	3.87E-08	0.93	3.38	-	1097.7
AHQ-1-13- , 4317 - 4389	R.M*YAPAWVAPEALQK.K	1591.85542	2	1.01E-05	0.87	3.05	-	710.5
AHQ-1-9, 4730	R.MYAPAWVAPEALQK.K	1575.85602	2	9.81E-12	0.94	3.84	-	1158.9
AHQ-1-13, 4196	R.M*YAPAWVAPEALQK.K	1591.85542	2	4.54E-05	0.89	3.31	-	820.5
AHQ-1-10, 4352	R.MYAPAWVAPEALQK.K	1575.85602	2	1.32E-04	0.89	3.29	-	864.3
AHQ-1-11, 4096	R.M*YAPAWVAPEALQK.K	1591.85542	2	8.28E-04	0.83	2.76	-	804.2
AHQ-1-11, 4491 - 4498	R.MYAPAWVAPEALQK.K	1575.85602	2	9.65E-06	0.94	3.66	-	1192.1
AHQ-1-7, 4838	R.SAVVEMLIMR.G	1149.45316	2	3.04E-07	0.96	4.15	-	1393.9
AHQ-1-7, 3026	R.SVMIDEDMTAR.I	1268.44340	2	7.63E-06	0.78	2.60	-	839.9
AHQ-1-7, 4656	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	3	6.10E-10	0.79	3.54	-	912.0
AHQ-1-7, 4649 - 4661	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	2	6.25E-04	0.94	4.98	-	613.0
AHQ-1-7, 2909	R.WQGNDIVVK.V	1059.20012	1	2.46E-04	0.75	2.34	-	955.3
gi|4506413|ref|NP_002875.1| RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				1.15E-11	5.49	60.28	33.20	20987.1
AHQ-1-11, 2442	K.CDLEDERVVGK.E	1321.43945	2	1.44E-05	0.92	3.54	-	1191.6
AHQ-1-14- , 5867 - 5871	K.INVNEIFYDLVR.Q	1495.70427	2	5.92E-04	0.92	3.88	-	1033.6
AHQ-1-13- , 6863	K.INVNEIFYDLVR.Q	1495.70427	2	4.41E-09	0.97	5.66	-	1374.5
AHQ-1-13, 6407	K.INVNEIFYDLVR.Q	1495.70427	2	1.12E-07	0.95	4.98	-	948.1
AHQ-1-12, 6534	K.INVNEIFYDLVR.Q	1495.70427	2	1.49E-05	0.93	4.03	-	1054.6
AHQ-1-11, 5527	K.INVNEIFYDLVR.Q	1495.70427	2	5.26E-07	0.89	3.71	-	876.0
AHQ-1-11, 6402	K.INVNEIFYDLVR.Q	1495.70427	2	1.01E-06	0.97	5.20	-	1524.9
AHQ-1-11, 5751 - 5790	K.INVNEIFYDLVR.Q	1495.70427	2	1.39E-08	0.95	4.52	-	965.3
AHQ-1-11, 6316	K.INVNEIFYDLVR.Q	1495.70427	1	1.59E-06	0.48	3.20	-	292.9
AHQ-1-11, 6314 - 6384	K.INVNEIFYDLVR.Q	1495.70427	1	4.34E-04	0.35	2.90	-	238.4
AHQ-1-11, 6311 - 6312	K.INVNEIFYDLVR.Q	1495.70427	2	4.63E-08	0.95	4.42	-	1105.1
AHQ-1-11, 6178 - 6180	K.INVNEIFYDLVR.Q	1495.70427	2	1.39E-06	0.95	4.14	-	1268.8
AHQ-1-14- , 6610	K.INVNEIFYDLVR.Q	1495.70427	2	3.89E-09	0.96	4.61	-	1373.1
AHQ-1-13- , 2879 - 2880	K.LVVLGSGGVGK.S	986.19059	2	4.31E-04	0.94	4.15	-	1083.8
AHQ-1-12, 2758 - 2763	K.LVVLGSGGVGK.S	986.19059	2	3.26E-06	0.88	3.38	-	948.1
AHQ-1-14- , 2823	K.LVVLGSGGVGK.S	986.19059	1	1.10E-04	0.54	2.85	-	199.5
AHQ-1-11, 5990 - 6048	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.78E-05	0.95	4.95	-	1215.0
AHQ-1-11, 5858 - 5928	K.SALTVQFVQGIFVEK.Y	1666.94196	2	8.36E-04	0.92	3.66	-	1375.2
AHQ-1-11, 5742 - 5803	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.79E-06	0.96	4.80	-	1387.9
AHQ-1-11, 5752 - 5754	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.15E-11	0.96	4.82	-	1124.6
AHQ-1-14- , 6142	K.SKINVNEIFYDLVR.Q	1710.95483	3	6.39E-08	0.92	4.19	-	1330.0
AHQ-1-11, 5171 - 5195	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.32E-07	0.95	4.41	-	1041.4
AHQ-1-11, 5756	K.SKINVNEIFYDLVR.Q	1710.95483	3	1.77E-06	0.93	4.04	-	1639.1
AHQ-1-11, 4979	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.30E-09	0.90	3.97	-	747.7
AHQ-1-11, 5939 - 6004	K.SKINVNEIFYDLVR.Q	1710.95483	2	6.45E-11	0.95	4.59	-	1138.1
AHQ-1-14- , 6068 - 6139	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.73E-10	0.95	4.26	-	1121.8
AHQ-1-11, 4747 - 4755	K.SKINVNEIFYDLVR.Q	1710.95483	2	5.38E-04	0.46	3.05	-	377.0
AHQ-1-11, 6111	K.SKINVNEIFYDLVR.Q	1710.95483	2	3.49E-08	0.95	4.13	-	1379.8
AHQ-1-11, 2730 - 2794	K.YDPTIEDSYR.K	1259.30338	2	2.24E-07	0.80	2.84	-	418.6
AHQ-1-13- , 2904	K.YDPTIEDSYR.K	1259.30338	2	4.01E-05	0.89	3.13	-	495.1
AHQ-1-12, 2795 - 2797	K.YDPTIEDSYR.K	1259.30338	2	3.02E-04	0.69	2.76	-	299.4
AHQ-1-13, 2885 - 2893	K.YDPTIEDSYR.K	1259.30338	2	3.95E-08	0.81	3.06	-	407.5
AHQ-1-14- , 2830 - 2851	K.YDPTIEDSYR.K	1259.30338	2	5.66E-05	0.75	2.61	-	400.9

gi|5031857|ref|NP_005557.1| lactate dehydrogenase A [Homo sapiens]				1.16E-11	5.10	60.29	19.00	36688.5
AHQ-1-14- , 6494 - 6554	K.DLADELALVDVIEDK.L	1658.82864	2	2.85E-05	0.89	4.02	-	774.8
AHQ-1-13, 6355 - 6356	K.DLADELALVDVIEDK.L	1658.82864	2	1.16E-11	0.98	5.71	-	1903.7
AHQ-1-11, 6287	K.DLADELALVDVIEDK.L	1658.82864	2	5.74E-04	0.45	2.74	-	368.7
AHQ-1-13- , 6803 - 6808	K.DLADELALVDVIEDK.L	1658.82864	2	1.86E-10	0.97	5.31	-	1505.5
AHQ-1-9, 7026 - 7048	K.DLADELALVDVIEDK.L	1658.82864	2	6.86E-06	0.96	3.78	-	1677.7
AHQ-1-9, 7147 - 7227	K.DLADELALVDVIEDKLK.G	1900.15980	2	1.29E-05	0.86	3.77	-	893.5
AHQ-1-9, 2602	K.LVIITAGAR.Q	914.12760	2	1.93E-06	0.89	2.90	-	1007.1
AHQ-1-13- , 2893	K.LVIITAGAR.Q	914.12760	2	3.01E-06	0.90	2.72	-	1105.0
AHQ-1-9, 3275 - 3344	K.QVVESAYEVIK.L	1265.43734	2	7.85E-04	0.66	3.08	-	303.9
AHQ-1-9, 2322	K.TLHPDLGTDKDKEQWK.E	1912.09245	2	3.39E-04	0.81	3.14	-	653.7
AHQ-1-11, 2118	K.VTLTSEEEAR.L	1135.20693	2	8.80E-05	0.88	2.96	-	1019.5
AHQ-1-9, 2003 - 2018	K.VTLTSEEEAR.L	1135.20693	2	1.49E-07	0.90	2.87	-	1143.2
gi|24431935|ref|NP_065393.1| reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sap				1.17E-11	1.82	20.40	3.90	129930.3
AHQ-1-1, 3335	R.GPLPAAPPVAPER.Q	1272.47793	2	2.26E-06	0.84	3.23	-	682.6
AHQ-1-13- , 6213 - 6220	K.YQFVREPEDEEEEEEEEEDEDEDLEELEVLER.K	4189.14063	3	1.17E-11	0.98	7.92	-	2303.3
gi|5031985|ref|NP_005787.1| nuclear transport factor 2; placental protein 15 [Homo sapiens]				1.48E-11	4.43	50.34	63.00	14478.4
AHQ-1-14- , 5770	K.ADEDPIM*GFHQMFLLK.N	1909.21859	2	1.42E-04	0.88	3.76	-	824.0
AHQ-1-14- , 5454 - 5519	K.IQHSITAQDHQPTPDSCIISM*VVGQLK.A	3022.40358	3	6.17E-07	0.98	6.71	-	2023.0
AHQ-1-14- , 6042 - 6086	K.IQHSITAQDHQPTPDSCIISMVVGQLK.A	3006.40418	3	1.48E-11	0.96	5.44	-	1496.5
AHQ-1-14- , 4536	K.NINDAWVCTNDM*FR.L	1773.92828	2	8.14E-05	0.91	3.73	-	962.4
AHQ-1-14- , 6331	R.TQLGAIYIDASCLTWEGQQFQGK.A	2616.88699	3	8.65E-06	0.71	3.14	-	763.9
gi|7657007|ref|NP_055210.1| dual adaptor of phosphotyrosine and 3-phosphoinositides [Homo sapiens]				1.57E-11	2.59	30.23	18.90	32044.2
AHQ-1-13- , 3989	R.DSNETTGLYSLSVR.A	1542.62982	2	6.77E-05	0.79	3.40	-	610.6
AHQ-1-13, 4964	R.HAAEALLLSNGCDGSYLLR.D	2062.29263	2	8.53E-04	0.85	3.39	-	814.5
AHQ-1-13- , 6140 - 6153	R.SDGEAELLQDLGWYHGNLTR.H	2275.41943	3	1.57E-11	0.95	4.70	-	1590.8
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				1.82E-11	12.95	150.28	48.70	49481.2
AHQ-1-7, 4709 - 4744	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	6.39E-04	0.73	3.03	-	501.5
AHQ-1-7, 4176	K.AIQLTYNPDESSKPNM*IDAATLK.S	2537.82826	3	1.44E-04	0.66	3.23	-	593.7
AHQ-1-7, 4848 - 4849	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	8.91E-06	0.83	4.01	-	443.1
AHQ-1-11, 3900	K.AIQLTYNPDESSKPNM*IDAATLK.S	2537.82826	3	9.62E-05	0.68	3.45	-	589.3
AHQ-1-9, 4612 - 4618	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	1.25E-06	0.84	4.08	-	553.2
AHQ-1-5, 4769 - 4770	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	3.29E-04	0.54	3.06	-	298.6
AHQ-1-7, 5897	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.08E-07	0.58	2.67	-	457.4
AHQ-1-14- , 5414 - 5479	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	5.75E-11	0.81	3.21	-	671.4
AHQ-1-7, 5650 - 5720	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	7.25E-06	0.82	3.44	-	572.8
AHQ-1-14- , 5550 - 5616	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	9.25E-08	0.65	2.90	-	402.4
AHQ-1-13, 5261	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	4.98E-08	0.53	2.55	-	411.6
AHQ-1-13- , 5555 - 5620	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	9.43E-10	0.78	3.37	-	518.3
AHQ-1-14, 6428	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	3.81E-06	0.54	2.64	-	333.5
AHQ-1-5, 5853 - 5862	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	8.96E-07	0.80	3.41	-	572.6
AHQ-1-1, 5848 - 5861	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.08E-05	0.63	2.52	-	517.3
AHQ-1-7, 2770	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	6.26E-06	0.95	4.80	-	1359.7
AHQ-1-9, 2606 - 2680	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.70E-04	0.89	4.03	-	747.5
AHQ-1-13- , 2820 - 2897	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	1.80E-04	0.89	4.04	-	1138.9
AHQ-1-5, 2643	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.38E-11	0.92	4.52	-	659.7
AHQ-1-7, 2764 - 2768	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	1.82E-11	0.98	5.28	-	1528.7
AHQ-1-4, 2812	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	8.66E-09	0.95	4.72	-	1016.2
AHQ-1-1, 3301	R.DNCCILDER.F	1197.27847	2	2.22E-05	0.86	3.16	-	936.2
AHQ-1-7, 5325 - 5380	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	4.04E-05	0.92	4.46	-	653.3
AHQ-1-7, 5334 - 5405	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	5.61E-04	0.94	4.49	-	1552.8
AHQ-1-5, 5513	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.33E-05	0.81	3.29	-	612.8
AHQ-1-12, 5102	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.59E-06	0.73	3.19	-	470.5
AHQ-1-3, 5421	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.59E-04	0.77	3.37	-	502.3
AHQ-1-2, 5614	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.75E-04	0.87	3.79	-	537.5
AHQ-1-9, 5323	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.48E-07	0.84	3.21	-	867.7
AHQ-1-9, 5196 - 5204	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	5.09E-05	0.96	4.38	-	2116.1
AHQ-1-9, 5188	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	7.76E-06	0.95	4.54	-	969.1
AHQ-1-1, 5541	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.75E-06	0.92	4.38	-	676.3
AHQ-1-8, 5200	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.41E-06	0.91	4.13	-	599.1
AHQ-1-5, 5402 - 5426	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	7.39E-07	0.95	4.96	-	840.7
AHQ-1-7, 5446 - 5516	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	4.19E-07	0.93	4.84	-	580.9
AHQ-1-12, 6314	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	2.57E-07	0.88	3.91	-	908.9
AHQ-1-13, 6233	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.09E-05	0.84	3.74	-	501.1
AHQ-1-14- , 6423 - 6435	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.08E-05	0.85	3.89	-	524.1
AHQ-1-13- , 6663	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	5.38E-05	0.66	2.94	-	480.1
AHQ-1-1, 6711	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	1.65E-04	0.60	3.05	-	530.5
AHQ-1-12, 6321	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	8.47E-05	0.86	4.25	-	443.5
AHQ-1-11, 6115	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	6.78E-05	0.78	3.50	-	457.4
AHQ-1-9, 4426 - 4434	K.IHLISTQSAIPYALR.V	1683.97576	2	1.15E-07	0.97	5.07	-	1269.2
AHQ-1-10, 4173	K.IHLISTQSAIPYALR.V	1683.97576	2	4.59E-08	0.91	3.70	-	813.5
AHQ-1-8, 4327 - 4332	K.IHLISTQSAIPYALR.V	1683.97576	2	1.86E-09	0.97	5.06	-	1182.5
AHQ-1-8, 4333	K.IHLISTQSAIPYALR.V	1683.97576	3	8.11E-05	0.63	3.00	-	644.3
AHQ-1-6, 4551 - 4619	K.IHLISTQSAIPYALR.V	1683.97576	2	2.09E-04	0.80	3.40	-	828.0
AHQ-1-7, 4538 - 4608	K.IHLISTQSAIPYALR.V	1683.97576	2	1.00E-08	0.97	5.31	-	1450.9
AHQ-1-4, 4768 - 4839	K.IHLISTQSAIPYALR.V	1683.97576	2	1.65E-05	0.93	4.31	-	960.9
AHQ-1-7, 1913 - 1918	R.LDGSVDFKK.N	1009.13788	2	1.56E-04	0.69	2.82	-	497.6
AHQ-1-7, 2040	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	6.30E-06	0.90	3.63	-	908.4
AHQ-1-7, 1940	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	6.15E-07	0.69	3.18	-	551.7
AHQ-1-11, 2092	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	5.33E-06	0.82	2.98	-	843.9
AHQ-1-14- , 2147	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	5.86E-07	0.84	3.28	-	903.9
AHQ-1-7, 4121	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	1.62E-04	0.83	4.02	-	565.3
AHQ-1-1, 4129	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	6.57E-06	0.92	4.62	-	925.0
AHQ-1-8, 3972	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	2	5.75E-05	0.36	2.67	-	288.4
AHQ-1-7, 3996	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	8.33E-04	0.89	3.91	-	1005.7
AHQ-1-11, 3752	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	7.95E-04	0.70	3.48	-	638.1
AHQ-1-5, 4226	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	8.87E-04	0.88	4.06	-	948.8
AHQ-1-9, 4103	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	5.76E-10	0.95	5.43	-	1324.2
AHQ-1-8, 4113	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	6.10E-04	0.89	4.51	-	916.2
AHQ-1-1, 4324	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	5.40E-06	0.96	5.67	-	1399.3
AHQ-1-7, 3208 - 3212	R.VELEDWNGR.T	1118.18129	2	3.40E-06	0.87	3.21	-	998.9
AHQ-1-7, 3324	R.VELEDWNGR.T	1118.18129	2	1.20E-04	0.81	2.97	-	800.0
AHQ-1-8, 3168 - 3170	R.VELEDWNGR.T	1118.18129	2	3.70E-04	0.84	2.76	-	1014.0
AHQ-1-12, 2985	K.YEASILTHDSSIR.Y	1492.61564	2	1.95E-08	0.83	3.09	-	663.0
AHQ-1-11, 2931	K.YEASILTHDSSIR.Y	1492.61564	2	2.91E-05	0.84	3.51	-	519.0
AHQ-1-7, 2937 - 3008	K.YEASILTHDSSIR.Y	1492.61564	2	1.70E-07	0.87	3.65	-	636.0
AHQ-1-7, 2946 - 2949	K.YEASILTHDSSIR.Y	1492.61564	1	3.68E-04	0.15	2.21	-	257.0
AHQ-1-9, 2854	K.YEASILTHDSSIR.Y	1492.61564	2	6.52E-09	0.89	3.27	-	820.8
AHQ-1-13, 3074	K.YEASILTHDSSIR.Y	1492.61564	2	5.30E-06	0.52	2.54	-	402.4
AHQ-1-10, 2851	K.YEASILTHDSSIR.Y	1492.61564	2	1.95E-06	0.79	2.75	-	709.3
AHQ-1-1, 3125 - 3195	K.YEASILTHDSSIR.Y	1492.61564	2	8.64E-04	0.70	2.80	-	487.8
AHQ-1-7, 2785 - 2802	R.YLQEIYNSNNQK.I	1514.62131	2	6.03E-06	0.93	4.21	-	1050.0
AHQ-1-7, 2646 - 2716	R.YLQEIYNSNNQK.I	1514.62131	2	8.87E-04	0.94	4.58	-	1072.6
AHQ-1-3, 2837	R.YLQEIYNSNNQK.I	1514.62131	2	3.94E-04	0.96	4.17	-	1931.0
gi|4557032|ref|NP_002291.1| lactate dehydrogenase B [Homo sapiens]				2.01E-11	9.19	110.27	36.50	36638.3
AHQ-1-9, 4423	K.FIIPQIVK.Y	958.22198	2	3.91E-04	0.80	2.66	-	755.6
AHQ-1-9, 7243 - 7314	K.GM*YGIENEVFLSLPCILNAR.G	2314.66682	2	2.57E-07	0.92	4.70	-	518.3

AHQ-1-9, 2008 - 2079	K.IVADKDYSVTANSK.I	1511.65887	2	2.01E-11	0.97	4.84	-	1868.3
AHQ-1-13- , 2600	K.IVVVTAGVR.Q	914.12760	2	1.27E-04	0.89	3.40	-	835.6
AHQ-1-13- , 3496	K.LIAPVAEEEATVPNNK.I	1695.89534	2	3.60E-04	0.87	3.39	-	767.0
AHQ-1-9, 3532	K.LIAPVAEEEATVPNNK.I	1695.89534	2	3.77E-06	0.65	2.85	-	490.2
AHQ-1-14- , 3548	K.LIAPVAEEEATVPNNK.I	1695.89534	2	1.61E-05	0.87	3.23	-	805.9
AHQ-1-9, 2039 - 2042	K.LKDDEVAQLK.K	1159.31477	1	4.06E-04	0.31	2.49	-	485.4
AHQ-1-14- , 2243	K.LKDDEVAQLK.K	1159.31477	2	1.52E-05	0.65	2.64	-	495.2
AHQ-1-9, 2038 - 2043	K.LKDDEVAQLK.K	1159.31477	2	7.92E-05	0.77	3.21	-	527.6
AHQ-1-9, 4026	K.LKGEMM*DLQHGSLFLQTPK.I	2190.57228	2	6.34E-05	0.53	3.83	-	423.9
AHQ-1-9, 4572	K.LKGEMMDLQHGSLFLQTPK.I	2174.57288	2	3.74E-04	0.94	4.08	-	1162.5
AHQ-1-9, 3814 - 3883	K.MVVESAYEVIK.L	1268.50463	2	7.66E-09	0.93	3.79	-	901.2
AHQ-1-14- , 3931	K.MVVESAYEVIK.L	1268.50463	2	7.68E-07	0.85	2.88	-	801.8
AHQ-1-13- , 4039	K.MVVESAYEVIK.L	1268.50463	2	4.47E-06	0.86	3.10	-	868.6
AHQ-1-14- , 6532	K.SLADELALVDVLEDK.L	1630.81843	2	3.58E-05	0.93	3.44	-	1455.5
AHQ-1-13- , 6780 - 6783	K.SLADELALVDVLEDK.L	1630.81843	2	5.20E-08	0.96	5.37	-	1374.0
AHQ-1-9, 6932 - 6938	K.SLADELALVDVLEDK.L	1630.81843	2	1.71E-04	0.96	4.48	-	1652.7
AHQ-1-9, 6506	K.SLADELALVDVLEDK.L	1630.81843	2	1.71E-04	0.80	2.87	-	872.3
AHQ-1-11, 6239 - 6246	K.SLADELALVDVLEDK.L	1630.81843	2	8.34E-06	0.86	3.96	-	716.9
AHQ-1-13, 6331	K.SLADELALVDVLEDK.L	1630.81843	2	4.39E-08	0.97	5.22	-	1483.1
AHQ-1-14- , 6603 - 6631	K.SLADELALVDVLEDKLK.G	1872.14959	2	3.52E-06	0.93	3.96	-	1196.0
AHQ-1-9, 7094 - 7172	K.SLADELALVDVLEDKLK.G	1872.14959	2	1.14E-05	0.84	3.42	-	745.7
gi|4759096|ref|NP_004252.1| 15 kDa selenoprotein [Homo sapiens]				2.17E-11	0.93	10.24	9.90	17640.3
AHQ-1-13, 5824	K.LLDDNGNIAEELSILK.W	1757.96344	2	8.87E-09	0.97	4.84	-	1416.0
AHQ-1-12, 5855 - 5886	K.LLDDNGNIAEELSILK.W	1757.96344	2	2.17E-11	0.93	4.30	-	872.4
gi|13775198|ref|NP_112576.1| SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr				2.22E-11	4.17	50.27	34.40	10437.7
AHQ-1-13- , 4920 - 4987	R.IQYQLVDISQDNALR.D	1776.97168	2	3.69E-11	0.98	5.19	-	2176.7
AHQ-1-14- , 4726 - 4804	R.IQYQLVDISQDNALR.D	1776.97168	2	2.48E-08	0.98	5.35	-	2015.8
AHQ-1-13- , 4823	R.IQYQLVDISQDNALR.D	1776.97168	2	2.22E-11	0.97	5.05	-	1824.6
AHQ-1-14, 5573 - 5584	R.IQYQLVDISQDNALR.D	1776.97168	2	7.08E-09	0.98	5.36	-	2097.5
AHQ-1-13, 4588	R.IQYQLVDISQDNALR.D	1776.97168	2	7.48E-04	0.94	4.08	-	1372.6
AHQ-1-13, 4675 - 4735	R.IQYQLVDISQDNALR.D	1776.97168	2	8.78E-06	0.97	5.13	-	1546.2
AHQ-1-13, 4685	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	9.97E-04	0.87	3.60	-	755.5
AHQ-1-13, 4447	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.29E-07	0.56	3.03	-	419.9
AHQ-1-13, 4159 - 4239	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	4.53E-08	0.87	4.26	-	609.3
AHQ-1-13- , 5255 - 5284	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	3.90E-06	0.79	3.38	-	836.3
AHQ-1-13- , 5241 - 5245	R.IQYQLVDISQDNALRDEMR.A	2308.55751	2	5.95E-04	0.89	4.08	-	617.1
AHQ-1-13- , 5119 - 5188	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	6.74E-06	0.88	3.45	-	965.7
AHQ-1-13- , 4981 - 5053	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	6.66E-06	0.71	3.66	-	459.3
AHQ-1-13- , 4351	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	5.39E-04	0.78	3.48	-	380.9
AHQ-1-14- , 5000 - 5063	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	6.23E-08	0.87	3.92	-	790.8
AHQ-1-13- , 4656 - 4719	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	7.78E-06	0.83	4.18	-	429.6
AHQ-1-14- , 4599	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.72E-07	0.73	3.04	-	691.7
AHQ-1-13- , 4825	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.89E-04	0.58	3.20	-	284.0
AHQ-1-13- , 4555 - 4557	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.68E-06	0.75	3.45	-	518.1
AHQ-1-14- , 1816	R.VYSTSVTGSR.E	1057.13940	2	8.18E-06	0.86	2.85	-	933.6
AHQ-1-13- , 2008	R.VYSTSVTGSR.E	1057.13940	2	5.67E-05	0.91	2.60	-	1337.2
AHQ-1-13- , 1883 - 1948	R.VYSTSVTGSR.E	1057.13940	2	1.34E-05	0.95	3.95	-	1270.8
AHQ-1-13- , 1759 - 1825	R.VYSTSVTGSR.E	1057.13940	2	7.21E-06	0.89	2.94	-	936.2
AHQ-1-13, 1958 - 2038	R.VYSTSVTGSR.E	1057.13940	2	1.80E-06	0.86	3.03	-	848.9
AHQ-1-13- , 1623 - 1703	R.VYSTSVTGSR.E	1057.13940	2	1.61E-05	0.83	2.64	-	826.0
AHQ-1-13, 2363	R.VYSTSVTGSREIK.S	1427.58510	2	3.10E-05	0.82	3.11	-	797.4
AHQ-1-13- , 2316	R.VYSTSVTGSREIK.S	1427.58510	2	1.07E-05	0.59	3.00	-	565.6
AHQ-1-14- , 2291	R.VYSTSVTGSREIK.S	1427.58510	2	6.05E-04	0.64	2.80	-	551.4
gi|4506005|ref|NP_002700.1| protein phosphatase 1, catalytic subunit, beta isoform [Homo sapiens] [				2.35E-11	2.88	30.30	16.50	37186.6
AHQ-1-9, 7230 - 7232	R.EIFLSQPILLELEAPLK.I	1954.33857	2	2.15E-07	0.96	5.77	-	707.9
AHQ-1-14- , 6671	R.EIFLSQPILLELEAPLK.I	1954.33857	2	2.74E-05	0.94	4.55	-	781.4
AHQ-1-13- , 6919	R.EIFLSQPILLELEAPLK.I	1954.33857	2	5.49E-08	0.95	5.01	-	700.4
AHQ-1-12, 6601	R.EIFLSQPILLELEAPLK.I	1954.33857	2	2.87E-07	0.95	5.38	-	598.7
AHQ-1-9, 5263	K.IFCCHGGLSPDLQSMEQIR.R	2251.54930	3	2.08E-05	0.89	4.38	-	1236.4
AHQ-1-9, 5259	K.IFCCHGGLSPDLQSMEQIR.R	2251.54930	2	1.24E-05	0.96	4.74	-	1480.4
AHQ-1-9, 7163 - 7164	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	2.44E-06	0.98	6.06	-	1212.3
AHQ-1-9, 7004	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	2.35E-11	0.97	4.57	-	1423.8
gi|4504349|ref|NP_000509.1| beta globin [Homo sapiens]				2.36E-11	8.99	100.28	70.70	15998.3
AHQ-1-13- , 3105 - 3175	K.EFTPPVQAAYQK.V	1379.54213	2	5.05E-07	0.82	2.85	-	680.1
AHQ-1-14- , 5046 - 5047	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	3.36E-07	0.95	5.14	-	850.1
AHQ-1-13- , 5732	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.15E-06	0.95	4.84	-	864.5
AHQ-1-13, 5499	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	8.83E-05	0.86	3.29	-	844.0
AHQ-1-13, 5403	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.07E-04	0.92	4.41	-	616.8
AHQ-1-13, 4903	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	5.89E-05	0.92	3.53	-	1545.4
AHQ-1-13- , 5140 - 5151	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	6.83E-05	0.90	4.29	-	598.5
AHQ-1-13, 3519 - 3525	K.GTFATLSELHCDK.L	1480.62492	2	3.80E-09	0.84	3.42	-	627.8
AHQ-1-13- , 3615	K.GTFATLSELHCDK.L	1480.62492	2	2.32E-08	0.77	3.40	-	496.6
AHQ-1-13- , 5173 - 5200	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	2.36E-11	0.96	5.38	-	1052.0
AHQ-1-13, 4885	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	3.06E-09	0.95	5.18	-	1133.8
AHQ-1-13, 4905	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	2	2.34E-06	0.76	3.04	-	561.7
AHQ-1-13- , 4963 - 5017	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	5.06E-06	0.94	4.46	-	1096.9
AHQ-1-13- , 4969	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	7.21E-06	0.93	4.99	-	908.2
AHQ-1-13- , 3584	K.SAVTALWGK.V	933.08624	2	6.18E-05	0.90	3.01	-	817.4
AHQ-1-13, 3474	K.SAVTALWGK.V	933.08624	2	1.58E-04	0.76	2.60	-	699.3
AHQ-1-13, 4999 - 5056	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	7.13E-11	0.97	5.65	-	1688.3
AHQ-1-13, 4767 - 4841	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.27E-10	0.97	4.91	-	1850.9
AHQ-1-13- , 5300	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	1.60E-07	0.84	3.50	-	596.9
AHQ-1-13- , 5111	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.97E-10	0.97	5.20	-	1548.1
AHQ-1-13- , 5293	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	3.92E-07	0.95	4.50	-	1393.9
AHQ-1-13- , 3345	K.VNVDEVGGEALGR.L	1315.41484	1	2.28E-05	0.46	2.51	-	360.1
AHQ-1-13- , 3343	K.VNVDEVGGEALGR.L	1315.41484	2	1.85E-04	0.97	4.52	-	1919.3
AHQ-1-13- , 3349	K.VNVDEVGGEALGR.L	1315.41484	1	2.81E-07	0.73	3.40	-	337.2
AHQ-1-13, 3273 - 3275	K.VNVDEVGGEALGR.L	1315.41484	1	9.10E-05	0.61	2.81	-	347.2
AHQ-1-13- , 2535 - 2543	K.VVAGVANALAHK.Y	1150.35593	2	7.77E-08	0.93	3.15	-	1455.5
gi|24119203|ref|NP_705935.1| tropomyosin 3 [Homo sapiens]				2.46E-11	5.63	60.29	20.20	29032.5
AHQ-1-9, 2278	R.AREQAEAEVASLNR.R	1544.65218	2	9.03E-06	0.98	5.70	-	3481.3
AHQ-1-1, 3887 - 3903	R.IQLVEEELDR.A	1244.37653	2	8.34E-05	0.79	2.66	-	643.8
AHQ-1-13- , 3827 - 3840	R.IQLVEEELDR.A	1244.37653	2	1.02E-06	0.90	3.70	-	843.0
AHQ-1-11, 3515	R.IQLVEEELDR.A	1244.37653	2	2.79E-05	0.87	2.94	-	969.8
AHQ-1-10, 3408 - 3425	R.IQLVEEELDR.A	1244.37653	2	8.76E-08	0.92	3.75	-	1017.8
AHQ-1-9, 3538	R.IQLVEEELDR.A	1244.37653	1	9.35E-04	0.71	2.94	-	682.4
AHQ-1-9, 3528 - 3598	R.IQLVEEELDR.A	1244.37653	1	1.80E-05	0.60	2.74	-	578.7
AHQ-1-9, 3510 - 3590	R.IQLVEEELDR.A	1244.37653	2	2.59E-07	0.91	3.63	-	855.9
AHQ-1-13- , 3829	R.IQLVEEELDR.A	1244.37653	1	8.14E-06	0.43	2.41	-	384.6
AHQ-1-10, 2672	K.IQVLQQQADDAEER.A	1643.73738	2	6.38E-07	0.96	4.29	-	1460.5
AHQ-1-9, 2706	K.IQVLQQQADDAEER.A	1643.73738	2	1.33E-08	0.97	4.51	-	1878.9
AHQ-1-9, 2423	R.KIQVLQQQADDAEER.A	1771.91030	2	6.49E-08	0.97	4.86	-	1724.3
AHQ-1-9, 2523	R.KIQVLQQQADDAEER.A	1771.91030	2	3.32E-05	0.96	4.90	-	1332.3
AHQ-1-9, 2427 - 2440	R.KIQVLQQQADDAEER.A	1771.91030	3	2.46E-11	0.98	5.30	-	2262.3
AHQ-1-10, 2449	R.KIQVLQQQADDAEER.A	1771.91030	2	4.38E-04	0.96	4.98	-	1225.9
AHQ-1-10, 3131	R.RIQLVEEELDR.A	1400.56288	2	2.57E-07	0.98	5.23	-	2012.3
AHQ-1-9, 3019 - 3026	K.TIDDLEDKLK.C	1190.32563	2	2.08E-05	0.81	3.07	-	639.6

gi|4506877|ref|NP_002996.1| selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;				2.52E-11	11.31	130.26	27.50	90844.7
AHQ-1-3, 4881 - 4895	K.AVQCQHLEAPSEGTM*DCVHPLTAFAYGSSCK.F	3472.80519	3	4.54E-10	0.94	5.24	-	900.3
AHQ-1-3, 6673	R.CDNLGQWTAPAPVCQALQCQDLPVPNEAR.V	3313.64431	3	4.75E-04	0.59	3.32	-	473.6
AHQ-1-4, 6852	R.CDNLGQWTAPAPVCQALQCQDLPVPNEAR.V	3313.64431	3	6.57E-06	0.83	4.23	-	604.8
AHQ-1-3, 5965	R.CIDSGHWSAPLPTCEAISCEPLESPVHGSM*DCSPSLR.A	4162.54346	3	1.28E-06	0.90	4.64	-	732.0
AHQ-1-3, 4591 - 4646	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	5.17E-04	0.91	4.15	-	536.2
AHQ-1-3, 2290 - 2294	K.FECQPGYR.V	1058.14914	2	5.24E-04	0.66	2.60	-	555.7
AHQ-1-3, 5953	K.LECLASGIWTNKPPQCLAAQCPPLK.I	2857.31818	3	2.52E-11	0.91	4.51	-	896.3
AHQ-1-3, 6153 - 6194	K.LECLASGIWTNKPPQCLAAQCPPLKIPER.G	3352.89300	3	1.09E-09	0.93	4.82	-	1211.0
AHQ-1-3, 3141	R.PSGQWTAVTPACR.A	1432.58672	2	1.65E-05	0.94	3.79	-	1080.3
AHQ-1-1, 4999	K.STCQFICDEGYSLSGPER.L	2109.23671	2	3.69E-06	0.87	3.21	-	982.6
AHQ-1-3, 4958 - 4961	K.STCQFICDEGYSLSGPER.L	2109.23671	2	2.91E-09	0.92	3.44	-	1110.4
AHQ-1-4, 5056	K.STCQFICDEGYSLSGPER.L	2109.23671	2	1.64E-06	0.89	3.96	-	703.9
AHQ-1-3, 6367 - 6379	K.VLPYYSSYYWIGIR.K	1781.04522	2	6.34E-09	0.88	4.08	-	450.6
AHQ-1-3, 2491	R.WSATPPTCK.G	1049.18216	2	6.18E-05	0.79	2.76	-	674.9
AHQ-1-3, 3949	R.WTDSPPMCEAIK.C	1436.63555	2	2.58E-06	0.80	2.79	-	558.2
AHQ-1-3, 2906 - 2913	R.YTDLVAIQNK.N	1165.32100	1	9.83E-04	0.62	2.86	-	697.4
AHQ-1-3, 2907	R.YTDLVAIQNK.N	1165.32100	2	1.11E-05	0.92	2.93	-	1276.9
gi|5031569|ref|NP_005727.1| ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r				2.63E-11	1.90	20.28	10.60	42613.4
AHQ-1-8, 3976	R.ACYLSINPQKDETLETEK.A	2141.34169	2	7.82E-05	0.94	4.52	-	794.1
AHQ-1-8, 5371 - 5384	K.DQLQTFSEEHPVLLTEAPLNPR.K	2535.79382	2	2.63E-11	0.96	5.57	-	853.0
gi|22749499|ref|NP_689979.1| hypothetical protein MGC40107 [Homo sapiens]				2.68E-11	0.97	10.29	24.80	11741.6
AHQ-1-14- , 5646 - 5648	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	2.68E-11	0.97	5.90	-	1551.7
gi|17986283|ref|NP_006000.2| tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu				2.95E-11	0.95	10.26	3.30	50135.3
AHQ-1-3, 5946	R.AVFVDLEPTVIDEVR.T	1702.92947	2	5.26E-09	0.95	4.87	-	877.4
AHQ-1-4, 6072	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.33E-07	0.96	4.37	-	1506.2
AHQ-1-7, 5906 - 5984	R.AVFVDLEPTVIDEVR.T	1702.92947	2	2.95E-11	0.95	5.24	-	685.9
AHQ-1-9, 5740	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.77E-06	0.83	3.69	-	612.4
AHQ-1-12, 5517	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.37E-05	0.93	4.19	-	1009.9
AHQ-1-14- , 5628 - 5659	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.78E-08	0.92	4.75	-	702.1
AHQ-1-1, 5943 - 5952	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.65E-06	0.88	4.34	-	605.0
gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				3.29E-11	17.42	200.29	38.70	55901.8
AHQ-1-7, 2284	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.28E-08	0.92	4.03	-	947.5
AHQ-1-11, 2344	K.AHYGGFTVQNEANK.Y	1536.63020	2	9.03E-07	0.92	4.16	-	676.2
AHQ-1-9, 2226	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.39E-06	0.96	4.20	-	1396.7
AHQ-1-6, 2278	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.89E-07	0.95	4.06	-	1277.3
AHQ-1-8, 2176	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.01E-05	0.93	3.64	-	1080.3
AHQ-1-7, 3213	R.DNDGWLTSDPR.K	1276.29403	2	6.90E-05	0.88	3.32	-	850.8
AHQ-1-6, 3422	K.DNENVVNEYSSELEK.H	1769.80167	2	3.79E-09	0.79	3.31	-	486.6
AHQ-1-3, 4298	K.DNENVVNEYSSELEK.H	1769.80167	2	1.99E-06	0.90	4.28	-	699.6
AHQ-1-9, 4172 - 4184	K.DNENVVNEYSSELEK.H	1769.80167	2	6.81E-10	0.89	3.88	-	734.3
AHQ-1-13- , 4225	K.DNENVVNEYSSELEK.H	1769.80167	2	7.44E-04	0.84	3.58	-	647.9
AHQ-1-13, 4061	K.DNENVVNEYSSELEK.H	1769.80167	2	4.61E-05	0.84	3.75	-	625.7
AHQ-1-6, 4091 - 4174	K.DNENVVNEYSSELEK.H	1769.80167	2	1.89E-05	0.67	3.48	-	587.0
AHQ-1-9, 4432	K.DNENVVNEYSSELEK.H	1769.80167	2	4.73E-05	0.80	3.44	-	681.3
AHQ-1-7, 3766	K.DNENVVNEYSSELEK.H	1769.80167	2	6.24E-06	0.94	4.37	-	989.6
AHQ-1-12, 4054	K.DNENVVNEYSSELEK.H	1769.80167	2	1.35E-06	0.74	2.94	-	727.2
AHQ-1-7, 3461 - 3534	K.DNENVVNEYSSELEK.H	1769.80167	2	4.35E-06	0.60	3.04	-	475.3
AHQ-1-8, 4189	K.DNENVVNEYSSELEK.H	1769.80167	2	5.11E-04	0.82	3.36	-	765.2
AHQ-1-7, 4220 - 4288	K.DNENVVNEYSSELEK.H	1769.80167	2	3.67E-08	0.94	4.66	-	931.5
AHQ-1-1, 4321	K.DNENVVNEYSSELEK.H	1769.80167	2	2.24E-05	0.85	3.74	-	742.5
AHQ-1-8, 4072	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	4.62E-06	0.73	3.16	-	756.8
AHQ-1-8, 4081	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	4.00E-07	0.90	4.48	-	547.0
AHQ-1-9, 4043	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.58E-05	0.84	3.75	-	490.7
AHQ-1-7, 4164	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	8.45E-05	0.79	3.51	-	550.0
AHQ-1-7, 4156	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	3.53E-05	0.86	3.88	-	927.3
AHQ-1-7, 4150	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	2.53E-06	0.73	3.41	-	363.8
AHQ-1-6, 4110 - 4119	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	9.69E-08	0.85	3.90	-	842.6
AHQ-1-6, 3619 - 3626	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	3	1.49E-07	0.87	3.90	-	881.7
AHQ-1-6, 4118	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.45E-06	0.86	4.11	-	492.6
AHQ-1-7, 3669	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	9.60E-04	0.33	2.99	-	278.2
AHQ-1-7, 3670	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	3	1.43E-05	0.77	3.30	-	899.6
AHQ-1-9, 4031	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	1.88E-07	0.85	3.13	-	1313.0
AHQ-1-11, 4068	K.HGTDDGVVWMNWK.G	1545.70374	2	7.81E-05	0.94	4.00	-	1044.4
AHQ-1-7, 4312	K.HGTDDGVVWMNWK.G	1545.70374	2	1.01E-05	0.93	3.67	-	1181.9
AHQ-1-6, 3183	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	4.95E-05	0.87	4.27	-	876.2
AHQ-1-8, 3086	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	5.17E-05	0.74	3.52	-	670.6
AHQ-1-6, 3651	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	2.58E-05	0.94	4.60	-	1148.4
AHQ-1-7, 3217	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	3.73E-04	0.87	4.38	-	625.3
AHQ-1-9, 3490	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	9.01E-04	0.71	3.26	-	443.9
AHQ-1-6, 3646 - 3727	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.09E-09	0.93	5.45	-	756.1
AHQ-1-8, 3405	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	3.91E-04	0.84	3.78	-	732.0
AHQ-1-7, 3666 - 3736	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	2.70E-10	0.85	3.98	-	689.2
AHQ-1-7, 2744	K.KREEAPSLRPAPPPISGGGYR.A	2236.51908	3	2.27E-06	0.92	3.57	-	1378.6
AHQ-1-6, 2547	K.LESDVSAQM*EYCR.T	1605.72945	2	3.08E-07	0.72	2.90	-	497.5
AHQ-1-7, 2561	K.LESDVSAQM*EYCR.T	1605.72945	2	2.31E-04	0.79	2.96	-	674.6
AHQ-1-11, 5887 - 5924	R.M*GPTELLIEMEDWK.G	1708.97776	2	3.84E-06	0.93	3.99	-	1036.7
AHQ-1-7, 6660 - 6678	R.M*GPTELLIEMEDWK.G	1708.97776	2	3.46E-08	0.95	4.39	-	1365.3
AHQ-1-7, 7189 - 7196	R.MGPTELLIEMEDWK.G	1692.97836	2	2.47E-07	0.96	4.48	-	1273.2
AHQ-1-9, 6507	R.M*GPTELLIEMEDWK.G	1708.97776	2	1.38E-07	0.93	3.77	-	1205.7
AHQ-1-7, 4957 - 5037	R.M*GPTELLIEM*EDWK.G	1724.97716	2	1.22E-04	0.80	3.21	-	736.3
AHQ-1-8, 7150	R.MGPTELLIEMEDWK.G	1692.97836	2	6.61E-06	0.89	3.46	-	883.3
AHQ-1-10, 5772 - 5788	R.M*GPTELLIEMEDWK.G	1708.97776	2	5.96E-05	0.91	4.00	-	953.1
AHQ-1-6, 7035	R.MGPTELLIEMEDWK.G	1692.97836	2	3.73E-05	0.92	3.87	-	1128.6
AHQ-1-6, 6526 - 6534	R.M*GPTELLIEMEDWK.G	1708.97776	2	1.89E-05	0.95	4.11	-	1297.1
AHQ-1-7, 5996	K.NYCGLPGEYWLGNDK.I	1787.92994	2	1.13E-04	0.83	3.86	-	273.1
AHQ-1-6, 5276	K.NYCGLPGEYWLGNDK.I	1787.92994	2	3.29E-05	0.84	3.60	-	390.7
AHQ-1-11, 4875	K.NYCGLPGEYWLGNDK.I	1787.92994	2	1.19E-05	0.71	3.09	-	322.8
AHQ-1-7, 3892 - 3914	R.TPCTVSCNIPVVSGK.E	1621.85811	2	6.55E-07	0.66	3.09	-	403.0
AHQ-1-8, 3884	R.TPCTVSCNIPVVSGK.E	1621.85811	2	4.93E-05	0.61	2.80	-	692.2
AHQ-1-7, 5054 - 5068	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.58E-06	0.76	3.66	-	414.4
AHQ-1-7, 5052 - 5072	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.44E-05	0.93	4.36	-	1147.1
AHQ-1-6, 5008	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	7.04E-06	0.91	4.16	-	853.4
AHQ-1-1, 5156	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	6.11E-06	0.74	3.29	-	821.3
AHQ-1-6, 5006	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.24E-05	0.80	3.57	-	290.3
AHQ-1-8, 4991	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	7.99E-08	0.96	5.01	-	1537.7
AHQ-1-9, 4952	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.97E-06	0.90	3.78	-	1185.0
AHQ-1-9, 4924	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.08E-04	0.77	3.14	-	345.5
AHQ-1-9, 4596	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	5.10E-09	0.92	4.62	-	713.5
AHQ-1-7, 4109 - 4182	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	5.90E-06	0.88	3.78	-	780.2
AHQ-1-8, 4668	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	3.29E-11	0.93	4.56	-	759.7
AHQ-1-7, 4642 - 4668	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	6.27E-10	0.93	4.61	-	980.9
AHQ-1-7, 4736 - 4810	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	7.27E-10	0.96	4.84	-	1217.0
AHQ-1-6, 4043 - 4056	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	5.25E-07	0.95	4.77	-	973.0
AHQ-1-6, 4127	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	1.01E-05	0.94	3.98	-	1168.7
AHQ-1-6, 4594 - 4667	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	9.01E-09	0.96	4.98	-	1120.9
AHQ-1-12, 4937 - 4945	R.YYWGGQYTWDMAK.H	1669.84009	2	1.30E-05	0.92	3.70	-	850.6

AHQ-1-7, 5200 - 5204	R.YYWGGQYTWDMAK.H	1669.84009	2	6.33E-04	0.89	3.20	-	826.9
AHQ-1-10, 4140	R.YYWGGQYTWDM*AK.H	1685.83949	2	3.69E-05	0.91	3.83	-	968.2
AHQ-1-14- , 4567 - 4598	R.YYWGGQYTWDM*AK.H	1685.83949	2	2.86E-06	0.86	3.11	-	733.8
AHQ-1-14- , 5086 - 5090	R.YYWGGQYTWDMAK.H	1669.84009	2	2.30E-04	0.96	4.18	-	1444.8
AHQ-1-7, 5285	R.YYWGGQYTWDMAK.H	1669.84009	2	7.44E-04	0.93	3.31	-	1286.8
gi|5031601|ref|NP_005711.1| actin related protein 2/3 complex subunit 1B; ARP2/3 protein complex su				3.35E-11	5.21	60.25	21.50	40949.5
AHQ-1-9, 2254 - 2256	K.ASSEGGTAAGAGLDSLHK.N	1629.71071	2	4.70E-05	0.51	2.98	-	500.9
AHQ-1-9, 4136	K.ASSEGGTAAGAGLDSLHKNSVSQISVLSGGK.A	2887.10986	3	3.35E-11	0.91	4.70	-	1073.1
AHQ-1-9, 2426	K.EVEERPAPTPWGSK.M	1583.72678	2	7.44E-08	0.94	4.27	-	962.9
AHQ-1-9, 3286	K.NSVSQISVLSGGK.A	1276.42175	1	2.86E-06	0.16	1.98	-	270.8
AHQ-1-9, 2926	K.NSVSQISVLSGGK.A	1276.42175	2	2.21E-06	0.95	3.71	-	1347.4
AHQ-1-9, 3452	R.TQIAICPNNHEVHIYEK.S	2068.29887	2	3.15E-05	0.93	4.46	-	1007.1
AHQ-1-9, 3338 - 3352	R.TQIAICPNNHEVHIYEK.S	2068.29887	2	1.87E-07	0.95	5.00	-	894.4
AHQ-1-9, 3192	R.VAWVSHDSTVCLADADKK.M	2004.20995	2	2.25E-06	0.95	4.82	-	1049.4
gi|22043610|ref|XP_171081.1| similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1; rh				3.49E-11	2.73	30.28	24.00	21543.1
AHQ-1-11, 2755	R.HHCPNTPIILVGTK.L	1588.85612	3	7.29E-04	0.87	3.39	-	1257.5
AHQ-1-11, 3814 - 3815	K.KLTPITYPQGLAMAK.E	1632.99216	2	7.56E-05	0.88	3.89	-	645.7
AHQ-1-11, 4595	K.PVNLGLWDTAGQEDYDR.L	1950.05441	2	3.49E-11	0.98	5.64	-	2428.8
gi|21624607|ref|NP_066972.1| coactosin-like 1 [Homo sapiens]				3.53E-11	5.00	60.28	52.80	15944.9
AHQ-1-13, 2357	R.AAYNLVR.D	806.93245	2	4.34E-04	0.82	2.72	-	823.2
AHQ-1-12, 2215 - 2217	R.AAYNLVR.D	806.93245	2	1.06E-04	0.84	2.72	-	650.8
AHQ-1-13- , 5429 - 5445	R.DDGSAVIWVTFK.Y	1338.49001	2	2.40E-07	0.93	4.00	-	985.9
AHQ-1-13- , 5459	R.DDGSAVIWVTFK.Y	1338.49001	2	1.84E-06	0.95	3.74	-	1311.3
AHQ-1-13- , 4301	K.ELEEDFIKSELK.K	1480.64154	2	8.27E-04	0.60	3.05	-	448.3
AHQ-1-13, 6435	K.FALITWIGENVSGLQR.A	1805.06986	2	2.67E-08	0.97	5.55	-	1889.2
AHQ-1-13- , 2944	R.KELEEDFIK.S	1151.29110	2	9.47E-05	0.75	2.91	-	711.4
AHQ-1-13- , 2947	R.KELEEDFIK.S	1151.29110	1	6.14E-04	0.37	2.43	-	479.3
AHQ-1-13, 2905	R.KELEEDFIK.S	1151.29110	1	2.15E-04	0.59	2.73	-	523.2
AHQ-1-13, 2902 - 2906	R.KELEEDFIK.S	1151.29110	2	3.70E-04	0.80	3.02	-	767.5
AHQ-1-12, 2815	R.KELEEDFIK.S	1151.29110	2	4.23E-04	0.84	2.92	-	902.7
AHQ-1-13- , 5568	K.YDGSTIVPGEQGAEYQHFIQQCTDDVR.L	3116.27790	3	1.34E-08	0.60	3.13	-	306.6
AHQ-1-13, 5159 - 5221	K.YDGSTIVPGEQGAEYQHFIQQCTDDVR.L	3116.27790	3	3.53E-11	0.90	4.93	-	570.0
gi|4759300|ref|NP_004772.1| vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated				3.55E-11	2.85	30.28	33.00	11309.0
AHQ-1-14- , 3604	R.ADALQAGASQFETSAAK.L	1666.77095	2	8.72E-09	0.93	4.07	-	968.7
AHQ-1-13- , 3679	R.ADALQAGASQFETSAAK.L	1666.77095	2	3.55E-11	0.94	4.74	-	931.3
AHQ-1-13, 3558	R.ADALQAGASQFETSAAK.L	1666.77095	2	3.12E-04	0.86	3.59	-	720.4
AHQ-1-13- , 3835	R.LQQTQNQVDEVVDIM*R.V	1933.13344	3	4.54E-08	0.93	4.20	-	1347.5
AHQ-1-13- , 4889	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	7.78E-04	0.55	3.22	-	546.8
AHQ-1-13- , 5025	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	3.63E-08	0.98	5.51	-	2464.4
AHQ-1-13- , 3823 - 3831	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	5.39E-06	0.96	5.06	-	1295.2
AHQ-1-13, 4768	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	1.51E-07	0.98	5.56	-	1839.6
gi|4885413|ref|NP_005331.1| histidine triad nucleotide binding protein 1; Histidine triad nucleotid				3.83E-11	2.68	30.25	42.10	13801.8
AHQ-1-13, 5373 - 5387	R.CLAFHDISPQAPTHFLVIPK.K	2293.67220	3	4.93E-06	0.94	4.73	-	1354.6
AHQ-1-13- , 4005	R.MVVNEGSDGGQSVYHVHLHVLGGR.Q	2548.82255	3	3.83E-11	0.84	3.63	-	718.4
AHQ-1-13- , 2465	R.PGGDTIFGK.I	891.99098	2	1.76E-06	0.89	3.36	-	676.3
gi|7657056|ref|NP_055415.1| EH-domain containing 3; EH domain containing 3 [Homo sapiens]				4.16E-11	8.07	90.34	34.00	60886.7
AHQ-1-7, 2836 - 2866	K.ADQIETQQLMR.V	1333.49681	2	3.40E-05	0.89	3.23	-	1399.8
AHQ-1-7, 6365	R.DKPMYDEIFYTLSPVDGK.I	2119.37953	2	4.14E-05	0.96	5.21	-	1107.3
AHQ-1-7, 5941	R.FHEFHSPALEDADFDNKPMVLLVGQYSTGK.T	3394.75749	3	4.16E-11	0.97	6.62	-	1389.2
AHQ-1-10, 6385	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	3.99E-04	0.87	3.78	-	724.8
AHQ-1-8, 7478 - 7479	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	2.44E-04	0.95	4.78	-	1113.0
AHQ-1-7, 5741	K.GGAFEGTLHGPFGHGYGEGAGEGIDDAEWVVAR.D	3317.48513	3	2.68E-06	0.98	6.75	-	1966.3
AHQ-1-7, 6033	K.LADIDKDGMLDDDEFALANHLIK.V	2573.86063	3	5.07E-05	0.57	3.12	-	634.2
AHQ-1-7, 5045	K.LFEAEEQDLFR.D	1397.51432	2	8.08E-07	0.95	3.33	-	1825.7
AHQ-1-7, 2857 - 2865	R.MQDQLQAQDFSK.F	1439.57624	2	5.92E-04	0.95	4.63	-	1427.9
AHQ-1-8, 6158 - 6162	R.VYIGSFWSHPLLIPDNR.K	2015.30234	2	3.09E-04	0.91	3.58	-	1046.6
AHQ-1-7, 6333 - 6338	R.VYIGSFWSHPLLIPDNR.K	2015.30234	2	1.63E-05	0.85	3.71	-	547.1
gi|7661678|ref|NP_056461.1| RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B				4.20E-11	8.75	100.30	28.80	20824.7
AHQ-1-11, 4171	K.DTDDVPMILVGNK.C	1417.61048	2	2.20E-07	0.85	3.48	-	796.8
AHQ-1-11, 6206 - 6279	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	2.02E-08	0.95	4.63	-	1518.2
AHQ-1-14- , 6447 - 6512	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	2.89E-06	0.93	4.61	-	1180.8
AHQ-1-11, 6560	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	4.18E-09	0.94	5.33	-	839.9
AHQ-1-13- , 6689 - 6759	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	4.78E-06	0.91	4.23	-	1386.8
AHQ-1-14- , 5268	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	2.19E-08	0.95	5.04	-	1339.6
AHQ-1-11, 6516 - 6590	K.QVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3019.33197	3	3.05E-04	0.73	3.26	-	644.2
AHQ-1-11, 3868 - 3927	R.QWNNCAFLESSAK.S	1556.68148	2	3.15E-05	0.51	2.86	-	394.2
AHQ-1-11, 3986 - 4058	R.QWNNCAFLESSAK.S	1556.68148	2	4.85E-05	0.55	2.89	-	204.5
AHQ-1-11, 3607 - 3620	R.VKDTDDVPMILVGNK.C	1644.91497	3	6.50E-06	0.94	4.34	-	1691.5
AHQ-1-11, 3598 - 3658	R.VKDTDDVPMILVGNK.C	1644.91497	2	4.41E-10	0.97	5.09	-	1904.1
AHQ-1-13- , 4003	R.VKDTDDVPMILVGNK.C	1644.91497	2	3.23E-07	0.97	5.13	-	1489.1
AHQ-1-13, 3839	R.VKDTDDVPMILVGNK.C	1644.91497	2	9.29E-06	0.98	4.89	-	1957.2
AHQ-1-12, 3759	R.VKDTDDVPMILVGNK.C	1644.91497	2	7.37E-07	0.97	4.71	-	1772.8
AHQ-1-11, 3202	R.VKDTDDVPM*ILVGNK.C	1660.91437	3	2.21E-04	0.89	3.77	-	1323.1
AHQ-1-11, 3218 - 3254	R.VKDTDDVPM*ILVGNK.C	1660.91437	2	1.37E-04	0.96	4.78	-	1229.9
AHQ-1-14- , 3900 - 3914	R.VKDTDDVPMILVGNK.C	1644.91497	2	3.45E-06	0.96	4.27	-	1534.0
AHQ-1-13- , 4012	R.VKDTDDVPMILVGNK.C	1644.91497	3	3.04E-06	0.95	4.56	-	1931.5
AHQ-1-11, 4351	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	7.35E-06	0.80	3.38	-	481.4
AHQ-1-11, 4278 - 4358	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	8.43E-09	0.93	4.79	-	1057.7
AHQ-1-13, 4073	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	1.08E-04	0.87	4.46	-	680.9
AHQ-1-14, 5009	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	2.29E-04	0.87	4.24	-	825.8
AHQ-1-11, 4200 - 4258	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	2.72E-05	0.85	3.21	-	892.0
AHQ-1-11, 4148 - 4219	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	4.20E-11	0.97	5.96	-	1809.7
AHQ-1-13- , 4612	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	3.15E-05	0.93	4.51	-	1010.3
AHQ-1-11, 4020 - 4092	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	7.39E-10	0.94	5.16	-	1557.4
AHQ-1-11, 3916	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	2	7.31E-04	0.79	3.38	-	524.5
AHQ-1-11, 3906 - 3954	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	9.85E-05	0.83	3.86	-	861.2
AHQ-1-11, 4378	R.VKDTDDVPMILVGNKCDLEDERVVGK.E	2947.33182	3	8.34E-08	0.93	5.30	-	1273.5
gi|20149570|ref|NP_005816.2| RAS guanyl releasing protein 2 isoform 1; calcium and diacylglycerol-r				4.53E-11	1.84	20.21	6.30	75547.0
AHQ-1-6, 5419	K.ILFQDYHSFVTHGCTVDNPVLER.F	2750.03824	3	4.53E-11	0.92	4.14	-	1030.0
AHQ-1-6, 6838	K.LWEGLTELVTATGNYGNYR.R	2158.35558	2	5.91E-04	0.92	3.40	-	1416.1
gi|5803225|ref|NP_006752.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon poly				4.64E-11	1.55	20.28	11.80	29173.7
AHQ-1-9, 6983 - 6986	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	4.64E-11	0.93	4.48	-	909.7
AHQ-1-10, 6183	K.AAFDDAIAELDTLSEESYK.D	2089.19882	3	1.06E-05	0.75	3.27	-	695.9
AHQ-1-10, 6179 - 6180	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	2.72E-07	0.97	5.05	-	1431.2
AHQ-1-13, 6263 - 6339	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	1.19E-08	0.98	5.64	-	1633.5
AHQ-1-10, 2464	K.EAAENSLVAYK.A	1195.30397	2	2.10E-05	0.62	3.02	-	698.2
AHQ-1-9, 2663	K.EAAENSLVAYK.A	1195.30397	1	7.05E-10	0.62	2.42	-	360.9
gi|5902128|ref|NP_008880.1| syntaxin binding protein 2; Hunc18b [Homo sapiens]				4.65E-11	9.20	100.27	25.10	66438.1
AHQ-1-6, 6418	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	2	4.65E-11	0.97	5.49	-	1143.1
AHQ-1-6, 6422 - 6438	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	3	1.73E-06	0.95	5.36	-	951.6
AHQ-1-6, 6694 - 6695	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	6.10E-07	0.92	4.32	-	838.8
AHQ-1-14- , 6351	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	7.45E-07	0.75	3.04	-	648.7
AHQ-1-6, 3175	R.KGPEDTAQLAHAVLAK.L	1649.87303	3	4.84E-06	0.96	5.10	-	1710.2
AHQ-1-6, 3180	R.KGPEDTAQLAHAVLAK.L	1649.87303	2	1.27E-10	0.85	3.52	-	718.9
AHQ-1-6, 3716	K.LCSVEQDLAM*GSDAEGEK.I	1957.08386	2	3.41E-10	0.95	4.15	-	1436.7
AHQ-1-6, 2332	K.LIQHANVQAHSSLIR.N	1687.92773	2	9.28E-08	0.95	4.34	-	1442.0
AHQ-1-6, 6488	K.LIVPVLLDAAVPAYDK.I	1698.03911	2	8.04E-11	0.97	4.59	-	2154.8

AHQ-1-6, 5542	R.NLWPFVSDPAPTASSQAAVSAR.F	2273.48981	2	1.13E-04	0.81	3.66	-	437.8
AHQ-1-6, 6044 - 6124	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	4.14E-04	0.96	5.06	-	1417.5
AHQ-1-6, 4858 - 4928	K.WEVLIGSSHILTPTR.F	1709.97007	2	2.25E-09	0.96	4.57	-	1333.2
AHQ-1-6, 2032	R.YETTGLSEAR.E	1127.18649	2	1.08E-04	0.85	2.54	-	815.5
gi|6005942|ref|NP_009057.1| valosin-containing protein; yeast Cdc48p homolog; transitional endoplas				4.74E-11	8.42	100.28	18.90	89321.3
AHQ-1-5, 4146 - 4219	K.AIANECQANFISIK.G	1580.78762	2	6.66E-05	0.81	3.87	-	827.5
AHQ-1-5, 3781	R.ELQELVQYPVEHPDK.F	1825.01157	2	1.12E-04	0.90	4.18	-	671.0
AHQ-1-5, 3789 - 3790	R.ELQELVQYPVEHPDK.F	1825.01157	3	1.72E-04	0.73	3.31	-	707.7
AHQ-1-5, 3631	R.GILLYGPPGTGK.T	1173.38627	2	8.86E-04	0.63	3.01	-	646.9
AHQ-1-5, 6945	R.IVSQLLTLMDGLK.Q	1431.76657	2	2.47E-08	0.97	4.72	-	1466.3
AHQ-1-5, 5895 - 5897	R.LDQLIYIPLPDEK.S	1557.81228	2	2.80E-06	0.85	3.71	-	651.4
AHQ-1-5, 3055	R.LEILQIHTK.N	1095.31705	1	2.66E-06	0.60	2.51	-	452.8
AHQ-1-5, 5155 - 5225	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	1.09E-04	0.97	5.67	-	879.5
AHQ-1-5, 7433 - 7434	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	4.74E-11	0.96	4.97	-	1275.3
AHQ-1-5, 5079	K.VVETDPSPYCIVAPDTVIHCEGEPIKR.E	3085.45473	3	2.42E-09	0.84	4.03	-	385.8
AHQ-1-5, 3491	R.WALSQSNPSALR.E	1330.47434	2	7.77E-06	0.90	3.75	-	1069.6
gi|4501893|ref|NP_001094.1| actinin, alpha 2 [Homo sapiens]				5.16E-11	9.18	100.28	11.40	103853.1
AHQ-1-4, 4695	K.AGTQIENIEEDFR.N	1522.59861	2	5.27E-04	0.81	3.25	-	775.5
AHQ-1-5, 5121 - 5189	K.CQLEINFNTLQTK.L	1610.81373	2	1.75E-09	0.98	5.54	-	1400.5
AHQ-1-6, 5027 - 5100	K.CQLEINFNTLQTK.L	1610.81373	2	5.68E-04	0.85	2.92	-	1037.4
AHQ-1-4, 5195 - 5196	K.CQLEINFNTLQTK.L	1610.81373	2	1.87E-09	0.96	4.65	-	1447.1
AHQ-1-1, 5140	K.CQLEINFNTLQTK.L	1610.81373	2	6.82E-07	0.90	4.12	-	663.9
AHQ-1-5, 4965	K.EGLLLWCQR.K	1176.37031	2	5.43E-06	0.94	3.62	-	1030.8
AHQ-1-9, 4123 - 4202	R.FAIQDISVEETSAK.E	1538.68108	2	1.53E-09	0.96	4.70	-	1215.8
AHQ-1-3, 4347	R.FAIQDISVEETSAK.E	1538.68108	2	1.15E-04	0.91	3.44	-	1031.2
AHQ-1-7, 4281 - 4293	R.FAIQDISVEETSAK.E	1538.68108	2	4.39E-04	0.79	3.41	-	604.6
AHQ-1-2, 4514	R.FAIQDISVEETSAK.E	1538.68108	2	9.84E-04	0.78	2.75	-	883.9
AHQ-1-6, 4211 - 4215	R.FAIQDISVEETSAK.E	1538.68108	2	5.14E-06	0.95	3.95	-	1404.1
AHQ-1-10, 3900	R.FAIQDISVEETSAK.E	1538.68108	2	1.56E-04	0.68	2.75	-	730.7
AHQ-1-1, 4383 - 4399	R.FAIQDISVEETSAK.E	1538.68108	2	8.92E-04	0.89	2.99	-	1132.6
AHQ-1-4, 4391	R.FAIQDISVEETSAK.E	1538.68108	2	4.64E-09	0.92	3.57	-	1094.7
AHQ-1-13, 4124 - 4183	R.FAIQDISVEETSAK.E	1538.68108	2	9.20E-05	0.86	3.47	-	794.7
AHQ-1-5, 4265 - 4333	R.FAIQDISVEETSAK.E	1538.68108	2	5.90E-07	0.96	3.98	-	1601.7
AHQ-1-5, 4150	R.FAIQDISVEETSAK.E	1538.68108	2	5.52E-05	0.94	3.64	-	1488.3
AHQ-1-5, 6377	K.GYEEWLLNEIR.R	1422.56701	2	3.33E-07	0.94	3.33	-	1507.5
AHQ-1-1, 6132	K.GYEEWLLNEIR.R	1422.56701	2	1.37E-06	0.95	3.73	-	1410.7
AHQ-1-5, 6234	K.GYEEWLLNEIR.R	1422.56701	1	2.29E-05	0.39	2.34	-	270.3
AHQ-1-4, 5711	K.GYEEWLLNEIR.R	1422.56701	2	4.28E-07	0.93	3.39	-	1366.0
AHQ-1-6, 6108	K.GYEEWLLNEIR.R	1422.56701	2	1.90E-07	0.96	4.32	-	1679.4
AHQ-1-6, 5518	K.GYEEWLLNEIR.R	1422.56701	2	3.60E-07	0.92	2.92	-	1519.3
AHQ-1-5, 6225	K.GYEEWLLNEIR.R	1422.56701	1	6.45E-05	0.18	2.05	-	261.9
AHQ-1-4, 6276	K.GYEEWLLNEIR.R	1422.56701	2	5.23E-08	0.97	4.73	-	1711.8
AHQ-1-5, 5586	K.GYEEWLLNEIR.R	1422.56701	2	1.31E-05	0.90	3.27	-	1142.3
AHQ-1-5, 6222	K.GYEEWLLNEIR.R	1422.56701	2	2.22E-07	0.97	4.75	-	1809.5
AHQ-1-4, 2306	K.HEAFESDLAAHQDR.V	1626.66861	2	6.70E-08	0.97	4.31	-	2081.3
AHQ-1-5, 2153	K.HEAFESDLAAHQDR.V	1626.66861	2	5.16E-11	0.97	4.67	-	1493.3
AHQ-1-5, 2157 - 2158	K.HEAFESDLAAHQDR.V	1626.66861	3	1.66E-08	0.98	5.22	-	2148.4
AHQ-1-5, 3883	R.KAGTQIENIEEDFR.N	1650.77152	2	4.55E-07	0.91	4.08	-	698.8
AHQ-1-5, 1877 - 1955	R.KHEAFESDLAAHQDR.V	1754.84152	2	1.96E-07	0.95	3.83	-	1429.4
AHQ-1-6, 1867 - 1938	R.KHEAFESDLAAHQDR.V	1754.84152	2	9.57E-09	0.96	4.43	-	1447.7
AHQ-1-7, 1924	R.KHEAFESDLAAHQDR.V	1754.84152	2	4.37E-08	0.95	4.35	-	1160.9
AHQ-1-5, 4843 - 4845	K.LVSIGAEEIVDGNVK.M	1543.74400	2	7.31E-04	0.90	3.18	-	1104.5
AHQ-1-5, 4613 - 4683	K.LVSIGAEEIVDGNVK.M	1543.74400	2	2.14E-05	0.95	4.05	-	1099.1
AHQ-1-5, 4381 - 4457	K.LVSIGAEEIVDGNVK.M	1543.74400	2	8.08E-05	0.87	4.15	-	971.2
AHQ-1-5, 4249	K.LVSIGAEEIVDGNVK.M	1543.74400	2	3.10E-06	0.80	3.90	-	513.7
AHQ-1-5, 3469	K.TFTAWCNSHLR.K	1394.54018	2	5.93E-08	0.89	2.99	-	980.2
AHQ-1-6, 3456	K.TFTAWCNSHLR.K	1394.54018	2	3.66E-06	0.83	2.93	-	806.2
AHQ-1-5, 3590	K.TFTAWCNSHLR.K	1394.54018	2	2.01E-06	0.88	2.74	-	901.3
gi|4504391|ref|NP_000179.1| hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]				5.26E-11	7.15	90.24	14.10	102502.4
AHQ-1-4, 4610	K.ATDCVGHDVVTLLR.D	1557.75406	2	5.26E-11	0.88	3.43	-	857.5
AHQ-1-4, 2800 - 2803	K.FLSQIESDR.L	1095.18763	1	3.02E-05	0.20	2.21	-	207.2
AHQ-1-4, 2799	K.FLSQIESDR.L	1095.18763	2	4.80E-05	0.77	2.93	-	687.3
AHQ-1-4, 3372	K.GAALITAVGVR.L	1028.23070	2	2.11E-04	0.97	4.06	-	2501.8
AHQ-1-4, 5830 - 5834	K.GDFIALDLGGSSFR.I	1455.59700	2	8.60E-09	0.97	4.63	-	1857.9
AHQ-1-4, 2200 - 2252	R.HIDLVEGDEGR.M	1240.30483	2	5.42E-06	0.94	3.84	-	1091.7
AHQ-1-4, 5940	R.LGVEPSDDDCVSVQHVCTIVSFR.S	2622.86999	3	8.13E-06	0.67	3.80	-	223.8
AHQ-1-4, 6170	K.LPVGFTFSFPCQQSK.I	1744.99134	2	5.70E-06	0.96	4.82	-	1023.5
AHQ-1-5, 6117 - 6175	K.LPVGFTFSFPCQQSK.I	1744.99134	2	6.75E-04	0.90	3.84	-	659.7
AHQ-1-4, 2822	R.LVNEYSLNAGK.Q	1208.34588	1	1.75E-07	0.61	2.20	-	576.3
AHQ-1-4, 6387 - 6391	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	2.48E-10	0.95	4.47	-	1107.3
AHQ-1-4, 6303 - 6322	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	2.26E-07	0.95	4.45	-	954.0
gi|4557597|ref|NP_001449.1| gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);				5.60E-11	1.83	30.28	1.70	288897.4
AHQ-1-1, 4776 - 4800	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.98E-08	0.89	4.56	-	516.6
AHQ-1-8, 4255	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	1.43E-04	0.92	4.64	-	816.7
AHQ-1-7, 4508	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	7.56E-06	0.87	4.29	-	500.9
AHQ-1-6, 4499	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	2.04E-08	0.92	4.62	-	485.2
AHQ-1-6, 4487	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	5.11E-05	0.87	4.35	-	516.2
AHQ-1-4, 4734 - 4738	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.06E-07	0.93	5.16	-	701.4
AHQ-1-4, 4735	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	3.38E-07	0.94	5.02	-	474.5
AHQ-1-5, 4537	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	5.60E-11	0.96	5.57	-	689.3
AHQ-1-8, 4260	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	2.44E-07	0.95	5.19	-	571.4
AHQ-1-3, 1906 - 1978	K.IECDDKGDGSCDVR.Y	1628.67809	2	2.65E-06	0.78	3.17	-	623.2
AHQ-1-2, 2011	K.IECDDKGDGSCDVR.Y	1628.67809	3	6.17E-06	0.69	3.39	-	335.8
AHQ-1-4, 1907	K.IECDDKGDGSCDVR.Y	1628.67809	2	5.94E-04	0.67	2.79	-	517.5
AHQ-1-3, 2006 - 2115	K.NDNDTFTVK.Y	1054.09237	1	6.01E-05	0.09	1.87	-	174.2
gi|4885609|ref|NP_005408.1| v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen				5.68E-11	3.03	40.23	15.10	59834.4
AHQ-1-7, 7496	R.KEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL	3998.26826	3	2.11E-08	0.68	3.30	-	277.6
AHQ-1-7, 4153 - 4157	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	5.68E-11	0.95	4.61	-	1067.1
AHQ-1-7, 3872	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	4.27E-07	0.93	4.00	-	956.3
AHQ-1-7, 2538	R.LTTVCPTSKPQTQGLAK.D	1832.11198	2	8.36E-05	0.55	2.85	-	270.1
AHQ-1-7, 6574 - 6644	R.TQFNSLQQLVAYYSK.H	1790.99681	2	2.91E-06	0.95	4.14	-	1250.8
AHQ-1-7, 6426	R.TQFNSLQQLVAYYSK.H	1790.99681	2	3.06E-07	0.85	3.23	-	766.8
gi|4759212|ref|NP_004598.1| beta-tubulin cofactor A [Homo sapiens]				5.78E-11	3.81	40.32	26.90	12854.8
AHQ-1-13, 3526	R.ILENEKDLEEAEEYK.E	1852.97372	2	1.87E-10	0.97	5.20	-	1833.3
AHQ-1-13- , 3460	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	4.83E-10	0.97	6.30	-	1441.7
AHQ-1-13, 3371	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	2.49E-09	0.96	4.85	-	1259.1
AHQ-1-13, 3367	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	5.78E-11	0.96	5.02	-	1436.8
AHQ-1-13- , 3845 - 3885	R.LEAAYLDLQR.I	1192.34645	2	5.90E-06	0.97	3.88	-	2016.9
AHQ-1-13- , 3508 - 3533	R.RLEAAYLDLQR.I	1348.53280	2	1.17E-07	0.92	4.16	-	645.2
AHQ-1-13, 3403	R.RLEAAYLDLQR.I	1348.53280	2	1.48E-05	0.89	3.95	-	553.4
gi|17986260|ref|NP_524147.1| smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo				5.88E-11	3.29	40.26	23.30	12969.7
AHQ-1-12, 5441	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	5.88E-11	0.94	4.72	-	1332.3
AHQ-1-12, 5769 - 5827	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	4.17E-05	0.76	4.69	-	609.7
AHQ-1-12, 5819 - 5899	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	3.06E-05	0.92	4.96	-	1123.7
AHQ-1-12, 5885 - 5957	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	2.24E-07	0.89	4.98	-	815.2
AHQ-1-12, 5902	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	5.72E-04	0.94	4.77	-	1566.8
AHQ-1-12, 5994	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	4.32E-04	0.65	3.29	-	764.4

AHQ-1-12, 6055 - 6135	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	8.64E-05	0.87	4.50	-	759.1
AHQ-1-12, 6631 - 6689	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	3.30E-06	0.87	4.61	-	708.8
AHQ-1-13- , 6057 - 6131	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	4.84E-04	0.53	3.30	-	683.7
AHQ-1-14- , 5504 - 5558	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	1.30E-09	0.96	5.25	-	1554.3
AHQ-1-14- , 5772 - 5854	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	4.19E-04	0.64	4.02	-	547.5
gi|4506713|ref|NP_002945.1| ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte				5.95E-11	0.80	10.21	10.30	17964.8
AHQ-1-14- , 4446 - 4464	K.TITLEVEPSDTIENVK.A	1788.97431	2	5.95E-11	0.80	4.14	-	673.0
AHQ-1-14- , 4352 - 4383	K.TITLEVEPSDTIENVK.A	1788.97431	2	3.87E-05	0.88	4.07	-	758.0
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				6.57E-11	20.77	230.28	21.90	138070.8
AHQ-1-3, 2358 - 2441	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	1.01E-07	0.93	4.85	-	917.3
AHQ-1-3, 2365 - 2370	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	3.63E-09	0.94	5.21	-	531.3
AHQ-1-2, 2459	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	1.71E-06	0.94	4.84	-	742.4
AHQ-1-3, 7129	K.CTSDMETILTFIPQFHR.L	2098.38838	2	8.01E-05	0.84	4.10	-	473.5
AHQ-1-3, 6425	K.CTSDM*ETILTFIPQFHR.L	2114.38778	3	2.87E-09	0.86	3.85	-	686.3
AHQ-1-4, 4186	R.DQALQLQVLNSR.F	1385.55144	2	6.22E-04	0.63	2.71	-	748.3
AHQ-1-3, 4318	R.DQALQLQVLNSR.F	1385.55144	2	4.40E-06	0.94	3.34	-	1549.5
AHQ-1-3, 2821	K.EVHEQLLSTEQVSDQK.N	1870.99550	2	7.05E-05	0.96	4.99	-	892.4
AHQ-1-14- , 6118	K.FPPVTTFSGYLLYR.T	1661.92388	2	1.61E-08	0.93	3.59	-	937.8
AHQ-1-10, 5683	K.FPPVTTFSGYLLYR.T	1661.92388	2	2.14E-09	0.93	3.52	-	911.2
AHQ-1-13, 5940	K.FPPVTTFSGYLLYR.T	1661.92388	2	5.78E-04	0.92	3.27	-	929.6
AHQ-1-13- , 6348 - 6353	K.FPPVTTFSGYLLYR.T	1661.92388	2	5.68E-04	0.93	4.36	-	793.9
AHQ-1-2, 6630 - 6642	K.FPPVTTFSGYLLYR.T	1661.92388	2	4.46E-06	0.90	3.63	-	659.7
AHQ-1-3, 6467 - 6479	K.FPPVTTFSGYLLYR.T	1661.92388	2	7.14E-10	0.93	4.05	-	789.4
AHQ-1-3, 5925	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	7.99E-09	0.91	4.41	-	950.3
AHQ-1-1, 5957	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	3.68E-05	0.95	4.35	-	1429.5
AHQ-1-3, 6165 - 6190	K.GLTEFVEPIIQIK.T	1487.76518	2	1.08E-05	0.93	4.34	-	1011.8
AHQ-1-1, 6167	K.GLTEFVEPIIQIK.T	1487.76518	2	9.68E-05	0.91	3.66	-	946.3
AHQ-1-3, 2445	R.GVAEQQQQQGCGDPEVMQK.M	2119.27971	2	1.05E-04	0.94	4.84	-	759.4
AHQ-1-3, 2114	R.GVAEQQQQQGCGDPEVM*QK.M	2135.27911	2	8.93E-04	0.81	3.67	-	462.0
AHQ-1-2, 4075	K.HSLPDIQLLQK.G	1292.50915	2	7.15E-07	0.87	3.16	-	683.9
AHQ-1-3, 3881	K.HSLPDIQLLQK.G	1292.50915	2	9.92E-07	0.90	3.42	-	779.5
AHQ-1-3, 6061	K.IENLTSAVNSLNFIIK.E	1777.05472	2	5.65E-05	0.94	4.67	-	821.0
AHQ-1-3, 5174	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.56E-05	0.89	3.69	-	1014.1
AHQ-1-1, 5405	K.IFQNDM*QETVAQLFK.T	1829.06683	2	6.08E-05	0.69	2.89	-	533.1
AHQ-1-1, 6541	K.IFQNDMQETVAQLFK.T	1813.06743	2	3.32E-04	0.94	4.21	-	1125.4
AHQ-1-3, 6606 - 6609	K.IFQNDMQETVAQLFK.T	1813.06743	2	8.18E-07	0.98	5.64	-	2024.2
AHQ-1-3, 6710 - 6717	K.IFQNDMQETVAQLFK.T	1813.06743	2	2.58E-06	0.96	4.81	-	1607.7
AHQ-1-5, 6701 - 6709	K.IFQNDMQETVAQLFK.T	1813.06743	2	2.08E-08	0.98	5.22	-	2012.9
AHQ-1-3, 6806	K.IFQNDMQETVAQLFK.T	1813.06743	2	2.76E-06	0.88	3.83	-	803.9
AHQ-1-3, 5347	K.IFQNDM*QETVAQLFK.T	1829.06683	2	8.31E-07	0.88	4.05	-	834.3
AHQ-1-13, 5289	R.IPYLGVYVFK.Y	1199.46532	2	6.11E-05	0.71	2.62	-	891.3
AHQ-1-10, 4941	R.IPYLGVYVFK.Y	1199.46532	2	1.39E-05	0.94	3.67	-	1187.0
AHQ-1-14- , 5476	R.IPYLGVYVFK.Y	1199.46532	2	8.92E-04	0.93	2.83	-	1333.3
AHQ-1-13- , 4013	K.LAFESENINSEIHCDR.V	1936.04933	2	7.35E-06	0.94	4.77	-	946.7
AHQ-1-10, 3620	K.LAFESENINSEIHCDR.V	1936.04933	2	1.91E-05	0.91	3.52	-	1132.0
AHQ-1-3, 2870	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	3	2.14E-04	0.95	5.19	-	1496.6
AHQ-1-3, 2865 - 2943	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	1.05E-06	0.97	5.38	-	1773.1
AHQ-1-10, 3417 - 3491	K.LVEENALAPDFSK.G	1433.58810	2	4.31E-05	0.94	4.20	-	964.2
AHQ-1-13- , 3872	K.LVEENALAPDFSK.G	1433.58810	2	5.85E-05	0.72	2.88	-	584.6
AHQ-1-1, 3940 - 3996	K.LVEENALAPDFSK.G	1433.58810	2	6.38E-05	0.90	2.94	-	1146.2
AHQ-1-3, 7155	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	1.30E-04	0.92	4.25	-	1130.8
AHQ-1-3, 2134	K.QTHLEGALEQEHSR.S	1635.72018	2	1.48E-08	0.76	3.06	-	341.8
AHQ-1-3, 6781 - 6799	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	4.04E-05	0.70	3.45	-	445.5
AHQ-1-3, 7034	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	1.97E-04	0.73	3.41	-	555.4
AHQ-1-3, 7234	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	6.57E-11	0.95	5.10	-	815.4
AHQ-1-4, 3524	K.TVSSLSEDLESTR.Q	1424.49324	2	5.81E-05	0.69	3.21	-	552.6
AHQ-1-3, 4103	R.YNFVLQVAK.T	1082.27683	2	1.97E-05	0.93	3.10	-	1338.6
gi|4885183|ref|NP_005210.1| diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS				6.73E-11	10.19	120.29	16.60	138977.7
AHQ-1-3, 6259 - 6271	R.DM*PLLSCLESLR.V	1451.69163	2	7.04E-05	0.90	3.59	-	721.8
AHQ-1-3, 3295	R.DVQNFPAATDEKDKFVEK.M	2082.25588	2	3.17E-06	0.57	3.22	-	285.5
AHQ-1-3, 4601	R.LGLHQVLQDLR.E	1292.51238	2	3.38E-07	0.78	2.90	-	710.2
AHQ-1-3, 2359	K.LQDLQGEKDALHSEK.Q	1711.85486	2	7.23E-05	0.91	3.78	-	916.2
AHQ-1-3, 6554	K.LQFSEQVENIKPEIVSVTAACEELR.K	2892.23121	3	2.24E-06	0.96	5.74	-	1514.2
AHQ-1-3, 5269	K.LVAEDLSQDCFWTK.V	1713.88927	2	1.45E-07	0.89	3.63	-	725.4
AHQ-1-4, 5376	K.LVAEDLSQDCFWTK.V	1713.88927	2	1.45E-07	0.86	3.56	-	618.0
AHQ-1-3, 7311	R.M*EM*DDFNEVFQILLNTVK.D	2219.52085	2	6.73E-11	0.97	4.86	-	1503.4
AHQ-1-3, 6283	K.MLSELKDEYDDLAESEQFGVVM*GTVPR.L	3076.40186	3	2.82E-04	0.65	3.48	-	412.3
AHQ-1-3, 5806 - 5874	K.QDLEAEVSQLTGEVAK.L	1717.85617	2	2.91E-05	0.87	4.19	-	958.5
AHQ-1-3, 6021	K.TAQNLSIFLGSFR.M	1454.65537	2	3.24E-06	0.88	3.56	-	653.3
AHQ-1-3, 7282	K.VGCLQLINALITPAEELDFR.V	2274.62236	2	9.40E-06	0.96	5.33	-	831.7
AHQ-1-3, 7135	K.VGCLQLINALITPAEELDFR.V	2274.62236	2	3.59E-07	0.89	4.23	-	628.5
AHQ-1-3, 5069	R.VQLNVFDEQGEEDSYDLK.G	2129.22304	2	1.04E-04	0.94	4.33	-	1124.2
gi|4557703|ref|NP_000414.1| keratin 2a [Homo sapiens]				6.80E-11	2.75	30.26	12.90	65864.9
AHQ-1-1, 6832	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	2.30E-04	0.91	4.56	-	954.4
AHQ-1-14- , 6502	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	6.80E-11	0.84	3.85	-	1006.2
AHQ-1-4, 3111 - 3112	R.FLEQQNQVLQTK.W	1476.65935	2	3.59E-07	0.97	4.82	-	2097.1
AHQ-1-5, 2998	R.FLEQQNQVLQTK.W	1476.65935	2	1.72E-06	0.97	5.22	-	2241.6
AHQ-1-6, 2988	R.FLEQQNQVLQTK.W	1476.65935	2	1.78E-06	0.98	4.82	-	2340.8
AHQ-1-11, 2928	R.FLEQQNQVLQTK.W	1476.65935	2	1.65E-04	0.92	3.46	-	1538.7
AHQ-1-12, 2962	R.FLEQQNQVLQTK.W	1476.65935	2	1.41E-08	0.96	4.00	-	2192.8
AHQ-1-13, 3046	R.FLEQQNQVLQTK.W	1476.65935	2	1.77E-04	0.95	4.22	-	1604.9
AHQ-1-13- , 3080 - 3088	R.FLEQQNQVLQTK.W	1476.65935	2	3.00E-07	0.97	5.03	-	2417.7
AHQ-1-14- , 3031	R.FLEQQNQVLQTK.W	1476.65935	2	7.75E-06	0.97	4.67	-	1825.4
AHQ-1-1, 3145	R.FLEQQNQVLQTK.W	1476.65935	2	2.99E-08	0.97	4.67	-	2005.0
AHQ-1-14- , 5647	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	9.83E-08	0.95	5.13	-	1440.8
gi|11321601|ref|NP_002618.1| phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom				7.18E-11	3.80	40.28	9.30	85595.6
AHQ-1-5, 3667	K.AIGVLTSGGDAQGMNAAVR.A	1789.00750	2	7.18E-11	0.97	5.58	-	1468.9
AHQ-1-5, 3449	R.DLQSNVEHLTEK.M	1413.51529	2	8.03E-05	0.93	3.95	-	1259.3
AHQ-1-5, 6238 - 6241	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	2.13E-04	0.95	4.69	-	954.4
AHQ-1-5, 6626	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	6.23E-10	0.95	5.36	-	691.7
gi|13518026|ref|NP_004978.2| LIM and senescent cell antigen-like domains 1 [Homo sapiens]				7.59E-11	4.11	50.24	20.00	37251.2
AHQ-1-9, 4810	K.AWCVNCFACSTCNTK.L	1884.08097	2	1.79E-04	0.58	2.75	-	315.5
AHQ-1-13- , 6956	R.CDLCQEVLADIGFVK.N	1770.01757	2	1.64E-07	0.85	2.56	-	1362.3
AHQ-1-11, 4314	K.CHAIIDEQPLIFK.N	1585.84900	2	9.49E-04	0.94	3.82	-	1406.7
AHQ-1-12, 4471	K.CHAIIDEQPLIFK.N	1585.84900	2	7.39E-04	0.90	3.57	-	971.6
AHQ-1-8, 4484	K.CHAIIDEQPLIFK.N	1585.84900	2	1.06E-05	0.96	4.32	-	1421.6
AHQ-1-10, 4164	K.CHAIIDEQPLIFK.N	1585.84900	2	4.98E-06	0.93	3.70	-	1109.3
AHQ-1-9, 3087	K.MGVPICGACR.R	1123.35250	2	4.76E-04	0.80	2.67	-	454.2
AHQ-1-12, 3497 - 3538	R.VIEGDVVSALNK.A	1244.41966	2	7.59E-11	0.96	3.93	-	1545.1
AHQ-1-8, 3374	R.VIEGDVVSALNK.A	1244.41966	2	1.38E-09	0.96	4.66	-	1228.8
AHQ-1-14, 4478	R.VIEGDVVSALNK.A	1244.41966	2	4.05E-07	0.96	4.36	-	1298.6
AHQ-1-13- , 3603	R.VIEGDVVSALNK.A	1244.41966	1	9.36E-05	0.31	1.97	-	493.5
AHQ-1-11, 3394	R.VIEGDVVSALNK.A	1244.41966	2	5.03E-09	0.93	4.26	-	913.6
AHQ-1-9, 3398 - 3411	R.VIEGDVVSALNK.A	1244.41966	2	5.29E-07	0.96	4.77	-	1274.5
AHQ-1-14- , 3574	R.VIEGDVVSALNK.A	1244.41966	2	3.46E-07	0.96	4.19	-	1367.7
gi|10863927|ref|NP_066953.1| peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]				7.61E-11	7.79	90.24	30.90	18012.4
AHQ-1-12, 4085 - 4098	K.EGMNIVEAMER.F	1279.46942	2	2.00E-04	0.85	3.18	-	713.6

AHQ-1-14, 4932	K.FEDENFILK.H	1155.28144	2	6.50E-05	0.74	3.01	-	590.2
AHQ-1-12, 3969 - 3970	K.FEDENFILK.H	1155.28144	2	1.29E-04	0.81	3.53	-	530.8
AHQ-1-13- , 4147	K.FEDENFILK.H	1155.28144	2	1.17E-04	0.75	2.86	-	500.0
AHQ-1-13, 3972	K.FEDENFILK.H	1155.28144	2	6.69E-04	0.77	3.19	-	538.8
AHQ-1-12, 3847 - 3909	K.FEDENFILK.H	1155.28144	2	5.18E-04	0.84	3.50	-	633.6
AHQ-1-12, 3767	K.ITIADCGQLE	1121.24345	2	1.87E-04	0.91	3.27	-	1525.7
AHQ-1-12, 3402 - 3478	K.KITIADCGQLE	1249.41637	2	8.04E-08	0.83	3.16	-	651.7
AHQ-1-14- , 3372	K.KITIADCGQLE	1249.41637	2	1.76E-05	0.90	3.84	-	1260.1
AHQ-1-12, 3277 - 3337	K.KITIADCGQLE	1249.41637	2	1.47E-06	0.92	3.81	-	1414.6
AHQ-1-13- , 4840	K.SIYGEKFEDENFILK.H	1833.03047	2	7.47E-08	0.94	4.19	-	1204.6
AHQ-1-14, 5580 - 5601	K.SIYGEKFEDENFILK.H	1833.03047	2	3.39E-06	0.94	4.28	-	1134.4
AHQ-1-12, 4551 - 4613	K.SIYGEKFEDENFILK.H	1833.03047	2	1.74E-08	0.96	4.57	-	1303.5
AHQ-1-12, 4762 - 4831	K.SIYGEKFEDENFILK.H	1833.03047	2	4.82E-06	0.88	3.68	-	998.2
AHQ-1-14- , 4735	K.SIYGEKFEDENFILK.H	1833.03047	2	7.61E-11	0.94	4.80	-	1014.7
AHQ-1-13, 4591	K.SIYGEKFEDENFILK.H	1833.03047	2	7.34E-08	0.93	4.09	-	1161.1
AHQ-1-12, 3791	K.VKEGMNIVEAMER.F	1506.77390	2	1.51E-05	0.87	3.68	-	1245.6
AHQ-1-12, 3613	K.VKEGMNIVEAMER.F	1506.77390	2	7.64E-07	0.94	3.85	-	1407.3
AHQ-1-14- , 2120	K.VKEGM*NIVEAM*ER.F	1538.77270	2	6.62E-04	0.83	3.01	-	689.9
AHQ-1-12, 2941	K.VKEGM*NIVEAMER.F	1522.77330	2	4.31E-04	0.87	3.36	-	941.6
AHQ-1-12, 4290	R.VSFELFADKVPK.T	1380.61317	2	1.28E-09	0.87	3.24	-	1017.6
AHQ-1-12, 4519	R.VSFELFADKVPK.T	1380.61317	3	5.31E-06	0.64	3.38	-	423.2
AHQ-1-12, 4513 - 4517	R.VSFELFADKVPK.T	1380.61317	2	2.07E-08	0.83	3.47	-	807.8
gi|5174393|ref|NP_006001.1|	arginine-rich, mutated in early stage tumors; arginine-rich protein [Ho			8.04E-11	3.44	40.30	25.20	26906.2
AHQ-1-12, 4545	K.DRDVTFSPATIENELIK.F	1949.15100	2	1.18E-08	0.97	4.98	-	1915.8
AHQ-1-12, 5435 - 5498	K.DRDVTFSPATIENELIK.F	1949.15100	2	1.98E-08	0.98	5.90	-	1921.3
AHQ-1-12, 2885	K.IINEVSKPLAHHIPVEK.I	1925.26378	2	9.81E-04	0.88	3.75	-	753.2
AHQ-1-12, 3186 - 3249	K.ILDDWGETCKGCAEK.S	1784.94596	2	8.04E-11	0.82	3.53	-	496.5
AHQ-1-12, 3765	K.QIDLSTVDLK.K	1132.28932	2	3.29E-04	0.77	2.55	-	604.9
gi|4507109|ref|NP_000336.1|	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor			8.26E-11	4.98	60.31	34.30	14460.1
AHQ-1-12, 2197 - 2267	K.EGVVHGVATVAEK.T	1296.45466	2	7.52E-06	0.84	2.81	-	769.5
AHQ-1-13- , 2291 - 2295	K.EGVVHGVATVAEK.T	1296.45466	2	6.89E-07	0.78	3.04	-	555.5
AHQ-1-13- , 4801	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.63E-06	0.91	3.77	-	842.6
AHQ-1-13, 4528	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	4.72E-08	0.95	5.12	-	790.4
AHQ-1-14, 5498	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.09E-06	0.96	5.13	-	1018.8
AHQ-1-12, 4557 - 4619	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	8.26E-11	0.97	5.69	-	1152.6
AHQ-1-14- , 4672 - 4676	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.89E-08	0.98	5.95	-	1532.9
AHQ-1-12, 2117	K.TKEGVLYVGSK.T	1181.36357	2	5.75E-06	0.83	3.03	-	703.6
AHQ-1-13- , 2177	K.TKEGVVHGVATVAEK.T	1525.73191	2	3.81E-06	0.95	3.94	-	1406.6
AHQ-1-12, 4181 - 4191	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	4.58E-04	0.93	5.06	-	1141.7
AHQ-1-13, 4173	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	8.12E-04	0.86	3.67	-	1112.6
AHQ-1-12, 4175	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.49E-05	0.96	4.72	-	1302.9
AHQ-1-13- , 4368	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.33E-07	0.98	6.28	-	1645.5
AHQ-1-14- , 4378	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	2.16E-05	0.97	5.72	-	1337.4
AHQ-1-14- , 4372 - 4379	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	1.83E-05	0.92	4.68	-	1107.3
AHQ-1-13, 4175	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.50E-06	0.96	4.80	-	1350.8
AHQ-1-12, 4094 - 4101	K.TVEGAGSIAAATGFVK.K	1479.66001	1	8.61E-04	0.48	2.78	-	421.1
gi|4505733|ref|NP_002610.1|	platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4			8.34E-11	5.57	60.29	38.60	10844.9
AHQ-1-14- , 4475	K.AGPHCPTAQLIATLK.N	1579.84600	2	7.10E-06	0.55	2.61	-	578.2
AHQ-1-13, 4121 - 4188	K.AGPHCPTAQLIATLK.N	1579.84600	2	8.63E-07	0.93	3.93	-	1026.6
AHQ-1-14- , 4242 - 4308	K.AGPHCPTAQLIATLK.N	1579.84600	2	3.01E-08	0.91	3.78	-	764.3
AHQ-1-14, 5030 - 5048	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.25E-06	0.94	4.06	-	828.4
AHQ-1-13- , 4316	K.AGPHCPTAQLIATLK.N	1579.84600	2	7.01E-04	0.91	3.41	-	924.2
AHQ-1-14- , 4111 - 4115	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.11E-04	0.95	4.23	-	1084.7
AHQ-1-14, 4944 - 4965	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	8.34E-11	0.97	5.22	-	1698.1
AHQ-1-14, 4948 - 5006	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	1.50E-06	0.90	4.28	-	638.7
AHQ-1-14- , 3926 - 3935	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	9.65E-10	0.98	5.83	-	2686.5
AHQ-1-14- , 4059	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	2.03E-09	0.94	4.51	-	942.5
AHQ-1-14- , 4044	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	3.62E-08	0.95	4.99	-	1408.6
AHQ-1-14, 4813	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	4.43E-08	0.94	4.64	-	1303.5
AHQ-1-14, 4808 - 4821	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.30E-10	0.97	4.95	-	1736.2
AHQ-1-14, 4686	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	5.86E-06	0.90	3.71	-	1333.5
AHQ-1-14- , 2534 - 2599	R.HITSLEVIK.A	1040.23825	2	1.11E-05	0.88	3.34	-	575.4
AHQ-1-14- , 2658 - 2735	R.HITSLEVIK.A	1040.23825	2	1.33E-06	0.88	3.48	-	469.8
AHQ-1-14, 3584 - 3640	R.HITSLEVIK.A	1040.23825	2	5.61E-05	0.88	3.35	-	568.7
AHQ-1-14, 3470 - 3528	R.HITSLEVIK.A	1040.23825	2	1.82E-04	0.85	2.95	-	554.1
AHQ-1-13, 2715	R.HITSLEVIK.A	1040.23825	2	7.03E-04	0.74	2.97	-	414.6
AHQ-1-13- , 2705	R.HITSLEVIK.A	1040.23825	2	4.97E-05	0.80	2.95	-	534.9
AHQ-1-14, 5812 - 5813	K.ICLDLQAPLYK.K	1335.59400	2	3.29E-05	0.94	4.20	-	1172.2
AHQ-1-14- , 4936	K.ICLDLQAPLYK.K	1335.59400	1	4.66E-04	0.60	2.87	-	532.9
AHQ-1-14- , 4926	K.ICLDLQAPLYK.K	1335.59400	2	1.20E-05	0.95	4.10	-	1414.8
AHQ-1-14- , 5139	K.ICLDLQAPLYK.K	1335.59400	2	4.03E-05	0.93	4.15	-	1185.6
AHQ-1-14- , 4546 - 4606	R.KICLDLQAPLYK.K	1463.76691	2	4.03E-07	0.97	5.19	-	1501.7
AHQ-1-14- , 4602	R.KICLDLQAPLYK.K	1463.76691	1	6.56E-06	0.87	3.75	-	741.0
AHQ-1-14, 5417 - 5482	R.KICLDLQAPLYK.K	1463.76691	2	6.98E-06	0.97	4.90	-	1575.7
AHQ-1-14, 5437 - 5444	R.KICLDLQAPLYK.K	1463.76691	1	4.79E-05	0.83	3.04	-	952.4
AHQ-1-14- , 4560 - 4624	R.KICLDLQAPLYK.K	1463.76691	1	8.48E-04	0.58	2.32	-	865.3
AHQ-1-14- , 4558 - 4559	R.KICLDLQAPLYK.K	1463.76691	3	1.13E-06	0.89	3.69	-	1171.7
gi|5729887|ref|NP_006624.1|	IQ motif containing GTPase activating protein 2 [Homo sapiens]			8.74E-11	10.73	120.27	14.30	180611.0
AHQ-1-3, 4035	K.AWVNQLETQTGEASK.L	1662.78230	2	1.47E-06	0.86	3.64	-	674.1
AHQ-1-5, 5786	K.GVLLDIDDLQTNQFK.N	1719.91690	2	7.23E-06	0.95	4.22	-	1281.7
AHQ-1-3, 7363	K.IGGILANELSVDEAALHAAVIAINEAVEK.G	2932.31842	3	7.11E-04	0.90	4.34	-	931.8
AHQ-1-3, 7130	K.KPEAQLPAVYPFAAAMYQNELFNLQK.Q	2983.43222	3	1.82E-04	0.76	3.65	-	594.4
AHQ-1-3, 5929	K.LGIAPQIQDLLGK.V	1366.63117	2	8.80E-08	0.88	3.53	-	572.1
AHQ-1-3, 4925 - 4937	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	1.14E-09	0.98	4.92	-	2106.5
AHQ-1-5, 4931	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	8.74E-11	0.96	4.52	-	1669.8
AHQ-1-3, 6046	R.NPNAVLTLVDDNLAPEYQK.E	2115.32901	2	5.58E-08	0.91	4.29	-	614.8
AHQ-1-3, 6957	R.NQPGNTLTEILETPATAQQEVDHATDMVSR.A	3268.51558	3	7.51E-08	0.72	3.05	-	510.0
AHQ-1-3, 4577	K.SLIINTNPVEVYK.A	1490.72593	2	1.62E-06	0.92	3.57	-	1115.3
AHQ-1-4, 4263	K.TLVGSENPPLTVIR.K	1496.73370	2	4.64E-06	0.92	3.61	-	1091.9
AHQ-1-3, 4238	K.TLVGSENPPLTVIR.K	1496.73370	2	1.35E-04	0.85	3.83	-	493.0
AHQ-1-5, 4257 - 4259	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	1.99E-04	0.89	3.72	-	975.5
AHQ-1-4, 4355 - 4359	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	1.33E-04	0.93	3.92	-	1219.1
AHQ-1-3, 4223 - 4294	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	2.21E-05	0.96	4.88	-	1357.5
AHQ-1-3, 5974	R.VVAVGYINEAIDEGNPLR.T	1930.15092	2	1.62E-07	0.98	5.32	-	1867.1
gi|6005727|ref|NP_006576.1|	chaperonin containing TCP1, subunit 8 (theta); T-complex protein 1, the			9.31E-11	1.77	20.19	5.70	59662.4
AHQ-1-7, 2709 - 2712	K.AIADTGANVVVTGGK.V	1373.53743	2	9.31E-11	0.92	3.28	-	1198.5
AHQ-1-7, 5424	K.IAVYSCPFDGMITETK.G	1834.10347	2	3.37E-04	0.86	3.72	-	487.9
gi|7661728|ref|NP_054736.1|	HSPC003 protein [Homo sapiens]			1.23E-10	0.93	10.25	21.60	13507.4
AHQ-1-14- , 5571	R.VTAAIASNIWAAYDRNGNQAFNEDNLK.F	2968.18636	3	1.23E-10	0.93	5.07	-	735.1
gi|4504183|ref|NP_000843.1|	glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s			1.26E-10	9.12	110.29	64.30	23355.7
AHQ-1-11, 5056	K.AFLASPEYVNLPINGNGK.Q	1905.14305	2	8.56E-06	0.83	3.14	-	882.1
AHQ-1-14, 6170	K.AFLASPEYVNLPINGNGKQ	2033.27283	2	6.72E-04	0.64	2.74	-	730.5
AHQ-1-13- , 5549	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	3.71E-05	0.20	2.56	-	234.3
AHQ-1-11, 5026 - 5086	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.08E-07	0.91	4.21	-	546.4
AHQ-1-11, 5028 - 5042	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	3	3.69E-06	0.81	3.75	-	628.6
AHQ-1-11, 5127	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	3.33E-06	0.80	3.48	-	408.9
AHQ-1-11, 3139	K.ASCLYGQLPK.F	1138.31884	1	4.78E-04	0.44	2.45	-	242.1

AHQ-1-11, 3062 - 3135	K.ASCLYGQLPK.F	1138.31884	2	1.38E-06	0.88	2.79	-	969.6
AHQ-1-11, 4962	K.DQQEAALVDM*VNDGVEDLR.C	2134.26783	2	8.37E-06	0.96	4.93	-	1056.4
AHQ-1-11, 4958	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	7.57E-09	0.93	4.49	-	730.0
AHQ-1-11, 6202 - 6271	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.63E-08	0.96	5.26	-	935.9
AHQ-1-11, 5784 - 5852	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.59E-05	0.92	4.11	-	948.1
AHQ-1-11, 5947 - 6022	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.26E-10	0.98	5.87	-	1370.1
AHQ-1-11, 4578 - 4644	K.FQDGDLTLYQSNTILR.H	1885.06701	2	7.51E-10	0.92	4.18	-	777.0
AHQ-1-11, 4702 - 4783	K.FQDGDLTLYQSNTILR.H	1885.06701	2	5.15E-09	0.97	5.24	-	1462.6
AHQ-1-14- , 4928 - 4955	K.FQDGDLTLYQSNTILR.H	1885.06701	2	9.37E-09	0.94	4.64	-	895.4
AHQ-1-11, 5726 - 5796	R.M*LLADQGQSWKEEVVTVETWQEGSLK.A	3009.33685	3	2.77E-08	0.95	5.81	-	1100.7
AHQ-1-11, 5866	R.MLLADQGQSWKEEVVTVETWQEGSLK.A	2993.33745	3	4.16E-04	0.68	3.38	-	533.6
AHQ-1-11, 2276	R.TLGLYGK.D	751.89356	1	2.74E-04	0.44	1.97	-	664.0
AHQ-1-11, 4304 - 4331	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	1.63E-06	0.90	4.09	-	674.2
AHQ-1-13- , 4740	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	6.66E-09	0.94	4.58	-	805.4
AHQ-1-11, 4420	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	5.84E-07	0.77	3.25	-	535.2
gi|13899317|ref|NP_113657.1| SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M				1.28E-10	6.37	70.30	72.00	12326.0
AHQ-1-14- , 5490 - 5492	K.ESNTVFSFLGLKPR.L	1595.82383	2	9.40E-08	0.81	3.42	-	574.6
AHQ-1-13- , 5665	K.ESNTVFSFLGLKPR.L	1595.82383	2	4.39E-08	0.73	3.43	-	394.8
AHQ-1-14- , 4982	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	2	2.06E-04	0.92	4.32	-	919.2
AHQ-1-14, 5865 - 5925	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	4.59E-04	0.96	5.08	-	1614.5
AHQ-1-14, 5874	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	2	3.51E-04	0.88	3.41	-	1097.6
AHQ-1-14- , 4974 - 5042	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	3.08E-08	0.98	5.95	-	2110.7
AHQ-1-14, 5141 - 5149	K.IEFEEVDITM*SEEQR.Q	1872.00051	2	1.14E-04	0.80	3.20	-	807.2
AHQ-1-14- , 4291	K.IEFEEVDITM*SEEQR.Q	1872.00051	2	1.28E-10	0.96	4.77	-	1161.1
AHQ-1-14, 4700	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	2.73E-04	0.90	3.68	-	831.9
AHQ-1-14- , 3756 - 3771	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	2.83E-04	0.85	3.32	-	741.0
AHQ-1-14- , 5722 - 5762	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	5.24E-05	0.86	4.13	-	845.2
AHQ-1-14- , 4454 - 4532	R.VFIASSSGFVAIK.K	1326.56551	2	3.80E-07	0.98	4.19	-	2584.6
AHQ-1-14, 5352	R.YCGDYDSFFESK.E	1519.57010	2	1.28E-06	0.96	3.88	-	1111.2
AHQ-1-14- , 4463	R.YCGDYDSFFESK.E	1519.57010	2	7.24E-07	0.96	4.16	-	1185.2
gi|18104989|ref|NP_002822.2| protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t				1.32E-10	2.59	30.24	9.40	67560.7
AHQ-1-14- , 6670	K.FATLTELVEYYTQQQGVLQDR.D	2503.74859	3	9.30E-07	0.94	4.71	-	1184.6
AHQ-1-6, 4443 - 4463	R.IQNSGDFYDLYGGEK.F	1706.79040	2	3.92E-05	0.73	3.54	-	333.3
AHQ-1-6, 4111 - 4188	R.IQNSGDFYDLYGGEK.F	1706.79040	2	1.45E-05	0.76	3.35	-	460.3
AHQ-1-6, 7219	R.YTVGGLETFDSLTDLVEHFK.K	2272.49536	2	1.32E-10	0.89	4.36	-	410.9
gi|4502051|ref|NP_000688.1| arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]				1.44E-10	7.74	90.21	17.60	75721.8
AHQ-1-6, 4966	R.AAAQLTYCSLCPPDDLADR.G	2140.33708	2	1.41E-08	0.86	3.93	-	346.3
AHQ-1-6, 2258	K.AVSTGGGGHVQLLR.R	1352.52468	2	1.44E-10	0.86	3.34	-	1004.6
AHQ-1-6, 3428	K.GDPELQAWCR.E	1233.33558	2	3.37E-07	0.61	2.78	-	395.2
AHQ-1-6, 5515	R.GLLGLPGALYAHDALR.L	1637.90708	2	2.06E-10	0.93	3.82	-	845.9
AHQ-1-6, 5207	R.ITVQGPGACAEVAFPCYR.W	1999.25659	2	1.24E-09	0.87	3.43	-	893.9
AHQ-1-6, 4634	R.LPGDNALDMFQK.H	1349.53784	2	3.30E-06	0.95	3.82	-	1365.5
AHQ-1-6, 3760	R.LPGDNALDM*FQK.H	1365.53724	2	1.48E-04	0.88	3.20	-	896.6
AHQ-1-6, 5098	R.WVQGEDILSLPEGTAR.L	1771.95190	2	4.96E-05	0.86	3.98	-	595.7
AHQ-1-6, 4995	R.YVEGIVHLFYQR.D	1524.74730	2	7.03E-07	0.92	3.11	-	1154.9
gi|4506925|ref|NP_003013.1| SH3 domain binding glutamic acid-rich protein like; SH3-binding domain				1.46E-10	2.83	30.33	50.00	12774.2
AHQ-1-13- , 6061 - 6135	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	3.09E-05	0.92	4.66	-	572.6
AHQ-1-13- , 6145 - 6207	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	1.58E-04	0.88	4.05	-	608.4
AHQ-1-13, 4915 - 4980	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	8.54E-08	0.89	4.43	-	713.9
AHQ-1-13- , 5291	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	4.19E-10	0.93	4.77	-	1007.9
AHQ-1-13- , 5068 - 5147	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.46E-10	0.97	6.52	-	1275.5
AHQ-1-13- , 5159 - 5227	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	4.75E-08	0.96	5.68	-	1277.1
AHQ-1-13, 4799 - 4859	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.87E-05	0.94	4.79	-	1174.9
AHQ-1-13- , 2432 - 2435	R.VYIASSSGSTAIK.K	1284.44065	2	1.50E-05	0.94	4.20	-	1512.8
AHQ-1-13- , 2524	R.VYIASSSGSTAIK.K	1284.44065	2	2.82E-05	0.92	3.73	-	1559.7
gi|21618359|ref|NP_004095.3| fatty acid synthase [Homo sapiens]				1.68E-10	1.81	20.31	1.60	273262.0
AHQ-1-1, 6439	R.LHLSGIDANPNALFPPVEFPAPR.G	2473.81368	2	1.99E-07	0.82	3.30	-	462.3
AHQ-1-2, 7122	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	1.68E-10	0.98	6.24	-	2232.4
AHQ-1-3, 6937 - 6959	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	1.68E-05	0.97	5.08	-	1556.8
AHQ-1-1, 6811 - 6817	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	4.00E-09	0.98	4.86	-	1931.8
gi|4506365|ref|NP_002856.1| RAB2, member RAS oncogene family [Homo sapiens]				1.88E-10	0.96	10.18	6.10	23545.4
AHQ-1-14, 5386	K.LQIWDTAGQESFR.S	1551.68478	2	2.30E-04	0.65	2.56	-	352.6
AHQ-1-11, 4218	K.LQIWDTAGQESFR.S	1551.68478	2	1.88E-10	0.96	3.56	-	1765.5
gi|4758304|ref|NP_004902.1| protein disulfide isomerase related protein (calcium-binding protein, i				1.93E-10	6.51	80.22	16.90	72931.9
AHQ-1-6, 4720	K.DLGLSESGEDVNAAILDESGKK.F	2248.38737	2	1.93E-10	0.95	4.42	-	1236.8
AHQ-1-6, 6166 - 6170	R.EVSQPDWTPPPEVTLVLTK.E	2137.41772	2	7.87E-04	0.39	3.19	-	220.1
AHQ-1-6, 4707	K.FAMEPEEFDSDTLR.E	1687.80890	2	1.44E-08	0.86	3.46	-	617.6
AHQ-1-6, 3686	R.FDVSGYPTIK.I	1127.27123	1	1.52E-04	0.26	2.10	-	437.8
AHQ-1-6, 3688	R.FDVSGYPTIK.I	1127.27123	2	6.40E-05	0.90	2.99	-	1162.7
AHQ-1-6, 3779	R.FDVSGYPTLK.I	1127.27123	2	2.54E-06	0.82	2.57	-	920.0
AHQ-1-6, 2882	K.IDATSASVLASR.F	1191.31686	2	1.76E-06	0.93	3.48	-	1278.9
AHQ-1-6, 1970 - 2034	K.RSPPIPLAK.V	979.20128	2	3.39E-04	0.81	2.52	-	654.7
AHQ-1-6, 2927	K.VSQGQLVVMQPEK.F	1443.69431	2	6.46E-05	0.85	2.68	-	1260.7
gi|12025678|ref|NP_004915.2| actinin, alpha 4 [Homo sapiens]				1.96E-10	10.60	130.27	22.30	104853.3
AHQ-1-5, 3462	R.ASFNHFDKDHGGALGPEEFK.A	2204.34290	2	1.88E-08	0.66	2.94	-	525.3
AHQ-1-5, 2077	R.EAILAIHK.E	895.08114	2	1.85E-04	0.89	2.94	-	952.0
AHQ-1-5, 2086	R.EAILAIHK.E	895.08114	1	4.54E-05	0.49	1.94	-	345.2
AHQ-1-6, 4724	R.ETTDTDTADQVIASFK.V	1742.81936	2	1.05E-05	0.90	3.18	-	1425.5
AHQ-1-4, 4908	R.ETTDTDTADQVIASFK.V	1742.81936	2	1.40E-07	0.95	4.53	-	1362.1
AHQ-1-14, 5558 - 5617	R.ETTDTDTADQVIASFK.V	1742.81936	2	7.34E-07	0.84	3.29	-	925.6
AHQ-1-5, 4811	R.ETTDTDTADQVIASFK.V	1742.81936	2	1.21E-07	0.91	4.20	-	1023.7
AHQ-1-5, 2159	K.GISQEQM*QEFR.A	1369.48598	2	5.66E-04	0.47	2.70	-	559.5
AHQ-1-5, 2445 - 2453	K.HRDYETATLSDIK.A	1549.66719	2	2.48E-04	0.92	3.65	-	891.3
AHQ-1-5, 4901	K.ICDQWDALGSLTHSR.R	1760.90926	2	5.57E-10	0.93	4.10	-	1009.3
AHQ-1-5, 3819	R.KDDPVTNLNNAFEVAEK.Y	1905.05509	2	3.69E-09	0.91	3.73	-	917.4
AHQ-1-5, 4443	R.KDDPVTNLNNAFEVAEK.Y	1905.05509	2	1.93E-05	0.97	5.36	-	1144.9
AHQ-1-4, 4104	R.M*APYQGPDAVPGALDYK.S	1810.02037	2	1.67E-05	0.87	3.30	-	752.2
AHQ-1-5, 4286	R.MAPYQGPDAVPGALDYK.S	1794.02097	2	4.78E-05	0.90	4.10	-	669.5
AHQ-1-5, 4217	K.MLDAEDIVNTARPDEK.A	1817.99924	2	3.95E-06	0.90	3.85	-	883.6
AHQ-1-5, 4095	K.MVSDINNGWQHLEQAEK.G	2000.18160	2	1.96E-10	0.90	4.27	-	593.5
AHQ-1-4, 7290	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	5.70E-04	0.83	4.30	-	664.0
AHQ-1-4, 6807	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	8.15E-05	0.83	4.08	-	518.0
AHQ-1-5, 6717 - 6729	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	2.73E-10	0.91	4.75	-	944.9
gi|21361370|ref|NP_002853.2| phosphorylase, glycogen; brain [Homo sapiens]				1.99E-10	5.67	60.24	10.60	96695.3
AHQ-1-5, 3813	R.GLAGLGDVAEVR.K	1157.30210	2	8.89E-06	0.96	4.39	-	1481.1
AHQ-1-5, 3635 - 3662	R.HLDHVAALFPGDVDR.L	1662.83036	2	7.76E-04	0.97	4.33	-	1936.3
AHQ-1-5, 6058 - 6059	K.LLPLVSDEVFIR.D	1401.67552	2	1.99E-10	0.90	3.47	-	647.1
AHQ-1-5, 7419	K.LQDFNVGDYIEAVLDR.N	1868.03645	2	2.59E-09	0.96	4.69	-	1199.0
AHQ-1-5, 4313	K.LVTSIGDVVNHDPVVGDR.L	1893.09067	2	1.25E-08	0.92	4.16	-	695.2
AHQ-1-5, 6769 - 6830	R.WLLLCNPGLADTIVEK.I	1844.16436	2	2.74E-05	0.96	4.83	-	1385.1
gi|28269681|ref|NP_783313.1| NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]				2.07E-10	1.35	20.28	27.00	14852.0
AHQ-1-13- , 6708	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	2.07E-10	0.96	5.67	-	1524.3
AHQ-1-14- , 6463	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	3.87E-05	0.94	4.25	-	1747.5
AHQ-1-13, 4800 - 4867	R.VTLNPPGTFLEGVAK.V	1543.78883	2	1.72E-04	0.39	2.51	-	273.2
gi|9257257|ref|NP_059830.1| WD repeat-containing protein 1 isoform 1 [Homo sapiens]				2.12E-10	1.73	20.24	7.90	66193.1
AHQ-1-10, 3935	R.LHHVSSLAWLDEHTLVTTSHDASVK.E	2785.06406	3	2.11E-06	0.91	4.09	-	1105.6
AHQ-1-6, 4203	R.LHHVSSLAWLDEHTLVTTSHDASVK.E	2785.06406	3	2.12E-10	0.94	4.74	-	1119.4

AHQ-1-6, 5087	K.VVTVFSVADGYSENNVFYGHHAK.I	2541.75861	3	3.91E-08	0.78	3.36	-	695.9
gi|4507383|ref|NP_001052.1| thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil				2.12E-10	7.17	90.23	21.50	60675.3
AHQ-1-7, 2414	R.DVFSSTGCKPNPSR.Q	1553.67913	2	3.87E-08	0.56	2.82	-	501.0
AHQ-1-7, 2477	R.EAAQDCEVLGQR.I	1377.46310	2	1.98E-04	0.86	3.61	-	1050.8
AHQ-1-7, 4476 - 4556	R.FQACPETQVPLQLESK.S	1877.10807	2	2.12E-10	0.96	4.50	-	1541.9
AHQ-1-10, 4033	R.FQACPETQVPLQLESK.S	1877.10807	2	1.54E-05	0.96	4.45	-	1276.9
AHQ-1-7, 3466	R.GALMSAFSPEK.L	1138.31906	1	1.08E-04	0.37	2.32	-	601.6
AHQ-1-7, 4101	R.HSASPMGVQDFDIVR.D	1659.84828	2	4.75E-06	0.95	3.98	-	1257.6
AHQ-1-7, 5273	K.LYGPLCGYYLGR.R	1433.65622	2	1.09E-05	0.89	2.92	-	1061.1
AHQ-1-7, 3544	K.NRDELNGFFNK.L	1354.45276	2	5.49E-04	0.87	3.17	-	888.9
AHQ-1-14- , 5974	K.PSPFIGNLTFFR.Q	1396.61752	2	2.50E-06	0.76	2.62	-	566.3
AHQ-1-7, 3092	R.YAESGDAFDIQR.C	1372.42172	2	4.83E-10	0.95	4.06	-	1383.6
gi|7661818|ref|NP_054900.1| HSPC159 protein [Homo sapiens]				2.16E-10	4.29	50.27	43.00	19011.6
AHQ-1-13, 6379	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	1.89E-05	0.84	3.91	-	279.2
AHQ-1-13- , 6835 - 6836	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	1.62E-05	0.84	3.58	-	384.7
AHQ-1-14- , 6586	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.99E-05	0.92	4.61	-	355.7
AHQ-1-12, 6502	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	4.19E-06	0.82	3.60	-	308.1
AHQ-1-11, 6310	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	2.15E-04	0.92	4.42	-	418.9
AHQ-1-13- , 3873 - 3884	R.IQTLSAIDTIK.I	1203.41068	2	7.81E-04	0.80	3.10	-	578.5
AHQ-1-11, 4623	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	2	2.10E-06	0.79	3.34	-	721.2
AHQ-1-11, 4736 - 4796	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	2	1.24E-06	0.97	5.34	-	1595.8
AHQ-1-13- , 6711	R.NSCISGERGEEQSAIPYFPFIPDQPFR.V	3144.41922	3	3.18E-04	0.67	3.37	-	421.9
AHQ-1-13- , 6844	R.NSCISGERGEEQSAIPYFPFIPDQPFR.V	3144.41922	3	1.14E-05	0.79	3.55	-	671.2
AHQ-1-11, 4594	R.VFVDGHQLFDFYHR.I	1780.96540	2	6.45E-10	0.96	4.62	-	1653.9
AHQ-1-11, 4704	R.VFVDGHQLFDFYHR.I	1780.96540	2	2.16E-10	0.91	3.47	-	1112.2
gi|21464101|ref|NP_036611.2| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein				2.18E-10	3.75	40.31	29.60	28302.4
AHQ-1-10, 6279	R.LGLALNYSVFYYEIQNAPEQACHLAK.T	3015.38773	3	2.18E-10	0.96	6.15	-	1136.4
AHQ-1-10, 3963 - 4036	R.NLLSVAYKNVVGAR.R	1504.75906	2	6.34E-06	0.95	4.18	-	1253.1
AHQ-1-10, 3768	R.NLLSVAYKNVVGAR.R	1504.75906	2	4.51E-07	0.92	3.31	-	1373.3
AHQ-1-13- , 3128	K.NVTELNEPLSNEER.N	1644.72215	2	9.25E-08	0.94	4.49	-	864.3
AHQ-1-14- , 3083	K.NVTELNEPLSNEER.N	1644.72215	2	7.71E-07	0.93	3.94	-	907.8
AHQ-1-10, 2876	K.NVTELNEPLSNEER.N	1644.72215	2	5.48E-04	0.91	3.53	-	875.1
AHQ-1-11, 2966 - 2968	K.NVTELNEPLSNEER.N	1644.72215	2	4.12E-04	0.81	3.03	-	682.5
AHQ-1-14, 3952	K.NVTELNEPLSNEER.N	1644.72215	2	5.85E-04	0.86	3.81	-	489.4
AHQ-1-10, 6012 - 6075	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	4.15E-05	0.64	3.36	-	627.1
AHQ-1-13- , 6668 - 6681	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	3.40E-05	0.87	3.99	-	808.6
AHQ-1-10, 5840	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	2.14E-09	0.83	3.91	-	656.4
AHQ-1-14- , 6451 - 6452	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	7.27E-06	0.93	4.23	-	1005.6
AHQ-1-13, 6229 - 6251	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	3.87E-10	0.93	3.94	-	1073.9
gi|30159310|ref|XP_301899.1| similar to beta-actin [Homo sapiens]				2.32E-10	1.46	20.18	9.20	32376.4
AHQ-1-8, 1475 - 2015	K.DSYVGNEAQSK.R	1198.22158	1	2.32E-10	0.59	2.71	-	357.5
AHQ-1-8, 1705	K.DSYVGNEAQSK.R	1198.22158	2	6.24E-06	0.72	3.27	-	532.9
AHQ-1-8, 1801 - 1873	K.DSYVGNEAQSK.R	1198.22158	2	2.56E-05	0.72	3.08	-	664.4
AHQ-1-13- , 1661 - 1737	K.DSYVGNEAQSK.R	1198.22158	2	8.15E-04	0.49	2.88	-	428.4
AHQ-1-13, 1819 - 1877	K.DSYVGNEAQSK.R	1198.22158	1	9.33E-07	0.38	2.17	-	406.8
AHQ-1-9, 1542 - 1602	K.DSYVGNEAQSK.R	1198.22158	1	5.21E-08	0.71	2.80	-	512.5
AHQ-1-9, 1856	K.DSYVGNEAQSK.R	1198.22158	1	1.17E-08	0.56	2.58	-	405.7
AHQ-1-13- , 1705	K.DSYVGNEAQSK.R	1198.22158	1	4.05E-04	0.05	1.81	-	209.2
AHQ-1-12, 1638 - 1702	K.DSYVGNEAQSK.R	1198.22158	2	2.30E-06	0.64	3.00	-	597.1
AHQ-1-12, 1707 - 1846	K.DSYVGNEAQSK.R	1198.22158	1	1.26E-08	0.42	2.49	-	338.2
AHQ-1-12, 1757 - 1821	K.DSYVGNEAQSK.R	1198.22158	2	3.47E-06	0.56	3.10	-	500.5
AHQ-1-8, 4723 - 4795	K.SYKLLDGQVITIGNER.F	1807.04092	2	1.22E-05	0.80	3.41	-	679.7
AHQ-1-9, 4570 - 4575	K.SYKLLDGQVITIGNER.F	1807.04092	2	4.23E-04	0.72	2.96	-	541.6
AHQ-1-8, 4892 - 4971	K.SYKLLDGQVITIGNER.F	1807.04092	2	2.25E-06	0.87	3.49	-	724.1
gi|4507745|ref|NP_003320.1| thioredoxin [Homo sapiens]				2.33E-10	0.93	10.17	12.40	11693.3
AHQ-1-13- , 4000	K.TAFQEALDAAGDK.L	1337.41728	1	7.56E-06	0.53	2.10	-	916.3
AHQ-1-14- , 3891 - 3898	K.TAFQEALDAAGDK.L	1337.41728	2	2.33E-10	0.93	3.48	-	1470.7
AHQ-1-14- , 3899	K.TAFQEALDAAGDK.L	1337.41728	1	3.57E-05	0.79	2.88	-	1010.6
AHQ-1-14, 4788	K.TAFQEALDAAGDK.L	1337.41728	2	6.39E-06	0.92	3.39	-	1275.0
gi|20127528|ref|NP_037459.2| parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]				2.41E-10	5.13	60.26	21.70	41714.0
AHQ-1-14- , 3544	K.ARPEDVVNLDLK.S	1369.54878	2	3.72E-04	0.94	4.26	-	998.1
AHQ-1-9, 3287 - 3290	K.ARPEDVVNLDLK.S	1369.54878	2	1.34E-05	0.93	4.14	-	875.9
AHQ-1-9, 3294	K.ARPEDVVNLDLK.S	1369.54878	1	3.93E-05	0.41	2.35	-	298.4
AHQ-1-9, 3306	K.ARPEDVVNLDLK.S	1369.54878	1	1.08E-06	0.67	3.12	-	318.0
AHQ-1-13, 3482	K.ARPEDVVNLDLK.S	1369.54878	2	1.86E-04	0.95	4.23	-	1216.2
AHQ-1-10, 3244	K.ARPEDVVNLDLK.S	1369.54878	2	6.54E-05	0.93	3.94	-	937.5
AHQ-1-13- , 3587	K.ARPEDVVNLDLK.S	1369.54878	2	1.35E-05	0.88	3.72	-	762.1
AHQ-1-14, 4438	K.ARPEDVVNLDLK.S	1369.54878	2	1.93E-05	0.93	3.99	-	1068.9
AHQ-1-9, 5438	R.DAFDTLFDHAPDKLSVVK.K	2019.24293	2	3.17E-05	0.83	3.63	-	667.2
AHQ-1-9, 3703	K.LNVAEVTQSEIGQK.Q	1516.67865	2	4.65E-06	0.96	4.75	-	1262.2
AHQ-1-13, 3748	K.LNVAEVTQSEIGQK.Q	1516.67865	2	1.08E-05	0.83	3.20	-	998.5
AHQ-1-13- , 3888	K.LNVAEVTQSEIGQK.Q	1516.67865	2	1.98E-08	0.95	4.27	-	1351.4
AHQ-1-9, 3464	R.LPEHVTVQVVVVR.K	1475.76086	2	5.40E-05	0.90	3.75	-	895.7
AHQ-1-9, 3223	K.SLITFVNK.H	922.10336	2	2.92E-05	0.83	2.60	-	781.5
AHQ-1-9, 6375 - 6444	K.VLLDWINDVLVEER.I	1713.95549	2	3.26E-08	0.90	4.11	-	795.5
AHQ-1-9, 7202 - 7220	K.VLLDWINDVLVEER.I	1713.95549	2	2.41E-10	0.95	5.14	-	1136.3
AHQ-1-9, 7464	K.VLLDWINDVLVEER.I	1713.95549	2	7.22E-04	0.59	3.01	-	664.4
gi|4758442|ref|NP_004115.1| glia maturation factor, beta [Homo sapiens]				2.47E-10	2.33	30.25	35.20	16713.1
AHQ-1-12, 5954	R.LVVLDEELEGISPDELKDELPER.Q	2638.90589	3	2.47E-10	0.96	5.06	-	1717.9
AHQ-1-12, 6257 - 6318	R.VSYPLCFIFSSPVGCKPEQQM*MYAGSK.N	3131.61197	3	7.04E-08	0.62	3.45	-	688.2
AHQ-1-12, 6101	R.VSYPLCFIFSSPVGCKPEQQM*M*YAGSK.N	3147.61137	3	1.40E-05	0.75	3.41	-	626.1
gi|4557361|ref|NP_001187.1| BH3 interacting domain death agonist; BH3-interacting domain death agon				2.52E-10	2.76	30.23	28.70	21994.6
AHQ-1-11, 5836	R.DVFHTTVNFINQNLR.T	1819.01348	2	1.98E-05	0.90	3.99	-	794.8
AHQ-1-11, 5880	R.ELDALGHELPVLAPQWEGYDELQTDGNR.S	3167.38790	3	6.27E-05	0.89	4.24	-	824.9
AHQ-1-11, 2715	R.IEADSESQEDIIR.N	1505.56635	2	2.52E-10	0.97	4.54	-	2071.1
gi|12707570|ref|NP_004083.2| mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor [Homo				2.61E-10	1.50	20.21	13.10	31371.2
AHQ-1-10, 4925	K.AQFAQPEILIGTIPGAGGTQR.L	2126.40140	2	2.94E-04	0.55	2.58	-	571.6
AHQ-1-10, 6400	K.ICPVETLVEEAIQCAEK.I	1992.25744	2	2.61E-10	0.96	4.23	-	1372.5
gi|27480104|ref|XP_208215.1| similar to triosephosphate isomerase 1 [Homo sapiens]				2.67E-10	5.27	60.24	27.70	26942.6
AHQ-1-13, 3070	R.HVFGESDELIGQK.V	1459.58565	2	4.36E-05	0.94	4.03	-	818.3
AHQ-1-10, 2816 - 2843	R.HVFGESDELIGQK.V	1459.58565	2	2.67E-10	0.96	4.73	-	839.3
AHQ-1-13- , 3113	R.HVFGESDELIGQK.V	1459.58565	2	6.95E-09	0.96	4.71	-	791.0
AHQ-1-13- , 2835	R.IIYGGSVTGATCK.E	1328.51672	2	2.13E-08	0.90	3.77	-	585.1
AHQ-1-10, 2625	R.IIYGGSVTGATCK.E	1328.51672	1	5.64E-05	0.42	2.57	-	335.1
AHQ-1-10, 2611	R.IIYGGSVTGATCK.E	1328.51672	2	1.34E-04	0.90	3.33	-	798.1
AHQ-1-13, 2826 - 2829	R.IIYGGSVTGATCK.E	1328.51672	2	2.87E-07	0.88	3.77	-	589.3
AHQ-1-13- , 2168 - 2236	K.SNVSDAVAQSTR.I	1235.28659	2	8.87E-04	0.88	3.26	-	1072.8
AHQ-1-10, 2039	K.SNVSDAVAQSTR.I	1235.28659	2	9.42E-06	0.96	3.78	-	2283.7
AHQ-1-10, 3971 - 4015	K.VTNGAFTGEISPGMIK.D	1622.86786	2	5.00E-06	0.83	3.34	-	818.4
AHQ-1-10, 3512 - 3571	K.VTNGAFTGEISPGM*IK.D	1638.86726	2	2.60E-07	0.75	3.03	-	700.7
AHQ-1-10, 3997	K.VTNGAFTGEISPGM*IK.D	1638.86726	2	2.79E-05	0.60	2.58	-	620.8
AHQ-1-10, 4936 - 5016	K.VVLAYEPVWAIGTGK.T	1603.88587	2	1.13E-05	0.87	3.51	-	775.0
gi|20357552|ref|NP_005222.2| cortactin isoform a; oncogene EMS1 [Homo sapiens]				2.80E-10	1.90	20.30	8.00	61585.7
AHQ-1-14- , 4707	K.ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK.E	3334.37643	3	2.64E-06	0.93	5.03	-	823.8
AHQ-1-14- , 4851 - 4922	K.ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK.E	3334.37643	3	1.27E-04	0.90	4.78	-	582.4
AHQ-1-14- , 4992	K.ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK.E	3334.37643	3	2.80E-10	0.95	5.98	-	789.3
AHQ-1-12, 5198 - 5257	R.YGLFPANYVELR.Q	1442.64306	2	9.98E-10	0.94	4.32	-	681.7

gi|30150448|ref|XP_293066.2| similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose				2.81E-10	0.97	10.29	2.90	58788.2
AHQ-1-6, 4686 - 4696	R.VINEPTAAALAYGLDK.S	1646.86592	2	2.81E-10	0.97	5.73	-	834.3
gi|4503987|ref|NP_003869.1| gamma-glutamyl hydrolase precursor; conjugase; folylpolygammaglutamyl h				3.22E-10	0.93	10.22	4.10	35964.1
AHQ-1-14- , 5311	R.LDLTEKDYEILFK.S	1627.85937	2	3.22E-10	0.93	4.44	-	869.6
gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre				3.22E-10	9.15	110.29	41.20	48141.1
AHQ-1-7, 6117 - 6185	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	1.32E-04	0.97	5.81	-	1484.9
AHQ-1-7, 6126 - 6138	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	2	1.01E-06	0.86	3.17	-	980.5
AHQ-1-14- , 3958	K.EQFLDGDGWTSR.W	1411.45795	2	4.12E-05	0.85	2.91	-	1042.1
AHQ-1-14, 6413 - 6448	R.FYALSASFEPFSNK.G	1608.77470	2	7.44E-04	0.85	3.12	-	1036.9
AHQ-1-7, 5581 - 5652	R.FYALSASFEPFSNK.G	1608.77470	2	2.78E-08	0.97	5.25	-	1595.2
AHQ-1-7, 3690	K.IDDPTDSKPEDWDKPEHIPDPDAK.K	2761.89139	3	1.69E-04	0.79	3.98	-	750.6
AHQ-1-7, 3693	K.IDDPTDSKPEDWDKPEHIPDPDAK.K	2761.89139	2	6.61E-06	0.44	2.80	-	353.0
AHQ-1-7, 5308 - 5381	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	2	4.80E-09	0.80	3.35	-	594.1
AHQ-1-7, 2432	K.IKDPDASKPEDWDER.A	1801.89173	2	2.62E-06	0.93	3.79	-	980.7
AHQ-1-7, 5638	K.KPEDWDEEMDGEWEPPVIQNPEYK.G	2962.14926	3	2.09E-06	0.87	4.27	-	767.6
AHQ-1-7, 5636	K.KPEDWDEEMDGEWEPPVIQNPEYK.G	2962.14926	2	4.88E-09	0.92	4.40	-	587.4
AHQ-1-7, 5026	K.KPEDWDEEM*DGEWEPPVIQNPEYK.G	2978.14866	3	3.40E-06	0.83	4.01	-	660.8
AHQ-1-7, 2262	K.KVHVIFNYK.G	1148.38164	2	1.74E-05	0.84	2.90	-	720.6
AHQ-1-7, 2254	K.KVHVIFNYK.G	1148.38164	1	2.82E-06	0.80	2.92	-	564.0
AHQ-1-7, 7448	K.SGTIFDNFLITNDEAYAEEFGNETWGVTK.A	3270.46022	3	3.22E-10	0.97	5.89	-	1790.0
AHQ-1-7, 2670	K.VHVIFNYK.G	1020.20872	1	1.95E-06	0.76	2.78	-	746.9
gi|17921989|ref|NP_005991.1| tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain				3.30E-10	13.63	170.29	46.90	49924.1
AHQ-1-13- , 4747 - 4812	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	8.13E-04	0.97	5.10	-	2323.8
AHQ-1-7, 4754	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	2.02E-05	0.93	3.67	-	1470.7
AHQ-1-14- , 4667 - 4739	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	5.12E-05	0.93	4.39	-	1610.2
AHQ-1-13, 5060 - 5125	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.25E-04	0.95	3.97	-	1592.4
AHQ-1-12, 5049 - 5105	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	6.30E-08	0.92	3.92	-	1289.5
AHQ-1-13- , 6167 - 6245	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	7.71E-07	0.96	4.66	-	1709.5
AHQ-1-14- , 5960 - 5980	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.66E-05	0.93	3.81	-	1445.7
AHQ-1-13- , 5583 - 5592	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	5.39E-05	0.96	4.21	-	1936.7
AHQ-1-13- , 5348	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	3.26E-06	0.94	3.97	-	1231.5
AHQ-1-7, 6084	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	6.23E-05	0.92	3.82	-	1182.6
AHQ-1-7, 6512	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.40E-05	0.77	2.86	-	1084.9
AHQ-1-7, 5772	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	4.41E-10	0.95	4.40	-	1192.4
AHQ-1-13- , 5840	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.61E-05	0.85	3.17	-	934.5
AHQ-1-7, 6377 - 6444	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	4.00E-08	0.95	4.38	-	1404.1
AHQ-1-14, 6117	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.50E-05	0.74	3.13	-	680.0
AHQ-1-13, 5849 - 5908	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	6.55E-05	0.62	2.79	-	529.6
AHQ-1-12, 5839	R.AVCMLSNTTAIAEAWAR.L	1867.13992	3	9.87E-06	0.96	4.25	-	2420.9
AHQ-1-3, 6355	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.52E-04	0.87	2.92	-	1272.4
AHQ-1-9, 6234 - 6235	R.AVFVDLEPTVIDEIR.N	1716.95615	2	4.13E-07	0.92	4.20	-	1242.3
AHQ-1-12, 5863	R.AVFVDLEPTVIDEIR.N	1716.95615	2	3.99E-05	0.78	3.24	-	826.0
AHQ-1-7, 6384 - 6409	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.96E-09	0.86	3.15	-	1201.8
AHQ-1-13, 5793	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.19E-07	0.65	2.65	-	936.4
AHQ-1-7, 5709 - 5770	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	2.13E-04	0.92	4.17	-	879.0
AHQ-1-7, 5564	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	2.35E-07	0.97	5.77	-	1269.3
AHQ-1-7, 5865	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	1.36E-07	0.91	3.90	-	887.2
AHQ-1-7, 3640	K.DVNAAIAAIK.T	986.14745	1	6.27E-05	0.93	3.27	-	1291.7
AHQ-1-12, 3353	K.DVNAAIAAIK.T	986.14745	2	1.91E-04	0.87	3.10	-	963.9
AHQ-1-7, 3421 - 3433	K.DVNAAIAAIK.T	986.14745	2	3.02E-05	0.93	3.98	-	1068.2
AHQ-1-12, 3029	K.DVNAAIAAIK.T	986.14745	1	1.51E-04	0.49	1.80	-	815.7
AHQ-1-7, 3096 - 3169	K.DVNAAIAAIK.T	986.14745	1	3.71E-04	0.71	2.36	-	890.7
AHQ-1-7, 1477	K.EDAANNYAR.G	1024.02636	1	1.50E-04	0.14	2.11	-	241.1
AHQ-1-12, 5047	R.IHFPLATYAPVISAEK.A	1758.05310	2	7.05E-05	0.79	3.31	-	450.7
AHQ-1-11, 4834	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.68E-04	0.93	3.93	-	754.4
AHQ-1-7, 5128 - 5196	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.04E-06	0.96	4.58	-	881.1
AHQ-1-10, 4643 - 4700	R.IHFPLATYAPVISAEK.A	1758.05310	2	9.05E-04	0.82	3.40	-	480.0
AHQ-1-9, 4947 - 5023	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.55E-06	0.87	3.61	-	503.6
AHQ-1-13, 4976 - 5040	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.61E-05	0.65	2.83	-	426.0
AHQ-1-7, 5224 - 5264	R.IHFPLATYAPVISAEK.A	1758.05310	2	7.26E-10	0.96	4.80	-	810.5
AHQ-1-7, 3052	R.LDHKFDLMYAK.R	1381.62467	2	5.72E-04	0.74	3.07	-	553.5
AHQ-1-7, 7088 - 7164	R.LISQIVSSITASLR.F	1488.75471	2	5.18E-09	0.97	4.98	-	1212.8
AHQ-1-7, 7225 - 7297	R.LISQIVSSITASLR.F	1488.75471	2	8.79E-08	0.95	4.70	-	1043.7
AHQ-1-14- , 6556	R.LISQIVSSITASLR.F	1488.75471	2	1.80E-08	0.95	4.64	-	1072.4
AHQ-1-9, 6934	R.LISQIVSSITASLR.F	1488.75471	2	2.90E-06	0.93	4.07	-	1087.5
AHQ-1-13- , 6812	R.LISQIVSSITASLR.F	1488.75471	2	1.35E-07	0.95	4.48	-	1031.2
AHQ-1-8, 7066	R.LISQIVSSITASLR.F	1488.75471	2	5.14E-09	0.92	4.05	-	862.8
AHQ-1-7, 6189	R.LISQIVSSITASLR.F	1488.75471	2	1.40E-04	0.94	4.37	-	962.9
AHQ-1-5, 3455	R.NLDIERPTYTNLNR.L	1719.88022	2	6.45E-05	0.43	2.82	-	284.6
AHQ-1-9, 3304	R.NLDIERPTYTNLNR.L	1719.88022	2	1.87E-04	0.60	3.06	-	439.2
AHQ-1-7, 3465 - 3488	R.NLDIERPTYTNLNR.L	1719.88022	3	7.80E-06	0.73	3.37	-	498.6
AHQ-1-14, 4358	R.NLDIERPTYTNLNR.L	1719.88022	2	1.01E-04	0.60	2.66	-	488.7
AHQ-1-7, 3540 - 3620	R.NLDIERPTYTNLNR.L	1719.88022	2	7.26E-05	0.36	2.77	-	244.1
AHQ-1-7, 3602 - 3676	R.NLDIERPTYTNLNR.L	1719.88022	2	3.88E-06	0.71	3.41	-	586.7
AHQ-1-13, 3463	R.NLDIERPTYTNLNR.L	1719.88022	2	4.48E-04	0.50	3.13	-	323.4
AHQ-1-6, 3424	R.NLDIERPTYTNLNR.L	1719.88022	2	1.95E-07	0.33	2.89	-	225.4
AHQ-1-7, 3441 - 3512	R.NLDIERPTYTNLNR.L	1719.88022	2	4.65E-05	0.65	3.20	-	383.6
AHQ-1-14- , 3523	R.NLDIERPTYTNLNR.L	1719.88022	2	2.08E-04	0.42	2.94	-	282.2
AHQ-1-7, 4276	R.QLFHPEQLITGK.E	1411.63050	2	6.81E-04	0.68	3.31	-	337.1
AHQ-1-3, 5970	R.SIQFVDWCPTGFK.V	1586.79232	2	4.75E-04	0.71	2.61	-	631.6
AHQ-1-11, 5371	R.SIQFVDWCPTGFK.V	1586.79232	2	2.99E-06	0.50	2.52	-	460.4
AHQ-1-4, 6094 - 6096	R.SIQFVDWCPTGFK.V	1586.79232	2	1.44E-05	0.96	4.86	-	1324.4
AHQ-1-6, 5910	R.SIQFVDWCPTGFK.V	1586.79232	2	2.11E-04	0.83	2.82	-	787.7
AHQ-1-1, 5967	R.SIQFVDWCPTGFK.V	1586.79232	2	1.50E-05	0.92	3.87	-	761.8
AHQ-1-7, 5928 - 6000	R.SIQFVDWCPTGFK.V	1586.79232	2	3.26E-09	0.96	4.70	-	1192.8
AHQ-1-7, 5878 - 5948	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.95E-08	0.91	3.98	-	831.7
AHQ-1-9, 5755 - 5828	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.70E-06	0.66	3.27	-	371.1
AHQ-1-12, 5462	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.38E-07	0.72	3.32	-	406.0
AHQ-1-7, 6016 - 6097	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.77E-08	0.89	3.97	-	593.3
AHQ-1-7, 6168 - 6240	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	7.34E-10	0.68	3.06	-	380.1
AHQ-1-14- , 5563 - 5623	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.30E-10	0.96	5.14	-	887.6
AHQ-1-4, 6031	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.48E-09	0.68	3.19	-	293.9
AHQ-1-13- , 5760	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.38E-10	0.86	3.74	-	595.2
AHQ-1-13- , 4595	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	3.33E-08	0.72	3.66	-	278.5
AHQ-1-13- , 4449 - 4521	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.70E-06	0.70	3.24	-	302.6
AHQ-1-13, 4344	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.20E-04	0.65	2.78	-	364.6
AHQ-1-6, 4514 - 4531	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.28E-05	0.57	3.22	-	259.5
AHQ-1-7, 4349 - 4352	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.19E-04	0.73	3.06	-	353.9
AHQ-1-7, 4444 - 4512	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	7.50E-07	0.78	3.41	-	397.6
AHQ-1-10, 4075	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	6.87E-04	0.62	3.31	-	304.2
AHQ-1-7, 4580 - 4648	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.50E-04	0.82	3.38	-	419.7
AHQ-1-12, 4406 - 4481	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.66E-06	0.83	3.36	-	481.1
AHQ-1-12, 4313 - 4377	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	7.52E-07	0.80	3.41	-	360.6
AHQ-1-7, 4560 - 4592	K.YMACCLLYR.G	1252.50864	2	4.14E-04	0.96	3.84	-	1136.7
AHQ-1-12, 4349	K.YMACCLLYR.G	1252.50864	2	1.56E-06	0.95	3.58	-	1012.3
AHQ-1-7, 4056 - 4058	K.YM*ACCLLYR.G	1268.50804	2	8.39E-04	0.74	2.79	-	494.9
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				3.32E-10	5.14	60.29	21.70	61986.9

AHQ-1-1, 6349 - 6427	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.27E-07	0.95	5.45	-	1103.2
AHQ-1-3, 6502 - 6514	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	6.98E-05	0.92	4.52	-	1063.6
AHQ-1-4, 6648	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.03E-04	0.92	4.68	-	766.1
AHQ-1-6, 6467	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	8.74E-08	0.93	4.76	-	1011.3
AHQ-1-14- , 6120 - 6127	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	5.15E-07	0.96	5.75	-	1587.4
AHQ-1-12, 6001	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.78E-04	0.94	4.79	-	1325.9
AHQ-1-14- , 5018	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	1.76E-09	0.92	4.49	-	742.8
AHQ-1-13- , 5292	R.HGVQELEIELQSQLSK.K	1839.03978	2	3.32E-10	0.96	5.10	-	1389.8
AHQ-1-14- , 6616	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	5.03E-06	0.88	4.00	-	636.0
AHQ-1-14- , 6484	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	9.60E-08	0.92	4.10	-	938.9
AHQ-1-12, 6411	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	3.19E-05	0.71	2.83	-	841.9
AHQ-1-8, 4847	K.TLNDMRQEYEQLIAK.N	1853.08996	2	6.43E-06	0.53	2.84	-	641.3
gi|5453832|ref|NP_006380.1| oxygen regulated protein precursor; oxygen regulated protein (150kD) [H				3.36E-10	2.58	30.22	6.20	111334.8
AHQ-1-3, 6667	R.VEFEELCADLFER.V	1658.81048	2	3.36E-10	0.96	4.40	-	1491.0
AHQ-1-3, 6487 - 6562	K.VLQLINDNTATALSYGVFR.R	2096.37206	2	2.26E-08	0.96	4.36	-	1409.0
AHQ-1-3, 7430	R.VPGPVQQALQSAEM*SLDEIEQVILVGGATR.V	3153.55387	3	6.80E-04	0.66	3.65	-	337.3
gi|5174727|ref|NP_005989.1| chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring				3.65E-10	3.53	40.23	9.20	60330.4
AHQ-1-6, 3802	R.AVAQALEVIPR.T	1167.38326	2	2.48E-04	0.89	3.41	-	1108.6
AHQ-1-6, 4502	K.IPGGIIEDSCVLR.G	1430.65218	2	4.12E-07	0.95	4.64	-	1147.9
AHQ-1-6, 2822	R.TLIQNCGASTIR.L	1335.51249	2	2.61E-04	0.73	2.88	-	561.8
AHQ-1-6, 5551 - 5568	R.WSSLACNIALDAVK.M	1549.77353	2	3.65E-10	0.96	4.60	-	1377.7
gi|4502201|ref|NP_001649.1| ADP-ribosylation factor 1 [Homo sapiens]				3.86E-10	8.06	90.30	46.40	20696.6
AHQ-1-12, 4523 - 4589	R.DAVLLVFANK.Q	1090.29726	1	4.84E-05	0.85	2.94	-	946.7
AHQ-1-12, 4515 - 4578	R.DAVLLVFANK.Q	1090.29726	2	5.86E-06	0.97	4.52	-	2175.5
AHQ-1-12, 4774	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	5.20E-07	0.98	5.61	-	1960.4
AHQ-1-12, 4919	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	3.97E-08	0.98	5.96	-	1855.0
AHQ-1-12, 5143 - 5211	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.64E-09	0.98	5.53	-	1813.3
AHQ-1-12, 4959 - 5029	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	3.63E-04	0.44	3.31	-	274.5
AHQ-1-12, 4445 - 4509	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	6.18E-08	0.92	4.26	-	1186.3
AHQ-1-12, 4871 - 4885	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	3.86E-10	0.94	4.94	-	1054.7
AHQ-1-11, 4606 - 4684	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	1.29E-04	0.80	3.79	-	673.4
AHQ-1-12, 3673	R.ILMVGLDAAGK.T	1088.34632	1	6.08E-05	0.78	2.59	-	1254.3
AHQ-1-12, 3127	R.ILM*VGLDAAGK.T	1104.34572	2	3.48E-04	0.92	3.44	-	1349.7
AHQ-1-12, 3667 - 3669	R.ILMVGLDAAGK.T	1088.34632	2	6.33E-06	0.95	4.04	-	1222.6
AHQ-1-12, 3683	R.ILMVGLDAAGK.T	1088.34632	1	9.58E-04	0.80	3.50	-	634.5
AHQ-1-14- , 6268	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	6.11E-04	0.48	2.79	-	188.7
AHQ-1-12, 6177 - 6234	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	4.32E-04	0.72	3.86	-	162.9
AHQ-1-13- , 6512 - 6523	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	3.69E-04	0.49	3.38	-	171.4
AHQ-1-12, 2609 - 2611	R.MLAEDELR.D	977.11769	2	7.61E-04	0.89	2.99	-	982.5
AHQ-1-12, 6567	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	3	7.82E-10	0.96	4.30	-	2039.8
AHQ-1-12, 6565 - 6625	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	2	1.01E-04	0.89	3.90	-	712.9
AHQ-1-13- , 5244 - 5252	K.NISFTVWDVGGQDK.I	1566.69621	2	3.48E-08	0.93	4.13	-	773.4
AHQ-1-11, 4780	K.NISFTVWDVGGQDK.I	1566.69621	2	1.53E-04	0.87	3.13	-	1002.0
AHQ-1-14- , 5110 - 5114	K.NISFTVWDVGGQDK.I	1566.69621	2	2.60E-06	0.87	3.77	-	624.3
AHQ-1-12, 4913 - 4969	K.NISFTVWDVGGQDK.I	1566.69621	2	6.80E-09	0.95	4.48	-	1006.4
AHQ-1-13, 4952 - 4963	K.NISFTVWDVGGQDK.I	1566.69621	2	4.47E-04	0.90	4.12	-	678.2
gi|11496277|ref|NP_068805.1| mitogen-activated protein kinase kinase 1 interacting protein 1; MEK p				4.48E-10	1.85	20.27	35.50	13622.6
AHQ-1-14- , 5451	K.SIICYYNTYQVVQFNR.L	2070.31322	2	3.19E-06	0.92	3.81	-	1113.8
AHQ-1-14- , 5274	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	4.48E-10	0.93	5.43	-	673.5
gi|14149680|ref|NP_056107.1| KIAA0747 protein [Homo sapiens]				4.59E-10	5.01	60.26	7.90	122855.6
AHQ-1-4, 5752	K.AVYSTNCPVWEEAFR.F	1830.99795	2	1.28E-04	0.82	2.99	-	819.2
AHQ-1-12, 5382	R.FEWELPLDEAQR.R	1533.66622	2	1.67E-07	0.82	3.49	-	537.8
AHQ-1-4, 3320 - 3391	R.GSNPHLQTFTFTR.V	1506.64724	2	4.04E-06	0.87	3.02	-	940.0
AHQ-1-4, 4020	R.IHVLEAQDLIAK.D	1350.58860	2	4.59E-10	0.74	2.84	-	534.9
AHQ-1-7, 7246	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	6.24E-06	0.79	3.51	-	416.4
AHQ-1-12, 3975	R.LTHVDSPLEAPAGPLGQVK.L	1930.19405	2	1.93E-06	0.97	5.13	-	1746.8
AHQ-1-4, 4219	R.LTHVDSPLEAPAGPLGQVK.L	1930.19405	2	2.07E-04	0.84	3.24	-	757.1
gi|4504521|ref|NP_002147.1| heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P				4.75E-10	3.46	40.31	11.30	61024.2
AHQ-1-14- , 6627	R.ALM*LQGVDLLADAVAVTM*GPK.G	2146.55768	3	4.75E-10	0.98	6.27	-	2329.6
AHQ-1-7, 5750	K.CEFQDAYVLLSEK.K	1603.77482	2	9.54E-07	0.95	3.68	-	1739.8
AHQ-1-7, 5537	K.ISSIQSIVPALEIANAHR.K	1920.20240	2	3.09E-04	0.69	3.19	-	346.4
AHQ-1-7, 5889	K.TLNDELEIIEGMK.F	1505.71604	2	3.11E-06	0.83	2.68	-	1124.8
gi|4504345|ref|NP_000508.1| alpha 2 globin [Homo sapiens]				5.00E-10	2.60	30.27	30.30	15257.4
AHQ-1-13- , 4388	K.FLASVSTVLTSK.Y	1253.46970	2	1.77E-06	0.91	3.45	-	1145.7
AHQ-1-13- , 4187	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	2.66E-05	0.88	4.16	-	573.4
AHQ-1-13- , 4115 - 4183	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	3.52E-04	0.75	3.17	-	641.8
AHQ-1-13, 4003	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	1.08E-05	0.72	3.26	-	464.6
AHQ-1-13- , 2651	K.VGAHAGEYGAEALER.M	1530.62397	3	2.50E-05	0.97	5.44	-	2334.9
AHQ-1-13- , 2647	K.VGAHAGEYGAEALER.M	1530.62397	2	3.69E-08	0.96	4.09	-	1657.5
AHQ-1-13, 2654 - 2657	K.VGAHAGEYGAEALER.M	1530.62397	2	5.00E-10	0.97	4.94	-	1594.8
gi|4758950|ref|NP_000933.1| peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]				5.24E-10	6.99	80.21	36.60	23742.4
AHQ-1-12, 4119	K.DFMIQGGDFTR.G	1287.42660	2	4.52E-04	0.87	2.90	-	934.1
AHQ-1-11, 4006	K.DFMIQGGDFTR.G	1287.42660	2	3.10E-04	0.89	3.19	-	1173.3
AHQ-1-11, 2882	R.DKPLKDVIIADCGK.I	1573.83653	2	2.71E-08	0.89	3.53	-	963.5
AHQ-1-12, 2946 - 2954	R.DKPLKDVIIADCGK.I	1573.83653	3	6.13E-07	0.94	4.23	-	1290.4
AHQ-1-12, 2951	R.DKPLKDVIIADCGK.I	1573.83653	2	4.30E-07	0.91	3.81	-	876.9
AHQ-1-11, 4122	K.DTNGSQFFITTVK.T	1458.59766	2	5.28E-07	0.92	3.59	-	1366.3
AHQ-1-11, 2396	K.DVIIADCGK.I	992.12891	1	1.18E-05	0.68	2.29	-	616.4
AHQ-1-12, 3103	K.HYGPGWVSMANAGK.D	1475.65664	2	5.24E-10	0.95	4.13	-	1232.4
AHQ-1-12, 3146 - 3158	K.IEVEKPFAIAK.E	1245.49240	2	1.83E-05	0.92	3.54	-	1274.3
AHQ-1-11, 4166	K.TVDNFVALATGEK.G	1365.51377	2	6.62E-05	0.92	3.67	-	1106.7
AHQ-1-11, 4172 - 4174	K.TVDNFVALATGEK.G	1365.51377	1	7.83E-04	0.25	2.09	-	308.0
AHQ-1-14, 5402	K.TVDNFVALATGEK.G	1365.51377	2	1.92E-04	0.88	3.89	-	648.7
AHQ-1-12, 4602	K.TVDNFVALATGEK.G	1365.51377	2	2.65E-06	0.90	3.23	-	880.6
AHQ-1-12, 4305	K.TVDNFVALATGEK.G	1365.51377	2	2.05E-05	0.87	3.52	-	826.3
AHQ-1-11, 3987	R.VIKDFMIQGGDFTR.G	1627.88933	2	1.27E-06	0.85	3.32	-	790.3
AHQ-1-12, 4133	R.VIKDFMIQGGDFTR.G	1627.88933	2	1.85E-06	0.88	3.54	-	901.7
gi|4758484|ref|NP_004823.1| glutathione-S-transferase like; glutathione transferase omega [Homo sap				5.27E-10	4.23	60.18	19.50	27565.7
AHQ-1-10, 3720	K.EDPTVSALLTSEK.D	1390.51840	1	1.27E-04	0.48	2.78	-	252.4
AHQ-1-10, 2955	K.EDYAGLKEEFR.K	1357.45019	2	5.27E-10	0.87	2.91	-	1012.5
AHQ-1-10, 2461	K.GSAPPGPVPEGSIR.I	1321.46422	1	1.86E-04	0.27	2.59	-	205.0
AHQ-1-13- , 2989 - 2992	R.HEVININLK.N	1080.26247	2	2.72E-07	0.92	3.24	-	993.9
AHQ-1-10, 2677	R.HEVININLK.N	1080.26247	1	2.48E-04	0.75	3.00	-	543.6
AHQ-1-13- , 2924	R.SQNKEDYAGLKEEFR.K	1814.93364	3	2.87E-08	0.82	3.62	-	780.9
AHQ-1-12, 4582	K.VPSLVGSFIR.S	1075.28583	2	1.90E-06	0.86	2.78	-	856.2
gi|24497612|ref|NP_116262.2| nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr				5.27E-10	2.86	30.28	9.20	72695.6
AHQ-1-6, 6752	K.LGCDWVATIFSR.D	1426.62208	2	5.46E-07	0.97	3.56	-	1988.0
AHQ-1-6, 6598	R.LVGEALLESNTIIDHVYCSPSLR.C	2588.91822	2	5.27E-10	0.96	4.72	-	1252.1
AHQ-1-6, 6210	R.RPYEDQGLGETTPLTIICQPMQPLR.V	2916.32264	3	6.94E-05	0.94	5.50	-	868.4
gi|7706497|ref|NP_057392.1| UMP-CMP kinase [Homo sapiens]				6.11E-10	4.48	50.23	27.60	25854.7
AHQ-1-11, 5740	R.IQTYLQSTKPIIDLYEEMGK.V	2371.73502	2	6.11E-10	0.90	4.67	-	362.2
AHQ-1-11, 2578	R.KNPDSQYGELIEK.Y	1521.65375	2	3.58E-07	0.93	4.36	-	755.6
AHQ-1-11, 6492	K.SVDEVFDEVVQIFDK.E	1769.92954	2	2.92E-04	0.79	3.07	-	681.2
AHQ-1-11, 6494	K.SVDEVFDEVVQIFDKEG	1956.09563	2	5.34E-04	0.93	4.31	-	916.4
AHQ-1-11, 3594 - 3667	K.YGYTHLSAGELLR.D	1480.64969	2	3.36E-07	0.93	3.75	-	1097.9
gi|4502011|ref|NP_000467.1| adenylate kinase 1 [Homo sapiens]				6.27E-10	5.76	70.24	47.90	21634.7
AHQ-1-11, 3680 - 3684	K.ATEPVIAFYEK.R	1268.43969	1	7.51E-05	0.31	2.09	-	463.5

AHQ-1-11, 6483	K.GQLVPLETVLDMLR.D	1584.90590	2	6.27E-10	0.95	4.79	-	693.2
AHQ-1-11, 6222 - 6303	K.GQLVPLETVLDM*LR.D	1600.90530	2	4.38E-06	0.87	4.11	-	396.5
AHQ-1-11, 5016	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	2	9.14E-05	0.85	3.61	-	703.8
AHQ-1-11, 3380 - 3460	K.IIFVVGGPGSGK.G	1131.34939	2	1.56E-04	0.91	3.59	-	1515.6
AHQ-1-11, 5900 - 5971	R.KVNAEGSVDSVFSQVCTHLDALK	2506.77407	3	9.80E-05	0.93	4.40	-	1359.8
AHQ-1-11, 3651	K.YGYTHLSTGDLLR.S	1496.64912	2	4.87E-04	0.93	3.76	-	1127.8
gi|19923437|ref|NP_057366.2| adenylate kinase 3 alpha like [Homo sapiens]				6.66E-10	2.24	30.21	19.40	25565.2
AHQ-1-10, 3119	K.AYEDQTKPVLEYYQK.K	1876.05535	2	3.05E-04	0.78	3.50	-	487.8
AHQ-1-10, 6024 - 6040	K.NLTQYSWLLDGFPR.T	1710.91339	2	6.66E-10	0.95	4.17	-	1440.8
AHQ-1-10, 4415 - 4417	K.TVGIDDLTGEPLIQR.E	1627.82100	2	6.16E-04	0.51	2.92	-	327.8
gi|4507907|ref|NP_000543.1| von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille				6.96E-10	22.80	260.30	12.90	309296.7
AHQ-1-1, 5053	K.AFVLSSVDELEQQR.D	1621.77332	2	7.68E-05	0.93	3.54	-	1835.0
AHQ-1-1, 4025	K.AHLLSLVDVM*QR.E	1398.65673	2	2.15E-08	0.94	3.68	-	1185.2
AHQ-1-1, 4201 - 4267	R.CLPTACTIQLR.G	1335.57568	2	2.39E-06	0.57	2.52	-	496.3
AHQ-1-1, 5109 - 5175	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	2.08E-06	0.63	3.18	-	504.7
AHQ-1-1, 5756	R.EQAPNLVYMVTGNPASDEIK.R	2177.42062	2	2.43E-05	0.93	4.12	-	685.8
AHQ-1-1, 4820	R.EQAPNLVYM*VTGNPASDEIK.R	2193.42002	2	4.35E-04	0.88	3.77	-	627.5
AHQ-1-1, 4187	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	2.02E-07	0.92	4.36	-	958.1
AHQ-1-1, 6273	R.IEDLPTMVTLGNSFLHK.L	1916.23079	2	4.24E-04	0.89	3.92	-	906.6
AHQ-1-1, 6867	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	2.76E-08	0.92	4.31	-	728.7
AHQ-1-1, 6968	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	1.28E-07	0.96	5.06	-	1029.3
AHQ-1-3, 7211	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	6.07E-06	0.90	4.14	-	582.5
AHQ-1-3, 2615	R.ILAGPAGDSNVVK.L	1241.41901	2	2.26E-04	0.87	2.89	-	1019.6
AHQ-1-2, 2695	R.ILAGPAGDSNVVK.L	1241.41901	2	2.75E-06	0.93	3.57	-	1064.2
AHQ-1-1, 2728	R.ILAGPAGDSNVVK.L	1241.41901	2	2.10E-07	0.88	3.54	-	823.3
AHQ-1-1, 6313	K.ILDELLQTCVDPEDCPVCEVAGR.R	2692.97859	2	1.82E-04	0.89	4.35	-	461.7
AHQ-1-1, 3780 - 3852	R.ILTSDVFQDCNK.L	1441.58869	2	7.04E-05	0.89	3.39	-	962.5
AHQ-1-1, 5849	R.LPGDIQVVPIGVGPNANVQELER.I	2415.73085	3	4.32E-06	0.86	3.49	-	1130.3
AHQ-1-1, 5845	R.LPGDIQVVPIGVGPNANVQELER.I	2415.73085	2	7.06E-08	0.72	3.09	-	377.0
AHQ-1-1, 4263	K.LTGSCSYVLFQNK.E	1518.71629	2	3.62E-04	0.94	3.68	-	1269.8
AHQ-1-1, 5555	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	7.06E-06	0.98	5.98	-	2701.3
AHQ-1-1, 5664	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	4.48E-04	0.96	5.49	-	1719.1
AHQ-1-1, 4077	R.SGFTYVLHEGECCGR.C	1774.91285	2	6.96E-10	0.90	3.35	-	932.6
AHQ-1-1, 3499	R.SKEFMEEVIQR.M	1396.59450	2	1.13E-05	0.91	3.03	-	1168.2
AHQ-1-1, 2588	R.SKEFM*EEVIQR.M	1412.59390	2	1.25E-05	0.94	3.55	-	1081.9
AHQ-1-1, 5051 - 5060	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	6.08E-06	0.95	4.80	-	749.4
AHQ-1-2, 5171 - 5201	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	3.73E-06	0.85	3.81	-	484.2
AHQ-1-3, 5025 - 5045	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	6.84E-07	0.82	3.81	-	330.2
AHQ-1-2, 6323	K.TYGLCGICDENGANDFMLR.D	2209.42291	2	5.91E-07	0.91	4.14	-	621.7
AHQ-1-1, 4584 - 4585	K.VIVIPVGIGPHANLK.Q	1527.87891	2	2.56E-07	0.89	4.00	-	435.6
AHQ-1-1, 4692	R.VTVFPIGIGDR.Y	1174.37426	2	4.49E-06	0.94	3.68	-	1097.1
AHQ-1-2, 3035	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.75E-06	0.93	3.85	-	982.0
AHQ-1-1, 3017 - 3023	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.15E-09	0.96	4.72	-	953.4
AHQ-1-1, 6641	K.YLFPGECQYVLVQDYCGSNPGTFR.I	2874.15305	2	1.90E-06	0.79	2.90	-	790.0
AHQ-1-1, 3472 - 3545	R.YLSDHSFLVSQGDR.E	1624.73576	2	7.84E-06	0.91	3.04	-	1444.4
AHQ-1-1, 6064	K.YTLFQIFSK.I	1147.34728	2	8.58E-08	0.93	3.21	-	1002.8
gi|4503643|ref|NP_000121.1| coagulation factor V precursor; labile factor; factor V Leiden [Homo sa				7.01E-10	4.33	50.22	3.00	251716.5
AHQ-1-3, 6026 - 6094	R.AADIEQQAVFAVFDENK.S	1896.04666	2	2.30E-06	0.95	4.36	-	1362.0
AHQ-1-1, 3309	R.AEVDDVIQVR.F	1144.26019	2	1.54E-04	0.97	4.00	-	2146.4
AHQ-1-1, 5268	R.DPDNIAAWYLR.S	1334.46145	2	7.71E-05	0.61	2.60	-	521.6
AHQ-1-1, 3277	K.EVIITGIQTQGAK.H	1358.56590	2	2.05E-05	0.88	3.00	-	1415.0
AHQ-1-5, 4986	R.GEYEEHLGILGPIIR.A	1696.92816	2	7.01E-10	0.93	3.58	-	1220.1
AHQ-1-2, 5207 - 5277	R.GEYEEHLGILGPIIR.A	1696.92816	2	3.30E-05	0.91	3.65	-	886.7
gi|4501993|ref|NP_003650.1| alkylglycerone phosphate synthase precursor [Homo sapiens]				7.10E-10	0.86	10.18	2.60	72911.4
AHQ-1-6, 6136	R.GISDPLTVFEQTEAAAR.E	1805.96665	2	7.10E-10	0.86	3.63	-	595.7
gi|14211923|ref|NP_115982.1| PKCI-1-related HIT protein [Homo sapiens]				7.27E-10	1.82	20.30	22.70	17161.6
AHQ-1-13, 5924	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	2.53E-09	0.95	4.65	-	1333.4
AHQ-1-13- , 6360	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	1.54E-06	0.97	5.93	-	1379.2
AHQ-1-13- , 6355 - 6364	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	2.98E-06	0.92	4.73	-	953.4
AHQ-1-13, 5920 - 5923	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	7.27E-10	0.88	4.21	-	826.1
AHQ-1-13, 5928	K.SLPADILYEDQQCLVFR.D	2069.32354	2	7.10E-06	0.94	3.89	-	1037.7
gi|30160191|ref|XP_294035.2| similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme				7.33E-10	0.94	10.21	2.80	50222.2
AHQ-1-7, 5188 - 5213	K.IYVDDGLISLQVK.Q	1463.70048	2	7.33E-10	0.94	3.94	-	1195.3
AHQ-1-7, 5292 - 5320	K.IYVDDGLISLQVK.Q	1463.70048	2	9.39E-09	0.96	4.26	-	1766.8
AHQ-1-7, 5048	K.IYVDDGLISLQVK.Q	1463.70048	2	1.97E-08	0.96	4.24	-	1758.2
gi|5803011|ref|NP_001966.1| enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron				7.35E-10	0.97	10.25	3.70	47268.3
AHQ-1-8, 6795	R.YITGDQLGALYQDFVR.D	1860.05915	2	7.35E-10	0.97	4.98	-	1199.3
gi|10346135|ref|NP_055083.1| microtubule-associated protein, RP/EB family, member 2; T-cell activat				7.51E-10	1.86	20.28	9.80	37031.1
AHQ-1-13, 6393	R.FQDNLDFIQWFK.K	1601.78539	2	8.73E-05	0.91	3.53	-	995.1
AHQ-1-9, 7056	R.FQDNLDFIQWFK.K	1601.78539	2	3.16E-07	0.96	4.32	-	1429.2
AHQ-1-12, 6510	R.FQDNLDFIQWFK.K	1601.78539	2	7.51E-10	0.95	4.55	-	1156.7
AHQ-1-13- , 6848	R.FQDNLDFIQWFK.K	1601.78539	2	1.17E-09	0.96	4.71	-	1137.7
AHQ-1-12, 4853	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	9.80E-08	0.90	4.08	-	1017.9
AHQ-1-9, 4859	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	3.00E-07	0.96	5.50	-	1412.6
AHQ-1-9, 4858	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	2	1.33E-04	0.92	4.32	-	767.1
gi|4507651|ref|NP_003281.1| tropomyosin 4 [Homo sapiens]				7.95E-10	6.20	70.28	25.40	28521.6
AHQ-1-9, 1894	K.AEGDVAALNR.R	1016.09051	2	1.62E-04	0.91	2.98	-	1466.3
AHQ-1-9, 4096	R.AEVSELKCGDLEEELK.N	1851.02256	2	1.27E-05	0.92	4.27	-	796.1
AHQ-1-9, 6216	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	9.16E-07	0.86	4.46	-	923.0
AHQ-1-9, 6114 - 6127	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	1.02E-08	0.92	4.75	-	1134.2
AHQ-1-9, 1718 - 1791	R.EKAEGDVAALNR.R	1273.37796	2	8.79E-05	0.79	2.71	-	925.0
AHQ-1-10, 2524	K.IQALQQQADEAEDR.A	1615.68404	2	3.99E-05	0.93	3.51	-	1224.2
AHQ-1-9, 2528 - 2535	K.IQALQQQADEAEDR.A	1615.68404	2	7.95E-10	0.98	5.59	-	1737.7
AHQ-1-11, 2560	K.IQALQQQADEAEDR.A	1615.68404	2	2.51E-07	0.97	4.31	-	1673.4
AHQ-1-9, 2251 - 2288	R.KIQALQQQADEAEDR.A	1743.85695	3	2.77E-08	0.94	4.67	-	1307.7
AHQ-1-9, 2574	R.KIQALQQQADEAEDR.A	1743.85695	2	1.43E-09	0.96	4.83	-	1317.8
AHQ-1-10, 2321	R.KIQALQQQADEAEDR.A	1743.85695	2	7.10E-07	0.96	5.03	-	1738.7
AHQ-1-9, 2484	R.KIQALQQQADEAEDR.A	1743.85695	2	8.12E-05	0.95	4.68	-	1257.6
AHQ-1-9, 1967	K.YSEKEDKYEEEIK.L	1690.78605	3	2.00E-06	0.73	3.41	-	889.6
AHQ-1-9, 2059	K.YSEKEDKYEEEIK.L	1690.78605	3	2.12E-05	0.85	3.65	-	1219.1
gi|4507869|ref|NP_003361.1| vasodilator-stimulated phosphoprotein [Homo sapiens]				8.05E-10	2.94	40.24	13.40	39829.4
AHQ-1-8, 2121	R.ATVMLYDDGNKR.W	1383.55582	2	1.36E-04	0.63	2.69	-	490.9
AHQ-1-8, 6258	K.VKEEIIEAFVQELR.K	1703.96061	2	8.05E-10	0.97	4.79	-	1636.3
AHQ-1-14- , 3035	R.VQIYHNPTANSFR.V	1547.69936	2	1.01E-05	0.48	2.76	-	415.1
AHQ-1-13- , 3137	K.YNQATPNFHQWR.D	1562.67258	2	7.37E-09	0.86	3.61	-	564.2
gi|4507951|ref|NP_003396.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept				8.07E-10	6.18	70.25	34.60	28218.5
AHQ-1-14- , 3019	K.AVTELNEPLSNEDR.N	1587.67060	2	2.78E-04	0.66	2.88	-	447.6
AHQ-1-10, 2795 - 2865	K.AVTELNEPLSNEDR.N	1587.67060	2	1.60E-06	0.95	4.93	-	915.1
AHQ-1-13- , 3053	K.AVTELNEPLSNEDR.N	1587.67060	2	1.38E-06	0.85	3.33	-	711.3
AHQ-1-10, 5495 - 5507	K.ELETVCNDVLSLLDK.F	1749.96137	2	8.07E-10	0.93	4.36	-	776.2
AHQ-1-13, 6403	K.ELETVCNDVLSLLDK.F	1749.96137	2	3.29E-07	0.79	3.50	-	495.7
AHQ-1-13- , 6864	K.ELETVCNDVLSLLDK.F	1749.96137	2	5.88E-07	0.93	4.31	-	855.1
AHQ-1-10, 6263	K.ELETVCNDVLSLLDK.F	1749.96137	2	4.37E-06	0.94	4.72	-	829.1
AHQ-1-10, 3889	K.FLIKNCNDFQYESK.V	1808.00430	2	1.09E-04	0.91	3.85	-	701.4
AHQ-1-13- , 2333	K.KNSVVEASEAAYK.E	1396.52786	2	2.82E-08	0.90	3.27	-	1061.8
AHQ-1-10, 2629	K.NSVVEASEAAYK.E	1268.35495	1	1.31E-05	0.63	2.21	-	578.2
AHQ-1-13- , 2672	K.NSVVEASEAAYK.E	1268.35495	2	1.20E-07	0.87	3.33	-	751.1

AHQ-1-10, 2468	K.NSVVEASEAAYK.E	1268.35495	2	1.36E-08	0.90	3.13	-	990.4
AHQ-1-13- , 6232 - 6235	K.QAFDDAIAELDTLNEDSYK.D	2159.24915	2	5.89E-07	0.94	4.61	-	761.3
AHQ-1-14- , 6040	K.QAFDDAIAELDTLNEDSYK.D	2159.24915	2	7.55E-05	0.84	3.77	-	565.3
AHQ-1-10, 5545 - 5619	K.QAFDDAIAELDTLNEDSYK.D	2159.24915	2	8.54E-06	0.29	2.63	-	153.9
AHQ-1-10, 2100	R.YLAEVASGEK.K	1067.17419	2	2.52E-05	0.87	2.99	-	1086.2
AHQ-1-10, 2099	R.YLAEVASGEK.K	1067.17419	1	1.72E-04	0.44	2.81	-	282.4
AHQ-1-10, 2093	R.YLAEVASGEK.K	1067.17419	1	1.16E-04	0.16	2.02	-	361.6
AHQ-1-13- , 2257 - 2267	R.YLAEVASGEK.K	1067.17419	2	6.49E-07	0.75	2.83	-	860.2
gi|4502565|ref|NP_001740.1| calpain, small subunit 1; calpain, small polypeptide; calcium-dependent				8.11E-10	3.95	50.24	36.20	28315.5
AHQ-1-12, 6597	R.LFAQLAGDDMEVSATELM*NILNK.V	2540.89556	3	5.53E-05	0.73	3.87	-	479.9
AHQ-1-12, 6413	R.SGTICSSELPGAFEAAGFHLNEHLYNM*IIR.R	3353.73016	3	8.41E-04	0.69	3.04	-	587.4
AHQ-1-12, 2819 - 2883	K.TDGFGIDTCR.S	1143.20921	2	9.15E-06	0.68	2.50	-	495.6
AHQ-1-11, 2307	R.THYSNIEANESEEVR.Q	1778.81502	2	2.42E-05	0.96	4.14	-	1668.1
AHQ-1-10, 2220 - 2281	R.THYSNIEANESEEVR.Q	1778.81502	2	5.89E-05	0.95	4.27	-	1290.5
AHQ-1-12, 6381 - 6418	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	2.75E-08	0.95	4.62	-	1171.8
AHQ-1-11, 6154 - 6210	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	4.97E-08	0.81	3.52	-	517.3
AHQ-1-10, 6120	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	3.29E-07	0.95	4.75	-	1214.7
AHQ-1-13, 6320	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	4.77E-06	0.83	3.52	-	577.4
AHQ-1-13- , 6773	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	2.68E-07	0.90	3.98	-	713.7
AHQ-1-14- , 6523	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	8.11E-10	0.90	3.77	-	887.1
gi|4505775|ref|NP_002626.1| phosphate carrier precursor isoform 1b; phosphate carrier, mitochondria				8.71E-10	2.43	30.21	15.20	39958.5
AHQ-1-9, 6559	K.GWAPTFLGYSMQGLCK.F	1818.10896	2	5.34E-06	0.94	4.15	-	979.3
AHQ-1-9, 2470	R.IQTQPGYANTLR.D	1362.51634	2	2.73E-04	0.67	3.02	-	393.8
AHQ-1-9, 7239	K.YYALCGFGGVLSCGLTHTAVVPLDLVK.C	2914.38804	2	8.71E-10	0.82	3.68	-	552.5
gi|17986258|ref|NP_066299.2| smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo				8.80E-10	7.08	80.27	42.40	16930.0
AHQ-1-14- , 4302	K.DQGTYEDYVEGLR.V	1545.58904	2	1.39E-05	0.85	3.46	-	1162.8
AHQ-1-13- , 4355	K.DQGTYEDYVEGLR.V	1545.58904	2	2.77E-06	0.95	3.76	-	1492.9
AHQ-1-12, 3913	K.EAFQLFDR.T	1026.12699	2	1.21E-04	0.77	2.93	-	701.5
AHQ-1-12, 2229 - 2273	R.HVLVTLGEK.M	996.18547	2	6.99E-07	0.88	3.30	-	638.9
AHQ-1-13- , 2359	R.HVLVTLGEK.M	996.18547	2	9.42E-07	0.82	2.88	-	608.8
AHQ-1-14, 3216	R.HVLVTLGEK.M	996.18547	1	7.00E-04	0.40	2.12	-	457.7
AHQ-1-13, 2414	R.HVLVTLGEK.M	996.18547	2	4.62E-06	0.86	3.27	-	682.5
AHQ-1-12, 2333	R.HVLVTLGEK.M	996.18547	2	4.72E-05	0.86	3.09	-	752.4
AHQ-1-12, 2239 - 2285	R.HVLVTLGEK.M	996.18547	1	2.00E-05	0.70	3.24	-	565.9
AHQ-1-14- , 2312 - 2366	R.HVLVTLGEK.M	996.18547	2	7.85E-05	0.85	2.74	-	736.0
AHQ-1-12, 2226 - 2374	R.HVLVTLGEK.M	996.18547	1	8.00E-04	0.74	2.48	-	803.9
AHQ-1-14- , 2320	R.HVLVTLGEK.M	996.18547	1	8.20E-04	0.79	2.84	-	726.5
AHQ-1-13- , 2356	R.HVLVTLGEK.M	996.18547	1	4.90E-04	0.61	2.52	-	661.2
AHQ-1-12, 3978 - 3990	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.53E-06	0.79	3.35	-	932.3
AHQ-1-14- , 3774	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.00E-07	0.94	3.84	-	1416.7
AHQ-1-12, 3967 - 3977	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.21E-09	0.89	3.82	-	910.7
AHQ-1-12, 3729	K.NKDQGTYEDYVEGLR.V	1787.86505	3	7.12E-06	0.83	3.69	-	1092.1
AHQ-1-12, 3723	K.NKDQGTYEDYVEGLR.V	1787.86505	2	6.10E-05	0.93	4.04	-	985.8
AHQ-1-12, 3601 - 3661	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.87E-09	0.96	4.38	-	1460.3
AHQ-1-13, 3729	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.56E-06	0.93	4.18	-	1106.9
AHQ-1-13, 4012	K.NKDQGTYEDYVEGLR.V	1787.86505	2	5.65E-09	0.86	3.40	-	806.2
AHQ-1-13- , 3876 - 3887	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.82E-09	0.95	4.25	-	1430.5
AHQ-1-12, 3594 - 3653	K.NKDQGTYEDYVEGLR.V	1787.86505	3	3.41E-04	0.93	4.38	-	1342.5
AHQ-1-14- , 3947	K.NKDQGTYEDYVEGLR.V	1787.86505	2	5.51E-06	0.89	3.69	-	1007.8
AHQ-1-14, 4652 - 4725	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.66E-07	0.91	4.11	-	1029.5
AHQ-1-12, 4057	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.81E-07	0.65	3.21	-	683.3
AHQ-1-14, 3504	R.VFDKEGNGTVM*GAEIR.H	1739.93168	2	1.98E-04	0.84	3.19	-	770.5
AHQ-1-13- , 3407 - 3429	R.VFDKEGNGTVMGAEIR.H	1723.93228	2	1.07E-08	0.94	4.38	-	1206.8
AHQ-1-12, 3257 - 3259	R.VFDKEGNGTVM*GAEIR.H	1739.93168	2	8.55E-04	0.94	3.92	-	1282.2
AHQ-1-14- , 2715	R.VFDKEGNGTVM*GAEIR.H	1739.93168	2	8.62E-05	0.81	2.63	-	838.2
AHQ-1-12, 3219 - 3281	R.VFDKEGNGTVMGAEIR.H	1723.93228	2	8.80E-10	0.95	4.33	-	1305.1
AHQ-1-12, 6186	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	5.82E-06	0.90	4.35	-	477.8
AHQ-1-12, 6525	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	8.59E-08	0.94	4.69	-	864.0
AHQ-1-12, 6087 - 6157	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	1.22E-05	0.89	3.80	-	1143.4
AHQ-1-13, 6048	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	9.57E-05	0.73	3.16	-	600.9
AHQ-1-12, 6386 - 6445	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	2.08E-05	0.88	3.74	-	771.9
AHQ-1-13- , 6865	K.VLDFEHFLPMLQTVAK.N	1889.25017	3	1.15E-05	0.88	3.90	-	1166.0
AHQ-1-14- , 6234 - 6264	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	6.78E-04	0.93	3.97	-	898.9
gi|4758638|ref|NP_004896.1| peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi				9.94E-10	8.82	110.33	53.10	25034.8
AHQ-1-10, 3669	R.DFTPVCTTELGR.A	1397.53591	1	1.04E-04	0.46	2.81	-	140.7
AHQ-1-10, 3660	R.DFTPVCTTELGR.A	1397.53591	1	9.40E-04	0.32	2.24	-	202.0
AHQ-1-13- , 3960 - 4007	R.DFTPVCTTELGR.A	1397.53591	2	5.53E-06	0.81	2.87	-	630.9
AHQ-1-10, 4481 - 4539	K.DGDSVMVLPTIPEEEAK.K	1831.03469	2	8.85E-05	0.74	2.99	-	784.0
AHQ-1-10, 3961 - 3984	K.DGDSVM*VLPTIPEEEAK.K	1847.03409	2	1.60E-05	0.48	2.52	-	375.2
AHQ-1-13- , 2683	K.DINAYNCEEPTEK.L	1584.64363	2	9.69E-05	0.66	2.77	-	645.8
AHQ-1-10, 5180 - 5249	K.DINAYNCEEPTEKLPFPIIDDR.N	2651.88650	2	5.85E-04	0.90	4.49	-	528.2
AHQ-1-10, 5651 - 5727	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	6.20E-08	0.97	5.14	-	1227.8
AHQ-1-13- , 6323 - 6387	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	1.80E-04	0.94	4.62	-	936.9
AHQ-1-10, 5860 - 5921	R.FHDFLGDSWGILFSHPR.D	2032.24831	2	1.91E-05	0.99	6.59	-	2624.4
AHQ-1-10, 5859 - 5861	R.FHDFLGDSWGILFSHPR.D	2032.24831	3	9.94E-10	0.97	5.80	-	1610.8
AHQ-1-14- , 5928 - 5995	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	1.38E-06	0.96	4.68	-	1062.5
AHQ-1-13- , 6124	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	3.80E-05	0.50	3.37	-	249.4
AHQ-1-10, 5524	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	2.84E-09	0.94	4.22	-	1178.8
AHQ-1-10, 5476	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	1.43E-05	0.53	3.48	-	346.5
AHQ-1-13- , 6123	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	2.52E-07	0.86	2.96	-	888.7
AHQ-1-14- , 5915	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	1.90E-04	0.54	3.17	-	356.4
AHQ-1-10, 5420 - 5475	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	9.90E-08	0.96	4.85	-	1332.6
AHQ-1-13, 4483	K.LPFPIIDDR.N	1086.26548	2	5.25E-05	0.86	3.25	-	611.8
AHQ-1-10, 4196	K.LPFPIIDDR.N	1086.26548	2	1.98E-05	0.92	3.36	-	896.1
AHQ-1-13- , 4693	K.LPFPIIDDR.N	1086.26548	2	4.08E-05	0.95	3.17	-	1463.3
AHQ-1-10, 4696	R.VATPVDWKDGDSVM*VLPTIPEEEAK.K	2744.06717	3	8.72E-04	0.56	3.16	-	297.3
AHQ-1-10, 3591	R.VVFVFGPDK.K	1008.19471	1	1.86E-04	0.76	2.33	-	969.7
AHQ-1-10, 3599	R.VVFVFGPDK.K	1008.19471	2	4.80E-06	0.88	3.19	-	654.1
gi|4507677|ref|NP_003290.1| tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu				9.94E-10	9.17	110.28	18.40	92468.2
AHQ-1-5, 6593	R.EAVEKEFEPLLNWMK.D	1864.15434	2	3.70E-04	0.86	3.30	-	879.2
AHQ-1-5, 3929	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	2.43E-08	0.98	5.53	-	2393.7
AHQ-1-5, 3927 - 3949	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	4.99E-06	0.96	4.94	-	1225.0
AHQ-1-5, 4047 - 4117	K.GVVDSDDLPLNVSR.E	1486.60940	1	7.51E-04	0.63	2.53	-	474.5
AHQ-1-6, 4038	K.GVVDSDDLPLNVSR.E	1486.60940	2	1.06E-09	0.93	4.18	-	881.3
AHQ-1-5, 7317 - 7318	K.GYEVIYLTEPVDEYCIQALPEFDGK.R	2951.24921	2	4.27E-05	0.62	2.85	-	310.6
AHQ-1-5, 7011 - 7074	K.GYEVIYLTEPVDEYCIQALPEFDGKR.F	3107.43557	3	9.94E-10	0.87	4.43	-	612.7
AHQ-1-5, 3365 - 3437	K.IADDKYNDTFWK.E	1516.63566	2	1.20E-04	0.88	3.39	-	861.8
AHQ-1-5, 6454 - 6521	K.KYSQFINFPIYVWSSK.T	2008.30657	2	1.04E-08	0.97	5.04	-	1841.0
AHQ-1-5, 5339	R.LISLTDENALSGNEELTVK.I	2047.24975	2	3.20E-05	0.90	4.11	-	793.6
AHQ-1-5, 5229	R.LISLTDENALSGNEELTVK.I	2047.24975	2	7.99E-07	0.95	5.20	-	1115.8
AHQ-1-5, 2653	R.SGYLLPDTK.A	994.12321	1	1.35E-06	0.70	2.89	-	629.0
AHQ-1-5, 2642	R.SGYLLPDTK.A	994.12321	1	6.92E-05	0.79	2.66	-	768.4
AHQ-1-5, 2649 - 2650	R.SGYLLPDTK.A	994.12321	2	2.71E-05	0.88	2.86	-	944.2
AHQ-1-5, 2662	K.TETVEEPMEEEEAAKEEK.E	2109.20871	2	5.87E-05	0.45	2.73	-	312.3
AHQ-1-5, 7065 - 7086	K.YSQFINFPIYVWSSK.T	1880.13366	2	5.79E-06	0.96	4.91	-	1035.7
gi|29739414|ref|XP_294015.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				1.03E-09	4.54	50.25	17.70	26916.7
AHQ-1-11, 3902	K.IISNASCTTNCLAPLAK.V	1837.10868	2	9.82E-08	0.80	3.73	-	806.7

<table>
<tr><td>AHQ-1-14- , 3995</td><td>K.IISNASCTTNCLAPLAK.V</td><td>1837.10868</td><td>2</td><td>3.71E-06</td><td>0.92</td><td>3.78</td><td>-</td><td>1519.4</td></tr>
<tr><td>AHQ-1-11, 3762 - 3822</td><td>K.IISNASCTTNCLAPLAK.V</td><td>1837.10868</td><td>2</td><td>1.46E-07</td><td>0.87</td><td>4.20</td><td>-</td><td>1282.1</td></tr>
<tr><td>AHQ-1-9, 3926 - 3947</td><td>K.IISNASCTTNCLAPLAK.V</td><td>1837.10868</td><td>2</td><td>3.54E-08</td><td>0.89</td><td>4.37</td><td>-</td><td>1202.3</td></tr>
<tr><td>AHQ-1-9, 4020 - 4087</td><td>K.IISNASCTTNCLAPLAK.V</td><td>1837.10868</td><td>2</td><td>3.26E-05</td><td>0.62</td><td>3.37</td><td>-</td><td>773.9</td></tr>
<tr><td>AHQ-1-9, 4142 - 4212</td><td>K.IISNASCTTNCLAPLAK.V</td><td>1837.10868</td><td>2</td><td>6.17E-09</td><td>0.81</td><td>4.06</td><td>-</td><td>961.5</td></tr>
<tr><td>AHQ-1-9, 5007 - 5038</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>2.13E-07</td><td>0.95</td><td>4.30</td><td>-</td><td>1243.8</td></tr>
<tr><td>AHQ-1-9, 5174 - 5242</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>9.49E-08</td><td>0.94</td><td>4.42</td><td>-</td><td>887.8</td></tr>
<tr><td>AHQ-1-9, 5363</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>2.62E-04</td><td>0.88</td><td>3.63</td><td>-</td><td>772.6</td></tr>
<tr><td>AHQ-1-9, 5495</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>1.56E-04</td><td>0.85</td><td>3.71</td><td>-</td><td>687.6</td></tr>
<tr><td>AHQ-1-14- , 5022 - 5102</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>1.10E-07</td><td>0.96</td><td>4.57</td><td>-</td><td>1510.2</td></tr>
<tr><td>AHQ-1-9, 4827</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>1.03E-09</td><td>0.94</td><td>4.35</td><td>-</td><td>716.4</td></tr>
<tr><td>AHQ-1-13- , 5137 - 5139</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>1.44E-09</td><td>0.97</td><td>4.55</td><td>-</td><td>1380.1</td></tr>
<tr><td>AHQ-1-10, 4591 - 4611</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>2.00E-08</td><td>0.95</td><td>4.70</td><td>-</td><td>992.7</td></tr>
<tr><td>AHQ-1-11, 4686 - 4751</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>1.29E-06</td><td>0.59</td><td>2.91</td><td>-</td><td>747.8</td></tr>
<tr><td>AHQ-1-11, 4827</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>3.97E-06</td><td>0.95</td><td>4.20</td><td>-</td><td>1075.7</td></tr>
<tr><td>AHQ-1-12, 4894</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>5.13E-04</td><td>0.75</td><td>2.53</td><td>-</td><td>998.3</td></tr>
<tr><td>AHQ-1-13, 4864</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>4.61E-09</td><td>0.93</td><td>4.25</td><td>-</td><td>829.3</td></tr>
<tr><td>AHQ-1-14, 5966 - 6028</td><td>K.LISWYDNEFGYSNR.V</td><td>1764.87478</td><td>2</td><td>2.20E-09</td><td>0.97</td><td>4.96</td><td>-</td><td>1345.2</td></tr>
<tr><td>AHQ-1-9, 2730</td><td>R.VVDLMAHMASK.E</td><td>1202.47292</td><td>2</td><td>2.35E-04</td><td>0.95</td><td>3.64</td><td>-</td><td>1160.3</td></tr>
<tr><td>AHQ-1-9, 2134</td><td>R.VVDLMAHM*ASKE</td><td>1347.58686</td><td>2</td><td>4.67E-04</td><td>0.87</td><td>3.97</td><td>-</td><td>1119.6</td></tr>
<tr><td>AHQ-1-9, 2942</td><td>R.VVDLMAHMASKE</td><td>1331.58746</td><td>2</td><td>1.55E-05</td><td>0.97</td><td>4.21</td><td>-</td><td>1881.0</td></tr>
<tr><td colspan="2">gi|13489087|ref|NP_109591.1| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member</td><td></td><td></td><td>1.07E-09</td><td>4.58</td><td>50.23</td><td>22.20</td><td>42741.5</td></tr>
<tr><td>AHQ-1-9, 4363</td><td>K.FAYGYIEDLK.C</td><td>1219.36713</td><td>2</td><td>2.39E-08</td><td>0.95</td><td>3.31</td><td>-</td><td>1327.2</td></tr>
<tr><td>AHQ-1-9, 4567</td><td>R.LGVQDLFNSSK.A</td><td>1208.34588</td><td>2</td><td>2.60E-05</td><td>0.91</td><td>2.71</td><td>-</td><td>1250.5</td></tr>
<tr><td>AHQ-1-9, 4036</td><td>K.TYGADLASVDFQHASEDAR.K</td><td>2054.11949</td><td>3</td><td>5.36E-09</td><td>0.88</td><td>4.09</td><td>-</td><td>640.2</td></tr>
<tr><td>AHQ-1-9, 4010 - 4078</td><td>K.TYGADLASVDFQHASEDAR.K</td><td>2054.11949</td><td>2</td><td>1.07E-09</td><td>0.93</td><td>4.06</td><td>-</td><td>953.7</td></tr>
<tr><td>AHQ-1-8, 4065 - 4144</td><td>K.TYGADLASVDFQHASEDAR.K</td><td>2054.11949</td><td>3</td><td>6.90E-05</td><td>0.61</td><td>3.26</td><td>-</td><td>418.8</td></tr>
<tr><td>AHQ-1-8, 4059</td><td>K.TYGADLASVDFQHASEDAR.K</td><td>2054.11949</td><td>2</td><td>3.14E-09</td><td>0.90</td><td>3.69</td><td>-</td><td>901.9</td></tr>
<tr><td>AHQ-1-9, 6340</td><td>K.TYNFLPEFLVSTQK.T</td><td>1687.91650</td><td>2</td><td>2.99E-04</td><td>0.94</td><td>4.67</td><td>-</td><td>578.9</td></tr>
<tr><td>AHQ-1-9, 7234 - 7306</td><td>R.VLELPYQGEELSMVILLPDDIEDESTGLKK.I</td><td>3375.82891</td><td>3</td><td>6.31E-09</td><td>0.86</td><td>4.57</td><td>-</td><td>557.5</td></tr>
<tr><td colspan="2">gi|5729997|ref|NP_004154.2| RAB27B, member RAS oncogene family [Homo sapiens]</td><td></td><td></td><td>1.07E-09</td><td>5.93</td><td>70.24</td><td>35.30</td><td>24607.7</td></tr>
<tr><td>AHQ-1-11, 6286</td><td>K.AVETLLDLIMK.R</td><td>1246.54211</td><td>2</td><td>1.96E-08</td><td>0.90</td><td>3.73</td><td>-</td><td>843.3</td></tr>
<tr><td>AHQ-1-10, 5295</td><td>K.AVETLLDLIM*K.R</td><td>1262.54151</td><td>2</td><td>5.79E-06</td><td>0.88</td><td>3.43</td><td>-</td><td>938.6</td></tr>
<tr><td>AHQ-1-10, 6160 - 6163</td><td>K.AVETLLDLIMK.R</td><td>1246.54211</td><td>2</td><td>9.83E-08</td><td>0.91</td><td>3.90</td><td>-</td><td>761.9</td></tr>
<tr><td>AHQ-1-10, 4917</td><td>K.AVETLLDLIM*KR.M</td><td>1418.72786</td><td>2</td><td>5.27E-04</td><td>0.71</td><td>2.67</td><td>-</td><td>647.2</td></tr>
<tr><td>AHQ-1-13- , 3132</td><td>K.LLALGDSGVGK.T</td><td>1030.20023</td><td>2</td><td>1.06E-06</td><td>0.84</td><td>2.68</td><td>-</td><td>1030.5</td></tr>
<tr><td>AHQ-1-13- , 3133</td><td>K.LLALGDSGVGK.T</td><td>1030.20023</td><td>1</td><td>5.74E-04</td><td>0.48</td><td>2.03</td><td>-</td><td>548.7</td></tr>
<tr><td>AHQ-1-11, 2930</td><td>K.LLALGDSGVGK.T</td><td>1030.20023</td><td>1</td><td>5.54E-04</td><td>0.30</td><td>2.07</td><td>-</td><td>354.9</td></tr>
<tr><td>AHQ-1-10, 2836</td><td>K.LLALGDSGVGK.T</td><td>1030.20023</td><td>1</td><td>1.67E-04</td><td>0.58</td><td>2.16</td><td>-</td><td>723.2</td></tr>
<tr><td>AHQ-1-13, 3097</td><td>K.LLALGDSGVGK.T</td><td>1030.20023</td><td>1</td><td>5.60E-04</td><td>0.57</td><td>2.35</td><td>-</td><td>704.7</td></tr>
<tr><td>AHQ-1-10, 5720 - 5767</td><td>R.NWMSQLQANAYCENPDIVLIGNK.A</td><td>2680.99772</td><td>2</td><td>1.20E-07</td><td>0.71</td><td>3.16</td><td>-</td><td>508.9</td></tr>
<tr><td>AHQ-1-11, 5987</td><td>R.NWMSQLQANAYCENPDIVLIGNK.A</td><td>2680.99772</td><td>2</td><td>5.95E-05</td><td>0.88</td><td>4.03</td><td>-</td><td>443.4</td></tr>
<tr><td>AHQ-1-10, 5887</td><td>R.NWMSQLQANAYCENPDIVLIGNK.A</td><td>2680.99772</td><td>2</td><td>8.68E-04</td><td>0.80</td><td>3.32</td><td>-</td><td>578.2</td></tr>
<tr><td>AHQ-1-10, 3399 - 3401</td><td>K.VHLQLWDTAGQER.F</td><td>1553.70390</td><td>2</td><td>2.76E-08</td><td>0.95</td><td>4.09</td><td>-</td><td>1209.2</td></tr>
<tr><td>AHQ-1-12, 3637</td><td>K.VHLQLWDTAGQER.F</td><td>1553.70390</td><td>2</td><td>5.54E-08</td><td>0.94</td><td>3.62</td><td>-</td><td>1245.9</td></tr>
<tr><td>AHQ-1-13, 3743</td><td>K.VHLQLWDTAGQER.F</td><td>1553.70390</td><td>2</td><td>6.59E-06</td><td>0.92</td><td>3.73</td><td>-</td><td>1159.7</td></tr>
<tr><td>AHQ-1-11, 3444 - 3510</td><td>K.VHLQLWDTAGQER.F</td><td>1553.70390</td><td>2</td><td>7.43E-06</td><td>0.92</td><td>3.62</td><td>-</td><td>821.8</td></tr>
<tr><td>AHQ-1-13- , 3868</td><td>K.VHLQLWDTAGQER.F</td><td>1553.70390</td><td>2</td><td>4.31E-08</td><td>0.96</td><td>3.87</td><td>-</td><td>1769.6</td></tr>
<tr><td>AHQ-1-10, 4272 - 4312</td><td>K.YGIPYFETSAATGQNVEK.A</td><td>1976.13177</td><td>2</td><td>4.54E-06</td><td>0.74</td><td>3.45</td><td>-</td><td>710.3</td></tr>
<tr><td>AHQ-1-10, 4124 - 4179</td><td>K.YGIPYFETSAATGQNVEK.A</td><td>1976.13177</td><td>2</td><td>1.07E-09</td><td>0.95</td><td>4.87</td><td>-</td><td>752.2</td></tr>
<tr><td>AHQ-1-11, 4302 - 4339</td><td>K.YGIPYFETSAATGQNVEK.A</td><td>1976.13177</td><td>2</td><td>4.93E-08</td><td>0.95</td><td>4.26</td><td>-</td><td>1179.8</td></tr>
<tr><td>AHQ-1-12, 4470</td><td>K.YGIPYFETSAATGQNVEK.A</td><td>1976.13177</td><td>2</td><td>4.48E-04</td><td>0.78</td><td>3.54</td><td>-</td><td>408.8</td></tr>
<tr><td>AHQ-1-13- , 4647 - 4711</td><td>K.YGIPYFETSAATGQNVEK.A</td><td>1976.13177</td><td>2</td><td>3.07E-08</td><td>0.91</td><td>4.12</td><td>-</td><td>757.7</td></tr>
<tr><td colspan="2">gi|4557395|ref|NP_000058.1| carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase;</td><td></td><td></td><td>1.07E-09</td><td>4.68</td><td>60.28</td><td>32.30</td><td>29245.8</td></tr>
<tr><td>AHQ-1-10, 6292</td><td>K.AVQQPDGLAVLGIFLK.V</td><td>1669.98899</td><td>2</td><td>3.16E-09</td><td>0.95</td><td>4.79</td><td>-</td><td>664.3</td></tr>
<tr><td>AHQ-1-13- , 6895</td><td>K.AVQQPDGLAVLGIFLK.V</td><td>1669.98899</td><td>2</td><td>1.68E-08</td><td>0.94</td><td>4.55</td><td>-</td><td>636.3</td></tr>
<tr><td>AHQ-1-10, 3048</td><td>K.EPISVSSEQVLK.F</td><td>1316.48265</td><td>1</td><td>9.76E-04</td><td>0.41</td><td>3.00</td><td>-</td><td>161.8</td></tr>
<tr><td>AHQ-1-10, 3931 - 4004</td><td>R.ILNNGHAFNVEFDDSQDK.A</td><td>2064.15751</td><td>2</td><td>1.07E-09</td><td>0.97</td><td>5.61</td><td>-</td><td>1757.9</td></tr>
<tr><td>AHQ-1-10, 3763</td><td>R.ILNNGHAFNVEFDDSQDK.A</td><td>2064.15751</td><td>2</td><td>2.39E-06</td><td>0.87</td><td>3.90</td><td>-</td><td>947.2</td></tr>
<tr><td>AHQ-1-10, 3129</td><td>K.SADFTNFDPR.G</td><td>1170.21306</td><td>2</td><td>1.66E-06</td><td>0.85</td><td>3.02</td><td>-</td><td>818.2</td></tr>
<tr><td>AHQ-1-10, 3559</td><td>K.VVDVLDSIK.T</td><td>988.16011</td><td>2</td><td>4.58E-05</td><td>0.87</td><td>3.66</td><td>-</td><td>436.7</td></tr>
<tr><td>AHQ-1-13, 4472</td><td>K.YDPSLKPLSVSYDQATSLR.I</td><td>2141.36647</td><td>2</td><td>4.61E-07</td><td>0.64</td><td>3.00</td><td>-</td><td>418.8</td></tr>
<tr><td colspan="2">gi|4505303|ref|NP_002466.1| myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m</td><td></td><td></td><td>1.09E-09</td><td>2.69</td><td>30.20</td><td>11.50</td><td>22763.8</td></tr>
<tr><td>AHQ-1-12, 2677 - 2757</td><td>R.ALGQNPTNAEVLK.V</td><td>1355.52211</td><td>2</td><td>1.09E-09</td><td>0.85</td><td>3.97</td><td>-</td><td>435.1</td></tr>
<tr><td>AHQ-1-12, 2779</td><td>R.ALGQNPTNAEVLK.V</td><td>1355.52211</td><td>2</td><td>5.10E-06</td><td>0.84</td><td>3.13</td><td>-</td><td>622.6</td></tr>
<tr><td>AHQ-1-12, 2877 - 2905</td><td>R.ALGQNPTNAEVLK.V</td><td>1355.52211</td><td>2</td><td>1.29E-07</td><td>0.84</td><td>3.71</td><td>-</td><td>425.2</td></tr>
<tr><td>AHQ-1-12, 2585</td><td>R.ALGQNPTNAEVLK.V</td><td>1355.52211</td><td>2</td><td>4.03E-07</td><td>0.70</td><td>3.32</td><td>-</td><td>350.9</td></tr>
<tr><td>AHQ-1-13- , 2743</td><td>K.ILYSQCGDVM*R.A</td><td>1359.55429</td><td>2</td><td>2.97E-06</td><td>0.92</td><td>3.11</td><td>-</td><td>1154.1</td></tr>
<tr><td>AHQ-1-13- , 3395</td><td>K.ILYSQCGDVMR.A</td><td>1343.55489</td><td>2</td><td>5.09E-07</td><td>0.90</td><td>3.09</td><td>-</td><td>975.6</td></tr>
<tr><td>AHQ-1-14- , 2694 - 2768</td><td>K.ILYSQCGDVM*R.A</td><td>1359.55429</td><td>2</td><td>1.17E-05</td><td>0.94</td><td>3.46</td><td>-</td><td>1192.3</td></tr>
<tr><td>AHQ-1-12, 3174 - 3237</td><td>K.ILYSQCGDVMR.A</td><td>1343.55489</td><td>2</td><td>1.74E-08</td><td>0.91</td><td>3.23</td><td>-</td><td>1020.1</td></tr>
<tr><td colspan="2">gi|4507645|ref|NP_000356.1| triosephosphate isomerase 1 [Homo sapiens]</td><td></td><td></td><td>1.18E-09</td><td>3.55</td><td>40.27</td><td>30.90</td><td>26669.3</td></tr>
<tr><td>AHQ-1-13- , 4023</td><td>K.DCGATWVVLGHSER.R</td><td>1588.72671</td><td>2</td><td>2.38E-07</td><td>0.89</td><td>3.78</td><td>-</td><td>701.4</td></tr>
<tr><td>AHQ-1-13, 3868</td><td>K.DCGATWVVLGHSER.R</td><td>1588.72671</td><td>2</td><td>8.03E-07</td><td>0.91</td><td>3.72</td><td>-</td><td>951.8</td></tr>
<tr><td>AHQ-1-10, 3581 - 3653</td><td>K.DCGATWVVLGHSER.R</td><td>1588.72671</td><td>2</td><td>1.18E-09</td><td>0.95</td><td>4.28</td><td>-</td><td>1256.3</td></tr>
<tr><td>AHQ-1-14- , 6574</td><td>K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q</td><td>3031.40532</td><td>3</td><td>1.78E-06</td><td>0.58</td><td>3.48</td><td>-</td><td>171.1</td></tr>
<tr><td>AHQ-1-10, 6007 - 6085</td><td>K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q</td><td>3031.40532</td><td>3</td><td>7.64E-07</td><td>0.80</td><td>3.84</td><td>-</td><td>238.4</td></tr>
<tr><td>AHQ-1-13- , 6684</td><td>K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q</td><td>3031.40532</td><td>3</td><td>7.58E-06</td><td>0.69</td><td>3.47</td><td>-</td><td>233.9</td></tr>
<tr><td>AHQ-1-10, 4815</td><td>K.QSLGELIGTLNAAK.V</td><td>1415.61746</td><td>2</td><td>8.42E-05</td><td>0.83</td><td>3.14</td><td>-</td><td>706.0</td></tr>
<tr><td>AHQ-1-13, 5349</td><td>K.VPADTEVVCAPPTAYIDFAR.Q</td><td>2194.44943</td><td>2</td><td>3.54E-07</td><td>0.96</td><td>5.31</td><td>-</td><td>871.4</td></tr>
<tr><td>AHQ-1-13- , 5656</td><td>K.VPADTEVVCAPPTAYIDFAR.Q</td><td>2194.44943</td><td>2</td><td>6.60E-06</td><td>0.93</td><td>4.28</td><td>-</td><td>763.8</td></tr>
<tr><td colspan="2">gi|4503573|ref|NP_001967.1| enolase 3; enolase-3, beta, muscle; muscle specific enolase; beta enola</td><td></td><td></td><td>1.25E-09</td><td>0.71</td><td>10.21</td><td>3.50</td><td>46958.5</td></tr>
<tr><td>AHQ-1-8, 3776</td><td>K.VNQIGSVTESIQACK.L</td><td>1635.82159</td><td>2</td><td>7.73E-06</td><td>0.90</td><td>4.19</td><td>-</td><td>582.5</td></tr>
<tr><td>AHQ-1-8, 3979</td><td>K.VNQIGSVTESIQACK.L</td><td>1635.82159</td><td>2</td><td>1.25E-09</td><td>0.71</td><td>3.24</td><td>-</td><td>632.4</td></tr>
<tr><td>AHQ-1-13, 3751</td><td>K.VNQIGSVTESIQACK.L</td><td>1635.82159</td><td>2</td><td>6.49E-04</td><td>0.89</td><td>3.59</td><td>-</td><td>745.3</td></tr>
<tr><td>AHQ-1-14, 4594 - 4648</td><td>K.VNQIGSVTESIQACK.L</td><td>1635.82159</td><td>2</td><td>2.88E-05</td><td>0.75</td><td>2.96</td><td>-</td><td>590.7</td></tr>
<tr><td>AHQ-1-13- , 3889</td><td>K.VNQIGSVTESIQACK.L</td><td>1635.82159</td><td>2</td><td>5.98E-07</td><td>0.83</td><td>3.02</td><td>-</td><td>796.8</td></tr>
<tr><td>AHQ-1-8, 3693</td><td>K.VNQIGSVTESIQACK.L</td><td>1635.82159</td><td>2</td><td>1.52E-06</td><td>0.94</td><td>3.99</td><td>-</td><td>1051.2</td></tr>
<tr><td colspan="2">gi|29568101|ref|NP_006467.3| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT</td><td></td><td></td><td>1.33E-09</td><td>2.44</td><td>30.22</td><td>14.60</td><td>11400.3</td></tr>
<tr><td>AHQ-1-14- , 3660 - 3731</td><td>K.TPALVNAAVTYSK.P</td><td>1335.53080</td><td>2</td><td>1.33E-09</td><td>0.93</td><td>4.19</td><td>-</td><td>869.6</td></tr>
<tr><td>AHQ-1-14- , 3678 - 3715</td><td>K.TPALVNAAVTYSKPR.L</td><td>1588.83283</td><td>2</td><td>4.85E-05</td><td>0.96</td><td>4.47</td><td>-</td><td>1196.4</td></tr>
<tr><td>AHQ-1-14, 4512 - 4570</td><td>K.TPALVNAAVTYSKPR.L</td><td>1588.83283</td><td>2</td><td>2.84E-06</td><td>0.91</td><td>4.03</td><td>-</td><td>869.5</td></tr>
<tr><td>AHQ-1-14- , 4388</td><td>K.VELVPPTPAEIPR.A</td><td>1418.66294</td><td>2</td><td>9.83E-05</td><td>0.60</td><td>2.53</td><td>-</td><td>259.6</td></tr>
<tr><td colspan="2">gi|16933567|ref|NP_005361.2| mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]</td><td></td><td></td><td>1.33E-09</td><td>0.92</td><td>10.20</td><td>6.80</td><td>23668.1</td></tr>
<tr><td>AHQ-1-11, 5723</td><td>K.ANINVENAFFTLAR.D</td><td>1580.76926</td><td>2</td><td>1.33E-09</td><td>0.92</td><td>3.92</td><td>-</td><td>909.7</td></tr>
<tr><td colspan="2">gi|29730023|ref|XP_291482.1| similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno</td><td></td><td></td><td>1.39E-09</td><td>5.31</td><td>60.25</td><td>13.30</td><td>63563.0</td></tr>
<tr><td>AHQ-1-5, 4902</td><td>R.IINKPTAAAIAYGLDK.R</td><td>1659.95097</td><td>2</td><td>3.59E-07</td><td>0.70</td><td>3.26</td><td>-</td><td>701.9</td></tr>
<tr><td>AHQ-1-7, 4874</td><td>R.IINKPTAAAIAYGLDK.R</td><td>1659.95097</td><td>2</td><td>1.15E-05</td><td>0.87</td><td>3.30</td><td>-</td><td>989.4</td></tr>
<tr><td>AHQ-1-6, 4782 - 4863</td><td>R.IINKPTAAAIAYGLDK.R</td><td>1659.95097</td><td>2</td><td>1.96E-08</td><td>0.82</td><td>4.16</td><td>-</td><td>774.9</td></tr>
<tr><td>AHQ-1-9, 4758</td><td>R.IINKPTAAAIAYGLDK.R</td><td>1659.95097</td><td>2</td><td>1.88E-05</td><td>0.83</td><td>4.32</td><td>-</td><td>726.1</td></tr>
<tr><td>AHQ-1-6, 3468 - 3523</td><td>K.KKELEEIVQPIISK.L</td><td>1654.97263</td><td>2</td><td>3.20E-07</td><td>0.96</td><td>4.79</td><td>-</td><td>1452.4</td></tr>
<tr><td>AHQ-1-5, 3595</td><td>K.LYGSAGPPPTGEEDTAEKDEL</td><td>2177.26447</td><td>2</td><td>8.47E-09</td><td>0.93</td><td>4.32</td><td>-</td><td>847.4</td></tr>
<tr><td>AHQ-1-6, 3512 - 3594</td><td>K.LYGSAGPPPTGEEDTAEKDEL</td><td>2177.26447</td><td>2</td><td>1.18E-05</td><td>0.96</td><td>5.02</td><td>-</td><td>866.5</td></tr>
<tr><td>AHQ-1-6, 3430</td><td>K.LYGSAGPPPTGEEDTAEKDEL</td><td>2177.26447</td><td>2</td><td>1.00E-03</td><td>0.83</td><td>3.32</td><td>-</td><td>787.3</td></tr>
<tr><td>AHQ-1-6, 4030</td><td>R.NELESYAYSLK.N</td><td>1317.42597</td><td>2</td><td>3.74E-04</td><td>0.87</td><td>2.79</td><td>-</td><td>1089.5</td></tr>
<tr><td>AHQ-1-5, 5855</td><td>K.TFAPKEISAMVLTK.M</td><td>1536.86124</td><td>2</td><td>9.24E-06</td><td>0.90</td><td>2.96</td><td>-</td><td>1300.7</td></tr>
<tr><td>AHQ-1-6, 5764</td><td>K.TFAPKEISAMVLTK.M</td><td>1536.86124</td><td>2</td><td>1.39E-09</td><td>0.87</td><td>3.12</td><td>-</td><td>1269.1</td></tr>
</table>

AHQ-1-6, 4919 - 4992	K.TFAPKEISAM*VLTK.M	1552.86064	2	1.19E-05	0.85	3.61	-	1115.2
gi|29742827|ref|XP_294099.1| similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]				1.43E-09	1.63	20.23	14.20	17094.0
AHQ-1-11, 2267 - 2339	K.EAFNM*IDQNR.D	1254.35498	2	6.81E-04	0.66	2.70	-	540.9
AHQ-1-11, 3132	R.FTDEEVDELYR.E	1416.47127	2	1.80E-04	0.94	3.69	-	1267.6
AHQ-1-11, 3615 - 3678	R.FTDEEVDELYR.E	1416.47127	2	3.58E-08	0.97	4.63	-	1707.0
AHQ-1-11, 3679 - 3739	R.FTDEEVDELYR.E	1416.47127	1	9.65E-06	0.37	1.82	-	427.7
AHQ-1-11, 3692	R.FTDEEVDELYR.E	1416.47127	1	4.78E-05	0.61	2.54	-	443.4
AHQ-1-11, 3738 - 3751	R.FTDEEVDELYR.E	1416.47127	2	1.43E-09	0.97	4.55	-	1901.3
AHQ-1-12, 3706 - 3769	R.FTDEEVDELYR.E	1416.47127	2	1.31E-08	0.97	4.56	-	1686.9
AHQ-1-13, 3847	R.FTDEEVDELYR.E	1416.47127	2	8.77E-08	0.95	3.44	-	1575.9
AHQ-1-14, 4760 - 4761	R.FTDEEVDELYR.E	1416.47127	2	5.83E-08	0.97	4.40	-	1664.6
AHQ-1-13- , 3991	R.FTDEEVDELYR.E	1416.47127	2	2.47E-09	0.96	3.57	-	1753.8
AHQ-1-14- , 3894 - 3895	R.FTDEEVDELYR.E	1416.47127	2	1.05E-08	0.97	4.64	-	1698.5
gi|21361621|ref|NP_002624.2| phosphoglucomutase 1 [Homo sapiens]				1.44E-09	1.45	20.17	5.00	61448.7
AHQ-1-7, 3806	K.FNISNGGPAPEAITDK.I	1631.76820	2	1.44E-09	0.93	3.44	-	1638.9
AHQ-1-7, 4078 - 4086	K.TIEEYAVCPDLK.V	1439.61271	2	6.11E-04	0.52	2.52	-	767.2
gi|5803227|ref|NP_006817.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype				1.58E-09	4.46	50.26	30.20	27764.1
AHQ-1-14- , 2287	K.AVTEQGAELSNEER.N	1533.57979	2	5.43E-06	0.89	2.92	-	1374.4
AHQ-1-13- , 2311	K.AVTEQGAELSNEER.N	1533.57979	2	1.58E-09	0.93	3.91	-	1172.7
AHQ-1-10, 2141 - 2165	K.AVTEQGAELSNEER.N	1533.57979	2	5.92E-07	0.84	3.16	-	950.0
AHQ-1-13- , 4217	K.QTIDNSQGAYQEAFDISK.K	2016.11116	2	1.50E-05	0.86	3.53	-	793.5
AHQ-1-10, 3823	K.QTIDNSQGAYQEAFDISK.K	2016.11116	2	3.20E-04	0.45	2.77	-	133.3
AHQ-1-13- , 6767	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	4.41E-09	0.95	4.72	-	1160.8
AHQ-1-10, 6127	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	2.59E-05	0.96	4.83	-	1082.8
AHQ-1-13, 6315 - 6316	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	4.10E-06	0.95	4.83	-	1004.4
AHQ-1-14- , 6522 - 6528	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	8.64E-06	0.95	5.14	-	989.2
AHQ-1-10, 2551	R.YLAEVACGDDR.K	1270.35099	2	7.22E-08	0.91	2.92	-	1249.9
AHQ-1-10, 2553	K.YLIANATNPESK.V	1321.46099	2	2.39E-04	0.94	3.37	-	1726.3
AHQ-1-10, 2643 - 2707	K.YLIANATNPESK.V	1321.46099	1	1.45E-07	0.81	3.03	-	814.2
AHQ-1-10, 2648	K.YLIANATNPESK.V	1321.46099	2	1.30E-04	0.92	3.60	-	1183.3
gi|12545410|ref|NP_031394.1| RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,				1.60E-09	1.77	20.24	4.30	95912.5
AHQ-1-5, 5375	K.SADVEPVSASAAHILGEVCR.E	2070.26993	2	1.60E-09	0.95	4.88	-	1055.6
AHQ-1-5, 6513	K.SLCPFYGEDFYCEIPR.S	2056.26024	2	1.90E-05	0.82	3.60	-	429.9
gi|20127408|ref|NP_000173.2| hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub				1.76E-09	4.81	60.25	12.70	82999.1
AHQ-1-6, 6556	R.DSIFSNLTGQLDYQGFEK.A	2063.20943	2	6.76E-08	0.96	4.92	-	1075.3
AHQ-1-6, 2616	K.DTSASAVAVGLK.Q	1119.25064	1	2.83E-04	0.20	2.22	-	392.8
AHQ-1-6, 4704	R.FGGGNPELLTQMVSK.G	1578.81508	2	4.98E-06	0.91	3.83	-	806.3
AHQ-1-6, 3094	K.TGIEQGSDAGYLCESQK.F	1844.93497	2	1.76E-09	0.92	3.83	-	875.2
AHQ-1-6, 3596	K.TLQEVTQLSQEAQR.I	1631.76974	2	1.18E-05	0.95	3.91	-	1896.1
AHQ-1-6, 6202	K.TVLGTPEVLLGALPGAGGTQR.L	2008.30795	3	1.65E-07	0.87	4.18	-	836.4
gi|8922673|ref|NP_060692.1| parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]				1.79E-09	0.96	10.20	3.50	42243.4
AHQ-1-9, 4644 - 4656	R.DAFDTLFDHAPDK.L	1492.57096	2	8.48E-08	0.93	3.89	-	1137.1
AHQ-1-9, 4654	R.DAFDTLFDHAPDK.L	1492.57096	1	1.82E-04	0.47	2.34	-	520.3
AHQ-1-9, 4664	R.DAFDTLFDHAPDK.L	1492.57096	1	2.60E-06	0.87	3.91	-	605.0
AHQ-1-13- , 4779	R.DAFDTLFDHAPDK.L	1492.57096	2	4.31E-09	0.93	3.47	-	1288.4
AHQ-1-9, 4307	R.DAFDTLFDHAPDK.L	1492.57096	2	1.79E-09	0.96	3.68	-	1632.3
gi|4505759|ref|NP_002622.1| phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo				1.79E-09	2.78	30.28	11.20	53151.7
AHQ-1-14, 5518	R.DYFGAHTYELLAK.P	1528.68958	2	1.67E-06	0.96	4.04	-	1603.4
AHQ-1-8, 6438	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	5.75E-05	0.97	5.51	-	1555.0
AHQ-1-8, 6622	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	1.79E-09	0.98	4.84	-	2241.5
AHQ-1-8, 4465	K.VGTGEPCCDWVGDEGAGHFVK.M	2280.43619	2	4.92E-05	0.81	3.31	-	587.9
AHQ-1-8, 4464	K.VGTGEPCCDWVGDEGAGHFVK.M	2280.43619	3	9.80E-09	0.84	4.12	-	352.1
gi|30150022|ref|XP_300862.1| similar to beta-tubulin 4Q [Homo sapiens]				1.85E-09	4.60	50.22	22.20	33545.2
AHQ-1-7, 6493	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	5.74E-06	0.93	4.49	-	1401.9
AHQ-1-13- , 6252	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	3.96E-04	0.85	3.86	-	944.0
AHQ-1-9, 3224 - 3236	R.FPGQLNADLR.K	1131.26634	2	1.26E-06	0.85	3.05	-	792.0
AHQ-1-8, 3197 - 3236	R.FPGQLNADLR.K	1131.26634	2	3.57E-05	0.90	3.13	-	852.8
AHQ-1-7, 3616	R.FPGQLNADLR.K	1131.26634	2	9.21E-07	0.85	3.06	-	714.8
AHQ-1-7, 3480 - 3496	R.FPGQLNADLR.K	1131.26634	2	6.19E-05	0.88	3.17	-	760.6
AHQ-1-7, 3340 - 3409	R.FPGQLNADLR.K	1131.26634	2	1.41E-04	0.91	3.54	-	888.3
AHQ-1-7, 3956	R.KLAVNMVPFPR.L	1272.58771	2	3.11E-07	0.95	4.07	-	1261.0
AHQ-1-8, 4329	K.LAVNMVPFPR.L	1144.41480	2	3.37E-05	0.94	3.83	-	899.1
AHQ-1-7, 4536	K.LAVNMVPFPR.L	1144.41480	2	3.23E-06	0.94	4.01	-	888.2
AHQ-1-10, 4116	K.LAVNMVPFPR.L	1144.41480	2	1.52E-06	0.90	3.41	-	731.2
AHQ-1-9, 4400 - 4406	K.LAVNMVPFPR.L	1144.41480	2	2.76E-08	0.94	4.29	-	773.3
AHQ-1-7, 5864 - 5892	R.LHFFMPGFAPLTSR.G	1621.92962	2	1.24E-08	0.94	3.67	-	895.7
AHQ-1-11, 5416	R.LHFFMPGFAPLTSR.G	1621.92962	2	6.91E-05	0.93	3.57	-	1037.1
AHQ-1-7, 5874	R.LHFFMPGFAPLTSR.G	1621.92962	3	7.20E-04	0.82	3.55	-	931.9
AHQ-1-9, 5695 - 5698	R.LHFFMPGFAPLTSR.G	1621.92962	2	1.85E-09	0.92	3.76	-	737.3
gi|19913424|ref|NP_001681.2| ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT				1.91E-09	2.85	30.25	7.10	68303.7
AHQ-1-6, 4318	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	1.12E-08	0.95	4.58	-	949.5
AHQ-1-6, 3078	R.TALVANTSNMPVAAR.E	1516.74852	2	1.91E-09	0.98	5.09	-	1974.1
AHQ-1-6, 3192	R.VGHSELVGEIIR.L	1309.49658	2	3.19E-08	0.92	3.38	-	1140.0
gi|4502097|ref|NP_001142.1| solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra				1.92E-09	2.74	30.18	12.10	33148.4
AHQ-1-10, 3176 - 3247	R.AAYFGVYDTAK.G	1206.32845	2	1.19E-06	0.92	3.62	-	802.5
AHQ-1-10, 4248	K.DFLAGAVAAAVSK.T	1220.39980	2	5.22E-04	0.93	3.34	-	2189.0
AHQ-1-10, 5240	R.YFPTQALNFAFK.D	1447.66130	1	3.20E-06	0.58	2.92	-	409.8
AHQ-1-13, 5519	R.YFPTQALNFAFK.D	1447.66130	2	1.92E-09	0.89	2.91	-	831.3
AHQ-1-13- , 5789 - 5855	R.YFPTQALNFAFK.D	1447.66130	2	3.08E-07	0.86	3.23	-	695.7
AHQ-1-10, 5231 - 5252	R.YFPTQALNFAFK.D	1447.66130	2	1.06E-07	0.92	3.08	-	868.8
gi|4503117|ref|NP_000091.1| cystatin B; stefin B; liver thiol proteinase inhibitor; CPI-B [Homo sap				2.16E-09	2.45	30.21	45.90	11139.5
AHQ-1-13- , 3600 - 3655	K.SQVVAGTNYFIK.V	1327.51036	2	1.59E-06	0.92	3.76	-	988.7
AHQ-1-13- , 3804	R.VFQSLPHENKPLTLSNYQTNK.A	2459.74218	3	5.10E-06	0.70	3.39	-	542.5
AHQ-1-13- , 3813	R.VFQSLPHENKPLTLSNYQTNK.A	2459.74218	2	6.97E-04	0.91	4.21	-	890.6
AHQ-1-13, 3295	K.VHVGDEDFVHLR.V	1423.55823	2	2.16E-09	0.83	2.94	-	515.5
gi|7657431|ref|NP_055205.1| EBNA-2 co-activator (100kD) [Homo sapiens]				2.17E-09	3.59	40.25	10.50	99689.7
AHQ-1-4, 6378 - 6402	R.DIQNTQCLLNVEHLSAGCPHVTLQFADSK.G	3299.63749	3	2.17E-09	0.96	5.00	-	1638.6
AHQ-1-4, 6574	K.DTNGENIAESLVAEGLATR.R	1961.07704	2	1.10E-08	0.96	4.36	-	1767.3
AHQ-1-4, 6680	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	3.24E-04	0.90	4.30	-	515.9
AHQ-1-4, 5043	K.VNVTVDYIRPASPATETVPAFSER.T	2620.89872	2	2.11E-04	0.61	2.83	-	376.9
AHQ-1-4, 5039	K.VNVTVDYIRPASPATETVPAFSER.T	2620.89872	3	3.90E-05	0.78	3.55	-	671.5
gi|4505773|ref|NP_002625.1| prohibitin [Homo sapiens]				2.21E-09	1.81	20.25	9.60	29803.9
AHQ-1-10, 3473	R.ILFRPVASQLPR.I	1397.69333	2	4.46E-04	0.84	3.09	-	778.5
AHQ-1-10, 3948	R.KLEAAEDIAYQLSR.S	1607.78978	2	2.21E-09	0.98	4.92	-	2169.0
gi|4507171|ref|NP_003109.1| secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec				2.22E-09	3.35	40.28	21.10	34632.0
AHQ-1-9, 3055	R.LEAGDHPVELLAR.D	1420.59579	2	1.32E-04	0.93	3.90	-	866.5
AHQ-1-8, 3057	R.LEAGDHPVELLAR.D	1420.59579	2	2.22E-09	0.94	4.37	-	1053.6
AHQ-1-9, 7126	K.NYNMYIFPVHWQFGQLDQHPIDGYLSHTELAPLR.A	4102.58560	3	2.69E-07	0.94	5.58	-	685.2
AHQ-1-9, 2723	K.RLEAGDHPVELLAR.D	1576.78214	2	2.29E-07	0.90	3.89	-	595.4
AHQ-1-9, 6550 - 6560	K.YIPPCLDSELTEFPLR.M	1952.21655	2	6.65E-08	0.58	2.94	-	199.1
gi|4504973|ref|NP_002292.1| lactate dehydrogenase C [Homo sapiens]				2.25E-09	0.91	10.18	3.60	36311.0
AHQ-1-9, 2475	R.VIGSGCNLDSAR.F	1250.36445	2	2.25E-09	0.91	3.63	-	721.7
AHQ-1-10, 2361	R.VIGSGCNLDSAR.F	1250.36445	2	3.67E-07	0.87	3.33	-	579.9
AHQ-1-11, 2348 - 2415	R.VIGSGCNLDSAR.F	1250.36445	2	7.77E-07	0.88	3.25	-	723.8
AHQ-1-9, 2379	R.VIGSGCNLDSAR.F	1250.36445	2	2.83E-06	0.85	3.48	-	788.2
gi|25188179|ref|NP_005653.3| voltage-dependent anion channel 3 [Homo sapiens]				2.34E-09	5.71	70.23	24.00	30658.4
AHQ-1-10, 3240	K.LSQNNFALGYK.A	1255.40424	1	1.09E-04	0.58	2.38	-	691.2

AHQ-1-13- , 3365 - 3431	K.LSQNNFALGYK.A	1255.40424	2	2.22E-04	0.82	3.05	-	749.8
AHQ-1-10, 3120	K.LSQNNFALGYK.A	1255.40424	2	3.44E-04	0.89	2.75	-	1228.6
AHQ-1-10, 4705	K.LTLDTIFVPNTGK.K	1419.64771	2	2.41E-07	0.93	3.72	-	1261.8
AHQ-1-10, 4596 - 4615	K.LTLDTIFVPNTGK.K	1419.64771	2	9.89E-05	0.92	3.89	-	816.8
AHQ-1-10, 4047	K.LTLDTIFVPNTGKK.S	1547.82062	2	4.90E-04	0.57	2.87	-	447.0
AHQ-1-10, 4288	K.LTLSALIDGK.N	1031.22813	2	8.34E-05	0.89	3.91	-	698.7
AHQ-1-13, 3696	K.VCNYGLTFTQK.W	1332.50706	2	5.10E-04	0.79	3.08	-	638.6
AHQ-1-10, 3423 - 3424	K.VCNYGLTFTQK.W	1332.50706	2	7.69E-05	0.94	4.33	-	958.5
AHQ-1-10, 4391	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	3	1.03E-06	0.88	4.36	-	755.3
AHQ-1-10, 4095	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	3	3.85E-07	0.89	3.99	-	1079.2
AHQ-1-10, 4093	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	1.77E-08	0.85	3.93	-	524.5
AHQ-1-10, 4223 - 4299	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.93E-09	0.85	3.76	-	637.0
AHQ-1-10, 4384	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.34E-09	0.85	3.88	-	517.3
AHQ-1-13, 4521	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	3	8.52E-07	0.79	4.10	-	587.5
AHQ-1-13, 4525	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	5.56E-07	0.86	3.63	-	642.1
AHQ-1-13- , 4744	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	8.64E-09	0.88	4.04	-	549.4
AHQ-1-10, 3619	K.YKVCNYGLTFTQK.W	1623.85410	2	3.02E-07	0.96	4.67	-	1350.3
gi|20539300|ref|XP_088391.4| similar to tropomyosin 4 [Homo sapiens]				2.40E-09	1.40	20.22	6.90	18592.1
AHQ-1-9, 3412 - 3488	R.KLVILEGELER.A	1299.54160	2	5.33E-06	0.95	4.10	-	1575.7
AHQ-1-9, 3576	R.KLVILEGELER.A	1299.54160	2	1.76E-06	0.90	3.75	-	934.4
AHQ-1-10, 3411	R.KLVILEGELER.A	1299.54160	2	1.45E-04	0.96	4.39	-	1529.8
AHQ-1-9, 3407 - 3484	R.KLVILEGELER.A	1299.54160	1	2.40E-09	0.45	2.48	-	388.4
AHQ-1-9, 4014	K.LVILEGELER.A	1171.36868	2	1.80E-08	0.95	3.70	-	1642.1
gi|4557419|ref|NP_000063.1| CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36				2.40E-09	3.65	40.25	12.90	53052.1
AHQ-1-6, 4755	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	9.03E-05	0.69	3.14	-	439.8
AHQ-1-5, 4857 - 4934	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	2.62E-06	0.90	3.85	-	621.5
AHQ-1-5, 4781 - 4849	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.76E-07	0.88	3.63	-	722.9
AHQ-1-1, 4831	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.26E-04	0.41	2.54	-	354.1
AHQ-1-5, 2818 - 2895	K.RLQVNLLVKPSEK.I	1524.83342	3	9.89E-04	0.83	3.64	-	903.5
AHQ-1-6, 5616 - 5635	K.SQVLQFFSSDICR.S	1588.76661	2	3.24E-05	0.94	3.48	-	1541.2
AHQ-1-5, 5681 - 5705	K.SQVLQFFSSDICR.S	1588.76661	2	4.02E-07	0.97	4.91	-	1717.6
AHQ-1-1, 5755	K.SQVLQFFSSDICR.S	1588.76661	2	4.51E-06	0.97	4.96	-	1477.0
AHQ-1-7, 5693	K.SQVLQFFSSDICR.S	1588.76661	2	1.66E-04	0.76	2.58	-	1037.8
AHQ-1-5, 7309 - 7314	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	2.40E-09	0.96	4.54	-	1328.8
gi|13129150|ref|NP_005339.1| heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H				2.43E-09	4.32	50.25	8.70	84659.1
AHQ-1-5, 2446	K.DQVANSAFVER.L	1236.31618	2	3.28E-04	0.94	3.55	-	1369.4
AHQ-1-5, 2382	K.FYEQFSK.N	949.04099	1	7.12E-04	0.73	2.51	-	732.4
AHQ-1-5, 6970	K.HGLEVIYMIEPIDEYCVQQLK.E	2579.97320	3	1.72E-05	0.87	4.04	-	1167.7
AHQ-1-5, 4137	R.NPDDITNEEYGEFYK.S	1834.87381	2	2.43E-09	0.97	4.99	-	1505.5
AHQ-1-6, 4080	R.NPDDITNEEYGEFYK.S	1834.87381	2	3.88E-07	0.92	4.35	-	694.6
AHQ-1-5, 4063	R.RAPFDLFENR.K	1265.40235	2	7.52E-05	0.80	3.17	-	544.5
gi|4507521|ref|NP_001055.1| transketolase [Homo sapiens]				2.64E-09	2.23	30.20	8.20	67877.3
AHQ-1-6, 4732	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	2.08E-06	0.91	4.05	-	410.6
AHQ-1-6, 3848 - 3894	R.SVPTSTVFYPSDGVATEK.A	1886.04854	2	5.61E-04	0.55	2.84	-	269.7
AHQ-1-6, 7174	R.TVPFCSTFAAFFTR.A	1653.88190	2	2.64E-09	0.77	3.16	-	312.9
gi|4504077|ref|NP_000165.1| glycoprotein IX (platelet) [Homo sapiens]				2.70E-09	5.34	60.22	30.50	19046.0
AHQ-1-11, 4750	R.ALETMGLWVDCR.G	1452.68135	2	3.19E-09	0.93	3.08	-	1241.4
AHQ-1-12, 4157	R.ALETM*GLWVDCR.G	1468.68075	2	2.88E-04	0.90	2.60	-	1108.2
AHQ-1-12, 4927	R.ALETMGLWVDCR.G	1452.68135	2	2.12E-04	0.93	3.87	-	941.2
AHQ-1-11, 4024 - 4035	R.ALETM*GLWVDCR.G	1468.68075	2	1.52E-04	0.87	3.66	-	781.8
AHQ-1-12, 2635 - 2715	R.CASPSLAAHGPLGR.L	1395.56962	2	2.70E-09	0.83	3.43	-	909.7
AHQ-1-11, 2604 - 2624	R.CASPSLAAHGPLGR.L	1395.56962	2	1.20E-06	0.92	3.35	-	1221.9
AHQ-1-14- , 2758	R.CASPSLAAHGPLGR.L	1395.56962	2	6.07E-07	0.93	3.43	-	1316.3
AHQ-1-11, 3232 - 3298	R.GHGLTALPALPAR.T	1274.49706	2	4.88E-05	0.96	4.35	-	1335.4
AHQ-1-12, 3427	R.GHGLTALPALPAR.T	1274.49706	2	2.80E-04	0.93	3.33	-	967.3
AHQ-1-11, 3295 - 3296	R.GHGLTALPALPAR.T	1274.49706	3	2.38E-05	0.89	3.30	-	1092.9
AHQ-1-11, 3299	R.GHGLTALPALPAR.T	1274.49706	1	9.71E-05	0.63	2.47	-	408.8
AHQ-1-11, 5108	R.LWLEDRTPEALLQVR.C	1840.11574	2	3.95E-05	0.89	4.13	-	735.1
AHQ-1-11, 3075 - 3098	R.TPEALLQVR.C	1027.19957	2	4.75E-04	0.84	3.00	-	832.1
AHQ-1-14- , 3228	R.TPEALLQVR.C	1027.19957	2	3.60E-06	0.94	3.02	-	1586.6
AHQ-1-14, 4189	R.TPEALLQVR.C	1027.19957	2	2.87E-05	0.92	3.27	-	1145.1
gi|4758756|ref|NP_004528.1| nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr				2.71E-09	4.18	50.24	15.10	45373.8
AHQ-1-7, 7370	K.GIPEFWLTVFK.N	1337.58999	2	2.71E-09	0.81	2.97	-	282.5
AHQ-1-7, 3786	R.KYAVLYQPLFDKR.F	1641.93733	2	5.64E-04	0.55	2.81	-	369.7
AHQ-1-7, 5757 - 5828	R.LDGLVETPTGYIESLPR.V	1861.08535	2	4.92E-05	0.93	3.98	-	952.6
AHQ-1-7, 5633 - 5676	K.NVDLLSDMVQEHDEPILK.H	2096.34751	2	3.07E-08	0.95	4.85	-	1000.5
AHQ-1-7, 4966	K.YAVLYQPLFDK.R	1357.57807	2	7.72E-06	0.94	3.35	-	1226.9
gi|5453990|ref|NP_006254.1| proteasome (prosome, macropain) activator subunit 1 (PA28 alpha); Prote				2.74E-09	1.72	20.19	13.70	28722.9
AHQ-1-10, 5637	K.ISELDAFLKEPALNEANLSNLK.A	2430.73906	2	2.74E-09	0.82	3.86	-	398.7
AHQ-1-10, 6105	R.NAYAVLYDIILK.N	1396.65574	2	3.71E-06	0.90	3.43	-	789.7
gi|4757766|ref|NP_004299.1| Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa				2.89E-09	2.05	30.24	8.70	50435.4
AHQ-1-11, 5663	K.FLLDHQGELFPSPDPSGL	1970.17037	2	3.74E-05	0.45	2.83	-	483.5
AHQ-1-7, 6412	K.FLLDHQGELFPSPDPSGL	1970.17037	2	1.03E-04	0.63	2.84	-	467.1
AHQ-1-8, 4060 - 4132	K.NPEQEPIPIVLR.E	1405.62426	2	2.43E-04	0.67	2.54	-	717.1
AHQ-1-8, 6391 - 6392	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	2.67E-06	0.93	4.68	-	712.1
AHQ-1-11, 5715	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	2.66E-04	0.74	3.50	-	331.8
AHQ-1-7, 6457	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	2.89E-09	0.93	4.80	-	619.0
gi|4502695|ref|NP_001779.1| cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c				3.05E-09	1.81	20.25	9.60	48786.6
AHQ-1-8, 5531	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	7.51E-06	0.95	4.91	-	1057.8
AHQ-1-13- , 6701	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	4.69E-05	0.68	3.14	-	430.1
AHQ-1-14- , 6215	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	2.58E-07	0.63	3.07	-	378.3
AHQ-1-14- , 6434	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	3.05E-09	0.86	4.03	-	587.5
AHQ-1-8, 6842	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	1.76E-05	0.75	3.32	-	698.1
gi|4505369|ref|NP_002486.1| NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q				3.38E-09	0.81	10.17	8.60	20107.8
AHQ-1-12, 4554	K.LDITTLTGVPEEHIK.T	1666.89713	2	3.38E-09	0.81	3.46	-	570.2
gi|22027538|ref|NP_037506.2| programmed cell death 6 interacting protein; ALG-2 interacting protein				3.45E-09	1.80	20.18	3.10	96022.6
AHQ-1-5, 4831	K.LANQAADYFGDAFK.Q	1531.65033	2	3.45E-09	0.89	3.57	-	810.6
AHQ-1-5, 3127 - 3133	R.LLDEEEATDNDLR.A	1533.57656	2	1.36E-06	0.91	3.56	-	1153.9
gi|10716563|ref|NP_001737.1| calnexin [Homo sapiens]				3.58E-09	1.74	20.22	4.20	67567.8
AHQ-1-5, 2329	K.AEEDEILNR.S	1089.13826	2	1.70E-04	0.85	2.79	-	1226.1
AHQ-1-4, 5167	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.69E-04	0.91	3.63	-	1018.8
AHQ-1-3, 5115	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.66E-06	0.87	3.28	-	820.9
AHQ-1-5, 5065	K.APVPTGEVYFADSFDR.G	1771.90722	2	3.58E-09	0.88	3.79	-	867.7
AHQ-1-6, 4998 - 5007	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.57E-07	0.93	4.42	-	1066.0
AHQ-1-1, 5160	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.96E-07	0.90	3.70	-	846.0
gi|8922835|ref|NP_060776.1| hypothetical protein FLJ11036 [Homo sapiens]				3.58E-09	0.97	10.22	6.90	22353.4
AHQ-1-13- , 6209	R.IHSVLQGFIPLFQK.F	1627.95380	2	3.58E-09	0.97	4.45	-	1552.8
gi|5032161|ref|NP_005639.1| elongin C; transcription elongation factor B (SIII), polypeptide 1 (15k				3.61E-09	1.75	20.24	28.60	12473.1
AHQ-1-13, 4651 - 4723	K.AMLSGPGQFAENETNEVNFR.E	2212.38515	2	2.43E-07	0.94	4.84	-	1206.5
AHQ-1-13- , 3180	K.LISSDGHEFIVK.R	1345.52569	2	3.61E-09	0.81	3.27	-	615.9
gi|27482573|ref|XP_208709.1| similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro				3.62E-09	1.90	20.26	26.00	17875.4
AHQ-1-12, 4801	K.GQVCLPVISAENWKPATK.T	2000.30757	2	7.08E-07	0.94	4.48	-	754.5
AHQ-1-12, 6491 - 6494	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	2	1.70E-06	0.93	5.00	-	547.0
AHQ-1-12, 6479 - 6490	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	3.62E-09	0.96	5.25	-	1430.0
gi|14149734|ref|NP_065174.1| coronin, actin binding protein, 1B [Homo sapiens]				3.68E-09	0.96	10.26	5.90	54234.4
AHQ-1-7, 7214	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	3.68E-09	0.96	5.25	-	1426.1
gi|29737978|ref|XP_290747.1| similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy				4.22E-09	4.49	50.24	2.10	191380.7

AHQ-1-3, 4037 - 4073	K.ADFCIIHYAGK.V	1296.47641	2	1.38E-04	0.87	2.71	-	1123.4
AHQ-1-2, 4185 - 4186	K.ADFCIIHYAGK.V	1296.47641	1	4.06E-04	0.76	3.09	-	696.3
AHQ-1-4, 4078	K.ADFCIIHYAGK.V	1296.47641	2	4.22E-09	0.92	3.70	-	970.0
AHQ-1-1, 4123	K.ADFCIIHYAGK.V	1296.47641	2	1.84E-04	0.87	3.24	-	882.8
AHQ-1-6, 3871 - 3884	K.ADFCIIHYAGK.V	1296.47641	2	1.40E-07	0.95	3.62	-	1328.7
AHQ-1-5, 3926	K.ADFCIIHYAGK.V	1296.47641	2	3.33E-05	0.88	3.50	-	724.7
AHQ-1-2, 4198	K.ADFCIIHYAGK.V	1296.47641	2	7.39E-06	0.96	3.95	-	1315.8
AHQ-1-5, 2781 - 2797	R.AGVLAHLEEER.D	1224.34854	2	3.15E-07	0.95	4.14	-	1590.9
AHQ-1-12, 2930	R.AGVLAHLEEER.D	1224.34854	2	1.05E-07	0.82	2.93	-	927.6
AHQ-1-1, 3124	R.AGVLAHLEEER.D	1224.34854	1	8.00E-05	0.36	1.84	-	657.3
AHQ-1-2, 3023 - 3102	R.AGVLAHLEEER.D	1224.34854	2	1.06E-06	0.96	4.14	-	1778.2
AHQ-1-6, 2758 - 2826	R.AGVLAHLEEER.D	1224.34854	2	4.89E-05	0.92	3.30	-	1288.0
AHQ-1-4, 2950 - 2963	R.AGVLAHLEEER.D	1224.34854	2	5.93E-07	0.96	4.42	-	1492.7
AHQ-1-13- , 3087	R.AGVLAHLEEER.D	1224.34854	2	2.54E-08	0.95	4.01	-	1388.6
AHQ-1-3, 2953	R.AGVLAHLEEER.D	1224.34854	2	5.58E-07	0.94	3.84	-	1464.5
AHQ-1-1, 3121	R.AGVLAHLEEER.D	1224.34854	2	1.64E-06	0.94	3.82	-	1390.1
AHQ-1-3, 3794	K.DKADFCIIHYAGK.V	1539.73719	3	1.07E-06	0.94	3.99	-	1761.0
AHQ-1-3, 3787	K.DKADFCIIHYAGK.V	1539.73719	2	4.25E-09	0.97	4.62	-	1699.6
AHQ-1-1, 3884	K.DKADFCIIHYAGK.V	1539.73719	2	1.41E-08	0.93	3.71	-	1176.6
AHQ-1-2, 3926	K.DKADFCIIHYAGK.V	1539.73719	2	4.85E-08	0.97	4.71	-	1896.5
AHQ-1-2, 3929	K.DKADFCIIHYAGK.V	1539.73719	3	4.81E-07	0.86	3.34	-	1107.2
AHQ-1-2, 4949 - 5017	K.LDPHLVLDQLR.C	1319.53460	2	9.67E-06	0.74	2.61	-	625.0
AHQ-1-1, 4860	K.LDPHLVLDQLR.C	1319.53460	3	2.98E-06	0.78	3.06	-	781.4
AHQ-1-1, 4843 - 4847	K.LDPHLVLDQLR.C	1319.53460	2	5.30E-05	0.73	2.77	-	542.7
AHQ-1-3, 4813	K.LDPHLVLDQLR.C	1319.53460	3	4.10E-06	0.79	3.64	-	668.6
AHQ-1-2, 4961 - 4965	K.LDPHLVLDQLR.C	1319.53460	3	2.86E-06	0.88	3.09	-	951.4
AHQ-1-2, 4127	K.VDYKADEWLMK.N	1398.60886	2	9.17E-09	0.77	3.03	-	645.8
gi|5031597|ref|NP_005710.1| actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub				4.60E-09	1.92	20.27	9.00	20546.5
AHQ-1-11, 6127	K.DTDIVDEAIYYFK.A	1592.72721	2	1.49E-06	0.94	3.79	-	1092.2
AHQ-1-12, 6317 - 6319	K.DTDIVDEAIYYFK.A	1592.72721	2	4.60E-09	0.97	5.44	-	1611.1
AHQ-1-14- , 6446	K.DTDIVDEAIYYFK.A	1592.72721	2	6.31E-06	0.92	3.62	-	1332.2
AHQ-1-11, 5651	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	1.37E-06	0.94	4.07	-	1148.0
gi|29740995|ref|XP_291768.1| similar to Proteasome activator complex subunit 2 (Proteasome activato				4.63E-09	0.96	10.25	9.60	19192.6
AHQ-1-10, 6231	R.AFYAELYHIISSNLEK.T	1899.13528	2	4.63E-09	0.96	5.06	-	1284.6
gi|6005846|ref|NP_009215.1| PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro				4.64E-09	4.82	50.29	26.90	39547.7
AHQ-1-12, 6230	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	6.82E-07	0.79	3.25	-	457.9
AHQ-1-13- , 6679	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	3.65E-07	0.96	4.98	-	863.7
AHQ-1-9, 6767 - 6768	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	4.64E-09	0.96	5.36	-	914.7
AHQ-1-13- , 6568 - 6632	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	7.20E-05	0.53	2.82	-	287.7
AHQ-1-12, 6334	R.AVLPLLDAQQPCYLLYR.L	2035.39506	3	1.09E-07	0.91	3.75	-	1250.6
AHQ-1-12, 6323	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	1.23E-05	0.94	4.57	-	780.9
AHQ-1-14- , 6422	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	1.10E-06	0.96	5.28	-	938.2
AHQ-1-11, 3970	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	7.28E-06	0.94	4.63	-	1009.1
AHQ-1-9, 4155	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	2.48E-04	0.94	4.40	-	947.9
AHQ-1-11, 4163	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	6.77E-09	0.97	5.15	-	1459.3
AHQ-1-9, 4311	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	9.88E-08	0.95	4.96	-	765.7
AHQ-1-11, 5959	K.KIEIGDGAELTAEFLYDEVHPK.Q	2475.73515	3	1.13E-08	0.96	5.83	-	1424.4
AHQ-1-13- , 4824	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	1.58E-05	0.97	4.50	-	2358.8
AHQ-1-13, 4600	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	1.43E-06	0.96	3.79	-	2003.4
AHQ-1-12, 4629	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	3	7.43E-04	0.97	4.92	-	2354.9
AHQ-1-12, 4642	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	4.14E-07	0.98	5.75	-	2160.3
gi|24797067|ref|NP_002107.3| major histocompatibility complex, class I, A precursor; HLA-A1 class I				4.70E-09	5.33	60.28	23.30	40840.5
AHQ-1-6, 5119	R.APWIEQEGPEYWDQETR.N	2135.23420	2	4.75E-07	0.90	4.10	-	617.4
AHQ-1-9, 5056	R.APWIEQEGPEYWDQETR.N	2135.23420	2	1.21E-05	0.92	4.01	-	840.5
AHQ-1-8, 5100	R.APWIEQEGPEYWDQETR.N	2135.23420	2	4.70E-09	0.97	5.59	-	1369.1
AHQ-1-5, 5195	R.APWIEQEGPEYWDQETR.N	2135.23420	2	2.88E-08	0.95	4.44	-	925.1
AHQ-1-8, 3314 - 3318	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	2	5.78E-08	0.84	4.06	-	411.4
AHQ-1-12, 4905	R.FIAVGYVDDTQFVR.F	1630.82504	2	1.65E-08	0.96	4.32	-	1616.5
AHQ-1-8, 3217	K.WAAVVVPSGEEQR.Y	1428.57478	1	2.80E-05	0.69	3.81	-	270.8
AHQ-1-8, 2044	R.YTCHVQHEGLPK.P	1470.63495	2	4.57E-04	0.92	3.68	-	812.7
AHQ-1-8, 3005 - 3076	R.YTCHVQHEGLPKPLTLR.W	2051.35781	2	8.49E-09	0.94	4.28	-	1495.1
AHQ-1-8, 3070	R.YTCHVQHEGLPKPLTLR.W	2051.35781	3	2.42E-06	0.93	4.99	-	1558.9
gi|9966867|ref|NP_065123.1| eIF-5A2 protein; eIF5AII [Homo sapiens]				4.79E-09	2.85	30.27	19.60	16793.1
AHQ-1-12, 3622	K.KYEDICPSTHNMDVPNIK.R	2163.41723	3	4.79E-09	0.95	4.97	-	1665.9
AHQ-1-12, 3626	K.KYEDICPSTHNMDVPNIK.R	2163.41723	2	2.39E-06	0.97	4.77	-	1445.3
AHQ-1-12, 3051	K.KYEDICPSTHNM*DVPNIK.R	2179.41663	3	1.07E-04	0.95	5.32	-	1212.8
AHQ-1-12, 4761	K.VHLVGIDIFTGK.K	1299.54329	2	1.47E-08	0.95	4.46	-	1079.3
gi|5803187|ref|NP_006746.1| transaldolase 1; dihydroxyacetone transferase; glycerone transferase [H				4.89E-09	2.49	30.20	10.70	37539.9
AHQ-1-9, 4860 - 4886	K.ALAGCDFLTISPK.L	1394.61830	2	4.89E-09	0.91	3.95	-	900.1
AHQ-1-9, 3015	K.LSSTWEGIQAGK.E	1277.40821	2	2.08E-04	0.94	3.69	-	1300.3
AHQ-1-9, 2698	K.SYEPLEDPGVK.S	1234.33696	2	6.85E-04	0.64	2.78	-	416.1
gi|17149842|ref|NP_004461.2| FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep				4.92E-09	3.48	40.21	19.00	15649.2
AHQ-1-13, 4119	K.GWDQGLLGM*CEGEK.R	1597.75215	2	8.50E-06	0.89	3.68	-	952.7
AHQ-1-13- , 5108	K.GWDQGLLGMCEGEK.R	1581.75275	2	1.34E-04	0.82	3.05	-	657.4
AHQ-1-13- , 4296	K.GWDQGLLGM*CEGEK.R	1597.75215	2	3.29E-04	0.75	2.63	-	800.6
AHQ-1-13- , 3993	R.KLVIPSELGYGER.G	1461.68782	2	2.67E-06	0.92	4.22	-	701.1
AHQ-1-13, 3755 - 3825	R.KLVIPSELGYGER.G	1461.68782	2	1.19E-04	0.75	3.12	-	425.5
AHQ-1-13- , 4325	K.LVIPSELGYGER.G	1333.51491	2	1.27E-07	0.79	3.00	-	412.7
AHQ-1-13, 4135 - 4140	K.LVIPSELGYGER.G	1333.51491	2	4.92E-09	0.84	2.99	-	540.6
gi|5031599|ref|NP_005722.1| actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub				5.08E-09	6.22	80.22	40.70	34332.8
AHQ-1-9, 2159 - 2167	R.ASHTAPQVLFSHR.E	1451.61481	2	3.47E-08	0.82	3.13	-	539.6
AHQ-1-9, 2558	K.DSIVHQAGMLK.R	1199.40563	1	5.08E-09	0.54	3.06	-	478.3
AHQ-1-9, 2582	K.ELQAHGADELLK.R	1324.46487	1	1.31E-05	0.34	2.01	-	439.3
AHQ-1-9, 2596	K.ELQAHGADELLK.R	1324.46487	2	3.49E-07	0.76	2.98	-	789.2
AHQ-1-14- , 2787	K.ELQAHGADELLK.R	1324.46487	2	1.57E-05	0.89	3.43	-	1128.8
AHQ-1-9, 2483 - 2559	K.ELQAHGADELLKR.V	1480.65123	2	7.91E-06	0.89	2.93	-	995.3
AHQ-1-14- , 6582	K.FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK.T	3638.89648	3	8.87E-06	0.86	3.84	-	699.9
AHQ-1-9, 3190	R.IIEETLALK.F	1030.24013	2	2.59E-05	0.73	2.67	-	534.6
AHQ-1-10, 6339 - 6340	R.VYGSFLVNPESGYNVSLLYDLENLPASK.D	3090.42808	3	5.44E-07	0.69	3.77	-	195.5
AHQ-1-9, 2607	K.YFQFQEEGKEGENR.A	1761.82929	2	1.91E-04	0.95	4.30	-	1329.1
AHQ-1-10, 2617	K.YFQFQEEGKEGENR.A	1761.82929	2	6.36E-05	0.93	3.82	-	1128.8
gi|4507725|ref|NP_000362.1| transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum				5.17E-09	4.73	50.33	49.00	15886.9
AHQ-1-13- , 3943 - 4015	K.AADDTWEPFASGK.T	1395.45529	2	2.22E-06	0.87	3.11	-	959.9
AHQ-1-13- , 4179 - 4184	R.GSPAINVAVHVFR.K	1367.58095	2	7.28E-08	0.95	4.54	-	1134.6
AHQ-1-13, 3999 - 4007	R.GSPAINVAVHVFR.K	1367.58095	2	1.27E-06	0.90	3.78	-	861.8
AHQ-1-13, 3199	R.KAADDTWEPFASGK.T	1523.62820	2	3.50E-04	0.97	4.92	-	1366.4
AHQ-1-13- , 3301	R.KAADDTWEPFASGK.T	1523.62820	2	8.43E-04	0.96	4.66	-	1390.4
AHQ-1-13- , 6051	R.RYTIAALLSPYSYSTTAVVTNPK.E	2517.86154	2	2.61E-06	0.98	5.85	-	2034.1
AHQ-1-13- , 5683 - 5693	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	9.95E-08	0.98	6.60	-	1653.9
AHQ-1-13- , 5687 - 5689	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	1.15E-06	0.98	6.16	-	1446.9
AHQ-1-13, 5273 - 5336	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	3.21E-06	0.97	5.97	-	1636.3
AHQ-1-13, 5331 - 5333	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	5.17E-09	0.96	5.23	-	1092.9
gi|5803133|ref|NP_006825.1| RAB32, member RAS oncogene family [Homo sapiens]				5.37E-09	1.70	20.20	12.40	24997.1
AHQ-1-10, 4485	K.VHLPNGSPIPAVLLANK.C	1741.07044	2	5.37E-09	0.77	2.88	-	366.3
AHQ-1-10, 3945	K.VLVIGELGVGK.T	1084.33417	2	4.49E-08	0.94	3.92	-	1275.1
gi|6912238|ref|NP_036226.1| peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]				5.46E-09	6.32	70.26	31.30	22026.2
AHQ-1-12, 6557	K.ETDLLLDDSLVSIFGNR.R	1908.09888	2	5.46E-09	0.97	5.08	-	1290.8

AHQ-1-12, 3839 - 3902	R.FSMVVQDGIVK.A	1223.46709	2	4.58E-05	0.86	3.46	-	626.9
AHQ-1-12, 2998	R.FSM*VVQDGIVK.A	1239.46649	2	6.80E-04	0.89	2.99	-	1222.4
AHQ-1-12, 5186 - 5191	K.GVLFGVPGAFTPGCSK.T	1595.84389	2	6.25E-04	0.88	4.10	-	542.9
AHQ-1-12, 4626 - 4633	K.KGVLFGVPGAFTPGCSK.T	1724.01680	2	1.88E-08	0.98	5.25	-	1850.7
AHQ-1-12, 4197	K.THLPGFVEQAEALK.A	1540.74504	3	7.24E-07	0.95	4.09	-	1862.6
AHQ-1-12, 4710	K.VNLAELFK.G	934.11414	2	2.75E-04	0.80	2.86	-	711.3
gi|21361322|ref|NP_006078.2|	tubulin, beta, 5 [Homo sapiens]			5.69E-09	2.46	30.28	13.70	49585.5
AHQ-1-7, 2940	R.EIVHLQAGQCGNQIGAK.F	1825.03962	3	3.94E-05	0.90	3.62	-	1544.2
AHQ-1-7, 3036	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	5.69E-09	0.90	4.27	-	770.2
AHQ-1-13, 3009	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	9.38E-06	0.88	3.86	-	868.4
AHQ-1-14- , 3011	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	2.98E-06	0.92	3.95	-	1138.3
AHQ-1-7, 2924 - 2932	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	1.55E-04	0.95	4.69	-	1256.2
AHQ-1-7, 5501 - 5577	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	5.54E-06	0.95	5.58	-	993.8
AHQ-1-7, 6884 - 6948	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	1.52E-04	0.61	3.29	-	320.6
gi|20149594|ref|NP_031381.2|	heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea			5.76E-09	5.85	70.26	11.50	83263.6
AHQ-1-5, 4075	R.ALLFIPR.R	830.05229	2	3.79E-04	0.80	2.54	-	949.6
AHQ-1-5, 2435	K.EDQTEYLEER.R	1312.32145	2	4.56E-05	0.51	2.57	-	495.3
AHQ-1-5, 5711	K.HSQFIGYPITLYLEK.E	1810.08487	2	7.90E-05	0.97	5.18	-	1623.9
AHQ-1-5, 3418 - 3431	K.IDIIPNPQER.T	1195.35034	2	4.39E-04	0.76	2.61	-	488.5
AHQ-1-6, 4151	R.NPDDITQEEYGEFYK.S	1848.90048	2	1.11E-08	0.96	4.82	-	1308.6
AHQ-1-5, 3979 - 3982	K.SLTNDWEDHLAVK.H	1528.64798	2	5.76E-09	0.88	3.71	-	834.2
AHQ-1-5, 4335 - 4343	R.TLTLVDTGIGMTK.A	1350.60718	2	1.04E-04	0.96	4.01	-	1283.9
gi|5803201|ref|NP_006818.1|	transmembrane trafficking protein [Homo sapiens]			6.41E-09	2.70	40.22	17.40	24975.8
AHQ-1-11, 2386	K.ITDSAGHILYSK.E	1305.46156	2	6.41E-09	0.97	4.31	-	1569.7
AHQ-1-11, 5951	R.LEDLSESIVNDFAYMK.K	1875.08916	2	9.81E-05	0.95	4.37	-	1377.4
AHQ-1-11, 2980	K.LKPLEVELR.R	1097.33294	1	2.62E-04	0.13	1.96	-	225.8
AHQ-1-11, 5243	R.RLEDLSESIVNDFAYM*K.K	2047.27492	2	6.24E-04	0.65	2.69	-	458.8
gi|27764873|ref|NP_057070.2|	cytokine receptor-like factor 3; cytokine receptor-like molecule 9; cy			7.06E-09	0.95	10.22	3.20	49737.6
AHQ-1-7, 3366	K.LIEHGVNTAEDLVR.E	1566.74089	2	7.06E-09	0.95	4.42	-	1140.2
gi|4757810|ref|NP_004037.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,			7.08E-09	8.13	90.26	21.50	59750.3
AHQ-1-7, 5809	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	3	7.08E-09	0.97	5.13	-	1769.3
AHQ-1-7, 3597	K.GIRPAINVGLSVSR.V	1439.68861	2	9.05E-06	0.94	3.98	-	962.6
AHQ-1-7, 6326	K.GMSLNLEPDNVGVVVFGNDK.L	2105.35763	2	3.85E-07	0.90	4.42	-	471.3
AHQ-1-7, 5677	K.GM*SLNLEPDNVGVVVFGNDK.L	2121.35703	2	3.80E-06	0.79	3.75	-	328.4
AHQ-1-7, 2842	R.GYLDKLEPSK.I	1150.30633	2	1.67E-05	0.80	2.70	-	859.8
AHQ-1-7, 3489	K.HALIIYDDLSK.Q	1288.47413	2	1.19E-06	0.95	3.57	-	1341.2
AHQ-1-7, 6846	K.LKEIVTNFLAGFEA	1552.79572	2	1.42E-05	0.89	3.28	-	1021.0
AHQ-1-14- , 5298 - 5376	R.TGAIVDVPVGEELLGR.V	1625.84824	2	5.99E-04	0.65	3.36	-	382.7
AHQ-1-7, 5476 - 5477	R.TGAIVDVPVGEELLGR.V	1625.84824	2	3.06E-06	0.95	4.81	-	839.4
AHQ-1-7, 3865	K.TGTAEMSSILEER.I	1424.55988	2	4.26E-06	0.96	4.07	-	1669.6
gi|4758714|ref|NP_004519.1|	microsomal glutathione S-transferase 3; microsomal glutathione S-transf			7.11E-09	0.95	10.22	9.20	16516.2
AHQ-1-12, 3702	R.VLYAYGYYTGEPSK.R	1611.77536	2	7.11E-09	0.95	4.33	-	1124.9
gi|29150259|ref|NP_803875.1|	fibrocystin L; polycystic kidney and hepatic disease-like 1 [Homo sapi			7.35E-09	0.73	10.15	0.40	465745.4
AHQ-1-1, 4696	K.IVGEDYPGWSEDSFGAR.V	1885.96719	2	7.35E-09	0.73	3.06	-	441.5
gi|4757768|ref|NP_004300.1|	Rho GDP dissociation inhibitor (GDI) alpha [Homo sapiens]			7.42E-09	2.78	30.25	15.70	23206.9
AHQ-1-13, 4527	R.AEEYEFLTPVEEAPK.G	1752.89898	2	7.42E-09	0.91	3.45	-	980.1
AHQ-1-10, 4243	R.AEEYEFLTPVEEAPK.G	1752.89898	2	5.56E-05	0.63	2.92	-	479.6
AHQ-1-12, 4565	R.AEEYEFLTPVEEAPK.G	1752.89898	2	5.88E-05	0.91	3.40	-	1116.7
AHQ-1-13- , 4753	R.AEEYEFLTPVEEAPK.G	1752.89898	2	8.61E-07	0.91	4.14	-	786.1
AHQ-1-13, 3848	K.SIQEIQELDKDDESLR.K	1919.03693	2	1.92E-05	0.94	4.46	-	1014.2
AHQ-1-13- , 4016	K.SIQEIQELDKDDESLR.K	1919.03693	2	9.78E-06	0.90	4.08	-	872.5
AHQ-1-10, 3588	K.SIQEIQELDKDDESLR.K	1919.03693	2	2.11E-07	0.92	4.10	-	963.6
AHQ-1-10, 3212	K.SIQEIQELDKDDESLRK.Y	2047.20984	2	1.06E-04	0.94	5.01	-	998.9
gi|4505763|ref|NP_000282.1|	phosphoglycerate kinase 1 [Homo sapiens]			7.65E-09	6.11	70.27	29.70	44614.4
AHQ-1-8, 5920	K.ACANPAAGSVILLENLR.F	1771.03187	2	3.92E-04	0.95	4.50	-	1283.0
AHQ-1-9, 5927	K.ACANPAAGSVILLENLR.F	1771.03187	2	7.65E-09	0.90	3.91	-	953.6
AHQ-1-8, 2285	R.AHSSMVGVNLPQK.A	1368.58752	1	3.70E-07	0.89	3.66	-	756.5
AHQ-1-8, 2283	R.AHSSMVGVNLPQK.A	1368.58752	2	4.38E-05	0.97	4.34	-	1876.0
AHQ-1-9, 5439	K.ALESPERPFLAILGGAK.V	1770.06542	2	9.53E-05	0.97	4.88	-	1641.9
AHQ-1-8, 5360	K.ALESPERPFLAILGGAK.V	1770.06542	2	1.64E-07	0.97	5.47	-	1736.1
AHQ-1-8, 4771 - 4843	K.DVLFLKDCVGPEVEK.A	1750.00620	2	1.28E-06	0.96	4.55	-	1452.4
AHQ-1-9, 5383	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	5.31E-07	0.83	3.76	-	514.3
AHQ-1-8, 5374	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	1.80E-08	0.85	3.94	-	498.1
AHQ-1-8, 4858 - 4860	K.TGQATVASGIPAGWMGLDCGPESSKK.Y	2607.90190	2	4.76E-05	0.64	3.34	-	181.6
AHQ-1-8, 5267	K.VLNNMEIGTSLFDEEGAK.I	1968.17459	2	9.99E-08	0.89	4.49	-	474.3
gi|4504041|ref|NP_002061.1|	guanine nucleotide binding protein (G protein), alpha inhibiting activi			7.74E-09	5.14	60.23	20.60	40450.7
AHQ-1-9, 4574	K.AMGNLQIDFADPSR.A	1535.70716	2	1.44E-04	0.72	2.85	-	764.9
AHQ-1-9, 5668	R.EYQLNDSAAYYLNDLER.I	2078.18096	2	7.74E-09	0.96	4.58	-	1294.7
AHQ-1-9, 2151	K.IIHEDGYSEEECR.Q	1638.69452	2	1.01E-05	0.86	2.99	-	919.7
AHQ-1-9, 4763	K.ITHSPLTICFPEYTGANK.Y	2051.30821	2	2.37E-04	0.80	3.56	-	487.9
AHQ-1-9, 5606	K.ITHSPLTICFPEYTGANKYDEAASYIQSK.F	3307.63156	3	3.54E-05	0.89	4.66	-	459.6
AHQ-1-9, 2520	K.YDEAASYIQSK.F	1275.34595	2	1.35E-04	0.91	3.19	-	1222.5
gi|4557731|ref|NP_000618.1|	latent transforming growth factor beta binding protein 1 precursor [Hom			7.98E-09	9.90	110.28	10.80	152790.9
AHQ-1-1, 3760	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	2.48E-06	0.96	5.01	-	1400.2
AHQ-1-3, 3721	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	3.01E-06	0.94	4.57	-	1311.5
AHQ-1-1, 4004	R.ASGLGDHCEDINECLEDKSVCQR.G	2696.84428	3	3.57E-06	0.85	3.69	-	925.5
AHQ-1-1, 2689 - 2709	R.CTCGQGYQLSAAK.D	1446.58862	2	1.14E-04	0.95	4.30	-	1015.1
AHQ-1-1, 4204	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	7.98E-09	0.97	4.62	-	1599.3
AHQ-1-3, 2135	K.DQCEDIDECQHR.H	1607.61898	2	1.35E-07	0.86	3.39	-	651.8
AHQ-1-1, 3447 - 3449	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	1.36E-05	0.94	4.17	-	940.7
AHQ-1-4, 6178	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	1.01E-04	0.74	4.06	-	292.4
AHQ-1-1, 5983 - 5987	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	3.24E-07	0.95	5.58	-	1150.4
AHQ-1-1, 3136	K.LCQIPVHGASVPK.L	1407.66344	2	7.52E-08	0.88	3.54	-	558.5
AHQ-1-3, 2927	R.TSTDLDVDVDQPK.E	1433.50014	2	5.22E-06	0.92	3.97	-	1034.6
AHQ-1-1, 2929 - 2987	R.TSTDLDVDVDQPK.E	1433.50014	2	4.65E-07	0.86	3.26	-	812.9
AHQ-1-3, 2686 - 2694	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	3.04E-07	0.91	3.99	-	1206.5
AHQ-1-4, 2691	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	2.98E-07	0.94	4.18	-	1484.6
AHQ-1-5, 2586	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	9.39E-08	0.78	2.97	-	1049.3
AHQ-1-2, 2770	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.87E-04	0.87	3.57	-	1183.9
AHQ-1-1, 3671	R.YTCICYEGYR.F	1387.51964	2	1.57E-06	0.90	3.08	-	719.5
gi|21361670|ref|NP_054782.2|	src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo			7.99E-09	3.49	40.23	16.00	48294.0
AHQ-1-11, 3302	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	5.35E-08	0.89	3.29	-	920.7
AHQ-1-12, 3413	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	2.81E-08	0.95	4.51	-	1027.9
AHQ-1-10, 3215 - 3217	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	7.99E-09	0.96	4.41	-	1263.4
AHQ-1-12, 5463	K.FVLINWTGEGVNDVR.K	1719.92182	2	4.28E-06	0.95	4.13	-	1263.0
AHQ-1-12, 5410 - 5479	K.SPTDWALFTYEGNSNDIR.V	2087.19108	2	2.20E-04	0.68	3.07	-	613.6
AHQ-1-13, 5500 - 5508	R.VAGTGEGGLEEMVEELNSGK.V	2007.16599	2	4.71E-04	0.82	3.56	-	557.1
AHQ-1-12, 5549	R.VAGTGEGGLEEMVEELNSGK.V	2007.16599	2	1.32E-05	0.91	4.33	-	801.3
gi|4557801|ref|NP_000261.1|	purine nucleoside phosphorylase [Homo sapiens]			8.52E-09	13.14	150.33	61.90	32147.7
AHQ-1-9, 1520	K.ANHEEVLAAGK.Q	1139.24364	1	3.55E-05	0.74	2.77	-	740.4
AHQ-1-9, 4402 - 4410	R.DHINLPGFSGQNPLR.G	1665.83425	2	2.84E-08	0.91	4.65	-	514.1
AHQ-1-9, 5662	K.FEVGDIMLIR.D	1193.44099	2	1.07E-05	0.92	3.57	-	1188.8
AHQ-1-9, 4556	R.FHMYEGYPLWK.V	1471.70636	2	2.33E-05	0.87	3.17	-	923.1
AHQ-1-9, 4558	R.FHMYEGYPLWK.V	1471.70636	1	3.58E-06	0.81	2.79	-	918.3
AHQ-1-9, 3068	R.FPAMSDAYDR.T	1173.28036	2	2.67E-04	0.94	3.35	-	1343.0
AHQ-1-13- , 4167	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	3	3.68E-06	0.98	5.31	-	4012.6
AHQ-1-9, 7312	K.LEQFVSILMASIPLPDK.A	1902.28716	2	4.34E-07	0.95	5.28	-	764.9

AHQ-1-9, 4871 - 4943	K.LGADAVGMSTVPEVIVAR.H	1786.08666	2	4.00E-04	0.92	3.87	-	953.8
AHQ-1-13, 4139	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	4.89E-05	0.94	4.67	-	851.8
AHQ-1-10, 3916	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	5.36E-04	0.89	3.62	-	869.9
AHQ-1-13- , 4321	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	7.64E-05	0.94	4.57	-	770.8
AHQ-1-9, 4222 - 4223	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	1.84E-05	0.95	4.15	-	1223.9
AHQ-1-11, 4656	K.LGADAVGMSTVPEVIVAR.H	1786.08666	2	9.80E-06	0.52	2.71	-	593.1
AHQ-1-11, 4027	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	4.21E-04	0.84	3.55	-	709.3
AHQ-1-13- , 6003 - 6015	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	1.18E-05	0.91	4.54	-	516.8
AHQ-1-9, 5996 - 6070	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	3.21E-05	0.79	3.52	-	427.8
AHQ-1-13- , 6025	K.LTQAQIFDYSEIPNFPR.S	2040.26383	3	8.46E-05	0.86	4.08	-	894.6
AHQ-1-9, 5115	R.LVFGFLNGR.A	1023.21261	2	3.15E-06	0.91	2.89	-	1386.7
AHQ-1-9, 4931	R.VFGFSLITNK.V	1126.32960	2	3.85E-05	0.92	3.84	-	777.1
AHQ-1-13- , 5180 - 5184	R.VFGFSLITNK.V	1126.32960	2	3.45E-04	0.92	3.60	-	731.1
AHQ-1-9, 6058 - 6096	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	8.52E-09	0.99	6.63	-	2850.1
AHQ-1-9, 2775	K.VIM*DYESLEK.A	1243.40878	2	3.83E-05	0.88	3.15	-	673.4
AHQ-1-9, 3506 - 3526	K.VIMDYESLEK.A	1227.40938	2	6.81E-05	0.81	2.80	-	458.6
gi|4507649|ref|NP_003280.1| tropomyosin 2 (beta) [Homo sapiens]				9.40E-09	1.91	20.23	4.90	32989.6
AHQ-1-9, 2650	K.ATDAEADVASLNR.R	1333.38703	2	4.40E-07	0.93	3.34	-	1654.1
AHQ-1-9, 2406	K.KATDAEADVASLNR.R	1461.55994	2	9.40E-09	0.97	4.58	-	2225.9
gi|5031593|ref|NP_005708.1| actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub				1.00E-08	6.39	70.34	53.60	16320.3
AHQ-1-12, 2978 - 3047	K.ALAAGGVGSIVR.V	1071.25558	2	1.73E-07	0.98	4.35	-	2384.6
AHQ-1-12, 3561	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	5.95E-06	0.89	3.84	-	632.5
AHQ-1-12, 4019 - 4082	K.AVQSLDKNGVDLLMK.Y	1631.91943	2	1.74E-06	0.97	5.29	-	1471.5
AHQ-1-12, 4026	K.AVQSLDKNGVDLLMK.Y	1631.91943	3	5.46E-04	0.89	3.43	-	1160.4
AHQ-1-12, 3469 - 3498	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	1.00E-08	0.92	4.12	-	628.4
AHQ-1-12, 4125	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	1.59E-06	0.95	4.35	-	1295.5
AHQ-1-12, 4210 - 4215	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	1.51E-07	0.66	2.98	-	472.4
AHQ-1-12, 4527	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	6.03E-07	0.93	4.68	-	865.5
AHQ-1-12, 4649 - 4663	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	1.12E-06	0.92	4.25	-	622.0
AHQ-1-12, 4271 - 4334	R.KVDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR.Q	3890.92031	3	1.46E-05	0.98	6.85	-	1849.6
AHQ-1-12, 4535 - 4598	K.VDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR.Q	3762.74739	3	8.02E-07	0.96	5.69	-	1379.1
gi|4758208|ref|NP_004081.1| dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;				1.02E-08	3.46	40.23	31.90	20478.2
AHQ-1-11, 4106	R.AADFIDQALAQK.N	1291.43488	2	5.78E-05	0.94	4.12	-	1236.4
AHQ-1-11, 5211 - 5283	K.ANDTQEFNLSAYFER.A	1805.88207	2	1.67E-05	0.76	3.06	-	753.5
AHQ-1-14- , 5539	K.ANDTQEFNLSAYFER.A	1805.88207	2	1.02E-08	0.63	3.25	-	366.5
AHQ-1-11, 5704 - 5724	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	4.49E-06	0.93	4.53	-	889.2
AHQ-1-11, 3962 - 3968	R.IYVGNASVAQDIPK.L	1475.67136	2	4.06E-05	0.95	4.56	-	1182.8
AHQ-1-11, 3619	R.IYVGNASVAQDIPK.L	1475.67136	2	3.54E-05	0.96	4.05	-	1439.6
gi|28077085|ref|NP_004559.3| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member				1.16E-08	1.82	20.22	10.10	42586.7
AHQ-1-9, 4783	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	3	1.16E-08	0.94	4.37	-	1422.4
AHQ-1-9, 4772	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	2	3.55E-05	0.84	3.76	-	692.0
AHQ-1-9, 7372	K.TYIGEIFTQILVLPYVGK.E	2055.44459	2	5.95E-07	0.89	4.01	-	918.3
gi|6598323|ref|NP_001485.2| GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom				1.19E-08	3.63	40.31	16.20	50662.9
AHQ-1-14, 6210	R.NPYYGGESASITPLEDLYK.R	2118.28499	2	1.29E-06	0.78	3.37	-	714.7
AHQ-1-9, 6907	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.96E-06	0.95	4.63	-	822.1
AHQ-1-8, 7022 - 7023	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	3.19E-05	0.97	5.68	-	1048.5
AHQ-1-7, 7089	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	4.16E-06	0.96	5.03	-	950.4
AHQ-1-6, 6954	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.44E-05	0.97	5.52	-	946.0
AHQ-1-8, 4157	R.TDDYLDQPCYETINR.I	1904.98887	2	2.28E-04	0.93	4.53	-	507.0
AHQ-1-8, 7511	K.VPSTEAEALASSLMGLFEK.R	1981.25641	2	1.19E-08	0.97	6.22	-	1414.6
gi|4502687|ref|NP_003865.1| CD84 antigen (leukocyte antigen); leukocyte antigen CD84 [Homo sapiens]				1.24E-08	1.56	20.26	11.60	36870.6
AHQ-1-7, 5030 - 5080	R.IHALGPNYNLVISDLR.M	1796.06296	2	1.24E-08	0.97	5.23	-	1577.4
AHQ-1-7, 3778	K.TSVAYVTPGDSETAPVVTVTHR.N	2288.49956	2	4.80E-04	0.58	3.10	-	327.2
gi|17318569|ref|NP_006112.2| keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]				1.27E-08	4.03	50.25	9.90	66066.3
AHQ-1-14- , 3951	K.LNDLEDALQQAK.E	1358.47963	2	1.54E-05	0.94	4.07	-	1579.8
AHQ-1-3, 4034	K.LNDLEDALQQAK.E	1358.47963	2	4.83E-04	0.92	3.48	-	1387.8
AHQ-1-4, 4080	K.LNDLEDALQQAK.E	1358.47963	2	6.58E-04	0.89	3.23	-	1429.0
AHQ-1-13- , 4048	K.LNDLEDALQQAK.E	1358.47963	2	5.73E-06	0.96	4.53	-	1647.6
AHQ-1-13, 5813	R.SLDLDSIIAEVK.A	1303.48388	2	4.00E-07	0.89	3.19	-	1062.6
AHQ-1-12, 5861	R.SLDLDSIIAEVK.A	1303.48388	2	4.71E-06	0.95	4.38	-	1291.6
AHQ-1-1, 6272	R.SLDLDSIIAEVK.A	1303.48388	2	8.35E-08	0.94	4.08	-	1394.5
AHQ-1-13- , 6197	R.SLDLDSIIAEVK.A	1303.48388	2	1.27E-08	0.97	5.08	-	1604.0
AHQ-1-14- , 5982 - 5992	R.SLDLDSIIAEVK.A	1303.48388	2	7.82E-05	0.93	3.37	-	1315.1
AHQ-1-14- , 4678 - 4706	K.SLNNQFASFIDK.V	1384.51877	2	3.82E-04	0.59	2.53	-	449.8
AHQ-1-14- , 6362	R.THNLEPYFESFINNLR.R	1995.18315	2	3.43E-05	0.68	3.10	-	334.9
AHQ-1-1, 4705 - 4748	K.WELLQQVDTSTR.T	1476.61621	2	3.75E-06	0.83	2.85	-	996.4
gi|4758970|ref|NP_004150.1| proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be				1.28E-08	1.59	20.17	9.60	29769.4
AHQ-1-11, 2496	K.FQHGVIAAVDSR.A	1300.44824	2	1.27E-04	0.76	2.60	-	885.3
AHQ-1-11, 3980 - 3983	K.VESTDVSDLLHQYR.E	1662.78230	2	1.28E-08	0.83	3.40	-	815.6
gi|21361399|ref|NP_055040.2| protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp				1.34E-08	3.66	40.29	11.70	65308.3
AHQ-1-6, 3911	R.AISHEHSPSDLEAHFVPLVK.R	2214.46551	3	1.65E-08	0.97	5.78	-	1596.3
AHQ-1-6, 5466 - 5538	K.IGPILDNSTLQSEVKPILEK.L	2195.54185	3	1.34E-08	0.90	3.68	-	1189.4
AHQ-1-6, 3708	R.LAGGDWFTSR.T	1110.20399	2	1.10E-06	0.87	2.93	-	698.8
AHQ-1-6, 5934	K.SEIIPMFSNLASDEQDSVR.L	2139.32924	2	7.18E-08	0.92	4.20	-	823.7
AHQ-1-6, 5868 - 5938	K.SEIIPMFSNLASDEQDSVR.L	2139.32924	2	1.88E-04	0.93	4.44	-	832.2
gi|29742410|ref|XP_291183.1| similar to TREM-like transcript 1 [Homo sapiens]				1.41E-08	2.33	30.22	16.70	32678.3
AHQ-1-13- , 4392 - 4456	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	8.09E-08	0.91	3.76	-	592.4
AHQ-1-11, 4131	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.41E-08	0.82	3.58	-	385.6
AHQ-1-13- , 4305	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	4.42E-06	0.87	3.78	-	429.6
AHQ-1-9, 5099	K.VLVCSKPVTYATVIFPGGNK.G	2152.54196	2	5.25E-05	0.88	3.97	-	517.4
AHQ-1-11, 3662	R.VSLNILPPEEEEETHK.I	1865.03087	3	5.79E-04	0.63	3.38	-	548.7
gi|4557014|ref|NP_001743.1| catalase [Homo sapiens]				1.51E-08	4.30	60.23	15.40	59755.8
AHQ-1-7, 2581	K.DAQIFIQK.K	963.11234	1	1.97E-05	0.48	2.29	-	673.1
AHQ-1-7, 5058	R.DPILFPSFIHSQK.R	1529.76385	2	1.75E-06	0.85	3.02	-	703.7
AHQ-1-7, 2576	R.FNTANDDNVTQVR.A	1494.54849	2	5.05E-04	0.16	2.53	-	303.6
AHQ-1-7, 2462	R.FNTANDDNVTQVR.A	1494.54849	2	4.17E-05	0.85	3.12	-	963.5
AHQ-1-7, 4692	K.GAGAFGYFEVTHDITK.Y	1713.87091	2	1.20E-05	0.93	4.41	-	819.6
AHQ-1-7, 4670 - 4730	R.LGPNYLHIPVNCPYR.A	1815.08803	2	4.16E-04	0.26	2.70	-	306.7
AHQ-1-7, 3974	K.NAIHTFVQSGSHLAAR.E	1709.89026	2	1.51E-08	0.95	4.65	-	1230.1
gi|5123454|ref|NP_005336.2| heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind				1.51E-08	2.65	40.19	10.50	70037.7
AHQ-1-6, 5354 - 5358	K.AAAIGIDLGTTYSCVGVFQHGK.V	2267.54677	3	3.57E-06	0.73	3.53	-	461.1
AHQ-1-6, 4163	K.NALESYAFNMK.S	1288.45450	2	4.55E-05	0.83	2.74	-	928.5
AHQ-1-6, 6828 - 6899	K.SINPDEAVAYGAAVQAAILM*GDK.S	2321.59293	2	1.51E-08	0.88	3.82	-	700.2
AHQ-1-6, 2168	K.VEIIANDQGNR.T	1229.32518	1	5.09E-04	0.21	1.86	-	307.8
gi|4506183|ref|NP_002779.1| proteasome alpha 3 subunit isoform 1; proteasome subunit C8; macropain				1.58E-08	0.95	10.21	5.50	28433.1
AHQ-1-10, 3881	R.HVGMAVAGLLADAR.S	1381.62943	2	1.58E-08	0.95	4.10	-	1022.0
gi|30154095|ref|XP_293967.2| similar to gamma actin-like protein [Homo sapiens]				1.61E-08	1.53	20.18	12.20	19259.0
AHQ-1-8, 5022 - 5098	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.61E-08	0.76	3.34	-	495.7
AHQ-1-8, 6374 - 6452	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	2.89E-06	0.34	2.86	-	371.9
AHQ-1-8, 6531 - 6532	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	1.12E-04	0.44	2.70	-	376.2
AHQ-1-10, 4423	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.41E-06	0.70	3.50	-	366.4
AHQ-1-13, 4724 - 4787	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.14E-05	0.46	3.09	-	345.5
AHQ-1-13, 4949	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	8.04E-05	0.64	3.38	-	486.4
AHQ-1-14, 5490 - 5560	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.76E-05	0.66	3.45	-	489.6
AHQ-1-14, 5652 - 5724	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.16E-05	0.57	3.08	-	376.6
AHQ-1-14, 5912	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.85E-05	0.55	3.10	-	449.0
AHQ-1-14, 6017	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	1.48E-07	0.77	3.34	-	397.4

AHQ-1-13- , 4992	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.55E-04	0.56	3.06	-	377.4
AHQ-1-13- , 5301	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	3.67E-06	0.42	3.46	-	413.8
AHQ-1-14- , 4758	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.52E-07	0.76	3.37	-	449.4
AHQ-1-14- , 4843	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	4.08E-06	0.55	3.13	-	452.3
AHQ-1-14- , 4968	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.37E-04	0.28	2.71	-	287.1
AHQ-1-14- , 5074 - 5091	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.61E-05	0.62	3.60	-	527.1
gi|4503747|ref|NP_001448.1| filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a				1.62E-08	4.10	60.24	2.00	278191.4
AHQ-1-1, 3701 - 3703	K.DLAEDAPWK.K	1045.12708	1	7.03E-06	0.48	2.42	-	616.2
AHQ-1-7, 3628	K.DLAEDAPWK.K	1045.12708	1	7.23E-04	0.27	2.10	-	445.1
AHQ-1-4, 3696	K.DLAEDAPWK.K	1045.12708	1	1.47E-05	0.26	2.15	-	465.1
AHQ-1-2, 3790	K.DLAEDAPWK.K	1045.12708	2	2.23E-04	0.80	3.14	-	768.2
AHQ-1-2, 3786	K.DLAEDAPWK.K	1045.12708	1	2.31E-06	0.52	1.84	-	819.0
AHQ-1-3, 3015	K.DLAEDAPWKK.I	1173.29999	2	6.50E-04	0.71	2.60	-	875.5
AHQ-1-13, 6001	R.LIALLEVLSQK.R	1227.51852	2	8.75E-05	0.94	3.71	-	1252.5
AHQ-1-2, 6678	R.LIALLEVLSQK.R	1227.51852	2	1.03E-07	0.97	4.12	-	1704.3
AHQ-1-6, 6475	R.LIALLEVLSQK.R	1227.51852	2	9.42E-08	0.96	4.44	-	1134.3
AHQ-1-3, 6509	R.LIALLEVLSQK.R	1227.51852	2	8.38E-08	0.97	4.28	-	1637.4
AHQ-1-1, 6491	R.LIALLEVLSQK.R	1227.51852	2	4.82E-07	0.97	4.25	-	1461.7
AHQ-1-4, 6671 - 6672	R.LIALLEVLSQK.R	1227.51852	2	1.79E-06	0.97	4.20	-	1458.1
AHQ-1-5, 6577	R.LIALLEVLSQK.R	1227.51852	2	1.62E-08	0.98	4.87	-	1680.1
AHQ-1-14- , 6219 - 6222	R.LIALLEVLSQK.R	1227.51852	2	4.66E-06	0.97	4.59	-	1270.2
AHQ-1-11, 5834	R.LIALLEVLSQK.R	1227.51852	2	8.35E-06	0.97	4.58	-	1229.6
AHQ-1-10, 5724	R.LIALLEVLSQK.R	1227.51852	2	2.86E-07	0.96	4.25	-	1292.7
AHQ-1-9, 6396	R.LIALLEVLSQK.R	1227.51852	2	9.63E-07	0.96	4.40	-	1256.8
AHQ-1-7, 3593	R.LLGWIQNK.I	972.16560	2	8.47E-04	0.78	2.74	-	633.2
AHQ-1-2, 1930	K.LVSIDSK.A	761.88676	1	4.19E-04	0.20	2.02	-	279.4
AHQ-1-2, 6719 - 6794	R.QM*QLENVSVALEFLDR.E	1909.15348	2	4.34E-05	0.89	3.92	-	832.3
AHQ-1-1, 6463	R.QM*QLENVSVALEFLDR.E	1909.15348	2	4.69E-06	0.91	4.03	-	1061.4
gi|4504743|ref|NP_002194.1| integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o				1.63E-08	3.40	40.25	5.80	129294.4
AHQ-1-3, 3765	K.AGDISCNADINPLK.I	1489.63335	2	2.07E-05	0.66	3.15	-	575.2
AHQ-1-3, 4847	K.KGILGQHQFLEGPEGIENTR.F	2224.46193	2	1.23E-05	0.95	4.94	-	699.7
AHQ-1-3, 3418	K.TQVGLIQYANNPR.V	1474.64668	2	1.63E-08	0.89	3.03	-	1061.0
AHQ-1-4, 5294	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	4.27E-06	0.91	4.16	-	688.8
AHQ-1-3, 5195	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	4.90E-08	0.91	4.35	-	706.6
gi|14745898|ref|XP_016144.2| similar to tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat				1.81E-08	0.97	10.25	7.50	18201.0
AHQ-1-10, 6164 - 6176	K.LLCCDILDVLDK.N	1479.74157	2	1.81E-08	0.97	4.99	-	979.7
AHQ-1-9, 6979 - 6998	K.LLCCDILDVLDK.N	1479.74157	2	2.79E-05	0.96	4.41	-	1139.2
gi|5453597|ref|NP_006126.1| F-actin capping protein alpha-1 subunit; Cap Z [Homo sapiens]				1.82E-08	4.14	50.25	26.20	32922.5
AHQ-1-9, 3180	K.DHYSNGFCTVYAK.T	1563.67248	2	5.84E-04	0.75	2.79	-	748.6
AHQ-1-13- , 5488	K.FTITPPTAQVVGVLK.I	1571.88532	2	3.27E-06	0.87	3.53	-	588.9
AHQ-1-9, 3170	K.IQVHYYEDGNVQLVSHK.D	2030.22904	2	1.67E-06	0.97	5.10	-	1638.1
AHQ-1-9, 4044	R.LLLNNDNLLR.E	1198.39736	2	1.62E-04	0.79	3.07	-	839.0
AHQ-1-9, 5514	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	3	3.19E-05	0.55	3.17	-	209.9
AHQ-1-9, 5510 - 5515	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	1.82E-08	0.76	3.89	-	295.7
gi|4502985|ref|NP_001854.1| cytochrome c oxidase subunit VIb; human cytochrome oxidase subunit VIb				1.84E-08	0.97	10.23	20.90	10192.3
AHQ-1-14- , 6138	R.VYQSLCPTSWVTDWDEQR.A	2272.43560	2	1.84E-08	0.97	4.68	-	1479.2
gi|14165439|ref|NP_002131.2| heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch bindin				1.85E-08	0.82	10.18	4.10	51027.9
AHQ-1-7, 5297 - 5368	R.GSYGDLGGPIITTQVTIPK.D	1918.18004	2	1.85E-08	0.82	3.38	-	634.5
AHQ-1-6, 5247 - 5312	R.GSYGDLGGPIITTQVTIPK.D	1918.18004	2	5.39E-05	0.82	3.69	-	582.5
gi|4759140|ref|NP_004243.1| solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulato				1.87E-08	0.93	10.19	3.90	38868.2
AHQ-1-13- , 3931	R.LLVVDPETDEQLQK.L	1627.81777	2	1.87E-08	0.93	3.83	-	745.1
AHQ-1-9, 3779	R.LLVVDPETDEQLQK.L	1627.81777	2	3.75E-05	0.78	3.01	-	596.4
gi|4507855|ref|NP_003472.1| Ubiquitin isopeptidase T; Ubiquitin-specific protease-5 (ubiquitin isop				1.89E-08	1.68	20.25	5.40	93393.2
AHQ-1-5, 4262	K.IFQNAPTDPTQDFSTQVAK.L	2109.28133	2	1.11E-04	0.72	2.85	-	678.4
AHQ-1-5, 7274	R.IGEWELIQESGVPLKPLFGPGYTGIR.N	2858.28283	3	1.89E-08	0.96	5.00	-	1737.2
gi|4757812|ref|NP_004880.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso				1.90E-08	2.73	30.22	25.50	10917.8
AHQ-1-13- , 6144	R.DFSPSGIFGAFQR.G	1429.56124	2	6.05E-08	0.94	3.90	-	1122.9
AHQ-1-14- , 5934	R.DFSPSGIFGAFQR.G	1429.56124	2	2.42E-06	0.94	3.94	-	1030.8
AHQ-1-13, 5752	R.DFSPSGIFGAFQR.G	1429.56124	2	1.90E-08	0.94	3.65	-	1301.7
AHQ-1-14- , 5970 - 5978	K.LGELPSWILMR.D	1315.60936	2	9.56E-07	0.93	4.36	-	656.5
AHQ-1-14- , 5534	K.LGELPSWILM*R.D	1331.60876	2	8.25E-06	0.86	3.32	-	581.9
gi|4505753|ref|NP_002620.1| phosphoglycerate mutase 1 (brain); Phosphoglycerate mutase A, nonmuscle				1.98E-08	1.69	20.22	16.50	28803.7
AHQ-1-10, 3809 - 3824	R.SYDVPPPPM*EPDHPFYSNISK.D	2434.66506	2	9.03E-05	0.78	3.32	-	374.4
AHQ-1-10, 4604	R.YADLTEDQLPSCESLKDTIAR.A	2427.62735	2	1.98E-08	0.91	4.49	-	513.2
AHQ-1-10, 4597	R.YADLTEDQLPSCESLKDTIAR.A	2427.62735	3	4.53E-05	0.76	3.59	-	502.9
gi|5031571|ref|NP_005713.1| actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog				2.02E-08	4.51	60.25	19.00	44760.5
AHQ-1-9, 5804 - 5819	K.CGYAGSNFPEHIFPALVGR.P	2094.33801	2	7.63E-04	0.35	2.82	-	379.5
AHQ-1-9, 6115	K.CGYAGSNFPEHIFPALVGRPIIR.S	2573.95654	3	5.82E-06	0.48	3.25	-	277.1
AHQ-1-8, 3853	K.DLMVGDEASELR.S	1335.46633	2	6.21E-08	0.95	3.89	-	1176.0
AHQ-1-9, 3768	K.DLMVGDEASELR.S	1335.46633	2	2.02E-08	0.90	2.97	-	1107.2
AHQ-1-9, 3355 - 3356	K.HIVLSGGSTM*YPGLPSR.L	1789.04907	2	6.42E-06	0.97	4.84	-	1802.2
AHQ-1-9, 4119	K.HLWDYTFGPEK.L	1393.52736	2	1.47E-06	0.92	3.47	-	697.8
AHQ-1-13- , 4357	K.HLWDYTFGPEK.L	1393.52736	2	4.79E-05	0.86	2.99	-	537.9
AHQ-1-8, 4140	K.HLWDYTFGPEK.L	1393.52736	2	3.18E-06	0.86	3.07	-	534.9
AHQ-1-8, 3441	K.ILLTEPPMNPTK.N	1354.64066	2	9.02E-04	0.70	3.14	-	439.9
AHQ-1-9, 3518 - 3556	K.ILLTEPPMNPTK.N	1354.64066	2	2.59E-04	0.89	3.56	-	577.1
gi|4557675|ref|NP_000201.1| integrin alpha chain, alpha 6 [Homo sapiens]				2.08E-08	2.65	30.22	4.90	119509.5
AHQ-1-4, 3515	K.FGSCQQGVAATFTK.D	1503.66172	2	6.25E-08	0.87	3.19	-	911.7
AHQ-1-4, 6227	R.NSYPDVAVGSLSDSVTIFR.S	2028.20822	2	2.08E-08	0.92	4.31	-	632.4
AHQ-1-4, 3960	R.VFIYHGSANGINTKPTQVLK.G	2188.51433	3	3.75E-05	0.85	3.55	-	1204.4
gi|5453603|ref|NP_006422.1| chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c				2.09E-08	1.91	30.18	7.90	57487.9
AHQ-1-7, 3145	R.EALLSSAVDHGSDEVK.F	1657.76083	2	2.09E-08	0.92	3.58	-	1156.9
AHQ-1-7, 3201 - 3210	R.GATQQILDEAER.S	1331.41427	1	7.20E-04	0.08	2.41	-	191.1
AHQ-1-7, 5820	R.SLHDALCVLAQTVK.D	1556.80920	2	3.73E-08	0.91	2.75	-	1568.3
gi|18570595|ref|XP_095590.1| similar to myosin regulatory light chain [Homo sapiens]				2.20E-08	0.92	10.18	8.90	13951.5
AHQ-1-11, 3086 - 3107	K.LNGTDPEDVIR.H	1229.32195	2	2.20E-08	0.92	3.59	-	998.9
AHQ-1-12, 3099	K.LNGTDPEDVIR.H	1229.32195	2	7.97E-08	0.90	3.30	-	954.7
AHQ-1-14, 4030	K.LNGTDPEDVIR.H	1229.32195	2	1.19E-04	0.91	3.53	-	974.6
AHQ-1-11, 2955 - 3026	K.LNGTDPEDVIR.H	1229.32195	2	8.39E-07	0.94	3.62	-	1360.1
gi|28376654|ref|NP_778250.1| hypothetical protein INM01 [Homo sapiens]				2.29E-08	0.92	10.25	10.90	28153.2
AHQ-1-13- , 5704 - 5708	K.LALEDISADPEDTVGGHPSWSGWEDDAK.G	2999.10449	3	2.29E-08	0.92	4.99	-	841.0
gi|25306267|ref|NP_001700.2| brain-derived neurotrophic factor isoform a preproprotein [Homo sapien				2.37E-08	0.95	10.22	6.10	27817.8
AHQ-1-13- , 3785	K.TAVDMSGGTVTVLEK.V	1508.71993	2	2.37E-08	0.95	4.45	-	1154.2
gi|4758076|ref|NP_004068.1| citrate synthase precursor; Citrate synthase, mitochondrial [Homo sapie				2.39E-08	0.88	10.15	2.40	51706.2
AHQ-1-8, 3392	K.IVPNVLLEQGK.A	1210.44805	2	2.39E-08	0.88	3.01	-	509.4
gi|5729842|ref|NP_006699.1| glyoxalase I; lactoyl glutathione lyase; lactoylglutathione lyase [Homo				2.44E-08	1.88	20.32	20.10	20719.6
AHQ-1-11, 4610 - 4614	R.GFGHIGIAVPDVYSACK.R	1793.03600	2	2.27E-05	0.91	3.62	-	1156.5
AHQ-1-11, 6382 - 6454	K.GLAFIQDPDGYWIEILNPNK.M	2304.58542	2	2.44E-08	0.98	6.30	-	1142.1
gi|20070125|ref|NP_000909.2| prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke				2.45E-08	8.47	100.29	27.00	57115.9
AHQ-1-7, 5217	K.HNQLPLVIEFTEQTAPK.I	1966.22639	2	5.90E-04	0.97	5.80	-	1258.0
AHQ-1-7, 3750 - 3822	K.IKPHLMSQELPEDWDKQPVK.V	2419.78460	3	1.35E-04	0.91	4.09	-	806.0
AHQ-1-7, 5404	R.ILEFFGLK.K	967.18573	2	5.41E-04	0.84	3.13	-	520.6
AHQ-1-7, 5317	K.ILFIFIDSDHTDNQR.I	1835.00968	2	6.83E-05	0.89	3.62	-	1023.7
AHQ-1-7, 2632	K.LGETYKDHENIVIAK.M	1730.94291	2	3.91E-05	0.93	3.76	-	1340.0
AHQ-1-7, 2682 - 2690	R.LITLEEEM*TK.Y	1223.41900	2	5.25E-04	0.77	2.55	-	767.6
AHQ-1-7, 2264	K.MDSTANEVEAVK.V	1294.41421	2	1.77E-06	0.81	3.37	-	831.4
AHQ-1-7, 3926 - 4006	K.VDATEESDLAQQYGVR.G	1781.85882	2	4.06E-05	0.88	3.29	-	1297.9

AHQ-1-7, 2142	K.YKPESEELTAER.I	1452.54828	1	3.45E-05	0.11	1.85	-	260.2
AHQ-1-7, 2140	K.YKPESEELTAER.I	1452.54828	2	2.45E-08	0.61	2.74	-	311.2
AHQ-1-7, 4057 - 4128	K.YQLDKDGVVLFK.K	1425.65394	2	7.25E-06	0.85	3.63	-	1014.1
gi|7657313|ref|NP_055277.1|	Lsm1 protein [Homo sapiens]			2.59E-08	0.88	10.21	12.00	15179.3
AHQ-1-12, 5755	R.SIDQFANLVLHQTVER.I	1871.08670	2	2.59E-08	0.88	4.13	-	662.6
gi|4504483|ref|NP_000185.1|	hypoxanthine phosphoribosyltransferase 1 [Homo sapiens]			2.60E-08	1.86	20.19	10.60	24579.2
AHQ-1-10, 6068	K.FFADLLDYIK.A	1245.44772	2	2.60E-08	0.94	3.86	-	871.4
AHQ-1-10, 5052	K.NVLIVEDIIDTGK.T	1429.64090	2	3.62E-04	0.92	3.37	-	1234.3
gi|28603830|ref|NP_776155.1|	hypothetical protein MGC51029 [Homo sapiens]			2.82E-08	0.89	10.21	11.00	17177.5
AHQ-1-12, 6634	K.AAPEINNLIEEATEFIK.Q	1903.12224	2	2.82E-08	0.89	4.16	-	540.0
gi|22042381|ref|XP_065237.3|	similar to FKSG30 [Homo sapiens]			2.86E-08	1.43	20.19	3.50	42016.0
AHQ-1-8, 2219	K.QEYDESGPSIVHR.K	1517.58206	3	3.15E-05	0.70	3.08	-	689.8
AHQ-1-13- , 2980	K.QEYDESGPSIVHR.K	1517.58206	2	1.56E-04	0.57	2.85	-	495.6
AHQ-1-13- , 2453 - 2492	K.QEYDESGPSIVHR.K	1517.58206	2	2.86E-08	0.63	2.75	-	311.1
AHQ-1-10, 2296 - 2299	K.QEYDESGPSIVHR.K	1517.58206	2	6.20E-08	0.83	3.46	-	451.1
AHQ-1-14, 3810	K.QEYDESGPSIVHR.K	1517.58206	2	4.84E-04	0.40	2.65	-	461.4
AHQ-1-13, 2457 - 2518	K.QEYDESGPSIVHR.K	1517.58206	2	6.20E-04	0.65	2.76	-	345.8
AHQ-1-14- , 2395 - 2408	K.QEYDESGPSIVHR.K	1517.58206	2	5.39E-05	0.40	2.56	-	244.2
AHQ-1-8, 3449 - 3524	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	2.40E-04	0.80	3.85	-	451.9
AHQ-1-8, 3660 - 3731	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	4.58E-04	0.73	3.43	-	415.8
AHQ-1-10, 3611	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	8.98E-04	0.21	2.52	-	179.6
gi|20070158|ref|NP_003567.2|	serine/threonine kinase 24 (STE20 homolog, yeast); STE20-like kinase 3			2.95E-08	0.72	10.16	3.40	49307.6
AHQ-1-7, 3949	K.SQACGGNLGSIEELR.G	1592.71366	2	2.95E-08	0.72	3.18	-	854.3
gi|5032041|ref|NP_005605.1|	Ras homolog enriched in brain 2 [Homo sapiens]			3.02E-08	0.92	10.18	8.70	20497.4
AHQ-1-12, 5070	K.ALAESWNAAFLESSAK.E	1695.85389	2	6.16E-05	0.81	3.54	-	459.9
AHQ-1-12, 4882	K.ALAESWNAAFLESSAK.E	1695.85389	2	3.02E-08	0.92	3.59	-	995.6
gi|5803217|ref|NP_006821.1|	ubiquinol-cytochrome c reductase (6.4kD) subunit [Homo sapiens]			3.05E-08	0.77	10.14	21.40	6569.6
AHQ-1-14- , 6286	R.LILDWVPYINGK.F	1431.70332	2	3.05E-08	0.77	2.73	-	766.5
AHQ-1-14- , 6140 - 6206	R.LILDWVPYINGK.F	1431.70332	2	2.18E-04	0.46	2.58	-	397.1
gi|18426915|ref|NP_004386.2|	drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [			3.38E-08	1.92	20.26	5.40	71438.9
AHQ-1-13- , 4199	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	2.61E-05	0.93	4.75	-	792.8
AHQ-1-8, 4031	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	3.38E-08	0.96	5.25	-	1098.5
AHQ-1-13- , 5715	K.YVLINWVGEDVPDAR.K	1746.94404	2	4.45E-04	0.95	3.98	-	1547.3
AHQ-1-13, 5376	K.YVLINWVGEDVPDAR.K	1746.94404	2	1.11E-05	0.96	4.61	-	1414.2
gi|9910542|ref|NP_064535.1|	SAR1a gene homolog 1; SAR1 protein [Homo sapiens]			3.53E-08	2.19	30.21	33.30	22366.6
AHQ-1-14- , 3863	R.EIFGLYGQTTGK.G	1314.46845	1	2.00E-04	0.40	2.48	-	227.8
AHQ-1-11, 3606 - 3611	R.EIFGLYGQTTGK.G	1314.46845	2	7.38E-04	0.93	3.50	-	1173.9
AHQ-1-11, 5895	R.LGQHVPTLHPTSEELTIAGMTFTTFDLGGHEQAR.R	3694.08659	3	3.53E-08	0.88	4.24	-	592.8
AHQ-1-11, 6451 - 6452	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	3.70E-06	0.91	4.05	-	728.2
AHQ-1-11, 6187	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	2.10E-04	0.34	2.50	-	314.8
gi|11968045|ref|NP_071934.1|	hypothetical protein FLJ22056 [Homo sapiens]			3.54E-08	0.94	10.24	8.00	36010.3
AHQ-1-11, 6431	K.DPTSLLGVLQAEADSTSEGLEDAVHSR.G	2798.95471	3	3.54E-08	0.94	4.87	-	1208.4
gi|5901944|ref|NP_008977.1|	elastin microfibril interface located protein; TNF? elastin microfibril			3.65E-08	4.31	50.27	9.60	106694.7
AHQ-1-3, 3610	R.APAPASAPPGPSEELLR.Q	1660.85268	2	3.65E-08	0.65	2.94	-	274.2
AHQ-1-3, 3029	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	2.00E-05	0.90	4.03	-	781.0
AHQ-1-3, 3131	R.GTELGGAAGQGGHPPGYTSLASR.L	2142.27464	2	6.36E-05	0.84	3.84	-	353.6
AHQ-1-3, 3687 - 3694	R.LDTVAGGLQGLR.E	1200.37012	2	2.65E-07	0.96	4.26	-	1571.0
AHQ-1-3, 3793	R.PARPNLSGSSAGSPLSGLGGEGPGESEK.V	2596.74928	3	3.60E-07	0.96	5.40	-	1493.1
gi|10863977|ref|NP_067000.1|	LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-			3.76E-08	0.97	10.26	20.00	10834.5
AHQ-1-14- , 5398 - 5400	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	3.76E-08	0.97	5.28	-	1366.2
AHQ-1-14, 6262 - 6325	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	1.61E-06	0.94	4.49	-	890.5
gi|15147250|ref|NP_150281.1|	protein phosphatase 1, regulatory (inhibitor) subunit 14A; 17-kDa PKC-			3.79E-08	0.86	10.20	10.90	16692.9
AHQ-1-12, 6497	K.SCGKPVEDFIQELLAK.L	1836.09909	2	3.79E-08	0.86	4.02	-	491.7
gi|21361198|ref|NP_000286.2|	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei			3.87E-08	1.91	20.24	7.90	46722.2
AHQ-1-7, 3738	K.LQHLENELTHDIITK.F	1805.02503	2	6.87E-04	0.95	4.20	-	1338.0
AHQ-1-7, 4681 - 4761	K.VFSNGADLSGVTEEAPLK.L	1835.00476	2	3.87E-08	0.96	4.75	-	1441.8
gi|23111030|ref|NP_037478.2|	sorting nexin 12 [Homo sapiens]			3.88E-08	0.95	10.25	8.60	18884.4
AHQ-1-12, 4923 - 4926	R.GDEGIFEESFIEER.R	1657.71615	2	3.88E-08	0.95	5.03	-	697.7
gi|8923114|ref|NP_060140.1|	ubiquitin-specific protease otubain 1 [Homo sapiens]			3.93E-08	0.52	10.15	6.60	31311.8
AHQ-1-9, 2603	R.GEGGTTNPHIFPEGSEPK.V	1854.95463	2	3.93E-08	0.52	2.96	-	367.8
gi|5031595|ref|NP_005709.1|	actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub			4.09E-08	3.75	40.26	31.00	19666.9
AHQ-1-11, 4179	R.AENFFILR.R	1010.17070	2	7.31E-04	0.97	4.25	-	1764.8
AHQ-1-12, 4219 - 4229	K.ELLLQPVTISR.N	1269.51549	2	2.01E-04	0.89	3.45	-	732.2
AHQ-1-12, 5583	R.KPVEGYDISFLITNFHTEQM*YK.H	2678.01211	3	2.83E-05	0.94	5.23	-	1210.3
AHQ-1-12, 3142	K.VLIEGSINSVR.V	1187.37134	2	2.01E-06	0.90	3.21	-	1118.7
AHQ-1-11, 3120	K.VLIEGSINSVR.V	1187.37134	2	4.09E-08	0.95	3.57	-	1610.5
gi|21361884|ref|NP_116235.2|	RAB2B [Homo sapiens]			4.23E-08	0.80	10.16	8.30	24214.2
AHQ-1-11, 2830	K.IGPQQSISTSVGPSASQR.N	1800.95164	2	4.23E-08	0.80	3.28	-	672.6
gi|5031973|ref|NP_005733.1|	protein disulfide isomerase-related protein [Homo sapiens]			4.54E-08	4.34	50.20	18.20	48121.0
AHQ-1-7, 7337	R.DGELPVEDDIDLSDVELDDLGKDEL	2759.86565	2	1.35E-05	0.84	3.14	-	997.3
AHQ-1-7, 2054	K.GESPVDYDGGR.T	1152.15291	2	3.13E-04	0.83	2.77	-	902.6
AHQ-1-7, 4940	K.GSFSEQGINEFLR.E	1484.59520	2	8.84E-08	0.86	3.13	-	884.5
AHQ-1-13- , 4192 - 4197	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	1.30E-06	0.86	3.90	-	736.6
AHQ-1-7, 4108 - 4126	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	2.66E-05	0.91	3.98	-	845.8
AHQ-1-8, 4052	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	1.11E-04	0.90	3.79	-	836.1
AHQ-1-11, 3866	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	5.58E-04	0.30	2.52	-	446.8
AHQ-1-12, 3997	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	5.05E-05	0.81	3.24	-	789.3
AHQ-1-13, 4015	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	1.53E-04	0.50	2.69	-	508.4
AHQ-1-13- , 6275	R.TGEAIVDAALSALR.Q	1387.56411	2	4.54E-08	0.94	3.45	-	1864.3
AHQ-1-7, 6442	R.TGEAIVDAALSALR.Q	1387.56411	2	4.83E-07	0.90	3.38	-	1329.1
gi|13128974|ref|NP_076933.1|	hypothetical protein MGC3265 [Homo sapiens]			4.64E-08	0.93	10.21	4.50	46867.3
AHQ-1-7, 4397	R.SYYSVQTAEWQAHPLYGSR.P	2244.40703	2	4.64E-08	0.93	4.22	-	1012.4
gi|27480842|ref|XP_208238.1|	similar to bA92K2.2 (similar to ubiquitin) [Homo sapiens]			4.76E-08	1.89	30.18	19.90	17966.9
AHQ-1-14, 4000 - 4001	K.ESTLHLVLR.L	1068.25169	2	1.62E-07	0.85	3.50	-	723.3
AHQ-1-14- , 3036	K.ESTLHLVLR.L	1068.25169	1	3.14E-04	0.37	2.25	-	211.2
AHQ-1-14- , 2039 - 2099	K.IQDKEGIPPDQQR.L	1524.66087	2	4.76E-08	0.79	3.00	-	653.8
AHQ-1-14, 3176 - 3232	R.TLSDYNIQK.E	1082.18886	1	2.42E-04	0.25	2.02	-	480.7
gi|30158844|ref|XP_292513.2|	similar to KIAA1879 protein [Homo sapiens]			4.81E-08	2.06	30.20	1.90	203894.8
AHQ-1-7, 3337	K.AVDSLVPIGR.G	1027.19957	1	1.21E-04	0.18	2.02	-	167.1
AHQ-1-7, 4253	K.TSIAIDTIINQK.H	1317.51378	2	1.07E-04	0.93	3.37	-	1565.3
AHQ-1-7, 3089	R.VVDALGNAIDGK.G	1172.31354	2	4.81E-08	0.95	3.91	-	1308.1
gi|4826848|ref|NP_004991.1|	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5; NADH dehydrogena			4.82E-08	0.98	10.35	22.40	13458.6
AHQ-1-14- , 6650	K.KLEDQLQGGQLEEVILQAEHELNLAR.K	2975.30339	3	4.82E-08	0.98	6.98	-	2166.7
gi|4507767|ref|NP_003326.1|	ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi			4.84E-08	3.44	40.25	7.70	111719.5
AHQ-1-5, 3510	R.APASAAASEDAPYPVCTVR.Y	1935.10448	2	1.02E-05	0.76	3.22	-	502.4
AHQ-1-5, 7333	R.GLNPDLQVIPLTYPLDPTTEHIYGDNFFSR.V	3434.79811	3	1.22E-04	0.73	3.70	-	279.7
AHQ-1-4, 4971	R.VDGVAAALDSFQAR.R	1420.55265	2	3.69E-05	0.97	3.88	-	2519.7
AHQ-1-4, 4814	R.VLVSGLQGLGAEVAK.N	1441.69805	2	4.84E-08	0.97	4.98	-	2049.8
gi|4502021|ref|NP_003680.1|	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase);			4.88E-08	1.86	20.22	10.30	36648.3
AHQ-1-9, 3811	K.ALQAAYGASAPSVTSAALR.W	1806.01302	2	4.88E-08	0.91	4.46	-	637.9
AHQ-1-9, 5610 - 5612	R.FYAYNPLAGGLLTGK.Y	1585.82741	2	8.13E-04	0.95	4.44	-	1002.0
gi|11128019|ref|NP_061820.1|	cytochrome c [Homo sapiens]			4.95E-08	0.91	10.17	13.30	11748.7
AHQ-1-13- , 2213 - 2216	K.TGQAPGYSYTAANK.N	1429.51641	2	4.95E-08	0.91	3.49	-	784.2
gi|4504557|ref|NP_000864.1|	intercellular adhesion molecule 2 precursor [Homo sapiens]			5.01E-08	0.94	10.24	5.80	30653.1
AHQ-1-7, 7536 - 7540	R.VPTVEPLDSLTLFLFR.G	1848.17455	2	5.01E-08	0.94	4.73	-	590.7
gi|4826657|ref|NP_004333.1|	caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]			5.07E-08	2.60	30.21	10.00	62662.9
AHQ-1-13- , 2687	K.GNVFSSPTAAGTPNK.E	1448.56286	2	1.16E-05	0.85	3.10	-	870.5

AHQ-1-6, 2667 - 2675	K.SAKPTKPAASDLPVPAEGVR.N	1992.26539	3	2.58E-04	0.89	3.96	-	982.9
AHQ-1-13, 3760	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	2.18E-04	0.86	3.76	-	784.5
AHQ-1-10, 3513	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	5.21E-06	0.95	4.28	-	1253.3
AHQ-1-6, 3751 - 3759	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	5.07E-08	0.86	3.91	-	657.5
gi|20270259|ref|NP_620061.1| phosphoglycerate kinase 2; phosphoglycerate kinase 1, pseudogene 2 [Ho				5.23E-08	0.93	10.21	3.60	44895.0
AHQ-1-8, 3384	K.LGDVYVNDAFGTAHR.A	1635.76178	2	5.23E-08	0.93	4.10	-	1024.8
gi|4504071|ref|NP_000164.1| platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA				5.26E-08	5.20	60.24	10.50	68955.0
AHQ-1-12, 5681 - 5690	R.AWLLFLR.G	919.14753	2	7.94E-05	0.92	3.22	-	997.4
AHQ-1-4, 5146	R.GLGELQELYLK.G	1263.46458	2	2.26E-05	0.92	3.72	-	1186.9
AHQ-1-1, 5157	R.GLGELQELYLK.G	1263.46458	2	1.33E-04	0.94	3.91	-	1380.1
AHQ-1-3, 5046	R.GLGELQELYLK.G	1263.46458	2	6.40E-06	0.95	4.03	-	1434.5
AHQ-1-9, 4887	R.GLGELQELYLK.G	1263.46458	2	4.71E-05	0.94	3.89	-	1374.7
AHQ-1-13, 4036 - 4053	R.GQDLLSTVSIR.Y	1189.34410	2	2.88E-07	0.94	3.62	-	1261.7
AHQ-1-14, 5014	R.GQDLLSTVSIR.Y	1189.34410	2	8.73E-05	0.95	3.40	-	1534.2
AHQ-1-12, 4001 - 4023	R.GQDLLSTVSIR.Y	1189.34410	2	5.26E-08	0.95	4.46	-	1113.8
AHQ-1-14- , 4082 - 4102	R.GQDLLSTVSIR.Y	1189.34410	2	9.40E-04	0.93	3.29	-	1393.9
AHQ-1-4, 4255	R.GQDLLSTVSIR.Y	1189.34410	2	2.31E-07	0.95	4.32	-	1170.9
AHQ-1-13- , 4215 - 4245	R.GQDLLSTVSIR.Y	1189.34410	2	1.40E-05	0.95	3.93	-	1406.1
AHQ-1-1, 4292	R.GQDLLSTVSIR.Y	1189.34410	2	2.70E-07	0.96	4.30	-	1300.6
AHQ-1-3, 4189	R.GQDLLSTVSIR.Y	1189.34410	2	2.27E-06	0.95	3.82	-	1397.6
AHQ-1-3, 2105	R.GVLQGHLESSR.N	1183.29965	2	2.87E-04	0.72	2.85	-	585.8
AHQ-1-4, 2103 - 2110	R.GVLQGHLESSR.N	1183.29965	2	6.74E-04	0.90	3.17	-	996.6
AHQ-1-3, 3697	R.LTQLNLDRCELTK.L	1605.83862	2	3.56E-04	0.69	3.86	-	399.1
AHQ-1-1, 5056	R.WLQDNAENVYVWK.Q	1665.82948	2	9.39E-07	0.97	4.58	-	1636.9
AHQ-1-3, 4981	R.WLQDNAENVYVWK.Q	1665.82948	2	1.04E-06	0.95	4.12	-	1423.1
AHQ-1-3, 5178 - 5253	R.WLQDNAENVYVWK.Q	1665.82948	2	1.58E-07	0.97	4.90	-	1697.7
gi|4507487|ref|NP_003238.1| thrombospondin 2 [Homo sapiens]				5.40E-08	1.34	20.18	2.60	129954.5
AHQ-1-1, 5317	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	5.40E-08	0.91	3.36	-	1337.6
AHQ-1-2, 5514	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.84E-07	0.78	3.37	-	640.3
AHQ-1-6, 2559	R.NALWHTGNTPGQVR.T	1551.69124	2	1.76E-04	0.90	3.51	-	1097.3
AHQ-1-7, 2570	R.NALWHTGNTPGQVR.T	1551.69124	2	1.19E-04	0.76	3.26	-	669.0
AHQ-1-8, 2446	R.NALWHTGNTPGQVR.T	1551.69124	2	6.38E-05	0.78	2.77	-	759.1
AHQ-1-9, 2507 - 2576	R.NALWHTGNTPGQVR.T	1551.69124	2	6.87E-06	0.43	2.66	-	565.2
AHQ-1-11, 2584 - 2587	R.NALWHTGNTPGQVR.T	1551.69124	2	1.45E-05	0.88	3.40	-	973.5
AHQ-1-1, 2844 - 2849	R.NALWHTGNTPGQVR.T	1551.69124	2	9.40E-04	0.87	3.30	-	909.9
gi|4505667|ref|NP_001074.1| phosphodiesterase 5A isoform 1; cGMP-binding cGMP-specific 3',5'-cyclic				5.70E-08	1.83	30.19	4.50	100012.4
AHQ-1-5, 3822 - 3830	R.FNAEVDQITGYK.T	1385.50354	2	3.64E-07	0.94	3.70	-	1165.4
AHQ-1-5, 4318	R.FPWTTENTGNVNQQCIR.S	2067.22783	2	1.45E-04	0.12	2.57	-	155.3
AHQ-1-5, 3863	K.VIGVCQLVNK.M	1131.37098	2	5.70E-08	0.77	3.05	-	527.7
gi|20532885|ref|XP_086931.2| similar to epsilon isoform of 14-3-3 protein [Homo sapiens]				5.75E-08	2.58	30.28	13.70	29380.0
AHQ-1-13- , 2680	K.EAAKNSIVAYK.A	1194.36234	2	7.62E-04	0.67	2.81	-	652.1
AHQ-1-11, 6264	K.LICCDILDVLDK.H	1479.74157	2	1.12E-04	0.92	3.88	-	873.9
AHQ-1-13, 6347	K.LICCDILDVLDK.H	1479.74157	2	2.84E-06	0.96	4.33	-	1067.1
AHQ-1-13- , 6797	K.LICCDILDVLDK.H	1479.74157	2	5.75E-08	0.97	5.57	-	1113.8
AHQ-1-10, 2513 - 2584	R.YLAEFATGNDRK.E	1385.50677	2	8.18E-07	0.94	3.71	-	1413.3
AHQ-1-10, 2379	R.YLAEFATGNDRK.E	1385.50677	2	1.78E-04	0.84	3.12	-	849.1
gi|30151001|ref|XP_170195.2| similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl				6.00E-08	0.89	10.18	2.60	46759.8
AHQ-1-10, 3500	R.AAYFGIYDTAK.G	1220.35512	2	2.66E-04	0.89	2.90	-	841.9
AHQ-1-13, 3804	R.AAYFGIYDTAK.G	1220.35512	2	6.00E-08	0.89	3.07	-	1041.9
AHQ-1-13- , 3952	R.AAYFGIYDTAK.G	1220.35512	2	4.41E-04	0.92	3.60	-	932.6
AHQ-1-10, 3496 - 3499	R.AAYFGIYDTAK.G	1220.35512	1	4.67E-04	0.72	2.39	-	890.0
gi|5454170|ref|NP_006393.1| hepatitis B virus x-interacting protein; hepatitis B virus x-interactin				6.16E-08	0.98	10.30	22.00	9613.9
AHQ-1-14- , 5874	K.NPSIVGVLCTDSQGLNLGCR.G	2163.41855	2	6.16E-08	0.98	5.94	-	2008.6
gi|20127517|ref|NP_009148.2| programmed cell death 10; apoptosis-related protein 15 [Homo sapiens]				6.35E-08	0.87	10.16	6.10	24701.4
AHQ-1-10, 3952	R.LIHQTNLILQTFK.T	1569.87265	2	6.35E-08	0.87	3.28	-	759.6
gi|29568111|ref|NP_006088.2| myosin, light polypeptide 9, regulatory; myosin regulatory light chain				6.37E-08	3.33	40.19	12.20	19827.1
AHQ-1-11, 2611 - 2686	R.FTDEEVDEM*YR.E	1450.50949	2	6.04E-06	0.94	3.59	-	1128.4
AHQ-1-11, 3350 - 3362	R.FTDEEVDEMYR.E	1434.51009	2	2.59E-07	0.86	3.12	-	907.6
AHQ-1-11, 3354	R.FTDEEVDEMYR.E	1434.51009	1	1.50E-05	0.04	1.81	-	265.5
AHQ-1-11, 3367	R.FTDEEVDEMYR.E	1434.51009	1	6.37E-08	0.68	2.66	-	476.1
AHQ-1-12, 2737	R.FTDEEVDEM*YR.E	1450.50949	2	1.26E-05	0.88	3.30	-	734.2
AHQ-1-12, 3446 - 3462	R.FTDEEVDEMYR.E	1434.51009	2	8.65E-06	0.90	3.07	-	1322.2
AHQ-1-12, 3798	K.GNFNYVEFTR.I	1247.34066	2	3.11E-05	0.82	2.93	-	765.3
AHQ-1-11, 3682 - 3710	K.GNFNYVEFTR.I	1247.34066	2	1.98E-06	0.93	3.74	-	893.3
AHQ-1-11, 3783 - 3796	K.GNFNYVEFTR.I	1247.34066	2	7.93E-05	0.76	2.79	-	520.1
AHQ-1-11, 3903	K.GNFNYVEFTR.I	1247.34066	2	8.89E-05	0.87	3.06	-	891.9
AHQ-1-12, 3734 - 3799	K.GNFNYVEFTR.I	1247.34066	2	1.48E-04	0.68	2.63	-	668.5
AHQ-1-14- , 3962	K.GNFNYVEFTR.I	1247.34066	2	5.55E-07	0.87	3.14	-	890.0
AHQ-1-11, 5598	R.NAFACFDEEASGFIHEDHLR.E	2367.49548	2	3.97E-05	0.84	3.58	-	615.0
gi|4503545|ref|NP_001961.1| eukaryotic translation initiation factor 5A; eIF5AI; eIF5A [Homo sapien				6.40E-08	0.93	10.20	11.00	16832.2
AHQ-1-12, 3937	R.EDLRLPEGDLGKEIEQK.Y	1970.17021	3	6.40E-08	0.93	4.01	-	1395.6
gi|4758984|ref|NP_004654.1| RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho				6.88E-08	6.14	70.30	30.60	24393.3
AHQ-1-12, 2802	K.AQIWDTAGQER.Y	1275.35241	2	3.69E-04	0.90	2.94	-	1204.3
AHQ-1-11, 2726 - 2744	K.AQIWDTAGQER.Y	1275.35241	2	2.48E-07	0.95	3.80	-	1370.4
AHQ-1-11, 4543 - 4622	R.DHADSNIVIMLVGNK.S	1626.85974	2	4.60E-07	0.97	4.73	-	1832.3
AHQ-1-11, 4054 - 4132	R.DHADSNIVIM*LVGNK.S	1642.85914	2	7.90E-06	0.96	4.72	-	1609.6
AHQ-1-14- , 5172	R.GAVGALLVYDIAK.H	1290.53317	2	1.58E-06	0.93	3.84	-	1291.5
AHQ-1-11, 4794	R.GAVGALLVYDIAK.H	1290.53317	2	6.88E-08	0.98	5.99	-	1990.7
AHQ-1-11, 2054	K.HLTYENVER.W	1161.24931	2	1.61E-06	0.78	2.58	-	563.2
AHQ-1-11, 2320	R.NEFNLESK.S	981.04139	1	1.17E-04	0.57	2.83	-	326.9
AHQ-1-11, 3016	K.STIGVEFATR.S	1081.20410	2	1.24E-06	0.92	3.21	-	991.2
gi|19913412|ref|NP_005106.2| major vault protein [Homo sapiens]				6.97E-08	0.80	10.16	1.80	99326.3
AHQ-1-4, 6012	R.LAQDPFPLYPGEVLEK.D	1817.07418	2	6.97E-08	0.80	3.24	-	730.9
gi|4507793|ref|NP_003339.1| ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast); ubiquitin-conj				7.12E-08	4.94	60.26	42.10	17137.7
AHQ-1-12, 5182 - 5203	K.LELFLPEEYPM*AAPK.V	1765.06265	2	1.72E-04	0.76	3.71	-	391.1
AHQ-1-13- , 5864 - 5865	K.LELFLPEEYPMAAPK.V	1749.06325	2	7.12E-08	0.85	4.11	-	593.0
AHQ-1-13, 5153	K.LELFLPEEYPM*AAPK.V	1765.06265	2	5.03E-04	0.47	3.03	-	382.8
AHQ-1-13- , 3501	R.LLAEPVPGIK.A	1037.27750	2	1.35E-04	0.66	2.73	-	493.6
AHQ-1-12, 2202 - 2203	K.TNEAQAIETAR.A	1204.27249	2	1.39E-06	0.92	3.96	-	1377.0
AHQ-1-12, 3517	K.WSPALQIR.T	971.13770	2	3.78E-05	0.78	2.94	-	538.8
AHQ-1-13- , 5415	R.YFHVVIAGPQDSPFEGGTFK.L	2197.43341	3	7.98E-07	0.96	5.23	-	1699.1
AHQ-1-12, 5133	R.YFHVVIAGPQDSPFEGGTFK.L	2197.43341	2	3.92E-05	0.95	4.54	-	1053.1
gi|4503823|ref|NP_002028.1| protein-tyrosine kinase fyn isoform a; proto-oncogene tyrosine-protein				7.16E-08	0.87	10.18	2.00	60761.5
AHQ-1-7, 3800 - 3805	K.WTAPEAALYGR.F	1235.37302	2	7.16E-08	0.87	3.55	-	635.7
gi|22748619|ref|NP_689476.1| tropomyosin 3 [Homo sapiens]				7.24E-08	4.30	50.23	21.80	28222.6
AHQ-1-9, 3771 - 3843	R.ALKDEEKMELQEIQLK.E	1946.25520	2	4.33E-04	0.94	4.16	-	1392.0
AHQ-1-10, 3159	R.KLVIIEGDLER.T	1285.51492	2	5.58E-05	0.90	3.52	-	980.3
AHQ-1-9, 3446 - 3503	R.LATALQKLEEAEK.A	1444.65557	2	1.56E-06	0.95	4.53	-	1435.0
AHQ-1-9, 3786	K.LVIIEGDLER.T	1157.34201	2	7.24E-08	0.81	2.72	-	904.5
AHQ-1-10, 2041 - 2117	K.YSQKEDKYEEEIK.I	1689.80129	2	6.33E-04	0.58	2.99	-	762.9
AHQ-1-9, 1979 - 2050	K.YSQKEDKYEEEIK.I	1689.80129	2	2.05E-05	0.69	3.20	-	618.0
gi|27436929|ref|NP_005518.2| heat shock 70kDa protein 1-like; heat shock 70kD protein-like 1 [Homo				7.57E-08	0.97	10.22	2.20	70404.7
AHQ-1-6, 3174	K.AKIHDIVLVGGSTR.I	1466.71083	2	7.57E-08	0.97	4.43	-	1985.9
gi|4507231|ref|NP_003134.1| single-stranded DNA binding protein; single-stranded DNA-binding protei				7.70E-08	3.24	40.28	25.70	17259.5
AHQ-1-13- , 2473	R.DVAYQYVK.K	986.10277	1	8.47E-04	0.49	2.16	-	717.8
AHQ-1-13, 2530	R.DVAYQYVK.K	986.10277	1	5.84E-05	0.47	1.96	-	728.6
AHQ-1-13, 5737 - 5801	K.NPVTIFSLATNEM*WR.S	1796.04007	2	1.00E-04	0.92	3.95	-	927.7

AHQ-1-13- , 6824	K.NPVTIFSLATNEMWR.S	1780.04067	2	7.70E-08	0.98	5.60	-	1896.7
AHQ-1-13- , 3304	R.SGDSEVYQLGDVSQK.T	1612.67692	2	8.91E-07	0.93	3.86	-	1003.4
AHQ-1-13, 3231	R.SGDSEVYQLGDVSQK.T	1612.67692	2	4.90E-07	0.87	3.74	-	808.6
gi|4503477|ref|NP_001950.1| eukaryotic translation elongation factor 1 beta 2; eukaryotic translati				7.85E-08	1.82	20.22	14.70	24763.6
AHQ-1-9, 5762 - 5768	K.SPAGLQVLNDYLADK.S	1604.78589	2	2.70E-05	0.89	3.72	-	920.6
AHQ-1-9, 5456 - 5522	K.SPAGLQVLNDYLADK.S	1604.78589	2	5.97E-07	0.93	4.06	-	924.0
AHQ-1-9, 4602	K.SPAGLQVLNDYLADK.S	1604.78589	2	7.85E-08	0.96	4.48	-	1296.2
AHQ-1-9, 5110	K.SSILLDVKPWDDETDMAK.L	2064.30228	2	1.21E-04	0.85	3.88	-	490.5
gi|30153515|ref|XP_293925.2| similar to phosphoglycerate mutase (EC 5.4.2.1) B chain - rat [Homo sa				8.25E-08	0.90	10.19	2.70	57163.7
AHQ-1-13- , 6316	R.ALPFWNEEIVPQIK.E	1684.95898	2	8.25E-08	0.90	3.84	-	565.4
gi|5031677|ref|NP_005681.1| dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [				8.40E-08	9.85	110.34	20.90	78060.6
AHQ-1-6, 4800	K.ALQGASQIIAEIR.E	1370.57991	2	2.83E-05	0.91	3.80	-	1223.1
AHQ-1-6, 2811	R.CVELVHEEMQR.I	1431.62054	2	5.61E-05	0.82	3.17	-	733.0
AHQ-1-13, 5031	K.DTLQSELVGQLYK.S	1494.67144	2	8.40E-08	0.90	3.19	-	1438.6
AHQ-1-14, 6074	K.DTLQSELVGQLYK.S	1494.67144	2	5.65E-05	0.71	2.63	-	893.5
AHQ-1-6, 4448	K.GHAVNLLDVPVPVAR.K	1557.82197	2	6.39E-06	0.92	3.61	-	1181.5
AHQ-1-6, 6494	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	7.11E-04	0.95	4.54	-	1262.8
AHQ-1-6, 7028 - 7034	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	1.62E-05	0.93	4.40	-	886.2
AHQ-1-7, 7208	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	8.42E-06	0.87	3.44	-	804.9
AHQ-1-7, 6646	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	6.90E-06	0.69	2.83	-	685.2
AHQ-1-5, 7193	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	9.28E-05	0.92	4.09	-	981.3
AHQ-1-6, 3383	K.LGIIGVVNR.S	941.15305	2	1.56E-05	0.92	3.07	-	1138.0
AHQ-1-6, 7254 - 7255	K.LQDVFNTVGADIIQLPQIVVVGTQSSGK.S	2928.32977	3	2.42E-06	0.97	6.78	-	1746.6
AHQ-1-14- , 6155	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	9.24E-08	0.96	5.04	-	1321.2
AHQ-1-13- , 6829 - 6901	K.SSLLDDLLTESEDMAQR.R	1924.07698	2	1.81E-05	0.92	3.94	-	990.0
AHQ-1-6, 7230	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	5.50E-06	0.96	5.15	-	1068.0
gi|4758018|ref|NP_004359.1| calponin 2; Calonin 2 [Homo sapiens]				8.59E-08	1.88	20.22	9.10	33696.9
AHQ-1-12, 2863 - 2865	K.GLQSGVDIGVK.Y	1073.22510	2	1.09E-05	0.92	3.65	-	1156.4
AHQ-1-11, 5950 - 6024	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.41E-05	0.94	4.15	-	1118.2
AHQ-1-9, 6604	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	5.65E-06	0.95	3.55	-	1637.1
AHQ-1-12, 6146 - 6173	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	8.59E-08	0.96	4.03	-	1637.3
AHQ-1-12, 6270	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	6.90E-04	0.56	2.80	-	424.6
AHQ-1-13- , 6449 - 6524	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.22E-05	0.95	4.26	-	1149.6
AHQ-1-14- , 6195 - 6267	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.37E-06	0.96	4.39	-	1293.6
AHQ-1-1, 6573	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.97E-05	0.94	3.72	-	1362.8
gi|5453599|ref|NP_006127.1| capping protein (actin filament) muscle Z-line, alpha 2; F-actin cappin				8.74E-08	2.54	30.35	12.20	32948.9
AHQ-1-9, 5279 - 5286	K.FTITPSTTQVVGILK.I	1605.90007	2	1.33E-04	0.92	4.27	-	527.1
AHQ-1-13- , 5436 - 5504	K.FTITPSTTQVVGILK.I	1605.90007	2	1.19E-06	0.81	3.29	-	428.9
AHQ-1-9, 5379	K.IDGQQTIIACIESHQFQAK.N	2189.43441	2	8.74E-08	0.75	3.32	-	504.1
AHQ-1-9, 4855	K.KIDGQQTIIACIESHQFQAK.N	2317.60733	3	9.28E-08	0.98	6.96	-	2682.1
gi|10835242|ref|NP_006249.1| protein kinase, cGMP-dependent, type I; Protein kinase, cGMP-dependent				9.35E-08	0.93	10.19	2.50	77803.3
AHQ-1-6, 6884	K.LSDFNIIDTLGVGGFGR.V	1781.98992	2	9.35E-08	0.93	3.90	-	1044.9
gi|7661922|ref|NP_055814.1| RAB21, member RAS oncogene family [Homo sapiens]				1.02E-07	0.97	10.28	7.60	24347.4
AHQ-1-10, 3999 - 4008	R.HVSIQEAESYAESVGAK.H	1805.92351	2	1.02E-07	0.97	5.58	-	1225.3
gi|4504073|ref|NP_000398.1| glycoprotein Ib beta polypeptide precursor [Homo sapiens]				1.05E-07	2.41	30.21	15.50	21717.6
AHQ-1-1, 4907	R.LLPYLAEDELR.A	1332.52691	2	1.05E-07	0.85	3.14	-	545.3
AHQ-1-3, 4869 - 4870	R.LLPYLAEDELR.A	1332.52691	2	4.13E-06	0.77	3.06	-	418.6
AHQ-1-4, 4942	R.LLPYLAEDELR.A	1332.52691	2	8.80E-07	0.81	3.03	-	632.4
AHQ-1-6, 4727 - 4738	R.LLPYLAEDELR.A	1332.52691	2	8.46E-05	0.78	2.78	-	590.2
AHQ-1-8, 4699	R.LLPYLAEDELR.A	1332.52691	2	2.74E-07	0.78	3.05	-	608.4
AHQ-1-9, 4666	R.LLPYLAEDELR.A	1332.52691	2	2.32E-06	0.69	2.89	-	330.2
AHQ-1-13, 4557	R.LLPYLAEDELR.A	1332.52691	2	5.41E-05	0.90	3.06	-	783.7
AHQ-1-10, 4259 - 4264	R.LLPYLAEDELR.A	1332.52691	2	2.62E-05	0.74	2.62	-	467.8
AHQ-1-12, 4590	R.LLPYLAEDELR.A	1332.52691	2	4.05E-05	0.69	2.62	-	356.0
AHQ-1-11, 4390 - 4422	R.LLPYLAEDELR.A	1332.52691	2	2.78E-07	0.88	3.51	-	467.8
AHQ-1-10, 3980	R.LSLTDPLVAER.A	1214.39356	2	2.75E-04	0.90	3.30	-	1287.4
AHQ-1-11, 4083 - 4094	R.LSLTDPLVAER.A	1214.39356	2	2.99E-06	0.96	4.13	-	1547.8
AHQ-1-11, 2319	R.TAHLGANPWR.C	1123.24913	2	2.68E-06	0.60	2.78	-	458.4
gi|29731325|ref|XP_293023.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				1.11E-07	0.88	10.19	6.00	28867.8
AHQ-1-13- , 4231 - 4235	K.AGPNTNGSQFFICTAK.T	1714.88050	2	8.02E-06	0.74	3.30	-	511.5
AHQ-1-12, 4045 - 4046	K.AGPNTNGSQFFICTAK.T	1714.88050	2	1.11E-07	0.88	3.72	-	644.5
gi|30148346|ref|XP_302059.1| similar to MLRQ subunit of the NADH: ubiquinone oxidoreductase complex				1.14E-07	0.88	10.15	6.60	17253.8
AHQ-1-14, 4233	K.FYSVNVDYSK.L	1222.32788	1	2.30E-06	0.49	2.46	-	547.4
AHQ-1-14- , 3403	K.FYSVNVDYSK.L	1222.32788	2	1.14E-07	0.88	3.10	-	646.5
AHQ-1-14, 4232	K.FYSVNVDYSK.L	1222.32788	2	2.14E-04	0.68	2.82	-	405.1
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				1.16E-07	5.31	60.22	44.00	22006.2
AHQ-1-13- , 4877 - 4887	K.HFCPNVPIILVGNK.K	1609.91693	2	6.35E-05	0.95	3.96	-	1565.8
AHQ-1-11, 4482	K.HFCPNVPIILVGNK.K	1609.91693	2	1.23E-04	0.95	3.63	-	1439.4
AHQ-1-10, 4316 - 4319	K.HFCPNVPIILVGNK.K	1609.91693	2	5.91E-04	0.97	4.31	-	1627.4
AHQ-1-10, 4000 - 4005	K.HFCPNVPIILVGNKK.D	1738.08985	2	5.01E-06	0.85	3.44	-	916.6
AHQ-1-10, 4096	R.ISAFGYLECSAK.T	1347.51850	2	4.93E-04	0.93	3.37	-	1063.0
AHQ-1-13- , 6833	R.LRPLSYPDTDVILM*CFSIDSPDSLENIPEK.W	3483.90759	3	3.87E-04	0.87	4.23	-	659.5
AHQ-1-10, 2604	K.LVIVGDGACGK.T	1090.27572	1	1.16E-07	0.75	3.23	-	533.1
AHQ-1-10, 2603 - 2605	K.LVIVGDGACGK.T	1090.27572	2	1.05E-04	0.85	3.33	-	816.3
AHQ-1-10, 2599	K.LVIVGDGACGK.T	1090.27572	1	7.78E-05	0.53	2.04	-	621.5
AHQ-1-13- , 5185 - 5212	K.QVELALWDTAGQEDYDR.L	2010.10662	2	4.35E-06	0.95	4.38	-	1148.8
AHQ-1-10, 4625	K.QVELALWDTAGQEDYDR.L	2010.10662	2	5.47E-04	0.94	3.88	-	1261.6
gi|28827809|ref|NP_789797.1| nucleoside diphosphate kinase B-like [Homo sapiens]				1.17E-07	3.03	40.21	29.20	15529.0
AHQ-1-12, 3317 - 3387	R.GDFCIQVGR.N	1053.17404	2	1.46E-05	0.89	3.25	-	993.5
AHQ-1-12, 3321	R.GDFCIQVGR.N	1053.17404	1	2.43E-04	0.34	1.82	-	253.5
AHQ-1-12, 2151	R.NIIHGSDSVKSAEK.E	1485.62464	1	4.06E-06	0.56	3.09	-	327.9
AHQ-1-12, 2137	R.NIIHGSDSVKSAEK.E	1485.62464	2	6.93E-06	0.63	3.43	-	553.9
AHQ-1-12, 2829 - 2906	R.VMLGETNPADSKPGTIR.G	1787.03151	2	1.61E-06	0.78	3.71	-	535.8
AHQ-1-12, 2830	R.VMLGETNPADSKPGTIR.G	1787.03151	3	7.97E-07	0.78	3.60	-	562.1
AHQ-1-12, 2649	R.VM*LGETNPADSKPGTIR.G	1803.03091	2	1.32E-06	0.79	3.49	-	666.3
AHQ-1-12, 2722	R.VMLGETNPADSKPGTIR.G	1787.03151	2	3.77E-05	0.76	3.34	-	565.2
AHQ-1-12, 2650	R.VM*LGETNPADSKPGTIR.G	1803.03091	3	1.17E-07	0.80	3.01	-	739.1
gi|4505735|ref|NP_002611.1| platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H				1.20E-07	2.81	30.24	26.00	11552.6
AHQ-1-14- , 3884	R.AEAEEDGDLQCLCVK.T	1739.86036	2	1.20E-07	0.97	4.81	-	1816.4
AHQ-1-14- , 3767 - 3784	R.AEAEEDGDLQCLCVK.T	1739.86036	2	2.27E-04	0.94	4.60	-	752.9
AHQ-1-14- , 4942	K.ICLDLQALLYK.K	1351.63656	2	9.51E-04	0.89	3.54	-	1145.9
AHQ-1-14- , 5834	R.KICLDLQALLYK.K	1479.80948	2	3.33E-04	0.94	4.21	-	956.6
gi|4507149|ref|NP_000445.1| superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult				1.20E-07	3.56	40.30	57.80	15935.7
AHQ-1-12, 5231	K.AVCVLKGDGPVQGIINFEQK.E	2174.50602	2	2.85E-05	0.93	4.46	-	901.4
AHQ-1-11, 3911	K.GDGPVQGIINFEQK.E	1502.65366	2	2.38E-05	0.73	2.95	-	697.8
AHQ-1-12, 4810	K.GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR.K	3522.76733	3	1.20E-07	0.95	4.82	-	1479.5
AHQ-1-12, 5778	R.HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR.T	3724.02282	3	1.55E-05	0.90	4.33	-	827.9
AHQ-1-11, 5587	R.HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR.T	3724.02282	3	3.95E-07	0.95	5.95	-	991.1
gi|4503971|ref|NP_001484.1| GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r				1.21E-07	0.86	10.28	4.30	50582.4
AHQ-1-7, 5450	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	1.05E-06	0.97	5.51	-	1138.6
AHQ-1-12, 5151	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	1.21E-07	0.86	3.83	-	709.1
AHQ-1-6, 5388	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	4.06E-05	0.93	4.49	-	917.4
gi|4503291|ref|NP_001346.1| D-dopachrome tautomerase [Homo sapiens]				1.37E-07	1.83	20.18	22.00	12711.7
AHQ-1-14- , 5624 - 5643	R.FFPLESWQIGK.I	1352.56151	2	1.37E-07	0.90	2.99	-	803.0
AHQ-1-14, 4525	R.LCAAAASILGKPADR.V	1515.76031	2	3.37E-05	0.92	3.68	-	1217.3
gi|29729950|ref|XP_293759.1| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				1.40E-07	0.86	10.17	5.00	39776.4
AHQ-1-5, 5113	K.CLELFTELAEDKENYKK.F	2132.37640	2	1.40E-07	0.86	3.45	-	963.9

gi|4758988|ref|NP_004152.1|	RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho			1.40E-07	3.21	40.23	25.40	22677.6
AHQ-1-14- , 6152	K.EFADSLGIPFLETSAK.N	1725.91990	2	2.21E-05	0.34	2.78	-	269.8
AHQ-1-13- , 6332 - 6409	K.EFADSLGIPFLETSAK.N	1725.91990	2	2.93E-06	0.80	3.48	-	399.6
AHQ-1-14- , 5890	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.37E-05	0.94	4.21	-	970.7
AHQ-1-11, 5564 - 5623	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.40E-07	0.96	4.59	-	1405.0
AHQ-1-11, 5943	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	6.48E-06	0.79	3.33	-	554.1
AHQ-1-11, 6603	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	6.13E-06	0.54	2.98	-	396.4
AHQ-1-13- , 6099	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.65E-06	0.96	4.69	-	1275.4
AHQ-1-11, 5810 - 5879	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.14E-07	0.93	4.43	-	809.8
AHQ-1-11, 5670 - 5743	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.07E-06	0.97	4.64	-	1821.6
AHQ-1-11, 5220	K.NATNVEQSFM*TMAAEIK.K	1902.13962	2	8.46E-04	0.78	3.74	-	801.3
AHQ-1-11, 5776 - 5835	K.NATNVEQSFMTMAAEIK.K	1886.14022	2	9.30E-04	0.66	3.44	-	741.2
gi|20070156|ref|NP_003565.2|	vessicle-associated membrane protein (VAMP)-associated protein of 33 k			1.42E-07	0.94	10.19	5.00	27317.4
AHQ-1-12, 4047	K.GPFTDVVTTNLK.L	1292.46278	2	1.42E-07	0.94	3.85	-	1421.3
gi|5902016|ref|NP_008939.1|	reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sapi			1.44E-07	1.71	20.23	14.10	22395.3
AHQ-1-1, 3263 - 3340	R.HQAQIDHYLGLANK.N	1608.78270	2	3.07E-04	0.90	3.52	-	769.3
AHQ-1-12, 3041	R.HQAQIDHYLGLANK.N	1608.78270	2	2.84E-06	0.96	4.58	-	1421.0
AHQ-1-1, 3072 - 3149	K.YSNSALGHVNCTIK.E	1565.73305	2	1.44E-07	0.75	3.23	-	557.5
gi|20536967|ref|XP_115812.1|	similar to Latent transforming growth factor beta binding protein 1L p			1.47E-07	0.35	10.13	12.00	13416.2
AHQ-1-1, 3631	K.GISGEQSTEGSFPLR.Y	1565.66662	2	1.47E-07	0.35	2.55	-	269.1
gi|4506181|ref|NP_002778.1|	proteasome alpha 2 subunit; proteasome subunit HC3; proteasome componen			1.56E-07	4.78	60.27	34.20	25898.4
AHQ-1-11, 2171	K.AANGVVLATEK.K	1073.22510	1	7.95E-04	0.40	2.26	-	407.8
AHQ-1-11, 4618	R.GYSFSLTTFSPSGK.L	1479.61533	2	7.33E-06	0.75	2.95	-	528.2
AHQ-1-11, 3495	K.HIGLVYSGMGPDYR.V	1565.77809	2	2.29E-04	0.96	4.24	-	1530.3
AHQ-1-11, 4934	R.KLAQQYYLVYQEPIPTAQLVQR.V	2651.05593	2	3.84E-05	0.95	4.94	-	910.8
AHQ-1-11, 5298	K.LAQQYYLVYQEPIPTAQLVQR.V	2522.88301	2	3.93E-04	0.75	2.93	-	695.7
AHQ-1-11, 6394	R.YNEDLELEDAIHTAILTLK.E	2202.44658	2	1.56E-07	0.96	5.18	-	1289.5
gi|7657486|ref|NP_055217.1|	low molecular mass ubiquinone-binding protein [Homo sapiens]			1.60E-07	0.97	10.27	14.00	11316.3
AHQ-1-14- , 3976	R.HVISYSLSPFEQR.A	1563.73870	2	1.60E-07	0.97	5.36	-	1353.8
gi|7305503|ref|NP_038470.1|	stomatin (EPB72)-like 2; stomatin-like protein 2; stomatin-like 2 [Homo			1.62E-07	0.91	10.18	4.20	38533.8
AHQ-1-9, 7106 - 7116	R.ILEPGLNILIPVLDR.I	1676.03667	2	1.62E-07	0.91	3.52	-	756.6
gi|6912494|ref|NP_036457.1|	microtubule-associated protein, RP/EB family, member 1; ADENOMATOUS POL			1.64E-07	4.32	50.27	25.40	29998.9
AHQ-1-12, 3918	K.FFDANYDGKDYDPVAAR.Q	1965.06754	2	2.25E-05	0.53	2.92	-	412.7
AHQ-1-12, 3915	K.FFDANYDGKDYDPVAAR.Q	1965.06754	3	6.08E-06	0.78	3.91	-	371.5
AHQ-1-12, 6341	K.FQDNFEFVQWFK.K	1635.80184	2	1.64E-07	0.95	3.87	-	1373.7
AHQ-1-12, 2673	K.LEHEYIQNFK.I	1321.46268	1	2.16E-04	0.50	2.13	-	758.4
AHQ-1-12, 2666	K.LEHEYIQNFK.I	1321.46268	2	3.70E-06	0.81	2.82	-	846.9
AHQ-1-13, 3234 - 3293	K.LTVEDLEKER.D	1232.36575	2	9.87E-05	0.81	2.70	-	953.8
AHQ-1-13, 4345	R.NIELICQENEGENDPVLQR.I	2272.43545	2	1.69E-07	0.97	5.33	-	1749.5
gi|29747201|ref|XP_290702.1|	similar to My016 protein [Homo sapiens]			1.68E-07	0.90	10.19	10.50	16932.3
AHQ-1-14- , 3535	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	6.47E-06	0.90	3.65	-	813.6
AHQ-1-14, 4362	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	1.68E-07	0.90	3.72	-	922.5
gi|4503531|ref|NP_001958.1|	eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens] [			1.68E-07	0.95	10.21	3.90	46393.9
AHQ-1-8, 3417	R.GIYAYGFEKPSAIQQR.A	1829.04828	2	1.68E-07	0.95	4.17	-	1198.9
gi|10864055|ref|NP_067069.1|	megakaryocyte-enhanced gene transcript 1 protein; lymphocyte antigen-6			1.79E-07	0.95	10.23	4.20	40891.9
AHQ-1-9, 4260	R.YWCAVLGQHHNYQNWR.V	2134.32402	2	1.79E-07	0.95	4.61	-	1289.7
gi|4502389|ref|NP_003851.1|	barrier to autointegration factor 1; breakpoint cluster region protein,			1.81E-07	0.96	10.23	13.50	10058.5
AHQ-1-14- , 6164	K.AYVVLGQFLVLK.K	1350.67334	2	1.81E-07	0.96	4.62	-	1598.2
gi|4508047|ref|NP_003452.1|	zyxin [Homo sapiens]			1.81E-07	1.84	30.21	9.80	61277.0
AHQ-1-8, 3936 - 3940	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	9.00E-06	0.84	4.30	-	626.7
AHQ-1-6, 3922	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	1.61E-05	0.76	3.16	-	717.3
AHQ-1-9, 2619 - 2626	R.SPGAPGPLTLK.E	1038.22236	1	7.66E-04	0.07	1.81	-	213.7
AHQ-1-9, 7362	K.VSSIDLEIDSLSSLLDDMTK.N	2182.43225	2	1.81E-07	0.93	4.22	-	1018.6
gi|21614499|ref|NP_003370.2|	villin 2; Villin-2; cytovillin [Homo sapiens]			1.83E-07	3.40	50.22	8.00	69412.3
AHQ-1-6, 4366	K.APDFVFYAPR.L	1183.33971	2	1.83E-07	0.97	4.34	-	1353.4
AHQ-1-6, 2440	K.FVIKPIDK.K	960.19473	1	2.53E-04	0.13	1.97	-	376.8
AHQ-1-6, 5198	K.IGFPWSEIR.N	1105.27049	2	1.28E-05	0.89	2.56	-	1265.3
AHQ-1-6, 3743	K.KAPDFVFYAPR.L	1311.51262	2	1.26E-06	0.68	2.65	-	558.7
AHQ-1-6, 4418	R.VTTM*DAELEFAIQPNTTGK.Q	2083.30556	2	8.20E-05	0.72	3.09	-	463.7
gi|10835189|ref|NP_000628.1|	glutathione reductase [Homo sapiens]			1.86E-07	2.66	30.23	10.60	51700.3
AHQ-1-7, 4910	K.ADFDNTVAIHPTSSEELVTLR	2316.50977	2	7.64E-06	0.81	4.07	-	373.7
AHQ-1-7, 4116	K.ALLTPVAIAAGR.K	1153.39973	2	2.04E-04	0.93	3.24	-	1418.4
AHQ-1-7, 2529	R.GHAAFTSDPKPTIEVSGK.K	1843.03012	2	1.86E-07	0.92	4.60	-	381.0
gi|4507287|ref|NP_003755.1|	syntaxin 11 [Homo sapiens]			1.89E-07	2.73	30.20	15.70	32955.3
AHQ-1-9, 4210 - 4214	R.DIQDENQLLVADVK.R	1600.75241	2	8.09E-05	0.93	3.54	-	1893.4
AHQ-1-9, 1971	K.ELSEAAEAQHGPHSAVAR.I	1860.96563	2	1.89E-07	0.84	3.44	-	748.6
AHQ-1-9, 6486 - 6492	K.WDVFSENLLADVK.G	1536.71002	2	4.69E-05	0.96	4.01	-	1411.3
gi|4507789|ref|NP_003338.1|	ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]			2.03E-07	1.69	20.17	15.60	17861.5
AHQ-1-12, 2163	R.ADLAEEYSK.D	1026.07893	2	6.90E-05	0.87	2.77	-	1065.0
AHQ-1-12, 5138	R.IEINFPAEYPFKPPK.I	1791.08155	3	2.03E-07	0.82	3.29	-	873.1
AHQ-1-12, 5081 - 5142	R.IEINFPAEYPFKPPK.I	1791.08155	2	2.63E-07	0.84	3.43	-	800.1
gi|30149327|ref|XP_293672.2|	similar to ebiP7687 [Homo sapiens]			2.06E-07	1.48	20.19	4.80	59404.3
AHQ-1-5, 3677	K.HLEINPNHPIVETLR.Q	1783.02428	2	2.06E-07	0.91	3.89	-	779.3
AHQ-1-5, 2761	K.SIYYITGESK.E	1161.28598	1	6.47E-04	0.57	1.88	-	1038.0
gi|4503725|ref|NP_000792.1|	FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei			2.19E-07	1.80	20.26	13.00	11950.6
AHQ-1-13- , 3091	R.GWEEGVAQM*SVGQR.A	1550.67866	2	2.19E-07	0.97	5.24	-	1159.8
AHQ-1-14- , 3039	R.GWEEGVAQM*SVGQR.A	1550.67866	2	2.85E-07	0.96	4.62	-	1119.7
AHQ-1-14- , 3922 - 3930	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.42E-06	0.83	3.20	-	1076.3
AHQ-1-13, 3876	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.70E-05	0.88	4.02	-	811.5
gi|4506363|ref|NP_002861.1|	RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s			2.24E-07	1.77	20.18	10.80	22774.0
AHQ-1-11, 3564 - 3590	K.LLLIGDSGVGK.T	1072.28025	2	2.24E-07	0.92	3.35	-	1013.1
AHQ-1-11, 3578	K.LLLIGDSGVGK.T	1072.28025	1	2.97E-04	0.76	2.70	-	628.1
AHQ-1-13, 3769 - 3776	K.LLLIGDSGVGK.T	1072.28025	2	1.23E-04	0.89	3.59	-	806.8
AHQ-1-11, 2948	K.LQVWDTAGQER.F	1303.40576	2	1.09E-06	0.86	3.54	-	992.9
gi|5902090|ref|NP_008862.1|	solute carrier family 2 (facilitated glucose transporter), member 3; GL			2.38E-07	1.33	20.25	4.00	53924.0
AHQ-1-1, 5271	R.LWGTQDVSQDIQEMK.D	1778.96471	2	2.38E-07	0.93	4.01	-	822.4
AHQ-1-1, 4183	R.LWGTQDVSQDIQEM*KDESAR.M	2353.50874	3	2.12E-04	0.40	3.24	-	164.9
gi|5031573|ref|NP_005712.1|	ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye			2.39E-07	6.35	70.25	28.70	47370.9
AHQ-1-8, 7516	R.DITYFIQQLLR.D	1410.64250	2	3.77E-06	0.97	4.76	-	1574.7
AHQ-1-8, 3614	K.DYEEIGPSICR.H	1340.44122	2	1.08E-05	0.85	2.59	-	1269.9
AHQ-1-8, 5936	K.GVDDLDFFIGDEAIEKPTYATK.W	2445.66268	2	2.39E-07	0.90	4.26	-	700.3
AHQ-1-8, 4289	R.HGIVEDWDLMER.F	1500.66127	2	2.19E-05	0.95	3.85	-	1290.5
AHQ-1-9, 6339	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	2.43E-05	0.80	3.82	-	367.4
AHQ-1-8, 6550 - 6615	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	4.06E-06	0.86	4.15	-	553.9
AHQ-1-8, 3719 - 3720	R.LPACVVDCGTGYTK.L	1543.74421	2	1.02E-04	0.91	3.99	-	866.6
AHQ-1-8, 6724	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	3.33E-04	0.91	4.73	-	719.3
gi|5802966|ref|NP_006861.1|	destrin (actin depolymerizing factor); destrin [Homo sapiens]			2.41E-07	1.76	20.17	14.50	18505.6
AHQ-1-12, 1985 - 2065	K.HECQANGPEDLNR.A	1541.58530	2	1.50E-05	0.87	3.12	-	878.7
AHQ-1-12, 3733	R.YALYDASFETK.E	1308.41754	1	2.41E-07	0.89	3.42	-	802.3
gi|10880989|ref|NP_067075.1|	RAB18, member RAS oncogene family; RAB18 small GTPase [Homo sapiens] [			2.55E-07	2.73	30.20	19.40	22976.9
AHQ-1-11, 3431	K.LAIWDTAGQER.F	1260.38088	2	3.38E-07	0.93	3.66	-	1279.1
AHQ-1-11, 5932 - 5938	K.LDNWLNELETYCTR.N	1828.98037	2	2.55E-07	0.92	4.09	-	802.4
AHQ-1-11, 5554	K.TCDGVQCAFEELVEK.I	1787.94661	2	1.68E-04	0.87	3.89	-	776.0
gi|5803181|ref|NP_006810.1|	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo			2.59E-07	0.85	10.19	3.50	62638.9
AHQ-1-14- , 6248	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	2.59E-07	0.85	3.58	-	491.6
gi|9910280|ref|NP_064505.1|	UDP-glucose ceramide glucosyltransferase-like 1; UDP-glucose:glycoprote			2.62E-07	0.97	10.22	0.90	177187.7
AHQ-1-3, 5687	K.VWQLQDLSFQTAAR.I	1663.85826	2	2.62E-07	0.97	4.39	-	2103.8

gi|4505813|ref|NP_003737.1|	cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain			2.65E-07	2.35	30.17	24.70	10365.8
AHQ-1-14- , 3866	K.NADM*SEEM*QQDSVECATQALEK.Y	2548.67874	2	4.45E-04	0.85	3.49	-	603.8
AHQ-1-14- , 3162	R.NFGSYVTHETK.H	1283.37131	2	2.65E-07	0.66	2.67	-	677.4
AHQ-1-14- , 2387	R.NFGSYVTHETK.H	1283.37131	2	3.88E-07	0.91	3.44	-	935.8
AHQ-1-14- , 3636 - 3671	K.YNPTWHCIVGR.N	1404.57820	2	3.43E-07	0.83	3.28	-	548.4
gi|18765729|ref|NP_003816.2|	synaptosomal-associated protein 23 isoform SNAP23A; synaptosomal-assoc			2.67E-07	2.37	30.20	19.40	23353.9
AHQ-1-10, 2497	R.IEEGLDQINK.D	1159.27163	2	5.42E-05	0.52	2.55	-	609.9
AHQ-1-12, 4386 - 4466	R.ILGLAIESQDAGIK.T	1428.65614	2	2.16E-06	0.93	3.70	-	1170.9
AHQ-1-11, 4239	R.ILGLAIESQDAGIK.T	1428.65614	2	5.64E-05	0.96	3.95	-	1639.9
AHQ-1-12, 3242	K.TTWGDGGENSPCNVVSK.Q	1809.89231	2	2.67E-07	0.92	3.91	-	1250.1
gi|4757714|ref|NP_004291.1|	acid phosphatase 1 isoform c; acid phosphatase of erythrocyte; red cell			2.72E-07	2.66	30.22	24.10	18042.4
AHQ-1-11, 3646 - 3647	K.IELLGSYDPQK.Q	1263.42144	2	2.16E-05	0.95	4.48	-	1027.6
AHQ-1-11, 3179	R.SPIAEAVFR.K	990.13779	2	2.72E-07	0.91	3.24	-	884.9
AHQ-1-11, 3382	R.VDSAATSGYEIGNPPDYR.G	1912.99094	2	1.91E-05	0.80	3.38	-	705.8
gi|6005854|ref|NP_009204.1|	repressor of estrogen receptor activity; B-cell associated protein [Hom			2.74E-07	2.72	30.24	16.40	33296.1
AHQ-1-9, 4900	R.IGGVQQDTILAEGLHFR.I	1855.08727	2	2.74E-07	0.90	3.72	-	911.8
AHQ-1-9, 7107	R.IPWFQYPIIYDIR.A	1725.02480	2	2.71E-04	0.97	4.73	-	1467.9
AHQ-1-9, 6658	R.IYLTADNLVLNLQDESFTR.G	2226.47137	2	3.02E-04	0.86	3.55	-	735.2
gi|17463729|ref|XP_069253.1|	similar to prohibitin [Homo sapiens]			2.74E-07	0.87	10.15	2.50	43846.2
AHQ-1-10, 3524	R.FDAGELITQR.E	1150.26643	2	2.74E-07	0.87	2.94	-	1215.7
gi|4557235|ref|NP_000009.1|	acyl-Coenzyme A dehydrogenase, very long chain precursor [Homo sapiens]			2.84E-07	0.93	10.20	2.30	70389.7
AHQ-1-6, 4523 - 4524	R.VPSENVLGEVGSGFK.V	1519.68100	2	2.84E-07	0.93	3.99	-	1008.0
gi|7705849|ref|NP_057215.1|	ras-related GTP-binding protein RAB10; ras-related GTP-binding protein			2.89E-07	1.90	20.23	11.50	22540.8
AHQ-1-11, 6008 - 6023	K.AFLTLAEDILR.K	1262.47982	2	2.89E-07	0.96	4.20	-	1791.3
AHQ-1-13- , 6631	K.AFLTLAEDILR.K	1262.47982	2	4.24E-07	0.95	4.13	-	1381.4
AHQ-1-14- , 6370 - 6372	K.AFLTLAEDILR.K	1262.47982	2	1.03E-06	0.95	4.54	-	1419.8
AHQ-1-11, 1787 - 1859	R.NIDEHANEDVER.M	1441.44245	2	4.51E-04	0.94	3.53	-	1322.7
gi|21361122|ref|NP_001440.2|	four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap			2.89E-07	3.64	40.26	18.90	31894.7
AHQ-1-9, 2388	K.AIVAGDQNVEYK.G	1307.43431	2	6.47E-06	0.91	3.67	-	862.9
AHQ-1-13- , 2552	K.AIVAGDQNVEYK.G	1307.43431	2	2.71E-05	0.90	3.78	-	703.1
AHQ-1-10, 2373	K.AIVAGDQNVEYK.G	1307.43431	2	6.61E-05	0.75	2.88	-	609.2
AHQ-1-9, 3210	K.CLHPLANETFVAK.D	1501.73210	2	2.73E-04	0.88	3.21	-	620.7
AHQ-1-13, 3707 - 3787	R.FVFHQEQVYCPDCAK.K	1931.13758	2	4.84E-05	0.80	3.41	-	729.6
AHQ-1-13- , 3933	R.FVFHQEQVYCPDCAK.K	1931.13758	2	1.06E-05	0.97	5.22	-	1391.7
AHQ-1-13- , 3927	R.FVFHQEQVYCPDCAK.K	1931.13758	3	8.19E-06	0.78	3.59	-	1032.9
AHQ-1-9, 3718 - 3754	R.FVFHQEQVYCPDCAK.K	1931.13758	2	2.89E-07	0.93	3.63	-	1138.8
AHQ-1-9, 3039	K.GEDFYCVTCHETK.F	1648.75260	2	4.20E-06	0.91	3.36	-	867.7
gi|4826659|ref|NP_004921.1|	F-actin capping protein beta subunit; Cap Z [Homo sapiens]			2.94E-07	3.48	40.24	19.10	30628.5
AHQ-1-10, 3832	K.GCWDSIHVVEVQEK.S	1687.85505	2	2.94E-07	0.95	4.80	-	1408.7
AHQ-1-10, 3296	R.KLEVEANNAFDQYR.D	1697.82988	2	1.61E-04	0.93	4.49	-	914.3
AHQ-1-10, 3213	R.KLEVEANNAFDQYR.D	1697.82988	2	5.20E-07	0.95	4.11	-	1463.7
AHQ-1-9, 3278 - 3279	R.KLEVEANNAFDQYR.D	1697.82988	2	3.36E-05	0.95	3.95	-	1655.2
AHQ-1-13- , 2999	K.SGSGTMNLGGSLTR.Q	1338.47345	2	1.53E-04	0.57	2.53	-	549.9
AHQ-1-9, 2716	K.SGSGTMNLGGSLTR.Q	1338.47345	2	6.93E-06	0.81	3.06	-	705.7
AHQ-1-10, 3449	R.STLNEIYFGK.T	1172.31200	2	1.21E-05	0.84	2.93	-	851.6
AHQ-1-9, 3552	R.STLNEIYFGK.T	1172.31200	2	3.34E-06	0.77	2.75	-	652.8
gi|30158852|ref|XP_301583.1|	similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa			2.96E-07	0.76	10.15	6.50	19197.0
AHQ-1-6, 2908	K.IWHHTFYNKLR.V	1515.74533	2	7.64E-05	0.46	2.85	-	512.8
AHQ-1-8, 2686	K.IWHHTFYNKLR.V	1515.74533	2	2.96E-07	0.76	2.83	-	848.5
AHQ-1-1, 3279 - 3356	K.IWHHTFYNKLR.V	1515.74533	2	1.34E-05	0.52	2.95	-	460.7
gi|4507509|ref|NP_003245.1|	tissue inhibitor of metalloproteinase 1 precursor; Erythroid-potentiati			2.98E-07	0.96	10.20	5.80	23170.8
AHQ-1-10, 3517	K.GFQALGDAADIR.F	1234.34342	2	2.98E-07	0.96	3.90	-	1774.1
gi|4507643|ref|NP_003279.1|	tumor protein D52-like 2; hD54 [Homo sapiens]			2.99E-07	1.70	20.23	14.60	22209.6
AHQ-1-10, 5073	R.TPAVEGLTEAEEEELRAELTK.V	2316.50485	3	2.99E-07	0.86	4.31	-	588.4
AHQ-1-10, 5072	R.TPAVEGLTEAEEEELRAELTK.V	2316.50485	2	7.86E-04	0.91	4.57	-	650.3
AHQ-1-10, 6372 - 6388	R.TPAVEGLTEAEEEELRAELTKVEEEIVTLR.Q	3385.71879	3	1.48E-05	0.84	4.14	-	613.1
gi|4503481|ref|NP_001395.1|	eukaryotic translation elongation factor 1 gamma; elongation factor 1-g			3.55E-07	1.25	20.20	6.40	50118.5
AHQ-1-12, 4909 - 4911	R.EYFSWEGAFQHVGK.A	1685.81925	2	3.55E-07	0.65	3.23	-	422.5
AHQ-1-14- , 2728	R.KLDPGSEETQTLVR.E	1573.73020	2	9.03E-07	0.60	3.25	-	321.8
AHQ-1-8, 2469 - 2471	R.KLDPGSEETQTLVR.E	1573.73020	2	1.13E-06	0.87	3.92	-	536.8
gi|12408675|ref|NP_036526.2|	prefoldin 2 [Homo sapiens]			3.59E-07	0.96	10.25	7.80	16647.7
AHQ-1-12, 3713 - 3715	K.IIETLTQQLQAK.G	1386.61925	2	3.59E-07	0.96	5.06	-	1509.6
gi|30153852|ref|XP_171113.3|	similar to Moesin (Membrane-organizing extension spike protein) [Homo			3.61E-07	0.97	10.24	9.30	15601.7
AHQ-1-6, 1866	R.RKPDTIEVQQMK.A	1473.72364	2	3.61E-07	0.97	4.71	-	1658.5
gi|22059949|ref|XP_114617.2|	similar to tubulin, beta 5 [Homo sapiens]			3.63E-07	1.87	20.34	18.80	22810.8
AHQ-1-10, 4839	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	1.70E-05	0.94	5.75	-	908.8
AHQ-1-13- , 5400	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	4.58E-04	0.82	4.27	-	602.3
AHQ-1-7, 5509 - 5536	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	3.63E-07	0.97	6.84	-	1587.6
AHQ-1-7, 5621	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	1.08E-04	0.93	5.26	-	1006.0
AHQ-1-14, 6116	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	7.47E-04	0.87	4.31	-	878.2
AHQ-1-9, 5371	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	7.34E-04	0.57	3.21	-	595.6
AHQ-1-14- , 5271	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	1.23E-05	0.97	6.33	-	1532.0
AHQ-1-12, 5178	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	6.50E-04	0.95	5.91	-	1006.4
AHQ-1-9, 2640 - 2642	R.ISVYYNEATGGK.Y	1302.41453	1	3.46E-05	0.05	1.86	-	221.9
AHQ-1-7, 2688 - 2696	R.ISVYYNEATGGK.Y	1302.41453	2	5.62E-07	0.90	3.66	-	752.9
AHQ-1-14- , 2742 - 2786	R.ISVYYNEATGGK.Y	1302.41453	2	1.31E-05	0.91	3.48	-	817.5
AHQ-1-7, 2685 - 2686	R.ISVYYNEATGGK.Y	1302.41453	1	1.90E-05	0.56	2.57	-	431.5
AHQ-1-13, 2825 - 2838	R.ISVYYNEATGGK.Y	1302.41453	2	1.08E-06	0.87	2.93	-	886.4
gi|16933542|ref|NP_002017.1|	fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s			3.67E-07	4.95	60.24	4.50	259222.8
AHQ-1-1, 4461 - 4472	R.EESPLLIGQQSTVSDVPR.D	1956.14354	2	2.65E-06	0.93	4.26	-	776.8
AHQ-1-1, 4525	R.ITYGETGGNSPVQEFTVPGSK.S	2169.33354	2	3.38E-05	0.73	3.19	-	394.6
AHQ-1-1, 6153 - 6165	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	1.66E-05	0.95	4.71	-	910.1
AHQ-1-1, 4416	R.PAQGVVTTLENVSPPR.R	1665.87246	2	6.65E-04	0.79	2.94	-	871.7
AHQ-1-1, 4819	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	3.91E-05	0.89	4.02	-	727.3
AHQ-1-1, 4105	R.VDVIPVNLPGEHGQR.L	1630.82981	2	3.67E-07	0.66	2.60	-	475.4
gi|28178832|ref|NP_002159.2|	isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat			3.68E-07	3.19	40.23	11.90	50909.0
AHQ-1-8, 4108 - 4180	K.DLAGCIHGLSNVK.L	1385.57150	1	8.35E-05	0.54	2.75	-	391.0
AHQ-1-8, 4024 - 4100	K.DLAGCIHGLSNVK.L	1385.57150	2	1.76E-04	0.95	3.76	-	1428.4
AHQ-1-8, 4832 - 4835	R.NILGGTVFREPIICK.N	1719.04170	2	3.68E-07	0.96	4.60	-	1431.4
AHQ-1-13- , 2167	K.TIEAEAAHGTVTR.H	1356.46696	2	8.40E-07	0.91	3.32	-	1179.6
AHQ-1-9, 1940	K.TIEAEAAHGTVTR.H	1356.46696	2	1.18E-06	0.77	2.81	-	669.2
AHQ-1-11, 2078	K.TIEAEAAHGTVTR.H	1356.46696	2	1.75E-06	0.75	3.00	-	917.3
AHQ-1-8, 1909	K.TIEAEAAHGTVTR.H	1356.46696	2	9.85E-06	0.92	3.53	-	1121.4
AHQ-1-8, 3106	K.VCVETVESGAMTK.D	1412.61230	2	6.33E-04	0.79	2.61	-	859.3
gi|7705614|ref|NP_057132.1|	CGI-111 protein [Homo sapiens]			3.73E-07	1.79	20.23	17.10	22087.6
AHQ-1-9, 7303	K.FSMVLPEVEAALAEIPGVR.S	2029.38904	2	3.73E-07	0.93	4.53	-	800.3
AHQ-1-9, 4291 - 4358	K.GLGSTVQEIDLTGVK.L	1517.70655	2	5.88E-04	0.85	3.21	-	805.8
gi|5453559|ref|NP_006347.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; ATP			3.74E-07	0.78	10.17	10.60	18491.1
AHQ-1-11, 5239	R.LAALPENPPAIDWAYYK.A	1933.19486	2	3.74E-07	0.78	3.36	-	349.7
gi|14043026|ref|NP_003752.2|	vesicle-associated membrane protein 8; endobrevin [Homo sapiens]			3.91E-07	0.91	10.21	14.00	11438.2
AHQ-1-13- , 2575	R.NKTEDLEATSEHFK.T	1649.74039	2	2.00E-05	0.95	3.87	-	1432.6
AHQ-1-13- , 2571	R.NKTEDLEATSEHFK.T	1649.74039	3	3.91E-07	0.91	4.22	-	1317.4
gi|4503821|ref|NP_001456.1|	FYN binding protein (FYB-120/130); FYN-binding protein (FYB-120/130) [H			4.06E-07	0.88	10.27	2.60	85450.5
AHQ-1-10, 3876 - 3877	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	6.59E-07	0.96	5.05	-	806.6
AHQ-1-12, 4111	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	4.06E-07	0.88	4.35	-	294.8
AHQ-1-13, 4091	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	1.34E-06	0.97	5.37	-	924.5
AHQ-1-13- , 4272	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	3.63E-04	0.93	4.54	-	721.1

AHQ-1-6, 4227	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	1.55E-05	0.88	4.09	-	484.3
gi|15553127|ref|NP_000180.2|	hexokinase 2; hexokinase-2, muscle [Homo sapiens]			4.16E-07	0.93	10.16	1.20	102379.3
AHQ-1-4, 2379	K.GAAM*VTAVAYR.L	1126.31148	2	4.16E-07	0.93	3.19	-	1532.9
gi|14249382|ref|NP_116139.1|	hypothetical protein MGC15429 [Homo sapiens]			4.17E-07	1.87	20.19	11.00	22345.5
AHQ-1-11, 3552	R.AVAIDLPGLGHSK.E	1278.48248	2	1.06E-05	0.94	3.80	-	1213.6
AHQ-1-11, 4243	R.FSVLLLHGIR.F	1155.41731	2	4.17E-07	0.93	3.31	-	1143.1
gi|10047092|ref|NP_037391.1|	neuronal protein [Homo sapiens]			4.33E-07	0.94	10.19	5.00	31454.0
AHQ-1-14- , 6022	R.TTDIFQTVDLWEGK.D	1653.81378	2	6.52E-05	0.89	3.44	-	1261.0
AHQ-1-12, 5878	R.TTDIFQTVDLWEGK.D	1653.81378	2	4.33E-07	0.94	3.89	-	1180.6
gi|29727565|ref|XP_291384.1|	similar to Cytochrome c, somatic [Homo sapiens]			4.36E-07	1.96	20.31	16.20	11621.4
AHQ-1-13- , 6556 - 6569	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	4.36E-07	0.98	5.62	-	1762.9
AHQ-1-13- , 6876	K.GIIWGEDTLMEYLENPK.K	2009.26831	2	5.73E-07	0.98	6.22	-	1834.2
AHQ-1-13, 6107 - 6112	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	1.42E-06	0.97	5.00	-	1542.4
gi|4506505|ref|NP_002916.1|	regulator of G-protein signaling 10 [Homo sapiens]			4.41E-07	1.35	20.18	16.20	19607.9
AHQ-1-11, 4558	K.LQDQIFNLMK.Y	1250.49254	2	3.55E-04	0.78	3.66	-	538.9
AHQ-1-11, 5175	K.WAASLENLLEDPEGVKR.F	1928.13502	2	4.41E-07	0.57	3.36	-	326.6
gi|21264318|ref|NP_004028.3|	adenosine monophosphate deaminase 2 (isoform L) [Homo sapiens]			4.50E-07	1.62	20.18	3.50	100687.2
AHQ-1-5, 6189	K.CGVPFTDLLDAAK.S	1408.60184	2	4.50E-07	0.80	3.06	-	522.6
AHQ-1-5, 5675	R.SAPYEFPEESPIEQLEER.R	2151.27185	2	1.37E-04	0.81	3.35	-	466.8
gi|17986001|ref|NP_005505.2|	major histocompatibility complex, class I, B; HLA class I histocompati			4.56E-07	2.78	30.25	13.30	40459.8
AHQ-1-8, 4867	R.APWIEQEGPEYWDR.N	1776.88556	2	4.56E-07	0.91	3.97	-	866.4
AHQ-1-12, 4770	R.APWIEQEGPEYWDR.N	1776.88556	2	5.11E-04	0.64	3.00	-	597.1
AHQ-1-9, 4875	R.APWIEQEGPEYWDR.N	1776.88556	2	6.52E-06	0.94	3.87	-	1342.0
AHQ-1-14, 5774	R.APWIEQEGPEYWDR.N	1776.88556	2	1.49E-05	0.72	3.11	-	674.5
AHQ-1-8, 5055 - 5088	R.FISVGYVDDTQFVR.F	1646.82447	2	5.10E-04	0.91	3.78	-	1054.2
AHQ-1-8, 4064	R.GHDQYAYDGKDYIALNEDLR.S	2357.47731	3	2.03E-06	0.95	5.03	-	1389.6
gi|7019375|ref|NP_037373.1|	formin homology 2 domain containing 1; FH1/FH2 domain-containing protei			4.65E-07	2.54	30.20	5.40	126496.5
AHQ-1-6, 6988	R.FGPCATLWASLDPVSVDTAR.L	2165.41131	2	4.65E-07	0.85	3.57	-	764.0
AHQ-1-6, 3927	K.FSGVAGEAPSNPSVPVAVSSGPGR.G	2227.41945	2	3.16E-04	0.79	3.85	-	310.4
AHQ-1-8, 5972	R.VQYLEDTDPFACANFPEPR.R	2271.44761	2	1.98E-05	0.90	3.92	-	861.7
gi|4502209|ref|NP_001653.1|	ADP-ribosylation factor 5 [Homo sapiens]			4.79E-07	0.79	10.13	7.80	20529.5
AHQ-1-11, 5079	K.NICFTVWDVGGQDK.I	1640.79838	2	4.79E-07	0.79	2.55	-	1078.8
gi|7019545|ref|NP_037481.1|	secreted protein of unknown function [Homo sapiens]			4.82E-07	0.74	10.17	8.70	18856.2
AHQ-1-12, 3954	R.YGGEEEDQPIYLAVK.G	1711.85009	2	4.82E-07	0.74	3.39	-	513.9
gi|23110942|ref|NP_002781.2|	proteasome alpha 5 subunit; proteasome component 5; macropain subunit			4.93E-07	1.79	20.20	12.90	26410.9
AHQ-1-10, 3041	R.AIGSASEGAQSSLQEVYHK.S	1963.09463	2	4.93E-07	0.83	3.98	-	531.7
AHQ-1-10, 5188	R.LFQVEYAIEAIK.L	1424.66595	2	6.50E-07	0.96	3.72	-	2086.0
gi|13376181|ref|NP_079079.1|	hypothetical protein FLJ21665 [Homo sapiens]			4.98E-07	0.63	10.15	3.80	49908.5
AHQ-1-7, 5096	R.SFGGGTGSGFTSLLM*ER.L	1720.88522	2	4.98E-07	0.63	3.07	-	577.9
gi|4557297|ref|NP_000022.1|	delta-aminolevulinic acid dehydratase; porphobilinogen synthase; aminol			5.01E-07	0.93	10.22	5.80	36294.7
AHQ-1-9, 5016 - 5047	R.GSAADSEESPAIEAIHLLR.K	1967.12642	2	5.01E-07	0.93	4.34	-	683.4
gi|7705819|ref|NP_057181.1|	HSPC039 protein [Homo sapiens]			5.05E-07	0.87	10.22	24.40	8968.7
AHQ-1-14- , 5116	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	5.05E-07	0.87	3.84	-	619.4
AHQ-1-14, 5996	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	3.44E-06	0.89	4.32	-	630.8
gi|4504505|ref|NP_000405.1|	hydroxysteroid (17-beta) dehydrogenase 4 [Homo sapiens]			5.42E-07	1.78	20.20	3.90	79685.9
AHQ-1-6, 2783	R.ATSTATSGFAGAIGQK.L	1468.59408	2	1.18E-05	0.78	3.10	-	703.8
AHQ-1-5, 2749	R.ATSTATSGFAGAIGQK.L	1468.59408	2	5.42E-07	0.82	3.24	-	877.6
AHQ-1-6, 3156	R.VVLVTGAGAGLGR.A	1170.38715	2	9.30E-06	0.96	4.01	-	1590.6
gi|4557697|ref|NP_000412.1|	keratin 10; Keratin-10 [Homo sapiens]			5.64E-07	2.63	30.20	10.30	57247.1
AHQ-1-5, 2654	R.ALEESNYELEGK.I	1382.45482	2	1.36E-06	0.92	3.82	-	1057.5
AHQ-1-13- , 2824	R.ALEESNYELEGK.I	1382.45482	2	1.72E-04	0.69	2.94	-	652.9
AHQ-1-14- , 2762	R.ALEESNYELEGK.I	1382.45482	2	5.64E-07	0.93	3.67	-	1278.6
AHQ-1-1, 4349	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	7.57E-06	0.84	3.38	-	646.7
AHQ-1-14- , 5591	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	9.38E-05	0.86	4.04	-	975.5
gi|5453605|ref|NP_006421.1|	chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-			5.69E-07	0.92	10.16	2.40	57838.8
AHQ-1-7, 3648	K.VIDPATATSVDLR.D	1358.52277	2	5.69E-07	0.92	3.07	-	1123.7
gi|8923812|ref|NP_060943.1|	uncharacterized hypothalamus protein HT012 [Homo sapiens]			6.29E-07	0.91	10.18	8.60	14960.4
AHQ-1-13- , 4248	K.TLAFTSVDLTNK.A	1310.47811	2	3.96E-06	0.93	3.62	-	1030.8
AHQ-1-13, 4068	K.TLAFTSVDLTNK.A	1310.47811	2	6.29E-07	0.91	2.79	-	1398.3
gi|4502219|ref|NP_001656.1|	ras homolog gene family, member G (rho G); RhoG [Homo sapiens]			6.46E-07	1.24	20.17	18.80	21338.4
AHQ-1-11, 4712	K.EYIPTVFDNYSAQSAVDGR.T	2133.25975	2	6.46E-07	0.80	3.35	-	478.0
AHQ-1-11, 4706	R.TVNLNLWDTAGQEEYDR.L	2025.12129	2	9.42E-04	0.44	2.63	-	339.4
gi|30157434|ref|XP_300550.1|	similar to cDNA sequence, BC023835 [Homo sapiens]			6.85E-07	1.17	20.18	20.10	23169.2
AHQ-1-11, 4512	K.DSGACFSASEPDAVHVVLDR.H	2134.26934	2	4.65E-04	0.27	2.74	-	198.5
AHQ-1-11, 5595	R.YHALLIPSCPGALTDLASSGSLAR.I	2472.80246	3	6.85E-07	0.90	3.62	-	1783.4
gi|30158489|ref|XP_301421.1|	similar to Chloride intracellular channel protein 1 (Nuclear chloride			7.31E-07	1.26	30.23	11.60	28267.5
AHQ-1-10, 5485 - 5539	K.FLNGNELTLADCNLLPK.L	1934.20276	2	1.89E-05	0.54	3.25	-	576.1
AHQ-1-13- , 6192	K.FLNGNELTLADCNLLPK.L	1934.20276	2	3.42E-05	0.90	4.63	-	1204.9
AHQ-1-12, 5550	R.KFLNGNELTLADCNLLPK.L	2062.37568	2	9.98E-04	0.58	3.57	-	612.5
AHQ-1-10, 2483	K.NSNPALNDNLQK.G	1328.41362	1	1.28E-04	0.16	2.21	-	260.1
AHQ-1-10, 2333	K.NSNPALNDNLQK.G	1328.41362	1	1.34E-04	0.09	2.36	-	199.2
AHQ-1-10, 2175	K.NSNPALNDNLQK.G	1328.41362	1	7.31E-07	0.13	2.06	-	222.6
gi|13489091|ref|NP_066949.1|	3-mercaptopyruvate sulfurtransferase [Homo sapiens]			7.40E-07	3.37	40.31	24.90	33178.2
AHQ-1-9, 3244	R.AFGHHAVSLLDGGLR.H	1550.74638	2	6.87E-05	0.85	3.41	-	926.8
AHQ-1-9, 6710	R.AGQPLQLLDASWYLPK.L	1801.07798	2	7.40E-07	0.97	4.87	-	1870.5
AHQ-1-9, 7071 - 7139	R.DGIEPGHIPGTVNIPFTDFLSQEGLEK.S	2912.19939	3	9.01E-04	0.96	6.27	-	1230.2
AHQ-1-9, 4779 - 4792	R.HIPGAAFFDIDQCSDR.T	1850.98926	2	4.29E-05	0.59	2.58	-	365.1
gi|4507207|ref|NP_003121.1|	sorcin; Sorcin (class 4 gene) [Homo sapiens]			7.57E-07	0.94	10.24	10.10	21676.3
AHQ-1-11, 4468 - 4470	R.CLTQSGIAGGYKPFNLETCR.L	2275.54736	2	7.57E-07	0.94	4.83	-	537.9
gi|24307939|ref|NP_036205.1|	chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]			7.81E-07	1.45	20.16	4.40	59670.7
AHQ-1-7, 4537	K.IAILTCPFEPPKPK.T	1612.95750	2	9.77E-04	0.70	3.15	-	401.1
AHQ-1-7, 3318	R.SLHDALCVIR.N	1185.37874	2	7.81E-07	0.74	2.72	-	650.4
gi|21314617|ref|NP_000433.2|	platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e			7.91E-07	3.97	50.30	9.90	82449.6
AHQ-1-3, 5995	R.CESISGTLPISYQLLK.T	1811.08954	2	4.94E-05	0.81	3.06	-	432.0
AHQ-1-4, 6103	R.CESISGTLPISYQLLK.T	1811.08954	2	1.37E-04	0.90	4.23	-	489.2
AHQ-1-1, 5948 - 5956	R.CESISGTLPISYQLLK.T	1811.08954	2	3.61E-04	0.73	3.20	-	296.4
AHQ-1-4, 6686	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	2.74E-04	0.97	5.97	-	1258.1
AHQ-1-5, 3442	K.EDTIVSQTQDFTK.I	1512.60049	2	5.38E-04	0.57	2.98	-	371.6
AHQ-1-4, 2491	R.IISGIHMQTSESTK.S	1532.74472	2	7.91E-07	0.95	4.13	-	977.3
AHQ-1-5, 4127	K.STESYFIPEVR.I	1328.45199	2	4.71E-04	0.68	2.58	-	498.4
gi|30147105|ref|XP_210550.2|	similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48			7.92E-07	0.91	10.19	2.20	61339.9
AHQ-1-5, 4271 - 4281	K.ADLINNLGTIAK.S	1243.43490	2	7.92E-07	0.91	3.80	-	832.5
AHQ-1-5, 4055	K.ADLINNLGTIAK.S	1243.43490	2	9.86E-06	0.86	3.54	-	548.4
gi|4502693|ref|NP_001760.1|	CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen			8.22E-07	2.17	30.20	9.60	25415.9
AHQ-1-11, 2228	K.EVQEFYK.D	943.03476	1	7.65E-04	0.57	2.93	-	286.4
AHQ-1-1, 2824	K.EVQEFYKDTYNK.L	1564.67709	2	2.84E-04	0.80	3.01	-	816.7
AHQ-1-10, 3163 - 3173	K.KDVLETFTVK.S	1180.37558	2	6.86E-05	0.79	3.16	-	691.0
AHQ-1-9, 3176	K.KDVLETFTVK.S	1180.37558	2	8.22E-07	0.79	2.85	-	882.5
AHQ-1-12, 3330	K.KDVLETFTVK.S	1180.37558	2	5.12E-05	0.87	3.31	-	882.1
AHQ-1-1, 3600	K.KDVLETFTVK.S	1180.37558	2	1.97E-05	0.92	3.43	-	1159.6
gi|4507143|ref|NP_003786.1|	sorting nexin 3 isoform a; sorting nexin 3A [Homo sapiens]			8.25E-07	1.78	20.19	14.80	18762.2
AHQ-1-12, 4886 - 4887	R.GDDGIFDDNFIEER.K	1642.66158	2	8.25E-07	0.91	3.74	-	963.2
AHQ-1-12, 2759	R.KQGLEQFINK.V	1205.38836	2	8.40E-05	0.87	3.41	-	895.9
gi|4503743|ref|NP_002009.1|	flightless I homolog [Homo sapiens]			8.28E-07	1.80	20.22	2.00	144750.1
AHQ-1-3, 4066	R.LLQSLLDTR.C	1059.24157	2	8.30E-05	0.84	2.92	-	980.6
AHQ-1-3, 6690	K.VGLGLGYLELPQINYK.L	1778.08432	2	8.28E-07	0.95	4.46	-	1180.6
gi|10835035|ref|NP_003157.1|	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3; t			8.32E-07	1.63	20.19	14.20	34196.0

AHQ-1-9, 5847	K.SHLPLALLPQTLLDQK.V	1788.12388	2	2.41E-06	0.85	3.11	-	773.2
AHQ-1-9, 6752	K.YFAEALGPLQSFQARPDDLLINTYPK.S	2969.33891	3	8.32E-07	0.78	3.49	-	472.3
gi|20330805|ref|NP_005263.1| guanine nucleotide binding protein, alpha transducing activity polypep				8.46E-07	0.94	10.19	3.10	40175.6
AHQ-1-9, 3143 - 3152	K.LLLLGAGESGK.S	1058.25357	2	8.46E-07	0.94	3.79	-	1329.2
gi|4506193|ref|NP_002784.1| proteasome beta 1 subunit; proteasome subunit HC5; proteasome component				8.50E-07	3.51	40.25	27.40	26489.2
AHQ-1-11, 5408 - 5418	K.AGGSASAMLQPLLDNQVGFK.N	2005.28443	2	7.07E-04	0.88	4.20	-	488.7
AHQ-1-11, 6419	R.FFPYYVYNIIGGLDEEGK.G	2125.36396	2	1.40E-04	0.97	5.05	-	1412.8
AHQ-1-11, 3892	K.GAVYSFDPVGSYQR.D	1546.66500	2	2.70E-04	0.85	3.38	-	735.9
AHQ-1-11, 3435	K.NMQNVEHVPLSLDR.A	1652.85728	2	8.50E-07	0.80	3.64	-	579.1
gi|5902726|ref|NP_005800.1| peroxiredoxin 2; thioredoxin-dependent peroxide reductase 1 (thiol-spec				8.55E-07	1.73	20.26	9.10	21856.8
AHQ-1-11, 6299	K.EGGLGPLNIPLLADVTR.R	1736.00583	2	5.71E-04	0.77	2.95	-	464.9
AHQ-1-11, 5820	R.KEGGLGPLNIPLLADVTR.R	1864.17875	2	8.55E-07	0.97	5.26	-	1109.8
gi|9966825|ref|NP_065089.1| HEF like Protein [Homo sapiens]				8.67E-07	1.53	20.29	4.30	86696.2
AHQ-1-13- , 4333	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	8.67E-07	0.97	5.86	-	1580.6
AHQ-1-13, 3457	K.LVDTLCMETQER.D	1496.68930	2	7.66E-04	0.56	2.66	-	404.6
gi|4759086|ref|NP_004883.1| vesicle trafficking protein sec22b [Homo sapiens]				9.05E-07	2.73	30.22	20.00	24740.4
AHQ-1-12, 2069	R.DLQQYQSQAK.Q	1209.29073	2	9.52E-04	0.93	3.39	-	1256.5
AHQ-1-12, 3921	R.NLGSINTELQDVQR.I	1587.71696	2	9.05E-07	0.92	4.46	-	823.3
AHQ-1-12, 3973	R.VADGLPLAASMQEDEQSGR.D	1975.12722	2	1.88E-04	0.88	3.44	-	747.5
gi|14042953|ref|NP_114420.1| FKSG17 [Homo sapiens]				9.67E-07	0.66	10.15	6.10	23305.9
AHQ-1-11, 4507	K.NILFVITKPDVYK.S	1550.86611	2	9.67E-07	0.66	2.90	-	651.6
gi|13637631|ref|XP_016625.1| similar to voltage-dependent anion channel isoform 2 [Homo sapiens] [M				9.72E-07	1.29	20.21	11.30	31479.2
AHQ-1-9, 4115 - 4183	K.VNNSSLIGVGYTQTLRPGVK.L	2104.39573	2	8.19E-04	0.33	2.72	-	297.3
AHQ-1-9, 4839	K.YKWCEYGLTFTEK.W	1726.92965	2	9.72E-07	0.97	4.29	-	1479.9
gi|4759044|ref|NP_004841.1| Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]				9.80E-07	2.27	30.20	4.00	160883.4
AHQ-1-3, 5218	K.EFINLQSALESER.R	1536.66842	2	9.80E-07	0.69	2.80	-	758.8
AHQ-1-3, 3725	R.GAFGEVQLVR.H	1076.23068	2	1.39E-04	0.82	2.96	-	1150.3
AHQ-1-3, 5427 - 5503	R.SQLQALHIGLDSSSIGSGPGDAEADDGFPESR.L	3215.34459	3	2.70E-04	0.76	3.91	-	808.3
gi|5453714|ref|NP_006448.1| LIM protein (similar to rat protein kinase C-binding enigma) [Homo sapi				1.01E-06	1.33	20.16	4.90	64027.9
AHQ-1-13- , 2049	R.ASAAPKPEPVPVQK.G	1419.65094	2	5.74E-05	0.69	3.12	-	481.8
AHQ-1-13- , 2951	K.EVVKPVPITSPAVSK.V	1551.85241	2	1.01E-06	0.63	2.73	-	322.2
AHQ-1-13, 2933	K.EVVKPVPITSPAVSK.V	1551.85241	2	3.48E-05	0.69	2.94	-	310.7
gi|19923457|ref|NP_057447.2| glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M				1.01E-06	0.92	10.20	3.20	67308.6
AHQ-1-7, 5773	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	2	4.39E-06	0.84	3.45	-	555.9
AHQ-1-7, 5756	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	1.01E-06	0.92	4.05	-	1177.1
gi|20547107|ref|XP_114482.1| similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN				1.01E-06	2.42	30.23	5.60	94330.3
AHQ-1-4, 7038	R.EFSITDVVPYPISLR.W	1736.98906	2	7.10E-06	0.67	3.07	-	317.4
AHQ-1-4, 3318	K.ELSTTLNADEAVTR.G	1520.62416	2	6.29E-04	0.82	3.14	-	670.0
AHQ-1-4, 6814 - 6831	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	1.01E-06	0.93	4.62	-	781.8
gi|4506675|ref|NP_002941.1| ribophorin I [Homo sapiens]				1.12E-06	0.93	10.21	2.80	68569.0
AHQ-1-1, 5880	R.FVDHVFDEQVIDSLTVK.I	1992.21748	2	1.12E-06	0.93	4.17	-	829.5
gi|11496891|ref|NP_000662.2| class III alcohol dehydrogenase 5 chi subunit; Alcohol dehydrogenase (				1.20E-06	0.95	10.26	5.90	39738.1
AHQ-1-11, 4932 - 4963	K.AAVAWEAGKPLSIEEIEVAPPK.A	2306.64276	2	2.72E-04	0.91	4.56	-	546.3
AHQ-1-9, 5200 - 5270	K.AAVAWEAGKPLSIEEIEVAPPK.A	2306.64276	2	1.20E-06	0.95	5.13	-	885.7
gi|30147623|ref|XP_293669.2| similar to actinin, alpha 4 [Homo sapiens]				1.22E-06	0.87	10.18	3.50	57794.4
AHQ-1-5, 4250	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	1.22E-06	0.87	3.58	-	724.0
gi|5901922|ref|NP_008996.1| CDC37 homolog [Homo sapiens]				1.25E-06	0.91	10.21	5.60	44468.0
AHQ-1-8, 6899	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	1.25E-06	0.91	4.25	-	514.3
gi|5454090|ref|NP_006271.1| signal sequence receptor, delta; translocon-associated protein delta [H				1.26E-06	1.70	20.18	17.30	18998.5
AHQ-1-12, 4725	R.FFDEESYSLLR.K	1406.52121	2	1.26E-06	0.91	3.62	-	917.4
AHQ-1-12, 5991	R.NNEDISIIPPLFTVSVDHR.G	2167.40715	3	1.58E-06	0.78	3.50	-	689.3
gi|4502171|ref|NP_000476.1| adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho				1.26E-06	4.31	50.28	41.10	19607.6
AHQ-1-11, 3666	R.DISPVLKDPASFR.A	1445.64525	2	5.60E-06	0.80	3.18	-	569.6
AHQ-1-11, 6506	R.GFLFGPSLAQELGLGCVLIR.K	2149.54130	2	2.98E-06	0.98	5.70	-	1753.0
AHQ-1-11, 4907	R.GKLPGPTLWASYSLEYGK.A	1968.24075	2	1.92E-05	0.81	3.26	-	543.0
AHQ-1-11, 3479	R.IDYIAGLDSR.G	1123.24098	2	1.37E-05	0.94	3.56	-	1235.7
AHQ-1-11, 5396 - 5402	R.SFPDFPTPGVVFR.D	1466.66462	2	1.26E-06	0.78	2.76	-	478.0
gi|29737976|ref|XP_290742.1| similar to Phosphoribosylformylglycinamidine synthase (FGAM synthase)				1.29E-06	0.68	10.18	2.10	144733.3
AHQ-1-3, 7087	R.LGGTALAQCFSQLGEHPPDLDLPENLVR.A	3050.39201	3	1.29E-06	0.68	3.51	-	403.5
gi|30149460|ref|XP_210540.2| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				1.34E-06	0.93	10.20	4.00	29287.8
AHQ-1-5, 2202 - 2210	K.HIYYITGETK.D	1225.37490	1	2.54E-04	0.81	2.63	-	879.9
AHQ-1-5, 2201	K.HIYYITGETK.D	1225.37490	2	1.34E-06	0.93	3.19	-	907.0
gi|5453722|ref|NP_006321.1| lysophospholipase I; lysophospholipase 1; lysophospholipid-specific lys				1.34E-06	1.71	20.21	12.60	24669.5
AHQ-1-11, 2962	K.ALIDQEVKNGIPSNR.I	1654.84968	2	1.34E-06	0.74	2.71	-	752.5
AHQ-1-11, 6196	K.LAGVTALSCWLPLR.A	1558.86992	2	1.19E-05	0.97	4.26	-	1779.6
gi|29788766|ref|NP_064424.2| tubulin, beta polypeptide 4, member Q [Homo sapiens]				1.40E-06	2.28	30.31	11.10	48377.2
AHQ-1-13- , 4045	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	2.69E-04	0.86	3.46	-	533.0
AHQ-1-14- , 3939 - 4016	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	2.56E-05	0.54	2.85	-	317.4
AHQ-1-9, 6335 - 6336	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	1.40E-06	0.76	3.90	-	649.0
AHQ-1-7, 5504 - 5513	R.KEAESCDCLQGFQLTHSLGGGTGSGM*GTLLLSK.I	3459.82781	3	4.04E-04	0.97	6.06	-	1816.5
gi|4505145|ref|NP_002387.1| malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochon				1.41E-06	2.69	30.20	6.30	65443.3
AHQ-1-7, 3644	K.ALTSQLTDEELAQGR.L	1632.75450	2	3.06E-04	0.89	3.91	-	932.8
AHQ-1-6, 3220	R.HISDSVFLEAAK.A	1317.47234	2	5.94E-06	0.94	3.74	-	843.7
AHQ-1-6, 2972	K.IETQDIQALR.F	1187.32821	2	1.41E-06	0.87	3.23	-	1049.5
gi|5729875|ref|NP_006658.1| progesterone receptor membrane component 1; progesterone binding protei				1.45E-06	2.41	30.17	17.90	21671.0
AHQ-1-11, 4343 - 4371	K.FYGPEGPYGVFAGR.D	1517.66849	2	4.41E-04	0.84	3.18	-	749.0
AHQ-1-11, 2818 - 2838	R.GDQPAASGDSDDDEPPPLPR.L	2037.04410	2	3.47E-05	0.73	3.22	-	295.7
AHQ-1-11, 3854 - 3915	R.KFYGPEGPYGVFAGR.D	1645.84140	2	1.45E-06	0.83	3.48	-	606.3
gi|4506045|ref|NP_002718.1| proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p				1.45E-06	2.79	30.20	17.10	17623.6
AHQ-1-1, 2449	R.CNPDSNSANCLEEK.G	1640.68887	2	9.56E-06	0.91	3.48	-	907.5
AHQ-1-1, 4816 - 4821	K.GPMFELLPGESNK.I	1419.62807	2	1.45E-06	0.94	3.87	-	1195.3
AHQ-1-1, 4209 - 4212	K.GPM*FELLPGESNK.I	1435.62747	2	4.18E-06	0.94	4.07	-	883.9
gi|4506381|ref|NP_002863.1| ras-related C3 botulinum toxin substrate 2; Ras-related C3 botulinum to				1.47E-06	1.71	20.20	7.80	21428.7
AHQ-1-11, 3946	K.KLAPITYPQGLALAK.E	1584.92723	2	2.21E-05	0.90	3.93	-	617.3
AHQ-1-11, 4347 - 4348	K.LAPITYPQGLALAK.E	1456.75431	2	1.47E-06	0.81	2.71	-	476.1
gi|29731000|ref|XP_291064.1| similar to KIAA0540 protein [Homo sapiens]				1.53E-06	1.71	20.23	2.10	224374.8
AHQ-1-1, 3721	K.LIVVVAGQPSEVR.S	1367.61917	2	1.53E-06	0.96	4.51	-	1433.3
AHQ-1-1, 6193	R.VLNTSSLESATDEAGSPLAAAAAAAAAER.C	2716.89684	3	1.35E-04	0.75	3.31	-	817.6
gi|17402865|ref|NP_003303.2| thiosulfate sulfurtransferase; rhodanese [Homo sapiens]				1.58E-06	2.56	30.20	14.80	33428.7
AHQ-1-9, 4038	R.FLGTEPEPDAVGLDSGHIR.G	2011.18089	2	4.05E-05	0.84	3.72	-	517.5
AHQ-1-9, 3335	K.KVDLSQPLIATCR.K	1502.76154	2	4.79E-04	0.80	2.96	-	694.8
AHQ-1-9, 4716	K.TYEQVLENLESK.R	1453.57618	2	1.58E-06	0.92	4.06	-	833.5
gi|9845502|ref|NP_002286.2| laminin receptor 1; Laminin receptor-1 (67kD); laminin receptor 1 (67kD				1.59E-06	0.83	10.16	5.10	32853.8
AHQ-1-10, 5175	R.FTPGTFTNQIQAAFR.E	1699.89060	2	1.59E-06	0.83	3.19	-	444.4
gi|29729857|ref|XP_293567.1| similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60)				1.62E-06	0.93	10.16	3.40	38427.8
AHQ-1-14- , 3583	R.TVIIEQSWGSPK.V	1345.52569	2	5.62E-04	0.93	3.28	-	1383.2
AHQ-1-7, 3516	R.TVIIEQSWGSPK.V	1345.52569	2	1.62E-06	0.93	3.00	-	1546.3
gi|5729991|ref|NP_006494.1| proteasome 26S ATPase subunit 4 isoform 1; protease 26S subunit 6; Tat-				1.69E-06	0.88	10.17	2.90	47365.9
AHQ-1-5, 3827	R.GVLM*YGPPGCGK.T	1253.47332	2	1.69E-06	0.88	3.35	-	950.7
gi|4504085|ref|NP_000399.1| glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA				1.71E-06	4.44	50.21	10.30	80814.1
AHQ-1-6, 3648	R.CKDVLTGQEFDVR.A	1568.73370	2	5.66E-06	0.89	3.34	-	952.7
AHQ-1-6, 6072 - 6082	R.LAFLNVQAAEEALPR.I	1642.88050	2	1.22E-04	0.89	3.82	-	851.1
AHQ-1-6, 5780	R.LVQDYGLESEVAQHLAATYGDK.A	2408.60567	3	1.11E-05	0.84	3.47	-	762.2
AHQ-1-6, 6291	R.VIFFLPWQK.M	1178.44934	2	1.71E-06	0.91	3.34	-	812.6
AHQ-1-6, 6342 - 6414	R.YGAATANYMEVVSLLK.K	1731.00632	2	1.00E-05	0.91	4.27	-	683.6
gi|10863873|ref|NP_000651.1| transforming growth factor, beta 1 (Camurati-Engelmann disease); trans				1.74E-06	2.74	30.21	11.00	44422.0
AHQ-1-13, 3349	R.ALDTNYCFSSTEK.N	1537.63010	2	2.37E-04	0.90	3.34	-	896.8

AHQ-1-13- , 3424	R.ALDTNYCFSSTEK.N	1537.63010	2	1.74E-06	0.93	3.85	-	1037.6
AHQ-1-9, 6827	R.LLAPSDSPEWLSFDVTGVVR.Q	2189.45272	2	2.18E-05	0.90	4.06	-	470.4
AHQ-1-13- , 3611	K.VEQLSNMIVR.S	1189.41074	2	3.29E-04	0.95	4.30	-	1325.9
AHQ-1-13, 3509	K.VEQLSNMIVR.S	1189.41074	2	5.10E-06	0.91	3.50	-	1206.7
gi|4557797|ref|NP_000260.1|	non-metastatic cells 1 protein [Homo sapiens]			1.79E-06	2.59	30.16	20.40	17148.6
AHQ-1-12, 4061	K.DRPFFAGLVK.Y	1150.35439	2	1.61E-04	0.91	3.28	-	1093.6
AHQ-1-12, 2917	R.GLVGEIIKR.F	985.20582	2	1.05E-04	0.87	2.56	-	1062.4
AHQ-1-14- , 3064	R.TFIAIKPDGVQR.G	1345.57205	2	1.79E-06	0.80	3.02	-	781.1
AHQ-1-12, 2949	R.TFIAIKPDGVQR.G	1345.57205	2	2.59E-05	0.85	3.14	-	808.8
gi|17450333|ref|XP_060887.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			1.89E-06	0.91	10.23	11.00	17503.9
AHQ-1-12, 6417	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	2.55E-04	0.93	4.47	-	1033.5
AHQ-1-13- , 6768	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	1.42E-05	0.95	4.56	-	1201.4
AHQ-1-12, 6198 - 6261	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	1.89E-06	0.91	3.65	-	1028.7
gi|19913414|ref|NP_055018.2|	adaptor-related protein complex 2, alpha 1 subunit isoform 1; adaptin,			1.92E-06	0.59	20.17	3.90	107545.3
AHQ-1-5, 5547 - 5551	K.TSVQFQNFSPTVVHPGDLQTQLAVQTK.R	2972.30119	3	1.01E-04	0.55	3.33	-	525.7
AHQ-1-12, 3757 - 3826	R.YGGAPQALTLK.L	1119.29547	1	1.92E-06	0.04	1.81	-	297.6
gi|4502297|ref|NP_001678.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit			1.96E-06	1.82	20.16	13.70	17489.8
AHQ-1-13, 2625	K.AQAELVGTADEATR.A	1432.51860	1	7.36E-04	0.22	2.29	-	208.4
AHQ-1-13- , 2611	K.AQAELVGTADEATR.A	1432.51860	1	2.72E-05	0.71	2.74	-	417.1
AHQ-1-13, 2621	K.AQAELVGTADEATR.A	1432.51860	2	1.96E-06	0.92	3.29	-	1150.6
AHQ-1-13- , 2368	R.IEANEALVK.A	987.13221	2	2.94E-04	0.90	2.94	-	891.4
gi|13569962|ref|NP_112243.1|	RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap			1.98E-06	2.43	30.29	18.90	22171.0
AHQ-1-11, 4336	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	1.98E-06	0.98	5.83	-	1912.9
AHQ-1-11, 4435	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	2.58E-05	0.96	4.92	-	1249.3
AHQ-1-11, 2059 - 2096	R.MGPGAASGGERPNLK.I	1442.62650	2	8.69E-04	0.48	2.70	-	451.2
AHQ-1-11, 6298 - 6302	K.NATNVEQAFMTMAAEIK.K	1870.14079	2	3.67E-06	0.97	5.29	-	1729.8
gi|15306356|ref|XP_035638.2|	similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan			2.05E-06	2.65	30.19	20.80	18795.1
AHQ-1-13, 3473	R.ESDVPLKTEEFEVTK.T	1751.91253	2	6.39E-05	0.76	3.32	-	462.2
AHQ-1-12, 3465	R.ESDVPLKTEEFEVTK.T	1751.91253	2	2.05E-06	0.78	3.48	-	384.5
AHQ-1-13- , 3596	R.GAEIEYAMAYSK.A	1333.49204	2	2.34E-04	0.94	3.85	-	1361.3
AHQ-1-13- , 4796	K.SYLYFTQFK.A	1197.36315	2	2.31E-05	0.93	3.55	-	1121.3
gi|8923579|ref|NP_060377.1|	hypothetical protein FLJ20625 [Homo sapiens]			2.05E-06	1.90	20.27	26.70	17744.7
AHQ-1-12, 6174 - 6175	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	1.88E-04	0.95	5.47	-	1157.5
AHQ-1-14- , 6250	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	5.99E-04	0.94	5.38	-	627.2
AHQ-1-12, 5265	R.TDEQALLSSILAK.T	1389.57677	2	2.05E-06	0.95	4.33	-	1219.9
gi|6041669|ref|NP_004538.2|	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd			2.10E-06	0.87	10.18	14.00	15208.5
AHQ-1-13, 4691	R.TLPETLDPAEYNISPETR.R	2047.20831	2	2.10E-06	0.87	3.54	-	545.3
gi|4504045|ref|NP_002063.1|	guanine nucleotide binding protein (G protein), q polypeptide [Homo sap			2.13E-06	3.37	40.27	15.90	42142.8
AHQ-1-9, 3183	K.LLLLGTGESGK.S	1088.27968	2	8.19E-04	0.82	3.37	-	794.8
AHQ-1-9, 4544 - 4592	K.SLWNDPGIQECYDR.R	1754.85835	2	2.13E-06	0.85	3.04	-	903.7
AHQ-1-9, 7228	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	3.50E-04	0.96	5.37	-	943.0
AHQ-1-9, 4539	K.VSAFENPYVDAIK.S	1453.62101	2	4.75E-04	0.74	2.64	-	818.7
gi|4506765|ref|NP_002952.1|	S100 calcium-binding protein A4; 18A2; 42A; S100 calcium-binding protei			2.26E-06	0.96	20.16	18.80	11728.5
AHQ-1-14- , 3514 - 3579	K.ALDVMVSTFHK.Y	1248.47665	2	2.26E-06	0.85	3.23	-	870.0
AHQ-1-14, 4718	R.ELPSFLGK.R	891.04613	1	7.06E-05	0.10	1.83	-	132.9
gi|4757952|ref|NP_001782.1|	cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p			2.28E-06	3.54	40.26	25.70	21258.5
AHQ-1-11, 2304	K.CVVVGDGAVGK.T	1062.22237	1	5.02E-04	0.77	2.61	-	745.1
AHQ-1-11, 2295 - 2298	K.CVVVGDGAVGK.T	1062.22237	2	6.76E-05	0.79	2.83	-	853.5
AHQ-1-11, 6300	K.NVFDEAILAALEPPEPK.K	1854.09282	3	2.28E-06	0.93	5.16	-	912.8
AHQ-1-11, 3790	K.TCLLISYTTNK.F	1315.51795	2	1.03E-05	0.92	3.19	-	1323.6
AHQ-1-11, 2530	K.YVECSALTQK.G	1200.34381	2	8.38E-06	0.90	3.68	-	602.1
gi|10835049|ref|NP_001655.1|	ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho			2.36E-06	0.90	10.18	6.20	21768.0
AHQ-1-13- , 3964	R.IGAFGYMECSAK.T	1335.53122	2	2.36E-06	0.90	3.54	-	746.6
AHQ-1-10, 3544	R.IGAFGYMECSAK.T	1335.53122	2	2.34E-05	0.57	2.80	-	505.2
gi|5803013|ref|NP_006808.1|	endoplasmic reticulum protein 29 precursor; endoplasmic reticulum lumen			2.39E-06	1.80	20.23	14.90	28993.2
AHQ-1-10, 3787	R.DGDFENPVPYTGAVK.V	1609.71786	2	2.39E-06	0.86	3.73	-	605.1
AHQ-1-10, 3655 - 3663	R.DGDFENPVPYTGAVK.V	1609.71786	2	5.44E-06	0.83	3.61	-	475.1
AHQ-1-10, 6380	K.GQGVYLGMPGCLPVYDALAGEFIR.A	2585.98267	2	3.16E-06	0.93	4.63	-	615.6
gi|13699868|ref|NP_005947.2|	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltet			2.40E-06	0.83	10.18	1.70	101530.5
AHQ-1-5, 4407 - 4462	K.YVVVTGITPTPLGEGK.S	1631.89439	2	2.40E-06	0.83	3.61	-	541.3
gi|30148456|ref|XP_293602.2|	similar to glutathione-S-transferase like; glutathione transferase ome			2.45E-06	0.91	10.18	3.90	29139.6
AHQ-1-13- , 4800	K.VPSLVGSFLR.T	1075.28583	2	4.87E-05	0.91	3.62	-	925.3
AHQ-1-10, 4239	K.VPSLVGSFLR.T	1075.28583	2	2.45E-06	0.91	3.38	-	1167.4
gi|4758790|ref|NP_004543.1|	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q			2.48E-06	0.97	10.26	11.30	12517.4
AHQ-1-13- , 6743	K.IEYDDFVECLLR.Q	1573.74872	2	2.48E-06	0.97	5.15	-	1092.7
AHQ-1-13, 6284	K.IEYDDFVECLLR.Q	1573.74872	2	3.12E-05	0.90	3.21	-	1163.6
gi|29729345|ref|XP_290995.1|	similar to speckle-type POZ protein [Homo sapiens]			2.54E-06	1.62	20.20	10.90	18703.4
AHQ-1-3, 6146	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	2.16E-04	0.67	3.08	-	859.5
AHQ-1-4, 6260 - 6274	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	2.54E-06	0.74	3.63	-	770.5
AHQ-1-5, 6214	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	6.13E-06	0.88	3.74	-	811.0
AHQ-1-6, 6107 - 6116	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	2.64E-04	0.87	3.76	-	887.1
AHQ-1-1, 6163	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	3.03E-04	0.79	4.02	-	867.3
gi|29727317|ref|XP_298144.1|	hypothetical protein XP_298144 [Homo sapiens]			2.64E-06	0.80	10.15	8.00	22108.6
AHQ-1-4, 6688 - 6704	K.GEYNLTLDTALTSNLK.T	1753.93165	2	2.64E-06	0.80	3.03	-	933.3
gi|4503529|ref|NP_001407.1|	eukaryotic translation initiation factor 4A, isoform 1 [Homo sapiens] [			2.68E-06	0.84	10.19	3.70	46153.7
AHQ-1-8, 3879	K.LQMEAPHIIVGTPGR.V	1619.91357	2	2.68E-06	0.84	3.78	-	677.0
gi|4759342|ref|NP_004808.1|	tight junction protein 2 (zona occludens 2); Friedreich ataxia region g			2.80E-06	0.97	10.25	1.60	124661.6
AHQ-1-7, 3769	R.TFLRPSPEDEAIYGPNTK.M	2036.23035	2	2.80E-06	0.97	4.98	-	1543.2
gi|4502861|ref|NP_001275.1|	adaptor-related protein complex 3, sigma 1 subunit; clathrin-associated			2.93E-06	0.94	10.20	7.80	21732.0
AHQ-1-11, 3748	K.FYQPYSEDTQQQIIR.E	1917.06756	2	2.93E-06	0.94	4.08	-	979.2
gi|11496885|ref|NP_005442.2|	enigma protein; LIM domain protein [Homo sapiens]			2.96E-06	0.94	10.19	2.60	49844.4
AHQ-1-11, 4576	K.VVLEGPAPWGFR.L	1328.54318	2	2.96E-06	0.94	3.83	-	1233.3
gi|30157216|ref|XP_292133.2|	similar to genethonin 1 [Homo sapiens]			3.01E-06	1.08	20.19	4.50	39693.8
AHQ-1-14, 5280	K.PSDTIENVK.A	1003.08850	1	4.49E-04	0.37	2.25	-	455.7
AHQ-1-5, 4582	K.TITLEVKPSDTIENVK.A	1788.03268	2	2.57E-05	0.57	3.00	-	579.3
AHQ-1-6, 4483	K.TITLEVKPSDTIENVK.A	1788.03268	2	9.20E-05	0.50	3.48	-	396.2
AHQ-1-9, 4414	K.TITLEVKPSDTIENVK.A	1788.03268	2	1.55E-04	0.25	2.53	-	236.3
AHQ-1-14, 5201 - 5277	K.TITLEVKPSDTIENVK.A	1788.03268	2	3.01E-06	0.71	3.74	-	565.2
AHQ-1-2, 4761	K.TITLEVKPSDTIENVK.A	1788.03268	2	5.12E-05	0.80	3.55	-	789.8
AHQ-1-1, 4637	K.TITLEVKPSDTIENVK.A	1788.03268	2	8.75E-05	0.37	2.58	-	315.8
gi|7656952|ref|NP_055227.1|	calcyclin binding protein [Homo sapiens]			3.03E-06	0.86	10.19	10.10	26209.8
AHQ-1-10, 4647	K.IYITLTGVHQVPTENVQVHFTER.S	2683.01488	3	3.03E-06	0.86	3.76	-	986.0
gi|7705632|ref|NP_057152.1|	CGI-135 protein [Homo sapiens]			3.27E-06	0.93	10.21	7.20	16979.6
AHQ-1-13- , 6777	K.GIVLLEELLPK.G	1224.51463	2	5.10E-06	0.94	4.11	-	1676.0
AHQ-1-12, 6383	K.GIVLLEELLPK.G	1224.51463	2	3.27E-06	0.93	3.24	-	1745.3
gi|5453998|ref|NP_006382.1|	importin 7; RAN-binding protein 7 [Homo sapiens]			3.31E-06	0.82	10.16	1.40	119515.7
AHQ-1-4, 6927	R.ENIVEAIIHSPELIR.V	1733.98994	2	3.31E-06	0.82	3.28	-	725.4
gi|19913373|ref|NP_079536.2|	G6B protein isoform G6b-A precursor; G6B protein; immunoglobulin recep			3.36E-06	2.52	30.16	13.90	25002.6
AHQ-1-12, 2510	R.TVLHVLGDR.T	1010.17224	2	3.36E-06	0.88	2.78	-	1080.5
AHQ-1-11, 2444	R.TVLHVLGDR.T	1010.17224	2	4.78E-05	0.94	3.13	-	1478.9
AHQ-1-12, 2643 - 2721	R.VNLSCGGVSHPIR.W	1397.58551	2	2.41E-05	0.89	2.93	-	1271.6
AHQ-1-11, 5018	R.WVWAPSFPACK.G	1350.56891	2	2.39E-04	0.75	2.87	-	531.2
gi|6005786|ref|NP_009214.1|	monoglyceride lipase; lysophospholipase-like [Homo sapiens]			3.38E-06	1.55	20.22	12.10	34292.3
AHQ-1-13- , 6260	K.LTVPFLLLQGSADR.L	1530.79329	2	3.38E-06	0.65	2.73	-	410.3
AHQ-1-14- , 6044 - 6046	K.LTVPFLLLQGSADR.L	1530.79329	2	5.87E-05	0.77	3.20	-	547.7
AHQ-1-9, 6428	R.TPQSIPYQDLPHLVNADGQYLFCR.Y	2835.14314	2	6.45E-04	0.79	3.41	-	504.4
AHQ-1-9, 6407 - 6438	R.TPQSIPYQDLPHLVNADGQYLFCR.Y	2835.14314	3	1.11E-05	0.89	4.50	-	621.3

gi|27500115|ref|XP_208901.1|	similar to ubiquitin-conjugating enzyme E2M; UBC12 homolog, yeast [Hom			3.44E-06	0.92	10.19	8.70	20964.0
AHQ-1-11, 5711	K.TCDISFSDPDDLLNFK.L	1889.02935	2	3.44E-06	0.92	3.81	-	940.8
gi|24307969|ref|NP_055423.1|	cytoplasmic FMR1 interacting protein 1; selective hybridizing clone (m			3.44E-06	0.79	10.17	1.00	145181.2
AHQ-1-3, 4581 - 4586	R.SSLEGPTILDIEK.F	1402.57231	2	3.44E-06	0.79	3.34	-	727.6
gi|6715607|ref|NP_000175.1|	G-gamma globin [Homo sapiens]			3.66E-06	0.89	10.19	6.80	16126.3
AHQ-1-13- , 5019 - 5032	R.LLVVYPWTQR.F	1275.52342	2	3.66E-06	0.89	3.20	-	972.0
gi|6005749|ref|NP_009193.1|	RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA			3.67E-06	2.51	30.22	30.20	19846.9
AHQ-1-11, 3330	R.DVVICPDASLEDAKK.E	1661.85581	2	3.67E-06	0.86	3.28	-	806.1
AHQ-1-11, 5082 - 5138	K.EGPYDVVVLPGGNLGAQNLSESAAVK.E	2585.85114	2	2.45E-04	0.86	4.31	-	315.8
AHQ-1-11, 3095 - 3158	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	3.69E-05	0.79	3.24	-	569.4
gi|7661948|ref|NP_055545.1|	KIAA0152 gene product [Homo sapiens]			3.71E-06	0.89	10.18	4.50	32233.6
AHQ-1-10, 3260 - 3303	R.SNPEDQILYQTER.Y	1593.67683	2	7.36E-06	0.81	3.57	-	505.0
AHQ-1-9, 3422	R.SNPEDQILYQTER.Y	1593.67683	2	3.71E-06	0.89	3.53	-	862.1
gi|19923483|ref|NP_057406.2|	GTPase Rab14 [Homo sapiens]			3.72E-06	2.97	40.23	17.20	23896.8
AHQ-1-10, 4039	R.GAAGALMVYDITR.R	1338.55819	2	1.78E-04	0.95	4.24	-	1498.9
AHQ-1-11, 4168	R.GAAGALMVYDITR.R	1338.55819	2	4.13E-06	0.95	3.65	-	1442.1
AHQ-1-11, 3650	R.GAAGALM*VYDITR.R	1354.55759	2	3.72E-06	0.94	3.72	-	1414.0
AHQ-1-11, 3180	K.SCLLHQFTEK.K	1264.43272	2	6.62E-05	0.91	3.25	-	838.5
AHQ-1-10, 3092	K.SCLLHQFTEK.K	1264.43272	2	1.93E-05	0.88	3.44	-	777.3
AHQ-1-10, 4215 - 4216	K.TGENVEDAFLEAAK.K	1494.58517	1	5.99E-04	0.22	2.41	-	460.1
AHQ-1-11, 4338	K.TGENVEDAFLEAAK.K	1494.58517	1	2.99E-04	0.20	2.23	-	624.9
AHQ-1-10, 4211 - 4256	K.TGENVEDAFLEAAK.K	1494.58517	2	8.00E-04	0.90	3.73	-	886.7
gi|19743813|ref|NP_002202.2|	integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib			3.86E-06	0.78	10.24	2.10	88414.9
AHQ-1-5, 5315	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	1.59E-04	0.78	3.65	-	411.0
AHQ-1-3, 5293 - 5295	K.LKPEDITQIQPQQLVLR.L	2020.36187	3	3.86E-06	0.78	3.87	-	731.1
gi|24111250|ref|NP_006563.2|	guanine nucleotide binding protein (G protein), alpha 13 [Homo sapiens			3.88E-06	0.34	10.13	4.50	44049.3
AHQ-1-9, 5172	K.LGEPDYIPSQQDILLAR.R	1929.16292	2	3.88E-06	0.34	2.63	-	254.1
gi|4885153|ref|NP_005198.1|	v-crk sarcoma virus CT10 oncogene homolog (avian)-like; v-crk avian sar			3.92E-06	1.90	20.22	9.60	33776.7
AHQ-1-9, 6632	K.IGDQEFDHLPALLEFYK.I	2036.27195	2	3.92E-06	0.93	4.43	-	931.1
AHQ-1-14- , 4799	K.TALALEVGDIVK.V	1229.44814	2	2.34E-05	0.96	4.14	-	1888.9
gi|9625002|ref|NP_000879.2|	integrin, beta 6 [Homo sapiens]			3.93E-06	0.91	10.13	1.10	85935.7
AHQ-1-3, 4002	R.LGFGSFVEK.P	984.13002	2	3.93E-06	0.91	2.59	-	1101.8
gi|4885405|ref|NP_005326.1|	hematopoietic cell-specific Lyn substrate 1 [Homo sapiens]			4.04E-06	0.96	10.20	2.70	53997.7
AHQ-1-12, 2375 - 2438	K.SAVGHEYVAEVEK.H	1418.53353	2	4.04E-06	0.96	4.04	-	1928.4
gi|22267436|ref|NP_056284.1|	DKFZp564D177 protein [Homo sapiens]			4.05E-06	2.62	30.21	18.20	28466.4
AHQ-1-11, 6114	K.DKEWQEQFLIPNLALIDK.Q	2201.50664	2	1.20E-04	0.92	4.28	-	753.6
AHQ-1-11, 3582 - 3644	K.LVGVFHTEYGALNR.V	1576.78061	2	1.65E-05	0.80	2.69	-	817.2
AHQ-1-11, 4080	R.VHVLWWNESADSR.A	1599.73113	2	4.05E-06	0.90	3.45	-	465.6
gi|4503609|ref|NP_001976.1|	electron-transfer-flavoprotein, beta polypeptide; electron-transferring			4.06E-06	1.71	20.20	11.40	27843.4
AHQ-1-10, 3540	K.EVIAVSCGPAQCQETIR.T	1921.14254	2	4.06E-06	0.90	4.04	-	823.1
AHQ-1-13, 3759	K.EVIAVSCGPAQCQETIR.T	1921.14254	2	4.52E-04	0.62	2.74	-	489.5
AHQ-1-10, 3139 - 3152	K.LSVISVEDPPQR.T	1340.50744	2	1.37E-04	0.81	3.05	-	777.5
gi|5803121|ref|NP_006801.1|	for protein disulfide isomerase-related [Homo sapiens]			4.09E-06	2.39	30.21	10.80	59594.0
AHQ-1-7, 4160	R.FHISEFPTLK.Y	1219.41350	2	4.09E-06	0.73	2.53	-	783.1
AHQ-1-7, 3174	K.GPPLWEEDPGAK.D	1296.40999	2	2.22E-04	0.77	2.59	-	652.4
AHQ-1-7, 6860 - 6930	K.NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK.E	3870.10181	3	9.89E-06	0.90	4.27	-	876.4
gi|4504111|ref|NP_002077.1|	growth factor receptor-bound protein 2 [Homo sapiens]			4.23E-06	0.67	10.16	5.50	25206.2
AHQ-1-10, 3277	K.VLNEECDQNWYK.A	1599.70313	2	4.23E-06	0.67	3.06	-	502.8
gi|20127450|ref|NP_002729.2|	protein kinase C, beta 1; Protein kinase C, beta 1 polypeptide [Homo s			4.23E-06	0.51	10.13	1.80	77011.7
AHQ-1-9, 4411	K.CSLNPEWNETFR.F	1554.66558	2	4.23E-06	0.51	2.60	-	373.3
gi|7706244|ref|NP_057005.1|	divalent cation tolerant protein CUTA [Homo sapiens]			4.26E-06	0.91	10.21	17.30	16832.5
AHQ-1-13, 6464	R.SVHPYEVAEVIALPVEQGNFPYLQWVR.Q	3142.55428	3	4.26E-06	0.91	4.10	-	1084.6
gi|29736026|ref|XP_085123.3|	similar to Ras-related protein Rab-15 [Homo sapiens]			4.36E-06	0.47	10.14	5.30	23517.8
AHQ-1-11, 3324	R.IQIWDTAGQER.Y	1317.43243	1	4.36E-06	0.47	2.79	-	315.4
gi|20070272|ref|NP_057110.2|	androgen-regulated short-chain dehydrogenase/reductase 1; prostate sho			4.41E-06	1.79	20.21	10.40	35414.1
AHQ-1-9, 3463	K.GSGVTTYSVHPGTVQSELVR.H	2075.26811	2	1.45E-05	0.83	3.43	-	537.5
AHQ-1-9, 2494 - 2500	K.VVVVTGANTGIGK.E	1215.42469	2	4.41E-06	0.96	4.29	-	1583.8
gi|19913441|ref|NP_002140.2|	hippocalcin-like 1; visinin-like protein 3; calcium-binding protein BD			4.44E-06	1.81	20.21	14.00	22313.1
AHQ-1-11, 4138	R.ENTEFTDHELQEWYK.G	1970.04095	2	6.63E-05	0.93	4.14	-	943.3
AHQ-1-11, 5615	R.SEMLEIVQAIYK.M	1424.68776	2	4.44E-06	0.89	2.93	-	1056.4
gi|4557251|ref|NP_001101.1|	a disintegrin and metalloprotease domain 10 [Homo sapiens]			4.60E-06	0.52	10.15	1.90	84141.7
AHQ-1-5, 4139	R.TITLQPGSPCNDFR.G	1607.76993	2	4.60E-06	0.52	2.99	-	256.3
gi|21281669|ref|NP_060899.1|	transcription factor-like nuclear regulator; putative transcription re			4.66E-06	0.31	10.16	0.80	252842.5
AHQ-1-2, 4895	K.NNSLEIDQTENVKPMLR.G	2002.23894	2	4.66E-06	0.31	3.15	-	386.1
AHQ-1-1, 4683	K.NNSLEIDQTENVKPMLR.G	2002.23894	2	5.78E-05	0.42	3.03	-	468.8
gi|4506265|ref|NP_000954.1|	prostaglandin-endoperoxide synthase 2 precursor; prostaglandin G/H synt			4.88E-06	0.81	10.17	1.50	68995.7
AHQ-1-6, 4106	R.LILIGETIK.I	1000.25717	2	4.88E-06	0.81	3.35	-	562.3
gi|4505989|ref|NP_000299.1|	protective protein for beta-galactosidase; Protective protein for beta-			4.91E-06	1.78	20.20	5.00	54495.8
AHQ-1-12, 4594	K.EFSHIAFLTIK.G	1306.53429	2	6.76E-04	0.81	3.14	-	595.4
AHQ-1-12, 3494	K.YGDSGEQIAGFVK.E	1371.47686	2	4.91E-06	0.97	4.00	-	1828.9
AHQ-1-14- , 3599	K.YGDSGEQIAGFVK.E	1371.47686	1	1.04E-04	0.37	2.56	-	342.5
AHQ-1-11, 3406	K.YGDSGEQIAGFVK.E	1371.47686	2	3.59E-04	0.97	3.88	-	2517.7
gi|4557871|ref|NP_001054.1|	transferrin [Homo sapiens]			5.27E-06	1.57	20.16	4.20	77049.5
AHQ-1-5, 4218	K.ADRDQYELLCLDNTR.K	1884.01756	2	5.27E-06	0.68	2.72	-	702.5
AHQ-1-5, 4235	R.FDEFFSEGCAPGSK.K	1579.66868	2	3.27E-05	0.89	3.20	-	1199.5
gi|5453607|ref|NP_006420.1|	chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co			5.29E-06	1.85	20.24	6.60	59366.3
AHQ-1-7, 5253	K.LPIGDVATQYFADR.D	1566.73935	2	1.63E-05	0.90	3.90	-	882.5
AHQ-1-7, 7276 - 7281	K.SQDAEVGDGTTSVTLLAAEFLK.Q	2253.44875	2	5.29E-06	0.95	4.87	-	838.9
gi|21361358|ref|NP_006365.2|	serine/threonine kinase 25 (STE20 homolog, yeast); sterile 20 (oxidant			5.35E-06	0.96	10.23	3.80	48111.3
AHQ-1-7, 4809	K.LADFGVAGQLTDTQIK.R	1677.88001	2	5.35E-06	0.96	4.55	-	1652.7
gi|4506189|ref|NP_002783.1|	proteasome alpha 7 subunit isoform 1; proteasome subunit RC6-1; proteas			5.45E-06	1.79	20.18	10.50	27886.7
AHQ-1-10, 2880 - 2943	K.ALLEVVQSGGK.N	1101.27845	2	5.45E-06	0.91	3.07	-	1234.3
AHQ-1-10, 3863	K.NYTDEAIETDDLTIK.L	1741.83137	2	5.97E-05	0.89	3.55	-	799.6
gi|22060072|ref|XP_088293.2|	similar to cytochrome c [Homo sapiens]			5.63E-06	1.58	20.15	18.10	11887.8
AHQ-1-13- , 4375	R.ADLIAYLK.K	907.08869	2	1.11E-05	0.89	2.95	-	948.7
AHQ-1-13, 4184	R.ADLIAYLK.K	907.08869	2	5.63E-06	0.83	2.76	-	865.6
AHQ-1-13- , 3567 - 3645	K.TGPNLHGLFGR.K	1169.31780	2	5.88E-05	0.76	2.69	-	590.3
gi|21361619|ref|NP_061882.2|	TOLLIP protein; Toll-interacting protein [Homo sapiens]			5.65E-06	1.70	20.22	9.90	30281.6
AHQ-1-11, 5463	R.GPVYIGELPQDFLR.I	1604.83072	2	5.65E-06	0.95	4.37	-	1231.1
AHQ-1-11, 4679 - 4742	R.IAWTHITIPESLR.Q	1537.78752	2	2.46E-04	0.75	2.83	-	762.0
gi|4557321|ref|NP_000030.1|	apolipoprotein A-I precursor [Homo sapiens]			5.69E-06	0.91	10.20	6.00	30777.6
AHQ-1-11, 5632 - 5643	R.EQLGPVTQEFWDNLEK.E	1934.09489	2	5.69E-06	0.91	3.91	-	711.4
gi|4505273|ref|NP_002442.1|	5'-methylthioadenosine phosphorylase [Homo sapiens]			5.79E-06	0.92	10.22	6.40	31249.9
AHQ-1-9, 5647	K.IGIIGGTGLDDPEILEGR.T	1826.04101	2	5.79E-06	0.92	4.35	-	707.8
gi|4501841|ref|NP_001596.1|	alanyl-tRNA synthetase [Homo sapiens]			5.83E-06	1.39	20.17	3.40	106800.7
AHQ-1-4, 7318	R.EIADLGEALATAVIPQWQK.D	2054.33195	2	5.83E-06	0.80	3.36	-	609.9
AHQ-1-4, 3492	K.ITCLCQVPQNAANR.G	1647.85889	2	4.44E-04	0.60	3.23	-	294.8
gi|8922804|ref|NP_060760.1|	hypothetical protein FLJ10983 [Homo sapiens]			6.01E-06	0.71	10.15	1.80	68268.9
AHQ-1-6, 2311	R.IVLANDPADR.L	1199.29585	2	6.01E-06	0.71	2.92	-	775.0
gi|4502553|ref|NP_003647.1|	calcium/calmodulin-dependent protein kinase I [Homo sapiens]			6.24E-06	0.55	10.14	4.60	41336.9
AHQ-1-9, 5487 - 5507	R.DLKPENLLYYSLDEDSK.I	2043.21643	2	6.24E-06	0.55	2.75	-	389.2
gi|21389549|ref|NP_653263.1|	hypothetical protein MGC26605 [Homo sapiens]			6.24E-06	1.31	20.17	14.90	26927.8
AHQ-1-10, 5156	R.AITVFSPDGHLFQVEYAQEAVK.K	2450.73052	2	4.40E-04	0.58	2.93	-	544.7
AHQ-1-10, 5157	R.AITVFSPDGHLFQVEYAQEAVK.K	2450.73052	3	6.24E-06	0.66	3.27	-	590.5
AHQ-1-10, 4245 - 4315	K.LTVEDPVTVEYITR.F	1635.83990	2	8.06E-05	0.65	3.17	-	640.8
gi|13027638|ref|NP_006750.2|	UDP-glucose pyrophosphorylase 2; UTP-glucose-1-phosphate uridyltransfe			6.37E-06	0.90	10.23	3.50	56964.9
AHQ-1-7, 6728	R.NENTFLDLTVQQIEHLNK.T	2157.36913	2	6.37E-06	0.90	4.52	-	856.5

<table>
<tr><td>gi|6005745|ref|NP_009165.1| dynactin 3 isoform 1; dynactin light chain [Homo sapiens]</td><td></td><td></td><td></td><td>6.51E-06</td><td>0.82</td><td>10.15</td><td>5.90</td><td>21119.3</td></tr>
<tr><td>AHQ-1-11, 2816</td><td>K.VQVALGNISSK.R</td><td>1116.29312</td><td>2</td><td>6.51E-06</td><td>0.82</td><td>2.93</td><td>-</td><td>671.4</td></tr>
<tr><td>gi|29734141|ref|XP_291117.1| similar to succinate dehydrogenase flavoprotein subunit [Homo sapiens]</td><td></td><td></td><td></td><td>6.60E-06</td><td>0.05</td><td>10.09</td><td>8.90</td><td>16590.8</td></tr>
<tr><td>AHQ-1-6, 2091</td><td>R.KHTLSYVDVGTGK.V</td><td>1405.58112</td><td>1</td><td>6.60E-06</td><td>0.05</td><td>1.81</td><td>-</td><td>327.2</td></tr>
<tr><td>gi|4506407|ref|NP_002873.1| RAN binding protein 1 [Homo sapiens]</td><td></td><td></td><td></td><td>6.65E-06</td><td>0.88</td><td>10.18</td><td>5.50</td><td>23310.0</td></tr>
<tr><td>AHQ-1-10, 4121</td><td>K.TLEEDEEELFK.M</td><td>1382.45159</td><td>2</td><td>6.65E-06</td><td>0.88</td><td>3.56</td><td>-</td><td>646.8</td></tr>
<tr><td>gi|13786129|ref|NP_112586.1| RAB33B, member RAS oncogene family; likely ortholog of mouse RAB33b [H</td><td></td><td></td><td></td><td>6.65E-06</td><td>0.35</td><td>10.16</td><td>4.80</td><td>25717.4</td></tr>
<tr><td>AHQ-1-13, 3485</td><td>K.IQLWDTAGQER.F</td><td>1317.43243</td><td>2</td><td>9.63E-04</td><td>0.88</td><td>3.26</td><td>-</td><td>792.9</td></tr>
<tr><td>AHQ-1-14- , 3667</td><td>K.IQLWDTAGQER.F</td><td>1317.43243</td><td>2</td><td>2.41E-05</td><td>0.90</td><td>3.14</td><td>-</td><td>1023.9</td></tr>
<tr><td>AHQ-1-11, 3439 - 3440</td><td>K.IQLWDTAGQER.F</td><td>1317.43243</td><td>1</td><td>6.65E-06</td><td>0.35</td><td>2.45</td><td>-</td><td>261.6</td></tr>
<tr><td>gi|29729329|ref|XP_291459.1| similar to Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18) [</td><td></td><td></td><td></td><td>6.88E-06</td><td>1.44</td><td>20.20</td><td>18.30</td><td>17172.9</td></tr>
<tr><td>AHQ-1-12, 5509 - 5571</td><td>K.EILVGDVGQTVNNLYATFVK.M</td><td>2181.47373</td><td>2</td><td>6.88E-06</td><td>0.92</td><td>4.09</td><td>-</td><td>965.2</td></tr>
<tr><td>AHQ-1-12, 2351</td><td>K.NIILEEGK.E</td><td>916.05399</td><td>1</td><td>3.15E-04</td><td>0.52</td><td>2.67</td><td>-</td><td>577.1</td></tr>
<tr><td>AHQ-1-12, 2345 - 2409</td><td>K.NIILEEGK.E</td><td>916.05399</td><td>1</td><td>2.37E-04</td><td>0.52</td><td>2.32</td><td>-</td><td>435.6</td></tr>
<tr><td>gi|7330335|ref|NP_039234.1| chloride intracellular channel 4; chloride intracellular channel 4 like</td><td></td><td></td><td></td><td>7.05E-06</td><td>3.00</td><td>40.18</td><td>24.50</td><td>28771.9</td></tr>
<tr><td>AHQ-1-10, 4424 - 4441</td><td>R.DEFTNTCPSDKEVEIAYSDVAK.R</td><td>2520.66487</td><td>2</td><td>1.16E-04</td><td>0.74</td><td>3.53</td><td>-</td><td>416.0</td></tr>
<tr><td>AHQ-1-10, 5393</td><td>K.FLDGNEMTLADCNLLPK.L</td><td>1953.22635</td><td>2</td><td>7.05E-06</td><td>0.69</td><td>3.18</td><td>-</td><td>505.0</td></tr>
<tr><td>AHQ-1-10, 5007</td><td>R.KFLDGNEMTLADCNLLPK.L</td><td>2081.39926</td><td>2</td><td>1.37E-05</td><td>0.83</td><td>3.65</td><td>-</td><td>711.8</td></tr>
<tr><td>AHQ-1-10, 5120</td><td>K.LDEYLNSPLPDEIDENSMEDIK.F</td><td>2580.76043</td><td>2</td><td>2.02E-04</td><td>0.74</td><td>2.83</td><td>-</td><td>530.4</td></tr>
<tr><td>gi|19923233|ref|NP_002970.2| sterol carrier protein 2 [Homo sapiens]</td><td></td><td></td><td></td><td>7.25E-06</td><td>0.85</td><td>10.18</td><td>2.20</td><td>58993.3</td></tr>
<tr><td>AHQ-1-13- , 2771 - 2836</td><td>K.LQNLQLQPGNAK.L</td><td>1324.51124</td><td>2</td><td>7.25E-06</td><td>0.85</td><td>3.55</td><td>-</td><td>811.6</td></tr>
<tr><td>gi|4501867|ref|NP_001089.1| aconitase 2 [Homo sapiens]</td><td></td><td></td><td></td><td>7.40E-06</td><td>0.85</td><td>10.19</td><td>2.10</td><td>85424.8</td></tr>
<tr><td>AHQ-1-5, 3434</td><td>K.IVYGHLDDPASQEIER.G</td><td>1842.98698</td><td>2</td><td>7.40E-06</td><td>0.85</td><td>3.77</td><td>-</td><td>644.6</td></tr>
<tr><td>gi|21614520|ref|NP_000393.2| glucose-6-phosphate dehydrogenase [Homo sapiens]</td><td></td><td></td><td></td><td>7.88E-06</td><td>2.49</td><td>30.23</td><td>9.10</td><td>59257.4</td></tr>
<tr><td>AHQ-1-14- , 5592</td><td>R.DGLLPENTFIVGYAR.S</td><td>1665.87093</td><td>2</td><td>1.18E-05</td><td>0.88</td><td>3.39</td><td>-</td><td>717.6</td></tr>
<tr><td>AHQ-1-7, 7096</td><td>R.LFYLALPPTVYEAVTK.N</td><td>1826.16735</td><td>2</td><td>7.88E-06</td><td>0.69</td><td>3.58</td><td>-</td><td>256.5</td></tr>
<tr><td>AHQ-1-7, 4473</td><td>R.LQFHDVAGDIFHQQCK.R</td><td>1945.14742</td><td>3</td><td>1.36E-05</td><td>0.92</td><td>4.53</td><td>-</td><td>855.0</td></tr>
<tr><td>AHQ-1-7, 4472</td><td>R.LQFHDVAGDIFHQQCK.R</td><td>1945.14742</td><td>2</td><td>1.62E-04</td><td>0.95</td><td>3.95</td><td>-</td><td>1207.5</td></tr>
<tr><td>gi|4505185|ref|NP_002406.1| macrophage migration inhibitory factor (glycosylation-inhibiting factor</td><td></td><td></td><td></td><td>8.17E-06</td><td>0.96</td><td>10.21</td><td>7.80</td><td>12476.2</td></tr>
<tr><td>AHQ-1-14- , 4618 - 4630</td><td>K.LLCGLLAER.L</td><td>1046.26608</td><td>2</td><td>8.17E-06</td><td>0.96</td><td>4.29</td><td>-</td><td>1328.8</td></tr>
<tr><td>gi|5902134|ref|NP_009005.1| coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin</td><td></td><td></td><td></td><td>8.35E-06</td><td>5.26</td><td>60.24</td><td>14.30</td><td>51026.0</td></tr>
<tr><td>AHQ-1-7, 1861 - 1866</td><td>R.AAPEASGTPSSDAVSR.L</td><td>1503.55369</td><td>2</td><td>1.25E-04</td><td>0.92</td><td>4.03</td><td>-</td><td>717.9</td></tr>
<tr><td>AHQ-1-7, 2045</td><td>K.ADQCYEDVR.V</td><td>1157.19275</td><td>2</td><td>1.90E-04</td><td>0.84</td><td>2.86</td><td>-</td><td>893.8</td></tr>
<tr><td>AHQ-1-7, 4460</td><td>R.DAGPLLISLK.D</td><td>1027.23948</td><td>2</td><td>1.46E-05</td><td>0.88</td><td>3.01</td><td>-</td><td>903.5</td></tr>
<tr><td>AHQ-1-7, 4456</td><td>R.DAGPLLISLK.D</td><td>1027.23948</td><td>1</td><td>1.60E-04</td><td>0.32</td><td>2.27</td><td>-</td><td>576.0</td></tr>
<tr><td>AHQ-1-7, 2197</td><td>R.KLQATVQELQK.R</td><td>1286.50292</td><td>2</td><td>3.89E-04</td><td>0.92</td><td>3.81</td><td>-</td><td>1325.7</td></tr>
<tr><td>AHQ-1-7, 2441</td><td>K.LQATVQELQK.R</td><td>1158.33000</td><td>2</td><td>1.09E-05</td><td>0.77</td><td>3.06</td><td>-</td><td>566.3</td></tr>
<tr><td>AHQ-1-7, 7437</td><td>R.YFEITSEAPFLHYLSMFSSK.E</td><td>2398.71748</td><td>3</td><td>2.48E-05</td><td>0.92</td><td>4.44</td><td>-</td><td>838.2</td></tr>
<tr><td>AHQ-1-7, 7436</td><td>R.YFEITSEAPFLHYLSMFSSK.E</td><td>2398.71748</td><td>2</td><td>8.35E-06</td><td>0.91</td><td>4.78</td><td>-</td><td>465.3</td></tr>
<tr><td>gi|11321585|ref|NP_002065.1| guanine nucleotide-binding protein, beta-1 subunit; G protein, beta-1</td><td></td><td></td><td></td><td>8.37E-06</td><td>2.38</td><td>30.19</td><td>12.10</td><td>37376.8</td></tr>
<tr><td>AHQ-1-9, 4963</td><td>R.KACADATLSQITNNIDPVGR.I</td><td>2146.36794</td><td>2</td><td>8.37E-06</td><td>0.68</td><td>3.07</td><td>-</td><td>444.4</td></tr>
<tr><td>AHQ-1-9, 4247</td><td>K.LIIWDSYTTNK.V</td><td>1354.53258</td><td>2</td><td>1.22E-04</td><td>0.84</td><td>3.14</td><td>-</td><td>807.5</td></tr>
<tr><td>AHQ-1-9, 1859</td><td>R.LLVSASQDGK.L</td><td>1018.14631</td><td>2</td><td>2.24E-05</td><td>0.87</td><td>2.88</td><td>-</td><td>944.3</td></tr>
<tr><td>gi|4506353|ref|NP_002854.1| phosphorylase, glycogen; liver (Hers disease, glycogen storage disease</td><td></td><td></td><td></td><td>8.61E-06</td><td>0.85</td><td>10.16</td><td>1.70</td><td>97147.8</td></tr>
<tr><td>AHQ-1-5, 5673 - 5691</td><td>K.LVIDQIDNGFFSPK.Q</td><td>1593.80471</td><td>2</td><td>8.61E-06</td><td>0.85</td><td>3.15</td><td>-</td><td>936.7</td></tr>
<tr><td>gi|21450721|ref|NP_659447.1| hypothetical protein MGC26778 [Homo sapiens]</td><td></td><td></td><td></td><td>8.81E-06</td><td>0.02</td><td>10.12</td><td>3.10</td><td>29454.0</td></tr>
<tr><td>AHQ-1-14- , 4064</td><td>K.KAQEDYDR.Y</td><td>1025.05426</td><td>1</td><td>8.81E-06</td><td>0.02</td><td>1.81</td><td>-</td><td>70.1</td></tr>
<tr><td>gi|27597085|ref|NP_000357.3| tropomyosin 1 (alpha) [Homo sapiens]</td><td></td><td></td><td></td><td>8.82E-06</td><td>2.44</td><td>30.17</td><td>8.50</td><td>32865.7</td></tr>
<tr><td>AHQ-1-9, 3164</td><td>R.KLVIIESDLER.A</td><td>1315.54103</td><td>1</td><td>2.89E-04</td><td>0.30</td><td>1.84</td><td>-</td><td>379.0</td></tr>
<tr><td>AHQ-1-9, 3150</td><td>R.KLVIIESDLER.A</td><td>1315.54103</td><td>2</td><td>8.82E-06</td><td>0.88</td><td>3.24</td><td>-</td><td>1004.1</td></tr>
<tr><td>AHQ-1-10, 3541</td><td>K.LVIIESDLER.A</td><td>1187.36811</td><td>2</td><td>2.05E-04</td><td>0.85</td><td>2.88</td><td>-</td><td>936.6</td></tr>
<tr><td>AHQ-1-10, 2049</td><td>K.YSQKEDRYEEEIK.V</td><td>1717.81473</td><td>2</td><td>2.10E-04</td><td>0.71</td><td>3.21</td><td>-</td><td>351.4</td></tr>
<tr><td>gi|30148492|ref|XP_293610.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]</td><td></td><td></td><td></td><td>8.94E-06</td><td>2.65</td><td>30.22</td><td>4.40</td><td>72113.4</td></tr>
<tr><td>AHQ-1-6, 4342</td><td>K.DAGTIAGLNVLR.I</td><td>1200.37012</td><td>2</td><td>3.49E-04</td><td>0.93</td><td>3.63</td><td>-</td><td>1249.6</td></tr>
<tr><td>AHQ-1-10, 4285 - 4361</td><td>R.IINEPTAAAIAYGLDK.K</td><td>1660.89259</td><td>2</td><td>8.94E-06</td><td>0.80</td><td>3.49</td><td>-</td><td>895.1</td></tr>
<tr><td>AHQ-1-6, 4291 - 4302</td><td>R.IINEPTAAAIAYGLDKK.V</td><td>1789.06550</td><td>3</td><td>1.69E-05</td><td>0.75</td><td>3.33</td><td>-</td><td>530.2</td></tr>
<tr><td>AHQ-1-7, 4377</td><td>R.IINEPTAAAIAYGLDKK.V</td><td>1789.06550</td><td>2</td><td>3.11E-04</td><td>0.64</td><td>2.94</td><td>-</td><td>422.3</td></tr>
<tr><td>AHQ-1-7, 4386</td><td>R.IINEPTAAAIAYGLDKK.V</td><td>1789.06550</td><td>3</td><td>3.63E-04</td><td>0.68</td><td>3.28</td><td>-</td><td>384.1</td></tr>
<tr><td>AHQ-1-6, 4287</td><td>R.IINEPTAAAIAYGLDKK.V</td><td>1789.06550</td><td>2</td><td>4.03E-05</td><td>0.83</td><td>3.74</td><td>-</td><td>693.4</td></tr>
<tr><td>AHQ-1-6, 4232 - 4303</td><td>R.IINEPTAAAIAYGLDKK.V</td><td>1789.06550</td><td>2</td><td>9.15E-06</td><td>0.92</td><td>4.44</td><td>-</td><td>612.5</td></tr>
<tr><td>gi|7705704|ref|NP_057001.1| glutathione S-transferase subunit 13 homolog [Homo sapiens]</td><td></td><td></td><td></td><td>8.95E-06</td><td>1.84</td><td>20.24</td><td>13.70</td><td>25496.7</td></tr>
<tr><td>AHQ-1-11, 4392</td><td>R.FLTAVNLEHPEMLEK.A</td><td>1772.05845</td><td>2</td><td>2.84E-05</td><td>0.96</td><td>4.70</td><td>-</td><td>1548.1</td></tr>
<tr><td>AHQ-1-11, 4382</td><td>R.NEDITEPQSILAAAEK.A</td><td>1729.86695</td><td>2</td><td>8.95E-06</td><td>0.88</td><td>3.71</td><td>-</td><td>613.3</td></tr>
<tr><td>gi|4503141|ref|NP_001805.1| cathepsin C isoform a preproprotein; dipeptidyl-peptidase I; dipeptidyl</td><td></td><td></td><td></td><td>9.04E-06</td><td>1.81</td><td>20.22</td><td>4.30</td><td>51841.5</td></tr>
<tr><td>AHQ-1-14- , 5427 - 5450</td><td>R.GTDECAIESIAVAATPIPK.L</td><td>1945.18072</td><td>2</td><td>9.04E-06</td><td>0.95</td><td>4.45</td><td>-</td><td>1210.4</td></tr>
<tr><td>AHQ-1-14, 5953</td><td>R.RGTDECAIESIAVAATPIPK.L</td><td>2101.36707</td><td>2</td><td>7.26E-05</td><td>0.86</td><td>4.00</td><td>-</td><td>606.1</td></tr>
<tr><td>gi|14149777|ref|NP_115500.1| hypothetical protein DKFZp564D1378 [Homo sapiens]</td><td></td><td></td><td></td><td>9.28E-06</td><td>0.96</td><td>10.26</td><td>8.10</td><td>28535.7</td></tr>
<tr><td>AHQ-1-10, 6301 - 6373</td><td>K.DGLALGPGPFVTALEYATDTK.A</td><td>2137.37459</td><td>2</td><td>9.28E-06</td><td>0.96</td><td>5.30</td><td>-</td><td>968.1</td></tr>
<tr><td>gi|21536449|ref|NP_002613.2| prefoldin 1; prefoldin subunit 1 [Homo sapiens]</td><td></td><td></td><td></td><td>9.62E-06</td><td>0.97</td><td>10.22</td><td>9.00</td><td>14210.4</td></tr>
<tr><td>AHQ-1-13- , 3917</td><td>K.LADIQIEQLNR.T</td><td>1313.48523</td><td>2</td><td>9.62E-06</td><td>0.97</td><td>4.35</td><td>-</td><td>1992.5</td></tr>
<tr><td>AHQ-1-13, 3783</td><td>K.LADIQIEQLNR.T</td><td>1313.48523</td><td>2</td><td>8.40E-05</td><td>0.95</td><td>4.50</td><td>-</td><td>1455.7</td></tr>
<tr><td>gi|4506191|ref|NP_002792.1| proteasome beta 10 subunit proprotein; proteasome subunit MECL1; protea</td><td></td><td></td><td></td><td>9.73E-06</td><td>0.90</td><td>10.22</td><td>7.30</td><td>28936.1</td></tr>
<tr><td>AHQ-1-13, 6089 - 6095</td><td>R.LPFTALGSGQDAALAVLEDR.F</td><td>2045.28192</td><td>2</td><td>4.14E-04</td><td>0.96</td><td>4.43</td><td>-</td><td>1443.1</td></tr>
<tr><td>AHQ-1-10, 5868</td><td>R.LPFTALGSGQDAALAVLEDR.F</td><td>2045.28192</td><td>2</td><td>9.73E-06</td><td>0.90</td><td>3.72</td><td>-</td><td>837.2</td></tr>
<tr><td>gi|4505591|ref|NP_002565.1| peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc</td><td></td><td></td><td></td><td>9.73E-06</td><td>2.40</td><td>30.16</td><td>14.60</td><td>22110.2</td></tr>
<tr><td>AHQ-1-11, 3782</td><td>R.GLFIIDDK.G</td><td>921.07223</td><td>1</td><td>6.70E-04</td><td>0.80</td><td>3.11</td><td>-</td><td>1103.6</td></tr>
<tr><td>AHQ-1-11, 3518 - 3543</td><td>R.LVQAFQFTDK.H</td><td>1197.36469</td><td>2</td><td>9.73E-06</td><td>0.89</td><td>3.09</td><td>-</td><td>1066.8</td></tr>
<tr><td>AHQ-1-11, 3363</td><td>R.QITVNDLPVGR.S</td><td>1212.38090</td><td>2</td><td>5.80E-04</td><td>0.71</td><td>3.00</td><td>-</td><td>404.9</td></tr>
<tr><td>gi|20270343|ref|NP_620150.1| hypothetical protein BC015408 [Homo sapiens]</td><td></td><td></td><td></td><td>9.86E-06</td><td>0.88</td><td>10.22</td><td>12.40</td><td>21415.8</td></tr>
<tr><td>AHQ-1-11, 5658 - 5662</td><td>K.NELHNLLDKPQLQGIPVLVLGNK.R</td><td>2553.98492</td><td>3</td><td>9.86E-06</td><td>0.88</td><td>4.37</td><td>-</td><td>343.3</td></tr>
<tr><td>gi|20543399|ref|XP_116396.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [</td><td></td><td></td><td></td><td>9.89E-06</td><td>0.86</td><td>10.17</td><td>5.00</td><td>19852.7</td></tr>
<tr><td>AHQ-1-12, 4335 - 4398</td><td>R.VSFKLFADK.F</td><td>1055.25138</td><td>2</td><td>9.89E-06</td><td>0.86</td><td>3.48</td><td>-</td><td>957.3</td></tr>
<tr><td>gi|18558709|ref|XP_087572.1| similar to bA291L22.2 (similar to CDC10 (cell division cycle 10, S. ce</td><td></td><td></td><td></td><td>9.94E-06</td><td>0.96</td><td>10.18</td><td>10.90</td><td>9988.5</td></tr>
<tr><td>AHQ-1-8, 3090</td><td>K.FEDYLNAESR.V</td><td>1244.29194</td><td>2</td><td>9.94E-06</td><td>0.96</td><td>3.58</td><td>-</td><td>1711.8</td></tr>
<tr><td>gi|4502211|ref|NP_001654.1| ADP-ribosylation factor 6 [Homo sapiens]</td><td></td><td></td><td></td><td>1.00E-05</td><td>3.26</td><td>40.20</td><td>24.60</td><td>20082.0</td></tr>
<tr><td>AHQ-1-12, 3998</td><td>K.FNVWDVGGQDK.I</td><td>1265.35598</td><td>2</td><td>1.00E-05</td><td>0.78</td><td>2.87</td><td>-</td><td>862.2</td></tr>
<tr><td>AHQ-1-12, 4193</td><td>R.ILMLGLDAAGK.T</td><td>1102.37299</td><td>2</td><td>1.59E-05</td><td>0.96</td><td>3.94</td><td>-</td><td>1508.0</td></tr>
<tr><td>AHQ-1-12, 3678</td><td>R.ILM*LGLDAAGK.T</td><td>1118.37239</td><td>2</td><td>1.90E-04</td><td>0.96</td><td>3.36</td><td>-</td><td>1998.1</td></tr>
<tr><td>AHQ-1-12, 5366</td><td>K.LGQSVTTIPTVGFNVETVTYK.N</td><td>2255.55261</td><td>2</td><td>1.07E-05</td><td>0.57</td><td>3.14</td><td>-</td><td>170.5</td></tr>
<tr><td>gi|4758038|ref|NP_004246.1| cytochrome c oxidase subunit Va precursor; cytochrome c oxidase polypep</td><td></td><td></td><td></td><td>1.02E-05</td><td>1.25</td><td>20.21</td><td>20.70</td><td>16774.1</td></tr>
<tr><td>AHQ-1-14, 5745</td><td>K.GINTLVTYDMVPEPK.I</td><td>1677.94342</td><td>2</td><td>4.87E-05</td><td>0.59</td><td>2.51</td><td>-</td><td>764.4</td></tr>
<tr><td>AHQ-1-13, 4677 - 4736</td><td>K.GINTLVTYDMVPEPK.I</td><td>1677.94342</td><td>2</td><td>7.85E-04</td><td>0.93</td><td>4.02</td><td>-</td><td>1131.9</td></tr>
<tr><td>AHQ-1-13, 5592</td><td>R.WVTYFNKPDIDAWELR.K</td><td>2054.29220</td><td>2</td><td>1.02E-05</td><td>0.66</td><td>3.20</td><td>-</td><td>306.9</td></tr>
<tr><td>gi|21361456|ref|NP_055425.2| alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph</td><td></td><td></td><td></td><td>1.02E-05</td><td>1.78</td><td>20.20</td><td>4.60</td><td>109437.2</td></tr>
<tr><td>AHQ-1-4, 6655</td><td>R.FSFSGNTLVSSSADPEGHFETPIWIER.V</td><td>3012.23437</td><td>3</td><td>9.23E-05</td><td>0.85</td><td>3.58</td><td>-</td><td>964.9</td></tr>
<tr><td>AHQ-1-5, 3871</td><td>R.VVIIGAGKPAAVVLQTK.G</td><td>1665.05702</td><td>2</td><td>1.02E-05</td><td>0.93</td><td>3.83</td><td>-</td><td>1010.5</td></tr>
<tr><td>AHQ-1-4, 4047</td><td>R.VVIIGAGKPAAVVLQTK.G</td><td>1665.05702</td><td>2</td><td>1.13E-05</td><td>0.90</td><td>3.97</td><td>-</td><td>879.1</td></tr>
<tr><td>gi|20551618|ref|XP_167021.1| similar to calponin 2; Calonin 2 [Homo sapiens]</td><td></td><td></td><td></td><td>1.03E-05</td><td>0.78</td><td>10.16</td><td>3.70</td><td>47327.9</td></tr>
<tr><td>AHQ-1-12, 5218</td><td>R.SM*QNWHQLENLSNFIK.A</td><td>2006.23095</td><td>3</td><td>1.03E-05</td><td>0.78</td><td>3.25</td><td>-</td><td>819.4</td></tr>
<tr><td>gi|23510451|ref|NP_001631.3| N-acylaminoacyl-peptide hydrolase; oxidized protein hydrolase; acylami</td><td></td><td></td><td></td><td>1.04E-05</td><td>0.90</td><td>10.15</td><td>1.80</td><td>81224.1</td></tr>
<tr><td>AHQ-1-6, 2960</td><td>K.ALDVSASDDEIAR.L</td><td>1362.42514</td><td>2</td><td>1.04E-05</td><td>0.90</td><td>2.91</td><td>-</td><td>1229.1</td></tr>
<tr><td>gi|21361478|ref|NP_055944.2| septin 6 isoform B; septin 2 [Homo sapiens]</td><td></td><td></td><td></td><td>1.08E-05</td><td>1.91</td><td>20.28</td><td>9.40</td><td>49716.3</td></tr>
<tr><td>AHQ-1-7, 3005</td><td>R.KTAAELLQSQGSQAGGSQTLK.R</td><td>2104.30776</td><td>2</td><td>1.08E-05</td><td>0.97</td><td>5.65</td><td>-</td><td>1322.8</td></tr>
<tr><td>AHQ-1-7, 5216</td><td>R.TVPLAGHVGFDSLPDQLVNK.S</td><td>2108.38284</td><td>2</td><td>5.48E-05</td><td>0.94</td><td>4.59</td><td>-</td><td>811.8</td></tr>
<tr><td>gi|29727204|ref|XP_290872.1| similar to Pyruvate kinase, M2 isozyme [Homo sapiens]</td><td></td><td></td><td></td><td>1.10E-05</td><td>1.80</td><td>20.21</td><td>14.80</td><td>16297.7</td></tr>
<tr><td>AHQ-1-7, 2297</td><td>R.APIIAVTR.N</td><td>841.03348</td><td>2</td><td>2.19E-04</td><td>0.90</td><td>3.04</td><td>-</td><td>973.2</td></tr>
<tr><td>AHQ-1-7, 5454</td><td>K.KGDVVIVLTGWRPGSGFTNTMR.V</td><td>2392.76561</td><td>3</td><td>1.10E-05</td><td>0.90</td><td>4.28</td><td>-</td><td>1004.0</td></tr>
</table>

gi|4758440|ref|NP_004868.1|	glia maturation factor, gamma [Homo sapiens]			1.10E-05	0.93	10.23	9.20	16801.2
AHQ-1-12, 4297	R.TTDDLTEAWLQEK.L	1550.64872	2	1.10E-05	0.93	4.04	-	1349.2
gi|10800412|ref|NP_036458.2|	microtubule-associated protein, RP/EB family, member 3; APC binding pr			1.13E-05	0.69	10.14	3.60	31982.0
AHQ-1-9, 2108	K.LEHEYIHNFK.V	1330.47280	2	1.13E-05	0.69	2.71	-	824.4
gi|5174539|ref|NP_005908.1|	cytosolic malate dehydrogenase; soluble malate dehydrogenase [Homo sapi			1.19E-05	1.88	20.22	9.00	36425.9
AHQ-1-13, 3065	K.DVIATDKEDVAFK.D	1451.60343	2	1.19E-05	0.94	3.54	-	1367.6
AHQ-1-9, 3594	K.VIVVGNPANTNCLTASK.S	1760.00585	2	9.80E-05	0.95	4.41	-	912.6
gi|11993943|ref|NP_055419.1|	Tax interaction protein 1 [Homo sapiens]			1.21E-05	0.96	10.23	13.70	13734.6
AHQ-1-13, 4072 - 4079	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	1.21E-05	0.96	4.68	-	1555.4
gi|4502981|ref|NP_001852.1|	cytochrome c oxidase subunit IV isoform 1 precursor; cytochrome c oxida			1.29E-05	2.48	30.18	21.30	19576.6
AHQ-1-13- , 2320	R.DHPLPEVAHVK.H	1242.40869	3	9.47E-05	0.91	3.53	-	1240.9
AHQ-1-12, 3534	K.HYVYGPLPQSFDK.E	1551.72638	2	1.29E-05	0.92	3.57	-	911.5
AHQ-1-13- , 3963	K.SEDFSLPAYM*DR.R	1447.55197	2	2.20E-04	0.66	2.73	-	358.5
gi|5729873|ref|NP_006656.1|	heparanase; heparanase-1 [Homo sapiens]			1.33E-05	0.95	10.19	1.70	61176.4
AHQ-1-14- , 5010	K.TDFLIFDPK.K	1096.25713	2	1.33E-05	0.95	3.89	-	1438.3
AHQ-1-14- , 5008	K.TDFLIFDPK.K	1096.25713	1	1.86E-04	0.44	2.27	-	536.6
gi|4557469|ref|NP_001273.1|	adaptor-related protein complex 2, beta 1 subunit; adaptin, beta 2 (bet			1.34E-05	0.93	10.21	1.30	104551.9
AHQ-1-6, 6235	R.CVSTLLDLIQTK.V	1392.64385	2	1.34E-05	0.93	4.20	-	945.5
gi|19923262|ref|NP_004153.2|	RAB5A, member RAS oncogene family; RAS-associated protein RAB5A [Homo			1.34E-05	1.79	20.17	10.20	23658.5
AHQ-1-10, 3676 - 3735	K.FEIWDTAGQER.Y	1352.43364	2	2.72E-04	0.90	2.52	-	1523.2
AHQ-1-10, 3319 - 3323	K.LVLLGESAVGK.S	1086.30692	2	1.34E-05	0.89	3.40	-	1037.6
gi|30149697|ref|XP_070805.2|	similar to prohibitin [Homo sapiens]			1.36E-05	0.93	10.18	3.30	33918.9
AHQ-1-10, 3456	K.DLQNVNLTLR.I	1186.34344	2	1.36E-05	0.93	3.67	-	1142.5
gi|21070997|ref|NP_003147.2|	stromal interaction molecule 1 precursor [Homo sapiens]			1.43E-05	0.94	10.21	2.30	77422.9
AHQ-1-7, 3650	K.ELESHSSWYAPEALQK.W	1876.01544	2	1.43E-05	0.94	4.28	-	974.8
gi|4505357|ref|NP_002480.1|	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa; NADH dehyd			1.44E-05	0.89	10.20	14.80	9369.8
AHQ-1-14- , 5555 - 5615	R.LALFNPDVCWDR.N	1507.69520	2	1.44E-05	0.89	3.99	-	577.5
gi|4557385|ref|NP_000055.1|	complement component 3 precursor; acylation-stimulating protein cleavag			1.48E-05	0.95	10.22	1.30	187162.3
AHQ-1-6, 4652	R.VPVAVQGEDTVQSLTQGDGVAK.L	2199.40432	2	1.48E-05	0.95	4.37	-	1062.2
gi|4502107|ref|NP_001145.1|	annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoag			1.49E-05	1.48	20.19	8.80	35936.5
AHQ-1-9, 6964	K.GLGTDEESILTLLTSR.S	1705.88853	2	1.49E-05	0.89	3.77	-	808.4
AHQ-1-9, 3878	R.GTVTDFPGFDER.A	1341.40762	2	8.18E-04	0.60	2.55	-	460.6
gi|18079216|ref|NP_065815.1|	CASK-interacting protein 1 [Homo sapiens]			1.50E-05	0.26	10.19	1.30	149812.6
AHQ-1-1, 6939 - 7007	R.PGSPQALGGPHGPAPATAK.V	1711.90292	2	1.50E-05	0.26	2.58	-	427.1
gi|22538465|ref|NP_002786.2|	proteasome beta 3 subunit; proteasome theta chain; proteasome chain 13			1.52E-05	1.87	20.22	16.60	22948.8
AHQ-1-10, 4784 - 4789	R.FGPYYTEPVIAGLDPK.T	1768.00162	2	1.52E-05	0.91	3.68	-	1132.7
AHQ-1-10, 5793	R.LYIGLAGLATDVQTVAQR.L	1890.17306	2	5.28E-05	0.96	4.45	-	1892.3
gi|4507747|ref|NP_003321.1|	thioredoxin reductase 1 [Homo sapiens]			1.54E-05	0.82	10.21	7.20	54419.1
AHQ-1-7, 7457	K.IPVTDEEQTNVPYIYAIGDILEDKVELTPVAIQAGR.L	3972.44634	3	1.54E-05	0.82	4.18	-	373.5
gi|4759270|ref|NP_004613.1|	translin; recombination hotspot associated factor; recombination hotspo			1.58E-05	0.83	10.18	6.60	26182.8
AHQ-1-10, 3919	R.EAVTEILGIEPDREK.G	1699.88399	2	1.58E-05	0.83	3.62	-	781.5
gi|6857820|ref|NP_005019.2|	phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl			1.73E-05	0.79	10.15	3.40	46224.3
AHQ-1-7, 4764 - 4766	R.FGIDDQDFQNSLTR.S	1656.73462	2	1.73E-05	0.79	3.06	-	904.3
gi|7706675|ref|NP_057661.1|	RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M			1.75E-05	2.28	30.23	16.30	23461.5
AHQ-1-11, 4515	R.GSDVIIMLVGNK.T	1246.50220	2	2.19E-04	0.98	4.60	-	2401.4
AHQ-1-11, 3400 - 3458	R.LQLWDTAGQER.F	1317.43243	2	1.75E-05	0.88	3.05	-	1003.3
AHQ-1-11, 3247 - 3319	R.LQLWDTAGQER.F	1317.43243	2	4.84E-05	0.88	3.40	-	763.2
AHQ-1-10, 3200 - 3255	R.LQLWDTAGQER.F	1317.43243	2	4.23E-05	0.83	3.07	-	786.3
AHQ-1-11, 3514	K.LVFLGEQSVGK.T	1177.37492	1	5.17E-04	0.43	2.38	-	428.5
gi|21361409|ref|NP_036515.2|	osteoclast stimulating factor 1 [Homo sapiens]			1.76E-05	0.31	10.13	11.50	24063.9
AHQ-1-10, 5008	R.TGLIPSNYVAEQAESIDNPLHEAAK.R	2668.89701	2	1.76E-05	0.31	2.69	-	275.6
gi|22538814|ref|NP_002976.2|	small inducible cytokine A5 precursor; T-cell specific protein p288; T			1.79E-05	0.87	10.15	12.10	9989.6
AHQ-1-14- , 3832	K.CSNPAVVFVTR.K	1251.43718	2	1.79E-05	0.87	2.97	-	793.3
gi|23110944|ref|NP_002782.1|	proteasome alpha 6 subunit; prosomal P27K protein; proteasome subunit			1.80E-05	0.69	10.14	3.70	27399.3
AHQ-1-10, 3580	R.LYQVEYAFK.A	1161.33081	2	1.80E-05	0.69	2.83	-	593.6
gi|29736622|ref|XP_293924.1|	similar to cytoplasmic beta-actin [Homo sapiens]			1.83E-05	1.52	20.25	9.80	42002.9
AHQ-1-8, 1477 - 1512	K.CDVDIRK.D	907.02724	2	4.46E-04	0.76	2.60	-	604.3
AHQ-1-8, 6956 - 7030	R.FRCPEAIFQPSFLGIESSGIHETTFNSIMK.C	3446.89713	3	1.83E-05	0.76	3.53	-	414.1
gi|7705501|ref|NP_057546.1|	hypothetical protein HSPC194 [Homo sapiens]			1.89E-05	1.90	20.21	15.20	11564.5
AHQ-1-14- , 6320 - 6394	K.FMPAGLIAGASLLM*VAK.V	1707.13765	2	8.37E-04	0.94	4.12	-	946.6
AHQ-1-14- , 5910 - 5979	K.FM*PAGLIAGASLLM*VAK.V	1723.13705	2	1.89E-05	0.97	3.83	-	2129.8
gi|29743626|ref|XP_297123.1|	hypothetical protein XP_297123 [Homo sapiens]			1.89E-05	0.63	10.15	13.80	13908.9
AHQ-1-13, 6477	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	1.89E-05	0.63	2.94	-	741.1
gi|4505237|ref|NP_002427.1|	palmitoylated membrane protein 1; membrane protein, palmitoylated 1 (55			1.91E-05	0.91	10.18	2.60	52296.2
AHQ-1-9, 4958	K.IAILDIEPQTLK.I	1354.61716	2	1.91E-05	0.91	3.57	-	1002.3
gi|5803009|ref|NP_006786.1|	EH-domain containing 1; homolog of Drosophila past; EH domain containin			2.11E-05	0.95	10.22	2.80	60844.7
AHQ-1-7, 5840 - 5913	K.LLDTVDDMLANDIAR.L	1675.88593	2	2.11E-05	0.95	3.94	-	1763.9
gi|4503377|ref|NP_001377.1|	dihydropyrimidinase-like 2; collapsin response mediator protein hCRMP-2			2.22E-05	1.45	20.16	7.30	62293.3
AHQ-1-7, 4245	R.GLYDGPVCEVSVTPK.T	1622.82128	2	2.22E-05	0.76	2.87	-	632.7
AHQ-1-7, 5314	R.ILDLGITGPEGHVLSRPEEVEAEAVNR.A	2902.20927	3	8.18E-05	0.69	3.28	-	506.2
gi|4759274|ref|NP_004777.1|	thioredoxin-like, 32kDa; thioredoxin-related 32 kDa protein; thioredoxi			2.27E-05	0.90	10.18	5.20	32251.1
AHQ-1-9, 3083	R.IDQYQGADAVGLEEK.I	1636.74162	2	2.27E-05	0.90	3.63	-	1107.6
gi|8922712|ref|NP_060713.1|	hypothetical protein FLJ10849 [Homo sapiens]			2.28E-05	1.57	20.18	8.60	49397.9
AHQ-1-7, 2546	K.AAAQLLQSQAQQSGAQQTK.K	1958.12276	2	2.53E-04	0.84	3.64	-	479.6
AHQ-1-7, 3649	K.DTDPDSKPFSLQETYEAK.R	2072.17149	2	2.28E-05	0.74	3.03	-	347.7
gi|4506417|ref|NP_002877.1|	RAP2B, member of RAS oncogene family [Homo sapiens]			2.30E-05	4.03	50.23	35.00	20494.2
AHQ-1-11, 4416	K.ALAEEWSCPFM*ETSAK.N	1875.06928	2	4.12E-04	0.49	2.92	-	531.3
AHQ-1-11, 4914 - 4916	K.ALAEEWSCPFMETSAK.N	1859.06988	2	4.82E-05	0.92	4.32	-	766.2
AHQ-1-11, 5838	K.ASVDELFAEIVR.Q	1349.51434	2	2.30E-05	0.89	3.71	-	1059.5
AHQ-1-11, 6294	K.EIEVDSSPSVLEILDTAGTEQFASM*R.D	2842.08287	3	9.85E-05	0.89	4.52	-	850.1
AHQ-1-11, 4078	K.YDPTIEDFYR.K	1319.40042	2	1.48E-04	0.84	2.88	-	414.4
gi|10190678|ref|NP_065691.1|	RP42 homolog; squamous cell carcinoma-related oncogene [Homo sapiens]			2.30E-05	0.87	10.21	6.60	30124.1
AHQ-1-10, 5708	K.LDVATDNFFQNPELYIR.E	2056.26326	2	2.30E-05	0.87	4.28	-	601.0
gi|21361565|ref|NP_001679.2|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, is			2.34E-05	1.81	20.19	9.00	28908.4
AHQ-1-11, 2903	R.HYLFDVQR.N	1078.20513	2	2.34E-05	0.95	3.43	-	1422.3
AHQ-1-11, 6510	R.YGLIPEEFFQFLYPK.T	1892.18434	2	3.43E-05	0.86	3.76	-	387.8
gi|4757818|ref|NP_004879.1|	ATPase, H+ transporting, lysosomal, V1 subunit G isoform 1; vacuolar H(			2.54E-05	0.92	10.18	9.30	13757.4
AHQ-1-13- , 2856 - 2863	K.EEAQAEIEQYR.L	1366.41548	2	2.54E-05	0.92	3.67	-	1083.6
gi|18543899|ref|XP_086916.1|	similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic			2.64E-05	0.85	10.21	11.80	21265.8
AHQ-1-11, 5002	R.YVWLVYEQDRPLKCDEPILSNR.S	2796.15005	3	2.64E-05	0.85	4.12	-	590.6
gi|4507657|ref|NP_003282.1|	tripeptidyl peptidase II [Homo sapiens]			2.66E-05	1.57	20.22	2.70	138447.8
AHQ-1-3, 4615	K.IVDIIDTTGSGDVNTATEVEPK.D	2275.45273	2	8.10E-04	0.95	4.33	-	1626.8
AHQ-1-3, 3379	R.LSTMETGTGLIR.A	1279.48905	2	2.66E-05	0.62	2.63	-	719.3
gi|13376282|ref|NP_079131.1|	hypothetical protein FLJ12785 [Homo sapiens]			2.72E-05	0.77	10.14	0.00	68298.1
AHQ-1-6, 3996	K.YPGHLAAITLSR.M	1299.50338	2	2.80E-04	0.54	2.52	-	776.0
AHQ-1-4, 4118 - 4135	K.YPGHLAAITLSR.M	1299.50338	2	2.72E-05	0.77	2.73	-	932.6
gi|5031691|ref|NP_004640.1|	chromosome 21 open reading frame 33; human HES1 protein, homolog to E.c			2.75E-05	1.83	20.24	19.00	28142.2
AHQ-1-11, 3791	R.GVEVTVGHEQEEGGKWPYAGTAEAIK.A	2743.96557	3	1.19E-04	0.92	4.88	-	857.8
AHQ-1-11, 5068	K.ITDLANLSAANHDAAIFPGGFGAAK.N	2443.69961	2	2.75E-05	0.91	4.35	-	635.0
AHQ-1-11, 5063	K.ITDLANLSAANHDAAIFPGGFGAAK.N	2443.69961	3	2.81E-04	0.85	3.95	-	896.5
gi|19913446|ref|NP_002134.2|	hippocalcin; neuron specific calcium-binding protein hippocalcin [Homo			2.79E-05	1.21	20.15	7.80	22427.3
AHQ-1-11, 2260	K.FAEHVFR.T	906.02258	1	2.79E-05	0.28	1.84	-	438.6
AHQ-1-11, 4807	K.LSLEEFIR.G	1007.16512	2	5.71E-04	0.93	3.04	-	1598.5
gi|21359955|ref|NP_076982.2|	SECIS binding protein 2 [Homo sapiens]			2.91E-05	0.17	10.15	2.10	95477.3
AHQ-1-12, 6026 - 6041	K.NVSIPSSEALSSDPSYNK.E	1896.00183	2	2.91E-05	0.17	2.61	-	295.6
gi|24308263|ref|NP_067045.1|	TcD37 homolog; prune [Homo sapiens]			2.93E-05	0.96	10.25	3.80	50199.3
AHQ-1-7, 7605	K.LLPLLQEALSAYFDSMK.I	1940.29226	2	2.93E-05	0.96	4.94	-	1415.5

gi|4504051|ref|NP_002064.1|	guanine nucleotide binding protein, alpha z polypeptide; transducin alp			3.00E-05	1.60	20.19	9.00	40923.5
AHQ-1-9, 5494 - 5500	R.AYDAVQLFALTGPAESK.G	1781.98669	2	3.00E-05	0.76	3.28	-	689.3
AHQ-1-9, 6627 - 6646	R.IAAADYIPTVEDILR.S	1660.89259	2	1.17E-04	0.83	3.84	-	354.4
gi|16950601|ref|NP_005956.2|	myosin light chain kinase isoform 6; myosin light chain kinase [Homo s			3.30E-05	1.62	20.17	2.90	110074.8
AHQ-1-12, 5402	K.IEGYPDPEVVWFK.D	1579.77650	2	1.32E-04	0.90	3.35	-	532.2
AHQ-1-6, 5080	R.STSFNVQDLLPDHEYK.F	1894.03076	2	3.30E-05	0.72	3.34	-	378.2
gi|4758158|ref|NP_004395.1|	neural precursor cell expressed, developmentally down-regulated 5 [Homo			3.30E-05	0.88	10.19	4.40	41487.2
AHQ-1-9, 6943	K.STLINSLFLTDLYPER.V	1883.13416	2	3.30E-05	0.88	3.85	-	784.4
gi|4506405|ref|NP_002872.1|	v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP			3.32E-05	2.79	30.25	15.50	23408.4
AHQ-1-10, 3761	K.AEEWGVQYVETSAK.T	1597.70708	2	5.05E-04	0.87	3.25	-	776.2
AHQ-1-10, 3345 - 3420	R.SKAEEWGVQYVETSAK.T	1812.95765	2	3.32E-05	0.97	5.01	-	1430.4
AHQ-1-10, 3332	R.VKAEEDKIPLLVVGNK.S	1753.07630	2	2.29E-04	0.96	4.90	-	1181.3
gi|4506285|ref|NP_003470.1|	protein tyrosine phosphatase type IVA, member 2 isoform 1; protein tyro			3.36E-05	0.93	10.17	8.40	19127.1
AHQ-1-11, 2895	R.FLITHNPTNATLNK.F	1584.80104	2	3.36E-05	0.93	3.46	-	1565.0
gi|5454152|ref|NP_006285.1|	ubiquinol-cytochrome c reductase binding protein [Homo sapiens]			3.37E-05	0.97	10.24	11.70	13530.4
AHQ-1-13- , 5352 - 5359	K.YEEENFYLEPYLK.E	1737.88601	2	3.37E-05	0.97	4.84	-	1798.2
gi|19923231|ref|NP_002860.2|	RAB6A, member RAS oncogene family; Oncogene RAB6; RAB6, member RAS onc			3.47E-05	0.73	10.17	6.70	23548.6
AHQ-1-11, 2870	R.VAAALPGMESTQDR.S	1446.61192	2	3.47E-05	0.73	3.00	-	456.5
gi|18105037|ref|NP_004709.2|	cytochrome c oxidase subunit VIIa polypeptide 2 like; estrogen recepto			3.55E-05	0.89	10.21	28.90	12614.6
AHQ-1-14- , 6048	K.LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK.L	3399.87995	3	3.55E-05	0.89	4.20	-	851.6
gi|4758032|ref|NP_004757.1|	coatomer protein complex, subunit beta 2 (beta prime); coatomer binding			3.61E-05	0.80	10.17	2.10	102486.5
AHQ-1-5, 6542	K.AAESLADPTEYENLFPGLK.E	2066.25322	2	3.61E-05	0.80	3.47	-	532.7
gi|4758504|ref|NP_004484.1|	hydroxyacyl-Coenzyme A dehydrogenase, type II [Homo sapiens]			3.64E-05	1.53	20.21	16.50	26922.9
AHQ-1-10, 4663	R.LVGQGASAVLLDLPNSGGEAQAK.K	2196.44680	2	3.64E-05	0.66	3.16	-	338.4
AHQ-1-10, 4463	R.LVGQGASAVLLDLPNSGGEAQAK.K	2196.44680	2	2.63E-04	0.89	4.17	-	669.8
AHQ-1-13- , 6827	R.VMTIAPGLFGTPLLTSLPEK.V	2086.52363	2	5.29E-05	0.87	3.71	-	695.4
gi|6005902|ref|NP_009043.1|	thrombospondin 3 [Homo sapiens]			3.70E-05	0.77	10.14	0.70	104200.6
AHQ-1-2, 4925	R.FYVVMWK.Q	973.21547	2	1.82E-04	0.92	2.80	-	961.8
AHQ-1-3, 4747	R.FYVVMWK.Q	973.21547	2	5.48E-04	0.81	2.67	-	664.9
AHQ-1-6, 4536	R.FYVVMWK.Q	973.21547	1	2.83E-04	0.80	2.10	-	1059.8
AHQ-1-7, 4566	R.FYVVMWK.Q	973.21547	1	3.70E-05	0.77	2.19	-	1001.3
AHQ-1-11, 4287	R.FYVVMWK.Q	973.21547	1	7.32E-04	0.75	2.00	-	1098.1
AHQ-1-2, 4906 - 4917	R.FYVVMWK.Q	973.21547	1	1.43E-04	0.74	2.03	-	991.5
gi|4826643|ref|NP_005130.1|	annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III,			3.87E-05	0.87	10.20	5.00	36375.0
AHQ-1-9, 6155	K.GAGTNEDALIEILTTR.T	1674.83453	2	3.87E-05	0.87	3.90	-	709.3
gi|30149555|ref|XP_301154.1|	similar to heat shock protein 86 [Homo sapiens]			3.91E-05	0.96	10.23	10.60	15781.6
AHQ-1-5, 5958	K.HSQFIGYPITLFVEK.E	1780.05877	2	3.91E-05	0.96	4.66	-	1193.2
gi|5453710|ref|NP_006139.1|	LIM and SH3 protein 1; Lasp-1 [Homo sapiens]			3.92E-05	0.71	10.16	5.00	29717.0
AHQ-1-13- , 4084	K.GFSVVADTPELQR.I	1419.56466	2	3.92E-05	0.71	2.65	-	855.9
AHQ-1-9, 3903 - 3912	K.GFSVVADTPELQR.I	1419.56466	1	9.70E-05	0.22	2.19	-	231.6
gi|4502923|ref|NP_001830.1|	calponin 3; calponin, acidic [Homo sapiens]			4.08E-05	0.90	10.16	3.30	36413.4
AHQ-1-12, 2641 - 2647	K.GPSYGLSAEVK.N	1108.22631	2	4.08E-05	0.90	3.16	-	888.6
gi|29728979|ref|XP_060316.2|	similar to Olfactory receptor 2T1 (Olfactory receptor 1-25) (OR1-25) [			4.39E-05	0.23	10.13	2.10	75271.9
AHQ-1-13- , 4620	R.FKGPQRVSGELWSR.A	1647.86206	2	4.39E-05	0.23	2.57	-	249.8
gi|4502989|ref|NP_001856.1|	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor; hepa			4.43E-05	0.95	10.19	15.70	9395.9
AHQ-1-14- , 5314 - 5370	K.LFQEDDEIPLYLK.G	1623.82758	2	4.43E-05	0.95	3.81	-	1547.4
gi|5729779|ref|NP_006701.1|	COP9 homolog [Homo sapiens]			4.61E-05	0.97	10.20	6.20	23225.5
AHQ-1-11, 2987	R.KPVAGALDVSFNK.F	1346.55682	2	4.61E-05	0.97	4.07	-	1703.8
gi|23200010|ref|NP_112585.2|	Williams Beuren syndrome chromosome region 21 isoform 4 [Homo sapiens]			4.69E-05	0.84	10.21	20.80	10639.1
AHQ-1-10, 6432	R.LLDGEAALPAVVFLHGLFGSK.T	2155.52425	2	4.69E-05	0.84	4.11	-	271.0
gi|4503785|ref|NP_000135.1|	frataxin; Friedreich ataxia (frataxin) [Homo sapiens]			4.78E-05	0.96	10.21	5.70	23218.1
AHQ-1-13- , 3869	K.LGGDLGTYVINK.Q	1250.42590	2	4.78E-05	0.96	4.13	-	1346.1
AHQ-1-13, 3741	K.LGGDLGTYVINK.Q	1250.42590	2	9.91E-05	0.93	3.81	-	985.6
gi|6996014|ref|NP_002100.2|	histidyl-tRNA synthetase; histidine-tRNA ligase; HisRS; histidine trans			4.80E-05	0.73	10.13	2.60	57410.2
AHQ-1-7, 2618	R.TTETQVLVASAQK.K	1376.53809	2	4.80E-05	0.73	2.68	-	1077.3
gi|17482508|ref|XP_058957.1|	similar to QIL1 [Homo sapiens]			4.87E-05	0.97	10.26	18.60	13087.2
AHQ-1-14- , 5683 - 5688	K.GSVAGGAVYLVYDQELLGPSDK.S	2239.46691	2	4.87E-05	0.97	5.27	-	1439.5
gi|4506237|ref|NP_002809.1|	proteasome (prosome, macropain) activator subunit 2 (PA28 beta); Protea			5.03E-05	0.89	10.22	6.70	27348.4
AHQ-1-10, 6275	K.VLSLLALVKPEVWTLK.E	1810.25573	2	5.03E-05	0.89	4.35	-	659.5
gi|4505621|ref|NP_002558.1|	prostatic binding protein; phosphatidylethanolamine binding protein [Ho			5.03E-05	2.85	30.25	37.40	21056.6
AHQ-1-11, 4762	R.APVAGTCYQAEWDDYVPK.L	2072.23961	2	5.03E-05	0.95	4.22	-	1440.3
AHQ-1-11, 4183	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	5.98E-05	0.95	4.29	-	1206.3
AHQ-1-11, 5111 - 5178	K.WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK.V	3473.79274	3	6.42E-04	0.95	5.03	-	1455.9
gi|4758784|ref|NP_004540.1|	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa; NADH			5.10E-05	0.72	10.13	7.60	14187.4
AHQ-1-13, 2818	K.REDYLYAVR.D	1185.31400	2	5.10E-05	0.72	2.69	-	698.2
gi|27477800|ref|XP_208313.1|	similar to tropomyosin 4 [Homo sapiens]			5.25E-05	1.43	20.23	15.20	18426.7
AHQ-1-9, 5227	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.53E-04	0.95	4.53	-	1121.9
AHQ-1-9, 5674 - 5682	K.CGDLEEELKNVTNNLK.S	1878.05124	2	5.25E-05	0.95	4.39	-	1515.4
AHQ-1-9, 1852 - 1916	K.TIDDLEEK.L	963.02115	2	2.75E-04	0.48	2.66	-	247.3
gi|4507195|ref|NP_003119.1|	spectrin, beta, non-erythrocytic 1; Spectrin, beta, nonerythrocytic-1 (			5.45E-05	0.89	10.21	0.80	274628.5
AHQ-1-1, 6420	R.DASVAEAWLLGQEPYLSSR.E	2093.28190	2	5.45E-05	0.89	4.13	-	590.1
gi|4758460|ref|NP_004479.1|	glycoprotein V (platelet) [Homo sapiens]			5.51E-05	1.65	20.21	6.30	60958.9
AHQ-1-5, 5671	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	9.27E-05	0.81	4.16	-	668.7
AHQ-1-5, 3371	R.YLGVTLSPR.L	1006.18036	2	5.51E-05	0.84	3.32	-	912.7
gi|5032137|ref|NP_005629.1|	synaptobrevin-like 1 [Homo sapiens]			5.53E-05	1.88	20.23	13.20	24934.9
AHQ-1-13- , 4755 - 4756	K.LTYSHGNYLFHYICQDR.I	2189.39466	2	5.53E-05	0.94	4.53	-	959.9
AHQ-1-13- , 2853	K.VMETQAQVDELK.G	1391.57303	2	5.21E-04	0.94	3.74	-	1426.8
gi|30148978|ref|XP_291520.2|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			5.53E-05	0.78	10.15	2.20	68413.1
AHQ-1-11, 4590 - 4620	R.DWSHYFKTIKDLR.A	1709.92863	2	5.53E-05	0.78	2.92	-	888.9
gi|4503447|ref|NP_001389.1|	peroxisomal enoyl-coenzyme A hydratase-like protein; delta3,5-delta2,4-			5.66E-05	0.90	10.16	3.40	35994.1
AHQ-1-9, 4262	R.YCAQDAFFQVK.E	1378.53429	2	5.66E-05	0.90	3.21	-	1066.1
gi|19923142|ref|NP_002256.2|	karyopherin beta 1; nuclear factor p97; importin 90; importin beta-1 s			5.77E-05	1.76	20.21	4.00	97169.7
AHQ-1-5, 7410	K.GALQYLVPILTQTLTK.Q	1760.11044	2	5.89E-05	0.83	3.83	-	523.6
AHQ-1-5, 6407	K.YLEVVLNTLQQASQAQVDK.S	2148.40214	2	5.77E-05	0.92	4.15	-	1380.2
gi|4757712|ref|NP_004026.1|	acyl-Coenzyme A oxidase isoform a; acyl-coenzyme A oxidase 1 [Homo sapi			6.02E-05	0.82	10.18	3.60	74745.4
AHQ-1-6, 6492	R.INEGIGQGDLSELPELHALTAGLK.A	2476.76782	3	6.02E-05	0.82	3.55	-	784.0
gi|4507295|ref|NP_003560.1|	syntaxin 7 [Homo sapiens]			6.40E-05	0.77	10.15	5.70	29845.3
AHQ-1-13- , 3453	R.TLNQLGTPQDSPELR.Q	1669.81798	2	6.40E-05	0.77	2.99	-	561.5
gi|6912536|ref|NP_036475.1|	nicotinamide nucleotide transhydrogenase [Homo sapiens]			6.43E-05	0.71	10.18	1.80	113946.9
AHQ-1-4, 6579	K.TSGTLISFIYPAQNPELLNK.L	2207.51119	2	6.43E-05	0.71	3.58	-	301.3
gi|22065448|ref|XP_084610.2|	similar to tubulin alpha-1 chain - Chinese hamster [Homo sapiens] [MAS			6.49E-05	0.79	10.16	2.40	41009.4
AHQ-1-11, 4694	K.EIIDLVLDR.I	1086.26378	2	6.49E-05	0.79	3.17	-	811.6
gi|7705827|ref|NP_057187.1|	GTP-binding protein Sara [Homo sapiens]			6.52E-05	0.85	10.15	5.60	22409.7
AHQ-1-11, 4102	K.LVFLGLDNAGK.T	1147.34882	2	6.52E-05	0.85	2.84	-	978.2
gi|4504215|ref|NP_000848.1|	guanylate cyclase 1, soluble, beta 3 [Homo sapiens]			7.68E-05	0.83	10.14	1.80	70514.1
AHQ-1-6, 4300	K.LTQELEILTDR.L	1331.49732	2	7.68E-05	0.83	2.53	-	1458.9
gi|18201911|ref|NP_000629.2|	vitronectin precursor; serum spreading factor; somatomedin B; compleme			8.03E-05	0.88	10.16	3.10	54335.4
AHQ-1-13, 5463	R.SIAQYWLGCPAPGHL	1671.90045	2	8.03E-05	0.88	3.24	-	765.4
gi|30158159|ref|XP_301350.1|	similar to 60S RIBOSOMAL PROTEIN L34 [Homo sapiens]			8.37E-05	0.63	10.16	21.00	14102.3
AHQ-1-9, 6866	R.SIVQFATNFMTINKWFKFSEKQQQK.I	3080.55113	3	8.37E-05	0.63	3.25	-	593.7
gi|4557377|ref|NP_000052.1|	Bruton agammaglobulinemia tyrosine kinase [Homo sapiens]			8.39E-05	1.25	20.24	4.70	76280.8
AHQ-1-6, 2994	K.ITCVETVVPEKNPPPER.Q	1967.23275	2	3.71E-04	0.50	2.70	-	319.0
AHQ-1-6, 3368 - 3414	R.YVLDDEYTSSVGSK.F	1563.64427	2	8.39E-05	0.75	3.55	-	302.2
gi|14249348|ref|NP_116120.1|	hypothetical protein MGC14353 [Homo sapiens]			8.58E-05	0.78	10.14	11.40	13940.7
AHQ-1-13, 4039	K.SWCPDCVQAEPVVR.E	1705.89366	2	8.58E-05	0.78	2.57	-	969.3
gi|4502285|ref|NP_001672.1|	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 2; ATP			8.67E-05	0.92	10.20	1.50	109690.3
AHQ-1-1, 4789 - 4799	K.VGEATETALTCLVEK.M	1622.81958	2	8.67E-05	0.92	3.98	-	935.7

gi|21389337|ref|NP_653164.1|	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase); RIBOSE			8.75E-05	0.90	10.21	7.60	26090.9
AHQ-1-10, 4496	R.VKQENLNLVCIPTSFQAR.Q	2119.43046	2	8.75E-05	0.90	4.11	-	639.8
gi|5730118|ref|NP_006514.1|	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble; X-prolyl aminope			8.91E-05	1.80	20.19	4.80	69858.4
AHQ-1-6, 6327 - 6403	R.GSLTFEPLTLVPIQTK.M	1745.05263	2	8.91E-05	0.87	3.83	-	648.9
AHQ-1-6, 6266 - 6268	R.VGVDPLIIPTDYWK.K	1616.88141	2	2.39E-04	0.94	3.89	-	962.6
gi|27481323|ref|XP_208234.1|	similar to unactive progesterone receptor, 23 kD; likely ortholog of m			9.31E-05	0.75	10.14	7.50	18694.3
AHQ-1-11, 5907	K.LNWLSVDFNNWK.D	1536.71494	2	9.31E-05	0.75	2.75	-	631.3
gi|19923264|ref|NP_004571.2|	RAB27A, member RAS oncogene family [Homo sapiens]			9.36E-05	0.85	10.16	4.50	24867.9
AHQ-1-10, 4372	K.FITTVGIDFR.E	1169.35448	2	9.36E-05	0.85	3.21	-	661.2
gi|7662651|ref|NP_054778.1|	RGC32 protein [Homo sapiens]			9.60E-05	1.86	20.21	26.50	12924.1
AHQ-1-12, 5162 - 5167	K.ELEAFIADLDK.T	1264.40621	2	1.88E-04	0.95	3.66	-	1475.9
AHQ-1-12, 4186 - 4249	K.LNSPTDSTPALLSATVTPQK.A	2042.27634	2	9.60E-05	0.91	4.23	-	559.5
gi|4502205|ref|NP_001651.1|	ADP-ribosylation factor 4 [Homo sapiens]			9.72E-05	0.77	10.15	5.60	20510.6
AHQ-1-11, 2476	R.IQEVADELQK.M	1173.29830	2	9.72E-05	0.77	3.05	-	666.4
gi|21245108|ref|NP_631960.1|	TGFB-induced factor 2-like, Y-linked [Homo sapiens]			9.87E-05	0.65	10.14	4.90	20813.6
AHQ-1-13, 5664	R.CQERSNQIR.S	1192.28823	2	9.87E-05	0.65	2.87	-	712.9
gi|10880136|ref|NP_004032.2|	arrestin beta 1 isoform A [Homo sapiens]			1.05E-04	0.59	10.16	4.30	47065.3
AHQ-1-7, 2374	K.VQYAPERPGPQPTAETTR.Q	1999.17334	2	1.05E-04	0.59	3.15	-	275.7
gi|28461290|ref|NP_443728.2|	TRALPUSH; no opposite paired repeat protein [Homo sapiens]			1.05E-04	0.55	10.14	0.40	240073.5
AHQ-1-8, 3526	K.KKPQVNAK.D	913.09970	1	1.16E-04	0.39	2.30	-	419.0
AHQ-1-9, 3550	K.KKPQVNAK.D	913.09970	1	3.73E-04	0.61	2.63	-	591.8
AHQ-1-10, 3377	K.KKPQVNAK.D	913.09970	1	1.05E-04	0.55	2.60	-	447.6
AHQ-1-11, 3463	K.KKPQVNAK.D	913.09970	1	4.42E-04	0.50	2.55	-	450.5
AHQ-1-7, 3692	K.KKPQVNAK.D	913.09970	1	3.25E-04	0.41	2.31	-	429.7
gi|7657548|ref|NP_055378.1|	spondyloepiphyseal dysplasia, late; sedlin [Homo sapiens]			1.07E-04	0.68	10.13	10.00	16444.6
AHQ-1-13, 4165	K.FSM*NPFYEPNSPIR.S	1715.91027	2	1.07E-04	0.68	2.61	-	695.8
gi|17444699|ref|XP_017966.4|	similar to Reticulon protein 3 (Neuroendocrine-specific protein-like 2			1.07E-04	0.88	10.15	4.70	25522.7
AHQ-1-1, 2960 - 2972	K.TQIDHYVGIAR.H	1273.42279	2	1.07E-04	0.88	2.97	-	1117.2
gi|6005848|ref|NP_009126.1|	polymerase (DNA directed) iota; RAD30 (S. cerevisiae) homolog B; polyme			1.08E-04	0.40	10.14	2.40	80345.8
AHQ-1-8, 4068 - 4123	K.QMQDIPINPRDHLSSSK.Q	1967.19629	2	1.08E-04	0.40	2.84	-	451.4
gi|4557773|ref|NP_000248.1|	myosin, heavy polypeptide 7, cardiac muscle, beta [Homo sapiens]			1.08E-04	0.76	10.16	0.50	223110.8
AHQ-1-2, 3350	R.CNGVLEGIR.I	1019.15759	1	7.31E-04	0.22	2.31	-	127.3
AHQ-1-1, 3328	R.CNGVLEGIR.I	1019.15759	2	1.08E-04	0.76	3.00	-	626.3
gi|19923750|ref|NP_002858.2|	RAB3B, member RAS oncogene family; Brain antigen RAB3B [Homo sapiens]			1.08E-04	0.75	10.13	5.00	24757.7
AHQ-1-12, 3406	K.LQIWDTAGQER.Y	1317.43243	2	1.08E-04	0.75	2.70	-	724.0
gi|8922699|ref|NP_060705.1|	hypothetical protein FLJ10830 [Homo sapiens]			1.10E-04	0.86	10.15	2.30	52779.0
AHQ-1-7, 3972	K.TVFGVEPDLTR.E	1234.38333	2	1.10E-04	0.86	2.82	-	1050.5
gi|20428652|ref|NP_005347.2|	lymphocyte-specific protein tyrosine kinase; oncogene LCK; membrane as			1.16E-04	0.74	10.17	2.00	57969.3
AHQ-1-7, 2317	R.LIEDNEYTAR.E	1224.30217	2	1.16E-04	0.74	3.43	-	477.3
gi|17448269|ref|XP_069750.1|	similar to GDP dissociation inhibitor isoform 2; GDI-2 [Homo sapiens]			1.19E-04	0.93	10.17	4.20	32024.9
AHQ-1-13, 4155	K.DLGTESQIFISR.A	1366.50176	2	1.19E-04	0.93	3.31	-	1485.1
gi|4507303|ref|NP_001045.1|	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2; th			1.20E-04	0.96	10.24	5.40	34310.4
AHQ-1-9, 5959 - 5971	K.THLPLALLPQTLLDQK.V	1802.15055	2	1.20E-04	0.96	4.88	-	1005.7
gi|29728414|ref|XP_290989.1|	similar to myosin-I, Myr 1c (alternatively spliced) - rat [Homo sapien			1.23E-04	0.85	10.21	1.90	124949.7
AHQ-1-2, 7273	K.CRTHFLLMKKSQIVIAAWYR.R	2524.05044	3	1.23E-04	0.85	4.11	-	992.7
gi|4557525|ref|NP_000099.1|	dihydrolipoamide dehydrogenase precursor; E3 component of pyruvate dehy			1.23E-04	0.94	10.18	2.60	54149.9
AHQ-1-7, 2485	K.SEEQLKEEGIEYK.V	1582.69072	2	1.23E-04	0.94	3.52	-	1352.5
gi|4885539|ref|NP_005380.1|	protein-L-isoaspartate (D-aspartate) O-methyltransferase [Homo sapiens]			1.25E-04	0.91	10.21	15.00	24636.2
AHQ-1-11, 5823	R.M*GYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR.L	3522.97505	3	1.25E-04	0.91	4.29	-	904.3
gi|4557241|ref|NP_001095.1|	skeletal muscle specific actinin, alpha 3 [Homo sapiens]			1.26E-04	0.92	10.17	0.90	103293.7
AHQ-1-6, 2884	K.ALDFIASK.G	865.00867	2	2.09E-04	0.83	2.78	-	622.3
AHQ-1-12, 2942	K.ALDFIASK.G	865.00867	1	2.40E-04	0.44	1.83	-	872.7
AHQ-1-5, 2830 - 2834	K.ALDFIASK.G	865.00867	2	1.26E-04	0.92	3.35	-	780.0
gi|13376187|ref|NP_079082.1|	hypothetical protein FLJ23554 [Homo sapiens]			1.27E-04	0.72	10.15	2.20	82410.2
AHQ-1-13- , 4837 - 4839	R.GNGM*EPDSLDEEESPR.W	1778.79043	3	1.27E-04	0.72	3.07	-	1139.6
gi|29743324|ref|XP_293276.1|	similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote			1.34E-04	0.86	10.27	16.00	21244.7
AHQ-1-13, 5151	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	1.34E-04	0.86	5.36	-	723.0
gi|13899297|ref|NP_113646.1|	B aggressive lymphoma gene [Homo sapiens]			1.35E-04	0.13	10.13	1.30	96282.7
AHQ-1-1, 3004	K.SILQQAGVEMK.S	1204.42218	1	1.35E-04	0.13	2.12	-	483.0
gi|15718761|ref|NP_004976.2|	c-K-ras2 protein isoform b; Kirsten rat sarcoma-2 viral (v-Ki-ras2) on			1.39E-04	0.95	10.20	8.00	21424.4
AHQ-1-11, 3612	R.VKDSEDVPM*VLVGNK.C	1646.88770	2	1.39E-04	0.95	4.08	-	1484.2
gi|6005886|ref|NP_009200.1|	syntaxin binding protein 3; syntaxin 4 binding protein [Homo sapiens] [			1.45E-04	0.91	10.20	2.50	67573.7
AHQ-1-6, 3767	K.SCEVIIGSTHVLTPK.K	1642.89886	2	1.45E-04	0.91	4.02	-	834.3
gi|5453629|ref|NP_006391.1|	dynactin 2; dynactin complex 50 kD subunit; dynamitin; 50 kD dynein-ass			1.46E-04	0.91	10.23	4.70	44819.3
AHQ-1-9, 5255	K.LLGPDAAINLTDPDGALAK.R	1866.10514	2	1.46E-04	0.91	4.52	-	766.2
gi|5803135|ref|NP_006852.1|	RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind			1.48E-04	0.91	10.20	5.50	23025.1
AHQ-1-14- , 3818 - 3819	K.LLIIGDSGVGK.S	1072.28025	2	1.48E-04	0.91	4.00	-	891.2
AHQ-1-11, 3566 - 3627	K.LLIIGDSGVGK.S	1072.28025	1	2.51E-04	0.21	1.89	-	500.1
gi|29725611|ref|NP_066954.2|	regulatory subunit PR 53 of protein phosphatase 2A isoform b; phosphot			1.51E-04	0.93	10.25	9.00	36775.0
AHQ-1-9, 7222	K.LDEEAENLVATVVPTHLAAAVPEVAVYLK.E	3063.49045	3	1.51E-04	0.93	4.97	-	1162.2
gi|14589893|ref|NP_001785.2|	cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-			1.55E-04	0.42	10.15	2.00	100279.9
AHQ-1-5, 4751 - 4823	K.VENPIDLYIYVIDM*NDNR.P	2213.45293	2	1.96E-04	0.33	3.07	-	315.7
AHQ-1-11, 4291	K.VENPIDLYIYVIDM*NDNR.P	2213.45293	2	3.37E-04	0.44	2.90	-	493.8
AHQ-1-1, 4911	K.VENPIDLYIYVIDM*NDNR.P	2213.45293	2	1.55E-04	0.42	2.65	-	495.0
gi|6005731|ref|NP_009167.1|	calcium binding protein P22; SLC9A1 binding protein; calcineurin homolo			1.57E-04	0.70	10.16	6.20	22456.0
AHQ-1-11, 4479	R.IPELAINPLGDR.I	1308.50858	2	1.57E-04	0.70	3.13	-	755.5
gi|4758788|ref|NP_004542.1|	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q			1.58E-04	0.70	10.17	6.40	30241.3
AHQ-1-10, 5852	K.TYTDELTPIESAVSVFK.A	1901.10311	2	1.58E-04	0.70	3.41	-	291.5
gi|20540302|ref|XP_166540.1|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			1.59E-04	0.43	10.10	6.10	12714.2
AHQ-1-6, 1623 - 1626	K.DNNLLGK.F	773.85763	1	1.59E-04	0.43	1.99	-	412.1
gi|29740132|ref|XP_299177.1|	hypothetical protein XP_299177 [Homo sapiens]			1.61E-04	0.56	10.16	2.70	114488.9
AHQ-1-3, 5285	R.RCHEEKLPLSAGTASHKGQASAQPITPR.Q	3030.36879	3	1.61E-04	0.56	3.23	-	460.7
gi|4503253|ref|NP_001335.1|	defender against cell death 1 [Homo sapiens]			1.62E-04	0.92	10.17	10.60	12496.6
AHQ-1-14, 4921	R.FLEEYLSSTPQR.L	1470.60844	2	1.62E-04	0.92	3.38	-	1399.3
gi|29732170|ref|XP_291550.1|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			1.64E-04	0.85	10.18	13.60	13262.9
AHQ-1-5, 3519	K.KHLEINPDHSIIETLR.Q	1916.17061	2	1.64E-04	0.85	3.50	-	1078.9
gi|30156394|ref|XP_062437.6|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			1.70E-04	0.18	10.13	3.30	44396.0
AHQ-1-13- , 5015	R.DWSHYFKIIDDLR.A	1708.89749	2	1.70E-04	0.18	2.51	-	299.5
gi|4503445|ref|NP_001944.1|	endothelial cell growth factor 1 (platelet-derived); thymidine phosphor			1.72E-04	0.96	10.25	3.90	49955.2
AHQ-1-7, 4404	R.AREQEELLAPADGTVELVR.A	2097.31523	2	1.72E-04	0.96	5.08	-	934.9
gi|12408677|ref|NP_002614.2|	prefoldin 4 [Homo sapiens]			1.76E-04	0.94	10.19	9.00	15314.1
AHQ-1-12, 4878	K.NLQEEIDALESR.V	1417.50394	2	1.76E-04	0.94	3.72	-	1386.3
gi|10140853|ref|NP_065438.1|	diazepam binding inhibitor; GABA receptor modulator; endozepine; acyl			1.77E-04	0.80	10.19	15.40	11793.3
AHQ-1-14- , 3815	K.TKPSDEEM*LFIYGHYK.Q	1975.21039	3	1.77E-04	0.80	3.77	-	406.3
gi|18491024|ref|NP_005691.2|	dipeptidylpeptidase III isoform 1; dipeptidylpeptidase III [Homo sapie			1.77E-04	0.73	10.14	2.30	82588.6
AHQ-1-6, 4672	K.LAQDFLDSQNLSAYNTR.L	1957.09009	2	1.77E-04	0.73	2.79	-	519.7
gi|29739581|ref|XP_084467.3|	similar to eukaryotic initiation factor 5A [Homo sapiens]			1.87E-04	0.90	10.19	8.40	16773.1
AHQ-1-12, 2967	R.LPEGDLGKEIEQK.Y	1456.62321	2	1.87E-04	0.90	3.85	-	1001.0
gi|4885281|ref|NP_005262.1|	glutamate dehydrogenase 1 [Homo sapiens]			1.95E-04	0.73	10.15	2.90	61397.5
AHQ-1-7, 3994	K.HGGTIPIVPTAEFQDR.I	1738.92514	2	1.95E-04	0.73	2.94	-	363.4
gi|4501889|ref|NP_001606.1|	actin, gamma 2 propeptide; actin, alpha-3 [Homo sapiens]			1.96E-04	0.21	10.17	5.60	41876.7
AHQ-1-14- , 4866 - 4882	K.DLYANNVLSGGTTM*YPGIADR.M	2245.45502	2	2.62E-04	0.74	3.36	-	532.6
AHQ-1-10, 4952	K.DLYANNVLSGGTTM*YPGIADR.M	2245.45502	2	1.96E-04	0.21	2.76	-	225.5
gi|4505329|ref|NP_003818.1|	N-ethylmaleimide-sensitive factor attachment protein, alpha; alpha-SNAP			1.98E-04	0.96	10.24	6.10	33246.6
AHQ-1-9, 3232	K.LLEAHEEQNVDSYTESVK.E	2092.20594	2	1.98E-04	0.96	4.85	-	1413.4
gi|4505755|ref|NP_000281.1|	phosphoglycerate mutase 2 (muscle); Phosphoglycerate mutase, muscle for			2.01E-04	0.37	10.15	5.10	28850.0
AHQ-1-6, 7244	K.M*EFDICYTSVLKR.A	1679.93944	2	2.01E-04	0.37	2.56	-	519.6

gi|8393638|ref|NP_058642.1|	F11 receptor isoform a precursor; platelet F11 receptor; platelet adhes			2.09E-04	0.80	10.15	3.70	32582.9
AHQ-1-9, 5247	R.VTFLPTGITFK.S	1224.47318	2	2.09E-04	0.80	3.08	-	477.3
gi|14765644|ref|XP_037574.1|	similar to PTPL1-associated RhoGAP 1 [Homo sapiens]			2.15E-04	0.67	10.14	1.70	124613.7
AHQ-1-13- , 6885	K.YPLLNTVETLTAAGTLIAK.V	1990.32931	2	2.15E-04	0.67	2.75	-	873.0
gi|4505409|ref|NP_002503.1|	non-metastatic cells 2, protein (NM23B) expressed in; Non-metastatic ce			2.17E-04	0.88	10.19	0.00	17297.9
AHQ-1-12, 5865 - 5941	K.EISLWFKPEELVDYK.S	1897.15929	2	2.17E-04	0.88	3.90	-	600.3
gi|7705300|ref|NP_057701.1|	hypothetical protein BM-002 [Homo sapiens]			2.18E-04	0.69	10.13	17.60	9117.5
AHQ-1-14- , 5394	K.VLSVPESTPFTAVLK.F	1588.86951	2	2.18E-04	0.69	2.64	-	330.1
gi|4506195|ref|NP_002785.1|	proteasome beta 2 subunit; proteasome subunit, beta type, 2; macropain			2.34E-04	0.78	10.17	5.50	22836.1
AHQ-1-11, 5782	R.FILNLPTFSVR.I	1307.56542	2	2.34E-04	0.78	3.41	-	501.7
gi|21361827|ref|NP_062826.2|	putative methyltransferase M6A; putative methyltransferase [Homo sapie			2.35E-04	0.64	10.17	3.10	64473.6
AHQ-1-2, 4489	K.YVHYEIDACMDSEAPGSK.D	2074.23418	2	2.35E-04	0.64	3.34	-	429.7
gi|4502013|ref|NP_001616.1|	adenylate kinase 2 isoform a; adenylate kinase, mitochondrial; adenylat			2.35E-04	0.80	10.17	10.50	26477.6
AHQ-1-13- , 6989	R.GIHSAIDASQTPDVVFASILAAFSK.A	2546.85974	3	2.35E-04	0.80	3.36	-	867.7
gi|4557609|ref|NP_000806.1|	gamma-aminobutyric acid (GABA) A receptor, delta [Homo sapiens]			2.41E-04	0.39	10.15	4.90	50689.0
AHQ-1-9, 2452 - 2455	R.NAIVLFSLSAAGVTQELAISRR.Q	2317.67354	3	2.41E-04	0.39	3.07	-	487.7
gi|4885079|ref|NP_005165.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypept			2.43E-04	0.77	10.15	4.00	32880.7
AHQ-1-12, 4967	R.IYGLGSLALYEK.A	1327.55027	2	2.43E-04	0.77	2.72	-	669.0
gi|21361822|ref|NP_057049.3|	cell death-regulatory protein GRIM19; CGI-39 protein [Homo sapiens] [M			2.48E-04	0.66	10.13	5.70	25864.7
AHQ-1-13- , 6904	R.WVPPLIGELYGLR.T	1513.80756	2	2.48E-04	0.66	2.61	-	354.7
gi|21624643|ref|NP_660202.1|	similar to CG3714 gene product [Homo sapiens]			2.56E-04	0.64	10.13	9.00	14620.8
AHQ-1-7, 3220 - 3294	R.SPAQYQVVLSER.L	1377.52778	2	2.56E-04	0.64	2.58	-	485.0
gi|27485813|ref|XP_208062.1|	similar to ARP2/3 complex 21 kDa subunit (P21-ARC) (Actin-related prot			2.61E-04	0.78	10.13	6.30	12870.0
AHQ-1-11, 2432	R.AYLQQLR.Q	892.03735	2	2.61E-04	0.78	2.63	-	731.5
gi|5454148|ref|NP_006368.1|	UNC13 (C. elegans)-like; homolog of rat Munc13 (diacylglycerol-binding)			2.61E-04	0.92	10.19	0.80	180682.0
AHQ-1-5, 4041	R.EDRVLGLAVMPLR.D	1469.77813	3	2.61E-04	0.92	3.87	-	1741.7
gi|7706485|ref|NP_057376.1|	tumor necrosis factor type 1 receptor associated protein [Homo sapiens]			2.70E-04	0.93	10.21	2.00	80010.4
AHQ-1-5, 4509 - 4510	R.GVVDSEDIPLNLSR.E	1514.66275	2	2.70E-04	0.93	4.14	-	877.8
gi|4501865|ref|NP_001087.1|	ATP citrate lyase [Homo sapiens]			2.78E-04	0.64	10.15	1.50	121419.0
AHQ-1-4, 5316	R.DEPSVAAMVYPFTGDHK.Q	1865.05606	2	2.78E-04	0.64	2.97	-	533.4
gi|30156116|ref|XP_301571.1|	similar to Dual specificity protein phosphatase 3 (Dual specificity pr			2.90E-04	0.74	10.13	1.70	64164.4
AHQ-1-11, 3604	K.DSGITYLGIK.A	1067.21733	2	2.90E-04	0.74	2.64	-	656.4
gi|7657649|ref|NP_055362.1|	tropomodulin 3 (ubiquitous) [Homo sapiens]			2.92E-04	0.53	10.14	5.70	39594.5
AHQ-1-9, 5314	K.ILPVFDEPPNPTNVEESLKR.T	2295.57683	2	2.92E-04	0.53	2.88	-	322.8
gi|11140817|ref|NP_068557.1|	retinoic acid induced 2 [Homo sapiens]			3.04E-04	0.37	10.17	3.40	57147.9
AHQ-1-12, 6335	R.HTVIKM*GSENEALDLSM*K.S	2036.31705	2	3.04E-04	0.37	3.05	-	261.5
gi|7705369|ref|NP_057535.1|	coatomer protein complex, subunit beta; beta coat protein [Homo sapiens			3.06E-04	0.88	10.18	1.90	107141.5
AHQ-1-5, 3439 - 3446	K.EAGELKPEEEITVGPVQK.L	1954.16755	2	3.06E-04	0.88	3.52	-	872.2
gi|18087855|ref|NP_542408.1|	dynein light chain 2 [Homo sapiens]			3.09E-04	0.43	10.09	0.00	10349.8
AHQ-1-14- , 3114	K.DIAAYIK.K	793.93045	1	3.09E-04	0.43	1.88	-	717.6
gi|8923582|ref|NP_060378.1|	hypothetical protein FLJ20626 [Homo sapiens]			3.12E-04	0.77	10.14	2.70	48956.7
AHQ-1-9, 2851 - 2918	R.AFDWKSQLVIHR.K	1500.72897	2	3.12E-04	0.77	2.87	-	600.3
gi|27500963|ref|XP_028810.2|	similar to KIAA1755 protein [Homo sapiens]			3.16E-04	0.33	10.11	1.90	53033.5
AHQ-1-7, 4357	K.DGSLETVEK.A	978.03581	1	3.16E-04	0.33	2.20	-	492.7
gi|7019485|ref|NP_037364.1|	programmed cell death 6; apoptosis-linked gene 2 [Homo sapiens]			3.22E-04	0.74	10.14	5.20	21868.3
AHQ-1-11, 4922	K.YITDWQNVFR.T	1342.48358	2	3.22E-04	0.74	2.86	-	638.8
gi|16357474|ref|NP_006026.2|	CDC42-binding protein kinase beta; CDC42-binding protein kinase beta (			3.24E-04	0.70	10.15	0.90	194327.5
AHQ-1-4, 4002	R.FQFPSHVTDVSEEAK.D	1721.84821	2	3.24E-04	0.70	2.91	-	543.1
gi|5174389|ref|NP_005882.1|	acetyl-Coenzyme A acetyltransferase 2; acetoacetyl Coenzyme A thiolase			3.38E-04	0.90	10.17	4.00	41295.5
AHQ-1-9, 3607	K.AGHFDKEIVPVLVSTR.K	1769.03752	2	3.38E-04	0.90	3.39	-	1334.0
gi|11386183|ref|NP_008921.1|	WAS protein family, member 2; suppressor of cyclic-AMP receptor (WASP-			3.40E-04	0.90	10.19	3.20	54283.7
AHQ-1-14- , 6095	R.SELECVTNITLANVIR.Q	1834.08473	2	3.40E-04	0.90	3.88	-	1011.3
gi|6912586|ref|NP_036220.1|	6-phosphogluconolactonase [Homo sapiens]			3.49E-04	0.63	10.21	8.10	27546.7
AHQ-1-10, 3955	R.ILEDQEENPLPAALVQPHTGK.L	2300.55348	2	3.49E-04	0.63	3.00	-	346.2
AHQ-1-10, 3939	R.ILEDQEENPLPAALVQPHTGK.L	2300.55348	3	4.08E-04	0.87	4.17	-	887.8
gi|5453854|ref|NP_006187.1|	poly(rC) binding protein 1; heterogenous nuclear ribonucleoprotein X; p			3.50E-04	0.71	10.26	3.90	37525.7
AHQ-1-13- , 4079 - 4151	R.LVVPATQCGSLIGK.G	1444.72199	2	3.50E-04	0.71	2.85	-	389.5
gi|4505695|ref|NP_002604.1|	3-phosphoinositide dependent protein kinase-1; PkB kinase [Homo sapiens			3.51E-04	0.52	10.11	1.60	63151.5
AHQ-1-4, 2396	R.EYAIKILEK.R	1107.32460	1	3.51E-04	0.52	2.28	-	691.7
gi|7305053|ref|NP_038479.1|	myoferlin isoform a; fer-1-like 3 [Homo sapiens]			3.55E-04	0.37	10.14	0.80	234705.6
AHQ-1-2, 5006	R.ILVELATFLEKTPPDK.K	1815.14287	2	3.55E-04	0.37	2.80	-	377.8
gi|30156971|ref|XP_301321.1|	similar to Tubulin alpha-4 chain (Alpha-tubulin 4) [Homo sapiens] [MAS			3.63E-04	0.40	10.12	3.80	20833.0
AHQ-1-8, 3229	K.FNLMYAK.R	887.08098	1	3.63E-04	0.40	2.01	-	459.5
gi|7524354|ref|NP_039268.1|	dimethylarginine dimethylaminohydrolase 2; dimethylarginine dimethylami			3.66E-04	0.33	10.13	5.60	29643.6
AHQ-1-10, 3495	R.DFAVSTVPVSGPSHLR.G	1669.86281	2	3.66E-04	0.33	2.60	-	379.7
gi|23097264|ref|NP_690870.1|	hypothetical protein DKFZp761P1121 [Homo sapiens]			3.67E-04	0.81	10.21	7.90	24194.3
AHQ-1-10, 5384	K.LAALTNYLQPQLDWQAR.G	2002.26196	2	3.67E-04	0.81	4.14	-	272.2
gi|4557896|ref|NP_000243.1|	myotubularin [Homo sapiens]			3.74E-04	0.30	10.13	2.30	69931.3
AHQ-1-12, 3727 - 3790	K.DDEKYLDVIRETNK.Q	1738.87708	2	3.74E-04	0.30	2.54	-	338.1
gi|30149013|ref|XP_302138.1|	similar to alpha tubulin [Homo sapiens]			3.81E-04	0.79	10.16	4.60	22444.5
AHQ-1-7, 5112 - 5124	R.EIINLVLDR.I	1085.27902	2	3.81E-04	0.79	3.29	-	846.6
AHQ-1-13- , 5131	R.EIINLVLDR.I	1085.27902	2	5.04E-04	0.80	2.97	-	792.9
AHQ-1-14- , 4996 - 5006	R.EIINLVLDR.I	1085.27902	2	7.17E-04	0.80	2.93	-	732.2
AHQ-1-7, 5108	R.EIINLVLDR.I	1085.27902	1	6.61E-04	0.32	2.05	-	245.2
gi|9845522|ref|NP_000365.2|	uroporphyrinogen decarboxylase; uroporphyrinogen III decarboxylase [Hom			3.82E-04	0.87	10.19	6.80	40802.7
AHQ-1-9, 7142	K.TVTLQGNLDPCALYASEEEIGQLVK.Q	2751.05952	2	3.82E-04	0.87	3.87	-	563.3
gi|4502905|ref|NP_001822.1|	clusterin; complement-associated protein SP-40 [Homo sapiens]			3.83E-04	0.89	10.23	3.80	52494.3
AHQ-1-11, 5087	K.LFDSDPITVTVPVEVSR.K	1875.11203	2	3.83E-04	0.89	3.78	-	816.9
gi|7705963|ref|NP_057454.1|	RAB9-like protein [Homo sapiens]			3.84E-04	0.87	10.17	7.00	22719.3
AHQ-1-11, 3784	R.FVTLQIWDTAGQER.F	1664.84302	2	3.84E-04	0.87	3.38	-	1197.0
gi|27478732|ref|XP_210750.1|	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, su			3.84E-04	0.81	10.15	7.10	16272.9
AHQ-1-11, 3427	K.SCAEWVSLSK.A	1168.30181	2	3.84E-04	0.81	2.85	-	785.1
gi|14161692|ref|NP_115706.1|	calpain small subunit 2 [Homo sapiens]			3.87E-04	0.80	10.14	2.80	27660.1
AHQ-1-12, 3379	K.LGFEEFK.Y	869.98378	2	3.87E-04	0.80	2.87	-	691.0
gi|4758986|ref|NP_004209.1|	RAB11B, member RAS oncogene family; RAB11B, member of RAS oncogene fami			3.95E-04	0.86	10.17	9.60	24573.4
AHQ-1-11, 5892	K.NNLSFIETSALDSTNVEEAFK.N	2330.49008	2	3.95E-04	0.86	3.36	-	739.0
gi|20149637|ref|NP_057526.2|	type 1 tumor necrosis factor receptor shedding aminopeptidase regulato			3.98E-04	0.26	10.18	1.90	107761.4
AHQ-1-4, 5775	R.SELLLLACVHNYQPCVQR.A	2203.52751	2	3.98E-04	0.26	2.70	-	305.8
gi|21361553|ref|NP_003168.2|	spleen tyrosine kinase [Homo sapiens]			4.03E-04	0.78	10.18	3.10	72065.7
AHQ-1-13- , 6481	R.EEAEDYLVQGGMSDGLYLLR.Q	2259.47849	2	4.03E-04	0.78	3.61	-	705.8
gi|4503101|ref|NP_001312.1|	cysteine and glycine-rich protein 2; LIM domain only 5, smooth muscle;			4.24E-04	0.39	10.16	9.30	20953.8
AHQ-1-14, 4172	K.GYGYGQGAGTLNM*DRGER.L	1919.02542	2	4.24E-04	0.39	3.16	-	265.7
gi|4503069|ref|NP_001306.1|	mitogen-activated protein kinase 14 isoform 1; cytokine suppressive ant			4.35E-04	0.85	10.18	4.20	41493.2
AHQ-1-9, 6894	K.LTDDHVQFLIYQILR.G	1875.16009	2	4.35E-04	0.85	3.56	-	724.5
gi|5729808|ref|NP_006557.1|	adhesion glycoprotein; platelet and T cell activation antigen 1; DNAX a			4.39E-04	0.67	10.16	5.40	38583.7
AHQ-1-6, 6718	R.WSVIVIPDVTVSDSGLYR.C	2007.27528	2	4.39E-04	0.67	3.12	-	406.7
gi|27479431|ref|XP_050793.2|	similar to KIAA1393 protein [Homo sapiens]			4.40E-04	0.30	10.10	1.60	58245.9
AHQ-1-5, 4846	-.M*VLWILWR.P	1133.43358	1	4.40E-04	0.30	1.93	-	553.7
gi|29734623|ref|XP_299768.1|	hypothetical protein XP_299768 [Homo sapiens]			4.42E-04	0.24	10.10	7.50	14905.7
AHQ-1-10, 3409	K.RMVPVKEIDR.L	1243.50477	1	4.42E-04	0.24	2.03	-	469.2
gi|14780596|ref|XP_033004.1|	hypothetical protein BC005107 [Homo sapiens]			4.42E-04	0.42	10.13	5.00	18127.9
AHQ-1-2, 1958 - 2025	R.EQIIAKAK.A	901.08569	1	4.42E-04	0.42	2.53	-	288.5
gi|6680033|ref|NP_031379.1|	guanine nucleotide binding protein (G protein) alpha 12 [Homo sapiens]			4.43E-04	0.57	10.13	2.90	44250.9
AHQ-1-9, 3140	K.ILLLGAGESGK.S	1058.25357	1	4.43E-04	0.57	2.22	-	738.5
gi|21618331|ref|NP_000746.2|	carnitine acetyltransferase isoform 1 precursor [Homo sapiens]			4.46E-04	0.43	10.15	4.00	70875.3
AHQ-1-9, 4536	R.FKAHQDALPRLPVPPLQQSLDHYLK.A	2913.36808	3	4.46E-04	0.43	3.03	-	517.3
gi|5174441|ref|NP_005886.1|	Golgi autoantigen, golgin subfamily a, 3; Golgin-160; male enhanced ant			4.51E-04	0.10	10.13	0.60	170266.8

<table>
<tr><td>AHQ-1-2, 2579</td><td>K.EEQVRLQAR.K</td><td>1129.25198</td><td>1</td><td>4.51E-04</td><td>0.10</td><td>1.96</td><td>-</td><td>127.9</td></tr>
<tr><td>gi|29729703|ref|XP_293563.1|</td><td>similar to huntingtin-associated protein interacting protein (duo) [Ho</td><td></td><td></td><td>4.59E-04</td><td>0.20</td><td>10.13</td><td>6.40</td><td>26758.5</td></tr>
<tr><td>AHQ-1-14- , 3936</td><td>K.ETDEERVLMDWEKVK.D</td><td>1908.12238</td><td>2</td><td>4.59E-04</td><td>0.20</td><td>2.63</td><td>-</td><td>259.6</td></tr>
<tr><td>gi|17439599|ref|XP_067423.1|</td><td>similar to destrin - pig [Homo sapiens]</td><td></td><td></td><td>4.71E-04</td><td>0.58</td><td>10.12</td><td>4.40</td><td>19819.2</td></tr>
<tr><td>AHQ-1-12, 2338 - 2341</td><td>K.CIIVEEGK.E</td><td>949.10404</td><td>1</td><td>4.71E-04</td><td>0.58</td><td>2.46</td><td>-</td><td>572.7</td></tr>
<tr><td>gi|30155280|ref|XP_294126.2|</td><td>similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK</td><td></td><td></td><td>4.72E-04</td><td>0.22</td><td>10.15</td><td>7.90</td><td>36155.8</td></tr>
<tr><td>AHQ-1-13, 4020 - 4024</td><td>R.RTVQSLEIDLDLMRNPKASLENSLR.E</td><td>2900.30469</td><td>3</td><td>4.72E-04</td><td>0.22</td><td>3.01</td><td>-</td><td>221.4</td></tr>
<tr><td>gi|30153966|ref|XP_293932.2|</td><td>similar to hypothetical protein BC013073 [Homo sapiens]</td><td></td><td></td><td>4.73E-04</td><td>0.66</td><td>10.18</td><td>9.00</td><td>21711.3</td></tr>
<tr><td>AHQ-1-3, 4018</td><td>R.MIFTLFTINVSKDIRHH</td><td>2073.44997</td><td>2</td><td>4.73E-04</td><td>0.66</td><td>3.48</td><td>-</td><td>321.9</td></tr>
<tr><td>AHQ-1-6, 4096</td><td>R.MIFTLFTINVSKDIRHH</td><td>2073.44997</td><td>2</td><td>8.43E-04</td><td>0.39</td><td>3.05</td><td>-</td><td>373.4</td></tr>
<tr><td>AHQ-1-2, 4350</td><td>R.MIFTLFTINVSKDIRHH</td><td>2073.44997</td><td>3</td><td>5.20E-04</td><td>0.80</td><td>3.54</td><td>-</td><td>1173.3</td></tr>
<tr><td>gi|28373103|ref|NP_005164.2|</td><td>sarco/endoplasmic reticulum Ca2+ -ATPase isoform a; ATPase, Ca(2+)-tra</td><td></td><td></td><td>4.76E-04</td><td>0.90</td><td>10.19</td><td>1.50</td><td>109255.5</td></tr>
<tr><td>AHQ-1-1, 3792</td><td>R.VDQSILTGESVSVTK.H</td><td>1563.73208</td><td>2</td><td>4.76E-04</td><td>0.90</td><td>3.73</td><td>-</td><td>773.5</td></tr>
<tr><td>gi|25777600|ref|NP_002798.2|</td><td>proteasome 26S non-ATPase subunit 1; 26S proteasome non-ATPase regulat</td><td></td><td></td><td>4.79E-04</td><td>0.93</td><td>10.20</td><td>2.20</td><td>105835.6</td></tr>
<tr><td>AHQ-1-4, 5664</td><td>R.TPEQCPSVVSLLSESYNPHVR.Y</td><td>2401.63796</td><td>3</td><td>4.79E-04</td><td>0.93</td><td>4.03</td><td>-</td><td>1964.5</td></tr>
<tr><td>gi|21361741|ref|NP_057569.2|</td><td>hypothetical protein HSPC228; My012 protein [Homo sapiens]</td><td></td><td></td><td>4.88E-04</td><td>0.63</td><td>10.15</td><td>6.50</td><td>33879.0</td></tr>
<tr><td>AHQ-1-9, 5082</td><td>K.YAGSALQYEDVSTAVQNLQK.A</td><td>2186.36410</td><td>2</td><td>4.88E-04</td><td>0.63</td><td>2.96</td><td>-</td><td>363.0</td></tr>
<tr><td>gi|24475861|ref|NP_054891.2|</td><td>phosphohistidine phosphatase; sex-regulated protein janus-a [Homo sapi</td><td></td><td></td><td>4.90E-04</td><td>0.87</td><td>10.20</td><td>16.80</td><td>13832.4</td></tr>
<tr><td>AHQ-1-13- , 4141</td><td>K.IHVYGYSMAYGPAQHAISTEK.I</td><td>2324.60023</td><td>3</td><td>4.90E-04</td><td>0.87</td><td>4.04</td><td>-</td><td>659.0</td></tr>
<tr><td>gi|10835121|ref|NP_000289.1|</td><td>pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H</td><td></td><td></td><td>4.90E-04</td><td>0.94</td><td>10.20</td><td>1.90</td><td>61829.8</td></tr>
<tr><td>AHQ-1-7, 3708 - 3754</td><td>R.GDLGIEIPAEK.V</td><td>1142.28420</td><td>2</td><td>4.90E-04</td><td>0.94</td><td>3.98</td><td>-</td><td>1116.8</td></tr>
<tr><td>gi|13027380|ref|NP_055864.1|</td><td>amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidat</td><td></td><td></td><td>5.12E-04</td><td>0.70</td><td>10.17</td><td>2.30</td><td>101432.5</td></tr>
<tr><td>AHQ-1-13, 4999 - 5056</td><td>R.VEQMTKTYNDIDMVTHLLAER.D</td><td>2508.85682</td><td>3</td><td>5.12E-04</td><td>0.70</td><td>3.39</td><td>-</td><td>754.7</td></tr>
<tr><td>gi|4759080|ref|NP_004159.1|</td><td>succinate dehydrogenase complex, subunit A, flavoprotein precursor; suc</td><td></td><td></td><td>5.57E-04</td><td>0.50</td><td>10.16</td><td>4.50</td><td>72689.1</td></tr>
<tr><td>AHQ-1-6, 7082</td><td>R.AGLPCQDLEFVQFHPTGIYGAGCLITEGCR.G</td><td>3371.76536</td><td>3</td><td>5.57E-04</td><td>0.50</td><td>3.12</td><td>-</td><td>427.0</td></tr>
<tr><td>gi|7661624|ref|NP_056202.1|</td><td>preimplantation protein 3; likely ortholog of preimplantation protein 3</td><td></td><td></td><td>5.77E-04</td><td>0.50</td><td>10.14</td><td>7.20</td><td>22256.6</td></tr>
<tr><td>AHQ-1-10, 3555</td><td>K.ILEPPEGQDEGVWK.Y</td><td>1597.75022</td><td>2</td><td>5.77E-04</td><td>0.50</td><td>2.71</td><td>-</td><td>216.5</td></tr>
<tr><td>gi|6996010|ref|NP_002038.1|</td><td>glycyl-tRNA synthetase; GlyRS; glycine tRNA ligase [Homo sapiens]</td><td></td><td></td><td>5.96E-04</td><td>1.18</td><td>20.18</td><td>5.70</td><td>77530.3</td></tr>
<tr><td>AHQ-1-6, 6566</td><td>K.SPITGNDLSPPVSFNLMFK.T</td><td>2065.37824</td><td>2</td><td>5.96E-04</td><td>0.39</td><td>3.15</td><td>-</td><td>245.3</td></tr>
<tr><td>AHQ-1-6, 6883</td><td>K.TLYVEEVVPNVIEPSFGLGR.I</td><td>2219.52197</td><td>2</td><td>7.46E-04</td><td>0.79</td><td>3.60</td><td>-</td><td>517.9</td></tr>
<tr><td>gi|5174737|ref|NP_006077.1|</td><td>tubulin, beta, 4 [Homo sapiens]</td><td></td><td></td><td>6.26E-04</td><td>0.70</td><td>10.16</td><td>3.30</td><td>50517.5</td></tr>
<tr><td>AHQ-1-7, 4652 - 4654</td><td>R.ALTVPELTQQM*FDAK.N</td><td>1708.95749</td><td>2</td><td>6.26E-04</td><td>0.70</td><td>3.12</td><td>-</td><td>425.6</td></tr>
<tr><td>gi|30156349|ref|XP_301652.1|</td><td>similar to Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) [</td><td></td><td></td><td>6.33E-04</td><td>0.23</td><td>10.14</td><td>9.30</td><td>21450.7</td></tr>
<tr><td>AHQ-1-8, 4379 - 4461</td><td>K.M*HAADLTVSALRGDM*DEK.E</td><td>1993.20912</td><td>2</td><td>6.33E-04</td><td>0.23</td><td>2.74</td><td>-</td><td>340.6</td></tr>
<tr><td>gi|4502417|ref|NP_000703.1|</td><td>biliverdin reductase A [Homo sapiens]</td><td></td><td></td><td>6.43E-04</td><td>0.46</td><td>10.14</td><td>4.70</td><td>33488.3</td></tr>
<tr><td>AHQ-1-9, 2911</td><td>K.SGSLENVPNVGVNK.N</td><td>1414.54642</td><td>2</td><td>6.43E-04</td><td>0.46</td><td>2.75</td><td>-</td><td>234.0</td></tr>
<tr><td>gi|6912396|ref|NP_036335.1|</td><td>glyoxylate reductase/hydroxypyruvate reductase [Homo sapiens]</td><td></td><td></td><td>6.74E-04</td><td>0.67</td><td>10.18</td><td>5.50</td><td>35668.0</td></tr>
<tr><td>AHQ-1-9, 4180</td><td>R.AADCEVEQWDSDEPIPAK.E</td><td>2062.15676</td><td>2</td><td>6.74E-04</td><td>0.67</td><td>2.82</td><td>-</td><td>509.3</td></tr>
<tr><td>gi|5902154|ref|NP_008994.1|</td><td>vascular Rab-GAP/TBC-containing [Homo sapiens]</td><td></td><td></td><td>6.74E-04</td><td>0.31</td><td>10.10</td><td>1.10</td><td>102676.0</td></tr>
<tr><td>AHQ-1-4, 2795</td><td>K.QM*IKDLAKEK.D</td><td>1220.46471</td><td>1</td><td>6.74E-04</td><td>0.31</td><td>1.93</td><td>-</td><td>628.4</td></tr>
<tr><td>gi|4506077|ref|NP_002734.1|</td><td>protein kinase C substrate 80K-H; glucosidase II, beta subunit; AGE-bin</td><td></td><td></td><td>6.80E-04</td><td>0.92</td><td>10.15</td><td>1.90</td><td>59296.0</td></tr>
<tr><td>AHQ-1-5, 4167</td><td>K.SLEDQVEMLR.T</td><td>1220.37847</td><td>2</td><td>6.80E-04</td><td>0.92</td><td>3.02</td><td>-</td><td>1500.4</td></tr>
<tr><td>gi|14249478|ref|NP_116189.1|</td><td>hypothetical protein FLJ14525 [Homo sapiens]</td><td></td><td></td><td>6.93E-04</td><td>0.08</td><td>10.14</td><td>2.40</td><td>36346.2</td></tr>
<tr><td>AHQ-1-2, 1962 - 2030</td><td>R.KIM*QDKEK.I</td><td>1036.22824</td><td>1</td><td>6.93E-04</td><td>0.08</td><td>2.01</td><td>-</td><td>289.7</td></tr>
<tr><td>gi|30157774|ref|XP_301845.1|</td><td>similar to Kunitz-type protease inhibitor 3 (HKIB9) [Homo sapiens] [MA</td><td></td><td></td><td>7.02E-04</td><td>0.41</td><td>10.15</td><td>12.00</td><td>24113.1</td></tr>
<tr><td>AHQ-1-12, 5435 - 5498</td><td>-.MQLQASLSFLLILTLCLELRSELAR.D</td><td>2921.51174</td><td>3</td><td>7.02E-04</td><td>0.41</td><td>3.04</td><td>-</td><td>435.0</td></tr>
<tr><td>gi|13385594|ref|NP_085056.1|</td><td>cytochrome b5 outer mitochondrial membrane precursor; type 2 cyt-b5 [H</td><td></td><td></td><td>7.20E-04</td><td>0.83</td><td>10.17</td><td>23.30</td><td>16332.0</td></tr>
<tr><td>AHQ-1-11, 5722</td><td>R.FLNEHPGGEEVLLEQAGVDASESFEDVGHSSDAR.E</td><td>3629.75848</td><td>3</td><td>7.20E-04</td><td>0.83</td><td>3.45</td><td>-</td><td>779.6</td></tr>
<tr><td>gi|28872728|ref|NP_002808.2|</td><td>proteasome 26S non-ATPase subunit 13 isoform 1; 26S proteasome subunit</td><td></td><td></td><td>7.50E-04</td><td>0.42</td><td>10.16</td><td>4.80</td><td>42918.2</td></tr>
<tr><td>AHQ-1-9, 4996</td><td>K.TAWGQQPDLAANEAQLLR.K</td><td>1983.17391</td><td>2</td><td>7.50E-04</td><td>0.42</td><td>3.11</td><td>-</td><td>230.9</td></tr>
<tr><td>gi|13376539|ref|NP_079295.1|</td><td>hypothetical protein FLJ13940 [Homo sapiens]</td><td></td><td></td><td>7.61E-04</td><td>0.49</td><td>10.14</td><td>5.00</td><td>27546.1</td></tr>
<tr><td>AHQ-1-11, 3862</td><td>R.QIFHPEQLITGK.E</td><td>1411.63050</td><td>2</td><td>7.61E-04</td><td>0.49</td><td>2.82</td><td>-</td><td>161.2</td></tr>
<tr><td>gi|11321611|ref|NP_006868.1|</td><td>guanosine monophosphate reductase; guanine monophosphate reductase [Ho</td><td></td><td></td><td>7.68E-04</td><td>0.90</td><td>10.23</td><td>7.50</td><td>37414.6</td></tr>
<tr><td>AHQ-1-9, 4174</td><td>K.LFATNHPECLQNVAVSSGSGQNDLEK.M</td><td>2818.02614</td><td>3</td><td>7.68E-04</td><td>0.90</td><td>4.57</td><td>-</td><td>1225.5</td></tr>
<tr><td>gi|22059372|ref|XP_113714.2|</td><td>similar to Density-regulated protein (DRP) (DRP1 protein) (Smooth musc</td><td></td><td></td><td>7.85E-04</td><td>0.49</td><td>10.15</td><td>8.60</td><td>22091.9</td></tr>
<tr><td>AHQ-1-10, 4371</td><td>K.WPEVDDDSIEDLGEVKK</td><td>1975.09895</td><td>2</td><td>7.85E-04</td><td>0.49</td><td>2.93</td><td>-</td><td>543.6</td></tr>
<tr><td>gi|24432013|ref|NP_078982.2|</td><td>hypothetical protein FLJ13479 [Homo sapiens]</td><td></td><td></td><td>7.96E-04</td><td>0.01</td><td>10.10</td><td>1.50</td><td>67976.0</td></tr>
<tr><td>AHQ-1-9, 2763</td><td>K.AYAELKDLR.N</td><td>1079.23134</td><td>1</td><td>7.96E-04</td><td>0.01</td><td>2.03</td><td>-</td><td>90.3</td></tr>
<tr><td>gi|6912662|ref|NP_036372.1|</td><td>sirtuin 4; sir2-like 4; sirtuin type 4; sirtuin silent mating type info</td><td></td><td></td><td>8.02E-04</td><td>0.47</td><td>10.16</td><td>8.60</td><td>35187.3</td></tr>
<tr><td>AHQ-1-9, 5234</td><td>K.AGSRRLTELHGCMDRVLCLDCGEQTPR.G</td><td>3192.57848</td><td>3</td><td>8.02E-04</td><td>0.47</td><td>3.13</td><td>-</td><td>476.4</td></tr>
<tr><td>gi|29745994|ref|XP_290546.1|</td><td>similar to KIAA0830 protein [Homo sapiens]</td><td></td><td></td><td>8.03E-04</td><td>0.95</td><td>10.21</td><td>2.60</td><td>55016.4</td></tr>
<tr><td>AHQ-1-9, 4200</td><td>K.ILEVVNQIQDEER.M</td><td>1585.74098</td><td>2</td><td>8.03E-04</td><td>0.95</td><td>4.26</td><td>-</td><td>1288.2</td></tr>
<tr><td>gi|20546215|ref|XP_115639.1|</td><td>similar to leukocyte immunoglobulin-like receptor, subfamily B (with T</td><td></td><td></td><td>8.20E-04</td><td>0.31</td><td>10.14</td><td>4.70</td><td>42748.2</td></tr>
<tr><td>AHQ-1-11, 4463 - 4476</td><td>R.CSREVNSREDNVLYRVVK.P</td><td>2225.47152</td><td>2</td><td>8.20E-04</td><td>0.31</td><td>2.74</td><td>-</td><td>501.9</td></tr>
<tr><td>gi|4504061|ref|NP_002067.1|</td><td>glucosamine (N-acetyl)-6-sulfatase precursor; N-acetylglucosamine-6-sul</td><td></td><td></td><td>8.21E-04</td><td>0.30</td><td>10.14</td><td>3.30</td><td>62081.8</td></tr>
<tr><td>AHQ-1-3, 5689 - 5761</td><td>K.RWQTLLSVDDLVEKLVKR.L</td><td>2199.58179</td><td>2</td><td>8.21E-04</td><td>0.30</td><td>2.66</td><td>-</td><td>321.3</td></tr>
<tr><td>gi|18588342|ref|XP_085748.1|</td><td>similar to KIAA1039 protein [Homo sapiens]</td><td></td><td></td><td>8.36E-04</td><td>0.65</td><td>10.14</td><td>14.40</td><td>10510.0</td></tr>
<tr><td>AHQ-1-7, 3578</td><td>K.LPFTDGDAQQLQR.K</td><td>1489.61498</td><td>2</td><td>8.36E-04</td><td>0.65</td><td>2.79</td><td>-</td><td>806.8</td></tr>
<tr><td>gi|7662502|ref|NP_054779.1|</td><td>MCT-1 protein [Homo sapiens]</td><td></td><td></td><td>8.37E-04</td><td>0.92</td><td>10.22</td><td>10.50</td><td>20555.2</td></tr>
<tr><td>AHQ-1-11, 5014</td><td>K.FVLSGANIMCPGLTSPGAK.L</td><td>1922.25862</td><td>2</td><td>8.37E-04</td><td>0.92</td><td>4.45</td><td>-</td><td>747.3</td></tr>
<tr><td>gi|5803003|ref|NP_006720.1|</td><td>diaphanous 2 isoform 156 [Homo sapiens]</td><td></td><td></td><td>8.71E-04</td><td>0.63</td><td>10.17</td><td>1.60</td><td>125568.3</td></tr>
<tr><td>AHQ-1-1, 5015</td><td>K.TAREQYEKLSTMHNNMMK.L</td><td>2213.54787</td><td>3</td><td>8.71E-04</td><td>0.63</td><td>3.38</td><td>-</td><td>764.9</td></tr>
<tr><td>gi|6912324|ref|NP_036266.1|</td><td>leiomodin 1 (smooth muscle); thyroid and eye muscle autoantigen D1 (64k</td><td></td><td></td><td>8.77E-04</td><td>0.38</td><td>10.13</td><td>3.00</td><td>63737.1</td></tr>
<tr><td>AHQ-1-14, 6114 - 6186</td><td>K.GEKKDLLEVPKAGAVAK.G</td><td>1754.06430</td><td>2</td><td>8.77E-04</td><td>0.38</td><td>2.69</td><td>-</td><td>557.0</td></tr>
<tr><td>gi|21361547|ref|NP_002930.2|</td><td>ribonuclease/angiogenin inhibitor; Placental ribonuclease inhibitor [H</td><td></td><td></td><td>8.83E-04</td><td>0.82</td><td>10.17</td><td>3.30</td><td>49973.3</td></tr>
<tr><td>AHQ-1-7, 6921</td><td>R.WAELLPLLQQCQVVR.L</td><td>1855.19360</td><td>2</td><td>8.83E-04</td><td>0.82</td><td>3.41</td><td>-</td><td>432.4</td></tr>
<tr><td>gi|4502167|ref|NP_000475.1|</td><td>amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disea</td><td></td><td></td><td>8.87E-04</td><td>0.42</td><td>10.13</td><td>2.30</td><td>86942.8</td></tr>
<tr><td>AHQ-1-4, 7012</td><td>R.CLVGEFVSDALLVPDKCK.F</td><td>2053.38561</td><td>2</td><td>8.87E-04</td><td>0.42</td><td>2.52</td><td>-</td><td>557.7</td></tr>
<tr><td>gi|4507947|ref|NP_003671.1|</td><td>tyrosyl-tRNA synthetase; tyrosyl-tRNA synthetase; tyrosyl tRNA ligase [</td><td></td><td></td><td>8.94E-04</td><td>0.90</td><td>10.19</td><td>3.40</td><td>59143.1</td></tr>
<tr><td>AHQ-1-7, 6225</td><td>K.AFCEPGNVENNGVLSFIK.H</td><td>1997.21741</td><td>2</td><td>8.94E-04</td><td>0.90</td><td>3.87</td><td>-</td><td>987.5</td></tr>
<tr><td>gi|4506185|ref|NP_002780.1|</td><td>proteasome alpha 4 subunit; proteasome component C9; proteasome subunit</td><td></td><td></td><td>9.35E-04</td><td>0.71</td><td>10.16</td><td>9.20</td><td>29483.6</td></tr>
<tr><td>AHQ-1-10, 6091</td><td>K.LNEDMACSVAGITSDANVLTNELR.L</td><td>2595.84629</td><td>2</td><td>9.35E-04</td><td>0.71</td><td>3.21</td><td>-</td><td>467.2</td></tr>
<tr><td>gi|11072091|ref|NP_057736.2|</td><td>Crn, crooked neck-like 1; CGI-201 protein; crooked neck protein (crn);</td><td></td><td></td><td>9.61E-04</td><td>0.47</td><td>10.10</td><td>1.10</td><td>99200.7</td></tr>
<tr><td>AHQ-1-4, 3214</td><td>R.FVLVHPDVK.N</td><td>1054.26662</td><td>1</td><td>9.61E-04</td><td>0.47</td><td>1.82</td><td>-</td><td>804.7</td></tr>
</table>

Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]				1.00E-30	31.15	370.29	32.80	129351.8
AHQ-2-2, 4316 - 4386	K.AGTLDLSLTVQGK.Q	1303.48711	2	8.12E-06	0.93	3.68	-	1377.6
AHQ-2-6, 2503	R.AQLYIDCEK.M	1141.27636	1	2.19E-04	0.15	2.57	-	218.1
AHQ-2-3, 6700	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	3	6.44E-06	0.95	5.68	-	899.4
AHQ-2-10, 5959	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	2	5.61E-08	0.78	3.23	-	496.8
AHQ-2-2, 6745	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	3	2.18E-05	0.93	4.94	-	1081.7
AHQ-2-2, 7069	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	3	1.17E-05	0.94	5.06	-	1038.1
AHQ-2-4, 4244	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.82E-12	0.91	3.94	-	551.4
AHQ-2-3, 4060 - 4072	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.61E-04	0.80	3.09	-	592.5
AHQ-2-1, 4209	R.CENTDPGYNCLPCPPR.F	1954.10800	2	9.99E-06	0.71	3.26	-	296.6
AHQ-2-1, 3929	R.CENTDPGYNCLPCPPR.F	1954.10800	2	8.00E-06	0.83	3.20	-	498.0
AHQ-2-2, 3945 - 4017	R.CENTDPGYNCLPCPPR.F	1954.10800	2	8.39E-09	0.94	4.43	-	735.7
AHQ-2-2, 4096	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.55E-05	0.61	3.13	-	276.5
AHQ-2-4, 3354	K.CNYLGHYSDPM*YR.C	1693.84162	2	4.87E-05	0.93	3.43	-	971.5
AHQ-2-2, 3389 - 3392	K.CNYLGHYSDPM*YR.C	1693.84162	2	1.47E-04	0.92	3.78	-	779.0
AHQ-2-2, 3917	K.CNYLGHYSDPMYR.C	1677.84222	2	3.51E-05	0.91	3.90	-	635.4
AHQ-2-4, 3872 - 3948	K.CNYLGHYSDPMYR.C	1677.84222	2	5.43E-04	0.72	2.91	-	742.7
AHQ-2-4, 3477 - 3554	K.DCVGDVTENQICNK.Q	1654.75869	2	5.76E-05	0.87	3.22	-	867.3
AHQ-2-3, 3464 - 3467	K.DCVGDVTENQICNK.Q	1654.75869	2	9.38E-07	0.96	4.44	-	1340.8
AHQ-2-2, 3525	K.DCVGDVTENQICNK.Q	1654.75869	2	5.37E-06	0.94	3.91	-	1192.7
AHQ-2-4, 6610	K.DDFDHDSVPDIDDICPENVDISETDFR.R	3183.22991	3	2.56E-04	0.73	3.58	-	785.8
AHQ-2-5, 2584	K.DHSGQVFSVVSNGK.A	1461.56164	2	5.86E-04	0.92	3.86	-	925.3
AHQ-2-6, 2521	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.05E-04	0.77	2.69	-	700.8
AHQ-2-2, 2693	K.DHSGQVFSVVSNGK.A	1461.56164	2	8.23E-07	0.94	3.24	-	1501.7
AHQ-2-10, 2496	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.93E-04	0.94	3.91	-	1152.5
AHQ-2-2, 2706	K.DHSGQVFSVVSNGK.A	1461.56164	1	2.18E-08	0.37	2.24	-	344.3
AHQ-2-4, 2653	K.DHSGQVFSVVSNGK.A	1461.56164	2	1.17E-08	0.95	4.12	-	1147.7
AHQ-2-1, 3189	R.DNCQYVYNVDQR.D	1575.64166	2	7.58E-07	0.92	4.39	-	781.8
AHQ-2-1, 3353	R.DNCQYVYNVDQR.D	1575.64166	2	5.51E-05	0.91	3.45	-	1363.2
AHQ-2-4, 3144	R.DNCQYVYNVDQR.D	1575.64166	2	2.03E-05	0.93	3.86	-	1047.1
AHQ-2-3, 3140	R.DNCQYVYNVDQR.D	1575.64166	2	1.47E-04	0.90	3.65	-	948.7
AHQ-2-2, 6294	K.DSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFR.R	4418.43100	3	7.42E-09	0.74	4.05	-	331.8
AHQ-2-3, 4309 - 4363	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	7.78E-11	0.90	4.37	-	665.2
AHQ-2-2, 3972 - 4040	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	5.96E-13	0.91	4.57	-	855.6
AHQ-2-5, 4288	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.46E-05	0.88	4.49	-	555.1
AHQ-2-7, 4275	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	2.68E-05	0.86	4.36	-	512.1
AHQ-2-2, 4346 - 4417	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.16E-13	0.92	5.05	-	570.8
AHQ-2-4, 4234	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	3.39E-09	0.92	4.49	-	836.3
AHQ-2-4, 3932 - 4008	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	4.01E-08	0.81	3.58	-	678.1
AHQ-2-3, 3917 - 3973	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.62E-10	0.91	5.34	-	523.3
AHQ-2-2, 4108	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.07E-04	0.76	3.45	-	608.5
AHQ-2-4, 4320	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.47E-07	0.80	3.65	-	449.2
AHQ-2-1, 3889 - 3890	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	6.04E-09	0.91	4.54	-	822.9
AHQ-2-2, 4545	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.90E-07	0.75	3.40	-	458.7
AHQ-2-1, 4310	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.87E-05	0.73	3.48	-	463.4
AHQ-2-2, 3644	K.FQDLVDAVR.A	1063.18877	1	2.79E-04	0.24	2.03	-	346.3
AHQ-2-2, 3645	K.FQDLVDAVR.A	1063.18877	2	2.87E-06	0.94	3.39	-	1279.7
AHQ-2-1, 3782	K.FQDLVDAVR.A	1063.18877	2	1.23E-04	0.86	2.57	-	998.3
AHQ-2-6, 3346	K.FQDLVDAVR.A	1063.18877	2	1.61E-05	0.88	2.84	-	1050.2
AHQ-2-9, 3299	K.FQDLVDAVR.A	1063.18877	1	2.72E-05	0.24	2.07	-	348.1
AHQ-2-7, 2455	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.20E-05	0.86	3.98	-	431.7
AHQ-2-1, 2962	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	5.11E-09	0.81	3.79	-	373.7
AHQ-2-3, 2925	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.31E-12	0.72	3.34	-	409.8
AHQ-2-2, 2833 - 2913	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.22E-06	0.90	4.17	-	513.9
AHQ-2-2, 2734	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	5.63E-04	0.60	3.25	-	481.2
AHQ-2-5, 2479	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.36E-04	0.87	3.90	-	542.3
AHQ-2-3, 2831	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.27E-07	0.78	3.67	-	337.0
AHQ-2-4, 2926	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.94E-06	0.88	4.14	-	452.8
AHQ-2-4, 5689	R.FVFGTTPEDILR.N	1395.58470	2	3.47E-04	0.84	3.11	-	708.8
AHQ-2-4, 5697	R.FVFGTTPEDILR.N	1395.58470	1	4.07E-07	0.08	2.12	-	88.6
AHQ-2-9, 5330 - 5331	R.FVFGTTPEDILR.N	1395.58470	1	4.86E-06	0.03	1.95	-	98.3
AHQ-2-9, 5326 - 5334	R.FVFGTTPEDILR.N	1395.58470	2	6.40E-04	0.81	3.31	-	697.9
AHQ-2-3, 5660 - 5661	R.FVFGTTPEDILR.N	1395.58470	1	1.23E-04	0.12	2.06	-	170.6
AHQ-2-12, 5465	R.FVFGTTPEDILR.N	1395.58470	2	3.05E-04	0.89	2.80	-	1036.5
AHQ-2-5, 5417	R.FVFGTTPEDILR.N	1395.58470	1	2.77E-05	0.15	2.00	-	132.9
AHQ-2-5, 5420	R.FVFGTTPEDILR.N	1395.58470	1	2.45E-06	0.12	2.25	-	69.2
AHQ-2-6, 5337 - 5418	R.FVFGTTPEDILR.N	1395.58470	1	2.53E-04	0.08	2.04	-	139.4
AHQ-2-6, 4425 - 4433	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.27E-10	0.92	4.37	-	868.7
AHQ-2-5, 4245	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.16E-04	0.78	3.07	-	642.9
AHQ-2-2, 4829 - 4908	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.09E-05	0.95	4.79	-	1083.8
AHQ-2-2, 4725 - 4752	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.74E-05	0.89	4.11	-	798.0
AHQ-2-2, 4581	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.71E-04	0.91	3.91	-	813.6
AHQ-2-6, 4190 - 4191	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.44E-05	0.94	4.24	-	1140.7
AHQ-2-1, 4653	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.06E-05	0.83	3.75	-	707.4
AHQ-2-4, 4890	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.57E-08	0.91	4.21	-	840.8
AHQ-2-4, 4716 - 4746	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.10E-08	0.86	3.53	-	776.9
AHQ-2-4, 4625 - 4701	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.36E-07	0.81	3.37	-	590.9
AHQ-2-4, 4530	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.40E-05	0.81	3.25	-	897.2
AHQ-2-7, 4039 - 4111	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.46E-04	0.73	3.58	-	408.4
AHQ-2-10, 4327 - 4330	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.85E-07	0.91	4.18	-	878.3
AHQ-2-2, 4422	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.26E-05	0.72	3.29	-	494.5
AHQ-2-7, 4401 - 4413	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.01E-08	0.88	4.17	-	770.3
AHQ-2-10, 3898	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.85E-07	0.74	3.09	-	686.3
AHQ-2-1, 4749	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.96E-06	0.90	4.16	-	717.7
AHQ-2-3, 4887	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.59E-05	0.88	4.02	-	728.1
AHQ-2-8, 3943	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.90E-05	0.63	3.12	-	497.8
AHQ-2-5, 4493 - 4544	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.51E-05	0.89	4.04	-	836.3
AHQ-2-9, 4166 - 4174	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.12E-04	0.76	3.76	-	470.6
AHQ-2-9, 4408 - 4442	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.44E-05	0.92	4.02	-	1089.1
AHQ-2-3, 4707 - 4783	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.78E-10	0.93	4.36	-	1019.6
AHQ-2-10, 3990	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.60E-04	0.67	3.50	-	529.9
AHQ-2-3, 4391	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.55E-04	0.84	3.55	-	904.9
AHQ-2-5, 4664	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.85E-06	0.82	3.57	-	652.4
AHQ-2-3, 4543	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.28E-06	0.86	3.67	-	719.2
AHQ-2-10, 4162 - 4163	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.77E-11	0.90	4.28	-	807.4
AHQ-2-1, 2234 - 2253	K.GPDPSSPAFR.I	1031.10364	2	6.05E-05	0.70	2.91	-	516.5
AHQ-2-2, 2074	K.GPDPSSPAFR.I	1031.10364	2	1.20E-05	0.87	3.06	-	686.1
AHQ-2-5, 1857 - 1868	K.GPDPSSPAFR.I	1031.10364	2	8.55E-04	0.77	3.19	-	409.9
AHQ-2-6, 1855 - 1881	K.GPDPSSPAFR.I	1031.10364	2	8.98E-05	0.75	3.00	-	455.9
AHQ-2-3, 2004 - 2083	K.GPDPSSPAFR.I	1031.10364	2	1.79E-05	0.84	3.11	-	570.4
AHQ-2-11, 2104	K.GPDPSSPAFR.I	1031.10364	2	4.15E-04	0.79	3.04	-	623.2
AHQ-2-4, 2073	K.GPDPSSPAFR.I	1031.10364	2	2.09E-05	0.87	3.13	-	683.1
AHQ-2-10, 2648 - 2656	R.GTLLALER.K	873.03234	2	1.89E-04	0.88	3.05	-	939.2
AHQ-2-2, 2910	R.GTLLALER.K	873.03234	2	3.77E-04	0.90	3.32	-	1022.9
AHQ-2-11, 2877 - 2878	R.GTLLALER.K	873.03234	2	5.53E-04	0.83	2.92	-	886.9

AHQ-2-4, 2910	R.GTLLALER.K	873.03234	2	6.52E-04	0.93	3.49	-	1149.8
AHQ-2-3, 2544 - 2608	K.GTSQNDPNWVVR.H	1373.45608	2	6.47E-04	0.47	2.73	-	588.2
AHQ-2-2, 2557 - 2586	K.GTSQNDPNWVVR.H	1373.45608	2	1.69E-04	0.72	3.13	-	810.7
AHQ-2-4, 2557 - 2566	K.GTSQNDPNWVVR.H	1373.45608	2	4.16E-05	0.72	3.40	-	601.4
AHQ-2-1, 2772	K.GTSQNDPNWVVR.H	1373.45608	2	2.11E-04	0.48	2.53	-	608.8
AHQ-2-13, 6260	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	6.37E-06	0.71	3.24	-	317.7
AHQ-2-5, 6659 - 6660	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.55E-07	0.76	3.32	-	316.2
AHQ-2-12, 6465 - 6539	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.23E-07	0.81	3.63	-	274.2
AHQ-2-12, 6399 - 6462	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.21E-05	0.85	4.17	-	447.4
AHQ-2-5, 6869	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.77E-04	0.84	4.02	-	416.7
AHQ-2-2, 6960 - 7038	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.59E-05	0.54	2.77	-	235.2
AHQ-2-13, 6261	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.46E-06	0.69	3.39	-	189.1
AHQ-2-11, 6261 - 6304	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	8.26E-06	0.69	3.17	-	310.2
AHQ-2-11, 6164 - 6184	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.14E-08	0.82	4.05	-	431.1
AHQ-2-11, 6162 - 6170	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.80E-04	0.48	2.97	-	215.9
AHQ-2-14-, 6304 - 6385	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	8.25E-07	0.76	3.12	-	630.2
AHQ-2-3, 6983	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.57E-05	0.80	4.01	-	360.5
AHQ-2-13-, 6445 - 6449	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.62E-07	0.67	3.04	-	448.4
AHQ-2-10, 6124 - 6199	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.33E-07	0.82	4.13	-	334.7
AHQ-2-10, 6042 - 6114	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.76E-05	0.63	3.29	-	186.2
AHQ-2-10, 6038 - 6050	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.15E-10	0.88	4.28	-	444.6
AHQ-2-3, 6791 - 6823	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.61E-06	0.68	3.45	-	418.4
AHQ-2-3, 6932 - 6984	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.60E-06	0.58	2.57	-	316.2
AHQ-2-1, 6273	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.56E-04	0.88	4.35	-	413.1
AHQ-2-3, 6892	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.99E-11	0.80	3.66	-	423.5
AHQ-2-6, 6393 - 6469	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	9.49E-06	0.34	2.55	-	164.4
AHQ-2-9, 6736	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	7.11E-08	0.79	3.93	-	341.8
AHQ-2-9, 6610 - 6612	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.81E-04	0.36	2.64	-	274.7
AHQ-2-1, 6612	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	9.04E-05	0.71	3.40	-	333.2
AHQ-2-1, 6722 - 6800	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.85E-08	0.87	4.14	-	462.9
AHQ-2-1, 6736 - 6801	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.31E-05	0.55	2.87	-	245.3
AHQ-2-1, 6865	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.94E-06	0.82	3.92	-	358.9
AHQ-2-4, 6844 - 6848	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.27E-09	0.68	3.03	-	472.8
AHQ-2-7, 6551	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.17E-08	0.72	3.47	-	356.4
AHQ-2-2, 7041	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.93E-06	0.79	3.81	-	436.7
AHQ-2-6, 6657	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.86E-04	0.69	3.22	-	353.2
AHQ-2-6, 6497 - 6570	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.46E-08	0.86	4.46	-	338.3
AHQ-2-2, 2309 - 2380	K.IM*ADSGPIYDK.T	1226.38144	2	1.53E-04	0.76	3.37	-	415.5
AHQ-2-8, 2250	K.IMADSGPIYDK.T	1210.38204	2	7.99E-06	0.91	3.18	-	945.0
AHQ-2-3, 2528	K.IMADSGPIYDK.T	1210.38204	2	5.10E-06	0.92	3.59	-	720.0
AHQ-2-2, 2542	K.IMADSGPIYDK.T	1210.38204	2	2.21E-04	0.91	3.55	-	716.3
AHQ-2-11, 2496	K.IMADSGPIYDK.T	1210.38204	2	7.49E-04	0.85	3.11	-	668.4
AHQ-2-4, 2536 - 2549	K.IMADSGPIYDK.T	1210.38204	2	1.24E-04	0.88	3.27	-	623.0
AHQ-2-6, 2379	K.IMADSGPIYDK.T	1210.38204	1	8.26E-04	0.73	2.64	-	720.9
AHQ-2-6, 2374	K.IMADSGPIYDK.T	1210.38204	2	7.40E-05	0.93	3.68	-	879.4
AHQ-2-12, 2542	K.IMADSGPIYDK.T	1210.38204	2	3.45E-06	0.87	3.50	-	771.0
AHQ-2-13, 2704 - 2715	K.IMADSGPIYDK.T	1210.38204	2	6.07E-05	0.83	3.04	-	660.3
AHQ-2-14-, 2263	K.IM*ADSGPIYDK.T	1226.38144	2	9.36E-06	0.83	3.55	-	471.0
AHQ-2-14-, 6687 - 6757	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.62E-08	0.97	5.74	-	1034.2
AHQ-2-1, 7092	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	9.03E-13	0.97	5.68	-	1367.0
AHQ-2-10, 6410 - 6471	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.03E-08	0.97	5.29	-	1243.5
AHQ-2-10, 6550 - 6615	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.00E-30	0.97	5.38	-	1313.0
AHQ-2-2, 7286 - 7352	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.43E-11	0.97	5.81	-	1285.4
AHQ-2-3, 7217 - 7285	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.18E-06	0.96	5.28	-	988.8
AHQ-2-3, 7353	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.82E-11	0.97	5.66	-	1425.2
AHQ-2-3, 7437	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.38E-05	0.91	4.24	-	817.6
AHQ-2-9, 7119 - 7186	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.74E-07	0.92	4.46	-	638.8
AHQ-2-13, 6616	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.23E-10	0.96	5.38	-	1071.4
AHQ-2-6, 7042	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.88E-05	0.92	4.20	-	829.5
AHQ-2-6, 6901 - 6911	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.20E-12	0.95	5.11	-	947.8
AHQ-2-9, 6996 - 6998	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.15E-05	0.94	4.77	-	903.4
AHQ-2-4, 7273 - 7316	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.88E-14	0.96	5.62	-	862.8
AHQ-2-11, 6509	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.05E-04	0.93	4.47	-	745.6
AHQ-2-12, 6863	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	9.07E-08	0.93	4.97	-	856.9
AHQ-2-4, 7378	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	6.93E-08	0.90	4.20	-	657.9
AHQ-2-5, 7071 - 7135	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.51E-06	0.96	5.63	-	958.2
AHQ-2-4, 7466	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.21E-08	0.85	3.58	-	711.0
AHQ-2-2, 7425	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	6.99E-12	0.97	5.63	-	1199.5
AHQ-2-4, 2214 - 2282	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.48E-11	0.90	3.63	-	997.4
AHQ-2-3, 2215 - 2289	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.28E-08	0.90	3.70	-	966.2
AHQ-2-2, 2230 - 2301	R.KDHSGQVFSVVSNGK.A	1589.73455	2	6.86E-11	0.94	3.80	-	1347.8
AHQ-2-1, 2438 - 2516	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.50E-05	0.26	2.52	-	303.4
AHQ-2-5, 2091	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.05E-07	0.89	3.44	-	937.6
AHQ-2-9, 2050 - 2127	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.40E-06	0.77	2.94	-	796.0
AHQ-2-2, 2322	K.KIMADSGPIYDK.T	1338.55496	2	5.23E-08	0.93	4.03	-	849.7
AHQ-2-4, 2341	R.KVTEENKELANELR.R	1673.84976	2	6.71E-09	0.95	4.73	-	1416.0
AHQ-2-5, 1956 - 2027	R.KVTEENKELANELR.R	1673.84976	3	5.03E-09	0.78	3.19	-	818.8
AHQ-2-3, 2233	R.KVTEENKELANELR.R	1673.84976	2	4.76E-06	0.81	3.62	-	769.9
AHQ-2-4, 2236 - 2237	R.KVTEENKELANELR.R	1673.84976	2	3.80E-09	0.94	4.97	-	1112.4
AHQ-2-2, 2368	R.KVTEENKELANELR.R	1673.84976	2	4.86E-10	0.97	5.23	-	1684.3
AHQ-2-6, 2031	R.KVTEENKELANELR.R	1673.84976	2	4.07E-08	0.95	5.39	-	1105.5
AHQ-2-5, 1964 - 2035	R.KVTEENKELANELR.R	1673.84976	2	2.24E-06	0.93	4.71	-	1062.1
AHQ-2-2, 1969	R.KVTEENKELANELR.R	1673.84976	2	1.05E-08	0.88	3.68	-	843.5
AHQ-2-6, 2171	R.KVTEENKELANELR.R	1673.84976	2	2.92E-04	0.93	4.68	-	671.7
AHQ-2-2, 2272	R.KVTEENKELANELR.R	1673.84976	2	3.28E-08	0.94	5.04	-	1309.6
AHQ-2-9, 2082	R.KVTEENKELANELR.R	1673.84976	2	1.11E-08	0.94	4.84	-	1282.4
AHQ-2-1, 2454	R.KVTEENKELANELR.R	1673.84976	2	4.06E-10	0.95	5.19	-	1369.8
AHQ-2-4, 1993	R.KVTEENKELANELR.R	1673.84976	2	1.57E-09	0.94	4.33	-	1435.6
AHQ-2-7, 1873 - 1951	R.KVTEENKELANELR.R	1673.84976	2	7.50E-06	0.93	4.54	-	1023.0
AHQ-2-3, 2345	R.KVTEENKELANELR.R	1673.84976	2	1.24E-07	0.94	4.61	-	1228.6
AHQ-2-1, 2637	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.98E-07	0.91	4.35	-	616.4
AHQ-2-5, 2388	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.93E-06	0.93	4.87	-	636.9
AHQ-2-3, 2513	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	2.72E-07	0.83	3.64	-	518.9
AHQ-2-2, 2532	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	8.94E-05	0.82	3.73	-	557.0
AHQ-2-3, 2148 - 2149	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	5.47E-06	0.87	3.71	-	533.6
AHQ-2-4, 2149	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	9.06E-04	0.72	2.65	-	538.6
AHQ-2-7, 5420 - 5421	K.MENAELDVPIQSVFTR.D	1850.08607	2	9.21E-07	0.93	4.66	-	571.8
AHQ-2-4, 5586	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	5.26E-05	0.40	2.58	-	274.2
AHQ-2-2, 5964	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.94E-05	0.94	4.91	-	604.2
AHQ-2-2, 5840	K.MENAELDVPIQSVFTR.D	1850.08607	2	9.57E-10	0.95	4.87	-	654.4
AHQ-2-3, 5811	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.36E-09	0.93	4.57	-	654.0
AHQ-2-4, 5812 - 5813	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.57E-09	0.80	3.73	-	416.6
AHQ-2-2, 5572	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	3.17E-09	0.94	4.86	-	734.4
AHQ-2-6, 5219	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	9.12E-04	0.96	5.14	-	807.5
AHQ-2-11, 5309	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.98E-05	0.87	3.87	-	456.5
AHQ-2-5, 5519 - 5552	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.03E-10	0.92	4.50	-	521.0
AHQ-2-3, 5544	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	6.73E-10	0.94	4.91	-	637.0

AHQ-2-4, 5946	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.62E-07	0.87	3.61	-	566.3
AHQ-2-3, 3060 - 3067	K.QVTQSYWDTNPTR.A	1596.68241	2	5.34E-08	0.91	3.74	-	953.6
AHQ-2-5, 2831 - 2832	K.QVTQSYWDTNPTR.A	1596.68241	2	1.71E-06	0.84	3.48	-	501.6
AHQ-2-4, 3054 - 3056	K.QVTQSYWDTNPTR.A	1596.68241	2	9.16E-07	0.90	3.77	-	670.8
AHQ-2-2, 3076 - 3088	K.QVTQSYWDTNPTR.A	1596.68241	2	1.84E-06	0.93	3.85	-	1019.7
AHQ-2-11, 2941	K.QVTQSYWDTNPTR.A	1596.68241	2	5.04E-08	0.89	3.76	-	677.5
AHQ-2-4, 2786	R.RPPLCYHNGVQYR.N	1661.86889	2	1.50E-06	0.88	3.40	-	642.5
AHQ-2-2, 2526 - 2604	R.RPPLCYHNGVQYR.N	1661.86889	2	4.00E-04	0.64	3.05	-	434.3
AHQ-2-6, 2525	R.RPPLCYHNGVQYR.N	1661.86889	2	1.75E-08	0.94	4.51	-	822.5
AHQ-2-4, 2684 - 2752	R.RPPLCYHNGVQYR.N	1661.86889	2	1.56E-06	0.91	3.81	-	764.5
AHQ-2-5, 2340	R.RPPLCYHNGVQYR.N	1661.86889	2	4.96E-04	0.85	3.46	-	555.4
AHQ-2-2, 2717 - 2794	R.RPPLCYHNGVQYR.N	1661.86889	2	9.12E-07	0.91	3.96	-	710.5
AHQ-2-3, 2711 - 2785	R.RPPLCYHNGVQYR.N	1661.86889	2	1.03E-08	0.94	4.14	-	737.1
AHQ-2-2, 3906	K.SITLFVQEDR.A	1208.34588	2	4.25E-06	0.94	3.70	-	1384.1
AHQ-2-3, 3853	K.SITLFVQEDR.A	1208.34588	2	6.45E-06	0.92	3.58	-	1107.7
AHQ-2-6, 3563	K.SITLFVQEDR.A	1208.34588	2	1.87E-06	0.86	2.71	-	1017.1
AHQ-2-12, 3747 - 3750	K.SITLFVQEDR.A	1208.34588	2	3.95E-05	0.90	3.25	-	1129.2
AHQ-2-4, 3840	K.SITLFVQEDR.A	1208.34588	2	1.93E-05	0.93	3.38	-	1283.5
AHQ-2-1, 4020	K.SITLFVQEDR.A	1208.34588	2	4.38E-04	0.90	3.46	-	1158.6
AHQ-2-5, 3647	K.SITLFVQEDR.A	1208.34588	2	8.63E-07	0.90	3.02	-	1145.3
AHQ-2-10, 3460	K.SITLFVQEDR.A	1208.34588	2	1.27E-06	0.88	3.08	-	1089.2
AHQ-2-2, 4013	K.SITLFVQEDR.A	1208.34588	2	4.88E-07	0.86	2.58	-	1063.0
AHQ-2-5, 3100	R.TIVTTLQDSIR.K	1247.42355	2	9.57E-06	0.97	3.15	-	2436.3
AHQ-2-4, 4461 - 4533	R.TIVTTLQDSIR.K	1247.42355	2	3.27E-06	0.96	3.70	-	1619.6
AHQ-2-1, 4628 - 4636	R.TIVTTLQDSIR.K	1247.42355	2	5.86E-06	0.97	4.32	-	1536.2
AHQ-2-7, 4047	R.TIVTTLQDSIR.K	1247.42355	2	1.58E-06	0.96	3.57	-	1650.1
AHQ-2-5, 4135 - 4179	R.TIVTTLQDSIR.K	1247.42355	2	3.27E-07	0.97	4.48	-	1511.3
AHQ-2-8, 3908	R.TIVTTLQDSIR.K	1247.42355	2	9.23E-07	0.97	3.76	-	1907.7
AHQ-2-2, 4524 - 4605	R.TIVTTLQDSIR.K	1247.42355	2	7.81E-07	0.97	4.17	-	1807.8
AHQ-2-3, 4603	R.TIVTTLQDSIR.K	1247.42355	2	3.19E-07	0.95	3.62	-	1551.7
AHQ-2-6, 4110 - 4141	R.TIVTTLQDSIR.K	1247.42355	2	1.35E-07	0.97	3.63	-	2298.3
AHQ-2-3, 4479 - 4485	R.TIVTTLQDSIR.K	1247.42355	2	2.83E-07	0.97	4.39	-	1552.9
AHQ-2-9, 4108 - 4128	R.TIVTTLQDSIR.K	1247.42355	2	7.23E-07	0.96	3.81	-	1326.4
AHQ-2-6, 4114	R.TIVTTLQDSIR.K	1247.42355	1	7.90E-04	0.22	2.02	-	139.5
AHQ-2-1, 6597	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	5.26E-10	0.81	3.77	-	898.2
AHQ-2-6, 2267 - 2274	K.VTEENKELANELR.R	1545.67685	2	3.84E-05	0.90	4.04	-	956.6
AHQ-2-4, 2444	K.VTEENKELANELR.R	1545.67685	2	8.93E-07	0.85	3.58	-	951.5
AHQ-2-7, 2215 - 2227	K.VTEENKELANELR.R	1545.67685	2	5.88E-04	0.68	3.33	-	525.4
AHQ-2-9, 2339	K.VTEENKELANELR.R	1545.67685	2	1.47E-04	0.78	3.24	-	786.7
AHQ-2-5, 2267	K.VTEENKELANELR.R	1545.67685	2	4.06E-08	0.93	3.93	-	1308.9
AHQ-2-1, 2673	K.VTEENKELANELR.R	1545.67685	2	2.93E-06	0.87	3.48	-	942.6
AHQ-2-5, 2273	K.VTEENKELANELR.R	1545.67685	3	4.87E-08	0.80	3.48	-	807.2
gi|4507729|ref|NP_001060.1| tubulin, beta polypeptide [Homo sapiens]				1.00E-30	7.27	90.36	30.80	49906.7
AHQ-2-11, 4684	R.AILVDLEPGTMDSVR.S	1616.86162	2	2.43E-04	0.62	2.71	-	494.0
AHQ-2-13, 3000	R.EIVHIQAGQCGNQIGAK.F	1825.03962	2	6.60E-04	0.66	2.58	-	556.2
AHQ-2-12, 2870	K.EVDEQMLNVQNK.N	1447.59668	2	8.20E-04	0.87	3.35	-	1150.8
AHQ-2-7, 2691	K.EVDEQMLNVQNK.N	1447.59668	1	5.86E-06	0.61	3.54	-	281.8
AHQ-2-7, 2687 - 2703	K.EVDEQMLNVQNK.N	1447.59668	2	6.05E-04	0.88	3.69	-	1217.8
AHQ-2-13-, 6419	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.78E-14	0.99	6.74	-	3027.6
AHQ-2-13, 6204	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	7.37E-04	0.92	4.58	-	1162.3
AHQ-2-7, 6236	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.36E-11	0.98	5.93	-	2544.0
AHQ-2-13, 6144 - 6203	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.66E-11	0.97	5.56	-	1656.4
AHQ-2-7, 6180	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	5.31E-05	0.92	4.76	-	1103.8
AHQ-2-12, 6331	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.68E-07	0.98	6.29	-	2617.9
AHQ-2-14-, 6283	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	1.26E-04	0.87	3.78	-	1057.1
AHQ-2-11, 6049 - 6056	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.37E-04	0.98	6.46	-	2699.9
AHQ-2-13, 6201	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.34E-09	0.99	6.52	-	2791.4
AHQ-2-10, 5886	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.75E-05	0.98	6.25	-	2496.6
AHQ-2-8, 6202	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.23E-05	0.97	4.52	-	1787.2
AHQ-2-14-, 6291	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.41E-06	0.98	6.31	-	2951.5
AHQ-2-9, 6262 - 6340	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.77E-07	0.98	6.01	-	1909.7
AHQ-2-9, 6406	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.20E-07	0.98	5.92	-	2358.1
AHQ-2-12, 4509	R.ISEQFTAMFR.R	1230.41818	2	1.44E-08	0.90	3.20	-	1191.4
AHQ-2-12, 4421 - 4435	R.ISEQFTAMFR.R	1230.41818	2	4.06E-05	0.68	3.07	-	744.3
AHQ-2-9, 7299	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	6.67E-06	0.84	3.63	-	930.0
AHQ-2-7, 6327	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	1.51E-05	0.84	4.00	-	617.1
AHQ-2-9, 7298 - 7300	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	8.29E-05	0.94	4.64	-	904.1
AHQ-2-8, 7263	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	1.69E-05	0.92	4.53	-	809.9
AHQ-2-7, 7355 - 7425	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	7.89E-05	0.76	3.35	-	569.4
AHQ-2-10, 6651	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	2.20E-04	0.73	3.55	-	559.6
AHQ-2-7, 7347 - 7419	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	4.35E-07	0.91	4.37	-	1186.9
AHQ-2-9, 6303 - 6384	K.LTTPTYGDLNHLVSATM*SGVTTCLR.F	2727.06467	2	1.98E-05	0.68	3.20	-	520.1
AHQ-2-12, 5473	K.NSSYFVEWIPNNVK.T	1697.87148	2	5.10E-05	0.84	3.56	-	623.0
AHQ-2-7, 6245 - 6316	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.71E-04	0.71	3.02	-	773.8
AHQ-2-13, 5549	K.NSSYFVEWIPNNVK.T	1697.87148	2	6.95E-04	0.55	2.54	-	574.0
AHQ-2-7, 5271 - 5348	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.64E-06	0.93	4.14	-	913.1
AHQ-2-12, 5583	K.NSSYFVEWIPNNVK.T	1697.87148	2	3.40E-05	0.49	2.60	-	449.3
AHQ-2-9, 6570	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.03E-05	0.89	4.16	-	911.6
AHQ-2-9, 6572 - 6582	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	7.81E-09	0.97	5.31	-	1185.3
AHQ-2-7, 6447 - 6517	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	2.23E-07	0.97	5.78	-	1098.4
AHQ-2-12, 6342	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	4.18E-08	0.96	5.34	-	1023.8
AHQ-2-7, 6681 - 6749	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.21E-07	0.94	5.28	-	1098.4
AHQ-2-7, 6384 - 6451	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.56E-09	0.96	5.71	-	1371.1
AHQ-2-7, 6599 - 6667	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	7.61E-08	0.95	5.28	-	990.3
AHQ-2-9, 6418	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	5.05E-05	0.87	4.01	-	1028.7
AHQ-2-7, 6307 - 6380	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	9.48E-06	0.95	4.71	-	1283.5
AHQ-2-7, 6281 - 6352	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	2.43E-05	0.97	7.10	-	1325.6
AHQ-2-13, 6239 - 6299	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.74E-13	0.97	5.82	-	1885.0
AHQ-2-11, 6160	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	6.98E-08	0.89	4.35	-	601.6
AHQ-2-14-, 6249 - 6315	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.00E-30	0.98	7.06	-	2425.8
AHQ-2-12, 6359 - 6438	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	1.90E-04	0.90	4.21	-	753.6
AHQ-2-11, 6096 - 6165	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.18E-13	0.98	7.13	-	2018.8
gi|21361399|ref|NP_055040.2| protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp				1.00E-30	0.99	10.38	3.90	65308.3
AHQ-2-6, 7233	K.DNTIEHLLPLFLAQLKDECPEVR.L	2753.12348	3	1.00E-30	0.99	7.60	-	3759.0
gi|4501885|ref|NP_001092.1| beta actin; beta cytoskeletal actin [Homo sapiens]				1.11E-16	13.78	150.46	36.80	41736.5
AHQ-2-8, 6187	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	6.87E-07	0.89	4.52	-	607.8
AHQ-2-14-, 6484 - 6544	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.92E-04	0.76	4.61	-	521.2
AHQ-2-13-, 6865 - 6907	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	6.61E-08	0.92	4.41	-	736.7
AHQ-2-13-, 6609 - 6669	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	6.23E-04	0.71	4.33	-	448.1
AHQ-2-1, 6962	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	2.02E-04	0.80	3.73	-	563.8
AHQ-2-13-, 6310	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	4.50E-07	0.88	4.08	-	733.2
AHQ-2-13, 6647	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	6.35E-08	0.90	4.44	-	619.4
AHQ-2-13, 6439 - 6508	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	1.53E-05	0.81	4.19	-	570.7
AHQ-2-13, 6313 - 6381	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	6.18E-07	0.68	3.78	-	510.5
AHQ-2-13, 6159	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.77E-05	0.78	3.47	-	503.3
AHQ-2-12, 6947 - 7013	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.79E-06	0.92	4.27	-	1025.6
AHQ-2-8, 6950 - 6984	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.20E-08	0.94	5.21	-	1016.7

AHQ-2-3, 7333 - 7337	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.20E-06	0.88	4.39	-	642.6
AHQ-2-11, 6620 - 6669	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.21E-09	0.93	4.85	-	690.0
AHQ-2-11, 6249 - 6317	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	7.60E-04	0.49	3.51	-	267.7
AHQ-2-7, 7191	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.39E-04	0.81	3.80	-	683.3
AHQ-2-10, 6610	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.41E-07	0.94	5.08	-	855.1
AHQ-2-8, 6998	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	4.05E-04	0.47	3.17	-	437.1
AHQ-2-8, 7047 - 7082	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	6.27E-06	0.94	5.02	-	880.4
AHQ-2-10, 6458 - 6520	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.41E-04	0.91	4.63	-	916.4
AHQ-2-8, 7154 - 7220	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.07E-07	0.94	5.49	-	855.5
AHQ-2-9, 7242 - 7311	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.27E-07	0.92	5.01	-	580.6
AHQ-2-9, 7139 - 7202	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.86E-08	0.89	4.57	-	641.7
AHQ-2-8, 7290 - 7359	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.34E-10	0.96	5.66	-	1210.6
AHQ-2-8, 7566 - 7586	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.01E-06	0.96	5.99	-	928.6
AHQ-2-8, 7426 - 7499	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.28E-11	0.96	5.69	-	1091.8
AHQ-2-8, 6730 - 6803	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.10E-06	0.83	4.49	-	653.4
AHQ-2-8, 7419 - 7490	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.63E-05	0.85	3.43	-	754.7
AHQ-2-8, 7574	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	7.76E-08	0.93	5.33	-	1028.0
AHQ-2-8, 7283 - 7362	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	3.59E-07	0.95	5.07	-	1438.9
AHQ-2-8, 7282 - 7350	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.43E-04	0.90	3.72	-	832.0
AHQ-2-8, 7179 - 7251	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	3.25E-05	0.93	5.29	-	1322.2
AHQ-2-9, 7326 - 7334	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	5.78E-08	0.91	4.42	-	779.3
AHQ-2-8, 7135 - 7212	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.30E-05	0.89	3.91	-	688.2
AHQ-2-4, 7482	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	7.46E-06	0.89	3.66	-	904.1
AHQ-2-10, 6591 - 6659	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.30E-04	0.90	4.29	-	636.3
AHQ-2-10, 6699 - 6712	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	5.09E-05	0.63	2.68	-	643.7
AHQ-2-11, 6684 - 6689	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.35E-07	0.95	4.73	-	1067.7
AHQ-2-14-, 6820	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.82E-04	0.51	2.53	-	287.3
AHQ-2-8, 7432 - 7502	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	4.35E-10	0.97	6.73	-	1343.0
AHQ-2-8, 5784 - 5850	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.32E-07	0.90	4.38	-	954.3
AHQ-2-8, 5634 - 5703	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	3.06E-04	0.88	4.17	-	1120.6
AHQ-2-8, 5435 - 5504	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	2.35E-05	0.70	3.12	-	892.2
AHQ-2-8, 7150 - 7219	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	1.89E-11	0.98	8.13	-	2448.3
AHQ-2-10, 6378 - 6455	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	2.02E-07	0.98	7.55	-	2016.5
AHQ-2-10, 6560 - 6619	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	4.72E-05	0.94	4.73	-	1157.9
AHQ-2-8, 7286 - 7366	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	4.01E-12	0.98	7.38	-	2161.4
AHQ-2-8, 7046 - 7115	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	2.12E-13	0.98	9.18	-	2466.9
AHQ-2-8, 7435 - 7508	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	3.79E-05	0.97	6.12	-	1464.4
AHQ-2-8, 6850 - 6868	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	6.81E-07	0.98	7.35	-	1924.3
AHQ-2-8, 6934 - 7006	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	2.26E-10	0.97	6.58	-	1407.4
AHQ-2-8, 7559	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	2.59E-04	0.92	5.01	-	854.7
AHQ-2-5, 2247 - 2255	R.GYSFTTTAER.E	1133.19273	2	6.00E-05	0.92	3.39	-	1168.9
AHQ-2-4, 2436	R.GYSFTTTAER.E	1133.19273	2	1.29E-04	0.91	3.13	-	1093.5
AHQ-2-8, 2242 - 2258	R.GYSFTTTAER.E	1133.19273	2	1.49E-04	0.90	3.01	-	1110.4
AHQ-2-7, 2201 - 2209	R.GYSFTTTAER.E	1133.19273	2	1.29E-04	0.93	3.52	-	1092.8
AHQ-2-8, 2104 - 2188	R.GYSFTTTAER.E	1133.19273	2	3.75E-04	0.90	3.49	-	853.1
AHQ-2-3, 2443 - 2444	R.GYSFTTTAER.E	1133.19273	2	1.31E-04	0.91	3.25	-	1089.4
AHQ-2-14-, 2415 - 2416	R.GYSFTTTAER.E	1133.19273	2	4.87E-06	0.93	3.26	-	1027.1
AHQ-2-10, 2266 - 2326	R.GYSFTTTAER.E	1133.19273	2	1.64E-04	0.92	3.50	-	1083.4
AHQ-2-13-, 2529 - 2530	R.GYSFTTTAER.E	1133.19273	2	7.86E-06	0.92	3.19	-	1025.4
AHQ-2-10, 4347 - 4358	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.53E-04	0.96	4.62	-	1389.1
AHQ-2-10, 4631	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	3.94E-04	0.73	3.01	-	502.4
AHQ-2-14-, 4255 - 4259	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	4.02E-06	0.90	3.59	-	1036.3
AHQ-2-14, 5725	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	5.49E-04	0.84	3.11	-	958.9
AHQ-2-11, 4130	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	2.73E-09	0.93	3.63	-	1277.9
AHQ-2-8, 4298	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	4.40E-04	0.90	4.51	-	1002.9
AHQ-2-8, 4295	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	2.87E-06	0.95	4.43	-	1302.8
AHQ-2-14-, 4752 - 4760	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	6.41E-04	0.92	3.87	-	970.3
AHQ-2-11, 4558	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.91E-05	0.89	3.48	-	915.3
AHQ-2-14, 5266 - 5329	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	4.92E-05	0.94	4.59	-	867.9
AHQ-2-14, 5830	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	3.12E-05	0.96	4.53	-	1487.1
AHQ-2-8, 7610 - 7611	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	6.25E-08	0.97	6.11	-	1902.5
AHQ-2-8, 7472 - 7544	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	2.51E-08	0.97	6.18	-	1678.9
AHQ-2-7, 5571 - 5583	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.99E-11	0.97	6.04	-	1719.6
AHQ-2-6, 5839 - 5915	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.55E-16	0.96	5.63	-	1501.7
AHQ-2-7, 5693 - 5767	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.03E-09	0.94	5.08	-	1390.9
AHQ-2-1, 6209	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.94E-07	0.94	4.94	-	1276.5
AHQ-2-6, 5477	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.67E-04	0.82	3.56	-	1111.3
AHQ-2-6, 5379	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.74E-05	0.90	4.60	-	872.4
AHQ-2-13-, 5815 - 5873	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.33E-09	0.97	5.84	-	1770.7
AHQ-2-7, 5836	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.25E-09	0.97	5.90	-	1432.7
AHQ-2-6, 5671 - 5685	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.08E-07	0.97	6.69	-	1383.7
AHQ-2-1, 5874	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.67E-07	0.95	5.58	-	1105.1
AHQ-2-5, 5893 - 5907	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.10E-13	0.97	5.99	-	1580.7
AHQ-2-8, 5944	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.03E-10	0.97	6.15	-	1810.2
AHQ-2-7, 5244 - 5255	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.78E-06	0.94	5.21	-	1231.5
AHQ-2-13-, 5722 - 5749	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.46E-06	0.97	6.80	-	1756.9
AHQ-2-13-, 5459 - 5538	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.53E-05	0.95	5.43	-	1168.6
AHQ-2-9, 5295 - 5366	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.72E-06	0.96	6.32	-	1243.9
AHQ-2-9, 5438 - 5507	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.86E-05	0.94	4.63	-	1284.4
AHQ-2-9, 5576 - 5648	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.90E-13	0.97	6.20	-	1741.0
AHQ-2-9, 5667 - 5699	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.76E-05	0.87	4.46	-	715.0
AHQ-2-9, 5718 - 5786	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.48E-11	0.96	6.25	-	1187.2
AHQ-2-9, 5807 - 5874	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.04E-09	0.97	6.18	-	1551.1
AHQ-2-9, 5943	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.46E-09	0.97	6.00	-	1574.3
AHQ-2-5, 5396	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.14E-07	0.94	5.08	-	1051.7
AHQ-2-1, 6128	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.01E-06	0.97	6.06	-	1784.0
AHQ-2-14, 6589	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	9.51E-08	0.95	5.18	-	1373.9
AHQ-2-8, 5674 - 5738	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.99E-14	0.96	6.29	-	1198.7
AHQ-2-14-, 5739 - 5803	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.18E-11	0.98	7.19	-	1671.7
AHQ-2-8, 5583 - 5650	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.55E-04	0.75	4.17	-	692.5
AHQ-2-8, 5530 - 5602	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.22E-14	0.97	6.15	-	1984.9
AHQ-2-10, 5019 - 5084	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.78E-07	0.94	5.35	-	999.3
AHQ-2-10, 5274 - 5338	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.91E-09	0.96	6.19	-	1251.5
AHQ-2-10, 5362 - 5434	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.11E-16	0.98	6.77	-	1704.8
AHQ-2-8, 5398 - 5470	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.67E-12	0.97	6.26	-	1660.9
AHQ-2-8, 5367 - 5426	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.11E-05	0.91	4.46	-	915.2
AHQ-2-8, 5231 - 5310	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.74E-12	0.97	6.46	-	1226.4
AHQ-2-4, 6249 - 6252	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.19E-09	0.97	6.64	-	1356.3
AHQ-2-4, 6088 - 6157	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.73E-08	0.96	5.49	-	1657.1
AHQ-2-4, 5721	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.05E-05	0.95	5.48	-	1223.8
AHQ-2-8, 5087 - 5170	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.80E-10	0.96	5.56	-	1546.1
AHQ-2-8, 4943 - 5015	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.55E-08	0.97	6.19	-	1494.4
AHQ-2-14-, 5416 - 5492	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.11E-10	0.96	5.85	-	1515.3
AHQ-2-11, 5278 - 5329	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.45E-04	0.93	4.68	-	1331.8
AHQ-2-11, 5536 - 5596	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.35E-13	0.98	6.04	-	2168.4
AHQ-2-14-, 5556 - 5559	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.46E-10	0.96	5.51	-	1722.6
AHQ-2-14-, 5717 - 5792	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.03E-04	0.78	3.95	-	548.6

AHQ-2-3, 6213	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.36E-11	0.97	6.38	-	1316.5
AHQ-2-2, 6049 - 6128	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.12E-04	0.91	4.38	-	1231.7
AHQ-2-2, 6241	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.02E-07	0.96	5.91	-	1171.9
AHQ-2-12, 5486	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.73E-04	0.93	5.08	-	767.7
AHQ-2-12, 5574	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.07E-05	0.93	5.14	-	917.1
AHQ-2-12, 5763	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.13E-05	0.83	3.91	-	728.9
AHQ-2-12, 5878 - 5959	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.15E-10	0.97	6.12	-	1380.1
AHQ-2-3, 6092	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.06E-09	0.97	6.13	-	1624.9
AHQ-2-5, 5713	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.51E-09	0.98	7.09	-	1800.2
AHQ-2-13, 5347	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.62E-08	0.92	4.43	-	1078.7
AHQ-2-13, 5428	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.52E-07	0.94	5.17	-	1142.8
AHQ-2-13, 5601	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.59E-09	0.96	5.30	-	1644.3
AHQ-2-13, 5725	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.23E-08	0.96	5.42	-	1892.6
AHQ-2-13, 5808	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.23E-06	0.96	5.02	-	1539.0
AHQ-2-3, 3935 - 3937	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.18E-04	0.88	4.12	-	559.4
AHQ-2-13, 3920	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.86E-06	0.93	4.34	-	966.4
AHQ-2-12, 3853	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.25E-04	0.92	4.34	-	750.1
AHQ-2-12, 3718 - 3785	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.09E-06	0.90	4.26	-	691.0
AHQ-2-14, 4794	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.12E-04	0.94	4.52	-	961.3
AHQ-2-4, 3916 - 3984	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.66E-04	0.85	3.94	-	597.3
AHQ-2-11, 3653	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.51E-05	0.84	4.01	-	492.0
AHQ-2-8, 3296 - 3366	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.07E-07	0.93	4.63	-	801.4
AHQ-2-5, 3591 - 3660	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.26E-06	0.85	3.82	-	575.1
AHQ-2-5, 3597 - 3639	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	7.90E-04	0.72	4.22	-	498.7
AHQ-2-13-, 3955 - 3969	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	7.30E-05	0.85	4.75	-	862.4
AHQ-2-13-, 3958	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.65E-04	0.87	4.07	-	683.1
AHQ-2-9, 3606	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.91E-05	0.94	4.07	-	1143.2
AHQ-2-9, 3522 - 3590	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.69E-04	0.91	4.26	-	815.6
AHQ-2-6, 3573	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.49E-06	0.94	4.86	-	768.9
AHQ-2-2, 3964 - 4033	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	9.99E-05	0.60	3.28	-	577.7
AHQ-2-7, 3456 - 3463	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.34E-04	0.92	4.28	-	794.0
AHQ-2-8, 3067 - 3138	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	8.06E-05	0.79	4.15	-	794.0
AHQ-2-8, 3170 - 3238	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	1.31E-04	0.85	4.10	-	875.8
AHQ-2-8, 3194 - 3266	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.73E-04	0.93	4.87	-	813.6
AHQ-2-8, 3768	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.41E-06	0.92	4.51	-	880.5
AHQ-2-8, 3546	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.25E-04	0.94	4.42	-	1098.3
AHQ-2-8, 3536 - 3616	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.32E-04	0.95	4.98	-	922.6
AHQ-2-8, 3407 - 3478	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.11E-06	0.94	5.05	-	879.7
AHQ-2-10, 3475 - 3542	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.07E-10	0.94	4.54	-	981.5
AHQ-2-1, 4053 - 4132	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.52E-04	0.93	4.57	-	920.7
AHQ-2-8, 2907	R.VAPEEHPVLLTEAPLNPKANR.E	2296.61120	2	1.48E-05	0.95	4.87	-	876.2
gi|4503571|ref|NP_001419.1| enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n				1.11E-16	11.77	150.34	44.90	47168.7
AHQ-2-14-, 5300	R.AAVPSGASTGIYEALELR.D	1806.00979	2	4.21E-11	0.94	4.58	-	698.0
AHQ-2-13-, 5343 - 5418	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.28E-08	0.96	5.00	-	811.0
AHQ-2-11, 5098 - 5114	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.59E-06	0.96	5.05	-	831.3
AHQ-2-12, 5345 - 5354	R.AAVPSGASTGIYEALELR.D	1806.00979	2	4.55E-13	0.96	5.18	-	911.7
AHQ-2-8, 4868 - 4935	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.11E-16	0.96	5.15	-	947.8
AHQ-2-14, 6454 - 6509	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.90E-11	0.96	5.58	-	567.8
AHQ-2-13, 5247 - 5309	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.71E-10	0.92	4.25	-	535.7
AHQ-2-9, 5175 - 5198	R.AAVPSGASTGIYEALELR.D	1806.00979	2	7.29E-04	0.82	4.00	-	370.3
AHQ-2-7, 4540	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	8.75E-06	0.94	4.69	-	801.8
AHQ-2-8, 6062	K.DATNVGDEGGFAPNILENKEGLELLK.T	2744.99178	3	3.45E-06	0.81	3.86	-	1041.8
AHQ-2-11, 6602	K.DYPVVSIEDPFDQDDWGAWQK.F	2511.63977	2	1.17E-07	0.79	2.99	-	677.4
AHQ-2-8, 5898 - 5930	K.FTASAGIQVVGDDLTVTNPK.R	2034.25590	2	7.80E-04	0.44	2.87	-	327.8
AHQ-2-13, 4239 - 4241	R.GNPTVEVDLFTSK.G	1407.55065	2	8.07E-04	0.68	3.18	-	544.4
AHQ-2-13-, 4286	R.GNPTVEVDLFTSK.G	1407.55065	1	2.31E-06	0.34	1.97	-	641.7
AHQ-2-13, 4240	R.GNPTVEVDLFTSK.G	1407.55065	1	1.29E-04	0.24	2.40	-	481.2
AHQ-2-8, 5940	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	1.06E-13	0.95	5.41	-	1400.7
AHQ-2-9, 2091 - 2092	R.IGAEVYHNLK.N	1144.30502	2	4.48E-04	0.88	3.36	-	1074.8
AHQ-2-9, 7015	K.LAMQEFMILPVGAANFR.E	1909.30812	2	1.89E-05	0.93	4.09	-	824.7
AHQ-2-10, 6443	K.LAMQEFMILPVGAANFR.E	1909.30812	2	3.41E-05	0.94	4.41	-	915.0
AHQ-2-8, 6200	K.LAMQEFM*ILPVGAANFR.E	1925.30752	2	1.18E-05	0.86	4.83	-	445.7
AHQ-2-7, 6999	K.LAMQEFMILPVGAANFR.E	1909.30812	2	5.14E-06	0.93	3.84	-	1006.0
AHQ-2-8, 6822 - 6895	K.LAMQEFMILPVGAANFR.E	1909.30812	2	4.77E-10	0.97	6.32	-	976.6
AHQ-2-8, 5830	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	7.17E-06	0.94	5.06	-	1195.4
AHQ-2-8, 6939 - 6951	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	3	2.98E-06	0.98	6.86	-	2364.9
AHQ-2-8, 6930 - 6938	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	2	9.56E-04	0.82	3.62	-	586.7
AHQ-2-7, 2017	K.TIAPALVSK.K	900.09769	1	9.31E-04	0.10	1.93	-	322.9
AHQ-2-8, 1940	K.TIAPALVSK.K	900.09769	1	1.29E-04	0.28	2.06	-	387.9
AHQ-2-7, 3504	K.VNQIGSVTESLQACK.L	1635.82159	2	4.54E-07	0.76	2.89	-	723.7
AHQ-2-13, 3808	K.VNQIGSVTESLQACK.L	1635.82159	2	3.20E-06	0.94	4.28	-	882.1
AHQ-2-7, 4755	R.YISPDQLADLYK.S	1426.59557	2	1.31E-08	0.85	3.33	-	603.2
AHQ-2-8, 4581 - 4589	R.YISPDQLADLYK.S	1426.59557	2	1.09E-06	0.93	3.80	-	826.2
gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act				2.22E-16	103.55	1210.34	56.40	280757.4
AHQ-2-5, 5131 - 5203	R.AEAGVPAEFSIWTR.E	1534.69735	2	5.58E-07	0.76	3.68	-	234.5
AHQ-2-5, 2252	K.AEISFEDR.K	967.01472	2	9.16E-04	0.91	2.80	-	1188.0
AHQ-2-5, 2355 - 2357	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.16E-11	0.96	4.65	-	1701.9
AHQ-2-7, 2319	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.87E-04	0.90	3.07	-	1419.9
AHQ-2-4, 2532 - 2533	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.49E-07	0.95	4.40	-	1340.0
AHQ-2-2, 2528 - 2552	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.71E-10	0.95	3.40	-	1472.1
AHQ-2-4, 2548	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	2.75E-07	0.53	2.94	-	178.1
AHQ-2-6, 2377	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.53E-08	0.95	3.79	-	1664.5
AHQ-2-1, 2872	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.53E-06	0.94	3.77	-	1182.4
AHQ-2-3, 2536	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	3.28E-06	0.28	2.69	-	218.7
AHQ-2-1, 2706 - 2777	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.15E-08	0.95	3.36	-	1626.9
AHQ-2-1, 2713 - 2717	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	6.94E-05	0.04	1.94	-	92.0
AHQ-2-3, 2523 - 2552	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.67E-06	0.92	3.65	-	1194.5
AHQ-2-14-, 3323 - 3363	K.AGNNMLLVGVHGPR.T	1435.68033	2	2.67E-06	0.87	3.70	-	717.4
AHQ-2-14, 3544 - 3614	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.47E-04	0.75	3.07	-	669.9
AHQ-2-14, 3761 - 3829	K.AGNNM*LLVGVHGPR.T	1451.67973	2	4.85E-06	0.70	2.70	-	624.2
AHQ-2-14-, 3032 - 3039	K.AGNNMLLVGVHGPR.T	1435.68033	2	7.32E-06	0.81	3.14	-	743.5
AHQ-2-13-, 2729	K.AGNNM*LLVGVHGPR.T	1451.67973	2	6.73E-05	0.80	3.08	-	887.0
AHQ-2-14, 4353	K.AGNNMLLVGVHGPR.T	1435.68033	2	1.34E-04	0.71	2.60	-	721.4
AHQ-2-14, 4314	K.AGNNMLLVGVHGPR.T	1435.68033	3	5.67E-07	0.89	3.58	-	1212.2
AHQ-2-14-, 2764	K.AGNNM*LLVGVHGPR.T	1451.67973	3	2.65E-07	0.81	3.22	-	1097.2
AHQ-2-14, 4233 - 4300	K.AGNNMLLVGVHGPR.T	1435.68033	2	2.16E-08	0.77	3.37	-	519.7
AHQ-2-14-, 2655 - 2733	K.AGNNM*LLVGVHGPR.T	1451.67973	2	9.38E-06	0.87	3.50	-	871.2
AHQ-2-14-, 3428 - 3499	K.AGNNMLLVGVHGPR.T	1435.68033	2	9.45E-06	0.75	2.77	-	714.0
AHQ-2-14-, 2652 - 2729	K.AGNNM*LLVGVHGPR.T	1451.67973	3	4.42E-05	0.83	3.60	-	1297.6
AHQ-2-14, 4046	K.AGNNMLLVGVHGPR.T	1435.68033	3	2.65E-07	0.93	4.03	-	1548.2
AHQ-2-4, 2188	K.AGVAPLQVK.V	883.07036	2	2.28E-05	0.78	2.73	-	615.6
AHQ-2-5, 1955	K.AGVAPLQVK.V	883.07036	2	8.19E-04	0.80	2.94	-	650.9
AHQ-2-2, 2157	K.AGVAPLQVK.V	883.07036	2	1.04E-05	0.79	2.76	-	596.0
AHQ-2-3, 2169 - 2172	K.AGVAPLQVK.V	883.07036	2	2.44E-04	0.68	2.82	-	405.0
AHQ-2-1, 2381	K.AGVAPLQVK.V	883.07036	2	1.89E-04	0.86	2.80	-	716.7
AHQ-2-2, 5194	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	2	4.81E-04	0.50	2.90	-	284.0
AHQ-2-2, 7677 - 7757	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	2	9.54E-04	0.92	3.60	-	1246.2

AHQ-2-1, 7428	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	1.62E-04	0.72	3.31	-	836.9
AHQ-2-1, 7310 - 7372	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	1.21E-05	0.96	5.09	-	1658.1
AHQ-2-4, 2514 - 2516	K.AHVVPCFDASK.V	1232.39073	2	1.10E-05	0.63	2.55	-	434.6
AHQ-2-3, 2500	K.AHVVPCFDASK.V	1232.39073	2	1.50E-04	0.63	2.54	-	690.8
AHQ-2-2, 2509 - 2510	K.AHVVPCFDASK.V	1232.39073	2	3.86E-06	0.89	3.10	-	922.3
AHQ-2-5, 2324	K.AHVVPCFDASK.V	1232.39073	2	8.49E-06	0.82	2.84	-	648.6
AHQ-2-1, 2728 - 2785	K.AHVVPCFDASK.V	1232.39073	2	4.24E-08	0.76	2.63	-	647.1
AHQ-2-4, 6490 - 6572	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.29E-09	0.91	4.82	-	631.9
AHQ-2-9, 6432	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.29E-05	0.90	4.68	-	643.4
AHQ-2-7, 6243 - 6321	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.41E-07	0.94	5.65	-	604.5
AHQ-2-2, 6512 - 6580	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.15E-12	0.93	5.42	-	624.9
AHQ-2-3, 6587 - 6661	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.30E-11	0.94	5.30	-	815.1
AHQ-2-3, 6429 - 6499	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.69E-11	0.89	4.61	-	682.8
AHQ-2-3, 6312 - 6356	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.73E-04	0.70	3.31	-	665.7
AHQ-2-10, 5778	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.16E-08	0.88	4.20	-	698.6
AHQ-2-2, 6648 - 6720	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.22E-16	0.95	5.78	-	774.1
AHQ-2-1, 6448 - 6516	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.38E-13	0.95	5.85	-	920.3
AHQ-2-1, 6357	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.49E-08	0.84	3.92	-	773.0
AHQ-2-1, 6222 - 6285	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.24E-06	0.85	4.24	-	623.3
AHQ-2-2, 6362 - 6444	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.02E-04	0.93	5.29	-	756.6
AHQ-2-8, 6096 - 6159	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.52E-08	0.84	3.99	-	541.6
AHQ-2-5, 6205 - 6276	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.19E-08	0.85	4.34	-	544.5
AHQ-2-5, 6473 - 6539	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.57E-09	0.90	4.60	-	572.6
AHQ-2-5, 6575	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.30E-07	0.75	4.07	-	407.0
AHQ-2-9, 6288	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.35E-09	0.92	5.28	-	648.2
AHQ-2-2, 1474	R.ALTQTGGPHVK.A	1109.26067	2	3.36E-04	0.85	3.29	-	750.9
AHQ-2-9, 3036	R.ANLPQSFQVDTSK.A	1435.56409	2	3.28E-04	0.44	2.57	-	299.5
AHQ-2-3, 3253 - 3265	R.ANLPQSFQVDTSK.A	1435.56409	2	5.58E-05	0.70	2.54	-	544.4
AHQ-2-3, 3507	R.ANLPQSFQVDTSK.A	1435.56409	1	2.45E-06	0.45	2.36	-	520.4
AHQ-2-1, 3608 - 3609	R.ANLPQSFQVDTSK.A	1435.56409	2	9.36E-06	0.70	3.39	-	364.9
AHQ-2-7, 2969	R.ANLPQSFQVDTSK.A	1435.56409	1	9.71E-06	0.28	2.68	-	272.2
AHQ-2-5, 3068	R.ANLPQSFQVDTSK.A	1435.56409	1	9.98E-08	0.65	3.02	-	393.1
AHQ-2-6, 3245	R.ANLPQSFQVDTSK.A	1435.56409	1	3.96E-04	0.33	2.27	-	376.8
AHQ-2-4, 3306	R.ANLPQSFQVDTSK.A	1435.56409	1	4.29E-08	0.61	2.97	-	349.3
AHQ-2-8, 2863 - 2878	R.ANLPQSFQVDTSK.A	1435.56409	2	1.09E-08	0.89	3.62	-	592.8
AHQ-2-5, 3051	R.ANLPQSFQVDTSK.A	1435.56409	2	4.59E-09	0.91	3.89	-	540.0
AHQ-2-1, 3330 - 3412	R.ANLPQSFQVDTSK.A	1435.56409	2	1.09E-04	0.88	3.27	-	754.4
AHQ-2-7, 2961 - 2984	R.ANLPQSFQVDTSK.A	1435.56409	2	4.74E-08	0.84	3.42	-	514.8
AHQ-2-4, 3284	R.ANLPQSFQVDTSK.A	1435.56409	2	3.29E-10	0.82	3.11	-	549.2
AHQ-2-6, 3042	R.ANLPQSFQVDTSK.A	1435.56409	2	3.09E-08	0.90	3.55	-	675.7
AHQ-2-2, 3264	R.ANLPQSFQVDTSK.A	1435.56409	1	2.49E-07	0.65	3.21	-	380.1
AHQ-2-1, 3450	R.ANLPQSFQVDTSK.A	1435.56409	1	5.65E-04	0.26	2.49	-	358.9
AHQ-2-2, 4690 - 4760	R.ANLPQSFQVDTSKAGVAPLQVK.V	2299.61185	2	3.36E-05	0.91	4.02	-	1055.9
AHQ-2-1, 3568 - 3626	R.APSVANVGSHCDLSLK.I	1656.84249	2	9.59E-05	0.83	3.44	-	507.2
AHQ-2-6, 3082	R.APSVANVGSHCDLSLK.I	1656.84249	2	1.65E-05	0.91	4.25	-	704.6
AHQ-2-5, 3087 - 3101	R.APSVANVGSHCDLSLK.I	1656.84249	2	2.22E-04	0.95	5.01	-	846.6
AHQ-2-1, 6116 - 6185	K.ASGPGLNTTGVPASLPVEFTIDAK.D	2343.61826	3	6.89E-05	0.83	3.98	-	622.6
AHQ-2-5, 1505	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	7.44E-05	0.88	3.71	-	668.2
AHQ-2-1, 1946	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	5.65E-07	0.95	4.74	-	945.6
AHQ-2-2, 3648 - 3718	R.AWGPGLEGGVVGK.S	1227.39403	2	3.21E-07	0.92	3.74	-	862.7
AHQ-2-1, 3792 - 3862	R.AWGPGLEGGVVGK.S	1227.39403	2	4.54E-04	0.94	4.10	-	990.8
AHQ-2-6, 3266 - 3341	R.AWGPGLEGGVVGK.S	1227.39403	2	1.19E-04	0.81	3.18	-	637.2
AHQ-2-6, 3351	R.AWGPGLEGGVVGK.S	1227.39403	2	1.52E-06	0.81	3.13	-	774.7
AHQ-2-3, 3623	R.AWGPGLEGGVVGK.S	1227.39403	2	9.20E-05	0.87	3.12	-	763.3
AHQ-2-7, 3257	R.AWGPGLEGGVVGK.S	1227.39403	2	1.42E-06	0.82	2.91	-	770.1
AHQ-2-2, 3653 - 3720	R.AWGPGLEGGVVGK.S	1227.39403	1	7.89E-06	0.73	2.86	-	676.9
AHQ-2-4, 3644	R.AWGPGLEGGVVGK.S	1227.39403	2	4.18E-05	0.95	4.11	-	1086.8
AHQ-2-5, 3352	R.AWGPGLEGGVVGK.S	1227.39403	2	2.17E-05	0.86	3.29	-	846.1
AHQ-2-3, 3171 - 3188	R.AYGPGIEPTGNMVK.K	1434.64274	2	5.52E-06	0.63	2.90	-	500.9
AHQ-2-1, 2692 - 2725	R.AYGPGIEPTGNM*VK.K	1450.64214	2	1.62E-04	0.52	2.51	-	425.2
AHQ-2-7, 2323 - 2372	R.AYGPGIEPTGNM*VK.K	1450.64214	2	3.38E-04	0.33	2.76	-	299.7
AHQ-2-7, 2837	R.AYGPGIEPTGNMVK.K	1434.64274	2	8.73E-04	0.57	2.54	-	435.9
AHQ-2-2, 3470 - 3541	R.AYGPGIEPTGNMVK.K	1434.64274	1	5.37E-05	0.31	2.81	-	380.2
AHQ-2-5, 3143 - 3221	R.AYGPGIEPTGNMVK.K	1434.64274	2	3.47E-05	0.81	2.95	-	544.9
AHQ-2-5, 2916	R.AYGPGIEPTGNMVK.K	1434.64274	2	6.17E-06	0.83	3.51	-	473.7
AHQ-2-4, 3105 - 3178	R.AYGPGIEPTGNMVK.K	1434.64274	1	2.92E-05	0.33	2.55	-	333.3
AHQ-2-6, 2883 - 2931	R.AYGPGIEPTGNMVK.K	1434.64274	2	7.77E-05	0.87	3.27	-	654.4
AHQ-2-4, 3372 - 3444	R.AYGPGIEPTGNMVK.K	1434.64274	2	9.57E-04	0.59	3.03	-	375.5
AHQ-2-1, 3429 - 3508	R.AYGPGIEPTGNMVK.K	1434.64274	2	4.76E-04	0.64	2.69	-	479.3
AHQ-2-2, 2529 - 2538	R.AYGPGIEPTGNM*VK.K	1450.64214	2	9.11E-04	0.62	2.97	-	334.3
AHQ-2-2, 2697 - 2742	R.AYGPGIEPTGNM*VK.K	1450.64214	2	8.04E-07	0.91	3.94	-	614.5
AHQ-2-3, 3368 - 3443	R.AYGPGIEPTGNMVK.K	1434.64274	2	3.20E-05	0.80	3.36	-	548.3
AHQ-2-4, 6474 - 6545	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.94E-05	0.86	3.65	-	622.8
AHQ-2-3, 6399 - 6467	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	3.44E-06	0.94	4.81	-	665.4
AHQ-2-2, 6433 - 6445	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.89E-06	0.93	4.23	-	806.6
AHQ-2-5, 6304 - 6323	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.15E-04	0.82	4.07	-	819.6
AHQ-2-2, 6516	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	8.39E-08	0.90	3.66	-	673.9
AHQ-2-6, 6154	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.21E-07	0.77	3.32	-	452.4
AHQ-2-2, 6281 - 6292	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.01E-07	0.96	4.71	-	947.8
AHQ-2-2, 6150	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	6.27E-05	0.82	3.27	-	576.3
AHQ-2-3, 6412	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.10E-09	0.97	5.08	-	1684.2
AHQ-2-1, 6328 - 6361	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.23E-05	0.93	4.35	-	684.0
AHQ-2-3, 6424 - 6500	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.08E-07	0.85	3.74	-	458.6
AHQ-2-3, 6489	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.72E-07	0.92	4.31	-	685.1
AHQ-2-1, 6149	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	9.16E-06	0.80	3.06	-	621.9
AHQ-2-1, 6338	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	3.14E-09	0.95	4.59	-	1372.4
AHQ-2-2, 6452	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.10E-07	0.95	4.63	-	1573.3
AHQ-2-3, 6241	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.68E-06	0.73	3.00	-	528.5
AHQ-2-2, 7320 - 7393	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	1.02E-05	0.73	3.62	-	422.3
AHQ-2-2, 6725 - 6800	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	2.39E-05	0.77	3.87	-	421.9
AHQ-2-3, 6629 - 6711	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	5.55E-06	0.85	4.44	-	419.8
AHQ-2-3, 7272 - 7345	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	7.21E-05	0.65	3.20	-	374.6
AHQ-2-1, 6501 - 6576	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	1.05E-04	0.74	3.80	-	540.9
AHQ-2-2, 2928 - 2944	K.CSGPGLSPGMVR.A	1219.41699	2	9.55E-07	0.77	3.09	-	556.5
AHQ-2-5, 2755	K.CSGPGLSPGMVR.A	1219.41699	2	8.47E-06	0.81	2.88	-	805.1
AHQ-2-3, 2932 - 2935	K.CSGPGLSPGMVR.A	1219.41699	2	1.18E-05	0.57	2.59	-	448.5
AHQ-2-4, 5537 - 5544	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	1.27E-11	0.97	5.17	-	1228.8
AHQ-2-4, 5000 - 5036	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	1.21E-06	0.88	4.37	-	544.2
AHQ-2-1, 5097	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	3.92E-05	0.68	2.59	-	405.2
AHQ-2-1, 5017 - 5088	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	4.19E-07	0.94	5.30	-	546.6
AHQ-2-5, 5227 - 5235	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	2.44E-10	0.97	5.21	-	1265.8
AHQ-2-3, 5009 - 5031	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	2.92E-05	0.87	4.61	-	402.5
AHQ-2-5, 5224 - 5244	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	8.83E-06	0.89	4.06	-	707.6
AHQ-2-2, 5517 - 5589	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	3.84E-13	0.97	5.33	-	1344.0
AHQ-2-2, 5034	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	8.03E-05	0.86	3.29	-	825.0
AHQ-2-1, 5590 - 5661	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	8.19E-10	0.82	3.59	-	709.9
AHQ-2-5, 4732 - 4743	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	1.25E-05	0.84	3.99	-	391.0

AHQ-2-3, 5015 - 5027	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	9.01E-07	0.87	3.85	-	524.4
AHQ-2-3, 4681 - 4721	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	1.94E-05	0.93	3.87	-	1128.1
AHQ-2-1, 4721	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	4.81E-07	0.93	4.01	-	1042.7
AHQ-2-5, 4439	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	1.16E-04	0.89	3.64	-	981.3
AHQ-2-1, 4117	R.DAEM*PATEKDLAEDAPWK.K	2034.18987	2	7.35E-06	0.90	3.84	-	696.0
AHQ-2-2, 4186	R.DAEMPATEKDLAEDAPWKK.I	2146.36338	3	3.92E-09	0.78	3.71	-	535.7
AHQ-2-13, 3959	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	2.37E-04	0.44	2.55	-	535.1
AHQ-2-8, 3779	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.34E-05	0.71	3.03	-	841.9
AHQ-2-1, 4118 - 4189	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	5.63E-06	0.96	4.83	-	1384.7
AHQ-2-3, 4113	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	3.53E-05	0.94	4.97	-	1181.7
AHQ-2-2, 4170	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	6.32E-04	0.85	3.44	-	962.8
AHQ-2-12, 3971	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	6.02E-05	0.87	3.55	-	964.0
AHQ-2-4, 4076 - 4146	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	3.60E-05	0.81	3.32	-	849.9
AHQ-2-1, 5048	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	4.99E-07	0.88	3.46	-	1050.1
AHQ-2-6, 4102 - 4117	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.43E-05	0.93	4.08	-	1224.0
AHQ-2-3, 4456 - 4527	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.89E-06	0.95	4.46	-	1280.1
AHQ-2-3, 4461 - 4469	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	7.81E-10	0.93	4.16	-	1280.4
AHQ-2-3, 4625 - 4699	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.81E-06	0.95	4.79	-	1195.6
AHQ-2-4, 4426 - 4508	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.34E-08	0.96	4.95	-	1259.6
AHQ-2-1, 4777 - 4796	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.00E-06	0.94	4.48	-	1190.5
AHQ-2-2, 4612 - 4680	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.48E-10	0.94	4.44	-	1099.8
AHQ-2-2, 4500 - 4569	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	7.12E-09	0.94	4.78	-	1264.5
AHQ-2-2, 4882	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.02E-05	0.87	3.78	-	972.3
AHQ-2-11, 4108	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.70E-07	0.96	4.85	-	1412.9
AHQ-2-2, 4470 - 4541	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.37E-07	0.94	4.09	-	1330.8
AHQ-2-1, 4513 - 4548	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.67E-07	0.90	3.72	-	1021.9
AHQ-2-5, 4185 - 4188	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.90E-09	0.94	4.32	-	1257.7
AHQ-2-7, 4065	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.65E-05	0.90	4.09	-	980.6
AHQ-2-8, 3912	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	9.16E-06	0.89	3.73	-	1125.5
AHQ-2-1, 4553 - 4626	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	2.94E-08	0.93	3.92	-	1298.3
AHQ-2-2, 4748 - 4754	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.48E-06	0.93	4.35	-	1175.9
AHQ-2-5, 4305	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	9.04E-06	0.73	2.84	-	847.7
AHQ-2-4, 4448	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	4.79E-08	0.90	3.84	-	954.6
AHQ-2-10, 3935	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.58E-05	0.86	3.89	-	822.5
AHQ-2-1, 4616	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.59E-06	0.88	3.80	-	968.6
AHQ-2-5, 4235	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.60E-04	0.77	2.99	-	955.0
AHQ-2-5, 4879	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.79E-06	0.58	2.83	-	958.6
AHQ-2-5, 4739 - 4809	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	2.52E-05	0.70	3.36	-	708.8
AHQ-2-1, 4688	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.16E-08	0.91	3.51	-	1265.6
AHQ-2-2, 1825	R.DAPQDFHPDR.V	1198.22650	2	4.10E-07	0.54	2.64	-	446.9
AHQ-2-1, 1973 - 2034	R.DAPQDFHPDR.V	1198.22650	2	2.20E-05	0.56	2.68	-	455.6
AHQ-2-3, 1695 - 1760	R.DAPQDFHPDR.V	1198.22650	2	9.67E-08	0.59	2.51	-	680.5
AHQ-2-2, 1692 - 1756	R.DAPQDFHPDR.V	1198.22650	2	8.83E-06	0.46	2.67	-	537.5
AHQ-2-5, 5060 - 5129	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.84E-04	0.88	4.23	-	657.7
AHQ-2-5, 4947 - 4989	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.50E-08	0.79	4.11	-	410.4
AHQ-2-4, 4992 - 5060	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	5.35E-04	0.89	4.31	-	567.1
AHQ-2-7, 5053	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.89E-05	0.79	3.83	-	405.8
AHQ-2-6, 4814 - 4891	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	4.97E-06	0.93	4.94	-	756.0
AHQ-2-10, 4536	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	5.36E-04	0.86	3.88	-	492.0
AHQ-2-14-, 2331	K.DKGEYTLVVK.W	1152.32223	1	1.54E-04	0.20	2.35	-	405.1
AHQ-2-14-, 2345	K.DKGEYTLVVK.W	1152.32223	1	3.40E-04	0.43	2.46	-	503.5
AHQ-2-14, 3368	K.DKGEYTLVVK.W	1152.32223	2	1.13E-04	0.72	2.81	-	502.2
AHQ-2-5, 2135 - 2139	K.DKGEYTLVVK.W	1152.32223	2	7.09E-06	0.65	2.62	-	457.8
AHQ-2-14, 3138 - 3424	K.DKGEYTLVVK.W	1152.32223	1	8.23E-04	0.17	2.19	-	402.7
AHQ-2-14-, 2328 - 2397	K.DKGEYTLVVK.W	1152.32223	2	3.59E-06	0.79	2.86	-	700.8
AHQ-2-14, 3248 - 3312	K.DKGEYTLVVK.W	1152.32223	2	1.97E-06	0.62	2.66	-	439.4
AHQ-2-13-, 2415	K.DKGEYTLVVK.W	1152.32223	1	5.96E-04	0.12	1.81	-	386.1
AHQ-2-4, 2348	K.DKGEYTLVVK.W	1152.32223	1	7.57E-07	0.54	2.80	-	511.9
AHQ-2-14, 3588 - 3636	K.DKGEYTLVVK.W	1152.32223	2	4.58E-05	0.61	2.52	-	437.9
AHQ-2-14, 3630	K.DKGEYTLVVK.W	1152.32223	1	8.66E-06	0.50	2.52	-	627.0
AHQ-2-1, 3384	K.DNGNGTYSCSYVPR.K	1591.64109	2	4.69E-06	0.83	3.04	-	909.4
AHQ-2-4, 3080	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.43E-06	0.94	4.43	-	947.6
AHQ-2-4, 3000 - 3008	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	2.91E-04	0.66	3.03	-	403.7
AHQ-2-6, 2786	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	9.98E-05	0.81	3.06	-	732.7
AHQ-2-2, 3246	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	7.81E-05	0.93	4.15	-	1072.5
AHQ-2-4, 2941 - 3012	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.47E-06	0.92	4.05	-	904.4
AHQ-2-2, 3154	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.02E-06	0.89	3.55	-	886.0
AHQ-2-2, 3028 - 3084	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.93E-10	0.97	4.93	-	1351.3
AHQ-2-1, 3292 - 3365	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	4.20E-06	0.72	3.02	-	411.4
AHQ-2-2, 2942 - 3016	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.19E-04	0.89	3.53	-	784.8
AHQ-2-4, 3272	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	9.85E-05	0.89	3.51	-	1067.7
AHQ-2-3, 3267 - 3344	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	4.49E-05	0.91	3.93	-	605.8
AHQ-2-3, 3083	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.47E-08	0.96	4.87	-	1134.3
AHQ-2-1, 3157 - 3224	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	4.96E-07	0.95	4.42	-	1247.8
AHQ-2-3, 2940 - 3012	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.06E-05	0.93	3.86	-	986.5
AHQ-2-9, 3110	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	2.72E-05	0.59	3.04	-	394.7
AHQ-2-7, 3109	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.02E-05	0.92	2.94	-	1743.7
AHQ-2-1, 3513 - 3517	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.15E-06	0.94	4.38	-	1098.0
AHQ-2-6, 3127	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	1.54E-08	0.65	3.36	-	315.9
AHQ-2-5, 3172	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	3.55E-08	0.79	3.42	-	412.3
AHQ-2-5, 3164 - 3305	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	6.87E-04	0.08	1.97	-	245.7
AHQ-2-4, 3401 - 3408	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.97E-05	0.96	4.50	-	1637.2
AHQ-2-2, 3030	R.EATTEFSVDAR.A	1226.27493	2	5.40E-04	0.75	2.71	-	648.6
AHQ-2-2, 2540 - 2609	R.EATTEFSVDAR.A	1226.27493	2	5.16E-06	0.87	3.42	-	807.3
AHQ-2-5, 6391 - 6456	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.79E-06	0.88	4.05	-	733.2
AHQ-2-3, 6483 - 6552	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.90E-08	0.96	6.30	-	690.4
AHQ-2-2, 6493 - 6560	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.08E-10	0.96	6.06	-	948.7
AHQ-2-2, 7241	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	9.94E-04	0.59	3.19	-	416.7
AHQ-2-3, 6619 - 6688	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.70E-10	0.96	6.19	-	939.1
AHQ-2-1, 6432 - 6512	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.68E-05	0.95	6.15	-	695.3
AHQ-2-5, 6523	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.96E-09	0.94	5.61	-	687.7
AHQ-2-6, 6301 - 6303	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	5.73E-07	0.93	5.23	-	763.8
AHQ-2-2, 6696 - 6765	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.11E-08	0.94	5.18	-	826.6
AHQ-2-1, 6572 - 6646	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.62E-07	0.90	4.73	-	586.2
AHQ-2-2, 6593 - 6660	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.01E-07	0.94	5.56	-	824.0
AHQ-2-4, 6696 - 6768	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.27E-08	0.92	5.34	-	520.5
AHQ-2-4, 6552 - 6628	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.29E-09	0.94	5.96	-	665.1
AHQ-2-1, 5301 - 5302	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	5.53E-07	0.96	4.81	-	1682.3
AHQ-2-2, 4976	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.88E-07	0.86	3.76	-	739.5
AHQ-2-1, 5230 - 5304	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	6.07E-08	0.93	4.08	-	1145.4
AHQ-2-2, 5252 - 5280	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	8.43E-05	0.92	4.02	-	1190.9
AHQ-2-8, 4773 - 4845	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.90E-06	0.93	4.23	-	778.4
AHQ-2-1, 5332	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.78E-05	0.84	3.68	-	846.9
AHQ-2-4, 5244 - 5313	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.42E-07	0.90	3.70	-	1145.3
AHQ-2-5, 5068	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.15E-07	0.93	4.14	-	1047.5
AHQ-2-6, 4962	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.08E-08	0.78	3.75	-	734.2
AHQ-2-7, 4956	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	7.79E-09	0.93	4.45	-	1073.8

AHQ-2-9, 4978	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	7.90E-05	0.82	3.24	-	719.2
AHQ-2-2, 5348 - 5352	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.88E-10	0.94	4.08	-	1321.0
AHQ-2-1, 5368	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.27E-05	0.94	4.37	-	1038.3
AHQ-2-3, 5220 - 5303	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.62E-08	0.96	4.93	-	1300.6
AHQ-2-3, 4032 - 4033	R.ENGVYLIDVK.F	1150.30633	1	2.63E-06	0.18	2.34	-	167.0
AHQ-2-6, 3781	R.ENGVYLIDVK.F	1150.30633	1	4.46E-04	0.14	1.90	-	264.5
AHQ-2-5, 3847	R.ENGVYLIDVK.F	1150.30633	1	1.33E-04	0.21	2.12	-	286.1
AHQ-2-5, 3701	R.ENGVYLIDVK.F	1150.30633	1	1.92E-04	0.16	2.28	-	290.0
AHQ-2-5, 3241	K.FADQHVPGSPFSVK.V	1516.68203	2	4.52E-04	0.48	2.57	-	314.7
AHQ-2-1, 3616 - 3689	K.FADQHVPGSPFSVK.V	1516.68203	2	3.00E-05	0.41	2.65	-	301.3
AHQ-2-13-, 3417	K.FADQHVPGSPFSVK.V	1516.68203	2	1.01E-05	0.73	2.88	-	470.5
AHQ-2-7, 2991	K.FADQHVPGSPFSVK.V	1516.68203	2	2.19E-06	0.53	2.86	-	323.6
AHQ-2-2, 3466	K.FADQHVPGSPFSVK.V	1516.68203	2	1.98E-06	0.87	3.41	-	642.4
AHQ-2-8, 2872	K.FADQHVPGSPFSVK.V	1516.68203	3	9.48E-06	0.90	3.72	-	1045.0
AHQ-2-1, 3628	K.FADQHVPGSPFSVK.V	1516.68203	3	1.25E-05	0.92	3.64	-	1356.9
AHQ-2-6, 3107	K.FADQHVPGSPFSVK.V	1516.68203	3	6.08E-05	0.92	4.03	-	1305.6
AHQ-2-6, 3106	K.FADQHVPGSPFSVK.V	1516.68203	2	2.35E-07	0.86	3.70	-	556.7
AHQ-2-5, 3121 - 3131	K.FADQHVPGSPFSVK.V	1516.68203	3	7.67E-08	0.95	4.41	-	1396.2
AHQ-2-3, 3441	K.FADQHVPGSPFSVK.V	1516.68203	2	2.63E-07	0.88	3.75	-	519.6
AHQ-2-5, 3103 - 3171	K.FADQHVPGSPFSVK.V	1516.68203	2	1.64E-05	0.79	3.39	-	500.4
AHQ-2-1, 5800	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.14E-08	0.96	5.38	-	1040.9
AHQ-2-1, 5724 - 5788	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.94E-08	0.93	5.09	-	782.9
AHQ-2-1, 5856 - 5921	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.15E-08	0.94	5.41	-	1053.1
AHQ-2-1, 5910	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.02E-05	0.95	5.22	-	720.7
AHQ-2-8, 5103	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.15E-06	0.97	5.55	-	1164.1
AHQ-2-2, 5542	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.29E-04	0.86	3.97	-	682.1
AHQ-2-11, 5181	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.04E-04	0.88	4.18	-	627.3
AHQ-2-5, 5392	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.93E-04	0.87	4.02	-	620.8
AHQ-2-11, 5222	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	5.42E-06	0.94	4.33	-	957.7
AHQ-2-5, 5407	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	5.02E-07	0.94	4.80	-	916.4
AHQ-2-2, 5652 - 5720	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.50E-09	0.93	5.16	-	751.4
AHQ-2-2, 5654 - 5669	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.50E-08	0.96	5.63	-	901.3
AHQ-2-8, 5088 - 5107	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.39E-05	0.93	4.65	-	997.4
AHQ-2-9, 5335 - 5360	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	7.53E-06	0.91	4.61	-	697.5
AHQ-2-2, 5740 - 5808	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	9.03E-07	0.95	5.52	-	846.9
AHQ-2-6, 5346	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.36E-08	0.92	4.42	-	924.0
AHQ-2-13-, 5407 - 5421	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.66E-10	0.93	4.94	-	788.9
AHQ-2-2, 5789 - 5856	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.38E-09	0.91	4.42	-	956.6
AHQ-2-4, 5672 - 5746	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.02E-05	0.96	5.57	-	1019.1
AHQ-2-4, 5665 - 5693	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.91E-06	0.92	5.13	-	658.6
AHQ-2-2, 5870 - 5876	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	7.58E-10	0.98	6.88	-	1290.0
AHQ-2-3, 5640 - 5711	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	6.04E-05	0.96	5.18	-	1354.5
AHQ-2-3, 5656 - 5723	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.01E-09	0.93	4.77	-	974.7
AHQ-2-12, 5453	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.14E-05	0.95	4.89	-	937.7
AHQ-2-3, 5729	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.10E-06	0.97	6.01	-	1008.8
AHQ-2-3, 5779 - 5847	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	6.70E-11	0.95	5.00	-	899.9
AHQ-2-12, 5443	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.59E-06	0.87	3.80	-	916.1
AHQ-2-13, 5328	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	8.21E-05	0.66	2.98	-	575.9
AHQ-2-7, 5277 - 5283	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.77E-06	0.93	4.86	-	941.1
AHQ-2-7, 5288	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.64E-06	0.95	5.13	-	919.1
AHQ-2-5, 5075 - 5077	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	2.29E-05	0.93	4.69	-	655.3
AHQ-2-5, 3219	K.FNGTHIPGSPFK.I	1302.46259	2	2.08E-05	0.84	3.21	-	665.6
AHQ-2-5, 3491 - 3495	K.FNGTHIPGSPFK.I	1302.46259	2	4.58E-06	0.85	3.29	-	708.1
AHQ-2-3, 3829	K.FNGTHIPGSPFK.I	1302.46259	2	1.47E-04	0.78	3.26	-	449.1
AHQ-2-6, 3362	K.FNGTHIPGSPFK.I	1302.46259	2	5.08E-04	0.80	2.85	-	724.4
AHQ-2-1, 3953	K.FNGTHIPGSPFK.I	1302.46259	2	2.79E-04	0.61	2.55	-	536.1
AHQ-2-5, 3672 - 3677	K.FNGTHIPGSPFK.I	1302.46259	1	1.33E-04	0.37	2.04	-	392.1
AHQ-2-3, 2927 - 2933	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.66E-11	0.92	3.84	-	777.6
AHQ-2-7, 2500 - 2572	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.39E-08	0.89	3.84	-	692.7
AHQ-2-1, 2470	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	2.92E-04	0.73	2.64	-	430.2
AHQ-2-2, 2912	R.FVPAEMGTHTVSVK.Y	1503.74821	2	2.71E-04	0.77	2.51	-	692.7
AHQ-2-5, 2617	R.FVPAEMGTHTVSVK.Y	1503.74821	2	4.49E-11	0.89	3.03	-	866.0
AHQ-2-1, 3113	R.FVPAEMGTHTVSVK.Y	1503.74821	2	9.05E-06	0.76	2.90	-	503.3
AHQ-2-2, 6430	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	6.27E-04	0.60	3.11	-	266.2
AHQ-2-3, 6952 - 7019	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	3.94E-04	0.76	3.98	-	571.5
AHQ-2-2, 6278 - 6358	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	2.12E-05	0.83	4.27	-	723.2
AHQ-2-2, 7057 - 7125	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	9.87E-05	0.93	4.32	-	845.3
AHQ-2-2, 7197 - 7273	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	1.11E-04	0.72	3.42	-	437.7
AHQ-2-2, 3341 - 3412	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.32E-06	0.87	3.48	-	806.2
AHQ-2-3, 3529	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	7.34E-05	0.69	2.96	-	550.6
AHQ-2-2, 3254 - 3325	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.31E-06	0.88	3.80	-	731.5
AHQ-2-2, 3768 - 3784	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	5.19E-05	0.80	2.84	-	929.0
AHQ-2-5, 3085	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	6.92E-06	0.93	3.91	-	1057.5
AHQ-2-1, 3552 - 3553	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.04E-04	0.85	3.46	-	783.2
AHQ-2-2, 3480 - 3553	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.28E-05	0.85	3.85	-	828.6
AHQ-2-4, 3344 - 3386	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.21E-04	0.65	2.89	-	544.7
AHQ-2-5, 3176	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.97E-05	0.70	3.14	-	692.2
AHQ-2-8, 2875	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	4.31E-05	0.73	3.05	-	696.8
AHQ-2-1, 3410 - 3481	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.40E-04	0.89	3.58	-	803.6
AHQ-2-3, 3327 - 3401	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	7.25E-08	0.94	4.87	-	746.2
AHQ-2-6, 3078 - 3085	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.90E-05	0.83	3.47	-	693.9
AHQ-2-2, 3597	K.GKLDVQFSGLTK.G	1293.49392	2	1.67E-04	0.91	3.59	-	860.0
AHQ-2-2, 3286	K.GKLDVQFSGLTK.G	1293.49392	2	6.02E-05	0.95	3.82	-	1381.9
AHQ-2-2, 3232 - 3374	K.GKLDVQFSGLTK.G	1293.49392	1	3.13E-06	0.59	3.04	-	432.3
AHQ-2-2, 3284	K.GKLDVQFSGLTK.G	1293.49392	2	5.54E-05	0.96	4.08	-	1520.9
AHQ-2-4, 3298 - 3314	K.GKLDVQFSGLTK.G	1293.49392	2	5.44E-04	0.91	3.50	-	930.5
AHQ-2-3, 5084 - 5152	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.14E-08	0.98	6.64	-	1294.7
AHQ-2-1, 5034 - 5105	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	3.50E-06	0.73	3.47	-	408.8
AHQ-2-1, 5168 - 5244	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.85E-10	0.96	5.42	-	1120.9
AHQ-2-2, 5220 - 5293	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.94E-06	0.97	5.81	-	1390.9
AHQ-2-1, 6676 - 6678	K.GLVEPVDVVDNADGTQTVNYVPSREGPYSISVLYGDEEVPR.S	4437.77937	3	1.24E-10	0.95	5.53	-	900.3
AHQ-2-1, 2292 - 2368	K.GTVEPQLEAR.G	1100.20741	2	1.36E-05	0.72	2.60	-	504.5
AHQ-2-3, 2124	K.GTVEPQLEAR.G	1100.20741	2	3.22E-04	0.82	3.08	-	525.7
AHQ-2-2, 2116 - 2132	K.GTVEPQLEAR.G	1100.20741	2	8.78E-05	0.84	3.05	-	585.1
AHQ-2-6, 1925 - 1929	K.GTVEPQLEAR.G	1100.20741	2	4.16E-05	0.81	3.26	-	528.6
AHQ-2-5, 1891 - 1907	K.GTVEPQLEAR.G	1100.20741	2	9.54E-04	0.76	2.58	-	711.8
AHQ-2-2, 5628 - 5629	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	1.19E-06	0.98	6.08	-	1290.8
AHQ-2-1, 5388	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	1.58E-04	0.71	3.83	-	455.4
AHQ-2-3, 5327	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	9.24E-05	0.93	4.12	-	1004.9
AHQ-2-2, 5248	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	1.40E-05	0.79	3.74	-	716.5
AHQ-2-5, 4905	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	6.82E-05	0.96	4.70	-	1356.6
AHQ-2-2, 5849	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	3.14E-09	0.94	4.56	-	915.7
AHQ-2-3, 5599 - 5600	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	7.04E-08	0.98	5.84	-	1651.9
AHQ-2-4, 5184 - 5185	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.82E-04	0.93	4.23	-	1020.9
AHQ-2-1, 5778 - 5784	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	2.67E-04	0.98	6.37	-	1163.6
AHQ-2-2, 5333	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.96E-05	0.89	3.35	-	953.5
AHQ-2-3, 5215 - 5255	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	8.70E-04	0.96	4.70	-	1282.0

AHQ-2-5, 5308	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	6.34E-05	0.98	6.16	-	1344.8
AHQ-2-3, 5236	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	2.48E-04	0.67	3.29	-	655.8
AHQ-2-2, 5237 - 5264	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	3.22E-07	0.97	5.67	-	1275.1
AHQ-2-4, 5622	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	1.03E-07	0.95	4.49	-	994.6
AHQ-2-11, 3970	R.IANLQTDLSDGLR.L	1416.56231	2	5.20E-07	0.87	3.31	-	798.9
AHQ-2-3, 3897 - 3907	R.IANLQTDLSDGLR.L	1416.56231	2	5.18E-06	0.93	4.04	-	981.2
AHQ-2-1, 4405 - 4472	R.IANLQTDLSDGLR.L	1416.56231	2	7.47E-06	0.94	4.38	-	978.6
AHQ-2-5, 3989 - 4015	R.IANLQTDLSDGLR.L	1416.56231	2	9.29E-06	0.94	4.04	-	1172.5
AHQ-2-2, 3920	R.IANLQTDLSDGLR.L	1416.56231	2	7.16E-07	0.97	4.23	-	1657.7
AHQ-2-2, 4008	R.IANLQTDLSDGLR.L	1416.56231	2	3.06E-06	0.95	4.83	-	990.2
AHQ-2-3, 3983	R.IANLQTDLSDGLR.L	1416.56231	2	1.01E-05	0.94	4.69	-	838.1
AHQ-2-12, 4119	R.IANLQTDLSDGLR.L	1416.56231	2	1.18E-07	0.94	4.77	-	790.4
AHQ-2-2, 4089 - 4162	R.IANLQTDLSDGLR.L	1416.56231	2	4.43E-06	0.74	2.59	-	835.6
AHQ-2-7, 3919 - 3935	R.IANLQTDLSDGLR.L	1416.56231	2	6.32E-06	0.85	3.40	-	738.0
AHQ-2-1, 4294	R.IANLQTDLSDGLR.L	1416.56231	2	9.43E-07	0.90	3.90	-	785.7
AHQ-2-2, 4281 - 4358	R.IANLQTDLSDGLR.L	1416.56231	2	2.04E-06	0.95	4.31	-	1191.0
AHQ-2-5, 3691	R.IANLQTDLSDGLR.L	1416.56231	2	1.79E-05	0.92	3.33	-	1271.9
AHQ-2-13, 4156	R.IANLQTDLSDGLR.L	1416.56231	2	3.46E-06	0.93	3.56	-	1231.2
AHQ-2-1, 4094	R.IANLQTDLSDGLR.L	1416.56231	2	2.18E-06	0.95	4.13	-	1339.1
AHQ-2-9, 3967	R.IANLQTDLSDGLR.L	1416.56231	2	8.84E-05	0.94	4.07	-	1081.3
AHQ-2-4, 3869 - 3905	R.IANLQTDLSDGLR.L	1416.56231	2	2.52E-08	0.93	4.00	-	1064.4
AHQ-2-9, 3646	R.IANLQTDLSDGLR.L	1416.56231	2	3.66E-09	0.85	3.32	-	706.2
AHQ-2-3, 4305 - 4307	R.IANLQTDLSDGLR.L	1416.56231	1	9.12E-05	0.53	2.97	-	345.3
AHQ-2-4, 4284	R.IANLQTDLSDGLR.L	1416.56231	2	1.11E-04	0.87	3.16	-	879.8
AHQ-2-1, 4000	R.IANLQTDLSDGLR.L	1416.56231	2	1.15E-07	0.94	4.15	-	1103.7
AHQ-2-1, 4546 - 4612	R.IANLQTDLSDGLR.L	1416.56231	2	3.19E-07	0.92	3.43	-	1120.1
AHQ-2-2, 4722	R.IANLQTDLSDGLR.L	1416.56231	2	3.98E-06	0.96	4.47	-	1353.7
AHQ-2-4, 4289 - 4290	R.IANLQTDLSDGLR.L	1416.56231	1	4.34E-05	0.74	3.26	-	309.6
AHQ-2-2, 4618	R.IANLQTDLSDGLR.L	1416.56231	1	6.78E-05	0.37	2.09	-	326.3
AHQ-2-2, 4598	R.IANLQTDLSDGLR.L	1416.56231	2	1.61E-06	0.94	3.91	-	1340.9
AHQ-2-4, 5685	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.91E-08	0.97	4.80	-	1861.3
AHQ-2-6, 5353	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.60E-10	0.97	4.74	-	1914.8
AHQ-2-6, 5369 - 5442	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.78E-11	0.99	6.79	-	2256.6
AHQ-2-13, 5325	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.71E-08	0.97	5.01	-	1659.2
AHQ-2-11, 5189	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.97E-10	0.97	4.69	-	1665.8
AHQ-2-5, 4815	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.62E-09	0.97	4.86	-	1874.0
AHQ-2-12, 5442 - 5449	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.91E-12	0.98	5.88	-	1925.1
AHQ-2-6, 3945	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.22E-08	0.97	5.55	-	1395.1
AHQ-2-1, 4285 - 4356	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	8.23E-10	0.98	5.56	-	1952.6
AHQ-2-13-, 5430	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	7.51E-05	0.96	5.45	-	1014.4
AHQ-2-3, 5659 - 5728	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.83E-06	0.94	4.28	-	1215.2
AHQ-2-8, 5190	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	8.63E-09	0.98	5.50	-	1705.4
AHQ-2-7, 3923	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	8.74E-07	0.95	4.55	-	1097.0
AHQ-2-4, 4224	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.57E-05	0.94	4.54	-	1040.1
AHQ-2-14, 6444	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.44E-04	0.97	4.98	-	1532.8
AHQ-2-7, 5347 - 5356	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.12E-09	0.98	5.63	-	1973.5
AHQ-2-1, 5740	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	8.01E-12	0.98	5.43	-	2033.0
AHQ-2-1, 5760	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	1.83E-05	0.88	4.09	-	924.3
AHQ-2-5, 5589 - 5623	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	9.93E-05	0.74	3.15	-	627.5
AHQ-2-4, 2468	K.IVGPSGAAVPCK.V	1157.36530	2	1.50E-08	0.70	2.60	-	574.7
AHQ-2-3, 2464	K.IVGPSGAAVPCK.V	1157.36530	2	2.17E-05	0.86	3.16	-	708.8
AHQ-2-2, 2480	K.IVGPSGAAVPCK.V	1157.36530	2	1.08E-08	0.92	3.45	-	940.3
AHQ-2-1, 2621 - 2622	K.IVGPSGAAVPCK.V	1157.36530	2	3.85E-07	0.88	3.38	-	689.6
AHQ-2-5, 2327	K.IVGPSGAAVPCK.V	1157.36530	2	2.92E-08	0.92	3.65	-	869.5
AHQ-2-2, 2617	K.IVGPSGAAVPCK.V	1157.36530	2	4.18E-09	0.92	3.67	-	985.3
AHQ-2-2, 4268 - 4336	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	5.14E-07	0.96	4.97	-	1703.6
AHQ-2-3, 4264 - 4336	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	2.08E-05	0.94	5.23	-	603.9
AHQ-2-5, 3999	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.22E-04	0.93	5.11	-	1175.3
AHQ-2-5, 4119	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	6.30E-07	0.94	4.56	-	1373.2
AHQ-2-3, 4369 - 4443	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.59E-04	0.72	3.35	-	640.2
AHQ-2-2, 4404 - 4482	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.53E-08	0.91	4.55	-	1017.5
AHQ-2-1, 4348 - 4416	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.79E-09	0.92	5.13	-	986.3
AHQ-2-3, 4260 - 4331	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.32E-07	0.91	4.08	-	1261.7
AHQ-2-2, 4277 - 4348	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	3.22E-07	0.90	4.41	-	492.4
AHQ-2-2, 4421 - 4449	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.23E-08	0.95	5.60	-	458.7
AHQ-2-6, 3954 - 3957	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.33E-06	0.97	5.38	-	1860.1
AHQ-2-1, 4353 - 4421	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	4.16E-06	0.95	5.06	-	704.9
AHQ-2-5, 4263	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	1.48E-07	0.73	3.40	-	519.6
AHQ-2-1, 4545	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.47E-04	0.81	3.01	-	651.4
AHQ-2-5, 3840 - 3911	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.94E-08	0.97	5.90	-	1860.8
AHQ-2-1, 4544	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.79E-09	0.96	5.15	-	1638.0
AHQ-2-6, 3995 - 4006	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.11E-04	0.80	3.30	-	531.6
AHQ-2-1, 3708	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	1.41E-06	0.88	3.21	-	1080.4
AHQ-2-3, 3263	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	2.43E-04	0.93	4.36	-	1167.2
AHQ-2-5, 2987	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	7.64E-05	0.84	3.59	-	1004.1
AHQ-2-4, 3402	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.23E-07	0.94	4.49	-	1318.9
AHQ-2-2, 3390 - 3462	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.96E-07	0.93	4.63	-	1229.1
AHQ-2-8, 2820	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.61E-04	0.86	3.72	-	819.4
AHQ-2-1, 3661	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	3.24E-05	0.93	4.06	-	1133.4
AHQ-2-2, 3233	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	8.25E-09	0.93	4.51	-	1167.3
AHQ-2-1, 3540 - 3565	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	2.36E-05	0.94	4.58	-	888.9
AHQ-2-1, 3506 - 3585	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.41E-09	0.93	4.40	-	1031.6
AHQ-2-1, 4086	K.LDVQFSGLTK.G	1108.26945	2	4.69E-05	0.88	3.28	-	826.2
AHQ-2-1, 4092	K.LDVQFSGLTK.G	1108.26945	1	7.73E-07	0.62	2.92	-	338.5
AHQ-2-3, 3955	K.LDVQFSGLTK.G	1108.26945	1	3.35E-05	0.31	2.43	-	266.3
AHQ-2-4, 3934	K.LDVQFSGLTK.G	1108.26945	2	7.61E-05	0.91	3.67	-	840.1
AHQ-2-3, 3951	K.LDVQFSGLTK.G	1108.26945	2	1.42E-05	0.93	4.01	-	825.2
AHQ-2-2, 3985	K.LDVQFSGLTK.G	1108.26945	1	3.86E-05	0.37	2.42	-	273.8
AHQ-2-2, 3984 - 3994	K.LDVQFSGLTK.G	1108.26945	2	8.39E-06	0.95	3.53	-	1569.9
AHQ-2-2, 7149	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	2	1.60E-07	0.84	4.05	-	442.0
AHQ-2-1, 5030 - 5100	K.LPQLPITNFSR.D	1286.50461	2	1.17E-04	0.90	3.04	-	900.5
AHQ-2-6, 4573 - 4581	K.LPQLPITNFSR.D	1286.50461	2	9.06E-04	0.85	2.92	-	617.7
AHQ-2-5, 4695	K.LPQLPITNFSR.D	1286.50461	2	5.30E-05	0.89	3.15	-	692.4
AHQ-2-2, 4961 - 5033	K.LPQLPITNFSR.D	1286.50461	2	2.13E-08	0.92	3.48	-	783.1
AHQ-2-2, 5285	K.LPQLPITNFSR.D	1286.50461	2	1.41E-07	0.89	3.20	-	786.5
AHQ-2-2, 4940 - 5008	K.LPQLPITNFSR.D	1286.50461	2	1.13E-07	0.90	3.13	-	778.1
AHQ-2-3, 5279	K.LPQLPITNFSR.D	1286.50461	2	7.42E-05	0.89	3.14	-	795.6
AHQ-2-11, 4573	K.LPQLPITNFSR.D	1286.50461	2	9.93E-04	0.82	3.08	-	595.4
AHQ-2-3, 5185	K.LPQLPITNFSR.D	1286.50461	2	5.72E-05	0.79	2.95	-	582.1
AHQ-2-3, 4935 - 5007	K.LPQLPITNFSR.D	1286.50461	2	1.10E-05	0.92	3.23	-	902.2
AHQ-2-2, 5618 - 5688	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.69E-07	0.94	4.98	-	777.3
AHQ-2-3, 5699 - 5767	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.01E-06	0.95	5.11	-	760.6
AHQ-2-2, 5637 - 5710	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	6.11E-15	0.98	6.33	-	2152.5
AHQ-2-2, 5724 - 5792	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	6.24E-05	0.81	3.42	-	598.7
AHQ-2-2, 5768 - 5837	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	7.57E-07	0.96	5.85	-	688.2
AHQ-2-3, 5557 - 5628	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	5.34E-06	0.93	4.77	-	740.6
AHQ-2-4, 5577 - 5652	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	6.41E-05	0.85	3.54	-	626.3

AHQ-2-1, 5736 - 5808	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	5.14E-08	0.94	4.66	-	752.8
AHQ-2-1, 5605 - 5673	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.31E-06	0.89	3.75	-	754.8
AHQ-2-1, 5604 - 5676	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	4.05E-12	0.98	6.58	-	2509.8
AHQ-2-6, 5318 - 5385	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.80E-07	0.97	5.68	-	990.6
AHQ-2-2, 5776 - 5852	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	1.30E-09	0.96	5.26	-	1518.0
AHQ-2-4, 5645 - 5720	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.34E-11	0.97	6.24	-	1165.1
AHQ-2-2, 5860	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.66E-08	0.93	4.94	-	633.5
AHQ-2-4, 5801	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.87E-05	0.75	3.11	-	504.7
AHQ-2-8, 2279	R.LRNGHVGISFVPK.E	1424.67564	2	1.72E-05	0.74	2.87	-	434.6
AHQ-2-5, 2643	R.LRNGHVGISFVPK.E	1424.67564	2	1.77E-04	0.78	2.69	-	651.5
AHQ-2-5, 2547	R.LRNGHVGISFVPK.E	1424.67564	2	2.42E-04	0.78	2.96	-	740.1
AHQ-2-4, 2993	R.LRNGHVGISFVPK.E	1424.67564	2	1.77E-04	0.75	2.74	-	809.8
AHQ-2-1, 3125	R.LRNGHVGISFVPK.E	1424.67564	3	7.56E-05	0.87	3.21	-	1410.8
AHQ-2-5, 2645	R.LRNGHVGISFVPK.E	1424.67564	3	3.03E-05	0.91	3.24	-	1694.8
AHQ-2-1, 4204	R.LSPFMADIR.D	1050.25664	2	1.82E-04	0.67	2.70	-	378.2
AHQ-2-6, 3110 - 3111	R.LTVSSLQESGLK.V	1262.43499	2	9.52E-05	0.91	3.50	-	961.3
AHQ-2-4, 3422 - 3428	R.LTVSSLQESGLK.V	1262.43499	2	6.87E-05	0.84	3.30	-	681.3
AHQ-2-8, 2887	R.LTVSSLQESGLK.V	1262.43499	2	6.92E-05	0.84	3.02	-	794.3
AHQ-2-7, 3012	R.LTVSSLQESGLK.V	1262.43499	2	1.09E-04	0.90	3.30	-	969.0
AHQ-2-11, 3873	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.92E-10	0.97	5.05	-	1754.4
AHQ-2-7, 3655	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.77E-08	0.97	5.96	-	1482.9
AHQ-2-7, 3651	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	5.80E-06	0.96	5.02	-	1130.5
AHQ-2-14-, 3980	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.77E-07	0.97	5.49	-	1679.1
AHQ-2-4, 4098 - 4101	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.32E-07	0.97	5.59	-	1365.4
AHQ-2-4, 4104 - 4105	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.08E-06	0.93	4.19	-	1147.5
AHQ-2-5, 3867 - 3944	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	4.07E-05	0.96	4.77	-	1734.8
AHQ-2-3, 4172	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.06E-04	0.95	4.70	-	1242.8
AHQ-2-3, 4167	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.52E-08	0.97	4.52	-	2422.6
AHQ-2-14, 5585	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.12E-05	0.89	3.98	-	552.5
AHQ-2-5, 4117 - 4183	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	4.05E-09	0.98	5.49	-	2260.2
AHQ-2-13-, 4139	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.43E-05	0.95	4.89	-	1395.2
AHQ-2-10, 3931	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.40E-05	0.91	4.53	-	594.0
AHQ-2-4, 4472 - 4474	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.67E-08	0.97	5.39	-	1317.5
AHQ-2-13, 4071	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.97E-07	0.93	4.83	-	713.8
AHQ-2-8, 3678	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.78E-04	0.96	5.08	-	1108.0
AHQ-2-14, 5322	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.35E-06	0.93	4.21	-	956.5
AHQ-2-7, 4024	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.28E-08	0.94	4.77	-	714.3
AHQ-2-5, 4120 - 4196	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.05E-09	0.96	5.55	-	913.4
AHQ-2-5, 3753 - 3835	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.19E-08	0.97	6.15	-	1029.8
AHQ-2-5, 3712 - 3784	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.21E-11	0.97	5.82	-	1614.3
AHQ-2-13, 4252	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.62E-04	0.84	4.09	-	411.0
AHQ-2-6, 4134	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	6.43E-09	0.95	4.64	-	990.6
AHQ-2-5, 4276	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.19E-07	0.95	4.77	-	940.4
AHQ-2-5, 3885	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.85E-05	0.94	4.65	-	955.6
AHQ-2-5, 4660 - 4735	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.92E-04	0.87	4.05	-	516.3
AHQ-2-1, 4652	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.10E-07	0.92	4.27	-	1009.2
AHQ-2-1, 4641	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	9.16E-09	0.98	5.47	-	1818.7
AHQ-2-6, 3763 - 3773	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.36E-04	0.96	5.07	-	1517.3
AHQ-2-1, 4350	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.30E-04	0.98	5.61	-	1721.7
AHQ-2-13-, 4137	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	5.83E-05	0.97	5.61	-	1363.5
AHQ-2-11, 3864	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.16E-05	0.94	4.49	-	856.9
AHQ-2-1, 4352 - 4368	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.49E-06	0.97	5.66	-	1627.8
AHQ-2-6, 3771	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.29E-07	0.96	5.08	-	1205.1
AHQ-2-5, 2383	K.MDCQECPEGYR.V	1447.55375	1	1.84E-05	0.17	2.07	-	151.8
AHQ-2-5, 2369	K.MDCQECPEGYR.V	1447.55375	2	5.53E-04	0.85	2.95	-	802.7
AHQ-2-4, 2482 - 2558	K.MDCQECPEGYR.V	1447.55375	2	2.98E-04	0.86	2.96	-	827.9
AHQ-2-6, 2358	K.MDCQECPEGYR.V	1447.55375	2	7.95E-04	0.72	3.01	-	618.5
AHQ-2-5, 2704	R.NGHVGISFVPK.E	1155.33104	1	6.28E-07	0.59	2.29	-	460.6
AHQ-2-4, 4882	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	5.81E-07	0.80	2.99	-	727.5
AHQ-2-5, 4595 - 4603	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	2.00E-04	0.91	3.84	-	590.7
AHQ-2-1, 4922 - 4924	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	4.98E-06	0.97	5.41	-	1290.9
AHQ-2-5, 4792 - 4793	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	3.60E-06	0.69	3.08	-	345.9
AHQ-2-8, 4324	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	1.32E-06	0.94	3.73	-	1540.5
AHQ-2-2, 1774 - 1797	K.RAEFTVETR.S	1109.21754	2	2.86E-06	0.94	3.60	-	1052.7
AHQ-2-1, 2106	K.RAEFTVETR.S	1109.21754	2	8.53E-06	0.94	3.23	-	1141.2
AHQ-2-2, 1870	K.RAEFTVETR.S	1109.21754	2	9.48E-05	0.90	3.40	-	783.0
AHQ-2-5, 2612 - 2615	R.RAPSVANVGSHCDLSLK.I	1813.02884	2	7.00E-04	0.95	4.47	-	1272.7
AHQ-2-1, 3984	K.RIANLQTDLSDGLR.L	1572.74866	2	1.36E-06	0.63	3.02	-	461.4
AHQ-2-9, 2655	R.RLTVSSLQESGLK.V	1418.62134	2	2.03E-04	0.97	4.69	-	1728.8
AHQ-2-5, 2540 - 2616	R.RLTVSSLQESGLK.V	1418.62134	2	1.78E-04	0.97	4.70	-	2080.6
AHQ-2-7, 2536 - 2539	R.RLTVSSLQESGLK.V	1418.62134	2	2.42E-04	0.95	4.40	-	1335.1
AHQ-2-2, 2924	R.RLTVSSLQESGLK.V	1418.62134	2	4.09E-05	0.95	4.40	-	1201.7
AHQ-2-3, 2948	R.RLTVSSLQESGLK.V	1418.62134	2	1.13E-05	0.97	4.57	-	2263.6
AHQ-2-2, 7712 - 7780	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	2.55E-05	0.96	5.76	-	1358.0
AHQ-2-4, 3885 - 3956	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.17E-06	0.87	3.98	-	557.4
AHQ-2-8, 3503	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	9.80E-11	0.86	4.14	-	477.8
AHQ-2-7, 3537	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.13E-07	0.91	4.48	-	489.7
AHQ-2-2, 3921 - 3992	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	5.93E-07	0.94	4.77	-	1212.2
AHQ-2-2, 4202	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	9.82E-10	0.93	4.15	-	1329.1
AHQ-2-2, 4181 - 4258	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.01E-06	0.94	4.99	-	637.1
AHQ-2-2, 3910 - 3981	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	6.92E-06	0.93	4.75	-	744.6
AHQ-2-4, 3890	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.69E-06	0.94	5.14	-	589.6
AHQ-2-1, 4056 - 4136	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	6.31E-06	0.94	5.05	-	865.6
AHQ-2-2, 4062 - 4132	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.17E-06	0.93	4.03	-	1419.4
AHQ-2-1, 4054 - 4129	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	4.00E-07	0.95	4.86	-	1406.5
AHQ-2-2, 4052 - 4109	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	7.65E-07	0.94	4.81	-	805.6
AHQ-2-4, 3902 - 3909	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	6.74E-09	0.91	4.14	-	1389.4
AHQ-2-2, 4410	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	8.81E-06	0.91	4.54	-	595.1
AHQ-2-1, 4205 - 4222	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.42E-07	0.93	4.96	-	673.2
AHQ-2-3, 3901 - 3972	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	4.27E-09	0.93	4.10	-	1343.2
AHQ-2-3, 3903 - 3971	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.41E-10	0.96	5.55	-	729.2
AHQ-2-6, 3606 - 3637	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.51E-07	0.90	4.29	-	1128.8
AHQ-2-3, 4045	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.77E-07	0.89	4.43	-	403.5
AHQ-2-3, 4173	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.46E-07	0.90	4.15	-	637.7
AHQ-2-3, 4256	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.54E-07	0.87	3.84	-	596.5
AHQ-2-2, 3320 - 3388	K.SPFEVYVDK.S	1084.20321	1	9.91E-05	0.79	3.06	-	786.7
AHQ-2-2, 3321 - 3400	K.SPFEVYVDK.S	1084.20321	2	8.23E-06	0.93	3.49	-	996.9
AHQ-2-7, 3029	K.SPFEVYVDK.S	1084.20321	1	3.12E-06	0.81	3.03	-	717.7
AHQ-2-3, 3337	K.SPFEVYVDK.S	1084.20321	1	1.25E-04	0.64	2.35	-	776.2
AHQ-2-1, 3466 - 3492	K.SPFEVYVDK.S	1084.20321	2	7.36E-06	0.87	2.84	-	1017.6
AHQ-2-1, 3485	K.SPFEVYVDK.S	1084.20321	1	9.71E-07	0.82	2.96	-	911.0
AHQ-2-4, 3352	K.SPFEVYVDK.S	1084.20321	1	8.40E-05	0.35	2.20	-	728.6
AHQ-2-3, 3343	K.SPFEVYVDK.S	1084.20321	2	3.10E-05	0.92	3.39	-	1080.1
AHQ-2-4, 3362	K.SPFEVYVDK.S	1084.20321	1	5.72E-05	0.71	2.93	-	656.7
AHQ-2-3, 3348	K.SPFEVYVDK.S	1084.20321	1	7.83E-06	0.78	3.04	-	745.5
AHQ-2-4, 3364	K.SPFEVYVDK.S	1084.20321	2	2.66E-06	0.91	3.39	-	916.0
AHQ-2-7, 3033	K.SPFEVYVDK.S	1084.20321	2	6.81E-06	0.92	3.12	-	1172.8

AHQ-2-2, 2968	K.SPFEVYVDKSQGDASK.V	1757.87886	2	1.42E-04	0.95	4.15	-	1349.9
AHQ-2-1, 5096 - 5173	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.26E-07	0.87	4.09	-	687.7
AHQ-2-2, 5308	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.52E-06	0.40	2.65	-	405.4
AHQ-2-3, 5076 - 5125	K.SPFSVAVSPSLDLSK.I	1534.73557	2	7.84E-06	0.79	3.49	-	522.0
AHQ-2-4, 5068 - 5080	K.SPFSVAVSPSLDLSK.I	1534.73557	2	9.52E-08	0.94	5.20	-	790.3
AHQ-2-2, 4944 - 5014	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.62E-04	0.83	3.49	-	563.2
AHQ-2-6, 4791	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.83E-06	0.93	4.23	-	1049.1
AHQ-2-4, 4932	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.13E-04	0.87	3.61	-	784.9
AHQ-2-2, 5184 - 5200	K.SPFSVAVSPSLDLSK.I	1534.73557	2	9.57E-07	0.94	4.65	-	942.9
AHQ-2-2, 5097 - 5132	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.03E-06	0.95	4.85	-	1080.6
AHQ-2-5, 4871	K.SPFSVAVSPSLDLSK.I	1534.73557	2	8.23E-06	0.90	3.55	-	948.9
AHQ-2-2, 3552	R.SPYTVTVGQACNPSACR.A	1871.04208	2	7.22E-07	0.91	4.43	-	538.1
AHQ-2-7, 3217	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.40E-05	0.81	3.76	-	472.1
AHQ-2-5, 3285	R.SPYTVTVGQACNPSACR.A	1871.04208	3	3.33E-04	0.88	3.86	-	875.2
AHQ-2-4, 3430 - 3488	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.92E-04	0.92	4.57	-	495.1
AHQ-2-5, 3272	R.SPYTVTVGQACNPSACR.A	1871.04208	2	6.12E-05	0.92	4.65	-	440.0
AHQ-2-2, 3468 - 3536	R.SPYTVTVGQACNPSACR.A	1871.04208	2	9.91E-07	0.91	4.57	-	427.0
AHQ-2-1, 3525 - 3596	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.93E-05	0.90	3.92	-	559.8
AHQ-2-1, 3698	R.SPYTVTVGQACNPSACR.A	1871.04208	2	3.57E-04	0.56	2.76	-	449.0
AHQ-2-3, 3435 - 3515	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.87E-06	0.88	4.21	-	415.6
AHQ-2-6, 3235	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.00E-05	0.91	4.20	-	470.5
AHQ-2-3, 3480	R.SPYTVTVGQACNPSACR.A	1871.04208	3	3.26E-04	0.92	4.21	-	1361.3
AHQ-2-5, 3233 - 3303	R.SPYTVTVGQACNPSACR.A	1871.04208	2	6.77E-04	0.58	2.94	-	319.8
AHQ-2-2, 2674	K.SQGDASKVTAQGPGLEPSGNIANK.T	2327.49419	2	1.50E-06	0.90	4.53	-	666.8
AHQ-2-14-, 2092 - 2152	K.SSFTVDCSK.A	1032.10676	1	7.17E-04	0.70	2.81	-	295.1
AHQ-2-14-, 4569 - 4648	K.SSFTVDCSKAGNNMLLVGVHGPR.T	2448.76449	3	6.09E-05	0.70	3.16	-	790.7
AHQ-2-2, 5065 - 5138	R.TFSVWYVPEVTGTHK.V	1751.96228	3	1.25E-05	0.72	3.22	-	480.5
AHQ-2-2, 5045 - 5124	R.TFSVWYVPEVTGTHK.V	1751.96228	2	3.72E-07	0.85	3.74	-	462.0
AHQ-2-5, 4704 - 4777	R.TFSVWYVPEVTGTHK.V	1751.96228	2	9.36E-04	0.54	2.69	-	314.8
AHQ-2-4, 2958	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	4.87E-06	0.85	3.54	-	713.5
AHQ-2-3, 2955	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	6.27E-06	0.92	3.96	-	1015.1
AHQ-2-2, 2861 - 2932	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	6.43E-06	0.95	4.51	-	1069.3
AHQ-2-1, 3142 - 3216	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	2.11E-06	0.85	3.55	-	806.0
AHQ-2-2, 2933	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	2.21E-06	0.74	3.12	-	623.9
AHQ-2-4, 2949	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	6.93E-05	0.92	3.95	-	747.4
AHQ-2-3, 2920 - 2991	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	6.95E-06	0.90	4.32	-	541.2
AHQ-2-2, 2673	R.TGVELGKPTHFTVNAK.A	1699.93205	3	6.77E-04	0.79	3.82	-	688.6
AHQ-2-4, 2817	R.TGVELGKPTHFTVNAK.A	1699.93205	2	3.22E-04	0.90	3.73	-	799.1
AHQ-2-3, 2679 - 2697	R.TGVELGKPTHFTVNAK.A	1699.93205	3	9.45E-06	0.52	3.30	-	484.6
AHQ-2-2, 2704 - 2773	R.TGVELGKPTHFTVNAK.A	1699.93205	2	5.86E-04	0.92	4.20	-	650.6
AHQ-2-1, 2940	R.TGVELGKPTHFTVNAK.A	1699.93205	2	7.22E-04	0.85	3.86	-	437.5
AHQ-2-1, 3044 - 3112	R.TGVELGKPTHFTVNAK.A	1699.93205	2	3.57E-06	0.82	3.50	-	455.0
AHQ-2-2, 2558 - 2636	R.TGVELGKPTHFTVNAK.A	1699.93205	2	3.04E-04	0.84	4.01	-	427.1
AHQ-2-7, 2760 - 2831	K.THEAEIVEGENHTYCIR.F	2060.19046	3	5.12E-05	0.88	3.54	-	1214.8
AHQ-2-7, 2755	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.74E-11	0.98	5.81	-	2375.2
AHQ-2-4, 2948 - 3018	K.THEAEIVEGENHTYCIR.F	2060.19046	3	4.50E-07	0.90	3.79	-	1105.1
AHQ-2-4, 2953 - 3028	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.00E-04	0.98	6.38	-	2488.8
AHQ-2-5, 2811 - 2812	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.28E-12	0.98	5.85	-	2174.1
AHQ-2-7, 2648	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.04E-05	0.98	5.34	-	1810.7
AHQ-2-3, 3045	K.THEAEIVEGENHTYCIR.F	2060.19046	2	6.77E-14	0.98	5.69	-	2083.4
AHQ-2-5, 2712	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.80E-05	0.93	4.12	-	1506.7
AHQ-2-5, 2711	K.THEAEIVEGENHTYCIR.F	2060.19046	2	1.39E-06	0.98	5.61	-	1695.0
AHQ-2-1, 3172 - 3246	K.THEAEIVEGENHTYCIR.F	2060.19046	3	4.20E-06	0.80	3.26	-	974.8
AHQ-2-6, 2817 - 2821	K.THEAEIVEGENHTYCIR.F	2060.19046	2	3.57E-13	0.99	6.61	-	2548.9
AHQ-2-1, 3301	K.THEAEIVEGENHTYCIR.F	2060.19046	2	9.27E-12	0.97	4.90	-	1691.2
AHQ-2-1, 3873	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	2	4.85E-08	0.94	4.07	-	1053.6
AHQ-2-14, 3840 - 3913	R.TPCEEILVK.H	1090.27249	2	1.48E-04	0.80	2.77	-	722.1
AHQ-2-13, 3088	R.TPCEEILVK.H	1090.27249	2	9.29E-07	0.85	3.30	-	770.6
AHQ-2-13-, 3045 - 3054	R.TPCEEILVK.H	1090.27249	2	9.10E-06	0.77	2.85	-	742.4
AHQ-2-4, 3092	R.TPCEEILVK.H	1090.27249	2	2.08E-05	0.86	3.06	-	680.3
AHQ-2-14-, 2967	R.TPCEEILVK.H	1090.27249	2	7.79E-05	0.82	3.00	-	683.0
AHQ-2-7, 2812	R.TPCEEILVK.H	1090.27249	2	3.38E-05	0.85	2.99	-	758.4
AHQ-2-14, 3937	R.TPCEEILVK.H	1090.27249	1	3.43E-05	0.38	2.64	-	344.2
AHQ-2-3, 3109	R.TPCEEILVK.H	1090.27249	2	2.77E-05	0.90	3.35	-	872.6
AHQ-2-10, 2811	R.TPCEEILVK.H	1090.27249	2	2.47E-04	0.66	2.80	-	467.2
AHQ-2-4, 3098	R.TPCEEILVK.H	1090.27249	1	4.95E-04	0.56	3.05	-	393.8
AHQ-2-14, 3976 - 4044	R.TPCEEILVK.H	1090.27249	2	1.52E-05	0.70	2.90	-	505.0
AHQ-2-11, 2972	R.TPCEEILVK.H	1090.27249	2	1.75E-06	0.74	2.85	-	625.2
AHQ-2-5, 2867	R.TPCEEILVK.H	1090.27249	2	8.91E-07	0.83	2.98	-	617.3
AHQ-2-6, 2871	R.TPCEEILVK.H	1090.27249	2	5.23E-06	0.74	2.52	-	636.6
AHQ-2-1, 3238	R.TPCEEILVK.H	1090.27249	2	1.77E-05	0.78	2.64	-	652.9
AHQ-2-6, 3033	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.35E-11	0.95	4.46	-	1160.3
AHQ-2-1, 3221 - 3244	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.41E-11	0.93	3.99	-	911.0
AHQ-2-2, 3593	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.85E-05	0.87	3.13	-	850.7
AHQ-2-4, 3438 - 3509	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.24E-12	0.95	4.25	-	1128.2
AHQ-2-4, 3242 - 3296	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.52E-08	0.92	4.17	-	718.3
AHQ-2-3, 3152	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.41E-10	0.96	4.54	-	1195.2
AHQ-2-2, 3242 - 3324	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.76E-11	0.95	4.73	-	987.6
AHQ-2-2, 3090 - 3160	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.83E-10	0.92	3.82	-	881.7
AHQ-2-6, 3211 - 3289	R.VANPSGNLTETYVQDR.G	1764.87462	2	9.64E-05	0.88	3.90	-	650.7
AHQ-2-3, 3240 - 3319	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.69E-11	0.96	4.82	-	997.5
AHQ-2-5, 3063	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.96E-13	0.93	4.36	-	795.2
AHQ-2-3, 3396 - 3469	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.65E-11	0.91	4.20	-	586.0
AHQ-2-2, 3376 - 3448	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.17E-12	0.92	3.90	-	805.4
AHQ-2-9, 3040	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.73E-07	0.84	3.71	-	495.2
AHQ-2-1, 3380 - 3448	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.50E-11	0.91	4.05	-	664.9
AHQ-2-7, 2971 - 2972	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.14E-07	0.94	4.50	-	905.1
AHQ-2-1, 3537 - 3612	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.03E-11	0.98	5.86	-	1248.8
AHQ-2-5, 2364	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.91E-04	0.85	3.63	-	606.3
AHQ-2-6, 2595	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	7.80E-08	0.92	3.98	-	876.5
AHQ-2-4, 2769	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	6.92E-05	0.83	3.42	-	589.1
AHQ-2-10, 2534	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.06E-06	0.76	2.97	-	505.9
AHQ-2-10, 2382 - 2451	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.33E-05	0.70	3.02	-	498.0
AHQ-2-13-, 2626	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.03E-05	0.72	3.12	-	506.6
AHQ-2-1, 2698	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	7.40E-05	0.79	3.27	-	616.6
AHQ-2-13, 2861	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.93E-04	0.79	3.24	-	569.5
AHQ-2-1, 2894	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.04E-06	0.89	3.63	-	860.0
AHQ-2-9, 2603	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	9.36E-04	0.79	3.68	-	389.0
AHQ-2-2, 2808 - 2809	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	6.52E-07	0.87	4.23	-	517.8
AHQ-2-5, 2524 - 2539	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	9.94E-10	0.90	4.21	-	599.1
AHQ-2-8, 2374	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.46E-05	0.57	2.79	-	330.1
AHQ-2-4, 2534	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.40E-04	0.81	3.84	-	392.6
AHQ-2-8, 2263	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.80E-05	0.84	3.46	-	615.1
AHQ-2-7, 3536	K.VDINTEDLEDGTCR.V	1638.69283	2	5.62E-06	0.93	3.75	-	1138.3
AHQ-2-1, 3542	K.VDINTEDLEDGTCR.V	1638.69283	2	5.80E-07	0.95	4.42	-	1091.8
AHQ-2-1, 3436	K.VDINTEDLEDGTCR.V	1638.69283	2	3.11E-11	0.95	4.23	-	1284.3
AHQ-2-5, 3559 - 3567	K.VDINTEDLEDGTCR.V	1638.69283	2	5.26E-06	0.94	4.58	-	925.1

AHQ-2-6, 3271	K.VDINTEDLEDGTCR.V	1638.69283	2	1.11E-05	0.85	3.33	-	882.3
AHQ-2-13, 3505 - 3569	K.VDINTEDLEDGTCR.V	1638.69283	2	7.37E-07	0.82	3.56	-	904.9
AHQ-2-4, 3442	K.VDINTEDLEDGTCR.V	1638.69283	2	6.73E-05	0.63	2.90	-	514.0
AHQ-2-6, 3363	K.VDINTEDLEDGTCR.V	1638.69283	2	1.83E-04	0.81	2.85	-	955.9
AHQ-2-3, 3679 - 3703	K.VDINTEDLEDGTCR.V	1638.69283	2	1.80E-05	0.85	3.10	-	757.6
AHQ-2-6, 3490	K.VDINTEDLEDGTCR.V	1638.69283	2	5.97E-08	0.89	3.74	-	855.6
AHQ-2-5, 3464 - 3473	K.VDINTEDLEDGTCR.V	1638.69283	2	9.48E-09	0.94	4.27	-	1285.5
AHQ-2-8, 3287	K.VDINTEDLEDGTCR.V	1638.69283	2	7.05E-04	0.92	3.45	-	1374.0
AHQ-2-1, 3721 - 3725	K.VDINTEDLEDGTCR.V	1638.69283	2	3.60E-05	0.91	3.62	-	1155.1
AHQ-2-12, 3554	K.VDINTEDLEDGTCR.V	1638.69283	2	6.14E-08	0.91	3.54	-	876.2
AHQ-2-1, 3838	K.VDINTEDLEDGTCR.V	1638.69283	2	5.90E-08	0.93	3.52	-	1228.3
AHQ-2-4, 3681	K.VDINTEDLEDGTCR.V	1638.69283	2	4.30E-09	0.93	3.57	-	1313.3
AHQ-2-5, 3349	K.VDINTEDLEDGTCR.V	1638.69283	2	3.30E-07	0.80	2.99	-	779.6
AHQ-2-3, 2451	K.VDVGKDQEFTVK.S	1365.51377	1	9.16E-06	0.39	2.72	-	282.8
AHQ-2-2, 2460 - 2533	K.VDVGKDQEFTVK.S	1365.51377	2	1.80E-07	0.91	3.69	-	778.8
AHQ-2-6, 2297	K.VDVGKDQEFTVK.S	1365.51377	2	2.02E-09	0.89	3.47	-	765.3
AHQ-2-1, 2632 - 2633	K.VDVGKDQEFTVK.S	1365.51377	2	6.20E-08	0.88	3.36	-	674.8
AHQ-2-2, 2466	K.VDVGKDQEFTVK.S	1365.51377	1	1.58E-04	0.59	3.34	-	334.2
AHQ-2-5, 2279	K.VDVGKDQEFTVK.S	1365.51377	2	6.63E-08	0.92	3.58	-	824.5
AHQ-2-1, 2800 - 2868	K.VEPGLGADNSVVR.F	1313.44209	2	2.26E-06	0.84	3.40	-	286.2
AHQ-2-2, 2864 - 2866	K.VEPGLGADNSVVR.F	1313.44209	2	3.99E-08	0.86	3.23	-	477.6
AHQ-2-4, 6604 - 6616	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	5.89E-06	0.89	4.62	-	594.2
AHQ-2-4, 6482 - 6549	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	9.77E-04	0.51	3.29	-	389.8
AHQ-2-1, 6488 - 6554	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	1.15E-04	0.88	4.65	-	593.8
AHQ-2-5, 6463 - 6545	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	3.00E-05	0.92	5.13	-	694.3
AHQ-2-3, 7528	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	4.89E-08	0.93	4.71	-	733.2
AHQ-2-3, 7531 - 7532	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	5.15E-07	0.87	4.35	-	599.0
AHQ-2-5, 7415	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	4.82E-12	0.95	4.87	-	809.4
AHQ-2-7, 7475	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.17E-06	0.85	3.81	-	516.2
AHQ-2-1, 7172 - 7237	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	9.77E-04	0.66	3.10	-	562.9
AHQ-2-6, 7219 - 7274	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	2.65E-06	0.86	3.52	-	920.8
AHQ-2-9, 7332 - 7402	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	8.12E-07	0.90	4.37	-	488.9
AHQ-2-1, 7168 - 7242	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	2.00E-07	0.92	4.69	-	592.8
AHQ-2-6, 4123	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	5.15E-05	0.95	4.98	-	963.4
AHQ-2-4, 4478	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	3.25E-04	0.95	5.10	-	1076.5
AHQ-2-1, 4580	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.21E-08	0.96	4.91	-	1305.3
AHQ-2-5, 4189	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	8.88E-10	0.96	5.18	-	1428.8
AHQ-2-7, 4075	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	4.03E-11	0.98	4.65	-	2160.6
AHQ-2-8, 4255	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	8.09E-10	0.84	4.10	-	559.2
AHQ-2-7, 4285 - 4356	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	4.39E-10	0.88	4.51	-	638.9
AHQ-2-6, 4445	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.85E-07	0.93	4.88	-	938.6
AHQ-2-5, 4471 - 4545	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.70E-08	0.93	5.33	-	627.9
AHQ-2-1, 4918	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	2.56E-09	0.95	4.46	-	1551.4
AHQ-2-1, 4912	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	4.21E-04	0.88	4.30	-	640.2
AHQ-2-3, 4837	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.65E-09	0.85	4.42	-	437.5
AHQ-2-11, 4444	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.12E-10	0.86	4.44	-	517.9
AHQ-2-8, 4263	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	2.73E-08	0.92	3.89	-	1162.0
AHQ-2-8, 3484	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.43E-06	0.79	3.13	-	552.5
AHQ-2-5, 3599 - 3668	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.31E-07	0.83	3.24	-	491.8
AHQ-2-4, 3844 - 3912	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.02E-08	0.76	3.19	-	464.1
AHQ-2-2, 3817 - 3889	K.VNQPASFAVSLNGAK.G	1503.68480	2	6.42E-05	0.86	3.40	-	692.2
AHQ-2-7, 3531	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.54E-07	0.89	3.82	-	633.9
AHQ-2-7, 3436	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.70E-08	0.79	3.53	-	434.8
AHQ-2-5, 3456 - 3527	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.96E-07	0.67	2.79	-	409.1
AHQ-2-6, 3462 - 3542	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.02E-07	0.93	4.03	-	678.9
AHQ-2-8, 3356	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.40E-04	0.93	4.13	-	694.9
AHQ-2-1, 3952 - 4016	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.13E-06	0.88	3.49	-	664.9
AHQ-2-2, 1477 - 1490	K.VPVHDVTDASK.V	1168.28175	2	3.33E-07	0.95	3.61	-	1495.0
AHQ-2-3, 1497	K.VPVHDVTDASK.V	1168.28175	2	9.94E-07	0.94	3.24	-	1249.3
AHQ-2-1, 4288 - 4358	R.VQVQDNEGCPVEALVK.D	1786.98493	2	8.89E-07	0.97	5.28	-	1598.4
AHQ-2-4, 4170 - 4248	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.01E-10	0.95	4.70	-	1068.6
AHQ-2-3, 4195 - 4263	R.VQVQDNEGCPVEALVK.D	1786.98493	2	6.07E-06	0.96	4.89	-	1363.4
AHQ-2-5, 3948 - 3964	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.89E-06	0.97	5.09	-	1468.5
AHQ-2-2, 4444 - 4448	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.23E-09	0.96	4.66	-	1807.8
AHQ-2-2, 4304 - 4373	R.VQVQDNEGCPVEALVK.D	1786.98493	2	8.03E-06	0.96	4.46	-	1399.1
AHQ-2-6, 3893 - 3898	R.VQVQDNEGCPVEALVK.D	1786.98493	2	2.77E-05	0.77	3.77	-	539.9
AHQ-2-1, 4404 - 4428	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.47E-10	0.94	4.97	-	956.1
AHQ-2-2, 4221 - 4232	R.VQVQDNEGCPVEALVK.D	1786.98493	2	5.48E-09	0.95	4.78	-	954.2
AHQ-2-3, 4332	R.VQVQDNEGCPVEALVK.D	1786.98493	2	7.22E-07	0.96	4.49	-	1741.0
AHQ-2-2, 5584	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.44E-05	0.87	3.73	-	1011.6
AHQ-2-4, 5524	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.33E-05	0.79	3.57	-	854.8
AHQ-2-1, 5276 - 5346	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	5.67E-07	0.93	4.77	-	1418.0
AHQ-2-2, 5312 - 5380	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	2.75E-12	0.90	4.42	-	1336.7
AHQ-2-1, 5552	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	4.78E-04	0.92	4.09	-	1562.9
AHQ-2-3, 5272	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	4.55E-14	0.94	4.56	-	1710.2
AHQ-2-3, 5483 - 5551	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.70E-06	0.94	4.78	-	1743.6
AHQ-2-5, 5319	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	3.60E-09	0.80	3.22	-	1111.4
AHQ-2-7, 4217	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.24E-09	0.97	5.65	-	1514.9
AHQ-2-13, 4639 - 4643	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.96E-10	0.95	5.55	-	1120.4
AHQ-2-8, 3947	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	4.14E-10	0.95	5.17	-	811.4
AHQ-2-13-, 4737	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.35E-04	0.86	3.43	-	1003.2
AHQ-2-8, 4235	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.39E-04	0.94	4.64	-	1199.4
AHQ-2-5, 4361 - 4443	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.89E-11	0.96	5.40	-	1283.5
AHQ-2-4, 4792 - 4804	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	3.05E-08	0.95	5.32	-	1318.7
AHQ-2-1, 4960 - 5033	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.43E-04	0.90	4.31	-	745.3
AHQ-2-6, 4373 - 4446	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.71E-09	0.97	6.15	-	1388.3
AHQ-2-10, 4120	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	3.42E-04	0.84	3.40	-	345.4
AHQ-2-8, 3946	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.49E-07	0.91	4.70	-	833.9
AHQ-2-1, 4964	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	4.21E-05	0.94	4.04	-	1161.9
AHQ-2-1, 2893 - 2934	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.83E-05	0.77	3.89	-	341.1
AHQ-2-4, 2740	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	9.48E-07	0.91	3.74	-	882.6
AHQ-2-3, 2753	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.69E-06	0.74	3.23	-	432.2
AHQ-2-1, 2748 - 2816	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	8.70E-04	0.82	3.28	-	727.2
AHQ-2-3, 2607 - 2675	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.39E-05	0.74	3.08	-	698.8
AHQ-2-5, 2435 - 2481	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	3.57E-05	0.93	5.00	-	530.7
AHQ-2-6, 2586	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.77E-05	0.85	3.86	-	503.8
AHQ-2-6, 2471 - 2483	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.43E-04	0.78	3.43	-	423.8
AHQ-2-8, 2290	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.66E-05	0.45	2.65	-	300.7
AHQ-2-2, 2601 - 2613	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.83E-05	0.82	3.90	-	424.2
AHQ-2-2, 2860	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.75E-11	0.91	3.92	-	624.0
AHQ-2-5, 2579	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	6.45E-09	0.82	3.79	-	444.7
AHQ-2-2, 2684 - 2776	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	6.12E-08	0.93	4.52	-	665.2
AHQ-2-6, 2777	K.VTVLFAGQHIAK.S	1284.53185	2	8.91E-05	0.81	3.67	-	518.6
AHQ-2-4, 3082	K.VTVLFAGQHIAK.S	1284.53185	1	8.38E-06	0.67	2.92	-	508.5
AHQ-2-2, 2978 - 3049	K.VTVLFAGQHIAK.S	1284.53185	2	5.96E-07	0.92	3.87	-	904.9
AHQ-2-7, 2627	K.VTVLFAGQHIAK.S	1284.53185	2	5.07E-05	0.83	3.29	-	689.8
AHQ-2-5, 2695	K.VTVLFAGQHIAK.S	1284.53185	2	4.14E-06	0.92	3.95	-	871.8

AHQ-2-4, 3033	K.VTVLFAGQHIAK.S	1284.53185	1	8.91E-05	0.29	1.81	-	443.4
AHQ-2-4, 3037	K.VTVLFAGQHIAK.S	1284.53185	2	2.78E-07	0.76	3.27	-	544.8
AHQ-2-3, 3043	K.VTVLFAGQHIAK.S	1284.53185	2	3.04E-04	0.69	3.02	-	501.5
AHQ-2-1, 3316 - 3317	K.VTVLFAGQHIAK.S	1284.53185	2	6.00E-05	0.97	4.47	-	1489.0
AHQ-2-4, 5194	R.VTYCPTEPGNYIINIK.F	1884.14221	2	8.10E-04	0.84	3.29	-	594.9
AHQ-2-9, 4930	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.17E-04	0.65	3.19	-	295.6
AHQ-2-6, 5066	R.VTYCPTEPGNYIINIK.F	1884.14221	2	5.29E-05	0.60	2.80	-	290.3
AHQ-2-8, 4739 - 4791	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.16E-08	0.92	3.70	-	694.6
AHQ-2-7, 4819 - 4887	R.VTYCPTEPGNYIINIK.F	1884.14221	2	9.57E-10	0.92	4.46	-	499.9
AHQ-2-5, 4835 - 4911	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.18E-09	0.93	4.28	-	645.2
AHQ-2-5, 5047	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.52E-06	0.93	4.33	-	560.3
AHQ-2-13-, 4899	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.63E-05	0.67	3.39	-	251.6
AHQ-2-2, 5240	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.77E-04	0.79	2.82	-	509.8
AHQ-2-5, 5169	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.41E-05	0.73	3.16	-	217.2
AHQ-2-1, 5073	R.VTYCPTEPGNYIINIK.F	1884.14221	2	4.41E-06	0.86	3.59	-	602.8
AHQ-2-5, 4933 - 5003	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.25E-09	0.92	4.59	-	396.7
AHQ-2-3, 5208	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.27E-05	0.88	3.83	-	480.4
AHQ-2-1, 5257	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.83E-04	0.67	2.89	-	359.5
AHQ-2-8, 4996	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.40E-05	0.82	3.11	-	730.5
AHQ-2-5, 4831	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	2.35E-05	0.88	3.68	-	654.2
AHQ-2-2, 5668	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.94E-04	0.67	2.86	-	555.8
AHQ-2-14-, 5379 - 5403	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.22E-04	0.72	3.03	-	703.0
AHQ-2-13, 5327	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.84E-04	0.72	2.96	-	522.3
AHQ-2-7, 5191 - 5227	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	5.89E-05	0.73	3.25	-	486.8
AHQ-2-3, 5639	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.06E-04	0.63	2.57	-	511.7
AHQ-2-13-, 5426	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.99E-05	0.88	3.28	-	731.4
AHQ-2-6, 4785	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	3.83E-05	0.71	3.12	-	387.7
AHQ-2-11, 5156 - 5162	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	7.06E-04	0.81	3.43	-	481.9
AHQ-2-10, 4915 - 4931	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.61E-04	0.79	3.45	-	588.3
AHQ-2-10, 3022	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.03E-04	0.81	3.29	-	657.6
AHQ-2-1, 3526 - 3536	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.07E-05	0.88	3.14	-	869.6
AHQ-2-2, 3333 - 3361	R.YAPSEAGLHEMDIR.Y	1589.75482	2	7.72E-05	0.41	2.50	-	385.1
AHQ-2-13-, 3375 - 3381	R.YAPSEAGLHEMDIR.Y	1589.75482	2	3.80E-05	0.91	3.59	-	946.0
AHQ-2-3, 3336	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.83E-05	0.85	3.01	-	748.8
AHQ-2-4, 3336 - 3368	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.71E-04	0.46	2.66	-	444.3
AHQ-2-5, 2363	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	7.03E-04	0.79	3.04	-	688.9
AHQ-2-5, 3015 - 3083	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.10E-06	0.89	3.23	-	906.4
AHQ-2-7, 2947	R.YAPSEAGLHEMDIR.Y	1589.75482	2	9.96E-05	0.89	3.16	-	1096.4
AHQ-2-6, 3974 - 4045	K.YGGDEIPFSPYR.V	1401.50466	2	1.38E-04	0.75	2.85	-	603.6
AHQ-2-12, 4185	K.YGGDEIPFSPYR.V	1401.50466	2	1.93E-05	0.80	3.27	-	552.8
AHQ-2-2, 4380	K.YGGDEIPFSPYR.V	1401.50466	1	9.93E-04	0.27	2.34	-	385.2
AHQ-2-10, 3887	K.YGGDEIPFSPYR.V	1401.50466	1	3.07E-05	0.22	2.19	-	398.7
AHQ-2-10, 3886	K.YGGDEIPFSPYR.V	1401.50466	2	4.12E-04	0.70	3.48	-	443.3
AHQ-2-9, 4054	K.YGGDEIPFSPYR.V	1401.50466	2	2.32E-04	0.52	2.59	-	419.7
AHQ-2-4, 4324 - 4393	K.YGGDEIPFSPYR.V	1401.50466	2	5.67E-04	0.65	3.00	-	360.0
AHQ-2-12, 4190 - 4193	K.YGGDEIPFSPYR.V	1401.50466	1	1.28E-04	0.36	2.43	-	433.1
AHQ-2-9, 2948	K.YGGPYHIGGSPFK.A	1380.53182	2	9.93E-04	0.89	3.25	-	1138.5
AHQ-2-7, 2763 - 2835	K.YGGPYHIGGSPFK.A	1380.53182	2	5.55E-04	0.82	3.17	-	867.3
AHQ-2-4, 3268	K.YGGPYHIGGSPFK.A	1380.53182	1	4.04E-09	0.90	3.83	-	521.5
AHQ-2-5, 2911 - 2984	K.YGGPYHIGGSPFK.A	1380.53182	2	2.89E-07	0.96	4.60	-	1623.9
AHQ-2-7, 2829	K.YGGPYHIGGSPFK.A	1380.53182	1	2.00E-05	0.82	3.11	-	429.5
AHQ-2-10, 2934	K.YGGPYHIGGSPFK.A	1380.53182	2	7.92E-07	0.95	3.91	-	1568.8
AHQ-2-5, 2919	K.YGGPYHIGGSPFK.A	1380.53182	3	1.15E-05	0.87	3.98	-	617.3
AHQ-2-1, 3461	K.YGGPYHIGGSPFK.A	1380.53182	2	2.19E-05	0.96	3.99	-	1486.6
AHQ-2-14-, 3277	K.YGGPYHIGGSPFK.A	1380.53182	2	1.65E-07	0.97	4.75	-	1927.9
AHQ-2-5, 2928	K.YGGPYHIGGSPFK.A	1380.53182	1	1.33E-06	0.86	3.53	-	578.7
AHQ-2-4, 3249	K.YGGPYHIGGSPFK.A	1380.53182	2	7.24E-07	0.89	3.16	-	1213.9
AHQ-2-13-, 3337 - 3347	K.YGGPYHIGGSPFK.A	1380.53182	2	1.15E-05	0.95	4.07	-	1151.8
AHQ-2-2, 2989 - 3062	K.YGGQPVPNFPSK.L	1291.43658	2	1.04E-05	0.84	3.60	-	374.2
AHQ-2-1, 3121	K.YGGQPVPNFPSK.L	1291.43658	2	8.52E-05	0.93	3.51	-	782.3
AHQ-2-4, 2989	K.YGGQPVPNFPSK.L	1291.43658	1	6.37E-04	0.34	2.52	-	219.5
AHQ-2-4, 2984 - 3016	K.YGGQPVPNFPSK.L	1291.43658	2	8.06E-07	0.92	3.69	-	564.7
AHQ-2-2, 3002	K.YGGQPVPNFPSK.L	1291.43658	1	3.14E-04	0.43	2.63	-	478.2
AHQ-2-3, 2993	K.YGGQPVPNFPSK.L	1291.43658	1	1.25E-04	0.17	2.28	-	239.6
AHQ-2-3, 2987 - 2992	K.YGGQPVPNFPSK.L	1291.43658	2	1.73E-05	0.90	3.28	-	560.3
AHQ-2-3, 4297	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	6.86E-08	0.90	4.79	-	798.2
AHQ-2-7, 3667	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.37E-06	0.87	4.06	-	762.2
AHQ-2-6, 3829	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	2	1.08E-06	0.90	4.44	-	372.9
AHQ-2-6, 3826	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	6.02E-09	0.95	5.57	-	1050.3
AHQ-2-5, 3791 - 3865	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	7.04E-07	0.91	4.50	-	819.0
AHQ-2-5, 2475	K.YNEQHVPGSPFTAR.V	1603.71978	2	5.57E-07	0.86	3.56	-	448.3
AHQ-2-5, 2485 - 2489	K.YNEQHVPGSPFTAR.V	1603.71978	3	4.68E-06	0.94	4.75	-	1151.2
AHQ-2-5, 2792 - 2795	K.YNEQHVPGSPFTAR.V	1603.71978	2	3.47E-09	0.91	3.46	-	798.7
AHQ-2-9, 2531	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.42E-07	0.83	3.65	-	451.4
AHQ-2-6, 2534	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.37E-06	0.75	2.99	-	471.6
AHQ-2-6, 2545 - 2579	K.YNEQHVPGSPFTAR.V	1603.71978	3	1.29E-04	0.89	3.91	-	912.8
AHQ-2-4, 2701	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.16E-05	0.66	3.37	-	382.6
AHQ-2-7, 2461	K.YNEQHVPGSPFTAR.V	1603.71978	2	9.00E-04	0.35	2.58	-	232.2
AHQ-2-1, 2932 - 2949	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.31E-05	0.88	3.35	-	608.5
AHQ-2-10, 2502	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.41E-04	0.89	3.25	-	661.5
AHQ-2-8, 2243 - 2291	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.09E-04	0.91	3.49	-	715.4
AHQ-2-4, 3030	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.22E-05	0.81	3.17	-	444.1
AHQ-2-3, 4632 - 4703	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.78E-07	0.89	4.10	-	527.1
AHQ-2-3, 4771 - 4839	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.30E-08	0.93	4.64	-	700.2
AHQ-2-7, 4340	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.96E-04	0.93	4.34	-	783.8
AHQ-2-8, 4258	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.90E-07	0.80	3.59	-	368.6
AHQ-2-6, 4406	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.71E-04	0.88	4.02	-	493.2
AHQ-2-5, 4643	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.25E-05	0.92	3.92	-	773.9
AHQ-2-1, 4558	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.51E-05	0.80	3.33	-	530.9
AHQ-2-4, 4660 - 4677	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.07E-04	0.92	4.61	-	657.1
AHQ-2-4, 4748 - 4749	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.49E-07	0.89	4.44	-	506.0
AHQ-2-1, 4808 - 4881	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.01E-06	0.93	4.87	-	575.4
AHQ-2-5, 4483 - 4499	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.76E-06	0.93	4.37	-	743.3
AHQ-2-2, 4884 - 4901	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.57E-07	0.92	4.13	-	642.5
AHQ-2-2, 4746 - 4816	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.11E-06	0.92	4.34	-	654.6
AHQ-2-2, 4658 - 4728	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.91E-06	0.92	4.21	-	894.1
AHQ-2-2, 4526 - 4532	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.58E-06	0.92	4.34	-	768.9
AHQ-2-4, 4836	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.68E-07	0.89	3.98	-	586.3
AHQ-2-3, 4492	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.13E-04	0.82	3.36	-	464.2
AHQ-2-4, 6988	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.75E-07	0.81	3.49	-	527.2
AHQ-2-2, 6570 - 6640	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	9.09E-09	0.95	3.92	-	1452.5
AHQ-2-1, 7022	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	7.80E-08	0.91	3.53	-	1115.4
AHQ-2-1, 7013	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	5.81E-10	0.72	3.05	-	448.4
AHQ-2-1, 6854 - 6925	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	5.88E-07	0.91	3.69	-	873.4
AHQ-2-1, 6810 - 6876	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	4.42E-09	0.85	3.33	-	559.7
AHQ-2-1, 6506 - 6526	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	6.42E-07	0.71	3.23	-	447.3
AHQ-2-2, 6572 - 6645	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	2.16E-12	0.81	3.53	-	582.8

AHQ-2-2, 6945 - 6990	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.44E-08	0.94	4.21	-	889.8
AHQ-2-2, 6957 - 7028	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	9.20E-12	0.84	3.48	-	490.7
AHQ-2-5, 6767 - 6784	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.53E-05	0.92	4.27	-	726.9
AHQ-2-2, 7004 - 7072	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	1.45E-09	0.88	3.99	-	514.9
AHQ-2-3, 6899 - 6967	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.00E-04	0.89	3.80	-	704.0
AHQ-2-3, 6889 - 6972	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	1.69E-10	0.78	3.22	-	567.0
AHQ-2-4, 6626 - 6649	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	4.69E-07	0.75	2.82	-	662.8
gi|16753233|ref|NP_006280.2| talin 1 [Homo sapiens]				1.11E-15	118.32	1330.37	57.10	269665.3
AHQ-2-1, 3198 - 3272	K.AAAFEEQENETVVVK.E	1664.79496	2	2.35E-04	0.89	3.79	-	928.7
AHQ-2-5, 3151	K.AAAFEEQENETVVVK.E	1664.79496	2	4.99E-09	0.94	4.30	-	1065.8
AHQ-2-2, 3854	K.AAAFEEQENETVVVK.E	1664.79496	2	5.44E-04	0.44	2.95	-	390.1
AHQ-2-2, 4010	K.AAAFEEQENETVVVK.E	1664.79496	2	6.08E-05	0.84	3.84	-	761.0
AHQ-2-3, 3205	K.AAAFEEQENETVVVK.E	1664.79496	2	8.46E-04	0.22	2.52	-	361.7
AHQ-2-1, 3473	K.AAAFEEQENETVVVK.E	1664.79496	2	7.66E-08	0.90	3.73	-	859.3
AHQ-2-4, 3213 - 3220	K.AAAFEEQENETVVVK.E	1664.79496	2	2.70E-09	0.92	4.52	-	927.1
AHQ-2-4, 3365	K.AAAFEEQENETVVVK.E	1664.79496	2	1.47E-08	0.87	3.83	-	877.9
AHQ-2-2, 3113 - 3193	K.AAAFEEQENETVVVK.E	1664.79496	2	2.71E-06	0.93	4.20	-	1554.8
AHQ-2-3, 2469	R.AAM*EPIVISAK.T	1146.38260	2	1.11E-05	0.80	2.69	-	679.2
AHQ-2-4, 3140	R.AAMEPIVISAK.T	1130.38320	2	2.16E-05	0.85	2.53	-	754.4
AHQ-2-4, 2469	R.AAM*EPIVISAK.T	1146.38260	1	1.99E-04	0.50	2.35	-	221.3
AHQ-2-5, 2291	R.AAM*EPIVISAK.T	1146.38260	2	2.58E-06	0.84	2.99	-	742.6
AHQ-2-4, 2465	R.AAM*EPIVISAK.T	1146.38260	2	3.31E-05	0.89	2.75	-	1156.6
AHQ-2-3, 2467 - 2471	R.AAM*EPIVISAK.T	1146.38260	1	4.00E-04	0.26	2.20	-	190.1
AHQ-2-1, 2678	R.AAM*EPIVISAK.T	1146.38260	2	1.82E-05	0.84	2.64	-	832.6
AHQ-2-1, 2693	R.AAM*EPIVISAK.T	1146.38260	1	1.65E-05	0.59	2.92	-	265.0
AHQ-2-10, 2824	R.AAMEPIVISAK.T	1130.38320	1	1.50E-04	0.33	1.97	-	658.5
AHQ-2-2, 2496	R.AAM*EPIVISAK.T	1146.38260	1	4.87E-05	0.46	2.81	-	190.3
AHQ-2-2, 2489	R.AAM*EPIVISAK.T	1146.38260	2	1.92E-07	0.92	3.07	-	1126.8
AHQ-2-2, 1833	K.ADAEGESDLENSR.K	1393.35296	2	5.98E-08	0.74	2.83	-	613.0
AHQ-2-1, 2037	K.ADAEGESDLENSR.K	1393.35296	2	5.30E-08	0.92	3.36	-	1096.7
AHQ-2-5, 2417 - 2419	K.AGALQCSPSDAYTK.K	1470.58689	2	2.33E-07	0.92	3.96	-	825.6
AHQ-2-2, 2594	K.AGALQCSPSDAYTK.K	1470.58689	1	1.44E-05	0.82	3.90	-	476.0
AHQ-2-5, 2428	K.AGALQCSPSDAYTK.K	1470.58689	1	2.76E-07	0.81	3.57	-	472.8
AHQ-2-4, 2565	K.AGALQCSPSDAYTK.K	1470.58689	2	5.20E-07	0.93	3.72	-	1010.1
AHQ-2-6, 2426	K.AGALQCSPSDAYTK.K	1470.58689	2	3.77E-06	0.90	3.59	-	799.6
AHQ-2-4, 2585	K.AGALQCSPSDAYTK.K	1470.58689	1	3.34E-05	0.73	3.17	-	492.3
AHQ-2-1, 2710 - 2712	K.AGALQCSPSDAYTK.K	1470.58689	2	1.83E-06	0.93	4.19	-	877.3
AHQ-2-3, 2587	K.AGALQCSPSDAYTK.K	1470.58689	1	9.53E-07	0.68	3.23	-	378.0
AHQ-2-1, 2526	K.AGALQCSPSDAYTK.K	1470.58689	2	9.53E-05	0.83	3.18	-	721.6
AHQ-2-2, 2312	K.AGALQCSPSDAYTKK.E	1598.75981	2	3.16E-04	0.89	3.72	-	736.6
AHQ-2-4, 2264 - 2281	K.AGALQCSPSDAYTKK.E	1598.75981	2	1.59E-04	0.79	3.25	-	583.9
AHQ-2-9, 6210	K.AGFLDLKDFLPK.E	1364.61374	2	4.53E-04	0.90	3.18	-	1389.6
AHQ-2-1, 4248	K.AIAVTVQEMVTK.S	1290.55498	2	2.23E-06	0.96	4.27	-	1329.8
AHQ-2-2, 4041 - 4053	K.AIAVTVQEMVTK.S	1290.55498	2	1.19E-04	0.96	5.29	-	1228.5
AHQ-2-4, 3980 - 4000	K.AIAVTVQEMVTK.S	1290.55498	2	2.10E-09	0.96	5.04	-	1121.8
AHQ-2-1, 3028	K.AIAVTVQEM*VTK.S	1306.55438	2	3.45E-05	0.91	3.60	-	812.9
AHQ-2-2, 4126 - 4196	K.AIAVTVQEMVTK.S	1290.55498	2	3.38E-09	0.94	4.12	-	1221.2
AHQ-2-3, 4005 - 4085	K.AIAVTVQEMVTK.S	1290.55498	2	5.38E-07	0.95	4.08	-	1265.5
AHQ-2-4, 2576 - 2582	K.ALDGAFTEENR.A	1223.27427	2	3.52E-07	0.94	3.92	-	1228.7
AHQ-2-3, 2441	K.ALDGAFTEENR.A	1223.27427	2	5.66E-06	0.93	3.57	-	1269.8
AHQ-2-2, 2458 - 2465	K.ALDGAFTEENR.A	1223.27427	2	5.68E-06	0.95	3.98	-	1758.7
AHQ-2-5, 2401 - 2404	K.ALDGAFTEENR.A	1223.27427	1	6.87E-04	0.22	1.96	-	233.6
AHQ-2-4, 2440 - 2510	K.ALDGAFTEENR.A	1223.27427	2	4.84E-07	0.94	3.49	-	1485.7
AHQ-2-12, 3799	K.ALDYYMLR.N	1045.23686	2	1.55E-04	0.90	2.68	-	1067.1
AHQ-2-13-, 3306	K.ALDYYM*LR.N	1061.23626	2	5.58E-06	0.82	2.55	-	732.4
AHQ-2-13, 3320	K.ALDYYM*LR.N	1061.23626	2	2.16E-06	0.92	3.03	-	1056.2
AHQ-2-13, 3952	K.ALDYYMLR.N	1045.23686	2	1.46E-06	0.95	4.13	-	942.1
AHQ-2-13-, 3994 - 3999	K.ALDYYMLR.N	1045.23686	2	3.56E-07	0.93	3.70	-	818.5
AHQ-2-7, 1573	R.ALEATTEHIR.Q	1141.25953	2	4.18E-05	0.93	3.51	-	1428.0
AHQ-2-5, 1559	R.ALEATTEHIR.Q	1141.25953	2	5.35E-04	0.73	3.01	-	742.6
AHQ-2-2, 1724 - 1792	R.ALEATTEHIR.Q	1141.25953	2	1.38E-05	0.92	3.44	-	1340.5
AHQ-2-4, 1741 - 1806	R.ALEATTEHIR.Q	1141.25953	2	2.10E-06	0.88	2.73	-	1309.1
AHQ-2-1, 2077	R.ALEATTEHIR.Q	1141.25953	1	3.85E-05	0.02	1.86	-	193.4
AHQ-2-1, 2062	R.ALEATTEHIR.Q	1141.25953	2	5.63E-07	0.85	3.00	-	1106.8
AHQ-2-4, 3440	K.ALGDLISATK.A	989.14811	2	6.11E-05	0.93	3.64	-	912.2
AHQ-2-2, 3433	K.ALGDLISATK.A	989.14811	2	5.58E-05	0.90	4.01	-	680.5
AHQ-2-7, 3113	K.ALGDLISATK.A	989.14811	2	3.40E-08	0.92	3.39	-	902.8
AHQ-2-5, 3199	K.ALGDLISATK.A	989.14811	2	1.08E-06	0.91	3.58	-	832.1
AHQ-2-1, 3564	K.ALGDLISATK.A	989.14811	2	5.31E-05	0.91	3.54	-	798.4
AHQ-2-6, 3178 - 3187	K.ALGDLISATK.A	989.14811	2	1.59E-07	0.95	4.41	-	954.9
AHQ-2-3, 3431 - 3432	K.ALGDLISATK.A	989.14811	2	3.08E-06	0.91	3.62	-	763.8
AHQ-2-1, 2729 - 2733	K.ALSTDPAAPNLK.S	1198.35099	2	4.82E-05	0.66	2.67	-	480.4
AHQ-2-4, 2485 - 2556	K.ALSTDPAAPNLK.S	1198.35099	2	1.48E-04	0.80	3.47	-	577.2
AHQ-2-2, 2553 - 2554	K.ALSTDPAAPNLK.S	1198.35099	2	1.24E-06	0.78	3.11	-	610.8
AHQ-2-5, 2377 - 2457	K.ALSTDPAAPNLK.S	1198.35099	2	4.91E-08	0.73	2.98	-	613.4
AHQ-2-6, 2389	K.ALSTDPAAPNLK.S	1198.35099	2	7.72E-07	0.59	2.63	-	581.8
AHQ-2-3, 2548 - 2565	K.ALSTDPAAPNLK.S	1198.35099	2	3.93E-07	0.84	3.27	-	775.7
AHQ-2-13-, 2653	K.ALSTDPAAPNLK.S	1198.35099	2	8.78E-05	0.69	2.73	-	638.0
AHQ-2-2, 3580	K.ALSTDPAAPNLKSQLAAAAR.A	1967.21592	2	1.09E-08	0.83	3.43	-	506.0
AHQ-2-3, 3555 - 3560	K.ALSTDPAAPNLKSQLAAAAR.A	1967.21592	2	9.62E-06	0.91	3.93	-	693.6
AHQ-2-3, 6676 - 6744	R.ANQAIQMACQSLGEPGCTQAQVLSAATIVAK.H	3220.64522	3	4.16E-04	0.90	4.69	-	833.0
AHQ-2-2, 7384 - 7456	R.ANQAIQMACQSLGEPGCTQAQVLSAATIVAK.H	3220.64522	3	3.49E-06	0.91	4.89	-	711.4
AHQ-2-1, 6600 - 6673	R.ANQAIQMACQSLGEPGCTQAQVLSAATIVAK.H	3220.64522	3	6.55E-05	0.94	4.88	-	1066.4
AHQ-2-2, 6498	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.35E-09	0.97	4.82	-	1445.7
AHQ-2-4, 6534	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.70E-07	0.97	5.26	-	1283.2
AHQ-2-5, 6295	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.94E-07	0.98	5.98	-	1546.8
AHQ-2-4, 5782	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.78E-05	0.68	3.46	-	434.7
AHQ-2-3, 5763 - 5768	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.65E-07	0.97	5.32	-	1187.6
AHQ-2-2, 5822	K.APGQLECETAIAALNSCLR.D	2077.32566	2	8.79E-09	0.96	4.61	-	1446.7
AHQ-2-1, 6424	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.48E-06	0.91	3.98	-	1172.5
AHQ-2-3, 6464	K.APGQLECETAIAALNSCLR.D	2077.32566	2	9.29E-05	0.96	4.85	-	1196.7
AHQ-2-1, 7002	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	5.64E-06	0.96	5.38	-	1257.6
AHQ-2-2, 7177 - 7178	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	2.93E-11	0.96	5.19	-	1853.4
AHQ-2-5, 2624 - 2625	K.ASAGPQPLLVQSCK.A	1457.67763	1	4.86E-04	0.25	2.07	-	326.8
AHQ-2-3, 2855 - 2895	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.03E-05	0.87	3.84	-	406.7
AHQ-2-2, 3118	K.ASAGPQPLLVQSCK.A	1457.67763	2	5.43E-09	0.77	2.88	-	455.8
AHQ-2-6, 2626 - 2677	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.40E-06	0.87	3.94	-	481.7
AHQ-2-7, 2568	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.02E-09	0.82	3.70	-	467.3
AHQ-2-2, 2878	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.45E-05	0.46	2.86	-	403.2
AHQ-2-2, 2846 - 2916	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.28E-09	0.90	4.32	-	475.4
AHQ-2-4, 2825 - 2896	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.24E-09	0.93	4.36	-	690.3
AHQ-2-4, 2872	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.04E-05	0.59	3.04	-	397.1
AHQ-2-4, 3186	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.95E-05	0.80	2.94	-	575.5
AHQ-2-7, 2577	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.10E-13	0.75	3.48	-	471.5
AHQ-2-1, 3001 - 3076	K.ASAGPQPLLVQSCK.A	1457.67763	2	3.17E-10	0.93	4.52	-	583.6
AHQ-2-6, 2673 - 2743	K.ASAGPQPLLVQSCK.A	1457.67763	1	2.71E-05	0.11	2.07	-	287.3
AHQ-2-5, 2608 - 2623	K.ASAGPQPLLVQSCK.A	1457.67763	2	6.52E-07	0.80	3.41	-	361.1

AHQ-2-3, 4079	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.49E-04	0.65	3.20	-	338.3
AHQ-2-4, 4352 - 4420	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.11E-14	0.95	5.30	-	665.7
AHQ-2-7, 4083	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	5.43E-07	0.93	4.25	-	1018.3
AHQ-2-2, 4412 - 4484	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.68E-07	0.94	4.80	-	737.1
AHQ-2-4, 4045 - 4049	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.40E-05	0.87	3.83	-	532.7
AHQ-2-3, 4515 - 4592	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.84E-08	0.96	5.10	-	857.8
AHQ-2-5, 4187	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	5.32E-06	0.92	3.97	-	934.7
AHQ-2-4, 3764	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	3.13E-05	0.57	2.74	-	393.0
AHQ-2-3, 4376 - 4447	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	7.20E-09	0.92	4.48	-	657.4
AHQ-2-6, 4258	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	4.25E-04	0.81	3.71	-	447.2
AHQ-2-2, 4548 - 4616	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.36E-08	0.89	4.24	-	418.5
AHQ-2-6, 4093	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.13E-10	0.90	4.29	-	590.3
AHQ-2-1, 4446 - 4460	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	9.18E-05	0.89	4.01	-	575.1
AHQ-2-5, 4343	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.22E-09	0.82	3.75	-	385.9
AHQ-2-6, 3530	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.63E-06	0.93	4.54	-	664.0
AHQ-2-2, 3966 - 3973	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	8.29E-07	0.95	5.00	-	872.9
AHQ-2-4, 4452 - 4520	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	6.78E-07	0.87	4.10	-	521.2
AHQ-2-1, 5150 - 5161	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.54E-06	0.75	3.08	-	499.8
AHQ-2-6, 4767	K.AVAEQIPLLVQGVR.G	1493.77619	1	5.94E-06	0.60	2.87	-	163.0
AHQ-2-6, 4725	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.46E-06	0.88	3.57	-	643.7
AHQ-2-3, 5071	K.AVAEQIPLLVQGVR.G	1493.77619	1	8.65E-07	0.77	3.56	-	385.8
AHQ-2-2, 5146	K.AVAEQIPLLVQGVR.G	1493.77619	3	6.34E-06	0.94	4.59	-	1492.9
AHQ-2-4, 5078	K.AVAEQIPLLVQGVR.G	1493.77619	1	1.31E-06	0.43	3.23	-	145.5
AHQ-2-4, 5044 - 5057	K.AVAEQIPLLVQGVR.G	1493.77619	2	8.21E-04	0.86	3.80	-	523.4
AHQ-2-3, 5044 - 5119	K.AVAEQIPLLVQGVR.G	1493.77619	2	5.33E-07	0.92	4.27	-	675.8
AHQ-2-5, 4773	K.AVAEQIPLLVQGVR.G	1493.77619	1	3.94E-07	0.41	2.70	-	189.5
AHQ-2-2, 5077 - 5098	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.19E-07	0.79	3.22	-	694.9
AHQ-2-1, 4042	K.AVASAAAALVLK.A	1085.32216	2	7.22E-06	0.96	4.36	-	1352.0
AHQ-2-2, 3902	K.AVASAAAALVLK.A	1085.32216	2	6.36E-08	0.97	4.24	-	1777.7
AHQ-2-2, 4012	K.AVASAAAALVLK.A	1085.32216	2	1.39E-05	0.96	4.19	-	1720.7
AHQ-2-1, 3914	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.66E-05	0.93	4.41	-	1054.9
AHQ-2-2, 5006	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.75E-06	0.88	3.81	-	960.3
AHQ-2-5, 4964	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.89E-04	0.46	2.77	-	591.9
AHQ-2-2, 3957 - 4034	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.42E-08	0.95	4.13	-	1532.3
AHQ-2-1, 4021	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.52E-07	0.79	3.36	-	940.2
AHQ-2-2, 4265 - 4338	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.91E-06	0.92	4.49	-	903.8
AHQ-2-2, 4838 - 4898	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.08E-06	0.94	4.33	-	1303.3
AHQ-2-1, 4388	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.58E-04	0.95	4.59	-	1455.6
AHQ-2-4, 4298	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.29E-04	0.77	3.37	-	732.1
AHQ-2-3, 4163 - 4231	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.37E-06	0.81	3.63	-	739.9
AHQ-2-2, 4409	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.13E-07	0.96	4.99	-	1477.7
AHQ-2-1, 4213 - 4245	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.26E-07	0.92	3.94	-	1051.5
AHQ-2-1, 4233	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	3	2.17E-05	0.87	3.80	-	1250.3
AHQ-2-3, 7449 - 7459	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.80E-08	0.97	5.78	-	2051.6
AHQ-2-6, 6010 - 6021	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.49E-06	0.86	4.14	-	589.3
AHQ-2-3, 4911	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	7.78E-06	0.72	3.66	-	384.9
AHQ-2-1, 6216 - 6225	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.87E-04	0.55	3.08	-	472.8
AHQ-2-4, 4929	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.52E-07	0.84	3.48	-	538.5
AHQ-2-2, 5904	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	7.05E-04	0.34	2.93	-	203.0
AHQ-2-2, 4962	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.03E-07	0.89	4.40	-	461.4
AHQ-2-4, 5897 - 5904	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	5.32E-04	0.63	3.23	-	286.3
AHQ-2-1, 6304 - 6372	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	8.48E-09	0.92	4.77	-	982.6
AHQ-2-7, 6077	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.16E-12	0.91	5.03	-	774.0
AHQ-2-3, 6347 - 6415	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	2.27E-11	0.96	6.11	-	1183.0
AHQ-2-1, 6004	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	2.84E-09	0.93	5.18	-	870.9
AHQ-2-5, 6268	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	4.10E-10	0.95	5.24	-	1329.8
AHQ-2-4, 6364 - 6432	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	2.81E-11	0.94	5.40	-	1085.9
AHQ-2-2, 5173	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	8.90E-08	0.84	4.41	-	590.9
AHQ-2-5, 6179	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.11E-15	0.93	4.77	-	1240.2
AHQ-2-4, 6017 - 6032	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	6.38E-10	0.92	5.09	-	890.5
AHQ-2-6, 6058	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	8.05E-10	0.92	4.54	-	1050.5
AHQ-2-2, 7389 - 7402	R.AVTDSINQLITMCTQQAPGQKECDNALRELETVR.E	3894.32086	3	8.58E-04	0.51	3.54	-	227.4
AHQ-2-2, 2416 - 2417	R.CVSCLPGQR.D	1079.23309	2	1.75E-05	0.89	3.14	-	927.0
AHQ-2-5, 2261 - 2263	R.CVSCLPGQR.D	1079.23309	1	1.82E-05	0.29	2.19	-	117.8
AHQ-2-2, 2406	R.CVSCLPGQR.D	1079.23309	1	6.86E-04	0.08	1.88	-	146.7
AHQ-2-3, 2380 - 2391	R.CVSCLPGQR.D	1079.23309	2	9.92E-05	0.83	2.95	-	724.6
AHQ-2-10, 3395	R.DDILNGSHPVSFDK.A	1544.64741	2	6.04E-08	0.96	3.95	-	1762.0
AHQ-2-11, 3358	R.DDILNGSHPVSFDK.A	1544.64741	2	2.59E-04	0.59	2.55	-	604.3
AHQ-2-10, 3227 - 3291	R.DDILNGSHPVSFDK.A	1544.64741	2	1.57E-07	0.87	3.66	-	890.3
AHQ-2-7, 3455 - 3508	R.DDILNGSHPVSFDK.A	1544.64741	2	4.14E-11	0.92	3.83	-	1030.4
AHQ-2-8, 3424	R.DDILNGSHPVSFDK.A	1544.64741	2	1.31E-07	0.90	3.59	-	977.8
AHQ-2-7, 3323 - 3335	R.DDILNGSHPVSFDK.A	1544.64741	2	9.79E-10	0.94	3.97	-	1036.0
AHQ-2-8, 3243	R.DDILNGSHPVSFDK.A	1544.64741	2	1.58E-07	0.91	3.77	-	910.4
AHQ-2-1, 3694	R.DDILNGSHPVSFDK.A	1544.64741	2	7.21E-04	0.66	2.72	-	489.5
AHQ-2-9, 3259 - 3330	R.DDILNGSHPVSFDK.A	1544.64741	2	3.51E-10	0.95	4.02	-	1318.7
AHQ-2-7, 4783	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	4.93E-04	0.84	3.60	-	752.8
AHQ-2-3, 5808 - 5875	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.19E-09	0.79	3.34	-	833.6
AHQ-2-3, 5491 - 5493	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.14E-10	0.95	4.66	-	1161.1
AHQ-2-7, 5960	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.26E-11	0.87	4.05	-	608.1
AHQ-2-4, 6013	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	7.60E-04	0.82	3.34	-	622.1
AHQ-2-1, 5512	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.03E-05	0.91	4.40	-	809.2
AHQ-2-6, 5953	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.13E-09	0.96	4.96	-	1207.8
AHQ-2-3, 6009	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.17E-05	0.91	4.34	-	761.4
AHQ-2-2, 5477 - 5549	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.99E-11	0.93	4.11	-	950.7
AHQ-2-1, 6232	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.73E-10	0.92	4.29	-	609.4
AHQ-2-9, 6024	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	8.03E-08	0.91	4.11	-	872.2
AHQ-2-4, 6310	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.26E-08	0.96	5.30	-	855.6
AHQ-2-2, 6042	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.06E-06	0.91	4.02	-	894.0
AHQ-2-3, 6255 - 6264	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.09E-06	0.97	5.20	-	1383.3
AHQ-2-4, 6565	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.22E-15	0.93	4.37	-	920.6
AHQ-2-1, 5853	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	8.08E-07	0.88	3.63	-	890.1
AHQ-2-2, 6304 - 6376	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.57E-10	0.96	4.77	-	1175.3
AHQ-2-5, 6068	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.38E-07	0.94	4.67	-	978.3
AHQ-2-5, 6325	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.59E-10	0.94	4.74	-	842.9
AHQ-2-3, 6417 - 6492	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.05E-14	0.95	5.09	-	927.1
AHQ-2-5, 5297	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.78E-15	0.93	4.53	-	946.9
AHQ-2-2, 6520	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.02E-11	0.92	3.96	-	786.6
AHQ-2-4, 6484	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.25E-08	0.95	4.44	-	1004.8
AHQ-2-4, 4848 - 4857	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.33E-06	0.85	3.58	-	757.8
AHQ-2-3, 5463 - 5535	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.79E-04	0.93	4.74	-	647.5
AHQ-2-2, 5506 - 5580	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.31E-04	0.93	4.48	-	745.9
AHQ-2-3, 5476	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	7.10E-06	0.90	3.94	-	1596.8
AHQ-2-2, 5528	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	3.62E-07	0.96	4.88	-	1940.0
AHQ-2-4, 5488 - 5568	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.74E-09	0.96	4.63	-	1550.3
AHQ-2-4, 5509	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	1.35E-05	0.95	4.47	-	1984.8
AHQ-2-11, 5032 - 5033	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.48E-04	0.43	2.88	-	395.1
AHQ-2-1, 5488 - 5493	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	1.83E-06	0.93	4.58	-	1587.1

AHQ-2-5, 3227	R.DPPSWSVLAGHSR.T	1409.53156	3	9.41E-07	0.90	4.30	-	753.1
AHQ-2-1, 3750	R.DPPSWSVLAGHSR.T	1409.53156	3	3.69E-07	0.84	3.66	-	577.9
AHQ-2-2, 3526 - 3606	R.DPPSWSVLAGHSR.T	1409.53156	2	6.56E-08	0.90	3.13	-	633.2
AHQ-2-4, 3524 - 3526	R.DPPSWSVLAGHSR.T	1409.53156	2	3.67E-10	0.95	3.97	-	881.3
AHQ-2-2, 3545	R.DPPSWSVLAGHSR.T	1409.53156	3	3.61E-08	0.92	4.10	-	980.6
AHQ-2-3, 3516 - 3539	R.DPPSWSVLAGHSR.T	1409.53156	2	4.08E-08	0.94	3.99	-	732.8
AHQ-2-10, 4790	R.DPVQLNLLYVQAR.D	1529.76539	2	1.02E-06	0.96	4.04	-	1725.9
AHQ-2-7, 5219	R.DPVQLNLLYVQAR.D	1529.76539	2	1.56E-05	0.96	3.63	-	2076.7
AHQ-2-9, 5152	R.DPVQLNLLYVQAR.D	1529.76539	2	3.57E-06	0.91	3.76	-	1141.7
AHQ-2-3, 2357	K.EAAYHPEVAPDVR.L	1454.56910	2	2.00E-04	0.89	2.77	-	1127.8
AHQ-2-7, 2152	K.EAAYHPEVAPDVR.L	1454.56910	1	3.11E-05	0.50	2.19	-	292.4
AHQ-2-4, 2352 - 2353	K.EAAYHPEVAPDVR.L	1454.56910	2	4.38E-06	0.78	3.02	-	622.9
AHQ-2-4, 2362	K.EAAYHPEVAPDVR.L	1454.56910	1	3.63E-10	0.83	3.27	-	526.1
AHQ-2-5, 2185	K.EAAYHPEVAPDVR.L	1454.56910	2	3.88E-05	0.73	2.66	-	734.3
AHQ-2-8, 2088 - 2096	K.EAAYHPEVAPDVR.L	1454.56910	2	1.12E-08	0.85	3.08	-	868.8
AHQ-2-1, 6245 - 6313	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.50E-05	0.91	3.85	-	1316.4
AHQ-2-10, 5518 - 5579	K.EADESLNFEEQILEAAK.S	1937.05072	2	8.77E-09	0.94	4.50	-	1302.6
AHQ-2-14-, 5820	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.94E-05	0.62	2.96	-	739.7
AHQ-2-3, 6397 - 6471	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.43E-07	0.83	3.65	-	925.7
AHQ-2-5, 6052 - 6132	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.24E-09	0.96	4.98	-	1282.8
AHQ-2-4, 6254 - 6328	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.38E-06	0.96	5.46	-	1309.1
AHQ-2-9, 6151	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.71E-06	0.72	3.01	-	618.1
AHQ-2-6, 5914	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.64E-06	0.82	3.50	-	853.2
AHQ-2-9, 5999 - 6075	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.28E-05	0.87	3.84	-	818.1
AHQ-2-5, 6201	K.EADESLNFEEQILEAAK.S	1937.05072	2	9.68E-04	0.89	4.15	-	761.7
AHQ-2-5, 6340	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.55E-08	0.95	5.23	-	1056.5
AHQ-2-6, 6029	K.EADESLNFEEQILEAAK.S	1937.05072	2	8.69E-07	0.97	4.75	-	1540.7
AHQ-2-2, 6714 - 6786	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.99E-04	0.28	2.58	-	424.5
AHQ-2-3, 6715	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.29E-04	0.62	3.74	-	361.4
AHQ-2-4, 6788	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.02E-04	0.79	3.55	-	559.6
AHQ-2-11, 5636	K.EADESLNFEEQILEAAK.S	1937.05072	2	8.08E-05	0.91	3.92	-	1258.3
AHQ-2-7, 6009	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.67E-04	0.82	3.91	-	800.3
AHQ-2-11, 5770 - 5789	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.37E-04	0.69	3.03	-	795.1
AHQ-2-2, 6252 - 6325	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.35E-08	0.96	4.90	-	1465.1
AHQ-2-1, 6122 - 6192	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.74E-09	0.96	5.39	-	1393.6
AHQ-2-2, 6344 - 6412	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.91E-09	0.98	5.76	-	1782.2
AHQ-2-2, 6484 - 6486	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.45E-06	0.95	4.99	-	1350.2
AHQ-2-4, 6396 - 6464	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.42E-06	0.97	5.43	-	1710.8
AHQ-2-3, 6208 - 6276	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.28E-07	0.96	5.02	-	1615.1
AHQ-2-4, 6018	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.76E-05	0.91	4.50	-	771.7
AHQ-2-3, 7561 - 7563	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	7.55E-10	0.96	5.10	-	1654.0
AHQ-2-8, 7427	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	7.39E-06	0.81	3.24	-	991.5
AHQ-2-2, 7606 - 7608	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	5.19E-12	0.96	5.43	-	1434.1
AHQ-2-9, 7450	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	6.90E-09	0.88	3.66	-	790.7
AHQ-2-4, 7620 - 7638	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	7.25E-11	0.97	5.87	-	1295.2
AHQ-2-6, 7262 - 7263	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	6.67E-10	0.91	4.66	-	934.4
AHQ-2-5, 7429 - 7509	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	2.94E-05	0.90	4.23	-	537.0
AHQ-2-5, 7507	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	2.81E-12	0.96	5.91	-	1252.5
AHQ-2-6, 7298 - 7318	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	3.33E-15	0.97	6.23	-	1822.7
AHQ-2-3, 7533 - 7607	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.11E-09	0.95	5.84	-	860.3
AHQ-2-3, 7627	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	6.89E-07	0.96	5.86	-	1193.2
AHQ-2-2, 7604 - 7674	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.87E-10	0.93	5.05	-	979.4
AHQ-2-1, 7274 - 7341	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	7.54E-04	0.73	3.77	-	436.7
AHQ-2-5, 7540 - 7600	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	6.45E-07	0.97	5.06	-	2291.9
AHQ-2-7, 7575	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.92E-08	0.93	5.04	-	1199.3
AHQ-2-9, 7515 - 7518	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	4.44E-06	0.95	5.57	-	1295.1
AHQ-2-4, 7618 - 7689	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.39E-12	0.96	6.21	-	1258.4
AHQ-2-5, 7427	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	8.49E-06	0.91	4.47	-	863.2
AHQ-2-4, 7516	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	3.36E-04	0.88	4.44	-	742.7
AHQ-2-2, 7469 - 7544	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.85E-06	0.95	5.38	-	1131.9
AHQ-2-8, 7486	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	7.23E-08	0.95	5.19	-	1449.1
AHQ-2-2, 7270 - 7349	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	2.53E-05	0.60	3.51	-	335.6
AHQ-2-4, 7342 - 7409	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	2.52E-05	0.65	4.25	-	330.8
AHQ-2-7, 2704	R.ELMEEKKEEITGTLR.K	1807.05950	2	2.53E-09	0.80	3.71	-	467.0
AHQ-2-7, 2147	R.ELM*EEKKEEITGTLR.K	1823.05890	2	5.73E-04	0.36	2.52	-	266.9
AHQ-2-7, 2613 - 2695	R.EQGVEEHETLLLR.R	1553.69898	2	7.17E-04	0.85	3.75	-	455.8
AHQ-2-7, 2860	R.EQGVEEHETLLLR.R	1553.69898	2	8.57E-09	0.58	3.00	-	257.9
AHQ-2-13-, 5557	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	4.03E-12	0.98	6.95	-	1421.2
AHQ-2-7, 5447	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	3.81E-09	0.97	6.45	-	1515.4
AHQ-2-13, 5436 - 5461	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	9.29E-08	0.97	6.03	-	1684.0
AHQ-2-13-, 5203 - 5205	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	2.33E-11	0.98	6.46	-	1843.3
AHQ-2-13, 5113	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	6.96E-11	0.97	6.23	-	1832.3
AHQ-2-7, 4903 - 4912	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	5.63E-12	0.98	6.71	-	1951.4
AHQ-2-4, 2278	K.EVANSTANLVK.T	1146.27608	2	2.75E-04	0.73	2.50	-	797.5
AHQ-2-2, 2046	K.EVANSTANLVK.T	1146.27608	2	4.47E-04	0.85	2.73	-	1015.9
AHQ-2-4, 2276	K.EVANSTANLVK.T	1146.27608	1	1.95E-04	0.25	1.89	-	279.4
AHQ-2-3, 2048 - 2071	K.EVANSTANLVK.T	1146.27608	2	5.35E-04	0.74	3.09	-	677.4
AHQ-2-8, 4340	K.EVIQEWNLTNIK.R	1487.68214	2	5.54E-05	0.93	3.75	-	1522.4
AHQ-2-7, 4457	K.EVIQEWNLTNIK.R	1487.68214	1	1.79E-05	0.72	3.64	-	260.5
AHQ-2-10, 4292	K.EVIQEWNLTNIK.R	1487.68214	2	1.68E-05	0.76	3.11	-	725.9
AHQ-2-12, 4709	K.EVIQEWNLTNIK.R	1487.68214	2	2.44E-04	0.86	3.48	-	982.4
AHQ-2-11, 4549	K.EVIQEWNLTNIK.R	1487.68214	2	3.70E-07	0.84	3.24	-	873.0
AHQ-2-7, 3748	K.EVIQEWNLTNIKR.W	1643.86849	2	5.29E-06	0.81	3.46	-	696.9
AHQ-2-8, 2735	K.FFYSDQNVDSR.D	1378.42795	2	6.39E-06	0.86	2.94	-	838.7
AHQ-2-7, 2872	K.FFYSDQNVDSR.D	1378.42795	2	3.37E-04	0.71	2.60	-	430.5
AHQ-2-8, 5936	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	1.10E-10	0.97	5.91	-	1672.6
AHQ-2-7, 5955 - 6025	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	3.82E-11	0.98	6.78	-	2150.9
AHQ-2-2, 7792	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	1.37E-08	0.83	4.40	-	660.3
AHQ-2-3, 6596 - 6665	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	1.09E-06	0.90	4.14	-	1046.1
AHQ-2-3, 7651 - 7727	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	5.24E-09	0.88	3.16	-	1184.8
AHQ-2-3, 7733	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	2.19E-05	0.78	3.77	-	609.4
AHQ-2-4, 6664 - 6738	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	1.33E-07	0.86	3.74	-	888.4
AHQ-2-1, 7145	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	2.11E-06	0.75	2.96	-	782.3
AHQ-2-1, 6505	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	9.09E-07	0.92	4.38	-	952.2
AHQ-2-1, 6497 - 6566	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	4.97E-08	0.92	5.09	-	684.0
AHQ-2-2, 7482	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	6.51E-04	0.68	2.58	-	1002.1
AHQ-2-2, 7497	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	8.42E-05	0.81	3.40	-	813.3
AHQ-2-1, 2890	K.FLPSELRDEH	1243.35032	2	1.89E-07	0.62	2.50	-	310.2
AHQ-2-5, 4903	K.GLAGAVSELLR.S	1086.26701	2	1.15E-06	0.98	5.11	-	2177.4
AHQ-2-3, 5231	K.GLAGAVSELLR.S	1086.26701	2	3.76E-05	0.97	4.28	-	1864.9
AHQ-2-2, 5265 - 5272	K.GLAGAVSELLR.S	1086.26701	2	1.72E-07	0.97	5.10	-	1793.0
AHQ-2-8, 4599	K.GLAGAVSELLR.S	1086.26701	2	1.77E-06	0.98	5.21	-	2090.9
AHQ-2-4, 5200	K.GLAGAVSELLR.S	1086.26701	2	2.08E-06	0.98	5.05	-	2326.4
AHQ-2-6, 4878	K.GLAGAVSELLR.S	1086.26701	2	8.09E-07	0.98	5.09	-	2219.0
AHQ-2-1, 5353	K.GLAGAVSELLR.S	1086.26701	2	7.23E-05	0.97	4.47	-	1728.0
AHQ-2-9, 4831	K.GLAGAVSELLR.S	1086.26701	2	3.73E-06	0.98	5.04	-	2189.9
AHQ-2-5, 6727 - 6799	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.44E-04	0.96	5.62	-	825.9

AHQ-2-2, 6972 - 7052	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.30E-05	0.92	4.97	-	717.5
AHQ-2-2, 7414	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	3.55E-04	0.92	4.37	-	730.1
AHQ-2-2, 7412 - 7420	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.12E-07	0.93	4.85	-	1040.4
AHQ-2-6, 6566 - 6633	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.51E-06	0.95	5.50	-	782.8
AHQ-2-4, 6948	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.55E-07	0.94	5.69	-	707.9
AHQ-2-3, 6869 - 6951	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	3.11E-05	0.94	5.03	-	725.7
AHQ-2-3, 7312 - 7335	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	7.17E-05	0.88	4.18	-	581.3
AHQ-2-2, 7256 - 7324	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.28E-04	0.72	3.10	-	503.8
AHQ-2-2, 6852 - 6928	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.23E-05	0.92	4.90	-	868.0
AHQ-2-1, 6817 - 6888	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	5.06E-07	0.95	5.39	-	1052.9
AHQ-2-6, 6506 - 6569	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	4.86E-08	0.94	5.11	-	866.4
AHQ-2-4, 6941 - 7012	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.77E-07	0.96	5.52	-	1096.5
AHQ-2-8, 6470 - 6479	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	5.03E-05	0.92	4.47	-	729.6
AHQ-2-2, 6988 - 6996	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.00E-05	0.94	5.39	-	1041.9
AHQ-2-7, 7611	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	3.33E-11	0.97	6.31	-	1852.5
AHQ-2-13-, 7101	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.73E-05	0.96	5.25	-	1979.9
AHQ-2-6, 7345 - 7346	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	8.07E-11	0.96	5.96	-	1231.5
AHQ-2-1, 7344	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.33E-05	0.92	4.82	-	1061.0
AHQ-2-5, 7603 - 7676	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.15E-13	0.97	6.45	-	1851.6
AHQ-2-4, 7560 - 7561	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	3.12E-08	0.97	6.46	-	969.8
AHQ-2-1, 7228	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.07E-11	0.98	7.22	-	2782.6
AHQ-2-2, 7556 - 7560	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	7.26E-04	0.98	6.40	-	3438.5
AHQ-2-5, 5515 - 5517	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.74E-07	0.95	5.16	-	972.1
AHQ-2-9, 7454 - 7456	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	6.15E-05	0.95	5.43	-	848.7
AHQ-2-8, 7420	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.13E-05	0.94	4.97	-	941.9
AHQ-2-8, 7418	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.62E-06	0.96	5.64	-	913.4
AHQ-2-10, 6779	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	8.23E-06	0.92	4.94	-	673.7
AHQ-2-7, 7515	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	8.92E-08	0.89	4.62	-	636.8
AHQ-2-14-, 6905	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.36E-06	0.94	5.41	-	843.6
AHQ-2-5, 7504 - 7505	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.07E-04	0.96	5.41	-	1184.6
AHQ-2-3, 7568	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.47E-05	0.89	3.36	-	1267.8
AHQ-2-2, 7613 - 7614	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	8.65E-10	0.96	5.58	-	1257.0
AHQ-2-2, 7612	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.13E-06	0.92	4.82	-	643.6
AHQ-2-7, 7516 - 7517	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.56E-05	0.93	5.42	-	746.8
AHQ-2-1, 7288	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.14E-07	0.86	3.92	-	930.5
AHQ-2-1, 7289	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.67E-08	0.95	5.48	-	1038.3
AHQ-2-6, 7265 - 7266	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.42E-09	0.96	5.57	-	1053.0
AHQ-2-6, 7261	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	3.64E-09	0.89	3.93	-	869.7
AHQ-2-3, 5892	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	7.03E-06	0.93	4.82	-	797.7
AHQ-2-3, 7567 - 7569	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	8.29E-06	0.93	4.99	-	759.1
AHQ-2-4, 7616 - 7625	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.44E-07	0.90	4.31	-	676.7
AHQ-2-4, 7624 - 7629	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.37E-07	0.93	4.40	-	1115.7
AHQ-2-14-, 6904	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.29E-06	0.95	4.94	-	1225.0
AHQ-2-5, 7503	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.15E-07	0.92	4.96	-	1147.7
AHQ-2-3, 2292	K.HRVQELGHGCAALVTK.A	1778.02933	2	9.17E-07	0.94	3.99	-	1248.0
AHQ-2-13, 3333	R.IGITNHDEYSLVR.E	1517.66833	2	3.37E-11	0.91	3.64	-	966.1
AHQ-2-13-, 3327	R.IGITNHDEYSLVR.E	1517.66833	3	6.58E-09	0.91	4.33	-	655.8
AHQ-2-13-, 3761 - 3834	R.IGITNHDEYSLVR.E	1517.66833	2	1.29E-06	0.81	3.57	-	527.8
AHQ-2-7, 3252 - 3324	R.IGITNHDEYSLVR.E	1517.66833	2	2.47E-04	0.87	3.21	-	1191.9
AHQ-2-13-, 3310 - 3329	R.IGITNHDEYSLVR.E	1517.66833	2	6.90E-06	0.95	4.06	-	1450.5
AHQ-2-8, 3302	R.IGITNHDEYSLVR.E	1517.66833	2	3.89E-06	0.85	3.07	-	857.1
AHQ-2-7, 2852 - 2923	R.IGITNHDEYSLVR.E	1517.66833	2	2.86E-05	0.93	3.86	-	1190.2
AHQ-2-10, 2999	R.IGITNHDEYSLVR.E	1517.66833	2	9.59E-05	0.91	3.74	-	1064.7
AHQ-2-2, 5216 - 5226	R.ILAQATSDLVNAIK.A	1457.69748	2	1.90E-08	0.98	5.25	-	1990.5
AHQ-2-5, 3965	R.ILAQATSDLVNAIK.A	1457.69748	2	1.38E-09	0.97	4.01	-	2108.9
AHQ-2-2, 5229	R.ILAQATSDLVNAIK.A	1457.69748	1	1.57E-05	0.73	3.33	-	511.6
AHQ-2-5, 4912 - 4983	R.ILAQATSDLVNAIK.A	1457.69748	2	2.11E-09	0.98	5.70	-	2170.3
AHQ-2-5, 4929	R.ILAQATSDLVNAIK.A	1457.69748	1	6.27E-04	0.78	3.56	-	726.3
AHQ-2-2, 4726	R.ILAQATSDLVNAIK.A	1457.69748	2	1.58E-08	0.98	5.59	-	2228.5
AHQ-2-1, 4334 - 4354	R.ILAQATSDLVNAIK.A	1457.69748	2	3.80E-04	0.96	4.17	-	1787.8
AHQ-2-2, 4542 - 4546	R.ILAQATSDLVNAIK.A	1457.69748	2	5.20E-08	0.95	4.04	-	1351.1
AHQ-2-3, 4259	R.ILAQATSDLVNAIK.A	1457.69748	1	6.55E-05	0.15	1.84	-	486.4
AHQ-2-9, 4830	R.ILAQATSDLVNAIK.A	1457.69748	2	4.98E-06	0.90	3.52	-	959.1
AHQ-2-2, 4249 - 4256	R.ILAQATSDLVNAIK.A	1457.69748	2	7.92E-06	0.97	4.37	-	2258.0
AHQ-2-8, 4607	R.ILAQATSDLVNAIK.A	1457.69748	2	4.53E-08	0.97	5.19	-	1651.4
AHQ-2-4, 4206	R.ILAQATSDLVNAIK.A	1457.69748	2	2.82E-08	0.97	4.16	-	1864.6
AHQ-2-14, 6148	R.ILAQATSDLVNAIK.A	1457.69748	2	7.38E-08	0.96	4.49	-	1522.9
AHQ-2-6, 4849	R.ILAQATSDLVNAIK.A	1457.69748	2	4.74E-05	0.96	3.74	-	1821.9
AHQ-2-7, 4795 - 4809	R.ILAQATSDLVNAIK.A	1457.69748	2	5.57E-08	0.98	4.77	-	1986.2
AHQ-2-1, 5250	R.ILAQATSDLVNAIK.A	1457.69748	2	1.71E-07	0.95	4.07	-	1569.0
AHQ-2-6, 3933	R.ILAQATSDLVNAIK.A	1457.69748	2	5.41E-09	0.96	4.00	-	1780.9
AHQ-2-3, 4236 - 4243	R.ILAQATSDLVNAIK.A	1457.69748	2	2.56E-06	0.98	4.61	-	2288.6
AHQ-2-4, 4498	R.ILAQATSDLVNAIK.A	1457.69748	2	1.70E-04	0.92	3.30	-	1365.1
AHQ-2-3, 5175 - 5179	R.ILAQATSDLVNAIK.A	1457.69748	2	7.50E-07	0.97	5.39	-	1661.5
AHQ-2-3, 5197	R.ILAQATSDLVNAIK.A	1457.69748	1	6.65E-06	0.78	3.97	-	440.9
AHQ-2-1, 6264	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	3.54E-04	0.87	3.73	-	705.7
AHQ-2-13, 5812 - 5871	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.93E-06	0.96	5.01	-	1353.2
AHQ-2-8, 5900 - 5924	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	7.96E-04	0.89	4.09	-	667.8
AHQ-2-7, 5951 - 5964	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	6.22E-05	0.92	4.43	-	694.3
AHQ-2-14-, 5795 - 5865	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	5.66E-07	0.96	5.52	-	864.1
AHQ-2-13-, 5403 - 5439	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	4.28E-13	0.94	4.36	-	1580.3
AHQ-2-8, 4997 - 5069	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.16E-04	0.94	4.06	-	1655.3
AHQ-2-13, 5379 - 5457	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	6.43E-04	0.77	3.35	-	1092.3
AHQ-2-7, 5264 - 5343	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.77E-12	0.96	5.36	-	1177.7
AHQ-2-14-, 5397 - 5417	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	3.94E-14	0.96	5.11	-	1529.4
AHQ-2-13, 2881	K.ISIGNVVK.T	830.00746	2	7.06E-05	0.74	2.69	-	425.4
AHQ-2-7, 1991	K.KGIWLEAGK.A	1002.19171	2	8.08E-05	0.90	3.70	-	912.1
AHQ-2-1, 2650 - 2653	K.LAQAAQSSVATITR.L	1417.59344	2	1.67E-05	0.94	3.70	-	1338.9
AHQ-2-9, 2503	K.LAQAAQSSVATITR.L	1417.59344	2	2.87E-08	0.93	3.62	-	1394.4
AHQ-2-4, 2614	K.LAQAAQSSVATITR.L	1417.59344	1	5.45E-04	0.14	2.69	-	97.2
AHQ-2-6, 2313	K.LAQAAQSSVATITR.L	1417.59344	2	2.68E-11	0.96	4.71	-	1278.3
AHQ-2-11, 2601	K.LAQAAQSSVATITR.L	1417.59344	2	5.01E-08	0.94	3.59	-	1565.5
AHQ-2-4, 2466	K.LAQAAQSSVATITR.L	1417.59344	2	1.46E-10	0.97	4.72	-	1761.5
AHQ-2-2, 2620 - 2688	K.LAQAAQSSVATITR.L	1417.59344	2	1.23E-09	0.97	5.32	-	1615.3
AHQ-2-2, 2485	K.LAQAAQSSVATITR.L	1417.59344	2	1.89E-07	0.96	4.60	-	1405.8
AHQ-2-7, 2403 - 2408	K.LAQAAQSSVATITR.L	1417.59344	2	7.96E-08	0.97	4.99	-	1829.0
AHQ-2-6, 2462 - 2465	K.LAQAAQSSVATITR.L	1417.59344	2	2.29E-07	0.97	5.18	-	1784.0
AHQ-2-14-, 2651	K.LAQAAQSSVATITR.L	1417.59344	2	2.21E-09	0.91	3.27	-	1411.2
AHQ-2-6, 2489	K.LAQAAQSSVATITR.L	1417.59344	1	2.39E-05	0.26	2.47	-	119.7
AHQ-2-1, 2796	K.LAQAAQSSVATITR.L	1417.59344	2	7.79E-09	0.97	4.54	-	1710.6
AHQ-2-3, 2456 - 2457	K.LAQAAQSSVATITR.L	1417.59344	2	1.26E-07	0.93	3.77	-	1304.0
AHQ-2-10, 2454	K.LAQAAQSSVATITR.L	1417.59344	2	1.59E-06	0.94	3.51	-	1455.3
AHQ-2-5, 2433 - 2443	K.LAQAAQSSVATITR.L	1417.59344	2	2.54E-09	0.97	4.70	-	1717.5
AHQ-2-4, 2604 - 2610	K.LAQAAQSSVATITR.L	1417.59344	2	9.98E-10	0.97	4.65	-	1656.1
AHQ-2-4, 3128 - 3164	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.33E-09	0.95	4.99	-	1538.1
AHQ-2-1, 3310 - 3357	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.10E-05	0.97	5.78	-	1916.9
AHQ-2-3, 3124	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.87E-07	0.96	5.88	-	1468.3

AHQ-2-3, 3120	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.06E-05	0.89	4.20	-	661.1
AHQ-2-6, 2855 - 2869	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	3.96E-05	0.96	5.31	-	1615.9
AHQ-2-3, 2937	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.98E-08	0.96	5.37	-	1111.2
AHQ-2-2, 2934	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.35E-05	0.96	5.01	-	1131.9
AHQ-2-9, 2851	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.27E-04	0.86	4.04	-	426.3
AHQ-2-9, 2846	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	5.68E-06	0.85	3.89	-	911.5
AHQ-2-2, 3128	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	6.84E-07	0.95	5.19	-	711.2
AHQ-2-6, 2879	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.44E-06	0.92	4.76	-	553.9
AHQ-2-5, 2839	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.14E-07	0.91	4.82	-	508.5
AHQ-2-4, 3133	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.18E-06	0.95	4.98	-	729.6
AHQ-2-13, 5124	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.80E-05	0.85	3.71	-	793.9
AHQ-2-7, 5117 - 5125	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.62E-10	0.94	4.58	-	758.6
AHQ-2-7, 5268 - 5272	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.65E-06	0.97	5.58	-	1251.4
AHQ-2-2, 5790 - 5865	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.85E-07	0.96	5.06	-	1054.8
AHQ-2-2, 5638 - 5641	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.09E-11	0.98	6.84	-	2644.4
AHQ-2-9, 5302	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.88E-05	0.64	3.21	-	464.5
AHQ-2-3, 5564 - 5643	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.53E-07	0.97	5.22	-	1343.3
AHQ-2-5, 5383 - 5453	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.37E-04	0.96	5.23	-	1161.8
AHQ-2-2, 5536 - 5610	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.20E-08	0.97	5.23	-	1277.3
AHQ-2-4, 5598 - 5676	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.31E-06	0.97	5.56	-	1402.1
AHQ-2-4, 5640 - 5662	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.14E-04	0.96	4.45	-	2318.4
AHQ-2-2, 5437 - 5465	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.69E-08	0.91	4.13	-	736.4
AHQ-2-1, 5857	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.47E-04	0.90	4.32	-	628.9
AHQ-2-5, 5225 - 5251	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.65E-06	0.97	5.17	-	1443.8
AHQ-2-4, 5748 - 5817	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.23E-08	0.97	5.61	-	1443.6
AHQ-2-3, 5615 - 5620	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.22E-05	0.89	3.60	-	1376.2
AHQ-2-1, 5700	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	8.75E-06	0.95	4.63	-	1743.3
AHQ-2-3, 5417 - 5487	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.12E-06	0.92	4.51	-	742.1
AHQ-2-1, 5541	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.03E-06	0.94	4.33	-	1015.3
AHQ-2-14-, 5116	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.45E-08	0.93	4.49	-	930.8
AHQ-2-3, 5841 - 5912	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.77E-08	0.92	4.27	-	805.6
AHQ-2-14-, 5296	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.47E-04	0.95	4.72	-	999.6
AHQ-2-1, 5688 - 5693	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.22E-06	0.97	5.32	-	1350.3
AHQ-2-6, 5303 - 5305	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.74E-08	0.95	5.24	-	913.1
AHQ-2-6, 5313 - 5325	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	6.26E-06	0.90	4.42	-	1411.4
AHQ-2-6, 5482	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.38E-06	0.91	4.44	-	763.2
AHQ-2-4, 5405 - 5457	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.88E-10	0.97	5.22	-	1607.8
AHQ-2-1, 4030	K.LHTDDELNWLDHGR.T	1721.81153	3	9.26E-06	0.85	3.72	-	688.7
AHQ-2-8, 3063	K.LHTDDELNWLDHGR.T	1721.81153	3	2.24E-06	0.92	4.23	-	1171.8
AHQ-2-9, 3354	K.LHTDDELNWLDHGR.T	1721.81153	2	8.09E-06	0.95	4.08	-	1428.8
AHQ-2-7, 3275 - 3343	K.LHTDDELNWLDHGR.T	1721.81153	2	3.19E-06	0.97	4.72	-	1649.3
AHQ-2-8, 3062	K.LHTDDELNWLDHGR.T	1721.81153	2	5.36E-06	0.96	4.65	-	1428.0
AHQ-2-7, 3327	K.LHTDDELNWLDHGR.T	1721.81153	3	3.65E-04	0.86	3.25	-	1196.4
AHQ-2-3, 4371 - 4439	K.LLAALLEDEGGSGR.P	1401.54764	2	1.32E-04	0.74	3.49	-	418.6
AHQ-2-1, 4530	K.LLAALLEDEGGSGR.P	1401.54764	2	2.06E-11	0.97	4.56	-	1584.3
AHQ-2-1, 5522	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	6.96E-09	0.98	6.31	-	1430.4
AHQ-2-1, 5521 - 5528	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	5.88E-09	0.93	4.53	-	1302.0
AHQ-2-3, 5256	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.17E-08	0.92	4.52	-	803.6
AHQ-2-2, 5388 - 5413	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.22E-12	0.97	6.02	-	1660.5
AHQ-2-8, 4609	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.40E-09	0.96	5.27	-	1671.1
AHQ-2-12, 5209 - 5214	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.48E-05	0.95	4.73	-	1509.2
AHQ-2-3, 5361	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.10E-09	0.98	6.46	-	1785.2
AHQ-2-3, 5363	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.34E-07	0.96	4.91	-	1666.8
AHQ-2-2, 5389	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	9.23E-11	0.97	6.04	-	1553.7
AHQ-2-10, 4710	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.72E-05	0.92	4.86	-	868.2
AHQ-2-8, 4608 - 4623	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.88E-10	0.98	6.85	-	1368.3
AHQ-2-6, 5001	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	6.70E-05	0.90	4.21	-	754.0
AHQ-2-9, 4982 - 4983	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	7.98E-09	0.98	6.65	-	1545.2
AHQ-2-9, 4990	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	6.44E-08	0.95	5.24	-	1163.3
AHQ-2-5, 5033 - 5103	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	7.72E-09	0.98	6.55	-	1411.4
AHQ-2-5, 5027 - 5039	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	8.08E-09	0.95	5.06	-	1319.7
AHQ-2-10, 4715	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.11E-07	0.96	5.53	-	1129.4
AHQ-2-7, 4875 - 4885	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	9.57E-10	0.98	6.21	-	1563.0
AHQ-2-4, 5236	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.93E-05	0.87	4.29	-	410.9
AHQ-2-4, 5372 - 5376	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.78E-09	0.98	7.40	-	1348.3
AHQ-2-4, 5360 - 5362	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.00E-10	0.96	5.23	-	1500.2
AHQ-2-3, 5375	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	1.59E-04	0.60	3.57	-	615.0
AHQ-2-2, 5402	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	5.30E-04	0.82	4.54	-	476.0
AHQ-2-5, 5411	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.69E-11	0.98	5.78	-	1864.5
AHQ-2-2, 4558 - 4589	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.20E-10	0.92	4.99	-	649.3
AHQ-2-3, 6079 - 6084	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.16E-12	0.98	5.69	-	2180.9
AHQ-2-4, 5633 - 5704	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.22E-09	0.98	5.92	-	2035.9
AHQ-2-5, 5419 - 5424	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	6.15E-05	0.98	5.88	-	2540.8
AHQ-2-5, 5888	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.78E-06	0.93	4.04	-	984.0
AHQ-2-11, 5242	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.13E-06	0.92	4.33	-	790.6
AHQ-2-4, 5710 - 5733	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.32E-06	0.98	5.74	-	3004.1
AHQ-2-4, 4529 - 4570	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.86E-13	0.97	5.41	-	1249.8
AHQ-2-3, 5460	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.21E-06	0.78	3.07	-	743.5
AHQ-2-1, 5369	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.87E-09	0.96	4.39	-	1678.7
AHQ-2-3, 6401	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.50E-09	0.91	4.13	-	740.6
AHQ-2-8, 5111	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.46E-07	0.96	4.59	-	1374.9
AHQ-2-3, 5827	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.17E-08	0.98	6.04	-	1795.6
AHQ-2-9, 5374	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.95E-13	0.98	6.15	-	1765.1
AHQ-2-6, 5358 - 5373	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.37E-11	0.98	5.75	-	1801.1
AHQ-2-1, 5592	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.66E-06	0.67	2.79	-	668.8
AHQ-2-5, 4347	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.64E-08	0.96	5.26	-	1081.1
AHQ-2-3, 5739 - 5740	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.42E-11	0.98	5.59	-	1816.1
AHQ-2-4, 6093 - 6098	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.26E-10	0.97	5.00	-	1632.2
AHQ-2-6, 5775	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.42E-09	0.95	4.96	-	994.2
AHQ-2-3, 5676 - 5696	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.14E-04	0.98	5.59	-	2692.2
AHQ-2-1, 5694	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.90E-04	0.94	4.31	-	900.0
AHQ-2-1, 5804 - 5872	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.91E-09	0.96	5.02	-	1352.1
AHQ-2-1, 5810 - 5824	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	6.21E-09	0.98	6.05	-	2302.0
AHQ-2-5, 5785	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.05E-13	0.98	5.50	-	1892.6
AHQ-2-3, 5604 - 5675	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.67E-11	0.98	5.97	-	1634.0
AHQ-2-1, 6009	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.21E-06	0.96	4.70	-	1331.7
AHQ-2-2, 5514	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.85E-08	0.94	4.37	-	1106.4
AHQ-2-1, 6129 - 6137	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.61E-14	0.98	6.08	-	2000.8
AHQ-2-10, 5011 - 5012	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.65E-09	0.96	4.16	-	1556.8
AHQ-2-7, 5700	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.86E-04	0.88	4.23	-	551.7
AHQ-2-2, 5657 - 5701	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.62E-09	0.97	5.82	-	1374.8
AHQ-2-2, 6129	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	4.87E-09	0.95	4.66	-	1820.0
AHQ-2-2, 5713 - 5729	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.36E-09	0.98	6.53	-	2105.4
AHQ-2-2, 6120	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.60E-09	0.97	5.10	-	1777.1
AHQ-2-2, 5769 - 5845	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.50E-08	0.97	5.73	-	1338.0
AHQ-2-7, 5313	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.97E-11	0.97	5.36	-	1474.9
AHQ-2-2, 5916 - 5986	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.77E-08	0.97	5.32	-	1409.9

AHQ-2-1, 4590 - 4592	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.95E-10	0.95	5.03	-	846.9
AHQ-2-3, 5928 - 5940	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.42E-09	0.98	5.99	-	1402.3
AHQ-2-3, 5456	R.LNEAAAGLNQAATELVQASRGTPQDLAR.A	2867.12501	3	3.07E-06	0.69	3.47	-	747.8
AHQ-2-4, 2040	R.MATNAAAQNAIK.K	1204.38227	2	4.40E-06	0.79	3.11	-	889.4
AHQ-2-2, 2017	R.MATNAAAQNAIK.K	1204.38227	2	4.36E-06	0.87	3.57	-	837.4
AHQ-2-2, 2102	R.MATNAAAQNAIK.K	1204.38227	2	2.27E-10	0.90	3.77	-	969.3
AHQ-2-2, 4297	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.01E-05	0.93	5.11	-	762.7
AHQ-2-2, 4182	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	7.20E-09	0.91	4.63	-	926.4
AHQ-2-4, 4100	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.20E-09	0.84	3.89	-	713.6
AHQ-2-2, 4477	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	1.34E-07	0.86	3.41	-	811.1
AHQ-2-2, 4488 - 4562	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	7.03E-10	0.96	5.60	-	1528.3
AHQ-2-1, 4257	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.21E-12	0.91	4.17	-	1045.7
AHQ-2-4, 4305 - 4376	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	4.16E-08	0.97	6.00	-	1641.4
AHQ-2-6, 4050 - 4051	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	8.61E-09	0.90	4.38	-	871.0
AHQ-2-7, 3967 - 3987	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	5.90E-06	0.91	4.48	-	908.5
AHQ-2-7, 4133	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	4.32E-06	0.77	3.47	-	520.2
AHQ-2-5, 4064 - 4075	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	6.06E-05	0.78	3.64	-	622.5
AHQ-2-3, 4152 - 4153	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	7.24E-09	0.96	5.56	-	1308.2
AHQ-2-3, 4339	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	5.64E-08	0.85	3.72	-	884.3
AHQ-2-10, 3695	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.09E-09	0.93	4.36	-	1106.9
AHQ-2-1, 4385 - 4400	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.00E-05	0.63	3.17	-	566.5
AHQ-2-3, 4368 - 4441	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	6.52E-06	0.58	2.77	-	579.8
AHQ-2-1, 4537 - 4540	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	3.70E-06	0.94	4.69	-	1085.9
AHQ-2-10, 3854 - 3914	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	9.44E-07	0.94	4.66	-	1276.9
AHQ-2-3, 4424 - 4425	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.88E-05	0.72	3.38	-	667.1
AHQ-2-10, 3991	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.32E-09	0.71	3.58	-	607.3
AHQ-2-8, 3848	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	7.23E-08	0.90	4.05	-	646.7
AHQ-2-8, 3840	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.35E-07	0.82	3.61	-	905.4
AHQ-2-4, 7236 - 7274	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.40E-06	0.96	4.43	-	1525.5
AHQ-2-5, 7019	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.15E-08	0.98	5.09	-	2197.6
AHQ-2-14-, 6567 - 6579	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.57E-04	0.71	3.43	-	533.3
AHQ-2-2, 6501	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	6.77E-04	0.91	3.53	-	1115.8
AHQ-2-4, 6529	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	1.19E-06	0.95	4.50	-	1365.9
AHQ-2-6, 6849 - 6854	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.02E-13	0.98	6.09	-	1893.6
AHQ-2-10, 6370	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	6.68E-09	0.97	5.46	-	1631.1
AHQ-2-10, 5783	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	2.07E-04	0.83	3.22	-	941.6
AHQ-2-9, 6914 - 6978	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.31E-06	0.96	4.73	-	1317.7
AHQ-2-7, 6893	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.38E-06	0.95	4.65	-	1415.9
AHQ-2-4, 6229	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.58E-04	0.67	2.59	-	772.8
AHQ-2-2, 6237 - 6238	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	8.36E-11	0.98	6.06	-	1643.6
AHQ-2-3, 6228	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.38E-07	0.97	5.23	-	1400.7
AHQ-2-13, 6359	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	3.59E-05	0.96	4.78	-	1392.9
AHQ-2-3, 7181 - 7192	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.44E-09	0.97	5.71	-	1492.0
AHQ-2-1, 6816 - 6837	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	4.17E-11	0.94	4.60	-	1022.9
AHQ-2-14-, 6383 - 6428	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.79E-05	0.97	5.09	-	1878.3
AHQ-2-3, 6547	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	1.98E-09	0.97	4.99	-	1598.9
AHQ-2-2, 7248 - 7312	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.27E-06	0.97	5.64	-	1814.8
AHQ-2-4, 6940 - 6950	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	2.50E-04	0.98	6.05	-	2100.4
AHQ-2-4, 6638	K.MVGGIAQIIAAQEEMLRK.E	1959.36698	2	1.23E-04	0.93	4.61	-	753.0
AHQ-2-7, 2095	K.NCGQMSEIEAK.V	1268.40005	2	8.94E-05	0.84	3.15	-	1028.7
AHQ-2-3, 4521 - 4591	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.85E-04	0.70	2.88	-	527.9
AHQ-2-3, 4793	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.40E-08	0.91	3.91	-	636.5
AHQ-2-2, 4593	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.06E-04	0.74	2.93	-	407.1
AHQ-2-5, 4669 - 4745	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.31E-10	0.85	3.66	-	472.3
AHQ-2-4, 4788 - 4856	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.78E-06	0.70	3.57	-	290.6
AHQ-2-1, 4576	K.NGNLPEFGDAISTASK.A	1621.73018	2	6.78E-05	0.50	2.85	-	286.3
AHQ-2-6, 4558 - 4578	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.98E-07	0.82	3.39	-	489.2
AHQ-2-1, 4344	K.NLGTALAELR.T	1058.21367	2	3.18E-04	0.86	3.09	-	948.4
AHQ-2-5, 3764	K.NLGTALAELR.T	1058.21367	2	2.87E-04	0.82	2.81	-	828.7
AHQ-2-4, 4093 - 4096	K.NLGTALAELR.T	1058.21367	2	3.01E-06	0.83	3.41	-	828.8
AHQ-2-1, 2833	K.PAAVAAENEEIGSHIK.H	1636.78798	3	3.06E-08	0.95	4.79	-	1481.6
AHQ-2-1, 2829	K.PAAVAAENEEIGSHIK.H	1636.78798	2	9.55E-06	0.97	4.41	-	1848.3
AHQ-2-4, 2584	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.48E-06	0.98	5.88	-	2076.7
AHQ-2-2, 2592	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.73E-10	0.98	5.75	-	2273.0
AHQ-2-4, 2588	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.12E-10	0.97	5.48	-	1829.0
AHQ-2-3, 2599	K.PAAVAAENEEIGSHIK.H	1636.78798	3	7.35E-11	0.98	5.42	-	2300.9
AHQ-2-6, 2407	K.PAAVAAENEEIGSHIK.H	1636.78798	2	4.16E-09	0.98	5.44	-	2304.0
AHQ-2-2, 2593	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.43E-11	0.97	5.27	-	1703.6
AHQ-2-5, 2385 - 2391	K.PAAVAAENEEIGSHIK.H	1636.78798	2	8.17E-05	0.98	5.55	-	1675.8
AHQ-2-6, 2405	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.60E-07	0.95	4.50	-	1812.9
AHQ-2-3, 2595	K.PAAVAAENEEIGSHIK.H	1636.78798	2	2.39E-07	0.98	5.69	-	1920.6
AHQ-2-6, 2911	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.56E-05	0.92	4.54	-	719.8
AHQ-2-2, 3413	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.10E-07	0.85	4.07	-	538.6
AHQ-2-2, 3189	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	6.99E-05	0.90	4.44	-	540.6
AHQ-2-5, 2887	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.93E-06	0.94	5.05	-	734.5
AHQ-2-5, 2872 - 2883	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	9.21E-04	0.61	3.03	-	654.8
AHQ-2-1, 3566	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	7.01E-06	0.90	4.21	-	700.8
AHQ-2-7, 2803	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.72E-04	0.77	3.66	-	418.1
AHQ-2-1, 3394	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	4.18E-06	0.83	3.66	-	820.1
AHQ-2-1, 3392	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	4.17E-06	0.86	4.04	-	603.6
AHQ-2-3, 3187	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	3.35E-06	0.85	4.11	-	559.3
AHQ-2-4, 3388	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	3.41E-10	0.93	4.73	-	744.5
AHQ-2-3, 3191	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	5.06E-04	0.84	3.86	-	782.1
AHQ-2-3, 3384	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.32E-06	0.81	4.29	-	586.7
AHQ-2-4, 3188 - 3190	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.19E-06	0.94	5.10	-	802.5
AHQ-2-1, 3069	R.QEDVIATANLSR.R	1317.43074	2	5.69E-04	0.75	2.91	-	513.5
AHQ-2-3, 4055 - 4133	R.QELAVFCSPEPPAK.T	1574.77985	2	4.12E-06	0.88	3.71	-	788.3
AHQ-2-4, 4064 - 4072	R.QELAVFCSPEPPAK.T	1574.77985	2	1.44E-08	0.92	3.64	-	1076.6
AHQ-2-1, 4106 - 4185	R.QELAVFCSPEPPAK.T	1574.77985	2	3.10E-05	0.74	2.97	-	701.4
AHQ-2-5, 3763 - 3843	R.QELAVFCSPEPPAK.T	1574.77985	2	1.94E-06	0.88	3.34	-	781.2
AHQ-2-2, 4088 - 4158	R.QELAVFCSPEPPAK.T	1574.77985	2	1.71E-05	0.92	4.05	-	805.8
AHQ-2-8, 7406	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	1.35E-13	0.92	5.61	-	556.9
AHQ-2-5, 7471 - 7473	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	1.13E-07	0.86	4.52	-	619.5
AHQ-2-5, 7495	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	1.14E-10	0.97	6.85	-	1156.2
AHQ-2-1, 7240	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	2.37E-06	0.83	4.16	-	594.8
AHQ-2-2, 7576	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	1.27E-05	0.92	5.36	-	807.1
AHQ-2-7, 7503	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	8.55E-07	0.92	5.34	-	518.4
AHQ-2-2, 3856 - 3857	K.QVAASTAQLLVACK.V	1461.70942	2	1.77E-05	0.94	3.93	-	879.8
AHQ-2-3, 3816 - 3817	K.QVAASTAQLLVACK.V	1461.70942	2	9.74E-08	0.94	4.21	-	738.2
AHQ-2-2, 2453	R.RAIADMLR.A	946.15319	2	1.83E-05	0.84	2.89	-	743.3
AHQ-2-3, 4951	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	2.64E-07	0.84	3.68	-	338.9
AHQ-2-4, 6002 - 6005	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	1.20E-05	0.98	5.56	-	1950.3
AHQ-2-1, 6142	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	6.35E-06	0.98	5.09	-	2215.8
AHQ-2-1, 5085	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	4.78E-06	0.92	4.38	-	689.1
AHQ-2-3, 5995	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	2.27E-06	0.97	5.20	-	1447.1
AHQ-2-5, 5581	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	3.32E-09	0.98	5.70	-	1723.6
AHQ-2-2, 6025	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	7.09E-07	0.98	6.13	-	2491.8

AHQ-2-2, 2888	K.SIAAATSALVK.A	1032.21612	2	3.38E-04	0.91	3.51	-	995.7
AHQ-2-3, 2896 - 2899	K.SIAAATSALVK.A	1032.21612	2	8.54E-04	0.87	3.16	-	802.5
AHQ-2-4, 2870 - 2888	K.SIAAATSALVK.A	1032.21612	2	2.67E-04	0.83	3.01	-	702.3
AHQ-2-6, 2667	K.SIAAATSALVK.A	1032.21612	2	5.57E-05	0.84	2.91	-	972.8
AHQ-2-5, 2620	K.SIAAATSALVK.A	1032.21612	2	5.02E-05	0.87	3.01	-	987.6
AHQ-2-7, 3603	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	2.02E-06	0.90	4.19	-	879.5
AHQ-2-10, 3572	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	5.95E-04	0.68	3.02	-	874.2
AHQ-2-7, 3985 - 4059	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	1.03E-09	0.89	3.89	-	664.2
AHQ-2-7, 3988 - 4055	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	5.73E-07	0.97	5.57	-	1849.9
AHQ-2-7, 4071	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	2.85E-06	0.81	2.99	-	882.5
AHQ-2-5, 5352	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.42E-07	0.94	4.74	-	638.9
AHQ-2-3, 5647	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.31E-07	0.90	4.15	-	489.3
AHQ-2-2, 5370 - 5441	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.89E-07	0.88	4.05	-	421.7
AHQ-2-3, 4767	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.44E-09	0.73	3.77	-	489.6
AHQ-2-4, 5558 - 5594	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.16E-05	0.51	2.58	-	246.5
AHQ-2-5, 5491 - 5568	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.03E-05	0.91	4.06	-	626.7
AHQ-2-1, 4769 - 4842	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.64E-06	0.92	4.22	-	719.4
AHQ-2-2, 5050	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.80E-08	0.89	4.32	-	573.7
AHQ-2-3, 5431 - 5511	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.84E-09	0.83	3.72	-	325.8
AHQ-2-9, 5111	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.22E-05	0.88	3.92	-	685.3
AHQ-2-6, 4489 - 4498	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.06E-09	0.84	3.79	-	484.6
AHQ-2-4, 5354 - 5425	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.07E-06	0.89	3.99	-	504.2
AHQ-2-4, 4780	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.87E-13	0.95	4.75	-	814.4
AHQ-2-4, 5204	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.32E-06	0.91	4.58	-	463.1
AHQ-2-4, 5664 - 5666	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.58E-07	0.88	4.09	-	493.2
AHQ-2-1, 5598 - 5670	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.20E-07	0.93	4.31	-	667.8
AHQ-2-5, 4583 - 4584	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.35E-11	0.94	4.47	-	843.1
AHQ-2-3, 5187 - 5199	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.84E-06	0.89	4.13	-	557.5
AHQ-2-6, 5059 - 5130	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.62E-07	0.87	3.67	-	643.0
AHQ-2-2, 4808	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.11E-07	0.85	3.75	-	379.7
AHQ-2-3, 5335 - 5403	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.26E-07	0.71	3.04	-	380.4
AHQ-2-2, 5217 - 5234	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.68E-06	0.81	3.71	-	389.5
AHQ-2-6, 5407	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.90E-06	0.82	3.20	-	625.6
AHQ-2-1, 5452 - 5516	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.09E-05	0.76	3.36	-	471.0
AHQ-2-2, 5617 - 5693	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.33E-07	0.92	4.22	-	644.1
AHQ-2-5, 5163	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.24E-07	0.89	3.86	-	619.4
AHQ-2-6, 7183 - 7185	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.11E-14	0.97	5.69	-	1833.9
AHQ-2-2, 7472 - 7542	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	8.79E-13	0.98	6.23	-	2128.7
AHQ-2-1, 7250 - 7286	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	5.43E-05	0.90	4.26	-	1192.1
AHQ-2-7, 3843 - 3912	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.29E-06	0.96	4.85	-	1418.0
AHQ-2-8, 3786	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.02E-05	0.93	4.58	-	1044.2
AHQ-2-9, 3955	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.58E-06	0.96	4.69	-	1631.7
AHQ-2-13, 4253 - 4257	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.37E-08	0.96	4.81	-	1476.4
AHQ-2-7, 3857	K.TKEVIQEWNLTNIK.R	1716.95938	3	4.75E-05	0.93	4.68	-	1175.8
AHQ-2-9, 6422	K.TLAESALQLLYTAK.E	1522.76793	2	3.78E-05	0.95	4.07	-	1242.4
AHQ-2-2, 6668 - 6748	K.TLAESALQLLYTAK.E	1522.76793	2	4.08E-08	0.97	5.25	-	1436.5
AHQ-2-3, 6639 - 6707	K.TLAESALQLLYTAK.E	1522.76793	2	6.76E-10	0.97	5.41	-	1388.8
AHQ-2-2, 6838	K.TLAESALQLLYTAK.E	1522.76793	2	4.84E-06	0.93	3.57	-	1047.3
AHQ-2-4, 6712 - 6780	K.TLAESALQLLYTAK.E	1522.76793	2	4.08E-11	0.97	4.91	-	1410.5
AHQ-2-1, 6650 - 6654	K.TLAESALQLLYTAK.E	1522.76793	2	7.81E-10	0.96	4.78	-	1039.5
AHQ-2-10, 5915	K.TLAESALQLLYTAK.E	1522.76793	2	8.83E-04	0.82	3.44	-	860.3
AHQ-2-3, 6904	K.TLAESALQLLYTAK.E	1522.76793	2	3.21E-07	0.94	4.16	-	1034.9
AHQ-2-11, 6064	K.TLAESALQLLYTAK.E	1522.76793	2	4.46E-04	0.92	3.87	-	861.4
AHQ-2-5, 6411 - 6491	K.TLAESALQLLYTAK.E	1522.76793	2	1.04E-05	0.97	4.82	-	1430.4
AHQ-2-2, 2420	K.TLSHPQQM*ALLDQTK.T	1727.96404	2	1.63E-05	0.89	3.71	-	582.7
AHQ-2-2, 3134	K.TLSHPQQMALLDQTK.T	1711.96464	3	4.26E-08	0.96	5.18	-	1801.4
AHQ-2-3, 3125	K.TLSHPQQMALLDQTK.T	1711.96464	3	2.30E-07	0.91	5.00	-	879.1
AHQ-2-10, 2820	K.TLSHPQQMALLDQTK.T	1711.96464	2	7.76E-04	0.78	3.28	-	394.1
AHQ-2-4, 3124	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.34E-05	0.94	5.11	-	647.7
AHQ-2-5, 2845	K.TLSHPQQMALLDQTK.T	1711.96464	3	1.49E-05	0.91	4.50	-	990.4
AHQ-2-2, 3125 - 3126	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.40E-04	0.95	5.08	-	735.3
AHQ-2-1, 3369	K.TLSHPQQMALLDQTK.T	1711.96464	3	4.75E-05	0.83	3.90	-	674.8
AHQ-2-4, 3129	K.TLSHPQQMALLDQTK.T	1711.96464	3	1.64E-07	0.93	4.93	-	997.6
AHQ-2-9, 2850	K.TLSHPQQMALLDQTK.T	1711.96464	2	6.67E-05	0.93	4.32	-	714.8
AHQ-2-3, 3087 - 3155	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.30E-04	0.95	4.64	-	821.2
AHQ-2-7, 2753 - 2792	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.55E-04	0.88	4.14	-	661.8
AHQ-2-6, 2861	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.25E-04	0.95	4.46	-	871.1
AHQ-2-5, 2835 - 2843	K.TLSHPQQMALLDQTK.T	1711.96464	2	7.55E-04	0.96	4.92	-	829.3
AHQ-2-5, 4085 - 4091	K.TMLESAGGLIQTAR.A	1448.67095	2	9.01E-07	0.95	3.82	-	1833.3
AHQ-2-4, 4349 - 4360	K.TMLESAGGLIQTAR.A	1448.67095	2	3.77E-05	0.86	3.56	-	850.8
AHQ-2-5, 3203	K.TM*LESAGGLIQTAR.A	1464.67035	2	2.32E-05	0.89	3.46	-	1174.0
AHQ-2-2, 3493 - 3494	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.17E-07	0.97	4.91	-	1655.7
AHQ-2-3, 3468 - 3549	K.TM*LESAGGLIQTAR.A	1464.67035	2	5.67E-04	0.95	4.04	-	1468.5
AHQ-2-6, 3173	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.15E-05	0.90	3.27	-	1091.7
AHQ-2-1, 3620	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.71E-05	0.95	4.17	-	1463.2
AHQ-2-2, 4514	K.TMLESAGGLIQTAR.A	1448.67095	2	2.20E-05	0.93	3.65	-	1599.4
AHQ-2-6, 4046	K.TMLESAGGLIQTAR.A	1448.67095	2	7.51E-07	0.89	2.57	-	1765.1
AHQ-2-1, 4418 - 4498	K.TMLESAGGLIQTAR.A	1448.67095	2	1.92E-06	0.95	4.02	-	1843.7
AHQ-2-2, 4428	K.TMLESAGGLIQTAR.A	1448.67095	2	8.93E-07	0.77	3.10	-	1005.7
AHQ-2-4, 4357	K.TMLESAGGLIQTAR.A	1448.67095	1	6.37E-04	0.09	1.82	-	296.4
AHQ-2-13-, 4883	K.TMQFEPSTMVYDACR.I	1838.07571	2	1.28E-05	0.92	4.52	-	608.1
AHQ-2-7, 4679	K.TMQFEPSTMVYDACR.I	1838.07571	2	4.70E-06	0.94	5.26	-	553.3
AHQ-2-7, 3859	K.TMQFEPSTM*VYDACR.I	1854.07511	2	3.66E-04	0.82	3.30	-	471.3
AHQ-2-12, 4838 - 4855	K.TMQFEPSTMVYDACR.I	1838.07571	2	2.90E-04	0.89	4.41	-	499.4
AHQ-2-13, 4235 - 4236	K.TM*QFEPSTMVYDACR.I	1854.07511	2	3.63E-06	0.93	4.64	-	738.2
AHQ-2-7, 4116 - 4123	K.TM*QFEPSTMVYDACR.I	1854.07511	2	3.89E-06	0.95	4.92	-	678.7
AHQ-2-14-, 4837	K.TMQFEPSTMVYDACR.I	1838.07571	2	1.24E-06	0.94	4.64	-	567.0
AHQ-2-13, 4789 - 4795	K.TMQFEPSTMVYDACR.I	1838.07571	2	6.65E-04	0.94	4.33	-	635.9
AHQ-2-13-, 4289	K.TM*QFEPSTMVYDACR.I	1854.07511	2	5.68E-06	0.91	4.64	-	658.6
AHQ-2-13-, 5394 - 5462	K.TVTDMLMTICAR.I	1413.71007	2	9.21E-04	0.86	3.24	-	804.3
AHQ-2-7, 3533 - 3608	K.TVTDM*LM*TICAR.I	1445.70887	2	3.56E-06	0.91	3.16	-	1014.8
AHQ-2-13-, 3737 - 3801	K.TVTDM*LM*TICAR.I	1445.70887	2	1.53E-06	0.91	3.34	-	805.4
AHQ-2-13, 5352	K.TVTDMLMTICAR.I	1413.71007	2	5.96E-05	0.86	2.62	-	1176.7
AHQ-2-13, 3719 - 3784	K.TVTDM*LM*TICAR.I	1445.70887	2	7.71E-08	0.90	3.77	-	764.2
AHQ-2-12, 5258	K.TYGVSFFLVK.E	1161.37395	2	1.66E-06	0.75	2.71	-	627.3
AHQ-2-7, 4923	K.TYGVSFFLVK.E	1161.37395	2	2.83E-06	0.89	3.62	-	581.3
AHQ-2-11, 5017	K.TYGVSFFLVK.E	1161.37395	2	1.83E-04	0.78	2.62	-	681.8
AHQ-2-9, 5132	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	1.86E-04	0.81	3.01	-	968.2
AHQ-2-9, 6278 - 6306	R.VAGSVTELIQAAEAMK.G	1618.87752	2	7.78E-06	0.94	3.87	-	1428.5
AHQ-2-3, 6553	R.VAGSVTELIQAAEAMK.G	1618.87752	2	6.03E-09	0.94	4.23	-	957.1
AHQ-2-5, 6337 - 6355	R.VAGSVTELIQAAEAMK.G	1618.87752	2	3.89E-11	0.98	5.85	-	1625.3
AHQ-2-13, 6132	R.VAGSVTELIQAAEAMK.G	1618.87752	2	8.18E-05	0.94	3.79	-	1535.7
AHQ-2-1, 6573 - 6593	R.VAGSVTELIQAAEAMK.G	1618.87752	2	5.50E-11	0.98	6.07	-	2033.3
AHQ-2-4, 6589 - 6666	R.VAGSVTELIQAAEAMK.G	1618.87752	2	3.58E-09	0.97	5.21	-	1452.4
AHQ-2-3, 5408 - 5479	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	8.37E-06	0.97	4.66	-	1763.9
AHQ-2-2, 5460 - 5496	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	9.45E-04	0.79	3.35	-	797.6
AHQ-2-6, 6234 - 6238	R.VAGSVTELIQAAEAMK.G	1618.87752	2	7.93E-07	0.97	4.73	-	1730.5

AHQ-2-2, 6526 - 6592	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.10E-10	0.98	6.26	-	1684.1
AHQ-2-2, 6781	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.39E-08	0.95	4.13	-	1463.6
AHQ-2-7, 6155	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.39E-06	0.76	2.80	-	903.2
AHQ-2-1, 6152 - 6217	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.05E-11	0.94	5.12	-	679.0
AHQ-2-12, 5865 - 5875	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.52E-08	0.95	5.58	-	745.8
AHQ-2-1, 6053 - 6082	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.74E-12	0.93	4.63	-	751.6
AHQ-2-2, 5836	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.19E-07	0.90	4.32	-	594.2
AHQ-2-1, 6254	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.99E-06	0.68	3.04	-	465.4
AHQ-2-4, 5917 - 5988	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.79E-09	0.96	5.34	-	961.1
AHQ-2-2, 5930 - 6000	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.64E-08	0.96	5.41	-	977.3
AHQ-2-11, 5446	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.55E-06	0.92	4.29	-	789.0
AHQ-2-3, 6075 - 6101	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.25E-10	0.95	4.79	-	1100.5
AHQ-2-1, 5901 - 5965	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.11E-05	0.86	3.99	-	517.4
AHQ-2-3, 6171 - 6243	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.42E-07	0.93	4.70	-	703.9
AHQ-2-3, 5899 - 5967	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.66E-04	0.88	3.99	-	579.2
AHQ-2-10, 5188 - 5262	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.75E-09	0.92	4.42	-	612.2
AHQ-2-10, 5582 - 5654	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.22E-08	0.90	4.23	-	621.7
AHQ-2-7, 5831	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.86E-09	0.91	4.34	-	585.2
AHQ-2-11, 5540 - 5601	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.62E-12	0.98	6.23	-	1460.8
AHQ-2-6, 5586 - 5633	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.42E-07	0.95	4.72	-	830.0
AHQ-2-5, 5884 - 5951	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.08E-11	0.96	5.47	-	922.9
AHQ-2-3, 5709 - 5787	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.63E-09	0.91	4.25	-	651.7
AHQ-2-2, 6068 - 6136	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.57E-09	0.95	4.93	-	790.3
AHQ-2-4, 6350 - 6429	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.37E-06	0.83	3.43	-	608.1
AHQ-2-5, 6125 - 6133	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.76E-10	0.96	5.44	-	980.3
AHQ-2-6, 5801 - 5853	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.39E-12	0.96	5.58	-	845.8
AHQ-2-7, 5672 - 5680	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.12E-06	0.92	4.37	-	834.9
AHQ-2-4, 6078 - 6149	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.41E-08	0.92	4.38	-	519.4
AHQ-2-12, 5998	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.14E-10	0.93	3.82	-	953.3
AHQ-2-2, 6172	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.29E-09	0.89	3.86	-	652.5
AHQ-2-14-, 5769	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.58E-09	0.94	4.98	-	646.0
AHQ-2-10, 5375 - 5439	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.60E-13	0.95	5.25	-	773.7
AHQ-2-10, 5279	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.18E-06	0.94	4.65	-	842.3
AHQ-2-9, 5887 - 5904	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.30E-08	0.97	5.21	-	1519.1
AHQ-2-9, 5690	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.55E-08	0.95	4.78	-	1006.0
AHQ-2-8, 5536	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.36E-07	0.82	3.61	-	559.8
AHQ-2-8, 5680	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.22E-09	0.95	5.05	-	696.5
AHQ-2-3, 5983	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.03E-06	0.96	5.23	-	940.8
AHQ-2-1, 3976	K.VGDDPAVWQLK.N	1228.37879	2	6.73E-09	0.94	4.09	-	965.4
AHQ-2-5, 3503	K.VGDDPAVWQLK.N	1228.37879	2	2.57E-08	0.91	3.71	-	885.0
AHQ-2-7, 3424	K.VGDDPAVWQLK.N	1228.37879	2	5.71E-06	0.90	3.49	-	854.5
AHQ-2-10, 3400	K.VGDDPAVWQLK.N	1228.37879	2	4.74E-07	0.85	3.25	-	664.2
AHQ-2-2, 3844	K.VGDDPAVWQLK.N	1228.37879	2	7.73E-09	0.94	4.28	-	929.4
AHQ-2-4, 3784	K.VGDDPAVWQLK.N	1228.37879	2	1.95E-09	0.90	3.29	-	832.8
AHQ-2-2, 3804 - 3881	K.VGDDPAVWQLK.N	1228.37879	2	2.43E-08	0.93	4.17	-	799.7
AHQ-2-6, 3491	K.VGDDPAVWQLK.N	1228.37879	2	6.32E-09	0.95	3.99	-	1057.0
AHQ-2-2, 3192	K.VGDDPAVWQLKNSAK.V	1628.81068	2	2.74E-08	0.79	3.39	-	682.9
AHQ-2-4, 3182	K.VGDDPAVWQLKNSAK.V	1628.81068	2	2.95E-11	0.80	3.34	-	583.2
AHQ-2-3, 3091 - 3160	K.VLGEAMTGISQNAK.N	1419.62961	1	2.28E-09	0.88	3.77	-	527.3
AHQ-2-4, 3084 - 3165	K.VLGEAMTGISQNAK.N	1419.62961	1	7.84E-05	0.49	2.38	-	370.1
AHQ-2-2, 3092	K.VLGEAMTGISQNAK.N	1419.62961	2	2.46E-10	0.98	4.92	-	2259.1
AHQ-2-4, 3270	K.VLGEAMTGISQNAK.N	1419.62961	2	3.30E-08	0.96	4.04	-	2056.1
AHQ-2-1, 2460	K.VLGEAM*TGISQNAK.N	1435.62901	2	5.81E-05	0.92	3.92	-	934.8
AHQ-2-2, 3108 - 3178	K.VLGEAMTGISQNAK.N	1419.62961	1	9.19E-08	0.63	3.12	-	342.8
AHQ-2-2, 2324 - 2396	K.VLGEAM*TGISQNAK.N	1435.62901	2	5.13E-06	0.97	5.06	-	1498.8
AHQ-2-3, 3156	K.VLGEAMTGISQNAK.N	1419.62961	2	3.03E-08	0.98	4.59	-	2529.5
AHQ-2-6, 2859 - 2862	K.VLGEAMTGISQNAK.N	1419.62961	2	1.62E-04	0.88	3.15	-	1078.9
AHQ-2-5, 2859 - 2860	K.VLGEAMTGISQNAK.N	1419.62961	2	9.35E-05	0.97	4.42	-	1702.0
AHQ-2-3, 4920 - 4932	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	5.89E-07	0.87	4.52	-	382.5
AHQ-2-5, 5408 - 5445	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	1.01E-09	0.84	3.92	-	613.7
AHQ-2-1, 4954	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	3.55E-05	0.89	4.39	-	669.1
AHQ-2-3, 5497 - 5567	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	8.12E-12	0.88	4.62	-	612.8
AHQ-2-2, 5088	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	2.03E-07	0.85	4.19	-	564.8
AHQ-2-2, 5538 - 5608	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	3.31E-04	0.89	4.78	-	686.0
AHQ-2-3, 1848	K.VLVQNAAGSQEK.L	1244.37976	2	2.18E-04	0.79	2.99	-	682.8
AHQ-2-3, 1661 - 1737	K.VLVQNAAGSQEK.L	1244.37976	2	5.68E-07	0.88	3.23	-	710.0
AHQ-2-5, 1459	K.VLVQNAAGSQEK.L	1244.37976	2	1.10E-04	0.74	3.18	-	527.4
AHQ-2-3, 1520 - 1579	K.VLVQNAAGSQEK.L	1244.37976	2	3.19E-04	0.91	3.49	-	964.9
AHQ-2-1, 1786 - 1845	K.VLVQNAAGSQEK.L	1244.37976	2	4.43E-05	0.88	3.53	-	670.0
AHQ-2-4, 1505 - 1577	K.VLVQNAAGSQEK.L	1244.37976	2	2.35E-08	0.93	3.51	-	1027.1
AHQ-2-4, 1754	K.VLVQNAAGSQEK.L	1244.37976	2	1.87E-04	0.95	4.13	-	1203.2
AHQ-2-6, 1486	K.VLVQNAAGSQEK.L	1244.37976	2	8.54E-07	0.83	3.41	-	577.2
AHQ-2-2, 1661 - 1730	K.VLVQNAAGSQEK.L	1244.37976	2	1.75E-08	0.93	4.04	-	927.6
AHQ-2-1, 1904	K.VLVQNAAGSQEK.L	1244.37976	2	5.71E-04	0.67	2.78	-	407.2
AHQ-2-2, 1614	K.VLVQNAAGSQEK.L	1244.37976	1	2.87E-04	0.24	1.99	-	423.0
AHQ-2-2, 1522 - 1592	K.VLVQNAAGSQEK.L	1244.37976	2	9.26E-05	0.88	3.49	-	892.3
AHQ-2-4, 4737 - 4738	K.VMVTNVTSLLK.T	1205.49322	2	1.24E-05	0.92	4.36	-	741.3
AHQ-2-3, 4759	K.VMVTNVTSLLK.T	1205.49322	2	7.13E-06	0.92	4.30	-	811.7
AHQ-2-3, 4375	K.VM*VTNVTSLLK.T	1221.49262	2	8.23E-05	0.79	3.13	-	679.9
AHQ-2-5, 4367 - 4371	K.VMVTNVTSLLK.T	1205.49322	2	2.10E-06	0.93	4.28	-	928.5
AHQ-2-1, 4896	K.VMVTNVTSLLK.T	1205.49322	2	2.80E-05	0.91	3.52	-	887.6
AHQ-2-1, 4528	K.VM*VTNVTSLLK.T	1221.49262	2	7.32E-04	0.86	3.41	-	718.0
AHQ-2-5, 4019	K.VM*VTNVTSLLK.T	1221.49262	2	2.22E-04	0.79	3.25	-	582.9
AHQ-2-2, 4388 - 4389	K.VM*VTNVTSLLK.T	1221.49262	2	7.40E-05	0.82	3.54	-	670.2
AHQ-2-6, 4333	K.VMVTNVTSLLK.T	1205.49322	2	2.56E-04	0.88	3.79	-	605.1
AHQ-2-2, 4772	K.VMVTNVTSLLK.T	1205.49322	2	2.24E-05	0.90	3.90	-	869.6
AHQ-2-7, 4208	K.VMVTNVTSLLK.T	1205.49322	2	4.87E-05	0.87	3.55	-	784.5
AHQ-2-4, 4341	K.VM*VTNVTSLLK.T	1221.49262	2	1.61E-05	0.80	3.39	-	611.1
AHQ-2-3, 2691 - 2693	R.VQELGHGCAALVTK.A	1484.70307	2	9.01E-06	0.97	4.54	-	1764.3
AHQ-2-2, 2705	R.VQELGHGCAALVTK.A	1484.70307	1	1.72E-05	0.91	4.06	-	854.2
AHQ-2-2, 2696 - 2708	R.VQELGHGCAALVTK.A	1484.70307	2	1.90E-04	0.97	4.47	-	1592.1
AHQ-2-3, 2703	R.VQELGHGCAALVTK.A	1484.70307	1	4.40E-05	0.86	3.72	-	585.9
AHQ-2-6, 2505	R.VQELGHGCAALVTK.A	1484.70307	2	2.46E-04	0.95	4.01	-	1346.0
AHQ-2-1, 2904	R.VQELGHGCAALVTK.A	1484.70307	2	1.68E-09	0.97	5.65	-	1386.2
AHQ-2-4, 2750	R.VQELGHGCAALVTK.A	1484.70307	2	4.03E-04	0.95	4.11	-	1200.1
AHQ-2-4, 2661 - 2672	R.VQELGHGCAALVTK.A	1484.70307	2	1.20E-05	0.97	4.21	-	1701.8
AHQ-2-3, 2511	K.VSHVLAALQAGNR.G	1336.52525	1	7.95E-05	0.85	3.47	-	513.7
AHQ-2-3, 2512 - 2592	K.VSHVLAALQAGNR.G	1336.52525	2	3.20E-11	0.97	4.68	-	1792.2
AHQ-2-7, 2276	K.VSHVLAALQAGNR.G	1336.52525	1	1.59E-05	0.72	3.11	-	378.8
AHQ-2-2, 2520 - 2598	K.VSHVLAALQAGNR.G	1336.52525	1	4.92E-04	0.30	2.66	-	227.8
AHQ-2-2, 2521 - 2522	K.VSHVLAALQAGNR.G	1336.52525	2	8.35E-11	0.97	5.15	-	1781.6
AHQ-2-3, 2525	K.VSHVLAALQAGNR.G	1336.52525	1	4.19E-06	0.91	4.13	-	520.4
AHQ-2-2, 2524	K.VSHVLAALQAGNR.G	1336.52525	1	5.20E-05	0.85	3.46	-	415.2
AHQ-2-5, 2308	K.VSHVLAALQAGNR.G	1336.52525	1	8.32E-05	0.77	3.18	-	356.8
AHQ-2-3, 2661	K.VSHVLAALQAGNR.G	1336.52525	1	1.73E-08	0.34	1.95	-	545.3
AHQ-2-1, 2810	K.VSHVLAALQAGNR.G	1336.52525	1	3.86E-04	0.65	2.45	-	462.6
AHQ-2-10, 2392	K.VSHVLAALQAGNR.G	1336.52525	1	8.38E-06	0.67	2.73	-	355.5

AHQ-2-5, 2325	K.VSHVLAALQAGNR.G	1336.52525	1	1.06E-05	0.67	2.97	-	214.9
AHQ-2-4, 2638	K.VSHVLAALQAGNR.G	1336.52525	2	1.26E-09	0.96	3.71	-	1663.0
AHQ-2-6, 2335 - 2339	K.VSHVLAALQAGNR.G	1336.52525	2	1.24E-06	0.97	4.39	-	1822.0
AHQ-2-9, 2395	K.VSHVLAALQAGNR.G	1336.52525	1	7.92E-04	0.51	2.51	-	328.7
AHQ-2-1, 2730 - 2809	K.VSHVLAALQAGNR.G	1336.52525	2	8.00E-11	0.97	4.59	-	1717.1
AHQ-2-4, 2525 - 2526	K.VSHVLAALQAGNR.G	1336.52525	1	1.03E-07	0.89	3.74	-	570.2
AHQ-2-5, 2307 - 2319	K.VSHVLAALQAGNR.G	1336.52525	2	3.38E-09	0.98	5.17	-	2143.9
AHQ-2-5, 5747	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.86E-04	0.87	3.79	-	683.5
AHQ-2-11, 6352 - 6354	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.31E-04	0.96	5.21	-	965.0
AHQ-2-3, 6037 - 6107	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	6.37E-06	0.94	4.56	-	887.0
AHQ-2-3, 6068	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	3.31E-05	0.93	4.58	-	1175.7
AHQ-2-3, 6876	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.94E-06	0.93	4.64	-	759.0
AHQ-2-3, 6959 - 7027	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.92E-06	0.97	5.78	-	1138.2
AHQ-2-3, 6969 - 6989	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	4.08E-09	0.97	6.15	-	1542.8
AHQ-2-3, 7116	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.23E-10	0.96	5.42	-	854.9
AHQ-2-5, 6825 - 6835	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.59E-06	0.98	6.63	-	1264.6
AHQ-2-9, 6786	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.13E-05	0.85	3.60	-	574.4
AHQ-2-6, 5705	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.80E-08	0.95	4.51	-	1257.4
AHQ-2-6, 6645 - 6653	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	8.73E-07	0.96	5.43	-	1061.9
AHQ-2-10, 6214 - 6226	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.08E-07	0.97	5.47	-	1157.5
AHQ-2-4, 7177	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.30E-06	0.93	4.42	-	875.0
AHQ-2-4, 7040 - 7042	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	2.69E-09	0.96	5.03	-	1581.8
AHQ-2-4, 7036 - 7100	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.06E-07	0.96	5.56	-	1106.0
AHQ-2-4, 6953 - 7032	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.11E-07	0.97	5.63	-	1278.3
AHQ-2-2, 6096	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	8.45E-08	0.95	4.89	-	1049.1
AHQ-2-4, 6222	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	6.20E-07	0.95	4.58	-	1232.6
AHQ-2-4, 6072	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.53E-06	0.94	4.18	-	1023.7
AHQ-2-2, 6921	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.40E-07	0.93	4.82	-	628.2
AHQ-2-2, 7020 - 7089	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.90E-06	0.96	5.64	-	882.1
AHQ-2-2, 7188	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.75E-09	0.96	5.50	-	931.2
AHQ-2-1, 7034	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.94E-07	0.96	5.28	-	805.8
AHQ-2-4, 6006 - 6076	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.51E-07	0.94	4.66	-	1004.8
AHQ-2-13-, 6662	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	8.68E-06	0.90	4.39	-	555.0
AHQ-2-1, 6924 - 6938	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	4.14E-07	0.97	5.72	-	1785.2
AHQ-2-8, 6528	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	8.70E-06	0.95	4.90	-	825.0
AHQ-2-7, 6675	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.98E-07	0.96	5.55	-	818.9
AHQ-2-1, 6860 - 6921	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	7.80E-07	0.95	4.67	-	1040.2
AHQ-2-1, 6048 - 6124	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	7.21E-05	0.85	3.94	-	618.4
AHQ-2-1, 6133	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	2.10E-10	0.96	4.91	-	1635.6
AHQ-2-7, 5639	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.39E-06	0.94	4.81	-	729.6
AHQ-2-12, 6667	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.69E-05	0.74	3.35	-	425.1
AHQ-2-4, 4664	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.89E-05	0.93	4.76	-	482.3
AHQ-2-4, 4800 - 4825	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.99E-06	0.96	5.26	-	992.4
AHQ-2-10, 4178 - 4246	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.06E-05	0.90	4.04	-	699.8
AHQ-2-13-, 4606	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.00E-07	0.94	4.42	-	749.7
AHQ-2-8, 4262	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.00E-07	0.92	4.71	-	456.3
AHQ-2-8, 4358 - 4427	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.06E-07	0.94	5.10	-	543.3
AHQ-2-8, 4448	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	8.70E-12	0.95	5.14	-	1275.6
AHQ-2-14, 5497	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.62E-05	0.45	2.65	-	400.4
AHQ-2-1, 4980	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.58E-05	0.82	3.66	-	280.4
AHQ-2-4, 4957	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.21E-09	0.91	4.70	-	400.2
AHQ-2-1, 4812	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.95E-06	0.96	5.17	-	972.4
AHQ-2-1, 4693	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.47E-05	0.83	3.96	-	278.4
AHQ-2-14-, 4572 - 4576	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.22E-13	0.95	4.89	-	789.4
AHQ-2-3, 4668 - 4671	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.02E-07	0.93	4.57	-	513.4
AHQ-2-6, 4501 - 4513	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.41E-11	0.98	6.30	-	1043.9
AHQ-2-3, 4791 - 4860	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.40E-05	0.95	5.07	-	769.8
AHQ-2-2, 4689	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.78E-04	0.77	4.13	-	166.7
AHQ-2-5, 4485	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.21E-05	0.88	4.46	-	423.7
AHQ-2-5, 4587 - 4600	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.33E-08	0.97	5.85	-	1079.4
AHQ-2-2, 5001 - 5002	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.66E-11	0.94	4.69	-	775.1
AHQ-2-3, 4953	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.40E-06	0.85	3.54	-	453.1
AHQ-2-12, 4605	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.56E-05	0.63	3.15	-	318.3
AHQ-2-2, 4824 - 4897	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.17E-04	0.97	5.77	-	901.4
AHQ-2-7, 4475 - 4487	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.02E-07	0.94	5.06	-	732.2
gi|21956645|ref|NP_665807.1| myotrophin; granule cell differentiation protein [Homo sapiens]				1.11E-15	4.72	50.34	66.90	12894.7
AHQ-2-14-, 4531	K.GADINAPDKHHITPLLSAVYEGHVSCVK.L	3031.39193	3	7.13E-09	0.98	6.61	-	1640.5
AHQ-2-13, 4357	K.GADINAPDKHHITPLLSAVYEGHVSCVK.L	3031.39193	3	7.81E-07	0.97	6.06	-	1765.6
AHQ-2-14, 5752	K.GADINAPDKHHITPLLSAVYEGHVSCVK.L	3031.39193	3	4.36E-08	0.97	6.10	-	1358.3
AHQ-2-13-, 3995 - 4069	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.80E-10	0.97	5.32	-	1781.4
AHQ-2-13, 4031 - 4111	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.11E-15	0.98	5.97	-	1427.5
AHQ-2-13, 3907 - 3967	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	4.18E-04	0.88	3.69	-	918.9
AHQ-2-14-, 4084	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.86E-05	0.95	4.94	-	1079.8
AHQ-2-14, 4860 - 4934	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.78E-06	0.97	5.17	-	1369.3
AHQ-2-14, 4992 - 5060	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	6.72E-04	0.94	4.21	-	1123.6
AHQ-2-13-, 4162	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	8.52E-09	0.97	5.41	-	1373.1
AHQ-2-13-, 4023 - 4093	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	6.10E-07	0.97	5.27	-	1512.6
AHQ-2-14-, 3876 - 3951	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.00E-09	0.98	5.91	-	1845.8
AHQ-2-13-, 4090	K.GPDGLTAFEATDNQAIK.A	1748.87196	3	1.99E-07	0.74	3.32	-	795.2
AHQ-2-13, 4003 - 4005	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	2	4.42E-05	0.97	5.13	-	1168.4
AHQ-2-13, 3999	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	4.56E-06	0.99	6.89	-	3169.8
AHQ-2-14, 5293 - 5365	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	7.76E-04	0.97	5.48	-	1758.3
AHQ-2-14-, 6836 - 6843	R.KPLHYAADCGQLEILEFLLLK.G	2473.91510	3	3.38E-05	0.86	3.53	-	1032.7
AHQ-2-14-, 3587	K.NGDLDEVKDYVAK.G	1466.57496	2	5.42E-08	0.95	3.83	-	1399.1
AHQ-2-14-, 3673	K.NGDLDEVKDYVAK.G	1466.57496	2	1.15E-08	0.94	3.71	-	1315.9
AHQ-2-13-, 3770	K.NGDLDEVKDYVAK.G	1466.57496	2	3.00E-08	0.93	3.66	-	1177.1
AHQ-2-14, 4537	K.NGDLDEVKDYVAK.G	1466.57496	2	5.53E-08	0.95	4.17	-	1456.6
AHQ-2-13-, 3658	K.NGDLDEVKDYVAK.G	1466.57496	2	1.58E-09	0.92	3.58	-	1103.8
AHQ-2-13-, 3777	K.NGDLDEVKDYVAK.G	1466.57496	1	1.30E-06	0.41	2.60	-	269.5
AHQ-2-13, 3751 - 3759	K.NGDLDEVKDYVAK.G	1466.57496	2	4.93E-09	0.93	3.98	-	1116.5
gi|4504165|ref|NP_000168.1| gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]				2.22E-15	21.02	230.37	35.30	85696.9
AHQ-2-5, 3572	K.AGALNSNDAFVLK.T	1320.47622	1	1.62E-07	0.40	2.42	-	406.7
AHQ-2-5, 3657 - 3727	K.AGALNSNDAFVLK.T	1320.47622	1	2.61E-06	0.40	2.28	-	414.7
AHQ-2-5, 3509 - 3587	K.AGALNSNDAFVLK.T	1320.47622	2	1.54E-06	0.87	3.74	-	711.4
AHQ-2-5, 3311 - 3347	K.AGALNSNDAFVLK.T	1320.47622	2	2.11E-05	0.75	3.12	-	619.0
AHQ-2-5, 3663 - 3716	K.AGALNSNDAFVLK.T	1320.47622	2	1.11E-07	0.88	3.49	-	722.7
AHQ-2-6, 3543	K.AGALNSNDAFVLK.T	1320.47622	2	3.99E-04	0.91	3.67	-	952.1
AHQ-2-6, 3627	K.AGALNSNDAFVLK.T	1320.47622	2	9.53E-05	0.40	3.00	-	375.1
AHQ-2-7, 3253	K.AGALNSNDAFVLK.T	1320.47622	2	3.45E-06	0.78	3.26	-	555.1
AHQ-2-6, 5497 - 5501	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	8.86E-08	0.96	5.69	-	715.4
AHQ-2-6, 5593 - 5673	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.89E-07	0.95	5.20	-	715.0
AHQ-2-11, 5494	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.02E-04	0.91	4.07	-	662.8
AHQ-2-5, 5575	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.39E-04	0.93	4.78	-	719.5
AHQ-2-10, 5124 - 5126	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.12E-05	0.94	5.06	-	623.5
AHQ-2-7, 5540	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.62E-05	0.94	4.97	-	635.4
AHQ-2-9, 5680 - 5711	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.04E-05	0.94	4.68	-	695.9
AHQ-2-5, 5715 - 5783	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.09E-06	0.96	5.60	-	850.4

AHQ-2-9, 5522	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.73E-10	0.91	4.73	-	464.4
AHQ-2-5, 5900 - 5979	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.66E-06	0.97	6.26	-	764.4
AHQ-2-7, 5657 - 5723	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.68E-08	0.95	5.50	-	563.2
AHQ-2-1, 6058	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.80E-04	0.75	3.67	-	284.0
AHQ-2-3, 6032	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.40E-05	0.89	4.12	-	619.5
AHQ-2-10, 5260 - 5322	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	8.37E-07	0.93	4.86	-	689.6
AHQ-2-8, 5511 - 5590	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	9.55E-06	0.92	4.17	-	765.3
AHQ-2-5, 6047	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.39E-08	0.96	5.40	-	786.4
AHQ-2-6, 5558	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.02E-05	0.94	4.41	-	1305.9
AHQ-2-5, 5641 - 5723	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.50E-04	0.56	3.05	-	337.4
AHQ-2-5, 2136	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.39E-07	0.84	3.30	-	858.6
AHQ-2-7, 1903	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.50E-10	0.94	3.50	-	1654.1
AHQ-2-11, 2149	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.35E-04	0.82	3.29	-	884.7
AHQ-2-9, 2034 - 2043	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.09E-05	0.88	3.39	-	1344.9
AHQ-2-5, 2043	K.DSQEEEKTEALTSAK.R	1666.72289	2	8.81E-04	0.91	3.74	-	1201.0
AHQ-2-13, 2311	K.DSQEEEKTEALTSAK.R	1666.72289	2	6.43E-05	0.87	3.59	-	894.4
AHQ-2-5, 1945	K.DSQEEEKTEALTSAK.R	1666.72289	3	4.70E-05	0.97	4.62	-	2225.1
AHQ-2-5, 1941 - 1968	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.24E-08	0.95	4.27	-	1434.7
AHQ-2-10, 2026	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.25E-05	0.88	3.50	-	1071.0
AHQ-2-13-, 2205	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.51E-07	0.96	4.24	-	1709.7
AHQ-2-13-, 2219	K.DSQEEEKTEALTSAK.R	1666.72289	3	3.58E-08	0.97	4.45	-	2372.4
AHQ-2-8, 1854	K.DSQEEEKTEALTSAK.R	1666.72289	2	9.00E-08	0.88	3.63	-	1050.9
AHQ-2-6, 1950	K.DSQEEEKTEALTSAK.R	1666.72289	3	1.72E-05	0.88	3.27	-	1253.1
AHQ-2-6, 1941	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.89E-08	0.91	3.59	-	1126.4
AHQ-2-5, 6363 - 6369	R.EVQGFESATFLGYFK.S	1723.90570	2	7.65E-10	0.96	4.13	-	1576.4
AHQ-2-13, 6087 - 6156	R.EVQGFESATFLGYFK.S	1723.90570	2	4.96E-05	0.80	2.74	-	1051.6
AHQ-2-12, 6238	R.EVQGFESATFLGYFK.S	1723.90570	2	8.87E-04	0.88	3.19	-	1027.5
AHQ-2-5, 6927	R.EVQGFESATFLGYFK.S	1723.90570	2	2.02E-04	0.86	2.95	-	912.6
AHQ-2-5, 7065	R.EVQGFESATFLGYFK.S	1723.90570	2	6.00E-07	0.88	3.28	-	1036.0
AHQ-2-13-, 6258 - 6331	R.EVQGFESATFLGYFK.S	1723.90570	2	4.91E-09	0.97	4.86	-	1760.0
AHQ-2-5, 2233	K.HVVPNEVVVQR.L	1276.46981	1	2.20E-06	0.75	2.59	-	640.6
AHQ-2-6, 2022	K.HVVPNEVVVQR.L	1276.46981	2	1.78E-06	0.84	3.12	-	546.8
AHQ-2-5, 2228	K.HVVPNEVVVQR.L	1276.46981	2	1.35E-04	0.83	2.90	-	572.7
AHQ-2-7, 1952	K.HVVPNEVVVQR.L	1276.46981	2	2.46E-07	0.86	3.02	-	560.6
AHQ-2-9, 2067	K.HVVPNEVVVQR.L	1276.46981	2	1.15E-07	0.84	2.95	-	470.7
AHQ-2-11, 2204 - 2212	K.HVVPNEVVVQR.L	1276.46981	2	3.76E-06	0.94	3.51	-	842.2
AHQ-2-11, 2208 - 2210	K.HVVPNEVVVQR.L	1276.46981	1	5.46E-06	0.60	2.47	-	427.3
AHQ-2-5, 2019	K.HVVPNEVVVQR.L	1276.46981	1	1.83E-06	0.27	2.53	-	204.7
AHQ-2-12, 2242 - 2243	K.HVVPNEVVVQR.L	1276.46981	1	9.70E-07	0.25	2.33	-	261.4
AHQ-2-12, 2237	K.HVVPNEVVVQR.L	1276.46981	2	4.67E-06	0.92	3.50	-	653.2
AHQ-2-5, 2007 - 2076	K.HVVPNEVVVQR.L	1276.46981	2	1.69E-08	0.90	3.44	-	545.2
AHQ-2-5, 6864	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	7.43E-04	0.78	3.66	-	543.2
AHQ-2-5, 6415 - 6431	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	3.62E-07	0.97	5.77	-	1617.7
AHQ-2-5, 5467 - 5535	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	4.24E-09	0.97	7.01	-	1209.9
AHQ-2-6, 5445	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	7.20E-06	0.98	7.40	-	2024.2
AHQ-2-5, 6172 - 6183	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	2.22E-15	0.95	5.56	-	1046.1
AHQ-2-5, 1760 - 1811	K.PALPAGTEDTAK.E	1171.28241	2	1.92E-08	0.83	2.90	-	512.6
AHQ-2-5, 2269	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	2.24E-08	0.81	3.58	-	412.9
AHQ-2-7, 2257	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	3.78E-05	0.38	2.77	-	123.6
AHQ-2-5, 2080	K.PALPAGTEDTAKEDAANRK.L	1956.10363	2	2.69E-04	0.86	3.61	-	524.2
AHQ-2-7, 4555	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	3.80E-05	0.76	3.38	-	308.4
AHQ-2-6, 4655	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	3.85E-07	0.93	4.35	-	576.0
AHQ-2-5, 4856	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	6.73E-06	0.84	3.45	-	423.3
AHQ-2-8, 4370	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	9.44E-04	0.82	3.24	-	424.6
AHQ-2-5, 4688 - 4763	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	4.52E-05	0.87	3.85	-	525.5
AHQ-2-5, 2697	K.SEDCFILDHGK.D	1322.42590	2	2.89E-06	0.95	3.71	-	1519.9
AHQ-2-7, 2661	K.SEDCFILDHGK.D	1322.42590	2	1.54E-06	0.92	3.21	-	1220.8
AHQ-2-6, 2749	K.SEDCFILDHGK.D	1322.42590	2	2.76E-06	0.96	3.58	-	1707.3
AHQ-2-5, 1881	K.TGAQELLR.V	888.00387	2	2.33E-04	0.89	3.02	-	1067.4
AHQ-2-8, 3938	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	6.63E-04	0.92	3.92	-	986.7
AHQ-2-5, 4252 - 4323	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.81E-10	0.98	5.17	-	1734.4
AHQ-2-5, 4693	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	6.91E-05	0.78	3.02	-	604.0
AHQ-2-7, 4135	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	2.04E-06	0.85	3.48	-	837.3
AHQ-2-6, 4371	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	8.02E-05	0.59	2.79	-	561.6
AHQ-2-5, 4391 - 4469	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.66E-10	0.96	4.51	-	1465.9
AHQ-2-9, 4646	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	2.55E-04	0.96	4.78	-	1103.5
AHQ-2-5, 3541 - 3563	R.VHVSEEGTEPEAM*LQVLGPK.P	2167.42570	2	1.14E-04	0.95	4.85	-	1119.5
AHQ-2-7, 4571	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	3.74E-06	0.94	4.43	-	772.8
AHQ-2-5, 4697 - 4767	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	6.50E-06	0.97	5.40	-	1211.2
AHQ-2-5, 5071	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	7.23E-06	0.86	4.10	-	653.0
AHQ-2-6, 5013	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	2.34E-09	0.92	4.89	-	718.5
AHQ-2-8, 4813	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	1.00E-05	0.87	4.04	-	607.9
AHQ-2-5, 4147	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	1.24E-04	0.89	4.66	-	694.3
AHQ-2-5, 4821	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAKEDAANR.K	3960.33442	3	9.41E-06	0.94	5.32	-	1043.1
AHQ-2-5, 3435	R.VPFDAATLHTSTAM*AAQHGMDDDGTGQK.Q	2891.10081	3	9.38E-04	0.94	5.46	-	1128.0
AHQ-2-5, 3804	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	1.20E-06	0.97	5.98	-	1573.3
AHQ-2-5, 6199 - 6267	K.VSNGAGTMSVSLVADENPFAQGALK.S	2464.73740	2	2.01E-09	0.80	3.23	-	691.6
gi|4503327|ref|NP_000389.1| cytochrome b5 reductase membrane-bound isoform; diaphorase (NADH) [Homo				2.22E-15	7.72	90.29	42.20	34234.6
AHQ-2-9, 5659 - 5732	R.APEAWDYGQGFVNEEMIR.D	2113.29517	2	1.02E-06	0.96	4.94	-	1139.9
AHQ-2-9, 5056 - 5058	R.APEAWDYGQGFVNEEM*IR.D	2129.29457	2	6.94E-04	0.97	4.77	-	1878.3
AHQ-2-9, 4650	K.DILLRPELEELR.N	1496.73370	2	4.01E-09	0.86	3.29	-	884.6
AHQ-2-9, 6116 - 6134	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	2	6.01E-05	0.89	4.37	-	539.1
AHQ-2-11, 5888 - 5913	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	3	8.25E-04	0.77	3.70	-	756.6
AHQ-2-12, 6146 - 6166	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	3	7.04E-09	0.95	5.33	-	1151.8
AHQ-2-9, 6115 - 6182	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	3	2.22E-15	0.97	5.88	-	1844.5
AHQ-2-9, 2707 - 2712	R.GPSGLLVYQGK.G	1119.29547	1	1.35E-05	0.81	3.61	-	381.4
AHQ-2-9, 2732	R.GPSGLLVYQGK.G	1119.29547	2	3.02E-04	0.93	3.41	-	1310.7
AHQ-2-12, 6003	R.IDGNLVVRPYTPISSDDDKGFVDLVIK.V	2977.35765	3	6.37E-05	0.49	3.12	-	398.3
AHQ-2-9, 6160 - 6239	R.IDGNLVVRPYTPISSDDDKGFVDLVIK.V	2977.35765	3	1.56E-05	0.93	5.49	-	878.4
AHQ-2-9, 6006 - 6076	R.IDGNLVVRPYTPISSDDDKGFVDLVIK.V	2977.35765	3	5.89E-05	0.95	5.38	-	1508.5
AHQ-2-9, 4479	R.STPAITLESPDIKYPLR.L	1902.18061	2	1.30E-08	0.88	4.13	-	554.1
AHQ-2-9, 5940 - 6008	K.SVGMIAGGTGITPMLQVIR.A	1902.31543	2	1.23E-04	0.63	3.49	-	538.6
AHQ-2-9, 5010	K.SVGMIAGGTGITPM*LQVIR.A	1918.31483	2	6.29E-06	0.71	3.24	-	442.8
gi|21361657|ref|NP_005304.3| glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom				3.33E-15	9.86	120.33	27.90	56782.0
AHQ-2-7, 5839	R.ELSDFISYLQR.E	1371.52000	2	2.03E-06	0.97	4.39	-	1588.1
AHQ-2-7, 7283 - 7292	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	3.33E-15	0.98	6.59	-	3103.6
AHQ-2-10, 6632	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	7.23E-06	0.89	4.84	-	691.9
AHQ-2-7, 4297	R.GFPTIYFSPANK.K	1342.52349	1	6.18E-04	0.46	2.75	-	504.8
AHQ-2-7, 5607 - 5611	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	3	3.13E-06	0.92	4.65	-	1080.2
AHQ-2-7, 2343	K.LNFAVASR.K	878.01067	2	2.19E-04	0.80	2.93	-	776.0
AHQ-2-7, 1955	K.LSKDPNIVIAK.M	1198.43727	2	1.02E-05	0.86	3.23	-	935.5
AHQ-2-7, 3269 - 3347	K.MDATANDVPSPYEVR.G	1665.80646	2	2.07E-04	0.84	3.86	-	476.1
AHQ-2-7, 2916	K.M*DATANDVPSPYEVR.G	1681.80586	2	4.52E-05	0.84	3.71	-	397.0
AHQ-2-7, 2131	K.SEPIPESNDGPVK.V	1369.45928	1	2.11E-04	0.47	2.59	-	467.8
AHQ-2-7, 1867	R.TADGIVSHLK.K	1041.18311	2	8.95E-05	0.84	2.77	-	919.1
AHQ-2-9, 6354	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	2	9.78E-08	0.97	4.93	-	1659.8
AHQ-2-7, 6263 - 6273	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	3	5.86E-05	0.89	4.33	-	740.4

AHQ-2-7, 2785 - 2799	K.YGVSGYPTLK.I	1085.23435	2	6.17E-04	0.92	3.39	-	666.1
gi|22043610|ref|XP_171081.1| similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1; rh				3.89E-15	2.86	40.26	21.40	21543.1
AHQ-2-11, 2538	R.AVLCPPPVK.K	982.22199	1	1.97E-04	0.15	1.97	-	289.5
AHQ-2-11, 3732 - 3800	K.KLTPITYPQGLAMAK.E	1632.99216	2	9.79E-05	0.87	3.72	-	591.4
AHQ-2-11, 3714 - 3717	K.LTPITYPQGLAM*AK.E	1520.81864	2	7.99E-05	0.86	3.03	-	553.3
AHQ-2-11, 4702 - 4705	K.PVNLGLWDTAGQEDYDR.L	1950.05441	2	3.89E-15	0.98	5.26	-	2272.8
gi|4502295|ref|NP_001677.1| ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti				4.44E-15	10.95	120.33	38.40	57955.2
AHQ-2-7, 2513	K.AHGGYSVFAGVGER.T	1407.51566	2	2.72E-08	0.80	2.97	-	519.0
AHQ-2-7, 5581 - 5596	R.AIAELGIYPAVDPLDSTSR.I	1989.21513	2	1.88E-07	0.90	4.03	-	539.5
AHQ-2-7, 7615	R.DQEGQDVLLFIDNIFR.F	1923.11524	2	2.12E-10	0.96	5.51	-	975.9
AHQ-2-7, 6035	R.FLSQPFQVAEVFTGHMGK.L	2024.33104	3	5.50E-08	0.76	3.86	-	506.2
AHQ-2-7, 6029 - 6107	R.FLSQPFQVAEVFTGHMGK.L	2024.33104	2	3.06E-07	0.85	3.69	-	605.0
AHQ-2-7, 4252 - 4256	R.FTQAGSEVSALLGR.I	1436.59522	2	1.72E-09	0.97	4.98	-	1359.8
AHQ-2-7, 7351	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	4.44E-15	0.97	6.65	-	1217.1
AHQ-2-7, 3369	R.IMDPNIVGSEHYDVAR.G	1817.01617	2	1.75E-10	0.95	4.37	-	1016.3
AHQ-2-7, 3563 - 3573	R.IMNVIGEPIDER.G	1386.59962	2	3.43E-04	0.93	4.28	-	979.8
AHQ-2-7, 4563	R.IPSAVGYQPTLATDMGTMQER.I	2267.56880	2	1.56E-05	0.88	4.20	-	415.1
AHQ-2-7, 3928 - 3943	R.LVLEVAQHLGESTVR.T	1651.88893	2	6.42E-09	0.97	5.19	-	1674.3
AHQ-2-7, 5588 - 5589	R.VALTGLTVAEYFR.D	1440.66861	2	5.53E-05	0.91	3.19	-	1301.6
AHQ-2-7, 4495 - 4507	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	8.79E-08	0.88	4.23	-	362.2
AHQ-2-7, 4496	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	3	5.51E-09	0.94	4.45	-	1519.2
gi|4827056|ref|NP_005103.1| WD repeat-containing protein 1 isoform 2 [Homo sapiens]				8.88E-15	11.37	130.38	45.90	58001.9
AHQ-2-9, 4774	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	4.13E-04	0.90	3.92	-	808.6
AHQ-2-6, 4813	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	6.60E-09	0.96	5.39	-	1170.0
AHQ-2-6, 4997	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	2.70E-04	0.95	5.41	-	1016.3
AHQ-2-10, 5288	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	5.72E-05	0.92	4.50	-	731.9
AHQ-2-6, 5769 - 5813	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	3.81E-11	0.94	5.37	-	870.0
AHQ-2-6, 5630 - 5701	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	8.88E-15	0.97	6.07	-	1235.5
AHQ-2-7, 5701	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	2.62E-09	0.71	3.48	-	516.9
AHQ-2-9, 5730	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	3.72E-09	0.95	5.06	-	940.2
AHQ-2-6, 7415 - 7437	K.CVAVGPGGYAVVVCIGQIVLLK.D	2275.75982	2	1.91E-05	0.48	2.88	-	370.7
AHQ-2-10, 4319	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	9.73E-10	0.93	4.19	-	1078.9
AHQ-2-6, 4533 - 4601	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	1.46E-09	0.98	5.55	-	1848.6
AHQ-2-13, 2427	K.IKDIAWTEDSKR.I	1462.63267	2	9.44E-06	0.90	3.61	-	830.0
AHQ-2-11, 5322	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.11E-07	0.89	3.51	-	932.1
AHQ-2-6, 5457 - 5521	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	3.78E-06	0.95	4.94	-	1053.5
AHQ-2-7, 5443	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	8.25E-07	0.81	3.55	-	846.5
AHQ-2-6, 5829	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.42E-08	0.79	3.31	-	698.1
AHQ-2-7, 3549	R.LYSILGTTLKDEGK.L	1538.76736	2	3.27E-08	0.85	3.44	-	740.3
AHQ-2-6, 3631	R.LYSILGTTLKDEGK.L	1538.76736	2	4.52E-06	0.86	3.29	-	794.3
AHQ-2-9, 3656	R.LYSILGTTLKDEGK.L	1538.76736	2	4.09E-04	0.80	2.92	-	820.2
AHQ-2-6, 4947 - 5010	R.MTVDESGQLISCSMDDTVR.Y	2146.36365	2	2.69E-04	0.87	3.60	-	791.2
AHQ-2-6, 4375	R.M*TVDESGQLISCSMDDTVR.Y	2162.36305	2	5.68E-04	0.90	4.06	-	605.4
AHQ-2-6, 4033	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	3	9.64E-04	0.73	3.16	-	409.5
AHQ-2-13, 4227	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	2.69E-09	0.96	5.20	-	1130.7
AHQ-2-6, 1635	K.SIQCLTVHKNGGK.S	1443.65418	2	1.31E-04	0.81	3.61	-	816.9
AHQ-2-6, 3998	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	1.41E-11	0.98	7.58	-	1743.0
AHQ-2-6, 4125	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	6.34E-08	0.96	6.09	-	1189.4
AHQ-2-12, 3939	K.YAPSGFYIASGDVSGK.L	1619.75589	2	5.10E-05	0.87	3.32	-	738.0
AHQ-2-1, 4173	K.YAPSGFYIASGDVSGK.L	1619.75589	2	3.27E-06	0.76	3.10	-	542.9
AHQ-2-6, 3699 - 3769	K.YAPSGFYIASGDVSGK.L	1619.75589	2	6.66E-09	0.96	4.73	-	920.4
gi|4757810|ref|NP_004037.1| ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,				8.88E-15	3.49	40.30	11.60	59750.3
AHQ-2-7, 5361 - 5365	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	2	1.31E-08	0.93	4.49	-	948.3
AHQ-2-7, 5349 - 5352	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	3	8.88E-15	0.97	5.91	-	1882.7
AHQ-2-7, 6184	K.GMSLNLEPDNVGVVVFGNDK.L	2105.35763	2	5.31E-04	0.87	4.49	-	383.7
AHQ-2-7, 3496 - 3499	K.TGTAEMSSILEER.I	1424.55988	2	3.09E-04	0.91	3.20	-	1546.3
AHQ-2-7, 2816	R.VLSIGDGIAR.V	1001.16212	2	9.86E-05	0.73	2.72	-	593.3
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				9.99E-15	109.21	1260.38	49.00	226529.8
AHQ-2-3, 2488	R.AKQTLENERGELANEVK.V	1930.10932	2	5.99E-05	0.95	4.87	-	950.8
AHQ-2-4, 1934	R.ALEEAMEQK.A	1049.18068	2	8.75E-06	0.90	3.44	-	1008.0
AHQ-2-3, 1911	R.ALEEAMEQK.A	1049.18068	2	3.03E-05	0.89	3.55	-	728.9
AHQ-2-2, 1777 - 1912	R.ALEEAMEQK.A	1049.18068	1	1.72E-04	0.27	2.17	-	548.1
AHQ-2-1, 3910 - 3912	K.ALELDSNLYR.I	1194.31920	1	2.43E-04	0.18	2.49	-	283.9
AHQ-2-4, 3745	K.ALELDSNLYR.I	1194.31920	2	1.46E-05	0.95	4.16	-	1246.4
AHQ-2-2, 3797	K.ALELDSNLYR.I	1194.31920	2	4.79E-06	0.94	3.71	-	1337.6
AHQ-2-6, 3469 - 3470	K.ALELDSNLYR.I	1194.31920	2	7.24E-07	0.90	3.44	-	973.9
AHQ-2-5, 3488	K.ALELDSNLYR.I	1194.31920	2	6.73E-07	0.96	4.09	-	1458.6
AHQ-2-3, 3747 - 3764	K.ALELDSNLYR.I	1194.31920	2	2.48E-06	0.95	4.02	-	1174.6
AHQ-2-1, 3908	K.ALELDSNLYR.I	1194.31920	2	6.39E-06	0.94	3.49	-	1290.1
AHQ-2-4, 2788	R.ALEQQVEEMK.T	1205.36380	2	4.95E-05	0.89	3.71	-	1015.1
AHQ-2-2, 2034	R.ALEQQVEEM*K.T	1221.36320	2	4.61E-05	0.81	3.26	-	898.3
AHQ-2-4, 2054	R.ALEQQVEEM*K.T	1221.36320	2	7.18E-04	0.74	2.81	-	631.8
AHQ-2-1, 2954	R.ALEQQVEEMK.T	1205.36380	2	4.54E-06	0.92	3.81	-	1296.9
AHQ-2-2, 2786 - 2796	R.ALEQQVEEMK.T	1205.36380	2	1.35E-07	0.93	3.99	-	1056.1
AHQ-2-1, 2196	R.ALEQQVEEM*K.T	1221.36320	2	4.31E-06	0.83	3.55	-	798.8
AHQ-2-5, 2541	R.ALEQQVEEMK.T	1205.36380	2	2.86E-05	0.90	3.63	-	1015.2
AHQ-2-3, 2789	R.ALEQQVEEMK.T	1205.36380	2	4.35E-05	0.91	3.82	-	1126.5
AHQ-2-5, 7456	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	2.12E-07	0.96	5.75	-	1239.8
AHQ-2-6, 6401	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.11E-10	0.98	6.25	-	2185.4
AHQ-2-3, 6708 - 6712	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	2.07E-10	0.97	6.38	-	1503.0
AHQ-2-1, 6712 - 6713	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.45E-09	0.96	5.92	-	1486.1
AHQ-2-1, 6585 - 6649	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	4.07E-05	0.97	6.95	-	1674.2
AHQ-2-5, 6585	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	2.06E-07	0.96	5.81	-	1518.2
AHQ-2-2, 6764	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	2.62E-12	0.98	7.60	-	1959.7
AHQ-2-2, 7568 - 7570	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	7.41E-05	0.97	5.89	-	1664.6
AHQ-2-3, 7519	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	2.61E-05	0.96	6.27	-	1270.0
AHQ-2-6, 7214	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	1.89E-06	0.96	6.02	-	1252.5
AHQ-2-4, 7572	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	3.54E-08	0.97	5.62	-	1939.6
AHQ-2-2, 5320 - 5390	K.ANLQIDQINTDLNLER.S	1871.04187	2	5.81E-04	0.97	5.76	-	1519.3
AHQ-2-2, 5474 - 5544	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.55E-11	0.97	5.49	-	1442.9
AHQ-2-1, 5037	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.37E-06	0.97	5.53	-	1233.2
AHQ-2-9, 4968	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.29E-07	0.96	4.98	-	1401.2
AHQ-2-2, 5210 - 5284	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.26E-08	0.98	5.70	-	1578.6
AHQ-2-5, 5052 - 5061	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.47E-06	0.97	5.66	-	1544.5
AHQ-2-2, 5084 - 5094	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.20E-05	0.95	4.74	-	835.5
AHQ-2-2, 4992 - 5004	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.58E-06	0.93	4.19	-	1012.4
AHQ-2-4, 5338	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.25E-04	0.94	4.24	-	1021.6
AHQ-2-6, 4941	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.30E-07	0.93	4.44	-	968.1
AHQ-2-3, 5039 - 5072	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.69E-05	0.93	4.72	-	765.6
AHQ-2-1, 5268 - 5344	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.13E-05	0.96	5.04	-	1066.4
AHQ-2-1, 5432	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.03E-04	0.95	4.83	-	1183.9
AHQ-2-3, 5184 - 5259	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.81E-06	0.97	5.28	-	1527.5
AHQ-2-3, 5324	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.81E-08	0.94	4.61	-	996.7
AHQ-2-4, 5230 - 5245	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.38E-04	0.97	4.81	-	1879.3
AHQ-2-7, 4931	K.ANLQIDQINTDLNLER.S	1871.04187	2	5.84E-04	0.94	4.63	-	922.0
AHQ-2-3, 5477	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.44E-08	0.97	4.78	-	1377.6
AHQ-2-10, 4654	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.64E-08	0.97	5.28	-	1707.6

AHQ-2-4, 2240	K.ASITALEAK.I	904.04321	2	1.26E-06	0.94	3.21	-	1269.1
AHQ-2-5, 2009 - 2012	K.ASITALEAK.I	904.04321	2	5.72E-04	0.88	3.10	-	809.4
AHQ-2-2, 2238	K.ASITALEAK.I	904.04321	2	3.11E-05	0.92	2.85	-	1118.4
AHQ-2-1, 2440 - 2466	K.ASITALEAK.I	904.04321	2	9.65E-05	0.92	3.37	-	971.2
AHQ-2-3, 2231	K.ASITALEAK.I	904.04321	2	2.76E-06	0.91	2.91	-	970.8
AHQ-2-6, 2023	K.ASITALEAK.I	904.04321	2	9.37E-06	0.78	2.54	-	764.6
AHQ-2-3, 1893 - 1901	R.ASREEILAQAK.E	1216.36955	2	1.78E-04	0.95	3.59	-	1888.8
AHQ-2-2, 1861 - 1930	R.ASREEILAQAK.E	1216.36955	2	1.71E-06	0.94	3.79	-	1624.5
AHQ-2-4, 1902	R.ASREEILAQAK.E	1216.36955	2	3.22E-06	0.89	3.03	-	1292.9
AHQ-2-2, 1906	R.ASREEILAQAK.E	1216.36955	1	5.56E-04	0.58	1.97	-	385.7
AHQ-2-1, 2129	R.ASREEILAQAK.E	1216.36955	2	1.27E-05	0.92	3.75	-	1355.1
AHQ-2-2, 3429	R.DELADEIANSSGK.G	1349.38323	1	6.52E-08	0.51	2.30	-	437.7
AHQ-2-3, 3391	R.DELADEIANSSGK.G	1349.38323	1	8.76E-06	0.40	2.45	-	352.6
AHQ-2-4, 3234	R.DELADEIANSSGK.G	1349.38323	1	2.10E-05	0.07	1.83	-	275.3
AHQ-2-4, 3241	R.DELADEIANSSGK.G	1349.38323	2	2.25E-05	0.96	4.35	-	1633.2
AHQ-2-2, 3208 - 3245	R.DELADEIANSSGK.G	1349.38323	2	3.03E-07	0.93	3.17	-	1310.1
AHQ-2-2, 2920	R.DELADEIANSSGK.G	1349.38323	1	1.40E-07	0.64	2.43	-	487.6
AHQ-2-3, 3229	R.DELADEIANSSGK.G	1349.38323	2	3.20E-05	0.94	3.92	-	1138.6
AHQ-2-1, 3281	R.DELADEIANSSGK.G	1349.38323	2	5.29E-07	0.96	4.42	-	1528.3
AHQ-2-1, 6972	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	5.10E-07	0.98	6.56	-	1691.1
AHQ-2-2, 7356 - 7422	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	8.18E-05	0.85	3.85	-	1085.6
AHQ-2-2, 7201 - 7268	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.11E-10	0.98	6.29	-	2119.2
AHQ-2-3, 7295	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	9.16E-07	0.95	4.75	-	1635.6
AHQ-2-3, 7131 - 7143	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	3.65E-04	0.96	4.72	-	2147.4
AHQ-2-3, 6872	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	4.59E-04	0.89	4.24	-	736.6
AHQ-2-4, 7192 - 7200	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	4.40E-12	0.97	6.21	-	2214.1
AHQ-2-1, 7096 - 7176	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	7.32E-13	0.97	5.47	-	1962.2
AHQ-2-5, 7043	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	5.05E-14	0.98	6.26	-	2141.0
AHQ-2-4, 7354	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	5.96E-06	0.94	4.79	-	1575.9
AHQ-2-2, 6762	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	2	3.66E-10	0.69	3.39	-	386.0
AHQ-2-3, 6697 - 6716	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	2.32E-11	0.94	5.13	-	869.9
AHQ-2-3, 6705	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	2	7.45E-05	0.86	3.73	-	568.2
AHQ-2-2, 6756 - 6780	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	4.52E-11	0.87	4.25	-	682.8
AHQ-2-3, 2021 - 2051	K.DLEAHIDSANK.N	1213.27938	2	7.46E-07	0.97	4.21	-	1837.6
AHQ-2-2, 2026 - 2101	K.DLEAHIDSANK.N	1213.27938	2	6.52E-07	0.98	4.11	-	2515.5
AHQ-2-2, 2024 - 2093	K.DLEAHIDSANK.N	1213.27938	1	4.45E-04	0.53	2.00	-	709.5
AHQ-2-4, 2032	K.DLEAHIDSANK.N	1213.27938	2	7.82E-08	0.98	3.93	-	2675.0
AHQ-2-1, 2216	K.DLEAHIDSANK.N	1213.27938	2	2.50E-06	0.98	4.39	-	2492.6
AHQ-2-3, 2431	K.DLEAHIDSANKNRDEAIK.Q	2040.18063	2	7.77E-05	0.90	4.39	-	699.9
AHQ-2-2, 2581	K.DLEAHIDSANKNRDEAIK.Q	2040.18063	2	4.94E-07	0.95	4.97	-	1011.3
AHQ-2-2, 2442 - 2449	K.DLEAHIDSANKNRDEAIK.Q	2040.18063	2	1.87E-04	0.95	4.94	-	934.1
AHQ-2-4, 2230	K.DLEGLSQR.H	917.98683	2	2.79E-04	0.79	2.68	-	905.3
AHQ-2-1, 7185	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	4.06E-12	0.98	6.47	-	2559.3
AHQ-2-5, 7571	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	7.49E-10	0.97	6.30	-	1859.9
AHQ-2-1, 7290	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.96E-05	0.85	3.87	-	1136.4
AHQ-2-7, 7579	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.54E-08	0.96	4.86	-	1887.5
AHQ-2-2, 7508	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.17E-14	0.98	7.05	-	2181.7
AHQ-2-6, 7317	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.77E-11	0.97	5.48	-	1974.4
AHQ-2-3, 7584 - 7621	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	3.97E-11	0.96	5.97	-	1141.4
AHQ-2-2, 7740	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	3.07E-07	0.95	5.43	-	1500.2
AHQ-2-2, 7632 - 7666	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.20E-13	0.97	6.19	-	1809.2
AHQ-2-3, 5359	K.DMFQETMEAMR.I	1389.60414	1	7.53E-05	0.48	2.63	-	258.7
AHQ-2-2, 3434 - 3454	K.DVLLQVDDER.R	1202.29650	2	8.87E-07	0.91	3.27	-	1289.5
AHQ-2-1, 3432	K.DVLLQVDDER.R	1202.29650	2	1.82E-04	0.88	3.00	-	1142.9
AHQ-2-4, 2813	K.DVLLQVDDERR.N	1358.48286	2	6.14E-04	0.49	2.90	-	546.6
AHQ-2-6, 2627	K.DVLLQVDDERR.N	1358.48286	2	4.91E-04	0.61	2.71	-	584.1
AHQ-2-1, 2054	R.EEILAQAK.E	902.02731	1	2.45E-05	0.11	1.94	-	234.8
AHQ-2-5, 2665 - 2740	R.ELEDATETADAMNR.E	1566.63006	2	4.26E-06	0.88	3.32	-	1055.7
AHQ-2-11, 2770	R.ELEDATETADAMNR.E	1566.63006	2	5.19E-05	0.48	2.76	-	333.3
AHQ-2-4, 2860 - 2934	R.ELEDATETADAMNR.E	1566.63006	2	2.74E-10	0.94	4.42	-	1008.5
AHQ-2-6, 2643 - 2717	R.ELEDATETADAMNR.E	1566.63006	2	1.24E-05	0.76	3.05	-	884.4
AHQ-2-2, 2877	R.ELEDATETADAMNR.E	1566.63006	2	3.47E-06	0.94	3.69	-	1385.1
AHQ-2-3, 2861 - 2867	R.ELEDATETADAMNR.E	1566.63006	2	1.97E-08	0.96	5.18	-	1275.7
AHQ-2-2, 3834	R.ELEDATETADAMNREVSSLK.N	2210.36264	2	1.47E-04	0.81	3.31	-	596.9
AHQ-2-3, 5571	R.ELESQISELQEDLESER.A	2035.10956	2	3.37E-06	0.84	3.27	-	625.4
AHQ-2-4, 6037 - 6112	R.ELESQISELQEDLESER.A	2035.10956	2	2.31E-04	0.90	3.92	-	974.1
AHQ-2-4, 6366 - 6436	R.ELESQISELQEDLESER.A	2035.10956	2	4.83E-05	0.83	3.64	-	651.7
AHQ-2-2, 5614 - 5616	R.ELESQISELQEDLESER.A	2035.10956	2	6.43E-10	0.95	4.72	-	1043.6
AHQ-2-6, 5710	R.ELESQISELQEDLESER.A	2035.10956	2	9.47E-06	0.82	3.22	-	920.2
AHQ-2-4, 5982 - 6048	R.ELESQISELQEDLESER.A	2035.10956	3	1.12E-05	0.97	5.96	-	2013.2
AHQ-2-3, 6033	R.ELESQISELQEDLESER.A	2035.10956	3	2.38E-08	0.98	6.03	-	2019.5
AHQ-2-3, 6083	R.ELESQISELQEDLESER.A	2035.10956	2	7.23E-06	0.87	3.92	-	780.1
AHQ-2-3, 6375	R.ELESQISELQEDLESER.A	2035.10956	2	7.50E-10	0.91	4.17	-	833.6
AHQ-2-3, 6475	R.ELESQISELQEDLESER.A	2035.10956	2	2.00E-04	0.96	4.72	-	1586.9
AHQ-2-2, 6070 - 6085	R.ELESQISELQEDLESER.A	2035.10956	2	1.72E-05	0.96	5.29	-	1123.0
AHQ-2-1, 5628	R.ELESQISELQEDLESER.A	2035.10956	2	3.01E-07	0.90	4.04	-	653.3
AHQ-2-1, 5945 - 6018	R.ELESQISELQEDLESER.A	2035.10956	2	4.89E-07	0.94	4.67	-	1101.6
AHQ-2-2, 6080 - 6094	R.ELESQISELQEDLESER.A	2035.10956	3	2.92E-11	0.98	6.16	-	2178.6
AHQ-2-2, 6428 - 6429	R.ELESQISELQEDLESER.A	2035.10956	2	2.18E-06	0.97	5.12	-	1448.5
AHQ-2-3, 6031 - 6059	R.ELESQISELQEDLESER.A	2035.10956	2	3.12E-07	0.97	5.59	-	1121.1
AHQ-2-3, 2485	R.EMEAELEDER.K	1251.30306	2	4.01E-04	0.76	2.73	-	755.4
AHQ-2-5, 1883	R.EMEAELEDERK.Q	1379.47597	2	5.83E-05	0.85	3.05	-	1025.2
AHQ-2-2, 2096	R.EMEAELEDERK.Q	1379.47597	2	1.15E-04	0.92	3.37	-	1371.3
AHQ-2-1, 2272	R.EMEAELEDERK.Q	1379.47597	2	1.82E-04	0.92	3.61	-	1170.4
AHQ-2-3, 2092	R.EMEAELEDERK.Q	1379.47597	2	2.66E-04	0.84	2.87	-	1022.3
AHQ-2-1, 4685	K.EQADFAIEALAK.A	1306.44632	2	7.26E-04	0.78	2.94	-	615.6
AHQ-2-2, 4570 - 4640	K.EQADFAIEALAK.A	1306.44632	1	1.22E-07	0.36	2.91	-	278.6
AHQ-2-2, 2325	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.98E-04	0.91	4.37	-	666.6
AHQ-2-4, 2292	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	5.04E-05	0.88	3.93	-	722.2
AHQ-2-1, 2484	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	2.24E-09	0.92	3.99	-	1017.3
AHQ-2-6, 2157	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	7.57E-07	0.82	3.66	-	440.1
AHQ-2-3, 2299	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.94E-04	0.83	3.74	-	525.3
AHQ-2-5, 2143	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	6.72E-05	0.88	4.39	-	436.2
AHQ-2-2, 3405 - 3478	R.FLSNGHVTIPGQQDK.D	1641.80946	2	1.72E-10	0.91	3.84	-	696.8
AHQ-2-5, 5848	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	1.32E-06	0.91	4.60	-	712.1
AHQ-2-2, 6148	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	7.31E-07	0.93	5.62	-	611.0
AHQ-2-2, 5289 - 5357	R.FLSNGHVTIPGQQDKDMFQETM*EAMR.I	3028.39040	3	1.57E-04	0.69	4.40	-	471.4
AHQ-2-6, 5781	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	7.33E-05	0.87	4.29	-	806.7
AHQ-2-7, 5752	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	1.32E-04	0.66	3.63	-	418.3
AHQ-2-3, 6135	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	1.66E-05	0.93	4.83	-	814.4
AHQ-2-6, 3298	K.FVSELWK.D	909.06314	1	2.02E-04	0.37	1.97	-	739.3
AHQ-2-2, 4270	R.GDLPFVVPR.R	1000.17581	2	2.09E-04	0.78	2.58	-	822.4
AHQ-2-3, 4252	R.GDLPFVVPR.R	1000.17581	2	1.91E-04	0.65	2.82	-	597.3
AHQ-2-1, 2512	K.HEAM*ITDLEER.L	1360.47586	2	9.93E-04	0.94	3.58	-	1194.1
AHQ-2-2, 2721	K.HEAMITDLEER.L	1344.47646	2	2.27E-05	0.90	3.22	-	790.9
AHQ-2-1, 2960	K.HEAMITDLEER.L	1344.47646	2	2.30E-08	0.97	4.46	-	1577.7
AHQ-2-3, 2724 - 2725	K.HEAMITDLEER.L	1344.47646	2	6.34E-04	0.94	3.53	-	1090.5

AHQ-2-5, 3157 - 3205	R.HEMPPHIYAITDTAYR.S	1916.14944	2	8.31E-05	0.92	3.99	-	833.8
AHQ-2-10, 3115	R.HEMPPHIYAITDTAYR.S	1916.14944	3	1.60E-05	0.97	3.89	-	2517.2
AHQ-2-2, 3170 - 3244	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	2.84E-04	0.95	4.05	-	1931.7
AHQ-2-10, 2870	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	3.67E-04	0.56	2.55	-	415.1
AHQ-2-5, 2861	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	6.17E-04	0.86	3.10	-	706.2
AHQ-2-10, 3112	R.HEMPPHIYAITDTAYR.S	1916.14944	2	2.46E-05	0.91	3.95	-	789.2
AHQ-2-2, 3492 - 3565	R.HEMPPHIYAITDTAYR.S	1916.14944	2	2.15E-06	0.93	3.84	-	814.6
AHQ-2-2, 3497	R.HEMPPHIYAITDTAYR.S	1916.14944	3	2.21E-09	0.98	4.62	-	3259.0
AHQ-2-3, 3652	R.HEMPPHIYAITDTAYR.S	1916.14944	3	7.28E-04	0.85	3.32	-	998.5
AHQ-2-1, 3790	R.HEMPPHIYAITDTAYR.S	1916.14944	2	1.36E-04	0.71	3.35	-	548.8
AHQ-2-1, 3406	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	5.29E-07	0.95	4.46	-	1761.6
AHQ-2-4, 3174	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	9.46E-07	0.97	5.03	-	1793.0
AHQ-2-6, 2897	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	6.66E-06	0.97	5.14	-	1942.9
AHQ-2-3, 3177	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	2.55E-06	0.97	5.05	-	2197.7
AHQ-2-2, 3582	R.HEMPPHIYAITDTAYR.S	1916.14944	3	1.57E-08	0.98	5.24	-	3224.8
AHQ-2-2, 3636 - 3637	R.HEMPPHIYAITDTAYR.S	1916.14944	2	1.27E-04	0.93	3.91	-	846.9
AHQ-2-2, 3664	R.HEMPPHIYAITDTAYR.S	1916.14944	3	2.88E-08	0.97	5.22	-	1830.0
AHQ-2-4, 3177	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	4.21E-04	0.83	3.20	-	555.8
AHQ-2-3, 3476 - 3556	R.HEMPPHIYAITDTAYR.S	1916.14944	2	3.32E-08	0.87	3.56	-	743.1
AHQ-2-6, 3143	R.HEMPPHIYAITDTAYR.S	1916.14944	3	2.62E-10	0.98	5.42	-	2630.5
AHQ-2-2, 4588	K.HSQAVEELAEQLEQTK.R	1840.96940	3	2.28E-04	0.96	5.22	-	1546.1
AHQ-2-4, 4532	K.HSQAVEELAEQLEQTK.R	1840.96940	2	5.58E-11	0.98	6.16	-	1842.4
AHQ-2-3, 4540 - 4615	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.87E-09	0.98	5.94	-	2390.4
AHQ-2-1, 4702	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.72E-09	0.98	5.94	-	1743.1
AHQ-2-2, 4580 - 4653	K.HSQAVEELAEQLEQTK.R	1840.96940	2	6.99E-12	0.98	6.65	-	2276.1
AHQ-2-1, 4706	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.31E-05	0.97	5.08	-	2147.2
AHQ-2-5, 4153 - 4223	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.12E-09	0.94	4.25	-	1244.1
AHQ-2-3, 4545 - 4561	K.HSQAVEELAEQLEQTK.R	1840.96940	3	4.68E-08	0.97	5.52	-	2163.4
AHQ-2-5, 3708	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	3.18E-09	0.99	7.27	-	2804.4
AHQ-2-5, 3692	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.90E-08	0.98	6.40	-	2377.6
AHQ-2-4, 4040 - 4057	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	7.27E-07	0.98	6.83	-	1951.0
AHQ-2-1, 4318	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	4.49E-09	0.98	6.29	-	2620.5
AHQ-2-4, 4041	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	8.86E-08	0.98	6.75	-	2218.7
AHQ-2-1, 4309	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.55E-05	0.97	5.84	-	1703.7
AHQ-2-3, 4053	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	2.30E-08	0.99	6.93	-	2772.8
AHQ-2-6, 3729	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	8.91E-06	0.93	4.73	-	1069.4
AHQ-2-2, 4073 - 4146	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	9.67E-11	0.98	5.77	-	1945.4
AHQ-2-2, 4076 - 4154	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.03E-08	0.98	7.09	-	2020.3
AHQ-2-1, 3869 - 3940	R.IAEFTTNLTEEEEK.S	1654.75371	2	8.41E-09	0.97	5.01	-	1850.7
AHQ-2-1, 4010 - 4082	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.01E-08	0.97	5.00	-	1760.2
AHQ-2-2, 4184	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.84E-07	0.95	4.12	-	1304.0
AHQ-2-2, 4036 - 4105	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.12E-10	0.97	4.75	-	2172.6
AHQ-2-2, 4284 - 4354	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.81E-05	0.87	3.56	-	729.0
AHQ-2-5, 3436 - 3516	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.42E-10	0.97	4.58	-	2148.8
AHQ-2-3, 4364	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.24E-05	0.60	2.75	-	854.7
AHQ-2-4, 4106	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.77E-06	0.77	2.95	-	611.3
AHQ-2-2, 3908 - 3976	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.79E-10	0.97	4.93	-	1794.1
AHQ-2-7, 3447	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.70E-05	0.91	3.01	-	1269.0
AHQ-2-4, 3828 - 3906	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.82E-07	0.90	2.86	-	1484.0
AHQ-2-3, 4221 - 4291	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.36E-04	0.84	3.26	-	904.5
AHQ-2-4, 3728 - 3796	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.61E-10	0.96	4.29	-	1717.7
AHQ-2-3, 4035 - 4103	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.65E-09	0.97	4.69	-	1780.3
AHQ-2-3, 3919 - 3967	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.83E-08	0.98	5.06	-	2000.8
AHQ-2-2, 3794 - 3864	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.71E-10	0.97	5.24	-	1871.6
AHQ-2-3, 3851 - 3892	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.96E-09	0.96	4.97	-	1570.9
AHQ-2-3, 3712 - 3792	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.24E-09	0.96	4.62	-	1650.9
AHQ-2-4, 3900 - 3977	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.26E-09	0.97	4.54	-	1819.5
AHQ-2-2, 3298	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	9.73E-10	0.82	3.57	-	686.7
AHQ-2-3, 3315	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	5.59E-04	0.81	3.59	-	645.9
AHQ-2-4, 3332	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	6.00E-05	0.67	3.16	-	468.3
AHQ-2-2, 5418 - 5501	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	4.88E-08	0.65	3.24	-	408.4
AHQ-2-3, 5721	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	9.11E-06	0.91	4.79	-	871.8
AHQ-2-1, 5718 - 5754	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	3.16E-06	0.83	3.35	-	910.0
AHQ-2-1, 3625	K.IAQLEEQLDNETK.E	1531.64695	2	7.34E-07	0.91	3.65	-	1165.4
AHQ-2-3, 3364	K.IAQLEEQLDNETK.E	1531.64695	2	1.22E-05	0.92	3.45	-	1333.0
AHQ-2-2, 3825 - 3848	K.IAQLEEQLDNETK.E	1531.64695	2	1.53E-07	0.94	4.50	-	855.2
AHQ-2-5, 3045	K.IAQLEEQLDNETK.E	1531.64695	2	1.42E-07	0.83	3.26	-	721.7
AHQ-2-7, 3067	K.IAQLEEQLDNETK.E	1531.64695	2	3.28E-06	0.94	3.89	-	1359.1
AHQ-2-3, 3449	K.IAQLEEQLDNETK.E	1531.64695	2	9.34E-05	0.84	3.33	-	999.1
AHQ-2-6, 2990	K.IAQLEEQLDNETK.E	1531.64695	2	3.77E-07	0.44	2.61	-	406.6
AHQ-2-2, 2926	K.IAQLEEQLDNETK.E	1531.64695	2	7.90E-09	0.95	4.14	-	1300.3
AHQ-2-11, 3194	K.IAQLEEQLDNETK.E	1531.64695	2	2.38E-08	0.95	3.98	-	1306.9
AHQ-2-2, 3110 - 3184	K.IAQLEEQLDNETK.E	1531.64695	2	1.20E-09	0.97	4.76	-	2038.2
AHQ-2-1, 3465 - 3494	K.IAQLEEQLDNETK.E	1531.64695	2	1.47E-09	0.97	4.55	-	1925.4
AHQ-2-4, 3173	K.IAQLEEQLDNETK.E	1531.64695	2	3.11E-08	0.96	4.60	-	1583.3
AHQ-2-10, 3062	K.IAQLEEQLDNETK.E	1531.64695	2	5.51E-09	0.96	4.90	-	1365.3
AHQ-2-2, 3529	K.IAQLEEQLDNETK.E	1531.64695	2	7.87E-08	0.95	4.60	-	1360.6
AHQ-2-6, 3113	K.IAQLEEQLDNETK.E	1531.64695	2	9.57E-05	0.97	4.75	-	1905.7
AHQ-2-9, 3048 - 3106	K.IAQLEEQLDNETK.E	1531.64695	2	2.93E-05	0.96	3.84	-	1784.0
AHQ-2-4, 3373	K.IAQLEEQLDNETK.E	1531.64695	2	1.65E-07	0.95	3.82	-	1667.8
AHQ-2-2, 3386 - 3457	K.IAQLEEQLDNETK.E	1531.64695	2	5.74E-08	0.94	4.06	-	1381.5
AHQ-2-3, 3097 - 3167	K.IAQLEEQLDNETK.E	1531.64695	2	1.87E-07	0.97	5.01	-	1586.5
AHQ-2-2, 3033 - 3065	K.IAQLEEQLDNETKER.Q	1816.94784	2	7.36E-09	0.95	4.26	-	1110.2
AHQ-2-2, 3489 - 3558	K.IAQLEEQLDNETKER.Q	1816.94784	2	5.66E-09	0.96	4.77	-	1338.7
AHQ-2-2, 3486	K.IAQLEEQLDNETKER.Q	1816.94784	3	5.42E-06	0.69	3.41	-	438.1
AHQ-2-2, 5976	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	2.01E-04	0.95	5.16	-	838.9
AHQ-2-5, 6695 - 6700	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.56E-05	0.96	5.01	-	1131.5
AHQ-2-8, 6458	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.67E-09	0.96	5.03	-	1100.2
AHQ-2-4, 5473 - 5513	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.09E-05	0.84	3.86	-	654.6
AHQ-2-1, 5500	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	8.51E-07	0.95	4.33	-	1156.8
AHQ-2-3, 6804 - 6815	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.42E-06	0.97	5.66	-	1478.9
AHQ-2-1, 6728 - 6746	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	8.40E-04	0.96	5.75	-	1056.5
AHQ-2-3, 5453	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.88E-07	0.96	4.94	-	1036.8
AHQ-2-2, 5492	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.02E-05	0.94	4.23	-	1051.3
AHQ-2-1, 6720 - 6789	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.38E-05	0.95	5.23	-	881.7
AHQ-2-6, 6495 - 6527	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.77E-07	0.97	5.62	-	1223.1
AHQ-2-1, 6121	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.64E-04	0.94	4.69	-	870.0
AHQ-2-2, 6848 - 6870	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	4.82E-04	0.94	5.43	-	895.6
AHQ-2-4, 6837 - 6904	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.70E-09	0.96	5.20	-	1215.2
AHQ-2-14-, 6285 - 6324	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.80E-04	0.97	5.46	-	1250.2
AHQ-2-13, 6277	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.85E-04	0.94	4.85	-	740.1
AHQ-2-7, 6607	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.50E-05	0.97	5.40	-	1289.3
AHQ-2-3, 4804	R.IM*GIPEEEQMGLLR.V	1632.92766	2	5.35E-04	0.66	2.70	-	619.0
AHQ-2-6, 4411 - 4454	R.IM*GIPEEEQMGLLR.V	1632.92766	2	6.39E-04	0.85	3.20	-	611.7
AHQ-2-1, 5497	R.IMGIPEEEQMGLLR.V	1616.92826	2	1.09E-04	0.54	2.54	-	297.7
AHQ-2-4, 5417	R.IMGIPEEEQMGLLR.V	1616.92826	2	6.52E-06	0.89	4.01	-	387.3
AHQ-2-8, 4893 - 4965	R.IMGIPEEEQMGLLR.V	1616.92826	2	3.44E-06	0.92	3.90	-	607.0

AHQ-2-2, 4724 - 4800	R.IMGIPEEEQM*GLLR.V	1632.92766	2	4.66E-04	0.86	3.84	-	515.9
AHQ-2-2, 6021	K.IRELESQISELQEDLESER.A	2304.45416	2	1.76E-04	0.98	6.55	-	1169.6
AHQ-2-3, 5889 - 5968	K.IRELESQISELQEDLESER.A	2304.45416	2	7.27E-08	0.98	6.43	-	1315.9
AHQ-2-3, 5976 - 6016	K.IRELESQISELQEDLESER.A	2304.45416	3	2.00E-10	0.98	6.64	-	2072.4
AHQ-2-1, 6050	K.IRELESQISELQEDLESER.A	2304.45416	2	2.08E-05	0.98	6.87	-	1408.7
AHQ-2-6, 5619	K.IRELESQISELQEDLESER.A	2304.45416	3	1.45E-07	0.97	5.83	-	2189.8
AHQ-2-6, 5618	K.IRELESQISELQEDLESER.A	2304.45416	2	4.89E-06	0.98	6.18	-	1753.2
AHQ-2-4, 5993 - 6004	K.IRELESQISELQEDLESER.A	2304.45416	3	8.42E-08	0.98	6.82	-	1774.7
AHQ-2-5, 5653 - 5671	K.IRELESQISELQEDLESER.A	2304.45416	2	1.47E-05	0.98	6.93	-	1762.2
AHQ-2-3, 6039	K.IRELESQISELQEDLESER.A	2304.45416	2	7.53E-07	0.98	6.21	-	1086.3
AHQ-2-4, 5985	K.IRELESQISELQEDLESER.A	2304.45416	2	2.56E-05	0.98	6.85	-	1818.7
AHQ-2-2, 6024 - 6030	K.IRELESQISELQEDLESER.A	2304.45416	3	1.92E-08	0.97	6.01	-	1569.2
AHQ-2-1, 6052	K.IRELESQISELQEDLESER.A	2304.45416	3	6.46E-09	0.98	6.41	-	2003.4
AHQ-2-3, 4624 - 4636	K.KANLQIDQINTDLNLER.S	1999.21478	3	1.61E-06	0.91	4.50	-	1175.6
AHQ-2-3, 4616	K.KANLQIDQINTDLNLER.S	1999.21478	2	5.46E-06	0.97	6.12	-	1394.5
AHQ-2-6, 4230 - 4237	K.KANLQIDQINTDLNLER.S	1999.21478	2	8.08E-05	0.98	5.97	-	2118.8
AHQ-2-5, 4283	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.94E-05	0.98	6.77	-	1456.7
AHQ-2-2, 4845 - 4921	K.KANLQIDQINTDLNLER.S	1999.21478	2	9.99E-15	0.98	6.08	-	2021.2
AHQ-2-2, 4494	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.83E-06	0.95	5.19	-	945.7
AHQ-2-3, 4380 - 4453	K.KANLQIDQINTDLNLER.S	1999.21478	2	5.77E-06	0.97	6.07	-	1279.2
AHQ-2-3, 4811	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.42E-04	0.97	5.42	-	1463.2
AHQ-2-3, 4909	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.45E-06	0.93	4.62	-	794.9
AHQ-2-2, 4721	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.23E-07	0.97	5.76	-	1371.0
AHQ-2-9, 4179	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.27E-06	0.96	5.05	-	1326.5
AHQ-2-2, 4654	K.KANLQIDQINTDLNLER.S	1999.21478	3	1.60E-04	0.91	4.20	-	1322.9
AHQ-2-1, 4720	K.KANLQIDQINTDLNLER.S	1999.21478	3	9.84E-04	0.89	4.16	-	1084.9
AHQ-2-2, 4638 - 4652	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.98E-10	0.98	5.96	-	1555.8
AHQ-2-1, 2642	R.KKVEAQLQELQVK.F	1541.81761	2	5.75E-08	0.97	5.10	-	1443.0
AHQ-2-4, 2389	R.KKVEAQLQELQVK.F	1541.81761	2	3.94E-04	0.97	5.01	-	1914.5
AHQ-2-2, 2408 - 2410	R.KKVEAQLQELQVK.F	1541.81761	2	3.12E-08	0.97	5.71	-	1509.0
AHQ-2-3, 3643	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.53E-04	0.92	4.51	-	700.5
AHQ-2-4, 3534	K.KLEEEQIILEDQNCK.L	1891.08992	2	3.19E-11	0.98	6.11	-	1933.9
AHQ-2-2, 3766	K.KLEEEQIILEDQNCK.L	1891.08992	2	3.87E-06	0.98	5.99	-	1861.4
AHQ-2-1, 3696 - 3697	K.KLEEEQIILEDQNCK.L	1891.08992	3	1.06E-06	0.90	4.39	-	1074.8
AHQ-2-1, 3684	K.KLEEEQIILEDQNCK.L	1891.08992	2	3.84E-09	0.98	5.74	-	2208.5
AHQ-2-1, 3518 - 3588	K.KLEEEQIILEDQNCK.L	1891.08992	2	4.39E-04	0.96	5.04	-	1494.0
AHQ-2-3, 3565 - 3633	K.KLEEEQIILEDQNCK.L	1891.08992	3	1.38E-04	0.92	4.09	-	1345.8
AHQ-2-3, 3776	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.12E-04	0.97	5.54	-	1673.1
AHQ-2-2, 3678	K.KLEEEQIILEDQNCK.L	1891.08992	2	6.14E-05	0.85	3.39	-	683.6
AHQ-2-3, 3531 - 3608	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.09E-11	0.97	5.63	-	1604.2
AHQ-2-3, 3416 - 3436	K.KLEEEQIILEDQNCK.L	1891.08992	3	6.21E-06	0.90	4.54	-	1240.7
AHQ-2-2, 3581 - 3652	K.KLEEEQIILEDQNCK.L	1891.08992	2	4.92E-11	0.98	6.33	-	1550.7
AHQ-2-3, 7364 - 7391	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	7.48E-10	0.88	4.59	-	791.0
AHQ-2-3, 7367 - 7431	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	3.01E-07	0.97	5.53	-	1192.2
AHQ-2-6, 7067	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	1.73E-09	0.91	5.00	-	814.9
AHQ-2-1, 7149 - 7225	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	6.49E-08	0.97	6.47	-	1151.3
AHQ-2-1, 7073 - 7148	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	4.28E-06	0.92	4.86	-	926.0
AHQ-2-4, 7382 - 7440	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	4.74E-06	0.97	5.68	-	1486.4
AHQ-2-5, 7264 - 7265	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	4.64E-06	0.90	5.06	-	1016.7
AHQ-2-4, 7424 - 7494	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	3.98E-06	0.95	5.51	-	1047.0
AHQ-2-4, 7492 - 7556	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.92E-05	0.92	4.78	-	621.1
AHQ-2-5, 7263	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	6.87E-08	0.96	5.63	-	1304.6
AHQ-2-2, 7436	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	3.75E-08	0.97	6.53	-	1234.0
AHQ-2-6, 2383	K.KLVWVPSDK.S	1072.28194	2	1.06E-05	0.77	2.69	-	736.5
AHQ-2-2, 2568	K.KLVWVPSDK.S	1072.28194	2	2.64E-04	0.83	3.03	-	896.5
AHQ-2-3, 2564	K.KLVWVPSDK.S	1072.28194	1	8.42E-04	0.52	2.58	-	484.4
AHQ-2-5, 2341	K.KLVWVPSDK.S	1072.28194	2	7.57E-05	0.69	2.71	-	711.4
AHQ-2-4, 3588	K.KMEDSVGCLETAEEVK.R	1827.02450	2	1.75E-06	0.82	3.69	-	793.1
AHQ-2-2, 3204	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	2.11E-06	0.93	4.77	-	919.1
AHQ-2-2, 3197	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	4.51E-07	0.92	3.65	-	1117.5
AHQ-2-2, 2817	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	2.20E-06	0.89	3.87	-	843.1
AHQ-2-2, 2805	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	3.91E-06	0.92	4.55	-	891.6
AHQ-2-4, 3208	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	1.35E-05	0.96	4.52	-	1601.6
AHQ-2-3, 3200	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	2.19E-09	0.97	5.16	-	1752.2
AHQ-2-5, 2529	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	2.62E-04	0.94	5.01	-	831.4
AHQ-2-6, 2947	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.41E-08	0.88	4.04	-	778.1
AHQ-2-1, 3388	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.07E-09	0.91	4.37	-	1019.7
AHQ-2-1, 3000	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	5.62E-04	0.93	4.54	-	1114.6
AHQ-2-3, 2816	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	3.22E-04	0.72	3.60	-	268.0
AHQ-2-2, 4964	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	2.53E-04	0.52	2.80	-	292.5
AHQ-2-3, 5379 - 5404	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	1.33E-05	0.91	4.14	-	1059.2
AHQ-2-1, 5578	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	5.04E-05	0.87	3.87	-	704.9
AHQ-2-2, 5428	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	2.94E-05	0.96	5.52	-	1162.5
AHQ-2-3, 4919	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	7.74E-04	0.63	2.99	-	348.3
AHQ-2-1, 5013	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	6.47E-06	0.58	2.83	-	380.1
AHQ-2-3, 4923	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	2.24E-04	0.85	3.92	-	1004.9
AHQ-2-4, 4922	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	1.67E-09	0.51	3.00	-	381.7
AHQ-2-4, 4065 - 4080	K.KQELEEICHDLEAR.V	1771.93036	3	9.81E-06	0.97	5.26	-	2036.8
AHQ-2-1, 4264 - 4273	K.KQELEEICHDLEAR.V	1771.93036	3	5.72E-04	0.97	5.77	-	1930.4
AHQ-2-6, 3759	K.KQELEEICHDLEAR.V	1771.93036	2	6.24E-04	0.98	5.09	-	2702.2
AHQ-2-4, 4048 - 4053	K.KQELEEICHDLEAR.V	1771.93036	2	3.86E-04	0.97	4.64	-	2430.9
AHQ-2-7, 3661	K.KQELEEICHDLEAR.V	1771.93036	2	2.53E-04	0.97	5.04	-	2065.9
AHQ-2-8, 3690	K.KQELEEICHDLEAR.V	1771.93036	2	6.93E-04	0.96	4.84	-	1703.7
AHQ-2-11, 3857 - 3920	K.KQELEEICHDLEAR.V	1771.93036	2	3.10E-04	0.70	3.13	-	595.5
AHQ-2-1, 3037	K.KVEAQLQELQVK.F	1413.64470	3	4.68E-06	0.81	3.66	-	1038.4
AHQ-2-4, 2705	K.KVEAQLQELQVK.F	1413.64470	2	1.07E-05	0.97	5.05	-	1757.4
AHQ-2-1, 3032	K.KVEAQLQELQVK.F	1413.64470	2	1.12E-07	0.95	4.39	-	1316.6
AHQ-2-5, 2492	K.KVEAQLQELQVK.F	1413.64470	2	1.04E-07	0.97	4.88	-	1857.5
AHQ-2-6, 2565	K.KVEAQLQELQVK.F	1413.64470	2	3.89E-07	0.97	4.97	-	1430.6
AHQ-2-3, 2743 - 2745	K.KVEAQLQELQVK.F	1413.64470	2	1.43E-04	0.98	5.52	-	2061.0
AHQ-2-3, 2761	K.KVEAQLQELQVK.F	1413.64470	1	1.52E-04	0.60	3.18	-	388.9
AHQ-2-2, 2753	K.KVEAQLQELQVK.F	1413.64470	2	1.64E-06	0.96	5.03	-	1319.4
AHQ-2-2, 2761	K.KVEAQLQELQVK.F	1413.64470	1	3.93E-06	0.56	2.98	-	384.6
AHQ-2-2, 3570	K.KVIQYLAYVASSHK.S	1607.87775	2	1.06E-08	0.97	4.73	-	1494.9
AHQ-2-6, 3182	K.KVIQYLAYVASSHK.S	1607.87775	2	9.80E-04	0.92	3.60	-	1012.4
AHQ-2-2, 3970 - 3996	K.LEEEQIILEDQNCK.L	1762.91700	2	4.04E-10	0.97	5.83	-	1233.5
AHQ-2-1, 3948 - 4022	K.LEEEQIILEDQNCK.L	1762.91700	2	1.23E-08	0.96	5.24	-	1237.0
AHQ-2-1, 4038	K.LEEEQIILEDQNCK.L	1762.91700	2	1.03E-07	0.94	3.81	-	1181.4
AHQ-2-2, 3888	K.LEEEQIILEDQNCK.L	1762.91700	2	1.45E-07	0.95	4.56	-	1355.3
AHQ-2-3, 3961 - 4008	K.LEEEQIILEDQNCK.L	1762.91700	2	3.67E-08	0.97	4.58	-	1473.3
AHQ-2-4, 3850	K.LEEEQIILEDQNCK.L	1762.91700	2	4.09E-07	0.93	4.16	-	936.0
AHQ-2-2, 4065 - 4136	K.LEEEQIILEDQNCK.L	1762.91700	2	1.22E-09	0.97	5.46	-	1438.5
AHQ-2-1, 7208	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	1.66E-12	0.97	5.49	-	1298.9
AHQ-2-4, 7548 - 7549	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	2.33E-07	0.91	3.81	-	846.8
AHQ-2-3, 7487 - 7489	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	5.07E-10	0.97	6.14	-	1277.0
AHQ-2-1, 7212	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	5.22E-06	0.77	4.16	-	628.8
AHQ-2-1, 3653	R.LEVNLQAMK.A	1046.26630	2	7.45E-05	0.90	3.52	-	780.2

AHQ-2-3, 2483	R.LEVNLQAM*K.A	1062.26570	2	9.18E-04	0.81	2.88	-	644.8
AHQ-2-4, 2472	R.LEVNLQAM*K.A	1062.26570	1	1.58E-04	0.14	1.80	-	80.2
AHQ-2-3, 3448	R.LEVNLQAMK.A	1046.26630	2	1.19E-04	0.90	3.59	-	666.5
AHQ-2-1, 2660 - 2677	R.LEVNLQAM*K.A	1062.26570	2	1.59E-05	0.76	2.77	-	538.9
AHQ-2-4, 3453	R.LEVNLQAMK.A	1046.26630	2	5.62E-06	0.85	3.06	-	770.8
AHQ-2-5, 3148	R.LEVNLQAMK.A	1046.26630	2	1.56E-04	0.69	2.72	-	586.1
AHQ-2-1, 3660	R.LEVNLQAMK.A	1046.26630	1	2.69E-04	0.65	2.72	-	646.7
AHQ-2-2, 3441 - 3444	R.LEVNLQAMK.A	1046.26630	2	9.64E-06	0.88	3.60	-	621.7
AHQ-2-4, 3382	K.LKDVLLQVDDER.R	1443.62767	2	8.14E-09	0.94	3.44	-	1544.0
AHQ-2-4, 3398	K.LKDVLLQVDDER.R	1443.62767	1	1.02E-05	0.66	3.20	-	405.4
AHQ-2-2, 3377	K.LKDVLLQVDDER.R	1443.62767	2	2.65E-09	0.95	4.00	-	1567.6
AHQ-2-1, 3621 - 3673	K.LKDVLLQVDDER.R	1443.62767	2	1.93E-09	0.92	3.75	-	1184.3
AHQ-2-3, 3373	K.LKDVLLQVDDER.R	1443.62767	2	1.05E-07	0.95	3.72	-	1558.3
AHQ-2-2, 3272	K.LKDVLLQVDDER.R	1443.62767	2	5.59E-07	0.95	3.63	-	1823.9
AHQ-2-6, 2654	K.LKDVLLQVDDERR.N	1599.81402	2	2.73E-04	0.88	3.35	-	1066.4
AHQ-2-2, 2900	K.LKDVLLQVDDERR.N	1599.81402	2	5.21E-05	0.88	3.60	-	951.6
AHQ-2-3, 2915 - 2916	K.LKDVLLQVDDERR.N	1599.81402	2	3.05E-06	0.93	4.02	-	1273.5
AHQ-2-6, 2655	K.LKDVLLQVDDERR.N	1599.81402	3	5.37E-07	0.93	3.99	-	1179.0
AHQ-2-4, 2836 - 2904	K.LKDVLLQVDDERR.N	1599.81402	2	3.03E-04	0.90	3.18	-	1266.3
AHQ-2-3, 2683	K.LKNKHEAMITDLEER.L	1828.08363	2	1.83E-05	0.91	3.65	-	1030.6
AHQ-2-3, 5616 - 5689	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.76E-05	0.90	4.12	-	733.9
AHQ-2-5, 5939 - 6011	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.13E-05	0.86	4.52	-	631.4
AHQ-2-1, 5845	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	7.07E-05	0.85	3.57	-	795.0
AHQ-2-2, 6236 - 6316	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	4.33E-05	0.93	5.02	-	802.6
AHQ-2-2, 6345	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.73E-10	0.97	5.48	-	1240.2
AHQ-2-6, 5885 - 5951	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.22E-10	0.97	5.43	-	1338.9
AHQ-2-1, 6284 - 6325	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.50E-06	0.82	3.75	-	660.9
AHQ-2-1, 6286 - 6289	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	8.80E-12	0.98	5.37	-	1998.0
AHQ-2-4, 6245 - 6256	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.84E-05	0.89	4.20	-	705.8
AHQ-2-4, 6238 - 6312	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.34E-11	0.97	5.01	-	1901.9
AHQ-2-3, 6319	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.04E-06	0.96	5.15	-	1189.0
AHQ-2-5, 5927 - 6008	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.00E-10	0.98	5.63	-	1688.4
AHQ-2-2, 5732	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.93E-07	0.95	4.85	-	1183.8
AHQ-2-2, 6197 - 6276	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.32E-09	0.96	5.13	-	1406.2
AHQ-2-3, 6400 - 6419	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	8.46E-07	0.98	5.12	-	2053.9
AHQ-2-3, 6176 - 6247	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.00E-11	0.97	4.99	-	1456.6
AHQ-2-2, 5966 - 6032	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.84E-07	0.96	5.34	-	1155.9
AHQ-2-4, 5970 - 6040	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	8.38E-07	0.97	5.45	-	1467.8
AHQ-2-2, 6982	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.62E-06	0.92	4.02	-	980.6
AHQ-2-3, 6167 - 6239	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.34E-08	0.97	6.11	-	1182.7
AHQ-2-2, 6209 - 6280	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.19E-13	0.98	6.84	-	1341.7
AHQ-2-5, 5781 - 5851	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.12E-07	0.97	5.46	-	1614.2
AHQ-2-3, 6309 - 6329	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.25E-07	0.97	5.06	-	1367.9
AHQ-2-3, 6019 - 6096	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.91E-08	0.98	6.01	-	1584.5
AHQ-2-4, 6244	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.96E-05	0.96	4.84	-	1227.5
AHQ-2-1, 5649	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.46E-04	0.97	5.69	-	1349.5
AHQ-2-4, 6325 - 6394	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.24E-05	0.87	3.98	-	544.9
AHQ-2-3, 6403	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.53E-12	0.97	5.41	-	1190.9
AHQ-2-1, 5952 - 6032	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.35E-07	0.98	5.80	-	1692.0
AHQ-2-3, 6532	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.75E-08	0.96	5.21	-	992.5
AHQ-2-5, 6031	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	7.18E-05	0.96	4.89	-	1131.2
AHQ-2-2, 6100	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.57E-11	0.97	6.47	-	1230.3
AHQ-2-2, 6072 - 6140	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.56E-07	0.98	5.92	-	1546.7
AHQ-2-2, 7346	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	7.77E-05	0.93	4.10	-	1006.8
AHQ-2-2, 6348 - 6418	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.59E-10	0.98	6.16	-	1976.0
AHQ-2-2, 7092	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.74E-08	0.96	5.61	-	1099.2
AHQ-2-3, 7383	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.67E-05	0.65	3.05	-	555.2
AHQ-2-2, 6448	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.45E-09	0.96	5.21	-	1125.7
AHQ-2-4, 6110 - 6158	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.18E-05	0.95	5.31	-	848.1
AHQ-2-4, 6478	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.44E-07	0.97	4.90	-	1385.1
AHQ-2-1, 6100	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.44E-07	0.97	5.84	-	1106.8
AHQ-2-3, 6995	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	8.86E-06	0.88	4.21	-	566.0
AHQ-2-1, 6204	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.88E-06	0.94	4.52	-	937.5
AHQ-2-2, 6542	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.65E-11	0.97	5.29	-	1208.6
AHQ-2-3, 5901 - 5975	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.24E-11	0.98	6.58	-	1454.3
AHQ-2-3, 5192 - 5195	R.LTEMETLQSQLMAEK.L	1753.03211	2	8.84E-09	0.98	5.44	-	1860.7
AHQ-2-2, 5232	R.LTEMETLQSQLMAEK.L	1753.03211	2	3.40E-08	0.97	5.59	-	1709.2
AHQ-2-3, 5205	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	2.24E-05	0.90	3.50	-	1099.3
AHQ-2-2, 5349 - 5366	R.LTEMETLQSQLMAEK.L	1753.03211	2	1.34E-04	0.94	3.76	-	1508.6
AHQ-2-4, 4630 - 4662	R.LTEMETLQSQLM*AEK.L	1769.03151	2	1.66E-06	0.93	3.81	-	1117.6
AHQ-2-3, 4039 - 4081	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	6.18E-05	0.96	4.07	-	2004.9
AHQ-2-2, 5149 - 5228	R.LTEMETLQSQLMAEK.L	1753.03211	2	2.37E-06	0.94	4.31	-	1211.2
AHQ-2-2, 4085 - 4156	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	4.58E-06	0.96	3.66	-	2294.6
AHQ-2-1, 5288	R.LTEMETLQSQLMAEK.L	1753.03211	2	6.74E-06	0.96	4.53	-	1510.2
AHQ-2-1, 3666	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	2.15E-04	0.89	3.39	-	1089.1
AHQ-2-4, 5180	R.LTEMETLQSQLMAEK.L	1753.03211	2	1.30E-05	0.96	4.86	-	1522.7
AHQ-2-1, 7028	K.LTKDFSALESQLQDTQELLQEENR.Q	2837.04608	3	3.03E-08	0.95	4.90	-	1592.4
AHQ-2-5, 2785	K.LVWVPSDK.S	944.10903	1	7.66E-04	0.33	2.07	-	394.3
AHQ-2-3, 3985	K.MEDSVGCLETAEEVK.R	1698.85159	2	3.25E-06	0.82	3.29	-	716.8
AHQ-2-2, 4025	K.MEDSVGCLETAEEVK.R	1698.85159	2	1.49E-04	0.74	3.03	-	580.6
AHQ-2-2, 3198	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	1.60E-07	0.92	3.99	-	772.8
AHQ-2-3, 3528	K.MEDSVGCLETAEEVKR.K	1855.03794	2	7.52E-05	0.76	3.28	-	458.9
AHQ-2-4, 3530	K.MEDSVGCLETAEEVKR.K	1855.03794	2	6.61E-08	0.91	3.96	-	768.6
AHQ-2-2, 3562 - 3568	K.MEDSVGCLETAEEVKR.K	1855.03794	3	7.09E-08	0.73	3.09	-	735.5
AHQ-2-6, 3250	K.MEDSVGCLETAEEVKR.K	1855.03794	2	7.76E-05	0.44	2.63	-	289.8
AHQ-2-2, 3554 - 3572	K.MEDSVGCLETAEEVKR.K	1855.03794	2	2.14E-07	0.72	3.29	-	461.7
AHQ-2-2, 5733 - 5801	K.MQQNIQELEEQLEEEESAR.Q	2334.46063	3	7.08E-08	0.82	4.09	-	514.0
AHQ-2-14-, 5192	K.NFINNPLAQADWAAK.K	1673.85315	2	1.83E-09	0.93	4.49	-	851.7
AHQ-2-5, 5167 - 5193	K.NFINNPLAQADWAAK.K	1673.85315	2	4.57E-06	0.96	4.82	-	1209.7
AHQ-2-1, 5525	K.NFINNPLAQADWAAK.K	1673.85315	2	1.93E-04	0.93	3.98	-	942.2
AHQ-2-13, 5116 - 5191	K.NFINNPLAQADWAAK.K	1673.85315	2	7.59E-06	0.95	5.05	-	881.8
AHQ-2-14, 6344	K.NFINNPLAQADWAAK.K	1673.85315	2	1.50E-06	0.93	4.60	-	819.3
AHQ-2-10, 4711 - 4779	K.NFINNPLAQADWAAK.K	1673.85315	2	7.52E-04	0.91	4.05	-	988.6
AHQ-2-3, 6144	K.NFINNPLAQADWAAK.K	1673.85315	2	7.74E-08	0.92	4.40	-	747.7
AHQ-2-11, 4997	K.NFINNPLAQADWAAK.K	1673.85315	2	1.76E-08	0.94	4.61	-	851.6
AHQ-2-7, 5027	K.NFINNPLAQADWAAK.K	1673.85315	2	1.14E-10	0.94	4.36	-	1003.0
AHQ-2-3, 5415 - 5416	K.NFINNPLAQADWAAK.K	1673.85315	2	2.06E-08	0.96	4.97	-	1270.6
AHQ-2-10, 4798	K.NFINNPLAQADWAAK.K	1673.85315	2	4.73E-06	0.93	3.91	-	1062.2
AHQ-2-9, 5098	K.NFINNPLAQADWAAK.K	1673.85315	2	2.19E-10	0.94	4.61	-	990.4
AHQ-2-12, 5238	K.NFINNPLAQADWAAK.K	1673.85315	2	3.48E-07	0.87	3.49	-	827.5
AHQ-2-2, 6160	K.NFINNPLAQADWAAK.K	1673.85315	2	1.67E-06	0.92	4.07	-	856.6
AHQ-2-4, 5430	K.NFINNPLAQADWAAK.K	1673.85315	2	6.66E-05	0.91	3.72	-	1015.6
AHQ-2-1, 6068	K.NFINNPLAQADWAAK.K	1673.85315	2	6.98E-07	0.94	4.15	-	1161.7
AHQ-2-4, 6164	K.NFINNPLAQADWAAK.K	1673.85315	2	2.55E-07	0.95	4.34	-	1357.7
AHQ-2-6, 5081 - 5089	K.NFINNPLAQADWAAK.K	1673.85315	2	2.42E-05	0.94	4.50	-	1013.1
AHQ-2-2, 5433	K.NFINNPLAQADWAAK.K	1673.85315	2	3.73E-06	0.96	5.18	-	1102.1
AHQ-2-3, 2908	K.NKHEAMITDLEER.L	1586.75247	2	1.81E-10	0.93	3.61	-	1252.1

AHQ-2-4, 2382 - 2384	K.NKHEAMITDLEER.L	1586.75247	2	4.69E-06	0.94	3.70	-	1204.5
AHQ-2-3, 2053	K.NKHEAM*ITDLEER.L	1602.75187	2	4.07E-04	0.90	3.86	-	820.7
AHQ-2-5, 2191	K.NKHEAMITDLEER.L	1586.75247	2	9.01E-10	0.94	3.79	-	1346.3
AHQ-2-3, 2383	K.NKHEAMITDLEER.L	1586.75247	2	3.52E-11	0.94	3.77	-	1284.4
AHQ-2-2, 2404 - 2405	K.NKHEAMITDLEER.L	1586.75247	2	7.84E-09	0.95	3.80	-	1358.2
AHQ-2-1, 2644	K.NKHEAMITDLEER.L	1586.75247	2	1.56E-05	0.96	3.70	-	1473.3
AHQ-2-2, 5294 - 5365	K.NLPIYSEEIVEM*YK.G	1744.98660	2	5.56E-06	0.94	4.58	-	924.3
AHQ-2-1, 5986	K.NLPIYSEEIVEMYK.G	1728.98720	2	3.83E-06	0.88	3.46	-	607.6
AHQ-2-4, 5278 - 5288	K.NLPIYSEEIVEM*YK.G	1744.98660	2	6.80E-06	0.95	4.41	-	1033.0
AHQ-2-3, 5273 - 5299	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.35E-06	0.93	3.97	-	929.6
AHQ-2-13, 5544	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.65E-05	0.90	3.83	-	596.8
AHQ-2-12, 5670	K.NLPIYSEEIVEMYK.G	1728.98720	2	3.30E-07	0.90	3.42	-	796.4
AHQ-2-2, 5933 - 6004	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.15E-09	0.94	4.64	-	635.7
AHQ-2-11, 5421 - 5422	K.NLPIYSEEIVEMYK.G	1728.98720	2	7.26E-07	0.92	4.22	-	719.1
AHQ-2-3, 5908 - 5939	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.71E-07	0.93	4.63	-	634.4
AHQ-2-7, 5484	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.14E-04	0.88	3.60	-	625.1
AHQ-2-10, 5162	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.80E-05	0.92	4.05	-	617.4
AHQ-2-3, 5896 - 5964	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.68E-04	0.92	4.55	-	720.4
AHQ-2-7, 5169	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	7.02E-04	0.89	3.68	-	1034.9
AHQ-2-2, 5141	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	5.11E-06	0.91	4.03	-	862.5
AHQ-2-6, 5253	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	4.97E-07	0.86	3.93	-	638.8
AHQ-2-5, 5311 - 5312	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	2.95E-08	0.94	4.88	-	748.3
AHQ-2-2, 5604	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.43E-04	0.77	3.45	-	560.4
AHQ-2-1, 5752	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.02E-06	0.91	4.25	-	711.6
AHQ-2-4, 5098	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	2.25E-05	0.63	2.79	-	660.1
AHQ-2-2, 5620 - 5621	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	3	4.08E-09	0.82	3.65	-	511.8
AHQ-2-3, 5585	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	8.07E-07	0.90	4.31	-	710.0
AHQ-2-3, 5237	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	2.89E-09	0.60	2.89	-	495.4
AHQ-2-3, 6211	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	5.31E-04	0.66	2.92	-	450.7
AHQ-2-3, 5743	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	3.49E-07	0.91	4.03	-	773.8
AHQ-2-1, 5209	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	2.62E-06	0.81	3.01	-	982.5
AHQ-2-2, 5144	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	8.52E-09	0.86	3.73	-	659.4
AHQ-2-4, 5605 - 5624	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	2.95E-06	0.93	4.92	-	729.1
AHQ-2-4, 5617	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	3	3.92E-08	0.77	3.34	-	393.2
AHQ-2-1, 5136 - 5217	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	8.40E-05	0.73	3.14	-	934.7
AHQ-2-2, 5929	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.27E-07	0.93	4.58	-	778.1
AHQ-2-2, 5760 - 5781	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	2.60E-07	0.94	4.71	-	904.9
AHQ-2-3, 5100	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	8.95E-04	0.74	2.73	-	854.3
AHQ-2-2, 5261	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	1.20E-08	0.92	3.63	-	1103.6
AHQ-2-3, 7603	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	4.15E-06	0.98	5.69	-	2107.6
AHQ-2-2, 7648	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	5.31E-06	0.98	6.05	-	1543.0
AHQ-2-2, 3068 - 3136	R.QAQQERDELADEIANSSGK.G	2090.15168	2	3.42E-06	0.94	4.16	-	1029.8
AHQ-2-4, 2770 - 2810	R.QAQQERDELADEIANSSGK.G	2090.15168	2	2.02E-04	0.21	2.77	-	160.6
AHQ-2-1, 3294 - 3302	R.QAQQERDELADEIANSSGK.G	2090.15168	3	9.73E-04	0.93	4.44	-	1264.6
AHQ-2-3, 3211	R.QAQQERDELADEIANSSGK.G	2090.15168	2	4.45E-05	0.87	4.35	-	316.4
AHQ-2-5, 2885	R.QAQQERDELADEIANSSGK.G	2090.15168	2	1.46E-04	0.79	3.90	-	360.4
AHQ-2-3, 2771	R.QAQQERDELADEIANSSGK.G	2090.15168	2	8.50E-04	0.29	2.98	-	160.0
AHQ-2-2, 3220	R.QAQQERDELADEIANSSGK.G	2090.15168	3	1.35E-04	0.73	3.32	-	646.4
AHQ-2-6, 2885	R.QAQQERDELADEIANSSGK.G	2090.15168	2	3.06E-04	0.78	3.99	-	351.7
AHQ-2-2, 3213	R.QAQQERDELADEIANSSGK.G	2090.15168	2	1.82E-05	0.86	3.78	-	499.4
AHQ-2-2, 4646	K.QELEEICHDLEAR.V	1643.75744	2	2.43E-06	0.84	3.76	-	466.3
AHQ-2-2, 2186	K.QIATLHAQVADM*K.K	1442.66637	2	4.22E-04	0.49	2.81	-	216.9
AHQ-2-4, 2628	K.QIATLHAQVADMK.K	1426.66697	2	1.20E-04	0.78	2.80	-	567.8
AHQ-2-2, 1946	R.QLEEAEEEAQR.A	1332.35590	2	8.16E-07	0.73	2.97	-	550.3
AHQ-2-3, 1933	R.QLEEAEEEAQR.A	1332.35590	2	1.14E-04	0.66	2.89	-	575.9
AHQ-2-1, 2104	R.QLEEAEEEAQR.A	1332.35590	2	4.04E-06	0.64	3.10	-	441.3
AHQ-2-2, 2432	K.RALEQQVEEMK.T	1361.55016	2	9.79E-04	0.90	3.41	-	1009.2
AHQ-2-3, 3407	R.RGDLPFVVPR.R	1156.36217	2	9.84E-07	0.92	3.56	-	1028.3
AHQ-2-12, 3295	R.RGDLPFVVPR.R	1156.36217	2	2.05E-05	0.90	3.39	-	956.9
AHQ-2-10, 3080	R.RGDLPFVVPR.R	1156.36217	2	7.18E-04	0.89	3.09	-	1106.2
AHQ-2-11, 3286	R.RGDLPFVVPR.R	1156.36217	2	9.38E-06	0.94	3.67	-	1319.5
AHQ-2-5, 3057 - 3067	R.RGDLPFVVPR.R	1156.36217	2	6.25E-05	0.93	3.52	-	1154.7
AHQ-2-4, 3346 - 3424	R.RGDLPFVVPR.R	1156.36217	2	3.71E-07	0.96	4.29	-	1272.9
AHQ-2-1, 3712	R.RGDLPFVVPR.R	1156.36217	2	2.46E-06	0.94	3.27	-	1564.1
AHQ-2-2, 3340 - 3409	R.RGDLPFVVPR.R	1156.36217	2	2.94E-05	0.95	3.74	-	1433.9
AHQ-2-6, 3109	R.RGDLPFVVPR.R	1156.36217	2	1.18E-05	0.92	3.65	-	924.1
AHQ-2-1, 6944	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.54E-05	0.96	6.31	-	1392.5
AHQ-2-2, 6997 - 7064	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.39E-11	0.96	5.67	-	1487.2
AHQ-2-3, 6968	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	5.85E-08	0.96	6.18	-	1295.8
AHQ-2-3, 7049	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	8.13E-05	0.93	5.01	-	1161.6
AHQ-2-4, 7048	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	8.33E-10	0.98	7.42	-	1597.8
AHQ-2-2, 2816	K.RQAQQERDELADEIANSSGK.G	2246.33803	3	2.29E-05	0.92	4.05	-	1122.2
AHQ-2-11, 1970	K.RQLEEAEEEAQR.A	1488.54225	2	2.09E-04	0.92	4.89	-	939.0
AHQ-2-2, 1829	K.RQLEEAEEEAQR.A	1488.54225	2	3.37E-04	0.97	4.95	-	2527.2
AHQ-2-3, 1852	K.RQLEEAEEEAQR.A	1488.54225	2	1.27E-06	0.96	4.87	-	1910.2
AHQ-2-1, 6490	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	4.68E-11	0.92	4.60	-	909.4
AHQ-2-14-, 5909	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.55E-11	0.96	5.42	-	1207.9
AHQ-2-1, 6394	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.46E-09	0.91	4.58	-	930.7
AHQ-2-3, 6371	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.25E-06	0.91	4.52	-	926.0
AHQ-2-2, 6825	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	7.87E-08	0.96	5.61	-	1425.4
AHQ-2-2, 7081	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	3.22E-10	0.95	5.11	-	1275.0
AHQ-2-2, 6372 - 6405	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.03E-09	0.95	5.43	-	1131.1
AHQ-2-2, 6917	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.36E-08	0.90	4.30	-	931.3
AHQ-2-1, 4889 - 4969	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	3.32E-11	0.98	5.26	-	1855.1
AHQ-2-2, 5081	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.99E-04	0.94	4.57	-	1125.4
AHQ-2-1, 6973	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	8.67E-07	0.96	5.31	-	1622.8
AHQ-2-2, 7496	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.71E-08	0.97	5.11	-	1512.7
AHQ-2-3, 7069	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	2.11E-04	0.92	4.74	-	1067.4
AHQ-2-2, 7269 - 7336	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	2.49E-05	0.89	3.84	-	1040.1
AHQ-2-4, 7142	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	1.62E-07	0.94	4.87	-	1677.2
AHQ-2-4, 4868 - 4874	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.70E-07	0.97	4.89	-	1722.4
AHQ-2-6, 6735 - 6758	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	9.84E-05	0.96	5.18	-	1648.1
AHQ-2-2, 7161	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.25E-06	0.97	5.40	-	1844.9
AHQ-2-3, 5880 - 5955	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	7.33E-08	0.94	4.97	-	1660.7
AHQ-2-3, 5948 - 6028	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	9.08E-07	0.95	4.43	-	1839.6
AHQ-2-2, 6076 - 6081	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	3.40E-04	0.88	4.41	-	916.1
AHQ-2-3, 6993 - 7065	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	6.98E-06	0.98	6.23	-	1778.9
AHQ-2-4, 7124 - 7128	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	2.32E-06	0.97	5.51	-	1897.3
AHQ-2-5, 6923 - 6931	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	6.78E-06	0.97	5.44	-	1759.2
AHQ-2-2, 7132 - 7200	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	2.08E-09	0.97	6.08	-	1421.8
AHQ-2-2, 7144 - 7145	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	1.57E-05	0.97	5.56	-	2108.5
AHQ-2-5, 3264	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	5.23E-05	0.96	5.64	-	1057.0
AHQ-2-3, 2952 - 2953	R.SMM*QDREDQSILCTGESGAGK.T	2318.50627	2	9.24E-04	0.88	3.86	-	729.1
AHQ-2-3, 3488	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	1.39E-04	0.94	4.80	-	1164.5
AHQ-2-9, 3210	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	3.48E-05	0.93	4.78	-	862.9
AHQ-2-4, 3497	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	7.31E-05	0.98	5.73	-	1652.6
AHQ-2-2, 3504	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	6.34E-05	0.96	5.90	-	1082.5

AHQ-2-6, 3241	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	2.63E-04	0.96	5.43	-	949.7
AHQ-2-2, 3685 - 3761	K.TDLLLEPYNK.Y	1206.36989	2	4.98E-05	0.92	4.09	-	1066.6
AHQ-2-2, 3694 - 3753	K.TDLLLEPYNK.Y	1206.36989	1	8.96E-04	0.06	2.13	-	215.8
AHQ-2-1, 3844	K.TDLLLEPYNK.Y	1206.36989	2	4.79E-06	0.93	3.87	-	1248.5
AHQ-2-5, 3408 - 3424	K.TDLLLEPYNK.Y	1206.36989	2	2.30E-05	0.86	3.35	-	946.5
AHQ-2-4, 3696	K.TDLLLEPYNK.Y	1206.36989	2	1.95E-06	0.92	4.03	-	968.4
AHQ-2-6, 3381 - 3382	K.TDLLLEPYNK.Y	1206.36989	2	9.73E-06	0.84	3.42	-	852.1
AHQ-2-3, 3676	K.TDLLLEPYNK.Y	1206.36989	2	2.78E-04	0.87	3.22	-	1229.6
AHQ-2-2, 3884	K.TDLLLEPYNKYR.F	1525.73037	2	6.76E-05	0.94	4.18	-	1104.6
AHQ-2-4, 4476	K.TELEDTLDSTAAQQELR.S	1921.00969	2	5.43E-06	0.94	3.75	-	1873.5
AHQ-2-5, 4301	K.TELEDTLDSTAAQQELR.S	1921.00969	2	2.45E-05	0.84	3.22	-	1354.8
AHQ-2-1, 4488	K.TELEDTLDSTAAQQELR.S	1921.00969	2	6.27E-10	0.97	4.84	-	1590.7
AHQ-2-2, 4517 - 4518	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.80E-07	0.93	4.06	-	1049.5
AHQ-2-2, 3104	R.TEMEDLMSSK.D	1171.32449	2	3.41E-05	0.89	3.58	-	821.5
AHQ-2-3, 3076 - 3085	R.TEMEDLMSSK.D	1171.32449	2	2.46E-04	0.91	3.54	-	833.1
AHQ-2-1, 3209	R.TEMEDLMSSK.D	1171.32449	2	2.62E-06	0.82	2.63	-	780.7
AHQ-2-1, 2584	R.TEMEDLM*SSKDDVGK.S	1701.85566	2	8.33E-05	0.70	3.03	-	574.0
AHQ-2-2, 3358	R.TEMEDLMSSKDDVGK.S	1685.85626	2	4.19E-06	0.90	3.69	-	1036.0
AHQ-2-5, 3137	R.TEMEDLMSSKDDVGK.S	1685.85626	2	2.19E-08	0.74	3.11	-	748.5
AHQ-2-1, 3457	R.TEMEDLMSSKDDVGK.S	1685.85626	2	5.50E-06	0.85	3.23	-	985.3
AHQ-2-4, 3350	R.TEMEDLMSSKDDVGK.S	1685.85626	2	9.72E-06	0.75	3.19	-	691.3
AHQ-2-3, 3340	R.TEMEDLMSSKDDVGK.S	1685.85626	2	3.16E-05	0.91	3.92	-	873.1
AHQ-2-2, 7257	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	4.01E-04	0.90	4.04	-	738.1
AHQ-2-3, 6693 - 6761	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	2.65E-04	0.95	4.58	-	1163.4
AHQ-2-5, 6243 - 6308	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	3.84E-08	0.97	5.19	-	1661.7
AHQ-2-7, 6019	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	8.33E-05	0.97	5.06	-	1421.0
AHQ-2-3, 6601	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	9.83E-06	0.97	5.15	-	1599.6
AHQ-2-2, 6558 - 6638	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.73E-05	0.98	6.33	-	1954.6
AHQ-2-5, 6252	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.10E-06	0.95	4.80	-	1343.6
AHQ-2-2, 6569	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	3.75E-08	0.92	4.25	-	1145.5
AHQ-2-6, 6241	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.57E-08	0.96	5.07	-	1484.3
AHQ-2-7, 6023	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	2.15E-05	0.96	5.48	-	1454.1
AHQ-2-2, 6817	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	6.36E-06	0.97	4.96	-	1690.5
AHQ-2-4, 3626	K.TLEEEAKTHEAQIQEMR.Q	2044.23269	2	3.80E-04	0.94	4.36	-	907.1
AHQ-2-2, 3733	K.TLEEEAKTHEAQIQEMR.Q	2044.23269	2	1.24E-04	0.96	4.54	-	1347.5
AHQ-2-4, 1730	K.VAAYDKLEK.T	1037.19123	2	7.40E-06	0.65	2.74	-	470.9
AHQ-2-5, 2979	K.VEAQLQELQVK.F	1285.47179	2	1.05E-04	0.94	3.74	-	1498.7
AHQ-2-2, 3225	K.VEAQLQELQVK.F	1285.47179	2	6.37E-05	0.96	4.32	-	1500.1
AHQ-2-4, 3229	K.VEAQLQELQVK.F	1285.47179	2	1.62E-05	0.94	3.82	-	1214.6
AHQ-2-1, 3404	K.VEAQLQELQVK.F	1285.47179	2	4.47E-06	0.95	4.00	-	1476.3
AHQ-2-4, 3240	K.VEAQLQELQVK.F	1285.47179	1	2.07E-04	0.53	2.92	-	474.4
AHQ-2-3, 3227	K.VEAQLQELQVK.F	1285.47179	2	2.47E-05	0.94	4.15	-	1240.3
AHQ-2-6, 5773	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.58E-06	0.94	4.77	-	648.7
AHQ-2-11, 5584 - 5585	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.57E-09	0.95	4.89	-	821.9
AHQ-2-3, 6137	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.01E-07	0.86	3.91	-	695.1
AHQ-2-3, 6139	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	7.63E-12	0.88	3.98	-	604.2
AHQ-2-10, 4766	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	5.19E-06	0.94	4.56	-	1222.9
AHQ-2-5, 5768 - 5784	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	3.41E-06	0.89	3.98	-	724.7
AHQ-2-12, 5838	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.21E-08	0.65	3.58	-	306.0
AHQ-2-2, 6394	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	8.80E-10	0.83	3.82	-	699.7
AHQ-2-5, 5152	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.02E-09	0.79	3.73	-	493.5
AHQ-2-9, 5766	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.07E-07	0.74	3.58	-	335.4
AHQ-2-10, 5364	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.82E-09	0.91	4.29	-	740.2
AHQ-2-13, 5639	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.25E-09	0.87	3.84	-	573.7
AHQ-2-1, 6157 - 6161	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.73E-11	0.96	5.18	-	940.1
AHQ-2-2, 6141	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.39E-08	0.88	4.44	-	617.5
AHQ-2-1, 5548	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	7.41E-13	0.94	4.79	-	770.5
AHQ-2-10, 4756	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.79E-13	0.92	3.97	-	982.4
AHQ-2-13-, 5250	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	5.65E-04	0.68	3.29	-	523.1
AHQ-2-10, 5368	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.21E-07	0.85	3.82	-	716.1
AHQ-2-2, 6410	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.20E-12	0.87	4.12	-	566.2
AHQ-2-2, 5417 - 5452	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	3.27E-10	0.96	5.86	-	1255.7
AHQ-2-7, 5691	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	7.74E-12	0.93	4.25	-	730.6
AHQ-2-6, 5061	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.07E-08	0.88	4.16	-	567.0
AHQ-2-9, 5062	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	4.39E-05	0.57	3.05	-	294.4
AHQ-2-6, 5751	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	8.01E-07	0.83	3.71	-	763.4
AHQ-2-2, 5382 - 5416	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.06E-09	0.91	4.25	-	732.2
AHQ-2-4, 6144 - 6150	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	6.74E-09	0.94	4.71	-	998.6
AHQ-2-4, 6140 - 6156	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	7.19E-10	0.94	4.95	-	687.3
AHQ-2-8, 5515 - 5582	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.76E-07	0.95	4.40	-	1023.2
AHQ-2-2, 6142 - 6217	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.94E-10	0.94	4.95	-	725.5
AHQ-2-1, 6102 - 6168	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	7.34E-07	0.87	3.99	-	618.4
AHQ-2-1, 5658	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	3.59E-09	0.87	3.69	-	1007.2
AHQ-2-1, 2089	R.VEEEEERCQHLQAEK.K	1916.01642	3	3.77E-04	0.84	4.05	-	759.6
AHQ-2-4, 1908	R.VEEEEERCQHLQAEK.K	1916.01642	2	8.64E-05	0.84	3.39	-	996.7
AHQ-2-3, 1907	R.VEEEEERCQHLQAEK.K	1916.01642	3	8.11E-05	0.80	3.66	-	592.5
AHQ-2-2, 3924	K.VIQYLAYVASSHK.S	1479.70484	3	7.03E-05	0.87	3.78	-	803.6
AHQ-2-1, 4121	K.VIQYLAYVASSHK.S	1479.70484	3	2.06E-06	0.81	3.75	-	474.8
AHQ-2-4, 3886	K.VIQYLAYVASSHK.S	1479.70484	3	1.97E-07	0.86	3.82	-	674.4
AHQ-2-3, 3879	K.VIQYLAYVASSHK.S	1479.70484	2	1.02E-05	0.75	2.92	-	736.4
AHQ-2-7, 3387	K.VIQYLAYVASSHK.S	1479.70484	2	7.44E-05	0.91	3.17	-	1061.9
AHQ-2-1, 4112 - 4128	K.VIQYLAYVASSHK.S	1479.70484	2	6.19E-07	0.94	3.88	-	1250.7
AHQ-2-2, 3909	K.VIQYLAYVASSHK.S	1479.70484	2	4.99E-08	0.94	4.05	-	1097.1
AHQ-2-5, 3499	K.VIQYLAYVASSHK.S	1479.70484	3	2.49E-05	0.83	3.71	-	552.2
AHQ-2-5, 3496	K.VIQYLAYVASSHK.S	1479.70484	2	5.10E-04	0.94	4.08	-	1288.2
AHQ-2-8, 3068	K.VIQYLAYVASSHK.S	1479.70484	2	9.87E-06	0.95	3.95	-	1131.7
AHQ-2-10, 3431	K.VIQYLAYVASSHK.S	1479.70484	2	7.49E-09	0.93	4.03	-	1094.3
AHQ-2-4, 6732 - 6804	R.VISGVLQLGNIVFK.K	1487.81155	2	5.28E-09	0.97	5.16	-	1701.4
AHQ-2-7, 6239 - 6319	R.VISGVLQLGNIVFK.K	1487.81155	2	1.12E-08	0.96	4.53	-	1453.3
AHQ-2-3, 6664 - 6731	R.VISGVLQLGNIVFK.K	1487.81155	2	6.90E-08	0.97	4.50	-	1981.1
AHQ-2-6, 6346 - 6413	R.VISGVLQLGNIVFK.K	1487.81155	2	2.11E-07	0.97	5.44	-	1775.3
AHQ-2-5, 6420 - 6488	R.VISGVLQLGNIVFK.K	1487.81155	2	2.95E-05	0.95	3.65	-	1502.5
AHQ-2-2, 6673 - 6744	R.VISGVLQLGNIVFK.K	1487.81155	2	3.52E-09	0.98	5.64	-	1820.7
AHQ-2-2, 6772 - 6842	R.VISGVLQLGNIVFK.K	1487.81155	2	8.63E-09	0.97	5.08	-	1635.7
AHQ-2-5, 6435 - 6444	R.VISGVLQLGNIVFK.K	1487.81155	1	6.49E-04	0.54	3.07	-	510.7
AHQ-2-2, 6857	R.VISGVLQLGNIVFK.K	1487.81155	2	4.56E-04	0.86	2.52	-	1187.5
AHQ-2-10, 5919	R.VISGVLQLGNIVFK.K	1487.81155	2	9.20E-07	0.92	3.67	-	1155.9
AHQ-2-3, 6681	R.VISGVLQLGNIVFK.K	1487.81155	1	2.69E-04	0.67	3.22	-	673.1
AHQ-2-6, 4561 - 4569	K.VSHLLGINVTDFTR.G	1572.79026	2	3.60E-11	0.97	5.33	-	1326.3
AHQ-2-5, 4608	K.VSHLLGINVTDFTR.G	1572.79026	2	1.35E-08	0.95	4.16	-	1424.7
AHQ-2-7, 4429 - 4500	K.VSHLLGINVTDFTR.G	1572.79026	2	2.41E-04	0.86	3.42	-	792.3
AHQ-2-1, 5054 - 5094	K.VSHLLGINVTDFTR.G	1572.79026	2	3.16E-10	0.97	4.47	-	1600.3
AHQ-2-1, 5101	K.VSHLLGINVTDFTR.G	1572.79026	3	7.28E-07	0.89	3.66	-	1084.6
AHQ-2-4, 4958 - 4960	K.VSHLLGINVTDFTR.G	1572.79026	2	2.68E-10	0.96	4.60	-	1449.5
AHQ-2-2, 4942 - 5012	K.VSHLLGINVTDFTR.G	1572.79026	2	5.73E-12	0.95	4.17	-	1242.2
AHQ-2-3, 4964	K.VSHLLGINVTDFTR.G	1572.79026	2	5.34E-11	0.95	4.21	-	1437.6
AHQ-2-5, 2753	R.VVFQEFR.Q	925.06580	2	8.12E-05	0.80	2.54	-	536.1

AHQ-2-1, 3270	R.VVFQEFR.Q	925.06580	2	2.57E-04	0.68	2.56	-	546.4
AHQ-2-2, 4044 - 4056	R.YEILTPNSIPK.G	1275.47536	2	3.16E-07	0.93	3.99	-	977.6
AHQ-2-2, 4172	R.YEILTPNSIPK.G	1275.47536	2	3.22E-05	0.80	2.80	-	939.3
AHQ-2-3, 4283 - 4285	R.YEILTPNSIPK.G	1275.47536	1	8.40E-04	0.36	2.17	-	644.1
AHQ-2-3, 4268	R.YEILTPNSIPK.G	1275.47536	2	1.64E-04	0.85	3.00	-	743.8
AHQ-2-3, 4019	R.YEILTPNSIPK.G	1275.47536	2	4.23E-06	0.90	3.44	-	1143.6
AHQ-2-4, 4009	R.YEILTPNSIPK.G	1275.47536	2	1.39E-05	0.78	3.13	-	659.3
AHQ-2-1, 4077 - 4158	R.YEILTPNSIPK.G	1275.47536	2	3.99E-05	0.84	2.97	-	825.2
AHQ-2-1, 4225	R.YEILTPNSIPK.G	1275.47536	2	1.64E-04	0.92	3.57	-	1001.7
AHQ-2-2, 6357 - 6369	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	3	2.97E-07	0.96	5.02	-	1701.8
AHQ-2-10, 5590	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	2	7.36E-08	0.77	3.22	-	529.3
gi|30159830|ref|XP_302246.1| similar to HSPC280 [Homo sapiens]				1.17E-14	1.95	20.30	3.90	45644.4
AHQ-2-13, 6799	K.CANLFEALVGTLK.A	1437.68632	2	8.46E-09	0.98	6.05	-	1854.5
AHQ-2-14-, 6861	K.CANLFEALVGTLK.A	1437.68632	2	1.25E-06	0.97	5.39	-	1363.7
AHQ-2-14-, 6808 - 6817	R.DDKCANLFEALVGTLK.A	1796.03496	2	2.83E-10	0.96	4.79	-	1277.6
AHQ-2-14-, 6811 - 6812	R.DDKCANLFEALVGTLK.A	1796.03496	3	1.21E-04	0.95	4.28	-	2137.2
AHQ-2-13-, 6955	R.DDKCANLFEALVGTLK.A	1796.03496	2	9.88E-14	0.96	4.50	-	1404.3
AHQ-2-13, 6735 - 6736	R.DDKCANLFEALVGTLK.A	1796.03496	2	1.17E-14	0.96	4.94	-	1285.9
gi|4507521|ref|NP_001055.1| transketolase [Homo sapiens]				1.28E-14	1.42	20.20	5.90	67877.3
AHQ-2-6, 4597	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	1.28E-14	0.89	3.97	-	429.0
AHQ-2-6, 3689 - 3702	R.SVPTSTVFYPSDGVATEK.A	1886.04854	2	1.74E-06	0.53	2.65	-	220.2
gi|4885609|ref|NP_005408.1| v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen				1.78E-14	4.56	50.37	20.10	59834.4
AHQ-2-7, 7007	R.AGPLAGGVTTFVALYDYESR.T	2088.30526	2	4.65E-05	0.84	3.65	-	530.0
AHQ-2-7, 7543	R.KEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL	3998.26826	3	4.53E-09	0.90	5.16	-	352.2
AHQ-2-7, 7523	R.LPQLVDMAAQIASGMAYVER.M	2164.53485	2	1.78E-14	0.99	7.30	-	4979.6
AHQ-2-7, 6323	R.MPCPPECPESLHDLMCQCWR.K	2608.97680	3	6.47E-12	0.90	4.23	-	588.1
AHQ-2-7, 6303	R.TQFNSLQQLVAYYSK.H	1790.99681	2	4.95E-08	0.97	4.95	-	1359.8
AHQ-2-7, 6204 - 6217	R.TQFNSLQQLVAYYSK.H	1790.99681	2	2.27E-10	0.93	3.81	-	1066.3
gi|4501881|ref|NP_001091.1| alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA				1.83E-14	15.20	200.27	46.70	42050.8
AHQ-2-13, 2043 - 2100	K.AGFAGDDAPR.A	977.01283	2	5.43E-04	0.90	3.16	-	1265.0
AHQ-2-8, 1594 - 1619	K.AGFAGDDAPR.A	977.01283	2	2.51E-04	0.92	3.61	-	1099.4
AHQ-2-12, 1901 - 1974	K.AGFAGDDAPR.A	977.01283	2	1.02E-04	0.87	3.09	-	969.3
AHQ-2-12, 1755 - 1834	K.AGFAGDDAPR.A	977.01283	2	1.08E-06	0.92	3.53	-	1158.5
AHQ-2-8, 1687 - 1762	K.AGFAGDDAPR.A	977.01283	2	3.89E-04	0.88	3.19	-	1053.0
AHQ-2-13-, 1925	K.AGFAGDDAPR.A	977.01283	2	4.77E-04	0.88	3.31	-	986.7
AHQ-2-8, 1449 - 1524	K.AGFAGDDAPR.A	977.01283	2	3.83E-07	0.88	3.48	-	882.4
AHQ-2-13-, 3541 - 3557	R.AVFPSIVGR.P	946.12815	2	2.38E-04	0.83	2.66	-	727.3
AHQ-2-8, 2742 - 2747	R.AVFPSIVGRPR.H	1199.43018	2	2.01E-04	0.70	2.69	-	626.3
AHQ-2-8, 2559 - 2610	R.AVFPSIVGRPR.H	1199.43018	2	1.94E-06	0.74	3.00	-	533.7
AHQ-2-8, 2344 - 2414	R.AVFPSIVGRPR.H	1199.43018	2	6.67E-04	0.56	2.57	-	380.9
AHQ-2-8, 2463 - 2534	R.AVFPSIVGRPR.H	1199.43018	2	5.75E-04	0.57	2.84	-	365.3
AHQ-2-9, 2822 - 2823	R.AVFPSIVGRPR.H	1199.43018	2	2.96E-05	0.60	2.65	-	524.8
AHQ-2-9, 3675	R.DLTDYLM*K.I	1015.16266	1	2.58E-04	0.25	2.52	-	97.8
AHQ-2-9, 4418	R.DLTDYLMK.I	999.16326	1	4.72E-04	0.43	2.71	-	294.0
AHQ-2-7, 4424	R.DLTDYLMK.I	999.16326	1	4.32E-05	0.39	2.47	-	383.9
AHQ-2-13, 4308 - 4384	R.DLTDYLMK.I	999.16326	1	5.67E-05	0.46	2.13	-	681.4
AHQ-2-9, 4430	R.DLTDYLMK.I	999.16326	2	9.76E-04	0.69	2.79	-	392.9
AHQ-2-11, 4285	R.DLTDYLMK.I	999.16326	2	7.02E-04	0.63	2.62	-	406.6
AHQ-2-8, 4043	R.DLTDYLMK.I	999.16326	1	4.54E-04	0.40	2.77	-	322.7
AHQ-2-8, 4346 - 4416	R.DLTDYLMK.I	999.16326	2	3.09E-04	0.86	3.10	-	483.4
AHQ-2-8, 3606	R.DLTDYLM*K.I	1015.16266	1	1.90E-05	0.49	2.35	-	173.4
AHQ-2-5, 4495	R.DLTDYLMK.I	999.16326	1	8.81E-06	0.63	2.19	-	721.9
AHQ-2-10, 3518	R.DLTDYLM*K.I	1015.16266	1	6.23E-04	0.18	1.92	-	122.1
AHQ-2-10, 3522 - 3534	R.DLTDYLM*K.I	1015.16266	2	8.39E-04	0.83	3.20	-	471.5
AHQ-2-10, 4122 - 4172	R.DLTDYLMK.I	999.16326	2	9.28E-04	0.69	2.90	-	375.2
AHQ-2-8, 4331 - 4461	R.DLTDYLMK.I	999.16326	1	1.26E-05	0.69	2.97	-	645.9
AHQ-2-8, 3822	R.DLTDYLMK.I	999.16326	1	8.47E-04	0.45	1.89	-	483.5
AHQ-2-13, 3781	R.DLTDYLM*K.I	1015.16266	1	3.90E-04	0.21	2.11	-	99.9
AHQ-2-10, 4999	K.DLYANNVMSGGTTMYPGIADR.M	2247.49444	2	3.47E-07	0.50	2.87	-	517.4
AHQ-2-8, 1480	K.DSYVGDEAQSK.R	1199.20634	1	7.37E-04	0.76	2.82	-	539.2
AHQ-2-13-, 1718	K.DSYVGDEAQSK.R	1199.20634	1	4.81E-06	0.30	1.94	-	431.9
AHQ-2-12, 1587 - 1649	K.DSYVGDEAQSK.R	1199.20634	2	1.04E-05	0.82	3.21	-	585.8
AHQ-2-8, 1453	K.DSYVGDEAQSKR.G	1355.39270	2	1.07E-06	0.53	2.52	-	551.8
AHQ-2-13, 2919 - 2992	K.EITALAPSTMK.I	1162.38206	2	3.77E-04	0.72	2.73	-	532.0
AHQ-2-9, 2586 - 2730	K.EITALAPSTMK.I	1162.38206	1	2.22E-04	0.40	2.34	-	294.6
AHQ-2-4, 2901	K.EITALAPSTMK.I	1162.38206	1	2.09E-05	0.19	1.98	-	277.6
AHQ-2-7, 2599	K.EITALAPSTMK.I	1162.38206	1	1.27E-05	0.25	2.24	-	277.4
AHQ-2-8, 1956 - 2026	K.EITALAPSTM*K.I	1178.38146	2	1.55E-06	0.89	3.24	-	840.2
AHQ-2-14, 3740 - 3864	K.EITALAPSTMK.I	1162.38206	1	4.72E-06	0.43	2.38	-	309.7
AHQ-2-8, 2330 - 2399	K.EITALAPSTMK.I	1162.38206	2	1.69E-04	0.74	2.78	-	526.2
AHQ-2-14, 3176 - 3217	K.EITALAPSTM*K.I	1178.38146	2	7.43E-04	0.71	2.66	-	659.4
AHQ-2-10, 2171 - 2244	K.EITALAPSTM*K.I	1178.38146	2	3.56E-04	0.80	2.89	-	688.5
AHQ-2-10, 2566 - 2643	K.EITALAPSTMK.I	1162.38206	2	5.02E-04	0.77	2.63	-	589.9
AHQ-2-10, 2607 - 2674	K.EITALAPSTMK.I	1162.38206	1	1.05E-04	0.31	2.66	-	221.9
AHQ-2-12, 2858 - 2859	K.EITALAPSTMK.I	1162.38206	2	8.24E-05	0.83	3.05	-	588.1
AHQ-2-8, 2732 - 2734	K.EITALAPSTMK.I	1162.38206	1	8.37E-05	0.24	2.35	-	166.8
AHQ-2-14-, 2275 - 2343	K.EITALAPSTM*K.I	1178.38146	2	1.04E-06	0.90	3.14	-	1045.3
AHQ-2-11, 2809	K.EITALAPSTMK.I	1162.38206	1	7.06E-06	0.33	2.21	-	310.0
AHQ-2-8, 2814	K.EITALAPSTMK.I	1162.38206	2	2.72E-04	0.72	2.55	-	593.7
AHQ-2-14-, 2763 - 2833	K.EITALAPSTMK.I	1162.38206	2	1.88E-04	0.81	3.21	-	525.1
AHQ-2-5, 2647	K.EITALAPSTMK.I	1162.38206	1	4.34E-04	0.20	2.12	-	258.1
AHQ-2-12, 2783 - 2857	K.EITALAPSTMK.I	1162.38206	1	5.38E-05	0.58	2.33	-	421.7
AHQ-2-8, 7271 - 7342	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	2	1.06E-04	0.59	3.45	-	361.1
AHQ-2-8, 7535 - 7572	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	3	4.66E-05	0.87	3.88	-	760.2
AHQ-2-8, 1532 - 1602	R.HQGVMVGMGQK.D	1172.40691	2	3.34E-04	0.89	3.57	-	618.0
AHQ-2-8, 2778 - 2852	K.IWHHTFYNELR.V	1516.68695	2	3.56E-08	0.90	3.49	-	886.9
AHQ-2-3, 2900	K.IWHHTFYNELR.V	1516.68695	2	6.08E-04	0.69	2.51	-	582.2
AHQ-2-6, 2629	K.IWHHTFYNELR.V	1516.68695	2	3.84E-06	0.77	3.16	-	899.4
AHQ-2-8, 2542 - 2614	K.IWHHTFYNELR.V	1516.68695	2	8.47E-10	0.94	4.17	-	1001.1
AHQ-2-12, 3017	K.IWHHTFYNELR.V	1516.68695	3	9.70E-06	0.92	3.53	-	1706.9
AHQ-2-10, 2539 - 2582	K.IWHHTFYNELR.V	1516.68695	2	2.96E-05	0.89	3.16	-	934.1
AHQ-2-2, 2881	K.IWHHTFYNELR.V	1516.68695	2	1.03E-05	0.58	3.02	-	529.7
AHQ-2-9, 2946	K.IWHHTFYNELR.V	1516.68695	2	1.88E-06	0.78	2.86	-	752.5
AHQ-2-12, 3142	K.IWHHTFYNELR.V	1516.68695	2	4.86E-09	0.94	3.36	-	1299.2
AHQ-2-8, 2208 - 2278	K.IWHHTFYNELR.V	1516.68695	2	1.87E-04	0.73	2.90	-	601.5
AHQ-2-13, 3044	K.IWHHTFYNELR.V	1516.68695	2	2.13E-05	0.76	3.22	-	802.6
AHQ-2-4, 2866	K.IWHHTFYNELR.V	1516.68695	2	3.08E-04	0.70	2.78	-	564.7
AHQ-2-12, 2829 - 2897	K.IWHHTFYNELR.V	1516.68695	3	1.98E-05	0.92	4.33	-	1530.8
AHQ-2-9, 2574 - 2646	K.IWHHTFYNELR.V	1516.68695	2	5.38E-07	0.89	4.22	-	963.3
AHQ-2-8, 2346 - 2415	K.IWHHTFYNELR.V	1516.68695	2	2.17E-06	0.87	3.55	-	919.2
AHQ-2-13-, 3006	K.IWHHTFYNELR.V	1516.68695	2	5.32E-06	0.89	3.11	-	837.6
AHQ-2-8, 4991 - 5059	R.LDLAGRDLTDYLMK.I	1624.88375	2	5.55E-05	0.89	3.73	-	866.3
AHQ-2-9, 5196	R.LDLAGRDLTDYLMK.I	1624.88375	2	1.91E-04	0.82	3.17	-	628.4
AHQ-2-8, 5004 - 5081	K.SYELPDGQVITIGNER.F	1791.93998	2	3.24E-06	0.96	4.99	-	1219.3
AHQ-2-8, 5150 - 5151	K.SYELPDGQVITIGNER.F	1791.93998	2	1.18E-08	0.96	4.51	-	1338.6
AHQ-2-14, 6138	K.SYELPDGQVITIGNER.F	1791.93998	2	3.06E-05	0.91	3.29	-	911.0
AHQ-2-8, 4851 - 4923	K.SYELPDGQVITIGNER.F	1791.93998	2	4.39E-11	0.97	5.02	-	1247.9

AHQ-2-1, 4697	K.SYELPDGQVITIGNER.F	1791.93998	2	3.76E-05	0.90	3.98	-	663.9
AHQ-2-8, 4735 - 4803	K.SYELPDGQVITIGNER.F	1791.93998	2	8.18E-13	0.95	4.54	-	1105.0
AHQ-2-3, 5344	K.SYELPDGQVITIGNER.F	1791.93998	2	3.91E-07	0.85	3.63	-	556.0
AHQ-2-8, 4729	K.SYELPDGQVITIGNER.F	1791.93998	3	1.15E-09	0.96	4.81	-	1877.4
AHQ-2-8, 4705 - 4783	K.SYELPDGQVITIGNER.F	1791.93998	2	1.62E-11	0.96	4.72	-	1060.2
AHQ-2-9, 4331 - 4410	K.SYELPDGQVITIGNER.F	1791.93998	2	5.40E-05	0.68	2.81	-	510.9
AHQ-2-3, 5153 - 5160	K.SYELPDGQVITIGNER.F	1791.93998	2	1.18E-07	0.96	4.80	-	1115.9
AHQ-2-3, 4769 - 4772	K.SYELPDGQVITIGNER.F	1791.93998	2	1.81E-08	0.93	4.23	-	880.0
AHQ-2-13, 5036 - 5095	K.SYELPDGQVITIGNER.F	1791.93998	2	6.50E-06	0.95	4.11	-	1168.4
AHQ-2-9, 4478 - 4528	K.SYELPDGQVITIGNER.F	1791.93998	2	8.05E-10	0.93	4.19	-	992.0
AHQ-2-13, 4869 - 4895	K.SYELPDGQVITIGNER.F	1791.93998	2	8.91E-07	0.96	4.84	-	956.2
AHQ-2-9, 4607	K.SYELPDGQVITIGNER.F	1791.93998	2	7.64E-10	0.91	3.90	-	797.7
AHQ-2-9, 4698 - 4708	K.SYELPDGQVITIGNER.F	1791.93998	2	7.57E-09	0.95	3.88	-	1446.9
AHQ-2-9, 4794 - 4862	K.SYELPDGQVITIGNER.F	1791.93998	2	1.83E-14	0.97	5.22	-	1397.2
AHQ-2-9, 5036 - 5106	K.SYELPDGQVITIGNER.F	1791.93998	2	3.57E-04	0.86	3.68	-	661.2
AHQ-2-9, 5144 - 5218	K.SYELPDGQVITIGNER.F	1791.93998	2	4.09E-12	0.95	4.28	-	1268.1
AHQ-2-14, 5956 - 6033	K.SYELPDGQVITIGNER.F	1791.93998	2	2.02E-04	0.92	4.22	-	869.4
AHQ-2-8, 4641	K.SYELPDGQVITIGNER.F	1791.93998	3	1.81E-06	0.95	4.61	-	1606.6
AHQ-2-8, 4603 - 4671	K.SYELPDGQVITIGNER.F	1791.93998	2	1.05E-11	0.97	5.33	-	1224.4
AHQ-2-8, 4516 - 4587	K.SYELPDGQVITIGNER.F	1791.93998	2	4.55E-11	0.96	5.18	-	1099.5
AHQ-2-8, 4366 - 4447	K.SYELPDGQVITIGNER.F	1791.93998	2	6.27E-13	0.96	4.46	-	1223.5
AHQ-2-3, 4680	K.SYELPDGQVITIGNER.F	1791.93998	2	8.11E-06	0.85	3.35	-	627.4
AHQ-2-4, 4666	K.SYELPDGQVITIGNER.F	1791.93998	2	2.35E-07	0.95	4.36	-	955.0
AHQ-2-13, 4504	K.SYELPDGQVITIGNER.F	1791.93998	2	1.53E-11	0.94	4.30	-	957.8
AHQ-2-10, 4104 - 4114	K.SYELPDGQVITIGNER.F	1791.93998	2	1.61E-04	0.86	3.50	-	577.1
AHQ-2-4, 4778 - 4784	K.SYELPDGQVITIGNER.F	1791.93998	2	1.66E-08	0.95	4.09	-	1149.4
AHQ-2-10, 4191 - 4202	K.SYELPDGQVITIGNER.F	1791.93998	2	1.78E-07	0.94	4.58	-	900.2
AHQ-2-10, 4302 - 4374	K.SYELPDGQVITIGNER.F	1791.93998	2	2.49E-10	0.94	4.10	-	1146.6
AHQ-2-10, 4515 - 4579	K.SYELPDGQVITIGNER.F	1791.93998	2	1.38E-08	0.95	4.71	-	1037.6
AHQ-2-10, 4750 - 4830	K.SYELPDGQVITIGNER.F	1791.93998	2	4.92E-04	0.76	3.09	-	531.1
AHQ-2-2, 5198	K.SYELPDGQVITIGNER.F	1791.93998	2	8.21E-06	0.90	3.54	-	914.5
AHQ-2-13-, 5129 - 5193	K.SYELPDGQVITIGNER.F	1791.93998	2	1.88E-13	0.97	5.10	-	1370.7
AHQ-2-2, 4818	K.SYELPDGQVITIGNER.F	1791.93998	2	2.72E-10	0.91	3.83	-	829.4
AHQ-2-8, 4226 - 4306	K.SYELPDGQVITIGNER.F	1791.93998	2	7.03E-11	0.96	4.82	-	1122.7
AHQ-2-11, 4306 - 4380	K.SYELPDGQVITIGNER.F	1791.93998	2	8.65E-10	0.90	3.93	-	742.8
AHQ-2-11, 4525	K.SYELPDGQVITIGNER.F	1791.93998	2	5.69E-11	0.95	4.44	-	1072.9
AHQ-2-11, 4697 - 4768	K.SYELPDGQVITIGNER.F	1791.93998	2	2.76E-12	0.92	4.22	-	752.6
AHQ-2-11, 4912 - 4990	K.SYELPDGQVITIGNER.F	1791.93998	2	1.68E-11	0.94	3.94	-	1041.9
AHQ-2-4, 5429	K.SYELPDGQVITIGNER.F	1791.93998	2	9.41E-09	0.93	4.16	-	930.0
AHQ-2-1, 5373 - 5441	K.SYELPDGQVITIGNER.F	1791.93998	2	3.80E-09	0.95	4.59	-	1042.3
AHQ-2-1, 5181 - 5197	K.SYELPDGQVITIGNER.F	1791.93998	2	2.54E-09	0.94	4.32	-	953.4
AHQ-2-13-, 4959 - 4981	K.SYELPDGQVITIGNER.F	1791.93998	2	4.30E-05	0.83	3.19	-	863.1
AHQ-2-5, 4563	K.SYELPDGQVITIGNER.F	1791.93998	2	5.55E-10	0.78	3.46	-	533.2
AHQ-2-6, 4471	K.SYELPDGQVITIGNER.F	1791.93998	2	3.71E-04	0.69	2.66	-	460.2
AHQ-2-6, 4838 - 4850	K.SYELPDGQVITIGNER.F	1791.93998	2	8.86E-07	0.83	3.15	-	674.2
AHQ-2-6, 5134 - 5138	K.SYELPDGQVITIGNER.F	1791.93998	2	2.45E-05	0.76	3.11	-	569.7
AHQ-2-1, 4790	K.SYELPDGQVITIGNER.F	1791.93998	2	1.55E-08	0.90	3.59	-	786.2
AHQ-2-13-, 4565	K.SYELPDGQVITIGNER.F	1791.93998	2	1.41E-09	0.94	4.02	-	957.0
AHQ-2-12, 4570	K.SYELPDGQVITIGNER.F	1791.93998	2	3.19E-07	0.87	3.40	-	770.5
AHQ-2-12, 4718	K.SYELPDGQVITIGNER.F	1791.93998	2	4.36E-12	0.93	4.06	-	924.9
AHQ-2-7, 5059 - 5075	K.SYELPDGQVITIGNER.F	1791.93998	2	2.05E-04	0.84	3.12	-	857.6
AHQ-2-12, 4930 - 4993	K.SYELPDGQVITIGNER.F	1791.93998	2	2.61E-13	0.96	4.77	-	1082.6
AHQ-2-12, 5111 - 5181	K.SYELPDGQVITIGNER.F	1791.93998	2	6.22E-08	0.93	4.53	-	746.1
AHQ-2-9, 4315 - 4394	K.SYELPDGQVITIGNER.F	1791.93998	2	8.52E-07	0.89	3.64	-	755.3
AHQ-2-14-, 4916	K.SYELPDGQVITIGNER.F	1791.93998	2	4.80E-06	0.91	3.88	-	972.6
AHQ-2-9, 3434 - 3502	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	8.33E-04	0.89	4.22	-	596.8
AHQ-2-8, 3142 - 3215	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	1.20E-04	0.85	3.67	-	642.5
AHQ-2-11, 4242	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.00E-04	0.85	3.88	-	655.7
AHQ-2-10, 4006 - 4039	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.11E-04	0.87	3.75	-	792.2
AHQ-2-9, 4548 - 4566	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.34E-04	0.90	4.52	-	725.7
AHQ-2-9, 4463 - 4474	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.44E-06	0.91	4.47	-	575.8
AHQ-2-9, 4139 - 4210	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.72E-04	0.89	4.34	-	668.3
AHQ-2-12, 4151	K.YPIEHGIITNWDDMEK.I	1962.17174	2	8.86E-04	0.78	3.88	-	607.0
AHQ-2-14, 5698	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.04E-04	0.43	2.58	-	535.7
AHQ-2-2, 4684	K.YPIEHGIITNWDDMEK.I	1962.17174	2	9.41E-04	0.81	3.64	-	692.9
AHQ-2-3, 4648	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.09E-04	0.73	3.44	-	666.2
AHQ-2-8, 4777	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.64E-08	0.91	4.46	-	683.2
AHQ-2-8, 4322	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.27E-04	0.91	4.38	-	698.4
AHQ-2-8, 3519 - 3563	K.YPIEHGIITNWDDM*EK.I	1978.17114	3	7.28E-04	0.78	3.29	-	918.4
AHQ-2-12, 4085	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	7.05E-05	0.78	3.30	-	562.9
AHQ-2-13-, 4454 - 4526	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.70E-06	0.88	4.10	-	713.9
AHQ-2-13-, 4457	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.70E-04	0.83	3.97	-	576.2
AHQ-2-7, 4172	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.44E-04	0.84	3.70	-	709.6
AHQ-2-13-, 4671	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.30E-08	0.83	3.63	-	632.7
AHQ-2-5, 4299	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.85E-05	0.79	3.27	-	662.1
AHQ-2-4, 4814	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.29E-04	0.37	2.65	-	525.6
AHQ-2-12, 4735	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.31E-04	0.87	3.96	-	648.1
AHQ-2-8, 6512 - 6578	K.YPIEHGIITNWDDMEKIWHHTFYNELR.V	3459.83609	3	1.14E-07	0.92	5.03	-	721.3
AHQ-2-8, 5200 - 5204	K.YPIEHGIITNWDDM*EKIWHHTFYNELR.V	3475.83549	3	2.89E-06	0.93	5.11	-	855.7
gi|27500274|ref|XP_113950.3| similar to Munc13-4 protein [Homo sapiens]				1.89E-14	9.17	120.33	17.60	123281.1
AHQ-2-5, 7631	K.AFGELCPNTAPLPQLVTEALQTGTTEWFHLK.Q	3472.91108	3	1.35E-11	0.74	3.49	-	442.7
AHQ-2-6, 7373	K.AFGELCPNTAPLPQLVTEALQTGTTEWFHLK.Q	3472.91108	3	9.41E-09	0.80	3.93	-	339.9
AHQ-2-4, 6670	R.ALLYEDALYTVLHR.L	1677.92484	2	1.04E-11	0.95	4.37	-	1236.4
AHQ-2-4, 4988 - 4993	R.AVQM*DELVPLGELTK.H	1659.92638	2	1.52E-05	0.78	2.96	-	719.4
AHQ-2-4, 2424	R.DLELQAASSR.E	1090.16939	1	6.59E-04	0.10	1.84	-	257.8
AHQ-2-4, 3417 - 3434	R.EVPGLSGSEEPGEVPQTR.L	1868.97961	2	8.41E-04	0.55	2.78	-	321.1
AHQ-2-4, 4754	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	1.89E-14	0.98	6.19	-	2344.4
AHQ-2-5, 4344	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	1.99E-07	0.96	5.35	-	1262.8
AHQ-2-4, 3517 - 3532	R.IQQQAETTSEELGAVTVK.A	1933.10674	2	7.70E-11	0.98	6.58	-	1572.0
AHQ-2-4, 3520	K.LGELTDLHGLR.R	1224.39168	2	4.54E-04	0.87	3.20	-	1088.4
AHQ-2-4, 3349	R.LGHPEPNHVTEASELLR.Y	1900.08490	2	5.78E-04	0.72	3.10	-	489.6
AHQ-2-4, 5610	K.LPAQLAWEALEQR.V	1525.73360	2	1.70E-09	0.96	4.15	-	1431.6
AHQ-2-4, 4169	R.SVFPLSVSDSPAR.L	1362.51311	2	5.69E-06	0.76	2.63	-	858.0
AHQ-2-4, 6480	R.WFQPAIPSWLQK.T	1501.75533	2	1.05E-05	0.79	3.14	-	516.7
gi|4505879|ref|NP_002655.1| pleckstrin; p47 [Homo sapiens]				2.94E-14	9.70	120.41	44.30	40082.5
AHQ-2-1, 6069	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	6.82E-06	0.96	5.95	-	1241.5
AHQ-2-13, 5573	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	2.72E-06	0.78	3.20	-	600.8
AHQ-2-12, 5718 - 5721	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.17E-09	0.96	5.88	-	1451.9
AHQ-2-11, 5468 - 5470	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	9.46E-09	0.95	5.66	-	1516.2
AHQ-2-13-, 5662 - 5673	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.28E-09	0.97	6.64	-	1779.8
AHQ-2-13, 5563 - 5577	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	3.39E-08	0.98	6.89	-	1834.9
AHQ-2-8, 5442	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	7.11E-12	0.97	6.48	-	1687.3
AHQ-2-8, 5448	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	1.47E-05	0.84	3.54	-	569.3
AHQ-2-14-, 5652	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	6.80E-09	0.95	5.52	-	1090.9
AHQ-2-12, 2451	R.GCVVTSVESNSNGR.K	1467.54464	2	5.50E-06	0.88	3.33	-	1081.4
AHQ-2-8, 2339	R.GCVVTSVESNSNGR.K	1467.54464	2	2.94E-06	0.92	3.42	-	1296.0
AHQ-2-11, 2442	R.GCVVTSVESNSNGR.K	1467.54464	2	7.57E-04	0.90	2.92	-	1605.0

AHQ-2-13-, 2463 - 2513	R.GCVVTSVESNSNGR.K	1467.54464	2	1.04E-05	0.92	3.87	-	1184.9
AHQ-2-8, 2156 - 2232	R.GCVVTSVESNSNGRK.S	1595.71755	2	3.32E-05	0.85	3.24	-	1149.0
AHQ-2-8, 2844	K.GSTLTSPCQDFGK.R	1399.50867	1	9.36E-06	0.07	2.07	-	204.7
AHQ-2-8, 2288 - 2302	K.GSTLTSPCQDFGKR.M	1555.69502	2	3.82E-07	0.40	2.66	-	322.6
AHQ-2-13-, 2865 - 2875	K.GSTLTSPCQDFGKR.M	1555.69502	2	7.79E-04	0.66	3.11	-	370.3
AHQ-2-8, 7367 - 7444	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	6.90E-07	0.98	5.72	-	1805.1
AHQ-2-10, 6535	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	9.65E-10	0.97	5.00	-	1425.2
AHQ-2-9, 7272 - 7351	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	2.21E-04	0.95	4.77	-	1193.6
AHQ-2-8, 7050 - 7055	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	3.23E-12	0.98	6.39	-	1803.4
AHQ-2-8, 7224 - 7295	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	5.70E-08	0.98	6.44	-	1793.2
AHQ-2-13-, 7061	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	6.35E-08	0.98	7.68	-	2039.8
AHQ-2-10, 6795	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	6.31E-08	0.98	7.80	-	2794.7
AHQ-2-8, 7452 - 7526	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	3.30E-06	0.99	8.20	-	3635.1
AHQ-2-9, 7478 - 7479	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	2.60E-06	0.98	7.82	-	2629.7
AHQ-2-14-, 6915	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	2.94E-14	0.99	7.89	-	3063.0
AHQ-2-12, 7194 - 7263	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	9.18E-12	0.98	6.64	-	2062.7
AHQ-2-10, 6162	R.LPETIDLGALYLSMK.D	1664.98779	2	2.89E-05	0.95	4.48	-	1321.3
AHQ-2-12, 6567 - 6585	R.LPETIDLGALYLSMK.D	1664.98779	2	1.29E-06	0.97	4.37	-	2018.7
AHQ-2-9, 6734 - 6760	R.LPETIDLGALYLSMK.D	1664.98779	2	1.58E-05	0.97	4.09	-	1936.0
AHQ-2-8, 6618 - 6686	R.LPETIDLGALYLSMK.D	1664.98779	2	7.65E-05	0.97	3.90	-	1863.5
AHQ-2-8, 6531 - 6598	R.LPETIDLGALYLSMK.D	1664.98779	2	7.47E-06	0.98	4.40	-	2673.0
AHQ-2-12, 5799 - 5801	R.LPETIDLGALYLSM*K.D	1680.98719	2	1.67E-06	0.95	4.73	-	997.5
AHQ-2-8, 6018 - 6019	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	3	5.51E-05	0.94	4.95	-	1049.1
AHQ-2-8, 5946 - 5986	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	2.41E-04	0.97	5.60	-	1654.7
AHQ-2-8, 6132	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	8.84E-05	0.91	4.29	-	668.0
AHQ-2-8, 5856 - 5882	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	1.59E-07	0.89	4.09	-	672.0
AHQ-2-8, 5886 - 5951	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	3	9.57E-04	0.86	4.28	-	514.0
AHQ-2-9, 6166	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	2.63E-05	0.92	4.46	-	536.5
AHQ-2-10, 4107	K.QQDHFFQAAFLEER.D	1766.89390	2	1.07E-10	0.80	3.36	-	254.4
AHQ-2-8, 3970 - 3972	K.QQDHFFQAAFLEER.D	1766.89390	2	4.77E-07	0.86	3.49	-	295.0
AHQ-2-11, 4381	K.QQDHFFQAAFLEER.D	1766.89390	2	4.69E-05	0.72	3.26	-	169.8
AHQ-2-12, 4515	K.QQDHFFQAAFLEER.D	1766.89390	2	4.95E-10	0.83	3.24	-	244.0
AHQ-2-12, 7255	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	5.60E-07	0.88	4.39	-	554.9
AHQ-2-12, 7253 - 7254	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.72E-09	0.91	5.18	-	779.7
AHQ-2-10, 6871	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	9.75E-09	0.93	5.16	-	818.1
AHQ-2-10, 6870	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	1.49E-05	0.88	4.68	-	490.2
AHQ-2-9, 7544 - 7610	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	3.43E-05	0.73	3.96	-	312.2
AHQ-2-8, 7615	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	1.48E-09	0.56	2.87	-	459.4
AHQ-2-13-, 7102 - 7106	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	7.46E-07	0.93	4.99	-	1158.4
AHQ-2-8, 7560	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	2.98E-11	0.91	4.06	-	1230.0
AHQ-2-8, 7474 - 7543	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	3.48E-04	0.27	2.53	-	389.2
AHQ-2-14-, 6960	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	5.91E-10	0.85	3.99	-	769.6
gi|4505839|ref|NP_002645.1| pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro				3.00E-14	14.83	160.36	40.90	57913.6
AHQ-2-7, 6127 - 6137	R.AGKPVICATQMLESMIK.K	1879.29869	3	2.03E-06	0.95	4.47	-	1732.7
AHQ-2-9, 6290	R.AGKPVICATQMLESMIK.K	1879.29869	2	6.44E-04	0.91	3.56	-	875.8
AHQ-2-7, 6119 - 6128	R.AGKPVICATQMLESMIK.K	1879.29869	2	7.60E-06	0.95	4.73	-	950.7
AHQ-2-7, 7567	K.FGVEQDVDMVFASFIR.K	1861.11055	2	6.58E-10	0.96	4.82	-	1342.1
AHQ-2-7, 7477	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	3.82E-08	0.96	4.59	-	1193.7
AHQ-2-7, 4877 - 4880	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.53E-10	0.95	4.72	-	1310.7
AHQ-2-7, 5123	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	5.88E-06	0.97	4.96	-	1402.4
AHQ-2-7, 2512	K.GDYPLEAVR.M	1020.12076	2	1.59E-05	0.78	2.73	-	705.7
AHQ-2-7, 6908 - 6972	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	3.69E-11	0.97	5.81	-	2010.1
AHQ-2-11, 6386 - 6393	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	2.30E-06	0.96	3.97	-	2564.0
AHQ-2-9, 6880	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	2.01E-06	0.93	4.45	-	1215.8
AHQ-2-7, 6815 - 6887	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	7.84E-11	0.98	6.08	-	2153.5
AHQ-2-7, 6811 - 6879	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	1.73E-05	0.95	4.48	-	1153.7
AHQ-2-9, 6870	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	8.16E-09	0.92	4.15	-	666.2
AHQ-2-11, 6389 - 6394	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	6.62E-06	0.93	4.47	-	810.4
AHQ-2-13-, 6717	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	3.00E-14	0.98	6.14	-	2377.6
AHQ-2-1, 4926	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	1.55E-04	0.87	4.08	-	409.6
AHQ-2-7, 2891 - 2893	K.ITLDNAYMEK.C	1198.37126	2	2.18E-06	0.86	3.47	-	617.4
AHQ-2-7, 3816	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	1.04E-06	0.90	4.22	-	1008.9
AHQ-2-9, 3879 - 3927	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	2.10E-04	0.96	5.05	-	1100.1
AHQ-2-7, 3805	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	2.84E-08	0.97	5.84	-	983.5
AHQ-2-7, 5036	K.KGVNLPGAAVDLPAVSEKDIQDLK.F	2478.82685	3	2.36E-09	0.98	7.22	-	2147.9
AHQ-2-7, 5413	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.95E-08	0.96	4.83	-	1346.7
AHQ-2-7, 6215	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	3.20E-07	0.96	4.73	-	1291.5
AHQ-2-7, 6300 - 6368	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.72E-10	0.97	5.31	-	1235.5
AHQ-2-11, 5580	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	8.94E-05	0.92	4.26	-	781.4
AHQ-2-7, 6071 - 6141	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	6.87E-09	0.97	6.06	-	1138.6
AHQ-2-7, 6637 - 6712	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	5.72E-06	0.94	4.75	-	742.7
AHQ-2-1, 6118	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.11E-08	0.94	4.53	-	870.3
AHQ-2-7, 5935 - 6004	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.20E-04	0.98	6.38	-	1262.7
AHQ-2-7, 6881	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.18E-05	0.92	3.69	-	1019.9
AHQ-2-9, 5855 - 5923	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	9.13E-04	0.67	2.97	-	527.4
AHQ-2-7, 7228 - 7300	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	4.71E-06	0.96	4.95	-	960.1
AHQ-2-7, 6441	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	9.54E-07	0.91	3.63	-	997.4
AHQ-2-7, 5828 - 5895	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.81E-11	0.97	5.87	-	1153.7
AHQ-2-7, 6552	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	4.14E-04	0.92	4.00	-	880.6
AHQ-2-7, 7321	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.53E-04	0.82	3.69	-	618.2
AHQ-2-7, 3172 - 3185	R.LDIDSPPITAR.N	1198.35099	2	3.12E-05	0.89	3.38	-	879.5
AHQ-2-7, 2003 - 2075	R.LNFSHGTHEYHAETIK.N	1885.02879	2	2.96E-06	0.86	3.58	-	655.8
AHQ-2-7, 3143 - 3160	R.NTGIICTIGPASR.S	1361.54994	2	1.47E-06	0.96	4.80	-	1287.4
AHQ-2-13-, 3446 - 3450	R.NTGIICTIGPASR.S	1361.54994	2	1.27E-04	0.93	3.67	-	1018.3
AHQ-2-11, 3292	R.NTGIICTIGPASR.S	1361.54994	2	3.91E-05	0.93	4.03	-	1082.0
AHQ-2-13, 3465	R.NTGIICTIGPASR.S	1361.54994	2	2.64E-05	0.89	3.53	-	953.4
AHQ-2-7, 3963 - 3983	R.NTGIICTIGPASR.S	1361.54994	2	4.47E-04	0.92	3.37	-	1362.4
AHQ-2-7, 5017 - 5029	R.RFDEILEASDGIMVAR.G	1823.06385	2	6.42E-12	0.97	5.22	-	1498.6
AHQ-2-7, 5392 - 5467	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	1.48E-04	0.78	3.17	-	800.4
AHQ-2-12, 5759 - 5829	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	2.70E-04	0.42	3.17	-	175.1
AHQ-2-13-, 5649 - 5717	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	6.20E-05	0.88	3.78	-	1161.2
AHQ-2-7, 5535 - 5537	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	2.38E-07	0.91	4.08	-	1020.9
AHQ-2-7, 5483 - 5551	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	9.30E-05	0.90	4.24	-	427.4
gi|21361670|ref|NP_054782.2| src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo				3.55E-14	1.50	20.25	8.80	48294.0
AHQ-2-13-, 6509	R.GYGPDGHFGM*FPANYVELIE	2230.44050	2	6.86E-04	0.53	3.06	-	178.0
AHQ-2-12, 5518	K.SPTDWALFTYEGNSNDIR.V	2087.19108	2	3.55E-14	0.97	4.76	-	1362.3
gi|4885387|ref|NP_005318.1| L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain; L-3-hydroxyacyl-				4.05E-14	0.95	10.28	9.60	34286.3
AHQ-2-9, 7558	K.TLSTIATSTDAASVVHSTDLVVEAIVENLK.V	3086.43759	3	4.05E-14	0.95	5.67	-	1083.7
gi|4507953|ref|NP_003397.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep				5.55E-14	9.23	110.28	46.90	27744.9
AHQ-2-10, 6818	R.EKIETELRDICNDVLSLLEK.F	2419.73463	2	3.13E-04	0.59	3.89	-	321.9
AHQ-2-10, 3134 - 3247	K.FLIPNASQAESK.V	1305.46156	1	4.03E-06	0.50	2.48	-	451.7
AHQ-2-10, 2912 - 2974	K.FLIPNASQAESK.V	1305.46156	1	8.24E-05	0.37	2.16	-	454.9
AHQ-2-9, 2983 - 3008	K.FLIPNASQAESK.V	1305.46156	2	1.83E-04	0.62	2.59	-	397.4
AHQ-2-9, 2986	K.FLIPNASQAESK.V	1305.46156	1	1.20E-06	0.64	2.77	-	455.6
AHQ-2-10, 2911 - 2975	K.FLIPNASQAESK.V	1305.46156	2	2.37E-06	0.78	2.81	-	435.7
AHQ-2-10, 3620	K.FLIPNASQAESK.V	1305.46156	1	4.30E-06	0.27	1.90	-	491.2
AHQ-2-12, 3135 - 3143	K.FLIPNASQAESK.V	1305.46156	2	7.54E-07	0.59	2.64	-	430.2

AHQ-2-10, 3356	K.FLIPNASQAESK.V	1305.46156	1	1.21E-06	0.27	1.80	-	491.6
AHQ-2-10, 5892	K.IETELRDICNDVLSLLEK.F	2162.44718	3	4.06E-08	0.91	4.19	-	1120.5
AHQ-2-9, 7458	K.IETELRDICNDVLSLLEK.F	2162.44718	2	4.51E-05	0.95	4.70	-	1179.6
AHQ-2-10, 6791 - 6799	R.LGLALNFSVFYYEILNSPEK.A	2318.65200	2	2.21E-05	0.85	4.35	-	361.9
AHQ-2-13-, 2307	K.SVTEQGAELSNEER.N	1549.57922	2	2.41E-07	0.91	3.60	-	1063.8
AHQ-2-9, 2151 - 2199	K.SVTEQGAELSNEER.N	1549.57922	2	1.65E-08	0.95	4.10	-	1528.5
AHQ-2-14-, 2259 - 2320	K.SVTEQGAELSNEER.N	1549.57922	2	5.35E-09	0.95	4.67	-	1272.8
AHQ-2-10, 2108 - 2178	K.SVTEQGAELSNEER.N	1549.57922	2	1.09E-07	0.93	3.68	-	1265.8
AHQ-2-1, 2425	K.SVTEQGAELSNEER.N	1549.57922	2	2.51E-05	0.85	2.93	-	1141.3
AHQ-2-10, 4166	K.SVTEQGAELSNEERNLLSVAYK.N	2438.63331	2	3.44E-05	0.71	3.26	-	333.5
AHQ-2-11, 6736	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.98E-10	0.96	5.31	-	931.0
AHQ-2-10, 5474 - 5476	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	5.40E-07	0.96	4.47	-	1490.7
AHQ-2-13-, 6957	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.52E-06	0.96	5.22	-	1409.8
AHQ-2-10, 5899	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	9.79E-08	0.57	3.34	-	404.1
AHQ-2-10, 6682	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	7.83E-09	0.96	4.79	-	1244.7
AHQ-2-10, 6688 - 6690	K.TAFDEAIAELDTLSEESYK.D	2133.25160	3	2.12E-06	0.94	4.41	-	1270.2
AHQ-2-13, 6739	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.94E-10	0.97	5.51	-	1252.8
AHQ-2-12, 7077 - 7081	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.86E-08	0.97	5.57	-	1515.6
AHQ-2-14-, 6815 - 6816	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	5.28E-07	0.97	5.49	-	1575.4
AHQ-2-9, 7526 - 7598	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	2.25E-08	0.91	4.81	-	914.1
AHQ-2-10, 6820 - 6854	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	4.77E-11	0.89	4.36	-	832.0
AHQ-2-10, 6878 - 6879	K.TAFDEAIAELDTLSEESYKDSTLIMQLLR.D	3304.66764	3	5.55E-14	0.94	5.08	-	1047.8
AHQ-2-13-, 2299	R.YLAEVAAGDDK.K	1152.23595	1	1.02E-05	0.33	1.92	-	769.6
AHQ-2-10, 2116	R.YLAEVAAGDDK.K	1152.23595	1	1.54E-06	0.88	2.44	-	1713.8
AHQ-2-10, 1743 - 1810	R.YLAEVAAGDDKK.G	1280.40887	1	8.90E-04	0.86	3.84	-	680.5
AHQ-2-13, 2171	R.YLAEVAAGDDKK.G	1280.40887	2	3.21E-04	0.87	3.02	-	1117.3
AHQ-2-10, 1732 - 1806	R.YLAEVAAGDDKK.G	1280.40887	2	4.06E-05	0.96	3.95	-	1674.1
AHQ-2-13-, 2037	R.YLAEVAAGDDKK.G	1280.40887	2	2.15E-04	0.96	3.63	-	1833.4
AHQ-2-12, 1957	R.YLAEVAAGDDKK.G	1280.40887	2	3.24E-07	0.96	3.53	-	2027.3
AHQ-2-11, 1972 - 1980	R.YLAEVAAGDDKK.G	1280.40887	2	2.94E-04	0.96	3.68	-	1878.2
AHQ-2-10, 1851	R.YLAEVAAGDDKK.G	1280.40887	2	7.70E-05	0.96	3.96	-	2041.4
AHQ-2-9, 1682 - 1706	R.YLAEVAAGDDKK.G	1280.40887	2	7.50E-07	0.91	3.11	-	1365.8
AHQ-2-10, 1812	R.YLAEVAAGDDKK.G	1280.40887	3	1.55E-06	0.91	3.33	-	1197.9
gi|17986260|ref|NP_524147.1| smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo				7.61E-14	3.64	40.36	23.30	12969.7
AHQ-2-12, 5726 - 5802	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	2.83E-06	0.96	5.40	-	1749.3
AHQ-2-12, 5874 - 5953	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	8.29E-05	0.45	3.60	-	324.4
AHQ-2-12, 6018 - 6067	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	2.58E-06	0.86	4.21	-	912.9
AHQ-2-12, 6133 - 6199	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	5.99E-10	0.95	7.08	-	1404.4
AHQ-2-12, 6262 - 6326	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	2.20E-04	0.84	4.70	-	1088.2
AHQ-2-12, 6329 - 6405	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	4.39E-10	0.98	7.21	-	2947.0
AHQ-2-12, 6346 - 6426	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	7.61E-14	0.74	3.43	-	636.5
AHQ-2-12, 6414 - 6481	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	2.77E-04	0.98	6.17	-	2657.7
AHQ-2-12, 6489 - 6551	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	2.43E-06	0.89	5.21	-	772.9
AHQ-2-12, 7178 - 7242	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	4.74E-08	0.71	3.50	-	570.8
AHQ-2-12, 7297	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	2.85E-05	0.96	5.01	-	1716.8
AHQ-2-12, 7311	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	3.05E-07	0.77	4.23	-	638.9
AHQ-2-14, 6552 - 6610	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	1.47E-07	0.94	4.42	-	1572.8
AHQ-2-14-, 5595	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	1.64E-12	0.96	6.10	-	1292.2
AHQ-2-14-, 5741 - 5817	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	9.57E-08	0.84	5.08	-	693.1
AHQ-2-14-, 5895 - 5928	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	1.64E-05	0.72	4.43	-	568.4
AHQ-2-14-, 5985 - 5992	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	2.28E-04	0.80	4.33	-	862.9
gi|27498267|ref|XP_209737.1| similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,				8.16E-14	2.38	40.32	41.10	11063.6
AHQ-2-10, 5720 - 5782	R.DICNDVLSLLEK.F	1420.61093	1	2.04E-06	0.79	2.79	-	823.8
AHQ-2-14-, 5933 - 6003	R.DICNDVLSLLEK.F	1420.61093	2	6.79E-05	0.83	2.78	-	1043.1
AHQ-2-11, 5869	R.DICNDVLSLLEK.F	1420.61093	1	1.71E-07	0.36	2.03	-	643.0
AHQ-2-10, 6686 - 6758	R.DICNDVLSLLEK.F	1420.61093	1	4.42E-04	0.88	3.56	-	765.0
AHQ-2-9, 6304	R.DICNDVLSLLEK.F	1420.61093	1	6.94E-12	0.39	1.88	-	700.5
AHQ-2-9, 6312	R.DICNDVLSLLEK.F	1420.61093	2	1.22E-04	0.96	3.97	-	1577.0
AHQ-2-9, 6316	R.DICNDVLSLLEK.F	1420.61093	1	2.33E-05	0.55	2.21	-	737.8
AHQ-2-9, 7371	R.DICNDVLSLLEK.F	1420.61093	1	1.34E-07	0.85	3.48	-	701.2
AHQ-2-9, 7374	R.DICNDVLSLLEK.F	1420.61093	2	1.72E-06	0.97	5.01	-	1714.5
AHQ-2-10, 6147	R.DICNDVLSLLEK.F	1420.61093	2	1.31E-06	0.94	3.76	-	1973.1
AHQ-2-10, 5766	R.DICNDVLSLLEK.F	1420.61093	2	1.26E-05	0.87	3.43	-	972.8
AHQ-2-10, 5764	R.DICNDVLSLLEK.F	1420.61093	1	5.23E-09	0.82	3.28	-	801.0
AHQ-2-14-, 6819 - 6832	R.DICNDVLSLLEK.F	1420.61093	2	1.39E-06	0.96	4.29	-	1703.4
AHQ-2-10, 1607 - 1666	R.EKIQTELR.D	1017.16155	1	1.70E-04	0.08	2.03	-	98.3
AHQ-2-10, 4795 - 4858	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	6.75E-10	0.98	5.60	-	1751.4
AHQ-2-10, 4870	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	3.14E-06	0.98	6.39	-	2301.0
AHQ-2-10, 4918 - 4998	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.12E-09	0.98	5.79	-	1672.0
AHQ-2-10, 5058 - 5122	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.27E-12	0.98	6.07	-	1588.2
AHQ-2-10, 5186 - 5264	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.95E-06	0.97	5.13	-	1208.1
AHQ-2-10, 5326 - 5386	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.16E-14	0.98	5.63	-	2265.2
AHQ-2-10, 5451 - 5530	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.04E-10	0.96	5.21	-	1190.7
AHQ-2-10, 5592 - 5660	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.10E-07	0.97	5.36	-	1259.0
AHQ-2-10, 4404 - 4466	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.54E-10	0.97	5.49	-	1625.0
AHQ-2-5, 5348	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.48E-06	0.93	4.35	-	1094.2
AHQ-2-14-, 5131 - 5139	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.05E-07	0.98	6.45	-	1938.6
AHQ-2-10, 4550	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.19E-10	0.98	5.15	-	1754.3
AHQ-2-10, 6179 - 6248	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.15E-05	0.94	4.17	-	1062.3
AHQ-2-10, 6238 - 6316	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.91E-08	0.97	5.51	-	1465.2
AHQ-2-10, 6380	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.28E-07	0.92	3.60	-	1152.9
AHQ-2-10, 6475	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.49E-08	0.95	4.53	-	1017.1
AHQ-2-10, 6595 - 6599	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.30E-06	0.88	4.09	-	555.7
AHQ-2-9, 5250 - 5251	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.35E-09	0.97	5.47	-	1320.5
AHQ-2-11, 4644	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.13E-07	0.96	5.09	-	1165.1
AHQ-2-11, 5012	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.86E-06	0.97	5.33	-	1491.7
AHQ-2-11, 5221 - 5273	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.22E-06	0.91	4.39	-	690.7
AHQ-2-9, 4888	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.40E-06	0.91	4.40	-	725.6
AHQ-2-12, 5245	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	7.89E-09	0.98	5.73	-	1719.4
AHQ-2-13, 5079 - 5128	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.29E-11	0.97	5.35	-	1540.2
AHQ-2-13, 5145	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	7.50E-08	0.98	6.09	-	2512.7
AHQ-2-14, 6120 - 6128	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.81E-08	0.97	5.25	-	1613.4
AHQ-2-13-, 5201	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.70E-07	0.95	4.62	-	1159.1
AHQ-2-13-, 5219 - 5299	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.25E-05	0.93	3.83	-	1290.1
AHQ-2-1, 5501	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.83E-07	0.94	4.52	-	990.5
AHQ-2-10, 4259	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	3	3.20E-08	0.92	4.81	-	1380.5
AHQ-2-10, 4250	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	1.26E-04	0.98	5.97	-	2223.3
gi|4505733|ref|NP_002610.1| platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4				8.22E-14	4.73	50.27	38.60	10844.9
AHQ-2-14, 5400 - 5460	K.AGPHCPTAQLIATLK.N	1579.84600	2	3.21E-04	0.84	3.64	-	620.5
AHQ-2-13-, 4143 - 4209	K.AGPHCPTAQLIATLK.N	1579.84600	3	3.80E-04	0.84	3.80	-	998.4
AHQ-2-13-, 4302 - 4366	K.AGPHCPTAQLIATLK.N	1579.84600	2	3.75E-06	0.90	4.22	-	761.3
AHQ-2-14-, 3997 - 4080	K.AGPHCPTAQLIATLK.N	1579.84600	2	6.40E-10	0.91	3.71	-	813.7
AHQ-2-13, 4127	K.AGPHCPTAQLIATLK.N	1579.84600	2	3.75E-05	0.89	3.88	-	719.5
AHQ-2-14-, 3999 - 4077	K.AGPHCPTAQLIATLK.N	1579.84600	3	9.05E-05	0.83	3.85	-	847.2
AHQ-2-14-, 4152 - 4215	K.AGPHCPTAQLIATLK.N	1579.84600	2	4.72E-08	0.92	3.90	-	777.6
AHQ-2-14-, 4243	K.AGPHCPTAQLIATLK.N	1579.84600	3	4.17E-04	0.91	4.32	-	1328.7
AHQ-2-14, 5280 - 5361	K.AGPHCPTAQLIATLK.N	1579.84600	3	4.47E-04	0.72	3.51	-	772.4

AHQ-2-14, 5272	K.AGPHCPTAQLIATLK.N	1579.84600	2	2.47E-06	0.83	3.26	-	632.0
AHQ-2-14, 5265 - 5338	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.42E-07	0.93	4.59	-	681.2
AHQ-2-13-, 4174 - 4210	K.AGPHCPTAQLIATLK.N	1579.84600	2	4.16E-07	0.89	3.82	-	736.7
AHQ-2-14, 5024 - 5028	K.AGPHCPTAQLIATLK.N	1579.84600	2	2.50E-09	0.92	4.13	-	694.7
AHQ-2-14, 4989	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	5.14E-09	0.96	4.85	-	1300.1
AHQ-2-14, 4941 - 5000	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	3.18E-10	0.98	5.41	-	3098.8
AHQ-2-14, 5153 - 5226	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.69E-06	0.94	4.32	-	923.9
AHQ-2-14, 4866 - 4938	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	5.70E-05	0.92	4.11	-	751.4
AHQ-2-14, 4781	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	6.80E-04	0.93	4.02	-	1046.9
AHQ-2-13-, 4113	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	2.11E-07	0.95	3.80	-	1165.9
AHQ-2-13-, 4081 - 4109	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	5.86E-08	0.98	5.32	-	2619.1
AHQ-2-14-, 3936	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.94E-12	0.95	4.72	-	1002.5
AHQ-2-14-, 3915	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.01E-09	0.95	4.50	-	1827.2
AHQ-2-13, 4045	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	8.22E-14	0.94	4.49	-	972.0
AHQ-2-14, 5213 - 5217	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	5.33E-09	0.98	5.32	-	2457.9
AHQ-2-14-, 2545 - 2615	R.HITSLEVIK.A	1040.23825	2	1.63E-04	0.90	3.65	-	523.1
AHQ-2-14, 3380 - 3690	R.HITSLEVIK.A	1040.23825	1	7.67E-04	0.26	2.03	-	367.1
AHQ-2-12, 2447	R.HITSLEVIK.A	1040.23825	2	8.27E-06	0.81	2.66	-	625.7
AHQ-2-13, 2639 - 2667	R.HITSLEVIK.A	1040.23825	2	2.48E-04	0.89	3.24	-	693.3
AHQ-2-13-, 2537 - 2607	R.HITSLEVIK.A	1040.23825	2	5.13E-06	0.91	3.26	-	646.8
AHQ-2-14, 3381 - 3441	R.HITSLEVIK.A	1040.23825	2	7.40E-04	0.81	2.92	-	580.8
AHQ-2-14, 3500 - 3562	R.HITSLEVIK.A	1040.23825	2	1.51E-04	0.76	2.91	-	414.5
AHQ-2-14-, 2391	R.HITSLEVIK.A	1040.23825	1	2.36E-05	0.40	2.22	-	431.8
AHQ-2-14-, 2387 - 2411	R.HITSLEVIK.A	1040.23825	2	4.16E-06	0.89	3.33	-	617.8
AHQ-2-14-, 2457 - 2535	R.HITSLEVIK.A	1040.23825	2	1.64E-06	0.93	4.01	-	663.7
AHQ-2-14, 6080 - 6140	K.ICLDLQAPLYK.K	1335.59400	2	5.80E-05	0.96	4.25	-	1753.6
AHQ-2-13, 4939 - 4951	K.ICLDLQAPLYK.K	1335.59400	2	1.70E-05	0.97	4.07	-	1916.1
AHQ-2-13-, 5013 - 5015	K.ICLDLQAPLYK.K	1335.59400	2	1.98E-06	0.97	4.64	-	2104.2
AHQ-2-14-, 4923 - 4936	K.ICLDLQAPLYK.K	1335.59400	2	3.23E-06	0.97	4.40	-	2089.6
AHQ-2-14-, 4929	K.ICLDLQAPLYK.K	1335.59400	1	1.37E-04	0.66	2.64	-	649.4
AHQ-2-14, 6093 - 6154	K.ICLDLQAPLYK.K	1335.59400	1	1.57E-05	0.70	2.97	-	596.4
AHQ-2-14, 6281	K.ICLDLQAPLYK.K	1335.59400	2	5.70E-04	0.75	3.21	-	681.5
AHQ-2-14-, 5148	K.ICLDLQAPLYK.K	1335.59400	2	2.66E-05	0.94	4.02	-	1348.9
AHQ-2-13-, 4477	R.KICLDLQAPLYK.K	1463.76691	3	4.98E-05	0.90	3.48	-	1572.4
AHQ-2-13-, 4473 - 4481	R.KICLDLQAPLYK.K	1463.76691	2	5.43E-09	0.98	5.07	-	1930.6
AHQ-2-14, 5965	R.KICLDLQAPLYK.K	1463.76691	2	1.15E-06	0.96	4.40	-	1417.9
AHQ-2-14, 5772 - 5773	R.KICLDLQAPLYK.K	1463.76691	2	5.43E-06	0.97	4.61	-	1605.8
AHQ-2-14, 5648 - 5708	R.KICLDLQAPLYK.K	1463.76691	2	2.34E-06	0.97	4.41	-	1870.1
AHQ-2-14, 5482 - 5560	R.KICLDLQAPLYK.K	1463.76691	2	3.11E-06	0.95	4.16	-	1305.7
AHQ-2-14-, 4295	R.KICLDLQAPLYK.K	1463.76691	2	1.06E-05	0.93	3.83	-	1137.0
AHQ-2-14-, 4435 - 4500	R.KICLDLQAPLYK.K	1463.76691	2	2.08E-05	0.97	4.73	-	1582.7
AHQ-2-14-, 4441 - 4507	R.KICLDLQAPLYK.K	1463.76691	3	8.81E-04	0.87	3.98	-	1282.9
AHQ-2-14-, 4563 - 4627	R.KICLDLQAPLYK.K	1463.76691	2	1.50E-04	0.95	4.72	-	1117.7
AHQ-2-13, 4415	R.KICLDLQAPLYK.K	1463.76691	2	1.55E-06	0.95	4.19	-	1261.4
AHQ-2-12, 4454 - 4477	R.KICLDLQAPLYK.K	1463.76691	2	2.21E-07	0.93	3.77	-	1107.2
AHQ-2-13-, 4478	R.KICLDLQAPLYK.K	1463.76691	1	8.98E-06	0.82	3.47	-	672.7
gi|4507949|ref|NP_003395.1| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,				1.17E-13	4.56	50.28	31.70	28082.2
AHQ-2-10, 6875	K.IEAELQDICNDVLELLDK.Y	2132.37471	2	8.95E-08	0.96	5.61	-	1133.0
AHQ-2-10, 4074	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	1.09E-05	0.81	3.61	-	447.7
AHQ-2-13-, 6813	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	5.23E-07	0.93	4.42	-	946.0
AHQ-2-10, 6200	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	1.00E-05	0.77	3.58	-	515.7
AHQ-2-14-, 6844 - 6903	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	1.44E-04	0.86	4.05	-	593.9
AHQ-2-14-, 6675 - 6744	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	1.19E-05	0.95	4.96	-	783.9
AHQ-2-10, 6419	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	3.50E-04	0.96	4.74	-	1451.5
AHQ-2-10, 6874 - 6876	K.TAFDEAIAELDTLNEESYKDSTLIM*QLLR.D	3347.69249	3	1.17E-13	0.94	5.09	-	1044.2
AHQ-2-10, 2732	K.YLIPNATQPESK.V	1361.52512	1	7.50E-05	0.67	2.29	-	749.8
AHQ-2-10, 2618 - 2628	K.YLIPNATQPESK.V	1361.52512	2	3.13E-06	0.92	3.62	-	827.0
AHQ-2-10, 2823	K.YLIPNATQPESK.V	1361.52512	1	2.92E-05	0.77	2.49	-	915.7
gi|5031987|ref|NP_005720.1| peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]				1.23E-13	4.87	60.31	41.50	22040.1
AHQ-2-12, 3727	R.FPDENFTLK.H	1111.22866	2	1.55E-05	0.63	2.66	-	606.5
AHQ-2-12, 3817	R.FPDENFTLK.H	1111.22866	2	4.89E-04	0.81	2.61	-	874.6
AHQ-2-12, 4081	R.FPDENFTLK.H	1111.22866	1	2.11E-04	0.17	2.07	-	226.8
AHQ-2-12, 5178 - 5241	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	1.23E-13	0.91	4.54	-	945.2
AHQ-2-12, 5195 - 5265	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	2	1.01E-06	0.52	2.58	-	292.3
AHQ-2-12, 6046 - 6111	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	2	1.44E-06	0.90	4.35	-	649.1
AHQ-2-14-, 5321	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	3	7.52E-06	0.92	4.95	-	775.7
AHQ-2-11, 5684	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	2	2.90E-05	0.90	4.73	-	450.3
AHQ-2-12, 5373 - 5375	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	2	2.74E-05	0.91	4.85	-	384.9
AHQ-2-12, 5374 - 5398	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	3	1.65E-05	0.94	4.66	-	1483.4
AHQ-2-12, 5525	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	2	1.07E-04	0.67	3.02	-	326.8
AHQ-2-12, 5909 - 5973	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	2	1.50E-07	0.93	4.78	-	577.5
AHQ-2-12, 5918 - 5983	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	3	1.26E-06	0.97	6.14	-	1742.4
AHQ-2-14-, 5857	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	3	2.56E-08	0.94	4.98	-	1351.8
AHQ-2-12, 4023	R.VIPSFM*CQAGDFTNHNGTGGK.S	2256.46118	2	2.58E-05	0.65	2.87	-	141.1
AHQ-2-12, 4651 - 4723	R.VIPSFMCQAGDFTNHNGTGGK.S	2240.46178	2	1.71E-05	0.83	3.73	-	463.7
gi|4505257|ref|NP_002435.1| moesin [Homo sapiens]				1.42E-13	7.53	90.29	23.10	67819.5
AHQ-2-6, 2283	K.ALTSELANAR.D	1046.15975	2	2.09E-05	0.93	3.24	-	1192.8
AHQ-2-6, 3921	R.EDAVLEYLK.I	1080.21287	1	8.46E-05	0.41	2.71	-	253.0
AHQ-2-7, 7456	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	2	9.73E-05	0.49	2.89	-	255.5
AHQ-2-10, 6658	K.FYPEDVSEELIQDITQR.L	2083.24065	2	3.31E-08	0.97	5.00	-	1980.1
AHQ-2-9, 7306	K.FYPEDVSEELIQDITQR.L	2083.24065	2	1.09E-09	0.95	4.57	-	1181.7
AHQ-2-11, 6710	K.FYPEDVSEELIQDITQR.L	2083.24065	2	1.77E-04	0.85	3.58	-	710.9
AHQ-2-6, 7133 - 7151	K.FYPEDVSEELIQDITQR.L	2083.24065	2	2.72E-11	0.96	5.20	-	1181.4
AHQ-2-7, 7361	K.FYPEDVSEELIQDITQR.L	2083.24065	2	7.28E-11	0.97	5.71	-	1101.1
AHQ-2-13, 6720	K.FYPEDVSEELIQDITQR.L	2083.24065	2	9.16E-11	0.97	5.22	-	1243.6
AHQ-2-6, 5486	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	4.36E-09	0.97	4.81	-	1801.8
AHQ-2-6, 1995	R.ISQLEMAR.Q	948.12272	2	1.42E-04	0.87	2.78	-	1168.8
AHQ-2-6, 4477	K.KTQEQLALEMAELTAR.I	1833.10018	2	3.98E-07	0.97	4.77	-	1510.0
AHQ-2-6, 3457	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	1.42E-13	0.94	5.21	-	1314.3
AHQ-2-6, 3310 - 3385	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	4.99E-09	0.93	4.89	-	1148.8
AHQ-2-6, 5185 - 5194	K.TQEQLALEMAELTAR.I	1704.92727	2	1.02E-10	0.98	5.59	-	2047.5
AHQ-2-7, 5148	K.TQEQLALEMAELTAR.I	1704.92727	2	3.74E-04	0.72	2.71	-	714.7
gi|13994151|ref|NP_066272.1| PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H				1.55E-13	15.15	200.26	55.00	36071.5
AHQ-2-14-, 6625	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	3.51E-07	0.80	4.25	-	424.7
AHQ-2-14-, 6375 - 6451	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	3.27E-09	0.93	4.98	-	976.0
AHQ-2-13-, 6917	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.55E-13	0.92	4.91	-	621.3
AHQ-2-13, 6697	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	2.04E-08	0.89	4.42	-	667.1
AHQ-2-13-, 6775 - 6810	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	4.71E-06	0.79	3.86	-	519.8
AHQ-2-12, 7022	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.07E-11	0.88	4.40	-	622.3
AHQ-2-14-, 6165	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	6.52E-05	0.92	4.69	-	791.3
AHQ-2-14-, 6024 - 6100	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	6.75E-07	0.87	4.28	-	472.1
AHQ-2-12, 6765	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.84E-08	0.74	3.68	-	305.8
AHQ-2-13, 6557	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.42E-04	0.80	3.90	-	418.4
AHQ-2-13-, 4490	K.CGTGIVGVFVK.L	1138.36198	2	6.06E-04	0.95	3.73	-	1354.1
AHQ-2-13, 4456	K.CGTGIVGVFVK.L	1138.36198	2	1.61E-04	0.92	3.24	-	1123.0
AHQ-2-14-, 4455	K.CGTGIVGVFVK.L	1138.36198	2	1.31E-04	0.94	3.12	-	1456.3
AHQ-2-14-, 3611 - 3619	K.DFEQPLAISR.V	1176.30388	1	6.36E-07	0.56	2.29	-	345.2

AHQ-2-12, 3610	K.DFEQPLAISR.V	1176.30388	2	3.08E-04	0.85	3.05	-	844.6
AHQ-2-13, 3700	K.DFEQPLAISR.V	1176.30388	2	2.05E-05	0.84	3.08	-	799.9
AHQ-2-14-, 3616 - 3617	K.DFEQPLAISR.V	1176.30388	2	7.50E-04	0.90	3.39	-	1183.0
AHQ-2-13, 3413	K.GCTDNLTLTVAR.S	1322.47058	2	4.31E-04	0.78	3.25	-	593.9
AHQ-2-13-, 3387	K.GCTDNLTLTVAR.S	1322.47058	2	3.70E-06	0.84	3.64	-	701.6
AHQ-2-14-, 3360	K.GCTDNLTLTVAR.S	1322.47058	2	1.19E-04	0.84	3.53	-	629.8
AHQ-2-12, 3997 - 4066	K.GHFFVEDQIYCEK.H	1673.82684	2	2.25E-04	0.95	4.50	-	1000.0
AHQ-2-13, 4025 - 4029	K.GHFFVEDQIYCEK.H	1673.82684	2	3.60E-05	0.96	4.40	-	1454.8
AHQ-2-14, 4910 - 4985	K.GHFFVEDQIYCEK.H	1673.82684	2	8.58E-06	0.93	3.55	-	912.1
AHQ-2-13-, 4077	K.GHFFVEDQIYCEK.H	1673.82684	2	4.51E-05	0.97	4.24	-	1669.3
AHQ-2-13-, 2999 - 3003	R.HPECYVCTDCGTNLK.Q	1858.02023	2	9.24E-04	0.93	3.77	-	789.3
AHQ-2-12, 2970	R.HPECYVCTDCGTNLK.Q	1858.02023	2	7.21E-05	0.81	2.90	-	601.5
AHQ-2-13, 2728	R.HRHPECYVCTDCGTNLK.Q	2151.34648	2	7.10E-06	0.82	3.49	-	419.7
AHQ-2-13-, 2671	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	1.17E-05	0.93	4.67	-	911.9
AHQ-2-11, 3022	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.44E-08	0.93	3.33	-	1175.4
AHQ-2-14, 4033 - 4085	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.11E-04	0.90	3.22	-	1074.2
AHQ-2-14, 3905 - 3956	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.04E-07	0.91	3.31	-	1075.5
AHQ-2-13-, 3073	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.23E-10	0.94	4.39	-	897.8
AHQ-2-12, 3057	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.10E-11	0.86	3.06	-	829.6
AHQ-2-14-, 3033	R.IKGCTDNLTLTVAR.S	1563.80174	3	6.73E-04	0.92	4.25	-	1549.3
AHQ-2-14-, 3031 - 3043	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.20E-10	0.96	4.98	-	1046.1
AHQ-2-13, 3111 - 3112	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.76E-07	0.86	3.42	-	752.6
AHQ-2-13-, 5302	K.LPMCDKCGTGIVGVFVK.L	1884.27358	3	8.88E-07	0.60	3.32	-	530.2
AHQ-2-12, 4781 - 4807	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	2	7.67E-05	0.80	2.94	-	604.0
AHQ-2-14-, 5248	K.LPMCDKCGTGIVGVFVK.L	1884.27358	3	7.17E-06	0.80	3.83	-	525.9
AHQ-2-13, 3803	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.00E-04	0.94	4.60	-	913.9
AHQ-2-14-, 3724	R.LVGGKDFEQPLAISR.V	1630.86972	2	4.24E-08	0.97	5.19	-	1746.7
AHQ-2-14, 4589 - 4658	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.60E-06	0.89	3.85	-	904.1
AHQ-2-13, 4079	K.MNLASEPQEVLHIGSAHNR.S	2104.33619	2	4.46E-05	0.89	4.08	-	623.8
AHQ-2-13-, 3523	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	1.97E-10	0.64	3.22	-	532.8
AHQ-2-12, 6771 - 6790	K.QSTSFLVLQEILESEEK.G	1981.18977	2	5.50E-09	0.96	4.98	-	1215.5
AHQ-2-13, 6573 - 6576	K.QSTSFLVLQEILESEEK.G	1981.18977	2	7.66E-10	0.97	4.73	-	1818.8
AHQ-2-13-, 6778	K.QSTSFLVLQEILESEEK.G	1981.18977	2	4.30E-07	0.96	4.62	-	1401.4
AHQ-2-13, 6095	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	5.91E-05	0.88	4.28	-	647.1
AHQ-2-13-, 6273 - 6275	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	2.22E-07	0.66	3.35	-	488.2
AHQ-2-12, 2365 - 2371	R.SAM*PFTASPASSTTAR.V	1599.74799	2	5.44E-04	0.77	3.08	-	637.4
AHQ-2-13, 3035	R.SAMPFTASPASSTTAR.V	1583.74859	2	3.59E-07	0.23	2.51	-	234.0
AHQ-2-12, 4813 - 4883	R.VTPPEGYEVVTVFPK	1662.90695	2	4.65E-04	0.30	2.62	-	111.4
AHQ-2-13-, 3061 - 3071	K.VWSPLVTEEGKR.H	1401.59247	2	5.39E-07	0.81	2.67	-	766.7
AHQ-2-14-, 2979	K.VWSPLVTEEGKR.H	1401.59247	2	6.24E-08	0.90	2.68	-	1197.6
AHQ-2-13, 3095	K.VWSPLVTEEGKR.H	1401.59247	2	5.10E-07	0.55	2.53	-	551.3
gi|5729770|ref|NP_000382.3| ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky				1.73E-13	1.91	20.32	7.30	61247.6
AHQ-2-8, 2615	R.LFGGNFAHQASVAR.V	1475.63637	2	2.98E-06	0.93	4.24	-	1116.0
AHQ-2-8, 7410 - 7412	R.VPIPWVSGTSASTPVFGGILSLINEHR.I	2836.23725	3	1.73E-13	0.98	6.41	-	1688.0
gi|7669492|ref|NP_002037.2| glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]				2.12E-13	9.27	120.36	48.40	36053.0
AHQ-2-11, 3485	R.GALQNIIPASTGAAK.A	1412.61680	1	5.89E-08	0.76	3.39	-	522.7
AHQ-2-9, 3290 - 3358	R.GALQNIIPASTGAAK.A	1412.61680	1	1.37E-06	0.64	3.38	-	284.2
AHQ-2-9, 7218 - 7291	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	6.17E-09	0.96	6.37	-	1207.8
AHQ-2-9, 6254 - 6327	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	3.46E-05	0.90	4.82	-	814.5
AHQ-2-9, 4260	K.RVIISAPSADAPMFVMGVNHEK.Y	2370.78022	3	5.97E-06	0.91	4.36	-	994.6
AHQ-2-9, 7530 - 7531	K.VDIVAINDPFIDLNYMVYM*FQYDSTHGK.F	3326.74330	3	2.87E-05	0.61	4.07	-	262.5
AHQ-2-10, 6662	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	5.01E-12	0.95	6.50	-	1441.2
AHQ-2-11, 6720 - 6724	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	2.12E-13	0.97	7.11	-	2408.2
AHQ-2-9, 7294 - 7372	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	3.99E-04	0.93	4.44	-	940.9
AHQ-2-9, 7286	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	3.22E-07	0.97	6.49	-	1653.7
AHQ-2-11, 6721 - 6722	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	3.93E-07	0.97	7.16	-	1781.4
AHQ-2-9, 6416 - 6474	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	2	6.84E-04	0.92	4.11	-	777.0
AHQ-2-9, 6466 - 6534	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	6.69E-13	0.98	6.56	-	1849.5
AHQ-2-9, 7268 - 7338	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	1.12E-11	0.92	5.38	-	1396.3
AHQ-2-10, 6666	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	1.63E-05	0.97	5.64	-	2279.0
AHQ-2-9, 6607 - 6660	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	1.15E-07	0.97	6.20	-	1494.0
AHQ-2-10, 4799 - 4800	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	4.98E-08	0.61	2.97	-	346.9
AHQ-2-10, 4524	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	1.60E-05	0.74	3.32	-	293.5
AHQ-2-10, 4328	R.VIISAPSADAPM*FVMGVNHEK.Y	2230.59327	2	9.96E-05	0.37	2.94	-	237.4
AHQ-2-12, 5261	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	5.44E-08	0.35	2.63	-	309.8
AHQ-2-12, 5067	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	6.67E-09	0.69	3.14	-	400.3
AHQ-2-9, 4454 - 4462	R.VIISAPSADAPMFVM*GVNHEK.Y	2230.59327	2	9.21E-05	0.48	3.23	-	472.1
AHQ-2-9, 5050	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	3.99E-04	0.81	3.55	-	550.3
AHQ-2-9, 4787 - 4790	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	2.08E-05	0.88	3.76	-	611.5
AHQ-2-9, 3802 - 3810	R.VPTANVSVVDLTCR.L	1532.74450	2	1.01E-07	0.90	3.52	-	961.3
AHQ-2-12, 4097 - 4166	R.VPTANVSVVDLTCR.L	1532.74450	2	2.71E-09	0.94	4.02	-	1145.0
AHQ-2-9, 4736	R.VPTANVSVVDLTCR.L	1532.74450	2	3.52E-04	0.87	2.86	-	849.9
AHQ-2-11, 3934 - 3960	R.VPTANVSVVDLTCR.L	1532.74450	2	3.65E-09	0.92	3.62	-	911.8
AHQ-2-9, 4070 - 4144	R.VPTANVSVVDLTCR.L	1532.74450	2	9.09E-09	0.94	4.16	-	1014.6
AHQ-2-10, 3770 - 3834	R.VPTANVSVVDLTCR.L	1532.74450	2	3.40E-07	0.93	3.78	-	883.5
AHQ-2-13, 4125 - 4141	R.VPTANVSVVDLTCR.L	1532.74450	2	1.10E-07	0.95	4.05	-	1020.7
AHQ-2-14, 4998	R.VPTANVSVVDLTCR.L	1532.74450	2	1.29E-10	0.94	4.08	-	979.6
AHQ-2-13-, 4163	R.VPTANVSVVDLTCR.L	1532.74450	2	7.06E-09	0.96	4.49	-	1290.7
AHQ-2-9, 3956 - 4002	R.VPTANVSVVDLTCR.L	1532.74450	2	4.52E-07	0.87	3.24	-	819.2
AHQ-2-9, 4162 - 4232	R.VPTANVSVVDLTCR.L	1532.74450	2	2.53E-10	0.89	3.51	-	706.6
AHQ-2-9, 7578	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	6.28E-07	0.92	4.51	-	707.1
AHQ-2-9, 7551	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	1.62E-06	0.64	3.01	-	441.2
AHQ-2-9, 7436 - 7508	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.13E-08	0.96	4.40	-	1308.0
AHQ-2-9, 7287 - 7363	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	9.18E-06	0.89	4.03	-	629.6
AHQ-2-9, 6519 - 6591	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.34E-06	0.90	4.29	-	695.2
AHQ-2-9, 6603 - 6672	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	8.01E-06	0.95	5.07	-	851.0
AHQ-2-9, 7171 - 7219	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	7.37E-05	0.91	4.45	-	686.7
AHQ-2-12, 6313	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.01E-05	0.87	4.22	-	543.7
AHQ-2-9, 7036 - 7103	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	5.18E-08	0.95	4.70	-	999.4
AHQ-2-13, 6080 - 6104	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.66E-05	0.89	3.68	-	832.1
AHQ-2-13, 6175 - 6237	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	4.21E-07	0.86	3.89	-	557.8
AHQ-2-9, 6954	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.06E-07	0.90	3.86	-	775.0
AHQ-2-9, 6747 - 6815	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	4.82E-05	0.96	4.30	-	1370.6
AHQ-2-13-, 5679	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	3.67E-04	0.92	4.05	-	921.9
AHQ-2-13-, 6245 - 6311	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.79E-05	0.95	4.62	-	1077.5
AHQ-2-13-, 6382 - 6434	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	4.27E-08	0.90	4.03	-	728.1
gi|4506353|ref|NP_002854.1| phosphorylase, glycogen; liver (Hers disease, glycogen storage disease				2.13E-13	2.22	30.27	7.30	97147.8
AHQ-2-5, 4808	K.EYAQNIWNVEPSDLK.I	1806.95311	2	1.04E-04	0.46	2.74	-	456.9
AHQ-2-5, 7431 - 7432	R.GAGTVFDAFPDQVAIQLNDTHPALAIPELMR.I	3309.74040	3	2.13E-13	0.84	4.17	-	473.8
AHQ-2-5, 6508	R.WLLLCNPGLAELIAEK.I	1842.19160	2	8.19E-10	0.92	4.55	-	1016.4
gi|27498332|ref|XP_212565.1| similar to tubulin, beta 5 [Homo sapiens]				2.14E-13	4.34	50.29	9.90	49670.5
AHQ-2-9, 5556 - 5558	R.ALTVPELTQQVFDAK.N	1660.89259	2	9.03E-04	0.83	3.57	-	412.8
AHQ-2-11, 5449	R.ALTVPELTQQVFDAK.N	1660.89259	2	1.55E-04	0.64	2.66	-	322.1
AHQ-2-7, 3256	R.IM*NTFSVVPSPK.V	1336.58217	2	3.48E-04	0.88	3.41	-	708.1
AHQ-2-7, 3503 - 3519	R.IMNTFSVVPSPK.V	1320.58277	2	3.74E-04	0.97	3.79	-	2236.7
AHQ-2-7, 6983	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.14E-13	0.96	4.87	-	866.0
AHQ-2-12, 6805	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	4.19E-05	0.95	4.29	-	1191.0

AHQ-2-13, 6575	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.33E-13	0.95	4.49	-	955.8
AHQ-2-14-, 6289 - 6351	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.09E-11	0.97	5.76	-	1363.2
AHQ-2-14-, 6517 - 6533	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.11E-07	0.95	4.43	-	1190.4
AHQ-2-14-, 6631 - 6639	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.70E-07	0.98	5.40	-	1551.4
AHQ-2-7, 7348	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	9.45E-07	0.90	3.98	-	674.9
gi|5453595|ref|NP_006358.1| adenylyl cyclase-associated protein [Homo sapiens]				2.59E-13	10.05	130.31	35.60	51672.7
AHQ-2-10, 2567 - 2570	R.ALLVTASQCQQPAENK.L	1759.96271	2	8.93E-04	0.95	4.69	-	1030.4
AHQ-2-9, 2630	R.ALLVTASQCQQPAENK.L	1759.96271	2	1.08E-07	0.90	3.92	-	790.3
AHQ-2-7, 2535 - 2547	R.ALLVTASQCQQPAENK.L	1759.96271	2	5.76E-05	0.97	5.38	-	1206.5
AHQ-2-13, 2867	R.ALLVTASQCQQPAENK.L	1759.96271	2	4.33E-05	0.93	3.98	-	1021.9
AHQ-2-7, 6641	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	2.40E-10	0.94	4.98	-	1149.9
AHQ-2-7, 3295 - 3308	K.EMNDAAMFYTNR.V	1463.62130	2	2.25E-04	0.34	2.58	-	334.2
AHQ-2-7, 1891	K.KEPAVLELEGKK.W	1341.57848	1	4.87E-04	0.42	2.36	-	318.1
AHQ-2-7, 7673	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	2.59E-13	0.98	6.26	-	1385.7
AHQ-2-13-, 5107	K.LSDLLAPISEQIK.E	1427.66814	2	5.53E-04	0.92	3.15	-	1135.7
AHQ-2-7, 4843 - 4921	K.LSDLLAPISEQIK.E	1427.66814	2	4.22E-05	0.86	3.52	-	821.0
AHQ-2-7, 4851	K.LSDLLAPISEQIK.E	1427.66814	1	1.11E-05	0.57	2.72	-	546.6
AHQ-2-12, 5090	K.LSDLLAPISEQIK.E	1427.66814	2	2.41E-05	0.69	2.85	-	676.9
AHQ-2-11, 4849	K.LSDLLAPISEQIK.E	1427.66814	2	2.61E-04	0.84	3.14	-	796.2
AHQ-2-9, 4907	K.LSDLLAPISEQIK.E	1427.66814	1	1.62E-07	0.55	2.93	-	434.9
AHQ-2-9, 4900 - 4904	K.LSDLLAPISEQIK.E	1427.66814	2	5.80E-07	0.90	4.07	-	720.2
AHQ-2-14-, 3007 - 3013	K.NSLDCEIVSAK.S	1237.36245	2	1.21E-06	0.88	3.17	-	902.1
AHQ-2-7, 3528	K.NSLDCEIVSAK.S	1237.36245	1	7.60E-05	0.29	2.05	-	304.1
AHQ-2-11, 3428	K.NSLDCEIVSAK.S	1237.36245	1	3.46E-05	0.29	2.05	-	412.4
AHQ-2-8, 4308	R.SALFAQINQGESITHALK.H	1929.16615	3	5.48E-06	0.73	3.47	-	552.3
AHQ-2-7, 4369 - 4440	R.SALFAQINQGESITHALK.H	1929.16615	2	1.92E-09	0.94	5.07	-	729.8
AHQ-2-9, 4515 - 4535	R.SALFAQINQGESITHALK.H	1929.16615	2	2.20E-07	0.93	4.93	-	882.7
AHQ-2-8, 4299	R.SALFAQINQGESITHALK.H	1929.16615	2	4.62E-05	0.90	4.46	-	556.0
AHQ-2-7, 1761 - 1767	R.SGPKPFSAPKPQTSPSPK.R	1839.08461	2	5.91E-04	0.75	3.37	-	596.8
AHQ-2-14-, 6640	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.19E-06	0.85	4.00	-	279.3
AHQ-2-14-, 6292	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	7.82E-04	0.64	3.29	-	189.9
AHQ-2-7, 6856 - 6936	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	2.33E-04	0.92	4.37	-	364.9
AHQ-2-14-, 6176	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	1.03E-06	0.82	3.79	-	274.9
AHQ-2-14-, 6071 - 6075	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	8.98E-05	0.82	3.91	-	246.4
AHQ-2-7, 6751 - 6767	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	4.95E-07	0.54	3.02	-	221.2
AHQ-2-14-, 6512 - 6515	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.33E-08	0.95	5.28	-	529.6
AHQ-2-7, 6421 - 6493	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	1.14E-04	0.32	2.78	-	123.1
AHQ-2-13, 6476 - 6479	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.64E-05	0.60	3.22	-	184.9
AHQ-2-11, 6045	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	9.68E-05	0.40	2.67	-	182.3
AHQ-2-11, 6297 - 6373	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	8.29E-06	0.71	3.08	-	397.9
AHQ-2-14-, 6424	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	5.31E-08	0.74	3.38	-	263.1
AHQ-2-12, 4814	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.16E-06	0.92	4.35	-	684.2
AHQ-2-7, 4827	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	3.73E-07	0.91	4.33	-	653.2
AHQ-2-13, 4767 - 4773	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	7.78E-07	0.90	3.99	-	817.2
AHQ-2-11, 4864	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.38E-09	0.94	4.77	-	892.2
AHQ-2-13-, 4861	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.42E-07	0.92	4.71	-	624.6
AHQ-2-7, 4580 - 4652	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	3.65E-08	0.95	5.00	-	774.4
AHQ-2-11, 4608	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.44E-09	0.93	4.90	-	624.8
AHQ-2-14-, 4803	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.07E-07	0.97	5.87	-	1159.5
AHQ-2-10, 4412	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.37E-07	0.94	4.69	-	999.4
AHQ-2-10, 4398	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.68E-04	0.92	4.05	-	860.3
AHQ-2-8, 4507	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.60E-08	0.94	4.70	-	768.3
AHQ-2-7, 4984 - 5057	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.20E-08	0.91	4.66	-	593.2
AHQ-2-9, 4676	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.93E-04	0.92	4.16	-	719.9
AHQ-2-7, 2163 - 2243	K.VPTISINK.T	872.04435	1	7.67E-06	0.64	3.12	-	360.9
gi|4501891|ref|NP_001093.1| actinin, alpha 1 [Homo sapiens]				2.93E-13	36.65	410.33	46.30	103056.9
AHQ-2-4, 5534	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	4.30E-05	0.70	3.46	-	296.8
AHQ-2-10, 4836	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	5.20E-06	0.82	4.02	-	907.4
AHQ-2-5, 4629	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.61E-05	0.89	4.69	-	1039.8
AHQ-2-11, 5088 - 5090	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	5.99E-05	0.89	4.91	-	877.5
AHQ-2-1, 5697	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	3.88E-05	0.43	3.24	-	462.5
AHQ-2-9, 5159	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	7.14E-05	0.57	3.77	-	345.6
AHQ-2-5, 5223	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	3.15E-04	0.79	3.98	-	820.1
AHQ-2-9, 4594	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	9.40E-04	0.50	2.70	-	316.0
AHQ-2-6, 5181	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	4.22E-06	0.80	4.39	-	630.1
AHQ-2-5, 5403	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	1.07E-06	0.82	3.71	-	502.3
AHQ-2-9, 6438 - 6510	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	7.75E-04	0.66	3.23	-	327.8
AHQ-2-5, 6407 - 6480	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	5.89E-09	0.93	4.66	-	772.7
AHQ-2-6, 6406	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	2.20E-04	0.77	3.70	-	412.9
AHQ-2-5, 2963	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	4.68E-04	0.92	3.75	-	1194.9
AHQ-2-5, 3240 - 3317	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	4.60E-04	0.70	2.67	-	584.2
AHQ-2-5, 2964 - 2972	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	4.88E-05	0.97	4.73	-	2593.0
AHQ-2-5, 1895	K.ASIHEAWTDGK.E	1215.29697	2	3.94E-05	0.79	3.04	-	882.2
AHQ-2-5, 1803 - 1880	K.ASIHEAWTDGK.E	1215.29697	2	5.19E-05	0.87	3.08	-	1025.9
AHQ-2-1, 5936	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	8.44E-07	0.81	3.46	-	656.7
AHQ-2-5, 5775 - 5855	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.82E-12	0.96	4.94	-	1363.8
AHQ-2-5, 6145	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	9.69E-13	0.96	4.73	-	1124.8
AHQ-2-6, 5646	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.64E-10	0.96	5.03	-	997.5
AHQ-2-4, 5978 - 5984	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.89E-10	0.95	4.84	-	1241.7
AHQ-2-5, 4781 - 4855	K.DGLGFCALIHR.H	1260.44730	2	4.97E-05	0.89	2.91	-	1292.0
AHQ-2-5, 5113	K.DGLGFCALIHR.H	1260.44730	2	1.83E-06	0.92	2.79	-	1428.4
AHQ-2-5, 2225 - 2227	R.DHSGTLGPEEFK.A	1317.38606	1	2.75E-06	0.63	2.80	-	385.6
AHQ-2-6, 2239	R.DHSGTLGPEEFK.A	1317.38606	2	3.22E-05	0.87	3.31	-	753.3
AHQ-2-5, 2223	R.DHSGTLGPEEFK.A	1317.38606	2	3.91E-04	0.91	3.49	-	893.3
AHQ-2-6, 3607	K.DYETATLSEIK.A	1270.36761	2	1.53E-04	0.77	2.53	-	843.2
AHQ-2-4, 4621	R.ETADTDTADQVMASFK.I	1730.83208	2	1.53E-07	0.86	3.40	-	737.5
AHQ-2-3, 4628 - 4635	R.ETADTDTADQVMASFK.I	1730.83208	2	8.67E-09	0.95	4.23	-	1185.3
AHQ-2-9, 4362 - 4376	R.ETADTDTADQVMASFK.I	1730.83208	2	2.30E-07	0.77	3.71	-	476.9
AHQ-2-11, 4237 - 4309	R.ETADTDTADQVMASFK.I	1730.83208	2	5.66E-09	0.88	3.51	-	860.8
AHQ-2-5, 3116 - 3195	R.ETADTDTADQVM*ASFK.I	1746.83148	2	8.42E-06	0.94	4.13	-	1114.2
AHQ-2-2, 4674	R.ETADTDTADQVMASFK.I	1730.83208	2	3.89E-04	0.79	2.86	-	678.1
AHQ-2-13, 4361	R.ETADTDTADQVMASFK.I	1730.83208	2	2.07E-04	0.65	2.92	-	643.1
AHQ-2-13-, 4430	R.ETADTDTADQVMASFK.I	1730.83208	2	2.58E-06	0.95	3.95	-	1396.0
AHQ-2-6, 4337	R.ETADTDTADQVMASFK.I	1730.83208	2	1.60E-05	0.96	4.26	-	1575.6
AHQ-2-1, 4650	R.ETADTDTADQVMASFK.I	1730.83208	2	1.26E-05	0.83	3.31	-	812.7
AHQ-2-5, 4399 - 4473	R.ETADTDTADQVMASFK.I	1730.83208	2	1.42E-05	0.94	3.65	-	1635.3
AHQ-2-5, 2685	K.GISQEQMNEFR.A	1339.45991	1	6.28E-04	0.40	2.41	-	176.5
AHQ-2-6, 2721	K.GISQEQMNEFR.A	1339.45991	2	2.34E-04	0.76	2.89	-	738.3
AHQ-2-5, 2675	K.GISQEQMNEFR.A	1339.45991	1	7.37E-04	0.11	2.12	-	146.8
AHQ-2-9, 2735	K.GISQEQMNEFR.A	1339.45991	2	2.66E-06	0.75	2.70	-	730.8
AHQ-2-5, 2673 - 2681	K.GISQEQMNEFR.A	1339.45991	2	4.37E-08	0.89	3.77	-	801.0
AHQ-2-11, 2845	K.GISQEQMNEFR.A	1339.45991	2	2.92E-05	0.85	3.31	-	816.7
AHQ-2-4, 2016	R.HRPELIDYGK.L	1228.38202	2	1.77E-04	0.89	3.46	-	609.5
AHQ-2-5, 1716	R.HRPELIDYGK.L	1228.38202	2	2.74E-04	0.88	3.26	-	564.5
AHQ-2-5, 1723	R.HRPELIDYGK.L	1228.38202	3	1.13E-04	0.88	3.46	-	801.7
AHQ-2-6, 4853 - 4854	K.ICDQWDNLGALTQK.R	1663.83349	2	2.00E-08	0.97	4.81	-	2339.9
AHQ-2-5, 4877 - 4955	K.ICDQWDNLGALTQK.R	1663.83349	2	8.16E-06	0.97	5.24	-	1948.6

AHQ-2-7, 4872 - 4881	K.ICDQWDNLGALTQK.R	1663.83349	2	3.35E-05	0.93	3.42	-	1742.6
AHQ-2-3, 5149 - 5155	K.ICDQWDNLGALTQK.R	1663.83349	2	3.53E-06	0.97	4.95	-	1758.9
AHQ-2-4, 5141 - 5145	K.ICDQWDNLGALTQK.R	1663.83349	2	9.41E-07	0.97	4.91	-	1914.0
AHQ-2-1, 5144	K.ICDQWDNLGALTQK.R	1663.83349	2	3.25E-07	0.93	3.89	-	1503.0
AHQ-2-5, 5388	K.ICDQWDNLGALTQK.R	1663.83349	2	9.58E-08	0.97	4.11	-	2084.3
AHQ-2-5, 4644	K.ICDQWDNLGALTQK.R	1663.83349	2	9.11E-08	0.93	4.58	-	994.2
AHQ-2-5, 5800 - 5872	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	7.63E-12	0.97	6.02	-	1873.4
AHQ-2-4, 6160	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	8.05E-05	0.90	3.95	-	1113.8
AHQ-2-6, 5793 - 5794	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	4.51E-07	0.96	5.48	-	1376.1
AHQ-2-5, 6032 - 6103	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	1.30E-04	0.93	4.54	-	1361.2
AHQ-2-5, 3941	K.ILAGDKNYITMDELR.R	1753.01353	2	2.89E-07	0.95	4.36	-	1286.4
AHQ-2-5, 3947 - 3955	K.ILAGDKNYITMDELR.R	1753.01353	3	4.21E-05	0.92	4.62	-	820.9
AHQ-2-5, 3248	K.ILAGDKNYITM*DELR.R	1769.01293	2	4.29E-05	0.91	4.38	-	522.7
AHQ-2-5, 2561	R.IMSIVDPNR.L	1045.23840	2	1.48E-04	0.80	3.12	-	623.3
AHQ-2-5, 4807 - 4833	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	2	3.00E-04	0.94	4.07	-	1477.8
AHQ-2-5, 4799 - 4868	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	3	3.11E-09	0.96	5.05	-	1738.7
AHQ-2-5, 4089	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	2	3.70E-08	0.79	3.45	-	432.0
AHQ-2-5, 4784	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	3	1.31E-07	0.77	3.86	-	352.0
AHQ-2-5, 4548 - 4549	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	1.68E-07	0.95	4.86	-	957.7
AHQ-2-5, 4789 - 4797	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	1.03E-05	0.85	3.94	-	524.5
AHQ-2-5, 4640 - 4712	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	3	2.84E-04	0.75	3.69	-	550.7
AHQ-2-5, 4659	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	1.04E-08	0.95	4.84	-	940.6
AHQ-2-5, 4547 - 4568	R.KAGTQIENIEEDFRDGLK.L	2064.24210	3	5.48E-05	0.95	6.56	-	1037.7
AHQ-2-11, 4624	R.KAGTQIENIEEDFRDGLK.L	2064.24210	3	9.37E-05	0.76	4.11	-	732.1
AHQ-2-5, 4520 - 4575	R.KAGTQIENIEEDFRDGLK.L	2064.24210	2	3.33E-04	0.90	4.82	-	1038.2
AHQ-2-4, 5041	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.37E-06	0.95	4.83	-	1050.1
AHQ-2-5, 4761 - 4771	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	5.93E-06	0.97	5.32	-	1335.0
AHQ-2-5, 5001	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	7.16E-05	0.97	5.53	-	1387.9
AHQ-2-4, 4336 - 4398	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	1.88E-04	0.85	3.46	-	755.3
AHQ-2-6, 4025	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	3.24E-04	0.94	4.37	-	1144.9
AHQ-2-5, 4044 - 4051	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	5.83E-06	0.93	4.36	-	979.9
AHQ-2-6, 3001	R.LAILGIHNEVSK.I	1294.52505	2	2.09E-05	0.93	3.74	-	985.5
AHQ-2-5, 3315	R.LAILGIHNEVSK.I	1294.52505	2	6.07E-07	0.92	3.32	-	1118.3
AHQ-2-5, 2933 - 3003	R.LAILGIHNEVSK.I	1294.52505	2	2.33E-07	0.92	3.40	-	1005.7
AHQ-2-5, 2943	R.LAILGIHNEVSK.I	1294.52505	3	2.15E-04	0.64	3.09	-	570.0
AHQ-2-5, 2957	R.LAILGIHNEVSK.I	1294.52505	1	7.34E-06	0.71	3.15	-	423.8
AHQ-2-5, 3521	R.LAILGIHNEVSK.I	1294.52505	1	2.32E-05	0.48	2.10	-	499.9
AHQ-2-5, 5948 - 6019	K.LASDLLEWIR.R	1216.41115	2	7.57E-08	0.98	4.93	-	2339.4
AHQ-2-4, 6313	K.LASDLLEWIR.R	1216.41115	2	5.05E-08	0.96	3.87	-	1490.0
AHQ-2-5, 6056	K.LASDLLEWIR.R	1216.41115	2	2.16E-08	0.97	4.38	-	2093.9
AHQ-2-7, 5921 - 5928	K.LASDLLEWIR.R	1216.41115	2	3.01E-06	0.96	4.20	-	1530.4
AHQ-2-1, 6340 - 6344	K.LASDLLEWIR.R	1216.41115	2	2.11E-07	0.97	4.48	-	1804.7
AHQ-2-6, 5905 - 5909	K.LASDLLEWIR.R	1216.41115	2	9.24E-08	0.97	4.27	-	2212.6
AHQ-2-4, 6924	K.LLETIDQLYLEYAK.R	1712.96427	2	3.25E-08	0.97	4.58	-	1691.9
AHQ-2-1, 6776	K.LLETIDQLYLEYAK.R	1712.96427	2	1.55E-07	0.96	4.53	-	1335.3
AHQ-2-2, 6909 - 6976	K.LLETIDQLYLEYAK.R	1712.96427	2	1.36E-04	0.95	4.03	-	1191.2
AHQ-2-5, 6717 - 6791	K.LLETIDQLYLEYAK.R	1712.96427	2	2.17E-08	0.98	5.96	-	1412.2
AHQ-2-5, 7105	K.LLETIDQLYLEYAK.R	1712.96427	2	2.50E-06	0.92	3.69	-	1081.4
AHQ-2-3, 6860	K.LLETIDQLYLEYAK.R	1712.96427	2	7.19E-04	0.94	3.68	-	1212.8
AHQ-2-5, 5405	K.LLETIDQLYLEYAK.R	1712.96427	2	1.54E-06	0.94	4.18	-	760.2
AHQ-2-7, 6644 - 6653	K.LLETIDQLYLEYAK.R	1712.96427	2	1.13E-05	0.95	3.95	-	1370.7
AHQ-2-5, 6955 - 7023	K.LLETIDQLYLEYAK.R	1712.96427	2	1.21E-06	0.97	4.85	-	1447.9
AHQ-2-14-, 6407 - 6419	K.LLETIDQLYLEYAK.R	1712.96427	2	1.36E-05	0.95	4.12	-	1302.5
AHQ-2-5, 6811 - 6875	K.LLETIDQLYLEYAK.R	1712.96427	2	1.43E-04	0.93	3.46	-	1186.8
AHQ-2-6, 6529 - 6597	K.LLETIDQLYLEYAK.R	1712.96427	2	4.22E-09	0.97	5.01	-	1415.5
AHQ-2-6, 2330 - 2354	R.LSNRPAFMPSEGR.M	1462.65941	2	3.54E-04	0.87	3.52	-	735.9
AHQ-2-1, 3784	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	7.83E-05	0.88	3.74	-	725.2
AHQ-2-5, 3779 - 3807	K.MLDAEDIVGTARPDEK.A	1760.94769	3	8.63E-05	0.79	3.70	-	678.8
AHQ-2-5, 3775 - 3776	K.MLDAEDIVGTARPDEK.A	1760.94769	2	1.99E-08	0.94	4.58	-	995.2
AHQ-2-7, 3692	K.MLDAEDIVGTARPDEK.A	1760.94769	2	9.87E-05	0.83	3.60	-	678.1
AHQ-2-8, 3686	K.MLDAEDIVGTARPDEK.A	1760.94769	3	5.49E-08	0.77	3.59	-	485.5
AHQ-2-6, 3753	K.MLDAEDIVGTARPDEK.A	1760.94769	3	1.27E-04	0.85	3.56	-	766.6
AHQ-2-6, 3719 - 3766	K.MLDAEDIVGTARPDEK.A	1760.94769	2	1.20E-06	0.94	4.62	-	1071.0
AHQ-2-5, 3355	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	7.79E-05	0.86	3.83	-	586.1
AHQ-2-9, 3758	K.MLDAEDIVGTARPDEK.A	1760.94769	2	4.89E-04	0.87	3.68	-	742.3
AHQ-2-4, 4025	K.MLDAEDIVGTARPDEK.A	1760.94769	2	5.95E-06	0.89	3.71	-	900.3
AHQ-2-4, 3620	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	2.77E-04	0.93	4.02	-	998.0
AHQ-2-8, 3683	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.22E-05	0.88	4.26	-	806.1
AHQ-2-6, 5166 - 5245	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	6.36E-05	0.69	2.87	-	656.5
AHQ-2-7, 5555 - 5557	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.80E-06	0.93	4.27	-	901.4
AHQ-2-4, 5912	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	4.27E-05	0.80	3.25	-	760.2
AHQ-2-5, 6159	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.12E-10	0.96	4.83	-	1258.3
AHQ-2-5, 5988	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.36E-07	0.94	4.30	-	1055.5
AHQ-2-6, 5795	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.36E-05	0.96	4.57	-	1217.2
AHQ-2-5, 5876	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.17E-08	0.98	5.25	-	2166.7
AHQ-2-5, 5617	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	7.62E-11	0.98	6.10	-	1273.4
AHQ-2-6, 5071	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	8.16E-08	0.95	4.42	-	906.9
AHQ-2-5, 5560 - 5580	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	7.19E-08	0.94	4.59	-	978.4
AHQ-2-5, 5300 - 5327	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.09E-08	0.97	5.15	-	1608.7
AHQ-2-6, 5533	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	3.66E-08	0.96	4.74	-	1446.7
AHQ-2-5, 5176 - 5180	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.08E-06	0.93	4.66	-	674.6
AHQ-2-6, 5405 - 5471	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.23E-07	0.97	4.93	-	1771.8
AHQ-2-6, 5323	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	9.18E-11	0.95	4.55	-	1140.8
AHQ-2-3, 5887 - 5893	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.61E-04	0.95	4.71	-	856.6
AHQ-2-9, 4388	K.NVNIQNFHISWK.D	1500.68583	2	6.69E-04	0.91	3.57	-	987.4
AHQ-2-5, 3460	K.NYITMDELR.R	1155.30648	2	8.59E-04	0.75	3.02	-	570.3
AHQ-2-5, 4941 - 5011	K.QFGAQANVIGPWIQTK.M	1759.00118	2	4.28E-05	0.83	3.43	-	652.8
AHQ-2-5, 2629 - 2631	R.QKDYETATLSEIK.A	1526.67030	2	1.46E-05	0.66	3.42	-	298.4
AHQ-2-3, 4011 - 4020	R.TINEVENQILTR.D	1430.58898	2	7.90E-06	0.87	3.71	-	876.6
AHQ-2-4, 3997	R.TINEVENQILTR.D	1430.58898	2	2.56E-05	0.93	4.16	-	1181.1
AHQ-2-6, 3726 - 3731	R.TINEVENQILTR.D	1430.58898	2	9.70E-08	0.86	3.72	-	889.5
AHQ-2-2, 4050	R.TINEVENQILTR.D	1430.58898	2	2.43E-06	0.81	3.41	-	704.6
AHQ-2-5, 3728 - 3743	R.TINEVENQILTR.D	1430.58898	2	1.59E-06	0.92	4.02	-	995.4
AHQ-2-10, 3606 - 3631	R.TINEVENQILTR.D	1430.58898	2	2.65E-05	0.88	3.50	-	1024.6
AHQ-2-5, 3936 - 4007	R.TINEVENQILTR.D	1430.58898	1	4.46E-06	0.29	2.07	-	262.0
AHQ-2-5, 3400 - 3428	R.TINEVENQILTR.D	1430.58898	2	2.65E-04	0.73	3.29	-	465.9
AHQ-2-7, 3672	R.TINEVENQILTR.D	1430.58898	2	4.48E-04	0.81	3.13	-	751.5
AHQ-2-5, 3737	R.TINEVENQILTR.D	1430.58898	1	4.83E-04	0.14	2.30	-	148.4
AHQ-2-5, 7091 - 7156	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	8.62E-05	0.97	6.14	-	1856.0
AHQ-2-1, 7108	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	8.72E-08	0.96	5.74	-	1309.1
AHQ-2-5, 7219 - 7223	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	2.64E-05	0.94	4.91	-	1397.2
AHQ-2-7, 6548	R.VGWEQLLTTIAR.T	1387.60894	2	6.37E-06	0.93	4.15	-	1121.3
AHQ-2-1, 6904	R.VGWEQLLTTIAR.T	1387.60894	2	8.08E-07	0.90	3.77	-	894.6
AHQ-2-5, 6647 - 6725	R.VGWEQLLTTIAR.T	1387.60894	2	4.59E-07	0.97	4.97	-	1704.7
AHQ-2-6, 6571 - 6591	R.VGWEQLLTTIAR.T	1387.60894	2	1.66E-06	0.95	3.81	-	1618.7
AHQ-2-11, 6306 - 6322	R.VGWEQLLTTIAR.T	1387.60894	2	1.85E-06	0.95	3.98	-	1299.1
AHQ-2-2, 7005 - 7006	R.VGWEQLLTTIAR.T	1387.60894	2	3.42E-08	0.96	4.78	-	1509.8

AHQ-2-4, 7000	R.VGWEQLLTTIAR.T	1387.60894	2	9.39E-08	0.95	3.88	-	1419.4
AHQ-2-10, 6139	R.VGWEQLLTTIAR.T	1387.60894	2	3.18E-06	0.88	3.28	-	1112.8
AHQ-2-9, 6678 - 6690	R.VGWEQLLTTIAR.T	1387.60894	2	2.90E-07	0.96	4.69	-	1438.2
AHQ-2-3, 6949	R.VGWEQLLTTIAR.T	1387.60894	2	3.52E-07	0.94	3.76	-	1393.9
AHQ-2-14-, 6507	R.VGWEQLLTTIAR.T	1387.60894	2	1.66E-06	0.93	3.55	-	1376.7
AHQ-2-5, 4231 - 4300	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.08E-06	0.94	5.04	-	801.7
AHQ-2-5, 4541 - 4612	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.93E-13	0.97	5.71	-	1283.8
AHQ-2-5, 4176	K.VLAVNQENEQLMEDYEK.L	2053.23635	3	5.90E-11	0.93	4.51	-	1038.2
AHQ-2-6, 4465	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.38E-09	0.95	4.56	-	1082.6
AHQ-2-3, 4431	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	5.30E-06	0.88	3.78	-	889.4
AHQ-2-9, 4098 - 4176	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	5.31E-06	0.85	3.78	-	626.4
AHQ-2-6, 4087	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.98E-08	0.96	5.45	-	928.0
AHQ-2-5, 4093 - 4163	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.15E-06	0.95	5.09	-	877.8
AHQ-2-2, 4485	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.30E-07	0.93	4.39	-	1133.9
AHQ-2-6, 3419 - 3426	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.76E-06	0.96	4.98	-	1169.6
AHQ-2-8, 3892	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	9.04E-09	0.95	5.05	-	1068.2
AHQ-2-5, 3417 - 3431	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.12E-07	0.97	5.56	-	1337.4
AHQ-2-5, 3665	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.45E-08	0.95	4.41	-	1049.2
AHQ-2-1, 4500	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.51E-06	0.97	5.10	-	1500.7
AHQ-2-5, 4377 - 4447	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.83E-09	0.97	5.49	-	1673.4
gi|4505981|ref|NP_002695.1| pro-platelet basic protein (includes platelet basic protein, bet; Pro-p				3.11E-13	7.76	90.33	40.60	13894.1
AHQ-2-14-, 5097 - 5173	K.EESLDSDLYAELR.C	1540.61070	2	6.17E-04	0.58	2.96	-	504.4
AHQ-2-14-, 4771 - 4839	K.EESLDSDLYAELR.C	1540.61070	2	1.02E-07	0.94	4.14	-	986.4
AHQ-2-14, 5833 - 5896	K.EESLDSDLYAELR.C	1540.61070	2	2.59E-07	0.95	4.01	-	1181.5
AHQ-2-14-, 4428	K.EESLDSDLYAELR.C	1540.61070	2	1.29E-06	0.75	2.98	-	389.2
AHQ-2-14-, 4431 - 4495	K.GKEESLDSDLYAELR.C	1725.83517	2	1.75E-10	0.98	5.62	-	2889.5
AHQ-2-14-, 4560 - 4623	K.GKEESLDSDLYAELR.C	1725.83517	2	4.94E-12	0.98	4.82	-	2295.6
AHQ-2-13, 4173 - 4175	K.GKEESLDSDLYAELR.C	1725.83517	2	6.76E-11	0.98	5.87	-	2484.8
AHQ-2-13, 4184	K.GKEESLDSDLYAELR.C	1725.83517	3	1.43E-04	0.91	4.28	-	1013.3
AHQ-2-14-, 4373 - 4436	K.GKEESLDSDLYAELR.C	1725.83517	3	1.35E-04	0.88	3.91	-	955.3
AHQ-2-14-, 4304	K.GKEESLDSDLYAELR.C	1725.83517	2	2.07E-11	0.98	5.60	-	2745.5
AHQ-2-14-, 4289 - 4368	K.GKEESLDSDLYAELR.C	1725.83517	2	2.19E-11	0.99	6.47	-	2861.7
AHQ-2-14-, 4219 - 4279	K.GKEESLDSDLYAELR.C	1725.83517	3	1.32E-04	0.92	4.50	-	1138.6
AHQ-2-14-, 4176 - 4240	K.GKEESLDSDLYAELR.C	1725.83517	2	3.11E-13	0.98	5.13	-	2478.0
AHQ-2-14-, 4104 - 4163	K.GKEESLDSDLYAELR.C	1725.83517	3	1.55E-07	0.94	4.77	-	1426.9
AHQ-2-14-, 4688	K.GKEESLDSDLYAELR.C	1725.83517	2	9.89E-08	0.97	4.88	-	2183.8
AHQ-2-14-, 3971 - 4041	K.GKEESLDSDLYAELR.C	1725.83517	3	5.06E-08	0.93	4.83	-	1159.3
AHQ-2-14-, 3895 - 3975	K.GKEESLDSDLYAELR.C	1725.83517	2	3.31E-12	0.98	6.54	-	2565.3
AHQ-2-14-, 3879 - 3955	K.GKEESLDSDLYAELR.C	1725.83517	3	2.54E-05	0.92	5.17	-	757.3
AHQ-2-14-, 3864 - 3903	K.GKEESLDSDLYAELR.C	1725.83517	2	5.28E-11	0.97	5.05	-	1751.5
AHQ-2-13-, 4242 - 4247	K.GKEESLDSDLYAELR.C	1725.83517	3	9.23E-10	0.91	4.58	-	955.1
AHQ-2-13-, 4239	K.GKEESLDSDLYAELR.C	1725.83517	2	1.40E-11	0.98	5.60	-	2349.5
AHQ-2-13-, 4029	K.GKEESLDSDLYAELR.C	1725.83517	2	3.85E-07	0.95	4.42	-	1261.7
AHQ-2-14, 6458	K.GKEESLDSDLYAELR.C	1725.83517	2	3.16E-07	0.92	3.90	-	1185.3
AHQ-2-14, 6188 - 6244	K.GKEESLDSDLYAELR.C	1725.83517	2	3.43E-05	0.97	4.95	-	1865.1
AHQ-2-14, 6089 - 6166	K.GKEESLDSDLYAELR.C	1725.83517	2	3.08E-04	0.97	5.16	-	1764.0
AHQ-2-14, 6040 - 6101	K.GKEESLDSDLYAELR.C	1725.83517	2	1.25E-05	0.97	4.16	-	2571.2
AHQ-2-14, 5937 - 6009	K.GKEESLDSDLYAELR.C	1725.83517	2	1.02E-06	0.97	4.71	-	2062.1
AHQ-2-14-, 4044 - 4115	K.GKEESLDSDLYAELR.C	1725.83517	2	2.16E-11	0.98	5.53	-	2304.4
AHQ-2-14, 5805 - 5854	K.GKEESLDSDLYAELR.C	1725.83517	2	3.12E-09	0.98	5.19	-	2453.6
AHQ-2-14, 5672 - 5732	K.GKEESLDSDLYAELR.C	1725.83517	2	2.59E-07	0.98	5.11	-	2403.4
AHQ-2-14, 5556 - 5612	K.GKEESLDSDLYAELR.C	1725.83517	2	5.45E-12	0.98	5.16	-	2737.1
AHQ-2-14, 5469	K.GKEESLDSDLYAELR.C	1725.83517	3	5.18E-04	0.79	3.71	-	827.1
AHQ-2-14, 4816 - 4876	K.GKEESLDSDLYAELR.C	1725.83517	2	5.12E-09	0.98	5.45	-	1880.9
AHQ-2-14, 4828 - 4896	K.GKEESLDSDLYAELR.C	1725.83517	3	3.14E-06	0.91	4.08	-	1064.2
AHQ-2-14, 5412 - 5492	K.GKEESLDSDLYAELR.C	1725.83517	2	4.23E-09	0.98	6.04	-	2277.3
AHQ-2-14, 4936 - 5001	K.GKEESLDSDLYAELR.C	1725.83517	2	2.51E-10	0.98	5.43	-	2225.4
AHQ-2-14, 4958 - 5036	K.GKEESLDSDLYAELR.C	1725.83517	3	6.83E-04	0.85	3.85	-	892.4
AHQ-2-14, 5333 - 5401	K.GKEESLDSDLYAELR.C	1725.83517	3	2.08E-05	0.87	4.12	-	829.1
AHQ-2-14, 5324 - 5388	K.GKEESLDSDLYAELR.C	1725.83517	2	6.15E-10	0.98	5.10	-	2716.9
AHQ-2-14, 5062 - 5129	K.GKEESLDSDLYAELR.C	1725.83517	3	1.89E-05	0.87	4.01	-	1135.7
AHQ-2-14, 5064 - 5137	K.GKEESLDSDLYAELR.C	1725.83517	2	8.69E-09	0.98	5.88	-	2398.0
AHQ-2-14, 5277 - 5340	K.GKEESLDSDLYAELR.C	1725.83517	3	4.30E-05	0.95	4.45	-	1631.8
AHQ-2-14, 5200 - 5281	K.GKEESLDSDLYAELR.C	1725.83517	2	1.98E-08	0.98	5.44	-	2463.3
AHQ-2-14, 5192 - 5268	K.GKEESLDSDLYAELR.C	1725.83517	3	2.54E-04	0.94	4.86	-	1352.2
AHQ-2-14, 5177 - 5249	K.GTHCNQVEVIATLK.D	1571.78073	2	3.08E-08	0.95	3.46	-	1819.4
AHQ-2-14-, 4799 - 4871	K.GTHCNQVEVIATLK.D	1571.78073	2	9.22E-05	0.92	4.04	-	852.0
AHQ-2-13, 3300 - 3376	K.GTHCNQVEVIATLK.D	1571.78073	2	5.30E-05	0.83	3.37	-	600.4
AHQ-2-14, 5312 - 5378	K.GTHCNQVEVIATLK.D	1571.78073	2	7.65E-06	0.92	3.88	-	1047.8
AHQ-2-14, 5050 - 5117	K.GTHCNQVEVIATLK.D	1571.78073	2	1.68E-05	0.97	4.83	-	1666.5
AHQ-2-14, 4970	K.GTHCNQVEVIATLK.D	1571.78073	3	8.53E-05	0.71	3.55	-	947.9
AHQ-2-14, 4916 - 4961	K.GTHCNQVEVIATLK.D	1571.78073	2	2.32E-06	0.96	4.56	-	1458.8
AHQ-2-14, 5440 - 5510	K.GTHCNQVEVIATLK.D	1571.78073	2	1.53E-05	0.96	4.62	-	1317.7
AHQ-2-14, 4796 - 4857	K.GTHCNQVEVIATLK.D	1571.78073	2	1.13E-09	0.96	4.65	-	1342.7
AHQ-2-14, 5552 - 5617	K.GTHCNQVEVIATLK.D	1571.78073	2	3.02E-06	0.93	3.91	-	1237.4
AHQ-2-14, 4660 - 4740	K.GTHCNQVEVIATLK.D	1571.78073	2	2.10E-11	0.97	4.86	-	1501.8
AHQ-2-14-, 4601	K.GTHCNQVEVIATLK.D	1571.78073	2	3.93E-05	0.96	3.92	-	1720.0
AHQ-2-14, 5681	K.GTHCNQVEVIATLK.D	1571.78073	2	1.47E-04	0.94	4.39	-	899.2
AHQ-2-14, 4536 - 4616	K.GTHCNQVEVIATLK.D	1571.78073	2	2.57E-08	0.98	5.39	-	1700.5
AHQ-2-14, 5822 - 5846	K.GTHCNQVEVIATLK.D	1571.78073	2	9.67E-06	0.95	4.24	-	1364.0
AHQ-2-14-, 3403 - 3476	K.GTHCNQVEVIATLK.D	1571.78073	2	7.15E-07	0.97	4.96	-	1611.7
AHQ-2-14, 4469 - 4540	K.GTHCNQVEVIATLK.D	1571.78073	2	5.01E-09	0.97	4.83	-	1956.1
AHQ-2-14, 5982 - 6045	K.GTHCNQVEVIATLK.D	1571.78073	2	4.72E-09	0.96	4.58	-	1504.6
AHQ-2-14, 4356 - 4420	K.GTHCNQVEVIATLK.D	1571.78073	2	2.10E-08	0.97	4.49	-	2149.0
AHQ-2-13, 3420	K.GTHCNQVEVIATLK.D	1571.78073	2	2.24E-04	0.94	3.83	-	1365.0
AHQ-2-14, 4224 - 4292	K.GTHCNQVEVIATLK.D	1571.78073	2	1.05E-07	0.97	4.79	-	1420.7
AHQ-2-14, 6304 - 6320	K.GTHCNQVEVIATLK.D	1571.78073	2	7.96E-04	0.87	3.24	-	1089.0
AHQ-2-14-, 3531 - 3552	K.GTHCNQVEVIATLK.D	1571.78073	2	3.57E-09	0.98	5.22	-	1808.7
AHQ-2-14, 6480	K.GTHCNQVEVIATLK.D	1571.78073	2	5.60E-04	0.89	3.68	-	850.1
AHQ-2-13, 3504	K.GTHCNQVEVIATLK.D	1571.78073	2	3.10E-06	0.92	4.08	-	1026.5
AHQ-2-14-, 4393 - 4460	K.GTHCNQVEVIATLK.D	1571.78073	2	8.36E-12	0.96	4.82	-	1422.4
AHQ-2-14-, 4247 - 4311	K.GTHCNQVEVIATLK.D	1571.78073	2	2.05E-06	0.98	5.33	-	1706.0
AHQ-2-14-, 4119 - 4184	K.GTHCNQVEVIATLK.D	1571.78073	2	2.53E-09	0.97	4.91	-	1480.6
AHQ-2-13-, 3358	K.GTHCNQVEVIATLK.D	1571.78073	2	1.35E-07	0.94	3.97	-	1187.0
AHQ-2-13-, 3491	K.GTHCNQVEVIATLK.D	1571.78073	2	1.01E-06	0.95	4.30	-	1211.2
AHQ-2-14-, 3269 - 3340	K.GTHCNQVEVIATLK.D	1571.78073	2	5.33E-08	0.98	4.90	-	1918.2
AHQ-2-14-, 3987 - 4059	K.GTHCNQVEVIATLK.D	1571.78073	2	1.23E-07	0.97	5.31	-	1575.3
AHQ-2-14-, 3615 - 3695	K.GTHCNQVEVIATLK.D	1571.78073	2	4.72E-09	0.98	5.05	-	2059.1
AHQ-2-14-, 3623 - 3701	K.GTHCNQVEVIATLK.D	1571.78073	3	1.12E-04	0.94	4.30	-	1572.4
AHQ-2-14-, 3763 - 3840	K.GTHCNQVEVIATLK.D	1571.78073	2	5.62E-10	0.98	5.54	-	2048.8
AHQ-2-14, 4084 - 4156	K.GTHCNQVEVIATLK.D	1571.78073	2	1.50E-05	0.97	4.64	-	1865.2
AHQ-2-14-, 3855 - 3921	K.GTHCNQVEVIATLK.D	1571.78073	2	5.63E-07	0.97	4.62	-	1735.9
AHQ-2-14-, 3387 - 3464	K.GTHCNQVEVIATLK.D	1571.78073	3	9.93E-04	0.90	4.39	-	1100.6
AHQ-2-14-, 3628	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	6.33E-07	0.94	4.35	-	1282.0
AHQ-2-14-, 2935 - 3012	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.85E-09	0.95	4.76	-	1206.8
AHQ-2-14-, 2940 - 3021	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	2.10E-08	0.98	5.20	-	1871.3
AHQ-2-14, 4010 - 4076	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.79E-07	0.92	4.01	-	905.6

AHQ-2-14, 3802 - 3869	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	3.19E-04	0.86	3.60	-	705.1
AHQ-2-14, 4161	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.17E-06	0.96	5.31	-	1321.5
AHQ-2-14, 4168	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	8.08E-10	0.97	4.90	-	1653.0
AHQ-2-14, 4533	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	9.52E-07	0.76	3.19	-	795.1
AHQ-2-14-, 3335	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.00E-05	0.87	3.90	-	750.4
AHQ-2-14, 4069	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	6.52E-07	0.96	5.04	-	1113.0
AHQ-2-14-, 2676	K.GTHCNQVEVIATLKDGRK.I	2028.27941	2	7.61E-05	0.94	4.82	-	710.4
AHQ-2-14-, 2668 - 2677	K.GTHCNQVEVIATLKDGRK.I	2028.27941	3	6.29E-04	0.89	3.91	-	1100.8
AHQ-2-13, 2932	K.ICLDPDAPR.I	1058.19059	2	1.12E-05	0.77	2.83	-	811.7
AHQ-2-13-, 2873 - 2877	K.ICLDPDAPR.I	1058.19059	2	2.38E-04	0.79	2.98	-	830.5
AHQ-2-14, 3669 - 3734	K.ICLDPDAPR.I	1058.19059	2	2.54E-05	0.79	2.90	-	908.5
AHQ-2-14-, 2916 - 2917	K.ICLDPDAPR.I	1058.19059	2	1.41E-04	0.87	3.02	-	1078.0
AHQ-2-14-, 2771 - 2820	K.ICLDPDAPR.I	1058.19059	2	6.68E-04	0.88	3.03	-	993.1
AHQ-2-14, 3013 - 3068	R.KICLDPDAPR.I	1186.36350	2	8.83E-06	0.63	2.89	-	522.4
AHQ-2-13-, 2567 - 2614	R.KICLDPDAPR.I	1186.36350	2	1.95E-06	0.92	3.39	-	1010.5
AHQ-2-14-, 2573	R.KICLDPDAPR.I	1186.36350	2	5.97E-04	0.86	3.18	-	858.6
AHQ-2-14-, 2445 - 2511	R.KICLDPDAPR.I	1186.36350	2	3.06E-05	0.85	3.15	-	809.6
AHQ-2-14, 3220 - 3282	R.KICLDPDAPR.I	1186.36350	2	2.60E-05	0.82	3.01	-	895.9
AHQ-2-14, 3340 - 3400	R.KICLDPDAPR.I	1186.36350	2	2.19E-05	0.87	3.66	-	707.0
AHQ-2-14, 3762 - 3825	R.KICLDPDAPR.I	1186.36350	2	1.62E-04	0.76	3.11	-	754.5
AHQ-2-14, 3674 - 3676	R.KICLDPDAPR.I	1186.36350	2	5.56E-05	0.67	2.87	-	527.7
AHQ-2-13, 2663	R.KICLDPDAPR.I	1186.36350	2	2.94E-06	0.84	3.33	-	785.8
AHQ-2-14, 1789	K.KLAGDESAD	905.92969	1	8.57E-04	0.39	1.98	-	441.5
AHQ-2-14, 4118 - 4188	K.NIQSLEVIGK.G	1101.27845	2	2.85E-06	0.94	3.86	-	1110.6
AHQ-2-13-, 3313	K.NIQSLEVIGK.G	1101.27845	2	2.23E-06	0.86	3.56	-	704.3
AHQ-2-14, 4090 - 4164	K.NIQSLEVIGK.G	1101.27845	2	1.52E-05	0.85	3.50	-	653.4
AHQ-2-14-, 3081 - 3143	K.NIQSLEVIGK.G	1101.27845	2	6.21E-06	0.87	3.51	-	728.7
AHQ-2-14-, 4180	K.NIQSLEVIGK.G	1101.27845	2	1.50E-04	0.93	3.10	-	1538.2
AHQ-2-13-, 3321	K.NIQSLEVIGK.G	1101.27845	1	7.56E-04	0.36	2.58	-	207.0
AHQ-2-14-, 3111 - 3171	K.NIQSLEVIGK.G	1101.27845	2	9.60E-06	0.86	3.63	-	653.9
AHQ-2-14-, 3289 - 3351	K.NIQSLEVIGK.G	1101.27845	2	2.70E-06	0.91	3.87	-	821.1
AHQ-2-14, 4252 - 4320	K.NIQSLEVIGK.G	1101.27845	2	1.78E-06	0.87	3.71	-	629.4
AHQ-2-13, 3340	K.NIQSLEVIGK.G	1101.27845	2	8.14E-06	0.85	3.33	-	762.9
AHQ-2-14, 4618 - 4682	K.NIQSLEVIGK.G	1101.27845	2	3.30E-04	0.83	3.26	-	757.6
AHQ-2-14, 5140 - 5205	K.NIQSLEVIGK.G	1101.27845	1	8.95E-04	0.71	2.59	-	653.4
AHQ-2-14-, 3416 - 3483	K.NIQSLEVIGK.G	1101.27845	2	3.82E-04	0.86	3.29	-	758.1
AHQ-2-14, 5141 - 5214	K.NIQSLEVIGK.G	1101.27845	2	9.03E-05	0.84	3.08	-	992.0
AHQ-2-14-, 3331	K.NIQSLEVIGK.G	1101.27845	2	1.06E-06	0.89	3.68	-	777.4
gi|4506877|ref|NP_002996.1| selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;				3.18E-13	5.28	60.32	11.10	90844.7
AHQ-2-3, 4760 - 4761	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	3.18E-13	0.94	4.44	-	787.4
AHQ-2-2, 4810 - 4868	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	3.17E-06	0.94	4.36	-	802.2
AHQ-2-3, 6089	K.LECLASGIWTNKPPQCLAAQCPPLK.I	2857.31818	3	3.55E-04	0.73	3.23	-	966.7
AHQ-2-3, 6308	K.LECLASGIWTNKPPQCLAAQCPPLKIPER.G	3352.89300	3	1.13E-05	0.97	6.47	-	1317.1
AHQ-2-2, 3081	R.PSGQWTAVTPACR.A	1432.58672	2	1.15E-07	0.95	4.06	-	1131.9
AHQ-2-3, 5077	K.STCQFICDEGYSLSGPER.L	2109.23671	2	6.89E-08	0.91	3.73	-	973.0
AHQ-2-2, 5126	K.STCQFICDEGYSLSGPER.L	2109.23671	2	3.43E-08	0.86	3.63	-	680.3
AHQ-2-1, 5052	K.STCQFICDEGYSLSGPER.L	2109.23671	2	1.15E-06	0.93	4.53	-	853.8
AHQ-2-4, 5092	K.STCQFICDEGYSLSGPER.L	2109.23671	2	4.06E-08	0.91	4.02	-	798.4
AHQ-2-3, 6508	K.VLPYYSSYYWIGIR.K	1781.04522	2	7.75E-08	0.83	3.64	-	463.2
gi|5031635|ref|NP_005498.1| cofilin 1 (non-muscle) [Homo sapiens]				3.53E-13	10.16	110.39	59.60	18502.4
AHQ-2-13, 3495 - 3499	K.AVLFCLSEDKK.N	1311.52930	2	5.41E-05	0.54	2.60	-	499.5
AHQ-2-13-, 3493 - 3494	K.AVLFCLSEDKK.N	1311.52930	2	8.21E-07	0.88	3.13	-	832.6
AHQ-2-12, 3297 - 3366	K.AVLFCLSEDKK.N	1311.52930	2	8.75E-05	0.88	2.97	-	799.2
AHQ-2-12, 7090	K.EDLVFIFWAPESAPLK.S	1863.14454	2	3.78E-06	0.96	4.35	-	1482.8
AHQ-2-13, 5607	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	8.88E-09	0.97	5.10	-	1345.4
AHQ-2-11, 5533	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.01E-05	0.96	4.82	-	1219.7
AHQ-2-12, 5867 - 5933	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.53E-13	0.97	5.48	-	1251.6
AHQ-2-12, 5730 - 5798	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.76E-12	0.98	5.78	-	1630.3
AHQ-2-13-, 5706 - 5737	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	9.53E-07	0.97	5.60	-	1449.3
AHQ-2-12, 5506	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.14E-06	0.88	3.63	-	911.6
AHQ-2-14-, 5683 - 5684	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	8.41E-08	0.97	5.99	-	1266.5
AHQ-2-12, 5622 - 5695	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	7.69E-08	0.97	5.14	-	1327.6
AHQ-2-12, 6055 - 6117	K.ESKKEDLVFIFWAPESAPLK.S	2335.68256	3	6.45E-04	0.85	4.14	-	672.1
AHQ-2-12, 2317 - 2382	K.HELQANCYEEVKDR.C	1792.90812	3	2.70E-12	0.98	5.83	-	2182.8
AHQ-2-12, 2415 - 2494	K.HELQANCYEEVKDR.C	1792.90812	2	9.87E-04	0.63	3.20	-	169.5
AHQ-2-13-, 2449	K.HELQANCYEEVKDR.C	1792.90812	2	5.13E-04	0.95	4.07	-	1328.6
AHQ-2-13-, 2446	K.HELQANCYEEVKDR.C	1792.90812	3	6.11E-07	0.95	4.84	-	1397.2
AHQ-2-12, 2274 - 2342	K.HELQANCYEEVKDR.C	1792.90812	2	1.78E-10	0.98	5.45	-	1959.9
AHQ-2-12, 2805	K.KAVLFCLSEDKK.N	1439.70221	1	3.69E-07	0.66	3.08	-	391.4
AHQ-2-12, 2797	K.KAVLFCLSEDKK.N	1439.70221	1	1.18E-05	0.48	2.45	-	609.1
AHQ-2-12, 6726	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	8.87E-06	0.91	4.10	-	856.1
AHQ-2-14-, 6467	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.11E-08	0.96	4.69	-	1212.0
AHQ-2-13-, 6618	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	2.80E-06	0.97	5.86	-	1459.8
AHQ-2-11, 6278 - 6356	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.21E-04	0.93	4.31	-	789.3
AHQ-2-13-, 6605	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	5.38E-07	0.97	5.91	-	1491.9
AHQ-2-13, 6379	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	5.79E-04	0.96	4.71	-	1125.3
AHQ-2-12, 6666	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	8.36E-05	0.95	5.21	-	1132.7
AHQ-2-12, 6493 - 6553	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	1.35E-10	0.98	5.50	-	1719.4
AHQ-2-12, 6494 - 6570	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	1.37E-09	0.97	5.70	-	1603.9
AHQ-2-12, 6581 - 6657	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	4.76E-09	0.98	5.69	-	1601.4
AHQ-2-12, 6626	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.88E-09	0.97	5.65	-	1366.0
AHQ-2-12, 6586 - 6593	K.KNIILEEGKEILVGDVGQTVDDPYATFVK.M	3192.60499	3	6.49E-09	0.98	7.79	-	2450.0
AHQ-2-12, 4029	K.LGGSAVISLEGKPL	1341.57848	2	5.49E-08	0.95	3.95	-	1589.3
AHQ-2-12, 5058 - 5121	K.LGGSAVISLEGKPL	1341.57848	2	2.60E-04	0.90	3.61	-	833.8
AHQ-2-12, 4331 - 4405	K.LGGSAVISLEGKPL	1341.57848	2	2.10E-06	0.96	4.29	-	1401.0
AHQ-2-12, 4961	K.LGGSAVISLEGKPL	1341.57848	2	9.08E-06	0.93	3.84	-	1153.6
AHQ-2-12, 4469 - 4545	K.LGGSAVISLEGKPL	1341.57848	2	2.54E-10	0.97	5.35	-	1264.2
AHQ-2-12, 4822 - 4894	K.LGGSAVISLEGKPL	1341.57848	2	8.51E-07	0.95	4.72	-	1073.3
AHQ-2-12, 4705 - 4773	K.LGGSAVISLEGKPL	1341.57848	2	7.20E-07	0.97	5.35	-	1292.6
AHQ-2-12, 4566 - 4637	K.LGGSAVISLEGKPL	1341.57848	2	4.66E-06	0.96	5.01	-	1289.8
AHQ-2-13, 6619	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	6.92E-08	0.97	7.08	-	1598.1
AHQ-2-12, 7217 - 7281	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	3.42E-09	0.98	7.15	-	1564.4
AHQ-2-12, 6949 - 7005	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	4.62E-11	0.98	7.07	-	2027.6
AHQ-2-1, 7113 - 7126	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	9.99E-04	0.88	3.72	-	1120.0
AHQ-2-13-, 6837 - 6838	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.49E-11	0.98	7.85	-	1614.7
AHQ-2-11, 6545 - 6612	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.90E-07	0.94	4.99	-	1238.9
AHQ-2-14-, 6691 - 6763	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.24E-09	0.96	5.45	-	1367.2
AHQ-2-12, 3118 - 3181	R.YALYDATYETK.E	1338.44364	1	7.39E-07	0.63	2.95	-	342.5
AHQ-2-12, 3117 - 3153	R.YALYDATYETK.E	1338.44364	2	4.77E-08	0.95	3.54	-	1189.7
AHQ-2-12, 3085 - 3158	R.YALYDATYETK.E	1338.44364	2	1.51E-07	0.92	3.40	-	973.6
AHQ-2-12, 3346	R.YALYDATYETK.E	1338.44364	2	2.27E-06	0.90	2.80	-	1062.9
AHQ-2-13, 3295	R.YALYDATYETK.E	1338.44364	1	2.03E-07	0.53	2.65	-	328.4
gi|4758638|ref|NP_004896.1| peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi				3.73E-13	8.23	110.29	48.20	25034.8
AHQ-2-10, 4035	K.DGDSVM*VLPTIPEEEAK.K	1847.03409	2	6.55E-06	0.56	2.91	-	440.2
AHQ-2-10, 2588 - 2590	K.DINAYNCEEPTEK.L	1584.64363	2	9.73E-05	0.88	3.39	-	878.9
AHQ-2-10, 2483 - 2487	K.DINAYNCEEPTEK.L	1584.64363	2	1.17E-06	0.89	3.69	-	721.7
AHQ-2-10, 5354	K.DINAYNCEEPTEKLPFPIIDDR.N	2651.88650	3	6.66E-05	0.87	3.74	-	881.5

AHQ-2-10, 5454	K.DINAYNCEEPTEKLPFPIIDDR.N	2651.88650	2	6.31E-05	0.31	2.58	-	213.0
AHQ-2-10, 5819 - 5895	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	2.71E-04	0.93	4.14	-	977.9
AHQ-2-12, 6257	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	7.20E-05	0.79	3.38	-	596.0
AHQ-2-10, 5699 - 5758	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	3.43E-06	0.96	4.78	-	1197.6
AHQ-2-10, 5998	R.FHDFLGDSWGILFSHPR.D	2032.24831	3	4.49E-09	0.96	4.91	-	1462.5
AHQ-2-10, 5995 - 6059	R.FHDFLGDSWGILFSHPR.D	2032.24831	2	1.13E-05	0.98	5.86	-	2124.4
AHQ-2-10, 6122	R.FHDFLGDSWGILFSHPR.D	2032.24831	2	4.26E-06	0.97	5.22	-	1462.8
AHQ-2-14-, 5968	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	3.73E-13	0.98	5.34	-	2020.7
AHQ-2-10, 5572 - 5647	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	1.30E-08	0.97	4.83	-	1607.3
AHQ-2-14-, 5979	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	9.04E-05	0.36	3.09	-	213.3
AHQ-2-10, 5747	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	4.63E-04	0.85	3.26	-	805.2
AHQ-2-10, 4143 - 4154	K.LPFPIIDDR.N	1086.26548	2	3.46E-05	0.91	3.26	-	825.4
AHQ-2-10, 5311	R.VATPVDWKDGDSVMVLPTIPEEEAK.K	2728.06777	2	4.48E-04	0.82	4.05	-	399.3
AHQ-2-10, 5214 - 5287	R.VATPVDWKDGDSVMVLPTIPEEEAK.K	2728.06777	2	1.22E-04	0.65	2.97	-	429.7
AHQ-2-10, 4735 - 4803	R.VATPVDWKDGDSVM*VLPTIPEEEAK.K	2744.06717	3	2.63E-04	0.35	3.02	-	205.3
AHQ-2-10, 3482 - 3484	R.VVFVFGPDK.K	1008.19471	1	1.36E-04	0.58	2.10	-	776.6
AHQ-2-10, 3502	R.VVFVFGPDK.K	1008.19471	2	3.25E-07	0.80	2.71	-	602.8
AHQ-2-10, 2682	R.VVFVFGPDKK.L	1136.36763	2	2.34E-05	0.88	3.18	-	890.4
gi|10863977|ref|NP_067000.1| LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-				3.96E-13	1.68	20.26	40.00	10834.5
AHQ-2-14-, 6707	K.NDLSICGTLHSVDQYLNIK.L	2192.43507	2	2.27E-07	0.94	4.38	-	999.4
AHQ-2-14-, 6709	K.NDLSICGTLHSVDQYLNIK.L	2192.43507	3	1.24E-07	0.76	3.47	-	478.4
AHQ-2-14-, 5420 - 5423	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	4.36E-09	0.97	5.26	-	1459.9
AHQ-2-14, 6508	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	3.96E-13	0.93	3.91	-	1268.2
AHQ-2-14, 6249	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	8.62E-05	0.57	2.61	-	525.3
gi|24431935|ref|NP_065393.1| reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sap				4.87E-13	0.97	10.30	2.80	129930.3
AHQ-2-14-, 6089	K.YQFVREPEDEEEEEEEEEDEDEDLEELEVLER.K	4189.14063	3	4.87E-13	0.97	6.06	-	1640.6
gi|13562114|ref|NP_110400.1| beta tubulin 1, class VI [Homo sapiens]				5.25E-13	20.69	230.36	57.40	50326.6
AHQ-2-1, 6625	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.80E-04	0.93	4.00	-	1221.2
AHQ-2-10, 5863	R.ALSVAELTQQMFDAR.N	1680.90740	2	6.94E-05	0.93	4.18	-	1450.3
AHQ-2-9, 6334	R.ALSVAELTQQMFDAR.N	1680.90740	2	7.00E-08	0.94	4.34	-	1194.1
AHQ-2-14-, 6225 - 6295	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.16E-04	0.82	2.99	-	1045.2
AHQ-2-9, 4567 - 4568	R.ALSVAELTQQM*FDAR.N	1696.90680	2	1.86E-05	0.90	3.81	-	994.0
AHQ-2-8, 6170 - 6188	R.ALSVAELTQQMFDAR.N	1680.90740	2	3.04E-06	0.96	4.86	-	1450.7
AHQ-2-13, 6169 - 6179	R.ALSVAELTQQMFDAR.N	1680.90740	2	4.48E-05	0.97	5.25	-	1849.3
AHQ-2-11, 6008 - 6028	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.77E-06	0.94	4.65	-	1094.5
AHQ-2-14, 4969 - 5029	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	6.36E-04	0.53	2.74	-	444.2
AHQ-2-7, 4687 - 4767	R.AVLVDLEPGTMDSIR.S	1616.86162	2	8.52E-08	0.90	4.59	-	590.7
AHQ-2-14-, 4692	R.AVLVDLEPGTMDSIR.S	1616.86162	2	7.03E-06	0.86	3.44	-	621.6
AHQ-2-12, 4965	R.AVLVDLEPGTMDSIR.S	1616.86162	2	2.14E-05	0.81	3.45	-	656.1
AHQ-2-14, 4869 - 4933	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	7.79E-05	0.71	3.59	-	431.5
AHQ-2-7, 3539 - 3541	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	7.97E-04	0.94	4.31	-	1100.4
AHQ-2-13, 3981	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	4.16E-07	0.91	4.14	-	726.0
AHQ-2-14-, 3781 - 3784	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	2.20E-08	0.95	5.44	-	809.7
AHQ-2-12, 3734	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	3.11E-04	0.80	3.39	-	419.2
AHQ-2-9, 2984 - 3054	K.EVDQQLLSVQTR.N	1416.56231	2	8.75E-04	0.74	3.22	-	540.5
AHQ-2-8, 2908 - 2979	K.EVDQQLLSVQTR.N	1416.56231	1	7.17E-04	0.12	1.82	-	119.4
AHQ-2-10, 3012	K.EVDQQLLSVQTR.N	1416.56231	2	2.45E-04	0.92	3.83	-	1059.9
AHQ-2-13-, 3206 - 3270	K.EVDQQLLSVQTR.N	1416.56231	2	6.87E-04	0.85	3.42	-	806.2
AHQ-2-7, 5287 - 5301	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	9.83E-05	0.71	3.35	-	326.8
AHQ-2-7, 5136 - 5216	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.56E-04	0.83	3.61	-	470.2
AHQ-2-7, 5453	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.50E-05	0.48	2.62	-	311.5
AHQ-2-14, 5821	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	2.93E-06	0.93	3.69	-	896.3
AHQ-2-12, 5179 - 5246	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	4.06E-08	0.97	5.99	-	1514.3
AHQ-2-14, 6337 - 6406	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.26E-11	0.97	5.00	-	1748.9
AHQ-2-13-, 5279	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	1.82E-09	0.95	4.18	-	1477.6
AHQ-2-14-, 5191	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.27E-09	0.98	6.57	-	2014.3
AHQ-2-14-, 5195 - 5276	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	1.25E-09	0.96	5.13	-	1408.4
AHQ-2-13, 5176	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.12E-07	0.98	5.72	-	1697.3
AHQ-2-13-, 5269	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.67E-05	0.91	3.87	-	849.4
AHQ-2-7, 5552	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	3.43E-07	0.95	4.07	-	1384.9
AHQ-2-8, 6650 - 6728	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.39E-06	0.98	6.02	-	2442.6
AHQ-2-12, 6833	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.98E-06	0.98	6.37	-	2489.4
AHQ-2-12, 6814 - 6815	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	2.96E-05	0.94	5.20	-	1457.0
AHQ-2-12, 6778 - 6813	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.62E-06	0.98	6.36	-	2400.9
AHQ-2-4, 7280	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.26E-04	0.94	4.02	-	1623.5
AHQ-2-13, 6621	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.22E-05	0.97	5.57	-	1643.2
AHQ-2-9, 6950	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	9.65E-07	0.99	7.03	-	2474.5
AHQ-2-7, 6775 - 6851	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	7.72E-04	0.85	4.40	-	1044.8
AHQ-2-7, 6772 - 6855	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.88E-12	0.98	6.61	-	2573.9
AHQ-2-11, 6506	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.85E-07	0.93	4.35	-	1960.1
AHQ-2-13-, 6850	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.25E-13	0.98	7.25	-	2187.3
AHQ-2-11, 6504	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.38E-10	0.98	6.58	-	2630.7
AHQ-2-1, 7134	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.73E-06	0.97	5.46	-	1673.6
AHQ-2-10, 6350	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.01E-08	0.98	5.56	-	2349.6
AHQ-2-13, 6635	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	4.10E-04	0.88	4.16	-	1423.2
AHQ-2-14-, 6703	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.18E-04	0.89	4.80	-	1219.3
AHQ-2-14-, 6443 - 6459	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	6.75E-09	0.92	4.49	-	811.0
AHQ-2-7, 7420	R.GLSMAATFIGNNTAIQEIFNR.V	2269.56611	2	2.84E-06	0.93	4.76	-	839.9
AHQ-2-7, 6659 - 6697	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	5.26E-09	0.92	4.26	-	810.0
AHQ-2-13-, 6594	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	9.45E-06	0.93	4.61	-	740.2
AHQ-2-13, 6391	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.33E-05	0.91	4.54	-	681.6
AHQ-2-11, 6036	R.HESESCDCLQGFQIVHSLGGGTGSGMGTLLMNK.I	3511.88634	3	2.80E-10	0.96	5.30	-	1656.1
AHQ-2-7, 3495 - 3524	R.IMNSFSVMPSPK.V	1338.62160	2	1.38E-06	0.91	3.59	-	1430.3
AHQ-2-7, 3760	R.IMNSFSVMPSPK.V	1338.62160	2	2.52E-06	0.92	3.42	-	816.4
AHQ-2-7, 3892	R.IMNSFSVMPSPK.V	1338.62160	2	6.15E-07	0.95	3.80	-	1448.4
AHQ-2-7, 2736	R.IMNSFSVM*PSPK.V	1354.62100	2	5.27E-04	0.81	3.29	-	783.8
AHQ-2-14, 3914 - 3988	R.ISVYYNEAYGR.K	1335.44622	2	3.34E-09	0.91	3.14	-	1002.7
AHQ-2-14-, 3219	R.ISVYYNEAYGR.K	1335.44622	2	3.74E-07	0.95	3.23	-	1484.6
AHQ-2-14-, 3055 - 3056	R.ISVYYNEAYGR.K	1335.44622	2	3.45E-06	0.92	3.22	-	1185.5
AHQ-2-13-, 3253	R.ISVYYNEAYGR.K	1335.44622	2	2.99E-06	0.95	3.41	-	1419.9
AHQ-2-14, 4020	R.ISVYYNEAYGR.K	1335.44622	2	8.27E-06	0.90	2.89	-	907.8
AHQ-2-7, 2895 - 2897	R.ISVYYNEAYGR.K	1335.44622	2	1.09E-07	0.95	3.40	-	1344.7
AHQ-2-13, 3264 - 3273	R.ISVYYNEAYGR.K	1335.44622	2	2.26E-05	0.71	2.52	-	767.9
AHQ-2-12, 5174	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	2.11E-06	0.83	3.36	-	813.5
AHQ-2-13, 5117 - 5184	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	4.08E-07	0.87	3.66	-	785.5
AHQ-2-7, 4688	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	3.32E-10	0.83	3.45	-	803.7
AHQ-2-13-, 5185 - 5197	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	9.80E-10	0.74	3.62	-	545.6
AHQ-2-7, 4811	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.14E-07	0.97	5.17	-	1075.7
AHQ-2-11, 5588	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	5.61E-04	0.97	4.99	-	1108.2
AHQ-2-9, 4903 - 4918	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	4.16E-06	0.97	5.78	-	937.4
AHQ-2-8, 5263	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	3.41E-06	0.96	5.38	-	807.1
AHQ-2-12, 5861	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	1.34E-06	0.93	4.55	-	1238.4
AHQ-2-10, 5267	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	3.70E-08	0.97	5.53	-	850.5
AHQ-2-11, 4950	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	2.79E-06	0.97	5.03	-	1221.6
AHQ-2-9, 5598 - 5603	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	3.98E-05	0.96	5.02	-	804.3
AHQ-2-12, 5862	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	1.95E-07	0.96	5.40	-	727.1
AHQ-2-9, 7414	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	7.90E-08	0.96	5.82	-	1259.6

AHQ-2-7, 7433 - 7509	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	6.86E-08	0.93	4.08	-	948.2
AHQ-2-7, 7479 - 7480	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	4.55E-08	0.96	5.53	-	1573.2
AHQ-2-4, 7597	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	8.42E-06	0.93	4.78	-	1147.8
AHQ-2-14-, 5879	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	1.71E-06	0.89	4.06	-	846.4
AHQ-2-14-, 6647	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	3.45E-07	0.84	4.03	-	643.0
AHQ-2-9, 7335 - 7410	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.37E-06	0.83	3.87	-	463.5
AHQ-2-8, 6806	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	2.36E-05	0.89	3.83	-	893.9
AHQ-2-8, 7387 - 7388	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	3.84E-08	0.95	5.45	-	795.3
AHQ-2-10, 6356 - 6360	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	2.16E-07	0.76	3.47	-	476.1
AHQ-2-14-, 6612 - 6681	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	5.56E-06	0.94	5.33	-	1181.6
AHQ-2-9, 6895 - 6960	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	5.27E-04	0.92	4.62	-	986.2
AHQ-2-12, 7143	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.42E-06	0.93	4.46	-	813.3
AHQ-2-10, 6680 - 6744	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	1.31E-06	0.92	4.65	-	1008.4
AHQ-2-7, 6981	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	2.79E-05	0.95	5.31	-	1216.3
AHQ-2-9, 6956	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	7.22E-09	0.85	4.14	-	564.1
AHQ-2-10, 6742	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.06E-06	0.95	4.86	-	1065.9
AHQ-2-7, 6099 - 6103	R.NSSCFVEWIPNNVK.V	1695.87718	2	3.59E-04	0.90	4.14	-	840.3
AHQ-2-11, 5108	R.NSSCFVEWIPNNVK.V	1695.87718	2	4.08E-04	0.89	3.92	-	672.2
AHQ-2-12, 2955	R.VSEHFSAMFK.R	1183.36152	2	5.09E-07	0.89	3.07	-	1010.6
AHQ-2-9, 5170	R.YLTVACIFR.G	1144.36822	2	5.48E-05	0.87	2.74	-	841.9
AHQ-2-13, 5259	R.YLTVACIFR.G	1144.36822	2	8.56E-04	0.87	3.02	-	784.0
AHQ-2-7, 5097	R.YLTVACIFR.G	1144.36822	2	8.10E-05	0.76	2.70	-	609.2
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				5.57E-13	24.84	290.35	56.60	75429.7
AHQ-2-6, 2933 - 2969	K.AGDALWLR.F	902.03223	2	3.61E-04	0.92	3.82	-	1132.9
AHQ-2-13, 6455	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	7.68E-06	0.90	3.77	-	850.8
AHQ-2-11, 6345 - 6346	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	5.75E-09	0.81	3.83	-	570.5
AHQ-2-12, 6643	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	6.82E-10	0.88	3.62	-	791.5
AHQ-2-10, 6232	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	1.44E-07	0.79	3.44	-	594.3
AHQ-2-14-, 6529	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	3.21E-08	0.96	4.79	-	1516.2
AHQ-2-9, 6744 - 6826	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.19E-07	0.96	4.96	-	864.5
AHQ-2-1, 6996	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.56E-05	0.88	3.61	-	681.2
AHQ-2-9, 6890 - 6891	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.33E-06	0.95	4.66	-	958.2
AHQ-2-6, 6698	R.ASFSQPLFQAVAAICR.L	1768.02967	3	6.84E-07	0.93	4.41	-	1044.0
AHQ-2-6, 6627 - 6649	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.95E-04	0.95	4.68	-	814.2
AHQ-2-12, 6722	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.69E-07	0.94	4.28	-	914.1
AHQ-2-6, 6973	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.74E-05	0.91	3.94	-	628.8
AHQ-2-3, 7073	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.14E-07	0.96	4.91	-	1001.9
AHQ-2-8, 6587	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.33E-05	0.92	3.33	-	1091.6
AHQ-2-5, 6903	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.42E-05	0.95	4.42	-	1154.1
AHQ-2-7, 6724 - 6735	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.08E-07	0.96	5.13	-	1016.7
AHQ-2-4, 7132	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.63E-05	0.92	3.83	-	782.6
AHQ-2-13, 6528	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.13E-08	0.80	2.94	-	489.7
AHQ-2-11, 6396 - 6476	R.ASFSQPLFQAVAAICR.L	1768.02967	2	7.24E-04	0.89	3.50	-	828.5
AHQ-2-6, 6713 - 6774	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.02E-05	0.96	5.57	-	904.0
AHQ-2-11, 3452	K.EKEPEEELYDLSK.V	1609.71294	2	8.81E-06	0.84	3.68	-	489.8
AHQ-2-6, 3282 - 3354	K.EKEPEEELYDLSK.V	1609.71294	2	9.89E-09	0.89	3.83	-	528.9
AHQ-2-1, 3840 - 3841	K.EKEPEEELYDLSK.V	1609.71294	2	4.48E-05	0.74	3.28	-	391.4
AHQ-2-9, 3303 - 3336	K.EKEPEEELYDLSK.V	1609.71294	2	1.58E-04	0.85	3.25	-	647.8
AHQ-2-10, 3294	K.EKEPEEELYDLSK.V	1609.71294	2	1.21E-06	0.80	3.32	-	445.8
AHQ-2-6, 3425	K.EKEPEEELYDLSK.V	1609.71294	2	1.69E-05	0.74	3.19	-	429.7
AHQ-2-9, 7128	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	9.60E-08	0.92	4.46	-	542.1
AHQ-2-9, 7362	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	2.28E-05	0.94	5.08	-	667.7
AHQ-2-12, 6921 - 6922	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	3.10E-06	0.93	4.77	-	606.1
AHQ-2-13, 6659	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	1.14E-04	0.88	4.15	-	514.1
AHQ-2-12, 3195 - 3198	K.GCEVVPDVNVSGQK.F	1489.63335	1	2.02E-05	0.70	2.36	-	752.2
AHQ-2-9, 3071	K.GCEVVPDVNVSGQK.F	1489.63335	1	3.46E-10	0.89	3.91	-	856.9
AHQ-2-12, 3189 - 3194	K.GCEVVPDVNVSGQK.F	1489.63335	2	2.50E-05	0.68	2.59	-	630.5
AHQ-2-13, 6711	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	1.52E-06	0.89	4.19	-	759.1
AHQ-2-14-, 6713 - 6787	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	6.33E-06	0.92	4.13	-	1074.4
AHQ-2-6, 7150	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	3.94E-06	0.80	3.55	-	565.3
AHQ-2-12, 7047 - 7115	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	1.33E-05	0.73	3.23	-	658.3
AHQ-2-6, 3765 - 3786	R.GMPAHFSDSAQTEACYHMLSR.P	2398.64117	3	6.15E-06	0.95	5.42	-	875.3
AHQ-2-10, 3562	R.IDLAVGDVVK.T	1029.21223	1	3.40E-04	0.57	2.15	-	636.3
AHQ-2-13, 3885	R.IDLAVGDVVK.T	1029.21223	2	1.08E-04	0.93	3.65	-	1275.2
AHQ-2-13-, 3910	R.IDLAVGDVVK.T	1029.21223	1	4.44E-05	0.64	2.61	-	582.4
AHQ-2-7, 3629	R.IDLAVGDVVK.T	1029.21223	1	7.50E-04	0.20	2.38	-	204.6
AHQ-2-6, 3635 - 3705	R.IDLAVGDVVK.T	1029.21223	1	4.38E-04	0.22	2.27	-	193.8
AHQ-2-12, 3773	R.IDLAVGDVVK.T	1029.21223	1	7.74E-04	0.28	2.12	-	516.5
AHQ-2-6, 3621 - 3697	R.IDLAVGDVVK.T	1029.21223	2	3.45E-04	0.90	3.81	-	918.2
AHQ-2-6, 3625 - 3693	R.IDLAVGDVVK.T	1029.21223	1	2.85E-04	0.22	1.91	-	488.9
AHQ-2-12, 3781	R.IDLAVGDVVK.T	1029.21223	1	2.62E-04	0.63	2.83	-	511.7
AHQ-2-12, 4437 - 4447	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.49E-08	0.99	6.99	-	2278.1
AHQ-2-12, 4434	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	1.18E-06	0.96	5.31	-	1846.4
AHQ-2-6, 4253 - 4321	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	7.49E-09	0.98	6.82	-	2138.3
AHQ-2-6, 4247 - 4319	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	5.09E-07	0.94	5.58	-	1158.9
AHQ-2-1, 4766	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.36E-11	0.98	5.59	-	1992.0
AHQ-2-9, 4375	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.00E-04	0.96	4.92	-	1503.5
AHQ-2-2, 4694	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.57E-13	0.98	6.59	-	1781.4
AHQ-2-9, 4223 - 4302	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.79E-12	0.98	7.01	-	2046.0
AHQ-2-11, 4249	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.83E-07	0.98	6.47	-	2525.1
AHQ-2-13-, 4463	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	8.01E-05	0.98	6.03	-	1485.5
AHQ-2-3, 4663	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.45E-05	0.97	4.79	-	1670.2
AHQ-2-13, 4401	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	6.07E-08	0.97	5.10	-	1913.5
AHQ-2-4, 4657	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	8.35E-11	0.98	5.61	-	1549.0
AHQ-2-7, 4179	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.73E-06	0.98	6.48	-	1909.8
AHQ-2-6, 4397	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	9.64E-12	0.98	5.93	-	1911.5
AHQ-2-13, 2724 - 2783	R.KDEILGIANNR.L	1243.39499	2	1.54E-05	0.96	3.96	-	1452.3
AHQ-2-6, 2305	R.KDEILGIANNR.L	1243.39499	1	1.32E-05	0.47	2.23	-	292.0
AHQ-2-9, 2355	R.KDEILGIANNR.L	1243.39499	2	2.09E-04	0.89	3.52	-	893.1
AHQ-2-6, 2301	R.KDEILGIANNR.L	1243.39499	2	5.33E-04	0.95	3.87	-	1342.8
AHQ-2-9, 2352	R.KDEILGIANNR.L	1243.39499	1	1.84E-04	0.29	2.05	-	231.6
AHQ-2-13-, 2659 - 2669	R.KDEILGIANNR.L	1243.39499	1	3.83E-05	0.58	2.24	-	381.8
AHQ-2-13-, 2658 - 2665	R.KDEILGIANNR.L	1243.39499	2	6.27E-04	0.92	3.65	-	1046.2
AHQ-2-12, 2525 - 2593	R.KDEILGIANNR.L	1243.39499	1	6.52E-09	0.62	2.38	-	372.4
AHQ-2-6, 2393 - 2395	R.KDEILGIANNR.L	1243.39499	2	1.47E-07	0.90	3.58	-	1161.1
AHQ-2-6, 3645 - 3646	R.KQDWSDHAIWWEQK.R	1858.00504	3	9.39E-04	0.70	3.43	-	721.4
AHQ-2-6, 3669 - 3677	R.KQDWSDHAIWWEQK.R	1858.00504	2	2.51E-04	0.90	4.15	-	909.6
AHQ-2-6, 6666 - 6737	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.02E-07	0.95	4.65	-	1010.3
AHQ-2-7, 6780	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.25E-06	0.86	3.84	-	620.8
AHQ-2-1, 6857 - 6937	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	6.32E-07	0.85	3.52	-	742.9
AHQ-2-14-, 6536	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.73E-04	0.87	3.94	-	555.7
AHQ-2-10, 6224 - 6264	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	9.02E-05	0.90	4.33	-	593.5
AHQ-2-8, 6648	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.68E-05	0.90	4.15	-	620.7
AHQ-2-6, 5599 - 5601	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.28E-06	0.95	4.59	-	1095.7
AHQ-2-6, 6253 - 6255	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.65E-07	0.94	4.84	-	753.0
AHQ-2-6, 6387 - 6454	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.43E-05	0.72	3.27	-	603.6
AHQ-2-9, 6840	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	4.32E-06	0.88	4.07	-	528.6

AHQ-2-6, 6554	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.49E-06	0.92	3.94	-	968.3
AHQ-2-6, 6141 - 6153	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	9.15E-11	0.93	5.24	-	693.7
AHQ-2-11, 4648	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	7.81E-07	0.51	2.64	-	174.9
AHQ-2-1, 5062	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	4.42E-04	0.37	2.61	-	182.1
AHQ-2-6, 5421	K.LLVPSPEGMSEIYLR.C	1705.01201	2	9.57E-07	0.63	2.61	-	443.2
AHQ-2-11, 5574 - 5576	K.LLVPSPEGMSEIYLR.C	1705.01201	2	5.01E-08	0.78	3.19	-	361.4
AHQ-2-6, 5721 - 5785	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.21E-10	0.88	3.36	-	599.2
AHQ-2-13, 5653	K.LLVPSPEGMSEIYLR.C	1705.01201	2	1.98E-05	0.66	2.75	-	352.0
AHQ-2-14-, 5776	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.77E-08	0.72	2.76	-	320.4
AHQ-2-6, 6913 - 6982	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	9.78E-06	0.95	5.21	-	1482.5
AHQ-2-7, 7068	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.19E-05	0.94	4.50	-	1501.2
AHQ-2-6, 7005	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	7.70E-07	0.91	4.30	-	1102.2
AHQ-2-7, 2056 - 2077	R.LTQLYEQAR.W	1122.25622	2	1.24E-06	0.91	3.35	-	1307.9
AHQ-2-12, 2298	R.LTQLYEQAR.W	1122.25622	2	8.15E-07	0.81	3.28	-	938.0
AHQ-2-13-, 2338	R.LTQLYEQAR.W	1122.25622	2	4.94E-05	0.84	3.51	-	892.2
AHQ-2-6, 2089 - 2165	R.LTQLYEQAR.W	1122.25622	2	5.01E-06	0.89	3.79	-	884.1
AHQ-2-9, 2140	R.LTQLYEQAR.W	1122.25622	2	8.72E-04	0.89	3.21	-	1134.4
AHQ-2-6, 4837	R.QWLLQTHWTLDK.Y	1569.78807	2	6.50E-05	0.31	2.70	-	200.4
AHQ-2-14-, 3979 - 3992	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	6.66E-08	0.90	4.16	-	575.5
AHQ-2-6, 3882 - 3949	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	6.29E-07	0.88	4.37	-	447.3
AHQ-2-11, 3853 - 3912	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	9.39E-05	0.86	3.72	-	577.3
AHQ-2-13, 4083 - 4087	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.01E-04	0.85	3.44	-	620.7
AHQ-2-6, 5343	K.SQDEAPGDPIQQLNLKGCEVVPDVNVSGQK.F	3224.50249	3	2.17E-07	0.86	4.45	-	611.4
AHQ-2-11, 4202	K.TASGDYIDSSWELR.V	1600.66783	2	9.20E-07	0.89	3.50	-	750.7
AHQ-2-9, 4256 - 4295	K.TASGDYIDSSWELR.V	1600.66783	2	2.12E-06	0.91	3.52	-	953.9
AHQ-2-6, 4229 - 4297	K.TASGDYIDSSWELR.V	1600.66783	2	4.21E-11	0.96	4.72	-	1077.2
AHQ-2-11, 3645	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	5.63E-04	0.96	5.86	-	1382.1
AHQ-2-6, 3678 - 3754	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	3.10E-04	0.84	3.97	-	488.3
AHQ-2-6, 3755 - 3831	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	3.74E-04	0.96	5.54	-	1565.0
AHQ-2-6, 3541 - 3562	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	8.19E-04	0.92	4.56	-	796.6
AHQ-2-6, 3534 - 3602	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	7.92E-12	0.95	5.79	-	1055.3
AHQ-2-10, 3532	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	3.42E-04	0.90	4.07	-	651.4
AHQ-2-9, 3559 - 3636	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.47E-05	0.91	4.79	-	472.2
AHQ-2-4, 3920	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	9.74E-04	0.96	5.73	-	1569.8
AHQ-2-11, 3652	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.64E-06	0.94	5.09	-	739.9
AHQ-2-8, 3774 - 3851	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.63E-04	0.91	4.18	-	942.4
AHQ-2-1, 4236 - 4244	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.67E-08	0.95	4.28	-	1286.6
AHQ-2-2, 4144 - 4212	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.21E-10	0.95	5.03	-	1221.8
AHQ-2-14, 4830 - 4909	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.35E-05	0.94	4.20	-	1313.1
AHQ-2-7, 3856	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.61E-07	0.91	3.60	-	1160.2
AHQ-2-4, 4133 - 4152	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.75E-10	0.96	4.21	-	1579.2
AHQ-2-10, 3734	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.04E-06	0.89	3.99	-	851.8
AHQ-2-14-, 3920 - 3923	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.87E-09	0.96	4.18	-	1727.2
AHQ-2-12, 4019 - 4021	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.94E-07	0.96	4.74	-	1181.5
AHQ-2-13, 4004	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.06E-08	0.92	4.07	-	1049.2
AHQ-2-11, 3860	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.53E-08	0.95	4.31	-	1417.3
AHQ-2-3, 4171	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.00E-11	0.97	5.03	-	1406.3
AHQ-2-13-, 4034	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.80E-10	0.94	4.35	-	1243.6
AHQ-2-9, 3863 - 3943	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.81E-06	0.94	4.13	-	1334.9
AHQ-2-6, 3861 - 3930	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.65E-11	0.97	5.07	-	1400.3
AHQ-2-5, 3937	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.68E-06	0.96	4.54	-	1466.2
AHQ-2-13, 2889	R.VTGESHIGGVLLK.I	1310.52448	2	3.31E-07	0.96	3.97	-	1935.8
AHQ-2-11, 2669 - 2737	R.VTGESHIGGVLLK.I	1310.52448	2	3.77E-04	0.77	3.04	-	923.9
AHQ-2-9, 2487	R.VTGESHIGGVLLK.I	1310.52448	1	2.59E-08	0.84	3.12	-	852.6
AHQ-2-13-, 2835	R.VTGESHIGGVLLK.I	1310.52448	1	2.01E-04	0.35	2.69	-	338.2
AHQ-2-13-, 2833	R.VTGESHIGGVLLK.I	1310.52448	2	3.76E-07	0.96	4.52	-	1634.8
AHQ-2-1, 2953	R.VTGESHIGGVLLK.I	1310.52448	2	1.19E-06	0.96	3.83	-	1896.5
AHQ-2-6, 2461	R.VTGESHIGGVLLK.I	1310.52448	1	4.67E-08	0.84	3.44	-	703.3
AHQ-2-6, 2453	R.VTGESHIGGVLLK.I	1310.52448	2	1.51E-07	0.95	4.17	-	1524.2
AHQ-2-9, 2478 - 2486	R.VTGESHIGGVLLK.I	1310.52448	2	4.58E-07	0.96	4.16	-	1744.9
AHQ-2-7, 2379	R.VTGESHIGGVLLK.I	1310.52448	2	4.34E-08	0.93	4.04	-	1322.2
AHQ-2-12, 2714	R.VTGESHIGGVLLK.I	1310.52448	2	1.31E-07	0.87	3.45	-	1144.7
AHQ-2-14-, 2743 - 2744	R.VTGESHIGGVLLK.I	1310.52448	2	2.28E-09	0.98	4.64	-	2316.6
AHQ-2-5, 4696	K.VVLAGGVAPALFR.G	1270.54832	2	7.96E-08	0.97	4.84	-	1811.2
AHQ-2-1, 5121	K.VVLAGGVAPALFR.G	1270.54832	2	1.01E-07	0.98	5.26	-	2067.4
AHQ-2-9, 4648	K.VVLAGGVAPALFR.G	1270.54832	2	4.26E-06	0.89	2.99	-	1433.8
AHQ-2-9, 4588	K.VVLAGGVAPALFR.G	1270.54832	1	6.40E-04	0.63	3.13	-	154.7
AHQ-2-3, 5036	K.VVLAGGVAPALFR.G	1270.54832	2	8.93E-06	0.94	3.73	-	1406.0
AHQ-2-11, 4630	K.VVLAGGVAPALFR.G	1270.54832	2	5.01E-07	0.96	4.60	-	1423.7
AHQ-2-6, 4593 - 4673	K.VVLAGGVAPALFR.G	1270.54832	2	1.82E-08	0.97	5.04	-	1849.4
AHQ-2-6, 4611	K.VVLAGGVAPALFR.G	1270.54832	1	7.67E-05	0.21	1.95	-	116.3
AHQ-2-7, 4493	K.VVLAGGVAPALFR.G	1270.54832	2	1.88E-08	0.97	4.86	-	1674.1
AHQ-2-10, 4366	K.VVLAGGVAPALFR.G	1270.54832	2	2.99E-07	0.95	4.12	-	1452.3
AHQ-2-6, 2282	K.YGILADAR.L	878.99544	2	2.74E-05	0.94	3.74	-	1146.1
AHQ-2-7, 5217	K.YYSFFDLDPK.T	1295.42046	2	5.47E-05	0.93	3.21	-	942.3
AHQ-2-6, 5226	K.YYSFFDLDPK.T	1295.42046	2	1.68E-04	0.87	3.92	-	798.5
AHQ-2-9, 5227	K.YYSFFDLDPK.T	1295.42046	2	1.84E-06	0.81	3.50	-	648.3
gi|5031857|ref|NP_005557.1| lactate dehydrogenase A [Homo sapiens]				5.59E-13	4.49	60.28	24.70	36688.5
AHQ-2-13, 6651	K.DLADELALVDVIEDK.L	1658.82864	2	1.62E-10	0.97	5.29	-	1370.3
AHQ-2-9, 7156 - 7236	K.DLADELALVDVIEDK.L	1658.82864	2	5.59E-13	0.97	5.12	-	1751.1
AHQ-2-13-, 6861	K.DLADELALVDVIEDK.L	1658.82864	2	5.90E-11	0.97	5.69	-	1327.0
AHQ-2-14-, 6717 - 6727	K.DLADELALVDVIEDK.L	1658.82864	2	5.41E-05	0.90	3.16	-	1569.1
AHQ-2-9, 7383	K.DLADELALVDVIEDKLK.G	1900.15980	2	2.72E-07	0.96	4.93	-	1662.9
AHQ-2-9, 4770	K.DQLIYNLLKEEQTPQNK.I	2075.30802	2	3.59E-06	0.93	4.49	-	1413.1
AHQ-2-9, 7419	K.GLYGIKDDVFLSVPCILGQNGISDLVK.V	2923.37318	2	6.73E-07	0.88	4.65	-	339.1
AHQ-2-9, 3128	K.QVVESAYEVIK.L	1265.43734	2	7.66E-04	0.59	2.71	-	337.5
AHQ-2-11, 2069 - 2072	K.VTLTSEEEAR.L	1135.20693	2	1.52E-04	0.85	2.79	-	979.2
AHQ-2-11, 2073 - 2074	K.VTLTSEEEAR.L	1135.20693	1	4.05E-06	0.15	2.20	-	161.8
gi|21361478|ref|NP_055944.2| septin 6 isoform B; septin 2 [Homo sapiens]				6.53E-13	3.80	40.33	15.90	49716.3
AHQ-2-7, 3781	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L	3147.31508	3	6.53E-13	0.98	6.64	-	1909.6
AHQ-2-7, 2673	R.KTAAELLQSQGSQAGGSQTLK.R	2104.30776	2	5.46E-04	0.91	4.21	-	631.0
AHQ-2-7, 2879 - 2880	K.TAAELLQSQGSQAGGSQTLK.R	1976.13485	2	1.25E-08	0.96	4.81	-	1320.2
AHQ-2-7, 4876	R.TVPLAGHVGFDSLPDQLVNK.S	2108.38284	2	6.46E-07	0.96	5.21	-	1011.5
gi|13124879|ref|NP_002465.1| smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]				8.93E-13	9.68	110.39	6.10	227336.7
AHQ-2-3, 4949	R.DLGEELEALK.T	1117.23151	2	1.78E-04	0.94	3.95	-	1089.3
AHQ-2-2, 4986	R.DLGEELEALK.T	1117.23151	2	4.61E-05	0.90	3.42	-	921.8
AHQ-2-3, 4948	R.DLGEELEALK.T	1117.23151	1	3.00E-04	0.32	2.72	-	354.2
AHQ-2-6, 2610	R.EDQSILCTGESGAGK.T	1553.63107	2	5.41E-04	0.66	3.09	-	413.1
AHQ-2-3, 2764	R.EDQSILCTGESGAGK.T	1553.63107	2	2.17E-04	0.90	3.80	-	839.3
AHQ-2-3, 2801	K.FDQLLAEEK.N	1093.21165	1	1.48E-06	0.64	2.47	-	660.4
AHQ-2-2, 2810	K.FDQLLAEEK.N	1093.21165	1	4.37E-05	0.69	2.67	-	755.9
AHQ-2-2, 2804	K.FDQLLAEEK.N	1093.21165	2	1.69E-05	0.92	3.24	-	1487.8
AHQ-2-3, 2796	K.FDQLLAEEK.N	1093.21165	2	1.61E-05	0.93	3.09	-	1569.4
AHQ-2-1, 2977	K.FDQLLAEEK.N	1093.21165	2	1.24E-04	0.93	3.18	-	1522.2
AHQ-2-4, 2332	K.KEEELQAALAR.L	1258.40643	2	4.40E-04	0.93	3.40	-	1591.0
AHQ-2-2, 2349	K.KEEELQAALAR.L	1258.40643	2	7.10E-05	0.86	3.53	-	971.6
AHQ-2-3, 2324 - 2335	K.KEEELQAALAR.L	1258.40643	2	3.28E-04	0.76	3.08	-	855.6

AHQ-2-1, 2564	K.KEEELQAALAR.L	1258.40643	3	1.49E-05	0.90	3.64	-	1465.1
AHQ-2-6, 2454	R.KFDQLLAEEK.N	1221.38456	2	6.46E-04	0.87	3.12	-	1131.2
AHQ-2-5, 2423	R.KFDQLLAEEK.N	1221.38456	1	2.22E-05	0.31	1.99	-	542.2
AHQ-2-6, 2414 - 2447	R.KFDQLLAEEK.N	1221.38456	1	4.50E-04	0.19	1.81	-	218.5
AHQ-2-2, 2576 - 2628	R.KFDQLLAEEK.N	1221.38456	2	1.97E-05	0.92	3.26	-	1274.8
AHQ-2-3, 2627	R.KFDQLLAEEK.N	1221.38456	2	5.51E-04	0.81	3.26	-	820.5
AHQ-2-2, 5386 - 5392	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	5.35E-12	0.99	7.79	-	3672.9
AHQ-2-2, 5384 - 5385	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	4.22E-07	0.93	4.62	-	642.5
AHQ-2-5, 5788 - 5868	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	4.12E-08	0.89	3.26	-	1133.5
AHQ-2-4, 6186	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	1.39E-07	0.96	4.30	-	1672.3
AHQ-2-4, 6185	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	5.24E-10	0.98	6.08	-	2523.6
AHQ-2-2, 6180	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	1.96E-08	0.94	4.03	-	1406.0
AHQ-2-2, 6184 - 6188	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	2.44E-11	0.98	6.45	-	2786.2
AHQ-2-2, 6270	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	2.29E-12	0.98	6.47	-	2733.8
AHQ-2-2, 6290 - 6370	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	2.93E-09	0.98	5.89	-	1842.8
AHQ-2-5, 5792	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	5.96E-06	0.97	4.54	-	2616.9
AHQ-2-2, 6450 - 6521	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	7.15E-09	0.98	5.70	-	2034.3
AHQ-2-2, 6506	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	2.32E-09	0.98	5.48	-	2685.3
AHQ-2-3, 5348	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	3.68E-07	0.98	6.43	-	2249.0
AHQ-2-5, 5983 - 6027	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	9.87E-11	0.97	5.50	-	1755.7
AHQ-2-1, 5430 - 5498	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	3.80E-10	0.98	6.48	-	3212.2
AHQ-2-3, 5343	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	8.41E-04	0.85	3.44	-	834.2
AHQ-2-5, 6219	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	5.23E-04	0.83	3.47	-	809.4
AHQ-2-1, 6229 - 6250	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.02E-11	0.98	5.90	-	2586.4
AHQ-2-1, 5745	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	3.94E-09	0.93	4.62	-	1374.9
AHQ-2-2, 5502	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	3.14E-10	0.98	6.21	-	2073.1
AHQ-2-3, 2572 - 2659	R.NCAAYLK.L	840.96726	1	7.70E-04	0.60	2.19	-	616.2
AHQ-2-1, 2421	R.NCAAYLK.L	840.96726	1	4.94E-04	0.72	1.87	-	996.7
AHQ-2-2, 1618	R.NTDQASMPDNTAAQK.V	1592.67074	2	2.28E-04	0.81	3.75	-	429.9
AHQ-2-2, 6573	K.QLLQANPILEAFGNAK.T	1727.98540	2	5.82E-06	0.92	4.02	-	836.8
AHQ-2-9, 6080 - 6146	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.95E-05	0.88	3.71	-	665.8
AHQ-2-3, 6416 - 6431	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.52E-06	0.94	4.27	-	808.4
AHQ-2-3, 6575	K.QLLQANPILEAFGNAK.T	1727.98540	2	5.16E-10	0.96	4.43	-	1120.0
AHQ-2-2, 6354 - 6432	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.95E-08	0.96	4.70	-	1033.3
AHQ-2-7, 5992 - 5997	K.QLLQANPILEAFGNAK.T	1727.98540	2	5.39E-07	0.94	4.14	-	927.6
AHQ-2-6, 6077	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.12E-08	0.96	4.77	-	1078.5
AHQ-2-5, 6352	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.04E-10	0.95	4.45	-	1035.0
AHQ-2-1, 6396 - 6476	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.52E-07	0.94	4.42	-	877.8
AHQ-2-4, 6450 - 6465	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.02E-07	0.95	4.72	-	925.6
AHQ-2-5, 6109 - 6119	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.94E-07	0.96	4.87	-	1103.5
AHQ-2-1, 6582	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.15E-08	0.89	4.07	-	583.6
AHQ-2-9, 6223 - 6296	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.46E-05	0.55	2.69	-	460.5
AHQ-2-2, 4166	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.54E-06	0.93	4.34	-	985.2
AHQ-2-5, 5651 - 5668	K.TQLEELEDELQATEDAK.L	1963.04334	2	6.78E-06	0.98	6.13	-	1926.0
AHQ-2-2, 5924 - 5996	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.30E-09	0.98	6.91	-	2060.3
AHQ-2-2, 5948	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.53E-05	0.96	5.74	-	1213.1
AHQ-2-2, 6145 - 6213	K.TQLEELEDELQATEDAK.L	1963.04334	2	8.91E-05	0.91	4.05	-	849.7
AHQ-2-1, 6112	K.TQLEELEDELQATEDAK.L	1963.04334	2	8.93E-13	0.98	5.90	-	1809.3
AHQ-2-1, 5928	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.44E-09	0.96	5.62	-	1448.5
AHQ-2-1, 5924	K.TQLEELEDELQATEDAK.L	1963.04334	2	5.15E-06	0.98	4.88	-	2195.2
AHQ-2-6, 5565 - 5566	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.08E-06	0.98	5.98	-	2223.6
AHQ-2-4, 5885 - 5956	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.60E-09	0.99	7.39	-	2442.5
AHQ-2-7, 5625	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.01E-11	0.98	6.37	-	2566.8
AHQ-2-4, 4117	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.27E-04	0.85	3.42	-	769.8
AHQ-2-3, 5904	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.68E-06	0.97	6.00	-	1283.3
AHQ-2-3, 4132	K.TQLEELEDELQATEDAK.L	1963.04334	2	3.75E-05	0.97	5.53	-	1712.2
gi|4557305|ref|NP_000025.1| aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho				9.87E-13	8.68	100.28	47.30	39419.7
AHQ-2-9, 2056	R.ALANSLACQGK.Y	1134.28859	2	1.64E-04	0.81	2.80	-	849.4
AHQ-2-8, 3880	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	1.10E-06	0.96	5.59	-	1283.8
AHQ-2-8, 3790	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	2.38E-09	0.94	5.59	-	709.0
AHQ-2-9, 6098 - 6103	K.CPLLKPWALTFSYGR.A	1811.13929	2	2.69E-04	0.93	4.42	-	641.1
AHQ-2-8, 5974 - 6044	K.CPLLKPWALTFSYGR.A	1811.13929	2	7.10E-06	0.94	4.55	-	712.9
AHQ-2-9, 4106	K.FSHEEIAMATVTALR.R	1676.91875	2	9.87E-13	0.97	5.14	-	1455.0
AHQ-2-8, 3883	K.FSHEEIAMATVTALR.R	1676.91875	2	5.56E-11	0.90	3.82	-	1073.6
AHQ-2-11, 2821	K.GILAADESTGSIAK.R	1333.47008	2	4.08E-06	0.95	3.54	-	1612.3
AHQ-2-8, 2543 - 2586	K.GILAADESTGSIAK.R	1333.47008	2	7.30E-10	0.97	4.99	-	1435.9
AHQ-2-9, 2720	K.GILAADESTGSIAK.R	1333.47008	1	2.62E-04	0.40	2.72	-	292.8
AHQ-2-12, 2861	K.GILAADESTGSIAK.R	1333.47008	2	2.12E-07	0.94	3.86	-	1219.9
AHQ-2-9, 4250	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	3.02E-06	0.65	3.77	-	469.9
AHQ-2-9, 5264	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	9.13E-05	0.96	4.99	-	951.8
AHQ-2-10, 4944	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.21E-04	0.80	3.56	-	551.2
AHQ-2-8, 4975 - 5003	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.08E-04	0.95	4.86	-	868.6
AHQ-2-9, 4966	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.16E-08	0.93	4.32	-	880.3
AHQ-2-8, 6206 - 6275	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	9.27E-08	0.93	4.29	-	805.8
AHQ-2-9, 5720	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	4.11E-04	0.69	3.66	-	250.8
AHQ-2-8, 4218 - 4288	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	3.96E-06	0.84	3.97	-	408.6
gi|20535366|ref|XP_053177.4| similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap				1.44E-12	2.78	30.23	9.60	49858.2
AHQ-2-7, 2847	K.DVNAAIATIK.T	1016.17355	2	1.20E-05	0.94	4.01	-	1199.5
AHQ-2-7, 3060	K.DVNAAIATIK.T	1016.17355	1	1.20E-05	0.25	1.98	-	378.0
AHQ-2-7, 3163	K.DVNAAIATIK.T	1016.17355	1	4.22E-04	0.46	2.07	-	629.7
AHQ-2-1, 5526	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.18E-06	0.52	2.68	-	409.4
AHQ-2-7, 4864	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.44E-12	0.89	4.27	-	413.5
AHQ-2-7, 5000	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.15E-07	0.89	4.11	-	578.8
AHQ-2-7, 5151 - 5225	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.52E-07	0.94	4.55	-	1007.6
AHQ-2-7, 5307 - 5372	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.03E-05	0.82	3.79	-	490.3
AHQ-2-7, 5375 - 5445	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.09E-04	0.72	3.18	-	428.4
AHQ-2-13-, 5270 - 5274	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.96E-08	0.91	4.20	-	694.4
AHQ-2-9, 5162	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.15E-06	0.83	3.72	-	492.5
AHQ-2-11, 5009 - 5080	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	6.54E-10	0.93	4.49	-	777.2
AHQ-2-12, 5249 - 5257	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.96E-08	0.90	3.63	-	861.2
AHQ-2-13-, 4877	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	9.76E-08	0.67	3.43	-	312.5
AHQ-2-13, 5175	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	6.80E-08	0.58	3.10	-	294.6
AHQ-2-14, 5856	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.73E-08	0.82	3.86	-	367.4
AHQ-2-14, 6205 - 6265	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.17E-07	0.92	4.12	-	803.2
AHQ-2-14, 6324	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.42E-08	0.93	4.49	-	849.4
AHQ-2-14, 6516	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.71E-09	0.96	4.60	-	1433.0
AHQ-2-14-, 5167 - 5215	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.62E-06	0.93	4.52	-	761.9
AHQ-2-7, 5739 - 5740	R.TIQFVDWCPTGFK.V	1600.81899	2	2.75E-06	0.94	4.56	-	784.5
AHQ-2-12, 5742 - 5809	R.TIQFVDWCPTGFK.V	1600.81899	2	9.38E-06	0.67	3.00	-	478.9
gi|4758606|ref|NP_004508.1| integrin-linked kinase [Homo sapiens]				1.57E-12	12.11	140.27	31.90	51418.9
AHQ-2-13-, 5710	R.EVPFADLSNMEIGMK.V	1681.95558	2	3.83E-04	0.91	3.64	-	545.8
AHQ-2-13, 5612 - 5689	R.EVPFADLSNMEIGMK.V	1681.95558	2	4.16E-06	0.91	4.13	-	555.9
AHQ-2-7, 4125 - 4195	R.EVPFADLSNM*EIGM*K.V	1713.95438	2	3.96E-05	0.70	2.89	-	489.0
AHQ-2-11, 5464 - 5532	R.EVPFADLSNMEIGMK.V	1681.95558	2	1.38E-05	0.88	4.39	-	579.0
AHQ-2-7, 4244 - 4279	K.FDM*IVPILEK.M	1221.49108	2	4.76E-05	0.85	2.76	-	749.1
AHQ-2-10, 5164	K.FDMIVPILEK.M	1205.49168	2	8.38E-04	0.65	2.51	-	619.2
AHQ-2-11, 2068 - 2077	R.GDDTPLHLAASHGHR.D	1584.67809	2	1.23E-07	0.93	3.95	-	1069.2

AHQ-2-7, 1651 - 1672	R.GDDTPLHLAASHGHR.D	1584.67809	2	3.42E-09	0.93	3.93	-	1099.2
AHQ-2-10, 1899 - 1903	R.GDDTPLHLAASHGHR.D	1584.67809	2	4.12E-07	0.92	3.86	-	1047.8
AHQ-2-9, 5722	R.GMAFLHTLEPLIPR.H	1595.93361	2	1.61E-05	0.91	3.66	-	915.1
AHQ-2-7, 4744	R.GM*AFLHTLEPLIPR.H	1611.93301	2	2.12E-05	0.90	3.54	-	869.8
AHQ-2-7, 5649	R.GMAFLHTLEPLIPR.H	1595.93361	3	9.44E-08	0.88	3.35	-	1247.5
AHQ-2-10, 4660	R.GM*AFLHTLEPLIPR.H	1611.93301	2	8.30E-05	0.87	3.48	-	619.0
AHQ-2-11, 4969	R.GM*AFLHTLEPLIPR.H	1611.93301	2	2.94E-05	0.89	3.48	-	773.6
AHQ-2-7, 1928 - 1936	K.LNENHSGELWK.G	1327.42732	2	2.28E-07	0.92	3.57	-	1292.8
AHQ-2-9, 6123	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	1.19E-04	0.80	3.44	-	1133.5
AHQ-2-7, 6048 - 6117	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	1.05E-05	0.95	5.35	-	1173.0
AHQ-2-11, 5796	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	1.57E-12	0.93	4.54	-	1259.7
AHQ-2-14-, 5963 - 5973	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	1.20E-09	0.95	5.48	-	1174.6
AHQ-2-11, 4146	R.M*YAPAWVAPEALQK.K	1591.85542	2	1.67E-04	0.91	3.38	-	830.2
AHQ-2-10, 3891 - 3956	R.M*YAPAWVAPEALQK.K	1591.85542	2	6.69E-05	0.89	3.37	-	637.0
AHQ-2-11, 4568 - 4576	R.MYAPAWVAPEALQK.K	1575.85602	2	8.29E-08	0.96	4.39	-	1070.3
AHQ-2-13-, 4805 - 4806	R.MYAPAWVAPEALQK.K	1575.85602	2	1.78E-06	0.94	3.72	-	1197.3
AHQ-2-13-, 4301	R.M*YAPAWVAPEALQK.K	1591.85542	2	2.56E-05	0.87	3.45	-	730.0
AHQ-2-10, 4338	R.MYAPAWVAPEALQK.K	1575.85602	2	2.48E-05	0.91	3.48	-	781.2
AHQ-2-12, 4294	R.M*YAPAWVAPEALQK.K	1591.85542	2	4.75E-04	0.61	2.55	-	441.8
AHQ-2-13, 4255	R.M*YAPAWVAPEALQK.K	1591.85542	2	6.33E-05	0.87	3.21	-	852.2
AHQ-2-11, 4014	R.SAVVEMLIM*R.G	1165.45256	2	1.81E-04	0.90	3.06	-	1388.4
AHQ-2-7, 4232 - 4307	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	2	5.05E-09	0.96	5.02	-	920.4
AHQ-2-7, 4227	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	3	8.90E-10	0.90	4.11	-	845.0
AHQ-2-11, 4385 - 4414	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	2	5.86E-04	0.74	3.67	-	512.2
AHQ-2-7, 2688	R.WQGNDIVVK.V	1059.20012	1	9.76E-05	0.79	2.46	-	1005.6
gi|4504745|ref|NP_000410.1| integrin alpha 2b precursor [Homo sapiens]				1.85E-12	34.27	380.35	38.30	113374.2
AHQ-2-4, 1737	R.AEAQVELR.G	916.01408	2	1.06E-04	0.91	2.97	-	1311.3
AHQ-2-13-, 5307	R.AEGGQCPSLLFDLR.D	1564.74505	2	9.94E-05	0.83	3.12	-	810.7
AHQ-2-13, 5207	R.AEGGQCPSLLFDLR.D	1564.74505	2	8.54E-05	0.77	3.00	-	572.2
AHQ-2-1, 5485 - 5556	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.04E-07	0.94	4.50	-	838.2
AHQ-2-11, 5020 - 5028	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.00E-07	0.94	3.60	-	1189.0
AHQ-2-1, 5561	R.AEGGQCPSLLFDLR.D	1564.74505	2	7.23E-04	0.83	2.71	-	821.0
AHQ-2-10, 4814	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.00E-09	0.96	4.85	-	1009.6
AHQ-2-4, 5653	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.04E-11	0.95	4.00	-	1344.6
AHQ-2-9, 5156	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.90E-04	0.85	3.61	-	533.6
AHQ-2-4, 5512	R.AEGGQCPSLLFDLR.D	1564.74505	2	6.33E-07	0.94	4.39	-	971.1
AHQ-2-4, 5130	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.94E-04	0.86	3.36	-	932.3
AHQ-2-7, 5121	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.17E-07	0.95	4.39	-	1113.6
AHQ-2-4, 5426 - 5496	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.48E-08	0.96	5.15	-	1051.9
AHQ-2-6, 5129 - 5137	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.45E-05	0.93	3.93	-	860.6
AHQ-2-5, 5140 - 5220	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.24E-07	0.95	4.36	-	996.6
AHQ-2-4, 5065	R.AEGGQCPSLLFDLRDETR.N	2066.23814	3	1.67E-05	0.73	3.16	-	719.4
AHQ-2-4, 4946	R.AEGGQCPSLLFDLRDETR.N	2066.23814	3	5.33E-06	0.75	3.42	-	824.7
AHQ-2-4, 4934	R.AEGGQCPSLLFDLRDETR.N	2066.23814	2	5.10E-04	0.83	3.53	-	807.7
AHQ-2-6, 2562	R.ALSNVEGFER.L	1122.21308	2	1.42E-06	0.86	3.17	-	874.4
AHQ-2-4, 2709 - 2780	R.ALSNVEGFER.L	1122.21308	1	1.96E-04	0.14	2.38	-	137.9
AHQ-2-4, 2712 - 2781	R.ALSNVEGFER.L	1122.21308	2	2.69E-06	0.90	3.65	-	935.3
AHQ-2-4, 2716 - 2785	R.ALSNVEGFER.L	1122.21308	1	1.88E-05	0.30	2.63	-	98.5
AHQ-2-4, 2808	R.ALSNVEGFER.L	1122.21308	2	4.00E-06	0.69	2.89	-	639.0
AHQ-2-6, 2561	R.ALSNVEGFER.L	1122.21308	1	2.88E-06	0.19	2.06	-	192.2
AHQ-2-5, 2519	R.ALSNVEGFER.L	1122.21308	1	2.96E-04	0.14	2.17	-	132.0
AHQ-2-5, 2520	R.ALSNVEGFER.L	1122.21308	2	4.81E-06	0.77	2.70	-	893.8
AHQ-2-4, 3132	R.ALSNVEGFER.L	1122.21308	1	4.43E-04	0.30	2.59	-	279.6
AHQ-2-5, 2523	R.ALSNVEGFER.L	1122.21308	1	9.36E-04	0.08	1.81	-	54.0
AHQ-2-7, 2492	R.ALSNVEGFER.L	1122.21308	2	7.33E-07	0.85	3.21	-	790.1
AHQ-2-1, 2948	R.ALSNVEGFER.L	1122.21308	2	2.85E-05	0.83	3.10	-	686.7
AHQ-2-4, 5440	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	4.33E-05	0.87	4.02	-	627.7
AHQ-2-4, 5280 - 5348	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.49E-06	0.92	4.81	-	660.8
AHQ-2-4, 5144 - 5212	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.41E-04	0.86	3.87	-	898.4
AHQ-2-4, 3224	R.DETRNVGSQTLQTFK.A	1724.85363	2	3.67E-06	0.73	2.90	-	586.0
AHQ-2-4, 3004	R.DETRNVGSQTLQTFK.A	1724.85363	2	4.16E-07	0.84	3.43	-	968.8
AHQ-2-3, 4047 - 4048	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.41E-05	0.71	3.41	-	520.3
AHQ-2-5, 3891 - 3892	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.46E-06	0.94	5.17	-	753.7
AHQ-2-6, 3813 - 3881	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.30E-04	0.71	3.54	-	468.5
AHQ-2-4, 4013 - 4033	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.38E-06	0.86	3.85	-	739.4
AHQ-2-4, 4225	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.28E-07	0.91	4.18	-	765.3
AHQ-2-4, 4578 - 4581	R.FGSAIAPLGDLDR.D	1332.48700	2	3.20E-06	0.91	3.59	-	1102.2
AHQ-2-7, 4191	R.FGSAIAPLGDLDR.D	1332.48700	2	2.06E-04	0.84	2.69	-	883.9
AHQ-2-4, 4586	R.FGSAIAPLGDLDR.D	1332.48700	1	3.98E-06	0.80	3.18	-	499.4
AHQ-2-4, 6014 - 6084	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.41E-07	0.94	5.38	-	864.0
AHQ-2-4, 6153 - 6224	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.50E-06	0.92	5.34	-	865.8
AHQ-2-4, 6292 - 6360	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.62E-04	0.87	4.39	-	798.1
AHQ-2-5, 6055 - 6085	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.83E-07	0.90	4.50	-	797.4
AHQ-2-5, 5887 - 5957	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	3.78E-11	0.93	4.12	-	1416.1
AHQ-2-4, 5889 - 5957	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.50E-05	0.90	4.87	-	575.6
AHQ-2-6, 5731 - 5797	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.16E-06	0.91	4.87	-	878.1
AHQ-2-7, 5732 - 5811	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	6.46E-05	0.93	4.94	-	942.6
AHQ-2-1, 6025 - 6080	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	3.75E-07	0.87	4.54	-	685.2
AHQ-2-5, 5804 - 5873	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	8.35E-11	0.91	4.59	-	907.3
AHQ-2-4, 6826 - 6870	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.02E-05	0.92	4.75	-	522.2
AHQ-2-4, 7037 - 7114	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	3.42E-08	0.94	5.54	-	479.8
AHQ-2-4, 7256 - 7324	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.13E-06	0.86	3.72	-	476.1
AHQ-2-4, 7532 - 7601	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	7.28E-04	0.85	3.43	-	714.1
AHQ-2-4, 7392 - 7461	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	6.31E-09	0.95	5.06	-	705.0
AHQ-2-4, 6585 - 6653	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.32E-07	0.90	4.78	-	549.6
AHQ-2-4, 6937 - 6969	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.00E-07	0.94	5.07	-	495.4
AHQ-2-10, 4500 - 4571	R.GEAQVWTQLLR.A	1301.47614	2	3.59E-05	0.93	3.81	-	1147.1
AHQ-2-10, 4822	R.GEAQVWTQLLR.A	1301.47614	1	8.19E-04	0.09	2.01	-	210.1
AHQ-2-1, 5341 - 5348	R.GEAQVWTQLLR.A	1301.47614	2	7.36E-05	0.94	3.80	-	1359.4
AHQ-2-10, 4498 - 4595	R.GEAQVWTQLLR.A	1301.47614	1	2.57E-05	0.17	2.35	-	168.2
AHQ-2-11, 4777	R.GEAQVWTQLLR.A	1301.47614	2	3.76E-07	0.88	3.68	-	771.7
AHQ-2-4, 5470 - 5549	R.GNSFPASLVVAAEEGER.E	1733.86053	2	5.87E-07	0.94	4.74	-	948.3
AHQ-2-4, 5722 - 5792	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.17E-09	0.96	5.09	-	1200.7
AHQ-2-4, 5878 - 5949	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.58E-04	0.82	3.10	-	880.0
AHQ-2-4, 6016	R.GNSFPASLVVAAEEGER.E	1733.86053	2	2.97E-12	0.90	4.22	-	747.4
AHQ-2-4, 5621 - 5696	R.GNSFPASLVVAAEEGER.E	1733.86053	2	6.12E-09	0.92	4.67	-	742.3
AHQ-2-4, 5385 - 5456	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.56E-04	0.89	3.97	-	691.2
AHQ-2-4, 6146	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.82E-06	0.73	2.94	-	676.1
AHQ-2-4, 6554 - 6625	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	6.73E-08	0.80	3.94	-	384.9
AHQ-2-4, 6662 - 6702	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	2	8.26E-05	0.72	3.26	-	554.8
AHQ-2-4, 6785 - 6856	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	6.75E-08	0.75	3.97	-	391.8
AHQ-2-4, 7092 - 7169	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	1.31E-10	0.87	4.60	-	481.5
AHQ-2-4, 6888 - 6913	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	2	3.04E-05	0.52	3.15	-	260.6
AHQ-2-4, 5201 - 5272	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.22E-05	0.97	6.00	-	1202.5
AHQ-2-4, 5205 - 5285	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	7.91E-04	0.91	3.86	-	1320.9
AHQ-2-1, 5517	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.72E-04	0.95	5.06	-	891.2
AHQ-2-6, 4913 - 4938	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	2.77E-04	0.85	3.63	-	1017.7

AHQ-2-6, 4918 - 4919	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	9.46E-06	0.98	6.42	-	1111.8
AHQ-2-7, 4709	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	9.09E-06	0.97	5.37	-	1098.6
AHQ-2-4, 5320 - 5388	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.97E-05	0.96	5.17	-	911.8
AHQ-2-7, 4711	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	1.16E-05	0.87	4.11	-	860.6
AHQ-2-4, 5358	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	5.62E-05	0.90	3.81	-	1287.9
AHQ-2-5, 4860 - 4932	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	4.68E-06	0.96	5.10	-	1068.3
AHQ-2-3, 5317 - 5325	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.52E-05	0.95	5.18	-	724.5
AHQ-2-4, 5406 - 5477	R.GQVLVFLGQSEGLR.S	1503.72793	2	2.34E-05	0.88	2.95	-	1251.1
AHQ-2-4, 5264 - 5334	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.20E-08	0.97	4.51	-	1622.5
AHQ-2-3, 5172	R.GQVLVFLGQSEGLR.S	1503.72793	2	3.51E-07	0.95	3.79	-	1509.4
AHQ-2-4, 5120 - 5196	R.GQVLVFLGQSEGLR.S	1503.72793	2	5.78E-08	0.97	5.31	-	1685.8
AHQ-2-5, 4108	R.HDLLVGAPLYMESR.A	1601.85188	2	1.46E-06	0.92	3.41	-	1306.4
AHQ-2-6, 4099 - 4153	R.HDLLVGAPLYMESR.A	1601.85188	2	2.18E-04	0.83	3.44	-	691.0
AHQ-2-4, 3829 - 3861	R.HDLLVGAPLYM*ESR.A	1617.85128	2	2.29E-06	0.97	4.60	-	1828.2
AHQ-2-4, 4416 - 4484	R.HDLLVGAPLYMESR.A	1601.85188	2	6.25E-06	0.96	4.80	-	1312.9
AHQ-2-5, 3267 - 3276	K.HSPICHTTMAFLR.D	1572.83705	2	6.31E-08	0.67	2.71	-	343.2
AHQ-2-4, 2966	K.HSPICHTTM*AFLR.D	1588.83645	2	4.61E-04	0.77	2.71	-	612.5
AHQ-2-5, 4159 - 4160	K.IVLLDVPVR.A	1024.28196	2	1.64E-04	0.95	3.97	-	1360.4
AHQ-2-4, 4424 - 4497	K.IVLLDVPVR.A	1024.28196	2	3.23E-04	0.90	3.96	-	830.9
AHQ-2-12, 4327	K.IVLLDVPVR.A	1024.28196	2	1.50E-04	0.88	3.33	-	835.4
AHQ-2-6, 4107	K.IVLLDVPVR.A	1024.28196	2	2.90E-04	0.88	3.22	-	902.4
AHQ-2-3, 4505	K.IVLLDVPVR.A	1024.28196	2	9.94E-05	0.93	3.68	-	1024.4
AHQ-2-11, 4162	K.IVLLDVPVR.A	1024.28196	2	2.68E-04	0.88	3.28	-	801.5
AHQ-2-4, 4566 - 4585	R.IYVENDFSWDK.R	1416.51610	2	4.40E-07	0.92	3.91	-	737.4
AHQ-2-4, 4569 - 4577	R.IYVENDFSWDK.R	1416.51610	1	7.52E-06	0.27	2.07	-	386.3
AHQ-2-4, 3925 - 3998	R.IYVENDFSWDKR.Y	1572.70245	2	7.03E-06	0.95	4.17	-	1467.2
AHQ-2-4, 4308	R.IYVENDFSWDKR.Y	1572.70245	2	7.50E-05	0.69	3.04	-	862.2
AHQ-2-4, 4213	R.IYVENDFSWDKR.Y	1572.70245	2	4.57E-07	0.85	3.69	-	699.7
AHQ-2-10, 6499	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	8.61E-04	0.72	3.26	-	242.5
AHQ-2-10, 6363 - 6434	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	1.85E-05	0.88	3.84	-	521.9
AHQ-2-4, 4652	K.LSLNAELQLDR.Q	1272.43310	2	3.25E-08	0.92	3.88	-	912.6
AHQ-2-4, 5177	K.LSLNAELQLDR.Q	1272.43310	2	2.25E-06	0.96	3.75	-	1815.0
AHQ-2-4, 4777 - 4854	K.LSLNAELQLDR.Q	1272.43310	2	1.10E-06	0.90	3.30	-	1002.8
AHQ-2-11, 2112	R.NRPPLEEDDEEGE	1529.50164	2	2.14E-09	0.91	3.28	-	1021.2
AHQ-2-11, 2706	R.NVGSQTLQTFK.A	1223.36055	2	3.41E-04	0.92	3.60	-	733.4
AHQ-2-4, 3262	R.NVGSQTLQTFK.A	1223.36055	1	7.68E-06	0.13	2.07	-	163.2
AHQ-2-6, 2547	R.NVGSQTLQTFK.A	1223.36055	2	2.34E-07	0.88	3.22	-	612.7
AHQ-2-4, 2950 - 2954	R.NVGSQTLQTFK.A	1223.36055	1	5.93E-05	0.17	2.33	-	170.1
AHQ-2-12, 2742	R.NVGSQTLQTFK.A	1223.36055	2	7.07E-04	0.83	3.03	-	468.7
AHQ-2-4, 2692 - 2766	R.NVGSQTLQTFK.A	1223.36055	2	5.10E-04	0.90	3.80	-	516.8
AHQ-2-7, 5812	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	3.98E-05	0.97	5.22	-	2055.9
AHQ-2-3, 6283	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.88E-06	0.89	4.30	-	1134.6
AHQ-2-4, 5925	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.58E-10	0.97	6.24	-	1805.8
AHQ-2-4, 6062 - 6136	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.50E-09	0.92	4.60	-	1281.4
AHQ-2-1, 6326	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	9.18E-12	0.96	5.55	-	1240.1
AHQ-2-4, 6284 - 6352	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	1.06E-07	0.95	4.99	-	708.9
AHQ-2-14-, 5917	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	9.22E-07	0.94	4.90	-	1111.5
AHQ-2-5, 5899 - 5967	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.67E-10	0.95	5.56	-	1494.4
AHQ-2-6, 5867 - 5933	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.44E-04	0.97	6.32	-	1415.2
AHQ-2-4, 6137 - 6213	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	7.30E-05	0.85	3.74	-	528.5
AHQ-2-4, 6348 - 6417	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	4.02E-08	0.98	7.03	-	1607.2
AHQ-2-4, 6209 - 6281	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.19E-09	0.97	6.46	-	1508.6
AHQ-2-6, 5877 - 5945	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	7.51E-07	0.84	3.59	-	614.6
AHQ-2-3, 3759	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.90E-05	0.90	4.37	-	615.3
AHQ-2-4, 3652 - 3721	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.28E-06	0.92	4.18	-	632.0
AHQ-2-11, 3510	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.61E-04	0.84	4.05	-	414.9
AHQ-2-7, 3407	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.72E-07	0.93	4.60	-	614.9
AHQ-2-5, 3472 - 3481	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	7.94E-06	0.94	4.89	-	568.0
AHQ-2-6, 3433	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	4.51E-05	0.88	4.13	-	527.8
AHQ-2-4, 3877	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	6.07E-11	0.90	3.95	-	581.1
AHQ-2-11, 5266 - 5333	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.82E-04	0.92	4.44	-	999.2
AHQ-2-5, 5555	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	8.54E-06	0.88	3.82	-	714.2
AHQ-2-7, 5385 - 5465	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	7.31E-10	0.93	4.28	-	787.9
AHQ-2-7, 5475	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.07E-07	0.96	5.30	-	1021.4
AHQ-2-4, 5972 - 6000	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.09E-05	0.43	2.91	-	301.0
AHQ-2-1, 5841 - 5908	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.12E-06	0.93	4.37	-	839.9
AHQ-2-3, 5828 - 5836	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.66E-07	0.66	3.29	-	672.8
AHQ-2-6, 5479 - 5511	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	6.97E-05	0.91	4.17	-	768.1
AHQ-2-10, 5106	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.40E-05	0.95	4.77	-	1019.5
AHQ-2-13-, 5562 - 5565	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.24E-10	0.97	6.03	-	1215.4
AHQ-2-9, 5495	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.46E-05	0.83	3.67	-	611.4
AHQ-2-4, 5900 - 5966	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.87E-07	0.94	4.65	-	948.6
AHQ-2-4, 5757 - 5833	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	5.32E-07	0.96	5.25	-	1155.0
AHQ-2-4, 5838	R.TLGPSQEETGGVFLCPWR.A	2036.25364	3	4.13E-04	0.94	4.80	-	1329.1
AHQ-2-12, 5571 - 5581	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.56E-07	0.94	4.74	-	836.7
AHQ-2-6, 3527	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.03E-07	0.92	3.86	-	831.4
AHQ-2-11, 3560 - 3564	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.58E-05	0.91	4.12	-	604.1
AHQ-2-5, 3575	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.63E-06	0.86	3.05	-	928.1
AHQ-2-4, 3964	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.05E-07	0.92	3.89	-	802.1
AHQ-2-1, 3933 - 3937	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.47E-06	0.83	3.76	-	643.2
AHQ-2-7, 3509	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.18E-06	0.87	4.14	-	592.4
AHQ-2-4, 3780 - 3814	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.28E-04	0.85	3.53	-	637.7
AHQ-2-10, 3426	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.68E-05	0.89	3.70	-	723.8
AHQ-2-4, 3665 - 3690	K.TPVGSCFLAQPESGR.R	1607.76993	2	7.39E-05	0.72	3.02	-	730.7
AHQ-2-4, 6384	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	8.01E-08	0.96	5.27	-	1347.6
AHQ-2-4, 5273 - 5346	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	6.68E-07	0.98	6.54	-	1882.8
AHQ-2-4, 4916	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.35E-04	0.97	4.79	-	2019.0
AHQ-2-4, 5413 - 5494	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	5.71E-10	0.96	5.29	-	1499.2
AHQ-2-4, 4646	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	2	1.62E-06	0.86	3.34	-	947.5
AHQ-2-4, 6125	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	2.01E-06	0.92	4.57	-	1022.9
AHQ-2-5, 4420	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	7.86E-04	0.91	3.89	-	1242.0
AHQ-2-4, 5932	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	4.70E-04	0.82	3.34	-	886.3
AHQ-2-4, 4741	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	1.62E-10	0.96	4.55	-	1873.3
AHQ-2-4, 4632 - 4640	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	4.14E-06	0.96	5.27	-	1319.4
AHQ-2-5, 2293	R.VAIVVGAPR.T	882.08560	2	5.09E-06	0.86	2.83	-	979.0
AHQ-2-4, 2478 - 2496	R.VAIVVGAPR.T	882.08560	2	8.33E-06	0.94	3.69	-	1400.5
AHQ-2-7, 2253	R.VAIVVGAPR.T	882.08560	2	2.27E-05	0.90	3.43	-	949.1
AHQ-2-13-, 2627	R.VAIVVGAPR.T	882.08560	2	3.10E-06	0.91	3.09	-	1163.7
AHQ-2-4, 6476 - 6514	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.61E-07	0.96	5.55	-	1234.1
AHQ-2-4, 6724 - 6793	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.05E-07	0.98	6.02	-	1851.4
AHQ-2-4, 6876 - 6944	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	3.40E-08	0.98	6.49	-	2093.7
AHQ-2-4, 7013 - 7069	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	9.97E-08	0.98	5.95	-	1800.6
AHQ-2-4, 6009	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.11E-09	0.98	6.57	-	1910.0
AHQ-2-4, 7238 - 7266	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.35E-08	0.98	6.48	-	2054.9
AHQ-2-4, 7298 - 7372	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	6.65E-10	0.97	5.85	-	1620.9
AHQ-2-4, 6332 - 6408	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.65E-08	0.98	6.18	-	1549.1
AHQ-2-4, 7446 - 7456	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.08E-11	0.94	4.72	-	1058.0

AHQ-2-4, 7533 - 7606	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.28E-07	0.98	5.91	-	1615.6
AHQ-2-4, 7685 - 7757	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.85E-12	0.98	6.38	-	1717.4
AHQ-2-5, 6188	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.50E-04	0.66	3.40	-	381.3
AHQ-2-4, 6241 - 6261	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.59E-08	0.98	6.11	-	1932.0
AHQ-2-4, 7136 - 7201	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.43E-09	0.98	6.10	-	1401.5
AHQ-2-4, 6096 - 6166	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.16E-05	0.97	5.23	-	1729.2
AHQ-2-5, 3940 - 3977	R.VVLCELGNPMK.K	1261.53692	2	4.47E-06	0.93	3.99	-	925.4
AHQ-2-4, 3341 - 3370	R.VVLCELGNPM*K.K	1277.53632	2	7.85E-07	0.95	3.86	-	1364.9
AHQ-2-4, 4188 - 4189	R.VVLCELGNPMK.K	1261.53692	2	1.71E-06	0.96	4.50	-	1268.7
AHQ-2-5, 3283	R.VVLCELGNPMKK.N	1389.70984	2	5.68E-05	0.88	2.97	-	1097.1
AHQ-2-4, 3568	R.VVLCELGNPMKK.N	1389.70984	2	2.71E-05	0.74	2.81	-	628.2
AHQ-2-5, 3863 - 3873	R.VYLFLQPR.G	1036.25129	2	2.11E-05	0.94	3.90	-	1192.2
AHQ-2-4, 4145 - 4216	R.VYLFLQPR.G	1036.25129	2	1.70E-05	0.94	3.64	-	1096.8
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				1.97E-12	10.87	130.29	44.60	49481.2
AHQ-2-7, 4385 - 4467	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	3.09E-06	0.87	4.38	-	350.4
AHQ-2-5, 4551 - 4580	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	1.64E-04	0.71	3.42	-	357.3
AHQ-2-9, 4490	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	1.68E-05	0.75	3.80	-	294.6
AHQ-2-7, 4535 - 4604	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	2.69E-06	0.91	4.72	-	635.0
AHQ-2-7, 4393 - 4463	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	1.71E-05	0.90	4.31	-	746.7
AHQ-2-5, 5779	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.98E-05	0.67	2.96	-	354.8
AHQ-2-1, 5825 - 5888	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	4.49E-04	0.75	3.35	-	463.9
AHQ-2-1, 5982	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.10E-10	0.65	2.73	-	385.2
AHQ-2-14-, 5445 - 5512	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.72E-06	0.89	3.44	-	726.5
AHQ-2-13-, 5641	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.74E-07	0.52	2.98	-	378.9
AHQ-2-7, 5655 - 5724	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	3.38E-11	0.65	3.05	-	479.8
AHQ-2-5, 5588	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.01E-05	0.39	2.60	-	350.2
AHQ-2-7, 2413 - 2491	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.13E-11	0.97	5.58	-	1307.3
AHQ-2-2, 2678	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.11E-07	0.96	4.70	-	1084.3
AHQ-2-7, 2437	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	9.68E-08	0.97	5.53	-	1805.9
AHQ-2-13-, 2717	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.08E-11	0.97	5.30	-	1165.1
AHQ-2-4, 2646	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.34E-08	0.92	3.94	-	988.2
AHQ-2-9, 2506	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	1.97E-04	0.81	3.72	-	433.1
AHQ-2-13, 2769 - 2773	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	4.47E-05	0.94	4.54	-	756.0
AHQ-2-1, 2838	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	7.73E-07	0.95	4.70	-	776.4
AHQ-2-9, 5254	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.68E-05	0.81	3.97	-	338.8
AHQ-2-8, 4856	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	5.33E-06	0.95	4.62	-	1018.8
AHQ-2-1, 5609 - 5629	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	2.22E-04	0.95	4.08	-	2123.0
AHQ-2-11, 5006	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.84E-04	0.85	3.73	-	418.1
AHQ-2-3, 5439	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	4.44E-04	0.86	3.76	-	555.7
AHQ-2-5, 5155	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	9.93E-06	0.93	4.39	-	650.9
AHQ-2-5, 5156	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	3.09E-05	0.93	4.55	-	1392.3
AHQ-2-5, 5279	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.61E-06	0.84	3.93	-	444.3
AHQ-2-1, 5704 - 5725	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.64E-06	0.73	3.34	-	438.0
AHQ-2-4, 5613	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.14E-08	0.93	3.77	-	1155.2
AHQ-2-7, 5223 - 5297	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.31E-06	0.94	4.78	-	854.1
AHQ-2-6, 5078	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	4.60E-04	0.94	4.57	-	847.7
AHQ-2-7, 5080 - 5152	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.31E-08	0.93	4.58	-	738.8
AHQ-2-7, 4968 - 5035	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.12E-05	0.96	5.48	-	689.7
AHQ-2-2, 5493	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.01E-07	0.94	4.69	-	847.7
AHQ-2-11, 6381 - 6461	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	7.08E-04	0.87	3.77	-	594.8
AHQ-2-7, 6901 - 6971	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	2.41E-04	0.77	3.27	-	556.8
AHQ-2-12, 6701 - 6769	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	5.80E-10	0.92	4.49	-	799.3
AHQ-2-12, 6706	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	2.49E-06	0.78	3.60	-	844.4
AHQ-2-14-, 6543	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	4.67E-05	0.54	2.91	-	346.8
AHQ-2-4, 4650 - 4720	K.IHLISTQSAIPYALR.V	1683.97576	2	4.52E-09	0.96	5.07	-	1124.4
AHQ-2-9, 4222 - 4230	K.IHLISTQSAIPYALR.V	1683.97576	2	6.44E-06	0.97	4.91	-	1435.0
AHQ-2-7, 4103 - 4171	K.IHLISTQSAIPYALR.V	1683.97576	2	1.97E-12	0.97	5.79	-	1406.1
AHQ-2-3, 4743	K.IHLISTQSAIPYALR.V	1683.97576	2	4.71E-06	0.96	4.64	-	1106.0
AHQ-2-8, 3936	K.IHLISTQSAIPYALR.V	1683.97576	2	2.24E-07	0.97	4.71	-	1394.4
AHQ-2-10, 4096	K.IHLISTQSAIPYALR.V	1683.97576	2	5.13E-07	0.93	3.60	-	980.8
AHQ-2-2, 4673 - 4753	K.IHLISTQSAIPYALR.V	1683.97576	2	1.16E-07	0.97	4.91	-	1251.9
AHQ-2-5, 4332	K.IHLISTQSAIPYALR.V	1683.97576	2	1.74E-08	0.97	4.72	-	1474.1
AHQ-2-5, 4345	K.IHLISTQSAIPYALR.V	1683.97576	3	1.54E-04	0.57	3.09	-	555.0
AHQ-2-13-, 2101 - 2105	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.11E-08	0.95	4.17	-	1357.6
AHQ-2-7, 1597 - 1603	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.09E-07	0.92	3.54	-	1415.9
AHQ-2-7, 1691 - 1756	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.44E-07	0.94	3.88	-	1493.7
AHQ-2-10, 1859	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.79E-07	0.55	2.61	-	416.5
AHQ-2-11, 2030	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	7.14E-06	0.86	3.26	-	854.9
AHQ-2-12, 2007	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.66E-07	0.88	3.71	-	776.7
AHQ-2-4, 1966	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.26E-04	0.85	3.05	-	882.3
AHQ-2-14-, 2085	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	2.34E-09	0.96	4.46	-	1074.6
AHQ-2-7, 2637	R.TSTADYAMFK.V	1135.27203	1	4.84E-05	0.12	2.08	-	235.1
AHQ-2-9, 3763 - 3770	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	4.34E-05	0.94	4.97	-	1189.9
AHQ-2-7, 3713 - 3752	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	3.86E-04	0.91	4.36	-	782.4
AHQ-2-7, 3715 - 3716	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	2	6.47E-04	0.60	2.99	-	205.3
AHQ-2-4, 4044	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	5.88E-04	0.91	4.64	-	802.7
AHQ-2-1, 4162	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	4.44E-05	0.89	4.32	-	850.9
AHQ-2-8, 3691	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	4.96E-06	0.73	3.50	-	590.6
AHQ-2-8, 3695	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	2	2.62E-04	0.27	2.54	-	192.2
AHQ-2-10, 3815	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	1.51E-05	0.94	5.05	-	1310.0
AHQ-2-1, 4380	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	9.41E-10	0.94	5.59	-	1012.9
AHQ-2-7, 3899 - 3925	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	2.90E-04	0.95	5.24	-	1536.8
AHQ-2-8, 3826	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	4.83E-04	0.86	4.32	-	730.4
AHQ-2-5, 3111 - 3180	R.VELEDWNGR.T	1118.18129	2	6.72E-05	0.86	2.66	-	1022.9
AHQ-2-8, 3000	R.VELEDWNGR.T	1118.18129	2	1.81E-04	0.88	2.91	-	1193.6
AHQ-2-7, 3079	R.VELEDWNGR.T	1118.18129	2	6.26E-07	0.90	3.07	-	1158.2
AHQ-2-12, 2919	K.YEASILTHDSSIR.Y	1492.61564	2	5.54E-06	0.86	2.93	-	846.0
AHQ-2-12, 2922	K.YEASILTHDSSIR.Y	1492.61564	1	3.64E-04	0.61	2.81	-	336.1
AHQ-2-11, 2888	K.YEASILTHDSSIR.Y	1492.61564	2	1.64E-05	0.78	2.99	-	537.9
AHQ-2-5, 2663 - 2671	K.YEASILTHDSSIR.Y	1492.61564	2	2.69E-05	0.91	3.83	-	819.7
AHQ-2-2, 2937	K.YEASILTHDSSIR.Y	1492.61564	2	3.60E-05	0.50	2.62	-	399.2
AHQ-2-6, 2727	K.YEASILTHDSSIR.Y	1492.61564	2	1.08E-04	0.73	2.62	-	585.6
AHQ-2-9, 2692 - 2710	K.YEASILTHDSSIR.Y	1492.61564	2	1.03E-06	0.93	3.82	-	986.1
AHQ-2-7, 2564 - 2635	K.YEASILTHDSSIR.Y	1492.61564	2	5.54E-06	0.89	3.65	-	705.2
AHQ-2-12, 2911	K.YEASILTHDSSIR.Y	1492.61564	2	1.19E-05	0.83	3.49	-	490.8
AHQ-2-3, 2889 - 2949	K.YEASILTHDSSIR.Y	1492.61564	2	2.16E-05	0.82	3.01	-	650.4
AHQ-2-1, 2896 - 2908	R.YLQEIYNSNNQK.I	1514.62131	2	1.66E-06	0.94	4.45	-	1227.3
gi|11386183|ref|NP_008921.1| WAS protein family, member 2; suppressor of cyclic-AMP receptor (WASP-				1.99E-12	1.82	20.31	7.60	54283.7
AHQ-2-10, 3660	K.VTQLDPKEEEVSLQGINTR.K	2157.36743	2	1.23E-06	0.84	3.73	-	483.1
AHQ-2-14-, 6841	K.YAEDIFGELFTQANTFASR.V	2181.34601	2	1.99E-12	0.98	6.20	-	2134.1
gi|4506925|ref|NP_003013.1| SH3 domain binding glutamic acid-rich protein like; SH3-binding domain				2.00E-12	3.83	40.33	64.00	12774.2
AHQ-2-13, 5897 - 5956	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	4.89E-04	0.84	4.25	-	407.1
AHQ-2-13-, 6425 - 6489	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	6.40E-08	0.93	4.13	-	920.6
AHQ-2-13, 4873 - 4941	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	3.47E-06	0.89	3.99	-	1010.9
AHQ-2-13, 5004 - 5067	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	5.44E-09	0.96	5.92	-	1159.5
AHQ-2-13-, 5265	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	7.32E-11	0.92	4.71	-	868.9
AHQ-2-13-, 5173 - 5241	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	6.91E-09	0.97	6.36	-	1380.2

AHQ-2-13-, 5081 - 5149	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.00E-12	0.97	6.60	-	1195.5
AHQ-2-13-, 4983 - 5014	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.31E-12	0.96	6.18	-	1074.3
AHQ-2-13, 2768 - 2831	K.IGFEEKDIAANEENRK.W	1864.00620	2	6.14E-05	0.97	4.70	-	2029.1
AHQ-2-13, 2433 - 2443	R.VYIASSSGSTAIK.K	1284.44065	2	7.77E-05	0.96	4.43	-	1985.5
AHQ-2-13, 2435	R.VYIASSSGSTAIK.K	1284.44065	1	8.97E-04	0.10	2.04	-	226.4
gi|4759212|ref|NP_004598.1| beta-tubulin cofactor A [Homo sapiens]				2.10E-12	0.97	10.31	16.70	12854.8
AHQ-2-13, 3365	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	8.61E-06	0.97	5.10	-	1468.2
AHQ-2-13-, 3359	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	3.12E-05	0.89	3.77	-	684.5
AHQ-2-13, 3359	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	2.10E-12	0.97	6.28	-	1427.2
gi|4557677|ref|NP_000203.1| integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu				2.24E-12	19.39	230.29	32.50	87185.6
AHQ-2-3, 2864 - 2873	R.AKWDTANNPLYK.E	1421.58225	2	7.24E-07	0.89	3.83	-	671.5
AHQ-2-3, 2868	R.AKWDTANNPLYK.E	1421.58225	1	6.15E-05	0.74	3.31	-	443.2
AHQ-2-6, 2834	R.AKWDTANNPLYK.E	1421.58225	1	5.44E-04	0.30	2.00	-	322.4
AHQ-2-1, 3097	R.AKWDTANNPLYK.E	1421.58225	2	1.49E-09	0.91	3.25	-	862.5
AHQ-2-4, 5600	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	2	4.53E-06	0.89	4.49	-	421.4
AHQ-2-3, 5461 - 5531	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	3.30E-04	0.92	4.57	-	962.5
AHQ-2-3, 5459 - 5516	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	2	1.06E-06	0.71	3.29	-	591.3
AHQ-2-5, 5303	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	3.86E-04	0.92	4.43	-	829.6
AHQ-2-4, 5542 - 5552	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	6.66E-05	0.94	5.21	-	1067.9
AHQ-2-3, 5608	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	3.56E-04	0.87	4.04	-	1008.3
AHQ-2-2, 4582	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.35E-07	0.87	4.09	-	716.1
AHQ-2-1, 4508 - 4512	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.40E-08	0.76	3.51	-	398.7
AHQ-2-3, 4468 - 4539	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	1.86E-07	0.73	3.47	-	579.1
AHQ-2-4, 4522 - 4602	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.22E-06	0.89	4.55	-	503.9
AHQ-2-6, 4298	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.63E-04	0.73	3.56	-	410.9
AHQ-2-5, 4411	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.24E-12	0.67	3.23	-	405.6
AHQ-2-1, 6045 - 6078	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.04E-06	0.93	4.51	-	770.9
AHQ-2-1, 4620 - 4634	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	5.34E-08	0.95	4.84	-	790.6
AHQ-2-4, 4698 - 4761	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	5.26E-05	0.85	3.44	-	709.2
AHQ-2-3, 7303	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	8.25E-05	0.84	3.44	-	470.8
AHQ-2-3, 4643 - 4716	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	6.76E-06	0.93	4.64	-	724.5
AHQ-2-3, 7087	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	4.71E-07	0.68	2.94	-	475.2
AHQ-2-3, 6863	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	3.27E-09	0.90	4.01	-	558.8
AHQ-2-3, 6579 - 6651	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	3.89E-06	0.96	5.14	-	1110.3
AHQ-2-3, 6439 - 6511	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.36E-04	0.95	4.80	-	1148.1
AHQ-2-3, 6296 - 6368	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.76E-07	0.96	5.66	-	851.6
AHQ-2-3, 6156 - 6224	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	9.14E-08	0.94	4.60	-	898.9
AHQ-2-4, 5104	K.DDLWSIQNLGTK.L	1390.52332	1	4.96E-04	0.53	2.76	-	366.7
AHQ-2-5, 4920 - 4921	K.DDLWSIQNLGTK.L	1390.52332	1	1.28E-06	0.15	1.93	-	272.8
AHQ-2-3, 5080 - 5099	K.DDLWSIQNLGTK.L	1390.52332	2	1.30E-05	0.94	4.57	-	871.1
AHQ-2-6, 4835	K.DDLWSIQNLGTK.L	1390.52332	1	5.51E-08	0.54	2.47	-	445.0
AHQ-2-3, 5088	K.DDLWSIQNLGTK.L	1390.52332	1	7.12E-07	0.74	2.90	-	560.0
AHQ-2-9, 4378	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.50E-04	0.76	3.05	-	696.2
AHQ-2-6, 4342 - 4354	K.DNCAPESIEFPVSEAR.V	1822.93099	2	2.48E-05	0.88	3.52	-	853.6
AHQ-2-3, 4785	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.22E-08	0.93	3.58	-	1470.0
AHQ-2-7, 4372	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.58E-05	0.36	2.56	-	374.6
AHQ-2-3, 4519 - 4587	K.DNCAPESIEFPVSEAR.V	1822.93099	2	4.40E-06	0.75	2.85	-	798.9
AHQ-2-4, 4596 - 4616	K.DNCAPESIEFPVSEAR.V	1822.93099	2	6.92E-07	0.93	3.71	-	1215.1
AHQ-2-1, 3464	K.EATSTFTNITYR.G	1404.50685	2	5.83E-07	0.83	2.87	-	755.2
AHQ-2-4, 3342	K.EATSTFTNITYR.G	1404.50685	2	7.41E-07	0.68	2.77	-	572.6
AHQ-2-3, 3325	K.EATSTFTNITYR.G	1404.50685	2	7.74E-07	0.70	2.86	-	480.6
AHQ-2-3, 2260 - 2283	R.FQYYEDSSGK.S	1224.25749	2	4.19E-06	0.72	2.72	-	500.5
AHQ-2-3, 3819	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.29E-05	0.63	2.79	-	528.5
AHQ-2-4, 3669 - 3749	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.76E-07	0.96	4.20	-	1719.1
AHQ-2-6, 3467	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	3.50E-05	0.97	4.46	-	1607.8
AHQ-2-1, 3736	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	9.91E-06	0.87	3.50	-	884.2
AHQ-2-5, 3524 - 3531	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	5.20E-07	0.94	3.81	-	1557.6
AHQ-2-3, 3735	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.36E-07	0.89	3.72	-	1066.3
AHQ-2-3, 3672 - 3687	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	3.48E-09	0.83	3.35	-	776.0
AHQ-2-3, 3587 - 3665	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	3.07E-05	0.91	4.20	-	907.6
AHQ-2-2, 3742 - 3790	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.68E-07	0.89	3.78	-	864.3
AHQ-2-5, 1577	K.GSGDSSQVTQVSPQR.I	1533.58302	2	7.80E-04	0.72	3.20	-	822.8
AHQ-2-4, 1716 - 1780	K.GSGDSSQVTQVSPQR.I	1533.58302	2	5.69E-04	0.79	3.13	-	801.6
AHQ-2-7, 1581	K.GSGDSSQVTQVSPQR.I	1533.58302	2	1.35E-04	0.53	2.84	-	664.7
AHQ-2-7, 2336 - 2349	K.HVLTLTDQVTR.F	1283.45912	2	2.21E-07	0.92	3.38	-	692.6
AHQ-2-4, 2561	K.HVLTLTDQVTR.F	1283.45912	2	5.26E-07	0.90	3.60	-	605.4
AHQ-2-6, 2385	K.HVLTLTDQVTR.F	1283.45912	2	2.67E-07	0.92	3.88	-	680.6
AHQ-2-3, 2624	K.HVLTLTDQVTR.F	1283.45912	2	8.62E-04	0.77	2.58	-	573.9
AHQ-2-3, 2540 - 2551	K.HVLTLTDQVTR.F	1283.45912	2	6.93E-06	0.90	3.67	-	511.8
AHQ-2-4, 2573	K.HVLTLTDQVTR.F	1283.45912	1	4.03E-06	0.63	3.02	-	289.7
AHQ-2-5, 2371	K.HVLTLTDQVTR.F	1283.45912	2	2.40E-09	0.94	3.64	-	900.1
AHQ-2-1, 2738 - 2808	K.HVLTLTDQVTR.F	1283.45912	2	1.40E-08	0.89	2.94	-	756.9
AHQ-2-3, 4997	K.IGDTVSFSIEAK.V	1267.41009	2	1.10E-06	0.93	3.20	-	1096.0
AHQ-2-3, 4287 - 4355	R.NDASHLLVFTTDAK.T	1532.67977	2	1.05E-04	0.75	2.70	-	536.9
AHQ-2-5, 3501	R.NDASHLLVFTTDAK.T	1532.67977	2	2.13E-08	0.97	4.35	-	1660.3
AHQ-2-3, 4459 - 4532	R.NDASHLLVFTTDAK.T	1532.67977	2	9.17E-10	0.97	4.69	-	1412.4
AHQ-2-6, 3454 - 3525	R.NDASHLLVFTTDAK.T	1532.67977	2	1.13E-09	0.96	4.46	-	1496.1
AHQ-2-7, 3403	R.NDASHLLVFTTDAK.T	1532.67977	2	4.74E-07	0.89	3.74	-	830.3
AHQ-2-3, 3540 - 3557	R.NDASHLLVFTTDAK.T	1532.67977	2	7.01E-08	0.87	3.75	-	858.6
AHQ-2-1, 4060 - 4125	R.NDASHLLVFTTDAK.T	1532.67977	2	6.84E-05	0.87	3.34	-	887.7
AHQ-2-3, 3788 - 3864	R.NDASHLLVFTTDAK.T	1532.67977	2	5.44E-09	0.98	5.49	-	1697.8
AHQ-2-3, 3771 - 3847	R.NDASHLLVFTTDAK.T	1532.67977	2	2.34E-10	0.97	5.19	-	1551.3
AHQ-2-1, 4554	R.NDASHLLVFTTDAK.T	1532.67977	2	2.00E-10	0.95	4.28	-	1249.6
AHQ-2-3, 3861	R.NDASHLLVFTTDAK.T	1532.67977	3	1.01E-09	0.95	4.58	-	1402.1
AHQ-2-4, 3845	R.NDASHLLVFTTDAK.T	1532.67977	2	9.22E-09	0.97	4.78	-	1545.6
AHQ-2-4, 4454 - 4492	R.NDASHLLVFTTDAK.T	1532.67977	2	6.82E-09	0.94	4.28	-	1083.6
AHQ-2-4, 3230 - 3257	K.SFTIKPVGFK.D	1124.35685	2	1.97E-05	0.88	2.87	-	1221.0
AHQ-2-3, 3215	K.SFTIKPVGFK.D	1124.35685	1	4.11E-04	0.37	2.47	-	573.9
AHQ-2-1, 4574	K.SILYVVEEPECPK.G	1564.78173	2	1.04E-04	0.83	2.85	-	864.1
AHQ-2-3, 4499 - 4508	K.SILYVVEEPECPK.G	1564.78173	2	1.28E-05	0.95	3.48	-	1572.7
AHQ-2-4, 3714	R.TDTCMSSNGLLCSGR.G	1661.81786	2	6.53E-07	0.69	3.08	-	891.0
AHQ-2-3, 3827	R.TDTCMSSNGLLCSGR.G	1661.81786	2	2.82E-07	0.72	2.52	-	834.6
AHQ-2-4, 2978 - 2981	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	4.04E-07	0.75	3.07	-	399.4
AHQ-2-4, 2876	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	6.69E-08	0.94	3.79	-	1311.9
AHQ-2-1, 2885	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	7.34E-08	0.96	3.95	-	1897.0
AHQ-2-1, 2984	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.09E-06	0.88	3.38	-	789.7
AHQ-2-5, 3545	R.TDTCMSSNGLLCSGR.G	1661.81786	2	4.69E-07	0.92	3.59	-	1026.7
AHQ-2-5, 3651	R.TDTCMSSNGLLCSGR.G	1661.81786	2	2.35E-08	0.86	3.32	-	1048.4
AHQ-2-2, 3778	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.94E-07	0.77	2.71	-	893.5
AHQ-2-1, 3722 - 3768	R.TDTCMSSNGLLCSGR.G	1661.81786	2	5.90E-06	0.83	2.85	-	942.5
AHQ-2-1, 3622	R.TDTCMSSNGLLCSGR.G	1661.81786	2	7.64E-10	0.91	3.53	-	947.5
AHQ-2-3, 2957 - 3037	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.33E-07	0.87	3.46	-	1103.2
AHQ-2-3, 2871 - 2881	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.12E-10	0.96	3.59	-	1714.3
AHQ-2-3, 1763 - 1837	R.VLEDRPLSDK.G	1172.31354	2	7.00E-04	0.88	3.29	-	930.2
AHQ-2-7, 2495 - 2551	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	1.28E-07	0.90	3.80	-	1309.9
AHQ-2-1, 2869	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	1.07E-04	0.90	4.14	-	1106.6
AHQ-2-3, 2680 - 2755	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	2.09E-09	0.96	5.44	-	1599.0

AHQ-2-3, 3264 - 3268	K.WDTANNPLYK.E	1222.33111	2	3.03E-06	0.76	3.36	-	463.2
AHQ-2-1, 3776	K.YCECDDFSCVR.Y	1514.59674	2	9.60E-07	0.95	3.61	-	1190.7
AHQ-2-2, 3842	K.YCECDDFSCVR.Y	1514.59674	2	1.49E-09	0.91	3.52	-	975.4
AHQ-2-3, 3763	K.YCECDDFSCVR.Y	1514.59674	2	4.98E-07	0.91	3.44	-	990.2
AHQ-2-4, 3768 - 3774	K.YCECDDFSCVR.Y	1514.59674	2	7.30E-05	0.85	2.59	-	1044.0
AHQ-2-1, 2382	R.YCRDEIESVK.E	1300.42023	2	3.30E-05	0.87	3.29	-	1002.6
AHQ-2-4, 2229 - 2232	R.YCRDEIESVK.E	1300.42023	2	8.40E-05	0.90	3.05	-	1173.3
gi|10346135|ref|NP_055083.1| microtubule-associated protein, RP/EB family, member 2; T-cell activat				2.35E-12	1.94	20.27	9.80	37031.1
AHQ-2-13, 6680	R.FQDNLDFIQWFK.K	1601.78539	2	1.15E-07	0.96	4.46	-	1284.0
AHQ-2-9, 7118 - 7122	R.FQDNLDFIQWFK.K	1601.78539	2	3.52E-08	0.97	4.59	-	1356.8
AHQ-2-12, 6946 - 6950	R.FQDNLDFIQWFK.K	1601.78539	2	5.20E-07	0.96	4.28	-	1266.6
AHQ-2-13-, 6903	R.FQDNLDFIQWFK.K	1601.78539	2	2.51E-10	0.97	5.16	-	1426.5
AHQ-2-12, 4953	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	3.30E-08	0.94	4.92	-	1171.6
AHQ-2-9, 4686 - 4694	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	2	2.35E-12	0.97	5.30	-	1277.3
AHQ-2-9, 4684 - 4688	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	2.14E-09	0.94	4.96	-	1141.1
gi|4507767|ref|NP_003326.1| ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi				3.29E-12	4.18	50.24	10.10	111719.5
AHQ-2-4, 5030 - 5101	K.FQHLHGRPPQPWDPVDAETVVGLAR.D	2824.14835	3	6.84E-05	0.83	3.59	-	670.4
AHQ-2-4, 7496	R.GLNPDLQVIPLTYPLDPTTEHIYGDNFFSR.V	3434.79811	3	1.45E-07	0.67	3.43	-	291.8
AHQ-2-5, 7376	R.GLNPDLQVIPLTYPLDPTTEHIYGDNFFSR.V	3434.79811	3	3.10E-05	0.75	3.62	-	308.6
AHQ-2-4, 4757	R.VLVSGLQGLGAEVAK.N	1441.69805	2	3.29E-12	0.98	4.70	-	2313.3
AHQ-2-4, 4316	R.VTELVQQLTGQAPAPGQR.V	1894.12181	2	8.12E-04	0.82	3.75	-	539.9
AHQ-2-4, 4124 - 4136	R.YFPSTAEHTLQWAR.H	1707.86959	2	5.66E-10	0.88	3.86	-	671.9
gi|23510338|ref|NP_003325.2| ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity				3.43E-12	6.96	80.28	11.80	117848.1
AHQ-2-4, 6693 - 6700	R.AAVATFLQSVQVPEFTPK.S	1934.22430	2	2.71E-04	0.67	2.93	-	522.3
AHQ-2-4, 4682 - 4693	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	3.43E-12	0.96	5.63	-	750.6
AHQ-2-4, 3682 - 3689	K.DNPGVVTCLDEAR.H	1447.55333	2	8.18E-04	0.90	3.49	-	855.3
AHQ-2-4, 2308	R.KPLLESGTLGTK.G	1244.46280	2	1.83E-06	0.92	3.31	-	1205.8
AHQ-2-4, 5474	R.LAGTQPLEVLEAVQR.S	1624.86348	2	4.33E-04	0.84	3.32	-	616.6
AHQ-2-4, 6124	R.NEEDAAELVALAQAVNAR.A	1885.02541	2	1.35E-06	0.95	4.18	-	1651.6
AHQ-2-5, 6667	K.SLVASLAEPDFVVTDFAK.F	1910.15638	2	3.29E-05	0.92	4.25	-	620.8
AHQ-2-4, 4201	R.YDGQVAVFGSDLQEK.L	1656.77453	2	1.09E-04	0.80	3.11	-	736.9
gi|29739414|ref|XP_294015.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				3.62E-12	3.72	40.24	17.70	26916.7
AHQ-2-11, 3868	K.IISNASCTTNCLAPLAK.V	1837.10868	2	3.57E-05	0.84	3.72	-	1019.3
AHQ-2-11, 4190	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.01E-04	0.46	2.68	-	676.6
AHQ-2-10, 3699 - 3759	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.44E-05	0.73	3.09	-	1025.7
AHQ-2-12, 4035	K.IISNASCTTNCLAPLAK.V	1837.10868	2	3.09E-06	0.90	3.96	-	1188.8
AHQ-2-9, 5090 - 5160	K.LISWYDNEFGYSNR.V	1764.87478	2	3.62E-12	0.96	3.92	-	1343.8
AHQ-2-9, 5236	K.LISWYDNEFGYSNR.V	1764.87478	2	1.05E-06	0.92	4.12	-	850.4
AHQ-2-9, 5323	K.LISWYDNEFGYSNR.V	1764.87478	2	3.53E-05	0.67	2.90	-	501.3
AHQ-2-9, 4735	K.LISWYDNEFGYSNR.V	1764.87478	2	1.33E-06	0.79	2.98	-	610.6
AHQ-2-10, 4658	K.LISWYDNEFGYSNR.V	1764.87478	2	3.38E-09	0.92	3.94	-	852.1
AHQ-2-10, 4748	K.LISWYDNEFGYSNR.V	1764.87478	2	1.06E-06	0.94	4.20	-	1085.6
AHQ-2-14-, 5031 - 5035	K.LISWYDNEFGYSNR.V	1764.87478	2	3.34E-09	0.96	4.77	-	1286.2
AHQ-2-13-, 5085	K.LISWYDNEFGYSNR.V	1764.87478	2	1.24E-11	0.95	4.24	-	1053.0
AHQ-2-11, 4806 - 4868	K.LISWYDNEFGYSNR.V	1764.87478	2	1.08E-08	0.95	4.07	-	1230.9
AHQ-2-11, 4933 - 4998	K.LISWYDNEFGYSNR.V	1764.87478	2	1.11E-05	0.84	3.07	-	662.1
AHQ-2-9, 4950 - 5018	K.LISWYDNEFGYSNR.V	1764.87478	2	3.61E-09	0.96	4.53	-	1368.2
AHQ-2-12, 5070	K.LISWYDNEFGYSNR.V	1764.87478	2	4.54E-07	0.94	3.71	-	1217.6
AHQ-2-13, 4987 - 4988	K.LISWYDNEFGYSNR.V	1764.87478	2	1.27E-06	0.95	4.20	-	1297.1
AHQ-2-14, 6212 - 6278	K.LISWYDNEFGYSNR.V	1764.87478	2	4.97E-08	0.96	4.22	-	1600.0
AHQ-2-9, 2579	R.VVDLMAHMASK.E	1202.47292	2	1.85E-06	0.97	4.05	-	1604.6
AHQ-2-9, 2719 - 2790	R.VVDLMAHMASKE	1331.58746	2	8.16E-05	0.90	3.42	-	1196.1
gi|5729997|ref|NP_004154.2| RAB27B, member RAS oncogene family [Homo sapiens]				4.10E-12	4.59	50.23	29.80	24607.7
AHQ-2-10, 6303 - 6367	K.AVETLLDLIMK.R	1246.54211	2	7.02E-04	0.72	3.03	-	623.2
AHQ-2-11, 5598	K.AVETLLDLIM*K.R	1262.54151	2	1.10E-05	0.90	3.68	-	796.2
AHQ-2-11, 6540	K.AVETLLDLIMK.R	1246.54211	2	7.10E-07	0.94	3.96	-	1206.3
AHQ-2-10, 5358	K.AVETLLDLIM*K.R	1262.54151	2	4.25E-05	0.93	3.74	-	1221.0
AHQ-2-11, 6254 - 6257	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	3.64E-05	0.92	3.99	-	845.3
AHQ-2-10, 5970	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	3.05E-06	0.85	3.51	-	602.4
AHQ-2-11, 3469	K.VHLQLWDTAGQER.F	1553.70390	2	4.10E-12	0.96	4.21	-	1307.6
AHQ-2-10, 3255	K.VHLQLWDTAGQER.F	1553.70390	2	8.92E-11	0.95	4.24	-	1194.8
AHQ-2-10, 4186 - 4263	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	4.62E-09	0.94	4.21	-	895.6
AHQ-2-11, 4329 - 4396	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	4.23E-08	0.97	4.65	-	1506.0
AHQ-2-10, 4326 - 4391	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	3.53E-07	0.69	3.60	-	540.3
gi|4758086|ref|NP_004069.1| cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain				4.34E-12	6.01	70.26	46.10	20567.3
AHQ-2-11, 4173	K.GFGFGQGAGALVHSE	1434.53788	2	2.21E-06	0.91	3.12	-	1118.0
AHQ-2-13, 4228 - 4237	K.GFGFGQGAGALVHSE	1434.53788	2	4.82E-07	0.95	4.17	-	1187.8
AHQ-2-13-, 4279	K.GFGFGQGAGALVHSE	1434.53788	2	2.33E-05	0.94	3.67	-	1235.8
AHQ-2-11, 4060 - 4086	K.GFGFGQGAGALVHSE	1434.53788	2	6.83E-05	0.93	3.87	-	934.3
AHQ-2-11, 3209 - 3217	K.GLESTTLADKDGEIYCK.G	1902.06957	3	5.53E-06	0.85	3.92	-	773.0
AHQ-2-12, 3279	K.GLESTTLADKDGEIYCK.G	1902.06957	2	9.15E-06	0.96	5.23	-	877.7
AHQ-2-13, 3371	K.GLESTTLADKDGEIYCK.G	1902.06957	2	4.36E-10	0.95	4.66	-	1151.8
AHQ-2-13-, 3369	K.GLESTTLADKDGEIYCK.G	1902.06957	2	2.13E-08	0.95	4.75	-	1042.0
AHQ-2-11, 3160 - 3220	K.GLESTTLADKDGEIYCK.G	1902.06957	2	7.15E-09	0.94	4.96	-	882.5
AHQ-2-11, 2477	K.GYGYGQGAGTLSTDK.G	1475.54194	2	1.96E-04	0.87	3.40	-	766.1
AHQ-2-12, 3519	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	1.40E-08	0.88	4.07	-	596.4
AHQ-2-12, 3521	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	4.68E-09	0.94	4.78	-	958.7
AHQ-2-13-, 3698	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	4.34E-12	0.87	4.63	-	462.8
AHQ-2-11, 3409 - 3474	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	2.55E-06	0.85	4.02	-	564.3
AHQ-2-13, 3640	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	4.93E-06	0.90	3.84	-	806.4
AHQ-2-10, 3276	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	1.53E-08	0.66	3.30	-	324.6
AHQ-2-11, 2922	K.KNLDSTTVAVHGEEIYCK.S	2066.27805	2	5.70E-04	0.56	2.51	-	313.8
AHQ-2-11, 3380 - 3457	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	5.17E-10	0.96	5.13	-	1106.1
AHQ-2-11, 3882	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	1.24E-04	0.84	3.63	-	551.0
gi|4506413|ref|NP_002875.1| RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				4.87E-12	7.01	80.29	33.20	20987.1
AHQ-2-11, 1854	K.CDLEDER.V	937.95183	2	3.97E-04	0.76	2.67	-	729.5
AHQ-2-11, 2408 - 2412	K.CDLEDERVVGK.E	1321.43945	2	8.40E-05	0.89	3.45	-	1124.7
AHQ-2-10, 6578	K.INVNEIFYDLVR.Q	1495.70427	2	1.04E-08	0.94	4.28	-	1018.8
AHQ-2-14-, 6767 - 6839	K.INVNEIFYDLVR.Q	1495.70427	2	1.07E-09	0.95	5.21	-	1019.5
AHQ-2-11, 6566 - 6648	K.INVNEIFYDLVR.Q	1495.70427	2	1.17E-09	0.96	5.04	-	1278.6
AHQ-2-14-, 6771	K.INVNEIFYDLVR.Q	1495.70427	1	4.21E-06	0.23	2.69	-	209.9
AHQ-2-14-, 6637	K.INVNEIFYDLVR.Q	1495.70427	2	2.73E-08	0.95	4.50	-	1338.8
AHQ-2-11, 6576 - 6640	K.INVNEIFYDLVR.Q	1495.70427	1	2.65E-06	0.30	3.14	-	218.2
AHQ-2-13-, 6919	K.INVNEIFYDLVR.Q	1495.70427	1	8.60E-07	0.08	1.85	-	78.7
AHQ-2-13-, 6918	K.INVNEIFYDLVR.Q	1495.70427	2	4.93E-08	0.94	4.83	-	894.9
AHQ-2-13, 6700 - 6701	K.INVNEIFYDLVR.Q	1495.70427	2	2.12E-07	0.95	4.92	-	1061.7
AHQ-2-11, 6010	K.INVNEIFYDLVR.Q	1495.70427	1	2.46E-04	0.41	2.69	-	270.0
AHQ-2-11, 5686 - 5748	K.INVNEIFYDLVR.Q	1495.70427	2	2.40E-06	0.92	3.99	-	1095.0
AHQ-2-11, 5692	K.INVNEIFYDLVR.Q	1495.70427	1	1.10E-04	0.07	1.96	-	127.6
AHQ-2-11, 6685 - 6749	K.INVNEIFYDLVR.Q	1495.70427	2	3.52E-08	0.94	4.65	-	1065.7
AHQ-2-11, 6584 - 6636	K.INVNEIFYDLVR.Q	1495.70427	1	3.15E-04	0.18	3.10	-	141.7
AHQ-2-11, 6004	K.INVNEIFYDLVR.Q	1495.70427	2	1.78E-07	0.95	5.13	-	829.1
AHQ-2-11, 6425	K.INVNEIFYDLVR.Q	1495.70427	2	1.43E-08	0.94	4.20	-	1346.9
AHQ-2-10, 2494	K.LVVLGSGGVGK.S	986.19059	2	1.34E-05	0.80	3.18	-	752.1
AHQ-2-11, 2573 - 2624	K.LVVLGSGGVGK.S	986.19059	2	2.12E-08	0.92	3.68	-	1009.7
AHQ-2-13, 2827	K.LVVLGSGGVGK.S	986.19059	2	2.73E-04	0.92	3.27	-	1230.5
AHQ-2-10, 2479	K.LVVLGSGGVGK.S	986.19059	1	5.15E-05	0.81	3.01	-	541.1

AHQ-2-11, 6202 - 6268	K.SALTVQFVQGIFVEK.Y	1666.94196	2	8.00E-05	0.97	5.31	-	1630.4
AHQ-2-11, 6464 - 6525	K.SALTVQFVQGIFVEK.Y	1666.94196	2	5.04E-05	0.94	3.85	-	1450.9
AHQ-2-11, 6529 - 6594	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.42E-04	0.97	5.45	-	1690.4
AHQ-2-11, 6148 - 6208	K.SALTVQFVQGIFVEK.Y	1666.94196	2	6.30E-06	0.97	4.86	-	2070.1
AHQ-2-11, 6328 - 6404	K.SALTVQFVQGIFVEK.Y	1666.94196	2	6.16E-06	0.97	5.71	-	1851.3
AHQ-2-11, 5664	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.85E-06	0.85	3.43	-	730.7
AHQ-2-11, 6654 - 6712	K.SALTVQFVQGIFVEK.Y	1666.94196	2	6.11E-04	0.95	4.81	-	1303.6
AHQ-2-11, 6874 - 6949	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.47E-04	0.96	4.68	-	1737.4
AHQ-2-11, 5698	K.SKINVNEIFYDLVR.Q	1710.95483	2	5.58E-08	0.93	4.05	-	1128.2
AHQ-2-11, 5917 - 5918	K.SKINVNEIFYDLVR.Q	1710.95483	2	7.91E-12	0.96	4.66	-	1281.0
AHQ-2-11, 6132 - 6206	K.SKINVNEIFYDLVR.Q	1710.95483	2	5.18E-09	0.91	4.03	-	831.2
AHQ-2-11, 5240 - 5265	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.25E-07	0.86	3.47	-	697.1
AHQ-2-14-, 6193 - 6212	K.SKINVNEIFYDLVR.Q	1710.95483	3	4.64E-04	0.83	3.88	-	958.0
AHQ-2-11, 5082 - 5084	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.40E-09	0.89	4.17	-	636.6
AHQ-2-14-, 6191	K.SKINVNEIFYDLVR.Q	1710.95483	2	4.87E-12	0.96	4.86	-	1175.2
AHQ-2-13-, 2818 - 2821	K.YDPTIEDSYR.K	1259.30338	2	6.30E-07	0.85	3.19	-	350.8
AHQ-2-11, 2677 - 2745	K.YDPTIEDSYR.K	1259.30338	2	1.41E-05	0.85	2.73	-	459.0
AHQ-2-11, 2532	K.YDPTIEDSYR.K	1259.30338	2	9.88E-07	0.87	2.89	-	542.4
AHQ-2-13, 2875	K.YDPTIEDSYR.K	1259.30338	2	1.52E-04	0.77	2.66	-	417.3
AHQ-2-11, 2301 - 2330	K.YDPTIEDSYRK.Q	1387.47629	2	1.88E-06	0.82	3.04	-	444.6
gi|17986273|ref|NP_524144.1| fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2				5.26E-12	0.96	10.23	8.20	21145.0
AHQ-2-13, 3356	R.VFDKEGNGTVMGAELR.H	1723.93228	2	6.35E-09	0.93	3.78	-	1063.0
AHQ-2-13-, 3345 - 3353	R.VFDKEGNGTVMGAELR.H	1723.93228	2	5.26E-12	0.96	4.59	-	1274.8
AHQ-2-12, 3305 - 3374	R.VFDKEGNGTVMGAELR.H	1723.93228	2	5.24E-06	0.93	3.84	-	1127.6
gi|5031855|ref|NP_005556.1| lymphocyte cytosolic protein 2; SH2 domain-containing leukocyte protein				5.41E-12	2.84	30.28	8.30	60187.8
AHQ-2-12, 4154	K.ESQVYLLGTGLR.G	1336.51879	2	2.64E-05	0.90	3.69	-	1293.3
AHQ-2-14-, 6823	R.GKEDFLSVSDIIDYFR.K	1905.09669	2	5.41E-12	0.98	5.64	-	2364.7
AHQ-2-10, 6580	R.SEVLGWDPDSLADYFK.K	1842.98222	2	3.16E-07	0.95	4.44	-	1011.8
gi|4504349|ref|NP_000509.1| beta globin [Homo sapiens]				6.03E-12	9.86	110.28	67.30	15998.3
AHQ-2-14-, 5640	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.94E-06	0.94	4.51	-	880.3
AHQ-2-13-, 5823	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	2.92E-05	0.77	2.93	-	824.1
AHQ-2-13-, 5639 - 5665	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	3.85E-06	0.95	4.81	-	953.3
AHQ-2-13-, 5125	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.97E-07	0.85	4.06	-	404.7
AHQ-2-14-, 5055	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	7.15E-09	0.89	4.00	-	706.0
AHQ-2-14, 6153 - 6232	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	8.14E-04	0.70	3.47	-	451.3
AHQ-2-13, 4960 - 5035	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	5.75E-06	0.90	4.27	-	539.0
AHQ-2-13, 5536 - 5599	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.83E-05	0.89	4.07	-	711.7
AHQ-2-13, 5380	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.47E-05	0.88	3.87	-	728.2
AHQ-2-13, 5043	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	3.38E-07	0.95	4.75	-	1501.2
AHQ-2-13, 3509	K.GTFATLSELHCDK.L	1480.62492	2	7.47E-08	0.72	3.25	-	338.4
AHQ-2-13-, 3505	K.GTFATLSELHCDK.L	1480.62492	2	1.12E-05	0.82	3.73	-	515.3
AHQ-2-13, 5001	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	2.58E-09	0.93	4.69	-	942.3
AHQ-2-13, 5011	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	2	1.98E-05	0.90	4.13	-	414.9
AHQ-2-13-, 5055 - 5121	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	5.44E-09	0.89	3.86	-	1099.2
AHQ-2-13-, 5119	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	2	8.58E-09	0.89	3.82	-	636.6
AHQ-2-13-, 4867	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	6.15E-09	0.97	5.62	-	1570.5
AHQ-2-13-, 2758	K.LHVDPENFR.L	1127.23455	2	3.44E-04	0.78	2.50	-	931.8
AHQ-2-13, 6459	R.LLGNVLVCVLAHHFGK.E	1779.14197	3	6.12E-08	0.84	3.80	-	529.4
AHQ-2-13, 3441	K.SAVTALWGK.V	933.08624	2	5.41E-04	0.92	2.65	-	1251.6
AHQ-2-14, 6349	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	9.82E-05	0.92	3.88	-	1228.5
AHQ-2-13, 5069 - 5131	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.58E-10	0.96	5.17	-	1269.0
AHQ-2-13-, 4973 - 5041	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.60E-08	0.95	4.66	-	1186.9
AHQ-2-13-, 5042	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	1.74E-09	0.87	3.53	-	768.0
AHQ-2-13, 4907 - 4931	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	7.73E-07	0.96	5.30	-	1227.4
AHQ-2-13, 5105 - 5107	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	8.37E-08	0.87	3.79	-	702.2
AHQ-2-13-, 5217	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	4.45E-07	0.84	3.13	-	603.2
AHQ-2-13-, 5209 - 5277	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	6.03E-12	0.96	5.53	-	1422.4
AHQ-2-13-, 3238 - 3269	K.VNVDEVGGEALGR.L	1315.41484	1	4.98E-06	0.65	2.95	-	333.9
AHQ-2-13, 3287	K.VNVDEVGGEALGR.L	1315.41484	1	9.63E-05	0.78	3.33	-	439.7
AHQ-2-13, 3281 - 3284	K.VNVDEVGGEALGR.L	1315.41484	2	4.38E-06	0.96	4.57	-	1601.6
AHQ-2-14-, 3243 - 3245	K.VNVDEVGGEALGR.L	1315.41484	2	8.18E-07	0.97	4.58	-	2112.5
AHQ-2-13-, 3265 - 3266	K.VNVDEVGGEALGR.L	1315.41484	2	1.87E-04	0.96	4.38	-	1459.3
AHQ-2-13-, 2662	K.VVAGVANALAHK.Y	1150.35593	2	2.17E-09	0.96	3.95	-	1649.5
AHQ-2-13, 2271	K.VVAGVANALAHK.Y	1150.35593	2	1.33E-04	0.86	2.96	-	961.7
gi|4507877|ref|NP_003364.1| vinculin isoform VCL [Homo sapiens]				6.61E-12	53.03	630.31	49.80	116721.6
AHQ-2-10, 3296 - 3306	K.AGEVINQPMMMAAR.Q	1519.83932	2	5.22E-04	0.91	4.02	-	819.1
AHQ-2-4, 3693	K.AGEVINQPMMMAAR.Q	1519.83932	2	1.25E-06	0.95	4.66	-	1089.0
AHQ-2-12, 7213	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.11E-08	0.95	4.37	-	988.2
AHQ-2-11, 6777 - 6856	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.52E-11	0.97	4.96	-	1260.6
AHQ-2-10, 6819 - 6822	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.34E-06	0.97	5.74	-	1308.0
AHQ-2-13, 6877	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.84E-08	0.97	5.52	-	1266.8
AHQ-2-13-, 7073	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.52E-06	0.96	5.22	-	864.8
AHQ-2-1, 7314	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.90E-08	0.96	4.51	-	1101.5
AHQ-2-9, 7498 - 7503	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.46E-07	0.97	5.11	-	1216.8
AHQ-2-8, 7467 - 7468	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.48E-05	0.97	5.68	-	1126.0
AHQ-2-7, 7544 - 7559	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.06E-07	0.93	4.35	-	741.2
AHQ-2-3, 7609 - 7689	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.54E-09	0.96	5.23	-	1006.8
AHQ-2-6, 7227 - 7306	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.54E-11	0.97	4.99	-	1446.5
AHQ-2-4, 7512 - 7589	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	6.16E-06	0.87	3.77	-	679.2
AHQ-2-5, 7639	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.53E-09	0.88	3.64	-	744.8
AHQ-2-5, 7548	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	6.61E-12	0.97	5.44	-	1261.9
AHQ-2-4, 7662	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.97E-06	0.97	5.05	-	1183.5
AHQ-2-14-, 6925 - 6927	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	8.35E-10	0.98	5.88	-	1275.4
AHQ-2-7, 2965 - 2973	R.ALASQLQDSLK.D	1174.32943	2	7.45E-04	0.83	2.91	-	839.3
AHQ-2-6, 3037	R.ALASQLQDSLK.D	1174.32943	2	2.05E-04	0.84	3.09	-	844.2
AHQ-2-5, 3035 - 3047	R.ALASQLQDSLK.D	1174.32943	2	8.83E-05	0.95	3.78	-	1436.9
AHQ-2-4, 3289 - 3361	R.ALASQLQDSLK.D	1174.32943	2	5.12E-04	0.88	3.22	-	952.3
AHQ-2-4, 3801	K.AQQVSQGLDVLTAK.V	1458.64233	1	7.34E-06	0.71	2.94	-	591.6
AHQ-2-6, 3281	K.AQQVSQGLDVLTAK.V	1458.64233	1	1.83E-05	0.64	3.76	-	294.8
AHQ-2-6, 3203 - 3269	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.22E-08	0.96	4.26	-	1570.9
AHQ-2-1, 3760	K.AQQVSQGLDVLTAK.V	1458.64233	2	4.59E-05	0.94	3.91	-	1064.8
AHQ-2-3, 3513 - 3593	K.AQQVSQGLDVLTAK.V	1458.64233	2	5.15E-04	0.95	3.77	-	1533.1
AHQ-2-4, 3561	K.AQQVSQGLDVLTAK.V	1458.64233	1	5.49E-04	0.63	3.25	-	397.6
AHQ-2-4, 3513 - 3585	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.25E-09	0.96	4.71	-	1431.4
AHQ-2-7, 3183 - 3195	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.14E-10	0.97	4.71	-	1478.7
AHQ-2-8, 3008	K.AQQVSQGLDVLTAK.V	1458.64233	2	7.37E-11	0.96	4.41	-	1307.5
AHQ-2-9, 3224	K.AQQVSQGLDVLTAK.V	1458.64233	2	7.05E-05	0.84	3.24	-	790.2
AHQ-2-2, 3556 - 3624	K.AQQVSQGLDVLTAK.V	1458.64233	2	6.39E-04	0.95	4.45	-	1205.4
AHQ-2-5, 3280	K.AQQVSQGLDVLTAK.V	1458.64233	1	4.29E-04	0.28	2.67	-	256.0
AHQ-2-7, 2211	K.AVAGNISDPGLQK.S	1270.41721	2	2.94E-05	0.87	3.45	-	682.1
AHQ-2-5, 2251	K.AVAGNISDPGLQK.S	1270.41721	2	6.60E-07	0.90	3.55	-	774.0
AHQ-2-6, 2255	K.AVAGNISDPGLQK.S	1270.41721	2	8.62E-07	0.87	3.66	-	713.3
AHQ-2-3, 2424	K.AVAGNISDPGLQK.S	1270.41721	2	3.57E-05	0.82	3.37	-	643.8
AHQ-2-5, 2259	K.AVAGNISDPGLQK.S	1270.41721	1	4.19E-05	0.53	3.20	-	305.8
AHQ-2-4, 2529	K.AVAGNISDPGLQK.S	1270.41721	2	8.83E-04	0.82	3.47	-	589.0
AHQ-2-4, 2416	K.AVAGNISDPGLQK.S	1270.41721	2	3.74E-05	0.90	3.61	-	812.8
AHQ-2-8, 2135	K.AVAGNISDPGLQK.S	1270.41721	2	2.28E-04	0.86	3.30	-	716.4

AHQ-2-6, 2261	K.AVAGNISDPGLQK.S	1270.41721	1	5.34E-06	0.68	2.81	-	435.1
AHQ-2-3, 6197	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	6.85E-05	0.92	3.69	-	1129.7
AHQ-2-4, 6201 - 6272	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	6.64E-06	0.92	4.04	-	937.5
AHQ-2-6, 5861 - 5862	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	3.33E-04	0.79	3.29	-	694.0
AHQ-2-4, 6228	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	4.77E-07	0.93	4.81	-	1315.5
AHQ-2-1, 6166	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	2.12E-06	0.84	3.50	-	758.2
AHQ-2-4, 6448	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	6.06E-05	0.76	3.05	-	719.9
AHQ-2-6, 5874 - 5882	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	2.05E-05	0.88	4.50	-	988.8
AHQ-2-5, 5991	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	1.82E-07	0.92	4.31	-	1425.1
AHQ-2-1, 6169	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	5.89E-05	0.91	4.64	-	1016.1
AHQ-2-4, 2233 - 2309	R.DPSASPGDAGEQAIR.Q	1471.51169	2	7.68E-08	0.94	4.48	-	756.7
AHQ-2-7, 2187	R.DPSASPGDAGEQAIR.Q	1471.51169	2	3.08E-06	0.90	3.76	-	682.2
AHQ-2-5, 2195 - 2209	R.DPSASPGDAGEQAIR.Q	1471.51169	2	4.41E-09	0.94	4.22	-	942.2
AHQ-2-1, 2416 - 2426	R.DPSASPGDAGEQAIR.Q	1471.51169	2	4.28E-07	0.88	3.55	-	720.7
AHQ-2-3, 2328	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.10E-08	0.92	3.65	-	861.9
AHQ-2-6, 2185	R.DPSASPGDAGEQAIR.Q	1471.51169	2	6.89E-07	0.93	4.55	-	650.3
AHQ-2-4, 2316 - 2320	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.66E-08	0.91	3.24	-	895.1
AHQ-2-5, 4504	K.ELLPVLISAM*K.I	1230.54265	2	3.32E-04	0.89	3.31	-	916.4
AHQ-2-4, 6068 - 6085	K.ELLPVLISAMK.I	1214.54325	2	1.73E-04	0.81	3.09	-	601.4
AHQ-2-4, 4833	K.ELLPVLISAM*K.I	1230.54265	2	1.59E-06	0.86	3.40	-	847.3
AHQ-2-5, 5695	K.ELLPVLISAMK.I	1214.54325	2	5.53E-05	0.82	3.27	-	601.5
AHQ-2-10, 2466	R.ELTPQVVSAAR.I	1171.32878	2	4.77E-04	0.87	2.57	-	1099.1
AHQ-2-11, 2960	K.ETVQTTEDQILK.R	1405.53306	2	3.47E-05	0.71	3.43	-	403.5
AHQ-2-5, 2875	K.ETVQTTEDQILK.R	1405.53306	1	1.80E-04	0.13	2.44	-	145.4
AHQ-2-4, 2916	K.ETVQTTEDQILKR.D	1561.71942	2	2.83E-05	0.67	2.74	-	601.3
AHQ-2-11, 2797 - 2874	K.ETVQTTEDQILKR.D	1561.71942	2	2.25E-04	0.54	3.03	-	373.3
AHQ-2-7, 2624	K.ETVQTTEDQILKR.D	1561.71942	2	2.95E-04	0.62	2.84	-	544.1
AHQ-2-5, 2660	K.ETVQTTEDQILKR.D	1561.71942	2	3.81E-04	0.71	2.64	-	673.4
AHQ-2-3, 2936	K.ETVQTTEDQILKR.D	1561.71942	2	9.10E-08	0.66	2.74	-	632.4
AHQ-2-4, 7749 - 7769	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	5.67E-05	0.80	3.96	-	460.1
AHQ-2-5, 7297 - 7365	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	7.88E-07	0.98	6.26	-	1266.1
AHQ-2-1, 7164 - 7166	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.16E-06	0.93	4.21	-	1033.0
AHQ-2-11, 6676 - 6745	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.86E-04	0.89	3.99	-	881.7
AHQ-2-4, 7368 - 7444	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.41E-09	0.97	5.64	-	1032.0
AHQ-2-5, 6627 - 6644	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	6.58E-05	0.82	3.38	-	632.7
AHQ-2-3, 6825	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	2.88E-05	0.72	3.44	-	474.9
AHQ-2-4, 6874 - 6880	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	1.07E-07	0.93	4.11	-	1093.8
AHQ-2-4, 1929 - 2065	K.GNDIIAAAK.R	872.98920	1	1.50E-05	0.39	2.01	-	472.5
AHQ-2-4, 1998	K.GNDIIAAAK.R	872.98920	1	6.91E-05	0.23	1.95	-	486.6
AHQ-2-5, 3313	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	1.27E-04	0.88	4.15	-	675.5
AHQ-2-4, 3572	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	3	2.06E-09	0.93	4.46	-	1492.2
AHQ-2-4, 3564 - 3580	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	4.10E-04	0.86	4.08	-	652.0
AHQ-2-4, 2142	K.IAELCDDPKER.D	1347.47690	2	8.77E-05	0.75	3.05	-	575.0
AHQ-2-5, 1932	K.IAELCDDPKER.D	1347.47690	2	1.24E-04	0.89	3.26	-	1011.8
AHQ-2-5, 3212	K.IAELCDDPKERDDILR.S	1960.15548	3	2.87E-07	0.90	3.79	-	1338.5
AHQ-2-4, 3468	K.IAELCDDPKERDDILR.S	1960.15548	3	2.45E-04	0.86	3.10	-	1290.1
AHQ-2-5, 3211	K.IAELCDDPKERDDILR.S	1960.15548	2	1.55E-04	0.65	3.01	-	543.1
AHQ-2-13, 3084	R.IPTISTQLK.I	1001.20202	2	2.61E-04	0.68	2.59	-	636.0
AHQ-2-4, 2014	R.KIAELCDDPKER.D	1475.64981	2	6.04E-06	0.91	3.06	-	1272.7
AHQ-2-4, 3136 - 3210	R.KIAELCDDPKERDDILR.S	2088.32839	3	4.23E-04	0.74	3.24	-	555.4
AHQ-2-4, 4512	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.46E-09	0.90	4.17	-	607.0
AHQ-2-5, 4191 - 4244	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	4.03E-05	0.94	5.45	-	994.4
AHQ-2-4, 4429 - 4444	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	5.64E-04	0.67	3.01	-	392.5
AHQ-2-6, 4071 - 4145	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	2.14E-05	0.92	4.23	-	1398.5
AHQ-2-5, 2544	R.LANVMM*GPYR.Q	1168.41500	2	1.76E-04	0.71	2.70	-	700.1
AHQ-2-4, 2824	R.LANVM*MGPYR.Q	1168.41500	2	8.54E-04	0.86	3.65	-	910.5
AHQ-2-6, 3053	R.LANVMMGPYR.Q	1152.41560	2	3.06E-04	0.90	3.42	-	950.4
AHQ-2-6, 2625	R.LANVM*MGPYR.Q	1168.41500	2	8.48E-05	0.87	3.18	-	1004.5
AHQ-2-5, 3027	R.LANVMMGPYR.Q	1152.41560	2	2.15E-04	0.90	3.89	-	695.1
AHQ-2-5, 2980 - 2983	K.LLAVAATAPPDAPNR.E	1477.69048	2	8.61E-04	0.92	4.46	-	573.4
AHQ-2-4, 4541	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	2	8.76E-05	0.83	3.58	-	419.8
AHQ-2-4, 4597 - 4668	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	4.96E-07	0.82	3.94	-	651.0
AHQ-2-4, 4736	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	5.65E-05	0.84	4.05	-	494.8
AHQ-2-5, 4372 - 4385	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	1.68E-04	0.79	4.11	-	542.7
AHQ-2-4, 3750 - 3820	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.11E-09	0.94	4.76	-	633.4
AHQ-2-6, 3535	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.91E-07	0.94	4.89	-	706.6
AHQ-2-5, 3555	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	8.47E-05	0.67	3.15	-	451.7
AHQ-2-4, 4684 - 4753	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	8.96E-07	0.91	4.37	-	673.4
AHQ-2-4, 4706	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	2.12E-04	0.80	3.07	-	1031.9
AHQ-2-7, 4293 - 4303	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	3.99E-06	0.84	4.06	-	601.2
AHQ-2-7, 3487	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	4.28E-04	0.87	3.61	-	783.3
AHQ-2-12, 4202	R.MALLMAEMSR.L	1153.46531	2	1.52E-07	0.96	4.52	-	1772.0
AHQ-2-12, 2167	R.M*ALLM*AEM*SR.L	1201.46351	2	5.19E-04	0.87	2.90	-	878.4
AHQ-2-4, 4353	R.MALLMAEMSR.L	1153.46531	2	9.43E-08	0.96	4.65	-	1548.0
AHQ-2-6, 3947	K.MLGQMTDQVADLR.A	1478.72055	2	2.22E-07	0.96	4.95	-	1512.4
AHQ-2-4, 3781	K.M*LGQMTDQVADLR.A	1494.71995	2	2.02E-06	0.70	2.52	-	652.7
AHQ-2-5, 3987	K.M*LGQM*TDQVADLR.A	1510.71935	2	9.38E-05	0.93	3.52	-	1519.1
AHQ-2-4, 3297	K.MLGQM*TDQVADLR.A	1494.71995	2	3.45E-06	0.92	3.85	-	1453.4
AHQ-2-4, 4233 - 4236	K.MLGQMTDQVADLR.A	1478.72055	2	4.85E-10	0.97	4.95	-	1638.2
AHQ-2-7, 3907	K.MLGQMTDQVADLR.A	1478.72055	2	1.26E-07	0.90	2.91	-	1693.0
AHQ-2-5, 3084	K.MLGQM*TDQVADLR.A	1494.71995	2	8.54E-07	0.93	3.86	-	1522.2
AHQ-2-8, 3811 - 3814	K.MLGQMTDQVADLR.A	1478.72055	2	1.84E-08	0.97	4.93	-	1876.3
AHQ-2-9, 3951	K.MLGQMTDQVADLR.A	1478.72055	2	2.67E-06	0.91	3.29	-	1267.0
AHQ-2-4, 2865	K.M*LGQM*TDQVADLR.A	1510.71935	2	8.97E-04	0.96	3.81	-	1966.1
AHQ-2-6, 3062	K.MLGQM*TDQVADLR.A	1494.71995	2	3.65E-04	0.73	2.87	-	827.7
AHQ-2-4, 4253	K.M*LGQM*TDQVADLR.A	1510.71935	2	2.41E-05	0.94	3.68	-	1347.3
AHQ-2-3, 4272	K.MLGQMTDQVADLR.A	1478.72055	2	4.15E-08	0.96	4.61	-	1725.6
AHQ-2-5, 3979 - 3983	K.MLGQMTDQVADLR.A	1478.72055	2	1.47E-06	0.97	4.70	-	1911.4
AHQ-2-4, 3101 - 3104	K.M*SAEINEIIR.V	1192.36823	2	9.40E-06	0.93	3.59	-	1116.5
AHQ-2-4, 3441	K.MSAEINEIIR.V	1176.36883	2	1.88E-04	0.86	2.67	-	949.4
AHQ-2-5, 3504	K.MSAEINEIIR.V	1176.36883	2	1.52E-04	0.81	3.02	-	800.8
AHQ-2-5, 2848	K.M*TGLVDEAIDTK.S	1309.46876	2	1.13E-07	0.96	3.84	-	1726.7
AHQ-2-4, 3593 - 3594	K.MTGLVDEAIDTK.S	1293.46936	1	1.40E-04	0.34	2.19	-	356.0
AHQ-2-4, 3086	K.M*TGLVDEAIDTK.S	1309.46876	2	3.20E-07	0.96	3.99	-	1535.7
AHQ-2-6, 3314	K.MTGLVDEAIDTK.S	1293.46936	2	2.20E-07	0.97	4.03	-	1663.6
AHQ-2-6, 2863	K.M*TGLVDEAIDTK.S	1309.46876	2	6.83E-06	0.89	3.05	-	1119.2
AHQ-2-5, 4041 - 4113	K.MTGLVDEAIDTK.S	1293.46936	2	4.91E-04	0.80	2.63	-	942.9
AHQ-2-6, 2659	R.NPGNQAAYEHFETMK.N	1737.87437	3	6.16E-07	0.68	3.05	-	475.9
AHQ-2-6, 2646 - 2651	R.NPGNQAAYEHFETMK.N	1737.87437	2	7.19E-05	0.89	3.90	-	520.7
AHQ-2-5, 2576	R.NPGNQAAYEHFETMK.N	1737.87437	2	1.20E-06	0.90	3.70	-	812.1
AHQ-2-4, 2381	R.NPGNQAAYEHFETM*K.N	1753.87377	2	4.21E-04	0.88	3.71	-	582.9
AHQ-2-4, 2886	R.NPGNQAAYEHFETMK.N	1737.87437	2	2.41E-05	0.93	3.82	-	1043.5
AHQ-2-5, 2577 - 2589	R.NPGNQAAYEHFETMK.N	1737.87437	3	1.53E-05	0.77	3.30	-	731.0
AHQ-2-5, 2648	K.NQWIDNVEK.M	1146.23464	1	2.96E-04	0.62	2.84	-	273.5
AHQ-2-6, 2671 - 2686	K.NQWIDNVEK.M	1146.23464	1	1.93E-06	0.26	2.22	-	225.9
AHQ-2-4, 2720 - 2800	K.QVATALQNLQTK.T	1315.50112	2	6.63E-05	0.89	3.76	-	515.1
AHQ-2-7, 2489 - 2505	K.QVATALQNLQTK.T	1315.50112	2	4.80E-06	0.85	3.03	-	657.9

AHQ-2-4, 3416	R.SLGEISALTSK.L	1106.25186	1	3.17E-09	0.68	3.35	-	297.3
AHQ-2-7, 3048	R.SLGEISALTSK.L	1106.25186	1	3.96E-06	0.33	2.49	-	170.7
AHQ-2-1, 3646	R.SLGEISALTSK.L	1106.25186	2	1.78E-04	0.81	2.68	-	693.1
AHQ-2-7, 3039	R.SLGEISALTSK.L	1106.25186	2	2.37E-04	0.90	3.41	-	728.0
AHQ-2-6, 3150	R.SLGEISALTSK.L	1106.25186	1	1.92E-06	0.63	3.02	-	183.5
AHQ-2-6, 3130 - 3149	R.SLGEISALTSK.L	1106.25186	2	3.39E-06	0.93	3.60	-	929.3
AHQ-2-8, 2842	K.SLLDASEEAIKK.D	1304.47187	2	3.34E-05	0.80	2.83	-	745.4
AHQ-2-4, 3276 - 3281	K.SLLDASEEAIKK.D	1304.47187	2	4.02E-05	0.89	3.13	-	1017.7
AHQ-2-5, 3007 - 3008	K.SLLDASEEAIKK.D	1304.47187	2	3.33E-06	0.79	2.89	-	751.0
AHQ-2-4, 2244 - 2312	K.STVEGIQASVK.T	1119.25064	2	3.21E-06	0.88	2.86	-	1065.0
AHQ-2-5, 2120	K.STVEGIQASVK.T	1119.25064	1	2.48E-05	0.15	2.11	-	103.5
AHQ-2-5, 2112 - 2119	K.STVEGIQASVK.T	1119.25064	2	1.26E-06	0.91	3.41	-	928.6
AHQ-2-4, 2392 - 2397	R.TDAGFTLR.W	880.96819	2	8.53E-05	0.84	2.52	-	873.3
AHQ-2-7, 7501	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	1.05E-06	0.74	3.59	-	495.7
AHQ-2-11, 6809 - 6814	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	6.71E-09	0.85	4.10	-	620.8
AHQ-2-14-, 6789 - 6860	R.TIESILEPVAQQISHLVIM*HEEGEVDGK.A	3119.49274	3	1.60E-05	0.68	3.52	-	261.7
AHQ-2-5, 7487	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	2.59E-06	0.82	3.79	-	457.7
AHQ-2-3, 7411	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	8.52E-04	0.66	3.12	-	641.9
AHQ-2-4, 7460 - 7477	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	4.65E-06	0.88	4.64	-	551.5
AHQ-2-12, 5930 - 6009	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	9.84E-08	0.94	5.31	-	940.7
AHQ-2-12, 5533 - 5597	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	4.78E-06	0.59	3.02	-	607.7
AHQ-2-4, 7105 - 7172	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	5.99E-04	0.63	3.39	-	639.2
AHQ-2-12, 5149 - 5182	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	1.22E-06	0.88	4.78	-	655.4
AHQ-2-4, 5380	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	6.25E-04	0.72	3.25	-	713.4
AHQ-2-12, 6001	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	5.70E-05	0.84	3.91	-	544.2
AHQ-2-6, 7093 - 7094	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.91E-10	0.90	4.80	-	574.4
AHQ-2-12, 6993	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.52E-09	0.88	4.75	-	439.4
AHQ-2-12, 5945	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	6.28E-06	0.77	3.94	-	488.9
AHQ-2-12, 6663 - 6725	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	1.00E-05	0.88	5.15	-	652.3
AHQ-2-4, 7374 - 7393	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	6.60E-04	0.69	3.78	-	391.4
AHQ-2-10, 5635	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.01E-07	0.64	3.29	-	464.0
AHQ-2-10, 6590	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	8.04E-05	0.92	4.49	-	1001.5
AHQ-2-10, 2926	R.TNLLQVCER.I	1134.28859	1	1.52E-05	0.34	2.34	-	66.0
AHQ-2-4, 3148 - 3217	R.TNLLQVCER.I	1134.28859	2	2.02E-05	0.92	3.38	-	1231.4
AHQ-2-12, 3101	R.TNLLQVCER.I	1134.28859	2	7.02E-06	0.87	3.29	-	925.3
AHQ-2-12, 4931	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	3.15E-05	0.47	2.94	-	365.8
AHQ-2-5, 5965 - 6023	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	3	1.89E-04	0.94	4.71	-	1439.3
AHQ-2-4, 5786	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	3	2.18E-05	0.93	4.94	-	1470.7
AHQ-2-6, 5881 - 5950	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	3.99E-05	0.89	4.30	-	599.2
AHQ-2-5, 5931 - 5999	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	7.59E-05	0.96	5.27	-	885.7
AHQ-2-5, 4987	R.VDQLTAQLADLAAR.G	1485.66778	2	6.14E-06	0.94	2.81	-	2229.1
AHQ-2-5, 4940 - 4993	R.VDQLTAQLADLAAR.G	1485.66778	1	5.66E-07	0.81	3.18	-	400.4
AHQ-2-5, 5296 - 5367	R.VLQLTSWDEDAWASK.D	1749.90156	2	8.27E-09	0.96	4.63	-	1384.0
AHQ-2-1, 5692	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.41E-05	0.92	3.65	-	889.3
AHQ-2-6, 5270 - 5281	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.11E-09	0.97	4.70	-	1396.4
AHQ-2-5, 5429	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.94E-04	0.75	2.84	-	718.5
AHQ-2-2, 5649	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.03E-08	0.94	4.29	-	1045.8
AHQ-2-4, 5608 - 5690	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.10E-08	0.96	5.09	-	1168.5
AHQ-2-3, 5595 - 5597	R.VLQLTSWDEDAWASK.D	1749.90156	2	5.11E-07	0.95	4.44	-	1058.4
AHQ-2-4, 2372	R.VMLVNSM*NTVK.E	1252.53021	2	4.35E-04	0.95	3.79	-	1159.0
AHQ-2-5, 2863	R.VMLVNSMNTVK.E	1236.53081	2	4.18E-05	0.95	3.68	-	1344.5
AHQ-2-5, 2995	R.VMLVNSMNTVK.E	1236.53081	2	3.68E-05	0.92	3.41	-	1120.1
AHQ-2-4, 3145	R.VMLVNSMNTVK.E	1236.53081	2	5.10E-04	0.93	3.47	-	1237.8
AHQ-2-5, 2689 - 2703	R.WIDNPTVDDR.G	1231.29640	2	3.17E-05	0.93	3.59	-	1190.6
AHQ-2-6, 2701	R.WIDNPTVDDR.G	1231.29640	2	2.34E-04	0.96	4.18	-	1409.3
gi|4505735|ref|NP_002611.1| platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H				6.69E-12	1.92	20.25	26.00	11552.6
AHQ-2-14-, 3843 - 3911	R.AEAEEDGDLQCLCVK.T	1739.86036	2	6.69E-12	0.96	4.91	-	1356.0
AHQ-2-14-, 3752	R.AEAEEDGDLQCLCVK.T	1739.86036	2	6.37E-06	0.92	3.44	-	1024.4
AHQ-2-14-, 5861	R.KICLDLQALLYK.K	1479.80948	2	2.29E-04	0.96	4.68	-	1124.4
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				6.73E-12	23.66	260.32	25.60	191612.6
AHQ-2-3, 6853	K.ADDPSSYMEVVQAANTSGNWEELVK.Y	2741.92512	2	6.55E-07	0.92	4.52	-	692.2
AHQ-2-3, 7599 - 7600	K.AFMTADLPNELIELLEK.I	1948.26956	2	7.93E-04	0.93	4.81	-	551.1
AHQ-2-3, 4488	R.ALEHFTDLYDIK.R	1465.63179	2	6.83E-06	0.93	3.66	-	1097.9
AHQ-2-1, 7308	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	1.54E-07	0.87	4.48	-	638.7
AHQ-2-3, 7596 - 7601	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	5.48E-05	0.91	5.03	-	792.1
AHQ-2-3, 4961	R.GQFSTDELVAEVEK.R	1552.66462	2	2.99E-04	0.87	3.57	-	915.7
AHQ-2-4, 4830 - 4844	R.GQFSTDELVAEVEKR.N	1708.85097	2	9.83E-09	0.93	3.99	-	1081.5
AHQ-2-3, 4827	R.GQFSTDELVAEVEKR.N	1708.85097	2	8.45E-09	0.95	3.83	-	1585.8
AHQ-2-3, 3207	K.HDVVFLITK.Y	1072.28194	2	4.10E-07	0.94	3.20	-	1181.5
AHQ-2-3, 3208	K.HDVVFLITK.Y	1072.28194	1	1.62E-04	0.59	2.19	-	680.2
AHQ-2-3, 5396 - 5413	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	2.42E-08	0.94	4.62	-	1101.8
AHQ-2-3, 3568	K.IVLDNSVFSEHR.N	1416.56400	2	5.01E-07	0.88	3.25	-	1055.1
AHQ-2-3, 7309	R.KFDVNTSAVQVLIEHIGNLDR.A	2369.66218	3	6.73E-12	0.98	6.12	-	2796.5
AHQ-2-3, 3500 - 3503	R.KFNALFAQGNYSEAAK.V	1759.94281	2	3.87E-07	0.98	5.79	-	1885.1
AHQ-2-3, 4551	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	1.91E-06	0.93	3.99	-	1180.1
AHQ-2-4, 4560	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	9.72E-05	0.94	4.67	-	1004.9
AHQ-2-1, 4692	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	2.06E-06	0.93	4.43	-	949.5
AHQ-2-3, 4381	K.LHIIEVGTPPTGNQPFPK.K	1946.23831	2	1.52E-04	0.91	4.09	-	633.7
AHQ-2-3, 7420	R.LLEMNLMHAPQVADAILGNQMFTHYDR.A	3130.61385	3	9.90E-10	0.98	6.48	-	2002.2
AHQ-2-3, 3737	K.LLYNNVSNFGR.L	1297.44435	2	7.15E-08	0.91	3.34	-	970.7
AHQ-2-1, 6953	R.LPVVIGGLLDVDCSEDVIK.N	2043.36744	2	4.61E-05	0.92	4.29	-	723.6
AHQ-2-3, 7205 - 7267	R.LPVVIGGLLDVDCSEDVIK.N	2043.36744	2	7.31E-07	0.98	5.76	-	1693.9
AHQ-2-3, 6456	R.NLQNLLILTAIK.A	1354.66353	2	4.83E-04	0.97	5.15	-	1791.4
AHQ-2-3, 4361	R.NNLAGAEELFAR.K	1305.42165	2	1.96E-06	0.89	3.36	-	894.5
AHQ-2-3, 2356	K.RDPHLACVAYER.G	1488.65351	2	2.70E-04	0.78	2.92	-	521.1
AHQ-2-3, 7128 - 7129	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	2	1.35E-05	0.93	5.24	-	477.9
AHQ-2-5, 6999	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	5.57E-04	0.81	3.87	-	810.5
AHQ-2-3, 7105 - 7112	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	1.90E-05	0.94	4.93	-	1097.0
AHQ-2-4, 5164	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	2.09E-08	0.91	4.17	-	530.5
AHQ-2-1, 5180	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	1.70E-07	0.97	5.44	-	1773.5
AHQ-2-3, 7253	K.VGYTPDWIFLLR.N	1480.73443	2	7.41E-08	0.69	2.79	-	448.4
AHQ-2-3, 3095	K.VIQCFAETGQVQK.I	1509.70940	2	1.09E-06	0.96	4.05	-	1744.4
AHQ-2-3, 3423 - 3493	K.VSQPIEGHAASFAQFK.M	1717.90593	2	4.53E-04	0.67	2.99	-	710.8
AHQ-2-3, 5016	K.WLKEDKLECSEELGDLVK.S	2193.45974	2	2.32E-09	0.98	5.61	-	2202.0
AHQ-2-3, 7523	K.YHEQLSTQSLIELFESFK.S	2200.43237	2	9.81E-07	0.98	5.60	-	1873.2
gi|21464101|ref|NP_036611.2| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein				8.16E-12	5.03	70.26	44.90	28302.4
AHQ-2-10, 6930	K.ELEAVCQDVLSLLDNYLIK.N	2237.55566	2	6.46E-09	0.96	5.21	-	1096.9
AHQ-2-10, 6668	R.LGLALNYSVFYYEIQNAPEQACHLAK.T	3015.38773	3	8.16E-12	0.92	4.97	-	682.6
AHQ-2-10, 3870	R.NLLSVAYKNVVGAR.R	1504.75906	2	3.43E-06	0.95	3.52	-	1720.8
AHQ-2-9, 3796	R.NLLSVAYKNVVGAR.R	1504.75906	2	4.21E-04	0.92	3.72	-	1097.1
AHQ-2-10, 2790	K.NVTELNEPLSNEER.N	1644.72215	2	1.22E-05	0.91	3.77	-	771.9
AHQ-2-10, 2915	K.NVTELNEPLSNEER.N	1644.72215	2	4.10E-06	0.76	3.28	-	524.1
AHQ-2-10, 6567	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	3.29E-04	0.79	3.62	-	574.4
AHQ-2-14-, 6521 - 6585	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	1.21E-07	0.68	2.84	-	765.0
AHQ-2-10, 6126	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	1.20E-05	0.78	3.66	-	595.7
AHQ-2-10, 6258 - 6330	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	4.22E-08	0.95	4.44	-	1173.3
AHQ-2-10, 6334	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	3	1.91E-06	0.76	3.52	-	711.7

AHQ-2-14-, 6548 - 6583	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	3.89E-07	0.97	5.00	-	1303.6
AHQ-2-10, 2138	R.YDDMAAAMK.N	1016.17419	1	1.11E-05	0.27	2.21	-	340.2
AHQ-2-10, 2082	R.YLAEVATGEK.R	1081.20087	1	1.98E-05	0.21	2.11	-	459.3
AHQ-2-10, 2084	R.YLAEVATGEK.R	1081.20087	2	8.09E-05	0.90	3.38	-	891.2
AHQ-2-10, 2090	R.YLAEVATGEK.R	1081.20087	1	1.77E-04	0.41	2.41	-	278.3
gi|4504391|ref|NP_000179.1| hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]				8.74E-12	11.01	120.25	15.50	102502.4
AHQ-2-4, 6378 - 6457	R.AILQQLGLNSTCDDSILVK.T	2090.38419	2	4.13E-11	0.93	4.46	-	725.1
AHQ-2-4, 4525 - 4538	K.ATDCVGHDVVTLLR.D	1557.75406	2	8.74E-12	0.92	3.53	-	949.5
AHQ-2-4, 2669 - 2749	K.FLSQIESDR.L	1095.18763	2	8.72E-05	0.87	3.47	-	724.5
AHQ-2-4, 3221	K.GAALITAVGVR.L	1028.23070	2	1.24E-06	0.96	4.25	-	1796.7
AHQ-2-4, 5809	K.GDFIALDLGGSSFR.I	1455.59700	2	8.78E-12	0.98	4.96	-	2145.6
AHQ-2-4, 2162	R.HIDLVEGDEGR.M	1240.30483	2	2.57E-07	0.97	4.75	-	1437.2
AHQ-2-4, 5561	K.KLPVGFTFSFPCQQSK.I	1873.16425	2	3.18E-07	0.91	3.77	-	949.2
AHQ-2-4, 6181 - 6182	K.LPVGFTFSFPCQQSK.I	1744.99134	2	6.57E-07	0.94	4.10	-	1042.4
AHQ-2-4, 6021	R.LSDETLIDIMTR.F	1407.61560	2	3.18E-08	0.95	4.05	-	1199.0
AHQ-2-4, 2729 - 2801	R.LVNEYSLNAGK.Q	1208.34588	2	3.26E-07	0.72	3.10	-	705.8
AHQ-2-4, 7521	R.SANLVAATLGAILNR.L	1484.72615	2	1.24E-07	0.95	4.93	-	1090.6
AHQ-2-4, 6416	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	1.04E-08	0.92	4.58	-	663.1
gi|9910542|ref|NP_064535.1| SAR1a gene homolog 1; SAR1 protein [Homo sapiens]				8.98E-12	4.46	50.31	46.00	22366.6
AHQ-2-11, 3620	R.EIFGLYGQTTGK.G	1314.46845	1	4.12E-05	0.66	3.05	-	283.2
AHQ-2-11, 6081	R.LGQHVPTLHPTSEELTIAGMTFTTFDLGGHEQAR.R	3694.08659	3	8.98E-12	0.96	6.10	-	1057.5
AHQ-2-11, 3654	K.LREIFGLYGQTTGK.G	1583.81305	2	1.06E-06	0.96	4.52	-	1230.8
AHQ-2-11, 6424	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	3.33E-09	0.95	4.39	-	1151.0
AHQ-2-11, 6560 - 6621	K.VELNALM*TDETISNVPILILGNK.I	2514.92088	2	5.88E-04	0.93	4.37	-	888.9
gi|4507907|ref|NP_000543.1| von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille				9.27E-12	30.36	340.33	14.60	309296.7
AHQ-2-1, 5082	K.AFVLSSVDELEQQR.D	1621.77332	2	1.85E-06	0.88	3.39	-	1085.0
AHQ-2-1, 4036	K.AHLLSLVDVM*QR.E	1398.65673	2	1.32E-09	0.95	3.62	-	1709.2
AHQ-2-1, 5038	K.AHLLSLVDVMQR.E	1382.65733	2	6.13E-09	0.95	4.00	-	1443.6
AHQ-2-1, 3081 - 3161	K.APTCGLCEVAR.L	1236.40097	2	8.42E-05	0.88	2.92	-	895.9
AHQ-2-1, 4324	R.CLPTACTIQLR.G	1335.57568	2	1.43E-04	0.54	2.63	-	494.7
AHQ-2-1, 5220	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	1.41E-08	0.72	2.92	-	649.0
AHQ-2-1, 4696	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	1.38E-06	0.69	3.05	-	639.5
AHQ-2-1, 4888	R.EQAPNLVYM*VTGNPASDEIK.R	2193.42002	2	6.98E-09	0.89	4.08	-	486.7
AHQ-2-1, 5813 - 5880	R.EQAPNLVYMVTGNPASDEIK.R	2177.42062	2	4.53E-04	0.82	3.54	-	445.8
AHQ-2-1, 4226	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	6.80E-10	0.87	3.81	-	562.7
AHQ-2-1, 4525 - 4598	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	8.11E-05	0.81	3.77	-	566.6
AHQ-2-1, 2420	R.GLRPSCPNSQSPVK.V	1528.71594	2	3.61E-05	0.73	3.47	-	499.7
AHQ-2-1, 6433	R.IEDLPTMVTLGNSFLHK.L	1916.23079	2	6.47E-06	0.96	5.20	-	1021.2
AHQ-2-1, 6426	R.IEDLPTMVTLGNSFLHK.L	1916.23079	3	2.19E-04	0.63	3.26	-	451.3
AHQ-2-1, 5260 - 5290	R.IEDLPTM*VTLGNSFLHK.L	1932.23019	2	5.48E-07	0.83	3.66	-	668.6
AHQ-2-2, 7564	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	2.19E-06	0.91	4.07	-	599.1
AHQ-2-1, 7120	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	1.11E-08	0.92	4.57	-	732.5
AHQ-2-1, 7234 - 7312	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	2.49E-08	0.95	4.67	-	888.3
AHQ-2-1, 2684	R.ILAGPAGDSNVVK.L	1241.41901	2	2.46E-07	0.95	3.56	-	1390.5
AHQ-2-1, 2773	R.ILAGPAGDSNVVK.L	1241.41901	2	9.55E-05	0.70	2.78	-	680.0
AHQ-2-3, 2504	R.ILAGPAGDSNVVK.L	1241.41901	2	2.40E-06	0.80	2.89	-	705.4
AHQ-2-1, 3876 - 3880	R.ILTSDVFQDCNK.L	1441.58869	2	4.21E-07	0.96	4.64	-	1155.6
AHQ-2-2, 3818	R.ILTSDVFQDCNK.L	1441.58869	2	6.04E-08	0.86	3.22	-	872.3
AHQ-2-1, 5988 - 6005	R.LPGDIQVVPIGVGPNANVQELER.I	2415.73085	3	2.38E-05	0.95	4.87	-	1575.5
AHQ-2-1, 4329 - 4330	R.LSEAEFEVLK.A	1165.31777	2	7.18E-08	0.95	3.99	-	1257.0
AHQ-2-1, 4272 - 4293	K.LTGSCSYVLFQNK.E	1518.71629	2	1.40E-06	0.95	4.34	-	1276.0
AHQ-2-1, 5798 - 5869	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	4.37E-04	0.97	5.57	-	2164.3
AHQ-2-2, 5600	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	1.95E-06	0.97	5.50	-	1914.5
AHQ-2-1, 5654 - 5730	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	5.59E-09	0.98	6.54	-	1902.6
AHQ-2-1, 4072	R.SGFTYVLHEGECCGR.C	1774.91285	2	3.23E-11	0.94	3.62	-	1416.7
AHQ-2-1, 2524 - 2534	R.SKEFM*EEVIQR.M	1412.59390	2	1.94E-05	0.92	3.28	-	1144.2
AHQ-2-1, 3456 - 3470	R.SKEFMEEVIQR.M	1396.59450	2	7.21E-07	0.92	3.53	-	1087.9
AHQ-2-3, 5032 - 5112	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	3.25E-05	0.82	3.63	-	396.8
AHQ-2-2, 5158	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	1.99E-05	0.87	4.02	-	425.6
AHQ-2-1, 5093	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	6.58E-05	0.91	4.16	-	588.2
AHQ-2-1, 4998 - 5021	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	1.18E-06	0.89	3.86	-	707.0
AHQ-2-1, 5790 - 5837	K.TYGLCGICDENGANDFM*LR.D	2225.42231	2	3.77E-10	0.95	4.52	-	1128.6
AHQ-2-1, 6241 - 6242	K.TYGLCGICDENGANDFMLR.D	2209.42291	2	1.09E-06	0.94	4.37	-	927.4
AHQ-2-1, 4613	K.VIVIPVGIGPHANLK.Q	1527.87891	3	1.41E-04	0.68	3.23	-	486.4
AHQ-2-1, 4609 - 4621	K.VIVIPVGIGPHANLK.Q	1527.87891	2	5.66E-07	0.91	4.09	-	652.9
AHQ-2-1, 2408 - 2476	R.VKEEVFIQQR.N	1276.46658	2	1.93E-07	0.85	3.00	-	799.8
AHQ-2-1, 4744	R.VTVFPIGIGDR.Y	1174.37426	2	3.49E-04	0.93	3.61	-	1129.4
AHQ-2-1, 3633	R.WTCPCVCTGSSTR.H	1575.72645	2	2.38E-07	0.87	2.93	-	814.1
AHQ-2-3, 2841	K.YAGSQVASTSEVLK.Y	1440.58064	2	9.40E-06	0.96	4.36	-	1332.6
AHQ-2-1, 3010	K.YAGSQVASTSEVLK.Y	1440.58064	1	6.65E-06	0.81	3.11	-	792.4
AHQ-2-2, 2852	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.31E-04	0.96	4.23	-	1181.1
AHQ-2-1, 2993 - 2994	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.27E-07	0.94	4.38	-	866.5
AHQ-2-3, 7500	R.YFTFSGICQYLLAR.D	1741.00269	2	1.09E-06	0.94	4.41	-	851.3
AHQ-2-1, 6848	K.YLFPGECQYVLVQDYCGSNPGTFR.I	2874.15305	2	9.27E-12	0.88	3.78	-	753.4
AHQ-2-1, 6782 - 6836	K.YLFPGECQYVLVQDYCGSNPGTFR.I	2874.15305	3	2.13E-08	0.86	3.71	-	1336.9
AHQ-2-2, 3257	R.YLSDHSFLVSQGDR.E	1624.73576	2	1.78E-09	0.97	4.86	-	1836.0
AHQ-2-1, 3452	R.YLSDHSFLVSQGDR.E	1624.73576	2	1.85E-09	0.94	3.98	-	1453.4
AHQ-2-1, 6172	K.YTLFQIFSK.I	1147.34728	2	1.10E-08	0.93	3.18	-	1091.9
gi|9507215|ref|NP_061816.1| tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]				9.36E-12	3.71	40.23	10.90	50093.2
AHQ-2-14-, 5289	R.AVMIDLEPTVVDEVR.A	1686.95185	2	8.48E-10	0.95	4.27	-	1436.8
AHQ-2-14, 6029	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	2.70E-05	0.90	3.69	-	1060.6
AHQ-2-7, 5291	R.IHFPLVTYAPIISAEK.A	1800.13312	2	6.73E-07	0.93	4.08	-	715.4
AHQ-2-14, 6325 - 6396	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	1.20E-10	0.47	2.55	-	170.6
AHQ-2-14-, 5308	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	9.36E-12	0.93	4.67	-	697.8
AHQ-2-13, 5293	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	3.06E-07	0.75	3.75	-	397.3
gi|29741246|ref|XP_294070.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				9.77E-12	4.26	50.25	14.60	35032.0
AHQ-2-9, 5291	K.AENGKLVINGNPITIFQER.D	2114.39062	2	1.01E-07	0.70	3.07	-	466.5
AHQ-2-9, 5471	K.AENGKLVINGNPITIFQER.D	2114.39062	2	6.09E-06	0.67	3.29	-	483.6
AHQ-2-13, 5295	K.AENGKLVINGNPITIFQER.D	2114.39062	2	5.97E-07	0.40	3.16	-	363.6
AHQ-2-9, 5706 - 5779	K.LVINGNPITIFQER.D	1614.87029	2	6.84E-09	0.96	4.64	-	1258.9
AHQ-2-14-, 5632 - 5705	K.LVINGNPITIFQER.D	1614.87029	2	1.28E-09	0.95	4.23	-	1112.7
AHQ-2-10, 5230	K.LVINGNPITIFQER.D	1614.87029	2	1.46E-05	0.82	2.77	-	1063.2
AHQ-2-9, 5550 - 5623	K.LVINGNPITIFQER.D	1614.87029	2	2.91E-10	0.92	3.92	-	947.8
AHQ-2-10, 5328	K.LVINGNPITIFQER.D	1614.87029	2	3.14E-11	0.94	3.52	-	1516.3
AHQ-2-13, 5652	K.LVINGNPITIFQER.D	1614.87029	2	1.25E-07	0.86	2.99	-	812.8
AHQ-2-12, 5711 - 5786	K.LVINGNPITIFQER.D	1614.87029	2	1.20E-09	0.92	3.42	-	1120.1
AHQ-2-13, 5525 - 5587	K.LVINGNPITIFQER.D	1614.87029	2	9.77E-12	0.92	3.63	-	1028.7
AHQ-2-9, 5112 - 5182	K.LVINGNPITIFQERDPSK.I	2042.32440	2	2.15E-08	0.86	3.46	-	616.3
AHQ-2-9, 6398	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	1.99E-04	0.94	4.95	-	1868.1
AHQ-2-14-, 6825	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	7.04E-09	0.90	4.77	-	1403.6
AHQ-2-10, 5962 - 6040	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	1.30E-05	0.88	5.01	-	1100.4
gi|18104967|ref|NP_000953.2| prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland				1.00E-11	6.22	70.28	20.20	68686.0
AHQ-2-6, 3730 - 3738	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	6.00E-05	0.95	4.46	-	859.0
AHQ-2-7, 3637	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	4.77E-07	0.91	3.80	-	807.3
AHQ-2-6, 3651 - 3653	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	3	2.87E-07	0.92	3.89	-	1187.6
AHQ-2-6, 3642 - 3663	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	2	1.00E-11	0.97	5.46	-	1576.7
AHQ-2-6, 4945	R.FGMKPYTSFQELVGEK.E	1862.13845	2	1.24E-06	0.91	3.84	-	513.0

AHQ-2-6, 7025 - 7090	K.GLLGNPICSPEYWKPSTFGGEVGFNIVK.T	3069.47853	3	1.15E-08	0.85	4.33	-	419.1
AHQ-2-6, 6935 - 7013	K.GLLGNPICSPEYWKPSTFGGEVGFNIVK.T	3069.47853	3	1.39E-07	0.81	4.27	-	495.6
AHQ-2-6, 3090	R.VPDASQDDGPAVERPSTEL	1984.06747	2	4.34E-05	0.76	2.61	-	768.6
AHQ-2-6, 3193 - 3267	R.VPDASQDDGPAVERPSTEL	1984.06747	2	9.93E-05	0.92	4.29	-	888.7
AHQ-2-6, 5802	K.YQVLDGEMYPPSVEEAPVLMHYPR.G	2822.20799	3	1.35E-09	0.95	5.62	-	818.9
AHQ-2-6, 5298	K.YQVLDGEMYPPSVEEAPVLM*HYPR.G	2838.20739	3	2.80E-11	0.87	4.16	-	643.9
gi|10835002|ref|NP_001166.1| Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]				1.22E-11	5.38	60.24	47.30	22987.8
AHQ-2-10, 2303	K.APEPHVEEDDDDELDSK.L	1940.90995	2	2.14E-07	0.94	4.14	-	1126.4
AHQ-2-10, 2263 - 2324	K.APEPHVEEDDDDELDSK.L	1940.90995	3	1.22E-11	0.95	4.29	-	1745.3
AHQ-2-13-, 5638	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.63E-04	0.88	3.98	-	826.1
AHQ-2-12, 5891	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	1.71E-04	0.81	3.96	-	435.8
AHQ-2-10, 5154 - 5172	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	5.64E-08	0.92	4.77	-	847.7
AHQ-2-10, 5394 - 5458	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	7.41E-04	0.67	3.35	-	520.4
AHQ-2-10, 5435 - 5502	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	2	4.02E-04	0.65	3.00	-	422.7
AHQ-2-14-, 5607	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	6.08E-05	0.83	4.03	-	825.4
AHQ-2-10, 2904	K.ELQEMDKDDESLIK.Y	1693.85489	2	3.86E-05	0.89	4.21	-	804.3
AHQ-2-11, 6465	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	3.82E-05	0.52	3.22	-	295.5
AHQ-2-10, 6343 - 6423	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	4.16E-08	0.84	4.15	-	627.4
AHQ-2-10, 3068 - 3119	K.TLLGDGPVVTDPK.A	1312.49400	2	5.53E-10	0.97	4.33	-	1753.2
gi|13775198|ref|NP_112576.1| SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr				1.26E-11	5.04	60.29	35.50	10437.7
AHQ-2-14-, 4748	R.IQYQLVDISQDNALR.D	1776.97168	2	1.26E-11	0.98	4.83	-	2260.5
AHQ-2-13-, 4893	R.IQYQLVDISQDNALR.D	1776.97168	2	1.33E-10	0.98	5.18	-	2065.1
AHQ-2-14, 5800	R.IQYQLVDISQDNALR.D	1776.97168	2	1.68E-10	0.98	5.26	-	2056.3
AHQ-2-13-, 4826 - 4898	R.IQYQLVDISQDNALR.D	1776.97168	2	7.83E-08	0.95	4.53	-	1527.7
AHQ-2-13, 4843 - 4868	R.IQYQLVDISQDNALR.D	1776.97168	2	2.78E-09	0.95	5.17	-	1333.2
AHQ-2-13-, 4802	R.IQYQLVDISQDNALR.D	1776.97168	3	2.19E-07	0.96	5.77	-	1986.2
AHQ-2-13, 4707 - 4779	R.IQYQLVDISQDNALR.D	1776.97168	2	1.24E-10	0.98	5.83	-	1721.2
AHQ-2-13-, 4713 - 4779	R.IQYQLVDISQDNALR.D	1776.97168	2	2.55E-10	0.98	5.83	-	2052.8
AHQ-2-13, 5063 - 5144	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	2.12E-07	0.80	3.65	-	550.7
AHQ-2-13-, 4845 - 4851	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	5.55E-04	0.78	3.26	-	772.8
AHQ-2-13, 4937 - 4999	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	4.38E-09	0.83	3.44	-	623.4
AHQ-2-14-, 4456 - 4529	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	6.60E-04	0.81	3.62	-	441.0
AHQ-2-13-, 4513 - 4577	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.08E-04	0.79	3.54	-	470.0
AHQ-2-13-, 5043 - 5109	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	6.93E-06	0.80	3.17	-	654.8
AHQ-2-13-, 4274	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	3.65E-04	0.82	3.32	-	535.9
AHQ-2-13-, 5045 - 5111	R.IQYQLVDISQDNALRDEMR.A	2308.55751	2	3.36E-04	0.92	4.29	-	665.8
AHQ-2-13-, 4298	K.RIQYQLVDISQDNALR.D	1933.15803	2	2.02E-08	0.97	5.45	-	1070.8
AHQ-2-13, 4244	K.RIQYQLVDISQDNALR.D	1933.15803	2	4.42E-07	0.96	4.71	-	1085.6
AHQ-2-13-, 1841 - 1855	R.VYSTSVTGSR.E	1057.13940	2	2.56E-07	0.91	3.23	-	1144.6
AHQ-2-13-, 1589 - 1649	R.VYSTSVTGSR.E	1057.13940	2	8.29E-06	0.88	2.98	-	1034.1
AHQ-2-13-, 1543 - 1969	R.VYSTSVTGSR.E	1057.13940	1	3.66E-04	0.09	1.85	-	72.1
AHQ-2-13-, 1930 - 1974	R.VYSTSVTGSR.E	1057.13940	2	4.79E-05	0.90	3.25	-	1013.1
AHQ-2-13, 2083 - 2145	R.VYSTSVTGSR.E	1057.13940	2	6.75E-07	0.75	2.80	-	743.4
AHQ-2-13, 1939 - 2005	R.VYSTSVTGSR.E	1057.13940	2	9.95E-06	0.89	3.30	-	914.5
AHQ-2-13, 1887 - 1987	R.VYSTSVTGSR.E	1057.13940	1	4.26E-05	0.24	2.38	-	71.1
AHQ-2-13-, 1709 - 1770	R.VYSTSVTGSR.E	1057.13940	2	1.38E-05	0.93	3.26	-	1261.5
AHQ-2-13, 1827 - 2279	R.VYSTSVTGSR.E	1057.13940	1	8.25E-04	0.02	1.91	-	41.7
AHQ-2-13, 2335	R.VYSTSVTGSREIK.S	1427.58510	2	2.90E-05	0.57	2.53	-	641.6
AHQ-2-13-, 2225	R.VYSTSVTGSREIK.S	1427.58510	2	8.76E-07	0.56	2.95	-	507.5
gi|4503689|ref|NP_000499.1| fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M				1.38E-11	18.48	220.27	29.10	94972.5
AHQ-2-6, 5849 - 5854	K.DSDWPFCSDEDWNYK.C	1965.98609	2	4.10E-06	0.94	4.21	-	737.5
AHQ-2-7, 6017	K.DSDWPFCSDEDWNYK.C	1965.98609	2	2.37E-05	0.91	3.27	-	713.9
AHQ-2-9, 5555	K.DSHSLTTNIMEILR.G	1630.84839	2	2.82E-05	0.95	3.99	-	1300.5
AHQ-2-10, 4455	K.DSHSLTTNIM*EILR.G	1646.84779	2	4.02E-06	0.86	3.35	-	801.1
AHQ-2-1, 5193	K.DSHSLTTNIM*EILR.G	1646.84779	2	8.98E-04	0.90	3.18	-	1261.6
AHQ-2-7, 5495	K.DSHSLTTNIMEILR.G	1630.84839	2	1.14E-04	0.85	2.70	-	1057.4
AHQ-2-12, 5771	K.DSHSLTTNIMEILR.G	1630.84839	2	2.62E-05	0.96	4.00	-	1573.3
AHQ-2-10, 5216 - 5252	K.DSHSLTTNIMEILR.G	1630.84839	2	6.74E-07	0.95	4.07	-	1178.2
AHQ-2-11, 5501 - 5506	K.DSHSLTTNIMEILR.G	1630.84839	2	5.29E-04	0.82	3.51	-	533.6
AHQ-2-13, 2403	K.ESSSHHPGIAEFPSR.G	1638.72252	2	9.57E-05	0.78	3.27	-	404.9
AHQ-2-13, 2696	R.EVDLKDYEDQQK.Q	1510.58460	2	2.69E-06	0.74	2.73	-	693.2
AHQ-2-1, 2694	R.EVDLKDYEDQQK.Q	1510.58460	2	3.19E-07	0.66	2.85	-	585.7
AHQ-2-6, 2365	R.EVDLKDYEDQQK.Q	1510.58460	2	6.22E-08	0.93	3.89	-	1023.3
AHQ-2-5, 2360	R.EVDLKDYEDQQK.Q	1510.58460	2	4.61E-05	0.81	2.82	-	681.1
AHQ-2-9, 2420	R.EVDLKDYEDQQK.Q	1510.58460	2	1.08E-06	0.78	2.90	-	666.8
AHQ-2-7, 2331	R.EVDLKDYEDQQK.Q	1510.58460	2	2.78E-05	0.77	3.09	-	574.2
AHQ-2-8, 2247 - 2255	R.EVDLKDYEDQQK.Q	1510.58460	2	2.66E-07	0.88	3.47	-	863.5
AHQ-2-13-, 2630	R.EVDLKDYEDQQK.Q	1510.58460	2	5.65E-09	0.90	3.32	-	906.9
AHQ-2-13, 6527	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	7.43E-06	0.72	3.24	-	760.4
AHQ-2-13, 6279 - 6285	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	2.66E-08	0.94	5.39	-	958.3
AHQ-2-1, 6721	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	3.50E-09	0.88	4.23	-	956.9
AHQ-2-11, 6212	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	2.07E-05	0.91	4.63	-	1015.4
AHQ-2-1, 6581 - 6606	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	1.10E-04	0.91	4.83	-	640.6
AHQ-2-7, 6752	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	3.17E-05	0.68	3.21	-	742.2
AHQ-2-7, 1495 - 1501	R.GGSTSYGTGSETESPR.N	1573.55765	2	3.64E-05	0.76	3.61	-	338.4
AHQ-2-1, 1886	R.GGSTSYGTGSETESPR.N	1573.55765	2	7.37E-07	0.76	2.67	-	664.0
AHQ-2-4, 4961 - 4974	K.GLIDEVNQDFTNR.I	1521.61384	2	6.18E-07	0.95	4.35	-	1089.9
AHQ-2-10, 4548	K.GLIDEVNQDFTNR.I	1521.61384	2	2.00E-07	0.72	2.51	-	830.9
AHQ-2-10, 4414 - 4426	K.GLIDEVNQDFTNR.I	1521.61384	2	5.54E-08	0.93	4.22	-	925.5
AHQ-2-12, 4758	K.GLIDEVNQDFTNR.I	1521.61384	2	2.54E-08	0.93	4.33	-	807.8
AHQ-2-9, 4627 - 4704	K.GLIDEVNQDFTNR.I	1521.61384	2	1.11E-06	0.74	3.19	-	713.9
AHQ-2-9, 5167	K.GLIDEVNQDFTNR.I	1521.61384	2	2.03E-08	0.86	3.45	-	876.0
AHQ-2-5, 4785 - 4788	K.GLIDEVNQDFTNR.I	1521.61384	2	6.35E-05	0.92	3.64	-	1100.9
AHQ-2-1, 4937 - 4940	K.GLIDEVNQDFTNR.I	1521.61384	2	1.70E-09	0.94	4.11	-	960.4
AHQ-2-6, 4671 - 4687	K.GLIDEVNQDFTNR.I	1521.61384	2	1.34E-09	0.92	3.84	-	860.9
AHQ-2-2, 5016	K.GLIDEVNQDFTNR.I	1521.61384	2	9.20E-11	0.91	3.78	-	883.2
AHQ-2-11, 4524 - 4585	K.GLIDEVNQDFTNR.I	1521.61384	2	1.46E-08	0.85	2.83	-	997.1
AHQ-2-3, 4971	K.GLIDEVNQDFTNR.I	1521.61384	2	1.39E-09	0.90	3.18	-	901.0
AHQ-2-8, 4571 - 4579	K.GLIDEVNQDFTNR.I	1521.61384	2	4.56E-08	0.92	4.12	-	863.0
AHQ-2-8, 4124	K.GLIDEVNQDFTNR.I	1521.61384	2	2.37E-05	0.87	3.02	-	712.2
AHQ-2-7, 4703	K.GLIDEVNQDFTNR.I	1521.61384	2	2.47E-07	0.82	3.26	-	753.1
AHQ-2-4, 2145 - 2150	R.GSESGIFTNTK.E	1141.21317	1	7.56E-04	0.51	2.22	-	426.0
AHQ-2-13, 2383	R.GSESGIFTNTK.E	1141.21317	2	4.29E-04	0.75	2.97	-	577.2
AHQ-2-6, 1910	R.GSESGIFTNTK.E	1141.21317	1	1.56E-04	0.20	2.09	-	255.8
AHQ-2-6, 1918	R.GSESGIFTNTK.E	1141.21317	1	8.48E-06	0.57	2.61	-	388.8
AHQ-2-13-, 2262	R.GSESGIFTNTK.E	1141.21317	1	1.77E-05	0.58	2.88	-	313.1
AHQ-2-13-, 3053	R.HPDEAAFFDTASTGK.T	1594.66329	2	3.38E-06	0.85	3.81	-	461.3
AHQ-2-13, 2669	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	2.45E-04	0.91	3.79	-	819.3
AHQ-2-4, 2404	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	8.91E-05	0.85	3.61	-	313.7
AHQ-2-7, 2168	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	7.11E-07	0.97	4.99	-	2083.1
AHQ-2-6, 2158 - 2230	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	1.55E-04	0.95	4.71	-	1518.9
AHQ-2-5, 2221	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	7.63E-06	0.94	4.49	-	844.3
AHQ-2-13-, 2594	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	2.24E-05	0.95	5.01	-	864.0
AHQ-2-9, 2258	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.90E-04	0.96	4.42	-	1420.0
AHQ-2-13-, 2613	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	2.65E-06	0.97	4.99	-	2382.7
AHQ-2-13, 2691	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	8.78E-07	0.94	4.19	-	1518.9
AHQ-2-11, 2414	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.41E-05	0.96	4.86	-	1139.8

AHQ-2-10, 2256	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	4.39E-05	0.95	4.28	-	1163.2
AHQ-2-9, 3123	K.M*KPVPDLVPGNFK.S	1458.75054	2	4.91E-07	0.84	3.39	-	571.9
AHQ-2-10, 3144 - 3159	K.M*KPVPDLVPGNFK.S	1458.75054	2	1.54E-04	0.63	3.07	-	358.0
AHQ-2-10, 3594	K.MKPVPDLVPGNFK.S	1442.75114	2	1.94E-04	0.80	3.15	-	469.0
AHQ-2-9, 5127	K.NNKDSHSLTTNIMEILR.G	1987.22751	2	1.31E-05	0.86	3.97	-	688.2
AHQ-2-9, 5020	K.NNKDSHSLTTNIMEILR.G	1987.22751	2	4.81E-06	0.95	4.36	-	1109.3
AHQ-2-4, 2133	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	6.75E-06	0.88	3.73	-	551.9
AHQ-2-6, 1938	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	6.05E-06	0.84	3.08	-	692.9
AHQ-2-7, 2031	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	1.01E-09	0.92	4.58	-	558.4
AHQ-2-9, 2123	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	1.20E-06	0.90	3.70	-	759.9
AHQ-2-7, 1876	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	6.70E-11	0.96	4.76	-	1106.5
AHQ-2-1, 2282	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	3.13E-05	0.43	3.02	-	289.8
AHQ-2-9, 2518	K.NSLFEYQK.N	1029.12765	1	3.83E-04	0.28	2.65	-	199.4
AHQ-2-8, 1816 - 1820	R.PGSTGTWNPGSSER.G	1433.46515	2	1.83E-06	0.86	3.86	-	502.2
AHQ-2-7, 1857	R.PGSTGTWNPGSSER.G	1433.46515	2	9.74E-05	0.67	3.21	-	490.4
AHQ-2-11, 2150	R.PGSTGTWNPGSSER.G	1433.46515	2	3.26E-04	0.66	2.84	-	623.6
AHQ-2-6, 1930 - 1934	R.PGSTGTWNPGSSER.G	1433.46515	2	3.98E-09	0.78	3.20	-	396.7
AHQ-2-7, 4683	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.73E-07	0.95	4.91	-	979.6
AHQ-2-7, 4665 - 4668	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.73E-06	0.89	3.59	-	906.5
AHQ-2-11, 4610 - 4649	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.46E-07	0.90	4.25	-	666.7
AHQ-2-10, 4435	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	9.22E-07	0.82	3.64	-	576.7
AHQ-2-6, 4637 - 4703	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.03E-04	0.79	3.47	-	357.2
AHQ-2-13, 6813 - 6875	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.26E-05	0.78	3.51	-	340.1
AHQ-2-13-, 7015 - 7085	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.80E-08	0.90	4.45	-	382.2
AHQ-2-2, 7313	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	9.62E-04	0.47	2.92	-	202.2
AHQ-2-10, 6747	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.45E-07	0.82	3.67	-	358.9
AHQ-2-3, 7543 - 7545	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.10E-06	0.87	4.06	-	351.6
AHQ-2-4, 7604	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.13E-06	0.83	3.33	-	505.4
AHQ-2-2, 7598	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.33E-08	0.88	3.89	-	434.1
AHQ-2-6, 7203 - 7237	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	6.97E-07	0.82	3.37	-	390.5
AHQ-2-9, 7380 - 7420	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.88E-04	0.62	2.82	-	292.2
AHQ-2-1, 7086	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	2.99E-04	0.52	2.74	-	163.9
AHQ-2-7, 7483	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.39E-06	0.84	3.76	-	287.9
AHQ-2-11, 6426 - 6493	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	8.01E-05	0.48	3.00	-	107.9
AHQ-2-11, 6792 - 6793	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.38E-11	0.93	4.88	-	531.1
AHQ-2-13-, 6827 - 6829	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	5.89E-07	0.87	4.37	-	219.7
AHQ-2-9, 6992 - 6994	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	7.40E-04	0.75	3.33	-	303.7
AHQ-2-1, 7260 - 7261	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.34E-05	0.86	3.63	-	472.6
AHQ-2-12, 6837	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.38E-05	0.77	3.51	-	184.5
AHQ-2-12, 7147 - 7153	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.82E-04	0.86	3.86	-	471.7
AHQ-2-5, 7079	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	5.10E-04	0.67	2.90	-	221.9
AHQ-2-12, 2254 - 2334	K.VQHIQLLQK.N	1107.33106	1	4.15E-04	0.48	2.61	-	499.5
AHQ-2-13, 2451	K.VQHIQLLQK.N	1107.33106	1	5.72E-04	0.61	2.47	-	647.3
AHQ-2-11, 2242	K.VQHIQLLQK.N	1107.33106	1	1.16E-04	0.36	2.33	-	584.5
AHQ-2-10, 2059	K.VQHIQLLQK.N	1107.33106	1	3.51E-04	0.65	2.57	-	600.3
AHQ-2-10, 2056	K.VQHIQLLQK.N	1107.33106	2	1.89E-04	0.83	3.00	-	820.9
AHQ-2-9, 2040 - 2046	K.VQHIQLLQK.N	1107.33106	2	4.51E-06	0.90	3.25	-	813.2
AHQ-2-9, 2038	K.VQHIQLLQK.N	1107.33106	1	8.36E-04	0.48	2.84	-	426.2
AHQ-2-8, 1842	K.VQHIQLLQK.N	1107.33106	1	5.72E-04	0.67	2.77	-	540.7
AHQ-2-8, 1834	K.VQHIQLLQK.N	1107.33106	1	3.26E-04	0.66	2.63	-	641.1
AHQ-2-13-, 2343	K.VQHIQLLQK.N	1107.33106	1	4.88E-04	0.29	2.48	-	441.2
AHQ-2-7, 1904	K.VQHIQLLQK.N	1107.33106	2	5.70E-04	0.76	2.79	-	618.1
AHQ-2-5, 1987	K.VQHIQLLQK.N	1107.33106	1	4.89E-04	0.32	2.37	-	489.8
AHQ-2-4, 2248 - 2253	K.VQHIQLLQK.N	1107.33106	1	8.47E-04	0.72	2.65	-	667.2
AHQ-2-2, 2261	K.VQHIQLLQK.N	1107.33106	1	1.89E-04	0.06	2.05	-	407.2
AHQ-2-1, 2492	K.VQHIQLLQK.N	1107.33106	1	3.40E-04	0.62	2.51	-	662.2
AHQ-2-9, 2030 - 2099	K.VQHIQLLQK.N	1107.33106	1	1.42E-04	0.27	2.19	-	540.3
gi|24119203|ref|NP_705935.1| tropomyosin 3 [Homo sapiens]				1.53E-11	5.55	60.27	20.20	29032.5
AHQ-2-9, 2202	R.AREQAEAEVASLNR.R	1544.65218	2	1.95E-04	0.98	5.46	-	3011.3
AHQ-2-9, 3391	R.IQLVEEELDR.A	1244.37653	2	5.15E-07	0.90	3.44	-	974.0
AHQ-2-10, 3354 - 3355	R.IQLVEEELDR.A	1244.37653	2	4.36E-06	0.84	3.33	-	811.1
AHQ-2-10, 2571	K.IQVLQQQADDAEER.A	1643.73738	2	1.53E-11	0.97	4.70	-	1659.5
AHQ-2-9, 2638	K.IQVLQQQADDAEER.A	1643.73738	2	3.62E-06	0.97	4.70	-	1842.6
AHQ-2-10, 2312	R.KIQVLQQQADDAEER.A	1771.91030	2	2.07E-06	0.98	5.05	-	2107.0
AHQ-2-9, 2332	R.KIQVLQQQADDAEER.A	1771.91030	2	7.98E-07	0.97	5.16	-	1416.7
AHQ-2-10, 2983	R.RIQLVEEELDR.A	1400.56288	2	1.45E-07	0.96	4.21	-	1295.8
AHQ-2-9, 2966	R.RIQLVEEELDR.A	1400.56288	2	4.50E-08	0.98	4.72	-	2021.1
AHQ-2-9, 2894	K.TIDDLEDKLK.C	1190.32563	2	4.63E-06	0.77	3.06	-	536.8
gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				1.65E-11	21.63	260.29	49.30	55901.8
AHQ-2-7, 2193 - 2195	K.AHYGGFTVQNEANK.Y	1536.63020	2	5.03E-08	0.94	4.17	-	1148.3
AHQ-2-6, 2077 - 2078	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.91E-07	0.95	4.52	-	1296.9
AHQ-2-7, 1983 - 1985	K.AHYGGFTVQNEANK.Y	1536.63020	2	6.16E-09	0.90	3.79	-	905.7
AHQ-2-11, 4001 - 4017	K.DNENVVNEYSSELEK.H	1769.80167	2	2.17E-06	0.93	4.54	-	1009.2
AHQ-2-4, 4332	K.DNENVVNEYSSELEK.H	1769.80167	2	2.94E-05	0.84	3.46	-	741.5
AHQ-2-1, 4381	K.DNENVVNEYSSELEK.H	1769.80167	2	1.71E-10	0.93	3.90	-	1094.2
AHQ-2-7, 4072 - 4079	K.DNENVVNEYSSELEK.H	1769.80167	2	2.66E-08	0.92	4.11	-	808.2
AHQ-2-7, 4365	K.DNENVVNEYSSELEK.H	1769.80167	2	4.88E-05	0.61	3.00	-	621.9
AHQ-2-7, 4452	K.DNENVVNEYSSELEK.H	1769.80167	2	1.41E-08	0.88	3.72	-	802.4
AHQ-2-12, 4165	K.DNENVVNEYSSELEK.H	1769.80167	2	2.88E-04	0.70	3.24	-	540.1
AHQ-2-6, 4363	K.DNENVVNEYSSELEK.H	1769.80167	2	1.80E-05	0.90	3.89	-	703.2
AHQ-2-6, 4063 - 4077	K.DNENVVNEYSSELEK.H	1769.80167	2	5.42E-08	0.92	4.29	-	841.8
AHQ-2-9, 4096	K.DNENVVNEYSSELEK.H	1769.80167	2	1.21E-05	0.86	3.42	-	829.3
AHQ-2-7, 3359 - 3439	K.DNENVVNEYSSELEK.H	1769.80167	2	4.95E-07	0.76	3.73	-	475.9
AHQ-2-7, 3381	K.EDGGGWWYNR.C	1240.26508	2	1.78E-04	0.57	2.76	-	402.7
AHQ-2-6, 3413	K.EDGGGWWYNR.C	1240.26508	2	3.62E-07	0.80	2.94	-	470.8
AHQ-2-6, 3137 - 3142	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	3	2.28E-05	0.76	3.07	-	695.5
AHQ-2-10, 3099	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	7.61E-05	0.27	2.73	-	143.1
AHQ-2-6, 3141 - 3153	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	1.34E-05	0.15	2.53	-	180.5
AHQ-2-6, 3867 - 3869	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.61E-04	0.88	4.30	-	561.6
AHQ-2-7, 3320	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	7.44E-07	0.67	3.37	-	389.1
AHQ-2-7, 3815	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	9.72E-06	0.82	3.66	-	454.6
AHQ-2-8, 3755	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.53E-04	0.82	3.87	-	483.5
AHQ-2-8, 3759	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	4.66E-09	0.86	3.81	-	950.9
AHQ-2-7, 3819	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	4.18E-05	0.71	3.16	-	624.0
AHQ-2-9, 3859 - 3862	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.02E-06	0.93	4.51	-	754.0
AHQ-2-7, 4044 - 4107	K.HGTDDGVVWMNWK.G	1545.70374	2	6.44E-06	0.94	4.34	-	964.0
AHQ-2-10, 3872 - 3920	K.HGTDDGVVWMNWK.G	1545.70374	2	8.35E-09	0.95	3.92	-	1359.3
AHQ-2-6, 3219 - 3290	K.HGTDDGVVWM*NWK.G	1561.70314	2	7.96E-05	0.95	3.75	-	1404.5
AHQ-2-7, 3880 - 3956	K.HGTDDGVVWMNWK.G	1545.70374	2	1.68E-08	0.98	5.63	-	1329.2
AHQ-2-6, 3939 - 3975	K.HGTDDGVVWMNWK.G	1545.70374	2	2.15E-08	0.98	5.03	-	1798.0
AHQ-2-12, 3251	K.IRPFFPQQ	1033.20750	2	2.08E-04	0.62	2.53	-	504.6
AHQ-2-7, 6237 - 6309	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	4089.58482	3	1.46E-04	0.81	4.10	-	350.3
AHQ-2-8, 3031	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	7.48E-06	0.96	5.80	-	1032.1
AHQ-2-9, 3279	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	4.17E-04	0.84	4.13	-	641.9
AHQ-2-8, 3027 - 3028	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	5.89E-10	0.93	5.16	-	730.4
AHQ-2-6, 2953	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	5.60E-04	0.83	3.68	-	881.6
AHQ-2-6, 3373 - 3386	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.65E-11	0.91	4.88	-	683.1

AHQ-2-7, 3241 - 3311	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	4.36E-05	0.91	4.69	-	674.2
AHQ-2-11, 6118	R.M*GPTELLIEMEDWK.G	1708.97776	2	1.08E-05	0.87	3.34	-	946.6
AHQ-2-9, 7052	R.MGPTELLIEMEDWK.G	1692.97836	2	5.41E-05	0.83	3.33	-	672.8
AHQ-2-10, 5947	R.M*GPTELLIEMEDWK.G	1708.97776	2	8.60E-04	0.83	3.36	-	627.6
AHQ-2-10, 6479	R.MGPTELLIEMEDWK.G	1692.97836	2	2.09E-06	0.95	4.57	-	1178.0
AHQ-2-6, 6955 - 6965	R.MGPTELLIEMEDWK.G	1692.97836	2	1.35E-07	0.96	4.85	-	1353.1
AHQ-2-11, 6549 - 6558	R.MGPTELLIEMEDWK.G	1692.97836	2	1.84E-04	0.96	4.79	-	1271.3
AHQ-2-11, 5109	R.MGPTELLIEM*EDWK.G	1708.97776	2	2.06E-04	0.87	3.74	-	743.1
AHQ-2-7, 7131	R.MGPTELLIEMEDWK.G	1692.97836	2	4.00E-06	0.90	3.36	-	1094.1
AHQ-2-7, 7037 - 7099	R.MGPTELLIEMEDWK.G	1692.97836	2	4.67E-08	0.96	5.16	-	1181.7
AHQ-2-7, 6388 - 6403	R.M*GPTELLIEMEDWK.G	1708.97776	2	1.30E-06	0.93	3.47	-	1244.3
AHQ-2-6, 5243	R.MGPTELLIEM*EDWK.G	1708.97776	2	6.38E-05	0.93	4.36	-	708.8
AHQ-2-7, 6165	R.MGPTELLIEMEDWKGDK.V	1993.29069	3	1.21E-05	0.67	3.16	-	592.3
AHQ-2-7, 6171	R.MGPTELLIEMEDWKGDK.V	1993.29069	2	1.20E-08	0.93	4.08	-	1079.0
AHQ-2-7, 5163	K.NYCGLPGEYWLGNDK.I	1787.92994	2	6.45E-10	0.93	4.49	-	448.3
AHQ-2-11, 5013	K.NYCGLPGEYWLGNDK.I	1787.92994	2	5.34E-04	0.87	3.82	-	435.9
AHQ-2-6, 5985	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	2	9.84E-09	0.80	3.43	-	387.2
AHQ-2-6, 5990	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	3	4.70E-08	0.81	3.59	-	392.6
AHQ-2-7, 2591	R.SILENLR.S	844.97899	2	9.01E-04	0.81	2.61	-	893.4
AHQ-2-8, 3672 - 3694	R.TPCTVSCNIPVVSGK.E	1621.85811	2	3.00E-05	0.86	3.54	-	735.6
AHQ-2-6, 3701	R.TPCTVSCNIPVVSGK.E	1621.85811	2	3.72E-04	0.90	4.10	-	626.7
AHQ-2-6, 4867 - 4869	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.53E-08	0.93	4.74	-	550.0
AHQ-2-7, 4805 - 4883	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.01E-09	0.93	4.49	-	1327.8
AHQ-2-7, 5047	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	2.39E-05	0.86	3.95	-	833.9
AHQ-2-9, 4912	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.20E-04	0.67	3.25	-	767.2
AHQ-2-7, 4964	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	4.13E-04	0.84	3.63	-	1130.4
AHQ-2-6, 4486 - 4525	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	3.60E-08	0.96	4.64	-	1204.8
AHQ-2-7, 4081	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	2.59E-05	0.93	4.20	-	958.5
AHQ-2-8, 4488 - 4500	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.26E-10	0.97	4.78	-	1590.2
AHQ-2-6, 4594 - 4595	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.48E-08	0.92	3.92	-	942.8
AHQ-2-7, 4693	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.13E-04	0.87	3.70	-	819.1
AHQ-2-7, 3981	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	1.82E-04	0.96	4.68	-	1318.3
AHQ-2-6, 4001	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	7.57E-06	0.95	4.40	-	1219.6
AHQ-2-9, 4563	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	5.95E-07	0.94	4.77	-	866.2
AHQ-2-7, 4548 - 4623	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.21E-07	0.94	4.74	-	1042.0
AHQ-2-7, 1695	K.YQISVNK.Y	851.96999	1	1.85E-04	0.36	2.70	-	339.3
AHQ-2-7, 4960 - 5041	R.YYWGGQYTWDMAK.H	1669.84009	2	1.71E-08	0.95	4.10	-	1077.5
AHQ-2-7, 4288	R.YYWGGQYTWDM*AK.H	1685.83949	2	2.44E-06	0.94	3.66	-	967.2
AHQ-2-11, 4354 - 4370	R.YYWGGQYTWDM*AK.H	1685.83949	2	2.10E-05	0.87	2.90	-	972.6
AHQ-2-11, 4897	R.YYWGGQYTWDMAK.H	1669.84009	2	8.09E-07	0.95	3.77	-	1331.5
AHQ-2-6, 4994 - 4995	R.YYWGGQYTWDMAK.H	1669.84009	2	2.90E-06	0.95	3.89	-	1337.0
AHQ-2-6, 4382	R.YYWGGQYTWDM*AK.H	1685.83949	2	1.96E-05	0.96	4.08	-	1337.1
AHQ-2-12, 5113	R.YYWGGQYTWDMAK.H	1669.84009	2	1.51E-06	0.95	3.76	-	1318.1
AHQ-2-14, 5588 - 5660	R.YYWGGQYTWDM*AK.H	1685.83949	2	2.36E-05	0.91	3.37	-	819.8
AHQ-2-14, 6257	R.YYWGGQYTWDMAK.H	1669.84009	2	5.51E-08	0.95	3.43	-	1395.6
AHQ-2-14-, 4544 - 4600	R.YYWGGQYTWDM*AK.H	1685.83949	2	4.05E-05	0.96	4.34	-	1073.0
gi|4501893|ref|NP_001094.1| actinin, alpha 2 [Homo sapiens]				1.69E-11	9.72	120.24	12.40	103853.1
AHQ-2-5, 4319	K.AGTQIENIEEDFR.N	1522.59861	2	1.70E-05	0.93	4.78	-	1007.1
AHQ-2-5, 4264 - 4335	K.AGTQIENIEEDFR.N	1522.59861	2	1.37E-05	0.87	3.76	-	827.7
AHQ-2-5, 5057 - 5127	K.CQLEINFNTLQTK.L	1610.81373	2	1.51E-06	0.96	4.57	-	1320.0
AHQ-2-6, 4939 - 5006	K.CQLEINFNTLQTK.L	1610.81373	2	4.23E-07	0.92	4.34	-	914.9
AHQ-2-5, 5299 - 5371	K.CQLEINFNTLQTK.L	1610.81373	2	8.87E-06	0.94	4.03	-	1244.3
AHQ-2-4, 4329	R.FAIQDISVEETSAK.E	1538.68108	2	1.50E-10	0.93	3.37	-	1178.7
AHQ-2-13-, 4217 - 4222	R.FAIQDISVEETSAK.E	1538.68108	2	4.90E-04	0.85	3.34	-	858.5
AHQ-2-11, 4016 - 4040	R.FAIQDISVEETSAK.E	1538.68108	2	3.75E-06	0.95	3.75	-	1514.2
AHQ-2-1, 4434	R.FAIQDISVEETSAK.E	1538.68108	2	4.03E-05	0.69	2.71	-	594.2
AHQ-2-6, 3950 - 4026	R.FAIQDISVEETSAK.E	1538.68108	2	3.77E-10	0.84	3.06	-	946.6
AHQ-2-5, 6065 - 6148	K.GYEEWLLNEIR.R	1422.56701	2	5.92E-06	0.95	4.24	-	1438.0
AHQ-2-1, 6277	K.GYEEWLLNEIR.R	1422.56701	2	1.09E-06	0.93	4.25	-	1162.5
AHQ-2-6, 5977 - 6054	K.GYEEWLLNEIR.R	1422.56701	1	3.86E-05	0.41	2.84	-	109.4
AHQ-2-6, 5347 - 5362	K.GYEEWLLNEIR.R	1422.56701	1	1.64E-04	0.42	2.49	-	410.9
AHQ-2-4, 6365	K.GYEEWLLNEIR.R	1422.56701	2	8.29E-05	0.95	3.96	-	1483.2
AHQ-2-5, 6261	K.GYEEWLLNEIR.R	1422.56701	1	5.69E-05	0.27	2.32	-	311.8
AHQ-2-5, 6071 - 6140	K.GYEEWLLNEIR.R	1422.56701	1	2.25E-10	0.37	2.61	-	134.3
AHQ-2-5, 6064 - 6131	K.GYEEWLLNEIR.R	1422.56701	1	6.94E-05	0.34	2.56	-	246.9
AHQ-2-5, 1976	K.HEAFESDLAAHQDR.V	1626.66861	2	2.20E-09	0.97	4.79	-	1823.6
AHQ-2-5, 2265	R.ISNRPAFMPSEGK.M	1434.64597	2	5.18E-07	0.81	3.25	-	693.5
AHQ-2-5, 3569	R.KAGTQIENIEEDFR.N	1650.77152	2	1.36E-05	0.96	4.85	-	1178.1
AHQ-2-5, 4257	R.KAGTQIENIEEDFRNGLK.L	2063.25733	2	7.21E-04	0.77	3.60	-	707.4
AHQ-2-5, 1611 - 1643	R.KHEAFESDLAAHQDR.V	1754.84152	2	1.81E-09	0.95	4.32	-	1099.8
AHQ-2-6, 1670	R.KHEAFESDLAAHQDR.V	1754.84152	2	5.59E-09	0.97	4.86	-	1797.2
AHQ-2-5, 1620	R.KHEAFESDLAAHQDR.V	1754.84152	3	1.69E-11	0.90	4.40	-	892.8
AHQ-2-11, 2950	R.KTFTAWCNSHLR.K	1522.71309	2	2.95E-06	0.43	2.70	-	344.8
AHQ-2-5, 2493	R.KTFTAWCNSHLR.K	1522.71309	2	3.08E-06	0.70	3.27	-	363.7
AHQ-2-5, 4476 - 4507	K.LVSIGAEEIVDGNVK.M	1543.74400	2	3.85E-07	0.89	3.35	-	944.2
AHQ-2-5, 4731 - 4812	K.LVSIGAEEIVDGNVK.M	1543.74400	2	4.85E-08	0.97	4.49	-	1636.3
AHQ-2-5, 4116	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.16E-04	0.94	3.87	-	1224.7
AHQ-2-5, 4588 - 4663	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.91E-06	0.93	3.69	-	1106.7
AHQ-2-5, 3388	K.TFTAWCNSHLR.K	1394.54018	2	2.22E-07	0.81	2.94	-	727.2
gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]				1.73E-11	15.40	190.28	88.40	22391.3
AHQ-2-11, 5745 - 5805	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.16E-05	0.90	3.14	-	1117.9
AHQ-2-12, 6017 - 6097	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.06E-06	0.97	4.86	-	1430.8
AHQ-2-12, 6162	R.DDGLFSGDPNWFPK.K	1595.69288	2	8.27E-08	0.96	4.40	-	1429.1
AHQ-2-11, 5992	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.20E-08	0.95	4.23	-	1232.0
AHQ-2-11, 5865 - 5880	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.91E-07	0.97	4.72	-	1566.8
AHQ-2-11, 5652 - 5721	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.81E-05	0.97	4.50	-	1589.5
AHQ-2-12, 5887 - 5967	R.DDGLFSGDPNWFPK.K	1595.69288	2	8.53E-07	0.94	4.00	-	1146.8
AHQ-2-13, 5732 - 5792	R.DDGLFSGDPNWFPK.K	1595.69288	2	3.13E-05	0.87	3.28	-	949.3
AHQ-2-13, 5869	R.DDGLFSGDPNWFPK.K	1595.69288	2	3.33E-04	0.89	3.05	-	972.0
AHQ-2-13, 6207	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.29E-04	0.83	3.78	-	579.1
AHQ-2-11, 6862	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	3	6.97E-05	0.91	4.12	-	1231.9
AHQ-2-11, 6106 - 6128	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	6.53E-06	0.93	4.64	-	676.1
AHQ-2-12, 7197 - 7199	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.91E-05	0.91	4.42	-	658.3
AHQ-2-13-, 6366	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.27E-09	0.94	4.98	-	698.0
AHQ-2-12, 6401 - 6463	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	8.98E-05	0.90	4.20	-	608.2
AHQ-2-13, 6863	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	8.62E-04	0.88	4.27	-	571.2
AHQ-2-11, 6324 - 6348	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.43E-04	0.63	3.18	-	485.2
AHQ-2-11, 5530 - 5592	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	5.32E-09	0.87	3.94	-	1072.6
AHQ-2-14-, 6867	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.26E-08	0.83	3.91	-	651.4
AHQ-2-11, 5801	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	6.04E-06	0.45	2.60	-	463.4
AHQ-2-12, 5841 - 5843	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	8.67E-07	0.84	3.60	-	630.9
AHQ-2-13, 6812	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	9.73E-07	0.84	4.11	-	522.4
AHQ-2-13, 6811	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.09E-09	0.90	4.56	-	795.0
AHQ-2-13-, 7014	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.80E-08	0.85	3.72	-	1083.7
AHQ-2-11, 5570	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.24E-06	0.68	2.87	-	513.2
AHQ-2-13-, 7018	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.10E-08	0.78	3.86	-	559.7
AHQ-2-12, 7129 - 7145	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.22E-09	0.91	4.34	-	833.7

AHQ-2-12, 5845	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	9.60E-05	0.78	3.22	-	937.9
AHQ-2-11, 6784	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	7.32E-06	0.83	4.23	-	568.2
AHQ-2-11, 6790	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.37E-08	0.93	4.54	-	1071.4
AHQ-2-12, 4542	R.ENFQNWLK.D	1079.18989	1	4.57E-04	0.07	2.00	-	142.8
AHQ-2-12, 2406	K.ENPRNFSDNQLQEGK.N	1776.84549	2	4.53E-05	0.87	3.38	-	662.4
AHQ-2-11, 2382	K.ENPRNFSDNQLQEGK.N	1776.84549	2	3.32E-05	0.61	2.69	-	663.7
AHQ-2-11, 2610	R.GASQAGMTGYGMPR.Q	1384.56732	2	2.48E-06	0.92	3.47	-	1211.0
AHQ-2-11, 1905	R.GPAYGLSR.E	820.91599	2	1.77E-04	0.91	2.99	-	1170.3
AHQ-2-12, 1833 - 1893	R.GPAYGLSR.E	820.91599	2	2.76E-05	0.90	3.23	-	855.9
AHQ-2-12, 2078 - 2081	R.GPAYGLSREVQQK.I	1433.59456	2	5.64E-05	0.93	4.17	-	1302.5
AHQ-2-11, 2426	K.IQASTMAFK.Q	997.19374	1	8.91E-04	0.68	2.48	-	678.0
AHQ-2-12, 2170 - 2174	K.KIQASTMAFK.Q	1125.36665	2	1.14E-04	0.81	3.10	-	815.4
AHQ-2-11, 2157	K.KIQASTMAFK.Q	1125.36665	2	6.15E-05	0.88	3.24	-	981.1
AHQ-2-11, 2564	R.NFSDNQLQEGK.N	1280.32582	1	6.61E-05	0.15	1.82	-	212.1
AHQ-2-12, 2586	R.NFSDNQLQEGK.N	1280.32582	2	4.29E-04	0.77	2.76	-	967.2
AHQ-2-12, 2583	R.NFSDNQLQEGK.N	1280.32582	1	3.68E-07	0.14	2.14	-	307.8
AHQ-2-12, 2177 - 2202	R.NFSDNQLQEGK.N	1280.32582	2	2.40E-05	0.83	3.54	-	625.8
AHQ-2-11, 2396	R.NFSDNQLQEGK.N	1280.32582	1	1.35E-05	0.43	2.09	-	459.6
AHQ-2-11, 2297	R.NFSDNQLQEGK.N	1280.32582	1	1.64E-05	0.20	2.24	-	228.8
AHQ-2-12, 2293	R.NFSDNQLQEGK.N	1280.32582	1	3.92E-08	0.28	2.39	-	214.9
AHQ-2-13, 2356	R.NFSDNQLQEGK.N	1280.32582	2	1.87E-05	0.72	3.25	-	518.8
AHQ-2-11, 2262 - 2264	K.NVIGLQM*GTNR.G	1219.39691	2	1.71E-05	0.94	4.03	-	1052.7
AHQ-2-12, 4906	K.QM*EQISQFLQAAER.Y	1695.87890	2	4.91E-04	0.88	3.68	-	751.8
AHQ-2-13-, 5509	K.QMEQISQFLQAAER.Y	1679.87950	2	3.25E-04	0.96	4.93	-	1223.5
AHQ-2-11, 5236 - 5269	K.QMEQISQFLQAAER.Y	1679.87950	2	4.32E-08	0.96	5.02	-	1197.2
AHQ-2-11, 5249	K.QMEQISQFLQAAER.Y	1679.87950	3	2.19E-04	0.97	4.69	-	2374.6
AHQ-2-14-, 4816 - 4817	K.QM*EQISQFLQAAER.Y	1695.87890	2	5.92E-04	0.89	4.05	-	669.4
AHQ-2-14-, 5461	K.QMEQISQFLQAAER.Y	1679.87950	2	1.06E-04	0.94	4.14	-	1057.5
AHQ-2-11, 4577 - 4613	K.QM*EQISQFLQAAER.Y	1695.87890	2	9.67E-04	0.55	2.64	-	426.5
AHQ-2-13, 5395	K.QMEQISQFLQAAER.Y	1679.87950	2	1.96E-05	0.94	4.07	-	1051.1
AHQ-2-12, 5509	K.QMEQISQFLQAAER.Y	1679.87950	3	3.22E-07	0.98	4.89	-	3133.3
AHQ-2-13-, 7081	K.QYDADLEQILIQWITTQCR.K	2396.66131	3	1.72E-07	0.96	5.29	-	2109.4
AHQ-2-12, 7234	K.QYDADLEQILIQWITTQCR.K	2396.66131	3	5.84E-04	0.90	3.80	-	1169.6
AHQ-2-11, 4638	R.TLMNLGGLAVAR.D	1216.47932	2	1.88E-04	0.93	3.70	-	1526.8
AHQ-2-12, 3545 - 3574	R.TLM*NLGGLAVAR.D	1232.47872	2	5.03E-04	0.92	4.23	-	897.7
AHQ-2-12, 4417 - 4450	R.TLMNLGGLAVAR.D	1216.47932	2	5.66E-07	0.94	4.30	-	1160.7
AHQ-2-13, 3553	R.TLM*NLGGLAVAR.D	1232.47872	2	8.50E-04	0.94	3.75	-	1295.6
AHQ-2-13, 4440 - 4443	R.TLMNLGGLAVAR.D	1216.47932	2	3.81E-06	0.91	4.25	-	822.1
AHQ-2-14-, 4509	R.TLMNLGGLAVAR.D	1216.47932	2	1.38E-06	0.93	3.71	-	1281.0
AHQ-2-12, 4841	R.TLMNLGGLAVAR.D	1216.47932	2	7.86E-05	0.94	3.73	-	1553.9
AHQ-2-11, 4277 - 4340	R.TLMNLGGLAVAR.D	1216.47932	2	9.47E-04	0.93	4.02	-	1206.6
AHQ-2-11, 3880	R.TLM*NLGGLAVAR.D	1232.47872	2	1.47E-05	0.88	3.50	-	856.9
AHQ-2-13-, 4495 - 4497	R.TLMNLGGLAVAR.D	1216.47932	2	1.42E-06	0.93	4.22	-	1089.0
AHQ-2-12, 4521	R.TLMNLGGLAVAR.D	1216.47932	2	4.09E-06	0.74	2.94	-	765.9
AHQ-2-12, 6810 - 6825	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.24E-10	0.95	4.47	-	1046.2
AHQ-2-14-, 6721 - 6791	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.02E-09	0.97	5.58	-	1503.5
AHQ-2-13, 6669 - 6744	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	8.01E-11	0.97	5.39	-	1302.0
AHQ-2-11, 6456 - 6490	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.86E-09	0.97	4.46	-	1990.2
AHQ-2-11, 6638 - 6696	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.03E-08	0.97	5.62	-	1386.3
AHQ-2-13-, 6933	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.65E-07	0.97	5.30	-	1630.7
AHQ-2-11, 6740	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.73E-11	0.97	5.51	-	1073.4
AHQ-2-11, 6916 - 6938	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.80E-07	0.91	3.98	-	1023.0
AHQ-2-12, 7305 - 7313	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.06E-11	0.88	3.77	-	764.0
AHQ-2-12, 7029 - 7103	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	6.50E-10	0.96	5.46	-	972.1
AHQ-2-12, 7170 - 7245	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.28E-09	0.93	4.08	-	900.2
AHQ-2-11, 6264 - 6338	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	9.32E-07	0.97	4.85	-	1527.4
AHQ-2-12, 6967	R.YGINTTDIFQTVDLWEGKNMACVQR.T	2962.30673	3	8.86E-08	0.90	4.17	-	975.9
AHQ-2-12, 7021	R.YGINTTDIFQTVDLWEGKNMACVQR.T	2962.30673	2	1.91E-09	0.82	3.72	-	469.5
gi|5453740|ref|NP_006462.1| myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat				1.78E-11	6.08	70.28	33.30	19794.0
AHQ-2-11, 6125 - 6192	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	3.94E-07	0.96	4.94	-	1307.5
AHQ-2-14-, 5459	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.20E-11	0.96	4.66	-	1427.2
AHQ-2-14, 6572 - 6597	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	5.63E-06	0.80	3.47	-	759.2
AHQ-2-13, 6129	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	3.46E-07	0.92	3.92	-	1005.6
AHQ-2-12, 5522 - 5538	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.94E-09	0.96	4.97	-	1190.2
AHQ-2-11, 6370	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	4.80E-05	0.94	4.45	-	905.2
AHQ-2-14-, 6179 - 6180	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	2.14E-10	0.98	5.44	-	1644.8
AHQ-2-11, 5224 - 5284	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.32E-05	0.97	5.08	-	1320.4
AHQ-2-11, 6001 - 6002	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	3	6.93E-05	0.87	3.79	-	981.2
AHQ-2-11, 5996 - 6065	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	4.19E-05	0.96	4.66	-	1556.0
AHQ-2-11, 5976 - 5982	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.07E-05	0.94	4.45	-	686.8
AHQ-2-11, 5932	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	3.41E-05	0.84	3.36	-	750.6
AHQ-2-11, 5813 - 5820	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	4.61E-09	0.95	4.51	-	1554.4
AHQ-2-11, 5809	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.08E-06	0.97	5.01	-	1615.9
AHQ-2-11, 5660 - 5685	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.78E-11	0.97	5.60	-	1527.1
AHQ-2-11, 5196	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	3.51E-07	0.75	3.42	-	776.9
AHQ-2-14-, 5860 - 5924	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	3.46E-11	0.97	5.01	-	1257.1
AHQ-2-11, 4405	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	3.58E-05	0.97	5.30	-	1045.6
AHQ-2-13-, 6038	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	3.17E-05	0.93	3.95	-	1129.2
AHQ-2-13, 5883	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.03E-07	0.95	4.48	-	1242.7
AHQ-2-12, 5993 - 6071	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	3.73E-07	0.98	5.15	-	1943.2
AHQ-2-12, 5994 - 5999	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.22E-09	0.92	3.76	-	1514.9
AHQ-2-11, 6141 - 6221	K.EAFNMIDQNRDGFIDKEDLHDMLASLGK.N	3224.57104	3	6.21E-05	0.92	5.09	-	884.7
AHQ-2-11, 4198 - 4256	K.GNFNYIEFTR.I	1261.36733	2	8.05E-05	0.77	3.16	-	797.8
AHQ-2-11, 3988 - 4048	K.GNFNYIEFTR.I	1261.36733	2	1.61E-05	0.84	3.18	-	840.6
AHQ-2-13-, 4273	K.GNFNYIEFTR.I	1261.36733	2	1.47E-04	0.76	2.94	-	682.5
AHQ-2-12, 4178	K.GNFNYIEFTR.I	1261.36733	2	3.96E-05	0.87	3.59	-	829.3
AHQ-2-11, 4246 - 4248	K.GNFNYIEFTR.I	1261.36733	1	3.23E-06	0.37	2.74	-	396.1
AHQ-2-13, 4217	K.GNFNYIEFTR.I	1261.36733	2	3.88E-05	0.78	3.22	-	709.3
AHQ-2-11, 3364	K.KGNFNYIEFTR.I	1389.54025	2	6.03E-07	0.92	3.65	-	992.3
AHQ-2-11, 3846	K.KGNFNYIEFTR.I	1389.54025	2	1.21E-04	0.83	3.16	-	703.8
gi|21361755|ref|NP_004090.3| stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie				1.84E-11	9.01	100.34	46.20	31708.5
AHQ-2-10, 3803 - 3824	K.EASM*VITESPAALQLR.Y	1732.98059	2	4.49E-06	0.57	2.51	-	750.8
AHQ-2-1, 4936	K.EASMVITESPAALQLR.Y	1716.98119	2	2.64E-05	0.92	4.06	-	971.3
AHQ-2-14-, 4699	K.EASMVITESPAALQLR.Y	1716.98119	2	2.18E-09	0.80	3.52	-	867.6
AHQ-2-12, 4686	K.EASMVITESPAALQLR.Y	1716.98119	2	5.28E-07	0.36	2.84	-	464.9
AHQ-2-1, 4369	K.EASM*VITESPAALQLR.Y	1732.98059	2	6.06E-07	0.86	3.33	-	794.2
AHQ-2-14, 5777	K.EASMVITESPAALQLR.Y	1716.98119	2	4.73E-06	0.71	3.06	-	539.0
AHQ-2-13, 4648	K.EASMVITESPAALQLR.Y	1716.98119	2	1.46E-05	0.72	3.13	-	810.3
AHQ-2-9, 4555 - 4570	K.EASMVITESPAALQLR.Y	1716.98119	2	1.39E-06	0.65	2.69	-	769.8
AHQ-2-9, 7406	K.GPGLFFILPCTDSFIK.V	1814.13672	2	6.04E-04	0.95	4.69	-	882.1
AHQ-2-2, 7585	K.GPGLFFILPCTDSFIK.V	1814.13672	2	6.28E-06	0.93	4.54	-	660.4
AHQ-2-10, 6730	K.GPGLFFILPCTDSFIK.V	1814.13672	2	1.71E-06	0.96	4.94	-	946.3
AHQ-2-1, 2480	R.LLAQTTLR.N	916.10035	2	3.46E-05	0.84	3.33	-	527.7
AHQ-2-1, 7190	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	3.93E-09	0.85	4.22	-	769.2
AHQ-2-1, 6212 - 6290	K.NLSQILSDREEIAHNM*QSTLDDATDAWGIK.V	3389.65279	3	5.14E-05	0.97	5.44	-	2523.3
AHQ-2-10, 6646	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	6.22E-07	0.97	5.77	-	1970.2
AHQ-2-9, 7302	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	6.19E-07	0.98	6.80	-	1661.3

AHQ-2-9, 7554	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	7.16E-04	0.75	3.45	-	400.7
AHQ-2-14-, 6968	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	2.51E-04	0.71	3.13	-	395.2
AHQ-2-13-, 7109	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	1.14E-04	0.85	4.04	-	493.4
AHQ-2-12, 7262	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	6.06E-04	0.81	3.52	-	565.9
AHQ-2-13-, 2235	K.VIAAEGEMNASR.A	1248.39191	2	2.63E-09	0.96	4.05	-	1537.6
AHQ-2-1, 2338	K.VIAAEGEMNASR.A	1248.39191	2	7.83E-10	0.97	4.23	-	1734.0
AHQ-2-10, 3712 - 3716	R.VQNATLAVANITNADSATR.L	1931.09731	2	8.24E-07	0.96	5.66	-	716.2
AHQ-2-10, 4127 - 4199	R.VQNATLAVANITNADSATR.L	1931.09731	2	5.01E-06	0.94	4.75	-	723.9
AHQ-2-10, 3624	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.11E-07	0.90	4.77	-	419.0
AHQ-2-10, 3519 - 3554	R.VQNATLAVANITNADSATR.L	1931.09731	2	3.31E-05	0.82	3.84	-	375.4
AHQ-2-1, 4709 - 4712	R.VQNATLAVANITNADSATR.L	1931.09731	2	2.07E-10	0.92	4.41	-	664.9
AHQ-2-1, 4414	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.91E-07	0.85	3.96	-	462.0
AHQ-2-1, 3960	R.VQNATLAVANITNADSATR.L	1931.09731	2	8.53E-10	0.93	4.48	-	761.2
AHQ-2-1, 4306	R.VQNATLAVANITNADSATR.L	1931.09731	2	2.74E-05	0.74	3.14	-	505.5
AHQ-2-1, 4201	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.84E-11	0.96	5.18	-	1169.5
AHQ-2-1, 4045 - 4064	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.56E-09	0.97	5.54	-	1463.9
AHQ-2-1, 4037 - 4040	R.YLQTLTTIAAEK.N	1352.55813	2	4.59E-05	0.94	4.27	-	1232.5
AHQ-2-13, 3851	R.YLQTLTTIAAEK.N	1352.55813	2	8.01E-05	0.93	3.38	-	1300.1
AHQ-2-10, 3454	R.YLQTLTTIAAEK.N	1352.55813	2	6.82E-04	0.92	3.63	-	1162.2
AHQ-2-13-, 3885	R.YLQTLTTIAAEK.N	1352.55813	2	6.98E-08	0.94	3.32	-	1477.0
gi|4826898|ref|NP_005013.1| profilin 1; profilin-1 [Homo sapiens]				1.88E-11	16.99	200.30	75.00	15054.2
AHQ-2-12, 1735	K.CYEM*ASHLR.R	1184.32794	2	2.96E-04	0.92	2.60	-	1695.0
AHQ-2-12, 2305	K.CYEMASHLR.R	1168.32854	2	2.38E-04	0.77	2.53	-	1019.9
AHQ-2-13-, 1607 - 1666	K.CYEM*ASHLR.R	1184.32794	2	1.85E-05	0.90	2.91	-	1351.8
AHQ-2-13-, 1754 - 1813	K.CYEM*ASHLR.R	1184.32794	2	1.37E-04	0.89	2.99	-	1153.6
AHQ-2-13-, 1873 - 1895	K.CYEM*ASHLR.R	1184.32794	2	1.39E-04	0.89	3.02	-	1177.3
AHQ-2-13-, 1961 - 2023	K.CYEM*ASHLR.R	1184.32794	2	2.89E-05	0.80	2.79	-	850.4
AHQ-2-13-, 2281 - 2354	K.CYEMASHLR.R	1168.32854	2	1.04E-04	0.95	3.28	-	1781.1
AHQ-2-13-, 2413 - 2485	K.CYEMASHLR.R	1168.32854	2	2.70E-05	0.97	3.74	-	2150.0
AHQ-2-13-, 2425	K.CYEMASHLR.R	1168.32854	2	4.42E-04	0.94	3.29	-	1392.9
AHQ-2-13-, 2701	K.CYEMASHLR.R	1168.32854	2	5.98E-04	0.94	3.52	-	1469.8
AHQ-2-13, 2389 - 2459	K.CYEMASHLR.R	1168.32854	2	1.54E-04	0.95	3.21	-	2003.0
AHQ-2-13, 2523 - 2587	K.CYEMASHLR.R	1168.32854	2	1.80E-04	0.92	2.80	-	1661.1
AHQ-2-13, 1951 - 2028	K.CYEM*ASHLR.R	1184.32794	2	1.89E-04	0.94	3.07	-	1593.3
AHQ-2-13-, 4263	K.DRSSFYVNGLTLGGQK.C	1742.91379	3	6.21E-07	0.95	4.54	-	1688.7
AHQ-2-13-, 4265	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.88E-11	0.97	5.42	-	1146.1
AHQ-2-13, 4075 - 4139	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	5.29E-09	0.96	5.16	-	1062.7
AHQ-2-13, 4201	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	6.33E-05	0.92	3.76	-	906.1
AHQ-2-13-, 4123 - 4126	K.DRSSFYVNGLTLGGQK.C	1742.91379	3	1.45E-05	0.83	3.54	-	954.1
AHQ-2-13-, 4121 - 4197	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.95E-10	0.97	5.73	-	1047.7
AHQ-2-12, 5633 - 5699	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.38E-09	0.97	4.54	-	1932.2
AHQ-2-12, 5810 - 5818	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.48E-09	0.97	5.13	-	1794.5
AHQ-2-13-, 5633 - 5701	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.36E-10	0.98	5.31	-	2089.7
AHQ-2-13-, 5585 - 5653	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.32E-10	0.98	5.39	-	2309.3
AHQ-2-13-, 5502 - 5578	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.45E-04	0.92	3.42	-	1517.5
AHQ-2-12, 5905 - 5971	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.72E-06	0.95	3.99	-	1730.1
AHQ-2-12, 6039	R.DSLLQDGEFSMDLR.T	1626.77023	2	8.69E-05	0.95	4.37	-	1333.4
AHQ-2-13-, 5449 - 5517	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.44E-10	0.97	4.81	-	2045.3
AHQ-2-12, 6237 - 6310	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.68E-05	0.90	3.83	-	912.7
AHQ-2-12, 5498 - 5561	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.11E-08	0.93	3.72	-	1121.8
AHQ-2-13-, 5893 - 5953	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.38E-06	0.90	2.85	-	1271.9
AHQ-2-12, 5365 - 5433	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.13E-09	0.95	4.42	-	1340.3
AHQ-2-13-, 5409	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.16E-04	0.92	3.48	-	1143.5
AHQ-2-13-, 5310 - 5381	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.00E-09	0.97	4.93	-	1548.2
AHQ-2-13-, 5065 - 5083	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.12E-05	0.92	3.48	-	1484.5
AHQ-2-13-, 4922 - 4947	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.54E-07	0.98	4.53	-	2548.1
AHQ-2-13-, 4821 - 4874	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.91E-07	0.97	5.10	-	1710.0
AHQ-2-13-, 4689 - 4757	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.53E-11	0.96	4.49	-	1674.6
AHQ-2-13-, 4566 - 4626	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.95E-10	0.95	4.52	-	1236.3
AHQ-2-13-, 4467	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.14E-04	0.93	3.96	-	1030.4
AHQ-2-12, 5275 - 5282	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.32E-06	0.90	3.73	-	831.2
AHQ-2-12, 4743 - 4769	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.81E-04	0.77	2.64	-	907.8
AHQ-2-12, 4617 - 4625	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.90E-06	0.93	4.14	-	1197.7
AHQ-2-13, 6183 - 6243	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.56E-09	0.97	4.49	-	1960.1
AHQ-2-13-, 5979 - 6050	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.65E-06	0.95	3.65	-	1805.2
AHQ-2-13, 6049 - 6107	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.19E-08	0.96	4.19	-	2194.0
AHQ-2-13, 5933 - 5997	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.67E-08	0.96	4.03	-	1744.7
AHQ-2-13, 5799 - 5859	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.79E-08	0.96	4.14	-	1778.2
AHQ-2-13, 6900	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.21E-07	0.95	3.53	-	1995.8
AHQ-2-14, 5662 - 5712	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.34E-05	0.96	3.87	-	1957.8
AHQ-2-13, 6429	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.29E-04	0.93	3.80	-	1436.2
AHQ-2-13-, 6113 - 6177	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.97E-09	0.98	4.85	-	2374.1
AHQ-2-13-, 6209 - 6274	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.87E-07	0.96	3.27	-	2485.5
AHQ-2-14, 6505 - 6564	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.74E-05	0.92	3.33	-	1361.4
AHQ-2-13-, 6341 - 6406	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.80E-04	0.97	4.96	-	2037.2
AHQ-2-13, 5580 - 5643	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.21E-08	0.97	4.74	-	1873.9
AHQ-2-13, 5451 - 5516	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.81E-09	0.97	5.00	-	1898.5
AHQ-2-13-, 6682	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.27E-09	0.94	3.71	-	1430.4
AHQ-2-13, 4508 - 4627	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.85E-08	0.93	4.02	-	1234.4
AHQ-2-14-, 4588	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.70E-09	0.91	3.60	-	1107.0
AHQ-2-14-, 4705	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.10E-08	0.96	4.33	-	1470.7
AHQ-2-13, 4691 - 4759	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.71E-08	0.95	3.68	-	1796.1
AHQ-2-13, 4824 - 4887	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.85E-07	0.96	4.16	-	1635.1
AHQ-2-14, 6512 - 6584	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.02E-08	0.92	3.28	-	1544.8
AHQ-2-13, 5245 - 5255	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.33E-07	0.92	3.79	-	1202.5
AHQ-2-13, 5323 - 5387	R.DSLLQDGEFSMDLR.T	1626.77023	2	8.50E-09	0.96	4.20	-	1447.2
AHQ-2-14-, 5264 - 5341	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.25E-09	0.97	4.96	-	1479.8
AHQ-2-14-, 5444 - 5513	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.17E-06	0.97	4.35	-	1809.1
AHQ-2-13, 4896	R.DSLLQDGEFSMDLRTK.S	1856.04748	2	2.71E-05	0.52	2.84	-	332.6
AHQ-2-12, 3573 - 3654	K.DSPSVWAAVPGK.T	1214.35211	2	2.83E-06	0.88	3.29	-	885.2
AHQ-2-12, 3854	K.DSPSVWAAVPGK.T	1214.35211	2	2.82E-07	0.80	2.50	-	1099.2
AHQ-2-13-, 3349 - 3374	K.DSPSVWAAVPGK.T	1214.35211	2	9.07E-06	0.85	2.73	-	1177.3
AHQ-2-13-, 3529 - 3598	K.DSPSVWAAVPGK.T	1214.35211	2	4.95E-05	0.89	3.54	-	944.5
AHQ-2-13, 3677 - 3753	K.DSPSVWAAVPGK.T	1214.35211	2	1.76E-05	0.84	2.99	-	935.3
AHQ-2-13-, 3625 - 3706	K.DSPSVWAAVPGK.T	1214.35211	2	1.63E-07	0.91	3.75	-	985.8
AHQ-2-13, 3392	K.DSPSVWAAVPGK.T	1214.35211	2	3.17E-05	0.86	3.13	-	1039.2
AHQ-2-13, 3548 - 3731	K.DSPSVWAAVPGK.T	1214.35211	1	4.46E-04	0.13	2.01	-	446.2
AHQ-2-13, 3547 - 3616	K.DSPSVWAAVPGK.T	1214.35211	2	1.29E-05	0.87	3.26	-	1066.8
AHQ-2-13, 3860 - 3921	K.DSPSVWAAVPGK.T	1214.35211	2	8.19E-04	0.87	2.81	-	1079.7
AHQ-2-13, 6652	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	3.78E-06	0.95	5.40	-	1399.2
AHQ-2-13, 6504	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	2	1.88E-04	0.56	3.27	-	211.7
AHQ-2-13, 6489 - 6492	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	1.21E-09	0.89	4.34	-	1298.1
AHQ-2-13-, 1538 - 1713	K.EGVHGGLINK.K	1024.15577	1	3.42E-04	0.43	2.03	-	200.3
AHQ-2-13-, 2153	K.KCYEMASHLR.R	1296.50145	3	1.18E-06	0.95	4.05	-	2020.1
AHQ-2-13-, 2155 - 2158	K.KCYEMASHLR.R	1296.50145	1	4.23E-04	0.24	1.95	-	272.3
AHQ-2-13-, 2154	K.KCYEMASHLR.R	1296.50145	2	2.09E-06	0.96	3.22	-	2103.2
AHQ-2-14, 5313	R.SSFYVNGLTLGGQK.C	1471.63957	2	5.86E-05	0.88	3.51	-	670.3

AHQ-2-14, 5328	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.43E-10	0.47	2.46	-	388.6
AHQ-2-14, 5630 - 5689	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.38E-09	0.96	4.29	-	1309.2
AHQ-2-13-, 4597 - 4657	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.48E-07	0.97	4.54	-	1586.5
AHQ-2-12, 4305	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.60E-05	0.92	3.87	-	816.6
AHQ-2-13-, 4471 - 4537	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.33E-08	0.97	4.67	-	1270.2
AHQ-2-12, 4306 - 4309	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.81E-09	0.43	2.95	-	394.7
AHQ-2-13, 4249 - 4311	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.96E-07	0.93	3.86	-	889.5
AHQ-2-14-, 4213 - 4293	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.64E-04	0.67	2.60	-	551.1
AHQ-2-13, 4564	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.71E-04	0.62	2.47	-	534.9
AHQ-2-13, 4563 - 4629	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.15E-07	0.86	3.11	-	748.4
AHQ-2-12, 4466 - 4601	R.SSFYVNGLTLGGQK.C	1471.63957	1	4.97E-09	0.37	2.61	-	324.7
AHQ-2-13-, 4305 - 4373	R.SSFYVNGLTLGGQK.C	1471.63957	2	5.14E-08	0.93	4.13	-	728.2
AHQ-2-14-, 4505 - 4571	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.89E-04	0.56	2.35	-	508.4
AHQ-2-13, 4471 - 4539	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.56E-10	0.96	4.55	-	1069.3
AHQ-2-13, 4332 - 4404	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.02E-05	0.84	3.05	-	682.0
AHQ-2-13, 4261 - 4628	R.SSFYVNGLTLGGQK.C	1471.63957	1	8.45E-09	0.48	2.72	-	368.0
AHQ-2-13, 4259 - 4315	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.65E-06	0.60	2.84	-	478.6
AHQ-2-13-, 4307 - 4694	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.08E-07	0.44	2.85	-	354.3
AHQ-2-14-, 4508 - 4575	R.SSFYVNGLTLGGQK.C	1471.63957	2	5.07E-09	0.96	4.48	-	1210.3
AHQ-2-12, 4463 - 4533	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.03E-09	0.96	4.79	-	1193.9
AHQ-2-13, 3317 - 3379	K.STGGAPTFNVTVTK.T	1380.52843	2	1.91E-05	0.84	3.27	-	630.1
AHQ-2-13-, 2934 - 3001	K.STGGAPTFNVTVTK.T	1380.52843	2	2.16E-06	0.88	3.79	-	510.4
AHQ-2-13, 3087 - 3168	K.STGGAPTFNVTVTK.T	1380.52843	2	1.47E-06	0.72	2.99	-	424.1
AHQ-2-13-, 3010 - 3293	K.STGGAPTFNVTVTK.T	1380.52843	1	8.64E-04	0.35	2.66	-	288.5
AHQ-2-13-, 3069 - 3137	K.STGGAPTFNVTVTK.T	1380.52843	2	3.33E-08	0.85	3.03	-	518.6
AHQ-2-13-, 3201 - 3267	K.STGGAPTFNVTVTK.T	1380.52843	2	6.12E-07	0.86	3.45	-	473.0
AHQ-2-12, 2913 - 3033	K.STGGAPTFNVTVTK.T	1380.52843	1	4.43E-05	0.17	1.92	-	412.7
AHQ-2-14-, 3023 - 3025	K.STGGAPTFNVTVTK.T	1380.52843	2	1.89E-05	0.73	2.68	-	424.3
AHQ-2-13, 3051 - 3315	K.STGGAPTFNVTVTK.T	1380.52843	1	4.21E-04	0.41	2.72	-	297.2
AHQ-2-13, 3216 - 3297	K.STGGAPTFNVTVTK.T	1380.52843	2	9.80E-05	0.89	3.37	-	549.1
AHQ-2-14, 3933 - 3957	K.STGGAPTFNVTVTK.T	1380.52843	2	1.70E-04	0.66	2.81	-	374.7
AHQ-2-13, 2997 - 3059	K.STGGAPTFNVTVTK.T	1380.52843	2	1.92E-08	0.89	3.78	-	539.7
AHQ-2-12, 3035	K.STGGAPTFNVTVTK.T	1380.52843	2	1.09E-04	0.84	3.18	-	480.7
AHQ-2-12, 2942	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	4.32E-05	0.88	3.22	-	843.1
AHQ-2-13, 2895	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	1.47E-06	0.89	3.62	-	653.3
AHQ-2-13-, 2847 - 2854	K.TDKTLVLLM*GK.E	1235.51929	2	1.66E-06	0.94	4.13	-	1056.0
AHQ-2-13-, 3533 - 3613	K.TDKTLVLLMGK.E	1219.51989	2	1.07E-06	0.95	4.13	-	1314.6
AHQ-2-13, 3541 - 3620	K.TDKTLVLLMGK.E	1219.51989	2	1.81E-06	0.95	4.02	-	1310.8
AHQ-2-13-, 6681 - 6693	K.TFVNITPAEVGVLVGK.D	1644.93630	2	4.96E-04	0.92	3.98	-	909.7
AHQ-2-13-, 5997 - 6069	K.TFVNITPAEVGVLVGK.D	1644.93630	2	7.68E-07	0.95	4.88	-	1062.4
AHQ-2-13, 5424 - 5503	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.00E-04	0.76	3.62	-	572.9
AHQ-2-13, 5644 - 5723	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.94E-06	0.95	4.75	-	944.6
AHQ-2-13, 5685 - 5749	K.TFVNITPAEVGVLVGK.D	1644.93630	3	1.46E-07	0.95	4.81	-	1448.8
AHQ-2-13, 5783 - 5843	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.90E-07	0.94	4.72	-	884.8
AHQ-2-13, 5895 - 5957	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.56E-04	0.82	3.33	-	547.9
AHQ-2-13, 5971 - 6023	K.TFVNITPAEVGVLVGK.D	1644.93630	2	5.78E-05	0.85	3.78	-	799.5
AHQ-2-13-, 5923	K.TFVNITPAEVGVLVGK.D	1644.93630	3	2.73E-07	0.98	5.93	-	1981.4
AHQ-2-13-, 5870 - 5935	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.19E-05	0.92	4.11	-	928.3
AHQ-2-13-, 5793 - 5818	K.TFVNITPAEVGVLVGK.D	1644.93630	3	1.32E-08	0.97	6.09	-	1503.6
AHQ-2-13-, 5781 - 5849	K.TFVNITPAEVGVLVGK.D	1644.93630	2	5.03E-07	0.95	4.32	-	1042.3
AHQ-2-12, 6073	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.63E-04	0.87	3.58	-	612.7
AHQ-2-12, 5897 - 5899	K.TFVNITPAEVGVLVGK.D	1644.93630	3	2.37E-08	0.96	5.23	-	1340.6
AHQ-2-12, 5885 - 5962	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.66E-05	0.89	3.92	-	734.5
AHQ-2-12, 5850 - 5921	K.TFVNITPAEVGVLVGK.D	1644.93630	2	4.48E-05	0.88	3.76	-	674.1
AHQ-2-14-, 5859	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.02E-04	0.91	4.11	-	734.8
AHQ-2-13, 5345 - 5353	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	1.72E-04	0.73	3.82	-	505.2
AHQ-2-13, 5336 - 5399	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	4.90E-07	0.92	4.50	-	576.2
AHQ-2-12, 5469	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	3.01E-06	0.85	3.90	-	476.5
AHQ-2-13-, 5438	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	4.88E-08	0.90	4.38	-	627.3
AHQ-2-13, 2731 - 2800	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	3.94E-04	0.95	4.34	-	1092.0
AHQ-2-13, 3349	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	4.97E-05	0.50	2.63	-	271.6
AHQ-2-13-, 2746 - 2795	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	2.07E-04	0.95	4.25	-	946.8
AHQ-2-13-, 2753 - 2785	R.TKSTGGAPTFNVTVTK.T	1609.80568	3	4.60E-04	0.83	3.72	-	789.6
AHQ-2-13, 2839	R.TKSTGGAPTFNVTVTK.T	1609.80568	3	1.57E-05	0.84	3.62	-	932.3
AHQ-2-13, 2859 - 2860	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	7.72E-06	0.92	3.72	-	757.6
AHQ-2-13, 3716	K.TLVLLMGK.E	875.15478	2	1.26E-05	0.85	2.66	-	787.5
AHQ-2-13-, 3005	K.TLVLLM*GK.E	891.15418	2	1.17E-05	0.75	2.75	-	728.8
AHQ-2-13-, 2907 - 2977	K.TLVLLM*GK.E	891.15418	2	4.39E-04	0.78	2.60	-	600.2
AHQ-2-13, 3587 - 3655	K.TLVLLMGK.E	875.15478	2	3.64E-05	0.88	3.19	-	601.3
AHQ-2-13-, 3701 - 3771	K.TLVLLMGK.E	875.15478	2	3.35E-05	0.89	3.37	-	626.9
AHQ-2-12, 3557	K.TLVLLMGK.E	875.15478	1	7.70E-05	0.40	2.14	-	556.7
AHQ-2-13-, 3578	K.TLVLLMGK.E	875.15478	1	8.91E-05	0.20	2.32	-	224.2
AHQ-2-13, 2960 - 3023	K.TLVLLM*GK.E	891.15418	2	2.82E-04	0.81	2.63	-	882.8
AHQ-2-12, 2831	K.TLVLLM*GK.E	891.15418	2	5.93E-04	0.86	2.61	-	762.5
AHQ-2-13-, 3574 - 3637	K.TLVLLMGK.E	875.15478	2	8.45E-06	0.85	2.79	-	619.8
gi|4759082|ref|NP_004648.1| serum deprivation response protein; serum deprivation response; phospha				1.93E-11	4.42	50.27	13.60	47172.9
AHQ-2-11, 6282	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	7.37E-04	0.95	4.25	-	1643.6
AHQ-2-14-, 6268 - 6331	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.57E-11	0.96	3.90	-	1803.5
AHQ-2-13-, 6426 - 6461	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.75E-09	0.97	5.15	-	1808.2
AHQ-2-13, 6360	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.06E-05	0.85	3.46	-	877.9
AHQ-2-13, 6264 - 6283	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.28E-08	0.98	5.41	-	1728.1
AHQ-2-9, 6575 - 6646	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.93E-05	0.97	4.75	-	1771.9
AHQ-2-12, 6369 - 6437	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.04E-07	0.96	4.58	-	1354.2
AHQ-2-14-, 6384 - 6436	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	3.09E-04	0.89	3.53	-	1309.5
AHQ-2-11, 6168	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.75E-07	0.97	5.07	-	1897.8
AHQ-2-11, 6077 - 6156	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.14E-09	0.96	5.10	-	1159.9
AHQ-2-11, 3356 - 3404	K.LVNMLDAVQENQHK.M	1639.85851	2	8.49E-08	0.92	3.91	-	1187.8
AHQ-2-12, 3443	K.LVNMLDAVQENQHK.M	1639.85851	2	9.10E-05	0.85	3.56	-	813.8
AHQ-2-11, 2089	K.RLENNHAQLLR.R	1364.53869	2	4.01E-06	0.83	2.86	-	874.5
AHQ-2-13-, 3386	R.SDGDPVQPAVLQVHQTS	1778.90130	2	3.95E-04	0.75	2.83	-	612.6
AHQ-2-12, 6169 - 6234	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.19E-07	0.96	5.21	-	829.1
AHQ-2-10, 5750	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.16E-06	0.89	3.78	-	612.4
AHQ-2-13, 6047	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.92E-10	0.96	5.44	-	912.4
AHQ-2-9, 6546	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.72E-08	0.96	4.92	-	1190.1
AHQ-2-9, 6394 - 6475	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.79E-08	0.93	4.59	-	826.0
AHQ-2-11, 5886 - 5928	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	6.97E-07	0.96	4.90	-	1186.2
AHQ-2-13-, 6213	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	5.32E-04	0.96	5.40	-	1036.0
AHQ-2-9, 6159 - 6236	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.80E-08	0.96	5.43	-	827.9
AHQ-2-14-, 6017 - 6091	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.93E-11	0.95	5.18	-	892.3
AHQ-2-8, 6114 - 6131	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.43E-06	0.95	4.80	-	1056.1
AHQ-2-6, 6205	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.67E-08	0.94	4.78	-	819.6
gi|5901944|ref|NP_008977.1| elastin microfibril interface located protein; TNF? elastin microfibril				1.94E-11	4.45	50.27	9.40	106694.7
AHQ-2-3, 3553	R.APAPASAPPGPSEELLR.Q	1660.85268	2	9.57E-10	0.71	3.27	-	328.6
AHQ-2-4, 3565 - 3638	R.APAPASAPPGPSEELLR.Q	1660.85268	2	2.91E-07	0.76	3.22	-	351.7
AHQ-2-3, 3033	R.GTELGGAAGQGGHPPGYTSLASR.L	2142.27464	2	1.35E-08	0.88	4.61	-	320.2
AHQ-2-4, 3013	R.GTELGGAAGQGGHPPGYTSLASR.L	2142.27464	2	6.08E-06	0.58	3.06	-	304.1
AHQ-2-3, 3611	R.LDTVAGGLQGLR.E	1200.37012	2	4.29E-06	0.97	4.53	-	1590.4

AHQ-2-4, 2762	R.LVGSGLHTVEAAGEAR.Q	1567.72888	2	1.66E-06	0.89	3.52	-	995.5
AHQ-2-3, 2765	R.LVGSGLHTVEAAGEAR.Q	1567.72888	2	1.94E-11	0.93	3.66	-	1297.4
AHQ-2-3, 3711	R.PARPNLSGSSAGSPLSGLGGEGPGESEK.V	2596.74928	3	3.02E-07	0.96	5.42	-	1274.3
gi|5729877|ref|NP_006588.1| heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD				2.04E-11	11.87	130.27	21.10	70897.6
AHQ-2-6, 4227	R.ARFEELNADLFR.G	1481.63768	2	3.77E-08	0.94	3.90	-	1020.2
AHQ-2-6, 4146	R.ARFEELNADLFR.G	1481.63768	3	1.54E-04	0.93	4.29	-	1201.1
AHQ-2-6, 4559	R.FEELNADLFR.G	1254.37310	2	3.91E-07	0.93	3.38	-	1236.4
AHQ-2-6, 5186	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	2.04E-11	0.90	4.33	-	1023.5
AHQ-2-6, 5182 - 5205	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	2	1.80E-07	0.97	5.32	-	1449.8
AHQ-2-6, 5535	K.ILDKCNEIINWLDK.N	1776.04688	2	1.25E-07	0.96	5.04	-	1499.3
AHQ-2-6, 3259	K.LDKSQIHDIVLVGGSTR.I	1839.08615	2	1.09E-04	0.85	3.63	-	633.6
AHQ-2-6, 2719	R.M*VNHFIAEFK.R	1252.46696	2	5.55E-05	0.91	2.86	-	1117.3
AHQ-2-6, 3722	K.NQVAMNPTNTVFDAK.R	1650.83816	2	2.06E-04	0.87	3.50	-	738.4
AHQ-2-6, 2765	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	1.07E-05	0.95	4.51	-	1084.5
AHQ-2-6, 3993	K.NQVAMNPTNTVFDAK.R	1650.83816	2	3.59E-07	0.90	4.39	-	558.8
AHQ-2-6, 3821 - 3865	K.NSLESYAFNMK.A	1304.45393	2	1.87E-05	0.86	3.36	-	772.7
AHQ-2-6, 3074	K.NSLESYAFNM*K.A	1320.45333	2	1.21E-05	0.78	2.75	-	664.7
AHQ-2-6, 2415	R.RFDDAVVQSDMK.H	1411.56603	2	4.76E-06	0.95	4.42	-	1320.9
AHQ-2-13, 2765	R.RFDDAVVQSDMK.H	1411.56603	2	9.18E-05	0.92	3.61	-	1179.8
AHQ-2-6, 6834 - 6905	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	6.78E-10	0.96	5.39	-	1043.7
AHQ-2-6, 6951 - 6987	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	4.65E-04	0.84	3.40	-	581.5
AHQ-2-7, 7003	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	1.09E-08	0.96	4.97	-	1021.4
AHQ-2-7, 2660	K.SQIHDIVLVGGSTR.I	1482.66712	2	1.92E-08	0.97	4.25	-	1812.0
AHQ-2-6, 2751	K.SQIHDIVLVGGSTR.I	1482.66712	2	3.72E-10	0.97	4.50	-	2004.5
AHQ-2-6, 2761	K.SQIHDIVLVGGSTR.I	1482.66712	1	9.36E-09	0.85	3.63	-	392.4
gi|4502027|ref|NP_000468.1| albumin precursor; PRO0883 protein [Homo sapiens]				2.13E-11	20.89	250.36	48.30	69366.4
AHQ-2-5, 2347 - 2348	K.AAFTECCQAADK.A	1374.47927	2	4.75E-05	0.87	3.31	-	794.5
AHQ-2-5, 5527 - 5528	K.AVMDDFAAFVEK.C	1343.53006	2	2.60E-07	0.97	4.54	-	1509.6
AHQ-2-6, 5429 - 5430	K.AVMDDFAAFVEK.C	1343.53006	2	1.01E-08	0.97	4.25	-	1836.4
AHQ-2-12, 5531	K.AVMDDFAAFVEK.C	1343.53006	2	7.50E-05	0.83	3.02	-	784.0
AHQ-2-5, 5541	K.AVMDDFAAFVEK.C	1343.53006	1	1.74E-06	0.87	3.63	-	900.0
AHQ-2-14-, 5448	K.AVMDDFAAFVEK.C	1343.53006	2	1.13E-09	0.96	4.00	-	1783.9
AHQ-2-6, 2298 - 2314	K.CCTESLVNR.R	1141.25805	2	4.33E-05	0.85	2.79	-	1035.9
AHQ-2-5, 2335	K.CCTESLVNR.R	1141.25805	1	7.95E-06	0.25	2.00	-	126.0
AHQ-2-5, 2328	K.CCTESLVNR.R	1141.25805	2	3.83E-05	0.84	2.68	-	1028.4
AHQ-2-6, 2537	R.ETYGEMADCCAK.Q	1437.55563	2	2.34E-05	0.51	2.94	-	355.0
AHQ-2-5, 2353	R.FKDLGEENFK.A	1227.34766	1	5.92E-04	0.27	1.85	-	492.8
AHQ-2-6, 2357 - 2362	R.FKDLGEENFK.A	1227.34766	2	9.91E-06	0.79	3.15	-	675.8
AHQ-2-13-, 2698 - 2707	R.FKDLGEENFK.A	1227.34766	2	1.50E-04	0.78	2.94	-	646.4
AHQ-2-5, 2275 - 2351	R.FKDLGEENFK.A	1227.34766	2	4.15E-06	0.83	3.17	-	714.3
AHQ-2-5, 2596	K.FQNALLVR.Y	961.14282	2	3.09E-05	0.84	2.71	-	947.1
AHQ-2-5, 2260	K.KQTALVELVK.H	1129.37494	2	2.56E-05	0.81	3.01	-	766.7
AHQ-2-5, 3209 - 3215	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.41E-07	0.89	3.83	-	648.6
AHQ-2-10, 3156 - 3162	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.54E-06	0.89	3.53	-	625.9
AHQ-2-6, 3151 - 3233	K.KVPQVSTPTLVEVSR.N	1640.90605	2	6.16E-09	0.93	3.71	-	1066.7
AHQ-2-7, 3072	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.62E-07	0.86	3.28	-	630.8
AHQ-2-2, 3610	K.KVPQVSTPTLVEVSR.N	1640.90605	2	6.11E-09	0.80	3.13	-	552.5
AHQ-2-4, 3470 - 3545	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.64E-05	0.55	2.95	-	491.8
AHQ-2-8, 2915	K.KVPQVSTPTLVEVSR.N	1640.90605	2	4.70E-06	0.52	2.73	-	443.5
AHQ-2-3, 3559	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.39E-09	0.82	2.99	-	721.6
AHQ-2-6, 2985 - 3051	K.LVNEVTEFAK.T	1150.30633	2	2.63E-07	0.77	3.06	-	520.6
AHQ-2-1, 3449	K.LVNEVTEFAK.T	1150.30633	2	2.16E-06	0.84	3.64	-	507.7
AHQ-2-6, 5605	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	7.27E-06	0.97	5.74	-	1719.8
AHQ-2-5, 5640	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	1.50E-06	0.98	7.13	-	2273.8
AHQ-2-5, 5253	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	1.77E-08	0.97	6.57	-	1148.2
AHQ-2-5, 5019	K.QNCELFEQLGEYK.F	1659.79847	2	5.15E-05	0.48	2.50	-	374.3
AHQ-2-6, 3630	R.RHPDYSVVLLLR.L	1468.72842	2	4.28E-07	0.93	3.51	-	1021.6
AHQ-2-5, 3609 - 3621	R.RHPDYSVVLLLR.L	1468.72842	2	8.71E-05	0.94	3.60	-	1189.6
AHQ-2-6, 5742	R.RHPYFYAPELLFFAK.R	1900.21293	2	4.51E-11	0.98	4.85	-	2456.0
AHQ-2-5, 5633	R.RHPYFYAPELLFFAK.R	1900.21293	3	4.24E-10	0.97	6.04	-	1954.3
AHQ-2-5, 5631	R.RHPYFYAPELLFFAK.R	1900.21293	2	2.54E-06	0.98	5.78	-	2733.8
AHQ-2-6, 7174	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	8.96E-04	0.95	5.63	-	1113.2
AHQ-2-6, 7213	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	3.82E-08	0.97	6.21	-	1828.1
AHQ-2-5, 7420	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	3.76E-05	0.96	6.09	-	1284.8
AHQ-2-5, 7455 - 7457	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	1.20E-05	0.98	6.47	-	1924.1
AHQ-2-7, 4523	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.01E-04	0.89	3.81	-	611.4
AHQ-2-1, 4994	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.98E-08	0.84	3.85	-	542.1
AHQ-2-5, 4636	R.RPCFSALEVDETYVPK.E	1913.14041	2	5.15E-06	0.91	4.37	-	645.3
AHQ-2-6, 6349 - 6357	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	1.06E-05	0.92	5.30	-	598.5
AHQ-2-7, 7025 - 7043	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	1.52E-04	0.95	5.77	-	756.2
AHQ-2-6, 6893 - 6963	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	5.02E-08	0.96	5.29	-	966.2
AHQ-2-5, 7059 - 7124	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	2.13E-11	0.96	6.10	-	975.7
AHQ-2-5, 7061	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	3.57E-05	0.94	4.82	-	847.8
AHQ-2-6, 6859 - 6922	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	2.08E-07	0.95	5.43	-	939.5
AHQ-2-5, 2248	K.SLHTLFGDK.L	1018.14800	1	3.46E-05	0.63	2.53	-	489.3
AHQ-2-7, 2196	K.SLHTLFGDK.L	1018.14800	1	2.11E-04	0.55	2.34	-	505.6
AHQ-2-6, 4846	K.SLHTLFGDKLCTVATLR.E	1934.24913	3	9.95E-08	0.86	3.65	-	822.9
AHQ-2-6, 4855	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	7.39E-06	0.93	4.28	-	870.8
AHQ-2-6, 5683 - 5765	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.36E-04	0.87	4.44	-	449.0
AHQ-2-6, 5711 - 5778	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.20E-06	0.95	4.38	-	1467.1
AHQ-2-1, 6126	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.30E-07	0.97	5.06	-	1530.8
AHQ-2-5, 5971	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.83E-05	0.73	3.60	-	413.3
AHQ-2-5, 5795 - 5805	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	5.33E-06	0.95	4.41	-	1581.9
AHQ-2-5, 5787 - 5864	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.23E-05	0.94	4.54	-	626.2
AHQ-2-9, 5776 - 5854	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.92E-05	0.90	4.40	-	443.2
AHQ-2-3, 6108	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.42E-04	0.89	4.00	-	555.2
AHQ-2-4, 6109	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	7.24E-04	0.66	3.20	-	297.6
AHQ-2-6, 5562	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.59E-06	0.90	4.13	-	1055.6
AHQ-2-7, 5711 - 5712	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.22E-05	0.85	4.44	-	371.7
AHQ-2-1, 6120	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.58E-06	0.91	4.30	-	466.9
AHQ-2-5, 3528	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	1.32E-04	0.94	5.40	-	826.7
AHQ-2-5, 3759 - 3760	K.VPQVSTPTLVEVSR.N	1512.73313	2	2.92E-04	0.88	3.21	-	894.7
AHQ-2-10, 3610	K.VPQVSTPTLVEVSR.N	1512.73313	2	1.56E-04	0.56	2.54	-	595.5
AHQ-2-6, 3725 - 3751	K.VPQVSTPTLVEVSR.N	1512.73313	2	1.61E-07	0.91	3.93	-	810.2
AHQ-2-6, 2177 - 2181	K.YICENQDSISSK.L	1445.53420	2	9.41E-07	0.95	4.81	-	735.5
AHQ-2-5, 2201	K.YICENQDSISSK.L	1445.53420	1	9.02E-07	0.44	2.74	-	323.9
AHQ-2-1, 2452	K.YICENQDSISSK.L	1445.53420	1	8.51E-04	0.05	1.96	-	183.0
AHQ-2-1, 2449	K.YICENQDSISSK.L	1445.53420	2	4.98E-07	0.93	3.99	-	759.1
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				2.28E-11	2.61	30.34	13.10	32164.8
AHQ-2-1, 5056	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.24E-05	0.95	4.15	-	1166.9
AHQ-2-1, 5584	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.16E-07	0.91	4.46	-	670.4
AHQ-2-2, 5286 - 5317	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.00E-04	0.91	4.40	-	727.1
AHQ-2-2, 5846	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.42E-04	0.67	3.08	-	495.9
AHQ-2-3, 5135	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.90E-06	0.85	3.58	-	541.9
AHQ-2-3, 5788	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.41E-04	0.92	4.84	-	723.7
AHQ-2-4, 5140	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.46E-07	0.93	4.48	-	757.5
AHQ-2-4, 5632 - 5644	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.30E-07	0.74	3.47	-	543.1

AHQ-2-5, 5497	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.84E-07	0.92	4.64	-	796.8
AHQ-2-6, 5002 - 5003	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.23E-06	0.92	4.21	-	812.3
AHQ-2-6, 5342	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.06E-05	0.91	4.28	-	913.0
AHQ-2-14-, 5523 - 5587	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.25E-05	0.92	4.21	-	893.2
AHQ-2-8, 4724	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.42E-08	0.89	4.53	-	515.4
AHQ-2-8, 4824 - 4903	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.88E-05	0.97	5.57	-	1114.7
AHQ-2-8, 4915 - 4987	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.52E-05	0.96	5.14	-	932.1
AHQ-2-8, 5055 - 5126	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.15E-09	0.96	4.98	-	1082.7
AHQ-2-8, 5159 - 5232	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.13E-04	0.79	3.51	-	599.2
AHQ-2-8, 5234 - 5302	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.24E-04	0.98	6.86	-	1120.3
AHQ-2-8, 5331 - 5399	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.70E-06	0.87	3.67	-	718.0
AHQ-2-8, 5427 - 5498	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.23E-07	0.85	3.69	-	634.8
AHQ-2-8, 5447 - 5514	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.11E-04	0.93	4.46	-	858.6
AHQ-2-8, 5656 - 5722	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.50E-05	0.91	4.44	-	623.7
AHQ-2-8, 5747 - 5826	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.21E-05	0.93	4.51	-	773.8
AHQ-2-8, 5878 - 5958	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.28E-06	0.97	5.83	-	1110.6
AHQ-2-8, 6026 - 6107	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.28E-04	0.97	5.86	-	1125.3
AHQ-2-8, 6174 - 6244	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.99E-06	0.95	5.02	-	834.2
AHQ-2-8, 6307 - 6371	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.03E-04	0.97	5.81	-	918.2
AHQ-2-8, 6438 - 6506	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.22E-05	0.95	5.23	-	828.9
AHQ-2-8, 6575 - 6642	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.17E-05	0.95	4.75	-	1034.5
AHQ-2-8, 6710 - 6790	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.23E-05	0.94	4.83	-	832.1
AHQ-2-8, 6848 - 6920	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.58E-06	0.96	5.73	-	855.2
AHQ-2-8, 7252 - 7323	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.57E-04	0.92	4.90	-	553.2
AHQ-2-9, 4951 - 4952	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.79E-05	0.95	5.02	-	1056.4
AHQ-2-9, 5034 - 5108	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.61E-05	0.94	4.50	-	934.2
AHQ-2-9, 5394	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.17E-05	0.89	4.29	-	695.7
AHQ-2-9, 6294 - 6366	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.80E-07	0.83	3.77	-	515.9
AHQ-2-10, 4583 - 4664	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.71E-08	0.94	4.99	-	780.4
AHQ-2-10, 4722 - 4786	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.24E-04	0.96	4.94	-	1008.7
AHQ-2-10, 4979 - 4994	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.99E-06	0.97	5.63	-	1328.6
AHQ-2-10, 5098 - 5166	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.56E-07	0.96	5.30	-	884.2
AHQ-2-10, 5351 - 5414	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.44E-04	0.96	4.92	-	1237.4
AHQ-2-10, 5478 - 5547	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.12E-04	0.77	3.68	-	500.8
AHQ-2-10, 6131	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.76E-06	0.82	3.74	-	635.8
AHQ-2-11, 4704	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.15E-11	0.97	5.75	-	1014.5
AHQ-2-11, 4810 - 4829	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.35E-04	0.79	3.38	-	546.0
AHQ-2-11, 5005	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.01E-05	0.90	4.37	-	602.7
AHQ-2-11, 5116	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.65E-08	0.95	4.53	-	1111.9
AHQ-2-11, 5262 - 5330	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.25E-06	0.93	4.57	-	780.5
AHQ-2-12, 4925 - 4926	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.36E-09	0.97	5.64	-	1413.6
AHQ-2-12, 5351	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.28E-11	0.96	5.18	-	1305.8
AHQ-2-12, 5501 - 5566	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.07E-04	0.92	4.35	-	812.4
AHQ-2-13, 4787 - 4849	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.74E-08	0.96	5.38	-	1065.2
AHQ-2-13, 4871 - 4935	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.09E-05	0.96	5.18	-	1166.1
AHQ-2-13, 5000 - 5073	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.89E-05	0.93	4.18	-	961.1
AHQ-2-13, 5139 - 5200	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.64E-07	0.90	4.33	-	769.5
AHQ-2-13, 5161 - 5231	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.14E-06	0.95	4.78	-	1092.4
AHQ-2-13, 5559 - 5624	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.96E-04	0.94	5.01	-	701.6
AHQ-2-14, 5668 - 5728	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.62E-09	0.96	4.79	-	1252.0
AHQ-2-14, 5944 - 6006	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.26E-05	0.97	5.01	-	1486.5
AHQ-2-14, 6068 - 6141	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.22E-05	0.95	5.17	-	897.6
AHQ-2-14, 6144 - 6184	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.17E-07	0.97	5.91	-	1248.3
AHQ-2-14, 6200 - 6268	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.03E-06	0.94	4.52	-	969.1
AHQ-2-14, 6248 - 6312	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.69E-05	0.94	4.76	-	923.1
AHQ-2-14, 6373 - 6436	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.43E-04	0.96	5.93	-	1011.3
AHQ-2-14, 6590 - 6609	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.36E-08	0.97	5.17	-	1379.6
AHQ-2-13-, 4942 - 5009	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.11E-05	0.96	5.44	-	1081.9
AHQ-2-13-, 5049	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.29E-05	0.84	3.52	-	753.3
AHQ-2-13-, 5135 - 5181	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.50E-04	0.92	4.45	-	822.9
AHQ-2-13-, 5243 - 5313	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.35E-05	0.95	5.12	-	963.0
AHQ-2-13-, 5386 - 5453	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.38E-05	0.96	5.80	-	928.3
AHQ-2-13-, 5518 - 5594	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.96E-04	0.95	5.41	-	835.3
AHQ-2-13-, 5658 - 5667	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.71E-05	0.96	5.25	-	884.8
AHQ-2-13-, 5811 - 5874	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.92E-06	0.94	4.82	-	780.5
AHQ-2-13-, 5951 - 6025	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.53E-04	0.91	4.07	-	790.5
AHQ-2-14-, 4677 - 4744	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.81E-06	0.93	4.51	-	836.3
AHQ-2-14-, 4851 - 4915	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.95E-05	0.96	5.06	-	1086.9
AHQ-2-14-, 4980 - 5044	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.09E-05	0.95	5.26	-	795.6
AHQ-2-14-, 5083 - 5145	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.61E-08	0.96	5.30	-	896.2
AHQ-2-14-, 5143 - 5211	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.35E-11	0.97	6.08	-	1439.6
AHQ-2-14-, 5212 - 5213	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.30E-04	0.88	3.78	-	819.6
AHQ-2-14-, 5255 - 5333	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.72E-05	0.97	5.27	-	1272.5
AHQ-2-14-, 5395 - 5467	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.75E-05	0.96	5.58	-	889.5
AHQ-2-14-, 5656	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.53E-07	0.93	4.44	-	970.7
AHQ-2-8, 3534 - 3602	K.YPIEHSIITNWDDM*EK.I	2008.19724	2	6.24E-04	0.67	2.88	-	425.1
gi|5729887|ref|NP_006624.1| IQ motif containing GTPase activating protein 2 [Homo sapiens]				2.31E-11	5.41	60.29	7.00	180611.0
AHQ-2-6, 5530	K.GVLLDIDDLQTNQFK.N	1719.91690	2	3.98E-06	0.85	3.14	-	846.6
AHQ-2-3, 5883	K.GVLLDIDDLQTNQFK.N	1719.91690	2	2.31E-11	0.98	5.83	-	1673.2
AHQ-2-3, 5992	K.LGIAPQIQDLLGK.V	1366.63117	2	4.19E-05	0.81	3.20	-	436.7
AHQ-2-6, 5609	K.LGIAPQIQDLLGK.V	1366.63117	1	2.22E-04	0.14	1.99	-	291.3
AHQ-2-4, 4989	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	2.95E-08	0.95	4.41	-	1530.2
AHQ-2-3, 4989	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	3.75E-10	0.97	4.68	-	1684.4
AHQ-2-3, 6159	R.NPNAVLTLVDDNLAPEYQK.E	2115.32901	2	3.67E-04	0.87	3.67	-	548.3
AHQ-2-3, 7135	R.NQPGNTLTEILETPATAQQEVDHATDMVSR.A	3268.51558	3	9.82E-06	0.83	3.85	-	533.8
AHQ-2-5, 6992	R.NQPGNTLTEILETPATAQQEVDHATDMVSR.A	3268.51558	3	2.77E-04	0.71	3.23	-	503.7
AHQ-2-6, 6827	R.NQPGNTLTEILETPATAQQEVDHATDMVSR.A	3268.51558	3	1.53E-07	0.82	3.87	-	506.1
AHQ-2-4, 4304	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	5.76E-06	0.91	3.86	-	1169.8
AHQ-2-3, 4313	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	3.06E-08	0.96	4.91	-	1385.5
gi|4502985|ref|NP_001854.1| cytochrome c oxidase subunit VIb; human cytochrome oxidase subunit VIb				2.36E-11	0.93	10.22	20.90	10192.3
AHQ-2-14-, 6223	R.VYQSLCPTSWVTDWDEQR.A	2272.43560	2	2.36E-11	0.93	4.43	-	868.5
gi|4504523|ref|NP_002148.1| heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (				2.40E-11	1.84	20.20	25.50	10931.6
AHQ-2-14-, 2720 - 2732	K.VLQATVVAVGSGSK.G	1316.52902	2	1.44E-09	0.96	3.50	-	1879.8
AHQ-2-14, 3660	K.VLQATVVAVGSGSK.G	1316.52902	2	1.66E-05	0.91	3.73	-	849.5
AHQ-2-14-, 5020 - 5027	K.VVLDDKDYFLFR.D	1530.74861	2	1.66E-10	0.94	4.00	-	964.5
AHQ-2-14, 6260	K.VVLDDKDYFLFR.D	1530.74861	2	2.40E-11	0.88	3.16	-	972.7
gi|7661818|ref|NP_054900.1| HSPC159 protein [Homo sapiens]				2.61E-11	3.80	50.24	43.60	19011.6
AHQ-2-13-, 6889 - 6890	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	4.82E-07	0.89	4.53	-	340.8
AHQ-2-13, 6671	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	9.91E-05	0.90	4.06	-	454.4
AHQ-2-11, 6617 - 6628	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	9.10E-06	0.91	4.35	-	463.5
AHQ-2-14-, 6747	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	5.71E-06	0.90	4.36	-	394.9
AHQ-2-11, 2492 - 2502	K.INGDLQITK.L	1002.14688	1	1.85E-04	0.32	2.05	-	393.4
AHQ-2-13, 3711	R.IQTLSAIDTIK.I	1203.41068	2	5.01E-04	0.70	2.88	-	469.0
AHQ-2-13-, 3722 - 3795	R.IQTLSAIDTIK.I	1203.41068	2	7.84E-04	0.71	2.71	-	599.6
AHQ-2-11, 4886 - 4952	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	2	2.61E-11	0.95	4.86	-	1366.3
AHQ-2-11, 4892	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	3	6.09E-07	0.92	4.60	-	1102.2
AHQ-2-11, 4737	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	2	1.34E-07	0.92	4.73	-	829.0

AHQ-2-11, 4993 - 5073	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	3	7.46E-05	0.69	3.22	-	825.7
AHQ-2-13, 4881	R.VFVDGHQLFDFYHR.I	1780.96540	2	1.52E-05	0.97	4.65	-	1682.6
AHQ-2-11, 4678 - 4742	R.VFVDGHQLFDFYHR.I	1780.96540	2	3.81E-11	0.94	4.40	-	1089.2
AHQ-2-12, 4885	R.VFVDGHQLFDFYHR.I	1780.96540	2	1.46E-10	0.96	4.74	-	1318.4
gi|6005846|ref|NP_009215.1| PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro				2.73E-11	5.51	60.28	29.80	39547.7
AHQ-2-12, 6690	R.AVLPLLDAQQPCYLLYR.L	2035.39506	3	5.14E-10	0.94	4.42	-	1254.7
AHQ-2-12, 6681	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	8.15E-06	0.95	4.64	-	897.0
AHQ-2-12, 6594	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	5.16E-06	0.85	3.59	-	516.5
AHQ-2-13, 6472 - 6484	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	2.73E-11	0.96	5.35	-	954.2
AHQ-2-12, 3183	K.DDLSFAGYQK.H	1144.21551	1	6.52E-06	0.68	2.54	-	523.4
AHQ-2-10, 3862 - 3863	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	3.33E-05	0.91	4.66	-	700.4
AHQ-2-11, 4020 - 4022	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	5.23E-06	0.95	4.83	-	940.7
AHQ-2-11, 4188 - 4189	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	9.76E-11	0.98	5.35	-	1418.2
AHQ-2-10, 3976	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	3.17E-10	0.97	4.60	-	1665.3
AHQ-2-11, 6178	K.KIEIGDGAELTAEFLYDEVHPK.Q	2475.73515	3	1.22E-10	0.97	5.59	-	1735.5
AHQ-2-12, 4789 - 4826	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	2.52E-07	0.97	4.74	-	2028.3
gi|5174727|ref|NP_005989.1| chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring				3.08E-11	3.70	40.22	9.20	60330.4
AHQ-2-6, 3553	R.AVAQALEVIPR.T	1167.38326	2	7.78E-05	0.95	4.37	-	1370.3
AHQ-2-6, 4353	K.IPGGIIEDSCVLR.G	1430.65218	2	3.08E-11	0.94	4.21	-	1191.6
AHQ-2-6, 2638	R.TLIQNCGASTIR.L	1335.51249	2	2.77E-04	0.88	3.45	-	821.0
AHQ-2-6, 5389	R.WSSLACNIALDAVK.M	1549.77353	2	1.71E-06	0.93	3.71	-	1188.0
gi|7661678|ref|NP_056461.1| RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B				3.39E-11	11.06	120.27	35.90	20824.7
AHQ-2-11, 4258 - 4260	K.DTDDVPMILVGNK.C	1417.61048	1	6.81E-05	0.31	2.63	-	489.6
AHQ-2-11, 4257	K.DTDDVPMILVGNK.C	1417.61048	2	7.01E-08	0.94	3.85	-	948.5
AHQ-2-11, 6686	R.KQVEVDAQQCMLEILDTAGTEQFTAMR.D	3115.50608	3	2.16E-05	0.67	3.25	-	661.1
AHQ-2-14, 6313	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	7.22E-04	0.90	4.16	-	1142.5
AHQ-2-11, 6437 - 6452	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	6.69E-09	0.94	4.72	-	1629.4
AHQ-2-11, 5117	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	3.51E-09	0.93	4.65	-	961.0
AHQ-2-14-, 5280	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	1.51E-08	0.83	3.39	-	974.3
AHQ-2-13-, 6925	R.KQVEVDAQQCMLEILDTAGTEQFTAMR.D	3115.50608	3	8.49E-08	0.92	4.99	-	818.2
AHQ-2-11, 5553	R.KQVEVDAQQCM*LEILDTAGTEQFTAMR.D	3131.50548	3	1.76E-04	0.93	4.54	-	1295.3
AHQ-2-11, 6770 - 6776	K.QVEVDAQQCMLEILDTAGTEQFTAMR.D	2987.33317	2	1.50E-07	0.89	4.49	-	453.2
AHQ-2-11, 4036 - 4102	R.QWNNCAFLESSAK.S	1556.68148	2	1.04E-06	0.61	2.73	-	246.3
AHQ-2-11, 3893 - 3973	R.QWNNCAFLESSAK.S	1556.68148	2	7.21E-07	0.80	3.81	-	220.4
AHQ-2-11, 3801	R.QWNNCAFLESSAK.S	1556.68148	2	1.38E-05	0.74	3.23	-	275.4
AHQ-2-14-, 3811 - 3823	R.VKDTDDVPMILVGNK.C	1644.91497	2	2.53E-06	0.93	3.27	-	1484.9
AHQ-2-13-, 3905	R.VKDTDDVPMILVGNK.C	1644.91497	3	9.13E-05	0.95	4.28	-	1849.5
AHQ-2-11, 3729 - 3758	R.VKDTDDVPMILVGNK.C	1644.91497	2	7.77E-09	0.98	5.36	-	2089.7
AHQ-2-11, 3576 - 3578	R.VKDTDDVPMILVGNK.C	1644.91497	3	8.89E-04	0.97	5.23	-	2422.7
AHQ-2-11, 3141 - 3200	R.VKDTDDVPM*ILVGNK.C	1660.91437	2	6.76E-04	0.95	4.54	-	1121.5
AHQ-2-11, 3533 - 3596	R.VKDTDDVPMILVGNK.C	1644.91497	2	2.11E-04	0.97	4.36	-	1911.7
AHQ-2-13, 3864	R.VKDTDDVPMILVGNK.C	1644.91497	2	6.61E-08	0.97	5.03	-	1836.0
AHQ-2-13-, 3902 - 3907	R.VKDTDDVPMILVGNK.C	1644.91497	2	4.41E-07	0.97	4.62	-	1976.2
AHQ-2-11, 4505 - 4554	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	5.80E-10	0.97	5.38	-	2296.6
AHQ-2-14-, 4580 - 4587	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	3.02E-08	0.93	4.17	-	1428.1
AHQ-2-11, 4422 - 4490	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	1.03E-08	0.92	3.98	-	918.6
AHQ-2-12, 4478	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	5.80E-05	0.84	3.62	-	812.3
AHQ-2-12, 4631	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	3.39E-11	0.92	4.85	-	847.1
AHQ-2-11, 4373 - 4436	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	1.19E-04	0.91	4.79	-	990.9
AHQ-2-13, 4481	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	4.13E-04	0.86	3.85	-	957.1
AHQ-2-13, 4601	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	1.37E-05	0.82	3.30	-	1173.1
AHQ-2-11, 4302	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	6.95E-04	0.70	3.47	-	637.8
AHQ-2-11, 4268 - 4333	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	2.02E-04	0.93	4.53	-	711.8
AHQ-2-11, 4229 - 4308	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	4.62E-08	0.92	5.12	-	753.1
AHQ-2-13-, 4559	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	4.06E-06	0.92	4.93	-	1026.2
AHQ-2-11, 4070 - 4145	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	1.27E-08	0.95	5.07	-	1242.4
AHQ-2-11, 3948	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	2	2.56E-04	0.44	2.76	-	340.6
AHQ-2-11, 4574	R.VKDTDDVPMILVGNKCDLEDERVVGK.E	2947.33182	3	1.68E-08	0.92	4.33	-	1508.6
AHQ-2-11, 4429	R.VKDTDDVPMILVGNKCDLEDERVVGK.E	2947.33182	3	7.01E-05	0.93	5.24	-	1180.7
gi|4502219|ref|NP_001656.1| ras homolog gene family, member G (rho G); RhoG [Homo sapiens]				3.51E-11	1.87	20.20	18.80	21338.4
AHQ-2-11, 4869	K.EYIPTVFDNYSAQSAVDGR.T	2133.25975	2	3.51E-11	0.93	3.89	-	904.9
AHQ-2-11, 4820	R.TVNLNLWDTAGQEEYDR.L	2025.12129	2	6.85E-08	0.94	4.06	-	1463.9
gi|10835187|ref|NP_000627.1| superoxide dismutase 2, mitochondrial [Homo sapiens]				3.70E-11	4.36	50.23	39.60	24733.0
AHQ-2-13-, 6309 - 6315	K.AIWNVINWENVTER.Y	1744.93137	2	3.92E-11	0.96	4.69	-	1426.6
AHQ-2-13, 6127	K.AIWNVINWENVTER.Y	1744.93137	2	9.69E-08	0.90	4.22	-	720.4
AHQ-2-11, 6289	K.AIWNVINWENVTER.Y	1744.93137	2	3.70E-11	0.93	3.63	-	1181.3
AHQ-2-11, 6012	K.AIWNVINWENVTER.Y	1744.93137	2	2.04E-06	0.89	3.12	-	1072.3
AHQ-2-11, 5885 - 5954	K.AIWNVINWENVTER.Y	1744.93137	2	2.42E-07	0.90	3.87	-	726.0
AHQ-2-14-, 6171	K.AIWNVINWENVTER.Y	1744.93137	2	1.28E-06	0.94	3.88	-	1146.8
AHQ-2-11, 4493 - 4516	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	2	3.09E-07	0.87	3.94	-	552.5
AHQ-2-11, 4389	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	2	4.45E-09	0.91	4.62	-	647.2
AHQ-2-11, 3748 - 3808	K.GDVTAQIALQPALK.F	1425.65548	2	1.04E-04	0.86	3.50	-	899.1
AHQ-2-11, 3720	K.GDVTAQIALQPALK.F	1425.65548	1	3.36E-06	0.80	3.33	-	858.6
AHQ-2-11, 3657 - 3724	K.GDVTAQIALQPALK.F	1425.65548	2	4.84E-06	0.77	3.50	-	585.4
AHQ-2-11, 3804	K.GDVTAQIALQPALK.F	1425.65548	1	2.41E-06	0.80	3.42	-	852.4
AHQ-2-11, 2293	K.HHAAYVNNLNVTEEK.Y	1739.86999	3	7.92E-06	0.95	4.44	-	2010.9
AHQ-2-11, 2205	K.HHAAYVNNLNVTEEK.Y	1739.86999	3	1.29E-04	0.94	4.39	-	1578.4
AHQ-2-11, 2292 - 2369	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	8.01E-07	0.93	3.99	-	1031.5
AHQ-2-11, 2198	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	2.00E-07	0.93	4.22	-	815.2
AHQ-2-11, 6893 - 6973	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	6.80E-06	0.78	3.47	-	619.1
gi|4507651|ref|NP_003281.1| tropomyosin 4 [Homo sapiens]				3.92E-11	4.49	50.27	20.20	28521.6
AHQ-2-9, 3896 - 3968	R.AEVSELKCGDLEEELK.N	1851.02256	2	3.12E-07	0.91	4.12	-	837.9
AHQ-2-9, 3895 - 3966	R.AEVSELKCGDLEEELK.N	1851.02256	2	3.39E-06	0.94	4.46	-	982.8
AHQ-2-9, 6031	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	3.92E-11	0.95	5.43	-	1344.0
AHQ-2-9, 1620	R.EKAEGDVAALNR.R	1273.37796	2	1.17E-05	0.73	2.76	-	681.8
AHQ-2-9, 2454 - 2483	K.IQALQQQADEAEDR.A	1615.68404	2	6.04E-11	0.97	4.73	-	1638.3
AHQ-2-11, 2508	K.IQALQQQADEAEDR.A	1615.68404	2	1.40E-04	0.97	3.61	-	2466.9
AHQ-2-9, 2592	K.IQALQQQADEAEDR.A	1615.68404	2	3.79E-06	0.80	2.84	-	488.7
AHQ-2-10, 2214	R.KIQALQQQADEAEDR.A	1743.85695	2	4.73E-07	0.93	4.29	-	1185.2
AHQ-2-9, 2230	R.KIQALQQQADEAEDR.A	1743.85695	3	3.86E-04	0.58	3.14	-	589.1
AHQ-2-9, 2351	R.KIQALQQQADEAEDR.A	1743.85695	2	5.45E-04	0.91	3.33	-	1320.5
gi|17986258|ref|NP_066299.2| smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo				4.01E-11	7.16	80.28	37.10	16930.0
AHQ-2-12, 4293 - 4310	K.DQGTYEDYVEGLR.V	1545.58904	2	1.28E-05	0.93	3.55	-	1101.4
AHQ-2-12, 3858 - 3927	K.EAFQLFDR.T	1026.12699	2	6.25E-04	0.73	2.87	-	640.6
AHQ-2-13, 2371	R.HVLVTLGEK.M	996.18547	2	3.73E-05	0.86	2.78	-	779.9
AHQ-2-13-, 2237	R.HVLVTLGEK.M	996.18547	2	4.46E-06	0.90	3.39	-	718.2
AHQ-2-14-, 2207	R.HVLVTLGEK.M	996.18547	2	7.56E-07	0.90	3.31	-	683.0
AHQ-2-14-, 2208 - 2209	R.HVLVTLGEK.M	996.18547	1	3.81E-04	0.71	3.01	-	430.1
AHQ-2-12, 2193	R.HVLVTLGEK.M	996.18547	2	2.60E-06	0.85	2.84	-	695.3
AHQ-2-12, 2105 - 2169	R.HVLVTLGEK.M	996.18547	1	3.47E-05	0.62	2.92	-	538.7
AHQ-2-13, 2376	R.HVLVTLGEK.M	996.18547	1	1.05E-05	0.66	2.85	-	582.1
AHQ-2-12, 2102 - 2166	R.HVLVTLGEK.M	996.18547	2	3.28E-06	0.88	3.50	-	588.0
AHQ-2-12, 3763 - 3770	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.53E-04	0.53	3.08	-	624.1
AHQ-2-12, 4171	K.NKDQGTYEDYVEGLR.V	1787.86505	2	7.01E-06	0.75	3.07	-	717.2
AHQ-2-12, 3743 - 3823	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.24E-08	0.86	3.68	-	708.1
AHQ-2-14-, 3709	K.NKDQGTYEDYVEGLR.V	1787.86505	2	5.23E-09	0.92	4.13	-	982.4
AHQ-2-12, 3601 - 3669	K.NKDQGTYEDYVEGLR.V	1787.86505	3	5.21E-06	0.95	4.90	-	1296.1

<table>
<tr><td>AHQ-2-12, 3598 - 3673</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>2</td><td>4.16E-09</td><td>0.95</td><td>4.03</td><td>-</td><td>1490.9</td></tr>
<tr><td>AHQ-2-13-, 3813 - 3819</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>2</td><td>1.36E-10</td><td>0.89</td><td>3.87</td><td>-</td><td>779.0</td></tr>
<tr><td>AHQ-2-14-, 3711 - 3716</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>3</td><td>1.42E-05</td><td>0.93</td><td>5.01</td><td>-</td><td>991.2</td></tr>
<tr><td>AHQ-2-14-, 3988</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>2</td><td>2.98E-08</td><td>0.80</td><td>3.17</td><td>-</td><td>782.0</td></tr>
<tr><td>AHQ-2-12, 3995 - 4065</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>2</td><td>1.43E-08</td><td>0.94</td><td>4.22</td><td>-</td><td>1175.0</td></tr>
<tr><td>AHQ-2-13, 3752 - 3775</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>2</td><td>6.77E-08</td><td>0.93</td><td>4.23</td><td>-</td><td>928.1</td></tr>
<tr><td>AHQ-2-14, 4805</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>2</td><td>3.58E-05</td><td>0.81</td><td>3.54</td><td>-</td><td>900.2</td></tr>
<tr><td>AHQ-2-14, 4594</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>3</td><td>1.05E-06</td><td>0.87</td><td>4.19</td><td>-</td><td>881.1</td></tr>
<tr><td>AHQ-2-14, 4592</td><td>K.NKDQGTYEDYVEGLR.V</td><td>1787.86505</td><td>2</td><td>1.56E-10</td><td>0.91</td><td>3.71</td><td>-</td><td>1067.7</td></tr>
<tr><td>AHQ-2-12, 3165 - 3234</td><td>R.VFDKEGNGTVMGAEIR.H</td><td>1723.93228</td><td>2</td><td>2.26E-10</td><td>0.94</td><td>4.21</td><td>-</td><td>1036.7</td></tr>
<tr><td>AHQ-2-14-, 3305</td><td>R.VFDKEGNGTVMGAEIR.H</td><td>1723.93228</td><td>2</td><td>4.01E-11</td><td>0.96</td><td>4.46</td><td>-</td><td>1553.3</td></tr>
<tr><td>AHQ-2-12, 3246 - 3254</td><td>R.VFDKEGNGTVM*GAEIR.H</td><td>1739.93168</td><td>2</td><td>1.65E-06</td><td>0.89</td><td>4.02</td><td>-</td><td>870.6</td></tr>
<tr><td>AHQ-2-12, 6973 - 7042</td><td>K.VLDFEHFLPMLQTVAK.N</td><td>1889.25017</td><td>2</td><td>6.76E-07</td><td>0.95</td><td>4.97</td><td>-</td><td>918.9</td></tr>
<tr><td>AHQ-2-13-, 6482</td><td>K.VLDFEHFLPM*LQTVAK.N</td><td>1905.24957</td><td>3</td><td>9.10E-06</td><td>0.88</td><td>3.77</td><td>-</td><td>861.6</td></tr>
<tr><td>AHQ-2-13-, 6922 - 6923</td><td>K.VLDFEHFLPMLQTVAK.N</td><td>1889.25017</td><td>2</td><td>3.16E-04</td><td>0.96</td><td>5.20</td><td>-</td><td>960.2</td></tr>
<tr><td>AHQ-2-12, 6975 - 6987</td><td>K.VLDFEHFLPMLQTVAK.N</td><td>1889.25017</td><td>3</td><td>1.24E-05</td><td>0.96</td><td>5.07</td><td>-</td><td>1385.9</td></tr>
<tr><td>AHQ-2-12, 6651</td><td>K.VLDFEHFLPM*LQTVAK.N</td><td>1905.24957</td><td>2</td><td>6.12E-06</td><td>0.88</td><td>3.71</td><td>-</td><td>655.8</td></tr>
<tr><td>AHQ-2-12, 6378 - 6449</td><td>K.VLDFEHFLPM*LQTVAK.N</td><td>1905.24957</td><td>3</td><td>5.56E-06</td><td>0.86</td><td>3.61</td><td>-</td><td>833.4</td></tr>
<tr><td>AHQ-2-13, 6256</td><td>K.VLDFEHFLPM*LQTVAK.N</td><td>1905.24957</td><td>2</td><td>3.12E-06</td><td>0.90</td><td>4.06</td><td>-</td><td>655.2</td></tr>
<tr><td>AHQ-2-12, 6366 - 6429</td><td>K.VLDFEHFLPM*LQTVAK.N</td><td>1905.24957</td><td>2</td><td>4.52E-06</td><td>0.91</td><td>4.28</td><td>-</td><td>694.1</td></tr>
<tr><td>AHQ-2-13-, 6927</td><td>K.VLDFEHFLPMLQTVAK.N</td><td>1889.25017</td><td>3</td><td>2.07E-05</td><td>0.92</td><td>4.06</td><td>-</td><td>1606.0</td></tr>
<tr><td>AHQ-2-13, 6699</td><td>K.VLDFEHFLPMLQTVAK.N</td><td>1889.25017</td><td>2</td><td>1.17E-06</td><td>0.91</td><td>4.20</td><td>-</td><td>658.8</td></tr>
<tr><td>AHQ-2-14-, 6312 - 6328</td><td>K.VLDFEHFLPM*LQTVAK.N</td><td>1905.24957</td><td>3</td><td>1.20E-04</td><td>0.78</td><td>3.38</td><td>-</td><td>914.2</td></tr>
<tr><td>AHQ-2-14-, 6316</td><td>K.VLDFEHFLPM*LQTVAK.N</td><td>1905.24957</td><td>2</td><td>4.82E-04</td><td>0.92</td><td>4.19</td><td>-</td><td>731.5</td></tr>
<tr><td>AHQ-2-14-, 6776 - 6777</td><td>K.VLDFEHFLPMLQTVAK.N</td><td>1889.25017</td><td>2</td><td>4.71E-06</td><td>0.97</td><td>5.52</td><td>-</td><td>1488.6</td></tr>
<tr><td>AHQ-2-14-, 6779 - 6780</td><td>K.VLDFEHFLPMLQTVAK.N</td><td>1889.25017</td><td>3</td><td>1.14E-05</td><td>0.96</td><td>4.78</td><td>-</td><td>1708.3</td></tr>
<tr><td colspan="2">gi|6857820|ref|NP_005019.2| phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl</td><td></td><td></td><td>4.25E-11</td><td>2.74</td><td>30.24</td><td>11.30</td><td>46224.3</td></tr>
<tr><td>AHQ-2-7, 4559</td><td>R.FGIDDQDFQNSLTR.S</td><td>1656.73462</td><td>2</td><td>3.71E-06</td><td>0.88</td><td>3.88</td><td>-</td><td>982.4</td></tr>
<tr><td>AHQ-2-7, 2449</td><td>K.HGAGAEISTVNPEQYSK.R</td><td>1788.89618</td><td>2</td><td>4.68E-10</td><td>0.97</td><td>4.89</td><td>-</td><td>2082.4</td></tr>
<tr><td>AHQ-2-7, 3947</td><td>K.TITSEDVAEMHNILK.K</td><td>1701.92338</td><td>2</td><td>4.25E-11</td><td>0.89</td><td>4.04</td><td>-</td><td>741.1</td></tr>
<tr><td colspan="2">gi|4757826|ref|NP_004039.1| beta-2-microglobulin [Homo sapiens]</td><td></td><td></td><td>4.87E-11</td><td>3.13</td><td>40.24</td><td>38.70</td><td>13714.5</td></tr>
<tr><td>AHQ-2-14-, 6653 - 6720</td><td>K.SNFLNCYVSGFHPSDIEVDLLK.N</td><td>2556.83155</td><td>3</td><td>3.25E-06</td><td>0.78</td><td>3.66</td><td>-</td><td>642.3</td></tr>
<tr><td>AHQ-2-14-, 6519 - 6581</td><td>K.SNFLNCYVSGFHPSDIEVDLLK.N</td><td>2556.83155</td><td>2</td><td>2.49E-09</td><td>0.80</td><td>3.98</td><td>-</td><td>356.9</td></tr>
<tr><td>AHQ-2-14-, 6716</td><td>K.SNFLNCYVSGFHPSDIEVDLLK.N</td><td>2556.83155</td><td>2</td><td>5.02E-06</td><td>0.93</td><td>4.73</td><td>-</td><td>750.1</td></tr>
<tr><td>AHQ-2-14-, 6491</td><td>K.SNFLNCYVSGFHPSDIEVDLLKNGER.I</td><td>3013.28710</td><td>3</td><td>4.87E-11</td><td>0.89</td><td>4.41</td><td>-</td><td>962.8</td></tr>
<tr><td>AHQ-2-14-, 6255 - 6257</td><td>K.SNFLNCYVSGFHPSDIEVDLLKNGER.I</td><td>3013.28710</td><td>3</td><td>4.70E-08</td><td>0.85</td><td>4.05</td><td>-</td><td>429.6</td></tr>
<tr><td>AHQ-2-14, 3076</td><td>K.VEHSDLSFSK.D</td><td>1149.23530</td><td>1</td><td>4.29E-04</td><td>0.35</td><td>2.38</td><td>-</td><td>415.3</td></tr>
<tr><td>AHQ-2-14-, 2059 - 2061</td><td>K.VEHSDLSFSK.D</td><td>1149.23530</td><td>1</td><td>3.06E-04</td><td>0.86</td><td>3.33</td><td>-</td><td>650.5</td></tr>
<tr><td>AHQ-2-14-, 1723</td><td>R.VNHVTLSQPK.I</td><td>1123.28735</td><td>1</td><td>6.53E-04</td><td>0.23</td><td>2.26</td><td>-</td><td>173.1</td></tr>
<tr><td>AHQ-2-14-, 1848</td><td>R.VNHVTLSQPK.I</td><td>1123.28735</td><td>1</td><td>4.10E-04</td><td>0.27</td><td>2.09</td><td>-</td><td>243.5</td></tr>
<tr><td>AHQ-2-14-, 1961 - 2037</td><td>R.VNHVTLSQPK.I</td><td>1123.28735</td><td>1</td><td>1.75E-06</td><td>0.58</td><td>2.73</td><td>-</td><td>338.7</td></tr>
<tr><td colspan="2">gi|27480104|ref|XP_208215.1| similar to triosephosphate isomerase 1 [Homo sapiens]</td><td></td><td></td><td>5.13E-11</td><td>3.55</td><td>40.27</td><td>17.30</td><td>26942.6</td></tr>
<tr><td>AHQ-2-10, 2686</td><td>R.HVFGESDELIGQK.V</td><td>1459.58565</td><td>1</td><td>3.52E-06</td><td>0.91</td><td>3.87</td><td>-</td><td>798.5</td></tr>
<tr><td>AHQ-2-10, 2676 - 2678</td><td>R.HVFGESDELIGQK.V</td><td>1459.58565</td><td>2</td><td>5.13E-11</td><td>0.97</td><td>5.19</td><td>-</td><td>1038.2</td></tr>
<tr><td>AHQ-2-10, 2679</td><td>R.HVFGESDELIGQK.V</td><td>1459.58565</td><td>1</td><td>9.63E-07</td><td>0.87</td><td>3.44</td><td>-</td><td>882.7</td></tr>
<tr><td>AHQ-2-11, 2900</td><td>R.HVFGESDELIGQK.V</td><td>1459.58565</td><td>2</td><td>2.27E-08</td><td>0.92</td><td>4.17</td><td>-</td><td>535.9</td></tr>
<tr><td>AHQ-2-10, 2506 - 2518</td><td>R.IIYGGSVTGATCK.E</td><td>1328.51672</td><td>2</td><td>4.78E-05</td><td>0.80</td><td>2.98</td><td>-</td><td>538.5</td></tr>
<tr><td>AHQ-2-10, 2378</td><td>R.RHVFGESDELIGQK.V</td><td>1615.77200</td><td>2</td><td>2.00E-09</td><td>0.98</td><td>5.40</td><td>-</td><td>2427.4</td></tr>
<tr><td>AHQ-2-10, 3440 - 3514</td><td>K.VTNGAFTGEISPGM*IK.D</td><td>1638.86726</td><td>2</td><td>4.93E-05</td><td>0.80</td><td>3.08</td><td>-</td><td>902.7</td></tr>
<tr><td colspan="2">gi|5031677|ref|NP_005681.1| dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [</td><td></td><td></td><td>5.49E-11</td><td>7.36</td><td>90.28</td><td>18.50</td><td>78060.6</td></tr>
<tr><td>AHQ-2-14-, 4833</td><td>K.ALQGASQIIAEIR.E</td><td>1370.57991</td><td>2</td><td>3.62E-08</td><td>0.96</td><td>4.50</td><td>-</td><td>1740.5</td></tr>
<tr><td>AHQ-2-14, 6032</td><td>K.ALQGASQIIAEIR.E</td><td>1370.57991</td><td>2</td><td>5.78E-08</td><td>0.95</td><td>4.05</td><td>-</td><td>1828.3</td></tr>
<tr><td>AHQ-2-14, 6293 - 6296</td><td>K.DTLQSELVGQLYK.S</td><td>1494.67144</td><td>2</td><td>6.64E-05</td><td>0.89</td><td>3.12</td><td>-</td><td>1041.1</td></tr>
<tr><td>AHQ-2-13, 5187</td><td>K.DTLQSELVGQLYK.S</td><td>1494.67144</td><td>2</td><td>1.78E-06</td><td>0.94</td><td>4.02</td><td>-</td><td>1400.2</td></tr>
<tr><td>AHQ-2-14-, 5199 - 5200</td><td>K.DTLQSELVGQLYK.S</td><td>1494.67144</td><td>1</td><td>1.59E-04</td><td>0.58</td><td>2.82</td><td>-</td><td>371.3</td></tr>
<tr><td>AHQ-2-6, 6941</td><td>K.IFSPNVVNLTLVDLPGMTK.V</td><td>2059.45828</td><td>2</td><td>9.48E-04</td><td>0.61</td><td>2.51</td><td>-</td><td>646.6</td></tr>
<tr><td>AHQ-2-6, 6399</td><td>K.IFSPNVVNLTLVDLPGM*TK.V</td><td>2075.45768</td><td>2</td><td>9.21E-06</td><td>0.87</td><td>3.69</td><td>-</td><td>833.2</td></tr>
<tr><td>AHQ-2-5, 7161</td><td>K.IFSPNVVNLTLVDLPGMTK.V</td><td>2059.45828</td><td>2</td><td>1.61E-06</td><td>0.76</td><td>3.00</td><td>-</td><td>744.0</td></tr>
<tr><td>AHQ-2-6, 7250 - 7251</td><td>K.LQDVFNTVGADIIQLPQIVVVGTQSSGK.S</td><td>2928.32977</td><td>2</td><td>1.94E-06</td><td>0.63</td><td>3.44</td><td>-</td><td>234.4</td></tr>
<tr><td>AHQ-2-6, 6155</td><td>K.LYTDFDEIRQEIENETER.I</td><td>2301.40883</td><td>2</td><td>1.66E-04</td><td>0.32</td><td>2.53</td><td>-</td><td>365.1</td></tr>
<tr><td>AHQ-2-13, 6755 - 6756</td><td>K.SSLLDDLLTESEDMAQR.R</td><td>1924.07698</td><td>2</td><td>1.55E-04</td><td>0.88</td><td>4.31</td><td>-</td><td>645.6</td></tr>
<tr><td>AHQ-2-14-, 6229 - 6235</td><td>K.SSLLDDLLTESEDM*AQR.R</td><td>1940.07638</td><td>2</td><td>5.49E-11</td><td>0.97</td><td>5.68</td><td>-</td><td>1343.2</td></tr>
<tr><td>AHQ-2-14-, 6827 - 6887</td><td>K.SSLLDDLLTESEDMAQR.R</td><td>1924.07698</td><td>2</td><td>1.76E-06</td><td>0.95</td><td>5.21</td><td>-</td><td>966.6</td></tr>
<tr><td>AHQ-2-7, 7471</td><td>R.TLESVDPLGGLNTIDILTAIR.N</td><td>2212.52928</td><td>2</td><td>9.10E-05</td><td>0.95</td><td>4.52</td><td>-</td><td>1146.0</td></tr>
<tr><td colspan="2">gi|6598323|ref|NP_001485.2| GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom</td><td></td><td></td><td>5.58E-11</td><td>1.95</td><td>20.32</td><td>8.50</td><td>50662.9</td></tr>
<tr><td>AHQ-2-8, 6763</td><td>K.SPYLYPLYGLGELPQGFAR.L</td><td>2142.44089</td><td>2</td><td>5.82E-08</td><td>0.96</td><td>4.98</td><td>-</td><td>987.1</td></tr>
<tr><td>AHQ-2-10, 6379</td><td>K.SPYLYPLYGLGELPQGFAR.L</td><td>2142.44089</td><td>2</td><td>8.54E-07</td><td>0.95</td><td>5.06</td><td>-</td><td>754.2</td></tr>
<tr><td>AHQ-2-9, 6966</td><td>K.SPYLYPLYGLGELPQGFAR.L</td><td>2142.44089</td><td>2</td><td>5.92E-05</td><td>0.97</td><td>5.43</td><td>-</td><td>1163.9</td></tr>
<tr><td>AHQ-2-7, 6925 - 6947</td><td>K.SPYLYPLYGLGELPQGFAR.L</td><td>2142.44089</td><td>2</td><td>8.65E-05</td><td>0.97</td><td>5.55</td><td>-</td><td>1111.4</td></tr>
<tr><td>AHQ-2-8, 7454</td><td>K.VPSTEAEALASSLMGLFEK.R</td><td>1981.25641</td><td>2</td><td>5.58E-11</td><td>0.98</td><td>6.38</td><td>-</td><td>1685.5</td></tr>
<tr><td colspan="2">gi|7656991|ref|NP_055140.1| coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;</td><td></td><td></td><td>6.27E-11</td><td>6.23</td><td>70.28</td><td>22.40</td><td>53248.7</td></tr>
<tr><td>AHQ-2-6, 5859 - 5897</td><td>R.AIFLADGNVFTTGFSR.M</td><td>1716.91793</td><td>2</td><td>1.87E-06</td><td>0.98</td><td>5.02</td><td>-</td><td>2162.8</td></tr>
<tr><td>AHQ-2-6, 3706</td><td>K.CDLISIPK.K</td><td>947.13128</td><td>2</td><td>1.86E-04</td><td>0.83</td><td>3.02</td><td>-</td><td>814.5</td></tr>
<tr><td>AHQ-2-7, 2888 - 2892</td><td>R.KCEPIIMTVPR.K</td><td>1345.65706</td><td>2</td><td>2.83E-04</td><td>0.86</td><td>3.34</td><td>-</td><td>704.8</td></tr>
<tr><td>AHQ-2-6, 3017 - 3021</td><td>R.KCEPIIMTVPR.K</td><td>1345.65706</td><td>2</td><td>1.68E-06</td><td>0.91</td><td>3.66</td><td>-</td><td>891.9</td></tr>
<tr><td>AHQ-2-7, 7391</td><td>R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N</td><td>3273.46087</td><td>3</td><td>2.20E-08</td><td>0.96</td><td>5.60</td><td>-</td><td>1575.4</td></tr>
<tr><td>AHQ-2-9, 7323</td><td>R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N</td><td>3273.46087</td><td>3</td><td>4.43E-08</td><td>0.96</td><td>5.52</td><td>-</td><td>1323.2</td></tr>
<tr><td>AHQ-2-7, 3632</td><td>K.NADPILISLK.H</td><td>1084.29103</td><td>1</td><td>4.45E-04</td><td>0.12</td><td>1.91</td><td>-</td><td>304.6</td></tr>
<tr><td>AHQ-2-6, 3707</td><td>K.NADPILISLK.H</td><td>1084.29103</td><td>1</td><td>4.38E-04</td><td>0.10</td><td>1.90</td><td>-</td><td>272.5</td></tr>
<tr><td>AHQ-2-6, 3714</td><td>K.NADPILISLK.H</td><td>1084.29103</td><td>2</td><td>8.39E-06</td><td>0.72</td><td>2.60</td><td>-</td><td>522.9</td></tr>
<tr><td>AHQ-2-6, 2201</td><td>K.SIKDTICNQDER.I</td><td>1480.58332</td><td>2</td><td>2.50E-06</td><td>0.90</td><td>2.81</td><td>-</td><td>1486.4</td></tr>
<tr><td>AHQ-2-7, 6028</td><td>R.YFEITDESPYVHYLNTFSSK.E</td><td>2441.63258</td><td>3</td><td>6.27E-11</td><td>0.92</td><td>4.46</td><td>-</td><td>874.7</td></tr>
<tr><td>AHQ-2-6, 6073</td><td>R.YFEITDESPYVHYLNTFSSK.E</td><td>2441.63258</td><td>3</td><td>1.19E-10</td><td>0.93</td><td>3.92</td><td>-</td><td>1095.3</td></tr>
<tr><td>AHQ-2-6, 6074 - 6085</td><td>R.YFEITDESPYVHYLNTFSSK.E</td><td>2441.63258</td><td>2</td><td>3.81E-08</td><td>0.95</td><td>4.49</td><td>-</td><td>1160.0</td></tr>
<tr><td>AHQ-2-7, 6024 - 6027</td><td>R.YFEITDESPYVHYLNTFSSK.E</td><td>2441.63258</td><td>2</td><td>5.59E-06</td><td>0.92</td><td>4.05</td><td>-</td><td>856.2</td></tr>
<tr><td>AHQ-2-10, 5659</td><td>R.YFEITDESPYVHYLNTFSSK.E</td><td>2441.63258</td><td>2</td><td>3.38E-04</td><td>0.94</td><td>4.13</td><td>-</td><td>1120.1</td></tr>
<tr><td colspan="2">gi|4557731|ref|NP_000618.1| latent transforming growth factor beta binding protein 1 precursor [Hom</td><td></td><td></td><td>6.98E-11</td><td>14.22</td><td>170.32</td><td>19.20</td><td>152790.9</td></tr>
<tr><td>AHQ-2-2, 3764</td><td>R.ASGLGDHCEDINECLEDK.S</td><td>2065.13910</td><td>2</td><td>3.37E-05</td><td>0.96</td><td>4.94</td><td>-</td><td>1579.7</td></tr>
<tr><td>AHQ-2-1, 3797</td><td>R.ASGLGDHCEDINECLEDK.S</td><td>2065.13910</td><td>2</td><td>6.85E-05</td><td>0.97</td><td>5.69</td><td>-</td><td>1538.7</td></tr>
<tr><td>AHQ-2-3, 3699 - 3708</td><td>R.ASGLGDHCEDINECLEDK.S</td><td>2065.13910</td><td>2</td><td>6.98E-11</td><td>0.98</td><td>6.32</td><td>-</td><td>2172.3</td></tr>
<tr><td>AHQ-2-1, 3793</td><td>R.ASGLGDHCEDINECLEDK.S</td><td>2065.13910</td><td>3</td><td>4.07E-07</td><td>0.90</td><td>4.12</td><td>-</td><td>1112.3</td></tr>
<tr><td>AHQ-2-1, 2892</td><td>R.CFQETIGSQCGK.A</td><td>1417.54728</td><td>2</td><td>5.09E-04</td><td>0.83</td><td>2.87</td><td>-</td><td>899.9</td></tr>
<tr><td>AHQ-2-1, 6716</td><td>K.CLCLPGYVPSDKPNYCTPLNTALNLEK.D</td><td>3142.56947</td><td>3</td><td>9.46E-04</td><td>0.84</td><td>3.98</td><td>-</td><td>507.6</td></tr>
<tr><td>AHQ-2-1, 3710</td><td>R.CTCGQGYQLSAAKDQCEDIDECQHR.H</td><td>3035.18500</td><td>3</td><td>2.42E-09</td><td>0.88</td><td>4.41</td><td>-</td><td>714.9</td></tr>
<tr><td>AHQ-2-3, 4253</td><td>K.CVDIDECTQVQHLCSQGR.C</td><td>2209.38110</td><td>2</td><td>7.11E-04</td><td>0.89</td><td>3.90</td><td>-</td><td>700.0</td></tr>
<tr><td>AHQ-2-1, 4256</td><td>K.CVDIDECTQVQHLCSQGR.C</td><td>2209.38110</td><td>2</td><td>3.02E-06</td><td>0.97</td><td>5.08</td><td>-</td><td>1501.6</td></tr>
<tr><td>AHQ-2-3, 2059</td><td>K.DQCEDIDECQHR.H</td><td>1607.61898</td><td>2</td><td>7.00E-04</td><td>0.69</td><td>2.74</td><td>-</td><td>488.8</td></tr>
<tr><td>AHQ-2-1, 2173 - 2174</td><td>K.DQCEDIDECQHR.H</td><td>1607.61898</td><td>2</td><td>7.09E-06</td><td>0.84</td><td>3.45</td><td>-</td><td>651.8</td></tr>
<tr><td>AHQ-2-1, 3298</td><td>K.EAQPGQSQVSYQGLPVQK.T</td><td>1945.12244</td><td>2</td><td>8.41E-04</td><td>0.93</td><td>3.87</td><td>-</td><td>907.4</td></tr>
<tr><td>AHQ-2-1, 3638</td><td>K.EAQPGQSQVSYQGLPVQK.T</td><td>1945.12244</td><td>2</td><td>7.89E-06</td><td>0.78</td><td>3.20</td><td>-</td><td>672.7</td></tr>
<tr><td>AHQ-2-1, 3460</td><td>K.EAQPGQSQVSYQGLPVQK.T</td><td>1945.12244</td><td>2</td><td>1.35E-08</td><td>0.91</td><td>4.09</td><td>-</td><td>662.6</td></tr>
<tr><td>AHQ-2-1, 4052</td><td>K.EEPVEALTFSR.E</td><td>1278.39297</td><td>2</td><td>6.02E-05</td><td>0.70</td><td>2.77</td><td>-</td><td>492.8</td></tr>
<tr><td>AHQ-2-1, 3601</td><td>K.EICPGGMGYTVSGVHR.R</td><td>1721.93967</td><td>2</td><td>3.95E-04</td><td>0.62</td><td>2.72</td><td>-</td><td>661.8</td></tr>
<tr><td>AHQ-2-1, 2876</td><td>K.GFVPAGESSSEAGGENYK.D</td><td>1786.83392</td><td>2</td><td>2.00E-05</td><td>0.93</td><td>4.27</td><td>-</td><td>789.7</td></tr>
<tr><td>AHQ-2-4, 5744</td><td>R.GRCEDIDECLNPSTCPDEQCVNSPGSYQCVPCTEGFR.G</td><td>4402.64921</td><td>3</td><td>1.35E-04</td><td>0.75</td><td>3.72</td><td>-</td><td>462.1</td></tr>
<tr><td>AHQ-2-3, 5715 - 5720</td><td>R.GRCEDIDECLNPSTCPDEQCVNSPGSYQCVPCTEGFR.G</td><td>4402.64921</td><td>3</td><td>1.76E-06</td><td>0.91</td><td>4.72</td><td>-</td><td>867.9</td></tr>
<tr><td>AHQ-2-1, 2224</td><td>K.HPPEASVQIHQVSR.I</td><td>1585.74913</td><td>3</td><td>8.93E-09</td><td>0.66</td><td>3.13</td><td>-</td><td>533.7</td></tr>
</table>

AHQ-2-1, 3102	K.LCQIPVHGASVPK.L	1407.66344	2	7.52E-04	0.83	3.51	-	421.6
AHQ-2-1, 3702	R.NTEGSFQCVCDQGYR.A	1823.89914	2	2.32E-06	0.93	4.35	-	679.0
AHQ-2-1, 2980	R.TSTDLDVDVDQPK.E	1433.50014	2	1.51E-06	0.88	3.27	-	943.8
AHQ-2-4, 2590	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	2.67E-04	0.76	3.31	-	805.6
AHQ-2-1, 3700	R.YTCICYEGYR.F	1387.51964	2	5.31E-04	0.74	3.01	-	405.2
gi|4502549|ref|NP_001734.1| calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta				7.54E-11	2.59	30.24	29.50	16837.5
AHQ-2-11, 3949 - 4012	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	4.17E-05	0.89	4.07	-	729.0
AHQ-2-12, 4113 - 4181	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	7.20E-10	0.95	3.81	-	1384.4
AHQ-2-12, 4249	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	2.85E-07	0.93	4.20	-	1005.8
AHQ-2-13, 4085 - 4165	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	1.64E-05	0.74	3.22	-	476.4
AHQ-2-12, 1630	K.MKDTDSEEEIR.E	1353.43852	2	2.05E-05	0.68	2.71	-	546.1
AHQ-2-12, 3933 - 4007	R.VFDKDGNGYISAAELR.H	1755.90933	2	9.57E-06	0.92	4.00	-	1160.1
AHQ-2-12, 3802 - 3835	R.VFDKDGNGYISAAELR.H	1755.90933	3	1.77E-06	0.88	3.76	-	1023.7
AHQ-2-12, 3798 - 3866	R.VFDKDGNGYISAAELR.H	1755.90933	2	7.54E-11	0.96	4.85	-	1380.7
AHQ-2-13, 3867	R.VFDKDGNGYISAAELR.H	1755.90933	2	9.57E-08	0.91	3.67	-	810.6
AHQ-2-11, 3621 - 3689	R.VFDKDGNGYISAAELR.H	1755.90933	2	4.80E-06	0.87	3.43	-	827.2
gi|17921989|ref|NP_005991.1| tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain				8.92E-11	14.03	170.28	45.10	49924.1
AHQ-2-7, 6369 - 6377	R.AFVHWYVGEGMEEGEFSEAR.E	2331.50495	2	1.01E-04	0.93	3.69	-	1066.6
AHQ-2-12, 4623	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	3.43E-06	0.97	5.38	-	1787.4
AHQ-2-12, 5202	R.AFVHWYVGEGMEEGEFSEAR.E	2331.50495	2	2.19E-08	0.90	3.55	-	805.9
AHQ-2-13, 5181	R.AFVHWYVGEGMEEGEFSEAR.E	2331.50495	2	4.97E-07	0.94	4.10	-	1130.8
AHQ-2-12, 6121 - 6187	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.84E-07	0.92	3.96	-	1333.5
AHQ-2-12, 5595 - 5599	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	9.27E-07	0.88	3.33	-	999.0
AHQ-2-14-, 6044	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.07E-06	0.95	4.37	-	1361.5
AHQ-2-13-, 5225 - 5293	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	6.55E-06	0.94	4.58	-	1125.8
AHQ-2-7, 6281 - 6352	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.22E-06	0.95	5.09	-	1305.9
AHQ-2-13-, 6297 - 6365	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.69E-04	0.95	4.06	-	1502.0
AHQ-2-13-, 5309 - 5378	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	4.57E-05	0.83	3.17	-	1201.2
AHQ-2-7, 6681 - 6749	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	5.94E-06	0.87	4.16	-	923.9
AHQ-2-7, 5181 - 5253	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	4.95E-05	0.86	3.58	-	1065.6
AHQ-2-7, 6833	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	3.35E-04	0.85	3.47	-	928.1
AHQ-2-13-, 6149 - 6157	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	4.90E-06	0.94	4.77	-	988.8
AHQ-2-13, 5987 - 6063	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	7.64E-10	0.91	4.08	-	930.0
AHQ-2-14, 6332	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	5.24E-04	0.94	3.89	-	1208.0
AHQ-2-11, 5941	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.88E-06	0.82	3.64	-	758.6
AHQ-2-13, 5167 - 5227	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	2.98E-04	0.88	3.49	-	833.8
AHQ-2-7, 6181	R.AVFVDLEPTVIDEIR.N	1716.95615	2	4.15E-07	0.93	3.92	-	1465.6
AHQ-2-7, 6041 - 6111	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.90E-07	0.74	2.99	-	981.0
AHQ-2-13-, 6173 - 6175	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.04E-05	0.90	3.64	-	1336.6
AHQ-2-12, 6150 - 6157	R.AVFVDLEPTVIDEIR.N	1716.95615	2	5.31E-08	0.90	3.53	-	1203.9
AHQ-2-7, 6199 - 6203	R.AVFVDLEPTVIDEIRNGPYR.Q	2304.58696	2	1.46E-04	0.36	2.70	-	167.7
AHQ-2-7, 5263	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	3.31E-05	0.68	2.79	-	614.4
AHQ-2-7, 3377	K.DVNAAIAAIK.T	986.14745	1	1.44E-04	0.90	3.18	-	1131.8
AHQ-2-11, 3288	K.DVNAAIAAIK.T	986.14745	1	1.47E-04	0.43	1.88	-	714.4
AHQ-2-12, 3037	K.DVNAAIAAIK.T	986.14745	1	1.13E-07	0.87	2.43	-	1368.1
AHQ-2-12, 3359	K.DVNAAIAAIK.T	986.14745	2	3.86E-06	0.91	3.60	-	1076.2
AHQ-2-7, 3023	K.FDLMYAK.R	888.06574	1	6.33E-04	0.51	2.45	-	415.7
AHQ-2-13, 3428	K.FDLMYAK.R	888.06574	2	2.69E-04	0.83	2.57	-	864.1
AHQ-2-12, 3258	K.FDLMYAK.R	888.06574	2	6.24E-04	0.82	2.82	-	686.7
AHQ-2-12, 5093 - 5173	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.91E-04	0.60	3.19	-	340.2
AHQ-2-7, 4636 - 4708	R.IHFPLATYAPVISAEK.A	1758.05310	2	2.21E-04	0.94	4.01	-	793.6
AHQ-2-11, 4896	R.IHFPLATYAPVISAEK.A	1758.05310	2	2.43E-07	0.89	3.85	-	493.1
AHQ-2-9, 4767 - 4839	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.67E-06	0.96	4.62	-	896.9
AHQ-2-7, 4779 - 4780	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.78E-06	0.96	4.56	-	976.5
AHQ-2-10, 4627 - 4702	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.10E-05	0.90	3.81	-	637.8
AHQ-2-7, 6935	R.LISQIVSSITASLR.F	1488.75471	2	8.92E-11	0.97	4.79	-	1248.9
AHQ-2-9, 6995	R.LISQIVSSITASLR.F	1488.75471	2	1.22E-08	0.94	4.11	-	1117.5
AHQ-2-7, 7031 - 7095	R.LISQIVSSITASLR.F	1488.75471	2	9.20E-08	0.94	4.67	-	860.0
AHQ-2-7, 7159 - 7239	R.LISQIVSSITASLR.F	1488.75471	2	8.73E-08	0.94	3.48	-	1245.3
AHQ-2-14-, 6697 - 6699	R.LISQIVSSITASLR.F	1488.75471	2	3.13E-08	0.97	5.51	-	1313.3
AHQ-2-13, 3443 - 3455	R.NLDIERPTYTNLNR.L	1719.88022	2	7.87E-08	0.67	3.15	-	435.7
AHQ-2-4, 3502 - 3512	R.NLDIERPTYTNLNR.L	1719.88022	2	3.65E-05	0.37	3.26	-	249.1
AHQ-2-13-, 3447 - 3453	R.NLDIERPTYTNLNR.L	1719.88022	2	6.98E-06	0.46	2.96	-	290.3
AHQ-2-9, 3148	R.NLDIERPTYTNLNR.L	1719.88022	2	5.83E-04	0.47	2.65	-	437.2
AHQ-2-8, 2922	R.NLDIERPTYTNLNR.L	1719.88022	2	9.58E-04	0.74	3.18	-	481.1
AHQ-2-5, 3232	R.NLDIERPTYTNLNR.L	1719.88022	2	7.75E-10	0.54	2.90	-	314.3
AHQ-2-6, 3214	R.NLDIERPTYTNLNR.L	1719.88022	2	5.67E-04	0.32	2.97	-	298.2
AHQ-2-7, 3083 - 3151	R.NLDIERPTYTNLNR.L	1719.88022	2	4.95E-04	0.65	3.59	-	427.4
AHQ-2-12, 3361	R.NLDIERPTYTNLNR.L	1719.88022	2	4.06E-06	0.55	3.33	-	285.6
AHQ-2-10, 3131	R.NLDIERPTYTNLNR.L	1719.88022	2	7.38E-04	0.61	3.21	-	405.7
AHQ-2-13-, 5725 - 5726	R.SIQFVDWCPTGFK.V	1586.79232	2	9.81E-07	0.89	3.00	-	854.8
AHQ-2-3, 6067	R.SIQFVDWCPTGFK.V	1586.79232	2	4.33E-04	0.86	3.25	-	808.8
AHQ-2-12, 5769 - 5791	R.SIQFVDWCPTGFK.V	1586.79232	2	4.43E-04	0.90	3.15	-	1029.6
AHQ-2-1, 6110	R.SIQFVDWCPTGFK.V	1586.79232	2	9.01E-06	0.93	3.47	-	1073.3
AHQ-2-7, 5868 - 5943	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.00E-10	0.94	4.62	-	809.7
AHQ-2-9, 5794	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	4.43E-09	0.79	3.28	-	584.2
AHQ-2-7, 5760 - 5799	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	8.09E-10	0.89	4.02	-	618.6
AHQ-2-13-, 5650 - 5689	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.26E-07	0.89	3.94	-	585.2
AHQ-2-14-, 5655	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.00E-10	0.93	4.61	-	680.6
AHQ-2-4, 6038	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.17E-06	0.35	2.65	-	199.0
AHQ-2-7, 5963 - 6037	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.39E-08	0.94	4.17	-	1093.6
AHQ-2-10, 5344 - 5350	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.83E-07	0.92	4.32	-	519.3
AHQ-2-13, 5551 - 5591	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	6.90E-07	0.66	3.15	-	424.2
AHQ-2-1, 6034	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	9.14E-06	0.50	2.68	-	426.6
AHQ-2-13, 4355 - 4408	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	7.81E-08	0.86	3.76	-	459.5
AHQ-2-12, 4569	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.22E-08	0.78	3.32	-	370.9
AHQ-2-2, 4692	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	9.55E-06	0.35	2.68	-	185.7
AHQ-2-12, 4430 - 4502	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	5.01E-05	0.83	3.33	-	507.1
AHQ-2-14, 5377 - 5452	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	3.93E-04	0.45	3.09	-	180.4
AHQ-2-3, 4669	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	5.36E-05	0.66	3.47	-	293.0
AHQ-2-11, 4266 - 4334	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.90E-06	0.74	3.04	-	367.1
AHQ-2-13-, 4417 - 4423	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.47E-04	0.92	4.42	-	527.3
AHQ-2-13-, 4499	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.82E-04	0.78	3.39	-	396.0
AHQ-2-9, 4488 - 4498	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	8.21E-08	0.55	2.95	-	256.8
AHQ-2-6, 4362	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	3.50E-06	0.60	3.97	-	235.0
AHQ-2-7, 4513	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	9.06E-04	0.54	2.75	-	300.2
AHQ-2-7, 4212 - 4291	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	3.03E-07	0.90	4.13	-	455.6
AHQ-2-7, 4360 - 4431	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.56E-06	0.88	4.17	-	361.9
AHQ-2-13, 4480	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.19E-06	0.66	2.77	-	446.3
AHQ-2-12, 3978	K.YM*ACCLLYR.G	1268.50804	2	9.69E-04	0.78	3.23	-	475.5
AHQ-2-12, 4462	K.YMACCLLYR.G	1252.50864	2	1.34E-05	0.96	3.64	-	1194.0
AHQ-2-9, 4406	K.YMACCLLYR.G	1252.50864	1	8.00E-04	0.50	2.49	-	357.8
AHQ-2-7, 4364 - 4371	K.YMACCLLYR.G	1252.50864	2	1.07E-05	0.96	3.84	-	1237.4
gi|4502201|ref|NP_001649.1| ADP-ribosylation factor 1 [Homo sapiens]				9.06E-11	9.93	110.30	54.70	20696.6
AHQ-2-12, 4681	R.DAVLLVFANK.Q	1090.29726	2	1.76E-06	0.96	4.28	-	1678.9
AHQ-2-12, 4803 - 4830	R.DAVLLVFANK.Q	1090.29726	1	4.92E-04	0.85	3.31	-	833.8
AHQ-2-12, 4663 - 4738	R.DAVLLVFANK.Q	1090.29726	1	1.67E-04	0.72	2.73	-	677.6

AHQ-2-12, 6285	R.DAVLLVFANKQDLPNAMNAAEITDK.L	2703.06468	2	8.63E-07	0.91	4.54	-	661.9
AHQ-2-12, 4911	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	8.16E-08	0.98	5.95	-	2171.7
AHQ-2-12, 5318	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	9.06E-11	0.97	5.42	-	1572.6
AHQ-2-12, 5402 - 5451	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	9.43E-06	0.98	5.88	-	2093.5
AHQ-2-12, 5602 - 5673	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.28E-08	0.95	5.03	-	769.9
AHQ-2-12, 4999	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	5.41E-06	0.98	5.90	-	1877.9
AHQ-2-12, 5094 - 5166	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	8.56E-07	0.98	6.01	-	1996.0
AHQ-2-12, 4899 - 4971	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	3.42E-05	0.93	5.26	-	846.0
AHQ-2-12, 4362	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	2.77E-06	0.84	3.82	-	469.3
AHQ-2-12, 4507 - 4573	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	1.37E-06	0.80	3.92	-	449.4
AHQ-2-12, 5057	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	4.19E-06	0.91	4.16	-	1023.1
AHQ-2-12, 3090	R.ILM*VGLDAAGK.T	1104.34572	2	8.68E-07	0.95	3.46	-	1705.1
AHQ-2-11, 3541	R.ILMVGLDAAGK.T	1088.34632	2	3.24E-05	0.94	3.11	-	1368.7
AHQ-2-12, 3659 - 3725	R.ILMVGLDAAGK.T	1088.34632	2	4.16E-04	0.95	3.50	-	1565.8
AHQ-2-12, 3683	R.ILMVGLDAAGK.T	1088.34632	1	4.16E-04	0.74	2.86	-	711.0
AHQ-2-12, 6537 - 6601	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	3	1.84E-04	0.91	4.28	-	1004.7
AHQ-2-13-, 6517 - 6519	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	6.49E-04	0.92	4.73	-	311.1
AHQ-2-12, 6727 - 6803	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	7.05E-06	0.45	2.99	-	164.8
AHQ-2-14-, 6379	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	2.89E-06	0.76	3.65	-	264.9
AHQ-2-11, 6353	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	2.21E-05	0.44	3.02	-	159.8
AHQ-2-11, 6232 - 6293	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	9.03E-08	0.64	3.35	-	172.5
AHQ-2-12, 6475 - 6545	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	4.61E-04	0.82	3.75	-	279.7
AHQ-2-12, 2545	R.MLAEDELR.D	977.11769	2	1.70E-04	0.92	3.43	-	1040.3
AHQ-2-12, 7067	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	3	1.36E-08	0.95	4.65	-	1813.7
AHQ-2-13-, 5183	K.NISFTVWDVGGQDK.I	1566.69621	2	2.92E-05	0.92	3.55	-	1044.7
AHQ-2-12, 5137 - 5206	K.NISFTVWDVGGQDK.I	1566.69621	2	7.64E-09	0.96	4.89	-	903.7
AHQ-2-14-, 5109 - 5112	K.NISFTVWDVGGQDK.I	1566.69621	2	1.53E-04	0.87	3.55	-	792.9
AHQ-2-12, 4794 - 4809	K.NISFTVWDVGGQDK.I	1566.69621	2	2.10E-04	0.39	2.67	-	354.9
AHQ-2-12, 3675 - 3749	K.QDLPNAMNAAEITDK.L	1631.79001	2	3.33E-07	0.92	3.87	-	964.3
gi|4885063|ref|NP_005156.1| aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase				9.34E-11	1.76	20.29	7.10	39455.6
AHQ-2-8, 4271 - 4348	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	9.34E-11	0.80	5.00	-	520.0
AHQ-2-8, 4449 - 4515	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.93E-10	0.95	4.95	-	720.1
AHQ-2-9, 4504 - 4546	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.05E-06	0.78	4.61	-	513.1
AHQ-2-9, 4634	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	8.55E-09	0.85	4.73	-	884.0
AHQ-2-10, 4340	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	9.96E-07	0.85	4.94	-	724.2
AHQ-2-12, 4349	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.79E-06	0.69	3.95	-	619.6
AHQ-2-12, 4693	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	3.62E-10	0.69	4.21	-	445.0
AHQ-2-8, 4127 - 4199	K.VDKGVVPLAGTDGETTTQGLDGLSER.C	2616.82041	3	7.32E-10	0.96	5.77	-	1083.4
gi|7705704|ref|NP_057001.1| glutathione S-transferase subunit 13 homolog [Homo sapiens]				1.03E-10	5.53	60.25	35.80	25496.7
AHQ-2-11, 3270 - 3334	K.AGMSAEQAQGLLEK.I	1433.61314	2	1.64E-05	0.92	4.17	-	1334.2
AHQ-2-11, 2557	K.AGM*SAEQAQGLLEK.I	1449.61254	2	1.28E-04	0.92	3.68	-	1241.5
AHQ-2-11, 4440	R.FLTAVNLEHPEMLEK.A	1772.05845	2	4.78E-06	0.94	4.84	-	942.5
AHQ-2-11, 4793	R.MELLAHLLGEK.W	1254.52433	2	2.12E-05	0.93	3.58	-	1235.5
AHQ-2-11, 4445 - 4494	R.NEDITEPQSILAAAEK.A	1729.86695	2	1.03E-10	0.88	3.60	-	645.2
AHQ-2-11, 5741	R.YGAFGLPITVAHVDGQTHMLFGSDR.M	2691.01737	3	7.48E-08	0.93	5.01	-	757.3
gi|5453607|ref|NP_006420.1| chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co				1.10E-10	2.73	30.24	11.20	59366.3
AHQ-2-14-, 6909	R.INALTAASEAACLIVSVDETIKNPR.S	2659.00999	3	1.10E-10	0.92	4.57	-	984.5
AHQ-2-7, 5008	K.LPIGDVATQYFADR.D	1566.73935	2	5.66E-05	0.85	2.73	-	1070.2
AHQ-2-7, 7175	K.SQDAEVGDGTTSVTLLAAEFLK.Q	2253.44875	2	3.62E-05	0.95	4.76	-	971.8
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				1.12E-10	5.50	60.32	20.30	61986.9
AHQ-2-5, 6531 - 6547	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	7.51E-07	0.97	5.37	-	2390.0
AHQ-2-14-, 6219	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.12E-10	0.95	4.89	-	1877.8
AHQ-2-5, 4472	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	4.63E-09	0.96	5.47	-	1803.5
AHQ-2-5, 5093	R.HGVQELEIELQSQLSK.K	1839.03978	2	2.25E-07	0.98	6.43	-	2179.0
AHQ-2-5, 7367 - 7369	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	2.02E-09	0.87	4.50	-	473.6
AHQ-2-5, 7368	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	2	1.53E-07	0.87	4.05	-	577.9
AHQ-2-5, 6587	K.SDLEMQYETLQEELMALKK.N	2300.63547	3	4.64E-08	0.75	3.31	-	556.3
AHQ-2-5, 6569 - 6584	K.SDLEMQYETLQEELMALKK.N	2300.63547	2	2.43E-05	0.85	3.97	-	536.2
AHQ-2-5, 2804 - 2805	K.VQALEEANNDLENK.I	1587.67060	2	3.07E-09	0.98	5.74	-	1789.2
gi|7705296|ref|NP_057271.1| bridging integrator 2; bridging integrator-2; breast cancer associated				1.12E-10	5.96	70.25	21.60	61746.8
AHQ-2-13, 5947	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	8.20E-09	0.88	3.88	-	676.2
AHQ-2-10, 5808 - 5880	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	5.80E-07	0.90	3.78	-	954.7
AHQ-2-10, 5674 - 5746	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	1.12E-10	0.96	4.82	-	1398.5
AHQ-2-10, 6778 - 6850	K.AQTVFEDLNQELLEELPILYNSR.I	2736.02649	2	4.20E-06	0.93	4.99	-	759.2
AHQ-2-10, 6843 - 6851	K.AQTVFEDLNQELLEELPILYNSR.I	2736.02649	3	5.81E-05	0.65	3.54	-	374.4
AHQ-2-10, 2522	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	2.09E-06	0.96	4.72	-	1340.2
AHQ-2-14-, 6587 - 6589	R.IGCYVTIFQNISNLR.D	1800.07167	2	4.63E-05	0.96	5.09	-	1037.3
AHQ-2-10, 6342	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.21E-05	0.86	3.66	-	735.7
AHQ-2-9, 6902 - 6919	R.IGCYVTIFQNISNLR.D	1800.07167	2	1.33E-05	0.90	3.89	-	761.5
AHQ-2-10, 6102	R.IGCYVTIFQNISNLR.D	1800.07167	2	7.37E-04	0.50	2.65	-	190.3
AHQ-2-12, 6751	R.IGCYVTIFQNISNLR.D	1800.07167	2	5.13E-05	0.76	3.60	-	509.4
AHQ-2-10, 2559	K.LNHNLYEVMSK.L	1348.55307	2	3.93E-08	0.79	2.94	-	859.1
AHQ-2-7, 4008	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	1.75E-05	0.72	3.37	-	559.4
AHQ-2-10, 4630	R.VSETLQEIYSSEWDGHEELK.A	2380.50595	2	2.04E-05	0.69	3.45	-	374.2
gi|5902134|ref|NP_009005.1| coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin				1.14E-10	3.75	40.28	16.30	51026.0
AHQ-2-7, 4145	R.DAGPLLISLK.D	1027.23948	2	3.18E-05	0.92	3.07	-	1159.1
AHQ-2-7, 7080 - 7148	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	1.07E-09	0.95	5.54	-	532.4
AHQ-2-1, 7133	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	3.23E-04	0.77	3.54	-	353.9
AHQ-2-7, 3999 - 4012	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	2.01E-06	0.93	4.42	-	976.9
AHQ-2-7, 7467	R.YFEITSEAPFLHYLSMFSSK.E	2398.71748	3	1.14E-10	0.96	5.32	-	1175.3
gi|20070125|ref|NP_000909.2| prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke				1.20E-10	3.95	50.28	16.30	57115.9
AHQ-2-7, 4715	K.HNQLPLVIEFTEQTAPK.I	1966.22639	2	1.19E-06	0.91	4.35	-	660.1
AHQ-2-7, 2359	K.LGETYKDHENIVIAK.M	1730.94291	2	5.70E-04	0.86	3.38	-	761.2
AHQ-2-13, 5656 - 5903	K.QPVKVLVGK.N	968.21840	1	2.86E-04	0.37	2.16	-	472.6
AHQ-2-7, 7709	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	3	1.20E-10	0.93	4.87	-	1084.6
AHQ-2-7, 7601	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	3	3.61E-06	0.97	5.53	-	2512.2
AHQ-2-7, 3757	K.YQLDKDGVVLFK.K	1425.65394	2	2.90E-05	0.88	3.98	-	774.1
gi|4758970|ref|NP_004150.1| proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be				1.43E-10	2.57	30.21	14.70	29769.4
AHQ-2-11, 2400	K.FQHGVIAAVDSR.A	1300.44824	1	9.02E-08	0.67	2.45	-	395.8
AHQ-2-11, 2300	K.KGPGLYYVDEHGTR.L	1592.73690	2	1.44E-07	0.96	4.23	-	1406.4
AHQ-2-11, 4008	K.VESTDVSDLLHQYR.E	1662.78230	2	1.43E-10	0.94	3.99	-	1299.4
gi|4503821|ref|NP_001456.1| FYN binding protein (FYB-120/130); FYN-binding protein (FYB-120/130) [H				1.44E-10	0.95	10.25	2.60	85450.5
AHQ-2-12, 4177	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	1.44E-10	0.95	4.97	-	576.7
AHQ-2-13, 4152	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	1.00E-07	0.95	4.95	-	788.2
AHQ-2-10, 3874	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	2.80E-09	0.92	4.32	-	566.7
gi|20357552|ref|NP_005222.2| cortactin isoform a; oncogene EMS1 [Homo sapiens]				1.45E-10	2.63	30.21	7.10	61585.7
AHQ-2-12, 3999	R.LPSSPVYEDAASFK.A	1511.65733	2	1.25E-04	0.60	2.72	-	455.8
AHQ-2-11, 3852 - 3905	R.LPSSPVYEDAASFK.A	1511.65733	2	9.22E-05	0.92	3.20	-	982.7
AHQ-2-13, 3099 - 3164	R.VDQSAVGFEYQGK.T	1428.52841	2	5.06E-05	0.77	2.84	-	799.3
AHQ-2-12, 5377 - 5381	R.YGLFPANYVELR.Q	1442.64306	2	1.45E-10	0.94	4.11	-	776.2
gi|4507231|ref|NP_003134.1| single-stranded DNA binding protein; single-stranded DNA-binding protei				1.77E-10	3.54	40.23	32.40	17259.5
AHQ-2-13, 5943	K.NPVTIFSLATNEM*WR.S	1796.04007	2	1.77E-10	0.93	4.34	-	855.8
AHQ-2-13, 6631	K.NPVTIFSLATNEMWR.S	1780.04067	2	1.50E-05	0.97	4.60	-	1963.7
AHQ-2-13, 6029 - 6100	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	8.01E-04	0.68	3.19	-	490.8
AHQ-2-13-, 3213	R.SGDSEVYQLGDVSQK.T	1612.67692	2	8.86E-07	0.95	4.61	-	1049.9
AHQ-2-13, 3228	R.SGDSEVYQLGDVSQK.T	1612.67692	2	9.11E-07	0.90	4.01	-	855.9
gi|4502051|ref|NP_000688.1| arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]				1.82E-10	5.71	70.23	16.10	75721.8

AHQ-2-6, 4877	R.AAAQLTYCSLCPPDDLADR.G	2140.33708	2	8.87E-10	0.92	4.53	-	443.2
AHQ-2-6, 2045	K.AVSTGGGGHVQLLR.R	1352.52468	2	6.69E-09	0.87	3.53	-	904.7
AHQ-2-6, 5289	R.GLLGLPGALYAHDALR.L	1637.90708	2	1.82E-10	0.92	3.64	-	774.7
AHQ-2-6, 5162	R.ITVQGPGACAEVAFPCYR.W	1999.25659	2	1.46E-07	0.88	3.81	-	951.0
AHQ-2-6, 4467	R.LPGDNALDMFQK.H	1349.53784	2	3.62E-08	0.92	3.84	-	828.0
AHQ-2-6, 3901 - 3902	R.TQLISDGGIFDK.A	1294.43554	1	2.43E-04	0.58	2.18	-	920.3
AHQ-2-6, 4933	R.WVQGEDILSLPEGTAR.L	1771.95190	2	6.92E-05	0.63	2.88	-	491.7
gi|4508047|ref|NP_003452.1| zyxin [Homo sapiens]				1.82E-10	2.46	30.27	8.90	61277.0
AHQ-2-8, 7340	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	3	1.82E-10	0.87	3.86	-	1230.1
AHQ-2-9, 7367	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	2	7.44E-07	0.92	4.51	-	593.2
AHQ-2-8, 7338 - 7402	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	2	1.71E-07	0.91	4.45	-	608.1
AHQ-2-9, 1959	K.FGPVVAPKPK.V	1040.28308	1	6.34E-04	0.62	2.27	-	676.6
AHQ-2-9, 7539	K.VSSIDLEIDSLSSLLDDMTK.N	2182.43225	2	1.78E-06	0.97	5.50	-	1095.5
gi|5803201|ref|NP_006818.1| transmembrane trafficking protein [Homo sapiens]				1.87E-10	3.83	50.28	17.40	24975.8
AHQ-2-11, 2314	K.ITDSAGHILYSK.E	1305.46156	1	4.49E-04	0.65	1.85	-	1002.8
AHQ-2-11, 2313	K.ITDSAGHILYSK.E	1305.46156	2	8.92E-09	0.96	4.55	-	1424.3
AHQ-2-11, 6209 - 6220	R.LEDLSESIVNDFAYMK.K	1875.08916	2	7.26E-07	0.95	4.82	-	1005.0
AHQ-2-11, 2902 - 2904	K.LKPLEVELR.R	1097.33294	1	1.05E-05	0.06	2.22	-	126.8
AHQ-2-11, 6090	R.RLEDLSESIVNDFAYMK.K	2031.27552	2	8.05E-08	0.98	5.59	-	2091.4
AHQ-2-11, 5414	R.RLEDLSESIVNDFAYM*K.K	2047.27492	2	4.04E-04	0.88	3.54	-	765.7
AHQ-2-11, 4989	R.RLEDLSESIVNDFAYMK.K	2031.27552	2	1.87E-10	0.97	4.90	-	1799.8
gi|21618359|ref|NP_004095.3| fatty acid synthase [Homo sapiens]				1.88E-10	5.69	70.24	4.60	273262.0
AHQ-2-1, 4250	K.CTVFHGAQVEDAFR.Y	1638.78572	2	2.64E-07	0.73	2.68	-	864.7
AHQ-2-1, 4246	R.FPQLDSTSFANSR.D	1470.56853	2	5.28E-08	0.90	3.65	-	882.8
AHQ-2-1, 6224	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	1.88E-10	0.93	4.71	-	1090.0
AHQ-2-1, 6628	R.LHLSGIDANPNALFPPVEFPAPR.G	2473.81368	3	4.77E-04	0.79	3.58	-	618.2
AHQ-2-3, 7121 - 7193	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	3.41E-04	0.94	3.69	-	1495.8
AHQ-2-1, 7033	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	7.88E-06	0.97	4.34	-	1646.4
AHQ-2-1, 3832	R.LQVVDQPLPVR.G	1264.49894	2	2.68E-05	0.84	3.23	-	1083.5
AHQ-2-1, 3950	K.VLQGDLVM*NVYR.D	1423.66306	2	3.75E-04	0.52	2.77	-	579.1
gi|4507207|ref|NP_003121.1| sorcin; Sorcin (class 4 gene) [Homo sapiens]				1.89E-10	0.93	10.23	10.10	21676.3
AHQ-2-11, 4501 - 4578	R.CLTQSGIAGGYKPFNLETCR.L	2275.54736	2	1.89E-10	0.93	4.54	-	555.6
gi|4504041|ref|NP_002061.1| guanine nucleotide binding protein (G protein), alpha inhibiting activi				1.94E-10	1.79	20.25	9.90	40450.7
AHQ-2-9, 5811	R.EYQLNDSAAYYLNDLER.I	2078.18096	2	1.94E-10	0.89	3.94	-	837.9
AHQ-2-14, 6136	K.ITHSPLTICFPEYTGANK.Y	2051.30821	2	1.59E-05	0.90	4.18	-	489.9
gi|4759300|ref|NP_004772.1| vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated				1.98E-10	3.82	40.31	40.00	11309.0
AHQ-2-13-, 3646	R.ADALQAGASQFETSAAK.L	1666.77095	2	3.19E-08	0.94	4.15	-	1048.0
AHQ-2-14-, 3556	R.ADALQAGASQFETSAAK.L	1666.77095	2	8.55E-10	0.95	4.37	-	1128.6
AHQ-2-13-, 3786	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	3.59E-07	0.98	6.26	-	1604.3
AHQ-2-13-, 4971	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	7.27E-08	0.97	5.40	-	1720.9
AHQ-2-13, 4879	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	1.98E-10	0.97	5.23	-	1371.2
AHQ-2-13-, 4673 - 4681	K.LSELDDRADALQAGASQFETSAAK.L	2495.64172	3	2.86E-05	0.92	4.45	-	1368.7
gi|29730023|ref|XP_291482.1| similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno				1.98E-10	4.51	50.23	13.30	63563.0
AHQ-2-6, 4605 - 4669	R.IINKPTAAAIAYGLDK.R	1659.95097	2	6.18E-09	0.87	4.03	-	875.3
AHQ-2-6, 3205	K.KKELEEIVQPIISK.L	1654.97263	2	3.51E-08	0.96	4.60	-	1466.0
AHQ-2-6, 3323 - 3405	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	8.52E-06	0.92	4.27	-	729.4
AHQ-2-6, 3833	R.NELESYAYSLK.N	1317.42597	2	5.12E-04	0.85	3.20	-	733.5
AHQ-2-6, 5525 - 5529	K.TFAPKEISAMVLTK.M	1536.86124	2	1.98E-10	0.92	4.37	-	1281.7
gi|10716563|ref|NP_001737.1| calnexin [Homo sapiens]				2.06E-10	4.53	50.21	12.30	67567.8
AHQ-2-5, 2204	K.AEEDEILNR.S	1089.13826	2	2.37E-04	0.93	3.06	-	1799.2
AHQ-2-1, 5200	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.61E-07	0.78	3.05	-	562.1
AHQ-2-6, 4833	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.25E-04	0.88	3.02	-	1109.5
AHQ-2-5, 4895 - 4969	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.06E-10	0.93	4.15	-	1119.9
AHQ-2-5, 4193	R.CESAPGCGVWQRPVIDNPNYK.G	2450.69236	2	3.48E-05	0.79	3.00	-	634.8
AHQ-2-9, 6211	R.KIPNPDFFEDLEPFR.M	1865.07739	2	1.89E-04	0.88	3.88	-	661.3
AHQ-2-6, 6183	R.KIPNPDFFEDLEPFR.M	1865.07739	2	3.49E-06	0.87	3.20	-	770.3
AHQ-2-5, 6235 - 6307	R.KIPNPDFFEDLEPFR.M	1865.07739	2	1.28E-06	0.93	3.61	-	1091.2
AHQ-2-5, 3271 - 3340	K.TPELNLDQFHDK.T	1457.56976	2	1.05E-05	0.94	3.95	-	1512.6
gi|4507677|ref|NP_003290.1| tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu				2.25E-10	6.14	80.30	14.40	92468.2
AHQ-2-5, 2297 - 2301	K.DISTNYYASQK.K	1290.36061	1	2.25E-10	0.37	2.26	-	345.0
AHQ-2-5, 6396	R.EAVEKEFEPLLNWMK.D	1864.15434	2	2.70E-04	0.94	4.48	-	991.6
AHQ-2-6, 3685	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	1.37E-04	0.97	5.45	-	2403.4
AHQ-2-6, 3691	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	1.12E-06	0.79	3.39	-	609.3
AHQ-2-5, 3655 - 3659	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	1.21E-04	0.93	4.43	-	962.4
AHQ-2-5, 6980 - 7041	K.GYEVIYLTEPVDEYCIQALPEFDGKR.F	3107.43557	3	1.11E-05	0.87	4.40	-	603.7
AHQ-2-5, 6260	K.KYSQFINFPIYVWSSK.T	2008.30657	2	2.15E-09	0.98	5.21	-	1865.4
AHQ-2-5, 5329	R.LISLTDENALSGNEELTVK.I	2047.24975	2	6.73E-06	0.84	3.33	-	486.5
AHQ-2-5, 3273	R.LSLNIDPDAK.V	1086.22065	1	4.56E-05	0.38	2.24	-	561.9
AHQ-2-5, 6940 - 7007	K.YSQFINFPIYVWSSK.T	1880.13366	2	1.56E-04	0.98	5.95	-	1445.3
gi|4504345|ref|NP_000508.1| alpha 2 globin [Homo sapiens]				2.31E-10	2.83	30.30	30.30	15257.4
AHQ-2-13, 4247	K.FLASVSTVLTSK.Y	1253.46970	2	2.42E-06	0.90	3.38	-	1124.7
AHQ-2-13-, 4293	K.FLASVSTVLTSK.Y	1253.46970	2	3.92E-06	0.92	3.46	-	1286.8
AHQ-2-13-, 4063 - 4073	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	5.03E-10	0.96	5.09	-	1160.3
AHQ-2-13, 3992 - 4007	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	2.75E-06	0.95	4.14	-	1205.9
AHQ-2-13-, 2539 - 2558	K.VGAHAGEYGAEALER.M	1530.62397	2	5.46E-09	0.96	3.93	-	1671.0
AHQ-2-13, 2604 - 2609	K.VGAHAGEYGAEALER.M	1530.62397	2	2.31E-10	0.97	4.15	-	1815.0
gi|12408656|ref|NP_005177.2| calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ				2.59E-10	8.22	100.26	19.90	81889.4
AHQ-2-6, 6702 - 6717	R.DMETIGFAVYEVPPELVGQPAVHLK.R	2741.15451	3	2.59E-10	0.87	4.20	-	775.0
AHQ-2-6, 6001	R.FRLPPGEYVVVPSTFEPNKEGDFVLR.F	2994.39160	3	1.99E-04	0.94	5.26	-	1024.4
AHQ-2-6, 4097 - 4109	R.KAPSDLYQIILK.A	1389.66474	2	4.01E-08	0.93	4.16	-	834.0
AHQ-2-10, 3992	R.KAPSDLYQIILK.A	1389.66474	2	8.31E-05	0.80	2.97	-	639.5
AHQ-2-6, 5645	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	3.19E-07	0.77	3.68	-	527.7
AHQ-2-6, 6433	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	2	9.69E-06	0.96	4.82	-	1355.4
AHQ-2-6, 5073	R.NYPATFWVNPQFK.I	1612.81141	2	3.96E-05	0.92	3.82	-	926.4
AHQ-2-6, 4335 - 4345	K.RPTELLSNPQFIVDGATR.T	2015.25904	3	6.52E-07	0.94	4.98	-	1254.4
AHQ-2-6, 2837 - 2842	R.SEQFINLR.E	1007.12521	1	4.65E-04	0.26	2.20	-	128.5
AHQ-2-6, 4161	K.WNTTLYEGTWR.R	1427.54534	2	5.81E-04	0.75	2.64	-	652.6
AHQ-2-6, 3123 - 3129	K.YLGQDYEQLR.V	1285.38720	2	3.60E-06	0.88	3.11	-	690.2
gi|27477800|ref|XP_208313.1| similar to tropomyosin 4 [Homo sapiens]				2.76E-10	0.95	10.25	10.10	18426.7
AHQ-2-9, 5234 - 5312	K.CGDLEEELKNVTNNLK.S	1878.05124	2	8.17E-07	0.92	4.32	-	1053.4
AHQ-2-9, 5506 - 5578	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.17E-07	0.80	3.72	-	648.4
AHQ-2-9, 5590 - 5652	K.CGDLEEELKNVTNNLK.S	1878.05124	2	2.76E-10	0.95	4.52	-	1406.7
AHQ-2-9, 4606 - 4614	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.11E-08	0.97	5.06	-	1673.5
gi|4757812|ref|NP_004880.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso				3.07E-10	2.63	30.20	25.50	10917.8
AHQ-2-13-, 6125 - 6139	R.DFSPSGIFGAFQR.G	1429.56124	2	2.96E-08	0.94	4.10	-	1153.2
AHQ-2-13, 5969 - 5975	R.DFSPSGIFGAFQR.G	1429.56124	2	5.35E-09	0.93	3.61	-	1182.9
AHQ-2-14-, 6007	R.DFSPSGIFGAFQR.G	1429.56124	2	3.07E-10	0.93	3.57	-	1048.0
AHQ-2-13-, 6118	K.LGELPSWILMR.D	1315.60936	2	4.91E-08	0.92	3.85	-	743.1
AHQ-2-13-, 5606 - 5611	K.LGELPSWILM*R.D	1331.60876	2	5.97E-06	0.89	3.63	-	529.7
AHQ-2-14-, 5551	K.LGELPSWILM*R.D	1331.60876	2	3.63E-06	0.89	3.29	-	661.8
AHQ-2-13, 5948	K.LGELPSWILMR.D	1315.60936	2	1.71E-04	0.90	3.58	-	686.0
AHQ-2-13, 5496	K.LGELPSWILM*R.D	1331.60876	2	5.74E-07	0.78	3.13	-	464.9
AHQ-2-14-, 6023	K.LGELPSWILMR.D	1315.60936	2	2.84E-05	0.92	3.69	-	783.0
gi|7657124|ref|NP_055165.1| TNF-induced protein [Homo sapiens]				3.13E-10	0.91	10.21	10.50	22047.4
AHQ-2-12, 7174 - 7241	K.SIATTLIDDTSSEVLDELYR.V	2242.42274	2	3.13E-10	0.91	4.14	-	861.4
gi|24234688|ref|NP_004125.3| heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre				3.57E-10	0.88	10.19	2.80	73680.1
AHQ-2-6, 6011	K.STNGDTFLGGEDFDQALLR.H	2057.16328	2	3.57E-10	0.88	3.70	-	588.6

gi|30159310|ref|XP_301899.1| similar to beta-actin [Homo sapiens]				3.59E-10	1.41	20.18	9.20	32376.4
AHQ-2-8, 1448 - 1791	K.DSYVGNEAQSK.R	1198.22158	1	3.59E-10	0.57	2.73	-	338.9
AHQ-2-8, 1454	K.DSYVGNEAQSK.R	1198.22158	2	1.01E-05	0.81	3.08	-	848.8
AHQ-2-8, 1545 - 1603	K.DSYVGNEAQSK.R	1198.22158	2	5.69E-05	0.79	3.19	-	693.1
AHQ-2-13, 1820	K.DSYVGNEAQSK.R	1198.22158	1	2.09E-06	0.63	2.63	-	453.1
AHQ-2-12, 1611 - 1671	K.DSYVGNEAQSK.R	1198.22158	1	1.64E-07	0.20	2.16	-	283.9
AHQ-2-9, 1490 - 1566	K.DSYVGNEAQSK.R	1198.22158	1	9.56E-09	0.36	2.32	-	286.7
AHQ-2-13, 1912	K.DSYVGNEAQSK.R	1198.22158	1	1.38E-08	0.19	1.86	-	321.5
AHQ-2-8, 4535	K.SYKLLDGQVITIGNER.F	1807.04092	2	3.67E-05	0.80	3.05	-	752.5
AHQ-2-8, 4617 - 4695	K.SYKLLDGQVITIGNER.F	1807.04092	2	2.54E-05	0.84	3.18	-	588.1
AHQ-2-9, 4846 - 4874	K.SYKLLDGQVITIGNER.F	1807.04092	2	6.55E-04	0.73	2.90	-	639.2
gi|18426915|ref|NP_004386.2| drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [				3.62E-10	3.54	40.26	11.70	71438.9
AHQ-2-14-, 5735	R.EESAADWALYTYEDGSDDLK.L	2279.31212	2	5.40E-04	0.84	3.61	-	668.8
AHQ-2-8, 3706	K.KSESEVEEAAAIIAQRPDNPR.E	2311.49476	3	1.87E-08	0.85	3.96	-	668.0
AHQ-2-12, 4006	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	2.59E-05	0.94	4.60	-	922.4
AHQ-2-12, 4010	K.LAASGEGGLQELSGHFENQK.V	2073.20908	3	3.53E-05	0.66	3.52	-	357.7
AHQ-2-13-, 4105	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	3.62E-10	0.96	5.22	-	1172.3
AHQ-2-13, 4024	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	4.10E-07	0.86	4.01	-	676.9
AHQ-2-8, 3702	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	8.14E-05	0.81	3.86	-	616.9
AHQ-2-13-, 5637	K.YVLINWVGEDVPDAR.K	1746.94404	2	1.90E-05	0.97	4.78	-	1760.6
AHQ-2-14-, 5589 - 5608	K.YVLINWVGEDVPDAR.K	1746.94404	2	2.73E-08	0.89	3.51	-	1062.6
AHQ-2-12, 5654	K.YVLINWVGEDVPDAR.K	1746.94404	2	2.34E-07	0.92	3.60	-	1290.9
AHQ-2-13, 5520	K.YVLINWVGEDVPDAR.K	1746.94404	2	5.20E-07	0.94	3.97	-	1197.3
gi|16507237|ref|NP_005338.1| heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he				3.90E-10	11.06	130.29	28.00	72332.5
AHQ-2-6, 4777	R.AKFEELNMDLFR.S	1513.74309	2	4.67E-08	0.92	3.67	-	918.4
AHQ-2-6, 5499	K.DNHLLGTFDLTGIPPAPR.G	1935.17239	2	2.42E-05	0.86	3.40	-	699.8
AHQ-2-6, 6017 - 6094	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	6.37E-06	0.77	3.22	-	687.9
AHQ-2-6, 6162 - 6231	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	3.98E-08	0.94	4.52	-	962.4
AHQ-2-6, 4626	K.IEWLESHQDADIEDFK.A	1976.08864	3	3.90E-10	0.85	3.60	-	820.7
AHQ-2-6, 4617	K.IEWLESHQDADIEDFK.A	1976.08864	2	1.23E-06	0.98	5.74	-	1602.6
AHQ-2-6, 4094 - 4173	R.IINEPTAAAIAYGLDKR.E	1817.07894	2	1.09E-05	0.93	3.90	-	1121.8
AHQ-2-6, 3641 - 3709	R.ITPSYVAFTPEGER.L	1567.72412	2	2.08E-06	0.92	3.79	-	841.5
AHQ-2-7, 3605	R.ITPSYVAFTPEGER.L	1567.72412	2	8.04E-05	0.46	2.52	-	344.8
AHQ-2-6, 3475	K.KSDIDEIVLVGGSTR.I	1589.77277	2	1.11E-07	0.97	4.71	-	2052.9
AHQ-2-6, 3002	K.KSQIFSTASDNQPTVTIK.V	1966.18156	2	1.50E-09	0.98	5.65	-	2027.3
AHQ-2-6, 2061	K.MKETAEAYLGK.K	1241.43928	2	7.42E-05	0.93	3.91	-	893.3
AHQ-2-6, 3069	K.NQLTSNPENTVFDAK.R	1678.78173	2	4.92E-09	0.91	3.88	-	756.6
AHQ-2-6, 3814	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	1.59E-07	0.92	3.93	-	1001.6
AHQ-2-7, 3544	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	2.39E-04	0.78	4.19	-	489.4
AHQ-2-6, 3605 - 3675	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	4.96E-08	0.96	5.63	-	909.3
AHQ-2-6, 2854	R.TWNDPSVQQDIK.F	1431.53230	1	3.57E-05	0.18	2.37	-	248.2
AHQ-2-6, 3661 - 3698	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	4.07E-07	0.70	3.24	-	511.5
gi|29732955|ref|XP_291603.1| similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA				4.08E-10	0.90	10.24	16.80	11173.0
AHQ-2-9, 3984 - 4034	K.NISNASCTTNCIAPLAK.M	1838.05353	2	6.65E-06	0.71	3.85	-	795.1
AHQ-2-9, 4074 - 4114	K.NISNASCTTNCIAPLAK.M	1838.05353	2	4.08E-10	0.90	4.53	-	1261.8
AHQ-2-9, 4186 - 4259	K.NISNASCTTNCIAPLAK.M	1838.05353	2	3.35E-09	0.92	4.06	-	1764.2
AHQ-2-9, 4332	K.NISNASCTTNCIAPLAK.M	1838.05353	2	6.52E-10	0.73	3.16	-	1040.0
AHQ-2-9, 4440 - 4516	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.22E-07	0.94	4.25	-	1285.0
AHQ-2-10, 3710	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.67E-08	0.96	4.73	-	1401.7
AHQ-2-10, 3979 - 4058	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.04E-06	0.71	2.98	-	1148.8
AHQ-2-9, 3820 - 3902	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.55E-08	0.93	4.31	-	804.4
gi|5453549|ref|NP_006397.1| thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho				4.25E-10	5.62	60.24	33.60	30539.7
AHQ-2-10, 3471	K.DYGVYLEDSGHTLR.G	1625.72052	2	8.81E-09	0.95	4.33	-	1169.4
AHQ-2-10, 3831	K.HGEVCPAGWKPGSETIIPDPAGK.L	2405.67144	2	2.69E-05	0.90	3.77	-	850.7
AHQ-2-10, 4546	R.IPLLSDLTHQISK.D	1465.71961	2	4.25E-10	0.96	4.16	-	1419.0
AHQ-2-10, 4454	K.ISKPAPYWEGTAVIDGEFK.E	2109.36607	2	2.31E-07	0.95	4.82	-	1169.3
AHQ-2-10, 2670	R.LVQAFQYTDK.H	1213.36412	2	8.78E-06	0.90	3.15	-	860.5
AHQ-2-10, 2104	R.VSVADHSLHLSK.A	1293.45401	2	1.73E-06	0.96	3.93	-	1493.2
gi|4504517|ref|NP_001531.1| heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M				4.36E-10	6.55	80.35	59.00	22782.3
AHQ-2-13-, 2229	K.DGVVEITGK.H	918.02674	1	1.60E-04	0.20	2.15	-	423.9
AHQ-2-13-, 2206	K.DGVVEITGK.H	918.02674	1	5.03E-04	0.49	2.55	-	403.1
AHQ-2-13-, 5334 - 5397	R.KYTLPPGVDPTQVSSSLSPEGTLTVEAPM*PK.L	3244.65854	3	1.39E-04	0.96	6.57	-	1087.1
AHQ-2-13-, 5630 - 5703	R.KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK.L	3228.65914	3	1.59E-04	0.95	7.03	-	1394.9
AHQ-2-14, 5930	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.97E-04	0.28	2.68	-	214.7
AHQ-2-11, 4636 - 4645	K.LATQSNEITIPVTFESR.A	1907.11412	2	3.66E-05	0.66	3.34	-	352.8
AHQ-2-11, 4762	K.LATQSNEITIPVTFESR.A	1907.11412	2	2.70E-05	0.61	3.29	-	253.0
AHQ-2-11, 4497	R.LFDQAFGLPR.L	1164.33793	2	3.04E-07	0.97	4.28	-	1616.7
AHQ-2-10, 4287	R.LFDQAFGLPR.L	1164.33793	2	2.83E-06	0.97	4.23	-	1645.0
AHQ-2-10, 6415 - 6432	R.LPEEWSQWLGGSSWPGYVR.P	2235.44173	2	4.15E-05	0.94	4.29	-	999.7
AHQ-2-10, 6638	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	1.09E-07	0.97	6.20	-	1359.2
AHQ-2-11, 6700	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	7.14E-04	0.87	3.78	-	957.1
AHQ-2-13-, 4701 - 4722	R.VSLDVNHFAPDELTVK.T	1784.99058	2	4.36E-10	0.96	4.80	-	1276.3
AHQ-2-13-, 4955	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.21E-08	0.95	4.63	-	962.4
AHQ-2-10, 4294 - 4295	R.VSLDVNHFAPDELTVK.T	1784.99058	2	3.35E-08	0.95	4.93	-	1047.8
AHQ-2-11, 4513 - 4522	R.VSLDVNHFAPDELTVK.T	1784.99058	2	2.04E-06	0.95	4.61	-	1228.3
AHQ-2-13, 4623	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.77E-07	0.93	4.43	-	1158.5
gi|22059949|ref|XP_114617.2| similar to tubulin, beta 5 [Homo sapiens]				4.70E-10	1.81	20.38	18.80	22810.8
AHQ-2-13, 5288	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	3.47E-06	0.90	4.85	-	847.8
AHQ-2-12, 5409	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	2.21E-04	0.93	5.49	-	870.6
AHQ-2-14-, 5283	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	4.70E-10	0.98	7.62	-	1742.7
AHQ-2-13, 2809	R.ISVYYNEATGGK.Y	1302.41453	2	7.36E-05	0.78	2.82	-	723.4
AHQ-2-13-, 2747	R.ISVYYNEATGGK.Y	1302.41453	2	2.07E-06	0.83	3.07	-	688.0
AHQ-2-7, 2435	R.ISVYYNEATGGK.Y	1302.41453	1	1.33E-05	0.50	2.96	-	293.7
AHQ-2-7, 2432	R.ISVYYNEATGGK.Y	1302.41453	2	9.63E-06	0.90	3.55	-	839.8
gi|7657007|ref|NP_055210.1| dual adaptor of phosphotyrosine and 3-phosphoinositides [Homo sapiens]				4.75E-10	0.89	10.21	7.10	32044.2
AHQ-2-12, 6047	R.SDGEAELLQDLGWYHGNLTR.H	2275.41943	2	4.75E-10	0.89	4.17	-	719.3
gi|6005749|ref|NP_009193.1| RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA				4.83E-10	2.72	30.24	26.50	19846.9
AHQ-2-10, 3184 - 3198	R.DVVICPDASLEDAKK.E	1661.85581	2	4.40E-04	0.88	3.37	-	993.7
AHQ-2-10, 6883	R.GPGTSFEFALAIVEALNGK.E	1922.17039	2	1.05E-07	0.94	4.73	-	977.3
AHQ-2-11, 3037	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	4.32E-05	0.86	3.53	-	623.7
AHQ-2-10, 2896	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	4.83E-10	0.90	3.64	-	703.6
gi|4507869|ref|NP_003361.1| vasodilator-stimulated phosphoprotein [Homo sapiens]				5.02E-10	3.78	40.27	14.20	39829.4
AHQ-2-7, 3444	R.KMQPDQQVVINCAIVR.G	1901.24418	2	7.42E-06	0.93	4.02	-	976.1
AHQ-2-7, 6000 - 6013	K.VKEEIIEAFVQELR.K	1703.96061	2	5.02E-10	0.97	5.34	-	1795.6
AHQ-2-7, 1789	R.VKQELLEEVKK.E	1343.59438	2	9.47E-05	0.94	4.35	-	1261.3
AHQ-2-7, 2508	R.VQIYHNPTANSFR.V	1547.69936	2	4.39E-08	0.93	3.72	-	923.8
AHQ-2-13-, 2807	R.VQIYHNPTANSFR.V	1547.69936	2	3.70E-06	0.89	3.11	-	1127.7
AHQ-2-7, 2409	R.VQIYHNPTANSFR.V	1547.69936	2	2.20E-09	0.94	3.46	-	1209.9
gi|21361370|ref|NP_002853.2| phosphorylase, glycogen; brain [Homo sapiens]				5.65E-10	6.16	70.25	12.00	96695.3
AHQ-2-5, 3565	R.GLAGLGDVAEVR.K	1157.30210	2	3.90E-05	0.96	4.39	-	1347.2
AHQ-2-5, 3344	R.HLDHVAALFPGDVDR.L	1662.83036	2	2.77E-08	0.97	4.91	-	1675.2
AHQ-2-5, 6227	K.IGEEFLTDLSQLK.K	1493.68345	2	1.39E-06	0.97	4.99	-	1669.7
AHQ-2-5, 5829	K.IVNGWQVEEADDWLR.Y	1830.97790	2	5.65E-10	0.96	4.78	-	1100.3
AHQ-2-5, 5771 - 5776	K.LLPLVSDEVFIR.D	1401.67552	2	7.38E-07	0.85	3.61	-	493.2
AHQ-2-5, 4099	K.LVTSIGDVVNHDPVVGDR.L	1893.09067	2	2.40E-05	0.88	3.88	-	649.9
AHQ-2-5, 6747	R.WLLLCNPGLADTIVEK.I	1844.16436	2	1.77E-05	0.57	3.07	-	477.3
gi|10863927|ref|NP_066953.1| peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]				5.75E-10	6.33	80.24	30.90	18012.4

AHQ-2-13-, 4250	K.EGMNIVEAMER.F	1279.46942	2	9.43E-04	0.59	2.81	-	486.9
AHQ-2-12, 4045 - 4046	K.FEDENFILK.H	1155.28144	2	2.88E-05	0.84	3.37	-	610.9
AHQ-2-12, 4162	K.FEDENFILK.H	1155.28144	1	5.72E-04	0.71	2.52	-	1024.0
AHQ-2-12, 3946	K.ITIADCGQLE	1121.24345	1	2.76E-04	0.46	2.31	-	393.4
AHQ-2-12, 3454	K.KITIADCGQLE	1249.41637	2	1.22E-06	0.88	3.91	-	980.0
AHQ-2-13-, 3378	K.KITIADCGQLE	1249.41637	2	4.37E-06	0.89	3.45	-	787.3
AHQ-2-12, 3277 - 3345	K.KITIADCGQLE	1249.41637	2	1.34E-07	0.69	3.33	-	662.9
AHQ-2-14, 5936 - 5997	K.SIYGEKFEDENFILK.H	1833.03047	2	5.31E-04	0.86	3.86	-	733.7
AHQ-2-13, 4649	K.SIYGEKFEDENFILK.H	1833.03047	2	8.99E-04	0.95	4.73	-	1106.7
AHQ-2-14-, 4757	K.SIYGEKFEDENFILK.H	1833.03047	2	3.27E-09	0.94	4.63	-	1106.8
AHQ-2-12, 4741 - 4811	K.SIYGEKFEDENFILK.H	1833.03047	2	3.69E-09	0.95	4.35	-	1347.2
AHQ-2-12, 4649 - 4670	K.SIYGEKFEDENFILK.H	1833.03047	2	5.75E-10	0.96	4.78	-	1268.7
AHQ-2-12, 3567	K.VKEGMNIVEAMER.F	1506.77390	2	1.69E-05	0.95	4.37	-	1608.2
AHQ-2-12, 4382	R.VSFELFADK.V	1056.19300	2	2.05E-05	0.83	3.17	-	854.1
AHQ-2-12, 4511	R.VSFELFADK.V	1056.19300	1	1.39E-04	0.46	2.60	-	581.1
AHQ-2-12, 4517	R.VSFELFADK.V	1056.19300	2	9.94E-06	0.95	3.96	-	1087.1
AHQ-2-12, 4514	R.VSFELFADKVPK.T	1380.61317	2	5.25E-07	0.89	3.98	-	893.6
AHQ-2-12, 4302	R.VSFELFADKVPK.T	1380.61317	2	9.31E-07	0.88	3.77	-	885.5
gi|7705501|ref|NP_057546.1| hypothetical protein HSPC194 [Homo sapiens]				5.93E-10	1.84	20.22	41.10	11564.5
AHQ-2-14-, 6947	K.AGSVPSLAAGLLFGSLAGLGAYQLSQDPR.N	2818.17710	2	1.07E-04	0.88	4.33	-	622.3
AHQ-2-14-, 5971	K.FM*PAGLIAGASLLM*VAK.V	1723.13705	2	5.93E-10	0.97	4.43	-	2003.2
gi|4557419|ref|NP_000063.1| CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36				5.96E-10	2.66	30.25	10.20	53052.1
AHQ-2-1, 4929	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	2.28E-06	0.74	3.43	-	382.0
AHQ-2-5, 5488	K.SQVLQFFSSDICR.S	1588.76661	2	5.96E-10	0.95	3.98	-	1410.5
AHQ-2-5, 7341 - 7343	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.88E-08	0.97	5.05	-	1461.9
gi|4557297|ref|NP_000022.1| delta-aminolevulinic acid dehydratase; porphobilinogen synthase; aminol				6.20E-10	1.73	20.21	10.00	36294.7
AHQ-2-9, 4843	R.GSAADSEESPAIEAIHLLR.K	1967.12642	2	2.97E-08	0.93	4.11	-	906.5
AHQ-2-9, 4866	R.GSAADSEESPAIEAIHLLR.K	1967.12642	3	6.20E-10	0.86	3.68	-	884.1
AHQ-2-9, 4683	R.LEEMLRPLVEEGLR.C	1684.98233	2	1.70E-04	0.87	3.36	-	1046.8
gi|4757786|ref|NP_004306.1| N-acylsphingosine amidohydrolase (acid ceramidase) 1; N-acylsphingosine				6.21E-10	0.98	10.28	4.30	44649.3
AHQ-2-13-, 6718 - 6785	K.LPGLLGNFPGPFEEEMK.G	1876.16512	2	3.90E-04	0.92	3.32	-	1211.3
AHQ-2-14-, 6513 - 6576	K.LPGLLGNFPGPFEEEMK.G	1876.16512	2	6.21E-10	0.98	5.58	-	1613.2
AHQ-2-13, 6437 - 6499	K.LPGLLGNFPGPFEEEMK.G	1876.16512	2	6.65E-07	0.97	4.76	-	1608.2
gi|4504515|ref|NP_002146.1| heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B				6.28E-10	4.62	60.23	10.70	70853.4
AHQ-2-6, 2229	K.ATAGDTHLGGEDFDNR.L	1676.68279	3	6.24E-07	0.64	3.02	-	338.8
AHQ-2-6, 2233	K.ATAGDTHLGGEDFDNR.L	1676.68279	2	6.32E-10	0.95	4.63	-	1197.3
AHQ-2-7, 4655	R.IINEPTAAAIAYGLDR.R	1688.90603	2	3.51E-06	0.92	3.24	-	1271.2
AHQ-2-6, 4753 - 4771	R.IINEPTAAAIAYGLDR.R	1688.90603	2	6.28E-10	0.95	4.67	-	1000.3
AHQ-2-6, 4341	K.LLQDFFNGK.E	1082.23369	2	8.39E-04	0.87	2.59	-	886.6
AHQ-2-6, 4206 - 4277	K.LLQDFFNGKELNK.S	1566.78249	2	5.13E-04	0.95	3.84	-	1750.7
AHQ-2-13-, 3457 - 3463	R.TTPSYVAFTDTER.L	1488.58062	2	3.23E-07	0.78	3.11	-	584.3
AHQ-2-13, 3467	R.TTPSYVAFTDTER.L	1488.58062	2	1.78E-04	0.87	2.79	-	922.1
AHQ-2-12, 3370	R.TTPSYVAFTDTER.L	1488.58062	2	6.40E-07	0.81	2.64	-	676.3
AHQ-2-6, 1985 - 2053	R.VEILANDQGNR.T	1229.32518	2	2.84E-04	0.94	3.94	-	1330.0
AHQ-2-6, 1989 - 2058	R.VEILANDQGNR.T	1229.32518	1	2.50E-04	0.12	1.90	-	237.7
gi|4758018|ref|NP_004359.1| calponin 2; Calonin 2 [Homo sapiens]				6.48E-10	2.77	30.27	12.60	33696.9
AHQ-2-12, 5155	K.DGTILCTLMNK.L	1267.49833	2	7.78E-04	0.88	3.35	-	947.4
AHQ-2-12, 2786	K.GLQSGVDIGVK.Y	1073.22510	2	1.85E-06	0.92	3.35	-	1178.1
AHQ-2-13-, 2861	K.GLQSGVDIGVK.Y	1073.22510	2	4.14E-05	0.91	2.87	-	1471.6
AHQ-2-10, 6028 - 6096	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.11E-06	0.74	3.18	-	337.5
AHQ-2-12, 6466 - 6525	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	6.48E-10	0.97	4.62	-	1720.9
AHQ-2-12, 6591	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	9.67E-05	0.79	2.87	-	953.9
AHQ-2-13, 6311 - 6315	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	3.30E-09	0.97	5.30	-	1334.3
AHQ-2-13, 6415 - 6480	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.40E-04	0.45	2.71	-	588.5
AHQ-2-1, 6770 - 6838	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	9.86E-06	0.94	3.99	-	1170.3
AHQ-2-13-, 6422 - 6494	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.05E-09	0.97	5.44	-	1418.0
AHQ-2-14-, 6360	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.30E-05	0.96	4.31	-	1447.9
gi|27478749|ref|XP_208411.1| similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit				6.81E-10	1.79	20.29	13.40	25628.5
AHQ-2-9, 4446	K.GEMMDLQHGSLFLR.T	1634.90537	2	1.30E-09	0.83	3.80	-	688.8
AHQ-2-9, 7474	K.LLIVSNPVDILTYVAWK.I	1945.33337	2	6.81E-10	0.96	5.90	-	913.9
gi|7657056|ref|NP_055415.1| EH-domain containing 3; EH domain containing 3 [Homo sapiens]				7.28E-10	5.66	60.30	20.20	60886.7
AHQ-2-7, 5517	R.FHEFHSPALEDADFDNKPMVLLVGQYSTGK.T	3394.75749	3	3.08E-08	0.94	5.11	-	843.2
AHQ-2-10, 6774 - 6775	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	3.12E-04	0.92	4.50	-	927.8
AHQ-2-7, 7519	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	1.13E-05	0.95	4.86	-	1034.5
AHQ-2-8, 7423	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	7.28E-10	0.97	6.04	-	1454.3
AHQ-2-13, 5303	K.LADIDKDGM*LDDDEFALANHLIK.V	2589.86003	3	6.75E-06	0.94	4.60	-	1434.0
AHQ-2-13, 5625 - 5693	K.LADIDKDGMLDDDEFALANHLIK.V	2573.86063	3	1.25E-06	0.96	4.60	-	2116.1
AHQ-2-7, 5936	R.VYIGSFWSHPLLIPDNR.K	2015.30234	2	1.64E-04	0.94	4.13	-	1106.0
AHQ-2-8, 4501	R.YLLEQDFPGMR.I	1369.57075	2	4.97E-05	0.92	3.43	-	1430.2
AHQ-2-13-, 4855	R.YLLEQDFPGMR.I	1369.57075	2	2.42E-04	0.84	3.47	-	1011.1
AHQ-2-8, 4508	R.YLLEQDFPGMR.I	1369.57075	1	2.67E-04	0.29	2.11	-	271.6
gi|16975484|ref|NP_056057.1| centaurin delta 2 isoform b; ARF-GAP, RHO-GAP, ankyrin repeat, and ple				8.11E-10	0.82	10.17	1.20	136262.7
AHQ-2-3, 5169	R.AVFPEGPCEEPLQLR.K	1743.96175	2	8.11E-10	0.82	3.35	-	461.7
gi|4758038|ref|NP_004246.1| cytochrome c oxidase subunit Va precursor; cytochrome c oxidase polypep				8.83E-10	1.81	20.28	30.00	16774.1
AHQ-2-13, 6731 - 6807	K.EIYPYVIQELRPTLNELGISTPEELGLDKV	3430.88913	3	8.83E-10	0.94	5.53	-	708.8
AHQ-2-13-, 6950	K.EIYPYVIQELRPTLNELGISTPEELGLDKV	3430.88913	3	1.59E-08	0.91	4.24	-	1127.4
AHQ-2-14-, 6868 - 6936	K.EIYPYVIQELRPTLNELGISTPEELGLDKV	3430.88913	3	1.77E-04	0.87	4.47	-	544.8
AHQ-2-13, 4207	K.GINTLVTYDM*VPEPK.I	1693.94282	2	1.36E-04	0.87	3.07	-	1246.8
gi|4504077|ref|NP_000165.1| glycoprotein IX (platelet) [Homo sapiens]				8.95E-10	5.03	60.22	30.50	19046.0
AHQ-2-11, 4076	R.ALETM*GLWVDCR.G	1468.68075	2	5.86E-04	0.89	3.10	-	1099.0
AHQ-2-11, 4902	R.ALETMGLWVDCR.G	1452.68135	2	1.47E-06	0.93	3.55	-	1034.8
AHQ-2-14, 3538 - 3596	R.CASPSLAAHGPLGR.L	1395.56962	2	7.56E-06	0.77	2.87	-	791.8
AHQ-2-12, 2610	R.CASPSLAAHGPLGR.L	1395.56962	2	2.56E-09	0.93	3.71	-	1249.8
AHQ-2-14-, 2660	R.CASPSLAAHGPLGR.L	1395.56962	2	4.08E-08	0.85	2.79	-	940.4
AHQ-2-11, 2614	R.CASPSLAAHGPLGR.L	1395.56962	1	6.67E-08	0.67	3.39	-	215.3
AHQ-2-11, 2572	R.CASPSLAAHGPLGR.L	1395.56962	2	8.95E-10	0.93	3.49	-	1082.6
AHQ-2-11, 3201 - 3265	R.GHGLTALPALPAR.T	1274.49706	2	5.59E-05	0.94	4.06	-	780.0
AHQ-2-11, 5229	R.LWLEDRTPEALLQVR.C	1840.11574	2	9.45E-04	0.90	4.35	-	641.0
AHQ-2-11, 3060	R.TPEALLQVR.C	1027.19957	1	3.37E-06	0.44	2.35	-	167.5
AHQ-2-11, 3057	R.TPEALLQVR.C	1027.19957	2	4.58E-05	0.94	3.73	-	1261.4
AHQ-2-14-, 3071	R.TPEALLQVR.C	1027.19957	2	4.46E-05	0.96	3.24	-	1787.2
AHQ-2-12, 3082	R.TPEALLQVR.C	1027.19957	2	2.99E-05	0.90	2.95	-	993.1
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				9.17E-10	17.27	190.33	21.60	138070.8
AHQ-2-1, 2522	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	1.46E-04	0.77	3.36	-	520.9
AHQ-2-3, 2259	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	6.09E-06	0.94	5.05	-	742.5
AHQ-2-3, 2351	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	2.67E-05	0.89	3.96	-	892.4
AHQ-2-2, 2293	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	3.44E-05	0.91	4.93	-	495.0
AHQ-2-3, 2261	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	5.16E-04	0.95	4.78	-	1693.7
AHQ-2-3, 7405 - 7412	K.CTSDMETILTFIPQFHR.L	2098.38838	3	2.11E-05	0.91	4.57	-	801.9
AHQ-2-3, 7397 - 7407	K.CTSDMETILTFIPQFHR.L	2098.38838	2	3.57E-04	0.90	3.88	-	834.7
AHQ-2-3, 4140	R.DQALQLQVLNSR.F	1385.55144	2	2.32E-06	0.96	3.88	-	2203.7
AHQ-2-10, 5850 - 5851	K.FPPVTTFSGYLLYR.T	1661.92388	2	3.11E-05	0.93	4.09	-	725.5
AHQ-2-14-, 6196	K.FPPVTTFSGYLLYR.T	1661.92388	2	7.61E-07	0.93	3.92	-	670.0
AHQ-2-3, 5971 - 6004	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	4.64E-04	0.78	3.88	-	574.3
AHQ-2-4, 6008	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	4.01E-07	0.92	4.23	-	896.7
AHQ-2-3, 5979	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.92E-06	0.94	4.16	-	1254.2
AHQ-2-6, 5989	K.GLTEFVEPIIQIK.T	1487.76518	2	8.16E-05	0.82	3.01	-	841.1

AHQ-2-1, 6312	K.GLTEFVEPIIQIK.T	1487.76518	2	1.75E-06	0.92	4.34	-	825.6
AHQ-2-3, 6288 - 6355	K.GLTEFVEPIIQIK.T	1487.76518	2	2.47E-04	0.93	3.48	-	1275.4
AHQ-2-3, 6311	K.GLTEFVEPIIQIK.T	1487.76518	1	1.02E-04	0.58	3.18	-	524.2
AHQ-2-3, 3748	K.HSLPDIQLLQK.G	1292.50915	2	2.05E-09	0.93	3.49	-	1041.9
AHQ-2-1, 4017 - 4028	K.HSLPDIQLLQK.G	1292.50915	2	2.59E-06	0.94	3.53	-	1066.2
AHQ-2-4, 3769	K.HSLPDIQLLQK.G	1292.50915	2	4.42E-06	0.50	2.68	-	516.0
AHQ-2-2, 3816	K.HSLPDIQLLQK.G	1292.50915	2	9.49E-04	0.93	3.37	-	1010.2
AHQ-2-3, 6195	K.IENLTSAVNSLNFIIK.E	1777.05472	2	4.00E-05	0.96	5.42	-	972.5
AHQ-2-3, 5209 - 5224	K.IFQNDM*QETVAQLFK.T	1829.06683	2	3.20E-07	0.95	4.19	-	1372.6
AHQ-2-5, 6571	K.IFQNDMQETVAQLFK.T	1813.06743	2	2.17E-05	0.96	4.16	-	1741.6
AHQ-2-3, 6771 - 6844	K.IFQNDMQETVAQLFK.T	1813.06743	2	1.42E-08	0.97	5.05	-	1885.4
AHQ-2-3, 6909	K.IFQNDMQETVAQLFK.T	1813.06743	2	3.28E-08	0.96	4.53	-	1586.2
AHQ-2-3, 5457	K.IFQNDM*QETVAQLFK.T	1829.06683	2	2.42E-08	0.92	4.09	-	910.8
AHQ-2-10, 3544 - 3546	K.LAFESENINSEIHCDR.V	1936.04933	2	8.80E-06	0.92	4.42	-	539.9
AHQ-2-3, 2735	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	5.29E-06	0.97	5.49	-	1335.3
AHQ-2-1, 2970	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	1.69E-06	0.96	4.96	-	1010.2
AHQ-2-5, 2507	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	2.47E-08	0.97	5.94	-	1259.9
AHQ-2-4, 2741	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	1.15E-06	0.97	5.91	-	1019.6
AHQ-2-3, 2740	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	3	2.43E-07	0.96	5.14	-	1865.4
AHQ-2-11, 3593	K.LVEENALAPDFSK.G	1433.58810	2	9.37E-04	0.86	3.44	-	770.6
AHQ-2-10, 3439 - 3442	K.LVEENALAPDFSK.G	1433.58810	1	1.40E-04	0.13	2.16	-	353.2
AHQ-2-10, 3423 - 3430	K.LVEENALAPDFSK.G	1433.58810	2	7.57E-06	0.94	3.74	-	1065.3
AHQ-2-3, 7571	K.M*SEQLNDLTYDMEILQPLLEQGASLR.Q	3025.40122	3	1.12E-06	0.96	6.50	-	1587.4
AHQ-2-3, 1971 - 1984	K.QTHLEGALEQEHSR.S	1635.72018	2	5.14E-05	0.50	2.62	-	279.6
AHQ-2-3, 7483	K.TM*TIINNAIDFIQDNYALK.E	2215.51196	2	9.17E-10	0.94	4.95	-	963.2
AHQ-2-4, 7605	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	3.97E-08	0.89	4.05	-	837.5
AHQ-2-3, 3403	K.TVSSLSEDLESTR.Q	1424.49324	2	1.89E-05	0.86	2.88	-	1105.0
AHQ-2-3, 3417	K.TVSSLSEDLESTR.Q	1424.49324	1	1.17E-04	0.22	2.36	-	157.8
AHQ-2-1, 3576	K.TVSSLSEDLESTR.Q	1424.49324	2	8.42E-05	0.45	2.93	-	381.7
AHQ-2-3, 4017	R.YNFVLQVAK.T	1082.27683	2	4.68E-05	0.92	3.05	-	1019.4
gi|5902128|ref|NP_008880.1| syntaxin binding protein 2; Hunc18b [Homo sapiens]				9.25E-10	7.13	80.32	21.40	66438.1
AHQ-2-6, 6293	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	2	1.91E-07	0.98	6.44	-	1964.5
AHQ-2-6, 6295 - 6309	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	3	6.34E-07	0.94	4.57	-	1207.5
AHQ-2-6, 6590 - 6601	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	7.00E-06	0.95	4.71	-	910.7
AHQ-2-6, 2906 - 2907	R.KGPEDTAQLAHAVLAK.L	1649.87303	3	1.76E-08	0.96	4.71	-	1672.9
AHQ-2-6, 2903	R.KGPEDTAQLAHAVLAK.L	1649.87303	2	9.25E-10	0.95	4.04	-	1477.8
AHQ-2-6, 2129	K.LIQHANVQAHSSLIR.N	1687.92773	2	4.60E-06	0.92	3.74	-	1099.1
AHQ-2-6, 6345 - 6358	K.LIVPVLLDAAVPAYDK.I	1698.03911	2	1.11E-05	0.98	5.08	-	1929.2
AHQ-2-6, 3055	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	5.38E-05	0.92	4.12	-	837.1
AHQ-2-6, 5410	R.NLWPFVSDPAPTASSQAAVSAR.F	2273.48981	2	1.03E-04	0.71	3.27	-	405.2
AHQ-2-6, 5865 - 5923	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	2.21E-05	0.98	6.03	-	1608.6
AHQ-2-6, 5866	R.REPIPSLEAIYLLSPTEK.S	2057.37574	3	1.24E-05	0.72	3.25	-	710.6
gi|12707570|ref|NP_004083.2| mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor [Homo				9.41E-10	0.97	10.26	5.90	31371.2
AHQ-2-10, 6787	K.ICPVETLVEEAIQCAEK.I	1992.25744	2	9.41E-10	0.97	5.24	-	1309.0
gi|29740995|ref|XP_291768.1| similar to Proteasome activator complex subunit 2 (Proteasome activato				9.54E-10	0.98	10.29	9.60	19192.6
AHQ-2-10, 6482 - 6483	R.AFYAELYHIISSNLEK.T	1899.13528	2	9.54E-10	0.98	5.75	-	1787.0
gi|4885413|ref|NP_005331.1| histidine triad nucleotide binding protein 1; Histidine triad nucleotid				9.74E-10	4.60	50.30	71.40	13801.8
AHQ-2-13-, 2705	K.AQVARPGGDTIFGK.I	1417.59513	2	1.57E-04	0.92	3.73	-	1234.0
AHQ-2-13, 2763	K.AQVARPGGDTIFGK.I	1417.59513	2	1.76E-04	0.81	3.30	-	895.9
AHQ-2-13-, 5621	R.CLAFHDISPQAPTHFLVIPK.K	2293.67220	2	8.02E-04	0.81	3.57	-	731.5
AHQ-2-13-, 5618	R.CLAFHDISPQAPTHFLVIPK.K	2293.67220	3	1.44E-06	0.94	4.49	-	1148.5
AHQ-2-13, 6041 - 6109	K.IIFEDDRCLAFHDISPQAPTHFLVIPK.K	3182.64001	3	3.03E-06	0.92	4.92	-	1172.5
AHQ-2-13-, 5543	K.KHISQISVAEDDDESLLGHLMIVGK.K	2736.09467	3	2.06E-06	0.98	6.05	-	2255.4
AHQ-2-13-, 3898	R.MVVNEGSDGGQSVYHVHLHVLGGR.Q	2548.82255	3	9.74E-10	0.85	3.84	-	793.0
gi|6912494|ref|NP_036457.1| microtubule-associated protein, RP/EB family, member 1; ADENOMATOUS POL				1.02E-09	3.12	40.24	15.30	29998.9
AHQ-2-12, 3990	K.FFDANYDGKDYDPVAAR.Q	1965.06754	2	5.69E-05	0.85	3.57	-	557.6
AHQ-2-12, 6686 - 6689	K.FQDNFEFVQWFK.K	1635.80184	2	1.02E-09	0.97	4.82	-	1419.8
AHQ-2-12, 6819	K.FQDNFEFVQWFK.K	1635.80184	2	6.86E-07	0.96	4.02	-	1320.0
AHQ-2-12, 6175	K.GKFQDNFEFVQWFK.K	1821.02630	2	1.96E-04	0.96	4.59	-	1270.2
AHQ-2-13-, 2709	K.LEHEYIQNFK.I	1321.46268	2	9.03E-04	0.67	2.58	-	951.4
AHQ-2-12, 2563	K.LEHEYIQNFK.I	1321.46268	1	1.01E-05	0.34	2.14	-	553.1
gi|29568111|ref|NP_006088.2| myosin, light polypeptide 9, regulatory; myosin regulatory light chain				1.07E-09	3.13	40.22	18.00	19827.1
AHQ-2-11, 3352	R.FTDEEVDEMYR.E	1434.51009	1	2.09E-07	0.47	2.18	-	470.5
AHQ-2-11, 3366	R.FTDEEVDEMYR.E	1434.51009	1	8.48E-05	0.33	2.31	-	347.2
AHQ-2-11, 2658	R.FTDEEVDEM*YR.E	1450.50949	2	7.24E-06	0.94	3.45	-	1257.9
AHQ-2-11, 3640 - 3704	K.GNFNYVEFTR.I	1247.34066	2	1.24E-05	0.84	3.34	-	792.5
AHQ-2-11, 3674	K.GNFNYVEFTR.I	1247.34066	2	2.14E-05	0.86	3.19	-	708.0
AHQ-2-11, 3820	K.GNFNYVEFTR.I	1247.34066	2	7.66E-04	0.73	2.75	-	515.4
AHQ-2-11, 3925	K.GNFNYVEFTR.I	1247.34066	2	1.71E-04	0.92	3.77	-	907.8
AHQ-2-11, 4129	K.GNFNYVEFTR.I	1247.34066	1	5.78E-06	0.21	1.85	-	221.1
AHQ-2-13-, 3935 - 3978	K.GNFNYVEFTR.I	1247.34066	2	1.83E-05	0.88	3.18	-	914.8
AHQ-2-12, 3766	K.GNFNYVEFTR.I	1247.34066	2	2.83E-07	0.78	2.95	-	614.3
AHQ-2-14-, 3867	K.GNFNYVEFTR.I	1247.34066	2	4.18E-05	0.84	2.97	-	909.8
AHQ-2-11, 5726 - 5765	R.NAFACFDEEASGFIHEDHLR.E	2367.49548	2	1.07E-09	0.94	4.38	-	1036.3
gi|17986283|ref|NP_006000.2| tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu				1.07E-09	0.96	10.29	3.30	50135.3
AHQ-2-1, 6081 - 6089	R.AVFVDLEPTVIDEVR.T	1702.92947	2	4.26E-06	0.88	4.05	-	737.9
AHQ-2-3, 6047	R.AVFVDLEPTVIDEVR.T	1702.92947	2	6.39E-07	0.72	3.70	-	502.2
AHQ-2-4, 6056	R.AVFVDLEPTVIDEVR.T	1702.92947	2	6.69E-09	0.94	4.53	-	1002.4
AHQ-2-6, 5686 - 5743	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.07E-05	0.89	4.16	-	726.1
AHQ-2-7, 5315	R.AVFVDLEPTVIDEVR.T	1702.92947	2	7.35E-05	0.89	3.36	-	888.3
AHQ-2-7, 5605 - 5675	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.07E-09	0.96	5.73	-	1039.3
AHQ-2-10, 5270 - 5291	R.AVFVDLEPTVIDEVR.T	1702.92947	2	4.25E-08	0.96	5.17	-	1265.0
AHQ-2-11, 5492	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.28E-06	0.91	4.36	-	868.5
AHQ-2-12, 5767 - 5846	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.80E-04	0.51	2.84	-	299.1
AHQ-2-13, 5605	R.AVFVDLEPTVIDEVR.T	1702.92947	2	5.86E-06	0.84	4.11	-	498.3
AHQ-2-13-, 5705	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.51E-07	0.94	4.95	-	887.9
AHQ-2-14-, 5671 - 5749	R.AVFVDLEPTVIDEVR.T	1702.92947	2	6.78E-09	0.96	5.21	-	987.3
gi|23110944|ref|NP_002782.1| proteasome alpha 6 subunit; prosomal P27K protein; proteasome subunit				1.09E-09	0.87	10.17	4.90	27399.3
AHQ-2-10, 4034 - 4036	K.LLDSSTVTHLFK.I	1361.56825	2	1.09E-09	0.87	3.38	-	704.4
gi|5032161|ref|NP_005639.1| elongin C; transcription elongation factor B (SIII), polypeptide 1 (15k				1.13E-09	2.50	30.24	28.60	12473.1
AHQ-2-13-, 4634	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	2.24E-06	0.74	3.20	-	787.2
AHQ-2-13-, 4935	K.AMLSGPGQFAENETNEVNFR.E	2212.38515	2	1.13E-09	0.95	4.74	-	1282.4
AHQ-2-13-, 3041	K.LISSDGHEFIVK.R	1345.52569	2	4.63E-06	0.81	3.17	-	616.8
AHQ-2-13, 3077	K.LISSDGHEFIVK.R	1345.52569	2	1.62E-04	0.75	2.90	-	646.5
gi|4507109|ref|NP_000336.1| alpha-synuclein isoform NACP140; non A4 component of amyloid precursor				1.14E-09	5.18	60.29	45.70	14460.1
AHQ-2-12, 2118 - 2119	K.EGVVHGVATVAEK.T	1296.45466	2	7.81E-07	0.91	3.47	-	957.2
AHQ-2-13-, 4715 - 4718	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	6.72E-09	0.96	5.36	-	873.0
AHQ-2-14, 5685	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	7.45E-08	0.95	4.86	-	1200.3
AHQ-2-14-, 4695	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.35E-07	0.94	4.87	-	773.4
AHQ-2-14-, 4640 - 4708	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	3	1.31E-05	0.91	4.25	-	1195.7
AHQ-2-13-, 4719	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	3	7.58E-04	0.97	5.50	-	1724.2
AHQ-2-12, 4699	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	3.39E-07	0.95	5.23	-	907.4
AHQ-2-12, 4939	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	2.88E-07	0.90	4.07	-	563.6
AHQ-2-13, 4633	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	6.93E-06	0.95	4.91	-	1042.7
AHQ-2-12, 1993	K.TKEGVLYVGSK.T	1181.36357	2	1.22E-05	0.77	2.71	-	618.9
AHQ-2-12, 1989	K.TKEGVVHGVATVAEK.T	1525.73191	3	5.21E-04	0.92	3.97	-	1177.7
AHQ-2-14-, 2052	K.TKEGVVHGVATVAEK.T	1525.73191	2	1.08E-06	0.96	4.44	-	1462.6

AHQ-2-12, 1985	K.TKEGVVHGVATVAEK.T	1525.73191	2	2.83E-06	0.94	3.95	-	1298.1
AHQ-2-14, 5386 - 5409	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	7.41E-04	0.85	3.77	-	1288.5
AHQ-2-14, 5393	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.88E-06	0.97	5.80	-	1296.0
AHQ-2-13, 4209	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.77E-05	0.95	4.63	-	1189.1
AHQ-2-14-, 4207 - 4223	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	4.35E-04	0.77	3.50	-	931.6
AHQ-2-14-, 4231	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.14E-09	0.97	5.17	-	1380.7
AHQ-2-12, 4209 - 4214	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	7.51E-05	0.91	4.57	-	1391.5
AHQ-2-13-, 4211	K.TVEGAGSIAAATGFVK.K	1479.66001	1	3.68E-04	0.37	2.66	-	257.5
AHQ-2-13, 4171	K.TVEGAGSIAAATGFVK.K	1479.66001	1	9.02E-06	0.61	3.08	-	444.8
AHQ-2-13, 4159	K.TVEGAGSIAAATGFVK.K	1479.66001	2	8.07E-05	0.49	2.65	-	543.0
AHQ-2-12, 4158	K.TVEGAGSIAAATGFVK.K	1479.66001	1	7.28E-05	0.34	2.73	-	333.4
AHQ-2-14, 5025	K.TVEGAGSIAAATGFVK.K	1479.66001	2	7.07E-04	0.67	2.50	-	876.0
gi|21361741|ref|NP_057569.2|	hypothetical protein HSPC228; My012 protein [Homo sapiens]			1.14E-09	0.37	10.14	6.50	33879.0
AHQ-2-9, 5040	K.YAGSALQYEDVSTAVQNLQK.A	2186.36410	2	1.14E-09	0.37	2.86	-	419.3
gi|12025678|ref|NP_004915.2|	actinin, alpha 4 [Homo sapiens]			1.15E-09	8.27	100.26	15.80	104853.3
AHQ-2-5, 4049	K.DGLAFNALIHR.H	1227.39726	2	3.10E-08	0.86	2.99	-	939.7
AHQ-2-5, 4685	R.ETTDTDTADQVIASFK.V	1742.81936	2	2.10E-05	0.94	3.96	-	1467.7
AHQ-2-14, 5658 - 5733	R.ETTDTDTADQVIASFK.V	1742.81936	2	2.45E-05	0.79	3.35	-	441.0
AHQ-2-5, 2719 - 2723	K.GISQEQMQEFR.A	1353.48658	2	8.61E-07	0.79	3.02	-	1094.7
AHQ-2-5, 3816 - 3819	R.M*APYQGPDAVPGALDYK.S	1810.02037	2	1.29E-07	0.94	3.82	-	1222.1
AHQ-2-5, 4088	R.MAPYQGPDAVPGALDYK.S	1794.02097	2	3.94E-07	0.93	3.80	-	1192.2
AHQ-2-5, 4009	K.MLDAEDIVNTARPDEK.A	1817.99924	2	1.98E-06	0.76	3.50	-	579.8
AHQ-2-5, 4509 - 4523	R.QFASQANVVGPWIQTK.M	1775.00061	2	1.15E-09	0.89	4.12	-	490.6
AHQ-2-1, 6788	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	6.77E-04	0.64	3.31	-	479.9
AHQ-2-5, 3627	K.VLAGDKNFITAEELR.R	1676.89525	2	7.94E-06	0.85	4.15	-	593.9
AHQ-2-5, 3455 - 3463	K.VLAVNQENEHLMEDYEK.L	2062.24648	2	4.50E-05	0.94	5.10	-	577.7
AHQ-2-5, 3459	K.VLAVNQENEHLMEDYEK.L	2062.24648	3	5.20E-08	0.66	3.05	-	413.2
gi|4506505|ref|NP_002916.1|	regulator of G-protein signaling 10 [Homo sapiens]			1.18E-09	2.70	30.22	23.40	19607.9
AHQ-2-11, 3518 - 3524	K.ILEEPHPLMFQK.L	1482.77213	2	4.46E-06	0.94	4.30	-	886.3
AHQ-2-11, 4628 - 4629	K.LQDQIFNLMK.Y	1250.49254	2	6.52E-05	0.89	3.65	-	732.7
AHQ-2-11, 5292 - 5308	K.WAASLENLLEDPEGVKR.F	1928.13502	2	1.18E-09	0.87	4.45	-	484.2
gi|10834976|ref|NP_000572.1|	glutathione peroxidase 1 [Homo sapiens]			1.18E-09	8.06	90.30	58.70	21909.0
AHQ-2-11, 5345	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	1.18E-09	0.93	4.08	-	1026.9
AHQ-2-11, 2738 - 2818	R.DYTQMNELQR.R	1298.40778	2	1.52E-05	0.83	3.10	-	816.1
AHQ-2-11, 3968	K.FLVGPDGVPLR.R	1170.38561	2	8.48E-06	0.94	3.61	-	1302.8
AHQ-2-11, 4846 - 4917	R.GLVVLGFPCNQFGHQENAK.N	2117.37312	2	6.26E-05	0.81	3.73	-	386.8
AHQ-2-11, 5938 - 6018	R.GLVVLGFPCNQFGHQENAKNEEILNSLK.Y	3158.53371	3	9.80E-07	0.88	4.58	-	604.9
AHQ-2-14, 4825	R.PLAGGEPVSLGSLR.G	1353.54935	2	6.49E-06	0.93	3.92	-	837.1
AHQ-2-11, 3646 - 3725	R.PLAGGEPVSLGSLR.G	1353.54935	2	8.24E-07	0.95	4.13	-	1332.3
AHQ-2-10, 3608 - 3619	R.PLAGGEPVSLGSLR.G	1353.54935	2	1.87E-06	0.94	4.10	-	980.5
AHQ-2-11, 6737	R.RFQTIDIEPDIEALLSQGPSCA	2462.71807	2	3.10E-07	0.95	4.77	-	1102.5
AHQ-2-11, 4865	K.YVRPGGGFEPNFM*LFEK.C	2005.28455	3	7.76E-04	0.81	3.71	-	763.2
AHQ-2-11, 5126	K.YVRPGGGFEPNFMLFEK.C	1989.28515	3	9.28E-08	0.95	4.47	-	1561.5
AHQ-2-11, 5124 - 5125	K.YVRPGGGFEPNFMLFEK.C	1989.28515	2	9.65E-05	0.98	6.01	-	2762.1
AHQ-2-11, 5234	K.YVRPGGGFEPNFMLFEK.C	1989.28515	2	2.05E-05	0.94	4.29	-	832.5
gi|4557395|ref|NP_000058.1|	carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase;			1.20E-09	4.66	60.25	28.80	29245.8
AHQ-2-10, 6650	K.AVQQPDGLAVLGIFLK.V	1669.98899	2	1.19E-05	0.95	4.55	-	724.1
AHQ-2-10, 2048 - 2052	K.GGPLDGTYR.L	936.00385	1	1.69E-04	0.08	1.97	-	144.7
AHQ-2-10, 3963	R.ILNNGHAFNVEFDDSQDK.A	2064.15751	2	3.07E-07	0.96	4.96	-	1197.7
AHQ-2-10, 3852	R.ILNNGHAFNVEFDDSQDK.A	2064.15751	2	3.50E-06	0.76	3.61	-	388.6
AHQ-2-10, 3071	K.SADFTNFDPR.G	1170.21306	2	1.24E-07	0.86	3.36	-	775.5
AHQ-2-10, 3483	K.VVDVLDSIK.T	988.16011	2	3.08E-04	0.84	3.49	-	467.7
AHQ-2-10, 3146	K.YAAELHLVHWNTK.Y	1582.78684	2	1.20E-09	0.98	4.21	-	2631.7
gi|6005942|ref|NP_009057.1|	valosin-containing protein; yeast Cdc48p homolog; transitional endoplas			1.34E-09	9.63	110.28	21.50	89321.3
AHQ-2-5, 3525 - 3539	R.ELQELVQYPVEHPDK.F	1825.01157	2	6.03E-04	0.90	3.86	-	905.6
AHQ-2-5, 3379	R.GILLYGPPGTGK.T	1173.38627	2	1.23E-04	0.84	3.42	-	891.3
AHQ-2-5, 6857	R.IVSQLLTLMDGLK.Q	1431.76657	2	5.91E-05	0.81	3.00	-	780.3
AHQ-2-5, 2988	R.KYEMFAQTLQQSR.G	1630.85008	2	8.24E-08	0.97	5.02	-	1808.7
AHQ-2-5, 2705	R.LEILQIHTK.N	1095.31705	1	1.43E-05	0.58	2.44	-	372.4
AHQ-2-5, 5181	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	3.05E-07	0.97	5.53	-	1350.1
AHQ-2-5, 4795	K.MTNGFSGADLTEICQR.A	1801.97996	2	2.78E-09	0.90	3.57	-	1049.0
AHQ-2-5, 7483 - 7484	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	2.04E-08	0.96	5.43	-	1269.0
AHQ-2-5, 4324	R.QTNPSAMEVEEDDPVPEIR.R	2157.30143	2	3.36E-07	0.95	4.58	-	1362.0
AHQ-2-5, 4885	K.VVETDPSPYCIVAPDTVIHCEGEPIKR.E	3085.45473	3	1.34E-09	0.83	3.86	-	615.2
AHQ-2-5, 3244 - 3252	R.WALSQSNPSALR.E	1330.47434	2	5.21E-05	0.92	3.67	-	1161.4
gi|21624607|ref|NP_066972.1|	coactosin-like 1 [Homo sapiens]			1.35E-09	4.06	60.30	31.70	15944.9
AHQ-2-13-, 2218	R.AAYNLVR.D	806.93245	2	5.88E-04	0.91	2.74	-	1110.2
AHQ-2-12, 5966	R.DDGSAVIWVTFK.Y	1338.49001	1	1.11E-05	0.43	2.44	-	488.6
AHQ-2-13, 2244	K.EVVQNFAK.E	935.05900	1	7.76E-05	0.02	2.15	-	87.3
AHQ-2-13-, 2082 - 2151	K.EVVQNFAK.E	935.05900	1	5.43E-05	0.22	2.52	-	138.7
AHQ-2-13, 6737	K.FALITWIGENVSGLQR.A	1805.06986	2	1.35E-09	0.98	6.05	-	2532.9
AHQ-2-12, 7053 - 7058	K.FALITWIGENVSGLQR.A	1805.06986	2	7.15E-05	0.98	5.71	-	2586.2
AHQ-2-12, 2670	R.KELEEDFIK.S	1151.29110	2	4.78E-04	0.80	2.90	-	791.0
AHQ-2-12, 5421 - 5487	K.YDGSTIVPGEQGAEYQHFIQQCTDDVR.L	3116.27790	3	7.61E-08	0.71	3.43	-	385.2
gi|21361322|ref|NP_006078.2|	tubulin, beta, 5 [Homo sapiens]			1.48E-09	2.44	30.25	13.70	49585.5
AHQ-2-7, 2807	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	1.48E-09	0.94	4.15	-	1128.0
AHQ-2-9, 2740	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	7.15E-04	0.72	3.07	-	594.6
AHQ-2-7, 2647	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	1.92E-06	0.95	4.60	-	1160.4
AHQ-2-7, 5359	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	1.88E-04	0.92	5.09	-	918.3
AHQ-2-12, 6459 - 6461	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	2.88E-04	0.53	3.10	-	584.1
AHQ-2-7, 6973	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	5.28E-05	0.59	3.53	-	516.7
gi|13569962|ref|NP_112243.1|	RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap			1.48E-09	3.63	40.33	18.90	22171.0
AHQ-2-11, 4541	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	1.47E-08	0.98	5.49	-	1941.9
AHQ-2-11, 4410 - 4478	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	2.32E-09	0.98	6.51	-	1917.9
AHQ-2-11, 6494 - 6553	K.NATNVEQAFMTMAAEIK.K	1870.14079	2	1.48E-09	0.97	5.24	-	1276.6
AHQ-2-11, 6658	K.NATNVEQAFM*TMAAEIK.K	1886.14019	2	5.74E-06	0.93	5.00	-	1296.8
AHQ-2-11, 6785 - 6786	K.NATNVEQAFMTMAAEIK.K	1870.14079	2	4.04E-08	0.96	4.96	-	1276.9
AHQ-2-11, 5061	K.NATNVEQAFM*TM*AAEIK.K	1902.13959	2	5.46E-06	0.75	3.27	-	845.0
gi|5031593|ref|NP_005708.1|	actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub			1.48E-09	4.55	50.27	30.50	16320.3
AHQ-2-12, 2909	K.ALAAGGVGSIVR.V	1071.25558	2	3.00E-07	0.97	4.75	-	1929.7
AHQ-2-14-, 2939	K.ALAAGGVGSIVR.V	1071.25558	2	1.37E-06	0.95	3.83	-	1610.3
AHQ-2-12, 3542 - 3614	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	2.34E-05	0.85	3.90	-	505.2
AHQ-2-12, 4069 - 4137	K.AVQSLDKNGVDLLMK.Y	1631.91943	2	1.48E-09	0.98	5.45	-	1871.9
AHQ-2-12, 4591	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	1.56E-07	0.93	4.43	-	886.9
AHQ-2-12, 4783 - 4806	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	1.56E-07	0.83	4.11	-	633.3
AHQ-2-12, 4791	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	3	2.10E-04	0.61	3.06	-	368.1
AHQ-2-12, 4271	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	8.56E-05	0.92	4.29	-	758.3
AHQ-2-12, 4174	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	6.80E-06	0.92	3.57	-	1069.9
gi|4504183|ref|NP_000843.1|	glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s			1.61E-09	5.26	60.25	51.90	23355.7
AHQ-2-11, 5268	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	7.61E-09	0.79	3.35	-	514.9
AHQ-2-13, 5331 - 5340	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	4.64E-06	0.62	3.10	-	281.7
AHQ-2-10, 4874	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.67E-07	0.81	3.34	-	454.2
AHQ-2-11, 5142 - 5206	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.86E-05	0.84	3.70	-	337.0
AHQ-2-11, 3020 - 3094	K.ASCLYGQLPK.F	1138.31884	2	9.35E-05	0.91	3.22	-	842.2
AHQ-2-13-, 6558	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	6.54E-06	0.91	3.92	-	1067.8
AHQ-2-11, 6470 - 6478	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	4.91E-08	0.90	4.26	-	706.9
AHQ-2-11, 6272 - 6337	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	6.68E-06	0.95	4.57	-	1067.4

AHQ-2-13, 6363 - 6367	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	3.24E-08	0.94	4.95	-	814.8
AHQ-2-10, 6187	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	7.47E-04	0.90	4.05	-	745.7
AHQ-2-14-, 6441	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	4.43E-06	0.95	4.79	-	894.8
AHQ-2-11, 6041	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	7.20E-04	0.95	4.67	-	1234.1
AHQ-2-11, 4944	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.61E-09	0.91	4.17	-	826.9
AHQ-2-11, 4840	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.21E-08	0.95	5.02	-	753.1
AHQ-2-11, 4720 - 4780	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.08E-04	0.92	4.23	-	800.3
AHQ-2-14-, 4981	K.FQDGDLTLYQSNTILR.H	1885.06701	2	7.81E-04	0.83	3.71	-	547.7
AHQ-2-14, 6062	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.37E-06	0.83	3.51	-	714.6
AHQ-2-10, 4622 - 4688	K.FQDGDLTLYQSNTILR.H	1885.06701	2	3.40E-07	0.94	4.93	-	838.7
AHQ-2-11, 6196 - 6269	R.MLLADQGQSWKEEVVTVETWQEGSLK.A	2993.33745	3	1.26E-05	0.85	4.61	-	665.3
AHQ-2-11, 4546	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	4.12E-04	0.85	3.73	-	618.1
AHQ-2-10, 4183	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	3.32E-07	0.85	3.83	-	621.6
gi|4507645|ref|NP_000356.1| triosephosphate isomerase 1 [Homo sapiens]				1.69E-09	4.58	50.33	32.90	26669.3
AHQ-2-10, 6612	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	1.69E-09	0.76	3.79	-	218.0
AHQ-2-10, 3998	R.KQSLGELIGTLNAAK.V	1543.79037	2	1.02E-05	0.96	4.18	-	1809.5
AHQ-2-10, 3760	R.KQSLGELIGTLNAAK.V	1543.79037	2	1.49E-04	0.94	4.03	-	1169.9
AHQ-2-10, 4852	K.QSLGELIGTLNAAK.V	1415.61746	2	3.27E-04	0.90	3.54	-	1013.1
AHQ-2-10, 4942 - 5022	K.VAHALAEGLGVIACIGEK.L	1810.10800	2	6.70E-06	0.99	6.67	-	3106.5
AHQ-2-10, 5108 - 5175	K.VPADTEVVCAPPTAYIDFAR.Q	2194.44943	2	1.79E-04	0.97	5.42	-	1030.2
gi|4502491|ref|NP_001203.1| complement component 1, q subcomponent binding protein precursor; hyalu				1.72E-09	0.87	10.20	5.00	31362.0
AHQ-2-9, 5352	K.AFVDFLSDEIKEER.K	1698.85455	2	1.72E-09	0.87	3.46	-	951.1
gi|4503423|ref|NP_001939.1| dUTP pyrophosphatase [Homo sapiens]				1.77E-09	0.95	10.22	10.40	17748.0
AHQ-2-11, 5458	R.IFYPEIEEVQALDDTER.G	2068.22598	2	1.77E-09	0.95	4.40	-	1135.5
gi|25188179|ref|NP_005653.3| voltage-dependent anion channel 3 [Homo sapiens]				1.79E-09	2.33	30.21	16.30	30658.4
AHQ-2-10, 4624 - 4648	K.LTLDTIFVPNTGK.K	1419.64771	2	1.92E-05	0.91	3.62	-	848.5
AHQ-2-10, 4619	K.LTLDTIFVPNTGK.K	1419.64771	1	1.04E-05	0.75	2.87	-	583.2
AHQ-2-11, 4856	K.LTLDTIFVPNTGK.K	1419.64771	2	1.32E-05	0.85	3.09	-	820.5
AHQ-2-9, 4154 - 4234	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	1.44E-06	0.88	4.30	-	801.7
AHQ-2-10, 4026 - 4028	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	3	6.38E-06	0.76	3.48	-	664.8
AHQ-2-14, 5690	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	1.52E-08	0.70	3.61	-	447.0
AHQ-2-10, 4410	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.72E-09	0.65	3.38	-	365.4
AHQ-2-10, 4022	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.13E-08	0.87	3.90	-	637.5
AHQ-2-9, 4674 - 4678	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	8.74E-07	0.67	3.14	-	379.9
AHQ-2-10, 4196	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	1.17E-05	0.71	2.93	-	655.1
AHQ-2-9, 3640	K.YKVCNYGLTFTQK.W	1623.85410	2	1.39E-05	0.95	4.14	-	1142.4
AHQ-2-10, 3564	K.YKVCNYGLTFTQK.W	1623.85410	2	1.79E-09	0.93	4.12	-	1006.3
gi|5803181|ref|NP_006810.1| stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo				1.81E-09	0.93	10.23	3.50	62638.9
AHQ-2-6, 6485	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	1.81E-09	0.93	4.38	-	785.9
AHQ-2-14-, 6348	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	8.50E-07	0.92	4.40	-	690.6
AHQ-2-6, 6402 - 6478	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	1.16E-08	0.94	4.64	-	876.8
gi|4503609|ref|NP_001976.1| electron-transfer-flavoprotein, beta polypeptide; electron-transferring				1.86E-09	1.91	20.23	12.50	27843.4
AHQ-2-10, 4776	K.HSMNPFCEIAVEEAVR.L	1891.11834	2	1.86E-09	0.96	4.59	-	1246.2
AHQ-2-10, 4188	K.IEVIKPGDLGVDLTSK.L	1684.95560	2	4.51E-07	0.94	4.12	-	853.0
gi|5031595|ref|NP_005709.1| actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub				1.95E-09	5.17	60.35	42.90	19666.9
AHQ-2-12, 4333	R.AENFFILR.R	1010.17070	2	5.60E-04	0.97	4.18	-	1810.6
AHQ-2-11, 6357	R.ATLQAALCLENFSSQVVER.H	2138.38741	2	1.92E-04	0.41	2.66	-	420.9
AHQ-2-11, 4105	K.ELLLQPVTISR.N	1269.51549	1	7.13E-04	0.44	2.47	-	171.7
AHQ-2-12, 4273 - 4281	K.ELLLQPVTISR.N	1269.51549	2	8.42E-05	0.92	3.90	-	846.6
AHQ-2-11, 5849	R.KPVEGYDISFLITNFHTEQMYK.H	2662.01271	3	5.29E-08	0.98	7.04	-	2055.4
AHQ-2-12, 5741	R.RKPVEGYDISFLITNFHTEQMYK.H	2818.19906	3	1.13E-04	0.97	6.68	-	1510.5
AHQ-2-12, 3191	K.VLIEGSINSVR.V	1187.37134	2	1.95E-09	0.92	3.34	-	1144.0
AHQ-2-12, 3109	K.VLIEGSINSVR.V	1187.37134	2	1.12E-08	0.90	3.07	-	1083.9
AHQ-2-11, 3062	K.VLIEGSINSVR.V	1187.37134	2	2.17E-07	0.93	3.30	-	1153.3
gi|21361198|ref|NP_000286.2| serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei				1.95E-09	1.93	20.27	7.90	46722.2
AHQ-2-7, 3189 - 3263	K.LQHLENELTHDIITK.F	1805.02503	2	1.07E-08	0.97	5.37	-	1650.3
AHQ-2-7, 4543 - 4611	K.VFSNGADLSGVTEEAPLK.L	1835.00476	2	1.95E-09	0.95	4.60	-	1084.0
gi|5031571|ref|NP_005713.1| actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog				2.13E-09	6.88	80.23	24.10	44760.5
AHQ-2-8, 3583 - 3655	K.DLMVGDEASELR.S	1335.46633	2	8.36E-08	0.83	3.13	-	779.1
AHQ-2-8, 2838	R.GYAFNHSADFETVR.M	1614.69943	2	2.13E-09	0.93	3.95	-	1016.1
AHQ-2-8, 3475	K.HIVLSGGSTMYPGLPSR.L	1773.04967	2	2.83E-04	0.97	4.58	-	1584.6
AHQ-2-8, 3794	K.HLWDYTFGPEK.L	1393.52736	2	1.99E-06	0.90	3.68	-	626.8
AHQ-2-8, 3796 - 3798	K.HLWDYTFGPEK.L	1393.52736	1	4.64E-04	0.68	2.80	-	672.5
AHQ-2-8, 2544	R.KVVVCDNGTGFVK.C	1424.64764	2	1.39E-04	0.89	3.64	-	960.7
AHQ-2-8, 3642	K.LCYVGYNIEQEQK.L	1645.81494	2	3.38E-07	0.96	3.77	-	1514.5
AHQ-2-8, 4809	R.SMLEVNYPMENGIVR.N	1753.03703	2	4.61E-05	0.79	3.21	-	553.8
AHQ-2-8, 3004	K.VVVCDNGTGFVK.C	1296.47472	2	1.79E-06	0.61	2.61	-	384.5
gi|13518026|ref|NP_004978.2| LIM and senescent cell antigen-like domains 1 [Homo sapiens]				2.17E-09	1.92	20.24	7.70	37251.2
AHQ-2-8, 4164 - 4166	K.CHAIIDEQPLIFK.N	1585.84900	2	7.63E-09	0.94	4.78	-	1060.0
AHQ-2-11, 4361	K.CHAIIDEQPLIFK.N	1585.84900	2	1.07E-04	0.94	4.07	-	1381.5
AHQ-2-9, 4358 - 4370	K.CHAIIDEQPLIFK.N	1585.84900	2	5.58E-05	0.94	4.20	-	1282.1
AHQ-2-10, 4112	K.CHAIIDEQPLIFK.N	1585.84900	2	6.97E-05	0.96	4.67	-	1390.6
AHQ-2-8, 3111 - 3127	R.VIEGDVVSALNK.A	1244.41966	2	1.81E-08	0.96	4.15	-	1286.9
AHQ-2-11, 3384	R.VIEGDVVSALNK.A	1244.41966	2	2.91E-07	0.95	4.12	-	1206.5
AHQ-2-9, 3295	R.VIEGDVVSALNK.A	1244.41966	1	2.45E-05	0.41	2.82	-	328.1
AHQ-2-9, 3286	R.VIEGDVVSALNK.A	1244.41966	2	6.40E-09	0.96	4.49	-	1343.3
AHQ-2-13-, 3498 - 3575	R.VIEGDVVSALNK.A	1244.41966	2	1.39E-08	0.96	4.48	-	1193.7
AHQ-2-14-, 3521	R.VIEGDVVSALNK.A	1244.41966	2	2.17E-09	0.97	4.85	-	1680.5
gi|4503747|ref|NP_001448.1| filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a				2.33E-09	4.75	60.26	1.70	278191.4
AHQ-2-2, 3712	K.DLAEDAPWK.K	1045.12708	2	5.07E-04	0.89	3.43	-	909.8
AHQ-2-1, 3737 - 3738	K.DLAEDAPWK.K	1045.12708	2	3.03E-04	0.87	3.38	-	753.3
AHQ-2-3, 3648	K.DLAEDAPWK.K	1045.12708	1	4.43E-05	0.49	2.01	-	662.8
AHQ-2-5, 3445	K.DLAEDAPWK.K	1045.12708	1	3.24E-06	0.31	2.07	-	502.8
AHQ-2-4, 3650	K.DLAEDAPWK.K	1045.12708	1	1.15E-04	0.29	2.00	-	483.0
AHQ-2-2, 3706	K.DLAEDAPWK.K	1045.12708	1	1.17E-05	0.48	2.44	-	501.1
AHQ-2-2, 2896	K.DLAEDAPWKK.I	1173.29999	2	1.89E-04	0.76	2.88	-	882.0
AHQ-2-1, 3084 - 3085	K.DLAEDAPWKK.I	1173.29999	2	6.35E-04	0.57	2.78	-	669.4
AHQ-2-11, 6024	R.LIALLEVLSQK.R	1227.51852	2	5.68E-08	0.96	4.87	-	1046.3
AHQ-2-1, 6657 - 6658	R.LIALLEVLSQK.R	1227.51852	2	9.63E-07	0.97	4.54	-	1545.7
AHQ-2-6, 6281	R.LIALLEVLSQK.R	1227.51852	2	2.33E-09	0.98	4.98	-	1723.2
AHQ-2-3, 6616	R.LIALLEVLSQK.R	1227.51852	2	3.98E-06	0.97	4.68	-	1499.8
AHQ-2-2, 6604 - 6672	R.LIALLEVLSQK.R	1227.51852	2	2.03E-06	0.97	4.36	-	1375.1
AHQ-2-5, 6311 - 6381	R.LIALLEVLSQK.R	1227.51852	2	8.01E-07	0.97	5.15	-	1280.1
AHQ-2-4, 6672 - 6680	R.LIALLEVLSQK.R	1227.51852	2	1.02E-08	0.97	4.82	-	1341.0
AHQ-2-2, 3596 - 3604	R.LLGWIQNK.I	972.16560	2	4.22E-04	0.85	3.30	-	655.5
AHQ-2-1, 6653	R.QM*QLENVSVALEFLDR.E	1909.15348	2	1.81E-08	0.94	4.34	-	1311.5
AHQ-2-2, 6757 - 6829	R.QM*QLENVSVALEFLDR.E	1909.15348	2	5.37E-04	0.92	3.97	-	848.4
AHQ-2-2, 7380	R.QMQLENVSVALEFLDR.E	1893.15408	2	1.53E-04	0.91	3.88	-	899.6
gi|4507725|ref|NP_000362.1| transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum				2.35E-09	3.75	40.33	36.70	15886.9
AHQ-2-13-, 3870	K.AADDTWEPFASGK.T	1395.45529	2	6.74E-09	0.92	4.12	-	782.3
AHQ-2-13, 3839	K.AADDTWEPFASGK.T	1395.45529	2	4.75E-08	0.92	3.51	-	1055.7
AHQ-2-12, 3729	K.AADDTWEPFASGK.T	1395.45529	2	5.74E-06	0.67	2.85	-	498.2
AHQ-2-13-, 4067 - 4075	R.GSPAINVAVHVFR.K	1367.58095	2	1.58E-08	0.96	4.54	-	1439.9
AHQ-2-13, 4013 - 4016	R.GSPAINVAVHVFR.K	1367.58095	2	8.33E-09	0.96	4.52	-	1246.1
AHQ-2-13, 5460	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	1.31E-07	0.92	4.43	-	808.0
AHQ-2-13-, 5601 - 5603	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	3.47E-09	0.98	6.56	-	2523.4
AHQ-2-12, 5577	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	2.96E-07	0.93	4.33	-	889.4

AHQ-2-13, 5453	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	6.79E-04	0.85	3.15	-	1568.8
AHQ-2-12, 5582	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	2.35E-09	0.97	5.79	-	1797.4
AHQ-2-13-, 5609 - 5677	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	1.73E-06	0.97	5.35	-	1514.5
AHQ-2-13, 6384	K.TSESGELHGLTTEEEFVEGIYKVEIDTK.S	3142.37019	3	9.96E-06	0.90	4.91	-	536.6
gi|4758442|ref|NP_004115.1|	glia maturation factor, beta [Homo sapiens]			2.36E-09	1.76	20.25	35.20	16713.1
AHQ-2-12, 6218 - 6291	R.LVVLDEELEGISPDELKDELPER.Q	2638.90589	3	1.05E-05	0.93	4.90	-	1095.0
AHQ-2-12, 6865 - 6931	R.VSYPLCFIFSSPVGCKPEQQMMYAGSK.N	3115.61257	3	2.36E-09	0.84	4.16	-	414.2
gi|5453832|ref|NP_006380.1|	oxygen regulated protein precursor; oxygen regulated protein (150kD) [H			2.38E-09	2.85	30.31	5.30	111334.8
AHQ-2-3, 6405	K.NINADEAAAMGAVYQAAALSK.A	2080.30817	2	6.59E-07	0.97	6.28	-	958.8
AHQ-2-3, 6861	R.VEFEELCADLFER.V	1658.81048	2	2.38E-09	0.95	4.19	-	1139.5
AHQ-2-3, 6768	K.VLQLINDNTATALSYGVFR.R	2096.37206	2	1.85E-07	0.93	3.69	-	1051.9
gi|4503631|ref|NP_000120.1|	coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,			2.60E-09	17.27	210.27	32.50	83232.8
AHQ-2-5, 5539 - 5616	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	1.80E-08	0.70	3.38	-	224.7
AHQ-2-5, 5399 - 5471	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	1.31E-07	0.59	2.89	-	228.8
AHQ-2-5, 2095 - 2096	R.CGPASVQAIK.H	1032.19627	2	2.81E-04	0.87	3.08	-	853.9
AHQ-2-6, 2386	R.CLGIPAR.I	787.95073	1	2.80E-04	0.43	2.19	-	209.2
AHQ-2-5, 2305	K.DGTHVVENVDATHIGK.L	1692.81163	2	2.60E-09	0.94	4.08	-	1144.1
AHQ-2-6, 2321	K.DGTHVVENVDATHIGK.L	1692.81163	2	9.02E-09	0.95	3.86	-	1388.1
AHQ-2-9, 2372	K.DGTHVVENVDATHIGK.L	1692.81163	2	4.89E-05	0.93	4.12	-	1021.3
AHQ-2-11, 4216	R.EIRPNSTVQWEEVCRPWVSGHR.K	2724.99524	3	1.36E-04	0.59	3.27	-	338.1
AHQ-2-5, 4445	R.EIRPNSTVQWEEVCRPWVSGHR.K	2724.99524	3	2.81E-04	0.78	3.29	-	652.6
AHQ-2-5, 4175	R.EIRPNSTVQWEEVCRPWVSGHR.K	2724.99524	3	9.59E-04	0.89	4.36	-	681.5
AHQ-2-11, 5493 - 5509	K.ETFDVTLEPLSFK.K	1526.71190	2	4.88E-06	0.90	3.67	-	853.1
AHQ-2-6, 5669 - 5677	K.ETFDVTLEPLSFK.K	1526.71190	2	2.11E-06	0.82	3.05	-	762.1
AHQ-2-5, 5751 - 5823	K.ETFDVTLEPLSFK.K	1526.71190	2	2.24E-08	0.89	3.78	-	836.9
AHQ-2-5, 4817	K.ETFDVTLEPLSFKK.E	1654.88482	2	4.26E-04	0.37	2.69	-	349.5
AHQ-2-7, 5391 - 5441	K.GTYIPVPIVSELQSGK.W	1688.94594	2	6.42E-06	0.65	3.19	-	263.4
AHQ-2-9, 5463 - 5478	K.GTYIPVPIVSELQSGK.W	1688.94594	2	3.93E-05	0.81	3.54	-	391.5
AHQ-2-5, 5523 - 5543	K.GTYIPVPIVSELQSGK.W	1688.94594	2	5.94E-04	0.86	3.64	-	493.7
AHQ-2-9, 7063	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	6.26E-08	0.95	4.41	-	1357.5
AHQ-2-9, 7076	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	1.56E-07	0.85	4.03	-	703.9
AHQ-2-10, 6495 - 6575	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.82E-05	0.91	4.32	-	861.5
AHQ-2-8, 6844	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.09E-06	0.94	4.34	-	1150.5
AHQ-2-7, 7036	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	7.74E-08	0.97	5.02	-	1522.6
AHQ-2-5, 7108 - 7125	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	8.75E-08	0.95	5.00	-	1085.3
AHQ-2-5, 7127 - 7164	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	8.27E-08	0.88	3.90	-	900.5
AHQ-2-5, 7191 - 7256	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.23E-08	0.96	4.60	-	1379.8
AHQ-2-5, 7324	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.91E-07	0.94	4.88	-	838.0
AHQ-2-14-, 6755	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	9.58E-07	0.96	5.00	-	1300.6
AHQ-2-11, 6565	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.35E-07	0.97	5.04	-	1431.3
AHQ-2-13, 6673	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.79E-08	0.97	5.24	-	1310.8
AHQ-2-13-, 6901	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.41E-07	0.97	4.48	-	1590.0
AHQ-2-6, 6989	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	3.16E-09	0.89	4.24	-	731.3
AHQ-2-2, 7437	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.18E-06	0.90	3.86	-	882.3
AHQ-2-6, 6978	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	8.78E-07	0.95	4.70	-	1107.0
AHQ-2-5, 3833	R.HVYGELDVQIQR.R	1457.61612	2	5.54E-05	0.80	2.93	-	573.2
AHQ-2-6, 1917	K.KDGTHVVENVDATHIGK.L	1820.98455	2	9.20E-08	0.95	4.50	-	1362.3
AHQ-2-5, 2100	K.KDGTHVVENVDATHIGK.L	1820.98455	3	6.44E-06	0.95	4.86	-	1605.4
AHQ-2-5, 1903	K.KDGTHVVENVDATHIGK.L	1820.98455	2	2.89E-07	0.96	4.18	-	1656.0
AHQ-2-5, 2367	R.KLIASMSSDSLR.H	1308.53039	2	3.36E-09	0.96	4.23	-	1420.7
AHQ-2-6, 4510 - 4527	R.LALETALMYGAK.K	1281.54655	2	9.69E-07	0.97	4.04	-	1762.9
AHQ-2-5, 2749 - 2829	K.LIASMSSDSLR.H	1180.35748	2	2.45E-05	0.95	3.80	-	1196.8
AHQ-2-5, 5473	R.M*YVAVWTPYGVLR.T	1571.86734	2	1.03E-05	0.97	5.12	-	1150.7
AHQ-2-5, 6093 - 6160	R.MYVAVWTPYGVLR.T	1555.86794	2	1.07E-06	0.95	4.34	-	998.6
AHQ-2-6, 5441 - 5446	R.M*YVAVWTPYGVLR.T	1571.86734	2	2.13E-04	0.93	3.58	-	944.9
AHQ-2-6, 6046 - 6053	R.MYVAVWTPYGVLR.T	1555.86794	2	3.04E-08	0.95	4.10	-	1100.7
AHQ-2-7, 6725	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	4.37E-04	0.70	3.07	-	868.5
AHQ-2-5, 6979	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	4.62E-07	0.88	4.22	-	564.7
AHQ-2-5, 6819	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	9.09E-09	0.94	5.48	-	841.5
AHQ-2-5, 3329 - 3332	R.NVWVHLDGPGVTR.P	1450.62682	2	3.15E-04	0.68	2.63	-	817.2
AHQ-2-5, 3297	R.NVWVHLDGPGVTRPMK.K	1807.11248	2	8.39E-06	0.94	4.56	-	883.5
AHQ-2-5, 4637	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.27E-08	0.96	4.62	-	1715.2
AHQ-2-11, 5486	K.STVLTIPEIIIK.V	1327.63485	2	1.93E-07	0.89	3.38	-	1142.7
AHQ-2-9, 5580	K.STVLTIPEIIIK.V	1327.63485	2	5.16E-04	0.83	2.81	-	1157.5
AHQ-2-8, 5275	K.STVLTIPEIIIK.V	1327.63485	2	8.06E-04	0.92	3.52	-	1290.3
gi|15147250|ref|NP_150281.1|	protein phosphatase 1, regulatory (inhibitor) subunit 14A; 17-kDa PKC-			2.66E-09	0.85	10.23	10.90	16692.9
AHQ-2-12, 6919	K.SCGKPVEDFIQELLAK.L	1836.09909	2	2.66E-09	0.85	4.55	-	503.4
gi|4505989|ref|NP_000299.1|	protective protein for beta-galactosidase; Protective protein for beta-			2.68E-09	1.73	20.21	6.90	54495.8
AHQ-2-10, 5068	K.CNFYDNKDLECVTNLQEVAR.I	2491.69642	2	1.54E-05	0.75	2.77	-	873.4
AHQ-2-12, 3494 - 3507	K.YGDSGEQIAGFVK.E	1371.47686	2	2.68E-09	0.98	4.14	-	2739.3
AHQ-2-11, 3400	K.YGDSGEQIAGFVK.E	1371.47686	2	5.32E-06	0.97	3.97	-	2410.8
gi|5803227|ref|NP_006817.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype			2.68E-09	3.63	40.26	23.30	27764.1
AHQ-2-12, 2210	K.AVTEQGAELSNEER.N	1533.57979	2	2.18E-06	0.80	3.48	-	721.0
AHQ-2-10, 2086	K.AVTEQGAELSNEER.N	1533.57979	2	2.68E-09	0.96	5.02	-	1292.1
AHQ-2-10, 6663	R.SICTTVLELLDK.Y	1393.62862	2	9.15E-09	0.94	4.46	-	878.8
AHQ-2-10, 6411	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	1.47E-08	0.96	5.15	-	1365.0
AHQ-2-14-, 6664	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	5.89E-07	0.94	4.81	-	834.4
AHQ-2-10, 2574	K.YLIANATNPESK.V	1321.46099	1	3.53E-09	0.77	2.61	-	808.5
AHQ-2-10, 2435	K.YLIANATNPESK.V	1321.46099	2	5.57E-06	0.96	3.79	-	1723.0
gi|13489087|ref|NP_109591.1|	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member			2.69E-09	1.78	20.20	8.70	42741.5
AHQ-2-9, 3892	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	1.36E-07	0.89	3.27	-	942.9
AHQ-2-11, 3896	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	2.69E-09	0.92	4.01	-	858.7
AHQ-2-13, 4051	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	1.12E-06	0.77	3.15	-	275.1
AHQ-2-13-, 4107	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	3.87E-06	0.72	3.41	-	374.8
AHQ-2-8, 3758	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	2.57E-05	0.79	3.18	-	648.5
AHQ-2-13, 6133	K.TYNFLPEFLVSTQK.T	1687.91650	2	7.49E-06	0.86	3.74	-	453.3
gi|7706497|ref|NP_057392.1|	UMP-CMP kinase [Homo sapiens]			2.77E-09	2.82	30.27	20.20	25854.7
AHQ-2-11, 5953	R.IQTYLQSTKPIIDLYEEMGK.V	2371.73502	3	4.54E-04	0.74	3.32	-	695.6
AHQ-2-11, 5948 - 5949	R.IQTYLQSTKPIIDLYEEMGK.V	2371.73502	2	4.30E-07	0.96	5.46	-	802.4
AHQ-2-11, 2501	R.KNPDSQYGELIEK.Y	1521.65375	2	8.97E-05	0.89	3.62	-	914.1
AHQ-2-11, 3649	K.YGYTHLSAGELLR.D	1480.64969	2	2.77E-09	0.96	4.02	-	1673.1
gi|4507951|ref|NP_003396.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept			2.81E-09	5.31	60.22	34.10	28218.5
AHQ-2-13-, 2958	K.AVTELNEPLSNEDR.N	1587.67060	2	1.01E-08	0.89	3.89	-	643.0
AHQ-2-13, 3007	K.AVTELNEPLSNEDR.N	1587.67060	2	6.02E-09	0.93	4.12	-	781.8
AHQ-2-10, 2694	K.AVTELNEPLSNEDR.N	1587.67060	2	6.80E-06	0.94	4.38	-	895.1
AHQ-2-10, 6622	K.ELETVCNDVLSLLDK.F	1749.96137	2	4.48E-06	0.75	3.54	-	513.8
AHQ-2-13, 6708	K.ELETVCNDVLSLLDK.F	1749.96137	2	9.89E-09	0.89	3.97	-	670.6
AHQ-2-14-, 6784	K.ELETVCNDVLSLLDK.F	1749.96137	2	4.26E-07	0.91	4.05	-	706.6
AHQ-2-14-, 5981	K.ELETVCNDVLSLLDK.F	1749.96137	2	5.70E-07	0.86	3.50	-	564.0
AHQ-2-10, 3888	K.FLIKNCNDFQYESK.V	1808.00430	2	5.40E-04	0.89	3.60	-	787.8
AHQ-2-10, 2556	K.NSVVEASEAAYK.E	1268.35495	1	4.48E-04	0.51	2.02	-	528.8
AHQ-2-10, 2350	K.NSVVEASEAAYK.E	1268.35495	2	2.81E-09	0.95	4.26	-	1021.8
AHQ-2-10, 2346 - 2354	K.NSVVEASEAAYK.E	1268.35495	1	1.37E-04	0.20	2.01	-	276.5
AHQ-2-10, 2772	K.NSVVEASEAAYK.E	1268.35495	1	3.29E-04	0.21	2.17	-	253.0
AHQ-2-14-, 6113	K.QAFDDAIAELDTLNEDSYK.D	2159.24915	2	3.04E-05	0.75	3.26	-	511.2
AHQ-2-10, 5846	K.QAFDDAIAELDTLNEDSYK.D	2159.24915	2	7.58E-07	0.80	3.88	-	421.2
AHQ-2-10, 1979	R.YLAEVASGEK.K	1067.17419	1	8.14E-06	0.74	3.00	-	512.6

AHQ-2-10, 1986	R.YLAEVASGEK.K	1067.17419	2	4.22E-06	0.86	3.15	-	945.5
gi|4502695|ref|NP_001779.1| cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c				2.94E-09	2.45	30.25	13.60	48786.6
AHQ-2-8, 3708	K.IYEFPETDDEEENKLVK.K	2099.23685	2	2.69E-04	0.71	3.33	-	348.7
AHQ-2-13, 5393	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	8.38E-05	0.91	4.21	-	729.8
AHQ-2-14-, 5393 - 5465	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	4.93E-07	0.91	3.92	-	882.7
AHQ-2-13-, 5494	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	4.25E-07	0.95	4.87	-	977.2
AHQ-2-8, 5220	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	1.82E-08	0.95	5.08	-	1086.5
AHQ-2-14-, 6299	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	3.33E-09	0.63	3.08	-	315.8
AHQ-2-14-, 6531	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	2.94E-09	0.78	3.35	-	629.2
AHQ-2-13, 6468	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	7.05E-04	0.53	3.13	-	453.2
gi|6912638|ref|NP_036557.1| ras suppressor protein 1 [Homo sapiens]				2.97E-09	6.21	80.29	48.70	31540.1
AHQ-2-12, 7181 - 7185	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	7.70E-08	0.81	3.69	-	503.4
AHQ-2-10, 5900 - 5958	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	2.06E-07	0.95	4.89	-	587.5
AHQ-2-10, 6010 - 6071	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	2.97E-09	0.87	4.03	-	464.7
AHQ-2-10, 1474 - 1536	K.ELHIQGNR.L	967.06432	1	2.08E-04	0.17	2.48	-	136.0
AHQ-2-14-, 6877	R.GISNM*LDVNGLFTLSHITQLVLSHNK.L	2869.28903	3	5.83E-04	0.80	3.73	-	708.7
AHQ-2-10, 6754	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	2	4.42E-08	0.82	3.89	-	314.6
AHQ-2-10, 5507 - 5576	K.LQILSLRDNDLISLPK.E	1839.16919	2	6.16E-08	0.95	5.06	-	1562.1
AHQ-2-10, 5408 - 5431	K.LQILSLRDNDLISLPK.E	1839.16919	2	3.78E-09	0.95	4.93	-	1538.4
AHQ-2-10, 5536 - 5598	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	5.70E-06	0.94	4.46	-	768.4
AHQ-2-11, 5669 - 5728	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	8.69E-07	0.91	4.17	-	602.1
AHQ-2-10, 5594	R.LTVLPPELGNLDLTGQK.Q	1809.09672	3	8.03E-07	0.96	5.83	-	1156.0
AHQ-2-10, 5658 - 5727	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	3.96E-05	0.92	4.06	-	595.6
AHQ-2-12, 6013 - 6078	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	2.83E-07	0.88	3.68	-	551.5
AHQ-2-14-, 5896 - 5969	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	2.29E-04	0.87	4.01	-	456.6
AHQ-2-11, 6764 - 6766	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	2	7.80E-09	0.90	4.60	-	606.0
AHQ-2-14-, 6873 - 6943	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	3	3.33E-05	0.90	5.00	-	550.1
AHQ-2-10, 6648 - 6719	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	2	4.99E-08	0.87	4.48	-	390.3
gi|21735621|ref|NP_005909.2| mitochondrial malate dehydrogenase precursor [Homo sapiens]				3.20E-09	5.00	60.27	32.50	35503.0
AHQ-2-9, 6462 - 6482	K.GYLGPEQLPDCLKGCDVVVIPAGVPR.K	2813.24211	3	6.91E-04	0.78	4.06	-	512.2
AHQ-2-9, 6467	K.GYLGPEQLPDCLKGCDVVVIPAGVPR.K	2813.24211	2	2.25E-07	0.90	4.69	-	376.8
AHQ-2-13, 6123	K.GYLGPEQLPDCLKGCDVVVIPAGVPR.K	2813.24211	3	2.36E-04	0.63	3.35	-	493.8
AHQ-2-9, 5560	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	3	7.56E-09	0.96	5.49	-	1424.9
AHQ-2-9, 5554	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	2	2.96E-06	0.56	2.76	-	324.9
AHQ-2-11, 5389	K.SQETECTYFSTPLLLGK.K	1976.19328	2	1.18E-07	0.96	4.84	-	1112.4
AHQ-2-9, 5527	K.SQETECTYFSTPLLLGK.K	1976.19328	2	2.54E-04	0.92	3.81	-	1117.7
AHQ-2-9, 6779 - 6782	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	2.05E-04	0.96	5.35	-	1036.2
AHQ-2-9, 4986	K.VDFPQDQLTALTGR.I	1561.72111	2	3.20E-09	0.81	2.75	-	963.7
AHQ-2-9, 2284	R.VNVPVIGGHAGK.T	1148.34004	1	1.80E-05	0.42	2.29	-	429.5
gi|4557675|ref|NP_000201.1| integrin alpha chain, alpha 6 [Homo sapiens]				3.26E-09	3.35	40.26	5.00	119509.5
AHQ-2-4, 6025	K.DFHYIVFGAPGTYNWK.G	1916.12609	2	1.46E-07	0.97	4.84	-	1538.9
AHQ-2-4, 3456 - 3464	K.FGSCQQGVAATFTK.D	1503.66172	2	3.26E-09	0.95	4.01	-	1212.9
AHQ-2-4, 3574	K.FSYLPIQK.G	996.18393	1	4.58E-04	0.50	2.07	-	645.5
AHQ-2-4, 4912	R.IEDDMDGGDWSFCDGR.L	1876.91588	2	2.01E-04	0.94	3.56	-	1452.9
gi|18860900|ref|NP_002834.2| protein tyrosine phosphatase, receptor type, J precursor; protein tyro				3.30E-09	13.37	150.25	16.60	145926.2
AHQ-2-1, 3505	R.AGSPTAPVHDESLVGPVDPSSGQQSR.D	2576.71806	2	2.67E-07	0.84	3.53	-	557.1
AHQ-2-1, 5976 - 5993	K.AVSISPTNVILTWK.S	1529.80530	2	3.04E-04	0.88	3.33	-	674.0
AHQ-2-1, 4476	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	3	3.30E-09	0.97	5.01	-	1831.7
AHQ-2-1, 5108	R.DTEVLLVGLEPGTR.Y	1499.69122	2	8.77E-04	0.65	2.86	-	632.5
AHQ-2-1, 2813 - 2820	K.FSGFEASHGPIK.A	1277.40990	2	4.32E-07	0.90	3.51	-	851.6
AHQ-2-1, 5366	K.GLIDGAESYVSFSR.Y	1501.62253	2	6.77E-09	0.88	3.18	-	1159.7
AHQ-2-1, 4885	K.GLIDGAESYVSFSR.Y	1501.62253	2	3.07E-07	0.89	3.31	-	973.2
AHQ-2-1, 3977	K.KDFIATQGPLPNTLK.D	1643.90840	2	6.03E-06	0.95	4.23	-	1403.7
AHQ-2-1, 5041	K.SFCTDPASM*ASFDCEVVPK.E	2167.37954	2	5.68E-05	0.94	4.27	-	942.1
AHQ-2-1, 5890	K.SFCTDPASMASFDCEVVPK.E	2151.38014	2	7.96E-04	0.87	3.72	-	631.6
AHQ-2-1, 5468	K.SPDGASEYVYHLVIESK.H	1895.05866	2	1.21E-08	0.95	4.79	-	1153.7
AHQ-2-1, 2754	K.TKGDPLGTEGGLDASNTER.S	1918.99702	2	7.65E-07	0.93	4.48	-	847.6
AHQ-2-1, 3741	K.TPSSTGPSPVFDIK.A	1433.58810	2	7.44E-05	0.87	3.15	-	1000.3
AHQ-2-1, 4560	R.VENFEAYFK.K	1147.26100	2	1.33E-05	0.93	3.93	-	748.8
AHQ-2-1, 4384	K.VITEPIPVSDLR.V	1339.56259	2	2.17E-05	0.87	3.50	-	623.1
AHQ-2-1, 3920	R.VLLESIGSHEELTQDSR.L	1914.06352	2	5.68E-09	0.93	4.35	-	883.5
AHQ-2-1, 3926	R.VLLESIGSHEELTQDSR.L	1914.06352	3	2.66E-06	0.92	4.18	-	971.2
AHQ-2-1, 4004	R.VLLESIGSHEELTQDSR.L	1914.06352	2	7.15E-04	0.77	3.03	-	670.9
gi|8922673|ref|NP_060692.1| parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]				3.31E-09	1.74	20.21	5.60	42243.4
AHQ-2-13, 4647 - 4725	R.DAFDTLFDHAPDK.L	1492.57096	2	1.92E-07	0.94	4.02	-	1067.2
AHQ-2-9, 4519	R.DAFDTLFDHAPDK.L	1492.57096	2	3.31E-09	0.96	4.27	-	1422.8
AHQ-2-9, 4526	R.DAFDTLFDHAPDK.L	1492.57096	1	3.11E-08	0.87	3.79	-	592.3
AHQ-2-13-, 4726	R.DAFDTLFDHAPDK.L	1492.57096	2	6.42E-09	0.95	4.06	-	1520.2
AHQ-2-13-, 4190	R.VLYNLFTK.Y	998.19983	2	2.95E-04	0.81	2.80	-	463.5
AHQ-2-9, 3854	R.VLYNLFTK.Y	998.19983	1	3.65E-04	0.34	2.32	-	397.2
AHQ-2-9, 3718	R.VLYNLFTK.Y	998.19983	2	3.22E-05	0.78	2.69	-	435.9
gi|4504743|ref|NP_002194.1| integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o				3.44E-09	3.96	50.24	7.40	129294.4
AHQ-2-3, 4661	K.EKNPLMYLTGVQTDK.A	1737.99886	2	1.03E-04	0.36	2.66	-	317.5
AHQ-2-3, 6851	K.GNWLLVGSPWSGFPENR.M	1917.11562	2	1.27E-04	0.91	4.22	-	662.3
AHQ-2-4, 4876	K.KGILGQHQFLEGPEGIENTR.F	2224.46193	2	1.73E-06	0.95	4.81	-	813.3
AHQ-2-3, 3312	K.TQVGLIQYANNPR.V	1474.64668	2	9.58E-06	0.90	3.03	-	1303.8
AHQ-2-4, 5304	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	3.44E-09	0.84	3.41	-	698.3
AHQ-2-3, 5288	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	1.91E-04	0.92	4.17	-	803.3
gi|4507143|ref|NP_003786.1| sorting nexin 3 isoform a; sorting nexin 3A [Homo sapiens]				3.70E-09	1.86	20.22	16.70	18762.2
AHQ-2-12, 4594	R.CLHM*FLQDEIIDK.S	1679.93944	2	3.39E-04	0.91	3.73	-	1259.3
AHQ-2-12, 5117 - 5119	R.GDDGIFDDNFIEER.K	1642.66158	2	3.70E-09	0.95	4.49	-	1081.3
gi|20070156|ref|NP_003565.2| vessicle-associated membrane protein (VAMP)-associated protein of 33 k				3.76E-09	1.86	20.19	5.80	27317.4
AHQ-2-12, 4267	K.FKGPFTDVVTTNLK.L	1567.81039	2	3.75E-04	0.91	3.42	-	1070.1
AHQ-2-12, 4098 - 4105	K.GPFTDVVTTNLK.L	1292.46278	2	3.76E-09	0.95	3.82	-	1561.4
gi|14149734|ref|NP_065174.1| coronin, actin binding protein, 1B [Homo sapiens]				4.17E-09	0.95	10.27	5.90	54234.4
AHQ-2-7, 7101	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	2.70E-07	0.93	4.82	-	1011.5
AHQ-2-6, 6967 - 6986	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	4.17E-09	0.95	5.49	-	1226.1
gi|29727565|ref|XP_291384.1| similar to Cytochrome c, somatic [Homo sapiens]				4.20E-09	3.62	40.29	17.10	11621.4
AHQ-2-13, 6344 - 6423	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	1.53E-04	0.96	4.41	-	1645.1
AHQ-2-13-, 6946	K.GIIWGEDTLMEYLENPK.K	2009.26831	2	7.59E-07	0.97	5.77	-	1792.2
AHQ-2-13-, 6746	K.GIIWGEDTLMEYLENPKK.Y	2137.44123	2	4.20E-09	0.97	4.82	-	1492.7
AHQ-2-13-, 6751	K.GIIWGEDTLMEYLENPKK.Y	2137.44123	3	2.39E-07	0.72	3.20	-	439.7
AHQ-2-13, 6523	K.GIIWGEDTLMEYLENPKK.Y	2137.44123	2	6.39E-05	0.92	4.22	-	754.6
AHQ-2-13, 5981	K.GIIWGEDTLM*EYLENPKK.Y	2153.44063	2	3.23E-06	0.72	3.34	-	501.0
gi|7657486|ref|NP_055217.1| low molecular mass ubiquinone-binding protein [Homo sapiens]				4.55E-09	0.95	10.21	14.00	11316.3
AHQ-2-14-, 3871	R.HVISYSLSPFEQR.A	1563.73870	2	4.55E-09	0.95	4.25	-	1067.1
gi|4502013|ref|NP_001616.1| adenylate kinase 2 isoform a; adenylate kinase, mitochondrial; adenylat				4.76E-09	3.65	40.29	34.70	26477.6
AHQ-2-10, 6814 - 6815	R.GIHSAIDASQTPDVVFASILAAFSK.A	2546.85974	2	3.09E-04	0.97	5.81	-	1435.4
AHQ-2-10, 3632	R.LQAYHTQTTPLIEYYR.K	1998.22695	3	2.22E-06	0.61	3.42	-	666.3
AHQ-2-10, 3618	R.LQAYHTQTTPLIEYYR.K	1998.22695	2	7.51E-08	0.97	5.25	-	1724.3
AHQ-2-10, 5670	K.NLETPLCKNGFLLDGFPR.T	2093.39146	2	4.76E-09	0.82	3.29	-	653.0
AHQ-2-10, 3807	R.SYHEEFNPPKEPMKDDITGEPLIR.R	2844.14855	2	5.43E-04	0.89	3.66	-	736.3
gi|29742827|ref|XP_294099.1| similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]				5.08E-09	2.63	30.22	14.20	17094.0
AHQ-2-11, 2890	K.EAFNM*IDQNR.D	1254.35498	2	3.93E-04	0.82	3.20	-	710.8
AHQ-2-11, 2828 - 2882	K.EAFNMIDQNR.D	1238.35558	2	1.34E-04	0.84	3.44	-	700.7
AHQ-2-12, 2927 - 2935	K.EAFNMIDQNR.D	1238.35558	2	8.03E-04	0.68	2.73	-	663.2
AHQ-2-10, 3639	R.FTDEEVDELYR.E	1416.47127	1	3.43E-06	0.39	2.00	-	441.8

AHQ-2-11, 3636 - 3712	R.FTDEEVDELYR.E	1416.47127	2	2.18E-08	0.97	4.37	-	1989.9
AHQ-2-11, 3716 - 3780	R.FTDEEVDELYR.E	1416.47127	1	4.48E-07	0.32	1.89	-	491.8
AHQ-2-11, 3722 - 3784	R.FTDEEVDELYR.E	1416.47127	1	1.50E-08	0.42	2.32	-	369.8
AHQ-2-11, 3792	R.FTDEEVDELYR.E	1416.47127	2	5.08E-09	0.97	4.44	-	1794.9
AHQ-2-10, 3630	R.FTDEEVDELYR.E	1416.47127	2	3.12E-04	0.92	3.51	-	802.0
AHQ-2-12, 3849 - 3850	R.FTDEEVDELYR.E	1416.47127	2	4.78E-07	0.96	4.19	-	1563.1
AHQ-2-13, 3828 - 3899	R.FTDEEVDELYR.E	1416.47127	2	5.51E-06	0.93	2.92	-	1580.2
AHQ-2-14, 4754	R.FTDEEVDELYR.E	1416.47127	2	7.07E-09	0.96	3.99	-	1625.0
AHQ-2-13-, 3937 - 3942	R.FTDEEVDELYR.E	1416.47127	2	1.23E-07	0.97	3.99	-	1896.2
AHQ-2-14-, 3839	R.FTDEEVDELYR.E	1416.47127	2	4.85E-07	0.96	4.02	-	1469.3
AHQ-2-14-, 3845	R.FTDEEVDELYR.E	1416.47127	1	7.34E-07	0.29	1.94	-	283.7
gi|9966825|ref|NP_065089.1| HEF like Protein [Homo sapiens]				5.08E-09	1.89	20.28	4.30	86696.2
AHQ-2-13-, 4233	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	1.75E-07	0.97	5.50	-	1530.1
AHQ-2-13-, 3454	K.LVDTLCMETQER.D	1496.68930	2	5.08E-09	0.92	3.60	-	877.3
gi|14149680|ref|NP_056107.1| KIAA0747 protein [Homo sapiens]				5.28E-09	2.71	30.19	4.30	122855.6
AHQ-2-12, 5591	R.FEWELPLDEAQR.R	1533.66622	2	5.28E-09	0.88	3.56	-	596.9
AHQ-2-7, 7067	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	1.99E-07	0.90	3.66	-	617.0
AHQ-2-6, 6998	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	5.21E-07	0.86	3.38	-	532.1
AHQ-2-4, 7384	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	1.01E-06	0.70	2.65	-	451.8
AHQ-2-12, 4022	R.LTHVDSPLEAPAGPLGQVK.L	1930.19405	2	2.39E-04	0.93	3.89	-	1141.9
gi|4506405|ref|NP_002872.1| v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP				5.40E-09	2.82	30.28	15.50	23408.4
AHQ-2-10, 3560	K.AEEDKIPLLVVGNK.S	1525.77182	2	2.21E-07	0.90	3.40	-	864.5
AHQ-2-10, 3322	R.SKAEEWGVQYVETSAK.T	1812.95765	3	3.08E-07	0.94	4.04	-	1147.8
AHQ-2-10, 3303	R.SKAEEWGVQYVETSAK.T	1812.95765	2	5.40E-09	0.98	5.61	-	1698.4
AHQ-2-10, 3152	R.VKAEEDKIPLLVVGNK.S	1753.07630	2	6.40E-05	0.95	4.87	-	927.7
gi|5031931|ref|NP_005585.1| nascent-polypeptide-associated complex alpha polypeptide [Homo sapiens]				5.64E-09	0.94	10.20	6.50	23383.7
AHQ-2-13, 4035	K.SPASDTYIVFGEAK.I	1485.61987	2	5.64E-09	0.94	4.07	-	1076.5
gi|4507789|ref|NP_003338.1| ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]				5.69E-09	0.93	10.19	9.70	17861.5
AHQ-2-12, 5279 - 5299	R.IEINFPAEYPFKPPK.I	1791.08155	3	5.69E-09	0.93	3.87	-	1345.4
AHQ-2-12, 5217 - 5294	R.IEINFPAEYPFKPPK.I	1791.08155	2	2.29E-06	0.80	3.65	-	581.7
gi|21361785|ref|NP_543010.2| histidyl-tRNA synthetase 2; histidyl-tRNA synthetase; bA379J5.3; chrom				5.94E-09	0.98	10.30	12.70	24013.4
AHQ-2-10, 6635	K.GNKPDFHLAMPTEQAEGFYNSFLEQLR.K	3141.46192	3	5.94E-09	0.98	6.09	-	2102.2
gi|4758460|ref|NP_004479.1| glycoprotein V (platelet) [Homo sapiens]				6.02E-09	2.95	40.27	14.80	60958.9
AHQ-2-5, 5487	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	3.63E-05	0.78	4.10	-	594.2
AHQ-2-1, 5861	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	5.84E-05	0.75	3.87	-	532.1
AHQ-2-5, 4611	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	2.19E-06	0.96	4.25	-	1895.0
AHQ-2-5, 3732	R.LTEVLLGHNSWR.C	1425.61726	1	4.06E-05	0.25	2.16	-	201.3
AHQ-2-5, 7575 - 7616	K.LVNLQELALNQNQLDFLPASLFTNLENLK.L	3314.77659	3	6.02E-09	0.95	5.33	-	1353.9
gi|17149842|ref|NP_004461.2| FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep				6.04E-09	2.25	30.18	19.00	15649.2
AHQ-2-13-, 5058	K.GWDQGLLGMCEGEK.R	1581.75275	2	1.89E-07	0.86	3.24	-	869.8
AHQ-2-13-, 4469	K.GWDQGLLGMCEGEKR.K	1737.93910	2	6.13E-04	0.60	2.80	-	384.9
AHQ-2-13-, 4229 - 4241	K.LVIPSELGYGER.G	1333.51491	2	6.04E-09	0.78	2.76	-	519.2
AHQ-2-13, 4183	K.LVIPSELGYGER.G	1333.51491	2	2.32E-07	0.73	2.90	-	399.9
gi|4502565|ref|NP_001740.1| calpain, small subunit 1; calpain, small polypeptide; calcium-dependent				6.05E-09	2.59	30.23	10.80	28315.5
AHQ-2-12, 2874	K.TDGFGIDTCR.S	1143.20921	2	4.77E-04	0.73	3.04	-	412.2
AHQ-2-12, 6785	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	6.05E-09	0.93	4.53	-	1133.3
AHQ-2-12, 7061	R.YSDESGNMDFDNFISCLVR.L	2271.42628	2	3.60E-08	0.93	4.52	-	933.3
AHQ-2-13, 6588	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	1.38E-04	0.74	3.16	-	588.0
AHQ-2-14-, 6596 - 6663	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	2.68E-08	0.87	3.82	-	808.1
AHQ-2-11, 6473	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	2.93E-05	0.81	3.56	-	610.3
gi|4504521|ref|NP_002147.1| heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P				6.11E-09	2.73	40.31	12.90	61024.2
AHQ-2-14-, 6907	R.ALM*LQGVDLLADAVAVTMGPK.G	2130.55828	2	6.11E-09	0.98	6.22	-	2455.4
AHQ-2-7, 3871 - 3876	R.GYISPYFINTSK.G	1390.56492	1	2.60E-05	0.22	2.22	-	290.4
AHQ-2-14-, 6979 - 6980	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D	2870.28530	3	3.25E-04	0.68	3.32	-	546.0
AHQ-2-7, 5643	K.TLNDELEIIEGMK.F	1505.71604	2	4.60E-04	0.84	3.34	-	712.7
gi|29568101|ref|NP_006467.3| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT				6.15E-09	3.28	40.21	23.30	11400.3
AHQ-2-14-, 4525	R.LATFWYYAK.V	1163.34840	2	2.42E-06	0.74	2.57	-	450.5
AHQ-2-14, 4566	K.TPALVNAAVTYSK.P	1335.53080	2	1.52E-05	0.84	3.33	-	726.3
AHQ-2-14-, 3659	K.TPALVNAAVTYSK.P	1335.53080	2	6.15E-09	0.97	4.28	-	1717.6
AHQ-2-14, 4504	K.TPALVNAAVTYSKPR.L	1588.83283	3	4.56E-04	0.88	3.43	-	1318.6
AHQ-2-14, 5292 - 5364	K.VELVPPTPAEIPR.A	1418.66294	2	8.10E-04	0.70	2.59	-	449.7
gi|4503725|ref|NP_000792.1| FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei				6.15E-09	3.75	40.29	29.60	11950.6
AHQ-2-13, 3380	R.GQTCVVHYTGMLEDGKK.F	1925.17623	2	1.28E-04	0.90	3.96	-	808.1
AHQ-2-13, 3924 - 3993	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.20E-05	0.93	4.18	-	1142.5
AHQ-2-13-, 3954 - 4027	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.40E-04	0.60	2.72	-	842.9
AHQ-2-13, 3403 - 3408	K.RGQTCVVHYTGMLEDGK.K	1953.18967	2	3.62E-08	0.98	5.85	-	1856.1
AHQ-2-13-, 3407 - 3411	K.RGQTCVVHYTGMLEDGK.K	1953.18967	2	3.47E-08	0.98	5.81	-	1710.1
AHQ-2-13-, 2987	K.RGQTCVVHYTGMLEDGKK.F	2081.36259	3	6.15E-09	0.94	4.44	-	1275.3
AHQ-2-13, 3021	K.RGQTCVVHYTGMLEDGKK.F	2081.36259	2	8.24E-05	0.96	4.47	-	1463.7
AHQ-2-13, 2923	K.RGQTCVVHYTGMLEDGKK.F	2081.36259	2	9.73E-04	0.94	4.62	-	814.0
gi|21314617|ref|NP_000433.2| platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e				6.27E-09	7.60	90.31	17.60	82449.6
AHQ-2-5, 5919	R.CESISGTLPISYQLLK.T	1811.08954	2	4.15E-06	0.93	4.24	-	685.8
AHQ-2-4, 6752	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	2.18E-07	0.98	6.14	-	1604.8
AHQ-2-3, 6701	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	5.82E-06	0.95	4.17	-	1227.3
AHQ-2-4, 6533 - 6548	R.DQNFVILEFPVEEQDR.V	1979.13566	2	9.25E-04	0.38	2.71	-	381.8
AHQ-2-5, 6351	R.DQNFVILEFPVEEQDR.V	1979.13566	2	3.14E-04	0.93	4.78	-	865.2
AHQ-2-6, 6191	R.DQNFVILEFPVEEQDR.V	1979.13566	2	2.00E-04	0.30	2.54	-	241.0
AHQ-2-4, 3489	K.EDTIVSQTQDFTK.I	1512.60049	2	2.43E-04	0.90	3.82	-	560.1
AHQ-2-4, 2361 - 2365	R.IISGIHMQTSESTK.S	1532.74472	2	1.86E-08	0.96	4.40	-	1190.3
AHQ-2-4, 4269	R.ISYDAQFEVIK.G	1313.48046	2	7.10E-06	0.87	3.33	-	709.8
AHQ-2-4, 3266	K.SDSGTYICTAGIDK.V	1489.58698	2	8.73E-05	0.91	3.91	-	904.9
AHQ-2-4, 4085 - 4162	K.STESYFIPEVR.I	1328.45199	2	3.68E-04	0.84	3.23	-	743.5
AHQ-2-3, 5667	K.VIAPVDEVQISILSSK.V	1698.98227	2	8.19E-07	0.84	3.34	-	443.4
AHQ-2-4, 5677 - 5684	K.VIAPVDEVQISILSSK.V	1698.98227	2	6.27E-09	0.91	3.82	-	682.1
gi|4503823|ref|NP_002028.1| protein-tyrosine kinase fyn isoform a; proto-oncogene tyrosine-protein				6.29E-09	0.90	10.18	2.00	60761.5
AHQ-2-7, 3409 - 3413	K.WTAPEAALYGR.F	1235.37302	2	6.29E-09	0.90	3.64	-	633.0
gi|18543899|ref|XP_086916.1| similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic				6.51E-09	0.95	10.22	8.00	21265.8
AHQ-2-11, 3229 - 3230	K.NRPTSISWDGLDSGK.L	1633.74419	2	6.51E-09	0.95	4.30	-	1080.2
gi|30150271|ref|XP_292964.2| similar to Heat shock protein HSP 90-beta (HSP 84) (Tumor specific tra				6.67E-09	0.92	10.21	4.10	47348.8
AHQ-2-5, 4667	K.CLELFSELAEDKKNYKK.F	2117.40810	2	6.67E-09	0.92	4.23	-	1518.2
gi|5031597|ref|NP_005710.1| actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub				6.77E-09	2.37	30.27	23.60	20546.5
AHQ-2-11, 6398 - 6408	K.DTDIVDEAIYYFK.A	1592.72721	2	1.39E-08	0.97	5.11	-	1444.5
AHQ-2-12, 6729 - 6730	K.DTDIVDEAIYYFK.A	1592.72721	2	6.77E-09	0.98	5.30	-	1674.0
AHQ-2-13-, 6709	K.DTDIVDEAIYYFK.A	1592.72721	2	2.02E-06	0.94	3.40	-	1561.6
AHQ-2-13, 6517	K.DTDIVDEAIYYFK.A	1592.72721	2	4.17E-05	0.95	4.93	-	867.8
AHQ-2-14-, 6568 - 6571	K.DTDIVDEAIYYFK.A	1592.72721	2	1.84E-05	0.88	2.55	-	1367.4
AHQ-2-12, 7123	K.EM*YTLGITNFPIPGEPGFPLNAIYAK.P	2871.29861	2	1.99E-04	0.47	2.76	-	176.5
AHQ-2-11, 5824 - 5828	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	4.11E-08	0.93	4.27	-	900.9
gi|4758504|ref|NP_004484.1| hydroxyacyl-Coenzyme A dehydrogenase, type II [Homo sapiens]				7.01E-09	3.44	40.23	26.40	26922.9
AHQ-2-10, 6806	R.LGDPAEYAHLVQAIIENPFLNGEVIR.L	2880.24689	2	7.01E-09	0.82	3.48	-	616.2
AHQ-2-10, 4747	R.LVGQGASAVLLDLPNSGGEAQAK.K	2196.44680	2	4.59E-05	0.87	4.07	-	693.3
AHQ-2-10, 6463 - 6470	R.VMTIAPGLFGTPLLTSLPEK.V	2086.52363	2	3.52E-05	0.87	3.72	-	673.6
AHQ-2-10, 6098	R.VM*TIAPGLFGTPLLTSLPEK.V	2102.52303	2	3.72E-06	0.88	4.35	-	401.6
gi|4758756|ref|NP_004528.1| nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr				7.68E-09	3.59	40.27	14.60	45373.8
AHQ-2-7, 7275	K.GIPEFWLTVFK.N	1337.58999	2	7.68E-09	0.75	2.99	-	239.4
AHQ-2-7, 5523	R.LDGLVETPTGYIESLPR.V	1861.08535	2	6.70E-07	0.95	4.52	-	1022.2
AHQ-2-7, 5609	R.LDGLVETPTGYIESLPR.V	1861.08535	2	2.85E-04	0.87	3.67	-	652.9

AHQ-2-7, 5337 - 5351	K.NVDLLSDMVQEHDEPILK.H	2096.34751	2	8.65E-08	0.97	5.40	-	1394.4
AHQ-2-7, 4589	K.YAVLYQPLFDK.R	1357.57807	2	3.53E-07	0.92	3.16	-	1143.0
AHQ-2-7, 4508 - 4585	K.YAVLYQPLFDK.R	1357.57807	1	8.70E-04	0.58	2.62	-	601.2
gi|4505763|ref|NP_000282.1| phosphoglycerate kinase 1 [Homo sapiens]				8.22E-09	7.67	100.28	42.20	44614.4
AHQ-2-8, 5586	K.ACANPAAGSVILLENLR.F	1771.03187	2	2.65E-06	0.95	4.77	-	1092.5
AHQ-2-11, 5562 - 5641	K.ACANPAAGSVILLENLR.F	1771.03187	2	2.02E-06	0.96	4.62	-	1508.3
AHQ-2-10, 4938	K.ALESPERPFLAILGGAK.V	1770.06542	2	5.19E-07	0.95	4.63	-	1125.7
AHQ-2-11, 5253	K.ALESPERPFLAILGGAK.V	1770.06542	2	1.32E-04	0.88	3.83	-	1135.4
AHQ-2-8, 4924	K.ALESPERPFLAILGGAK.V	1770.06542	2	4.98E-06	0.96	4.94	-	1527.1
AHQ-2-8, 4932	K.ALESPERPFLAILGGAK.V	1770.06542	2	8.22E-09	0.97	5.19	-	1762.0
AHQ-2-9, 5255	K.ALESPERPFLAILGGAK.V	1770.06542	2	6.52E-06	0.95	4.58	-	1395.1
AHQ-2-8, 4496	K.DVLFLKDCVGPEVEK.A	1750.00620	2	7.56E-08	0.92	3.75	-	1035.4
AHQ-2-8, 4495	K.DVLFLKDCVGPEVEK.A	1750.00620	2	1.95E-06	0.97	5.16	-	1373.6
AHQ-2-11, 5198	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	2.55E-05	0.51	2.77	-	400.0
AHQ-2-8, 5216	K.SVVLMSHLGRPDGVPMPDKYSLEPVAVELK.S	3265.83562	3	2.33E-06	0.96	5.54	-	1692.0
AHQ-2-8, 4547	K.TGQATVASGIPAGWMGLDCGPESSKK.Y	2607.90190	3	4.09E-05	0.83	3.85	-	487.2
AHQ-2-8, 4993	K.VLNNMEIGTSLFDEEGAK.I	1968.17459	2	1.61E-04	0.74	3.67	-	296.3
AHQ-2-8, 5315 - 5316	K.VLPGVDALSNI	1098.27456	1	8.89E-04	0.27	1.89	-	340.8
AHQ-2-8, 3834	K.WNTEDKVSHVSTGGGASLELLEGK.V	2515.71777	2	8.31E-04	0.73	3.01	-	697.5
AHQ-2-13-, 4291 - 4294	K.YSLEPVAVELK.S	1248.44991	2	1.28E-06	0.78	2.66	-	716.6
gi|20127528|ref|NP_037459.2| parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]				8.59E-09	4.74	60.28	27.20	41714.0
AHQ-2-9, 3130 - 3134	K.ARPEDVVNLDLK.S	1369.54878	1	5.13E-07	0.27	2.65	-	192.8
AHQ-2-9, 3131	K.ARPEDVVNLDLK.S	1369.54878	2	2.75E-05	0.91	4.32	-	806.9
AHQ-2-13, 3468	K.ARPEDVVNLDLK.S	1369.54878	2	8.94E-05	0.93	4.60	-	777.1
AHQ-2-11, 3297	K.ARPEDVVNLDLK.S	1369.54878	2	4.73E-05	0.91	3.47	-	961.7
AHQ-2-13-, 3413 - 3482	K.ARPEDVVNLDLK.S	1369.54878	2	5.24E-06	0.88	3.80	-	622.8
AHQ-2-9, 5311	R.DAFDTLFDHAPDKLSVVK.K	2019.24293	2	9.57E-05	0.84	4.00	-	500.2
AHQ-2-1, 3989	K.LNVAEVTQSEIGQK.Q	1516.67865	2	3.41E-06	0.94	4.60	-	802.2
AHQ-2-13, 3807	K.LNVAEVTQSEIGQK.Q	1516.67865	2	3.91E-06	0.90	4.00	-	824.4
AHQ-2-9, 4559	K.NAINSPMSPALVDVHPEDTQLEENEER.T	3036.23445	3	4.06E-08	0.78	3.64	-	422.4
AHQ-2-9, 3731	K.QLEEDLYDGQVLQK.L	1678.82164	2	4.06E-04	0.73	3.14	-	780.9
AHQ-2-9, 3938 - 3939	K.QLEEDLYDGQVLQK.L	1678.82164	2	1.61E-06	0.95	4.45	-	1086.6
AHQ-2-9, 7354 - 7364	K.VLLDWINDVLVEER.I	1713.95549	2	8.59E-09	0.97	5.65	-	1370.2
AHQ-2-9, 6579	K.VLLDWINDVLVEER.I	1713.95549	2	3.95E-06	0.79	3.40	-	607.0
gi|28827809|ref|NP_789797.1| nucleoside diphosphate kinase B-like [Homo sapiens]				8.67E-09	5.25	60.26	43.10	15529.0
AHQ-2-12, 3357 - 3367	R.GDFCIQVGR.N	1053.17404	2	2.37E-05	0.88	3.35	-	1016.5
AHQ-2-12, 2057	R.NIIHGSDSVKSAEK.E	1485.62464	1	7.62E-08	0.81	3.53	-	659.0
AHQ-2-12, 2049	R.NIIHGSDSVKSAEK.E	1485.62464	2	1.88E-07	0.88	4.14	-	986.7
AHQ-2-12, 2751	R.VMLGETNPADSKPGTIR.G	1787.03151	2	4.32E-08	0.81	3.86	-	478.4
AHQ-2-12, 2566	R.VM*LGETNPADSKPGTIR.G	1803.03091	2	7.52E-05	0.84	3.34	-	716.1
AHQ-2-12, 7109	K.YM*NSGPVVAMVWEGLNVVK.T	2110.48562	2	8.67E-09	0.96	5.27	-	1220.3
AHQ-2-12, 7106 - 7134	K.YMNSGPVVAMVWEGLNVVK.T	2094.48622	2	1.28E-05	0.94	4.88	-	576.6
gi|5902016|ref|NP_008939.1| reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sapi				8.76E-09	1.72	20.18	14.10	22395.3
AHQ-2-1, 3174	R.HQAQIDHYLGLANK.N	1608.78270	2	3.54E-04	0.91	3.65	-	837.4
AHQ-2-1, 3038	K.YSNSALGHVNCTIK.E	1565.73305	2	8.76E-09	0.82	3.15	-	715.1
gi|5803225|ref|NP_006752.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon poly				1.01E-08	3.32	40.25	20.40	29173.7
AHQ-2-13-, 6842 - 6849	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	5.73E-07	0.96	4.97	-	1215.8
AHQ-2-9, 7070 - 7078	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	4.07E-04	0.93	4.42	-	849.0
AHQ-2-13, 6627	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	3.17E-07	0.93	3.52	-	1297.6
AHQ-2-14-, 6629 - 6708	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	1.01E-08	0.95	4.53	-	1249.5
AHQ-2-10, 6898 - 6962	K.AAFDDAIAELDTLSEESYKDSTLIMQLLR.D	3260.61486	3	5.62E-08	0.91	4.72	-	801.2
AHQ-2-9, 2370	K.EAAENSLVAYK.A	1195.30397	2	4.91E-06	0.76	3.15	-	546.8
AHQ-2-9, 1552	K.HLIPAANTGESK.V	1238.37521	2	6.99E-04	0.71	2.61	-	576.8
gi|13899317|ref|NP_113657.1| SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M				1.02E-08	4.31	50.22	72.00	12326.0
AHQ-2-14-, 5479 - 5484	K.ESNTVFSFLGLKPR.L	1595.82383	2	5.55E-08	0.67	3.10	-	359.4
AHQ-2-13, 5392 - 5443	K.ESNTVFSFLGLKPR.L	1595.82383	2	4.32E-06	0.90	3.78	-	745.9
AHQ-2-14, 6081	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	2	8.02E-04	0.78	3.26	-	685.7
AHQ-2-14-, 5071 - 5075	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	1.02E-08	0.90	4.03	-	1260.6
AHQ-2-13-, 3830	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	2.69E-06	0.90	3.78	-	786.5
AHQ-2-13-, 6034	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	3.96E-04	0.74	3.35	-	692.7
AHQ-2-13-, 5903 - 5966	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	1.84E-06	0.88	4.36	-	729.8
AHQ-2-13, 5739 - 5801	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	1.67E-05	0.86	4.40	-	923.0
AHQ-2-14-, 5871 - 5937	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	1.59E-04	0.85	4.43	-	686.0
AHQ-2-14, 5601 - 5604	R.VFIASSSGFVAIK.K	1326.56551	2	1.11E-06	0.97	4.35	-	2021.9
AHQ-2-14-, 4555 - 4629	R.VFIASSSGFVAIK.K	1326.56551	2	2.99E-05	0.95	3.17	-	2063.4
gi|30150022|ref|XP_300862.1| similar to beta-tubulin 4Q [Homo sapiens]				1.10E-08	6.54	70.29	22.50	33545.2
AHQ-2-11, 5970	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	9.68E-07	0.94	4.66	-	1666.0
AHQ-2-7, 6267 - 6337	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	1.29E-08	0.95	5.38	-	998.0
AHQ-2-13-, 3403	R.FPGQLNADLR.K	1131.26634	2	3.35E-05	0.68	2.51	-	694.2
AHQ-2-8, 2882 - 2959	R.FPGQLNADLR.K	1131.26634	2	4.72E-04	0.88	2.91	-	978.2
AHQ-2-7, 3133	R.FPGQLNADLR.K	1131.26634	2	1.27E-05	0.89	2.82	-	1048.7
AHQ-2-7, 2995 - 3063	R.FPGQLNADLR.K	1131.26634	2	8.36E-04	0.85	3.06	-	686.4
AHQ-2-7, 5800 - 5804	R.KEAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3443.82841	3	1.10E-08	0.97	5.75	-	2083.2
AHQ-2-7, 3419 - 3432	R.KLAVNMVPFPR.L	1272.58771	2	2.26E-05	0.95	4.32	-	1167.9
AHQ-2-7, 4140 - 4216	K.LAVNMVPFPR.L	1144.41480	2	2.06E-06	0.92	3.57	-	823.2
AHQ-2-8, 3975	K.LAVNMVPFPR.L	1144.41480	2	4.75E-06	0.95	3.77	-	948.4
AHQ-2-9, 4212	K.LAVNMVPFPR.L	1144.41480	2	7.49E-04	0.89	3.06	-	732.6
AHQ-2-13-, 4486	K.LAVNMVPFPR.L	1144.41480	2	2.76E-06	0.69	2.57	-	648.7
AHQ-2-10, 4072	K.LAVNMVPFPR.L	1144.41480	2	1.63E-06	0.93	4.10	-	890.1
AHQ-2-11, 4272	K.LAVNMVPFPR.L	1144.41480	2	2.15E-06	0.88	3.41	-	663.9
AHQ-2-7, 3460	K.LAVNM*VPFPR.L	1160.41420	2	3.80E-04	0.93	3.88	-	965.9
AHQ-2-9, 5523	R.LHFFMPGFAPLTSR.G	1621.92962	2	2.59E-04	0.88	3.31	-	635.6
AHQ-2-7, 5405 - 5407	R.LHFFMPGFAPLTSR.G	1621.92962	2	1.86E-06	0.92	3.47	-	881.2
gi|21361553|ref|NP_003168.2| spleen tyrosine kinase [Homo sapiens]				1.10E-08	0.79	10.26	2.00	72065.7
AHQ-2-13, 4476	K.TGPFEDLKENLIR.E	1532.72291	2	1.10E-08	0.79	3.29	-	693.1
gi|4506005|ref|NP_002700.1| protein phosphatase 1, catalytic subunit, beta isoform [Homo sapiens] [				1.10E-08	4.11	50.27	24.20	37186.6
AHQ-2-9, 3703	R.AHQVVEDGYEFFAK.R	1640.77679	2	1.37E-04	0.92	3.54	-	1021.7
AHQ-2-13, 6787	R.EIFLSQPILLELEAPLK.I	1954.33857	2	1.71E-06	0.95	5.04	-	686.6
AHQ-2-9, 7387 - 7388	R.EIFLSQPILLELEAPLK.I	1954.33857	2	1.10E-08	0.95	5.32	-	749.5
AHQ-2-9, 5212 - 5222	K.IFCCHGGLSPDLQSMEQIR.R	2251.54930	2	3.93E-07	0.97	4.83	-	1653.8
AHQ-2-9, 4759 - 4760	K.IKYPENFFLLR.G	1440.71344	2	5.50E-04	0.30	2.72	-	246.0
AHQ-2-9, 7310	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	2.41E-07	0.97	5.25	-	1137.4
gi|11496885|ref|NP_005442.2| enigma protein; LIM domain protein [Homo sapiens]				1.13E-08	3.61	40.25	16.40	49844.4
AHQ-2-13, 6205	K.AAQAGVAVGDWVLSIDGENAGSLTHIEAQNK.I	3123.37980	3	1.64E-04	0.81	4.20	-	549.5
AHQ-2-14-, 6263	K.AAQAGVAVGDWVLSIDGENAGSLTHIEAQNK.I	3123.37980	3	1.13E-08	0.91	4.82	-	619.6
AHQ-2-10, 3396	K.VLEEGGFFEEK.G	1284.39598	2	2.38E-08	0.77	3.06	-	642.6
AHQ-2-14-, 4887	K.VVLEGPAPWGFR.L	1328.54318	2	6.47E-08	0.96	3.77	-	1752.0
AHQ-2-14, 6185	K.VVLEGPAPWGFR.L	1328.54318	2	3.19E-07	0.93	3.50	-	1099.0
AHQ-2-13-, 4917	K.VVLEGPAPWGFR.L	1328.54318	2	9.45E-07	0.92	3.86	-	886.6
AHQ-2-11, 4657	K.VVLEGPAPWGFR.L	1328.54318	2	2.34E-05	0.92	3.51	-	1104.0
AHQ-2-9, 4464 - 4466	R.YLVALGHAYHPEEFVCSQCGK.V	2468.74928	2	1.15E-07	0.97	4.97	-	1384.3
AHQ-2-9, 4468	R.YLVALGHAYHPEEFVCSQCGK.V	2468.74928	3	1.86E-04	0.96	4.97	-	1479.5
gi|28178832|ref|NP_002159.2| isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat				1.18E-08	4.54	50.24	15.00	50909.0
AHQ-2-8, 3767	K.DLAGCIHGLSNVK.L	1385.57150	2	2.47E-06	0.97	4.10	-	1914.2
AHQ-2-8, 1862 - 1932	R.GKLDGNQDLIR.F	1229.36832	2	1.89E-04	0.90	3.00	-	1189.2
AHQ-2-8, 5235	K.LNEHFLNTTDFLDTIK.S	1922.12725	2	1.18E-08	0.97	4.82	-	1465.2
AHQ-2-8, 4491	R.NILGGTVFREPIICK.N	1719.04170	2	1.97E-04	0.93	4.29	-	927.7

AHQ-2-8, 1620	K.TIEAEAAHGTVTR.H	1356.46696	2	4.11E-04	0.78	3.03	-	685.0
gi|4758988|ref|NP_004152.1|	RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho			1.20E-08	4.05	50.24	35.60	22677.6
AHQ-2-14-, 6236 - 6261	K.EFADSLGIPFLETSAK.N	1725.91990	2	1.46E-05	0.61	3.27	-	354.6
AHQ-2-11, 6076 - 6085	K.EFADSLGIPFLETSAK.N	1725.91990	2	1.16E-04	0.80	3.59	-	592.4
AHQ-2-12, 6362	K.EFADSLGIPFLETSAK.N	1725.91990	2	7.01E-05	0.72	3.58	-	431.0
AHQ-2-11, 5989 - 6048	K.EFADSLGIPFLETSAK.N	1725.91990	2	6.48E-05	0.72	3.73	-	403.3
AHQ-2-11, 5908	K.EFADSLGIPFLETSAK.N	1725.91990	2	7.24E-05	0.62	2.74	-	385.4
AHQ-2-11, 5973 - 6052	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.09E-07	0.97	4.85	-	1619.9
AHQ-2-11, 5866 - 5930	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.46E-06	0.88	3.24	-	1005.2
AHQ-2-11, 5561 - 5634	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.07E-08	0.97	4.37	-	1666.4
AHQ-2-14-, 6040 - 6105	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.20E-08	0.91	3.55	-	986.9
AHQ-2-11, 6112 - 6172	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	4.29E-08	0.95	4.35	-	1007.5
AHQ-2-11, 6241 - 6316	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	5.83E-06	0.94	4.15	-	1040.2
AHQ-2-11, 6842 - 6913	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.08E-06	0.93	3.76	-	1075.2
AHQ-2-11, 6976	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.86E-07	0.94	4.61	-	938.6
AHQ-2-14-, 5904 - 5977	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.59E-08	0.94	4.02	-	1291.4
AHQ-2-13, 6025	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	4.54E-05	0.69	3.21	-	636.1
AHQ-2-11, 5037	R.GAHGIIVVYDVTDQESFNNVK.Q	2306.51658	2	1.18E-04	0.91	4.08	-	744.6
AHQ-2-11, 4794	K.NATNVEQSFMTM*AAEIK.K	1902.13962	2	2.86E-04	0.79	3.67	-	814.1
AHQ-2-11, 6032	K.NATNVEQSFMTMAAEIK.K	1886.14022	2	7.20E-06	0.83	3.92	-	944.5
gi|4503971|ref|NP_001484.1|	GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r			1.26E-08	3.56	40.27	14.80	50582.4
AHQ-2-7, 4151	R.FQLLEGPPESMGR.G	1461.66818	2	9.71E-05	0.89	3.96	-	908.5
AHQ-2-7, 5160	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	8.10E-06	0.79	3.44	-	585.8
AHQ-2-6, 5217 - 5218	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	1.35E-04	0.96	5.44	-	965.4
AHQ-2-6, 4274	R.TDDYLDQPCLETVNR.I	1840.94632	2	1.26E-08	0.90	4.32	-	626.8
AHQ-2-7, 7235	K.VPSTETEALASNLMGMFEK.R	2056.34679	2	4.81E-08	0.97	5.15	-	1191.0
AHQ-2-6, 7114	K.VPSTETEALASNLMGMFEK.R	2056.34679	2	3.51E-08	0.97	4.90	-	1764.8
gi|4505585|ref|NP_002563.1|	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30			1.33E-08	1.80	20.22	17.00	25569.1
AHQ-2-10, 5584 - 5587	R.ELFSPLHALNFGIGGDTTR.H	2046.27160	2	1.49E-05	0.83	3.50	-	611.4
AHQ-2-10, 6598	K.ICKPLHELIMQLLEETPEEK.Q	2452.87287	2	1.33E-08	0.96	4.46	-	1883.6
gi|5453760|ref|NP_006147.1|	neural precursor cell expressed, developmentally down-regulated 8 [Homo			1.36E-08	0.86	10.17	17.30	9071.5
AHQ-2-14-, 3675	K.EIEIDIEPTDKVER.I	1686.84208	2	1.36E-08	0.86	3.39	-	821.6
gi|6679056|ref|NP_031387.1|	nidogen 2 (osteonidogen); nidogen 2 [Homo sapiens]			1.39E-08	0.77	10.18	2.10	151153.0
AHQ-2-1, 6780 - 6809	R.AGLELGAEPETIVNSGLISPEGLAIDHIR.R	2973.32740	3	1.39E-08	0.77	3.70	-	682.6
gi|21361547|ref|NP_002930.2|	ribonuclease/angiogenin inhibitor; Placental ribonuclease inhibitor [H			1.42E-08	0.90	10.20	3.30	49973.3
AHQ-2-14-, 6503	R.WAELLPLLQQCQVVR.L	1855.19360	2	1.42E-08	0.90	4.04	-	544.5
gi|22042381|ref|XP_065237.3|	similar to FKSG30 [Homo sapiens]			1.42E-08	1.59	20.19	8.30	42016.0
AHQ-2-14-, 2301 - 2324	K.QEYDESGPSIVHR.K	1517.58206	2	2.12E-04	0.59	2.66	-	342.2
AHQ-2-13-, 2893	K.QEYDESGPSIVHR.K	1517.58206	2	1.96E-04	0.35	2.74	-	476.1
AHQ-2-13-, 2377 - 2443	K.QEYDESGPSIVHR.K	1517.58206	2	4.88E-08	0.87	3.42	-	527.6
AHQ-2-13, 2477	K.QEYDESGPSIVHR.K	1517.58206	2	1.42E-08	0.79	3.20	-	399.9
AHQ-2-8, 2022 - 2090	K.QEYDESGPSIVHR.K	1517.58206	2	1.44E-07	0.56	2.63	-	290.6
AHQ-2-9, 3435 - 3514	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	1.07E-04	0.65	3.14	-	428.4
AHQ-2-8, 3219 - 3286	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	1.35E-04	0.61	3.17	-	385.3
AHQ-2-8, 3098 - 3140	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	1.22E-05	0.79	3.65	-	485.9
gi|4505705|ref|NP_003759.1|	phosphoprotein enriched in astrocytes 15; Phosphoprotein enriched in as			1.50E-08	0.88	10.21	13.10	15040.0
AHQ-2-12, 6109 - 6177	K.LDKDNLSYIEHIFEISR.R	2093.32504	2	1.50E-08	0.88	4.25	-	591.2
gi|4504483|ref|NP_000185.1|	hypoxanthine phosphoribosyltransferase 1 [Homo sapiens]			1.61E-08	1.90	20.33	21.10	24579.2
AHQ-2-10, 6623	R.SPGVVISDDEPGYDLDLFCIPNHYAEDLER.V	3438.67572	3	1.61E-08	0.96	6.57	-	793.2
AHQ-2-10, 4422	R.SVGYKPDFVGFEIPDK.F	1799.01571	2	1.30E-07	0.93	4.50	-	738.4
gi|28077085|ref|NP_004559.3|	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member			1.62E-08	0.92	10.22	5.30	42586.7
AHQ-2-9, 4624	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	2	1.62E-08	0.92	4.48	-	849.8
AHQ-2-8, 4371	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	2	1.57E-04	0.82	3.50	-	873.5
gi|6005854|ref|NP_009204.1|	repressor of estrogen receptor activity; B-cell associated protein [Hom			1.65E-08	1.86	20.24	10.70	33296.1
AHQ-2-9, 7182 - 7235	R.IPWFQYPIIYDIR.A	1725.02480	2	1.10E-04	0.95	3.82	-	1459.0
AHQ-2-9, 6743	R.IYLTADNLVLNLQDESFTR.G	2226.47137	2	1.65E-08	0.91	4.75	-	579.0
gi|4507295|ref|NP_003560.1|	syntaxin 7 [Homo sapiens]			1.69E-08	0.91	10.20	5.70	29845.3
AHQ-2-13-, 3366	R.TLNQLGTPQDSPELR.Q	1669.81798	2	1.76E-07	0.85	3.41	-	538.0
AHQ-2-13, 3385 - 3391	R.TLNQLGTPQDSPELR.Q	1669.81798	2	1.69E-08	0.91	4.02	-	724.8
gi|4758790|ref|NP_004543.1|	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q			1.69E-08	2.57	30.23	34.90	12517.4
AHQ-2-13-, 3827	K.EWIECAHGIGYTR.A	1593.74495	2	7.43E-07	0.84	2.97	-	684.8
AHQ-2-13-, 6761	K.IEYDDFVECLLR.Q	1573.74872	2	2.69E-07	0.96	4.66	-	910.4
AHQ-2-13, 6552	K.IEYDDFVECLLR.Q	1573.74872	2	1.69E-08	0.88	3.31	-	809.8
AHQ-2-13-, 3897	R.WLTIQSGEQPYK.M	1450.62036	2	1.82E-04	0.85	3.56	-	728.4
gi|27436929|ref|NP_005518.2|	heat shock 70kDa protein 1-like; heat shock 70kD protein-like 1 [Homo			1.73E-08	0.97	10.21	2.20	70404.7
AHQ-2-6, 2927	K.AKIHDIVLVGGSTR.I	1466.71083	2	1.73E-08	0.97	4.12	-	2243.4
gi|4557032|ref|NP_002291.1|	lactate dehydrogenase B [Homo sapiens]			1.74E-08	11.71	160.29	43.70	36638.3
AHQ-2-13-, 4554	K.FIIPQIVK.Y	958.22198	1	4.10E-04	0.28	2.02	-	430.5
AHQ-2-9, 4084	K.GEM*MDLQHGSLFLQTPK.I	1949.24111	2	4.22E-04	0.67	3.61	-	687.0
AHQ-2-9, 4654	K.GEMMDLQHGSLFLQTPK.I	1933.24171	2	9.28E-06	0.95	4.64	-	941.7
AHQ-2-9, 2212	R.GLTSVINQK.L	960.10999	2	2.28E-04	0.60	2.57	-	536.1
AHQ-2-14-, 2380	R.GLTSVINQK.L	960.10999	2	9.43E-05	0.51	2.59	-	325.3
AHQ-2-9, 7407 - 7464	K.GMYGIENEVFLSLPCILNAR.G	2298.66742	2	6.28E-06	0.77	3.74	-	412.1
AHQ-2-9, 1600	R.IHPVSTMVK.G	1012.25154	1	1.57E-05	0.13	2.29	-	212.9
AHQ-2-9, 7611	K.ITVVGVGQVGMACAISILGK.S	1975.40611	2	6.63E-04	0.92	4.25	-	687.0
AHQ-2-13, 2248	K.IVADKDYSVTANSK.I	1511.65887	2	6.80E-06	0.93	3.67	-	1225.1
AHQ-2-9, 1982	K.IVADKDYSVTANSK.I	1511.65887	2	8.10E-05	0.87	3.62	-	749.7
AHQ-2-13-, 2127	K.IVADKDYSVTANSK.I	1511.65887	2	9.09E-07	0.90	3.09	-	948.8
AHQ-2-13-, 2611	K.IVVVTAGVR.Q	914.12760	2	2.38E-07	0.89	3.43	-	818.5
AHQ-2-14-, 3511	K.LIAPVAEEEATVPNNK.I	1695.89534	2	4.68E-05	0.91	3.61	-	1031.1
AHQ-2-14-, 3597	K.LIAPVAEEEATVPNNK.I	1695.89534	2	2.50E-06	0.70	2.69	-	626.7
AHQ-2-14-, 3313 - 3385	K.LIAPVAEEEATVPNNK.I	1695.89534	2	8.01E-04	0.93	3.86	-	1009.6
AHQ-2-9, 1922	K.LKDDEVAQLK.K	1159.31477	2	4.01E-05	0.69	2.61	-	489.7
AHQ-2-9, 3826	K.LKGEM*MDLQHGSLFLQTPK.I	2190.57228	3	8.92E-04	0.69	3.93	-	495.7
AHQ-2-11, 3713	K.MVVESAYEVIK.L	1268.50463	2	8.48E-05	0.94	3.95	-	1086.0
AHQ-2-9, 3664 - 3668	K.MVVESAYEVIK.L	1268.50463	2	1.46E-07	0.93	4.01	-	985.5
AHQ-2-10, 3592	K.MVVESAYEVIK.L	1268.50463	2	1.48E-07	0.92	3.48	-	1160.4
AHQ-2-14-, 3853	K.MVVESAYEVIK.L	1268.50463	2	4.73E-06	0.92	3.39	-	923.3
AHQ-2-9, 3378	K.SADTLWDIQK.D	1177.28864	2	7.51E-07	0.77	3.04	-	683.2
AHQ-2-13-, 6821 - 6830	K.SLADELALVDVLEDK.L	1630.81843	2	1.74E-08	0.97	5.75	-	1370.0
AHQ-2-14-, 6600 - 6671	K.SLADELALVDVLEDK.L	1630.81843	2	1.69E-04	0.91	4.04	-	864.6
AHQ-2-9, 7104 - 7176	K.SLADELALVDVLEDK.L	1630.81843	2	2.04E-05	0.94	3.92	-	1370.7
AHQ-2-9, 7014 - 7026	K.SLADELALVDVLEDK.L	1630.81843	2	3.05E-08	0.97	5.18	-	1520.7
AHQ-2-10, 6436	K.SLADELALVDVLEDK.L	1630.81843	2	1.26E-04	0.94	4.79	-	1070.8
AHQ-2-11, 6508	K.SLADELALVDVLEDK.L	1630.81843	2	8.25E-04	0.89	3.52	-	832.9
AHQ-2-13, 6612	K.SLADELALVDVLEDK.L	1630.81843	2	3.21E-07	0.96	4.37	-	1578.3
AHQ-2-14-, 6805	K.SLADELALVDVLEDKLK.G	1872.14959	2	2.97E-05	0.96	4.57	-	1665.5
AHQ-2-9, 7266 - 7315	K.SLADELALVDVLEDKLK.G	1872.14959	2	1.22E-06	0.94	3.92	-	1415.8
gi|19923142|ref|NP_002256.2|	karyopherin beta 1; nuclear factor p97; importin 90; importin beta-1 s			1.78E-08	3.39	40.21	7.90	97169.7
AHQ-2-5, 6877	R.AAVENLPTFLVELSR.V	1659.90783	2	3.56E-04	0.75	2.98	-	354.3
AHQ-2-5, 7452 - 7453	K.GALQYLVPILTQTLTK.Q	1760.11044	2	1.84E-06	0.80	3.77	-	453.0
AHQ-2-5, 7672	R.IQFNDLQSLLCATLQNVLR.K	2248.58813	2	3.27E-07	0.89	4.14	-	880.1
AHQ-2-5, 6315	K.YLEVVLNTLQQASQAQVDK.S	2148.40214	2	1.78E-08	0.95	3.85	-	2159.4
gi|5031573|ref|NP_005712.1|	ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye			1.88E-08	5.80	80.29	31.10	47370.9
AHQ-2-9, 7490 - 7491	R.DITYFIQQLLR.D	1410.64250	1	3.58E-04	0.39	2.49	-	261.3
AHQ-2-7, 7555	R.DITYFIQQLLR.D	1410.64250	1	1.33E-05	0.12	2.12	-	221.2
AHQ-2-7, 7557	R.DITYFIQQLLR.D	1410.64250	1	3.01E-05	0.18	2.00	-	109.2

AHQ-2-7, 5803 - 5877	K.GVDDLDFFIGDEAIEKPTYATK.W	2445.66268	2	1.04E-05	0.76	2.94	-	868.2
AHQ-2-7, 4189 - 4260	R.HGIVEDWDLMER.F	1500.66127	2	4.43E-06	0.90	3.27	-	1090.0
AHQ-2-7, 2112	R.HNPVFGVM*S	1004.14480	1	9.69E-05	0.31	1.83	-	293.1
AHQ-2-7, 6516	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	2.35E-06	0.88	3.87	-	765.3
AHQ-2-7, 6395 - 6407	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	1.88E-08	0.93	4.79	-	575.2
AHQ-2-12, 6245 - 6259	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	2.02E-04	0.73	3.55	-	423.1
AHQ-2-10, 5818	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	5.09E-04	0.68	3.57	-	341.1
AHQ-2-13, 6088	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	4.42E-04	0.44	3.25	-	271.9
AHQ-2-9, 3576	R.LPACVVDCGTGYTK.L	1543.74421	2	3.28E-04	0.91	3.59	-	975.7
AHQ-2-7, 3669	K.NIVLSGGSTMFR.D	1282.49463	2	1.25E-06	0.94	3.91	-	1387.5
AHQ-2-13, 4055	K.NIVLSGGSTMFR.D	1282.49463	2	6.45E-04	0.87	2.99	-	1371.6
AHQ-2-9, 6692	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	7.38E-04	0.90	4.30	-	1006.2
AHQ-2-8, 6492	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	2.52E-04	0.83	3.80	-	801.9
AHQ-2-7, 6768	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	1.18E-04	0.94	4.83	-	1228.1
gi|21389549|ref|NP_653263.1|	hypothetical protein MGC26605 [Homo sapiens]			2.00E-08	1.59	20.22	14.90	26927.8
AHQ-2-10, 5203	R.AITVFSPDGHLFQVEYAQEAVK.K	2450.73052	3	6.56E-05	0.66	3.06	-	556.0
AHQ-2-10, 4370 - 4371	K.LTVEDPVTVEYITR.F	1635.83990	2	2.00E-08	0.93	4.25	-	749.4
gi|4557361|ref|NP_001187.1|	BH3 interacting domain death agonist; BH3-interacting domain death agon			2.02E-08	2.87	30.30	29.70	21994.6
AHQ-2-11, 6861	R.DLATALEQLLQAYPR.D	1702.93270	2	3.67E-08	0.96	4.81	-	1138.5
AHQ-2-11, 6037	R.DVFHTTVNFINQNLR.T	1819.01348	2	7.01E-04	0.95	4.45	-	1406.4
AHQ-2-11, 6124 - 6129	R.ELDALGHELPVLAPQWEGYDELQTDGNR.S	3167.38790	3	2.02E-08	0.96	5.92	-	1328.1
gi|4758208|ref|NP_004081.1|	dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;			2.17E-08	4.11	50.25	38.90	20478.2
AHQ-2-11, 4168	R.AADFIDQALAQK.N	1291.43488	1	7.25E-05	0.41	3.09	-	511.3
AHQ-2-11, 4152	R.AADFIDQALAQK.N	1291.43488	2	5.66E-04	0.90	3.82	-	922.0
AHQ-2-11, 5369	K.ANDTQEFNLSAYFER.A	1805.88207	2	2.65E-07	0.89	3.63	-	933.9
AHQ-2-11, 5912 - 5952	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	2.17E-08	0.94	4.97	-	860.7
AHQ-2-11, 6097	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	4.36E-05	0.61	3.11	-	422.5
AHQ-2-11, 3616	R.IYVGNASVAQDIPK.L	1475.67136	2	1.02E-05	0.96	4.77	-	1434.7
AHQ-2-11, 4046 - 4049	R.IYVGNASVAQDIPK.L	1475.67136	2	4.20E-08	0.96	4.18	-	1594.5
AHQ-2-11, 3266	K.LGITHVLNAAEGR.S	1351.53669	2	1.04E-06	0.91	3.24	-	1256.6
AHQ-2-11, 3277	K.LGITHVLNAAEGR.S	1351.53669	1	9.57E-05	0.50	2.48	-	467.3
gi|5802974|ref|NP_006784.1|	peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide			2.21E-08	4.92	60.29	36.70	27692.5
AHQ-2-10, 4223	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	2.21E-08	0.96	5.73	-	1246.3
AHQ-2-11, 3937	K.DLSLDDFK.G	953.02795	1	1.17E-05	0.46	2.15	-	519.1
AHQ-2-10, 5116	R.DYGVLLEGSGLALR.G	1463.66058	1	2.81E-04	0.06	2.10	-	152.8
AHQ-2-11, 5312	R.DYGVLLEGSGLALR.G	1463.66058	2	6.21E-07	0.96	3.90	-	1895.8
AHQ-2-11, 5485	R.GLFIIDPNGVIK.H	1286.54452	1	2.64E-05	0.40	2.16	-	521.8
AHQ-2-11, 5342	R.GLFIIDPNGVIK.H	1286.54452	2	9.99E-06	0.72	2.61	-	858.0
AHQ-2-10, 2662	K.HLSVNDLPVGR.S	1207.36435	2	7.58E-07	0.90	3.30	-	780.0
AHQ-2-10, 4882	R.KNGGLGHMNIALLSDLTK.Q	1883.20557	2	1.74E-04	0.93	4.25	-	827.3
gi|5453599|ref|NP_006127.1|	capping protein (actin filament) muscle Z-line, alpha 2; F-actin cappin			2.23E-08	2.70	30.26	18.90	32948.9
AHQ-2-9, 4630	R.EGAAHAFAQYNLDQFTPVK.I	2108.29826	2	3.98E-05	0.93	4.26	-	924.7
AHQ-2-9, 5171 - 5186	K.FTITPSTTQVVGILK.I	1605.90007	2	2.23E-08	0.81	3.28	-	472.1
AHQ-2-9, 4700	K.KIDGQQTIIACIESHQFQAK.N	2317.60733	2	1.74E-05	0.95	5.22	-	743.7
gi|5453555|ref|NP_006316.1|	ras-related nuclear protein [Homo sapiens]			2.23E-08	1.71	20.20	14.80	24422.9
AHQ-2-10, 5250 - 5258	K.SNYNFEKPFLWLAR.K	1786.02509	2	2.23E-08	0.90	3.98	-	620.5
AHQ-2-10, 3970 - 3994	K.YVATLGVEVHPLVFHTNR.G	2053.35211	2	2.05E-06	0.81	3.70	-	419.5
gi|16933567|ref|NP_005361.2|	mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]			2.43E-08	0.88	10.19	6.80	23668.1
AHQ-2-11, 5680	K.ANINVENAFFTLAR.D	1580.76926	2	6.88E-05	0.89	3.52	-	925.3
AHQ-2-11, 5049	K.ANINVENAFFTLAR.D	1580.76926	2	2.43E-08	0.88	3.72	-	805.6
gi|27597085|ref|NP_000357.3|	tropomyosin 1 (alpha) [Homo sapiens]			2.50E-08	2.71	30.24	16.90	32865.7
AHQ-2-9, 2835	K.ALMAAEDKYSQKEDRYEEEIK.V	2547.78004	2	2.50E-08	0.85	3.61	-	835.5
AHQ-2-9, 2864	R.AQKDEEKMEIQEIQLK.E	1961.22673	2	2.67E-05	0.95	4.76	-	1173.3
AHQ-2-10, 2955	R.KLVIIESDLER.A	1315.54103	1	2.14E-04	0.14	2.00	-	202.7
AHQ-2-9, 2958 - 2979	R.KLVIIESDLER.A	1315.54103	2	5.51E-05	0.91	3.84	-	1047.8
gi|4507649|ref|NP_003280.1|	tropomyosin 2 (beta) [Homo sapiens]			2.66E-08	0.93	10.19	4.60	32989.6
AHQ-2-9, 2588	K.ATDAEADVASLNR.R	1333.38703	2	2.66E-08	0.93	3.77	-	1371.4
gi|4826643|ref|NP_005130.1|	annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III,			2.67E-08	0.91	10.21	5.00	36375.0
AHQ-2-9, 6074	K.GAGTNEDALIEILTTR.T	1674.83453	2	2.67E-08	0.91	4.26	-	908.3
gi|13385594|ref|NP_085056.1|	cytochrome b5 outer mitochondrial membrane precursor; type 2 cyt-b5 [H			2.69E-08	0.86	10.22	23.30	16332.0
AHQ-2-11, 5934	R.FLNEHPGGEEVLLEQAGVDASESFEDVGHSSDAR.E	3629.75848	3	2.69E-08	0.86	4.32	-	604.6
gi|4505813|ref|NP_003737.1|	cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain			2.74E-08	2.74	40.17	49.40	10365.8
AHQ-2-14, 5373	K.NADM*SEEMQQDSVECATQALEK.Y	2532.67934	2	5.60E-04	0.58	3.10	-	556.4
AHQ-2-14, 5010	K.NADMSEEM*QQDSVECATQALEK.Y	2532.67934	2	7.57E-06	0.46	3.23	-	481.2
AHQ-2-14-, 2273	R.NFGSYVTHETK.H	1283.37131	2	1.09E-06	0.86	3.29	-	708.8
AHQ-2-14-, 3567 - 3568	K.YNPTWHCIVGR.N	1404.57820	2	2.74E-08	0.84	3.46	-	399.4
AHQ-2-13-, 3514	K.YNPTWHCIVGR.N	1404.57820	2	1.97E-05	0.83	3.40	-	527.2
gi|4504071|ref|NP_000164.1|	platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA			2.96E-08	4.53	50.23	9.40	68955.0
AHQ-2-1, 5176	R.GLGELQELYLK.G	1263.46458	2	2.43E-05	0.94	4.10	-	1346.2
AHQ-2-4, 5090	R.GLGELQELYLK.G	1263.46458	2	3.67E-04	0.95	4.52	-	1252.8
AHQ-2-3, 5091 - 5095	R.GLGELQELYLK.G	1263.46458	2	2.79E-05	0.94	4.24	-	1144.5
AHQ-2-3, 4192	R.GQDLLSTVSIR.Y	1189.34410	2	6.02E-07	0.96	4.46	-	1308.0
AHQ-2-4, 4173	R.GQDLLSTVSIR.Y	1189.34410	2	2.96E-08	0.96	3.97	-	1635.6
AHQ-2-12, 4047	R.GQDLLSTVSIR.Y	1189.34410	2	6.74E-08	0.96	4.42	-	1377.6
AHQ-2-1, 4312 - 4316	R.GQDLLSTVSIR.Y	1189.34410	2	1.30E-07	0.96	4.54	-	1397.6
AHQ-2-14, 5009	R.GQDLLSTVSIR.Y	1189.34410	2	2.85E-04	0.86	2.71	-	1057.3
AHQ-2-4, 1973 - 1976	R.GVLQGHLESSR.N	1183.29965	1	2.32E-04	0.25	2.43	-	358.6
AHQ-2-3, 1955 - 1987	R.GVLQGHLESSR.N	1183.29965	2	3.85E-05	0.89	3.46	-	843.9
AHQ-2-4, 1964 - 1970	R.GVLQGHLESSR.N	1183.29965	2	2.38E-05	0.88	3.03	-	998.7
AHQ-2-3, 3607 - 3609	R.LTQLNLDRCELTK.L	1605.83862	2	2.16E-05	0.79	3.84	-	606.1
AHQ-2-4, 3616 - 3628	R.LTQLNLDRCELTK.L	1605.83862	2	2.92E-04	0.86	4.08	-	703.3
AHQ-2-4, 5364	R.WLQDNAENVYVWK.Q	1665.82948	2	3.73E-04	0.68	2.69	-	463.6
AHQ-2-3, 5019	R.WLQDNAENVYVWK.Q	1665.82948	2	6.00E-08	0.94	3.93	-	1217.1
AHQ-2-3, 5347	R.WLQDNAENVYVWK.Q	1665.82948	2	4.36E-08	0.96	3.88	-	1603.6
gi|4758076|ref|NP_004068.1|	citrate synthase precursor; Citrate synthase, mitochondrial [Homo sapie			2.99E-08	1.77	20.19	5.80	51706.2
AHQ-2-8, 4499 - 4504	K.GLVYETSVLDPDEGIR.F	1763.92654	2	2.99E-08	0.87	3.70	-	667.4
AHQ-2-8, 3048 - 3056	K.IVPNVLLEQGK.A	1210.44805	2	5.36E-06	0.90	3.17	-	593.8
gi|4885183|ref|NP_005210.1|	diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS			2.99E-08	1.80	20.25	3.10	138977.7
AHQ-2-3, 6748	K.LQFSEQVENIKPEIVSVTAACEELR.K	2892.23121	3	3.88E-05	0.87	3.75	-	1300.3
AHQ-2-4, 5394	K.LVAEDLSQDCFWTK.V	1713.88927	2	6.00E-07	0.95	4.09	-	1127.6
AHQ-2-3, 5364	K.LVAEDLSQDCFWTK.V	1713.88927	2	2.99E-08	0.92	3.88	-	944.6
gi|6912240|ref|NP_036227.1|	adaptor-related protein complex 3, mu 1 subunit; mu-adaptin 3A; AP-3 ad			3.24E-08	0.90	10.20	5.50	46938.9
AHQ-2-10, 4434	K.GLVNLQSGAPKPEENPSLNIQFK.I	2481.78929	2	3.24E-08	0.90	4.10	-	659.6
gi|4557597|ref|NP_001449.1|	gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);			3.29E-08	1.76	30.28	1.70	288897.4
AHQ-2-1, 4826 - 4836	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.24E-04	0.95	5.70	-	546.8
AHQ-2-4, 4608 - 4613	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	1.26E-07	0.83	4.07	-	391.1
AHQ-2-6, 4165	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	6.09E-05	0.88	4.36	-	363.0
AHQ-2-3, 4660	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	1.39E-05	0.89	4.47	-	608.9
AHQ-2-5, 4136 - 4213	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	4.35E-05	0.94	5.49	-	453.7
AHQ-2-2, 1705 - 1760	K.IECDDKGDGSCDVR.Y	1628.67809	2	3.29E-08	0.87	3.00	-	942.6
AHQ-2-1, 1993	K.IECDDKGDGSCDVR.Y	1628.67809	2	3.38E-04	0.86	3.35	-	829.5
AHQ-2-2, 1793 - 2009	K.NDNDTFTVK.Y	1054.09237	1	2.79E-04	0.06	1.96	-	165.8
gi|11321601|ref|NP_002618.1|	phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom			3.43E-08	3.66	40.29	8.80	85595.6
AHQ-2-5, 3200 - 3207	R.DLQSNVEHLTEK.M	1413.51529	2	3.60E-06	0.87	3.62	-	856.4
AHQ-2-5, 6129	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	1.40E-05	0.83	3.72	-	585.7
AHQ-2-5, 6595	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	3.43E-08	0.97	5.84	-	1016.3
AHQ-2-5, 4907	R.LPLMECVQMTQDVQK.A	1822.16087	2	1.60E-05	0.98	4.93	-	2422.1

gi|4507509|ref|NP_003245.1| tissue inhibitor of metalloproteinase 1 precursor; Erythroid-potentiati				3.48E-08	1.66	20.23	16.90	23170.8
AHQ-2-9, 5534	R.FVYTPAMESVCGYFHR.S	1966.22851	2	3.48E-08	0.73	2.93	-	682.0
AHQ-2-10, 4216	K.LQSGTHCLWTDQLLQGSEK.G	2203.41795	2	3.84E-04	0.93	4.54	-	927.0
gi|5174393|ref|NP_006001.1| arginine-rich, mutated in early stage tumors; arginine-rich protein [Ho				3.52E-08	2.47	30.29	13.70	26906.2
AHQ-2-12, 4678	K.DRDVTFSPATIENELIK.F	1949.15100	2	1.02E-05	0.94	4.53	-	1126.2
AHQ-2-12, 5651 - 5723	K.DRDVTFSPATIENELIK.F	1949.15100	2	8.12E-06	0.97	5.49	-	1648.8
AHQ-2-12, 5745	K.DRDVTFSPATIENELIK.F	1949.15100	2	3.52E-08	0.98	5.76	-	2252.9
AHQ-2-12, 6273 - 6305	R.DVTFSPATIENELIK.F	1677.87678	2	2.70E-04	0.65	2.81	-	476.7
AHQ-2-12, 3223	K.ILDDWGETCKGCAEK.S	1784.94596	2	3.70E-04	0.84	3.14	-	680.1
gi|5901922|ref|NP_008996.1| CDC37 homolog [Homo sapiens]				3.61E-08	0.94	10.24	5.60	44468.0
AHQ-2-7, 6733 - 6807	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	3.61E-08	0.94	4.79	-	572.1
gi|19913441|ref|NP_002140.2| hippocalcin-like 1; visinin-like protein 3; calcium-binding protein BD				3.67E-08	2.80	30.22	22.30	22313.1
AHQ-2-11, 4174 - 4181	R.ENTEFTDHELQEWYK.G	1970.04095	2	3.67E-08	0.91	4.14	-	903.4
AHQ-2-11, 5752	R.SEMLEIVQAIYK.M	1424.68776	2	8.51E-04	0.93	2.75	-	1468.6
AHQ-2-11, 5920	K.WAFSMYDLDGNGYISR.S	1896.07185	2	8.42E-08	0.96	4.24	-	1714.4
gi|20070158|ref|NP_003567.2| serine/threonine kinase 24 (STE20 homolog, yeast); STE20-like kinase 3				3.70E-08	0.92	10.18	3.40	49307.6
AHQ-2-7, 3641	K.SQACGGNLGSIEELR.G	1592.71366	2	3.70E-08	0.92	3.53	-	1541.3
gi|29737978|ref|XP_290747.1| similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy				3.70E-08	4.37	50.25	3.80	191380.7
AHQ-2-3, 3975 - 3991	K.ADFCIIHYAGK.V	1296.47641	2	7.08E-07	0.94	3.22	-	1369.4
AHQ-2-4, 3965	K.ADFCIIHYAGK.V	1296.47641	2	6.94E-06	0.95	3.68	-	1628.8
AHQ-2-4, 3978	K.ADFCIIHYAGK.V	1296.47641	1	7.60E-06	0.71	2.75	-	622.3
AHQ-2-7, 3609	K.ADFCIIHYAGK.V	1296.47641	2	1.75E-07	0.89	2.78	-	1360.8
AHQ-2-6, 3650	K.ADFCIIHYAGK.V	1296.47641	2	1.71E-06	0.96	4.04	-	1404.8
AHQ-2-5, 3687	K.ADFCIIHYAGK.V	1296.47641	2	2.94E-06	0.95	3.47	-	1406.8
AHQ-2-2, 4000 - 4002	K.ADFCIIHYAGK.V	1296.47641	2	3.70E-08	0.97	4.16	-	1651.8
AHQ-2-1, 3066	R.AGVLAHLEEER.D	1224.34854	1	6.10E-07	0.51	2.65	-	546.3
AHQ-2-1, 3056 - 3061	R.AGVLAHLEEER.D	1224.34854	2	6.74E-07	0.94	4.35	-	1383.8
AHQ-2-2, 2806	R.AGVLAHLEEER.D	1224.34854	2	4.18E-07	0.95	4.04	-	1451.4
AHQ-2-2, 2762 - 2832	R.AGVLAHLEEER.D	1224.34854	2	7.13E-04	0.87	3.08	-	1104.0
AHQ-2-1, 3017 - 3089	R.AGVLAHLEEER.D	1224.34854	1	3.77E-04	0.20	1.84	-	544.9
AHQ-2-9, 2558	R.AGVLAHLEEER.D	1224.34854	1	7.87E-04	0.27	2.40	-	340.1
AHQ-2-3, 2744 - 2815	R.AGVLAHLEEER.D	1224.34854	2	1.16E-07	0.94	3.85	-	1297.1
AHQ-2-3, 2772 - 2775	R.AGVLAHLEEER.D	1224.34854	1	1.09E-04	0.63	2.85	-	573.6
AHQ-2-1, 6757 - 6794	R.ALEQQVEEM*RTQLEELEDELQATEDAK.L	3193.39738	3	6.73E-04	0.62	3.43	-	528.6
AHQ-2-2, 3762	K.DKADFCIIHYAGK.V	1539.73719	3	2.54E-06	0.95	4.58	-	1414.8
AHQ-2-2, 3750 - 3757	K.DKADFCIIHYAGK.V	1539.73719	2	3.86E-06	0.96	4.91	-	1395.1
AHQ-2-5, 3389	K.DKADFCIIHYAGK.V	1539.73719	3	9.67E-08	0.91	3.72	-	1491.8
AHQ-2-1, 3886	K.DKADFCIIHYAGK.V	1539.73719	2	1.08E-06	0.96	4.41	-	1623.5
AHQ-2-3, 3689	K.DKADFCIIHYAGK.V	1539.73719	2	3.71E-08	0.94	3.85	-	1455.6
AHQ-2-2, 4798 - 4837	K.LDPHLVLDQLR.C	1319.53460	2	1.18E-06	0.87	2.97	-	722.4
AHQ-2-2, 4822	K.LDPHLVLDQLR.C	1319.53460	3	1.06E-06	0.89	3.38	-	963.0
AHQ-2-1, 4916	K.LDPHLVLDQLR.C	1319.53460	3	8.66E-06	0.84	3.74	-	727.8
gi|14251209|ref|NP_001279.2| chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo				3.92E-08	6.48	80.30	46.10	26922.5
AHQ-2-9, 6487 - 6550	K.FLDGNELTLADCNLLPK.L	1935.18752	2	3.20E-06	0.85	4.78	-	679.7
AHQ-2-9, 6402	K.FLDGNELTLADCNLLPK.L	1935.18752	2	9.85E-05	0.23	2.59	-	350.2
AHQ-2-9, 3591	K.FSAYIKNSNPALNDNLEK.G	2039.23424	2	4.43E-04	0.87	4.19	-	771.4
AHQ-2-13-, 3418	K.GVTFNVTTVDTK.R	1282.42476	2	3.11E-06	0.89	3.61	-	916.3
AHQ-2-13, 3431 - 3436	K.GVTFNVTTVDTK.R	1282.42476	2	6.36E-06	0.95	3.96	-	1098.0
AHQ-2-10, 3087	K.GVTFNVTTVDTK.R	1282.42476	2	1.92E-05	0.92	3.75	-	1005.4
AHQ-2-14-, 3365	K.GVTFNVTTVDTK.R	1282.42476	2	4.40E-05	0.77	3.03	-	527.9
AHQ-2-9, 3111	K.GVTFNVTTVDTK.R	1282.42476	2	4.72E-06	0.90	3.26	-	959.2
AHQ-2-9, 2260	K.IGNCPFSQR.L	1080.19948	2	1.03E-04	0.76	3.06	-	484.5
AHQ-2-9, 5792 - 5822	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	4.20E-06	0.95	5.34	-	1211.6
AHQ-2-9, 5535 - 5611	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.92E-08	0.97	6.02	-	999.2
AHQ-2-13, 5311	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.04E-05	0.91	4.20	-	705.9
AHQ-2-9, 5282 - 5350	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	4.80E-05	0.93	4.74	-	637.1
AHQ-2-10, 4930	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	7.93E-06	0.96	5.18	-	958.6
AHQ-2-10, 5167	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	8.54E-04	0.90	3.94	-	629.1
AHQ-2-11, 5169 - 5192	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.02E-04	0.92	4.26	-	737.1
AHQ-2-14-, 5369	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.73E-05	0.95	5.26	-	758.6
AHQ-2-12, 5430	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.75E-06	0.92	3.95	-	792.3
AHQ-2-9, 2442 - 2462	K.LHIVQVVCK.K	1097.35623	1	3.16E-04	0.59	2.39	-	449.1
AHQ-2-10, 2439	K.LHIVQVVCK.K	1097.35623	1	1.42E-05	0.76	2.62	-	780.3
AHQ-2-9, 2459	K.LHIVQVVCK.K	1097.35623	1	1.05E-05	0.78	2.79	-	574.5
AHQ-2-12, 2653	K.LHIVQVVCK.K	1097.35623	1	1.82E-05	0.73	2.41	-	830.8
AHQ-2-9, 5414 - 5482	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	5.80E-04	0.65	3.01	-	381.5
AHQ-2-12, 5358	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	4.98E-06	0.41	2.60	-	319.1
gi|4758484|ref|NP_004823.1| glutathione-S-transferase like; glutathione transferase omega [Homo sap				3.97E-08	2.67	50.19	24.10	27565.7
AHQ-2-10, 3682	K.EDPTVSALLTSEK.D	1390.51840	1	2.62E-06	0.55	2.70	-	263.9
AHQ-2-10, 3774	K.EFTKLEEVLTNK.K	1451.64657	2	3.97E-08	0.77	3.88	-	430.3
AHQ-2-10, 2328 - 2331	K.GSAPPGPVPEGSIR.I	1321.46422	1	8.31E-05	0.23	2.65	-	159.0
AHQ-2-10, 2475	R.HEVININLK.N	1080.26247	1	4.94E-05	0.85	3.57	-	490.9
AHQ-2-10, 2459 - 2463	R.HEVININLK.N	1080.26247	2	1.07E-06	0.89	3.25	-	727.1
AHQ-2-10, 2458	R.HEVININLK.N	1080.26247	1	4.94E-05	0.64	2.72	-	499.7
AHQ-2-9, 4344	K.VPSLVGSFIR.S	1075.28583	1	4.18E-04	0.24	1.88	-	237.7
gi|14249348|ref|NP_116120.1| hypothetical protein MGC14353 [Homo sapiens]				4.23E-08	0.99	20.18	19.50	13940.7
AHQ-2-13-, 4145	K.SWCPDCVQAEPVVR.E	1705.89366	2	4.23E-08	0.95	3.56	-	1525.1
AHQ-2-13, 4715 - 4781	K.TIFAYFTGSK.D	1135.29336	1	3.44E-05	0.04	1.96	-	77.5
gi|4505303|ref|NP_002466.1| myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m				4.26E-08	2.66	30.20	11.50	22763.8
AHQ-2-12, 2971	R.ALGQNPTNAEVLK.V	1355.52211	1	6.29E-06	0.21	2.37	-	290.9
AHQ-2-12, 2598 - 2665	R.ALGQNPTNAEVLK.V	1355.52211	2	3.44E-07	0.86	3.94	-	567.9
AHQ-2-12, 2609 - 2673	R.ALGQNPTNAEVLK.V	1355.52211	1	9.97E-04	0.35	2.86	-	319.8
AHQ-2-12, 2963 - 2967	R.ALGQNPTNAEVLK.V	1355.52211	2	2.28E-04	0.81	3.28	-	619.8
AHQ-2-12, 2515	R.ALGQNPTNAEVLK.V	1355.52211	2	3.55E-05	0.88	3.76	-	588.4
AHQ-2-12, 3269	K.ILYSQCGDVMR.A	1343.55489	2	4.26E-08	0.91	2.92	-	1063.0
AHQ-2-14-, 3260	K.ILYSQCGDVMR.A	1343.55489	2	6.48E-05	0.90	2.80	-	1076.7
AHQ-2-12, 2581 - 2651	K.ILYSQCGDVM*R.A	1359.55429	2	1.49E-04	0.89	3.33	-	885.1
gi|30158489|ref|XP_301421.1| similar to Chloride intracellular channel protein 1 (Nuclear chloride				4.39E-08	1.64	20.22	6.90	28267.5
AHQ-2-9, 6250 - 6319	K.FLNGNELTLADCNLLPK.L	1934.20276	2	2.05E-06	0.86	4.27	-	977.7
AHQ-2-10, 5795 - 5859	K.FLNGNELTLADCNLLPK.L	1934.20276	2	2.80E-05	0.50	3.03	-	555.1
AHQ-2-12, 6203	K.FLNGNELTLADCNLLPK.L	1934.20276	2	4.39E-08	0.81	3.90	-	896.7
AHQ-2-9, 5708 - 5754	R.KFLNGNELTLADCNLLPK.L	2062.37568	2	2.76E-07	0.83	4.34	-	795.3
gi|18571222|ref|XP_088393.1| similar to destrin - pig [Homo sapiens]				4.48E-08	1.85	20.20	11.70	11560.5
AHQ-2-12, 2509	K.HFVGMLPEKDCR.C	1490.73281	3	4.48E-08	0.90	3.70	-	1150.1
AHQ-2-12, 2199	K.HFVGM*LPEKDCR.C	1506.73221	2	3.83E-04	0.95	3.98	-	1167.6
gi|4758304|ref|NP_004902.1| protein disulfide isomerase related protein (calcium-binding protein, i				4.49E-08	3.82	50.20	12.40	72931.9
AHQ-2-6, 4603	K.DLGLSESGEDVNAAILDESGKK.F	2248.38737	2	5.60E-08	0.92	4.05	-	1110.0
AHQ-2-6, 6047 - 6057	R.EVSQPDWTPPPEVTLVLTK.E	2137.41772	2	8.92E-04	0.35	2.94	-	143.4
AHQ-2-6, 4574	K.FAMEPEEFDSDTLR.E	1687.80890	2	4.49E-08	0.78	3.12	-	497.9
AHQ-2-6, 2753	K.IDATSASVLASR.F	1191.31686	2	2.05E-05	0.92	3.42	-	1129.0
AHQ-2-6, 2725 - 2734	K.VSQGQLVVMQPEK.F	1443.69431	2	3.74E-06	0.84	3.18	-	1324.3
gi|4506063|ref|NP_002725.1| protein kinase, cAMP-dependent, regulatory, type I, alpha; tissue-speci				4.53E-08	1.41	20.16	7.60	42981.4
AHQ-2-9, 5120	R.LTVADALEPVQFEDGQK.I	1861.04222	2	9.47E-05	0.49	2.66	-	281.1
AHQ-2-7, 2823	K.NVLFSHLDDNER.S	1459.54574	2	4.53E-08	0.92	3.15	-	1352.6
gi|27478053|ref|XP_015334.4| similar to heat shock 70kD protein binding protein; progesterone recep				4.71E-08	0.98	10.26	11.60	16603.8
AHQ-2-7, 4677	R.LLGHWEEAAHDLALACK.L	1936.18044	2	4.71E-08	0.98	5.24	-	2060.5
gi|24797067|ref|NP_002107.3| major histocompatibility complex, class I, A precursor; HLA-A1 class I				4.80E-08	4.09	50.23	21.60	40840.5

AHQ-2-8, 3178	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	3	5.38E-06	0.62	3.18	-	477.3
AHQ-2-8, 3171	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	2	9.92E-06	0.68	3.84	-	376.5
AHQ-2-14-, 5008	R.FIAVGYVDDTQFVR.F	1630.82504	2	1.18E-06	0.92	3.57	-	1249.1
AHQ-2-14, 6130 - 6208	R.FIAVGYVDDTQFVR.F	1630.82504	2	2.78E-04	0.93	3.08	-	1534.2
AHQ-2-8, 2902 - 2916	K.WAAVVVPSGEEQR.Y	1428.57478	2	2.39E-04	0.95	3.98	-	1182.1
AHQ-2-8, 1858	R.YLENGKETLQR.T	1351.49032	2	6.15E-05	0.66	2.57	-	721.8
AHQ-2-8, 2754	R.YTCHVQHEGLPKPLTLR.W	2051.35781	3	4.80E-08	0.94	4.68	-	1908.2
gi|4758950|ref|NP_000933.1| peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]				4.92E-08	7.72	90.24	39.80	23742.4
AHQ-2-12, 4231 - 4287	K.DFMIQGGDFTR.G	1287.42660	2	3.17E-04	0.81	2.95	-	891.9
AHQ-2-11, 2852	R.DKPLKDVIIADCGK.I	1573.83653	3	1.01E-05	0.95	4.71	-	1740.5
AHQ-2-11, 2830	R.DKPLKDVIIADCGK.I	1573.83653	2	4.92E-08	0.93	3.57	-	1147.6
AHQ-2-12, 4453	K.DTNGSQFFITTVK.T	1458.59766	2	1.95E-04	0.86	2.99	-	1039.2
AHQ-2-13-, 4438	K.DTNGSQFFITTVK.T	1458.59766	2	1.04E-06	0.84	3.09	-	826.3
AHQ-2-11, 4201 - 4270	K.DTNGSQFFITTVK.T	1458.59766	1	6.84E-05	0.17	2.28	-	349.7
AHQ-2-12, 4449	K.DTNGSQFFITTVK.T	1458.59766	1	5.18E-06	0.07	1.86	-	207.9
AHQ-2-11, 2388	K.DVIIADCGK.I	992.12891	1	4.17E-07	0.45	2.11	-	544.8
AHQ-2-12, 2426	K.DVIIADCGK.I	992.12891	1	3.38E-05	0.71	2.14	-	814.7
AHQ-2-12, 3003	K.HYGPGWVSMANAGK.D	1475.65664	2	9.79E-08	0.96	4.70	-	1063.5
AHQ-2-12, 3042 - 3049	K.IEVEKPFAIAK.E	1245.49240	2	6.50E-05	0.86	3.32	-	860.1
AHQ-2-11, 3004 - 3074	K.IEVEKPFAIAK.E	1245.49240	2	1.28E-05	0.93	3.61	-	1484.6
AHQ-2-11, 3193	K.IEVEKPFAIAKE	1374.60693	2	6.67E-04	0.97	4.39	-	2010.5
AHQ-2-12, 4366	K.TVDNFVALATGEK.G	1365.51377	2	5.15E-06	0.93	4.04	-	995.7
AHQ-2-12, 4371	K.TVDNFVALATGEK.G	1365.51377	1	2.72E-06	0.06	2.13	-	273.0
AHQ-2-12, 4350 - 4353	K.TVDNFVALATGEK.G	1365.51377	2	3.19E-04	0.91	3.78	-	786.6
AHQ-2-11, 4240	K.TVDNFVALATGEK.G	1365.51377	1	1.31E-05	0.46	3.00	-	329.7
AHQ-2-11, 4594 - 4666	K.TVDNFVALATGEK.G	1365.51377	2	5.51E-07	0.90	3.36	-	790.2
AHQ-2-14-, 4361	K.TVDNFVALATGEK.G	1365.51377	2	1.25E-04	0.76	3.00	-	603.8
AHQ-2-11, 2838 - 2913	K.VLEGMEVVR.K	1032.23962	2	3.11E-05	0.93	3.45	-	1211.9
gi|5174539|ref|NP_005908.1| cytosolic malate dehydrogenase; soluble malate dehydrogenase [Homo sapi				5.03E-08	2.29	30.20	12.00	36425.9
AHQ-2-13-, 2994	K.DVIATDKEDVAFK.D	1451.60343	2	5.03E-08	0.95	3.90	-	1619.9
AHQ-2-9, 5142	K.EVGVYEALKDDSWLK.G	1752.94535	2	7.14E-05	0.83	3.28	-	857.4
AHQ-2-9, 4632	K.FVEGLPINDFSR.E	1394.55680	1	8.95E-05	0.50	2.82	-	279.3
gi|22538814|ref|NP_002976.2| small inducible cytokine A5 precursor; T-cell specific protein p288; T				5.32E-08	1.41	20.20	20.90	9989.6
AHQ-2-14-, 3772 - 3780	K.CSNPAVVFVTR.K	1251.43718	2	5.32E-08	0.93	3.99	-	779.1
AHQ-2-14-, 2271	K.EYFYTSGK.C	995.06653	1	2.16E-04	0.48	2.25	-	253.9
gi|6912238|ref|NP_036226.1| peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]				6.64E-08	6.43	70.27	44.90	22026.2
AHQ-2-12, 7069	K.ETDLLLDDSLVSIFGNR.R	1908.09888	2	8.49E-08	0.97	5.39	-	1416.7
AHQ-2-12, 3906 - 3982	R.FSMVVQDGIVK.A	1223.46709	2	4.13E-06	0.95	4.10	-	1302.6
AHQ-2-12, 4683	K.KGVLFGVPGAFTPGCSK.T	1724.01680	2	6.64E-08	0.94	4.28	-	908.6
AHQ-2-13-, 3490 - 3525	R.LLADPTGAFGK.E	1090.25413	2	1.22E-04	0.79	2.59	-	797.7
AHQ-2-12, 4206	K.THLPGFVEQAEALK.A	1540.74504	3	5.02E-05	0.94	3.97	-	2161.2
AHQ-2-12, 4886 - 4967	K.VGDAIPAVEVFEGEPGNK.V	1829.00022	2	5.30E-07	0.94	4.67	-	565.3
AHQ-2-12, 4765 - 4777	K.VNLAELFK.G	934.11414	2	8.05E-05	0.90	3.38	-	764.4
gi|5031985|ref|NP_005787.1| nuclear transport factor 2; placental protein 15 [Homo sapiens]				6.72E-08	3.95	50.30	63.00	14478.4
AHQ-2-14-, 6128	K.ADEDPIMGFHQMFLLK.N	1893.21919	3	1.92E-05	0.60	3.21	-	450.1
AHQ-2-14-, 6107 - 6119	K.IQHSITAQDHQPTPDSCIISMVVGQLK.A	3006.40418	3	1.39E-07	0.97	5.90	-	1857.0
AHQ-2-14-, 5387 - 5391	K.NINDAWVCTNDMFR.L	1757.92888	2	6.72E-08	0.97	4.98	-	1178.4
AHQ-2-14, 5550	K.NINDAWVCTNDM*FR.L	1773.92828	2	1.77E-05	0.46	2.89	-	381.1
AHQ-2-14-, 6445 - 6468	R.TQLGAIYIDASCLTWEGQQFQGK.A	2616.88699	2	1.54E-07	0.95	4.76	-	999.1
gi|14211923|ref|NP_115982.1| PKCI-1-related HIT protein [Homo sapiens]				7.12E-08	3.50	40.25	41.70	17161.6
AHQ-2-13-, 3277	K.AQQATPGGAAPTIFSR.I	1573.73512	2	6.26E-07	0.93	4.33	-	565.4
AHQ-2-13, 4753	R.DVAPQAPVHFLVIPK.K	1631.94245	2	9.11E-04	0.79	3.30	-	575.6
AHQ-2-13-, 6318	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	1.12E-05	0.95	4.92	-	1278.1
AHQ-2-13-, 6247 - 6314	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	7.12E-08	0.88	3.99	-	975.6
AHQ-2-13, 6119	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	8.12E-07	0.93	4.42	-	1150.9
AHQ-2-13-, 6333 - 6398	K.SLPADILYEDQQCLVFR.D	2069.32354	2	4.50E-04	0.92	3.70	-	1054.7
AHQ-2-13, 6172	K.SLPADILYEDQQCLVFR.D	2069.32354	2	2.96E-05	0.90	3.90	-	825.1
gi|4507745|ref|NP_003320.1| thioredoxin [Homo sapiens]				7.73E-08	0.94	10.19	12.40	11693.3
AHQ-2-14, 4769 - 4784	K.TAFQEALDAAGDK.L	1337.41728	2	4.20E-07	0.77	3.00	-	918.0
AHQ-2-13-, 2809	K.TAFQEALDAAGDK.L	1337.41728	2	2.02E-05	0.76	2.62	-	1161.1
AHQ-2-13-, 3837 - 3909	K.TAFQEALDAAGDK.L	1337.41728	2	2.30E-06	0.93	3.49	-	1682.1
AHQ-2-13-, 3914 - 3930	K.TAFQEALDAAGDK.L	1337.41728	1	7.54E-05	0.49	2.22	-	888.7
AHQ-2-14-, 3815 - 3816	K.TAFQEALDAAGDK.L	1337.41728	2	7.73E-08	0.94	3.72	-	1429.5
AHQ-2-14-, 3820 - 3896	K.TAFQEALDAAGDK.L	1337.41728	1	6.68E-07	0.75	2.84	-	829.2
AHQ-2-13, 3863	K.TAFQEALDAAGDK.L	1337.41728	2	1.14E-06	0.93	3.29	-	1477.0
gi|4505759|ref|NP_002622.1| phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo				8.12E-08	3.73	40.33	15.50	53151.7
AHQ-2-8, 2923	R.HEMLPASLIQAQR.D	1494.74454	2	2.05E-04	0.88	3.10	-	753.2
AHQ-2-8, 6563	K.IKDAFDRNPELQNLLLDDFFK.S	2552.86598	3	1.36E-05	0.94	4.88	-	1151.4
AHQ-2-8, 6208	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	3.54E-07	0.91	4.28	-	958.2
AHQ-2-7, 6304	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	8.12E-08	0.98	6.56	-	1979.8
AHQ-2-8, 4223 - 4224	K.VGTGEPCCDWVGDEGAGHFVK.M	2280.43619	3	1.48E-06	0.92	4.72	-	697.7
AHQ-2-8, 4222	K.VGTGEPCCDWVGDEGAGHFVK.M	2280.43619	2	3.43E-05	0.46	2.57	-	349.3
gi|4557801|ref|NP_000261.1| purine nucleoside phosphorylase [Homo sapiens]				8.16E-08	8.01	100.33	46.70	32147.7
AHQ-2-9, 1478	K.ANHEEVLAAGK.Q	1139.24364	1	8.29E-05	0.39	2.52	-	381.9
AHQ-2-9, 4298 - 4303	R.FHMYEGYPLWK.V	1471.70636	1	7.16E-05	0.62	2.55	-	716.1
AHQ-2-9, 4299	R.FHMYEGYPLWK.V	1471.70636	2	1.82E-04	0.92	3.14	-	1175.1
AHQ-2-13-, 3993 - 4066	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	3	8.16E-08	0.98	5.51	-	2889.7
AHQ-2-13, 4023 - 4039	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	2	1.41E-06	0.93	4.19	-	992.9
AHQ-2-13-, 4082	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	2	1.04E-06	0.91	4.07	-	712.8
AHQ-2-13, 6867	K.LEQFVSILMASIPLPDK.A	1902.28716	2	2.36E-06	0.94	4.60	-	846.9
AHQ-2-13-, 7058 - 7135	K.LEQFVSILMASIPLPDK.A	1902.28716	2	9.01E-04	0.93	4.35	-	725.1
AHQ-2-9, 7483 - 7484	K.LEQFVSILMASIPLPDK.A	1902.28716	2	7.35E-06	0.96	5.05	-	1082.0
AHQ-2-9, 4126	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	2.09E-07	0.91	3.71	-	817.2
AHQ-2-13-, 4243 - 4246	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	1.31E-06	0.94	4.62	-	832.8
AHQ-2-13, 4855 - 4920	K.LGADAVGMSTVPEVIVAR.H	1786.08666	2	4.24E-04	0.55	2.91	-	774.3
AHQ-2-11, 4096	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	1.60E-04	0.89	3.79	-	859.8
AHQ-2-13, 5851 - 5853	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	9.01E-07	0.90	4.46	-	555.3
AHQ-2-13-, 5987	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	1.03E-05	0.94	4.54	-	807.1
AHQ-2-9, 6034 - 6060	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	1.09E-04	0.91	4.54	-	477.2
AHQ-2-9, 4792	R.VFGFSLITNK.V	1126.32960	2	3.94E-05	0.93	3.81	-	768.5
AHQ-2-9, 5986 - 5995	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	6.10E-06	0.99	6.67	-	3631.5
AHQ-2-9, 6095	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	4.31E-07	0.92	4.04	-	1058.0
AHQ-2-9, 3371 - 3380	K.VIMDYESLEK.A	1227.40938	2	3.57E-05	0.87	3.37	-	501.2
gi|24497612|ref|NP_116262.2| nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr				8.26E-08	2.56	30.22	5.70	72695.6
AHQ-2-6, 6658	K.LGCDWVATIFSR.D	1426.62208	2	8.26E-08	0.93	3.42	-	1304.0
AHQ-2-6, 6066	R.RPYEDQGLGETTPLTIICQPMQPLR.V	2916.32264	3	1.45E-04	0.90	4.41	-	768.2
AHQ-2-6, 5295	R.RPYEDQGLGETTPLTIICQPM*QPLR.V	2932.32204	3	1.25E-04	0.73	4.05	-	557.1
gi|30147105|ref|XP_210550.2| similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48				8.40E-08	0.92	10.21	2.20	61339.9
AHQ-2-5, 4033	K.ADLINNLGTIAK.S	1243.43490	2	8.40E-08	0.92	4.14	-	997.8
AHQ-2-6, 4003	K.ADLINNLGTIAK.S	1243.43490	2	9.11E-05	0.87	3.08	-	885.0
AHQ-2-5, 3896	K.ADLINNLGTIAK.S	1243.43490	2	7.68E-04	0.81	3.38	-	408.8
gi|4503743|ref|NP_002009.1| flightless I homolog [Homo sapiens]				8.75E-08	2.65	30.23	4.50	144750.1
AHQ-2-4, 3185	K.AVQGAQQPSLYQIR.T	1559.75158	2	4.46E-07	0.92	3.76	-	817.5
AHQ-2-3, 7323	R.TQSNLPTSLEGLSNLADVDLSCNDLTR.V	2936.15611	2	1.62E-05	0.77	3.13	-	674.1
AHQ-2-3, 6871	K.VGLGLGYLELPQINYK.L	1778.08432	2	8.75E-08	0.96	4.66	-	1318.6
gi|4502097|ref|NP_001142.1| solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra				9.02E-08	0.80	10.17	4.00	33148.4
AHQ-2-10, 5271	R.YFPTQALNFAFK.D	1447.66130	1	9.02E-08	0.80	3.29	-	594.0

AHQ-2-10, 5266 - 5275	R.YFPTQALNFAFK.D	1447.66130	2	4.42E-06	0.86	3.40	-	546.9
gi|5802966|ref|NP_006861.1| destrin (actin depolymerizing factor); destrin [Homo sapiens]				9.11E-08	2.72	30.22	24.80	18505.6
AHQ-2-12, 1875 - 1907	K.HECQANGPEDLNR.A	1541.58530	2	1.47E-05	0.92	4.05	-	858.5
AHQ-2-12, 7065 - 7125	R.KEELMFFLWAPELAPLK.S	2063.49022	2	1.05E-04	0.91	4.39	-	837.5
AHQ-2-13-, 3857 - 3881	R.YALYDASFETK.E	1308.41754	2	9.11E-08	0.88	2.99	-	979.6
AHQ-2-12, 3714 - 3733	R.YALYDASFETK.E	1308.41754	2	1.79E-06	0.95	3.83	-	1201.6
gi|30160191|ref|XP_294035.2| similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme				9.24E-08	0.70	10.16	2.80	50222.2
AHQ-2-7, 5184	K.IYVDDGLISLQVK.Q	1463.70048	1	9.24E-08	0.70	3.17	-	618.2
AHQ-2-7, 5112 - 5188	K.IYVDDGLISLQVK.Q	1463.70048	2	3.72E-06	0.91	2.84	-	1607.1
gi|16950601|ref|NP_005956.2| myosin light chain kinase isoform 6; myosin light chain kinase [Homo s				9.35E-08	2.78	30.20	3.20	110074.8
AHQ-2-12, 2523	R.DLEVVEGSAAR.F	1146.23295	2	4.86E-06	0.92	4.02	-	1168.9
AHQ-2-6, 3429 - 3430	K.LVQCVDAFEEK.A	1339.49637	2	8.70E-04	0.92	2.91	-	1221.2
AHQ-2-6, 3329	K.VSDFYDIEER.L	1273.33005	2	9.35E-08	0.94	3.30	-	1215.4
gi|19913373|ref|NP_079536.2| G6B protein isoform G6b-A precursor; G6B protein; immunoglobulin recep				9.44E-08	1.82	20.21	9.30	25002.6
AHQ-2-11, 2365	R.TVLHVLGDR.T	1010.17224	2	6.07E-05	0.88	2.86	-	1301.2
AHQ-2-12, 2391	R.TVLHVLGDR.T	1010.17224	2	5.01E-04	0.92	3.31	-	1399.1
AHQ-2-12, 2394	R.TVLHVLGDR.T	1010.17224	1	8.47E-04	0.64	2.19	-	606.3
AHQ-2-10, 2187	R.TVLHVLGDR.T	1010.17224	1	6.03E-04	0.57	2.28	-	486.0
AHQ-2-12, 2574	R.VNLSCGGVSHPIR.W	1397.58551	2	9.44E-08	0.94	4.22	-	1399.5
gi|18104989|ref|NP_002822.2| protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t				9.44E-08	2.67	30.19	7.10	67560.7
AHQ-2-6, 5893	K.AGFWEEFESLQK.Q	1471.59489	2	2.17E-06	0.94	3.72	-	1543.0
AHQ-2-14, 6066	R.DLSGLDAETLLK.G	1275.43053	2	9.44E-08	0.94	3.61	-	1539.4
AHQ-2-6, 3030	R.WYHGHMSGGQAETLLQAK.G	2015.24110	2	7.87E-07	0.79	3.87	-	557.3
gi|9966867|ref|NP_065123.1| eIF-5A2 protein; eIF5AII [Homo sapiens]				9.60E-08	2.66	30.30	19.60	16793.1
AHQ-2-12, 3631 - 3638	K.KYEDICPSTHNMDVPNIK.R	2163.41723	3	3.63E-06	0.97	6.00	-	1676.2
AHQ-2-12, 4823 - 4825	K.VHLVGIDIFTGK.K	1299.54329	1	9.60E-08	0.93	3.67	-	1142.2
AHQ-2-12, 4821	K.VHLVGIDIFTGK.K	1299.54329	2	4.04E-07	0.93	3.40	-	1254.4
AHQ-2-11, 4656	K.VHLVGIDIFTGK.K	1299.54329	2	9.32E-05	0.91	3.32	-	1185.8
AHQ-2-12, 3973	K.YEDICPSTHNMDVPNIK.R	2035.24432	2	1.36E-04	0.75	3.45	-	560.1
gi|4503377|ref|NP_001377.1| dihydropyrimidinase-like 2; collapsin response mediator protein hCRMP-2				9.93E-08	2.32	30.19	8.00	62293.3
AHQ-2-7, 5521	R.FQMPDQGMTSADDFFQGTK.A	2152.34998	2	8.20E-04	0.82	2.77	-	1006.3
AHQ-2-7, 2540	R.GSPLVVISQGK.I	1085.27902	1	9.93E-08	0.59	2.46	-	621.3
AHQ-2-7, 3031	K.IVLEDGTLHVTEGSGR.Y	1683.84465	2	9.66E-06	0.91	3.87	-	860.5
gi|4506417|ref|NP_002877.1| RAP2B, member of RAS oncogene family [Homo sapiens]				1.01E-07	3.98	50.21	37.20	20494.2
AHQ-2-11, 6062 - 6073	K.ASVDELFAEIVR.Q	1349.51434	2	1.01E-07	0.95	4.08	-	1338.8
AHQ-2-11, 6752	K.EIEVDSSPSVLEILDTAGTEQFASMR.D	2826.08347	2	1.76E-05	0.79	3.76	-	425.4
AHQ-2-11, 3033	R.VPMILVGNK.V	971.24256	2	4.23E-06	0.92	2.95	-	982.1
AHQ-2-11, 2304	K.VVVLGSGGVGK.S	972.16391	1	2.82E-04	0.50	2.28	-	552.0
AHQ-2-11, 4138	K.YDPTIEDFYR.K	1319.40042	2	3.16E-05	0.82	2.59	-	470.2
gi|5453605|ref|NP_006421.1| chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-				1.02E-07	1.89	20.23	4.80	57838.8
AHQ-2-7, 6536	R.DALSDLALHFLNK.M	1457.65603	2	1.02E-07	0.97	4.51	-	2145.6
AHQ-2-7, 3356	K.VIDPATATSVDLR.D	1358.52277	2	1.40E-05	0.92	3.38	-	1066.7
gi|4757768|ref|NP_004300.1| Rho GDP dissociation inhibitor (GDI) alpha [Homo sapiens]				1.07E-07	3.67	40.24	22.50	23206.9
AHQ-2-12, 4658 - 4674	R.AEEYEFLTPVEEAPK.G	1752.89898	2	3.28E-06	0.91	4.26	-	743.3
AHQ-2-10, 4262 - 4267	R.AEEYEFLTPVEEAPK.G	1752.89898	2	1.39E-05	0.92	3.84	-	984.5
AHQ-2-10, 2810	K.IDKTDYMVGSYGPR.A	1602.79350	2	5.53E-06	0.91	3.32	-	1296.0
AHQ-2-10, 3556	K.SIQEIQELDKDDESLR.K	1919.03693	2	1.07E-07	0.95	4.81	-	943.0
AHQ-2-10, 3098 - 3104	K.SIQEIQELDKDDESLRK.Y	2047.20984	3	1.02E-06	0.86	4.09	-	786.2
AHQ-2-10, 3084 - 3102	K.SIQEIQELDKDDESLRK.Y	2047.20984	2	4.60E-07	0.90	4.45	-	646.8
gi|7657431|ref|NP_055205.1| EBNA-2 co-activator (100kD) [Homo sapiens]				1.08E-07	0.88	10.22	2.40	99689.7
AHQ-2-5, 6572 - 6580	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	2.24E-06	0.92	4.35	-	550.5
AHQ-2-6, 6405	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	1.08E-07	0.88	3.74	-	600.3
AHQ-2-4, 6772	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	8.17E-06	0.89	4.33	-	425.9
gi|19913426|ref|NP_001683.2| ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1; A				1.09E-07	0.91	10.21	3.90	56832.7
AHQ-2-7, 5409	K.IPIFSAAGLPHNEIAAQICR.Q	2180.51549	3	1.09E-07	0.91	4.17	-	907.2
gi|13129150|ref|NP_005339.1| heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H				1.18E-07	3.51	40.25	6.10	84659.1
AHQ-2-5, 2684	K.ELHINLIPNKQDR.T	1590.80882	2	7.17E-04	0.92	3.81	-	787.1
AHQ-2-6, 2218	K.FYEQFSK.N	949.04099	1	4.69E-04	0.45	2.30	-	279.3
AHQ-2-5, 2203	K.FYEQFSK.N	949.04099	1	4.40E-04	0.77	2.53	-	676.8
AHQ-2-5, 4012	R.NPDDITNEEYGEFYK.S	1834.87381	2	3.26E-06	0.95	4.94	-	843.7
AHQ-2-6, 3951	R.NPDDITNEEYGEFYK.S	1834.87381	2	1.18E-07	0.97	5.00	-	1213.4
AHQ-2-5, 3749	R.RAPFDLFENR.K	1265.40235	2	4.25E-06	0.86	3.48	-	634.3
gi|4505753|ref|NP_002620.1| phosphoglycerate mutase 1 (brain); Phosphoglycerate mutase A, nonmuscle				1.19E-07	4.51	60.24	28.30	28803.7
AHQ-2-10, 3696	R.FSGWYDADLSPAGHEEAK.R	1981.06697	2	2.35E-07	0.93	4.18	-	1020.1
AHQ-2-10, 3304	R.FSGWYDADLSPAGHEEAKR.G	2137.25332	2	1.19E-07	0.96	4.87	-	1088.1
AHQ-2-10, 1852	R.HYGGLTGLNK.A	1060.18811	1	8.33E-04	0.68	2.80	-	395.6
AHQ-2-10, 3795 - 3860	R.RSYDVPPPPMEPDHPFYSNISK.D	2574.85201	3	2.62E-05	0.71	3.08	-	656.0
AHQ-2-10, 4130	R.SYDVPPPPMEPDHPFYSNISK.D	2418.66566	2	2.78E-05	0.36	2.79	-	253.4
AHQ-2-10, 4695	R.YADLTEDQLPSCESLKDTIAR.A	2427.62735	3	9.19E-06	0.86	3.44	-	892.3
gi|8923812|ref|NP_060943.1| uncharacterized hypothalamus protein HT012 [Homo sapiens]				1.21E-07	0.93	10.18	8.60	14960.4
AHQ-2-13-, 4166	K.TLAFTSVDLTNK.A	1310.47811	2	1.21E-07	0.93	3.63	-	1211.6
gi|4507171|ref|NP_003109.1| secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec				1.22E-07	2.18	30.20	9.90	34632.0
AHQ-2-9, 2882	R.LEAGDHPVELLAR.D	1420.59579	2	1.04E-06	0.96	4.06	-	1498.2
AHQ-2-8, 2244 - 2307	K.RLEAGDHPVELLAR.D	1576.78214	2	2.10E-07	0.78	3.46	-	427.9
AHQ-2-11, 6186	K.YIPPCLDSELTEFPLR.M	1952.21655	2	1.22E-07	0.44	2.94	-	123.8
AHQ-2-9, 6616 - 6622	K.YIPPCLDSELTEFPLR.M	1952.21655	2	2.55E-06	0.64	2.67	-	280.6
gi|11993943|ref|NP_055419.1| Tax interaction protein 1 [Homo sapiens]				1.24E-07	0.95	10.21	13.70	13734.6
AHQ-2-13-, 4167	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	1.24E-07	0.95	4.12	-	1504.0
AHQ-2-13, 4121 - 4195	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	2.01E-06	0.94	3.66	-	1415.9
gi|7657313|ref|NP_055277.1| Lsm1 protein [Homo sapiens]				1.24E-07	0.86	10.21	12.00	15179.3
AHQ-2-12, 5955 - 6034	R.SIDQFANLVLHQTVER.I	1871.08670	2	1.24E-07	0.86	4.17	-	555.2
gi|4757766|ref|NP_004299.1| Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa				1.25E-07	3.33	40.23	11.40	50435.4
AHQ-2-7, 6247	K.FLLDHQGELFPSPDPSGL	1970.17037	2	4.49E-07	0.85	3.60	-	704.2
AHQ-2-11, 3965	K.NPEQEPIPIVLR.E	1405.62426	2	4.60E-07	0.89	3.36	-	974.1
AHQ-2-8, 6120	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	4.23E-04	0.64	2.85	-	484.4
AHQ-2-11, 5926	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	1.25E-07	0.93	4.63	-	806.7
AHQ-2-7, 6172	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	6.34E-04	0.68	3.06	-	513.2
AHQ-2-11, 6678	K.YNMGLPVDFDQYNELHLPAVILK.T	2691.09719	3	5.13E-05	0.66	3.08	-	258.5
gi|30148346|ref|XP_302059.1| similar to MLRQ subunit of the NADH: ubiquinone oxidoreductase complex				1.30E-07	0.32	10.11	6.60	17253.8
AHQ-2-14-, 3349 - 3376	K.FYSVNVDYSK.L	1222.32788	1	1.30E-07	0.32	2.19	-	246.1
gi|5902090|ref|NP_008862.1| solute carrier family 2 (facilitated glucose transporter), member 3; GL				1.40E-07	0.83	10.18	3.00	53924.0
AHQ-2-1, 5361	R.LWGTQDVSQDIQEMK.D	1778.96471	2	1.40E-07	0.83	3.51	-	481.6
gi|7661922|ref|NP_055814.1| RAB21, member RAS oncogene family [Homo sapiens]				1.45E-07	0.96	10.25	7.60	24347.4
AHQ-2-10, 3946	R.HVSIQEAESYAESVGAK.H	1805.92351	2	1.45E-07	0.96	5.06	-	1244.7
gi|8923541|ref|NP_060357.1| hypothetical protein FLJ20580 [Homo sapiens]				1.52E-07	0.92	10.21	10.00	18048.3
AHQ-2-10, 4110	K.AQESVGIYEVTHQFVK.C	1836.03759	2	1.52E-07	0.92	4.24	-	823.7
gi|4502021|ref|NP_003680.1| aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase);				1.55E-07	0.81	10.17	5.80	36648.3
AHQ-2-9, 3694	K.ALQAAYGASAPSVTSAALR.W	1806.01302	2	1.55E-07	0.81	3.34	-	685.8
gi|10337595|ref|NP_066283.1| protein phosphatase 1A isoform 1; protein phosphatase 2C alpha isoform				1.64E-07	0.89	10.19	4.70	42447.5
AHQ-2-7, 3401	K.GPTEQLVSPEPEVHDIER.S	2033.18486	3	1.64E-07	0.89	3.85	-	1097.9
gi|4505621|ref|NP_002558.1| prostatic binding protein; phosphatidylethanolamine binding protein [Ho				1.67E-07	1.91	20.24	20.30	21056.6
AHQ-2-11, 4916	R.APVAGTCYQAEWDDYVPK.L	2072.23961	2	6.31E-05	0.96	4.46	-	1273.5
AHQ-2-11, 4262	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	1.67E-07	0.95	4.44	-	1110.2
gi|4507487|ref|NP_003238.1| thrombospondin 2 [Homo sapiens]				1.71E-07	1.74	20.19	2.60	129954.5
AHQ-2-1, 5418	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.61E-04	0.87	3.49	-	920.8
AHQ-2-1, 5502	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.88E-04	0.86	3.05	-	1023.0
AHQ-2-1, 3041 - 3045	R.NALWHTGNTPGQVR.T	1551.69124	2	1.71E-07	0.86	3.43	-	844.9

AHQ-2-2, 2516	R.NALWHTGNTPGQVR.T	1551.69124	2	5.73E-05	0.70	2.55	-	737.4
AHQ-2-3, 2509	R.NALWHTGNTPGQVR.T	1551.69124	3	7.06E-04	0.87	3.76	-	785.8
AHQ-2-3, 3063	R.NALWHTGNTPGQVR.T	1551.69124	2	1.37E-04	0.73	2.78	-	778.8
AHQ-2-4, 2449 - 2520	R.NALWHTGNTPGQVR.T	1551.69124	2	2.91E-04	0.76	3.44	-	872.1
AHQ-2-5, 2296	R.NALWHTGNTPGQVR.T	1551.69124	2	6.45E-07	0.88	3.04	-	1003.7
AHQ-2-11, 2493 - 2494	R.NALWHTGNTPGQVR.T	1551.69124	2	1.19E-05	0.92	3.17	-	1303.5
AHQ-2-13-, 2690	R.NALWHTGNTPGQVR.T	1551.69124	2	1.46E-05	0.86	3.24	-	982.4
AHQ-2-14-, 2644	R.NALWHTGNTPGQVR.T	1551.69124	2	3.13E-06	0.87	3.26	-	978.4
gi|10863873|ref|NP_000651.1| transforming growth factor, beta 1 (Camurati-Engelmann disease); trans				1.72E-07	3.00	40.21	16.90	44422.0
AHQ-2-13, 3368	R.ALDTNYCFSSTEK.N	1537.63010	2	2.74E-06	0.85	3.30	-	730.8
AHQ-2-13-, 3350	R.ALDTNYCFSSTEK.N	1537.63010	2	1.72E-07	0.92	3.90	-	788.9
AHQ-2-13-, 6602	K.GYHANFCLGPCPYIWSLDTQYSK.V	2781.07085	2	3.47E-04	0.59	2.63	-	395.3
AHQ-2-9, 6959	R.LLAPSDSPEWLSFDVTGVVR.Q	2189.45272	2	7.65E-06	0.57	3.19	-	317.8
AHQ-2-13, 3481	K.VEQLSNMIVR.S	1189.41074	2	1.90E-05	0.92	3.40	-	1328.5
gi|23308579|ref|NP_006592.3| unactive progesterone receptor, 23 kD; likely ortholog of mouse telome				1.72E-07	0.93	10.22	10.60	18697.3
AHQ-2-11, 4689	K.HLNEIDLFHCIDPNDSK.H	2069.24049	3	1.72E-07	0.93	4.34	-	1117.2
gi|4759140|ref|NP_004243.1| solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulato				1.77E-07	0.93	10.21	3.90	38868.2
AHQ-2-13-, 3861 - 3862	R.LLVVDPETDEQLQK.L	1627.81777	2	1.77E-07	0.93	4.17	-	740.1
AHQ-2-13, 3843	R.LLVVDPETDEQLQK.L	1627.81777	2	1.98E-07	0.91	3.76	-	694.9
gi|10047092|ref|NP_037391.1| neuronal protein [Homo sapiens]				1.79E-07	0.96	10.23	5.00	31454.0
AHQ-2-14-, 6087	R.TTDIFQTVDLWEGK.D	1653.81378	2	1.79E-07	0.96	4.69	-	1554.1
gi|27480253|ref|XP_208225.1| similar to hypothetical protein FLJ20420 [Homo sapiens]				1.81E-07	0.96	10.19	10.90	11294.5
AHQ-2-10, 2524	R.VAEELALEQAK.K	1201.35165	1	6.08E-04	0.63	2.70	-	892.6
AHQ-2-10, 2523	R.VAEELALEQAK.K	1201.35165	2	1.81E-07	0.96	3.71	-	2068.8
gi|4502303|ref|NP_001688.1| mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m				1.82E-07	5.06	60.25	40.80	23277.2
AHQ-2-11, 6652 - 6714	R.FSPLTTNLINLLAENGR.L	1874.13050	2	6.48E-07	0.66	2.89	-	758.8
AHQ-2-11, 5398 - 5472	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	1.30E-04	0.92	5.05	-	647.5
AHQ-2-13, 5564	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	5.08E-06	0.82	3.26	-	754.1
AHQ-2-14-, 5619	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	9.40E-04	0.62	3.14	-	409.6
AHQ-2-11, 3481	K.LVRPPVQVYGIEGR.Y	1583.85942	3	1.82E-07	0.97	4.55	-	2007.8
AHQ-2-11, 4369	K.TDPSILGGMIVR.I	1259.50097	2	3.35E-04	0.89	3.58	-	542.0
AHQ-2-11, 3130	K.VAASVLNPYVK.R	1161.37549	2	7.09E-07	0.90	3.79	-	704.1
AHQ-2-11, 2404	R.YATALYSAASK.Q	1146.27455	2	4.91E-04	0.82	2.54	-	1042.1
gi|18572267|ref|XP_088476.1| similar to thioredoxin domain containing 4; endoplasmic reticulum resi				1.89E-07	0.91	10.18	3.40	46970.9
AHQ-2-7, 4844	K.TPADCPVIAIDSFR.H	1563.75706	2	1.89E-07	0.91	3.52	-	916.4
gi|4503573|ref|NP_001967.1| enolase 3; enolase-3, beta, muscle; muscle specific enolase; beta enola				2.05E-07	0.94	10.20	3.50	46958.5
AHQ-2-8, 3447	K.VNQIGSVTESIQACK.L	1635.82159	2	3.71E-05	0.86	3.29	-	774.6
AHQ-2-14, 4590	K.VNQIGSVTESIQACK.L	1635.82159	2	9.83E-07	0.90	3.61	-	845.7
AHQ-2-8, 2991	K.VNQIGSVTESIQACK.L	1635.82159	2	2.05E-07	0.94	4.00	-	1127.3
gi|7657647|ref|NP_055363.1| tropomodulin 2 (neuronal) [Homo sapiens]				2.15E-07	0.87	10.15	3.10	39594.8
AHQ-2-11, 3168	K.FGYQFTKQGPR.T	1329.48804	2	2.15E-07	0.87	3.10	-	938.7
gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre				2.16E-07	8.10	90.27	28.30	48141.1
AHQ-2-7, 5721 - 5736	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	2	2.08E-05	0.83	3.46	-	766.0
AHQ-2-9, 5842	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	3.46E-07	0.95	5.37	-	1174.9
AHQ-2-7, 5719	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	7.34E-05	0.94	4.90	-	873.4
AHQ-2-12, 5435 - 5511	R.FYALSASFEPFSNK.G	1608.77470	2	3.13E-06	0.93	3.80	-	1349.8
AHQ-2-7, 5364 - 5435	R.FYALSASFEPFSNK.G	1608.77470	2	1.87E-06	0.96	3.25	-	1874.4
AHQ-2-7, 2252	K.FYGDEEKDKGLQTSQDAR.F	2088.17738	2	2.16E-07	0.90	3.69	-	970.0
AHQ-2-7, 1817	K.HEQNIDCGGGYVK.L	1478.56912	1	1.33E-04	0.86	4.19	-	552.6
AHQ-2-13, 2309	K.HEQNIDCGGGYVK.L	1478.56912	2	1.13E-04	0.95	4.17	-	1290.2
AHQ-2-7, 5060	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	3.81E-05	0.92	4.64	-	716.7
AHQ-2-7, 5341 - 5417	K.KPEDWDEEMDGEWEPPVIQNPEYK.G	2962.14926	3	9.51E-07	0.93	5.00	-	964.5
AHQ-2-7, 1907	K.KVHVIFNYK.G	1148.38164	1	1.20E-05	0.87	3.04	-	697.0
AHQ-2-7, 1905	K.KVHVIFNYK.G	1148.38164	2	1.46E-04	0.80	3.00	-	646.2
AHQ-2-7, 2129	K.NVLINKDIR.C	1085.28225	2	2.06E-05	0.86	2.87	-	807.8
AHQ-2-7, 2313	K.VHVIFNYK.G	1020.20872	1	1.35E-06	0.76	2.42	-	727.3
gi|15451907|ref|NP_006301.2| aminopeptidase puromycin sensitive; puromycin-sensitive aminopeptidase				2.19E-07	1.61	20.19	3.90	98502.8
AHQ-2-5, 7073	R.TIQQCCENILLNAAWLK.R	2078.39839	2	2.19E-07	0.90	3.82	-	1266.1
AHQ-2-5, 4897	K.VTLSFPSTLQTGTGTLK.I	1752.00203	2	5.64E-04	0.71	2.88	-	474.9
gi|4759044|ref|NP_004841.1| Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]				2.22E-07	3.24	40.21	4.60	160883.4
AHQ-2-3, 6337	K.ELQDQLEAEQYFSTLYK.T	2106.27421	2	1.86E-05	0.94	4.09	-	1103.9
AHQ-2-3, 3099	K.LFHVRPVTQTDVYR.A	1731.97897	2	8.45E-05	0.58	2.75	-	443.9
AHQ-2-4, 2889	R.SIAEEQYSDLEKEK.I	1669.76838	2	3.52E-05	0.82	2.99	-	959.9
AHQ-2-3, 4312	R.TLTSDVANLANEKEELNNK.L	2104.26140	2	2.22E-07	0.90	4.17	-	1020.5
gi|28269681|ref|NP_783313.1| NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]				2.24E-07	2.62	30.25	40.40	14852.0
AHQ-2-13, 5148 - 5188	K.AYSTTSIASVAGLTAAAYR.V	1875.07212	2	3.17E-05	0.89	4.01	-	515.3
AHQ-2-13, 6493 - 6496	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	2.24E-07	0.92	4.50	-	1261.7
AHQ-2-13-, 6710	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	9.07E-07	0.97	5.00	-	2314.3
AHQ-2-13-, 4966 - 5031	R.VTLNPPGTFLEGVAK.V	1543.78883	2	6.51E-06	0.81	3.14	-	480.7
AHQ-2-13, 4912 - 4952	R.VTLNPPGTFLEGVAK.V	1543.78883	2	3.79E-04	0.38	2.63	-	200.2
gi|5729808|ref|NP_006557.1| adhesion glycoprotein; platelet and T cell activation antigen 1; DNAX a				2.45E-07	0.98	10.25	6.00	38583.7
AHQ-2-6, 4797 - 4873	K.IGTQQDSIAIFSPTHGMVIR.K	2172.49357	2	2.05E-05	0.78	3.28	-	409.0
AHQ-2-6, 4789	K.IGTQQDSIAIFSPTHGMVIR.K	2172.49357	3	2.45E-07	0.98	5.08	-	2888.2
gi|19923483|ref|NP_057406.2| GTPase Rab14 [Homo sapiens]				2.51E-07	4.33	50.23	31.20	23896.8
AHQ-2-10, 3975	K.FMADCPHTIGVEFGTR.I	1840.07303	2	9.05E-04	0.70	3.37	-	482.7
AHQ-2-10, 4015	R.GAAGALMVYDITR.R	1338.55819	2	7.34E-07	0.95	4.59	-	1068.4
AHQ-2-11, 3117	K.SCLLHQFTEK.K	1264.43272	1	8.12E-04	0.36	2.21	-	468.5
AHQ-2-10, 2940	K.SCLLHQFTEK.K	1264.43272	2	4.08E-06	0.94	4.04	-	861.3
AHQ-2-11, 3982	R.STYNHLSSWLTDAR.N	1651.76121	2	1.22E-04	0.80	2.86	-	778.8
AHQ-2-10, 3798	R.STYNHLSSWLTDAR.N	1651.76121	2	8.53E-05	0.89	3.06	-	1000.6
AHQ-2-10, 4212	K.TGENVEDAFLEAAK.K	1494.58517	1	1.41E-06	0.77	3.59	-	726.5
AHQ-2-10, 4210	K.TGENVEDAFLEAAK.K	1494.58517	2	2.51E-07	0.86	3.69	-	620.1
AHQ-2-11, 4416 - 4425	K.TGENVEDAFLEAAK.K	1494.58517	2	3.43E-05	0.91	4.09	-	718.7
gi|19923457|ref|NP_057447.2| glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M				2.63E-07	2.32	30.25	6.60	67308.6
AHQ-2-7, 3188	R.CQGPPGVDLYR.L	1263.40482	2	8.96E-05	0.51	2.50	-	534.7
AHQ-2-7, 5355	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	4.80E-06	0.95	5.03	-	1317.1
AHQ-2-7, 5368	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	2	2.21E-06	0.85	3.88	-	425.0
AHQ-2-7, 4653	R.YGFDQFALYK.E	1252.39881	2	2.63E-07	0.95	3.77	-	1206.0
gi|4758984|ref|NP_004654.1| RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho				2.79E-07	5.25	60.28	31.90	24393.3
AHQ-2-10, 2551	K.AQIWDTAGQER.Y	1275.35241	2	2.76E-05	0.95	3.23	-	1428.2
AHQ-2-12, 2731	K.AQIWDTAGQER.Y	1275.35241	2	3.78E-06	0.90	2.76	-	1143.7
AHQ-2-13-, 2825	K.AQIWDTAGQER.Y	1275.35241	2	2.41E-06	0.92	3.07	-	1370.1
AHQ-2-11, 2693 - 2766	K.AQIWDTAGQER.Y	1275.35241	2	2.79E-07	0.97	3.98	-	1783.6
AHQ-2-11, 4696 - 4756	R.DHADSNIVIMLVGNK.S	1626.85974	2	4.70E-06	0.97	4.64	-	1823.3
AHQ-2-11, 4900 - 4974	R.GAVGALLVYDIAK.H	1290.53317	2	3.12E-07	0.98	5.70	-	1833.6
AHQ-2-11, 1998	K.HLTYENVER.W	1161.24931	2	1.00E-05	0.80	2.87	-	506.0
AHQ-2-11, 2989	K.STIGVEFATR.S	1081.20410	2	5.06E-07	0.93	3.08	-	1069.6
AHQ-2-11, 2720	K.VVLIGDSGVGK.S	1044.22690	1	1.51E-04	0.53	2.14	-	877.3
AHQ-2-10, 2560	K.VVLIGDSGVGK.S	1044.22690	2	5.08E-04	0.79	2.97	-	1027.2
AHQ-2-11, 2725	K.VVLIGDSGVGK.S	1044.22690	1	7.67E-05	0.60	2.87	-	747.7
AHQ-2-11, 2717	K.VVLIGDSGVGK.S	1044.22690	2	1.34E-04	0.66	3.25	-	705.1
gi|23110942|ref|NP_002781.2| proteasome alpha 5 subunit; proteasome component 5; macropain subunit				2.84E-07	2.66	30.22	21.20	26410.9
AHQ-2-10, 2950	R.AIGSASEGAQSSLQEVYHK.S	1963.09463	2	2.84E-07	0.92	4.13	-	818.0
AHQ-2-10, 4387	K.GPQLFHMDPSGTFVQCDAR.A	2165.39491	2	3.17E-04	0.94	4.42	-	938.7
AHQ-2-10, 3339 - 3346	R.ITSPLMEPSSIEK.I	1432.66506	2	2.61E-05	0.80	2.70	-	1000.4
gi|4885153|ref|NP_005198.1| v-crk sarcoma virus CT10 oncogene homolog (avian)-like; v-crk avian sar				2.92E-07	2.66	30.23	18.50	33776.7
AHQ-2-11, 3945	K.IHYLDTTTLIEPAPR.Y	1740.98094	2	3.71E-07	0.90	3.57	-	930.1

AHQ-2-10, 5130 - 5131	R.TLYDFPGNDAEDLPFK.K	1842.98222	2	2.92E-07	0.85	3.63	-	529.1
AHQ-2-10, 5020 - 5023	R.YPSPPMGSVSAPNLPTAEDNLEYVR.T	2705.98075	2	3.30E-07	0.91	4.65	-	451.5
gi|4507149|ref|NP_000445.1| superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult				3.01E-07	3.27	40.29	57.80	15935.7
AHQ-2-12, 5378 - 5386	K.AVCVLKGDGPVQGIINFEQK.E	2174.50602	2	4.46E-05	0.97	5.55	-	1289.5
AHQ-2-12, 4561	K.GDGPVQGIINFEQK.E	1502.65366	2	3.01E-07	0.69	3.33	-	522.4
AHQ-2-12, 4338 - 4357	K.GDGPVQGIINFEQK.E	1502.65366	2	1.20E-05	0.36	2.67	-	499.0
AHQ-2-12, 4887	K.GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR.K	3522.76733	3	3.14E-04	0.96	5.39	-	1514.2
AHQ-2-11, 4664	K.GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR.K	3522.76733	3	1.29E-05	0.96	5.71	-	1550.3
AHQ-2-13, 5913	R.HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR.T	3724.02282	3	9.38E-06	0.65	3.18	-	547.0
gi|10880989|ref|NP_067075.1| RAB18, member RAS oncogene family; RAB18 small GTPase [Homo sapiens] [				3.04E-07	1.81	20.21	14.10	22976.9
AHQ-2-11, 6180	K.LDNWLNELETYCTR.N	1828.98037	2	6.51E-06	0.88	3.61	-	729.5
AHQ-2-11, 5768 - 5769	K.TCDGVQCAFEELVEK.I	1787.94661	2	3.04E-07	0.92	4.29	-	920.4
gi|4502107|ref|NP_001145.1| annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoag				3.15E-07	1.87	20.21	9.10	35936.5
AHQ-2-9, 6714	R.DLLDDLKSELTGK.F	1447.61309	2	3.15E-07	0.94	3.93	-	1153.3
AHQ-2-9, 7030 - 7048	K.GLGTDEESILTLLTSR.S	1705.88853	2	3.65E-06	0.93	4.19	-	945.7
gi|4504073|ref|NP_000398.1| glycoprotein Ib beta polypeptide precursor [Homo sapiens]				3.16E-07	2.54	30.21	15.50	21717.6
AHQ-2-1, 4957	R.LLPYLAEDELR.A	1332.52691	2	4.83E-07	0.78	2.95	-	478.2
AHQ-2-5, 4597	R.LLPYLAEDELR.A	1332.52691	2	2.79E-05	0.80	2.68	-	611.7
AHQ-2-6, 4537	R.LLPYLAEDELR.A	1332.52691	2	6.44E-07	0.88	3.51	-	613.6
AHQ-2-13, 4668	R.LLPYLAEDELR.A	1332.52691	2	2.37E-05	0.89	2.83	-	883.2
AHQ-2-10, 4234 - 4266	R.LLPYLAEDELR.A	1332.52691	2	1.78E-06	0.88	3.16	-	609.1
AHQ-2-10, 4252	R.LLPYLAEDELR.A	1332.52691	1	8.21E-06	0.48	3.28	-	176.2
AHQ-2-12, 4682	R.LLPYLAEDELR.A	1332.52691	2	1.07E-05	0.73	2.71	-	351.9
AHQ-2-11, 4484	R.LLPYLAEDELR.A	1332.52691	1	8.79E-04	0.70	3.01	-	438.9
AHQ-2-13-, 4741	R.LLPYLAEDELR.A	1332.52691	2	2.94E-06	0.81	2.85	-	557.2
AHQ-2-11, 4121 - 4124	R.LSLTDPLVAER.A	1214.39356	2	3.16E-07	0.94	4.25	-	1080.5
AHQ-2-10, 2074	R.TAHLGANPWR.C	1123.24913	2	5.09E-05	0.82	2.91	-	707.4
gi|4557703|ref|NP_000414.1| keratin 2a [Homo sapiens]				3.28E-07	2.30	30.26	10.50	65864.9
AHQ-2-14-, 6635	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	3.32E-05	0.93	5.05	-	1188.4
AHQ-2-14-, 2931 - 2933	R.FLEQQNQVLQTK.W	1476.65935	2	3.28E-07	0.97	5.15	-	2319.0
AHQ-2-4, 3014	R.FLEQQNQVLQTK.W	1476.65935	2	2.41E-04	0.59	2.74	-	477.1
AHQ-2-1, 3154	R.FLEQQNQVLQTK.W	1476.65935	2	1.26E-05	0.78	2.96	-	1041.6
AHQ-2-14-, 5905	K.VDLLNQEIEFLK.V	1461.68459	2	6.01E-04	0.40	2.65	-	412.0
gi|9910280|ref|NP_064505.1| UDP-glucose ceramide glucosyltransferase-like 1; UDP-glucose:glycoprote				3.29E-07	2.14	30.16	4.10	177187.7
AHQ-2-5, 6924	R.AVYLGELPHDQDVVEYIMNQPNVVPR.I	2997.37416	2	4.13E-05	0.80	3.23	-	486.7
AHQ-2-3, 7605	R.IIGPLEDSELFNQDDFHLLENIILK.T	2927.29710	3	1.92E-04	0.70	3.08	-	715.0
AHQ-2-3, 4687	R.IVPEWQDYDQEIK.Q	1663.80866	2	3.29E-07	0.63	2.94	-	289.0
gi|30148456|ref|XP_293602.2| similar to glutathione-S-transferase like; glutathione transferase ome				3.31E-07	0.91	10.17	3.90	29139.6
AHQ-2-11, 4433	K.VPSLVGSFLR.T	1075.28583	2	3.31E-07	0.91	3.09	-	1144.2
AHQ-2-10, 4136 - 4138	K.VPSLVGSFLR.T	1075.28583	2	1.46E-05	0.94	3.33	-	1318.7
gi|29729616|ref|XP_292963.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				3.36E-07	1.86	20.28	16.40	18025.4
AHQ-2-12, 4919 - 4945	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	6.05E-06	0.93	5.05	-	1167.5
AHQ-2-12, 5009 - 5089	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	7.54E-06	0.91	4.96	-	973.0
AHQ-2-12, 5066 - 5129	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	4.04E-04	0.85	4.16	-	592.5
AHQ-2-12, 5541 - 5621	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	2.29E-05	0.93	4.53	-	734.3
AHQ-2-12, 5629 - 5701	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	9.74E-05	0.93	5.04	-	1225.8
AHQ-2-12, 5853 - 5931	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	2.66E-06	0.82	3.11	-	943.5
AHQ-2-13, 4880	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	4.24E-06	0.91	4.50	-	1088.6
AHQ-2-13, 4888	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	1.78E-04	0.62	3.25	-	313.9
AHQ-2-13, 5005	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	7.10E-04	0.73	3.49	-	673.2
AHQ-2-13-, 4953	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	3.78E-06	0.92	4.62	-	1086.9
AHQ-2-13-, 5554 - 5587	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	3.36E-07	0.94	5.66	-	1300.7
gi|20149594|ref|NP_031381.2| heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea				3.42E-07	3.61	40.25	7.30	83263.6
AHQ-2-14-, 3019	R.ELISNASDALDK.I	1276.37539	2	9.02E-04	0.66	3.06	-	432.7
AHQ-2-5, 2959 - 2971	R.ELISNASDALDK.I	1276.37539	2	7.72E-07	0.87	3.31	-	761.8
AHQ-2-5, 4107 - 4121	R.NPDDITQEEYGEFYK.S	1848.90048	2	3.42E-07	0.97	4.95	-	1358.8
AHQ-2-5, 3731 - 3733	K.SLTNDWEDHLAVK.H	1528.64798	2	3.83E-06	0.84	3.29	-	1017.0
AHQ-2-5, 4105	R.TLTLVDTGIGMTK.A	1350.60718	2	4.97E-06	0.94	3.70	-	1103.2
gi|16933542|ref|NP_002017.1| fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s				3.75E-07	6.26	90.20	6.70	259222.8
AHQ-2-1, 6274	K.FTQVTPTSLSAQWTPPNVQLTGYR.V	2693.99453	2	6.18E-06	0.69	3.47	-	297.6
AHQ-2-1, 2780	R.GDSPASSKPISINYR.T	1592.73521	2	1.57E-04	0.41	2.55	-	244.2
AHQ-2-1, 4601	R.ITYGETGGNSPVQEFTVPGSK.S	2169.33354	2	1.03E-06	0.83	3.94	-	422.6
AHQ-2-1, 5126	R.NLQPASEYTVSLVAIK.G	1733.98671	2	1.05E-05	0.81	2.88	-	484.2
AHQ-2-2, 6400	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	6.12E-05	0.64	2.86	-	423.1
AHQ-2-1, 6796	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	1.99E-04	0.71	3.29	-	448.7
AHQ-2-1, 4892	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	5.09E-04	0.91	4.03	-	961.4
AHQ-2-1, 3482	R.VPGTSTSATLTGLTR.G	1462.63098	2	2.07E-06	0.77	2.92	-	664.5
AHQ-2-1, 7160	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	3.75E-07	0.89	3.32	-	647.9
AHQ-2-2, 7448	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	9.37E-07	0.86	3.34	-	518.2
AHQ-2-1, 3946	K.WLPSSSPVTGYR.V	1350.50402	2	8.97E-04	0.32	2.65	-	233.7
gi|4506185|ref|NP_002780.1| proteasome alpha 4 subunit; proteasome component C9; proteasome subunit				3.75E-07	1.87	20.25	12.30	29483.6
AHQ-2-10, 4444	K.LLDEVFFSEK.I	1227.38757	2	3.75E-07	0.94	3.52	-	918.9
AHQ-2-10, 6738 - 6739	R.YLLQYQEPIPCEQLVTALCDIK.Q	2698.10465	2	2.26E-06	0.93	4.93	-	590.2
gi|7705849|ref|NP_057215.1| ras-related GTP-binding protein RAB10; ras-related GTP-binding protein				3.85E-07	1.85	30.24	15.50	22540.8
AHQ-2-14-, 6463	K.AFLTLAEDILR.K	1262.47982	2	1.01E-06	0.95	4.22	-	1557.7
AHQ-2-11, 6236 - 6244	K.AFLTLAEDILR.K	1262.47982	2	3.85E-07	0.96	4.88	-	1393.2
AHQ-2-10, 6092	K.AFLTLAEDILR.K	1262.47982	2	4.89E-07	0.94	3.92	-	1397.0
AHQ-2-11, 2996 - 3012	K.KTYDLLFK.L	1028.22593	2	3.00E-04	0.72	2.68	-	544.5
AHQ-2-11, 1960	R.NIDEHANEDVER.M	1441.44245	1	2.05E-06	0.18	2.32	-	168.4
AHQ-2-11, 1826	R.NIDEHANEDVER.M	1441.44245	1	3.35E-04	0.63	2.77	-	307.9
AHQ-2-11, 1792	R.NIDEHANEDVER.M	1441.44245	2	5.16E-04	0.66	2.86	-	550.1
gi|22060072|ref|XP_088293.2| similar to cytochrome c [Homo sapiens]				3.86E-07	1.98	30.18	24.80	11887.8
AHQ-2-13-, 4267	R.ADLIAYLK.K	907.08869	2	4.09E-04	0.91	3.43	-	961.7
AHQ-2-13, 4220	R.ADLIAYLK.K	907.08869	2	1.09E-04	0.83	2.74	-	802.5
AHQ-2-13, 2956	K.M*IFVGIK.K	824.06630	1	5.94E-04	0.23	1.91	-	174.8
AHQ-2-13-, 3519	K.TGPNLHGLFGR.K	1169.31780	1	2.69E-05	0.37	2.24	-	162.6
AHQ-2-13-, 3513 - 3518	K.TGPNLHGLFGR.K	1169.31780	2	9.04E-07	0.92	3.64	-	820.4
AHQ-2-13, 3513 - 3515	K.TGPNLHGLFGR.K	1169.31780	2	3.86E-07	0.92	3.49	-	813.9
gi|29727317|ref|XP_298144.1| hypothetical protein XP_298144 [Homo sapiens]				3.87E-07	1.04	20.16	15.90	22108.6
AHQ-2-7, 5201	K.CAAM*SKVLTAMPNM*GK.A	1744.11508	2	4.14E-04	0.26	2.67	-	252.5
AHQ-2-5, 6477	K.GEYNLTLDTALTSNLK.T	1753.93165	2	1.21E-06	0.78	3.00	-	1074.4
AHQ-2-4, 6753	K.GEYNLTLDTALTSNLK.T	1753.93165	2	3.87E-07	0.78	3.24	-	779.4
gi|20149637|ref|NP_057526.2| type 1 tumor necrosis factor receptor shedding aminopeptidase regulato				4.07E-07	0.79	10.13	1.40	107761.4
AHQ-2-4, 3194	R.ILASTQFEPTAAR.M	1405.58112	2	4.07E-07	0.79	2.66	-	929.7
gi|5453722|ref|NP_006321.1| lysophospholipase I; lysophospholipase 1; lysophospholipid-specific lys				4.11E-07	2.66	30.22	16.50	24669.5
AHQ-2-11, 2716 - 2750	R.ASFPQGPIGGANR.D	1272.39489	2	4.11E-07	0.82	3.22	-	520.6
AHQ-2-11, 6438 - 6442	K.LAGVTALSCWLPLR.A	1558.86992	2	6.50E-04	0.96	4.48	-	1255.7
AHQ-2-11, 3493	K.TLVNPANVTFK.T	1204.40037	2	5.95E-05	0.88	3.56	-	599.9
gi|4758906|ref|NP_004146.1| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member				4.21E-07	0.88	10.17	3.20	42403.4
AHQ-2-8, 2894	R.HLGIVDAFQQGK.A	1313.48692	2	4.21E-07	0.88	3.27	-	865.9
gi|5803187|ref|NP_006746.1| transaldolase 1; dihydroxyacetone transferase; glycerone transferase [H				4.24E-07	0.95	10.20	3.30	37539.9
AHQ-2-9, 3667	K.LLGELLQDNAK.L	1214.39356	2	4.24E-07	0.95	3.98	-	1229.6
AHQ-2-9, 3658 - 3659	K.LLGELLQDNAK.L	1214.39356	1	9.67E-05	0.34	2.22	-	462.6
gi|5031973|ref|NP_005733.1| protein disulfide isomerase-related protein [Homo sapiens]				4.39E-07	4.42	50.22	21.80	48121.0
AHQ-2-7, 7367 - 7369	R.DGELPVEDDIDLSDVELDDLGKDEL	2759.86565	2	6.88E-05	0.90	3.88	-	881.5
AHQ-2-7, 3695 - 3764	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	4.39E-07	0.84	3.23	-	888.0
AHQ-2-7, 4641 - 4644	K.LAAVDATVNQVLASR.Y	1528.73579	2	4.51E-06	0.94	3.68	-	1532.4

AHQ-2-7, 6151 - 6152	R.TGEAIVDAALSALR.Q	1387.56411	2	2.78E-06	0.97	4.40	-	1958.5
AHQ-2-7, 3367 - 3397	K.VGAVDADKHHSLGGQYGVQGFPTIK.I	2582.85541	2	1.49E-06	0.76	3.39	-	389.5
gi|4502171|ref|NP_000476.1| adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho				4.90E-07	3.45	40.23	30.00	19607.6
AHQ-2-11, 3672	R.DISPVLKDPASFR.A	1445.64525	2	1.38E-05	0.78	3.19	-	541.6
AHQ-2-11, 4985	R.GKLPGPTLWASYSLEYGK.A	1968.24075	2	3.34E-05	0.94	4.65	-	771.2
AHQ-2-11, 3497 - 3500	R.IDYIAGLDSR.G	1123.24098	2	4.90E-07	0.96	4.04	-	1689.1
AHQ-2-11, 5548 - 5614	R.SFPDFPTPGVVFR.D	1466.66462	2	1.43E-04	0.76	3.03	-	506.8
gi|7330335|ref|NP_039234.1| chloride intracellular channel 4; chloride intracellular channel 4 like				4.91E-07	3.34	40.26	28.90	28771.9
AHQ-2-10, 2862	K.AGSDGESIGNCPFSQR.L	1683.73852	2	4.91E-07	0.91	3.92	-	782.3
AHQ-2-10, 5580 - 5588	K.FLDGNEMTLADCNLLPK.L	1953.22635	2	7.86E-06	0.90	3.84	-	975.9
AHQ-2-10, 5318	K.LDEYLNSPLPDEIDENSMEDIK.F	2580.76043	2	7.47E-04	0.56	2.78	-	566.6
AHQ-2-10, 6726 - 6798	K.TDVNKIEEFLEEVLCPPK.Y	2162.44564	2	6.15E-07	0.96	5.18	-	1084.0
gi|4504505|ref|NP_000405.1| hydroxysteroid (17-beta) dehydrogenase 4 [Homo sapiens]				4.94E-07	0.90	10.19	2.20	79685.9
AHQ-2-6, 2590	R.ATSTATSGFAGAIGQK.L	1468.59408	2	4.94E-07	0.90	3.71	-	1165.7
gi|27500115|ref|XP_208901.1| similar to ubiquitin-conjugating enzyme E2M; UBC12 homolog, yeast [Hom				4.95E-07	0.82	10.16	8.70	20964.0
AHQ-2-11, 5968 - 6042	K.TCDISFSDPDDLLNFK.L	1889.02935	2	4.95E-07	0.82	3.18	-	632.4
gi|5729875|ref|NP_006658.1| progesterone receptor membrane component 1; progesterone binding protei				4.99E-07	2.27	30.23	11.80	21671.0
AHQ-2-10, 4236 - 4239	K.FYGPEGPYGVFAGR.D	1517.66849	2	1.67E-06	0.96	4.57	-	1392.6
AHQ-2-10, 2536	R.ILMAINGK.V	860.10021	1	6.99E-05	0.35	1.88	-	599.8
AHQ-2-11, 3921	R.KFYGPEGPYGVFAGR.D	1645.84140	2	5.26E-05	0.92	3.39	-	1182.0
AHQ-2-10, 3746	R.KFYGPEGPYGVFAGR.D	1645.84140	2	4.99E-07	0.96	4.35	-	1316.8
gi|5454152|ref|NP_006285.1| ubiquinol-cytochrome c reductase binding protein [Homo sapiens]				5.03E-07	0.98	10.26	11.70	13530.4
AHQ-2-13-, 5289 - 5290	K.YEEENFYLEPYLK.E	1737.88601	2	5.03E-07	0.98	5.28	-	2166.6
AHQ-2-13, 5183	K.YEEENFYLEPYLK.E	1737.88601	2	5.52E-04	0.96	4.51	-	1353.0
gi|27481323|ref|XP_208234.1| similar to unactive progesterone receptor, 23 kD; likely ortholog of m				5.41E-07	0.97	20.15	15.60	18694.3
AHQ-2-11, 6122	K.LNWLSVDFNNWK.D	1536.71494	2	6.33E-06	0.80	3.03	-	604.1
AHQ-2-11, 4413	K.LTFSCLGGSDNFK.H	1447.59493	1	5.41E-07	0.17	1.88	-	276.7
AHQ-2-11, 4400 - 4448	K.LTFSCLGGSDNFK.H	1447.59493	2	2.22E-04	0.79	2.56	-	873.1
gi|4503785|ref|NP_000135.1| frataxin; Friedreich ataxia (frataxin) [Homo sapiens]				5.46E-07	0.96	10.22	5.70	23218.1
AHQ-2-13-, 3818	K.LGGDLGTYVINK.Q	1250.42590	2	5.46E-07	0.96	4.37	-	1218.1
gi|5729804|ref|NP_006694.1| nudix (nucleoside diphosphate linked moiety X)-type motif 3; diphosphoi				5.66E-07	0.57	10.16	11.60	19470.8
AHQ-2-11, 4356	R.WIVPGGGM*EPEEEPSVAAVR.E	2127.36326	2	5.66E-07	0.57	3.07	-	164.1
gi|13489091|ref|NP_066949.1| 3-mercaptopyruvate sulfurtransferase [Homo sapiens]				5.78E-07	0.97	10.26	5.40	33178.2
AHQ-2-9, 6772	R.AGQPLQLLDASWYLPK.L	1801.07798	2	1.31E-04	0.93	3.70	-	1337.7
AHQ-2-9, 6680 - 6754	R.AGQPLQLLDASWYLPK.L	1801.07798	2	5.78E-07	0.97	4.54	-	2133.6
gi|4826848|ref|NP_004991.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5; NADH dehydrogena				5.90E-07	0.83	10.29	13.80	13458.6
AHQ-2-13, 3748	K.TTGLVGLAVCNTPHER.L	1726.93595	2	5.90E-07	0.83	3.46	-	717.4
gi|5032041|ref|NP_005605.1| Ras homolog enriched in brain 2 [Homo sapiens]				5.97E-07	0.95	10.24	8.70	20497.4
AHQ-2-12, 5030 - 5107	K.ALAESWNAAFLESSAK.E	1695.85389	2	5.97E-07	0.95	4.84	-	973.4
gi|7705819|ref|NP_057181.1| HSPC039 protein [Homo sapiens]				6.00E-07	0.95	10.25	24.40	8968.7
AHQ-2-14-, 5117	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	6.00E-07	0.95	5.00	-	1110.2
AHQ-2-14, 6221	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	7.63E-05	0.76	3.35	-	546.2
gi|22267436|ref|NP_056284.1| DKFZp564D177 protein [Homo sapiens]				6.01E-07	0.95	10.18	5.30	28466.4
AHQ-2-10, 3896	R.VHVLWWNESADSR.A	1599.73113	2	6.01E-07	0.95	3.52	-	1610.3
gi|17318569|ref|NP_006112.2| keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]				6.17E-07	3.89	50.22	9.50	66066.3
AHQ-2-5, 2775	R.DYQELMNTK.L	1142.26457	1	2.58E-04	0.66	2.38	-	498.0
AHQ-2-5, 6253 - 6272	R.SLDLDSIIAEVK.A	1303.48388	2	6.17E-07	0.96	4.31	-	1553.9
AHQ-2-14-, 6060 - 6061	R.SLDLDSIIAEVK.A	1303.48388	2	2.31E-06	0.95	4.36	-	1305.8
AHQ-2-5, 6619	R.THNLEPYFESFINNLR.R	1995.18315	2	1.27E-05	0.91	4.12	-	541.2
AHQ-2-5, 2224	R.TNAENEFVTIKK.D	1394.55511	2	2.42E-05	0.53	2.59	-	407.6
AHQ-2-14, 5670	K.WELLQQVDTSTR.T	1476.61621	2	5.47E-06	0.83	2.66	-	1131.8
gi|21618338|ref|NP_003141.2| signal transducer and activator of transcription 3 isoform 2; acute-ph				6.19E-07	1.51	20.16	5.20	87980.2
AHQ-2-6, 3427	R.FLQESNVLYQHNLR.R	1761.96193	2	6.19E-07	0.76	3.13	-	741.0
AHQ-2-6, 2841	R.LLQTAATAAQQGGQANHPTAAVVTEK.Q	2577.83547	3	9.66E-04	0.75	3.25	-	543.8
gi|21614499|ref|NP_003370.2| villin 2; Villin-2; cytovillin [Homo sapiens]				6.26E-07	1.91	20.22	3.20	69412.3
AHQ-2-7, 4084	K.APDFVFYAPR.L	1183.33971	2	3.82E-06	0.97	3.22	-	2000.6
AHQ-2-6, 4155 - 4158	K.APDFVFYAPR.L	1183.33971	2	6.26E-07	0.97	4.50	-	1577.0
AHQ-2-6, 4950 - 4963	K.IGFPWSEIR.N	1105.27049	2	1.01E-04	0.93	3.26	-	1111.1
gi|27544939|ref|NP_060932.2| uncharacterized hematopoietic stem/progenitor cells protein MDS027 [Ho				6.26E-07	0.95	10.23	17.30	8744.9
AHQ-2-14-, 5667	K.IADFLNSFDMSCR.S	1577.76410	2	6.26E-07	0.95	4.52	-	1220.9
AHQ-2-14-, 5303	K.IADFLNSFDMSCR.S	1577.76410	2	4.06E-04	0.92	3.19	-	1038.0
gi|4757952|ref|NP_001782.1| cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p				6.30E-07	4.24	50.28	31.40	21258.5
AHQ-2-11, 2273	K.CVVVGDGAVGK.T	1062.22237	1	1.44E-04	0.86	2.87	-	1004.1
AHQ-2-11, 2272	K.CVVVGDGAVGK.T	1062.22237	2	3.90E-05	0.86	2.91	-	1186.4
AHQ-2-11, 6573 - 6577	K.NVFDEAILAALEPPEPK.K	1854.09282	3	6.30E-07	0.96	5.69	-	1271.8
AHQ-2-11, 3821 - 3840	K.TCLLISYTTNK.F	1315.51795	2	2.64E-05	0.83	2.73	-	1254.4
AHQ-2-11, 2457	K.WVPEITHHCPK.T	1405.60610	1	7.69E-07	0.71	3.40	-	440.2
AHQ-2-11, 2478 - 2486	K.YVECSALTQK.G	1200.34381	2	1.47E-05	0.88	3.81	-	477.2
gi|4507793|ref|NP_003339.1| ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast); ubiquitin-conj				6.35E-07	3.34	40.24	30.30	17137.7
AHQ-2-12, 5873	K.LELFLPEEYPMAAPK.V	1749.06325	2	6.35E-07	0.87	4.17	-	607.3
AHQ-2-12, 5355 - 5379	K.LELFLPEEYPM*AAPK.V	1765.06265	2	1.94E-04	0.76	3.85	-	326.0
AHQ-2-12, 2126	K.TNEAQAIETAR.A	1204.27249	2	3.73E-04	0.75	2.87	-	998.8
AHQ-2-12, 5273	R.YFHVVIAGPQDSPFEGGTFK.L	2197.43341	2	8.78E-05	0.97	4.73	-	1492.8
gi|4502285|ref|NP_001672.1| ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 2; ATP				6.48E-07	0.92	10.21	1.50	109690.3
AHQ-2-1, 4868	K.VGEATETALTCLVEK.M	1622.81958	2	6.48E-07	0.92	4.12	-	847.5
gi|18570595|ref|XP_095590.1| similar to myosin regulatory light chain [Homo sapiens]				6.68E-07	0.91	10.18	0.00	13951.5
AHQ-2-11, 3041 - 3108	K.LNGTDPEDVIR.H	1229.32195	2	3.67E-05	0.93	3.00	-	1461.9
AHQ-2-12, 3159	K.LNGTDPEDVIR.H	1229.32195	2	3.32E-06	0.91	3.33	-	1030.8
AHQ-2-13-, 3221	K.LNGTDPEDVIR.H	1229.32195	2	5.58E-04	0.85	3.38	-	714.8
AHQ-2-11, 2952	K.LNGTDPEDVIR.H	1229.32195	2	6.68E-07	0.91	3.51	-	1075.7
gi|7657548|ref|NP_055378.1| spondyloepiphyseal dysplasia, late; sedlin [Homo sapiens]				6.70E-07	0.72	10.16	10.00	16444.6
AHQ-2-13, 5072 - 5080	K.FSMNPFYEPNSPIR.S	1699.91087	2	6.70E-07	0.72	3.25	-	519.2
gi|14745898|ref|XP_016144.2| similar to tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat				6.77E-07	0.96	10.23	7.50	18201.0
AHQ-2-11, 6541 - 6542	K.LLCCDILDVLDK.N	1479.74157	2	6.77E-07	0.96	4.61	-	1074.9
AHQ-2-10, 6478	K.LLCCDILDVLDK.N	1479.74157	2	7.45E-07	0.96	4.48	-	1055.7
gi|20551618|ref|XP_167021.1| similar to calponin 2; Calonin 2 [Homo sapiens]				6.89E-07	1.64	20.22	3.70	47327.9
AHQ-2-12, 5274 - 5341	R.SM*QNWHQLENLSNFIK.A	2006.23095	2	1.67E-06	0.82	3.75	-	497.4
AHQ-2-12, 5682	R.SMQNWHQLENLSNFIK.A	1990.23155	2	1.19E-04	0.93	4.26	-	885.9
AHQ-2-13, 5572	R.SMQNWHQLENLSNFIK.A	1990.23155	2	6.89E-07	0.82	3.60	-	635.1
AHQ-2-13-, 5702	R.SMQNWHQLENLSNFIK.A	1990.23155	2	8.43E-05	0.94	4.38	-	1187.9
AHQ-2-11, 5453	R.SMQNWHQLENLSNFIK.A	1990.23155	2	4.21E-04	0.95	4.35	-	1206.5
gi|5453597|ref|NP_006126.1| F-actin capping protein alpha-1 subunit; Cap Z [Homo sapiens]				7.00E-07	2.59	40.20	22.00	32922.5
AHQ-2-9, 4723 - 4731	K.FITHAPPGEFNEVFNDVR.L	2090.28294	2	1.62E-05	0.79	3.48	-	342.9
AHQ-2-10, 4896	K.FTITPPTAQVVGVLK.I	1571.88532	2	5.08E-06	0.51	2.73	-	184.7
AHQ-2-9, 4480	R.LLLNNDNLLR.E	1198.39736	2	2.28E-04	0.48	2.58	-	386.8
AHQ-2-9, 3876	R.LLLNNDNLLR.E	1198.39736	2	7.51E-04	0.84	3.80	-	702.4
AHQ-2-9, 5403	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	3	7.00E-07	0.81	4.04	-	320.2
AHQ-2-10, 5040	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	1.50E-06	0.63	2.96	-	303.1
AHQ-2-9, 5398 - 5466	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	3.31E-06	0.81	3.85	-	347.2
gi|11496277|ref|NP_068805.1| mitogen-activated protein kinase kinase 1 interacting protein 1; MEK p				7.01E-07	1.89	20.29	35.50	13622.6
AHQ-2-14, 6556 - 6569	K.SIICYYNTYQVVQFNR.L	2070.31322	2	7.01E-07	0.94	4.52	-	1074.5
AHQ-2-14-, 5243	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	2.02E-05	0.96	5.77	-	1095.8
gi|4502693|ref|NP_001760.1| CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen				7.09E-07	3.03	40.31	24.10	25415.9
AHQ-2-11, 6805	K.AIHYALNCCGLAGGVEQFISDICPK.K	2798.16446	3	1.34E-06	0.91	4.36	-	810.5
AHQ-2-11, 6806 - 6810	K.AIHYALNCCGLAGGVEQFISDICPK.K	2798.16446	2	7.09E-07	0.98	6.17	-	1810.1
AHQ-2-11, 2168	K.EVQEFYK.D	943.03476	1	4.80E-04	0.30	2.37	-	234.4
AHQ-2-11, 3137 - 3174	K.KDVLETFTVK.S	1180.37558	2	2.27E-04	0.90	3.61	-	922.4

AHQ-2-13-, 3383	K.KDVLETFTVK.S	1180.37558	2	2.29E-05	0.84	2.89	-	783.9
AHQ-2-11, 3132 - 3192	K.KDVLETFTVK.S	1180.37558	1	3.21E-05	0.38	1.90	-	500.6
AHQ-2-10, 2962	K.KDVLETFTVK.S	1180.37558	2	3.10E-05	0.91	3.42	-	1035.6
AHQ-2-1, 3541 - 3549	K.KDVLETFTVK.S	1180.37558	2	5.24E-06	0.89	3.31	-	922.9
AHQ-2-13, 3389	K.KDVLETFTVK.S	1180.37558	2	1.27E-06	0.81	3.15	-	735.6
AHQ-2-11, 3685	K.SCPDAIKEVFDNK.F	1524.67770	2	1.23E-04	0.95	3.86	-	1319.9
gi|10835035|ref|NP_003157.1| sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3; t				7.60E-07	1.84	30.19	20.70	34196.0
AHQ-2-9, 5640	K.SHLPLALLPQTLLDQK.V	1788.12388	2	1.67E-04	0.91	3.85	-	862.6
AHQ-2-9, 5382 - 5450	R.VPFLEVNDPGEPSGLETLK.D	2042.27480	2	6.75E-04	0.25	3.10	-	243.6
AHQ-2-9, 6814	K.YFAEALGPLQSFQARPDDLLINTYPK.S	2969.33891	3	7.60E-07	0.68	3.38	-	327.7
gi|4506025|ref|NP_000936.1| protein phosphatase 3, regulatory subunit B, alpha isoform 1; protein p				7.69E-07	0.79	10.14	11.80	19299.8
AHQ-2-12, 5963	R.IYDMDKDGYISNGELFQVLK.M	2349.64477	2	7.69E-07	0.79	2.81	-	737.4
gi|4505591|ref|NP_002565.1| peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc				8.04E-07	4.17	60.23	45.70	22110.2
AHQ-2-10, 3622	R.GLFIIDDK.G	921.07223	1	2.19E-04	0.63	2.57	-	947.9
AHQ-2-11, 2966	K.HGEVCPAGWKPGSDTIKPDVQK.S	2408.67532	2	6.32E-06	0.25	3.19	-	115.2
AHQ-2-11, 5457	K.LNCQVIGASVDSHFCHLAWVNTPK.K	2757.09720	3	3.27E-04	0.62	3.46	-	447.7
AHQ-2-11, 3492 - 3536	R.LVQAFQFTDK.H	1197.36469	2	8.04E-07	0.92	3.43	-	1049.3
AHQ-2-11, 4758	K.QGGLGPMNIPLVSDPK.R	1623.89899	2	1.08E-05	0.92	3.87	-	958.9
AHQ-2-11, 3365 - 3368	R.QITVNDLPVGR.S	1212.38090	2	5.18E-06	0.83	3.33	-	481.5
gi|5453970|ref|NP_006245.1| protein kinase C, delta [Homo sapiens]				8.18E-07	0.86	10.16	1.80	77476.6
AHQ-2-6, 3905	K.LLAEALNQVTQR.A	1356.55324	2	8.18E-07	0.86	3.28	-	941.1
gi|4506077|ref|NP_002734.1| protein kinase C substrate 80K-H; glucosidase II, beta subunit; AGE-bin				8.22E-07	1.82	20.17	4.40	59296.0
AHQ-2-5, 2976	K.AQQEQELAADAFK.E	1449.54763	2	8.22E-07	0.92	3.41	-	1245.6
AHQ-2-5, 3177	K.LWEEQLAAAK.A	1159.31646	2	3.94E-05	0.91	3.50	-	780.5
gi|20452464|ref|NP_620411.1| similar to endothelial cell-selective adhesion molecule; likely orthol				8.28E-07	0.94	10.23	6.70	41208.1
AHQ-2-7, 3813	R.LPTTDGAHPQPISPIPGGVSSSGLSR.M	2529.79081	3	8.28E-07	0.94	4.61	-	1504.2
gi|5453998|ref|NP_006382.1| importin 7; RAN-binding protein 7 [Homo sapiens]				8.30E-07	0.90	10.20	1.40	119515.7
AHQ-2-4, 6997	R.ENIVEAIIHSPELIR.V	1733.98994	2	8.30E-07	0.90	4.07	-	789.2
gi|7661624|ref|NP_056202.1| preimplantation protein 3; likely ortholog of preimplantation protein 3				8.49E-07	0.64	10.14	7.20	22256.6
AHQ-2-10, 3550 - 3555	K.ILEPPEGQDEGVWK.Y	1597.75022	2	8.49E-07	0.64	2.76	-	555.9
gi|6715607|ref|NP_000175.1| G-gamma globin [Homo sapiens]				8.81E-07	0.92	10.18	6.80	16126.3
AHQ-2-13-, 4921 - 4925	R.LLVVYPWTQR.F	1275.52342	2	6.84E-06	0.90	3.38	-	966.1
AHQ-2-14, 6261	R.LLVVYPWTQR.F	1275.52342	2	8.81E-07	0.92	3.59	-	1029.0
gi|20539300|ref|XP_088391.4| similar to tropomyosin 4 [Homo sapiens]				8.87E-07	1.87	20.20	6.90	18592.1
AHQ-2-9, 3215 - 3250	R.KLVILEGELER.A	1299.54160	1	3.98E-04	0.34	2.09	-	441.3
AHQ-2-9, 3344	R.KLVILEGELER.A	1299.54160	2	1.39E-04	0.92	3.92	-	1108.8
AHQ-2-9, 3214 - 3218	R.KLVILEGELER.A	1299.54160	2	7.14E-04	0.88	3.16	-	1229.2
AHQ-2-9, 3944	K.LVILEGELER.A	1171.36868	2	8.87E-07	0.95	3.77	-	1693.8
gi|4504973|ref|NP_002292.1| lactate dehydrogenase C [Homo sapiens]				9.00E-07	0.82	10.18	3.60	36311.0
AHQ-2-11, 2372	R.VIGSGCNLDSAR.F	1250.36445	2	1.07E-06	0.84	3.54	-	506.8
AHQ-2-9, 2310	R.VIGSGCNLDSAR.F	1250.36445	2	9.00E-07	0.82	3.35	-	465.8
gi|5902726|ref|NP_005800.1| peroxiredoxin 2; thioredoxin-dependent peroxide reductase 1 (thiol-spec				9.08E-07	1.90	20.30	9.10	21856.8
AHQ-2-11, 6568	K.EGGLGPLNIPLLADVTR.R	1736.00583	2	1.48E-06	0.92	4.34	-	667.5
AHQ-2-11, 5990 - 5998	R.KEGGLGPLNIPLLADVTR.R	1864.17875	2	9.08E-07	0.97	5.94	-	1279.9
gi|29732788|ref|XP_297707.1| hypothetical protein XP_297707 [Homo sapiens]				9.30E-07	0.58	10.16	5.70	55232.0
AHQ-2-9, 5056 - 5058	R.KYEPSSLTAMLKHSGEPVQHKLSTTAVVR.T	3196.66997	3	9.30E-07	0.58	3.22	-	477.2
gi|5123454|ref|NP_005336.2| heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind				9.31E-07	4.35	50.32	16.10	70037.7
AHQ-2-6, 5435	K.AAAIGIDLGTTYSCVGVFQHGK.V	2267.54677	2	1.88E-04	0.85	3.86	-	607.4
AHQ-2-6, 4733	K.DAGVIAGLNVLR.I	1198.39736	2	4.68E-06	0.95	3.00	-	1981.2
AHQ-2-6, 6233	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G	3058.37100	3	9.31E-07	0.98	6.35	-	1993.9
AHQ-2-13, 3809	K.NQVALNPQNTVFDAK.R	1659.82478	2	3.30E-04	0.37	2.54	-	503.3
AHQ-2-6, 3506 - 3511	K.NQVALNPQNTVFDAK.R	1659.82478	2	6.83E-05	0.94	4.52	-	739.8
AHQ-2-6, 7167	K.SINPDEAVAYGAAVQAAILMGDK.S	2305.59353	2	4.17E-04	0.63	2.69	-	547.5
gi|30147623|ref|XP_293669.2| similar to actinin, alpha 4 [Homo sapiens]				9.66E-07	0.83	10.22	3.50	57794.4
AHQ-2-5, 4052	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	9.66E-07	0.83	3.45	-	663.8
AHQ-2-6, 3934	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	2.93E-05	0.50	2.69	-	466.8
AHQ-2-5, 3908 - 3980	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	4.39E-05	0.88	4.34	-	739.5
gi|8922712|ref|NP_060713.1| hypothetical protein FLJ10849 [Homo sapiens]				9.66E-07	2.69	30.19	9.10	49397.9
AHQ-2-7, 2327	K.AAAQLLQSQAQQSGAQQTK.K	1958.12276	2	2.02E-06	0.91	3.75	-	964.3
AHQ-2-7, 2453	K.RNEFLGELQK.K	1234.38656	2	1.23E-04	0.94	3.65	-	1361.5
AHQ-2-7, 2084	R.SYELQESNVR.L	1225.29016	2	9.66E-07	0.84	2.93	-	972.6
gi|18201905|ref|NP_000166.2| glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras				9.69E-07	4.41	60.27	17.40	63146.7
AHQ-2-7, 1665	K.HFVALSTNTTK.V	1219.37190	1	1.81E-04	0.64	2.12	-	511.7
AHQ-2-7, 2769	K.NLVTEDVMR.M	1077.23726	1	5.12E-05	0.15	1.91	-	179.1
AHQ-2-7, 2719	K.TFTTQETITNAETAK.E	1656.77283	2	9.69E-07	0.91	3.84	-	939.3
AHQ-2-7, 6021	K.TLAQLNPESSLFIIASK.T	1833.11828	2	3.21E-06	0.86	3.75	-	550.3
AHQ-2-7, 5400 - 5479	R.VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK.M	3317.61777	3	1.33E-04	0.95	5.35	-	1241.5
AHQ-2-7, 2968	K.VFEGNRPTNSIVFTK.L	1709.92693	2	1.12E-06	0.90	3.91	-	956.3
gi|17450333|ref|XP_060887.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				1.01E-06	0.95	10.22	11.00	17503.9
AHQ-2-12, 6787 - 6854	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	1.01E-06	0.95	4.32	-	1307.7
AHQ-2-12, 6915	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	1.34E-05	0.84	3.54	-	862.8
AHQ-2-12, 6569 - 6633	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	7.53E-06	0.92	4.13	-	931.3
gi|21361565|ref|NP_001679.2| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, is				1.02E-06	1.75	20.21	9.00	28908.4
AHQ-2-11, 2829	R.HYLFDVQR.N	1078.20513	2	1.02E-06	0.83	2.84	-	854.7
AHQ-2-13-, 7083	R.YGLIPEEFFQFLYPK.T	1892.18434	2	3.05E-04	0.71	2.91	-	338.2
AHQ-2-11, 6872	R.YGLIPEEFFQFLYPK.T	1892.18434	2	3.69E-05	0.92	4.16	-	430.3
gi|4506365|ref|NP_002856.1| RAB2, member RAS oncogene family [Homo sapiens]				1.03E-06	2.12	30.22	16.50	23545.4
AHQ-2-11, 4274 - 4293	K.LQIWDTAGQESFR.S	1551.68478	2	1.03E-06	0.96	4.34	-	1588.8
AHQ-2-11, 4184	K.SCLLLQFTDKR.F	1382.61075	2	3.38E-04	0.71	3.02	-	661.7
AHQ-2-11, 3376	K.YIIIGDTGVGK.S	1136.32280	1	2.51E-04	0.45	2.46	-	499.0
gi|21361122|ref|NP_001440.2| four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap				1.13E-06	4.09	50.23	21.80	31894.7
AHQ-2-12, 2427	K.AIVAGDQNVEYK.G	1307.43431	2	7.11E-05	0.79	2.98	-	633.5
AHQ-2-11, 2390	K.AIVAGDQNVEYK.G	1307.43431	2	2.84E-04	0.89	3.59	-	876.6
AHQ-2-9, 2996 - 3067	K.CLHPLANETFVAK.D	1501.73210	2	9.24E-06	0.91	3.96	-	524.1
AHQ-2-9, 3620 - 3695	R.FVFHQEQVYCPDCAK.K	1931.13758	2	1.29E-05	0.96	4.64	-	988.9
AHQ-2-13-, 3874	R.FVFHQEQVYCPDCAK.K	1931.13758	2	9.47E-06	0.96	4.00	-	1583.1
AHQ-2-10, 2800 - 2879	K.GEDFYCVTCHETK.F	1648.75260	2	6.71E-06	0.86	3.32	-	713.6
AHQ-2-9, 2926	K.GEDFYCVTCHETK.F	1648.75260	2	1.13E-06	0.91	3.33	-	912.1
AHQ-2-9, 2131	K.NPITGFGK.G	833.95467	1	2.26E-06	0.53	2.33	-	292.7
gi|4506677|ref|NP_002942.1| ribophorin II [Homo sapiens]				1.20E-06	1.77	20.21	5.50	69301.6
AHQ-2-1, 5124	R.LQVTNVLSQPLTQATVK.L	1841.14195	2	1.20E-06	0.92	4.26	-	761.7
AHQ-2-1, 6773	K.TSFTPVGDVFELNFM*NVK.F	2062.33118	2	9.67E-05	0.84	3.66	-	547.4
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				1.21E-06	4.47	50.23	29.00	22006.2
AHQ-2-10, 4238 - 4258	K.HFCPNVPIILVGNK.K	1609.91693	2	1.21E-06	0.97	4.67	-	1913.1
AHQ-2-10, 3762 - 3764	K.HFCPNVPIILVGNKK.D	1738.08985	2	6.95E-06	0.97	4.64	-	1427.2
AHQ-2-10, 6586	R.LRPLSYPDTDVILM*CFSIDSPDSLENIPEK.W	3483.90759	3	4.95E-04	0.92	4.59	-	961.1
AHQ-2-10, 6678	R.LRPLSYPDTDVILMCFSIDSPDSLENIPEK.W	3467.90819	3	5.70E-05	0.84	4.05	-	655.9
AHQ-2-10, 2498	K.LVIVGDGACGK.T	1090.27572	2	2.30E-05	0.76	2.98	-	787.4
AHQ-2-10, 2495	K.LVIVGDGACGK.T	1090.27572	1	7.45E-04	0.62	2.11	-	772.9
gi|4504085|ref|NP_000399.1| glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA				1.25E-06	1.81	20.22	4.00	80814.1
AHQ-2-6, 3458	R.CKDVLTGQEFDVR.A	1568.73370	2	1.25E-06	0.95	4.28	-	1408.1
AHQ-2-6, 6170 - 6243	R.YGAATANYMEVVSLLK.K	1731.00632	2	2.18E-04	0.85	3.57	-	968.0
gi|15306356|ref|XP_035638.2| similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan				1.28E-06	1.79	20.18	13.90	18795.1
AHQ-2-13-, 3473	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.28E-06	0.86	3.50	-	619.8
AHQ-2-13, 3475	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.43E-06	0.77	3.08	-	629.1
AHQ-2-12, 3389	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.94E-06	0.89	3.62	-	707.9
AHQ-2-12, 4610	K.SYLYFTQFK.A	1197.36315	2	4.35E-06	0.93	3.21	-	1258.8

gi|7657649|ref|NP_055362.1| tropomodulin 3 (ubiquitous) [Homo sapiens]				1.31E-06	0.96	10.24	5.40	39594.5
AHQ-2-11, 5052	K.YKDLDEDELLGNLSETELK.Q	2225.39217	2	1.31E-06	0.96	4.70	-	1210.2
gi|4503291|ref|NP_001346.1| D-dopachrome tautomerase [Homo sapiens]				1.32E-06	0.88	10.18	9.30	12711.7
AHQ-2-14-, 5639	R.FFPLESWQIGK.I	1352.56151	2	1.32E-06	0.88	3.40	-	558.1
gi|4557871|ref|NP_001054.1| transferrin [Homo sapiens]				1.33E-06	0.86	10.22	2.70	77049.5
AHQ-2-5, 7344 - 7419	R.SAGWNIPIGLLYCDLPEPR.K	2173.47658	2	1.33E-06	0.86	4.37	-	441.8
gi|20070272|ref|NP_057110.2| androgen-regulated short-chain dehydrogenase/reductase 1; prostate sho				1.36E-06	2.12	30.19	15.40	35414.1
AHQ-2-13, 3735	K.GSGVTTYSVHPGTVQSELVR.H	2075.26811	2	1.36E-06	0.74	3.10	-	490.1
AHQ-2-9, 3272	K.GSGVTTYSVHPGTVQSELVR.H	2075.26811	2	7.31E-06	0.90	3.86	-	744.6
AHQ-2-9, 3779	K.MLSSGVCTSTVQLPGK.V	1666.94223	2	1.76E-04	0.80	3.33	-	657.2
AHQ-2-13-, 2633 - 2643	K.VVVVTGANTGIGK.E	1215.42469	2	2.23E-04	0.58	3.04	-	495.3
AHQ-2-13, 2712	K.VVVVTGANTGIGK.E	1215.42469	2	3.83E-04	0.86	3.01	-	947.8
gi|4758030|ref|NP_004362.1| coatomer protein complex, subunit alpha; alpha coat protein; xenin [Hom				1.40E-06	0.50	10.13	1.20	138330.6
AHQ-2-14, 6025	R.VTTVTEIGKDVIGLR.I	1601.86982	2	1.40E-06	0.50	2.63	-	318.2
gi|30148492|ref|XP_293610.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				1.40E-06	2.68	30.22	4.40	72113.4
AHQ-2-6, 4185	K.DAGTIAGLNVLR.I	1200.37012	2	1.29E-04	0.94	3.29	-	1489.0
AHQ-2-7, 4541	R.IINEPTAAAIAYGLDK.K	1660.89259	2	1.01E-05	0.81	3.79	-	885.5
AHQ-2-9, 4618	R.IINEPTAAAIAYGLDK.K	1660.89259	2	1.49E-04	0.47	2.99	-	361.4
AHQ-2-10, 4376 - 4384	R.IINEPTAAAIAYGLDK.K	1660.89259	2	1.29E-05	0.89	3.97	-	629.9
AHQ-2-6, 4023	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	1.40E-06	0.93	4.36	-	758.6
gi|4502905|ref|NP_001822.1| clusterin; complement-associated protein SP-40 [Homo sapiens]				1.44E-06	2.64	40.28	15.10	52494.3
AHQ-2-9, 5871	R.ASSIIDELFQDR.F	1394.51197	1	2.51E-05	0.07	2.37	-	165.0
AHQ-2-9, 2875	R.EILSVDCSTNNPSQAK.L	1764.89299	2	4.43E-04	0.77	3.21	-	634.3
AHQ-2-8, 2792	R.EILSVDCSTNNPSQAK.L	1764.89299	2	6.19E-04	0.49	2.66	-	443.4
AHQ-2-11, 5276	K.LFDSDPITVTVPVEVSR.K	1875.11203	2	4.97E-05	0.84	3.56	-	922.2
AHQ-2-11, 3392	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	1.44E-06	0.96	5.70	-	912.8
AHQ-2-9, 3234	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	3.40E-05	0.95	4.79	-	1123.8
gi|21361619|ref|NP_061882.2| TOLLIP protein; Toll-interacting protein [Homo sapiens]				1.50E-06	1.76	20.20	9.90	30281.6
AHQ-2-11, 5554 - 5629	R.GPVYIGELPQDFLR.I	1604.83072	2	1.50E-06	0.92	4.08	-	959.0
AHQ-2-11, 5637	R.GPVYIGELPQDFLR.I	1604.83072	2	1.87E-06	0.95	4.04	-	1409.4
AHQ-2-11, 4740 - 4745	R.IAWTHITIPESLR.Q	1537.78752	2	5.90E-05	0.83	3.47	-	626.3
gi|4505145|ref|NP_002387.1| malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochon				1.59E-06	2.64	30.25	8.90	65443.3
AHQ-2-6, 2967	R.HISDSVFLEAAK.A	1317.47234	2	1.88E-05	0.84	3.43	-	479.3
AHQ-2-6, 2799	K.IETQDIQALR.F	1187.32821	2	1.59E-06	0.91	3.59	-	1006.2
AHQ-2-6, 7217 - 7287	R.ILQDDIESLMPIVYTPTVGLACSQYGHIFR.R	3439.94604	3	3.71E-06	0.90	5.07	-	493.7
gi|17444699|ref|XP_017966.4| similar to Reticulon protein 3 (Neuroendocrine-specific protein-like 2				1.60E-06	0.90	10.16	4.70	25522.7
AHQ-2-1, 2901 - 2905	K.TQIDHYVGIAR.H	1273.42279	2	1.60E-06	0.90	3.25	-	1055.7
gi|30149460|ref|XP_210540.2| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				1.61E-06	1.70	20.17	11.10	29287.8
AHQ-2-5, 1979	K.EGLELPEDEEEKKKQEEK.K	2188.33193	2	1.30E-04	0.83	3.46	-	712.0
AHQ-2-5, 1996	K.HIYYITGETK.D	1225.37490	2	1.61E-06	0.87	3.08	-	673.3
gi|5729873|ref|NP_006656.1| heparanase; heparanase-1 [Homo sapiens]				1.62E-06	1.78	20.19	4.20	61176.4
AHQ-2-14-, 4999	K.TDFLIFDPK.K	1096.25713	1	1.29E-04	0.37	2.20	-	468.3
AHQ-2-14-, 5005	K.TDFLIFDPK.K	1096.25713	2	1.62E-06	0.94	3.81	-	1369.8
AHQ-2-7, 3296 - 3301	K.YLLRPLGPHGLLSK.S	1564.89924	2	9.10E-04	0.83	2.89	-	931.1
gi|29736026|ref|XP_085123.3| similar to Ras-related protein Rab-15 [Homo sapiens]				1.67E-06	0.35	10.18	5.30	23517.8
AHQ-2-13-, 3470 - 3489	R.IQIWDTAGQER.Y	1317.43243	2	1.53E-05	0.92	3.61	-	952.8
AHQ-2-10, 3160	R.IQIWDTAGQER.Y	1317.43243	1	1.67E-06	0.35	2.83	-	234.8
gi|4505775|ref|NP_002626.1| phosphate carrier precursor isoform 1b; phosphate carrier, mitochondria				1.73E-06	0.81	10.18	7.50	39958.5
AHQ-2-9, 7403 - 7404	K.YYALCGFGGVLSCGLTHTAVVPLDLVK.C	2914.38804	2	1.73E-06	0.81	3.65	-	605.2
gi|5803013|ref|NP_006808.1| endoplasmic reticulum protein 29 precursor; endoplasmic reticulum lumen				1.74E-06	2.19	30.20	15.30	28993.2
AHQ-2-10, 3864 - 3868	R.DGDFENPVPYTGAVK.V	1609.71786	2	7.48E-04	0.32	2.75	-	437.6
AHQ-2-10, 3727	K.ILDQGEDFPASEMTR.I	1709.85924	2	3.98E-05	0.94	4.06	-	980.0
AHQ-2-10, 4476	K.SLNILTAFQK.K	1135.33804	2	1.74E-06	0.92	3.33	-	1321.6
gi|29742410|ref|XP_291183.1| similar to TREM-like transcript 1 [Homo sapiens]				1.79E-06	0.72	10.21	5.10	32678.3
AHQ-2-10, 4027	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	8.45E-06	0.74	3.21	-	348.7
AHQ-2-11, 4205	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.79E-06	0.72	2.94	-	384.9
AHQ-2-13-, 4230 - 4238	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	5.87E-06	0.89	4.22	-	472.5
AHQ-2-9, 4288	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	2.21E-04	0.51	3.10	-	135.1
gi|5803135|ref|NP_006852.1| RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind				1.81E-06	0.88	10.18	5.50	23025.1
AHQ-2-13-, 3814 - 3829	K.LLIIGDSGVGK.S	1072.28025	2	5.65E-05	0.89	3.49	-	1052.4
AHQ-2-10, 3406	K.LLIIGDSGVGK.S	1072.28025	2	1.81E-06	0.88	3.38	-	902.6
gi|7706244|ref|NP_057005.1| divalent cation tolerant protein CUTA [Homo sapiens]				1.82E-06	0.97	10.34	17.30	16832.5
AHQ-2-13, 6773	R.SVHPYEVAEVIALPVEQGNFPYLQWVR.Q	3142.55428	3	1.82E-06	0.97	6.78	-	1780.9
gi|18375652|ref|NP_002826.2| protein tyrosine phosphatase, non-receptor type 12; protein-tyrosine p				1.87E-06	0.93	10.22	2.10	88119.9
AHQ-2-9, 7195	R.YWPLYGEDPITFAPFK.I	1945.20411	2	4.27E-04	0.76	3.46	-	329.3
AHQ-2-7, 7128 - 7192	R.YWPLYGEDPITFAPFK.I	1945.20411	2	1.87E-06	0.93	4.37	-	661.7
gi|7019485|ref|NP_037364.1| programmed cell death 6; apoptosis-linked gene 2 [Homo sapiens]				1.89E-06	1.68	20.18	20.90	21868.3
AHQ-2-11, 5445	K.AGVNFSEFTGVWK.Y	1442.59992	2	1.89E-06	0.90	3.56	-	1055.0
AHQ-2-11, 6524	R.SGVISDTELQQALSNGTWTPFNPVTVR.S	2919.19515	2	2.38E-06	0.78	3.52	-	541.8
gi|5174613|ref|NP_005960.1| nucleosome assembly protein 1-like 4; nucleosome assembly protein 2 [Ho				1.89E-06	0.95	10.17	2.70	42823.1
AHQ-2-7, 2619	K.FYEEVHDLER.K	1337.41897	2	1.89E-06	0.95	3.40	-	1659.1
gi|4506205|ref|NP_002791.1| proteasome beta 9 subunit isoform 1 proprotein; proteasome subunit, bet				1.96E-06	0.93	10.16	5.50	23264.2
AHQ-2-11, 4417	R.FTTDAIALAMSR.D	1297.50607	2	1.96E-06	0.93	3.30	-	1431.5
gi|18201911|ref|NP_000629.2| vitronectin precursor; serum spreading factor; somatomedin B; compleme				2.06E-06	0.94	10.21	3.10	54335.4
AHQ-2-13-, 5713 - 5715	R.SIAQYWLGCPAPGHL	1671.90045	2	2.06E-06	0.94	4.17	-	968.9
AHQ-2-13, 5603	R.SIAQYWLGCPAPGHL	1671.90045	2	1.97E-04	0.77	2.88	-	616.2
gi|22748619|ref|NP_689476.1| tropomyosin 3 [Homo sapiens]				2.07E-06	1.82	20.25	11.10	28222.6
AHQ-2-9, 3634	R.ALKDEEKMELQEIQLK.E	1946.25520	2	2.07E-06	0.95	4.92	-	1238.0
AHQ-2-9, 3011 - 3078	R.KLVIIEGDLER.T	1285.51492	2	1.47E-04	0.87	3.40	-	873.6
gi|27413156|ref|NP_000338.2| spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)				2.09E-06	0.90	10.21	1.40	246320.0
AHQ-2-2, 7465	R.DASVAEAWLIAQEPYLASGDFGHTVDSVEK.L	3207.44880	3	2.09E-06	0.90	4.12	-	1098.5
gi|4506363|ref|NP_002861.1| RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s				2.12E-06	1.74	20.19	10.80	22774.0
AHQ-2-11, 3550	K.LLLIGDSGVGK.T	1072.28025	1	2.90E-05	0.82	3.19	-	626.9
AHQ-2-13, 3792	K.LLLIGDSGVGK.T	1072.28025	2	3.69E-04	0.89	3.35	-	964.8
AHQ-2-14-, 3755	K.LLLIGDSGVGK.T	1072.28025	2	2.12E-06	0.93	3.75	-	1259.1
AHQ-2-11, 2930	K.LQVWDTAGQER.F	1303.40576	2	5.05E-05	0.81	3.15	-	812.2
gi|4503359|ref|NP_003965.1| docking protein 2, 56kD [Homo sapiens]				2.13E-06	1.52	20.14	6.30	45547.8
AHQ-2-13, 4000	R.FGASLYGGSDCALAR.L	1546.68659	2	2.13E-06	0.62	2.73	-	621.7
AHQ-2-13-, 3915	R.LYLLAAPAAER.G	1188.40094	2	5.08E-04	0.90	2.89	-	1186.2
gi|4759342|ref|NP_004808.1| tight junction protein 2 (zona occludens 2); Friedreich ataxia region g				2.15E-06	0.76	10.19	2.90	124661.6
AHQ-2-13, 6296	R.DNPHFENGETSIVISDVLPGGPADGLLQENDR.V	3407.60319	3	2.15E-06	0.76	3.89	-	663.7
gi|7706675|ref|NP_057661.1| RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M				2.15E-06	2.74	40.24	23.10	23461.5
AHQ-2-11, 4600	R.GSDVIIMLVGNK.T	1246.50220	2	9.59E-06	0.96	4.15	-	1961.4
AHQ-2-11, 3425	R.LQLWDTAGQER.F	1317.43243	1	8.52E-05	0.20	2.55	-	217.9
AHQ-2-12, 3315 - 3394	R.LQLWDTAGQER.F	1317.43243	2	2.45E-04	0.62	2.54	-	595.2
AHQ-2-11, 3489	K.LVFLGEQSVGK.T	1177.37492	2	8.48E-05	0.94	3.60	-	1242.9
AHQ-2-11, 3000	R.VASALPGMENVQEK.S	1473.67727	1	2.15E-06	0.64	3.56	-	307.5
gi|30154095|ref|XP_293967.2| similar to gamma actin-like protein [Homo sapiens]				2.15E-06	1.41	20.20	12.20	19259.0
AHQ-2-8, 5073	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.13E-04	0.37	2.80	-	334.7
AHQ-2-8, 5208	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.31E-04	0.31	2.72	-	257.0
AHQ-2-10, 4680 - 4694	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.29E-05	0.37	2.75	-	376.9
AHQ-2-13, 4911 - 4919	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.62E-05	0.33	2.73	-	306.8
AHQ-2-13, 5213	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	6.74E-05	0.63	2.70	-	572.8
AHQ-2-14, 5700	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.66E-05	0.74	3.36	-	526.8
AHQ-2-14, 5824 - 5885	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.00E-05	0.64	3.31	-	441.7
AHQ-2-14, 6076	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	6.86E-05	0.85	3.74	-	725.2
AHQ-2-14, 6196	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	3.40E-05	0.84	4.08	-	488.9

AHQ-2-13-, 4847	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	7.68E-06	0.80	3.53	-	602.6
AHQ-2-13-, 4950 - 5018	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.87E-04	0.69	3.21	-	484.1
AHQ-2-13-, 5177	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.25E-05	0.82	3.11	-	886.2
AHQ-2-13-, 5273	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	1.79E-04	0.75	3.59	-	420.8
AHQ-2-14-, 4775 - 4843	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.00E-04	0.74	3.20	-	730.6
AHQ-2-14-, 4907 - 4979	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.21E-04	0.35	3.02	-	363.5
AHQ-2-14-, 5096 - 5111	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.15E-06	0.56	3.05	-	400.1
gi|19923437|ref|NP_057366.2| adenylate kinase 3 alpha like [Homo sapiens]				2.15E-06	1.79	20.22	12.80	25565.2
AHQ-2-10, 3038	K.AYEDQTKPVLEYYQK.K	1876.05535	2	1.09E-04	0.92	4.36	-	613.9
AHQ-2-10, 6246 - 6286	K.NLTQYSWLLDGFPR.T	1710.91339	2	2.15E-06	0.87	3.20	-	1180.3
gi|5453603|ref|NP_006422.1| chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c				2.18E-06	3.63	40.20	11.40	57487.9
AHQ-2-7, 2856	R.EALLSSAVDHGSDEVK.F	1657.76083	2	8.35E-06	0.90	4.03	-	886.8
AHQ-2-7, 2919	R.GATQQILDEAER.S	1331.41427	2	2.18E-06	0.91	3.77	-	1136.4
AHQ-2-7, 5433	K.LGGSLADSYLDEGFLLDKK.I	2042.27480	2	9.27E-05	0.92	3.69	-	1091.2
AHQ-2-7, 5481 - 5545	R.SLHDALCVLAQTVK.D	1556.80920	2	3.87E-06	0.90	3.27	-	1047.5
gi|4759270|ref|NP_004613.1| translin; recombination hotspot associated factor; recombination hotspo				2.19E-06	1.84	20.23	15.80	26182.8
AHQ-2-10, 5059 - 5134	R.EILTLLQGVHQGAGFQDIPK.R	2165.47753	2	2.76E-05	0.87	4.10	-	540.5
AHQ-2-10, 6079	R.PLHISTFINELDSGFR.L	1847.06360	2	2.19E-06	0.97	4.61	-	1797.2
gi|4503481|ref|NP_001395.1| eukaryotic translation elongation factor 1 gamma; elongation factor 1-g				2.25E-06	1.68	20.20	8.20	50118.5
AHQ-2-12, 7026	R.GQELAFPLSPDWQVDYESYTWR.K	2688.88693	2	1.26E-04	0.79	3.33	-	383.5
AHQ-2-12, 2571	R.KLDPGSEETQTLVR.E	1573.73020	2	2.25E-06	0.89	4.00	-	546.1
gi|4504351|ref|NP_000510.1| delta globin [Homo sapiens]				2.27E-06	0.93	10.19	12.90	16055.4
AHQ-2-13-, 5626	R.FFESFGDLSSPDAVMGNPK.V	2046.24551	2	2.27E-06	0.93	3.83	-	1245.9
AHQ-2-13, 5449 - 5528	R.FFESFGDLSSPDAVMGNPK.V	2046.24551	2	8.73E-04	0.85	3.32	-	1030.6
gi|24308263|ref|NP_067045.1| TcD37 homolog; prune [Homo sapiens]				2.33E-06	0.97	10.25	3.80	50199.3
AHQ-2-7, 7660	K.LLPLLQEALSAYFDSMK.I	1940.29226	2	2.33E-06	0.97	5.02	-	1760.3
gi|4504045|ref|NP_002063.1| guanine nucleotide binding protein (G protein), q polypeptide [Homo sap				2.39E-06	1.66	20.24	9.50	42142.8
AHQ-2-8, 3850	R.VADPAYLPTQQDVLR.V	1686.89014	2	2.39E-06	0.71	3.05	-	504.6
AHQ-2-9, 7386 - 7390	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	7.66E-04	0.94	4.77	-	691.4
AHQ-2-8, 7355	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	1.89E-05	0.95	4.72	-	980.9
gi|4758792|ref|NP_004544.1| NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q				2.44E-06	0.59	10.13	9.70	13711.5
AHQ-2-13-, 3931	K.TGTCGYCGLQFR.Q	1422.56875	2	2.44E-06	0.59	2.62	-	665.0
gi|6680033|ref|NP_031379.1| guanine nucleotide binding protein (G protein) alpha 12 [Homo sapiens]				2.45E-06	0.61	10.13	2.90	44250.9
AHQ-2-9, 2971	K.ILLLGAGESGK.S	1058.25357	1	2.95E-04	0.66	2.57	-	622.1
AHQ-2-8, 2807	K.ILLLGAGESGK.S	1058.25357	1	2.45E-06	0.61	2.60	-	503.6
gi|30149013|ref|XP_302138.1| similar to alpha tubulin [Homo sapiens]				2.46E-06	0.85	10.14	4.60	22444.5
AHQ-2-13, 4989	R.EIINLVLDR.I	1085.27902	1	1.63E-04	0.13	2.08	-	134.3
AHQ-2-14-, 5011	R.EIINLVLDR.I	1085.27902	2	3.82E-04	0.76	2.66	-	852.9
AHQ-2-7, 4932 - 4936	R.EIINLVLDR.I	1085.27902	2	2.46E-06	0.85	2.89	-	1050.7
gi|4502011|ref|NP_000467.1| adenylate kinase 1 [Homo sapiens]				2.61E-06	3.97	50.31	35.10	21634.7
AHQ-2-11, 6554 - 6557	K.GQLVPLETVLDM*LR.D	1600.90530	2	6.61E-04	0.92	4.61	-	486.2
AHQ-2-11, 5644	R.IGQPTLLLYVDAGPETMTQR.L	2204.53234	2	3.00E-06	0.95	4.46	-	1087.9
AHQ-2-11, 5148	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	2	2.61E-06	0.86	4.13	-	595.4
AHQ-2-11, 3346	K.IIFVVGGPGSGK.G	1131.34939	1	3.52E-04	0.75	2.46	-	934.2
AHQ-2-11, 6321 - 6390	K.VNAEGSVDSVFSQVCTHLDALK	2378.60116	2	4.40E-04	0.49	2.88	-	381.4
gi|5453714|ref|NP_006448.1| LIM protein (similar to rat protein kinase C-binding enigma) [Homo sapi				2.64E-06	0.79	10.16	2.50	64027.9
AHQ-2-13-, 2829 - 2894	K.EVVKPVPITSPAVSK.V	1551.85241	2	2.64E-06	0.79	3.10	-	371.5
AHQ-2-13, 2888 - 2937	K.EVVKPVPITSPAVSK.V	1551.85241	2	8.52E-05	0.68	3.02	-	262.1
gi|4506181|ref|NP_002778.1| proteasome alpha 2 subunit; proteasome subunit HC3; proteasome componen				2.84E-06	1.18	20.22	15.40	25898.4
AHQ-2-10, 4490	R.GYSFSLTTFSPSGK.L	1479.61533	1	7.54E-04	0.26	2.42	-	284.4
AHQ-2-10, 4812	R.KLAQQYYLVYQEPIPTAQLVQR.V	2651.05593	2	2.84E-06	0.92	4.43	-	674.9
gi|4506359|ref|NP_000311.1| quinoid dihydropteridine reductase; dihydropteridine reductase [Homo sa				2.87E-06	0.98	10.26	7.00	25803.4
AHQ-2-10, 3280	K.NRPSSGSLIQVVTTEGR.T	1801.98277	2	2.87E-06	0.98	5.12	-	1874.6
gi|4757714|ref|NP_004291.1| acid phosphatase 1 isoform c; acid phosphatase of erythrocyte; red cell				3.29E-06	0.64	10.18	5.70	18042.4
AHQ-2-11, 3112	R.SPIAEAVFR.K	990.13779	1	3.29E-06	0.64	2.29	-	413.1
gi|21361456|ref|NP_055425.2| alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph				3.37E-06	3.33	40.20	7.20	109437.2
AHQ-2-5, 5947	K.HHGPQTLYLPVTLSSIPVFQR.G	2391.75581	2	4.49E-06	0.76	3.03	-	646.8
AHQ-2-5, 4280	R.LSFQHDPETSVLVLR.K	1741.96893	2	4.91E-04	0.84	3.72	-	519.6
AHQ-2-5, 3629	K.MMDYLQGSGETPQTDVR.W	1929.12196	2	3.37E-06	0.94	4.10	-	1097.2
AHQ-2-4, 3893	R.VVIIGAGKPAAVVLQTK.G	1665.05702	2	6.35E-04	0.79	3.35	-	652.3
gi|4506285|ref|NP_003470.1| protein tyrosine phosphatase type IVA, member 2 isoform 1; protein tyro				3.41E-06	0.88	10.17	8.40	19127.1
AHQ-2-11, 2837 - 2897	R.FLITHNPTNATLNK.F	1584.80104	2	3.41E-06	0.88	3.30	-	1159.4
gi|20127408|ref|NP_000173.2| hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub				3.56E-06	3.63	50.21	12.70	82999.1
AHQ-2-6, 6475	R.DSIFSNLTGQLDYQGFEK.A	2063.20943	2	1.10E-04	0.92	4.15	-	915.8
AHQ-2-6, 2481	K.DTSASAVAVGLK.Q	1119.25064	1	5.72E-05	0.18	2.21	-	367.7
AHQ-2-6, 6621 - 6629	K.EVEAVIPDHCIFASNTSALPISEIAAVSK.R	3071.44790	3	3.10E-04	0.79	3.91	-	440.7
AHQ-2-6, 2975	K.TGIEQGSDAGYLCESQK.F	1844.93497	2	3.56E-06	0.93	4.15	-	880.0
AHQ-2-6, 6045	K.TVLGTPEVLLGALPGAGGTQR.L	2008.30795	3	1.49E-04	0.81	3.45	-	948.4
gi|9845511|ref|NP_008839.2| ras-related C3 botulinum toxin substrate 1 isoform Rac1; rho family, sm				3.95E-06	0.96	10.21	5.20	21450.0
AHQ-2-11, 3052	K.YLECSALTQR.G	1242.38392	2	3.95E-06	0.96	4.18	-	1668.5
gi|8923579|ref|NP_060377.1| hypothetical protein FLJ20625 [Homo sapiens]				4.01E-06	1.84	20.27	26.70	17744.7
AHQ-2-13, 6301	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	7.24E-04	0.87	4.25	-	626.1
AHQ-2-14-, 6339	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	6.89E-04	0.93	5.38	-	718.7
AHQ-2-12, 5445	R.TDEQALLSSILAK.T	1389.57677	2	4.01E-06	0.91	3.19	-	1195.8
gi|29736622|ref|XP_293924.1| similar to cytoplasmic beta-actin [Homo sapiens]				4.02E-06	1.87	20.24	13.60	42002.9
AHQ-2-8, 7187	R.FRCPEAIFQPSFLGIESSGIHETTFNSIMK.C	3446.89713	3	5.02E-05	0.93	4.78	-	1168.7
AHQ-2-8, 3762	R.VAPDEHPILLTEAPLNPKINR.E	2338.69122	3	4.02E-06	0.94	4.71	-	1399.8
gi|22063113|ref|XP_171447.1| similar to elongin B; transcription elongation factor B (SIII), polype				4.36E-06	1.30	20.16	21.20	13156.8
AHQ-2-12, 3470	R.PQAPATVGLAFR.A	1228.42516	2	4.36E-06	0.88	3.20	-	742.6
AHQ-2-12, 4897	K.TLGECGFTSQTARPQAPATVGLAFR.A	2638.94056	2	6.63E-05	0.41	2.82	-	241.3
gi|27482573|ref|XP_208709.1| similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro				4.49E-06	0.96	10.27	11.70	17875.4
AHQ-2-12, 4917	K.GQVCLPVISAENWKPATK.T	2000.30757	2	4.49E-06	0.96	5.38	-	878.0
gi|25306267|ref|NP_001700.2| brain-derived neurotrophic factor isoform a preproprotein [Homo sapien				4.58E-06	1.68	20.20	6.10	27817.8
AHQ-2-13-, 2858	K.TAVDM*SGGTVTVLEK.V	1524.71933	2	4.58E-06	0.73	2.59	-	1013.9
AHQ-2-13-, 3754 - 3758	K.TAVDMSGGTVTVLEK.V	1508.71993	2	7.97E-04	0.80	3.34	-	841.4
AHQ-2-13, 3740 - 3743	K.TAVDMSGGTVTVLEK.V	1508.71993	2	8.34E-05	0.95	3.91	-	1659.7
gi|4505395|ref|NP_002499.1| nidogen (enactin); Nidogen; nidogen (entactin) [Homo sapiens]				4.59E-06	0.95	10.18	0.90	136488.3
AHQ-2-3, 4536	R.VLFETDLVNPR.G	1303.48880	2	4.59E-06	0.95	3.56	-	1467.7
gi|5031569|ref|NP_005727.1| ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r				4.59E-06	0.93	10.23	5.90	42613.4
AHQ-2-8, 5052	K.DQLQTFSEEHPVLLTEAPLNPR.K	2535.79382	2	4.59E-06	0.93	4.42	-	748.7
gi|19923262|ref|NP_004153.2| RAB5A, member RAS oncogene family; RAS-associated protein RAB5A [Homo				4.76E-06	1.84	20.19	10.20	23658.5
AHQ-2-10, 3691	K.FEIWDTAGQER.Y	1352.43364	2	4.37E-05	0.93	3.80	-	1250.9
AHQ-2-10, 3204 - 3206	K.LVLLGESAVGK.S	1086.30692	2	4.76E-06	0.90	3.53	-	1143.8
gi|8393638|ref|NP_058642.1| F11 receptor isoform a precursor; platelet F11 receptor; platelet adhes				5.09E-06	0.68	10.13	3.70	32582.9
AHQ-2-12, 5326	R.VTFLPTGITFK.S	1224.47318	2	5.09E-06	0.68	2.55	-	374.5
gi|4557251|ref|NP_001101.1| a disintegrin and metalloprotease domain 10 [Homo sapiens]				5.12E-06	0.87	10.17	2.00	84141.7
AHQ-2-5, 4676	K.AIDTIYQTTDFSGIR.N	1701.85844	2	5.12E-06	0.87	3.31	-	869.0
gi|20149570|ref|NP_005816.2| RAS guanyl releasing protein 2 isoform 1; calcium and diacylglycerol-r				5.28E-06	0.80	10.14	2.80	75547.0
AHQ-2-7, 6844	K.LWEGLTELVTATGNYGNYR.R	2158.35558	2	5.28E-06	0.80	2.76	-	1014.2
gi|6005786|ref|NP_009214.1| monoglyceride lipase; lysophospholipase-like [Homo sapiens]				5.49E-06	3.47	40.26	19.20	34292.3
AHQ-2-9, 1966	K.ALIFVSHGAGEHSGR.Y	1538.69246	2	5.49E-06	0.95	4.20	-	1159.4
AHQ-2-14-, 6103	K.LTVPFLLLQGSADR.L	1530.79329	2	5.48E-04	0.70	2.88	-	491.7
AHQ-2-9, 6430	R.TPQSIPYQDLPHLVNADGQYLFCR.Y	2835.14314	3	4.62E-04	0.87	4.46	-	400.1
AHQ-2-9, 7346	K.VLNLVLPNLSLGPIDSSVLSR.N	2207.59900	2	5.03E-04	0.95	5.20	-	718.2
gi|8922601|ref|NP_060654.1| hypothetical protein FLJ10702 [Homo sapiens]				6.17E-06	1.04	20.18	13.40	21538.9
AHQ-2-11, 2597 - 2629	R.DLPNALDEK.Q	1015.09928	1	3.53E-04	0.20	1.83	-	463.5
AHQ-2-11, 5433	R.GVNAIVYMIDAADREK.I	1766.01230	2	6.17E-06	0.83	3.56	-	677.3

gi|4826657|ref|NP_004333.1| caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]				6.37E-06	3.55	40.20	13.00	62662.9
AHQ-2-10, 4634 - 4640	K.EFDPTITDASLSLPSR.R	1749.89986	2	2.63E-05	0.87	3.52	-	786.4
AHQ-2-12, 2503	K.GNVFSSPTAAGTPNK.E	1448.56286	2	5.22E-04	0.71	2.67	-	884.8
AHQ-2-13, 2668	K.GNVFSSPTAAGTPNK.E	1448.56286	2	7.40E-04	0.72	2.85	-	553.1
AHQ-2-13-, 2601	K.GNVFSSPTAAGTPNK.E	1448.56286	2	6.37E-06	0.92	3.81	-	918.8
AHQ-2-12, 2694	K.SAKPTKPAASDLPVPAEGVR.N	1992.26539	2	2.46E-04	0.88	4.10	-	593.8
AHQ-2-10, 3516	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	4.98E-05	0.87	3.06	-	980.4
gi|4505329|ref|NP_003818.1| N-ethylmaleimide-sensitive factor attachment protein, alpha; alpha-SNAP				6.55E-06	1.94	20.24	11.20	33246.6
AHQ-2-9, 3974	K.HDAATCFVDAGNAFK.K	1625.74381	2	6.55E-06	0.97	4.58	-	2068.3
AHQ-2-9, 3118	K.LLEAHEEQNVDSYTESVK.E	2092.20594	2	9.22E-05	0.97	4.83	-	1535.2
gi|4759086|ref|NP_004883.1| vesicle trafficking protein sec22b [Homo sapiens]				6.69E-06	2.65	30.20	20.00	24740.4
AHQ-2-12, 1987	R.DLQQYQSQAK.Q	1209.29073	2	3.08E-05	0.83	2.97	-	763.3
AHQ-2-12, 3970	R.NLGSINTELQDVQR.I	1587.71696	2	6.69E-06	0.91	3.48	-	1333.7
AHQ-2-13-, 4089	R.VADGLPLAASMQEDEQSGR.D	1975.12722	2	2.58E-04	0.63	2.94	-	554.4
AHQ-2-12, 4041	R.VADGLPLAASMQEDEQSGR.D	1975.12722	2	4.81E-05	0.91	4.04	-	639.7
gi|4502211|ref|NP_001654.1| ADP-ribosylation factor 6 [Homo sapiens]				6.72E-06	0.81	10.17	6.30	20082.0
AHQ-2-12, 4079	K.FNVWDVGGQDK.I	1265.35598	2	6.72E-06	0.81	2.77	-	1144.5
gi|20270343|ref|NP_620150.1| hypothetical protein BC015408 [Homo sapiens]				6.72E-06	1.88	20.32	17.20	21415.8
AHQ-2-11, 2709	K.MNLSAIQDR.E	1048.19914	2	4.76E-04	0.92	3.23	-	1348.4
AHQ-2-11, 5833 - 5836	K.NELHNLLDKPQLQGIPVLVLGNK.R	2553.98492	2	6.72E-06	0.96	5.28	-	834.7
AHQ-2-11, 5832 - 5897	K.NELHNLLDKPQLQGIPVLVLGNK.R	2553.98492	3	1.16E-05	0.97	6.36	-	1323.7
gi|30148978|ref|XP_291520.2| similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK				6.80E-06	0.72	10.16	2.20	68413.1
AHQ-2-11, 4888	R.DWSHYFKTIKDLR.A	1709.92863	2	2.24E-04	0.37	2.59	-	379.0
AHQ-2-13-, 4963	R.DWSHYFKTIKDLR.A	1709.92863	2	1.05E-04	0.63	3.14	-	663.3
AHQ-2-11, 4754 - 4830	R.DWSHYFKTIKDLR.A	1709.92863	2	6.80E-06	0.72	3.10	-	663.6
gi|22129786|ref|NP_059980.1| gp25L2 protein [Homo sapiens]				6.83E-06	0.76	10.19	5.10	25104.5
AHQ-2-10, 2875	R.QLVEQVEQIQK.E	1342.52334	2	6.83E-06	0.76	3.39	-	653.5
gi|4504221|ref|NP_000849.1| guanylate kinase 1 [Homo sapiens]				7.08E-06	0.97	10.21	6.10	21725.4
AHQ-2-11, 5065	R.ICVLDVDLQGVR.N	1388.61530	2	7.08E-06	0.97	4.10	-	2374.2
gi|6996010|ref|NP_002038.1| glycyl-tRNA synthetase; GlyRS; glycine tRNA ligase [Homo sapiens]				7.13E-06	1.57	20.17	4.50	77530.3
AHQ-2-6, 6805	K.TLYVEEVVPNVIEPSFGLGR.I	2219.52197	2	7.13E-06	0.85	3.47	-	757.3
AHQ-2-6, 2991 - 3010	K.TVNVVQFEPSK.G	1248.41001	2	6.57E-05	0.72	2.54	-	837.4
gi|27480842|ref|XP_208238.1| similar to bA92K2.2 (similar to ubiquitin) [Homo sapiens]				7.23E-06	0.88	10.14	5.80	17966.9
AHQ-2-14-, 2283	R.TLSDYNIQK.E	1082.18886	2	7.23E-06	0.88	2.83	-	642.7
gi|4502297|ref|NP_001678.1| ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit				7.35E-06	0.65	10.21	8.30	17489.8
AHQ-2-13-, 2515	K.AQAELVGTADEATR.A	1432.51860	2	8.18E-04	0.94	4.11	-	1171.8
AHQ-2-13-, 2535	K.AQAELVGTADEATR.A	1432.51860	1	7.35E-06	0.65	3.20	-	204.4
AHQ-2-12, 2471	K.AQAELVGTADEATR.A	1432.51860	2	6.00E-04	0.81	3.06	-	569.9
gi|4503531|ref|NP_001958.1| eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens] [				7.50E-06	0.38	10.12	3.40	46393.9
AHQ-2-8, 2576	K.GYDVIAQAQSGTGK.T	1395.49996	1	7.50E-06	0.38	2.47	-	550.3
gi|5803217|ref|NP_006821.1| ubiquinol-cytochrome c reductase (6.4kD) subunit [Homo sapiens]				7.63E-06	0.90	10.14	21.40	6569.6
AHQ-2-14-, 6288	R.LILDWVPYINGK.F	1431.70332	2	7.63E-06	0.90	2.89	-	895.3
gi|19743813|ref|NP_002202.2| integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib				7.67E-06	0.66	10.16	2.10	88414.9
AHQ-2-5, 5124	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	7.67E-06	0.66	3.02	-	680.1
gi|7706371|ref|NP_057190.1| vesicle transport-related protein [Homo sapiens]				7.69E-06	0.89	10.19	3.00	72479.5
AHQ-2-6, 6641	K.GSPFPEVAESVQQELESYR.A	2153.29097	2	7.69E-06	0.89	3.87	-	779.2
gi|29729950|ref|XP_293759.1| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				7.75E-06	0.95	10.21	5.00	39776.4
AHQ-2-5, 4823	K.CLELFTELAEDKENYKK.F	2132.37640	2	7.75E-06	0.95	4.16	-	1482.2
gi|29730354|ref|XP_298663.1| hypothetical protein XP_298663 [Homo sapiens]				7.81E-06	0.34	10.15	15.90	19365.2
AHQ-2-6, 6857	K.QLGAIPSWLARRTVNTKPTTFLGGSDLR.T	3057.49883	3	7.81E-06	0.34	3.02	-	259.0
gi|4505185|ref|NP_002406.1| macrophage migration inhibitory factor (glycosylation-inhibiting factor				7.85E-06	0.94	10.20	7.80	12476.2
AHQ-2-14-, 4592 - 4595	K.LLCGLLAER.L	1046.26608	2	4.15E-04	0.94	4.09	-	940.8
AHQ-2-14, 5762	K.LLCGLLAER.L	1046.26608	2	7.85E-06	0.94	3.49	-	1037.8
gi|14249382|ref|NP_116139.1| hypothetical protein MGC15429 [Homo sapiens]				8.31E-06	0.63	10.14	10.50	22345.5
AHQ-2-11, 4918	K.TPALIVYGDQDPMGQTSFEHLK.Q	2448.73644	2	8.31E-06	0.63	2.82	-	331.6
gi|11496891|ref|NP_000662.2| class III alcohol dehydrogenase 5 chi subunit; Alcohol dehydrogenase (				8.69E-06	0.94	10.24	5.90	39738.1
AHQ-2-14, 6409	K.AAVAWEAGKPLSIEEIEVAPPK.A	2306.64276	2	9.15E-06	0.49	2.84	-	242.3
AHQ-2-9, 5147	K.AAVAWEAGKPLSIEEIEVAPPK.A	2306.64276	2	8.69E-06	0.94	4.85	-	834.3
gi|5031601|ref|NP_005711.1| actin related protein 2/3 complex subunit 1B; ARP2/3 protein complex su				8.93E-06	2.17	30.26	14.20	40949.5
AHQ-2-9, 2180	K.ASSEGGTAAGAGLDSLHK.N	1629.71071	2	1.87E-05	0.34	2.61	-	354.3
AHQ-2-9, 3188	K.EHNGQVTGIDWAPESNR.I	1910.98151	2	8.93E-06	0.86	3.60	-	619.8
AHQ-2-8, 2843	R.VAWVSHDSTVCLADADKK.M	2004.20995	2	9.24E-06	0.96	5.27	-	1225.4
gi|4502599|ref|NP_001748.1| carbonyl reductase 1; carbonyl reductase (NADPH); carbonyl reductase (N				8.95E-06	0.71	10.15	5.40	30374.7
AHQ-2-9, 5515	R.DVCTELLPLIKPQGR.V	1741.04567	2	8.95E-06	0.71	3.09	-	335.6
gi|19913424|ref|NP_001681.2| ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT				9.07E-06	0.93	10.21	2.80	68303.7
AHQ-2-6, 4149 - 4154	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	9.07E-06	0.93	4.14	-	1082.3
gi|5031599|ref|NP_005722.1| actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub				9.26E-06	3.87	50.21	23.30	34332.8
AHQ-2-10, 3679	R.DNTINLIHTFR.D	1344.50101	2	3.00E-04	0.84	2.98	-	772.9
AHQ-2-9, 2423	K.DSIVHQAGMLK.R	1199.40563	2	3.07E-05	0.90	3.28	-	947.8
AHQ-2-9, 2255	R.DYLHYHIK.C	1089.22792	1	1.03E-04	0.43	2.36	-	526.3
AHQ-2-9, 2480 - 2500	K.ELQAHGADELLK.R	1324.46487	2	9.26E-06	0.90	3.68	-	942.5
AHQ-2-9, 7398 - 7400	R.VYGSFLVNPESGYNVSLLYDLENLPASK.D	3090.42808	3	3.44E-05	0.80	3.92	-	402.9
gi|4506713|ref|NP_002945.1| ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte				9.68E-06	0.83	10.21	10.30	17964.8
AHQ-2-14-, 4188	K.TITLEVEPSDTIENVK.A	1788.97431	2	8.63E-04	0.71	3.10	-	292.5
AHQ-2-14-, 4375 - 4439	K.TITLEVEPSDTIENVK.A	1788.97431	2	1.08E-04	0.80	4.17	-	545.7
AHQ-2-4, 4648	K.TITLEVEPSDTIENVK.A	1788.97431	2	9.68E-06	0.83	3.96	-	614.4
gi|30158852|ref|XP_301583.1| similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa				9.72E-06	0.69	10.15	6.50	19197.0
AHQ-2-8, 2458 - 2472	K.IWHHTFYNKLR.V	1515.74533	2	9.72E-06	0.69	2.92	-	785.9
gi|4826659|ref|NP_004921.1| F-actin capping protein beta subunit; Cap Z [Homo sapiens]				1.05E-05	2.29	30.21	13.20	30628.5
AHQ-2-9, 3980 - 4012	K.GCWDSIHVVEVQEK.S	1687.85505	2	1.05E-05	0.92	4.26	-	1340.1
AHQ-2-9, 3274	R.KLEVEANNAFDQYR.D	1697.82988	2	3.18E-04	0.95	3.79	-	1717.7
AHQ-2-10, 3114 - 3126	R.KLEVEANNAFDQYR.D	1697.82988	2	9.26E-05	0.96	4.15	-	1892.4
AHQ-2-9, 2632 - 2636	K.NDLVEALK.R	902.02731	1	5.78E-04	0.40	2.09	-	438.1
gi|4507383|ref|NP_001052.1| thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil				1.08E-05	2.81	30.22	5.80	60675.3
AHQ-2-7, 4231 - 4305	R.FQACPETQVPLQLESK.S	1877.10807	2	1.08E-05	0.93	4.00	-	879.3
AHQ-2-7, 3636 - 3663	R.HSASPMGVQDFDIVR.D	1659.84828	2	1.87E-04	0.95	4.33	-	1211.6
AHQ-2-7, 2956	R.HSASPM*GVQDFDIVR.D	1675.84768	2	4.29E-05	0.94	3.85	-	1174.7
gi|7705614|ref|NP_057132.1| CGI-111 protein [Homo sapiens]				1.11E-05	1.66	20.24	17.10	22087.6
AHQ-2-9, 7468 - 7472	K.FSMVLPEVEAALAEIPGVR.S	2029.38904	2	1.11E-05	0.95	4.84	-	834.3
AHQ-2-9, 4158 - 4238	K.GLGSTVQEIDLTGVK.L	1517.70655	2	8.12E-04	0.72	2.62	-	788.0
gi|7706351|ref|NP_057161.1| CGI-147 protein [Homo sapiens]				1.15E-05	0.82	10.20	12.80	19193.4
AHQ-2-11, 5241	R.TQIAPGSQTVLGIGPGPADLIDK.V	2249.54961	2	1.15E-05	0.82	3.91	-	599.1
gi|24308123|ref|NP_056505.1| serine/threonine kinase 36 (fused homolog, Drosophila); serine/threoni				1.17E-05	0.48	10.16	2.10	143995.0
AHQ-2-7, 6635 - 6655	R.IQSQLHEAGGQILNGILEGASHILPAFR.V	2971.36280	3	1.17E-05	0.48	3.16	-	307.6
gi|4501841|ref|NP_001596.1| alanyl-tRNA synthetase [Homo sapiens]				1.19E-05	1.86	20.24	3.40	106800.7
AHQ-2-4, 7493	R.EIADLGEALATAVIPQWQK.D	2054.33195	2	3.55E-04	0.90	4.33	-	863.2
AHQ-2-4, 3614	K.KAEEIANEMIEAAK.A	1547.75615	2	1.19E-05	0.96	4.76	-	1252.2
gi|4557321|ref|NP_000030.1| apolipoprotein A-I precursor [Homo sapiens]				1.20E-05	2.71	30.25	16.50	30777.6
AHQ-2-11, 5078	K.LLDNWDSVTSTFSK.L	1613.74965	2	1.20E-05	0.83	3.48	-	660.7
AHQ-2-11, 5541	K.LREQLGPVTQEFWDNLEK.E	2203.43949	2	2.01E-04	0.96	4.99	-	1020.7
AHQ-2-14-, 6247	K.VSFLSALEEYTK.K	1387.55934	2	3.54E-05	0.92	3.39	-	1111.0
gi|7705827|ref|NP_057187.1| GTP-binding protein Sara [Homo sapiens]				1.23E-05	0.52	10.19	5.60	22409.7
AHQ-2-11, 4136 - 4137	K.LVFLGLDNAGK.T	1147.34882	1	1.23E-05	0.52	2.59	-	514.7
AHQ-2-11, 4132	K.LVFLGLDNAGK.T	1147.34882	2	1.43E-04	0.95	3.86	-	1194.5
gi|7706563|ref|NP_057614.1| RAB-8b protein [Homo sapiens]				1.27E-05	0.87	10.22	7.20	23584.0
AHQ-2-11, 5230	R.GAM*GIMLVYDITNEK.S	1671.96066	2	1.27E-05	0.87	4.32	-	869.6
gi|4885569|ref|NP_005393.1| v-ral simian leukemia viral oncogene homolog A (ras related); RAS-like				1.27E-05	0.93	10.24	7.20	23986.1

AHQ-2-10, 3846	R.VKEDENVPFLLVGNK.S	1701.94471	2	1.27E-05	0.93	4.81	-	773.2
gi|29725611|ref|NP_066954.2|	regulatory subunit PR 53 of protein phosphatase 2A isoform b; phosphot			1.29E-05	0.93	10.24	9.00	36775.0
AHQ-2-9, 7382	K.LDEEAENLVATVVPTHLAAAVPEVAVYLK.E	3063.49045	3	1.29E-05	0.93	4.73	-	1360.3
gi|4503643|ref|NP_000121.1|	coagulation factor V precursor; labile factor; factor V Leiden [Homo sa			1.37E-05	2.52	30.21	2.00	251716.5
AHQ-2-6, 2847	K.EVIITGIQTQGAK.H	1358.56590	2	9.19E-05	0.83	3.14	-	767.3
AHQ-2-1, 3265	K.EVIITGIQTQGAK.H	1358.56590	2	7.73E-05	0.86	3.60	-	880.9
AHQ-2-3, 4983 - 5043	R.GEYEEHLGILGPIIR.A	1696.92816	2	1.28E-04	0.91	3.81	-	1065.1
AHQ-2-6, 4681	R.GEYEEHLGILGPIIR.A	1696.92816	2	1.37E-05	0.72	3.16	-	582.4
AHQ-2-3, 3709	K.LSEGASYLDHTFPAEK.M	1765.90099	2	9.61E-04	0.93	4.10	-	1202.0
gi|4502989|ref|NP_001856.1|	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor; hepa			1.39E-05	0.89	10.18	15.70	9395.9
AHQ-2-14-, 5319 - 5339	K.LFQEDDEIPLYLK.G	1623.82758	2	1.39E-05	0.89	3.62	-	1098.0
AHQ-2-14, 6485 - 6561	K.LFQEDDEIPLYLK.G	1623.82758	2	5.42E-05	0.94	3.60	-	1539.8
gi|6552299|ref|NP_009225.1|	breast cancer 1, early onset; breast-ovarian cancer, included [Homo sap			1.42E-05	0.33	10.19	1.60	207718.7
AHQ-2-10, 6783	K.TPEM*INQGTNQTEQNGQVM*NITNSGHENK.T	3248.42306	3	1.42E-05	0.33	3.75	-	261.7
gi|7662651|ref|NP_054778.1|	RGC32 protein [Homo sapiens]			1.42E-05	0.89	10.16	9.40	12924.1
AHQ-2-12, 5353	K.ELEAFIADLDK.T	1264.40621	2	1.42E-05	0.89	3.17	-	998.9
gi|24475861|ref|NP_054891.2|	phosphohistidine phosphatase; sex-regulated protein janus-a [Homo sapi			1.47E-05	0.93	10.16	8.80	13832.4
AHQ-2-13-, 3009 - 3079	K.WAEYHADIYDK.V	1411.49955	2	1.47E-05	0.93	3.25	-	1168.3
gi|22538465|ref|NP_002786.2|	proteasome beta 3 subunit; proteasome theta chain; proteasome chain 13			1.50E-05	0.94	10.20	7.80	22948.8
AHQ-2-10, 4844	R.FGPYYTEPVIAGLDPK.T	1768.00162	2	3.26E-05	0.88	3.20	-	891.3
AHQ-2-10, 4840	R.FGPYYTEPVIAGLDPK.T	1768.00162	2	1.50E-05	0.94	4.08	-	1031.8
gi|29729345|ref|XP_290995.1|	similar to speckle-type POZ protein [Homo sapiens]			1.53E-05	1.53	20.19	10.90	18703.4
AHQ-2-2, 6258 - 6341	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	1.53E-05	0.74	3.71	-	772.1
AHQ-2-3, 6232 - 6304	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	9.30E-05	0.79	3.75	-	911.7
AHQ-2-1, 6288	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	6.73E-05	0.80	3.33	-	705.0
gi|18640750|ref|NP_570138.1|	regulator of G-protein signalling 18; regulator of G-protein signaling			1.58E-05	0.88	10.21	8.90	27582.0
AHQ-2-11, 4110	K.EVITNSITQPTLHSFDAAQSR.V	2316.51300	2	1.58E-05	0.88	4.27	-	357.2
gi|4502553|ref|NP_003647.1|	calcium/calmodulin-dependent protein kinase I [Homo sapiens]			1.75E-05	0.94	10.27	5.40	41336.9
AHQ-2-9, 4940 - 4944	R.FTCEQALQHPWIAGDTALDK.N	2303.53598	2	1.75E-05	0.94	5.38	-	657.8
gi|24308400|ref|NP_612366.1|	hypothetical protein BC010682 [Homo sapiens]			1.75E-05	1.08	20.16	10.30	39866.6
AHQ-2-9, 6664	R.CQFTLKPISDSVGVFLR.Q	1969.29348	2	1.42E-04	0.54	2.87	-	258.7
AHQ-2-9, 7016	K.TLVQQLYTTLCIEQHQLNK.E	2332.66190	3	1.75E-05	0.54	3.25	-	393.4
gi|10835049|ref|NP_001655.1|	ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho			1.76E-05	0.95	10.17	6.20	21768.0
AHQ-2-10, 3515	R.IGAFGYMECSAK.T	1335.53122	2	1.76E-05	0.95	3.39	-	1274.1
gi|13786129|ref|NP_112586.1|	RAB33B, member RAS oncogene family; likely ortholog of mouse RAB33b [H			1.79E-05	0.90	10.17	4.80	25717.4
AHQ-2-11, 3257 - 3320	K.IQLWDTAGQER.F	1317.43243	2	2.65E-05	0.81	3.21	-	680.7
AHQ-2-14-, 3465 - 3468	K.IQLWDTAGQER.F	1317.43243	2	1.79E-05	0.90	3.43	-	809.6
AHQ-2-10, 3100 - 3174	K.IQLWDTAGQER.F	1317.43243	2	4.70E-04	0.91	3.23	-	1053.2
gi|4557377|ref|NP_000052.1|	Bruton agammaglobulinemia tyrosine kinase [Homo sapiens]			1.88E-05	0.97	10.24	2.60	76280.8
AHQ-2-6, 3414	R.HYVVCSTPQSQYYLAEK.H	2075.28663	2	1.88E-05	0.97	4.74	-	1140.5
gi|4504107|ref|NP_002076.1|	glutathione peroxidase 4; phospholipid hydroperoxidase; sperm nucleus g			1.92E-05	0.68	10.16	0.00	22137.7
AHQ-2-11, 3878 - 3881	R.YGPMEEPLVIEK.D	1405.64130	2	1.92E-05	0.68	3.21	-	432.1
gi|8922804|ref|NP_060760.1|	hypothetical protein FLJ10983 [Homo sapiens]			1.93E-05	0.93	10.23	2.90	68268.9
AHQ-2-6, 7189	K.ELNELVSAIEEHFFQPQK.Y	2159.38348	2	1.93E-05	0.93	4.69	-	744.6
gi|11128019|ref|NP_061820.1|	cytochrome c [Homo sapiens]			1.93E-05	0.90	10.16	13.30	11748.7
AHQ-2-13-, 2139	K.TGQAPGYSYTAANK.N	1429.51641	2	1.93E-05	0.90	3.29	-	759.4
gi|12545410|ref|NP_031394.1|	RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,			1.93E-05	0.88	10.20	1.90	95912.5
AHQ-2-5, 6447	K.SLCPFYGEDFYCEIPR.S	2056.26024	2	1.93E-05	0.88	3.53	-	767.7
gi|5454028|ref|NP_006261.1|	related RAS viral (r-ras) oncogene homolog; Oncogene RRAS [Homo sapiens			1.98E-05	0.94	10.24	9.20	23480.3
AHQ-2-10, 2874	R.SEASAFGASHHVAYFEASAK.L	2068.19099	2	1.98E-05	0.94	4.79	-	684.1
gi|6912586|ref|NP_036220.1|	6-phosphogluconolactonase [Homo sapiens]			2.00E-05	2.24	30.23	24.00	27546.7
AHQ-2-10, 3926	R.ILEDQEENPLPAALVQPHTGK.L	2300.55348	2	2.00E-05	0.87	4.12	-	495.5
AHQ-2-10, 2371	K.IVAPISDSPKPPPQR.V	1602.85951	2	5.67E-04	0.48	2.57	-	435.8
AHQ-2-10, 6307 - 6308	R.LPIPESQVITINPELPVEEAAEDYAK.K	2867.19683	2	1.71E-04	0.88	4.63	-	492.3
gi|29788766|ref|NP_064424.2|	tubulin, beta polypeptide 4, member Q [Homo sapiens]			2.03E-05	1.31	20.19	10.90	48377.2
AHQ-2-13-, 3977	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	4.21E-04	0.70	3.35	-	349.5
AHQ-2-13, 4893	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	1.94E-04	0.49	2.72	-	370.9
AHQ-2-13-, 6241 - 6242	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	2.03E-05	0.82	3.60	-	1101.4
gi|15149476|ref|NP_002878.2|	arginyl-tRNA synthetase [Homo sapiens]			2.08E-05	0.75	10.14	2.30	75378.5
AHQ-2-6, 6193	K.IVFVPGCSIPLTIVK.S	1645.04263	2	2.08E-05	0.75	2.79	-	679.0
gi|5730118|ref|NP_006514.1|	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble; X-prolyl aminope			2.12E-05	1.72	20.20	4.80	69858.4
AHQ-2-6, 6209 - 6277	R.GSLTFEPLTLVPIQTK.M	1745.05263	2	2.12E-05	0.86	3.93	-	482.6
AHQ-2-6, 6117	R.VGVDPLIIPTDYWK.K	1616.88141	2	1.91E-04	0.86	3.44	-	602.0
gi|4758158|ref|NP_004395.1|	neural precursor cell expressed, developmentally down-regulated 5 [Homo			2.20E-05	0.62	10.17	4.40	41487.2
AHQ-2-9, 7008 - 7010	K.STLINSLFLTDLYPER.V	1883.13416	2	2.20E-05	0.62	3.16	-	604.7
gi|8922671|ref|NP_060691.1|	chromosome 2 open reading frame 6 [Homo sapiens]			2.35E-05	0.67	10.15	5.10	25007.5
AHQ-2-11, 4877	R.ELAPLQELIEK.L	1283.49580	2	2.35E-05	0.67	2.83	-	451.6
gi|30147857|ref|XP_293007.2|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			2.35E-05	0.30	10.10	5.90	20789.8
AHQ-2-12, 3282 - 3349	K.KITIADCGQLQ	1248.43160	1	2.35E-05	0.30	2.01	-	469.6
gi|5453710|ref|NP_006139.1|	LIM and SH3 protein 1; Lasp-1 [Homo sapiens]			2.46E-05	0.74	10.16	5.00	29717.0
AHQ-2-12, 3941	K.GFSVVADTPELQR.I	1419.56466	2	2.46E-05	0.74	2.94	-	785.7
AHQ-2-12, 3967	K.GFSVVADTPELQR.I	1419.56466	1	4.09E-04	0.17	2.32	-	173.3
AHQ-2-13, 3972 - 3980	K.GFSVVADTPELQR.I	1419.56466	2	5.28E-04	0.80	3.12	-	889.6
AHQ-2-11, 3809	K.GFSVVADTPELQR.I	1419.56466	1	3.76E-04	0.22	2.19	-	262.6
gi|20532885|ref|XP_086931.2|	similar to epsilon isoform of 14-3-3 protein [Homo sapiens]			2.52E-05	0.90	10.20	4.70	29380.0
AHQ-2-9, 7096	K.LICCDILDVLDK.H	1479.74157	1	8.54E-05	0.60	3.26	-	620.3
AHQ-2-10, 6484	K.LICCDILDVLDK.H	1479.74157	1	3.44E-05	0.91	3.99	-	884.8
AHQ-2-9, 7082	K.LICCDILDVLDK.H	1479.74157	2	2.52E-05	0.90	3.23	-	798.4
gi|29746056|ref|XP_296036.1|	hypothetical protein XP_296036 [Homo sapiens]			2.57E-05	0.46	10.13	7.70	21908.1
AHQ-2-6, 3890	K.MKRLFIPENSTGNQR.E	1792.05622	2	2.57E-05	0.46	2.57	-	664.1
gi|30157216|ref|XP_292133.2|	similar to genethonin 1 [Homo sapiens]			2.62E-05	0.73	10.20	4.50	39693.8
AHQ-2-5, 4407	K.TITLEVKPSDTIENVK.A	1788.03268	2	4.79E-04	0.61	3.81	-	396.5
AHQ-2-10, 4068	K.TITLEVKPSDTIENVK.A	1788.03268	2	4.57E-04	0.35	2.92	-	276.0
AHQ-2-13, 4371	K.TITLEVKPSDTIENVK.A	1788.03268	2	7.04E-04	0.60	3.41	-	435.0
AHQ-2-14, 5017	K.TITLEVKPSDTIENVK.A	1788.03268	2	6.54E-05	0.22	2.57	-	305.3
AHQ-2-14, 5432 - 5496	K.TITLEVKPSDTIENVK.A	1788.03268	2	2.62E-05	0.73	3.87	-	577.1
AHQ-2-14-, 4280	K.TITLEVKPSDTIENVK.A	1788.03268	2	5.25E-05	0.74	3.84	-	548.4
AHQ-2-14-, 4476	K.TITLEVKPSDTIENVK.A	1788.03268	2	4.17E-05	0.73	3.48	-	546.2
AHQ-2-1, 4704	K.TITLEVKPSDTIENVK.A	1788.03268	2	4.83E-04	0.61	3.50	-	492.4
gi|21361416|ref|NP_036382.2|	related RAS viral (r-ras) oncogene homolog 2; oncogene TC21 [Homo sapi			2.63E-05	0.58	10.13	7.80	23399.4
AHQ-2-10, 4936	R.LDILDTAGQEEFGAMR.E	1766.95393	2	2.63E-05	0.58	2.59	-	629.0
gi|5803009|ref|NP_006786.1|	EH-domain containing 1; homolog of Drosophila past; EH domain containin			2.64E-05	1.75	20.22	7.10	60844.7
AHQ-2-7, 7533	R.FMCAQLPNPVLDSISIIDTPGILSGEK.Q	2918.37521	2	1.60E-04	0.87	3.96	-	695.1
AHQ-2-7, 2985	R.HLIEQDFPGMR.I	1343.53652	2	2.64E-05	0.88	3.21	-	825.2
gi|11072091|ref|NP_057736.2|	Crn, crooked neck-like 1; CGI-201 protein; crooked neck protein (crn);			2.82E-05	0.55	10.12	1.10	99200.7
AHQ-2-1, 3250	R.FVLVHPDVK.N	1054.26662	1	2.82E-05	0.55	2.35	-	649.2
gi|22749499|ref|NP_689979.1|	hypothetical protein MGC40107 [Homo sapiens]			2.85E-05	0.96	10.27	24.80	11741.6
AHQ-2-14-, 5681 - 5696	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	2.85E-05	0.96	5.43	-	1431.1
gi|18105037|ref|NP_004709.2|	cytochrome c oxidase subunit VIIa polypeptide 2 like; estrogen recepto			2.95E-05	0.85	10.30	28.90	12614.6
AHQ-2-14-, 6120 - 6136	K.LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK.L	3399.87995	3	7.03E-04	0.95	5.90	-	876.7
AHQ-2-13, 6103	K.LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK.L	3399.87995	3	2.95E-05	0.85	3.97	-	602.0
gi|16904381|ref|NP_006717.1|	LPS-responsive vesicle trafficking, beach and anchor containing; vesic			3.54E-05	1.36	20.15	1.50	319158.3
AHQ-2-4, 4968	K.FPSNSPVTHVAANTQPGLATPAVITVTANR.L	3033.38776	3	7.22E-04	0.62	3.09	-	750.9
AHQ-2-4, 2285	R.NPLGSTHPEATLK.T	1365.51700	2	3.54E-05	0.74	3.03	-	481.3
gi|24307955|ref|NP_055191.1|	p53 inducible protein [Homo sapiens]			3.64E-05	0.88	10.13	1.00	145660.2
AHQ-2-3, 4865	K.YAPLHLVPLIER.L	1421.71166	2	3.64E-05	0.88	2.62	-	1249.2
gi|4502981|ref|NP_001852.1|	cytochrome c oxidase subunit IV isoform 1 precursor; cytochrome c oxida			3.66E-05	0.60	10.14	7.10	19576.6

AHQ-2-12, 4505	K.SEDFSLPAYMDR.R	1431.55257	2	3.66E-05	0.60	2.87	-	376.9
gi|4557773|ref|NP_000248.1|	myosin, heavy polypeptide 7, cardiac muscle, beta [Homo sapiens]			3.66E-05	1.29	20.17	1.20	223110.8
AHQ-2-5, 3183	R.CNGVLEGIR.I	1019.15759	2	1.07E-04	0.63	2.93	-	426.6
AHQ-2-3, 3492	R.CNGVLEGIR.I	1019.15759	2	1.05E-04	0.90	2.94	-	896.2
AHQ-2-3, 4240	R.IEELEEELESERTAR.A	1833.93203	2	3.66E-05	0.39	2.71	-	655.9
gi|5803121|ref|NP_006801.1|	for protein disulfide isomerase-related [Homo sapiens]			3.68E-05	0.86	10.15	2.30	59594.0
AHQ-2-7, 2845	K.GPPLWEEDPGAK.D	1296.40999	2	3.68E-05	0.86	3.04	-	858.3
gi|4502205|ref|NP_001651.1|	ADP-ribosylation factor 4 [Homo sapiens]			3.72E-05	1.67	20.19	13.30	20510.6
AHQ-2-11, 2438	R.IQEVADELQK.M	1173.29830	2	2.44E-04	0.80	3.06	-	758.2
AHQ-2-11, 5338 - 5349	K.NICFTVWDVGGQDR.I	1668.81182	2	3.72E-05	0.87	3.78	-	733.7
gi|13027638|ref|NP_006750.2|	UDP-glucose pyrophosphorylase 2; UTP-glucose-1-phosphate uridyltransfe			3.79E-05	0.92	10.16	2.40	56964.9
AHQ-2-7, 3949	K.SFENSLGINVPR.S	1333.47500	2	3.79E-05	0.92	3.10	-	1335.6
gi|21361409|ref|NP_036515.2|	osteoclast stimulating factor 1 [Homo sapiens]			3.85E-05	0.70	10.17	8.80	24063.9
AHQ-2-10, 6335	K.DIVEMLFTQPNIELNQQNK.L	2275.56743	2	3.85E-05	0.70	3.33	-	339.4
gi|4505417|ref|NP_000895.1|	NAD(P)H dehydrogenase, quinone 2; NAD(P)H menadione oxidoreductase-1, d			3.91E-05	0.61	10.14	7.80	25952.4
AHQ-2-10, 4807	K.VLAPQISFAPEIASEEER.K	1987.19924	2	3.91E-05	0.61	2.73	-	551.2
gi|21264318|ref|NP_004028.3|	adenosine monophosphate deaminase 2 (isoform L) [Homo sapiens]			3.91E-05	0.80	10.17	2.00	100687.2
AHQ-2-5, 5533	R.SAPYEFPEESPIEQLEER.R	2151.27185	2	3.91E-05	0.80	3.49	-	458.5
gi|21536449|ref|NP_002613.2|	prefoldin 1; prefoldin subunit 1 [Homo sapiens]			3.94E-05	0.12	10.20	9.00	14210.4
AHQ-2-13-, 3849 - 3850	K.LADIQIEQLNR.T	1313.48523	2	2.99E-04	0.95	3.98	-	1556.8
AHQ-2-13, 3831	K.LADIQIEQLNR.T	1313.48523	1	3.94E-05	0.12	1.82	-	290.4
gi|18491024|ref|NP_005691.2|	dipeptidylpeptidase III isoform 1; dipeptidylpeptidase III [Homo sapie			3.98E-05	0.94	10.20	2.30	82588.6
AHQ-2-6, 4549	K.LAQDFLDSQNLSAYNTR.L	1957.09009	2	3.98E-05	0.94	4.05	-	1345.1
gi|5454170|ref|NP_006393.1|	hepatitis B virus x-interacting protein; hepatitis B virus x-interactin			3.98E-05	1.57	20.19	44.00	9613.9
AHQ-2-14, 5666	R.GTLSDEHAGVISVLAQQAAK.L	1996.21090	2	3.98E-05	0.70	3.00	-	740.0
AHQ-2-14-, 5948 - 5983	K.NPSIVGVLCTDSQGLNLGCR.G	2163.41855	2	4.75E-05	0.87	3.71	-	692.3
gi|13027380|ref|NP_055864.1|	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidat			3.98E-05	0.77	10.19	2.30	101432.5
AHQ-2-13-, 5209 - 5277	R.VEQMTKTYNDIDMVTHLLAER.D	2508.85682	3	3.98E-05	0.77	3.73	-	904.3
gi|14780596|ref|XP_033004.1|	hypothetical protein BC005107 [Homo sapiens]			3.99E-05	0.24	10.14	5.00	18127.9
AHQ-2-2, 1674 - 1877	R.EQIIAKAK.A	901.08569	1	7.17E-05	0.45	2.68	-	327.1
AHQ-2-2, 1986	R.EQIIAKAK.A	901.08569	1	3.99E-05	0.24	2.50	-	243.6
AHQ-2-3, 1673 - 1883	R.EQIIAKAK.A	901.08569	1	3.85E-04	0.52	2.72	-	343.7
AHQ-2-1, 1920 - 2057	R.EQIIAKAK.A	901.08569	1	2.91E-04	0.33	2.74	-	288.0
gi|4506765|ref|NP_002952.1|	S100 calcium-binding protein A4; 18A2; 42A; S100 calcium-binding protei			4.01E-05	1.75	20.17	10.90	11728.5
AHQ-2-14-, 3372	K.ALDVMVSTFHK.Y	1248.47665	2	4.01E-05	0.85	2.99	-	938.0
AHQ-2-14-, 2795	K.ALDVM*VSTFHK.Y	1264.47605	2	3.43E-04	0.90	3.49	-	982.6
gi|16753212|ref|NP_003921.2|	src family associated phosphoprotein 2; src kinase-associated phosphop			4.03E-05	0.86	10.17	2.80	41216.5
AHQ-2-12, 3038	K.RGDVIYILSK.E	1164.37938	2	4.03E-05	0.86	3.32	-	1006.1
gi|4506193|ref|NP_002784.1|	proteasome beta 1 subunit; proteasome subunit HC5; proteasome component			4.06E-05	1.82	20.24	13.70	26489.2
AHQ-2-11, 2942	K.NM*QNVEHVPLSLDR.A	1668.85668	2	1.14E-04	0.88	3.43	-	995.5
AHQ-2-11, 6613	R.RFFPYYVYNIIGGLDEEGK.G	2281.55031	2	4.06E-05	0.95	4.74	-	1129.1
gi|4505409|ref|NP_002503.1|	non-metastatic cells 2, protein (NM23B) expressed in; Non-metastatic ce			4.12E-05	0.86	10.25	9.90	17297.9
AHQ-2-14-, 6163	K.EISLWFKPEELVDYK.S	1897.15929	2	4.12E-05	0.86	3.57	-	649.2
AHQ-2-12, 6182 - 6250	K.EISLWFKPEELVDYK.S	1897.15929	2	8.54E-05	0.97	4.97	-	1369.9
gi|5454090|ref|NP_006271.1|	signal sequence receptor, delta; translocon-associated protein delta [H			4.15E-05	1.48	20.16	17.30	18998.5
AHQ-2-12, 4913	R.FFDEESYSLLR.K	1406.52121	2	1.54E-04	0.84	3.19	-	802.4
AHQ-2-12, 6258	R.NNEDISIIPPLFTVSVDHR.G	2167.40715	3	4.15E-05	0.64	3.03	-	535.6
gi|7019375|ref|NP_037373.1|	formin homology 2 domain containing 1; FH1/FH2 domain-containing protei			4.34E-05	0.93	10.23	1.60	126496.5
AHQ-2-7, 5845 - 5856	R.VQYLEDTDPFACANFPEPR.R	2271.44761	2	4.34E-05	0.93	4.58	-	1007.9
gi|19923750|ref|NP_002858.2|	RAB3B, member RAS oncogene family; Brain antigen RAB3B [Homo sapiens]			4.46E-05	0.88	10.17	5.00	24757.7
AHQ-2-13, 3476	K.LQIWDTAGQER.Y	1317.43243	1	1.07E-04	0.15	2.11	-	333.2
AHQ-2-13, 3483	K.LQIWDTAGQER.Y	1317.43243	2	4.46E-05	0.88	3.34	-	800.7
AHQ-2-11, 3345 - 3420	K.LQIWDTAGQER.Y	1317.43243	2	4.90E-05	0.84	3.23	-	675.5
gi|10800412|ref|NP_036458.2|	microtubule-associated protein, RP/EB family, member 3; APC binding pr			4.67E-05	0.42	10.15	3.60	31982.0
AHQ-2-9, 1970	K.LEHEYIHNFK.V	1330.47280	1	4.67E-05	0.42	1.81	-	584.7
gi|30149221|ref|XP_291446.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			4.70E-05	0.91	10.19	3.90	45688.5
AHQ-2-6, 2205	R.STAGDTHLGGEDFDNR.M	1692.68222	2	4.70E-05	0.91	3.81	-	1033.9
gi|27764873|ref|NP_057070.2|	cytokine receptor-like factor 3; cytokine receptor-like molecule 9; cy			4.80E-05	0.94	10.22	3.20	49737.6
AHQ-2-7, 3085	K.LIEHGVNTAEDLVR.E	1566.74089	2	4.80E-05	0.94	3.61	-	1305.2
gi|29747201|ref|XP_290702.1|	similar to My016 protein [Homo sapiens]			4.88E-05	0.89	10.21	10.50	16932.3
AHQ-2-14-, 3500	R.DLEAEHVEVEDTTLNR.C	1870.95236	3	6.39E-04	0.93	4.02	-	1508.6
AHQ-2-14-, 3497	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	4.88E-05	0.89	4.17	-	739.8
gi|13637631|ref|XP_016625.1|	similar to voltage-dependent anion channel isoform 2 [Homo sapiens] [M			4.99E-05	0.91	10.16	4.40	31479.2
AHQ-2-9, 4679 - 4711	K.YKWCEYGLTFTEK.W	1726.92965	2	4.99E-05	0.91	3.16	-	992.0
gi|6005902|ref|NP_009043.1|	thrombospondin 3 [Homo sapiens]			5.12E-05	0.64	10.14	0.70	104200.6
AHQ-2-3, 4679	R.FYVVMWK.Q	973.21547	1	2.19E-04	0.75	2.16	-	1013.4
AHQ-2-4, 4665	R.FYVVMWK.Q	973.21547	1	1.33E-04	0.75	2.31	-	895.9
AHQ-2-5, 4303	R.FYVVMWK.Q	973.21547	1	4.07E-04	0.64	2.13	-	755.8
AHQ-2-6, 4265	R.FYVVMWK.Q	973.21547	1	7.88E-04	0.73	2.30	-	840.0
AHQ-2-7, 4097 - 4143	R.FYVVMWK.Q	973.21547	1	3.27E-04	0.65	2.04	-	771.1
AHQ-2-10, 4082	R.FYVVMWK.Q	973.21547	1	5.12E-05	0.64	1.98	-	916.4
AHQ-2-1, 4866	R.FYVVMWK.Q	973.21547	1	9.53E-04	0.82	2.46	-	970.2
gi|19923748|ref|NP_001924.2|	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarat			5.18E-05	0.95	10.26	4.60	48755.0
AHQ-2-7, 5980 - 6016	K.ASAFALQEQPVVNAVIDDTTK.E	2218.44924	2	5.18E-05	0.95	5.21	-	962.5
gi|4507913|ref|NP_003922.1|	WAS protein family, member 1; WASP family Verprolin-homologous protein;			5.48E-05	0.90	10.16	1.60	61652.0
AHQ-2-11, 2529 - 2540	R.SVLLEAIRK.G	1029.25860	2	5.48E-05	0.90	3.20	-	1290.6
gi|11321585|ref|NP_002065.1|	guanine nucleotide-binding protein, beta-1 subunit; G protein, beta-1			5.48E-05	0.75	10.17	5.90	37376.8
AHQ-2-9, 4726	R.KACADATLSQITNNIDPVGR.I	2146.36794	2	5.48E-05	0.75	3.36	-	384.6
gi|30152366|ref|XP_294234.2|	similar to chromosome condensation-related SMC-associated protein 1 [H			5.52E-05	0.32	10.16	2.90	52674.0
AHQ-2-1, 2837 - 2878	R.VLREEQEHKTKDPK.E	1737.93868	2	5.52E-05	0.32	3.17	-	175.6
gi|9910470|ref|NP_064542.1|	otoraplin precursor; fibrocyte-derived protein; melanoma inhibitory act			5.63E-05	0.13	10.10	7.00	14332.3
AHQ-2-8, 2815 - 2824	K.GQQIYVYSK.L	1086.22234	1	5.63E-05	0.13	2.03	-	308.2
gi|4503477|ref|NP_001950.1|	eukaryotic translation elongation factor 1 beta 2; eukaryotic translati			5.89E-05	0.85	10.20	8.00	24763.6
AHQ-2-9, 5024	K.SSILLDVKPWDDETDMAK.L	2064.30228	2	5.89E-05	0.85	4.03	-	406.4
gi|6005727|ref|NP_006576.1|	chaperonin containing TCP1, subunit 8 (theta); T-complex protein 1, the			5.94E-05	1.43	20.16	5.30	59662.4
AHQ-2-7, 2983	R.KAHEILPNLVCCSAK.N	1743.04172	2	3.13E-04	0.66	2.72	-	688.1
AHQ-2-7, 3104 - 3107	R.LVPGGGATEIELAK.Q	1355.56202	2	5.94E-05	0.77	3.03	-	385.8
gi|14589893|ref|NP_001785.2|	cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-			6.00E-05	0.67	10.18	2.00	100279.9
AHQ-2-1, 4933	K.VENPIDLYIYVIDM*NDNR.P	2213.45293	2	6.00E-05	0.67	3.63	-	450.1
gi|30153966|ref|XP_293932.2|	similar to hypothetical protein BC013073 [Homo sapiens]			6.29E-05	0.59	10.19	9.00	21711.3
AHQ-2-2, 4060 - 4130	R.MIFTLFTINVSKDIRHH	2073.44997	2	9.51E-05	0.77	3.72	-	546.3
AHQ-2-2, 4264	R.MIFTLFTINVSKDIRHH	2073.44997	2	6.85E-04	0.63	3.13	-	535.3
AHQ-2-2, 4278 - 4353	R.MIFTLFTINVSKDIRHH	2073.44997	2	5.56E-04	0.65	3.71	-	330.1
AHQ-2-3, 3731	R.MIFTLFTINVSKDIRHH	2073.44997	2	7.29E-04	0.37	2.83	-	344.2
AHQ-2-3, 4227 - 4247	R.MIFTLFTINVSKDIRHH	2073.44997	2	9.46E-04	0.62	3.31	-	436.8
AHQ-2-4, 4006	R.MIFTLFTINVSKDIRHH	2073.44997	2	6.29E-05	0.59	3.13	-	377.7
AHQ-2-6, 3961	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.34E-04	0.42	3.17	-	339.8
AHQ-2-1, 4270 - 4341	R.MIFTLFTINVSKDIRHH	2073.44997	2	1.45E-04	0.67	3.57	-	442.4
gi|30159103|ref|XP_296859.2|	hypothetical protein XP_296859 [Homo sapiens]			6.47E-05	0.52	10.13	6.40	31013.7
AHQ-2-5, 7387	R.FLRHPWLEAGAAALRGEK.L	2023.32923	2	6.47E-05	0.52	2.55	-	435.9
gi|5803167|ref|NP_006793.1|	splicing factor 3a, subunit 3, 60kDa; pre-mRNA splicing factor SF3a (60			6.56E-05	0.41	10.15	4.40	58848.5
AHQ-2-8, 6091	R.TRAMQDRYMEVSGNLRDLYDDK.D	2677.95567	3	6.56E-05	0.41	3.02	-	235.7
gi|10864055|ref|NP_067069.1|	megakaryocyte-enhanced gene transcript 1 protein; lymphocyte antigen-6			6.68E-05	0.64	10.16	4.70	40891.9
AHQ-2-1, 5721	R.AADGSPCNVLLCSVVPSR.R	1905.14311	2	6.68E-05	0.64	3.21	-	501.7
gi|29731325|ref|XP_293023.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			6.76E-05	0.76	10.17	6.00	28867.8
AHQ-2-12, 4058 - 4131	K.AGPNTNGSQFFICTAK.T	1714.88050	2	6.76E-05	0.76	3.38	-	479.9
gi|29731460|ref|XP_293027.1|	similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl			6.78E-05	0.54	10.14	4.70	23572.2

AHQ-2-10, 1999 - 2000	K.LLLQVQHASK.Q	1137.35716	1	6.78E-05	0.54	2.37	-	489.4
gi|4501859|ref|NP_001600.1|	acyl-Coenzyme A dehydrogenase, short/branched chain precursor [Homo sap			6.79E-05	0.88	10.19	5.10	47485.1
AHQ-2-8, 6612	R.LFDFQGLQHQVAHVATQLEAAR.L	2480.76631	3	6.79E-05	0.88	3.78	-	803.9
gi|30151001|ref|XP_170195.2|	similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl			7.00E-05	0.86	10.16	2.60	46759.8
AHQ-2-10, 3428 - 3446	R.AAYFGIYDTAK.G	1220.35512	2	7.00E-05	0.86	3.18	-	835.8
gi|6681764|ref|NP_004993.1|	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 9, 39kDa; NADH dehy			7.15E-05	0.79	10.18	4.50	42509.3
AHQ-2-9, 6218	R.DAFPEAIIVKPSDIFGR.E	1876.14485	2	7.15E-05	0.79	3.50	-	634.2
gi|5453854|ref|NP_006187.1|	poly(rC) binding protein 1; heterogenous nuclear ribonucleoprotein X; p			7.93E-05	0.64	10.16	3.90	37525.7
AHQ-2-10, 3726	R.LVVPATQCGSLIGK.G	1444.72199	2	7.93E-05	0.64	3.18	-	259.3
gi|21361427|ref|NP_055182.2|	hypothetical protein, estradiol-induced [Homo sapiens]			8.48E-05	0.94	10.23	8.90	21551.0
AHQ-2-13-, 5723 - 5727	K.EDEIPETVSLEMLDAAK.N	1891.08690	2	8.48E-05	0.94	4.54	-	669.7
AHQ-2-13, 5631 - 5641	K.EDEIPETVSLEMLDAAK.N	1891.08690	2	6.61E-04	0.90	4.32	-	478.5
gi|18104998|ref|NP_001119.2|	adaptor-related protein complex 1, gamma 1 subunit; gamma adaptin; cla			8.55E-05	0.92	10.22	3.30	91679.3
AHQ-2-13, 6759	K.TFQLQLLSPSSSIVPAFNTGTITQVIK.V	2892.33903	3	8.55E-05	0.92	4.44	-	1281.2
gi|8393147|ref|NP_058625.1|	chloride intracellular channel 5 [Homo sapiens]			8.82E-05	0.93	10.22	7.20	28109.7
AHQ-2-10, 5378	R.KFLDGDELTLADCNLLPK.L	2064.34520	2	8.82E-05	0.93	4.33	-	916.9
gi|20543399|ref|XP_116396.1|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			9.15E-05	0.78	10.12	5.00	19852.7
AHQ-2-12, 4375 - 4589	R.VSFKLFADK.F	1055.25138	1	9.15E-05	0.78	2.43	-	1199.0
gi|19923231|ref|NP_002860.2|	RAB6A, member RAS oncogene family; Oncogene RAB6; RAB6, member RAS onc			1.02E-04	0.66	10.14	6.70	23548.6
AHQ-2-11, 2850	R.VAAALPGMESTQDR.S	1446.61192	2	1.02E-04	0.66	2.79	-	349.8
gi|4507249|ref|NP_003464.1|	signal transducing adaptor molecule 1; signal transducing adaptor molec			1.03E-04	0.65	10.15	5.00	59179.3
AHQ-2-14-, 6132	K.GETHQGIGLFPSNFVTADLTAEPEM*IK.T	2920.24330	3	1.03E-04	0.65	3.08	-	642.8
gi|5729991|ref|NP_006494.1|	proteasome 26S ATPase subunit 4 isoform 1; protease 26S subunit 6; Tat-			1.03E-04	0.90	10.17	2.90	47365.9
AHQ-2-5, 3589	R.GVLM*YGPPGCGK.T	1253.47332	2	1.03E-04	0.90	3.42	-	984.7
gi|10190678|ref|NP_065691.1|	RP42 homolog; squamous cell carcinoma-related oncogene [Homo sapiens]			1.05E-04	0.89	10.20	6.60	30124.1
AHQ-2-10, 5911 - 5928	K.LDVATDNFFQNPELYIR.E	2056.26326	2	1.05E-04	0.89	4.05	-	843.1
gi|4758330|ref|NP_004448.1|	long-chain fatty-acid-Coenzyme A ligase 3; lignoceroyl-CoA synthase [Ho			1.06E-04	0.65	10.15	2.50	80345.5
AHQ-2-5, 6116	R.LSPEPWTPETGLVTDAFK.L	1989.21359	2	1.06E-04	0.65	3.04	-	395.7
gi|20547107|ref|XP_114482.1|	similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN			1.07E-04	1.88	20.27	4.40	94330.3
AHQ-2-4, 5589	K.KPVVDCVVSVPCFYTDAER.R	2244.53004	2	1.07E-04	0.92	4.15	-	672.3
AHQ-2-4, 6892 - 6894	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	7.26E-04	0.96	5.43	-	936.3
gi|4885417|ref|NP_005330.1|	huntingtin interacting protein 2; ubiquitin-conjugating enzyme E2-25 KD			1.08E-04	0.96	10.21	9.00	22406.5
AHQ-2-11, 3666	R.LWAHVYAGAPVSSPEYTK.K	1977.20773	2	1.08E-04	0.96	4.25	-	1531.2
gi|11559923|ref|NP_071496.1|	eukaryotic translation initiation factor 4H isoform 1 [Homo sapiens] [			1.12E-04	0.89	10.23	11.70	27384.8
AHQ-2-11, 6844 - 6912	K.ELPTEPPYTAYVGNLPFNTVQGDIDAIFK.D	3211.56532	3	1.12E-04	0.89	4.57	-	863.9
gi|14765644|ref|XP_037574.1|	similar to PTPL1-associated RhoGAP 1 [Homo sapiens]			1.16E-04	0.94	10.29	2.90	124613.7
AHQ-2-13, 6892 - 6893	R.SPLTAASPGELPTEGAGPDVVEDISHLLADVAR.F	3286.59214	3	1.16E-04	0.94	5.76	-	717.3
gi|27363461|ref|NP_057153.8|	mitochondria-associated GM-CSF signaling molecule [Homo sapiens]			1.20E-04	0.92	10.24	18.40	13824.6
AHQ-2-13, 6136	R.SAAASNLSGLSLQEAQQILNVSK.L	2330.58112	2	1.20E-04	0.92	4.86	-	612.3
gi|18765729|ref|NP_003816.2|	synaptosomal-associated protein 23 isoform SNAP23A; synaptosomal-assoc			1.22E-04	1.28	20.19	11.40	23353.9
AHQ-2-10, 2391	R.IEEGLDQINK.D	1159.27163	1	4.26E-04	0.37	2.31	-	614.8
AHQ-2-10, 4103	R.ILGLAIESQDAGIK.T	1428.65614	2	1.22E-04	0.91	3.64	-	985.4
gi|19923534|ref|NP_060988.2|	MCM10 minichromosome maintenance deficient 10; homolog of yeast MCM10			1.23E-04	0.60	10.15	2.10	96134.1
AHQ-2-13-, 6609 - 6669	R.EQLAYLESEEFQKILKAK.S	2168.47496	2	1.23E-04	0.60	3.06	-	243.1
AHQ-2-8, 7534	R.EQLAYLESEEFQKILKAK.S	2168.47496	2	5.38E-04	0.29	2.53	-	162.0
gi|4502601|ref|NP_001227.1|	carbonyl reductase 3; carbonyl reductase (NADPH) 3 [Homo sapiens]			1.24E-04	0.97	10.25	5.80	30850.1
AHQ-2-9, 3160 - 3163	R.GQAAVQQLQAEGLSPR.F	1653.82178	2	1.24E-04	0.97	4.92	-	1578.4
gi|5031611|ref|NP_005859.1|	BET1 homolog; Golgi vesicular membrane trafficking protein p18; Bet1p h			1.26E-04	0.71	10.16	15.30	13289.4
AHQ-2-13-, 4846	K.LLAEM*DSQFDSTTGFLGK.T	1977.18145	2	1.26E-04	0.71	3.22	-	216.6
gi|5453559|ref|NP_006347.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; ATP			1.30E-04	0.75	10.19	8.10	18491.1
AHQ-2-11, 4182	K.KYPYWPHQPIENL	1685.90553	2	1.30E-04	0.75	2.92	-	600.6
gi|22065448|ref|XP_084610.2|	similar to tubulin alpha-1 chain - Chinese hamster [Homo sapiens] [MAS			1.34E-04	0.76	10.17	2.40	41009.4
AHQ-2-13, 4985	K.EIIDLVLDR.I	1086.26378	2	1.34E-04	0.76	2.87	-	829.9
AHQ-2-14, 6270 - 6272	K.EIIDLVLDR.I	1086.26378	2	3.23E-04	0.80	3.31	-	800.2
AHQ-2-13-, 5070	K.EIIDLVLDR.I	1086.26378	2	3.71E-04	0.85	3.38	-	823.4
AHQ-2-11, 4828	K.EIIDLVLDR.I	1086.26378	2	2.09E-04	0.73	2.82	-	756.8
gi|17440821|ref|XP_060398.1|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			1.36E-04	0.40	10.13	2.90	26761.9
AHQ-2-12, 2266	K.TEWLDGK.H	848.92297	1	1.36E-04	0.40	2.34	-	494.1
AHQ-2-12, 2265	K.TEWLDGK.H	848.92297	2	6.34E-04	0.71	2.52	-	582.3
gi|14043026|ref|NP_003752.2|	vesicle-associated membrane protein 8; endobrevin [Homo sapiens]			1.38E-04	0.92	10.17	14.00	11438.2
AHQ-2-13-, 2462	R.NKTEDLEATSEHFK.T	1649.74039	3	1.38E-04	0.92	3.47	-	1620.4
AHQ-2-13, 2548	R.NKTEDLEATSEHFK.T	1649.74039	2	3.76E-04	0.65	2.51	-	418.5
gi|5453704|ref|NP_006398.1|	cytoskeleton related vitamin A responsive protein; glutamate transporte			1.40E-04	0.88	10.20	10.10	21614.6
AHQ-2-1, 6125	R.TPM*GIVLDALEQQEEGINR.L	2130.36546	2	1.40E-04	0.88	4.09	-	767.0
gi|4503141|ref|NP_001805.1|	cathepsin C isoform a preproprotein; dipeptidyl-peptidase I; dipeptidyl			1.42E-04	1.87	20.28	4.30	51841.5
AHQ-2-14-, 5463	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	2.64E-04	0.90	3.49	-	1152.3
AHQ-2-14-, 5029	R.RGTDECAIESIAVAATPIPK.L	2101.36707	2	1.42E-04	0.97	5.62	-	1485.2
AHQ-2-14, 6186	R.RGTDECAIESIAVAATPIPK.L	2101.36707	2	2.89E-04	0.95	4.69	-	1045.3
gi|21359896|ref|NP_009177.2|	kelch-like 2, Mayven; mayven; kelch (Drosophila)-like 2 (Mayven) [Homo			1.42E-04	0.04	10.14	1.70	66075.5
AHQ-2-12, 2929 - 2930	K.KAFKVMNELR.S	1236.51223	1	1.42E-04	0.04	1.94	-	98.2
gi|4758440|ref|NP_004868.1|	glia maturation factor, gamma [Homo sapiens]			1.43E-04	0.93	10.21	9.20	16801.2
AHQ-2-12, 4311 - 4381	R.TTDDLTEAWLQEK.L	1550.64872	2	1.43E-04	0.93	4.30	-	1261.5
gi|4506045|ref|NP_002718.1|	proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p			1.45E-04	0.93	10.19	8.20	17623.6
AHQ-2-1, 4877	K.GPMFELLPGESNK.I	1419.62807	2	1.45E-04	0.93	3.74	-	1136.2
gi|14150155|ref|NP_115729.1|	hypothetical protein MGC10540 [Homo sapiens]			1.45E-04	0.95	10.20	8.00	20747.6
AHQ-2-11, 5626	R.FPPFFTLQPNVDTR.Q	1679.89929	2	1.45E-04	0.95	4.01	-	1434.5
gi|20373153|ref|NP_115997.4|	myosin XVIIIB; myosin 18B [Homo sapiens]			1.47E-04	0.89	10.21	0.70	285231.7
AHQ-2-13, 6629	R.ITAAQLQTMLLEKSRVAR.Q	2030.42494	2	1.47E-04	0.89	4.12	-	1173.8
gi|8922974|ref|NP_060849.1|	hypothetical protein FLJ11280 [Homo sapiens]			1.56E-04	0.41	10.15	7.30	36538.0
AHQ-2-9, 6715	K.EVITSDELMAHLGNCLLSIKPQEK.S	2728.13573	3	1.56E-04	0.41	3.04	-	463.1
gi|13376539|ref|NP_079295.1|	hypothetical protein FLJ13940 [Homo sapiens]			1.58E-04	0.68	10.17	0.00	27546.1
AHQ-2-11, 3849	R.QIFHPEQLITGK.E	1411.63050	2	1.58E-04	0.68	2.97	-	259.3
gi|17482508|ref|XP_058957.1|	similar to QIL1 [Homo sapiens]			1.61E-04	0.93	10.22	18.60	13087.2
AHQ-2-14-, 5753	K.GSVAGGAVYLVYDQELLGPSDK.S	2239.46691	2	1.61E-04	0.93	4.43	-	902.6
gi|7661728|ref|NP_054736.1|	HSPC003 protein [Homo sapiens]			1.64E-04	0.83	10.19	14.40	13507.4
AHQ-2-14-, 6616 - 6617	K.AQALVQYLEEPLTQVAAS	1932.16358	2	1.64E-04	0.83	3.81	-	376.7
gi|15718761|ref|NP_004976.2|	c-K-ras2 protein isoform b; Kirsten rat sarcoma-2 viral (v-Ki-ras2) on			1.66E-04	0.89	10.17	8.00	21424.4
AHQ-2-11, 3561 - 3626	R.VKDSEDVPM*VLVGNK.C	1646.88770	2	1.66E-04	0.89	3.45	-	1309.8
gi|29150259|ref|NP_803875.1|	fibrocystin L; polycystic kidney and hepatic disease-like 1 [Homo sapi			1.67E-04	1.68	20.18	0.70	465745.4
AHQ-2-1, 3870	R.IDGEPCPGQFNPVEK.W	1688.83981	2	3.32E-04	0.80	3.43	-	524.6
AHQ-2-1, 4865	R.IEYVEVFHAGQAFR.L	1666.86061	2	1.67E-04	0.88	3.05	-	1051.7
gi|4557471|ref|NP_001274.1|	adaptor-related protein complex 1, sigma 1 subunit isoform 1; clathrin-			1.68E-04	0.97	10.26	10.10	18732.9
AHQ-2-12, 3593	K.AIEQADLLQEEDESPR.S	1843.92692	2	1.68E-04	0.97	5.11	-	1693.6
gi|4885235|ref|NP_005239.1|	Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog; Gardner-			1.69E-04	0.78	10.19	3.80	59478.3
AHQ-2-7, 5460	K.TLKPGTMSPKAFLEEAQVMK.L	2207.64277	2	1.69E-04	0.78	3.87	-	870.1
gi|24497435|ref|NP_002796.4|	proteasome 26S ATPase subunit 5; thyroid receptor interactor 1; protea			1.72E-04	0.92	10.20	5.20	45625.7
AHQ-2-12, 6239	R.LLREELQLLQEQGSYVGEVVR.A	2459.78363	2	1.72E-04	0.92	3.95	-	974.8
gi|29727204|ref|XP_290872.1|	similar to Pyruvate kinase, M2 isozyme [Homo sapiens]			1.72E-04	0.93	10.18	5.40	16297.7
AHQ-2-7, 2009 - 2033	R.APIIAVTR.N	841.03348	2	1.72E-04	0.93	3.04	-	1227.5
gi|5803011|ref|NP_001966.1|	enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron			1.81E-04	0.65	10.16	3.70	47268.3
AHQ-2-8, 6519	R.YITGDQLGALYQDFVR.D	1860.05915	2	1.81E-04	0.65	3.15	-	741.9
gi|4505273|ref|NP_002442.1|	5'-methylthioadenosine phosphorylase [Homo sapiens]			1.82E-04	1.36	20.17	12.70	31249.9
AHQ-2-9, 6827 - 6852	R.TWGADVINMTTVPEVVLAK.E	2045.38847	2	6.48E-04	0.56	2.78	-	486.5
AHQ-2-9, 4619	K.YVDTPFGKPSDALILGK.I	1822.09396	2	1.82E-04	0.80	3.46	-	665.3
gi|9257195|ref|NP_004733.1|	BAI1-associated protein 1; WW domain-containing protein 3; atrophin-1 i			1.83E-04	0.61	10.15	1.30	136980.0
AHQ-2-13-, 7113 - 7171	R.CRGLKEGDLIVEVNKK.N	1860.16856	2	1.83E-04	0.61	2.98	-	503.0
gi|22041780|ref|XP_059066.2|	similar to 14-3-3 protein sigma (Stratifin) (Epithelial cell marker pr			1.89E-04	0.93	10.20	4.00	27773.9

AHQ-2-13, 5815 - 5816	K.DSTLIMQLLR.D	1190.43864	2	1.89E-04	0.93	3.84	-	1403.7
gi|29730632|ref|XP_293786.1|	similar to RAN, member RAS oncogene family [Homo sapiens]			1.90E-04	0.52	10.10	7.70	16426.8
AHQ-2-10, 2230	K.LVLVGDGGTGK.T	1016.17355	1	1.90E-04	0.52	2.06	-	481.4
gi|5729779|ref|NP_006701.1|	COP9 homolog [Homo sapiens]			1.92E-04	0.84	10.18	6.70	23225.5
AHQ-2-11, 3389 - 3464	K.GILEQGWQADSTTR.M	1562.66596	2	1.92E-04	0.84	3.53	-	664.7
gi|4759302|ref|NP_004729.1|	VAMP (vesicle-associated membrane protein)-associated protein B and C;			1.96E-04	0.51	10.15	5.80	27228.2
AHQ-2-12, 3395 - 3407	K.VEQVLSLEPQHELK.F	1649.86980	2	1.96E-04	0.51	2.90	-	471.9
gi|4758986|ref|NP_004209.1|	RAB11B, member RAS oncogene family; RAB11B, member of RAS oncogene fami			2.07E-04	0.24	10.12	3.70	24573.4
AHQ-2-10, 3858	K.NILTEIYR.I	1022.17979	1	2.07E-04	0.24	2.47	-	164.6
gi|18087855|ref|NP_542408.1|	dynein light chain 2 [Homo sapiens]			2.08E-04	0.46	10.12	7.90	10349.8
AHQ-2-14-, 2925 - 2995	K.DIAAYIK.K	793.93045	1	2.08E-04	0.46	2.31	-	322.3
gi|4504375|ref|NP_000177.1|	H factor 1 (complement); H factor-1 (complement) [Homo sapiens]			2.12E-04	0.22	10.13	1.10	139124.7
AHQ-2-7, 3673	K.SCDIPVFM*NARTK.N	1556.78953	2	2.12E-04	0.22	2.51	-	306.5
gi|4506675|ref|NP_002941.1|	ribophorin I [Homo sapiens]			2.21E-04	0.87	10.19	4.10	68569.0
AHQ-2-1, 6989 - 7048	K.THYIVGYNLPSYEYLYNLGDQYALK.M	2999.32033	3	2.21E-04	0.87	3.85	-	847.4
gi|13259510|ref|NP_004073.2|	dynactin 1 isoform 1; dynactin 1 (p150, Glued (Drosophila) homolog); p			2.42E-04	0.87	10.17	1.00	141693.7
AHQ-2-11, 3705	K.YFTCDEGHGIFVR.Q	1602.75184	2	2.42E-04	0.87	3.33	-	901.2
gi|27481006|ref|XP_117198.2|	hypothetical protein XP_117198 [Homo sapiens]			2.45E-04	0.28	20.13	0.90	251738.6
AHQ-2-4, 3228	K.EDELQEM*M*VK.D	1284.43954	1	2.45E-04	0.19	1.97	-	457.8
AHQ-2-7, 3228	K.ESKSNKGISK.T	1078.20175	1	2.62E-04	0.09	2.13	-	310.1
gi|29729329|ref|XP_291459.1|	similar to Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18) [			2.46E-04	0.37	10.16	5.20	17172.9
AHQ-2-12, 2261	K.NIILEEGK.E	916.05399	1	5.46E-04	0.67	3.14	-	576.5
AHQ-2-13-, 2337	K.NIILEEGK.E	916.05399	1	2.46E-04	0.37	2.25	-	417.4
AHQ-2-12, 2253 - 2393	K.NIILEEGK.E	916.05399	1	5.97E-04	0.34	2.20	-	378.7
gi|4758476|ref|NP_004801.1|	GRB2-related adaptor protein 2; growth factor receptor-bound protein 2-			2.50E-04	0.42	10.15	3.00	37908.9
AHQ-2-11, 2117	R.HQAENLLMGK.E	1141.32617	1	2.50E-04	0.42	2.44	-	424.7
gi|5453629|ref|NP_006391.1|	dynactin 2; dynactin complex 50 kD subunit; dynamitin; 50 kD dynein-ass			2.52E-04	1.61	20.23	8.10	44819.3
AHQ-2-12, 5310	K.LLGPDAAINLTDPDGALAK.R	1866.10514	2	9.67E-04	0.68	3.03	-	530.0
AHQ-2-9, 4146	R.LLHEVQELTTEVEK.I	1668.86989	2	2.52E-04	0.93	4.21	-	1146.5
gi|4758032|ref|NP_004757.1|	coatomer protein complex, subunit beta 2 (beta prime); coatomer binding			2.55E-04	0.92	10.23	2.10	102486.5
AHQ-2-5, 6481 - 6557	K.AAESLADPTEYENLFPGLK.E	2066.25322	2	2.55E-04	0.92	4.61	-	562.8
gi|8923932|ref|NP_060935.1|	uncharacterized hematopoietic stem/progenitor cells protein MDS030 [Hom			2.62E-04	0.92	10.19	8.80	17229.3
AHQ-2-12, 2710	R.MKGEAEDILETEK.S	1493.66212	2	2.62E-04	0.92	3.86	-	912.1
gi|4507797|ref|NP_003341.1|	ubiquitin-conjugating enzyme E2 variant 2; 1 alpha,25-dihydroxyvitamin			2.72E-04	0.92	10.19	6.90	16362.7
AHQ-2-12, 2990	R.LLEELEEGQK.G	1188.30974	2	2.72E-04	0.92	3.89	-	1153.4
gi|4757818|ref|NP_004879.1|	ATPase, H+ transporting, lysosomal, V1 subunit G isoform 1; vacuolar H(			2.80E-04	0.93	10.20	9.30	13757.4
AHQ-2-13-, 2769	K.EEAQAEIEQYR.L	1366.41548	2	2.80E-04	0.93	4.03	-	1057.7
gi|29734916|ref|XP_294215.1|	similar to argininosuccinate synthetase [Homo sapiens]			2.81E-04	0.68	10.17	3.80	48038.6
AHQ-2-9, 5263	K.EQGYDVTAYLANIGQK.E	1770.92077	2	2.81E-04	0.68	3.45	-	562.6
gi|30152971|ref|XP_301494.1|	similar to RIKEN cDNA C730036D15 [Homo sapiens]			2.81E-04	0.73	10.18	10.70	31692.4
AHQ-2-8, 5815 - 5888	R.PISTSSFFSQKAATLTVTPKTGLADKCLDMK.A	3346.86046	3	2.81E-04	0.73	3.65	-	646.8
gi|4505881|ref|NP_000292.1|	plasminogen [Homo sapiens]			3.02E-04	0.89	10.20	2.10	90568.6
AHQ-2-4, 4078	R.NPDGDVGGPWCYTTNPR.K	1907.99768	2	3.02E-04	0.89	4.07	-	667.4
gi|14165439|ref|NP_002131.2|	heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch bindin			3.04E-04	0.74	10.17	4.10	51027.9
AHQ-2-14, 6165	R.GSYGDLGGPIITTQVTIPK.D	1918.18004	2	3.04E-04	0.74	3.46	-	402.9
gi|30155919|ref|XP_292814.2|	similar to zinc finger protein 433 [Homo sapiens]			3.11E-04	0.47	10.14	1.60	108732.0
AHQ-2-14-, 4753 - 4829	K.CKQCGKGFNLPSSIR.Y	1755.01259	2	3.11E-04	0.47	2.87	-	623.6
gi|4505127|ref|NP_000520.1|	melanocortin 2 receptor; Melanocortin-2 receptor (ACTH receptor); melan			3.21E-04	0.35	10.13	3.40	33926.5
AHQ-2-12, 5187 - 5193	K.ILENILIILR.N	1210.53432	1	3.21E-04	0.35	2.58	-	247.1
gi|29731000|ref|XP_291064.1|	similar to KIAA0540 protein [Homo sapiens]			3.34E-04	0.91	10.20	1.40	224374.8
AHQ-2-1, 6377	R.VLNTSSLESATDEAGSPLAAAAAAAAER.C	2716.89684	3	3.34E-04	0.91	4.05	-	1434.8
gi|4506427|ref|NP_002880.1|	retinoic acid receptor responder (tazarotene induced) 2 [Homo sapiens]			3.39E-04	0.32	10.13	7.40	18617.5
AHQ-2-12, 3402	R.LVHCPIETQVLR.E	1466.73089	1	3.39E-04	0.32	2.42	-	347.6
gi|4507657|ref|NP_003282.1|	tripeptidyl peptidase II [Homo sapiens]			3.40E-04	1.86	20.23	4.00	138447.8
AHQ-2-3, 4908	R.DPVQVAAPSDHGVGIEPVFPENTENSEK.I	2964.14642	3	3.40E-04	0.91	4.25	-	1038.6
AHQ-2-3, 4676	K.IVDIIDTTGSGDVNTATEVEPK.D	2275.45273	2	9.35E-04	0.94	4.60	-	979.8
gi|4506311|ref|NP_002831.1|	protein tyrosine phosphatase, receptor type, F isoform 1 precursor; pro			3.46E-04	0.46	10.15	2.00	211842.5
AHQ-2-7, 6463	R.TGEQAPSSPPRRVQARMLSASTMLVQWEPPEEPNGLVR.G	4204.74426	3	3.46E-04	0.46	3.08	-	264.6
gi|10835242|ref|NP_006249.1|	protein kinase, cGMP-dependent, type I; Protein kinase, cGMP-dependent			3.50E-04	0.93	10.20	2.50	77803.3
AHQ-2-6, 6797	K.LSDFNIIDTLGVGGFGR.V	1781.98992	2	3.50E-04	0.93	3.93	-	958.6
gi|13376689|ref|NP_079390.1|	hypothetical protein FLJ13615 [Homo sapiens]			3.63E-04	0.22	10.10	2.30	67925.5
AHQ-2-9, 4382	R.LDLKKKNSSNGSR.K	1447.62278	1	3.63E-04	0.22	2.05	-	537.0
gi|28373103|ref|NP_005164.2|	sarco/endoplasmic reticulum Ca2+ -ATPase isoform a; ATPase, Ca(2+)-tra			3.67E-04	0.84	10.17	2.10	109255.5
AHQ-2-11, 5961	R.DIVPGDIVEVAVGDKVPADLR.L	2178.47138	2	3.67E-04	0.84	3.37	-	658.0
gi|10835121|ref|NP_000289.1|	pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H			3.72E-04	0.82	10.15	1.90	61829.8
AHQ-2-7, 3393 - 3417	R.GDLGIEIPAEK.V	1142.28420	2	3.72E-04	0.82	2.95	-	870.9
AHQ-2-7, 3389 - 3391	R.GDLGIEIPAEK.V	1142.28420	1	8.64E-04	0.50	2.28	-	565.8
gi|4507795|ref|NP_003340.1|	ubiquitin-conjugating enzyme E2 variant 1 isoform b; DNA-binding protei			3.75E-04	0.65	10.15	4.10	25796.6
AHQ-2-12, 3362 - 3363	K.YPEAPPFVR.F	1076.22914	2	3.75E-04	0.65	2.95	-	418.4
gi|13375985|ref|NP_078975.1|	hypothetical protein FLJ14007 [Homo sapiens]			3.77E-04	0.23	10.12	4.90	30753.1
AHQ-2-9, 4392	K.RWKGAKNSETAAK.V	1447.62447	1	3.77E-04	0.23	2.36	-	390.6
gi|18254478|ref|NP_543152.1|	dual specificity phosphatase 19; protein phosphatase; stress-activated			3.88E-04	0.01	10.13	5.50	24194.3
AHQ-2-7, 4943	R.KQCTRVTTLTGK.K	1394.62307	1	3.88E-04	0.01	1.83	-	183.8
gi|21614520|ref|NP_000393.2|	glucose-6-phosphate dehydrogenase [Homo sapiens]			3.93E-04	0.53	10.13	3.10	59257.4
AHQ-2-7, 6897 - 6911	R.LFYLALPPTVYEAVTK.N	1826.16735	2	3.93E-04	0.53	2.57	-	361.4
gi|4506381|ref|NP_002863.1|	ras-related C3 botulinum toxin substrate 2; Ras-related C3 botulinum to			3.97E-04	1.44	20.20	12.00	21428.7
AHQ-2-11, 2088	R.AVLCPQPTR.Q	1043.22229	2	3.97E-04	0.64	2.81	-	517.4
AHQ-2-11, 2700 - 2705	R.HHCPSTPIILVGTK.L	1561.83067	2	3.99E-04	0.80	2.96	-	571.6
gi|4507879|ref|NP_003365.1|	voltage-dependent anion channel 1 [Homo sapiens]			4.01E-04	0.36	10.14	7.10	30772.3
AHQ-2-9, 4579	K.VNNSSLIGLGYTQTLKPGIK.L	2104.43564	2	4.01E-04	0.36	2.74	-	298.9
gi|4557797|ref|NP_000260.1|	non-metastatic cells 1 protein [Homo sapiens]			4.02E-04	0.79	10.17	0.00	17148.6
AHQ-2-12, 2893	R.TFIAIKPDGVQR.G	1345.57205	2	4.02E-04	0.79	3.23	-	481.7
AHQ-2-12, 2882 - 2950	R.TFIAIKPDGVQR.G	1345.57205	2	9.43E-04	0.85	3.31	-	722.2
gi|4827050|ref|NP_005142.1|	ubiquitin specific protease 14 [Homo sapiens]			4.04E-04	1.66	20.18	6.30	56068.8
AHQ-2-7, 4001	K.AQLFALTGVQPAR.Q	1372.59750	2	8.34E-04	0.85	3.23	-	1045.2
AHQ-2-7, 7311	K.FPLMLDMYELCTPELQEK.M	2259.64823	2	4.04E-04	0.81	3.51	-	642.5
gi|24308201|ref|NP_065392.1|	chromosome 20 open reading frame 3; chromosome 20open reading frame 3			4.20E-04	0.79	10.14	2.90	46480.1
AHQ-2-8, 2995	K.LLLSSETPIEGK.N	1287.48445	2	4.20E-04	0.79	2.79	-	692.6
gi|28461290|ref|NP_443728.2|	TRALPUSH; no opposite paired repeat protein [Homo sapiens]			4.31E-04	0.42	10.15	0.40	240073.5
AHQ-2-7, 3464	K.KKPQVNAK.D	913.09970	1	4.31E-04	0.42	2.82	-	393.9
gi|4506237|ref|NP_002809.1|	proteasome (prosome, macropain) activator subunit 2 (PA28 beta); Protea			4.47E-04	0.94	10.22	6.70	27348.4
AHQ-2-10, 6618	K.VLSLLALVKPEVWTLK.E	1810.25573	2	4.47E-04	0.94	4.49	-	946.4
gi|4557241|ref|NP_001095.1|	skeletal muscle specific actinin, alpha 3 [Homo sapiens]			4.62E-04	0.54	10.15	0.90	103293.7
AHQ-2-5, 2587	K.ALDFIASK.G	865.00867	1	9.47E-04	0.45	2.67	-	690.8
AHQ-2-5, 2588	K.ALDFIASK.G	865.00867	2	6.22E-04	0.86	3.04	-	565.0
AHQ-2-11, 2834	K.ALDFIASK.G	865.00867	1	4.62E-04	0.54	2.40	-	669.1
AHQ-2-5, 2580 - 2651	K.ALDFIASK.G	865.00867	1	5.23E-04	0.36	1.81	-	792.0
gi|5729980|ref|NP_006547.1|	phosphomevalonate kinase [Homo sapiens]			4.64E-04	1.36	20.21	13.50	21994.8
AHQ-2-11, 2634 - 2681	K.EQYAQEHGLNFQR.L	1620.70720	2	4.89E-04	0.45	2.76	-	275.1
AHQ-2-11, 6629	R.LEEQLENLIEFIR.S	1646.86592	2	4.64E-04	0.90	4.16	-	897.8
gi|4505237|ref|NP_002427.1|	palmitoylated membrane protein 1; membrane protein, palmitoylated 1 (55			4.75E-04	0.40	10.19	2.10	52296.2
AHQ-2-9, 1936	K.NALLSQNPEK.F	1114.23409	1	4.75E-04	0.40	2.58	-	328.3
gi|21281669|ref|NP_060899.1|	transcription factor-like nuclear regulator; putative transcription re			4.82E-04	0.56	10.15	0.80	252842.5
AHQ-2-1, 4925	K.NNSLEIDQTENVKPMLR.G	2002.23894	2	4.82E-04	0.56	3.02	-	700.4
gi|4505877|ref|NP_000436.1|	plectin 1, intermediate filament binding protein 500kDa; plectin 1, int			5.30E-04	0.56	10.13	0.40	518488.0
AHQ-2-1, 6308	K.EQELQQTLQQEQSVLDQLR.G	2314.49541	2	5.30E-04	0.56	2.68	-	508.7
gi|13899253|ref|NP_113620.1|	uridine-cytidine kinase 1 [Homo sapiens]			5.31E-04	0.17	10.11	4.30	31434.5

AHQ-2-12, 6535 - 6602	R.KVVILSQDRFYK.V	1496.77853	1	5.31E-04	0.17	2.20	-	334.1
gi|22065231|ref|XP_035037.2| similar to MEGF7 [Homo sapiens]				5.33E-04	0.46	10.15	2.10	171294.3
AHQ-2-9, 5430	R.TVLIWENLDRPRDIVVEPM*GGYMYWTDWGASPK.I	3913.43248	3	5.33E-04	0.46	3.04	-	240.1
gi|21361687|ref|NP_060521.2| hypothetical protein FLJ10300 [Homo sapiens]				5.44E-04	0.25	10.13	2.70	60917.0
AHQ-2-4, 3705 - 3709	K.RRWAAPEVDECNRLR.L	1930.14076	2	5.44E-04	0.25	2.62	-	366.7
gi|4501889|ref|NP_001606.1| actin, gamma 2 propeptide; actin, alpha-3 [Homo sapiens]				5.55E-04	0.28	10.15	5.60	41876.7
AHQ-2-8, 5307 - 5375	K.DLYANNVLSGGTTM*YPGIADR.M	2245.45502	2	5.55E-04	0.28	2.78	-	282.4
gi|4506985|ref|NP_003043.1| solute carrier family 34 (sodium phosphate), member 1; solute carrier f				5.56E-04	0.19	10.09	1.90	68937.1
AHQ-2-10, 5742	K.MLNSLLKGQVAK.V	1302.61212	1	5.56E-04	0.19	1.82	-	460.2
gi|17486695|ref|XP_066916.1| similar to cytosolic malate dehydrogenase [Homo sapiens]				5.57E-04	0.22	10.12	4.40	17725.8
AHQ-2-10, 2462	K.YVIAADK.E	779.90377	1	5.57E-04	0.22	2.03	-	395.9
gi|21618342|ref|NP_003143.2| signal transducer and activator of transcription 5A; signal transducer				5.60E-04	0.74	10.14	1.50	90646.4
AHQ-2-5, 3479	K.HLQINQTFEELR.L	1528.69435	2	5.60E-04	0.74	2.78	-	329.0
gi|15100168|ref|NP_150094.1| CUB and Sushi multiple domains 1 [Homo sapiens]				5.69E-04	0.43	10.16	0.70	382827.5
AHQ-2-2, 3221 - 3262	R.LLSSLSGSHSGETLPLATSNQILLR.F	2595.93384	3	5.69E-04	0.43	3.23	-	294.6
gi|20270259|ref|NP_620061.1| phosphoglycerate kinase 2; phosphoglycerate kinase 1, pseudogene 2 [Ho				5.69E-04	0.25	10.14	1.90	44895.0
AHQ-2-8, 2870	R.VDFNVPMK.K	950.13707	1	5.69E-04	0.25	1.98	-	393.3
gi|6715568|ref|NP_000935.1| protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform (				5.71E-04	1.47	20.17	8.30	58687.5
AHQ-2-7, 7356	R.FKEPPAYGPMCDILWSDPLEDFGNEK.T	3058.38651	3	9.99E-04	0.67	3.34	-	814.2
AHQ-2-7, 4657	K.GLTPTGMLPSGVLSGGK.Q	1572.85198	2	5.71E-04	0.80	3.29	-	552.7
gi|6005717|ref|NP_009031.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e; ATP				5.96E-04	0.18	10.13	14.50	7933.1
AHQ-2-14-, 2919	R.ELAEDDSILK	1133.23094	1	5.96E-04	0.18	2.34	-	164.3
gi|8393120|ref|NP_059139.1| polymerase (DNA directed), epsilon 3 (p17 subunit); histone fold protei				6.18E-04	0.42	10.15	12.20	16859.5
AHQ-2-10, 4219	K.TLNASDVLSAM*EEM*EFQR.F	2104.30511	3	6.18E-04	0.42	3.09	-	381.8
gi|4507303|ref|NP_001045.1| sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2; th				6.30E-04	0.83	10.20	8.80	34310.4
AHQ-2-9, 6858 - 6868	K.YFAEALGPLQSFQARPDDLLISTYPK.S	2942.31346	2	6.30E-04	0.83	3.92	-	376.8
gi|4504111|ref|NP_002077.1| growth factor receptor-bound protein 2 [Homo sapiens]				6.32E-04	0.11	10.15	6.50	25206.2
AHQ-2-10, 3279	R.ESESAPGDFSLSVK.F	1453.53305	1	6.32E-04	0.11	2.24	-	137.2
gi|4503101|ref|NP_001312.1| cysteine and glycine-rich protein 2; LIM domain only 5, smooth muscle;				6.34E-04	0.77	10.18	9.30	20953.8
AHQ-2-13, 3377	K.GYGYGQGAGTLNM*DRGER.L	1919.02542	2	6.34E-04	0.77	3.12	-	636.7
gi|4502501|ref|NP_000583.1| complement component 4B proprotein [Homo sapiens]				6.42E-04	0.01	10.13	0.50	192795.6
AHQ-2-8, 4600 - 4605	K.SCGLHQLLR.G	1085.26240	1	6.42E-04	0.01	1.91	-	50.3
gi|13775186|ref|NP_112567.1| ring finger protein 17 isoform long [Homo sapiens]				6.61E-04	0.67	10.16	1.70	73736.0
AHQ-2-14-, 5433	K.TADQLTTGLER.S	1205.30039	2	6.61E-04	0.67	3.10	-	768.2
gi|21359960|ref|NP_112186.2| hypothetical protein PRTD-NY3 [Homo sapiens]				6.84E-04	0.13	10.13	2.70	74412.9
AHQ-2-14, 4952	K.GVM*LSHDNITWIAGAVTK.D	1930.21753	2	6.84E-04	0.13	2.52	-	134.0
gi|19424120|ref|NP_061846.2| dolichyl-phosphate mannosyltransferase polypeptide 3 isoform 1; prosti				6.92E-04	0.80	10.16	8.20	13276.6
AHQ-2-14-, 2164	R.ELQSQIQEAR.A	1202.29973	2	6.92E-04	0.80	3.15	-	794.1
gi|29743324|ref|XP_293276.1| similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote				6.98E-04	0.94	10.33	16.00	21244.7
AHQ-2-14-, 5285 - 5361	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	6.98E-04	0.94	6.53	-	1267.5
gi|5453545|ref|NP_006454.1| associated molecule with the SH3 domain of STAM [Homo sapiens]				7.02E-04	0.16	10.14	6.40	48076.6
AHQ-2-13, 6317	R.SLKPGALSNSESIPTIDGLRHVVVPGR.L	2801.19445	2	7.02E-04	0.16	2.73	-	140.8
gi|4502879|ref|NP_003268.1| transmembrane protein claudin 5; androgen withdrawal and apoptosis indu				7.06E-04	0.83	10.13	5.50	23147.3
AHQ-2-11, 3210	R.EFYDPSVPVSQK.Y	1396.52632	2	7.06E-04	0.83	2.69	-	748.6
gi|23065535|ref|NP_690007.1| hypoxia-inducible factor-3 alpha isoform a; inhibitory PAS domain prot				7.10E-04	0.28	10.13	1.90	72404.1
AHQ-2-12, 2483	-.MDWQDHRSTTELR.K	1675.80781	2	7.10E-04	0.28	2.69	-	319.7
gi|11321581|ref|NP_003840.1| succinate-CoA ligase, GDP-forming, alpha subunit [Homo sapiens]				7.22E-04	0.88	10.16	4.80	35059.2
AHQ-2-8, 3711	R.LIGPNCPGVINPGECK.I	1727.98391	2	7.22E-04	0.88	3.21	-	787.4
gi|30150448|ref|XP_293066.2| similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose				7.41E-04	0.95	10.18	2.90	58788.2
AHQ-2-6, 4493	R.VINEPTAAALAYGLDK.S	1646.86592	2	7.41E-04	0.95	3.63	-	1402.7
gi|21361621|ref|NP_002624.2| phosphoglucomutase 1 [Homo sapiens]				7.53E-04	0.91	10.19	4.40	61448.7
AHQ-2-13-, 7105	K.VFQSSANYAENFIQSIISTVEPAQR.Q	2801.06026	3	7.53E-04	0.91	3.79	-	1308.3
gi|29742841|ref|XP_294103.1| similar to 60S ribosomal protein L35 [Homo sapiens]				7.61E-04	0.85	10.14	7.40	11374.4
AHQ-2-5, 1875	K.TQKENLR.K	888.99186	2	7.61E-04	0.85	2.86	-	887.8
gi|4506243|ref|NP_002810.1| polypyrimidine tract-binding protein 1 isoform a; RNA-binding protein;				7.66E-04	0.85	10.20	4.10	59632.7
AHQ-2-10, 6160 - 6231	R.IAIPGLAGAGNSVLLVSNLNPER.V	2276.62142	2	7.66E-04	0.85	3.90	-	434.0
gi|17440554|ref|XP_067503.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				8.00E-04	0.80	10.16	7.90	18110.6
AHQ-2-12, 2817	R.VKEGM*DIVEAMER.F	1523.75807	2	8.00E-04	0.80	3.14	-	727.3
gi|6912324|ref|NP_036266.1| leiomodin 1 (smooth muscle); thyroid and eye muscle autoantigen D1 (64k				8.14E-04	0.46	10.17	3.00	63737.1
AHQ-2-14, 6382 - 6413	K.GEKKDLLEVPKAGAVAK.G	1754.06430	2	8.14E-04	0.46	3.34	-	459.0
gi|21450838|ref|NP_659501.1| hypothetical protein MGC2793 [Homo sapiens]				8.19E-04	0.24	10.12	2.50	41506.7
AHQ-2-10, 2702 - 2768	R.EIGQITLKK.D	1030.24336	1	8.19E-04	0.24	2.39	-	142.1
gi|29734552|ref|XP_291269.1| similar to KIAA1875 protein [Homo sapiens]				8.33E-04	0.50	10.14	1.70	93320.7
AHQ-2-13-, 4786	R.M*LAPKRSWGTPQLR.L	1657.96500	2	8.33E-04	0.50	2.75	-	659.5
gi|4502643|ref|NP_001753.1| chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing				8.51E-04	0.42	10.20	3.00	58023.9
AHQ-2-7, 4757 - 4803	K.VLAQNSGFDLQETLVK.I	1762.98491	2	8.51E-04	0.42	2.55	-	554.8
gi|29743107|ref|XP_297088.1| hypothetical protein XP_297088 [Homo sapiens]				8.60E-04	0.18	10.11	1.90	59382.3
AHQ-2-11, 3009 - 3082	R.HSTQNKVDTR.K	1186.26040	1	8.60E-04	0.18	2.15	-	275.6
gi|29732368|ref|XP_297653.1| hypothetical protein XP_297653 [Homo sapiens]				8.63E-04	0.20	10.15	2.40	79792.2
AHQ-2-2, 4122	R.QGAM*TRQLQGQEETVM*K.R	1968.20280	2	8.63E-04	0.20	2.53	-	369.1
gi|29730163|ref|XP_297463.1| hypothetical protein XP_297463 [Homo sapiens]				8.72E-04	0.31	10.09	5.10	21238.0
AHQ-2-9, 5026 - 5027	R.M*RDWEELLER.A	1393.55068	1	8.72E-04	0.31	1.82	-	604.0
gi|6912532|ref|NP_036473.1| G protein-binding protein CRFG; GTP-binding protein [Homo sapiens] [MAS				8.97E-04	0.55	10.18	3.30	73832.8
AHQ-2-5, 4023 - 4031	K.VKFTQQNYHDRLSQILTDFPK.L	2579.89466	3	8.97E-04	0.55	3.67	-	445.6
gi|19923178|ref|NP_003669.2| chromosome 22 open reading frame 19; gene from NF2/meningioma region o				8.98E-04	0.78	10.15	2.30	78521.4
AHQ-2-14-, 6855	R.ECLSNKEKILKEIEVK.K	1962.29756	2	8.98E-04	0.78	2.93	-	841.0
gi|17439599|ref|XP_067423.1| similar to destrin - pig [Homo sapiens]				9.16E-04	0.77	10.12	4.40	19819.2
AHQ-2-12, 2301	K.CIIVEEGK.E	949.10404	1	9.16E-04	0.77	2.49	-	884.7
gi|5174427|ref|NP_006085.1| deleted in liver cancer 1; ortholog of mouse Arhgap7; START domain cont				9.22E-04	0.18	10.11	0.90	122815.9
AHQ-2-9, 2675	K.ELSSFSFSMK.G	1163.32538	1	9.22E-04	0.18	2.25	-	212.3
gi|7661602|ref|NP_056230.1| DKFZP564B167 protein [Homo sapiens]				9.31E-04	0.77	10.17	9.40	14278.8
AHQ-2-13, 2233	K.LRPLYNHPAGPR.T	1391.60574	2	9.31E-04	0.77	2.95	-	602.0
gi|5174525|ref|NP_005900.1| microtubule-associated protein 1B isoform 1 [Homo sapiens]				9.39E-04	0.35	10.13	0.60	270617.4
AHQ-2-4, 3946 - 3986	K.ESVEKAAKPTTTPEVK.A	1715.92656	2	9.39E-04	0.35	2.62	-	551.8
gi|4506801|ref|NP_003460.1| secretogranin II precursor; Chromogranin C (secretogranin II); secreton				9.62E-04	0.15	10.14	2.80	70868.2
AHQ-2-8, 4239 - 4310	R.DSKENIGKNEQINDEM*K.R	2009.14194	2	9.62E-04	0.15	2.78	-	198.3
gi|4503179|ref|NP_003602.1| oral-facial-digital syndrome 1; chromosome X open reading frame 5; oral				9.75E-04	0.17	10.14	0.00	116670.5
AHQ-2-5, 5961 - 6037	K.KEELNQSVNR.V	1217.31440	1	9.75E-04	0.17	2.11	-	301.0
gi|18079216|ref|NP_065815.1| CASK-interacting protein 1 [Homo sapiens]				9.83E-04	0.15	10.16	1.30	149812.6
AHQ-2-6, 7191 - 7198	R.PGSPQALGGPHGPAPATAK.V	1711.90292	2	9.83E-04	0.15	2.57	-	328.7
gi|18379346|ref|NP_055793.1| VPS10 domain receptor protein SORCS 3 [Homo sapiens]				9.84E-04	0.07	10.12	1.00	135754.0
AHQ-2-6, 4781	R.GIPAPAKLGGAR.R	1108.31905	1	9.84E-04	0.07	1.84	-	227.9
gi|13325064|ref|NP_001399.1| cadherin EGF LAG seven-pass G-type receptor 2; EGF-like-domain, multip				9.93E-04	0.11	10.13	0.70	317449.8
AHQ-2-9, 5190 - 5267	R.GNELSLVLLNASTGELKLSR.A	2115.41683	2	9.93E-04	0.11	2.62	-	216.8

Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|4507485|ref|NP_003237.1|	thrombospondin 1 [Homo sapiens]			1.00E-30	29.99	350.33	30.40	129351.8
AHQ-3-2, 6755 - 6778	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	3	6.21E-06	0.93	5.07	-	930.7
AHQ-3-10, 5799	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	2	4.41E-05	0.80	3.55	-	506.8
AHQ-3-1, 4040 - 4068	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.85E-04	0.87	3.65	-	547.4
AHQ-3-2, 4097 - 4150	R.CENTDPGYNCLPCPPR.F	1954.10800	2	6.98E-04	0.73	3.22	-	345.3
AHQ-3-5, 3909 - 3917	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.74E-08	0.87	3.52	-	545.6
AHQ-3-4, 4017	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.43E-04	0.86	3.65	-	521.0
AHQ-3-2, 4279	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.27E-06	0.89	3.44	-	648.3
AHQ-3-1, 3940	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.23E-09	0.93	4.38	-	758.6
AHQ-3-2, 3394 - 3395	K.CNYLGHYSDPM*YR.C	1693.84162	2	6.93E-05	0.93	3.72	-	793.6
AHQ-3-2, 3946	K.CNYLGHYSDPMYR.C	1677.84222	2	1.75E-06	0.94	4.05	-	931.9
AHQ-3-3, 3356	K.CNYLGHYSDPM*YR.C	1693.84162	2	5.06E-04	0.93	3.42	-	1129.3
AHQ-3-4, 3316	K.CNYLGHYSDPM*YR.C	1693.84162	2	2.75E-04	0.93	3.54	-	990.0
AHQ-3-3, 3884	K.CNYLGHYSDPMYR.C	1677.84222	2	4.28E-06	0.95	3.95	-	930.3
AHQ-3-4, 3450	K.DCVGDVTENQICNK.Q	1654.75869	2	1.03E-04	0.80	3.74	-	494.9
AHQ-3-1, 3449 - 3450	K.DCVGDVTENQICNK.Q	1654.75869	2	5.04E-06	0.93	4.27	-	975.6
AHQ-3-2, 3531	K.DCVGDVTENQICNK.Q	1654.75869	2	2.92E-04	0.95	4.25	-	1377.4
AHQ-3-3, 3466 - 3473	K.DCVGDVTENQICNK.Q	1654.75869	2	3.90E-05	0.97	4.95	-	1487.4
AHQ-3-4, 6545	K.DDFDHDSVPDIDDICPENVDISETDFR.R	3183.22991	3	9.15E-04	0.84	4.00	-	682.6
AHQ-3-11, 2599	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.02E-09	0.94	4.10	-	1031.6
AHQ-3-10, 2536	K.DHSGQVFSVVSNGK.A	1461.56164	1	1.22E-06	0.43	2.07	-	476.9
AHQ-3-2, 2698	K.DHSGQVFSVVSNGK.A	1461.56164	2	9.68E-06	0.91	3.13	-	1129.5
AHQ-3-5, 2540	K.DHSGQVFSVVSNGK.A	1461.56164	2	1.04E-06	0.95	3.47	-	1523.0
AHQ-3-10, 2588	K.DHSGQVFSVVSNGK.A	1461.56164	2	1.39E-06	0.95	3.79	-	1225.4
AHQ-3-9, 2497	K.DHSGQVFSVVSNGK.A	1461.56164	1	3.77E-06	0.07	1.85	-	247.6
AHQ-3-3, 3126 - 3128	R.DNCQYVYNVDQR.D	1575.64166	2	2.37E-05	0.90	4.00	-	814.2
AHQ-3-1, 3361	R.DNCQYVYNVDQR.D	1575.64166	2	1.67E-05	0.90	3.55	-	1134.4
AHQ-3-5, 3031	R.DNCQYVYNVDQR.D	1575.64166	2	2.58E-04	0.89	3.59	-	911.7
AHQ-3-4, 3117	R.DNCQYVYNVDQR.D	1575.64166	2	9.94E-05	0.80	3.33	-	759.7
AHQ-3-3, 6174 - 6248	K.DSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFR.R	4418.43100	3	4.72E-05	0.81	4.07	-	517.6
AHQ-3-2, 6237 - 6307	K.DSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFR.R	4418.43100	3	6.68E-06	0.96	5.92	-	1105.0
AHQ-3-2, 4255 - 4335	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	2.25E-07	0.88	4.11	-	680.5
AHQ-3-2, 4139	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.03E-07	0.87	4.41	-	691.4
AHQ-3-4, 3910	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.16E-08	0.89	4.21	-	758.1
AHQ-3-3, 3910	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.64E-04	0.74	3.52	-	589.7
AHQ-3-2, 3981	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.60E-09	0.87	4.18	-	606.3
AHQ-3-1, 3905 - 3976	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.00E-30	0.90	4.50	-	830.5
AHQ-3-6, 3787	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.23E-09	0.84	3.93	-	802.2
AHQ-3-1, 4318	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	2.83E-04	0.90	4.48	-	624.7
AHQ-3-2, 4405	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	7.28E-12	0.88	4.53	-	497.6
AHQ-3-4, 4310	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	5.03E-11	0.95	5.41	-	802.4
AHQ-3-2, 3671	K.FQDLVDAVR.A	1063.18877	2	1.37E-06	0.90	3.15	-	1001.5
AHQ-3-10, 3254	K.FQDLVDAVR.A	1063.18877	1	7.83E-06	0.42	2.25	-	357.5
AHQ-3-1, 2984	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	5.48E-04	0.83	3.60	-	550.6
AHQ-3-2, 2770 - 2847	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.06E-08	0.85	4.41	-	343.6
AHQ-3-1, 2970	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	7.21E-05	0.83	3.96	-	353.9
AHQ-3-4, 2792	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	7.11E-06	0.88	3.68	-	845.1
AHQ-3-4, 2922	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	5.79E-07	0.79	3.30	-	505.6
AHQ-3-2, 2922	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.25E-05	0.83	3.78	-	410.2
AHQ-3-6, 2547	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.65E-04	0.62	2.98	-	345.5
AHQ-3-4, 5638	R.FVFGTTPEDILR.N	1395.58470	1	4.67E-06	0.18	2.47	-	113.1
AHQ-3-10, 4874 - 4934	R.FVFGTTPEDILR.N	1395.58470	1	8.81E-05	0.09	1.83	-	139.1
AHQ-3-1, 5790 - 5864	R.FVFGTTPEDILR.N	1395.58470	1	6.88E-06	0.02	1.83	-	93.6
AHQ-3-3, 5669	R.FVFGTTPEDILR.N	1395.58470	1	4.49E-06	0.17	2.61	-	127.0
AHQ-3-9, 5021	R.FVFGTTPEDILR.N	1395.58470	1	5.55E-07	0.12	2.42	-	68.3
AHQ-3-6, 5377 - 5378	R.FVFGTTPEDILR.N	1395.58470	1	2.99E-04	0.06	2.03	-	115.6
AHQ-3-10, 4891	R.FVFGTTPEDILR.N	1395.58470	1	4.37E-07	0.34	2.94	-	135.1
AHQ-3-12, 5400	R.FVFGTTPEDILR.N	1395.58470	2	9.42E-04	0.75	2.90	-	419.8
AHQ-3-5, 5445	R.FVFGTTPEDILR.N	1395.58470	1	1.44E-04	0.08	2.02	-	111.1
AHQ-3-5, 5449	R.FVFGTTPEDILR.N	1395.58470	1	1.63E-06	0.27	2.52	-	93.8
AHQ-3-2, 4989 - 5045	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.11E-07	0.88	3.63	-	949.7
AHQ-3-2, 4902	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.12E-04	0.91	4.19	-	916.2
AHQ-3-2, 4735 - 4810	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.25E-07	0.91	3.94	-	774.5
AHQ-3-6, 4163 - 4233	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.77E-06	0.88	4.21	-	537.0
AHQ-3-5, 4519 - 4588	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.22E-06	0.88	3.96	-	836.0
AHQ-3-2, 4594	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.34E-09	0.89	4.30	-	691.9
AHQ-3-7, 4052 - 4132	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.18E-05	0.87	4.30	-	629.1
AHQ-3-6, 4589	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.37E-05	0.70	2.93	-	651.4
AHQ-3-10, 3982 - 4048	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.14E-04	0.61	3.24	-	427.6
AHQ-3-10, 4114 - 4188	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.46E-08	0.92	4.27	-	909.1
AHQ-3-9, 4171	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.33E-09	0.90	3.99	-	829.5
AHQ-3-7, 4387	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.04E-04	0.87	3.64	-	836.2
AHQ-3-4, 4829	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.31E-08	0.95	4.34	-	1477.1
AHQ-3-4, 4582 - 4652	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.71E-10	0.91	3.67	-	1025.3
AHQ-3-11, 4142	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.22E-06	0.83	3.46	-	650.9
AHQ-3-9, 3940	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.23E-04	0.56	2.83	-	515.2
AHQ-3-1, 4680 - 4749	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.46E-08	0.87	3.75	-	819.3
AHQ-3-1, 4660	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.03E-04	0.89	3.98	-	794.0
AHQ-3-10, 4267	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.14E-09	0.91	4.04	-	851.9
AHQ-3-9, 3851 - 3927	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.12E-04	0.88	3.85	-	692.5
AHQ-3-5, 4296	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.68E-04	0.89	4.28	-	691.3
AHQ-3-6, 4375 - 4445	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.81E-08	0.94	4.58	-	1108.7
AHQ-3-6, 4071	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.37E-06	0.70	3.11	-	566.6
AHQ-3-3, 4390	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.79E-05	0.78	3.84	-	484.1
AHQ-3-11, 4075 - 4147	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.39E-04	0.57	2.96	-	426.9
AHQ-3-3, 4552 - 4553	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.24E-04	0.94	4.45	-	1030.2
AHQ-3-3, 4704 - 4784	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.58E-04	0.90	4.03	-	776.3
AHQ-3-3, 4880 - 4896	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.80E-07	0.94	4.34	-	1155.7
AHQ-3-10, 3896 - 3904	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.99E-07	0.82	3.44	-	827.0
AHQ-3-2, 2081 - 2105	K.GPDPSSPAFR.I	1031.10364	2	2.11E-04	0.83	3.21	-	573.9
AHQ-3-10, 2010	K.GPDPSSPAFR.I	1031.10364	2	6.94E-04	0.77	3.04	-	560.2
AHQ-3-3, 2082	K.GPDPSSPAFR.I	1031.10364	2	1.17E-04	0.78	3.04	-	528.0
AHQ-3-1, 2253	K.GPDPSSPAFR.I	1031.10364	2	1.24E-05	0.78	2.71	-	582.2
AHQ-3-4, 2098	K.GPDPSSPAFR.I	1031.10364	2	4.56E-05	0.65	2.85	-	451.3
AHQ-3-6, 2709	R.GTLLALER.K	873.03234	2	2.13E-04	0.92	3.43	-	1160.0
AHQ-3-3, 2952	R.GTLLALER.K	873.03234	2	3.66E-04	0.90	3.11	-	1029.6
AHQ-3-2, 2933	R.GTLLALER.K	873.03234	2	5.39E-04	0.89	3.46	-	969.7
AHQ-3-1, 3194	R.GTLLALER.K	873.03234	2	5.15E-04	0.87	3.01	-	849.8
AHQ-3-2, 2585	K.GTSQNDPNWVVR.H	1373.45608	1	9.00E-04	0.09	1.89	-	117.0
AHQ-3-12, 6334	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.02E-08	0.76	3.40	-	254.4
AHQ-3-11, 6239	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.08E-05	0.80	3.83	-	339.7
AHQ-3-11, 6098 - 6174	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.91E-04	0.67	3.19	-	222.7
AHQ-3-11, 6095	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.30E-10	0.65	3.39	-	451.9
AHQ-3-13, 6346 - 6365	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.38E-06	0.68	3.66	-	343.7
AHQ-3-3, 6772 - 6841	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	8.91E-06	0.74	4.08	-	302.8

AHQ-3-13-, 6319 - 6331	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.28E-09	0.70	3.04	-	478.2
AHQ-3-1, 6733 - 6776	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.27E-10	0.76	3.34	-	538.6
AHQ-3-1, 6744 - 6764	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	7.76E-05	0.55	2.92	-	202.5
AHQ-3-1, 6880	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.07E-07	0.63	3.23	-	315.0
AHQ-3-9, 6209 - 6216	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.97E-06	0.82	4.13	-	446.1
AHQ-3-8, 6275	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.66E-06	0.72	3.20	-	213.8
AHQ-3-14-, 6252	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.32E-04	0.71	3.17	-	258.5
AHQ-3-7, 6483	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.20E-04	0.72	3.38	-	233.0
AHQ-3-7, 6479 - 6510	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.34E-06	0.79	3.60	-	357.9
AHQ-3-6, 6511 - 6539	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	6.36E-09	0.73	3.65	-	330.4
AHQ-3-3, 6777	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.20E-05	0.33	2.61	-	143.6
AHQ-3-10, 5875 - 5934	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	8.26E-06	0.41	2.94	-	173.5
AHQ-3-3, 6965 - 6972	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.58E-07	0.76	3.27	-	412.5
AHQ-3-5, 6657 - 6663	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	8.26E-06	0.70	3.36	-	254.0
AHQ-3-4, 6730 - 6801	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.82E-08	0.82	3.78	-	296.9
AHQ-3-4, 6784 - 6785	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	9.36E-08	0.85	3.83	-	465.8
AHQ-3-2, 6845 - 6915	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.06E-11	0.75	3.64	-	433.2
AHQ-3-2, 6982 - 7053	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.29E-08	0.63	3.18	-	342.9
AHQ-3-2, 6995 - 7051	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.25E-06	0.71	2.99	-	431.4
AHQ-3-6, 2386	K.IMADSGPIYDK.T	1210.38204	2	4.65E-06	0.88	3.31	-	653.1
AHQ-3-2, 2303	K.IM*ADSGPIYDK.T	1226.38144	2	1.99E-04	0.84	3.21	-	654.6
AHQ-3-14-, 2561 - 2571	K.IMADSGPIYDK.T	1210.38204	2	1.12E-05	0.90	3.66	-	874.2
AHQ-3-12, 2234 - 2274	K.IM*ADSGPIYDK.T	1226.38144	2	7.94E-04	0.52	2.56	-	404.6
AHQ-3-2, 2551	K.IMADSGPIYDK.T	1210.38204	2	3.07E-05	0.95	3.95	-	1004.6
AHQ-3-12, 2559	K.IMADSGPIYDK.T	1210.38204	2	1.59E-06	0.93	3.94	-	846.6
AHQ-3-13-, 2630	K.IMADSGPIYDK.T	1210.38204	2	3.79E-06	0.76	2.94	-	596.5
AHQ-3-13, 2615 - 2670	K.IMADSGPIYDK.T	1210.38204	2	5.25E-04	0.58	2.69	-	653.1
AHQ-3-11, 2455	K.IMADSGPIYDK.T	1210.38204	2	7.22E-04	0.76	2.97	-	474.1
AHQ-3-4, 7208 - 7286	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.65E-07	0.97	5.79	-	1116.4
AHQ-3-13, 6723	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.18E-10	0.97	5.66	-	1151.8
AHQ-3-6, 6913	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.93E-09	0.97	5.58	-	1134.3
AHQ-3-2, 7281 - 7345	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.04E-10	0.97	5.12	-	1234.6
AHQ-3-6, 7073 - 7142	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.12E-10	0.97	5.66	-	1261.7
AHQ-3-5, 7065 - 7075	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.37E-09	0.96	5.27	-	1078.8
AHQ-3-5, 7164 - 7231	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	6.85E-09	0.96	4.99	-	1321.9
AHQ-3-3, 7256 - 7328	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.14E-11	0.97	5.73	-	1040.7
AHQ-3-2, 7417	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.31E-10	0.97	5.71	-	1138.3
AHQ-3-11, 6571	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.85E-05	0.88	4.01	-	525.7
AHQ-3-14-, 6592 - 6660	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.08E-11	0.98	6.54	-	1819.4
AHQ-3-11, 6440 - 6511	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.46E-08	0.97	5.67	-	1230.3
AHQ-3-3, 7192 - 7265	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.59E-09	0.97	5.48	-	1354.7
AHQ-3-9, 6564 - 6576	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.21E-11	0.96	5.51	-	822.6
AHQ-3-4, 7362	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.27E-06	0.95	5.28	-	770.0
AHQ-3-10, 6384	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.60E-13	0.95	5.03	-	917.0
AHQ-3-10, 6240 - 6307	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.04E-10	0.97	5.87	-	1161.7
AHQ-3-1, 7105 - 7168	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.50E-12	0.98	6.05	-	1782.6
AHQ-3-9, 6676 - 6741	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.33E-06	0.87	3.89	-	473.3
AHQ-3-6, 6930 - 7009	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.03E-10	0.97	5.90	-	1264.5
AHQ-3-1, 2488	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.06E-07	0.90	3.34	-	1068.9
AHQ-3-4, 2229	R.KDHSGQVFSVVSNGK.A	1589.73455	2	4.08E-06	0.88	3.44	-	938.0
AHQ-3-6, 2018	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.12E-11	0.82	3.46	-	777.7
AHQ-3-5, 2040	R.KDHSGQVFSVVSNGK.A	1589.73455	2	6.81E-08	0.94	4.06	-	1294.1
AHQ-3-2, 2314	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.37E-09	0.90	3.74	-	1062.6
AHQ-3-7, 1936	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.39E-09	0.57	2.57	-	624.1
AHQ-3-12, 2314	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.45E-04	0.59	2.86	-	261.7
AHQ-3-13, 2381	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.04E-06	0.90	3.84	-	971.5
AHQ-3-10, 2103 - 2174	R.KDHSGQVFSVVSNGK.A	1589.73455	2	3.72E-13	0.91	3.59	-	1113.0
AHQ-3-2, 2322	K.KIMADSGPIYDK.T	1338.55496	2	4.82E-07	0.94	4.17	-	933.8
AHQ-3-2, 1981 - 1990	K.KIM*ADSGPIYDK.T	1354.55436	2	5.64E-04	0.94	3.95	-	1125.2
AHQ-3-1, 2456	R.KVTEENKELANELR.R	1673.84976	2	1.61E-06	0.93	4.05	-	1515.5
AHQ-3-3, 1989	R.KVTEENKELANELR.R	1673.84976	2	2.14E-07	0.94	4.18	-	1482.0
AHQ-3-4, 2013	R.KVTEENKELANELR.R	1673.84976	2	5.40E-06	0.89	4.00	-	960.5
AHQ-3-6, 2049 - 2059	R.KVTEENKELANELR.R	1673.84976	2	2.22E-08	0.94	5.22	-	1116.8
AHQ-3-4, 2257	R.KVTEENKELANELR.R	1673.84976	3	8.30E-05	0.75	3.43	-	768.0
AHQ-3-5, 1759	R.KVTEENKELANELR.R	1673.84976	2	7.94E-05	0.89	3.91	-	907.2
AHQ-3-2, 2379	R.KVTEENKELANELR.R	1673.84976	2	6.37E-10	0.96	5.11	-	1416.4
AHQ-3-5, 2099	R.KVTEENKELANELR.R	1673.84976	3	1.79E-06	0.77	3.80	-	683.9
AHQ-3-3, 2358	R.KVTEENKELANELR.R	1673.84976	2	4.22E-06	0.95	4.52	-	1549.6
AHQ-3-3, 2245	R.KVTEENKELANELR.R	1673.84976	2	2.68E-06	0.92	4.55	-	1158.4
AHQ-3-2, 2274 - 2305	R.KVTEENKELANELR.R	1673.84976	2	3.24E-09	0.94	4.54	-	1323.5
AHQ-3-2, 2283	R.KVTEENKELANELR.R	1673.84976	3	4.04E-07	0.86	3.91	-	959.1
AHQ-3-4, 2144 - 2158	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	7.46E-05	0.85	3.39	-	579.2
AHQ-3-5, 2420	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	2.35E-04	0.84	4.04	-	529.9
AHQ-3-4, 2150	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	3	5.97E-05	0.79	3.72	-	701.1
AHQ-3-3, 2501 - 2506	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.83E-06	0.88	4.06	-	479.5
AHQ-3-2, 2166	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	5.29E-05	0.66	3.14	-	293.1
AHQ-3-2, 2535	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.75E-05	0.82	3.74	-	445.8
AHQ-3-4, 2496	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.05E-06	0.88	3.79	-	571.1
AHQ-3-6, 5479	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.60E-04	0.86	3.51	-	561.7
AHQ-3-9, 5068 - 5135	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.01E-05	0.72	3.04	-	508.4
AHQ-3-6, 5621	K.MENAELDVPIQSVFTR.D	1850.08607	2	7.69E-08	0.76	3.38	-	456.9
AHQ-3-2, 5951	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.31E-04	0.39	2.52	-	269.8
AHQ-3-4, 5744 - 5745	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.62E-07	0.91	4.67	-	412.9
AHQ-3-3, 5545 - 5556	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	9.23E-08	0.95	4.41	-	945.7
AHQ-3-6, 5422 - 5493	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.66E-04	0.92	4.16	-	607.4
AHQ-3-1, 5889	K.MENAELDVPIQSVFTR.D	1850.08607	2	4.00E-06	0.86	3.75	-	430.0
AHQ-3-2, 5590 - 5597	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	3.49E-10	0.96	5.22	-	958.9
AHQ-3-4, 5512	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	9.56E-09	0.84	3.81	-	612.1
AHQ-3-6, 5242	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	4.92E-04	0.87	3.65	-	568.9
AHQ-3-10, 5130	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.81E-05	0.85	3.44	-	511.2
AHQ-3-3, 5808 - 5828	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.44E-07	0.92	4.64	-	499.9
AHQ-3-5, 5544	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.31E-04	0.79	3.08	-	560.9
AHQ-3-2, 3089	K.QVTQSYWDTNPTR.A	1596.68241	2	3.46E-08	0.91	4.21	-	717.7
AHQ-3-5, 2875	K.QVTQSYWDTNPTR.A	1596.68241	2	2.00E-06	0.78	3.20	-	471.5
AHQ-3-3, 3069	K.QVTQSYWDTNPTR.A	1596.68241	2	3.02E-05	0.82	3.56	-	420.7
AHQ-3-1, 3236	K.QVTQSYWDTNPTR.A	1596.68241	2	2.01E-07	0.80	3.27	-	476.8
AHQ-3-11, 2894	K.QVTQSYWDTNPTR.A	1596.68241	2	2.15E-06	0.63	2.68	-	444.2
AHQ-3-4, 3024	K.QVTQSYWDTNPTR.A	1596.68241	2	6.97E-07	0.87	3.29	-	737.3
AHQ-3-3, 2725 - 2798	R.RPPLCYHNGVQYR.N	1661.86889	2	1.23E-06	0.95	3.81	-	1175.2
AHQ-3-6, 2574 - 2594	R.RPPLCYHNGVQYR.N	1661.86889	3	3.33E-05	0.95	3.89	-	1767.0
AHQ-3-2, 2783	R.RPPLCYHNGVQYR.N	1661.86889	2	5.15E-05	0.88	3.47	-	663.3
AHQ-3-6, 3571	K.SITLFVQEDR.A	1208.34588	2	6.99E-05	0.91	2.80	-	1484.9
AHQ-3-2, 3861 - 3921	K.SITLFVQEDR.A	1208.34588	2	3.23E-07	0.92	3.35	-	1255.7
AHQ-3-3, 3858	K.SITLFVQEDR.A	1208.34588	2	1.74E-06	0.94	3.59	-	1339.2
AHQ-3-10, 3464	K.SITLFVQEDR.A	1208.34588	2	1.36E-07	0.94	3.64	-	1497.1
AHQ-3-1, 4021	K.SITLFVQEDR.A	1208.34588	2	2.41E-05	0.95	3.64	-	1530.8
AHQ-3-7, 4066 - 4072	R.TIVTTLQDSIR.K	1247.42355	2	9.01E-07	0.97	3.90	-	1790.4

AHQ-3-12, 4292	R.TIVTTLQDSIR.K	1247.42355	2	2.21E-07	0.94	3.82	-	1123.2
AHQ-3-2, 4534 - 4606	R.TIVTTLQDSIR.K	1247.42355	2	7.71E-05	0.95	3.78	-	1421.1
AHQ-3-1, 3458	R.TIVTTLQDSIR.K	1247.42355	2	5.97E-04	0.94	3.33	-	1499.7
AHQ-3-8, 3864	R.TIVTTLQDSIR.K	1247.42355	2	1.25E-07	0.93	3.19	-	1340.2
AHQ-3-3, 4494 - 4501	R.TIVTTLQDSIR.K	1247.42355	2	6.01E-07	0.97	4.09	-	1639.5
AHQ-3-6, 4126 - 4149	R.TIVTTLQDSIR.K	1247.42355	2	1.06E-05	0.97	4.05	-	2182.2
AHQ-3-5, 4196 - 4204	R.TIVTTLQDSIR.K	1247.42355	2	1.71E-05	0.97	4.26	-	2011.9
AHQ-3-1, 4628 - 4636	R.TIVTTLQDSIR.K	1247.42355	2	1.05E-06	0.96	3.81	-	1602.7
AHQ-3-9, 3879	R.TIVTTLQDSIR.K	1247.42355	2	1.08E-05	0.95	3.88	-	1445.9
AHQ-3-7, 2244 - 2246	K.VTEENKELANELR.R	1545.67685	2	1.33E-09	0.91	4.02	-	853.7
AHQ-3-1, 2681	K.VTEENKELANELR.R	1545.67685	2	8.16E-07	0.77	3.26	-	630.5
AHQ-3-6, 2290	K.VTEENKELANELR.R	1545.67685	2	1.80E-08	0.88	3.60	-	923.0
gi|4507729|ref|NP_001060.1|	tubulin, beta polypeptide [Homo sapiens]			1.00E-30	8.71	100.36	34.60	49906.7
AHQ-3-14-, 4827 - 4851	R.AILVDLEPGTMDSVR.S	1616.86162	2	3.70E-06	0.89	3.68	-	670.1
AHQ-3-7, 2811	R.EIVHIQAGQCGNQIGAK.F	1825.03962	2	1.01E-06	0.95	4.64	-	1195.4
AHQ-3-11, 2823	R.EIVHIQAGQCGNQIGAK.F	1825.03962	2	2.46E-04	0.88	3.35	-	911.8
AHQ-3-7, 2703	K.EVDEQMLNVQNK.N	1447.59668	1	9.08E-09	0.62	3.44	-	254.8
AHQ-3-7, 2702	K.EVDEQMLNVQNK.N	1447.59668	2	5.54E-05	0.92	3.90	-	1036.7
AHQ-3-14-, 6188	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	2.48E-04	0.84	3.67	-	1103.5
AHQ-3-14-, 6193 - 6195	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.05E-13	0.99	6.96	-	2947.9
AHQ-3-7, 6162 - 6230	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.65E-08	0.99	6.88	-	3091.6
AHQ-3-7, 6166 - 6238	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	6.70E-05	0.92	5.19	-	1026.0
AHQ-3-11, 5990	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.93E-05	0.99	6.68	-	3046.4
AHQ-3-13-, 6298	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	9.51E-04	0.88	3.86	-	1193.3
AHQ-3-9, 5915 - 5944	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	7.60E-05	0.97	5.19	-	1803.9
AHQ-3-12, 6180 - 6219	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.15E-13	0.98	6.33	-	2642.1
AHQ-3-13-, 6297	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	6.64E-09	0.99	7.19	-	3475.8
AHQ-3-13, 6282	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	6.61E-14	0.99	6.98	-	2813.3
AHQ-3-13, 6281	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	3.55E-05	0.62	3.14	-	728.3
AHQ-3-10, 5778	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.84E-07	0.98	5.87	-	2760.6
AHQ-3-13, 3685 - 3735	R.ISEQFTAM*FR.R	1246.41758	2	9.52E-06	0.72	2.89	-	648.1
AHQ-3-7, 7198 - 7246	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	1.95E-11	0.93	4.74	-	616.7
AHQ-3-7, 7234	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	2.40E-08	0.89	4.40	-	967.3
AHQ-3-8, 7112	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	1.30E-06	0.94	4.13	-	1669.0
AHQ-3-7, 6262	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	3.20E-11	0.72	3.30	-	674.8
AHQ-3-9, 5956 - 5960	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	3.79E-04	0.40	2.53	-	366.3
AHQ-3-7, 6187	K.LTTPTYGDLNHLVSATM*SGVTTCLR.F	2727.06467	3	8.47E-06	0.85	3.56	-	879.0
AHQ-3-7, 6099 - 6104	K.LTTPTYGDLNHLVSATM*SGVTTCLR.F	2727.06467	3	8.22E-05	0.88	4.22	-	894.6
AHQ-3-9, 6869 - 6875	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	1.45E-04	0.89	4.51	-	887.8
AHQ-3-7, 6258	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	8.47E-07	0.89	4.17	-	679.6
AHQ-3-14-, 5983	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	7.88E-06	0.19	2.66	-	297.7
AHQ-3-7, 6554 - 6555	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	1.45E-10	0.91	4.79	-	1100.4
AHQ-3-12, 6004 - 6072	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	1.84E-05	0.66	3.30	-	736.4
AHQ-3-7, 5996	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	2.25E-07	0.75	3.50	-	885.6
AHQ-3-12, 5422 - 5471	R.NSSYFVEWIPNNVK.T	1697.87148	2	1.53E-04	0.89	4.26	-	743.3
AHQ-3-11, 6084	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	2.18E-09	0.97	5.81	-	2069.7
AHQ-3-11, 6083	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	8.00E-08	0.96	5.29	-	919.0
AHQ-3-9, 6123 - 6161	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	4.68E-08	0.92	4.19	-	869.2
AHQ-3-12, 6130 - 6200	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.59E-04	0.67	3.62	-	781.9
AHQ-3-10, 5866	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	2.81E-07	0.90	4.41	-	618.3
AHQ-3-12, 6320	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	1.06E-06	0.95	5.20	-	694.7
AHQ-3-7, 6528 - 6542	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	6.42E-06	0.93	4.67	-	666.3
AHQ-3-13, 6270 - 6341	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	2.20E-05	0.91	4.24	-	751.5
AHQ-3-7, 6434 - 6502	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	5.85E-12	0.95	6.07	-	979.7
AHQ-3-7, 6387 - 6450	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	1.64E-05	0.93	4.88	-	692.7
AHQ-3-13, 6309 - 6377	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.89E-07	0.94	5.36	-	1155.8
AHQ-3-7, 6338 - 6406	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.90E-12	0.98	6.93	-	1851.5
AHQ-3-7, 6240 - 6314	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	3.06E-04	0.95	5.21	-	671.2
AHQ-3-9, 6007	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	5.05E-04	0.93	4.57	-	899.0
AHQ-3-3, 6768	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.23E-06	0.84	4.08	-	643.1
AHQ-3-14-, 6156 - 6223	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.00E-30	0.98	7.22	-	1814.5
AHQ-3-14-, 6169 - 6229	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	3.72E-06	0.95	4.95	-	1021.9
AHQ-3-4, 6781	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	4.74E-05	0.74	3.59	-	401.0
AHQ-3-9, 6153	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.02E-08	0.95	5.23	-	1338.3
AHQ-3-14-, 6297 - 6375	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	5.81E-05	0.95	5.86	-	1227.9
gi|4504517|ref|NP_001531.1|	heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M			1.00E-30	7.02	90.33	60.00	22782.3
AHQ-3-13, 2521	K.DGVVEITGK.H	918.02674	1	4.03E-04	0.30	2.16	-	298.8
AHQ-3-13-, 2267	K.DGVVEITGK.H	918.02674	1	9.76E-06	0.19	2.06	-	408.6
AHQ-3-11, 5426 - 5487	R.KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK.L	3228.65914	3	2.92E-06	0.95	6.59	-	1551.8
AHQ-3-11, 4728 - 4730	K.LATQSNEITIPVTFESR.A	1907.11412	2	7.21E-10	0.88	3.91	-	461.1
AHQ-3-13-, 4781 - 4849	K.LATQSNEITIPVTFESR.A	1907.11412	2	2.82E-04	0.19	2.67	-	193.1
AHQ-3-11, 4594	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.02E-04	0.56	2.81	-	240.2
AHQ-3-14-, 4760 - 4767	K.LATQSNEITIPVTFESR.A	1907.11412	2	7.48E-04	0.68	3.36	-	235.6
AHQ-3-11, 4432 - 4439	R.LFDQAFGLPR.L	1164.33793	2	1.52E-07	0.97	4.37	-	1585.5
AHQ-3-10, 4254	R.LFDQAFGLPR.L	1164.33793	2	1.13E-06	0.97	4.14	-	1759.3
AHQ-3-10, 6242 - 6256	R.LPEEWSQWLGGSSWPGYVR.P	2235.44173	2	3.13E-07	0.95	4.61	-	975.5
AHQ-3-11, 6428 - 6508	R.LPEEWSQWLGGSSWPGYVR.P	2235.44173	2	5.87E-07	0.94	4.09	-	1031.6
AHQ-3-10, 6442 - 6443	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	1.00E-30	0.97	6.33	-	1193.9
AHQ-3-11, 6596 - 6634	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	1.00E-30	0.97	5.89	-	1417.6
AHQ-3-14-, 6709	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	8.92E-05	0.82	3.68	-	497.8
AHQ-3-11, 3983	R.PLPPAAIESPAVAAPAYSR.A	1879.14874	2	9.38E-10	0.96	4.81	-	933.3
AHQ-3-10, 3828 - 3839	R.PLPPAAIESPAVAAPAYSR.A	1879.14874	2	9.65E-12	0.93	4.33	-	648.7
AHQ-3-11, 1775	K.TKDGVVEITGK.H	1147.30399	1	8.04E-04	0.23	2.07	-	367.4
AHQ-3-13, 4854 - 4929	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.88E-08	0.94	4.33	-	1008.7
AHQ-3-14, 5699 - 5700	R.VSLDVNHFAPDELTVK.T	1784.99058	2	3.52E-10	0.97	5.51	-	1281.3
AHQ-3-11, 4444 - 4506	R.VSLDVNHFAPDELTVK.T	1784.99058	2	8.17E-09	0.96	4.84	-	1128.5
AHQ-3-13-, 4603 - 4614	R.VSLDVNHFAPDELTVK.T	1784.99058	2	3.64E-10	0.97	5.35	-	1568.1
AHQ-3-13, 4621	R.VSLDVNHFAPDELTVK.T	1784.99058	3	1.58E-07	0.79	3.65	-	525.6
AHQ-3-13, 4595	R.VSLDVNHFAPDELTVK.T	1784.99058	2	6.95E-09	0.94	4.26	-	1253.5
AHQ-3-14-, 4564 - 4635	R.VSLDVNHFAPDELTVK.T	1784.99058	2	7.00E-05	0.95	5.05	-	998.0
AHQ-3-14-, 4591 - 4639	R.VSLDVNHFAPDELTVK.T	1784.99058	3	1.53E-05	0.67	3.26	-	408.2
AHQ-3-10, 4240	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.48E-05	0.89	3.67	-	818.7
AHQ-3-11, 4630	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.77E-07	0.89	4.04	-	889.7
gi|4507149|ref|NP_000445.1|	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult			1.00E-30	4.69	50.42	57.80	15935.7
AHQ-3-12, 5327	K.AVCVLKGDGPVQGIINFEQK.E	2174.50602	2	3.78E-07	0.96	5.07	-	996.7
AHQ-3-11, 5070	K.AVCVLKGDGPVQGIINFEQK.E	2174.50602	2	2.80E-07	0.95	4.68	-	952.9
AHQ-3-12, 4340 - 4354	K.GDGPVQGIINFEQK.E	1502.65366	2	3.95E-07	0.85	3.31	-	687.5
AHQ-3-12, 4483 - 4496	K.GDGPVQGIINFEQK.E	1502.65366	2	1.87E-05	0.71	3.17	-	505.1
AHQ-3-12, 4851 - 4875	K.GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR.K	3522.76733	3	9.44E-13	0.98	8.37	-	2732.0
AHQ-3-12, 2055 - 2060	R.HVGDLGNVTADK.D	1226.32129	2	5.17E-06	0.93	3.96	-	709.6
AHQ-3-11, 5726 - 5730	R.HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR.T	3724.02282	3	1.00E-30	0.98	8.42	-	1675.4
gi|5729770|ref|NP_000382.3|	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky			1.00E-30	1.88	20.31	7.30	61247.6
AHQ-3-8, 2574 - 2581	R.LFGGNFAHQASVAR.V	1475.63637	2	5.46E-04	0.90	3.89	-	712.5
AHQ-3-8, 7252	R.VPIPWVSGTSASTPVFGGILSLINEHR.I	2836.23725	3	1.00E-30	0.97	6.14	-	1977.3
gi|16753233|ref|NP_006280.2|	talin 1 [Homo sapiens]			5.55E-16	110.44	1270.39	56.60	269665.3
AHQ-3-1, 3284	K.AAAFEEQENETVVVK.E	1664.79496	2	2.66E-05	0.85	3.60	-	939.4
AHQ-3-1, 3482 - 3541	K.AAAFEEQENETVVVK.E	1664.79496	2	2.85E-05	0.84	3.74	-	755.0

AHQ-3-1, 3621	K.AAAFEEQENETVVVK.E	1664.79496	2	4.63E-05	0.87	3.75	-	777.4
AHQ-3-2, 3343 - 3413	K.AAAFEEQENETVVVK.E	1664.79496	2	1.93E-07	0.92	4.64	-	893.5
AHQ-3-13, 3187	K.AAAFEEQENETVVVK.E	1664.79496	2	3.85E-05	0.55	2.79	-	347.3
AHQ-3-1, 2692	R.AAM*EPIVISAK.T	1146.38260	2	1.05E-05	0.72	2.68	-	613.8
AHQ-3-5, 2335	R.AAM*EPIVISAK.T	1146.38260	1	1.30E-04	0.52	2.34	-	258.8
AHQ-3-5, 2943 - 2948	R.AAMEPIVISAK.T	1130.38320	2	1.67E-04	0.65	2.70	-	414.8
AHQ-3-6, 2902	R.AAMEPIVISAK.T	1130.38320	2	3.31E-04	0.56	2.66	-	357.0
AHQ-3-3, 2482 - 2486	R.AAM*EPIVISAK.T	1146.38260	2	1.08E-05	0.87	3.03	-	823.9
AHQ-3-3, 2480	R.AAM*EPIVISAK.T	1146.38260	1	9.24E-05	0.23	2.36	-	125.0
AHQ-3-2, 2485 - 2502	R.AAM*EPIVISAK.T	1146.38260	1	9.64E-04	0.11	1.84	-	158.2
AHQ-3-2, 2490	R.AAM*EPIVISAK.T	1146.38260	2	8.72E-06	0.88	3.00	-	919.9
AHQ-3-4, 2466	R.AAM*EPIVISAK.T	1146.38260	2	4.10E-07	0.87	2.89	-	835.0
AHQ-3-2, 1835	K.ADAEGESDLENSR.K	1393.35296	2	1.67E-06	0.87	3.35	-	759.8
AHQ-3-4, 1901	K.ADAEGESDLENSR.K	1393.35296	2	2.39E-06	0.91	3.56	-	1017.5
AHQ-3-5, 1693	K.ADAEGESDLENSR.K	1393.35296	2	6.35E-04	0.86	3.07	-	850.6
AHQ-3-4, 2562	K.AGALQCSPSDAYTK.K	1470.58689	2	7.75E-04	0.92	3.56	-	887.0
AHQ-3-3, 2580	K.AGALQCSPSDAYTK.K	1470.58689	2	1.65E-06	0.83	3.57	-	610.6
AHQ-3-3, 2589	K.AGALQCSPSDAYTK.K	1470.58689	1	8.29E-05	0.78	3.87	-	471.5
AHQ-3-4, 2558 - 2564	K.AGALQCSPSDAYTK.K	1470.58689	1	4.51E-05	0.83	3.01	-	761.8
AHQ-3-1, 2453	K.AGALQCSPSDAYTKK.E	1598.75981	2	6.13E-05	0.72	3.10	-	513.7
AHQ-3-7, 6039	K.AGFLDLKDFLPK.E	1364.61374	2	4.04E-04	0.92	3.83	-	1270.3
AHQ-3-4, 4050	K.AIAVTVQEMVTK.S	1290.55498	2	1.90E-04	0.84	2.89	-	792.6
AHQ-3-2, 4065	K.AIAVTVQEMVTK.S	1290.55498	2	6.67E-06	0.96	4.73	-	1075.7
AHQ-3-1, 4210	K.AIAVTVQEMVTK.S	1290.55498	2	5.17E-05	0.94	3.77	-	1236.2
AHQ-3-3, 4014 - 4022	K.AIAVTVQEMVTK.S	1290.55498	2	4.57E-04	0.95	4.45	-	1181.5
AHQ-3-2, 4157 - 4158	K.AIAVTVQEMVTK.S	1290.55498	2	3.47E-04	0.92	3.56	-	1284.4
AHQ-3-4, 3932	K.AIAVTVQEMVTK.S	1290.55498	2	1.21E-04	0.89	3.39	-	1047.3
AHQ-3-1, 3029	K.AIAVTVQEM*VTK.S	1306.55438	2	5.52E-05	0.94	3.73	-	1142.0
AHQ-3-2, 2461 - 2462	K.ALDGAFTEENR.A	1223.27427	2	6.63E-05	0.95	3.69	-	1423.2
AHQ-3-1, 2589	K.ALDGAFTEENR.A	1223.27427	2	1.91E-07	0.94	3.50	-	1436.9
AHQ-3-4, 2445	K.ALDGAFTEENR.A	1223.27427	2	1.52E-06	0.92	3.40	-	1301.8
AHQ-3-3, 2445	K.ALDGAFTEENR.A	1223.27427	2	3.64E-06	0.94	3.69	-	1424.3
AHQ-3-4, 2566 - 2568	K.ALDGAFTEENR.A	1223.27427	2	8.91E-06	0.94	3.72	-	1413.7
AHQ-3-1, 2746	K.ALDGAFTEENR.A	1223.27427	2	5.29E-07	0.93	3.54	-	1534.3
AHQ-3-7, 3602	K.ALDYYMLR.N	1045.23686	2	8.42E-05	0.92	3.04	-	1003.6
AHQ-3-13, 3918 - 3921	K.ALDYYMLR.N	1045.23686	1	2.23E-04	0.32	1.95	-	258.8
AHQ-3-13-, 3935	K.ALDYYMLR.N	1045.23686	2	2.50E-06	0.93	3.28	-	928.9
AHQ-3-7, 4210	K.ALDYYMLRNGDTMEYR.K	2012.25579	2	6.45E-04	0.54	2.70	-	514.3
AHQ-3-3, 1801 - 1874	R.ALEATTEHIR.Q	1141.25953	2	2.25E-05	0.66	2.73	-	728.4
AHQ-3-2, 1738 - 1805	R.ALEATTEHIR.Q	1141.25953	1	4.36E-05	0.07	2.04	-	251.0
AHQ-3-5, 1616	R.ALEATTEHIR.Q	1141.25953	2	4.71E-04	0.85	3.26	-	951.1
AHQ-3-1, 3565	K.ALGDLISATK.A	989.14811	2	2.05E-04	0.93	3.34	-	947.1
AHQ-3-5, 3243	K.ALGDLISATK.A	989.14811	2	7.60E-07	0.92	4.02	-	713.2
AHQ-3-7, 3127	K.ALGDLISATK.A	989.14811	2	2.45E-04	0.82	2.65	-	729.0
AHQ-3-2, 3447	K.ALGDLISATK.A	989.14811	2	8.98E-07	0.91	3.73	-	829.4
AHQ-3-4, 3408	K.ALGDLISATK.A	989.14811	2	6.20E-06	0.94	3.65	-	958.2
AHQ-3-3, 3440	K.ALGDLISATK.A	989.14811	2	2.92E-06	0.88	3.18	-	777.9
AHQ-3-6, 3189	K.ALGDLISATK.A	989.14811	2	6.43E-07	0.92	3.57	-	859.9
AHQ-3-7, 2358	K.ALSTDPAAPNLK.S	1198.35099	2	3.87E-06	0.72	2.82	-	727.4
AHQ-3-1, 2733	K.ALSTDPAAPNLK.S	1198.35099	2	3.62E-07	0.79	3.02	-	620.7
AHQ-3-3, 2550	K.ALSTDPAAPNLK.S	1198.35099	2	1.27E-06	0.65	2.73	-	604.2
AHQ-3-6, 2406 - 2410	K.ALSTDPAAPNLK.S	1198.35099	2	1.57E-06	0.77	3.06	-	618.0
AHQ-3-2, 2557 - 2566	K.ALSTDPAAPNLK.S	1198.35099	2	1.29E-07	0.82	3.44	-	593.6
AHQ-3-3, 3568	K.ALSTDPAAPNLKSQLAAAAR.A	1967.21592	2	6.86E-08	0.80	3.33	-	469.6
AHQ-3-2, 7750	R.ANQAIQMACQSLGEPGCTQAQVLSAATIVAK.H	3220.64522	3	7.59E-04	0.92	5.08	-	844.2
AHQ-3-1, 6232 - 6304	R.ANQAIQM*ACQSLGEPGCTQAQVLSAATIVAK.H	3236.64462	3	1.72E-04	0.88	4.53	-	817.5
AHQ-3-1, 6450	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.21E-04	0.72	2.85	-	604.8
AHQ-3-2, 6515	K.APGQLECETAIAALNSCLR.D	2077.32566	2	4.57E-07	0.95	4.80	-	1164.0
AHQ-3-3, 6448	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.94E-07	0.96	4.31	-	1518.8
AHQ-3-3, 6721	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.99E-10	0.93	4.11	-	821.8
AHQ-3-3, 5758	K.APGQLECETAIAALNSCLR.D	2077.32566	2	5.15E-08	0.95	4.42	-	1119.8
AHQ-3-4, 6461	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.64E-07	0.96	5.04	-	1253.4
AHQ-3-2, 5821 - 5826	K.APGQLECETAIAALNSCLR.D	2077.32566	2	6.03E-09	0.97	4.65	-	1483.2
AHQ-3-1, 6676	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.13E-05	0.56	3.24	-	482.7
AHQ-3-2, 7178	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	5.62E-04	0.91	4.42	-	1227.5
AHQ-3-1, 6169	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	1.77E-04	0.89	4.51	-	856.5
AHQ-3-3, 7085 - 7089	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.09E-05	0.96	5.05	-	1997.5
AHQ-3-4, 7096 - 7097	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.36E-04	0.96	5.39	-	1629.4
AHQ-3-1, 7004	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	2	3.60E-06	0.77	3.14	-	768.6
AHQ-3-1, 7012	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	9.31E-06	0.96	5.15	-	1639.9
AHQ-3-3, 7084	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	2	1.24E-04	0.77	3.17	-	601.0
AHQ-3-5, 2684	K.ASAGPQPLLVQSCK.A	1457.67763	1	8.13E-10	0.67	3.65	-	342.2
AHQ-3-6, 2691	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.00E-06	0.58	3.08	-	377.7
AHQ-3-2, 2879 - 2883	K.ASAGPQPLLVQSCK.A	1457.67763	1	7.86E-04	0.17	2.13	-	465.2
AHQ-3-4, 2810	K.ASAGPQPLLVQSCK.A	1457.67763	2	4.94E-05	0.81	3.45	-	392.2
AHQ-3-3, 2864	K.ASAGPQPLLVQSCK.A	1457.67763	2	3.82E-05	0.86	3.39	-	506.4
AHQ-3-2, 2859 - 2937	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.22E-06	0.86	3.47	-	456.5
AHQ-3-4, 2834	K.ASAGPQPLLVQSCK.A	1457.67763	1	3.16E-07	0.65	3.44	-	383.9
AHQ-3-1, 3014 - 3084	K.ASAGPQPLLVQSCK.A	1457.67763	2	5.85E-07	0.83	3.26	-	453.9
AHQ-3-1, 3073 - 3078	K.ASAGPQPLLVQSCK.A	1457.67763	1	2.90E-05	0.19	2.22	-	403.6
AHQ-3-3, 2886	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.84E-05	0.65	3.10	-	457.3
AHQ-3-5, 2644 - 2715	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.11E-05	0.65	2.85	-	371.6
AHQ-3-7, 2528 - 2584	K.ASAGPQPLLVQSCK.A	1457.67763	2	8.44E-04	0.43	2.67	-	356.9
AHQ-3-3, 4605	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.07E-09	0.91	4.19	-	650.9
AHQ-3-3, 4881	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	4.74E-08	0.84	3.83	-	418.2
AHQ-3-2, 4938	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.40E-11	0.83	3.75	-	401.4
AHQ-3-7, 4079	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	4.99E-05	0.90	4.62	-	494.7
AHQ-3-1, 4454	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.59E-04	0.70	2.80	-	641.9
AHQ-3-3, 4389 - 4461	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.48E-06	0.82	3.84	-	404.0
AHQ-3-2, 4425 - 4493	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.87E-06	0.96	4.77	-	1321.2
AHQ-3-2, 4561 - 4629	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	9.54E-10	0.96	5.51	-	736.5
AHQ-3-3, 3776	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.08E-04	0.92	3.97	-	1082.8
AHQ-3-4, 4325 - 4396	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	8.17E-04	0.85	3.55	-	541.6
AHQ-3-4, 4464	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	6.45E-06	0.90	4.05	-	713.9
AHQ-3-2, 3633	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	5.11E-05	0.70	2.89	-	455.9
AHQ-3-6, 4107	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.37E-08	0.87	3.82	-	588.9
AHQ-3-2, 3983 - 3990	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.82E-05	0.95	4.77	-	858.2
AHQ-3-2, 4093	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	7.94E-06	0.83	3.80	-	380.0
AHQ-3-5, 4376	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.41E-05	0.75	3.69	-	376.0
AHQ-3-5, 4203	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.49E-04	0.88	3.84	-	539.7
AHQ-3-5, 3599	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	5.14E-06	0.72	3.23	-	342.1
AHQ-3-6, 3538	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	6.08E-07	0.85	3.51	-	615.6
AHQ-3-1, 3857 - 3872	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.29E-04	0.87	3.72	-	548.5
AHQ-3-3, 5058 - 5076	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.94E-08	0.93	4.56	-	719.7
AHQ-3-4, 4985 - 5013	K.AVAEQIPLLVQGVR.G	1493.77619	2	4.50E-11	0.93	4.49	-	703.5
AHQ-3-2, 5007 - 5085	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.33E-04	0.90	4.10	-	632.8
AHQ-3-5, 4815	K.AVAEQIPLLVQGVR.G	1493.77619	1	2.81E-04	0.43	2.79	-	324.5

AHQ-3-5, 4829	K.AVAEQIPLLVQGVR.G	1493.77619	1	1.12E-08	0.34	2.35	-	158.6
AHQ-3-2, 5394	K.AVAEQIPLLVQGVR.G	1493.77619	2	5.08E-04	0.74	2.77	-	716.6
AHQ-3-5, 4803 - 4873	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.03E-05	0.83	3.50	-	537.8
AHQ-3-3, 5064 - 5066	K.AVAEQIPLLVQGVR.G	1493.77619	1	3.85E-04	0.54	3.14	-	374.9
AHQ-3-2, 3917	K.AVASAAAALVLK.A	1085.32216	2	4.28E-05	0.96	4.27	-	1577.6
AHQ-3-1, 4046	K.AVASAAAALVLK.A	1085.32216	2	1.10E-05	0.95	4.22	-	1347.6
AHQ-3-2, 4985 - 5055	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.79E-06	0.93	4.25	-	1032.0
AHQ-3-2, 4369 - 4399	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.76E-06	0.89	3.80	-	1052.2
AHQ-3-2, 3963	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.28E-05	0.87	3.91	-	770.8
AHQ-3-1, 4216 - 4292	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.81E-06	0.66	2.94	-	1047.1
AHQ-3-2, 4455 - 4475	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.71E-06	0.95	4.57	-	1361.9
AHQ-3-2, 4265 - 4298	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.98E-07	0.94	4.77	-	1164.3
AHQ-3-4, 4244	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.23E-08	0.59	2.87	-	670.7
AHQ-3-1, 3992	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	8.64E-05	0.96	4.61	-	1522.2
AHQ-3-1, 4233	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	3	5.45E-07	0.90	3.80	-	1354.2
AHQ-3-6, 7201 - 7206	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.52E-13	0.97	5.59	-	1594.6
AHQ-3-3, 7414 - 7416	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	4.97E-07	0.96	4.91	-	1856.4
AHQ-3-1, 5877 - 5886	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	5.61E-04	0.88	4.48	-	486.9
AHQ-3-4, 4873	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	6.09E-06	0.58	2.96	-	308.6
AHQ-3-2, 5921	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	8.72E-06	0.82	3.73	-	459.4
AHQ-3-6, 6037	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	2.41E-04	0.74	3.66	-	479.1
AHQ-3-2, 4894 - 4965	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	2.44E-09	0.86	4.08	-	393.5
AHQ-3-3, 5804 - 5873	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	2.18E-04	0.56	3.70	-	397.5
AHQ-3-3, 4912	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	6.92E-08	0.78	3.90	-	398.3
AHQ-3-1, 6012 - 6090	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.86E-07	0.93	5.29	-	887.1
AHQ-3-5, 6327	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	9.20E-13	0.92	4.73	-	1123.5
AHQ-3-2, 6065	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	8.52E-10	0.95	5.07	-	1272.7
AHQ-3-4, 5890 - 5952	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.93E-05	0.93	5.40	-	961.3
AHQ-3-3, 6340 - 6422	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.22E-11	0.94	5.24	-	915.2
AHQ-3-4, 6294 - 6364	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	8.68E-09	0.90	4.30	-	946.0
AHQ-3-1, 6302 - 6346	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	4.97E-11	0.86	4.04	-	706.4
AHQ-3-5, 6219	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.95E-08	0.87	4.50	-	839.6
AHQ-3-3, 2385	R.CVSCLPGQR.D	1079.23309	1	5.70E-04	0.10	2.11	-	89.2
AHQ-3-5, 2285 - 2291	R.CVSCLPGQR.D	1079.23309	1	6.14E-04	0.15	1.97	-	93.6
AHQ-3-4, 2380	R.CVSCLPGQR.D	1079.23309	1	7.70E-05	0.43	2.02	-	222.6
AHQ-3-10, 3403 - 3404	R.DDILNGSHPVSFDK.A	1544.64741	2	8.80E-06	0.89	3.75	-	791.8
AHQ-3-9, 3139	R.DDILNGSHPVSFDK.A	1544.64741	2	9.56E-09	0.91	3.90	-	877.7
AHQ-3-10, 3234 - 3239	R.DDILNGSHPVSFDK.A	1544.64741	2	1.02E-09	0.85	3.30	-	724.6
AHQ-3-7, 3448 - 3463	R.DDILNGSHPVSFDK.A	1544.64741	2	7.31E-09	0.93	4.22	-	1053.6
AHQ-3-7, 3314 - 3322	R.DDILNGSHPVSFDK.A	1544.64741	2	9.61E-09	0.95	4.18	-	1199.2
AHQ-3-4, 3541	R.DDILNGSHPVSFDK.A	1544.64741	2	7.98E-07	0.72	3.13	-	553.3
AHQ-3-2, 6458 - 6529	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.16E-12	0.97	5.10	-	1460.9
AHQ-3-2, 6318 - 6326	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	2.16E-06	0.84	4.24	-	1027.8
AHQ-3-2, 5471 - 5541	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.33E-09	0.90	4.30	-	775.3
AHQ-3-6, 5981 - 6050	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.06E-07	0.91	3.80	-	889.7
AHQ-3-2, 6537	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	6.18E-04	0.68	3.74	-	634.7
AHQ-3-3, 5382 - 5454	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	9.13E-06	0.86	3.45	-	980.7
AHQ-3-2, 5979 - 6053	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	8.51E-10	0.93	4.19	-	1000.0
AHQ-3-4, 5366 - 5437	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.42E-11	0.93	4.09	-	1235.8
AHQ-3-3, 6249 - 6274	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.29E-07	0.93	4.15	-	992.7
AHQ-3-3, 6005	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.29E-04	0.78	2.96	-	759.6
AHQ-3-5, 6403	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	7.22E-15	0.91	3.71	-	1003.1
AHQ-3-4, 6225 - 6292	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.68E-12	0.93	4.45	-	676.8
AHQ-3-4, 6244	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.74E-08	0.85	3.57	-	619.9
AHQ-3-9, 5643	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.50E-08	0.89	3.55	-	1010.9
AHQ-3-5, 6115 - 6124	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	2.20E-04	0.85	3.75	-	1120.6
AHQ-3-5, 6107	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	9.60E-12	0.96	4.98	-	1126.0
AHQ-3-3, 6372	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.82E-06	0.76	3.35	-	636.5
AHQ-3-2, 5870 - 5937	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.90E-10	0.94	4.37	-	1173.3
AHQ-3-1, 5517	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.74E-09	0.91	4.15	-	908.8
AHQ-3-4, 6410 - 6488	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.40E-11	0.97	5.21	-	1226.9
AHQ-3-3, 6481	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.35E-09	0.72	2.98	-	517.6
AHQ-3-1, 6241	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	9.89E-08	0.96	4.78	-	1027.4
AHQ-3-5, 5308	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.79E-11	0.93	4.22	-	975.8
AHQ-3-2, 5594	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.27E-06	0.90	3.95	-	1108.2
AHQ-3-3, 5413 - 5472	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.54E-07	0.90	3.25	-	1291.2
AHQ-3-2, 5542	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.71E-08	0.94	4.25	-	1796.5
AHQ-3-4, 5516 - 5590	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.07E-10	0.85	3.27	-	1295.6
AHQ-3-2, 5486 - 5523	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.42E-04	0.94	4.45	-	1123.3
AHQ-3-4, 5398 - 5468	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	7.28E-07	0.97	5.64	-	1042.8
AHQ-3-1, 5494	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	1.16E-06	0.91	4.70	-	1406.5
AHQ-3-3, 5489	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.70E-07	0.90	3.89	-	1685.7
AHQ-3-1, 3737	R.DPPSWSVLAGHSR.T	1409.53156	3	2.30E-06	0.84	3.43	-	741.6
AHQ-3-6, 3219 - 3221	R.DPPSWSVLAGHSR.T	1409.53156	2	3.48E-06	0.84	3.46	-	485.0
AHQ-3-3, 3528 - 3561	R.DPPSWSVLAGHSR.T	1409.53156	2	2.38E-08	0.87	3.12	-	462.7
AHQ-3-1, 3729	R.DPPSWSVLAGHSR.T	1409.53156	2	6.26E-10	0.86	3.34	-	484.1
AHQ-3-2, 3553 - 3599	R.DPPSWSVLAGHSR.T	1409.53156	2	9.30E-11	0.92	3.73	-	654.4
AHQ-3-4, 3482	R.DPPSWSVLAGHSR.T	1409.53156	2	7.52E-07	0.84	2.81	-	585.3
AHQ-3-10, 4715	R.DPVQLNLLYVQAR.D	1529.76539	2	9.13E-08	0.97	5.34	-	1495.7
AHQ-3-7, 5128 - 5206	R.DPVQLNLLYVQAR.D	1529.76539	2	7.34E-06	0.96	4.26	-	1706.7
AHQ-3-9, 4861	R.DPVQLNLLYVQAR.D	1529.76539	2	2.88E-04	0.93	4.34	-	1110.6
AHQ-3-2, 2381	K.EAAYHPEVAPDVR.L	1454.56910	1	1.73E-05	0.20	1.88	-	252.3
AHQ-3-3, 2369 - 2370	K.EAAYHPEVAPDVR.L	1454.56910	1	1.26E-04	0.76	2.88	-	574.8
AHQ-3-4, 2353	K.EAAYHPEVAPDVR.L	1454.56910	1	2.85E-04	0.13	1.90	-	242.0
AHQ-3-4, 2356	K.EAAYHPEVAPDVR.L	1454.56910	1	1.34E-07	0.56	2.48	-	347.0
AHQ-3-4, 2350 - 2352	K.EAAYHPEVAPDVR.L	1454.56910	2	2.73E-06	0.81	2.83	-	786.8
AHQ-3-2, 2390	K.EAAYHPEVAPDVR.L	1454.56910	1	9.59E-10	0.86	3.40	-	485.1
AHQ-3-4, 6181 - 6252	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.32E-05	0.95	4.72	-	1299.2
AHQ-3-3, 6205 - 6276	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.93E-09	0.97	5.23	-	1498.9
AHQ-3-4, 5948	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.82E-06	0.92	4.28	-	976.0
AHQ-3-4, 6320 - 6388	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.08E-08	0.95	4.74	-	1099.6
AHQ-3-3, 6345 - 6392	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.71E-05	0.97	5.29	-	1619.6
AHQ-3-2, 6635	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.04E-08	0.96	4.78	-	1205.6
AHQ-3-2, 6743 - 6781	K.EADESLNFEEQILEAAK.S	1937.05072	2	9.35E-05	0.62	3.28	-	555.0
AHQ-3-2, 6855	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.48E-05	0.95	4.40	-	1268.5
AHQ-3-3, 6461	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.39E-05	0.84	3.64	-	784.1
AHQ-3-2, 7334	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.11E-05	0.48	2.89	-	547.1
AHQ-3-2, 6145 - 6198	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.07E-06	0.91	4.61	-	953.9
AHQ-3-1, 6329 - 6398	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.21E-05	0.94	5.11	-	848.6
AHQ-3-1, 6181 - 6248	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.16E-08	0.97	5.29	-	1587.8
AHQ-3-5, 6152	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.57E-05	0.95	4.70	-	1361.0
AHQ-3-5, 6297	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.55E-08	0.94	4.12	-	1419.9
AHQ-3-9, 5631	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.17E-09	0.94	4.18	-	1494.0
AHQ-3-1, 5908 - 5968	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.24E-04	0.48	2.69	-	485.5
AHQ-3-2, 6246 - 6313	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.98E-08	0.97	5.59	-	1779.9
AHQ-3-2, 7801	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.45E-06	0.70	3.05	-	635.8
AHQ-3-2, 6269	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.86E-05	0.92	4.85	-	960.2

AHQ-3-14-, 5752	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.44E-07	0.96	5.50	-	1290.5
AHQ-3-2, 6382 - 6453	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.43E-09	0.97	5.93	-	1278.9
AHQ-3-6, 6031	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.02E-04	0.88	3.79	-	1013.2
AHQ-3-4, 6412 - 6480	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.94E-05	0.82	3.52	-	734.7
AHQ-3-2, 6489 - 6561	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.23E-10	0.96	4.88	-	1484.9
AHQ-3-6, 7313	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	3.85E-06	0.95	4.91	-	1181.2
AHQ-3-2, 7617	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	8.22E-06	0.85	3.73	-	547.1
AHQ-3-9, 7008	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	3.24E-04	0.69	3.55	-	441.7
AHQ-3-5, 7503	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	9.83E-14	0.96	5.77	-	1268.3
AHQ-3-2, 7609	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	2.43E-08	0.93	4.98	-	1194.1
AHQ-3-4, 7548 - 7554	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	9.92E-08	0.96	5.73	-	1451.1
AHQ-3-3, 7528	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	2.25E-08	0.94	5.15	-	1165.3
AHQ-3-6, 7315 - 7327	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	1.96E-04	0.86	3.75	-	721.9
AHQ-3-3, 7521 - 7592	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	2.66E-08	0.96	6.01	-	1264.5
AHQ-3-4, 7545 - 7616	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	2.46E-04	0.94	5.37	-	1087.1
AHQ-3-7, 7446 - 7448	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	2.05E-12	0.95	5.90	-	1154.6
AHQ-3-3, 7420	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	9.52E-07	0.96	5.87	-	1341.7
AHQ-3-1, 7357	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.73E-10	0.96	5.79	-	1762.5
AHQ-3-10, 6635	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	4.63E-07	0.82	4.03	-	908.1
AHQ-3-11, 6808	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	5.76E-05	0.96	5.34	-	1580.6
AHQ-3-6, 7370	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	8.85E-07	0.95	5.52	-	1281.8
AHQ-3-2, 7509	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	7.77E-08	0.92	4.60	-	1050.2
AHQ-3-2, 7605 - 7678	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.01E-05	0.93	5.02	-	1085.7
AHQ-3-5, 7527	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.87E-07	0.93	5.04	-	970.7
AHQ-3-5, 7367 - 7412	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	4.29E-06	0.95	5.26	-	1210.2
AHQ-3-4, 7436 - 7480	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	4.22E-06	0.97	6.41	-	1236.6
AHQ-3-2, 7239 - 7305	R.ELLENPVQPINDMSYFGCLDSVM*ENSK.V	3148.48814	3	9.65E-05	0.76	3.89	-	389.1
AHQ-3-11, 2898	R.EQGVEEHETLLLR.R	1553.69898	2	7.28E-04	0.50	2.74	-	278.9
AHQ-3-7, 2714 - 2790	R.EQGVEEHETLLLR.R	1553.69898	2	4.85E-09	0.87	3.17	-	665.2
AHQ-3-8, 2570 - 2636	R.EQGVEEHETLLLR.R	1553.69898	2	1.63E-07	0.63	2.90	-	271.1
AHQ-3-1, 3252	R.EQGVEEHETLLLR.R	1553.69898	2	1.58E-04	0.74	3.00	-	509.8
AHQ-3-7, 5414	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	3.12E-07	0.97	6.54	-	1303.2
AHQ-3-13-, 5478 - 5494	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	1.07E-12	0.98	6.69	-	1956.8
AHQ-3-13, 5495 - 5509	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	5.40E-11	0.96	5.65	-	1377.1
AHQ-3-14-, 5487	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	4.60E-08	0.98	6.42	-	1963.5
AHQ-3-14-, 5083	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.47E-06	0.98	6.75	-	1726.3
AHQ-3-13-, 5121	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	3.83E-09	0.98	6.76	-	2165.6
AHQ-3-13, 5143 - 5154	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	5.27E-13	0.98	6.38	-	2535.6
AHQ-3-7, 4908 - 4930	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.23E-08	0.98	7.81	-	1875.9
AHQ-3-8, 4720	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	4.73E-04	0.97	5.63	-	1909.6
AHQ-3-3, 2282	K.EVANSTANLVK.T	1146.27608	1	1.99E-04	0.13	2.27	-	201.3
AHQ-3-4, 2177	K.EVANSTANLVK.T	1146.27608	1	2.12E-04	0.19	2.03	-	217.7
AHQ-3-4, 2292	K.EVANSTANLVK.T	1146.27608	1	8.06E-07	0.30	2.30	-	193.3
AHQ-3-1, 2310	K.EVANSTANLVK.T	1146.27608	1	9.83E-05	0.07	2.10	-	132.2
AHQ-3-7, 4470	K.EVIQEWNLTNIK.R	1487.68214	1	5.37E-04	0.71	3.71	-	244.1
AHQ-3-13, 4591 - 4669	K.EVIQEWNLTNIK.R	1487.68214	2	6.00E-05	0.54	2.76	-	549.2
AHQ-3-11, 4491 - 4510	K.EVIQEWNLTNIK.R	1487.68214	2	5.62E-06	0.67	2.98	-	680.5
AHQ-3-7, 4458 - 4478	K.EVIQEWNLTNIK.R	1487.68214	2	6.86E-07	0.91	3.94	-	1153.2
AHQ-3-7, 3799	K.EVIQEWNLTNIKR.W	1643.86849	2	3.49E-05	0.71	3.07	-	520.4
AHQ-3-7, 2782	K.FFYSDQNVDSR.D	1378.42795	1	2.26E-04	0.34	2.45	-	192.7
AHQ-3-7, 2775 - 2778	K.FFYSDQNVDSR.D	1378.42795	2	7.42E-09	0.92	3.72	-	1028.7
AHQ-3-9, 2680	K.FFYSDQNVDSR.D	1378.42795	2	4.17E-04	0.90	2.83	-	1261.8
AHQ-3-8, 2706	K.FFYSDQNVDSR.D	1378.42795	2	1.23E-05	0.91	3.24	-	1125.9
AHQ-3-7, 5915 - 5943	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	6.77E-09	0.95	4.73	-	1543.0
AHQ-3-7, 6014	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	1.30E-08	0.97	5.45	-	2064.5
AHQ-3-1, 6500 - 6580	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	4.16E-09	0.92	5.51	-	595.2
AHQ-3-5, 7557	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	3.01E-04	0.42	2.83	-	310.5
AHQ-3-3, 6573 - 6645	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	2.77E-05	0.84	3.58	-	804.8
AHQ-3-3, 6576 - 6644	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	5.78E-08	0.92	4.69	-	758.4
AHQ-3-2, 6647 - 6714	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	3.08E-10	0.95	5.35	-	1101.6
AHQ-3-2, 7479	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	7.53E-06	0.56	3.27	-	546.5
AHQ-3-2, 6642 - 6721	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	4.48E-06	0.86	3.70	-	898.2
AHQ-3-1, 2901	K.FLPSELRDEH	1243.35032	2	5.54E-06	0.55	2.67	-	375.8
AHQ-3-3, 5246 - 5252	K.GLAGAVSELLR.S	1086.26701	2	8.50E-06	0.98	5.12	-	2012.1
AHQ-3-8, 4520	K.GLAGAVSELLR.S	1086.26701	2	1.29E-04	0.97	5.06	-	1923.7
AHQ-3-4, 5138	K.GLAGAVSELLR.S	1086.26701	2	1.47E-06	0.98	5.32	-	2081.3
AHQ-3-7, 4735	K.GLAGAVSELLR.S	1086.26701	2	1.32E-06	0.97	4.23	-	1926.8
AHQ-3-5, 4961 - 4991	K.GLAGAVSELLR.S	1086.26701	2	4.18E-07	0.98	5.16	-	1956.7
AHQ-3-2, 5265	K.GLAGAVSELLR.S	1086.26701	2	2.11E-05	0.97	4.79	-	1814.2
AHQ-3-6, 4902	K.GLAGAVSELLR.S	1086.26701	2	1.69E-06	0.98	5.29	-	1966.0
AHQ-3-1, 5353 - 5386	K.GLAGAVSELLR.S	1086.26701	2	3.94E-06	0.98	5.21	-	2014.6
AHQ-3-2, 7410	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.13E-08	0.94	5.11	-	700.0
AHQ-3-2, 7355 - 7422	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.17E-08	0.79	3.68	-	770.9
AHQ-3-4, 6866 - 6944	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	7.50E-05	0.94	5.33	-	629.2
AHQ-3-4, 6869 - 6945	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.81E-08	0.91	4.83	-	869.8
AHQ-3-2, 7233 - 7311	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	3.98E-07	0.92	4.84	-	723.5
AHQ-3-3, 7206 - 7212	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.68E-07	0.82	3.82	-	398.8
AHQ-3-6, 6593 - 6657	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.05E-05	0.88	4.40	-	738.6
AHQ-3-11, 6208	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.28E-04	0.83	3.81	-	519.6
AHQ-3-2, 7005 - 7073	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.15E-05	0.93	4.76	-	1109.1
AHQ-3-2, 6993 - 7074	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	7.09E-07	0.97	6.25	-	1115.5
AHQ-3-1, 6825 - 6893	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.44E-04	0.85	4.00	-	650.3
AHQ-3-1, 6584	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	7.52E-07	0.52	3.49	-	577.8
AHQ-3-1, 6884 - 6950	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.28E-04	0.83	4.37	-	492.8
AHQ-3-5, 6717 - 6783	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.39E-04	0.88	4.09	-	633.3
AHQ-3-3, 7312	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.43E-05	0.90	3.93	-	844.8
AHQ-3-2, 6867 - 6937	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	6.15E-06	0.90	4.30	-	895.9
AHQ-3-2, 6861 - 6926	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.88E-04	0.92	3.87	-	1040.5
AHQ-3-3, 7316	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.18E-07	0.75	3.58	-	692.6
AHQ-3-5, 6731 - 6805	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.19E-04	0.91	4.23	-	1143.6
AHQ-3-10, 6662	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	7.61E-07	0.97	6.10	-	1665.0
AHQ-3-7, 7482 - 7483	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	8.33E-15	0.97	6.67	-	1421.3
AHQ-3-2, 7713 - 7789	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.54E-04	0.87	3.78	-	1561.2
AHQ-3-1, 7376	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	6.00E-14	0.96	5.87	-	1375.6
AHQ-3-4, 7602 - 7640	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	7.08E-11	0.95	5.27	-	1518.8
AHQ-3-6, 7401 - 7474	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.34E-11	0.96	5.84	-	1457.9
AHQ-3-3, 7472 - 7476	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	2.61E-11	0.98	6.59	-	3054.4
AHQ-3-4, 7492 - 7493	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.31E-09	0.98	7.13	-	2905.4
AHQ-3-1, 7256	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	2.44E-04	0.89	4.27	-	1009.9
AHQ-3-5, 7429 - 7435	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	5.02E-06	0.95	4.97	-	1522.1
AHQ-3-2, 7559 - 7563	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	6.88E-14	0.97	6.27	-	1534.7
AHQ-3-8, 7260 - 7261	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	7.73E-08	0.93	4.69	-	1088.5
AHQ-3-2, 7614	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.62E-07	0.95	5.04	-	1169.0
AHQ-3-3, 5900	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.17E-06	0.88	3.84	-	806.9
AHQ-3-11, 6758	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.64E-06	0.86	4.30	-	670.6
AHQ-3-2, 7537 - 7613	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.05E-07	0.93	4.88	-	718.9
AHQ-3-5, 5553	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.94E-05	0.88	4.27	-	803.9

AHQ-3-2, 5930	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.59E-08	0.93	4.98	-	726.8
AHQ-3-5, 7491	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	3.53E-08	0.92	4.29	-	1226.0
AHQ-3-7, 7386	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.17E-06	0.91	4.56	-	820.6
AHQ-3-9, 7011 - 7013	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.20E-04	0.93	5.04	-	675.3
AHQ-3-1, 7317	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.39E-05	0.93	5.17	-	687.7
AHQ-3-3, 7533 - 7534	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	8.42E-07	0.95	4.78	-	1227.7
AHQ-3-4, 7552	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	8.91E-05	0.88	3.98	-	827.2
AHQ-3-1, 6030	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.43E-04	0.90	4.14	-	939.1
AHQ-3-1, 7316	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.69E-06	0.84	3.36	-	899.3
AHQ-3-7, 7387	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.59E-09	0.94	4.79	-	1072.6
AHQ-3-3, 7532	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.74E-07	0.97	6.01	-	1139.7
AHQ-3-4, 5816	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	6.54E-05	0.81	4.05	-	483.4
AHQ-3-6, 7317 - 7318	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.88E-07	0.94	4.82	-	1229.7
AHQ-3-6, 7314	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.80E-05	0.94	5.50	-	744.2
AHQ-3-6, 5550	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.12E-07	0.94	4.64	-	868.8
AHQ-3-5, 7487	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	9.05E-06	0.96	5.65	-	976.9
AHQ-3-14-, 6829	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.35E-05	0.96	5.62	-	1033.3
AHQ-3-13-, 3302	R.IGITNHDEYSLVR.E	1517.66833	2	5.59E-08	0.95	4.15	-	1274.7
AHQ-3-10, 3048	R.IGITNHDEYSLVR.E	1517.66833	2	1.39E-08	0.91	3.06	-	1179.7
AHQ-3-4, 3232	R.IGITNHDEYSLVR.E	1517.66833	2	1.81E-04	0.52	2.65	-	724.6
AHQ-3-13-, 3697	R.IGITNHDEYSLVR.E	1517.66833	2	1.92E-08	0.89	3.53	-	738.0
AHQ-3-10, 3360	R.IGITNHDEYSLVR.E	1517.66833	2	3.91E-05	0.90	3.40	-	1016.3
AHQ-3-7, 2934	R.IGITNHDEYSLVR.E	1517.66833	3	8.29E-08	0.85	3.54	-	696.2
AHQ-3-7, 3272 - 3350	R.IGITNHDEYSLVR.E	1517.66833	2	4.14E-09	0.94	3.60	-	1505.7
AHQ-3-7, 3411	R.IGITNHDEYSLVR.E	1517.66833	3	1.95E-06	0.61	3.14	-	487.2
AHQ-3-13, 3298 - 3327	R.IGITNHDEYSLVR.E	1517.66833	2	8.89E-08	0.95	4.15	-	1383.9
AHQ-3-13, 3689	R.IGITNHDEYSLVR.E	1517.66833	2	2.12E-05	0.92	3.66	-	981.7
AHQ-3-7, 4774 - 4783	R.ILAQATSDLVNAIK.A	1457.69748	2	4.09E-06	0.96	4.16	-	1648.6
AHQ-3-6, 4870 - 4877	R.ILAQATSDLVNAIK.A	1457.69748	2	1.10E-08	0.97	4.79	-	1525.9
AHQ-3-6, 3931	R.ILAQATSDLVNAIK.A	1457.69748	2	4.64E-06	0.97	4.69	-	1625.0
AHQ-3-2, 4530	R.ILAQATSDLVNAIK.A	1457.69748	2	3.38E-06	0.97	4.50	-	2094.9
AHQ-3-3, 4236	R.ILAQATSDLVNAIK.A	1457.69748	2	3.98E-07	0.97	4.26	-	2000.3
AHQ-3-2, 4635	R.ILAQATSDLVNAIK.A	1457.69748	2	1.02E-08	0.96	4.44	-	1270.2
AHQ-3-2, 4257 - 4262	R.ILAQATSDLVNAIK.A	1457.69748	2	2.15E-06	0.96	4.30	-	1587.9
AHQ-3-2, 4734	R.ILAQATSDLVNAIK.A	1457.69748	2	1.71E-06	0.97	4.57	-	1687.0
AHQ-3-4, 4153	R.ILAQATSDLVNAIK.A	1457.69748	2	6.46E-06	0.97	4.56	-	1846.9
AHQ-3-5, 4955	R.ILAQATSDLVNAIK.A	1457.69748	2	5.49E-08	0.96	4.57	-	1513.3
AHQ-3-4, 4162	R.ILAQATSDLVNAIK.A	1457.69748	1	3.11E-05	0.69	2.59	-	695.8
AHQ-3-1, 4328	R.ILAQATSDLVNAIK.A	1457.69748	2	8.60E-08	0.75	2.75	-	917.6
AHQ-3-8, 4519	R.ILAQATSDLVNAIK.A	1457.69748	2	3.07E-09	0.96	4.45	-	1597.4
AHQ-3-2, 5225	R.ILAQATSDLVNAIK.A	1457.69748	1	1.60E-05	0.79	3.61	-	560.7
AHQ-3-4, 5084 - 5104	R.ILAQATSDLVNAIK.A	1457.69748	2	9.06E-04	0.93	3.07	-	1391.4
AHQ-3-4, 5100	R.ILAQATSDLVNAIK.A	1457.69748	1	1.77E-04	0.84	3.66	-	707.0
AHQ-3-1, 4585	R.ILAQATSDLVNAIK.A	1457.69748	2	1.83E-05	0.72	2.50	-	886.6
AHQ-3-7, 3887	R.ILAQATSDLVNAIK.A	1457.69748	2	3.12E-07	0.87	3.18	-	1079.2
AHQ-3-2, 5171 - 5251	R.ILAQATSDLVNAIK.A	1457.69748	2	1.79E-09	0.97	5.36	-	1536.5
AHQ-3-5, 4973	R.ILAQATSDLVNAIK.A	1457.69748	1	1.49E-04	0.82	3.68	-	751.1
AHQ-3-3, 5184	R.ILAQATSDLVNAIK.A	1457.69748	2	1.26E-11	0.97	4.96	-	1835.9
AHQ-3-3, 5201	R.ILAQATSDLVNAIK.A	1457.69748	1	8.00E-04	0.70	2.97	-	538.1
AHQ-3-14, 6017	R.ILAQATSDLVNAIK.A	1457.69748	2	2.88E-04	0.92	3.70	-	1079.6
AHQ-3-1, 5244	R.ILAQATSDLVNAIK.A	1457.69748	2	1.44E-08	0.98	5.10	-	2325.4
AHQ-3-13, 5882 - 5885	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.18E-04	0.95	5.32	-	817.5
AHQ-3-1, 6266	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	5.07E-04	0.82	3.43	-	495.0
AHQ-3-13-, 5786 - 5855	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	8.88E-06	0.98	5.68	-	1470.0
AHQ-3-12, 5872	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	5.09E-05	0.90	4.33	-	633.9
AHQ-3-14-, 5785	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	4.13E-04	0.95	4.62	-	906.0
AHQ-3-10, 5371 - 5450	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	9.75E-05	0.92	4.08	-	859.7
AHQ-3-7, 5902 - 5966	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.87E-06	0.95	4.77	-	939.8
AHQ-3-13-, 5329 - 5393	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.07E-11	0.94	5.00	-	1361.9
AHQ-3-12, 5408 - 5487	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	7.66E-08	0.89	3.76	-	1448.6
AHQ-3-11, 5156	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	8.67E-13	0.95	4.83	-	1435.6
AHQ-3-14-, 5343 - 5408	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	3.88E-05	0.97	5.52	-	2118.4
AHQ-3-13, 5409 - 5437	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	6.18E-05	0.93	4.18	-	1694.7
AHQ-3-7, 5263 - 5292	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	5.20E-09	0.97	5.60	-	1905.3
AHQ-3-7, 1476	K.KEEITGTLR.K	1047.18765	1	6.46E-05	0.28	2.24	-	350.9
AHQ-3-7, 2024	K.KGIWLEAGK.A	1002.19171	2	1.11E-04	0.88	3.33	-	794.3
AHQ-3-7, 2367	R.KIFQAHKNCGQMSEIEAK.V	2121.42671	2	8.44E-05	0.87	3.99	-	775.0
AHQ-3-4, 1456	K.KLEQLKPR.A	1012.23127	1	5.55E-04	0.16	2.22	-	195.0
AHQ-3-1, 2808 - 2824	K.LAQAAQSSVATITR.L	1417.59344	2	7.56E-11	0.94	4.09	-	1345.5
AHQ-3-3, 2632 - 2633	K.LAQAAQSSVATITR.L	1417.59344	2	2.59E-10	0.98	5.39	-	2014.8
AHQ-3-12, 2683 - 2762	K.LAQAAQSSVATITR.L	1417.59344	2	1.28E-09	0.96	3.85	-	1680.6
AHQ-3-6, 2471	K.LAQAAQSSVATITR.L	1417.59344	2	2.63E-07	0.98	5.09	-	1741.9
AHQ-3-3, 2637	K.LAQAAQSSVATITR.L	1417.59344	1	1.65E-05	0.52	3.37	-	159.2
AHQ-3-8, 2268	K.LAQAAQSSVATITR.L	1417.59344	2	3.83E-07	0.96	4.56	-	1370.6
AHQ-3-10, 2504	K.LAQAAQSSVATITR.L	1417.59344	2	2.32E-04	0.83	3.31	-	715.0
AHQ-3-11, 2572	K.LAQAAQSSVATITR.L	1417.59344	2	2.28E-09	0.95	3.54	-	1742.2
AHQ-3-6, 2478	K.LAQAAQSSVATITR.L	1417.59344	1	3.96E-04	0.25	2.66	-	159.4
AHQ-3-7, 2282	K.LAQAAQSSVATITR.L	1417.59344	2	5.17E-06	0.93	4.03	-	1137.9
AHQ-3-14-, 2641 - 2648	K.LAQAAQSSVATITR.L	1417.59344	2	5.23E-06	0.92	2.89	-	1336.9
AHQ-3-2, 2630 - 2702	K.LAQAAQSSVATITR.L	1417.59344	2	8.66E-14	0.97	5.58	-	1465.5
AHQ-3-5, 2483 - 2551	K.LAQAAQSSVATITR.L	1417.59344	2	4.37E-05	0.97	4.57	-	1715.4
AHQ-3-4, 2596 - 2598	K.LAQAAQSSVATITR.L	1417.59344	2	5.39E-11	0.98	5.28	-	1731.9
AHQ-3-7, 2415 - 2486	K.LAQAAQSSVATITR.L	1417.59344	2	8.43E-04	0.86	3.67	-	888.4
AHQ-3-4, 2901	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.34E-09	0.95	4.73	-	1042.1
AHQ-3-4, 3084 - 3106	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	7.67E-13	0.98	6.71	-	2822.5
AHQ-3-4, 3089	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.14E-07	0.90	4.35	-	480.4
AHQ-3-2, 3498	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.05E-09	0.93	4.67	-	1717.2
AHQ-3-5, 2899	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.51E-06	0.95	4.97	-	809.4
AHQ-3-3, 2932	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.50E-07	0.93	4.43	-	913.2
AHQ-3-9, 2699	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.80E-06	0.89	4.26	-	874.2
AHQ-3-2, 3151	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.52E-10	0.96	5.74	-	854.9
AHQ-3-2, 2947	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	8.46E-04	0.96	5.06	-	1190.3
AHQ-3-6, 2883	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.03E-09	0.97	6.06	-	1716.6
AHQ-3-1, 3358	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	7.43E-05	0.89	4.12	-	479.8
AHQ-3-6, 2895	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.91E-06	0.94	4.45	-	795.1
AHQ-3-3, 3142	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.66E-05	0.96	5.26	-	919.2
AHQ-3-3, 3144	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	6.12E-06	0.96	5.64	-	1594.8
AHQ-3-1, 3357 - 3390	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	4.30E-07	0.94	4.84	-	1428.3
AHQ-3-7, 2739 - 2814	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.78E-04	0.95	4.37	-	1854.9
AHQ-3-5, 2897	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.70E-09	0.96	5.84	-	1526.7
AHQ-3-2, 5423 - 5497	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.13E-11	0.96	5.11	-	1210.4
AHQ-3-7, 5431	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.89E-06	0.92	4.55	-	748.5
AHQ-3-2, 5779 - 5798	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.39E-04	0.96	5.05	-	1255.4
AHQ-3-2, 5863 - 5869	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.16E-14	0.97	5.52	-	1357.6
AHQ-3-6, 5509	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.56E-07	0.94	4.51	-	1043.7
AHQ-3-3, 5657 - 5733	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.23E-04	0.95	4.78	-	1087.8
AHQ-3-1, 5849 - 5870	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.01E-06	0.94	4.24	-	1056.4

AHQ-3-6, 5329 - 5361	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.80E-07	0.96	5.13	-	1152.1
AHQ-3-2, 5457	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.85E-05	0.94	4.74	-	1013.1
AHQ-3-6, 5099 - 5165	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.11E-07	0.93	4.25	-	913.5
AHQ-3-2, 5645	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	7.54E-09	0.97	5.52	-	2395.2
AHQ-3-3, 5506 - 5585	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.39E-06	0.96	5.16	-	1207.2
AHQ-3-5, 5588	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.35E-08	0.96	5.00	-	1151.1
AHQ-3-2, 5975 - 6047	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.65E-07	0.93	4.68	-	737.4
AHQ-3-2, 5589 - 5657	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.80E-10	0.96	4.98	-	1162.3
AHQ-3-4, 5344 - 5412	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.96E-10	0.97	5.51	-	1622.8
AHQ-3-5, 5415	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.09E-05	0.96	5.45	-	1079.8
AHQ-3-1, 5700 - 5709	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	3.18E-05	0.92	3.78	-	1602.7
AHQ-3-1, 5442 - 5509	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.93E-13	0.93	4.45	-	853.7
AHQ-3-10, 4864	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.20E-05	0.94	4.44	-	922.3
AHQ-3-2, 6058 - 6131	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.67E-04	0.70	3.25	-	479.6
AHQ-3-4, 5820	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.35E-05	0.82	3.88	-	430.0
AHQ-3-5, 5260 - 5333	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.11E-10	0.97	5.53	-	1116.1
AHQ-3-14-, 5251	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.64E-04	0.92	4.31	-	958.4
AHQ-3-4, 5541 - 5576	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.43E-08	0.97	5.69	-	1439.5
AHQ-3-4, 5454	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.23E-07	0.94	4.60	-	978.1
AHQ-3-1, 5690 - 5704	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.90E-04	0.96	4.81	-	1089.3
AHQ-3-7, 5094	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.17E-07	0.91	4.00	-	833.5
AHQ-3-7, 5262	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.60E-06	0.95	4.82	-	927.6
AHQ-3-5, 5385 - 5455	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.09E-04	0.97	5.22	-	1356.6
AHQ-3-3, 5422 - 5492	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.72E-08	0.96	5.10	-	1011.6
AHQ-3-3, 5797 - 5821	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.55E-10	0.95	4.58	-	1091.7
AHQ-3-7, 3368 - 3438	K.LHTDDELNWLDHGR.T	1721.81153	3	9.21E-04	0.81	3.81	-	532.3
AHQ-3-9, 3172 - 3176	K.LHTDDELNWLDHGR.T	1721.81153	2	1.74E-06	0.98	5.36	-	2226.1
AHQ-3-10, 3331 - 3408	K.LHTDDELNWLDHGR.T	1721.81153	2	1.19E-04	0.95	4.65	-	1154.5
AHQ-3-1, 4541	K.LLAALLEDEGGSGR.P	1401.54764	2	1.31E-04	0.98	4.46	-	2388.7
AHQ-3-1, 5512 - 5581	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.62E-06	0.96	5.90	-	1174.9
AHQ-3-4, 5302	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	8.24E-08	0.96	5.30	-	1594.4
AHQ-3-4, 5300	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.71E-08	0.97	5.76	-	1292.0
AHQ-3-5, 5095 - 5137	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.14E-08	0.98	6.58	-	1455.8
AHQ-3-9, 4696	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.05E-09	0.94	4.60	-	1131.8
AHQ-3-9, 4685	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	8.90E-07	0.97	5.75	-	1496.5
AHQ-3-7, 4892	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.87E-08	0.98	6.36	-	2348.3
AHQ-3-2, 5273	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.16E-05	0.91	4.42	-	522.3
AHQ-3-12, 5158 - 5159	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.84E-08	0.97	5.35	-	1548.3
AHQ-3-6, 5037 - 5039	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.44E-06	0.96	5.06	-	1648.5
AHQ-3-6, 5038 - 5049	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.58E-10	0.98	6.82	-	1546.6
AHQ-3-3, 5376	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.73E-07	0.95	5.46	-	1309.7
AHQ-3-10, 4666 - 4668	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.39E-08	0.98	6.64	-	1458.7
AHQ-3-8, 4531	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	9.35E-08	0.97	5.74	-	1826.1
AHQ-3-1, 5516	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.11E-14	0.98	6.82	-	1818.3
AHQ-3-2, 5401	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.42E-08	0.98	6.46	-	1700.7
AHQ-3-2, 5398 - 5433	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.31E-07	0.97	5.99	-	1429.8
AHQ-3-3, 5372	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	7.26E-09	0.97	5.71	-	1346.2
AHQ-3-12, 5162	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.77E-04	0.97	5.67	-	1619.1
AHQ-3-11, 4842 - 4914	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	7.23E-06	0.96	5.45	-	1079.5
AHQ-3-8, 4529 - 4544	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.85E-10	0.98	6.70	-	1288.9
AHQ-3-5, 5152	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	1.03E-04	0.69	3.77	-	466.7
AHQ-3-3, 5381	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	3.26E-07	0.84	4.68	-	615.6
AHQ-3-2, 5406	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	2.06E-07	0.66	3.61	-	605.1
AHQ-3-4, 4137 - 4209	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.11E-07	0.87	4.01	-	362.2
AHQ-3-1, 4400 - 4468	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.32E-09	0.93	4.21	-	607.3
AHQ-3-2, 4413 - 4481	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.22E-08	0.80	3.72	-	256.7
AHQ-3-4, 4280 - 4348	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.66E-05	0.83	3.62	-	388.7
AHQ-3-3, 4424 - 4496	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	4.54E-04	0.92	4.73	-	399.3
AHQ-3-2, 4550 - 4621	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	5.95E-06	0.79	3.78	-	246.2
AHQ-3-7, 3924	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	6.70E-04	0.67	3.07	-	231.5
AHQ-3-2, 4277 - 4345	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.59E-10	0.86	3.74	-	363.8
AHQ-3-2, 4183 - 4254	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	6.26E-13	0.94	4.93	-	420.4
AHQ-3-5, 3969 - 4021	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.32E-04	0.85	3.66	-	364.9
AHQ-3-1, 4260 - 4332	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.40E-04	0.89	3.84	-	478.4
AHQ-3-3, 4288 - 4356	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.99E-09	0.87	4.03	-	413.9
AHQ-3-1, 4484 - 4553	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.81E-05	0.70	2.99	-	317.9
AHQ-3-1, 5814	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.01E-07	0.97	5.71	-	2127.3
AHQ-3-5, 5921	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.97E-07	0.90	4.62	-	611.4
AHQ-3-5, 5832	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.39E-09	0.98	5.72	-	1720.2
AHQ-3-5, 5687	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.52E-06	0.93	4.27	-	934.8
AHQ-3-7, 5318	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.51E-09	0.98	6.16	-	1591.7
AHQ-3-11, 5158	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.01E-04	0.93	4.31	-	919.0
AHQ-3-5, 5599	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.22E-08	0.95	4.41	-	1203.7
AHQ-3-1, 6142	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.81E-13	0.97	5.25	-	1626.3
AHQ-3-2, 5649 - 5717	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.77E-12	0.98	6.31	-	1563.4
AHQ-3-9, 5040	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.07E-06	0.79	3.56	-	560.0
AHQ-3-9, 5520	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.26E-04	0.45	2.79	-	345.7
AHQ-3-2, 5874 - 5894	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.52E-13	0.98	5.23	-	2061.3
AHQ-3-1, 5801 - 5840	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.57E-07	0.98	5.71	-	2086.3
AHQ-3-2, 5977	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.85E-11	0.98	5.94	-	1507.8
AHQ-3-1, 5590	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.35E-08	0.95	4.53	-	1226.0
AHQ-3-4, 4493 - 4496	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.42E-11	0.97	5.46	-	1135.9
AHQ-3-3, 4482 - 4560	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.03E-13	0.97	5.45	-	1364.8
AHQ-3-2, 5522	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.21E-10	0.97	5.69	-	1387.3
AHQ-3-2, 5303	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.74E-05	0.68	3.12	-	452.1
AHQ-3-2, 6121	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.23E-12	0.97	5.23	-	1418.2
AHQ-3-4, 5629 - 5706	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.03E-07	0.96	4.76	-	1635.9
AHQ-3-4, 5654	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	6.86E-04	0.97	5.11	-	2155.7
AHQ-3-5, 5252	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.27E-08	0.95	4.36	-	1456.7
AHQ-3-3, 6076 - 6080	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.26E-12	0.95	4.48	-	1039.3
AHQ-3-3, 5672 - 5740	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.65E-09	0.98	6.21	-	1467.4
AHQ-3-2, 5714 - 5783	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	3.97E-10	0.97	5.61	-	1737.0
AHQ-3-2, 5769	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.11E-07	0.97	5.76	-	1313.1
AHQ-3-4, 5876	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.37E-10	0.97	5.35	-	1377.3
AHQ-3-6, 4295	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.90E-05	0.46	2.81	-	283.2
AHQ-3-2, 6127	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.45E-05	0.95	4.97	-	1585.2
AHQ-3-1, 5912	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.73E-10	0.96	4.60	-	1695.6
AHQ-3-13, 5423	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.24E-04	0.93	4.16	-	922.7
AHQ-3-2, 4593 - 4673	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.58E-09	0.89	4.22	-	593.3
AHQ-3-6, 5401 - 5413	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.80E-10	0.98	5.96	-	1728.4
AHQ-3-5, 4365 - 4444	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.87E-05	0.93	4.29	-	857.4
AHQ-3-3, 5928	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.23E-08	0.95	4.97	-	981.6
AHQ-3-3, 5824	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.70E-08	0.97	5.44	-	1552.3
AHQ-3-5, 5447	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.92E-10	0.98	6.23	-	1574.7
AHQ-3-14, 6313	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.26E-06	0.95	4.39	-	1236.0
AHQ-3-2, 1846 - 1922	R.MATNAAAQNAIK.K	1204.38227	2	2.73E-04	0.81	3.45	-	649.2
AHQ-3-2, 1685 - 1741	R.MATNAAAQNAIK.K	1204.38227	2	6.15E-05	0.63	2.94	-	718.4

AHQ-3-3, 1885	R.MATNAAAQNAIK.K	1204.38227	2	7.47E-06	0.58	2.67	-	695.7
AHQ-3-5, 4111 - 4143	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	2.97E-10	0.96	4.91	-	1839.0
AHQ-3-7, 3766	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	3.11E-04	0.79	3.48	-	946.8
AHQ-3-8, 3790	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.17E-06	0.86	3.82	-	959.5
AHQ-3-4, 4242 - 4312	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	8.64E-05	0.95	5.54	-	1350.5
AHQ-3-4, 4053 - 4056	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	2	8.90E-07	0.69	3.30	-	346.9
AHQ-3-5, 3879	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	3.39E-11	0.87	4.03	-	865.0
AHQ-3-3, 4069 - 4148	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	3.00E-08	0.93	5.09	-	822.5
AHQ-3-1, 4266	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.47E-07	0.94	5.08	-	1107.4
AHQ-3-9, 3832	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	6.24E-05	0.73	3.36	-	730.3
AHQ-3-2, 4190 - 4209	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.93E-08	0.96	5.66	-	1349.5
AHQ-3-2, 4191 - 4201	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	2	3.11E-05	0.76	3.33	-	452.2
AHQ-3-6, 3817	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	5.85E-11	0.93	4.90	-	841.1
AHQ-3-2, 4397 - 4402	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.00E-06	0.92	4.40	-	1035.1
AHQ-3-1, 4182 - 4185	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	3.50E-10	0.91	4.39	-	1002.5
AHQ-3-6, 4061	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	4.29E-07	0.89	4.34	-	696.2
AHQ-3-2, 4675	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	3.09E-04	0.85	3.69	-	1005.3
AHQ-3-2, 4433 - 4501	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	5.80E-06	0.65	2.87	-	747.9
AHQ-3-2, 4482 - 4495	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	4.58E-04	0.86	4.40	-	656.0
AHQ-3-3, 4546	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.23E-04	0.78	3.23	-	1143.8
AHQ-3-2, 4587 - 4661	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	4.67E-08	0.92	4.30	-	1078.2
AHQ-3-1, 6824 - 6840	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	2.40E-06	0.95	4.77	-	1238.7
AHQ-3-4, 6066 - 6138	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	2.74E-04	0.96	4.71	-	1515.8
AHQ-3-3, 7154 - 7162	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	3.08E-06	0.97	5.12	-	1491.9
AHQ-3-4, 7164	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.67E-10	0.97	4.97	-	1543.8
AHQ-3-6, 6883	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	7.85E-07	0.98	5.48	-	1979.9
AHQ-3-3, 6546	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	5.37E-11	0.95	4.66	-	1398.1
AHQ-3-2, 6178 - 6243	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.88E-09	0.97	5.40	-	1699.1
AHQ-3-2, 6894 - 6943	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	3.68E-05	0.97	5.11	-	1424.8
AHQ-3-14-, 6488	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	8.22E-04	0.52	2.79	-	475.2
AHQ-3-7, 6800	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	4.66E-09	0.96	4.97	-	1382.5
AHQ-3-1, 6174 - 6190	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	2.77E-05	0.97	4.90	-	1523.9
AHQ-3-2, 7246 - 7322	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.29E-12	0.98	5.98	-	1659.6
AHQ-3-7, 6484	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	5.52E-04	0.88	3.61	-	1086.6
AHQ-3-5, 7029 - 7032	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.91E-07	0.97	5.77	-	1520.5
AHQ-3-3, 6458	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	2.57E-04	0.94	4.29	-	1155.4
AHQ-3-3, 6820 - 6874	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	7.22E-06	0.97	5.10	-	1953.5
AHQ-3-4, 6860 - 6872	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	4.63E-06	0.98	5.44	-	2122.9
AHQ-3-9, 6528 - 6540	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	4.47E-08	0.97	4.85	-	1498.1
AHQ-3-3, 6234 - 6237	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	6.62E-07	0.98	5.68	-	2146.1
AHQ-3-1, 6270 - 6341	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	7.68E-08	0.98	5.56	-	1662.1
AHQ-3-10, 6215	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	3.30E-07	0.97	4.85	-	1701.8
AHQ-3-7, 2662	K.NCGQMSEIEAK.V	1268.40005	1	4.32E-05	0.35	2.20	-	403.9
AHQ-3-7, 2668	K.NCGQMSEIEAK.V	1268.40005	2	3.30E-06	0.79	2.92	-	876.8
AHQ-3-4, 4733 - 4804	K.NGNLPEFGDAISTASK.A	1621.73018	2	8.45E-08	0.48	2.74	-	317.8
AHQ-3-2, 4713	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.07E-05	0.78	3.32	-	406.8
AHQ-3-1, 4774 - 4784	K.NGNLPEFGDAISTASK.A	1621.73018	2	4.38E-07	0.91	4.55	-	542.8
AHQ-3-3, 4780	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.02E-08	0.94	4.13	-	916.1
AHQ-3-2, 4818 - 4890	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.30E-07	0.81	3.71	-	332.1
AHQ-3-2, 4169 - 4173	K.NLGTALAELR.T	1058.21367	2	7.89E-04	0.89	3.36	-	983.4
AHQ-3-1, 4348 - 4361	K.NLGTALAELR.T	1058.21367	2	6.99E-04	0.91	3.60	-	995.2
AHQ-3-6, 3805	K.NLGTALAELR.T	1058.21367	2	5.41E-06	0.83	2.95	-	771.9
AHQ-3-5, 3836	K.NLGTALAELR.T	1058.21367	2	1.01E-05	0.88	3.34	-	841.3
AHQ-3-4, 2577	K.PAAVAAENEEIGSHIK.H	1636.78798	2	7.37E-09	0.97	5.51	-	1636.3
AHQ-3-2, 2609	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.32E-05	0.98	5.14	-	2186.3
AHQ-3-6, 2425 - 2426	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.08E-10	0.98	6.12	-	1637.0
AHQ-3-2, 2881	K.PAAVAAENEEIGSHIK.H	1636.78798	2	7.55E-08	0.95	3.48	-	1715.7
AHQ-3-5, 2443	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.21E-10	0.97	5.33	-	1641.8
AHQ-3-1, 2762 - 2842	K.PAAVAAENEEIGSHIK.H	1636.78798	2	6.12E-07	0.98	5.41	-	1915.0
AHQ-3-4, 2588	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.65E-08	0.98	5.92	-	2035.2
AHQ-3-7, 2374	K.PAAVAAENEEIGSHIK.H	1636.78798	2	6.42E-05	0.96	4.92	-	1327.8
AHQ-3-3, 2612 - 2624	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.98E-04	0.97	4.64	-	1738.8
AHQ-3-5, 2440	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.02E-06	0.96	5.03	-	1249.1
AHQ-3-3, 2616	K.PAAVAAENEEIGSHIK.H	1636.78798	3	9.65E-08	0.96	4.84	-	1610.3
AHQ-3-2, 3217	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.17E-08	0.92	4.41	-	765.8
AHQ-3-3, 3204 - 3213	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	1.71E-05	0.82	3.36	-	957.4
AHQ-3-1, 3389	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	4.26E-06	0.86	3.70	-	677.5
AHQ-3-2, 3430	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.12E-07	0.92	4.31	-	851.5
AHQ-3-6, 2925	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	1.34E-05	0.82	3.39	-	604.7
AHQ-3-2, 3442	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	8.21E-05	0.67	3.00	-	862.5
AHQ-3-3, 3404 - 3406	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.85E-06	0.91	4.42	-	726.9
AHQ-3-3, 3200	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	3.42E-07	0.71	3.56	-	444.9
AHQ-3-5, 2939	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.75E-06	0.84	4.01	-	445.0
AHQ-3-4, 3136 - 3140	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.81E-08	0.93	4.82	-	740.2
AHQ-3-13-, 3973	R.QELAVFCSPEPPAK.T	1574.77985	2	2.67E-05	0.71	2.55	-	586.4
AHQ-3-1, 4193	R.QELAVFCSPEPPAK.T	1574.77985	2	5.13E-05	0.87	2.81	-	1087.0
AHQ-3-3, 4054 - 4125	R.QELAVFCSPEPPAK.T	1574.77985	2	7.70E-04	0.92	3.38	-	1099.0
AHQ-3-2, 4101 - 4105	R.QELAVFCSPEPPAK.T	1574.77985	2	5.12E-07	0.94	4.25	-	1038.4
AHQ-3-5, 3867	R.QELAVFCSPEPPAK.T	1574.77985	2	3.74E-07	0.87	2.90	-	995.6
AHQ-3-5, 7455	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	2.36E-04	0.87	4.23	-	716.7
AHQ-3-4, 7537	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	9.45E-11	0.94	5.54	-	769.1
AHQ-3-8, 7243	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	2.48E-08	0.89	4.88	-	566.6
AHQ-3-3, 7492	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	8.56E-10	0.90	4.67	-	779.1
AHQ-3-7, 7374	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	2.93E-05	0.89	4.63	-	583.4
AHQ-3-2, 7581	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	9.09E-07	0.90	4.57	-	918.7
AHQ-3-6, 7221 - 7302	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	2.59E-08	0.92	5.10	-	665.3
AHQ-3-4, 7516	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	3.58E-09	0.89	4.11	-	959.2
AHQ-3-5, 7479	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	1.55E-11	0.96	6.08	-	930.6
AHQ-3-2, 3869 - 3922	K.QVAASTAQLLVACK.V	1461.70942	2	2.57E-10	0.87	3.79	-	567.6
AHQ-3-3, 3813 - 3826	K.QVAASTAQLLVACK.V	1461.70942	2	1.45E-04	0.92	3.86	-	700.8
AHQ-3-1, 3968 - 3973	K.QVAASTAQLLVACK.V	1461.70942	2	2.27E-05	0.82	2.95	-	783.0
AHQ-3-2, 6026	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	6.41E-06	0.98	6.28	-	2199.2
AHQ-3-3, 5996	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	2.79E-05	0.98	5.69	-	2275.0
AHQ-3-3, 4996	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	4.19E-06	0.66	3.71	-	222.8
AHQ-3-4, 5912	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	1.40E-06	0.98	5.32	-	2089.5
AHQ-3-5, 5637	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	9.55E-07	0.98	5.89	-	2645.3
AHQ-3-2, 4954 - 5025	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	5.25E-06	0.91	4.26	-	541.1
AHQ-3-2, 2901	K.SIAAATSALVK.A	1032.21612	2	7.87E-05	0.90	3.15	-	945.7
AHQ-3-1, 3140 - 3141	K.SIAAATSALVK.A	1032.21612	2	2.09E-04	0.92	3.55	-	1014.8
AHQ-3-7, 3623	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	4.04E-07	0.93	4.76	-	1357.0
AHQ-3-7, 4074 - 4082	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	8.15E-10	0.97	5.99	-	1953.9
AHQ-3-7, 4084 - 4107	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	8.53E-05	0.89	4.48	-	472.7
AHQ-3-6, 5090 - 5093	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.67E-06	0.91	3.93	-	711.2
AHQ-3-4, 5316 - 5388	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.94E-07	0.92	4.06	-	690.2
AHQ-3-1, 4780	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.03E-06	0.87	3.78	-	478.3
AHQ-3-5, 5357 - 5376	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.68E-08	0.90	4.40	-	432.8
AHQ-3-3, 5517 - 5534	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.21E-04	0.77	3.56	-	364.9

AHQ-3-5, 4599 - 4600	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.50E-09	0.95	4.88	-	931.4
AHQ-3-2, 5217	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.51E-05	0.79	3.48	-	404.2
AHQ-3-4, 5597 - 5674	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.86E-08	0.91	4.21	-	606.9
AHQ-3-4, 5238 - 5317	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.75E-06	0.66	3.27	-	241.3
AHQ-3-6, 4501	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.51E-07	0.84	3.50	-	538.9
AHQ-3-3, 5617	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.83E-06	0.80	3.82	-	353.8
AHQ-3-2, 4805 - 4806	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.10E-07	0.91	4.35	-	522.8
AHQ-3-4, 5153	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.76E-06	0.81	3.29	-	603.1
AHQ-3-3, 5432	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.53E-07	0.82	3.62	-	348.3
AHQ-3-4, 4952	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.48E-05	0.78	3.33	-	592.3
AHQ-3-4, 4716	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.89E-07	0.84	3.51	-	508.9
AHQ-3-2, 5377 - 5453	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.82E-06	0.91	4.36	-	591.8
AHQ-3-3, 5208 - 5221	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.39E-05	0.77	3.67	-	349.0
AHQ-3-5, 5184 - 5191	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.24E-08	0.92	4.39	-	558.2
AHQ-3-2, 5051	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.65E-07	0.84	3.83	-	367.4
AHQ-3-3, 4764 - 4772	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.26E-07	0.92	4.41	-	643.9
AHQ-3-2, 5738	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.41E-05	0.86	3.73	-	437.1
AHQ-3-1, 5646	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.72E-06	0.86	3.89	-	476.3
AHQ-3-2, 5510 - 5582	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.78E-04	0.65	3.05	-	358.9
AHQ-3-7, 5043	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.28E-06	0.64	2.99	-	405.3
AHQ-3-1, 5421 - 5488	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.52E-05	0.78	3.33	-	426.7
AHQ-3-1, 5554 - 5636	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.64E-07	0.82	3.39	-	427.3
AHQ-3-3, 5340 - 5416	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.15E-07	0.90	4.24	-	481.0
AHQ-3-7, 7302 - 7303	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	5.00E-13	0.97	6.05	-	1637.8
AHQ-3-13, 6807 - 6875	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.46E-05	0.90	3.93	-	1255.8
AHQ-3-2, 7541 - 7550	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.22E-15	0.97	6.00	-	1727.7
AHQ-3-5, 7411 - 7419	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.36E-11	0.97	5.92	-	1811.6
AHQ-3-3, 7380 - 7457	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.31E-12	0.98	6.48	-	1884.2
AHQ-3-12, 4226	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.62E-08	0.94	3.92	-	1257.5
AHQ-3-10, 3898	K.TKEVIQEWNLTNIK.R	1716.95938	2	2.45E-06	0.96	4.34	-	1843.2
AHQ-3-13, 4227	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.03E-08	0.95	4.14	-	1460.5
AHQ-3-12, 4231	K.TKEVIQEWNLTNIK.R	1716.95938	3	7.82E-06	0.94	4.28	-	1460.3
AHQ-3-11, 4026	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.02E-04	0.96	4.48	-	1572.7
AHQ-3-7, 3902 - 3904	K.TKEVIQEWNLTNIK.R	1716.95938	3	3.10E-07	0.96	4.98	-	1630.7
AHQ-3-8, 3680 - 3746	K.TKEVIQEWNLTNIK.R	1716.95938	2	5.21E-08	0.96	4.48	-	1474.5
AHQ-3-1, 6644 - 6710	K.TLAESALQLLYTAK.E	1522.76793	2	3.72E-05	0.97	4.94	-	1491.0
AHQ-3-3, 6716	K.TLAESALQLLYTAK.E	1522.76793	2	8.54E-05	0.95	4.42	-	1085.3
AHQ-3-3, 6632 - 6700	K.TLAESALQLLYTAK.E	1522.76793	2	3.41E-08	0.97	4.96	-	1259.2
AHQ-3-4, 6644 - 6716	K.TLAESALQLLYTAK.E	1522.76793	2	4.02E-07	0.97	4.85	-	1504.2
AHQ-3-2, 6685 - 6757	K.TLAESALQLLYTAK.E	1522.76793	2	9.33E-09	0.96	4.81	-	1185.7
AHQ-3-1, 6852	K.TLAESALQLLYTAK.E	1522.76793	2	8.56E-04	0.87	3.05	-	970.4
AHQ-3-11, 6010	K.TLAESALQLLYTAK.E	1522.76793	2	2.40E-06	0.92	3.92	-	909.2
AHQ-3-13, 6303	K.TLAESALQLLYTAK.E	1522.76793	2	1.73E-05	0.92	3.45	-	939.3
AHQ-3-9, 6011	K.TLAESALQLLYTAK.E	1522.76793	2	2.42E-06	0.88	3.74	-	678.9
AHQ-3-2, 6825 - 6842	K.TLAESALQLLYTAK.E	1522.76793	2	6.93E-04	0.96	4.46	-	1112.2
AHQ-3-4, 3046 - 3122	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.72E-05	0.97	5.54	-	1010.4
AHQ-3-1, 3362 - 3369	K.TLSHPQQMALLDQTK.T	1711.96464	2	4.01E-06	0.93	4.42	-	685.8
AHQ-3-5, 2895	K.TLSHPQQMALLDQTK.T	1711.96464	2	7.37E-05	0.96	5.08	-	990.0
AHQ-3-3, 3154	K.TLSHPQQMALLDQTK.T	1711.96464	3	4.61E-08	0.95	4.71	-	1884.4
AHQ-3-3, 3060 - 3134	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.12E-08	0.93	4.35	-	680.3
AHQ-3-6, 2873	K.TLSHPQQMALLDQTK.T	1711.96464	2	3.43E-07	0.95	4.88	-	929.9
AHQ-3-2, 3149	K.TLSHPQQMALLDQTK.T	1711.96464	2	3.07E-06	0.93	4.42	-	705.7
AHQ-3-1, 3384	K.TLSHPQQMALLDQTK.T	1711.96464	3	6.36E-04	0.95	4.71	-	1591.6
AHQ-3-2, 4427 - 4453	K.TMLESAGGLIQTAR.A	1448.67095	1	3.83E-04	0.19	2.32	-	196.4
AHQ-3-6, 4069	K.TMLESAGGLIQTAR.A	1448.67095	2	2.92E-10	0.92	3.80	-	1522.4
AHQ-3-3, 3481 - 3557	K.TM*LESAGGLIQTAR.A	1464.67035	2	5.58E-07	0.95	4.78	-	1193.0
AHQ-3-5, 3245	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.96E-05	0.97	4.26	-	1958.8
AHQ-3-2, 3513 - 3514	K.TM*LESAGGLIQTAR.A	1464.67035	2	4.37E-08	0.98	5.01	-	2043.2
AHQ-3-5, 4132 - 4147	K.TMLESAGGLIQTAR.A	1448.67095	2	3.15E-07	0.93	3.76	-	1526.7
AHQ-3-1, 3625 - 3642	K.TM*LESAGGLIQTAR.A	1464.67035	2	2.85E-08	0.95	4.08	-	1314.4
AHQ-3-4, 4285 - 4289	K.TMLESAGGLIQTAR.A	1448.67095	2	3.56E-07	0.82	3.39	-	716.2
AHQ-3-1, 4418 - 4493	K.TMLESAGGLIQTAR.A	1448.67095	2	1.89E-07	0.94	4.16	-	1466.1
AHQ-3-3, 4402	K.TMLESAGGLIQTAR.A	1448.67095	1	1.23E-06	0.11	2.08	-	242.9
AHQ-3-3, 4388 - 4408	K.TMLESAGGLIQTAR.A	1448.67095	2	2.06E-06	0.92	3.72	-	1524.4
AHQ-3-4, 3438 - 3440	K.TM*LESAGGLIQTAR.A	1464.67035	2	4.75E-09	0.98	5.33	-	1830.7
AHQ-3-2, 4503	K.TMLESAGGLIQTAR.A	1448.67095	2	1.11E-05	0.89	3.09	-	1701.3
AHQ-3-13-, 4221	K.TM*QFEPSTMVYDACR.I	1854.07511	2	8.36E-05	0.92	4.20	-	715.5
AHQ-3-13, 4791	K.TMQFEPSTMVYDACR.I	1838.07571	2	3.80E-05	0.89	4.22	-	571.1
AHQ-3-13-, 4789	K.TMQFEPSTMVYDACR.I	1838.07571	2	6.76E-04	0.88	3.58	-	582.0
AHQ-3-14, 5203	K.TM*QFEPSTMVYDACR.I	1854.07511	2	4.81E-04	0.91	4.14	-	754.1
AHQ-3-13-, 3999	K.TMQFEPSTM*VYDACR.I	1854.07511	2	3.97E-04	0.84	3.64	-	382.9
AHQ-3-8, 4452	K.TMQFEPSTMVYDACR.I	1838.07571	2	2.46E-04	0.85	3.98	-	474.1
AHQ-3-13, 4213	K.TM*QFEPSTMVYDACR.I	1854.07511	2	4.23E-06	0.89	3.57	-	664.7
AHQ-3-13-, 3673 - 3741	K.TVTDM*LM*TICAR.I	1445.70887	2	9.01E-04	0.88	3.21	-	831.5
AHQ-3-13, 3682 - 3746	K.TVTDM*LM*TICAR.I	1445.70887	2	5.99E-05	0.82	3.10	-	609.8
AHQ-3-13, 5334 - 5401	K.TVTDMLMTICAR.I	1413.71007	2	2.13E-05	0.61	2.66	-	479.6
AHQ-3-7, 4927	K.TYGVSFFLVK.E	1161.37395	2	1.54E-07	0.88	3.24	-	688.1
AHQ-3-11, 4963	K.TYGVSFFLVK.E	1161.37395	2	5.64E-06	0.91	3.97	-	663.0
AHQ-3-7, 5010	K.TYGVSFFLVK.E	1161.37395	2	1.55E-05	0.91	3.56	-	746.1
AHQ-3-12, 5214	K.TYGVSFFLVK.E	1161.37395	2	2.01E-07	0.85	3.26	-	570.4
AHQ-3-5, 6401 - 6428	R.VAGSVTELIQAAEAMK.G	1618.87752	2	6.64E-07	0.97	4.48	-	1581.6
AHQ-3-4, 6552 - 6568	R.VAGSVTELIQAAEAMK.G	1618.87752	2	8.68E-09	0.96	4.39	-	1494.1
AHQ-3-2, 5469 - 5537	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.17E-08	0.97	5.44	-	1622.6
AHQ-3-2, 6779	R.VAGSVTELIQAAEAMK.G	1618.87752	2	3.12E-04	0.96	4.21	-	1634.5
AHQ-3-1, 6561 - 6569	R.VAGSVTELIQAAEAMK.G	1618.87752	2	4.45E-08	0.96	4.83	-	1224.5
AHQ-3-4, 5385 - 5456	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	7.15E-06	0.96	4.94	-	1339.3
AHQ-3-3, 5437 - 5510	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	3.57E-06	0.91	3.90	-	1077.1
AHQ-3-9, 5887 - 5893	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.81E-07	0.95	4.58	-	1247.1
AHQ-3-1, 5582	R.VAGSVTELIQAAEAM*K.G	1634.87692	3	3.12E-05	0.96	5.59	-	1566.2
AHQ-3-2, 6539 - 6614	R.VAGSVTELIQAAEAMK.G	1618.87752	2	6.86E-09	0.98	6.14	-	1465.6
AHQ-3-3, 6500 - 6568	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.04E-09	0.98	5.72	-	1627.2
AHQ-3-10, 5691 - 5695	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.26E-08	0.91	4.07	-	954.1
AHQ-3-1, 5566	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	2.45E-05	0.81	2.80	-	847.9
AHQ-3-7, 6139	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.82E-08	0.98	4.69	-	2249.7
AHQ-3-3, 6132 - 6164	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.33E-09	0.94	5.11	-	863.4
AHQ-3-3, 5988 - 6064	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.52E-06	0.88	4.19	-	669.1
AHQ-3-10, 5287 - 5322	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.11E-09	0.95	5.12	-	711.5
AHQ-3-10, 5107 - 5170	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.59E-05	0.91	4.57	-	753.9
AHQ-3-3, 5852 - 5920	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.84E-06	0.53	3.17	-	276.8
AHQ-3-11, 5542	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.05E-08	0.96	5.41	-	1058.2
AHQ-3-12, 5870	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.00E-07	0.93	4.23	-	884.9
AHQ-3-5, 5775 - 5788	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.11E-06	0.92	4.40	-	773.4
AHQ-3-5, 5963 - 5984	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.13E-11	0.97	5.45	-	994.3
AHQ-3-1, 6150	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.21E-05	0.88	3.86	-	517.7
AHQ-3-5, 6159 - 6160	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.65E-11	0.96	5.01	-	1011.2
AHQ-3-9, 5465 - 5532	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.03E-09	0.95	5.30	-	596.0
AHQ-3-1, 6068 - 6148	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.56E-10	0.92	4.13	-	705.1

AHQ-3-6, 5837 - 5877	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.55E-16	0.96	5.22	-	729.3
AHQ-3-1, 5921 - 5988	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.06E-07	0.95	5.08	-	849.4
AHQ-3-8, 5593	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.46E-11	0.95	4.89	-	834.0
AHQ-3-13, 5763	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.80E-05	0.52	2.85	-	385.5
AHQ-3-2, 5827 - 5897	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.91E-07	0.93	4.52	-	845.3
AHQ-3-2, 5970 - 6015	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.88E-10	0.97	5.67	-	1365.8
AHQ-3-7, 5638	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.04E-09	0.90	4.33	-	659.0
AHQ-3-7, 5803 - 5826	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.05E-11	0.97	5.61	-	1082.9
AHQ-3-2, 6093 - 6161	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.58E-09	0.93	4.41	-	857.8
AHQ-3-14-, 5701	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.65E-05	0.94	4.29	-	945.9
AHQ-3-7, 5952	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.49E-05	0.85	3.23	-	700.1
AHQ-3-4, 5721	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.44E-04	0.84	3.95	-	568.1
AHQ-3-6, 5669	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.84E-05	0.73	3.13	-	346.3
AHQ-3-11, 5386	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.25E-04	0.81	3.60	-	387.6
AHQ-3-4, 5802 - 5872	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.08E-10	0.94	4.13	-	1126.6
AHQ-3-4, 5873 - 5941	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.32E-06	0.49	2.77	-	237.2
AHQ-3-4, 5965 - 6037	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.81E-05	0.91	4.51	-	593.6
AHQ-3-4, 6108	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.62E-09	0.97	5.79	-	813.2
AHQ-3-3, 3810 - 3820	K.VGDDPAVWQLK.N	1228.37879	2	1.31E-08	0.93	4.10	-	870.0
AHQ-3-4, 3741 - 3752	K.VGDDPAVWQLK.N	1228.37879	2	1.39E-06	0.92	3.82	-	796.6
AHQ-3-1, 3981	K.VGDDPAVWQLK.N	1228.37879	2	4.85E-08	0.93	4.03	-	811.2
AHQ-3-6, 3509	K.VGDDPAVWQLK.N	1228.37879	2	2.27E-07	0.88	3.39	-	778.3
AHQ-3-5, 3548 - 3576	K.VGDDPAVWQLK.N	1228.37879	2	1.43E-07	0.93	3.72	-	842.1
AHQ-3-2, 3850	K.VGDDPAVWQLK.N	1228.37879	2	1.09E-07	0.91	3.69	-	838.6
AHQ-3-3, 3278 - 3286	K.VLGEAMTGISQNAK.N	1419.62961	2	4.57E-04	0.80	2.65	-	935.0
AHQ-3-2, 2325 - 2399	K.VLGEAM*TGISQNAK.N	1435.62901	2	6.37E-06	0.96	4.73	-	1160.2
AHQ-3-2, 3099 - 3178	K.VLGEAMTGISQNAK.N	1419.62961	2	6.85E-11	0.98	5.13	-	1808.3
AHQ-3-1, 3260	K.VLGEAMTGISQNAK.N	1419.62961	2	1.94E-10	0.97	4.32	-	2161.7
AHQ-3-3, 3104	K.VLGEAMTGISQNAK.N	1419.62961	1	1.44E-06	0.74	3.07	-	358.3
AHQ-3-1, 2465 - 2477	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.52E-05	0.96	4.12	-	1467.3
AHQ-3-3, 2305 - 2377	K.VLGEAM*TGISQNAK.N	1435.62901	2	2.77E-04	0.97	4.56	-	1456.8
AHQ-3-4, 3048 - 3126	K.VLGEAMTGISQNAK.N	1419.62961	2	1.28E-08	0.98	5.07	-	2101.3
AHQ-3-4, 3049 - 3134	K.VLGEAMTGISQNAK.N	1419.62961	1	1.58E-04	0.42	2.23	-	367.4
AHQ-3-3, 2314	K.VLGEAM*TGISQNAK.N	1435.62901	1	2.29E-05	0.14	2.04	-	135.5
AHQ-3-2, 3119	K.VLGEAMTGISQNAK.N	1419.62961	1	3.69E-06	0.76	3.38	-	334.3
AHQ-3-2, 3270	K.VLGEAMTGISQNAK.N	1419.62961	2	3.36E-09	0.98	4.49	-	2051.1
AHQ-3-4, 2293 - 2310	K.VLGEAM*TGISQNAK.N	1435.62901	2	8.34E-05	0.92	3.96	-	1054.5
AHQ-3-5, 2196 - 2205	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.95E-06	0.98	5.30	-	1830.1
AHQ-3-2, 4970	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	1.73E-04	0.73	3.97	-	463.3
AHQ-3-3, 5013 - 5060	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	2.68E-05	0.70	3.51	-	543.2
AHQ-3-1, 5577	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	4.24E-05	0.88	4.21	-	696.7
AHQ-3-1, 4969 - 5042	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	4.43E-08	0.90	5.08	-	449.0
AHQ-3-6, 1458 - 1490	K.VLVQNAAGSQEK.L	1244.37976	2	1.45E-05	0.67	2.91	-	562.9
AHQ-3-4, 1568 - 1574	K.VLVQNAAGSQEK.L	1244.37976	2	2.39E-09	0.92	3.61	-	1001.9
AHQ-3-2, 1719	K.VLVQNAAGSQEK.L	1244.37976	2	4.93E-08	0.84	3.15	-	692.2
AHQ-3-3, 1680 - 1754	K.VLVQNAAGSQEK.L	1244.37976	2	1.23E-07	0.84	3.16	-	802.6
AHQ-3-2, 1494 - 1563	K.VLVQNAAGSQEK.L	1244.37976	2	1.02E-06	0.89	3.69	-	794.3
AHQ-3-5, 1472	K.VLVQNAAGSQEK.L	1244.37976	2	6.11E-07	0.92	3.29	-	1119.1
AHQ-3-3, 1558	K.VLVQNAAGSQEK.L	1244.37976	1	2.44E-05	0.44	2.82	-	294.9
AHQ-3-4, 1773	K.VLVQNAAGSQEK.L	1244.37976	1	5.61E-08	0.58	2.37	-	498.5
AHQ-3-2, 1566 - 1733	K.VLVQNAAGSQEK.L	1244.37976	1	6.13E-05	0.38	2.61	-	284.0
AHQ-3-4, 1548 - 1684	K.VLVQNAAGSQEK.L	1244.37976	1	1.20E-05	0.36	2.61	-	240.3
AHQ-3-3, 1546 - 1608	K.VLVQNAAGSQEK.L	1244.37976	2	6.06E-06	0.87	3.26	-	769.3
AHQ-3-2, 1631 - 1645	K.VLVQNAAGSQEK.L	1244.37976	2	7.55E-08	0.85	3.53	-	603.2
AHQ-3-5, 4431	K.VMVTNVTSLLK.T	1205.49322	2	4.69E-06	0.89	3.85	-	849.1
AHQ-3-2, 4401 - 4403	K.VM*VTNVTSLLK.T	1221.49262	2	1.53E-04	0.84	3.82	-	626.3
AHQ-3-6, 4361	K.VMVTNVTSLLK.T	1205.49322	2	3.12E-06	0.95	4.25	-	1065.1
AHQ-3-1, 4529 - 4533	K.VM*VTNVTSLLK.T	1221.49262	2	5.83E-04	0.79	3.22	-	623.8
AHQ-3-6, 4017	K.VM*VTNVTSLLK.T	1221.49262	2	2.62E-04	0.66	2.57	-	612.3
AHQ-3-4, 4268	K.VM*VTNVTSLLK.T	1221.49262	2	3.70E-05	0.84	3.33	-	633.8
AHQ-3-4, 4654 - 4657	K.VMVTNVTSLLK.T	1205.49322	2	7.72E-07	0.91	4.28	-	668.6
AHQ-3-3, 4380	K.VM*VTNVTSLLK.T	1221.49262	2	2.29E-04	0.74	3.08	-	759.2
AHQ-3-1, 4904	K.VMVTNVTSLLK.T	1205.49322	2	3.24E-04	0.89	3.60	-	732.9
AHQ-3-7, 4238 - 4252	K.VMVTNVTSLLK.T	1205.49322	2	5.57E-07	0.88	3.68	-	622.2
AHQ-3-2, 4781	K.VMVTNVTSLLK.T	1205.49322	2	1.26E-07	0.90	4.18	-	706.1
AHQ-3-3, 4774 - 4806	K.VMVTNVTSLLK.T	1205.49322	2	2.42E-04	0.88	3.94	-	670.6
AHQ-3-5, 4084	K.VM*VTNVTSLLK.T	1221.49262	2	4.22E-04	0.82	3.33	-	605.3
AHQ-3-4, 2649	R.VQELGHGCAALVTK.A	1484.70307	2	3.20E-07	0.95	4.56	-	1011.9
AHQ-3-6, 2517	R.VQELGHGCAALVTK.A	1484.70307	2	3.13E-04	0.97	4.00	-	1780.7
AHQ-3-5, 2524	R.VQELGHGCAALVTK.A	1484.70307	1	2.38E-07	0.88	3.66	-	641.4
AHQ-3-1, 2913	R.VQELGHGCAALVTK.A	1484.70307	2	2.66E-06	0.97	4.88	-	1383.5
AHQ-3-3, 2701	R.VQELGHGCAALVTK.A	1484.70307	2	1.25E-04	0.94	4.61	-	901.9
AHQ-3-3, 2708	R.VQELGHGCAALVTK.A	1484.70307	1	1.29E-05	0.89	3.68	-	736.2
AHQ-3-2, 2737	R.VQELGHGCAALVTK.A	1484.70307	1	2.61E-10	0.86	3.58	-	655.0
AHQ-3-7, 2466	R.VQELGHGCAALVTK.A	1484.70307	2	1.87E-04	0.94	4.11	-	1289.7
AHQ-3-2, 2711 - 2715	R.VQELGHGCAALVTK.A	1484.70307	2	1.97E-04	0.96	4.13	-	1528.7
AHQ-3-4, 2660	R.VQELGHGCAALVTK.A	1484.70307	1	3.46E-10	0.88	3.85	-	617.6
AHQ-3-5, 2515	R.VQELGHGCAALVTK.A	1484.70307	2	3.41E-05	0.98	5.10	-	2076.8
AHQ-3-2, 2539	K.VSHVLAALQAGNR.G	1336.52525	1	2.15E-06	0.88	3.93	-	428.5
AHQ-3-7, 2311	K.VSHVLAALQAGNR.G	1336.52525	2	4.80E-05	0.96	3.95	-	1612.7
AHQ-3-3, 2689	K.VSHVLAALQAGNR.G	1336.52525	2	5.03E-10	0.97	4.08	-	1840.1
AHQ-3-6, 2358	K.VSHVLAALQAGNR.G	1336.52525	1	2.11E-04	0.77	2.98	-	427.9
AHQ-3-3, 2534	K.VSHVLAALQAGNR.G	1336.52525	1	2.89E-06	0.88	3.72	-	442.3
AHQ-3-3, 2528 - 2600	K.VSHVLAALQAGNR.G	1336.52525	1	1.97E-04	0.39	2.47	-	284.5
AHQ-3-5, 2361	K.VSHVLAALQAGNR.G	1336.52525	2	2.05E-09	0.98	4.95	-	2113.9
AHQ-3-2, 2538 - 2542	K.VSHVLAALQAGNR.G	1336.52525	2	2.03E-09	0.97	4.96	-	1832.6
AHQ-3-4, 2516	K.VSHVLAALQAGNR.G	1336.52525	1	1.40E-07	0.84	3.45	-	442.3
AHQ-3-5, 2359	K.VSHVLAALQAGNR.G	1336.52525	1	7.74E-08	0.81	2.99	-	485.0
AHQ-3-1, 2821	K.VSHVLAALQAGNR.G	1336.52525	1	5.34E-08	0.79	3.13	-	405.8
AHQ-3-4, 2638	K.VSHVLAALQAGNR.G	1336.52525	1	1.02E-08	0.66	2.18	-	500.9
AHQ-3-1, 2822	K.VSHVLAALQAGNR.G	1336.52525	2	1.33E-08	0.96	4.40	-	1310.3
AHQ-3-11, 6274	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.85E-04	0.77	3.29	-	503.2
AHQ-3-11, 5500	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	4.83E-05	0.85	3.29	-	868.6
AHQ-3-4, 6132 - 6142	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.19E-06	0.96	5.26	-	966.3
AHQ-3-4, 6972	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	1.37E-10	0.93	4.59	-	1297.4
AHQ-3-4, 7102	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.42E-08	0.94	4.92	-	633.1
AHQ-3-8, 6420	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.43E-05	0.96	4.97	-	1152.6
AHQ-3-4, 6878	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.11E-05	0.96	5.24	-	1127.2
AHQ-3-7, 5618	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	4.96E-06	0.96	4.82	-	1249.2
AHQ-3-2, 6101 - 6125	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.82E-07	0.97	5.50	-	1306.8
AHQ-3-9, 6369	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.88E-05	0.79	3.64	-	397.5
AHQ-3-6, 6678	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.46E-04	0.95	4.67	-	996.0
AHQ-3-13-, 6546	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.99E-04	0.50	3.00	-	391.4
AHQ-3-14-, 6428	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.61E-05	0.97	6.19	-	1062.7
AHQ-3-12, 6528	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.34E-04	0.86	3.75	-	664.0
AHQ-3-6, 5694 - 5761	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.11E-08	0.94	4.40	-	1143.7
AHQ-3-2, 7169 - 7238	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.05E-05	0.90	4.46	-	593.2

AHQ-3-1, 6245 - 6262	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.08E-06	0.87	3.64	-	643.0
AHQ-3-5, 5796	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.99E-04	0.85	3.35	-	964.4
AHQ-3-3, 6001 - 6072	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	5.50E-06	0.95	5.08	-	995.7
AHQ-3-2, 7034	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	2.89E-06	0.84	3.35	-	1156.7
AHQ-3-7, 6626 - 6630	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.26E-04	0.97	6.27	-	1125.1
AHQ-3-3, 7142 - 7210	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.33E-05	0.92	4.29	-	703.3
AHQ-3-4, 5957 - 6028	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.13E-05	0.95	4.88	-	995.6
AHQ-3-10, 6066 - 6070	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.40E-05	0.91	4.15	-	936.5
AHQ-3-1, 6138	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	9.70E-08	0.97	5.87	-	2036.3
AHQ-3-2, 7031 - 7102	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.60E-05	0.97	5.44	-	1137.5
AHQ-3-3, 7016 - 7092	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.36E-07	0.96	5.69	-	883.4
AHQ-3-3, 6953	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	9.97E-06	0.82	3.43	-	1002.0
AHQ-3-1, 6925	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.63E-04	0.93	4.66	-	739.5
AHQ-3-5, 6839 - 6840	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.86E-06	0.97	6.09	-	882.3
AHQ-3-2, 6939	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.39E-08	0.87	4.02	-	579.4
AHQ-3-1, 7041	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.78E-07	0.97	5.20	-	1173.6
AHQ-3-4, 6965 - 7032	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.53E-07	0.96	5.02	-	1082.2
AHQ-3-3, 6869 - 6949	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.30E-05	0.97	6.03	-	881.5
AHQ-3-2, 6238	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	5.49E-04	0.87	3.42	-	790.7
AHQ-3-1, 4993	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.60E-09	0.80	3.43	-	392.9
AHQ-3-13, 4522	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.59E-07	0.95	5.00	-	661.9
AHQ-3-5, 4965	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.06E-05	0.76	3.46	-	409.4
AHQ-3-1, 4820	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.34E-08	0.95	5.03	-	617.8
AHQ-3-5, 4705	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.32E-05	0.74	3.51	-	315.2
AHQ-3-5, 4604 - 4623	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.23E-11	0.96	5.40	-	847.6
AHQ-3-12, 4546 - 4620	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.43E-05	0.95	5.02	-	819.5
AHQ-3-3, 4672	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.87E-07	0.94	4.49	-	658.4
AHQ-3-3, 4788 - 4789	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.22E-06	0.91	4.87	-	390.2
AHQ-3-3, 4966	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.41E-11	0.93	4.64	-	669.2
AHQ-3-3, 5116 - 5124	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.04E-06	0.75	4.13	-	354.6
AHQ-3-2, 5001 - 5079	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.11E-15	0.83	4.02	-	394.1
AHQ-3-5, 4504 - 4505	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.27E-06	0.95	5.33	-	580.4
AHQ-3-6, 4402	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.65E-07	0.91	4.44	-	569.6
AHQ-3-2, 4914	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.41E-05	0.94	5.06	-	828.7
AHQ-3-1, 4701	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.96E-05	0.90	4.50	-	349.8
AHQ-3-14-, 4437 - 4491	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.72E-12	0.95	4.82	-	999.8
AHQ-3-2, 4822 - 4839	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.31E-05	0.90	4.51	-	439.6
AHQ-3-7, 4450 - 4492	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.49E-04	0.67	3.28	-	437.5
AHQ-3-2, 4689 - 4701	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.06E-05	0.90	4.39	-	413.7
AHQ-3-4, 4530 - 4609	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.39E-05	0.92	4.77	-	466.5
AHQ-3-8, 4357	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	3.03E-05	0.89	4.44	-	849.5
AHQ-3-8, 4347	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.16E-07	0.92	4.25	-	659.2
AHQ-3-6, 4509 - 4517	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.72E-08	0.96	5.35	-	944.8
AHQ-3-8, 4173	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.41E-04	0.88	4.25	-	412.8
AHQ-3-4, 4740	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.53E-10	0.97	5.29	-	1060.2
AHQ-3-14, 5443	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.95E-09	0.93	4.69	-	641.1
gi|4885387|ref|NP_005318.1| L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain; L-3-hydroxyacyl-				1.11E-15	0.96	10.27	9.60	34286.3
AHQ-3-9, 7115	K.TLSTIATSTDAASVVHSTDLVVEAIVENLK.V	3086.43759	3	1.11E-15	0.96	5.30	-	1389.8
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				3.89E-15	105.73	1200.38	47.60	226529.8
AHQ-3-3, 1925	R.ALEEAMEQK.A	1049.18068	1	7.69E-05	0.77	3.36	-	622.5
AHQ-3-4, 1930	R.ALEEAMEQK.A	1049.18068	1	2.70E-05	0.38	2.14	-	565.0
AHQ-3-2, 1862 - 1942	R.ALEEAMEQK.A	1049.18068	2	6.03E-05	0.87	3.39	-	728.6
AHQ-3-2, 3925	K.ALELDSNLYR.I	1194.31920	2	7.58E-06	0.91	3.13	-	1244.7
AHQ-3-3, 3750 - 3753	K.ALELDSNLYR.I	1194.31920	2	3.11E-07	0.92	3.87	-	1036.1
AHQ-3-4, 3704	K.ALELDSNLYR.I	1194.31920	2	4.19E-06	0.93	3.75	-	1117.6
AHQ-3-2, 3814 - 3829	K.ALELDSNLYR.I	1194.31920	2	4.80E-06	0.95	4.07	-	1311.5
AHQ-3-5, 3525	K.ALELDSNLYR.I	1194.31920	2	4.37E-06	0.94	3.65	-	1378.5
AHQ-3-6, 3487	K.ALELDSNLYR.I	1194.31920	2	2.58E-06	0.89	2.96	-	1135.2
AHQ-3-6, 3481	K.ALELDSNLYR.I	1194.31920	1	5.40E-07	0.19	1.86	-	299.0
AHQ-3-3, 3732 - 3801	K.ALELDSNLYR.I	1194.31920	1	4.53E-04	0.30	2.56	-	223.4
AHQ-3-2, 2803	R.ALEQQVEEMK.T	1205.36380	2	5.77E-07	0.89	3.30	-	1152.0
AHQ-3-3, 2793 - 2801	R.ALEQQVEEMK.T	1205.36380	2	2.31E-05	0.92	3.94	-	1095.9
AHQ-3-4, 2772	R.ALEQQVEEMK.T	1205.36380	2	8.97E-05	0.88	3.52	-	939.7
AHQ-3-5, 2595 - 2613	R.ALEQQVEEMK.T	1205.36380	2	2.32E-05	0.88	3.41	-	920.5
AHQ-3-6, 2606	R.ALEQQVEEMK.T	1205.36380	2	7.55E-06	0.88	3.22	-	1038.4
AHQ-3-1, 2969 - 2980	R.ALEQQVEEMK.T	1205.36380	2	2.67E-05	0.92	3.78	-	1135.7
AHQ-3-3, 2041	R.ALEQQVEEM*K.T	1221.36320	2	9.26E-06	0.82	2.95	-	920.4
AHQ-3-3, 7484	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	1.14E-08	0.96	5.82	-	1500.9
AHQ-3-1, 6645 - 6708	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	5.62E-09	0.97	6.43	-	1786.1
AHQ-3-5, 7444	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	9.28E-08	0.97	5.96	-	1709.2
AHQ-3-2, 6766 - 6841	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	6.11E-15	0.98	7.16	-	2221.3
AHQ-3-3, 6685 - 6765	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.40E-08	0.96	6.50	-	1267.6
AHQ-3-1, 7264	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	4.67E-08	0.95	5.34	-	1513.7
AHQ-3-1, 6896 - 6930	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	9.19E-12	0.96	5.21	-	1472.4
AHQ-3-4, 7504	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	1.64E-10	0.97	5.72	-	1812.6
AHQ-3-6, 7265	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	5.13E-09	0.95	5.36	-	1292.3
AHQ-3-3, 5032	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.21E-07	0.86	3.88	-	646.5
AHQ-3-6, 4962	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.67E-05	0.89	3.78	-	879.1
AHQ-3-2, 5495 - 5570	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.62E-05	0.95	4.62	-	1121.4
AHQ-3-1, 5529	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.95E-06	0.94	4.59	-	918.6
AHQ-3-3, 5480	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.30E-07	0.96	5.09	-	1169.0
AHQ-3-7, 4903	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.22E-05	0.96	4.97	-	1455.6
AHQ-3-3, 5176 - 5245	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.57E-05	0.97	5.35	-	1333.6
AHQ-3-1, 5349 - 5425	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.89E-11	0.95	5.11	-	1054.1
AHQ-3-2, 5349 - 5417	K.ANLQIDQINTDLNLER.S	1871.04187	2	5.38E-06	0.97	5.47	-	1424.9
AHQ-3-10, 4584	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.34E-07	0.96	5.17	-	1353.0
AHQ-3-2, 5219 - 5289	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.83E-08	0.98	5.93	-	1393.5
AHQ-3-9, 4665	K.ANLQIDQINTDLNLER.S	1871.04187	2	5.95E-07	0.96	4.97	-	1211.2
AHQ-3-2, 5089 - 5119	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.28E-06	0.96	5.49	-	1021.0
AHQ-3-3, 5296 - 5368	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.26E-06	0.98	5.65	-	1688.8
AHQ-3-2, 2255 - 2266	K.ASITALEAK.I	904.04321	2	1.67E-04	0.93	3.39	-	1080.4
AHQ-3-1, 2446	K.ASITALEAK.I	904.04321	2	6.84E-07	0.92	3.25	-	1011.6
AHQ-3-5, 2064	K.ASITALEAK.I	904.04321	2	4.63E-06	0.90	3.17	-	930.0
AHQ-3-5, 1695	R.ASREEILAQAK.E	1216.36955	2	4.66E-04	0.83	3.08	-	1055.3
AHQ-3-3, 1905	R.ASREEILAQAK.E	1216.36955	2	2.80E-06	0.93	3.52	-	1548.7
AHQ-3-2, 1883 - 1953	R.ASREEILAQAK.E	1216.36955	2	1.12E-05	0.93	3.33	-	1611.5
AHQ-3-4, 1953	R.ASREEILAQAK.E	1216.36955	2	2.74E-06	0.87	3.02	-	1326.5
AHQ-3-1, 2158	R.ASREEILAQAK.E	1216.36955	2	5.47E-05	0.94	3.43	-	1780.7
AHQ-3-1, 3290	R.DELADEIANSSGK.G	1349.38323	2	9.40E-08	0.94	4.00	-	1296.5
AHQ-3-2, 3247	R.DELADEIANSSGK.G	1349.38323	2	7.23E-06	0.96	4.62	-	1306.9
AHQ-3-3, 3226	R.DELADEIANSSGK.G	1349.38323	2	1.61E-06	0.93	3.70	-	1266.8
AHQ-3-6, 2782	R.DELADEIANSSGK.G	1349.38323	1	1.63E-05	0.28	1.99	-	407.7
AHQ-3-2, 3434	R.DELADEIANSSGK.G	1349.38323	2	8.65E-06	0.93	3.22	-	1436.7
AHQ-3-2, 3431	R.DELADEIANSSGK.G	1349.38323	1	3.10E-09	0.83	3.12	-	648.2
AHQ-3-2, 2914	R.DELADEIANSSGK.G	1349.38323	1	1.25E-09	0.65	2.29	-	611.7
AHQ-3-3, 2878	R.DELADEIANSSGK.G	1349.38323	1	2.85E-05	0.72	2.89	-	489.5
AHQ-3-3, 3224	R.DELADEIANSSGK.G	1349.38323	1	4.15E-06	0.34	1.90	-	444.2

AHQ-3-1, 7118	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	3.64E-04	0.91	4.08	-	1371.7
AHQ-3-4, 7128 - 7144	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	7.93E-08	0.96	5.56	-	1712.0
AHQ-3-3, 7276	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.64E-06	0.92	4.32	-	1380.6
AHQ-3-6, 6881	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	4.14E-12	0.97	6.27	-	1503.3
AHQ-3-2, 7362 - 7369	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.27E-07	0.94	5.01	-	1016.2
AHQ-3-2, 7199 - 7235	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.20E-11	0.98	6.78	-	2380.9
AHQ-3-5, 7031	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.48E-05	0.96	4.99	-	1594.8
AHQ-3-3, 7108 - 7138	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	8.38E-04	0.77	3.20	-	1135.4
AHQ-3-3, 6676	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	4.68E-08	0.77	3.59	-	549.9
AHQ-3-3, 6688	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	2	8.08E-08	0.84	3.62	-	390.9
AHQ-3-1, 6558 - 6624	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	4.87E-09	0.86	4.14	-	573.3
AHQ-3-4, 6610 - 6690	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	1.27E-07	0.85	4.34	-	568.2
AHQ-3-2, 6769	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	2	9.23E-11	0.76	3.62	-	328.6
AHQ-3-2, 6759	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	1.51E-10	0.68	3.31	-	527.1
AHQ-3-2, 2045	K.DLEAHIDSANK.N	1213.27938	2	1.45E-06	0.98	4.61	-	3186.1
AHQ-3-1, 2245	K.DLEAHIDSANK.N	1213.27938	2	3.22E-06	0.97	4.25	-	2505.5
AHQ-3-3, 2050	K.DLEAHIDSANK.N	1213.27938	2	2.46E-06	0.98	4.62	-	2524.4
AHQ-3-2, 2451	K.DLEAHIDSANKNRDEAIK.Q	2040.18063	2	1.01E-04	0.92	4.31	-	833.6
AHQ-3-2, 7741	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	6.37E-08	0.97	5.46	-	2267.3
AHQ-3-2, 7633	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	4.52E-12	0.97	6.12	-	1619.0
AHQ-3-6, 7369	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.18E-10	0.97	6.06	-	2175.2
AHQ-3-4, 7572 - 7614	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.48E-10	0.97	5.69	-	1960.5
AHQ-3-7, 7450	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.56E-05	0.93	4.40	-	1378.6
AHQ-3-5, 7551	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	4.05E-10	0.97	5.80	-	2286.0
AHQ-3-1, 3436	K.DVLLQVDDER.R	1202.29650	2	2.40E-05	0.85	2.93	-	837.7
AHQ-3-2, 3455	K.DVLLQVDDER.R	1202.29650	1	1.47E-07	0.26	2.00	-	301.3
AHQ-3-2, 3458	K.DVLLQVDDER.R	1202.29650	2	5.46E-07	0.92	3.29	-	1355.0
AHQ-3-1, 3001 - 3005	K.DVLLQVDDERR.N	1358.48286	2	1.71E-05	0.80	3.01	-	1027.1
AHQ-3-3, 2848	K.DVLLQVDDERR.N	1358.48286	2	5.17E-04	0.52	3.06	-	451.7
AHQ-3-2, 1655 - 1806	R.EEILAQAK.E	902.02731	1	1.30E-04	0.60	2.88	-	280.5
AHQ-3-6, 2717	R.ELEDATETADAMNR.E	1566.63006	2	2.52E-07	0.91	3.37	-	1388.5
AHQ-3-4, 2848 - 2908	R.ELEDATETADAMNR.E	1566.63006	2	1.77E-09	0.94	4.21	-	1043.3
AHQ-3-3, 2858	R.ELEDATETADAMNR.E	1566.63006	2	2.00E-05	0.92	3.64	-	1163.0
AHQ-3-2, 2877	R.ELEDATETADAMNR.E	1566.63006	2	4.76E-10	0.92	3.69	-	1112.3
AHQ-3-5, 2763	R.ELEDATETADAMNR.E	1566.63006	2	2.16E-06	0.89	3.64	-	942.5
AHQ-3-1, 2370	R.ELEDATETADAM*NR.E	1582.62946	2	9.90E-07	0.84	3.50	-	687.9
AHQ-3-4, 5917 - 5988	R.ELESQISELQEDLESER.A	2035.10956	2	2.72E-06	0.95	4.82	-	1324.3
AHQ-3-5, 5859 - 5879	R.ELESQISELQEDLESER.A	2035.10956	2	2.30E-04	0.91	3.92	-	907.0
AHQ-3-3, 6046	R.ELESQISELQEDLESER.A	2035.10956	3	2.27E-08	0.98	6.11	-	2476.9
AHQ-3-9, 5459	R.ELESQISELQEDLESER.A	2035.10956	2	4.88E-04	0.85	3.78	-	492.7
AHQ-3-7, 5736	R.ELESQISELQEDLESER.A	2035.10956	2	1.70E-07	0.95	4.43	-	1024.0
AHQ-3-3, 6593 - 6660	R.ELESQISELQEDLESER.A	2035.10956	2	7.67E-05	0.83	3.60	-	348.4
AHQ-3-3, 6360	R.ELESQISELQEDLESER.A	2035.10956	2	1.13E-04	0.71	2.85	-	736.1
AHQ-3-2, 6077	R.ELESQISELQEDLESER.A	2035.10956	3	1.49E-06	0.97	5.37	-	1911.0
AHQ-3-2, 6521	R.ELESQISELQEDLESER.A	2035.10956	2	9.06E-08	0.95	4.35	-	1335.8
AHQ-3-1, 6044	R.ELESQISELQEDLESER.A	2035.10956	3	4.03E-07	0.97	5.33	-	2147.2
AHQ-3-1, 6014 - 6058	R.ELESQISELQEDLESER.A	2035.10956	2	1.30E-04	0.90	3.51	-	1049.2
AHQ-3-3, 6020 - 6049	R.ELESQISELQEDLESER.A	2035.10956	2	4.61E-07	0.94	4.43	-	1100.9
AHQ-3-2, 5622	R.ELESQISELQEDLESER.A	2035.10956	2	9.25E-07	0.93	4.64	-	770.5
AHQ-3-1, 6313	R.ELESQISELQEDLESER.A	2035.10956	2	1.08E-07	0.92	4.08	-	944.8
AHQ-3-2, 6089 - 6122	R.ELESQISELQEDLESER.A	2035.10956	2	6.73E-08	0.93	4.23	-	1002.5
AHQ-3-1, 5630	R.ELESQISELQEDLESER.A	2035.10956	2	2.84E-06	0.89	3.90	-	781.5
AHQ-3-2, 6431	R.ELESQISELQEDLESER.A	2035.10956	2	8.70E-07	0.97	5.40	-	1281.5
AHQ-3-3, 2492	R.EMEAELEDER.K	1251.30306	2	5.25E-04	0.75	2.70	-	755.3
AHQ-3-5, 1933	R.EMEAELEDERK.Q	1379.47597	2	9.43E-06	0.79	2.72	-	976.1
AHQ-3-2, 4649 - 4674	K.EQADFAIEALAK.A	1306.44632	2	6.78E-04	0.84	2.99	-	637.1
AHQ-3-3, 2338	R.EQEVNILK.K	973.10554	1	6.38E-04	0.14	2.28	-	174.7
AHQ-3-5, 2183	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.48E-06	0.87	4.26	-	506.9
AHQ-3-6, 2159 - 2162	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	9.04E-04	0.92	4.12	-	865.0
AHQ-3-1, 2494	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.66E-05	0.87	3.98	-	618.9
AHQ-3-4, 2297	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.30E-04	0.83	3.75	-	550.3
AHQ-3-2, 3501	R.FLSNGHVTIPGQQDK.D	1641.80946	2	1.54E-04	0.90	3.65	-	854.3
AHQ-3-3, 3472	R.FLSNGHVTIPGQQDK.D	1641.80946	2	2.53E-09	0.93	3.70	-	1142.4
AHQ-3-3, 6136	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	3.56E-05	0.94	5.38	-	994.6
AHQ-3-4, 6053	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	7.15E-04	0.87	4.23	-	639.2
AHQ-3-3, 3608	K.FVSELWK.D	909.06314	1	3.92E-04	0.33	2.32	-	505.8
AHQ-3-1, 2977	K.HEAMITDLEER.L	1344.47646	2	1.10E-07	0.97	4.12	-	1488.1
AHQ-3-2, 2755 - 2761	K.HEAMITDLEER.L	1344.47646	2	6.27E-09	0.96	3.97	-	1319.7
AHQ-3-1, 2522	K.HEAM*ITDLEER.L	1360.47586	2	7.01E-04	0.96	4.04	-	1395.3
AHQ-3-3, 2740 - 2742	K.HEAMITDLEER.L	1344.47646	2	1.87E-04	0.95	3.80	-	1115.9
AHQ-3-3, 3497 - 3537	R.HEMPPHIYAITDTAYR.S	1916.14944	2	3.67E-05	0.87	3.54	-	610.6
AHQ-3-3, 3538	R.HEMPPHIYAITDTAYR.S	1916.14944	3	4.63E-04	0.97	3.92	-	2626.2
AHQ-3-2, 3589	R.HEMPPHIYAITDTAYR.S	1916.14944	3	4.96E-11	0.98	5.58	-	2774.2
AHQ-3-2, 3506 - 3587	R.HEMPPHIYAITDTAYR.S	1916.14944	2	4.87E-06	0.95	3.78	-	1169.2
AHQ-3-10, 2904	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	3.86E-04	0.79	2.83	-	540.4
AHQ-3-1, 3836	R.HEMPPHIYAITDTAYR.S	1916.14944	3	7.52E-04	0.91	4.01	-	1458.5
AHQ-3-4, 3128	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	6.86E-06	0.80	2.88	-	627.8
AHQ-3-3, 3194	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	9.57E-08	0.95	4.36	-	1381.4
AHQ-3-1, 3398	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	2.18E-05	0.90	3.34	-	787.2
AHQ-3-10, 3159	R.HEMPPHIYAITDTAYR.S	1916.14944	2	5.16E-05	0.89	3.66	-	596.2
AHQ-3-2, 3183 - 3257	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	2.62E-06	0.96	4.11	-	1883.9
AHQ-3-5, 2933 - 2941	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	2.81E-05	0.96	4.95	-	1516.4
AHQ-3-1, 3329 - 3401	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	1.13E-04	0.94	4.13	-	1619.2
AHQ-3-6, 2910	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	1.28E-05	0.97	4.62	-	1892.3
AHQ-3-2, 3659 - 3661	R.HEMPPHIYAITDTAYR.S	1916.14944	2	5.03E-06	0.90	3.51	-	751.7
AHQ-3-6, 4181 - 4234	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.39E-04	0.91	4.18	-	1307.8
AHQ-3-4, 4482	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.85E-06	0.94	4.98	-	1395.8
AHQ-3-4, 4461	K.HSQAVEELAEQLEQTK.R	1840.96940	2	4.97E-06	0.98	5.64	-	2093.1
AHQ-3-2, 4597 - 4665	K.HSQAVEELAEQLEQTK.R	1840.96940	2	4.99E-09	0.98	5.41	-	2086.4
AHQ-3-3, 4561 - 4633	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.13E-10	0.98	6.28	-	2384.9
AHQ-3-3, 4572	K.HSQAVEELAEQLEQTK.R	1840.96940	3	2.16E-07	0.96	4.85	-	1994.8
AHQ-3-2, 4899	K.HSQAVEELAEQLEQTK.R	1840.96940	2	3.50E-07	0.96	4.40	-	1544.6
AHQ-3-3, 4853	K.HSQAVEELAEQLEQTK.R	1840.96940	2	4.67E-08	0.98	4.72	-	2715.1
AHQ-3-1, 4714	K.HSQAVEELAEQLEQTK.R	1840.96940	3	6.24E-07	0.97	5.16	-	2509.6
AHQ-3-1, 4706	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.21E-04	0.93	4.31	-	1109.5
AHQ-3-5, 4187 - 4260	K.HSQAVEELAEQLEQTK.R	1840.96940	2	4.89E-07	0.93	4.26	-	1404.7
AHQ-3-2, 4599 - 4605	K.HSQAVEELAEQLEQTK.R	1840.96940	3	7.77E-07	0.96	5.24	-	1656.2
AHQ-3-1, 4316	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	9.53E-05	0.97	5.76	-	1760.4
AHQ-3-3, 4062	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	5.43E-11	0.98	6.31	-	2233.8
AHQ-3-4, 3988	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	2.13E-10	0.98	6.52	-	2056.1
AHQ-3-7, 3680	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.29E-06	0.98	5.92	-	1963.7
AHQ-3-4, 3989	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	5.15E-06	0.97	5.74	-	1698.5
AHQ-3-2, 4110	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	5.50E-14	0.99	7.25	-	3194.7
AHQ-3-2, 4109	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	3.19E-06	0.98	6.83	-	2024.5
AHQ-3-3, 4060 - 4072	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	5.78E-13	0.98	6.79	-	1696.6
AHQ-3-6, 3765	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	6.42E-05	0.97	5.87	-	1618.1
AHQ-3-1, 4317	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	2.71E-13	0.98	5.77	-	1850.0

AHQ-3-5, 3769	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	6.12E-06	0.96	5.52	-	1253.4
AHQ-3-5, 3776 - 3777	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.17E-13	0.98	6.62	-	2374.7
AHQ-3-2, 4882 - 4957	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.55E-04	0.49	2.81	-	655.1
AHQ-3-7, 3470	R.IAEFTTNLTEEEEK.S	1654.75371	2	6.11E-06	0.85	3.07	-	1278.3
AHQ-3-4, 3680 - 3756	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.76E-09	0.96	4.42	-	1739.2
AHQ-3-5, 3537 - 3608	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.53E-05	0.96	4.09	-	1839.2
AHQ-3-3, 4020 - 4097	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.95E-08	0.96	4.57	-	1962.0
AHQ-3-4, 3838	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.89E-05	0.64	2.92	-	619.2
AHQ-3-2, 3809 - 3877	R.IAEFTTNLTEEEEK.S	1654.75371	2	7.19E-11	0.97	5.19	-	2005.6
AHQ-3-1, 3869 - 3944	R.IAEFTTNLTEEEEK.S	1654.75371	2	7.60E-07	0.97	5.00	-	2002.0
AHQ-3-3, 3734 - 3804	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.25E-06	0.97	4.93	-	1701.2
AHQ-3-1, 4012 - 4088	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.60E-07	0.97	4.76	-	1954.8
AHQ-3-2, 4114 - 4185	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.71E-08	0.96	4.58	-	1806.0
AHQ-3-2, 3945 - 3975	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.45E-06	0.96	4.42	-	1782.8
AHQ-3-6, 3486	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.61E-09	0.97	4.78	-	2078.1
AHQ-3-2, 4387 - 4415	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.41E-04	0.92	3.08	-	1341.9
AHQ-3-2, 4022 - 4045	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.71E-10	0.97	5.23	-	1832.1
AHQ-3-3, 3872 - 3949	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.28E-07	0.97	4.69	-	2303.9
AHQ-3-1, 4160	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.76E-04	0.80	3.19	-	919.4
AHQ-3-1, 4014	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.48E-06	0.83	3.03	-	1251.9
AHQ-3-2, 4294	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.49E-05	0.92	3.61	-	1319.2
AHQ-3-3, 3330	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	6.20E-08	0.86	3.80	-	772.5
AHQ-3-4, 3289	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	4.35E-06	0.78	3.06	-	769.9
AHQ-3-2, 3321 - 3327	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	1.70E-09	0.89	4.15	-	706.7
AHQ-3-2, 5789 - 5795	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	1.54E-08	0.95	4.60	-	1243.3
AHQ-3-1, 5721	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	2.95E-07	0.86	3.73	-	639.4
AHQ-3-6, 3117	K.IAQLEEQLDNETK.E	1531.64695	2	1.03E-09	0.97	4.88	-	1757.3
AHQ-3-5, 3167 - 3172	K.IAQLEEQLDNETK.E	1531.64695	2	1.98E-04	0.89	3.59	-	917.5
AHQ-3-1, 3620 - 3698	K.IAQLEEQLDNETK.E	1531.64695	2	7.95E-04	0.96	4.32	-	1532.8
AHQ-3-2, 2927	K.IAQLEEQLDNETK.E	1531.64695	2	2.17E-08	0.96	4.72	-	1230.1
AHQ-3-3, 3169	K.IAQLEEQLDNETK.E	1531.64695	2	1.05E-05	0.96	4.66	-	1622.3
AHQ-3-7, 3084	K.IAQLEEQLDNETK.E	1531.64695	2	2.11E-09	0.97	4.79	-	1708.6
AHQ-3-3, 2922	K.IAQLEEQLDNETK.E	1531.64695	2	2.61E-05	0.85	2.74	-	1232.0
AHQ-3-3, 3368 - 3372	K.IAQLEEQLDNETK.E	1531.64695	2	6.84E-05	0.92	3.33	-	1536.7
AHQ-3-2, 3550 - 3551	K.IAQLEEQLDNETK.E	1531.64695	2	4.99E-10	0.96	4.94	-	1445.5
AHQ-3-4, 3334	K.IAQLEEQLDNETK.E	1531.64695	2	3.15E-07	0.96	4.18	-	1761.7
AHQ-3-6, 2982	K.IAQLEEQLDNETK.E	1531.64695	2	2.13E-06	0.57	2.90	-	296.4
AHQ-3-1, 3472	K.IAQLEEQLDNETK.E	1531.64695	2	2.70E-06	0.92	3.53	-	1234.0
AHQ-3-1, 3920	K.IAQLEEQLDNETK.E	1531.64695	2	1.28E-07	0.80	3.18	-	573.0
AHQ-3-1, 3249	K.IAQLEEQLDNETK.E	1531.64695	2	1.24E-06	0.95	4.36	-	1506.5
AHQ-3-9, 2933	K.IAQLEEQLDNETK.E	1531.64695	2	1.02E-10	0.96	4.63	-	1601.4
AHQ-3-1, 3037	K.IAQLEEQLDNETK.E	1531.64695	2	1.07E-05	0.93	3.71	-	1266.5
AHQ-3-11, 3154	K.IAQLEEQLDNETK.E	1531.64695	2	1.03E-04	0.94	3.65	-	1555.4
AHQ-3-10, 3078	K.IAQLEEQLDNETK.E	1531.64695	2	1.55E-04	0.92	3.56	-	1137.6
AHQ-3-2, 3114 - 3189	K.IAQLEEQLDNETK.E	1531.64695	2	4.87E-08	0.97	5.11	-	1769.0
AHQ-3-2, 3505	K.IAQLEEQLDNETKER.Q	1816.94784	2	1.58E-08	0.96	4.95	-	1282.1
AHQ-3-1, 3189 - 3192	K.IAQLEEQLDNETKER.Q	1816.94784	2	8.30E-07	0.75	3.22	-	748.5
AHQ-3-3, 3465	K.IAQLEEQLDNETKER.Q	1816.94784	2	8.19E-09	0.93	4.63	-	904.7
AHQ-3-2, 3333	K.IAQLEEQLDNETKER.Q	1816.94784	2	7.91E-05	0.36	2.88	-	347.7
AHQ-3-2, 6142 - 6209	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.07E-05	0.96	4.96	-	1037.5
AHQ-3-2, 6837 - 6910	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.07E-08	0.97	5.13	-	1459.2
AHQ-3-1, 6745	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	2.61E-04	0.91	4.61	-	962.1
AHQ-3-3, 6166 - 6169	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.57E-04	0.94	4.42	-	963.7
AHQ-3-5, 6691 - 6693	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.05E-06	0.97	5.32	-	1327.2
AHQ-3-6, 5646	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	6.22E-06	0.94	4.47	-	846.3
AHQ-3-1, 6732	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.19E-04	0.96	4.59	-	1341.3
AHQ-3-3, 5936	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	3.66E-04	0.90	4.00	-	633.5
AHQ-3-3, 6788 - 6856	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.47E-05	0.95	4.52	-	1226.7
AHQ-3-3, 5452	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	4.57E-04	0.83	3.54	-	549.1
AHQ-3-6, 6465 - 6545	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.09E-09	0.97	5.76	-	1329.9
AHQ-3-14, 6347	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.56E-04	0.93	4.52	-	681.5
AHQ-3-13, 6367	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.14E-04	0.89	4.12	-	640.3
AHQ-3-2, 5505	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.57E-06	0.96	5.05	-	1126.6
AHQ-3-4, 6765 - 6833	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.69E-05	0.97	5.39	-	1208.5
AHQ-3-1, 5873 - 5944	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	2.35E-04	0.86	4.26	-	552.7
AHQ-3-7, 6534 - 6535	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.88E-06	0.97	5.59	-	1455.3
AHQ-3-6, 6549 - 6550	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.54E-06	0.97	5.62	-	1302.2
AHQ-3-1, 5496 - 5500	R.IMGIPEEEQMGLLR.V	1616.92826	2	5.19E-08	0.88	4.20	-	387.7
AHQ-3-6, 4414 - 4481	R.IM*GIPEEEQMGLLR.V	1632.92766	2	2.53E-06	0.85	3.37	-	667.4
AHQ-3-7, 5006 - 5074	R.IMGIPEEEQMGLLR.V	1616.92826	2	5.53E-04	0.35	2.63	-	236.9
AHQ-3-7, 4392	R.IM*GIPEEEQMGLLR.V	1632.92766	2	1.35E-05	0.94	4.04	-	1012.3
AHQ-3-2, 4053 - 4055	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	4.37E-04	0.94	4.53	-	919.2
AHQ-3-7, 3702	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	6.58E-05	0.75	3.32	-	511.4
AHQ-3-5, 5219 - 5220	R.IMGIPEEEQMGLLR.V	1616.92826	2	2.36E-08	0.84	3.25	-	487.3
AHQ-3-3, 4013	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	8.20E-05	0.78	3.23	-	524.6
AHQ-3-3, 5412 - 5430	R.IMGIPEEEQMGLLR.V	1616.92826	2	1.25E-04	0.67	2.92	-	302.7
AHQ-3-2, 4821	R.IM*GIPEEEQMGLLR.V	1632.92766	2	1.43E-08	0.93	3.62	-	905.9
AHQ-3-2, 4731 - 4811	R.IMGIPEEEQM*GLLR.V	1632.92766	2	2.23E-06	0.92	4.04	-	626.4
AHQ-3-5, 4571 - 4643	R.IM*GIPEEEQMGLLR.V	1632.92766	2	1.03E-06	0.81	3.44	-	619.9
AHQ-3-3, 5972	K.IRELESQISELQEDLESER.A	2304.45416	2	1.06E-06	0.98	6.57	-	1653.3
AHQ-3-3, 5477	K.IRELESQISELQEDLESER.A	2304.45416	2	5.98E-04	0.63	2.65	-	517.6
AHQ-3-4, 5905 - 5906	K.IRELESQISELQEDLESER.A	2304.45416	2	6.16E-12	0.98	6.93	-	1610.8
AHQ-3-6, 5662	K.IRELESQISELQEDLESER.A	2304.45416	3	7.65E-10	0.97	5.47	-	2231.4
AHQ-3-3, 5970 - 5984	K.IRELESQISELQEDLESER.A	2304.45416	3	1.05E-06	0.97	5.71	-	1647.2
AHQ-3-5, 5632 - 5695	K.IRELESQISELQEDLESER.A	2304.45416	2	6.86E-05	0.98	5.67	-	1323.6
AHQ-3-2, 6014	K.IRELESQISELQEDLESER.A	2304.45416	3	9.07E-12	0.98	6.23	-	2373.7
AHQ-3-7, 5564	K.IRELESQISELQEDLESER.A	2304.45416	3	9.58E-04	0.90	3.72	-	1496.5
AHQ-3-1, 6053 - 6062	K.IRELESQISELQEDLESER.A	2304.45416	3	1.15E-08	0.97	5.98	-	1904.5
AHQ-3-1, 6054 - 6057	K.IRELESQISELQEDLESER.A	2304.45416	2	2.89E-07	0.98	7.19	-	1412.8
AHQ-3-2, 6013 - 6079	K.IRELESQISELQEDLESER.A	2304.45416	2	2.71E-07	0.99	7.59	-	2539.1
AHQ-3-4, 5910 - 5924	K.IRELESQISELQEDLESER.A	2304.45416	3	1.78E-10	0.98	6.08	-	2144.7
AHQ-3-2, 4657 - 4729	K.KANLQIDQINTDLNLER.S	1999.21478	2	4.34E-07	0.98	5.94	-	1533.1
AHQ-3-3, 4468	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.69E-05	0.93	4.61	-	840.3
AHQ-3-3, 4630 - 4708	K.KANLQIDQINTDLNLER.S	1999.21478	2	4.97E-05	0.98	5.76	-	1810.5
AHQ-3-6, 4250	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.82E-08	0.98	5.76	-	1934.0
AHQ-3-2, 4445 - 4507	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.36E-05	0.94	4.74	-	750.2
AHQ-3-2, 4518	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.97E-05	0.91	4.84	-	723.3
AHQ-3-5, 4335	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.50E-06	0.97	5.97	-	1229.7
AHQ-3-2, 5039	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.38E-07	0.96	5.01	-	1345.4
AHQ-3-2, 4851	K.KANLQIDQINTDLNLER.S	1999.21478	2	4.89E-08	0.97	5.87	-	1529.4
AHQ-3-2, 4666	K.KANLQIDQINTDLNLER.S	1999.21478	3	7.25E-05	0.93	4.86	-	1158.7
AHQ-3-1, 4549	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.45E-05	0.94	4.60	-	1053.5
AHQ-3-3, 4744	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.08E-06	0.90	4.60	-	575.7
AHQ-3-1, 4902	K.KANLQIDQINTDLNLER.S	1999.21478	2	5.35E-06	0.97	5.66	-	1189.3
AHQ-3-3, 4814 - 4830	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.13E-07	0.95	4.86	-	1129.4
AHQ-3-2, 2707	K.KKM*EDSVGCLETAEEVK.R	1971.19681	2	7.32E-05	0.91	3.53	-	1131.7
AHQ-3-6, 2237	R.KKVEAQLQELQVK.F	1541.81761	2	1.08E-06	0.96	5.11	-	1120.8

AHQ-3-4, 2388	R.KKVEAQLQELQVK.F	1541.81761	2	7.69E-06	0.98	5.38	-	2056.2
AHQ-3-2, 2417 - 2437	R.KKVEAQLQELQVK.F	1541.81761	2	8.62E-08	0.98	5.57	-	1734.6
AHQ-3-3, 2409 - 2428	R.KKVEAQLQELQVK.F	1541.81761	2	5.99E-08	0.97	5.29	-	1577.4
AHQ-3-5, 2239 - 2247	R.KKVEAQLQELQVK.F	1541.81761	2	1.33E-07	0.98	5.02	-	2178.4
AHQ-3-4, 3370	K.KLEEEQIILEDQNCK.L	1891.08992	2	9.04E-05	0.98	5.78	-	1749.1
AHQ-3-3, 3520 - 3588	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.39E-12	0.98	5.48	-	1783.5
AHQ-3-3, 3657 - 3660	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.92E-04	0.92	4.09	-	525.0
AHQ-3-2, 3698 - 3778	K.KLEEEQIILEDQNCK.L	1891.08992	2	6.38E-08	0.97	5.11	-	1000.3
AHQ-3-2, 3545 - 3613	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.46E-10	0.98	6.11	-	2123.8
AHQ-3-6, 3150	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.08E-04	0.97	4.86	-	1536.8
AHQ-3-2, 3474	K.KLEEEQIILEDQNCK.L	1891.08992	3	5.99E-07	0.95	5.04	-	1534.8
AHQ-3-1, 3684	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.92E-08	0.98	5.42	-	1957.6
AHQ-3-2, 3407 - 3477	K.KLEEEQIILEDQNCK.L	1891.08992	2	7.38E-06	0.98	6.08	-	2124.8
AHQ-3-3, 3417	K.KLEEEQIILEDQNCK.L	1891.08992	2	9.77E-11	0.97	5.55	-	1612.4
AHQ-3-4, 3485 - 3516	K.KLEEEQIILEDQNCK.L	1891.08992	2	8.73E-07	0.98	6.00	-	1926.9
AHQ-3-1, 4049	K.KLEEEQIILEDQNCKLAK.E	2203.49930	3	6.47E-05	0.95	4.61	-	1513.0
AHQ-3-5, 7252 - 7267	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.79E-06	0.96	5.02	-	1587.6
AHQ-3-4, 7356 - 7365	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.17E-07	0.89	5.04	-	681.1
AHQ-3-1, 7172	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.67E-09	0.90	4.76	-	802.2
AHQ-3-4, 7352 - 7420	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.17E-08	0.95	4.79	-	1139.6
AHQ-3-2, 7441 - 7518	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	5.15E-07	0.97	6.62	-	1121.3
AHQ-3-3, 7336 - 7400	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	6.42E-08	0.97	6.38	-	1364.3
AHQ-3-2, 7435 - 7439	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	1.16E-07	0.93	5.81	-	848.3
AHQ-3-6, 7109 - 7115	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	4.23E-05	0.91	4.64	-	1019.0
AHQ-3-6, 7114	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	5.53E-05	0.97	5.32	-	1322.3
AHQ-3-3, 7337 - 7348	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	1.27E-05	0.86	4.87	-	698.9
AHQ-3-2, 2578	K.KLVWVPSDK.S	1072.28194	1	5.19E-05	0.61	2.79	-	510.5
AHQ-3-10, 2487	K.KLVWVPSDK.S	1072.28194	2	3.21E-04	0.64	2.84	-	536.7
AHQ-3-4, 2584	K.KLVWVPSDK.S	1072.28194	1	8.44E-05	0.76	2.67	-	674.0
AHQ-3-2, 2594	K.KLVWVPSDK.S	1072.28194	2	5.46E-04	0.84	3.19	-	780.2
AHQ-3-13, 2783	K.KLVWVPSDK.S	1072.28194	1	3.19E-05	0.60	2.75	-	506.0
AHQ-3-3, 3113	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	6.49E-05	0.76	2.69	-	903.9
AHQ-3-2, 3129	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	1.11E-06	0.86	3.17	-	869.7
AHQ-3-3, 3600	K.KMEDSVGCLETAEEVK.R	1827.02450	2	4.14E-06	0.96	4.65	-	1467.5
AHQ-3-3, 2816	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	3.08E-05	0.86	3.24	-	841.6
AHQ-3-2, 2825	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	2.26E-05	0.95	5.08	-	1320.8
AHQ-3-1, 3012	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	4.17E-04	0.57	3.01	-	468.8
AHQ-3-1, 3385	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	8.02E-11	0.94	4.98	-	969.8
AHQ-3-3, 3220	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	4.81E-06	0.96	5.04	-	1729.6
AHQ-3-2, 3221	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	1.36E-07	0.96	4.72	-	1526.2
AHQ-3-2, 3227	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	3.21E-10	0.97	6.66	-	1376.0
AHQ-3-2, 2815 - 2827	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	2.66E-04	0.87	3.74	-	569.4
AHQ-3-3, 5405	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	3.10E-05	0.95	4.62	-	1031.7
AHQ-3-1, 5568 - 5573	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	1.45E-04	0.97	5.60	-	1399.1
AHQ-3-2, 4981	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	1.17E-04	0.91	4.62	-	925.9
AHQ-3-3, 4940	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	5.56E-08	0.90	4.32	-	1153.9
AHQ-3-1, 5014	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	2.26E-06	0.90	4.36	-	574.7
AHQ-3-4, 4016	K.KQELEEICHDLEAR.V	1771.93036	3	3.23E-04	0.93	4.46	-	1403.6
AHQ-3-7, 3719	K.KQELEEICHDLEAR.V	1771.93036	2	6.73E-05	0.92	3.72	-	1524.7
AHQ-3-2, 4135 - 4189	K.KQELEEICHDLEAR.V	1771.93036	2	1.59E-05	0.97	5.52	-	1837.5
AHQ-3-5, 3815 - 3816	K.KQELEEICHDLEAR.V	1771.93036	2	1.52E-07	0.96	5.08	-	1674.8
AHQ-3-4, 3993 - 4029	K.KQELEEICHDLEAR.V	1771.93036	2	2.45E-05	0.95	4.69	-	1307.1
AHQ-3-2, 4134 - 4205	K.KQELEEICHDLEAR.V	1771.93036	3	1.81E-06	0.96	5.42	-	1886.8
AHQ-3-2, 4374	K.KQELEEICHDLEAR.V	1771.93036	2	1.30E-10	0.94	3.97	-	1453.4
AHQ-3-1, 4272	K.KQELEEICHDLEAR.V	1771.93036	3	8.84E-04	0.93	4.90	-	1056.5
AHQ-3-2, 2769	K.KVEAQLQELQVK.F	1413.64470	2	9.68E-06	0.97	5.00	-	1543.5
AHQ-3-3, 2764 - 2765	K.KVEAQLQELQVK.F	1413.64470	2	2.90E-06	0.97	5.15	-	1652.7
AHQ-3-4, 2705	K.KVEAQLQELQVK.F	1413.64470	2	3.12E-07	0.97	4.90	-	1685.7
AHQ-3-6, 2575	K.KVEAQLQELQVK.F	1413.64470	2	5.23E-07	0.95	4.40	-	1386.5
AHQ-3-3, 2777	K.KVEAQLQELQVK.F	1413.64470	1	1.71E-05	0.65	2.93	-	460.2
AHQ-3-5, 2561	K.KVEAQLQELQVK.F	1413.64470	2	1.08E-04	0.95	4.32	-	1527.5
AHQ-3-2, 3614	K.KVIQYLAYVASSHK.S	1607.87775	2	8.49E-10	0.98	5.64	-	2485.4
AHQ-3-2, 4070	K.LEEEQIILEDQNCK.L	1762.91700	2	1.37E-07	0.96	5.02	-	1174.2
AHQ-3-3, 3932 - 4000	K.LEEEQIILEDQNCK.L	1762.91700	2	1.00E-07	0.94	4.44	-	1005.9
AHQ-3-1, 4032	K.LEEEQIILEDQNCK.L	1762.91700	2	1.36E-08	0.95	4.72	-	1006.6
AHQ-3-4, 3809	K.LEEEQIILEDQNCK.L	1762.91700	2	7.78E-05	0.89	3.57	-	914.3
AHQ-3-3, 3850	K.LEEEQIILEDQNCK.L	1762.91700	2	3.93E-09	0.95	4.47	-	1323.6
AHQ-3-1, 3949 - 3960	K.LEEEQIILEDQNCK.L	1762.91700	2	1.01E-08	0.96	5.10	-	1327.5
AHQ-3-2, 3978	K.LEEEQIILEDQNCK.L	1762.91700	2	5.72E-09	0.94	4.71	-	893.3
AHQ-3-1, 7237	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	1.02E-06	0.96	5.48	-	1551.1
AHQ-3-4, 7473	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	5.13E-11	0.97	6.22	-	1260.6
AHQ-3-2, 7545	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	4.85E-05	0.56	2.88	-	448.5
AHQ-3-1, 3662	R.LEVNLQAMK.A	1046.26630	2	7.77E-04	0.91	3.71	-	754.6
AHQ-3-2, 3473	R.LEVNLQAMK.A	1046.26630	2	7.77E-04	0.83	3.10	-	548.3
AHQ-3-1, 2677	R.LEVNLQAM*K.A	1062.26570	2	9.11E-05	0.82	3.16	-	564.6
AHQ-3-4, 3685	R.LEVNLQAMK.A	1046.26630	1	3.40E-04	0.09	2.05	-	218.7
AHQ-3-2, 3802	R.LEVNLQAMK.A	1046.26630	1	1.13E-05	0.47	2.34	-	522.4
AHQ-3-5, 3125	K.LKDVLLQVDDER.R	1443.62767	2	8.15E-05	0.87	2.98	-	1032.7
AHQ-3-2, 3319 - 3399	K.LKDVLLQVDDER.R	1443.62767	2	8.31E-08	0.97	4.70	-	1775.4
AHQ-3-1, 3618 - 3690	K.LKDVLLQVDDER.R	1443.62767	2	5.39E-06	0.88	3.58	-	968.2
AHQ-3-3, 3401 - 3405	K.LKDVLLQVDDER.R	1443.62767	2	1.46E-08	0.95	3.81	-	1582.8
AHQ-3-3, 2925 - 2926	K.LKDVLLQVDDERR.N	1599.81402	2	8.08E-05	0.89	3.72	-	959.4
AHQ-3-2, 2917 - 2918	K.LKDVLLQVDDERR.N	1599.81402	2	7.07E-05	0.96	4.57	-	1562.7
AHQ-3-4, 2877	K.LKDVLLQVDDERR.N	1599.81402	2	3.92E-05	0.74	3.23	-	790.6
AHQ-3-1, 3148	K.LKDVLLQVDDERR.N	1599.81402	2	1.49E-05	0.95	3.86	-	1885.7
AHQ-3-2, 7717 - 7781	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	3	3.06E-04	0.90	4.36	-	1024.8
AHQ-3-1, 7458	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	4.95E-07	0.90	3.71	-	681.6
AHQ-3-2, 6470 - 6474	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.08E-08	0.86	3.73	-	934.7
AHQ-3-6, 5945	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.09E-10	0.97	5.25	-	1788.3
AHQ-3-4, 6152 - 6165	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.55E-08	0.97	5.04	-	1815.9
AHQ-3-5, 6003 - 6023	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	4.29E-05	0.95	5.24	-	1032.6
AHQ-3-2, 5729	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.29E-10	0.96	4.57	-	1364.2
AHQ-3-2, 6354	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	8.96E-05	0.91	4.03	-	1043.1
AHQ-3-6, 5942	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.24E-07	0.88	4.15	-	768.6
AHQ-3-5, 5997 - 6069	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.60E-10	0.97	5.32	-	1431.2
AHQ-3-4, 6156	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	2.01E-04	0.83	3.91	-	583.8
AHQ-3-2, 6349	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.67E-06	0.96	4.70	-	1534.9
AHQ-3-2, 6249 - 6317	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.42E-06	0.91	4.37	-	755.2
AHQ-3-1, 5136	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	8.04E-10	0.92	3.71	-	1203.9
AHQ-3-1, 6289	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	7.66E-10	0.96	5.39	-	1226.9
AHQ-3-5, 6087	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.51E-06	0.91	4.32	-	962.7
AHQ-3-3, 6170 - 6241	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.60E-12	0.96	5.15	-	1229.3
AHQ-3-2, 6214 - 6281	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.11E-09	0.97	5.49	-	1435.9
AHQ-3-3, 5698	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.76E-07	0.94	4.41	-	956.1
AHQ-3-3, 5882 - 5956	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.26E-10	0.97	5.64	-	1633.9
AHQ-3-1, 5654 - 5656	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.47E-09	0.97	5.59	-	1383.0
AHQ-3-1, 5973 - 6042	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.94E-10	0.98	6.32	-	2312.5

AHQ-3-2, 5925 - 5994	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.14E-06	0.96	5.20	-	1282.3
AHQ-3-3, 5948 - 6025	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.87E-12	0.97	6.09	-	1232.8
AHQ-3-2, 6062 - 6134	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.06E-08	0.98	6.77	-	1754.8
AHQ-3-2, 6325 - 6338	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.40E-05	0.91	4.07	-	860.6
AHQ-3-2, 6409 - 6478	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.23E-11	0.95	5.32	-	835.5
AHQ-3-4, 6017 - 6085	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.62E-07	0.96	5.43	-	983.4
AHQ-3-1, 6108	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.70E-08	0.97	5.67	-	1334.0
AHQ-3-3, 6092 - 6160	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.90E-07	0.97	6.33	-	1192.9
AHQ-3-1, 6254	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.89E-15	0.96	4.67	-	1365.9
AHQ-3-2, 6205 - 6277	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.77E-04	0.89	3.60	-	996.3
AHQ-3-3, 6501	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.07E-06	0.95	4.81	-	965.0
AHQ-3-2, 6746	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.52E-04	0.96	5.48	-	1172.5
AHQ-3-4, 5896 - 5936	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.90E-11	0.97	5.62	-	1488.8
AHQ-3-5, 5812 - 5857	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.57E-06	0.96	5.19	-	1101.8
AHQ-3-3, 6228 - 6301	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.77E-08	0.97	6.19	-	1277.8
AHQ-3-3, 6314 - 6382	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.85E-06	0.96	5.07	-	1162.8
AHQ-3-5, 6240	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.96E-06	0.95	5.29	-	939.8
AHQ-3-2, 7273 - 7350	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.92E-08	0.97	5.50	-	1231.4
AHQ-3-2, 3627	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	1.15E-05	0.94	4.06	-	1251.7
AHQ-3-2, 3730	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	3.66E-04	0.93	4.45	-	944.5
AHQ-3-2, 4681	R.LTEMETLQSQLM*AEK.L	1769.03151	2	1.73E-04	0.93	4.12	-	1151.1
AHQ-3-3, 3501 - 3574	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	7.41E-04	0.94	4.17	-	1162.3
AHQ-3-2, 4794 - 4866	R.LTEMETLQSQLM*AEK.L	1769.03151	2	5.14E-06	0.88	3.02	-	1402.6
AHQ-3-1, 4705 - 4776	R.LTEMETLQSQLM*AEK.L	1769.03151	2	7.24E-04	0.93	3.96	-	1249.4
AHQ-3-3, 4636 - 4637	R.LTEMETLQSQLM*AEK.L	1769.03151	2	1.69E-05	0.90	3.86	-	882.8
AHQ-3-3, 5200 - 5216	R.LTEMETLQSQLMAEK.L	1753.03211	2	5.99E-06	0.96	5.05	-	1396.4
AHQ-3-1, 4181 - 4254	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	1.17E-04	0.95	4.16	-	1603.3
AHQ-3-1, 3732	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	3.82E-04	0.91	3.66	-	943.0
AHQ-3-2, 4035	K.MEDSVGCLETAEEVK.R	1698.85159	2	7.70E-07	0.94	4.53	-	844.9
AHQ-3-3, 3980	K.MEDSVGCLETAEEVK.R	1698.85159	2	5.23E-04	0.86	3.31	-	575.2
AHQ-3-2, 3581	K.MEDSVGCLETAEEVKR.K	1855.03794	2	7.32E-07	0.82	3.54	-	462.6
AHQ-3-3, 3544	K.MEDSVGCLETAEEVKR.K	1855.03794	2	7.09E-07	0.83	3.53	-	573.7
AHQ-3-2, 3590	K.MEDSVGCLETAEEVKR.K	1855.03794	3	1.09E-07	0.82	3.89	-	466.5
AHQ-3-1, 3605 - 3678	K.MEDSVGCLETAEEVKR.K	1855.03794	2	1.44E-04	0.34	2.55	-	448.0
AHQ-3-2, 3214	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	1.10E-11	0.94	4.26	-	771.9
AHQ-3-2, 5737 - 5809	K.MQQNIQELEEQLEEEESAR.Q	2334.46063	3	2.64E-08	0.89	3.84	-	1162.5
AHQ-3-13, 5111 - 5181	K.NFINNPLAQADWAAK.K	1673.85315	2	4.31E-05	0.90	3.63	-	1020.9
AHQ-3-3, 5425	K.NFINNPLAQADWAAK.K	1673.85315	2	1.25E-05	0.95	4.67	-	1118.6
AHQ-3-1, 5526 - 5548	K.NFINNPLAQADWAAK.K	1673.85315	2	1.27E-06	0.96	5.07	-	1230.8
AHQ-3-14, 6168	K.NFINNPLAQADWAAK.K	1673.85315	2	8.07E-07	0.95	4.65	-	1016.6
AHQ-3-10, 4718	K.NFINNPLAQADWAAK.K	1673.85315	2	4.15E-05	0.93	4.12	-	938.6
AHQ-3-9, 4793 - 4803	K.NFINNPLAQADWAAK.K	1673.85315	2	1.01E-05	0.93	4.47	-	942.4
AHQ-3-2, 6170	K.NFINNPLAQADWAAK.K	1673.85315	2	8.80E-07	0.94	4.47	-	905.5
AHQ-3-2, 5627	K.NFINNPLAQADWAAK.K	1673.85315	2	4.77E-08	0.87	3.96	-	651.2
AHQ-3-4, 5372	K.NFINNPLAQADWAAK.K	1673.85315	2	1.19E-05	0.94	4.50	-	1067.0
AHQ-3-1, 6084	K.NFINNPLAQADWAAK.K	1673.85315	2	1.06E-06	0.95	4.80	-	1028.7
AHQ-3-3, 6138	K.NFINNPLAQADWAAK.K	1673.85315	2	2.98E-08	0.91	4.24	-	795.4
AHQ-3-5, 5207	K.NFINNPLAQADWAAK.K	1673.85315	2	2.08E-05	0.95	4.29	-	1130.3
AHQ-3-2, 5449 - 5454	K.NFINNPLAQADWAAK.K	1673.85315	2	4.00E-07	0.95	4.58	-	1021.3
AHQ-3-7, 5030	K.NFINNPLAQADWAAK.K	1673.85315	2	1.67E-08	0.92	3.94	-	1055.8
AHQ-3-6, 5110 - 5142	K.NFINNPLAQADWAAK.K	1673.85315	2	3.69E-05	0.92	4.01	-	884.1
AHQ-3-1, 2654	K.NKHEAMITDLEER.L	1586.75247	2	2.14E-08	0.91	3.59	-	918.8
AHQ-3-2, 2414	K.NKHEAMITDLEER.L	1586.75247	2	3.08E-09	0.93	4.10	-	1242.7
AHQ-3-2, 2115	K.NKHEAM*ITDLEER.L	1602.75187	3	2.92E-04	0.94	4.12	-	1463.2
AHQ-3-3, 2400	K.NKHEAMITDLEER.L	1586.75247	2	1.45E-06	0.93	3.63	-	1169.7
AHQ-3-4, 2385 - 2386	K.NKHEAMITDLEER.L	1586.75247	2	1.42E-08	0.94	4.03	-	1275.9
AHQ-3-2, 2423	K.NKHEAM*ITDLEER.L	1602.75187	2	1.91E-04	0.87	3.29	-	886.5
AHQ-3-1, 5365 - 5368	K.NLPIYSEEIVEM*YK.G	1744.98660	2	4.59E-08	0.93	4.41	-	659.6
AHQ-3-11, 5354	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.65E-05	0.85	3.04	-	623.0
AHQ-3-2, 5938 - 5957	K.NLPIYSEEIVEMYK.G	1728.98720	2	7.72E-07	0.94	4.28	-	834.1
AHQ-3-5, 5049 - 5071	K.NLPIYSEEIVEM*YK.G	1744.98660	2	3.46E-06	0.92	3.55	-	856.1
AHQ-3-2, 5293 - 5362	K.NLPIYSEEIVEM*YK.G	1744.98660	2	5.99E-07	0.96	4.56	-	1110.9
AHQ-3-4, 5213 - 5224	K.NLPIYSEEIVEM*YK.G	1744.98660	2	5.57E-04	0.89	3.61	-	685.5
AHQ-3-1, 5997	K.NLPIYSEEIVEMYK.G	1728.98720	2	8.04E-06	0.89	3.51	-	604.4
AHQ-3-5, 5639 - 5661	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.98E-05	0.86	3.05	-	711.7
AHQ-3-3, 5908 - 5916	K.NLPIYSEEIVEMYK.G	1728.98720	2	5.12E-05	0.94	4.63	-	906.9
AHQ-3-7, 5475	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.28E-04	0.73	2.69	-	480.2
AHQ-3-4, 5852 - 5893	K.NLPIYSEEIVEMYK.G	1728.98720	2	6.01E-04	0.70	2.68	-	469.3
AHQ-3-6, 5583 - 5590	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.11E-05	0.95	4.58	-	833.0
AHQ-3-2, 5635	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	3	6.21E-07	0.87	4.04	-	534.7
AHQ-3-1, 5761	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.03E-06	0.80	4.01	-	423.3
AHQ-3-5, 5352	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	4.80E-04	0.92	3.94	-	992.6
AHQ-3-4, 5028	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	6.21E-06	0.91	3.78	-	973.1
AHQ-3-1, 5217	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	9.44E-09	0.92	4.34	-	1148.8
AHQ-3-2, 5149	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	1.43E-04	0.93	3.89	-	1167.4
AHQ-3-3, 5229	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	1.05E-04	0.92	3.81	-	1142.2
AHQ-3-3, 5598 - 5610	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	5.09E-05	0.88	3.95	-	654.3
AHQ-3-2, 5775	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	4.23E-06	0.93	4.15	-	854.7
AHQ-3-3, 5897	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	3.28E-07	0.86	3.84	-	555.6
AHQ-3-2, 5625	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	3.47E-05	0.84	3.96	-	633.8
AHQ-3-6, 5231 - 5305	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.31E-06	0.87	4.05	-	650.4
AHQ-3-2, 5150 - 5174	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	1.86E-06	0.74	3.22	-	685.6
AHQ-3-3, 7570	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	8.27E-07	0.97	5.38	-	1607.8
AHQ-3-1, 7338	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	1.50E-09	0.98	6.29	-	2154.6
AHQ-3-2, 7653	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	6.45E-06	0.98	6.30	-	2726.2
AHQ-3-2, 3230	R.QAQQERDELADEIANSSGK.G	2090.15168	2	6.00E-06	0.86	3.71	-	735.3
AHQ-3-2, 2799 - 2843	R.QAQQERDELADEIANSSGK.G	2090.15168	2	4.77E-04	0.64	3.60	-	193.2
AHQ-3-1, 2905	R.QAQQERDELADEIANSSGK.G	2090.15168	2	6.76E-06	0.44	2.80	-	386.3
AHQ-3-1, 3302 - 3376	R.QAQQERDELADEIANSSGK.G	2090.15168	2	6.79E-05	0.93	4.79	-	569.3
AHQ-3-2, 4662	K.QELEEICHDLEAR.V	1643.75744	2	9.06E-07	0.81	3.32	-	556.8
AHQ-3-3, 4620	K.QELEEICHDLEAR.V	1643.75744	2	2.60E-05	0.58	2.99	-	366.2
AHQ-3-4, 2618	K.QIATLHAQVADMK.K	1426.66697	2	2.05E-04	0.59	2.71	-	176.5
AHQ-3-3, 2162 - 2165	K.QIATLHAQVADM*K.K	1442.66637	2	3.61E-05	0.88	3.77	-	609.2
AHQ-3-2, 1949	R.QLEEAEEEAQR.A	1332.35590	2	5.15E-05	0.64	2.63	-	503.6
AHQ-3-9, 2892	R.RGDLPFVVPR.R	1156.36217	2	5.04E-06	0.93	3.33	-	1241.8
AHQ-3-6, 3061 - 3133	R.RGDLPFVVPR.R	1156.36217	2	9.23E-07	0.92	3.62	-	1069.5
AHQ-3-6, 3118	R.RGDLPFVVPR.R	1156.36217	2	9.99E-05	0.89	3.20	-	790.3
AHQ-3-3, 3433	R.RGDLPFVVPR.R	1156.36217	1	4.93E-04	0.19	1.83	-	180.4
AHQ-3-11, 3242	R.RGDLPFVVPR.R	1156.36217	2	1.77E-04	0.87	3.22	-	1017.3
AHQ-3-3, 3429 - 3437	R.RGDLPFVVPR.R	1156.36217	2	1.59E-06	0.95	4.13	-	1308.9
AHQ-3-4, 3369	R.RGDLPFVVPR.R	1156.36217	2	5.48E-06	0.93	3.54	-	1129.4
AHQ-3-2, 3373 - 3449	R.RGDLPFVVPR.R	1156.36217	2	3.40E-06	0.96	3.96	-	1706.8
AHQ-3-5, 3147 - 3169	R.RGDLPFVVPR.R	1156.36217	2	5.05E-07	0.95	4.04	-	1266.2
AHQ-3-1, 3712	R.RGDLPFVVPR.R	1156.36217	2	2.97E-07	0.92	3.15	-	1408.5
AHQ-3-3, 6945 - 6994	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	7.80E-07	0.93	5.50	-	1164.7
AHQ-3-1, 6944 - 6973	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.34E-06	0.97	6.24	-	1712.4
AHQ-3-1, 6958	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	2	2.88E-04	0.81	3.71	-	537.6

AHQ-3-2, 7069	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.25E-06	0.98	6.67	-	2177.1
AHQ-3-4, 6982	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.43E-06	0.97	6.41	-	1364.9
AHQ-3-2, 2830	K.RQAQQERDELADEIANSSGK.G	2246.33803	2	1.96E-04	0.82	3.95	-	335.7
AHQ-3-2, 1839	K.RQLEEAEEEAQR.A	1488.54225	2	1.41E-05	0.96	4.75	-	1473.7
AHQ-3-2, 7390	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.68E-05	0.80	3.62	-	705.2
AHQ-3-2, 7298	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	5.88E-08	0.94	4.44	-	1733.2
AHQ-3-2, 6485 - 6501	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.09E-07	0.95	5.00	-	1390.8
AHQ-3-2, 6342 - 6413	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.15E-08	0.81	3.86	-	633.7
AHQ-3-14-, 6000	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	5.72E-08	0.88	4.30	-	610.9
AHQ-3-5, 6369	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.14E-05	0.79	3.87	-	568.4
AHQ-3-1, 6404	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	5.35E-08	0.91	4.12	-	1238.0
AHQ-3-6, 6198	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	6.41E-09	0.92	4.27	-	943.4
AHQ-3-3, 6444	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.31E-06	0.88	4.26	-	758.3
AHQ-3-2, 7083 - 7149	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	3.76E-10	0.98	6.47	-	1658.7
AHQ-3-3, 7040 - 7066	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	6.71E-04	0.84	3.43	-	1091.3
AHQ-3-3, 7052	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	1.08E-05	0.94	4.81	-	1382.2
AHQ-3-5, 6924 - 6932	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	8.39E-07	0.95	4.18	-	1830.4
AHQ-3-2, 4885 - 4917	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	6.14E-08	0.98	5.83	-	2272.4
AHQ-3-1, 5018	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	3.63E-07	0.96	4.85	-	1356.6
AHQ-3-4, 7053	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	7.84E-06	0.94	4.27	-	1273.5
AHQ-3-1, 4893 - 4922	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	5.94E-11	0.98	5.70	-	1831.7
AHQ-3-2, 7245	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.13E-06	0.97	5.36	-	1491.5
AHQ-3-2, 7146 - 7165	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	7.30E-04	0.97	5.70	-	2300.4
AHQ-3-2, 4987	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.54E-05	0.89	3.86	-	994.1
AHQ-3-2, 5186	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	4.40E-07	0.95	4.22	-	1429.4
AHQ-3-2, 5799	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	5.76E-05	0.80	3.18	-	1146.2
AHQ-3-6, 6775 - 6793	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	7.53E-08	0.97	5.13	-	1908.1
AHQ-3-2, 5971 - 6042	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	1.23E-04	0.54	3.25	-	641.2
AHQ-3-1, 7002	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	3.04E-05	0.95	4.59	-	1680.5
AHQ-3-2, 7114 - 7181	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.12E-05	0.97	5.87	-	1486.4
AHQ-3-3, 5957 - 6026	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	2.24E-06	0.92	4.21	-	1516.1
AHQ-3-4, 4809	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	7.57E-06	0.90	4.28	-	814.6
AHQ-3-6, 3239	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	1.59E-06	0.97	5.53	-	1578.6
AHQ-3-5, 3297	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	1.64E-05	0.96	4.92	-	1798.4
AHQ-3-7, 3215	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	3.68E-05	0.92	4.35	-	972.5
AHQ-3-10, 3171	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	3.21E-07	0.97	5.73	-	1779.8
AHQ-3-2, 3526	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	2.36E-10	0.98	6.82	-	1620.0
AHQ-3-4, 3453	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	4.37E-05	0.97	5.30	-	1594.1
AHQ-3-5, 3299	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	4.01E-06	0.95	4.45	-	1325.4
AHQ-3-1, 3850 - 3852	K.TDLLLEPYNK.Y	1206.36989	1	5.80E-05	0.31	2.31	-	405.0
AHQ-3-3, 3685 - 3697	K.TDLLLEPYNK.Y	1206.36989	2	4.66E-04	0.94	3.89	-	1298.4
AHQ-3-4, 3656	K.TDLLLEPYNK.Y	1206.36989	2	1.01E-06	0.94	3.86	-	1389.5
AHQ-3-1, 3845	K.TDLLLEPYNK.Y	1206.36989	2	8.68E-06	0.88	3.41	-	997.1
AHQ-3-7, 3326	K.TDLLLEPYNK.Y	1206.36989	2	2.19E-05	0.71	2.69	-	949.3
AHQ-3-6, 3390 - 3409	K.TDLLLEPYNK.Y	1206.36989	2	1.00E-04	0.92	3.69	-	1168.7
AHQ-3-2, 3703 - 3774	K.TDLLLEPYNK.Y	1206.36989	2	3.76E-05	0.94	4.26	-	1083.9
AHQ-3-5, 3448 - 3464	K.TDLLLEPYNK.Y	1206.36989	2	5.97E-04	0.85	3.54	-	895.4
AHQ-3-2, 3894 - 3897	K.TDLLLEPYNKYR.F	1525.73037	2	6.52E-07	0.83	3.42	-	735.7
AHQ-3-5, 4316	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.18E-05	0.88	3.51	-	1240.6
AHQ-3-2, 4521 - 4525	K.TELEDTLDSTAAQQELR.S	1921.00969	2	8.57E-06	0.74	3.02	-	1015.2
AHQ-3-1, 4494 - 4500	K.TELEDTLDSTAAQQELR.S	1921.00969	2	9.84E-12	0.97	4.88	-	1905.6
AHQ-3-2, 3111	R.TEMEDLMSSK.D	1171.32449	2	1.84E-06	0.91	3.35	-	772.8
AHQ-3-2, 3382	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.71E-08	0.91	3.71	-	1067.7
AHQ-3-3, 3349 - 3353	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.42E-04	0.85	3.25	-	1043.8
AHQ-3-4, 3317	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.53E-07	0.87	3.45	-	1026.1
AHQ-3-2, 3131	R.TEMEDLMSSKDDVGK.S	1685.85626	2	7.16E-04	0.87	3.54	-	947.0
AHQ-3-2, 6571	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.95E-06	0.95	4.59	-	1127.9
AHQ-3-7, 6035	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	4.40E-06	0.97	5.04	-	1626.9
AHQ-3-6, 6286 - 6297	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.70E-06	0.98	5.87	-	2155.7
AHQ-3-2, 6594	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	8.74E-11	0.97	5.45	-	1639.1
AHQ-3-4, 6626 - 6704	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.90E-06	0.87	3.90	-	1209.5
AHQ-3-2, 6667 - 6731	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.48E-05	0.98	5.48	-	1931.5
AHQ-3-5, 6335	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.15E-12	0.95	4.69	-	1312.8
AHQ-3-3, 6597 - 6630	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	3.13E-07	0.98	5.43	-	1987.4
AHQ-3-2, 7250	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	4.97E-06	0.94	4.05	-	1126.1
AHQ-3-3, 6604	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.24E-08	0.96	5.10	-	1303.4
AHQ-3-7, 6044	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.00E-07	0.97	5.37	-	1642.7
AHQ-3-5, 3027	K.VEAQLQELQVK.F	1285.47179	2	3.16E-05	0.95	4.16	-	1308.2
AHQ-3-6, 2997	K.VEAQLQELQVK.F	1285.47179	2	5.94E-05	0.89	3.24	-	1164.7
AHQ-3-4, 3189 - 3197	K.VEAQLQELQVK.F	1285.47179	2	3.89E-05	0.95	4.10	-	1370.2
AHQ-3-2, 3245	K.VEAQLQELQVK.F	1285.47179	2	2.27E-05	0.95	4.49	-	1362.6
AHQ-3-3, 3232	K.VEAQLQELQVK.F	1285.47179	2	1.83E-05	0.95	4.30	-	1277.4
AHQ-3-6, 5089 - 5102	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.75E-06	0.86	4.03	-	715.3
AHQ-3-6, 5091 - 5167	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	3.52E-09	0.94	5.18	-	1264.7
AHQ-3-5, 6195 - 6273	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	6.97E-04	0.87	3.55	-	711.7
AHQ-3-5, 5847 - 5868	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	6.24E-04	0.92	4.44	-	995.6
AHQ-3-9, 5361 - 5431	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.25E-05	0.58	3.04	-	384.0
AHQ-3-10, 5298	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.99E-10	0.88	4.03	-	716.6
AHQ-3-1, 5522 - 5542	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.17E-07	0.94	4.35	-	916.3
AHQ-3-6, 5731 - 5801	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.20E-08	0.80	3.87	-	363.9
AHQ-3-6, 5791	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.63E-06	0.87	4.12	-	781.0
AHQ-3-5, 5952	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	6.25E-10	0.91	4.48	-	676.4
AHQ-3-10, 5282	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.25E-04	0.90	4.05	-	713.7
AHQ-3-2, 6157 - 6158	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.13E-07	0.90	4.42	-	786.5
AHQ-3-3, 5338 - 5408	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	3.09E-07	0.90	3.96	-	802.5
AHQ-3-10, 5514	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.94E-10	0.93	4.16	-	835.9
AHQ-3-2, 6151 - 6169	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.01E-11	0.95	4.86	-	1028.7
AHQ-3-4, 5358	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	3.89E-05	0.91	4.05	-	944.1
AHQ-3-5, 5789 - 5855	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.42E-09	0.94	4.33	-	812.1
AHQ-3-4, 6050	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.86E-08	0.94	4.49	-	867.1
AHQ-3-2, 5390 - 5425	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.86E-04	0.73	3.41	-	510.7
AHQ-3-7, 5707	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.36E-08	0.89	3.83	-	842.3
AHQ-3-4, 6070	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	3.45E-08	0.69	3.15	-	499.2
AHQ-3-3, 5409 - 5436	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	4.46E-05	0.94	4.73	-	1419.5
AHQ-3-3, 6140	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	5.96E-08	0.91	4.13	-	701.0
AHQ-3-13-, 5151	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.95E-06	0.91	3.89	-	873.7
AHQ-3-5, 5176 - 5249	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.23E-07	0.89	3.89	-	610.6
AHQ-3-13-, 5597 - 5662	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.68E-08	0.91	4.09	-	771.5
AHQ-3-13, 5162 - 5217	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.02E-05	0.74	3.14	-	599.7
AHQ-3-3, 6146	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	3.29E-08	0.92	4.48	-	904.9
AHQ-3-3, 6368	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.05E-11	0.76	3.63	-	446.2
AHQ-3-10, 4699 - 4712	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	8.88E-09	0.95	4.78	-	1089.7
AHQ-3-2, 1887 - 1963	R.VEEEEERCQHLQAEK.K	1916.01642	2	3.74E-04	0.81	3.40	-	822.7
AHQ-3-1, 2120 - 2122	R.VEEEEERCQHLQAEK.K	1916.01642	2	6.06E-04	0.91	3.87	-	1057.3
AHQ-3-2, 4033	K.VIQYLAYVASSHK.S	1479.70484	2	2.22E-05	0.91	3.48	-	1105.7
AHQ-3-4, 3829	K.VIQYLAYVASSHK.S	1479.70484	2	2.75E-04	0.94	3.85	-	1206.0
AHQ-3-7, 3436 - 3442	K.VIQYLAYVASSHK.S	1479.70484	2	1.78E-04	0.94	3.71	-	1191.2

AHQ-3-2, 3953	K.VIQYLAYVASSHK.S	1479.70484	3	9.93E-05	0.72	3.34	-	564.0
AHQ-3-2, 3937 - 3939	K.VIQYLAYVASSHK.S	1479.70484	2	2.08E-05	0.96	4.18	-	1440.6
AHQ-3-1, 4124	K.VIQYLAYVASSHK.S	1479.70484	2	1.97E-04	0.94	3.82	-	1355.1
AHQ-3-6, 6385 - 6405	R.VISGVLQLGNIVFK.K	1487.81155	2	3.70E-05	0.96	4.21	-	1723.0
AHQ-3-4, 6689 - 6764	R.VISGVLQLGNIVFK.K	1487.81155	1	1.04E-06	0.81	3.58	-	573.1
AHQ-3-2, 6587	R.VISGVLQLGNIVFK.K	1487.81155	2	2.31E-08	0.97	4.81	-	1431.8
AHQ-3-7, 6134 - 6210	R.VISGVLQLGNIVFK.K	1487.81155	2	2.16E-05	0.97	4.22	-	1810.2
AHQ-3-2, 6694 - 6761	R.VISGVLQLGNIVFK.K	1487.81155	2	2.56E-08	0.97	4.94	-	1840.4
AHQ-3-2, 6715 - 6807	R.VISGVLQLGNIVFK.K	1487.81155	1	2.03E-06	0.68	3.53	-	445.0
AHQ-3-4, 6661 - 6734	R.VISGVLQLGNIVFK.K	1487.81155	2	1.20E-05	0.97	5.27	-	1703.3
AHQ-3-13, 6310 - 6318	R.VISGVLQLGNIVFK.K	1487.81155	2	6.51E-05	0.96	4.15	-	1637.4
AHQ-3-2, 6829	R.VISGVLQLGNIVFK.K	1487.81155	2	3.35E-09	0.97	4.95	-	1935.8
AHQ-3-1, 6684	R.VISGVLQLGNIVFK.K	1487.81155	1	1.34E-06	0.25	2.56	-	388.3
AHQ-3-12, 6255	R.VISGVLQLGNIVFK.K	1487.81155	2	1.95E-08	0.97	4.83	-	1521.3
AHQ-3-1, 6668 - 6696	R.VISGVLQLGNIVFK.K	1487.81155	2	1.36E-06	0.68	2.50	-	568.4
AHQ-3-1, 6578	R.VISGVLQLGNIVFK.K	1487.81155	2	1.30E-08	0.94	4.49	-	869.2
AHQ-3-5, 6505 - 6507	R.VISGVLQLGNIVFK.K	1487.81155	2	2.23E-07	0.93	3.43	-	1187.2
AHQ-3-5, 6516	R.VISGVLQLGNIVFK.K	1487.81155	1	3.06E-04	0.66	3.35	-	401.2
AHQ-3-5, 6603	R.VISGVLQLGNIVFK.K	1487.81155	2	1.10E-06	0.93	3.23	-	1570.0
AHQ-3-5, 6607	R.VISGVLQLGNIVFK.K	1487.81155	1	2.71E-05	0.74	3.40	-	455.9
AHQ-3-2, 6958	R.VISGVLQLGNIVFK.K	1487.81155	2	3.88E-05	0.96	3.94	-	1442.9
AHQ-3-1, 6008 - 6086	R.VISGVLQLGNIVFKK.E	1615.98446	2	5.47E-04	0.88	3.70	-	1085.9
AHQ-3-1, 6085	R.VISGVLQLGNIVFKK.E	1615.98446	2	1.08E-05	0.95	4.91	-	1030.1
AHQ-3-3, 4988 - 5037	K.VSHLLGINVTDFTR.G	1572.79026	2	3.55E-07	0.96	4.47	-	1388.9
AHQ-3-4, 4854 - 4912	K.VSHLLGINVTDFTR.G	1572.79026	2	1.64E-08	0.94	4.11	-	1311.4
AHQ-3-2, 4949 - 5017	K.VSHLLGINVTDFTR.G	1572.79026	2	3.04E-08	0.96	4.74	-	1275.9
AHQ-3-1, 5053 - 5125	K.VSHLLGINVTDFTR.G	1572.79026	2	4.15E-11	0.96	4.85	-	1319.4
AHQ-3-10, 4348	K.VSHLLGINVTDFTR.G	1572.79026	2	1.11E-06	0.70	2.64	-	748.1
AHQ-3-1, 5114	K.VSHLLGINVTDFTR.G	1572.79026	3	2.90E-04	0.85	3.42	-	1056.7
AHQ-3-2, 5331	K.VSHLLGINVTDFTR.G	1572.79026	2	3.44E-04	0.92	3.63	-	1091.9
AHQ-3-6, 4587 - 4614	K.VSHLLGINVTDFTR.G	1572.79026	2	2.11E-09	0.96	4.46	-	1442.7
AHQ-3-7, 4452	K.VSHLLGINVTDFTR.G	1572.79026	2	2.55E-08	0.96	4.13	-	1429.4
AHQ-3-5, 4659 - 4669	K.VSHLLGINVTDFTR.G	1572.79026	2	2.74E-10	0.96	5.03	-	1209.5
AHQ-3-2, 3017 - 3085	R.VVFQEFR.Q	925.06580	2	8.92E-05	0.70	2.68	-	503.9
AHQ-3-1, 3276	R.VVFQEFR.Q	925.06580	2	1.74E-05	0.74	2.76	-	537.7
AHQ-3-3, 4012 - 4044	R.YEILTPNSIPK.G	1275.47536	2	5.28E-08	0.92	3.75	-	1130.9
AHQ-3-2, 4063 - 4102	R.YEILTPNSIPK.G	1275.47536	2	4.54E-06	0.95	3.83	-	1317.9
AHQ-3-4, 3965 - 3973	R.YEILTPNSIPK.G	1275.47536	2	1.49E-04	0.91	3.35	-	1061.2
AHQ-3-1, 4142 - 4217	R.YEILTPNSIPK.G	1275.47536	2	6.20E-04	0.88	3.61	-	957.2
AHQ-3-3, 4017 - 4018	R.YEILTPNSIPK.G	1275.47536	1	7.60E-06	0.65	2.64	-	543.2
AHQ-3-2, 6401	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	3	9.28E-05	0.89	3.93	-	1075.3
gi|17986260|ref|NP_524147.1|	smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo			5.55E-15	3.74	40.30	23.30	12969.7
AHQ-3-12, 5602 - 5676	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	1.34E-11	0.94	4.84	-	1304.5
AHQ-3-12, 5819 - 5899	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	1.55E-08	0.90	4.95	-	1108.5
AHQ-3-12, 5947 - 6026	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	4.70E-07	0.92	5.62	-	1285.8
AHQ-3-12, 6056 - 6118	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	3.75E-07	0.79	4.78	-	612.6
AHQ-3-12, 6286	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	1.00E-04	0.96	4.99	-	1946.5
AHQ-3-12, 6494	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	1.84E-04	0.81	3.82	-	694.0
AHQ-3-12, 7068	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	3.90E-05	0.55	3.52	-	440.9
AHQ-3-13-, 6009	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	1.78E-06	0.95	5.70	-	1691.3
AHQ-3-14-, 5531 - 5597	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	7.01E-07	0.97	5.55	-	1831.9
AHQ-3-14-, 5908 - 5921	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	5.55E-15	0.93	5.98	-	1114.2
gi|4501885|ref|NP_001092.1|	beta actin; beta cytoskeletal actin [Homo sapiens]			6.66E-15	13.00	150.42	36.00	41736.5
AHQ-3-8, 7265 - 7336	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	4.29E-13	0.94	5.14	-	827.6
AHQ-3-8, 6603 - 6679	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	6.05E-05	0.78	4.88	-	453.0
AHQ-3-13-, 6707 - 6758	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	6.66E-15	0.94	4.98	-	973.3
AHQ-3-13-, 6587 - 6650	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	2.83E-05	0.71	3.88	-	471.9
AHQ-3-13-, 6373 - 6399	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	4.20E-06	0.82	4.18	-	637.7
AHQ-3-13-, 6047 - 6113	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.55E-08	0.92	4.90	-	573.6
AHQ-3-8, 6368 - 6401	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.48E-04	0.84	4.93	-	412.8
AHQ-3-8, 6193 - 6255	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	8.72E-04	0.76	3.33	-	492.3
AHQ-3-13, 6758 - 6827	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.12E-07	0.91	4.40	-	792.2
AHQ-3-13, 6217	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.65E-05	0.84	4.03	-	454.0
AHQ-3-8, 6800 - 6868	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.37E-04	0.90	4.70	-	829.6
AHQ-3-13, 6062 - 6085	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	4.13E-06	0.94	5.14	-	767.6
AHQ-3-8, 6827 - 6899	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	7.20E-07	0.63	3.88	-	320.0
AHQ-3-8, 6913 - 6979	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.18E-07	0.92	4.86	-	814.0
AHQ-3-8, 7043 - 7119	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.15E-13	0.93	5.18	-	618.5
AHQ-3-4, 7320 - 7396	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.68E-05	0.91	4.64	-	769.2
AHQ-3-8, 7175 - 7244	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.00E-11	0.93	5.23	-	614.9
AHQ-3-8, 7403	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.11E-14	0.95	5.35	-	986.5
AHQ-3-10, 6346 - 6414	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.27E-09	0.94	4.84	-	983.6
AHQ-3-8, 6651 - 6719	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	6.21E-04	0.64	3.48	-	240.3
AHQ-3-9, 6713 - 6781	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.24E-10	0.91	4.71	-	759.8
AHQ-3-10, 5647 - 5702	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	8.45E-06	0.78	3.84	-	558.9
AHQ-3-8, 6992 - 7008	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	5.90E-04	0.78	3.98	-	672.8
AHQ-3-8, 7075 - 7117	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	6.94E-07	0.85	4.48	-	743.3
AHQ-3-8, 7088 - 7109	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.38E-06	0.95	5.53	-	914.0
AHQ-3-8, 5592 - 5659	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	3.22E-06	0.83	3.86	-	760.5
AHQ-3-9, 6899	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.75E-04	0.85	3.64	-	824.2
AHQ-3-9, 6764 - 6833	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	4.16E-08	0.87	3.26	-	966.2
AHQ-3-8, 7155 - 7223	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.26E-05	0.89	3.68	-	879.4
AHQ-3-8, 7171 - 7187	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	9.34E-08	0.92	4.61	-	1365.6
AHQ-3-11, 6618	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.52E-06	0.80	3.18	-	684.0
AHQ-3-10, 6432	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	3.00E-06	0.87	3.93	-	974.6
AHQ-3-8, 7255 - 7323	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	6.69E-05	0.86	3.41	-	760.7
AHQ-3-10, 6430 - 6495	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	6.09E-05	0.93	4.34	-	871.3
AHQ-3-8, 7391	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	3.14E-04	0.79	3.23	-	626.0
AHQ-3-8, 7347 - 7420	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.66E-07	0.95	5.91	-	1076.8
AHQ-3-8, 7256 - 7279	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	7.02E-06	0.89	4.95	-	862.5
AHQ-3-8, 7296 - 7363	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.09E-08	0.91	4.39	-	922.6
AHQ-3-8, 5360 - 5423	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	4.47E-09	0.83	3.75	-	955.0
AHQ-3-8, 5288 - 5339	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	3.31E-07	0.87	3.58	-	1153.7
AHQ-3-8, 7321 - 7339	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	6.72E-04	0.80	3.19	-	612.3
AHQ-3-8, 7407 - 7408	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	3.11E-04	0.69	3.08	-	320.4
AHQ-3-8, 7180 - 7251	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	9.51E-05	0.89	4.42	-	726.9
AHQ-3-10, 6296 - 6326	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	3.79E-07	0.98	6.86	-	1512.9
AHQ-3-8, 6811 - 6891	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	5.44E-14	0.99	8.34	-	2596.3
AHQ-3-10, 6170 - 6232	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	4.63E-06	0.97	6.95	-	1423.3
AHQ-3-8, 6683 - 6749	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	1.03E-12	0.97	6.64	-	1150.3
AHQ-3-10, 6095	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	1.40E-05	0.83	3.72	-	778.5
AHQ-3-8, 7273	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	2.39E-04	0.75	3.86	-	396.2
AHQ-3-10, 5839 - 5912	R.FRCPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3555.03753	3	3.85E-04	0.51	3.20	-	405.7
AHQ-3-11, 2362 - 2363	R.GYSFTTTAER.E	1133.19273	2	7.49E-04	0.88	3.22	-	834.2
AHQ-3-1, 2624	R.GYSFTTTAER.E	1133.19273	2	2.35E-05	0.86	2.94	-	894.6
AHQ-3-8, 2002 - 2074	R.GYSFTTTAER.E	1133.19273	2	2.70E-04	0.79	2.69	-	672.1
AHQ-3-13, 2571 - 2577	R.GYSFTTTAER.E	1133.19273	2	8.03E-05	0.89	3.15	-	892.6

AHQ-3-9, 2195 - 2256	R.GYSFTTTAER.E	1133.19273	2	2.67E-04	0.86	3.17	-	702.8
AHQ-3-7, 2218	R.GYSFTTTAER.E	1133.19273	2	1.25E-04	0.92	3.18	-	1046.1
AHQ-3-4, 2436	R.GYSFTTTAER.E	1133.19273	2	5.73E-04	0.90	3.08	-	1039.9
AHQ-3-10, 2318 - 2378	R.GYSFTTTAER.E	1133.19273	2	1.55E-04	0.95	3.27	-	1286.1
AHQ-3-13-, 2529 - 2554	R.GYSFTTTAER.E	1133.19273	2	8.37E-04	0.91	3.14	-	997.0
AHQ-3-3, 2449	R.GYSFTTTAER.E	1133.19273	2	1.25E-04	0.92	3.18	-	1144.9
AHQ-3-14-, 2415	R.GYSFTTTAER.E	1133.19273	2	7.62E-05	0.95	3.21	-	1278.5
AHQ-3-8, 2289	R.GYSFTTTAER.E	1133.19273	2	9.84E-05	0.84	2.58	-	1220.5
AHQ-3-13, 4201	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	1.43E-04	0.88	3.88	-	919.3
AHQ-3-11, 4520	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	4.65E-07	0.94	4.04	-	1215.6
AHQ-3-14, 5752	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	5.19E-04	0.94	4.28	-	978.0
AHQ-3-10, 4303	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	3.59E-08	0.88	3.47	-	749.2
AHQ-3-12, 4719	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	3.20E-06	0.93	3.76	-	1140.0
AHQ-3-13-, 4213 - 4229	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	2.09E-09	0.91	4.30	-	1126.8
AHQ-3-14-, 4199 - 4219	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	3.97E-04	0.80	4.30	-	534.5
AHQ-3-8, 3856 - 3857	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	8.06E-08	0.97	6.09	-	1417.3
AHQ-3-8, 4153	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	1.22E-04	0.76	3.44	-	585.0
AHQ-3-8, 4208 - 4217	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	4.25E-07	0.89	3.28	-	1080.3
AHQ-3-8, 4685	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	2.11E-04	0.89	4.75	-	833.7
AHQ-3-8, 4377 - 4399	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	1.24E-04	0.95	5.60	-	1098.1
AHQ-3-8, 7293 - 7371	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	9.58E-09	0.96	6.19	-	1755.9
AHQ-3-8, 7387 - 7388	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	1.15E-06	0.96	5.52	-	1742.5
AHQ-3-14-, 5367 - 5447	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.48E-07	0.95	5.60	-	959.6
AHQ-3-8, 5115 - 5183	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.99E-08	0.95	5.68	-	1093.4
AHQ-3-8, 5001 - 5071	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.28E-09	0.96	5.88	-	1335.5
AHQ-3-1, 5802 - 5869	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.36E-06	0.87	4.27	-	784.9
AHQ-3-1, 5936	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.76E-06	0.91	5.14	-	1002.5
AHQ-3-1, 6146 - 6225	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.10E-10	0.95	5.10	-	1416.4
AHQ-3-8, 4863 - 4931	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.18E-09	0.96	5.89	-	1535.2
AHQ-3-8, 5109 - 5179	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.76E-07	0.96	5.34	-	1620.7
AHQ-3-2, 6063 - 6141	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.65E-07	0.94	4.86	-	1217.1
AHQ-3-13-, 5805 - 5866	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.32E-09	0.97	5.41	-	2104.0
AHQ-3-13-, 5642	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.02E-05	0.94	5.59	-	1042.9
AHQ-3-7, 5787 - 5854	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.00E-11	0.97	5.91	-	1738.3
AHQ-3-13-, 5467	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.02E-10	0.95	5.05	-	1358.0
AHQ-3-13-, 5373	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.63E-06	0.96	5.81	-	1316.3
AHQ-3-8, 5247 - 5315	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.16E-10	0.97	6.53	-	1418.9
AHQ-3-9, 4928 - 4995	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.38E-06	0.96	5.57	-	1185.9
AHQ-3-9, 5039 - 5107	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.79E-07	0.96	5.87	-	1332.9
AHQ-3-9, 5193 - 5263	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.69E-12	0.97	5.96	-	1535.5
AHQ-3-8, 5403 - 5471	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.78E-05	0.86	4.24	-	895.6
AHQ-3-9, 5415 - 5440	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.82E-10	0.98	6.38	-	1819.7
AHQ-3-9, 5507 - 5527	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.07E-10	0.97	6.03	-	1693.5
AHQ-3-9, 5591	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.32E-10	0.97	6.22	-	1759.1
AHQ-3-7, 5578	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.76E-07	0.94	5.47	-	881.3
AHQ-3-7, 5266 - 5307	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.27E-06	0.94	4.99	-	1149.6
AHQ-3-3, 5705 - 5776	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.52E-07	0.91	4.82	-	829.2
AHQ-3-6, 5879 - 5959	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.08E-07	0.96	5.87	-	942.6
AHQ-3-8, 5483 - 5503	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.76E-12	0.98	7.50	-	1498.9
AHQ-3-10, 4931 - 4991	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.96E-09	0.97	6.74	-	1030.7
AHQ-3-10, 4990 - 5068	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.19E-07	0.97	6.22	-	1386.3
AHQ-3-10, 5178 - 5226	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.04E-08	0.98	6.37	-	2357.8
AHQ-3-10, 5194 - 5254	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.95E-04	0.75	3.80	-	676.8
AHQ-3-10, 5286 - 5346	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.29E-10	0.98	6.59	-	2140.4
AHQ-3-10, 5408	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.58E-12	0.96	5.35	-	1470.6
AHQ-3-6, 5706 - 5717	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.87E-11	0.96	5.52	-	1500.3
AHQ-3-6, 5503 - 5527	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.76E-06	0.84	4.03	-	969.0
AHQ-3-6, 5393 - 5405	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.64E-07	0.95	5.73	-	1147.1
AHQ-3-14, 6387	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.04E-08	0.96	6.04	-	1375.9
AHQ-3-5, 6060	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.79E-04	0.94	4.60	-	1488.1
AHQ-3-5, 5960	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.16E-06	0.96	5.83	-	1295.6
AHQ-3-5, 5764 - 5784	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.94E-09	0.98	6.66	-	1919.7
AHQ-3-5, 5431	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.97E-09	0.97	5.97	-	1433.5
AHQ-3-4, 6113 - 6188	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.41E-08	0.97	5.65	-	1818.7
AHQ-3-8, 5567 - 5636	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.27E-14	0.98	6.72	-	1615.2
AHQ-3-8, 5700 - 5765	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.46E-09	0.96	5.66	-	1545.1
AHQ-3-11, 5170	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.66E-07	0.96	5.70	-	1578.6
AHQ-3-11, 5470 - 5546	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.83E-11	0.96	5.57	-	1504.8
AHQ-3-11, 5608	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.17E-05	0.94	5.06	-	1069.5
AHQ-3-4, 5976 - 6029	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.96E-09	0.97	6.84	-	1672.3
AHQ-3-3, 5844	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.73E-06	0.60	3.21	-	455.0
AHQ-3-3, 6209	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.08E-08	0.97	6.10	-	1251.4
AHQ-3-9, 5279 - 5347	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.72E-11	0.97	6.16	-	1409.7
AHQ-3-12, 5432 - 5506	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.29E-08	0.92	4.73	-	983.4
AHQ-3-12, 5704 - 5780	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.56E-05	0.97	6.06	-	1809.2
AHQ-3-4, 5788	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.24E-06	0.89	4.34	-	1057.7
AHQ-3-8, 5836	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.66E-08	0.95	5.23	-	1256.8
AHQ-3-13, 5397 - 5477	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.58E-05	0.96	5.70	-	1442.5
AHQ-3-13, 5803	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.06E-07	0.93	4.51	-	1221.3
AHQ-3-4, 5646 - 5717	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.70E-08	0.97	6.16	-	1207.4
AHQ-3-14-, 5647 - 5716	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.16E-14	0.97	6.33	-	1589.7
AHQ-3-12, 3750 - 3775	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	4.95E-04	0.51	3.09	-	495.4
AHQ-3-14, 4771	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.18E-04	0.93	4.63	-	825.0
AHQ-3-11, 3626 - 3634	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	5.84E-04	0.56	3.21	-	419.5
AHQ-3-6, 3599	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.85E-05	0.94	4.67	-	824.8
AHQ-3-7, 3502 - 3570	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.64E-05	0.90	4.18	-	707.2
AHQ-3-13-, 3891 - 3897	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.48E-08	0.93	4.39	-	1060.3
AHQ-3-9, 3391	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.71E-05	0.85	3.82	-	514.9
AHQ-3-9, 3363 - 3427	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.06E-04	0.93	4.49	-	931.5
AHQ-3-9, 3247 - 3327	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.65E-06	0.94	4.83	-	972.8
AHQ-3-8, 3112 - 3188	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.59E-04	0.93	4.59	-	884.9
AHQ-3-8, 3120 - 3145	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	4.42E-04	0.49	3.32	-	517.3
AHQ-3-8, 3204 - 3268	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.43E-08	0.92	4.04	-	1031.3
AHQ-3-8, 3212 - 3280	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	9.13E-04	0.80	4.45	-	865.9
AHQ-3-8, 3292 - 3360	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.01E-06	0.94	4.78	-	919.9
AHQ-3-8, 3424 - 3500	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.36E-07	0.92	4.54	-	814.9
AHQ-3-1, 4136	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.08E-05	0.91	4.15	-	801.7
AHQ-3-14-, 3812	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.80E-04	0.86	3.37	-	698.4
AHQ-3-8, 3492 - 3569	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.73E-08	0.91	4.34	-	793.0
AHQ-3-8, 3662 - 3714	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.01E-04	0.90	4.33	-	812.9
AHQ-3-12, 3774 - 3842	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.34E-04	0.93	4.60	-	839.4
gi|21361399|ref|NP_055040.2| protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp				6.66E-15	1.79	20.38	7.10	65308.3
AHQ-3-6, 7282	K.DNTIEHLLPLFLAQLKDECPEVR.L	2753.12348	3	6.66E-15	0.99	7.58	-	4081.7
AHQ-3-6, 5793	K.SEIIPMFSNLASDEQDSVR.L	2139.32924	2	6.86E-04	0.80	3.62	-	632.0
gi|4557597|ref|NP_001449.1| gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);				7.77E-15	2.41	40.30	2.50	288897.4
AHQ-3-1, 3509 - 3529	R.GAGTGGLGLAIEGPSEAK.M	1585.74098	2	5.93E-04	0.55	3.13	-	329.4
AHQ-3-7, 4004 - 4076	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	7.06E-04	0.92	4.51	-	822.1

AHQ-3-1, 4817	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.01E-05	0.73	3.75	-	349.5
AHQ-3-1, 4824	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.15E-05	0.89	4.37	-	394.0
AHQ-3-6, 4109 - 4182	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	7.35E-06	0.93	4.90	-	787.2
AHQ-3-2, 4617 - 4694	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	5.23E-04	0.88	4.18	-	438.0
AHQ-3-3, 4680 - 4758	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	6.09E-06	0.88	4.12	-	463.8
AHQ-3-5, 4235 - 4255	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	7.77E-15	0.95	5.58	-	529.9
AHQ-3-4, 4500	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.07E-08	0.90	4.54	-	387.0
AHQ-3-4, 4502	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	7.83E-07	0.81	4.14	-	401.6
AHQ-3-6, 4183 - 4189	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	2.77E-04	0.96	5.93	-	538.0
AHQ-3-2, 1710 - 1791	K.IECDDKGDGSCDVR.Y	1628.67809	2	8.28E-05	0.87	3.19	-	979.4
AHQ-3-1, 2026	K.IECDDKGDGSCDVR.Y	1628.67809	2	5.20E-05	0.80	3.12	-	723.7
AHQ-3-4, 4260 - 4264	K.YGGDEIPYSPFR.I	1401.50466	1	3.51E-04	0.12	2.16	-	239.5
gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act				8.33E-15	100.37	1200.37	55.60	280757.4
AHQ-3-6, 2261	K.AEISFEDR.K	967.01472	2	9.51E-04	0.91	2.81	-	1276.6
AHQ-3-6, 2389	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.90E-05	0.95	3.63	-	1759.0
AHQ-3-4, 2538	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	4.96E-04	0.35	2.99	-	112.7
AHQ-3-4, 2520	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.69E-04	0.91	3.23	-	1327.0
AHQ-3-2, 2710	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	6.23E-04	0.30	2.22	-	232.5
AHQ-3-3, 2696 - 2734	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.74E-06	0.93	3.47	-	1561.1
AHQ-3-5, 2404	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.33E-07	0.87	3.25	-	1036.8
AHQ-3-3, 2530	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	8.34E-08	0.89	2.68	-	1246.2
AHQ-3-3, 2541	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	4.40E-07	0.75	3.54	-	187.9
AHQ-3-1, 2718 - 2788	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	5.41E-04	0.90	2.98	-	1291.4
AHQ-3-1, 2880	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.28E-05	0.91	3.13	-	1089.3
AHQ-3-2, 2541 - 2611	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.39E-05	0.90	2.90	-	1224.6
AHQ-3-14, 3651 - 3711	K.AGNNM*LLVGVHGPR.T	1451.67973	2	7.34E-06	0.76	3.00	-	677.9
AHQ-3-14-, 2635 - 2653	K.AGNNM*LLVGVHGPR.T	1451.67973	3	1.70E-04	0.88	3.70	-	1292.6
AHQ-3-14, 3588	K.AGNNM*LLVGVHGPR.T	1451.67973	3	3.90E-04	0.85	3.12	-	1238.3
AHQ-3-14, 3509 - 3587	K.AGNNM*LLVGVHGPR.T	1451.67973	2	2.13E-04	0.76	3.16	-	719.7
AHQ-3-14-, 2636 - 2647	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.67E-05	0.92	3.72	-	944.6
AHQ-3-14-, 2717	K.AGNNM*LLVGVHGPR.T	1451.67973	3	2.59E-08	0.85	3.27	-	1153.0
AHQ-3-14-, 2720 - 2759	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.27E-04	0.82	3.28	-	598.6
AHQ-3-14-, 3019 - 3055	K.AGNNMLLVGVHGPR.T	1435.68033	3	3.80E-07	0.87	3.42	-	1254.2
AHQ-3-14-, 3303 - 3365	K.AGNNMLLVGVHGPR.T	1435.68033	2	3.37E-07	0.83	3.22	-	656.2
AHQ-3-14-, 3308	K.AGNNMLLVGVHGPR.T	1435.68033	3	1.44E-05	0.85	3.20	-	1280.0
AHQ-3-14, 4296 - 4359	K.AGNNMLLVGVHGPR.T	1435.68033	2	4.49E-07	0.82	3.38	-	711.5
AHQ-3-1, 1824 - 1889	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	9.65E-04	0.60	2.97	-	426.1
AHQ-3-2, 2170	K.AGVAPLQVK.V	883.07036	2	2.86E-05	0.82	2.80	-	649.7
AHQ-3-1, 2392	K.AGVAPLQVK.V	883.07036	2	1.09E-05	0.84	2.97	-	603.3
AHQ-3-2, 7715 - 7782	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	2.37E-09	0.97	5.36	-	1878.5
AHQ-3-1, 7346 - 7409	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	3.37E-05	0.93	4.84	-	1130.4
AHQ-3-1, 7466 - 7468	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	8.77E-05	0.93	4.73	-	1362.5
AHQ-3-2, 2626	K.AHVVPCFDASK.V	1232.39073	1	1.09E-04	0.68	2.75	-	499.6
AHQ-3-7, 6319	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.77E-10	0.90	4.35	-	565.0
AHQ-3-5, 6332 - 6408	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.29E-13	0.92	4.88	-	592.8
AHQ-3-5, 6231	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.19E-12	0.93	5.33	-	575.7
AHQ-3-2, 6385 - 6455	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.69E-11	0.93	5.36	-	699.0
AHQ-3-7, 6186	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.05E-08	0.94	5.40	-	720.9
AHQ-3-2, 6622 - 6689	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.99E-11	0.92	4.81	-	953.7
AHQ-3-9, 5891	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.08E-05	0.82	3.87	-	626.0
AHQ-3-2, 6763 - 6833	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.03E-07	0.61	3.52	-	359.2
AHQ-3-4, 6577 - 6654	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.50E-04	0.87	4.52	-	444.2
AHQ-3-4, 6426 - 6505	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.96E-11	0.93	4.90	-	822.2
AHQ-3-6, 6350	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.61E-09	0.95	5.29	-	861.3
AHQ-3-4, 6318 - 6350	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.87E-04	0.71	3.56	-	488.6
AHQ-3-9, 6053	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.70E-10	0.80	3.91	-	482.1
AHQ-3-1, 6593 - 6621	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.24E-06	0.79	4.07	-	437.9
AHQ-3-2, 6469 - 6545	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.07E-11	0.95	5.74	-	936.9
AHQ-3-3, 6413 - 6488	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.79E-08	0.94	5.26	-	809.4
AHQ-3-1, 6452 - 6528	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.36E-11	0.97	7.18	-	1302.4
AHQ-3-6, 6239	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.61E-12	0.92	5.13	-	487.8
AHQ-3-3, 6572 - 6646	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.04E-05	0.92	4.86	-	935.2
AHQ-3-1, 6324 - 6388	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.09E-08	0.92	4.75	-	772.4
AHQ-3-2, 1450	R.ALTQTGGPHVK.A	1109.26067	1	1.34E-04	0.13	1.96	-	267.4
AHQ-3-7, 2982	R.ANLPQSFQVDTSK.A	1435.56409	2	4.13E-07	0.79	2.70	-	510.8
AHQ-3-4, 3245	R.ANLPQSFQVDTSK.A	1435.56409	2	3.57E-04	0.71	2.91	-	398.2
AHQ-3-1, 3337 - 3412	R.ANLPQSFQVDTSK.A	1435.56409	2	2.64E-06	0.78	3.01	-	540.4
AHQ-3-1, 3426	R.ANLPQSFQVDTSK.A	1435.56409	1	8.14E-09	0.50	2.83	-	319.1
AHQ-3-2, 3273 - 3342	R.ANLPQSFQVDTSK.A	1435.56409	2	1.29E-08	0.89	3.92	-	465.6
AHQ-3-5, 3083	R.ANLPQSFQVDTSK.A	1435.56409	2	1.98E-04	0.76	2.85	-	483.1
AHQ-3-2, 3274	R.ANLPQSFQVDTSK.A	1435.56409	1	2.24E-05	0.14	2.13	-	340.6
AHQ-3-3, 3513	R.ANLPQSFQVDTSK.A	1435.56409	1	4.08E-08	0.49	2.66	-	514.7
AHQ-3-2, 3279	R.ANLPQSFQVDTSK.A	1435.56409	1	3.78E-06	0.59	2.80	-	406.3
AHQ-3-2, 3419	R.ANLPQSFQVDTSK.A	1435.56409	1	3.90E-05	0.72	2.77	-	649.9
AHQ-3-2, 3547	R.ANLPQSFQVDTSK.A	1435.56409	1	7.59E-08	0.44	3.09	-	347.3
AHQ-3-3, 3274 - 3284	R.ANLPQSFQVDTSK.A	1435.56409	2	1.66E-11	0.86	3.43	-	446.5
AHQ-3-1, 3612	R.ANLPQSFQVDTSK.A	1435.56409	2	4.68E-08	0.63	2.64	-	370.2
AHQ-3-3, 4681 - 4682	R.ANLPQSFQVDTSKAGVAPLQVK.V	2299.61185	2	4.55E-04	0.92	4.05	-	829.4
AHQ-3-2, 4702 - 4775	R.ANLPQSFQVDTSKAGVAPLQVK.V	2299.61185	2	1.34E-04	0.94	5.41	-	719.3
AHQ-3-2, 4699	R.ANLPQSFQVDTSKAGVAPLQVK.V	2299.61185	3	1.88E-04	0.65	3.00	-	415.0
AHQ-3-5, 3143	R.APSVANVGSHCDLSLK.I	1656.84249	2	7.13E-06	0.91	3.93	-	762.9
AHQ-3-4, 3341	R.APSVANVGSHCDLSLK.I	1656.84249	2	1.45E-10	0.94	4.57	-	601.7
AHQ-3-5, 1524	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	4.97E-04	0.94	4.80	-	669.1
AHQ-3-1, 1989	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	3.17E-04	0.67	2.92	-	426.9
AHQ-3-3, 3632 - 3642	R.AWGPGLEGGVVGK.S	1227.39403	2	1.28E-06	0.93	3.90	-	1018.7
AHQ-3-6, 3353	R.AWGPGLEGGVVGK.S	1227.39403	2	1.88E-04	0.93	3.79	-	917.4
AHQ-3-1, 3797 - 3820	R.AWGPGLEGGVVGK.S	1227.39403	2	4.11E-06	0.93	3.84	-	1082.2
AHQ-3-5, 3396 - 3401	R.AWGPGLEGGVVGK.S	1227.39403	2	3.63E-05	0.89	3.28	-	752.6
AHQ-3-2, 3670 - 3749	R.AWGPGLEGGVVGK.S	1227.39403	2	1.74E-07	0.92	4.07	-	839.1
AHQ-3-4, 3606	R.AWGPGLEGGVVGK.S	1227.39403	2	5.71E-04	0.89	3.71	-	777.5
AHQ-3-3, 3188	R.AYGPGIEPTGNMVK.K	1434.64274	1	2.58E-04	0.37	2.99	-	328.4
AHQ-3-2, 2537 - 2565	R.AYGPGIEPTGNM*VK.K	1450.64214	2	9.76E-05	0.79	2.83	-	673.0
AHQ-3-3, 3370 - 3450	R.AYGPGIEPTGNMVK.K	1434.64274	2	4.79E-04	0.71	2.96	-	524.0
AHQ-3-3, 3381 - 3454	R.AYGPGIEPTGNMVK.K	1434.64274	1	1.19E-04	0.40	2.24	-	477.4
AHQ-3-3, 3461	R.AYGPGIEPTGNMVK.K	1434.64274	2	6.11E-07	0.61	2.75	-	537.6
AHQ-3-2, 3191	R.AYGPGIEPTGNMVK.K	1434.64274	1	5.22E-04	0.78	3.27	-	479.4
AHQ-3-6, 2397	R.AYGPGIEPTGNM*VK.K	1450.64214	2	8.61E-04	0.59	3.04	-	328.5
AHQ-3-5, 6347	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.00E-09	0.88	4.18	-	658.7
AHQ-3-3, 6389 - 6469	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.24E-05	0.91	4.37	-	529.9
AHQ-3-3, 6410	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	2.73E-09	0.94	4.49	-	1328.9
AHQ-3-2, 6283	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	5.53E-06	0.95	4.92	-	826.7
AHQ-3-3, 6217	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.18E-05	0.81	3.52	-	496.2
AHQ-3-2, 6445 - 6514	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.64E-07	0.95	4.95	-	890.9
AHQ-3-3, 6542	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	9.20E-05	0.79	3.45	-	398.8
AHQ-3-4, 6402 - 6472	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	7.76E-07	0.87	3.87	-	589.6
AHQ-3-2, 6585	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	4.48E-04	0.84	4.36	-	344.6
AHQ-3-11, 5768 - 5779	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	3.72E-04	0.50	2.87	-	365.9

AHQ-3-2, 6463	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.04E-10	0.96	4.87	-	1438.3
AHQ-3-1, 6353	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	4.23E-10	0.97	5.17	-	1685.7
AHQ-3-1, 6332 - 6396	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	6.10E-06	0.96	4.92	-	908.3
AHQ-3-3, 6662	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	3.56E-04	0.50	3.02	-	372.4
AHQ-3-1, 6514 - 6582	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	4.52E-06	0.88	4.00	-	695.7
AHQ-3-3, 7262 - 7297	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	4.73E-04	0.60	3.20	-	399.0
AHQ-3-2, 6814 - 6889	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	1.85E-05	0.74	4.04	-	441.0
AHQ-3-4, 2920 - 2921	K.CSGPGLSPGMVR.A	1219.41699	2	3.58E-04	0.56	2.53	-	456.1
AHQ-3-2, 2938 - 2959	K.CSGPGLSPGMVR.A	1219.41699	2	5.41E-05	0.74	2.83	-	454.1
AHQ-3-5, 5268	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	6.08E-06	0.94	4.23	-	1098.7
AHQ-3-5, 4784	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	3.03E-05	0.81	3.18	-	435.1
AHQ-3-3, 5478 - 5528	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	4.91E-08	0.87	4.02	-	608.7
AHQ-3-1, 5097 - 5106	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	2.94E-05	0.92	4.51	-	664.8
AHQ-3-1, 5102 - 5104	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	4.23E-08	0.88	4.01	-	583.1
AHQ-3-4, 5490	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	4.43E-05	0.85	2.87	-	1027.8
AHQ-3-5, 4768 - 4787	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	6.91E-05	0.44	3.50	-	134.0
AHQ-3-3, 5516 - 5536	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	3.28E-09	0.95	4.41	-	1104.1
AHQ-3-2, 5581	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	3.50E-14	0.93	4.75	-	595.7
AHQ-3-2, 5550	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	5.02E-10	0.94	4.16	-	1143.5
AHQ-3-3, 5021 - 5025	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	1.83E-05	0.92	4.81	-	615.7
AHQ-3-2, 5037 - 5111	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	2.82E-05	0.86	3.83	-	764.8
AHQ-3-5, 5267	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	6.48E-05	0.90	3.94	-	1142.9
AHQ-3-2, 5493 - 5513	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	1.14E-05	0.68	3.12	-	523.2
AHQ-3-1, 4134	R.DAEM*PATEKDLAEDAPWK.K	2034.18987	2	5.19E-05	0.86	3.37	-	666.0
AHQ-3-1, 4720	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	1.93E-05	0.74	3.46	-	613.2
AHQ-3-13, 3929	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	7.10E-06	0.92	3.56	-	1246.5
AHQ-3-1, 4258	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	4.87E-06	0.92	4.31	-	876.3
AHQ-3-10, 3663	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	4.02E-06	0.82	3.20	-	927.6
AHQ-3-3, 4090	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	7.61E-06	0.84	3.87	-	788.6
AHQ-3-5, 3932 - 4003	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.76E-06	0.93	4.11	-	1217.6
AHQ-3-1, 4118 - 4188	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.13E-05	0.80	3.18	-	793.8
AHQ-3-1, 4382	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	2.85E-06	0.64	2.91	-	674.6
AHQ-3-2, 4161 - 4223	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	7.31E-05	0.67	3.04	-	677.6
AHQ-3-2, 5158 - 5191	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	1.88E-05	0.91	3.52	-	1308.8
AHQ-3-1, 5062 - 5065	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	1.14E-09	0.93	4.32	-	1148.9
AHQ-3-5, 4279	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.33E-04	0.93	4.29	-	979.1
AHQ-3-2, 4598 - 4671	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.46E-09	0.95	4.19	-	1445.3
AHQ-3-3, 4473 - 4545	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	8.63E-08	0.92	4.25	-	1046.3
AHQ-3-1, 4781	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.68E-07	0.92	4.07	-	994.7
AHQ-3-3, 4562	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.85E-09	0.90	4.04	-	945.9
AHQ-3-2, 4517 - 4585	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	2.03E-09	0.91	4.03	-	1107.5
AHQ-3-8, 3858 - 3869	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.28E-06	0.95	4.49	-	1263.9
AHQ-3-3, 4462 - 4533	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	9.83E-07	0.95	4.48	-	1163.3
AHQ-3-11, 4067	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.21E-05	0.89	4.14	-	795.3
AHQ-3-1, 4569 - 4645	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	5.10E-08	0.76	3.38	-	760.0
AHQ-3-3, 4661 - 4732	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.82E-05	0.85	3.55	-	866.5
AHQ-3-4, 4352 - 4432	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.57E-07	0.92	3.96	-	1108.5
AHQ-3-1, 4554 - 4632	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.61E-06	0.95	4.48	-	1267.1
AHQ-3-7, 4056	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.19E-05	0.94	4.55	-	1085.3
AHQ-3-2, 5050	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.06E-06	0.74	2.70	-	1096.7
AHQ-3-2, 4741 - 4819	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.14E-11	0.97	5.14	-	1521.1
AHQ-3-9, 3880	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.68E-05	0.92	4.09	-	1197.0
AHQ-3-5, 4136 - 4208	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.30E-04	0.59	3.18	-	553.5
AHQ-3-2, 4898	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.84E-04	0.94	3.90	-	1367.6
AHQ-3-3, 4894	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.91E-04	0.53	2.62	-	493.4
AHQ-3-2, 4477 - 4549	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.25E-08	0.91	3.81	-	1106.6
AHQ-3-1, 4806	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.16E-05	0.76	3.28	-	676.2
AHQ-3-4, 4785	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.67E-04	0.43	2.54	-	529.7
AHQ-3-5, 4851	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	6.73E-08	0.93	3.74	-	1304.0
AHQ-3-5, 4655 - 4724	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	8.87E-07	0.83	3.47	-	937.6
AHQ-3-1, 4704	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.91E-12	0.97	5.21	-	1302.9
AHQ-3-5, 4556 - 4628	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.99E-09	0.96	5.09	-	1359.2
AHQ-3-3, 4757	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.72E-05	0.76	3.07	-	914.9
AHQ-3-1, 2033	R.DAPQDFHPDR.V	1198.22650	2	3.10E-05	0.62	2.95	-	407.9
AHQ-3-2, 1681 - 1722	R.DAPQDFHPDR.V	1198.22650	2	2.84E-07	0.69	2.87	-	561.6
AHQ-3-2, 1790	R.DAPQDFHPDR.V	1198.22650	2	6.47E-08	0.77	3.13	-	481.3
AHQ-3-3, 1702 - 1769	R.DAPQDFHPDR.V	1198.22650	2	2.64E-07	0.34	2.52	-	407.3
AHQ-3-1, 5194	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.36E-04	0.64	3.41	-	374.4
AHQ-3-7, 4866 - 4879	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	4.48E-05	0.91	4.66	-	525.4
AHQ-3-1, 4988	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	5.13E-06	0.86	4.29	-	524.8
AHQ-3-5, 5112 - 5145	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	4.01E-05	0.84	3.72	-	567.3
AHQ-3-6, 4829 - 4903	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	3.08E-05	0.90	4.70	-	505.6
AHQ-3-14-, 2339 - 2417	K.DKGEYTLVVK.W	1152.32223	2	1.68E-06	0.79	2.79	-	651.9
AHQ-3-14, 3272 - 3332	K.DKGEYTLVVK.W	1152.32223	2	1.55E-06	0.67	2.78	-	507.0
AHQ-3-4, 2345 - 2346	K.DKGEYTLVVK.W	1152.32223	2	2.54E-06	0.86	2.59	-	845.2
AHQ-3-4, 2344 - 2360	K.DKGEYTLVVK.W	1152.32223	1	3.70E-05	0.24	2.40	-	399.3
AHQ-3-14-, 2340 - 2360	K.DKGEYTLVVK.W	1152.32223	1	1.56E-06	0.27	2.63	-	349.6
AHQ-3-14, 3233 - 3413	K.DKGEYTLVVK.W	1152.32223	1	3.29E-04	0.14	2.27	-	332.7
AHQ-3-2, 3502	K.DNGNGTYSCSYVPR.K	1591.64109	2	1.95E-05	0.75	3.05	-	709.9
AHQ-3-3, 3185 - 3234	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.51E-06	0.74	3.35	-	278.8
AHQ-3-2, 3289 - 3367	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.60E-04	0.85	3.54	-	681.9
AHQ-3-2, 3037 - 3105	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	3.94E-06	0.96	4.75	-	1319.6
AHQ-3-3, 3077 - 3149	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.44E-07	0.93	3.91	-	1209.1
AHQ-3-3, 2944 - 3016	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.42E-04	0.89	3.90	-	725.7
AHQ-3-4, 2934 - 2990	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.85E-04	0.77	2.91	-	806.7
AHQ-3-3, 3020	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	4.67E-06	0.66	3.31	-	405.2
AHQ-3-2, 3143 - 3215	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.35E-07	0.88	3.76	-	626.3
AHQ-3-1, 3188 - 3258	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	8.57E-04	0.93	3.81	-	1096.7
AHQ-3-6, 2797	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.98E-05	0.71	2.89	-	343.1
AHQ-3-4, 3352	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	5.21E-06	0.82	3.81	-	372.5
AHQ-3-5, 3207	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	7.06E-06	0.81	3.38	-	451.8
AHQ-3-1, 3517 - 3597	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	7.21E-08	0.96	4.63	-	1404.4
AHQ-3-7, 3107 - 3179	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	6.01E-06	0.63	3.27	-	285.6
AHQ-3-2, 3465 - 3467	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.73E-04	0.80	3.07	-	912.6
AHQ-3-6, 3142	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	8.48E-07	0.60	3.07	-	285.9
AHQ-3-13-, 3362	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.17E-05	0.91	3.32	-	1273.9
AHQ-3-3, 2533	R.EATTEFSVDAR.A	1226.27493	2	3.77E-04	0.69	2.62	-	680.8
AHQ-3-2, 2550 - 2622	R.EATTEFSVDAR.A	1226.27493	2	6.62E-05	0.88	3.47	-	923.4
AHQ-3-2, 6643 - 6709	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.62E-07	0.94	5.51	-	754.1
AHQ-3-2, 6785 - 6858	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	9.69E-12	0.96	6.39	-	990.4
AHQ-3-4, 6489 - 6557	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.64E-04	0.92	5.29	-	420.1
AHQ-3-5, 6411 - 6487	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	7.31E-11	0.97	6.64	-	957.1
AHQ-3-6, 6342 - 6371	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	9.92E-10	0.95	6.11	-	668.5
AHQ-3-1, 6436 - 6504	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.08E-09	0.91	4.59	-	814.5
AHQ-3-3, 6613 - 6681	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	5.74E-07	0.93	5.06	-	864.9
AHQ-3-7, 6250 - 6311	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.41E-06	0.76	3.70	-	451.3
AHQ-3-3, 6468 - 6548	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.17E-09	0.93	5.52	-	672.4

AHQ-3-1, 5166 - 5236	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.92E-10	0.87	3.76	-	1132.6
AHQ-3-9, 4676 - 4679	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	8.17E-07	0.88	3.76	-	658.2
AHQ-3-2, 4991	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.56E-06	0.81	3.31	-	646.1
AHQ-3-2, 5393	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	6.86E-11	0.92	3.53	-	1124.1
AHQ-3-6, 4977	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.40E-07	0.83	3.62	-	737.3
AHQ-3-7, 4918	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.78E-06	0.29	2.58	-	349.8
AHQ-3-2, 5253 - 5325	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.10E-09	0.95	4.33	-	1001.9
AHQ-3-1, 5304 - 5374	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.38E-10	0.93	4.30	-	1232.1
AHQ-3-5, 5092	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	6.03E-06	0.88	3.91	-	775.4
AHQ-3-8, 4695 - 4743	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.37E-04	0.76	3.09	-	629.3
AHQ-3-3, 5224 - 5292	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	7.60E-08	0.92	4.29	-	963.8
AHQ-3-5, 3733 - 3741	R.ENGVYLIDVK.F	1150.30633	1	8.74E-04	0.23	2.42	-	301.1
AHQ-3-4, 3969	R.ENGVYLIDVK.F	1150.30633	1	3.35E-04	0.22	2.16	-	246.9
AHQ-3-7, 3679 - 3750	R.ENGVYLIDVK.F	1150.30633	1	1.93E-04	0.24	2.32	-	257.1
AHQ-3-6, 3794	R.ENGVYLIDVK.F	1150.30633	1	7.45E-05	0.24	2.33	-	309.8
AHQ-3-2, 4089	R.ENGVYLIDVK.F	1150.30633	1	5.32E-04	0.45	2.32	-	409.7
AHQ-3-5, 1437	K.ETGEHLVHVK.K	1149.28166	1	1.87E-05	0.37	2.09	-	242.8
AHQ-3-5, 3159 - 3179	K.FADQHVPGSPFSVK.V	1516.68203	2	5.98E-06	0.54	3.06	-	508.8
AHQ-3-1, 3616	K.FADQHVPGSPFSVK.V	1516.68203	2	3.27E-08	0.84	2.56	-	803.7
AHQ-3-12, 3348	K.FADQHVPGSPFSVK.V	1516.68203	2	7.68E-08	0.82	3.08	-	503.5
AHQ-3-5, 3168 - 3185	K.FADQHVPGSPFSVK.V	1516.68203	3	6.68E-05	0.94	4.21	-	1284.1
AHQ-3-1, 3633	K.FADQHVPGSPFSVK.V	1516.68203	3	2.77E-06	0.90	3.64	-	1191.2
AHQ-3-13-, 3407 - 3411	K.FADQHVPGSPFSVK.V	1516.68203	2	4.01E-05	0.82	3.51	-	489.2
AHQ-3-6, 3119	K.FADQHVPGSPFSVK.V	1516.68203	2	4.49E-07	0.53	2.56	-	318.2
AHQ-3-5, 3283	K.FADQHVPGSPFSVK.V	1516.68203	2	4.72E-04	0.77	3.05	-	516.8
AHQ-3-4, 3376	K.FADQHVPGSPFSVK.V	1516.68203	2	1.73E-04	0.63	2.84	-	385.0
AHQ-3-2, 3478	K.FADQHVPGSPFSVK.V	1516.68203	2	2.68E-09	0.86	3.47	-	564.9
AHQ-3-2, 5745 - 5817	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.28E-05	0.96	5.57	-	1022.7
AHQ-3-2, 5697 - 5765	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	6.25E-07	0.89	4.24	-	827.1
AHQ-3-2, 5659 - 5734	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.13E-10	0.98	6.75	-	1508.6
AHQ-3-1, 5812 - 5878	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.73E-11	0.95	5.32	-	980.1
AHQ-3-4, 5616 - 5685	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.54E-09	0.97	5.75	-	1503.7
AHQ-3-12, 5370 - 5398	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.17E-04	0.93	4.61	-	1117.0
AHQ-3-1, 5777 - 5796	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.16E-06	0.97	6.25	-	1104.6
AHQ-3-4, 5704 - 5772	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.93E-06	0.96	4.98	-	1099.1
AHQ-3-12, 5390	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	6.44E-06	0.96	5.05	-	1055.8
AHQ-3-2, 5833 - 5913	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	7.01E-10	0.94	4.70	-	1426.0
AHQ-3-1, 5916	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.71E-08	0.97	5.66	-	1334.0
AHQ-3-12, 5500	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.09E-05	0.86	4.34	-	580.9
AHQ-3-4, 5612 - 5688	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.13E-07	0.91	4.74	-	778.7
AHQ-3-9, 5025	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.72E-07	0.89	4.26	-	852.5
AHQ-3-11, 5136 - 5152	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	6.53E-05	0.88	4.24	-	783.8
AHQ-3-3, 5741	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	6.02E-05	0.97	5.34	-	1291.6
AHQ-3-3, 5658 - 5732	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.77E-10	0.98	7.03	-	1309.4
AHQ-3-3, 5640 - 5721	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.42E-06	0.91	4.79	-	727.1
AHQ-3-5, 5428	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.61E-08	0.93	4.89	-	925.9
AHQ-3-7, 5278 - 5280	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.63E-04	0.94	4.29	-	1009.3
AHQ-3-5, 5601	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.26E-06	0.85	3.51	-	602.9
AHQ-3-9, 5019	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.40E-04	0.96	4.72	-	1298.2
AHQ-3-13-, 5291 - 5363	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.62E-08	0.79	3.94	-	424.0
AHQ-3-2, 5885	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.63E-12	0.96	5.68	-	848.9
AHQ-3-3, 5829	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.98E-04	0.94	4.38	-	942.5
AHQ-3-4, 5194 - 5264	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	1.23E-09	0.95	5.42	-	717.1
AHQ-3-5, 5233 - 5287	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	3	3.06E-06	0.69	3.13	-	768.6
AHQ-3-6, 4959	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	4.77E-04	0.83	3.81	-	499.1
AHQ-3-5, 5033 - 5104	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	6.92E-09	0.94	5.49	-	512.9
AHQ-3-5, 3436	K.FNGTHIPGSPFK.I	1302.46259	2	6.61E-04	0.80	3.06	-	602.7
AHQ-3-1, 3854	K.FNGTHIPGSPFK.I	1302.46259	2	4.44E-05	0.82	3.06	-	664.9
AHQ-3-1, 3962 - 3965	K.FNGTHIPGSPFK.I	1302.46259	2	6.30E-06	0.60	3.01	-	321.9
AHQ-3-4, 3904	K.FNGTHIPGSPFK.I	1302.46259	1	1.96E-04	0.32	2.06	-	370.0
AHQ-3-5, 3529	K.FNGTHIPGSPFK.I	1302.46259	2	1.26E-05	0.91	3.79	-	772.8
AHQ-3-7, 3312	K.FNGTHIPGSPFK.I	1302.46259	2	2.56E-04	0.83	3.04	-	733.2
AHQ-3-7, 3647	K.FNGTHIPGSPFK.I	1302.46259	2	2.00E-07	0.67	2.70	-	470.0
AHQ-3-5, 2688	R.FVPAEMGTHTVSVK.Y	1503.74821	2	9.24E-06	0.87	3.24	-	644.8
AHQ-3-6, 2697	R.FVPAEMGTHTVSVK.Y	1503.74821	2	3.59E-07	0.89	3.79	-	653.2
AHQ-3-1, 3124	R.FVPAEMGTHTVSVK.Y	1503.74821	2	2.60E-10	0.92	3.42	-	719.7
AHQ-3-2, 2315	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	8.43E-04	0.75	3.23	-	289.5
AHQ-3-4, 2878 - 2952	R.FVPAEMGTHTVSVK.Y	1503.74821	2	4.45E-08	0.86	3.83	-	537.5
AHQ-3-3, 6928 - 6997	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	1.22E-04	0.74	3.51	-	566.6
AHQ-3-2, 6441	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	3.45E-06	0.89	4.03	-	609.9
AHQ-3-2, 6297 - 6373	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	2.22E-04	0.86	3.99	-	644.0
AHQ-3-1, 3417 - 3488	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	8.87E-06	0.78	3.03	-	717.2
AHQ-3-2, 3919	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.06E-09	0.36	2.68	-	256.5
AHQ-3-9, 2880	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	5.32E-05	0.59	2.96	-	476.5
AHQ-3-4, 3300	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.52E-04	0.79	3.37	-	568.7
AHQ-3-3, 3432	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	5.77E-05	0.78	3.60	-	593.1
AHQ-3-5, 3135 - 3139	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	6.17E-04	0.82	3.31	-	682.5
AHQ-3-3, 3340 - 3364	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	4.22E-07	0.86	3.33	-	860.8
AHQ-3-7, 3010 - 3015	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	6.42E-06	0.92	4.00	-	786.5
AHQ-3-2, 3285 - 3353	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	7.83E-05	0.77	3.41	-	588.6
AHQ-3-2, 3489 - 3563	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.80E-07	0.70	2.69	-	797.6
AHQ-3-1, 3484 - 3557	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.35E-06	0.93	4.06	-	908.3
AHQ-3-6, 3086	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.20E-06	0.88	3.69	-	685.8
AHQ-3-3, 3337	K.GKLDVQFSGLTK.G	1293.49392	2	3.67E-04	0.93	3.75	-	1091.0
AHQ-3-3, 3422	K.GKLDVQFSGLTK.G	1293.49392	1	9.84E-04	0.70	2.79	-	552.4
AHQ-3-4, 3282	K.GKLDVQFSGLTK.G	1293.49392	2	1.04E-04	0.93	3.80	-	1018.6
AHQ-3-2, 3658	K.GKLDVQFSGLTK.G	1293.49392	1	6.83E-04	0.21	2.20	-	296.5
AHQ-3-1, 5169 - 5196	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	8.33E-15	0.98	6.48	-	1565.0
AHQ-3-1, 4968 - 5040	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.07E-08	0.94	5.30	-	804.4
AHQ-3-3, 5196 - 5264	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	6.88E-05	0.60	2.63	-	599.1
AHQ-3-2, 5094 - 5162	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	4.54E-08	0.98	6.62	-	1302.9
AHQ-3-2, 5233 - 5373	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	8.53E-07	0.94	5.16	-	996.0
AHQ-3-2, 6798 - 6823	K.GLVEPVDVVDNADGTQTVNYVPSREGPYSISVLYGDEEVPR.S	4437.77937	3	4.94E-06	0.73	3.26	-	516.3
AHQ-3-1, 6681	K.GLVEPVDVVDNADGTQTVNYVPSREGPYSISVLYGDEEVPR.S	4437.77937	3	4.47E-09	0.94	4.92	-	1026.8
AHQ-3-3, 2132 - 2133	K.GTVEPQLEAR.G	1100.20741	2	3.57E-04	0.62	2.93	-	384.4
AHQ-3-2, 2129	K.GTVEPQLEAR.G	1100.20741	1	8.49E-06	0.09	2.08	-	203.4
AHQ-3-2, 2125	K.GTVEPQLEAR.G	1100.20741	2	2.40E-06	0.73	3.15	-	461.5
AHQ-3-1, 2304	K.GTVEPQLEAR.G	1100.20741	2	5.47E-06	0.78	2.81	-	589.7
AHQ-3-1, 5778 - 5786	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	5.34E-07	0.97	5.40	-	1316.8
AHQ-3-4, 5561 - 5565	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	3.56E-06	0.97	5.29	-	1270.6
AHQ-3-2, 5535 - 5607	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.19E-07	0.94	4.13	-	1338.2
AHQ-3-3, 5226 - 5305	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	4.88E-05	0.93	3.93	-	1062.6
AHQ-3-3, 5240	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	2.17E-04	0.69	3.73	-	451.8
AHQ-3-2, 5638 - 5703	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	1.02E-06	0.98	5.49	-	1651.9
AHQ-3-2, 5647	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	3	3.56E-04	0.69	3.70	-	481.5
AHQ-3-1, 5373 - 5384	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.27E-06	0.96	5.06	-	1115.2
AHQ-3-2, 5243 - 5314	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.57E-04	0.97	5.35	-	1147.9

AHQ-3-5, 4956	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.21E-04	0.95	4.32	-	1057.5
AHQ-3-2, 5035	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	3.11E-04	0.97	4.47	-	1847.6
AHQ-3-4, 5117	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.71E-04	0.94	4.38	-	1016.2
AHQ-3-3, 5606 - 5616	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	6.41E-05	0.96	4.99	-	1150.3
AHQ-3-1, 5380	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	3.31E-04	0.82	3.87	-	958.6
AHQ-3-3, 4300 - 4377	R.IANLQTDLSDGLR.L	1416.56231	2	9.03E-04	0.96	4.37	-	1242.8
AHQ-3-1, 4758	R.IANLQTDLSDGLR.L	1416.56231	2	9.08E-04	0.39	2.57	-	262.4
AHQ-3-7, 3936	R.IANLQTDLSDGLR.L	1416.56231	2	7.02E-08	0.92	3.88	-	899.4
AHQ-3-11, 3922	R.IANLQTDLSDGLR.L	1416.56231	2	6.19E-08	0.93	4.15	-	990.8
AHQ-3-3, 4314	R.IANLQTDLSDGLR.L	1416.56231	1	1.27E-04	0.39	2.96	-	216.7
AHQ-3-2, 3933 - 3959	R.IANLQTDLSDGLR.L	1416.56231	2	5.69E-05	0.92	4.01	-	957.1
AHQ-3-1, 4408 - 4476	R.IANLQTDLSDGLR.L	1416.56231	2	8.31E-05	0.85	3.39	-	820.1
AHQ-3-5, 4052	R.IANLQTDLSDGLR.L	1416.56231	1	1.16E-04	0.50	2.91	-	315.6
AHQ-3-13, 4133 - 4143	R.IANLQTDLSDGLR.L	1416.56231	2	3.83E-05	0.96	4.49	-	1254.9
AHQ-3-4, 4241	R.IANLQTDLSDGLR.L	1416.56231	1	7.88E-04	0.61	3.08	-	363.4
AHQ-3-2, 4497 - 4577	R.IANLQTDLSDGLR.L	1416.56231	2	5.10E-08	0.93	3.42	-	1147.4
AHQ-3-2, 4267 - 4338	R.IANLQTDLSDGLR.L	1416.56231	2	4.94E-08	0.95	4.42	-	1142.7
AHQ-3-14, 5009	R.IANLQTDLSDGLR.L	1416.56231	2	2.92E-08	0.88	3.60	-	816.6
AHQ-3-10, 3831 - 3855	R.IANLQTDLSDGLR.L	1416.56231	2	2.41E-05	0.92	3.85	-	965.9
AHQ-3-2, 4029 - 4031	R.IANLQTDLSDGLR.L	1416.56231	2	1.99E-09	0.96	4.28	-	1248.9
AHQ-3-1, 4106	R.IANLQTDLSDGLR.L	1416.56231	2	7.43E-08	0.90	4.20	-	660.3
AHQ-3-13-, 4150	R.IANLQTDLSDGLR.L	1416.56231	2	1.78E-04	0.88	3.17	-	1095.3
AHQ-3-5, 4047	R.IANLQTDLSDGLR.L	1416.56231	2	9.11E-06	0.95	4.05	-	1312.2
AHQ-3-9, 3747 - 3753	R.IANLQTDLSDGLR.L	1416.56231	2	5.88E-08	0.94	4.54	-	933.5
AHQ-3-4, 3850	R.IANLQTDLSDGLR.L	1416.56231	2	6.47E-09	0.94	4.05	-	1101.1
AHQ-3-1, 4001 - 4025	R.IANLQTDLSDGLR.L	1416.56231	2	9.03E-06	0.94	3.87	-	1261.8
AHQ-3-3, 3986	R.IANLQTDLSDGLR.L	1416.56231	2	4.82E-06	0.88	3.64	-	653.6
AHQ-3-1, 4414	R.IANLQTDLSDGLR.L	1416.56231	1	5.24E-04	0.47	2.88	-	220.8
AHQ-3-4, 4224	R.IANLQTDLSDGLR.L	1416.56231	2	2.90E-07	0.93	3.80	-	1022.6
AHQ-3-1, 4604 - 4608	R.IANLQTDLSDGLR.L	1416.56231	2	2.58E-07	0.95	4.00	-	1284.2
AHQ-3-12, 4095	R.IANLQTDLSDGLR.L	1416.56231	2	1.66E-09	0.96	4.64	-	1138.4
AHQ-3-3, 4550	R.IANLQTDLSDGLR.L	1416.56231	2	1.01E-06	0.93	3.78	-	1203.6
AHQ-3-6, 3989 - 3994	R.IANLQTDLSDGLR.L	1416.56231	2	1.87E-08	0.93	3.95	-	1101.4
AHQ-3-5, 5452 - 5531	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.56E-05	0.96	4.69	-	1043.0
AHQ-3-6, 5381	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.88E-07	0.94	5.08	-	768.9
AHQ-3-5, 4023 - 4068	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.25E-07	0.97	5.10	-	1890.3
AHQ-3-7, 3922 - 3923	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	6.24E-05	0.97	5.28	-	1596.8
AHQ-3-1, 5736 - 5785	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.37E-04	0.96	4.57	-	1430.6
AHQ-3-1, 4341	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	3	6.58E-05	0.72	3.10	-	810.4
AHQ-3-5, 5475	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	4.75E-06	0.85	4.20	-	779.1
AHQ-3-6, 5415	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	6.02E-05	0.87	3.81	-	929.5
AHQ-3-4, 5624 - 5692	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	8.01E-11	0.98	6.00	-	2132.4
AHQ-3-5, 4847	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	6.78E-05	0.85	3.21	-	943.6
AHQ-3-4, 4160 - 4230	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	7.17E-06	0.96	5.61	-	1230.0
AHQ-3-7, 5323 - 5326	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.02E-10	0.97	5.25	-	1553.9
AHQ-3-2, 4270	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	3.66E-07	0.94	3.95	-	1106.8
AHQ-3-3, 5661	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	8.27E-10	0.95	4.64	-	1033.2
AHQ-3-1, 4288 - 4356	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	8.05E-06	0.97	5.32	-	1703.2
AHQ-3-6, 3963 - 3967	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	7.95E-07	0.98	4.93	-	2167.2
AHQ-3-3, 4230	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	5.66E-07	0.97	4.91	-	1475.3
AHQ-3-2, 2486	K.IVGPSGAAVPCK.V	1157.36530	2	3.61E-06	0.92	3.66	-	950.9
AHQ-3-3, 2476 - 2496	K.IVGPSGAAVPCK.V	1157.36530	2	1.96E-10	0.93	4.29	-	736.1
AHQ-3-1, 2632	K.IVGPSGAAVPCK.V	1157.36530	2	2.43E-05	0.90	3.68	-	880.4
AHQ-3-4, 2473	K.IVGPSGAAVPCK.V	1157.36530	2	4.74E-05	0.88	3.59	-	669.9
AHQ-3-1, 4360	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	3.01E-05	0.91	4.62	-	352.3
AHQ-3-3, 4264 - 4336	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	7.55E-07	0.93	4.97	-	498.2
AHQ-3-3, 4345 - 4420	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.21E-06	0.96	5.10	-	1349.4
AHQ-3-1, 4352 - 4424	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.45E-11	0.93	4.99	-	1331.6
AHQ-3-2, 4423	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	2.23E-05	0.81	3.15	-	600.9
AHQ-3-3, 4254 - 4276	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.69E-11	0.96	5.64	-	1225.2
AHQ-3-5, 4149	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.29E-04	0.91	4.06	-	1041.9
AHQ-3-2, 4274 - 4353	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.64E-08	0.93	4.78	-	1247.0
AHQ-3-1, 4469	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.54E-05	0.88	3.85	-	577.3
AHQ-3-6, 3973	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.32E-04	0.92	4.25	-	1462.5
AHQ-3-2, 4362 - 4429	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	9.40E-10	0.92	4.67	-	1067.8
AHQ-3-2, 4281 - 4350	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	6.74E-06	0.83	3.71	-	411.0
AHQ-3-4, 4194 - 4276	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	5.91E-05	0.90	4.36	-	1085.8
AHQ-3-4, 4196	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	2.04E-07	0.87	4.00	-	415.5
AHQ-3-5, 4044	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.07E-06	0.93	4.75	-	1296.3
AHQ-3-1, 4558 - 4637	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	6.60E-07	0.94	4.52	-	1028.3
AHQ-3-5, 4399	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	5.42E-04	0.51	3.16	-	564.0
AHQ-3-5, 4280 - 4295	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	2.31E-04	0.89	4.13	-	686.2
AHQ-3-5, 3956 - 3968	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.54E-05	0.93	4.73	-	658.4
AHQ-3-6, 4025 - 4029	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.49E-06	0.89	4.34	-	522.8
AHQ-3-5, 4075 - 4087	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.34E-11	0.98	7.40	-	2107.9
AHQ-3-9, 3763	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	2.08E-05	0.82	3.38	-	488.9
AHQ-3-8, 3760	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.68E-06	0.86	3.61	-	627.4
AHQ-3-2, 4461	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	9.59E-09	0.95	5.02	-	1709.5
AHQ-3-5, 4181	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	5.07E-05	0.93	4.42	-	1673.9
AHQ-3-1, 4480 - 4552	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	4.31E-08	0.97	5.75	-	1897.3
AHQ-3-1, 4592	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.81E-12	0.95	4.98	-	1431.7
AHQ-3-1, 4486 - 4556	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.29E-06	0.73	3.26	-	404.1
AHQ-3-4, 4205 - 4288	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	7.16E-07	0.96	5.84	-	1601.5
AHQ-3-2, 3393 - 3462	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	2.59E-08	0.96	5.60	-	1467.4
AHQ-3-6, 3025	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	6.34E-07	0.85	3.76	-	741.9
AHQ-3-2, 3411 - 3482	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	5.56E-05	0.96	5.39	-	1024.8
AHQ-3-3, 3290 - 3369	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	4.94E-04	0.94	4.89	-	687.7
AHQ-3-2, 3638	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.10E-06	0.89	3.89	-	1050.5
AHQ-3-3, 3302 - 3382	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	2.77E-04	0.84	3.61	-	916.5
AHQ-3-1, 3661 - 3730	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	5.37E-08	0.96	4.71	-	1758.4
AHQ-3-2, 3262 - 3305	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.06E-06	0.92	4.51	-	1209.9
AHQ-3-3, 3442 - 3516	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	2.39E-04	0.88	4.13	-	483.5
AHQ-3-4, 3442	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	5.22E-04	0.39	2.56	-	263.3
AHQ-3-1, 3546	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	7.09E-07	0.96	5.06	-	1010.3
AHQ-3-1, 3544	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	6.43E-08	0.92	4.16	-	1087.0
AHQ-3-1, 3550	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	5.40E-04	0.75	3.19	-	462.9
AHQ-3-4, 3896	K.LDVQFSGLTK.G	1108.26945	1	5.04E-06	0.31	2.14	-	342.4
AHQ-3-2, 3993 - 4062	K.LDVQFSGLTK.G	1108.26945	1	1.63E-06	0.10	1.91	-	298.1
AHQ-3-2, 4003	K.LDVQFSGLTK.G	1108.26945	1	1.09E-04	0.17	2.10	-	217.5
AHQ-3-2, 3995	K.LDVQFSGLTK.G	1108.26945	2	5.39E-06	0.94	3.90	-	1113.4
AHQ-3-3, 3960	K.LDVQFSGLTK.G	1108.26945	1	1.19E-05	0.19	2.31	-	190.4
AHQ-3-3, 3957	K.LDVQFSGLTK.G	1108.26945	2	3.66E-05	0.86	3.09	-	912.4
AHQ-3-3, 3945	K.LDVQFSGLTK.G	1108.26945	1	3.63E-04	0.11	2.04	-	201.2
AHQ-3-1, 4093	K.LDVQFSGLTK.G	1108.26945	2	2.03E-06	0.94	3.81	-	1065.2
AHQ-3-2, 7150	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	4.41E-04	0.96	5.27	-	1335.0
AHQ-3-2, 7162	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	2	7.82E-05	0.83	4.11	-	393.4
AHQ-3-2, 4969	K.LPQLPITNFSR.D	1286.50461	1	6.22E-07	0.77	2.94	-	265.2

AHQ-3-6, 4597 - 4607	K.LPQLPITNFSR.D	1286.50461	2	3.24E-05	0.76	2.93	-	480.6
AHQ-3-2, 5299	K.LPQLPITNFSR.D	1286.50461	1	4.55E-05	0.22	1.82	-	233.2
AHQ-3-1, 5048 - 5050	K.LPQLPITNFSR.D	1286.50461	2	2.93E-05	0.88	3.16	-	693.1
AHQ-3-2, 5294	K.LPQLPITNFSR.D	1286.50461	2	1.50E-06	0.85	2.95	-	692.0
AHQ-3-4, 4886	K.LPQLPITNFSR.D	1286.50461	2	5.30E-05	0.77	2.98	-	538.6
AHQ-3-2, 4950 - 5021	K.LPQLPITNFSR.D	1286.50461	2	8.61E-06	0.82	2.87	-	553.0
AHQ-3-9, 4291 - 4299	K.LPQLPITNFSR.D	1286.50461	2	5.48E-06	0.78	2.87	-	498.0
AHQ-3-3, 4960	K.LPQLPITNFSR.D	1286.50461	2	9.98E-07	0.92	3.16	-	826.3
AHQ-3-1, 5312	K.LPQLPITNFSR.D	1286.50461	2	4.89E-07	0.72	2.72	-	536.7
AHQ-3-2, 5206	K.LPQLPITNFSR.D	1286.50461	2	1.62E-04	0.54	2.54	-	356.9
AHQ-3-5, 5105	K.LPQLPITNFSR.D	1286.50461	2	3.96E-05	0.82	2.90	-	647.8
AHQ-3-3, 5736 - 5788	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	7.33E-09	0.91	4.29	-	635.5
AHQ-3-3, 5688	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	2.94E-08	0.98	6.63	-	1786.5
AHQ-3-5, 5503 - 5516	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	2.52E-06	0.96	4.93	-	1561.3
AHQ-3-12, 5331	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.31E-09	0.95	4.47	-	1028.7
AHQ-3-2, 5746 - 5813	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.82E-07	0.92	4.43	-	667.4
AHQ-3-2, 5642 - 5723	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	1.48E-09	0.98	7.00	-	2428.4
AHQ-3-2, 5623 - 5693	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	8.15E-09	0.96	5.73	-	920.8
AHQ-3-1, 5613 - 5692	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	2.93E-11	0.97	6.33	-	1776.2
AHQ-3-3, 5586 - 5664	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.43E-06	0.97	5.81	-	904.8
AHQ-3-1, 5580 - 5648	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	5.83E-07	0.90	3.61	-	962.0
AHQ-3-4, 5621 - 5622	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	4.91E-05	0.79	3.60	-	605.9
AHQ-3-4, 2822	R.LRNGHVGISFVPK.E	1424.67564	2	4.78E-04	0.86	3.35	-	730.9
AHQ-3-5, 2616	R.LRNGHVGISFVPK.E	1424.67564	2	1.55E-04	0.80	2.81	-	727.6
AHQ-3-1, 3133	R.LRNGHVGISFVPK.E	1424.67564	2	2.11E-05	0.82	2.95	-	750.4
AHQ-3-1, 3490 - 3496	R.LSPFM*ADIR.D	1066.25604	2	6.70E-04	0.78	2.63	-	598.0
AHQ-3-2, 4049 - 4057	R.LSPFMADIR.D	1050.25664	2	4.45E-04	0.77	2.79	-	393.9
AHQ-3-6, 3121	R.LTVSSLQESGLK.V	1262.43499	2	9.66E-06	0.70	2.57	-	694.7
AHQ-3-4, 3356 - 3388	R.LTVSSLQESGLK.V	1262.43499	2	9.80E-07	0.90	3.37	-	898.3
AHQ-3-7, 3707	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.40E-04	0.96	4.82	-	1639.6
AHQ-3-7, 3703 - 3706	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.02E-04	0.98	5.86	-	1384.2
AHQ-3-6, 4155 - 4161	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.10E-07	0.95	4.71	-	1011.5
AHQ-3-1, 4662	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.57E-08	0.95	4.99	-	1411.8
AHQ-3-1, 4649 - 4665	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.12E-09	0.96	5.28	-	1128.8
AHQ-3-6, 3790	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.75E-06	0.97	5.93	-	1807.7
AHQ-3-3, 4185	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.78E-05	0.95	4.84	-	1133.5
AHQ-3-13-, 4081	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.34E-07	0.96	4.99	-	1735.2
AHQ-3-8, 3645	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.22E-06	0.95	4.61	-	1075.4
AHQ-3-4, 4034 - 4041	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	7.13E-09	0.98	6.17	-	1861.7
AHQ-3-7, 4038	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.31E-06	0.95	5.00	-	1024.3
AHQ-3-10, 3708	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.21E-06	0.91	4.24	-	697.4
AHQ-3-5, 3699	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.20E-06	0.90	3.97	-	757.2
AHQ-3-11, 3819	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	6.08E-06	0.90	4.12	-	457.5
AHQ-3-4, 4026	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.90E-04	0.91	4.18	-	753.0
AHQ-3-5, 3767 - 3820	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	5.73E-04	0.97	4.95	-	1980.8
AHQ-3-11, 3830	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.97E-06	0.94	4.50	-	1335.1
AHQ-3-5, 3819 - 3892	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.76E-06	0.98	5.71	-	1858.1
AHQ-3-5, 3893	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	7.11E-07	0.97	4.70	-	2179.5
AHQ-3-11, 4111	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	9.14E-05	0.64	3.22	-	568.9
AHQ-3-13, 4057	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	9.65E-06	0.95	5.30	-	873.1
AHQ-3-1, 4344	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.84E-08	0.97	5.43	-	1529.0
AHQ-3-5, 4299	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	8.99E-06	0.83	3.20	-	844.4
AHQ-3-1, 4354	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.13E-04	0.96	4.55	-	1710.3
AHQ-3-2, 4213 - 4215	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.50E-07	0.98	6.34	-	2129.5
AHQ-3-14-, 3931	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.49E-08	0.96	4.79	-	1608.9
AHQ-3-14-, 4271	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.44E-05	0.93	4.31	-	730.9
AHQ-3-5, 4168 - 4240	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	5.41E-08	0.98	5.68	-	1820.1
AHQ-3-13, 4058	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	3.22E-04	0.94	4.26	-	1186.5
AHQ-3-6, 3781	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.67E-07	0.96	4.87	-	1327.7
AHQ-3-4, 4404 - 4481	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	9.19E-13	0.96	5.65	-	863.0
AHQ-3-14, 5280	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.85E-08	0.97	4.95	-	1878.7
AHQ-3-3, 4540	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	6.04E-08	0.95	4.35	-	1167.4
AHQ-3-14, 5424 - 5492	R.LYSVSYLLK.D	1086.30538	2	9.00E-04	0.47	2.91	-	266.4
AHQ-3-6, 2359 - 2395	K.MDCQECPEGYR.V	1447.55375	2	6.17E-06	0.86	3.47	-	698.0
AHQ-3-5, 2971	R.NGHVGISFVPK.E	1155.33104	1	3.52E-04	0.31	2.13	-	381.6
AHQ-3-4, 2970	R.NGHVGISFVPK.E	1155.33104	1	8.29E-07	0.70	2.46	-	499.9
AHQ-3-4, 3172	R.NGHVGISFVPK.E	1155.33104	1	8.79E-05	0.28	2.17	-	381.9
AHQ-3-5, 2768	R.NGHVGISFVPK.E	1155.33104	1	1.63E-06	0.61	2.61	-	421.8
AHQ-3-5, 4617 - 4631	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	8.24E-09	0.94	4.17	-	944.9
AHQ-3-4, 4812	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	1.16E-04	0.95	4.04	-	1310.4
AHQ-3-1, 4929	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	5.60E-05	0.95	4.29	-	1076.1
AHQ-3-2, 1811 - 1879	K.RAEFTVETR.S	1109.21754	2	5.87E-07	0.92	3.30	-	935.1
AHQ-3-1, 2146	K.RAEFTVETR.S	1109.21754	2	2.87E-06	0.96	3.73	-	1258.8
AHQ-3-1, 3146	R.RAPSVANVGSHCDLSLK.I	1813.02884	2	9.16E-05	0.96	4.95	-	1097.5
AHQ-3-7, 2572	R.RLTVSSLQESGLK.V	1418.62134	2	3.58E-04	0.92	3.98	-	993.4
AHQ-3-3, 2953	R.RLTVSSLQESGLK.V	1418.62134	2	5.22E-04	0.97	4.72	-	2067.8
AHQ-3-1, 7334 - 7416	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	9.23E-08	0.89	4.16	-	948.1
AHQ-3-3, 7681	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	1.52E-05	0.79	3.45	-	822.8
AHQ-3-1, 7440	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	2.83E-04	0.92	3.84	-	1334.8
AHQ-3-2, 7686 - 7755	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	3.78E-04	0.82	4.23	-	551.9
AHQ-3-1, 7345 - 7408	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	4.74E-06	0.92	4.76	-	1099.7
AHQ-3-2, 3941 - 4009	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.46E-06	0.87	4.33	-	516.5
AHQ-3-3, 3870 - 3942	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.67E-04	0.84	3.99	-	792.3
AHQ-3-2, 3949 - 4021	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	5.43E-07	0.92	4.45	-	947.5
AHQ-3-1, 4101 - 4128	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.81E-06	0.92	4.86	-	515.3
AHQ-3-2, 4103	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.53E-06	0.85	3.53	-	906.2
AHQ-3-2, 4193	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	5.09E-08	0.92	4.43	-	876.8
AHQ-3-4, 3834 - 3916	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.17E-07	0.87	3.98	-	706.3
AHQ-3-2, 4411 - 4483	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.40E-07	0.87	4.19	-	664.4
AHQ-3-2, 4567	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	7.00E-06	0.80	3.75	-	444.3
AHQ-3-1, 4060 - 4082	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	7.91E-07	0.93	4.43	-	1080.8
AHQ-3-4, 4010	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	7.08E-04	0.23	2.76	-	263.7
AHQ-3-7, 3550	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.85E-05	0.93	4.67	-	713.4
AHQ-3-8, 3418	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.98E-05	0.71	3.59	-	297.3
AHQ-3-1, 4294	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.95E-05	0.92	4.77	-	554.5
AHQ-3-5, 3755	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.07E-05	0.86	3.85	-	628.7
AHQ-3-5, 3665	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.96E-07	0.92	4.77	-	641.9
AHQ-3-6, 3626 - 3641	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	7.42E-11	0.92	4.63	-	591.5
AHQ-3-5, 3589 - 3664	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.54E-07	0.84	3.51	-	813.1
AHQ-3-3, 3896 - 3976	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.08E-06	0.94	4.94	-	643.8
AHQ-3-2, 4218 - 4291	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.31E-07	0.95	5.27	-	837.4
AHQ-3-4, 3868	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	4.13E-09	0.92	3.92	-	1360.6
AHQ-3-3, 4049 - 4056	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.39E-06	0.96	5.55	-	851.0
AHQ-3-3, 4177	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.61E-04	0.88	3.96	-	593.3
AHQ-3-6, 3639	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.11E-06	0.88	3.80	-	1063.8
AHQ-3-2, 4077 - 4146	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.13E-05	0.94	4.74	-	714.6
AHQ-3-1, 4129 - 4200	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	8.75E-08	0.88	4.26	-	605.1

AHQ-3-5, 3849	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.66E-07	0.82	3.57	-	505.5
AHQ-3-3, 3350	K.SPFEVYVDK.S	1084.20321	1	1.50E-05	0.69	2.79	-	598.3
AHQ-3-1, 3489	K.SPFEVYVDK.S	1084.20321	1	2.95E-05	0.82	2.99	-	952.2
AHQ-3-5, 3151	K.SPFEVYVDK.S	1084.20321	2	7.69E-06	0.89	2.97	-	985.8
AHQ-3-4, 3322	K.SPFEVYVDK.S	1084.20321	1	4.40E-05	0.83	3.35	-	819.0
AHQ-3-2, 3338 - 3409	K.SPFEVYVDK.S	1084.20321	2	6.61E-06	0.93	3.24	-	1211.0
AHQ-3-3, 3357	K.SPFEVYVDK.S	1084.20321	2	6.81E-06	0.92	3.31	-	1028.3
AHQ-3-7, 3030 - 3035	K.SPFEVYVDK.S	1084.20321	1	1.20E-05	0.49	2.33	-	554.8
AHQ-3-2, 3271 - 3483	K.SPFEVYVDK.S	1084.20321	1	4.47E-04	0.73	2.49	-	903.3
AHQ-3-1, 3481	K.SPFEVYVDK.S	1084.20321	2	1.15E-06	0.90	2.94	-	1054.9
AHQ-3-4, 3332	K.SPFEVYVDK.S	1084.20321	2	8.86E-06	0.92	3.33	-	1079.0
AHQ-3-4, 2961	K.SPFEVYVDKSQGDASK.V	1757.87886	2	6.43E-04	0.69	2.83	-	497.9
AHQ-3-6, 4810	K.SPFSVAVSPSLDLSK.I	1534.73557	2	4.36E-04	0.84	2.94	-	907.1
AHQ-3-1, 4977 - 4997	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.26E-04	0.76	3.20	-	677.0
AHQ-3-5, 4911	K.SPFSVAVSPSLDLSK.I	1534.73557	2	4.39E-05	0.92	3.95	-	1090.9
AHQ-3-1, 5109 - 5145	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.10E-05	0.88	3.48	-	1029.4
AHQ-3-2, 5118 - 5201	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.19E-06	0.94	4.66	-	953.6
AHQ-3-2, 4951	K.SPFSVAVSPSLDLSK.I	1534.73557	2	5.93E-08	0.88	3.42	-	920.8
AHQ-3-4, 5014 - 5036	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.67E-05	0.93	4.20	-	1025.4
AHQ-3-3, 5073 - 5148	K.SPFSVAVSPSLDLSK.I	1534.73557	2	4.46E-06	0.92	4.36	-	788.5
AHQ-3-2, 5189	K.SPFSVAVSPSLDLSKIK.V	1776.06673	2	4.86E-05	0.29	2.56	-	447.0
AHQ-3-2, 3457 - 3525	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.19E-04	0.91	4.70	-	443.8
AHQ-3-6, 3241	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.89E-04	0.86	3.59	-	596.3
AHQ-3-3, 3645	R.SPYTVTVGQACNPSACR.A	1871.04208	2	9.95E-06	0.72	2.95	-	626.9
AHQ-3-7, 3224	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.19E-04	0.90	4.05	-	582.5
AHQ-3-2, 3645 - 3725	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.66E-04	0.79	3.69	-	347.1
AHQ-3-5, 3255 - 3324	R.SPYTVTVGQACNPSACR.A	1871.04208	2	5.30E-05	0.87	3.98	-	461.2
AHQ-3-4, 3373 - 3444	R.SPYTVTVGQACNPSACR.A	1871.04208	2	8.01E-04	0.87	3.66	-	560.3
AHQ-3-3, 3438 - 3517	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.41E-04	0.92	4.21	-	559.3
AHQ-3-1, 3521 - 3596	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.91E-07	0.87	3.90	-	546.2
AHQ-3-2, 2679	K.SQGDASKVTAQGPGLEPSGNIANK.T	2327.49419	2	1.01E-06	0.90	4.51	-	651.4
AHQ-3-2, 5049 - 5117	R.TFSVWYVPEVTGTHK.V	1751.96228	2	1.04E-04	0.75	3.48	-	319.2
AHQ-3-3, 2964	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	7.32E-09	0.90	3.72	-	845.2
AHQ-3-4, 2945	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	8.90E-07	0.90	3.95	-	1014.9
AHQ-3-7, 2671	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	2.59E-04	0.90	3.74	-	817.1
AHQ-3-2, 2954	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	2.27E-05	0.92	3.67	-	1365.9
AHQ-3-5, 2775	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	6.21E-06	0.80	3.13	-	840.2
AHQ-3-6, 2749	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	2.08E-05	0.90	4.32	-	561.3
AHQ-3-1, 3157 - 3226	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	9.65E-05	0.70	3.15	-	571.9
AHQ-3-5, 2609	R.TGVELGKPTHFTVNAK.A	1699.93205	2	4.55E-05	0.88	3.44	-	787.8
AHQ-3-1, 2953	R.TGVELGKPTHFTVNAK.A	1699.93205	3	2.93E-05	0.59	3.23	-	548.7
AHQ-3-4, 2641 - 2642	R.TGVELGKPTHFTVNAK.A	1699.93205	2	9.87E-06	0.93	4.46	-	609.6
AHQ-3-5, 2485	R.TGVELGKPTHFTVNAK.A	1699.93205	2	5.75E-05	0.94	4.28	-	917.1
AHQ-3-3, 2688 - 2706	R.TGVELGKPTHFTVNAK.A	1699.93205	2	2.76E-04	0.90	3.86	-	704.9
AHQ-3-3, 2774 - 2844	R.TGVELGKPTHFTVNAK.A	1699.93205	2	4.97E-05	0.91	3.62	-	869.3
AHQ-3-2, 2657 - 2725	R.TGVELGKPTHFTVNAK.A	1699.93205	2	3.63E-04	0.91	3.96	-	691.9
AHQ-3-6, 2746	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.11E-10	0.94	4.64	-	1047.2
AHQ-3-5, 2848	K.THEAEIVEGENHTYCIR.F	2060.19046	2	1.57E-11	0.98	5.38	-	2462.2
AHQ-3-5, 2753	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.28E-04	0.88	3.63	-	971.4
AHQ-3-3, 3050 - 3052	K.THEAEIVEGENHTYCIR.F	2060.19046	2	5.22E-12	0.98	5.54	-	1782.7
AHQ-3-5, 2764 - 2840	K.THEAEIVEGENHTYCIR.F	2060.19046	2	6.76E-09	0.98	5.82	-	1725.2
AHQ-3-7, 2690	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.57E-05	0.93	4.02	-	1214.9
AHQ-3-7, 2692 - 2772	K.THEAEIVEGENHTYCIR.F	2060.19046	2	8.47E-05	0.98	5.32	-	1793.9
AHQ-3-7, 2780 - 2855	K.THEAEIVEGENHTYCIR.F	2060.19046	3	5.85E-04	0.84	3.41	-	951.2
AHQ-3-6, 2822 - 2823	K.THEAEIVEGENHTYCIR.F	2060.19046	2	3.74E-12	0.99	6.46	-	2705.3
AHQ-3-6, 2829	K.THEAEIVEGENHTYCIR.F	2060.19046	3	6.46E-05	0.94	4.75	-	1129.3
AHQ-3-5, 2929	K.THEAEIVEGENHTYCIR.F	2060.19046	2	4.87E-07	0.95	4.43	-	717.1
AHQ-3-2, 3078	K.THEAEIVEGENHTYCIR.F	2060.19046	2	6.95E-07	0.97	4.76	-	1783.5
AHQ-3-1, 3161 - 3190	K.THEAEIVEGENHTYCIR.F	2060.19046	3	5.69E-05	0.94	4.42	-	1241.3
AHQ-3-1, 3238 - 3308	K.THEAEIVEGENHTYCIR.F	2060.19046	2	9.44E-15	0.98	5.84	-	2169.3
AHQ-3-1, 3870	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	2	9.04E-06	0.88	3.72	-	661.5
AHQ-3-2, 4014	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	3	2.51E-08	0.90	3.98	-	858.4
AHQ-3-14-, 2929 - 2991	R.TPCEEILVK.H	1090.27249	2	2.42E-05	0.89	3.49	-	739.3
AHQ-3-14, 3932 - 3935	R.TPCEEILVK.H	1090.27249	1	5.27E-04	0.50	2.85	-	495.3
AHQ-3-5, 2911	R.TPCEEILVK.H	1090.27249	2	1.44E-04	0.85	2.90	-	676.6
AHQ-3-14, 3856 - 3923	R.TPCEEILVK.H	1090.27249	2	1.06E-05	0.76	2.85	-	653.7
AHQ-3-4, 3058	R.TPCEEILVK.H	1090.27249	2	5.58E-07	0.83	3.21	-	669.2
AHQ-3-14-, 2953 - 2995	R.TPCEEILVK.H	1090.27249	1	3.90E-04	0.57	2.56	-	414.1
AHQ-3-13-, 3034 - 3038	R.TPCEEILVK.H	1090.27249	2	4.51E-06	0.83	3.18	-	696.4
AHQ-3-14, 4025 - 4088	R.TPCEEILVK.H	1090.27249	2	9.75E-06	0.80	2.59	-	841.8
AHQ-3-6, 2877	R.TPCEEILVK.H	1090.27249	2	3.78E-05	0.87	2.95	-	762.6
AHQ-3-4, 3060	R.TPCEEILVK.H	1090.27249	1	1.35E-05	0.65	2.82	-	587.5
AHQ-3-13, 3057	R.TPCEEILVK.H	1090.27249	2	1.26E-06	0.86	3.10	-	667.7
AHQ-3-5, 3341	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.68E-11	0.95	4.40	-	1252.3
AHQ-3-7, 2995 - 2998	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.36E-11	0.96	4.94	-	1133.7
AHQ-3-3, 3477	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.53E-04	0.51	2.87	-	376.4
AHQ-3-5, 3041 - 3115	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.27E-07	0.90	3.98	-	687.0
AHQ-3-3, 3160	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.00E-07	0.65	2.61	-	587.1
AHQ-3-6, 3031 - 3038	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.11E-07	0.91	4.26	-	758.2
AHQ-3-1, 3640	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.04E-10	0.96	4.60	-	1102.6
AHQ-3-2, 3259 - 3341	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.06E-12	0.95	4.57	-	1077.9
AHQ-3-4, 3188 - 3261	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.39E-13	0.93	4.32	-	812.9
AHQ-3-1, 3540 - 3610	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.59E-10	0.94	4.46	-	1007.1
AHQ-3-1, 3372 - 3440	R.VANPSGNLTETYVQDR.G	1764.87462	2	9.73E-10	0.87	3.63	-	611.2
AHQ-3-2, 3354	R.VANPSGNLTETYVQDR.G	1764.87462	3	9.01E-04	0.92	4.04	-	1326.4
AHQ-3-3, 3393 - 3464	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.52E-09	0.95	5.32	-	748.1
AHQ-3-6, 3254	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.14E-12	0.88	3.89	-	779.8
AHQ-3-2, 3163	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.80E-09	0.94	4.13	-	979.7
AHQ-3-4, 3396 - 3465	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.05E-13	0.91	3.79	-	954.5
AHQ-3-1, 3225	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.51E-04	0.54	2.77	-	380.5
AHQ-3-2, 3410 - 3423	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.39E-13	0.96	5.08	-	983.9
AHQ-3-3, 3248 - 3316	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.94E-12	0.94	4.15	-	960.0
AHQ-3-2, 2806	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	7.65E-05	0.88	3.92	-	576.3
AHQ-3-1, 2850 - 2914	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.63E-07	0.84	3.55	-	613.6
AHQ-3-5, 2516 - 2580	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.91E-07	0.86	4.03	-	526.4
AHQ-3-8, 2354	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	9.47E-04	0.80	3.11	-	511.2
AHQ-3-8, 2245	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.90E-05	0.88	3.92	-	571.7
AHQ-3-5, 2603	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.70E-06	0.84	3.49	-	510.5
AHQ-3-13-, 2614	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.81E-04	0.76	3.39	-	309.2
AHQ-3-5, 2409 - 2435	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.88E-04	0.82	3.33	-	614.3
AHQ-3-4, 2521 - 2529	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.11E-04	0.95	4.27	-	1189.7
AHQ-3-13-, 2787	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.46E-07	0.72	3.22	-	449.0
AHQ-3-3, 2796	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.91E-05	0.87	3.78	-	662.0
AHQ-3-10, 2582	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	7.11E-05	0.85	3.68	-	458.7
AHQ-3-6, 2603	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.77E-04	0.78	3.72	-	343.2
AHQ-3-4, 2745 - 2752	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.00E-07	0.91	4.14	-	760.8
AHQ-3-1, 3444 - 3445	K.VDINTEDLEDGTCR.V	1638.69283	2	2.23E-09	0.95	4.32	-	1260.8

AHQ-3-2, 3746	K.VDINTEDLEDGTCR.V	1638.69283	2	1.19E-06	0.93	3.96	-	1192.6
AHQ-3-8, 3397	K.VDINTEDLEDGTCR.V	1638.69283	2	7.42E-06	0.71	3.20	-	777.9
AHQ-3-5, 3443 - 3451	K.VDINTEDLEDGTCR.V	1638.69283	2	1.26E-05	0.93	4.27	-	1029.5
AHQ-3-4, 3640 - 3645	K.VDINTEDLEDGTCR.V	1638.69283	2	4.17E-05	0.95	4.29	-	1300.6
AHQ-3-1, 3728	K.VDINTEDLEDGTCR.V	1638.69283	2	5.12E-07	0.91	3.80	-	973.0
AHQ-3-5, 3559	K.VDINTEDLEDGTCR.V	1638.69283	2	5.35E-08	0.94	3.79	-	1165.1
AHQ-3-1, 3832	K.VDINTEDLEDGTCR.V	1638.69283	2	1.65E-07	0.86	3.05	-	846.0
AHQ-3-6, 3485	K.VDINTEDLEDGTCR.V	1638.69283	2	9.37E-06	0.87	3.08	-	1042.0
AHQ-3-6, 3667	K.VDINTEDLEDGTCR.V	1638.69283	2	2.77E-07	0.61	2.61	-	533.5
AHQ-3-3, 3682	K.VDINTEDLEDGTCR.V	1638.69283	2	2.83E-06	0.85	3.03	-	877.0
AHQ-3-7, 3494	K.VDINTEDLEDGTCR.V	1638.69283	2	3.33E-07	0.90	3.46	-	911.4
AHQ-3-1, 3538 - 3549	K.VDINTEDLEDGTCR.V	1638.69283	2	2.42E-05	0.84	3.50	-	824.4
AHQ-3-5, 3748	K.VDINTEDLEDGTCR.V	1638.69283	2	6.41E-08	0.92	3.52	-	1077.6
AHQ-3-2, 2473	K.VDVGKDQEFTVK.S	1365.51377	1	7.65E-06	0.49	3.05	-	297.1
AHQ-3-1, 2644 - 2684	K.VDVGKDQEFTVK.S	1365.51377	2	1.68E-07	0.84	3.46	-	538.1
AHQ-3-1, 2670	K.VDVGKDQEFTVK.S	1365.51377	1	9.00E-04	0.38	2.90	-	335.9
AHQ-3-3, 2384 - 2460	K.VDVGKDQEFTVK.S	1365.51377	2	6.10E-08	0.92	3.63	-	890.5
AHQ-3-2, 2466 - 2489	K.VDVGKDQEFTVK.S	1365.51377	2	6.34E-07	0.90	3.59	-	812.6
AHQ-3-7, 2258	K.VDVGKDQEFTVK.S	1365.51377	2	3.49E-04	0.75	2.97	-	603.6
AHQ-3-6, 2310	K.VDVGKDQEFTVK.S	1365.51377	2	6.21E-08	0.81	3.49	-	478.8
AHQ-3-3, 2458	K.VDVGKDQEFTVK.S	1365.51377	1	4.67E-06	0.59	3.14	-	383.8
AHQ-3-4, 2453	K.VDVGKDQEFTVK.S	1365.51377	1	6.48E-04	0.41	3.00	-	326.0
AHQ-3-1, 2813 - 2884	K.VEPGLGADNSVVR.F	1313.44209	2	8.40E-06	0.82	3.35	-	407.5
AHQ-3-2, 2793 - 2873	K.VEPGLGADNSVVR.F	1313.44209	2	1.43E-05	0.55	2.63	-	297.9
AHQ-3-4, 2626 - 2630	K.VEPGLGADNSVVR.F	1313.44209	2	2.56E-05	0.70	2.78	-	245.5
AHQ-3-3, 2645 - 2681	K.VEPGLGADNSVVR.F	1313.44209	2	1.14E-05	0.72	2.62	-	282.7
AHQ-3-3, 6600 - 6605	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	1.67E-05	0.85	4.31	-	535.2
AHQ-3-3, 6453 - 6532	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	9.02E-07	0.93	5.69	-	602.7
AHQ-3-4, 6556	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.94E-05	0.92	5.19	-	781.9
AHQ-3-6, 6237 - 6313	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	5.50E-04	0.93	5.49	-	589.3
AHQ-3-1, 6540	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	1.51E-06	0.57	3.01	-	438.7
AHQ-3-2, 6573 - 6641	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	8.03E-06	0.95	6.11	-	952.2
AHQ-3-1, 7272	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.49E-06	0.93	4.88	-	632.1
AHQ-3-2, 7583	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	6.01E-07	0.96	5.28	-	1050.1
AHQ-3-3, 7490 - 7502	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	2.72E-06	0.94	4.85	-	758.5
AHQ-3-5, 4211 - 4281	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.04E-05	0.96	5.27	-	1382.4
AHQ-3-4, 4402	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	4.69E-07	0.92	3.97	-	946.2
AHQ-3-9, 3891	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.16E-06	0.95	4.20	-	1360.0
AHQ-3-6, 4137	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.08E-09	0.97	5.47	-	1517.7
AHQ-3-3, 4500 - 4520	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	9.09E-08	0.94	4.00	-	1063.6
AHQ-3-7, 4086 - 4099	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	6.87E-08	0.93	4.18	-	1067.0
AHQ-3-4, 4737 - 4742	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.71E-11	0.95	5.92	-	698.8
AHQ-3-6, 4457	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.19E-11	0.86	3.94	-	517.7
AHQ-3-1, 4917 - 4953	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.62E-08	0.87	4.11	-	640.6
AHQ-3-7, 4303 - 4375	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	4.07E-09	0.81	4.16	-	424.6
AHQ-3-4, 4824	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.91E-08	0.81	3.66	-	497.6
AHQ-3-6, 4465 - 4478	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	3.62E-07	0.53	2.87	-	576.6
AHQ-3-8, 4168	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.43E-06	0.93	5.43	-	515.2
AHQ-3-3, 4852	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	4.24E-13	0.93	4.85	-	715.3
AHQ-3-1, 4920	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	3.24E-07	0.90	4.07	-	1007.6
AHQ-3-7, 4370 - 4371	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.46E-07	0.92	4.47	-	1039.9
AHQ-3-5, 4525	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.32E-09	0.93	4.16	-	1333.5
AHQ-3-5, 4516 - 4589	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.45E-11	0.92	4.81	-	618.1
AHQ-3-6, 3621	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.60E-09	0.81	3.67	-	332.6
AHQ-3-8, 3422	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.54E-07	0.80	3.21	-	371.6
AHQ-3-1, 3878 - 3957	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.41E-10	0.90	3.99	-	654.8
AHQ-3-6, 3477 - 3550	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.51E-07	0.90	3.50	-	719.9
AHQ-3-5, 3635 - 3707	K.VNQPASFAVSLNGAK.G	1503.68480	2	9.49E-06	0.89	3.65	-	614.1
AHQ-3-7, 3446 - 3447	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.72E-07	0.84	3.15	-	612.6
AHQ-3-4, 3688 - 3700	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.87E-07	0.78	3.24	-	632.4
AHQ-3-4, 3793 - 3801	K.VNQPASFAVSLNGAK.G	1503.68480	2	7.29E-06	0.59	2.62	-	436.6
AHQ-3-7, 3546	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.04E-06	0.86	3.62	-	384.9
AHQ-3-5, 3241	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.01E-06	0.68	2.89	-	506.0
AHQ-3-3, 3770 - 3842	K.VNQPASFAVSLNGAK.G	1503.68480	2	6.23E-05	0.85	3.50	-	449.5
AHQ-3-3, 1493	K.VPVHDVTDASK.V	1168.28175	2	3.48E-06	0.94	2.99	-	1580.8
AHQ-3-2, 1457	K.VPVHDVTDASK.V	1168.28175	2	1.52E-06	0.95	3.23	-	1602.8
AHQ-3-3, 1460 - 1464	K.VPVHDVTDASK.V	1168.28175	1	6.39E-04	0.33	2.07	-	469.1
AHQ-3-4, 4248 - 4294	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.57E-04	0.96	4.47	-	1581.8
AHQ-3-2, 4153 - 4234	R.VQVQDNEGCPVEALVK.D	1786.98493	2	2.42E-08	0.95	4.73	-	1042.0
AHQ-3-2, 4310	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.49E-06	0.95	4.51	-	1241.6
AHQ-3-2, 4395	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.08E-04	0.75	3.27	-	671.1
AHQ-3-4, 4120	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.10E-07	0.95	4.70	-	1186.9
AHQ-3-3, 4188 - 4257	R.VQVQDNEGCPVEALVK.D	1786.98493	2	2.07E-06	0.97	5.50	-	1322.7
AHQ-3-1, 4286	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.56E-07	0.94	4.33	-	1102.0
AHQ-3-1, 4398 - 4421	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.71E-11	0.94	4.45	-	977.3
AHQ-3-2, 5446	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.63E-05	0.93	4.83	-	1238.8
AHQ-3-2, 5305 - 5374	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	7.41E-10	0.97	5.48	-	1875.3
AHQ-3-5, 5247	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	8.81E-08	0.89	4.14	-	1154.7
AHQ-3-1, 5269 - 5332	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	4.66E-09	0.94	4.59	-	1761.9
AHQ-3-1, 5400 - 5468	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.20E-05	0.90	4.49	-	818.3
AHQ-3-1, 5621	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	3.18E-04	0.88	3.72	-	1159.9
AHQ-3-3, 5269	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	7.20E-08	0.91	4.14	-	1499.4
AHQ-3-2, 5546 - 5615	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	4.31E-04	0.74	3.53	-	820.2
AHQ-3-13, 4623 - 4629	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	9.12E-07	0.91	4.64	-	827.4
AHQ-3-13, 4622	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	4.08E-06	0.94	4.85	-	675.7
AHQ-3-2, 4834	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	7.63E-04	0.87	3.74	-	841.5
AHQ-3-3, 4797 - 4873	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	3.55E-07	0.95	5.33	-	1006.9
AHQ-3-1, 4964	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	4.99E-06	0.87	4.25	-	529.6
AHQ-3-5, 4423 - 4492	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	5.14E-11	0.96	5.72	-	952.7
AHQ-3-5, 4425 - 4495	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	8.00E-09	0.94	4.64	-	1171.5
AHQ-3-1, 4965 - 5034	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.31E-04	0.96	5.99	-	1126.6
AHQ-3-6, 4403	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	3.81E-07	0.95	4.81	-	1507.7
AHQ-3-8, 3918	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.18E-09	0.94	4.92	-	1034.9
AHQ-3-12, 4626 - 4628	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	5.47E-05	0.93	4.81	-	720.5
AHQ-3-4, 4705 - 4720	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.64E-05	0.96	5.36	-	1133.3
AHQ-3-11, 4375	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.96E-06	0.91	4.16	-	1054.3
AHQ-3-7, 4250	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.91E-10	0.92	4.52	-	886.4
AHQ-3-6, 2479	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.30E-04	0.57	2.74	-	513.0
AHQ-3-6, 2589	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	3.26E-06	0.76	3.60	-	341.9
AHQ-3-5, 2560 - 2631	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	9.58E-05	0.78	3.53	-	448.8
AHQ-3-2, 2753 - 2821	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.31E-06	0.91	4.64	-	478.9
AHQ-3-4, 2718	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.15E-07	0.87	3.94	-	624.0
AHQ-3-2, 2615 - 2685	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.48E-04	0.90	4.30	-	595.8
AHQ-3-3, 2614 - 2661	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.41E-05	0.66	3.13	-	464.4
AHQ-3-3, 2785	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.12E-05	0.90	4.37	-	602.3
AHQ-3-5, 2465 - 2488	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.34E-05	0.79	3.99	-	387.1
AHQ-3-4, 2601	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	5.22E-06	0.72	3.25	-	410.3

AHQ-3-1, 3324 - 3404	K.VTVLFAGQHIAK.S	1284.53185	2	3.01E-06	0.85	3.46	-	786.1
AHQ-3-2, 3095	K.VTVLFAGQHIAK.S	1284.53185	1	9.06E-04	0.39	2.90	-	331.9
AHQ-3-5, 2783 - 2787	K.VTVLFAGQHIAK.S	1284.53185	2	6.78E-06	0.93	3.80	-	876.8
AHQ-3-2, 3014	K.VTVLFAGQHIAK.S	1284.53185	1	1.30E-04	0.35	2.59	-	357.1
AHQ-3-2, 3009 - 3077	K.VTVLFAGQHIAK.S	1284.53185	1	9.76E-04	0.20	1.92	-	486.6
AHQ-3-4, 3001	K.VTVLFAGQHIAK.S	1284.53185	2	5.25E-08	0.88	3.23	-	797.5
AHQ-3-6, 2798 - 2801	K.VTVLFAGQHIAK.S	1284.53185	2	3.77E-05	0.90	4.00	-	646.1
AHQ-3-2, 3010 - 3081	K.VTVLFAGQHIAK.S	1284.53185	2	6.71E-07	0.94	4.27	-	1020.0
AHQ-3-7, 4771 - 4844	R.VTYCPTEPGNYIINIK.F	1884.14221	2	5.58E-05	0.94	4.40	-	584.5
AHQ-3-1, 5396 - 5409	R.VTYCPTEPGNYIINIK.F	1884.14221	2	4.00E-06	0.79	3.18	-	474.8
AHQ-3-8, 4649 - 4699	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.47E-04	0.89	3.90	-	473.4
AHQ-3-3, 5212	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.96E-06	0.85	3.65	-	432.7
AHQ-3-5, 5007 - 5019	R.VTYCPTEPGNYIINIK.F	1884.14221	2	8.57E-06	0.65	3.03	-	292.2
AHQ-3-5, 5167	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.75E-06	0.82	3.25	-	501.9
AHQ-3-4, 5337	R.VTYCPTEPGNYIINIK.F	1884.14221	2	8.11E-06	0.79	3.65	-	352.3
AHQ-3-2, 5238	R.VTYCPTEPGNYIINIK.F	1884.14221	2	7.87E-04	0.77	3.48	-	338.2
AHQ-3-4, 5133	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.55E-04	0.78	3.32	-	351.9
AHQ-3-14-, 5332 - 5335	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.17E-04	0.79	3.12	-	680.0
AHQ-3-14-, 4845 - 4864	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	5.44E-04	0.89	3.98	-	581.5
AHQ-3-10, 4436 - 4439	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	7.66E-06	0.62	2.73	-	397.5
AHQ-3-4, 5592	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	6.80E-04	0.91	3.65	-	920.1
AHQ-3-5, 5407	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.48E-05	0.91	3.78	-	976.5
AHQ-3-5, 5321 - 5399	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	7.33E-04	0.91	3.96	-	788.6
AHQ-3-13-, 5341	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	8.85E-04	0.88	3.23	-	846.1
AHQ-3-6, 4814	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	6.61E-05	0.66	3.10	-	261.9
AHQ-3-3, 5644	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	7.05E-06	0.74	3.02	-	399.8
AHQ-3-6, 5325 - 5349	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.73E-04	0.73	3.15	-	558.9
AHQ-3-5, 4883 - 4927	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	6.06E-05	0.63	2.65	-	408.8
AHQ-3-13, 4894 - 4895	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	6.96E-05	0.53	2.58	-	261.6
AHQ-3-9, 4944 - 4948	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.80E-05	0.59	2.99	-	342.7
AHQ-3-7, 2987 - 2988	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.17E-06	0.90	3.34	-	1146.9
AHQ-3-1, 3534	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.91E-06	0.92	3.24	-	1061.8
AHQ-3-1, 2752	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	6.86E-05	0.74	2.94	-	727.7
AHQ-3-6, 3049	R.YAPSEAGLHEMDIR.Y	1589.75482	2	6.35E-04	0.71	2.70	-	579.1
AHQ-3-10, 3058	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.14E-04	0.90	3.20	-	911.1
AHQ-3-5, 3036 - 3091	R.YAPSEAGLHEMDIR.Y	1589.75482	2	5.36E-04	0.91	3.69	-	959.1
AHQ-3-7, 2362	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	8.05E-05	0.58	2.57	-	542.0
AHQ-3-3, 4349	K.YGGDEIPFSPYR.V	1401.50466	1	3.79E-06	0.42	2.59	-	486.8
AHQ-3-3, 4337 - 4370	K.YGGDEIPFSPYR.V	1401.50466	2	6.98E-05	0.72	3.16	-	466.8
AHQ-3-4, 4265 - 4340	K.YGGDEIPFSPYR.V	1401.50466	2	1.12E-04	0.51	2.61	-	377.5
AHQ-3-2, 4373 - 4441	K.YGGDEIPFSPYR.V	1401.50466	2	7.86E-06	0.81	3.40	-	581.0
AHQ-3-1, 4432 - 4460	K.YGGDEIPFSPYR.V	1401.50466	2	6.83E-06	0.85	3.30	-	734.5
AHQ-3-2, 4377 - 4449	K.YGGDEIPFSPYR.V	1401.50466	1	1.18E-06	0.34	2.34	-	516.5
AHQ-3-12, 4154	K.YGGDEIPFSPYR.V	1401.50466	1	1.10E-04	0.54	2.52	-	610.3
AHQ-3-5, 4124	K.YGGDEIPFSPYR.V	1401.50466	1	1.08E-04	0.24	2.01	-	359.2
AHQ-3-10, 3878 - 3882	K.YGGDEIPFSPYR.V	1401.50466	1	4.20E-04	0.28	2.18	-	377.3
AHQ-3-1, 4449	K.YGGDEIPFSPYR.V	1401.50466	1	1.50E-05	0.24	2.45	-	345.6
AHQ-3-5, 2973 - 2975	K.YGGPYHIGGSPFK.A	1380.53182	2	1.82E-09	0.97	4.41	-	1812.9
AHQ-3-3, 3265 - 3273	K.YGGPYHIGGSPFK.A	1380.53182	2	1.75E-05	0.97	4.86	-	1549.3
AHQ-3-1, 3469	K.YGGPYHIGGSPFK.A	1380.53182	2	4.42E-06	0.96	4.35	-	1699.3
AHQ-3-11, 3062	K.YGGPYHIGGSPFK.A	1380.53182	2	3.83E-09	0.97	4.27	-	1931.3
AHQ-3-7, 2882 - 2922	K.YGGPYHIGGSPFK.A	1380.53182	2	1.20E-05	0.95	3.75	-	1362.3
AHQ-3-4, 3213	K.YGGPYHIGGSPFK.A	1380.53182	1	1.13E-07	0.77	3.33	-	383.5
AHQ-3-5, 2991	K.YGGPYHIGGSPFK.A	1380.53182	3	1.38E-04	0.64	3.08	-	347.1
AHQ-3-2, 3267	K.YGGPYHIGGSPFK.A	1380.53182	2	6.53E-05	0.96	4.23	-	1555.6
AHQ-3-5, 2992	K.YGGPYHIGGSPFK.A	1380.53182	1	1.12E-05	0.82	3.44	-	432.1
AHQ-3-4, 3208 - 3209	K.YGGPYHIGGSPFK.A	1380.53182	2	6.43E-10	0.98	4.91	-	2014.3
AHQ-3-1, 3132 - 3204	K.YGGQPVPNFPSK.L	1291.43658	2	1.67E-06	0.94	4.04	-	731.3
AHQ-3-2, 3069 - 3147	K.YGGQPVPNFPSK.L	1291.43658	1	1.19E-04	0.45	2.71	-	262.4
AHQ-3-1, 3156	K.YGGQPVPNFPSK.L	1291.43658	1	1.49E-06	0.37	2.51	-	233.8
AHQ-3-3, 2990	K.YGGQPVPNFPSK.L	1291.43658	2	3.49E-05	0.86	3.56	-	367.8
AHQ-3-2, 3002 - 3073	K.YGGQPVPNFPSK.L	1291.43658	2	4.41E-07	0.93	3.40	-	698.0
AHQ-3-4, 2957 - 2964	K.YGGQPVPNFPSK.L	1291.43658	2	1.62E-05	0.82	3.25	-	376.6
AHQ-3-2, 3145	K.YGGQPVPNFPSK.L	1291.43658	2	1.05E-04	0.87	3.65	-	434.0
AHQ-3-6, 3850	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	8.52E-04	0.88	3.79	-	1015.6
AHQ-3-5, 3825 - 3900	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	7.33E-06	0.70	3.20	-	658.2
AHQ-3-6, 3851 - 3862	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	2	2.25E-06	0.80	3.74	-	280.8
AHQ-3-7, 3754 - 3787	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	2.68E-05	0.91	4.22	-	922.8
AHQ-3-3, 4317	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.71E-07	0.87	3.78	-	1213.4
AHQ-3-1, 4521 - 4540	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.37E-04	0.79	3.49	-	854.8
AHQ-3-13, 2838	K.YNEQHVPGSPFTAR.V	1603.71978	2	8.75E-05	0.77	2.86	-	402.7
AHQ-3-5, 2843 - 2852	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.35E-07	0.89	3.93	-	435.0
AHQ-3-5, 2535	K.YNEQHVPGSPFTAR.V	1603.71978	3	5.62E-09	0.93	4.51	-	1349.2
AHQ-3-5, 2531	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.16E-06	0.86	3.42	-	488.9
AHQ-3-4, 2678	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.72E-06	0.76	2.79	-	441.2
AHQ-3-2, 2754	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.82E-06	0.81	3.28	-	395.4
AHQ-3-4, 2988 - 2989	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.75E-05	0.78	3.12	-	487.5
AHQ-3-6, 2545	K.YNEQHVPGSPFTAR.V	1603.71978	2	9.84E-05	0.86	3.18	-	500.5
AHQ-3-7, 2483	K.YNEQHVPGSPFTAR.V	1603.71978	2	8.06E-04	0.61	3.21	-	302.5
AHQ-3-10, 2570	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.87E-09	0.88	3.36	-	570.2
AHQ-3-8, 2280	K.YNEQHVPGSPFTAR.V	1603.71978	3	5.41E-06	0.90	3.72	-	1190.2
AHQ-3-9, 2423	K.YNEQHVPGSPFTAR.V	1603.71978	2	5.52E-04	0.42	2.55	-	284.3
AHQ-3-2, 3083	K.YNEQHVPGSPFTAR.V	1603.71978	2	3.95E-04	0.68	2.98	-	363.1
AHQ-3-2, 4542	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.89E-06	0.82	3.44	-	451.2
AHQ-3-2, 4669 - 4715	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.12E-07	0.94	4.47	-	1049.3
AHQ-3-7, 4338	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.04E-06	0.89	3.89	-	619.9
AHQ-3-2, 4785	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	8.49E-08	0.94	4.77	-	835.0
AHQ-3-2, 4869 - 4937	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	7.45E-11	0.94	4.84	-	709.7
AHQ-3-4, 4594 - 4620	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.86E-06	0.93	4.62	-	814.8
AHQ-3-4, 4688 - 4768	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	7.13E-06	0.94	4.30	-	883.7
AHQ-3-5, 4503 - 4523	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.78E-05	0.94	4.60	-	767.2
AHQ-3-3, 4498	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.46E-06	0.88	3.82	-	714.4
AHQ-3-4, 4836	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.33E-04	0.43	2.74	-	330.3
AHQ-3-6, 4409 - 4438	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	8.85E-06	0.89	4.27	-	434.6
AHQ-3-9, 4123	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.69E-07	0.90	4.41	-	461.8
AHQ-3-3, 4768 - 4840	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.46E-07	0.94	4.73	-	668.8
AHQ-3-1, 4848	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.99E-05	0.90	4.21	-	582.1
AHQ-3-3, 4954 - 5034	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	8.25E-05	0.57	2.96	-	361.0
AHQ-3-1, 4681 - 4752	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.70E-07	0.94	4.62	-	699.6
AHQ-3-3, 4629 - 4700	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.02E-06	0.87	3.95	-	574.4
AHQ-3-3, 6892 - 6913	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	6.07E-07	0.64	3.17	-	386.0
AHQ-3-1, 7050 - 7062	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	5.20E-08	0.82	3.06	-	552.8
AHQ-3-1, 6861 - 6929	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	5.42E-08	0.94	4.67	-	778.8
AHQ-3-4, 6576	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.09E-06	0.84	3.18	-	899.5
AHQ-3-2, 7119 - 7198	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	7.54E-10	0.93	4.51	-	856.8
AHQ-3-2, 6967 - 7050	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.06E-06	0.96	5.14	-	938.7
AHQ-3-4, 6914 - 6966	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	6.30E-04	0.86	3.54	-	741.3

AHQ-3-3, 6901	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	8.78E-06	0.60	2.78	-	432.3
AHQ-3-2, 6959 - 7030	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	6.64E-05	0.82	3.50	-	530.3
AHQ-3-2, 6819	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	3.08E-09	0.73	3.36	-	480.3
AHQ-3-2, 6589 - 6605	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	7.20E-08	0.93	4.61	-	1072.8
AHQ-3-3, 6528 - 6566	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	6.38E-08	0.66	2.54	-	607.7
gi|4504745|ref|NP_000410.1| integrin alpha 2b precursor [Homo sapiens]				8.33E-15	30.83	360.38	41.50	113374.2
AHQ-3-4, 5376 - 5452	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.12E-09	0.96	5.06	-	998.3
AHQ-3-13-, 5195	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.12E-04	0.80	3.07	-	696.4
AHQ-3-5, 5200 - 5253	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.98E-06	0.95	4.40	-	980.2
AHQ-3-3, 5464	R.AEGGQCPSLLFDLR.D	1564.74505	2	4.24E-07	0.89	3.43	-	898.0
AHQ-3-1, 5481 - 5550	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.73E-06	0.90	3.45	-	834.6
AHQ-3-10, 4762	R.AEGGQCPSLLFDLR.D	1564.74505	2	9.64E-08	0.92	4.01	-	840.0
AHQ-3-13, 5179 - 5225	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.59E-05	0.94	3.72	-	1006.5
AHQ-3-4, 5589	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.08E-05	0.95	4.27	-	1032.2
AHQ-3-6, 5123 - 5153	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.50E-05	0.83	2.93	-	763.0
AHQ-3-5, 2567	R.ALSNVEGFER.L	1122.21308	2	3.20E-05	0.90	3.13	-	1055.2
AHQ-3-3, 2762	R.ALSNVEGFER.L	1122.21308	2	3.13E-04	0.86	2.96	-	793.0
AHQ-3-4, 2701	R.ALSNVEGFER.L	1122.21308	2	4.82E-06	0.92	3.50	-	1393.2
AHQ-3-4, 2798	R.ALSNVEGFER.L	1122.21308	2	5.68E-05	0.80	2.71	-	817.5
AHQ-3-1, 2965	R.ALSNVEGFER.L	1122.21308	2	7.30E-07	0.82	3.09	-	725.1
AHQ-3-7, 2511	R.ALSNVEGFER.L	1122.21308	2	6.85E-07	0.86	3.17	-	957.3
AHQ-3-6, 2569	R.ALSNVEGFER.L	1122.21308	2	7.26E-06	0.87	3.00	-	1140.7
AHQ-3-4, 5374 - 5453	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.03E-04	0.87	3.95	-	728.8
AHQ-3-4, 5088 - 5164	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	8.57E-06	0.94	4.91	-	938.5
AHQ-3-4, 5526 - 5601	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	7.32E-04	0.82	3.58	-	733.7
AHQ-3-4, 5232 - 5301	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.31E-05	0.90	4.39	-	611.7
AHQ-3-4, 2980	R.DETRNVGSQTLQTFK.A	1724.85363	2	7.44E-05	0.90	3.91	-	1052.8
AHQ-3-4, 3185	R.DETRNVGSQTLQTFK.A	1724.85363	2	1.02E-04	0.56	2.65	-	460.3
AHQ-3-6, 3813 - 3893	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	4.51E-06	0.83	4.01	-	605.7
AHQ-3-4, 4181	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	9.81E-06	0.84	3.65	-	570.3
AHQ-3-5, 3903 - 3911	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	4.52E-11	0.93	4.70	-	733.2
AHQ-3-4, 3976 - 4024	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.27E-04	0.63	3.17	-	689.2
AHQ-3-4, 2829	R.EQNSLDSWGPK.V	1261.32250	1	1.16E-05	0.05	2.04	-	96.1
AHQ-3-4, 4509 - 4536	R.FGSAIAPLGDLDR.D	1332.48700	2	9.86E-05	0.91	3.27	-	1074.9
AHQ-3-5, 4364	R.FGSAIAPLGDLDR.D	1332.48700	2	4.05E-07	0.88	3.07	-	1039.1
AHQ-3-4, 5860 - 5933	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.43E-10	0.92	4.98	-	737.8
AHQ-3-3, 6057 - 6078	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.07E-05	0.76	3.70	-	653.6
AHQ-3-4, 6116 - 6184	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	7.34E-09	0.87	4.14	-	941.1
AHQ-3-5, 5911 - 5975	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.44E-05	0.94	5.23	-	884.4
AHQ-3-6, 5757 - 5825	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.35E-07	0.84	4.20	-	778.1
AHQ-3-6, 5667 - 5741	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.68E-08	0.92	4.91	-	953.8
AHQ-3-4, 5996 - 6046	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	3.85E-09	0.93	5.45	-	811.9
AHQ-3-4, 7016 - 7080	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.58E-09	0.96	5.61	-	653.7
AHQ-3-4, 6590 - 6660	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	8.98E-04	0.96	5.72	-	685.9
AHQ-3-4, 7120 - 7184	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.19E-06	0.96	5.02	-	909.1
AHQ-3-4, 7249 - 7316	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.09E-08	0.97	5.68	-	862.2
AHQ-3-4, 7384 - 7460	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.34E-06	0.93	4.66	-	722.2
AHQ-3-4, 6452 - 6521	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.42E-04	0.67	3.31	-	215.1
AHQ-3-4, 7629 - 7697	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	7.30E-05	0.93	4.88	-	462.3
AHQ-3-4, 7530 - 7558	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.82E-05	0.94	5.29	-	576.8
AHQ-3-4, 6877 - 6952	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.45E-05	0.95	5.11	-	676.2
AHQ-3-11, 4719 - 4727	R.GEAQVWTQLLR.A	1301.47614	2	1.38E-06	0.92	3.86	-	946.0
AHQ-3-1, 5344	R.GEAQVWTQLLR.A	1301.47614	2	2.50E-05	0.86	3.09	-	894.3
AHQ-3-10, 4467	R.GEAQVWTQLLR.A	1301.47614	2	2.92E-06	0.95	4.27	-	1045.5
AHQ-3-12, 5008	R.GEAQVWTQLLR.A	1301.47614	2	7.89E-06	0.92	3.56	-	961.9
AHQ-3-4, 5656 - 5728	R.GNSFPASLVVAAEEGER.E	1733.86053	2	3.03E-09	0.93	4.35	-	924.8
AHQ-3-4, 5792 - 5868	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.69E-07	0.88	3.86	-	702.8
AHQ-3-4, 5508 - 5577	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.71E-06	0.91	3.69	-	900.5
AHQ-3-4, 5420 - 5488	R.GNSFPASLVVAAEEGER.E	1733.86053	2	6.57E-08	0.90	4.35	-	629.6
AHQ-3-4, 5944	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.03E-08	0.89	3.91	-	791.9
AHQ-3-4, 5313 - 5349	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.63E-07	0.88	4.08	-	699.0
AHQ-3-3, 5857	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.00E-05	0.83	3.52	-	627.5
AHQ-3-4, 6852 - 6894	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	6.68E-08	0.50	3.12	-	351.3
AHQ-3-4, 6665 - 6692	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	5.88E-11	0.88	4.42	-	521.4
AHQ-3-4, 6761 - 6762	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	1.26E-08	0.83	3.74	-	600.4
AHQ-3-4, 5240	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	7.11E-05	0.92	3.98	-	1334.0
AHQ-3-3, 5329 - 5378	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	8.80E-04	0.71	3.19	-	655.4
AHQ-3-2, 5371	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.58E-04	0.84	4.04	-	390.5
AHQ-3-7, 4742	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	8.74E-07	0.95	5.18	-	739.0
AHQ-3-4, 5152 - 5233	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	7.07E-06	0.82	3.52	-	843.6
AHQ-3-4, 5142 - 5212	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	6.39E-06	0.97	5.82	-	1150.7
AHQ-3-4, 5442	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.99E-07	0.81	3.53	-	545.8
AHQ-3-7, 4740	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	9.47E-06	0.77	3.03	-	1007.5
AHQ-3-5, 5008 - 5020	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	1.02E-04	0.93	4.15	-	1202.2
AHQ-3-4, 5038	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.87E-08	0.92	4.15	-	731.1
AHQ-3-3, 5242 - 5322	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	9.90E-06	0.93	5.04	-	450.1
AHQ-3-5, 5001	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.13E-05	0.96	5.10	-	876.6
AHQ-3-1, 5504	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	3.49E-04	0.81	3.58	-	838.9
AHQ-3-6, 4947	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	3.20E-04	0.90	4.05	-	1240.9
AHQ-3-6, 4941 - 4949	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.81E-07	0.97	5.92	-	969.8
AHQ-3-1, 5493	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	7.36E-04	0.79	3.62	-	391.3
AHQ-3-4, 5228 - 5298	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	9.50E-10	0.98	6.05	-	1456.0
AHQ-3-3, 5332 - 5346	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	6.68E-06	0.97	5.23	-	1141.3
AHQ-3-4, 5269 - 5312	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.11E-04	0.88	3.25	-	1125.9
AHQ-3-4, 5504 - 5538	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.59E-04	0.86	3.43	-	702.3
AHQ-3-4, 5188	R.GQVLVFLGQSEGLR.S	1503.72793	2	4.08E-08	0.96	4.82	-	1362.0
AHQ-3-5, 4176	R.HDLLVGAPLYMESR.A	1601.85188	2	5.90E-08	0.97	4.45	-	1664.0
AHQ-3-4, 4353 - 4429	R.HDLLVGAPLYMESR.A	1601.85188	2	2.15E-07	0.95	4.21	-	1258.5
AHQ-3-5, 3332	K.HSPICHTTMAFLR.D	1572.83705	2	5.73E-05	0.73	2.76	-	496.2
AHQ-3-6, 4129	K.IVLLDVPVR.A	1024.28196	2	4.54E-05	0.90	3.69	-	932.4
AHQ-3-4, 4362 - 4437	K.IVLLDVPVR.A	1024.28196	2	1.08E-04	0.91	3.58	-	927.9
AHQ-3-1, 4685	K.IVLLDVPVR.A	1024.28196	2	2.54E-04	0.92	3.77	-	930.3
AHQ-3-12, 4324	K.IVLLDVPVR.A	1024.28196	2	1.87E-05	0.90	3.50	-	823.0
AHQ-3-4, 4520	R.IYVENDFSWDK.R	1416.51610	1	5.96E-06	0.34	2.09	-	496.0
AHQ-3-4, 4060	R.IYVENDFSWDKR.Y	1572.70245	2	7.73E-07	0.94	3.70	-	1167.4
AHQ-3-4, 4226 - 4270	R.IYVENDFSWDKR.Y	1572.70245	2	1.92E-06	0.83	2.95	-	921.2
AHQ-3-10, 6334	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	1.87E-04	0.86	3.96	-	389.6
AHQ-3-10, 6171 - 6250	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	2.57E-08	0.94	5.06	-	369.6
AHQ-3-4, 4926	K.LSLNAELQLDR.Q	1272.43310	1	1.50E-04	0.10	2.05	-	300.2
AHQ-3-4, 4605	K.LSLNAELQLDR.Q	1272.43310	2	3.81E-07	0.80	3.21	-	696.4
AHQ-3-10, 2036 - 2095	R.NRPPLEEDDEEGE	1529.50164	2	1.65E-04	0.73	2.55	-	939.6
AHQ-3-11, 2059 - 2132	R.NRPPLEEDDEEGE	1529.50164	2	2.11E-08	0.85	3.04	-	862.8
AHQ-3-7, 2492	R.NVGSQTLQTFK.A	1223.36055	2	6.46E-07	0.92	3.48	-	798.0
AHQ-3-4, 3217	R.NVGSQTLQTFK.A	1223.36055	1	3.31E-07	0.27	2.20	-	283.5
AHQ-3-12, 2776	R.NVGSQTLQTFK.A	1223.36055	2	2.08E-04	0.78	2.97	-	440.0
AHQ-3-4, 2681 - 2761	R.NVGSQTLQTFK.A	1223.36055	2	8.70E-04	0.87	3.44	-	670.5
AHQ-3-4, 7546	R.QGLGASVVSWSDVIVACAPWQHWNVLEK.T	3139.53208	3	3.67E-07	0.91	4.90	-	649.6

AHQ-3-3, 6277	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	6.86E-05	0.96	5.46	-	1439.4
AHQ-3-5, 5980 - 5981	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.74E-11	0.98	7.42	-	1502.3
AHQ-3-6, 5921 - 5993	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	8.33E-15	0.96	5.96	-	1249.0
AHQ-3-4, 6129 - 6276	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	7.35E-11	0.98	7.53	-	1615.1
AHQ-3-4, 6212 - 6284	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	7.32E-09	0.97	6.12	-	704.8
AHQ-3-1, 6321 - 6340	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.02E-11	0.97	5.91	-	1641.7
AHQ-3-4, 5856	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.72E-04	0.96	5.90	-	1614.4
AHQ-3-4, 6346	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.61E-06	0.93	4.55	-	1378.8
AHQ-3-14-, 5844	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.90E-07	0.91	4.43	-	1273.9
AHQ-3-4, 3830	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	3.55E-09	0.80	3.72	-	380.2
AHQ-3-6, 3458	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.55E-04	0.93	4.26	-	819.5
AHQ-3-4, 3621 - 3692	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.21E-06	0.95	4.73	-	694.0
AHQ-3-11, 3478 - 3482	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.47E-06	0.92	4.62	-	468.0
AHQ-3-5, 3511 - 3513	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	6.13E-05	0.96	5.06	-	857.5
AHQ-3-3, 3744 - 3749	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	3.09E-07	0.91	4.03	-	638.4
AHQ-3-12, 5494	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.12E-07	0.94	4.26	-	1105.0
AHQ-3-6, 5517 - 5541	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.44E-09	0.95	4.37	-	1053.2
AHQ-3-4, 5666 - 5736	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.03E-08	0.88	4.03	-	521.6
AHQ-3-11, 5274	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.22E-08	0.84	3.55	-	683.4
AHQ-3-3, 5790 - 5848	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.26E-06	0.94	4.49	-	977.1
AHQ-3-4, 5776 - 5848	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.64E-08	0.91	4.14	-	823.9
AHQ-3-2, 5851 - 5922	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.09E-06	0.79	3.39	-	805.0
AHQ-3-4, 5804	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.46E-05	0.94	4.97	-	787.3
AHQ-3-5, 5591 - 5607	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.70E-05	0.97	5.57	-	1102.1
AHQ-3-10, 5030 - 5032	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.77E-05	0.97	5.57	-	1049.8
AHQ-3-13, 5493 - 5566	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	7.91E-06	0.84	3.89	-	617.8
AHQ-3-7, 5435 - 5439	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.99E-07	0.97	5.31	-	1144.8
AHQ-3-9, 5168	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.49E-08	0.96	4.82	-	1208.4
AHQ-3-13-, 5470 - 5471	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.02E-05	0.97	5.25	-	1274.5
AHQ-3-1, 3933	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.49E-06	0.76	3.53	-	577.5
AHQ-3-10, 3424	K.TPVGSCFLAQPESGR.R	1607.76993	2	8.91E-05	0.94	3.85	-	1044.3
AHQ-3-4, 3742 - 3748	K.TPVGSCFLAQPESGR.R	1607.76993	2	9.50E-08	0.97	4.95	-	1318.7
AHQ-3-4, 3922	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.10E-08	0.93	4.17	-	883.1
AHQ-3-11, 3527	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.16E-08	0.89	3.81	-	686.2
AHQ-3-3, 3806	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.15E-04	0.92	3.82	-	985.4
AHQ-3-5, 3612	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.91E-07	0.95	4.16	-	1036.2
AHQ-3-7, 3516 - 3518	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.54E-05	0.93	3.95	-	857.2
AHQ-3-4, 5200 - 5268	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.23E-09	0.96	5.39	-	1254.8
AHQ-3-4, 4689	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	1.75E-06	0.89	3.85	-	978.5
AHQ-3-4, 4569	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	5.61E-14	0.94	5.02	-	1040.9
AHQ-3-4, 6312	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	5.60E-04	0.90	4.07	-	872.3
AHQ-3-4, 5336 - 5409	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	7.36E-04	0.71	3.52	-	757.8
AHQ-3-4, 5509	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	5.23E-04	0.96	4.89	-	1581.7
AHQ-3-3, 2513	R.VAIVVGAPR.T	882.08560	2	2.52E-06	0.93	3.49	-	1128.1
AHQ-3-5, 2349	R.VAIVVGAPR.T	882.08560	2	3.70E-05	0.95	3.70	-	1382.7
AHQ-3-4, 2476 - 2480	R.VAIVVGAPR.T	882.08560	2	1.98E-05	0.94	3.58	-	1418.9
AHQ-3-13-, 2607	R.VAIVVGAPR.T	882.08560	2	5.75E-05	0.92	3.24	-	1176.7
AHQ-3-4, 6100 - 6172	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	6.74E-06	0.98	6.59	-	1783.6
AHQ-3-4, 7256 - 7321	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	3.15E-07	0.98	6.10	-	1881.6
AHQ-3-4, 6101	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.80E-07	0.92	3.89	-	1350.4
AHQ-3-4, 6240 - 6321	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.70E-08	0.98	5.81	-	1890.5
AHQ-3-4, 7126 - 7192	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.97E-09	0.97	5.75	-	1587.8
AHQ-3-4, 6996 - 7060	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.01E-08	0.98	6.20	-	1974.2
AHQ-3-5, 6229 - 6249	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	6.77E-04	0.95	4.44	-	1222.0
AHQ-3-4, 5953 - 6030	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	9.74E-07	0.96	5.05	-	1202.8
AHQ-3-4, 6368 - 6437	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.07E-12	0.98	6.19	-	1801.7
AHQ-3-4, 7645 - 7714	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	3.84E-07	0.98	6.56	-	1732.4
AHQ-3-4, 6733 - 6788	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.52E-11	0.97	5.40	-	1266.2
AHQ-3-4, 6856 - 6930	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	9.58E-10	0.97	5.78	-	1376.5
AHQ-3-4, 6596 - 6664	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.11E-05	0.96	5.53	-	1204.2
AHQ-3-5, 3993 - 4008	R.VVLCELGNPMK.K	1261.53692	2	1.05E-04	0.94	3.84	-	1266.3
AHQ-3-4, 3305	R.VVLCELGNPM*K.K	1277.53632	2	6.51E-06	0.91	3.58	-	1076.0
AHQ-3-6, 3921	R.VVLCELGNPMK.K	1261.53692	2	9.41E-05	0.94	3.63	-	1299.8
AHQ-3-4, 4140 - 4144	R.VVLCELGNPMK.K	1261.53692	2	8.38E-08	0.95	4.04	-	1195.4
AHQ-3-5, 3164	R.VVLCELGNPM*K.K	1277.53632	2	5.84E-05	0.82	2.62	-	922.3
AHQ-3-4, 3530	R.VVLCELGNPMKK.N	1389.70984	2	7.89E-06	0.85	3.01	-	941.8
AHQ-3-6, 3894	R.VYLFLQPR.G	1036.25129	2	6.82E-06	0.92	3.39	-	1212.5
AHQ-3-5, 3931 - 3940	R.VYLFLQPR.G	1036.25129	2	3.09E-05	0.94	3.85	-	1251.3
AHQ-3-4, 4128	R.VYLFLQPR.G	1036.25129	2	5.09E-06	0.95	3.81	-	1110.9
gi|7669492|ref|NP_002037.2|	glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]			9.99E-15	8.74	110.41	40.00	36053.0
AHQ-3-10, 3346	R.GALQNIIPASTGAAK.A	1412.61680	1	1.02E-07	0.87	4.09	-	467.4
AHQ-3-9, 3091 - 3235	R.GALQNIIPASTGAAK.A	1412.61680	1	2.31E-04	0.53	3.01	-	360.3
AHQ-3-9, 3109 - 3175	R.GALQNIIPASTGAAK.A	1412.61680	1	1.07E-06	0.84	3.84	-	558.3
AHQ-3-11, 3486	R.GALQNIIPASTGAAK.A	1412.61680	2	5.32E-04	0.57	3.70	-	290.0
AHQ-3-11, 3459	R.GALQNIIPASTGAAK.A	1412.61680	1	3.17E-08	0.66	3.40	-	352.6
AHQ-3-9, 3491	R.GALQNIIPASTGAAK.A	1412.61680	1	2.13E-04	0.17	2.15	-	168.7
AHQ-3-9, 6635 - 6703	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	3.73E-04	0.90	4.37	-	1156.5
AHQ-3-9, 6852 - 6901	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	2.45E-06	0.68	3.14	-	642.1
AHQ-3-9, 3625	K.RVIISAPSADAPMFVM*GVNHEK.Y	2386.77962	3	1.12E-04	0.92	4.61	-	1148.0
AHQ-3-9, 6856 - 6932	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	1.32E-07	0.98	6.86	-	2902.3
AHQ-3-10, 6466	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	3.31E-07	0.95	5.10	-	925.2
AHQ-3-9, 6855 - 6928	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	9.99E-15	0.97	8.15	-	2225.4
AHQ-3-9, 6192 - 6272	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	3.70E-05	0.95	4.92	-	1119.2
AHQ-3-9, 6047 - 6112	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	2	7.80E-06	0.96	6.42	-	1472.5
AHQ-3-9, 6040 - 6119	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	4.66E-14	0.98	6.00	-	1875.4
AHQ-3-10, 6396 - 6467	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	2.38E-08	0.97	6.16	-	2039.4
AHQ-3-10, 4720 - 4727	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	2.10E-12	0.88	3.77	-	555.7
AHQ-3-9, 4279	R.VIISAPSADAPM*FVMGVNHEK.Y	2230.59327	2	1.43E-08	0.69	3.42	-	551.2
AHQ-3-9, 4749 - 4824	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	3.15E-13	0.85	3.63	-	517.4
AHQ-3-9, 4184	R.VIISAPSADAPMFVM*GVNHEK.Y	2230.59327	2	2.28E-06	0.37	3.10	-	405.5
AHQ-3-13, 4106	R.VPTANVSVVDLTCR.L	1532.74450	2	3.63E-08	0.95	4.30	-	1170.4
AHQ-3-12, 4107	R.VPTANVSVVDLTCR.L	1532.74450	2	1.39E-09	0.94	4.12	-	1084.8
AHQ-3-11, 3930 - 3996	R.VPTANVSVVDLTCR.L	1532.74450	2	1.40E-08	0.94	4.00	-	1068.8
AHQ-3-9, 4181 - 4185	R.VPTANVSVVDLTCR.L	1532.74450	2	2.84E-07	0.89	3.43	-	872.4
AHQ-3-14-, 4005	R.VPTANVSVVDLTCR.L	1532.74450	2	1.99E-07	0.96	4.61	-	1254.7
AHQ-3-14, 4921 - 4972	R.VPTANVSVVDLTCR.L	1532.74450	2	2.10E-04	0.68	2.86	-	591.3
AHQ-3-9, 3961 - 3988	R.VPTANVSVVDLTCR.L	1532.74450	2	2.19E-10	0.92	3.94	-	845.3
AHQ-3-9, 3901	R.VPTANVSVVDLTCR.L	1532.74450	2	9.82E-05	0.84	3.19	-	749.8
AHQ-3-11, 3748	R.VPTANVSVVDLTCR.L	1532.74450	2	1.08E-06	0.80	2.89	-	780.1
AHQ-3-9, 3725 - 3831	R.VPTANVSVVDLTCR.L	1532.74450	2	1.68E-08	0.94	3.88	-	1027.3
AHQ-3-9, 3575	R.VPTANVSVVDLTCR.L	1532.74450	2	6.57E-07	0.95	4.09	-	1158.5
AHQ-3-6, 4019	R.VPTANVSVVDLTCR.L	1532.74450	2	1.78E-05	0.78	2.58	-	684.9
AHQ-3-10, 3818 - 3886	R.VPTANVSVVDLTCR.L	1532.74450	2	2.31E-08	0.67	2.98	-	475.0
AHQ-3-13-, 4111 - 4114	R.VPTANVSVVDLTCR.L	1532.74450	2	5.50E-08	0.96	4.89	-	1057.1
AHQ-3-9, 4061	R.VPTANVSVVDLTCR.L	1532.74450	2	1.23E-08	0.93	4.14	-	1028.5
AHQ-3-1, 4404	R.VPTANVSVVDLTCR.L	1532.74450	2	3.40E-04	0.71	2.91	-	694.7
AHQ-3-9, 7204	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.49E-06	0.94	4.88	-	794.3

AHQ-3-9, 7067 - 7139	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	9.14E-09	0.95	4.75	-	990.8
AHQ-3-9, 6917 - 6999	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.00E-09	0.94	4.05	-	1159.6
AHQ-3-9, 6516 - 6584	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.66E-08	0.90	3.88	-	697.1
AHQ-3-9, 6348 - 6425	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.58E-05	0.88	3.73	-	855.0
AHQ-3-9, 6200	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	9.43E-07	0.75	3.20	-	545.3
AHQ-3-13, 6214 - 6290	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.91E-07	0.94	4.32	-	847.6
AHQ-3-9, 6175 - 6240	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	3.56E-05	0.89	3.89	-	719.0
AHQ-3-9, 6045 - 6115	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	4.79E-05	0.85	3.78	-	503.2
AHQ-3-13-, 6061 - 6138	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.50E-05	0.95	4.72	-	988.3
AHQ-3-13-, 6211 - 6281	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	3.92E-09	0.96	5.07	-	946.3
AHQ-3-9, 6665 - 6727	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	5.44E-06	0.86	4.15	-	416.2
gi|4505257|ref|NP_002435.1| moesin [Homo sapiens]				1.17E-14	10.28	110.32	23.70	67819.5
AHQ-3-6, 2298 - 2303	K.ALTSELANAR.D	1046.15975	2	9.89E-06	0.92	3.66	-	813.4
AHQ-3-6, 7257 - 7258	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	3	2.10E-08	0.94	5.13	-	1236.7
AHQ-3-6, 7254	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	2	6.12E-05	0.74	3.52	-	258.9
AHQ-3-6, 6279	R.EVWFFGLQYQDTK.G	1661.83760	2	1.60E-06	0.92	3.48	-	1025.5
AHQ-3-10, 6460	K.FYPEDVSEELIQDITQR.L	2083.24065	2	2.25E-08	0.95	4.44	-	1009.4
AHQ-3-6, 7191	K.FYPEDVSEELIQDITQR.L	2083.24065	3	5.51E-11	0.96	5.20	-	1172.4
AHQ-3-6, 7173	K.FYPEDVSEELIQDITQR.L	2083.24065	2	1.70E-08	0.96	4.87	-	1124.2
AHQ-3-14-, 6716	K.FYPEDVSEELIQDITQR.L	2083.24065	2	2.38E-07	0.96	4.76	-	1089.1
AHQ-3-9, 6876 - 6880	K.FYPEDVSEELIQDITQR.L	2083.24065	2	6.20E-06	0.90	3.98	-	806.8
AHQ-3-6, 5521	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	3.05E-05	0.88	3.16	-	1028.5
AHQ-3-6, 2009	R.ISQLEMAR.Q	948.12272	2	1.70E-04	0.91	2.68	-	1415.0
AHQ-3-6, 3362	K.KTQEQLALEM*AELTAR.I	1849.09958	2	3.44E-05	0.95	4.16	-	974.7
AHQ-3-6, 4505	K.KTQEQLALEMAELTAR.I	1833.10018	2	2.00E-04	0.98	4.84	-	2327.0
AHQ-3-6, 3269 - 3319	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	2.46E-10	0.88	4.45	-	737.9
AHQ-3-6, 3107	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	1.17E-14	0.98	6.32	-	2285.9
AHQ-3-6, 3389 - 3418	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	3.52E-10	0.95	5.10	-	1601.2
AHQ-3-6, 5217	K.TQEQLALEMAELTAR.I	1704.92727	2	2.01E-09	0.98	5.37	-	2211.4
gi|4757826|ref|NP_004039.1| beta-2-microglobulin [Homo sapiens]				1.17E-14	3.33	40.25	38.70	13714.5
AHQ-3-14-, 6569 - 6636	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	3	6.53E-08	0.90	5.07	-	481.9
AHQ-3-14-, 6429	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	2	1.84E-07	0.88	4.16	-	487.3
AHQ-3-14-, 6171	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	4.91E-07	0.53	3.11	-	431.9
AHQ-3-14-, 6329 - 6403	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	1.17E-14	0.88	4.26	-	793.6
AHQ-3-14-, 6593	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	3.64E-10	0.81	3.74	-	779.7
AHQ-3-14-, 2069	K.VEHSDLSFSK.D	1149.23530	1	1.08E-04	0.79	3.37	-	492.6
AHQ-3-14-, 2019 - 2075	K.VEHSDLSFSK.D	1149.23530	1	1.57E-06	0.79	3.10	-	533.2
AHQ-3-14-, 2071	K.VEHSDLSFSK.D	1149.23530	2	7.08E-06	0.80	3.01	-	679.4
AHQ-3-14-, 1835 - 1909	R.VNHVTLSQPK.I	1123.28735	1	2.79E-06	0.76	2.83	-	379.4
gi|6598323|ref|NP_001485.2| GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom				1.22E-14	5.69	60.34	25.20	50662.9
AHQ-3-7, 7252	K.KFDLGQDVIDFTGHALALYR.T	2280.56709	3	1.22E-14	0.99	6.85	-	2931.2
AHQ-3-7, 7180 - 7250	K.KFDLGQDVIDFTGHALALYR.T	2280.56709	2	2.23E-07	0.97	5.20	-	1536.8
AHQ-3-7, 5628	R.KSDIYVCMISFAHNVAAQGK.Y	2241.57596	2	2.03E-05	0.88	3.38	-	929.9
AHQ-3-7, 5255	R.NPYYGGESASITPLEDLYK.R	2118.28499	2	1.51E-09	0.96	4.96	-	1254.6
AHQ-3-6, 6838 - 6909	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	6.54E-07	0.97	5.74	-	1125.1
AHQ-3-7, 6826	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	5.50E-08	0.96	4.91	-	946.9
AHQ-3-9, 6531	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.72E-04	0.95	4.55	-	887.0
AHQ-3-10, 6214	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	5.15E-06	0.97	5.48	-	1262.7
AHQ-3-7, 4030	R.TDDYLDQPCYETINR.I	1904.98887	2	2.18E-07	0.92	4.23	-	547.0
AHQ-3-7, 7419	K.VPSTEAEALASSLMGLFEK.R	1981.25641	2	5.29E-09	0.98	6.50	-	1752.2
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				1.33E-14	25.82	300.35	59.90	75429.7
AHQ-3-6, 2949 - 2950	K.AGDALWLR.F	902.03223	2	4.69E-04	0.93	3.97	-	1448.6
AHQ-3-12, 6499	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	2.29E-05	0.89	3.70	-	877.8
AHQ-3-14-, 6425	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	2.33E-12	0.96	4.68	-	1451.9
AHQ-3-13, 6537	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	5.97E-07	0.91	3.98	-	1057.6
AHQ-3-6, 6679 - 6755	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	2.44E-08	0.95	4.44	-	1449.5
AHQ-3-13, 6614	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.40E-05	0.92	4.07	-	739.2
AHQ-3-6, 6722	R.ASFSQPLFQAVAAICR.L	1768.02967	3	7.33E-04	0.93	4.38	-	1130.7
AHQ-3-6, 6677 - 6753	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.69E-08	0.96	5.07	-	886.4
AHQ-3-6, 6811 - 6817	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.28E-10	0.96	4.81	-	915.5
AHQ-3-6, 6990 - 7019	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.00E-08	0.94	4.40	-	844.1
AHQ-3-12, 6583	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.47E-06	0.89	3.61	-	693.3
AHQ-3-2, 7139	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.20E-07	0.92	4.22	-	700.5
AHQ-3-4, 7057	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.89E-08	0.92	3.98	-	751.3
AHQ-3-5, 6907	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.77E-05	0.91	3.81	-	771.4
AHQ-3-1, 7008	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.19E-08	0.94	4.11	-	860.0
AHQ-3-11, 6314 - 6395	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.15E-06	0.90	3.86	-	692.3
AHQ-3-3, 7038	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.53E-06	0.93	4.27	-	789.9
AHQ-3-9, 6459	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.44E-06	0.92	3.62	-	900.5
AHQ-3-7, 6672	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.72E-05	0.91	3.59	-	993.2
AHQ-3-10, 6103 - 6115	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.58E-06	0.94	4.65	-	789.1
AHQ-3-9, 6317 - 6397	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.89E-05	0.90	3.52	-	810.6
AHQ-3-11, 3380	K.EKEPEEELYDLSK.V	1609.71294	2	4.22E-08	0.79	3.15	-	406.6
AHQ-3-6, 3347 - 3421	K.EKEPEEELYDLSK.V	1609.71294	2	1.33E-10	0.92	3.99	-	595.1
AHQ-3-9, 3124	K.EKEPEEELYDLSK.V	1609.71294	2	3.53E-05	0.91	4.07	-	639.6
AHQ-3-9, 6853 - 6927	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	7.03E-06	0.89	4.79	-	400.4
AHQ-3-13-, 6717 - 6719	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	1.68E-06	0.96	6.01	-	587.8
AHQ-3-11, 6548	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	5.76E-06	0.84	4.35	-	275.1
AHQ-3-13, 6769 - 6771	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	5.12E-06	0.96	5.69	-	572.7
AHQ-3-6, 7238	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	1.96E-04	0.94	4.96	-	698.6
AHQ-3-14-, 6651	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	4.40E-05	0.92	4.69	-	552.2
AHQ-3-6, 7038 - 7103	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	1.77E-04	0.94	5.07	-	542.7
AHQ-3-1, 7165	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	8.18E-04	0.64	3.27	-	245.7
AHQ-3-12, 6766	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	2.71E-04	0.86	4.13	-	372.8
AHQ-3-6, 2999 - 3071	K.GCEVVPDVNVSGQK.F	1489.63335	2	6.47E-05	0.80	2.71	-	826.7
AHQ-3-7, 3044	K.GCEVVPDVNVSGQK.F	1489.63335	2	5.19E-04	0.78	2.69	-	694.5
AHQ-3-11, 3110	K.GCEVVPDVNVSGQK.F	1489.63335	1	5.82E-04	0.62	2.11	-	896.7
AHQ-3-6, 3078	K.GCEVVPDVNVSGQK.F	1489.63335	1	7.22E-09	0.92	3.80	-	1073.7
AHQ-3-13, 6831 - 6834	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	4.65E-07	0.91	4.34	-	862.8
AHQ-3-13-, 6767	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	6.52E-04	0.75	3.19	-	683.9
AHQ-3-6, 7147 - 7177	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	3.13E-08	0.97	5.03	-	1371.2
AHQ-3-14-, 6704 - 6707	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	4.97E-07	0.96	5.20	-	1246.5
AHQ-3-12, 6862	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	9.08E-04	0.83	3.51	-	757.7
AHQ-3-6, 2835	R.GM*PAHFSDSAQTEACYHM*LSR.P	2430.63997	3	1.59E-05	0.94	4.45	-	1502.8
AHQ-3-11, 3650	R.IDLAVGDVVK.T	1029.21223	1	4.24E-04	0.11	2.02	-	347.5
AHQ-3-10, 3546	R.IDLAVGDVVK.T	1029.21223	1	7.97E-04	0.23	1.97	-	419.6
AHQ-3-13, 3853	R.IDLAVGDVVK.T	1029.21223	1	3.02E-04	0.66	2.31	-	648.8
AHQ-3-13, 3858	R.IDLAVGDVVK.T	1029.21223	1	5.21E-04	0.62	3.03	-	398.7
AHQ-3-9, 3448	R.IDLAVGDVVK.T	1029.21223	1	3.28E-04	0.16	2.39	-	234.0
AHQ-3-1, 4096	R.IDLAVGDVVK.T	1029.21223	1	6.53E-04	0.20	1.99	-	594.2
AHQ-3-1, 4769	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	9.15E-12	0.97	5.78	-	1500.6
AHQ-3-5, 4384 - 4455	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.87E-07	0.98	6.97	-	1715.7
AHQ-3-4, 4581	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.37E-07	0.98	6.09	-	2621.6
AHQ-3-6, 4265 - 4334	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	3.77E-12	0.98	6.46	-	1824.4
AHQ-3-14, 5565	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.05E-11	0.98	5.93	-	1862.2
AHQ-3-6, 4446	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.65E-10	0.98	6.60	-	2355.4
AHQ-3-9, 3945 - 4016	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.86E-06	0.97	6.01	-	1520.9

AHQ-3-6, 4547	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	8.06E-11	0.98	6.62	-	2422.9
AHQ-3-11, 4210	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	8.05E-07	0.98	5.72	-	1612.2
AHQ-3-13, 4386	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	4.34E-06	0.97	5.49	-	1432.5
AHQ-3-3, 4677	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.33E-14	0.98	6.05	-	1524.3
AHQ-3-12, 4418	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	4.46E-05	0.77	3.62	-	941.1
AHQ-3-12, 4411 - 4479	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.35E-05	0.96	5.10	-	1240.7
AHQ-3-12, 2550	R.KDEILGIANNR.L	1243.39499	2	9.19E-05	0.88	3.44	-	906.9
AHQ-3-6, 2555 - 2561	R.KDEILGIANNR.L	1243.39499	1	1.09E-08	0.44	2.11	-	416.6
AHQ-3-13, 2674 - 2733	R.KDEILGIANNR.L	1243.39499	2	5.30E-05	0.95	3.99	-	1450.1
AHQ-3-13, 2679	R.KDEILGIANNR.L	1243.39499	1	3.64E-05	0.62	2.56	-	349.2
AHQ-3-9, 2267	R.KDEILGIANNR.L	1243.39499	2	2.75E-06	0.93	3.95	-	1049.9
AHQ-3-6, 2326 - 2403	R.KDEILGIANNR.L	1243.39499	1	1.48E-06	0.50	2.27	-	312.4
AHQ-3-10, 2420	R.KDEILGIANNR.L	1243.39499	2	1.87E-04	0.88	3.32	-	937.0
AHQ-3-13-, 2645 - 2710	R.KDEILGIANNR.L	1243.39499	2	5.55E-05	0.94	3.90	-	1270.5
AHQ-3-13-, 2822	R.KDEILGIANNR.L	1243.39499	2	3.54E-04	0.67	2.72	-	1003.9
AHQ-3-6, 2325 - 2329	R.KDEILGIANNR.L	1243.39499	2	7.10E-06	0.93	3.61	-	1234.4
AHQ-3-6, 3702	R.KQDWSDHAIWWEQK.R	1858.00504	3	2.06E-06	0.92	4.33	-	1180.7
AHQ-3-6, 3622 - 3701	R.KQDWSDHAIWWEQK.R	1858.00504	2	6.39E-05	0.88	3.73	-	867.6
AHQ-3-7, 3662	R.KQDWSDHAIWWEQK.R	1858.00504	2	8.57E-07	0.95	4.48	-	1087.7
AHQ-3-6, 3715 - 3795	R.KQDWSDHAIWWEQK.R	1858.00504	2	8.99E-05	0.78	3.12	-	908.5
AHQ-3-9, 3453	R.KQDWSDHAIWWEQK.R	1858.00504	2	4.59E-05	0.95	4.44	-	1313.3
AHQ-3-6, 6597	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.64E-05	0.85	3.76	-	597.3
AHQ-3-6, 5625	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	4.91E-06	0.90	4.38	-	526.2
AHQ-3-6, 6294 - 6311	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.39E-09	0.95	4.71	-	939.8
AHQ-3-14-, 6452	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.51E-06	0.71	3.49	-	476.1
AHQ-3-13, 6570 - 6634	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	9.12E-04	0.63	2.93	-	405.9
AHQ-3-6, 6431 - 6501	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.65E-05	0.89	3.70	-	712.1
AHQ-3-4, 7044	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.10E-04	0.88	4.34	-	583.0
AHQ-3-5, 6915	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.82E-04	0.43	2.73	-	282.0
AHQ-3-9, 6419	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.48E-04	0.91	3.95	-	848.8
AHQ-3-3, 6982 - 7048	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.26E-04	0.85	3.90	-	427.4
AHQ-3-6, 6709 - 6789	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.32E-06	0.95	4.88	-	934.2
AHQ-3-8, 6511	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.87E-07	0.68	3.05	-	443.0
AHQ-3-7, 6695 - 6702	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.90E-06	0.93	5.05	-	601.5
AHQ-3-6, 6377	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	1.67E-07	0.71	3.19	-	422.1
AHQ-3-1, 6194	K.LLVPSPEGMSEIYLR.C	1705.01201	2	1.02E-04	0.46	2.52	-	283.6
AHQ-3-6, 5457	K.LLVPSPEGMSEIYLR.C	1705.01201	2	7.02E-07	0.61	2.56	-	515.1
AHQ-3-11, 5531	K.LLVPSPEGMSEIYLR.C	1705.01201	2	3.40E-09	0.65	2.50	-	515.9
AHQ-3-6, 5753 - 5821	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.07E-09	0.56	2.73	-	266.0
AHQ-3-12, 4771 - 4842	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	6.22E-11	0.65	2.51	-	341.5
AHQ-3-13-, 6697	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.05E-07	0.81	3.21	-	1102.8
AHQ-3-6, 7111 - 7129	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.43E-04	0.84	3.79	-	1075.0
AHQ-3-6, 6927 - 7006	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	3.40E-11	0.96	5.22	-	1537.3
AHQ-3-1, 7128 - 7140	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.96E-07	0.93	4.52	-	1247.0
AHQ-3-6, 6382 - 6401	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	7.24E-04	0.51	3.18	-	482.7
AHQ-3-4, 7252	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	5.39E-05	0.89	4.29	-	916.4
AHQ-3-6, 2101 - 2109	R.LTQLYEQAR.W	1122.25622	2	3.96E-06	0.95	4.04	-	1442.8
AHQ-3-9, 2071	R.LTQLYEQAR.W	1122.25622	2	4.51E-05	0.88	3.25	-	1097.7
AHQ-3-6, 2203	R.LTQLYEQAR.W	1122.25622	2	5.53E-05	0.91	2.75	-	1304.6
AHQ-3-6, 4867	R.QWLLQTHWTLDK.Y	1569.78807	2	1.12E-05	0.54	2.88	-	202.7
AHQ-3-13-, 4065	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	9.23E-09	0.90	3.67	-	707.2
AHQ-3-1, 4330	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	9.25E-06	0.87	3.85	-	463.6
AHQ-3-11, 3868 - 3938	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	6.35E-09	0.91	4.50	-	530.1
AHQ-3-7, 3867 - 3882	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.45E-04	0.76	3.96	-	280.6
AHQ-3-6, 3975 - 4051	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	4.96E-08	0.85	3.55	-	493.3
AHQ-3-12, 4042	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.10E-05	0.51	2.62	-	316.9
AHQ-3-6, 3891 - 3905	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	5.10E-09	0.84	3.77	-	447.7
AHQ-3-6, 4493 - 4494	K.TASGDYIDSSWELR.V	1600.66783	2	2.63E-05	0.73	2.64	-	770.3
AHQ-3-11, 4148	K.TASGDYIDSSWELR.V	1600.66783	2	2.72E-05	0.76	3.19	-	515.6
AHQ-3-14-, 4265 - 4293	K.TASGDYIDSSWELR.V	1600.66783	2	7.95E-10	0.92	3.79	-	1199.2
AHQ-3-9, 4000 - 4069	K.TASGDYIDSSWELR.V	1600.66783	2	4.02E-05	0.76	2.97	-	566.3
AHQ-3-6, 4314 - 4325	K.TASGDYIDSSWELR.V	1600.66783	2	7.32E-10	0.96	4.70	-	1036.4
AHQ-3-6, 4167 - 4242	K.TASGDYIDSSWELR.V	1600.66783	2	1.61E-11	0.96	4.71	-	1080.9
AHQ-3-4, 3865	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	9.46E-04	0.65	3.16	-	416.0
AHQ-3-10, 3542	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.44E-04	0.89	4.16	-	654.1
AHQ-3-6, 3566 - 3618	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	3.53E-05	0.93	4.50	-	774.3
AHQ-3-3, 3937	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	2.08E-05	0.96	6.16	-	952.9
AHQ-3-6, 3695	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	7.92E-04	0.63	3.01	-	310.4
AHQ-3-11, 3618	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	1.34E-06	0.96	5.75	-	1245.4
AHQ-3-11, 3627	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	1.94E-04	0.89	4.35	-	552.7
AHQ-3-6, 3565 - 3645	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	7.09E-04	0.97	6.81	-	1305.7
AHQ-3-6, 7382	R.TMADSSYTSEVQAILAFLSLQR.T	2432.73531	3	2.07E-07	0.96	5.58	-	1533.0
AHQ-3-6, 7366	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	8.07E-07	0.95	4.97	-	1474.4
AHQ-3-12, 3974	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.78E-05	0.88	3.82	-	819.2
AHQ-3-5, 3971	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.17E-12	0.97	4.93	-	1631.7
AHQ-3-13-, 3981 - 3994	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.22E-08	0.93	4.35	-	1222.1
AHQ-3-9, 3727 - 3797	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.22E-05	0.73	2.99	-	709.3
AHQ-3-10, 3718	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.39E-06	0.94	4.25	-	1323.5
AHQ-3-6, 3873 - 3942	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.22E-10	0.95	4.82	-	1360.1
AHQ-3-2, 4211	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.99E-05	0.84	3.21	-	955.2
AHQ-3-14, 4804 - 4841	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.59E-07	0.88	3.74	-	961.7
AHQ-3-8, 3713	R.VFVGEEDPEAESVTLR.V	1777.91007	2	8.92E-07	0.88	3.89	-	844.1
AHQ-3-13, 3977 - 3982	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.83E-09	0.93	4.16	-	991.4
AHQ-3-4, 4105 - 4113	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.72E-07	0.95	4.56	-	1138.1
AHQ-3-9, 3585 - 3652	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.09E-06	0.89	3.96	-	887.1
AHQ-3-11, 3823 - 3826	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.43E-10	0.95	4.85	-	1489.4
AHQ-3-14-, 3871	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.48E-10	0.92	3.93	-	1194.9
AHQ-3-12, 2752	R.VTGESHIGGVLLK.I	1310.52448	2	4.99E-08	0.55	2.93	-	801.0
AHQ-3-11, 2636 - 2684	R.VTGESHIGGVLLK.I	1310.52448	1	8.52E-06	0.76	2.72	-	816.0
AHQ-3-11, 2632	R.VTGESHIGGVLLK.I	1310.52448	2	9.23E-09	0.92	4.09	-	1066.2
AHQ-3-6, 2549	R.VTGESHIGGVLLK.I	1310.52448	2	2.54E-04	0.90	3.01	-	1489.5
AHQ-3-6, 2469	R.VTGESHIGGVLLK.I	1310.52448	1	9.08E-08	0.62	2.92	-	449.8
AHQ-3-9, 2380	R.VTGESHIGGVLLK.I	1310.52448	1	2.75E-05	0.72	2.98	-	720.6
AHQ-3-9, 2376	R.VTGESHIGGVLLK.I	1310.52448	2	1.62E-07	0.97	4.37	-	1986.3
AHQ-3-6, 2465 - 2477	R.VTGESHIGGVLLK.I	1310.52448	2	3.75E-08	0.96	4.44	-	1517.3
AHQ-3-7, 2407	R.VTGESHIGGVLLK.I	1310.52448	2	1.69E-06	0.97	4.07	-	1971.1
AHQ-3-13-, 2810	R.VTGESHIGGVLLK.I	1310.52448	2	2.00E-05	0.79	2.70	-	1011.8
AHQ-3-14-, 2729	R.VTGESHIGGVLLK.I	1310.52448	2	1.39E-06	0.92	3.11	-	1524.5
AHQ-3-1, 2964	R.VTGESHIGGVLLK.I	1310.52448	2	1.84E-10	0.96	4.32	-	1512.6
AHQ-3-7, 4515	K.VVLAGGVAPALFR.G	1270.54832	2	7.66E-08	0.97	4.63	-	1994.2
AHQ-3-1, 5134	K.VVLAGGVAPALFR.G	1270.54832	2	2.50E-07	0.95	4.19	-	1391.4
AHQ-3-6, 4669 - 4739	K.VVLAGGVAPALFR.G	1270.54832	2	2.34E-07	0.97	5.10	-	1686.2
AHQ-3-6, 4621 - 4689	K.VVLAGGVAPALFR.G	1270.54832	1	9.65E-04	0.42	2.11	-	156.5
AHQ-3-6, 4617 - 4685	K.VVLAGGVAPALFR.G	1270.54832	2	6.19E-09	0.96	5.04	-	1507.8
AHQ-3-9, 4308 - 4319	K.VVLAGGVAPALFR.G	1270.54832	2	4.43E-07	0.97	4.84	-	1725.1
AHQ-3-5, 4756	K.VVLAGGVAPALFR.G	1270.54832	2	3.22E-09	0.97	4.80	-	1572.6
AHQ-3-3, 5033	K.VVLAGGVAPALFR.G	1270.54832	2	7.96E-08	0.94	4.17	-	1317.6

AHQ-3-6, 2297	K.YGILADAR.L	878.99544	2	6.49E-04	0.92	3.23	-	1286.6
AHQ-3-6, 5254 - 5257	K.YYSFFDLDPK.T	1295.42046	2	1.17E-05	0.86	3.64	-	700.4
AHQ-3-1, 5738	K.YYSFFDLDPK.T	1295.42046	2	6.66E-06	0.55	3.16	-	485.3
gi|4827056|ref|NP_005103.1|	WD repeat-containing protein 1 isoform 2 [Homo sapiens]			1.50E-14	11.63	140.33	42.30	58001.9
AHQ-3-6, 4834 - 4835	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	1.70E-05	0.93	4.36	-	874.9
AHQ-3-6, 5795 - 5869	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	2.33E-11	0.92	4.98	-	732.7
AHQ-3-7, 5654 - 5658	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.50E-14	0.94	4.82	-	1003.2
AHQ-3-9, 5372	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.64E-12	0.94	4.70	-	1027.6
AHQ-3-10, 5168	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	8.53E-12	0.94	5.41	-	869.9
AHQ-3-6, 5615 - 5658	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.50E-12	0.85	3.58	-	932.8
AHQ-3-6, 5561	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	3	2.85E-05	0.80	3.75	-	698.5
AHQ-3-6, 5573	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	2	2.03E-08	0.92	4.30	-	714.6
AHQ-3-10, 4278 - 4279	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	4.67E-05	0.96	4.62	-	1183.5
AHQ-3-12, 4667	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	2.61E-05	0.97	5.34	-	1706.9
AHQ-3-6, 4533 - 4602	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	3.48E-07	0.98	5.57	-	1692.7
AHQ-3-6, 4699	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	1.24E-06	0.90	3.75	-	954.9
AHQ-3-9, 4305	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	1.43E-04	0.90	3.70	-	970.0
AHQ-3-6, 2311	K.IKDIAWTEDSK.R	1306.44632	2	9.05E-07	0.91	3.89	-	807.7
AHQ-3-6, 2014	K.IKDIAWTEDSKR.I	1462.63267	2	3.29E-06	0.89	3.60	-	1095.4
AHQ-3-6, 5569 - 5643	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.04E-08	0.94	4.91	-	1071.9
AHQ-3-3, 5793	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.33E-05	0.69	3.29	-	871.1
AHQ-3-6, 5454 - 5501	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	7.88E-09	0.95	4.87	-	1150.5
AHQ-3-11, 5208 - 5260	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	8.65E-07	0.78	3.49	-	650.4
AHQ-3-7, 3632	R.LYSILGTTLKDEGK.L	1538.76736	2	9.71E-04	0.82	3.07	-	926.7
AHQ-3-6, 3657	R.LYSILGTTLKDEGK.L	1538.76736	2	1.82E-09	0.85	3.63	-	717.2
AHQ-3-6, 4955	R.MTVDESGQLISCSMDDTVR.Y	2146.36365	2	3.47E-07	0.81	3.67	-	522.2
AHQ-3-6, 4057 - 4087	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	3	9.08E-05	0.63	3.19	-	291.0
AHQ-3-13, 4211	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	5.07E-05	0.58	2.53	-	531.2
AHQ-3-6, 4011	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	3.14E-06	0.98	6.56	-	1967.5
AHQ-3-6, 4131	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	1.67E-14	0.97	6.37	-	1502.7
AHQ-3-6, 2086 - 2158	K.VINSVDIK.Q	888.04378	1	6.63E-05	0.32	2.31	-	403.7
AHQ-3-6, 3829	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.23E-08	0.91	3.86	-	671.3
AHQ-3-1, 4190	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.39E-09	0.92	4.07	-	673.3
AHQ-3-11, 3760	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.14E-08	0.91	3.90	-	637.7
AHQ-3-13-, 2842	K.YEYQPFAGK.I	1103.20822	2	1.22E-05	0.58	2.61	-	489.2
AHQ-3-13, 2869	K.YEYQPFAGK.I	1103.20822	2	2.03E-07	0.66	2.57	-	623.8
gi|4507953|ref|NP_003397.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep			1.78E-14	8.46	110.31	46.90	27744.9
AHQ-3-10, 5664 - 5679	R.EKIETELRDICNDVLSLLEK.F	2419.73463	2	1.10E-04	0.23	2.84	-	194.5
AHQ-3-11, 3067 - 3082	K.FLIPNASQAESK.V	1305.46156	2	5.35E-05	0.74	3.00	-	398.9
AHQ-3-10, 3166 - 3351	K.FLIPNASQAESK.V	1305.46156	1	2.47E-05	0.62	2.63	-	449.7
AHQ-3-9, 2825	K.FLIPNASQAESK.V	1305.46156	1	1.15E-06	0.39	2.59	-	361.3
AHQ-3-9, 2824	K.FLIPNASQAESK.V	1305.46156	2	6.32E-06	0.73	2.53	-	561.7
AHQ-3-10, 2934 - 2998	K.FLIPNASQAESK.V	1305.46156	2	3.03E-06	0.77	2.78	-	498.2
AHQ-3-10, 6522	K.IETELRDICNDVLSLLEK.F	2162.44718	2	3.69E-07	0.93	4.87	-	805.4
AHQ-3-9, 7015	K.IETELRDICNDVLSLLEK.F	2162.44718	2	7.38E-06	0.92	4.57	-	1439.8
AHQ-3-10, 5754 - 5812	K.IETELRDICNDVLSLLEK.F	2162.44718	2	1.32E-09	0.96	5.15	-	1110.6
AHQ-3-10, 6583	R.LGLALNFSVFYYEILNSPEK.A	2318.65200	2	2.84E-08	0.84	4.32	-	432.5
AHQ-3-13, 2362	K.SVTEQGAELSNEER.N	1549.57922	2	1.89E-07	0.92	4.05	-	1055.7
AHQ-3-14, 3005 - 3064	K.SVTEQGAELSNEER.N	1549.57922	2	7.16E-04	0.23	2.50	-	305.4
AHQ-3-10, 2246	K.SVTEQGAELSNEER.N	1549.57922	2	2.45E-07	0.84	3.33	-	1059.5
AHQ-3-10, 2154 - 2218	K.SVTEQGAELSNEER.N	1549.57922	2	1.84E-09	0.97	4.79	-	1768.4
AHQ-3-13-, 2318	K.SVTEQGAELSNEER.N	1549.57922	2	1.77E-09	0.92	3.40	-	1417.1
AHQ-3-14-, 2191 - 2260	K.SVTEQGAELSNEER.N	1549.57922	2	3.37E-13	0.96	4.48	-	1666.2
AHQ-3-12, 2288	K.SVTEQGAELSNEER.N	1549.57922	2	1.17E-05	0.91	3.56	-	1331.3
AHQ-3-10, 4550 - 4562	K.SVTEQGAELSNEERNLLSVAYK.N	2438.63331	2	2.72E-05	0.82	3.74	-	609.4
AHQ-3-10, 6422 - 6483	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	8.95E-07	0.97	5.80	-	1406.3
AHQ-3-9, 6915	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.07E-06	0.97	5.86	-	1108.7
AHQ-3-14-, 6735	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.10E-08	0.98	6.14	-	1331.6
AHQ-3-13-, 6790	K.TAFDEAIAELDTLSEESYK.D	2133.25160	3	1.32E-04	0.96	5.65	-	1166.8
AHQ-3-13-, 6789	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	2.11E-06	0.97	5.23	-	1260.0
AHQ-3-13, 6865	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.45E-07	0.97	5.79	-	1362.9
AHQ-3-11, 6670 - 6672	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.16E-09	0.97	5.37	-	1190.0
AHQ-3-9, 7159	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	1.78E-14	0.95	5.48	-	1289.4
AHQ-3-10, 6602 - 6680	K.TAFDEAIAELDTLSEESYKDSTLIMQLLR.D	3304.66764	3	1.27E-12	0.95	5.12	-	1432.7
AHQ-3-10, 6706 - 6707	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	1.53E-13	0.96	5.74	-	1434.5
AHQ-3-10, 2399 - 2460	R.YDDMAACMK.S	1106.27579	1	1.62E-05	0.44	2.04	-	435.3
AHQ-3-13-, 2019 - 2034	R.YLAEVAAGDDKK.G	1280.40887	2	2.83E-05	0.95	3.37	-	1723.5
AHQ-3-10, 1806 - 1866	R.YLAEVAAGDDKK.G	1280.40887	2	3.08E-05	0.96	3.76	-	1701.6
AHQ-3-11, 1879 - 1900	R.YLAEVAAGDDKK.G	1280.40887	2	2.06E-06	0.94	3.69	-	1341.9
AHQ-3-13, 2102	R.YLAEVAAGDDKK.G	1280.40887	2	1.05E-04	0.85	3.04	-	1022.9
gi|4885609|ref|NP_005408.1|	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen			1.78E-14	4.24	50.35	15.90	59834.4
AHQ-3-7, 6902	R.AGPLAGGVTTFVALYDYESR.T	2088.30526	2	4.19E-04	0.83	3.59	-	714.4
AHQ-3-7, 3888 - 3934	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	2.63E-05	0.88	3.51	-	924.8
AHQ-3-7, 3598	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	1.52E-04	0.85	2.90	-	944.8
AHQ-3-7, 2294	R.LLLNAENPR.G	1040.19834	2	2.58E-04	0.85	2.91	-	814.0
AHQ-3-7, 7395	R.LPQLVDMAAQIASGMAYVER.M	2164.53485	2	1.78E-14	0.99	7.04	-	4800.5
AHQ-3-7, 4639	K.TLKPGTM*SPEAFLQEAQVMK.K	2223.59904	2	1.99E-04	0.68	3.50	-	658.6
gi|4502051|ref|NP_000688.1|	arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]			1.94E-14	5.49	60.34	13.60	75721.8
AHQ-3-6, 2054	K.AVSTGGGGHVQLLR.R	1352.52468	2	1.70E-06	0.76	3.02	-	770.8
AHQ-3-6, 3013 - 3094	R.EITEVGLCQAQDR.G	1520.64745	2	1.53E-07	0.96	4.89	-	923.0
AHQ-3-6, 7205	R.GEEEEFDHDVAEDLGLLQFVR.L	2448.58352	2	1.94E-14	0.98	6.83	-	2267.5
AHQ-3-6, 5171	R.ITVQGPGACAEVAFPCYR.W	1999.25659	2	1.57E-05	0.92	3.68	-	1324.3
AHQ-3-6, 4482	R.LPGDNALDMFQK.H	1349.53784	2	1.78E-07	0.95	3.97	-	1350.4
AHQ-3-6, 3911	R.TQLISDGGIFDK.A	1294.43554	2	1.83E-06	0.92	3.41	-	1274.3
gi|4826898|ref|NP_005013.1|	profilin 1; profilin-1 [Homo sapiens]			2.16E-14	16.22	180.30	70.70	15054.2
AHQ-3-13, 5582 - 5649	K.CSVIRDSLLQDGEFSMDLR.T	2243.50389	3	3.65E-05	0.91	3.89	-	1239.8
AHQ-3-13, 5027 - 5054	K.CSVIRDSLLQDGEFSM*DLR.T	2259.50329	3	5.32E-05	0.94	4.80	-	1481.7
AHQ-3-13-, 4923 - 5005	K.CSVIRDSLLQDGEFSM*DLR.T	2259.50329	3	1.69E-07	0.96	5.25	-	1690.0
AHQ-3-13, 1957 - 2018	K.CYEM*ASHLR.R	1184.32794	2	5.51E-05	0.92	3.12	-	1301.9
AHQ-3-13, 2347 - 2413	K.CYEMASHLR.R	1168.32854	2	4.66E-04	0.96	3.22	-	2063.5
AHQ-3-13-, 1597 - 1659	K.CYEM*ASHLR.R	1184.32794	2	3.93E-06	0.92	3.04	-	1208.9
AHQ-3-13-, 1717 - 1793	K.CYEM*ASHLR.R	1184.32794	2	2.64E-04	0.90	3.04	-	1255.9
AHQ-3-13-, 1853 - 1913	K.CYEM*ASHLR.R	1184.32794	2	8.15E-06	0.91	3.37	-	1185.2
AHQ-3-13-, 1949 - 2023	K.CYEM*ASHLR.R	1184.32794	2	1.12E-04	0.85	2.88	-	1074.4
AHQ-3-13-, 2402 - 2465	K.CYEMASHLR.R	1168.32854	2	1.84E-04	0.95	3.51	-	1542.3
AHQ-3-13-, 2429	K.CYEMASHLR.R	1168.32854	2	4.81E-05	0.97	3.88	-	2137.6
AHQ-3-12, 1786	K.CYEM*ASHLR.R	1184.32794	2	2.64E-04	0.78	2.50	-	1003.3
AHQ-3-13, 1866 - 1925	K.CYEM*ASHLR.R	1184.32794	2	3.27E-05	0.89	3.28	-	923.2
AHQ-3-13, 4185	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.87E-10	0.97	5.34	-	1285.5
AHQ-3-13, 4053 - 4123	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	3.38E-10	0.96	5.29	-	1153.3
AHQ-3-13-, 4077	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	2.16E-14	0.98	5.85	-	1388.0
AHQ-3-12, 5415 - 5479	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.87E-07	0.95	4.36	-	1357.5
AHQ-3-14-, 5161 - 5227	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.50E-05	0.96	4.37	-	1600.5
AHQ-3-12, 5542 - 5620	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.69E-05	0.95	3.89	-	1461.2
AHQ-3-12, 5688 - 5750	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.55E-04	0.96	4.60	-	1396.2
AHQ-3-13-, 4721 - 4795	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.05E-08	0.94	3.72	-	1557.8
AHQ-3-12, 5816 - 5891	R.DSLLQDGEFSMDLR.T	1626.77023	2	6.82E-07	0.76	3.37	-	546.5

AHQ-3-13-, 4653	R.DSLLQDGEFSM*DLR.T	1642.76963	3	3.49E-07	0.98	5.60	-	2420.5
AHQ-3-12, 5271 - 5346	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.86E-09	0.96	4.79	-	1312.7
AHQ-3-13-, 4867 - 4926	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.87E-07	0.96	4.37	-	1980.8
AHQ-3-12, 4662 - 4696	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.49E-06	0.88	2.95	-	1251.0
AHQ-3-14-, 4612	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.27E-09	0.96	3.68	-	1810.1
AHQ-3-12, 4558	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.27E-06	0.92	3.57	-	1100.0
AHQ-3-13-, 4469 - 4533	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.69E-09	0.96	5.11	-	1214.5
AHQ-3-13-, 4363	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.78E-05	0.64	2.60	-	761.7
AHQ-3-13-, 5653 - 5713	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.39E-04	0.92	3.53	-	1340.1
AHQ-3-13-, 6101 - 6123	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.93E-06	0.97	4.69	-	2263.7
AHQ-3-13-, 4995 - 5070	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.78E-07	0.70	2.76	-	1084.6
AHQ-3-13-, 5115	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.27E-11	0.96	4.41	-	1496.3
AHQ-3-13-, 5211 - 5274	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.61E-10	0.97	4.84	-	1496.5
AHQ-3-13-, 6038	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.05E-05	0.93	3.05	-	1775.2
AHQ-3-14-, 5376 - 5455	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.13E-09	0.97	4.36	-	2202.8
AHQ-3-13-, 5414 - 5479	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.00E-04	0.77	3.01	-	956.6
AHQ-3-14-, 4487	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.64E-04	0.93	3.26	-	1361.2
AHQ-3-14, 6315	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.18E-10	0.97	4.20	-	2197.9
AHQ-3-14, 5592 - 5652	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.18E-07	0.95	4.03	-	1749.2
AHQ-3-14, 5445 - 5509	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.36E-06	0.73	3.08	-	736.2
AHQ-3-13, 6130 - 6198	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.60E-09	0.96	4.25	-	1807.5
AHQ-3-13-, 5429 - 5501	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.36E-10	0.98	4.91	-	2128.5
AHQ-3-13-, 5521 - 5587	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.51E-09	0.97	4.92	-	1756.1
AHQ-3-13, 6001 - 6065	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.11E-07	0.95	3.95	-	1693.6
AHQ-3-13-, 5893 - 5974	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.93E-10	0.98	5.10	-	2352.5
AHQ-3-13, 4385	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.52E-04	0.94	4.04	-	1418.3
AHQ-3-13, 4471 - 4534	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.68E-08	0.93	3.62	-	1069.7
AHQ-3-13, 5637 - 5705	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.58E-10	0.97	4.63	-	2042.3
AHQ-3-13, 4597 - 4665	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.35E-07	0.96	4.89	-	1607.0
AHQ-3-13, 4666 - 4729	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.50E-09	0.95	4.20	-	1627.2
AHQ-3-13, 4793 - 4861	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.36E-09	0.96	4.28	-	1893.4
AHQ-3-13, 4930 - 4997	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.77E-10	0.96	4.34	-	1627.5
AHQ-3-13-, 4531 - 4593	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.07E-10	0.97	4.99	-	1929.7
AHQ-3-13, 5161	R.DSLLQDGEFSMDLR.T	1626.77023	2	8.11E-08	0.94	3.95	-	1296.2
AHQ-3-13, 5261 - 5325	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.40E-04	0.95	3.98	-	1492.7
AHQ-3-13, 6702	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.60E-04	0.87	3.38	-	1041.8
AHQ-3-13, 5389 - 5461	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.58E-09	0.97	4.81	-	2112.5
AHQ-3-13, 5505 - 5573	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.30E-09	0.98	5.70	-	2157.9
AHQ-3-13-, 3497 - 3530	K.DSPSVWAAVPGK.T	1214.35211	2	2.20E-07	0.88	2.84	-	972.9
AHQ-3-13-, 3593 - 3667	K.DSPSVWAAVPGK.T	1214.35211	2	2.41E-07	0.90	3.64	-	950.6
AHQ-3-13, 3353 - 3361	K.DSPSVWAAVPGK.T	1214.35211	2	6.73E-05	0.87	3.09	-	1062.9
AHQ-3-13, 3519 - 3589	K.DSPSVWAAVPGK.T	1214.35211	2	2.96E-05	0.89	3.54	-	922.0
AHQ-3-13, 3525 - 3649	K.DSPSVWAAVPGK.T	1214.35211	1	2.98E-07	0.23	2.52	-	369.8
AHQ-3-12, 3554 - 3620	K.DSPSVWAAVPGK.T	1214.35211	2	6.05E-04	0.79	2.91	-	961.2
AHQ-3-12, 3555	K.DSPSVWAAVPGK.T	1214.35211	1	6.67E-04	0.56	2.68	-	651.3
AHQ-3-13, 3613 - 3686	K.DSPSVWAAVPGK.T	1214.35211	2	6.11E-08	0.87	3.04	-	1022.2
AHQ-3-13-, 3501 - 3626	K.DSPSVWAAVPGK.T	1214.35211	1	5.81E-05	0.34	2.46	-	367.6
AHQ-3-13, 3738	K.DSPSVWAAVPGK.T	1214.35211	2	1.64E-04	0.82	2.93	-	1046.1
AHQ-3-13, 3833	K.DSPSVWAAVPGK.T	1214.35211	2	5.25E-05	0.91	3.29	-	1130.2
AHQ-3-13-, 6557	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	2.82E-10	0.95	4.36	-	2033.7
AHQ-3-12, 4447 - 4518	R.SSFYVNGLTLGGQK.C	1471.63957	1	5.08E-06	0.38	2.94	-	320.3
AHQ-3-14, 5255	R.SSFYVNGLTLGGQK.C	1471.63957	2	7.16E-06	0.91	3.85	-	742.9
AHQ-3-14, 5263	R.SSFYVNGLTLGGQK.C	1471.63957	1	9.19E-08	0.28	2.18	-	302.6
AHQ-3-13, 4233 - 4293	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.56E-08	0.94	4.17	-	808.7
AHQ-3-12, 4288	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.45E-07	0.26	2.04	-	388.4
AHQ-3-12, 4282 - 4287	R.SSFYVNGLTLGGQK.C	1471.63957	2	7.04E-09	0.95	4.37	-	978.8
AHQ-3-13-, 4241 - 4602	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.61E-07	0.70	3.17	-	360.0
AHQ-3-12, 4522	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.36E-05	0.94	3.65	-	1229.0
AHQ-3-13, 4234 - 4593	R.SSFYVNGLTLGGQK.C	1471.63957	1	9.47E-09	0.70	3.20	-	377.3
AHQ-3-13, 4481 - 4545	R.SSFYVNGLTLGGQK.C	1471.63957	2	8.34E-05	0.97	4.49	-	1597.6
AHQ-3-13-, 4333 - 4394	R.SSFYVNGLTLGGQK.C	1471.63957	2	6.23E-08	0.93	3.86	-	869.6
AHQ-3-13-, 4237 - 4303	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.99E-09	0.94	4.44	-	765.8
AHQ-3-14-, 4252	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.81E-09	0.53	2.38	-	383.8
AHQ-3-12, 4663	R.SSFYVNGLTLGGQK.C	1471.63957	1	4.89E-05	0.22	2.05	-	356.2
AHQ-3-13-, 4783	R.SSFYVNGLTLGGQK.C	1471.63957	1	6.28E-05	0.09	1.96	-	264.8
AHQ-3-14-, 4419 - 4499	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.30E-07	0.33	2.09	-	397.5
AHQ-3-12, 4408 - 4455	R.SSFYVNGLTLGGQK.C	1471.63957	2	9.39E-05	0.94	4.27	-	1041.5
AHQ-3-14-, 4495 - 4513	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.16E-08	0.97	4.21	-	1612.3
AHQ-3-13-, 4461 - 4537	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.50E-07	0.97	4.99	-	1404.3
AHQ-3-14-, 4453	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.16E-05	0.25	2.07	-	316.7
AHQ-3-14-, 4401	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.22E-06	0.91	3.10	-	1271.7
AHQ-3-14-, 3013	K.STGGAPTFNVTVTK.T	1380.52843	1	1.23E-04	0.63	2.72	-	482.3
AHQ-3-13-, 3161 - 3185	K.STGGAPTFNVTVTK.T	1380.52843	2	3.53E-05	0.79	3.26	-	374.4
AHQ-3-13-, 3037 - 3118	K.STGGAPTFNVTVTK.T	1380.52843	2	4.02E-06	0.72	2.95	-	414.8
AHQ-3-13-, 3001 - 3269	K.STGGAPTFNVTVTK.T	1380.52843	1	1.95E-05	0.59	2.90	-	359.7
AHQ-3-13-, 2922	K.STGGAPTFNVTVTK.T	1380.52843	2	3.02E-05	0.76	2.78	-	443.5
AHQ-3-13-, 2921 - 2986	K.STGGAPTFNVTVTK.T	1380.52843	2	3.22E-10	0.92	4.27	-	572.7
AHQ-3-13, 3026 - 3198	K.STGGAPTFNVTVTK.T	1380.52843	1	1.90E-04	0.59	2.77	-	381.6
AHQ-3-13, 2950 - 3013	K.STGGAPTFNVTVTK.T	1380.52843	2	3.56E-04	0.83	3.18	-	550.8
AHQ-3-13, 3063 - 3129	K.STGGAPTFNVTVTK.T	1380.52843	2	1.59E-08	0.87	3.32	-	631.2
AHQ-3-12, 3050 - 3051	K.STGGAPTFNVTVTK.T	1380.52843	2	2.52E-06	0.87	3.19	-	575.1
AHQ-3-13, 3166 - 3246	K.STGGAPTFNVTVTK.T	1380.52843	2	2.32E-10	0.87	3.78	-	492.8
AHQ-3-13-, 2834 - 2843	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	9.79E-07	0.82	3.58	-	454.2
AHQ-3-13, 2846	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	7.57E-04	0.73	2.69	-	483.9
AHQ-3-13-, 2991	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	3.31E-05	0.90	4.05	-	652.0
AHQ-3-13, 3014	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	1.67E-06	0.87	3.61	-	521.1
AHQ-3-13-, 2829 - 2831	K.TDKTLVLLM*GK.E	1235.51929	2	3.80E-05	0.92	3.59	-	1032.2
AHQ-3-13, 3521 - 3590	K.TDKTLVLLMGK.E	1219.51989	2	3.70E-06	0.93	3.51	-	1229.9
AHQ-3-13-, 3505 - 3571	K.TDKTLVLLMGK.E	1219.51989	2	6.18E-07	0.94	4.35	-	1080.6
AHQ-3-12, 5863 - 5926	K.TFVNITPAEVGVLVGK.D	1644.93630	2	4.01E-08	0.89	4.19	-	673.4
AHQ-3-12, 5739 - 5802	K.TFVNITPAEVGVLVGK.D	1644.93630	2	9.83E-06	0.95	4.70	-	1054.9
AHQ-3-11, 5598 - 5600	K.TFVNITPAEVGVLVGK.D	1644.93630	2	9.65E-05	0.61	2.94	-	538.6
AHQ-3-13, 6093 - 6159	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.12E-04	0.88	4.12	-	596.3
AHQ-3-13, 5953 - 6017	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.22E-09	0.93	4.20	-	979.3
AHQ-3-13, 5854	K.TFVNITPAEVGVLVGK.D	1644.93630	3	7.12E-09	0.97	5.12	-	1806.7
AHQ-3-13, 5845 - 5909	K.TFVNITPAEVGVLVGK.D	1644.93630	2	4.42E-07	0.95	4.31	-	1060.3
AHQ-3-13, 5751 - 5787	K.TFVNITPAEVGVLVGK.D	1644.93630	3	4.47E-09	0.97	5.53	-	1645.4
AHQ-3-13-, 5477	K.TFVNITPAEVGVLVGK.D	1644.93630	2	5.02E-05	0.93	3.75	-	1074.8
AHQ-3-13, 5745	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.48E-05	0.94	4.48	-	828.6
AHQ-3-14-, 5677 - 5756	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.70E-04	0.92	3.93	-	830.1
AHQ-3-13-, 5698	K.TFVNITPAEVGVLVGK.D	1644.93630	3	1.00E-08	0.97	6.03	-	1583.1
AHQ-3-13-, 5761 - 5841	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.21E-07	0.93	4.00	-	1008.8
AHQ-3-13-, 5785	K.TFVNITPAEVGVLVGK.D	1644.93630	3	1.43E-07	0.95	5.02	-	1129.2
AHQ-3-13-, 5889 - 5957	K.TFVNITPAEVGVLVGK.D	1644.93630	2	5.13E-10	0.95	4.48	-	972.5
AHQ-3-13, 5711 - 5782	K.TFVNITPAEVGVLVGK.D	1644.93630	2	7.63E-04	0.86	3.79	-	842.7
AHQ-3-13-, 6021 - 6025	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.78E-06	0.93	4.45	-	1027.9
AHQ-3-14-, 5920	K.TFVNITPAEVGVLVGK.D	1644.93630	2	7.67E-04	0.92	3.42	-	1240.1

AHQ-3-12, 5424	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	6.66E-07	0.91	4.17	-	694.6
AHQ-3-13-, 6217	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	6.82E-06	0.56	2.83	-	742.3
AHQ-3-13-, 5367 - 5446	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	1.76E-09	0.91	4.25	-	743.7
AHQ-3-13, 5383 - 5386	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	2.14E-05	0.59	3.18	-	550.7
AHQ-3-13, 5393 - 5466	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	2.01E-08	0.90	4.22	-	678.7
AHQ-3-13-, 2699 - 2761	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	7.30E-05	0.96	4.66	-	956.4
AHQ-3-13-, 3303	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	4.52E-04	0.74	2.67	-	448.5
AHQ-3-12, 2680	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	9.98E-05	0.92	3.91	-	894.5
AHQ-3-13, 2726 - 2790	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	2.38E-10	0.96	5.35	-	961.0
AHQ-3-13, 2817	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	6.21E-05	0.94	4.47	-	927.9
AHQ-3-13-, 3714 - 3757	K.TLVLLMGK.E	875.15478	2	6.10E-06	0.86	3.28	-	487.0
AHQ-3-12, 3596	K.TLVLLMGK.E	875.15478	1	1.13E-04	0.21	2.36	-	255.1
AHQ-3-13-, 3563 - 3637	K.TLVLLMGK.E	875.15478	2	1.43E-05	0.78	3.27	-	492.7
AHQ-3-13, 3665 - 3727	K.TLVLLMGK.E	875.15478	2	7.31E-06	0.83	2.92	-	538.2
AHQ-3-13, 3579 - 3643	K.TLVLLMGK.E	875.15478	2	1.26E-05	0.72	2.81	-	468.3
gi|21361755|ref|NP_004090.3|	stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie			4.33E-14	9.73	110.36	46.20	31708.5
AHQ-3-14-, 4607	K.EASMVITESPAALQLR.Y	1716.98119	2	1.45E-04	0.67	2.97	-	735.5
AHQ-3-13, 4627	K.EASMVITESPAALQLR.Y	1716.98119	2	4.03E-05	0.83	3.41	-	759.1
AHQ-3-1, 4948 - 4949	K.EASMVITESPAALQLR.Y	1716.98119	2	8.83E-05	0.93	4.78	-	1033.1
AHQ-3-13-, 4098	K.EASM*VITESPAALQLR.Y	1732.98059	2	3.62E-05	0.92	4.20	-	1014.8
AHQ-3-9, 4284 - 4285	K.EASMVITESPAALQLR.Y	1716.98119	2	9.06E-04	0.84	3.45	-	915.6
AHQ-3-1, 4376	K.EASM*VITESPAALQLR.Y	1732.98059	2	7.92E-04	0.89	3.91	-	796.7
AHQ-3-13-, 6842	K.GPGLFFILPCTDSFIK.V	1814.13672	2	2.87E-04	0.91	3.73	-	760.3
AHQ-3-9, 6963	K.GPGLFFILPCTDSFIK.V	1814.13672	2	3.72E-05	0.93	4.56	-	729.4
AHQ-3-13, 6934	K.GPGLFFILPCTDSFIK.V	1814.13672	2	8.89E-04	0.46	2.55	-	351.1
AHQ-3-1, 7280	K.GPGLFFILPCTDSFIK.V	1814.13672	2	3.16E-04	0.95	4.50	-	928.1
AHQ-3-1, 2486	R.LLAQTTLR.N	916.10035	2	8.88E-05	0.58	2.56	-	392.3
AHQ-3-1, 6277 - 6325	K.NLSQILSDREEIAHNM*QSTLDDATDAWGIK.V	3389.65279	3	3.74E-05	0.94	4.72	-	1531.9
AHQ-3-9, 6872	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	4.50E-06	0.96	6.08	-	1256.6
AHQ-3-10, 5495	K.NLSQILSDREEIAHNM*QSTLDDATDAWGIK.V	3389.65279	3	3.38E-05	0.96	4.95	-	2237.4
AHQ-3-1, 7210 - 7282	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	2.27E-11	0.98	7.18	-	1643.1
AHQ-3-10, 6451	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	3.78E-09	0.97	6.71	-	1198.9
AHQ-3-10, 6667	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	4.35E-04	0.87	4.04	-	482.6
AHQ-3-1, 7420	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	6.01E-06	0.86	3.63	-	517.8
AHQ-3-13, 6955	K.NSTIVFPLPIDM*LQGIIGAK.H	2144.56315	2	9.55E-06	0.79	3.37	-	368.4
AHQ-3-1, 2341	K.VIAAEGEMNASR.A	1248.39191	2	1.09E-08	0.97	4.31	-	1810.2
AHQ-3-10, 3888	R.VQNATLAVANITNADSATR.L	1931.09731	2	3.59E-08	0.91	4.32	-	707.2
AHQ-3-1, 3913 - 3980	R.VQNATLAVANITNADSATR.L	1931.09731	2	8.57E-12	0.95	4.78	-	1055.3
AHQ-3-1, 4052 - 4064	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.33E-14	0.97	5.83	-	1281.9
AHQ-3-10, 3666	R.VQNATLAVANITNADSATR.L	1931.09731	2	2.93E-09	0.94	4.38	-	927.2
AHQ-3-1, 4713	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.94E-09	0.94	3.97	-	1048.9
AHQ-3-1, 4166 - 4245	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.34E-12	0.97	5.12	-	1169.3
AHQ-3-10, 3570 - 3571	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.12E-05	0.91	3.62	-	1116.6
AHQ-3-12, 3667 - 3740	R.YLQTLTTIAAEK.N	1352.55813	2	1.55E-04	0.76	2.54	-	875.5
AHQ-3-14-, 3744	R.YLQTLTTIAAEK.N	1352.55813	2	2.91E-07	0.92	3.54	-	1206.0
AHQ-3-13, 3822	R.YLQTLTTIAAEK.N	1352.55813	2	2.38E-04	0.94	4.18	-	1037.3
AHQ-3-13-, 3833	R.YLQTLTTIAAEK.N	1352.55813	2	2.82E-07	0.94	3.63	-	1343.5
gi|4757810|ref|NP_004037.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,			6.27E-14	5.32	60.30	16.30	59750.3
AHQ-3-11, 5328 - 5402	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	2	9.13E-04	0.76	3.31	-	470.7
AHQ-3-7, 5375 - 5400	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	3	6.27E-14	0.98	5.91	-	2146.2
AHQ-3-7, 6103	K.GMSLNLEPDNVGVVVFGNDK.L	2105.35763	2	1.10E-08	0.89	4.40	-	424.6
AHQ-3-7, 3066 - 3134	K.HALIIYDDLSK.Q	1288.47413	2	6.01E-06	0.86	3.00	-	788.2
AHQ-3-7, 3664 - 3712	R.ILGADTSVDLEETGR.V	1576.68772	2	4.65E-06	0.89	3.80	-	816.5
AHQ-3-7, 2322	K.TGTAEM*SSILEER.I	1440.55928	2	8.16E-06	0.86	3.32	-	855.4
AHQ-3-7, 2838	R.VLSIGDGIAR.V	1001.16212	2	8.12E-04	0.84	2.63	-	789.9
gi|6857820|ref|NP_005019.2|	phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl			7.83E-14	1.92	20.33	7.60	46224.3
AHQ-3-7, 4531	R.FGIDDQDFQNSLTR.S	1656.73462	2	1.02E-07	0.93	4.41	-	1227.9
AHQ-3-7, 2470 - 2479	K.HGAGAEISTVNPEQYSK.R	1788.89618	2	7.83E-14	0.98	6.55	-	2174.5
gi|4505879|ref|NP_002655.1|	pleckstrin; p47 [Homo sapiens]			8.22E-14	9.09	110.40	45.40	40082.5
AHQ-3-1, 6081	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	5.51E-05	0.95	5.37	-	1106.3
AHQ-3-10, 5176	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	3.28E-08	0.98	6.03	-	2895.6
AHQ-3-13, 5621	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	9.81E-10	0.97	6.26	-	1551.8
AHQ-3-12, 5611	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.97E-05	0.97	6.06	-	1626.2
AHQ-3-9, 5312 - 5339	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	4.14E-05	0.86	3.99	-	786.3
AHQ-3-8, 5351	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.60E-04	0.95	6.00	-	1009.2
AHQ-3-13-, 5578	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	3.63E-05	0.96	5.80	-	1394.2
AHQ-3-8, 2296	R.GCVVTSVESNSNGR.K	1467.54464	2	2.33E-06	0.86	3.11	-	1097.4
AHQ-3-13-, 2447 - 2510	R.GCVVTSVESNSNGR.K	1467.54464	2	2.79E-05	0.89	3.64	-	1114.7
AHQ-3-12, 2434	R.GCVVTSVESNSNGR.K	1467.54464	2	1.84E-07	0.86	3.56	-	790.6
AHQ-3-8, 2282 - 2285	K.GSTLTSPCQDFGKR.M	1555.69502	2	1.67E-07	0.57	2.93	-	300.6
AHQ-3-10, 6356	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	5.21E-11	0.98	6.04	-	1662.9
AHQ-3-8, 7079 - 7147	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	2.65E-09	0.97	6.18	-	1280.5
AHQ-3-8, 6907 - 6912	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	8.41E-12	0.98	6.55	-	1694.4
AHQ-3-11, 6543	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	1.54E-04	0.76	3.52	-	412.3
AHQ-3-8, 7291 - 7368	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	2.42E-08	0.99	7.61	-	2940.9
AHQ-3-13, 7005	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.29E-08	0.98	6.91	-	2478.7
AHQ-3-13-, 6886 - 6954	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.86E-12	0.98	7.28	-	2334.6
AHQ-3-7, 7411	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	4.28E-08	0.98	7.11	-	2231.9
AHQ-3-10, 6591	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.11E-13	0.98	7.95	-	2717.0
AHQ-3-9, 7035	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.56E-08	0.98	7.06	-	2098.8
AHQ-3-12, 7010 - 7090	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	6.17E-10	0.98	8.01	-	2505.3
AHQ-3-9, 6324	R.LPETIDLGALYLSMK.D	1664.98779	2	6.44E-06	0.97	4.27	-	1898.4
AHQ-3-8, 5464 - 5480	R.LPETIDLGALYLSM*K.D	1680.98719	2	1.16E-05	0.95	4.75	-	1017.6
AHQ-3-8, 6528 - 6596	R.LPETIDLGALYLSMK.D	1664.98779	2	1.78E-06	0.97	4.41	-	2431.7
AHQ-3-10, 6003	R.LPETIDLGALYLSMK.D	1664.98779	2	4.11E-06	0.96	4.20	-	1566.3
AHQ-3-12, 6427 - 6492	R.LPETIDLGALYLSMK.D	1664.98779	2	6.71E-05	0.98	5.20	-	2238.8
AHQ-3-13, 5702 - 5758	R.LPETIDLGALYLSM*K.D	1680.98719	2	2.07E-04	0.95	4.70	-	1063.0
AHQ-3-12, 5260 - 5295	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	3	1.49E-04	0.83	3.74	-	662.4
AHQ-3-8, 5867	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	2.28E-06	0.98	6.26	-	2764.7
AHQ-3-8, 6449	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	1.39E-06	0.38	2.56	-	246.6
AHQ-3-10, 5576	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	1.39E-04	0.95	4.61	-	1212.4
AHQ-3-11, 4316	K.QQDHFFQAAFLEER.D	1766.89390	2	9.27E-04	0.40	2.58	-	126.9
AHQ-3-12, 4507 - 4584	K.QQDHFFQAAFLEER.D	1766.89390	2	2.74E-09	0.74	3.02	-	207.5
AHQ-3-8, 4156	K.QQDHFFQAAFLEER.D	1766.89390	2	4.56E-10	0.67	2.65	-	187.3
AHQ-3-10, 6660	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.75E-10	0.85	3.47	-	934.7
AHQ-3-11, 6834	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	3.00E-11	0.83	3.82	-	860.5
AHQ-3-12, 7060	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	8.22E-14	0.92	4.43	-	976.8
AHQ-3-13-, 6930	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	4.09E-09	0.92	4.84	-	831.9
AHQ-3-14-, 6880	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.81E-08	0.69	3.44	-	458.9
gi|27498332|ref|XP_212565.1|	similar to tubulin, beta 5 [Homo sapiens]			1.43E-13	4.71	50.27	9.90	49670.5
AHQ-3-11, 5399 - 5403	R.ALTVPELTQQVFDAK.N	1660.89259	2	2.46E-04	0.88	3.82	-	497.4
AHQ-3-8, 5209 - 5224	R.ALTVPELTQQVFDAK.N	1660.89259	2	5.55E-11	0.92	4.30	-	466.2
AHQ-3-1, 6074	R.ALTVPELTQQVFDAK.N	1660.89259	2	1.58E-04	0.58	2.56	-	365.7
AHQ-3-11, 3223	R.IM*NTFSVVPSPK.V	1336.58217	2	6.60E-04	0.91	3.51	-	929.9
AHQ-3-7, 3530 - 3604	R.IMNTFSVVPSPK.V	1320.58277	2	1.13E-06	0.96	4.48	-	1608.4
AHQ-3-7, 7000 - 7016	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	7.20E-07	0.96	5.33	-	1251.8
AHQ-3-7, 7118	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	2.24E-08	0.95	4.44	-	971.6

AHQ-3-7, 7227	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	1.80E-06	0.96	5.15	-	867.0
AHQ-3-7, 6918	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	3.51E-05	0.95	4.42	-	1211.7
AHQ-3-7, 6879 - 6882	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.43E-13	0.97	5.02	-	1196.9
AHQ-3-1, 7048	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	4.79E-12	0.96	4.83	-	1128.0
AHQ-3-11, 6404	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	3.22E-08	0.82	3.76	-	518.4
AHQ-3-12, 6720	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	4.70E-04	0.78	3.39	-	959.2
AHQ-3-13, 6350 - 6431	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.27E-04	0.93	4.56	-	657.7
AHQ-3-13, 6665 - 6673	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.64E-10	0.96	4.75	-	1117.8
AHQ-3-13, 6733 - 6798	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	7.91E-04	0.81	3.06	-	918.2
AHQ-3-13-, 6341 - 6422	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.62E-07	0.96	4.72	-	1108.9
AHQ-3-13-, 6665 - 6677	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	6.75E-07	0.93	3.88	-	1232.1
AHQ-3-14-, 6536	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	3.24E-13	0.95	4.72	-	815.8
gi|13124879|ref|NP_002465.1| smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]				1.51E-13	7.86	100.36	5.30	227336.7
AHQ-3-2, 4998	R.DLGEELEALK.T	1117.23151	2	9.59E-05	0.92	3.71	-	904.9
AHQ-3-3, 4946	R.DLGEELEALK.T	1117.23151	2	1.85E-04	0.93	3.64	-	862.2
AHQ-3-3, 4953	R.DLGEELEALK.T	1117.23151	1	2.58E-05	0.15	2.23	-	345.2
AHQ-3-1, 4970	R.DLGEELEALK.T	1117.23151	2	6.21E-07	0.92	3.77	-	907.5
AHQ-3-2, 4994	R.DLGEELEALK.T	1117.23151	1	1.44E-05	0.16	2.26	-	388.2
AHQ-3-6, 2611 - 2613	R.EDQSILCTGESGAGK.T	1553.63107	2	1.46E-05	0.74	3.44	-	479.5
AHQ-3-4, 2748	R.EDQSILCTGESGAGK.T	1553.63107	2	5.62E-04	0.54	2.63	-	462.1
AHQ-3-2, 2777	R.EDQSILCTGESGAGK.T	1553.63107	2	6.11E-04	0.87	4.14	-	507.3
AHQ-3-2, 2801	K.FDQLLAEEK.N	1093.21165	1	3.39E-05	0.51	1.97	-	803.3
AHQ-3-2, 2810	K.FDQLLAEEK.N	1093.21165	1	1.28E-05	0.58	2.54	-	619.2
AHQ-3-3, 2804	K.FDQLLAEEK.N	1093.21165	1	1.30E-05	0.66	2.70	-	622.8
AHQ-3-1, 2990 - 2993	K.FDQLLAEEK.N	1093.21165	1	5.28E-04	0.70	2.36	-	1155.3
AHQ-3-4, 2778	K.FDQLLAEEK.N	1093.21165	1	2.10E-04	0.72	2.62	-	840.6
AHQ-3-1, 2998	K.FDQLLAEEK.N	1093.21165	2	4.78E-07	0.87	2.97	-	1161.1
AHQ-3-4, 2334 - 2337	K.KEEELQAALAR.L	1258.40643	2	9.66E-04	0.92	3.36	-	1494.0
AHQ-3-5, 2203	K.KEEELQAALAR.L	1258.40643	1	9.42E-07	0.27	1.89	-	504.8
AHQ-3-5, 2197	K.KEEELQAALAR.L	1258.40643	2	8.68E-06	0.92	3.52	-	1376.7
AHQ-3-3, 2570 - 2648	R.KFDQLLAEEK.N	1221.38456	2	5.12E-06	0.88	2.86	-	1265.4
AHQ-3-2, 2577 - 2645	R.KFDQLLAEEK.N	1221.38456	1	9.33E-04	0.34	2.24	-	432.6
AHQ-3-2, 2582 - 2654	R.KFDQLLAEEK.N	1221.38456	2	2.44E-05	0.87	3.22	-	960.9
AHQ-3-1, 2896	R.KFDQLLAEEK.N	1221.38456	2	4.60E-04	0.89	3.31	-	1110.5
AHQ-3-2, 5387	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	3.48E-04	0.77	2.97	-	762.5
AHQ-3-2, 5518 - 5521	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	1.34E-08	0.96	5.11	-	1025.3
AHQ-3-2, 5633	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	8.55E-04	0.70	2.60	-	584.9
AHQ-3-1, 5480	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.01E-05	0.97	5.45	-	1928.9
AHQ-3-3, 5360 - 5370	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	7.82E-06	0.98	5.47	-	2744.3
AHQ-3-5, 5848 - 5853	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	1.10E-09	0.98	6.14	-	1728.0
AHQ-3-5, 6223	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	4.43E-04	0.81	3.87	-	565.2
AHQ-3-2, 6194 - 6219	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	8.48E-09	0.99	6.58	-	2531.2
AHQ-3-2, 6289 - 6359	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	6.71E-11	0.98	6.29	-	1577.0
AHQ-3-3, 6190	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.11E-10	0.98	7.03	-	2446.7
AHQ-3-2, 6523	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	1.62E-10	0.93	3.58	-	1324.0
AHQ-3-2, 6530	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.51E-13	0.97	6.07	-	2293.6
AHQ-3-3, 6184 - 6252	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	1.01E-04	0.93	3.73	-	1399.8
AHQ-3-3, 5356	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	3.38E-04	0.64	2.67	-	515.8
AHQ-3-5, 6252 - 6320	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	3.16E-05	0.94	4.06	-	1363.2
AHQ-3-1, 6250	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	6.63E-06	0.97	5.64	-	2077.3
AHQ-3-2, 5389	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	3.43E-09	0.98	6.84	-	2109.3
AHQ-3-1, 5593	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	1.25E-05	0.68	2.90	-	538.4
AHQ-3-3, 5482	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.49E-09	0.97	5.41	-	1721.9
AHQ-3-2, 2581	R.NCAAYLK.L	840.96726	1	8.21E-04	0.84	2.66	-	852.6
AHQ-3-3, 1938 - 2017	R.NCAAYLK.L	840.96726	1	7.06E-04	0.34	2.20	-	379.2
AHQ-3-9, 5727	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.78E-04	0.81	3.36	-	619.9
AHQ-3-6, 6111	K.QLLQANPILEAFGNAK.T	1727.98540	2	6.74E-08	0.94	4.13	-	956.9
AHQ-3-1, 6334 - 6405	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.99E-07	0.95	3.73	-	1442.1
AHQ-3-2, 6597	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.10E-12	0.93	4.37	-	823.2
AHQ-3-2, 6379 - 6450	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.17E-10	0.96	4.89	-	1002.8
AHQ-3-3, 6412	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.63E-04	0.95	4.25	-	988.9
AHQ-3-3, 6570	K.QLLQANPILEAFGNAK.T	1727.98540	2	5.25E-09	0.94	4.41	-	860.0
AHQ-3-1, 6474	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.38E-05	0.91	3.79	-	716.1
AHQ-3-5, 6179 - 6247	K.QLLQANPILEAFGNAK.T	1727.98540	2	6.80E-09	0.96	4.45	-	1169.4
AHQ-3-1, 6581	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.37E-06	0.94	4.33	-	849.3
AHQ-3-4, 6574 - 6645	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.14E-04	0.91	3.81	-	937.3
AHQ-3-4, 6392 - 6398	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.36E-06	0.94	4.71	-	726.3
AHQ-3-7, 5990	K.QLLQANPILEAFGNAK.T	1727.98540	2	6.93E-04	0.87	2.92	-	879.4
AHQ-3-2, 5933 - 6005	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.02E-07	0.98	6.49	-	2078.2
AHQ-3-2, 4166	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.85E-11	0.97	5.60	-	1379.8
AHQ-3-5, 5652 - 5723	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.95E-08	0.98	6.39	-	1835.1
AHQ-3-2, 5947 - 5961	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.60E-04	0.96	5.53	-	1139.9
AHQ-3-2, 6078	K.TQLEELEDELQATEDAK.L	1963.04334	2	7.04E-05	0.89	3.93	-	598.9
AHQ-3-2, 6165	K.TQLEELEDELQATEDAK.L	1963.04334	2	6.17E-06	0.96	4.77	-	1447.1
AHQ-3-3, 6130 - 6142	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.34E-07	0.92	4.30	-	809.5
AHQ-3-1, 5934	K.TQLEELEDELQATEDAK.L	1963.04334	3	6.19E-07	0.96	5.12	-	1394.9
AHQ-3-6, 5605 - 5613	K.TQLEELEDELQATEDAK.L	1963.04334	2	3.41E-07	0.99	7.27	-	2441.4
AHQ-3-3, 5896	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.47E-04	0.90	3.99	-	1019.8
AHQ-3-7, 5590	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.60E-09	0.97	5.71	-	1398.9
AHQ-3-4, 5844	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.56E-05	0.95	4.91	-	1208.3
AHQ-3-3, 5880 - 5958	K.TQLEELEDELQATEDAK.L	1963.04334	2	6.56E-07	0.96	4.78	-	1513.5
gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				1.62E-13	23.15	270.26	48.30	55901.8
AHQ-3-6, 2085 - 2091	K.AHYGGFTVQNEANK.Y	1536.63020	2	3.61E-06	0.92	4.40	-	923.9
AHQ-3-6, 2253	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.56E-06	0.95	4.21	-	1339.8
AHQ-3-7, 2216	K.AHYGGFTVQNEANK.Y	1536.63020	2	6.31E-08	0.89	3.54	-	806.9
AHQ-3-7, 2019	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.53E-04	0.90	3.73	-	928.9
AHQ-3-13, 4109	K.DNENVVNEYSSELEK.H	1769.80167	2	1.61E-04	0.75	3.24	-	710.0
AHQ-3-7, 3395	K.DNENVVNEYSSELEK.H	1769.80167	2	9.47E-09	0.77	3.36	-	558.5
AHQ-3-11, 3954 - 3970	K.DNENVVNEYSSELEK.H	1769.80167	2	8.49E-05	0.80	3.36	-	868.4
AHQ-3-7, 4043 - 4059	K.DNENVVNEYSSELEK.H	1769.80167	2	6.06E-04	0.82	4.17	-	452.9
AHQ-3-9, 3856 - 3857	K.DNENVVNEYSSELEK.H	1769.80167	2	1.23E-05	0.91	4.28	-	691.8
AHQ-3-6, 4339	K.DNENVVNEYSSELEK.H	1769.80167	2	1.63E-04	0.59	3.02	-	526.8
AHQ-3-6, 4070 - 4093	K.DNENVVNEYSSELEK.H	1769.80167	2	1.68E-09	0.94	4.58	-	1020.2
AHQ-3-1, 4377	K.DNENVVNEYSSELEK.H	1769.80167	2	3.57E-06	0.93	4.08	-	1055.7
AHQ-3-6, 3413	K.EDGGGWWYNR.C	1240.26508	2	1.45E-04	0.73	2.74	-	493.6
AHQ-3-6, 3151 - 3191	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	4.79E-06	0.18	2.57	-	217.6
AHQ-3-7, 3083 - 3090	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	3	9.09E-04	0.82	3.69	-	637.0
AHQ-3-7, 3358 - 3359	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	6.37E-06	0.77	3.81	-	320.7
AHQ-3-8, 3704	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	3.31E-06	0.86	3.65	-	678.8
AHQ-3-6, 3427	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	4.31E-05	0.75	3.45	-	444.0
AHQ-3-6, 3878	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	2.53E-04	0.87	4.17	-	562.3
AHQ-3-9, 3635 - 3639	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	9.10E-08	0.89	4.07	-	716.2
AHQ-3-7, 3839 - 3856	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.78E-04	0.87	3.83	-	588.8
AHQ-3-6, 3879 - 3947	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	3.00E-07	0.87	3.87	-	1021.0
AHQ-3-6, 4194	K.HGTDDGVVWMNWK.G	1545.70374	2	1.49E-06	0.97	4.41	-	1546.5
AHQ-3-6, 3993 - 3997	K.HGTDDGVVWMNWK.G	1545.70374	2	6.07E-12	0.97	4.90	-	1618.2
AHQ-3-7, 3154	K.HGTDDGVVWM*NWK.G	1561.70314	2	1.92E-04	0.98	5.25	-	2064.6

AHQ-3-6, 3225	K.HGTDDGVVWM*NWK.G	1561.70314	2	1.47E-05	0.94	4.18	-	1123.1
AHQ-3-7, 3916	K.HGTDDGVVWMNWK.G	1545.70374	2	1.19E-07	0.90	3.70	-	839.6
AHQ-3-11, 3998	K.HGTDDGVVWMNWK.G	1545.70374	2	2.06E-04	0.96	3.98	-	1804.4
AHQ-3-8, 3770 - 3845	K.HGTDDGVVWMNWK.G	1545.70374	2	9.07E-10	0.97	4.52	-	1267.0
AHQ-3-6, 6317	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	4089.58482	3	3.00E-05	0.80	3.90	-	297.9
AHQ-3-6, 3186	R.KGGETSEMYLIQPDSSVK.P	1970.19049	2	1.70E-04	0.89	3.96	-	755.2
AHQ-3-7, 3302	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.27E-05	0.91	4.65	-	703.8
AHQ-3-6, 3323 - 3395	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	4.00E-08	0.82	4.24	-	429.5
AHQ-3-8, 2981	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.39E-04	0.92	4.49	-	956.2
AHQ-3-6, 3387	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	2.73E-07	0.95	5.19	-	961.3
AHQ-3-6, 2519 - 2529	K.KREEAPSLRPAPPPISGGGYR.A	2236.51908	3	8.76E-08	0.87	3.46	-	1195.9
AHQ-3-6, 6957	R.MGPTELLIEMEDWK.G	1692.97836	2	9.36E-06	0.89	3.46	-	1095.3
AHQ-3-10, 6312	R.MGPTELLIEMEDWK.G	1692.97836	2	5.82E-05	0.91	3.69	-	1219.4
AHQ-3-11, 6474	R.MGPTELLIEMEDWK.G	1692.97836	2	5.49E-06	0.95	4.41	-	1226.8
AHQ-3-6, 5227 - 5294	R.MGPTELLIEM*EDWK.G	1708.97776	2	3.59E-04	0.89	3.82	-	720.5
AHQ-3-7, 4647	R.M*GPTELLIEM*EDWK.G	1724.97716	2	2.75E-05	0.92	4.27	-	652.7
AHQ-3-7, 6950 - 6962	R.MGPTELLIEMEDWK.G	1692.97836	2	4.94E-05	0.96	4.56	-	1435.3
AHQ-3-7, 6342	R.M*GPTELLIEMEDWK.G	1708.97776	2	6.96E-09	0.95	4.47	-	1285.9
AHQ-3-6, 6433 - 6438	R.M*GPTELLIEMEDWK.G	1708.97776	2	5.73E-07	0.97	5.16	-	1664.2
AHQ-3-6, 5674	R.M*GPTELLIEMEDWKGDK.V	2009.29009	2	1.96E-04	0.81	3.82	-	377.8
AHQ-3-6, 5301 - 5317	K.NYCGLPGEYWLGNDK.I	1787.92994	2	1.03E-09	0.91	4.13	-	388.2
AHQ-3-7, 5288 - 5368	K.NYCGLPGEYWLGNDK.I	1787.92994	2	3.54E-07	0.91	3.94	-	490.0
AHQ-3-6, 5826	K.NYCGLPGEYWLGNDK.I	1787.92994	2	6.60E-09	0.90	3.95	-	472.8
AHQ-3-6, 5166 - 5245	K.NYCGLPGEYWLGNDK.I	1787.92994	2	1.79E-06	0.86	4.12	-	320.7
AHQ-3-7, 5946 - 5948	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	2	2.72E-06	0.88	4.32	-	457.5
AHQ-3-6, 6001	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	2	9.32E-09	0.85	3.71	-	436.2
AHQ-3-6, 2813 - 2893	K.REEAPSLRPAPPPISGGGYR.A	2108.34617	3	6.80E-06	0.96	4.50	-	1862.0
AHQ-3-7, 2736	K.REEAPSLRPAPPPISGGGYR.A	2108.34617	3	5.03E-07	0.96	4.80	-	1692.4
AHQ-3-6, 4722	R.TMTIHNGMFFSTYDR.D	1822.05792	2	3.23E-04	0.91	3.57	-	926.3
AHQ-3-6, 3709 - 3761	R.TPCTVSCNIPVVSGK.E	1621.85811	2	1.23E-05	0.91	3.81	-	813.1
AHQ-3-8, 3604	R.TPCTVSCNIPVVSGK.E	1621.85811	2	3.79E-05	0.81	3.37	-	535.5
AHQ-3-7, 3670 - 3698	R.TPCTVSCNIPVVSGK.E	1621.85811	2	1.22E-08	0.62	2.61	-	422.1
AHQ-3-7, 4811	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	4.43E-05	0.47	2.73	-	289.5
AHQ-3-7, 4939 - 4966	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	5.99E-04	0.75	3.38	-	808.0
AHQ-3-7, 4784 - 4856	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	6.55E-13	0.93	4.36	-	1277.7
AHQ-3-8, 4665	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.43E-04	0.48	2.58	-	340.5
AHQ-3-6, 4871 - 4942	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.08E-06	0.61	2.92	-	331.2
AHQ-3-6, 4874 - 4919	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.62E-13	0.94	4.52	-	1300.0
AHQ-3-6, 4969	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	8.29E-09	0.95	4.64	-	1459.1
AHQ-3-7, 4672 - 4676	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.79E-04	0.81	3.25	-	867.3
AHQ-3-8, 4660 - 4673	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	7.55E-10	0.94	4.74	-	1229.8
AHQ-3-6, 4762	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.01E-07	0.94	5.02	-	1191.9
AHQ-3-8, 4397	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.50E-10	0.94	4.68	-	967.1
AHQ-3-6, 4111 - 4186	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	5.71E-05	0.79	3.59	-	500.1
AHQ-3-7, 4675	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	9.15E-07	0.95	4.40	-	1206.6
AHQ-3-7, 4506 - 4574	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	4.99E-07	0.96	4.69	-	1290.6
AHQ-3-9, 3749	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	5.54E-06	0.70	3.34	-	394.5
AHQ-3-6, 4661 - 4695	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	9.82E-09	0.96	5.03	-	1252.2
AHQ-3-9, 4272 - 4281	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	5.97E-06	0.94	4.47	-	908.2
AHQ-3-6, 4525 - 4594	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	2.75E-11	0.95	4.29	-	1201.1
AHQ-3-7, 3943 - 4011	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	2.85E-08	0.91	4.11	-	730.7
AHQ-3-11, 4822 - 4832	R.YYWGGQYTWDMAK.H	1669.84009	2	1.12E-07	0.92	3.37	-	986.3
AHQ-3-7, 4298	R.YYWGGQYTWDM*AK.H	1685.83949	2	4.24E-04	0.76	2.74	-	737.6
AHQ-3-12, 4452	R.YYWGGQYTWDM*AK.H	1685.83949	2	8.79E-05	0.89	3.04	-	1106.5
AHQ-3-12, 5052	R.YYWGGQYTWDMAK.H	1669.84009	2	4.38E-04	0.89	3.48	-	882.6
AHQ-3-6, 5013 - 5025	R.YYWGGQYTWDMAK.H	1669.84009	2	1.46E-06	0.96	4.44	-	1158.4
AHQ-3-14, 5579 - 5656	R.YYWGGQYTWDM*AK.H	1685.83949	2	1.85E-09	0.98	4.51	-	1878.4
AHQ-3-14-, 4455 - 4489	R.YYWGGQYTWDM*AK.H	1685.83949	2	1.07E-05	0.97	4.46	-	1436.0
AHQ-3-6, 4379	R.YYWGGQYTWDM*AK.H	1685.83949	2	4.33E-06	0.94	3.71	-	988.4
gi|29741246|ref|XP_294070.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			1.75E-13	4.34	50.31	14.60	35032.0
AHQ-3-13-, 5299 - 5323	K.AENGKLVINGNPITIFQER.D	2114.39062	2	1.58E-07	0.72	3.57	-	389.6
AHQ-3-9, 5219 - 5291	K.LVINGNPITIFQER.D	1614.87029	2	3.18E-09	0.93	4.08	-	1012.1
AHQ-3-9, 5307 - 5387	K.LVINGNPITIFQER.D	1614.87029	2	4.48E-09	0.94	3.94	-	974.3
AHQ-3-13-, 5581 - 5657	K.LVINGNPITIFQER.D	1614.87029	2	1.15E-10	0.95	4.36	-	1222.7
AHQ-3-10, 5159 - 5235	K.LVINGNPITIFQER.D	1614.87029	2	8.13E-04	0.62	2.63	-	667.3
AHQ-3-11, 5336 - 5406	K.LVINGNPITIFQER.D	1614.87029	2	5.69E-04	0.77	2.86	-	796.5
AHQ-3-14-, 5581 - 5648	K.LVINGNPITIFQER.D	1614.87029	2	1.75E-13	0.95	3.98	-	1404.2
AHQ-3-13, 5693	K.LVINGNPITIFQER.D	1614.87029	2	5.55E-11	0.93	3.75	-	1023.4
AHQ-3-12, 5746	K.LVINGNPITIFQER.D	1614.87029	2	2.50E-07	0.88	3.69	-	674.8
AHQ-3-12, 5619 - 5684	K.LVINGNPITIFQER.D	1614.87029	2	4.65E-09	0.93	3.72	-	1010.1
AHQ-3-13, 5559 - 5625	K.LVINGNPITIFQER.D	1614.87029	2	1.02E-10	0.93	3.67	-	983.1
AHQ-3-9, 4819 - 4889	K.LVINGNPITIFQERDPSK.I	2042.32440	2	2.14E-07	0.84	3.75	-	584.7
AHQ-3-11, 6091	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	2	2.85E-05	0.87	4.45	-	1067.8
AHQ-3-9, 5968 - 6048	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	2	1.20E-04	0.89	4.07	-	975.9
AHQ-3-11, 6654	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	1.09E-10	0.95	6.22	-	1548.3
AHQ-3-11, 6650	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	2	1.12E-05	0.91	3.98	-	1537.3
gi|4557305|ref|NP_000025.1|	aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho			1.93E-13	8.86	100.26	50.30	39419.7
AHQ-3-8, 3749	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	9.04E-07	0.96	5.30	-	1365.4
AHQ-3-9, 5661 - 5723	K.CPLLKPWALTFSYGR.A	1811.13929	2	1.34E-05	0.60	3.05	-	303.5
AHQ-3-11, 5772 - 5803	K.CPLLKPWALTFSYGR.A	1811.13929	2	1.76E-06	0.75	3.11	-	374.1
AHQ-3-8, 5851 - 5920	K.CPLLKPWALTFSYGR.A	1811.13929	2	5.78E-05	0.66	3.07	-	399.5
AHQ-3-8, 3840	K.FSHEEIAMATVTALR.R	1676.91875	2	1.05E-08	0.95	4.12	-	1491.4
AHQ-3-9, 3889	K.FSHEEIAMATVTALR.R	1676.91875	2	4.22E-09	0.96	4.55	-	1325.2
AHQ-3-8, 2549	K.GILAADESTGSIAK.R	1333.47008	1	3.69E-06	0.58	2.91	-	388.0
AHQ-3-9, 2588	K.GILAADESTGSIAK.R	1333.47008	2	1.67E-04	0.93	3.39	-	1321.9
AHQ-3-13-, 2870 - 2871	K.GILAADESTGSIAK.R	1333.47008	2	3.09E-11	0.97	4.15	-	1750.4
AHQ-3-8, 2505 - 2548	K.GILAADESTGSIAK.R	1333.47008	2	7.29E-10	0.97	4.78	-	1686.7
AHQ-3-13, 2902	K.GILAADESTGSIAK.R	1333.47008	2	4.05E-11	0.97	4.77	-	1857.3
AHQ-3-9, 4339	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	4.61E-12	0.74	4.39	-	525.2
AHQ-3-8, 4360 - 4427	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	2.18E-13	0.81	4.88	-	544.4
AHQ-3-10, 4272 - 4275	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	4.52E-07	0.66	4.36	-	274.1
AHQ-3-9, 4005 - 4077	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	1.64E-06	0.78	4.27	-	587.9
AHQ-3-9, 4177 - 4249	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	8.41E-09	0.74	4.27	-	438.3
AHQ-3-8, 4892	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	6.34E-07	0.94	4.72	-	803.7
AHQ-3-9, 4667 - 4677	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.00E-06	0.92	4.09	-	782.2
AHQ-3-9, 4959 - 4968	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.03E-06	0.95	4.68	-	827.3
AHQ-3-8, 4559	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.93E-13	0.97	5.02	-	1404.4
AHQ-3-8, 6084	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	3.57E-05	0.91	3.88	-	748.7
AHQ-3-8, 5875 - 5884	R.YASICQQNGIVPIVEPEILPDGDHDLK.R	3023.36334	3	1.05E-05	0.86	4.76	-	496.8
AHQ-3-11, 5356	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	9.79E-05	0.81	3.98	-	557.4
AHQ-3-8, 5976	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	4.59E-07	0.83	3.52	-	492.8
AHQ-3-8, 4361	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	4.75E-12	0.87	3.80	-	724.5
AHQ-3-8, 4588	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	1.77E-04	0.69	2.82	-	481.5
AHQ-3-8, 4132 - 4205	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	2.35E-07	0.92	4.51	-	713.1
AHQ-3-8, 5825	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	6.88E-04	0.34	2.58	-	346.0
AHQ-3-9, 4063	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	2.34E-05	0.58	2.67	-	414.5
gi|4501891|ref|NP_001093.1|	actinin, alpha 1 [Homo sapiens]			2.93E-13	42.36	480.33	53.40	103056.9

AHQ-3-6, 7409	R.AAPFNNWM*EGAMEDLQDTFIVHTIEEIQGLTTAHEQFK.A	4380.81962	3	1.36E-04	0.84	4.73	-	856.3
AHQ-3-5, 7665 - 7667	R.AAPFNNWMEGAMEDLQDTFIVHTIEEIQGLTTAHEQFK.A	4364.82022	3	9.74E-11	0.95	6.21	-	1048.7
AHQ-3-5, 7588 - 7609	R.AAPFNNWMEGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4380.81962	3	1.10E-07	0.87	5.60	-	902.7
AHQ-3-6, 5215	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.47E-05	0.70	3.61	-	782.1
AHQ-3-5, 5257 - 5263	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.22E-05	0.78	4.36	-	709.4
AHQ-3-12, 5268	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.01E-06	0.69	4.05	-	593.2
AHQ-3-9, 4843 - 4849	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	3.42E-04	0.42	3.50	-	245.8
AHQ-3-9, 6023	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	3.24E-07	0.88	3.89	-	625.1
AHQ-3-5, 5433 - 5435	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	9.77E-08	0.93	4.56	-	763.0
AHQ-3-6, 6439 - 6490	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	3.44E-06	0.95	4.96	-	756.7
AHQ-3-7, 6288	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.00E-05	0.52	2.53	-	502.2
AHQ-3-5, 6517 - 6585	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.42E-07	0.96	5.05	-	992.0
AHQ-3-5, 3287 - 3288	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	1.23E-04	0.68	2.74	-	514.6
AHQ-3-5, 3023	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	1.49E-05	0.96	4.31	-	2219.3
AHQ-3-6, 3003	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	7.41E-04	0.81	3.26	-	691.9
AHQ-3-4, 3229	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	2.74E-04	0.71	3.19	-	397.8
AHQ-3-5, 3293	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	3.00E-05	0.93	4.04	-	1782.7
AHQ-3-5, 1935	K.ASIHEAWTDGK.E	1215.29697	1	7.05E-07	0.74	3.01	-	547.8
AHQ-3-5, 1869 - 1939	K.ASIHEAWTDGK.E	1215.29697	2	1.64E-04	0.92	3.57	-	1022.7
AHQ-3-6, 1925	K.ASIHEAWTDGK.E	1215.29697	2	2.64E-09	0.64	2.57	-	724.6
AHQ-3-6, 1922 - 1926	K.ASIHEAWTDGK.E	1215.29697	1	7.09E-06	0.39	2.00	-	619.4
AHQ-3-5, 4995	R.CQKICDQWDNLGALTQK.R	2081.31600	2	1.47E-09	0.84	3.61	-	649.8
AHQ-3-3, 5946	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	9.07E-06	0.88	3.67	-	860.2
AHQ-3-5, 5271	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.24E-06	0.88	3.73	-	786.6
AHQ-3-5, 5901	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.43E-05	0.88	3.52	-	886.5
AHQ-3-5, 5791 - 5863	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	9.81E-11	0.97	5.44	-	1416.9
AHQ-3-5, 6156 - 6157	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.02E-11	0.97	4.82	-	1496.8
AHQ-3-6, 5671	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	7.02E-07	0.94	4.78	-	899.1
AHQ-3-1, 5945	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	6.04E-06	0.74	3.18	-	504.1
AHQ-3-4, 5901	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.61E-06	0.92	3.70	-	1052.4
AHQ-3-6, 4794	K.DGLGFCALIHR.H	1260.44730	2	6.06E-09	0.93	2.88	-	1601.3
AHQ-3-5, 4932	K.DGLGFCALIHR.H	1260.44730	2	1.33E-06	0.92	3.09	-	1234.5
AHQ-3-5, 2273	R.DHSGTLGPEEFK.A	1317.38606	1	5.06E-04	0.60	2.95	-	325.5
AHQ-3-6, 2262	R.DHSGTLGPEEFK.A	1317.38606	2	9.07E-05	0.92	3.23	-	985.3
AHQ-3-5, 2269 - 2281	R.DHSGTLGPEEFK.A	1317.38606	2	6.50E-05	0.92	3.47	-	924.2
AHQ-3-5, 3671	K.DYETATLSEIK.A	1270.36761	2	6.24E-06	0.94	3.61	-	1289.4
AHQ-3-4, 3486 - 3560	R.ELPPDQAEYCIAR.M	1563.71392	2	1.41E-05	0.55	2.86	-	318.9
AHQ-3-5, 3471 - 3539	R.ELPPDQAEYCIAR.M	1563.71392	2	8.71E-08	0.65	2.60	-	224.4
AHQ-3-13, 4331 - 4337	R.ETADTDTADQVMASFK.I	1730.83208	2	7.62E-04	0.85	3.20	-	823.1
AHQ-3-5, 4557	R.ETADTDTADQVMASFK.I	1730.83208	2	2.84E-04	0.68	2.68	-	640.1
AHQ-3-5, 4411 - 4436	R.ETADTDTADQVMASFK.I	1730.83208	2	8.32E-11	0.95	4.14	-	1296.6
AHQ-3-6, 4345 - 4362	R.ETADTDTADQVMASFK.I	1730.83208	2	1.04E-06	0.96	4.50	-	1471.8
AHQ-3-13-, 4354	R.ETADTDTADQVMASFK.I	1730.83208	2	4.24E-09	0.92	3.72	-	1194.7
AHQ-3-4, 4565 - 4577	R.ETADTDTADQVMASFK.I	1730.83208	2	4.66E-08	0.96	4.64	-	1225.8
AHQ-3-11, 4192 - 4262	R.ETADTDTADQVMASFK.I	1730.83208	2	1.04E-06	0.74	2.80	-	673.1
AHQ-3-3, 4634	R.ETADTDTADQVMASFK.I	1730.83208	2	1.76E-05	0.92	3.76	-	1030.6
AHQ-3-14, 3949	R.ETADTDTADQVM*ASFK.I	1746.83148	2	5.08E-05	0.50	2.87	-	180.5
AHQ-3-13-, 3203	R.ETADTDTADQVM*ASFK.I	1746.83148	2	9.43E-09	0.96	5.11	-	1030.0
AHQ-3-5, 2723 - 2724	K.GISQEQMNEFR.A	1339.45991	2	3.60E-07	0.90	3.22	-	947.9
AHQ-3-4, 2202	K.GISQEQM*NEFR.A	1355.45931	2	4.51E-05	0.76	3.01	-	655.8
AHQ-3-6, 2734	K.GISQEQMNEFR.A	1339.45991	2	1.02E-05	0.86	3.03	-	902.0
AHQ-3-1, 2365	K.GISQEQM*NEFR.A	1355.45931	2	1.57E-06	0.88	3.35	-	891.4
AHQ-3-5, 2493	K.GISQEQMNEFR.A	1339.45991	2	7.05E-05	0.78	2.99	-	660.7
AHQ-3-5, 1784	R.HRPELIDYGK.L	1228.38202	2	3.16E-04	0.85	3.41	-	555.3
AHQ-3-4, 2049 - 2056	R.HRPELIDYGK.L	1228.38202	2	3.05E-04	0.92	3.81	-	645.3
AHQ-3-6, 4869 - 4873	K.ICDQWDNLGALTQK.R	1663.83349	2	6.38E-07	0.97	4.63	-	2065.0
AHQ-3-5, 4660 - 4668	K.ICDQWDNLGALTQK.R	1663.83349	2	5.08E-06	0.95	4.49	-	1089.0
AHQ-3-5, 4899 - 4967	K.ICDQWDNLGALTQK.R	1663.83349	2	7.69E-06	0.98	5.29	-	2440.0
AHQ-3-3, 5129 - 5156	K.ICDQWDNLGALTQK.R	1663.83349	2	7.31E-07	0.97	4.42	-	2233.3
AHQ-3-7, 4826	K.ICDQWDNLGALTQK.R	1663.83349	2	6.44E-05	0.74	2.91	-	1052.6
AHQ-3-4, 5076	K.ICDQWDNLGALTQK.R	1663.83349	2	3.68E-07	0.97	4.75	-	2267.2
AHQ-3-6, 5842 - 5853	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	1.35E-09	0.97	5.87	-	1649.1
AHQ-3-4, 6072	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	1.91E-09	0.97	5.27	-	2048.8
AHQ-3-5, 5849 - 5915	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	1.13E-07	0.98	6.70	-	1177.8
AHQ-3-5, 5856 - 5929	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	6.41E-07	0.96	5.46	-	1768.2
AHQ-3-5, 3227 - 3292	K.ILAGDKNYITM*DELR.R	1769.01293	2	5.41E-04	0.90	4.08	-	633.4
AHQ-3-6, 3271	K.ILAGDKNYITM*DELR.R	1769.01293	2	2.38E-04	0.65	3.51	-	353.8
AHQ-3-5, 3984 - 3991	K.ILAGDKNYITMDELR.R	1753.01353	2	7.39E-11	0.96	5.02	-	1247.0
AHQ-3-5, 2611 - 2619	R.IMSIVDPNR.L	1045.23840	2	1.81E-04	0.87	3.41	-	746.2
AHQ-3-6, 4807	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	2	3.05E-07	0.59	2.59	-	839.5
AHQ-3-5, 4852 - 4923	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	2	7.56E-09	0.94	4.71	-	978.9
AHQ-3-5, 4155	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	2	5.45E-08	0.89	4.29	-	450.0
AHQ-3-5, 4015 - 4055	K.IVQTYHVNM*AGTNPYTTITPQEINGK.W	2908.23575	3	1.18E-04	0.82	3.92	-	586.1
AHQ-3-5, 4704	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	9.99E-05	0.80	3.78	-	443.5
AHQ-3-5, 4579 - 4583	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	6.29E-10	0.96	5.26	-	1159.9
AHQ-3-5, 4607	R.KAGTQIENIEEDFRDGLK.L	2064.24210	3	6.97E-06	0.93	5.94	-	1161.6
AHQ-3-1, 5137	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	2.61E-07	0.95	4.78	-	1153.8
AHQ-3-5, 4807	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	6.95E-08	0.95	4.53	-	964.6
AHQ-3-4, 4972	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	9.83E-09	0.95	4.75	-	1069.0
AHQ-3-8, 4461	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	4.20E-06	0.95	4.45	-	1051.0
AHQ-3-6, 4761	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	3.22E-06	0.97	5.22	-	1282.4
AHQ-3-5, 4827 - 4895	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	8.00E-13	0.97	6.18	-	1217.9
AHQ-3-4, 4258 - 4328	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	5.98E-04	0.94	4.02	-	1194.6
AHQ-3-5, 4039 - 4107	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	5.16E-05	0.89	4.06	-	823.5
AHQ-3-5, 3509 - 3580	R.LAILGIHNEVSK.I	1294.52505	2	2.98E-04	0.93	3.14	-	1141.2
AHQ-3-5, 3011 - 3081	R.LAILGIHNEVSK.I	1294.52505	1	1.04E-04	0.25	1.95	-	355.3
AHQ-3-6, 2889 - 3030	R.LAILGIHNEVSK.I	1294.52505	1	1.22E-04	0.74	3.31	-	381.3
AHQ-3-6, 3009 - 3017	R.LAILGIHNEVSK.I	1294.52505	2	2.23E-08	0.95	4.00	-	1136.5
AHQ-3-7, 2912	R.LAILGIHNEVSK.I	1294.52505	2	1.65E-04	0.80	2.61	-	828.6
AHQ-3-5, 3008 - 3079	R.LAILGIHNEVSK.I	1294.52505	2	7.26E-07	0.91	3.80	-	874.0
AHQ-3-4, 3246	R.LAILGIHNEVSK.I	1294.52505	2	3.59E-07	0.96	4.38	-	1311.8
AHQ-3-1, 6344	K.LASDLLEWIR.R	1216.41115	2	5.64E-07	0.97	4.40	-	1910.1
AHQ-3-5, 6007 - 6077	K.LASDLLEWIR.R	1216.41115	2	3.47E-08	0.98	4.71	-	2383.8
AHQ-3-4, 6220	K.LASDLLEWIR.R	1216.41115	2	1.50E-06	0.96	3.88	-	1748.8
AHQ-3-6, 5953	K.LASDLLEWIR.R	1216.41115	2	3.31E-07	0.96	3.90	-	1761.5
AHQ-3-1, 6706 - 6782	K.LLETIDQLYLEYAK.R	1712.96427	2	2.28E-08	0.94	3.98	-	1191.2
AHQ-3-5, 5437	K.LLETIDQLYLEYAK.R	1712.96427	2	1.69E-08	0.93	4.04	-	877.8
AHQ-3-3, 6850	K.LLETIDQLYLEYAK.R	1712.96427	2	7.62E-07	0.93	4.16	-	866.8
AHQ-3-5, 6936	K.LLETIDQLYLEYAK.R	1712.96427	2	6.39E-07	0.97	4.62	-	1339.2
AHQ-3-5, 6793 - 6867	K.LLETIDQLYLEYAK.R	1712.96427	2	2.02E-05	0.97	4.98	-	1206.0
AHQ-3-5, 6708 - 6727	K.LLETIDQLYLEYAK.R	1712.96427	2	4.22E-09	0.97	5.15	-	1377.8
AHQ-3-4, 6848	K.LLETIDQLYLEYAK.R	1712.96427	2	2.97E-07	0.97	5.08	-	1241.6
AHQ-3-7, 6567	K.LLETIDQLYLEYAK.R	1712.96427	2	2.01E-04	0.95	3.69	-	1404.0
AHQ-3-6, 6577 - 6641	K.LLETIDQLYLEYAK.R	1712.96427	2	5.53E-07	0.96	4.58	-	1308.7
AHQ-3-5, 7025 - 7101	K.LLETIDQLYLEYAK.R	1712.96427	2	2.35E-07	0.94	3.89	-	1310.4
AHQ-3-5, 1923	R.LSNRPAFM*PSEGR.M	1478.65881	3	1.90E-05	0.82	3.56	-	880.4
AHQ-3-5, 3817	K.MLDAEDIVGTARPDEK.A	1760.94769	2	9.48E-05	0.86	3.66	-	874.9

AHQ-3-6, 3762	K.MLDAEDIVGTARPDEK.A	1760.94769	2	8.90E-06	0.85	3.83	-	825.5
AHQ-3-5, 3821	K.MLDAEDIVGTARPDEK.A	1760.94769	3	5.95E-06	0.89	4.23	-	795.1
AHQ-3-4, 3568 - 3570	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	5.15E-04	0.89	3.51	-	831.1
AHQ-3-7, 3722	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.20E-05	0.84	3.35	-	1030.9
AHQ-3-4, 3972	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.66E-05	0.91	4.06	-	1075.9
AHQ-3-5, 3391	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	8.69E-04	0.87	4.08	-	556.3
AHQ-3-6, 3345 - 3346	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	6.40E-04	0.94	4.51	-	872.4
AHQ-3-1, 3774	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	4.53E-06	0.84	3.58	-	634.3
AHQ-3-1, 3790	K.M*LDAEDIVGTARPDEK.A	1776.94709	3	2.13E-04	0.74	3.20	-	904.5
AHQ-3-8, 3630 - 3633	K.MLDAEDIVGTARPDEK.A	1760.94769	2	1.45E-06	0.93	4.39	-	1019.6
AHQ-3-8, 3636	K.MLDAEDIVGTARPDEK.A	1760.94769	3	3.09E-06	0.66	3.23	-	554.7
AHQ-3-9, 3469 - 3535	K.MLDAEDIVGTARPDEK.A	1760.94769	2	3.75E-04	0.82	3.38	-	761.4
AHQ-3-5, 6176	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	8.00E-06	0.91	3.77	-	1014.3
AHQ-3-1, 5642	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.56E-09	0.95	4.50	-	1061.5
AHQ-3-5, 6032	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.65E-10	0.97	5.13	-	1590.5
AHQ-3-5, 5301 - 5371	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.18E-10	0.98	5.89	-	1595.2
AHQ-3-5, 5448	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.43E-04	0.93	4.07	-	980.9
AHQ-3-5, 5777	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.49E-05	0.90	3.76	-	714.8
AHQ-3-4, 5836 - 5838	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	3.59E-05	0.92	4.31	-	900.4
AHQ-3-6, 5839	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	8.80E-08	0.85	3.28	-	981.4
AHQ-3-6, 5582	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.17E-05	0.93	4.39	-	806.2
AHQ-3-6, 5518	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	4.92E-07	0.86	3.48	-	935.4
AHQ-3-6, 5494 - 5513	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.66E-07	0.96	4.69	-	1453.7
AHQ-3-5, 5667	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.58E-08	0.97	5.53	-	1513.6
AHQ-3-6, 5350	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.24E-10	0.96	4.29	-	1697.4
AHQ-3-6, 5281	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	2.58E-04	0.58	3.03	-	543.5
AHQ-3-5, 5453	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	2.82E-04	0.47	2.64	-	400.9
AHQ-3-5, 5587 - 5613	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.05E-10	0.97	5.32	-	1294.9
AHQ-3-4, 5524	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	5.40E-04	0.85	3.97	-	610.2
AHQ-3-3, 5885	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	9.40E-06	0.84	3.33	-	798.8
AHQ-3-5, 5560 - 5596	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	5.47E-08	0.93	4.09	-	1233.1
AHQ-3-5, 5188 - 5216	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	8.29E-07	0.94	4.43	-	930.4
AHQ-3-6, 4466	K.NVNIQNFHISWK.D	1500.68583	2	2.03E-08	0.96	4.11	-	1389.5
AHQ-3-5, 4463 - 4536	K.NVNIQNFHISWK.D	1500.68583	2	1.09E-07	0.96	4.46	-	1333.4
AHQ-3-4, 4780	K.NVNIQNFHISWK.D	1500.68583	2	1.93E-04	0.95	4.27	-	1243.8
AHQ-3-5, 4800	K.NVNIQNFHISWK.D	1500.68583	2	9.30E-06	0.96	4.10	-	1319.4
AHQ-3-10, 4211	K.NVNIQNFHISWK.D	1500.68583	2	1.12E-04	0.90	3.47	-	959.4
AHQ-3-5, 3504	K.NYITMDELR.R	1155.30648	2	7.72E-05	0.83	3.39	-	632.8
AHQ-3-5, 2687	R.QKDYETATLSEIK.A	1526.67030	2	6.43E-04	0.46	2.85	-	272.2
AHQ-3-10, 3630	R.TINEVENQILTR.D	1430.58898	2	2.70E-06	0.87	3.34	-	966.7
AHQ-3-5, 2947 - 3004	R.TINEVENQILTR.D	1430.58898	1	4.71E-04	0.08	1.98	-	124.0
AHQ-3-5, 3960 - 4036	R.TINEVENQILTR.D	1430.58898	2	7.59E-05	0.90	3.60	-	1044.4
AHQ-3-8, 3617 - 3692	R.TINEVENQILTR.D	1430.58898	2	2.96E-04	0.81	2.98	-	988.1
AHQ-3-6, 3741 - 3745	R.TINEVENQILTR.D	1430.58898	2	1.01E-07	0.90	3.98	-	898.3
AHQ-3-2, 4059	R.TINEVENQILTR.D	1430.58898	2	2.62E-05	0.82	3.38	-	880.4
AHQ-3-4, 3952	R.TINEVENQILTR.D	1430.58898	1	8.13E-05	0.20	2.42	-	139.1
AHQ-3-4, 3937 - 3940	R.TINEVENQILTR.D	1430.58898	2	1.05E-07	0.95	4.58	-	1214.6
AHQ-3-4, 3573	R.TINEVENQILTR.D	1430.58898	2	6.53E-05	0.73	3.05	-	485.9
AHQ-3-7, 3704	R.TINEVENQILTR.D	1430.58898	1	4.89E-05	0.22	2.54	-	118.2
AHQ-3-7, 3690	R.TINEVENQILTR.D	1430.58898	2	2.21E-04	0.71	3.20	-	586.1
AHQ-3-3, 4009	R.TINEVENQILTR.D	1430.58898	2	2.76E-06	0.91	3.64	-	946.0
AHQ-3-6, 3365	R.TINEVENQILTR.D	1430.58898	2	2.05E-04	0.71	2.63	-	487.1
AHQ-3-5, 3784	R.TINEVENQILTR.D	1430.58898	1	1.54E-04	0.51	2.70	-	164.7
AHQ-3-5, 7083 - 7147	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.53E-09	0.98	6.68	-	2239.9
AHQ-3-5, 7051 - 7116	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	1.29E-06	0.97	5.59	-	1238.7
AHQ-3-5, 7143 - 7207	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	1.24E-05	0.82	3.30	-	728.1
AHQ-3-10, 5998	R.VGWEQLLTTIAR.T	1387.60894	2	1.20E-04	0.86	3.01	-	1047.7
AHQ-3-6, 6613	R.VGWEQLLTTIAR.T	1387.60894	2	1.01E-05	0.94	3.99	-	1353.5
AHQ-3-2, 7018 - 7019	R.VGWEQLLTTIAR.T	1387.60894	2	2.95E-09	0.97	4.91	-	2005.9
AHQ-3-14-, 6408	R.VGWEQLLTTIAR.T	1387.60894	2	2.59E-07	0.94	3.61	-	1457.1
AHQ-3-9, 6247 - 6263	R.VGWEQLLTTIAR.T	1387.60894	2	5.68E-08	0.96	4.42	-	1689.9
AHQ-3-1, 6908 - 6910	R.VGWEQLLTTIAR.T	1387.60894	2	5.33E-08	0.97	5.04	-	1784.0
AHQ-3-8, 6317	R.VGWEQLLTTIAR.T	1387.60894	2	2.98E-04	0.94	3.57	-	1617.5
AHQ-3-4, 6908 - 6910	R.VGWEQLLTTIAR.T	1387.60894	2	7.97E-08	0.96	4.73	-	1353.0
AHQ-3-5, 6695 - 6771	R.VGWEQLLTTIAR.T	1387.60894	2	1.58E-07	0.95	4.12	-	1404.8
AHQ-3-7, 6527 - 6530	R.VGWEQLLTTIAR.T	1387.60894	2	3.02E-08	0.97	4.58	-	1730.9
AHQ-3-3, 6924	R.VGWEQLLTTIAR.T	1387.60894	2	9.92E-10	0.95	3.96	-	1500.2
AHQ-3-11, 6224	R.VGWEQLLTTIAR.T	1387.60894	2	2.05E-07	0.95	4.21	-	1488.2
AHQ-3-4, 4700	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.90E-06	0.76	3.76	-	366.2
AHQ-3-3, 4430	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.20E-07	0.88	4.01	-	767.7
AHQ-3-8, 3850	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.79E-08	0.95	4.67	-	1042.6
AHQ-3-5, 3435 - 3463	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	5.10E-07	0.95	4.85	-	1133.9
AHQ-3-7, 4050 - 4128	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.45E-05	0.94	4.33	-	984.5
AHQ-3-4, 3792	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	9.32E-07	0.72	2.60	-	532.6
AHQ-3-5, 4637	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	6.86E-08	0.97	5.70	-	1687.6
AHQ-3-5, 4167 - 4247	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.63E-08	0.97	5.56	-	1469.0
AHQ-3-4, 3605 - 3620	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.12E-04	0.91	3.73	-	925.1
AHQ-3-6, 4411 - 4485	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	5.45E-09	0.89	3.84	-	596.3
AHQ-3-5, 4315 - 4391	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.39E-07	0.98	5.66	-	1671.6
AHQ-3-2, 4490	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.53E-05	0.88	3.27	-	1057.3
AHQ-3-6, 3410	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.42E-05	0.95	4.36	-	1238.3
AHQ-3-5, 4460 - 4531	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.93E-13	0.96	4.91	-	1395.6
AHQ-3-6, 4102	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.64E-09	0.95	4.42	-	1349.5
AHQ-3-5, 4264	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.96E-05	0.87	3.34	-	867.1
AHQ-3-1, 4504	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	5.17E-08	0.96	4.33	-	1562.0
AHQ-3-4, 4324 - 4392	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.53E-04	0.91	4.05	-	804.2
AHQ-3-5, 3675	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.48E-09	0.94	4.48	-	877.5
AHQ-3-5, 1549	R.VPENTMHAMQQK.L	1414.63656	1	1.65E-05	0.45	2.70	-	273.6
gi|5902128|ref|NP_008880.1|	syntaxin binding protein 2; Hunc18b [Homo sapiens]			3.66E-13	6.53	70.34	18.90	66438.1
AHQ-3-6, 6331	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	2	4.79E-07	0.97	5.36	-	1287.0
AHQ-3-6, 6626	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	1.22E-07	0.90	3.36	-	949.1
AHQ-3-6, 2931	R.KGPEDTAQLAHAVLAK.L	1649.87303	3	2.19E-09	0.97	5.44	-	1678.4
AHQ-3-6, 2921	R.KGPEDTAQLAHAVLAK.L	1649.87303	2	3.00E-08	0.93	4.13	-	1003.1
AHQ-3-6, 6383 - 6389	K.LIVPVLLDAAVPAYDK.I	1698.03911	2	3.66E-13	0.98	5.31	-	2135.0
AHQ-3-6, 3063	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	8.54E-06	0.96	5.13	-	1013.8
AHQ-3-6, 5354 - 5425	R.NLWPFVSDPAPTASSQAAVSAR.F	2273.48981	2	7.69E-04	0.78	3.20	-	555.5
AHQ-3-6, 5909 - 5933	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	5.95E-06	0.98	6.76	-	1841.4
gi|4501881|ref|NP_001091.1|	alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA			4.05E-13	14.46	190.28	46.20	42050.8
AHQ-3-12, 1822 - 1882	K.AGFAGDDAPR.A	977.01283	2	2.62E-05	0.90	2.89	-	1272.7
AHQ-3-13-, 1777 - 1846	K.AGFAGDDAPR.A	977.01283	2	9.86E-04	0.88	2.94	-	1066.4
AHQ-3-13-, 1905 - 1933	K.AGFAGDDAPR.A	977.01283	2	2.86E-04	0.91	3.16	-	1171.9
AHQ-3-8, 1447 - 1529	K.AGFAGDDAPR.A	977.01283	2	1.07E-05	0.85	2.66	-	1111.4
AHQ-3-8, 2850 - 2920	R.AVFPSIVGR.P	946.12815	2	4.52E-05	0.78	2.65	-	649.8
AHQ-3-8, 2704	R.AVFPSIVGRPR.H	1199.43018	2	2.60E-04	0.63	2.76	-	459.4
AHQ-3-7, 2644 - 2724	R.AVFPSIVGRPR.H	1199.43018	2	4.03E-04	0.56	2.65	-	407.7
AHQ-3-10, 2834 - 2851	R.AVFPSIVGRPR.H	1199.43018	2	1.60E-04	0.54	2.54	-	508.4
AHQ-3-1, 3937	R.DLTDYLM*K.I	1015.16266	2	1.03E-04	0.67	2.71	-	427.0

AHQ-3-14, 5331	R.DLTDYLMK.I	999.16326	1	7.72E-04	0.20	1.91	-	502.7
AHQ-3-8, 3720	R.DLTDYLMK.I	999.16326	1	1.88E-04	0.19	2.10	-	237.4
AHQ-3-8, 4331	R.DLTDYLMK.I	999.16326	2	5.53E-04	0.74	3.01	-	379.6
AHQ-3-12, 4387	R.DLTDYLMK.I	999.16326	1	7.02E-04	0.43	2.57	-	554.2
AHQ-3-14, 5335	R.DLTDYLMK.I	999.16326	1	2.19E-04	0.15	2.18	-	326.3
AHQ-3-14-, 4308	R.DLTDYLMK.I	999.16326	1	8.88E-05	0.31	2.12	-	515.5
AHQ-3-9, 3455	R.DLTDYLM*K.I	1015.16266	1	1.19E-04	0.30	1.97	-	123.5
AHQ-3-4, 3832	R.DLTDYLM*K.I	1015.16266	1	6.62E-04	0.64	2.76	-	160.6
AHQ-3-10, 3147	R.DLTDYLMK.I	999.16326	1	7.67E-06	0.34	2.03	-	392.2
AHQ-3-9, 4157	R.DLTDYLM*K.I	1015.16266	1	2.49E-04	0.46	2.24	-	257.7
AHQ-3-10, 4398	R.DLTDYLMK.I	999.16326	1	1.36E-04	0.18	1.94	-	384.8
AHQ-3-9, 4159 - 4163	R.DLTDYLMK.I	999.16326	1	4.72E-04	0.20	2.74	-	358.6
AHQ-3-8, 5153 - 5235	K.DLYANNVMSGGTTMYPGIADR.M	2247.49444	2	5.51E-04	0.65	3.06	-	504.3
AHQ-3-14-, 5311 - 5312	K.DLYANNVMSGGTTMYPGIADR.M	2247.49444	2	2.54E-05	0.73	3.58	-	347.3
AHQ-3-12, 1714	K.DSYVGDEAQSK.R	1199.20634	2	2.08E-05	0.82	2.86	-	555.3
AHQ-3-8, 1449 - 1516	K.DSYVGDEAQSK.R	1199.20634	1	7.18E-05	0.59	2.91	-	429.7
AHQ-3-8, 1448 - 1528	K.DSYVGDEAQSK.R	1199.20634	2	7.46E-06	0.87	2.82	-	835.3
AHQ-3-8, 1733 - 1769	K.DSYVGDEAQSK.R	1199.20634	2	4.91E-04	0.78	3.09	-	483.3
AHQ-3-8, 1432	K.DSYVGDEAQSKR.G	1355.39270	2	1.09E-06	0.85	2.75	-	713.9
AHQ-3-13, 2335 - 2415	K.EITALAPSTM*K.I	1178.38146	2	7.77E-04	0.78	3.11	-	667.2
AHQ-3-13, 2882 - 2957	K.EITALAPSTMK.I	1162.38206	2	2.78E-04	0.69	2.59	-	513.9
AHQ-3-13-, 2850 - 2914	K.EITALAPSTMK.I	1162.38206	2	5.13E-04	0.88	3.11	-	932.0
AHQ-3-14-, 2279 - 2355	K.EITALAPSTM*K.I	1178.38146	2	2.06E-05	0.84	3.32	-	673.1
AHQ-3-6, 2725	K.EITALAPSTMK.I	1162.38206	1	4.83E-05	0.23	2.21	-	228.5
AHQ-3-14-, 2751 - 2795	K.EITALAPSTMK.I	1162.38206	2	1.03E-04	0.83	2.94	-	649.8
AHQ-3-8, 2517 - 2552	K.EITALAPSTM*K.I	1178.38146	2	7.16E-05	0.85	3.04	-	786.9
AHQ-3-8, 2246 - 2316	K.EITALAPSTMK.I	1162.38206	2	3.13E-04	0.92	3.33	-	987.5
AHQ-3-12, 2879	K.EITALAPSTMK.I	1162.38206	1	8.18E-04	0.28	2.56	-	250.4
AHQ-3-14-, 2859 - 2860	K.EITALAPSTMK.I	1162.38206	2	4.48E-04	0.90	3.33	-	814.3
AHQ-3-1, 3109	K.EITALAPSTMK.I	1162.38206	2	2.26E-04	0.82	3.10	-	625.0
AHQ-3-12, 2874	K.EITALAPSTMK.I	1162.38206	2	8.77E-05	0.72	2.80	-	484.2
AHQ-3-7, 2606	K.EITALAPSTMK.I	1162.38206	1	5.63E-04	0.55	2.44	-	312.7
AHQ-3-8, 1956 - 2028	K.EITALAPSTM*K.I	1178.38146	2	2.60E-07	0.83	3.01	-	702.1
AHQ-3-8, 2266 - 2297	R.HQGVMVGMGQKDSYVGDEAQSK.R	2352.59065	3	1.27E-05	0.82	3.35	-	1205.7
AHQ-3-8, 2256 - 2328	K.IWHHTFYNELR.V	1516.68695	2	2.22E-07	0.90	3.63	-	1011.8
AHQ-3-9, 2628 - 2687	K.IWHHTFYNELR.V	1516.68695	2	2.16E-06	0.81	3.05	-	721.1
AHQ-3-8, 2293 - 2308	K.IWHHTFYNELR.V	1516.68695	3	8.75E-06	0.91	4.45	-	1260.3
AHQ-3-8, 2377 - 2445	K.IWHHTFYNELR.V	1516.68695	3	7.16E-05	0.97	4.81	-	1747.8
AHQ-3-12, 3175	K.IWHHTFYNELR.V	1516.68695	2	4.04E-05	0.88	3.36	-	852.8
AHQ-3-7, 2558 - 2576	K.IWHHTFYNELR.V	1516.68695	2	1.39E-07	0.82	3.16	-	802.3
AHQ-3-8, 2717 - 2744	K.IWHHTFYNELR.V	1516.68695	2	2.46E-09	0.92	3.68	-	884.9
AHQ-3-8, 2738 - 2748	K.IWHHTFYNELR.V	1516.68695	3	1.06E-05	0.96	4.28	-	2017.7
AHQ-3-7, 2547	K.IWHHTFYNELR.V	1516.68695	3	1.10E-04	0.96	4.32	-	1793.6
AHQ-3-12, 3040	K.IWHHTFYNELR.V	1516.68695	3	5.81E-06	0.92	3.45	-	1736.1
AHQ-3-1, 3162	K.IWHHTFYNELR.V	1516.68695	2	8.56E-04	0.60	3.03	-	596.4
AHQ-3-12, 3038	K.IWHHTFYNELR.V	1516.68695	2	3.99E-07	0.93	3.62	-	1106.3
AHQ-3-12, 2878 - 2891	K.IWHHTFYNELR.V	1516.68695	3	4.86E-07	0.91	4.39	-	1394.4
AHQ-3-12, 2875 - 2942	K.IWHHTFYNELR.V	1516.68695	2	7.64E-05	0.77	3.39	-	735.7
AHQ-3-13-, 2981	K.IWHHTFYNELR.V	1516.68695	2	4.11E-06	0.85	3.40	-	914.2
AHQ-3-13-, 2987	K.IWHHTFYNELR.V	1516.68695	3	5.61E-06	0.97	4.53	-	1761.6
AHQ-3-3, 2909	K.IWHHTFYNELR.V	1516.68695	2	3.53E-06	0.78	3.40	-	740.3
AHQ-3-9, 2788	K.IWHHTFYNELR.V	1516.68695	2	3.87E-06	0.85	3.19	-	825.1
AHQ-3-6, 2653	K.IWHHTFYNELR.V	1516.68695	2	4.25E-04	0.65	2.93	-	691.4
AHQ-3-9, 2401 - 2464	K.IWHHTFYNELR.V	1516.68695	2	1.58E-05	0.72	3.23	-	750.7
AHQ-3-8, 7440	K.LCYVALDFENEM*ATAASSSSLEK.S	2554.78938	3	1.25E-04	0.95	5.09	-	1567.8
AHQ-3-10, 4814 - 4844	R.LDLAGRDLTDYLMK.I	1624.88375	2	3.38E-05	0.84	3.72	-	696.9
AHQ-3-8, 4844 - 4917	K.SYELPDGQVITIGNER.F	1791.93998	2	6.06E-12	0.96	5.22	-	1055.5
AHQ-3-8, 4993 - 5069	K.SYELPDGQVITIGNER.F	1791.93998	2	8.42E-05	0.81	3.35	-	525.6
AHQ-3-13-, 4873	K.SYELPDGQVITIGNER.F	1791.93998	2	6.70E-05	0.94	4.13	-	1121.6
AHQ-3-13-, 4589	K.SYELPDGQVITIGNER.F	1791.93998	2	4.80E-09	0.92	3.67	-	860.1
AHQ-3-13-, 5026 - 5074	K.SYELPDGQVITIGNER.F	1791.93998	2	2.27E-10	0.96	5.12	-	1054.5
AHQ-3-8, 4707 - 4776	K.SYELPDGQVITIGNER.F	1791.93998	2	4.16E-11	0.97	5.36	-	1073.9
AHQ-3-8, 4607 - 4679	K.SYELPDGQVITIGNER.F	1791.93998	2	1.14E-11	0.96	4.88	-	1014.4
AHQ-3-8, 4576 - 4605	K.SYELPDGQVITIGNER.F	1791.93998	3	6.35E-08	0.96	5.11	-	1376.2
AHQ-3-1, 4898	K.SYELPDGQVITIGNER.F	1791.93998	2	6.98E-10	0.86	3.70	-	668.6
AHQ-3-5, 5264	K.SYELPDGQVITIGNER.F	1791.93998	2	4.97E-06	0.94	4.20	-	918.5
AHQ-3-5, 4917 - 4987	K.SYELPDGQVITIGNER.F	1791.93998	2	7.01E-06	0.93	4.16	-	968.1
AHQ-3-5, 4576 - 4652	K.SYELPDGQVITIGNER.F	1791.93998	2	5.65E-04	0.77	2.75	-	808.8
AHQ-3-13-, 4473 - 4486	K.SYELPDGQVITIGNER.F	1791.93998	2	2.12E-11	0.95	4.39	-	983.4
AHQ-3-9, 4196 - 4267	K.SYELPDGQVITIGNER.F	1791.93998	2	4.98E-06	0.85	3.53	-	543.3
AHQ-3-9, 4201	K.SYELPDGQVITIGNER.F	1791.93998	2	1.34E-07	0.75	2.85	-	664.3
AHQ-3-8, 4475 - 4543	K.SYELPDGQVITIGNER.F	1791.93998	2	4.08E-12	0.95	4.18	-	1157.8
AHQ-3-9, 4493 - 4563	K.SYELPDGQVITIGNER.F	1791.93998	2	9.42E-08	0.92	4.19	-	768.4
AHQ-3-9, 4619	K.SYELPDGQVITIGNER.F	1791.93998	2	6.22E-09	0.88	3.39	-	821.8
AHQ-3-9, 4737 - 4780	K.SYELPDGQVITIGNER.F	1791.93998	2	7.31E-05	0.92	3.88	-	962.2
AHQ-3-9, 4847 - 4848	K.SYELPDGQVITIGNER.F	1791.93998	2	2.85E-04	0.95	4.30	-	1225.0
AHQ-3-6, 4861 - 4875	K.SYELPDGQVITIGNER.F	1791.93998	2	6.06E-12	0.95	4.75	-	944.2
AHQ-3-8, 4280 - 4359	K.SYELPDGQVITIGNER.F	1791.93998	2	4.05E-13	0.95	4.24	-	1094.3
AHQ-3-10, 4078 - 4150	K.SYELPDGQVITIGNER.F	1791.93998	2	4.58E-06	0.95	4.67	-	918.7
AHQ-3-10, 4284	K.SYELPDGQVITIGNER.F	1791.93998	2	1.57E-07	0.90	3.52	-	823.5
AHQ-3-4, 5314 - 5384	K.SYELPDGQVITIGNER.F	1791.93998	2	2.10E-10	0.90	3.81	-	765.9
AHQ-3-10, 4454 - 4530	K.SYELPDGQVITIGNER.F	1791.93998	2	1.36E-10	0.97	5.04	-	1234.4
AHQ-3-10, 4650 - 4714	K.SYELPDGQVITIGNER.F	1791.93998	2	1.48E-10	0.91	3.84	-	901.2
AHQ-3-1, 5188 - 5209	K.SYELPDGQVITIGNER.F	1791.93998	2	1.98E-08	0.94	4.01	-	1035.3
AHQ-3-7, 4582 - 4654	K.SYELPDGQVITIGNER.F	1791.93998	2	3.69E-06	0.90	3.91	-	758.9
AHQ-3-1, 5385 - 5428	K.SYELPDGQVITIGNER.F	1791.93998	2	1.75E-09	0.95	4.33	-	1071.9
AHQ-3-11, 4252 - 4326	K.SYELPDGQVITIGNER.F	1791.93998	2	1.61E-07	0.89	3.80	-	646.6
AHQ-3-11, 4335	K.SYELPDGQVITIGNER.F	1791.93998	2	6.40E-08	0.93	3.74	-	840.1
AHQ-3-11, 4478 - 4490	K.SYELPDGQVITIGNER.F	1791.93998	2	5.80E-12	0.95	4.28	-	1048.2
AHQ-3-11, 4840 - 4907	K.SYELPDGQVITIGNER.F	1791.93998	2	5.01E-09	0.94	3.93	-	1024.5
AHQ-3-4, 4714	K.SYELPDGQVITIGNER.F	1791.93998	2	1.11E-07	0.86	3.61	-	695.2
AHQ-3-4, 4610	K.SYELPDGQVITIGNER.F	1791.93998	2	1.63E-04	0.84	3.05	-	789.0
AHQ-3-3, 5344 - 5361	K.SYELPDGQVITIGNER.F	1791.93998	2	1.59E-06	0.78	3.38	-	380.1
AHQ-3-1, 4801	K.SYELPDGQVITIGNER.F	1791.93998	2	4.72E-08	0.84	3.62	-	452.9
AHQ-3-8, 4141 - 4212	K.SYELPDGQVITIGNER.F	1791.93998	2	1.94E-10	0.98	5.68	-	1391.0
AHQ-3-3, 5153 - 5172	K.SYELPDGQVITIGNER.F	1791.93998	2	4.92E-13	0.95	4.38	-	1162.0
AHQ-3-6, 5083 - 5162	K.SYELPDGQVITIGNER.F	1791.93998	2	4.47E-08	0.93	4.07	-	1013.4
AHQ-3-14-, 4871	K.SYELPDGQVITIGNER.F	1791.93998	2	8.43E-10	0.94	4.09	-	936.4
AHQ-3-14-, 5041	K.SYELPDGQVITIGNER.F	1791.93998	2	3.29E-07	0.92	3.90	-	967.3
AHQ-3-3, 4904	K.SYELPDGQVITIGNER.F	1791.93998	2	1.02E-06	0.80	3.05	-	528.4
AHQ-3-2, 4809	K.SYELPDGQVITIGNER.F	1791.93998	2	1.27E-09	0.93	4.06	-	850.0
AHQ-3-12, 4514	K.SYELPDGQVITIGNER.F	1791.93998	2	2.70E-06	0.70	2.69	-	542.2
AHQ-3-2, 5202 - 5214	K.SYELPDGQVITIGNER.F	1791.93998	2	3.63E-09	0.96	4.79	-	1108.0
AHQ-3-12, 4887 - 4914	K.SYELPDGQVITIGNER.F	1791.93998	2	6.52E-13	0.95	4.43	-	1014.0
AHQ-3-14, 6007	K.SYELPDGQVITIGNER.F	1791.93998	2	5.91E-07	0.87	3.74	-	763.5
AHQ-3-12, 5056 - 5118	K.SYELPDGQVITIGNER.F	1791.93998	2	7.79E-13	0.95	4.43	-	1058.4
AHQ-3-3, 4765	K.SYELPDGQVITIGNER.F	1791.93998	2	4.31E-07	0.85	3.36	-	626.5

AHQ-3-14, 5880 - 5919	K.SYELPDGQVITIGNER.F	1791.93998	2	6.20E-04	0.54	2.83	-	627.9
AHQ-3-2, 5399	K.SYELPDGQVITIGNER.F	1791.93998	2	1.98E-05	0.89	3.64	-	734.4
AHQ-3-9, 4337 - 4405	K.SYELPDGQVITIGNER.F	1791.93998	2	1.99E-09	0.92	3.70	-	958.9
AHQ-3-13, 5006 - 5078	K.SYELPDGQVITIGNER.F	1791.93998	2	3.11E-04	0.90	3.49	-	834.2
AHQ-3-13, 4469	K.SYELPDGQVITIGNER.F	1791.93998	2	6.68E-09	0.89	3.26	-	836.9
AHQ-3-13, 4590 - 4598	K.SYELPDGQVITIGNER.F	1791.93998	2	8.03E-07	0.88	3.56	-	865.2
AHQ-3-13, 4885 - 4925	K.SYELPDGQVITIGNER.F	1791.93998	2	5.33E-07	0.96	4.55	-	1241.0
AHQ-3-11, 3670	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	4.89E-06	0.85	3.59	-	679.4
AHQ-3-5, 3681	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	2.58E-04	0.93	4.23	-	933.4
AHQ-3-7, 3519	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	1.29E-04	0.75	3.10	-	670.4
AHQ-3-3, 4654 - 4658	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.45E-04	0.56	3.14	-	557.3
AHQ-3-12, 5031	K.YPIEHGIITNWDDMEK.I	1962.17174	2	6.20E-04	0.83	3.38	-	636.7
AHQ-3-12, 4700	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.39E-06	0.79	3.72	-	535.9
AHQ-3-13, 3991 - 4014	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	3.86E-04	0.76	3.32	-	437.4
AHQ-3-11, 4203 - 4212	K.YPIEHGIITNWDDMEK.I	1962.17174	3	5.13E-04	0.63	3.36	-	860.1
AHQ-3-13, 4078	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	4.97E-04	0.84	3.30	-	699.2
AHQ-3-5, 4351 - 4389	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.00E-04	0.87	3.98	-	696.2
AHQ-3-9, 4195 - 4271	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.66E-06	0.80	3.90	-	409.4
AHQ-3-6, 4261 - 4274	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.21E-04	0.90	4.18	-	850.2
AHQ-3-12, 4491 - 4555	K.YPIEHGIITNWDDMEK.I	1962.17174	2	6.04E-04	0.85	3.95	-	568.0
AHQ-3-8, 3584 - 3657	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	4.66E-05	0.81	3.89	-	452.2
AHQ-3-8, 4705	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.96E-08	0.83	3.80	-	621.9
AHQ-3-8, 4571	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.17E-06	0.71	3.68	-	434.4
AHQ-3-8, 4206 - 4276	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.33E-04	0.84	3.85	-	640.4
AHQ-3-8, 3653 - 3733	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	6.67E-04	0.87	4.09	-	639.7
AHQ-3-13, 4350 - 4362	K.YPIEHGIITNWDDMEK.I	1962.17174	3	5.72E-04	0.78	3.84	-	698.0
AHQ-3-8, 5113 - 5136	K.YPIEHGIITNWDDM*EKIWHHTFYNELR.V	3475.83549	3	6.70E-04	0.88	4.38	-	629.0
AHQ-3-8, 4783	K.YPIEHGIITNWDDM*EKIWHHTFYNELR.V	3475.83549	3	1.01E-04	0.81	4.42	-	625.2
gi|5803011|ref|NP_001966.1|	enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron			5.11E-13	0.96	10.27	3.70	47268.3
AHQ-3-8, 6392	R.YITGDQLGALYQDFVR.D	1860.05915	2	3.34E-11	0.97	5.31	-	1426.6
AHQ-3-7, 6598	R.YITGDQLGALYQDFVR.D	1860.05915	2	5.11E-13	0.96	5.02	-	1206.7
gi|10346135|ref|NP_055083.1|	microtubule-associated protein, RP/EB family, member 2; T-cell activat			5.72E-13	1.93	20.28	9.80	37031.1
AHQ-3-12, 6790	R.FQDNLDFIQWFK.K	1601.78539	2	3.21E-06	0.96	5.00	-	1168.6
AHQ-3-9, 6680	R.FQDNLDFIQWFK.K	1601.78539	2	2.48E-08	0.97	4.63	-	1480.0
AHQ-3-13, 6789	R.FQDNLDFIQWFK.K	1601.78539	2	2.68E-06	0.97	4.52	-	1852.8
AHQ-3-9, 4411	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	2	5.72E-13	0.97	5.08	-	1398.3
AHQ-3-9, 4404 - 4416	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	4.87E-04	0.97	5.61	-	1729.9
gi|4503571|ref|NP_001419.1|	enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n			5.94E-13	9.78	110.29	36.20	47168.7
AHQ-3-14-, 5247 - 5265	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.25E-06	0.93	4.53	-	617.4
AHQ-3-8, 4779 - 4852	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.24E-12	0.96	5.33	-	686.4
AHQ-3-13-, 5246 - 5266	R.AAVPSGASTGIYEALELR.D	1806.00979	2	8.82E-13	0.94	4.87	-	800.9
AHQ-3-7, 5232	R.AAVPSGASTGIYEALELR.D	1806.00979	2	8.37E-04	0.81	3.33	-	444.0
AHQ-3-11, 5036	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.71E-10	0.96	4.62	-	1016.5
AHQ-3-12, 5275	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.10E-08	0.71	3.28	-	242.8
AHQ-3-14, 6237	R.AAVPSGASTGIYEALELR.D	1806.00979	2	5.19E-06	0.94	4.68	-	685.8
AHQ-3-13, 5190 - 5270	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.24E-09	0.90	3.96	-	498.8
AHQ-3-9, 4880 - 4888	R.AAVPSGASTGIYEALELR.D	1806.00979	2	4.04E-11	0.92	4.40	-	715.6
AHQ-3-10, 4199	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	8.98E-04	0.92	4.76	-	751.4
AHQ-3-8, 4348 - 4391	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	3.70E-05	0.89	4.78	-	730.6
AHQ-3-7, 4498	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	1.73E-06	0.92	4.74	-	669.1
AHQ-3-13-, 4222	R.GNPTVEVDLFTSK.G	1407.55065	2	2.21E-06	0.57	2.68	-	490.3
AHQ-3-8, 3849	R.GNPTVEVDLFTSK.G	1407.55065	1	5.45E-08	0.68	3.26	-	601.7
AHQ-3-13, 4214 - 4218	R.GNPTVEVDLFTSK.G	1407.55065	2	4.43E-06	0.77	3.16	-	607.9
AHQ-3-7, 5823	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	5.03E-04	0.79	3.47	-	1009.6
AHQ-3-7, 1966 - 1968	R.IGAEVYHNLK.N	1144.30502	2	7.85E-05	0.95	3.61	-	1688.4
AHQ-3-7, 6892	K.LAMQEFMILPVGAANFR.E	1909.30812	2	9.16E-04	0.91	4.26	-	779.5
AHQ-3-7, 5447	K.LAM*QEFM*ILPVGAANFR.E	1941.30692	2	9.27E-04	0.91	3.84	-	971.4
AHQ-3-8, 5157	K.LAM*QEFM*ILPVGAANFR.E	1941.30692	2	3.34E-05	0.95	4.82	-	958.4
AHQ-3-9, 5173	K.LAM*QEFM*ILPVGAANFR.E	1941.30692	2	9.99E-04	0.93	4.12	-	783.4
AHQ-3-9, 6588 - 6592	K.LAMQEFMILPVGAANFR.E	1909.30812	2	1.16E-04	0.94	4.55	-	822.3
AHQ-3-8, 6701	K.LAMQEFMILPVGAANFR.E	1909.30812	2	8.50E-05	0.94	4.84	-	698.7
AHQ-3-8, 2824	K.SCNCLLLK.V	1010.21066	2	8.71E-04	0.80	2.77	-	653.2
AHQ-3-8, 6805	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	3	5.94E-13	0.97	5.78	-	1972.5
AHQ-3-8, 6804	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	2	1.25E-07	0.89	4.13	-	743.3
AHQ-3-8, 3665	K.VNQIGSVTESLQACK.L	1635.82159	2	3.21E-06	0.83	3.32	-	628.9
AHQ-3-13-, 3782	K.VNQIGSVTESLQACK.L	1635.82159	2	2.25E-04	0.80	3.07	-	765.7
AHQ-3-8, 3373	K.VNQIGSVTESLQACK.L	1635.82159	2	1.62E-07	0.92	3.96	-	828.3
AHQ-3-9, 4507	R.YISPDQLADLYK.S	1426.59557	2	3.67E-05	0.88	3.21	-	711.1
AHQ-3-7, 4722 - 4738	R.YISPDQLADLYK.S	1426.59557	2	5.35E-07	0.94	4.20	-	768.4
AHQ-3-8, 4513	R.YISPDQLADLYK.S	1426.59557	1	7.85E-04	0.75	3.32	-	623.5
AHQ-3-8, 4500 - 4507	R.YISPDQLADLYK.S	1426.59557	2	9.12E-09	0.93	4.21	-	722.3
gi|4557677|ref|NP_000203.1|	integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu			6.81E-13	18.65	240.26	36.80	87185.6
AHQ-3-3, 2873 - 2888	R.AKWDTANNPLYK.E	1421.58225	2	9.40E-07	0.85	3.21	-	669.0
AHQ-3-3, 5638	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	2	1.08E-04	0.79	2.86	-	781.0
AHQ-3-5, 5403	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	1.29E-08	0.92	4.34	-	1153.5
AHQ-3-3, 5628	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	6.44E-04	0.85	4.25	-	680.6
AHQ-3-4, 5497	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	8.70E-04	0.85	3.82	-	973.9
AHQ-3-3, 5520 - 5588	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	2	2.03E-06	0.92	5.10	-	497.4
AHQ-3-3, 5481 - 5560	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	2.25E-06	0.93	4.89	-	1200.7
AHQ-3-3, 4616	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	6.81E-13	0.69	3.42	-	437.0
AHQ-3-4, 4476	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.61E-10	0.81	3.76	-	434.3
AHQ-3-5, 4403	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	7.68E-05	0.73	3.52	-	393.0
AHQ-3-3, 4464 - 4532	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	9.97E-05	0.68	3.55	-	433.5
AHQ-3-3, 6656 - 6724	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.48E-05	0.93	4.13	-	1117.6
AHQ-3-1, 6045 - 6076	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.37E-09	0.83	3.89	-	527.5
AHQ-3-3, 6564 - 6634	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	4.77E-05	0.94	4.49	-	955.7
AHQ-3-3, 6421 - 6497	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	5.71E-06	0.86	3.81	-	562.4
AHQ-3-3, 6281 - 6350	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	4.85E-06	0.94	4.40	-	947.1
AHQ-3-3, 6149	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	8.18E-05	0.96	4.36	-	1246.0
AHQ-3-3, 6744 - 6812	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.48E-06	0.92	4.45	-	671.7
AHQ-3-3, 4632 - 4705	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.71E-05	0.92	3.59	-	1134.2
AHQ-3-1, 4633	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.27E-04	0.92	3.70	-	890.2
AHQ-3-3, 4782	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	3.26E-04	0.88	3.90	-	589.3
AHQ-3-3, 5084	K.DDLWSIQNLGTK.L	1390.52332	1	4.20E-04	0.61	2.74	-	387.3
AHQ-3-3, 5081 - 5096	K.DDLWSIQNLGTK.L	1390.52332	2	6.34E-06	0.95	4.64	-	951.0
AHQ-3-4, 5045	K.DDLWSIQNLGTK.L	1390.52332	1	6.61E-08	0.73	2.99	-	428.7
AHQ-3-1, 5120	K.DDLWSIQNLGTK.L	1390.52332	2	5.30E-05	0.93	3.86	-	1069.1
AHQ-3-11, 4184	K.DNCAPESIEFPVSEAR.V	1822.93099	2	6.20E-05	0.65	2.69	-	729.6
AHQ-3-6, 4347	K.DNCAPESIEFPVSEAR.V	1822.93099	2	4.49E-06	0.66	3.04	-	520.6
AHQ-3-3, 4778	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.10E-04	0.77	3.15	-	779.2
AHQ-3-4, 4542 - 4549	K.DNCAPESIEFPVSEAR.V	1822.93099	2	9.56E-05	0.88	3.30	-	1059.0
AHQ-3-3, 3325 - 3332	K.EATSTFTNITYR.G	1404.50685	2	1.50E-04	0.84	3.12	-	778.4
AHQ-3-1, 3464 - 3470	K.EATSTFTNITYR.G	1404.50685	2	2.26E-06	0.85	3.36	-	688.7
AHQ-3-3, 2241 - 2252	R.FQYYEDSSGK.S	1224.25749	1	8.13E-04	0.27	2.29	-	450.8
AHQ-3-4, 3578 - 3648	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.68E-05	0.94	3.96	-	1302.0
AHQ-3-3, 3681	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	2.18E-04	0.74	3.29	-	663.9
AHQ-3-3, 3664 - 3737	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	6.65E-05	0.92	4.28	-	1004.1

AHQ-3-3, 3821	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.34E-08	0.92	4.56	-	827.7
AHQ-3-2, 3750 - 3758	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	5.94E-09	0.97	4.26	-	2047.0
AHQ-3-6, 3473 - 3482	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.38E-05	0.92	3.36	-	1267.2
AHQ-3-5, 3531 - 3535	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	9.88E-05	0.97	4.68	-	2019.0
AHQ-3-3, 4426	R.GKCECGSCVCIQPGSYGDTCEKCPTCPDACTFKK.E	4028.42584	3	2.33E-04	0.93	5.20	-	792.3
AHQ-3-4, 4372	R.GKCECGSCVCIQPGSYGDTCEKCPTCPDACTFKK.E	4028.42584	3	9.31E-05	0.76	3.76	-	539.1
AHQ-3-3, 1952 - 2020	K.GSGDSSQVTQVSPQR.I	1533.58302	2	1.40E-04	0.79	3.21	-	817.7
AHQ-3-3, 1800 - 1884	K.GSGDSSQVTQVSPQR.I	1533.58302	2	7.88E-04	0.71	2.88	-	623.9
AHQ-3-3, 2560 - 2630	K.HVLTLTDQVTR.F	1283.45912	2	6.96E-07	0.92	3.32	-	776.7
AHQ-3-4, 2560	K.HVLTLTDQVTR.F	1283.45912	2	1.23E-06	0.88	3.13	-	730.5
AHQ-3-6, 2405 - 2413	K.HVLTLTDQVTR.F	1283.45912	1	2.74E-04	0.22	1.87	-	228.8
AHQ-3-2, 2590	K.HVLTLTDQVTR.F	1283.45912	2	4.90E-05	0.89	3.37	-	666.1
AHQ-3-5, 2431	K.HVLTLTDQVTR.F	1283.45912	2	1.99E-06	0.91	3.38	-	786.5
AHQ-3-1, 2809	K.HVLTLTDQVTR.F	1283.45912	2	2.17E-04	0.90	3.24	-	806.2
AHQ-3-8, 2252	K.HVLTLTDQVTR.F	1283.45912	2	2.24E-04	0.92	3.43	-	876.1
AHQ-3-3, 5449	R.LAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEK.L	3997.35517	3	6.53E-09	0.73	3.55	-	474.3
AHQ-3-4, 5529	R.LAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEK.L	3997.35517	3	5.88E-04	0.48	3.11	-	503.7
AHQ-3-3, 5537 - 5609	R.LAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEK.L	3997.35517	3	1.29E-04	0.84	3.85	-	733.9
AHQ-3-3, 3845 - 3909	R.NDASHLLVFTTDAK.T	1532.67977	2	3.70E-07	0.97	5.11	-	1241.3
AHQ-3-4, 3781	R.NDASHLLVFTTDAK.T	1532.67977	2	6.45E-06	0.92	4.01	-	1009.1
AHQ-3-1, 4562	R.NDASHLLVFTTDAK.T	1532.67977	2	3.51E-07	0.94	4.55	-	937.8
AHQ-3-4, 4400 - 4410	R.NDASHLLVFTTDAK.T	1532.67977	2	6.28E-10	0.97	4.91	-	1338.5
AHQ-3-6, 3449 - 3525	R.NDASHLLVFTTDAK.T	1532.67977	2	8.01E-08	0.96	4.49	-	1249.4
AHQ-3-3, 4460 - 4469	R.NDASHLLVFTTDAK.T	1532.67977	2	6.84E-09	0.94	4.48	-	926.1
AHQ-3-6, 4158	R.NDASHLLVFTTDAK.T	1532.67977	2	6.96E-04	0.80	2.63	-	928.5
AHQ-3-2, 3926	R.NDASHLLVFTTDAK.T	1532.67977	2	1.88E-09	0.92	4.14	-	847.8
AHQ-3-9, 3231	R.NDASHLLVFTTDAK.T	1532.67977	2	2.37E-07	0.93	4.28	-	946.1
AHQ-3-1, 4065 - 4074	R.NDASHLLVFTTDAK.T	1532.67977	2	1.36E-09	0.97	4.85	-	1423.4
AHQ-3-5, 2959	K.SFTIKPVGFK.D	1124.35685	1	7.17E-04	0.43	2.28	-	692.2
AHQ-3-3, 3242	K.SFTIKPVGFK.D	1124.35685	1	2.50E-04	0.71	2.89	-	541.3
AHQ-3-3, 3690 - 3772	R.TDTCMSSNGLLCSGR.G	1661.81786	2	2.68E-08	0.91	3.57	-	776.0
AHQ-3-1, 3630	R.TDTCMSSNGLLCSGR.G	1661.81786	2	7.17E-09	0.85	3.32	-	843.5
AHQ-3-4, 3506 - 3584	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.91E-08	0.86	3.27	-	902.5
AHQ-3-3, 2958 - 3034	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.34E-08	0.88	3.74	-	771.7
AHQ-3-4, 2966	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.60E-06	0.75	2.98	-	462.5
AHQ-3-3, 2856	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.90E-07	0.96	4.19	-	1442.3
AHQ-3-1, 2894	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	9.10E-07	0.95	3.89	-	1592.9
AHQ-3-3, 1542	K.THIALDGR.L	882.98732	1	2.35E-04	0.00	2.02	-	91.4
AHQ-3-3, 1728 - 1796	R.VLEDRPLSDK.G	1172.31354	2	4.18E-05	0.89	3.17	-	932.9
AHQ-3-1, 2066	R.VLEDRPLSDK.G	1172.31354	2	1.84E-06	0.87	2.97	-	1019.3
AHQ-3-1, 2882	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	8.27E-06	0.94	4.60	-	1328.1
AHQ-3-3, 2738	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	2.52E-08	0.94	4.89	-	1242.1
AHQ-3-1, 3420	K.WDTANNPLYK.E	1222.33111	2	1.19E-04	0.75	2.86	-	662.1
AHQ-3-3, 3206 - 3276	K.WDTANNPLYK.E	1222.33111	2	5.10E-04	0.65	2.79	-	461.7
AHQ-3-6, 3614	K.YCECDDFSCVR.Y	1514.59674	2	1.51E-04	0.90	3.21	-	963.8
AHQ-3-2, 3843	K.YCECDDFSCVR.Y	1514.59674	2	2.16E-04	0.94	3.82	-	1268.5
AHQ-3-1, 3780	K.YCECDDFSCVR.Y	1514.59674	2	8.73E-07	0.95	3.69	-	1328.6
AHQ-3-5, 3680	K.YCECDDFSCVR.Y	1514.59674	2	9.32E-06	0.96	3.89	-	1300.5
AHQ-3-3, 3760	K.YCECDDFSCVR.Y	1514.59674	2	1.63E-07	0.96	3.95	-	1323.8
AHQ-3-4, 3750	K.YCECDDFSCVR.Y	1514.59674	2	4.93E-09	0.93	3.34	-	1005.4
AHQ-3-3, 2224	R.YCRDEIESVK.E	1300.42023	2	1.04E-04	0.86	3.45	-	984.6
gi|4504165|ref|NP_000168.1| gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]				7.64E-13	22.16	260.35	39.30	85696.9
AHQ-3-5, 3611 - 3613	K.AGALNSNDAFVLK.T	1320.47622	1	6.63E-06	0.70	3.04	-	522.1
AHQ-3-5, 3712	K.AGALNSNDAFVLK.T	1320.47622	1	6.13E-07	0.41	2.41	-	454.1
AHQ-3-5, 3721 - 3744	K.AGALNSNDAFVLK.T	1320.47622	2	2.24E-07	0.85	3.83	-	456.4
AHQ-3-5, 3393 - 3405	K.AGALNSNDAFVLK.T	1320.47622	2	7.12E-07	0.90	3.96	-	708.2
AHQ-3-5, 2668	K.AGKEPGLQIWR.V	1255.45060	2	4.62E-05	0.57	2.57	-	412.0
AHQ-3-6, 5531 - 5546	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.13E-04	0.92	4.86	-	498.1
AHQ-3-6, 5673 - 5683	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.32E-04	0.95	4.55	-	897.9
AHQ-3-7, 5488	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.63E-11	0.94	5.09	-	582.8
AHQ-3-7, 5642	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.64E-07	0.96	5.50	-	808.3
AHQ-3-5, 5939 - 6015	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.85E-08	0.96	5.29	-	766.0
AHQ-3-8, 5425	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.26E-05	0.91	4.56	-	594.8
AHQ-3-11, 5435	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	7.21E-05	0.93	4.28	-	626.5
AHQ-3-5, 5604	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.00E-07	0.95	5.22	-	675.4
AHQ-3-4, 5960	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.69E-05	0.92	4.53	-	647.9
AHQ-3-5, 5755 - 5823	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.79E-06	0.96	5.54	-	938.0
AHQ-3-10, 5190	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.56E-06	0.91	4.55	-	521.0
AHQ-3-1, 6061 - 6064	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.40E-06	0.96	5.49	-	701.9
AHQ-3-9, 5359 - 5379	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.77E-07	0.95	5.08	-	664.4
AHQ-3-8, 5264 - 5340	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	7.73E-05	0.94	4.95	-	588.7
AHQ-3-9, 5191	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.60E-04	0.86	4.01	-	403.0
AHQ-3-6, 5597	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	7.64E-13	0.95	4.85	-	1570.2
AHQ-3-5, 5928	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	3.91E-06	0.89	3.84	-	1283.1
AHQ-3-5, 2167	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.01E-06	0.86	3.24	-	933.4
AHQ-3-5, 2080 - 2085	K.DSQEEEKTEALTSAK.R	1666.72289	2	6.03E-06	0.95	4.15	-	1496.6
AHQ-3-12, 2171	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.15E-05	0.86	3.38	-	932.8
AHQ-3-3, 2150	K.DSQEEEKTEALTSAK.R	1666.72289	2	7.96E-07	0.87	3.18	-	1106.8
AHQ-3-5, 1989	K.DSQEEEKTEALTSAK.R	1666.72289	3	4.98E-05	0.96	4.42	-	1999.0
AHQ-3-5, 1983 - 1995	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.54E-08	0.95	4.16	-	1462.0
AHQ-3-7, 1890	K.DSQEEEKTEALTSAK.R	1666.72289	2	5.16E-06	0.94	3.83	-	1477.9
AHQ-3-13, 2261	K.DSQEEEKTEALTSAK.R	1666.72289	2	4.63E-06	0.91	3.71	-	1137.6
AHQ-3-11, 2094	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.07E-06	0.92	3.58	-	1147.1
AHQ-3-10, 2070	K.DSQEEEKTEALTSAK.R	1666.72289	2	6.47E-08	0.95	3.95	-	1560.8
AHQ-3-6, 1961	K.DSQEEEKTEALTSAK.R	1666.72289	2	5.85E-10	0.94	3.62	-	1591.6
AHQ-3-13-, 2225	K.DSQEEEKTEALTSAK.R	1666.72289	2	8.89E-06	0.96	4.54	-	1568.5
AHQ-3-5, 6432 - 6496	R.EVQGFESATFLGYFK.S	1723.90570	2	1.06E-08	0.97	5.05	-	1410.3
AHQ-3-5, 6953	R.EVQGFESATFLGYFK.S	1723.90570	2	4.21E-04	0.90	3.21	-	1175.5
AHQ-3-13-, 6143	R.EVQGFESATFLGYFK.S	1723.90570	2	2.18E-05	0.93	3.40	-	1372.8
AHQ-3-12, 6111	R.EVQGFESATFLGYFK.S	1723.90570	2	4.16E-07	0.92	3.77	-	874.9
AHQ-3-13, 6154	R.EVQGFESATFLGYFK.S	1723.90570	2	1.34E-04	0.94	4.07	-	1005.0
AHQ-3-5, 6532	R.EVQGFESATFLGYFK.S	1723.90570	2	1.02E-06	0.90	3.17	-	1162.1
AHQ-3-14-, 6035	R.EVQGFESATFLGYFK.S	1723.90570	2	8.50E-06	0.89	3.69	-	831.8
AHQ-3-8, 1913	K.HVVPNEVVVQR.L	1276.46981	2	1.70E-04	0.87	3.11	-	669.3
AHQ-3-5, 2055 - 2075	K.HVVPNEVVVQR.L	1276.46981	2	1.27E-07	0.90	3.34	-	566.4
AHQ-3-9, 2004	K.HVVPNEVVVQR.L	1276.46981	2	7.76E-06	0.87	3.16	-	598.8
AHQ-3-12, 2266	K.HVVPNEVVVQR.L	1276.46981	1	5.45E-06	0.54	2.50	-	480.9
AHQ-3-5, 2276 - 2277	K.HVVPNEVVVQR.L	1276.46981	1	2.21E-08	0.70	2.53	-	543.6
AHQ-3-12, 2258	K.HVVPNEVVVQR.L	1276.46981	2	8.06E-08	0.92	3.52	-	555.8
AHQ-3-5, 2059 - 2065	K.HVVPNEVVVQR.L	1276.46981	1	2.85E-05	0.25	2.12	-	295.3
AHQ-3-5, 2069	K.HVVPNEVVVQR.L	1276.46981	1	9.20E-04	0.34	2.73	-	255.0
AHQ-3-6, 2035	K.HVVPNEVVVQR.L	1276.46981	2	4.15E-09	0.86	2.86	-	620.0
AHQ-3-11, 2172	K.HVVPNEVVVQR.L	1276.46981	1	7.94E-06	0.63	2.77	-	370.6
AHQ-3-11, 2168	K.HVVPNEVVVQR.L	1276.46981	1	3.77E-04	0.14	1.85	-	265.5
AHQ-3-11, 2163	K.HVVPNEVVVQR.L	1276.46981	2	1.67E-08	0.87	3.03	-	535.4
AHQ-3-5, 2272	K.HVVPNEVVVQR.L	1276.46981	2	2.71E-07	0.89	2.88	-	860.5
AHQ-3-7, 1958	K.HVVPNEVVVQR.L	1276.46981	2	1.35E-05	0.82	2.60	-	713.4

AHQ-3-5, 6439	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	2.24E-05	0.95	4.79	-	1541.8
AHQ-3-6, 6285	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	1.09E-04	0.90	4.18	-	1221.4
AHQ-3-5, 6563	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	2.60E-04	0.87	4.17	-	920.6
AHQ-3-5, 5507 - 5576	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.29E-11	0.98	6.72	-	1676.2
AHQ-3-5, 6081 - 6108	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	7.48E-09	0.96	5.11	-	1303.4
AHQ-3-6, 5491	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.47E-05	0.95	5.33	-	1260.0
AHQ-3-5, 1769 - 1831	K.PALPAGTEDTAK.E	1171.28241	2	1.22E-04	0.49	2.53	-	325.6
AHQ-3-6, 2283 - 2295	K.PALPAGTEDTAKEDAANR.K	1827.93072	3	1.64E-06	0.71	3.04	-	392.7
AHQ-3-5, 2307	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	2.91E-05	0.87	3.71	-	445.6
AHQ-3-5, 4736 - 4760	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	4.57E-05	0.79	3.52	-	366.2
AHQ-3-7, 4559	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	6.64E-04	0.73	3.21	-	312.8
AHQ-3-5, 2428	K.SEDCFILDHGKDGK.I	1622.73823	2	1.06E-04	0.53	2.55	-	647.2
AHQ-3-5, 1851 - 1852	K.TASDFITK.M	882.98086	2	5.52E-05	0.75	2.62	-	434.4
AHQ-3-5, 1912 - 1928	K.TGAQELLR.V	888.00387	2	5.67E-05	0.90	3.18	-	1048.3
AHQ-3-5, 4313 - 4383	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	2.37E-06	0.98	5.91	-	1890.3
AHQ-3-5, 4452 - 4497	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.34E-07	0.94	3.96	-	1053.8
AHQ-3-7, 4154	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	6.60E-04	0.89	3.89	-	868.8
AHQ-3-5, 4709	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.80E-04	0.85	3.30	-	802.4
AHQ-3-5, 4845 - 4921	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	9.71E-05	0.89	3.69	-	857.5
AHQ-3-5, 4731 - 4799	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	3.64E-07	0.97	5.76	-	1075.5
AHQ-3-9, 4361	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	7.88E-04	0.89	3.76	-	714.6
AHQ-3-6, 4747	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	6.26E-07	0.97	5.70	-	1097.0
AHQ-3-5, 5121	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	2.47E-10	0.93	4.97	-	833.5
AHQ-3-5, 4213	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	6.11E-05	0.94	5.15	-	796.6
AHQ-3-5, 4889	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAKEDAANR.K	3960.33442	3	4.12E-04	0.94	5.37	-	761.4
AHQ-3-5, 2984 - 2987	R.VPFDAATLHTSTAM*AAQHGM*DDDGTGQK.Q	2907.10021	3	3.45E-06	0.95	5.65	-	899.6
AHQ-3-6, 3429	R.VPFDAATLHTSTAM*AAQHGMDDDGTGQK.Q	2891.10081	3	1.34E-04	0.95	5.18	-	1644.8
AHQ-3-6, 2951	R.VPFDAATLHTSTAM*AAQHGM*DDDGTGQK.Q	2907.10021	3	1.05E-05	0.95	5.66	-	965.7
AHQ-3-5, 3856	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	1.45E-04	0.98	7.09	-	2074.4
AHQ-3-5, 6891 - 6903	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	2	1.25E-06	0.76	3.28	-	458.7
AHQ-3-5, 5237	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	3.96E-06	0.58	2.55	-	502.6
AHQ-3-5, 5500	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	3	4.54E-07	0.95	5.41	-	1330.5
AHQ-3-5, 1608 - 1688	R.YIETDPANR.D	1079.14506	2	5.19E-07	0.68	2.89	-	445.7
gi|27498267|ref|XP_209737.1|	similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,			9.48E-13	3.31	40.33	33.70	11063.6
AHQ-3-10, 5607 - 5608	R.DICNDVLSLLEK.F	1420.61093	1	4.89E-09	0.77	3.09	-	877.8
AHQ-3-11, 6688	R.DICNDVLSLLEK.F	1420.61093	2	2.33E-06	0.97	4.62	-	2134.3
AHQ-3-9, 5924	R.DICNDVLSLLEK.F	1420.61093	1	1.06E-08	0.40	2.12	-	684.3
AHQ-3-9, 5929	R.DICNDVLSLLEK.F	1420.61093	1	1.59E-06	0.85	3.13	-	884.6
AHQ-3-9, 5937	R.DICNDVLSLLEK.F	1420.61093	2	5.63E-06	0.94	3.52	-	1260.9
AHQ-3-9, 6936	R.DICNDVLSLLEK.F	1420.61093	1	3.83E-10	0.80	3.51	-	583.6
AHQ-3-9, 6937	R.DICNDVLSLLEK.F	1420.61093	2	4.53E-07	0.97	4.99	-	1960.2
AHQ-3-11, 5811	R.DICNDVLSLLEK.F	1420.61093	1	1.60E-10	0.42	2.20	-	574.1
AHQ-3-10, 6486 - 6546	R.DICNDVLSLLEK.F	1420.61093	1	9.45E-07	0.81	3.39	-	617.1
AHQ-3-10, 6484 - 6498	R.DICNDVLSLLEK.F	1420.61093	2	1.10E-05	0.97	5.03	-	1782.0
AHQ-3-10, 5978	R.DICNDVLSLLEK.F	1420.61093	2	2.35E-05	0.94	3.60	-	1731.2
AHQ-3-14-, 6736 - 6751	R.DICNDVLSLLEK.F	1420.61093	2	2.28E-06	0.97	4.96	-	2013.3
AHQ-3-10, 4818 - 4898	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.92E-09	0.98	5.59	-	1689.2
AHQ-3-10, 4835	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.08E-08	0.97	5.11	-	1603.0
AHQ-3-10, 4958 - 5022	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.03E-09	0.98	6.68	-	1599.6
AHQ-3-10, 5082 - 5143	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.65E-07	0.97	5.27	-	1432.8
AHQ-3-10, 5202 - 5271	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.02E-08	0.98	5.99	-	1435.2
AHQ-3-10, 5332 - 5395	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.53E-07	0.94	5.02	-	942.3
AHQ-3-10, 5416 - 5474	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.72E-05	0.97	4.81	-	1793.1
AHQ-3-10, 4771 - 4798	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	8.46E-07	0.97	5.09	-	2046.6
AHQ-3-10, 5635 - 5711	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.40E-08	0.97	5.27	-	1363.0
AHQ-3-10, 4710 - 4778	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.09E-08	0.98	5.90	-	1793.9
AHQ-3-10, 6315 - 6355	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.19E-04	0.95	4.80	-	1048.4
AHQ-3-10, 4476 - 4546	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.10E-11	0.98	5.81	-	1671.9
AHQ-3-10, 4334 - 4394	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.92E-10	0.98	6.49	-	1626.7
AHQ-3-10, 6704	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.50E-08	0.88	3.94	-	639.6
AHQ-3-11, 4675	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.36E-12	0.95	4.85	-	1087.0
AHQ-3-11, 4946 - 4952	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.03E-10	0.97	5.57	-	1427.5
AHQ-3-11, 4974	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	2.88E-06	0.97	5.34	-	2208.2
AHQ-3-14-, 5076	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.53E-08	0.97	5.21	-	1334.5
AHQ-3-9, 4951 - 5031	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	7.67E-08	0.98	6.17	-	1522.3
AHQ-3-12, 5080 - 5148	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	6.76E-10	0.96	4.84	-	1367.9
AHQ-3-13, 5086 - 5153	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	9.54E-09	0.98	6.60	-	1559.4
AHQ-3-13, 5155	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	3.00E-07	0.97	5.35	-	1930.8
AHQ-3-14, 5992 - 5993	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.56E-09	0.97	4.97	-	1648.1
AHQ-3-13-, 5103 - 5125	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	9.48E-13	0.98	5.60	-	1505.1
AHQ-3-10, 4322 - 4403	K.GIVDQSQQAYQEAFEISKK.E	2170.36467	2	2.65E-05	0.95	4.42	-	1288.1
AHQ-3-9, 4239	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	6.46E-08	0.97	5.27	-	1417.8
gi|4507877|ref|NP_003364.1|	vinculin isoform VCL [Homo sapiens]			1.12E-12	44.72	530.32	44.60	116721.6
AHQ-3-14-, 6781 - 6847	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.80E-06	0.90	3.62	-	827.2
AHQ-3-13-, 6901 - 6903	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.77E-05	0.94	4.47	-	905.4
AHQ-3-3, 7576	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	9.20E-07	0.96	4.80	-	1091.4
AHQ-3-13, 7013 - 7017	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.22E-11	0.97	5.50	-	1205.9
AHQ-3-12, 7026 - 7028	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.75E-08	0.96	4.97	-	1034.2
AHQ-3-11, 6796 - 6868	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	9.71E-05	0.97	5.35	-	1177.4
AHQ-3-6, 7353 - 7357	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.48E-07	0.96	4.94	-	1168.9
AHQ-3-7, 7415 - 7430	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.82E-06	0.94	4.79	-	964.0
AHQ-3-10, 6614 - 6615	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.55E-11	0.98	6.44	-	1288.6
AHQ-3-9, 7053	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.47E-09	0.96	5.02	-	1072.8
AHQ-3-1, 7340 - 7405	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.73E-08	0.95	4.38	-	1050.4
AHQ-3-1, 7344	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	3	4.22E-04	0.88	3.92	-	1024.9
AHQ-3-2, 7582 - 7657	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.50E-06	0.92	4.13	-	994.1
AHQ-3-5, 7535	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	6.57E-11	0.97	5.25	-	1412.7
AHQ-3-8, 7307 - 7308	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	9.71E-11	0.97	5.83	-	1310.2
AHQ-3-4, 7592 - 7672	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.00E-11	0.97	5.01	-	1221.0
AHQ-3-7, 2990	R.ALASQLQDSLK.D	1174.32943	2	1.59E-04	0.94	3.53	-	1250.0
AHQ-3-4, 3325	R.ALASQLQDSLK.D	1174.32943	2	7.96E-05	0.89	3.04	-	938.4
AHQ-3-3, 3314	R.ALASQLQDSLK.D	1174.32943	2	2.37E-04	0.60	2.98	-	512.6
AHQ-3-6, 3047 - 3053	R.ALASQLQDSLK.D	1174.32943	2	1.21E-04	0.91	3.73	-	934.8
AHQ-3-1, 3473	R.ALASQLQDSLK.D	1174.32943	2	3.30E-04	0.88	3.15	-	939.1
AHQ-3-4, 3734 - 3746	K.AQQVSQGLDVLTAK.V	1458.64233	2	9.63E-05	0.76	3.23	-	758.1
AHQ-3-6, 3310	K.AQQVSQGLDVLTAK.V	1458.64233	1	1.24E-06	0.77	3.55	-	362.6
AHQ-3-6, 3286	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.45E-08	0.96	4.04	-	1840.5
AHQ-3-8, 2961	K.AQQVSQGLDVLTAK.V	1458.64233	2	5.53E-09	0.95	4.22	-	1254.3
AHQ-3-11, 3340	K.AQQVSQGLDVLTAK.V	1458.64233	2	5.80E-04	0.93	4.12	-	1013.3
AHQ-3-7, 3235	K.AQQVSQGLDVLTAK.V	1458.64233	1	9.51E-09	0.80	3.73	-	454.4
AHQ-3-7, 3223	K.AQQVSQGLDVLTAK.V	1458.64233	1	8.42E-05	0.19	2.40	-	320.3
AHQ-3-7, 3219 - 3220	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.63E-10	0.97	5.08	-	1554.4
AHQ-3-4, 3733	K.AQQVSQGLDVLTAK.V	1458.64233	1	7.07E-05	0.35	2.47	-	434.7
AHQ-3-2, 3571 - 3641	K.AQQVSQGLDVLTAK.V	1458.64233	2	4.23E-05	0.97	4.17	-	1947.7
AHQ-3-4, 3461 - 3532	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.63E-10	0.97	4.69	-	1594.1
AHQ-3-2, 2383 - 2454	K.AVAGNISDPGLQK.S	1270.41721	2	1.32E-04	0.87	3.39	-	782.7
AHQ-3-5, 2288 - 2299	K.AVAGNISDPGLQK.S	1270.41721	2	1.39E-05	0.90	3.72	-	943.9

AHQ-3-7, 2222 - 2234	K.AVAGNISDPGLQK.S	1270.41721	2	6.09E-05	0.85	3.44	-	647.0
AHQ-3-4, 2405 - 2424	K.AVAGNISDPGLQK.S	1270.41721	2	3.25E-07	0.82	3.33	-	622.2
AHQ-3-6, 2270	K.AVAGNISDPGLQK.S	1270.41721	2	8.07E-06	0.85	3.59	-	592.3
AHQ-3-8, 2129	K.AVAGNISDPGLQK.S	1270.41721	2	7.06E-06	0.85	3.39	-	672.1
AHQ-3-3, 2436	K.AVAGNISDPGLQK.S	1270.41721	2	1.27E-08	0.83	3.21	-	668.6
AHQ-3-6, 5907 - 5910	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	2.61E-04	0.92	3.69	-	1211.2
AHQ-3-2, 6233	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	3.86E-04	0.92	3.70	-	1081.9
AHQ-3-7, 5882	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	2.81E-04	0.87	3.38	-	879.1
AHQ-3-1, 6172	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	9.39E-04	0.96	4.29	-	1499.9
AHQ-3-4, 6120 - 6173	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	1.79E-08	0.93	3.80	-	1212.3
AHQ-3-5, 6027 - 6039	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	6.50E-05	0.93	4.80	-	1152.2
AHQ-3-5, 6012 - 6089	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	1.06E-05	0.92	3.60	-	1164.1
AHQ-3-4, 6150 - 6182	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	7.32E-06	0.85	4.05	-	986.0
AHQ-3-8, 5773	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	1.91E-06	0.94	4.00	-	1319.5
AHQ-3-9, 5605	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	1.29E-05	0.87	3.48	-	925.5
AHQ-3-7, 2166	R.DPSASPGDAGEQAIR.Q	1471.51169	2	5.74E-04	0.86	3.41	-	668.7
AHQ-3-4, 2305 - 2378	R.DPSASPGDAGEQAIR.Q	1471.51169	2	4.21E-08	0.91	3.76	-	773.9
AHQ-3-2, 2342	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.05E-05	0.86	3.39	-	554.9
AHQ-3-6, 2186	R.DPSASPGDAGEQAIR.Q	1471.51169	2	4.42E-06	0.92	3.78	-	797.8
AHQ-3-4, 2304	R.DPSASPGDAGEQAIR.Q	1471.51169	1	2.52E-04	0.11	2.09	-	138.8
AHQ-3-1, 2422	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.34E-06	0.83	3.26	-	572.6
AHQ-3-11, 5514	K.ELLPVLISAMK.I	1214.54325	2	1.82E-04	0.61	2.77	-	381.3
AHQ-3-5, 2908	K.ETVQTTEDQILK.R	1405.53306	1	7.12E-06	0.06	2.42	-	81.8
AHQ-3-14, 3821	K.ETVQTTEDQILKR.D	1561.71942	2	2.12E-05	0.52	2.54	-	464.6
AHQ-3-14-, 2892	K.ETVQTTEDQILKR.D	1561.71942	2	4.44E-06	0.79	2.89	-	572.1
AHQ-3-5, 2716	K.ETVQTTEDQILKR.D	1561.71942	2	4.22E-05	0.85	3.55	-	828.1
AHQ-3-7, 2664	K.ETVQTTEDQILKR.D	1561.71942	2	1.33E-04	0.78	3.01	-	652.1
AHQ-3-6, 2733 - 2743	K.ETVQTTEDQILKR.D	1561.71942	2	4.82E-05	0.88	3.53	-	826.1
AHQ-3-11, 2806	K.ETVQTTEDQILKR.D	1561.71942	2	2.50E-04	0.61	2.69	-	536.4
AHQ-3-4, 2897 - 2905	K.ETVQTTEDQILKR.D	1561.71942	2	1.66E-06	0.85	3.30	-	781.3
AHQ-3-1, 7185	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.12E-05	0.93	4.40	-	707.1
AHQ-3-11, 6602	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	3.26E-06	0.95	4.83	-	961.9
AHQ-3-4, 7364 - 7378	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.46E-10	0.94	4.81	-	881.9
AHQ-3-6, 7402 - 7473	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.18E-04	0.84	3.99	-	526.0
AHQ-3-6, 7117	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.17E-07	0.91	4.46	-	597.4
AHQ-3-5, 7043	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.20E-06	0.89	4.58	-	573.9
AHQ-3-5, 7269 - 7332	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.84E-08	0.97	5.24	-	1367.5
AHQ-3-4, 7710	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.45E-05	0.53	2.76	-	473.6
AHQ-3-4, 7122 - 7188	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	7.45E-07	0.89	4.01	-	737.4
AHQ-3-5, 6621 - 6637	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	4.52E-05	0.64	2.83	-	576.3
AHQ-3-14-, 6284	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	5.62E-08	0.89	3.32	-	1168.5
AHQ-3-11, 6120	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	1.09E-05	0.89	3.57	-	1085.4
AHQ-3-1, 6806	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	8.74E-04	0.58	2.74	-	562.4
AHQ-3-6, 6522	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	7.99E-04	0.80	3.31	-	786.9
AHQ-3-7, 3259	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	5.48E-07	0.83	3.72	-	553.9
AHQ-3-5, 3344 - 3352	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	5.05E-05	0.93	4.75	-	877.8
AHQ-3-4, 3520	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	7.19E-05	0.91	4.10	-	760.6
AHQ-3-4, 2149	K.IAELCDDPKER.D	1347.47690	2	5.28E-07	0.88	3.25	-	1058.5
AHQ-3-4, 3437	K.IAELCDDPKERDDILR.S	1960.15548	3	3.66E-06	0.90	3.96	-	1240.5
AHQ-3-5, 3248 - 3252	K.IAELCDDPKERDDILR.S	1960.15548	3	3.91E-05	0.87	3.89	-	1108.4
AHQ-3-5, 3239 - 3240	K.IAELCDDPKERDDILR.S	1960.15548	2	5.22E-04	0.42	3.07	-	429.5
AHQ-3-12, 2831	R.IPTISTQLK.I	1001.20202	1	3.25E-05	0.24	2.10	-	264.2
AHQ-3-12, 2994	R.IPTISTQLK.I	1001.20202	2	1.33E-05	0.80	2.72	-	685.6
AHQ-3-5, 4212 - 4284	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.97E-04	0.71	3.47	-	261.4
AHQ-3-6, 4166	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	1.20E-08	0.90	4.34	-	1372.7
AHQ-3-4, 4350 - 4425	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	2.13E-08	0.89	4.28	-	372.2
AHQ-3-4, 2785	R.LANVMM*GPYR.Q	1168.41500	2	1.40E-06	0.76	3.13	-	699.9
AHQ-3-5, 2020	R.LANVM*M*GPYR.Q	1184.41440	2	4.58E-04	0.88	3.29	-	782.1
AHQ-3-5, 3019	K.LLAVAATAPPDAPNR.E	1477.69048	2	8.73E-05	0.87	3.32	-	743.6
AHQ-3-4, 4474	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	2	1.69E-04	0.40	2.51	-	315.5
AHQ-3-2, 4463	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	2	2.96E-04	0.72	3.60	-	239.9
AHQ-3-4, 4274 - 4344	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	7.95E-05	0.76	3.54	-	694.7
AHQ-3-1, 4508	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	9.97E-05	0.77	3.46	-	638.8
AHQ-3-6, 4343	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	1.48E-04	0.52	3.04	-	369.8
AHQ-3-5, 4401 - 4483	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	6.75E-06	0.87	4.47	-	501.5
AHQ-3-3, 3802	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	7.35E-06	0.79	3.05	-	576.5
AHQ-3-4, 3728 - 3732	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	9.49E-07	0.93	4.05	-	916.5
AHQ-3-4, 3777	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	3	4.01E-07	0.95	3.95	-	2006.4
AHQ-3-8, 4172	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	3.55E-04	0.92	4.47	-	680.2
AHQ-3-2, 3853	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	3.08E-04	0.88	4.07	-	532.0
AHQ-3-5, 3591 - 3595	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	5.83E-08	0.95	4.87	-	758.0
AHQ-3-5, 3603 - 3619	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	3	1.16E-04	0.94	4.54	-	1646.0
AHQ-3-5, 4475 - 4476	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	3.62E-05	0.88	4.34	-	386.7
AHQ-3-6, 3534 - 3542	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	7.37E-06	0.95	4.83	-	778.4
AHQ-3-12, 4194	R.MALLMAEMSR.L	1153.46531	2	3.82E-04	0.93	3.73	-	1350.8
AHQ-3-5, 4033 - 4112	K.M*LGQM*TDQVADLR.A	1510.71935	2	8.61E-05	0.91	3.48	-	1198.5
AHQ-3-5, 4019 - 4020	K.MLGQMTDQVADLR.A	1478.72055	2	1.32E-06	0.96	4.93	-	1446.0
AHQ-3-3, 2898	K.M*LGQM*TDQVADLR.A	1510.71935	2	9.60E-04	0.81	2.71	-	917.9
AHQ-3-4, 4176	K.MLGQMTDQVADLR.A	1478.72055	2	1.97E-07	0.97	4.31	-	1865.5
AHQ-3-6, 3527 - 3531	K.M*LGQMTDQVADLR.A	1494.71995	2	2.46E-04	0.94	3.35	-	1770.6
AHQ-3-4, 3737	K.M*LGQMTDQVADLR.A	1494.71995	2	2.47E-06	0.95	3.85	-	1845.6
AHQ-3-7, 3920	K.MLGQMTDQVADLR.A	1478.72055	2	3.30E-06	0.90	3.10	-	1268.6
AHQ-3-6, 3965	K.MLGQMTDQVADLR.A	1478.72055	2	5.63E-05	0.97	4.74	-	2274.4
AHQ-3-4, 2846 - 2866	K.M*LGQM*TDQVADLR.A	1510.71935	2	5.82E-06	0.96	4.20	-	1761.1
AHQ-3-4, 4189	K.M*LGQM*TDQVADLR.A	1510.71935	2	1.60E-04	0.87	2.99	-	1166.5
AHQ-3-5, 3121 - 3156	K.MLGQM*TDQVADLR.A	1494.71995	2	5.36E-07	0.92	3.24	-	1542.7
AHQ-3-3, 4272	K.MLGQMTDQVADLR.A	1478.72055	2	5.85E-07	0.97	4.06	-	1993.4
AHQ-3-4, 3254 - 3257	K.MLGQM*TDQVADLR.A	1494.71995	2	3.51E-06	0.93	3.69	-	1543.5
AHQ-3-2, 3882	K.M*LGQMTDQVADLR.A	1494.71995	2	9.33E-05	0.96	3.73	-	1831.8
AHQ-3-1, 3033	K.M*LGQM*TDQVADLR.A	1510.71935	2	1.39E-04	0.92	3.67	-	1298.4
AHQ-3-8, 3764	K.MLGQMTDQVADLR.A	1478.72055	2	2.64E-07	0.95	3.63	-	1727.1
AHQ-3-4, 3068	K.M*SAEINEIIR.V	1192.36823	2	1.52E-05	0.92	3.59	-	1077.5
AHQ-3-4, 3766	K.MSAEINEIIR.V	1176.36883	2	7.12E-05	0.93	3.38	-	1575.9
AHQ-3-5, 3544	K.MSAEINEIIR.V	1176.36883	2	1.55E-05	0.91	3.57	-	1323.5
AHQ-3-5, 2900	K.M*SAEINEIIR.V	1192.36823	2	3.23E-05	0.89	3.29	-	997.8
AHQ-3-5, 2912	K.M*TGLVDEAIDTK.S	1309.46876	1	9.81E-05	0.53	2.54	-	251.8
AHQ-3-5, 2887	K.M*TGLVDEAIDTK.S	1309.46876	2	8.67E-06	0.84	2.84	-	963.8
AHQ-3-6, 3325	K.MTGLVDEAIDTK.S	1293.46936	2	9.12E-07	0.96	3.63	-	1748.5
AHQ-3-4, 3044	K.M*TGLVDEAIDTK.S	1309.46876	1	6.28E-05	0.26	2.36	-	174.9
AHQ-3-4, 3045	K.M*TGLVDEAIDTK.S	1309.46876	2	3.88E-07	0.94	3.62	-	1307.5
AHQ-3-6, 3261 - 3334	K.MTGLVDEAIDTK.S	1293.46936	1	4.87E-04	0.31	2.21	-	286.0
AHQ-3-4, 2854	R.NPGNQAAYEHFETMK.N	1737.87437	2	2.32E-07	0.94	3.97	-	1024.4
AHQ-3-5, 2640	R.NPGNQAAYEHFETMK.N	1737.87437	2	2.68E-05	0.93	3.87	-	1064.0
AHQ-3-4, 2861	K.NQWIDNVEK.M	1146.23464	1	1.67E-04	0.45	2.44	-	266.3
AHQ-3-6, 3153	R.SLGEISALTSK.L	1106.25186	2	1.29E-05	0.93	3.45	-	1031.9
AHQ-3-4, 3368	R.SLGEISALTSK.L	1106.25186	1	4.03E-05	0.23	2.33	-	187.5
AHQ-3-4, 3372	R.SLGEISALTSK.L	1106.25186	2	2.37E-04	0.84	3.18	-	668.3

AHQ-3-1, 3628	R.SLGEISALTSK.L	1106.25186	2	2.62E-04	0.91	3.48	-	783.7
AHQ-3-5, 3177	R.SLGEISALTSK.L	1106.25186	1	6.15E-05	0.10	2.07	-	105.3
AHQ-3-5, 3063	K.SLLDASEEAIKK.D	1304.47187	2	4.54E-06	0.76	2.82	-	713.8
AHQ-3-4, 3236 - 3237	K.SLLDASEEAIKK.D	1304.47187	2	3.43E-07	0.87	2.82	-	1006.5
AHQ-3-7, 2950 - 2967	K.SLLDASEEAIKK.D	1304.47187	2	6.75E-07	0.92	3.54	-	1186.4
AHQ-3-4, 2301	K.STVEGIQASVK.T	1119.25064	2	8.33E-09	0.91	3.32	-	951.9
AHQ-3-5, 2163 - 2213	K.STVEGIQASVK.T	1119.25064	2	6.41E-05	0.80	2.63	-	819.3
AHQ-3-12, 2424	R.TDAGFTLR.W	880.96819	2	5.34E-04	0.83	2.56	-	827.1
AHQ-3-11, 6738 - 6740	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	7.07E-04	0.84	4.47	-	444.5
AHQ-3-5, 7475 - 7481	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	3.60E-06	0.90	4.41	-	578.8
AHQ-3-5, 7284 - 7299	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	5.73E-06	0.86	4.17	-	605.4
AHQ-3-4, 5329	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	4.16E-04	0.61	3.47	-	329.0
AHQ-3-4, 5748 - 5797	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	1.83E-04	0.42	3.01	-	349.8
AHQ-3-13, 5950	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	1.73E-04	0.52	3.50	-	383.6
AHQ-3-13, 6739 - 6805	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.79E-07	0.85	4.37	-	471.7
AHQ-3-12, 5884	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.63E-06	0.85	3.88	-	679.1
AHQ-3-12, 4679	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	3.67E-09	0.77	3.77	-	373.8
AHQ-3-13-, 5947	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	6.13E-04	0.79	3.57	-	601.9
AHQ-3-12, 5458 - 5460	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	8.55E-10	0.91	5.50	-	727.5
AHQ-3-2, 7477	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.53E-05	0.88	4.74	-	483.8
AHQ-3-4, 7040 - 7117	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	6.50E-04	0.68	3.74	-	499.7
AHQ-3-14-, 6688	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	8.54E-04	0.85	4.29	-	500.0
AHQ-3-12, 6558 - 6619	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	1.01E-06	0.46	3.61	-	345.7
AHQ-3-4, 6332 - 6406	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	9.47E-05	0.77	3.50	-	572.8
AHQ-3-12, 6775 - 6818	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	3.31E-07	0.88	4.32	-	612.9
AHQ-3-4, 7386 - 7390	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.25E-08	0.86	3.98	-	670.0
AHQ-3-4, 6336 - 6362	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	3.57E-05	0.66	3.66	-	306.2
AHQ-3-12, 5830 - 5894	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	5.22E-08	0.70	4.45	-	443.2
AHQ-3-12, 3115	R.TNLLQVCER.I	1134.28859	2	2.46E-06	0.87	3.48	-	785.0
AHQ-3-4, 3174	R.TNLLQVCER.I	1134.28859	2	1.22E-05	0.93	3.12	-	1488.6
AHQ-3-5, 5999 - 6068	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	1.40E-04	0.94	4.92	-	650.8
AHQ-3-5, 5345	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	6.05E-07	0.91	4.69	-	1310.2
AHQ-3-4, 5525	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	6.40E-08	0.83	3.77	-	1168.4
AHQ-3-1, 5154	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	5.26E-04	0.85	3.89	-	411.4
AHQ-3-3, 5773 - 5786	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	2	8.11E-05	0.77	3.62	-	476.1
AHQ-3-7, 5148	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	8.28E-04	0.58	3.13	-	449.8
AHQ-3-7, 5843	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	2.53E-05	0.87	4.31	-	513.9
AHQ-3-4, 5002	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	2.82E-06	0.93	4.77	-	721.8
AHQ-3-6, 4791	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	1.67E-04	0.82	3.62	-	584.2
AHQ-3-5, 5317 - 5339	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	2.03E-05	0.90	4.32	-	847.3
AHQ-3-4, 5474 - 5548	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	1.55E-07	0.91	4.68	-	777.6
AHQ-3-4, 6130 - 6204	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	7.02E-04	0.87	4.60	-	385.8
AHQ-3-5, 5024 - 5025	R.VDQLTAQLADLAAR.G	1485.66778	2	1.52E-08	0.98	5.86	-	2894.6
AHQ-3-4, 5321	R.VDQLTAQLADLAAR.G	1485.66778	2	5.65E-04	0.97	4.79	-	1731.2
AHQ-3-1, 5282 - 5285	R.VDQLTAQLADLAAR.G	1485.66778	2	9.67E-08	0.97	4.06	-	2355.3
AHQ-3-4, 5132	R.VDQLTAQLADLAAR.G	1485.66778	2	5.67E-07	0.84	2.81	-	1355.1
AHQ-3-7, 5258	R.VLQLTSWDEDAWASK.D	1749.90156	2	6.50E-07	0.95	4.06	-	1084.7
AHQ-3-3, 5608	R.VLQLTSWDEDAWASK.D	1749.90156	2	3.20E-05	0.94	4.14	-	1015.0
AHQ-3-4, 5476 - 5549	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.20E-04	0.92	3.78	-	838.3
AHQ-3-5, 5331 - 5400	R.VLQLTSWDEDAWASK.D	1749.90156	2	8.12E-06	0.97	4.88	-	1739.7
AHQ-3-2, 5661	R.VLQLTSWDEDAWASK.D	1749.90156	2	6.56E-08	0.94	3.87	-	1043.6
AHQ-3-6, 5314 - 5321	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.12E-12	0.97	4.90	-	1323.7
AHQ-3-4, 2138	R.VM*LVNSM*NTVK.E	1268.52961	2	1.24E-04	0.71	2.91	-	779.1
AHQ-3-4, 3112 - 3121	R.VMLVNSMNTVK.E	1236.53081	2	2.92E-05	0.93	3.42	-	1337.6
AHQ-3-5, 2720	R.WIDNPTVDDR.G	1231.29640	2	7.94E-04	0.94	3.45	-	1533.5
AHQ-3-4, 2830 - 2902	R.WIDNPTVDDR.G	1231.29640	1	2.08E-04	0.19	1.87	-	313.0
AHQ-3-4, 2838	R.WIDNPTVDDR.G	1231.29640	2	5.07E-04	0.93	3.88	-	1022.1
gi|4759212|ref|NP_004598.1|	beta-tubulin cofactor A [Homo sapiens]			1.13E-12	0.98	10.37	16.70	12854.8
AHQ-3-13-, 3339	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	1.41E-06	0.90	4.23	-	653.7
AHQ-3-13-, 3329 - 3334	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	1.13E-12	0.98	7.46	-	1361.6
gi|4557419|ref|NP_000063.1|	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36			1.32E-12	2.80	30.24	10.20	53052.1
AHQ-3-2, 4975	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	3.65E-04	0.36	2.68	-	178.4
AHQ-3-6, 4662 - 4743	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.08E-04	0.56	2.88	-	344.7
AHQ-3-1, 4938 - 4940	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	7.67E-07	0.87	4.09	-	485.0
AHQ-3-1, 5872	K.SQVLQFFSSDICR.S	1588.76661	2	2.50E-05	0.92	3.31	-	1330.0
AHQ-3-6, 5473	K.SQVLQFFSSDICR.S	1588.76661	2	3.61E-08	0.94	4.30	-	1029.1
AHQ-3-5, 5519 - 5520	K.SQVLQFFSSDICR.S	1588.76661	2	2.47E-09	0.97	4.81	-	1432.8
AHQ-3-1, 7201	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.35E-10	0.95	4.20	-	1268.4
AHQ-3-3, 7398	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	6.49E-07	0.94	4.08	-	1088.3
AHQ-3-5, 7323 - 7327	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.32E-12	0.97	4.88	-	1403.6
gi|10835187|ref|NP_000627.1|	superoxide dismutase 2, mitochondrial [Homo sapiens]			1.38E-12	6.49	70.34	59.90	24733.0
AHQ-3-11, 5902 - 5966	K.AIWNVINWENVTER.Y	1744.93137	2	1.63E-10	0.95	4.70	-	1168.5
AHQ-3-13-, 6190	K.AIWNVINWENVTER.Y	1744.93137	2	9.40E-06	0.94	3.61	-	1383.2
AHQ-3-13, 6197	K.AIWNVINWENVTER.Y	1744.93137	2	5.03E-04	0.95	4.13	-	1302.5
AHQ-3-12, 6147	K.AIWNVINWENVTER.Y	1744.93137	2	2.01E-10	0.90	3.98	-	803.8
AHQ-3-11, 6039 - 6051	K.AIWNVINWENVTER.Y	1744.93137	2	6.02E-10	0.96	4.49	-	1254.9
AHQ-3-11, 5956	K.AIWNVINWENVTER.Y	1744.93137	2	1.89E-11	0.96	4.66	-	1335.1
AHQ-3-14-, 6083	K.AIWNVINWENVTER.Y	1744.93137	2	1.12E-08	0.95	4.33	-	1278.8
AHQ-3-11, 5824 - 5888	K.AIWNVINWENVTER.Y	1744.93137	2	1.38E-12	0.93	3.98	-	910.7
AHQ-3-11, 5603	K.AIWNVINWENVTER.Y	1744.93137	2	2.33E-07	0.90	3.29	-	941.9
AHQ-3-11, 4324 - 4398	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	2	9.11E-07	0.95	4.73	-	1001.2
AHQ-3-11, 4467	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	2	5.18E-06	0.90	3.81	-	895.1
AHQ-3-11, 3904	K.GDVTAQIALQPALK.F	1425.65548	2	5.60E-05	0.83	3.32	-	828.7
AHQ-3-11, 3704 - 3766	K.GDVTAQIALQPALK.F	1425.65548	1	2.37E-04	0.83	3.25	-	903.5
AHQ-3-11, 3687 - 3759	K.GDVTAQIALQPALK.F	1425.65548	2	1.35E-06	0.95	4.68	-	1182.5
AHQ-3-11, 3691 - 3754	K.GDVTAQIALQPALK.F	1425.65548	1	6.27E-04	0.56	2.62	-	868.1
AHQ-3-11, 6775	R.GHLQIAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYK.N	4296.85327	3	4.66E-11	0.97	6.71	-	1390.8
AHQ-3-11, 2244	K.HHAAYVNNLNVTEEK.Y	1739.86999	3	3.62E-04	0.90	3.76	-	1337.7
AHQ-3-11, 2150	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	1.76E-10	0.96	4.33	-	1229.9
AHQ-3-11, 3447	K.HHAAYVNNLNVTEEKYQEALAK.G	2543.77604	3	3.76E-07	0.90	4.70	-	820.8
AHQ-3-11, 5976 - 6056	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	5.44E-06	0.84	3.91	-	528.3
AHQ-3-11, 6387 - 6388	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	6.15E-04	0.78	3.65	-	485.0
AHQ-3-11, 6816	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	1.58E-05	0.79	3.37	-	608.0
gi|13562114|ref|NP_110400.1|	beta tubulin 1, class VI [Homo sapiens]			2.85E-12	18.79	220.35	55.20	50326.6
AHQ-3-1, 6625	R.ALSVAELTQQMFDAR.N	1680.90740	2	4.24E-04	0.88	3.35	-	1136.8
AHQ-3-9, 5935 - 5952	R.ALSVAELTQQMFDAR.N	1680.90740	2	8.55E-05	0.95	4.57	-	1238.1
AHQ-3-10, 5746	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.44E-06	0.93	4.23	-	1131.1
AHQ-3-7, 6190 - 6270	R.ALSVAELTQQMFDAR.N	1680.90740	2	3.36E-06	0.96	5.33	-	1353.0
AHQ-3-11, 5950 - 5954	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.14E-06	0.97	4.95	-	1811.0
AHQ-3-7, 4427 - 4502	R.ALSVAELTQQM*FDAR.N	1696.90680	2	2.41E-07	0.94	4.68	-	843.9
AHQ-3-4, 6636 - 6638	R.ALSVAELTQQMFDAR.N	1680.90740	2	4.34E-05	0.83	3.06	-	1099.9
AHQ-3-7, 4491	R.ALSVAELTQQM*FDAR.N	1696.90680	2	3.11E-05	0.97	5.01	-	1565.5
AHQ-3-7, 4750	R.AVLVDLEPGTMDSIR.S	1616.86162	2	9.11E-10	0.93	4.46	-	799.1
AHQ-3-7, 3558 - 3634	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	3.03E-04	0.89	4.15	-	563.5
AHQ-3-7, 3006	K.EVDQQLLSVQTR.N	1416.56231	2	4.41E-05	0.93	4.55	-	903.6
AHQ-3-9, 2873	K.EVDQQLLSVQTR.N	1416.56231	1	2.92E-05	0.19	2.17	-	116.3
AHQ-3-14, 5740	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	3	4.40E-06	0.87	3.62	-	770.9

AHQ-3-14, 5739 - 5747	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	1.00E-04	0.96	4.88	-	968.3
AHQ-3-14, 6172	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	7.42E-07	0.98	5.86	-	1891.9
AHQ-3-10, 4744	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	7.79E-04	0.94	4.23	-	1180.1
AHQ-3-13, 5201 - 5202	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.49E-07	0.98	6.17	-	1853.0
AHQ-3-13-, 5181	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	3.12E-12	0.98	6.31	-	2203.8
AHQ-3-14-, 5115 - 5172	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.20E-06	0.98	6.17	-	2166.0
AHQ-3-11, 4962	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	7.93E-05	0.95	4.70	-	1069.5
AHQ-3-14-, 4609	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	8.91E-07	0.95	4.77	-	809.7
AHQ-3-12, 5182	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	3.39E-07	0.98	5.46	-	1946.2
AHQ-3-12, 5319	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	9.58E-04	0.76	3.40	-	562.9
AHQ-3-7, 5122 - 5190	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.85E-12	0.98	6.12	-	2394.6
AHQ-3-12, 2218	R.GASALQLER.I	945.05542	2	2.83E-04	0.63	2.76	-	786.7
AHQ-3-11, 6426	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	7.52E-04	0.82	3.75	-	1284.8
AHQ-3-13-, 6705	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.22E-10	0.98	6.93	-	2422.6
AHQ-3-13-, 6702	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	4.23E-04	0.90	4.12	-	1604.7
AHQ-3-3, 7176	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	8.21E-09	0.98	6.65	-	2144.2
AHQ-3-10, 6207 - 6216	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.41E-07	0.98	6.00	-	2185.1
AHQ-3-5, 7024	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.41E-04	0.98	5.60	-	2463.1
AHQ-3-7, 6730 - 6798	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.73E-11	0.99	7.00	-	2531.3
AHQ-3-7, 6732	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.03E-04	0.95	5.19	-	1657.2
AHQ-3-13, 6713 - 6719	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	9.66E-09	0.99	6.36	-	3025.3
AHQ-3-14-, 6599 - 6600	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.48E-07	0.98	6.93	-	2452.0
AHQ-3-9, 6511	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.10E-05	0.97	5.23	-	1832.6
AHQ-3-14-, 6597 - 6603	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.72E-06	0.88	4.67	-	1072.8
AHQ-3-11, 6419	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.53E-08	0.98	6.75	-	2252.3
AHQ-3-8, 6537 - 6609	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.88E-04	0.95	4.23	-	1947.7
AHQ-3-7, 6768	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.77E-09	0.91	4.20	-	748.1
AHQ-3-10, 6040	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	6.62E-04	0.64	3.14	-	392.4
AHQ-3-12, 6456	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	4.91E-07	0.88	3.98	-	645.7
AHQ-3-1, 6882 - 6894	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	7.58E-04	0.80	3.29	-	676.2
AHQ-3-14-, 6355 - 6371	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.19E-09	0.94	5.22	-	736.1
AHQ-3-14-, 6220	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	4.48E-04	0.78	3.23	-	620.7
AHQ-3-7, 6586 - 6662	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	2.76E-09	0.94	4.68	-	859.3
AHQ-3-13, 6478 - 6481	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	9.25E-07	0.96	5.32	-	936.7
AHQ-3-9, 6337 - 6401	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.25E-04	0.91	4.10	-	795.1
AHQ-3-7, 7243 - 7315	R.GLSMAATFIGNNTAIQEIFNR.V	2269.56611	2	2.28E-07	0.93	4.77	-	799.0
AHQ-3-12, 6187	R.HESESCDCLQGFQIVHSLGGGTGSGMGTLLMNK.I	3511.88634	3	5.52E-08	0.96	4.82	-	2119.6
AHQ-3-11, 5974	R.HESESCDCLQGFQIVHSLGGGTGSGMGTLLMNK.I	3511.88634	3	7.61E-05	0.79	3.63	-	651.7
AHQ-3-7, 3767	R.IMNSFSVMPSPK.V	1338.62160	2	1.35E-06	0.84	2.94	-	717.2
AHQ-3-7, 3780 - 3784	R.IMNSFSVMPSPK.V	1338.62160	1	1.01E-07	0.52	2.32	-	571.7
AHQ-3-7, 3490 - 3538	R.IMNSFSVMPSPK.V	1338.62160	2	3.85E-06	0.92	3.35	-	1333.8
AHQ-3-7, 3232	R.IM*NSFSVMPSPK.V	1354.62100	2	6.50E-04	0.84	3.48	-	565.2
AHQ-3-7, 3008	R.IM*NSFSVMPSPK.V	1354.62100	2	5.90E-06	0.87	3.81	-	749.2
AHQ-3-13-, 3223	R.ISVYYNEAYGR.K	1335.44622	2	8.14E-09	0.87	2.82	-	961.4
AHQ-3-7, 2908	R.ISVYYNEAYGR.K	1335.44622	2	7.13E-08	0.94	3.39	-	1326.4
AHQ-3-14-, 3173	R.ISVYYNEAYGR.K	1335.44622	2	3.41E-07	0.93	3.32	-	1219.2
AHQ-3-13, 3226	R.ISVYYNEAYGR.K	1335.44622	2	2.15E-08	0.88	2.68	-	1126.4
AHQ-3-12, 3090	R.ISVYYNEAYGR.K	1335.44622	2	3.96E-07	0.91	3.42	-	978.4
AHQ-3-14-, 3031 - 3032	R.ISVYYNEAYGR.K	1335.44622	2	3.32E-07	0.96	3.69	-	1685.8
AHQ-3-14, 3967 - 4011	R.ISVYYNEAYGR.K	1335.44622	2	7.51E-07	0.92	3.00	-	1095.4
AHQ-3-12, 5115	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	2.23E-06	0.85	3.61	-	634.8
AHQ-3-7, 4714	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	1.91E-09	0.87	4.14	-	681.3
AHQ-3-13, 5099	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	8.12E-08	0.80	3.35	-	618.1
AHQ-3-13-, 5093	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	1.68E-09	0.87	4.21	-	585.0
AHQ-3-12, 5012 - 5015	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	7.71E-06	0.89	3.81	-	887.4
AHQ-3-13-, 5182	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	7.82E-07	0.82	3.59	-	755.6
AHQ-3-7, 4834 - 4855	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	3.57E-06	0.98	6.12	-	2994.7
AHQ-3-9, 5271	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	3.53E-06	0.97	5.81	-	995.9
AHQ-3-7, 5552 - 5558	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	2.37E-09	0.97	6.09	-	689.0
AHQ-3-10, 5262	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	3.63E-05	0.93	4.46	-	597.9
AHQ-3-12, 5151	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	2.72E-06	0.96	5.04	-	1005.4
AHQ-3-7, 4827	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	6.08E-04	0.95	4.33	-	1055.3
AHQ-3-14-, 5109 - 5124	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	8.19E-05	0.89	4.02	-	1197.9
AHQ-3-11, 5547	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	3.56E-06	0.96	5.81	-	723.9
AHQ-3-12, 5776	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	6.37E-04	0.96	5.06	-	859.9
AHQ-3-9, 4609 - 4611	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	5.55E-07	0.95	4.97	-	838.4
AHQ-3-8, 4515	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.84E-04	0.96	5.17	-	927.5
AHQ-3-8, 5199	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	2.54E-04	0.95	4.56	-	741.9
AHQ-3-11, 4894 - 4906	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	3.92E-05	0.97	5.69	-	1054.7
AHQ-3-8, 4521	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	8.06E-05	0.90	3.43	-	1722.7
AHQ-3-10, 4651 - 4654	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.57E-04	0.96	5.20	-	1055.9
AHQ-3-8, 6597	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.96E-04	0.68	3.21	-	645.4
AHQ-3-14-, 6551	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	9.61E-06	0.90	4.03	-	1111.4
AHQ-3-14-, 6524 - 6583	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	8.24E-07	0.94	5.08	-	931.9
AHQ-3-7, 5964	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	7.49E-04	0.59	3.17	-	356.8
AHQ-3-8, 7227	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.15E-06	0.92	4.84	-	757.4
AHQ-3-7, 7350 - 7351	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	7.75E-08	0.95	5.40	-	1220.2
AHQ-3-10, 6534	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	5.27E-08	0.95	4.97	-	1030.8
AHQ-3-7, 6700 - 6770	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.77E-04	0.77	3.63	-	442.8
AHQ-3-7, 6866 - 6888	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	5.02E-08	0.91	4.70	-	780.3
AHQ-3-9, 6975 - 6976	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	2.21E-06	0.93	4.65	-	1231.8
AHQ-3-9, 6971 - 7003	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.23E-09	0.96	5.59	-	984.3
AHQ-3-4, 7524 - 7526	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	2.01E-06	0.95	5.36	-	824.4
AHQ-3-3, 7506	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	7.72E-05	0.90	3.96	-	1190.9
AHQ-3-9, 6519 - 6533	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	8.33E-06	0.93	4.70	-	1098.6
AHQ-3-7, 6874 - 6875	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.19E-05	0.93	4.74	-	1042.0
AHQ-3-3, 7504	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	6.63E-05	0.86	3.48	-	801.5
AHQ-3-1, 7064	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.93E-05	0.88	4.43	-	583.4
AHQ-3-12, 6622	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	3.69E-05	0.93	4.64	-	1147.4
AHQ-3-7, 6022	R.NSSCFVEWIPNNVK.V	1695.87718	2	9.11E-05	0.67	2.70	-	690.7
AHQ-3-7, 5383 - 5391	R.NSSCFVEWIPNNVK.V	1695.87718	2	7.54E-04	0.41	3.05	-	472.4
AHQ-3-9, 4920	R.NSSCFVEWIPNNVK.V	1695.87718	2	1.17E-04	0.77	3.36	-	552.9
AHQ-3-13, 5287	R.YLTVACIFR.G	1144.36822	2	5.03E-05	0.86	2.95	-	654.2
AHQ-3-12, 5252	R.YLTVACIFR.G	1144.36822	2	9.86E-04	0.88	2.81	-	805.6
AHQ-3-11, 5010	R.YLTVACIFR.G	1144.36822	2	1.45E-04	0.88	2.93	-	879.6
gi|5729877|ref|NP_006588.1| heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD				2.87E-12	13.51	150.27	26.90	70897.6
AHQ-3-6, 4575	R.FEELNADLFR.G	1254.37310	2	1.30E-05	0.91	3.66	-	1008.6
AHQ-3-6, 5218 - 5290	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	2	2.59E-08	0.96	5.43	-	1399.2
AHQ-3-6, 5209	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	2.87E-12	0.94	4.98	-	1088.1
AHQ-3-6, 2938	K.HWPFM*VVNDAGRPK.V	1670.91910	3	8.50E-07	0.93	4.08	-	1150.0
AHQ-3-6, 5571 - 5639	K.ILDKCNEIINWLDK.N	1776.04688	2	3.97E-04	0.94	4.19	-	1282.5
AHQ-3-6, 3010 - 3067	R.MVNHFIAEFK.R	1236.46756	2	1.22E-07	0.95	3.64	-	1521.7
AHQ-3-14-, 2897	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	1.72E-05	0.91	3.83	-	644.4
AHQ-3-6, 2773 - 2774	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	1.17E-05	0.95	4.56	-	1023.9
AHQ-3-6, 3321	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	3.28E-05	0.92	4.06	-	968.6
AHQ-3-6, 3737	K.NQVAMNPTNTVFDAK.R	1650.83816	2	3.81E-06	0.74	3.21	-	678.7
AHQ-3-6, 3886	K.NSLESYAFNMK.A	1304.45393	2	9.54E-05	0.86	2.95	-	869.9

AHQ-3-6, 2427	R.RFDDAVVQSDMK.H	1411.56603	2	4.10E-06	0.96	3.92	-	1511.4
AHQ-3-6, 1903 - 1913	R.RFDDAVVQSDM*K.H	1427.56543	2	4.69E-05	0.90	3.69	-	788.0
AHQ-3-6, 4390 - 4393	K.SFYPEEVSSM*VLTK.M	1633.84425	2	3.20E-04	0.85	3.26	-	600.1
AHQ-3-6, 7079	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	8.48E-05	0.70	3.65	-	445.1
AHQ-3-7, 6906	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	1.62E-06	0.95	4.47	-	1209.5
AHQ-3-6, 6861 - 6934	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	1.04E-06	0.96	4.94	-	1210.2
AHQ-3-6, 2775	K.SQIHDIVLVGGSTR.I	1482.66712	1	4.98E-04	0.87	3.49	-	767.2
AHQ-3-6, 2771	K.SQIHDIVLVGGSTR.I	1482.66712	2	6.67E-10	0.96	4.26	-	1590.0
AHQ-3-6, 2786	K.SQIHDIVLVGGSTR.I	1482.66712	1	4.47E-07	0.69	2.83	-	377.0
AHQ-3-7, 2694	K.SQIHDIVLVGGSTR.I	1482.66712	2	1.54E-08	0.98	4.59	-	2253.2
AHQ-3-6, 4759	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	1.78E-08	0.82	3.71	-	346.0
AHQ-3-6, 2181 - 2191	K.VCNPIITK.L	946.14652	2	1.56E-04	0.85	2.81	-	661.9
gi|9507215|ref|NP_061816.1| tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]				3.02E-12	3.48	40.22	10.90	50093.2
AHQ-3-14, 5936	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	3.61E-04	0.94	3.98	-	1166.8
AHQ-3-13, 4921	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	1.71E-07	0.90	3.71	-	864.6
AHQ-3-7, 5204 - 5207	R.AVMIDLEPTVVDEVR.A	1686.95185	2	9.79E-06	0.81	3.96	-	604.4
AHQ-3-9, 5092	R.IHFPLVTYAPIISAEK.A	1800.13312	2	2.00E-05	0.76	2.97	-	425.8
AHQ-3-7, 5338	R.IHFPLVTYAPIISAEK.A	1800.13312	2	9.12E-07	0.85	3.28	-	566.3
AHQ-3-14-, 5243	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	3.02E-12	0.92	4.48	-	711.9
AHQ-3-13, 5317 - 5331	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	1.28E-10	0.90	4.24	-	749.3
gi|17986258|ref|NP_066299.2| smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo				3.17E-12	5.59	60.28	37.10	16930.0
AHQ-3-12, 4182 - 4251	K.DQGTYEDYVEGLR.V	1545.58904	2	2.30E-10	0.94	4.20	-	1091.0
AHQ-3-13-, 4234	K.DQGTYEDYVEGLR.V	1545.58904	2	1.02E-06	0.87	2.56	-	1374.9
AHQ-3-14-, 4204	K.DQGTYEDYVEGLR.V	1545.58904	2	7.77E-05	0.73	2.68	-	722.9
AHQ-3-13, 4243 - 4307	K.DQGTYEDYVEGLR.V	1545.58904	2	1.29E-05	0.70	2.86	-	394.1
AHQ-3-12, 2231	R.HVLVTLGEK.M	996.18547	2	2.42E-06	0.88	2.77	-	854.8
AHQ-3-13, 2318 - 2325	R.HVLVTLGEK.M	996.18547	2	1.21E-06	0.89	3.42	-	748.1
AHQ-3-12, 2146 - 2203	R.HVLVTLGEK.M	996.18547	1	9.59E-04	0.75	3.29	-	603.4
AHQ-3-13-, 2258	R.HVLVTLGEK.M	996.18547	1	2.56E-04	0.78	2.89	-	695.1
AHQ-3-13, 2330	R.HVLVTLGEK.M	996.18547	1	2.26E-05	0.55	2.67	-	531.3
AHQ-3-13-, 2259 - 2265	R.HVLVTLGEK.M	996.18547	2	1.49E-04	0.85	2.84	-	666.2
AHQ-3-12, 2140 - 2168	R.HVLVTLGEK.M	996.18547	2	8.28E-06	0.91	3.10	-	935.3
AHQ-3-12, 4022 - 4023	K.NKDQGTYEDYVEGLR.V	1787.86505	3	4.26E-05	0.52	3.10	-	599.2
AHQ-3-12, 3952 - 4018	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.06E-09	0.87	3.70	-	914.4
AHQ-3-14-, 3632	K.NKDQGTYEDYVEGLR.V	1787.86505	3	7.42E-05	0.87	3.81	-	1029.2
AHQ-3-12, 3894	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.28E-04	0.90	4.04	-	1455.8
AHQ-3-13-, 3758	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.46E-07	0.93	4.10	-	1199.1
AHQ-3-12, 3691 - 3758	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.35E-04	0.94	4.38	-	1555.0
AHQ-3-12, 3678 - 3743	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.15E-06	0.93	4.22	-	980.2
AHQ-3-12, 3598 - 3614	K.NKDQGTYEDYVEGLR.V	1787.86505	3	4.01E-05	0.94	4.77	-	1424.4
AHQ-3-13, 3742	K.NKDQGTYEDYVEGLR.V	1787.86505	2	8.58E-09	0.93	4.21	-	982.6
AHQ-3-13, 3743 - 3745	K.NKDQGTYEDYVEGLR.V	1787.86505	3	5.27E-05	0.82	3.23	-	1041.3
AHQ-3-13, 4047 - 4051	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.17E-12	0.92	3.78	-	1088.1
AHQ-3-12, 3591 - 3654	K.NKDQGTYEDYVEGLR.V	1787.86505	2	5.99E-09	0.93	3.94	-	1049.6
AHQ-3-14-, 3635	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.93E-08	0.92	4.05	-	1009.7
AHQ-3-14, 4571	K.NKDQGTYEDYVEGLR.V	1787.86505	2	6.90E-08	0.94	4.19	-	1226.1
AHQ-3-13, 3325 - 3346	R.VFDKEGNGTVMGAEIR.H	1723.93228	2	1.67E-09	0.94	4.21	-	1118.1
AHQ-3-13, 6337	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	6.45E-07	0.92	4.35	-	747.8
AHQ-3-13, 6817 - 6819	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	8.05E-08	0.93	4.99	-	584.3
AHQ-3-12, 6816 - 6820	K.VLDFEHFLPMLQTVAK.N	1889.25017	3	1.94E-06	0.95	4.68	-	1881.9
AHQ-3-12, 6518	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	4.32E-04	0.81	3.79	-	529.6
AHQ-3-13-, 6337 - 6347	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	3.82E-05	0.90	4.13	-	648.3
AHQ-3-13-, 6354	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	9.65E-05	0.88	4.13	-	673.1
AHQ-3-13-, 6757	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	3.14E-07	0.95	5.15	-	809.3
AHQ-3-13-, 6762 - 6763	K.VLDFEHFLPMLQTVAK.N	1889.25017	3	2.63E-04	0.97	5.67	-	1777.6
AHQ-3-12, 6342	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	4.38E-09	0.95	4.66	-	849.8
AHQ-3-12, 6246 - 6319	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	1.82E-04	0.80	3.48	-	777.2
AHQ-3-12, 6208 - 6280	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	2.61E-06	0.95	4.68	-	864.0
AHQ-3-14-, 6227 - 6248	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	4.80E-05	0.90	4.11	-	696.6
AHQ-3-14-, 6235 - 6239	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	3.41E-05	0.90	4.46	-	730.4
AHQ-3-14-, 6695 - 6700	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	1.27E-09	0.96	4.95	-	1061.7
gi|16933542|ref|NP_002017.1| fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s				3.21E-12	7.37	90.24	6.50	259222.8
AHQ-3-1, 6278	K.FTQVTPTSLSAQWTPPNVQLTGYR.V	2693.99453	2	2.27E-05	0.91	4.37	-	451.5
AHQ-3-1, 2800	R.GDSPASSKPISINYR.T	1592.73521	2	3.21E-12	0.83	3.70	-	410.6
AHQ-3-1, 5142	R.NLQPASEYTVSLVAIK.G	1733.98671	2	3.11E-04	0.91	3.92	-	542.4
AHQ-3-2, 6403 - 6406	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	6.31E-07	0.91	4.26	-	726.3
AHQ-3-1, 6320	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	3.25E-07	0.95	4.87	-	837.4
AHQ-3-1, 4901 - 4914	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	1.04E-05	0.92	4.20	-	1231.5
AHQ-3-1, 3898 - 3916	R.SYTITGLQPGTDYK.I	1544.68732	2	4.04E-04	0.36	2.71	-	403.2
AHQ-3-1, 4114	R.VDVIPVNLPGEHGQR.L	1630.82981	2	4.86E-09	0.81	3.06	-	608.0
AHQ-3-1, 7180	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	2.24E-06	0.77	2.91	-	472.8
AHQ-3-2, 7446	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	3.18E-05	0.62	2.86	-	229.1
AHQ-3-1, 4010	K.YSFCTDHTVLVQTR.G	1728.90717	2	9.30E-07	0.92	3.95	-	1186.1
gi|13994151|ref|NP_066272.1| PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H				3.76E-12	16.89	190.31	73.30	36071.5
AHQ-3-13, 6637 - 6697	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.14E-07	0.88	4.59	-	369.1
AHQ-3-14-, 6555 - 6615	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.98E-07	0.96	6.21	-	764.7
AHQ-3-14-, 6465 - 6527	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.88E-08	0.93	5.14	-	650.8
AHQ-3-14-, 6279 - 6351	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	2.42E-10	0.96	5.84	-	958.3
AHQ-3-14-, 5940 - 6009	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	5.86E-05	0.88	4.48	-	688.0
AHQ-3-11, 6616	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	7.87E-07	0.94	4.87	-	973.7
AHQ-3-13-, 6751	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	8.96E-09	0.92	5.00	-	887.5
AHQ-3-13-, 6642	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.22E-06	0.90	4.57	-	579.1
AHQ-3-13, 6813	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	8.09E-10	0.83	4.25	-	424.6
AHQ-3-14-, 6681	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.58E-06	0.72	3.30	-	330.2
AHQ-3-12, 6843	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	3.76E-12	0.92	4.87	-	777.0
AHQ-3-12, 6626	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.01E-09	0.93	5.06	-	798.7
AHQ-3-13, 4431	K.CGTGIVGVFVK.L	1138.36198	2	8.73E-05	0.93	3.26	-	1185.6
AHQ-3-14-, 4409	K.CGTGIVGVFVK.L	1138.36198	2	1.83E-04	0.93	2.86	-	1355.5
AHQ-3-13-, 3627 - 3690	K.DFEQPLAISR.V	1176.30388	2	2.05E-04	0.91	3.25	-	1149.2
AHQ-3-14-, 3563 - 3583	K.DFEQPLAISR.V	1176.30388	2	2.40E-04	0.74	2.68	-	743.8
AHQ-3-12, 3587	K.DFEQPLAISR.V	1176.30388	2	1.87E-05	0.90	3.52	-	955.3
AHQ-3-12, 3590	K.DFEQPLAISR.V	1176.30388	1	8.29E-05	0.17	1.96	-	343.8
AHQ-3-13, 3651 - 3662	K.DFEQPLAISR.V	1176.30388	2	4.73E-05	0.94	3.56	-	1147.9
AHQ-3-13, 3654 - 3658	K.DFEQPLAISR.V	1176.30388	1	4.04E-04	0.12	2.29	-	175.4
AHQ-3-13-, 3361 - 3369	K.GCTDNLTLTVAR.S	1322.47058	2	1.80E-04	0.82	3.42	-	648.3
AHQ-3-13, 3381 - 3385	K.GCTDNLTLTVAR.S	1322.47058	2	5.62E-04	0.85	3.51	-	755.1
AHQ-3-14, 4892 - 4956	K.GHFFVEDQIYCEK.H	1673.82684	2	1.29E-04	0.90	3.03	-	885.0
AHQ-3-13, 4005 - 4066	K.GHFFVEDQIYCEK.H	1673.82684	2	1.89E-05	0.95	4.37	-	1100.6
AHQ-3-12, 3966 - 4039	K.GHFFVEDQIYCEK.H	1673.82684	2	5.54E-04	0.96	4.13	-	1227.3
AHQ-3-13-, 4015	K.GHFFVEDQIYCEK.H	1673.82684	2	1.21E-04	0.96	4.23	-	1214.7
AHQ-3-13-, 2665	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	4.95E-09	0.96	5.36	-	1193.1
AHQ-3-14, 3911 - 3976	R.IKGCTDNLTLTVAR.S	1563.80174	2	3.29E-10	0.91	3.55	-	874.8
AHQ-3-11, 3192	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.77E-04	0.65	2.52	-	795.5
AHQ-3-11, 2983 - 2986	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.77E-08	0.95	3.96	-	1240.4
AHQ-3-13-, 2975 - 3054	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.04E-08	0.95	4.21	-	1155.9
AHQ-3-13, 3079	R.IKGCTDNLTLTVAR.S	1563.80174	2	7.32E-11	0.96	4.66	-	1156.7
AHQ-3-14-, 3015	R.IKGCTDNLTLTVAR.S	1563.80174	2	6.97E-10	0.95	4.63	-	990.0

AHQ-3-14, 4036	R.IKGCTDNLTLTVAR.S	1563.80174	2	7.36E-06	0.89	3.15	-	981.9
AHQ-3-14-, 4769	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	3	3.56E-04	0.86	3.61	-	776.9
AHQ-3-12, 4707 - 4752	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	2	3.84E-04	0.79	3.40	-	483.6
AHQ-3-13-, 3785	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.90E-08	0.96	4.61	-	1379.0
AHQ-3-14-, 3663 - 3740	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.48E-08	0.96	5.12	-	1196.7
AHQ-3-13, 3781	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.85E-05	0.92	3.74	-	1146.5
AHQ-3-14, 4588 - 4607	R.LVGGKDFEQPLAISR.V	1630.86972	2	2.06E-08	0.95	4.50	-	1258.6
AHQ-3-13, 4054	K.MNLASEPQEVLHIGSAHNR.S	2104.33619	2	3.75E-09	0.91	4.28	-	642.1
AHQ-3-13-, 3710	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	1.98E-05	0.90	4.45	-	536.4
AHQ-3-13, 3497	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	3.92E-05	0.78	3.63	-	455.5
AHQ-3-12, 3530	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	8.76E-06	0.90	4.28	-	531.2
AHQ-3-13, 3499	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	3.33E-06	0.90	3.91	-	629.8
AHQ-3-12, 6630	K.QSTSFLVLQEILESEEK.G	1981.18977	2	1.93E-07	0.97	4.75	-	1632.6
AHQ-3-13-, 6639	K.QSTSFLVLQEILESEEK.G	1981.18977	2	6.08E-06	0.97	5.05	-	1780.4
AHQ-3-13, 6657	K.QSTSFLVLQEILESEEK.G	1981.18977	2	4.44E-10	0.95	4.01	-	1397.2
AHQ-3-13, 6163	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	7.37E-06	0.87	3.86	-	834.8
AHQ-3-12, 6084	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	3.41E-05	0.65	3.34	-	412.8
AHQ-3-14-, 6072	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	2.25E-04	0.70	3.57	-	383.9
AHQ-3-13, 2477	R.SAM*PFTASPASSTTAR.V	1599.74799	2	3.62E-06	0.90	3.58	-	990.7
AHQ-3-13-, 2969 - 2971	R.SAMPFTASPASSTTAR.V	1583.74859	2	1.45E-04	0.40	2.67	-	455.4
AHQ-3-12, 2387	R.SAM*PFTASPASSTTAR.V	1599.74799	2	7.32E-06	0.90	3.37	-	922.5
AHQ-3-11, 2876 - 2948	R.SAMPFTASPASSTTAR.V	1583.74859	2	2.95E-04	0.32	2.56	-	351.4
AHQ-3-11, 3864	K.TAASGVEANSRPLDHAQPPSSLVIDKESEVYK.M	3397.69458	3	1.35E-04	0.95	6.05	-	1059.0
AHQ-3-12, 5443	R.VITNQYNNPAGLYSSENISNFNNALESK.T	3103.30221	3	4.77E-05	0.90	4.42	-	885.2
AHQ-3-11, 2892 - 2899	K.VWSPLVTEEGKR.H	1401.59247	2	5.56E-09	0.89	3.14	-	1073.6
AHQ-3-14-, 2959	K.VWSPLVTEEGKR.H	1401.59247	2	5.45E-10	0.92	3.35	-	1151.7
AHQ-3-12, 3002	K.VWSPLVTEEGKR.H	1401.59247	2	5.40E-06	0.61	2.70	-	509.1
gi|7706497|ref|NP_057392.1|	UMP-CMP kinase [Homo sapiens]			4.03E-12	2.75	30.24	20.20	25854.7
AHQ-3-11, 5886	R.IQTYLQSTKPIIDLYEEMGK.V	2371.73502	2	2.54E-08	0.93	4.43	-	640.5
AHQ-3-11, 2458	R.KNPDSQYGELIEK.Y	1521.65375	2	6.03E-05	0.86	3.59	-	609.8
AHQ-3-11, 3614	K.YGYTHLSAGELLR.D	1480.64969	2	4.03E-12	0.96	4.71	-	1272.8
gi|7657007|ref|NP_055210.1|	dual adaptor of phosphotyrosine and 3-phosphoinositides [Homo sapiens]			4.12E-12	3.57	40.24	22.50	32044.2
AHQ-3-13-, 3877	R.DSNETTGLYSLSVR.A	1542.62982	2	2.94E-06	0.78	2.99	-	866.7
AHQ-3-13, 5094	R.HAAEALLLSNGCDGSYLLR.D	2062.29263	2	5.46E-11	0.97	4.87	-	1677.3
AHQ-3-13, 6010	R.SDGEAELLQDLGWYHGNLTR.H	2275.41943	3	4.12E-12	0.95	4.45	-	1702.7
AHQ-3-13-, 3402 - 3403	K.TGVEADEWIK.I	1148.24730	2	1.30E-04	0.87	3.04	-	771.4
gi|5729887|ref|NP_006624.1|	IQ motif containing GTPase activating protein 2 [Homo sapiens]			4.23E-12	7.44	80.30	6.80	180611.0
AHQ-3-5, 3492	K.AWVNQLETQTGEASK.L	1662.78230	2	1.54E-06	0.97	5.68	-	1274.7
AHQ-3-4, 3672	K.AWVNQLETQTGEASK.L	1662.78230	2	3.86E-05	0.92	4.15	-	1043.2
AHQ-3-6, 5567	K.GVLLDIDDLQTNQFK.N	1719.91690	2	1.92E-05	0.94	4.30	-	1401.5
AHQ-3-13-, 5497	K.GVLLDIDDLQTNQFK.N	1719.91690	2	3.77E-05	0.94	4.66	-	1274.2
AHQ-3-3, 5881 - 5888	K.GVLLDIDDLQTNQFK.N	1719.91690	2	9.14E-10	0.98	6.09	-	1638.0
AHQ-3-3, 2293	R.KSFLHEQEENVVK.I	1587.75856	2	4.72E-06	0.92	3.62	-	1277.4
AHQ-3-4, 4933	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	4.23E-12	0.97	4.94	-	1493.0
AHQ-3-3, 4989 - 4998	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	2.79E-07	0.94	3.93	-	1213.0
AHQ-3-6, 6845	R.NQPGNTLTEILETPATAQQEVDHATDMVSR.A	3268.51558	3	1.86E-04	0.83	3.84	-	499.5
AHQ-3-3, 4205	K.TLVGSENPPLTVIR.K	1496.73370	2	1.83E-04	0.87	3.50	-	807.6
AHQ-3-3, 4312	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	5.35E-08	0.97	5.60	-	1550.7
AHQ-3-4, 4236	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	1.28E-05	0.92	3.89	-	925.5
AHQ-3-3, 7482	K.VLNSIISSLDLLPYGLR.Y	1874.21354	2	9.02E-08	0.93	4.48	-	725.9
gi|7661678|ref|NP_056461.1|	RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B			4.53E-12	7.52	90.33	33.70	20824.7
AHQ-3-11, 4223	K.DTDDVPMILVGNK.C	1417.61048	2	9.58E-09	0.84	3.34	-	639.2
AHQ-3-11, 4787 - 4806	K.DTDDVPMILVGNKCDLEDER.V	2336.53972	2	7.79E-04	0.42	2.57	-	488.7
AHQ-3-11, 6444	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	1.31E-05	0.89	4.61	-	869.3
AHQ-3-11, 6611	R.KQVEVDAQQCMLEILDTAGTEQFTAMR.D	3115.50608	3	1.05E-04	0.91	4.52	-	844.8
AHQ-3-13-, 6643	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	3.38E-05	0.65	3.29	-	684.2
AHQ-3-11, 6360 - 6378	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	1.96E-07	0.94	5.01	-	1047.5
AHQ-3-14-, 5233 - 5237	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	1.58E-08	0.98	6.62	-	2385.1
AHQ-3-11, 4162 - 4164	R.QWNNCAFLESSAK.S	1556.68148	2	1.42E-06	0.28	2.70	-	165.2
AHQ-3-11, 3955 - 3971	R.QWNNCAFLESSAK.S	1556.68148	2	3.21E-06	0.61	2.72	-	304.6
AHQ-3-11, 4052	R.QWNNCAFLESSAK.S	1556.68148	2	1.00E-05	0.64	2.84	-	286.4
AHQ-3-11, 3803 - 3867	R.QWNNCAFLESSAK.S	1556.68148	2	6.93E-08	0.62	3.11	-	185.8
AHQ-3-13-, 3854	R.VKDTDDVPMILVGNK.C	1644.91497	2	7.76E-05	0.97	4.72	-	1747.9
AHQ-3-13, 3827 - 3843	R.VKDTDDVPMILVGNK.C	1644.91497	2	1.23E-08	0.96	4.13	-	1691.8
AHQ-3-13-, 3851	R.VKDTDDVPMILVGNK.C	1644.91497	3	3.35E-04	0.95	4.62	-	1752.0
AHQ-3-11, 3506 - 3570	R.VKDTDDVPMILVGNK.C	1644.91497	2	8.02E-08	0.96	4.68	-	1500.8
AHQ-3-14, 4699 - 4759	R.VKDTDDVPMILVGNK.C	1644.91497	2	3.33E-07	0.85	3.32	-	894.1
AHQ-3-11, 4470	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	2.95E-06	0.59	2.65	-	623.7
AHQ-3-11, 4376 - 4438	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	6.60E-11	0.95	5.27	-	1143.6
AHQ-3-11, 4311 - 4388	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	7.34E-10	0.95	4.87	-	868.5
AHQ-3-11, 4274	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	8.22E-09	0.83	3.96	-	835.6
AHQ-3-11, 4222	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	4.53E-12	0.93	4.47	-	694.1
AHQ-3-13, 4031 - 4095	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	1.55E-06	0.92	5.15	-	1091.8
AHQ-3-11, 4186 - 4258	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	1.86E-11	0.95	5.56	-	941.7
AHQ-3-11, 4183 - 4250	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	7.37E-04	0.91	3.93	-	775.2
AHQ-3-11, 4030 - 4050	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	8.91E-04	0.93	4.63	-	1462.8
AHQ-3-13-, 4115 - 4122	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	3.40E-09	0.92	4.63	-	960.3
AHQ-3-13-, 4466 - 4471	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	2.95E-08	0.85	4.45	-	622.4
AHQ-3-11, 3902 - 3903	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	2	1.44E-04	0.79	3.19	-	613.1
AHQ-3-11, 4404 - 4471	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	1.31E-05	0.70	2.94	-	476.2
gi|5031987|ref|NP_005720.1|	peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]			4.58E-12	4.09	50.25	41.50	22040.1
AHQ-3-12, 3979	R.FPDENFTLK.H	1111.22866	2	2.66E-06	0.82	2.78	-	720.0
AHQ-3-11, 4912 - 4975	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	4.58E-12	0.90	4.57	-	654.0
AHQ-3-12, 5131	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	2	3.74E-07	0.60	2.77	-	320.5
AHQ-3-12, 5112 - 5174	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	8.98E-11	0.85	3.93	-	1094.3
AHQ-3-12, 5298	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	2	2.31E-05	0.61	3.00	-	431.5
AHQ-3-12, 5404	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	2	6.32E-05	0.54	2.84	-	343.4
AHQ-3-12, 5855 - 5927	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	2	3.14E-09	0.93	5.02	-	612.5
AHQ-3-14, 6236	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	3	2.12E-04	0.90	4.12	-	1304.2
AHQ-3-12, 4618 - 4691	R.VIPSFMCQAGDFTNHNGTGGK.S	2240.46178	2	1.98E-08	0.83	3.59	-	491.9
gi|4505839|ref|NP_002645.1|	pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro			5.35E-12	14.94	170.33	41.20	57913.6
AHQ-3-7, 6118 - 6143	R.AGKPVICATQMLESMIK.K	1879.29869	2	7.97E-06	0.96	4.25	-	1204.6
AHQ-3-7, 6126	R.AGKPVICATQMLESMIK.K	1879.29869	3	1.49E-07	0.92	4.00	-	1387.4
AHQ-3-7, 4996 - 5036	R.AGKPVICATQM*LESMIK.K	1895.29809	2	2.98E-04	0.86	4.03	-	694.0
AHQ-3-7, 5396	K.CDENILWLDYK.N	1470.62849	2	1.77E-04	0.90	2.90	-	1062.3
AHQ-3-7, 7436	K.FGVEQDVDMVFASFIR.K	1861.11055	2	1.42E-10	0.96	4.96	-	1357.6
AHQ-3-7, 7348	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	3.44E-09	0.97	4.62	-	1675.8
AHQ-3-7, 4767 - 4838	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	4.11E-09	0.98	5.46	-	2130.9
AHQ-3-7, 5091 - 5096	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	5.25E-09	0.97	5.26	-	1445.9
AHQ-3-9, 4301	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.95E-05	0.34	2.68	-	343.5
AHQ-3-7, 4862	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.73E-07	0.96	4.67	-	1520.1
AHQ-3-7, 4510 - 4547	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.62E-06	0.94	4.36	-	1149.4
AHQ-3-7, 6718 - 6786	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	5.35E-12	0.98	6.49	-	1989.3
AHQ-3-9, 6447	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	3.33E-05	0.87	3.95	-	600.9
AHQ-3-11, 6315	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.81E-04	0.95	4.47	-	1685.7
AHQ-3-14-, 6431 - 6479	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.97E-07	0.94	4.56	-	1305.2
AHQ-3-10, 6119 - 6122	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	7.26E-04	0.81	3.47	-	573.7

AHQ-3-7, 2910 - 2980	K.ITLDNAYMEK.C	1198.37126	2	1.33E-04	0.49	2.63	-	471.2
AHQ-3-7, 3840	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	2.37E-04	0.85	3.70	-	1027.0
AHQ-3-7, 3831	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	2.28E-09	0.97	5.58	-	1036.8
AHQ-3-7, 5046 - 5047	K.KGVNLPGAAVDLPAVSEKDIQDLK.F	2478.82685	3	1.95E-07	0.98	6.67	-	1745.8
AHQ-3-7, 6414	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	4.98E-07	0.94	3.91	-	1065.2
AHQ-3-7, 7062	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	5.44E-06	0.89	3.71	-	799.4
AHQ-3-7, 5792 - 5858	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.42E-06	0.97	4.90	-	1279.3
AHQ-3-7, 5926 - 6007	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.24E-08	0.98	5.78	-	1436.3
AHQ-3-7, 6074 - 6150	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	3.77E-05	0.97	5.32	-	1361.7
AHQ-3-11, 5520	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.40E-04	0.94	3.89	-	1174.2
AHQ-3-12, 5747	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.40E-08	0.95	5.03	-	931.0
AHQ-3-7, 6242	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	4.03E-07	0.96	4.71	-	1124.0
AHQ-3-7, 6706 - 6756	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.67E-07	0.95	4.47	-	1107.8
AHQ-3-7, 6504 - 6578	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	5.49E-07	0.96	4.54	-	1017.6
AHQ-3-7, 5378	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.51E-07	0.97	5.40	-	1286.5
AHQ-3-13-, 3417	R.LDIDSPPITAR.N	1198.35099	2	1.06E-05	0.93	3.35	-	1247.1
AHQ-3-13, 3422 - 3427	R.LDIDSPPITAR.N	1198.35099	2	5.10E-06	0.88	3.59	-	797.9
AHQ-3-7, 3138 - 3207	R.LDIDSPPITAR.N	1198.35099	2	2.62E-06	0.94	3.99	-	1210.8
AHQ-3-11, 3279	R.LDIDSPPITAR.N	1198.35099	2	5.29E-05	0.94	3.43	-	1213.5
AHQ-3-7, 2056	R.LNFSHGTHEYHAETIK.N	1885.02879	2	1.53E-07	0.91	3.50	-	950.8
AHQ-3-7, 2064	R.LNFSHGTHEYHAETIK.N	1885.02879	3	5.14E-05	0.92	4.31	-	1249.2
AHQ-3-7, 2359	R.LNFSHGTHEYHAETIK.N	1885.02879	2	8.68E-06	0.78	3.11	-	514.7
AHQ-3-11, 3266	R.NTGIICTIGPASR.S	1361.54994	2	6.39E-05	0.92	3.79	-	1077.1
AHQ-3-14-, 3396	R.NTGIICTIGPASR.S	1361.54994	2	5.35E-05	0.80	3.21	-	677.0
AHQ-3-7, 3158 - 3239	R.NTGIICTIGPASR.S	1361.54994	2	9.85E-05	0.92	3.96	-	951.0
AHQ-3-13-, 3429 - 3431	R.NTGIICTIGPASR.S	1361.54994	2	2.80E-06	0.92	3.77	-	958.5
AHQ-3-13, 3431	R.NTGIICTIGPASR.S	1361.54994	2	3.49E-05	0.88	3.44	-	928.5
AHQ-3-7, 3930	R.NTGIICTIGPASR.S	1361.54994	2	1.09E-08	0.91	3.78	-	755.7
AHQ-3-7, 4978	R.RFDEILEASDGIMVAR.G	1823.06385	2	1.21E-07	0.97	5.66	-	1172.3
AHQ-3-7, 4682	R.RFDEILEASDGIMVAR.G	1823.06385	2	3.45E-07	0.96	5.00	-	1161.4
AHQ-3-7, 3870	R.TATESFASDPILYR.P	1571.71277	2	2.83E-05	0.64	2.84	-	478.8
AHQ-3-13-, 5573 - 5638	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	7.43E-04	0.56	3.11	-	504.9
AHQ-3-7, 5452 - 5523	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	1.01E-04	0.88	4.07	-	1039.0
AHQ-3-7, 5458 - 5534	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	3.41E-08	0.61	3.36	-	185.4
gi|4501893|ref|NP_001094.1|	actinin, alpha 2 [Homo sapiens]			5.38E-12	10.47	120.29	12.60	103853.1
AHQ-3-5, 4353 - 4360	K.AGTQIENIEEDFR.N	1522.59861	2	2.27E-04	0.87	3.50	-	852.9
AHQ-3-5, 5204 - 5277	K.CQLEINFNTLQTK.L	1610.81373	2	1.03E-07	0.96	4.84	-	1163.2
AHQ-3-6, 4950 - 5018	K.CQLEINFNTLQTK.L	1610.81373	2	1.24E-04	0.96	4.56	-	1154.3
AHQ-3-4, 5161	K.CQLEINFNTLQTK.L	1610.81373	2	9.00E-04	0.84	3.18	-	827.8
AHQ-3-5, 5064 - 5135	K.CQLEINFNTLQTK.L	1610.81373	2	3.80E-04	0.96	4.56	-	1276.9
AHQ-3-5, 4864	R.DLLLDPAWEK.Q	1200.36535	2	8.87E-05	0.81	3.10	-	902.2
AHQ-3-4, 4993	K.EGLLLWCQR.K	1176.37031	2	2.84E-04	0.92	3.20	-	930.0
AHQ-3-5, 4811 - 4819	K.EGLLLWCQR.K	1176.37031	2	3.67E-06	0.94	3.95	-	919.1
AHQ-3-10, 3868	R.FAIQDISVEETSAK.E	1538.68108	2	5.38E-12	0.91	3.59	-	1075.1
AHQ-3-1, 4436	R.FAIQDISVEETSAK.E	1538.68108	2	4.33E-07	0.77	3.16	-	647.3
AHQ-3-4, 4257	R.FAIQDISVEETSAK.E	1538.68108	2	8.55E-04	0.74	3.01	-	760.5
AHQ-3-8, 3822	R.FAIQDISVEETSAK.E	1538.68108	2	5.99E-06	0.95	3.96	-	1315.7
AHQ-3-5, 3996	R.FAIQDISVEETSAK.E	1538.68108	2	7.62E-08	0.94	3.53	-	1506.4
AHQ-3-5, 4101	R.FAIQDISVEETSAK.E	1538.68108	2	1.10E-06	0.87	3.28	-	890.2
AHQ-3-6, 3970 - 4041	R.FAIQDISVEETSAK.E	1538.68108	2	1.14E-05	0.95	4.39	-	1237.1
AHQ-3-11, 3982	R.FAIQDISVEETSAK.E	1538.68108	2	4.70E-04	0.90	3.57	-	955.5
AHQ-3-1, 6286	K.GYEEWLLNEIR.R	1422.56701	2	2.85E-06	0.95	4.35	-	1436.6
AHQ-3-4, 6288	K.GYEEWLLNEIR.R	1422.56701	2	9.70E-06	0.97	4.38	-	1790.9
AHQ-3-6, 6015	K.GYEEWLLNEIR.R	1422.56701	1	1.88E-05	0.43	2.40	-	189.6
AHQ-3-5, 6285	K.GYEEWLLNEIR.R	1422.56701	1	1.25E-08	0.50	2.60	-	423.2
AHQ-3-5, 5456 - 5535	K.GYEEWLLNEIR.R	1422.56701	1	6.68E-06	0.33	2.16	-	336.1
AHQ-3-5, 5467 - 5529	K.GYEEWLLNEIR.R	1422.56701	2	2.02E-06	0.82	2.54	-	994.7
AHQ-3-5, 6099 - 6168	K.GYEEWLLNEIR.R	1422.56701	1	3.08E-04	0.44	2.89	-	248.2
AHQ-3-5, 6100 - 6169	K.GYEEWLLNEIR.R	1422.56701	2	1.68E-06	0.96	4.47	-	1532.8
AHQ-3-5, 6103	K.GYEEWLLNEIR.R	1422.56701	1	4.36E-06	0.42	2.48	-	170.3
AHQ-3-5, 6284	K.GYEEWLLNEIR.R	1422.56701	2	3.29E-07	0.88	2.86	-	1185.9
AHQ-3-5, 2021 - 2027	K.HEAFESDLAAHQDR.V	1626.66861	2	9.60E-10	0.98	5.24	-	1889.2
AHQ-3-6, 2007	K.HEAFESDLAAHQDR.V	1626.66861	2	3.26E-06	0.92	3.83	-	778.4
AHQ-3-5, 2024	K.HEAFESDLAAHQDR.V	1626.66861	3	1.72E-10	0.98	5.55	-	2755.9
AHQ-3-5, 3631	R.KAGTQIENIEEDFR.N	1650.77152	2	6.54E-06	0.95	4.56	-	922.5
AHQ-3-5, 1676	R.KHEAFESDLAAHQDR.V	1754.84152	2	4.37E-07	0.97	4.50	-	1423.3
AHQ-3-6, 1707	R.KHEAFESDLAAHQDR.V	1754.84152	3	1.13E-09	0.97	5.79	-	1331.2
AHQ-3-5, 2801	R.KTFTAWCNSHLR.K	1522.71309	2	2.75E-09	0.93	3.35	-	1073.9
AHQ-3-5, 4833	K.LVSIGAEEIVDGNVK.M	1543.74400	2	5.70E-06	0.85	3.03	-	1061.1
AHQ-3-5, 3249	K.TFTAWCNSHLR.K	1394.54018	2	3.55E-07	0.80	3.26	-	640.0
gi|4504345|ref|NP_000508.1|	alpha 2 globin [Homo sapiens]			5.57E-12	3.72	40.25	50.70	15257.4
AHQ-3-13, 4226	K.FLASVSTVLTSK.Y	1253.46970	2	5.34E-04	0.88	3.19	-	930.3
AHQ-3-13, 3989	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	8.22E-09	0.92	3.87	-	863.8
AHQ-3-13, 3997	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	1.11E-06	0.85	3.90	-	676.1
AHQ-3-14, 4899 - 4912	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	1.16E-07	0.96	4.06	-	1624.2
AHQ-3-13-, 4017 - 4021	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	3.41E-10	0.95	4.26	-	983.7
AHQ-3-14, 6441	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	6.61E-05	0.92	4.83	-	929.0
AHQ-3-14, 3284	K.VGAHAGEYGAEALER.M	1530.62397	2	1.03E-05	0.83	3.03	-	764.2
AHQ-3-13, 2581	K.VGAHAGEYGAEALER.M	1530.62397	3	8.28E-04	0.97	4.98	-	2206.6
AHQ-3-13-, 2534 - 2537	K.VGAHAGEYGAEALER.M	1530.62397	2	5.57E-12	0.97	5.06	-	1398.8
AHQ-3-13, 2574	K.VGAHAGEYGAEALER.M	1530.62397	2	6.09E-11	0.98	4.71	-	2130.0
gi|4507109|ref|NP_000336.1|	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor			5.77E-12	5.59	60.33	45.70	14460.1
AHQ-3-12, 2132	K.EGVVHGVATVAEK.T	1296.45466	2	3.47E-06	0.69	2.62	-	574.3
AHQ-3-13-, 2218	K.EGVVHGVATVAEK.T	1296.45466	2	1.04E-07	0.93	3.70	-	960.8
AHQ-3-12, 4659	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	3	1.48E-04	0.96	4.91	-	1682.9
AHQ-3-12, 4880	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.90E-11	0.94	4.46	-	845.3
AHQ-3-14-, 4617	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	3	1.32E-04	0.95	4.44	-	1546.4
AHQ-3-14-, 4628	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	3.44E-09	0.95	4.43	-	1153.1
AHQ-3-14, 5620	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	3.56E-07	0.94	5.03	-	668.2
AHQ-3-12, 4643	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	6.56E-06	0.92	3.83	-	1000.1
AHQ-3-13, 4614	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.02E-05	0.96	5.23	-	1233.1
AHQ-3-12, 2035 - 2039	K.TKEGVLYVGSK.T	1181.36357	2	1.12E-05	0.83	2.83	-	768.9
AHQ-3-12, 2024	K.TKEGVVHGVATVAEK.T	1525.73191	3	2.32E-06	0.88	3.73	-	957.5
AHQ-3-12, 2022	K.TKEGVVHGVATVAEK.T	1525.73191	2	3.16E-10	0.96	4.32	-	1821.3
AHQ-3-13, 4190 - 4191	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	5.77E-12	0.98	6.65	-	1953.5
AHQ-3-14, 5351	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.50E-06	0.96	5.45	-	920.0
AHQ-3-12, 4206 - 4218	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	1.20E-05	0.93	5.04	-	1042.0
AHQ-3-13-, 4206	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	6.06E-05	0.97	4.88	-	1681.7
AHQ-3-14-, 4181	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	2.43E-06	0.97	5.85	-	1247.7
AHQ-3-13-, 4205 - 4210	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	5.34E-09	0.98	6.01	-	2342.4
AHQ-3-12, 4138	K.TVEGAGSIAAATGFVK.K	1479.66001	1	7.74E-07	0.66	3.11	-	437.2
AHQ-3-13-, 4087 - 4154	K.TVEGAGSIAAATGFVK.K	1479.66001	2	2.78E-04	0.73	3.22	-	607.4
AHQ-3-13-, 4153	K.TVEGAGSIAAATGFVK.K	1479.66001	1	1.09E-04	0.46	2.64	-	275.5
AHQ-3-12, 4127 - 4135	K.TVEGAGSIAAATGFVK.K	1479.66001	2	6.90E-10	0.93	3.86	-	1159.9
AHQ-3-13, 4142	K.TVEGAGSIAAATGFVK.K	1479.66001	1	7.58E-04	0.23	2.68	-	316.8
gi|5902016|ref|NP_008939.1|	reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sapi			6.13E-12	1.91	20.25	14.10	22395.3
AHQ-3-1, 3125 - 3205	R.HQAQIDHYLGLANK.N	1608.78270	2	9.54E-07	0.84	3.58	-	334.4

AHQ-3-1, 3200	R.HQAQIDHYLGLANK.N	1608.78270	2	8.32E-07	0.97	5.02	-	1456.0
AHQ-3-1, 3394	R.HQAQIDHYLGLANK.N	1608.78270	2	1.83E-05	0.87	3.74	-	735.2
AHQ-3-12, 2967	R.HQAQIDHYLGLANK.N	1608.78270	2	1.88E-05	0.95	4.48	-	938.3
AHQ-3-1, 3046 - 3117	K.YSNSALGHVNCTIK.E	1565.73305	2	6.13E-12	0.94	4.23	-	1094.8
gi|5729980|ref|NP_006547.1| phosphomevalonate kinase [Homo sapiens]				6.55E-12	0.90	10.23	8.30	21994.8
AHQ-3-11, 5206	K.IVEGISQPIWLVSDTR.R	1814.07506	2	6.55E-12	0.90	4.53	-	434.6
gi|4557361|ref|NP_001187.1| BH3 interacting domain death agonist; BH3-interacting domain death agon				6.96E-12	3.77	40.27	36.40	21994.6
AHQ-3-11, 6791	R.DLATALEQLLQAYPR.D	1702.93270	2	6.96E-12	0.94	4.32	-	1060.3
AHQ-3-11, 5972	R.DVFHTTVNFINQNLR.T	1819.01348	2	9.66E-07	0.92	3.91	-	1190.5
AHQ-3-11, 6063 - 6075	R.ELDALGHELPVLAPQWEGYDELQTDGNR.S	3167.38790	3	9.74E-11	0.95	5.41	-	988.0
AHQ-3-11, 2655	R.IEADSESQEDIIR.N	1505.56635	2	2.37E-10	0.96	4.28	-	1789.0
gi|4502549|ref|NP_001734.1| calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta				7.02E-12	3.57	40.25	25.50	16837.5
AHQ-3-12, 5867 - 5880	R.EADIDGDGQVNYEEFVQM*MTAK	2507.69302	3	5.61E-05	0.86	4.77	-	1140.4
AHQ-3-12, 4666	R.EADIDGDGQVNYEEFVQM*M*TAK	2523.69242	2	3.37E-05	0.80	3.39	-	475.7
AHQ-3-12, 4094 - 4166	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	2.82E-04	0.94	4.51	-	1072.2
AHQ-3-11, 3919 - 3926	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	4.11E-04	0.88	3.53	-	865.1
AHQ-3-12, 3895	R.VFDKDGNGYISAAELR.H	1755.90933	3	6.37E-05	0.90	4.41	-	1039.4
AHQ-3-12, 3902 - 3976	R.VFDKDGNGYISAAELR.H	1755.90933	2	6.48E-05	0.92	3.83	-	1051.6
AHQ-3-11, 3679 - 3742	R.VFDKDGNGYISAAELR.H	1755.90933	2	7.02E-12	0.96	4.91	-	1273.8
AHQ-3-12, 3768 - 3830	R.VFDKDGNGYISAAELR.H	1755.90933	3	1.75E-08	0.89	4.41	-	891.3
AHQ-3-12, 3767 - 3835	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.57E-08	0.96	4.97	-	1142.6
AHQ-3-11, 3592 - 3659	R.VFDKDGNGYISAAELR.H	1755.90933	2	8.40E-07	0.91	3.66	-	1053.7
gi|27500274|ref|XP_113950.3| similar to Munc13-4 protein [Homo sapiens]				9.16E-12	9.36	110.29	19.40	123281.1
AHQ-3-4, 7664	K.AFGELCPNTAPLPQLVTEALQTGTTEWFHLK.Q	3472.91108	3	9.16E-12	0.81	4.23	-	403.5
AHQ-3-4, 7448	K.ALLGLVQDVIGDLHQCQR.T	2037.32944	2	6.74E-08	0.96	5.45	-	1129.6
AHQ-3-4, 7450	K.ALLGLVQDVIGDLHQCQR.T	2037.32944	3	5.39E-07	0.93	4.15	-	1242.1
AHQ-3-4, 3169	R.GQCHLQFQLIHK.R	1510.74545	2	8.64E-04	0.90	3.46	-	1074.6
AHQ-3-5, 4421	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	2.69E-06	0.95	4.18	-	1683.1
AHQ-3-4, 3418 - 3488	R.IQQQAETTSEELGAVTVK.A	1933.10674	2	1.77E-04	0.93	4.19	-	1009.9
AHQ-3-4, 3306	R.LGHPEPNHVTEASELLR.Y	1900.08490	2	4.29E-04	0.61	2.83	-	448.3
AHQ-3-4, 5545	K.LPAQLAWEALEQR.V	1525.73360	2	4.13E-05	0.91	3.24	-	1164.4
AHQ-3-5, 5365	K.LPAQLAWEALEQR.V	1525.73360	2	6.61E-09	0.96	4.08	-	1452.9
AHQ-3-4, 7506	R.LYQSLEFPSSCLLHPITSIEYQWIQGR.L	3268.68653	3	1.64E-04	0.90	4.54	-	709.1
AHQ-3-4, 4112	R.SVFPLSVSDSPAR.L	1362.51311	2	5.26E-06	0.85	3.05	-	997.2
AHQ-3-4, 7344	R.VGAVLEQGQLQNTLHAQLQSALAGLGHEIR.T	3153.54178	3	3.03E-05	0.93	5.20	-	1037.8
AHQ-3-4, 6405	R.WFQPAIPSWLQK.T	1501.75533	2	3.72E-05	0.56	2.56	-	395.2
gi|27480104|ref|XP_208215.1| similar to triosephosphate isomerase 1 [Homo sapiens]				9.25E-12	5.10	60.26	22.10	26942.6
AHQ-3-10, 2723	R.HVFGESDELIGQK.V	1459.58565	1	1.58E-06	0.89	3.81	-	921.2
AHQ-3-11, 2855	R.HVFGESDELIGQK.V	1459.58565	2	8.97E-08	0.94	3.82	-	833.7
AHQ-3-10, 2718	R.HVFGESDELIGQK.V	1459.58565	1	8.29E-04	0.84	2.89	-	1133.4
AHQ-3-10, 2722	R.HVFGESDELIGQK.V	1459.58565	2	9.25E-12	0.95	4.34	-	868.6
AHQ-3-10, 2259	K.IAVAAQNCYK.V	1139.30684	1	1.94E-05	0.51	2.57	-	325.4
AHQ-3-10, 2439 - 2442	R.RHVFGESDELIGQK.V	1615.77200	2	1.19E-08	0.98	5.22	-	2451.2
AHQ-3-10, 3970 - 3991	K.VTNGAFTGEISPGMIK.D	1622.86786	2	1.59E-05	0.87	3.69	-	745.7
AHQ-3-10, 3511	K.VTNGAFTGEISPGM*IK.D	1638.86726	2	1.74E-04	0.91	3.87	-	886.6
AHQ-3-10, 4910 - 4974	K.VVLAYEPVWAIGTGK.T	1603.88587	2	1.77E-04	0.87	3.52	-	788.2
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				9.49E-12	1.94	20.34	7.40	32164.8
AHQ-3-1, 5080 - 5160	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.28E-06	0.91	4.46	-	693.3
AHQ-3-1, 5228	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.62E-04	0.94	4.69	-	1021.6
AHQ-3-2, 5838 - 5841	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.69E-05	0.91	4.36	-	621.7
AHQ-3-3, 5593 - 5604	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.00E-05	0.94	4.88	-	908.7
AHQ-3-4, 5092	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.80E-10	0.96	5.21	-	1076.5
AHQ-3-4, 5216 - 5222	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.18E-04	0.88	3.89	-	770.8
AHQ-3-4, 5573 - 5580	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.23E-04	0.93	3.99	-	1034.3
AHQ-3-5, 5056 - 5136	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.19E-05	0.94	4.98	-	807.1
AHQ-3-5, 5508	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.82E-05	0.96	4.84	-	1115.2
AHQ-3-6, 4915	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.44E-07	0.87	3.61	-	685.7
AHQ-3-6, 5370	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.67E-06	0.94	4.87	-	867.7
AHQ-3-6, 5515	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.58E-04	0.87	3.69	-	880.7
AHQ-3-7, 4904	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.94E-07	0.84	3.78	-	460.5
AHQ-3-7, 4995	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.66E-05	0.93	4.35	-	999.5
AHQ-3-8, 4732 - 4803	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.31E-06	0.95	5.29	-	773.4
AHQ-3-8, 4871 - 4943	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.85E-05	0.95	5.22	-	923.1
AHQ-3-8, 5013 - 5085	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.59E-06	0.96	5.33	-	1055.2
AHQ-3-8, 5045	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.25E-04	0.95	5.00	-	987.5
AHQ-3-8, 5151 - 5231	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.05E-05	0.85	3.93	-	463.0
AHQ-3-8, 5227 - 5307	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.95E-09	0.96	5.28	-	1002.5
AHQ-3-8, 5375 - 5439	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.36E-04	0.96	5.73	-	837.1
AHQ-3-8, 5484 - 5560	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.55E-04	0.92	4.36	-	744.2
AHQ-3-8, 5507 - 5571	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.40E-04	0.95	4.92	-	933.9
AHQ-3-8, 5635 - 5699	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.58E-07	0.96	5.36	-	933.2
AHQ-3-8, 5764 - 5832	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.22E-04	0.93	4.74	-	764.7
AHQ-3-8, 5899 - 5964	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.29E-06	0.97	6.46	-	736.9
AHQ-3-8, 6163 - 6227	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.32E-04	0.95	4.98	-	860.3
AHQ-3-8, 6291 - 6355	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.48E-04	0.95	4.74	-	884.0
AHQ-3-8, 6423 - 6497	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.45E-05	0.94	5.39	-	667.0
AHQ-3-8, 6563 - 6635	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.51E-05	0.94	5.10	-	766.6
AHQ-3-8, 6808 - 6873	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.17E-04	0.91	4.46	-	700.4
AHQ-3-8, 7212 - 7277	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.12E-04	0.93	4.56	-	752.1
AHQ-3-8, 7348 - 7419	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.84E-04	0.96	5.56	-	805.5
AHQ-3-9, 4639 - 4720	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.08E-07	0.94	4.82	-	685.7
AHQ-3-9, 5195 - 5269	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.61E-04	0.81	3.70	-	634.7
AHQ-3-9, 5335 - 5408	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.83E-05	0.91	4.28	-	777.4
AHQ-3-10, 4482 - 4543	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.09E-08	0.96	5.07	-	936.0
AHQ-3-10, 4602 - 4631	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.93E-06	0.96	5.42	-	934.3
AHQ-3-10, 4680 - 4750	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.62E-05	0.96	5.20	-	1235.2
AHQ-3-10, 4994 - 5054	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.75E-06	0.95	4.62	-	1147.0
AHQ-3-10, 5114 - 5179	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.03E-04	0.88	3.89	-	773.8
AHQ-3-11, 4659	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.47E-09	0.96	4.93	-	1074.4
AHQ-3-11, 4770 - 4798	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.42E-06	0.94	4.66	-	910.3
AHQ-3-11, 5066	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.75E-08	0.94	4.88	-	801.2
AHQ-3-11, 5218 - 5292	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.51E-07	0.94	4.86	-	855.0
AHQ-3-12, 4830	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.79E-09	0.96	4.95	-	934.9
AHQ-3-12, 5254	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.05E-10	0.97	6.30	-	1388.1
AHQ-3-13, 4739 - 4801	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.34E-09	0.97	5.62	-	1377.7
AHQ-3-13, 4866 - 4937	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.89E-06	0.95	4.93	-	1047.0
AHQ-3-13, 5005	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.27E-05	0.95	5.47	-	755.5
AHQ-3-13, 5109 - 5178	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.33E-08	0.94	4.67	-	952.7
AHQ-3-13, 5185 - 5250	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.25E-06	0.96	4.91	-	1140.4
AHQ-3-13, 5359 - 5441	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.30E-07	0.97	6.14	-	900.7
AHQ-3-14, 5553 - 5619	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.23E-06	0.95	4.93	-	1026.7
AHQ-3-14, 5669 - 5731	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.31E-07	0.90	4.53	-	508.9
AHQ-3-14, 5741 - 5792	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.42E-04	0.97	6.01	-	1177.3
AHQ-3-14, 5855 - 5915	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.32E-06	0.96	5.21	-	987.7
AHQ-3-14, 6003 - 6063	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.40E-10	0.96	5.24	-	1086.2
AHQ-3-14, 6008 - 6068	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.79E-05	0.90	3.89	-	737.3
AHQ-3-14, 6056 - 6128	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.38E-09	0.89	4.42	-	588.5

AHQ-3-14, 6348	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.25E-04	0.58	3.09	-	322.0
AHQ-3-13-, 4745 - 4822	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.36E-07	0.96	5.63	-	873.5
AHQ-3-13-, 4885 - 4955	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.07E-06	0.97	5.51	-	1254.3
AHQ-3-13-, 4990 - 5057	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.17E-04	0.93	4.45	-	841.1
AHQ-3-13-, 5141 - 5166	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.85E-06	0.95	4.44	-	1222.3
AHQ-3-13-, 5425 - 5506	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.71E-05	0.98	6.71	-	1132.8
AHQ-3-13-, 5569 - 5645	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.17E-04	0.95	5.04	-	911.0
AHQ-3-14-, 4693 - 4755	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.49E-12	0.96	5.83	-	983.9
AHQ-3-14-, 4815 - 4879	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.48E-04	0.97	5.58	-	1162.3
AHQ-3-14-, 4940 - 5017	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.02E-04	0.93	4.67	-	887.2
AHQ-3-14-, 5081 - 5148	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.95E-04	0.97	5.58	-	1118.7
AHQ-3-14-, 5105 - 5167	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.91E-05	0.98	6.32	-	1358.0
AHQ-3-14-, 5200 - 5271	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.39E-05	0.95	4.87	-	970.8
AHQ-3-14-, 5319 - 5383	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.77E-04	0.95	5.35	-	806.7
AHQ-3-14-, 5451 - 5516	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.55E-04	0.96	5.66	-	999.3
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				1.14E-11	10.98	130.34	46.50	49481.2
AHQ-3-7, 4396 - 4415	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	1.56E-05	0.61	3.18	-	389.4
AHQ-3-7, 4483 - 4495	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	7.55E-07	0.83	3.93	-	681.7
AHQ-3-5, 4593 - 4595	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	2.57E-06	0.75	3.72	-	355.6
AHQ-3-8, 4218	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	4.46E-04	0.54	3.24	-	212.0
AHQ-3-7, 4532 - 4602	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	6.27E-04	0.31	2.58	-	282.0
AHQ-3-1, 5824 - 5888	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.14E-11	0.87	3.43	-	657.7
AHQ-3-13, 5453	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.13E-09	0.80	3.46	-	511.6
AHQ-3-5, 5603	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.15E-10	0.67	3.13	-	364.5
AHQ-3-4, 5741	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.28E-08	0.59	2.91	-	338.1
AHQ-3-13-, 5407	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	3.68E-05	0.76	3.24	-	511.1
AHQ-3-14, 6384 - 6439	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.72E-10	0.70	3.04	-	501.7
AHQ-3-6, 2497	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	2.66E-06	0.83	3.16	-	1231.8
AHQ-3-7, 2431 - 2508	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.60E-07	0.96	4.86	-	1102.1
AHQ-3-9, 2389	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	5.25E-07	0.93	4.41	-	787.3
AHQ-3-7, 2434 - 2512	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	9.10E-10	0.92	3.90	-	1552.4
AHQ-3-4, 2637	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	1.41E-06	0.93	4.50	-	746.3
AHQ-3-3, 5468	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	4.53E-06	0.87	3.97	-	584.1
AHQ-3-4, 5396 - 5413	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	6.53E-06	0.87	3.79	-	684.9
AHQ-3-4, 5553	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.79E-04	0.79	3.30	-	562.3
AHQ-3-1, 5616	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.56E-07	0.92	4.10	-	720.6
AHQ-3-7, 4990 - 5062	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	4.50E-06	0.94	5.13	-	600.2
AHQ-3-1, 5612	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	1.43E-06	0.95	4.63	-	1714.4
AHQ-3-7, 5138	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.05E-09	0.91	4.36	-	631.6
AHQ-3-6, 5109 - 5117	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.92E-04	0.94	4.52	-	856.7
AHQ-3-5, 5193 - 5199	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.83E-06	0.90	4.17	-	617.1
AHQ-3-9, 4868 - 4940	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.05E-07	0.87	4.06	-	565.0
AHQ-3-10, 4730 - 4734	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.07E-06	0.93	4.56	-	726.6
AHQ-3-7, 5219	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.23E-07	0.94	4.42	-	973.3
AHQ-3-9, 4763 - 4764	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	6.72E-04	0.90	4.28	-	656.8
AHQ-3-10, 6086 - 6143	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	7.34E-04	0.73	3.25	-	550.5
AHQ-3-1, 6952 - 6956	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	1.91E-06	0.72	3.38	-	677.9
AHQ-3-1, 6948 - 7024	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	9.84E-06	0.72	3.20	-	395.5
AHQ-3-14-, 6443	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	6.13E-05	0.70	2.77	-	618.6
AHQ-3-13, 6566 - 6646	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	8.48E-05	0.52	2.64	-	368.4
AHQ-3-11, 6298	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.73E-04	0.60	2.73	-	613.8
AHQ-3-3, 4754	K.IHLISTQSAIPYALR.V	1683.97576	2	1.14E-04	0.88	3.51	-	803.6
AHQ-3-9, 3928 - 3997	K.IHLISTQSAIPYALR.V	1683.97576	2	2.44E-04	0.95	4.03	-	1405.8
AHQ-3-10, 4075	K.IHLISTQSAIPYALR.V	1683.97576	2	1.74E-08	0.93	3.77	-	1109.8
AHQ-3-8, 3908 - 3913	K.IHLISTQSAIPYALR.V	1683.97576	2	2.16E-09	0.97	4.98	-	1265.1
AHQ-3-7, 4158 - 4230	K.IHLISTQSAIPYALR.V	1683.97576	2	2.37E-07	0.97	4.93	-	1316.6
AHQ-3-8, 3909	K.IHLISTQSAIPYALR.V	1683.97576	3	7.51E-04	0.48	3.11	-	459.4
AHQ-3-7, 4399 - 4479	K.IHLISTQSAIPYALR.V	1683.97576	2	7.36E-06	0.79	3.52	-	476.8
AHQ-3-2, 4766	K.IHLISTQSAIPYALR.V	1683.97576	2	1.43E-07	0.93	4.09	-	964.5
AHQ-3-5, 4407	K.IHLISTQSAIPYALR.V	1683.97576	2	8.13E-09	0.97	5.04	-	1275.0
AHQ-3-4, 4637	K.IHLISTQSAIPYALR.V	1683.97576	2	8.16E-08	0.97	5.51	-	1173.7
AHQ-3-13, 2146 - 2186	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	4.88E-05	0.90	4.01	-	958.0
AHQ-3-7, 1590 - 1599	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	9.10E-07	0.94	4.11	-	1285.5
AHQ-3-11, 1966	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.31E-06	0.80	3.40	-	647.0
AHQ-3-7, 1679 - 1747	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.58E-09	0.94	4.19	-	1058.2
AHQ-3-13-, 2125 - 2127	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.57E-09	0.94	3.80	-	1446.6
AHQ-3-4, 2557	K.NWIQYK.E	851.97168	1	1.72E-04	0.41	1.82	-	519.0
AHQ-3-8, 2894	K.QSGLYFIKPLK.A	1294.56665	2	5.33E-06	0.82	3.10	-	442.8
AHQ-3-1, 4116	K.QSGLYFIKPLK.A	1294.56665	2	3.25E-07	0.69	2.95	-	374.6
AHQ-3-7, 3298 - 3299	K.QSGLYFIKPLK.A	1294.56665	2	2.89E-04	0.63	2.53	-	350.6
AHQ-3-7, 3734	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	2	1.56E-04	0.72	3.40	-	236.1
AHQ-3-1, 4170	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	2.51E-07	0.85	3.57	-	825.3
AHQ-3-5, 3845 - 3863	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	6.48E-11	0.89	4.04	-	920.0
AHQ-3-7, 3727 - 3742	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	2.45E-04	0.83	3.66	-	826.6
AHQ-3-8, 3640	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	2	9.56E-05	0.62	3.28	-	390.3
AHQ-3-9, 3775	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	2.29E-08	0.96	6.73	-	1041.4
AHQ-3-1, 4392 - 4397	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	2.87E-07	0.88	4.58	-	868.2
AHQ-3-8, 3773 - 3774	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	1.74E-06	0.95	5.19	-	1524.1
AHQ-3-7, 3907 - 3974	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	6.62E-04	0.96	5.91	-	1372.7
AHQ-3-8, 2510	K.YEASILTHDSSIR.Y	1492.61564	2	4.51E-08	0.91	3.32	-	1010.3
AHQ-3-11, 2843	K.YEASILTHDSSIR.Y	1492.61564	2	2.39E-06	0.86	3.75	-	553.4
AHQ-3-7, 2648	K.YEASILTHDSSIR.Y	1492.61564	1	6.62E-05	0.46	2.64	-	268.6
AHQ-3-9, 2567	K.YEASILTHDSSIR.Y	1492.61564	2	7.13E-05	0.87	3.32	-	799.4
AHQ-3-7, 2612 - 2638	K.YEASILTHDSSIR.Y	1492.61564	2	5.40E-07	0.84	3.34	-	628.7
AHQ-3-6, 2745	K.YEASILTHDSSIR.Y	1492.61564	2	7.71E-07	0.87	3.66	-	698.1
AHQ-3-4, 2893 - 2913	K.YEASILTHDSSIR.Y	1492.61564	2	4.13E-05	0.70	2.91	-	626.1
AHQ-3-3, 2950	K.YEASILTHDSSIR.Y	1492.61564	2	7.68E-04	0.67	2.62	-	564.4
AHQ-3-2, 2946 - 2957	K.YEASILTHDSSIR.Y	1492.61564	2	2.22E-04	0.71	2.88	-	530.7
AHQ-3-12, 2936	K.YEASILTHDSSIR.Y	1492.61564	2	3.06E-05	0.86	3.38	-	534.5
AHQ-3-1, 2840 - 2918	R.YLQEIYNSNNQK.I	1514.62131	2	1.33E-04	0.96	4.36	-	1433.6
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				1.32E-11	20.03	220.31	20.00	191612.6
AHQ-3-3, 7452 - 7525	K.AFM*TADLPNELIELLEK.I	1964.26896	2	2.19E-04	0.95	5.02	-	743.4
AHQ-3-3, 7568	K.AFMTADLPNELIELLEK.I	1948.26956	2	1.32E-11	0.95	4.92	-	812.0
AHQ-3-3, 4508	R.ALEHFTDLYDIK.R	1465.63179	2	2.32E-08	0.96	4.10	-	1123.0
AHQ-3-3, 7620 - 7622	K.DTELAEELLQWFLQEEK.R	2122.31678	2	1.72E-06	0.97	5.25	-	1561.9
AHQ-3-3, 7564	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	3.61E-06	0.91	4.48	-	1076.8
AHQ-3-1, 7336 - 7337	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	3.43E-05	0.94	4.83	-	1542.9
AHQ-3-3, 4969 - 4976	R.GQFSTDELVAEVEK.R	1552.66462	2	3.16E-07	0.95	4.28	-	1180.4
AHQ-3-4, 4765	R.GQFSTDELVAEVEKR.N	1708.85097	2	4.82E-10	0.94	3.83	-	1331.9
AHQ-3-5, 4548	R.GQFSTDELVAEVEKR.N	1708.85097	2	6.63E-07	0.91	3.59	-	1175.9
AHQ-3-3, 4822	R.GQFSTDELVAEVEKR.N	1708.85097	2	1.26E-07	0.77	3.28	-	575.1
AHQ-3-3, 1953	R.IHEGCEEPATHNALAK.I	1778.92458	2	7.49E-04	0.91	4.13	-	780.8
AHQ-3-3, 3581	K.IVLDNSVFSEHR.N	1416.56400	2	4.38E-08	0.90	3.35	-	1061.4
AHQ-3-3, 7284	R.KFDVNTSAVQVLIEHIGNLDR.A	2369.66218	3	8.17E-06	0.97	6.16	-	1361.9
AHQ-3-3, 3512	R.KFNALFAQGNYSEAAK.V	1759.94281	2	4.40E-07	0.97	5.54	-	1418.3
AHQ-3-3, 4577 - 4626	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	1.10E-08	0.91	3.95	-	892.3
AHQ-3-3, 4586	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	3	3.82E-06	0.87	4.49	-	809.0

AHQ-3-3, 4398	K.LHIIEVGTPPTGNQPFPK.K	1946.23831	2	4.86E-04	0.68	3.38	-	290.4
AHQ-3-3, 3890	K.LLYNNVSNFGR.L	1297.44435	2	7.71E-05	0.79	2.75	-	656.5
AHQ-3-3, 7233	R.LPVVIGGLLDVDCSEDVIK.N	2043.36744	2	5.38E-04	0.93	3.90	-	1158.3
AHQ-3-3, 6457	R.NLQNLLILTAIK.A	1354.66353	2	5.71E-07	0.97	4.85	-	1969.1
AHQ-3-3, 2526	R.RPISADSAIMNPASK.V	1558.78540	2	6.41E-07	0.98	5.23	-	1657.4
AHQ-3-4, 7129	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	2	3.59E-04	0.84	3.84	-	345.0
AHQ-3-3, 7088 - 7097	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	7.09E-07	0.96	6.01	-	1336.1
AHQ-3-3, 7101	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	2	9.82E-05	0.94	4.85	-	592.1
AHQ-3-4, 7121 - 7134	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	1.02E-04	0.95	5.28	-	1454.0
AHQ-3-4, 5062 - 5112	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	1.99E-08	0.79	3.86	-	285.3
AHQ-3-5, 7093	K.VGYTPDWIFLLR.N	1480.73443	2	3.89E-09	0.85	3.68	-	509.1
AHQ-3-3, 7230	K.VGYTPDWIFLLR.N	1480.73443	2	4.93E-11	0.77	3.12	-	450.2
AHQ-3-3, 3094	K.VIQCFAETGQVQK.I	1509.70940	2	1.41E-05	0.93	3.21	-	1889.3
AHQ-3-3, 5018	K.WLKEDKLECSEELGDLVK.S	2193.45974	2	7.26E-07	0.96	4.49	-	1579.4
gi|4759082|ref|NP_004648.1| serum deprivation response protein; serum deprivation response; phospha				1.37E-11	2.85	30.27	11.10	47172.9
AHQ-3-9, 6380 - 6384	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.26E-07	0.94	4.08	-	1116.4
AHQ-3-12, 6291	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.94E-05	0.96	4.97	-	1372.4
AHQ-3-9, 6155 - 6223	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.47E-05	0.98	5.32	-	1718.8
AHQ-3-11, 6175 - 6235	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	7.71E-08	0.95	4.23	-	1482.0
AHQ-3-11, 6086 - 6090	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	7.56E-11	0.95	4.69	-	1224.0
AHQ-3-10, 5888	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.13E-04	0.94	3.97	-	1148.7
AHQ-3-12, 3494	K.LVNMLDAVQENQHK.M	1639.85851	2	3.67E-05	0.90	4.08	-	807.9
AHQ-3-13, 3514	K.LVNMLDAVQENQHK.M	1639.85851	2	7.12E-06	0.94	4.24	-	1110.5
AHQ-3-13-, 3502	K.LVNMLDAVQENQHK.M	1639.85851	2	2.53E-08	0.94	4.39	-	1044.0
AHQ-3-10, 5626	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.23E-04	0.96	4.75	-	1211.6
AHQ-3-11, 5828 - 5894	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.35E-05	0.93	4.40	-	741.2
AHQ-3-9, 6063 - 6143	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.37E-11	0.96	5.10	-	1049.9
AHQ-3-9, 5979 - 6052	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.75E-09	0.95	4.83	-	1021.0
AHQ-3-9, 5805 - 5879	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	7.30E-10	0.95	5.01	-	855.3
AHQ-3-12, 6054 - 6059	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.54E-05	0.96	5.20	-	915.4
AHQ-3-8, 5983	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.58E-06	0.91	4.30	-	873.4
AHQ-3-7, 6100 - 6123	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.25E-05	0.94	4.21	-	1174.6
AHQ-3-3, 6521	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.03E-04	0.93	4.36	-	845.0
AHQ-3-13-, 6097	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.58E-04	0.96	5.12	-	984.2
AHQ-3-14-, 6016	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.53E-04	0.92	3.83	-	954.5
gi|10863927|ref|NP_066953.1| peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]				1.50E-11	5.35	70.28	30.90	18012.4
AHQ-3-12, 4132	K.FEDENFILK.H	1155.28144	1	8.11E-05	0.70	2.89	-	944.1
AHQ-3-13, 3981	K.FEDENFILK.H	1155.28144	2	6.40E-04	0.76	3.30	-	555.7
AHQ-3-12, 3447 - 3524	K.KITIADCGQLE	1249.41637	2	9.52E-04	0.77	3.18	-	942.5
AHQ-3-12, 3279 - 3362	K.KITIADCGQLE	1249.41637	2	7.36E-07	0.87	4.11	-	923.4
AHQ-3-14, 5860 - 5883	K.SIYGEKFEDENFILK.H	1833.03047	2	1.06E-07	0.87	3.77	-	852.6
AHQ-3-13, 4626	K.SIYGEKFEDENFILK.H	1833.03047	2	4.71E-09	0.96	4.92	-	1181.0
AHQ-3-12, 4723	K.SIYGEKFEDENFILK.H	1833.03047	2	4.57E-08	0.63	2.68	-	694.4
AHQ-3-14-, 4648 - 4657	K.SIYGEKFEDENFILK.H	1833.03047	2	1.50E-11	0.97	5.61	-	1242.9
AHQ-3-12, 4831 - 4894	K.SIYGEKFEDENFILK.H	1833.03047	2	5.06E-08	0.87	3.86	-	754.4
AHQ-3-12, 4604 - 4670	K.SIYGEKFEDENFILK.H	1833.03047	2	2.59E-06	0.95	5.02	-	1041.4
AHQ-3-12, 2426	K.VKEGMNIVEAM*ER.F	1522.77330	3	2.47E-04	0.86	3.98	-	1288.9
AHQ-3-12, 2850 - 2922	K.VKEGM*NIVEAMER.F	1522.77330	2	8.13E-04	0.57	2.61	-	504.6
AHQ-3-12, 4464 - 4544	R.VSFELFADK.V	1056.19300	1	9.33E-04	0.77	2.99	-	735.7
AHQ-3-12, 4459	R.VSFELFADK.V	1056.19300	2	4.11E-06	0.88	3.54	-	1002.9
AHQ-3-12, 4372	R.VSFELFADK.V	1056.19300	1	2.12E-05	0.70	2.86	-	685.8
AHQ-3-12, 4370 - 4371	R.VSFELFADK.V	1056.19300	2	7.52E-06	0.95	3.42	-	1052.9
AHQ-3-13-, 4410	R.VSFELFADK.V	1056.19300	2	8.65E-05	0.84	3.24	-	769.7
AHQ-3-12, 4295	R.VSFELFADKVPK.T	1380.61317	2	1.70E-04	0.90	3.77	-	993.2
AHQ-3-12, 4502 - 4578	R.VSFELFADKVPK.T	1380.61317	2	8.15E-06	0.91	3.75	-	983.4
AHQ-3-12, 4520	R.VSFELFADKVPK.T	1380.61317	3	4.51E-06	0.50	3.15	-	343.0
gi|10834976|ref|NP_000572.1| glutathione peroxidase 1 [Homo sapiens]				1.60E-11	5.38	60.24	43.30	21909.0
AHQ-3-11, 5282	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	1.60E-11	0.94	3.98	-	1051.9
AHQ-3-11, 5191 - 5204	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	3.96E-10	0.90	4.35	-	554.1
AHQ-3-11, 2714 - 2776	R.DYTQMNELQR.R	1298.40778	2	1.54E-04	0.81	2.61	-	902.3
AHQ-3-11, 3935	K.FLVGPDGVPLR.R	1170.38561	2	4.91E-05	0.89	2.94	-	1231.5
AHQ-3-11, 4802 - 4811	R.GLVVLGFPCNQFGHQENAK.N	2117.37312	2	2.30E-04	0.89	4.76	-	306.4
AHQ-3-14-, 3836	R.PLAGGEPVSLGSLR.G	1353.54935	2	5.80E-06	0.96	4.09	-	1340.6
AHQ-3-11, 3692 - 3699	R.PLAGGEPVSLGSLR.G	1353.54935	2	1.77E-07	0.94	4.13	-	979.2
AHQ-3-11, 5071	K.YVRPGGGFEPNFMLFEK.C	1989.28515	3	1.68E-07	0.89	3.97	-	975.9
gi|5729997|ref|NP_004154.2| RAB27B, member RAS oncogene family [Homo sapiens]				1.61E-11	4.69	70.24	29.40	24607.7
AHQ-3-11, 5544	K.AVETLLDLIM*K.R	1262.54151	2	8.25E-06	0.94	4.53	-	788.0
AHQ-3-10, 5272	K.AVETLLDLIM*K.R	1262.54151	2	5.87E-06	0.85	3.28	-	664.0
AHQ-3-11, 6456	K.AVETLLDLIMK.R	1246.54211	2	4.24E-08	0.94	3.68	-	1194.7
AHQ-3-10, 6227	K.AVETLLDLIMK.R	1246.54211	2	7.09E-08	0.92	3.80	-	886.5
AHQ-3-10, 4854	K.AVETLLDLIM*KR.M	1418.72786	2	1.50E-05	0.40	2.58	-	394.6
AHQ-3-11, 2874	K.LLALGDSGVGK.T	1030.20023	1	8.96E-04	0.29	1.91	-	476.1
AHQ-3-13, 3030	K.LLALGDSGVGK.T	1030.20023	1	6.14E-07	0.31	2.09	-	414.3
AHQ-3-10, 5810	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	7.05E-07	0.81	3.77	-	469.1
AHQ-3-11, 6180	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	1.71E-04	0.87	3.98	-	638.2
AHQ-3-10, 5274	R.NWM*SQLQANAYCENPDIVLIGNK.A	2696.99712	2	7.17E-04	0.42	2.54	-	531.8
AHQ-3-10, 5931 - 5995	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	2.29E-04	0.72	3.02	-	612.7
AHQ-3-10, 4162 - 4166	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	1.61E-11	0.96	4.74	-	1099.1
AHQ-3-12, 4488 - 4559	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	4.36E-05	0.45	2.90	-	325.1
gi|4758606|ref|NP_004508.1| integrin-linked kinase [Homo sapiens]				1.64E-11	12.77	150.29	31.90	51418.9
AHQ-3-7, 4704	R.EVPFADLSNM*EIGMK.V	1697.95498	2	6.80E-05	0.92	5.21	-	517.5
AHQ-3-7, 4178	R.EVPFADLSNM*EIGM*K.V	1713.95438	2	5.15E-04	0.74	3.09	-	523.0
AHQ-3-10, 5240	R.EVPFADLSNMEIGMK.V	1681.95558	2	7.22E-04	0.59	3.28	-	402.0
AHQ-3-7, 5107 - 5116	R.EVPFADLSNMEIGM*K.V	1697.95498	2	4.61E-06	0.91	4.01	-	719.8
AHQ-3-7, 5442 - 5454	K.FDMIVPILEK.M	1205.49168	2	5.53E-06	0.87	3.24	-	763.5
AHQ-3-7, 1631 - 1659	R.GDDTPLHLAASHGHR.D	1584.67809	2	1.37E-08	0.87	3.42	-	947.3
AHQ-3-13-, 2186	R.GDDTPLHLAASHGHR.D	1584.67809	2	1.65E-04	0.86	2.60	-	1349.6
AHQ-3-7, 1648	R.GDDTPLHLAASHGHR.D	1584.67809	3	1.16E-04	0.78	3.54	-	711.4
AHQ-3-11, 4904	R.GM*AFLHTLEPLIPR.H	1611.93301	2	1.78E-04	0.91	3.38	-	1048.1
AHQ-3-10, 4644	R.GM*AFLHTLEPLIPR.H	1611.93301	2	4.47E-05	0.88	3.35	-	838.1
AHQ-3-9, 5401	R.GMAFLHTLEPLIPR.H	1595.93361	2	2.53E-10	0.97	4.66	-	1621.3
AHQ-3-7, 4752 - 4831	R.GM*AFLHTLEPLIPR.H	1611.93301	2	3.02E-05	0.77	2.76	-	637.9
AHQ-3-7, 4768	R.GM*AFLHTLEPLIPR.H	1611.93301	3	1.79E-07	0.91	3.99	-	1128.5
AHQ-3-7, 5671	R.GMAFLHTLEPLIPR.H	1595.93361	3	9.95E-06	0.90	3.90	-	1255.5
AHQ-3-7, 5599 - 5667	R.GMAFLHTLEPLIPR.H	1595.93361	2	1.74E-06	0.95	4.12	-	1363.2
AHQ-3-7, 1944 - 1959	K.LNENHSGELWK.G	1327.42732	2	6.68E-05	0.83	3.17	-	828.3
AHQ-3-7, 2184	K.LNENHSGELWK.G	1327.42732	2	3.98E-05	0.90	3.58	-	973.7
AHQ-3-7, 6102	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	8.41E-09	0.94	4.79	-	1182.9
AHQ-3-7, 6004	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	1.28E-06	0.93	4.62	-	1085.0
AHQ-3-8, 4258	R.MYAPAWVAPEALQK.K	1575.85602	2	1.82E-07	0.92	3.50	-	959.3
AHQ-3-13, 4230	R.M*YAPAWVAPEALQK.K	1591.85542	2	9.92E-06	0.90	3.68	-	631.2
AHQ-3-7, 4480	R.MYAPAWVAPEALQK.K	1575.85602	2	2.56E-05	0.84	2.77	-	812.8
AHQ-3-13-, 4233	R.M*YAPAWVAPEALQK.K	1591.85542	2	8.82E-09	0.93	3.58	-	881.3
AHQ-3-7, 4054 - 4078	R.M*YAPAWVAPEALQK.K	1591.85542	2	7.87E-08	0.95	4.66	-	750.7
AHQ-3-11, 4530	R.MYAPAWVAPEALQK.K	1575.85602	2	9.14E-07	0.96	3.95	-	1310.6
AHQ-3-7, 4440 - 4444	R.SAVVEMLIMR.G	1149.45316	2	3.60E-07	0.91	3.38	-	1213.9
AHQ-3-7, 4254 - 4263	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	3	1.64E-11	0.96	5.77	-	905.3

AHQ-3-7, 4346	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	2	7.48E-04	0.89	4.39	-	959.4
AHQ-3-7, 2698	R.WQGNDIVVK.V	1059.20012	1	2.11E-04	0.43	2.02	-	625.1
gi|5031635|ref|NP_005498.1|	cofilin 1 (non-muscle) [Homo sapiens]			1.85E-11	12.24	130.39	63.90	18502.4
AHQ-3-12, 3320 - 3386	K.AVLFCLSEDKK.N	1311.52930	2	4.42E-07	0.88	3.83	-	799.1
AHQ-3-13, 3465	K.AVLFCLSEDKK.N	1311.52930	2	9.70E-07	0.87	3.26	-	816.8
AHQ-3-12, 3344 - 3414	K.AVLFCLSEDKK.N	1311.52930	2	3.27E-06	0.79	2.73	-	845.5
AHQ-3-12, 6908	K.EDLVFIFWAPESAPLK.S	1863.14454	2	3.19E-05	0.95	4.10	-	1229.4
AHQ-3-12, 5642 - 5706	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.89E-06	0.97	5.29	-	1751.1
AHQ-3-11, 5484 - 5499	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	2.35E-07	0.97	4.96	-	1675.9
AHQ-3-13, 5651 - 5681	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	4.25E-05	0.96	5.16	-	1168.0
AHQ-3-14-, 5621	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.93E-07	0.97	5.56	-	1462.9
AHQ-3-12, 5858 - 5888	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.45E-04	0.82	3.24	-	374.5
AHQ-3-12, 5403	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	4.95E-07	0.97	4.83	-	1433.8
AHQ-3-12, 5514 - 5574	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.29E-04	0.96	5.27	-	1012.8
AHQ-3-13-, 5618	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	2.79E-06	0.97	5.90	-	1159.0
AHQ-3-14, 6495 - 6576	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.29E-10	0.97	5.35	-	1340.8
AHQ-3-12, 5730 - 5799	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.40E-10	0.98	5.64	-	1488.7
AHQ-3-12, 6014	K.ESKKEDLVFIFWAPESAPLK.S	2335.68256	2	6.06E-07	0.87	3.27	-	961.2
AHQ-3-12, 2374	K.HELQANCYEEVKDR.C	1792.90812	3	1.56E-10	0.98	5.82	-	2089.2
AHQ-3-12, 2294 - 2323	K.HELQANCYEEVKDR.C	1792.90812	2	4.86E-04	0.90	3.47	-	713.7
AHQ-3-13-, 2455 - 2519	K.HELQANCYEEVKDR.C	1792.90812	3	3.61E-05	0.95	4.61	-	1575.5
AHQ-3-12, 2526 - 2530	K.HELQANCYEEVKDR.C	1792.90812	2	1.65E-04	0.96	4.00	-	1271.5
AHQ-3-12, 2455 - 2527	K.HELQANCYEEVKDR.C	1792.90812	3	8.21E-10	0.98	5.58	-	2033.2
AHQ-3-12, 2390 - 2458	K.HELQANCYEEVKDR.C	1792.90812	2	4.20E-07	0.98	5.37	-	1972.2
AHQ-3-12, 2838 - 2839	K.KAVLFCLSEDKK.N	1439.70221	2	1.05E-06	0.94	4.43	-	982.4
AHQ-3-12, 2840	K.KAVLFCLSEDKK.N	1439.70221	3	4.09E-05	0.95	4.63	-	1462.5
AHQ-3-12, 6368 - 6434	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	4.81E-06	0.98	6.17	-	1480.7
AHQ-3-12, 6383 - 6452	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	7.22E-06	0.96	5.16	-	1203.1
AHQ-3-13, 6451 - 6466	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	3.41E-05	0.95	4.74	-	1047.7
AHQ-3-13, 6470	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	2.35E-08	0.88	4.20	-	790.6
AHQ-3-14-, 6385	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	9.63E-07	0.96	4.39	-	1275.6
AHQ-3-11, 6131 - 6195	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	3.21E-07	0.98	5.65	-	1553.8
AHQ-3-12, 6471 - 6532	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	1.68E-08	0.97	5.34	-	1566.2
AHQ-3-12, 5716 - 5796	K.KEDLVFIFWAPESAPLKSK.M	2206.56802	2	6.99E-06	0.96	5.35	-	1056.0
AHQ-3-12, 5127	K.LGGSAVISLEGKPL	1341.57848	2	8.50E-04	0.91	3.35	-	1109.0
AHQ-3-12, 4899 - 4966	K.LGGSAVISLEGKPL	1341.57848	2	2.36E-07	0.94	3.69	-	1216.6
AHQ-3-12, 4642 - 4710	K.LGGSAVISLEGKPL	1341.57848	2	6.40E-07	0.94	4.31	-	1061.4
AHQ-3-12, 4508 - 4575	K.LGGSAVISLEGKPL	1341.57848	2	7.22E-09	0.97	5.06	-	1196.5
AHQ-3-12, 4423 - 4554	K.LGGSAVISLEGKPL	1341.57848	1	2.11E-05	0.52	2.99	-	304.9
AHQ-3-13-, 4373	K.LGGSAVISLEGKPL	1341.57848	2	1.42E-04	0.87	3.81	-	698.5
AHQ-3-12, 4007 - 4028	K.LGGSAVISLEGKPL	1341.57848	2	3.30E-08	0.96	3.91	-	1878.3
AHQ-3-12, 4420 - 4486	K.LGGSAVISLEGKPL	1341.57848	2	1.91E-05	0.96	4.58	-	1201.9
AHQ-3-12, 4331 - 4402	K.LGGSAVISLEGKPL	1341.57848	2	1.62E-05	0.96	4.45	-	1522.1
AHQ-3-12, 4336	K.LGGSAVISLEGKPL	1341.57848	1	3.42E-04	0.10	2.30	-	249.5
AHQ-3-12, 2962	K.LTGIKHELQANCYEEVKDR.C	2305.55341	2	3.56E-09	0.97	5.44	-	1179.3
AHQ-3-12, 6966	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.91E-04	0.94	5.13	-	1189.3
AHQ-3-12, 6806 - 6887	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	3.05E-10	0.98	7.35	-	1816.1
AHQ-3-12, 6680 - 6744	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	3.77E-10	0.97	7.04	-	1537.6
AHQ-3-13, 6725	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	3.95E-07	0.98	7.35	-	1857.9
AHQ-3-13-, 6681 - 6682	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.85E-11	0.98	7.70	-	1929.9
AHQ-3-13-, 3247	R.YALYDATYETK.E	1338.44364	2	1.13E-06	0.95	3.86	-	1204.9
AHQ-3-13-, 3255	R.YALYDATYETK.E	1338.44364	1	3.51E-07	0.45	2.82	-	315.4
AHQ-3-12, 3272 - 3338	R.YALYDATYETK.E	1338.44364	2	2.47E-04	0.80	2.90	-	704.3
AHQ-3-12, 3158 - 3184	R.YALYDATYETK.E	1338.44364	2	4.84E-09	0.91	3.54	-	827.7
AHQ-3-12, 3116 - 3174	R.YALYDATYETK.E	1338.44364	1	4.77E-08	0.58	2.85	-	340.0
AHQ-3-13, 3265	R.YALYDATYETK.E	1338.44364	1	4.24E-04	0.59	2.90	-	319.6
AHQ-3-11, 3075 - 3092	R.YALYDATYETK.E	1338.44364	2	1.70E-06	0.85	3.09	-	679.4
AHQ-3-12, 2794	R.YALYDATYETKESK.K	1682.80875	2	5.39E-06	0.91	3.55	-	918.7
gi|4757900|ref|NP_004334.1|	calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre			1.88E-11	6.42	80.28	28.50	48141.1
AHQ-3-7, 5890	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	4.38E-06	0.92	4.33	-	1165.2
AHQ-3-7, 5743	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	3.87E-08	0.96	5.50	-	1322.0
AHQ-3-7, 3786	K.EQFLDGDGWTSR.W	1411.45795	1	6.86E-04	0.20	1.85	-	202.1
AHQ-3-7, 5362 - 5434	R.FYALSASFEPFSNK.G	1608.77470	2	1.88E-11	0.97	4.88	-	1656.1
AHQ-3-14, 6399	R.FYALSASFEPFSNK.G	1608.77470	2	1.79E-10	0.92	3.36	-	1156.2
AHQ-3-7, 5052 - 5059	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	2.21E-09	0.91	4.21	-	801.3
AHQ-3-7, 2227	K.IKDPDASKPEDWDER.A	1801.89173	2	2.13E-07	0.90	3.95	-	754.9
AHQ-3-7, 5387	K.KPEDWDEEMDGEWEPPVIQNPEYK.G	2962.14926	3	2.12E-04	0.83	4.11	-	528.6
AHQ-3-7, 1934	K.KVHVIFNYK.G	1148.38164	1	1.86E-06	0.82	2.92	-	596.7
AHQ-3-7, 2344	K.VHVIFNYK.G	1020.20872	1	7.67E-06	0.83	2.81	-	689.5
gi|4504349|ref|NP_000509.1|	beta globin [Homo sapiens]			1.94E-11	7.20	80.27	66.70	15998.3
AHQ-3-14, 6493	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.07E-07	0.94	4.42	-	931.5
AHQ-3-14-, 4995	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.23E-04	0.73	3.49	-	394.3
AHQ-3-13-, 5571 - 5577	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	5.15E-08	0.97	5.34	-	990.1
AHQ-3-13-, 5021 - 5091	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	6.71E-08	0.93	4.64	-	606.7
AHQ-3-14-, 5576	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	8.37E-08	0.96	4.51	-	1210.1
AHQ-3-14, 6015 - 6081	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	4.97E-06	0.91	4.23	-	748.6
AHQ-3-13, 4967 - 5042	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	6.50E-05	0.81	3.53	-	436.8
AHQ-3-13, 5578 - 5646	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	4.00E-07	0.95	4.97	-	781.3
AHQ-3-13, 5051	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	5.82E-06	0.92	4.39	-	586.5
AHQ-3-13, 5055	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	4.39E-05	0.95	4.11	-	1771.6
AHQ-3-13-, 3478	K.GTFATLSELHCDK.L	1480.62492	2	3.71E-09	0.74	3.19	-	451.4
AHQ-3-13, 3485 - 3487	K.GTFATLSELHCDK.L	1480.62492	2	3.54E-07	0.91	4.36	-	668.6
AHQ-3-13, 5014 - 5021	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	5.85E-11	0.95	4.77	-	1262.3
AHQ-3-13-, 5006	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	9.45E-08	0.94	4.56	-	1451.0
AHQ-3-13-, 6583	R.LLGNVLVCVLAHHFGK.E	1779.14197	3	3.24E-05	0.73	3.07	-	630.7
AHQ-3-14-, 5097	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	4.01E-10	0.96	4.79	-	1573.5
AHQ-3-13, 4919 - 4954	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	6.96E-09	0.94	4.23	-	1195.3
AHQ-3-13-, 4957	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	9.20E-09	0.97	5.30	-	1566.8
AHQ-3-13, 5113	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.94E-11	0.96	4.70	-	1300.4
AHQ-3-13-, 5117	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	4.79E-11	0.98	5.42	-	2100.8
AHQ-3-13, 3249 - 3251	K.VNVDEVGGEALGR.L	1315.41484	1	8.78E-04	0.21	2.20	-	255.9
AHQ-3-13-, 3237	K.VNVDEVGGEALGR.L	1315.41484	2	1.68E-05	0.97	5.11	-	1533.7
AHQ-3-13, 3250	K.VNVDEVGGEALGR.L	1315.41484	2	5.48E-04	0.96	4.44	-	1730.3
AHQ-3-13-, 2162	K.VVAGVANALAHK.Y	1150.35593	2	5.23E-08	0.96	3.85	-	1776.8
AHQ-3-13, 2223	K.VVAGVANALAHK.Y	1150.35593	2	2.63E-04	0.95	3.95	-	1442.9
AHQ-3-13, 2691	K.VVAGVANALAHK.Y	1150.35593	2	1.07E-04	0.93	3.57	-	1281.2
gi|30159830|ref|XP_302246.1|	similar to HSPC280 [Homo sapiens]			1.96E-11	1.92	20.27	3.90	45644.4
AHQ-3-14-, 6783	K.CANLFEALVGTLK.A	1437.68632	2	5.77E-08	0.97	5.50	-	1372.6
AHQ-3-14-, 6721 - 6727	R.DDKCANLFEALVGTLK.A	1796.03496	2	6.01E-11	0.97	5.13	-	1489.2
AHQ-3-13, 6862	R.DDKCANLFEALVGTLK.A	1796.03496	2	1.96E-11	0.94	4.32	-	1072.2
gi|4505981|ref|NP_002695.1|	pro-platelet basic protein (includes platelet basic protein, bet; Pro-p			1.98E-11	9.26	110.30	50.00	13894.1
AHQ-3-14, 5408 - 5447	K.EESLDSDLYAELR.C	1540.61070	2	5.13E-06	0.42	2.65	-	286.7
AHQ-3-14-, 4448 - 4528	K.EESLDSDLYAELR.C	1540.61070	2	3.22E-05	0.84	2.88	-	958.7
AHQ-3-14-, 4811 - 4836	K.EESLDSDLYAELR.C	1540.61070	2	6.20E-05	0.97	4.69	-	1483.2
AHQ-3-14, 5751 - 5817	K.EESLDSDLYAELR.C	1540.61070	2	4.05E-05	0.88	3.53	-	851.1
AHQ-3-14, 5795	K.EESLDSDLYAELR.C	1540.61070	2	4.09E-08	0.97	4.82	-	1361.8
AHQ-3-14, 5879 - 5889	K.EESLDSDLYAELR.C	1540.61070	2	1.49E-07	0.79	3.20	-	828.4

AHQ-3-14-, 4688 - 4751	K.EESLDSDLYAELR.C	1540.61070	2	2.11E-09	0.95	4.49	-	1008.7
AHQ-3-14-, 4351	K.EESLDSDLYAELR.C	1540.61070	2	4.98E-05	0.83	3.35	-	513.6
AHQ-3-14, 5292 - 5307	K.EESLDSDLYAELR.C	1540.61070	2	1.55E-06	0.87	3.76	-	670.1
AHQ-3-14-, 4328 - 4407	K.GKEESLDSDLYAELR.C	1725.83517	2	8.39E-11	0.98	5.40	-	2468.7
AHQ-3-14-, 4079 - 4139	K.GKEESLDSDLYAELR.C	1725.83517	2	2.25E-10	0.98	5.58	-	2489.3
AHQ-3-13-, 4162 - 4179	K.GKEESLDSDLYAELR.C	1725.83517	2	1.39E-05	0.98	5.34	-	2895.4
AHQ-3-14, 6061	K.GKEESLDSDLYAELR.C	1725.83517	2	3.15E-05	0.97	4.51	-	2172.9
AHQ-3-14, 5928 - 6000	K.GKEESLDSDLYAELR.C	1725.83517	2	2.04E-10	0.98	5.16	-	2056.6
AHQ-3-14-, 3980 - 4064	K.GKEESLDSDLYAELR.C	1725.83517	3	8.94E-06	0.93	5.02	-	1135.1
AHQ-3-14, 5832	K.GKEESLDSDLYAELR.C	1725.83517	2	1.42E-06	0.98	5.83	-	2585.9
AHQ-3-13, 4157	K.GKEESLDSDLYAELR.C	1725.83517	2	1.71E-08	0.98	5.16	-	2318.7
AHQ-3-13, 3966	K.GKEESLDSDLYAELR.C	1725.83517	2	1.72E-06	0.94	4.00	-	1272.5
AHQ-3-14, 5715 - 5763	K.GKEESLDSDLYAELR.C	1725.83517	2	3.83E-09	0.96	4.87	-	1487.0
AHQ-3-14, 5581 - 5653	K.GKEESLDSDLYAELR.C	1725.83517	2	1.76E-07	0.98	4.91	-	2703.6
AHQ-3-14-, 4667 - 4700	K.GKEESLDSDLYAELR.C	1725.83517	2	1.05E-09	0.96	4.38	-	1837.0
AHQ-3-14, 5467 - 5547	K.GKEESLDSDLYAELR.C	1725.83517	2	8.65E-09	0.98	5.96	-	2443.1
AHQ-3-14, 5455	K.GKEESLDSDLYAELR.C	1725.83517	3	5.10E-05	0.82	3.62	-	727.8
AHQ-3-14-, 4952	K.GKEESLDSDLYAELR.C	1725.83517	2	2.69E-07	0.97	4.95	-	1989.8
AHQ-3-14-, 4472 - 4535	K.GKEESLDSDLYAELR.C	1725.83517	2	4.43E-07	0.98	5.51	-	2688.5
AHQ-3-14, 5343 - 5404	K.GKEESLDSDLYAELR.C	1725.83517	2	2.06E-10	0.98	5.71	-	2769.0
AHQ-3-14-, 3825 - 3907	K.GKEESLDSDLYAELR.C	1725.83517	2	5.27E-08	0.97	5.49	-	1730.9
AHQ-3-14-, 4203 - 4263	K.GKEESLDSDLYAELR.C	1725.83517	2	1.98E-11	0.98	5.58	-	2328.6
AHQ-3-14, 5281 - 5347	K.GKEESLDSDLYAELR.C	1725.83517	3	3.64E-07	0.86	3.73	-	926.6
AHQ-3-14, 5223 - 5283	K.GKEESLDSDLYAELR.C	1725.83517	2	7.71E-09	0.98	5.59	-	2945.0
AHQ-3-14, 4628	K.GKEESLDSDLYAELR.C	1725.83517	2	1.07E-04	0.97	5.01	-	2074.9
AHQ-3-14, 5160 - 5219	K.GKEESLDSDLYAELR.C	1725.83517	3	2.38E-07	0.85	3.89	-	785.1
AHQ-3-14, 4760 - 4819	K.GKEESLDSDLYAELR.C	1725.83517	2	8.07E-10	0.98	5.72	-	1583.1
AHQ-3-14, 4847 - 4909	K.GKEESLDSDLYAELR.C	1725.83517	2	9.56E-11	0.98	5.46	-	2496.9
AHQ-3-14, 5103 - 5167	K.GKEESLDSDLYAELR.C	1725.83517	2	1.87E-10	0.98	5.18	-	2676.6
AHQ-3-14, 4924	K.GKEESLDSDLYAELR.C	1725.83517	3	5.87E-07	0.90	4.30	-	975.7
AHQ-3-14, 4971 - 5040	K.GKEESLDSDLYAELR.C	1725.83517	2	6.89E-07	0.98	5.42	-	2449.0
AHQ-3-14, 5023 - 5095	K.GKEESLDSDLYAELR.C	1725.83517	3	2.05E-06	0.90	4.43	-	855.9
AHQ-3-14-, 3979 - 4059	K.GKEESLDSDLYAELR.C	1725.83517	2	9.35E-11	0.98	5.87	-	2734.0
AHQ-3-14, 5073 - 5148	K.GTHCNQVEVIATLK.D	1571.78073	2	2.77E-07	0.97	4.66	-	2019.5
AHQ-3-14, 4859 - 4919	K.GTHCNQVEVIATLK.D	1571.78073	2	3.51E-09	0.97	4.82	-	1938.5
AHQ-3-14, 4739	K.GTHCNQVEVIATLK.D	1571.78073	2	7.31E-06	0.97	4.84	-	1627.2
AHQ-3-14, 5207 - 5275	K.GTHCNQVEVIATLK.D	1571.78073	2	4.02E-07	0.97	5.01	-	1929.3
AHQ-3-14, 4616	K.GTHCNQVEVIATLK.D	1571.78073	2	7.14E-07	0.97	4.25	-	1721.2
AHQ-3-14-, 4404 - 4471	K.GTHCNQVEVIATLK.D	1571.78073	2	1.18E-04	0.97	4.78	-	1884.4
AHQ-3-14, 4483 - 4555	K.GTHCNQVEVIATLK.D	1571.78073	2	6.28E-06	0.98	5.39	-	1688.2
AHQ-3-14, 5337 - 5400	K.GTHCNQVEVIATLK.D	1571.78073	2	2.38E-07	0.94	3.91	-	1310.1
AHQ-3-14, 4435 - 4495	K.GTHCNQVEVIATLK.D	1571.78073	2	5.32E-08	0.96	4.27	-	1745.7
AHQ-3-14, 4331 - 4365	K.GTHCNQVEVIATLK.D	1571.78073	2	7.18E-05	0.97	5.04	-	1577.6
AHQ-3-14-, 4488	K.GTHCNQVEVIATLK.D	1571.78073	2	8.97E-05	0.95	4.07	-	1353.8
AHQ-3-14, 4219 - 4268	K.GTHCNQVEVIATLK.D	1571.78073	2	3.17E-07	0.96	4.52	-	1328.8
AHQ-3-14, 5485 - 5525	K.GTHCNQVEVIATLK.D	1571.78073	2	8.48E-09	0.95	4.01	-	1551.1
AHQ-3-14, 4091 - 4155	K.GTHCNQVEVIATLK.D	1571.78073	2	5.44E-06	0.95	4.30	-	1501.7
AHQ-3-14, 5585 - 5613	K.GTHCNQVEVIATLK.D	1571.78073	2	1.43E-07	0.96	4.33	-	1539.6
AHQ-3-14, 5685 - 5759	K.GTHCNQVEVIATLK.D	1571.78073	2	3.02E-08	0.98	5.01	-	2270.1
AHQ-3-14-, 3945 - 3975	K.GTHCNQVEVIATLK.D	1571.78073	2	3.66E-08	0.96	4.87	-	1237.1
AHQ-3-14-, 3839 - 3904	K.GTHCNQVEVIATLK.D	1571.78073	2	4.76E-11	0.98	5.41	-	1897.4
AHQ-3-14-, 3800 - 3865	K.GTHCNQVEVIATLK.D	1571.78073	2	3.25E-07	0.97	4.54	-	1958.4
AHQ-3-14-, 3711	K.GTHCNQVEVIATLK.D	1571.78073	2	6.13E-08	0.97	4.95	-	1880.2
AHQ-3-14-, 3707 - 3775	K.GTHCNQVEVIATLK.D	1571.78073	2	6.99E-08	0.98	5.81	-	1995.6
AHQ-3-14-, 4705 - 4731	K.GTHCNQVEVIATLK.D	1571.78073	2	2.41E-05	0.91	4.14	-	982.8
AHQ-3-14-, 4069 - 4136	K.GTHCNQVEVIATLK.D	1571.78073	2	1.42E-07	0.97	5.13	-	1658.6
AHQ-3-14-, 3580 - 3647	K.GTHCNQVEVIATLK.D	1571.78073	2	8.69E-11	0.97	5.14	-	1692.7
AHQ-3-14, 6140	K.GTHCNQVEVIATLK.D	1571.78073	2	8.46E-05	0.87	3.24	-	693.1
AHQ-3-14, 6555	K.GTHCNQVEVIATLK.D	1571.78073	2	2.87E-04	0.84	3.25	-	659.3
AHQ-3-14-, 3471 - 3548	K.GTHCNQVEVIATLK.D	1571.78073	2	3.65E-08	0.97	5.11	-	1682.6
AHQ-3-13-, 3350	K.GTHCNQVEVIATLK.D	1571.78073	2	1.26E-06	0.94	3.91	-	1276.0
AHQ-3-14, 4980 - 4981	K.GTHCNQVEVIATLK.D	1571.78073	2	1.77E-06	0.97	4.85	-	1708.8
AHQ-3-14-, 4165 - 4235	K.GTHCNQVEVIATLK.D	1571.78073	2	3.36E-06	0.95	4.29	-	1364.9
AHQ-3-14-, 3339 - 3420	K.GTHCNQVEVIATLK.D	1571.78073	2	1.10E-06	0.97	4.71	-	1633.1
AHQ-3-14-, 3227 - 3295	K.GTHCNQVEVIATLK.D	1571.78073	2	1.56E-05	0.98	5.67	-	1961.7
AHQ-3-14-, 4315	K.GTHCNQVEVIATLK.D	1571.78073	2	5.15E-06	0.97	5.06	-	1875.5
AHQ-3-14, 4047 - 4109	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	2.19E-05	0.96	4.87	-	1313.9
AHQ-3-14-, 2888 - 2961	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.59E-10	0.92	4.34	-	1014.6
AHQ-3-14-, 2997	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	4.80E-07	0.98	5.67	-	1868.3
AHQ-3-14, 4009 - 4081	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.77E-08	0.94	4.45	-	1280.9
AHQ-3-14, 3885 - 3948	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.72E-06	0.90	3.98	-	961.3
AHQ-3-14-, 3176 - 3189	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	4.15E-06	0.94	4.35	-	1158.4
AHQ-3-14-, 3564	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	5.08E-05	0.91	4.14	-	859.0
AHQ-3-14-, 3401	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.01E-06	0.93	4.31	-	1066.2
AHQ-3-14, 3873 - 3936	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	1.74E-06	0.97	5.72	-	1579.6
AHQ-3-14-, 2640 - 2716	K.GTHCNQVEVIATLKDGRK.I	2028.27941	3	1.17E-06	0.91	4.40	-	1034.0
AHQ-3-14-, 2655	K.GTHCNQVEVIATLKDGRK.I	2028.27941	2	2.72E-05	0.96	5.42	-	1094.9
AHQ-3-14, 3568 - 3628	K.GTHCNQVEVIATLKDGRK.I	2028.27941	3	2.72E-04	0.82	3.66	-	757.3
AHQ-3-14-, 2760 - 2829	K.ICLDPDAPR.I	1058.19059	2	1.63E-05	0.85	3.15	-	929.4
AHQ-3-13-, 2582 - 2609	R.KICLDPDAPR.I	1186.36350	2	1.37E-05	0.48	2.83	-	414.2
AHQ-3-14-, 2427 - 2503	R.KICLDPDAPR.I	1186.36350	2	6.25E-05	0.83	3.23	-	812.4
AHQ-3-14-, 2519 - 2580	R.KICLDPDAPR.I	1186.36350	2	2.37E-04	0.87	3.32	-	842.6
AHQ-3-14, 3655	R.KICLDPDAPR.I	1186.36350	2	2.74E-04	0.46	2.58	-	454.1
AHQ-3-14, 3853	R.KICLDPDAPR.I	1186.36350	2	5.59E-05	0.77	3.15	-	764.9
AHQ-3-14, 3215 - 3271	R.KICLDPDAPR.I	1186.36350	2	3.65E-05	0.69	2.78	-	576.8
AHQ-3-14, 3331 - 3396	R.KICLDPDAPR.I	1186.36350	2	4.56E-06	0.90	3.40	-	954.3
AHQ-3-12, 2484 - 2522	R.KICLDPDAPR.I	1186.36350	2	3.76E-05	0.68	2.73	-	619.4
AHQ-3-13, 2625	R.KICLDPDAPR.I	1186.36350	2	1.27E-04	0.86	3.43	-	675.6
AHQ-3-14, 3452 - 3512	R.KICLDPDAPR.I	1186.36350	2	7.76E-05	0.81	3.10	-	735.3
AHQ-3-14, 3083 - 3157	R.KICLDPDAPR.I	1186.36350	2	7.71E-04	0.61	2.60	-	553.6
AHQ-3-14, 3455 - 3511	R.KICLDPDAPR.I	1186.36350	2	5.96E-05	0.88	3.48	-	786.9
AHQ-3-14, 1369 - 2623	K.KLAGDESAD	905.92969	1	7.96E-05	0.21	2.00	-	301.0
AHQ-3-14, 2852 - 2873	K.KLAGDESAD	905.92969	1	5.18E-04	0.22	1.86	-	277.2
AHQ-3-13, 3311 - 3321	K.NIQSLEVIGK.G	1101.27845	2	1.06E-06	0.84	3.27	-	659.0
AHQ-3-14-, 3427 - 3499	K.NIQSLEVIGK.G	1101.27845	2	2.79E-04	0.79	3.28	-	645.6
AHQ-3-14-, 3327 - 3332	K.NIQSLEVIGK.G	1101.27845	2	1.06E-06	0.87	3.23	-	776.5
AHQ-3-14-, 3204 - 3268	K.NIQSLEVIGK.G	1101.27845	2	2.66E-05	0.89	3.73	-	826.3
AHQ-3-14-, 3135 - 3203	K.NIQSLEVIGK.G	1101.27845	2	3.21E-05	0.89	4.01	-	640.0
AHQ-3-14-, 3667	K.NIQSLEVIGK.G	1101.27845	1	8.57E-04	0.67	2.52	-	654.8
AHQ-3-14, 4599 - 4629	K.NIQSLEVIGK.G	1101.27845	2	6.98E-04	0.83	3.34	-	748.5
AHQ-3-14, 4479 - 4539	K.NIQSLEVIGK.G	1101.27845	2	4.70E-04	0.84	3.28	-	647.6
AHQ-3-14, 4395 - 4455	K.NIQSLEVIGK.G	1101.27845	2	3.02E-05	0.81	3.24	-	563.3
AHQ-3-14, 4255 - 4332	K.NIQSLEVIGK.G	1101.27845	2	3.08E-06	0.90	3.81	-	763.5
AHQ-3-14, 4112 - 4191	K.NIQSLEVIGK.G	1101.27845	2	8.42E-06	0.89	3.77	-	645.2
AHQ-3-14-, 3072 - 3393	K.NIQSLEVIGK.G	1101.27845	1	8.25E-04	0.36	2.31	-	339.8
AHQ-3-14-, 3675	K.NIQSLEVIGK.G	1101.27845	1	5.99E-04	0.42	2.51	-	296.1
AHQ-3-14, 5777	R.NLAKGKEESLDSDLYAELR.C	2152.34765	2	4.17E-05	0.77	3.58	-	499.9

AHQ-3-14-, 3461	K.TTSGIHPKNIQSLEVIGK.G	1923.20305	2	7.30E-06	0.91	4.13	-	664.9
gi|4502985|ref|NP_001854.1| cytochrome c oxidase subunit VIb; human cytochrome oxidase subunit VIb				1.99E-11	2.54	30.20	31.40	10192.3
AHQ-3-14-, 6073 - 6137	R.VYQSLCPTSWVTDWDEQR.A	2272.43560	2	1.99E-11	0.93	3.99	-	1108.1
AHQ-3-14-, 6124 - 6147	R.VYQSLCPTSWVTDWDEQRAEGTFPGK.I	3060.29908	3	8.49E-06	0.78	3.61	-	363.0
AHQ-3-14-, 6531	R.VYQSLCPTSWVTDWDEQRAEGTFPGKI	3173.45733	3	9.14E-04	0.83	3.73	-	588.1
gi|7705296|ref|NP_057271.1| bridging integrator 2; bridging integrator-2; breast cancer associated				2.22E-11	5.25	60.25	18.10	61746.8
AHQ-3-10, 5630 - 5686	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	2.22E-11	0.95	4.36	-	1240.0
AHQ-3-10, 5518 - 5594	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	4.06E-11	0.95	4.44	-	1212.4
AHQ-3-9, 7009 - 7079	K.AQTVFEDLNQELLEELPILYNSR.I	2736.02649	2	1.91E-07	0.90	4.71	-	478.6
AHQ-3-10, 2578 - 2579	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	9.07E-06	0.96	4.94	-	1033.0
AHQ-3-14-, 6481 - 6485	R.IGCYVTIFQNISNLR.D	1800.07167	2	6.43E-06	0.93	4.65	-	956.8
AHQ-3-13, 6615	R.IGCYVTIFQNISNLR.D	1800.07167	2	1.94E-05	0.92	4.07	-	829.0
AHQ-3-9, 6471	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.38E-06	0.94	4.30	-	1061.5
AHQ-3-10, 6074 - 6130	R.IGCYVTIFQNISNLR.D	1800.07167	2	4.27E-04	0.94	4.81	-	897.8
AHQ-3-11, 6330	R.IGCYVTIFQNISNLR.D	1800.07167	2	1.08E-06	0.94	4.51	-	1143.6
AHQ-3-10, 2051	K.LNHNLYEVM*SK.L	1364.55247	2	4.24E-04	0.86	3.22	-	655.2
AHQ-3-7, 4028	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	4.27E-06	0.64	3.11	-	412.8
gi|4758086|ref|NP_004069.1| cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain				2.36E-11	6.82	80.25	51.30	20567.3
AHQ-3-11, 1667 - 1742	R.CSQAVYAAEK.V	1128.23768	1	5.48E-06	0.41	2.56	-	428.9
AHQ-3-13, 4210	K.GFGFGQGAGALVHSE	1434.53788	2	9.88E-06	0.95	4.29	-	1041.6
AHQ-3-11, 4024	K.GFGFGQGAGALVHSE	1434.53788	1	8.38E-04	0.58	2.69	-	522.1
AHQ-3-11, 4018	K.GFGFGQGAGALVHSE	1434.53788	2	8.83E-09	0.95	3.59	-	1363.2
AHQ-3-11, 3130 - 3198	K.GLESTTLADKDGEIYCK.G	1902.06957	2	7.36E-09	0.95	4.54	-	1187.3
AHQ-3-11, 2440	K.GYGYGQGAGTLSTDK.G	1475.54194	2	1.11E-06	0.94	4.26	-	921.0
AHQ-3-10, 3299	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	7.61E-06	0.54	3.07	-	225.9
AHQ-3-12, 3515 - 3516	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	1.10E-10	0.91	4.55	-	603.1
AHQ-3-11, 3330 - 3390	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	2.36E-11	0.87	4.31	-	501.1
AHQ-3-13, 3626	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	7.89E-10	0.84	3.76	-	648.5
AHQ-3-11, 2884	K.KNLDSTTVAVHGEEIYCK.S	2066.27805	3	6.82E-05	0.95	4.37	-	1490.8
AHQ-3-11, 3339 - 3419	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	2.46E-10	0.97	5.07	-	1372.2
AHQ-3-11, 3824	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	1.35E-05	0.95	4.71	-	983.6
AHQ-3-11, 4014	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	5.69E-05	0.89	3.96	-	699.1
AHQ-3-14, 5273	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	7.11E-06	0.78	3.78	-	447.4
gi|24431935|ref|NP_065393.1| reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sap				2.46E-11	0.97	10.31	2.80	129930.3
AHQ-3-14-, 6008	K.YQFVREPEDEEEEEEEEEEDEDEDLEELEVLER.K	4189.14063	3	2.46E-11	0.97	6.18	-	1726.4
gi|13775198|ref|NP_112576.1| SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr				2.98E-11	5.36	60.28	35.50	10437.7
AHQ-3-13, 4813 - 4850	R.IQYQLVDISQDNALR.D	1776.97168	2	1.93E-07	0.97	5.05	-	1936.9
AHQ-3-13-, 4717	R.IQYQLVDISQDNALR.D	1776.97168	3	1.15E-06	0.96	4.85	-	2099.0
AHQ-3-14-, 4684	R.IQYQLVDISQDNALR.D	1776.97168	2	1.93E-10	0.97	5.59	-	1850.0
AHQ-3-13-, 4846 - 4854	R.IQYQLVDISQDNALR.D	1776.97168	2	4.53E-11	0.95	4.75	-	1259.1
AHQ-3-13-, 4693 - 4757	R.IQYQLVDISQDNALR.D	1776.97168	2	2.98E-11	0.96	5.13	-	1631.3
AHQ-3-13, 4961 - 5041	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	5.02E-07	0.91	4.32	-	897.4
AHQ-3-13, 5114 - 5142	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	4.31E-06	0.50	3.01	-	452.8
AHQ-3-13-, 4962 - 5025	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.20E-06	0.79	3.65	-	701.2
AHQ-3-14-, 4355 - 4381	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	7.91E-05	0.61	3.04	-	358.0
AHQ-3-14-, 4935 - 5007	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.53E-05	0.81	3.75	-	439.4
AHQ-3-13, 4809 - 4877	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.97E-07	0.94	4.77	-	1192.4
AHQ-3-13-, 4214	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.13E-10	0.88	3.71	-	833.0
AHQ-3-13-, 4329 - 4393	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	8.27E-05	0.74	3.12	-	387.8
AHQ-3-13, 4223	K.RIQYQLVDISQDNALR.D	1933.15803	2	3.94E-07	0.95	4.95	-	793.9
AHQ-3-13-, 1623 - 1689	R.VYSTSVTGSR.E	1057.13940	2	6.95E-06	0.92	3.06	-	1120.7
AHQ-3-13, 1885 - 1945	R.VYSTSVTGSR.E	1057.13940	2	9.45E-07	0.91	3.27	-	973.3
AHQ-3-13-, 1749 - 1810	R.VYSTSVTGSR.E	1057.13940	2	1.31E-05	0.91	3.04	-	979.3
AHQ-3-13, 1765 - 1827	R.VYSTSVTGSR.E	1057.13940	2	1.19E-04	0.72	2.59	-	634.8
AHQ-3-13-, 2246	R.VYSTSVTGSREIK.S	1427.58510	2	1.09E-06	0.82	3.29	-	718.4
AHQ-3-13, 2281 - 2289	R.VYSTSVTGSREIK.S	1427.58510	2	1.09E-06	0.73	3.29	-	633.3
gi|4502027|ref|NP_000468.1| albumin precursor; PRO0883 protein [Homo sapiens]				3.01E-11	24.67	290.38	52.50	69366.4
AHQ-3-6, 2353	K.AAFTECCQAADK.A	1374.47927	1	1.33E-04	0.63	3.09	-	490.2
AHQ-3-6, 2346 - 2347	K.AAFTECCQAADK.A	1374.47927	2	9.87E-04	0.92	3.68	-	986.5
AHQ-3-5, 2375	K.AAFTECCQAADK.A	1374.47927	1	1.03E-04	0.56	2.79	-	425.9
AHQ-3-5, 2372	K.AAFTECCQAADK.A	1374.47927	2	2.30E-04	0.91	3.85	-	978.0
AHQ-3-6, 4302	K.AVM*DDFAAFVEK.C	1359.52946	2	1.93E-08	0.87	3.38	-	730.6
AHQ-3-5, 4395 - 4468	K.AVM*DDFAAFVEK.C	1359.52946	2	1.88E-07	0.95	3.65	-	1407.3
AHQ-3-5, 5541 - 5545	K.AVMDDFAAFVEK.C	1343.53006	2	4.49E-07	0.96	4.48	-	1249.6
AHQ-3-6, 5461 - 5463	K.AVMDDFAAFVEK.C	1343.53006	2	9.35E-08	0.95	3.84	-	1528.9
AHQ-3-6, 5469 - 5539	K.AVMDDFAAFVEK.C	1343.53006	1	5.60E-05	0.90	3.86	-	945.5
AHQ-3-14-, 5388 - 5391	K.AVMDDFAAFVEK.C	1343.53006	2	1.66E-09	0.95	4.17	-	1201.1
AHQ-3-5, 5548	K.AVMDDFAAFVEK.C	1343.53006	1	6.62E-06	0.88	3.94	-	895.3
AHQ-3-12, 5447	K.AVMDDFAAFVEK.C	1343.53006	2	3.75E-06	0.87	3.35	-	977.1
AHQ-3-14, 6396	K.AVMDDFAAFVEK.C	1343.53006	2	9.35E-08	0.94	3.36	-	1423.8
AHQ-3-5, 2029	K.CCAAADPHECYAK.V	1556.67999	2	4.89E-05	0.87	3.29	-	922.5
AHQ-3-6, 2305 - 2313	K.CCTESLVNR.R	1141.25805	2	2.94E-06	0.88	2.66	-	1211.2
AHQ-3-5, 2344	K.CCTESLVNR.R	1141.25805	2	1.16E-04	0.89	2.99	-	1053.4
AHQ-3-1, 7054	K.DVFLGM*FLYEYAR.R	1640.88331	2	1.43E-04	0.86	3.24	-	901.1
AHQ-3-6, 2539	R.ETYGEMADCCAK.Q	1437.55563	1	1.78E-06	0.34	2.50	-	104.7
AHQ-3-5, 2569	R.ETYGEMADCCAK.Q	1437.55563	1	4.62E-08	0.65	3.47	-	100.0
AHQ-3-13, 2711	R.FKDLGEENFK.A	1227.34766	2	6.94E-06	0.73	3.14	-	560.2
AHQ-3-6, 2373 - 2418	R.FKDLGEENFK.A	1227.34766	2	2.10E-05	0.81	3.43	-	593.2
AHQ-3-6, 2374	R.FKDLGEENFK.A	1227.34766	1	1.53E-04	0.18	1.90	-	424.6
AHQ-3-7, 2328	R.FKDLGEENFK.A	1227.34766	2	2.32E-05	0.50	2.54	-	511.6
AHQ-3-5, 2393	R.FKDLGEENFK.A	1227.34766	2	9.03E-07	0.82	2.80	-	776.1
AHQ-3-13, 2714 - 2715	R.FKDLGEENFK.A	1227.34766	1	3.01E-04	0.45	2.33	-	494.6
AHQ-3-14-, 2564 - 2621	R.FKDLGEENFK.A	1227.34766	2	3.25E-06	0.78	3.17	-	641.7
AHQ-3-5, 2664	K.FQNALLVR.Y	961.14282	2	1.42E-04	0.77	2.68	-	818.8
AHQ-3-6, 2675	K.FQNALLVR.Y	961.14282	2	3.08E-04	0.79	2.68	-	744.2
AHQ-3-6, 2231 - 2306	K.KQTALVELVK.H	1129.37494	1	1.26E-04	0.19	2.13	-	306.0
AHQ-3-2, 3609	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.40E-07	0.91	3.81	-	794.2
AHQ-3-5, 3263 - 3337	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.37E-04	0.84	3.12	-	649.0
AHQ-3-5, 3272	K.KVPQVSTPTLVEVSR.N	1640.90605	3	5.62E-06	0.94	5.14	-	1109.3
AHQ-3-8, 2866	K.KVPQVSTPTLVEVSR.N	1640.90605	2	9.93E-07	0.85	3.31	-	554.7
AHQ-3-7, 3122 - 3130	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.01E-09	0.94	4.14	-	871.8
AHQ-3-6, 2975	K.KVPQVSTPTLVEVSR.N	1640.90605	2	7.64E-09	0.82	3.16	-	502.8
AHQ-3-9, 2980 - 3033	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.76E-04	0.89	3.58	-	924.9
AHQ-3-10, 3191	K.KVPQVSTPTLVEVSR.N	1640.90605	2	5.83E-10	0.91	4.08	-	656.4
AHQ-3-6, 3213 - 3267	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.92E-07	0.91	3.71	-	843.4
AHQ-3-1, 3781	K.KVPQVSTPTLVEVSR.N	1640.90605	3	2.36E-06	0.93	4.26	-	1239.0
AHQ-3-3, 3564 - 3594	K.KVPQVSTPTLVEVSR.N	1640.90605	2	8.38E-10	0.88	3.49	-	746.1
AHQ-3-1, 3452	K.LVNEVTEFAK.T	1150.30633	2	2.19E-05	0.89	3.47	-	679.9
AHQ-3-14-, 3208	K.LVNEVTEFAK.T	1150.30633	2	3.79E-07	0.86	2.95	-	876.3
AHQ-3-13-, 3275	K.LVNEVTEFAK.T	1150.30633	2	2.75E-06	0.68	2.85	-	462.3
AHQ-3-5, 3035 - 3088	K.LVNEVTEFAK.T	1150.30633	2	1.95E-06	0.61	2.89	-	355.8
AHQ-3-6, 5642 - 5653	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	1.25E-05	0.98	6.50	-	1995.9
AHQ-3-5, 5684	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	7.59E-06	0.98	7.64	-	2057.2
AHQ-3-5, 5297	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	9.33E-08	0.98	6.87	-	1605.6
AHQ-3-6, 5250	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	3.01E-11	0.97	5.91	-	1478.5
AHQ-3-5, 5063	K.QNCELFEQLGEYK.F	1659.79847	2	1.26E-08	0.93	3.92	-	717.2
AHQ-3-5, 3704	R.RHPDYSVVLLLR.L	1468.72842	3	5.81E-05	0.97	4.93	-	2060.5

AHQ-3-3, 4086	R.RHPDYSVVLLLR.L	1468.72842	2	2.85E-07	0.89	3.62	-	740.2
AHQ-3-6, 3663	R.RHPDYSVVLLLR.L	1468.72842	3	2.20E-07	0.95	4.86	-	1810.5
AHQ-3-6, 3661	R.RHPDYSVVLLLR.L	1468.72842	2	3.53E-08	0.93	3.63	-	1016.1
AHQ-3-6, 5782	R.RHPYFYAPELLFFAK.R	1900.21293	3	7.51E-07	0.97	5.43	-	1970.2
AHQ-3-6, 5781 - 5790	R.RHPYFYAPELLFFAK.R	1900.21293	2	2.42E-05	0.98	5.12	-	2141.4
AHQ-3-5, 5675 - 5679	R.RHPYFYAPELLFFAK.R	1900.21293	2	6.77E-09	0.98	5.11	-	2932.8
AHQ-3-6, 7223	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	5.92E-06	0.95	5.72	-	1358.3
AHQ-3-5, 7439	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	5.34E-04	0.98	7.14	-	1564.2
AHQ-3-5, 7399 - 7400	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	9.67E-04	0.96	5.75	-	1438.2
AHQ-3-6, 7263	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	3.18E-04	0.98	6.39	-	2326.5
AHQ-3-1, 4989 - 4990	R.RPCFSALEVDETYVPK.E	1913.14041	2	6.66E-05	0.77	3.43	-	486.8
AHQ-3-6, 4609	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.31E-05	0.91	4.03	-	674.5
AHQ-3-4, 4853	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.66E-04	0.91	4.43	-	612.1
AHQ-3-3, 4932 - 4933	R.RPCFSALEVDETYVPK.E	1913.14041	2	4.14E-04	0.86	4.07	-	574.7
AHQ-3-10, 4292 - 4352	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.27E-04	0.84	3.16	-	702.2
AHQ-3-11, 4502	R.RPCFSALEVDETYVPK.E	1913.14041	2	3.04E-04	0.90	4.03	-	603.3
AHQ-3-5, 4667 - 4735	R.RPCFSALEVDETYVPK.E	1913.14041	2	9.09E-04	0.96	4.46	-	1047.0
AHQ-3-5, 6184	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	1.34E-05	0.53	3.36	-	299.5
AHQ-3-7, 6923	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	7.09E-04	0.87	4.73	-	356.8
AHQ-3-5, 7035 - 7115	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	2.04E-07	0.95	5.61	-	923.9
AHQ-3-5, 7037 - 7117	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	2.13E-07	0.95	5.09	-	926.2
AHQ-3-4, 7214 - 7220	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	2.34E-05	0.88	4.54	-	556.7
AHQ-3-1, 6596 - 6632	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	1.05E-04	0.95	5.55	-	983.7
AHQ-3-1, 6626	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	2	6.21E-05	0.78	3.43	-	521.1
AHQ-3-6, 6853 - 6918	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	2.01E-09	0.96	6.04	-	844.3
AHQ-3-6, 6905 - 6915	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	3.96E-04	0.93	4.52	-	857.4
AHQ-3-5, 2300	K.SLHTLFGDK.L	1018.14800	1	1.19E-05	0.56	2.55	-	449.4
AHQ-3-5, 2313	K.SLHTLFGDK.L	1018.14800	1	4.40E-05	0.54	2.50	-	431.8
AHQ-3-5, 4937	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	5.33E-06	0.96	5.24	-	1159.4
AHQ-3-6, 4865	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	1.32E-04	0.96	4.64	-	1402.4
AHQ-3-1, 6125	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.25E-04	0.91	4.26	-	570.1
AHQ-3-6, 5749 - 5817	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.55E-05	0.97	5.71	-	1684.0
AHQ-3-5, 6009 - 6083	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	7.57E-08	0.81	3.75	-	531.5
AHQ-3-2, 6138	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.34E-05	0.92	4.48	-	520.3
AHQ-3-5, 5840 - 5908	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	6.26E-06	0.94	4.47	-	1004.4
AHQ-3-6, 5357 - 5434	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	4.61E-05	0.76	3.85	-	456.5
AHQ-3-1, 6132	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.97E-07	0.97	5.43	-	1893.7
AHQ-3-6, 5718 - 5798	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.56E-04	0.93	4.84	-	533.6
AHQ-3-7, 5694	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.09E-06	0.92	4.81	-	492.0
AHQ-3-7, 5708	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	7.26E-09	0.95	4.67	-	1209.2
AHQ-3-5, 5660	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.44E-07	0.88	3.75	-	575.6
AHQ-3-3, 6030 - 6108	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.53E-06	0.81	3.60	-	377.4
AHQ-3-5, 5835 - 5913	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.98E-05	0.92	4.27	-	516.4
AHQ-3-9, 5417	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.79E-04	0.76	3.38	-	306.3
AHQ-3-10, 5259	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.54E-04	0.72	3.21	-	379.6
AHQ-3-6, 2887	K.VHTECCHGDLLECADDR.A	2091.20307	2	2.11E-06	0.96	4.60	-	1634.0
AHQ-3-3, 3797	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	7.59E-04	0.89	4.85	-	580.7
AHQ-3-5, 3564	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	1.24E-06	0.88	4.59	-	600.9
AHQ-3-6, 3514	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	4.94E-05	0.79	3.85	-	524.8
AHQ-3-5, 3740 - 3811	K.VPQVSTPTLVEVSR.N	1512.73313	2	9.64E-07	0.86	3.44	-	614.4
AHQ-3-5, 3797	K.VPQVSTPTLVEVSR.N	1512.73313	2	1.19E-07	0.93	3.62	-	951.6
AHQ-3-3, 2329	K.YICENQDSISSK.L	1445.53420	2	1.07E-06	0.86	3.81	-	569.5
AHQ-3-5, 2076 - 2224	K.YICENQDSISSK.L	1445.53420	1	1.03E-05	0.58	2.92	-	323.5
AHQ-3-6, 2189	K.YICENQDSISSK.L	1445.53420	2	6.56E-05	0.91	3.82	-	651.7
AHQ-3-5, 2216	K.YICENQDSISSK.L	1445.53420	2	5.62E-05	0.90	3.35	-	736.3
AHQ-3-1, 2449 - 2457	K.YICENQDSISSK.L	1445.53420	2	3.40E-04	0.82	3.46	-	483.5
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				3.24E-11	17.09	190.31	20.40	138070.8
AHQ-3-3, 2356	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	1.67E-09	0.93	4.81	-	781.6
AHQ-3-3, 2261 - 2272	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	2.75E-08	0.96	5.78	-	812.1
AHQ-3-2, 2301	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	3.68E-09	0.94	5.15	-	632.9
AHQ-3-3, 7369	K.CTSDMETILTFIPQFHR.L	2098.38838	2	1.25E-05	0.83	3.84	-	576.3
AHQ-3-4, 7394	K.CTSDMETILTFIPQFHR.L	2098.38838	2	5.65E-08	0.87	3.66	-	550.5
AHQ-3-3, 7376	K.CTSDMETILTFIPQFHR.L	2098.38838	3	1.30E-05	0.91	4.23	-	1239.5
AHQ-3-3, 4117	R.DQALQLQVLNSR.F	1385.55144	2	1.60E-05	0.96	4.08	-	1717.6
AHQ-3-3, 2729	K.EVHEQLLSTEQVSDQK.N	1870.99550	2	6.40E-04	0.95	4.65	-	928.3
AHQ-3-14-, 6115 - 6144	K.FPPVTTFSGYLLYR.T	1661.92388	2	3.58E-11	0.96	4.80	-	856.8
AHQ-3-10, 5732	K.FPPVTTFSGYLLYR.T	1661.92388	2	4.58E-05	0.88	3.38	-	567.5
AHQ-3-5, 5703	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	7.02E-06	0.81	3.63	-	485.8
AHQ-3-3, 5980	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	6.90E-04	0.89	4.33	-	501.6
AHQ-3-3, 5982	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	3.20E-07	0.95	4.41	-	1354.1
AHQ-3-4, 5920	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	3.96E-04	0.65	3.66	-	338.0
AHQ-3-1, 6317	K.GLTEFVEPIIQIK.T	1487.76518	2	9.09E-05	0.81	3.70	-	625.4
AHQ-3-3, 6302	K.GLTEFVEPIIQIK.T	1487.76518	1	5.11E-04	0.23	2.48	-	440.6
AHQ-3-6, 6027	K.GLTEFVEPIIQIK.T	1487.76518	2	5.18E-06	0.94	4.22	-	1148.5
AHQ-3-3, 2629	K.GPCGWTGGSCPQR.S	1422.52885	2	1.07E-07	0.86	3.47	-	696.6
AHQ-3-2, 3839	K.HSLPDIQLLQK.G	1292.50915	2	8.57E-06	0.91	3.42	-	740.3
AHQ-3-1, 4028	K.HSLPDIQLLQK.G	1292.50915	2	8.73E-07	0.88	2.82	-	831.6
AHQ-3-3, 3756	K.HSLPDIQLLQK.G	1292.50915	2	3.52E-08	0.91	3.45	-	740.5
AHQ-3-3, 6884 - 6957	K.IFQNDMQETVAQLFK.T	1813.06743	2	1.06E-06	0.94	4.26	-	1339.1
AHQ-3-3, 6708 - 6776	K.IFQNDMQETVAQLFK.T	1813.06743	2	1.61E-09	0.97	4.93	-	1666.3
AHQ-3-3, 5213	K.IFQNDM*QETVAQLFK.T	1829.06683	2	4.10E-05	0.88	4.09	-	660.7
AHQ-3-5, 6620	K.IFQNDMQETVAQLFK.T	1813.06743	2	3.24E-11	0.97	5.27	-	1610.5
AHQ-3-3, 5457	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.10E-08	0.95	3.92	-	1364.7
AHQ-3-3, 4970	R.KKIENLTSAVNSLNFIIK.E	2033.40055	2	6.00E-04	0.75	3.38	-	541.0
AHQ-3-4, 2724	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	4.09E-04	0.88	3.87	-	801.6
AHQ-3-1, 2989	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	5.15E-06	0.95	4.80	-	825.3
AHQ-3-3, 2690 - 2745	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	2.81E-06	0.98	6.23	-	1603.4
AHQ-3-10, 3419	K.LVEENALAPDFSK.G	1433.58810	2	2.60E-04	0.73	2.86	-	569.9
AHQ-3-11, 3546	K.LVEENALAPDFSK.G	1433.58810	2	4.18E-04	0.45	2.59	-	425.7
AHQ-3-10, 3412 - 3442	K.LVEENALAPDFSK.G	1433.58810	1	4.04E-05	0.52	2.34	-	582.0
AHQ-3-1, 7136 - 7214	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	5.26E-06	0.89	4.56	-	829.5
AHQ-3-3, 7512 - 7513	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	6.60E-09	0.95	5.19	-	877.3
AHQ-3-3, 7448	K.TM*TIINNAIDFIQDNYALK.E	2215.51196	2	1.14E-08	0.91	4.66	-	567.5
AHQ-3-4, 7532	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	6.99E-10	0.96	5.00	-	1075.0
AHQ-3-3, 3414 - 3436	K.TVSSLSEDLESTR.Q	1424.49324	2	7.14E-08	0.94	3.76	-	1074.9
AHQ-3-4, 3384	K.TVSSLSEDLESTR.Q	1424.49324	2	1.09E-04	0.62	2.59	-	649.6
AHQ-3-3, 4028	R.YNFVLQVAK.T	1082.27683	2	2.12E-05	0.91	3.33	-	796.6
gi|4505733|ref|NP_002610.1| platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4				3.36E-11	5.63	60.27	38.60	10844.9
AHQ-3-12, 4096	K.AGPHCPTAQLIATLK.N	1579.84600	2	7.12E-04	0.90	3.76	-	835.3
AHQ-3-14-, 3957 - 3965	K.AGPHCPTAQLIATLK.N	1579.84600	3	2.78E-04	0.88	3.94	-	1020.1
AHQ-3-14-, 3959 - 3960	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.36E-07	0.93	4.22	-	824.9
AHQ-3-14-, 4137 - 4215	K.AGPHCPTAQLIATLK.N	1579.84600	2	3.61E-08	0.87	3.52	-	707.1
AHQ-3-14, 5360 - 5436	K.AGPHCPTAQLIATLK.N	1579.84600	2	7.09E-04	0.92	3.97	-	895.8
AHQ-3-14, 5239 - 5300	K.AGPHCPTAQLIATLK.N	1579.84600	2	7.31E-04	0.93	4.29	-	827.3
AHQ-3-14, 5100 - 5179	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.63E-04	0.95	4.40	-	931.9
AHQ-3-14-, 3765	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	4.24E-06	0.97	4.91	-	1443.7
AHQ-3-14-, 3895	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	9.00E-09	0.94	4.72	-	802.4

AHQ-3-14-, 3879 - 3943	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	2.96E-09	0.97	5.39	-	2034.3
AHQ-3-14, 4740	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	6.80E-05	0.92	3.91	-	1014.3
AHQ-3-14, 4751	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.71E-08	0.94	4.89	-	1279.2
AHQ-3-14, 4865 - 4939	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.36E-11	0.96	4.97	-	1150.4
AHQ-3-14, 4944 - 4945	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	3.02E-09	0.96	5.19	-	1472.3
AHQ-3-14, 4452	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	3.61E-04	0.94	4.41	-	1417.2
AHQ-3-14, 4473	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	2	5.82E-06	0.95	4.07	-	1264.8
AHQ-3-14-, 2395 - 2459	R.HITSLEVIK.A	1040.23825	2	2.16E-07	0.90	3.53	-	649.6
AHQ-3-13, 2606	R.HITSLEVIK.A	1040.23825	2	2.91E-05	0.64	2.75	-	400.0
AHQ-3-14-, 2520 - 2599	R.HITSLEVIK.A	1040.23825	2	3.31E-06	0.90	3.28	-	659.3
AHQ-3-14, 3483 - 3552	R.HITSLEVIK.A	1040.23825	2	5.13E-06	0.85	3.27	-	531.8
AHQ-3-14, 3363 - 3423	R.HITSLEVIK.A	1040.23825	2	1.49E-04	0.83	3.36	-	470.0
AHQ-3-13-, 2557	R.HITSLEVIK.A	1040.23825	2	6.18E-05	0.68	2.74	-	446.4
AHQ-3-14, 3611 - 3621	R.HITSLEVIK.A	1040.23825	2	8.34E-04	0.72	2.65	-	466.8
AHQ-3-14-, 4883 - 4907	K.ICLDLQAPLYK.K	1335.59400	2	1.13E-06	0.96	4.57	-	1665.3
AHQ-3-13-, 4935	K.ICLDLQAPLYK.K	1335.59400	2	6.21E-06	0.97	4.53	-	2205.9
AHQ-3-14-, 4761	K.ICLDLQAPLYK.K	1335.59400	2	1.42E-05	0.91	3.15	-	1326.4
AHQ-3-13, 4953	K.ICLDLQAPLYK.K	1335.59400	2	2.21E-05	0.94	3.93	-	1218.7
AHQ-3-14, 5979 - 5980	K.ICLDLQAPLYK.K	1335.59400	2	2.66E-05	0.97	4.84	-	1975.4
AHQ-3-14, 5988	K.ICLDLQAPLYK.K	1335.59400	1	9.75E-06	0.71	3.17	-	552.8
AHQ-3-13-, 4405	R.KICLDLQAPLYK.K	1463.76691	2	1.61E-05	0.98	4.88	-	2045.5
AHQ-3-14, 5616	R.KICLDLQAPLYK.K	1463.76691	1	1.86E-06	0.89	3.53	-	800.4
AHQ-3-14, 5568 - 5627	R.KICLDLQAPLYK.K	1463.76691	2	1.09E-05	0.97	4.78	-	1592.7
AHQ-3-14, 5468	R.KICLDLQAPLYK.K	1463.76691	2	2.10E-06	0.97	4.90	-	1556.2
AHQ-3-13, 4402	R.KICLDLQAPLYK.K	1463.76691	1	2.28E-04	0.77	2.97	-	808.2
AHQ-3-14-, 4383 - 4460	R.KICLDLQAPLYK.K	1463.76691	2	4.77E-04	0.98	5.44	-	1597.2
AHQ-3-14-, 4385 - 4503	R.KICLDLQAPLYK.K	1463.76691	1	8.19E-04	0.84	3.53	-	637.6
AHQ-3-14-, 4392 - 4459	R.KICLDLQAPLYK.K	1463.76691	3	7.90E-05	0.91	4.35	-	1267.5
AHQ-3-14-, 4511 - 4589	R.KICLDLQAPLYK.K	1463.76691	2	1.65E-05	0.97	5.25	-	1667.0
AHQ-3-13, 4397	R.KICLDLQAPLYK.K	1463.76691	2	1.92E-04	0.95	4.00	-	1335.3
AHQ-3-14, 5687 - 5691	R.KICLDLQAPLYK.K	1463.76691	2	2.55E-08	0.98	5.07	-	1794.6
gi|7656991|ref|NP_055140.1| coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;				3.41E-11	6.11	70.28	24.30	53248.7
AHQ-3-7, 5898 - 5974	R.AIFLADGNVFTTGFSR.M	1716.91793	2	4.71E-04	0.78	2.63	-	959.0
AHQ-3-6, 6047 - 6123	R.AIFLADGNVFTTGFSR.M	1716.91793	2	7.20E-08	0.94	4.18	-	1150.4
AHQ-3-6, 5906 - 5937	R.AIFLADGNVFTTGFSR.M	1716.91793	2	3.41E-11	0.97	5.22	-	1465.4
AHQ-3-6, 2911	R.HVFGQAVKNDQCYDDIR.V	2067.22783	2	1.80E-07	0.96	4.70	-	1332.5
AHQ-3-6, 3029	R.KCEPIIMTVPR.K	1345.65706	2	2.86E-06	0.90	3.58	-	739.4
AHQ-3-7, 7262 - 7272	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	4.77E-06	0.94	5.00	-	1075.4
AHQ-3-6, 7194	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	9.81E-10	0.95	5.51	-	1013.9
AHQ-3-6, 2414	R.NGSLICTASK.D	1052.18435	1	1.23E-04	0.47	2.21	-	328.0
AHQ-3-6, 2197	K.SIKDTICNQDER.I	1480.58332	2	5.86E-04	0.92	2.83	-	1592.9
AHQ-3-7, 5999	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	9.01E-06	0.94	4.74	-	879.0
AHQ-3-6, 6109 - 6129	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	2.01E-09	0.95	4.91	-	811.1
AHQ-3-6, 6110 - 6121	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	5.08E-07	0.92	4.48	-	840.1
gi|27482573|ref|XP_208709.1| similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro				3.52E-11	1.93	20.29	26.00	17875.4
AHQ-3-12, 4890	K.GQVCLPVISAENWKPATK.T	2000.30757	3	4.96E-04	0.49	3.03	-	235.1
AHQ-3-12, 4879 - 4882	K.GQVCLPVISAENWKPATK.T	2000.30757	2	3.48E-07	0.97	5.83	-	1147.0
AHQ-3-12, 6740	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	3.52E-11	0.95	5.14	-	1141.3
AHQ-3-12, 6739	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	2	7.83E-11	0.90	4.89	-	401.3
gi|27764873|ref|NP_057070.2| cytokine receptor-like factor 3; cytokine receptor-like molecule 9; cy				3.59E-11	0.95	10.21	3.20	49737.6
AHQ-3-7, 3102	K.LIEHGVNTAEDLVR.E	1566.74089	2	3.59E-11	0.95	4.15	-	1340.6
gi|5031857|ref|NP_005557.1| lactate dehydrogenase A [Homo sapiens]				4.18E-11	5.05	60.30	19.30	36688.5
AHQ-3-9, 6987 - 6988	K.DDVFLSVPCILGQNGISDLVK.V	2291.60655	2	2.56E-05	0.92	4.29	-	648.5
AHQ-3-13, 6761	K.DLADELALVDVIEDK.L	1658.82864	2	3.45E-10	0.96	4.88	-	1364.6
AHQ-3-9, 6723 - 6784	K.DLADELALVDVIEDK.L	1658.82864	2	1.87E-06	0.96	4.32	-	1333.3
AHQ-3-13-, 6698	K.DLADELALVDVIEDK.L	1658.82864	2	4.18E-11	0.97	5.68	-	1407.1
AHQ-3-9, 6944	K.DLADELALVDVIEDKLK.G	1900.15980	2	1.96E-04	0.96	4.69	-	1297.6
AHQ-3-9, 6977	K.GLYGIKDDVFLSVPCILGQNGISDLVK.V	2923.37318	2	3.90E-09	0.86	4.33	-	339.7
AHQ-3-9, 2912	K.SADTLWGIQK.E	1119.25233	2	9.89E-04	0.88	2.81	-	1479.6
AHQ-3-9, 2913	K.SADTLWGIQK.E	1119.25233	1	3.13E-05	0.43	2.65	-	337.0
AHQ-3-9, 1837	K.VTLTSEEEAR.L	1135.20693	1	7.75E-04	0.19	1.88	-	269.8
AHQ-3-11, 2023	K.VTLTSEEEAR.L	1135.20693	2	2.16E-05	0.91	3.00	-	1265.9
gi|4557395|ref|NP_000058.1| carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase;				4.40E-11	4.62	50.24	22.30	29245.8
AHQ-3-10, 6454	K.AVQQPDGLAVLGIFLK.V	1669.98899	2	3.08E-05	0.94	4.59	-	668.2
AHQ-3-10, 3843 - 3903	R.ILNNGHAFNVEFDDSQDK.A	2064.15751	2	1.03E-10	0.95	4.80	-	1000.9
AHQ-3-10, 2832	K.KYAAELHLVHWNTK.Y	1710.95976	2	1.04E-08	0.98	4.64	-	2770.4
AHQ-3-10, 3102	K.SADFTNFDPR.G	1170.21306	2	4.39E-05	0.78	2.96	-	691.6
AHQ-3-10, 3206 - 3210	K.YAAELHLVHWNTK.Y	1582.78684	2	4.40E-11	0.97	4.64	-	1708.1
gi|18201905|ref|NP_000166.2| glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras				5.16E-11	4.36	50.23	16.80	63146.7
AHQ-3-7, 6587	K.ILLANFLAQTEALM*R.G	1721.05778	2	3.59E-05	0.92	3.62	-	1064.1
AHQ-3-7, 2758 - 2759	K.TFTTQETITNAETAK.E	1656.77283	2	1.10E-08	0.96	4.57	-	1192.9
AHQ-3-7, 7330	K.TITDVINIGIGGSDLGPLMVTEALKPYSSGGPR.V	3330.79783	3	2.93E-08	0.63	3.68	-	435.8
AHQ-3-7, 6000 - 6006	K.TLAQLNPESSLFIIASK.T	1833.11828	2	5.73E-04	0.90	4.32	-	561.1
AHQ-3-7, 3587	R.VWYVSNIDGTHIAK.T	1603.80282	2	5.16E-11	0.96	4.24	-	1287.5
gi|4758442|ref|NP_004115.1| glia maturation factor, beta [Homo sapiens]				5.44E-11	0.88	10.21	16.20	16713.1
AHQ-3-12, 6146	R.LVVLDEELEGISPDELKDELPER.Q	2638.90589	2	5.44E-11	0.88	4.09	-	571.8
AHQ-3-12, 6074 - 6144	R.LVVLDEELEGISPDELKDELPER.Q	2638.90589	3	5.71E-04	0.90	4.19	-	962.1
gi|18104967|ref|NP_000953.2| prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland				5.47E-11	4.61	50.29	12.90	68686.0
AHQ-3-6, 3749	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	1.44E-05	0.94	4.26	-	896.7
AHQ-3-6, 3758	K.AEHPTWGDEQLFQTTR.L	1917.02765	3	1.04E-06	0.89	4.30	-	1072.3
AHQ-3-6, 3675 - 3686	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	2	2.28E-06	0.98	5.72	-	2030.8
AHQ-3-6, 3162 - 3237	R.VPDASQDDGPAVERPSTEL	1984.06747	2	8.25E-06	0.96	5.36	-	971.4
AHQ-3-6, 5850 - 5857	K.YQVLDGEMYPPSVEEAPVLMHYPR.G	2822.20799	3	5.47E-11	0.94	5.74	-	783.6
AHQ-3-6, 5318	K.YQVLDGEMYPPSVEEAPVLM*HYPR.G	2838.20739	3	1.55E-04	0.83	3.68	-	878.8
gi|4502295|ref|NP_001677.1| ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti				5.70E-11	14.94	180.30	41.20	57955.2
AHQ-3-7, 2543	K.AHGGYSVFAGVGER.T	1407.51566	1	1.59E-04	0.34	2.21	-	249.1
AHQ-3-7, 5540 - 5546	R.AIAELGIYPAVDPLDSTSR.I	1989.21513	2	7.85E-08	0.91	4.21	-	505.2
AHQ-3-7, 7486	R.DQEGQDVLLFIDNIFR.F	1923.11524	2	4.75E-09	0.98	5.60	-	1524.1
AHQ-3-7, 5370	R.FLSQPFQVAEVFTGHM*GK.L	2040.33044	3	6.08E-05	0.78	3.50	-	543.1
AHQ-3-7, 6031	R.FLSQPFQVAEVFTGHMGK.L	2024.33104	3	3.01E-06	0.82	4.00	-	513.0
AHQ-3-7, 4266 - 4294	R.FTQAGSEVSALLGR.I	1436.59522	2	1.62E-06	0.94	3.99	-	1217.4
AHQ-3-7, 4292	R.FTQAGSEVSALLGR.I	1436.59522	1	2.32E-06	0.40	2.33	-	93.5
AHQ-3-7, 7228	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	5.70E-11	0.96	6.04	-	1031.4
AHQ-3-7, 7360 - 7362	K.GFQQILAGEYDHLPEQAFYMVGPIEEAVAK.A	3352.76051	3	4.58E-06	0.78	3.79	-	374.2
AHQ-3-7, 3386	R.IMDPNIVGSEHYDVAR.G	1817.01617	2	1.06E-08	0.90	3.92	-	694.4
AHQ-3-7, 2968	R.IM*DPNIVGSEHYDVAR.G	1833.01557	3	3.24E-09	0.86	3.59	-	969.7
AHQ-3-7, 2895 - 2976	R.IM*NVIGEPIDER.G	1402.59902	2	9.00E-05	0.57	2.83	-	698.3
AHQ-3-7, 3858	R.IPSAVGYQPTLATDM*GTMQER.I	2283.56820	2	1.59E-04	0.81	4.70	-	442.2
AHQ-3-7, 4560	R.IPSAVGYQPTLATDMGTMQER.I	2267.56880	2	5.99E-05	0.94	4.53	-	613.0
AHQ-3-7, 2628	K.IPVGPETLGR.I	1039.21035	2	7.37E-05	0.93	3.11	-	1008.5
AHQ-3-7, 3946	R.LVLEVAQHLGESTVR.T	1651.88893	2	1.51E-06	0.96	4.69	-	1155.6
AHQ-3-7, 5563	R.VALTGLTVAEYFR.D	1440.66861	2	9.27E-07	0.88	3.39	-	951.0
AHQ-3-7, 3236 - 3311	K.VALVYGQMNQPPGAR.A	1601.85511	2	2.81E-08	0.82	3.18	-	545.8
AHQ-3-7, 4490	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	4.41E-05	0.78	3.45	-	407.3
gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]				6.16E-11	12.99	160.29	67.30	22391.3
AHQ-3-12, 6103 - 6114	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.07E-07	0.96	4.15	-	1342.4
AHQ-3-12, 5942 - 6020	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.27E-07	0.96	4.73	-	1289.5

AHQ-3-12, 5692 - 5755	R.DDGLFSGDPNWFPK.K	1595.69288	2	5.31E-05	0.89	3.22	-	988.5
AHQ-3-11, 5763 - 5826	R.DDGLFSGDPNWFPK.K	1595.69288	2	5.31E-08	0.97	5.15	-	1691.1
AHQ-3-12, 5803 - 5883	R.DDGLFSGDPNWFPK.K	1595.69288	2	8.77E-10	0.96	4.04	-	1458.8
AHQ-3-11, 5914	R.DDGLFSGDPNWFPK.K	1595.69288	2	4.71E-07	0.95	4.27	-	1096.6
AHQ-3-11, 5610 - 5678	R.DDGLFSGDPNWFPK.K	1595.69288	2	3.57E-08	0.96	4.35	-	1562.0
AHQ-3-12, 7007	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	3.98E-05	0.74	3.21	-	567.7
AHQ-3-13, 6997	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	3	3.18E-04	0.81	3.83	-	695.3
AHQ-3-13-, 6241 - 6247	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.84E-05	0.94	4.67	-	854.5
AHQ-3-12, 6258	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	5.63E-07	0.87	4.07	-	534.6
AHQ-3-11, 6794	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	3	1.58E-07	0.88	4.63	-	710.9
AHQ-3-14-, 6165 - 6233	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.39E-05	0.70	3.42	-	264.1
AHQ-3-13, 6291 - 6313	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.01E-04	0.65	3.49	-	349.7
AHQ-3-11, 6042 - 6080	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.34E-04	0.63	3.18	-	325.1
AHQ-3-11, 5522	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	3.09E-08	0.72	3.67	-	351.1
AHQ-3-11, 5752 - 5764	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	2.52E-04	0.87	3.88	-	619.9
AHQ-3-11, 5754 - 5760	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.82E-06	0.62	3.07	-	636.7
AHQ-3-12, 6943 - 6982	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	2.77E-07	0.56	3.30	-	451.2
AHQ-3-12, 6948 - 6956	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.92E-08	0.86	4.24	-	680.2
AHQ-3-13, 6935	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.32E-08	0.83	3.46	-	621.0
AHQ-3-11, 6722	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.11E-07	0.92	4.28	-	1122.8
AHQ-3-12, 5723	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.45E-05	0.66	3.37	-	396.1
AHQ-3-13-, 6845 - 6846	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.12E-10	0.90	4.21	-	990.0
AHQ-3-14-, 6792 - 6793	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	7.61E-07	0.88	4.46	-	591.0
AHQ-3-11, 6716	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	5.70E-08	0.93	4.80	-	777.3
AHQ-3-11, 2574 - 2576	R.GASQAGMTGYGMPR.Q	1384.56732	2	1.20E-05	0.94	4.11	-	1141.4
AHQ-3-11, 1798 - 1855	R.GPAYGLSR.E	820.91599	2	2.90E-04	0.83	2.99	-	755.8
AHQ-3-12, 2115	R.GPAYGLSREVQQK.I	1433.59456	2	1.57E-04	0.96	4.72	-	1493.5
AHQ-3-12, 2486	K.IQASTMAFK.Q	997.19374	1	8.38E-04	0.37	2.16	-	467.3
AHQ-3-12, 2492	K.IQASTMAFK.Q	997.19374	1	2.60E-04	0.60	2.49	-	665.1
AHQ-3-12, 2210	K.KIQASTMAFK.Q	1125.36665	2	3.23E-04	0.89	2.85	-	1118.4
AHQ-3-12, 2206	K.KIQASTMAFK.Q	1125.36665	1	1.97E-04	0.36	2.18	-	561.0
AHQ-3-11, 2232	R.NFSDNQLQEGK.N	1280.32582	2	2.35E-07	0.71	2.97	-	419.7
AHQ-3-12, 2322	R.NFSDNQLQEGK.N	1280.32582	1	6.21E-05	0.21	2.34	-	226.2
AHQ-3-12, 2410	R.NFSDNQLQEGK.N	1280.32582	1	1.29E-09	0.25	2.09	-	299.4
AHQ-3-12, 2416	R.NFSDNQLQEGK.N	1280.32582	2	1.07E-04	0.85	3.25	-	809.5
AHQ-3-12, 2190 - 2267	R.NFSDNQLQEGK.N	1280.32582	2	8.18E-04	0.75	3.05	-	737.9
AHQ-3-11, 2518	R.NFSDNQLQEGK.N	1280.32582	1	1.22E-06	0.12	1.87	-	288.7
AHQ-3-11, 2080 - 2140	R.NFSDNQLQEGK.N	1280.32582	2	2.13E-05	0.90	3.56	-	858.4
AHQ-3-13, 4698 - 4726	K.QM*EQISQFLQAAER.Y	1695.87890	2	3.44E-05	0.87	3.78	-	620.7
AHQ-3-11, 4504	K.QM*EQISQFLQAAER.Y	1695.87890	2	7.95E-04	0.88	3.69	-	715.8
AHQ-3-14-, 5399	K.QMEQISQFLQAAER.Y	1679.87950	2	1.61E-05	0.94	4.50	-	953.0
AHQ-3-13, 5446	K.QMEQISQFLQAAER.Y	1679.87950	2	1.60E-05	0.92	4.19	-	796.7
AHQ-3-13-, 5413 - 5417	K.QMEQISQFLQAAER.Y	1679.87950	2	2.18E-04	0.96	5.14	-	1047.3
AHQ-3-14-, 4707 - 4715	K.QM*EQISQFLQAAER.Y	1695.87890	2	2.30E-04	0.81	3.45	-	499.3
AHQ-3-11, 5166 - 5187	K.QMEQISQFLQAAER.Y	1679.87950	2	6.72E-05	0.96	4.56	-	1304.6
AHQ-3-11, 5184	K.QMEQISQFLQAAER.Y	1679.87950	3	1.40E-05	0.96	4.78	-	1776.6
AHQ-3-11, 5398 - 5476	K.QMEQISQFLQAAER.Y	1679.87950	2	1.51E-06	0.92	3.83	-	1058.5
AHQ-3-12, 3550 - 3551	R.TLM*NLGGLAVAR.D	1232.47872	2	1.98E-04	0.89	3.86	-	775.1
AHQ-3-13-, 4447	R.TLMNLGGLAVAR.D	1216.47932	2	7.62E-05	0.93	4.19	-	1012.4
AHQ-3-13-, 4361 - 4431	R.TLMNLGGLAVAR.D	1216.47932	2	1.18E-04	0.94	4.40	-	1077.5
AHQ-3-12, 4788	R.TLMNLGGLAVAR.D	1216.47932	2	3.10E-05	0.92	3.77	-	1365.8
AHQ-3-11, 3404 - 3406	R.TLM*NLGGLAVAR.D	1232.47872	2	8.40E-06	0.94	4.31	-	1079.2
AHQ-3-11, 4230 - 4288	R.TLMNLGGLAVAR.D	1216.47932	2	1.45E-06	0.91	3.95	-	973.5
AHQ-3-12, 4430 - 4439	R.TLMNLGGLAVAR.D	1216.47932	2	1.62E-04	0.89	4.18	-	883.5
AHQ-3-11, 4240	R.TLM*NLGGLAVAR.D	1232.47872	2	3.23E-05	0.85	3.29	-	782.3
AHQ-3-11, 4587 - 4596	R.TLMNLGGLAVAR.D	1216.47932	2	2.05E-07	0.94	3.96	-	1245.8
AHQ-3-12, 3990	R.TLM*NLGGLAVAR.D	1232.47872	2	6.81E-05	0.91	3.41	-	1128.8
AHQ-3-11, 4318	R.TLMNLGGLAVAR.D	1216.47932	2	9.04E-08	0.91	3.83	-	1036.1
AHQ-3-13, 4417 - 4419	R.TLMNLGGLAVAR.D	1216.47932	2	2.22E-06	0.90	4.28	-	874.2
AHQ-3-12, 3812	R.TLM*NLGGLAVAR.D	1232.47872	2	1.51E-05	0.92	2.90	-	1396.5
AHQ-3-14-, 3585	R.TLM*NLGGLAVAR.D	1232.47872	2	5.91E-05	0.91	3.30	-	1410.8
AHQ-3-12, 6918 - 6986	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	9.66E-10	0.95	4.81	-	747.7
AHQ-3-13, 6833 - 6835	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.44E-05	0.97	5.31	-	1219.9
AHQ-3-12, 6771 - 6850	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.47E-08	0.96	5.28	-	1176.1
AHQ-3-12, 6671	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	6.17E-06	0.90	3.99	-	972.5
AHQ-3-11, 6572 - 6626	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	6.16E-11	0.97	5.66	-	1421.1
AHQ-3-11, 6406 - 6468	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	5.33E-05	0.79	3.18	-	776.4
AHQ-3-14-, 6711 - 6712	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	5.42E-10	0.97	5.72	-	1073.1
AHQ-3-11, 6824 - 6894	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.95E-06	0.95	4.42	-	1048.5
AHQ-3-13-, 6766	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	4.51E-10	0.97	5.31	-	1602.3
AHQ-3-11, 6632	R.YGINTTDIFQTVDLWEGK.N	2101.30080	3	2.30E-05	0.75	3.46	-	692.8
AHQ-3-11, 6192 - 6258	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	7.84E-06	0.95	4.67	-	1210.7
AHQ-3-12, 6354 - 6423	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.92E-04	0.91	4.34	-	923.5
AHQ-3-11, 6695	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.78E-06	0.94	4.27	-	1201.7
AHQ-3-11, 6622	R.YGINTTDIFQTVDLWEGKNMACVQR.T	2962.30673	3	2.31E-08	0.85	3.87	-	699.1
AHQ-3-12, 6639	R.YGINTTDIFQTVDLWEGKNM*ACVQR.T	2978.30613	3	1.56E-07	0.84	4.23	-	615.6
AHQ-3-12, 6842	R.YGINTTDIFQTVDLWEGKNMACVQR.T	2962.30673	3	7.46E-08	0.91	4.89	-	988.0
gi|28827809|ref|NP_789797.1|	nucleoside diphosphate kinase B-like [Homo sapiens]			6.33E-11	5.14	60.26	50.40	15529.0
AHQ-3-12, 3786	K.DRPFFPGLVK.Y	1176.39185	2	2.52E-04	0.85	3.01	-	976.7
AHQ-3-12, 3340	R.GDFCIQVGR.N	1053.17404	2	1.16E-04	0.93	3.54	-	1284.8
AHQ-3-12, 3352	R.GDFCIQVGR.N	1053.17404	1	7.69E-04	0.37	2.00	-	250.8
AHQ-3-12, 3334	R.GDFCIQVGR.N	1053.17404	1	6.95E-04	0.36	1.98	-	393.4
AHQ-3-12, 2086	R.NIIHGSDSVKSAEK.E	1485.62464	1	1.16E-06	0.75	3.81	-	548.6
AHQ-3-12, 2079 - 2082	R.NIIHGSDSVKSAEK.E	1485.62464	2	1.15E-08	0.88	3.96	-	1016.4
AHQ-3-12, 2579	R.VM*LGETNPADSKPGTIR.G	1803.03091	2	8.73E-05	0.77	3.52	-	713.9
AHQ-3-12, 2479	R.VM*LGETNPADSKPGTIR.G	1803.03091	2	2.50E-06	0.72	3.18	-	476.7
AHQ-3-12, 2688 - 2768	R.VMLGETNPADSKPGTIR.G	1787.03151	2	6.33E-11	0.81	3.44	-	744.2
AHQ-3-12, 6924	K.YM*NSGPVVAMVWEGLNVVK.T	2110.48562	2	3.50E-08	0.95	5.11	-	1002.5
gi|7657486|ref|NP_055217.1|	low molecular mass ubiquinone-binding protein [Homo sapiens]			6.71E-11	0.97	10.23	14.00	11316.3
AHQ-3-14-, 3821	R.HVISYSLSPFEQR.A	1563.73870	2	6.71E-11	0.97	4.53	-	1572.8
gi|27478749|ref|XP_208411.1|	similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit			6.86E-11	1.93	20.31	13.40	25628.5
AHQ-3-9, 4211	K.GEMMDLQHGSLFLR.T	1634.90537	2	6.86E-11	0.97	4.96	-	1474.1
AHQ-3-9, 7031 - 7032	K.LLIVSNPVDILTYVAWK.I	1945.33337	2	4.75E-07	0.96	6.29	-	920.3
gi|5453595|ref|NP_006358.1|	adenylyl cyclase-associated protein [Homo sapiens]			6.88E-11	9.21	130.32	31.80	51672.7
AHQ-3-7, 2546 - 2548	R.ALLVTASQCQQPAENK.L	1759.96271	2	6.79E-07	0.96	5.14	-	1151.2
AHQ-3-14-, 2711	R.ALLVTASQCQQPAENK.L	1759.96271	2	1.10E-04	0.94	4.28	-	899.6
AHQ-3-11, 2666	R.ALLVTASQCQQPAENK.L	1759.96271	2	4.86E-06	0.93	4.09	-	983.8
AHQ-3-13-, 2785	R.ALLVTASQCQQPAENK.L	1759.96271	2	2.44E-04	0.97	4.92	-	1288.7
AHQ-3-13, 2830 - 2831	R.ALLVTASQCQQPAENK.L	1759.96271	2	2.33E-05	0.96	4.83	-	1182.9
AHQ-3-7, 6779	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	6.25E-06	0.88	3.96	-	1097.2
AHQ-3-7, 6563	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	5.49E-06	0.95	5.27	-	1075.2
AHQ-3-7, 2452	K.CVNTTLQIK.G	1078.26494	1	2.39E-04	0.20	2.76	-	146.9
AHQ-3-7, 3306	K.EMNDAAMFYTNR.V	1463.62130	2	9.37E-04	0.49	2.71	-	520.9
AHQ-3-7, 2931	K.EPAVLELEGK.K	1085.23265	1	4.74E-05	0.18	2.12	-	232.4
AHQ-3-11, 2502	K.KEPAVLELEGK.K	1213.40557	2	9.66E-05	0.65	2.80	-	343.8
AHQ-3-10, 2492	K.KEPAVLELEGK.K	1213.40557	1	2.87E-08	0.33	2.33	-	352.7
AHQ-3-7, 7512 - 7550	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	6.88E-11	0.98	6.31	-	1993.7

AHQ-3-7, 4830	K.LSDLLAPISEQIK.E	1427.66814	1	2.80E-05	0.48	2.57	-	501.4
AHQ-3-13, 5038	K.LSDLLAPISEQIK.E	1427.66814	2	8.70E-06	0.86	3.17	-	866.2
AHQ-3-12, 5034	K.LSDLLAPISEQIK.E	1427.66814	2	3.95E-04	0.72	3.32	-	546.0
AHQ-3-11, 4799	K.LSDLLAPISEQIK.E	1427.66814	2	1.59E-04	0.87	3.45	-	847.0
AHQ-3-9, 4612	K.LSDLLAPISEQIK.E	1427.66814	1	1.21E-06	0.61	2.81	-	531.2
AHQ-3-7, 2848	K.NSLDCEIVSAK.S	1237.36245	2	2.64E-05	0.93	3.41	-	1151.6
AHQ-3-9, 4255 - 4257	R.SALFAQINQGESITHALK.H	1929.16615	2	5.03E-06	0.93	4.65	-	854.4
AHQ-3-7, 4684	R.SALFAQINQGESITHALK.H	1929.16615	2	7.35E-07	0.87	4.21	-	522.9
AHQ-3-8, 4225	R.SALFAQINQGESITHALK.H	1929.16615	2	4.71E-08	0.96	5.39	-	1134.9
AHQ-3-7, 4402 - 4435	R.SALFAQINQGESITHALK.H	1929.16615	2	8.31E-07	0.95	5.35	-	908.9
AHQ-3-7, 6607 - 6671	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	9.58E-06	0.87	3.83	-	413.0
AHQ-3-14-, 6099	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	2.45E-05	0.77	3.61	-	215.3
AHQ-3-14-, 6349	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.50E-06	0.60	2.80	-	263.7
AHQ-3-14-, 6212	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	1.64E-05	0.74	3.70	-	231.3
AHQ-3-7, 6910 - 6926	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	5.28E-05	0.65	3.20	-	186.5
AHQ-3-14-, 6544	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	6.99E-05	0.52	2.71	-	225.3
AHQ-3-14-, 6436 - 6509	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.08E-06	0.92	4.50	-	451.5
AHQ-3-7, 4790 - 4815	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.87E-05	0.94	4.50	-	846.2
AHQ-3-7, 4952	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.48E-07	0.85	3.66	-	580.6
AHQ-3-13, 4755 - 4761	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.48E-04	0.86	4.04	-	613.2
AHQ-3-7, 4576 - 4650	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.82E-05	0.92	4.53	-	731.3
AHQ-3-11, 4570	R.VENQENVSNLVIEDTELK.Q	2074.23206	3	5.37E-05	0.91	4.31	-	1142.4
AHQ-3-13-, 4771	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.47E-04	0.91	3.89	-	735.5
AHQ-3-11, 4554 - 4634	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.74E-07	0.90	4.16	-	681.0
AHQ-3-7, 5035 - 5044	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.12E-08	0.95	4.54	-	1131.1
AHQ-3-10, 4354 - 4356	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	9.15E-09	0.96	5.39	-	1025.0
AHQ-3-9, 4387	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.58E-05	0.68	3.12	-	476.0
AHQ-3-12, 4755	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.15E-05	0.89	3.78	-	816.9
AHQ-3-8, 4425 - 4435	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.56E-09	0.95	5.50	-	803.0
gi|17921989|ref|NP_005991.1| tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain				7.43E-11	11.64	140.28	33.00	49924.1
AHQ-3-12, 4595	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	2	2.11E-05	0.73	2.73	-	791.3
AHQ-3-13-, 4594 - 4666	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	7.63E-05	0.96	4.59	-	1735.4
AHQ-3-12, 4596	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	1.24E-05	0.95	4.44	-	1573.6
AHQ-3-12, 5994 - 6062	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.76E-09	0.96	4.79	-	1781.3
AHQ-3-14-, 5179 - 5180	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	3.23E-06	0.91	4.15	-	1094.1
AHQ-3-13-, 5989 - 6057	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.76E-07	0.96	4.65	-	1707.4
AHQ-3-14-, 5956 - 5959	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.89E-05	0.97	5.26	-	1692.7
AHQ-3-7, 6338 - 6406	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	4.35E-04	0.74	3.59	-	811.3
AHQ-3-13-, 5439 - 5443	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.26E-08	0.97	5.66	-	1473.3
AHQ-3-13-, 5194 - 5217	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.46E-09	0.97	5.13	-	1426.2
AHQ-3-13, 5218	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.48E-04	0.93	3.11	-	1825.7
AHQ-3-7, 6704	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.58E-06	0.76	3.74	-	519.7
AHQ-3-14, 6153	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	2.51E-07	0.92	3.42	-	1389.3
AHQ-3-7, 6203 - 6272	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.68E-06	0.96	4.72	-	1503.8
AHQ-3-13, 5415 - 5491	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	4.00E-08	0.95	4.18	-	1380.8
AHQ-3-13, 6081 - 6087	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.59E-06	0.89	3.54	-	1290.8
AHQ-3-11, 5818 - 5822	R.AVFVDLEPTVIDEIR.N	1716.95615	2	3.06E-08	0.92	3.64	-	1609.2
AHQ-3-9, 5828 - 5845	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.93E-08	0.68	2.72	-	920.0
AHQ-3-10, 5598 - 5606	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.01E-05	0.86	3.31	-	1151.2
AHQ-3-12, 6031	R.AVFVDLEPTVIDEIR.N	1716.95615	2	3.27E-06	0.69	2.82	-	863.2
AHQ-3-7, 6070 - 6148	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.15E-06	0.93	3.92	-	1471.1
AHQ-3-7, 3383 - 3391	K.DVNAAIAAIK.T	986.14745	1	3.37E-05	0.85	3.03	-	951.0
AHQ-3-7, 3480	K.DVNAAIAAIK.T	986.14745	1	1.66E-04	0.92	2.81	-	1618.7
AHQ-3-7, 3160	K.DVNAAIAAIK.T	986.14745	2	4.65E-05	0.87	3.03	-	1237.6
AHQ-3-2, 3159	K.DVNAAIAAIK.T	986.14745	1	2.19E-04	0.25	2.21	-	437.7
AHQ-3-7, 3151	K.DVNAAIAAIK.T	986.14745	1	6.91E-04	0.24	1.99	-	464.2
AHQ-3-11, 3252	K.DVNAAIAAIK.T	986.14745	2	5.43E-05	0.94	3.59	-	1260.7
AHQ-3-4, 3458	K.DVNAAIAAIK.T	986.14745	1	2.53E-04	0.17	1.91	-	490.4
AHQ-3-12, 3023	K.DVNAAIAAIK.T	986.14745	1	1.20E-04	0.64	2.30	-	714.0
AHQ-3-7, 2916	K.DVNAAIAAIK.T	986.14745	1	4.07E-04	0.61	2.19	-	914.4
AHQ-3-12, 3360 - 3367	K.DVNAAIAAIK.T	986.14745	2	9.30E-05	0.94	3.83	-	1278.0
AHQ-3-12, 3547	K.DVNAAIAAIK.T	986.14745	1	4.79E-04	0.73	2.24	-	874.8
AHQ-3-3, 3136	K.DVNAAIAAIK.T	986.14745	1	1.57E-04	0.54	2.38	-	598.3
AHQ-3-9, 4608	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.18E-05	0.84	2.96	-	587.9
AHQ-3-7, 4663 - 4734	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.58E-06	0.96	4.34	-	987.5
AHQ-3-3, 5325	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.38E-06	0.86	3.38	-	535.8
AHQ-3-7, 4748 - 4818	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.29E-07	0.93	4.10	-	676.1
AHQ-3-11, 4870	R.IHFPLATYAPVISAEK.A	1758.05310	2	2.55E-05	0.88	3.90	-	585.0
AHQ-3-9, 4471 - 4543	R.IHFPLATYAPVISAEK.A	1758.05310	2	7.64E-05	0.93	3.80	-	837.0
AHQ-3-7, 6930 - 6990	R.LISQIVSSITASLR.F	1488.75471	2	1.02E-07	0.96	4.53	-	1333.8
AHQ-3-7, 7055 - 7114	R.LISQIVSSITASLR.F	1488.75471	2	3.71E-06	0.87	3.15	-	1026.7
AHQ-3-9, 6555	R.LISQIVSSITASLR.F	1488.75471	2	1.27E-07	0.96	4.23	-	1406.2
AHQ-3-14-, 6591	R.LISQIVSSITASLR.F	1488.75471	2	1.03E-05	0.92	4.00	-	966.5
AHQ-3-7, 6815 - 6878	R.LISQIVSSITASLR.F	1488.75471	2	3.64E-07	0.92	4.07	-	798.0
AHQ-3-2, 3559	R.NLDIERPTYTNLNR.L	1719.88022	2	5.83E-05	0.53	3.10	-	379.9
AHQ-3-6, 3217	R.NLDIERPTYTNLNR.L	1719.88022	2	3.95E-07	0.34	2.70	-	288.1
AHQ-3-7, 3118 - 3186	R.NLDIERPTYTNLNR.L	1719.88022	2	1.21E-07	0.80	3.55	-	472.6
AHQ-3-13, 3418 - 3421	R.NLDIERPTYTNLNR.L	1719.88022	2	5.18E-05	0.74	3.41	-	556.8
AHQ-3-8, 2877	R.NLDIERPTYTNLNR.L	1719.88022	2	1.60E-05	0.38	2.55	-	258.6
AHQ-3-5, 3268	R.NLDIERPTYTNLNR.L	1719.88022	2	2.15E-04	0.21	2.56	-	167.6
AHQ-3-1, 3604 - 3680	R.NLDIERPTYTNLNR.L	1719.88022	2	2.04E-04	0.40	2.82	-	290.1
AHQ-3-9, 3493 - 3495	R.QLFHPEQLITGK.E	1411.63050	2	7.74E-04	0.21	2.98	-	103.6
AHQ-3-4, 6002	R.SIQFVDWCPTGFK.V	1586.79232	2	3.46E-04	0.90	3.98	-	671.0
AHQ-3-3, 6060	R.SIQFVDWCPTGFK.V	1586.79232	2	1.85E-06	0.91	3.83	-	832.4
AHQ-3-12, 5663 - 5671	R.SIQFVDWCPTGFK.V	1586.79232	2	1.41E-07	0.93	3.98	-	982.2
AHQ-3-7, 5626 - 5695	R.SIQFVDWCPTGFK.V	1586.79232	2	1.12E-07	0.96	5.01	-	1094.3
AHQ-3-5, 5829	R.SIQFVDWCPTGFK.V	1586.79232	2	1.32E-05	0.91	3.64	-	869.9
AHQ-3-13-, 5633 - 5643	R.SIQFVDWCPTGFK.V	1586.79232	2	6.70E-04	0.88	3.25	-	948.1
AHQ-3-1, 6112	R.SIQFVDWCPTGFK.V	1586.79232	2	2.76E-04	0.79	2.75	-	730.4
AHQ-3-7, 5740 - 5814	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.41E-07	0.82	3.69	-	520.3
AHQ-3-7, 5886	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	8.01E-08	0.80	3.35	-	501.8
AHQ-3-7, 5983 - 5992	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.55E-09	0.84	3.96	-	517.6
AHQ-3-7, 5683 - 5750	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	9.71E-09	0.92	4.05	-	868.2
AHQ-3-14-, 5607	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	7.43E-11	0.95	4.84	-	904.4
AHQ-3-12, 5626	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	4.07E-08	0.68	3.20	-	385.0
AHQ-3-9, 5436 - 5439	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	5.02E-09	0.84	3.61	-	469.9
AHQ-3-3, 5962 - 6040	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.90E-04	0.39	2.94	-	249.6
AHQ-3-1, 6028	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.13E-06	0.63	3.30	-	354.9
AHQ-3-10, 5212	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	8.25E-04	0.59	3.25	-	279.1
AHQ-3-9, 5543	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.14E-04	0.73	3.18	-	327.8
AHQ-3-13-, 5591	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.41E-10	0.82	3.69	-	378.8
AHQ-3-7, 4176 - 4246	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	7.47E-06	0.66	3.28	-	296.9
AHQ-3-13, 4465 - 4530	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.68E-05	0.61	2.92	-	323.8
AHQ-3-13, 4333 - 4401	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.47E-04	0.63	3.03	-	392.6
AHQ-3-4, 4712	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.58E-05	0.59	3.15	-	258.5
AHQ-3-13-, 4341 - 4406	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	8.72E-06	0.86	3.72	-	433.7
AHQ-3-4, 4556 - 4624	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.87E-06	0.49	3.19	-	282.3

AHQ-3-7, 4314 - 4391	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	9.10E-05	0.76	3.67	-	316.5
AHQ-3-11, 4246 - 4306	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	9.69E-04	0.68	2.99	-	414.0
AHQ-3-12, 4523 - 4524	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.77E-06	0.76	3.54	-	277.4
AHQ-3-8, 4070 - 4152	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.09E-04	0.73	3.37	-	398.3
AHQ-3-2, 4703	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	8.31E-06	0.47	2.83	-	235.3
AHQ-3-12, 4390 - 4458	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.50E-05	0.80	3.29	-	419.7
AHQ-3-7, 4354 - 4355	K.YMACCLLYR.G	1252.50864	2	7.36E-04	0.96	3.61	-	1063.3
AHQ-3-12, 4406	K.YMACCLLYR.G	1252.50864	2	3.10E-05	0.93	3.43	-	820.8
AHQ-3-7, 3804	K.YM*ACCLLYR.G	1268.50804	2	3.10E-04	0.72	2.84	-	489.6
gi|4504391|ref|NP_000179.1| hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]				7.53E-11	7.30	90.26	14.20	102502.4
AHQ-3-4, 6396	R.AILQQLGLNSTCDDSILVK.T	2090.38419	2	5.45E-07	0.89	4.38	-	692.1
AHQ-3-4, 4453 - 4470	K.ATDCVGHDVVTLLR.D	1557.75406	2	7.53E-11	0.85	3.30	-	774.0
AHQ-3-4, 2462	R.FLLSESGSGK.G	1025.13731	1	2.83E-04	0.41	2.67	-	198.9
AHQ-3-4, 5746	K.GDFIALDLGGSSFR.I	1455.59700	2	3.67E-10	0.97	5.19	-	1635.5
AHQ-3-4, 2174	R.HIDLVEGDEGR.M	1240.30483	2	9.98E-08	0.94	3.81	-	1051.2
AHQ-3-4, 2176	R.HIDLVEGDEGR.M	1240.30483	1	1.27E-06	0.55	2.35	-	529.0
AHQ-3-4, 6098	K.LPVGFTFSFPCQQSK.I	1744.99134	2	2.78E-05	0.94	3.89	-	1094.1
AHQ-3-4, 2717 - 2721	R.LVNEYSLNAGK.Q	1208.34588	1	1.38E-06	0.51	2.16	-	536.0
AHQ-3-4, 2726	R.LVNEYSLNAGK.Q	1208.34588	2	8.70E-04	0.59	2.67	-	634.9
AHQ-3-4, 7446	R.SANLVAATLGAILNR.L	1484.72615	2	1.18E-04	0.96	5.04	-	1422.5
AHQ-3-4, 6470 - 6549	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	1.34E-06	0.83	3.93	-	441.2
AHQ-3-4, 6348 - 6356	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	1.58E-06	0.91	4.07	-	869.5
gi|4507907|ref|NP_000543.1| von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille				8.12E-11	28.15	320.32	15.50	309296.7
AHQ-3-1, 5096	K.AFVLSSVDELEQQR.D	1621.77332	2	8.59E-04	0.90	3.71	-	1451.0
AHQ-3-1, 5045	K.AHLLSLVDVMQR.E	1382.65733	1	9.06E-06	0.59	2.75	-	459.1
AHQ-3-1, 5054	K.AHLLSLVDVMQR.E	1382.65733	2	2.57E-08	0.96	4.02	-	1500.1
AHQ-3-1, 4037	K.AHLLSLVDVM*QR.E	1398.65673	2	9.19E-06	0.96	3.77	-	1834.7
AHQ-3-3, 5521	R.CHPLVDPEPFVALCEK.T	1914.19160	2	4.39E-04	0.93	3.80	-	971.6
AHQ-3-3, 4036	R.CLPSACEVVTGSPR.G	1535.72531	2	1.21E-05	0.76	3.57	-	508.3
AHQ-3-1, 4058	R.CLPSACEVVTGSPR.G	1535.72531	2	2.31E-04	0.91	3.71	-	767.1
AHQ-3-3, 5194	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	7.65E-04	0.45	2.72	-	429.0
AHQ-3-2, 5222	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	9.40E-04	0.21	2.56	-	420.3
AHQ-3-1, 5230	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	5.50E-07	0.79	3.32	-	577.0
AHQ-3-1, 4894 - 4897	R.EQAPNLVYM*VTGNPASDEIK.R	2193.42002	2	9.89E-06	0.90	4.20	-	598.8
AHQ-3-1, 4172 - 4240	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	1.48E-04	0.89	3.79	-	800.1
AHQ-3-1, 4536 - 4605	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	4.75E-06	0.71	3.34	-	523.9
AHQ-3-1, 3134 - 3210	R.HIVTFDGQNFK.L	1306.45124	2	3.81E-04	0.88	3.16	-	735.5
AHQ-3-1, 6425	R.IEDLPTMVTLGNSFLHK.L	1916.23079	2	1.88E-05	0.89	3.55	-	838.3
AHQ-3-1, 5977	R.IEDLPTMVTLGNSFLHK.L	1916.23079	2	1.97E-06	0.97	5.03	-	1451.3
AHQ-3-2, 7565	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	5.26E-05	0.93	4.82	-	629.6
AHQ-3-1, 7262	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	8.23E-07	0.93	4.76	-	645.1
AHQ-3-1, 2693	R.ILAGPAGDSNVVK.L	1241.41901	2	2.10E-06	0.92	3.83	-	1005.2
AHQ-3-2, 2526	R.ILAGPAGDSNVVK.L	1241.41901	2	1.34E-05	0.89	3.63	-	833.6
AHQ-3-1, 6513	K.ILDELLQTCVDPEDCPVCEVAGR.R	2692.97859	2	7.23E-06	0.85	4.05	-	416.1
AHQ-3-1, 3873	R.ILTSDVFQDCNK.L	1441.58869	2	6.57E-08	0.94	3.60	-	1253.0
AHQ-3-2, 3831	R.ILTSDVFQDCNK.L	1441.58869	2	2.91E-10	0.94	3.50	-	1237.7
AHQ-3-1, 5996	R.LPGDIQVVPIGVGPNANVQELER.I	2415.73085	2	3.33E-05	0.38	2.62	-	212.8
AHQ-3-1, 4336	R.LSEAEFEVLK.A	1165.31777	2	1.15E-05	0.91	3.54	-	1074.5
AHQ-3-1, 4305	K.LTGSCSYVLFQNK.E	1518.71629	2	8.08E-04	0.95	4.12	-	1404.7
AHQ-3-1, 5653	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	2.14E-10	0.98	6.45	-	2206.0
AHQ-3-1, 5294	K.RPGDVWTLPDQCHTVTCQPDGQTLLK.S	3026.35060	3	3.95E-04	0.91	4.18	-	1098.4
AHQ-3-1, 2532	R.SKEFM*EEVIQR.M	1412.59390	2	1.43E-05	0.84	2.81	-	856.2
AHQ-3-1, 3461	R.SKEFMEEVIQR.M	1396.59450	2	6.07E-09	0.95	4.25	-	1237.1
AHQ-3-3, 5106	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	3.00E-05	0.93	4.64	-	540.8
AHQ-3-1, 5098 - 5108	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	1.48E-06	0.89	4.33	-	538.9
AHQ-3-2, 6417	K.TYGLCGICDENGANDFMLR.D	2209.42291	2	1.60E-06	0.67	3.16	-	524.8
AHQ-3-1, 5848 - 5922	K.TYGLCGICDENGANDFM*LR.D	2225.42231	2	1.33E-07	0.95	4.98	-	732.7
AHQ-3-1, 6258	K.TYGLCGICDENGANDFMLR.D	2209.42291	2	8.12E-11	0.90	3.60	-	864.0
AHQ-3-1, 4614	K.VIVIPVGIGPHANLK.Q	1527.87891	2	4.96E-08	0.80	3.23	-	500.5
AHQ-3-1, 2469	R.VKEEVFIQQR.N	1276.46658	2	6.35E-07	0.88	3.58	-	731.0
AHQ-3-1, 4750	R.VTVFPIGIGDR.Y	1174.37426	2	1.70E-07	0.95	3.85	-	1363.2
AHQ-3-1, 3645	R.WTCPCVCTGSSTR.H	1575.72645	2	3.74E-06	0.73	2.85	-	497.5
AHQ-3-1, 3004	K.YAGSQVASTSEVLK.Y	1440.58064	2	2.68E-09	0.94	4.13	-	1065.6
AHQ-3-1, 3021	K.YAGSQVASTSEVLK.Y	1440.58064	1	2.86E-06	0.58	2.78	-	552.9
AHQ-3-2, 2861	K.YAGSQVASTSEVLK.Y	1440.58064	2	3.71E-08	0.96	4.60	-	989.3
AHQ-3-3, 2845	K.YAGSQVASTSEVLK.Y	1440.58064	2	3.52E-07	0.95	4.28	-	1042.0
AHQ-3-1, 6841 - 6844	K.YLFPGECQYVLVQDYCGSNPGTFR.I	2874.15305	2	1.13E-09	0.88	3.59	-	807.2
AHQ-3-2, 3282	R.YLSDHSFLVSQGDR.E	1624.73576	2	2.31E-07	0.96	4.35	-	1633.7
AHQ-3-1, 3454	R.YLSDHSFLVSQGDR.E	1624.73576	2	1.62E-07	0.96	4.05	-	1661.0
AHQ-3-1, 6180	K.YTLFQIFSK.I	1147.34728	2	9.69E-08	0.94	3.13	-	1154.9
gi|10835002|ref|NP_001166.1| Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]				8.33E-11	6.24	70.28	34.80	22987.8
AHQ-3-10, 2351	K.APEPHVEEDDDDELDSK.L	1940.90995	2	1.44E-07	0.97	5.67	-	953.4
AHQ-3-10, 2348	K.APEPHVEEDDDDELDSK.L	1940.90995	3	2.74E-09	0.94	4.61	-	1379.5
AHQ-3-13-, 5551	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.91E-06	0.85	4.05	-	626.6
AHQ-3-13, 5565	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.29E-05	0.68	3.31	-	507.2
AHQ-3-12, 5791	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	2	8.90E-05	0.86	4.03	-	578.6
AHQ-3-10, 5312 - 5374	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	2	3.97E-07	0.94	4.36	-	997.6
AHQ-3-14-, 5543	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	6.70E-05	0.86	3.92	-	786.2
AHQ-3-11, 5379	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.20E-05	0.77	3.52	-	546.0
AHQ-3-10, 2920 - 2922	K.ELQEMDKDDESLIK.Y	1693.85489	2	8.33E-11	0.92	4.03	-	1195.0
AHQ-3-10, 2418	K.ELQEM*DKDDESLIK.Y	1709.85429	2	2.24E-05	0.84	4.32	-	433.9
AHQ-3-10, 6182 - 6263	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	1.30E-04	0.76	3.52	-	534.4
AHQ-3-10, 6184	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	2	2.43E-07	0.81	3.74	-	263.8
AHQ-3-10, 3118 - 3139	K.TLLGDGPVVTDPK.A	1312.49400	2	2.90E-07	0.94	4.06	-	1202.6
gi|17986273|ref|NP_524144.1| fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2				8.34E-11	1.78	20.22	8.20	21145.0
AHQ-3-12, 2603 - 2666	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	2.57E-06	0.89	3.88	-	870.5
AHQ-3-12, 3178 - 3254	R.VFDKEGNGTVMGAELR.H	1723.93228	2	6.86E-10	0.94	4.35	-	959.8
AHQ-3-12, 3190 - 3266	R.VFDKEGNGTVMGAELR.H	1723.93228	3	6.92E-06	0.88	3.57	-	1331.0
AHQ-3-12, 3247	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	8.37E-04	0.84	3.53	-	785.1
AHQ-3-12, 3267	R.VFDKEGNGTVMGAELR.H	1723.93228	2	3.05E-10	0.93	3.63	-	1226.0
AHQ-3-12, 3351 - 3368	R.VFDKEGNGTVMGAELR.H	1723.93228	2	1.79E-09	0.88	3.35	-	971.0
AHQ-3-13-, 2581 - 2654	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	1.40E-04	0.82	3.32	-	720.9
AHQ-3-13-, 3326	R.VFDKEGNGTVMGAELR.H	1723.93228	2	8.34E-11	0.95	4.22	-	1370.6
AHQ-3-14-, 2596	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	9.60E-11	0.83	3.38	-	608.5
gi|4506877|ref|NP_002996.1| selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;				8.48E-11	8.90	110.27	23.70	90844.7
AHQ-3-3, 4937	K.AVQCQHLEAPSEGTM*DCVHPLTAFAYGSSCK.F	3472.80519	3	8.26E-06	0.71	3.61	-	495.0
AHQ-3-3, 3318	R.CAEGFMLR.G	985.16311	1	1.82E-04	0.23	1.80	-	231.7
AHQ-3-3, 6900 - 6981	R.CDNLGQWTAPAPVCQALQCQDLPVPNEAR.V	3313.64431	3	2.36E-05	0.77	3.53	-	619.6
AHQ-3-2, 6393	R.CIDSGHWSAPLPTCEAISCEPLESPVHGSMDCSPSLR.A	4146.54406	3	1.66E-05	0.96	5.31	-	1555.7
AHQ-3-3, 6113	R.CIDSGHWSAPLPTCEAISCEPLESPVHGSM*DCSPSLR.A	4162.54346	3	5.99E-04	0.83	3.79	-	736.0
AHQ-3-3, 6326	R.CIDSGHWSAPLPTCEAISCEPLESPVHGSMDCSPSLR.A	4146.54406	3	3.24E-04	0.77	3.59	-	419.4
AHQ-3-2, 4803	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	6.15E-04	0.91	4.27	-	578.8
AHQ-3-3, 6110	K.LECLASGIWTNKPPQCLAAQCPPLK.I	2857.31818	3	1.73E-04	0.89	3.93	-	1159.3
AHQ-3-3, 6310	K.LECLASGIWTNKPPQCLAAQCPPLKIPER.G	3352.89300	3	1.24E-06	0.93	5.23	-	838.9
AHQ-3-3, 3082	R.PSGQWTAVTPACR.A	1432.58672	2	4.05E-07	0.92	3.65	-	1018.2
AHQ-3-3, 5062 - 5138	K.STCQFICDEGYSLSGPER.L	2109.23671	2	2.99E-10	0.95	4.49	-	1082.6
AHQ-3-1, 5056	K.STCQFICDEGYSLSGPER.L	2109.23671	2	1.84E-07	0.85	3.65	-	659.9

AHQ-3-2, 5129	K.STCQFICDEGYSLSGPER.L	2109.23671	2	8.48E-11	0.92	3.76	-	1083.8
AHQ-3-4, 5034	K.STCQFICDEGYSLSGPER.L	2109.23671	2	1.83E-04	0.76	3.37	-	667.9
AHQ-3-2, 6554	K.VLPYYSSYYWIGIR.K	1781.04522	2	2.80E-05	0.91	3.79	-	770.2
AHQ-3-3, 6508	K.VLPYYSSYYWIGIR.K	1781.04522	2	8.85E-06	0.85	3.27	-	639.1
gi|4505989|ref|NP_000299.1| protective protein for beta-galactosidase; Protective protein for beta-				9.52E-11	0.97	10.21	2.70	54495.8
AHQ-3-12, 3487 - 3491	K.YGDSGEQIAGFVK.E	1371.47686	2	9.52E-11	0.97	4.27	-	2309.8
AHQ-3-11, 3356	K.YGDSGEQIAGFVK.E	1371.47686	2	1.67E-10	0.95	3.81	-	1407.2
gi|4502097|ref|NP_001142.1| solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra				9.57E-11	1.50	20.17	13.10	33148.4
AHQ-3-10, 6472 - 6544	R.YFAGNLASGGAAGATSLCFVYPLDFAR.T	2799.10926	2	2.36E-04	0.60	2.74	-	425.2
AHQ-3-10, 5218	R.YFPTQALNFAFK.D	1447.66130	1	6.17E-08	0.79	3.46	-	522.1
AHQ-3-11, 5491	R.YFPTQALNFAFK.D	1447.66130	2	1.36E-05	0.68	2.57	-	436.5
AHQ-3-14-, 5712	R.YFPTQALNFAFK.D	1447.66130	2	9.57E-11	0.91	3.21	-	771.0
AHQ-3-10, 5214 - 5215	R.YFPTQALNFAFK.D	1447.66130	2	1.22E-07	0.91	3.46	-	859.1
gi|5032161|ref|NP_005639.1| elongin C; transcription elongation factor B (SIII), polypeptide 1 (15k				1.03E-10	3.66	40.28	41.10	12473.1
AHQ-3-13, 4462 - 4466	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	1.03E-10	0.98	5.69	-	1562.6
AHQ-3-13, 4847	K.AMLSGPGQFAENETNEVNFR.E	2212.38515	2	1.86E-08	0.96	4.96	-	1193.1
AHQ-3-13-, 4857	K.AMLSGPGQFAENETNEVNFR.E	2212.38515	2	1.02E-09	0.93	4.60	-	815.2
AHQ-3-13-, 3030	K.LISSDGHEFIVK.R	1345.52569	2	3.41E-08	0.90	3.84	-	630.4
AHQ-3-13, 2735	K.TYGGCEGPDAM*YVK.L	1565.70692	2	6.29E-05	0.86	3.34	-	629.7
gi|5803227|ref|NP_006817.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype				1.10E-10	4.40	60.26	34.70	27764.1
AHQ-3-10, 2042 - 2116	K.AVTEQGAELSNEER.N	1533.57979	2	1.82E-06	0.82	3.59	-	577.7
AHQ-3-14-, 2201	K.AVTEQGAELSNEER.N	1533.57979	2	4.76E-06	0.91	3.24	-	1387.4
AHQ-3-10, 1542	K.EMQPTHPIR.L	1109.28418	1	1.07E-04	0.07	1.85	-	84.2
AHQ-3-10, 1496 - 1554	K.EMQPTHPIR.L	1109.28418	1	7.42E-04	0.10	1.91	-	167.9
AHQ-3-10, 3587	R.KQTIDNSQGAYQEAFDISK.K	2144.28408	2	3.04E-05	0.94	4.59	-	734.3
AHQ-3-10, 6468	R.SICTTVLELLDK.Y	1393.62862	2	1.07E-04	0.68	2.70	-	550.5
AHQ-3-10, 6234	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	1.03E-06	0.87	3.48	-	896.4
AHQ-3-13, 6693	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	1.10E-10	0.97	5.20	-	1452.2
AHQ-3-13-, 6655	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	4.23E-06	0.96	5.25	-	1126.4
AHQ-3-10, 2483	K.YLIANATNPESK.V	1321.46099	1	1.17E-06	0.92	4.19	-	803.1
AHQ-3-10, 2600 - 2606	K.YLIANATNPESK.V	1321.46099	1	2.50E-06	0.82	2.94	-	843.2
AHQ-3-10, 2484 - 2491	K.YLIANATNPESK.V	1321.46099	2	2.75E-04	0.96	3.53	-	2165.1
gi|10863977|ref|NP_067000.1| LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-				1.11E-10	1.92	20.26	40.00	10834.5
AHQ-3-14-, 6616	K.NDLSICGTLHSVDQYLNIK.L	2192.43507	2	1.14E-09	0.95	4.81	-	1071.9
AHQ-3-14-, 5364 - 5375	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	1.88E-08	0.97	5.06	-	1268.5
AHQ-3-14, 6264	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	1.11E-10	0.97	5.28	-	1436.6
gi|4504523|ref|NP_002148.1| heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (				1.11E-10	1.87	20.28	25.50	10931.6
AHQ-3-14-, 2712	K.VLQATVVAVGSGSK.G	1316.52902	2	6.15E-08	0.98	5.57	-	1759.6
AHQ-3-14, 3612 - 3675	K.VLQATVVAVGSGSK.G	1316.52902	2	8.19E-06	0.83	3.09	-	838.0
AHQ-3-14-, 4965	K.VVLDDKDYFLFR.D	1530.74861	2	2.04E-09	0.91	3.37	-	977.1
AHQ-3-14-, 4968	K.VVLDDKDYFLFR.D	1530.74861	3	8.42E-09	0.91	3.78	-	765.7
AHQ-3-14, 6107	K.VVLDDKDYFLFR.D	1530.74861	2	1.11E-10	0.89	3.68	-	769.7
gi|4505759|ref|NP_002622.1| phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo				1.23E-10	3.66	40.29	15.50	53151.7
AHQ-3-7, 4316	R.DYFGAHTYELLAK.P	1528.68958	2	5.38E-06	0.96	3.56	-	1832.2
AHQ-3-7, 6692	K.IKDAFDRNPELQNLLLDDFFK.S	2552.86598	3	4.15E-09	0.97	5.78	-	1738.3
AHQ-3-7, 6467	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	1.23E-10	0.89	3.77	-	780.8
AHQ-3-13, 6297	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	1.59E-06	0.94	3.91	-	1008.5
AHQ-3-7, 6251	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	2.24E-06	0.98	5.49	-	2181.3
AHQ-3-8, 4140	K.VGTGEPCCDWVGDEGAGHFVK.M	2280.43619	2	2.53E-04	0.81	3.72	-	609.3
AHQ-3-8, 4137	K.VGTGEPCCDWVGDEGAGHFVK.M	2280.43619	3	2.11E-06	0.83	3.88	-	451.2
gi|4507869|ref|NP_003361.1| vasodilator-stimulated phosphoprotein [Homo sapiens]				1.25E-10	3.64	40.26	14.20	39829.4
AHQ-3-7, 3471	R.KMQPDQQVVINCAIVR.G	1901.24418	2	4.51E-06	0.94	4.76	-	788.9
AHQ-3-7, 5998	K.VKEEIIEAFVQELR.K	1703.96061	2	7.50E-10	0.97	5.12	-	1514.1
AHQ-3-7, 1795	R.VKQELLEEVKK.E	1343.59438	2	1.91E-04	0.83	3.60	-	881.1
AHQ-3-7, 2536 - 2615	R.VQIYHNPTANSFR.V	1547.69936	2	1.25E-10	0.90	3.43	-	894.2
AHQ-3-7, 2443 - 2444	R.VQIYHNPTANSFR.V	1547.69936	2	1.24E-04	0.92	3.71	-	819.6
gi|4506413|ref|NP_002875.1| RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				1.33E-10	5.73	70.28	40.80	20987.1
AHQ-3-10, 6402	K.INVNEIFYDLVR.Q	1495.70427	2	5.62E-10	0.94	3.87	-	1141.0
AHQ-3-14-, 6529	K.INVNEIFYDLVR.Q	1495.70427	2	1.51E-05	0.89	3.58	-	854.8
AHQ-3-14-, 5852	K.INVNEIFYDLVR.Q	1495.70427	2	9.79E-04	0.94	3.78	-	1209.4
AHQ-3-12, 6822	K.INVNEIFYDLVR.Q	1495.70427	2	3.40E-07	0.95	4.40	-	1060.9
AHQ-3-11, 6582 - 6662	K.INVNEIFYDLVR.Q	1495.70427	2	6.25E-07	0.95	4.71	-	1085.1
AHQ-3-11, 6503 - 6562	K.INVNEIFYDLVR.Q	1495.70427	1	9.05E-08	0.65	3.48	-	231.1
AHQ-3-11, 6491 - 6550	K.INVNEIFYDLVR.Q	1495.70427	2	1.67E-08	0.95	5.55	-	974.9
AHQ-3-11, 6348	K.INVNEIFYDLVR.Q	1495.70427	2	3.08E-08	0.91	3.67	-	1088.7
AHQ-3-11, 6280 - 6354	K.INVNEIFYDLVR.Q	1495.70427	1	6.86E-08	0.16	2.16	-	182.7
AHQ-3-11, 5947	K.INVNEIFYDLVR.Q	1495.70427	2	7.87E-05	0.87	3.10	-	1004.1
AHQ-3-11, 5646 - 5706	K.INVNEIFYDLVR.Q	1495.70427	2	4.42E-04	0.94	4.35	-	1088.0
AHQ-3-11, 5650	K.INVNEIFYDLVR.Q	1495.70427	1	3.96E-05	0.04	1.80	-	128.6
AHQ-3-11, 5920	K.INVNEIFYDLVR.Q	1495.70427	2	9.22E-06	0.93	4.29	-	989.8
AHQ-3-14-, 6680 - 6760	K.INVNEIFYDLVR.Q	1495.70427	2	4.41E-07	0.95	4.81	-	1142.6
AHQ-3-11, 2544 - 2606	K.LVVLGSGGVGK.S	986.19059	1	1.44E-06	0.65	3.16	-	437.0
AHQ-3-12, 2702	K.LVVLGSGGVGK.S	986.19059	1	1.80E-04	0.84	3.44	-	530.3
AHQ-3-11, 2746	K.LVVLGSGGVGK.S	986.19059	1	3.79E-04	0.83	2.89	-	706.5
AHQ-3-11, 2530 - 2595	K.LVVLGSGGVGK.S	986.19059	2	1.03E-04	0.89	3.06	-	1109.4
AHQ-3-13, 2781	K.LVVLGSGGVGK.S	986.19059	2	8.06E-07	0.91	3.77	-	1011.9
AHQ-3-13-, 2745 - 2747	K.LVVLGSGGVGK.S	986.19059	2	2.36E-04	0.84	2.82	-	1063.6
AHQ-3-13, 2795 - 2871	K.LVVLGSGGVGK.S	986.19059	1	8.01E-04	0.67	3.11	-	491.5
AHQ-3-12, 2699 - 2706	K.LVVLGSGGVGK.S	986.19059	2	2.32E-07	0.88	3.72	-	857.0
AHQ-3-11, 6811 - 6875	K.NGQGFALVYSITAQSTFNDLQDLR.E	2659.89181	3	8.18E-04	0.75	3.64	-	458.5
AHQ-3-11, 6058 - 6119	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.68E-06	0.97	5.50	-	1811.5
AHQ-3-11, 5604	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.02E-07	0.93	4.44	-	958.1
AHQ-3-11, 6367 - 6400	K.SALTVQFVQGIFVEK.Y	1666.94196	2	9.46E-04	0.85	3.29	-	1215.1
AHQ-3-11, 6427 - 6462	K.SALTVQFVQGIFVEK.Y	1666.94196	2	4.97E-05	0.97	5.14	-	1844.2
AHQ-3-11, 6178 - 6242	K.SALTVQFVQGIFVEK.Y	1666.94196	2	5.73E-04	0.97	5.18	-	1583.2
AHQ-3-11, 5918 - 5998	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.20E-06	0.97	4.59	-	1758.1
AHQ-3-11, 6535 - 6556	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.00E-05	0.97	4.90	-	1681.8
AHQ-3-14-, 6052 - 6117	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.14E-05	0.96	5.10	-	1437.3
AHQ-3-11, 6620 - 6683	K.SALTVQFVQGIFVEK.Y	1666.94196	2	6.87E-04	0.90	4.22	-	811.0
AHQ-3-11, 5699	K.SALTVQFVQGIFVEK.Y	1666.94196	2	9.39E-07	0.91	3.61	-	945.2
AHQ-3-11, 6843	K.SALTVQFVQGIFVEK.Y	1666.94196	2	6.16E-05	0.97	5.13	-	1677.9
AHQ-3-11, 6211 - 6287	K.SALTVQFVQGIFVEK.Y	1666.94196	2	9.38E-04	0.83	3.20	-	1149.6
AHQ-3-11, 5802 - 5867	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.14E-09	0.95	4.65	-	1036.7
AHQ-3-11, 5026 - 5048	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.30E-08	0.87	3.82	-	582.5
AHQ-3-14-, 6091 - 6109	K.SKINVNEIFYDLVR.Q	1710.95483	3	2.66E-08	0.95	4.53	-	1883.1
AHQ-3-11, 5151 - 5202	K.SKINVNEIFYDLVR.Q	1710.95483	2	9.56E-09	0.91	4.16	-	847.7
AHQ-3-11, 6262	K.SKINVNEIFYDLVR.Q	1710.95483	2	7.92E-08	0.91	3.56	-	997.7
AHQ-3-11, 6143	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.33E-10	0.96	4.84	-	1448.3
AHQ-3-11, 5862	K.SKINVNEIFYDLVR.Q	1710.95483	3	3.47E-06	0.92	4.60	-	1078.8
AHQ-3-14-, 6087	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.09E-09	0.97	4.97	-	1367.1
AHQ-3-13-, 2795 - 2798	K.YDPTIEDSYR.K	1259.30338	2	5.55E-07	0.78	2.62	-	365.4
AHQ-3-11, 2487	K.YDPTIEDSYR.K	1259.30338	2	1.63E-05	0.86	3.01	-	446.7
AHQ-3-14-, 2724	K.YDPTIEDSYR.K	1259.30338	2	8.75E-07	0.80	2.77	-	405.4
AHQ-3-11, 2668 - 2731	K.YDPTIEDSYR.K	1259.30338	2	4.99E-06	0.82	2.83	-	326.8
AHQ-3-11, 2167 - 2171	K.YDPTIEDSYRK.Q	1387.47629	2	2.68E-07	0.49	2.53	-	258.9
AHQ-3-13, 2463	K.YDPTIEDSYRK.Q	1387.47629	2	4.18E-05	0.80	3.21	-	399.4
gi|7661922|ref|NP_055814.1| RAB21, member RAS oncogene family [Homo sapiens]				1.39E-10	1.75	20.27	12.90	24347.4

AHQ-3-10, 5736	K.GIEELFLDLCKR.M	1494.73787	2	7.42E-04	0.78	2.58	-	837.9
AHQ-3-10, 3954 - 3962	R.HVSIQEAESYAESVGAK.H	1805.92351	2	1.39E-10	0.97	5.33	-	1139.4
gi|4758484|ref|NP_004823.1|	glutathione-S-transferase like; glutathione transferase omega [Homo sap			1.43E-10	3.77	60.24	41.10	27565.7
AHQ-3-10, 3680	K.EDPTVSALLTSEK.D	1390.51840	1	3.21E-04	0.19	2.19	-	167.9
AHQ-3-10, 3774	K.EFTKLEEVLTNK.K	1451.64657	2	1.65E-06	0.91	3.97	-	683.1
AHQ-3-10, 2386	K.GSAPPGPVPEGSIR.I	1321.46422	1	9.36E-05	0.27	2.47	-	236.4
AHQ-3-10, 2540	R.HEVININLK.N	1080.26247	1	2.89E-04	0.80	3.27	-	407.4
AHQ-3-10, 6458	K.KNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKK.L	4074.56041	3	1.43E-10	0.91	4.87	-	737.5
AHQ-3-10, 2500	R.SQNKEDYAGLKEEFR.K	1814.93364	2	7.37E-05	0.71	2.93	-	721.1
gi|12545410|ref|NP_031394.1|	RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,			1.49E-10	2.82	30.28	6.40	95912.5
AHQ-3-5, 4809	K.FGDEFLGELR.I	1183.29488	2	1.21E-06	0.95	3.76	-	1450.8
AHQ-3-5, 7391	K.SKGDQPLYSIPIENILAVEKLEEESFK.M	3078.45875	3	1.49E-10	0.96	5.64	-	1220.0
AHQ-3-5, 6475	K.SLCPFYGEDFYCEIPR.S	2056.26024	2	5.26E-08	0.91	3.60	-	894.6
gi|6005846|ref|NP_009215.1|	PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro			1.49E-10	8.40	90.30	49.30	39547.7
AHQ-3-13-, 6550 - 6558	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	3.65E-05	0.96	5.08	-	1179.4
AHQ-3-12, 6455 - 6523	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	2.21E-04	0.57	2.60	-	428.0
AHQ-3-13, 6585	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	5.72E-09	0.96	5.24	-	954.1
AHQ-3-12, 6547	R.AVLPLLDAQQPCYLLYR.L	2035.39506	3	5.75E-09	0.96	4.81	-	1451.7
AHQ-3-14-, 6447	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	5.36E-07	0.96	5.23	-	1028.2
AHQ-3-12, 5900	K.EFGGGHIKDELFGTVKDDLSFAGYQK.H	2860.12617	3	5.31E-04	0.94	4.85	-	1366.0
AHQ-3-11, 3990 - 4006	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	1.71E-05	0.95	5.07	-	1056.1
AHQ-3-10, 3863	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	1.55E-04	0.83	3.62	-	588.1
AHQ-3-12, 2570 - 2587	K.HLSSCAAPAPLTSAER.E	1669.84126	2	3.30E-06	0.94	4.50	-	743.9
AHQ-3-11, 4146	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	1.49E-10	0.97	5.31	-	983.8
AHQ-3-10, 3923 - 3986	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	3.42E-05	0.90	3.90	-	738.2
AHQ-3-11, 5495	K.HTHEGDPLESVVFIYSMPGYK.C	2407.68601	2	7.39E-05	0.75	2.86	-	494.2
AHQ-3-11, 6102	K.KIEIGDGAELTAEFLYDEVHPK.Q	2475.73515	3	2.50E-07	0.96	5.56	-	1949.6
AHQ-3-11, 5030 - 5035	R.LLDSVEQDFHLEIAK.K	1757.96513	2	3.47E-09	0.97	5.05	-	1546.2
AHQ-3-12, 4814	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	9.51E-06	0.95	4.46	-	1550.9
AHQ-3-13-, 4702	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	1.26E-07	0.96	4.42	-	1737.7
AHQ-3-12, 4720 - 4740	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	2.00E-07	0.96	4.47	-	1806.9
AHQ-3-13, 4710	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	1.64E-07	0.95	3.62	-	1794.1
AHQ-3-12, 4728 - 4730	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	3	2.82E-04	0.98	5.97	-	3033.1
gi|29739414|ref|XP_294015.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			1.56E-10	3.66	40.25	17.70	26916.7
AHQ-3-10, 3819	K.IISNASCTTNCLAPLAK.V	1837.10868	2	5.35E-09	0.52	2.94	-	766.0
AHQ-3-11, 3787 - 3846	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.93E-08	0.82	4.07	-	979.0
AHQ-3-9, 3601 - 3676	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.56E-10	0.93	4.70	-	1464.5
AHQ-3-9, 4068 - 4135	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.16E-07	0.85	3.43	-	1315.8
AHQ-3-10, 4006	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.37E-05	0.57	3.01	-	677.6
AHQ-3-10, 3727	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.40E-05	0.81	3.31	-	1041.9
AHQ-3-12, 3992	K.IISNASCTTNCLAPLAK.V	1837.10868	2	4.78E-07	0.83	3.37	-	1215.8
AHQ-3-14-, 4963 - 4972	K.LISWYDNEFGYSNR.V	1764.87478	2	2.28E-08	0.96	4.67	-	1223.9
AHQ-3-9, 4651 - 4723	K.LISWYDNEFGYSNR.V	1764.87478	2	2.00E-07	0.95	4.91	-	886.3
AHQ-3-10, 4599 - 4675	K.LISWYDNEFGYSNR.V	1764.87478	2	5.75E-09	0.96	4.51	-	1474.1
AHQ-3-13-, 4994	K.LISWYDNEFGYSNR.V	1764.87478	2	8.47E-09	0.94	4.32	-	885.3
AHQ-3-9, 4984 - 5052	K.LISWYDNEFGYSNR.V	1764.87478	2	4.44E-05	0.73	3.07	-	586.6
AHQ-3-9, 4791 - 4799	K.LISWYDNEFGYSNR.V	1764.87478	2	1.61E-07	0.97	4.74	-	1364.5
AHQ-3-13, 5001	K.LISWYDNEFGYSNR.V	1764.87478	2	1.66E-08	0.92	4.12	-	763.3
AHQ-3-9, 2457	R.VVDLMAHMASK.E	1202.47292	2	1.18E-05	0.95	3.61	-	1408.3
AHQ-3-9, 1877 - 1951	R.VVDLMAHM*ASKE	1347.58686	2	6.68E-04	0.81	3.64	-	637.2
gi|5031597|ref|NP_005710.1|	actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub			1.67E-10	2.87	30.27	15.20	20546.5
AHQ-3-13, 6610	K.DTDIVDEAIYYFK.A	1592.72721	2	1.67E-10	0.96	4.76	-	1355.0
AHQ-3-11, 6318 - 6319	K.DTDIVDEAIYYFK.A	1592.72721	2	1.13E-09	0.97	5.48	-	1409.6
AHQ-3-12, 6571 - 6582	K.DTDIVDEAIYYFK.A	1592.72721	2	3.73E-05	0.97	5.22	-	1473.7
AHQ-3-14-, 6467 - 6471	K.DTDIVDEAIYYFK.A	1592.72721	2	6.94E-09	0.96	4.47	-	1290.4
AHQ-3-12, 5976	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	2.49E-04	0.59	2.75	-	598.0
AHQ-3-11, 5771	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	2.06E-05	0.94	4.28	-	1048.3
AHQ-3-11, 4878	K.LIGNMALLPIR.S	1211.54582	2	6.81E-04	0.97	4.01	-	2206.7
gi|6912638|ref|NP_036557.1|	ras suppressor protein 1 [Homo sapiens]			1.69E-10	5.65	90.25	56.00	31540.1
AHQ-3-10, 6574 - 6582	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	3.03E-09	0.75	3.78	-	493.9
AHQ-3-10, 5712 - 5770	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	2.42E-06	0.93	4.62	-	515.0
AHQ-3-10, 5826 - 5886	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	1.97E-10	0.92	4.49	-	524.9
AHQ-3-10, 1479	K.ELHIQGNR.L	967.06432	1	6.32E-04	0.34	2.40	-	140.7
AHQ-3-10, 6550	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	2	5.19E-06	0.75	3.46	-	309.4
AHQ-3-10, 6552	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	3	1.69E-10	0.82	4.41	-	404.5
AHQ-3-10, 1868	K.HLNLGMNR.L	955.12018	1	8.43E-04	0.14	1.83	-	127.7
AHQ-3-10, 5320	K.LQILSLRDNDLISLPK.E	1839.16919	2	4.12E-07	0.94	5.06	-	1357.6
AHQ-3-10, 5410 - 5419	K.LQILSLRDNDLISLPK.E	1839.16919	2	7.68E-09	0.94	5.09	-	1534.8
AHQ-3-10, 4263 - 4368	K.LTMVPPNIAELK.N	1326.63045	1	6.42E-04	0.21	2.38	-	271.4
AHQ-3-13, 5867 - 5929	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	4.78E-04	0.72	2.86	-	457.0
AHQ-3-10, 5423 - 5482	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	4.38E-06	0.91	3.86	-	618.7
AHQ-3-11, 5643 - 5702	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	3.16E-08	0.91	4.07	-	706.5
AHQ-3-10, 5538 - 5611	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	1.43E-05	0.89	3.93	-	468.8
AHQ-3-14-, 6724 - 6796	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	2	6.97E-04	0.64	3.47	-	192.9
AHQ-3-10, 6566	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	2	5.58E-05	0.62	2.92	-	445.1
gi|21956645|ref|NP_665807.1|	myotrophin; granule cell differentiation protein [Homo sapiens]			1.86E-10	3.70	40.30	49.20	12894.7
AHQ-3-13, 4339 - 4354	K.GADINAPDKHHITPLLSAVYEGHVSCVK.L	3031.39193	3	7.62E-05	0.80	4.22	-	493.6
AHQ-3-14, 4975 - 5003	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.71E-06	0.97	5.53	-	1342.8
AHQ-3-13, 4090	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.10E-07	0.96	4.60	-	1461.0
AHQ-3-13, 3946 - 4021	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.64E-04	0.97	5.21	-	1502.1
AHQ-3-14-, 4001	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	5.34E-04	0.95	3.99	-	1385.5
AHQ-3-14-, 3855 - 3919	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.53E-09	0.97	5.33	-	1471.1
AHQ-3-13-, 4086	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	6.91E-05	0.97	5.42	-	1534.5
AHQ-3-14, 4851 - 4931	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.93E-05	0.98	5.76	-	1516.8
AHQ-3-13-, 3938 - 4011	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	6.95E-08	0.98	5.89	-	1995.1
AHQ-3-13-, 4003	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	8.97E-09	0.98	6.04	-	2572.1
AHQ-3-14, 5321	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	2.25E-10	0.98	5.63	-	3081.4
AHQ-3-13, 3987	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	7.50E-08	0.97	4.87	-	2064.3
AHQ-3-14, 4511	K.NGDLDEVKDYVAK.G	1466.57496	2	5.26E-05	0.87	3.34	-	841.4
AHQ-3-14-, 3519	K.NGDLDEVKDYVAK.G	1466.57496	2	3.60E-09	0.95	4.10	-	1352.6
AHQ-3-14-, 3527 - 3600	K.NGDLDEVKDYVAK.G	1466.57496	1	6.46E-07	0.48	2.22	-	353.7
AHQ-3-14-, 3624	K.NGDLDEVKDYVAK.G	1466.57496	2	3.46E-09	0.96	3.77	-	1654.2
AHQ-3-14, 4417	K.NGDLDEVKDYVAK.G	1466.57496	2	5.03E-07	0.96	3.97	-	1580.4
AHQ-3-13, 3723	K.NGDLDEVKDYVAK.G	1466.57496	2	1.86E-10	0.95	4.17	-	1337.1
AHQ-3-13-, 3718 - 3719	K.NGDLDEVKDYVAK.G	1466.57496	2	2.46E-08	0.94	3.94	-	1446.0
gi|11321601|ref|NP_002618.1|	phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom			1.93E-10	7.69	80.32	15.60	85595.6
AHQ-3-5, 3527	K.AIGVLTSGGDAQGMNAAVR.A	1789.00750	2	1.40E-08	0.98	6.33	-	1843.8
AHQ-3-5, 2804	K.AIGVLTSGGDAQGM*NAAVR.A	1805.00690	2	4.98E-06	0.97	5.17	-	1682.7
AHQ-3-5, 3247	R.DLQSNVEHLTEK.M	1413.51529	2	3.14E-08	0.94	4.21	-	1166.8
AHQ-3-5, 6163 - 6175	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	2.63E-06	0.96	4.90	-	1345.7
AHQ-3-5, 6595	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	1.93E-10	0.96	5.33	-	942.0
AHQ-3-5, 5393	R.IIEVVDAIMTTAQSHQR.T	1913.18853	2	1.20E-08	0.97	5.08	-	1572.0
AHQ-3-5, 4945	R.LPLMECVQMTQDVQK.A	1822.16087	2	1.96E-05	0.98	5.04	-	2785.2
AHQ-3-5, 3312	K.NVLGHMQQGGAPSPFDR.N	1812.00285	2	1.53E-06	0.93	3.75	-	1309.9
gi|5453740|ref|NP_006462.1|	myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat			2.02E-10	6.22	70.29	32.70	19794.0
AHQ-3-11, 5935	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	3	7.18E-06	0.91	3.98	-	1383.0
AHQ-3-14-, 5396 - 5413	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	8.66E-07	0.98	5.49	-	1705.0

AHQ-3-14, 6300	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	4.41E-06	0.85	3.55	-	560.4
AHQ-3-12, 6080 - 6143	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.25E-04	0.96	4.68	-	1400.3
AHQ-3-12, 5446	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.17E-04	0.86	3.27	-	651.8
AHQ-3-11, 6294	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	8.63E-07	0.93	4.23	-	794.0
AHQ-3-11, 5159 - 5222	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	9.15E-09	0.97	5.03	-	1861.2
AHQ-3-11, 5323 - 5387	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.70E-07	0.96	4.55	-	1457.4
AHQ-3-11, 6023	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.56E-08	0.98	5.25	-	1812.9
AHQ-3-14-, 6088 - 6095	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	5.91E-05	0.97	5.13	-	1451.3
AHQ-3-11, 5900 - 5958	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	7.66E-06	0.98	5.81	-	1957.3
AHQ-3-11, 5816	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.65E-04	0.94	4.17	-	967.7
AHQ-3-11, 5758 - 5762	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	6.09E-09	0.97	5.27	-	1573.6
AHQ-3-11, 5766	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.43E-09	0.89	3.69	-	1104.0
AHQ-3-14-, 5851	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.97E-08	0.97	5.51	-	1450.1
AHQ-3-11, 5662	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	2.02E-10	0.98	5.62	-	1672.7
AHQ-3-11, 5614 - 5676	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.02E-06	0.92	4.09	-	1245.6
AHQ-3-11, 5526 - 5602	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	4.26E-07	0.85	4.60	-	633.1
AHQ-3-14-, 5840	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	3.89E-08	0.78	3.07	-	1046.0
AHQ-3-11, 5138 - 5147	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	4.13E-04	0.88	3.41	-	979.9
AHQ-3-13-, 4578	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	7.90E-06	0.84	4.08	-	358.1
AHQ-3-11, 4480 - 4482	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	1.89E-04	0.92	4.36	-	901.6
AHQ-3-11, 4884	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	2.00E-05	0.88	4.01	-	802.9
AHQ-3-12, 5886 - 5887	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	7.99E-10	0.97	5.52	-	1531.9
AHQ-3-12, 5890	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.49E-05	0.91	4.29	-	1014.9
AHQ-3-11, 6071 - 6148	K.EAFNMIDQNRDGFIDKEDLHDMLASLGK.N	3224.57104	3	1.10E-07	0.96	5.78	-	1355.6
AHQ-3-11, 5742 - 5810	K.EAFNM*IDQNRDGFIDKEDLHDMLASLGK.N	3240.57044	3	4.35E-04	0.71	3.34	-	789.3
AHQ-3-12, 4164 - 4170	K.GNFNYIEFTR.I	1261.36733	2	1.16E-04	0.81	3.29	-	740.0
AHQ-3-11, 4007	K.GNFNYIEFTR.I	1261.36733	2	2.15E-05	0.78	3.14	-	773.9
AHQ-3-11, 4187 - 4188	K.GNFNYIEFTR.I	1261.36733	1	1.12E-04	0.29	2.16	-	402.4
AHQ-3-13, 4193	K.GNFNYIEFTR.I	1261.36733	2	2.90E-04	0.82	2.99	-	967.5
AHQ-3-11, 3872 - 3944	K.GNFNYIEFTR.I	1261.36733	2	1.42E-04	0.79	3.29	-	657.1
AHQ-3-12, 4171 - 4175	K.GNFNYIEFTR.I	1261.36733	1	2.96E-05	0.26	2.55	-	188.1
gi|4504515|ref|NP_002146.1| heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B				2.03E-10	2.55	40.25	6.40	70853.4
AHQ-3-6, 2239	K.ATAGDTHLGGEDFDNR.L	1676.68279	2	1.54E-04	0.82	3.30	-	642.0
AHQ-3-6, 4778 - 4789	R.IINEPTAAAIAYGLDR.R	1688.90603	2	2.03E-10	0.96	4.97	-	1131.7
AHQ-3-6, 4277 - 4383	K.LLQDFFNGK.E	1082.23369	1	1.26E-05	0.16	2.14	-	224.3
AHQ-3-13-, 3430 - 3441	R.TTPSYVAFTDTER.L	1488.58062	2	8.33E-07	0.61	2.68	-	571.7
AHQ-3-13, 3375 - 3438	R.TTPSYVAFTDTER.L	1488.58062	2	4.08E-04	0.53	2.63	-	299.1
gi|21624607|ref|NP_066972.1| coactosin-like 1 [Homo sapiens]				2.08E-10	4.54	70.31	58.50	15944.9
AHQ-3-12, 2134	R.AAYNLVR.D	806.93245	2	2.90E-04	0.64	2.56	-	580.1
AHQ-3-13-, 5307	R.DDGSAVIWVTFK.Y	1338.49001	1	4.45E-06	0.73	3.15	-	553.2
AHQ-3-13, 4137	K.ELEEDFIKSELK.K	1480.64154	2	5.74E-05	0.84	3.52	-	654.3
AHQ-3-13-, 2105 - 2165	K.EVVQNFAK.E	935.05900	1	2.00E-05	0.23	2.30	-	147.0
AHQ-3-12, 6879	K.FALITWIGENVSGLQR.A	1805.06986	2	5.26E-05	0.96	5.21	-	1310.8
AHQ-3-13, 6857	K.FALITWIGENVSGLQR.A	1805.06986	2	4.03E-06	0.97	5.84	-	1571.5
AHQ-3-13-, 6785	K.FALITWIGENVSGLQR.A	1805.06986	2	2.91E-08	0.98	6.11	-	2202.1
AHQ-3-13, 2813	R.KELEEDFIK.S	1151.29110	2	8.78E-04	0.83	3.22	-	772.5
AHQ-3-13-, 2793	R.KELEEDFIK.S	1151.29110	2	2.52E-04	0.65	2.69	-	572.0
AHQ-3-12, 2735	R.KELEEDFIK.S	1151.29110	1	1.11E-04	0.13	2.16	-	377.6
AHQ-3-13, 2818	R.KELEEDFIK.S	1151.29110	1	5.82E-05	0.46	2.76	-	476.2
AHQ-3-12, 5263 - 5342	K.YDGSTIVPGEQGAEYQHFIQQCTDDVR.L	3116.27790	3	2.08E-10	0.65	3.14	-	356.3
gi|4503631|ref|NP_000120.1| coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,				2.08E-10	22.67	260.30	37.30	83232.8
AHQ-3-5, 5427 - 5459	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	5.41E-07	0.45	3.07	-	150.8
AHQ-3-5, 2136	R.CGPASVQAIK.H	1032.19627	1	2.68E-04	0.48	2.93	-	259.7
AHQ-3-7, 2283	K.DGTHVVENVDATHIGK.L	1692.81163	2	1.90E-06	0.88	3.73	-	752.2
AHQ-3-5, 2472	K.DGTHVVENVDATHIGK.L	1692.81163	2	4.25E-09	0.94	4.00	-	1056.8
AHQ-3-5, 2340 - 2341	K.DGTHVVENVDATHIGK.L	1692.81163	2	5.91E-10	0.95	4.99	-	753.2
AHQ-3-5, 2353	K.DGTHVVENVDATHIGK.L	1692.81163	3	6.94E-08	0.87	4.37	-	781.1
AHQ-3-5, 4228	R.EIRPNSTVQWEEVCRPWVSGHR.K	2724.99524	3	1.47E-04	0.80	3.24	-	789.7
AHQ-3-11, 5400 - 5438	K.ETFDVTLEPLSFK.K	1526.71190	2	1.11E-05	0.64	2.64	-	611.2
AHQ-3-5, 5712 - 5792	K.ETFDVTLEPLSFK.K	1526.71190	2	4.58E-06	0.90	4.16	-	912.3
AHQ-3-8, 4467	K.ETFDVTLEPLSFKK.E	1654.88482	2	1.20E-07	0.77	2.89	-	545.6
AHQ-3-5, 5559 - 5628	K.GTYIPVPIVSELQSGK.W	1688.94594	2	1.94E-06	0.93	4.03	-	688.7
AHQ-3-8, 6733	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	9.66E-07	0.95	4.92	-	1004.4
AHQ-3-10, 6342	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	6.29E-08	0.95	4.85	-	1126.5
AHQ-3-7, 6951	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	2.09E-06	0.92	4.76	-	979.0
AHQ-3-7, 6942	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.68E-09	0.98	6.07	-	1702.9
AHQ-3-11, 6490	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.20E-08	0.97	5.43	-	1437.6
AHQ-3-6, 7086	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.23E-07	0.85	3.77	-	929.9
AHQ-3-12, 6791	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.17E-06	0.96	4.81	-	1305.1
AHQ-3-6, 7010	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	2.08E-10	0.93	4.71	-	838.4
AHQ-3-6, 6987	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.31E-06	0.93	4.34	-	893.5
AHQ-3-5, 7247 - 7317	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	8.28E-07	0.97	4.95	-	1608.9
AHQ-3-5, 7120 - 7187	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	3.54E-09	0.87	4.21	-	621.2
AHQ-3-14-, 6653 - 6667	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.06E-08	0.96	4.80	-	1382.2
AHQ-3-3, 7329	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.19E-07	0.93	4.58	-	956.0
AHQ-3-9, 6623 - 6700	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.12E-06	0.96	5.38	-	1120.8
AHQ-3-5, 7119 - 7184	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	5.15E-09	0.97	5.77	-	1297.8
AHQ-3-5, 3416	R.HVYGELDVQIQR.R	1457.61612	2	3.73E-06	0.88	2.96	-	836.3
AHQ-3-5, 7325	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	1.09E-08	0.94	5.29	-	1050.4
AHQ-3-5, 7243	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	2.76E-07	0.94	5.01	-	1135.6
AHQ-3-6, 1931	K.KDGTHVVENVDATHIGK.L	1820.98455	2	9.18E-07	0.95	4.43	-	1133.8
AHQ-3-5, 1953	K.KDGTHVVENVDATHIGK.L	1820.98455	2	8.76E-06	0.96	4.18	-	1688.0
AHQ-3-6, 2138	K.KDGTHVVENVDATHIGK.L	1820.98455	2	6.49E-04	0.94	4.12	-	1019.7
AHQ-3-5, 5004 - 5021	K.KETFDVTLEPLSFK.K	1654.88482	2	2.75E-08	0.97	4.75	-	1888.6
AHQ-3-11, 4834	K.KETFDVTLEPLSFK.K	1654.88482	2	5.72E-08	0.96	4.41	-	1801.5
AHQ-3-5, 2425 - 2427	R.KLIASMSSDSLR.H	1308.53039	2	2.15E-09	0.96	4.35	-	1594.4
AHQ-3-5, 4592 - 4664	R.LALETALMYGAK.K	1281.54655	2	2.67E-05	0.94	3.69	-	1292.1
AHQ-3-5, 4609	R.LALETALMYGAK.K	1281.54655	1	2.03E-04	0.70	3.02	-	371.5
AHQ-3-5, 4665	R.LALETALMYGAK.K	1281.54655	2	1.95E-04	0.94	3.57	-	1592.7
AHQ-3-5, 4095 - 4099	R.LALETALM*YGAK.K	1297.54595	2	2.06E-04	0.93	3.89	-	1083.4
AHQ-3-11, 2850	K.LIASMSSDSLR.H	1180.35748	2	3.39E-04	0.95	3.51	-	1398.8
AHQ-3-5, 2796 - 2821	K.LIASMSSDSLR.H	1180.35748	2	1.22E-07	0.97	3.72	-	1947.6
AHQ-3-6, 2779	K.LIASMSSDSLR.H	1180.35748	2	7.32E-05	0.95	3.73	-	1184.5
AHQ-3-5, 6143 - 6207	R.MYVAVWTPYGVLR.T	1555.86794	2	1.33E-06	0.97	5.22	-	1181.6
AHQ-3-5, 5504 - 5505	R.M*YVAVWTPYGVLR.T	1571.86734	2	1.07E-06	0.96	5.16	-	915.6
AHQ-3-6, 5998 - 6078	R.MYVAVWTPYGVLR.T	1555.86794	2	1.79E-05	0.93	4.14	-	921.1
AHQ-3-6, 5474	R.M*YVAVWTPYGVLR.T	1571.86734	2	4.55E-06	0.95	4.36	-	1003.1
AHQ-3-9, 5719	R.MYVAVWTPYGVLR.T	1555.86794	2	7.36E-05	0.91	3.48	-	848.1
AHQ-3-7, 5975	R.MYVAVWTPYGVLR.T	1555.86794	2	1.44E-07	0.95	4.37	-	912.6
AHQ-3-5, 6779 - 6843	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	2.20E-06	0.95	5.55	-	1193.9
AHQ-3-5, 3376 - 3377	R.NVWVHLDGPGVTR.P	1450.62682	2	6.23E-08	0.91	3.65	-	1009.3
AHQ-3-5, 2955	R.NVWVHLDGPGVTRPM*K.K	1823.11188	2	2.68E-04	0.89	3.62	-	852.2
AHQ-3-5, 2961	R.NVWVHLDGPGVTRPM*K.K	1823.11188	3	4.66E-06	0.68	3.14	-	518.6
AHQ-3-7, 3247	R.NVWVHLDGPGVTRPMK.K	1807.11248	2	6.36E-05	0.80	3.14	-	579.2
AHQ-3-5, 3356 - 3379	R.NVWVHLDGPGVTRPMK.K	1807.11248	2	2.51E-10	0.92	3.94	-	842.3
AHQ-3-5, 2537	R.NVWVHLDGPGVTRPM*KK.M	1951.28480	3	9.84E-04	0.84	3.62	-	917.3
AHQ-3-5, 2539	R.NVWVHLDGPGVTRPM*KK.M	1951.28480	2	2.60E-04	0.81	3.42	-	439.2

AHQ-3-5, 4627	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.65E-08	0.97	4.70	-	1912.7
AHQ-3-5, 4559 - 4636	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	3.78E-08	0.95	3.96	-	1496.5
AHQ-3-1, 4828 - 4900	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.06E-05	0.80	3.25	-	801.2
AHQ-3-5, 5949	R.SNVDMDFEVENAVLGK.D	1767.93869	2	6.68E-04	0.85	3.06	-	1156.5
AHQ-3-6, 4546	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	5.81E-08	0.94	3.85	-	1525.4
AHQ-3-13-, 5661	K.STVLTIPEIIIK.V	1327.63485	2	3.03E-04	0.88	3.28	-	1073.3
AHQ-3-9, 5249 - 5251	K.STVLTIPEIIIK.V	1327.63485	2	4.68E-06	0.91	3.53	-	1120.5
gi|4503689|ref|NP_000499.1| fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M				2.14E-10	18.78	240.28	29.20	94972.5
AHQ-3-7, 5960	K.DSDWPFCSDEDWNYK.C	1965.98609	2	1.02E-05	0.93	4.05	-	668.1
AHQ-3-1, 6066	K.DSDWPFCSDEDWNYK.C	1965.98609	2	9.66E-07	0.44	2.58	-	189.0
AHQ-3-6, 5897	K.DSDWPFCSDEDWNYK.C	1965.98609	2	8.21E-07	0.90	3.35	-	687.1
AHQ-3-1, 5197	K.DSHSLTTNIM*EILR.G	1646.84779	2	5.88E-04	0.89	3.66	-	930.9
AHQ-3-10, 4414 - 4422	K.DSHSLTTNIM*EILR.G	1646.84779	2	2.06E-05	0.90	3.85	-	1027.5
AHQ-3-9, 5224	K.DSHSLTTNIMEILR.G	1630.84839	2	2.80E-04	0.97	4.78	-	1518.1
AHQ-3-11, 5440	K.DSHSLTTNIMEILR.G	1630.84839	2	2.81E-05	0.95	3.85	-	1440.0
AHQ-3-10, 5172	K.DSHSLTTNIMEILR.G	1630.84839	2	2.70E-05	0.93	3.63	-	1212.9
AHQ-3-6, 5641	K.DSHSLTTNIMEILR.G	1630.84839	2	8.22E-06	0.95	4.08	-	1419.6
AHQ-3-13, 2363	K.ESSSHHPGIAEFPSR.G	1638.72252	2	2.44E-06	0.89	3.37	-	766.7
AHQ-3-1, 2697	R.EVDLKDYEDQQK.Q	1510.58460	2	4.06E-05	0.80	2.90	-	737.3
AHQ-3-13-, 2613	R.EVDLKDYEDQQK.Q	1510.58460	2	6.25E-06	0.90	3.60	-	867.9
AHQ-3-8, 2237	R.EVDLKDYEDQQK.Q	1510.58460	2	9.09E-06	0.53	2.63	-	525.9
AHQ-3-13, 2649	R.EVDLKDYEDQQK.Q	1510.58460	2	4.50E-07	0.83	3.40	-	528.6
AHQ-3-14-, 2560	R.EVDLKDYEDQQK.Q	1510.58460	2	4.81E-08	0.87	2.94	-	982.2
AHQ-3-10, 2430	R.EVDLKDYEDQQK.Q	1510.58460	2	5.38E-07	0.84	3.31	-	728.9
AHQ-3-9, 2304 - 2309	R.EVDLKDYEDQQK.Q	1510.58460	2	3.10E-07	0.85	3.22	-	720.0
AHQ-3-13, 6374 - 6454	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	4.29E-06	0.86	3.58	-	1047.6
AHQ-3-13, 6229	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	3.59E-07	0.95	5.66	-	938.2
AHQ-3-13-, 5925	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	1.25E-05	0.96	5.41	-	1257.3
AHQ-3-6, 6858 - 6865	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	4.48E-10	0.93	4.73	-	1383.9
AHQ-3-6, 6605 - 6671	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	7.43E-05	0.81	3.86	-	762.6
AHQ-3-13-, 6317	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	9.81E-08	0.86	3.65	-	1027.6
AHQ-3-1, 6737	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	1.32E-05	0.86	3.81	-	984.5
AHQ-3-1, 6997	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	4.72E-05	0.76	3.75	-	688.5
AHQ-3-11, 6146	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	2.60E-07	0.93	5.06	-	1026.7
AHQ-3-7, 1484	R.GGSTSYGTGSETESPR.N	1573.55765	2	7.29E-05	0.76	3.37	-	543.6
AHQ-3-6, 1503 - 1530	R.GGSTSYGTGSETESPR.N	1573.55765	2	6.72E-06	0.56	3.21	-	299.2
AHQ-3-4, 4905	K.GLIDEVNQDFTNR.I	1521.61384	2	9.71E-10	0.93	3.93	-	878.5
AHQ-3-2, 5011	K.GLIDEVNQDFTNR.I	1521.61384	2	7.78E-06	0.92	3.72	-	989.1
AHQ-3-13, 4678 - 4679	K.GLIDEVNQDFTNR.I	1521.61384	2	2.67E-08	0.89	2.92	-	1068.8
AHQ-3-9, 4853	K.GLIDEVNQDFTNR.I	1521.61384	2	2.14E-05	0.82	3.10	-	802.5
AHQ-3-1, 4946	K.GLIDEVNQDFTNR.I	1521.61384	2	1.32E-08	0.95	4.31	-	1249.7
AHQ-3-12, 4672 - 4683	K.GLIDEVNQDFTNR.I	1521.61384	2	3.17E-07	0.88	3.47	-	778.2
AHQ-3-10, 4342	K.GLIDEVNQDFTNR.I	1521.61384	2	7.44E-08	0.89	3.67	-	776.9
AHQ-3-3, 4956	K.GLIDEVNQDFTNR.I	1521.61384	2	1.08E-06	0.90	3.66	-	787.7
AHQ-3-9, 4336	K.GLIDEVNQDFTNR.I	1521.61384	2	1.08E-08	0.86	2.99	-	951.7
AHQ-3-7, 4603 - 4674	K.GLIDEVNQDFTNR.I	1521.61384	2	8.01E-07	0.85	3.23	-	675.6
AHQ-3-13, 2315	R.GSESGIFTNTK.E	1141.21317	1	5.64E-05	0.25	2.13	-	333.7
AHQ-3-13, 2327	R.GSESGIFTNTK.E	1141.21317	1	6.23E-05	0.46	2.51	-	285.4
AHQ-3-6, 1938	R.GSESGIFTNTK.E	1141.21317	2	4.34E-05	0.76	2.74	-	825.8
AHQ-3-4, 2157	R.GSESGIFTNTK.E	1141.21317	1	6.66E-04	0.19	2.15	-	268.5
AHQ-3-13, 2326	R.GSESGIFTNTK.E	1141.21317	2	7.85E-05	0.84	2.97	-	999.0
AHQ-3-13, 3065	R.HPDEAAFFDTASTGK.T	1594.66329	2	2.36E-04	0.75	3.04	-	429.8
AHQ-3-13-, 3039	R.HPDEAAFFDTASTGK.T	1594.66329	2	2.00E-09	0.69	3.03	-	285.7
AHQ-3-13-, 2601	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	2.17E-05	0.96	4.96	-	1117.9
AHQ-3-10, 2332	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.95E-06	0.96	4.70	-	1172.4
AHQ-3-1, 2686	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	1.72E-05	0.94	4.70	-	1351.8
AHQ-3-6, 2177 - 2247	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.20E-07	0.96	4.95	-	1226.9
AHQ-3-2, 2449	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	7.53E-04	0.96	5.10	-	1204.7
AHQ-3-9, 2176	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	7.55E-06	0.96	4.35	-	1413.2
AHQ-3-6, 2169 - 2242	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	6.97E-05	0.95	4.39	-	1727.7
AHQ-3-12, 2494	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	6.72E-07	0.94	4.17	-	1520.7
AHQ-3-12, 2495	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	8.83E-04	0.96	4.80	-	1436.1
AHQ-3-11, 2355	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	6.00E-04	0.95	4.20	-	1218.8
AHQ-3-13-, 2606	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	8.92E-04	0.94	4.41	-	1462.1
AHQ-3-6, 2369	R.MELERPGGNEITR.G	1502.67870	2	4.18E-07	0.64	3.04	-	541.3
AHQ-3-9, 2285	R.MELERPGGNEITR.G	1502.67870	2	7.33E-05	0.87	3.54	-	794.4
AHQ-3-10, 3632	K.MKPVPDLVPGNFK.S	1442.75114	2	1.84E-06	0.71	2.75	-	514.9
AHQ-3-9, 2959	K.M*KPVPDLVPGNFK.S	1458.75054	2	7.08E-04	0.84	3.35	-	593.8
AHQ-3-9, 4831	K.NNKDSHSLTTNIMEILR.G	1987.22751	2	2.57E-05	0.93	4.13	-	986.1
AHQ-3-9, 2049	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	9.47E-04	0.84	3.65	-	483.6
AHQ-3-7, 1999	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	2.57E-08	0.94	4.46	-	771.0
AHQ-3-6, 1943	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	1.73E-08	0.94	4.91	-	799.1
AHQ-3-9, 2693	K.NSLFEYQK.N	1029.12765	1	1.21E-05	0.17	1.82	-	253.2
AHQ-3-6, 3122	K.NSLFEYQK.N	1029.12765	1	4.45E-05	0.23	1.89	-	264.2
AHQ-3-8, 2272	K.NSLFEYQK.N	1029.12765	1	5.09E-05	0.07	1.84	-	166.2
AHQ-3-9, 2400	K.NSLFEYQK.N	1029.12765	1	3.44E-04	0.18	2.51	-	176.1
AHQ-3-6, 1941	R.PGSTGTWNPGSSER.G	1433.46515	2	2.14E-10	0.85	3.18	-	659.3
AHQ-3-8, 1850	R.PGSTGTWNPGSSER.G	1433.46515	2	1.73E-05	0.88	3.56	-	745.4
AHQ-3-6, 4729	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.24E-08	0.97	5.63	-	1316.0
AHQ-3-10, 4367	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	2.56E-07	0.95	4.63	-	1090.0
AHQ-3-7, 4664	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	4.01E-09	0.95	4.66	-	1007.0
AHQ-3-9, 4425	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	2.61E-05	0.83	3.40	-	609.1
AHQ-3-3, 5004	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	2.67E-05	0.63	3.11	-	359.9
AHQ-3-10, 6542 - 6543	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.76E-05	0.88	3.77	-	490.4
AHQ-3-2, 7599	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.62E-05	0.69	3.21	-	211.5
AHQ-3-7, 7358 - 7359	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.04E-04	0.69	3.00	-	290.4
AHQ-3-3, 7510	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	4.84E-06	0.76	3.23	-	356.1
AHQ-3-12, 6682	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.24E-05	0.37	2.71	-	140.2
AHQ-3-12, 6962	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.05E-06	0.84	3.63	-	387.2
AHQ-3-11, 6723	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.96E-04	0.89	3.58	-	564.1
AHQ-3-14-, 6604	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	8.29E-05	0.50	2.59	-	208.3
AHQ-3-13-, 6687 - 6691	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	7.38E-05	0.91	4.37	-	419.8
AHQ-3-6, 7285	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.95E-05	0.82	3.65	-	409.8
AHQ-3-6, 6902	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	4.24E-04	0.70	3.33	-	180.1
AHQ-3-9, 6557 - 6575	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	2.28E-04	0.61	2.73	-	297.0
AHQ-3-13-, 6849	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	9.05E-06	0.89	4.00	-	500.9
AHQ-3-9, 6979	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.05E-05	0.75	3.42	-	327.3
AHQ-3-5, 7465	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.79E-04	0.69	2.76	-	362.0
AHQ-3-5, 7067	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	8.90E-05	0.52	2.90	-	168.6
AHQ-3-13, 6726	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.19E-04	0.81	3.42	-	308.4
AHQ-3-13, 6942 - 7018	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	7.47E-08	0.79	3.44	-	410.9
AHQ-3-13-, 2362	K.VQHIQLLQK.N	1107.33106	1	2.75E-04	0.52	2.33	-	327.5
AHQ-3-10, 2118	K.VQHIQLLQK.N	1107.33106	1	2.59E-04	0.68	2.77	-	530.3
AHQ-3-10, 2110	K.VQHIQLLQK.N	1107.33106	1	2.48E-04	0.40	2.17	-	522.5
AHQ-3-9, 1987 - 1988	K.VQHIQLLQK.N	1107.33106	2	2.01E-04	0.82	3.17	-	673.7
AHQ-3-2, 2285	K.VQHIQLLQK.N	1107.33106	1	7.21E-04	0.48	2.33	-	609.9
AHQ-3-8, 1876	K.VQHIQLLQK.N	1107.33106	1	2.39E-05	0.20	2.52	-	207.1

AHQ-3-8, 1872	K.VQHIQLLQK.N	1107.33106	2	1.32E-05	0.77	2.78	-	583.5
AHQ-3-7, 1919	K.VQHIQLLQK.N	1107.33106	1	1.16E-04	0.14	2.39	-	203.4
AHQ-3-6, 2023	K.VQHIQLLQK.N	1107.33106	1	2.96E-04	0.42	2.58	-	349.0
AHQ-3-1, 2506	K.VQHIQLLQK.N	1107.33106	2	2.47E-04	0.73	2.67	-	593.3
AHQ-3-9, 1979	K.VQHIQLLQKNVR.A	1476.75208	2	6.40E-05	0.54	2.68	-	375.5
gi|4505775|ref|NP_002626.1| phosphate carrier precursor isoform 1b; phosphate carrier, mitochondria				2.37E-10	0.88	10.20	4.40	39958.5
AHQ-3-9, 5473	K.VLYSNMLGEENTYLWR.T	1989.24032	2	2.37E-10	0.88	3.94	-	776.4
gi|4504071|ref|NP_000164.1| platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA				3.37E-10	5.31	60.23	10.70	68955.0
AHQ-3-9, 4465	R.GLGELQELYLK.G	1263.46458	2	9.71E-06	0.85	2.93	-	1030.9
AHQ-3-3, 5097 - 5100	R.GLGELQELYLK.G	1263.46458	2	5.02E-06	0.93	3.98	-	1075.7
AHQ-3-1, 5182	R.GLGELQELYLK.G	1263.46458	2	9.00E-06	0.93	3.88	-	1219.3
AHQ-3-4, 5029	R.GLGELQELYLK.G	1263.46458	2	2.80E-05	0.92	3.33	-	1213.4
AHQ-3-4, 4117	R.GQDLLSTVSIR.Y	1189.34410	2	5.69E-05	0.95	3.77	-	1255.6
AHQ-3-3, 4182	R.GQDLLSTVSIR.Y	1189.34410	2	8.64E-05	0.95	3.90	-	1186.7
AHQ-3-13, 4062 - 4077	R.GQDLLSTVSIR.Y	1189.34410	2	1.90E-06	0.95	3.94	-	1463.4
AHQ-3-13-, 4073 - 4093	R.GQDLLSTVSIR.Y	1189.34410	2	2.07E-07	0.95	3.43	-	1451.5
AHQ-3-14-, 3953	R.GQDLLSTVSIR.Y	1189.34410	2	5.30E-05	0.95	3.41	-	1567.6
AHQ-3-3, 1966 - 1973	R.GVLQGHLESSR.N	1183.29965	2	9.86E-07	0.90	3.47	-	895.8
AHQ-3-4, 2005	R.GVLQGHLESSR.N	1183.29965	2	1.30E-05	0.84	3.07	-	742.4
AHQ-3-3, 3617	R.LTQLNLDRCELTK.L	1605.83862	2	9.34E-04	0.81	3.52	-	719.6
AHQ-3-1, 3833	R.LTQLNLDRCELTK.L	1605.83862	2	2.92E-04	0.90	3.99	-	832.6
AHQ-3-4, 3580 - 3590	R.LTQLNLDRCELTK.L	1605.83862	2	8.86E-04	0.91	3.79	-	1084.8
AHQ-3-3, 1852	R.VGPLVAGR.R	768.92735	1	4.94E-04	0.66	3.00	-	369.6
AHQ-3-1, 5101 - 5152	R.WLQDNAENVYVWK.Q	1665.82948	2	1.39E-04	0.92	3.75	-	1171.4
AHQ-3-3, 5285 - 5358	R.WLQDNAENVYVWK.Q	1665.82948	2	3.37E-10	0.96	4.55	-	1619.0
AHQ-3-3, 5048	R.WLQDNAENVYVWK.Q	1665.82948	2	1.46E-05	0.92	3.32	-	1430.2
gi|29568101|ref|NP_006467.3| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT				3.53E-10	0.94	10.21	14.60	11400.3
AHQ-3-14-, 3509	K.TPALVNAAVTYSKPR.L	1588.83283	3	3.53E-10	0.94	4.30	-	1331.1
gi|5803225|ref|NP_006752.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon poly				4.18E-10	2.07	30.22	15.70	29173.7
AHQ-3-9, 6645 - 6655	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	5.45E-10	0.95	4.37	-	1228.9
AHQ-3-10, 6300 - 6302	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	4.18E-10	0.95	4.44	-	1195.8
AHQ-3-9, 7191 - 7192	K.AAFDDAIAELDTLSEESYKDSTLIMQLLR.D	3260.61486	3	1.90E-05	0.82	3.83	-	807.3
AHQ-3-9, 2439	K.EAAENSLVAYK.A	1195.30397	1	8.74E-06	0.30	2.38	-	255.7
gi|4502303|ref|NP_001688.1| mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m				4.21E-10	3.36	40.23	29.10	23277.2
AHQ-3-11, 6584 - 6627	R.FSPLTTNLINLLAENGR.L	1874.13050	2	4.21E-10	0.88	3.71	-	963.8
AHQ-3-11, 5363 - 5418	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	1.18E-09	0.93	4.61	-	889.9
AHQ-3-14, 6444	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	3.61E-08	0.92	4.69	-	673.5
AHQ-3-14-, 5577	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	1.49E-05	0.88	3.99	-	712.9
AHQ-3-11, 3487	K.TDPSILGGM*IVR.I	1275.50037	2	9.33E-06	0.64	2.65	-	420.3
AHQ-3-11, 3100	K.VAASVLNPYVK.R	1161.37549	2	2.09E-04	0.90	3.31	-	945.7
gi|23510338|ref|NP_003325.2| ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity				4.77E-10	3.14	40.24	5.60	117848.1
AHQ-3-4, 4618	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	4.77E-10	0.90	3.83	-	565.0
AHQ-3-4, 4769	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	1.16E-04	0.66	2.91	-	314.0
AHQ-3-4, 4081	R.FEVQGLQPNGEEM*TLK.Q	1837.04413	2	1.97E-04	0.55	3.40	-	231.1
AHQ-3-4, 5429 - 5430	R.LAGTQPLEVLEAVQR.S	1624.86348	2	3.43E-06	0.90	4.01	-	592.6
AHQ-3-4, 3638	R.LQTSSVLVSGLR.G	1260.46546	2	5.32E-05	0.79	2.69	-	823.2
gi|4757812|ref|NP_004880.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso				4.84E-10	2.72	30.21	25.50	10917.8
AHQ-3-13, 6042	R.DFSPSGIFGAFQR.G	1429.56124	2	1.18E-05	0.87	3.02	-	920.1
AHQ-3-13-, 6010	R.DFSPSGIFGAFQR.G	1429.56124	2	5.65E-09	0.95	4.02	-	1292.1
AHQ-3-14-, 5927	R.DFSPSGIFGAFQR.G	1429.56124	2	4.84E-10	0.96	4.23	-	1185.9
AHQ-3-13-, 5522	K.LGELPSWILM*R.D	1331.60876	2	2.13E-06	0.84	3.53	-	416.9
AHQ-3-14-, 5495	K.LGELPSWILM*R.D	1331.60876	2	1.95E-05	0.91	3.42	-	679.5
AHQ-3-14, 6565	K.LGELPSWILM*R.D	1331.60876	2	1.30E-04	0.69	2.76	-	381.6
AHQ-3-14-, 5949 - 5955	K.LGELPSWILMR.D	1315.60936	2	7.39E-07	0.91	3.77	-	763.1
AHQ-3-13, 5537	K.LGELPSWILM*R.D	1331.60876	2	7.55E-05	0.90	3.45	-	600.2
gi|4758038|ref|NP_004246.1| cytochrome c oxidase subunit Va precursor; cytochrome c oxidase polypep				6.15E-10	0.90	10.25	20.00	16774.1
AHQ-3-14-, 6787 - 6849	K.EIYPYVIQELRPTLNELGISTPEELGLDKV	3430.88913	3	6.15E-10	0.90	4.68	-	731.4
AHQ-3-13, 6937 - 6998	K.EIYPYVIQELRPTLNELGISTPEELGLDKV	3430.88913	3	9.60E-07	0.94	4.94	-	1175.4
gi|4507521|ref|NP_001055.1| transketolase [Homo sapiens]				6.77E-10	2.46	30.19	8.20	67877.3
AHQ-3-6, 4603 - 4610	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	6.77E-10	0.91	3.90	-	671.8
AHQ-3-6, 3705	R.SVPTSTVFYPSDGVATEK.A	1886.04854	2	9.12E-05	0.80	3.09	-	536.9
AHQ-3-6, 7207	R.TVPFCSTFAAFFTR.A	1653.88190	2	8.15E-09	0.75	2.51	-	382.7
gi|4502565|ref|NP_001740.1| calpain, small subunit 1; calpain, small polypeptide; calcium-dependent				6.92E-10	4.44	50.23	27.20	28315.5
AHQ-3-14-, 6520 - 6601	R.ILGGVISAISEAAAQYNPEPPPPR.T	2448.75930	3	6.03E-04	0.87	3.62	-	893.8
AHQ-3-12, 6606	R.SGTICSSELPGAFEAAGFHLNEHLYNM*IIR.R	3353.73016	3	3.65E-04	0.88	4.58	-	368.9
AHQ-3-12, 2842 - 2844	K.TDGFGIDTCR.S	1143.20921	2	9.25E-04	0.90	3.49	-	684.4
AHQ-3-11, 6386	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	1.13E-05	0.86	3.70	-	647.1
AHQ-3-12, 6878	R.YSDESGNMDFDNFISCLVR.L	2271.42628	2	6.92E-10	0.92	4.28	-	785.7
AHQ-3-13, 6686	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	2.24E-06	0.87	3.15	-	857.7
AHQ-3-11, 6376	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	6.08E-05	0.66	3.22	-	500.2
AHQ-3-10, 6210	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	1.32E-05	0.67	3.36	-	333.9
gi|18860900|ref|NP_002834.2| protein tyrosine phosphatase, receptor type, J precursor; protein tyro				6.93E-10	10.12	120.28	12.50	145926.2
AHQ-3-1, 3502 - 3508	R.AGSPTAPVHDESLVGPVDPSSGQQSR.D	2576.71806	3	2.67E-04	0.94	5.19	-	1104.0
AHQ-3-1, 3504	R.AGSPTAPVHDESLVGPVDPSSGQQSR.D	2576.71806	2	5.59E-05	0.85	3.92	-	520.9
AHQ-3-1, 5989	K.AVSISPTNVILTWK.S	1529.80530	2	1.16E-06	0.81	2.97	-	552.5
AHQ-3-1, 4464 - 4489	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	2	2.05E-05	0.98	5.64	-	2710.8
AHQ-3-1, 3229	K.GDPLGTEGGLDASNTER.S	1689.71978	2	5.18E-07	0.74	3.04	-	579.5
AHQ-3-1, 5461	K.GLIDGAESYVSFSR.Y	1501.62253	2	9.91E-06	0.77	2.98	-	722.4
AHQ-3-1, 5900	K.SFCTDPASMASFDCEVVPK.E	2151.38014	2	7.90E-06	0.88	3.68	-	742.0
AHQ-3-1, 5041	K.SFCTDPASM*ASFDCEVVPK.E	2167.37954	2	5.07E-04	0.65	3.06	-	427.2
AHQ-3-1, 5472	K.SPDGASEYVYHLVIESK.H	1895.05866	3	5.52E-09	0.94	4.81	-	1136.6
AHQ-3-1, 5458	K.SPDGASEYVYHLVIESK.H	1895.05866	2	2.57E-09	0.95	4.86	-	1041.0
AHQ-3-1, 2758	K.TKGDPLGTEGGLDASNTER.S	1918.99702	2	1.50E-04	0.94	4.29	-	944.9
AHQ-3-1, 2766	K.TKGDPLGTEGGLDASNTER.S	1918.99702	3	4.26E-05	0.87	3.88	-	1076.6
AHQ-3-1, 4568	R.VENFEAYFK.K	1147.26100	2	5.80E-06	0.92	3.69	-	765.4
AHQ-3-1, 4384	K.VITEPIPVSDLR.V	1339.56259	2	6.79E-05	0.85	2.80	-	657.9
AHQ-3-1, 3921	R.VLLESIGSHEELTQDSR.L	1914.06352	2	1.56E-07	0.94	4.46	-	972.4
AHQ-3-1, 3926	R.VLLESIGSHEELTQDSR.L	1914.06352	3	6.93E-10	0.84	3.56	-	719.6
gi|4504183|ref|NP_000843.1| glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s				6.93E-10	7.40	80.27	51.90	23355.7
AHQ-3-13, 5370	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.18E-04	0.87	4.23	-	313.1
AHQ-3-11, 5086	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	1.42E-06	0.94	4.43	-	673.5
AHQ-3-10, 4843 - 4923	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.38E-07	0.92	4.58	-	436.8
AHQ-3-11, 5404	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	1.36E-06	0.78	3.69	-	282.9
AHQ-3-11, 5176 - 5238	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	1.73E-06	0.79	3.85	-	333.9
AHQ-3-11, 3054	K.ASCLYGQLPK.F	1138.31884	2	2.06E-06	0.90	3.50	-	749.9
AHQ-3-11, 6383	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	6.80E-08	0.93	4.18	-	920.5
AHQ-3-11, 6198 - 6275	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	3.31E-08	0.97	5.32	-	1118.4
AHQ-3-10, 6024	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	9.00E-05	0.86	3.67	-	738.8
AHQ-3-11, 5079	K.DQQEAALVDM*VNDGVEDLR.C	2134.26783	2	5.16E-07	0.95	5.11	-	806.4
AHQ-3-13-, 6421	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	6.54E-06	0.91	4.39	-	711.2
AHQ-3-11, 5242	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	3.51E-06	0.97	5.24	-	1435.0
AHQ-3-13, 6455	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	5.81E-04	0.80	3.31	-	862.2
AHQ-3-14-, 6337	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.72E-06	0.94	4.22	-	1181.5
AHQ-3-11, 4883 - 4899	K.FQDGDLTLYQSNTILR.H	1885.06701	2	6.93E-10	0.93	4.59	-	658.0
AHQ-3-10, 4558 - 4566	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.00E-05	0.89	3.90	-	835.6
AHQ-3-11, 4786	K.FQDGDLTLYQSNTILR.H	1885.06701	2	8.37E-05	0.92	4.49	-	665.4
AHQ-3-11, 4666 - 4726	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.46E-09	0.94	4.70	-	976.6

AHQ-3-14, 5952 - 6029	K.FQDGDLTLYQSNTILR.H	1885.06701	2	3.43E-07	0.75	3.22	-	541.0
AHQ-3-13, 4943	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.18E-05	0.86	3.82	-	630.7
AHQ-3-14-, 4923 - 4928	K.FQDGDLTLYQSNTILR.H	1885.06701	2	6.37E-07	0.91	4.30	-	772.1
AHQ-3-11, 2782	R.M*LLADQGQSWK.E	1293.47425	2	1.44E-05	0.89	3.21	-	995.6
AHQ-3-11, 6030 - 6100	R.MLLADQGQSWKEEVVTVETWQEGSLK.A	2993.33745	3	7.76E-06	0.91	4.91	-	725.1
AHQ-3-13, 4575	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	2.05E-07	0.42	2.75	-	357.8
AHQ-3-11, 4458	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	5.11E-08	0.92	3.97	-	832.1
AHQ-3-10, 4155 - 4164	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	4.50E-04	0.49	2.93	-	145.1
gi|4505735|ref|NP_002611.1| platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H				7.03E-10	1.91	20.28	26.00	11552.6
AHQ-3-14-, 3692 - 3699	R.AEAEEDGDLQCLCVK.T	1739.86036	2	1.00E-09	0.95	4.40	-	1056.2
AHQ-3-14-, 3783 - 3789	R.AEAEEDGDLQCLCVK.T	1739.86036	2	7.03E-10	0.98	5.65	-	1524.8
AHQ-3-14, 4604 - 4667	R.AEAEEDGDLQCLCVK.T	1739.86036	2	1.87E-04	0.89	3.49	-	796.3
AHQ-3-14-, 4417 - 4463	R.KICLDLQALLYK.K	1479.80948	2	3.41E-04	0.93	4.49	-	1030.5
gi|14149734|ref|NP_065174.1| coronin, actin binding protein, 1B [Homo sapiens]				7.77E-10	0.96	10.28	5.90	54234.4
AHQ-3-6, 6994 - 7017	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	7.77E-10	0.96	5.65	-	1109.8
gi|11993943|ref|NP_055419.1| Tax interaction protein 1 [Homo sapiens]				7.81E-10	0.95	10.21	13.70	13734.6
AHQ-3-13-, 4117 - 4126	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	7.81E-10	0.95	4.22	-	1424.3
AHQ-3-13, 4102	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	3.03E-05	0.94	3.92	-	1138.6
gi|4503445|ref|NP_001944.1| endothelial cell growth factor 1 (platelet-derived); thymidine phosphor				7.82E-10	3.66	40.25	12.70	49955.2
AHQ-3-7, 6514	R.ALPLALVLHELGAGR.S	1530.83966	2	7.82E-10	0.97	5.00	-	1494.3
AHQ-3-7, 7318	R.DVTATVDSLPLITASILSK.K	1945.24371	2	3.61E-05	0.93	4.48	-	637.9
AHQ-3-7, 2484	R.VAAALDDGSALGR.F	1216.32641	2	1.16E-04	0.84	2.96	-	918.4
AHQ-3-7, 2847	R.VAAALTAMDKPLGR.C	1414.69933	2	5.26E-04	0.92	3.42	-	1359.9
gi|21361370|ref|NP_002853.2| phosphorylase, glycogen; brain [Homo sapiens]				8.11E-10	5.64	60.25	10.70	96695.3
AHQ-3-5, 3615 - 3621	R.GLAGLGDVAEVR.K	1157.30210	2	3.82E-08	0.97	4.68	-	1383.6
AHQ-3-5, 3385	R.HLDHVAALFPGDVDR.L	1662.83036	2	8.11E-10	0.95	4.08	-	1269.9
AHQ-3-5, 6264 - 6267	K.IGEEFLTDLSQLK.K	1493.68345	2	9.14E-08	0.97	4.99	-	1569.6
AHQ-3-5, 7459	K.LQDFNVGDYIEAVLDR.N	1868.03645	2	2.86E-08	0.96	4.98	-	1135.7
AHQ-3-5, 4133 - 4139	K.LVTSIGDVVNHDPVVGDR.L	1893.09067	2	8.87E-09	0.82	3.90	-	605.8
AHQ-3-6, 6573 - 6578	R.WLLLCNPGLADTIVEK.I	1844.16436	2	4.66E-05	0.97	5.10	-	1448.4
gi|14211923|ref|NP_115982.1| PKCI-1-related HIT protein [Homo sapiens]				8.17E-10	2.70	30.30	32.50	17161.6
AHQ-3-13-, 3257	K.AQQATPGGAAPTIFSR.I	1573.73512	2	1.06E-04	0.79	3.27	-	389.2
AHQ-3-13, 3258	K.AQQATPGGAAPTIFSR.I	1573.73512	2	6.01E-06	0.80	3.22	-	379.9
AHQ-3-13-, 6209	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	1.70E-07	0.96	5.42	-	1553.5
AHQ-3-13, 6189 - 6190	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	8.17E-10	0.95	5.34	-	1146.9
AHQ-3-13-, 6202	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	1.84E-07	0.80	3.72	-	856.9
AHQ-3-13, 6186 - 6191	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	9.48E-08	0.97	6.00	-	1456.3
AHQ-3-13-, 6175 - 6238	K.SLPADILYEDQQCLVFR.D	2069.32354	2	8.15E-05	0.92	4.09	-	905.7
AHQ-3-13, 6233 - 6294	K.SLPADILYEDQQCLVFR.D	2069.32354	2	1.85E-06	0.95	4.27	-	1003.2
gi|4502693|ref|NP_001760.1| CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen				8.67E-10	2.77	40.22	24.10	25415.9
AHQ-3-11, 6747	K.AIHYALNCCGLAGGVEQFISDICPK.K	2798.16446	3	8.67E-10	0.91	4.43	-	921.6
AHQ-3-11, 2107	K.EVQEFYK.D	943.03476	1	1.67E-04	0.31	2.26	-	221.1
AHQ-3-12, 3234	K.KDVLETFTVK.S	1180.37558	2	5.15E-05	0.89	3.18	-	1126.2
AHQ-3-11, 3094 - 3106	K.KDVLETFTVK.S	1180.37558	2	1.37E-04	0.92	3.49	-	1089.4
AHQ-3-1, 3554	K.KDVLETFTVK.S	1180.37558	2	1.14E-05	0.62	3.00	-	425.0
AHQ-3-11, 3639	K.SCPDAIKEVFDNK.F	1524.67770	2	3.22E-05	0.93	4.05	-	1018.2
gi|4557871|ref|NP_001054.1| transferrin [Homo sapiens]				8.93E-10	1.86	20.27	5.90	77049.5
AHQ-3-5, 2791	R.KPVDEYKDCHLAQVPSHTVVAR.S	2551.86290	3	3.56E-05	0.90	4.64	-	549.6
AHQ-3-5, 7401	R.SAGWNIPIGLLYCDLPEPR.K	2173.47658	2	8.93E-10	0.96	5.41	-	932.0
gi|29742827|ref|XP_294099.1| similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]				9.73E-10	1.46	20.24	14.20	17094.0
AHQ-3-11, 2772 - 2839	K.EAFNMIDQNR.D	1238.35558	2	7.11E-04	0.93	3.98	-	996.7
AHQ-3-11, 3090 - 3091	R.FTDEEVDELYR.E	1416.47127	2	5.68E-07	0.95	4.01	-	1365.3
AHQ-3-11, 3336	R.FTDEEVDELYR.E	1416.47127	2	2.46E-09	0.94	3.84	-	1145.3
AHQ-3-11, 3660 - 3722	R.FTDEEVDELYR.E	1416.47127	2	8.37E-09	0.96	4.32	-	1692.3
AHQ-3-11, 3663 - 3726	R.FTDEEVDELYR.E	1416.47127	1	1.09E-06	0.54	1.97	-	494.5
AHQ-3-11, 3671 - 3734	R.FTDEEVDELYR.E	1416.47127	1	9.73E-10	0.53	2.79	-	339.3
AHQ-3-12, 3800	R.FTDEEVDELYR.E	1416.47127	2	3.99E-09	0.97	4.34	-	2015.9
AHQ-3-12, 3815	R.FTDEEVDELYR.E	1416.47127	1	1.24E-06	0.34	2.51	-	292.3
AHQ-3-13, 3869 - 3950	R.FTDEEVDELYR.E	1416.47127	2	1.74E-05	0.96	3.51	-	1621.0
AHQ-3-13, 3875 - 3879	R.FTDEEVDELYR.E	1416.47127	1	5.50E-09	0.44	1.95	-	484.5
AHQ-3-14, 4723	R.FTDEEVDELYR.E	1416.47127	1	3.27E-07	0.49	1.89	-	497.4
AHQ-3-13-, 3878	R.FTDEEVDELYR.E	1416.47127	2	6.88E-08	0.98	4.77	-	2222.9
AHQ-3-14-, 3777	R.FTDEEVDELYR.E	1416.47127	2	1.53E-08	0.97	4.72	-	1813.1
gi|29730023|ref|XP_291482.1| similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno				1.03E-09	5.69	70.22	15.90	63563.0
AHQ-3-6, 4381	K.ELEEIVQPIISK.L	1398.62680	1	4.61E-08	0.65	2.91	-	226.7
AHQ-3-6, 4622	R.IINKPTAAAIAYGLDK.R	1659.95097	2	1.03E-09	0.79	3.65	-	709.0
AHQ-3-10, 4340	R.IINKPTAAAIAYGLDK.R	1659.95097	2	1.80E-05	0.73	3.14	-	797.8
AHQ-3-6, 3234 - 3242	K.KKELEEIVQPIISK.L	1654.97263	2	7.71E-04	0.90	4.41	-	843.9
AHQ-3-5, 3465	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	2.84E-05	0.89	4.38	-	489.5
AHQ-3-6, 3845 - 3855	R.NELESYAYSLK.N	1317.42597	2	4.19E-04	0.91	3.34	-	932.2
AHQ-3-6, 3875	K.NQLTSNPKNTVFDAK.R	1677.84011	2	2.53E-04	0.53	3.28	-	333.5
AHQ-3-5, 3347	K.NQLTSNPKNTVFDAK.R	1677.84011	2	6.26E-09	0.70	3.31	-	655.9
AHQ-3-6, 5570 - 5578	K.TFAPKEISAMVLTK.M	1536.86124	2	1.73E-07	0.85	3.76	-	1074.5
gi|7657313|ref|NP_055277.1| Lsm1 protein [Homo sapiens]				1.04E-09	0.91	10.20	12.00	15179.3
AHQ-3-12, 5878 - 5920	R.SIDQFANLVLHQTVER.I	1871.08670	2	1.04E-09	0.91	3.92	-	886.0
gi|30159310|ref|XP_301899.1| similar to beta-actin [Homo sapiens]				1.05E-09	1.64	30.17	9.60	32376.4
AHQ-3-8, 1431 - 1833	K.DSYVGNEAQSK.R	1198.22158	1	2.11E-07	0.51	2.75	-	320.1
AHQ-3-12, 1666 - 1739	K.DSYVGNEAQSK.R	1198.22158	1	2.13E-07	0.38	2.27	-	356.8
AHQ-3-8, 1568 - 1641	K.DSYVGNEAQSK.R	1198.22158	2	2.78E-05	0.71	3.22	-	579.7
AHQ-3-8, 1834	K.DSYVGNEAQSK.R	1198.22158	2	5.80E-05	0.67	2.71	-	585.9
AHQ-3-8, 2014	K.DSYVGNEAQSK.R	1198.22158	1	7.91E-09	0.66	2.49	-	558.9
AHQ-3-12, 1602 - 1658	K.DSYVGNEAQSK.R	1198.22158	2	5.47E-05	0.61	2.95	-	562.2
AHQ-3-13, 1714 - 1790	K.DSYVGNEAQSK.R	1198.22158	1	1.39E-07	0.72	2.36	-	691.2
AHQ-3-9, 1463 - 1527	K.DSYVGNEAQSK.R	1198.22158	1	3.38E-08	0.49	2.55	-	317.3
AHQ-3-8, 1453	K.DSYVGNEAQSKR.G	1354.40793	1	1.05E-09	0.15	2.04	-	234.7
AHQ-3-8, 4193 - 4270	K.SYKLLDGQVITIGNER.F	1807.04092	2	5.67E-07	0.82	3.50	-	524.1
AHQ-3-8, 4537 - 4608	K.SYKLLDGQVITIGNER.F	1807.04092	2	3.11E-07	0.83	3.37	-	399.6
AHQ-3-10, 4160 - 4180	K.SYKLLDGQVITIGNER.F	1807.04092	2	6.11E-05	0.74	2.89	-	551.4
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				1.13E-09	3.38	40.27	16.10	61986.9
AHQ-3-14-, 6127	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.15E-05	0.96	5.47	-	1196.1
AHQ-3-12, 6186 - 6194	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.98E-06	0.95	5.29	-	1330.2
AHQ-3-1, 6609	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.57E-08	0.91	4.06	-	1140.8
AHQ-3-12, 5042	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	6.12E-07	0.72	3.36	-	392.3
AHQ-3-14-, 6708	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	1.13E-09	0.80	3.62	-	409.4
AHQ-3-1, 7208 - 7218	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	8.31E-07	0.89	4.35	-	567.0
AHQ-3-12, 2938	K.VQALEEANNDLENK.I	1587.67060	2	1.26E-06	0.95	3.97	-	1493.2
gi|4503821|ref|NP_001456.1| FYN binding protein (FYB-120/130); FYN-binding protein (FYB-120/130) [H				1.18E-09	0.95	10.24	2.60	85450.5
AHQ-3-12, 4143	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	1.19E-07	0.92	4.38	-	522.8
AHQ-3-13, 4126	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	1.18E-09	0.95	4.79	-	805.1
AHQ-3-10, 3862	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	3.14E-04	0.90	4.24	-	396.6
gi|7661818|ref|NP_054900.1| HSPC159 protein [Homo sapiens]				1.20E-09	5.08	60.25	48.30	19011.6
AHQ-3-12, 6716 - 6786	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	8.52E-05	0.84	3.84	-	289.4
AHQ-3-13-, 6729 - 6730	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	1.12E-04	0.86	4.23	-	348.9
AHQ-3-13, 6781	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	1.68E-06	0.81	3.82	-	325.0
AHQ-3-11, 6542	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	1.45E-04	0.33	2.84	-	123.6
AHQ-3-14-, 6664 - 6672	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	4.57E-06	0.79	3.44	-	394.0
AHQ-3-13-, 2577	K.INGDLQITK.L	1002.14688	2	7.03E-04	0.81	2.73	-	511.2

AHQ-3-13-, 3717 - 3754	R.IQTLSAIDTIK.I	1203.41068	2	6.88E-07	0.82	3.05	-	644.2
AHQ-3-11, 4874	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	2	4.49E-07	0.94	3.53	-	1579.1
AHQ-3-13, 6806	R.NSCISGERGEEQSAIPYFPFIPDQPFR.V	3144.41922	3	1.86E-04	0.71	3.58	-	461.3
AHQ-3-11, 6607	R.NSCISGERGEEQSAIPYFPFIPDQPFR.V	3144.41922	3	4.26E-06	0.73	3.73	-	515.1
AHQ-3-11, 4640	R.VFVDGHQLFDFYHR.I	1780.96540	3	1.50E-08	0.76	3.53	-	408.0
AHQ-3-11, 4627	R.VFVDGHQLFDFYHR.I	1780.96540	2	1.20E-09	0.97	5.07	-	1570.6
AHQ-3-12, 4878	R.VFVDGHQLFDFYHR.I	1780.96540	2	3.22E-07	0.95	4.25	-	1380.8
gi|13569962|ref|NP_112243.1|	RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap			1.38E-09	4.88	60.35	26.40	22171.0
AHQ-3-11, 4344 - 4411	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	1.05E-06	0.98	6.93	-	1764.6
AHQ-3-11, 2019 - 2020	R.M*GPGAASGGERPNLK.I	1458.62590	2	8.01E-05	0.44	2.67	-	600.7
AHQ-3-11, 2002	R.MGPGAASGGERPNLK.I	1442.62650	2	7.88E-08	0.89	3.73	-	906.7
AHQ-3-11, 4991 - 5064	K.NATNVEQAFMTM*AAEIK.K	1886.14019	2	1.23E-05	0.68	3.20	-	767.5
AHQ-3-11, 5778	K.NATNVEQAFMTM*AAEIK.K	1886.14019	2	5.28E-05	0.80	3.67	-	776.1
AHQ-3-11, 6475	K.NATNVEQAFMTMAAEIK.K	1870.14079	2	1.38E-09	0.96	5.11	-	1294.7
AHQ-3-11, 4300 - 4302	K.NATNVEQAFM*TM*AAEIK.K	1902.13959	2	1.26E-04	0.93	4.61	-	1454.9
gi|4507789|ref|NP_003338.1|	ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]			1.41E-09	0.93	10.20	0.00	17861.5
AHQ-3-12, 5191 - 5259	R.IEINFPAEYPFKPPK.I	1791.08155	2	1.41E-09	0.93	3.98	-	1118.4
AHQ-3-12, 5184 - 5255	R.IEINFPAEYPFKPPK.I	1791.08155	2	3.12E-08	0.88	3.16	-	1056.6
gi|21314617|ref|NP_000433.2|	platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e			1.53E-09	4.39	60.27	12.60	82449.6
AHQ-3-5, 5964	R.CESISGTLPISYQLLK.T	1811.08954	2	5.76E-04	0.77	3.67	-	353.7
AHQ-3-4, 6060	R.CESISGTLPISYQLLK.T	1811.08954	2	4.61E-04	0.21	2.52	-	243.1
AHQ-3-1, 6130	R.CESISGTLPISYQLLK.T	1811.08954	2	6.10E-04	0.77	3.26	-	367.4
AHQ-3-4, 6684	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	1.00E-07	0.96	5.20	-	1225.8
AHQ-3-5, 6576	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	3.40E-06	0.97	5.41	-	1334.1
AHQ-3-1, 6428	R.DQNFVILEFPVEEQDR.V	1979.13566	2	1.03E-04	0.66	3.36	-	441.6
AHQ-3-3, 6474	R.DQNFVILEFPVEEQDR.V	1979.13566	2	2.61E-04	0.63	3.36	-	566.4
AHQ-3-5, 6380	R.DQNFVILEFPVEEQDR.V	1979.13566	2	2.58E-04	0.82	3.94	-	580.9
AHQ-3-4, 3454 - 3474	K.EDTIVSQTQDFTK.I	1512.60049	2	4.89E-06	0.93	4.55	-	722.1
AHQ-3-4, 3602	K.EQEGEYYCTAFNR.A	1668.72232	2	1.19E-05	0.71	2.94	-	519.2
AHQ-3-4, 5625 - 5633	K.VIAPVDEVQISILSSK.V	1698.98227	2	1.53E-09	0.92	4.04	-	769.6
gi|5031573|ref|NP_005712.1|	ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye			1.58E-09	6.68	90.26	36.60	47370.9
AHQ-3-7, 4739 - 4812	R.AEPEDHYFLLTEPPLNTPENR.E	2483.67423	2	2.55E-08	0.95	4.99	-	898.9
AHQ-3-7, 7427 - 7428	R.DITYFIQQLLR.D	1410.64250	2	3.97E-07	0.95	4.24	-	1274.8
AHQ-3-9, 7051 - 7052	R.DITYFIQQLLR.D	1410.64250	1	3.03E-04	0.07	1.88	-	149.5
AHQ-3-7, 7426	R.DITYFIQQLLR.D	1410.64250	1	3.66E-05	0.40	2.75	-	240.5
AHQ-3-7, 3498	K.DYEEIGPSICR.H	1340.44122	1	5.76E-05	0.11	1.87	-	211.2
AHQ-3-7, 5790	K.GVDDLDFFIGDEAIEKPTYATK.W	2445.66268	3	7.94E-05	0.76	3.58	-	603.9
AHQ-3-7, 4174	R.HGIVEDWDLMER.F	1500.66127	2	1.58E-09	0.96	4.11	-	1425.9
AHQ-3-13, 6155	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	2.51E-05	0.55	3.05	-	365.6
AHQ-3-7, 6443 - 6444	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	3.14E-05	0.93	4.56	-	854.2
AHQ-3-13-, 3683	R.LPACVVDCGTGYTK.L	1543.74421	2	6.73E-04	0.63	2.63	-	577.6
AHQ-3-7, 3715	K.NIVLSGGSTMFR.D	1282.49463	2	1.31E-06	0.85	3.17	-	1035.8
AHQ-3-9, 6287	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	4.78E-04	0.90	4.14	-	1149.7
gi|7657431|ref|NP_055205.1|	EBNA-2 co-activator (100kD) [Homo sapiens]			1.75E-09	2.69	30.22	7.10	99689.7
AHQ-3-4, 6380	R.DIQNTQCLLNVEHLSAGCPHVTLQFADSK.G	3299.63749	3	3.99E-06	0.83	4.08	-	694.8
AHQ-3-4, 6696	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	1.75E-09	0.91	4.39	-	478.5
AHQ-3-6, 6446	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	3.00E-05	0.90	3.87	-	673.9
AHQ-3-4, 3017	R.SSHYDELLAAEAR.A	1462.54640	2	2.30E-08	0.95	3.70	-	1984.0
gi|17986283|ref|NP_006000.2|	tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu			1.77E-09	0.96	10.28	3.30	50135.3
AHQ-3-1, 6089	R.AVFVDLEPTVIDEVR.T	1702.92947	2	4.41E-05	0.84	3.72	-	653.9
AHQ-3-2, 6090	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.46E-07	0.89	3.83	-	724.1
AHQ-3-3, 6042 - 6044	R.AVFVDLEPTVIDEVR.T	1702.92947	2	7.19E-07	0.94	5.17	-	719.2
AHQ-3-4, 5977	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.18E-07	0.94	4.64	-	973.0
AHQ-3-7, 5555 - 5623	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.77E-09	0.96	5.47	-	981.7
AHQ-3-7, 5690 - 5758	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.89E-06	0.96	5.35	-	931.4
AHQ-3-12, 5662 - 5738	R.AVFVDLEPTVIDEVR.T	1702.92947	2	7.11E-05	0.89	3.26	-	853.6
AHQ-3-13, 5665	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.27E-05	0.86	4.35	-	508.9
AHQ-3-13-, 5617	R.AVFVDLEPTVIDEVR.T	1702.92947	2	8.21E-04	0.49	2.64	-	505.9
AHQ-3-14-, 5613 - 5631	R.AVFVDLEPTVIDEVR.T	1702.92947	2	2.23E-08	0.97	5.65	-	1141.4
gi|5174539|ref|NP_005908.1|	cytosolic malate dehydrogenase; soluble malate dehydrogenase [Homo sapi			1.80E-09	2.31	30.22	12.00	36425.9
AHQ-3-13-, 2977	K.DVIATDKEDVAFK.D	1451.60343	2	9.13E-08	0.94	3.76	-	1305.4
AHQ-3-9, 4839 - 4852	K.EVGVYEALKDDSWLK.G	1752.94535	2	1.80E-09	0.92	4.43	-	839.4
AHQ-3-9, 4344 - 4351	K.FVEGLPINDFSR.E	1394.55680	1	6.70E-07	0.45	2.59	-	253.0
gi|16507237|ref|NP_005338.1|	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he			1.87E-09	11.48	130.32	25.70	72332.5
AHQ-3-6, 4818	R.AKFEELNMDLFR.S	1513.74309	2	2.67E-09	0.95	4.05	-	1270.0
AHQ-3-6, 3919	R.AKFEELNM*DLFR.S	1529.74249	2	2.55E-06	0.88	3.39	-	769.7
AHQ-3-6, 3811	K.DAGTIAGLNVMR.I	1218.40894	2	2.98E-05	0.96	3.98	-	1493.1
AHQ-3-6, 5481	K.DNHLLGTFDLTGIPPAPR.G	1935.17239	2	1.60E-07	0.93	3.75	-	950.6
AHQ-3-6, 5598	K.DNHLLGTFDLTGIPPAPR.G	1935.17239	2	7.07E-06	0.94	4.71	-	624.1
AHQ-3-6, 6683	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	1.08E-04	0.84	3.59	-	613.2
AHQ-3-6, 6187 - 6253	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	4.84E-04	0.63	2.99	-	494.6
AHQ-3-6, 6082	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	1.51E-06	0.89	3.78	-	888.9
AHQ-3-5, 4719	K.IEWLESHQDADIEDFK.A	1976.08864	2	3.07E-05	0.96	5.68	-	1074.9
AHQ-3-6, 4641	K.IEWLESHQDADIEDFK.A	1976.08864	2	1.87E-09	0.98	6.45	-	1599.2
AHQ-3-6, 4193	R.IINEPTAAAIAYGLDKR.E	1817.07894	3	8.00E-05	0.55	3.36	-	333.1
AHQ-3-6, 3671 - 3697	R.ITPSYVAFTPEGER.L	1567.72412	2	1.14E-06	0.71	2.75	-	576.0
AHQ-3-5, 3731	R.ITPSYVAFTPEGER.L	1567.72412	2	2.92E-04	0.89	3.75	-	750.7
AHQ-3-6, 3506	K.KSDIDEIVLVGGSTR.I	1589.77277	2	2.42E-07	0.96	4.97	-	1357.6
AHQ-3-6, 3011 - 3082	K.KSQIFSTASDNQPTVTIK.V	1966.18156	2	1.04E-06	0.96	5.15	-	1380.9
AHQ-3-6, 2082	K.MKETAEAYLGK.K	1241.43928	2	1.76E-04	0.92	3.76	-	967.0
AHQ-3-6, 3690	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	6.42E-04	0.92	3.65	-	1013.1
AHQ-3-6, 3819	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	9.37E-06	0.87	3.54	-	616.2
AHQ-3-6, 3630 - 3707	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	3	4.95E-04	0.60	3.32	-	504.1
gi|4503327|ref|NP_000389.1|	cytochrome b5 reductase membrane-bound isoform; diaphorase (NADH) [Homo			1.98E-09	6.90	80.30	42.20	34234.6
AHQ-3-9, 4747 - 4748	R.APEAWDYGQGFVNEEM*IR.D	2129.29457	2	5.35E-06	0.96	4.34	-	1775.4
AHQ-3-9, 4372	K.DILLRPELEELR.N	1496.73370	2	2.04E-05	0.83	3.45	-	681.6
AHQ-3-9, 5743 - 5811	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	2	2.96E-07	0.94	4.70	-	782.7
AHQ-3-9, 5759	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	3	1.98E-09	0.93	4.70	-	1227.8
AHQ-3-9, 2595	R.GPSGLLVYQGK.G	1119.29547	2	2.23E-05	0.96	4.12	-	1310.7
AHQ-3-9, 2585	R.GPSGLLVYQGK.G	1119.29547	1	4.22E-06	0.73	3.35	-	268.6
AHQ-3-9, 5629	R.IDGNLVVRPYTPISSDDDKGFVDLVIK.V	2977.35765	3	9.20E-05	0.91	4.76	-	896.3
AHQ-3-9, 5712 - 5713	R.IDGNLVVRPYTPISSDDDKGFVDLVIK.V	2977.35765	3	3.34E-07	0.94	5.90	-	661.3
AHQ-3-9, 3252	R.STPAITLESPDIK.Y	1372.54621	1	1.07E-04	0.73	3.18	-	453.8
AHQ-3-12, 3718	R.STPAITLESPDIK.Y	1372.54621	2	1.80E-05	0.86	3.21	-	927.9
AHQ-3-9, 4207	R.STPAITLESPDIKYPLR.L	1902.18061	2	7.08E-08	0.80	3.57	-	508.5
AHQ-3-9, 4704	K.SVGMIAGGTGITPM*LQVIR.A	1918.31483	2	1.10E-05	0.85	3.73	-	611.8
gi|6005942|ref|NP_009057.1|	valosin-containing protein; yeast Cdc48p homolog; transitional endoplas			2.06E-09	7.58	90.24	13.80	89321.3
AHQ-3-5, 6885	R.IVSQLLTLMDGLK.Q	1431.76657	2	2.06E-09	0.96	4.75	-	1364.7
AHQ-3-5, 3039	R.KYEMFAQTLQQSR.G	1630.85008	2	2.12E-05	0.97	4.65	-	1736.9
AHQ-3-5, 2573	R.KYEM*FAQTLQQSR.G	1646.84948	2	3.42E-06	0.76	2.98	-	575.8
AHQ-3-5, 5705 - 5735	R.LDQLIYIPLPDEK.S	1557.81228	2	2.30E-09	0.94	4.33	-	805.1
AHQ-3-5, 2789 - 2864	R.LEILQIHTK.N	1095.31705	1	6.50E-06	0.65	2.66	-	370.5
AHQ-3-6, 4151	R.LGDVISIQPCPDVK.Y	1542.77930	2	7.19E-04	0.56	2.81	-	492.9
AHQ-3-5, 5113 - 5157	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	3.01E-04	0.96	4.78	-	1160.7
AHQ-3-6, 7294	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	1.65E-04	0.84	2.91	-	920.2
AHQ-3-5, 3291	R.WALSQSNPSALR.E	1330.47434	2	1.08E-04	0.93	3.67	-	1343.9
gi|4505763|ref|NP_000282.1|	phosphoglycerate kinase 1 [Homo sapiens]			2.07E-09	5.73	70.30	26.90	44614.4

AHQ-3-8, 5491	K.ACANPAAGSVILLENLR.F	1771.03187	2	3.20E-05	0.93	4.19	-	1107.9
AHQ-3-10, 5347	K.ACANPAAGSVILLENLR.F	1771.03187	2	6.13E-04	0.93	4.39	-	1101.2
AHQ-3-11, 5586 - 5592	K.ACANPAAGSVILLENLR.F	1771.03187	2	5.11E-06	0.95	5.01	-	945.4
AHQ-3-8, 4855	K.ALESPERPFLAILGGAK.V	1770.06542	2	8.26E-06	0.97	5.48	-	1437.4
AHQ-3-10, 4894 - 4903	K.ALESPERPFLAILGGAK.V	1770.06542	2	2.19E-09	0.97	6.05	-	1744.7
AHQ-3-11, 5188	K.ALESPERPFLAILGGAK.V	1770.06542	2	6.50E-05	0.95	4.57	-	1274.5
AHQ-3-9, 4873 - 4953	K.ALESPERPFLAILGGAK.V	1770.06542	2	1.36E-04	0.97	4.96	-	1613.5
AHQ-3-8, 4412	K.DVLFLKDCVGPEVEK.A	1750.00620	2	2.07E-09	0.96	4.59	-	1395.3
AHQ-3-11, 5139	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	1.73E-05	0.58	3.25	-	315.1
AHQ-3-10, 4863	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	2.93E-05	0.65	3.07	-	465.9
AHQ-3-8, 3521	K.SVVLMSHLGRPDGVPMPDK.Y	2036.40831	3	2.48E-04	0.83	3.95	-	1035.6
AHQ-3-8, 3894	K.TGQATVASGIPAGWM*GLDCGPESSKK.Y	2623.90130	3	6.59E-04	0.75	3.56	-	514.4
AHQ-3-8, 4468 - 4481	K.TGQATVASGIPAGWMGLDCGPESSKK.Y	2607.90190	2	5.14E-04	0.69	3.02	-	261.6
gi|21464101|ref|NP_036611.2| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein				2.08E-09	4.59	60.27	30.80	28302.4
AHQ-3-10, 6711 - 6712	K.ELEAVCQDVLSLLDNYLIK.N	2237.55566	2	2.08E-09	0.98	5.47	-	1745.0
AHQ-3-10, 3891 - 3894	R.NLLSVAYKNVVGAR.R	1504.75906	2	9.36E-07	0.95	3.92	-	1434.3
AHQ-3-10, 2902	K.NVTELNEPLSNEER.N	1644.72215	2	4.24E-04	0.93	3.88	-	957.4
AHQ-3-14, 3883	K.NVTELNEPLSNEER.N	1644.72215	2	1.05E-04	0.76	2.93	-	698.9
AHQ-3-14-, 2963	K.NVTELNEPLSNEER.N	1644.72215	2	2.13E-07	0.94	4.43	-	954.4
AHQ-3-10, 4868	K.NVTELNEPLSNEERNLLSVAYK.N	2533.77623	2	6.11E-06	0.55	3.33	-	201.2
AHQ-3-10, 6083 - 6148	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	8.19E-08	0.94	4.18	-	1108.1
AHQ-3-10, 5960	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	6.87E-05	0.76	3.48	-	513.3
AHQ-3-13-, 6570	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	1.53E-04	0.77	2.94	-	890.4
AHQ-3-10, 2127	R.YLAEVATGEK.R	1081.20087	1	7.70E-05	0.23	2.50	-	271.6
gi|4506925|ref|NP_003013.1| SH3 domain binding glutamic acid-rich protein like; SH3-binding domain				2.15E-09	3.01	40.27	61.40	12774.2
AHQ-3-13, 6321 - 6399	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.18E-05	0.87	3.32	-	850.1
AHQ-3-13, 4998 - 5065	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	9.85E-04	0.95	5.17	-	1131.2
AHQ-3-13, 5129 - 5198	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	3.47E-07	0.88	4.47	-	786.2
AHQ-3-13, 4859 - 4927	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	7.20E-04	0.80	3.92	-	667.5
AHQ-3-13-, 4925 - 4997	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.15E-09	0.93	5.42	-	878.7
AHQ-3-13-, 5061 - 5130	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	6.67E-08	0.94	5.23	-	1015.2
AHQ-3-13-, 4302	K.KQQDVLGFLEANK.I	1490.68602	2	9.05E-08	0.95	4.35	-	1594.6
AHQ-3-13, 2411	R.VYIASSSGSTAIK.K	1284.44065	1	1.50E-04	0.26	2.58	-	293.1
gi|9966867|ref|NP_065123.1| eIF-5A2 protein; eIF5AII [Homo sapiens]				2.19E-09	2.88	30.30	19.60	16793.1
AHQ-3-12, 3615 - 3623	K.KYEDICPSTHNMDVPNIK.R	2163.41723	3	6.33E-06	0.98	5.96	-	2291.3
AHQ-3-12, 3015	K.KYEDICPSTHNM*DVPNIK.R	2179.41663	3	3.25E-05	0.97	5.56	-	1701.1
AHQ-3-12, 4802	K.VHLVGIDIFTGK.K	1299.54329	2	2.19E-09	0.93	3.58	-	1095.7
AHQ-3-12, 4800	K.VHLVGIDIFTGK.K	1299.54329	1	1.72E-04	0.69	2.01	-	1117.8
gi|5031571|ref|NP_005713.1| actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog				2.35E-09	6.46	80.27	27.20	44760.5
AHQ-3-8, 3566 - 3576	K.DLMVGDEASELR.S	1335.46633	2	1.79E-07	0.94	3.93	-	1061.5
AHQ-3-8, 2814	R.GYAFNHSADFETVR.M	1614.69943	2	2.35E-09	0.93	3.87	-	979.3
AHQ-3-8, 3428	K.HIVLSGGSTMYPGLPSR.L	1773.04967	2	1.64E-05	0.98	5.31	-	2509.8
AHQ-3-8, 3742	K.HLWDYTFGPEK.L	1393.52736	2	3.68E-07	0.89	3.33	-	692.7
AHQ-3-8, 3750	K.HLWDYTFGPEK.L	1393.52736	1	1.95E-04	0.75	2.49	-	706.3
AHQ-3-8, 2602	K.ILLTEPPM*NPTK.N	1370.64006	2	1.06E-04	0.73	3.54	-	518.2
AHQ-3-8, 2508	R.KVVVCDNGTGFVK.C	1424.64764	2	2.54E-05	0.72	3.03	-	823.7
AHQ-3-8, 3578	K.LCYVGYNIEQEQK.L	1645.81494	2	9.12E-08	0.97	4.66	-	1666.2
AHQ-3-8, 4148	R.SMLEVNYPM*ENGIVR.N	1769.03643	2	2.08E-04	0.30	2.71	-	367.0
gi|4507951|ref|NP_003396.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept				2.36E-09	3.49	50.20	28.50	28218.5
AHQ-3-14-, 2884	K.AVTELNEPLSNEDR.N	1587.67060	2	2.36E-09	0.90	3.47	-	852.8
AHQ-3-10, 2727	K.AVTELNEPLSNEDR.N	1587.67060	2	2.30E-05	0.59	2.61	-	563.1
AHQ-3-13-, 2942 - 2967	K.AVTELNEPLSNEDR.N	1587.67060	2	2.88E-08	0.87	4.02	-	555.0
AHQ-3-10, 2866	K.AVTELNEPLSNEDR.N	1587.67060	2	5.54E-07	0.89	4.03	-	832.5
AHQ-3-13, 2970	K.AVTELNEPLSNEDR.N	1587.67060	2	4.31E-07	0.80	3.30	-	583.8
AHQ-3-10, 5572	K.ELETVCNDVLSLLDK.F	1749.96137	2	2.63E-05	0.71	3.07	-	451.3
AHQ-3-10, 6348 - 6426	K.ELETVCNDVLSLLDK.F	1749.96137	2	9.40E-05	0.88	3.68	-	831.6
AHQ-3-14-, 6699	K.ELETVCNDVLSLLDK.F	1749.96137	2	7.48E-05	0.90	3.96	-	694.7
AHQ-3-10, 2779	K.NSVVEASEAAYK.E	1268.35495	1	2.61E-05	0.28	1.90	-	376.4
AHQ-3-10, 5707	K.QAFDDAIAELDTLNEDSYK.D	2159.24915	2	5.88E-04	0.59	3.29	-	357.2
AHQ-3-13-, 6114	K.QAFDDAIAELDTLNEDSYK.D	2159.24915	2	3.35E-04	0.88	3.76	-	595.0
AHQ-3-13, 2247	R.YLAEVASGEK.K	1067.17419	1	3.07E-05	0.22	1.87	-	541.3
AHQ-3-10, 2028 - 2030	R.YLAEVASGEK.K	1067.17419	2	2.71E-05	0.91	3.32	-	848.1
AHQ-3-10, 2022	R.YLAEVASGEK.K	1067.17419	1	2.12E-06	0.72	3.10	-	385.6
AHQ-3-13, 2245	R.YLAEVASGEK.K	1067.17419	2	2.68E-04	0.76	2.99	-	623.1
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				2.42E-09	5.47	60.26	38.30	22006.2
AHQ-3-10, 4238 - 4243	K.HFCPNVPIILVGNK.K	1609.91693	2	2.42E-09	0.97	4.90	-	1528.7
AHQ-3-11, 4514	K.HFCPNVPIILVGNK.K	1609.91693	2	4.70E-04	0.95	3.52	-	1400.3
AHQ-3-10, 3936	K.HFCPNVPIILVGNKK.D	1738.08985	2	3.75E-05	0.94	3.37	-	1466.8
AHQ-3-10, 2175	K.KLVIVGDGACGK.T	1218.44864	2	4.11E-06	0.94	3.39	-	1591.4
AHQ-3-10, 6398 - 6403	R.LRPLSYPDTDVILM*CFSIDSPDSLENIPEK.W	3483.90759	3	9.90E-04	0.93	5.19	-	788.3
AHQ-3-10, 2551	K.LVIVGDGACGK.T	1090.27572	1	5.94E-07	0.75	3.33	-	423.7
AHQ-3-10, 2543	K.LVIVGDGACGK.T	1090.27572	2	4.28E-04	0.91	3.24	-	1037.4
AHQ-3-10, 4646 - 4684	K.QVELALWDTAGQEDYDR.L	2010.10662	2	4.41E-04	0.95	4.11	-	1513.3
gi|4503747|ref|NP_001448.1| filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a				2.43E-09	4.24	50.24	1.40	278191.4
AHQ-3-1, 3740	K.DLAEDAPWK.K	1045.12708	1	8.01E-06	0.37	2.06	-	527.4
AHQ-3-3, 3636	K.DLAEDAPWK.K	1045.12708	1	3.93E-06	0.58	2.00	-	819.1
AHQ-3-2, 3715	K.DLAEDAPWK.K	1045.12708	2	5.94E-04	0.88	3.14	-	962.9
AHQ-3-2, 3706	K.DLAEDAPWK.K	1045.12708	1	2.73E-05	0.50	2.57	-	434.6
AHQ-3-2, 3689	K.DLAEDAPWK.K	1045.12708	1	1.35E-05	0.49	2.46	-	520.8
AHQ-3-5, 3472	K.DLAEDAPWK.K	1045.12708	1	1.03E-04	0.24	1.83	-	572.6
AHQ-3-2, 2894	K.DLAEDAPWKK.I	1173.29999	2	5.18E-04	0.87	2.83	-	1297.7
AHQ-3-1, 3096	K.DLAEDAPWKK.I	1173.29999	2	5.60E-05	0.79	2.93	-	1081.6
AHQ-3-6, 6321	R.LIALLEVLSQK.R	1227.51852	2	2.46E-08	0.98	4.90	-	1628.8
AHQ-3-11, 5948	R.LIALLEVLSQK.R	1227.51852	2	3.69E-07	0.97	4.58	-	1266.1
AHQ-3-7, 6168	R.LIALLEVLSQK.R	1227.51852	2	7.58E-07	0.97	4.16	-	1664.2
AHQ-3-3, 6620	R.LIALLEVLSQK.R	1227.51852	2	8.13E-07	0.97	4.84	-	1391.0
AHQ-3-5, 6381	R.LIALLEVLSQK.R	1227.51852	2	2.43E-09	0.98	4.83	-	1617.7
AHQ-3-4, 6621	R.LIALLEVLSQK.R	1227.51852	2	2.45E-08	0.97	4.67	-	1456.7
AHQ-3-2, 6625 - 6705	R.LIALLEVLSQK.R	1227.51852	2	2.17E-08	0.97	4.49	-	1670.1
AHQ-3-1, 6656 - 6657	R.LIALLEVLSQK.R	1227.51852	2	6.29E-09	0.97	4.49	-	1382.0
AHQ-3-2, 6773 - 6847	R.QM*QLENVSVALEFLDR.E	1909.15348	2	1.71E-05	0.94	4.66	-	1042.7
AHQ-3-1, 6654	R.QM*QLENVSVALEFLDR.E	1909.15348	2	4.17E-09	0.93	4.66	-	899.9
AHQ-3-2, 7342 - 7407	R.QMQLENVSVALEFLDR.E	1893.15408	2	5.32E-06	0.96	4.63	-	1180.4
AHQ-3-3, 7261	R.QMQLENVSVALEFLDR.E	1893.15408	2	3.82E-04	0.54	2.72	-	544.2
gi|5453549|ref|NP_006397.1| thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho				2.46E-09	3.71	40.22	25.50	30539.7
AHQ-3-10, 3470	K.DYGVYLEDSGHTLR.G	1625.72052	2	2.46E-09	0.95	3.86	-	1291.5
AHQ-3-10, 3854	K.HGEVCPAGWKPGSETIIPDPAGK.L	2405.67144	3	2.45E-05	0.93	4.46	-	1381.7
AHQ-3-10, 4507	R.IPLLSDLTHQISK.D	1465.71961	2	3.71E-07	0.95	3.45	-	1465.7
AHQ-3-10, 4419	K.ISKPAPYWEGTAVIDGEFK.E	2109.36607	2	9.05E-07	0.88	3.49	-	851.6
gi|13518026|ref|NP_004978.2| LIM and senescent cell antigen-like domains 1 [Homo sapiens]				2.52E-09	2.80	30.25	12.30	37251.2
AHQ-3-9, 7016	R.CDLCQEVLADIGFVK.N	1770.01757	2	2.44E-05	0.95	3.78	-	1703.9
AHQ-3-11, 4310	K.CHAIIDEQPLIFK.N	1585.84900	2	2.52E-09	0.95	4.76	-	1271.6
AHQ-3-9, 4104 - 4107	K.CHAIIDEQPLIFK.N	1585.84900	2	2.57E-06	0.95	5.01	-	1228.1
AHQ-3-8, 4097 - 4105	K.CHAIIDEQPLIFK.N	1585.84900	2	1.30E-04	0.95	4.40	-	1302.7
AHQ-3-11, 3346 - 3418	R.VIEGDVVSALNK.A	1244.41966	2	2.55E-06	0.96	4.04	-	1567.7
AHQ-3-8, 3020	R.VIEGDVVSALNK.A	1244.41966	2	3.74E-08	0.90	3.87	-	858.9
AHQ-3-9, 3096	R.VIEGDVVSALNK.A	1244.41966	2	2.14E-05	0.91	3.78	-	916.8

AHQ-3-13, 3483	R.VIEGDVVSALNK.A	1244.41966	1	4.95E-04	0.25	1.91	-	542.7
AHQ-3-14-, 3479	R.VIEGDVVSALNK.A	1244.41966	2	5.81E-08	0.96	4.44	-	1203.2
gi|4507645|ref|NP_000356.1|	triosephosphate isomerase 1 [Homo sapiens]			2.59E-09	5.11	60.27	33.30	26669.3
AHQ-3-10, 6270 - 6350	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	2.59E-09	0.77	4.06	-	231.9
AHQ-3-10, 6370 - 6428	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	1.33E-08	0.69	3.16	-	257.7
AHQ-3-10, 6010 - 6090	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	7.02E-05	0.78	4.06	-	300.4
AHQ-3-10, 6228	K.ELASQPDVDGFLVGGASLKPEFVDIINAKQ	3159.53509	3	4.07E-05	0.50	3.15	-	179.1
AHQ-3-10, 3998	R.KQSLGELIGTLNAAK.V	1543.79037	2	4.83E-05	0.96	3.94	-	1956.1
AHQ-3-10, 4796 - 4802	K.QSLGELIGTLNAAK.V	1415.61746	2	3.81E-07	0.93	3.93	-	911.9
AHQ-3-10, 4920 - 4998	K.VAHALAEGLGVIACIGEK.L	1810.10800	2	1.95E-08	0.98	5.38	-	2194.3
AHQ-3-11, 5364	K.VPADTEVVCAPPTAYIDFAR.Q	2194.44943	2	7.67E-04	0.96	5.44	-	847.9
gi|13489087|ref|NP_109591.1|	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member			2.65E-09	5.49	60.22	22.20	42741.5
AHQ-3-8, 3914 - 3926	K.FAYGYIEDLK.C	1219.36713	2	1.25E-05	0.95	3.89	-	1089.9
AHQ-3-8, 4045	R.LGVQDLFNSSK.A	1208.34588	2	1.15E-06	0.90	3.27	-	932.1
AHQ-3-8, 3709	K.TYGADLASVDFQHASEDAR.K	2054.11949	3	1.33E-05	0.88	4.14	-	510.2
AHQ-3-9, 3681	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	6.20E-07	0.82	3.46	-	522.6
AHQ-3-8, 3705	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	2.65E-09	0.94	3.93	-	1140.5
AHQ-3-13, 6206	K.TYNFLPEFLVSTQK.T	1687.91650	2	4.46E-06	0.92	4.33	-	479.3
AHQ-3-8, 7211	R.VLELPYQGEELSMVILLPDDIEDESTGLKK.I	3375.82891	3	5.49E-08	0.91	4.49	-	840.0
AHQ-3-8, 7123	R.VLELPYQGEELSM*VILLPDDIEDESTGLKK.I	3391.82831	3	5.70E-05	0.88	4.24	-	528.2
gi|29736622|ref|XP_293924.1|	similar to cytoplasmic beta-actin [Homo sapiens]			2.70E-09	3.55	40.29	16.00	42002.9
AHQ-3-8, 7135 - 7136	R.CPEAIFQPSFLGIESSGIHETTFNSIMK.C	3143.53608	3	4.35E-05	0.88	3.76	-	844.0
AHQ-3-8, 7029 - 7033	R.FRCPEAIFQPSFLGIESSGIHETTFNSIMK.C	3446.89713	3	2.70E-09	0.97	5.75	-	1933.1
AHQ-3-9, 6087	R.TTGIVMDSGDGVTHIVPIYEGYALPHAILR.L	3197.65320	3	1.87E-04	0.82	3.54	-	888.9
AHQ-3-10, 5700 - 5763	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	3.87E-04	0.78	3.85	-	475.8
AHQ-3-8, 5988 - 5999	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	1.15E-04	0.88	4.11	-	1062.8
gi|4505753|ref|NP_002620.1|	phosphoglycerate mutase 1 (brain); Phosphoglycerate mutase A, nonmuscle			2.72E-09	4.05	60.21	31.10	28803.7
AHQ-3-10, 3715 - 3743	R.FSGWYDADLSPAGHEEAK.R	1981.06697	2	1.07E-04	0.91	3.55	-	1279.2
AHQ-3-10, 3330	R.FSGWYDADLSPAGHEEAKR.G	2137.25332	2	7.27E-08	0.76	3.22	-	768.2
AHQ-3-10, 2155	R.HGESAWNLENR.F	1313.36073	1	5.94E-05	0.26	2.28	-	266.4
AHQ-3-10, 1907	R.HYGGLTGLNK.A	1060.18811	1	9.97E-04	0.43	2.44	-	284.8
AHQ-3-10, 3892	K.NLKPIKPMQFLGDEETVR.K	2116.46992	3	2.31E-08	0.80	3.53	-	495.9
AHQ-3-10, 3879	K.NLKPIKPMQFLGDEETVR.K	2116.46992	2	8.35E-04	0.92	4.15	-	622.1
AHQ-3-10, 4627	R.YADLTEDQLPSCESLKDTIAR.A	2427.62735	3	2.72E-09	0.90	4.11	-	1032.0
gi|21361198|ref|NP_000286.2|	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei			2.73E-09	1.77	20.23	7.70	46722.2
AHQ-3-7, 6894	K.ITPNLAEFAFSLYR.Q	1642.87896	2	1.01E-06	0.81	2.87	-	618.7
AHQ-3-7, 4507 - 4578	K.VFSNGADLSGVTEEAPLK.L	1835.00476	2	4.97E-07	0.90	4.51	-	722.6
AHQ-3-7, 4400	K.VFSNGADLSGVTEEAPLK.L	1835.00476	2	2.73E-09	0.95	4.43	-	1110.4
gi|4507725|ref|NP_000362.1|	transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum			2.84E-09	3.75	40.27	48.30	15886.9
AHQ-3-13-, 3813 - 3830	K.AADDTWEPFASGK.T	1395.45529	2	9.67E-06	0.84	2.89	-	875.6
AHQ-3-13, 3807 - 3809	K.AADDTWEPFASGK.T	1395.45529	2	4.04E-06	0.91	4.32	-	677.7
AHQ-3-13-, 4013	R.GSPAINVAVHVFR.K	1367.58095	2	3.32E-09	0.94	4.14	-	1255.6
AHQ-3-13, 3990	R.GSPAINVAVHVFR.K	1367.58095	2	2.84E-09	0.91	3.71	-	887.7
AHQ-3-13, 3978	R.GSPAINVAVHVFR.K	1367.58095	2	5.16E-06	0.82	3.59	-	832.0
AHQ-3-13, 5906	R.RYTIAALLSPYSYSTTAVVTNPK.E	2517.86154	2	3.91E-06	0.97	5.43	-	1518.7
AHQ-3-13, 5507 - 5583	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	3.27E-07	0.97	5.17	-	1272.6
AHQ-3-13, 5501	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	2.04E-05	0.96	5.17	-	1818.2
AHQ-3-13-, 5498	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	6.13E-06	0.78	2.86	-	846.3
gi|4502011|ref|NP_000467.1|	adenylate kinase 1 [Homo sapiens]			3.03E-09	5.33	60.27	42.30	21634.7
AHQ-3-11, 6766	K.GQLVPLETVLDMLR.D	1584.90590	2	3.03E-09	0.90	4.26	-	419.6
AHQ-3-11, 5596	R.IGQPTLLLYVDAGPETMTQR.L	2204.53234	2	2.73E-04	0.95	4.84	-	865.0
AHQ-3-11, 5095	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	2	1.21E-05	0.70	3.05	-	743.5
AHQ-3-11, 5588	R.IGQPTLLLYVDAGPETMTQR.L	2204.53234	2	1.37E-05	0.88	3.28	-	907.3
AHQ-3-11, 3307	K.IIFVVGGPGSGK.G	1131.34939	2	1.49E-05	0.97	4.13	-	2552.3
AHQ-3-11, 5850	R.KVNAEGSVDSVFSQVCTHLDALK	2506.77407	3	3.20E-04	0.96	5.47	-	1520.0
AHQ-3-11, 3600	K.YGYTHLSTGDLLR.S	1496.64912	1	6.89E-05	0.46	2.20	-	383.9
AHQ-3-11, 3590	K.YGYTHLSTGDLLR.S	1496.64912	2	2.90E-08	0.92	3.42	-	1112.1
gi|4759044|ref|NP_004841.1|	Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]			3.04E-09	4.19	50.27	6.60	160883.4
AHQ-3-3, 6974	K.AFVGNQLPFIGFTYYR.E	1894.16356	2	3.04E-09	0.92	4.49	-	542.9
AHQ-3-3, 3066	R.DLQDKNCLLETAK.L	1549.72870	2	2.32E-06	0.80	3.28	-	608.8
AHQ-3-3, 6321	K.ELQDQLEAEQYFSTLYK.T	2106.27421	2	6.98E-04	0.81	3.05	-	703.0
AHQ-3-3, 2902	R.SIAEEQYSDLEKEK.I	1669.76838	2	4.30E-04	0.70	3.11	-	583.1
AHQ-3-3, 5542	R.SQLQALHIGLDSSSIGSGPGDAEADDGFPESR.L	3215.34459	3	1.82E-05	0.96	5.48	-	1525.3
gi|5453555|ref|NP_006316.1|	ras-related nuclear protein [Homo sapiens]			3.23E-09	1.69	20.20	14.80	24422.9
AHQ-3-10, 5208	K.SNYNFEKPFLWLAR.K	1786.02509	2	3.23E-09	0.87	3.60	-	527.3
AHQ-3-10, 5666 - 5676	K.SNYNFEKPFLWLAR.K	1786.02509	2	8.48E-07	0.67	3.13	-	540.6
AHQ-3-10, 3983	K.YVATLGVEVHPLVFHTNR.G	2053.35211	2	2.90E-05	0.82	3.95	-	445.0
gi|5453714|ref|NP_006448.1|	LIM protein (similar to rat protein kinase C-binding enigma) [Homo sapi			3.31E-09	0.86	10.21	2.50	64027.9
AHQ-3-13-, 2817 - 2894	K.EVVKPVPITSPAVSK.V	1551.85241	2	2.69E-08	0.88	4.30	-	354.9
AHQ-3-13, 2858 - 2906	K.EVVKPVPITSPAVSK.V	1551.85241	2	3.31E-09	0.86	3.78	-	319.7
gi|24497612|ref|NP_116262.2|	nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr			3.32E-09	3.43	40.28	11.60	72695.6
AHQ-3-6, 4089	R.EYVLYLRPTGPLAQK.L	1749.04621	2	4.99E-05	0.90	3.66	-	703.6
AHQ-3-6, 6697	K.LGCDWVATIFSR.D	1426.62208	2	3.32E-09	0.94	3.68	-	1096.8
AHQ-3-6, 6527	R.LVGEALLESNTIIDHVYCSPSLR.C	2588.91822	2	6.06E-07	0.96	5.57	-	932.4
AHQ-3-6, 5335	R.RPYEDQGLGETTPLTIICQPM*QPLR.V	2932.32204	3	5.10E-04	0.64	3.72	-	434.0
gi|4507855|ref|NP_003472.1|	Ubiquitin isopeptidase T; Ubiquitin-specific protease-5 (ubiquitin isop			3.47E-09	0.97	10.30	3.10	93393.2
AHQ-3-5, 7239	R.IGEWELIQESGVPLKPLFGPGYTGIR.N	2858.28283	3	3.47E-09	0.97	5.98	-	1792.2
gi|19913424|ref|NP_001681.2|	ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT			3.48E-09	2.72	30.20	5.20	68303.7
AHQ-3-6, 4159	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	3.48E-09	0.92	4.09	-	861.3
AHQ-3-6, 2886	R.TALVANTSNMPVAAR.E	1516.74852	2	7.62E-05	0.86	2.95	-	1483.6
AHQ-3-6, 2178	R.TALVANTSNM*PVAAR.E	1532.74792	2	7.28E-04	0.94	3.93	-	1597.8
gi|4507677|ref|NP_003290.1|	tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu			3.67E-09	8.20	110.25	18.20	92468.2
AHQ-3-5, 4473 - 4477	K.EEASDYLELDTIK.N	1526.62393	2	2.41E-05	0.92	3.83	-	1056.9
AHQ-3-6, 3706	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	4.36E-04	0.95	4.56	-	1142.1
AHQ-3-5, 3708	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	2.31E-04	0.87	3.40	-	898.4
AHQ-3-5, 3989 - 4067	K.GVVDSDDLPLNVSR.E	1486.60940	2	1.89E-04	0.93	4.27	-	906.2
AHQ-3-5, 6977 - 7048	K.GYEVIYLTEPVDEYCIQALPEFDGKR.F	3107.43557	3	1.47E-07	0.91	4.96	-	555.5
AHQ-3-5, 3473	K.IADDKYNDTFWK.E	1516.63566	2	1.83E-06	0.93	3.58	-	1087.5
AHQ-3-5, 6336 - 6337	K.KYSQFINFPIYVWSSK.T	2008.30657	2	1.51E-07	0.96	4.52	-	1635.1
AHQ-3-5, 3581	K.LIINSLYK.N	964.18338	1	9.29E-04	0.30	1.87	-	502.1
AHQ-3-5, 5316 - 5367	R.LISLTDENALSGNEELTVK.I	2047.24975	2	3.30E-07	0.62	3.05	-	444.1
AHQ-3-5, 3303	R.LSLNIDPDAK.V	1086.22065	1	1.56E-04	0.23	1.96	-	661.1
AHQ-3-5, 2479	R.SGYLLPDTK.A	994.12321	1	1.73E-04	0.59	2.07	-	689.6
AHQ-3-5, 6999	K.YSQFINFPIYVWSSK.T	1880.13366	2	3.67E-09	0.95	4.54	-	860.8
gi|5453603|ref|NP_006422.1|	chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c			3.72E-09	1.67	20.17	5.60	57487.9
AHQ-3-7, 2871	R.EALLSSAVDHGSDEVK.F	1657.76083	2	3.72E-09	0.89	3.35	-	1313.9
AHQ-3-7, 5470	R.SLHDALCVLAQTVK.D	1556.80920	2	5.39E-04	0.78	2.51	-	1242.4
gi|4557032|ref|NP_002291.1|	lactate dehydrogenase B [Homo sapiens]			3.96E-09	9.53	110.28	37.10	36638.3
AHQ-3-9, 4373	K.GEMMDLQHGSLFLQTPK.I	1933.24171	2	1.02E-04	0.86	3.81	-	618.7
AHQ-3-9, 6965 - 7044	K.GM*YGIENEVFLSLPCILNAR.G	2314.66682	2	1.50E-05	0.94	4.81	-	748.6
AHQ-3-9, 6968	K.GMYGIENEVFLSLPCILNAR.G	2298.66742	2	1.80E-07	0.92	4.59	-	647.2
AHQ-3-13-, 2141	K.IVADKDYSVTANSK.I	1511.65887	2	3.96E-09	0.93	3.40	-	1273.7
AHQ-3-13, 2199	K.IVADKDYSVTANSK.I	1511.65887	2	4.08E-04	0.92	3.48	-	888.3
AHQ-3-9, 1923	K.IVADKDYSVTANSK.I	1511.65887	2	2.61E-04	0.90	3.47	-	948.4
AHQ-3-13, 2643	K.IVVVTAGVR.Q	914.12760	2	1.70E-05	0.88	3.04	-	980.1
AHQ-3-13-, 2502	K.IVVVTAGVR.Q	914.12760	2	3.51E-05	0.85	3.24	-	768.3
AHQ-3-13-, 3487	K.LIAPVAEEEATVPNNK.I	1695.89534	2	8.73E-04	0.92	3.84	-	945.2

AHQ-3-9, 3224	K.LIAPVAEEEATVPNNK.I	1695.89534	2	5.12E-05	0.85	2.96	-	831.1
AHQ-3-9, 1864 - 1867	K.LKDDEVAQLK.K	1159.31477	1	6.38E-04	0.23	2.64	-	338.7
AHQ-3-9, 1871	K.LKDDEVAQLK.K	1159.31477	2	1.29E-05	0.63	2.77	-	544.5
AHQ-3-9, 3459	K.MVVESAYEVIK.L	1268.50463	2	1.03E-08	0.95	4.14	-	1078.0
AHQ-3-9, 3188	K.SADTLWDIQK.D	1177.28864	2	6.61E-07	0.77	2.82	-	666.7
AHQ-3-9, 6587 - 6595	K.SLADELALVDVLEDK.L	1630.81843	2	8.55E-08	0.97	5.63	-	1433.2
AHQ-3-13, 6711 - 6722	K.SLADELALVDVLEDK.L	1630.81843	2	2.91E-08	0.98	5.05	-	1968.1
AHQ-3-14-, 6587	K.SLADELALVDVLEDK.L	1630.81843	2	1.68E-05	0.96	4.40	-	1527.9
AHQ-3-13-, 6670	K.SLADELALVDVLEDK.L	1630.81843	2	9.92E-07	0.96	4.86	-	1366.1
AHQ-3-11, 6438	K.SLADELALVDVLEDK.L	1630.81843	2	1.64E-04	0.82	3.05	-	761.9
AHQ-3-9, 6871	K.SLADELALVDVLEDKLK.G	1872.14959	2	1.13E-05	0.82	3.17	-	845.8
gi|4507949|ref|NP_003395.1| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,				4.32E-09	2.53	30.29	20.30	28082.2
AHQ-3-10, 4031	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	8.86E-04	0.80	3.55	-	474.2
AHQ-3-10, 6251 - 6252	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	3.18E-07	0.97	5.73	-	1544.4
AHQ-3-13, 6981	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	7.86E-04	0.30	2.79	-	256.9
AHQ-3-14-, 6575 - 6644	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	4.32E-09	0.97	5.57	-	1192.7
AHQ-3-10, 2847 - 2855	K.YLIPNATQPESK.V	1361.52512	1	1.77E-05	0.82	2.93	-	842.9
AHQ-3-10, 2688 - 2758	K.YLIPNATQPESK.V	1361.52512	1	2.16E-07	0.76	3.01	-	758.2
AHQ-3-10, 2674	K.YLIPNATQPESK.V	1361.52512	2	3.97E-05	0.88	3.22	-	795.2
gi|4502013|ref|NP_001616.1| adenylate kinase 2 isoform a; adenylate kinase, mitochondrial; adenylat				4.63E-09	1.81	20.22	14.20	26477.6
AHQ-3-10, 3640 - 3700	R.LQAYHTQTTPLIEYYR.K	1998.22695	2	2.15E-05	0.94	4.30	-	985.4
AHQ-3-10, 5555	K.NLETPLCKNGFLLDGFPR.T	2093.39146	2	4.63E-09	0.88	4.03	-	524.1
gi|4758208|ref|NP_004081.1| dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;				4.83E-09	3.65	40.23	32.40	20478.2
AHQ-3-11, 5288 - 5315	K.ANDTQEFNLSAYFER.A	1805.88207	2	2.94E-07	0.94	4.64	-	1091.0
AHQ-3-11, 5838 - 5898	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	3.60E-06	0.93	4.56	-	773.5
AHQ-3-11, 6034	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	4.83E-09	0.91	4.67	-	574.4
AHQ-3-11, 3591	R.IYVGNASVAQDIPK.L	1475.67136	2	3.04E-06	0.88	3.58	-	829.7
AHQ-3-11, 3224 - 3272	K.LGITHVLNAAEGR.S	1351.53669	2	5.83E-04	0.92	3.31	-	1283.2
gi|24119203|ref|NP_705935.1| tropomyosin 3 [Homo sapiens]				4.91E-09	6.92	80.26	21.80	29032.5
AHQ-3-9, 2121	R.AREQAEAEVASLNR.R	1544.65218	2	6.38E-08	0.97	5.19	-	2438.6
AHQ-3-9, 3199	R.IQLVEEELDR.A	1244.37653	2	1.43E-06	0.90	3.29	-	973.5
AHQ-3-6, 3479	R.IQLVEEELDR.A	1244.37653	2	1.25E-04	0.83	2.76	-	878.6
AHQ-3-9, 3593 - 3641	R.IQLVEEELDRAQER.L	1728.88542	2	9.03E-05	0.65	2.75	-	721.6
AHQ-3-10, 2611	K.IQVLQQQADDAEER.A	1643.73738	2	1.32E-05	0.94	3.58	-	1420.9
AHQ-3-9, 2499	K.IQVLQQQADDAEER.A	1643.73738	2	9.43E-09	0.97	4.89	-	1906.2
AHQ-3-9, 2231	R.KIQVLQQQADDAEER.A	1771.91030	2	1.75E-06	0.98	5.17	-	1897.5
AHQ-3-9, 2244	R.KIQVLQQQADDAEER.A	1771.91030	3	4.91E-09	0.88	3.19	-	1397.0
AHQ-3-9, 2799	R.RIQLVEEELDR.A	1400.56288	2	1.91E-05	0.98	4.88	-	1856.2
AHQ-3-10, 3044	R.RIQLVEEELDR.A	1400.56288	2	1.23E-07	0.97	4.64	-	1725.2
AHQ-3-9, 3219	R.RIQLVEEELDRAQER.L	1885.07177	3	1.98E-05	0.83	3.24	-	1276.6
AHQ-3-9, 2727 - 2731	K.TIDDLEDKLK.C	1190.32563	2	1.25E-04	0.75	2.97	-	506.4
gi|20535366|ref|XP_053177.4| similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap				5.02E-09	3.19	40.23	9.80	49858.2
AHQ-3-12, 2872	K.DVNAAIATIK.T	1016.17355	1	9.85E-06	0.41	2.09	-	549.7
AHQ-3-9, 2667	K.DVNAAIATIK.T	1016.17355	1	3.52E-05	0.40	2.12	-	331.3
AHQ-3-7, 3062	K.DVNAAIATIK.T	1016.17355	1	8.83E-06	0.48	2.05	-	446.8
AHQ-3-7, 2863	K.DVNAAIATIK.T	1016.17355	1	4.53E-04	0.28	2.67	-	214.8
AHQ-3-7, 2862	K.DVNAAIATIK.T	1016.17355	2	5.65E-05	0.92	3.82	-	957.4
AHQ-3-7, 4887 - 4898	K.RTIQFVDWCPTGFK.V	1757.00535	2	8.82E-04	0.94	3.98	-	1025.4
AHQ-3-3, 5470	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.38E-06	0.71	3.13	-	532.9
AHQ-3-4, 5438	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.60E-08	0.68	3.12	-	463.4
AHQ-3-6, 5185 - 5189	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.75E-06	0.84	3.39	-	712.4
AHQ-3-7, 4968	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.13E-09	0.92	4.35	-	884.1
AHQ-3-7, 5124 - 5195	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.89E-07	0.94	4.34	-	1039.4
AHQ-3-7, 5274 - 5346	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.88E-08	0.92	4.60	-	642.6
AHQ-3-14-, 5039 - 5108	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.83E-09	0.92	4.52	-	663.4
AHQ-3-7, 4795	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.02E-09	0.89	4.11	-	488.6
AHQ-3-9, 4851	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	9.91E-06	0.83	3.81	-	451.0
AHQ-3-10, 4754 - 4828	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.08E-07	0.88	4.27	-	710.3
AHQ-3-11, 4950	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.81E-07	0.87	3.75	-	714.1
AHQ-3-1, 5513	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.26E-06	0.93	4.53	-	854.3
AHQ-3-12, 5170	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.86E-07	0.90	3.84	-	766.6
AHQ-3-14, 6285	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.69E-08	0.84	3.30	-	699.7
AHQ-3-13, 4797	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.16E-08	0.81	4.03	-	322.2
AHQ-3-13, 5182	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.43E-07	0.78	3.53	-	554.9
AHQ-3-14, 6059 - 6119	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.02E-07	0.64	3.10	-	431.5
AHQ-3-14, 5783	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.32E-08	0.82	3.55	-	525.6
AHQ-3-14-, 5171	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.91E-08	0.92	4.44	-	721.4
AHQ-3-7, 5636 - 5706	R.TIQFVDWCPTGFK.V	1600.81899	2	3.21E-06	0.88	3.64	-	684.9
AHQ-3-12, 5675 - 5722	R.TIQFVDWCPTGFK.V	1600.81899	2	2.78E-04	0.79	3.14	-	577.3
AHQ-3-13, 5699 - 5707	R.TIQFVDWCPTGFK.V	1600.81899	2	3.26E-05	0.66	2.95	-	512.5
gi|25188179|ref|NP_005653.3| voltage-dependent anion channel 3 [Homo sapiens]				5.02E-09	2.80	40.24	16.30	30658.4
AHQ-3-10, 3008 - 3016	K.LSQNNFALGYK.A	1255.40424	1	6.38E-04	0.38	2.44	-	324.8
AHQ-3-10, 4572	K.LTLDTIFVPNTGK.K	1419.64771	2	8.27E-04	0.72	2.85	-	527.2
AHQ-3-9, 4396	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	7.36E-05	0.53	2.72	-	548.2
AHQ-3-9, 4215	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.10E-08	0.65	3.34	-	457.4
AHQ-3-9, 3935	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	1.42E-08	0.87	3.85	-	560.0
AHQ-3-10, 4022 - 4023	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	1.16E-07	0.89	4.43	-	493.0
AHQ-3-10, 4028	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	3	5.29E-08	0.93	4.78	-	1379.0
AHQ-3-10, 4203	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.41E-07	0.86	3.84	-	665.7
AHQ-3-10, 4366 - 4375	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	5.02E-09	0.73	3.46	-	463.7
AHQ-3-14, 5595	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	4.46E-04	0.75	3.44	-	468.2
AHQ-3-10, 3574	K.YKVCNYGLTFTQK.W	1623.85410	2	1.68E-06	0.97	4.36	-	1582.7
gi|29737978|ref|XP_290747.1| similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy				5.17E-09	3.62	40.24	2.10	191380.7
AHQ-3-4, 3925 - 3926	K.ADFCIIHYAGK.V	1296.47641	2	2.54E-07	0.95	3.74	-	1301.4
AHQ-3-3, 3972	K.ADFCIIHYAGK.V	1296.47641	2	2.67E-06	0.94	3.42	-	1232.5
AHQ-3-2, 4017 - 4050	K.ADFCIIHYAGK.V	1296.47641	2	3.39E-06	0.96	3.99	-	1511.0
AHQ-3-5, 3732	K.ADFCIIHYAGK.V	1296.47641	2	7.60E-07	0.93	3.81	-	1036.0
AHQ-3-2, 2789 - 2835	R.AGVLAHLEEER.D	1224.34854	2	5.17E-09	0.96	4.34	-	1558.1
AHQ-3-3, 2753 - 2824	R.AGVLAHLEEER.D	1224.34854	2	4.59E-07	0.95	3.73	-	1529.1
AHQ-3-2, 2543 - 2842	R.AGVLAHLEEER.D	1224.34854	1	1.34E-05	0.30	2.72	-	217.5
AHQ-3-3, 2790	R.AGVLAHLEEER.D	1224.34854	1	9.05E-04	0.40	2.40	-	457.4
AHQ-3-1, 3060 - 3082	R.AGVLAHLEEER.D	1224.34854	2	1.67E-06	0.95	4.35	-	1302.1
AHQ-3-2, 3770	K.DKADFCIIHYAGK.V	1539.73719	2	1.87E-06	0.96	4.42	-	1698.7
AHQ-3-5, 3440	K.DKADFCIIHYAGK.V	1539.73719	2	5.24E-06	0.94	3.96	-	1176.7
AHQ-3-3, 3702	K.DKADFCIIHYAGK.V	1539.73719	2	3.68E-05	0.95	4.23	-	1273.5
AHQ-3-1, 3881 - 3885	K.DKADFCIIHYAGK.V	1539.73719	2	5.82E-08	0.97	4.90	-	1718.1
AHQ-3-2, 3779	K.DKADFCIIHYAGK.V	1539.73719	3	4.47E-08	0.91	4.08	-	1176.3
AHQ-3-4, 3650	K.DKADFCIIHYAGK.V	1539.73719	2	2.26E-04	0.97	4.43	-	1706.6
AHQ-3-1, 4928	K.LDPHLVLDQLR.C	1319.53460	3	1.42E-05	0.82	3.19	-	613.9
AHQ-3-3, 4796 - 4820	K.LDPHLVLDQLR.C	1319.53460	2	2.28E-07	0.81	2.63	-	617.1
AHQ-3-1, 4913 - 4916	K.LDPHLVLDQLR.C	1319.53460	2	3.33E-06	0.82	2.53	-	702.5
gi|4826657|ref|NP_004333.1| caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]				5.33E-09	1.33	20.19	5.80	62662.9
AHQ-3-12, 2744	R.LEQYTSAIEGTK.S	1340.46107	2	3.68E-04	0.41	2.53	-	612.5
AHQ-3-6, 2583	R.LEQYTSAIEGTK.S	1340.46107	2	4.16E-04	0.89	3.23	-	1107.2
AHQ-3-9, 3411	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	1.92E-07	0.92	3.88	-	957.1
AHQ-3-8, 3461	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	2.53E-08	0.84	3.48	-	678.7
AHQ-3-6, 3638	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	5.33E-09	0.92	3.77	-	1078.1

gi|4885417|ref|NP_005330.1| huntingtin interacting protein 2; ubiquitin-conjugating enzyme E2-25 KD				5.44E-09	0.92	10.18	6.00	22406.5
AHQ-3-11, 4568 - 4575	K.VDLVDENFTELR.G	1450.57553	2	5.44E-09	0.92	3.65	-	858.3
gi|4758970|ref|NP_004150.1| proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be				5.90E-09	2.82	30.22	14.70	29769.4
AHQ-3-11, 2347	K.FQHGVIAAVDSR.A	1300.44824	2	2.31E-05	0.91	3.09	-	1275.4
AHQ-3-11, 2247	K.KGPGLYYVDEHGTR.L	1592.73690	2	1.61E-07	0.96	4.45	-	1156.4
AHQ-3-11, 3964	K.VESTDVSDLLHQYR.E	1662.78230	2	5.90E-09	0.95	3.89	-	1503.3
gi|5453599|ref|NP_006127.1| capping protein (actin filament) muscle Z-line, alpha 2; F-actin cappin				6.05E-09	1.60	20.27	13.30	32948.9
AHQ-3-9, 5072	K.FIIHAPPGEFNEVFNDVR.L	2102.33685	2	8.99E-05	0.63	3.17	-	312.6
AHQ-3-9, 4413	K.KIDGQQTIIACIESHQFQAK.N	2317.60733	2	6.05E-09	0.96	5.34	-	956.3
gi|14249348|ref|NP_116120.1| hypothetical protein MGC14353 [Homo sapiens]				6.13E-09	0.92	10.19	11.40	13940.7
AHQ-3-13-, 4085	K.SWCPDCVQAEPVVR.E	1705.89366	2	6.13E-09	0.92	3.84	-	884.9
AHQ-3-13, 4085	K.SWCPDCVQAEPVVR.E	1705.89366	2	1.09E-07	0.95	3.71	-	1346.9
gi|11496277|ref|NP_068805.1| mitogen-activated protein kinase kinase 1 interacting protein 1; MEK p				6.20E-09	1.77	20.23	30.60	13622.6
AHQ-3-14, 6349	K.ELAPLFEELR.Q	1217.39591	2	2.53E-06	0.83	2.70	-	746.2
AHQ-3-14-, 5203	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	6.20E-09	0.94	4.52	-	1215.3
AHQ-3-14, 6279	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	2.75E-04	0.92	4.45	-	896.2
gi|14745898|ref|XP_016144.2| similar to tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat				6.48E-09	0.94	10.21	7.50	18201.0
AHQ-3-9, 6653 - 6660	K.LLCCDILDVLDK.N	1479.74157	2	6.48E-09	0.94	4.26	-	797.3
gi|4758984|ref|NP_004654.1| RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho				6.50E-09	5.50	80.26	30.60	24393.3
AHQ-3-11, 2646 - 2700	K.AQIWDTAGQER.Y	1275.35241	1	5.96E-04	0.31	2.07	-	318.5
AHQ-3-11, 4020	R.DHADSNIVIM*LVGNK.S	1642.85914	2	6.50E-09	0.97	4.96	-	1977.2
AHQ-3-11, 4643 - 4720	R.DHADSNIVIMLVGNK.S	1626.85974	2	5.54E-08	0.97	4.77	-	1970.5
AHQ-3-11, 4850 - 4915	R.GAVGALLVYDIAK.H	1290.53317	2	3.55E-07	0.98	5.23	-	1926.3
AHQ-3-11, 4862	R.GAVGALLVYDIAK.H	1290.53317	1	1.08E-04	0.62	3.17	-	576.9
AHQ-3-11, 1918	K.HLTYENVER.W	1161.24931	2	1.68E-05	0.71	2.69	-	393.1
AHQ-3-11, 1922 - 1924	K.HLTYENVER.W	1161.24931	1	6.33E-04	0.44	2.33	-	337.1
AHQ-3-11, 2207	R.NEFNLESK.S	981.04139	1	7.86E-07	0.49	2.21	-	306.4
AHQ-3-11, 2946	K.STIGVEFATR.S	1081.20410	2	5.77E-05	0.88	2.76	-	884.8
AHQ-3-11, 2688	K.VVLIGDSGVGK.S	1044.22690	1	7.86E-06	0.18	2.30	-	452.9
gi|4506181|ref|NP_002778.1| proteasome alpha 2 subunit; proteasome subunit HC3; proteasome componen				6.91E-09	1.90	20.24	17.50	25898.4
AHQ-3-11, 5007	R.KLAQQYYLVYQEPIPTAQLVQR.V	2651.05593	2	1.04E-06	0.93	4.43	-	836.5
AHQ-3-10, 6478	R.YNEDLELEDAIHTAILTLK.E	2202.44658	2	6.91E-09	0.97	4.87	-	1467.8
gi|4504077|ref|NP_000165.1| glycoprotein IX (platelet) [Homo sapiens]				7.00E-09	3.76	40.21	19.80	19046.0
AHQ-3-11, 4836 - 4855	R.ALETMGLWVDCR.G	1452.68135	2	7.00E-09	0.95	3.93	-	1268.2
AHQ-3-11, 2555	R.CASPSLAAHGPLGR.L	1395.56962	1	2.66E-07	0.54	3.08	-	204.1
AHQ-3-11, 2527	R.CASPSLAAHGPLGR.L	1395.56962	2	9.53E-08	0.92	3.42	-	1080.6
AHQ-3-11, 3195	R.GHGLTALPALPAR.T	1274.49706	1	4.54E-04	0.48	2.82	-	180.8
AHQ-3-11, 3162 - 3222	R.GHGLTALPALPAR.T	1274.49706	2	6.30E-05	0.95	4.17	-	962.7
AHQ-3-12, 3252 - 3318	R.GHGLTALPALPAR.T	1274.49706	2	5.72E-05	0.94	3.71	-	942.3
AHQ-3-11, 3012	R.TPEALLQVR.C	1027.19957	2	5.48E-05	0.95	3.79	-	1333.8
AHQ-3-14-, 3059	R.TPEALLQVR.C	1027.19957	2	5.77E-07	0.95	3.30	-	1781.0
AHQ-3-12, 3067 - 3108	R.TPEALLQVR.C	1027.19957	2	9.04E-05	0.85	3.16	-	909.2
gi|21735621|ref|NP_005909.2| mitochondrial malate dehydrogenase precursor [Homo sapiens]				7.37E-09	4.46	50.27	24.60	35503.0
AHQ-3-9, 4897	K.IFGVTTLDIVR.A	1234.46961	2	5.64E-08	0.96	3.87	-	1440.7
AHQ-3-9, 5163 - 5231	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	2	6.16E-06	0.88	3.98	-	504.8
AHQ-3-9, 5243	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	3	7.73E-06	0.97	5.44	-	1812.2
AHQ-3-9, 5203	K.SQETECTYFSTPLLLGK.K	1976.19328	2	8.49E-09	0.95	4.63	-	1079.0
AHQ-3-9, 6351	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	1.08E-06	0.97	5.13	-	1373.1
AHQ-3-9, 4673	K.VDFPQDQLTALTGR.I	1561.72111	2	7.37E-09	0.71	2.57	-	778.0
gi|4505303|ref|NP_002466.1| myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m				7.47E-09	3.52	40.22	15.90	22763.8
AHQ-3-12, 2534 - 2614	R.ALGQNPTNAEVLK.V	1355.52211	2	2.63E-04	0.75	3.59	-	326.1
AHQ-3-13, 2734 - 2801	R.ALGQNPTNAEVLK.V	1355.52211	2	8.12E-06	0.89	4.24	-	628.8
AHQ-3-12, 2630 - 2694	R.ALGQNPTNAEVLK.V	1355.52211	1	8.73E-04	0.07	2.51	-	223.0
AHQ-3-12, 2647 - 2711	R.ALGQNPTNAEVLK.V	1355.52211	2	2.02E-05	0.80	3.56	-	532.9
AHQ-3-12, 2778 - 2846	R.ALGQNPTNAEVLK.V	1355.52211	2	1.14E-04	0.88	4.43	-	376.0
AHQ-3-13-, 2701 - 2705	R.ALGQNPTNAEVLK.V	1355.52211	2	1.53E-05	0.88	3.97	-	662.9
AHQ-3-12, 2142 - 2202	R.HVLTTLGEK.M	998.15823	2	7.70E-04	0.81	2.65	-	504.2
AHQ-3-13, 2685 - 2703	K.ILYSQCGDVM*R.A	1359.55429	2	4.41E-05	0.52	2.50	-	526.4
AHQ-3-12, 2590 - 2658	K.ILYSQCGDVM*R.A	1359.55429	2	1.67E-06	0.91	3.45	-	993.4
AHQ-3-13-, 2659	K.ILYSQCGDVM*R.A	1359.55429	2	2.19E-04	0.92	3.27	-	1133.2
AHQ-3-12, 3212	K.ILYSQCGDVMR.A	1343.55489	1	9.24E-05	0.49	2.80	-	236.7
AHQ-3-12, 3262 - 3316	K.ILYSQCGDVMR.A	1343.55489	2	6.79E-06	0.91	3.24	-	1093.5
AHQ-3-14-, 2603	K.ILYSQCGDVM*R.A	1359.55429	2	7.47E-09	0.91	3.36	-	1063.2
gi|7657056|ref|NP_055415.1| EH-domain containing 3; EH domain containing 3 [Homo sapiens]				7.53E-09	2.80	30.32	10.30	60886.7
AHQ-3-7, 2571 - 2624	K.ADQIETQQLMR.V	1333.49681	2	1.63E-05	0.92	3.56	-	1434.5
AHQ-3-7, 7320 - 7390	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	3.78E-06	0.96	5.61	-	1291.5
AHQ-3-10, 6567 - 6568	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	5.66E-07	0.92	4.11	-	1083.5
AHQ-3-7, 5942 - 5955	R.VYIGSFWSHPLLIPDNR.K	2015.30234	2	7.53E-09	0.96	4.61	-	1210.8
gi|28178832|ref|NP_002159.2| isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat				7.85E-09	3.73	40.26	12.60	50909.0
AHQ-3-8, 3712	K.DLAGCIHGLSNVK.L	1385.57150	2	3.75E-05	0.94	4.10	-	1130.6
AHQ-3-8, 5161 - 5164	K.LNEHFLNTTDFLDTIK.S	1922.12725	2	3.84E-07	0.97	5.11	-	1656.9
AHQ-3-14-, 5608	K.LNEHFLNTTDFLDTIK.S	1922.12725	2	7.85E-09	0.96	4.45	-	1577.8
AHQ-3-8, 4419 - 4423	R.NILGGTVFREPIICK.N	1719.04170	2	3.84E-05	0.96	4.81	-	1212.4
AHQ-3-13, 2150	K.TIEAEAAHGTVTR.H	1356.46696	2	1.19E-05	0.86	3.37	-	769.7
AHQ-3-8, 1566 - 1601	K.TIEAEAAHGTVTR.H	1356.46696	2	6.55E-04	0.86	2.95	-	608.6
gi|10880989|ref|NP_067075.1| RAB18, member RAS oncogene family; RAB18 small GTPase [Homo sapiens] [				7.88E-09	1.76	20.21	14.10	22976.9
AHQ-3-11, 6094	K.LDNWLNELETYCTR.N	1828.98037	2	7.88E-09	0.93	4.11	-	977.5
AHQ-3-11, 5640 - 5715	K.TCDGVQCAFEELVEK.I	1787.94661	2	1.20E-05	0.83	3.90	-	814.5
gi|8922673|ref|NP_060692.1| parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]				8.24E-09	0.97	10.26	3.50	42243.4
AHQ-3-9, 4263	R.DAFDTLFDHAPDK.L	1492.57096	1	1.02E-08	0.90	4.05	-	644.8
AHQ-3-13, 4634	R.DAFDTLFDHAPDK.L	1492.57096	2	3.59E-04	0.83	2.77	-	975.0
AHQ-3-9, 4252	R.DAFDTLFDHAPDK.L	1492.57096	2	8.24E-09	0.97	5.13	-	1603.2
gi|4885413|ref|NP_005331.1| histidine triad nucleotide binding protein 1; Histidine triad nucleotid				8.44E-09	2.85	30.29	32.50	13801.8
AHQ-3-13, 2722	K.AQVARPGGDTIFGK.I	1417.59513	2	1.75E-08	0.94	3.73	-	1366.5
AHQ-3-13-, 5537 - 5566	R.CLAFHDISPQAPTHFLVIPK.K	2293.67220	3	8.44E-09	0.97	5.76	-	1847.5
AHQ-3-13, 5555 - 5598	R.CLAFHDISPQAPTHFLVIPK.K	2293.67220	3	4.70E-07	0.94	4.68	-	1062.1
AHQ-3-13-, 6121	K.IIFEDDRCLAFHDISPQAPTHFLVIPK.K	3182.64001	3	1.53E-07	0.94	5.06	-	1165.4
AHQ-3-13, 6114	K.IIFEDDRCLAFHDISPQAPTHFLVIPK.K	3182.64001	3	5.38E-05	0.92	4.93	-	1026.8
gi|5031593|ref|NP_005708.1| actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub				8.51E-09	5.52	60.29	62.30	16320.3
AHQ-3-12, 2930	K.ALAAGGVGSIVR.V	1071.25558	2	6.26E-06	0.97	4.30	-	2114.3
AHQ-3-12, 4038 - 4106	K.AVQSLDKNGVDLLMK.Y	1631.91943	2	1.34E-07	0.96	4.96	-	1227.3
AHQ-3-12, 4731	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	1.07E-08	0.88	4.35	-	532.6
AHQ-3-12, 4246	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	9.97E-07	0.92	3.57	-	924.6
AHQ-3-12, 4566	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	2.75E-08	0.94	4.60	-	956.5
AHQ-3-12, 4148	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	8.51E-09	0.87	3.75	-	520.2
AHQ-3-12, 4414	R.KVDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR.Q	3890.92031	3	2.59E-05	0.96	5.85	-	1408.1
AHQ-3-12, 4172	R.QGNMTAALQAALK.N	1317.54052	2	1.06E-05	0.88	3.34	-	716.5
gi|5031595|ref|NP_005709.1| actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub				8.72E-09	5.27	60.27	47.60	19666.9
AHQ-3-11, 4126	R.AENFFILR.R	1010.17070	2	2.46E-04	0.96	3.78	-	1846.9
AHQ-3-12, 4335 - 4347	R.AENFFILR.R	1010.17070	2	1.49E-05	0.96	3.70	-	1727.6
AHQ-3-11, 4071 - 4079	K.ELLLQPVTISR.N	1269.51549	2	2.37E-04	0.91	3.71	-	741.0
AHQ-3-12, 3431	R.IVAEEFLK.N	949.12558	2	4.26E-04	0.58	2.90	-	260.0
AHQ-3-11, 5795	R.KPVEGYDISFLITNFHTEQMYK.H	2662.01271	3	1.31E-08	0.95	5.50	-	1039.4
AHQ-3-11, 6815	K.LVDFVIHFMEEIDKEISEM*K.L	2469.85893	3	9.94E-04	0.92	5.30	-	785.6
AHQ-3-12, 3119	K.VLIEGSINSVR.V	1187.37134	2	8.72E-09	0.96	3.79	-	1441.8
AHQ-3-11, 3034 - 3103	K.VLIEGSINSVR.V	1187.37134	2	2.95E-06	0.92	3.36	-	1135.8
gi|20357552|ref|NP_005222.2| cortactin isoform a; oncogene EMS1 [Homo sapiens]				9.08E-09	2.72	40.18	9.50	61585.7

AHQ-3-14, 4715	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	2.22E-05	0.84	3.28	-	887.8
AHQ-3-12, 2407	K.SAVGFEYQGK.T	1086.17920	1	1.46E-04	0.12	1.92	-	328.0
AHQ-3-13-, 3027 - 3093	K.VDKSAVGFEYQGK.T	1428.57155	2	1.18E-06	0.89	3.62	-	668.9
AHQ-3-12, 5412	R.YGLFPANYVELR.Q	1442.64306	2	9.08E-09	0.87	3.45	-	509.8
AHQ-3-12, 5318	R.YGLFPANYVELR.Q	1442.64306	2	3.05E-07	0.83	2.96	-	484.4
gi|4557731|ref|NP_000618.1|	latent transforming growth factor beta binding protein 1 precursor [Hom			1.00E-08	11.13	130.25	14.30	152790.9
AHQ-3-2, 3775	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	1.41E-05	0.95	5.01	-	968.8
AHQ-3-1, 3792	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	4.10E-08	0.96	4.69	-	1458.0
AHQ-3-1, 6728	K.CLCLPGYVPSDKPNYCTPLNTALNLEK.D	3142.56947	3	3.20E-08	0.87	4.08	-	481.8
AHQ-3-1, 2661 - 2741	R.CTCGQGYQLSAAK.D	1446.58862	2	1.00E-08	0.93	4.10	-	830.9
AHQ-3-1, 3718	R.CTCGQGYQLSAAKDQCEDIDECQHR.H	3035.18500	3	1.38E-04	0.92	4.27	-	1092.2
AHQ-3-1, 4273	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	2.50E-07	0.95	5.06	-	789.1
AHQ-3-1, 4270 - 4282	K.CVDIDECTQVQHLCSQGR.C	2209.38110	3	1.66E-04	0.73	3.45	-	575.4
AHQ-3-1, 2198 - 2201	K.DQCEDIDECQHR.H	1607.61898	2	4.67E-04	0.83	3.21	-	645.4
AHQ-3-1, 3468	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	7.66E-05	0.89	3.82	-	670.5
AHQ-3-3, 3193	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	7.65E-04	0.55	3.16	-	311.2
AHQ-3-1, 4056 - 4057	K.EEPVEALTFSR.E	1278.39297	2	1.02E-04	0.84	3.21	-	658.2
AHQ-3-2, 5773 - 5782	R.GRCEDIDECLNPSTCPDEQCVNSPGSYQCVPCTEGFR.G	4402.64921	3	1.67E-04	0.85	3.95	-	620.3
AHQ-3-1, 3120	K.LCQIPVHGASVPK.L	1407.66344	2	5.90E-06	0.63	3.12	-	345.9
AHQ-3-1, 4466	K.NGFCLNTRPGYECYCK.Q	2043.24638	2	4.82E-04	0.85	3.84	-	441.5
AHQ-3-1, 2988	R.TSTDLDVDVDQPK.E	1433.50014	2	4.41E-07	0.77	3.02	-	879.0
AHQ-3-3, 2590	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.26E-07	0.85	3.67	-	953.4
AHQ-3-2, 2598	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	5.82E-04	0.92	3.97	-	1312.1
AHQ-3-1, 2756	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	6.61E-07	0.65	2.99	-	615.6
gi|27477800|ref|XP_208313.1|	similar to tropomyosin 4 [Homo sapiens]			1.06E-08	1.86	20.25	10.10	18426.7
AHQ-3-9, 2733	K.CGDLEEELK.N	1094.17487	2	9.91E-04	0.92	3.70	-	1036.4
AHQ-3-9, 4833 - 4903	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.06E-08	0.94	4.62	-	1291.2
AHQ-3-9, 5248	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.21E-04	0.84	3.88	-	732.8
AHQ-3-9, 5272	K.CGDLEEELKNVTNNLK.S	1878.05124	3	1.51E-07	0.92	4.25	-	1145.0
AHQ-3-9, 5485 - 5556	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.31E-06	0.78	3.43	-	835.9
AHQ-3-9, 4315 - 4327	K.CGDLEEELKNVTNNLK.S	1878.05124	2	5.46E-06	0.96	5.04	-	1488.0
gi|4504981|ref|NP_002296.1|	beta-galactosidase binding lectin precursor; Lectin, galactose-binding,			1.09E-08	0.83	10.15	8.90	14715.6
AHQ-3-13, 3731	K.DSNNLCLHFNPR.F	1488.61037	2	1.09E-08	0.83	3.02	-	918.1
gi|14210536|ref|NP_115914.1|	similar to chicken tubulin beta 5 [Homo sapiens]			1.10E-08	0.65	10.19	3.80	49856.8
AHQ-3-13-, 5999 - 6077	K.M*ASTFIGNSTAIQELFK.R	1875.13550	2	1.10E-08	0.65	3.85	-	675.9
gi|12408656|ref|NP_005177.2|	calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ			1.15E-08	14.90	170.27	26.10	81889.4
AHQ-3-6, 5055	K.APSDLYQIILK.A	1261.49183	2	6.24E-07	0.94	3.50	-	1306.8
AHQ-3-6, 6726	R.DMETIGFAVYEVPPELVGQPAVHLK.R	2741.15451	3	2.91E-06	0.90	3.94	-	1326.5
AHQ-3-6, 6435	R.DM*ETIGFAVYEVPPELVGQPAVHLK.R	2757.15391	3	8.74E-06	0.80	3.49	-	728.6
AHQ-3-6, 6347 - 6362	R.DM*ETIGFAVYEVPPELVGQPAVHLK.R	2757.15391	3	7.51E-05	0.75	3.26	-	545.8
AHQ-3-6, 6002 - 6011	R.FRLPPGEYVVVPSTFEPNKEGDFVLR.F	2994.39160	3	1.54E-07	0.95	5.47	-	1305.1
AHQ-3-6, 2811	K.IRLDETDDPDDYGDR.E	1795.79921	2	4.37E-05	0.80	3.72	-	440.9
AHQ-3-6, 4117	R.KAPSDLYQIILK.A	1389.66474	2	6.78E-05	0.87	3.23	-	880.2
AHQ-3-6, 3173	K.KLYELIITR.Y	1149.40785	2	1.58E-04	0.86	3.32	-	676.1
AHQ-3-6, 3511	R.KWNTTLYEGTWR.R	1555.71826	2	1.21E-05	0.89	3.10	-	830.1
AHQ-3-6, 4694	R.LPPGEYVVVPSTFEPNK.E	1874.12573	2	3.97E-06	0.90	4.07	-	575.4
AHQ-3-6, 5686	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	2.29E-07	0.80	3.59	-	571.2
AHQ-3-6, 5689	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	2	6.04E-04	0.71	3.04	-	271.1
AHQ-3-6, 6485	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	2	9.48E-06	0.97	5.27	-	1525.2
AHQ-3-6, 3766	K.LYELIITR.Y	1021.23493	2	4.66E-04	0.95	3.95	-	1458.5
AHQ-3-6, 5085	R.NYPATFWVNPQFK.I	1612.81141	2	6.51E-08	0.96	3.96	-	1462.9
AHQ-3-6, 4349 - 4357	K.RPTELLSNPQFIVDGATR.T	2015.25904	3	2.14E-05	0.95	4.85	-	1238.4
AHQ-3-6, 2854	R.SEQFINLR.E	1007.12521	2	1.00E-04	0.89	2.83	-	1026.7
AHQ-3-6, 3130	K.YLGQDYEQLR.V	1285.38720	2	1.53E-06	0.88	3.05	-	682.6
AHQ-3-14-, 6864	R.YSEPDLAVDFDNFVCCLVR.L	2322.55612	2	1.15E-08	0.60	2.96	-	258.6
AHQ-3-6, 7377	R.YSEPDLAVDFDNFVCCLVR.L	2322.55612	2	8.38E-07	0.96	5.42	-	879.6
gi|17318569|ref|NP_006112.2|	keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]			1.23E-08	2.73	30.22	5.90	66066.3
AHQ-3-1, 3894	K.QISNLQQSISDAEQR.G	1717.81950	2	1.23E-08	0.90	3.78	-	803.5
AHQ-3-1, 6444	R.SLDLDSIIAEVK.A	1303.48388	2	3.75E-07	0.94	3.76	-	1412.2
AHQ-3-12, 6036	R.SLDLDSIIAEVK.A	1303.48388	2	2.30E-06	0.96	4.32	-	1420.4
AHQ-3-14-, 5975 - 5987	R.SLDLDSIIAEVK.A	1303.48388	2	1.01E-05	0.94	4.06	-	1216.1
AHQ-3-1, 3256	R.TNAENEFVTIK.K	1266.38219	2	1.74E-04	0.88	3.35	-	735.6
gi|12707570|ref|NP_004083.2|	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor [Homo			1.29E-08	0.97	10.27	6.20	31371.2
AHQ-3-10, 4682 - 4683	K.IFEEDPAVGAIVLTGGDK.A	1832.04401	2	1.29E-08	0.97	5.38	-	1733.4
gi|5803133|ref|NP_006825.1|	RAB32, member RAS oncogene family [Homo sapiens]			1.33E-08	0.79	10.16	7.60	24997.1
AHQ-3-10, 4444	K.VHLPNGSPIPAVLLANK.C	1741.07044	2	1.33E-08	0.79	3.29	-	411.2
gi|5802966|ref|NP_006861.1|	destrin (actin depolymerizing factor); destrin [Homo sapiens]			1.35E-08	2.56	30.27	26.70	18505.6
AHQ-3-12, 6212	K.EILVGDVGVTITDPFK.H	1703.95738	2	3.57E-06	0.94	3.77	-	1217.0
AHQ-3-12, 6810	R.KEELM*FFLWAPELAPLK.S	2079.48962	2	2.79E-04	0.98	5.46	-	2294.9
AHQ-3-12, 3724	R.YALYDASFETK.E	1308.41754	1	1.35E-08	0.64	2.92	-	435.5
AHQ-3-12, 3710 - 3788	R.YALYDASFETK.E	1308.41754	2	5.14E-06	0.89	3.13	-	846.8
gi|30158844|ref|XP_292513.2|	similar to KIAA1879 protein [Homo sapiens]			1.36E-08	0.95	10.20	0.70	203894.8
AHQ-3-7, 2818 - 2819	R.VVDALGNAIDGK.G	1172.31354	2	1.36E-08	0.95	3.93	-	1380.1
gi|30160191|ref|XP_294035.2|	similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme			1.42E-08	0.96	10.18	2.80	50222.2
AHQ-3-7, 5071 - 5142	K.IYVDDGLISLQVK.Q	1463.70048	1	2.44E-04	0.65	3.14	-	514.4
AHQ-3-7, 5066 - 5123	K.IYVDDGLISLQVK.Q	1463.70048	2	1.42E-08	0.96	3.52	-	2448.9
gi|12025678|ref|NP_004915.2|	actinin, alpha 4 [Homo sapiens]			1.42E-08	5.80	70.25	14.30	104853.3
AHQ-3-5, 4408	K.AGTQIENIDEDFRDGLK.L	1922.04251	2	5.33E-05	0.88	4.15	-	658.2
AHQ-3-4, 4841	R.ETTDTDTADQVIASFK.V	1742.81936	2	1.42E-08	0.93	4.12	-	1165.7
AHQ-3-5, 2772	K.GISQEQMQEFR.A	1353.48658	2	2.45E-07	0.62	3.02	-	741.0
AHQ-3-5, 3843	R.M*APYQGPDAVPGALDYK.S	1810.02037	2	6.48E-04	0.97	4.60	-	1410.9
AHQ-3-5, 3633	K.M*LDAEDIVNTARPDEK.A	1833.99864	2	3.59E-05	0.70	3.20	-	491.9
AHQ-3-6, 7118	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	2.10E-05	0.90	5.07	-	667.4
AHQ-3-6, 6449 - 6510	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	5.09E-07	0.81	3.44	-	810.6
gi|10716563|ref|NP_001737.1|	calnexin [Homo sapiens]			1.46E-08	4.43	50.21	10.50	67567.8
AHQ-3-5, 4929 - 4980	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.19E-08	0.93	3.55	-	1131.2
AHQ-3-11, 4698	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.46E-08	0.84	3.10	-	717.7
AHQ-3-5, 3880	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	2	7.39E-05	0.89	3.71	-	757.9
AHQ-3-5, 6947	K.IPNPDFFEDLEPFR.M	1736.90447	2	4.05E-05	0.88	3.34	-	750.3
AHQ-3-9, 5848	R.KIPNPDFFEDLEPFR.M	1865.07739	2	3.56E-06	0.88	3.50	-	689.8
AHQ-3-5, 6311 - 6389	R.KIPNPDFFEDLEPFR.M	1865.07739	2	2.91E-05	0.90	3.79	-	712.2
AHQ-3-5, 3317 - 3319	K.TPELNLDQFHDK.T	1457.56976	2	9.84E-07	0.95	4.22	-	1429.3
gi|4826774|ref|NP_005092.1|	interferon, alpha-inducible protein (clone IFI-15K); interferon-stimula			1.58E-08	0.86	10.23	18.20	17887.4
AHQ-3-13, 6877	R.VPLASQGLGPGSTVLLVVDKCDEPLSILVR.N	3135.66454	3	1.58E-08	0.86	4.51	-	571.9
gi|4759140|ref|NP_004243.1|	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulato			1.58E-08	0.89	10.16	3.90	38868.2
AHQ-3-13-, 3806	R.LLVVDPETDEQLQK.L	1627.81777	2	1.58E-08	0.89	3.20	-	833.0
gi|6679056|ref|NP_031387.1|	nidogen 2 (osteonidogen); nidogen 2 [Homo sapiens]			1.61E-08	0.84	10.20	2.10	151153.0
AHQ-3-2, 7190	R.AGLELGAEPETIVNSGLISPEGLAIDHIR.R	2973.32740	3	1.61E-08	0.84	4.10	-	569.0
gi|4758988|ref|NP_004152.1|	RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho			1.66E-08	1.62	20.23	17.10	22677.6
AHQ-3-14-, 6157 - 6163	K.EFADSLGIPFLETSAK.N	1725.91990	2	1.45E-05	0.77	3.71	-	396.6
AHQ-3-12, 6226	K.EFADSLGIPFLETSAK.N	1725.91990	2	2.18E-04	0.50	2.95	-	348.9
AHQ-3-11, 5851 - 5908	K.EFADSLGIPFLETSAK.N	1725.91990	2	8.25E-06	0.60	3.00	-	221.3
AHQ-3-13-, 6257 - 6258	K.EFADSLGIPFLETSAK.N	1725.91990	2	2.68E-04	0.57	3.09	-	381.4
AHQ-3-11, 5967 - 6038	K.EFADSLGIPFLETSAK.N	1725.91990	2	1.11E-07	0.81	4.08	-	399.6
AHQ-3-11, 6838 - 6915	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	6.41E-05	0.94	4.27	-	1108.8
AHQ-3-11, 5783 - 5806	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.46E-07	0.61	2.87	-	766.2
AHQ-3-13, 6034	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.66E-08	0.80	3.28	-	586.2

AHQ-3-13-, 6015	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	5.57E-05	0.83	3.42	-	580.2
AHQ-3-11, 5995 - 6066	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.74E-06	0.96	4.61	-	1459.8
AHQ-3-11, 5866 - 5927	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.44E-06	0.96	4.31	-	1351.0
AHQ-3-14-, 5881 - 5945	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.66E-04	0.96	4.02	-	1628.6
AHQ-3-11, 5619	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	6.62E-06	0.83	3.45	-	584.9
gi|14251209|ref|NP_001279.2| chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo				1.73E-08	7.23	100.30	58.50	26922.5
AHQ-3-9, 6013 - 6077	K.FLDGNELTLADCNLLPK.L	1935.18752	2	9.61E-04	0.64	3.68	-	599.6
AHQ-3-9, 6140	K.FLDGNELTLADCNLLPK.L	1935.18752	2	1.73E-08	0.69	3.77	-	745.7
AHQ-3-9, 5875 - 5943	K.FLDGNELTLADCNLLPK.L	1935.18752	2	5.49E-08	0.93	4.81	-	1255.2
AHQ-3-9, 3375	K.FSAYIKNSNPALNDNLEK.G	2039.23424	2	1.92E-06	0.63	3.45	-	449.0
AHQ-3-13-, 3367 - 3397	K.GVTFNVTTVDTK.R	1282.42476	2	2.33E-04	0.93	3.67	-	1429.2
AHQ-3-13, 3402	K.GVTFNVTTVDTK.R	1282.42476	2	2.73E-06	0.96	4.34	-	1383.7
AHQ-3-10, 3123	K.GVTFNVTTVDTK.R	1282.42476	2	1.11E-06	0.84	3.15	-	821.6
AHQ-3-13, 2506	K.IGNCPFSQR.L	1080.19948	2	2.79E-05	0.81	2.86	-	588.5
AHQ-3-9, 5617 - 5628	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	1.35E-05	0.79	4.09	-	774.9
AHQ-3-9, 5447	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	2.89E-05	0.78	3.64	-	958.7
AHQ-3-9, 4971 - 5044	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.57E-05	0.96	4.78	-	1073.7
AHQ-3-9, 5201 - 5205	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.75E-08	0.96	5.06	-	1070.4
AHQ-3-13, 5311 - 5345	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	5.57E-08	0.94	4.69	-	669.2
AHQ-3-13-, 5451	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	4.33E-04	0.93	4.56	-	711.2
AHQ-3-13-, 5318	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.10E-05	0.94	5.15	-	716.3
AHQ-3-10, 4858	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	4.43E-07	0.94	4.37	-	908.3
AHQ-3-13, 5481 - 5489	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.73E-06	0.82	3.30	-	522.2
AHQ-3-14, 6283	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.40E-04	0.93	4.45	-	850.6
AHQ-3-11, 5119 - 5123	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.39E-05	0.97	6.01	-	930.1
AHQ-3-10, 5275	K.LCPGGQLPFLLYGTEVHTDTNK.I	2462.76290	2	3.73E-06	0.78	3.42	-	563.1
AHQ-3-9, 5171	R.LFM*VLWLK.G	1066.38391	1	8.67E-04	0.25	2.12	-	199.0
AHQ-3-10, 2511	K.LHIVQVVCK.K	1097.35623	1	9.30E-05	0.75	2.65	-	622.7
AHQ-3-9, 2355	K.LHIVQVVCK.K	1097.35623	2	5.59E-06	0.77	2.56	-	648.3
AHQ-3-9, 2365	K.LHIVQVVCK.K	1097.35623	1	6.38E-06	0.73	3.15	-	484.8
AHQ-3-10, 2506	K.LHIVQVVCK.K	1097.35623	2	4.37E-05	0.89	3.06	-	754.8
AHQ-3-10, 4839 - 4906	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	2.80E-04	0.46	2.80	-	240.8
AHQ-3-12, 5264	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	3	5.00E-05	0.70	3.42	-	539.8
AHQ-3-9, 5056 - 5091	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	1.84E-04	0.91	4.70	-	411.2
gi|4506005|ref|NP_002700.1| protein phosphatase 1, catalytic subunit, beta isoform [Homo sapiens] [				1.74E-08	3.81	40.28	20.80	37186.6
AHQ-3-9, 3511	R.AHQVVEDGYEFFAK.R	1640.77679	2	2.06E-04	0.96	4.14	-	1487.7
AHQ-3-14-, 6773 - 6840	R.EIFLSQPILLELEAPLK.I	1954.33857	2	3.11E-06	0.94	4.80	-	700.4
AHQ-3-13, 6913 - 6915	R.EIFLSQPILLELEAPLK.I	1954.33857	2	1.94E-07	0.96	5.60	-	651.5
AHQ-3-9, 6947	R.EIFLSQPILLELEAPLK.I	1954.33857	2	7.76E-06	0.95	5.06	-	807.2
AHQ-3-9, 4905	K.IFCCHGGLSPDLQSMEQIR.R	2251.54930	2	9.74E-04	0.96	5.39	-	1480.6
AHQ-3-9, 6879 - 6884	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	8.58E-07	0.97	5.36	-	1260.3
AHQ-3-9, 6681	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	1.74E-08	0.93	3.75	-	1159.7
gi|30158852|ref|XP_301583.1| similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa				1.88E-08	0.76	10.17	6.50	19197.0
AHQ-3-10, 2584 - 2647	K.IWHHTFYNKLR.V	1515.74533	2	2.95E-06	0.91	3.46	-	1253.2
AHQ-3-8, 2376 - 2398	K.IWHHTFYNKLR.V	1515.74533	2	1.88E-08	0.76	2.98	-	858.4
gi|4759300|ref|NP_004772.1| vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated				1.88E-08	2.89	30.28	33.00	11309.0
AHQ-3-14-, 3451 - 3503	R.ADALQAGASQFETSAAK.L	1666.77095	2	1.49E-04	0.86	3.69	-	691.8
AHQ-3-14, 4411	R.ADALQAGASQFETSAAK.L	1666.77095	2	1.92E-04	0.88	3.69	-	672.9
AHQ-3-13, 3562	R.ADALQAGASQFETSAAK.L	1666.77095	2	1.88E-08	0.94	4.34	-	959.2
AHQ-3-13-, 3733	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	4.60E-08	0.97	5.21	-	1725.0
AHQ-3-13-, 4881	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	5.38E-07	0.98	5.67	-	2089.1
AHQ-3-13, 4881	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	6.01E-08	0.98	5.49	-	2237.5
AHQ-3-13, 3733	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	2.13E-06	0.96	4.92	-	1230.4
gi|5802974|ref|NP_006784.1| peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide				1.93E-08	1.98	30.30	19.50	27692.5
AHQ-3-11, 4391	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	1.93E-08	0.96	6.09	-	1251.7
AHQ-3-11, 3890	K.DLSLDDFK.G	953.02795	1	1.08E-04	0.37	2.25	-	472.5
AHQ-3-11, 2863 - 2882	K.HLSVNDLPVGR.S	1207.36435	2	3.23E-04	0.65	2.66	-	358.8
gi|29731325|ref|XP_293023.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				1.95E-08	0.80	10.17	6.00	28867.8
AHQ-3-12, 4078 - 4080	K.AGPNTNGSQFFICTAK.T	1714.88050	2	1.95E-08	0.80	3.33	-	539.9
gi|4557385|ref|NP_000055.1| complement component 3 precursor; acylation-stimulating protein cleavag				2.10E-08	1.88	20.28	2.40	187162.3
AHQ-3-6, 5183	R.AYYENSPQQVFSTEFEVK.E	2167.31611	2	1.36E-05	0.91	3.98	-	822.6
AHQ-3-6, 4523	R.VPVAVQGEDTVQSLTQGDGVAK.L	2199.40432	2	2.10E-08	0.97	5.64	-	1303.0
gi|5174393|ref|NP_006001.1| arginine-rich, mutated in early stage tumors; arginine-rich protein [Ho				2.16E-08	3.29	40.28	25.60	26906.2
AHQ-3-12, 5640	K.DRDVTFSPATIENELIK.F	1949.15100	3	3.48E-04	0.76	3.17	-	899.0
AHQ-3-12, 5643	K.DRDVTFSPATIENELIK.F	1949.15100	2	2.16E-08	0.98	5.63	-	2612.3
AHQ-3-12, 2722	K.DSQICELKYDK.Q	1400.53657	2	6.70E-07	0.80	2.90	-	683.2
AHQ-3-12, 2803	K.IINEVSKPLAHHIPVEK.I	1925.26378	3	1.68E-07	0.82	3.81	-	885.6
AHQ-3-12, 3160 - 3230	K.ILDDWGETCKGCAEK.S	1784.94596	2	3.68E-05	0.69	2.84	-	472.9
gi|5031677|ref|NP_005681.1| dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [				2.18E-08	9.48	110.27	20.70	78060.6
AHQ-3-14, 5941	K.ALQGASQIIAEIR.E	1370.57991	2	2.18E-08	0.91	3.86	-	1312.0
AHQ-3-14, 6135	K.DTLQSELVGQLYK.S	1494.67144	2	9.03E-06	0.91	3.35	-	1273.8
AHQ-3-13, 5206	K.DTLQSELVGQLYK.S	1494.67144	2	3.81E-04	0.85	3.42	-	791.8
AHQ-3-6, 6887 - 6961	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	3.08E-07	0.92	3.86	-	1095.2
AHQ-3-6, 6434	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	1.22E-05	0.88	3.62	-	846.0
AHQ-3-11, 6484	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	1.41E-05	0.40	2.53	-	442.5
AHQ-3-6, 3033	R.IIQHCSNYSTQELLR.F	1864.07262	2	3.59E-04	0.63	2.77	-	448.6
AHQ-3-6, 7034	K.LHDAIVEVVTCLLR.K	1639.94134	2	1.64E-05	0.97	4.21	-	2119.9
AHQ-3-6, 6203	K.LYTDFDEIRQEIENETER.I	2301.40883	2	4.19E-06	0.47	2.95	-	377.7
AHQ-3-7, 6115	K.LYTDFDEIRQEIENETER.I	2301.40883	2	6.22E-05	0.53	2.67	-	357.4
AHQ-3-14-, 6140 - 6141	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	2.53E-08	0.96	4.72	-	1313.5
AHQ-3-13-, 6801	K.SSLLDDLLTESEDMAQR.R	1924.07698	2	7.96E-05	0.96	5.35	-	974.8
AHQ-3-14-, 6747 - 6748	K.SSLLDDLLTESEDMAQR.R	1924.07698	2	1.51E-04	0.96	4.86	-	1128.5
AHQ-3-6, 4677	K.SVTDSIRDEYAFLQK.K	1772.93666	2	7.79E-06	0.91	3.86	-	1039.5
AHQ-3-6, 7277	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	5.31E-06	0.97	5.28	-	1202.3
gi|4503481|ref|NP_001395.1| eukaryotic translation elongation factor 1 gamma; elongation factor 1-g				2.26E-08	1.83	20.19	6.20	50118.5
AHQ-3-7, 2768	K.ALIAAQYSGAQVR.V	1348.53280	2	2.26E-08	0.93	3.10	-	1678.3
AHQ-3-14, 6137	R.EYFSWEGAFQHVGK.A	1685.81925	2	2.73E-06	0.90	3.56	-	932.8
AHQ-3-12, 4996	R.EYFSWEGAFQHVGK.A	1685.81925	2	3.30E-06	0.85	3.77	-	583.6
gi|4503545|ref|NP_001961.1| eukaryotic translation initiation factor 5A; eIF5AI; eIF5A [Homo sapien				2.48E-08	1.82	20.24	26.00	16832.2
AHQ-3-12, 3960 - 3962	R.EDLRLPEGDLGKEIEQK.Y	1970.17021	2	2.48E-08	0.86	4.32	-	338.7
AHQ-3-12, 6896	R.NDFQLIGIQDGYLSLLQDSGEVR.E	2581.81935	2	1.76E-07	0.96	4.89	-	1196.1
gi|19923483|ref|NP_057406.2| GTPase Rab14 [Homo sapiens]				2.48E-08	5.94	70.23	45.10	23896.8
AHQ-3-10, 4004	R.GAAGALMVYDITR.R	1338.55819	2	1.82E-04	0.92	3.87	-	901.7
AHQ-3-11, 3739	K.IYQNIQDGSLDLNAAESGVQHKPSAPQGGR.L	3152.38123	3	2.93E-05	0.82	3.67	-	596.6
AHQ-3-10, 3604 - 3646	K.IYQNIQDGSLDLNAAESGVQHKPSAPQGGR.L	3152.38123	3	3.78E-04	0.79	3.79	-	399.3
AHQ-3-10, 4606	R.NLTNPNTVIILIGNK.A	1624.90662	2	3.93E-04	0.86	3.30	-	680.0
AHQ-3-11, 4851 - 4854	R.NLTNPNTVIILIGNK.A	1624.90662	2	4.17E-05	0.95	4.57	-	919.4
AHQ-3-11, 3063 - 3064	K.SCLLHQFTEK.K	1264.43272	2	9.24E-06	0.76	2.90	-	664.5
AHQ-3-10, 3931	R.STYNHLSSWLTDAR.N	1651.76121	2	2.95E-04	0.57	2.84	-	295.2
AHQ-3-11, 3916	R.STYNHLSSWLTDAR.N	1651.76121	2	1.08E-04	0.72	2.89	-	678.7
AHQ-3-11, 4352 - 4408	K.TGENVEDAFLEAAK.K	1494.58517	2	1.68E-04	0.62	2.92	-	420.2
AHQ-3-10, 4184 - 4186	K.TGENVEDAFLEAAK.K	1494.58517	2	3.52E-07	0.93	4.27	-	788.4
AHQ-3-10, 4187	K.TGENVEDAFLEAAK.K	1494.58517	1	6.66E-05	0.63	3.22	-	517.9
AHQ-3-10, 3810	K.TGENVEDAFLEAAKK.I	1622.75808	2	6.93E-04	0.80	3.62	-	499.4
AHQ-3-11, 3907	K.TGENVEDAFLEAAKK.I	1622.75808	3	2.48E-08	0.85	3.70	-	976.7
gi|4885063|ref|NP_005156.1| aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase				2.55E-08	1.76	20.29	7.10	39455.6
AHQ-3-8, 4176 - 4245	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.65E-07	0.92	5.47	-	1010.4

AHQ-3-12, 4610	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.53E-07	0.82	4.97	-	466.9
AHQ-3-8, 4093	K.VDKGVVPLAGTDGETTTQGLDGLSER.C	2616.82041	2	2.89E-06	0.93	4.62	-	458.8
AHQ-3-8, 4090	K.VDKGVVPLAGTDGETTTQGLDGLSER.C	2616.82041	3	2.55E-08	0.94	5.73	-	1167.9
gi|4504085|ref|NP_000399.1|	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA			2.58E-08	3.29	40.19	6.50	80814.1
AHQ-3-6, 5574	R.LVQDYGLESEVAQHLAATYGDK.A	2408.60567	3	2.58E-08	0.82	3.11	-	1180.3
AHQ-3-6, 6105	R.VIFFLPWQK.M	1178.44934	2	3.86E-05	0.85	3.07	-	745.2
AHQ-3-6, 6202 - 6281	R.YGAATANYMEVVSLLK.K	1731.00632	2	1.28E-04	0.81	2.83	-	814.1
AHQ-3-6, 5470	R.YGAATANYM*EVVSLLK.K	1747.00572	2	2.05E-04	0.81	3.78	-	445.6
gi|17450333|ref|XP_060887.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			2.59E-08	0.94	10.21	11.00	17503.9
AHQ-3-12, 6418 - 6483	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	2.59E-08	0.94	4.15	-	1105.1
AHQ-3-12, 6638 - 6706	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	1.95E-06	0.93	3.92	-	1190.8
AHQ-3-12, 6643 - 6659	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	3	4.32E-06	0.89	3.49	-	1347.9
AHQ-3-13, 6674	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	1.18E-04	0.88	3.77	-	752.4
AHQ-3-12, 5958	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	5.72E-04	0.44	2.56	-	445.0
gi|4507767|ref|NP_003326.1|	ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi			2.65E-08	2.36	40.21	6.70	111719.5
AHQ-3-4, 7424	R.GLNPDLQVIPLTYPLDPTTEHIYGDNFFSR.V	3434.79811	3	1.68E-05	0.45	3.02	-	232.2
AHQ-3-4, 3358	K.LLDEELYSR.Q	1138.25242	1	1.43E-04	0.17	2.19	-	244.9
AHQ-3-4, 4686 - 4697	R.VLVSGLQGLGAEVAK.N	1441.69805	2	2.65E-08	0.92	4.22	-	931.3
AHQ-3-4, 4061	R.YFPSTAEHTLQWAR.H	1707.86959	2	2.72E-05	0.81	3.28	-	471.6
gi|4506365|ref|NP_002856.1|	RAB2, member RAS oncogene family [Homo sapiens]			2.67E-08	0.96	10.21	6.10	23545.4
AHQ-3-11, 4231	K.LQIWDTAGQESFR.S	1551.68478	2	2.67E-08	0.96	4.25	-	1548.4
gi|4502297|ref|NP_001678.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit			2.72E-08	0.89	10.19	8.30	17489.8
AHQ-3-13-, 2517	K.AQAELVGTADEATR.A	1432.51860	2	2.72E-08	0.89	3.56	-	743.4
AHQ-3-13, 2557	K.AQAELVGTADEATR.A	1432.51860	2	2.79E-07	0.90	3.74	-	832.4
gi|4758304|ref|NP_004902.1|	protein disulfide isomerase related protein (calcium-binding protein, i			2.79E-08	4.34	50.22	9.50	72931.9
AHQ-3-6, 4611	K.DLGLSESGEDVNAAILDESGKK.F	2248.38737	2	3.67E-08	0.92	4.47	-	1105.0
AHQ-3-6, 3730	K.FAM*EPEEFDSDTLR.E	1703.80830	2	2.79E-08	0.86	3.40	-	604.4
AHQ-3-6, 4581	K.FAMEPEEFDSDTLR.E	1687.80890	2	2.52E-07	0.75	2.89	-	602.0
AHQ-3-6, 2761	K.IDATSASVLASR.F	1191.31686	2	1.17E-07	0.95	4.07	-	1574.4
AHQ-3-6, 2738	K.VSQGQLVVMQPEK.F	1443.69431	2	1.96E-07	0.85	3.04	-	1282.5
gi|4758906|ref|NP_004146.1|	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member			2.80E-08	1.80	20.20	8.50	42403.4
AHQ-3-8, 3686	R.AFQSLLTEVNK.A	1250.42590	2	2.80E-08	0.91	3.20	-	1186.5
AHQ-3-8, 4226 - 4232	K.GNTATQMAQALSLNTEEDIHR.A	2301.48023	3	2.28E-04	0.89	3.91	-	1056.4
gi|4557471|ref|NP_001274.1|	adaptor-related protein complex 1, sigma 1 subunit isoform 1; clathrin-			2.88E-08	0.95	10.25	10.10	18732.9
AHQ-3-12, 3575	K.AIEQADLLQEEDESPR.S	1843.92692	2	2.88E-08	0.95	4.93	-	1286.2
gi|4503291|ref|NP_001346.1|	D-dopachrome tautomerase [Homo sapiens]			2.97E-08	1.83	20.20	22.90	12711.7
AHQ-3-14-, 5579 - 5592	R.FFPLESWQIGK.I	1352.56151	2	2.97E-08	0.90	3.10	-	757.7
AHQ-3-14-, 3441	K.RLCAAAASILGKPADR.V	1671.94666	3	6.14E-05	0.93	4.00	-	1698.4
gi|21362062|ref|NP_115744.2|	leucine zipper and CTNNBIP1 domain containing [Homo sapiens]			2.98E-08	0.95	10.21	11.60	21494.4
AHQ-3-11, 6658 - 6703	K.LTADDEAFLSANAGAILSQFEK.V	2312.51789	2	2.98E-08	0.95	4.18	-	1298.9
gi|22042381|ref|XP_065237.3|	similar to FKSG30 [Homo sapiens]			3.14E-08	1.48	20.20	3.50	42016.0
AHQ-3-10, 2247	K.QEYDESGPSIVHR.K	1517.58206	3	8.69E-04	0.81	3.14	-	908.3
AHQ-3-8, 2025 - 2036	K.QEYDESGPSIVHR.K	1517.58206	2	1.06E-06	0.78	3.28	-	361.7
AHQ-3-13-, 2386	K.QEYDESGPSIVHR.K	1517.58206	2	1.18E-07	0.57	3.05	-	271.2
AHQ-3-13, 2438	K.QEYDESGPSIVHR.K	1517.58206	3	2.70E-07	0.72	3.01	-	847.0
AHQ-3-13, 2437 - 2445	K.QEYDESGPSIVHR.K	1517.58206	2	3.14E-08	0.69	2.85	-	349.3
AHQ-3-14-, 2293 - 2315	K.QEYDESGPSIVHR.K	1517.58206	2	4.78E-07	0.77	3.20	-	363.6
AHQ-3-8, 3113 - 3185	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	3.29E-05	0.79	3.68	-	414.4
AHQ-3-8, 3048 - 3117	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	3.98E-04	0.78	3.46	-	465.3
AHQ-3-7, 3531	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	1.57E-04	0.62	3.24	-	257.5
AHQ-3-8, 3253 - 3320	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	6.37E-04	0.74	3.16	-	448.8
gi|5031973|ref|NP_005733.1|	protein disulfide isomerase-related protein [Homo sapiens]			3.29E-08	5.37	60.24	24.50	48121.0
AHQ-3-7, 7398	R.ALDLFSDNAPPPELLEIINEDIAK.R	2638.95072	2	3.29E-08	0.91	4.41	-	585.4
AHQ-3-7, 7242	R.DGELPVEDDIDLSDVELDDLGKDEL	2759.86565	2	3.97E-08	0.91	4.14	-	961.9
AHQ-3-7, 4586 - 4612	K.GSFSEQGINEFLR.E	1484.59520	2	4.93E-05	0.84	3.18	-	694.3
AHQ-3-7, 3792	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	1.06E-05	0.77	2.78	-	883.3
AHQ-3-7, 4640 - 4648	K.LAAVDATVNQVLASR.Y	1528.73579	2	7.58E-07	0.97	4.88	-	1653.2
AHQ-3-7, 6119	R.TGEAIVDAALSALR.Q	1387.56411	2	1.19E-07	0.97	4.82	-	1837.4
gi|22043610|ref|XP_171081.1|	similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1; rh			3.30E-08	4.07	50.24	28.10	21543.1
AHQ-3-11, 2630	R.HHCPNTPIILVGTK.L	1588.85612	2	3.16E-04	0.69	2.62	-	575.9
AHQ-3-11, 3716	K.KLTPITYPQGLAMAK.E	1632.99216	2	8.75E-05	0.71	3.18	-	440.7
AHQ-3-11, 3684 - 3694	K.LTPITYPQGLAM*AK.E	1520.81864	2	2.53E-05	0.85	3.32	-	481.2
AHQ-3-11, 4607 - 4650	K.PVNLGLWDTAGQEDYDR.L	1950.05441	2	3.30E-08	0.97	4.74	-	1809.1
AHQ-3-11, 2866	K.TVFDEAIR.A	951.05843	1	1.40E-04	0.06	1.99	-	120.9
AHQ-3-11, 2858 - 2859	K.TVFDEAIR.A	951.05843	2	1.31E-05	0.86	3.25	-	640.4
gi|29732955|ref|XP_291603.1|	similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA			3.33E-08	0.92	10.21	16.80	11173.0
AHQ-3-9, 3843 - 3912	K.NISNASCTTNCIAPLAK.M	1838.05353	2	3.99E-07	0.83	4.30	-	992.4
AHQ-3-9, 3979 - 4049	K.NISNASCTTNCIAPLAK.M	1838.05353	2	3.33E-08	0.92	3.97	-	1514.1
AHQ-3-11, 4159	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.43E-06	0.60	2.92	-	861.7
AHQ-3-9, 3745 - 3811	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.58E-07	0.76	4.00	-	866.9
gi|4502201|ref|NP_001649.1|	ADP-ribosylation factor 1 [Homo sapiens]			3.34E-08	8.95	100.33	58.60	20696.6
AHQ-3-12, 4648	R.DAVLLVFANK.Q	1090.29726	1	2.86E-05	0.63	3.01	-	512.1
AHQ-3-12, 4616 - 4762	R.DAVLLVFANK.Q	1090.29726	1	8.74E-07	0.87	2.74	-	1057.2
AHQ-3-12, 4780	R.DAVLLVFANK.Q	1090.29726	2	1.21E-05	0.94	3.73	-	1403.3
AHQ-3-11, 4512	R.DAVLLVFANK.Q	1090.29726	1	1.59E-04	0.61	2.50	-	681.6
AHQ-3-12, 4640	R.DAVLLVFANK.Q	1090.29726	2	3.34E-08	0.97	4.04	-	1750.1
AHQ-3-12, 5163	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.18E-07	0.98	5.20	-	1903.8
AHQ-3-12, 4856	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	2.34E-05	0.98	5.26	-	2006.5
AHQ-3-12, 5059 - 5132	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	8.36E-05	0.99	6.53	-	2869.4
AHQ-3-12, 4950	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	2.79E-05	0.97	5.28	-	1473.9
AHQ-3-12, 5244 - 5283	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	3.38E-04	0.98	5.33	-	2355.7
AHQ-3-12, 5499 - 5572	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	2.63E-07	0.95	5.50	-	398.6
AHQ-3-12, 4480 - 4552	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	7.43E-04	0.93	4.60	-	977.4
AHQ-3-12, 5096 - 5176	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	1.44E-04	0.76	3.89	-	503.8
AHQ-3-12, 4874 - 4944	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	1.08E-06	0.92	4.80	-	833.9
AHQ-3-12, 4622 - 4678	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	1.16E-04	0.95	5.29	-	1231.9
AHQ-3-11, 3514	R.ILMVGLDAAGK.T	1088.34632	2	3.56E-04	0.93	3.48	-	1052.5
AHQ-3-12, 3659 - 3723	R.ILMVGLDAAGK.T	1088.34632	2	4.54E-07	0.93	3.71	-	1136.4
AHQ-3-12, 3672	R.ILMVGLDAAGK.T	1088.34632	1	9.65E-06	0.76	3.49	-	428.7
AHQ-3-12, 3098	R.ILM*VGLDAAGK.T	1104.34572	2	8.10E-06	0.96	3.85	-	1692.5
AHQ-3-11, 3011	R.ILM*VGLDAAGK.T	1104.34572	2	2.14E-05	0.94	3.55	-	1455.0
AHQ-3-11, 6179 - 6260	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	3	4.63E-04	0.55	3.13	-	476.6
AHQ-3-12, 6316 - 6387	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	6.37E-06	0.72	3.42	-	231.6
AHQ-3-12, 6570 - 6595	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	8.86E-08	0.55	3.26	-	212.2
AHQ-3-12, 6160	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	5.10E-04	0.20	2.57	-	124.8
AHQ-3-11, 6230 - 6286	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	3.46E-04	0.54	3.15	-	202.9
AHQ-3-12, 6450 - 6510	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	8.66E-07	0.91	4.51	-	388.1
AHQ-3-12, 6395 - 6458	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	3	1.71E-06	0.88	4.26	-	666.7
AHQ-3-11, 6135 - 6194	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	1.70E-04	0.91	4.59	-	359.6
AHQ-3-12, 2102	K.LGLHSLR.H	795.95280	2	4.81E-04	0.86	3.03	-	901.2
AHQ-3-12, 6883	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	3	7.59E-08	0.94	4.40	-	1646.4
AHQ-3-12, 5062 - 5122	K.NISFTVWDVGGQDK.I	1566.69621	2	4.64E-07	0.95	4.77	-	970.2
AHQ-3-14-, 5055	K.NISFTVWDVGGQDK.I	1566.69621	2	4.92E-05	0.72	2.72	-	699.5
AHQ-3-11, 4866	K.NISFTVWDVGGQDK.I	1566.69621	2	5.64E-04	0.90	3.62	-	835.4
AHQ-3-13-, 5090	K.NISFTVWDVGGQDK.I	1566.69621	2	5.87E-08	0.93	4.41	-	831.3
AHQ-3-12, 3731 - 3748	K.QDLPNAMNAAEITDK.L	1631.79001	2	5.00E-06	0.94	4.48	-	918.6
AHQ-3-12, 3650	K.QDLPNAMNAAEITDK.L	1631.79001	2	6.86E-08	0.91	4.06	-	714.9

AHQ-3-11, 3615	K.QDLPNAMNAAEITDK.L	1631.79001	2	8.88E-05	0.41	2.99	-	271.3
AHQ-3-12, 3867 - 3947	K.QDLPNAMNAAEITDK.L	1631.79001	2	3.67E-05	0.91	3.66	-	915.2
gi|9910542|ref|NP_064535.1| SAR1a gene homolog 1; SAR1 protein [Homo sapiens]				3.39E-08	2.53	30.33	33.30	22366.6
AHQ-3-11, 3556	R.EIFGLYGQTTGK.G	1314.46845	1	2.86E-07	0.66	3.29	-	223.9
AHQ-3-11, 6014	R.LGQHVPTLHPTSEELTIAGMTFTTFDLGGHEQAR.R	3694.08659	3	4.19E-08	0.96	6.69	-	713.1
AHQ-3-11, 6726	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	3.39E-08	0.91	4.19	-	699.2
AHQ-3-11, 6344	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	2.04E-05	0.90	4.18	-	644.4
gi|30154095|ref|XP_293967.2| similar to gamma actin-like protein [Homo sapiens]				3.46E-08	1.00	20.20	12.20	19259.0
AHQ-3-8, 4739 - 4807	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.22E-04	0.53	3.32	-	321.9
AHQ-3-8, 4976 - 5012	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	6.37E-06	0.45	2.64	-	475.0
AHQ-3-8, 5759 - 5831	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	1.29E-05	0.12	2.69	-	235.3
AHQ-3-10, 4494	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	8.15E-05	0.53	2.91	-	408.8
AHQ-3-10, 4582 - 4643	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	7.92E-05	0.48	2.81	-	406.8
AHQ-3-10, 4875	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	7.48E-05	0.70	3.31	-	487.6
AHQ-3-13, 4782	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.46E-08	0.87	3.85	-	681.8
AHQ-3-14, 5797 - 5859	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.21E-04	0.44	2.81	-	424.3
AHQ-3-14, 5945 - 5981	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.63E-04	0.33	2.77	-	349.3
AHQ-3-13-, 5085	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.66E-05	0.70	3.07	-	557.3
AHQ-3-14-, 4732	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	9.84E-05	0.51	3.18	-	429.5
AHQ-3-14-, 4828 - 4891	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.66E-05	0.85	3.67	-	616.4
gi|16933567|ref|NP_005361.2| mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]				3.53E-08	0.92	10.21	6.80	23668.1
AHQ-3-11, 5626	K.ANINVENAFFTLAR.D	1580.76926	2	7.52E-05	0.91	3.54	-	817.1
AHQ-3-11, 5848 - 5911	K.ANINVENAFFTLAR.D	1580.76926	2	1.04E-06	0.87	3.36	-	793.4
AHQ-3-11, 4996	K.ANINVENAFFTLAR.D	1580.76926	2	3.53E-08	0.92	4.19	-	928.6
gi|22059949|ref|XP_114617.2| similar to tubulin, beta 5 [Homo sapiens]				3.76E-08	1.89	20.30	18.80	22810.8
AHQ-3-11, 4994 - 5072	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	2.86E-04	0.89	4.52	-	695.8
AHQ-3-14-, 5232 - 5300	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	1.86E-06	0.96	6.08	-	1321.5
AHQ-3-7, 5320	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	1.65E-04	0.94	5.20	-	1031.4
AHQ-3-7, 5407	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	5.51E-04	0.91	4.07	-	1352.9
AHQ-3-13, 2755	R.ISVYYNEATGGK.Y	1302.41453	2	3.93E-04	0.83	3.14	-	700.6
AHQ-3-13-, 2725	R.ISVYYNEATGGK.Y	1302.41453	2	3.28E-05	0.77	2.78	-	667.0
AHQ-3-14-, 2675	R.ISVYYNEATGGK.Y	1302.41453	2	1.28E-06	0.79	2.54	-	767.3
AHQ-3-7, 2451 - 2454	R.ISVYYNEATGGK.Y	1302.41453	2	3.76E-08	0.92	3.57	-	920.4
AHQ-3-7, 2462	R.ISVYYNEATGGK.Y	1302.41453	1	6.40E-04	0.57	2.85	-	415.7
gi|4505813|ref|NP_003737.1| cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain				3.90E-08	2.34	30.18	49.40	10365.8
AHQ-3-14, 4940	K.NADMSEEM*QQDSVECATQALEK.Y	2532.67934	2	1.41E-05	0.74	3.54	-	653.1
AHQ-3-14-, 2267	R.NFGSYVTHETK.H	1283.37131	2	3.90E-08	0.87	3.36	-	721.9
AHQ-3-13-, 3485	K.YNPTWHCIVGR.N	1404.57820	2	1.58E-07	0.74	2.64	-	509.4
AHQ-3-14-, 3511	K.YNPTWHCIVGR.N	1404.57820	2	1.08E-06	0.80	3.12	-	372.0
AHQ-3-14, 4472	K.YNPTWHCIVGR.N	1404.57820	2	1.07E-05	0.74	2.54	-	596.0
gi|21361478|ref|NP_055944.2| septin 6 isoform B; septin 2 [Homo sapiens]				3.97E-08	3.86	50.26	18.20	49716.3
AHQ-3-7, 3782	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L	3147.31508	3	3.97E-08	0.93	5.30	-	1133.2
AHQ-3-7, 2719	R.KTAAELLQSQGSQAGGSQTLK.R	2104.30776	2	1.39E-04	0.89	4.01	-	594.0
AHQ-3-7, 3450	K.SLDDEVNAFK.Q	1138.20928	1	9.53E-07	0.14	1.85	-	356.8
AHQ-3-7, 2900	K.TAAELLQSQGSQAGGSQTLK.R	1976.13485	2	1.46E-04	0.96	4.95	-	1177.5
AHQ-3-7, 4886	R.TVPLAGHVGFDSLPDQLVNK.S	2108.38284	2	5.50E-05	0.93	4.52	-	829.7
gi|7705827|ref|NP_057187.1| GTP-binding protein Sara [Homo sapiens]				4.04E-08	0.70	10.19	5.60	22409.7
AHQ-3-11, 4094	K.LVFLGLDNAGK.T	1147.34882	1	5.65E-05	0.85	2.66	-	1140.2
AHQ-3-11, 4095	K.LVFLGLDNAGK.T	1147.34882	1	4.04E-08	0.70	2.98	-	356.2
AHQ-3-11, 4360	K.LVFLGLDNAGK.T	1147.34882	2	1.72E-05	0.95	3.75	-	1479.2
AHQ-3-11, 4090 - 4107	K.LVFLGLDNAGK.T	1147.34882	2	1.69E-06	0.94	3.70	-	1263.0
gi|13129150|ref|NP_005339.1| heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H				4.06E-08	2.82	40.26	6.10	84659.1
AHQ-3-5, 2767	K.ELHINLIPNKQDR.T	1590.80882	2	3.31E-06	0.43	2.59	-	385.2
AHQ-3-5, 2187 - 2260	K.FYEQFSK.N	949.04099	1	2.50E-04	0.58	2.33	-	446.2
AHQ-3-5, 4027	R.NPDDITNEEYGEFYK.S	1834.87381	2	4.06E-08	0.97	5.11	-	1443.8
AHQ-3-6, 3974	R.NPDDITNEEYGEFYK.S	1834.87381	2	6.31E-05	0.90	4.22	-	1005.2
AHQ-3-5, 3808	R.RAPFDLFENR.K	1265.40235	2	3.57E-07	0.84	3.66	-	521.8
gi|20149594|ref|NP_031381.2| heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea				4.70E-08	5.12	60.23	10.20	83263.6
AHQ-3-5, 2352	K.EDQTEYLEER.R	1312.32145	2	1.03E-04	0.66	2.96	-	449.5
AHQ-3-5, 2985 - 2988	R.ELISNASDALDK.I	1276.37539	2	6.33E-05	0.91	3.29	-	1029.1
AHQ-3-5, 5439	K.HSQFIGYPITLYLEK.E	1810.08487	2	4.41E-06	0.96	4.56	-	1115.2
AHQ-3-5, 4117	R.NPDDITQEEYGEFYK.S	1848.90048	2	4.70E-08	0.87	3.63	-	711.2
AHQ-3-5, 3487	R.TLTLVDTGIGM*TK.A	1366.60658	2	1.00E-05	0.91	2.99	-	1190.9
AHQ-3-5, 2033	K.YIDQEELNK.T	1152.23595	2	2.15E-04	0.80	3.16	-	669.7
gi|19923457|ref|NP_057447.2| glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M				4.73E-08	0.96	10.26	3.20	67308.6
AHQ-3-7, 5390	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	2	6.71E-05	0.92	4.41	-	775.7
AHQ-3-7, 5379	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	4.73E-08	0.96	5.30	-	1732.9
gi|28269681|ref|NP_783313.1| NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]				4.98E-08	1.59	20.22	27.00	14852.0
AHQ-3-13, 6577 - 6586	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	1.87E-04	0.94	4.33	-	1500.8
AHQ-3-13-, 4918 - 4989	R.VTLNPPGTFLEGVAK.V	1543.78883	2	4.98E-08	0.65	3.13	-	280.3
AHQ-3-13, 4923 - 4945	R.VTLNPPGTFLEGVAK.V	1543.78883	2	1.03E-05	0.84	3.56	-	475.2
gi|21614499|ref|NP_003370.2| villin 2; Villin-2; cytovillin [Homo sapiens]				5.06E-08	1.57	20.23	1.90	69412.3
AHQ-3-6, 4165	K.APDFVFYAPR.L	1183.33971	2	3.97E-06	0.97	4.57	-	1317.4
AHQ-3-6, 3457 - 3467	K.KAPDFVFYAPR.L	1311.51262	2	5.06E-08	0.60	2.97	-	396.9
gi|21361657|ref|NP_005304.3| glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom				5.19E-08	8.49	110.36	26.10	56782.0
AHQ-3-7, 1752	R.EATNPPVIQEEKPK.K	1580.76433	2	1.01E-04	0.75	3.18	-	522.5
AHQ-3-7, 5796 - 5806	R.ELSDFISYLQR.E	1371.52000	2	8.10E-06	0.96	4.27	-	1319.2
AHQ-3-7, 4759 - 4764	K.FIQENIFGICPHM*TEDNKDLIQGK.D	2866.21892	3	3.24E-04	0.33	3.04	-	274.9
AHQ-3-7, 4608	R.FLQDYFDGNLK.R	1360.49568	1	7.35E-06	0.29	2.32	-	426.9
AHQ-3-7, 4528 - 4606	R.FLQDYFDGNLK.R	1360.49568	2	3.60E-04	0.94	3.36	-	1505.6
AHQ-3-7, 3910	R.FLQDYFDGNLKR.Y	1516.68203	2	1.92E-04	0.87	3.85	-	792.3
AHQ-3-7, 4352	R.GFPTIYFSPANK.K	1342.52349	1	5.69E-07	0.84	3.66	-	529.8
AHQ-3-7, 5602 - 5607	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	2	3.03E-05	0.93	4.18	-	780.0
AHQ-3-7, 2366	K.LNFAVASR.K	878.01067	2	6.44E-05	0.86	3.14	-	918.3
AHQ-3-7, 1964 - 1976	K.LSKDPNIVIAK.M	1198.43727	2	3.08E-06	0.89	2.98	-	1034.4
AHQ-3-7, 3271 - 3342	K.MDATANDVPSPYEVR.G	1665.80646	2	2.76E-07	0.79	3.44	-	484.8
AHQ-3-7, 6218 - 6235	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	3	9.67E-07	0.90	4.08	-	1095.5
AHQ-3-7, 6147 - 6223	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	2	5.19E-08	0.98	7.29	-	1502.7
gi|18570595|ref|XP_095590.1| similar to myosin regulatory light chain [Homo sapiens]				5.24E-08	0.94	10.20	8.90	13951.5
AHQ-3-11, 3008 - 3086	K.LNGTDPEDVIR.H	1229.32195	2	3.49E-04	0.87	3.42	-	790.6
AHQ-3-11, 3136	K.LNGTDPEDVIR.H	1229.32195	2	1.08E-04	0.83	3.11	-	865.6
AHQ-3-12, 2992	K.LNGTDPEDVIR.H	1229.32195	2	1.76E-04	0.90	3.10	-	1114.6
AHQ-3-12, 3188	K.LNGTDPEDVIR.H	1229.32195	2	1.10E-04	0.92	3.56	-	1090.8
AHQ-3-11, 2910 - 2918	K.LNGTDPEDVIR.H	1229.32195	2	5.24E-08	0.94	4.02	-	1127.4
gi|20357529|ref|NP_005264.2| guanine nucleotide-binding protein, beta-2 subunit; G protein, beta-2				5.51E-08	0.94	10.23	5.90	37330.8
AHQ-3-9, 4583 - 4585	R.KACGDSTLTQITAGLDPVGR.I	2062.29094	2	5.51E-08	0.94	4.60	-	868.6
gi|4507745|ref|NP_003320.1| thioredoxin [Homo sapiens]				5.72E-08	1.90	20.20	22.90	11693.3
AHQ-3-14-, 4620 - 4633	K.EKLEATINELV	1259.43110	2	5.30E-04	0.95	3.71	-	1481.9
AHQ-3-14, 4731	K.TAFQEALDAAGDK.L	1337.41728	2	1.99E-05	0.86	3.03	-	1060.2
AHQ-3-13-, 3850 - 3873	K.TAFQEALDAAGDK.L	1337.41728	2	5.72E-08	0.95	3.97	-	1468.7
AHQ-3-14-, 3748 - 3759	K.TAFQEALDAAGDK.L	1337.41728	2	9.82E-06	0.93	3.62	-	1516.7
AHQ-3-13, 3841 - 3842	K.TAFQEALDAAGDK.L	1337.41728	1	4.06E-04	0.44	2.23	-	812.5
AHQ-3-13, 3837	K.TAFQEALDAAGDK.L	1337.41728	2	8.23E-04	0.87	3.17	-	1303.6
gi|4758638|ref|NP_004896.1| peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi				5.79E-08	6.62	90.32	48.20	25034.8
AHQ-3-10, 3990	K.DGDSVM*VLPTIPEEEAK.K	1847.03409	2	2.98E-05	0.56	2.83	-	473.0
AHQ-3-10, 5327	K.DINAYNCEEPTEKLPFPIIDDR.N	2651.88650	2	5.79E-08	0.33	2.81	-	376.5
AHQ-3-10, 5670	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	5.56E-06	0.91	3.81	-	943.0

AHQ-3-10, 5584 - 5646	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	1.82E-04	0.87	3.80	-	769.3
AHQ-3-10, 5883	R.FHDFLGDSWGILFSHPR.D	2032.24831	2	1.04E-07	0.98	6.30	-	2215.5
AHQ-3-14-, 5899	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	1.44E-04	0.63	3.49	-	380.2
AHQ-3-10, 5487 - 5542	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	8.81E-05	0.96	4.87	-	1175.2
AHQ-3-10, 4140	K.LPFPIIDDR.N	1086.26548	2	1.03E-05	0.93	3.22	-	1185.3
AHQ-3-10, 5151	R.VATPVDWKDGDSVMVLPTIPEEEAK.K	2728.06777	2	1.33E-06	0.82	3.96	-	545.5
AHQ-3-10, 3495	R.VVFVFGPDK.K	1008.19471	1	7.85E-05	0.46	1.81	-	883.3
AHQ-3-10, 2763	R.VVFVFGPDKK.L	1136.36763	1	2.53E-04	0.67	2.89	-	744.9
gi|22027655|ref|NP_003907.3| adaptor-related protein complex 1 sigma 2 subunit; clathrin adaptor co				6.30E-08	0.97	10.27	10.20	18614.6
AHQ-3-12, 3927 - 3928	K.AIEQADLLQEEAETPR.S	1813.94395	2	6.30E-08	0.97	5.42	-	1431.4
gi|4758460|ref|NP_004479.1| glycoprotein V (platelet) [Homo sapiens]				6.39E-08	1.74	20.26	9.80	60958.9
AHQ-3-5, 5515 - 5523	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	6.39E-08	0.79	4.10	-	687.9
AHQ-3-1, 5858	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	1.91E-04	0.87	4.25	-	823.0
AHQ-3-6, 7410	K.LVNLQELALNQNQLDFLPASLFTNLENLK.L	3314.77659	3	2.01E-07	0.95	5.24	-	1125.0
gi|4557697|ref|NP_000412.1| keratin 10; Keratin-10 [Homo sapiens]				6.44E-08	2.45	30.25	8.60	57247.1
AHQ-3-14-, 2661	R.ALEESNYELEGK.I	1382.45482	2	1.06E-04	0.72	3.02	-	577.0
AHQ-3-1, 5698	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	6.44E-08	0.78	3.34	-	705.9
AHQ-3-13-, 4123	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.12E-07	0.95	4.91	-	990.1
gi|5453605|ref|NP_006421.1| chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-				6.79E-08	0.89	10.16	2.40	57838.8
AHQ-3-7, 3379 - 3380	K.VIDPATATSVDLR.D	1358.52277	2	6.79E-08	0.89	3.27	-	1106.2
gi|4503643|ref|NP_000121.1| coagulation factor V precursor; labile factor; factor V Leiden [Homo sa				6.95E-08	3.53	40.23	2.10	251716.5
AHQ-3-1, 3641	R.ETDIEDSDDIPEDTTYK.K	1986.97539	2	1.01E-05	0.84	3.80	-	445.4
AHQ-3-5, 2873	R.ETDIEDSDDIPEDTTYKK.V	2115.14831	2	1.82E-07	0.80	3.55	-	564.5
AHQ-3-6, 2863	K.EVIITGIQTQGAK.H	1358.56590	2	6.95E-08	0.94	4.03	-	982.9
AHQ-3-3, 3713 - 3722	K.LSEGASYLDHTFPAEK.M	1765.90099	2	3.23E-07	0.94	4.67	-	1139.1
gi|5032041|ref|NP_005605.1| Ras homolog enriched in brain 2 [Homo sapiens]				7.14E-08	0.78	10.23	8.70	20497.4
AHQ-3-12, 5199	K.ALAESWNAAFLESSAK.E	1695.85389	2	7.14E-08	0.78	3.41	-	367.6
AHQ-3-12, 4974 - 4983	K.ALAESWNAAFLESSAK.E	1695.85389	2	1.38E-05	0.95	4.62	-	1079.3
gi|4757768|ref|NP_004300.1| Rho GDP dissociation inhibitor (GDI) alpha [Homo sapiens]				7.26E-08	2.68	30.24	15.70	23206.9
AHQ-3-11, 4447 - 4451	R.AEEYEFLTPVEEAPK.G	1752.89898	2	1.46E-04	0.89	3.51	-	972.9
AHQ-3-10, 4156 - 4234	R.AEEYEFLTPVEEAPK.G	1752.89898	2	1.89E-06	0.92	3.93	-	862.6
AHQ-3-12, 4634	R.AEEYEFLTPVEEAPK.G	1752.89898	2	1.55E-06	0.81	2.89	-	798.0
AHQ-3-10, 3562 - 3563	K.SIQEIQELDKDDESLR.K	1919.03693	2	7.26E-08	0.95	4.85	-	1018.4
AHQ-3-10, 3134	K.SIQEIQELDKDDESLRK.Y	2047.20984	2	2.00E-05	0.92	4.61	-	883.9
gi|19923437|ref|NP_057366.2| adenylate kinase 3 alpha like [Homo sapiens]				7.60E-08	0.97	10.21	6.20	25565.2
AHQ-3-10, 6092	K.NLTQYSWLLDGFPR.T	1710.91339	2	7.60E-08	0.97	4.27	-	1954.0
gi|5453597|ref|NP_006126.1| F-actin capping protein alpha-1 subunit; Cap Z [Homo sapiens]				8.03E-08	1.86	30.19	16.10	32922.5
AHQ-3-13-, 2821	K.DVQDSLTVSNEAQTAK.E	1706.79025	2	3.78E-05	0.92	3.78	-	1015.5
AHQ-3-9, 4109	R.LLLNNDNLLR.E	1198.39736	1	2.89E-04	0.30	2.31	-	302.8
AHQ-3-9, 5165 - 5169	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	2.88E-04	0.30	2.83	-	219.5
AHQ-3-9, 5069 - 5075	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	8.03E-08	0.65	3.34	-	269.1
gi|30147857|ref|XP_293007.2| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				8.15E-08	0.34	10.14	5.90	20789.8
AHQ-3-13-, 3353	K.KITIADCGQLQ	1248.43160	2	2.64E-06	0.75	2.88	-	830.3
AHQ-3-12, 3278 - 3342	K.KITIADCGQLQ	1248.43160	1	8.15E-08	0.34	2.24	-	472.7
gi|4506063|ref|NP_002725.1| protein kinase, cAMP-dependent, regulatory, type I, alpha; tissue-speci				8.16E-08	1.82	20.20	7.60	42981.4
AHQ-3-7, 5060 - 5072	R.LTVADALEPVQFEDGQK.I	1861.04222	2	6.51E-06	0.88	3.89	-	502.5
AHQ-3-7, 2779 - 2858	K.NVLFSHLDDNER.S	1459.54574	2	8.16E-08	0.94	3.36	-	1486.8
gi|8923579|ref|NP_060377.1| hypothetical protein FLJ20625 [Homo sapiens]				8.40E-08	3.57	40.31	34.80	17744.7
AHQ-3-14-, 5989 - 6055	K.KLPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3411.89550	3	5.74E-05	0.94	5.09	-	1136.9
AHQ-3-14, 5017	R.LAVLSSSLTHWK.K	1342.56817	2	2.33E-05	0.76	2.96	-	554.2
AHQ-3-12, 6371	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	1.32E-04	0.94	5.09	-	869.8
AHQ-3-14-, 6277 - 6283	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	1.69E-04	0.96	6.10	-	1219.1
AHQ-3-12, 5375	R.TDEQALLSSILAK.T	1389.57677	2	8.40E-08	0.93	3.96	-	1077.1
gi|24234688|ref|NP_004125.3| heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre				8.86E-08	0.95	10.20	1.80	73680.1
AHQ-3-6, 5585	R.AQFEGIVTDLIR.R	1362.55625	2	8.86E-08	0.95	4.00	-	1874.4
gi|4502211|ref|NP_001654.1| ADP-ribosylation factor 6 [Homo sapiens]				8.89E-08	2.69	30.23	28.00	20082.0
AHQ-3-12, 4030	K.FNVWDVGGQDK.I	1265.35598	2	5.15E-07	0.85	3.28	-	921.4
AHQ-3-12, 3682	R.ILM*LGLDAAGK.T	1118.37239	2	4.98E-04	0.91	3.08	-	1381.9
AHQ-3-12, 6930	R.NWYVQPSCATSGDGLYEGLTWLTSNYK.S	3113.35876	3	8.89E-08	0.93	4.50	-	1128.7
gi|4507231|ref|NP_003134.1| single-stranded DNA binding protein; single-stranded DNA-binding protei				9.82E-08	3.23	40.23	37.84	17259.5
AHQ-3-13, 2487	R.DVAYQYVK.K	986.10277	1	2.56E-04	0.63	2.06	-	822.7
AHQ-3-13, 6009 - 6027	K.NPVTIFSLATNEM*WR.S	1796.04007	2	3.15E-07	0.92	4.26	-	747.9
AHQ-3-13-, 6098	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	3.85E-05	0.72	3.34	-	613.5
AHQ-3-13-, 3194	R.SGDSEVYQLGDVSQK.T	1612.67692	2	9.82E-08	0.95	4.67	-	1224.4
AHQ-3-13, 3193	R.SGDSEVYQLGDVSQK.T	1612.67692	2	3.68E-07	0.92	4.19	-	843.9
gi|30150022|ref|XP_300862.1| similar to beta-tubulin 4Q [Homo sapiens]				9.87E-08	3.72	40.30	11.59	33545.2
AHQ-3-7, 3028 - 3106	R.FPGQLNADLR.K	1131.26634	2	7.93E-06	0.88	3.25	-	796.5
AHQ-3-7, 3246	R.FPGQLNADLR.K	1131.26634	2	9.87E-08	0.93	3.13	-	1215.2
AHQ-3-7, 3351	R.FPGQLNADLR.K	1131.26634	2	2.75E-07	0.92	3.02	-	1043.5
AHQ-3-9, 2939	R.FPGQLNADLR.K	1131.26634	2	1.92E-05	0.80	3.16	-	593.1
AHQ-3-11, 3220	R.FPGQLNADLR.K	1131.26634	2	1.09E-05	0.74	2.63	-	667.7
AHQ-3-7, 3491	R.KLAVNMVPFPR.L	1272.58771	2	3.26E-06	0.93	3.60	-	1194.4
AHQ-3-8, 3924	K.LAVNMVPFPR.L	1144.41480	2	6.28E-05	0.92	3.36	-	907.1
AHQ-3-9, 3995	K.LAVNMVPFPR.L	1144.41480	2	1.73E-04	0.92	3.21	-	938.1
AHQ-3-7, 4431	K.LAVNMVPFPR.L	1144.41480	1	3.31E-07	0.23	2.17	-	245.6
AHQ-3-7, 4163 - 4191	K.LAVNMVPFPR.L	1144.41480	2	1.39E-07	0.93	3.86	-	851.0
AHQ-3-14-, 4411	K.LAVNMVPFPR.L	1144.41480	2	2.83E-04	0.91	3.33	-	964.2
AHQ-3-9, 5199	R.LHFFMPGFAPLTSR.G	1621.92962	2	5.00E-07	0.92	4.07	-	744.0
gi|10835189|ref|NP_000628.1| glutathione reductase [Homo sapiens]				1.08E-07	1.80	20.25	8.14	51700.3
AHQ-3-7, 4618	K.ADFDNTVAIHPTSSEELVTLR	2316.50977	2	1.08E-07	0.84	4.25	-	412.0
AHQ-3-7, 2276	R.GHAAFTSDPKPTIEVSGK.K	1843.03012	2	1.03E-04	0.96	5.07	-	729.7
gi|29729616|ref|XP_292963.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				1.08E-07	1.67	20.30	16.36	18025.4
AHQ-3-12, 4832 - 4911	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	3.69E-05	0.94	5.48	-	844.5
AHQ-3-12, 4926 - 4988	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	9.36E-05	0.95	5.06	-	1337.1
AHQ-3-12, 4975 - 5038	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	4.17E-04	0.81	3.31	-	598.1
AHQ-3-12, 5490 - 5554	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	7.74E-05	0.92	4.75	-	633.0
AHQ-3-12, 5618	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	1.08E-07	0.91	4.73	-	730.6
AHQ-3-13, 4874	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	2.55E-04	0.92	4.45	-	1066.6
AHQ-3-13, 4889	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	3.43E-05	0.75	3.33	-	432.8
AHQ-3-13-, 4869	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	3.11E-04	0.55	2.82	-	309.9
AHQ-3-13-, 5485	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	1.45E-07	0.96	6.03	-	1522.3
gi|5901944|ref|NP_008977.1| elastin microfibril interface located protein; TNF? elastin microfibril				1.15E-07	4.38	50.26	10.04	106694.7
AHQ-3-3, 3560	R.APAPASAPPGPSEELLR.Q	1660.85268	2	9.20E-05	0.78	3.14	-	377.2
AHQ-3-4, 2984	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	1.94E-05	0.89	4.05	-	821.8
AHQ-3-3, 3032	R.GTELGGAAGQGGHPPGYTSLASR.L	2142.27464	2	2.30E-04	0.81	3.78	-	352.4
AHQ-3-3, 2773	R.LVGSGLHTVEAAGEAR.Q	1567.72888	2	1.15E-07	0.96	4.29	-	1270.3
AHQ-3-3, 3720	R.PARPNLSGSSAGSPLSGLGGEGPGESEK.V	2596.74928	3	1.55E-06	0.94	5.13	-	1108.2
gi|4507651|ref|NP_003281.1| tropomyosin 4 [Homo sapiens]				1.17E-07	6.38	70.26	25.40	28521.6
AHQ-3-9, 1709	K.AEGDVAALNR.R	1016.09051	2	2.05E-06	0.94	2.59	-	2132.1
AHQ-3-9, 3669 - 3735	R.AEVSELKCGDLEEELK.N	1851.02256	2	5.90E-04	0.82	3.48	-	818.8
AHQ-3-9, 5653	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	1.30E-06	0.95	4.90	-	1608.9
AHQ-3-9, 1581 - 1608	R.EKAEGDVAALNR.R	1273.37796	2	1.77E-04	0.78	2.85	-	820.3
AHQ-3-9, 2335	K.IQALQQQADEAEDR.A	1615.68404	2	1.17E-07	0.97	4.56	-	1736.0
AHQ-3-11, 2474	K.IQALQQQADEAEDR.A	1615.68404	2	8.58E-06	0.93	3.49	-	1331.0
AHQ-3-10, 2255	R.KIQALQQQADEAEDR.A	1743.85695	2	1.03E-06	0.97	5.25	-	1904.2
AHQ-3-9, 1895	K.YSEKEDKYEEEIK.L	1690.78605	2	1.32E-07	0.94	4.64	-	1044.3
gi|5901922|ref|NP_008996.1| CDC37 homolog [Homo sapiens]				1.17E-07	0.95	10.26	5.56	44468.0

AHQ-3-7, 6712	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	1.17E-07	0.95	5.24	-	613.8
gi|7657176|ref|NP_055070.1|	transmembrane protein 4 [Homo sapiens]			1.25E-07	0.61	10.20	8.79	20652.1
AHQ-3-11, 3488	R.INPDGSQSVVEVPYAR.S	1731.88777	2	1.25E-07	0.61	3.03	-	348.5
gi|4503725|ref|NP_000792.1|	FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei			1.28E-07	2.78	30.22	29.63	11950.6
AHQ-3-13-, 2962	R.GWEEGVAQM*SVGQR.A	1550.67866	2	8.79E-06	0.94	4.10	-	943.9
AHQ-3-14-, 3805 - 3811	R.GWEEGVAQMSVGQR.A	1534.67926	2	9.24E-06	0.83	3.08	-	1121.3
AHQ-3-14-, 2911	R.GWEEGVAQM*SVGQR.A	1550.67866	2	1.54E-06	0.90	3.35	-	965.8
AHQ-3-14, 4741	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.28E-07	0.94	3.89	-	1283.3
AHQ-3-13-, 2983	K.RGQTCVVHYTGMLEDGKK.F	2081.36259	3	6.77E-06	0.95	3.99	-	1768.8
gi|6912494|ref|NP_036457.1|	microtubule-associated protein, RP/EB family, member 1; ADENOMATOUS POL			1.31E-07	3.32	40.28	21.64	29998.9
AHQ-3-12, 3950	K.FFDANYDGKDYDPVAAR.Q	1965.06754	2	1.50E-06	0.92	4.49	-	651.8
AHQ-3-12, 6542	K.FQDNFEFVQWFK.K	1635.80184	2	1.31E-07	0.95	4.40	-	960.3
AHQ-3-12, 2586	K.LEHEYIQNFK.I	1321.46268	2	8.06E-06	0.48	2.65	-	575.2
AHQ-3-13-, 4439	R.NIELICQENEGENDPVLQR.I	2272.43545	2	5.19E-05	0.98	5.70	-	1720.5
AHQ-3-13-, 4555	R.NIELICQENEGENDPVLQR.I	2272.43545	2	1.94E-06	0.97	5.55	-	1608.7
AHQ-3-13, 4565	R.NIELICQENEGENDPVLQR.I	2272.43545	2	1.62E-05	0.93	4.68	-	824.3
gi|4758950|ref|NP_000933.1|	peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]			1.31E-07	7.55	90.22	40.74	23742.4
AHQ-3-11, 4039	K.DFMIQGGDFTR.G	1287.42660	2	2.42E-07	0.93	3.42	-	1305.0
AHQ-3-12, 4179 - 4180	K.DFMIQGGDFTR.G	1287.42660	2	6.72E-06	0.88	3.45	-	1009.9
AHQ-3-11, 2790	R.DKPLKDVIIADCGK.I	1573.83653	3	1.45E-06	0.89	4.31	-	976.0
AHQ-3-11, 2751 - 2819	R.DKPLKDVIIADCGK.I	1573.83653	2	1.23E-04	0.91	3.47	-	982.1
AHQ-3-12, 2894	R.DKPLKDVIIADCGK.I	1573.83653	2	1.31E-07	0.96	3.53	-	1801.7
AHQ-3-11, 4108	K.DTNGSQFFITTVK.T	1458.59766	2	2.90E-05	0.96	3.82	-	1895.5
AHQ-3-11, 4191 - 4238	K.DTNGSQFFITTVK.T	1458.59766	2	1.98E-06	0.94	4.06	-	1350.5
AHQ-3-12, 4382	K.DTNGSQFFITTVK.T	1458.59766	1	3.38E-04	0.18	2.08	-	291.0
AHQ-3-12, 4352	K.DTNGSQFFITTVK.T	1458.59766	2	1.34E-07	0.94	3.67	-	1279.5
AHQ-3-11, 4150 - 4220	K.DTNGSQFFITTVK.T	1458.59766	1	4.10E-06	0.28	2.42	-	324.4
AHQ-3-11, 2328	K.DVIIADCGK.I	992.12891	1	8.34E-07	0.37	1.95	-	496.7
AHQ-3-12, 2403	K.DVIIADCGK.I	992.12891	1	7.01E-05	0.73	2.20	-	826.1
AHQ-3-12, 2950 - 3030	K.HYGPGWVSMANAGK.D	1475.65664	2	3.46E-04	0.80	2.96	-	857.0
AHQ-3-12, 3074	K.IEVEKPFAIAK.E	1245.49240	2	2.00E-05	0.88	3.52	-	906.1
AHQ-3-12, 4346 - 4351	K.TVDNFVALATGEK.G	1365.51377	2	4.87E-07	0.92	4.22	-	798.2
AHQ-3-14-, 4320	K.TVDNFVALATGEK.G	1365.51377	2	2.25E-04	0.92	3.80	-	1025.1
AHQ-3-11, 4172	K.TVDNFVALATGEK.G	1365.51377	1	1.87E-04	0.33	2.56	-	259.2
AHQ-3-12, 3707	R.VIKDFM*IQGGDFTR.G	1643.88873	2	2.62E-05	0.87	3.72	-	783.6
AHQ-3-12, 2978 - 3016	K.VLEGMEVVR.K	1032.23962	2	2.42E-06	0.88	2.83	-	874.9
gi|4504073|ref|NP_000398.1|	glycoprotein Ib beta polypeptide precursor [Homo sapiens]			1.36E-07	2.08	30.18	10.68	21717.6
AHQ-3-10, 4218	R.LLPYLAEDELR.A	1332.52691	1	1.13E-04	0.51	2.58	-	540.8
AHQ-3-1, 4966	R.LLPYLAEDELR.A	1332.52691	2	6.39E-05	0.88	2.94	-	585.1
AHQ-3-4, 4840	R.LLPYLAEDELR.A	1332.52691	2	4.04E-06	0.67	2.60	-	486.8
AHQ-3-6, 4559	R.LLPYLAEDELR.A	1332.52691	2	9.83E-07	0.90	3.14	-	969.7
AHQ-3-7, 4443	R.LLPYLAEDELR.A	1332.52691	2	5.02E-07	0.79	3.03	-	380.7
AHQ-3-10, 4214 - 4244	R.LLPYLAEDELR.A	1332.52691	2	1.96E-07	0.81	2.69	-	654.9
AHQ-3-13-, 4635 - 4642	R.LLPYLAEDELR.A	1332.52691	2	8.07E-06	0.91	3.43	-	762.2
AHQ-3-13, 4638	R.LLPYLAEDELR.A	1332.52691	2	2.86E-06	0.76	2.74	-	449.7
AHQ-3-11, 4403 - 4430	R.LLPYLAEDELR.A	1332.52691	2	1.01E-04	0.87	3.33	-	568.0
AHQ-3-1, 4598	R.LSLTDPLVAER.A	1214.39356	2	9.62E-06	0.96	3.48	-	1695.4
AHQ-3-11, 4082	R.LSLTDPLVAER.A	1214.39356	2	1.36E-07	0.95	3.65	-	1426.2
AHQ-3-11, 2174	R.TAHLGANPWR.C	1123.24913	1	3.16E-04	0.31	2.15	-	292.0
gi|15306356|ref|XP_035638.2|	similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan			1.40E-07	2.67	30.20	20.81	18795.1
AHQ-3-13, 3447 - 3451	R.ESDVPLKTEEFEVTK.T	1751.91253	2	5.82E-05	0.92	3.96	-	623.0
AHQ-3-13-, 3445	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.40E-07	0.84	3.39	-	498.8
AHQ-3-12, 3458	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.55E-04	0.91	3.59	-	740.8
AHQ-3-13-, 2794	R.GAEIEYAM*AYSK.A	1349.49144	2	1.11E-05	0.93	3.78	-	1239.3
AHQ-3-13-, 4605	K.SYLYFTQFK.A	1197.36315	2	3.89E-04	0.81	2.53	-	1054.9
AHQ-3-13, 4586	K.SYLYFTQFK.A	1197.36315	2	3.56E-05	0.90	2.77	-	1216.4
gi|18104998|ref|NP_001119.2|	adaptor-related protein complex 1, gamma 1 subunit; gamma adaptin; cla			1.57E-07	0.97	10.32	3.27	91679.3
AHQ-3-13-, 6802	K.TFQLQLLSPSSSIVPAFNTGTITQVIK.V	2892.33903	3	1.57E-07	0.97	6.36	-	1838.7
AHQ-3-13, 6887	K.TFQLQLLSPSSSIVPAFNTGTITQVIK.V	2892.33903	3	7.09E-05	0.94	4.99	-	1482.3
gi|21389549|ref|NP_653263.1|	hypothetical protein MGC26605 [Homo sapiens]			1.58E-07	1.81	20.23	14.88	26927.8
AHQ-3-10, 5152	R.AITVFSPDGHLFQVEYAQEAVK.K	2450.73052	2	1.58E-07	0.93	4.51	-	801.8
AHQ-3-10, 4316 - 4323	K.LTVEDPVTVEYITR.F	1635.83990	2	4.01E-04	0.88	3.52	-	728.5
gi|4507171|ref|NP_003109.1|	secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec			1.59E-07	1.60	20.20	4.62	34632.0
AHQ-3-8, 2290	K.RLEAGDHPVELLAR.D	1576.78214	3	1.00E-05	0.92	3.38	-	1521.5
AHQ-3-9, 6203 - 6241	K.YIPPCLDSELTEFPLR.M	1952.21655	2	1.59E-07	0.69	3.20	-	183.7
gi|4507143|ref|NP_003786.1|	sorting nexin 3 isoform a; sorting nexin 3A [Homo sapiens]			1.59E-07	1.86	20.20	16.67	18762.2
AHQ-3-12, 5064	R.CLHMFLQDEIIDK.S	1663.94004	2	1.59E-07	0.93	4.07	-	1104.5
AHQ-3-12, 5022 - 5040	R.GDDGIFDDNFIEER.K	1642.66158	2	3.65E-07	0.94	3.88	-	894.4
gi|19923993|ref|NP_612469.1|	chemokine-like factor super family 5 [Homo sapiens]			1.62E-07	0.91	10.22	12.18	17444.2
AHQ-3-12, 4908 - 4971	R.DRHPEEGVVAELQGFAVDK.A	2097.27378	2	1.62E-07	0.91	4.33	-	759.2
gi|4557801|ref|NP_000261.1|	purine nucleoside phosphorylase [Homo sapiens]			1.65E-07	2.57	30.36	19.72	32147.7
AHQ-3-13, 7001	K.LEQFVSILMASIPLPDK.A	1902.28716	2	9.97E-04	0.86	3.87	-	551.6
AHQ-3-11, 4740	K.LGADAVGMSTVPEVIVAR.H	1786.08666	2	1.35E-05	0.77	3.33	-	606.6
AHQ-3-9, 5813	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	1.65E-07	0.95	4.96	-	978.0
AHQ-3-9, 5616 - 5623	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	3.76E-07	0.99	7.17	-	2997.4
gi|5453710|ref|NP_006139.1|	LIM and SH3 protein 1; Lasp-1 [Homo sapiens]			1.70E-07	0.89	10.18	4.60	29717.0
AHQ-3-12, 1982	R.LKQQSELQSQVR.Y	1444.61889	2	1.70E-07	0.89	3.59	-	1066.8
gi|29568111|ref|NP_006088.2|	myosin, light polypeptide 9, regulatory; myosin regulatory light chain			1.71E-07	3.60	40.22	23.84	19827.1
AHQ-3-11, 3315	R.FTDEEVDEMYR.E	1434.51009	1	7.33E-05	0.56	2.36	-	413.3
AHQ-3-13, 3458	R.FTDEEVDEMYR.E	1434.51009	2	3.80E-07	0.89	2.94	-	1028.8
AHQ-3-14-, 3440	R.FTDEEVDEMYR.E	1434.51009	2	1.71E-07	0.94	3.35	-	1502.1
AHQ-3-11, 2614 - 2626	R.FTDEEVDEM*YR.E	1450.50949	2	7.85E-07	0.96	4.33	-	1231.5
AHQ-3-11, 3878	K.GNFNYVEFTR.I	1247.34066	2	6.24E-05	0.92	3.64	-	992.9
AHQ-3-11, 3774 - 3776	K.GNFNYVEFTR.I	1247.34066	2	1.71E-06	0.84	3.14	-	609.4
AHQ-3-11, 3631	K.GNFNYVEFTR.I	1247.34066	2	4.25E-06	0.93	3.85	-	1025.7
AHQ-3-11, 5690	R.NAFACFDEEASGFIHEDHLR.E	2367.49548	2	2.74E-07	0.86	2.94	-	1217.3
gi|29788766|ref|NP_064424.2|	tubulin, beta polypeptide 4, member Q [Homo sapiens]			1.78E-07	1.69	20.26	7.39	48377.2
AHQ-3-7, 6255 - 6322	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	2.04E-06	0.91	4.37	-	1138.0
AHQ-3-9, 5972	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	1.09E-04	0.67	3.20	-	930.3
AHQ-3-12, 6123	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	1.78E-07	0.94	5.22	-	1093.1
AHQ-3-7, 5722	K.EAESCDCLQGFQLTHSLGGGTGSGM*GTLLLSK.I	3331.65490	3	1.77E-04	0.75	3.47	-	751.4
gi|4503743|ref|NP_002009.1|	flightless I homolog [Homo sapiens]			1.78E-07	3.43	40.23	5.67	144750.1
AHQ-3-4, 3138	K.AVQGAQQPSLYQIR.T	1559.75158	2	4.74E-04	0.84	3.79	-	503.2
AHQ-3-3, 3190	K.AVQGAQQPSLYQIR.T	1559.75158	2	3.48E-04	0.74	3.06	-	595.5
AHQ-3-3, 6541 - 6554	R.TGLCYLPEELAALQK.L	1707.96931	2	3.04E-04	0.84	3.69	-	393.2
AHQ-3-3, 7292	R.TQSNLPTSLEGLSNLADVDLSCNDLTR.V	2936.15611	2	4.00E-06	0.92	4.39	-	840.9
AHQ-3-4, 6849	K.VGLGLGYLELPQINYK.L	1778.08432	2	1.78E-07	0.93	4.38	-	912.6
AHQ-3-3, 6852 - 6921	K.VGLGLGYLELPQINYK.L	1778.08432	2	8.31E-05	0.93	4.59	-	907.1
gi|18105037|ref|NP_004709.2|	cytochrome c oxidase subunit VIIa polypeptide 2 like; estrogen recepto			1.87E-07	0.95	10.27	28.95	12614.6
AHQ-3-14-, 6053 - 6067	K.LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK.L	3399.87995	3	1.87E-07	0.95	5.45	-	1053.9
gi|21618359|ref|NP_004095.3|	fatty acid synthase [Homo sapiens]			1.87E-07	2.79	30.28	2.11	273262.0
AHQ-3-1, 6226 - 6237	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	2.78E-05	0.97	5.60	-	1657.1
AHQ-3-1, 7037 - 7053	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	4.88E-04	0.98	5.44	-	2881.0
AHQ-3-2, 7187	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	1.87E-07	0.98	5.12	-	1811.1
AHQ-3-1, 3840	R.LQVVDQPLPVR.G	1264.49894	2	6.86E-04	0.85	3.30	-	1008.5
gi|5174613|ref|NP_005960.1|	nucleosome assembly protein 1-like 4; nucleosome assembly protein 2 [Ho			1.90E-07	0.97	10.18	2.67	42823.1
AHQ-3-7, 2635 - 2636	K.FYEEVHDLER.K	1337.41897	2	1.90E-07	0.97	3.56	-	1956.3

gi|20270343|ref|NP_620150.1|	hypothetical protein BC015408 [Homo sapiens]			1.96E-07	1.87	20.33	12.90	21415.8
AHQ-3-11, 5788 - 5858	K.NELHNLLDKPQLQGIPVLVLGNK.R	2553.98492	3	1.96E-07	0.96	6.62	-	996.3
AHQ-3-11, 5791	K.NELHNLLDKPQLQGIPVLVLGNK.R	2553.98492	2	2.36E-05	0.97	5.49	-	1150.9
AHQ-3-11, 5538	K.NELHNLLDKPQLQGIPVLVLGNKR.D	2710.17128	3	9.44E-04	0.90	4.16	-	978.7
gi|4502219|ref|NP_001656.1|	ras homolog gene family, member G (rho G); RhoG [Homo sapiens]			2.09E-07	1.54	20.23	16.75	21338.4
AHQ-3-11, 4810	K.EYIPTVFDNYSAQSAVDGR.T	2133.25975	2	1.36E-05	0.56	2.84	-	348.1
AHQ-3-11, 3331	R.YLECSALQQDGVK.E	1512.66692	2	2.09E-07	0.97	4.64	-	2063.2
gi|21361388|ref|NP_008868.2|	SMT3 suppressor of mif two 3 homolog 2; SMT3 (suppressor of mif two 3,			2.15E-07	0.87	10.17	12.63	10870.2
AHQ-3-12, 2568	K.VAGQDGSVVQFK.I	1235.37133	2	2.15E-07	0.87	3.43	-	816.3
gi|4757952|ref|NP_001782.1|	cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p			2.17E-07	3.66	40.24	25.65	21258.5
AHQ-3-11, 2195 - 2260	K.CVVVGDGAVGK.T	1062.22237	1	1.06E-04	0.43	2.54	-	535.6
AHQ-3-11, 2227	K.CVVVGDGAVGK.T	1062.22237	1	1.02E-05	0.88	3.38	-	965.7
AHQ-3-11, 2184 - 2256	K.CVVVGDGAVGK.T	1062.22237	2	4.54E-04	0.88	3.21	-	1070.9
AHQ-3-11, 6502	K.NVFDEAILAALEPPEPK.K	1854.09282	3	2.61E-05	0.94	4.86	-	1145.1
AHQ-3-11, 3779	K.TCLLISYTTNK.F	1315.51795	2	6.04E-04	0.91	3.34	-	1446.8
AHQ-3-11, 2434 - 2436	K.YVECSALTQK.G	1200.34381	2	2.17E-07	0.93	3.75	-	841.6
gi|5803217|ref|NP_006821.1|	ubiquinol-cytochrome c reductase (6.4kD) subunit [Homo sapiens]			2.25E-07	0.91	10.18	21.43	6569.6
AHQ-3-14-, 6216 - 6295	R.LILDWVPYINGK.F	1431.70332	2	2.25E-07	0.91	3.52	-	963.1
gi|4557703|ref|NP_000414.1|	keratin 2a [Homo sapiens]			2.27E-07	2.71	30.28	10.54	65864.9
AHQ-3-14-, 6556	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	8.98E-06	0.79	4.03	-	534.4
AHQ-3-1, 7085	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	1.45E-04	0.96	5.56	-	1514.5
AHQ-3-3, 3028	R.FLEQQNQVLQTK.W	1476.65935	2	1.07E-06	0.96	4.29	-	1885.8
AHQ-3-13, 2997	R.FLEQQNQVLQTK.W	1476.65935	2	3.21E-05	0.95	3.82	-	1902.5
AHQ-3-13-, 2963 - 2973	R.FLEQQNQVLQTK.W	1476.65935	2	8.51E-07	0.97	5.02	-	2190.6
AHQ-3-14-, 2907	R.FLEQQNQVLQTK.W	1476.65935	2	2.27E-07	0.97	4.74	-	2114.1
AHQ-3-1, 3138 - 3217	R.FLEQQNQVLQTK.W	1476.65935	2	4.06E-07	0.97	4.38	-	2100.5
AHQ-3-1, 6446	R.NLDLDSIIAEVK.A	1330.50933	2	5.25E-07	0.95	4.66	-	1024.8
gi|5729875|ref|NP_006658.1|	progesterone receptor membrane component 1; progesterone binding protei			2.37E-07	2.79	30.22	17.95	21671.0
AHQ-3-11, 4395	K.FYGPEGPYGVFAGR.D	1517.66849	2	4.47E-06	0.95	3.91	-	1094.4
AHQ-3-11, 2831	R.GDQPAASGDSDDDEPPPLPR.L	2037.04410	2	2.37E-07	0.90	3.52	-	909.8
AHQ-3-11, 3883	R.KFYGPEGPYGVFAGR.D	1645.84140	2	5.49E-04	0.96	4.48	-	1307.3
AHQ-3-10, 3770	R.KFYGPEGPYGVFAGR.D	1645.84140	2	4.92E-05	0.95	4.29	-	1095.8
gi|4507487|ref|NP_003238.1|	thrombospondin 2 [Homo sapiens]			2.43E-07	1.66	20.19	2.56	129954.5
AHQ-3-1, 5426 - 5473	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	4.60E-05	0.89	3.58	-	906.4
AHQ-3-2, 2870	R.NALWHTGNTPGQVR.T	1551.69124	2	3.46E-05	0.68	2.96	-	603.9
AHQ-3-2, 3094	R.NALWHTGNTPGQVR.T	1551.69124	2	7.13E-04	0.73	2.77	-	653.6
AHQ-3-11, 2452	R.NALWHTGNTPGQVR.T	1551.69124	2	5.67E-04	0.90	3.50	-	1113.5
AHQ-3-11, 2720	R.NALWHTGNTPGQVR.T	1551.69124	2	2.51E-04	0.90	3.42	-	1056.2
AHQ-3-13-, 2683	R.NALWHTGNTPGQVR.T	1551.69124	2	2.43E-07	0.77	3.18	-	811.1
AHQ-3-14-, 2624	R.NALWHTGNTPGQVR.T	1551.69124	2	1.83E-04	0.69	2.65	-	647.0
AHQ-3-2, 2527 - 2529	R.NALWHTGNTPGQVR.T	1551.69124	2	8.36E-05	0.94	3.75	-	1226.5
gi|21361621|ref|NP_002624.2|	phosphoglucomutase 1 [Homo sapiens]			2.45E-07	1.83	20.22	7.83	61448.7
AHQ-3-6, 6394 - 6467	R.LVIGQNGILSTPAVSCIIR.K	2013.39093	2	2.80E-06	0.93	4.45	-	772.6
AHQ-3-6, 7403	K.VFQSSANYAENFIQSIISTVEPAQR.Q	2801.06026	2	2.45E-07	0.90	3.81	-	1056.4
gi|21914881|ref|NP_005597.2|	legumain; protease, cysteine, 1 (legumain) [Homo sapiens]			2.48E-07	0.78	10.16	3.93	49425.0
AHQ-3-9, 6315	K.DYTGEDVTPQNFLAVLR.G	1939.11467	2	2.48E-07	0.78	3.27	-	503.4
gi|11496885|ref|NP_005442.2|	enigma protein; LIM domain protein [Homo sapiens]			2.81E-07	1.83	20.25	7.22	49844.4
AHQ-3-13-, 4838	K.VVLEGPAPWGFR.L	1328.54318	2	3.95E-06	0.94	3.25	-	1195.3
AHQ-3-11, 4555 - 4619	K.VVLEGPAPWGFR.L	1328.54318	2	5.63E-04	0.85	2.55	-	886.1
AHQ-3-13, 4849	K.VVLEGPAPWGFR.L	1328.54318	2	3.60E-06	0.71	2.91	-	596.4
AHQ-3-14, 6039	K.VVLEGPAPWGFR.L	1328.54318	2	2.81E-07	0.89	3.39	-	982.6
AHQ-3-14-, 4821	K.VVLEGPAPWGFR.L	1328.54318	2	1.15E-06	0.95	3.72	-	1428.8
AHQ-3-10, 4206	R.YLVALGHAYHPEEFVCSQCGK.V	2468.74928	2	1.91E-04	0.96	5.01	-	1114.5
AHQ-3-9, 4199	R.YLVALGHAYHPEEFVCSQCGK.V	2468.74928	2	5.45E-05	0.93	4.57	-	956.2
gi|21361456|ref|NP_055425.2|	alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph			2.94E-07	1.81	20.22	3.52	109437.2
AHQ-3-4, 3798	K.MMDYLQGSGETPQTDVR.W	1929.12196	2	1.48E-06	0.95	4.32	-	1354.1
AHQ-3-5, 3616	R.VVIIGAGKPAAVVLQTK.G	1665.05702	2	2.94E-07	0.86	3.41	-	694.6
gi|14211943|ref|NP_115992.1|	lysyl oxidase-like 3 [Homo sapiens]			3.07E-07	0.83	10.16	1.73	83166.0
AHQ-3-4, 3522	R.RPLPVTEGLVEVR.L	1465.72284	2	3.07E-07	0.83	3.23	-	670.3
gi|4759096|ref|NP_004252.1|	15 kDa selenoprotein [Homo sapiens]			3.15E-07	0.87	10.16	8.02	17640.3
AHQ-3-12, 5544	K.WNTDSVEEFLSEK.L	1584.66517	2	3.15E-07	0.87	3.15	-	770.4
gi|30147623|ref|XP_293669.2|	similar to actinin, alpha 4 [Homo sapiens]			3.25E-07	0.98	20.24	5.64	57794.4
AHQ-3-5, 2784	K.GISQEQMQQFR.A	1352.50182	1	7.81E-04	0.03	1.92	-	65.7
AHQ-3-5, 3951 - 4025	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	3.25E-07	0.95	4.89	-	841.4
gi|24432022|ref|NP_115956.2|	testis-specific protein NYD-TSP1 [Homo sapiens]			3.29E-07	0.46	10.16	4.88	49458.7
AHQ-3-13-, 5129	K.FNNLLKEIKDILKNM*AGFEEK.I	2511.92191	3	3.29E-07	0.46	3.20	-	510.6
gi|4504107|ref|NP_002076.1|	glutathione peroxidase 4; phospholipid hydroperoxidase; sperm nucleus g			3.37E-07	0.89	10.18	6.09	22137.7
AHQ-3-11, 3216	R.YGPM*EEPLVIEK.D	1421.64070	2	3.37E-07	0.89	3.67	-	813.6
gi|30147105|ref|XP_210550.2|	similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48			3.37E-07	0.80	10.21	2.21	61339.9
AHQ-3-5, 4081	K.ADLINNLGTIAK.S	1243.43490	2	6.60E-07	0.93	4.27	-	957.9
AHQ-3-5, 3907	K.ADLINNLGTIAK.S	1243.43490	2	3.37E-07	0.80	3.25	-	495.0
gi|20428652|ref|NP_005347.2|	lymphocyte-specific protein tyrosine kinase; oncogene LCK; membrane as			3.41E-07	0.90	10.18	1.96	57969.3
AHQ-3-7, 2120	R.LIEDNEYTAR.E	1224.30217	2	3.41E-07	0.90	3.63	-	867.5
gi|4885287|ref|NP_005265.1|	guanine nucleotide binding protein (G protein), gamma 5 [Homo sapiens]			3.42E-07	0.90	10.27	39.71	7318.4
AHQ-3-14-, 5216 - 5229	K.QFCLQNAQHDPLLTGVSSSTNPFRPQK.V	3073.38890	3	3.42E-07	0.90	5.36	-	222.6
gi|13489091|ref|NP_066949.1|	3-mercaptopyruvate sulfurtransferase [Homo sapiens]			3.47E-07	0.94	10.19	5.39	33178.2
AHQ-3-9, 6275 - 6327	R.AGQPLQLLDASWYLPK.L	1801.07798	2	3.47E-07	0.94	3.86	-	1278.3
gi|27436929|ref|NP_005518.2|	heat shock 70kDa protein 1-like; heat shock 70kD protein-like 1 [Homo			3.51E-07	0.96	10.19	2.18	70404.7
AHQ-3-6, 2937	K.AKIHDIVLVGGSTR.I	1466.71083	2	3.51E-07	0.96	3.76	-	1929.2
gi|5174727|ref|NP_005989.1|	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring			3.55E-07	2.79	30.19	6.99	60330.4
AHQ-3-6, 3573 - 3574	R.AVAQALEVIPR.T	1167.38326	2	3.76E-05	0.94	3.76	-	1350.0
AHQ-3-6, 4366	K.IPGGIIEDSCVLR.G	1430.65218	2	4.08E-06	0.92	3.89	-	1095.7
AHQ-3-6, 5427	R.WSSLACNIALDAVK.M	1549.77353	2	3.55E-07	0.93	3.22	-	1510.7
gi|19923142|ref|NP_002256.2|	karyopherin beta 1; nuclear factor p97; importin 90; importin beta-1 s			3.61E-07	1.81	20.24	3.88	97169.7
AHQ-3-5, 6893	R.AAVENLPTFLVELSR.V	1659.90783	2	6.48E-05	0.85	3.42	-	606.8
AHQ-3-5, 7651	R.IQFNDLQSLLCATLQNVLR.K	2248.58813	2	3.61E-07	0.96	4.78	-	1267.6
gi|18543899|ref|XP_086916.1|	similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic			3.65E-07	2.76	30.21	26.74	21265.8
AHQ-3-11, 3176	K.NRPTSISWDGLDSGK.L	1633.74419	2	8.61E-06	0.96	4.23	-	1385.9
AHQ-3-11, 3354	K.YREWHHFLVVNMK.G	1760.05751	2	2.28E-05	0.92	3.77	-	852.8
AHQ-3-11, 5018 - 5078	R.YVWLVYEQDRPLKCDEPILSNR.S	2796.15005	3	3.65E-07	0.88	3.83	-	749.0
gi|4506505|ref|NP_002916.1|	regulator of G-protein signaling 10 [Homo sapiens]			3.72E-07	0.78	10.21	10.18	19607.9
AHQ-3-11, 5231	K.WAASLENLLEDPEGVKR.F	1928.13502	3	2.86E-06	0.58	3.04	-	484.3
AHQ-3-11, 5226 - 5227	K.WAASLENLLEDPEGVKR.F	1928.13502	2	3.72E-07	0.78	4.12	-	336.0
gi|5031985|ref|NP_005787.1|	nuclear transport factor 2; placental protein 15 [Homo sapiens]			3.75E-07	1.84	20.30	39.37	14478.4
AHQ-3-14-, 6031	K.IQHSITAQDHQPTPDSCIISMVVGQLK.A	3006.40418	3	3.75E-07	0.97	6.01	-	1642.8
AHQ-3-14-, 6372 - 6383	R.TQLGAIYIDASCLTWEGQQFQGK.A	2616.88699	2	1.42E-05	0.87	3.54	-	873.2
gi|4507383|ref|NP_001052.1|	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil			3.78E-07	1.92	20.24	5.81	60675.3
AHQ-3-7, 4219 - 4267	R.FQACPETQVPLQLESK.S	1877.10807	2	1.44E-06	0.95	4.20	-	1062.4
AHQ-3-7, 3714	R.HSASPMGVQDFDIVR.D	1659.84828	2	3.78E-07	0.98	4.80	-	1941.8
gi|10863873|ref|NP_000651.1|	transforming growth factor, beta 1 (Camurati-Engelmann disease); trans			3.87E-07	4.31	50.22	15.86	44422.0
AHQ-3-13, 3338 - 3339	R.ALDTNYCFSSTEK.N	1537.63010	2	3.87E-07	0.94	4.48	-	760.1
AHQ-3-13-, 3321 - 3322	R.ALDTNYCFSSTEK.N	1537.63010	2	3.88E-07	0.88	3.29	-	828.9
AHQ-3-14-, 6401 - 6469	R.LLAPSDSPEWLSFDVTGVVR.Q	2189.45272	2	3.00E-04	0.81	3.91	-	374.1
AHQ-3-8, 2768	R.VAGESAEPEPEPEADYYAK.E	2053.12504	2	6.28E-05	0.83	3.96	-	318.0
AHQ-3-13-, 3463	K.VEQLSNMIVR.S	1189.41074	2	5.06E-04	0.95	4.09	-	1397.7
AHQ-3-13, 3461	K.VEQLSNMIVR.S	1189.41074	2	7.90E-05	0.82	2.95	-	1015.1
AHQ-3-13, 2669 - 2677	K.VEQLSNM*IVR.S	1205.41014	2	1.07E-05	0.91	3.52	-	1020.6

gi|5123454|ref|NP_005336.2|	heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind			3.95E-07	3.72	50.34	14.51	70037.7
AHQ-3-6, 5670 - 5698	K.AFYPEEISSMVLTK.M	1615.87209	2	3.95E-07	0.89	3.30	-	846.3
AHQ-3-6, 5823	K.CQEVISWLDANTLAEKDEFEHK.R	2664.88528	3	7.36E-07	0.66	3.43	-	424.5
AHQ-3-6, 6275 - 6293	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G	3058.37100	3	2.57E-05	0.98	6.71	-	2575.6
AHQ-3-6, 4153	K.NQVALNPQNTVFDAK.R	1659.82478	2	2.31E-04	0.69	3.43	-	305.2
AHQ-3-6, 2027	K.VEIIANDQGNR.T	1229.32518	1	6.86E-05	0.49	2.31	-	366.5
gi|20149570|ref|NP_005816.2|	RAS guanyl releasing protein 2 isoform 1; calcium and diacylglycerol-r			3.99E-07	1.75	20.24	4.62	75547.0
AHQ-3-6, 3005	K.LDQALVVEHIEK.M	1394.59824	2	7.41E-06	0.79	3.15	-	769.2
AHQ-3-6, 6794	K.LWEGLTELVTATGNYGNYR.R	2158.35558	2	3.99E-07	0.96	4.72	-	1416.0
gi|4503141|ref|NP_001805.1|	cathepsin C isoform a preproprotein; dipeptidyl-peptidase I; dipeptidyl			4.19E-07	1.94	20.27	4.32	51841.5
AHQ-3-14, 6303 - 6304	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	1.08E-04	0.94	4.42	-	1186.7
AHQ-3-14-, 5412 - 5421	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	4.19E-07	0.97	5.36	-	1613.5
AHQ-3-14-, 4984	R.RGTDECAIESIAVAATPIPK.L	2101.36707	2	2.35E-05	0.97	5.24	-	1263.2
AHQ-3-14, 6041	R.RGTDECAIESIAVAATPIPK.L	2101.36707	2	4.64E-05	0.95	4.95	-	1004.4
gi|4758644|ref|NP_004511.1|	kinesin heavy chain member 2; Kinesin, heavy chain, 2 [Homo sapiens] [M			4.29E-07	0.76	10.20	2.36	76926.6
AHQ-3-6, 4859	R.FDYAFDDSAPNEMVYR.F	1941.06625	2	4.29E-07	0.76	3.32	-	489.0
gi|22538814|ref|NP_002976.2|	small inducible cytokine A5 precursor; T-cell specific protein p288; T			4.36E-07	0.82	10.16	12.09	9989.6
AHQ-3-14-, 3732	K.CSNPAVVFVTR.K	1251.43718	2	1.75E-06	0.83	3.12	-	605.6
AHQ-3-14-, 3715 - 3723	K.CSNPAVVFVTR.K	1251.43718	2	4.36E-07	0.82	2.66	-	711.6
gi|11128019|ref|NP_061820.1|	cytochrome c [Homo sapiens]			4.57E-07	0.92	10.17	13.33	11748.7
AHQ-3-13-, 2161	K.TGQAPGYSYTAANK.N	1429.51641	2	4.57E-07	0.92	3.48	-	841.8
gi|4758756|ref|NP_004528.1|	nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr			4.73E-07	3.57	40.29	19.95	45373.8
AHQ-3-7, 6390	R.FEIINAIYEPTEEECEWKPDEEDEISEELKEK.A	3974.21701	3	3.99E-04	0.78	3.74	-	461.6
AHQ-3-7, 7186	K.GIPEFWLTVFK.N	1337.58999	2	4.73E-07	0.87	3.25	-	309.4
AHQ-3-7, 5479 - 5486	R.LDGLVETPTGYIESLPR.V	1861.08535	2	1.16E-06	0.95	5.04	-	926.6
AHQ-3-7, 5348 - 5354	K.NVDLLSDMVQEHDEPILK.H	2096.34751	2	1.35E-06	0.98	5.71	-	1587.2
gi|18426915|ref|NP_004386.2|	drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [			4.73E-07	2.71	30.24	8.63	71438.9
AHQ-3-7, 3751	K.KSESEVEEAAAIIAQRPDNPR.E	2311.49476	3	2.77E-06	0.84	3.18	-	1072.6
AHQ-3-13, 4003 - 4025	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	3.23E-05	0.90	3.91	-	999.5
AHQ-3-13-, 3974 - 4049	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	1.92E-04	0.87	3.95	-	666.1
AHQ-3-12, 3996	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	4.73E-07	0.93	4.78	-	729.7
AHQ-3-13, 5562	K.YVLINWVGEDVPDAR.K	1746.94404	2	8.88E-06	0.94	4.02	-	1390.6
gi|4504111|ref|NP_002077.1|	growth factor receptor-bound protein 2 [Homo sapiens]			4.99E-07	0.80	20.15	11.98	25206.2
AHQ-3-11, 3371	R.ESESAPGDFSLSVK.F	1453.53305	2	1.08E-04	0.16	2.63	-	111.6
AHQ-3-11, 3375	R.ESESAPGDFSLSVK.F	1453.53305	1	7.71E-04	0.20	2.01	-	152.0
AHQ-3-11, 3844	K.FNSLNELVDYHR.S	1507.63200	2	1.09E-05	0.83	2.91	-	873.8
AHQ-3-10, 3671 - 3736	K.FNSLNELVDYHR.S	1507.63200	2	4.99E-07	0.64	2.71	-	598.8
gi|10835242|ref|NP_006249.1|	protein kinase, cGMP-dependent, type I; Protein kinase, cGMP-dependent			5.18E-07	0.96	10.23	2.48	77803.3
AHQ-3-6, 6835	K.LSDFNIIDTLGVGGFGR.V	1781.98992	2	5.18E-07	0.96	4.63	-	1349.5
gi|19913441|ref|NP_002140.2|	hippocalcin-like 1; visinin-like protein 3; calcium-binding protein BD			5.27E-07	0.94	10.23	7.77	22313.1
AHQ-3-11, 4119	R.ENTEFTDHELQEWYK.G	1970.04095	2	5.27E-07	0.94	4.62	-	967.2
gi|4758504|ref|NP_004484.1|	hydroxyacyl-Coenzyme A dehydrogenase, type II [Homo sapiens]			5.28E-07	0.93	10.26	8.81	26922.9
AHQ-3-10, 4430	R.LVGQGASAVLLDLPNSGGEAQAK.K	2196.44680	2	5.28E-07	0.93	5.23	-	614.7
gi|13899317|ref|NP_113657.1|	SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M			5.31E-07	4.45	50.26	71.96	12326.0
AHQ-3-14-, 5407 - 5419	K.ESNTVFSFLGLKPR.L	1595.82383	2	5.31E-07	0.68	3.03	-	406.3
AHQ-3-13-, 5441 - 5449	K.ESNTVFSFLGLKPR.L	1595.82383	2	1.11E-04	0.54	2.70	-	398.4
AHQ-3-14-, 5411 - 5433	K.ESNTVFSFLGLKPR.L	1595.82383	3	7.36E-04	0.68	3.03	-	621.2
AHQ-3-13-, 4961	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	1.90E-06	0.96	4.60	-	1976.0
AHQ-3-14-, 4927 - 5001	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	1.03E-05	0.96	5.19	-	1505.7
AHQ-3-14, 5955	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	2	1.26E-05	0.93	4.11	-	991.2
AHQ-3-14, 5933 - 5959	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	2.93E-04	0.96	5.22	-	1936.5
AHQ-3-14-, 5759 - 5823	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	3.63E-04	0.87	4.34	-	653.2
AHQ-3-14-, 4283	R.VFIASSSGFVAIK.K	1326.56551	2	6.05E-05	0.97	3.46	-	2309.9
AHQ-3-14-, 4475 - 4536	R.VFIASSSGFVAIK.K	1326.56551	2	7.86E-07	0.98	4.17	-	3313.3
AHQ-3-14, 5356	R.YCGDYDSFFESK.E	1519.57010	2	9.00E-07	0.95	3.75	-	1141.1
gi|7705849|ref|NP_057215.1|	ras-related GTP-binding protein RAB10; ras-related GTP-binding protein			5.35E-07	1.46	20.22	15.00	22540.8
AHQ-3-14-, 6360	K.AFLTLAEDILR.K	1262.47982	2	1.76E-06	0.95	4.17	-	1614.2
AHQ-3-11, 6154	K.AFLTLAEDILR.K	1262.47982	2	5.35E-07	0.95	4.44	-	1475.9
AHQ-3-11, 6892	R.FSDDAFNTTFISTIGIDFK.I	2140.33380	2	7.11E-06	0.50	3.26	-	607.9
gi|5902134|ref|NP_009005.1|	coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin			5.53E-07	4.14	50.28	18.87	51026.0
AHQ-3-7, 6991	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	1.09E-04	0.94	5.03	-	860.7
AHQ-3-6, 7013	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	1.79E-05	0.95	5.60	-	676.5
AHQ-3-7, 2191	K.LQATVQELQK.R	1158.33000	2	6.94E-05	0.77	2.76	-	724.2
AHQ-3-7, 1935	K.RGLEVNKCEIAR.F	1446.65807	2	5.53E-07	0.96	4.53	-	1078.8
AHQ-3-13-, 4163	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	1.83E-04	0.77	3.57	-	380.1
AHQ-3-7, 3999 - 4027	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	2.50E-06	0.90	3.98	-	803.6
AHQ-3-7, 7288 - 7338	R.YFEITSEAPFLHYLSMFSSK.E	2398.71748	2	2.60E-04	0.57	2.57	-	315.6
gi|17149842|ref|NP_004461.2|	FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep			5.60E-07	0.70	10.22	8.45	15649.2
AHQ-3-13-, 4173	K.LVIPSELGYGER.G	1333.51491	2	5.60E-07	0.70	3.05	-	303.3
AHQ-3-13, 4162	K.LVIPSELGYGER.G	1333.51491	2	1.62E-06	0.77	2.70	-	473.0
gi|21361070|ref|NP_002617.2|	phosphofructokinase, liver; Phosphofructokinase, liver type; human liv			5.98E-07	0.97	10.19	1.81	90202.5
AHQ-3-5, 7260	R.SEWGSLLEELVAEGK.I	1647.80754	2	5.98E-07	0.97	3.89	-	2144.5
gi|4506363|ref|NP_002861.1|	RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s			6.12E-07	1.75	20.16	10.84	22774.0
AHQ-3-13, 3769	K.LLLIGDSGVGK.T	1072.28025	2	7.62E-04	0.77	3.01	-	914.7
AHQ-3-14-, 3708	K.LLLIGDSGVGK.T	1072.28025	2	6.12E-07	0.90	3.17	-	1246.3
AHQ-3-11, 2887	K.LQVWDTAGQER.F	1303.40576	2	2.67E-04	0.86	2.67	-	1053.3
gi|4758440|ref|NP_004868.1|	glia maturation factor, gamma [Homo sapiens]			6.16E-07	1.85	20.23	21.83	16801.2
AHQ-3-12, 5996 - 5999	R.QMVVLEEEFQNISPEELK.M	2163.43385	2	2.14E-04	0.90	4.30	-	879.1
AHQ-3-12, 4362 - 4363	R.TTDDLTEAWLQEK.L	1550.64872	2	6.16E-07	0.95	4.60	-	1480.7
gi|5031599|ref|NP_005722.1|	actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub			6.46E-07	3.94	50.20	20.00	34332.8
AHQ-3-9, 2321	K.DSIVHQAGMLK.R	1199.40563	2	5.02E-06	0.81	2.72	-	785.6
AHQ-3-9, 2172 - 2175	R.DYLHYHIK.C	1089.22792	1	8.38E-04	0.50	2.39	-	491.8
AHQ-3-9, 2372	K.ELQAHGADELLK.R	1324.46487	2	6.46E-07	0.91	3.60	-	912.3
AHQ-3-9, 2264	K.ELQAHGADELLKR.V	1480.65123	2	1.82E-06	0.90	3.09	-	1121.8
AHQ-3-9, 6959	R.VYGSFLVNPESGYNVSLLYDLENLPASK.D	3090.42808	3	8.92E-05	0.82	3.95	-	401.4
gi|5454090|ref|NP_006271.1|	signal sequence receptor, delta; translocon-associated protein delta [H			6.89E-07	1.79	20.18	13.87	18998.5
AHQ-3-12, 4858	R.FFDEESYSLLR.K	1406.52121	2	6.89E-07	0.91	3.50	-	1094.1
AHQ-3-12, 3300	R.VQNMALYADVGGK.Q	1366.56840	2	1.79E-05	0.88	3.19	-	1152.4
gi|5803201|ref|NP_006818.1|	transmembrane trafficking protein [Homo sapiens]			7.22E-07	3.02	40.23	16.89	24975.8
AHQ-3-11, 4856	R.IPDQLVILDMK.H	1285.57833	2	2.37E-05	0.96	3.80	-	1751.4
AHQ-3-11, 6123	R.LEDLSESIVNDFAYMK.K	1875.08916	2	1.21E-05	0.91	3.52	-	1303.2
AHQ-3-11, 2864	K.LKPLEVELR.R	1097.33294	1	1.34E-04	0.18	2.17	-	282.4
AHQ-3-11, 6015	R.RLEDLSESIVNDFAYMK.K	2031.27552	2	7.22E-07	0.96	4.51	-	1172.5
gi|4507793|ref|NP_003339.1|	ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast); ubiquitin-conj			7.23E-07	4.33	50.24	36.84	17137.7
AHQ-3-12, 5288 - 5300	K.LELFLPEEYPM*AAPK.V	1765.06265	2	1.96E-06	0.80	3.78	-	454.1
AHQ-3-12, 5778 - 5782	K.LELFLPEEYPMAAPK.V	1749.06325	2	7.23E-07	0.88	4.45	-	589.0
AHQ-3-13, 5290	K.LELFLPEEYPM*AAPK.V	1765.06265	2	1.89E-05	0.66	3.50	-	341.1
AHQ-3-13, 5730	K.LELFLPEEYPMAAPK.V	1749.06325	2	1.05E-04	0.59	2.97	-	454.8
AHQ-3-13, 3350	R.LLAEPVPGIK.A	1037.27750	2	9.11E-05	0.71	2.88	-	582.9
AHQ-3-12, 3270	R.LLAEPVPGIK.A	1037.27750	2	1.91E-05	0.75	2.96	-	521.4
AHQ-3-13-, 2222	K.TNEAQAIETAR.A	1204.27249	2	7.03E-06	0.93	3.73	-	1623.8
AHQ-3-13-, 5213	R.YFHVVIAGPQDSPFEGGTFK.L	2197.43341	2	1.24E-05	0.96	4.79	-	1384.2
gi|11321611|ref|NP_006868.1|	guanosine monophosphate reductase; guanine monophosphate reductase [Ho			7.49E-07	0.91	10.20	6.38	37414.6
AHQ-3-9, 6953 - 7007	K.TVEVPYKGDVENTILDILGGLR.S	2402.72885	2	7.49E-07	0.91	3.96	-	845.5
gi|4505591|ref|NP_002565.1|	peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc			7.71E-07	2.53	30.22	15.58	22110.2
AHQ-3-11, 3456	R.LVQAFQFTDK.H	1197.36469	2	1.82E-04	0.92	3.59	-	1089.9
AHQ-3-11, 3344	R.QITVNDLPVGR.S	1212.38090	2	6.16E-04	0.79	3.29	-	434.0

AHQ-3-11, 2972	R.TIAQDYGVLK.A	1108.26945	2	7.71E-07	0.82	3.24	-	567.4
gi|20127528|ref|NP_037459.2|	parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]			7.95E-07	4.42	60.23	22.25	41714.0
AHQ-3-14-, 3428	K.ARPEDVVNLDLK.S	1369.54878	2	7.19E-05	0.86	3.41	-	718.0
AHQ-3-9, 2955	K.ARPEDVVNLDLK.S	1369.54878	2	3.13E-06	0.93	4.10	-	971.4
AHQ-3-9, 2972	K.ARPEDVVNLDLK.S	1369.54878	1	8.27E-05	0.34	2.87	-	235.1
AHQ-3-13, 3450	K.ARPEDVVNLDLK.S	1369.54878	2	1.65E-04	0.93	4.39	-	874.4
AHQ-3-10, 3168	K.ARPEDVVNLDLK.S	1369.54878	2	1.29E-04	0.92	4.13	-	773.1
AHQ-3-13-, 3447 - 3450	K.ARPEDVVNLDLK.S	1369.54878	2	7.95E-07	0.95	4.56	-	916.0
AHQ-3-9, 5000	R.DAFDTLFDHAPDKLSVVK.K	2019.24293	2	1.33E-04	0.88	3.92	-	658.2
AHQ-3-9, 3288 - 3303	K.LNVAEVTQSEIGQK.Q	1516.67865	2	2.54E-06	0.93	3.87	-	995.1
AHQ-3-13, 3775	K.LNVAEVTQSEIGQK.Q	1516.67865	2	2.71E-06	0.95	3.81	-	1525.0
AHQ-3-9, 3707 - 3723	K.QLEEDLYDGQVLQK.L	1678.82164	2	1.22E-05	0.90	3.94	-	1026.5
AHQ-3-9, 6065 - 6135	K.VLLDWINDVLVEER.I	1713.95549	2	2.94E-04	0.72	2.82	-	682.1
AHQ-3-9, 6913	K.VLLDWINDVLVEER.I	1713.95549	2	5.02E-04	0.94	4.07	-	1197.9
AHQ-3-9, 2111	R.WSVDSIHGK.N	1029.13088	1	8.14E-04	0.05	1.85	-	214.5
gi|4506765|ref|NP_002952.1|	S100 calcium-binding protein A4; 18A2; 42A; S100 calcium-binding protei			8.32E-07	1.82	20.18	10.89	11728.5
AHQ-3-14-, 3369	K.ALDVMVSTFHK.Y	1248.47665	2	8.32E-07	0.87	3.33	-	822.0
AHQ-3-14-, 2791	K.ALDVM*VSTFHK.Y	1264.47605	2	1.23E-04	0.94	3.59	-	1302.1
gi|4758018|ref|NP_004359.1|	calponin 2; Calonin 2 [Homo sapiens]			8.41E-07	1.82	20.25	9.06	33696.9
AHQ-3-13, 2886	K.GLQSGVDIGVK.Y	1073.22510	2	1.31E-04	0.90	2.83	-	1203.0
AHQ-3-12, 2807	K.GLQSGVDIGVK.Y	1073.22510	2	2.38E-06	0.89	3.08	-	1124.3
AHQ-3-13-, 2845	K.GLQSGVDIGVK.Y	1073.22510	2	2.46E-05	0.84	2.62	-	1131.5
AHQ-3-12, 6332 - 6394	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.83E-06	0.96	4.92	-	1319.0
AHQ-3-12, 6360	R.TWIEGLTGLSIGPDFQK.G	1863.10294	3	3.65E-04	0.86	4.07	-	870.8
AHQ-3-12, 6472	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.93E-04	0.89	3.21	-	1224.9
AHQ-3-11, 6139 - 6160	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	8.35E-04	0.93	4.29	-	908.1
AHQ-3-9, 6269	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	8.02E-04	0.90	3.56	-	952.9
AHQ-3-1, 6726 - 6785	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.43E-04	0.83	3.11	-	1004.1
AHQ-3-13-, 6349 - 6415	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	8.41E-07	0.93	3.97	-	1068.0
AHQ-3-14-, 6276	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.07E-04	0.85	3.12	-	1254.9
gi|5803181|ref|NP_006810.1|	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo			8.44E-07	0.94	10.24	3.50	62638.9
AHQ-3-13, 6362	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	6.35E-05	0.64	3.41	-	330.2
AHQ-3-6, 6525 - 6526	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	8.44E-07	0.94	4.87	-	846.7
gi|4506195|ref|NP_002785.1|	proteasome beta 2 subunit; proteasome subunit, beta type, 2; macropain			8.79E-07	0.86	10.17	5.47	22836.1
AHQ-3-11, 5846 - 5924	R.FILNLPTFSVR.I	1307.56542	2	8.79E-07	0.86	3.39	-	769.5
gi|4757766|ref|NP_004299.1|	Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa			9.02E-07	1.75	20.21	7.29	50435.4
AHQ-3-7, 3871	K.NPEQEPIPIVLR.E	1405.62426	2	1.81E-05	0.84	3.16	-	783.9
AHQ-3-11, 5878	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	2.41E-05	0.88	4.25	-	510.6
AHQ-3-7, 6127	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	9.02E-07	0.91	4.25	-	558.8
gi|4557553|ref|NP_000108.1|	emerin [Homo sapiens]			9.05E-07	0.82	10.18	8.27	28993.6
AHQ-3-13, 4125	R.LSPPSSSAASSYSFSDLNSTR.G	2162.25626	2	9.05E-07	0.82	3.58	-	276.0
gi|21361794|ref|NP_060918.2|	TIP120 protein [Homo sapiens]			9.28E-07	0.89	10.21	1.46	136374.7
AHQ-3-4, 4561 - 4562	K.VIRPLDQPSSFDATPYIK.D	2048.32741	2	9.28E-07	0.89	4.12	-	596.0
gi|21361547|ref|NP_002930.2|	ribonuclease/angiogenin inhibitor; Placental ribonuclease inhibitor [H			9.43E-07	0.88	10.20	3.25	49973.3
AHQ-3-14-, 6405	R.WAELLPLLQQCQVVR.L	1855.19360	2	7.14E-06	0.72	3.08	-	480.7
AHQ-3-7, 6628	R.WAELLPLLQQCQVVR.L	1855.19360	2	9.43E-07	0.88	3.73	-	604.8
gi|4508047|ref|NP_003452.1|	zyxin [Homo sapiens]			9.59E-07	1.92	30.22	11.54	61277.0
AHQ-3-8, 7183	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	3	3.49E-04	0.82	3.48	-	848.6
AHQ-3-9, 6931	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	2	9.59E-07	0.65	2.70	-	587.4
AHQ-3-10, 3623 - 3627	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	2	2.88E-05	0.82	3.70	-	510.4
AHQ-3-8, 3606	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	2	1.24E-04	0.92	4.39	-	620.2
AHQ-3-9, 7025 - 7097	K.VSSIDLEIDSLSSLLDDMTK.N	2182.43225	2	6.11E-04	0.45	2.59	-	485.8
gi|5453898|ref|NP_006212.1|	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1; dod;			9.70E-07	1.55	20.22	21.47	18243.2
AHQ-3-12, 5428	K.SGEEDFESLASQFSDCSSAK.A	2183.20603	2	2.84E-05	0.60	2.64	-	566.7
AHQ-3-12, 4003 - 4068	R.TKEEALELINGYIQK.I	1749.98614	2	9.70E-07	0.95	4.32	-	1257.0
gi|4502695|ref|NP_001779.1|	cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c			9.81E-07	2.16	30.27	8.13	48786.6
AHQ-3-8, 3648	K.IYEFPETDDEEENKLVK.K	2099.23685	2	2.65E-04	0.54	3.07	-	298.5
AHQ-3-14-, 5401	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	9.81E-07	0.95	4.34	-	1158.2
AHQ-3-14, 6305	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	4.41E-06	0.96	5.43	-	1037.7
AHQ-3-14-, 6449	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	2	6.85E-05	0.67	2.50	-	511.6
gi|4506417|ref|NP_002877.1|	RAP2B, member of RAS oncogene family [Homo sapiens]			1.01E-06	4.44	50.25	43.72	20494.2
AHQ-3-11, 4986	K.ALAEEWSCPFMETSAK.N	1859.06988	2	2.36E-05	0.96	5.05	-	965.7
AHQ-3-11, 5992 - 6004	K.ASVDELFAEIVR.Q	1349.51434	2	1.01E-06	0.94	4.35	-	1283.2
AHQ-3-11, 6002	K.ASVDELFAEIVR.Q	1349.51434	1	1.26E-05	0.36	2.36	-	300.5
AHQ-3-11, 6463	R.KEIEVDSSPSVLEILDTAGTEQFASMR.D	2954.25639	3	6.05E-05	0.90	4.82	-	736.2
AHQ-3-11, 2616	K.VDLEGEREVSYGEGK.A	1667.75571	2	5.23E-04	0.88	3.77	-	816.0
AHQ-3-11, 4083	K.YDPTIEDFYR.K	1319.40042	2	1.27E-04	0.78	2.85	-	330.2
gi|8923812|ref|NP_060943.1|	uncharacterized hypothalamus protein HT012 [Homo sapiens]			1.02E-06	0.96	10.21	8.57	14960.4
AHQ-3-13-, 4106	K.TLAFTSVDLTNK.A	1310.47811	2	1.02E-06	0.96	4.16	-	1245.9
AHQ-3-13, 4099	K.TLAFTSVDLTNK.A	1310.47811	2	4.73E-04	0.94	3.52	-	1146.9
gi|27597085|ref|NP_000357.3|	tropomyosin 1 (alpha) [Homo sapiens]			1.02E-06	0.94	20.20	7.04	32865.7
AHQ-3-9, 1512	R.AELSEGQVR.Q	989.06506	1	2.88E-05	0.27	1.92	-	300.8
AHQ-3-9, 2817	R.KLVIIESDLER.A	1315.54103	2	8.38E-06	0.95	3.98	-	1534.5
AHQ-3-9, 2815	R.KLVIIESDLER.A	1315.54103	1	1.02E-06	0.67	2.46	-	623.5
gi|4557675|ref|NP_000201.1|	integrin alpha chain, alpha 6 [Homo sapiens]			1.13E-06	1.87	20.25	2.80	119509.5
AHQ-3-4, 5942	K.DFHYIVFGAPGTYNWK.G	1916.12609	2	1.13E-06	0.94	4.14	-	1030.1
AHQ-3-4, 3422	K.FGSCQQGVAATFTK.D	1503.66172	2	1.62E-05	0.93	3.85	-	1098.7
gi|4758076|ref|NP_004068.1|	citrate synthase precursor; Citrate synthase, mitochondrial [Homo sapie			1.17E-06	1.62	20.16	5.79	51706.2
AHQ-3-8, 4420	K.GLVYETSVLDPDEGIR.F	1763.92654	2	2.31E-05	0.81	3.11	-	782.2
AHQ-3-8, 2994	K.IVPNVLLEQGK.A	1210.44805	2	1.17E-06	0.81	2.52	-	526.1
gi|4507295|ref|NP_003560.1|	syntaxin 7 [Homo sapiens]			1.20E-06	0.86	10.18	5.75	29845.3
AHQ-3-13, 3354	R.TLNQLGTPQDSPELR.Q	1669.81798	2	3.57E-05	0.71	3.34	-	341.1
AHQ-3-13-, 3345 - 3375	R.TLNQLGTPQDSPELR.Q	1669.81798	2	1.20E-06	0.86	3.56	-	691.9
AHQ-3-10, 3107	R.TLNQLGTPQDSPELR.Q	1669.81798	2	3.39E-04	0.70	2.88	-	506.4
gi|4502905|ref|NP_001822.1|	clusterin; complement-associated protein SP-40 [Homo sapiens]			1.21E-06	2.73	30.28	11.36	52494.3
AHQ-3-9, 5537	R.ASSIIDELFQDR.F	1394.51197	2	2.18E-05	0.92	3.61	-	1089.0
AHQ-3-9, 2712	R.EILSVDCSTNNPSQAK.L	1764.89299	2	2.11E-05	0.86	3.52	-	726.6
AHQ-3-11, 3359	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	4.42E-05	0.96	5.53	-	1103.3
AHQ-3-9, 3064	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	1.21E-06	0.94	4.71	-	912.4
gi|11496891|ref|NP_000662.2|	class III alcohol dehydrogenase 5 chi subunit; Alcohol dehydrogenase (			1.22E-06	0.95	10.25	5.88	39738.1
AHQ-3-9, 4845	K.AAVAWEAGKPLSIEEIEVAPPK.A	2306.64276	2	1.22E-06	0.95	4.98	-	921.4
gi|4502167|ref|NP_000475.1|	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disea			1.22E-06	0.67	10.19	2.34	86942.8
AHQ-3-4, 7050 - 7118	R.CLVGEFVSDALLVPDKCK.F	2053.38561	2	1.22E-06	0.67	3.79	-	451.5
gi|21361122|ref|NP_001440.2|	four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap			1.25E-06	3.45	40.22	18.93	31894.7
AHQ-3-9, 2233	K.AIVAGDQNVEYK.G	1307.43431	2	3.28E-05	0.91	3.26	-	1018.4
AHQ-3-9, 2883	K.CLHPLANETFVAK.D	1501.73210	2	6.83E-06	0.68	2.75	-	336.9
AHQ-3-13, 3805	R.FVFHQEQVYCPDCAK.K	1931.13758	3	6.80E-05	0.72	3.43	-	799.9
AHQ-3-14, 4609	R.FVFHQEQVYCPDCAK.K	1931.13758	2	3.28E-05	0.95	4.32	-	1216.1
AHQ-3-9, 2760 - 2767	K.GEDFYCVTCHETK.F	1648.75260	2	1.25E-06	0.92	3.99	-	917.9
gi|7706675|ref|NP_057661.1|	RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M			1.26E-06	2.80	30.21	16.35	23461.5
AHQ-3-11, 4547	R.GSDVIIMLVGNK.T	1246.50220	2	1.26E-06	0.96	4.20	-	1887.5
AHQ-3-14-, 3411	R.LQLWDTAGQER.F	1317.43243	2	3.27E-04	0.84	2.94	-	735.8
AHQ-3-11, 3206 - 3271	R.LQLWDTAGQER.F	1317.43243	2	4.68E-05	0.94	4.03	-	988.7
AHQ-3-11, 3450 - 3460	K.LVFLGEQSVGK.T	1177.37492	2	1.24E-05	0.90	3.26	-	1013.6
gi|6715607|ref|NP_000175.1|	G-gamma globin [Homo sapiens]			1.28E-06	0.91	10.18	6.80	16126.3
AHQ-3-13-, 4835 - 4845	R.LLVVYPWTQR.F	1275.52342	2	1.28E-06	0.91	3.53	-	922.5
AHQ-3-13, 4742 - 4819	R.LLVVYPWTQR.F	1275.52342	2	8.97E-04	0.91	3.11	-	1035.4

gi|5803009|ref|NP_006786.1|	EH-domain containing 1; homolog of Drosophila past; EH domain containin			1.37E-06	2.64	30.31	13.30	60844.7
AHQ-3-7, 7406	R.FMCAQLPNPVLDSISIIDTPGILSGEK.Q	2918.37521	2	1.37E-06	0.93	4.39	-	1037.8
AHQ-3-7, 6228 - 6231	R.IGPEPTTDSFIAVMHGPTEGVVPGNALVVDPR.R	3274.69283	3	3.62E-04	0.95	6.20	-	642.0
AHQ-3-7, 3958	R.KLFEAEEQDLFK.D	1497.67379	2	1.33E-04	0.76	3.55	-	562.4
gi|20149545|ref|NP_002717.2|	prolyl endopeptidase [Homo sapiens]			1.44E-06	0.96	10.22	2.39	80733.0
AHQ-3-6, 6039	R.VFLDPNILSDDGTVALR.G	1846.07392	2	1.44E-06	0.96	4.46	-	1600.1
gi|6912238|ref|NP_036226.1|	peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]			1.46E-06	5.14	60.28	30.37	22026.2
AHQ-3-12, 6882	K.ETDLLLDDSLVSIFGNR.R	1908.09888	2	1.46E-06	0.97	5.58	-	1266.1
AHQ-3-12, 3876 - 3944	R.FSMVVQDGIVK.A	1223.46709	2	3.88E-06	0.90	3.76	-	798.7
AHQ-3-12, 3416	R.LLADPTGAFGK.E	1090.25413	2	2.18E-04	0.86	3.20	-	739.2
AHQ-3-12, 4839 - 4903	K.VGDAIPAVEVFEGEPGNK.V	1829.00022	2	2.36E-05	0.93	4.70	-	500.0
AHQ-3-12, 6847	K.VGDAIPAVEVFEGEPGNKVNLAELFK.G	2744.09176	2	1.94E-06	0.58	2.76	-	271.2
AHQ-3-12, 4748	K.VNLAELFK.G	934.11414	2	2.40E-04	0.89	3.09	-	832.8
gi|30148978|ref|XP_291520.2|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			1.47E-06	0.74	10.17	2.15	68413.1
AHQ-3-11, 4772 - 4831	R.DWSHYFKTIKDLR.A	1709.92863	2	1.47E-06	0.74	3.39	-	653.7
AHQ-3-13-, 4875	R.DWSHYFKTIKDLR.A	1709.92863	2	9.41E-04	0.56	2.96	-	530.9
AHQ-3-11, 4632 - 4654	R.DWSHYFKTIKDLR.A	1709.92863	2	1.72E-04	0.70	3.29	-	599.4
gi|20547663|ref|XP_166266.1|	similar to Esterase D [Homo sapiens]			1.50E-06	1.53	20.22	14.18	31462.6
AHQ-3-9, 2589	K.SGYHQSASEHGLVVIAPDTSPR.G	2309.48055	2	1.50E-06	0.93	4.37	-	858.0
AHQ-3-9, 6085	K.SVSAFAPICNPVLCPWGK.K	2006.33387	2	4.68E-06	0.60	3.08	-	268.8
gi|4505621|ref|NP_002558.1|	prostatic binding protein; phosphatidylethanolamine binding protein [Ho			1.50E-06	1.91	20.25	20.32	21056.6
AHQ-3-11, 4859	R.APVAGTCYQAEWDDYVPK.L	2072.23961	2	1.32E-04	0.95	4.54	-	1130.8
AHQ-3-11, 4472	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	3.06E-06	0.94	4.20	-	1056.6
AHQ-3-11, 4219	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	1.50E-06	0.96	4.91	-	1055.2
gi|29745994|ref|XP_290546.1|	similar to KIAA0830 protein [Homo sapiens]			1.57E-06	0.82	10.14	2.60	55016.4
AHQ-3-1, 4472	K.ILEVVNQIQDEER.M	1585.74098	2	1.57E-06	0.82	2.79	-	974.7
gi|4507777|ref|NP_003331.1|	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast); UbcH5C; ubi			1.62E-06	0.56	10.13	12.24	16687.1
AHQ-3-13, 5350	R.IYHPNINSNGSICLDILR.S	2101.37199	2	1.62E-06	0.56	2.66	-	304.5
gi|18640750|ref|NP_570138.1|	regulator of G-protein signalling 18; regulator of G-protein signaling			1.72E-06	0.83	10.19	8.94	27582.0
AHQ-3-10, 3922	K.EVITNSITQPTLHSFDAAQSR.V	2316.51300	2	1.72E-06	0.83	3.76	-	350.2
gi|14780596|ref|XP_033004.1|	hypothetical protein BC005107 [Homo sapiens]			1.86E-06	0.47	10.13	5.00	18127.9
AHQ-3-1, 2154	R.EQIIAKAK.A	901.08569	1	7.01E-05	0.06	1.92	-	208.4
AHQ-3-2, 1669 - 1857	R.EQIIAKAK.A	901.08569	1	4.19E-05	0.41	2.56	-	314.2
AHQ-3-3, 1696 - 1828	R.EQIIAKAK.A	901.08569	1	1.58E-04	0.24	2.26	-	275.7
AHQ-3-3, 2009	R.EQIIAKAK.A	901.08569	1	1.86E-06	0.47	2.50	-	298.0
AHQ-3-4, 1752 - 1888	R.EQIIAKAK.A	901.08569	1	6.05E-04	0.31	2.45	-	241.8
AHQ-3-1, 1972 - 2038	R.EQIIAKAK.A	901.08569	1	4.20E-04	0.26	2.42	-	273.9
gi|18600882|ref|XP_089309.1|	similar to Cyclophilin-LC [Homo sapiens]			2.03E-06	0.25	10.15		18166.6
AHQ-3-12, 5044 - 5106	R.IIPGFMCQGGDFTR.P	1600.84403	2	2.03E-06	0.25	2.55	-	75.0
AHQ-3-14-, 4784 - 4793	R.IIPGFMCQGGDFTR.P	1600.84403	2	3.71E-05	0.73	2.55	-	262.3
AHQ-3-12, 4742 - 4822	R.IIPGFMCQGGDFTR.P	1600.84403	2	2.76E-05	0.86	3.06	-	407.6
gi|4503013|ref|NP_003906.1|	copine I [Homo sapiens]			2.10E-06	0.95	10.26	3.72	59058.5
AHQ-3-13, 6969	R.EALAQTVLAEVPTQLVSYFR.A	2236.55253	2	3.08E-04	0.50	2.63	-	369.8
AHQ-3-6, 7319	R.EALAQTVLAEVPTQLVSYFR.A	2236.55253	2	2.10E-06	0.95	5.29	-	628.7
gi|14149680|ref|NP_056107.1|	KIAA0747 protein [Homo sapiens]			2.23E-06	3.41	40.23	5.71	122855.6
AHQ-3-12, 5512 - 5532	R.FEWELPLDEAQR.R	1533.66622	2	1.65E-05	0.71	3.11	-	360.7
AHQ-3-6, 7023	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	1.34E-05	0.85	3.58	-	523.8
AHQ-3-4, 7317	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	2.23E-06	0.78	3.57	-	487.7
AHQ-3-12, 3998	R.LTHVDSPLEAPAGPLGQVK.L	1930.19405	2	4.11E-06	0.96	4.37	-	1462.1
AHQ-3-12, 4487	K.VQLDLAETDLSQGVAR.W	1715.88665	2	2.86E-04	0.95	4.57	-	1676.4
gi|4507669|ref|NP_003286.1|	tumor protein, translationally-controlled 1; fortilin; histamine-releas			2.28E-06	0.98	10.24	8.14	19595.2
AHQ-3-11, 4644 - 4694	R.DLISHDEMFSDIYK.I	1713.88949	2	2.28E-06	0.98	4.70	-	2318.8
gi|21361322|ref|NP_006078.2|	tubulin, beta, 5 [Homo sapiens]			2.33E-06	2.61	30.28	13.74	49585.5
AHQ-3-9, 2597	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	8.78E-05	0.90	3.72	-	938.0
AHQ-3-7, 2670	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	3.27E-05	0.91	4.06	-	844.8
AHQ-3-7, 5302	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	2.33E-06	0.95	5.53	-	856.8
AHQ-3-7, 6876	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	8.97E-05	0.75	4.06	-	617.7
gi|20070156|ref|NP_003565.2|	vessicle-associated membrane protein (VAMP)-associated protein of 33 k			2.37E-06	0.89	10.16	4.96	27317.4
AHQ-3-12, 4086	K.GPFTDVVTTNLK.L	1292.46278	2	2.37E-06	0.89	3.10	-	1125.7
gi|4503423|ref|NP_001939.1|	dUTP pyrophosphatase [Homo sapiens]			2.41E-06	0.97	10.24	10.37	17748.0
AHQ-3-11, 5351 - 5412	R.IFYPEIEEVQALDDTER.G	2068.22598	2	2.41E-06	0.97	4.77	-	1808.8
gi|28178825|ref|NP_005887.2|	isocitrate dehydrogenase 1 (NADP+), soluble; oxalosuccinate decarboxyl			2.50E-06	0.90	10.19	4.11	46659.0
AHQ-3-8, 6549	K.GQETSTNPIASIFAWTR.G	1880.05046	2	2.50E-06	0.90	3.71	-	851.2
gi|21361670|ref|NP_054782.2|	src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo			2.51E-06	2.43	30.19	12.53	48294.0
AHQ-3-12, 3388	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	1.04E-04	0.73	3.12	-	719.0
AHQ-3-12, 5392 - 5435	K.SPTDWALFTYEGNSNDIR.V	2087.19108	2	2.51E-06	0.91	3.88	-	824.3
AHQ-3-12, 5507 - 5583	K.SPTDWALFTYEGNSNDIR.V	2087.19108	2	2.93E-06	0.51	2.80	-	588.2
AHQ-3-12, 4240	R.VAGTGEGGLEEM*VEELNSGK.V	2023.16539	2	7.08E-06	0.80	3.59	-	471.9
gi|4507195|ref|NP_003119.1|	spectrin, beta, non-erythrocytic 1; Spectrin, beta, nonerythrocytic-1 (			2.54E-06	0.77	10.18	0.80	274628.5
AHQ-3-3, 6156	R.LVSQDNFGFDLPAVEAATK.K	2023.23158	2	2.54E-06	0.77	3.60	-	327.1
gi|4504041|ref|NP_002061.1|	guanine nucleotide binding protein (G protein), alpha inhibiting activi			2.57E-06	3.48	40.21	17.18	40450.7
AHQ-3-9, 5443 - 5519	R.EYQLNDSAAYYLNDLER.I	2078.18096	2	2.57E-06	0.86	3.42	-	1006.8
AHQ-3-8, 3729 - 3730	R.IAQSDYIPTQQDVLR.T	1747.93034	2	5.26E-06	0.89	3.96	-	469.4
AHQ-3-9, 4341	K.ITHSPLTICFPEYTGANK.Y	2051.30821	2	1.75E-04	0.93	4.23	-	780.1
AHQ-3-9, 5152	K.ITHSPLTICFPEYTGANKYDEAASYIQSK.F	3307.63156	3	3.30E-04	0.80	3.71	-	371.7
gi|20539300|ref|XP_088391.4|	similar to tropomyosin 4 [Homo sapiens]			2.60E-06	1.81	20.19	6.88	18592.1
AHQ-3-9, 3159	R.KLVILEGELER.A	1299.54160	2	3.96E-05	0.92	3.50	-	1216.1
AHQ-3-11, 3411	R.KLVILEGELER.A	1299.54160	2	2.60E-06	0.94	3.75	-	1263.1
AHQ-3-9, 3040 - 3047	R.KLVILEGELER.A	1299.54160	2	8.53E-04	0.90	3.81	-	1032.6
AHQ-3-9, 3657	K.LVILEGELER.A	1171.36868	2	1.02E-04	0.88	3.19	-	1053.4
gi|4504973|ref|NP_002292.1|	lactate dehydrogenase C [Homo sapiens]			2.68E-06	0.91	10.19	3.61	36311.0
AHQ-3-11, 2330	R.VIGSGCNLDSAR.F	1250.36445	2	1.36E-05	0.80	3.15	-	549.5
AHQ-3-9, 2211 - 2212	R.VIGSGCNLDSAR.F	1250.36445	2	2.68E-06	0.91	3.73	-	643.4
gi|4504483|ref|NP_000185.1|	hypoxanthine phosphoribosyltransferase 1 [Homo sapiens]			2.69E-06	0.90	10.18	7.34	24579.2
AHQ-3-10, 4386	R.SVGYKPDFVGFEIPDK.F	1799.01571	2	2.69E-06	0.90	3.55	-	833.8
gi|30158489|ref|XP_301421.1|	similar to Chloride intracellular channel protein 1 (Nuclear chloride			2.81E-06	1.64	30.22	11.58	28267.5
AHQ-3-10, 5642 - 5722	K.FLNGNELTLADCNLLPK.L	1934.20276	2	2.81E-06	0.80	3.48	-	996.1
AHQ-3-12, 6067	K.FLNGNELTLADCNLLPK.L	1934.20276	2	6.60E-04	0.63	3.40	-	688.1
AHQ-3-9, 5353 - 5423	R.KFLNGNELTLADCNLLPK.L	2062.37568	2	3.65E-05	0.77	4.39	-	714.3
AHQ-3-10, 2112	K.NSNPALNDNLQK.G	1328.41362	1	7.00E-05	0.26	2.11	-	213.5
AHQ-3-9, 1993	K.NSNPALNDNLQK.G	1328.41362	1	6.37E-05	0.08	1.94	-	130.3
gi|15718761|ref|NP_004976.2|	c-K-ras2 protein isoform b; Kirsten rat sarcoma-2 viral (v-Ki-ras2) on			2.93E-06	0.91	10.22	7.98	21424.4
AHQ-3-11, 3543 - 3607	R.VKDSEDVPM*VLVGNK.C	1646.88770	2	2.93E-06	0.91	4.34	-	958.2
gi|30149460|ref|XP_210540.2|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			2.97E-06	0.93	10.17	3.95	29287.8
AHQ-3-5, 2052 - 2116	K.HIYYITGETK.D	1225.37490	1	1.70E-04	0.45	1.90	-	686.1
AHQ-3-5, 2049	K.HIYYITGETK.D	1225.37490	2	2.97E-06	0.93	3.42	-	862.8
gi|7330335|ref|NP_039234.1|	chloride intracellular channel 4; chloride intracellular channel 4 like			2.99E-06	3.11	40.25	31.23	28771.9
AHQ-3-10, 2870	K.AGSDGESIGNCPFSQR.L	1683.73852	2	5.25E-06	0.45	2.92	-	275.4
AHQ-3-10, 4442 - 4443	R.DEFTNTCPSDKEVEIAYSDVAK.R	2520.66487	2	2.99E-06	0.83	3.83	-	636.9
AHQ-3-10, 5459	K.FLDGNEMTLADCNLLPK.L	1953.22635	2	6.25E-06	0.88	3.82	-	915.0
AHQ-3-10, 4440	R.KPADLQNLAPGTHPPFITFNSEVK.T	2622.95944	3	5.77E-05	0.95	4.95	-	1139.8
gi|23110942|ref|NP_002781.2|	proteasome alpha 5 subunit; proteasome component 5; macropain subunit			3.25E-06	1.79	20.21	15.77	26410.9
AHQ-3-10, 2963	R.AIGSASEGAQSSLQEVYHK.S	1963.09463	2	4.28E-05	0.85	3.49	-	743.0
AHQ-3-10, 4346	K.GPQLFHMDPSGTFVQCDAR.A	2165.39491	2	3.25E-06	0.94	4.11	-	1062.2
gi|5453607|ref|NP_006420.1|	chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co			3.35E-06	2.08	30.16	9.76	59366.3
AHQ-3-7, 7196	K.EGTDSSQGIPQLVSNISACQVIAEAVR.T	2832.09426	2	6.37E-04	0.54	2.50	-	407.7
AHQ-3-7, 2830	R.GGAEQFMEETER.S	1384.45431	2	9.33E-04	0.63	2.71	-	788.0

AHQ-3-7, 4982	K.LPIGDVATQYFADR.D	1566.73935	2	3.35E-06	0.90	3.09	-	1125.0
gi|5031601|ref|NP_005711.1|	actin related protein 2/3 complex subunit 1B; ARP2/3 protein complex su			3.49E-06	1.42	20.22	9.41	40949.5
AHQ-3-8, 1962	K.ASSEGGTAAGAGLDSLHK.N	1629.71071	2	3.49E-06	0.50	2.60	-	627.6
AHQ-3-8, 2885	R.TQIAICPNNHEVHIYEK.S	2068.29887	2	2.00E-04	0.92	4.37	-	770.8
gi|18104989|ref|NP_002822.2|	protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t			3.51E-06	1.46	20.19	4.03	67560.7
AHQ-3-6, 5941 - 6013	K.AGFWEEFESLQK.Q	1471.59489	1	1.02E-05	0.54	2.98	-	465.2
AHQ-3-6, 4997	R.DLSGLDAETLLK.G	1275.43053	2	3.51E-06	0.92	3.07	-	1372.3
gi|4826659|ref|NP_004921.1|	F-actin capping protein beta subunit; Cap Z [Homo sapiens]			3.62E-06	1.91	20.23	10.29	30628.5
AHQ-3-9, 3748 - 3816	K.GCWDSIHVVEVQEK.S	1687.85505	2	4.19E-06	0.96	4.52	-	1502.0
AHQ-3-10, 3806 - 3820	K.GCWDSIHVVEVQEK.S	1687.85505	2	4.22E-04	0.85	3.83	-	877.0
AHQ-3-10, 3150 - 3160	R.KLEVEANNAFDQYR.D	1697.82988	2	1.17E-05	0.96	4.15	-	1620.9
AHQ-3-9, 2953 - 2979	R.KLEVEANNAFDQYR.D	1697.82988	2	3.62E-06	0.95	4.13	-	1466.5
gi|15147250|ref|NP_150281.1|	protein phosphatase 1, regulatory (inhibitor) subunit 14A; 17-kDa PKC-			3.66E-06	0.84	10.20	10.88	16692.9
AHQ-3-12, 6768	K.SCGKPVEDFIQELLAK.L	1836.09909	2	3.66E-06	0.84	4.05	-	409.9
gi|24307969|ref|NP_055423.1|	cytoplasmic FMR1 interacting protein 1; selective hybridizing clone (m			3.72E-06	0.89	10.18	1.04	145181.2
AHQ-3-3, 4564	R.SSLEGPTILDIEK.F	1402.57231	2	3.72E-06	0.89	3.58	-	928.0
gi|6005854|ref|NP_009204.1|	repressor of estrogen receptor activity; B-cell associated protein [Hom			3.86E-06	0.95	10.21	4.35	33296.1
AHQ-3-9, 6737	R.IPWFQYPIIYDIR.A	1725.02480	2	3.86E-06	0.95	4.12	-	1353.8
gi|4557469|ref|NP_001273.1|	adaptor-related protein complex 2, beta 1 subunit; adaptin, beta 2 (bet			4.26E-06	0.70	10.15	2.77	104551.9
AHQ-3-6, 7178	K.KPSETQELVQQVLSLATQDSDNPDLR.D	2913.14409	2	4.26E-06	0.70	2.97	-	546.1
gi|28872786|ref|NP_060719.3|	CDK5 regulatory subunit associated protein 2; CDK5 activator-binding p			4.28E-06	0.29	10.15	0.95	215034.1
AHQ-3-7, 6094 - 6171	R.SEGLITEKCSSQQPPGSK.T	1935.10279	2	4.28E-06	0.29	2.54	-	346.3
gi|29727204|ref|XP_290872.1|	similar to Pyruvate kinase, M2 isozyme [Homo sapiens]			4.33E-06	0.92	10.18	5.37	16297.7
AHQ-3-13-, 2381	R.APIIAVTR.N	841.03348	2	3.52E-04	0.92	2.83	-	1297.5
AHQ-3-7, 2010 - 2079	R.APIIAVTR.N	841.03348	2	4.33E-06	0.92	2.70	-	1223.3
gi|4502285|ref|NP_001672.1|	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 2; ATP			4.37E-06	0.81	10.17	1.50	109690.3
AHQ-3-1, 4876	K.VGEATETALTCLVEK.M	1622.81958	2	4.37E-06	0.81	3.44	-	632.7
gi|7019545|ref|NP_037481.1|	secreted protein of unknown function [Homo sapiens]			4.67E-06	0.87	10.16	8.72	18856.2
AHQ-3-12, 3968	R.YGGEEEDQPIYLAVK.G	1711.85009	2	4.67E-06	0.87	3.29	-	727.4
gi|4507509|ref|NP_003245.1|	tissue inhibitor of metalloproteinase 1 precursor; Erythroid-potentiati			4.71E-06	0.94	10.27	9.18	23170.8
AHQ-3-10, 4202	K.LQSGTHCLWTDQLLQGSEK.G	2203.41795	2	4.71E-06	0.94	4.77	-	853.0
AHQ-3-9, 4203	K.LQSGTHCLWTDQLLQGSEK.G	2203.41795	2	4.60E-04	0.97	5.48	-	1146.5
gi|7705963|ref|NP_057454.1|	RAB9-like protein [Homo sapiens]			4.90E-06	0.85	10.17	6.97	22719.3
AHQ-3-11, 3763	R.FVTLQIWDTAGQER.F	1664.84302	2	4.90E-06	0.85	3.30	-	1186.7
AHQ-3-10, 3651 - 3724	R.FVTLQIWDTAGQER.F	1664.84302	2	8.11E-05	0.86	3.45	-	860.9
gi|7705501|ref|NP_057546.1|	hypothetical protein HSPC194 [Homo sapiens]			5.07E-06	1.75	20.20	41.07	11564.5
AHQ-3-14-, 6869 - 6873	K.AGSVPSLAAGLLFGSLAGLGAYQLSQDPR.N	2818.17710	2	6.22E-05	0.89	4.07	-	551.1
AHQ-3-14-, 5913 - 5980	K.FM*PAGLIAGASLLM*VAK.V	1723.13705	2	5.07E-06	0.87	3.34	-	1097.8
gi|4885539|ref|NP_005380.1|	protein-L-isoaspartate (D-aspartate) O-methyltransferase [Homo sapiens]			5.43E-06	2.66	30.23	30.84	24636.2
AHQ-3-11, 5114 - 5180	K.ALDVGSGSGILTACFAR.M	1696.90662	2	5.98E-05	0.90	3.67	-	1121.2
AHQ-3-11, 4476 - 4503	R.LILPVGPAGGNQM*LEQYDK.L	2060.35997	2	6.88E-06	0.93	4.50	-	550.7
AHQ-3-10, 5775	R.M*GYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGR.L	3522.97505	3	5.43E-06	0.83	3.62	-	542.8
gi|4885425|ref|NP_005334.1|	v-Ha-ras Harvey rat sarcoma viral oncogene homolog; H-RasIDX [Homo sapi			5.47E-06	0.88	10.19	7.94	21298.0
AHQ-3-11, 5630	R.TGEGFLCVFAINNTK.S	1672.88352	2	5.47E-06	0.88	3.85	-	745.7
gi|7705704|ref|NP_057001.1|	glutathione S-transferase subunit 13 homolog [Homo sapiens]			5.52E-06	2.76	30.26	19.91	25496.7
AHQ-3-11, 3287 - 3291	K.AGMSAEQAQGLLEK.I	1433.61314	2	5.52E-06	0.94	4.17	-	1364.8
AHQ-3-11, 4372	R.FLTAVNLEHPEMLEK.A	1772.05845	2	2.54E-05	0.95	5.15	-	1021.0
AHQ-3-11, 4440	R.NEDITEPQSILAAAEK.A	1729.86695	2	9.62E-05	0.88	3.89	-	547.3
gi|9966825|ref|NP_065089.1|	HEF like Protein [Homo sapiens]			5.59E-06	0.98	10.29	2.80	86696.2
AHQ-3-13-, 4109 - 4174	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	3.38E-05	0.98	5.74	-	2048.2
AHQ-3-13, 4154	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	5.59E-06	0.98	5.71	-	1695.8
gi|7305303|ref|NP_038464.1|	NCK-associated protein 1 [Homo sapiens]			5.80E-06	0.80	10.16	1.42	128789.1
AHQ-3-4, 4950	K.ELATVLSDQPGLLGPK.A	1638.88692	2	5.80E-06	0.80	3.22	-	625.4
gi|7669501|ref|NP_005552.2|	lysosomal-associated membrane protein 1 [Homo sapiens]			5.81E-06	0.47	10.21	2.64	44772.8
AHQ-3-4, 2213	R.ALQATVGNSYK.C	1152.28232	1	5.81E-06	0.47	2.09	-	441.6
gi|29743324|ref|XP_293276.1|	similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote			5.94E-06	1.46	20.33	15.98	21244.7
AHQ-3-13, 5293 - 5357	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	2.09E-04	0.91	6.45	-	815.6
AHQ-3-14-, 5236 - 5307	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	1.59E-04	0.93	6.32	-	1052.8
AHQ-3-11, 5130 - 5198	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	1.83E-04	0.93	5.01	-	834.4
AHQ-3-13, 5961 - 5963	K.YTLPPGVDPTKVSSSLSPEGTLTVEAPMPK.L	3100.52936	3	5.94E-06	0.53	3.14	-	723.3
gi|21361565|ref|NP_001679.2|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, is			6.01E-06	1.82	20.21	8.98	28908.4
AHQ-3-11, 2774	R.HYLFDVQR.N	1078.20513	2	4.48E-05	0.90	3.02	-	1043.1
AHQ-3-11, 6802 - 6803	R.YGLIPEEFFQFLYPK.T	1892.18434	2	6.01E-06	0.91	4.24	-	396.9
gi|4557797|ref|NP_000260.1|	non-metastatic cells 1 protein [Homo sapiens]			6.01E-06	3.48	40.19	20.39	17148.6
AHQ-3-12, 4034	K.DRPFFAGLVK.Y	1150.35439	2	5.47E-04	0.83	3.03	-	992.7
AHQ-3-12, 3199	R.GLVGEIIK.R	829.01947	2	4.61E-05	0.82	2.95	-	753.3
AHQ-3-12, 2819 - 2820	R.GLVGEIIKR.F	985.20582	2	1.30E-04	0.92	3.08	-	1126.0
AHQ-3-12, 2900	R.TFIAIKPDGVQR.G	1345.57205	2	6.01E-06	0.91	3.73	-	926.6
gi|30148492|ref|XP_293610.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			6.03E-06	1.66	20.22	4.44	72113.4
AHQ-3-6, 4197 - 4213	K.DAGTIAGLNVLR.I	1200.37012	2	2.08E-04	0.95	3.57	-	1650.4
AHQ-3-7, 4160	K.DAGTIAGLNVLR.I	1200.37012	2	5.24E-04	0.91	2.90	-	1443.3
AHQ-3-7, 3996	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	5.46E-04	0.82	3.33	-	589.3
AHQ-3-6, 4045 - 4049	R.IINEPTAAAIAYGLDKK.V	1789.06550	3	6.03E-06	0.70	3.24	-	385.1
gi|4759086|ref|NP_004883.1|	vesicle trafficking protein sec22b [Homo sapiens]			6.05E-06	0.87	10.17	6.51	24740.4
AHQ-3-12, 3946	R.NLGSINTELQDVQR.I	1587.71696	2	6.05E-06	0.87	3.37	-	1067.2
gi|5453722|ref|NP_006321.1|	lysophospholipase I; lysophospholipase 1; lysophospholipid-specific lys			6.18E-06	1.86	20.19	12.61	24669.5
AHQ-3-11, 2908	K.ALIDQEVKNGIPSNR.I	1654.84968	2	9.79E-05	0.94	3.81	-	1248.8
AHQ-3-11, 6371	K.LAGVTALSCWLPLR.A	1558.86992	2	6.18E-06	0.92	3.76	-	1134.6
gi|4557321|ref|NP_000030.1|	apolipoprotein A-I precursor [Homo sapiens]			6.24E-06	2.72	30.22	14.61	30777.6
AHQ-3-11, 4364 - 4368	R.DYVSQFEGSALGK.Q	1401.50297	2	3.05E-05	0.94	3.77	-	1182.2
AHQ-3-14, 6167	K.LLDNWDSVTSTFSK.L	1613.74965	2	6.24E-06	0.84	3.73	-	594.8
AHQ-3-14-, 5193	K.LLDNWDSVTSTFSK.L	1613.74965	2	2.66E-05	0.94	4.34	-	1017.5
AHQ-3-11, 5014 - 5062	K.LLDNWDSVTSTFSK.L	1613.74965	2	3.43E-05	0.85	2.97	-	906.8
AHQ-3-14-, 6153	K.VSFLSALEEYTK.K	1387.55934	2	6.10E-04	0.93	3.34	-	1222.6
gi|7705819|ref|NP_057181.1|	HSPC039 protein [Homo sapiens]			6.43E-06	0.94	10.23	24.39	8968.7
AHQ-3-14-, 5053	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	6.43E-06	0.94	4.60	-	900.6
AHQ-3-1, 5465	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	2.70E-04	0.68	2.94	-	501.7
gi|10864055|ref|NP_067069.1|	megakaryocyte-enhanced gene transcript 1 protein; lymphocyte antigen-6			6.49E-06	0.92	10.24	4.71	40891.9
AHQ-3-9, 5083	R.AADGSPCNVLLCSVVPSR.R	1905.14311	2	9.60E-05	0.39	2.55	-	544.4
AHQ-3-1, 5724	R.AADGSPCNVLLCSVVPSR.R	1905.14311	2	6.49E-06	0.92	4.85	-	750.4
gi|4504557|ref|NP_000864.1|	intercellular adhesion molecule 2 precursor [Homo sapiens]			6.55E-06	0.94	10.23	5.82	30653.1
AHQ-3-6, 7379	R.VPTVEPLDSLTLFLFR.G	1848.17455	2	6.55E-06	0.94	4.56	-	703.9
gi|29740995|ref|XP_291768.1|	similar to Proteasome activator complex subunit 2 (Proteasome activato			6.74E-06	0.98	10.28	9.64	19192.6
AHQ-3-10, 6327 - 6330	R.AFYAELYHIISSNLEK.T	1899.13528	2	6.74E-06	0.98	5.51	-	1832.4
gi|29742410|ref|XP_291183.1|	similar to TREM-like transcript 1 [Homo sapiens]			7.04E-06	0.78	10.26	5.14	32678.3
AHQ-3-13-, 4170 - 4247	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	4.37E-04	0.86	3.85	-	503.2
AHQ-3-13-, 4309 - 4311	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	3.27E-04	0.82	3.32	-	406.5
AHQ-3-11, 4102 - 4163	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	7.04E-06	0.78	3.09	-	529.5
gi|20536967|ref|XP_115812.1|	similar to Latent transforming growth factor beta binding protein 1L p			7.08E-06	0.81	10.13	12.00	13416.2
AHQ-3-1, 3466	K.GISGEQSTEGSFPLR.Y	1565.66662	2	7.08E-06	0.81	2.56	-	1077.8
gi|16950601|ref|NP_005956.2|	myosin light chain kinase isoform 6; myosin light chain kinase [Homo s			7.10E-06	1.19	20.21	2.72	110074.8
AHQ-3-12, 2528	R.DLEVVEGSAAR.F	1146.23295	1	2.42E-04	0.50	2.32	-	440.3
AHQ-3-6, 4883	R.STSFNVQDLLPDHEYK.F	1894.03076	2	7.10E-06	0.69	3.16	-	476.5
gi|4507207|ref|NP_003121.1|	sorcin; Sorcin (class 4 gene) [Homo sapiens]			7.19E-06	0.84	10.21	10.10	21676.3
AHQ-3-11, 4459 - 4522	R.CLTQSGIAGGYKPFNLETCR.L	2275.54736	2	7.19E-06	0.84	4.23	-	465.4
gi|11321585|ref|NP_002065.1|	guanine nucleotide-binding protein, beta-1 subunit; G protein, beta-1			7.20E-06	1.34	20.18	9.12	37376.8
AHQ-3-9, 4436	R.KACADATLSQITNNIDPVGR.I	2146.36794	2	1.09E-04	0.81	3.48	-	468.0

AHQ-3-9, 3783	R.KACADATLSQITNNIDPVGR.I	2146.36794	2	8.71E-06	0.79	3.51	-	521.8
AHQ-3-9, 3871	K.LIIWDSYTTNK.V	1354.53258	1	7.20E-06	0.56	2.93	-	253.9
gi|27484737|ref|XP_210664.1|	similar to MRDS1 protein [Homo sapiens]			7.56E-06	0.55	10.15	4.68	45171.8
AHQ-3-11, 6760	K.FEGEGLNEYIPMSLLKTGK.T	2127.44634	2	7.56E-06	0.55	3.09	-	357.5
gi|4506405|ref|NP_002872.1|	v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP			7.70E-06	1.59	20.28	14.56	23408.4
AHQ-3-10, 3728	K.AEEWGVQYVETSAK.T	1597.70708	2	3.07E-05	0.62	2.74	-	562.7
AHQ-3-10, 3202 - 3211	R.VKAEEDKIPLLVVGNK.S	1753.07630	2	7.70E-06	0.97	5.68	-	1306.9
gi|4757714|ref|NP_004291.1|	acid phosphatase 1 isoform c; acid phosphatase of erythrocyte; red cell			7.71E-06	1.85	20.19	12.66	18042.4
AHQ-3-11, 3620	K.IELLGSYDPQK.Q	1263.42144	2	6.52E-05	0.92	3.84	-	935.4
AHQ-3-11, 3074	R.SPIAEAVFR.K	990.13779	1	3.91E-05	0.59	2.46	-	311.7
AHQ-3-11, 3072	R.SPIAEAVFR.K	990.13779	2	7.71E-06	0.93	3.30	-	1041.5
gi|4502171|ref|NP_000476.1|	adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho			7.72E-06	2.56	30.20	22.78	19607.6
AHQ-3-11, 3644	R.DISPVLKDPASFR.A	1445.64525	2	1.93E-05	0.72	2.54	-	616.9
AHQ-3-11, 4936	R.GKLPGPTLWASYSLEYGK.A	1968.24075	2	1.11E-05	0.88	3.91	-	676.9
AHQ-3-11, 3443	R.IDYIAGLDSR.G	1123.24098	2	7.72E-06	0.96	4.06	-	1615.6
gi|4505185|ref|NP_002406.1|	macrophage migration inhibitory factor (glycosylation-inhibiting factor			7.85E-06	0.92	10.18	7.83	12476.2
AHQ-3-14-, 4515	K.LLCGLLAER.L	1046.26608	2	7.85E-06	0.92	3.63	-	886.6
gi|29729329|ref|XP_291459.1|	similar to Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18) [			8.04E-06	1.42	20.20	18.30	17172.9
AHQ-3-12, 5655 - 5664	K.EILVGDVGQTVNNLYATFVK.M	2181.47373	2	8.04E-06	0.84	3.96	-	613.8
AHQ-3-12, 2282	K.NIILEEGK.E	916.05399	1	1.08E-04	0.58	2.83	-	399.9
AHQ-3-12, 2275 - 2415	K.NIILEEGK.E	916.05399	1	5.66E-04	0.18	2.26	-	275.6
gi|4507783|ref|NP_003335.1|	ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast); ubiquitin-conju			8.08E-06	0.77	10.18	8.20	20655.0
AHQ-3-11, 4010	K.FYGPQGTPYEGGVWK.V	1686.84715	2	8.08E-06	0.77	3.60	-	374.6
gi|5729804|ref|NP_006694.1|	nudix (nucleoside diphosphate linked moiety X)-type motif 3; diphosphoi			8.30E-06	0.82	10.15	11.63	19470.8
AHQ-3-11, 4742 - 4746	R.WIVPGGGMEPEEEPSVAAVR.E	2111.36386	2	8.30E-06	0.82	3.09	-	547.7
gi|22749499|ref|NP_689979.1|	hypothetical protein MGC40107 [Homo sapiens]			8.48E-06	0.97	10.27	24.78	11741.6
AHQ-3-14-, 5615 - 5627	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	8.48E-06	0.97	5.49	-	1885.2
gi|13786129|ref|NP_112586.1|	RAB33B, member RAS oncogene family; likely ortholog of mouse RAB33b [H			9.32E-06	0.92	10.18	4.80	25717.4
AHQ-3-12, 3323 - 3391	K.IQLWDTAGQER.F	1317.43243	2	6.58E-04	0.82	2.90	-	810.9
AHQ-3-13, 3455 - 3457	K.IQLWDTAGQER.F	1317.43243	2	9.32E-06	0.92	3.55	-	1069.3
AHQ-3-11, 3374	K.IQLWDTAGQER.F	1317.43243	1	6.08E-04	0.16	2.23	-	243.9
gi|24797067|ref|NP_002107.3|	major histocompatibility complex, class I, A precursor; HLA-A1 class I			9.41E-06	0.95	10.26	4.66	40840.5
AHQ-3-8, 2728	R.YTCHVQHEGLPKPLTLR.W	2051.35781	2	9.41E-06	0.95	5.16	-	1183.9
gi|5453760|ref|NP_006147.1|	neural precursor cell expressed, developmentally down-regulated 8 [Homo			9.45E-06	1.02	20.20	17.28	9071.5
AHQ-3-14-, 3608	K.EIEIDIEPTDK.V	1302.40961	1	5.93E-05	0.13	2.24	-	119.9
AHQ-3-14-, 3615 - 3681	K.EIEIDIEPTDKVER.I	1686.84208	2	1.08E-04	0.66	2.96	-	626.1
AHQ-3-14, 4547	K.EIEIDIEPTDKVER.I	1686.84208	2	9.45E-06	0.89	3.96	-	652.6
gi|4757856|ref|NP_004321.1|	BCL2/adenovirus E1B 19kD interacting protein 2; BCL2/adenovirus E1B 19k			9.46E-06	0.90	10.17	4.14	36017.6
AHQ-3-11, 3832 - 3876	R.TLLAVTRPFISSK.F	1433.72075	2	9.46E-06	0.90	3.35	-	1160.5
gi|20551618|ref|XP_167021.1|	similar to calponin 2; Calonin 2 [Homo sapiens]			9.55E-06	1.81	20.24	3.71	47327.9
AHQ-3-11, 5384	R.SMQNWHQLENLSNFIK.A	1990.23155	2	9.59E-04	0.95	4.72	-	1095.2
AHQ-3-12, 5272 - 5278	R.SM*QNWHQLENLSNFIK.A	2006.23095	2	9.55E-06	0.88	3.92	-	558.9
AHQ-3-12, 5610	R.SMQNWHQLENLSNFIK.A	1990.23155	2	6.33E-04	0.93	4.53	-	1046.2
AHQ-3-11, 5027	R.SM*QNWHQLENLSNFIK.A	2006.23095	2	4.21E-05	0.74	3.04	-	544.7
gi|5803135|ref|NP_006852.1|	RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind			9.60E-06	0.72	10.18	5.47	23025.1
AHQ-3-11, 3523 - 3595	K.LLIIGDSGVGK.S	1072.28025	2	4.85E-05	0.93	3.68	-	1196.1
AHQ-3-11, 3528	K.LLIIGDSGVGK.S	1072.28025	1	3.25E-05	0.76	2.63	-	472.8
AHQ-3-11, 3522 - 3587	K.LLIIGDSGVGK.S	1072.28025	1	9.60E-06	0.72	2.68	-	682.2
gi|5902726|ref|NP_005800.1|	peroxiredoxin 2; thioredoxin-dependent peroxide reductase 1 (thiol-spec			9.67E-06	1.79	20.23	9.09	21856.8
AHQ-3-11, 6494	K.EGGLGPLNIPLLADVTR.R	1736.00583	2	9.67E-06	0.84	3.73	-	461.0
AHQ-3-11, 5942	R.KEGGLGPLNIPLLADVTR.R	1864.17875	2	3.34E-04	0.95	4.65	-	975.1
gi|5729808|ref|NP_006557.1|	adhesion glycoprotein; platelet and T cell activation antigen 1; DNAX a			9.68E-06	1.69	20.21	11.31	38583.7
AHQ-3-6, 4822	K.IGTQQDSIAIFSPTHGMVIR.K	2172.49357	3	9.68E-06	0.96	4.21	-	2225.8
AHQ-3-6, 6687	R.WSVIVIPDVTVSDSGLYR.C	2007.27528	2	5.24E-04	0.73	3.32	-	511.2
gi|7706244|ref|NP_057005.1|	divalent cation tolerant protein CUTA [Homo sapiens]			9.68E-06	0.96	10.27	17.31	16832.5
AHQ-3-13-, 6741 - 6815	R.SVHPYEVAEVIALPVEQGNFPYLQWVR.Q	3142.55428	3	9.68E-06	0.96	5.33	-	1888.6
gi|17017988|ref|NP_001853.2|	cytochrome c oxidase subunit Vb precursor; cytochrome c oxidase polype			9.79E-06	0.91	10.18	9.30	13695.6
AHQ-3-13, 3489	K.KGLDPYNVLAPK.G	1315.54272	2	9.79E-06	0.91	3.54	-	901.3
gi|18201911|ref|NP_000629.2|	vitronectin precursor; serum spreading factor; somatomedin B; compleme			1.01E-05	1.61	20.20	6.49	54335.4
AHQ-3-6, 3867	R.DWHGVPGQVDAAMAGR.I	1667.83051	2	1.01E-05	0.72	2.64	-	512.5
AHQ-3-13-, 5626	R.SIAQYWLGCPAPGHL	1671.90045	2	7.72E-05	0.88	3.92	-	687.5
gi|30149327|ref|XP_293672.2|	similar to ebiP7687 [Homo sapiens]			1.01E-05	0.83	10.19	2.88	59404.3
AHQ-3-5, 3423	K.HLEINPNHPIVETLR.Q	1783.02428	2	1.01E-05	0.83	3.79	-	952.1
gi|6996010|ref|NP_002038.1|	glycyl-tRNA synthetase; GlyRS; glycine tRNA ligase [Homo sapiens]			1.04E-05	0.62	10.15	2.92	77530.3
AHQ-3-6, 6839	K.TLYVEEVVPNVIEPSFGLGR.I	2219.52197	2	1.04E-05	0.62	3.04	-	405.3
gi|4504521|ref|NP_002147.1|	heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P			1.07E-05	1.08	20.16	6.98	61024.2
AHQ-3-7, 3892 - 3896	R.GYISPYFINTSK.G	1390.56492	1	4.20E-05	0.35	2.41	-	385.8
AHQ-3-14-, 6900	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D	2870.28530	3	1.07E-05	0.73	3.05	-	687.5
gi|24475861|ref|NP_054891.2|	phosphohistidine phosphatase; sex-regulated protein janus-a [Homo sapi			1.08E-05	0.96	10.21	8.80	13832.4
AHQ-3-13, 3019	K.WAEYHADIYDK.V	1411.49955	2	1.08E-05	0.96	4.14	-	1241.8
gi|23065552|ref|NP_000840.2|	glutathione S-transferase M3; glutathione S-transferase, Mu-3; brain G			1.09E-05	0.80	10.17	6.22	26559.4
AHQ-3-10, 3875	K.LKPQYLEELPGQLK.Q	1656.94708	2	1.09E-05	0.80	3.35	-	571.8
gi|5453704|ref|NP_006398.1|	cytoskeleton related vitamin A responsive protein; glutamate transporte			1.11E-05	0.75	10.15	5.85	21614.6
AHQ-3-1, 5218	R.AWDDFFPGSDR.F	1313.35597	2	1.11E-05	0.75	3.03	-	611.5
gi|20452464|ref|NP_620411.1|	similar to endothelial cell-selective adhesion molecule; likely orthol			1.11E-05	0.72	10.17	4.36	41208.1
AHQ-3-7, 7378	R.QLPSFQTFFAPALDVIR.G	1951.25656	2	1.11E-05	0.72	3.43	-	343.3
gi|6005749|ref|NP_009193.1|	RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA			1.13E-05	2.42	30.21	24.34	19846.9
AHQ-3-10, 3212	R.DVVICPDASLEDAKK.E	1661.85581	2	1.13E-05	0.82	3.49	-	617.5
AHQ-3-11, 4091 - 4092	K.GAEEM*ETVIPVDVMR.R	1692.93673	2	8.73E-04	0.87	3.70	-	654.2
AHQ-3-11, 3026 - 3102	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	9.14E-04	0.73	3.33	-	424.6
gi|4557773|ref|NP_000248.1|	myosin, heavy polypeptide 7, cardiac muscle, beta [Homo sapiens]			1.14E-05	1.29	20.17	1.24	223110.8
AHQ-3-2, 3234 - 3307	R.CNGVLEGIR.I	1019.15759	2	8.76E-04	0.88	3.26	-	752.1
AHQ-3-2, 4275	R.IEELEEELESERTAR.A	1833.93203	2	1.14E-05	0.41	3.08	-	518.1
gi|29734623|ref|XP_299768.1|	hypothetical protein XP_299768 [Homo sapiens]			1.22E-05	0.22	10.12	7.46	14905.7
AHQ-3-10, 3367	K.RMVPVKEIDR.L	1243.50477	1	1.22E-05	0.22	2.12	-	458.0
AHQ-3-9, 3193 - 3423	K.RMVPVKEIDR.L	1243.50477	1	1.11E-04	0.39	2.37	-	417.5
gi|8922712|ref|NP_060713.1|	hypothetical protein FLJ10849 [Homo sapiens]			1.22E-05	0.95	10.22	4.43	49397.9
AHQ-3-7, 2346	K.AAAQLLQSQAQQSGAQQTK.K	1958.12276	2	1.22E-05	0.95	4.43	-	1241.5
gi|4506045|ref|NP_002718.1|	proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p			1.23E-05	1.64	20.16	8.23	17623.6
AHQ-3-1, 4884	K.GPMFELLPGESNK.I	1419.62807	2	1.23E-05	0.82	3.18	-	750.0
AHQ-3-1, 4225	K.GPM*FELLPGESNK.I	1435.62747	2	4.87E-05	0.82	2.88	-	822.3
gi|4503971|ref|NP_001484.1|	GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r			1.23E-05	2.62	30.26	11.41	50582.4
AHQ-3-7, 3522	R.FQLLEGPPESM*GR.G	1477.66758	2	3.00E-05	0.72	3.15	-	523.9
AHQ-3-6, 5211 - 5283	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	5.14E-04	0.92	4.24	-	791.7
AHQ-3-6, 7151	K.VPSTETEALASNLMGMFEK.R	2056.34679	2	1.23E-05	0.98	5.28	-	1834.5
gi|29727317|ref|XP_298144.1|	hypothetical protein XP_298144 [Homo sapiens]			1.25E-05	0.61	10.14	7.96	22108.6
AHQ-3-1, 6669	K.GEYNLTLDTALTSNLK.T	1753.93165	2	1.25E-05	0.61	2.74	-	808.6
gi|4504045|ref|NP_002063.1|	guanine nucleotide binding protein (G protein), q polypeptide [Homo sap			1.27E-05	1.77	20.27	8.91	42142.8
AHQ-3-8, 7199 - 7200	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	1.33E-04	0.96	5.40	-	983.9
AHQ-3-9, 6948	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	1.27E-05	0.96	5.18	-	1112.2
AHQ-3-8, 4178	K.VSAFENPYVDAIK.S	1453.62101	2	1.06E-04	0.80	2.93	-	900.8
gi|4506191|ref|NP_002792.1|	proteasome beta 10 subunit proprotein; proteasome subunit MECL1; protea			1.28E-05	0.96	10.26	7.33	28936.1
AHQ-3-10, 5943	R.LPFTALGSGQDAALAVLEDR.F	2045.28192	2	1.28E-05	0.96	5.20	-	1203.2
gi|4757776|ref|NP_004303.1|	arrestin 3, retinal (X-arrestin); Arrestin 3, retinal [Homo sapiens] [M			1.31E-05	0.66	10.13	3.87	42751.8
AHQ-3-7, 2390	K.LKHEDTNLASSTIIR.P	1698.90245	2	1.31E-05	0.66	2.69	-	373.0
gi|19923262|ref|NP_004153.2|	RAB5A, member RAS oncogene family; RAS-associated protein RAB5A [Homo			1.37E-05	1.32	20.16	10.23	23658.5
AHQ-3-11, 3796	K.FEIWDTAGQER.Y	1352.43364	2	7.42E-05	0.92	3.13	-	1345.0

AHQ-3-10, 3248	K.LVLLGESAVGK.S	1086.30692	1	1.37E-05	0.40	2.81	-	203.3
gi|5454152|ref|NP_006285.1|	ubiquinol-cytochrome c reductase binding protein [Homo sapiens]			1.38E-05	0.97	10.22	11.71	13530.4
AHQ-3-13-, 5185 - 5193	K.YEEENFYLEPYLK.E	1737.88601	2	1.38E-05	0.97	4.44	-	1908.9
AHQ-3-13, 5205	K.YEEENFYLEPYLK.E	1737.88601	2	3.99E-04	0.97	4.50	-	1896.8
gi|5453629|ref|NP_006391.1|	dynactin 2; dynactin complex 50 kD subunit; dynamitin; 50 kD dynein-ass			1.55E-05	0.86	10.19	4.68	44819.3
AHQ-3-9, 4904	K.LLGPDAAINLTDPDGALAK.R	1866.10514	2	6.93E-05	0.37	3.21	-	391.7
AHQ-3-7, 5187	K.LLGPDAAINLTDPDGALAK.R	1866.10514	2	1.55E-05	0.86	3.70	-	715.4
gi|4506185|ref|NP_002780.1|	proteasome alpha 4 subunit; proteasome component C9; proteasome subunit			1.56E-05	0.88	10.21	8.43	29483.6
AHQ-3-10, 6464 - 6531	R.YLLQYQEPIPCEQLVTALCDIK.Q	2698.10465	2	1.56E-05	0.88	4.18	-	548.7
gi|29729345|ref|XP_290995.1|	similar to speckle-type POZ protein [Homo sapiens]			1.58E-05	1.44	20.17	10.91	18703.4
AHQ-3-2, 6258	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	1.55E-04	0.66	3.41	-	678.9
AHQ-3-1, 6285	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	1.58E-05	0.78	3.23	-	738.1
gi|20330805|ref|NP_005263.1|	guanine nucleotide binding protein, alpha transducing activity polypep			1.59E-05	0.72	10.15	3.11	40175.6
AHQ-3-8, 2778 - 2782	K.LLLLGAGESGK.S	1058.25357	1	1.59E-05	0.72	2.87	-	440.8
AHQ-3-9, 2811	K.LLLLGAGESGK.S	1058.25357	1	2.31E-04	0.33	2.09	-	484.1
AHQ-3-8, 2769	K.LLLLGAGESGK.S	1058.25357	2	3.53E-04	0.88	3.03	-	1175.0
gi|28077085|ref|NP_004559.3|	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member			1.62E-05	0.95	10.23	5.32	42586.7
AHQ-3-9, 4345	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	2	1.62E-05	0.95	4.46	-	1264.5
AHQ-3-8, 4286	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	2	2.93E-05	0.93	4.50	-	1080.7
gi|6912540|ref|NP_036357.1|	nucleotide binding protein 2 (MinD homolog, E. coli); nucleotide bindin			1.66E-05	0.67	10.17	9.96	28825.1
AHQ-3-10, 6394	R.TLEEGHDFIQEFPGSPAFAALTSIAQK.I	2906.19484	2	1.66E-05	0.67	3.43	-	469.0
gi|7705632|ref|NP_057152.1|	CGI-135 protein [Homo sapiens]			1.68E-05	0.63	10.14	8.55	16979.6
AHQ-3-13, 2322	R.GLLQTEPQNNQAK.E	1441.57186	2	1.68E-05	0.63	2.77	-	403.1
gi|11545906|ref|NP_071441.1|	fructosamine-3-kinase [Homo sapiens]			1.87E-05	0.73	10.14	4.53	35171.0
AHQ-3-9, 2553	R.AFGGPGAGCISEGR.A	1337.44380	2	1.87E-05	0.73	2.76	-	532.4
gi|22027538|ref|NP_037506.2|	programmed cell death 6 interacting protein; ALG-2 interacting protein			1.89E-05	0.94	10.20	1.84	96022.6
AHQ-3-5, 5229 - 5232	R.SVIEQGGIQTVDQLIK.E	1728.96847	2	1.89E-05	0.94	4.01	-	1271.1
gi|20127408|ref|NP_000173.2|	hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub			1.92E-05	3.43	50.25	12.19	82999.1
AHQ-3-6, 2499	K.DTSASAVAVGLK.Q	1119.25064	1	8.23E-04	0.06	2.07	-	241.4
AHQ-3-6, 4513	R.FGGGNPELLTQMVSK.G	1578.81508	2	4.73E-04	0.62	2.82	-	487.6
AHQ-3-6, 7214	K.KLDSLTTSFGFPVGAATLVDEVGVDVAK.H	2838.20186	3	2.18E-04	0.93	5.08	-	883.5
AHQ-3-6, 2977	K.TGIEQGSDAGYLCESQK.F	1844.93497	2	2.67E-04	0.90	3.76	-	820.0
AHQ-3-6, 6071	K.TVLGTPEVLLGALPGAGGTQR.L	2008.30795	3	1.92E-05	0.91	4.40	-	1139.3
gi|5803013|ref|NP_006808.1|	endoplasmic reticulum protein 29 precursor; endoplasmic reticulum lumen			2.07E-05	0.71	10.17	5.75	28993.2
AHQ-3-10, 3656	R.DGDFENPVPYTGAVK.V	1609.71786	2	2.07E-05	0.71	3.25	-	463.8
gi|6005902|ref|NP_009043.1|	thrombospondin 3 [Homo sapiens]			2.09E-05	0.77	10.14	0.73	104200.6
AHQ-3-4, 4588	R.FYVVMWK.Q	973.21547	1	6.14E-04	0.83	2.36	-	965.9
AHQ-3-5, 4367	R.FYVVMWK.Q	973.21547	1	1.86E-04	0.66	1.98	-	778.8
AHQ-3-11, 4244	R.FYVVMWK.Q	973.21547	1	2.09E-05	0.77	2.21	-	934.1
AHQ-3-2, 4730 - 4802	R.FYVVMWK.Q	973.21547	1	2.82E-05	0.90	2.81	-	1037.2
gi|6005890|ref|NP_009039.1|	elongin B; transcription elongation factor B (SIII), polypeptide 2 (18k			2.10E-05	0.92	10.17	10.17	13132.7
AHQ-3-12, 2588	R.LYKDDQLLDDGK.T	1423.55008	2	2.10E-05	0.92	3.32	-	1383.6
gi|4506713|ref|NP_002945.1|	ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte			2.13E-05	0.77	10.25	10.26	17964.8
AHQ-3-14-, 4236 - 4316	K.TITLEVEPSDTIENVK.A	1788.97431	2	2.13E-05	0.77	3.88	-	469.4
AHQ-3-13, 4342	K.TITLEVEPSDTIENVK.A	1788.97431	2	1.69E-04	0.55	3.48	-	394.4
gi|4505093|ref|NP_000889.1|	monoamine oxidase B [Homo sapiens]			2.17E-05	0.91	10.21	2.88	58762.6
AHQ-3-7, 3108	K.YVDLGGSYVGPTQNR.I	1626.75165	2	2.17E-05	0.91	4.12	-	673.1
gi|22060072|ref|XP_088293.2|	similar to cytochrome c [Homo sapiens]			2.17E-05	0.94	10.18	7.62	11887.8
AHQ-3-13-, 4202 - 4218	R.ADLIAYLK.K	907.08869	2	2.17E-05	0.94	3.53	-	1103.8
gi|21361741|ref|NP_057569.2|	hypothetical protein HSPC228; My012 protein [Homo sapiens]			2.21E-05	0.91	10.22	6.51	33879.0
AHQ-3-9, 4732 - 4773	K.YAGSALQYEDVSTAVQNLQK.A	2186.36410	2	2.21E-05	0.91	4.36	-	682.3
gi|19913373|ref|NP_079536.2|	G6B protein isoform G6b-A precursor; G6B protein; immunoglobulin recep			2.22E-05	1.83	20.18	9.28	25002.6
AHQ-3-12, 2432	R.TVLHVLGDR.T	1010.17224	2	2.22E-05	0.91	2.99	-	1255.3
AHQ-3-11, 2308	R.TVLHVLGDR.T	1010.17224	2	9.78E-05	0.90	3.26	-	1229.8
AHQ-3-12, 2428	R.TVLHVLGDR.T	1010.17224	1	4.64E-04	0.16	2.17	-	283.5
AHQ-3-9, 2112 - 2177	R.TVLHVLGDR.T	1010.17224	1	1.17E-04	0.12	2.05	-	256.8
AHQ-3-10, 2468	R.VNLSCGGVSHPIR.W	1397.58551	2	2.88E-05	0.93	3.50	-	1303.2
gi|23110944|ref|NP_002782.1|	proteasome alpha 6 subunit; prosomal P27K protein; proteasome subunit			2.23E-05	1.07	20.15	8.94	27399.3
AHQ-3-10, 2524	R.HITIFSPEGR.L	1157.30379	2	3.12E-05	0.77	3.08	-	435.0
AHQ-3-10, 4824	K.YGYEIPVDMLCK.R	1489.73836	1	2.23E-05	0.30	2.28	-	343.5
gi|6912304|ref|NP_036256.1|	cysteine and histidine-rich domain (CHORD)-containing, zinc binding pro			2.33E-05	0.42	10.14	5.72	37436.5
AHQ-3-8, 6572	K.RRTTDFSDFLSIVGCTKGR.H	2218.47898	2	2.33E-05	0.42	2.82	-	391.5
gi|21359896|ref|NP_009177.2|	kelch-like 2, Mayven; mayven; kelch (Drosophila)-like 2 (Mayven) [Homo			2.40E-05	0.12	10.10	1.69	66075.5
AHQ-3-11, 2775 - 2822	K.KAFKVMNELR.S	1236.51223	1	2.40E-05	0.12	1.87	-	122.3
gi|18152767|ref|NP_542775.1|	synaptotagmin-like 4 (granuphilin-a) [Homo sapiens]			2.44E-05	0.90	10.16	1.94	76009.1
AHQ-3-7, 2266	K.YEQQTQSLVVHVK.E	1559.74835	2	2.44E-05	0.90	3.29	-	957.6
gi|20070125|ref|NP_000909.2|	prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke			2.63E-05	1.73	20.19	5.51	57115.9
AHQ-3-7, 3720 - 3798	K.VDATEESDLAQQYGVR.G	1781.85882	2	2.63E-05	0.92	3.80	-	1369.8
AHQ-3-7, 3691 - 3770	K.YQLDKDGVVLFK.K	1425.65394	2	7.37E-05	0.81	3.70	-	756.7
gi|4503823|ref|NP_002028.1|	protein-tyrosine kinase fyn isoform a; proto-oncogene tyrosine-protein			2.63E-05	0.85	10.16	2.05	60761.5
AHQ-3-7, 3460	K.WTAPEAALYGR.F	1235.37302	2	2.63E-05	0.85	3.16	-	604.9
gi|29727565|ref|XP_291384.1|	similar to Cytochrome c, somatic [Homo sapiens]			2.69E-05	1.80	20.25	17.14	11621.4
AHQ-3-13, 6433	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	2.69E-05	0.96	4.95	-	1316.8
AHQ-3-13, 6601	K.GIIWGEDTLMEYLENPKK.Y	2137.44123	2	5.41E-05	0.84	3.64	-	575.0
gi|30147267|ref|XP_304295.1|	hypothetical protein XP_304295 [Homo sapiens]			2.79E-05	0.45	10.16	3.37	38558.9
AHQ-3-13, 6037 - 6038	K.PLGWIGQMQGEK.A	1344.56442	2	2.79E-05	0.45	2.63	-	533.4
gi|8922835|ref|NP_060776.1|	hypothetical protein FLJ11036 [Homo sapiens]			2.81E-05	0.82	10.16	5.42	22353.4
AHQ-3-11, 2954	K.AGLFSQEQYER.N	1328.41208	2	2.81E-05	0.82	3.17	-	771.7
gi|4502981|ref|NP_001852.1|	cytochrome c oxidase subunit IV isoform 1 precursor; cytochrome c oxida			2.99E-05	0.35	10.18	7.10	19576.6
AHQ-3-13-, 3845	K.SEDFSLPAYM*DR.R	1447.55197	2	2.99E-05	0.35	2.57	-	257.3
gi|23110925|ref|NP_002789.1|	proteasome beta 6 subunit; proteasome subunit Y; proteasome subunit be			3.01E-05	0.80	10.19	16.32	25357.6
AHQ-3-11, 6691	R.SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK.E	4058.45788	3	3.01E-05	0.80	3.78	-	600.7
gi|30158950|ref|XP_301585.1|	similar to natural killer cell transcript 4 [Homo sapiens]			3.10E-05	0.75	10.17	15.43	18547.1
AHQ-3-13-, 4823	R.EPTVNKDIHQRTCDLSKTIEAPAER.Q	2911.19785	3	3.10E-05	0.75	3.47	-	533.7
gi|30149013|ref|XP_302138.1|	similar to alpha tubulin [Homo sapiens]			3.19E-05	0.23	10.13	4.62	22444.5
AHQ-3-14-, 4947	R.EIINLVLDR.I	1085.27902	2	4.94E-05	0.81	2.53	-	811.7
AHQ-3-7, 4895	R.EIINLVLDR.I	1085.27902	1	3.19E-05	0.23	2.48	-	141.5
gi|17444699|ref|XP_017966.4|	similar to Reticulon protein 3 (Neuroendocrine-specific protein-like 2			3.19E-05	0.90	10.16	4.66	25522.7
AHQ-3-1, 2909	K.TQIDHYVGIAR.H	1273.42279	2	3.19E-05	0.90	3.22	-	1222.7
gi|4503377|ref|NP_001377.1|	dihydropyrimidinase-like 2; collapsin response mediator protein hCRMP-2			3.25E-05	0.78	10.14	3.32	62293.3
AHQ-3-7, 5472	R.FQMPDQGMTSADDFFQGTK.A	2152.34998	2	3.25E-05	0.78	2.87	-	755.7
gi|21361427|ref|NP_055182.2|	hypothetical protein, estradiol-induced [Homo sapiens]			3.28E-05	0.87	10.20	8.95	21551.0
AHQ-3-13, 5697	K.EDEIPETVSLEMLDAAK.N	1891.08690	2	3.28E-05	0.87	3.94	-	440.2
gi|21361619|ref|NP_061882.2|	TOLLIP protein; Toll-interacting protein [Homo sapiens]			3.30E-05	0.95	10.25	5.11	30281.6
AHQ-3-11, 5576 - 5578	R.GPVYIGELPQDFLR.I	1604.83072	2	3.30E-05	0.95	4.91	-	1009.3
gi|30153966|ref|XP_293932.2|	similar to hypothetical protein BC013073 [Homo sapiens]			3.31E-05	0.22	10.20	9.04	21711.3
AHQ-3-1, 4289	R.MIFTLFTINVSKDIRHH	2073.44997	3	2.53E-04	0.75	3.27	-	1049.2
AHQ-3-2, 4266 - 4293	R.MIFTLFTINVSKDIRHH	2073.44997	2	7.70E-04	0.46	3.07	-	436.4
AHQ-3-4, 3957	R.MIFTLFTINVSKDIRHH	2073.44997	2	3.31E-05	0.22	2.77	-	247.5
AHQ-3-5, 4037	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.56E-04	0.77	3.64	-	573.7
AHQ-3-1, 3862 - 3864	R.MIFTLFTINVSKDIRHH	2073.44997	2	6.58E-04	0.47	3.02	-	316.9
gi|4507287|ref|NP_003755.1|	syntaxin 11 [Homo sapiens]			3.42E-05	1.14	20.19	7.67	32955.3
AHQ-3-9, 3592	R.LAELLDLSK.Q	1002.18679	1	5.06E-04	0.34	2.63	-	332.3
AHQ-3-9, 6084	K.WDVFSENLLADVK.G	1536.71002	2	3.42E-05	0.80	3.09	-	803.2
gi|4502099|ref|NP_001143.1|	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra			3.56E-05	0.94	10.20	5.03	32895.0
AHQ-3-10, 4116	R.KGTDIMYTGTLDCWR.K	1819.05212	2	3.56E-05	0.94	4.00	-	1083.9
gi|5730031|ref|NP_005688.2|	secretory carrier membrane protein 2 [Homo sapiens]			3.64E-05	0.94	10.25	6.08	36648.6

AHQ-3-1, 5969	R.TGASFQQAQEEFSQGIFSSR.T	2206.31396	2	3.64E-05	0.94	4.92	-	873.5
gi|21614520|ref|NP_000393.2|	glucose-6-phosphate dehydrogenase [Homo sapiens]			3.70E-05	2.46	30.20	8.16	59257.4
AHQ-3-7, 2898	K.GYLDDPTVPR.G	1133.23587	2	5.15E-05	0.72	2.55	-	664.1
AHQ-3-7, 6810 - 6822	R.LFYLALPPTVYEAVTK.N	1826.16735	2	6.00E-05	0.82	3.81	-	336.0
AHQ-3-7, 4124	R.LQFHDVAGDIFHQQCK.R	1945.14742	3	3.70E-05	0.91	4.07	-	1196.9
gi|4502107|ref|NP_001145.1|	annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoag			3.85E-05	0.95	10.22	5.00	35936.5
AHQ-3-9, 6591	K.GLGTDEESILTLLTSR.S	1705.88853	2	3.85E-05	0.95	4.47	-	1271.2
gi|30157216|ref|XP_292133.2|	similar to genethonin 1 [Homo sapiens]			3.85E-05	0.43	10.19	4.51	39693.8
AHQ-3-9, 4071	K.TITLEVKPSDTIENVK.A	1788.03268	2	2.61E-04	0.18	2.64	-	236.1
AHQ-3-14, 5457 - 5529	K.TITLEVKPSDTIENVK.A	1788.03268	2	2.72E-04	0.41	3.31	-	310.8
AHQ-3-14-, 4323 - 4388	K.TITLEVKPSDTIENVK.A	1788.03268	2	1.10E-04	0.19	2.70	-	276.6
AHQ-3-2, 4685 - 4693	K.TITLEVKPSDTIENVK.A	1788.03268	2	3.85E-05	0.43	3.19	-	370.4
gi|20336761|ref|NP_057071.2|	heme binding protein 1 [Homo sapiens]			4.33E-05	0.62	10.16	8.47	21096.9
AHQ-3-11, 3647	K.FATVEVTDKPVDEALR.E	1790.99512	2	4.33E-05	0.62	3.22	-	347.6
gi|5453990|ref|NP_006254.1|	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha); Prote			4.34E-05	0.89	10.17	8.84	28722.9
AHQ-3-10, 5716	K.ISELDAFLKEPALNEANLSNLK.A	2430.73906	2	4.34E-05	0.89	3.42	-	1159.1
gi|18375652|ref|NP_002826.2|	protein tyrosine phosphatase, non-receptor type 12; protein-tyrosine p			4.35E-05	0.93	10.20	2.05	88119.9
AHQ-3-7, 7026 - 7087	R.YWPLYGEDPITFAPFK.I	1945.20411	2	4.35E-05	0.93	3.99	-	732.6
gi|5453559|ref|NP_006347.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; ATP			4.46E-05	0.86	10.17	10.56	18491.1
AHQ-3-11, 5283 - 5359	R.LAALPENPPAIDWAYYK.A	1933.19486	2	4.46E-05	0.86	3.43	-	568.3
gi|30149555|ref|XP_301154.1|	similar to heat shock protein 86 [Homo sapiens]			4.52E-05	0.97	10.21	10.56	15781.6
AHQ-3-5, 5645	K.HSQFIGYPITLFVEK.E	1780.05877	2	4.52E-05	0.97	4.27	-	1728.7
gi|7706563|ref|NP_057614.1|	RAB-8b protein [Homo sapiens]			4.76E-05	1.16	20.15	14.01	23584.0
AHQ-3-11, 5143	R.GAM*GIMLVYDITNEK.S	1671.96066	2	4.76E-05	0.38	2.79	-	412.7
AHQ-3-11, 5280 - 5344	K.SSANVEEAFFTLAR.D	1542.67465	2	1.41E-04	0.78	3.04	-	834.6
gi|29743626|ref|XP_297123.1|	hypothetical protein XP_297123 [Homo sapiens]			4.82E-05	0.84	10.18	13.79	13908.9
AHQ-3-12, 6946 - 6947	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	4.82E-05	0.84	3.69	-	1066.4
gi|5453916|ref|NP_006311.1|	progesterone membrane binding protein [Homo sapiens]			4.89E-05	0.88	10.17	6.28	23818.3
AHQ-3-10, 4556	K.FYGPAGPYGIFAGR.D	1473.65885	2	4.89E-05	0.88	3.31	-	809.5
gi|6041669|ref|NP_004538.2|	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd			4.99E-05	0.72	10.14		15208.5
AHQ-3-13-, 4811	R.TLPETLDPAEYNISPETR.R	2047.20831	2	4.99E-05	0.72	2.90	-	495.2
gi|14165439|ref|NP_002131.2|	heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch bindin			5.02E-05	0.86	10.19	4.09	51027.9
AHQ-3-6, 5107	R.GSYGDLGGPIITTQVTIPK.D	1918.18004	2	5.02E-05	0.86	3.86	-	664.9
gi|27413156|ref|NP_000338.2|	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)			5.05E-05	0.86	10.19	0.75	246320.0
AHQ-3-2, 5067	K.VIQGQTDPEYLLLGQR.L	1831.06248	2	5.05E-05	0.86	3.72	-	734.7
gi|24429572|ref|NP_722516.1|	TBP-associated factor RNA polymerase 1-like [Homo sapiens]			5.10E-05	0.63	10.14	0.60	207299.7
AHQ-3-8, 2750	R.EWEEQERKELR.R	1532.63986	2	5.10E-05	0.63	2.57	-	678.0
gi|6005786|ref|NP_009214.1|	monoglyceride lipase; lysophospholipase-like [Homo sapiens]			5.20E-05	1.59	20.29	9.27	34292.3
AHQ-3-9, 1916	K.ALIFVSHGAGEHSGR.Y	1538.69246	2	3.83E-04	0.83	2.91	-	890.1
AHQ-3-13-, 6106	K.LTVPFLLLQGSADR.L	1530.79329	2	8.60E-05	0.81	2.53	-	756.2
AHQ-3-9, 5780 - 5787	K.LTVPFLLLQGSADR.L	1530.79329	2	5.20E-05	0.76	2.64	-	751.4
gi|7662651|ref|NP_054778.1|	RGC32 protein [Homo sapiens]			5.57E-05	0.93	10.24	17.09	12924.1
AHQ-3-12, 4302 - 4307	K.LNSPTDSTPALLSATVTPQK.A	2042.27634	2	5.57E-05	0.93	4.77	-	616.4
gi|5031569|ref|NP_005727.1|	ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r			5.64E-05	1.79	20.20	9.31	42613.4
AHQ-3-8, 3632	R.ACYLSINPQKDETLETEK.A	2141.34169	2	5.64E-05	0.90	4.04	-	635.3
AHQ-3-8, 5072	K.AQYYLPDGSTIEIGPSR.F	1868.03645	2	2.39E-04	0.89	3.57	-	621.1
gi|20547107|ref|XP_114482.1|	similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN			5.68E-05	1.50	20.23	3.93	94330.3
AHQ-3-4, 7069	R.EFSITDVVPYPISLR.W	1736.98906	2	5.68E-05	0.58	2.76	-	300.8
AHQ-3-4, 6817 - 6820	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	3.56E-04	0.91	4.64	-	588.1
gi|4507795|ref|NP_003340.1|	ubiquitin-conjugating enzyme E2 variant 1 isoform b; DNA-binding protei			5.75E-05	0.79	10.16	4.07	25796.6
AHQ-3-12, 3376	K.YPEAPPFVR.F	1076.22914	2	5.75E-05	0.79	3.16	-	531.1
gi|21361346|ref|NP_002443.2|	nudix (nucleoside diphosphate linked moiety X)-type motif 1; mutT (E.			5.95E-05	0.72	10.16	7.26	20295.9
AHQ-3-12, 4936 - 4962	K.FQGQDTILDYTLR.E	1570.72800	2	5.95E-05	0.72	3.16	-	610.2
gi|4758790|ref|NP_004543.1|	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q			5.97E-05	1.68	20.20	22.64	12517.4
AHQ-3-13, 6635	K.IEYDDFVECLLR.Q	1573.74872	2	5.97E-05	0.83	3.19	-	739.9
AHQ-3-13, 3826 - 3834	R.WLTIQSGEQPYK.M	1450.62036	2	9.15E-04	0.85	3.76	-	612.0
gi|5031947|ref|NP_005591.1|	nitrilase 1 [Homo sapiens]			6.23E-05	0.73	10.14	4.59	35896.3
AHQ-3-9, 3233	R.DPAETLHLSEPLGGK.L	1564.72177	2	6.23E-05	0.73	2.75	-	693.2
gi|17402865|ref|NP_003303.2|	thiosulfate sulfurtransferase; rhodanese [Homo sapiens]			6.26E-05	0.90	20.14	10.77	33428.7
AHQ-3-9, 3697	R.FLGTEPEPDAVGLDSGHIR.G	2011.18089	2	6.26E-05	0.41	2.72	-	378.2
AHQ-3-9, 3920	K.TYEQVLENLESKR.F	1609.76254	2	6.53E-04	0.49	2.85	-	609.0
gi|4506381|ref|NP_002863.1|	ras-related C3 botulinum toxin substrate 2; Ras-related C3 botulinum to			6.30E-05	0.81	10.18	7.29	21428.7
AHQ-3-11, 4370 - 4371	K.LAPITYPQGLALAK.E	1456.75431	2	6.30E-05	0.81	3.37	-	391.6
gi|4507931|ref|NP_003384.1|	wingless-type MMTV integration site family, member 8B precursor [Homo s			6.76E-05	0.49	10.16	8.26	38691.8
AHQ-3-13-, 6673 - 6683	R.EVGAHLKEKYHAALKVDLLQGAGNSAAAR.G	3019.40746	3	6.76E-05	0.49	3.11	-	324.1
gi|4507657|ref|NP_003282.1|	tripeptidyl peptidase II [Homo sapiens]			6.78E-05	0.76	10.18	2.24	138447.8
AHQ-3-4, 4850	R.DPVQVAAPSDHGVGIEPVFPENTENSEK.I	2964.14642	3	6.78E-05	0.76	3.50	-	570.0
gi|30150448|ref|XP_293066.2|	similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose			6.84E-05	0.94	10.20	2.91	58788.2
AHQ-3-6, 4515	R.VINEPTAAALAYGLDK.S	1646.86592	2	6.84E-05	0.94	4.04	-	954.4
gi|29729950|ref|XP_293759.1|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			7.03E-05	0.93	10.21	5.00	39776.4
AHQ-3-5, 4892	K.CLELFTELAEDKENYKK.F	2132.37640	2	7.03E-05	0.93	4.22	-	1014.9
gi|11321581|ref|NP_003840.1|	succinate-CoA ligase, GDP-forming, alpha subunit [Homo sapiens]			7.21E-05	0.79	10.15	4.80	35059.2
AHQ-3-8, 3644	R.LIGPNCPGVINPGECK.I	1727.98391	2	7.21E-05	0.79	3.07	-	543.2
gi|13376719|ref|NP_079413.1|	hypothetical protein FLJ21439 [Homo sapiens]			7.22E-05	0.73	10.16	2.35	48893.8
AHQ-3-11, 4179 - 4195	K.GDFNYLEEFK.Q	1262.34887	2	7.22E-05	0.73	2.83	-	672.0
gi|22065448|ref|XP_084610.2|	similar to tubulin alpha-1 chain - Chinese hamster [Homo sapiens] [MAS			7.31E-05	0.74	10.18	2.41	41009.4
AHQ-3-13, 4999	K.EIIDLVLDR.I	1086.26378	2	7.31E-05	0.74	3.10	-	728.0
AHQ-3-7, 4894 - 4896	K.EIIDLVLDR.I	1086.26378	2	9.95E-05	0.85	3.63	-	727.3
gi|29732170|ref|XP_291550.1|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			7.42E-05	1.74	20.25	13.56	13262.9
AHQ-3-5, 3885	K.HLEINPDHSIIETLR.Q	1787.99770	3	5.75E-04	0.97	4.98	-	1824.3
AHQ-3-5, 3244	K.KHLEINPDHSIIETLR.Q	1916.17061	2	7.42E-05	0.78	3.21	-	751.6
gi|4503529|ref|NP_001407.1|	eukaryotic translation initiation factor 4A, isoform 1 [Homo sapiens] [			7.45E-05	0.93	10.23	3.69	46153.7
AHQ-3-8, 3477	K.LQMEAPHIIVGTPGR.V	1619.91357	2	7.45E-05	0.93	4.51	-	962.7
gi|7019485|ref|NP_037364.1|	programmed cell death 6; apoptosis-linked gene 2 [Homo sapiens]			7.57E-05	1.00	20.18	10.99	21868.3
AHQ-3-11, 3700	R.LSDQFHDILIR.K	1357.53970	2	1.05E-04	0.89	3.55	-	1003.9
AHQ-3-11, 4987	K.YITDWQNVFR.T	1342.48358	1	7.57E-05	0.11	1.92	-	138.6
gi|14161692|ref|NP_115706.1|	calpain small subunit 2 [Homo sapiens]			7.67E-05	0.04	10.15		27660.1
AHQ-3-12, 3526	K.YLWNNIK.K	951.10326	1	7.67E-05	0.04	1.94	-	228.6
gi|4504051|ref|NP_002064.1|	guanine nucleotide binding protein, alpha z polypeptide; transducin alp			7.70E-05	0.47	10.18	4.79	40923.5
AHQ-3-9, 5099	R.AYDAVQLFALTGPAESK.G	1781.98669	2	7.70E-05	0.47	2.64	-	256.4
gi|19923231|ref|NP_002860.2|	RAB6A, member RAS oncogene family; Oncogene RAB6; RAB6, member RAS onc			7.97E-05	0.80	10.14	6.73	23548.6
AHQ-3-11, 2824	R.VAAALPGMESTQDR.S	1446.61192	2	7.97E-05	0.80	2.85	-	507.1
gi|4557241|ref|NP_001095.1|	skeletal muscle specific actinin, alpha 3 [Homo sapiens]			8.11E-05	0.92	10.17	0.89	103293.7
AHQ-3-5, 2651	K.ALDFIASK.G	865.00867	2	8.11E-05	0.92	3.48	-	758.1
gi|27544939|ref|NP_060932.2|	uncharacterized hematopoietic stem/progenitor cells protein MDS027 [Ho			8.19E-05	0.70	10.14	10.67	8744.9
AHQ-3-14-, 2111 - 2125	R.RIEYIEAR.V	1050.19323	2	8.19E-05	0.70	2.86	-	412.8
gi|30157848|ref|XP_293411.2|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			8.27E-05	0.46	10.16	8.54	31231.0
AHQ-3-1, 4948 - 4949	K.GLQAQIASSELTVEDLAKIMADIR.A	2573.94845	3	8.27E-05	0.46	3.12	-	475.8
gi|10834992|ref|NP_000631.1|	interleukin 13 receptor, alpha 2 precursor; interleukin 13 binding pro			8.29E-05	0.22	10.14	4.74	44176.2
AHQ-3-14, 6275	R.NIGSETWKTIITKNLHYK.D	2147.46221	2	8.29E-05	0.22	2.72	-	252.2
gi|4506065|ref|NP_002727.1|	protein kinase, cAMP-dependent, regulatory, type II, beta [Homo sapiens			8.43E-05	0.93	10.22	4.07	46345.9
AHQ-3-7, 7247	K.NLDPEQMSQVLDAMFEK.L	1996.25144	2	8.43E-05	0.93	4.48	-	1425.1
gi|4758750|ref|NP_004136.1|	myosin IXB [Homo sapiens]			8.50E-05	0.41	10.14	0.45	228621.8
AHQ-3-13, 3983 - 3985	K.YLDEFLLNK.I	1155.32458	1	8.50E-05	0.41	2.64	-	528.9
gi|20532885|ref|XP_086931.2|	similar to epsilon isoform of 14-3-3 protein [Homo sapiens]			8.66E-05	0.96	20.20	9.02	29380.0
AHQ-3-10, 2400	K.EAAKNSIVAYK.A	1194.36234	2	8.66E-05	0.04	2.54	-	269.8
AHQ-3-13, 6747	K.LICCDILDVLDK.H	1479.74157	2	1.54E-04	0.94	3.99	-	988.2

AHQ-3-10, 6298	K.LICCDILDVLDK.H	1479.74157	2	1.03E-04	0.92	3.76	-	845.6
gi|4885281|ref|NP_005262.1|	glutamate dehydrogenase 1 [Homo sapiens]			8.75E-05	0.81	10.15	2.87	61397.5
AHQ-3-7, 3640	K.HGGTIPIVPTAEFQDR.I	1738.92514	2	8.75E-05	0.81	3.00	-	427.2
gi|22267436|ref|NP_056284.1|	DKFZp564D177 protein [Homo sapiens]			8.77E-05	0.80	10.17	7.29	28466.4
AHQ-3-11, 6292	K.DKEWQEQFLIPNLALIDK.Q	2201.50664	2	8.77E-05	0.80	3.48	-	456.8
gi|29727772|ref|XP_209234.2|	similar to hypothetical protein [Homo sapiens]			9.02E-05	0.13	10.10	0.98	125139.7
AHQ-3-13, 2134	R.M*KQLRESDGAK.V	1279.44911	1	9.02E-05	0.13	2.03	-	377.7
gi|30149221|ref|XP_291446.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			9.12E-05	0.91	10.20	3.86	45688.5
AHQ-3-7, 2183 - 2190	R.STAGDTHLGGEDFDNR.M	1692.68222	2	9.12E-05	0.91	4.02	-	866.7
gi|13376539|ref|NP_079295.1|	hypothetical protein FLJ13940 [Homo sapiens]			9.22E-05	0.70	10.13	4.98	27546.1
AHQ-3-8, 3532	R.QIFHPEQLITGK.E	1411.63050	2	9.22E-05	0.70	2.61	-	239.4
gi|4505145|ref|NP_002387.1|	malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochon			9.51E-05	1.77	20.22	4.28	65443.3
AHQ-3-6, 3402	K.ALTSQLTDEELAQGR.L	1632.75450	2	9.51E-05	0.86	4.32	-	654.6
AHQ-3-6, 2809	K.IETQDIQALR.F	1187.32821	2	1.16E-04	0.92	3.65	-	1100.1
gi|21264318|ref|NP_004028.3|	adenosine monophosphate deaminase 2 (isoform L) [Homo sapiens]			9.59E-05	0.84	10.21	2.05	100687.2
AHQ-3-5, 5543 - 5557	R.SAPYEFPEESPIEQLEER.R	2151.27185	2	9.59E-05	0.84	3.63	-	557.5
gi|4505409|ref|NP_002503.1|	non-metastatic cells 2, protein (NM23B) expressed in; Non-metastatic ce			1.06E-04	0.94	10.21		17297.9
AHQ-3-12, 6086 - 6106	K.EISLWFKPEELVDYK.S	1897.15929	2	1.06E-04	0.94	4.22	-	912.7
gi|13375985|ref|NP_078975.1|	hypothetical protein FLJ14007 [Homo sapiens]			1.06E-04	0.24	10.14	4.85	30753.1
AHQ-3-9, 4116	K.RWKGAKNSETAAK.V	1447.62447	1	1.06E-04	0.24	2.72	-	301.7
gi|12597635|ref|NP_075049.1|	B-cell CLL/lymphoma 11B isoform 2; B-cell lymphoma/leukaemia 11B; zinc			1.06E-04	0.33	10.14	1.82	88475.8
AHQ-3-14, 5165	R.PESSFSMDSELSRNR.E	1742.84932	2	1.06E-04	0.33	2.72	-	426.9
gi|7705777|ref|NP_057095.1|	CGI-63 protein [Homo sapiens]			1.11E-04	0.03	10.10	3.49	40057.0
AHQ-3-7, 3976	K.QPVVASVSLLIFK.D	1401.71866	1	1.11E-04	0.03	1.97	-	198.7
gi|4758784|ref|NP_004540.1|	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa; NADH			1.12E-04	0.83	10.16	7.56	14187.4
AHQ-3-13, 2730	K.REDYLYAVR.D	1185.31400	2	1.12E-04	0.83	3.13	-	868.4
gi|29747201|ref|XP_290702.1|	similar to My016 protein [Homo sapiens]			1.12E-04	0.91	10.21	10.53	16932.3
AHQ-3-14-, 3443	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	1.12E-04	0.91	4.16	-	846.3
AHQ-3-14, 4309	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	9.08E-04	0.93	3.92	-	1044.2
gi|10835121|ref|NP_000289.1|	pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H			1.13E-04	0.95	10.21	1.92	61829.8
AHQ-3-7, 3422	R.GDLGIEIPAEK.V	1142.28420	1	7.81E-04	0.56	2.77	-	512.5
AHQ-3-7, 3415 - 3430	R.GDLGIEIPAEK.V	1142.28420	2	1.13E-04	0.95	4.11	-	1145.6
gi|30151001|ref|XP_170195.2|	similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl			1.13E-04	0.75	10.14	2.55	46759.8
AHQ-3-10, 3436 - 3438	R.AAYFGIYDTAK.G	1220.35512	1	1.13E-04	0.75	2.60	-	684.4
gi|8922511|ref|NP_060605.1|	mitochondrial ribosomal protein S18A; mitochondrial ribosomal protein S			1.19E-04	0.34	10.14	8.16	22183.8
AHQ-3-5, 3999	R.EVVETQEGKTTIIEGR.I	1789.96553	2	1.19E-04	0.34	2.68	-	413.2
gi|4557235|ref|NP_000009.1|	acyl-Coenzyme A dehydrogenase, very long chain precursor [Homo sapiens]			1.22E-04	0.92	10.17	1.83	70389.7
AHQ-3-6, 3839	R.ALEQFATVVEAK.L	1306.48946	2	1.22E-04	0.92	3.46	-	1341.7
gi|18571222|ref|XP_088393.1|	similar to destrin - pig [Homo sapiens]			1.28E-04	0.97	10.23	11.65	11560.5
AHQ-3-12, 2467 - 2539	K.HFVGMLPEKDCR.C	1490.73281	2	1.28E-04	0.97	4.68	-	1698.4
gi|21389337|ref|NP_653164.1|	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase); RIBOSE			1.29E-04	0.93	10.22	7.59	26090.9
AHQ-3-10, 4446	R.VKQENLNLVCIPTSFQAR.Q	2119.43046	2	1.29E-04	0.93	4.44	-	798.0
gi|30148456|ref|XP_293602.2|	similar to glutathione-S-transferase like; glutathione transferase ome			1.29E-04	0.34	10.17	3.88	29139.6
AHQ-3-10, 4148	K.VPSLVGSFLR.T	1075.28583	1	1.29E-04	0.34	2.21	-	189.1
AHQ-3-10, 4147	K.VPSLVGSFLR.T	1075.28583	2	3.59E-04	0.93	3.43	-	1316.9
gi|20553919|ref|XP_033811.2|	similar to hypothetical protein FLJ14775 [Homo sapiens]			1.34E-04	0.62	10.14	9.87	17460.4
AHQ-3-13-, 6022	R.NGSKEGNHHSTQPKR.N	1677.76352	2	1.34E-04	0.62	2.83	-	706.5
gi|7656952|ref|NP_055227.1|	calcyclin binding protein [Homo sapiens]			1.36E-04	0.93	10.24	10.53	26209.8
AHQ-3-10, 3911	K.KAELLDNEKPAAVVAPITTGYTVK.I	2529.91377	2	1.36E-04	0.93	4.72	-	670.4
gi|4506189|ref|NP_002783.1|	proteasome alpha 7 subunit isoform 1; proteasome subunit RC6-1; proteas			1.38E-04	1.12	20.14	10.08	27886.7
AHQ-3-10, 2784 - 2788	K.ALLEVVQSGGK.N	1101.27845	1	1.38E-04	0.68	2.71	-	647.4
AHQ-3-10, 1923	K.YVAEIEKEKEENEK.K	1738.87385	2	7.14E-04	0.45	2.77	-	281.3
gi|19743813|ref|NP_002202.2|	integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib			1.43E-04	0.86	10.18	2.13	88414.9
AHQ-3-4, 5334	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	1.43E-04	0.86	3.63	-	783.7
gi|8923289|ref|NP_060227.1|	hypothetical protein FLJ20307 [Homo sapiens]			1.43E-04	0.47	10.13	1.40	111692.1
AHQ-3-10, 4286	K.WALNNHM*KLHTGEK.P	1695.92696	2	1.43E-04	0.47	2.60	-	367.7
gi|4506285|ref|NP_003470.1|	protein tyrosine phosphatase type IVA, member 2 isoform 1; protein tyro			1.47E-04	0.80	10.16	7.78	19127.1
AHQ-3-11, 2090	R.VCDATYDKAPVEK.E	1497.65225	2	1.47E-04	0.80	3.28	-	592.4
gi|29739581|ref|XP_084467.3|	similar to eukaryotic initiation factor 5A [Homo sapiens]			1.57E-04	0.87	10.16	8.44	16773.1
AHQ-3-12, 2927	R.LPEGDLGKEIEQK.Y	1456.62321	2	1.57E-04	0.87	3.11	-	889.3
gi|4504743|ref|NP_002194.1|	integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o			1.58E-04	0.07	10.20	0.68	129294.4
AHQ-3-3, 2113	R.SHLQYFGR.S	1008.11490	1	1.58E-04	0.07	1.85	-	202.7
gi|4501889|ref|NP_001606.1|	actin, gamma 2 propeptide; actin, alpha-3 [Homo sapiens]			1.60E-04	0.18	10.14	5.59	41876.7
AHQ-3-14-, 4853	K.DLYANNVLSGGTTM*YPGIADR.M	2245.45502	2	1.60E-04	0.18	2.52	-	313.2
gi|16936530|ref|NP_439892.1|	cyclin-dependent kinase 2 isoform 2; cdc2-related protein kinase; cell			1.62E-04	0.66	10.17	8.71	30083.7
AHQ-3-3, 4434	K.LADFGLARAFGVPVRTYTHEVTR.R	2577.92513	3	1.62E-04	0.66	3.41	-	688.5
gi|4506677|ref|NP_002942.1|	ribophorin II [Homo sapiens]			1.65E-04	1.54	20.18	5.55	69301.6
AHQ-3-1, 5133	R.LQVTNVLSQPLTQATVK.L	1841.14195	2	8.47E-04	0.90	3.61	-	869.6
AHQ-3-1, 6770	K.TSFTPVGDVFELNFM*NVK.F	2062.33118	2	1.65E-04	0.64	3.26	-	301.2
gi|4885183|ref|NP_005210.1|	diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS			1.70E-04	0.79	10.17	1.20	138977.7
AHQ-3-3, 2264	K.LQDLQGEKDALHSEK.Q	1711.85486	2	1.70E-04	0.79	3.38	-	559.4
gi|4502021|ref|NP_003680.1|	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase);			1.75E-04	0.84	10.17	5.76	36648.3
AHQ-3-9, 3480 - 3492	K.ALQAAYGASAPSVTSAALR.W	1806.01302	2	1.75E-04	0.84	3.39	-	562.0
gi|19923559|ref|NP_064578.2|	EMSY protein [Homo sapiens]			1.91E-04	0.48	10.14	1.29	141466.9
AHQ-3-12, 6262 - 6266	K.QQKLSQPPLEQTQLQVK.T	1994.28128	2	1.91E-04	0.48	2.85	-	404.9
gi|5729991|ref|NP_006494.1|	proteasome 26S ATPase subunit 4 isoform 1; protease 26S subunit 6; Tat-			1.99E-04	0.91	10.18	2.87	47365.9
AHQ-3-5, 3644	R.GVLM*YGPPGCGK.T	1253.47332	2	1.99E-04	0.91	3.50	-	1089.8
gi|21361900|ref|NP_068595.2|	hypothetical protein MDS018 [Homo sapiens]			2.02E-04	0.75	10.15	8.33	22429.1
AHQ-3-11, 6326	R.WADLLLVAPLDANTLGK.V	1811.11431	2	2.02E-04	0.75	3.06	-	582.9
gi|27498357|ref|XP_029179.2|	similar to filamin-interacting protein L-Filip; filamin-interacting pr			2.03E-04	0.56	10.16	1.07	138108.1
AHQ-3-11, 4711	K.PISELDRLEEKQK.E	1585.78412	2	2.03E-04	0.56	3.20	-	521.0
gi|4502491|ref|NP_001203.1|	complement component 1, q subcomponent binding protein precursor; hyalu			2.05E-04	0.53	10.17	4.96	31362.0
AHQ-3-14, 6415	K.AFVDFLSDEIKEER.K	1698.85455	2	2.05E-04	0.53	2.67	-	502.3
gi|4507513|ref|NP_000353.1|	tissue inhibitor of metalloproteinase 3; Tissue inhibitor of metallopro			2.16E-04	0.14	10.09	3.79	24144.9
AHQ-3-11, 2830	K.YQYLLTGR.V	1014.15935	1	2.16E-04	0.14	1.89	-	212.1
gi|4506359|ref|NP_000311.1|	quinoid dihydropteridine reductase; dihydropteridine reductase [Homo sa			2.24E-04	0.95	10.25	6.97	25803.4
AHQ-3-10, 3328	K.NRPSSGSLIQVVTTEGR.T	1801.98277	2	2.24E-04	0.95	4.90	-	1025.1
gi|13385594|ref|NP_085056.1|	cytochrome b5 outer mitochondrial membrane precursor; type 2 cyt-b5 [H			2.32E-04	0.91	10.22	23.29	16332.0
AHQ-3-11, 5868	R.FLNEHPGGEEVLLEQAGVDASESFEDVGHSSDAR.E	3629.75848	3	2.32E-04	0.91	4.50	-	967.3
gi|5031855|ref|NP_005556.1|	lymphocyte cytosolic protein 2; SH2 domain-containing leukocyte protein			2.36E-04	0.91	10.19	2.25	60187.8
AHQ-3-12, 4139 - 4142	K.ESQVYLLGTGLR.G	1336.51879	2	2.36E-04	0.91	3.79	-	1128.9
gi|22538465|ref|NP_002786.2|	proteasome beta 3 subunit; proteasome theta chain; proteasome chain 13			2.37E-04	0.91	10.19	7.80	22948.8
AHQ-3-10, 4772 - 4776	R.FGPYYTEPVIAGLDPK.T	1768.00162	2	2.37E-04	0.91	3.76	-	1018.8
gi|20070158|ref|NP_003567.2|	serine/threonine kinase 24 (STE20 homolog, yeast); STE20-like kinase 3			2.44E-04	0.90	10.18	4.29	49307.6
AHQ-3-7, 7332	K.RPFSQCLSTIISPLFAELK.E	2209.59351	2	2.44E-04	0.90	3.67	-	867.6
gi|4885173|ref|NP_005427.1|	DNA segment on chromosome 10 (unique) 170; DNA segment, single copy, pr			2.48E-04	0.70	10.18	4.79	65916.5
AHQ-3-14, 6097 - 6136	R.QLSESESSLEM*DDERYFNEMSAQGLRPR.T	3322.54357	3	2.48E-04	0.70	3.62	-	414.1
gi|4502923|ref|NP_001830.1|	calponin 3; calponin, acidic [Homo sapiens]			2.51E-04	0.86	10.16	3.34	36413.4
AHQ-3-13-, 2673	K.GPSYGLSAEVK.N	1108.22631	2	7.86E-04	0.93	3.19	-	1351.1
AHQ-3-12, 2582	K.GPSYGLSAEVK.N	1108.22631	2	2.51E-04	0.86	3.07	-	973.1
gi|6912536|ref|NP_036475.1|	nicotinamide nucleotide transhydrogenase [Homo sapiens]			2.61E-04	0.71	10.17	1.84	113946.9
AHQ-3-4, 6553	K.TSGTLISFIYPAQNPELLNK.L	2207.51119	2	2.61E-04	0.71	3.41	-	400.5
gi|18087855|ref|NP_542408.1|	dynein light chain 2 [Homo sapiens]			2.65E-04	0.54	10.13		10349.8
AHQ-3-14-, 2972	K.DIAAYIK.K	793.93045	1	2.65E-04	0.54	2.22	-	416.5
gi|29736026|ref|XP_085123.3|	similar to Ras-related protein Rab-15 [Homo sapiens]			2.66E-04	0.90	10.18	5.29	23517.8
AHQ-3-11, 3370	R.IQIWDTAGQER.Y	1317.43243	2	2.66E-04	0.90	3.51	-	933.7
AHQ-3-13-, 3446	R.IQIWDTAGQER.Y	1317.43243	2	2.89E-04	0.80	3.34	-	559.2

AHQ-3-11, 3255	R.IQIWDTAGQER.Y	1317.43243	1	7.45E-04	0.14	2.30	-	243.4
gi|28461290|ref|NP_443728.2| TRALPUSH; no opposite paired repeat protein [Homo sapiens]				2.66E-04	0.68	10.15	0.37	240073.5
AHQ-3-7, 3466	K.KKPQVNAK.D	913.09970	1	6.87E-04	0.52	2.84	-	426.1
AHQ-3-9, 3255	K.KKPQVNAK.D	913.09970	1	9.40E-04	0.58	2.67	-	574.6
AHQ-3-6, 3497	K.KKPQVNAK.D	913.09970	1	2.66E-04	0.68	2.93	-	492.8
gi|30148409|ref|XP_037817.5| similar to hypothetical protein FLJ20035 [Homo sapiens]				2.67E-04	0.19	10.15	3.20	90407.8
AHQ-3-7, 5490 - 5550	R.AEYINFLENLKILEISEDCTYADVK.A	2993.33077	3	2.67E-04	0.19	3.06	-	245.4
gi|20373153|ref|NP_115997.4| myosin XVIIIB; myosin 18B [Homo sapiens]				2.73E-04	0.83	10.23	0.70	285231.7
AHQ-3-11, 6430	R.ITAAQLQTMLLEKSRVAR.Q	2030.42494	2	2.73E-04	0.83	3.92	-	967.4
gi|6005717|ref|NP_009031.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e; ATP				3.07E-04	0.13	10.11	14.49	7933.1
AHQ-3-14-, 2900 - 2904	R.ELAEDDSILK	1133.23094	1	3.07E-04	0.13	2.11	-	74.3
gi|4503785|ref|NP_000135.1| frataxin; Friedreich ataxia (frataxin) [Homo sapiens]				3.19E-04	0.94	10.21	5.71	23218.1
AHQ-3-13, 3766	K.LGGDLGTYVINK.Q	1250.42590	2	3.19E-04	0.94	4.17	-	989.0
gi|6912398|ref|NP_036218.1| general transcription factor IIIC, polypeptide 3, 102kDa; general trans				3.22E-04	0.50	10.17	2.60	101271.5
AHQ-3-2, 6026	R.RILNLLSPSDGERFMQLARDMAK.S	2663.11679	3	3.22E-04	0.50	3.45	-	519.3
gi|29730275|ref|XP_067176.7| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				3.26E-04	0.45	10.11	6.11	19225.0
AHQ-3-12, 5206 - 5207	K.EGINIVEAMER.F	1261.43059	1	3.26E-04	0.45	2.24	-	478.4
gi|4502227|ref|NP_001168.1| ADP-ribosylation factor-like 1 [Homo sapiens]				3.36E-04	0.80	10.16	7.73	20417.4
AHQ-3-11, 4595	K.SELVAMLEEEELRK.A	1676.91383	2	3.36E-04	0.80	3.15	-	626.1
gi|20070272|ref|NP_057110.2| androgen-regulated short-chain dehydrogenase/reductase 1; prostate sho				3.58E-04	1.51	20.17	10.38	35414.1
AHQ-3-9, 3092	K.GSGVTTYSVHPGTVQSELVR.H	2075.26811	2	3.58E-04	0.71	3.46	-	371.9
AHQ-3-9, 2307	K.VVVVTGANTGIGK.E	1215.42469	2	8.51E-04	0.80	3.12	-	732.6
gi|14149767|ref|NP_115492.1| hypothetical protein MGC2599 similar to katanin p60 subunit A 1 2599 [				3.80E-04	0.80	10.16	2.45	55392.0
AHQ-3-7, 2539	R.RRINGLSPEEIR.A	1440.63347	2	3.80E-04	0.80	3.18	-	732.1
gi|20543399|ref|XP_116396.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				4.33E-04	0.78	10.15	5.00	19852.7
AHQ-3-12, 4556	R.VSFKLFADK.F	1055.25138	1	4.33E-04	0.78	2.99	-	842.3
gi|5729779|ref|NP_006701.1| COP9 homolog [Homo sapiens]				4.34E-04	0.54	10.15	10.05	23225.5
AHQ-3-11, 5246	K.FIPLSEPAPVPPIPNEQQLAR.L	2314.66812	2	4.34E-04	0.54	2.87	-	275.6
gi|16945970|ref|NP_066967.2| PC4 and SFRS1 interacting protein 1; transcriptional coactivator p52/p				4.37E-04	0.39	10.12	3.00	37652.8
AHQ-3-12, 2990	K.QPKKDEEGQK.E	1187.28507	1	4.37E-04	0.39	2.32	-	586.0
gi|20127454|ref|NP_004035.2| 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cy				4.45E-04	0.95	10.20	2.87	64615.5
AHQ-3-6, 4702	K.AFTHTAQYDEAISDYFR.K	2036.14577	2	4.45E-04	0.95	4.03	-	1346.4
gi|4557593|ref|NP_000131.1| ferrochelatase [Homo sapiens]				4.49E-04	0.45	10.16	6.86	47833.9
AHQ-3-6, 4641	R.WKSGAAAAAVTTETAQHAQGAKPQVQPQK.R	2962.26963	3	4.49E-04	0.45	3.16	-	319.0
gi|22048001|ref|XP_033371.2| similar to DKFZP564O092 protein [Homo sapiens]				4.58E-04	0.47	10.14	5.71	35893.9
AHQ-3-7, 6491	K.DQLLLMYLMDLTHLILDK.A	2189.66736	2	4.58E-04	0.47	2.84	-	221.6
gi|5729873|ref|NP_006656.1| heparanase; heparanase-1 [Homo sapiens]				4.65E-04	0.86	10.14	1.84	61176.4
AHQ-3-7, 2278	K.LYGPDVGQPR.R	1102.22500	2	4.65E-04	0.86	2.86	-	702.5
gi|7657649|ref|NP_055362.1| tropomodulin 3 (ubiquitous) [Homo sapiens]				4.73E-04	0.65	10.14	3.13	39594.5
AHQ-3-11, 3124	K.FGYQFTQQGPR.T	1329.44490	2	4.73E-04	0.65	2.73	-	622.2
gi|14043026|ref|NP_003752.2| vesicle-associated membrane protein 8; endobrevin [Homo sapiens]				4.82E-04	0.95	10.21	14.00	11438.2
AHQ-3-13-, 2473	R.NKTEDLEATSEHFK.T	1649.74039	3	4.82E-04	0.95	4.20	-	1747.5
gi|17452829|ref|XP_071133.1| similar to ATP synthase, H+ transporting, mitochondrial F0 complex, su				4.82E-04	0.86	10.16	6.25	16522.7
AHQ-3-11, 2976	K.AGLVDDFEK.K	994.08007	2	4.82E-04	0.86	3.19	-	799.9
gi|4503117|ref|NP_000091.1| cystatin B; stefin B; liver thiol proteinase inhibitor; CPI-B [Homo sap				4.83E-04	0.76	10.18	12.24	11139.5
AHQ-3-13, 3107	K.VHVGDEDFVHLR.V	1423.55823	2	4.83E-04	0.76	2.79	-	470.7
gi|4507797|ref|NP_003341.1| ubiquitin-conjugating enzyme E2 variant 2; 1 alpha,25-dihydroxyvitamin				4.88E-04	1.67	20.18	13.79	16362.7
AHQ-3-12, 2986	R.LLEELEEGQK.G	1188.30974	2	4.88E-04	0.87	3.67	-	801.1
AHQ-3-12, 3120 - 3180	R.WTGM*IIGPPR.T	1144.37163	2	5.40E-04	0.80	2.60	-	1077.7
gi|21361409|ref|NP_036515.2| osteoclast stimulating factor 1 [Homo sapiens]				4.99E-04	1.07	20.15	20.28	24063.9
AHQ-3-10, 6167	K.DIVEMLFTQPNIELNQQNK.L	2275.56743	2	5.34E-04	0.36	2.75	-	232.8
AHQ-3-10, 4988	R.TGLIPSNYVAEQAESIDNPLHEAAK.R	2668.89701	2	4.99E-04	0.71	3.09	-	432.4
gi|22748945|ref|NP_689663.1| hypothetical protein MGC26690 [Homo sapiens]				5.02E-04	0.46	10.15	4.66	42016.9
AHQ-3-11, 6000	K.KLSQMSARLDKIEEGQK.K	1962.26109	2	5.02E-04	0.46	2.90	-	608.0
gi|11140819|ref|NP_006843.1| tousled-like kinase 2; serine/threonine kinase; tousled-like kinase [H				5.15E-04	0.23	10.13	1.47	85366.9
AHQ-3-3, 5202	R.SIIMQIVNALK.Y	1230.54591	1	5.15E-04	0.23	1.98	-	411.8
gi|4503477|ref|NP_001950.1| eukaryotic translation elongation factor 1 beta 2; eukaryotic translati				5.21E-04	0.94	10.21	8.00	24763.6
AHQ-3-9, 4711 - 4725	K.SSILLDVKPWDDETDMAK.L	2064.30228	2	5.21E-04	0.94	4.15	-	825.9
gi|10864021|ref|NP_067033.1| MUM2 protein [Homo sapiens]				5.21E-04	0.83	10.18	11.03	16831.5
AHQ-3-13, 5991 - 6059	K.NPLCPLGQTVQSELFR.S	1861.11187	2	5.21E-04	0.83	3.59	-	484.2
gi|27485813|ref|XP_208062.1| similar to ARP2/3 complex 21 kDa subunit (P21-ARC) (Actin-related prot				5.26E-04	0.74	10.14	6.31	12870.0
AHQ-3-11, 2310 - 2314	R.AYLQQLR.Q	892.03735	2	5.26E-04	0.74	2.73	-	680.7
gi|17440554|ref|XP_067503.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				5.30E-04	0.14	10.16	6.71	18110.6
AHQ-3-12, 4108	K.EGMDIVEAMER.F	1280.45418	1	5.30E-04	0.14	2.35	-	126.8
gi|30159103|ref|XP_296859.2| hypothetical protein XP_296859 [Homo sapiens]				5.30E-04	0.30	10.13	6.36	31013.7
AHQ-3-3, 7422	R.FLRHPWLEAGAAALRGEK.L	2023.32923	2	5.30E-04	0.30	2.53	-	352.4
gi|20143916|ref|NP_596870.1| titin isoform novex-3; connectin; CMH9, included; cardiomyopathy, dila				5.31E-04	0.45	10.15	0.54	631586.8
AHQ-3-8, 4739 - 4807	K.PKDVTALENATVAFEVSVSHDTVPVKWFHK.S	3353.77137	3	5.31E-04	0.45	3.03	-	481.3
gi|5174737|ref|NP_006077.1| tubulin, beta, 4 [Homo sapiens]				5.31E-04	0.78	10.14	3.33	50517.5
AHQ-3-7, 5600	R.ALTVPELTQQMFDAK.N	1692.95809	2	5.31E-04	0.78	2.72	-	572.2
gi|4505451|ref|NP_002515.1| neuroblastoma RAS viral (v-ras) oncogene homolog; v-ras neuroblastoma R				5.35E-04	0.59	10.15	6.35	21229.1
AHQ-3-11, 4402	K.SYGIPFIETSAK.T	1313.48046	2	5.35E-04	0.59	2.94	-	276.9
gi|16950611|ref|NP_444253.1| myosin light chain kinase isoform 1; myosin light chain kinase [Homo s				5.37E-04	0.90	10.21	1.46	210771.9
AHQ-3-5, 6212	K.LESEEDVSQAFLEAVAEEKPHVKPYFSK.T	3208.51984	3	5.37E-04	0.90	4.21	-	808.7
gi|16904381|ref|NP_006717.1| LPS-responsive vesicle trafficking, beach and anchor containing; vesic				5.53E-04	0.76	10.15	0.45	319158.3
AHQ-3-4, 3778	R.VGVGTSFGLPQTR.R	1319.49146	2	5.53E-04	0.76	3.07	-	675.4
gi|4505357|ref|NP_002480.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa; NADH dehyd				5.57E-04	0.83	10.15	14.81	9369.8
AHQ-3-14-, 5564 - 5575	R.LALFNPDVCWDR.N	1507.69520	2	5.57E-04	0.83	2.99	-	728.1
gi|6912586|ref|NP_036220.1| 6-phosphogluconolactonase [Homo sapiens]				5.58E-04	0.90	10.25	10.08	27546.7
AHQ-3-10, 6154	R.LPIPESQVITINPELPVEEAAEDYAK.K	2867.19683	2	5.58E-04	0.90	5.09	-	471.2
gi|4503173|ref|NP_001329.1| coxsackie virus and adenovirus receptor; 46 kD coxsackievirus and adeno				5.66E-04	0.33	10.15	5.75	40029.7
AHQ-3-9, 6368	K.VAAPNLSRM*GAIPVM*IPAQSK.D	2184.61238	2	5.66E-04	0.33	2.95	-	156.6
gi|9910554|ref|NP_064425.1| solute carrier family 2 (facilitated glucose transporter), member 9; SL				5.66E-04	0.59	10.16	5.74	58816.7
AHQ-3-1, 5098 - 5108	K.HNEARAVKAFQTFLGKADVSQEVEEVLAESR.V	3460.79874	3	5.66E-04	0.59	3.28	-	300.7
gi|4758032|ref|NP_004757.1| coatomer protein complex, subunit beta 2 (beta prime); coatomer binding				5.67E-04	0.81	10.18	2.10	102486.5
AHQ-3-5, 6512	K.AAESLADPTEYENLFPGLK.E	2066.25322	2	5.67E-04	0.81	3.70	-	461.0
gi|4506353|ref|NP_002854.1| phosphorylase, glycogen; liver (Hers disease, glycogen storage disease				5.75E-04	0.93	10.18	1.53	97147.8
AHQ-3-5, 3051	R.GIVGVENVAELKK.S	1356.59315	2	5.75E-04	0.93	3.51	-	1174.1
gi|16418391|ref|NP_443114.1| zinc finger, imprinted 3 [Homo sapiens]				5.85E-04	0.08	10.09	2.33	54497.6
AHQ-3-13, 4019	K.CSICEKAFSQK.S	1360.53887	1	5.85E-04	0.08	1.80	-	354.4
gi|4505395|ref|NP_002499.1| nidogen (enactin); Nidogen; nidogen (entactin) [Homo sapiens]				5.88E-04	0.87	10.20		136488.3
AHQ-3-1, 5622 - 5696	K.ALEGLQYPFAVTSYGK.N	1744.96805	2	5.88E-04	0.87	4.05	-	559.1
gi|27481006|ref|XP_117198.2| hypothetical protein XP_117198 [Homo sapiens]				5.92E-04	0.30	10.12	0.45	251738.6
AHQ-3-5, 3021	K.EDELQEM*M*VK.D	1284.43954	1	5.92E-04	0.30	2.03	-	505.4
gi|7661620|ref|NP_054775.1| DKFZP564K247 protein [Homo sapiens]				5.95E-04	0.96	10.27	23.66	10143.8
AHQ-3-13-, 6974 - 6975	K.EAPFVPVGIAGFAAIVAYGLYK.L	2254.65428	2	5.95E-04	0.96	5.39	-	986.4
gi|5032009|ref|NP_005600.1| glycogen phosphorylase; phosphorylase, glycogen, muscle; myophosphoryla				6.12E-04	0.19	10.11	1.07	97091.4
AHQ-3-5, 4077	R.YEFGIFNQK.I	1146.27624	1	6.12E-04	0.19	2.18	-	312.6
gi|27500008|ref|XP_208872.1| similar to tropomyosin 3 [Homo sapiens]				6.17E-04	0.96	10.24	6.45	28954.4
AHQ-3-9, 3432	R.ALKDEEKMELQELQLK.E	1946.25520	2	6.17E-04	0.96	4.87	-	1544.6
gi|11386183|ref|NP_008921.1| WAS protein family, member 2; suppressor of cyclic-AMP receptor (WASP-				6.43E-04	0.51	10.14	3.82	54283.7
AHQ-3-13, 6899	K.YAEDIFGELFTQANTFASR.V	2181.34601	2	6.43E-04	0.51	2.87	-	508.1
gi|5453998|ref|NP_006382.1| importin 7; RAN-binding protein 7 [Homo sapiens]				6.61E-04	0.91	10.20	1.45	119515.7
AHQ-3-4, 6906	R.ENIVEAIIHSPELIR.V	1733.98994	2	6.61E-04	0.91	3.95	-	854.3
gi|4885153|ref|NP_005198.1| v-crk sarcoma virus CT10 oncogene homolog (avian)-like; v-crk avian sar				6.62E-04	1.32	20.18	13.86	33776.7
AHQ-3-10, 5908 - 5947	K.IGDQEFDHLPALLEFYK.I	2036.27195	2	6.62E-04	0.65	3.12	-	497.7
AHQ-3-9, 4701	R.YPSPPM*GSVSAPNLPTAEDNLEYVR.T	2721.98015	2	6.72E-04	0.67	3.51	-	231.2

gi|20127517|ref|NP_009148.2| programmed cell death 10; apoptosis-related protein 15 [Homo sapiens]				6.64E-04	0.73	10.14	6.13	24701.4
AHQ-3-10, 3871	R.LIHQTNLILQTFK.T	1569.87265	2	6.64E-04	0.73	2.79	-	586.2
gi|27485697|ref|XP_097771.2| similar to hypothetical protein [Homo sapiens]				6.64E-04	0.15	10.14	14.41	12705.1
AHQ-3-13-, 4615 - 4679	K.NTTKNLYHVELRLAEK.H	1930.19728	2	6.64E-04	0.15	2.69	-	169.4
gi|29150259|ref|NP_803875.1| fibrocystin L; polycystic kidney and hepatic disease-like 1 [Homo sapi				6.74E-04	0.02	10.09	0.24	465745.4
AHQ-3-1, 3000	R.SPELPVYGAK.T	1061.21279	1	6.74E-04	0.02	1.84	-	270.8
gi|29741322|ref|XP_086001.2| similar to placental protein 13; galectin-13 [Homo sapiens]				6.78E-04	0.06	10.10	8.45	16576.0
AHQ-3-3, 3412	R.VHLGRRVVMNSR.E	1424.70391	1	6.78E-04	0.06	2.02	-	139.7
gi|5174697|ref|NP_006091.1| alpha2,3-sialyltransferase VI [Homo sapiens]				6.85E-04	0.07	10.10	2.11	38213.3
AHQ-3-6, 1890 - 1893	K.YNFSDLK.S	886.97120	1	6.85E-04	0.07	2.00	-	83.5
gi|9257257|ref|NP_059830.1| WD repeat-containing protein 1 isoform 1 [Homo sapiens]				6.96E-04	0.95	10.25		66193.1
AHQ-3-6, 3865	R.LHHVSSLAWLDEHTLVTTSHDASVK.E	2785.06406	3	6.96E-04	0.95	5.09	-	1234.8
gi|4502139|ref|NP_001156.1| baculoviral IAP repeat-containing protein 3; apoptosis inhibitor 2; TNF				6.97E-04	0.37	10.13	1.49	68371.2
AHQ-3-14-, 4155	R.ELIDTILVK.G	1044.26681	1	6.97E-04	0.37	1.89	-	532.1
gi|30149984|ref|XP_210576.2| similar to RIKEN cDNA 4921517D21 [Homo sapiens]				7.04E-04	0.09	10.11	0.83	116840.3
AHQ-3-13, 3397	K.QVITLGPER.F	1013.17290	1	7.04E-04	0.09	2.11	-	80.6
gi|29730632|ref|XP_293786.1| similar to RAN, member RAS oncogene family [Homo sapiens]				7.13E-04	0.67	10.12	7.69	16426.8
AHQ-3-10, 2274	K.LVLVGDGGTGK.T	1016.17355	1	7.13E-04	0.67	2.43	-	658.2
gi|27499555|ref|XP_051091.3| similar to SF21 protein [Homo sapiens]				7.38E-04	0.54	10.15	0.93	190356.9
AHQ-3-4, 3941 - 3944	K.FPPVKEAAESGIIKVK.T	1714.04177	2	7.38E-04	0.54	2.94	-	663.7
gi|8393147|ref|NP_058625.1| chloride intracellular channel 5 [Homo sapiens]				7.48E-04	0.69	10.18	6.77	28109.7
AHQ-3-10, 5815	K.FLDGDELTLADCNLLPK.L	1936.17229	2	7.48E-04	0.69	3.54	-	424.0
gi|27754771|ref|NP_002578.2| protocadherin 1 isoform 1 precursor; protocadherin 42; cadherin-like p				7.54E-04	0.51	10.17	1.32	114742.6
AHQ-3-14, 5097 - 5159	K.KYFLQTTTPLDYEK.V	1747.96871	2	7.54E-04	0.51	3.30	-	379.8
gi|22749429|ref|NP_689936.1| hypothetical protein FLJ38159 [Homo sapiens]				7.84E-04	0.80	10.20	4.28	43808.3
AHQ-3-7, 6731	R.SRIEEQSQLICILKRR.S	2031.36958	2	7.84E-04	0.80	4.02	-	790.2
gi|21618338|ref|NP_003141.2| signal transducer and activator of transcription 3 isoform 2; acute-ph				7.97E-04	0.58	10.14	1.82	87980.2
AHQ-3-6, 3445	R.FLQESNVLYQHNLR.R	1761.96193	2	7.97E-04	0.58	2.83	-	500.5
gi|22748825|ref|NP_689598.1| hypothetical protein FLJ31438 [Homo sapiens]				8.02E-04	0.11	10.14	2.90	67291.5
AHQ-3-2, 6130	R.TIQLEAKMRIIESNSSK.I	1949.26232	2	8.02E-04	0.11	2.72	-	174.8
gi|4506193|ref|NP_002784.1| proteasome beta 1 subunit; proteasome subunit HC5; proteasome component				8.14E-04	0.88	10.22	8.30	26489.2
AHQ-3-11, 4631	K.AGGSASAM*LQPLLDNQVGFK.N	2021.28383	2	8.14E-04	0.88	4.31	-	336.6
gi|24158492|ref|NP_699179.1| F-box only protein 29; F-box protein Fbx29 [Homo sapiens]				8.23E-04	0.52	10.16	2.51	67296.3
AHQ-3-13-, 5394	R.RRWQEELAQAQAPKK.R	1840.07906	2	8.23E-04	0.52	2.53	-	593.9
gi|9845496|ref|NP_002283.2| laminin, beta 2 precursor; laminin S [Homo sapiens]				8.49E-04	0.04	10.10	0.56	195993.7
AHQ-3-10, 3434	R.DRLALNLTLR.Q	1185.40182	1	8.49E-04	0.04	2.04	-	140.0
gi|13899253|ref|NP_113620.1| uridine-cytidine kinase 1 [Homo sapiens]				8.56E-04	0.21	10.16	4.33	31434.5
AHQ-3-12, 6398 - 6399	R.KVVILSQDRFYK.V	1496.77853	1	8.56E-04	0.21	2.31	-	357.1
gi|20143964|ref|NP_597702.1| glutamate receptor, ionotropic, N-methyl-D-aspartate 3A [Homo sapiens]				8.60E-04	0.21	10.16	2.42	125436.3
AHQ-3-2, 4339 - 4363	R.YNVPATPDGVEYLKNDPEKLDAFIM*DK.A	3100.44475	3	8.60E-04	0.21	3.12	-	295.1
gi|4507879|ref|NP_003365.1| voltage-dependent anion channel 1 [Homo sapiens]				8.72E-04	0.49	10.14	3.89	30772.3
AHQ-3-9, 4076	R.WTEYGLTFTEK.W	1375.50711	1	8.72E-04	0.49	2.79	-	227.3
gi|16753212|ref|NP_003921.2| src family associated phosphoprotein 2; src kinase-associated phosphop				8.80E-04	0.93	10.18	2.79	41216.5
AHQ-3-12, 3078	K.RGDVIYILSK.E	1164.37938	2	8.80E-04	0.93	3.65	-	1234.7
gi|29736279|ref|XP_296484.1| hypothetical protein XP_296484 [Homo sapiens]				8.82E-04	0.10	10.14	6.35	27690.3
AHQ-3-4, 3705	K.TGSSRGKGPEDRQIPK.S	1713.87721	2	8.82E-04	0.10	2.90	-	264.9
gi|13994351|ref|NP_114159.1| MSTP043 protein [Homo sapiens]				8.99E-04	0.04	10.10	2.42	62669.3
AHQ-3-12, 4687	K.KVQLPSLSKLPFK.S	1485.83879	1	8.99E-04	0.04	1.95	-	144.5
gi|5730118|ref|NP_006514.1| X-prolyl aminopeptidase (aminopeptidase P) 1, soluble; X-prolyl aminope				9.70E-04	0.86	10.19	2.57	69858.4
AHQ-3-6, 6235 - 6306	R.GSLTFEPLTLVPIQTK.M	1745.05263	2	9.70E-04	0.86	3.30	-	607.3
gi|22538455|ref|NP_003734.3| nuclear receptor coactivator 1 isoform 1 [Homo sapiens]				9.72E-04	0.31	10.13	1.04	156755.4
AHQ-3-6, 4831	K.KESKDHQLLRYLLDK.D	1887.17241	2	9.72E-04	0.31	2.59	-	205.4
gi|30155338|ref|XP_303366.1| hypothetical protein XP_303366 [Homo sapiens]				9.74E-04	0.61	10.14	6.17	17471.0
AHQ-3-11, 2006	K.ASVIILAGRR.G	1056.28728	2	9.74E-04	0.61	2.88	-	662.1
gi|30156349|ref|XP_301652.1| similar to Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) [				9.98E-04	0.29	10.13	9.33	21450.7
AHQ-3-8, 4080	K.M*HAADLTVSALRGDM*DEK.E	1993.20912	2	9.98E-04	0.29	2.53	-	329.5

Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|4501885|ref|NP_001092.1| beta actin; beta cytoskeletal actin [Homo sapiens]				1.00E-30	14.77	170.38	36.80	41736.5
AHQ-4-8, 6733 - 6797	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	4.78E-11	0.96	5.58	-	1041.5
AHQ-4-8, 6945 - 6995	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	9.44E-09	0.92	4.69	-	939.5
AHQ-4-13-, 6580 - 6645	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	3.73E-05	0.64	4.28	-	321.5
AHQ-4-13-, 6354 - 6401	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	2.26E-04	0.55	3.13	-	382.4
AHQ-4-1, 6827 - 6893	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.46E-04	0.46	3.12	-	480.5
AHQ-4-13-, 6017 - 6084	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.47E-04	0.86	3.95	-	535.9
AHQ-4-13, 6820 - 6886	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.14E-06	0.82	3.98	-	634.7
AHQ-4-8, 7209 - 7278	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	9.88E-11	0.94	5.19	-	948.5
AHQ-4-13, 6729	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	6.66E-04	0.65	3.66	-	355.8
AHQ-4-8, 7345	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.42E-09	0.92	4.76	-	714.7
AHQ-4-13, 6457 - 6461	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	7.36E-07	0.74	3.76	-	420.4
AHQ-4-13, 6101 - 6168	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.00E-04	0.87	3.92	-	663.6
AHQ-4-11, 6598 - 6660	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.35E-04	0.93	4.84	-	897.6
AHQ-4-8, 6011	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	4.96E-10	0.83	3.85	-	598.0
AHQ-4-8, 6859 - 6921	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.93E-13	0.94	5.46	-	664.3
AHQ-4-10, 6284 - 6345	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.15E-08	0.95	4.98	-	1077.5
AHQ-4-8, 6559 - 6641	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	2.91E-04	0.63	4.00	-	402.7
AHQ-4-10, 6047 - 6125	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.19E-04	0.52	3.27	-	275.9
AHQ-4-10, 5927 - 5991	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	8.02E-05	0.75	4.49	-	524.9
AHQ-4-8, 7061 - 7137	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	8.02E-08	0.93	4.72	-	991.2
AHQ-4-10, 5581 - 5640	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	9.33E-04	0.71	3.67	-	385.1
AHQ-4-5, 7154	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.05E-07	0.82	4.09	-	657.8
AHQ-4-8, 6791 - 6853	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.71E-05	0.62	3.47	-	447.4
AHQ-4-9, 6500	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	4.82E-04	0.88	4.14	-	668.9
AHQ-4-9, 6471 - 6531	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	5.23E-06	0.85	3.70	-	809.0
AHQ-4-10, 6337 - 6396	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	8.91E-04	0.80	3.14	-	729.6
AHQ-4-8, 6918 - 6985	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	9.38E-05	0.85	3.96	-	908.3
AHQ-4-8, 5302 - 5337	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.00E-07	0.63	3.19	-	831.7
AHQ-4-8, 7337 - 7338	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.68E-08	0.91	4.13	-	843.6
AHQ-4-8, 5410 - 5478	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	7.42E-08	0.93	4.45	-	1201.3
AHQ-4-8, 7309 - 7377	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	5.81E-12	0.92	5.05	-	1041.8
AHQ-4-8, 5707	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	7.37E-05	0.82	3.65	-	899.9
AHQ-4-8, 5606 - 5638	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	9.07E-06	0.82	3.70	-	857.5
AHQ-4-8, 6954 - 7022	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.74E-09	0.91	4.93	-	718.7
AHQ-4-8, 7021 - 7098	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	7.30E-06	0.92	4.87	-	1174.1
AHQ-4-8, 7201 - 7269	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	8.65E-08	0.87	3.87	-	811.5
AHQ-4-8, 7163 - 7242	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	3.89E-08	0.95	5.72	-	1293.7
AHQ-4-8, 7062 - 7133	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	3.14E-07	0.89	3.69	-	902.0
AHQ-4-8, 6930 - 6994	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	3.83E-04	0.82	3.57	-	617.6
AHQ-4-8, 7317 - 7381	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	9.13E-04	0.83	3.40	-	918.2
AHQ-4-8, 6158 - 6293	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	1.05E-08	0.97	7.28	-	1264.4
AHQ-4-10, 6263 - 6320	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	1.97E-04	0.98	7.55	-	1455.6
AHQ-4-8, 6666 - 6729	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	3.33E-14	0.98	7.11	-	1778.2
AHQ-4-10, 5916 - 5981	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	1.12E-08	0.95	6.44	-	1130.3
AHQ-4-8, 6901 - 6966	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	2.75E-11	0.98	7.66	-	2026.7
AHQ-4-8, 6793 - 6857	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	1.00E-30	0.98	7.60	-	2267.7
AHQ-4-8, 6831 - 6906	R.FRCPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3555.03753	3	6.37E-04	0.49	3.19	-	541.1
AHQ-4-13, 6490 - 6560	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	1.96E-05	0.73	3.49	-	558.4
AHQ-4-7, 2238 - 2243	R.GYSFTTTAER.E	1133.19273	2	2.12E-04	0.91	3.14	-	1043.1
AHQ-4-1, 2610	R.GYSFTTTAER.E	1133.19273	2	4.38E-04	0.90	2.91	-	906.3
AHQ-4-8, 2051 - 2119	R.GYSFTTTAER.E	1133.19273	2	1.75E-04	0.88	3.25	-	781.5
AHQ-4-8, 2124 - 2199	R.GYSFTTTAER.E	1133.19273	2	8.44E-05	0.89	2.85	-	1351.6
AHQ-4-11, 2389 - 2392	R.GYSFTTTAER.E	1133.19273	2	3.79E-04	0.91	3.34	-	1008.3
AHQ-4-6, 2279	R.GYSFTTTAER.E	1133.19273	2	1.11E-04	0.89	3.08	-	884.2
AHQ-4-9, 2172 - 2179	R.GYSFTTTAER.E	1133.19273	2	3.88E-05	0.88	3.06	-	967.2
AHQ-4-3, 2439	R.GYSFTTTAER.E	1133.19273	2	3.94E-05	0.93	3.14	-	1208.4
AHQ-4-14-, 2383	R.GYSFTTTAER.E	1133.19273	2	3.98E-05	0.90	2.70	-	828.5
AHQ-4-8, 2183 - 2263	R.GYSFTTTAER.E	1133.19273	2	6.55E-05	0.90	3.14	-	887.5
AHQ-4-13, 4342 - 4356	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	2.50E-06	0.82	3.56	-	866.7
AHQ-4-11, 4565	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.13E-05	0.86	3.74	-	605.6
AHQ-4-10, 4259 - 4316	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	3.33E-05	0.91	3.55	-	1039.7
AHQ-4-13, 4778 - 4816	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	8.61E-04	0.87	3.73	-	719.4
AHQ-4-14, 5433	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	1.21E-07	0.84	3.57	-	542.2
AHQ-4-13-, 4224	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	6.91E-05	0.95	5.84	-	1340.1
AHQ-4-14-, 4615 - 4658	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	5.16E-04	0.94	3.93	-	1121.9
AHQ-4-8, 3833 - 3841	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	3.03E-05	0.94	5.09	-	780.8
AHQ-4-8, 3997 - 4071	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	3.73E-05	0.94	4.86	-	753.9
AHQ-4-8, 4637	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	3.93E-04	0.77	3.82	-	593.3
AHQ-4-8, 4553	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	6.96E-05	0.88	4.35	-	872.7
AHQ-4-8, 4339 - 4389	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	3.38E-07	0.98	5.23	-	1889.0
AHQ-4-8, 4187	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	2.96E-04	0.97	5.76	-	1700.2
AHQ-4-8, 4181	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	4.92E-05	0.75	2.79	-	915.7
AHQ-4-8, 7365 - 7394	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	3.41E-06	0.98	6.89	-	2348.6
AHQ-4-8, 5298 - 5323	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.03E-04	0.75	3.79	-	513.4
AHQ-4-14-, 5574 - 5633	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.61E-14	0.98	6.98	-	1542.5
AHQ-4-14-, 5359 - 5427	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.50E-07	0.96	5.75	-	1299.8
AHQ-4-8, 5869	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.35E-04	0.87	4.01	-	1085.2
AHQ-4-1, 5809 - 5879	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.44E-07	0.93	4.70	-	1335.5
AHQ-4-2, 6066 - 6082	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.13E-08	0.94	5.01	-	1088.5
AHQ-4-13-, 5769	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.96E-06	0.96	5.93	-	1110.8
AHQ-4-13-, 5652	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.42E-08	0.97	5.71	-	1699.1
AHQ-4-13-, 5465	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.22E-07	0.94	5.23	-	1234.3
AHQ-4-13-, 5378	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.71E-05	0.92	4.98	-	1111.7
AHQ-4-8, 5721 - 5797	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.64E-12	0.97	5.81	-	1835.8
AHQ-4-7, 5842	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.65E-09	0.94	4.87	-	1299.6
AHQ-4-7, 5761	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.74E-09	0.95	5.27	-	1307.0
AHQ-4-7, 5573 - 5578	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.20E-11	0.97	6.15	-	1507.6
AHQ-4-7, 5269 - 5283	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.11E-10	0.94	5.28	-	968.5
AHQ-4-8, 5366 - 5445	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.33E-14	0.97	6.50	-	1614.5
AHQ-4-8, 5134 - 5205	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.82E-12	0.97	5.93	-	1660.0
AHQ-4-8, 5390 - 5473	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.58E-04	0.85	4.28	-	777.1
AHQ-4-2, 6171	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.74E-06	0.96	5.38	-	1333.8
AHQ-4-3, 5681 - 5749	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.66E-06	0.88	4.16	-	919.3
AHQ-4-9, 4695 - 4767	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.90E-07	0.94	5.38	-	1039.1
AHQ-4-9, 4835 - 4911	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.99E-09	0.94	5.21	-	1282.3
AHQ-4-9, 5119 - 5183	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.42E-10	0.96	5.59	-	1373.9
AHQ-4-9, 5279 - 5339	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.88E-15	0.98	6.29	-	2056.1
AHQ-4-6, 5360	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.85E-08	0.90	4.97	-	635.3
AHQ-4-3, 6165	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.02E-07	0.95	5.46	-	1255.1
AHQ-4-4, 5642	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	9.79E-07	0.96	5.48	-	1364.1
AHQ-4-8, 5591 - 5657	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.00E-15	0.98	6.78	-	2350.1
AHQ-4-10, 4799 - 4859	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.32E-06	0.96	5.33	-	1602.5
AHQ-4-10, 4893 - 4951	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.35E-10	0.96	5.94	-	1472.8
AHQ-4-10, 5011 - 5013	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.74E-13	0.97	6.01	-	1640.1

AHQ-4-10, 5148 - 5211	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.21E-12	0.96	5.95	-	1238.3
AHQ-4-10, 5301 - 5363	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.14E-07	0.96	5.36	-	1647.2
AHQ-4-10, 5433 - 5507	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.27E-05	0.93	5.03	-	899.1
AHQ-4-5, 5913 - 5981	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.15E-07	0.96	5.23	-	1585.3
AHQ-4-5, 5818 - 5894	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.52E-06	0.93	4.67	-	1431.4
AHQ-4-5, 5707 - 5730	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.84E-12	0.97	6.24	-	1835.7
AHQ-4-5, 5511 - 5515	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.37E-06	0.96	5.78	-	1489.2
AHQ-4-13, 5844	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.57E-08	0.97	5.51	-	1553.1
AHQ-4-13, 5701 - 5757	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.11E-04	0.96	5.53	-	1694.8
AHQ-4-4, 6142	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.47E-07	0.96	5.73	-	1520.5
AHQ-4-4, 6003 - 6070	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.91E-08	0.95	5.29	-	1280.9
AHQ-4-13, 5558 - 5565	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.51E-04	0.76	3.64	-	448.6
AHQ-4-8, 5542 - 5581	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.71E-04	0.80	4.13	-	583.8
AHQ-4-11, 5213	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.98E-09	0.94	5.02	-	1092.2
AHQ-4-11, 5516 - 5596	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.26E-07	0.96	6.05	-	1296.2
AHQ-4-11, 5600 - 5660	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.87E-11	0.97	6.09	-	1264.5
AHQ-4-4, 5727 - 5803	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.26E-05	0.94	4.67	-	1274.3
AHQ-4-6, 5675 - 5744	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.16E-09	0.96	5.69	-	1380.0
AHQ-4-12, 5453	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.97E-05	0.93	4.97	-	1028.4
AHQ-4-12, 5534	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.08E-09	0.95	5.52	-	1244.8
AHQ-4-12, 5689 - 5754	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.55E-04	0.92	4.76	-	1005.0
AHQ-4-12, 5866	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.27E-07	0.94	4.75	-	1296.3
AHQ-4-8, 5509 - 5574	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.37E-12	0.97	5.48	-	2306.2
AHQ-4-14-, 5622 - 5694	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.00E-30	0.98	6.98	-	1736.5
AHQ-4-11, 3673	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.06E-07	0.91	4.17	-	857.5
AHQ-4-5, 3634 - 3709	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	4.10E-04	0.67	4.15	-	539.9
AHQ-4-5, 3637 - 3639	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.07E-04	0.92	4.42	-	820.8
AHQ-4-10, 3512 - 3567	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.49E-10	0.93	4.80	-	830.3
AHQ-4-6, 3576 - 3580	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.97E-06	0.92	4.43	-	789.0
AHQ-4-9, 3247 - 3319	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.71E-07	0.90	4.28	-	772.5
AHQ-4-3, 3923 - 3935	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.53E-04	0.60	3.35	-	492.7
AHQ-4-9, 3153 - 3223	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.84E-06	0.94	4.76	-	850.3
AHQ-4-7, 3494	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.02E-06	0.91	4.62	-	503.2
AHQ-4-13-, 3902	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.81E-04	0.94	4.68	-	1110.5
AHQ-4-8, 3683	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.18E-04	0.68	2.62	-	602.8
AHQ-4-8, 3109 - 3177	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.71E-05	0.92	4.34	-	805.6
AHQ-4-8, 3209 - 3277	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.78E-07	0.95	5.17	-	1087.9
AHQ-4-8, 3270 - 3337	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	2.98E-04	0.66	3.83	-	684.1
AHQ-4-8, 3318 - 3385	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.20E-06	0.93	4.76	-	813.2
AHQ-4-8, 3321	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.25E-09	0.90	4.17	-	788.2
AHQ-4-8, 3401 - 3477	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	1.78E-06	0.76	4.26	-	678.3
AHQ-4-1, 4166	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.05E-04	0.83	3.36	-	499.7
AHQ-4-1, 4153	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	9.18E-04	0.57	3.29	-	712.3
AHQ-4-14-, 3786	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.26E-05	0.84	3.98	-	633.8
AHQ-4-8, 3453	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.74E-05	0.90	3.59	-	762.3
AHQ-4-8, 3590 - 3594	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.60E-05	0.93	4.15	-	812.1
AHQ-4-12, 3749 - 3817	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.03E-04	0.92	4.71	-	842.1
AHQ-4-8, 2787 - 2861	R.VAPEEHPVLLTEAPLNPKANR.E	2296.61120	3	8.01E-07	0.78	3.89	-	342.4
gi|5729770|ref|NP_000382.3|	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky			1.00E-30	0.97	10.27	4.80	61247.6
AHQ-4-8, 7191	R.VPIPWVSGTSASTPVFGGILSLINEHR.I	2836.23725	3	1.00E-30	0.97	5.45	-	2057.8
gi|16753233|ref|NP_006280.2|	talin 1 [Homo sapiens]			5.55E-16	108.19	1240.38	54.80	269665.3
AHQ-4-3, 3361	K.AAAFEEQENETVVVK.E	1664.79496	2	9.99E-05	0.91	3.81	-	970.2
AHQ-4-1, 3431 - 3441	K.AAAFEEQENETVVVK.E	1664.79496	2	3.75E-06	0.81	3.58	-	678.4
AHQ-4-2, 3523 - 3552	K.AAAFEEQENETVVVK.E	1664.79496	2	3.96E-04	0.95	4.79	-	1258.4
AHQ-4-2, 3370	K.AAAFEEQENETVVVK.E	1664.79496	2	1.14E-04	0.90	3.67	-	1211.8
AHQ-4-6, 3002	K.AAAFEEQENETVVVK.E	1664.79496	2	4.89E-07	0.94	4.50	-	1204.3
AHQ-4-13, 3299	K.AAAFEEQENETVVVK.E	1664.79496	2	4.29E-04	0.92	3.90	-	1084.9
AHQ-4-2, 3124 - 3196	K.AAAFEEQENETVVVK.E	1664.79496	2	5.39E-05	0.60	2.80	-	478.8
AHQ-4-1, 2671	R.AAM*EPIVISAK.T	1146.38260	2	2.96E-06	0.87	2.93	-	920.1
AHQ-4-2, 2490	R.AAM*EPIVISAK.T	1146.38260	2	7.50E-06	0.78	2.74	-	643.3
AHQ-4-3, 3155	R.AAMEPIVISAK.T	1130.38320	2	1.74E-06	0.70	2.71	-	515.0
AHQ-4-4, 2459	R.AAM*EPIVISAK.T	1146.38260	1	6.10E-05	0.62	2.68	-	283.4
AHQ-4-4, 2460	R.AAM*EPIVISAK.T	1146.38260	2	1.86E-05	0.80	2.85	-	738.9
AHQ-4-2, 3167 - 3180	R.AAMEPIVISAK.T	1130.38320	2	8.14E-06	0.89	3.15	-	928.8
AHQ-4-2, 2496	R.AAM*EPIVISAK.T	1146.38260	1	1.20E-04	0.55	2.67	-	190.9
AHQ-4-3, 2441 - 2468	R.AAM*EPIVISAK.T	1146.38260	1	8.20E-04	0.47	2.28	-	246.3
AHQ-4-5, 2326	R.AAM*EPIVISAK.T	1146.38260	2	1.12E-04	0.83	2.57	-	786.4
AHQ-4-4, 3138 - 3148	R.AAMEPIVISAK.T	1130.38320	2	3.49E-05	0.74	2.64	-	669.3
AHQ-4-3, 2476 - 2479	R.AAM*EPIVISAK.T	1146.38260	2	1.76E-06	0.84	2.97	-	660.7
AHQ-4-5, 1641	K.ADAEGESDLENSR.K	1393.35296	2	2.60E-07	0.83	2.94	-	753.1
AHQ-4-1, 2043 - 2047	K.ADAEGESDLENSR.K	1393.35296	2	7.65E-07	0.93	4.11	-	1040.7
AHQ-4-2, 1804 - 1882	K.ADAEGESDLENSR.K	1393.35296	2	2.13E-06	0.95	4.83	-	1101.1
AHQ-4-3, 2571	K.AGALQCSPSDAYTK.K	1470.58689	2	2.00E-04	0.88	3.61	-	721.8
AHQ-4-6, 2435	K.AGALQCSPSDAYTK.K	1470.58689	2	4.43E-04	0.67	2.91	-	494.7
AHQ-4-2, 2600	K.AGALQCSPSDAYTK.K	1470.58689	1	6.06E-07	0.75	3.31	-	502.1
AHQ-4-4, 2555	K.AGALQCSPSDAYTK.K	1470.58689	1	3.17E-05	0.83	3.38	-	517.2
AHQ-4-4, 2546 - 2558	K.AGALQCSPSDAYTK.K	1470.58689	2	2.52E-04	0.92	3.93	-	770.6
AHQ-4-3, 2589	K.AGALQCSPSDAYTK.K	1470.58689	1	7.05E-08	0.67	3.47	-	445.3
AHQ-4-2, 2303	K.AGALQCSPSDAYTKK.E	1598.75981	2	3.01E-04	0.59	3.18	-	375.3
AHQ-4-7, 6069	K.AGFLDLKDFLPK.E	1364.61374	2	5.26E-04	0.91	3.57	-	1304.7
AHQ-4-2, 4180	K.AIAVTVQEMVTK.S	1290.55498	2	2.09E-04	0.96	4.27	-	1516.3
AHQ-4-4, 3963	K.AIAVTVQEMVTK.S	1290.55498	2	6.05E-05	0.96	4.38	-	1376.2
AHQ-4-3, 4011	K.AIAVTVQEMVTK.S	1290.55498	2	5.00E-08	0.94	4.01	-	1177.2
AHQ-4-3, 2437	K.ALDGAFTEENR.A	1223.27427	2	5.51E-08	0.94	3.34	-	1482.6
AHQ-4-1, 2571	K.ALDGAFTEENR.A	1223.27427	2	7.28E-04	0.93	3.22	-	1344.8
AHQ-4-2, 2451	K.ALDGAFTEENR.A	1223.27427	2	1.91E-06	0.91	3.34	-	1162.2
AHQ-4-1, 2723	K.ALDGAFTEENR.A	1223.27427	2	1.77E-05	0.95	3.79	-	1763.4
AHQ-4-4, 2416 - 2424	K.ALDGAFTEENR.A	1223.27427	2	5.24E-05	0.88	3.07	-	963.6
AHQ-4-7, 3605	K.ALDYYMLR.N	1045.23686	2	2.50E-04	0.92	3.10	-	901.1
AHQ-4-13-, 3306 - 3308	K.ALDYYM*LR.N	1061.23626	2	9.39E-06	0.90	2.52	-	1019.7
AHQ-4-13, 3449	K.ALDYYM*LR.N	1061.23626	2	1.52E-05	0.91	2.92	-	940.9
AHQ-4-13, 4088	K.ALDYYMLR.N	1045.23686	2	5.98E-05	0.91	2.99	-	836.2
AHQ-4-7, 2962	K.ALDYYM*LR.N	1061.23626	2	1.15E-04	0.90	2.54	-	1013.0
AHQ-4-13-, 3944	K.ALDYYMLR.N	1045.23686	2	1.80E-05	0.87	2.55	-	805.2
AHQ-4-1, 2063	R.ALEATTEHIR.Q	1141.25953	2	6.95E-06	0.85	3.14	-	1041.7
AHQ-4-2, 1802	R.ALEATTEHIR.Q	1141.25953	1	4.20E-04	0.12	2.17	-	137.1
AHQ-4-3, 1760	R.ALEATTEHIR.Q	1141.25953	2	6.91E-06	0.79	3.09	-	880.9
AHQ-4-6, 1644	R.ALEATTEHIR.Q	1141.25953	2	2.30E-07	0.80	3.10	-	927.4
AHQ-4-2, 1783 - 1862	R.ALEATTEHIR.Q	1141.25953	2	9.31E-07	0.79	3.16	-	929.9
AHQ-4-1, 2098	R.ALEATTEHIR.Q	1141.25953	1	1.73E-04	0.05	1.87	-	205.1
AHQ-4-4, 1799 - 1830	R.ALEATTEHIR.Q	1141.25953	2	7.95E-04	0.80	2.95	-	973.7
AHQ-4-1, 3546	K.ALGDLISATK.A	989.14811	2	1.35E-06	0.92	3.30	-	986.3
AHQ-4-4, 3408	K.ALGDLISATK.A	989.14811	2	2.35E-06	0.92	4.10	-	731.9
AHQ-4-4, 3406	K.ALGDLISATK.A	989.14811	1	1.70E-04	0.31	2.30	-	459.3
AHQ-4-5, 3233	K.ALGDLISATK.A	989.14811	2	2.83E-06	0.93	3.92	-	750.5
AHQ-4-6, 3182 - 3204	K.ALGDLISATK.A	989.14811	2	2.02E-04	0.93	3.69	-	862.4
AHQ-4-2, 3426	K.ALGDLISATK.A	989.14811	2	2.73E-07	0.92	3.55	-	788.0

AHQ-4-3, 3432	K.ALGDLISATK.A	989.14811	2	4.70E-05	0.92	3.61	-	857.2
AHQ-4-7, 2367	K.ALSTDPAAPNLK.S	1198.35099	2	6.64E-07	0.71	3.09	-	528.9
AHQ-4-4, 2539	K.ALSTDPAAPNLK.S	1198.35099	2	8.06E-07	0.70	3.18	-	472.2
AHQ-4-3, 2556	K.ALSTDPAAPNLK.S	1198.35099	2	3.62E-07	0.69	2.56	-	648.9
AHQ-4-2, 2403	K.ALSTDPAAPNLK.S	1198.35099	2	2.29E-04	0.67	2.57	-	609.5
AHQ-4-2, 2554	K.ALSTDPAAPNLK.S	1198.35099	2	4.29E-06	0.76	3.44	-	549.0
AHQ-4-6, 2407 - 2411	K.ALSTDPAAPNLK.S	1198.35099	2	1.13E-06	0.82	2.80	-	724.8
AHQ-4-1, 2715 - 2726	K.ALSTDPAAPNLK.S	1198.35099	2	3.88E-06	0.79	3.20	-	658.9
AHQ-4-2, 3582	K.ALSTDPAAPNLKSQLAAAAR.A	1967.21592	2	2.62E-06	0.76	3.04	-	570.5
AHQ-4-4, 5674	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.35E-09	0.94	4.48	-	1087.7
AHQ-4-2, 6426	K.APGQLECETAIAALNSCLR.D	2077.32566	2	7.36E-10	0.97	5.40	-	1117.8
AHQ-4-5, 6287	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.79E-05	0.95	4.48	-	1341.3
AHQ-4-3, 6420	K.APGQLECETAIAALNSCLR.D	2077.32566	2	7.98E-08	0.95	4.74	-	1147.9
AHQ-4-2, 5744	K.APGQLECETAIAALNSCLR.D	2077.32566	2	4.37E-08	0.95	5.05	-	882.8
AHQ-4-6, 6163	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.96E-04	0.60	2.66	-	585.0
AHQ-4-1, 6306 - 6369	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.23E-06	0.93	4.09	-	1006.4
AHQ-4-3, 5723	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.38E-10	0.94	4.18	-	1048.7
AHQ-4-4, 6403	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.87E-08	0.96	5.09	-	1052.5
AHQ-4-3, 7059	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	7.90E-10	0.92	4.20	-	1259.3
AHQ-4-6, 6763	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	4.81E-04	0.93	4.78	-	1320.5
AHQ-4-3, 7049 - 7131	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	2	4.64E-07	0.89	4.26	-	807.1
AHQ-4-1, 6930	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.44E-08	0.94	4.65	-	1389.4
AHQ-4-2, 7070	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	3.29E-04	0.92	4.04	-	1627.4
AHQ-4-5, 6903	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	2.16E-04	0.84	3.88	-	831.9
AHQ-4-4, 7011	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	4.04E-06	0.77	3.51	-	945.3
AHQ-4-1, 2987 - 3066	K.ASAGPQPLLVQSCK.A	1457.67763	2	7.68E-07	0.82	3.33	-	488.8
AHQ-4-2, 3135	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.08E-07	0.50	2.78	-	345.1
AHQ-4-2, 2867 - 2872	K.ASAGPQPLLVQSCK.A	1457.67763	1	5.42E-05	0.26	2.10	-	315.7
AHQ-4-5, 2687	K.ASAGPQPLLVQSCK.A	1457.67763	1	4.46E-09	0.75	3.68	-	352.8
AHQ-4-5, 2643 - 2681	K.ASAGPQPLLVQSCK.A	1457.67763	2	4.81E-09	0.84	3.57	-	466.5
AHQ-4-2, 2848 - 2918	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.60E-05	0.85	3.56	-	458.9
AHQ-4-4, 2868	K.ASAGPQPLLVQSCK.A	1457.67763	1	5.03E-07	0.49	2.91	-	326.9
AHQ-4-3, 2883	K.ASAGPQPLLVQSCK.A	1457.67763	1	6.43E-08	0.77	3.62	-	521.5
AHQ-4-6, 2699	K.ASAGPQPLLVQSCK.A	1457.67763	1	4.00E-10	0.70	3.36	-	317.8
AHQ-4-6, 2667 - 2686	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.31E-08	0.88	3.62	-	543.6
AHQ-4-3, 2849 - 2884	K.ASAGPQPLLVQSCK.A	1457.67763	2	5.01E-05	0.70	3.22	-	477.8
AHQ-4-2, 4059	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	6.40E-05	0.69	3.16	-	324.8
AHQ-4-2, 4387 - 4467	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	7.84E-07	0.94	4.69	-	604.1
AHQ-4-2, 4560	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.54E-09	0.91	4.43	-	556.3
AHQ-4-7, 4083	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	8.89E-06	0.63	3.07	-	380.6
AHQ-4-2, 4880	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	6.37E-09	0.89	3.40	-	808.7
AHQ-4-3, 4384 - 4425	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.23E-06	0.78	3.44	-	416.3
AHQ-4-3, 3928	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	4.09E-04	0.91	3.89	-	826.4
AHQ-4-1, 4419	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.00E-07	0.94	4.34	-	964.3
AHQ-4-4, 3736 - 3754	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.41E-05	0.89	4.09	-	538.1
AHQ-4-5, 3577	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.73E-05	0.74	3.16	-	502.4
AHQ-4-6, 4086	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.56E-09	0.90	4.25	-	546.4
AHQ-4-6, 3507	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.33E-04	0.80	3.42	-	532.6
AHQ-4-4, 4331 - 4355	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	5.45E-09	0.93	4.35	-	769.7
AHQ-4-6, 4730	K.AVAEQIPLLVQGVR.G	1493.77619	1	2.72E-04	0.47	2.81	-	269.9
AHQ-4-2, 5359	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.07E-06	0.90	3.86	-	746.6
AHQ-4-2, 5075	K.AVAEQIPLLVQGVR.G	1493.77619	1	1.33E-08	0.59	3.19	-	233.4
AHQ-4-2, 5042 - 5111	K.AVAEQIPLLVQGVR.G	1493.77619	2	6.39E-08	0.94	4.44	-	859.4
AHQ-4-3, 5036 - 5051	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.34E-06	0.94	4.90	-	649.0
AHQ-4-3, 5043	K.AVAEQIPLLVQGVR.G	1493.77619	1	5.57E-05	0.44	2.89	-	199.3
AHQ-4-3, 5351	K.AVAEQIPLLVQGVR.G	1493.77619	1	1.43E-04	0.25	2.07	-	232.9
AHQ-4-4, 5010 - 5014	K.AVAEQIPLLVQGVR.G	1493.77619	1	9.65E-05	0.39	2.80	-	304.1
AHQ-4-6, 4726 - 4728	K.AVAEQIPLLVQGVR.G	1493.77619	2	4.73E-06	0.89	3.82	-	620.6
AHQ-4-4, 3871	K.AVASAAAALVLK.A	1085.32216	2	4.60E-05	0.94	3.20	-	1454.0
AHQ-4-2, 3986 - 4063	K.AVASAAAALVLK.A	1085.32216	2	1.65E-05	0.96	4.20	-	1590.6
AHQ-4-2, 3882	K.AVASAAAALVLK.A	1085.32216	2	4.31E-06	0.95	4.11	-	1166.8
AHQ-4-1, 4013	K.AVASAAAALVLK.A	1085.32216	2	2.97E-06	0.96	3.72	-	2030.0
AHQ-4-2, 5216 - 5288	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.61E-05	0.51	2.99	-	636.8
AHQ-4-2, 4843	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.01E-07	0.88	3.68	-	1015.1
AHQ-4-2, 4739	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.45E-06	0.31	2.66	-	523.4
AHQ-4-1, 4185 - 4262	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.84E-07	0.93	4.03	-	1380.8
AHQ-4-2, 4354 - 4427	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.80E-06	0.93	4.04	-	1399.0
AHQ-4-8, 3702	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.45E-04	0.91	4.36	-	738.1
AHQ-4-4, 4268 - 4300	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.60E-04	0.92	4.27	-	1153.3
AHQ-4-1, 4357 - 4433	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.48E-06	0.89	3.56	-	1174.1
AHQ-4-2, 3888 - 3959	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.07E-07	0.95	4.24	-	1554.5
AHQ-4-1, 3887 - 3962	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	9.97E-08	0.86	3.79	-	796.8
AHQ-4-2, 4242 - 4319	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.05E-09	0.94	4.15	-	1442.4
AHQ-4-8, 3541	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.17E-04	0.41	2.66	-	143.0
AHQ-4-6, 7130 - 7132	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	4.51E-07	0.96	5.36	-	1578.2
AHQ-4-2, 4816 - 4898	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.62E-04	0.55	2.93	-	290.6
AHQ-4-4, 4844 - 4856	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	5.61E-06	0.74	3.40	-	439.6
AHQ-4-3, 6255 - 6263	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	4.86E-05	0.61	2.91	-	432.7
AHQ-4-3, 4891	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	3.25E-06	0.90	4.15	-	580.3
AHQ-4-6, 5995	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.53E-04	0.53	2.73	-	467.5
AHQ-4-1, 6161 - 6162	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	8.24E-07	0.80	3.62	-	435.6
AHQ-4-2, 5846	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	3.18E-06	0.85	4.04	-	466.4
AHQ-4-5, 6114	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	3.95E-05	0.85	3.53	-	566.4
AHQ-4-3, 6313 - 6383	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.08E-10	0.91	4.74	-	1017.9
AHQ-4-4, 6358	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.10E-08	0.96	5.40	-	1382.8
AHQ-4-5, 6153	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.72E-12	0.93	5.28	-	942.5
AHQ-4-1, 6234 - 6299	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.59E-12	0.94	4.88	-	1203.3
AHQ-4-4, 6272 - 6290	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.05E-14	0.77	3.61	-	733.5
AHQ-4-4, 5856 - 5926	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	2.48E-08	0.94	5.09	-	1110.8
AHQ-4-6, 6042 - 6111	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	3.86E-13	0.84	4.00	-	881.8
AHQ-4-2, 6312 - 6382	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	2.16E-11	0.93	4.62	-	1242.8
AHQ-4-5, 6234 - 6265	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	2.28E-09	0.89	4.40	-	849.0
AHQ-4-1, 5949	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	7.35E-06	0.70	3.49	-	639.7
AHQ-4-2, 2406	R.CVSCLPGQR.D	1079.23309	1	4.06E-07	0.17	2.13	-	107.1
AHQ-4-1, 3767	R.DDILNGSHPVSFDK.A	1544.64741	2	5.69E-04	0.75	2.70	-	800.7
AHQ-4-1, 3637 - 3655	R.DDILNGSHPVSFDK.A	1544.64741	2	9.46E-04	0.71	2.99	-	595.0
AHQ-4-10, 3380	R.DDILNGSHPVSFDK.A	1544.64741	2	1.03E-08	0.85	3.14	-	964.3
AHQ-4-7, 3238 - 3309	R.DDILNGSHPVSFDK.A	1544.64741	2	1.21E-06	0.92	3.74	-	982.7
AHQ-4-10, 3208	R.DDILNGSHPVSFDK.A	1544.64741	2	2.39E-07	0.88	3.58	-	754.6
AHQ-4-7, 3441 - 3509	R.DDILNGSHPVSFDK.A	1544.64741	2	5.82E-09	0.97	4.31	-	1873.8
AHQ-4-7, 3321	R.DDILNGSHPVSFDK.A	1544.64741	2	3.51E-07	0.92	3.75	-	935.2
AHQ-4-9, 3040	R.DDILNGSHPVSFDK.A	1544.64741	2	8.40E-08	0.94	3.90	-	1178.5
AHQ-4-7, 4741	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	4.68E-06	0.92	4.07	-	1037.0
AHQ-4-12, 4811	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	8.00E-07	0.96	5.27	-	1296.8
AHQ-4-4, 6446	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.31E-12	0.93	4.07	-	851.4
AHQ-4-10, 5399	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.23E-06	0.86	3.30	-	735.1
AHQ-4-5, 6051	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	1.79E-04	0.77	3.42	-	859.1

AHQ-4-2, 6394 - 6464	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.21E-05	0.90	4.09	-	754.5
AHQ-4-4, 6196	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.88E-08	0.89	4.04	-	765.2
AHQ-4-2, 5796 - 5862	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.87E-08	0.72	3.48	-	763.9
AHQ-4-2, 5442 - 5446	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.25E-05	0.76	3.19	-	643.1
AHQ-4-6, 5958	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.15E-10	0.94	4.74	-	879.5
AHQ-4-3, 6455 - 6456	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.53E-11	0.94	4.16	-	1137.8
AHQ-4-3, 6219 - 6287	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.49E-08	0.95	4.95	-	916.2
AHQ-4-1, 5466	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.16E-08	0.94	4.46	-	1021.8
AHQ-4-3, 5396 - 5467	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.63E-13	0.92	4.32	-	820.3
AHQ-4-3, 5771 - 5839	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.57E-05	0.65	3.42	-	558.2
AHQ-4-11, 5677	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.22E-06	0.94	4.20	-	1032.9
AHQ-4-2, 6234	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	1.71E-05	0.72	3.56	-	810.4
AHQ-4-2, 6232	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	8.74E-12	0.97	5.89	-	1152.4
AHQ-4-5, 6045 - 6057	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.64E-13	0.95	5.51	-	753.6
AHQ-4-1, 6177 - 6247	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.37E-09	0.96	5.35	-	1088.6
AHQ-4-5, 5269 - 5270	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.37E-10	0.97	5.07	-	1491.8
AHQ-4-3, 6365	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.61E-04	0.40	2.56	-	433.4
AHQ-4-5, 6311	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.44E-09	0.89	3.59	-	766.8
AHQ-4-7, 5926	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.41E-08	0.75	3.24	-	484.1
AHQ-4-4, 5410 - 5435	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.15E-04	0.90	3.48	-	1003.8
AHQ-4-2, 5470	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	4.48E-07	0.97	5.11	-	2178.9
AHQ-4-3, 5447 - 5483	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	6.23E-05	0.95	4.58	-	1094.3
AHQ-4-3, 5469	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.44E-07	0.95	4.35	-	1750.4
AHQ-4-11, 5017	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.23E-04	0.81	3.43	-	712.2
AHQ-4-2, 3544 - 3570	R.DPPSWSVLAGHSR.T	1409.53156	2	8.31E-11	0.92	3.33	-	688.9
AHQ-4-1, 3705	R.DPPSWSVLAGHSR.T	1409.53156	2	1.10E-07	0.90	3.37	-	587.2
AHQ-4-2, 3556	R.DPPSWSVLAGHSR.T	1409.53156	3	8.51E-08	0.86	3.65	-	796.0
AHQ-4-3, 3520	R.DPPSWSVLAGHSR.T	1409.53156	2	4.28E-09	0.85	3.11	-	549.7
AHQ-4-10, 4671	R.DPVQLNLLYVQAR.D	1529.76539	2	7.48E-07	0.97	5.12	-	1610.5
AHQ-4-4, 2344	K.EAAYHPEVAPDVR.L	1454.56910	2	1.21E-07	0.73	2.53	-	714.1
AHQ-4-4, 2358	K.EAAYHPEVAPDVR.L	1454.56910	1	1.63E-05	0.73	2.90	-	396.0
AHQ-4-2, 2383 - 2386	K.EAAYHPEVAPDVR.L	1454.56910	1	1.98E-06	0.68	2.50	-	523.0
AHQ-4-4, 6262 - 6332	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.05E-09	0.96	5.05	-	1357.5
AHQ-4-4, 6127 - 6194	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.09E-08	0.91	4.13	-	1218.5
AHQ-4-6, 5972 - 6047	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.08E-07	0.96	5.02	-	1577.8
AHQ-4-4, 5919 - 5922	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.11E-09	0.88	4.06	-	581.1
AHQ-4-5, 6159	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.08E-06	0.91	4.05	-	1275.8
AHQ-4-5, 6013 - 6085	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.33E-05	0.94	4.85	-	879.4
AHQ-4-2, 6654 - 6734	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.10E-08	0.92	4.40	-	968.3
AHQ-4-4, 6411 - 6463	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.79E-06	0.95	4.71	-	1223.0
AHQ-4-1, 6279	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.37E-05	0.79	3.29	-	951.4
AHQ-4-1, 6129 - 6209	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.77E-08	0.95	4.72	-	1318.6
AHQ-4-6, 5840 - 5907	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.20E-08	0.95	4.36	-	1497.6
AHQ-4-4, 6644	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.44E-05	0.63	3.24	-	571.0
AHQ-4-7, 5921	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.32E-05	0.83	3.76	-	725.2
AHQ-4-11, 5632	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.01E-06	0.96	5.35	-	1183.4
AHQ-4-3, 5964	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.08E-05	0.38	2.54	-	351.8
AHQ-4-2, 6391	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.55E-06	0.94	4.52	-	1187.1
AHQ-4-2, 6095 - 6175	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.37E-06	0.97	5.33	-	1476.5
AHQ-4-3, 6177 - 6196	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.89E-08	0.95	4.77	-	1168.6
AHQ-4-3, 6268 - 6335	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.72E-08	0.96	5.06	-	1527.8
AHQ-4-2, 6242 - 6311	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.07E-09	0.97	5.46	-	1483.0
AHQ-4-1, 5833 - 5903	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.31E-08	0.94	4.45	-	855.7
AHQ-4-2, 6484	K.EADESLNFEEQILEAAK.S	1937.05072	2	9.38E-08	0.95	4.73	-	1384.9
AHQ-4-1, 6113 - 6145	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.70E-07	0.95	4.96	-	1282.7
AHQ-4-10, 5325 - 5389	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.95E-06	0.86	3.80	-	915.7
AHQ-4-14-, 5722	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.74E-10	0.97	5.39	-	1602.6
AHQ-4-2, 7494	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	9.29E-05	0.93	4.93	-	1248.1
AHQ-4-4, 7442	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	2.73E-06	0.90	4.17	-	516.1
AHQ-4-3, 7501	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	2.85E-09	0.94	5.13	-	1077.0
AHQ-4-3, 7503	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	3.62E-04	0.78	3.55	-	495.7
AHQ-4-7, 7442	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	3.22E-06	0.84	3.68	-	930.8
AHQ-4-9, 6687 - 6691	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	5.13E-05	0.74	3.41	-	413.7
AHQ-4-3, 7388	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.45E-05	0.89	4.06	-	1133.2
AHQ-4-7, 7501	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	3.55E-06	0.95	5.23	-	1423.3
AHQ-4-6, 7288	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	3.92E-11	0.97	5.96	-	1600.0
AHQ-4-2, 7328 - 7395	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	3.44E-05	0.96	5.64	-	1265.5
AHQ-4-11, 6870	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.37E-09	0.96	5.95	-	1421.5
AHQ-4-2, 7430	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	5.79E-05	0.90	4.62	-	950.9
AHQ-4-5, 7455 - 7478	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	6.21E-10	0.98	7.27	-	1692.9
AHQ-4-4, 7506	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.19E-10	0.96	6.22	-	1384.3
AHQ-4-4, 7338	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	5.27E-06	0.93	4.86	-	955.0
AHQ-4-2, 7490 - 7556	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	4.80E-08	0.93	5.31	-	883.0
AHQ-4-5, 7297	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	4.48E-07	0.90	3.99	-	1248.9
AHQ-4-10, 6556 - 6572	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	7.19E-06	0.70	3.16	-	740.5
AHQ-4-3, 7567	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	2.21E-08	0.97	6.15	-	1542.1
AHQ-4-3, 7472 - 7544	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	8.31E-05	0.84	3.97	-	681.5
AHQ-4-4, 7411 - 7438	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	2.41E-04	0.87	4.41	-	644.2
AHQ-4-1, 7099 - 7169	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	8.98E-07	0.94	5.52	-	996.0
AHQ-4-2, 7266	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	2.88E-04	0.87	4.42	-	657.8
AHQ-4-4, 7186	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	1.05E-04	0.90	4.58	-	719.6
AHQ-4-2, 7142 - 7202	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	1.12E-06	0.75	4.71	-	420.8
AHQ-4-7, 2733	R.ELMEEKKEEITGTLR.K	1807.05950	2	1.72E-10	0.83	3.58	-	550.7
AHQ-4-12, 5563	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	8.78E-07	0.94	4.68	-	1218.7
AHQ-4-13-, 5481 - 5549	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	1.80E-11	0.97	6.30	-	1370.8
AHQ-4-7, 5422 - 5429	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	4.44E-10	0.98	6.55	-	2107.0
AHQ-4-13-, 5128	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	5.26E-06	0.98	6.46	-	2902.8
AHQ-4-13, 5218	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.77E-07	0.98	6.69	-	2484.2
AHQ-4-7, 4921 - 4989	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	8.30E-06	0.97	5.90	-	1478.5
AHQ-4-7, 4934	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	2	1.29E-04	0.73	2.93	-	372.5
AHQ-4-14-, 5077	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	8.06E-08	0.98	6.72	-	2381.1
AHQ-4-4, 2042 - 2270	K.EVANSTANLVK.T	1146.27608	1	4.67E-06	0.11	2.23	-	131.4
AHQ-4-4, 2143	K.EVANSTANLVK.T	1146.27608	1	8.68E-05	0.22	2.52	-	154.8
AHQ-4-4, 2262	K.EVANSTANLVK.T	1146.27608	2	6.76E-04	0.82	2.62	-	903.8
AHQ-4-2, 2308	K.EVANSTANLVK.T	1146.27608	2	6.30E-05	0.84	2.79	-	918.9
AHQ-4-3, 2113 - 2269	K.EVANSTANLVK.T	1146.27608	1	1.36E-07	0.17	2.25	-	151.9
AHQ-4-2, 2300	K.EVANSTANLVK.T	1146.27608	1	7.39E-05	0.24	2.02	-	218.8
AHQ-4-7, 4477	K.EVIQEWNLTNIK.R	1487.68214	1	8.62E-07	0.74	3.17	-	368.1
AHQ-4-12, 4677 - 4707	K.EVIQEWNLTNIK.R	1487.68214	2	9.61E-05	0.77	3.31	-	652.2
AHQ-4-13-, 4674 - 4736	K.EVIQEWNLTNIK.R	1487.68214	2	2.29E-06	0.69	2.68	-	784.0
AHQ-4-11, 4536 - 4538	K.EVIQEWNLTNIK.R	1487.68214	2	3.36E-06	0.91	3.88	-	1028.1
AHQ-4-7, 3797	K.EVIQEWNLTNIKR.W	1643.86849	2	1.89E-05	0.88	3.31	-	1015.6
AHQ-4-8, 2690 - 2691	K.FFYSDQNVDSR.D	1378.42795	2	1.23E-05	0.93	3.42	-	1075.1
AHQ-4-7, 2775	K.FFYSDQNVDSR.D	1378.42795	2	6.33E-07	0.90	3.22	-	962.8
AHQ-4-7, 5937 - 5993	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	8.33E-06	0.97	5.34	-	1917.3
AHQ-4-3, 6551 - 6565	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	6.50E-06	0.79	3.19	-	753.8
AHQ-4-2, 7640	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	3.53E-08	0.90	4.61	-	609.9

AHQ-4-1, 6443 - 6505	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	2.05E-05	0.57	2.71	-	505.9
AHQ-4-2, 6547 - 6623	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	8.84E-06	0.87	3.47	-	1058.6
AHQ-4-2, 6543 - 6612	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	1.31E-06	0.86	4.08	-	669.9
AHQ-4-2, 7372 - 7452	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	1.19E-05	0.90	4.00	-	695.2
AHQ-4-3, 6639	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	4.90E-07	0.71	3.67	-	396.5
AHQ-4-4, 6522 - 6599	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	2.65E-06	0.76	3.16	-	796.0
AHQ-4-3, 6555 - 6629	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	6.17E-06	0.83	4.23	-	591.4
AHQ-4-1, 2878	K.FLPSELRDEH	1243.35032	2	1.43E-05	0.61	2.73	-	277.6
AHQ-4-1, 5297 - 5298	K.GLAGAVSELLR.S	1086.26701	2	1.11E-06	0.97	4.92	-	1887.6
AHQ-4-5, 4919	K.GLAGAVSELLR.S	1086.26701	2	1.37E-05	0.98	5.33	-	2245.6
AHQ-4-4, 5154	K.GLAGAVSELLR.S	1086.26701	2	2.70E-07	0.97	4.87	-	1771.3
AHQ-4-7, 4757	K.GLAGAVSELLR.S	1086.26701	2	3.61E-06	0.98	5.02	-	2068.7
AHQ-4-2, 5230	K.GLAGAVSELLR.S	1086.26701	2	1.38E-06	0.97	4.87	-	1735.6
AHQ-4-8, 4501 - 4502	K.GLAGAVSELLR.S	1086.26701	2	6.20E-07	0.97	5.05	-	1847.6
AHQ-4-6, 4862 - 4867	K.GLAGAVSELLR.S	1086.26701	2	2.18E-06	0.98	5.31	-	1985.8
AHQ-4-5, 6661 - 6737	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.31E-06	0.89	4.40	-	459.4
AHQ-4-2, 6778 - 6842	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	7.99E-07	0.92	4.72	-	626.1
AHQ-4-2, 6839 - 6922	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	4.27E-06	0.93	5.13	-	1026.0
AHQ-4-2, 7195 - 7196	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.53E-07	0.89	4.39	-	753.9
AHQ-4-4, 6822 - 6870	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	5.47E-06	0.92	4.87	-	589.8
AHQ-4-5, 6618 - 6685	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.55E-05	0.73	3.67	-	455.5
AHQ-4-4, 6810 - 6874	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.26E-06	0.96	5.40	-	1719.3
AHQ-4-6, 6531 - 6598	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	7.23E-05	0.84	3.94	-	842.4
AHQ-4-1, 7041	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.28E-05	0.43	2.95	-	306.0
AHQ-4-2, 6991 - 7059	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	8.55E-06	0.85	4.51	-	643.8
AHQ-4-1, 6693 - 6753	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	4.36E-09	0.96	5.78	-	1330.2
AHQ-4-3, 6577	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	5.29E-04	0.85	3.91	-	531.5
AHQ-4-3, 7160	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.20E-05	0.83	3.71	-	536.0
AHQ-4-2, 7018 - 7019	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.12E-06	0.94	5.41	-	657.7
AHQ-4-3, 6837 - 6907	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.07E-08	0.91	4.83	-	634.8
AHQ-4-3, 6912 - 6987	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.89E-07	0.80	4.36	-	630.6
AHQ-4-5, 7513 - 7582	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	9.80E-13	0.96	6.06	-	1453.9
AHQ-4-2, 7514 - 7583	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	9.62E-11	0.97	6.38	-	1529.2
AHQ-4-1, 7277 - 7350	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.62E-09	0.97	5.89	-	1643.4
AHQ-4-9, 6787 - 6788	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	2.68E-12	0.96	5.29	-	1732.1
AHQ-4-7, 7533	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	6.05E-12	0.97	6.05	-	1788.7
AHQ-4-5, 7357	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	6.71E-11	0.98	7.53	-	2626.9
AHQ-4-4, 7308 - 7383	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	4.15E-11	0.98	6.85	-	1231.6
AHQ-4-2, 7443 - 7444	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	4.79E-12	0.98	7.11	-	2264.5
AHQ-4-10, 6439	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	1.58E-04	0.72	3.08	-	503.5
AHQ-4-3, 7444 - 7445	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	3.63E-12	0.98	6.77	-	2054.3
AHQ-4-4, 7386 - 7387	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.36E-06	0.98	7.23	-	2718.8
AHQ-4-6, 7178 - 7179	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	3.51E-12	0.97	6.84	-	704.4
AHQ-4-2, 7442	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	6.92E-12	0.97	6.19	-	1122.0
AHQ-4-7, 7441	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.25E-09	0.92	4.23	-	1000.9
AHQ-4-3, 5869	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.57E-08	0.92	4.80	-	785.6
AHQ-4-5, 7413 - 7419	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.33E-06	0.81	3.65	-	810.7
AHQ-4-4, 7446 - 7448	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.10E-09	0.95	5.06	-	1119.8
AHQ-4-2, 5868	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.83E-08	0.95	4.99	-	1005.7
AHQ-4-8, 7197	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	9.53E-04	0.94	4.83	-	1010.5
AHQ-4-4, 7447 - 7460	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.56E-06	0.94	5.21	-	678.8
AHQ-4-2, 5867	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.54E-07	0.95	5.38	-	1049.6
AHQ-4-2, 7499 - 7500	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	8.44E-11	0.97	5.64	-	1216.2
AHQ-4-2, 7498	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.32E-09	0.95	5.31	-	1143.3
AHQ-4-3, 7507	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	9.15E-05	0.95	5.20	-	821.7
AHQ-4-1, 7234	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	7.47E-07	0.94	4.99	-	966.7
AHQ-4-5, 7414 - 7415	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.64E-05	0.95	5.27	-	937.1
AHQ-4-8, 7203	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	8.35E-06	0.94	4.80	-	1069.4
AHQ-4-3, 7508	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.12E-09	0.94	4.94	-	1161.9
AHQ-4-7, 7439	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	8.14E-05	0.93	4.76	-	818.6
AHQ-4-4, 5819	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.23E-07	0.95	4.71	-	1036.7
AHQ-4-13, 7030	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	8.60E-04	0.74	3.55	-	534.1
AHQ-4-4, 5827	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.34E-09	0.93	4.56	-	1044.6
AHQ-4-14-, 6766 - 6771	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.57E-06	0.96	5.50	-	1284.2
AHQ-4-9, 6696	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.16E-06	0.87	4.13	-	539.4
AHQ-4-5, 5513	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	8.92E-09	0.92	4.35	-	805.1
AHQ-4-6, 7239 - 7242	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.78E-05	0.95	4.90	-	1280.6
AHQ-4-1, 7233	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	3.67E-07	0.89	3.77	-	1057.9
AHQ-4-6, 7238	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.59E-06	0.93	5.29	-	733.1
AHQ-4-7, 2571	K.IFQAHKNCGQMSEIEAK.V	1993.25380	2	7.84E-06	0.40	2.76	-	301.1
AHQ-4-13-, 3326 - 3340	R.IGITNHDEYSLVR.E	1517.66833	2	2.16E-11	0.96	4.26	-	1471.9
AHQ-4-7, 3239	R.IGITNHDEYSLVR.E	1517.66833	2	9.88E-07	0.83	3.24	-	858.4
AHQ-4-7, 2919 - 2943	R.IGITNHDEYSLVR.E	1517.66833	2	3.52E-08	0.94	3.74	-	1289.7
AHQ-4-13, 3821	R.IGITNHDEYSLVR.E	1517.66833	2	5.06E-05	0.87	2.88	-	963.7
AHQ-4-13-, 3685	R.IGITNHDEYSLVR.E	1517.66833	2	1.97E-06	0.86	2.96	-	780.7
AHQ-4-7, 3346 - 3421	R.IGITNHDEYSLVR.E	1517.66833	2	7.26E-04	0.95	3.61	-	1459.4
AHQ-4-10, 3040	R.IGITNHDEYSLVR.E	1517.66833	2	1.25E-10	0.94	3.77	-	1343.5
AHQ-4-11, 3140	R.IGITNHDEYSLVR.E	1517.66833	2	4.94E-08	0.95	3.92	-	1506.9
AHQ-4-2, 5190	R.ILAQATSDLVNAIK.A	1457.69748	1	6.73E-06	0.74	3.59	-	570.2
AHQ-4-3, 5177	R.ILAQATSDLVNAIK.A	1457.69748	1	9.48E-07	0.59	3.37	-	352.3
AHQ-4-3, 4229	R.ILAQATSDLVNAIK.A	1457.69748	1	6.95E-06	0.10	1.86	-	273.9
AHQ-4-3, 5155 - 5171	R.ILAQATSDLVNAIK.A	1457.69748	2	1.31E-07	0.97	5.00	-	1848.4
AHQ-4-4, 5119	R.ILAQATSDLVNAIK.A	1457.69748	1	2.00E-04	0.81	3.77	-	559.4
AHQ-4-5, 4947	R.ILAQATSDLVNAIK.A	1457.69748	1	8.13E-04	0.75	3.56	-	579.4
AHQ-4-7, 4794 - 4806	R.ILAQATSDLVNAIK.A	1457.69748	2	6.49E-09	0.98	4.79	-	2825.6
AHQ-4-2, 4226	R.ILAQATSDLVNAIK.A	1457.69748	2	7.00E-08	0.98	4.50	-	2168.1
AHQ-4-4, 4435 - 4446	R.ILAQATSDLVNAIK.A	1457.69748	2	1.41E-10	0.97	4.18	-	2246.7
AHQ-4-2, 5174 - 5176	R.ILAQATSDLVNAIK.A	1457.69748	2	1.60E-10	0.98	5.94	-	1862.3
AHQ-4-2, 4506	R.ILAQATSDLVNAIK.A	1457.69748	2	9.05E-10	0.97	4.58	-	1755.6
AHQ-4-3, 4495 - 4564	R.ILAQATSDLVNAIK.A	1457.69748	2	2.92E-04	0.96	4.42	-	1593.4
AHQ-4-5, 4909 - 4929	R.ILAQATSDLVNAIK.A	1457.69748	2	1.43E-08	0.98	4.96	-	2016.6
AHQ-4-4, 4180	R.ILAQATSDLVNAIK.A	1457.69748	1	2.93E-08	0.25	1.82	-	564.6
AHQ-4-4, 4152 - 4168	R.ILAQATSDLVNAIK.A	1457.69748	2	1.58E-09	0.97	4.68	-	2207.7
AHQ-4-6, 4838 - 4854	R.ILAQATSDLVNAIK.A	1457.69748	2	1.21E-09	0.98	5.27	-	2092.9
AHQ-4-2, 4704	R.ILAQATSDLVNAIK.A	1457.69748	2	1.82E-09	0.96	4.31	-	1407.9
AHQ-4-1, 4539	R.ILAQATSDLVNAIK.A	1457.69748	2	4.53E-07	0.89	3.51	-	1108.5
AHQ-4-1, 5194	R.ILAQATSDLVNAIK.A	1457.69748	2	1.91E-09	0.97	4.52	-	2022.2
AHQ-4-1, 4299 - 4306	R.ILAQATSDLVNAIK.A	1457.69748	2	1.27E-06	0.97	4.07	-	2423.3
AHQ-4-8, 4495	R.ILAQATSDLVNAIK.A	1457.69748	2	3.40E-08	0.96	4.61	-	1279.7
AHQ-4-7, 5929 - 5998	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.02E-04	0.96	5.09	-	1176.5
AHQ-4-13, 5912 - 5973	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	8.39E-06	0.97	5.61	-	1085.0
AHQ-4-14-, 5743 - 5749	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	2.03E-04	0.97	5.59	-	1181.6
AHQ-4-12, 5906 - 5985	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.02E-04	0.83	3.93	-	475.7
AHQ-4-8, 5741 - 5749	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	5.58E-05	0.96	5.10	-	1172.1
AHQ-4-10, 5377	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.28E-04	0.47	2.63	-	333.9
AHQ-4-13-, 5829 - 5864	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	8.17E-07	0.95	4.44	-	1180.4
AHQ-4-12, 5443 - 5509	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	9.23E-04	0.89	4.07	-	1112.7

AHQ-4-10, 4865 - 4939	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	9.40E-05	0.83	3.23	-	1064.7
AHQ-4-13, 5473 - 5540	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	4.18E-07	0.85	3.72	-	1120.8
AHQ-4-14-, 5317 - 5381	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.30E-08	0.91	3.72	-	1483.1
AHQ-4-7, 5265 - 5345	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	4.08E-13	0.95	4.70	-	1313.9
AHQ-4-13-, 5334 - 5382	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	7.69E-13	0.94	4.51	-	1380.0
AHQ-4-13, 2963	K.ISIGNVVK.T	830.00746	2	7.32E-04	0.78	2.58	-	516.2
AHQ-4-7, 1507 - 1522	K.KEEITGTLR.K	1047.18765	1	5.99E-04	0.17	1.98	-	269.3
AHQ-4-7, 2338 - 2341	R.KFFYSDQNVDSR.D	1506.60087	2	1.24E-04	0.94	4.27	-	924.3
AHQ-4-7, 5290 - 5363	R.KFFYSDQNVDSRDPVQLNLLYVQAR.D	3017.34366	3	1.34E-04	0.76	3.66	-	536.8
AHQ-4-14-, 2618	K.LAQAAQSSVATITR.L	1417.59344	2	7.16E-07	0.92	3.05	-	1269.6
AHQ-4-7, 2414 - 2466	K.LAQAAQSSVATITR.L	1417.59344	2	1.17E-06	0.97	4.82	-	1528.7
AHQ-4-11, 2589	K.LAQAAQSSVATITR.L	1417.59344	2	1.96E-09	0.96	4.03	-	1691.6
AHQ-4-10, 2509	K.LAQAAQSSVATITR.L	1417.59344	2	1.56E-04	0.80	2.77	-	902.7
AHQ-4-2, 2474	K.LAQAAQSSVATITR.L	1417.59344	2	1.89E-06	0.94	4.08	-	1113.7
AHQ-4-12, 2675	K.LAQAAQSSVATITR.L	1417.59344	2	1.81E-07	0.89	3.60	-	980.2
AHQ-4-5, 2469 - 2501	K.LAQAAQSSVATITR.L	1417.59344	2	9.26E-13	0.97	5.34	-	1514.2
AHQ-4-1, 2791 - 2870	K.LAQAAQSSVATITR.L	1417.59344	2	7.58E-08	0.96	4.74	-	1383.8
AHQ-4-5, 2331	K.LAQAAQSSVATITR.L	1417.59344	2	1.63E-11	0.96	4.10	-	1778.4
AHQ-4-4, 2450	K.LAQAAQSSVATITR.L	1417.59344	2	1.70E-07	0.94	4.18	-	1339.6
AHQ-4-6, 2323 - 2326	K.LAQAAQSSVATITR.L	1417.59344	2	5.10E-10	0.97	4.47	-	1710.6
AHQ-4-1, 2643	K.LAQAAQSSVATITR.L	1417.59344	2	7.89E-07	0.94	3.65	-	1602.2
AHQ-4-3, 2623 - 2625	K.LAQAAQSSVATITR.L	1417.59344	2	1.57E-10	0.98	5.27	-	1904.3
AHQ-4-2, 2631	K.LAQAAQSSVATITR.L	1417.59344	1	7.02E-05	0.50	3.07	-	194.6
AHQ-4-2, 2622 - 2690	K.LAQAAQSSVATITR.L	1417.59344	2	3.19E-11	0.98	5.24	-	1888.1
AHQ-4-6, 2474 - 2550	K.LAQAAQSSVATITR.L	1417.59344	2	6.23E-08	0.97	4.46	-	1619.0
AHQ-4-4, 2598	K.LAQAAQSSVATITR.L	1417.59344	2	1.32E-12	0.97	5.26	-	1584.7
AHQ-4-1, 3106	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.57E-07	0.67	3.25	-	858.5
AHQ-4-4, 3124 - 3130	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.54E-07	0.96	5.35	-	794.6
AHQ-4-1, 3345 - 3378	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	3.27E-05	0.94	5.03	-	1179.0
AHQ-4-4, 3123 - 3160	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.56E-04	0.95	4.96	-	1474.4
AHQ-4-2, 3150	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.26E-06	0.95	5.08	-	691.6
AHQ-4-5, 2894 - 2918	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.94E-09	0.98	6.13	-	2551.8
AHQ-4-6, 2890 - 2898	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.10E-06	0.95	4.96	-	810.9
AHQ-4-4, 3426	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.67E-06	0.87	4.30	-	512.7
AHQ-4-3, 3132 - 3133	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.02E-06	0.94	5.07	-	758.2
AHQ-4-2, 3142	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.03E-07	0.97	5.73	-	2198.5
AHQ-4-3, 2924	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.63E-06	0.94	4.49	-	845.8
AHQ-4-3, 3128	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	6.02E-10	0.97	6.04	-	1927.8
AHQ-4-6, 2887 - 2903	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	3.10E-08	0.98	6.67	-	2442.1
AHQ-4-12, 5370	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.73E-04	0.93	4.28	-	1017.7
AHQ-4-5, 5182 - 5209	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.20E-06	0.96	5.23	-	1009.5
AHQ-4-5, 5281	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.96E-09	0.91	4.21	-	829.4
AHQ-4-5, 5365 - 5366	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.31E-05	0.97	5.40	-	1236.6
AHQ-4-5, 5541	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.46E-07	0.97	5.25	-	1238.8
AHQ-4-4, 5742 - 5799	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.41E-10	0.95	5.12	-	892.6
AHQ-4-2, 5975 - 6026	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.76E-06	0.91	4.38	-	744.4
AHQ-4-4, 5658 - 5726	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.39E-10	0.96	4.84	-	1198.6
AHQ-4-7, 5267	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.09E-05	0.96	4.83	-	1186.8
AHQ-4-7, 5111	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.11E-06	0.80	3.76	-	546.5
AHQ-4-1, 5637	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	2.84E-08	0.96	4.79	-	1873.6
AHQ-4-4, 5518 - 5586	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.65E-07	0.96	4.87	-	1192.8
AHQ-4-2, 5790 - 5863	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.77E-13	0.96	5.25	-	1151.3
AHQ-4-4, 5340 - 5414	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.02E-05	0.81	3.83	-	544.6
AHQ-4-2, 5699 - 5726	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.41E-06	0.95	4.70	-	1004.9
AHQ-4-3, 5371 - 5419	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.85E-07	0.92	4.44	-	813.3
AHQ-4-2, 5558 - 5602	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.30E-08	0.95	4.69	-	1060.6
AHQ-4-1, 5798	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.55E-07	0.93	4.83	-	665.6
AHQ-4-11, 5142	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.03E-06	0.94	4.30	-	1064.8
AHQ-4-2, 5368 - 5438	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.84E-07	0.96	4.97	-	1227.1
AHQ-4-13-, 5268	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.50E-04	0.97	5.04	-	1413.1
AHQ-4-3, 5487 - 5568	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.47E-04	0.93	4.78	-	723.5
AHQ-4-13-, 5406	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.00E-04	0.18	2.65	-	267.4
AHQ-4-1, 5603 - 5669	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.38E-05	0.94	4.53	-	862.5
AHQ-4-6, 5120 - 5200	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.58E-13	0.96	4.97	-	1229.5
AHQ-4-6, 5291	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.25E-06	0.95	4.83	-	1117.0
AHQ-4-3, 5708 - 5785	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.45E-04	0.96	5.26	-	1015.3
AHQ-4-6, 5466	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.95E-08	0.95	4.47	-	1166.1
AHQ-4-1, 5479	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.01E-05	0.94	4.30	-	1149.8
AHQ-4-7, 3365 - 3434	K.LHTDDELNWLDHGR.T	1721.81153	3	1.09E-04	0.90	3.68	-	1045.6
AHQ-4-8, 3022	K.LHTDDELNWLDHGR.T	1721.81153	2	5.26E-06	0.95	4.12	-	1456.1
AHQ-4-9, 3088	K.LHTDDELNWLDHGR.T	1721.81153	2	2.61E-04	0.97	4.76	-	1794.3
AHQ-4-2, 4442 - 4460	K.LLAALLEDEGGSGR.P	1401.54764	2	3.72E-04	0.96	4.71	-	1069.4
AHQ-4-4, 4368	K.LLAALLEDEGGSGR.P	1401.54764	2	9.96E-05	0.93	4.00	-	1141.8
AHQ-4-5, 5051 - 5075	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.56E-10	0.98	7.11	-	1334.4
AHQ-4-10, 4643	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.50E-06	0.91	4.13	-	1140.2
AHQ-4-12, 5183	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.01E-05	0.94	4.97	-	844.0
AHQ-4-9, 4500 - 4504	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.97E-06	0.98	6.67	-	1618.4
AHQ-4-12, 5181	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.02E-10	0.94	4.75	-	1312.4
AHQ-4-3, 5352	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.70E-09	0.97	6.00	-	1261.3
AHQ-4-7, 4898 - 4899	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.31E-06	0.98	5.87	-	1902.9
AHQ-4-4, 5306 - 5307	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.79E-09	0.98	6.76	-	1248.4
AHQ-4-1, 5461	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.10E-08	0.97	5.78	-	1148.7
AHQ-4-6, 5022	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.20E-07	0.98	6.84	-	1486.9
AHQ-4-4, 5304	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	6.71E-08	0.96	5.17	-	1517.7
AHQ-4-6, 5014 - 5031	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.48E-09	0.95	5.32	-	1183.2
AHQ-4-5, 5050	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.33E-07	0.97	5.46	-	1841.3
AHQ-4-10, 4635	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.24E-09	0.96	5.13	-	1183.2
AHQ-4-3, 5356 - 5363	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.36E-09	0.96	5.35	-	1475.1
AHQ-4-2, 5355 - 5378	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.72E-06	0.98	6.82	-	1347.3
AHQ-4-1, 5458 - 5478	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.02E-08	0.94	4.98	-	1308.4
AHQ-4-2, 5356 - 5363	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.48E-07	0.97	5.31	-	1992.9
AHQ-4-8, 4505	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.18E-07	0.97	5.81	-	1365.1
AHQ-4-11, 4946	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.33E-08	0.95	4.88	-	1635.6
AHQ-4-7, 4893	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.81E-04	0.83	3.22	-	1076.8
AHQ-4-3, 5360	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	1.18E-04	0.81	4.30	-	650.9
AHQ-4-8, 4509	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	7.84E-04	0.88	4.66	-	997.1
AHQ-4-10, 4641	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	1.94E-04	0.61	3.89	-	578.9
AHQ-4-5, 4087 - 4157	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	7.82E-08	0.78	3.62	-	292.4
AHQ-4-5, 3950 - 4017	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.77E-04	0.83	3.87	-	359.4
AHQ-4-2, 4270 - 4339	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.58E-10	0.92	4.51	-	446.1
AHQ-4-7, 3917 - 3933	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.17E-05	0.44	2.90	-	223.7
AHQ-4-5, 4225	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	5.91E-06	0.63	3.14	-	222.8
AHQ-4-1, 4213 - 4281	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.11E-05	0.82	3.59	-	380.2
AHQ-4-3, 4383 - 4451	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	7.22E-07	0.80	3.67	-	281.8
AHQ-4-5, 4070 - 4085	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.56E-11	0.93	4.57	-	452.2
AHQ-4-2, 4139 - 4211	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.69E-05	0.77	3.28	-	240.8
AHQ-4-2, 4410 - 4484	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.09E-08	0.92	4.79	-	395.3

AHQ-4-4, 4254 - 4335	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	5.40E-07	0.85	3.83	-	330.5
AHQ-4-4, 4194 - 4262	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.26E-05	0.80	3.38	-	355.4
AHQ-4-4, 4108 - 4178	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.40E-04	0.82	3.57	-	347.7
AHQ-4-1, 4273 - 4349	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	8.54E-09	0.90	4.24	-	396.8
AHQ-4-3, 5988 - 6055	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.85E-12	0.97	5.64	-	1616.1
AHQ-4-3, 5657	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.29E-04	0.95	4.71	-	1444.1
AHQ-4-2, 4534 - 4550	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.53E-06	0.86	3.47	-	848.9
AHQ-4-4, 5428 - 5432	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.74E-08	0.97	5.84	-	1280.0
AHQ-4-1, 5941 - 5986	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.85E-10	0.96	5.32	-	1307.6
AHQ-4-2, 5818 - 5822	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.40E-13	0.98	5.53	-	1935.7
AHQ-4-1, 5630	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.05E-04	0.71	3.55	-	471.8
AHQ-4-2, 5904 - 5919	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.49E-05	0.94	4.62	-	1098.4
AHQ-4-4, 5571 - 5624	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.28E-07	0.97	5.13	-	1540.2
AHQ-4-4, 5639 - 5646	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	3.26E-08	0.97	5.99	-	1624.5
AHQ-4-7, 5321	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.41E-09	0.97	5.32	-	1800.3
AHQ-4-3, 5569 - 5649	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.10E-10	0.97	5.60	-	1496.9
AHQ-4-2, 6047	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.95E-11	0.94	4.18	-	1013.0
AHQ-4-10, 4900	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.63E-04	0.92	4.20	-	948.0
AHQ-4-3, 5667	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.74E-12	0.97	5.30	-	1587.1
AHQ-4-3, 5795	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.61E-13	0.98	5.76	-	1654.9
AHQ-4-5, 5873 - 5897	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.27E-14	0.98	6.16	-	1622.2
AHQ-4-5, 5782	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.38E-14	0.97	5.03	-	1751.4
AHQ-4-4, 5858	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.14E-10	0.97	5.34	-	1257.9
AHQ-4-12, 5435	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.39E-08	0.98	5.60	-	2198.1
AHQ-4-1, 6077	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.55E-15	0.97	5.91	-	1597.4
AHQ-4-1, 5743 - 5819	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.84E-09	0.98	5.44	-	1870.6
AHQ-4-2, 5650 - 5720	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	8.64E-04	0.98	6.23	-	1841.0
AHQ-4-4, 5991	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.18E-05	0.89	3.80	-	710.1
AHQ-4-6, 5366	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.17E-09	0.98	5.15	-	2281.8
AHQ-4-1, 5750	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.32E-06	0.96	5.60	-	1245.2
AHQ-4-2, 4574	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.77E-08	0.95	4.58	-	1614.4
AHQ-4-3, 5895	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.16E-12	0.97	5.03	-	1363.6
AHQ-4-14-, 5342	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.85E-09	0.93	4.15	-	1122.8
AHQ-4-6, 5703 - 5770	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.42E-07	0.93	4.41	-	846.4
AHQ-4-1, 4555	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.58E-09	0.93	4.04	-	880.6
AHQ-4-5, 4342	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.52E-08	0.94	4.87	-	874.8
AHQ-4-2, 5643 - 5722	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.81E-12	0.98	5.98	-	1561.8
AHQ-4-2, 5458	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.58E-08	0.97	5.25	-	1532.3
AHQ-4-6, 4263	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.72E-05	0.84	3.54	-	585.8
AHQ-4-11, 5200	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.01E-06	0.89	4.35	-	668.1
AHQ-4-3, 5459	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.03E-09	0.97	5.70	-	1486.1
AHQ-4-4, 4492	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.94E-09	0.96	5.31	-	985.4
AHQ-4-8, 5010	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.06E-08	0.98	5.32	-	2270.8
AHQ-4-9, 4832	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.38E-07	0.95	4.64	-	1185.4
AHQ-4-13, 5518	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.59E-04	0.93	3.77	-	1285.0
AHQ-4-5, 1661	R.MATNAAAQNAIK.K	1204.38227	2	9.89E-04	0.80	3.46	-	770.3
AHQ-4-2, 1823 - 1890	R.MATNAAAQNAIK.K	1204.38227	2	3.38E-04	0.66	2.92	-	655.2
AHQ-4-6, 4040	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	8.83E-07	0.92	4.36	-	1052.4
AHQ-4-8, 3757	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	9.42E-09	0.95	4.98	-	1171.7
AHQ-4-4, 4267 - 4343	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	8.72E-08	0.94	5.02	-	1204.5
AHQ-4-4, 4007 - 4068	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.22E-09	0.87	4.31	-	732.6
AHQ-4-2, 4375	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	4.75E-04	0.81	3.02	-	647.9
AHQ-4-2, 4367	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.16E-05	0.69	3.42	-	557.7
AHQ-4-2, 4454 - 4455	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.47E-07	0.97	5.88	-	1503.0
AHQ-4-2, 4466	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	4.81E-08	0.68	3.09	-	552.1
AHQ-4-1, 4510 - 4511	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.07E-09	0.93	4.75	-	1006.4
AHQ-4-1, 4229	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.78E-11	0.95	5.29	-	1208.0
AHQ-4-2, 4552 - 4576	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	3.01E-08	0.89	4.00	-	1042.0
AHQ-4-5, 3858	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.56E-07	0.92	4.22	-	1097.6
AHQ-4-8, 3621	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	4.49E-11	0.91	4.53	-	946.1
AHQ-4-10, 3872	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	2.04E-05	0.61	2.55	-	518.4
AHQ-4-2, 6846	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	8.18E-05	0.98	5.44	-	1869.8
AHQ-4-7, 6557	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	5.28E-04	0.94	4.17	-	1267.5
AHQ-4-7, 6917	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	3.50E-04	0.95	4.13	-	1393.6
AHQ-4-2, 6502	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	1.36E-11	0.97	5.10	-	1593.9
AHQ-4-4, 6799 - 6814	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	6.94E-05	0.97	5.12	-	1676.6
AHQ-4-2, 6183	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	3.10E-06	0.98	5.82	-	1621.0
AHQ-4-3, 6429	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	5.67E-04	0.63	2.88	-	558.7
AHQ-4-2, 7143	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.89E-07	0.97	5.09	-	1669.4
AHQ-4-3, 6793 - 6835	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.63E-04	0.97	5.60	-	1842.5
AHQ-4-4, 6148	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	9.75E-05	0.94	4.22	-	1205.8
AHQ-4-2, 7259	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	3.10E-06	0.96	5.18	-	1263.6
AHQ-4-14-, 6281	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.02E-04	0.98	5.68	-	1994.5
AHQ-4-3, 7121	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.19E-06	0.98	5.90	-	1760.0
AHQ-4-5, 6958 - 6965	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.32E-09	0.98	5.75	-	1709.6
AHQ-4-1, 6210 - 6275	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.26E-09	0.97	5.71	-	1469.0
AHQ-4-8, 6575	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.47E-08	0.97	5.27	-	1490.5
AHQ-4-1, 6750 - 6765	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.97E-04	0.95	4.46	-	1290.9
AHQ-4-14-, 5695 - 5701	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	2.36E-07	0.92	4.03	-	877.0
AHQ-4-4, 7091 - 7110	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.04E-13	0.98	5.63	-	2344.7
AHQ-4-4, 6502	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	2.54E-07	0.96	4.78	-	1273.2
AHQ-4-6, 6830	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.53E-13	0.98	5.44	-	1736.1
AHQ-4-10, 6153	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	1.26E-05	0.97	5.16	-	1352.0
AHQ-4-7, 2126	K.NCGQMSEIEAK.V	1268.40005	1	3.44E-06	0.49	3.21	-	279.8
AHQ-4-5, 4643	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.57E-09	0.93	4.25	-	600.0
AHQ-4-6, 4527	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.05E-07	0.79	3.11	-	449.5
AHQ-4-1, 4725	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.16E-04	0.82	3.59	-	494.1
AHQ-4-2, 4538	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.30E-04	0.67	3.02	-	371.4
AHQ-4-3, 4767	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.43E-09	0.88	3.48	-	694.4
AHQ-4-3, 4656	K.NGNLPEFGDAISTASK.A	1621.73018	2	8.60E-06	0.78	2.93	-	479.6
AHQ-4-2, 4778 - 4800	K.NGNLPEFGDAISTASK.A	1621.73018	2	7.05E-07	0.81	3.75	-	436.4
AHQ-4-4, 4070 - 4076	K.NLGTALAELR.T	1058.21367	2	2.30E-04	0.91	3.47	-	1097.8
AHQ-4-2, 4146 - 4191	K.NLGTALAELR.T	1058.21367	2	2.33E-05	0.90	3.62	-	840.6
AHQ-4-6, 3794 - 3795	K.NLGTALAELR.T	1058.21367	2	1.88E-05	0.89	3.20	-	915.8
AHQ-4-5, 3822	K.NLGTALAELR.T	1058.21367	2	1.38E-06	0.90	3.62	-	936.1
AHQ-4-3, 4109 - 4128	K.NLGTALAELR.T	1058.21367	2	7.73E-05	0.88	3.24	-	865.8
AHQ-4-6, 2431	K.PAAVAAENEEIGSHIK.H	1636.78798	2	2.17E-06	0.96	4.63	-	1438.7
AHQ-4-4, 2582 - 2583	K.PAAVAAENEEIGSHIK.H	1636.78798	2	6.01E-05	0.98	5.97	-	1898.5
AHQ-4-3, 2603 - 2609	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.16E-11	0.98	5.48	-	2325.3
AHQ-4-5, 2431 - 2434	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.22E-13	0.98	5.85	-	1810.7
AHQ-4-6, 2430	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.01E-10	0.97	5.99	-	1735.7
AHQ-4-5, 2429	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.25E-12	0.97	5.79	-	1848.3
AHQ-4-1, 2837	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.42E-07	0.98	5.18	-	1772.0
AHQ-4-1, 2830	K.PAAVAAENEEIGSHIK.H	1636.78798	3	7.91E-07	0.97	5.16	-	1814.8
AHQ-4-2, 2611	K.PAAVAAENEEIGSHIK.H	1636.78798	2	3.84E-11	0.98	5.53	-	2037.1
AHQ-4-3, 2608	K.PAAVAAENEEIGSHIK.H	1636.78798	3	3.74E-08	0.97	5.81	-	2122.8
AHQ-4-2, 2612	K.PAAVAAENEEIGSHIK.H	1636.78798	3	5.86E-10	0.97	5.45	-	1698.8

AHQ-4-3, 3195	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	7.95E-07	0.91	4.49	-	668.9
AHQ-4-3, 3388 - 3391	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.45E-10	0.89	4.62	-	599.5
AHQ-4-5, 3133	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.34E-05	0.90	4.14	-	792.6
AHQ-4-4, 3366	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.06E-07	0.88	4.64	-	463.4
AHQ-4-6, 2926	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	2.44E-05	0.79	3.46	-	638.9
AHQ-4-2, 3423	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.84E-07	0.85	4.19	-	432.4
AHQ-4-5, 2942	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	4.08E-05	0.85	4.03	-	530.4
AHQ-4-3, 3197	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	1.19E-05	0.82	3.39	-	847.8
AHQ-4-1, 3381	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	4.53E-06	0.82	3.47	-	752.7
AHQ-4-4, 3175	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	3.10E-04	0.78	3.56	-	492.4
AHQ-4-2, 3210	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.94E-05	0.86	3.76	-	628.0
AHQ-4-6, 3782	R.QELAVFCSPEPPAK.T	1574.77985	2	2.07E-06	0.78	3.39	-	725.8
AHQ-4-1, 4154 - 4158	R.QELAVFCSPEPPAK.T	1574.77985	2	1.20E-05	0.85	3.04	-	849.7
AHQ-4-3, 4047 - 4051	R.QELAVFCSPEPPAK.T	1574.77985	2	2.82E-09	0.88	3.60	-	891.5
AHQ-4-2, 4070	R.QELAVFCSPEPPAK.T	1574.77985	2	1.54E-06	0.93	3.62	-	1060.7
AHQ-4-5, 3869	R.QELAVFCSPEPPAK.T	1574.77985	2	1.14E-07	0.96	4.13	-	1424.9
AHQ-4-4, 7406 - 7486	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	1.32E-09	0.94	5.42	-	1005.6
AHQ-4-5, 7367 - 7405	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	1.97E-11	0.95	5.60	-	835.6
AHQ-4-4, 7426 - 7471	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	1.78E-11	0.96	6.24	-	865.5
AHQ-4-3, 3768 - 3801	K.QVAASTAQLLVACK.V	1461.70942	2	3.32E-06	0.85	3.37	-	501.8
AHQ-4-1, 3933 - 3934	K.QVAASTAQLLVACK.V	1461.70942	2	9.69E-07	0.89	3.78	-	544.9
AHQ-4-13-, 3764 - 3841	K.QVAASTAQLLVACK.V	1461.70942	2	5.31E-04	0.80	3.34	-	685.7
AHQ-4-2, 3839	K.QVAASTAQLLVACK.V	1461.70942	2	1.76E-04	0.93	3.86	-	715.9
AHQ-4-4, 5916	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	7.28E-05	0.98	5.52	-	1877.0
AHQ-4-5, 5606	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	5.04E-05	0.96	4.71	-	1232.5
AHQ-4-2, 5982 - 5987	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	4.95E-07	0.98	5.66	-	2275.0
AHQ-4-3, 5965 - 5972	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	1.05E-05	0.98	6.42	-	2205.1
AHQ-4-1, 3125	K.SIAAATSALVK.A	1032.21612	2	5.32E-05	0.91	3.33	-	969.7
AHQ-4-4, 2886	K.SIAAATSALVK.A	1032.21612	2	1.43E-04	0.85	3.12	-	800.4
AHQ-4-3, 2908	K.SIAAATSALVK.A	1032.21612	2	3.24E-04	0.84	3.33	-	733.2
AHQ-4-5, 2595 - 2665	K.SIAAATSALVK.A	1032.21612	2	1.96E-04	0.95	3.96	-	1165.1
AHQ-4-7, 4089	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	1.17E-07	0.86	3.93	-	663.4
AHQ-4-7, 3614 - 3649	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	1.33E-07	0.96	5.16	-	1572.6
AHQ-4-7, 3994 - 4073	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	4.21E-11	0.96	5.13	-	1809.5
AHQ-4-3, 5317 - 5387	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.56E-08	0.91	4.22	-	600.3
AHQ-4-1, 4738	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.06E-09	0.83	3.69	-	538.9
AHQ-4-4, 5566	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.34E-06	0.89	3.77	-	594.8
AHQ-4-7, 5067	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.56E-07	0.83	3.62	-	497.3
AHQ-4-2, 4762	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.03E-07	0.87	3.97	-	463.8
AHQ-4-4, 5478 - 5498	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.20E-06	0.90	4.25	-	511.9
AHQ-4-2, 5298 - 5338	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.41E-07	0.56	3.48	-	243.7
AHQ-4-6, 5244	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.10E-07	0.56	3.11	-	353.9
AHQ-4-1, 5330 - 5393	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.66E-05	0.77	3.44	-	392.7
AHQ-4-1, 5693	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.88E-07	0.78	3.58	-	352.7
AHQ-4-2, 5184	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.28E-09	0.74	3.21	-	399.1
AHQ-4-2, 4984	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.61E-07	0.91	4.46	-	564.3
AHQ-4-6, 5052 - 5075	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.31E-06	0.91	4.47	-	512.9
AHQ-4-4, 5280 - 5362	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.06E-05	0.89	3.84	-	631.1
AHQ-4-4, 5120	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.85E-06	0.83	3.60	-	550.7
AHQ-4-1, 5555 - 5625	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.59E-06	0.91	4.39	-	469.7
AHQ-4-3, 4743	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.34E-09	0.72	3.28	-	408.2
AHQ-4-4, 4932	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.77E-08	0.87	3.68	-	560.1
AHQ-4-3, 5516 - 5597	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.88E-06	0.93	4.63	-	683.4
AHQ-4-5, 4567	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.99E-06	0.88	4.02	-	498.1
AHQ-4-2, 5607 - 5611	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.11E-06	0.90	4.34	-	414.8
AHQ-4-2, 5382 - 5451	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.90E-09	0.86	4.09	-	407.2
AHQ-4-5, 5443 - 5471	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.05E-09	0.92	4.53	-	638.9
AHQ-4-3, 5415	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.30E-04	0.87	3.90	-	459.9
AHQ-4-2, 5471 - 5538	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.84E-08	0.85	3.86	-	378.2
AHQ-4-9, 4589	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.31E-07	0.62	3.12	-	333.0
AHQ-4-5, 5330 - 5338	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.10E-11	0.89	4.52	-	441.7
AHQ-4-3, 5189	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.91E-04	0.81	3.63	-	605.8
AHQ-4-12, 5163	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.23E-07	0.43	2.85	-	198.6
AHQ-4-6, 4475	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.43E-11	0.89	3.81	-	668.7
AHQ-4-4, 4710	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.52E-07	0.81	3.59	-	436.8
AHQ-4-5, 5142 - 5167	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.96E-07	0.92	4.42	-	596.9
AHQ-4-3, 7427	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	3.89E-15	0.98	6.90	-	2091.5
AHQ-4-5, 7341	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	8.04E-12	0.97	6.24	-	1499.7
AHQ-4-13, 6821 - 6893	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	9.96E-05	0.94	4.75	-	1647.3
AHQ-4-2, 7424	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	5.55E-16	0.98	6.97	-	1769.2
AHQ-4-1, 4571	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.03E-04	0.88	3.33	-	1233.1
AHQ-4-7, 3895	K.TKEVIQEWNLTNIK.R	1716.95938	3	3.66E-04	0.96	4.38	-	2079.4
AHQ-4-8, 3715	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.27E-05	0.95	4.42	-	1396.9
AHQ-4-13, 4306 - 4381	K.TKEVIQEWNLTNIK.R	1716.95938	2	9.53E-05	0.94	3.90	-	1471.6
AHQ-4-12, 4209 - 4223	K.TKEVIQEWNLTNIK.R	1716.95938	2	4.07E-06	0.95	4.26	-	1545.9
AHQ-4-9, 3604	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.68E-06	0.94	4.38	-	1441.2
AHQ-4-2, 6686 - 6759	K.TLAESALQLLYTAK.E	1522.76793	2	2.70E-06	0.92	4.04	-	920.1
AHQ-4-2, 6872	K.TLAESALQLLYTAK.E	1522.76793	2	1.05E-06	0.95	3.85	-	1197.8
AHQ-4-1, 6585 - 6602	K.TLAESALQLLYTAK.E	1522.76793	2	1.57E-10	0.96	4.62	-	1115.7
AHQ-4-4, 6591 - 6659	K.TLAESALQLLYTAK.E	1522.76793	2	4.26E-07	0.95	4.57	-	1128.0
AHQ-4-11, 6046	K.TLAESALQLLYTAK.E	1522.76793	2	3.69E-05	0.96	4.55	-	1082.0
AHQ-4-14-, 6146 - 6149	K.TLAESALQLLYTAK.E	1522.76793	2	4.49E-04	0.89	3.02	-	925.8
AHQ-4-3, 6604 - 6671	K.TLAESALQLLYTAK.E	1522.76793	2	1.71E-08	0.96	4.70	-	1169.8
AHQ-4-13, 6366	K.TLAESALQLLYTAK.E	1522.76793	2	7.78E-07	0.95	3.69	-	1369.0
AHQ-4-1, 6786	K.TLAESALQLLYTAK.E	1522.76793	2	7.67E-07	0.88	3.46	-	790.4
AHQ-4-4, 3128	K.TLSHPQQMALLDQTK.T	1711.96464	3	5.78E-05	0.92	4.40	-	1064.0
AHQ-4-1, 3354	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.34E-05	0.95	4.68	-	833.0
AHQ-4-2, 3146	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.91E-04	0.94	4.94	-	604.8
AHQ-4-2, 3152	K.TLSHPQQMALLDQTK.T	1711.96464	3	7.40E-04	0.86	4.16	-	901.7
AHQ-4-6, 2882	K.TLSHPQQMALLDQTK.T	1711.96464	2	5.14E-04	0.93	4.23	-	686.9
AHQ-4-1, 3371	K.TLSHPQQMALLDQTK.T	1711.96464	3	1.64E-04	0.91	4.21	-	1196.1
AHQ-4-2, 2431 - 2446	K.TLSHPQQM*ALLDQTK.T	1727.96404	3	5.61E-04	0.90	4.41	-	893.8
AHQ-4-1, 2589	K.TLSHPQQM*ALLDQTK.T	1727.96404	2	1.92E-04	0.84	3.43	-	482.7
AHQ-4-4, 3114 - 3142	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.06E-04	0.91	4.14	-	644.6
AHQ-4-9, 2647 - 2649	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.29E-04	0.94	4.49	-	724.2
AHQ-4-3, 2416	K.TLSHPQQM*ALLDQTK.T	1727.96404	3	2.63E-04	0.88	4.02	-	860.2
AHQ-4-3, 4345 - 4415	K.TMLESAGGLIQTAR.A	1448.67095	2	1.01E-06	0.94	4.10	-	1777.4
AHQ-4-1, 4391 - 4459	K.TMLESAGGLIQTAR.A	1448.67095	2	9.81E-05	0.92	3.54	-	1471.7
AHQ-4-2, 3490 - 3512	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.74E-08	0.97	5.13	-	1430.4
AHQ-4-6, 4038	K.TMLESAGGLIQTAR.A	1448.67095	2	8.68E-06	0.90	3.70	-	1109.6
AHQ-4-3, 4375	K.TMLESAGGLIQTAR.A	1448.67095	1	7.85E-04	0.24	2.44	-	220.9
AHQ-4-5, 4117	K.TMLESAGGLIQTAR.A	1448.67095	2	4.03E-07	0.93	4.08	-	1254.7
AHQ-4-3, 3475 - 3504	K.TM*LESAGGLIQTAR.A	1464.67035	2	3.61E-07	0.93	4.55	-	930.3
AHQ-4-2, 4327 - 4406	K.TMLESAGGLIQTAR.A	1448.67095	2	9.42E-05	0.77	2.91	-	909.7
AHQ-4-4, 4310	K.TMLESAGGLIQTAR.A	1448.67095	2	1.82E-05	0.87	3.06	-	1389.9
AHQ-4-1, 3603	K.TM*LESAGGLIQTAR.A	1464.67035	2	2.19E-05	0.96	4.15	-	1714.2
AHQ-4-7, 3859 - 3863	K.TMQFEPSTM*VYDACR.I	1854.07511	2	5.44E-07	0.93	4.34	-	514.3

AHQ-4-13-, 4786	K.TMQFEPSTMVYDACR.I	1838.07571	2	9.26E-07	0.93	4.37	-	623.2
AHQ-4-7, 4113	K.TM*QFEPSTMVYDACR.I	1854.07511	2	1.64E-04	0.88	3.82	-	565.9
AHQ-4-13-, 4233	K.TM*QFEPSTMVYDACR.I	1854.07511	2	3.42E-04	0.90	3.95	-	592.2
AHQ-4-13, 4897	K.TMQFEPSTMVYDACR.I	1838.07571	2	1.13E-06	0.88	3.97	-	437.7
AHQ-4-13, 4368	K.TM*QFEPSTMVYDACR.I	1854.07511	2	3.37E-04	0.90	3.94	-	703.0
AHQ-4-7, 4651 - 4675	K.TMQFEPSTMVYDACR.I	1838.07571	2	1.17E-05	0.96	5.50	-	650.6
AHQ-4-13-, 3662 - 3729	K.TVTDM*LM*TICAR.I	1445.70887	2	1.98E-06	0.86	3.52	-	649.7
AHQ-4-13, 3816 - 3885	K.TVTDM*LM*TICAR.I	1445.70887	2	5.87E-04	0.91	3.50	-	852.6
AHQ-4-12, 5239 - 5241	K.TYGVSFFLVK.E	1161.37395	2	9.43E-07	0.79	3.41	-	458.7
AHQ-4-7, 4945	K.TYGVSFFLVK.E	1161.37395	2	7.11E-06	0.85	3.33	-	603.2
AHQ-4-6, 6234 - 6259	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.26E-07	0.96	4.91	-	1404.6
AHQ-4-2, 6454 - 6522	R.VAGSVTELIQAAEAMK.G	1618.87752	2	4.71E-09	0.97	5.36	-	1460.9
AHQ-4-5, 6318	R.VAGSVTELIQAAEAMK.G	1618.87752	2	7.68E-08	0.97	4.51	-	2026.5
AHQ-4-4, 6510 - 6519	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.18E-06	0.97	5.65	-	1491.0
AHQ-4-9, 5644	R.VAGSVTELIQAAEAMK.G	1618.87752	2	8.41E-07	0.88	3.46	-	1032.4
AHQ-4-3, 5428	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	8.73E-07	0.92	3.85	-	1145.7
AHQ-4-10, 5672	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.82E-09	0.93	3.94	-	1092.6
AHQ-4-3, 6527 - 6528	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.08E-09	0.98	6.02	-	1543.9
AHQ-4-4, 5390 - 5444	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	7.99E-06	0.91	4.14	-	1088.5
AHQ-4-1, 6509	R.VAGSVTELIQAAEAMK.G	1618.87752	2	5.37E-09	0.94	4.02	-	1212.4
AHQ-4-1, 5513 - 5542	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	4.90E-04	0.75	2.70	-	735.1
AHQ-4-2, 5424 - 5495	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	2.91E-04	0.87	3.69	-	837.9
AHQ-4-3, 6271 - 6340	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.06E-06	0.56	3.39	-	356.5
AHQ-4-3, 6135 - 6203	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.01E-11	0.94	4.91	-	793.7
AHQ-4-3, 5992 - 6065	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.39E-11	0.96	5.49	-	765.2
AHQ-4-6, 5999 - 6007	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.78E-12	0.96	4.83	-	1034.8
AHQ-4-6, 5776 - 5858	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.75E-10	0.93	4.84	-	456.9
AHQ-4-10, 5407	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.06E-08	0.94	4.25	-	878.0
AHQ-4-6, 5619	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.50E-06	0.95	4.43	-	1089.1
AHQ-4-3, 5865 - 5923	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.71E-05	0.90	4.23	-	687.4
AHQ-4-11, 5540 - 5604	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.91E-09	0.92	4.80	-	520.5
AHQ-4-2, 5760	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.02E-06	0.93	4.85	-	638.2
AHQ-4-14-, 5671	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.38E-14	0.98	5.52	-	1731.1
AHQ-4-1, 6081 - 6149	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.37E-06	0.93	4.68	-	759.3
AHQ-4-2, 5859 - 5926	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.24E-09	0.91	4.39	-	622.6
AHQ-4-2, 5946 - 6019	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.18E-09	0.95	5.02	-	1000.7
AHQ-4-4, 5688 - 5708	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.19E-04	0.90	4.45	-	542.2
AHQ-4-2, 6084 - 6150	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.39E-09	0.90	3.81	-	867.4
AHQ-4-4, 5822 - 5890	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.98E-07	0.96	5.22	-	1015.9
AHQ-4-5, 6106 - 6125	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.75E-10	0.96	4.67	-	1182.9
AHQ-4-9, 5437	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.35E-04	0.61	3.16	-	449.3
AHQ-4-5, 5905 - 5906	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.66E-08	0.92	4.30	-	750.1
AHQ-4-5, 5682 - 5739	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.27E-07	0.96	4.82	-	1191.6
AHQ-4-4, 5988 - 6060	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.13E-07	0.92	4.64	-	537.3
AHQ-4-4, 6082 - 6150	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.41E-09	0.95	5.01	-	930.6
AHQ-4-10, 5228 - 5287	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.18E-10	0.94	4.71	-	730.5
AHQ-4-7, 5810 - 5825	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.19E-08	0.93	4.80	-	552.6
AHQ-4-12, 5793 - 5795	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.76E-04	0.55	3.54	-	526.0
AHQ-4-4, 6240	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.21E-06	0.79	2.82	-	702.3
AHQ-4-8, 5391	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.08E-04	0.74	3.11	-	535.0
AHQ-4-8, 5545 - 5557	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.45E-11	0.97	5.98	-	1321.9
AHQ-4-7, 5974	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.74E-04	0.74	3.34	-	446.2
AHQ-4-9, 5120	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.02E-08	0.87	3.89	-	610.0
AHQ-4-13, 5849	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.09E-04	0.34	2.59	-	310.8
AHQ-4-9, 5263 - 5287	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.30E-09	0.93	4.96	-	529.7
AHQ-4-1, 5991	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.60E-08	0.95	4.63	-	1009.7
AHQ-4-1, 5855 - 5894	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.76E-05	0.88	4.09	-	444.1
AHQ-4-5, 3533	K.VGDDPAVWQLK.N	1228.37879	2	7.73E-09	0.91	3.80	-	784.3
AHQ-4-6, 3495 - 3498	K.VGDDPAVWQLK.N	1228.37879	2	7.61E-09	0.93	3.88	-	847.6
AHQ-4-1, 3946	K.VGDDPAVWQLK.N	1228.37879	2	1.25E-06	0.94	3.99	-	962.4
AHQ-4-4, 3758	K.VGDDPAVWQLK.N	1228.37879	2	3.84E-09	0.94	4.03	-	844.4
AHQ-4-7, 3449	K.VGDDPAVWQLK.N	1228.37879	2	8.05E-08	0.86	3.16	-	749.2
AHQ-4-2, 3834 - 3875	K.VGDDPAVWQLK.N	1228.37879	2	9.17E-09	0.92	3.75	-	857.0
AHQ-4-3, 3797	K.VGDDPAVWQLK.N	1228.37879	2	3.91E-08	0.93	3.68	-	909.3
AHQ-4-2, 2318 - 2392	K.VLGEAM*TGISQNAK.N	1435.62901	2	9.12E-06	0.96	4.60	-	1227.0
AHQ-4-1, 3391	K.VLGEAMTGISQNAK.N	1419.62961	2	4.86E-07	0.96	3.80	-	1879.7
AHQ-4-4, 3080	K.VLGEAMTGISQNAK.N	1419.62961	1	6.58E-06	0.84	3.49	-	512.7
AHQ-4-4, 3071	K.VLGEAMTGISQNAK.N	1419.62961	2	7.98E-08	0.97	4.08	-	2044.2
AHQ-4-2, 2328	K.VLGEAM*TGISQNAK.N	1435.62901	1	3.75E-04	0.59	2.69	-	157.3
AHQ-4-2, 3106	K.VLGEAMTGISQNAK.N	1419.62961	2	2.16E-10	0.97	4.64	-	2107.9
AHQ-4-6, 2860	K.VLGEAMTGISQNAK.N	1419.62961	2	2.55E-06	0.97	4.36	-	1953.1
AHQ-4-3, 3264	K.VLGEAMTGISQNAK.N	1419.62961	2	4.97E-10	0.98	4.06	-	2254.8
AHQ-4-3, 3088	K.VLGEAMTGISQNAK.N	1419.62961	1	2.81E-06	0.87	3.81	-	571.4
AHQ-4-3, 3083 - 3151	K.VLGEAMTGISQNAK.N	1419.62961	2	2.08E-09	0.97	4.64	-	2061.8
AHQ-4-4, 2282 - 2352	K.VLGEAM*TGISQNAK.N	1435.62901	2	4.57E-04	0.90	3.00	-	1270.0
AHQ-4-5, 2187 - 2190	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.85E-05	0.95	4.63	-	1274.6
AHQ-4-3, 4829 - 4908	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	4.21E-08	0.73	3.88	-	263.9
AHQ-4-3, 5489 - 5563	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	3.13E-07	0.93	5.39	-	616.9
AHQ-4-4, 5450 - 5523	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	7.56E-06	0.90	4.93	-	632.2
AHQ-4-2, 5023	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	3.08E-06	0.91	4.79	-	593.3
AHQ-4-1, 4919 - 4991	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	1.29E-07	0.95	5.90	-	767.4
AHQ-4-2, 5492 - 5563	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	7.16E-11	0.89	4.98	-	532.4
AHQ-4-1, 5522	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	1.88E-04	0.85	4.75	-	380.3
AHQ-4-2, 1647 - 1660	K.VLVQNAAGSQEK.L	1244.37976	1	1.47E-05	0.43	1.96	-	620.2
AHQ-4-3, 1516 - 1587	K.VLVQNAAGSQEK.L	1244.37976	2	5.84E-10	0.89	3.51	-	797.9
AHQ-4-5, 1484	K.VLVQNAAGSQEK.L	1244.37976	2	1.32E-04	0.86	3.23	-	710.1
AHQ-4-1, 1803	K.VLVQNAAGSQEK.L	1244.37976	2	3.00E-06	0.88	3.26	-	843.9
AHQ-4-6, 1498	K.VLVQNAAGSQEK.L	1244.37976	2	1.15E-04	0.89	3.25	-	916.9
AHQ-4-2, 1504 - 1580	K.VLVQNAAGSQEK.L	1244.37976	2	1.03E-05	0.93	3.70	-	1102.8
AHQ-4-2, 1644	K.VLVQNAAGSQEK.L	1244.37976	2	9.23E-05	0.86	3.23	-	846.8
AHQ-4-1, 1891	K.VLVQNAAGSQEK.L	1244.37976	2	7.41E-05	0.50	2.54	-	472.7
AHQ-4-3, 1691 - 1717	K.VLVQNAAGSQEK.L	1244.37976	2	1.96E-04	0.84	3.34	-	798.7
AHQ-4-4, 1578 - 1620	K.VLVQNAAGSQEK.L	1244.37976	1	3.51E-05	0.06	1.91	-	162.9
AHQ-4-4, 1786	K.VLVQNAAGSQEK.L	1244.37976	1	1.17E-04	0.22	1.97	-	289.1
AHQ-4-4, 1654	K.VLVQNAAGSQEK.L	1244.37976	2	1.07E-06	0.89	3.43	-	835.6
AHQ-4-6, 4010	K.VM*VTNVTSLLK.T	1221.49262	2	3.12E-05	0.90	3.28	-	895.1
AHQ-4-3, 4753	K.VMVTNVTSLLK.T	1205.49322	2	9.58E-06	0.93	4.02	-	907.4
AHQ-4-4, 4311	K.VM*VTNVTSLLK.T	1221.49262	2	7.40E-06	0.93	3.95	-	1007.1
AHQ-4-3, 4364	K.VM*VTNVTSLLK.T	1221.49262	2	8.16E-04	0.66	3.15	-	525.0
AHQ-4-1, 4499 - 4501	K.VM*VTNVTSLLK.T	1221.49262	2	1.85E-04	0.82	3.32	-	697.2
AHQ-4-5, 4403 - 4406	K.VMVTNVTSLLK.T	1205.49322	2	1.24E-06	0.95	4.38	-	1029.7
AHQ-4-1, 4861	K.VMVTNVTSLLK.T	1205.49322	2	1.44E-05	0.87	3.67	-	762.3
AHQ-4-4, 4702	K.VMVTNVTSLLK.T	1205.49322	2	3.31E-04	0.86	3.71	-	722.9
AHQ-4-6, 4350	K.VMVTNVTSLLK.T	1205.49322	2	1.80E-07	0.89	3.70	-	768.6
AHQ-4-2, 4766	K.VMVTNVTSLLK.T	1205.49322	2	6.19E-05	0.88	3.62	-	786.8
AHQ-4-2, 4382	K.VM*VTNVTSLLK.T	1221.49262	2	4.07E-04	0.73	2.92	-	690.4
AHQ-4-7, 4242	K.VMVTNVTSLLK.T	1205.49322	2	2.27E-04	0.91	3.98	-	763.5

AHQ-4-8, 2287	R.VQELGHGCAALVTK.A	1484.70307	2	5.38E-06	0.96	4.05	-	1577.1
AHQ-4-1, 2889	R.VQELGHGCAALVTK.A	1484.70307	2	9.40E-06	0.97	4.94	-	1441.4
AHQ-4-3, 2717	R.VQELGHGCAALVTK.A	1484.70307	1	2.66E-05	0.87	3.65	-	757.4
AHQ-4-4, 2663	R.VQELGHGCAALVTK.A	1484.70307	1	2.23E-06	0.89	3.95	-	689.0
AHQ-4-6, 2523 - 2526	R.VQELGHGCAALVTK.A	1484.70307	2	4.87E-08	0.98	5.18	-	1890.6
AHQ-4-3, 2685	R.VQELGHGCAALVTK.A	1484.70307	2	4.16E-09	0.97	5.13	-	1654.8
AHQ-4-4, 2654	R.VQELGHGCAALVTK.A	1484.70307	2	1.56E-05	0.96	4.37	-	1596.6
AHQ-4-2, 2704	R.VQELGHGCAALVTK.A	1484.70307	2	4.79E-05	0.96	4.72	-	1200.7
AHQ-4-2, 2724	R.VQELGHGCAALVTK.A	1484.70307	1	7.47E-06	0.86	3.58	-	633.1
AHQ-4-11, 2654	R.VQELGHGCAALVTK.A	1484.70307	2	4.67E-05	0.96	4.36	-	1470.8
AHQ-4-5, 2518	R.VQELGHGCAALVTK.A	1484.70307	1	4.47E-07	0.91	3.95	-	588.1
AHQ-4-5, 2505 - 2579	R.VQELGHGCAALVTK.A	1484.70307	2	6.00E-11	0.98	4.97	-	2676.9
AHQ-4-7, 2454	R.VQELGHGCAALVTK.A	1484.70307	2	2.30E-05	0.97	4.39	-	1834.7
AHQ-4-5, 2346	K.VSHVLAALQAGNR.G	1336.52525	2	1.51E-09	0.97	4.60	-	1897.9
AHQ-4-5, 2345 - 2349	K.VSHVLAALQAGNR.G	1336.52525	1	1.16E-06	0.83	3.29	-	404.0
AHQ-4-3, 2660	K.VSHVLAALQAGNR.G	1336.52525	1	1.36E-05	0.15	1.86	-	288.2
AHQ-4-2, 2675	K.VSHVLAALQAGNR.G	1336.52525	1	1.52E-06	0.62	2.20	-	663.5
AHQ-4-4, 2524	K.VSHVLAALQAGNR.G	1336.52525	1	3.37E-05	0.92	3.45	-	784.3
AHQ-4-4, 2528 - 2564	K.VSHVLAALQAGNR.G	1336.52525	2	5.31E-11	0.97	4.48	-	1765.1
AHQ-4-4, 2531	K.VSHVLAALQAGNR.G	1336.52525	1	3.29E-06	0.85	3.58	-	392.6
AHQ-4-3, 2523 - 2525	K.VSHVLAALQAGNR.G	1336.52525	2	6.48E-09	0.98	5.25	-	1894.3
AHQ-4-1, 2802	K.VSHVLAALQAGNR.G	1336.52525	2	1.36E-08	0.97	4.64	-	1967.8
AHQ-4-3, 2519	K.VSHVLAALQAGNR.G	1336.52525	1	4.39E-08	0.76	3.28	-	385.1
AHQ-4-2, 2536 - 2538	K.VSHVLAALQAGNR.G	1336.52525	1	6.74E-07	0.88	3.49	-	494.7
AHQ-4-6, 2512	K.VSHVLAALQAGNR.G	1336.52525	2	1.11E-10	0.95	4.03	-	1370.3
AHQ-4-6, 2372	K.VSHVLAALQAGNR.G	1336.52525	1	1.95E-07	0.52	2.36	-	177.0
AHQ-4-2, 2531 - 2595	K.VSHVLAALQAGNR.G	1336.52525	2	2.98E-04	0.90	3.31	-	959.0
AHQ-4-6, 2363	K.VSHVLAALQAGNR.G	1336.52525	1	1.34E-05	0.79	3.07	-	413.6
AHQ-4-4, 2655	K.VSHVLAALQAGNR.G	1336.52525	1	1.75E-06	0.39	1.95	-	512.8
AHQ-4-9, 2267	K.VSHVLAALQAGNR.G	1336.52525	1	6.25E-04	0.55	2.82	-	305.8
AHQ-4-1, 2803	K.VSHVLAALQAGNR.G	1336.52525	1	3.09E-06	0.72	2.61	-	510.4
AHQ-4-3, 2536	K.VSHVLAALQAGNR.G	1336.52525	1	1.87E-06	0.88	3.57	-	412.7
AHQ-4-6, 2366	K.VSHVLAALQAGNR.G	1336.52525	2	1.82E-08	0.97	4.28	-	1967.3
AHQ-4-5, 6698 - 6773	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.16E-09	0.97	5.92	-	927.9
AHQ-4-2, 6179	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	6.63E-06	0.91	3.97	-	850.3
AHQ-4-2, 6860 - 6892	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	7.71E-04	0.86	3.83	-	492.7
AHQ-4-2, 6940	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	3.99E-08	0.96	5.06	-	1680.4
AHQ-4-2, 6962 - 7026	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.75E-06	0.96	5.18	-	972.1
AHQ-4-5, 5737 - 5757	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.13E-07	0.93	4.30	-	988.5
AHQ-4-2, 7119	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.31E-08	0.96	5.26	-	1120.2
AHQ-4-3, 6185	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.47E-06	0.95	4.25	-	1213.0
AHQ-4-2, 6042	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.31E-05	0.96	4.73	-	1113.1
AHQ-4-1, 6759	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.75E-04	0.86	3.44	-	683.3
AHQ-4-14-, 6383	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	8.95E-06	0.94	5.33	-	668.4
AHQ-4-8, 6371	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.17E-06	0.96	5.45	-	966.9
AHQ-4-1, 6061 - 6063	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.45E-08	0.95	4.92	-	1059.5
AHQ-4-3, 7072	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.19E-08	0.96	5.25	-	1127.8
AHQ-4-6, 5702	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	5.87E-05	0.89	3.84	-	770.1
AHQ-4-6, 6622 - 6638	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.52E-06	0.96	5.51	-	978.5
AHQ-4-1, 6842 - 6853	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.15E-06	0.96	5.24	-	1048.9
AHQ-4-3, 6839	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.00E-06	0.94	4.79	-	814.1
AHQ-4-3, 6932	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	1.07E-11	0.96	5.60	-	1606.4
AHQ-4-1, 6851 - 6855	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	1.04E-08	0.96	5.94	-	1221.0
AHQ-4-3, 6923 - 6991	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.10E-08	0.96	5.43	-	879.9
AHQ-4-7, 5639	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.42E-06	0.94	4.57	-	964.1
AHQ-4-7, 6741	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.19E-08	0.96	5.29	-	895.1
AHQ-4-4, 6946	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.49E-06	0.94	4.90	-	774.1
AHQ-4-4, 6851 - 6918	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.28E-04	0.96	5.80	-	820.6
AHQ-4-1, 6070 - 6095	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	6.29E-11	0.96	5.34	-	1717.0
AHQ-4-1, 6961	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.29E-07	0.83	3.67	-	545.7
AHQ-4-9, 6075 - 6076	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.36E-05	0.94	4.29	-	890.6
AHQ-4-4, 6140	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.19E-06	0.87	3.76	-	676.3
AHQ-4-4, 5982	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.63E-06	0.96	4.83	-	1189.4
AHQ-4-2, 6043 - 6062	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	3.21E-07	0.97	5.06	-	1872.7
AHQ-4-3, 4939	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.45E-11	0.90	4.36	-	477.5
AHQ-4-4, 5046 - 5050	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.14E-05	0.82	3.76	-	425.4
AHQ-4-4, 4902	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.35E-09	0.89	4.55	-	435.4
AHQ-4-4, 4738 - 4746	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.03E-07	0.97	5.61	-	1091.0
AHQ-4-3, 4771 - 4773	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.72E-08	0.95	5.81	-	688.8
AHQ-4-4, 4598	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.31E-04	0.81	3.53	-	413.2
AHQ-4-3, 4652	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.73E-04	0.70	3.58	-	189.0
AHQ-4-5, 4467 - 4471	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.25E-05	0.94	4.82	-	605.0
AHQ-4-5, 4573	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.42E-08	0.93	4.39	-	833.1
AHQ-4-5, 4911	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.30E-07	0.93	4.70	-	488.3
AHQ-4-1, 4663	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.28E-04	0.53	3.15	-	179.6
AHQ-4-1, 4773 - 4787	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.66E-06	0.69	3.17	-	336.0
AHQ-4-14-, 4401 - 4465	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.12E-05	0.97	5.46	-	1262.5
AHQ-4-12, 4562 - 4566	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.67E-07	0.90	4.73	-	452.1
AHQ-4-6, 4476 - 4483	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.57E-06	0.97	5.80	-	1033.9
AHQ-4-2, 4872 - 4954	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.86E-11	0.95	5.33	-	628.8
AHQ-4-2, 4775 - 4782	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.92E-07	0.95	5.00	-	697.2
AHQ-4-11, 4413	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.40E-04	0.41	3.19	-	275.9
AHQ-4-2, 4654	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.28E-06	0.93	4.51	-	588.6
AHQ-4-7, 4457 - 4486	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.37E-09	0.96	5.48	-	797.6
AHQ-4-10, 4095 - 4155	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.78E-04	0.59	3.45	-	191.2
AHQ-4-8, 4143	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.75E-08	0.90	4.44	-	467.5
AHQ-4-8, 4298 - 4313	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.34E-06	0.96	5.30	-	895.3
AHQ-4-9, 4055	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.37E-07	0.92	4.29	-	748.4
gi|4827056|ref|NP_005103.1|	WD repeat-containing protein 1 isoform 2 [Homo sapiens]			5.55E-16	10.72	130.36	46.40	58001.9
AHQ-4-9, 4299	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	5.67E-04	0.87	3.79	-	605.8
AHQ-4-6, 4987	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	2.63E-05	0.97	5.67	-	1665.8
AHQ-4-6, 4810	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	2.05E-12	0.98	7.21	-	2146.0
AHQ-4-10, 5111	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	2.16E-13	0.96	5.38	-	1262.1
AHQ-4-9, 5133	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	8.63E-11	0.71	3.32	-	445.4
AHQ-4-11, 5438	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	2.02E-11	0.89	4.32	-	730.2
AHQ-4-4, 5955	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.70E-04	0.73	3.20	-	542.3
AHQ-4-6, 5766	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	5.81E-08	0.88	4.00	-	840.9
AHQ-4-7, 5666	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	5.03E-08	0.71	3.24	-	515.2
AHQ-4-6, 5624 - 5690	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	5.55E-16	0.94	5.05	-	929.1
AHQ-4-6, 5543	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	2	2.41E-05	0.87	3.67	-	731.4
AHQ-4-9, 4119	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	8.11E-08	0.92	4.04	-	1004.7
AHQ-4-10, 4227	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	5.33E-05	0.93	4.01	-	1190.3
AHQ-4-3, 4880	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	2.82E-04	0.79	3.53	-	594.1
AHQ-4-6, 4548 - 4619	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	2.70E-06	0.97	5.22	-	1684.9
AHQ-4-6, 4696	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	6.67E-07	0.97	5.53	-	1404.1
AHQ-4-6, 2031	K.IKDIAWTEDSKR.I	1462.63267	2	8.10E-08	0.93	3.77	-	1206.9
AHQ-4-6, 2026	K.IKDIAWTEDSKR.I	1462.63267	3	4.76E-09	0.82	3.71	-	624.8

AHQ-4-12, 2273	K.IKDIAWTEDSKR.I	1462.63267	2	3.70E-04	0.84	3.37	-	905.1
AHQ-4-11, 5369	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	3.14E-04	0.88	3.96	-	664.4
AHQ-4-11, 5226 - 5273	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	6.72E-10	0.81	3.74	-	634.9
AHQ-4-6, 5327 - 5395	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	2.59E-06	0.89	3.86	-	880.6
AHQ-4-6, 5570	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	6.01E-07	0.91	4.34	-	875.2
AHQ-4-6, 5423 - 5498	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	4.79E-09	0.92	4.60	-	867.9
AHQ-4-6, 3638	R.LYSILGTTLKDEGK.L	1538.76736	2	2.43E-07	0.89	3.81	-	763.6
AHQ-4-10, 3611 - 3620	R.LYSILGTTLKDEGK.L	1538.76736	2	3.23E-10	0.90	4.10	-	787.1
AHQ-4-13, 4141 - 4197	R.LYSILGTTLKDEGK.L	1538.76736	2	4.24E-04	0.74	2.79	-	851.0
AHQ-4-6, 4899	R.MTVDESGQLISCSMDDTVR.Y	2146.36365	2	4.19E-04	0.52	3.22	-	268.2
AHQ-4-13, 4364	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	2.88E-08	0.87	3.33	-	897.3
AHQ-4-10, 3884	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	2.31E-08	0.77	3.40	-	496.7
AHQ-4-6, 3979	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	7.54E-10	0.97	6.53	-	1558.3
AHQ-4-6, 2088 - 2166	K.VINSVDIK.Q	888.04378	1	6.05E-04	0.46	2.34	-	521.4
AHQ-4-13-, 3905 - 3929	K.YAPSGFYIASGDVSGK.L	1619.75589	2	2.54E-06	0.89	3.89	-	782.4
AHQ-4-6, 3683 - 3766	K.YAPSGFYIASGDVSGK.L	1619.75589	2	8.15E-08	0.94	4.55	-	687.9
AHQ-4-12, 3910	K.YAPSGFYIASGDVSGK.L	1619.75589	2	2.32E-10	0.95	4.51	-	897.4
AHQ-4-6, 2588 - 2596	K.YEYQPFAGK.I	1103.20822	2	7.74E-05	0.80	3.02	-	460.9
gi|4502027|ref|NP_000468.1| albumin precursor; PRO0883 protein [Homo sapiens]				1.11E-15	22.95	270.37	50.40	69366.4
AHQ-4-6, 2356	K.AAFTECCQAADK.A	1374.47927	1	2.28E-04	0.71	3.06	-	539.0
AHQ-4-5, 2369	K.AAFTECCQAADK.A	1374.47927	1	8.02E-04	0.64	3.10	-	411.8
AHQ-4-5, 4458	K.AVM*DDFAAFVEK.C	1359.52946	2	1.07E-07	0.95	3.69	-	1189.8
AHQ-4-5, 5494 - 5517	K.AVMDDFAAFVEK.C	1343.53006	2	3.24E-08	0.97	4.31	-	1892.4
AHQ-4-12, 5477	K.AVMDDFAAFVEK.C	1343.53006	2	6.61E-05	0.87	2.95	-	1196.5
AHQ-4-14-, 5358	K.AVMDDFAAFVEK.C	1343.53006	2	8.40E-09	0.94	3.83	-	1297.4
AHQ-4-6, 5424 - 5431	K.AVMDDFAAFVEK.C	1343.53006	2	1.66E-08	0.97	4.35	-	1754.9
AHQ-4-6, 5430	K.AVMDDFAAFVEK.C	1343.53006	1	1.88E-05	0.89	4.23	-	827.6
AHQ-4-5, 2330	K.CCTESLVNR.R	1141.25805	2	3.51E-05	0.91	2.73	-	1243.5
AHQ-4-5, 6395	K.EFNAETFTFHADICTLSEK.E	2262.43749	2	2.50E-07	0.58	3.25	-	347.7
AHQ-4-13-, 2661 - 2716	R.FKDLGEENFK.A	1227.34766	2	1.99E-07	0.76	2.77	-	700.8
AHQ-4-5, 2385 - 2466	R.FKDLGEENFK.A	1227.34766	2	4.13E-05	0.85	3.30	-	682.5
AHQ-4-6, 2688	K.FQNALLVR.Y	961.14282	2	8.47E-04	0.73	2.77	-	653.7
AHQ-4-6, 6506	R.HPYFYAPELLFFAK.R	1744.02658	2	1.22E-05	0.49	2.52	-	253.8
AHQ-4-5, 6591	R.HPYFYAPELLFFAK.R	1744.02658	3	4.26E-08	0.95	4.28	-	1299.7
AHQ-4-5, 2319	K.KQTALVELVK.H	1129.37494	2	1.90E-05	0.73	2.75	-	796.3
AHQ-4-13-, 2753	K.KQTALVELVK.H	1129.37494	2	1.58E-06	0.77	2.93	-	632.9
AHQ-4-2, 3586 - 3590	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.88E-08	0.89	3.59	-	673.7
AHQ-4-10, 3181	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.06E-07	0.80	3.03	-	578.5
AHQ-4-3, 3549	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.90E-07	0.80	2.67	-	755.8
AHQ-4-6, 3208 - 3234	K.KVPQVSTPTLVEVSR.N	1640.90605	2	6.01E-07	0.91	3.34	-	883.3
AHQ-4-6, 3226	K.KVPQVSTPTLVEVSR.N	1640.90605	3	4.77E-09	0.94	4.45	-	1404.4
AHQ-4-5, 3257 - 3281	K.KVPQVSTPTLVEVSR.N	1640.90605	2	5.40E-07	0.93	3.96	-	869.1
AHQ-4-5, 3267 - 3277	K.KVPQVSTPTLVEVSR.N	1640.90605	3	4.90E-08	0.97	5.82	-	1774.2
AHQ-4-4, 3527	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.05E-04	0.73	2.59	-	640.5
AHQ-4-7, 3117	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.32E-06	0.81	3.36	-	383.6
AHQ-4-8, 2863	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.90E-10	0.70	2.85	-	413.2
AHQ-4-13-, 3300	K.LVNEVTEFAK.T	1150.30633	2	7.20E-04	0.82	2.63	-	672.4
AHQ-4-6, 2987 - 3043	K.LVNEVTEFAK.T	1150.30633	2	1.77E-05	0.77	3.27	-	497.5
AHQ-4-5, 3405	K.LVNEVTEFAK.T	1150.30633	1	2.28E-05	0.85	3.00	-	910.6
AHQ-4-13, 3439 - 3441	K.LVNEVTEFAK.T	1150.30633	2	1.42E-05	0.85	2.78	-	708.3
AHQ-4-5, 3042 - 3077	K.LVNEVTEFAK.T	1150.30633	1	6.22E-06	0.67	2.25	-	810.2
AHQ-4-7, 2991	K.LVNEVTEFAK.T	1150.30633	2	1.87E-04	0.79	2.85	-	599.2
AHQ-4-11, 5464	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	4.73E-04	0.86	4.37	-	873.5
AHQ-4-6, 5611 - 5655	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	2.11E-05	0.98	6.29	-	2035.8
AHQ-4-5, 7422	R.MPCAEDYLSVVLNQLCVLHEK.T	2521.91535	3	6.13E-05	0.97	5.45	-	1910.4
AHQ-4-1, 5278 - 5299	K.QNCELFEQLGEYK.F	1659.79847	2	1.77E-06	0.74	3.21	-	418.7
AHQ-4-6, 3650	R.RHPDYSVVLLLR.L	1468.72842	3	1.58E-04	0.96	4.55	-	1928.2
AHQ-4-5, 3678	R.RHPDYSVVLLLR.L	1468.72842	2	2.07E-04	0.89	3.56	-	734.9
AHQ-4-6, 3648	R.RHPDYSVVLLLR.L	1468.72842	2	2.42E-06	0.90	3.17	-	954.7
AHQ-4-5, 3703	R.RHPDYSVVLLLR.L	1468.72842	3	1.13E-05	0.96	4.84	-	2009.4
AHQ-4-3, 6215	R.RHPYFYAPELLFFAK.R	1900.21293	2	8.79E-04	0.95	3.56	-	1643.9
AHQ-4-10, 5299	R.RHPYFYAPELLFFAK.R	1900.21293	2	1.57E-04	0.98	5.25	-	2542.1
AHQ-4-5, 5645	R.RHPYFYAPELLFFAK.R	1900.21293	2	8.07E-10	0.98	5.47	-	2388.2
AHQ-4-6, 5774	R.RHPYFYAPELLFFAK.R	1900.21293	3	6.56E-06	0.98	5.67	-	2391.9
AHQ-4-6, 5762	R.RHPYFYAPELLFFAK.R	1900.21293	2	1.42E-08	0.98	5.37	-	2931.6
AHQ-4-6, 7191	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	9.72E-06	0.98	6.39	-	2194.9
AHQ-4-6, 7151	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	4.50E-04	0.94	5.00	-	1349.4
AHQ-4-5, 7329	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	3.39E-06	0.92	4.89	-	825.5
AHQ-4-5, 7365	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	1.19E-06	0.97	6.14	-	1928.5
AHQ-4-3, 4904 - 4905	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.03E-05	0.93	4.85	-	579.6
AHQ-4-11, 4544	R.RPCFSALEVDETYVPK.E	1913.14041	2	8.83E-06	0.76	3.44	-	462.5
AHQ-4-6, 4562	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.40E-04	0.93	4.49	-	596.9
AHQ-4-1, 4951	R.RPCFSALEVDETYVPK.E	1913.14041	2	3.42E-05	0.86	3.56	-	637.7
AHQ-4-10, 4253 - 4255	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.05E-04	0.94	4.62	-	740.3
AHQ-4-4, 4870	R.RPCFSALEVDETYVPK.E	1913.14041	2	9.16E-04	0.84	3.56	-	554.4
AHQ-4-12, 4694	R.RPCFSALEVDETYVPK.E	1913.14041	2	4.31E-04	0.92	4.05	-	684.5
AHQ-4-13, 4809	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.79E-05	0.80	3.85	-	381.4
AHQ-4-5, 6481 - 6485	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	2	7.17E-06	0.93	4.62	-	822.9
AHQ-4-1, 7029	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	4.04E-04	0.75	3.94	-	515.0
AHQ-4-5, 6975 - 7038	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	8.19E-05	0.96	4.84	-	1384.2
AHQ-4-5, 6963 - 7025	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	1.11E-15	0.95	5.43	-	1152.1
AHQ-4-6, 6767 - 6842	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	2.96E-04	0.90	4.08	-	654.3
AHQ-4-6, 6839 - 6916	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	3.42E-07	0.96	5.73	-	993.9
AHQ-4-7, 6997 - 7007	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	9.24E-13	0.92	4.76	-	765.0
AHQ-4-6, 4831	K.SLHTLFGDKLCTVATLR.E	1934.24913	3	4.11E-04	0.81	3.18	-	847.5
AHQ-4-5, 3662	K.TYETTLEKCCAAADPHECYAK.V	2522.72734	3	2.94E-04	0.78	3.35	-	716.1
AHQ-4-3, 6072	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	7.75E-04	0.77	3.51	-	342.3
AHQ-4-7, 5695	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.57E-04	0.91	4.50	-	432.3
AHQ-4-7, 5714	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.45E-07	0.94	4.26	-	1208.7
AHQ-4-3, 6079	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.80E-06	0.93	4.28	-	1087.4
AHQ-4-6, 5718 - 5788	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.61E-05	0.97	5.46	-	1710.2
AHQ-4-9, 5195 - 5197	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.11E-05	0.90	4.12	-	451.8
AHQ-4-6, 5656 - 5738	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.50E-05	0.90	4.38	-	843.4
AHQ-4-4, 6030 - 6107	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	7.48E-05	0.79	3.25	-	451.9
AHQ-4-5, 5618 - 5626	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.60E-09	0.92	4.28	-	694.8
AHQ-4-5, 5781 - 5851	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.92E-04	0.93	4.87	-	491.1
AHQ-4-5, 5785	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.82E-06	0.96	5.27	-	1418.1
AHQ-4-1, 6066	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	3.38E-06	0.94	4.63	-	1273.8
AHQ-4-1, 6073	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.09E-05	0.89	4.01	-	420.1
AHQ-4-5, 2863 - 2919	K.VHTECCHGDLLECADDR.A	2091.20307	2	9.13E-06	0.84	3.78	-	615.3
AHQ-4-5, 3777 - 3781	K.VPQVSTPTLVEVSR.N	1512.73313	2	3.57E-08	0.91	3.51	-	878.9
AHQ-4-6, 3716 - 3719	K.VPQVSTPTLVEVSR.N	1512.73313	2	5.21E-06	0.88	3.26	-	837.9
AHQ-4-5, 2207	K.YICENQDSISSK.L	1445.53420	2	1.24E-04	0.83	3.17	-	608.7
AHQ-4-6, 2192	K.YICENQDSISSK.L	1445.53420	2	6.18E-04	0.89	3.25	-	688.0
AHQ-4-1, 2441	K.YICENQDSISSK.L	1445.53420	2	1.20E-07	0.92	3.64	-	854.9
gi|4507729|ref|NP_001060.1| tubulin, beta polypeptide [Homo sapiens]				1.11E-15	8.29	100.40	29.40	49906.7
AHQ-4-7, 2665 - 2673	R.EIVHIQAGQCGNQIGAK.F	1825.03962	2	1.22E-04	0.96	4.35	-	1463.5

AHQ-4-7, 2701	K.EVDEQMLNVQNK.N	1447.59668	2	4.72E-06	0.88	3.66	-	891.0
AHQ-4-7, 2855	K.EVDEQMLNVQNK.N	1447.59668	1	6.31E-07	0.51	2.99	-	251.7
AHQ-4-7, 2702	K.EVDEQMLNVQNK.N	1447.59668	1	3.48E-06	0.63	3.60	-	253.6
AHQ-4-7, 2090	K.EVDEQM*LNVQNK.N	1463.59608	2	5.70E-05	0.73	3.16	-	685.2
AHQ-4-13-, 6284 - 6294	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.18E-07	0.98	6.28	-	2814.7
AHQ-4-13, 6349	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.26E-09	0.98	6.67	-	2611.0
AHQ-4-7, 4430	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.54E-04	0.96	4.80	-	1210.8
AHQ-4-7, 5270	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.33E-06	0.97	5.35	-	1574.6
AHQ-4-13, 6344 - 6357	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	1.34E-05	0.87	4.50	-	745.6
AHQ-4-7, 6191 - 6261	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	8.01E-06	0.99	7.18	-	3122.1
AHQ-4-7, 6202	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	6.22E-06	0.92	5.06	-	1060.5
AHQ-4-12, 6257	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	6.56E-04	0.84	4.50	-	713.3
AHQ-4-12, 6254	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.56E-08	0.99	7.07	-	3498.1
AHQ-4-11, 6032	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.19E-06	0.98	6.66	-	2371.4
AHQ-4-10, 5728	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	6.04E-06	0.98	5.16	-	2144.7
AHQ-4-9, 5692 - 5751	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	8.60E-06	0.98	6.06	-	2520.7
AHQ-4-14-, 6159	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.61E-13	0.99	7.40	-	2971.3
AHQ-4-7, 2701	R.GRM*SM*KEVDEQMLNVQNK.N	2170.47810	3	1.54E-04	0.48	3.11	-	463.5
AHQ-4-7, 4335	R.ISEQFTAMFR.R	1230.41818	2	4.90E-06	0.94	3.25	-	1522.5
AHQ-4-10, 6380	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	5.49E-09	0.92	4.45	-	608.3
AHQ-4-7, 6129	K.LTTPTYGDLNHLVSATM*SGVTTCLR.F	2727.06467	3	2.95E-05	0.91	4.63	-	791.5
AHQ-4-7, 7285 - 7286	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	1.47E-05	0.94	4.88	-	1240.0
AHQ-4-12, 6050	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	2.61E-07	0.80	3.66	-	945.9
AHQ-4-7, 6637	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	1.24E-08	0.88	4.39	-	1015.9
AHQ-4-14-, 5946	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	2.13E-05	0.67	3.61	-	635.8
AHQ-4-7, 6393 - 6461	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.18E-11	0.96	6.14	-	1555.3
AHQ-4-7, 6337 - 6401	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	7.91E-08	0.95	5.36	-	915.0
AHQ-4-11, 6065 - 6125	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.11E-15	0.97	6.50	-	1839.8
AHQ-4-9, 5708 - 5755	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	8.44E-04	0.94	4.92	-	926.3
AHQ-4-12, 6243	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	8.77E-09	0.96	5.39	-	1528.2
AHQ-4-7, 6259 - 6329	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	5.26E-07	0.97	5.85	-	1605.0
AHQ-4-7, 6255 - 6326	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.12E-05	0.97	6.73	-	1644.4
AHQ-4-12, 6367	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	5.25E-05	0.81	3.59	-	444.8
AHQ-4-13, 6306 - 6381	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	7.06E-04	0.69	3.17	-	838.3
AHQ-4-7, 6458 - 6525	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	3.49E-07	0.96	6.14	-	948.4
AHQ-4-7, 6583 - 6650	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.01E-09	0.96	6.06	-	1488.6
AHQ-4-13-, 6272 - 6334	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	6.88E-07	0.98	6.51	-	1857.4
AHQ-4-7, 6735 - 6763	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.87E-07	0.94	5.03	-	1327.0
AHQ-4-10, 5813	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	5.32E-08	0.94	4.55	-	994.2
AHQ-4-14-, 6118 - 6187	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.91E-12	0.98	8.10	-	2411.2
AHQ-4-7, 6598 - 6665	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	1.02E-04	0.80	3.44	-	513.1
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				1.11E-15	3.56	40.32	14.60	61986.9
AHQ-4-1, 6559 - 6561	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.11E-15	0.98	6.39	-	2491.3
AHQ-4-14-, 6097	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.26E-08	0.95	5.15	-	1287.8
AHQ-4-1, 4767	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	2.47E-06	0.95	5.21	-	1362.7
AHQ-4-1, 7126 - 7193	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	1.58E-04	0.85	4.12	-	572.7
AHQ-4-1, 3110	K.VQALEEANNDLENK.I	1587.67060	2	1.18E-04	0.78	3.25	-	585.5
gi|4504165|ref|NP_000168.1| gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]				1.67E-15	22.05	260.36	40.80	85696.9
AHQ-4-5, 3685	K.AGALNSNDAFVLK.T	1320.47622	1	6.05E-07	0.30	2.29	-	387.6
AHQ-4-6, 3530	K.AGALNSNDAFVLK.T	1320.47622	2	1.11E-05	0.76	3.08	-	649.4
AHQ-4-5, 3594	K.AGALNSNDAFVLK.T	1320.47622	1	7.21E-09	0.28	2.22	-	372.5
AHQ-4-5, 3593	K.AGALNSNDAFVLK.T	1320.47622	2	2.35E-07	0.85	3.67	-	582.4
AHQ-4-5, 3390	K.AGALNSNDAFVLK.T	1320.47622	2	9.41E-07	0.86	3.88	-	629.8
AHQ-4-5, 3687	K.AGALNSNDAFVLK.T	1320.47622	2	3.78E-05	0.89	3.57	-	773.2
AHQ-4-6, 3536	K.AGALNSNDAFVLK.T	1320.47622	1	3.77E-05	0.13	2.08	-	249.9
AHQ-4-7, 3283	K.AGALNSNDAFVLK.T	1320.47622	2	5.63E-04	0.90	3.52	-	936.5
AHQ-4-5, 2667	K.AGKEPGLQIWR.V	1255.45060	2	6.54E-04	0.61	2.63	-	423.5
AHQ-4-5, 5566 - 5597	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.09E-08	0.97	6.22	-	839.2
AHQ-4-11, 5477	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.19E-04	0.85	3.82	-	456.4
AHQ-4-6, 5486 - 5506	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.56E-06	0.94	4.82	-	637.0
AHQ-4-6, 5639	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.42E-07	0.89	4.18	-	471.2
AHQ-4-7, 5654	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.26E-06	0.93	4.74	-	688.6
AHQ-4-10, 5147	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.28E-05	0.97	5.72	-	958.9
AHQ-4-5, 5678 - 5710	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.97E-07	0.95	4.96	-	767.3
AHQ-4-10, 4999 - 5000	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.09E-06	0.96	5.27	-	766.8
AHQ-4-5, 5777	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.72E-06	0.96	5.43	-	743.5
AHQ-4-5, 5885 - 5955	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.70E-06	0.93	4.72	-	573.3
AHQ-4-4, 5766	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	9.26E-04	0.61	3.25	-	348.2
AHQ-4-7, 5501	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.86E-04	0.96	5.44	-	705.1
AHQ-4-8, 5386	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.18E-04	0.88	3.77	-	707.1
AHQ-4-9, 5109	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.61E-04	0.90	4.33	-	509.3
AHQ-4-9, 4897 - 4967	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.13E-04	0.91	4.49	-	499.7
AHQ-4-5, 6023	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.15E-06	0.95	4.84	-	779.1
AHQ-4-5, 5622	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.03E-07	0.96	5.39	-	1550.4
AHQ-4-11, 2114	K.DSQEEEKTEALTSAK.R	1666.72289	2	8.57E-07	0.83	3.17	-	1117.2
AHQ-4-12, 2182	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.28E-06	0.91	3.85	-	1116.4
AHQ-4-10, 2065	K.DSQEEEKTEALTSAK.R	1666.72289	2	7.03E-06	0.90	3.55	-	1086.0
AHQ-4-13, 2341	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.52E-05	0.92	3.78	-	1149.9
AHQ-4-7, 1954	K.DSQEEEKTEALTSAK.R	1666.72289	2	8.68E-07	0.94	4.12	-	1248.9
AHQ-4-13-, 2232	K.DSQEEEKTEALTSAK.R	1666.72289	2	4.72E-08	0.95	4.02	-	1682.7
AHQ-4-5, 2077 - 2085	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.21E-06	0.91	3.54	-	1400.5
AHQ-4-8, 1872	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.64E-06	0.87	3.51	-	990.2
AHQ-4-5, 1982	K.DSQEEEKTEALTSAK.R	1666.72289	3	1.10E-06	0.96	4.89	-	1718.5
AHQ-4-5, 1979 - 2009	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.41E-06	0.91	3.95	-	1052.8
AHQ-4-13-, 2238	K.DSQEEEKTEALTSAK.R	1666.72289	3	7.46E-07	0.92	3.72	-	1352.6
AHQ-4-9, 1947	K.DSQEEEKTEALTSAK.R	1666.72289	2	8.34E-05	0.68	2.97	-	742.6
AHQ-4-6, 1976	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.95E-09	0.95	4.30	-	1722.8
AHQ-4-5, 5078	K.EPAHLMSLFGGKPMIIYK.G	2033.48916	2	9.35E-05	0.87	3.92	-	463.9
AHQ-4-6, 5070	K.EPAHLMSLFGGKPMIIYK.G	2033.48916	2	1.58E-05	0.91	3.64	-	886.3
AHQ-4-12, 6163	R.EVQGFESATFLGYFK.S	1723.90570	2	9.23E-09	0.93	3.94	-	1045.2
AHQ-4-5, 6434 - 6483	R.EVQGFESATFLGYFK.S	1723.90570	2	2.93E-08	0.97	4.37	-	1677.6
AHQ-4-5, 6967	R.EVQGFESATFLGYFK.S	1723.90570	2	1.79E-05	0.82	3.01	-	686.2
AHQ-4-13, 6214 - 6282	R.EVQGFESATFLGYFK.S	1723.90570	2	1.63E-04	0.96	3.99	-	1675.0
AHQ-4-13-, 6124	R.EVQGFESATFLGYFK.S	1723.90570	2	1.09E-08	0.97	4.77	-	1967.4
AHQ-4-5, 6343	R.EVQGFESATFLGYFK.S	1723.90570	2	2.41E-07	0.95	4.26	-	1309.4
AHQ-4-5, 6549 - 6617	R.EVQGFESATFLGYFK.S	1723.90570	2	1.66E-04	0.90	3.12	-	1133.7
AHQ-4-14-, 5993	R.EVQGFESATFLGYFK.S	1723.90570	2	2.44E-06	0.92	2.99	-	1435.2
AHQ-4-5, 7449 - 7529	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	2	8.81E-04	0.90	3.63	-	738.5
AHQ-4-5, 2045 - 2123	K.HVVPNEVVVQR.L	1276.46981	2	1.38E-06	0.88	2.96	-	595.9
AHQ-4-6, 2044	K.HVVPNEVVVQR.L	1276.46981	2	3.82E-09	0.87	3.11	-	718.4
AHQ-4-5, 2047	K.HVVPNEVVVQR.L	1276.46981	1	9.20E-04	0.35	2.03	-	326.8
AHQ-4-5, 2057	K.HVVPNEVVVQR.L	1276.46981	1	5.63E-05	0.24	2.41	-	198.2
AHQ-4-5, 2255 - 2262	K.HVVPNEVVVQR.L	1276.46981	2	6.05E-09	0.89	3.14	-	680.8
AHQ-4-12, 2261	K.HVVPNEVVVQR.L	1276.46981	2	2.14E-07	0.89	3.26	-	555.0
AHQ-4-11, 2182	K.HVVPNEVVVQR.L	1276.46981	2	2.37E-05	0.80	2.90	-	441.5
AHQ-4-11, 2189 - 2190	K.HVVPNEVVVQR.L	1276.46981	1	2.60E-05	0.49	2.45	-	334.6
AHQ-4-7, 1995	K.HVVPNEVVVQR.L	1276.46981	2	2.90E-04	0.83	2.81	-	552.5

AHQ-4-5, 6757 - 6827	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	5.64E-04	0.94	4.93	-	1088.8
AHQ-4-5, 6634	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	6.19E-04	0.80	3.24	-	879.0
AHQ-4-5, 6370	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	5.54E-08	0.95	5.01	-	1138.2
AHQ-4-6, 5434 - 5442	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	3.19E-05	0.96	5.05	-	1747.1
AHQ-4-5, 5467 - 5539	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.67E-15	0.96	5.97	-	1053.5
AHQ-4-6, 1854	K.PALPAGTEDTAK.E	1171.28241	2	3.87E-07	0.68	2.61	-	429.4
AHQ-4-5, 2295	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	1.41E-07	0.88	3.79	-	446.9
AHQ-4-5, 4697 - 4701	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	1.22E-04	0.83	3.50	-	427.1
AHQ-4-8, 4255	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	5.91E-06	0.82	3.43	-	402.8
AHQ-4-6, 4642	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	9.01E-04	0.84	3.55	-	477.4
AHQ-4-5, 4846	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	4.40E-05	0.85	3.30	-	527.5
AHQ-4-6, 2759 - 2771	K.SEDCFILDHGK.D	1322.42590	2	1.94E-06	0.94	3.46	-	1229.3
AHQ-4-5, 2746 - 2753	K.SEDCFILDHGK.D	1322.42590	2	5.91E-04	0.96	3.88	-	1429.0
AHQ-4-5, 2422	K.SEDCFILDHGKDGK.I	1622.73823	2	2.45E-04	0.56	2.67	-	604.3
AHQ-4-5, 1894 - 1970	K.TGAQELLR.V	888.00387	2	1.30E-05	0.90	2.92	-	1163.3
AHQ-4-5, 4683	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	5.75E-05	0.93	4.29	-	819.8
AHQ-4-5, 4454 - 4525	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.60E-04	0.96	4.58	-	1355.0
AHQ-4-5, 4305 - 4373	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	9.86E-04	0.93	3.85	-	932.2
AHQ-4-5, 7387	R.VEKFDLVPVPTNLYGDFFTGDAYVILK.T	3062.50261	3	2.39E-04	0.72	3.66	-	520.8
AHQ-4-5, 3570 - 3607	R.VHVSEEGTEPEAM*LQVLGPK.P	2167.42570	2	3.29E-06	0.96	5.14	-	1047.8
AHQ-4-9, 4191 - 4269	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	4.92E-04	0.90	4.11	-	588.7
AHQ-4-6, 4687	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	5.25E-06	0.96	5.20	-	915.6
AHQ-4-5, 4702 - 4782	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	4.26E-04	0.95	5.02	-	984.9
AHQ-4-9, 4508	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	8.94E-04	0.83	3.94	-	606.2
AHQ-4-6, 5023	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	2.22E-09	0.96	6.00	-	801.6
AHQ-4-5, 5073	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	4.89E-08	0.95	5.83	-	1058.3
AHQ-4-5, 4838	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAKEDAANR.K	3960.33442	3	9.14E-04	0.78	3.64	-	428.6
AHQ-4-5, 3373 - 3450	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	8.88E-04	0.90	5.70	-	966.6
AHQ-4-5, 3837 - 3849	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	1.32E-10	0.98	7.29	-	1700.1
AHQ-4-5, 1571	R.YIETDPANR.D	1079.14506	2	4.13E-05	0.78	2.62	-	603.7
gi|13899317|ref|NP_113657.1| SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M				1.67E-15	5.51	60.32	72.00	12326.0
AHQ-4-14-, 5394 - 5398	K.ESNTVFSFLGLKPR.L	1595.82383	2	2.59E-10	0.82	3.63	-	483.5
AHQ-4-13-, 5432 - 5454	K.ESNTVFSFLGLKPR.L	1595.82383	2	2.16E-06	0.49	2.79	-	371.4
AHQ-4-13-, 5680	K.ESNTVFSFLGLKPR.L	1595.82383	2	3.32E-08	0.71	2.71	-	452.3
AHQ-4-14-, 5401	K.ESNTVFSFLGLKPR.L	1595.82383	3	8.76E-04	0.69	3.02	-	785.7
AHQ-4-13-, 4940	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	2	9.55E-05	0.91	4.00	-	916.2
AHQ-4-13-, 4932 - 4934	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	8.84E-11	0.98	6.38	-	3146.2
AHQ-4-14-, 4911	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	2	2.62E-06	0.95	5.16	-	912.6
AHQ-4-13, 5050	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	2.08E-04	0.91	4.81	-	1117.2
AHQ-4-13, 4350	K.IEFEEVDITM*SEEQR.Q	1872.00051	2	6.02E-05	0.89	3.12	-	1242.8
AHQ-4-13, 3961	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	3.37E-06	0.90	3.83	-	710.6
AHQ-4-13, 3876	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	1.10E-04	0.91	3.51	-	987.3
AHQ-4-13-, 3781	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	1.67E-15	0.91	4.01	-	887.5
AHQ-4-14-, 5758	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	1.10E-05	0.91	4.70	-	791.5
AHQ-4-14-, 5665 - 5738	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	1.82E-07	0.94	5.12	-	973.2
AHQ-4-13, 5852 - 5916	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	3.22E-04	0.90	4.88	-	844.2
AHQ-4-13-, 5766 - 5826	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	4.43E-04	0.90	4.58	-	823.4
AHQ-4-13-, 4366	R.VFIASSSGFVAIK.K	1326.56551	1	4.13E-04	0.04	1.89	-	186.3
AHQ-4-13-, 4369	R.VFIASSSGFVAIK.K	1326.56551	2	1.31E-05	0.97	4.24	-	2087.0
gi|4505879|ref|NP_002655.1| pleckstrin; p47 [Homo sapiens]				2.78E-15	12.66	140.42	45.40	40082.5
AHQ-4-8, 5311	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.05E-04	0.96	5.56	-	1467.6
AHQ-4-4, 5930	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	4.61E-04	0.92	4.34	-	1330.4
AHQ-4-12, 5651	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.97E-05	0.97	5.99	-	2146.6
AHQ-4-13-, 5578 - 5589	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.76E-09	0.97	6.20	-	1673.7
AHQ-4-8, 5315	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	4.50E-06	0.71	2.86	-	567.5
AHQ-4-10, 5132	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	2.22E-08	0.69	3.18	-	359.9
AHQ-4-14-, 5565 - 5627	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.79E-09	0.96	5.30	-	1663.1
AHQ-4-13, 5712	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.69E-04	0.98	6.81	-	1730.7
AHQ-4-11, 5458	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.71E-04	0.90	4.59	-	1117.9
AHQ-4-8, 2257 - 2272	R.GCVVTSVESNSNGR.K	1467.54464	2	1.16E-07	0.90	3.14	-	1300.3
AHQ-4-12, 2439	R.GCVVTSVESNSNGR.K	1467.54464	2	9.82E-04	0.89	3.32	-	934.6
AHQ-4-13-, 2458	R.GCVVTSVESNSNGR.K	1467.54464	2	4.52E-07	0.90	3.60	-	1147.6
AHQ-4-8, 1853	R.GCVVTSVESNSNGRK.S	1595.71755	2	1.24E-06	0.57	2.68	-	523.4
AHQ-4-8, 2068 - 2072	R.GCVVTSVESNSNGRK.S	1595.71755	2	5.92E-08	0.78	3.23	-	724.3
AHQ-4-13-, 2876	K.GSTLTSPCQDFGKR.M	1555.69502	2	5.66E-07	0.74	3.16	-	421.8
AHQ-4-8, 7010 - 7073	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	1.15E-08	0.97	5.14	-	1392.5
AHQ-4-8, 6869	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	3.47E-09	0.98	5.94	-	1607.1
AHQ-4-8, 7150 - 7223	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	1.49E-05	0.87	3.51	-	920.4
AHQ-4-10, 6373	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	4.22E-06	0.72	3.09	-	600.6
AHQ-4-8, 7233	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	3.41E-09	0.98	7.13	-	2341.2
AHQ-4-10, 6511	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	7.92E-11	0.98	8.31	-	2694.5
AHQ-4-13, 7032	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.05E-06	0.99	8.23	-	3055.4
AHQ-4-13-, 6876 - 6937	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.85E-10	0.98	7.45	-	2481.6
AHQ-4-9, 6716	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.04E-09	0.98	7.64	-	2120.9
AHQ-4-14-, 6777 - 6793	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.13E-07	0.99	7.40	-	3286.4
AHQ-4-12, 7077 - 7078	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	2.78E-15	0.98	7.52	-	2815.5
AHQ-4-11, 6829	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	3.51E-11	0.99	7.82	-	2921.9
AHQ-4-12, 5671 - 5737	R.LPETIDLGALYLSM*K.D	1680.98719	2	3.85E-07	0.95	4.39	-	1095.2
AHQ-4-8, 6542 - 6615	R.LPETIDLGALYLSMK.D	1664.98779	2	1.26E-07	0.97	4.75	-	1961.4
AHQ-4-8, 6445 - 6477	R.LPETIDLGALYLSMK.D	1664.98779	2	2.71E-04	0.98	4.68	-	2066.5
AHQ-4-8, 6355 - 6413	R.LPETIDLGALYLSMK.D	1664.98779	2	1.02E-04	0.97	3.73	-	2248.1
AHQ-4-13-, 5654	R.LPETIDLGALYLSM*K.D	1680.98719	2	6.77E-05	0.96	4.83	-	1258.0
AHQ-4-11, 6256	R.LPETIDLGALYLSMK.D	1664.98779	2	4.46E-04	0.97	4.06	-	2030.6
AHQ-4-1, 6053	R.LPETIDLGALYLSM*K.D	1680.98719	2	3.83E-05	0.93	4.29	-	1009.6
AHQ-4-10, 5947 - 5955	R.LPETIDLGALYLSMK.D	1664.98779	2	3.99E-06	0.98	5.47	-	2218.3
AHQ-4-8, 4811	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	3	6.00E-07	0.93	3.90	-	1246.5
AHQ-4-8, 4814 - 4885	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	2	1.15E-04	0.95	4.99	-	747.8
AHQ-4-12, 5334	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	3	8.24E-06	0.86	3.91	-	824.9
AHQ-4-8, 5042	R.NRQEGLM*IASSLLNEGYLQPAGDM*SK.S	2856.18262	3	1.11E-05	0.92	5.01	-	611.6
AHQ-4-10, 5509 - 5545	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	3.69E-07	0.97	4.93	-	1525.1
AHQ-4-10, 5279	R.NRQEGLMIASSLLNEGYLQPAGDM*SK.S	2840.18322	2	4.61E-06	0.89	4.05	-	494.0
AHQ-4-8, 5883 - 5953	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	2.07E-07	0.97	5.86	-	1235.3
AHQ-4-8, 6027	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	1.78E-04	0.83	3.58	-	569.6
AHQ-4-8, 5773 - 5818	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	3.98E-04	0.94	4.50	-	889.2
AHQ-4-12, 4506	K.QQDHFFQAAFLEER.D	1766.89390	2	2.60E-08	0.80	3.40	-	206.7
AHQ-4-12, 7133	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	2.70E-05	0.83	4.06	-	460.8
AHQ-4-12, 7130	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	2.40E-09	0.91	4.73	-	836.4
AHQ-4-8, 7306 - 7318	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	9.91E-11	0.92	4.57	-	881.7
AHQ-4-8, 7363	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	2.53E-07	0.89	4.60	-	433.0
AHQ-4-10, 6577	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	4.31E-08	0.90	4.86	-	623.6
AHQ-4-13-, 6917	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	2.54E-09	0.78	3.91	-	644.9
AHQ-4-8, 7391	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	9.30E-11	0.87	3.94	-	857.5
AHQ-4-10, 6587	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	9.59E-08	0.71	3.83	-	471.1
AHQ-4-14-, 6817	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	4.09E-10	0.91	4.44	-	768.7
AHQ-4-14-, 6819	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	2.25E-04	0.77	3.55	-	466.9
gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act				4.44E-15	95.91	1150.35	54.70	280757.4
AHQ-4-5, 5125 - 5197	R.AEAGVPAEFSIWTR.E	1534.69735	2	3.32E-07	0.71	3.11	-	328.2

AHQ-4-6, 1788	K.AEISFEDRK.D	1095.18763	2	2.96E-04	0.87	2.70	-	1259.8
AHQ-4-3, 2527 - 2601	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.07E-07	0.90	3.52	-	1122.6
AHQ-4-3, 2683	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.97E-06	0.96	3.79	-	1716.2
AHQ-4-4, 2518	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.32E-05	0.91	3.37	-	1264.6
AHQ-4-4, 2536	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	1.47E-04	0.07	2.14	-	119.7
AHQ-4-2, 2696 - 2706	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	6.91E-07	0.97	4.23	-	1916.4
AHQ-4-1, 2705	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	8.34E-09	0.95	3.71	-	1616.4
AHQ-4-5, 2393 - 2394	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.01E-06	0.93	3.72	-	1239.2
AHQ-4-2, 2530 - 2560	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	6.63E-09	0.91	3.59	-	1190.5
AHQ-4-1, 2862	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.09E-06	0.86	3.23	-	903.0
AHQ-4-4, 2526	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	8.34E-04	0.09	2.10	-	118.4
AHQ-4-14, 3541 - 3601	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.41E-06	0.78	3.34	-	660.9
AHQ-4-14, 4062 - 4120	K.AGNNMLLVGVHGPR.T	1435.68033	2	4.54E-06	0.86	3.16	-	858.1
AHQ-4-14, 3912	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.05E-07	0.73	2.54	-	737.7
AHQ-4-14, 4100 - 4116	K.AGNNMLLVGVHGPR.T	1435.68033	2	1.24E-04	0.87	3.83	-	840.5
AHQ-4-14, 3773 - 3850	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.09E-06	0.86	3.19	-	735.1
AHQ-4-14-, 2621 - 2689	K.AGNNM*LLVGVHGPR.T	1451.67973	3	6.72E-04	0.91	3.85	-	1528.7
AHQ-4-14, 3648 - 3708	K.AGNNM*LLVGVHGPR.T	1451.67973	2	2.03E-05	0.90	3.85	-	957.5
AHQ-4-14-, 3295 - 3357	K.AGNNMLLVGVHGPR.T	1435.68033	2	1.20E-08	0.80	3.01	-	710.2
AHQ-4-14, 3633	K.AGNNM*LLVGVHGPR.T	1451.67973	3	2.24E-05	0.78	3.03	-	1006.9
AHQ-4-14, 4350 - 4428	K.AGNNMLLVGVHGPR.T	1435.68033	2	1.85E-10	0.77	3.25	-	591.9
AHQ-4-14-, 3001 - 3005	K.AGNNMLLVGVHGPR.T	1435.68033	2	2.74E-06	0.89	3.66	-	843.8
AHQ-4-14-, 3002	K.AGNNMLLVGVHGPR.T	1435.68033	3	4.27E-05	0.93	3.85	-	1563.2
AHQ-4-14-, 2617 - 2694	K.AGNNM*LLVGVHGPR.T	1451.67973	2	7.08E-06	0.80	3.31	-	623.9
AHQ-4-1, 1746 - 1805	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	7.32E-04	0.64	2.74	-	638.3
AHQ-4-2, 2175 - 2182	K.AGVAPLQVK.V	883.07036	2	1.43E-05	0.82	2.69	-	699.2
AHQ-4-1, 2385	K.AGVAPLQVK.V	883.07036	2	9.81E-04	0.87	2.96	-	731.3
AHQ-4-1, 7270 - 7329	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	4.16E-04	0.96	4.91	-	1804.2
AHQ-4-2, 7588 - 7656	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	1.52E-07	0.91	4.16	-	1165.7
AHQ-4-2, 2518 - 2546	K.AHVVPCFDASK.V	1232.39073	2	8.09E-08	0.67	2.79	-	543.8
AHQ-4-1, 2717 - 2750	K.AHVVPCFDASK.V	1232.39073	2	7.41E-04	0.66	2.53	-	520.9
AHQ-4-4, 2510	K.AHVVPCFDASK.V	1232.39073	2	6.20E-04	0.81	2.62	-	719.0
AHQ-4-1, 6489 - 6569	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.44E-15	0.87	4.62	-	531.2
AHQ-4-5, 6149 - 6155	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.45E-11	0.94	5.48	-	1101.3
AHQ-4-4, 6458 - 6526	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.83E-13	0.96	6.31	-	963.4
AHQ-4-3, 6533 - 6559	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.53E-09	0.93	5.21	-	804.7
AHQ-4-6, 6299	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.05E-08	0.90	4.95	-	447.1
AHQ-4-6, 6186	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.78E-11	0.92	5.04	-	589.3
AHQ-4-8, 6134	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.77E-09	0.69	3.63	-	463.2
AHQ-4-5, 6431	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.61E-14	0.87	4.43	-	546.4
AHQ-4-5, 6261 - 6330	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.62E-12	0.90	4.97	-	505.8
AHQ-4-9, 5631 - 5635	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.48E-07	0.83	4.40	-	558.9
AHQ-4-2, 6520 - 6602	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.27E-14	0.96	6.06	-	829.3
AHQ-4-7, 6222	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.12E-10	0.81	3.92	-	685.5
AHQ-4-2, 6375 - 6448	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.89E-12	0.95	5.66	-	885.9
AHQ-4-3, 6627	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.59E-06	0.91	5.02	-	602.2
AHQ-4-1, 6365 - 6422	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.52E-08	0.95	5.02	-	1132.6
AHQ-4-3, 1447	R.ALTQTGGPHVK.A	1109.26067	1	2.72E-04	0.04	1.82	-	224.2
AHQ-4-3, 3285	R.ANLPQSFQVDTSK.A	1435.56409	1	1.21E-10	0.72	3.56	-	378.3
AHQ-4-3, 3503	R.ANLPQSFQVDTSK.A	1435.56409	1	2.12E-05	0.07	1.97	-	240.4
AHQ-4-4, 3264 - 3266	R.ANLPQSFQVDTSK.A	1435.56409	1	1.11E-04	0.20	2.10	-	313.1
AHQ-4-5, 3115	R.ANLPQSFQVDTSK.A	1435.56409	1	4.78E-08	0.71	2.98	-	386.6
AHQ-4-1, 3511 - 3589	R.ANLPQSFQVDTSK.A	1435.56409	2	3.12E-04	0.78	3.27	-	472.7
AHQ-4-8, 2813 - 2858	R.ANLPQSFQVDTSK.A	1435.56409	2	1.54E-07	0.87	3.08	-	616.7
AHQ-4-7, 2985 - 2989	R.ANLPQSFQVDTSK.A	1435.56409	2	3.71E-10	0.90	3.63	-	646.4
AHQ-4-2, 3270	R.ANLPQSFQVDTSK.A	1435.56409	1	4.38E-06	0.77	3.37	-	419.6
AHQ-4-2, 3518	R.ANLPQSFQVDTSK.A	1435.56409	2	4.63E-08	0.90	3.22	-	695.3
AHQ-4-6, 3044 - 3046	R.ANLPQSFQVDTSK.A	1435.56409	1	1.32E-06	0.54	2.55	-	422.4
AHQ-4-1, 3409	R.ANLPQSFQVDTSK.A	1435.56409	1	7.90E-05	0.45	2.46	-	392.4
AHQ-4-2, 3208 - 3282	R.ANLPQSFQVDTSK.A	1435.56409	2	7.45E-08	0.77	3.04	-	476.1
AHQ-4-2, 3526	R.ANLPQSFQVDTSK.A	1435.56409	1	3.18E-06	0.67	3.18	-	391.7
AHQ-4-5, 3083 - 3117	R.ANLPQSFQVDTSK.A	1435.56409	2	1.03E-09	0.84	3.54	-	439.7
AHQ-4-4, 3480	R.ANLPQSFQVDTSK.A	1435.56409	1	1.35E-05	0.37	2.17	-	314.7
AHQ-4-6, 3039 - 3047	R.ANLPQSFQVDTSK.A	1435.56409	2	7.92E-11	0.83	3.62	-	505.5
AHQ-4-2, 4672	R.ANLPQSFQVDTSKAGVAPLQVK.V	2299.61185	3	1.38E-08	0.80	3.24	-	663.3
AHQ-4-6, 3104	R.APSVANVGSHCDLSLK.I	1656.84249	2	4.81E-04	0.86	4.05	-	441.5
AHQ-4-5, 3138	R.APSVANVGSHCDLSLK.I	1656.84249	2	3.62E-06	0.93	4.23	-	908.1
AHQ-4-4, 1636	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	3.52E-04	0.84	3.83	-	319.6
AHQ-4-1, 3787	R.AWGPGLEGGVVGK.S	1227.39403	2	1.29E-05	0.93	3.81	-	936.7
AHQ-4-4, 3614	R.AWGPGLEGGVVGK.S	1227.39403	2	1.10E-04	0.88	3.78	-	665.4
AHQ-4-3, 3625	R.AWGPGLEGGVVGK.S	1227.39403	2	2.55E-08	0.93	3.91	-	981.9
AHQ-4-1, 3769 - 3773	R.AWGPGLEGGVVGK.S	1227.39403	2	1.12E-06	0.93	3.59	-	889.6
AHQ-4-6, 3271 - 3342	R.AWGPGLEGGVVGK.S	1227.39403	2	9.25E-07	0.88	3.34	-	824.2
AHQ-4-5, 3394	R.AWGPGLEGGVVGK.S	1227.39403	2	4.62E-05	0.85	3.42	-	679.2
AHQ-4-6, 3344 - 3346	R.AWGPGLEGGVVGK.S	1227.39403	1	4.54E-04	0.22	1.97	-	544.4
AHQ-4-2, 3730 - 3806	R.AWGPGLEGGVVGK.S	1227.39403	2	7.82E-06	0.91	3.65	-	922.7
AHQ-4-2, 3642 - 3715	R.AWGPGLEGGVVGK.S	1227.39403	2	1.14E-05	0.88	3.61	-	717.5
AHQ-4-2, 3118 - 3186	R.AYGPGIEPTGNMVK.K	1434.64274	2	1.57E-05	0.65	3.33	-	425.2
AHQ-4-5, 2971	R.AYGPGIEPTGNMVK.K	1434.64274	1	5.08E-04	0.46	2.51	-	381.1
AHQ-4-2, 2523	R.AYGPGIEPTGNM*VK.K	1450.64214	2	3.13E-04	0.60	2.70	-	379.5
AHQ-4-6, 3183	R.AYGPGIEPTGNMVK.K	1434.64274	2	3.27E-04	0.85	3.30	-	748.6
AHQ-4-3, 3183	R.AYGPGIEPTGNMVK.K	1434.64274	1	7.15E-04	0.75	3.25	-	416.0
AHQ-4-2, 3368 - 3448	R.AYGPGIEPTGNMVK.K	1434.64274	2	5.12E-04	0.69	2.96	-	604.1
AHQ-4-3, 3444	R.AYGPGIEPTGNMVK.K	1434.64274	2	7.38E-05	0.70	2.78	-	496.8
AHQ-4-1, 2834	R.AYGPGIEPTGNM*VK.K	1450.64214	2	1.16E-04	0.72	2.92	-	467.4
AHQ-4-7, 2858 - 2863	R.AYGPGIEPTGNMVK.K	1434.64274	2	6.09E-04	0.51	3.20	-	295.8
AHQ-4-4, 3090 - 3166	R.AYGPGIEPTGNMVK.K	1434.64274	2	4.24E-06	0.85	4.04	-	405.5
AHQ-4-3, 6361 - 6431	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	3.71E-08	0.92	4.32	-	627.7
AHQ-4-6, 6098 - 6134	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	3.71E-06	0.93	4.77	-	555.7
AHQ-4-5, 6254	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.79E-05	0.77	3.50	-	394.9
AHQ-4-1, 6263	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	7.83E-05	0.76	3.15	-	528.1
AHQ-4-2, 6194	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.99E-08	0.93	3.93	-	915.3
AHQ-4-2, 6354 - 6422	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	5.55E-08	0.91	3.81	-	748.4
AHQ-4-2, 6376	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	4.55E-11	0.97	5.41	-	2004.0
AHQ-4-1, 6283 - 6285	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.36E-09	0.97	6.11	-	1512.9
AHQ-4-4, 6346 - 6414	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.15E-07	0.86	3.74	-	605.6
AHQ-4-3, 6593	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	2.76E-05	0.83	3.90	-	406.2
AHQ-4-2, 6583 - 6614	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	9.53E-05	0.55	3.12	-	358.1
AHQ-4-3, 6675 - 6741	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	1.92E-06	0.75	4.14	-	368.0
AHQ-4-3, 2940 - 2941	K.CSGPGLSPGMVR.A	1219.41699	2	8.05E-06	0.61	2.59	-	501.4
AHQ-4-2, 2926 - 2934	K.CSGPGLSPGMVR.A	1219.41699	2	4.08E-06	0.75	3.05	-	479.4
AHQ-4-5, 4733 - 4747	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	8.17E-04	0.93	5.41	-	524.2
AHQ-4-2, 5087 - 5088	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	1.47E-05	0.61	3.15	-	291.2
AHQ-4-3, 5003 - 5029	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	4.93E-04	0.90	4.25	-	617.8
AHQ-4-2, 5450 - 5518	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	2.03E-06	0.88	4.23	-	481.8
AHQ-4-1, 5589	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	1.39E-08	0.97	5.37	-	1152.6
AHQ-4-3, 5496	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	4.98E-06	0.67	2.83	-	482.1

AHQ-4-2, 5003 - 5076	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	2.42E-09	0.93	5.22	-	562.1
AHQ-4-1, 5062 - 5063	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	2.18E-04	0.88	4.13	-	490.7
AHQ-4-1, 5535 - 5601	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	4.17E-06	0.92	4.72	-	787.0
AHQ-4-5, 5213 - 5230	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	1.85E-04	0.90	4.09	-	680.3
AHQ-4-4, 5463	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	1.45E-04	0.85	2.99	-	747.7
AHQ-4-2, 5496	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	6.47E-08	0.96	4.71	-	1217.5
AHQ-4-5, 5229	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	7.01E-04	0.91	4.24	-	801.6
AHQ-4-2, 5011 - 5014	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	9.28E-08	0.91	4.40	-	538.5
AHQ-4-2, 5516	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	8.82E-05	0.66	3.54	-	450.7
AHQ-4-1, 4105	R.DAEM*PATEKDLAEDAPWK.K	2034.18987	2	2.53E-05	0.71	3.33	-	503.5
AHQ-4-2, 4016 - 4038	R.DAEM*PATEKDLAEDAPWK.K	2034.18987	2	7.97E-05	0.89	3.85	-	525.3
AHQ-4-3, 4659	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	6.21E-05	0.62	2.69	-	561.2
AHQ-4-2, 4614 - 4684	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	8.49E-04	0.81	3.14	-	814.0
AHQ-4-2, 4680	R.DAEMPATEKDLAEDAPWK.K	2018.19047	3	2.38E-05	0.73	3.41	-	549.0
AHQ-4-1, 4693	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	4.65E-06	0.87	3.83	-	851.1
AHQ-4-2, 4156	R.DAEMPATEKDLAEDAPWKK.I	2146.36338	3	3.09E-06	0.83	3.76	-	500.9
AHQ-4-2, 4158	R.DAEMPATEKDLAEDAPWKK.I	2146.36338	2	4.84E-05	0.81	3.56	-	581.9
AHQ-4-3, 4084	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	4.13E-05	0.89	4.01	-	1026.4
AHQ-4-5, 3917 - 3986	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	9.48E-06	0.94	4.76	-	1046.2
AHQ-4-4, 4031 - 4050	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.98E-04	0.92	4.09	-	1350.4
AHQ-4-10, 3632 - 3688	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	5.29E-04	0.44	2.83	-	637.8
AHQ-4-1, 4081 - 4150	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	5.26E-07	0.93	4.20	-	1328.7
AHQ-4-1, 5018	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	1.41E-05	0.89	3.63	-	1204.0
AHQ-4-2, 4687 - 4712	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.13E-06	0.93	4.35	-	1108.9
AHQ-4-1, 4535	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.34E-06	0.91	3.94	-	1106.7
AHQ-4-3, 4691	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.14E-11	0.93	4.52	-	1082.4
AHQ-4-10, 3896	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.58E-05	0.83	3.60	-	762.2
AHQ-4-2, 4752	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	7.82E-06	0.83	3.97	-	890.4
AHQ-4-4, 4655	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.69E-07	0.90	3.57	-	914.0
AHQ-4-1, 4533 - 4598	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	7.75E-08	0.96	4.67	-	1553.3
AHQ-4-4, 4376 - 4426	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.91E-08	0.95	4.54	-	1338.4
AHQ-4-5, 4122 - 4197	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.21E-07	0.96	4.54	-	1488.5
AHQ-4-8, 3830	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.84E-06	0.89	4.19	-	867.3
AHQ-4-2, 4478 - 4487	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	5.04E-08	0.88	3.72	-	1088.1
AHQ-4-7, 4074	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.23E-06	0.92	3.99	-	1105.9
AHQ-4-2, 4471 - 4542	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.77E-09	0.93	4.32	-	1173.7
AHQ-4-3, 4533 - 4603	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.54E-06	0.85	3.67	-	927.4
AHQ-4-11, 4109 - 4182	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.15E-04	0.62	3.20	-	566.0
AHQ-4-2, 4972	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	7.44E-06	0.96	4.20	-	1511.5
AHQ-4-1, 4675 - 4745	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.98E-06	0.91	3.92	-	1191.5
AHQ-4-1, 4411 - 4490	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.84E-05	0.83	3.09	-	871.4
AHQ-4-2, 4598 - 4610	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.41E-07	0.95	4.90	-	1185.3
AHQ-4-3, 4439 - 4507	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.59E-06	0.96	5.08	-	1288.4
AHQ-4-3, 4453 - 4524	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	1.36E-07	0.89	3.44	-	1238.0
AHQ-4-9, 3715	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.82E-06	0.90	4.01	-	1034.6
AHQ-4-6, 4072 - 4122	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.04E-04	0.92	4.17	-	1214.0
AHQ-4-5, 4539 - 4610	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	5.57E-10	0.95	4.68	-	1306.2
AHQ-4-5, 4230	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.62E-08	0.88	3.50	-	821.1
AHQ-4-3, 4680	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.37E-04	0.90	3.28	-	1376.6
AHQ-4-1, 4661	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.58E-10	0.93	4.57	-	1024.0
AHQ-4-2, 1844	R.DAPQDFHPDR.V	1198.22650	2	5.36E-08	0.59	2.55	-	387.7
AHQ-4-1, 2002 - 2011	R.DAPQDFHPDR.V	1198.22650	2	5.35E-07	0.87	3.55	-	661.5
AHQ-4-2, 5024	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	9.31E-05	0.64	3.42	-	322.0
AHQ-4-6, 4782	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.14E-05	0.79	3.83	-	413.1
AHQ-4-5, 4913 - 4985	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.31E-06	0.91	4.26	-	703.0
AHQ-4-6, 4883	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	7.48E-06	0.84	3.51	-	610.3
AHQ-4-1, 4914 - 4937	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	5.12E-05	0.88	4.39	-	532.9
AHQ-4-7, 4887 - 4911	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	4.73E-05	0.89	4.49	-	576.3
AHQ-4-4, 4966 - 5042	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.59E-07	0.82	4.17	-	494.3
AHQ-4-5, 5009 - 5077	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.01E-06	0.92	4.58	-	758.5
AHQ-4-4, 2339	K.DKGEYTLVVK.W	1152.32223	1	3.83E-04	0.40	2.77	-	415.4
AHQ-4-14, 3288 - 3348	K.DKGEYTLVVK.W	1152.32223	2	2.39E-05	0.81	3.23	-	476.8
AHQ-4-14-, 2305 - 2377	K.DKGEYTLVVK.W	1152.32223	2	5.90E-05	0.85	3.29	-	709.5
AHQ-4-14, 3190 - 3566	K.DKGEYTLVVK.W	1152.32223	1	1.87E-06	0.34	2.57	-	381.0
AHQ-4-14-, 2306 - 2381	K.DKGEYTLVVK.W	1152.32223	1	3.20E-04	0.22	2.27	-	406.9
AHQ-4-2, 3387 - 3462	K.DNGNGTYSCSYVPR.K	1591.64109	2	2.93E-07	0.86	3.06	-	933.9
AHQ-4-3, 3253	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.82E-06	0.89	3.47	-	1028.2
AHQ-4-2, 3092	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	7.53E-05	0.93	3.75	-	1045.0
AHQ-4-5, 2823	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.76E-04	0.64	2.72	-	494.8
AHQ-4-3, 3087 - 3164	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.65E-06	0.87	3.58	-	720.8
AHQ-4-2, 3259	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.72E-05	0.91	4.25	-	707.6
AHQ-4-1, 3213 - 3281	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.55E-09	0.95	4.38	-	1010.5
AHQ-4-3, 3011 - 3079	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	8.45E-06	0.64	3.20	-	491.4
AHQ-4-6, 3118 - 3186	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	2.77E-08	0.96	4.20	-	1545.2
AHQ-4-5, 3907	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	1.90E-04	0.58	2.89	-	266.5
AHQ-4-4, 3382	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	8.57E-10	0.84	3.85	-	396.7
AHQ-4-6, 3142	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	1.92E-08	0.81	3.84	-	346.9
AHQ-4-7, 3082	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	9.11E-09	0.80	3.49	-	371.2
AHQ-4-3, 3409	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.63E-05	0.92	3.66	-	1216.8
AHQ-4-5, 3177 - 3245	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.95E-07	0.95	4.38	-	1211.9
AHQ-4-1, 3681	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	6.12E-08	0.92	3.57	-	1261.7
AHQ-4-7, 3029 - 3105	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.41E-05	0.85	3.10	-	1018.4
AHQ-4-9, 2864	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	2.53E-05	0.72	3.62	-	314.8
AHQ-4-1, 3467 - 3505	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	2.03E-06	0.94	4.38	-	1087.9
AHQ-4-2, 2456 - 2534	R.EATTEFSVDAR.A	1226.27493	2	3.32E-05	0.86	3.08	-	786.4
AHQ-4-2, 6430 - 6498	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.33E-08	0.93	4.88	-	906.2
AHQ-4-3, 6523 - 6603	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	6.77E-07	0.91	4.88	-	731.6
AHQ-4-2, 6566 - 6634	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.60E-07	0.95	5.63	-	828.0
AHQ-4-4, 6434 - 6506	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.98E-08	0.96	6.33	-	1013.1
AHQ-4-4, 6574 - 6587	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	8.23E-08	0.91	4.87	-	588.8
AHQ-4-1, 6469 - 6533	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.42E-05	0.90	4.60	-	782.1
AHQ-4-1, 6381 - 6449	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	7.70E-08	0.95	5.57	-	1005.8
AHQ-4-5, 6477	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.10E-05	0.94	5.71	-	727.4
AHQ-4-6, 6211 - 6282	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	7.28E-07	0.94	5.40	-	739.3
AHQ-4-5, 6331 - 6410	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.17E-05	0.88	4.25	-	781.3
AHQ-4-6, 4939	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.55E-04	0.80	3.50	-	562.2
AHQ-4-2, 5290 - 5312	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.97E-09	0.93	4.44	-	1045.3
AHQ-4-2, 5204 - 5223	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.87E-11	0.92	3.87	-	1098.8
AHQ-4-9, 4472 - 4487	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	6.94E-08	0.96	4.99	-	1260.1
AHQ-4-7, 4942	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.33E-04	0.69	3.30	-	553.3
AHQ-4-2, 4928 - 4940	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.93E-10	0.83	3.43	-	639.2
AHQ-4-4, 5166 - 5239	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.11E-08	0.89	3.57	-	776.3
AHQ-4-3, 5204 - 5275	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.02E-07	0.92	3.64	-	952.4
AHQ-4-5, 5045	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.97E-06	0.90	4.10	-	899.0
AHQ-4-10, 4537	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.21E-07	0.76	3.09	-	737.9
AHQ-4-1, 5267	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.15E-05	0.91	3.65	-	1231.1
AHQ-4-1, 5185 - 5253	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.07E-06	0.90	3.70	-	999.3

AHQ-4-8, 4649 - 4722	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	7.24E-05	0.82	3.31	-	757.4
AHQ-4-5, 3719	R.ENGVYLIDVK.F	1150.30633	2	1.90E-04	0.82	2.89	-	718.0
AHQ-4-7, 3885	R.ENGVYLIDVK.F	1150.30633	1	2.36E-04	0.25	2.11	-	365.1
AHQ-4-3, 4029	R.ENGVYLIDVK.F	1150.30633	1	2.19E-05	0.12	2.02	-	219.0
AHQ-4-1, 4082	R.ENGVYLIDVK.F	1150.30633	2	9.53E-04	0.58	2.58	-	426.4
AHQ-4-3, 3441 - 3451	K.FADQHVPGSPFSVK.V	1516.68203	2	4.62E-06	0.81	3.20	-	502.3
AHQ-4-4, 3415 - 3440	K.FADQHVPGSPFSVK.V	1516.68203	2	4.94E-07	0.80	3.21	-	554.8
AHQ-4-7, 3043	K.FADQHVPGSPFSVK.V	1516.68203	2	2.57E-07	0.90	3.55	-	738.9
AHQ-4-12, 3311	K.FADQHVPGSPFSVK.V	1516.68203	2	3.78E-04	0.80	3.19	-	360.1
AHQ-4-6, 3128 - 3131	K.FADQHVPGSPFSVK.V	1516.68203	3	7.37E-06	0.91	3.90	-	1056.7
AHQ-4-13-, 3429 - 3430	K.FADQHVPGSPFSVK.V	1516.68203	2	2.78E-05	0.85	3.52	-	534.0
AHQ-4-5, 3279	K.FADQHVPGSPFSVK.V	1516.68203	2	2.61E-04	0.65	2.52	-	435.4
AHQ-4-13, 3547 - 3554	K.FADQHVPGSPFSVK.V	1516.68203	2	3.03E-05	0.84	3.09	-	588.2
AHQ-4-8, 2829	K.FADQHVPGSPFSVK.V	1516.68203	3	3.25E-05	0.92	3.75	-	1309.2
AHQ-4-1, 3601	K.FADQHVPGSPFSVK.V	1516.68203	2	2.25E-10	0.86	3.04	-	681.2
AHQ-4-6, 3114 - 3146	K.FADQHVPGSPFSVK.V	1516.68203	2	8.84E-08	0.83	3.30	-	550.6
AHQ-4-12, 5409	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.97E-06	0.96	4.63	-	1340.2
AHQ-4-4, 5598 - 5635	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	7.40E-08	0.96	5.59	-	1134.5
AHQ-4-2, 5784 - 5852	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.68E-05	0.94	4.44	-	769.7
AHQ-4-7, 5297 - 5299	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	8.85E-06	0.96	5.29	-	892.5
AHQ-4-6, 5359	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.70E-08	0.97	5.20	-	1527.7
AHQ-4-6, 5342	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.46E-04	0.91	4.40	-	941.2
AHQ-4-3, 5625 - 5687	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.00E-04	0.95	4.48	-	1301.8
AHQ-4-3, 5715 - 5784	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.56E-08	0.95	5.58	-	945.2
AHQ-4-11, 5201	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.41E-09	0.95	5.11	-	939.4
AHQ-4-3, 5623 - 5647	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.34E-08	0.96	5.43	-	1391.1
AHQ-4-8, 4979	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.58E-07	0.94	5.91	-	699.9
AHQ-4-11, 5192 - 5193	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.82E-06	0.85	3.96	-	754.7
AHQ-4-1, 5703 - 5725	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.26E-05	0.95	4.98	-	808.3
AHQ-4-8, 5002	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.76E-05	0.94	4.29	-	1236.2
AHQ-4-4, 5583 - 5655	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.01E-09	0.93	5.26	-	774.3
AHQ-4-2, 5694	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	7.51E-05	0.96	5.09	-	1091.8
AHQ-4-7, 5278 - 5293	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.85E-05	0.95	5.57	-	1105.6
AHQ-4-3, 5800 - 5811	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	8.12E-06	0.97	6.16	-	890.2
AHQ-4-13-, 5322	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.68E-05	0.95	5.25	-	1115.6
AHQ-4-5, 5393	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	7.76E-08	0.97	5.36	-	1343.2
AHQ-4-2, 5595 - 5619	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	5.91E-06	0.91	4.09	-	991.8
AHQ-4-1, 5843	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.27E-10	0.98	5.93	-	1476.8
AHQ-4-2, 5624 - 5695	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.20E-05	0.90	4.54	-	694.2
AHQ-4-1, 5670 - 5737	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.88E-12	0.94	5.21	-	845.3
AHQ-4-6, 4935 - 4936	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	2.62E-06	0.85	3.91	-	505.5
AHQ-4-5, 4983 - 5065	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	2.13E-04	0.90	3.72	-	707.9
AHQ-4-1, 3929	K.FNGTHIPGSPFK.I	1302.46259	2	1.03E-07	0.54	2.56	-	528.1
AHQ-4-5, 3521	K.FNGTHIPGSPFK.I	1302.46259	2	9.00E-06	0.89	3.32	-	719.7
AHQ-4-5, 3721	K.FNGTHIPGSPFK.I	1302.46259	2	4.61E-04	0.57	2.82	-	394.2
AHQ-4-5, 3705 - 3715	K.FNGTHIPGSPFK.I	1302.46259	1	2.68E-04	0.36	1.93	-	468.6
AHQ-4-5, 3411	K.FNGTHIPGSPFK.I	1302.46259	2	2.51E-04	0.84	3.33	-	540.9
AHQ-4-6, 3359	K.FNGTHIPGSPFK.I	1302.46259	2	8.46E-05	0.86	3.23	-	779.0
AHQ-4-1, 3758 - 3834	K.FNGTHIPGSPFK.I	1302.46259	2	4.65E-04	0.63	2.98	-	370.8
AHQ-4-5, 2683 - 2703	R.FVPAEMGTHTVSVK.Y	1503.74821	2	6.24E-10	0.90	3.82	-	599.0
AHQ-4-6, 2704	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.05E-07	0.88	3.36	-	706.1
AHQ-4-4, 2914 - 2922	R.FVPAEMGTHTVSVK.Y	1503.74821	2	4.36E-05	0.80	3.44	-	396.7
AHQ-4-3, 2287 - 2341	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	8.39E-04	0.85	3.64	-	368.8
AHQ-4-1, 3113	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.40E-05	0.90	3.25	-	647.3
AHQ-4-7, 2577	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.05E-05	0.90	3.79	-	574.1
AHQ-4-2, 6176 - 6219	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	2.63E-04	0.88	4.42	-	533.6
AHQ-4-2, 3478 - 3551	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.73E-05	0.86	3.93	-	609.7
AHQ-4-3, 3328 - 3399	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.45E-06	0.93	4.16	-	1004.4
AHQ-4-2, 3267 - 3339	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	9.99E-07	0.92	4.09	-	831.9
AHQ-4-8, 2823	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.39E-05	0.77	3.13	-	687.4
AHQ-4-4, 3323	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.22E-05	0.80	2.70	-	896.7
AHQ-4-2, 3410 - 3414	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	6.43E-04	0.92	4.02	-	980.9
AHQ-4-5, 3131 - 3210	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.23E-07	0.92	4.15	-	755.2
AHQ-4-2, 3718 - 3763	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	7.33E-07	0.83	3.73	-	673.8
AHQ-4-1, 3453 - 3521	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.19E-05	0.90	3.90	-	693.9
AHQ-4-6, 3078	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.10E-05	0.82	3.33	-	651.9
AHQ-4-1, 3575	K.GKLDVQFSGLTK.G	1293.49392	2	1.32E-06	0.93	3.73	-	1112.0
AHQ-4-3, 3317 - 3395	K.GKLDVQFSGLTK.G	1293.49392	2	6.55E-05	0.88	3.61	-	794.0
AHQ-4-2, 2128 - 2142	K.GTVEPQLEAR.G	1100.20741	2	6.30E-04	0.82	3.08	-	559.5
AHQ-4-7, 1914	K.GTVEPQLEAR.G	1100.20741	2	2.35E-04	0.77	2.89	-	438.3
AHQ-4-1, 2294	K.GTVEPQLEAR.G	1100.20741	2	1.62E-05	0.82	2.91	-	583.9
AHQ-4-6, 1951 - 1955	K.GTVEPQLEAR.G	1100.20741	2	1.57E-05	0.88	3.27	-	653.2
AHQ-4-5, 4915	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.70E-07	0.97	5.18	-	1351.5
AHQ-4-5, 5318	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	4.98E-06	0.97	5.07	-	1329.1
AHQ-4-2, 5206 - 5276	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	7.76E-06	0.96	4.66	-	1492.4
AHQ-4-4, 5144	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.95E-04	0.94	4.71	-	836.5
AHQ-4-4, 5554	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	1.92E-05	0.97	4.76	-	1626.3
AHQ-4-1, 5329	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	2.80E-05	0.63	3.50	-	483.7
AHQ-4-3, 5201 - 5273	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	7.03E-07	0.94	4.62	-	993.0
AHQ-4-2, 5579	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	9.46E-06	0.97	5.30	-	1392.4
AHQ-4-2, 5215	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	2.78E-05	0.82	3.91	-	844.5
AHQ-4-1, 5317	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	8.62E-05	0.86	3.57	-	807.3
AHQ-4-3, 5589 - 5591	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	9.66E-06	0.97	4.73	-	1514.9
AHQ-4-1, 5715	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	4.08E-07	0.97	5.22	-	1116.8
AHQ-4-3, 5295	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	6.43E-05	0.93	4.29	-	917.7
AHQ-4-6, 3966 - 3968	R.IANLQTDLSDGLR.L	1416.56231	2	1.40E-06	0.95	4.33	-	1071.2
AHQ-4-11, 3958	R.IANLQTDLSDGLR.L	1416.56231	2	1.45E-06	0.94	4.21	-	1026.9
AHQ-4-13-, 4152	R.IANLQTDLSDGLR.L	1416.56231	2	2.41E-04	0.90	3.66	-	942.6
AHQ-4-1, 3966	R.IANLQTDLSDGLR.L	1416.56231	2	5.32E-06	0.94	3.87	-	1214.0
AHQ-4-4, 4242	R.IANLQTDLSDGLR.L	1416.56231	2	4.96E-08	0.89	3.77	-	723.2
AHQ-4-10, 3792	R.IANLQTDLSDGLR.L	1416.56231	2	2.50E-07	0.88	3.58	-	849.0
AHQ-4-1, 4063	R.IANLQTDLSDGLR.L	1416.56231	2	4.65E-07	0.92	4.04	-	904.7
AHQ-4-4, 3848	R.IANLQTDLSDGLR.L	1416.56231	2	5.84E-04	0.87	3.12	-	1048.6
AHQ-4-9, 3596	R.IANLQTDLSDGLR.L	1416.56231	2	7.03E-05	0.94	3.73	-	1054.3
AHQ-4-7, 3935	R.IANLQTDLSDGLR.L	1416.56231	2	7.06E-05	0.72	2.74	-	934.7
AHQ-4-2, 3998 - 4068	R.IANLQTDLSDGLR.L	1416.56231	2	2.01E-06	0.93	4.02	-	934.2
AHQ-4-1, 4566	R.IANLQTDLSDGLR.L	1416.56231	2	7.79E-05	0.93	3.55	-	1112.0
AHQ-4-3, 3876	R.IANLQTDLSDGLR.L	1416.56231	2	7.33E-05	0.52	2.51	-	738.4
AHQ-4-3, 4307	R.IANLQTDLSDGLR.L	1416.56231	1	2.75E-06	0.59	3.10	-	266.8
AHQ-4-3, 4292	R.IANLQTDLSDGLR.L	1416.56231	1	5.27E-04	0.09	2.35	-	144.5
AHQ-4-5, 4029	R.IANLQTDLSDGLR.L	1416.56231	2	1.82E-07	0.92	3.65	-	1014.4
AHQ-4-3, 4289 - 4360	R.IANLQTDLSDGLR.L	1416.56231	2	6.70E-09	0.93	3.78	-	970.9
AHQ-4-1, 4377 - 4393	R.IANLQTDLSDGLR.L	1416.56231	2	9.35E-06	0.88	3.86	-	673.5
AHQ-4-2, 4463 - 4535	R.IANLQTDLSDGLR.L	1416.56231	2	9.23E-07	0.77	2.59	-	736.6
AHQ-4-3, 4560	R.IANLQTDLSDGLR.L	1416.56231	2	5.65E-05	0.87	3.42	-	819.5
AHQ-4-2, 3898	R.IANLQTDLSDGLR.L	1416.56231	2	2.04E-05	0.90	3.75	-	827.2
AHQ-4-12, 4089	R.IANLQTDLSDGLR.L	1416.56231	2	2.51E-06	0.92	4.25	-	923.7

AHQ-4-13, 4280 - 4293	R.IANLQTDLSDGLR.L	1416.56231	2	9.63E-05	0.86	3.43	-	859.4
AHQ-4-1, 5681 - 5687	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.71E-06	0.97	4.84	-	1926.6
AHQ-4-5, 5414 - 5491	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.18E-09	0.98	5.44	-	2259.5
AHQ-4-3, 4236 - 4265	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	6.20E-06	0.96	4.60	-	1520.6
AHQ-4-11, 5180 - 5184	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.73E-09	0.89	3.96	-	937.2
AHQ-4-4, 5536 - 5614	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.21E-09	0.96	4.91	-	1520.2
AHQ-4-1, 4223 - 4294	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.06E-04	0.97	4.87	-	1746.0
AHQ-4-5, 5430	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	2.61E-08	0.93	4.75	-	844.2
AHQ-4-5, 4005 - 4082	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.01E-05	0.97	4.72	-	1973.9
AHQ-4-7, 5285 - 5353	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.77E-10	0.98	6.45	-	1948.0
AHQ-4-6, 4910	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.15E-04	0.89	3.97	-	699.6
AHQ-4-4, 4167 - 4212	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	6.68E-04	0.97	4.75	-	1565.2
AHQ-4-7, 3922	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.88E-06	0.96	4.86	-	1572.5
AHQ-4-6, 5350	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.49E-08	0.95	4.81	-	1161.7
AHQ-4-6, 3934 - 4008	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	3.10E-06	0.96	4.64	-	1253.5
AHQ-4-8, 5057	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	7.80E-06	0.92	4.02	-	1018.0
AHQ-4-5, 5563	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	8.56E-06	0.84	4.27	-	540.5
AHQ-4-4, 5607	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.75E-11	0.98	5.62	-	1750.1
AHQ-4-1, 2613	K.IVGPSGAAVPCK.V	1157.36530	2	3.74E-08	0.82	3.03	-	604.5
AHQ-4-2, 2476	K.IVGPSGAAVPCK.V	1157.36530	2	2.70E-09	0.93	4.20	-	941.5
AHQ-4-5, 2339	K.IVGPSGAAVPCK.V	1157.36530	2	7.06E-05	0.48	2.50	-	482.6
AHQ-4-4, 2463 - 2467	K.IVGPSGAAVPCK.V	1157.36530	2	2.00E-07	0.90	4.05	-	695.2
AHQ-4-3, 2465	K.IVGPSGAAVPCK.V	1157.36530	2	6.46E-09	0.75	2.69	-	693.6
AHQ-4-4, 4204 - 4218	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	9.54E-06	0.95	5.71	-	1284.8
AHQ-4-3, 4248 - 4327	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	5.51E-09	0.96	5.27	-	1717.8
AHQ-4-2, 4256 - 4326	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	7.40E-04	0.93	4.55	-	1384.9
AHQ-4-2, 4402	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	7.94E-06	0.87	3.68	-	551.3
AHQ-4-4, 4202 - 4270	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	4.41E-06	0.79	3.17	-	600.5
AHQ-4-2, 4258 - 4334	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	4.68E-05	0.94	4.50	-	834.8
AHQ-4-3, 4251 - 4319	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.45E-06	0.94	4.97	-	527.8
AHQ-4-5, 4025 - 4026	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	7.38E-10	0.94	4.64	-	1546.0
AHQ-4-1, 4317 - 4385	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	7.95E-07	0.89	4.65	-	905.7
AHQ-4-5, 4379 - 4382	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	1.34E-04	0.70	2.63	-	842.3
AHQ-4-4, 4315	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	8.12E-04	0.85	3.79	-	481.6
AHQ-4-9, 3621	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.26E-06	0.83	3.46	-	525.5
AHQ-4-1, 4519	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.04E-09	0.90	4.11	-	733.6
AHQ-4-8, 3734	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	7.79E-07	0.89	3.82	-	629.0
AHQ-4-4, 4244 - 4322	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.14E-10	0.91	4.39	-	1230.4
AHQ-4-3, 4419 - 4465	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	3.08E-09	0.96	5.52	-	1453.7
AHQ-4-1, 4481 - 4549	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	9.79E-08	0.86	3.60	-	1012.1
AHQ-4-5, 3885 - 3959	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.41E-10	0.97	5.02	-	2173.3
AHQ-4-5, 4053	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	2.16E-06	0.92	4.77	-	563.3
AHQ-4-6, 4002 - 4016	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	2.30E-08	0.94	4.73	-	750.5
AHQ-4-2, 3575	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	3.88E-05	0.90	4.12	-	1143.4
AHQ-4-1, 3526	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	8.16E-05	0.94	4.48	-	890.7
AHQ-4-3, 3484 - 3485	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	7.11E-06	0.94	4.67	-	1030.9
AHQ-4-2, 3258 - 3335	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.12E-04	0.94	4.76	-	1090.9
AHQ-4-2, 3444	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	1.74E-09	0.92	4.95	-	554.0
AHQ-4-2, 3344	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	4.99E-04	0.81	3.85	-	399.5
AHQ-4-1, 3614 - 3683	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	6.23E-05	0.92	4.17	-	1125.3
AHQ-4-2, 3407 - 3484	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.02E-06	0.94	4.90	-	1038.3
AHQ-4-2, 3440 - 3516	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	3.98E-06	0.92	4.19	-	816.2
AHQ-4-1, 3519	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.19E-04	0.90	4.05	-	1003.2
AHQ-4-3, 3572	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.57E-06	0.95	4.88	-	1359.9
AHQ-4-4, 3907	K.LDVQFSGLTK.G	1108.26945	1	3.72E-05	0.09	2.13	-	214.8
AHQ-4-1, 4050	K.LDVQFSGLTK.G	1108.26945	2	2.25E-05	0.92	3.38	-	1010.7
AHQ-4-2, 3916 - 3967	K.LDVQFSGLTK.G	1108.26945	1	2.29E-05	0.54	2.64	-	313.8
AHQ-4-2, 3962	K.LDVQFSGLTK.G	1108.26945	1	6.35E-04	0.13	1.82	-	249.7
AHQ-4-3, 3939 - 3943	K.LDVQFSGLTK.G	1108.26945	1	1.10E-04	0.10	1.97	-	235.5
AHQ-4-2, 3966 - 3970	K.LDVQFSGLTK.G	1108.26945	2	1.06E-04	0.94	3.55	-	1128.1
AHQ-4-4, 3915	K.LDVQFSGLTK.G	1108.26945	2	7.27E-07	0.93	4.05	-	1022.4
AHQ-4-3, 3947 - 3949	K.LDVQFSGLTK.G	1108.26945	2	5.51E-07	0.93	3.75	-	951.0
AHQ-4-1, 6963	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	2.65E-10	0.96	5.37	-	1319.6
AHQ-4-9, 4123	K.LPQLPITNFSR.D	1286.50461	2	5.38E-04	0.74	2.97	-	384.1
AHQ-4-3, 5245	K.LPQLPITNFSR.D	1286.50461	2	8.21E-06	0.87	3.18	-	715.6
AHQ-4-4, 4908 - 4931	K.LPQLPITNFSR.D	1286.50461	2	1.35E-04	0.90	2.96	-	773.0
AHQ-4-11, 4578	K.LPQLPITNFSR.D	1286.50461	2	6.54E-04	0.79	2.83	-	569.8
AHQ-4-1, 5003	K.LPQLPITNFSR.D	1286.50461	2	2.63E-05	0.87	3.01	-	769.7
AHQ-4-2, 5170 - 5239	K.LPQLPITNFSR.D	1286.50461	2	1.19E-04	0.80	2.87	-	611.2
AHQ-4-6, 4578 - 4596	K.LPQLPITNFSR.D	1286.50461	2	1.37E-05	0.84	2.90	-	672.6
AHQ-4-2, 4918 - 4994	K.LPQLPITNFSR.D	1286.50461	2	1.01E-04	0.88	3.03	-	707.8
AHQ-4-3, 4927	K.LPQLPITNFSR.D	1286.50461	2	2.92E-05	0.69	2.83	-	444.0
AHQ-4-3, 5571 - 5640	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.53E-12	0.97	5.88	-	1124.6
AHQ-4-3, 5565 - 5636	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	1.51E-04	0.98	6.09	-	1893.1
AHQ-4-2, 5567 - 5646	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	6.64E-12	0.98	7.00	-	2339.6
AHQ-4-3, 5707 - 5777	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.57E-09	0.96	4.90	-	1010.1
AHQ-4-6, 5351	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.15E-09	0.94	4.97	-	792.6
AHQ-4-12, 5365	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.17E-05	0.87	3.86	-	524.7
AHQ-4-4, 5544 - 5618	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.28E-06	0.91	4.08	-	805.7
AHQ-4-10, 4877	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.69E-05	0.80	3.36	-	452.0
AHQ-4-6, 5310 - 5374	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.19E-08	0.96	5.74	-	836.8
AHQ-4-11, 5169	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.16E-07	0.92	4.06	-	817.9
AHQ-4-4, 5520 - 5603	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	2.33E-14	0.97	6.40	-	1634.6
AHQ-4-1, 5510 - 5573	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.55E-08	0.96	4.94	-	1158.4
AHQ-4-1, 5546 - 5614	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	2.47E-10	0.98	6.45	-	2335.2
AHQ-4-4, 5700	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.31E-05	0.88	3.66	-	708.6
AHQ-4-5, 5446 - 5461	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.85E-06	0.94	4.51	-	912.6
AHQ-4-5, 5453 - 5478	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.53E-07	0.94	4.94	-	1321.4
AHQ-4-2, 5690 - 5758	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.67E-10	0.96	5.46	-	749.0
AHQ-4-2, 5554 - 5623	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.57E-06	0.96	5.07	-	961.6
AHQ-4-1, 5605 - 5641	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	5.41E-07	0.97	6.24	-	1043.1
AHQ-4-1, 5709 - 5735	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	7.97E-07	0.95	4.91	-	1011.9
AHQ-4-5, 2722	R.LRNGHVGISFVPK.E	1424.67564	2	4.51E-05	0.61	2.62	-	558.0
AHQ-4-6, 2656	R.LRNGHVGISFVPK.E	1424.67564	3	1.52E-05	0.89	3.54	-	1411.4
AHQ-4-5, 2606	R.LRNGHVGISFVPK.E	1424.67564	2	4.18E-04	0.71	2.98	-	470.3
AHQ-4-7, 3045	R.LTVSSLQESGLK.V	1262.43499	2	4.23E-04	0.81	3.02	-	621.4
AHQ-4-4, 3399	R.LTVSSLQESGLK.V	1262.43499	2	5.03E-05	0.91	3.23	-	1005.6
AHQ-4-1, 3571	R.LTVSSLQESGLK.V	1262.43499	2	4.25E-04	0.81	2.63	-	810.1
AHQ-4-6, 3115	R.LTVSSLQESGLK.V	1262.43499	2	3.82E-04	0.87	3.24	-	933.2
AHQ-4-13-, 4076	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.78E-04	0.89	3.52	-	1112.8
AHQ-4-13-, 4084	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.48E-09	0.98	6.20	-	1927.8
AHQ-4-14, 5441	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.09E-06	0.96	4.87	-	1350.2
AHQ-4-4, 4056 - 4079	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	3.69E-05	0.96	5.07	-	1443.1
AHQ-4-4, 4067	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.72E-06	0.96	5.19	-	1164.0
AHQ-4-8, 3609	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.52E-05	0.93	4.60	-	836.2
AHQ-4-7, 4039	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.54E-08	0.96	5.31	-	930.0
AHQ-4-5, 4149 - 4150	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.79E-10	0.97	6.01	-	1407.3

AHQ-4-3, 4155	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.38E-06	0.95	5.10	-	973.2
AHQ-4-13, 4201	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.69E-05	0.96	5.21	-	1451.5
AHQ-4-13, 4200	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.16E-07	0.97	5.00	-	1462.9
AHQ-4-5, 3799 - 3871	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.33E-08	0.98	6.07	-	1666.1
AHQ-4-1, 4623	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.46E-08	0.96	5.06	-	1286.9
AHQ-4-6, 3776 - 3791	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.84E-06	0.97	5.73	-	1679.8
AHQ-4-7, 3694	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	5.41E-09	0.96	4.93	-	1331.5
AHQ-4-11, 3854 - 3862	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.62E-05	0.95	4.87	-	1031.2
AHQ-4-6, 3774	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.94E-06	0.97	5.29	-	1423.8
AHQ-4-1, 4637	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.43E-06	0.95	5.08	-	979.6
AHQ-4-7, 3690 - 3705	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.49E-06	0.95	4.58	-	1103.9
AHQ-4-11, 3853	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.54E-05	0.96	5.45	-	1202.6
AHQ-4-5, 4234 - 4309	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.30E-08	0.97	4.99	-	1260.5
AHQ-4-13, 4550	R.LYSVSYLLK.D	1086.30538	2	9.67E-04	0.53	2.75	-	326.3
AHQ-4-4, 2444 - 2522	K.MDCQECPEGYR.V	1447.55375	2	1.83E-04	0.71	2.95	-	466.9
AHQ-4-7, 2355 - 2357	K.MDCQECPEGYR.V	1447.55375	2	2.31E-08	0.84	2.92	-	803.6
AHQ-4-5, 2974	R.NGHVGISFVPK.E	1155.33104	1	3.40E-07	0.41	2.21	-	357.6
AHQ-4-5, 2763	R.NGHVGISFVPK.E	1155.33104	1	2.28E-07	0.56	2.36	-	404.5
AHQ-4-1, 4890 - 4894	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	3.68E-07	0.96	5.38	-	1081.5
AHQ-4-1, 2119	K.RAEFTVETR.S	1109.21754	2	5.92E-06	0.95	3.65	-	1183.5
AHQ-4-2, 1858	K.RAEFTVETR.S	1109.21754	2	4.50E-07	0.90	3.20	-	751.1
AHQ-4-6, 2722	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	1.02E-04	0.97	5.19	-	1917.7
AHQ-4-4, 3720	K.RIANLQTDLSDGLR.L	1572.74866	2	1.33E-04	0.69	2.76	-	448.2
AHQ-4-8, 2347	R.RLTVSSLQESGLK.V	1418.62134	2	1.91E-05	0.95	4.07	-	1162.3
AHQ-4-1, 3159 - 3239	R.RLTVSSLQESGLK.V	1418.62134	2	2.19E-04	0.96	4.30	-	1645.1
AHQ-4-2, 7555 - 7627	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	1.69E-06	0.96	5.55	-	1801.8
AHQ-4-3, 4145	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.86E-04	0.67	3.35	-	339.3
AHQ-4-1, 4346	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.76E-05	0.86	3.74	-	508.3
AHQ-4-1, 4161	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.19E-07	0.93	5.49	-	648.4
AHQ-4-6, 3595	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.61E-06	0.91	4.13	-	692.2
AHQ-4-3, 3891 - 3927	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.35E-06	0.89	4.08	-	650.7
AHQ-4-3, 3892 - 3969	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	5.46E-06	0.96	4.54	-	1736.9
AHQ-4-1, 4119	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	4.58E-05	0.87	3.47	-	1081.3
AHQ-4-8, 3411	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.34E-09	0.83	3.72	-	511.7
AHQ-4-4, 4092	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.04E-05	0.68	3.25	-	373.4
AHQ-4-2, 4432	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.49E-08	0.91	4.35	-	725.5
AHQ-4-2, 4328	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.36E-05	0.68	3.24	-	420.1
AHQ-4-7, 3538	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.75E-07	0.85	4.00	-	542.1
AHQ-4-2, 4228	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.65E-08	0.89	4.29	-	543.8
AHQ-4-2, 4056	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	7.14E-06	0.88	3.99	-	954.5
AHQ-4-2, 4054 - 4135	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.09E-10	0.95	5.31	-	816.7
AHQ-4-2, 3914 - 3983	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.61E-06	0.92	4.44	-	1005.5
AHQ-4-2, 3911 - 3984	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.45E-06	0.94	4.80	-	694.1
AHQ-4-1, 4022 - 4089	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.60E-05	0.94	4.94	-	780.2
AHQ-4-5, 3654 - 3658	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	5.10E-08	0.95	4.59	-	1531.0
AHQ-4-1, 4021 - 4095	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	8.71E-09	0.94	4.60	-	1211.0
AHQ-4-3, 3995	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	8.94E-05	0.82	3.83	-	535.9
AHQ-4-3, 3335 - 3404	K.SPFEVYVDK.S	1084.20321	1	5.77E-04	0.55	2.50	-	587.6
AHQ-4-2, 3326 - 3394	K.SPFEVYVDK.S	1084.20321	2	5.21E-06	0.94	3.27	-	1210.2
AHQ-4-6, 3038 - 3107	K.SPFEVYVDK.S	1084.20321	1	1.39E-05	0.60	2.39	-	526.5
AHQ-4-1, 3477	K.SPFEVYVDK.S	1084.20321	1	2.91E-05	0.82	3.25	-	838.9
AHQ-4-3, 3343	K.SPFEVYVDK.S	1084.20321	1	3.07E-04	0.70	2.56	-	693.5
AHQ-4-2, 3330	K.SPFEVYVDK.S	1084.20321	1	7.94E-06	0.78	3.02	-	682.9
AHQ-4-1, 3470 - 3486	K.SPFEVYVDK.S	1084.20321	2	5.18E-05	0.92	3.07	-	1115.7
AHQ-4-5, 3145	K.SPFEVYVDK.S	1084.20321	2	3.67E-06	0.88	2.55	-	1170.9
AHQ-4-3, 3347 - 3360	K.SPFEVYVDK.S	1084.20321	2	7.94E-06	0.94	3.45	-	1297.4
AHQ-4-4, 3339	K.SPFEVYVDK.S	1084.20321	2	8.82E-06	0.93	3.35	-	1239.8
AHQ-4-4, 3347	K.SPFEVYVDK.S	1084.20321	1	3.47E-05	0.83	3.17	-	712.6
AHQ-4-1, 4934	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.63E-05	0.77	3.24	-	611.7
AHQ-4-3, 4900	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.36E-05	0.51	2.85	-	415.0
AHQ-4-3, 5055 - 5092	K.SPFSVAVSPSLDLSK.I	1534.73557	2	6.21E-06	0.89	3.83	-	766.1
AHQ-4-4, 5016 - 5090	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.87E-07	0.90	4.38	-	867.1
AHQ-4-2, 5066 - 5134	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.19E-05	0.93	4.66	-	833.6
AHQ-4-2, 4911	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.27E-06	0.81	3.40	-	677.1
AHQ-4-5, 4871	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.50E-07	0.88	3.51	-	941.0
AHQ-4-2, 3691	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.64E-05	0.88	4.02	-	558.8
AHQ-4-2, 3603	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.91E-05	0.73	3.40	-	401.1
AHQ-4-2, 3442 - 3514	R.SPYTVTVGQACNPSACR.A	1871.04208	2	6.13E-04	0.94	4.86	-	515.1
AHQ-4-4, 3446	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.12E-05	0.92	3.97	-	577.8
AHQ-4-1, 3493 - 3561	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.12E-04	0.93	4.80	-	510.0
AHQ-4-1, 3726	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.16E-04	0.81	3.17	-	469.9
AHQ-4-3, 3471 - 3516	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.29E-05	0.81	3.56	-	406.2
AHQ-4-6, 3222	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.45E-05	0.89	4.16	-	413.1
AHQ-4-5, 3290	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.67E-07	0.93	4.49	-	640.2
AHQ-4-14, 2929	K.SSFTVDCSK.A	1032.10676	1	4.00E-05	0.39	2.60	-	282.3
AHQ-4-14-, 2041 - 2101	K.SSFTVDCSK.A	1032.10676	1	4.13E-06	0.26	2.38	-	142.5
AHQ-4-14, 3116	K.SSFTVDCSK.A	1032.10676	1	1.30E-05	0.16	2.07	-	221.5
AHQ-4-3, 5060	R.TFSVWYVPEVTGTHK.V	1751.96228	3	1.31E-04	0.71	3.06	-	552.6
AHQ-4-5, 4734	R.TFSVWYVPEVTGTHK.V	1751.96228	3	2.07E-05	0.82	3.48	-	589.9
AHQ-4-9, 2551	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	1.36E-04	0.90	3.99	-	800.8
AHQ-4-1, 3095 - 3165	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	1.03E-04	0.92	4.38	-	701.2
AHQ-4-3, 2961 - 2973	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.95E-08	0.91	3.85	-	919.1
AHQ-4-2, 3002 - 3071	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	2.41E-04	0.89	4.04	-	723.6
AHQ-4-5, 2761	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	1.03E-04	0.81	3.76	-	505.3
AHQ-4-4, 2966	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.75E-10	0.89	3.50	-	958.2
AHQ-4-4, 2938 - 2954	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	1.76E-04	0.91	4.07	-	867.9
AHQ-4-5, 2770	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.44E-07	0.87	3.55	-	747.9
AHQ-4-1, 3150	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.18E-06	0.84	3.63	-	714.2
AHQ-4-2, 2954	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.28E-06	0.84	3.49	-	846.1
AHQ-4-1, 2958	R.TGVELGKPTHFTVNAK.A	1699.93205	3	1.02E-04	0.57	3.26	-	457.4
AHQ-4-1, 2941	R.TGVELGKPTHFTVNAK.A	1699.93205	2	6.39E-05	0.87	3.99	-	543.5
AHQ-4-2, 2839 - 2910	R.TGVELGKPTHFTVNAK.A	1699.93205	2	6.04E-06	0.87	3.64	-	674.9
AHQ-4-7, 2773	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.53E-09	0.98	5.40	-	1733.6
AHQ-4-4, 3103	K.THEAEIVEGENHTYCIR.F	2060.19046	2	7.95E-06	0.97	5.01	-	1523.7
AHQ-4-5, 2849	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.61E-11	0.98	5.24	-	2154.1
AHQ-4-6, 2743	K.THEAEIVEGENHTYCIR.F	2060.19046	3	4.64E-06	0.91	4.37	-	863.6
AHQ-4-4, 3014 - 3022	K.THEAEIVEGENHTYCIR.F	2060.19046	2	7.55E-14	0.98	5.12	-	2202.9
AHQ-4-6, 2820	K.THEAEIVEGENHTYCIR.F	2060.19046	2	1.71E-07	0.98	6.69	-	1962.2
AHQ-4-5, 2762 - 2839	K.THEAEIVEGENHTYCIR.F	2060.19046	2	5.10E-11	0.98	5.85	-	1699.1
AHQ-4-5, 2755	K.THEAEIVEGENHTYCIR.F	2060.19046	3	7.94E-04	0.82	3.69	-	830.7
AHQ-4-1, 3930	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	2	3.19E-07	0.81	3.00	-	705.9
AHQ-4-13, 3189	R.TPCEEILVK.H	1090.27249	2	4.75E-07	0.86	3.54	-	770.1
AHQ-4-13-, 3058	R.TPCEEILVK.H	1090.27249	2	4.74E-05	0.86	3.27	-	854.9
AHQ-4-12, 3011	R.TPCEEILVK.H	1090.27249	2	5.39E-06	0.89	3.10	-	838.0
AHQ-4-5, 2907 - 2909	R.TPCEEILVK.H	1090.27249	2	1.24E-05	0.90	3.10	-	825.5
AHQ-4-14-, 2927 - 2959	R.TPCEEILVK.H	1090.27249	2	2.20E-04	0.91	3.21	-	1063.3
AHQ-4-4, 3082	R.TPCEEILVK.H	1090.27249	1	9.99E-04	0.35	2.19	-	523.8

AHQ-4-4, 3078 - 3079	R.TPCEEILVK.H	1090.27249	2	1.55E-06	0.86	3.02	-	751.1
AHQ-4-6, 2879	R.TPCEEILVK.H	1090.27249	2	2.30E-04	0.81	2.97	-	718.4
AHQ-4-1, 3229 - 3237	R.TPCEEILVK.H	1090.27249	2	1.26E-05	0.81	2.83	-	640.4
AHQ-4-13, 3194	R.TPCEEILVK.H	1090.27249	1	5.41E-04	0.50	2.73	-	322.1
AHQ-4-11, 2956	R.TPCEEILVK.H	1090.27249	2	3.08E-05	0.81	2.95	-	622.7
AHQ-4-14-, 2934	R.TPCEEILVK.H	1090.27249	1	2.50E-05	0.08	2.17	-	178.4
AHQ-4-14, 4080 - 4134	R.TPCEEILVK.H	1090.27249	2	5.33E-06	0.78	2.78	-	694.9
AHQ-4-7, 2990	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.69E-07	0.93	4.44	-	975.9
AHQ-4-2, 3131	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.74E-07	0.93	4.10	-	858.0
AHQ-4-4, 3451	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.23E-11	0.92	4.04	-	745.6
AHQ-4-2, 3471 - 3542	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.79E-11	0.96	4.98	-	973.9
AHQ-4-1, 3507 - 3581	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.95E-11	0.93	4.13	-	927.1
AHQ-4-13, 3410	R.VANPSGNLTETYVQDR.G	1764.87462	2	9.82E-08	0.93	4.17	-	788.9
AHQ-4-1, 3230	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.17E-08	0.92	3.88	-	844.4
AHQ-4-1, 3377 - 3379	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.91E-10	0.94	4.61	-	651.7
AHQ-4-10, 3029	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.15E-05	0.74	3.03	-	555.8
AHQ-4-3, 3428 - 3499	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.26E-12	0.95	4.80	-	1104.3
AHQ-4-3, 3244 - 3315	R.VANPSGNLTETYVQDR.G	1764.87462	2	9.91E-06	0.92	3.87	-	871.8
AHQ-4-5, 3051 - 3122	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.20E-07	0.94	3.70	-	1221.2
AHQ-4-3, 3073 - 3145	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.13E-04	0.44	2.73	-	471.4
AHQ-4-2, 3242 - 3310	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.18E-08	0.95	4.43	-	982.4
AHQ-4-2, 3378 - 3446	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.78E-11	0.96	4.51	-	1127.3
AHQ-4-4, 3214 - 3282	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.93E-10	0.93	4.06	-	1042.3
AHQ-4-5, 3222	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.06E-05	0.89	3.76	-	750.3
AHQ-4-4, 2514	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.43E-05	0.73	3.33	-	570.1
AHQ-4-3, 2795	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.38E-07	0.90	3.74	-	774.4
AHQ-4-13-, 2820	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	7.83E-05	0.77	3.30	-	480.8
AHQ-4-10, 2427	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.52E-05	0.81	3.57	-	445.5
AHQ-4-10, 2603	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	8.73E-08	0.91	3.73	-	685.6
AHQ-4-5, 2397	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	9.46E-07	0.90	3.75	-	757.1
AHQ-4-1, 2905	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.25E-04	0.84	3.80	-	454.6
AHQ-4-2, 2802	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.78E-04	0.87	3.72	-	561.5
AHQ-4-7, 2526	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.15E-04	0.68	3.27	-	379.9
AHQ-4-8, 2339	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.22E-08	0.90	3.73	-	711.0
AHQ-4-5, 2561 - 2605	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.55E-05	0.89	4.15	-	587.0
AHQ-4-4, 2755	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.76E-04	0.77	3.31	-	403.1
AHQ-4-4, 3776 - 3779	K.VDINTEDLEDGTCR.V	1638.69283	2	1.53E-05	0.42	2.57	-	599.1
AHQ-4-3, 3645 - 3683	K.VDINTEDLEDGTCR.V	1638.69283	2	7.64E-07	0.90	3.19	-	1061.5
AHQ-4-4, 3635	K.VDINTEDLEDGTCR.V	1638.69283	2	3.92E-05	0.94	3.80	-	1254.9
AHQ-4-1, 3514	K.VDINTEDLEDGTCR.V	1638.69283	2	2.00E-08	0.91	4.07	-	821.2
AHQ-4-8, 3377 - 3454	K.VDINTEDLEDGTCR.V	1638.69283	2	6.19E-04	0.80	3.09	-	895.1
AHQ-4-5, 3683	K.VDINTEDLEDGTCR.V	1638.69283	2	1.13E-05	0.91	3.40	-	1084.3
AHQ-4-1, 3801	K.VDINTEDLEDGTCR.V	1638.69283	2	3.53E-09	0.90	3.74	-	866.7
AHQ-4-2, 3710 - 3712	K.VDINTEDLEDGTCR.V	1638.69283	2	8.05E-07	0.94	4.77	-	1005.9
AHQ-4-7, 3506	K.VDINTEDLEDGTCR.V	1638.69283	2	5.82E-06	0.93	3.18	-	1526.6
AHQ-4-1, 3697	K.VDINTEDLEDGTCR.V	1638.69283	2	1.79E-06	0.97	4.92	-	1519.4
AHQ-4-5, 3555	K.VDINTEDLEDGTCR.V	1638.69283	2	1.21E-05	0.70	3.11	-	589.5
AHQ-4-6, 3454	K.VDINTEDLEDGTCR.V	1638.69283	2	1.70E-05	0.89	3.95	-	642.7
AHQ-4-5, 3349 - 3427	K.VDINTEDLEDGTCR.V	1638.69283	2	1.22E-10	0.97	5.04	-	1376.9
AHQ-4-1, 3421	K.VDINTEDLEDGTCR.V	1638.69283	2	4.84E-07	0.96	4.28	-	1391.7
AHQ-4-5, 2310	K.VDVGKDQEFTVK.S	1365.51377	2	1.27E-08	0.84	3.22	-	542.8
AHQ-4-6, 2318	K.VDVGKDQEFTVK.S	1365.51377	2	3.87E-10	0.70	2.92	-	521.4
AHQ-4-2, 2462	K.VDVGKDQEFTVK.S	1365.51377	2	4.70E-06	0.86	3.56	-	591.1
AHQ-4-3, 2448	K.VDVGKDQEFTVK.S	1365.51377	1	2.34E-05	0.80	3.51	-	618.9
AHQ-4-1, 2629	K.VDVGKDQEFTVK.S	1365.51377	2	6.62E-07	0.83	3.25	-	679.5
AHQ-4-3, 2529	K.VDVGKDQEFTVK.S	1365.51377	2	8.19E-05	0.68	2.88	-	496.3
AHQ-4-2, 2467	K.VDVGKDQEFTVK.S	1365.51377	1	2.27E-07	0.52	2.93	-	298.6
AHQ-4-4, 2443	K.VDVGKDQEFTVK.S	1365.51377	1	1.15E-07	0.65	3.61	-	363.0
AHQ-4-2, 2630 - 2656	K.VEPGLGADNSVVR.F	1313.44209	2	2.62E-06	0.75	3.07	-	239.6
AHQ-4-4, 2619 - 2628	K.VEPGLGADNSVVR.F	1313.44209	2	6.24E-08	0.74	2.51	-	312.5
AHQ-4-2, 2876	K.VEPGLGADNSVVR.F	1313.44209	1	3.21E-04	0.15	2.01	-	153.0
AHQ-4-1, 2793 - 2865	K.VEPGLGADNSVVR.F	1313.44209	2	9.95E-06	0.85	3.21	-	363.8
AHQ-4-2, 2726 - 2736	K.VEPGLGADNSVVR.F	1313.44209	2	2.70E-06	0.76	2.86	-	345.0
AHQ-4-3, 2647 - 2728	K.VEPGLGADNSVVR.F	1313.44209	2	3.38E-07	0.74	2.74	-	318.6
AHQ-4-3, 2643 - 2719	K.VEPGLGADNSVVR.F	1313.44209	1	3.15E-04	0.16	2.21	-	179.0
AHQ-4-1, 6490	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.24E-06	0.91	4.54	-	845.6
AHQ-4-3, 6581	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.47E-04	0.88	4.50	-	463.9
AHQ-4-4, 6422 - 6490	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	3.72E-06	0.87	4.54	-	438.2
AHQ-4-6, 6246	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	6.10E-05	0.88	4.80	-	508.9
AHQ-4-5, 6274 - 6341	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	6.20E-05	0.80	4.17	-	436.6
AHQ-4-3, 6443 - 6511	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.19E-06	0.88	4.37	-	846.3
AHQ-4-1, 6401 - 6423	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	1.19E-07	0.97	6.72	-	899.1
AHQ-4-1, 7114 - 7182	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	8.85E-04	0.88	4.78	-	522.2
AHQ-4-6, 7198 - 7248	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	3.44E-05	0.72	3.59	-	522.8
AHQ-4-10, 6451 - 6452	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.17E-05	0.91	4.41	-	711.6
AHQ-4-7, 7393	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	9.35E-07	0.69	3.06	-	399.4
AHQ-4-1, 7186	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	2.64E-04	0.79	3.00	-	642.4
AHQ-4-3, 7465 - 7469	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	9.00E-06	0.86	4.58	-	457.4
AHQ-4-2, 7466 - 7467	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	3.45E-05	0.96	5.93	-	813.2
AHQ-4-1, 4554	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	7.32E-11	0.96	4.91	-	1181.6
AHQ-4-5, 4198 - 4278	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	4.21E-10	0.97	5.49	-	1622.9
AHQ-4-4, 4430	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	2.79E-05	0.97	6.05	-	1334.9
AHQ-4-6, 4118	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.82E-05	0.96	5.42	-	1177.3
AHQ-4-7, 4081	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.73E-05	0.92	4.42	-	822.1
AHQ-4-6, 4127	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	4.77E-04	0.91	3.63	-	1558.0
AHQ-4-7, 4357 - 4379	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.74E-10	0.89	3.82	-	1075.8
AHQ-4-9, 4011	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.26E-04	0.89	4.35	-	619.1
AHQ-4-1, 4882	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.78E-11	0.81	3.94	-	486.3
AHQ-4-5, 4490 - 4501	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.07E-06	0.48	2.95	-	695.1
AHQ-4-6, 4456	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	2.68E-06	0.93	4.47	-	1034.0
AHQ-4-3, 4832	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.28E-05	0.91	4.19	-	1033.1
AHQ-4-4, 4796	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.46E-04	0.89	3.67	-	1007.4
AHQ-4-5, 4489 - 4497	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	4.05E-07	0.89	4.61	-	527.3
AHQ-4-8, 4142	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	6.23E-12	0.92	4.76	-	659.0
AHQ-4-4, 4790 - 4859	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	4.59E-06	0.77	3.75	-	514.6
AHQ-4-7, 4351 - 4354	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.33E-09	0.94	5.27	-	744.4
AHQ-4-6, 4446 - 4514	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.80E-08	0.93	5.23	-	690.0
AHQ-4-7, 3533 - 3558	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.94E-07	0.82	3.60	-	354.7
AHQ-4-7, 3442	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.54E-06	0.73	2.91	-	464.2
AHQ-4-1, 3851 - 3925	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.75E-07	0.93	4.37	-	644.9
AHQ-4-2, 3779	K.VNQPASFAVSLNGAK.G	1503.68480	2	9.02E-05	0.59	2.51	-	485.9
AHQ-4-6, 3463 - 3539	K.VNQPASFAVSLNGAK.G	1503.68480	2	6.50E-08	0.92	4.13	-	689.7
AHQ-4-5, 3237	K.VNQPASFAVSLNGAK.G	1503.68480	2	9.98E-10	0.73	3.02	-	505.8
AHQ-4-8, 3403	K.VNQPASFAVSLNGAK.G	1503.68480	2	8.33E-06	0.88	3.19	-	721.9
AHQ-4-5, 3474 - 3539	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.07E-07	0.81	3.11	-	676.7
AHQ-4-5, 3611 - 3681	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.19E-06	0.85	3.89	-	435.0
AHQ-4-4, 3810 - 3878	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.33E-07	0.92	4.05	-	646.2

AHQ-4-1, 3990	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.51E-07	0.85	3.28	-	562.7
AHQ-4-2, 1560	K.VPVHDVTDASK.V	1168.28175	2	5.80E-05	0.94	3.27	-	1312.6
AHQ-4-3, 1468	K.VPVHDVTDASK.V	1168.28175	2	4.45E-07	0.88	2.95	-	1055.6
AHQ-4-2, 1478	K.VPVHDVTDASK.V	1168.28175	2	2.15E-06	0.96	3.54	-	1872.2
AHQ-4-4, 4124	R.VQVQDNEGCPVEALVK.D	1786.98493	2	2.92E-06	0.96	4.66	-	1203.3
AHQ-4-4, 4287	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.31E-07	0.93	3.93	-	1050.7
AHQ-4-2, 4315 - 4386	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.83E-08	0.97	5.00	-	1407.1
AHQ-4-1, 4358 - 4434	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.34E-10	0.92	4.20	-	925.0
AHQ-4-3, 4335	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.08E-08	0.94	4.11	-	1233.7
AHQ-4-5, 3966 - 3969	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.47E-07	0.94	4.88	-	981.1
AHQ-4-2, 4128 - 4202	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.52E-07	0.97	5.44	-	1435.9
AHQ-4-2, 4152 - 4223	R.VQVQDNEGCPVEALVK.D	1786.98493	2	6.20E-06	0.97	5.16	-	1496.5
AHQ-4-1, 5202 - 5269	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	3.68E-12	0.92	4.45	-	1344.6
AHQ-4-1, 5462 - 5509	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.04E-05	0.89	3.98	-	1236.9
AHQ-4-2, 5348 - 5418	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	2.91E-06	0.94	5.13	-	1341.1
AHQ-4-1, 5333 - 5397	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	3.40E-04	0.95	4.84	-	1460.6
AHQ-4-2, 4875	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	1.25E-04	0.75	3.35	-	555.8
AHQ-4-6, 4398	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.74E-10	0.93	4.97	-	1053.6
AHQ-4-9, 3960	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	8.14E-06	0.90	4.44	-	912.7
AHQ-4-1, 4941 - 4975	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	5.86E-11	0.96	5.86	-	1180.6
AHQ-4-5, 4401 - 4470	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.23E-09	0.94	5.19	-	1049.5
AHQ-4-2, 4795 - 4866	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.18E-05	0.96	5.44	-	1470.4
AHQ-4-13, 4746	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	2.80E-04	0.93	4.96	-	637.0
AHQ-4-8, 3901	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	8.23E-10	0.94	5.19	-	1023.5
AHQ-4-8, 4126	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.12E-04	0.87	3.78	-	883.8
AHQ-4-4, 4742 - 4810	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.32E-04	0.97	5.73	-	1606.8
AHQ-4-6, 2583	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	3.27E-05	0.81	3.33	-	630.2
AHQ-4-3, 2755	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.66E-11	0.82	3.54	-	562.7
AHQ-4-1, 2913	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.87E-10	0.84	3.79	-	458.4
AHQ-4-4, 2604 - 2615	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.61E-04	0.69	3.17	-	479.2
AHQ-4-7, 2413	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	5.38E-06	0.85	3.52	-	650.5
AHQ-4-4, 2726 - 2731	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.61E-06	0.77	3.66	-	525.8
AHQ-4-7, 2529	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.52E-05	0.83	3.98	-	508.8
AHQ-4-2, 2738 - 2815	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.64E-08	0.88	3.76	-	657.5
AHQ-4-1, 2761 - 2842	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	8.16E-06	0.92	4.81	-	544.0
AHQ-4-3, 2848 - 2853	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	8.11E-07	0.91	3.91	-	775.0
AHQ-4-5, 2597	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.58E-07	0.80	3.94	-	436.1
AHQ-4-5, 2779 - 2801	K.VTVLFAGQHIAK.S	1284.53185	2	1.40E-06	0.92	3.77	-	923.0
AHQ-4-2, 3114 - 3115	K.VTVLFAGQHIAK.S	1284.53185	2	2.14E-07	0.94	3.82	-	1041.8
AHQ-4-6, 2802	K.VTVLFAGQHIAK.S	1284.53185	2	1.43E-05	0.88	3.44	-	770.0
AHQ-4-7, 2658	K.VTVLFAGQHIAK.S	1284.53185	2	4.42E-07	0.84	3.22	-	653.5
AHQ-4-2, 3090	K.VTVLFAGQHIAK.S	1284.53185	1	5.82E-04	0.63	3.05	-	398.8
AHQ-4-2, 3031 - 3043	K.VTVLFAGQHIAK.S	1284.53185	2	8.16E-07	0.92	4.12	-	893.2
AHQ-4-2, 3058	K.VTVLFAGQHIAK.S	1284.53185	3	1.52E-05	0.79	3.38	-	678.8
AHQ-4-3, 3069 - 3072	K.VTVLFAGQHIAK.S	1284.53185	2	5.54E-04	0.90	3.66	-	818.8
AHQ-4-1, 5398	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.56E-06	0.80	3.11	-	420.7
AHQ-4-1, 5039	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.10E-05	0.77	2.91	-	518.0
AHQ-4-5, 4823 - 4893	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.16E-10	0.92	4.33	-	586.0
AHQ-4-4, 5138	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.81E-10	0.88	3.94	-	411.9
AHQ-4-2, 5195 - 5203	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.60E-10	0.87	3.82	-	414.6
AHQ-4-8, 4605 - 4653	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.96E-04	0.85	3.47	-	528.3
AHQ-4-5, 4962 - 5033	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.98E-07	0.92	4.47	-	458.2
AHQ-4-13, 5461 - 5464	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.47E-04	0.51	2.78	-	502.6
AHQ-4-2, 5614	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.52E-05	0.82	3.09	-	693.0
AHQ-4-8, 4874 - 4875	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	8.22E-04	0.73	2.72	-	703.8
AHQ-4-3, 5624	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.91E-05	0.90	3.44	-	919.3
AHQ-4-10, 4391	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	8.10E-04	0.78	2.96	-	482.8
AHQ-4-11, 5145 - 5152	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.30E-04	0.82	3.22	-	582.1
AHQ-4-5, 5283 - 5353	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.31E-08	0.91	4.14	-	696.1
AHQ-4-13-, 5344	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	8.10E-04	0.88	3.44	-	819.3
AHQ-4-7, 5219 - 5221	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.09E-04	0.87	4.11	-	564.3
AHQ-4-6, 5296 - 5299	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.07E-04	0.79	3.54	-	432.2
AHQ-4-14-, 5297	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	5.74E-06	0.79	3.00	-	580.2
AHQ-4-8, 2793	R.YAPSEAGLHEMDIR.Y	1589.75482	2	9.49E-05	0.76	2.54	-	732.4
AHQ-4-5, 2405 - 2406	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	2.88E-05	0.86	3.48	-	897.6
AHQ-4-10, 3047	R.YAPSEAGLHEMDIR.Y	1589.75482	2	8.83E-04	0.69	2.98	-	653.9
AHQ-4-6, 4022	K.YGGDEIPFSPYR.V	1401.50466	1	3.98E-05	0.19	1.83	-	431.2
AHQ-4-11, 4022	K.YGGDEIPFSPYR.V	1401.50466	1	7.96E-04	0.13	1.84	-	329.5
AHQ-4-2, 4344 - 4347	K.YGGDEIPFSPYR.V	1401.50466	1	5.61E-04	0.42	2.32	-	565.9
AHQ-4-11, 4021 - 4093	K.YGGDEIPFSPYR.V	1401.50466	2	3.36E-05	0.87	3.77	-	586.6
AHQ-4-3, 4331 - 4365	K.YGGDEIPFSPYR.V	1401.50466	2	5.28E-05	0.80	3.46	-	500.6
AHQ-4-3, 4339	K.YGGDEIPFSPYR.V	1401.50466	1	3.57E-07	0.26	2.27	-	394.6
AHQ-4-4, 4284 - 4298	K.YGGDEIPFSPYR.V	1401.50466	2	1.52E-06	0.85	3.77	-	575.7
AHQ-4-2, 4303 - 4374	K.YGGDEIPFSPYR.V	1401.50466	2	5.81E-06	0.79	3.38	-	497.3
AHQ-4-4, 4292	K.YGGDEIPFSPYR.V	1401.50466	1	1.53E-05	0.26	2.39	-	387.0
AHQ-4-1, 4425	K.YGGDEIPFSPYR.V	1401.50466	1	3.40E-05	0.50	2.79	-	554.5
AHQ-4-8, 3809	K.YGGDEIPFSPYR.V	1401.50466	2	3.13E-04	0.76	3.25	-	467.8
AHQ-4-11, 3082	K.YGGPYHIGGSPFK.A	1380.53182	2	1.03E-05	0.94	4.02	-	1340.6
AHQ-4-7, 2899	K.YGGPYHIGGSPFK.A	1380.53182	1	8.50E-07	0.86	3.81	-	385.7
AHQ-4-7, 2889	K.YGGPYHIGGSPFK.A	1380.53182	2	8.70E-06	0.96	4.56	-	1613.3
AHQ-4-5, 2986	K.YGGPYHIGGSPFK.A	1380.53182	3	1.28E-05	0.77	3.17	-	463.7
AHQ-4-6, 2990 - 3040	K.YGGPYHIGGSPFK.A	1380.53182	2	2.68E-07	0.96	4.41	-	1398.6
AHQ-4-5, 2977 - 3001	K.YGGPYHIGGSPFK.A	1380.53182	2	3.51E-07	0.97	4.77	-	1737.9
AHQ-4-3, 3255	K.YGGPYHIGGSPFK.A	1380.53182	2	2.09E-04	0.96	3.90	-	2105.6
AHQ-4-4, 3243	K.YGGPYHIGGSPFK.A	1380.53182	1	5.05E-08	0.90	3.73	-	672.0
AHQ-4-1, 3461	K.YGGPYHIGGSPFK.A	1380.53182	2	2.72E-06	0.93	3.83	-	1215.9
AHQ-4-4, 3232	K.YGGPYHIGGSPFK.A	1380.53182	2	4.72E-04	0.97	4.44	-	1895.1
AHQ-4-2, 2991 - 3018	K.YGGQPVPNFPSK.L	1291.43658	2	1.44E-07	0.93	4.06	-	631.0
AHQ-4-4, 2974 - 2980	K.YGGQPVPNFPSK.L	1291.43658	2	6.60E-04	0.84	3.24	-	395.8
AHQ-4-3, 2991 - 2993	K.YGGQPVPNFPSK.L	1291.43658	2	2.72E-04	0.86	3.42	-	446.7
AHQ-4-1, 3267	K.YGGQPVPNFPSK.L	1291.43658	2	3.20E-04	0.67	3.11	-	234.9
AHQ-4-5, 2807	K.YGGQPVPNFPSK.L	1291.43658	2	8.56E-04	0.45	2.51	-	251.6
AHQ-4-1, 3114	K.YGGQPVPNFPSK.L	1291.43658	2	4.82E-05	0.83	3.33	-	376.2
AHQ-4-2, 2992 - 3063	K.YGGQPVPNFPSK.L	1291.43658	1	4.48E-04	0.06	1.87	-	203.5
AHQ-4-6, 3832	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.97E-04	0.91	4.16	-	941.7
AHQ-4-5, 3881	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	3.12E-04	0.92	4.26	-	1343.0
AHQ-4-4, 4234	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.08E-05	0.89	4.07	-	1000.5
AHQ-4-3, 4283	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	2.90E-06	0.74	3.46	-	559.2
AHQ-4-7, 3729 - 3791	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	6.17E-05	0.92	4.27	-	1011.9
AHQ-4-7, 2478	K.YNEQHVPGSPFTAR.V	1603.71978	2	5.24E-06	0.73	3.22	-	334.3
AHQ-4-10, 2575 - 2579	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.49E-05	0.79	2.57	-	592.1
AHQ-4-6, 2563	K.YNEQHVPGSPFTAR.V	1603.71978	2	3.51E-04	0.79	3.25	-	488.7
AHQ-4-5, 2845	K.YNEQHVPGSPFTAR.V	1603.71978	3	4.36E-07	0.92	4.30	-	1502.6
AHQ-4-2, 2748	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.81E-04	0.62	2.68	-	390.5
AHQ-4-4, 2703	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.08E-06	0.83	3.09	-	530.6
AHQ-4-4, 2722	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.72E-06	0.92	4.14	-	483.8
AHQ-4-3, 2731	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.34E-06	0.87	3.79	-	514.3

AHQ-4-5, 2833	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.43E-04	0.73	3.10	-	414.8
AHQ-4-5, 2521 - 2522	K.YNEQHVPGSPFTAR.V	1603.71978	2	9.28E-08	0.91	3.74	-	637.9
AHQ-4-4, 3010	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.74E-04	0.86	3.39	-	502.3
AHQ-4-6, 4386	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.20E-07	0.87	3.64	-	550.5
AHQ-4-2, 4922	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.18E-07	0.87	3.74	-	617.3
AHQ-4-2, 4830 - 4851	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.40E-08	0.96	5.32	-	843.3
AHQ-4-2, 4710 - 4780	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.05E-06	0.85	3.75	-	504.9
AHQ-4-2, 4626 - 4694	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.92E-07	0.93	4.37	-	714.2
AHQ-4-2, 4502 - 4515	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.89E-05	0.85	3.75	-	644.6
AHQ-4-5, 4474 - 4477	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.18E-04	0.93	4.38	-	748.2
AHQ-4-3, 4480	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.26E-06	0.87	3.75	-	585.2
AHQ-4-3, 4624 - 4699	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.23E-05	0.90	4.02	-	594.6
AHQ-4-3, 4719 - 4792	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.63E-08	0.89	3.92	-	598.8
AHQ-4-8, 4135	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.25E-06	0.88	3.85	-	566.8
AHQ-4-3, 4805 - 4883	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.19E-08	0.93	4.77	-	587.2
AHQ-4-4, 4700 - 4778	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.38E-07	0.93	4.47	-	712.2
AHQ-4-10, 4060	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.39E-07	0.88	3.81	-	637.6
AHQ-4-4, 4582 - 4650	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.64E-06	0.94	4.75	-	744.7
AHQ-4-1, 4514	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	9.42E-06	0.76	3.24	-	480.7
AHQ-4-1, 4641 - 4709	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.40E-07	0.94	4.51	-	736.2
AHQ-4-1, 4805	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.20E-06	0.93	4.53	-	768.1
AHQ-4-7, 4337	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.88E-06	0.92	4.12	-	738.5
AHQ-4-9, 3952	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.59E-05	0.87	4.01	-	493.5
AHQ-4-5, 6723	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.89E-05	0.72	3.04	-	440.9
AHQ-4-1, 6971	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.46E-12	0.76	3.02	-	505.3
AHQ-4-3, 6849 - 6920	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	2.34E-06	0.82	3.50	-	620.3
AHQ-4-3, 6508 - 6521	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.89E-06	0.92	4.45	-	814.5
AHQ-4-2, 7071 - 7076	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.34E-08	0.91	3.52	-	1027.2
AHQ-4-3, 6831 - 6900	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.48E-08	0.94	4.57	-	807.8
AHQ-4-1, 6462 - 6463	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.24E-04	0.81	3.14	-	755.7
AHQ-4-2, 6938 - 6958	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	4.34E-08	0.94	4.55	-	923.7
gi|7669492|ref|NP_002037.2| glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]				5.00E-15	8.82	110.37	40.00	36053.0
AHQ-4-9, 3029 - 3067	R.GALQNIIPASTGAAK.A	1412.61680	1	6.27E-07	0.87	3.68	-	793.9
AHQ-4-9, 3211	R.GALQNIIPASTGAAK.A	1412.61680	1	9.63E-05	0.49	2.29	-	484.2
AHQ-4-9, 3371	R.GALQNIIPASTGAAK.A	1412.61680	1	8.54E-07	0.23	2.25	-	202.2
AHQ-4-10, 3317 - 3327	R.GALQNIIPASTGAAK.A	1412.61680	1	3.47E-05	0.47	2.70	-	423.4
AHQ-4-11, 3524	R.GALQNIIPASTGAAK.A	1412.61680	2	5.63E-06	0.76	3.17	-	575.1
AHQ-4-9, 6412 - 6473	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	2.57E-05	0.90	5.35	-	408.9
AHQ-4-9, 5899 - 5963	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	3.09E-04	0.81	4.08	-	486.9
AHQ-4-9, 3896	K.RVIISAPSADAPMFVMGVNHEK.Y	2370.78022	3	1.41E-07	0.94	5.24	-	844.8
AHQ-4-9, 6544 - 6617	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	7.22E-15	0.98	6.82	-	2194.5
AHQ-4-11, 6705 - 6708	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	1.53E-08	0.97	6.84	-	1958.7
AHQ-4-9, 6543 - 6608	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	9.81E-09	0.97	6.46	-	1642.7
AHQ-4-11, 6130	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	2	8.39E-04	0.90	5.08	-	993.0
AHQ-4-10, 5789	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	2.12E-06	0.97	5.52	-	1606.2
AHQ-4-9, 5791 - 5860	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	5.00E-15	0.96	6.59	-	1555.8
AHQ-4-10, 6399 - 6405	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	4.44E-08	0.95	6.13	-	1762.1
AHQ-4-11, 6704 - 6710	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	1.05E-10	0.96	7.38	-	1498.9
AHQ-4-9, 4108	R.VIISAPSADAPM*FVMGVNHEK.Y	2230.59327	2	1.34E-05	0.64	3.17	-	454.2
AHQ-4-9, 3911	R.VIISAPSADAPM*FVMGVNHEK.Y	2230.59327	2	4.86E-04	0.67	3.57	-	466.1
AHQ-4-9, 3657	R.VIISAPSADAPM*FVM*GVNHEK.Y	2246.59267	2	6.55E-05	0.40	2.84	-	223.7
AHQ-4-9, 4323 - 4401	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	1.82E-05	0.82	3.69	-	328.3
AHQ-4-9, 4560 - 4567	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	2.18E-07	0.38	2.60	-	320.9
AHQ-4-12, 4113	R.VPTANVSVVDLTCR.L	1532.74450	2	6.59E-09	0.93	4.22	-	964.8
AHQ-4-3, 4309	R.VPTANVSVVDLTCR.L	1532.74450	2	4.69E-05	0.70	2.89	-	750.2
AHQ-4-13, 4205 - 4244	R.VPTANVSVVDLTCR.L	1532.74450	2	7.37E-09	0.96	4.41	-	1212.1
AHQ-4-11, 4024	R.VPTANVSVVDLTCR.L	1532.74450	2	6.11E-04	0.72	3.01	-	367.8
AHQ-4-11, 3882 - 3960	R.VPTANVSVVDLTCR.L	1532.74450	2	1.44E-08	0.92	3.63	-	941.1
AHQ-4-9, 3439 - 3453	R.VPTANVSVVDLTCR.L	1532.74450	2	1.05E-09	0.94	3.83	-	1209.6
AHQ-4-10, 3637	R.VPTANVSVVDLTCR.L	1532.74450	2	6.59E-04	0.89	3.33	-	915.8
AHQ-4-9, 3717 - 3792	R.VPTANVSVVDLTCR.L	1532.74450	2	2.51E-09	0.94	4.05	-	859.0
AHQ-4-13-, 4102	R.VPTANVSVVDLTCR.L	1532.74450	2	2.01E-09	0.92	3.73	-	1029.6
AHQ-4-9, 3879	R.VPTANVSVVDLTCR.L	1532.74450	2	5.13E-09	0.90	3.41	-	861.1
AHQ-4-11, 3781	R.VPTANVSVVDLTCR.L	1532.74450	2	6.93E-04	0.92	3.72	-	949.3
AHQ-4-9, 6793 - 6860	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.33E-09	0.93	4.32	-	755.4
AHQ-4-9, 6775 - 6848	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	8.58E-06	0.87	3.63	-	740.7
AHQ-4-9, 6672 - 6755	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.90E-06	0.95	4.66	-	905.8
AHQ-4-9, 6445 - 6524	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	4.49E-07	0.85	3.59	-	501.2
AHQ-4-9, 6248 - 6280	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	3.50E-08	0.83	3.95	-	624.6
AHQ-4-9, 6101 - 6181	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	7.00E-05	0.88	3.48	-	859.7
AHQ-4-9, 5960 - 6025	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	4.18E-09	0.91	3.85	-	808.0
AHQ-4-13, 6238 - 6304	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	5.86E-04	0.90	4.04	-	808.6
AHQ-4-9, 5817 - 5891	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	3.74E-06	0.94	3.84	-	1246.0
AHQ-4-13-, 6041 - 6120	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.93E-04	0.95	4.72	-	897.7
AHQ-4-13-, 6177 - 6257	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.43E-06	0.93	4.81	-	659.2
AHQ-4-14-, 6005	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.24E-07	0.96	4.88	-	1074.1
gi|4758460|ref|NP_004479.1| glycoprotein V (platelet) [Homo sapiens]				6.66E-15	5.48	60.26	24.50	60958.9
AHQ-4-5, 5465	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	8.35E-08	0.84	3.77	-	805.8
AHQ-4-5, 4611	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	3.59E-05	0.95	3.75	-	1657.8
AHQ-4-5, 5495	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	2	4.76E-05	0.93	4.60	-	794.8
AHQ-4-5, 4522	R.LPNLSSLTLSR.N	1201.39802	2	2.49E-04	0.95	3.52	-	1838.2
AHQ-4-5, 7381 - 7429	R.LSALPQGAFQGLGELQVLALHSNGLTALPDGLLR.G	3471.99408	3	6.66E-15	0.91	5.11	-	528.5
AHQ-4-1, 7293	K.LVNLQELALNQNQLDFLPASLFTNLENLK.L	3314.77659	3	1.93E-05	0.90	4.65	-	738.7
gi|21361755|ref|NP_004090.3| stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie				7.22E-15	9.42	110.29	48.30	31708.5
AHQ-4-1, 4905	K.EASMVITESPAALQLR.Y	1716.98119	2	7.60E-05	0.86	3.75	-	912.4
AHQ-4-14, 5017 - 5072	K.EASM*VITESPAALQLR.Y	1732.98059	2	2.89E-04	0.54	2.74	-	414.8
AHQ-4-10, 3767 - 3772	K.EASM*VITESPAALQLR.Y	1732.98059	2	9.93E-06	0.83	3.24	-	1033.9
AHQ-4-14, 5858	K.EASMVITESPAALQLR.Y	1716.98119	2	4.68E-07	0.75	3.15	-	779.0
AHQ-4-13-, 4609	K.EASMVITESPAALQLR.Y	1716.98119	2	7.42E-04	0.90	4.50	-	741.0
AHQ-4-1, 4342 - 4354	K.EASM*VITESPAALQLR.Y	1732.98059	2	4.64E-04	0.91	3.76	-	1214.7
AHQ-4-13-, 4104 - 4134	K.EASM*VITESPAALQLR.Y	1732.98059	2	4.01E-08	0.91	4.20	-	941.2
AHQ-4-9, 4099	K.EASMVITESPAALQLR.Y	1716.98119	2	2.47E-05	0.85	3.38	-	902.0
AHQ-4-13, 6953 - 6954	K.GPGLFFILPCTDSFIK.V	1814.13672	2	9.41E-06	0.94	4.89	-	662.1
AHQ-4-3, 7471	K.GPGLFFILPCTDSFIK.V	1814.13672	2	9.77E-05	0.91	4.51	-	614.0
AHQ-4-1, 7197	K.GPGLFFILPCTDSFIK.V	1814.13672	2	2.00E-04	0.95	4.35	-	861.1
AHQ-4-10, 6455	K.GPGLFFILPCTDSFIK.V	1814.13672	2	8.46E-05	0.94	4.89	-	731.3
AHQ-4-13-, 6832 - 6833	K.GPGLFFILPCTDSFIK.V	1814.13672	2	3.89E-06	0.96	5.21	-	903.8
AHQ-4-1, 7134 - 7199	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	5.34E-05	0.86	4.44	-	986.0
AHQ-4-1, 6217 - 6221	K.NLSQILSDREEIAHNM*QSTLDDATDAWGIK.V	3389.65279	3	8.32E-05	0.96	5.30	-	1821.3
AHQ-4-2, 7591	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	2.83E-04	0.68	3.41	-	327.5
AHQ-4-14-, 6745	K.NSTIVFPLPIDM*LQGIIGAK.H	2144.56315	2	6.02E-04	0.79	3.71	-	305.0
AHQ-4-13-, 6924	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	2.05E-04	0.89	4.03	-	568.7
AHQ-4-14-, 6825	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	3.33E-05	0.67	3.47	-	326.4
AHQ-4-1, 5651 - 5721	R.TISFDIPPQEILTK.D	1602.85305	2	3.87E-05	0.67	2.56	-	329.2
AHQ-4-1, 2323	K.VIAAEGEMNASR.A	1248.39191	2	4.55E-09	0.96	4.06	-	1476.7
AHQ-4-1, 4155	R.VQNATLAVANITNADSATR.L	1931.09731	2	9.48E-07	0.76	3.35	-	491.5
AHQ-4-10, 4092	R.VQNATLAVANITNADSATR.L	1931.09731	2	2.92E-08	0.90	4.25	-	626.9

AHQ-4-1, 3923	R.VQNATLAVANITNADSATR.L	1931.09731	2	7.22E-15	0.96	5.06	-	1046.4
AHQ-4-1, 4681	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.74E-07	0.93	4.54	-	730.8
AHQ-4-10, 3679	R.VQNATLAVANITNADSATR.L	1931.09731	2	7.88E-04	0.30	2.61	-	184.1
AHQ-4-1, 4005 - 4025	R.VQNATLAVANITNADSATR.L	1931.09731	2	2.20E-12	0.97	5.89	-	1115.0
AHQ-4-13-, 3825	R.YLQTLTTIAAEK.N	1352.55813	2	6.54E-05	0.92	3.69	-	1088.7
AHQ-4-13, 3970 - 3978	R.YLQTLTTIAAEK.N	1352.55813	2	8.43E-04	0.91	3.55	-	995.9
AHQ-4-1, 3970 - 4030	R.YLQTLTTIAAEK.N	1352.55813	2	4.95E-08	0.93	3.34	-	1513.1
gi|4504517|ref|NP_001531.1| heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M				9.44E-15	5.61	60.35	39.50	22782.3
AHQ-4-14-, 4735 - 4745	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.37E-05	0.86	4.15	-	394.6
AHQ-4-10, 4481	K.LATQSNEITIPVTFESR.A	1907.11412	2	8.61E-04	0.56	3.12	-	257.0
AHQ-4-13, 4984 - 4992	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.31E-07	0.90	4.24	-	505.8
AHQ-4-13-, 4853 - 4917	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.07E-07	0.71	3.25	-	398.3
AHQ-4-13-, 4760 - 4780	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.79E-04	0.80	3.74	-	346.5
AHQ-4-11, 4754	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.11E-10	0.90	4.16	-	486.9
AHQ-4-14, 5996 - 6066	K.LATQSNEITIPVTFESR.A	1907.11412	2	3.66E-05	0.76	3.80	-	359.1
AHQ-4-11, 4628 - 4684	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.26E-04	0.61	2.93	-	397.7
AHQ-4-11, 4477	R.LFDQAFGLPR.L	1164.33793	2	1.32E-07	0.96	4.39	-	1487.8
AHQ-4-10, 6188	R.LPEEWSQWLGGSSWPGYVR.P	2235.44173	2	8.37E-04	0.74	3.45	-	542.5
AHQ-4-11, 6472 - 6480	R.LPEEWSQWLGGSSWPGYVR.P	2235.44173	2	7.08E-08	0.96	4.90	-	999.9
AHQ-4-11, 6688 - 6697	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	9.44E-15	0.97	7.03	-	1091.1
AHQ-4-10, 6376	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	2.60E-06	0.92	4.86	-	808.7
AHQ-4-11, 4025	R.PLPPAAIESPAVAAPAYSR.A	1879.14874	2	9.41E-07	0.84	3.44	-	418.1
AHQ-4-13, 4708 - 4709	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.30E-07	0.95	5.08	-	1038.3
AHQ-4-13-, 4596 - 4612	R.VSLDVNHFAPDELTVK.T	1784.99058	3	1.61E-07	0.80	3.50	-	509.5
AHQ-4-11, 4486 - 4549	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.53E-10	0.96	4.39	-	1499.2
AHQ-4-13-, 4845	R.VSLDVNHFAPDELTVK.T	1784.99058	2	8.73E-10	0.96	5.16	-	1211.0
AHQ-4-13-, 4593 - 4613	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.08E-11	0.97	5.08	-	1517.0
AHQ-4-11, 4665	R.VSLDVNHFAPDELTVK.T	1784.99058	2	5.80E-11	0.95	4.62	-	1067.6
AHQ-4-10, 4207 - 4208	R.VSLDVNHFAPDELTVK.T	1784.99058	2	3.12E-08	0.90	4.02	-	988.3
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				1.17E-14	103.36	1180.37	45.70	226529.8
AHQ-4-2, 2507	K.AKQTLENERGELANEVK.V	1930.10932	2	5.63E-05	0.89	4.06	-	1033.5
AHQ-4-3, 1809 - 1875	R.ALEEAMEQK.A	1049.18068	1	6.67E-04	0.45	2.38	-	744.0
AHQ-4-2, 1868 - 1943	R.ALEEAMEQK.A	1049.18068	2	6.68E-04	0.83	3.24	-	787.3
AHQ-4-2, 3784	K.ALELDSNLYR.I	1194.31920	2	1.07E-06	0.95	4.01	-	1245.3
AHQ-4-5, 3515 - 3517	K.ALELDSNLYR.I	1194.31920	2	8.95E-06	0.90	3.55	-	980.3
AHQ-4-2, 3899	K.ALELDSNLYR.I	1194.31920	2	4.09E-05	0.94	3.65	-	1182.6
AHQ-4-1, 3878 - 3891	K.ALELDSNLYR.I	1194.31920	2	1.88E-07	0.95	4.00	-	1366.6
AHQ-4-3, 3873	K.ALELDSNLYR.I	1194.31920	2	8.49E-07	0.89	3.12	-	1063.4
AHQ-4-4, 3719	K.ALELDSNLYR.I	1194.31920	2	2.70E-05	0.94	3.65	-	1288.6
AHQ-4-3, 3736 - 3737	K.ALELDSNLYR.I	1194.31920	2	1.03E-05	0.94	4.01	-	1127.0
AHQ-4-1, 2947	R.ALEQQVEEMK.T	1205.36380	2	3.54E-05	0.88	3.35	-	1070.2
AHQ-4-3, 2785 - 2800	R.ALEQQVEEMK.T	1205.36380	2	4.66E-05	0.92	3.69	-	1098.5
AHQ-4-2, 2792	R.ALEQQVEEMK.T	1205.36380	2	1.33E-05	0.88	3.61	-	890.7
AHQ-4-5, 2586	R.ALEQQVEEMK.T	1205.36380	2	5.56E-05	0.92	3.93	-	1062.0
AHQ-4-1, 2190	R.ALEQQVEEM*K.T	1221.36320	2	7.16E-05	0.79	3.13	-	882.4
AHQ-4-4, 2774	R.ALEQQVEEMK.T	1205.36380	2	1.33E-04	0.86	3.35	-	1042.1
AHQ-4-3, 2013	R.ALEQQVEEM*K.T	1221.36320	2	6.02E-04	0.81	3.13	-	987.9
AHQ-4-6, 2614	R.ALEQQVEEMK.T	1205.36380	2	3.42E-04	0.86	3.28	-	912.4
AHQ-4-5, 6513	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	2.12E-07	0.95	5.23	-	1440.8
AHQ-4-6, 6392	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	4.95E-06	0.91	4.35	-	1214.3
AHQ-4-3, 6595 - 6668	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	7.27E-14	0.98	7.44	-	2810.3
AHQ-4-1, 6571 - 6633	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.52E-06	0.97	6.68	-	1534.3
AHQ-4-5, 7370	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	4.74E-04	0.94	4.96	-	1239.2
AHQ-4-4, 7394	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	5.66E-11	0.96	6.09	-	1384.8
AHQ-4-2, 7455	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	1.94E-07	0.96	5.55	-	1701.6
AHQ-4-6, 7190	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	3.31E-12	0.97	6.18	-	1400.5
AHQ-4-3, 7456	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	3.14E-06	0.96	6.12	-	1504.9
AHQ-4-2, 6664 - 6738	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	3.52E-11	0.97	5.82	-	2068.6
AHQ-4-1, 6710	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.75E-04	0.76	3.65	-	758.9
AHQ-4-3, 5148 - 5219	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.46E-06	0.97	5.14	-	1588.6
AHQ-4-1, 5399	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.06E-07	0.97	5.78	-	1514.2
AHQ-4-2, 5416 - 5487	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.09E-05	0.97	5.76	-	1624.6
AHQ-4-2, 5270 - 5340	K.ANLQIDQINTDLNLER.S	1871.04187	2	8.37E-07	0.98	5.62	-	1852.3
AHQ-4-1, 5209 - 5277	K.ANLQIDQINTDLNLER.S	1871.04187	2	8.69E-04	0.94	5.14	-	810.7
AHQ-4-1, 5493 - 5567	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.14E-05	0.94	4.49	-	881.9
AHQ-4-7, 4918	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.64E-05	0.96	4.74	-	1190.3
AHQ-4-2, 4934	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.27E-06	0.94	4.43	-	1022.5
AHQ-4-5, 5029 - 5046	K.ANLQIDQINTDLNLER.S	1871.04187	2	8.03E-07	0.97	5.68	-	1398.0
AHQ-4-1, 4997	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.62E-08	0.91	4.13	-	555.0
AHQ-4-2, 5027 - 5034	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.13E-09	0.96	5.19	-	1089.7
AHQ-4-9, 4461	K.ANLQIDQINTDLNLER.S	1871.04187	2	7.74E-07	0.81	3.52	-	577.9
AHQ-4-2, 5162 - 5231	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.04E-06	0.97	5.44	-	1515.0
AHQ-4-3, 5400	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.04E-09	0.97	5.65	-	1585.0
AHQ-4-2, 2242	K.ASITALEAK.I	904.04321	2	1.31E-04	0.88	2.78	-	984.1
AHQ-4-3, 2224	K.ASITALEAK.I	904.04321	2	4.88E-05	0.93	3.10	-	1239.9
AHQ-4-1, 2437	K.ASITALEAK.I	904.04321	2	1.16E-04	0.93	3.33	-	1120.8
AHQ-4-5, 2049	K.ASITALEAK.I	904.04321	2	1.61E-06	0.93	2.90	-	1303.4
AHQ-4-3, 1881	R.ASREEILAQAK.E	1216.36955	2	1.43E-04	0.91	3.41	-	1278.8
AHQ-4-2, 1906 - 1976	R.ASREEILAQAK.E	1216.36955	2	7.03E-06	0.95	3.54	-	1837.5
AHQ-4-5, 1666	R.ASREEILAQAK.E	1216.36955	2	8.11E-05	0.87	3.39	-	1120.6
AHQ-4-1, 2154	R.ASREEILAQAK.E	1216.36955	2	1.17E-05	0.91	3.55	-	1307.7
AHQ-4-2, 3400	R.DELADEIANSSGK.G	1349.38323	1	8.83E-10	0.70	2.55	-	462.2
AHQ-4-4, 3208	R.DELADEIANSSGK.G	1349.38323	2	5.25E-04	0.89	3.46	-	789.0
AHQ-4-3, 3215	R.DELADEIANSSGK.G	1349.38323	2	4.71E-06	0.96	3.90	-	1758.9
AHQ-4-1, 3265	R.DELADEIANSSGK.G	1349.38323	2	7.13E-07	0.96	4.11	-	1783.3
AHQ-4-5, 3127	R.DELADEIANSSGK.G	1349.38323	2	5.91E-06	0.94	3.66	-	1413.9
AHQ-4-2, 3230	R.DELADEIANSSGK.G	1349.38323	2	2.45E-06	0.93	3.79	-	1252.7
AHQ-4-2, 3231	R.DELADEIANSSGK.G	1349.38323	1	2.26E-08	0.31	2.13	-	401.4
AHQ-4-2, 7248 - 7254	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.22E-14	0.96	5.11	-	1626.1
AHQ-4-3, 7079 - 7100	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	4.16E-08	0.98	6.53	-	2279.2
AHQ-4-4, 7038 - 7062	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.36E-06	0.97	5.26	-	2087.5
AHQ-4-1, 7038 - 7039	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.13E-10	0.97	6.18	-	1493.8
AHQ-4-2, 7086 - 7150	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	8.54E-05	0.98	6.39	-	1883.2
AHQ-4-2, 6840	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	5.80E-05	0.91	4.65	-	1023.3
AHQ-4-3, 6659	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	2	8.49E-06	0.41	2.62	-	269.5
AHQ-4-2, 6671 - 6672	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	2	1.29E-10	0.73	3.26	-	416.5
AHQ-4-3, 2021 - 2052	K.DLEAHIDSANK.N	1213.27938	2	5.18E-05	0.97	3.88	-	2162.7
AHQ-4-2, 2046	K.DLEAHIDSANK.N	1213.27938	1	8.86E-05	0.65	1.94	-	862.9
AHQ-4-1, 2222	K.DLEAHIDSANK.N	1213.27938	1	3.25E-08	0.73	2.95	-	579.6
AHQ-4-4, 2038	K.DLEAHIDSANK.N	1213.27938	2	2.92E-07	0.97	4.07	-	2225.0
AHQ-4-1, 2223	K.DLEAHIDSANK.N	1213.27938	2	1.36E-06	0.96	4.06	-	1759.3
AHQ-4-2, 2044	K.DLEAHIDSANK.N	1213.27938	2	1.29E-07	0.97	4.19	-	2044.4
AHQ-4-1, 7265	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	7.07E-10	0.96	4.90	-	1935.6
AHQ-4-3, 7631	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.05E-08	0.97	6.32	-	1874.7
AHQ-4-3, 7523 - 7560	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	8.67E-12	0.97	6.28	-	1837.8
AHQ-4-1, 7130 - 7131	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	6.09E-12	0.97	6.50	-	1768.2
AHQ-4-6, 7290 - 7291	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.50E-10	0.96	5.08	-	1930.1

AHQ-4-4, 7462	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	4.65E-11	0.97	5.90	-	1597.9
AHQ-4-7, 7502	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	8.55E-10	0.95	5.43	-	1263.3
AHQ-4-2, 7518	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.41E-11	0.97	5.82	-	1710.3
AHQ-4-5, 7481	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	8.10E-09	0.96	5.14	-	1769.9
AHQ-4-2, 3411 - 3419	K.DVLLQVDDER.R	1202.29650	1	8.55E-04	0.19	1.99	-	261.2
AHQ-4-3, 2827 - 2828	K.DVLLQVDDERR.N	1358.48286	2	1.49E-04	0.48	2.74	-	495.5
AHQ-4-2, 1819	R.EEILAQAK.E	902.02731	1	9.37E-04	0.55	2.82	-	302.7
AHQ-4-4, 2830	R.ELEDATETADAMNR.E	1566.63006	2	3.16E-05	0.90	3.59	-	1018.1
AHQ-4-6, 2714 - 2716	R.ELEDATETADAMNR.E	1566.63006	2	9.83E-08	0.95	4.05	-	1446.0
AHQ-4-3, 2772 - 2851	R.ELEDATETADAMNR.E	1566.63006	2	1.34E-05	0.89	3.96	-	1048.9
AHQ-4-2, 2862 - 2863	R.ELEDATETADAMNR.E	1566.63006	2	1.23E-11	0.97	5.48	-	985.3
AHQ-4-1, 6242	R.ELESQISELQEDLESER.A	2035.10956	2	1.59E-05	0.82	2.96	-	886.9
AHQ-4-3, 6432	R.ELESQISELQEDLESER.A	2035.10956	2	4.23E-04	0.91	4.31	-	771.5
AHQ-4-3, 6332	R.ELESQISELQEDLESER.A	2035.10956	2	1.11E-05	0.74	3.39	-	522.1
AHQ-4-4, 5975 - 6026	R.ELESQISELQEDLESER.A	2035.10956	2	5.49E-09	0.96	4.38	-	1502.6
AHQ-4-4, 5515	R.ELESQISELQEDLESER.A	2035.10956	2	2.92E-04	0.92	4.06	-	906.4
AHQ-4-3, 5991 - 6060	R.ELESQISELQEDLESER.A	2035.10956	2	1.05E-06	0.96	5.12	-	1071.4
AHQ-4-1, 5470	R.ELESQISELQEDLESER.A	2035.10956	2	1.19E-05	0.61	2.91	-	497.7
AHQ-4-3, 5549	R.ELESQISELQEDLESER.A	2035.10956	2	2.72E-05	0.77	3.54	-	640.3
AHQ-4-2, 6338	R.ELESQISELQEDLESER.A	2035.10956	2	1.80E-07	0.94	4.69	-	957.0
AHQ-4-2, 6064	R.ELESQISELQEDLESER.A	2035.10956	2	2.77E-05	0.64	3.57	-	743.7
AHQ-4-2, 6012	R.ELESQISELQEDLESER.A	2035.10956	3	3.07E-05	0.98	5.65	-	3017.0
AHQ-4-6, 5692 - 5694	R.ELESQISELQEDLESER.A	2035.10956	2	5.18E-06	0.96	5.05	-	1128.2
AHQ-4-1, 5577	R.ELESQISELQEDLESER.A	2035.10956	2	1.58E-06	0.89	3.90	-	684.5
AHQ-4-7, 5746	R.ELESQISELQEDLESER.A	2035.10956	2	1.64E-08	0.96	4.91	-	1197.0
AHQ-4-3, 6000 - 6003	R.ELESQISELQEDLESER.A	2035.10956	3	9.36E-06	0.98	6.35	-	2377.2
AHQ-4-1, 5898 - 5965	R.ELESQISELQEDLESER.A	2035.10956	2	6.14E-09	0.96	5.48	-	931.8
AHQ-4-2, 2495	R.EMEAELEDER.K	1251.30306	2	3.34E-04	0.71	2.53	-	726.8
AHQ-4-4, 2098 - 2106	R.EMEAELEDERK.Q	1379.47597	2	1.00E-07	0.93	3.62	-	1230.3
AHQ-4-5, 1933	R.EMEAELEDERK.Q	1379.47597	2	6.67E-04	0.91	3.39	-	1137.3
AHQ-4-1, 2275	R.EMEAELEDERK.Q	1379.47597	2	2.54E-04	0.85	2.97	-	1002.4
AHQ-4-2, 2107 - 2108	R.EMEAELEDERK.Q	1379.47597	2	2.14E-05	0.93	3.62	-	1205.4
AHQ-4-3, 4613	K.EQADFAIEALAK.A	1306.44632	2	3.88E-04	0.60	2.55	-	564.0
AHQ-4-4, 4447	K.EQADFAIEALAK.A	1306.44632	2	6.48E-04	0.76	2.66	-	745.0
AHQ-4-1, 2474	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.59E-04	0.82	3.58	-	726.9
AHQ-4-6, 2175	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	2.77E-05	0.68	3.64	-	294.0
AHQ-4-4, 2287	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	2.13E-05	0.87	3.94	-	627.4
AHQ-4-3, 2295	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.70E-04	0.92	4.57	-	845.7
AHQ-4-2, 3466	R.FLSNGHVTIPGQQDK.D	1641.80946	2	1.37E-07	0.90	3.64	-	737.3
AHQ-4-1, 3570	R.FLSNGHVTIPGQQDK.D	1641.80946	2	1.09E-04	0.59	2.93	-	518.1
AHQ-4-3, 3456	R.FLSNGHVTIPGQQDK.D	1641.80946	2	3.60E-09	0.92	3.48	-	1115.2
AHQ-4-2, 5242 - 5310	R.FLSNGHVTIPGQQDKDMFQETMEAM*R.I	3028.39040	3	4.45E-06	0.84	4.91	-	898.8
AHQ-4-7, 5727	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	1.94E-04	0.65	3.61	-	370.3
AHQ-4-4, 2682	K.HEAMITDLEER.L	1344.47646	2	5.96E-05	0.97	4.14	-	1661.2
AHQ-4-1, 2965	K.HEAMITDLEER.L	1344.47646	2	2.52E-07	0.94	3.60	-	1088.4
AHQ-4-3, 2723 - 2735	K.HEAMITDLEER.L	1344.47646	2	2.31E-08	0.96	3.83	-	1122.0
AHQ-4-3, 2725	K.HEAMITDLEER.L	1344.47646	1	2.27E-05	0.62	3.10	-	436.4
AHQ-4-4, 2683	K.HEAMITDLEER.L	1344.47646	1	1.17E-06	0.83	3.04	-	785.4
AHQ-4-2, 2758	K.HEAMITDLEER.L	1344.47646	2	1.53E-07	0.97	4.72	-	1610.4
AHQ-4-2, 2759	K.HEAMITDLEER.L	1344.47646	1	1.56E-06	0.49	1.97	-	727.2
AHQ-4-3, 3171 - 3173	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	7.49E-04	0.92	3.43	-	938.4
AHQ-4-1, 3334 - 3405	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	3.26E-04	0.87	3.51	-	1129.0
AHQ-4-3, 3176	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	1.12E-05	0.98	5.02	-	2433.0
AHQ-4-10, 2925	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	4.25E-07	0.95	4.45	-	1792.7
AHQ-4-2, 3500 - 3555	R.HEMPPHIYAITDTAYR.S	1916.14944	2	1.11E-04	0.93	3.52	-	941.5
AHQ-4-4, 3511	R.HEMPPHIYAITDTAYR.S	1916.14944	2	9.26E-06	0.83	3.68	-	460.3
AHQ-4-1, 3393	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	7.10E-05	0.71	2.68	-	547.9
AHQ-4-2, 3547	R.HEMPPHIYAITDTAYR.S	1916.14944	3	2.89E-11	0.97	4.51	-	2224.3
AHQ-4-2, 3628	R.HEMPPHIYAITDTAYR.S	1916.14944	2	1.65E-04	0.83	3.20	-	683.3
AHQ-4-2, 3662 - 3680	R.HEMPPHIYAITDTAYR.S	1916.14944	3	5.51E-05	0.95	3.67	-	1916.8
AHQ-4-6, 2916	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	2.33E-05	0.90	3.44	-	808.9
AHQ-4-6, 2914	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	9.18E-04	0.97	4.60	-	2150.3
AHQ-4-5, 2930	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	1.24E-04	0.87	3.15	-	714.3
AHQ-4-2, 3175 - 3179	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	9.84E-04	0.95	4.08	-	1009.4
AHQ-4-1, 3742	R.HEMPPHIYAITDTAYR.S	1916.14944	2	1.45E-04	0.81	2.86	-	860.3
AHQ-4-2, 3754	R.HEMPPHIYAITDTAYR.S	1916.14944	2	1.95E-04	0.66	3.12	-	496.4
AHQ-4-2, 3183	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	5.42E-06	0.96	4.64	-	1748.9
AHQ-4-2, 4915	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.08E-12	0.97	5.28	-	1764.4
AHQ-4-5, 4206 - 4251	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.99E-05	0.96	4.67	-	1311.3
AHQ-4-3, 4537 - 4583	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.17E-14	0.98	5.93	-	2171.8
AHQ-4-3, 4547	K.HSQAVEELAEQLEQTK.R	1840.96940	3	7.22E-08	0.96	5.10	-	2031.5
AHQ-4-2, 4575	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.57E-06	0.95	4.31	-	1801.9
AHQ-4-2, 4567 - 4646	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.46E-08	0.98	5.80	-	2240.1
AHQ-4-4, 4495	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.86E-08	0.98	5.59	-	2135.6
AHQ-4-1, 4679	K.HSQAVEELAEQLEQTK.R	1840.96940	3	9.36E-09	0.96	4.94	-	1858.8
AHQ-4-10, 3969	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.77E-04	0.81	3.45	-	512.0
AHQ-4-1, 4378	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	7.44E-14	0.97	5.43	-	1955.1
AHQ-4-2, 4091	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.07E-07	0.98	5.71	-	1949.4
AHQ-4-6, 3744	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.75E-05	0.97	5.49	-	1452.5
AHQ-4-1, 4295 - 4374	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	6.58E-07	0.96	5.25	-	913.8
AHQ-4-1, 4277 - 4283	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.02E-05	0.97	5.61	-	1504.4
AHQ-4-4, 4023 - 4026	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	3.89E-12	0.98	6.77	-	1644.4
AHQ-4-4, 4018 - 4020	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	2.00E-04	0.98	5.35	-	2489.4
AHQ-4-2, 4090	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.35E-09	0.97	5.38	-	1585.7
AHQ-4-3, 4048	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	4.69E-06	0.97	5.23	-	1548.1
AHQ-4-3, 4055	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	9.30E-08	0.96	5.48	-	1544.3
AHQ-4-2, 4207	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	4.29E-07	0.97	5.42	-	1724.9
AHQ-4-5, 3758	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	7.84E-07	0.98	5.97	-	1805.1
AHQ-4-3, 3727 - 3795	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.74E-10	0.97	4.62	-	1873.5
AHQ-4-4, 3691 - 3763	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.64E-09	0.96	4.50	-	1492.9
AHQ-4-4, 3795 - 3872	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.49E-06	0.96	4.17	-	1837.2
AHQ-4-6, 3464	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.41E-04	0.88	3.14	-	1291.7
AHQ-4-2, 4143	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.06E-05	0.90	3.26	-	1160.9
AHQ-4-3, 3863 - 3931	R.IAEFTTNLTEEEEK.S	1654.75371	2	8.43E-09	0.96	4.11	-	2114.5
AHQ-4-2, 3756 - 3826	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.74E-11	0.97	4.55	-	2007.0
AHQ-4-1, 4206	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.60E-05	0.87	2.69	-	1457.0
AHQ-4-3, 4000 - 4041	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.72E-05	0.96	4.48	-	1770.5
AHQ-4-2, 3895	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.50E-06	0.98	5.07	-	2008.3
AHQ-4-2, 3892 - 3963	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.06E-07	0.92	3.50	-	1729.6
AHQ-4-5, 3534	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.92E-06	0.96	4.12	-	1568.9
AHQ-4-1, 3838 - 3909	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.10E-08	0.97	4.87	-	1752.4
AHQ-4-1, 4067	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.76E-07	0.97	4.56	-	1875.1
AHQ-4-3, 3320 - 3400	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	8.26E-06	0.86	3.65	-	754.4
AHQ-4-2, 3311	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	1.17E-06	0.73	3.49	-	530.9
AHQ-4-1, 5307 - 5373	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	5.73E-06	0.92	4.57	-	1311.1
AHQ-4-1, 5665	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	1.96E-07	0.87	3.95	-	827.5
AHQ-4-2, 3799 - 3831	K.IAQLEEQLDNETK.E	1531.64695	2	1.08E-06	0.95	4.40	-	1008.0

AHQ-4-10, 3076 - 3088	K.IAQLEEQLDNETK.E	1531.64695	2	5.90E-05	0.92	3.88	-	1154.1
AHQ-4-2, 3607	K.IAQLEEQLDNETK.E	1531.64695	2	2.71E-09	0.97	4.95	-	1645.6
AHQ-4-9, 2855	K.IAQLEEQLDNETK.E	1531.64695	2	1.59E-07	0.94	3.98	-	1399.2
AHQ-4-11, 3174 - 3244	K.IAQLEEQLDNETK.E	1531.64695	2	8.26E-05	0.93	3.96	-	1391.7
AHQ-4-4, 3475	K.IAQLEEQLDNETK.E	1531.64695	2	3.23E-08	0.95	4.26	-	1403.0
AHQ-4-4, 3346 - 3359	K.IAQLEEQLDNETK.E	1531.64695	2	4.44E-05	0.93	3.32	-	1368.2
AHQ-4-1, 3022	K.IAQLEEQLDNETK.E	1531.64695	2	1.08E-07	0.88	3.72	-	891.3
AHQ-4-7, 3081	K.IAQLEEQLDNETK.E	1531.64695	2	7.58E-08	0.97	4.33	-	1850.8
AHQ-4-2, 3519	K.IAQLEEQLDNETK.E	1531.64695	2	7.45E-06	0.96	4.67	-	1435.8
AHQ-4-5, 3163 - 3178	K.IAQLEEQLDNETK.E	1531.64695	2	3.16E-04	0.93	3.92	-	1149.4
AHQ-4-2, 3383 - 3422	K.IAQLEEQLDNETK.E	1531.64695	2	9.89E-07	0.91	3.64	-	1023.8
AHQ-4-2, 3107 - 3178	K.IAQLEEQLDNETK.E	1531.64695	2	1.77E-07	0.96	4.70	-	1720.2
AHQ-4-1, 3457	K.IAQLEEQLDNETK.E	1531.64695	2	1.44E-05	0.97	4.19	-	1672.8
AHQ-4-6, 3106	K.IAQLEEQLDNETK.E	1531.64695	2	7.46E-06	0.97	3.79	-	2076.8
AHQ-4-6, 2982	K.IAQLEEQLDNETK.E	1531.64695	2	1.11E-04	0.37	2.61	-	175.9
AHQ-4-1, 3602 - 3610	K.IAQLEEQLDNETK.E	1531.64695	2	1.37E-05	0.77	3.44	-	734.6
AHQ-4-3, 3163	K.IAQLEEQLDNETK.E	1531.64695	2	7.80E-07	0.96	4.37	-	1663.2
AHQ-4-3, 3452	K.IAQLEEQLDNETKER.Q	1816.94784	2	1.82E-05	0.84	3.96	-	750.9
AHQ-4-2, 3475	K.IAQLEEQLDNETKER.Q	1816.94784	2	1.33E-08	0.93	4.37	-	944.8
AHQ-4-4, 3430	K.IAQLEEQLDNETKER.Q	1816.94784	2	1.76E-08	0.89	4.04	-	710.1
AHQ-4-2, 3050 - 3062	K.IAQLEEQLDNETKER.Q	1816.94784	2	6.47E-07	0.85	3.44	-	886.5
AHQ-4-2, 5447 - 5527	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	4.08E-06	0.94	4.51	-	1043.4
AHQ-4-2, 5439	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	2.79E-04	0.91	4.16	-	729.7
AHQ-4-2, 6762 - 6838	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	6.03E-08	0.98	6.63	-	1539.7
AHQ-4-2, 6696 - 6775	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	7.30E-04	0.96	5.58	-	1040.0
AHQ-4-6, 5610 - 5618	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	3.26E-04	0.96	5.57	-	903.1
AHQ-4-2, 6119 - 6122	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.29E-06	0.97	5.49	-	1354.2
AHQ-4-4, 6738 - 6758	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.12E-06	0.97	5.81	-	1205.2
AHQ-4-1, 6638 - 6665	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	6.31E-06	0.97	5.39	-	1110.0
AHQ-4-3, 6764 - 6833	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.44E-05	0.94	4.80	-	970.1
AHQ-4-1, 5990 - 6067	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.57E-04	0.81	3.19	-	713.1
AHQ-4-6, 6478	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.39E-04	0.95	4.64	-	1063.5
AHQ-4-7, 6625	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.45E-05	0.97	4.88	-	1425.6
AHQ-4-2, 5802	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.65E-05	0.94	4.45	-	900.8
AHQ-4-14-, 5475	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	2.42E-06	0.96	5.18	-	865.9
AHQ-4-5, 6622 - 6653	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.66E-05	0.98	5.62	-	1579.6
AHQ-4-14-, 6199 - 6279	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.76E-04	0.96	5.13	-	1275.0
AHQ-4-2, 5894 - 5971	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	7.98E-04	0.88	4.20	-	562.1
AHQ-4-8, 4766 - 4785	R.IMGIPEEEQMGLLR.V	1616.92826	2	3.51E-06	0.65	3.22	-	300.3
AHQ-4-4, 4656 - 4667	R.IMGIPEEEQM*GLLR.V	1632.92766	2	5.87E-04	0.87	3.57	-	470.4
AHQ-4-4, 5363 - 5364	R.IMGIPEEEQMGLLR.V	1616.92826	2	6.87E-06	0.86	3.26	-	514.1
AHQ-4-2, 4018	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	2.00E-06	0.73	2.76	-	465.7
AHQ-4-2, 4810	R.IM*GIPEEEQMGLLR.V	1632.92766	2	6.91E-05	0.93	3.82	-	961.8
AHQ-4-5, 5173	R.IMGIPEEEQMGLLR.V	1616.92826	2	2.76E-08	0.87	3.26	-	521.5
AHQ-4-5, 4542	R.IM*GIPEEEQMGLLR.V	1632.92766	2	8.09E-09	0.92	3.73	-	972.3
AHQ-4-2, 5386 - 5387	R.IMGIPEEEQMGLLR.V	1616.92826	2	6.14E-07	0.91	4.07	-	524.5
AHQ-4-2, 4791 - 4798	R.IM*GIPEEEQMGLLR.V	1632.92766	2	1.44E-06	0.96	4.29	-	1082.6
AHQ-4-1, 4086	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	2.72E-04	0.70	2.75	-	471.4
AHQ-4-5, 4413 - 4481	R.IMGIPEEEQM*GLLR.V	1632.92766	2	8.87E-06	0.85	3.35	-	520.5
AHQ-4-2, 4698 - 4727	R.IMGIPEEEQM*GLLR.V	1632.92766	2	1.19E-06	0.88	3.89	-	443.5
AHQ-4-3, 5933	K.IRELESQISELQEDLESER.A	2304.45416	3	3.23E-05	0.97	5.65	-	1837.4
AHQ-4-5, 5659 - 5735	K.IRELESQISELQEDLESER.A	2304.45416	2	3.15E-04	0.98	6.93	-	1694.4
AHQ-4-6, 5606	K.IRELESQISELQEDLESER.A	2304.45416	2	9.80E-05	0.96	5.78	-	661.1
AHQ-4-4, 5911	K.IRELESQISELQEDLESER.A	2304.45416	3	1.65E-06	0.94	4.81	-	1394.1
AHQ-4-1, 5987 - 6005	K.IRELESQISELQEDLESER.A	2304.45416	3	7.28E-08	0.96	5.43	-	1790.0
AHQ-4-2, 5966 - 5970	K.IRELESQISELQEDLESER.A	2304.45416	2	5.06E-06	0.98	7.04	-	1523.1
AHQ-4-1, 5985	K.IRELESQISELQEDLESER.A	2304.45416	2	1.43E-05	0.98	7.23	-	1369.9
AHQ-4-3, 5932	K.IRELESQISELQEDLESER.A	2304.45416	2	2.00E-13	0.98	6.66	-	1492.1
AHQ-4-2, 4847	K.KANLQIDQINTDLNLER.S	1999.21478	2	7.12E-08	0.98	6.59	-	1881.4
AHQ-4-6, 4226	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.39E-06	0.97	5.18	-	1653.4
AHQ-4-3, 4611	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.32E-05	0.97	5.63	-	1410.2
AHQ-4-1, 4862 - 4867	K.KANLQIDQINTDLNLER.S	1999.21478	2	8.78E-05	0.93	4.68	-	1060.0
AHQ-4-1, 4694	K.KANLQIDQINTDLNLER.S	1999.21478	3	4.37E-04	0.87	4.17	-	943.8
AHQ-4-3, 4701	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.33E-05	0.97	5.96	-	1430.1
AHQ-4-3, 4811 - 4885	K.KANLQIDQINTDLNLER.S	1999.21478	2	7.50E-04	0.93	4.28	-	1039.0
AHQ-4-9, 3787	K.KANLQIDQINTDLNLER.S	1999.21478	2	5.54E-05	0.98	6.37	-	2162.8
AHQ-4-1, 4630 - 4697	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.93E-05	0.97	5.76	-	1242.5
AHQ-4-5, 4310	K.KANLQIDQINTDLNLER.S	1999.21478	2	7.86E-09	0.96	5.57	-	1209.8
AHQ-4-2, 4764	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.32E-05	0.89	4.85	-	688.8
AHQ-4-2, 2416	R.KKVEAQLQELQVK.F	1541.81761	2	3.08E-07	0.96	4.56	-	1369.1
AHQ-4-6, 2248	R.KKVEAQLQELQVK.F	1541.81761	2	9.90E-04	0.95	4.30	-	1458.5
AHQ-4-2, 2422	R.KKVEAQLQELQVK.F	1541.81761	3	1.49E-04	0.86	3.63	-	883.6
AHQ-4-3, 2396 - 2420	R.KKVEAQLQELQVK.F	1541.81761	2	1.40E-07	0.97	5.05	-	1992.8
AHQ-4-1, 2582 - 2642	R.KKVEAQLQELQVK.F	1541.81761	2	3.10E-05	0.97	4.97	-	1628.1
AHQ-4-4, 2390 - 2391	R.KKVEAQLQELQVK.F	1541.81761	2	1.07E-08	0.98	5.17	-	2035.4
AHQ-4-5, 2229 - 2245	R.KKVEAQLQELQVK.F	1541.81761	2	2.92E-06	0.98	5.17	-	2042.7
AHQ-4-1, 3555 - 3563	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.52E-04	0.97	5.35	-	1405.9
AHQ-4-5, 3209	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.43E-05	0.97	5.17	-	1523.9
AHQ-4-3, 3641 - 3643	K.KLEEEQIILEDQNCK.L	1891.08992	2	3.84E-04	0.94	4.53	-	607.2
AHQ-4-3, 3352 - 3427	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.01E-11	0.98	6.39	-	1581.4
AHQ-4-3, 3783	K.KLEEEQIILEDQNCK.L	1891.08992	2	3.78E-06	0.98	4.91	-	2061.4
AHQ-4-2, 3380 - 3452	K.KLEEEQIILEDQNCK.L	1891.08992	2	3.41E-09	0.98	6.31	-	1999.1
AHQ-4-2, 3530 - 3598	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.25E-10	0.98	5.61	-	1464.0
AHQ-4-4, 3528	K.KLEEEQIILEDQNCK.L	1891.08992	3	9.44E-04	0.73	3.14	-	921.8
AHQ-4-3, 3491 - 3559	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.06E-05	0.97	5.26	-	1226.1
AHQ-4-4, 3386 - 3387	K.KLEEEQIILEDQNCK.L	1891.08992	2	7.06E-05	0.97	5.72	-	1560.2
AHQ-4-2, 3450	K.KLEEEQIILEDQNCK.L	1891.08992	3	7.92E-09	0.91	4.56	-	1155.7
AHQ-4-1, 3661	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.44E-09	0.98	6.27	-	1916.4
AHQ-4-4, 3494 - 3563	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.35E-07	0.97	5.25	-	1252.3
AHQ-4-2, 3675 - 3752	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.64E-05	0.97	5.29	-	1378.2
AHQ-4-3, 3525	K.KLEEEQIILEDQNCK.L	1891.08992	3	1.09E-06	0.92	3.83	-	1539.6
AHQ-4-6, 7042	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	1.39E-04	0.89	4.51	-	889.4
AHQ-4-5, 7186 - 7187	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	8.57E-07	0.97	5.33	-	1768.6
AHQ-4-3, 7297 - 7371	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	8.36E-08	0.92	5.18	-	872.0
AHQ-4-4, 7259	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.27E-07	0.98	6.42	-	1537.1
AHQ-4-1, 7093 - 7103	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.24E-07	0.89	5.08	-	727.3
AHQ-4-6, 7040 - 7086	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.61E-06	0.91	4.30	-	847.7
AHQ-4-5, 7185	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	9.44E-09	0.96	5.88	-	1273.4
AHQ-4-2, 7318	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	7.73E-08	0.89	4.93	-	545.6
AHQ-4-2, 7319	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	4.31E-07	0.97	5.72	-	1335.2
AHQ-4-1, 7094 - 7161	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	7.62E-09	0.98	6.35	-	1402.9
AHQ-4-4, 7258 - 7266	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.20E-06	0.90	5.23	-	768.3
AHQ-4-2, 2603	K.KLVWVPSDK.S	1072.28194	2	3.30E-04	0.87	3.39	-	856.9
AHQ-4-13-, 2801	K.KLVWVPSDK.S	1072.28194	1	2.02E-04	0.47	2.35	-	394.7
AHQ-4-4, 2600	K.KLVWVPSDK.S	1072.28194	1	1.61E-04	0.73	2.67	-	680.8
AHQ-4-7, 2334	K.KLVWVPSDK.S	1072.28194	1	3.43E-04	0.38	2.36	-	492.7
AHQ-4-2, 3620 - 3622	K.KMEDSVGCLETAEEVK.R	1827.02450	2	2.35E-08	0.96	4.97	-	1326.3

AHQ-4-3, 3585	K.KMEDSVGCLETAEEVK.R	1827.02450	2	4.63E-04	0.90	4.12	-	826.2
AHQ-4-1, 3275	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	2.23E-04	0.84	3.20	-	742.8
AHQ-4-2, 3122 - 3123	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	1.84E-05	0.93	3.93	-	1102.1
AHQ-4-4, 2784 - 2786	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	2.66E-06	0.85	3.20	-	567.2
AHQ-4-3, 3199	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	1.98E-05	0.96	4.78	-	1273.1
AHQ-4-4, 3199	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	9.81E-09	0.93	4.92	-	1023.1
AHQ-4-2, 3211	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	2.67E-04	0.94	5.04	-	1154.5
AHQ-4-1, 3001	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	5.70E-06	0.82	3.73	-	335.4
AHQ-4-2, 2823	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	1.46E-06	0.75	3.43	-	474.0
AHQ-4-5, 2574	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	5.04E-05	0.87	3.88	-	1051.3
AHQ-4-2, 3212	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	2.26E-08	0.92	4.18	-	883.4
AHQ-4-2, 2819	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	2.66E-04	0.96	4.90	-	1607.1
AHQ-4-1, 2998	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	1.06E-05	0.97	5.12	-	2136.3
AHQ-4-3, 3205	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	6.35E-05	0.95	5.17	-	1167.5
AHQ-4-3, 2811	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	2.02E-07	0.92	4.86	-	890.4
AHQ-4-4, 5360 - 5382	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	8.24E-07	0.96	4.70	-	1288.3
AHQ-4-1, 4973	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	8.51E-07	0.74	3.25	-	418.5
AHQ-4-1, 5521	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	7.45E-08	0.95	5.19	-	926.4
AHQ-4-2, 4930	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	2.20E-04	0.49	2.81	-	267.8
AHQ-4-1, 4231	K.KQELEEICHDLEAR.V	1771.93036	2	8.37E-06	0.95	4.46	-	1540.4
AHQ-4-3, 4071 - 4087	K.KQELEEICHDLEAR.V	1771.93036	3	2.92E-04	0.97	5.52	-	1869.0
AHQ-4-5, 3798	K.KQELEEICHDLEAR.V	1771.93036	3	5.27E-04	0.95	4.83	-	1634.2
AHQ-4-2, 4108 - 4178	K.KQELEEICHDLEAR.V	1771.93036	3	3.39E-07	0.95	4.84	-	1887.4
AHQ-4-4, 4019 - 4039	K.KQELEEICHDLEAR.V	1771.93036	2	8.86E-04	0.97	4.68	-	1877.2
AHQ-4-4, 4032	K.KQELEEICHDLEAR.V	1771.93036	3	4.55E-04	0.96	5.41	-	1807.1
AHQ-4-9, 3415	K.KQELEEICHDLEAR.V	1771.93036	2	2.95E-04	0.98	5.21	-	2352.7
AHQ-4-8, 3605	K.KQELEEICHDLEAR.V	1771.93036	2	3.29E-05	0.97	4.96	-	1911.7
AHQ-4-5, 3731 - 3797	K.KQELEEICHDLEAR.V	1771.93036	2	5.93E-05	0.97	5.06	-	2022.8
AHQ-4-3, 4053 - 4127	K.KQELEEICHDLEAR.V	1771.93036	2	3.69E-06	0.96	5.19	-	1496.4
AHQ-4-5, 2539	K.KVEAQLQELQVK.F	1413.64470	2	3.90E-04	0.96	4.83	-	1337.0
AHQ-4-1, 3023 - 3042	K.KVEAQLQELQVK.F	1413.64470	2	1.25E-05	0.97	4.84	-	1736.2
AHQ-4-4, 2744	K.KVEAQLQELQVK.F	1413.64470	2	2.94E-06	0.94	4.42	-	1141.6
AHQ-4-3, 2751	K.KVEAQLQELQVK.F	1413.64470	2	6.54E-05	0.95	4.83	-	1066.7
AHQ-4-2, 2766	K.KVEAQLQELQVK.F	1413.64470	2	5.81E-07	0.95	4.73	-	1107.8
AHQ-4-2, 2791	K.KVEAQLQELQVK.F	1413.64470	1	1.25E-06	0.74	3.25	-	506.4
AHQ-4-6, 2575	K.KVEAQLQELQVK.F	1413.64470	2	6.31E-05	0.95	4.48	-	1168.0
AHQ-4-3, 2760	K.KVEAQLQELQVK.F	1413.64470	1	3.08E-04	0.82	3.34	-	620.2
AHQ-4-2, 3604	K.KVIQYLAYVASSHK.S	1607.87775	2	9.87E-09	0.96	4.08	-	1689.5
AHQ-4-1, 4070	K.LEEEQIILEDQNCK.L	1762.91700	2	2.99E-04	0.85	3.83	-	634.8
AHQ-4-3, 3847 - 3912	K.LEEEQIILEDQNCK.L	1762.91700	2	2.78E-06	0.96	4.70	-	1254.7
AHQ-4-1, 3913 - 3991	K.LEEEQIILEDQNCK.L	1762.91700	2	8.81E-08	0.97	5.60	-	1290.3
AHQ-4-2, 3971 - 4043	K.LEEEQIILEDQNCK.L	1762.91700	2	2.29E-06	0.97	5.01	-	1382.1
AHQ-4-4, 3819	K.LEEEQIILEDQNCK.L	1762.91700	2	1.09E-07	0.93	3.97	-	1209.2
AHQ-4-3, 3952 - 3996	K.LEEEQIILEDQNCK.L	1762.91700	2	1.36E-09	0.95	4.65	-	1193.7
AHQ-4-4, 7366 - 7368	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	1.73E-09	0.95	4.76	-	1179.3
AHQ-4-2, 7426	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	1.68E-10	0.97	6.19	-	1105.6
AHQ-4-1, 3642	R.LEVNLQAMK.A	1046.26630	2	5.41E-05	0.88	3.47	-	677.5
AHQ-4-3, 3469	R.LEVNLQAMK.A	1046.26630	2	2.39E-05	0.80	3.56	-	506.2
AHQ-4-2, 3459 - 3468	R.LEVNLQAMK.A	1046.26630	2	1.98E-05	0.88	3.58	-	626.7
AHQ-4-2, 2498 - 2508	R.LEVNLQAM*K.A	1062.26570	2	6.01E-06	0.85	3.17	-	707.6
AHQ-4-2, 3371	K.LKDVLLQVDDER.R	1443.62767	2	1.20E-07	0.95	3.95	-	1418.1
AHQ-4-5, 3130	K.LKDVLLQVDDER.R	1443.62767	2	9.70E-09	0.95	4.27	-	1463.6
AHQ-4-3, 3381 - 3392	K.LKDVLLQVDDER.R	1443.62767	2	8.74E-10	0.96	4.03	-	1905.3
AHQ-4-11, 3220	K.LKDVLLQVDDER.R	1443.62767	2	1.53E-05	0.91	3.22	-	1640.4
AHQ-4-1, 3606	K.LKDVLLQVDDER.R	1443.62767	2	1.38E-05	0.96	4.18	-	1614.6
AHQ-4-4, 2911 - 2918	K.LKDVLLQVDDERR.N	1599.81402	2	4.01E-04	0.87	3.55	-	928.9
AHQ-4-1, 3147 - 3209	K.LKDVLLQVDDERR.N	1599.81402	2	2.23E-06	0.94	4.03	-	1430.2
AHQ-4-2, 2875 - 2947	K.LKDVLLQVDDERR.N	1599.81402	2	9.41E-06	0.91	3.76	-	1198.9
AHQ-4-3, 2920	K.LKDVLLQVDDERR.N	1599.81402	2	1.14E-04	0.89	3.52	-	1131.3
AHQ-4-5, 2645	K.LKDVLLQVDDERR.N	1599.81402	2	1.06E-04	0.83	3.43	-	886.5
AHQ-4-2, 2616	K.LKNKHEAMITDLEER.L	1828.08363	2	1.88E-08	0.94	4.20	-	974.5
AHQ-4-5, 6019 - 6042	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.11E-09	0.97	5.49	-	1719.3
AHQ-4-1, 6226	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.18E-11	0.95	4.75	-	1209.1
AHQ-4-4, 6154	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.67E-08	0.95	4.55	-	1450.1
AHQ-4-6, 5927	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	2.20E-06	0.91	4.45	-	760.6
AHQ-4-2, 6358 - 6415	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.03E-06	0.95	4.89	-	1215.9
AHQ-4-2, 5671	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.20E-07	0.97	5.02	-	1450.5
AHQ-4-2, 6274	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.04E-04	0.91	4.30	-	822.3
AHQ-4-3, 5040	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.05E-07	0.96	4.82	-	1335.5
AHQ-4-2, 6192 - 6262	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	9.43E-11	0.98	5.34	-	2091.7
AHQ-4-2, 6190 - 6258	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	6.18E-04	0.91	4.09	-	975.1
AHQ-4-1, 6383	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.46E-06	0.94	4.54	-	1151.8
AHQ-4-3, 6199 - 6207	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.84E-08	0.98	5.48	-	1942.5
AHQ-4-5, 5959	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.27E-06	0.88	4.01	-	668.4
AHQ-4-6, 5900	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.53E-09	0.97	5.10	-	1479.0
AHQ-4-7, 5890	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.01E-08	0.97	4.72	-	1800.1
AHQ-4-4, 5656	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	7.13E-05	0.71	3.12	-	253.2
AHQ-4-1, 6229	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	4.62E-05	0.86	4.15	-	734.8
AHQ-4-5, 5871 - 5950	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.57E-11	0.96	4.95	-	1543.4
AHQ-4-4, 6164	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	5.47E-04	0.93	4.40	-	1019.0
AHQ-4-3, 6201 - 6223	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	5.64E-05	0.90	4.34	-	846.7
AHQ-4-3, 5683 - 5692	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.43E-06	0.82	3.59	-	452.7
AHQ-4-1, 5902 - 5969	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.04E-06	0.97	5.68	-	1367.2
AHQ-4-3, 5860 - 5927	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.04E-07	0.98	6.17	-	1409.6
AHQ-4-2, 5910 - 5978	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.00E-09	0.97	5.76	-	1150.5
AHQ-4-2, 5955	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	7.79E-05	0.96	5.12	-	1888.0
AHQ-4-1, 6033	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.13E-07	0.97	5.60	-	1383.4
AHQ-4-14-, 5518	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.06E-08	0.96	5.23	-	1179.3
AHQ-4-3, 5996 - 6071	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.52E-06	0.98	5.88	-	1709.5
AHQ-4-2, 6046 - 6118	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.66E-14	0.98	5.91	-	1813.2
AHQ-4-1, 6151	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.19E-05	0.93	3.82	-	1152.5
AHQ-4-2, 6326	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.77E-07	0.96	5.25	-	1065.6
AHQ-4-5, 6087	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.46E-05	0.96	5.27	-	968.3
AHQ-4-1, 5591	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.24E-08	0.97	5.69	-	1393.8
AHQ-4-3, 6139 - 6220	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.59E-09	0.98	6.67	-	1927.1
AHQ-4-5, 5895	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.08E-05	0.90	3.52	-	934.0
AHQ-4-5, 5734 - 5803	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	8.45E-05	0.96	5.02	-	1102.0
AHQ-4-3, 6289	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.01E-07	0.95	5.71	-	756.1
AHQ-4-3, 6317 - 6388	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.40E-04	0.82	3.65	-	508.5
AHQ-4-4, 5560	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.78E-04	0.92	4.36	-	705.1
AHQ-4-4, 5931	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.05E-06	0.97	5.27	-	1217.9
AHQ-4-4, 6014	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.25E-04	0.88	3.74	-	952.6
AHQ-4-2, 7127	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.06E-04	0.93	4.35	-	882.3
AHQ-4-2, 7324	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.91E-04	0.81	3.82	-	925.0
AHQ-4-2, 5192 - 5210	R.LTEMETLQSQLMAEK.L	1753.03211	2	2.10E-09	0.97	5.50	-	1749.7
AHQ-4-2, 4558 - 4638	R.LTEMETLQSQLM*AEK.L	1769.03151	2	4.28E-04	0.80	3.51	-	701.9
AHQ-4-3, 5175 - 5184	R.LTEMETLQSQLMAEK.L	1753.03211	2	1.59E-07	0.97	4.84	-	1882.2

AHQ-4-3, 3501 - 3571	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	2.57E-04	0.62	3.03	-	520.5
AHQ-4-2, 4743	R.LTEMETLQSQLM*AEK.L	1769.03151	2	5.67E-06	0.91	3.94	-	944.6
AHQ-4-3, 5293	R.LTEMETLQSQLMAEK.L	1753.03211	2	2.92E-04	0.63	2.78	-	707.3
AHQ-4-2, 3532 - 3602	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	1.84E-05	0.85	3.87	-	731.9
AHQ-4-1, 3622 - 3690	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	7.28E-05	0.92	3.96	-	1110.4
AHQ-4-4, 4571 - 4572	R.LTEMETLQSQLM*AEK.L	1769.03151	2	2.74E-08	0.91	3.49	-	1221.0
AHQ-4-5, 4945	R.LTEMETLQSQLMAEK.L	1753.03211	2	2.01E-04	0.93	3.34	-	1423.6
AHQ-4-2, 4067 - 4134	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	1.24E-06	0.98	5.49	-	1911.4
AHQ-4-3, 4619	R.LTEMETLQSQLM*AEK.L	1769.03151	2	1.36E-06	0.96	5.11	-	1454.2
AHQ-4-2, 5211	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	2.12E-05	0.92	3.34	-	1258.4
AHQ-4-4, 5122 - 5124	R.LTEMETLQSQLMAEK.L	1753.03211	2	6.07E-06	0.98	5.41	-	1939.5
AHQ-4-1, 4145	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	7.74E-04	0.96	3.72	-	2305.3
AHQ-4-2, 3022	K.LVWVPSDK.S	944.10903	1	9.62E-04	0.44	2.17	-	412.1
AHQ-4-2, 3996	K.MEDSVGCLETAEEVK.R	1698.85159	2	2.98E-10	0.92	3.98	-	847.2
AHQ-4-2, 3559	K.MEDSVGCLETAEEVKR.K	1855.03794	3	4.46E-06	0.80	3.94	-	411.6
AHQ-4-2, 3578	K.MEDSVGCLETAEEVKR.K	1855.03794	2	1.25E-04	0.79	3.47	-	462.2
AHQ-4-2, 3202	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	4.65E-07	0.68	2.80	-	394.8
AHQ-4-3, 3531	K.MEDSVGCLETAEEVKR.K	1855.03794	2	4.61E-07	0.87	3.82	-	543.8
AHQ-4-4, 3503	K.MEDSVGCLETAEEVKR.K	1855.03794	2	1.84E-06	0.81	3.45	-	576.5
AHQ-4-1, 3577 - 3654	K.MEDSVGCLETAEEVKR.K	1855.03794	2	1.30E-06	0.19	2.57	-	246.5
AHQ-4-1, 5702	K.MQQNIQELEEQLEEEESAR.Q	2334.46063	3	2.85E-08	0.89	3.98	-	938.1
AHQ-4-2, 5666 - 5735	K.MQQNIQELEEQLEEEESAR.Q	2334.46063	3	1.51E-04	0.87	4.41	-	827.4
AHQ-4-13, 5278 - 5280	K.NFINNPLAQADWAAK.K	1673.85315	2	2.60E-07	0.92	4.22	-	881.9
AHQ-4-4, 6072	K.NFINNPLAQADWAAK.K	1673.85315	2	3.60E-06	0.94	4.13	-	1170.0
AHQ-4-1, 5474 - 5503	K.NFINNPLAQADWAAK.K	1673.85315	2	5.13E-07	0.93	4.28	-	1065.1
AHQ-4-13-, 5637 - 5709	K.NFINNPLAQADWAAK.K	1673.85315	2	2.15E-06	0.89	3.81	-	711.4
AHQ-4-2, 5396	K.NFINNPLAQADWAAK.K	1673.85315	2	2.82E-07	0.95	4.76	-	1014.3
AHQ-4-2, 6094	K.NFINNPLAQADWAAK.K	1673.85315	2	5.89E-10	0.93	4.21	-	881.3
AHQ-4-6, 5086 - 5102	K.NFINNPLAQADWAAK.K	1673.85315	2	9.50E-05	0.96	5.05	-	1116.6
AHQ-4-4, 5367 - 5398	K.NFINNPLAQADWAAK.K	1673.85315	2	2.20E-09	0.95	4.62	-	1093.6
AHQ-4-3, 5403	K.NFINNPLAQADWAAK.K	1673.85315	2	7.70E-10	0.96	5.16	-	1156.3
AHQ-4-2, 5559	K.NFINNPLAQADWAAK.K	1673.85315	2	2.54E-08	0.89	3.94	-	792.1
AHQ-4-10, 4680 - 4683	K.NFINNPLAQADWAAK.K	1673.85315	2	4.13E-07	0.95	4.87	-	966.4
AHQ-4-7, 5046	K.NFINNPLAQADWAAK.K	1673.85315	2	4.92E-06	0.93	3.91	-	1134.3
AHQ-4-11, 4982	K.NFINNPLAQADWAAK.K	1673.85315	2	2.07E-05	0.97	5.28	-	1250.7
AHQ-4-5, 5157	K.NFINNPLAQADWAAK.K	1673.85315	2	7.29E-07	0.89	4.04	-	758.5
AHQ-4-12, 5211	K.NFINNPLAQADWAAK.K	1673.85315	2	8.78E-08	0.91	4.38	-	788.2
AHQ-4-13-, 5172	K.NFINNPLAQADWAAK.K	1673.85315	2	1.37E-10	0.97	5.86	-	1376.3
AHQ-4-3, 6101	K.NFINNPLAQADWAAK.K	1673.85315	2	2.16E-09	0.95	4.49	-	971.9
AHQ-4-1, 2647	K.NKHEAMITDLEER.L	1586.75247	2	1.65E-04	0.90	3.50	-	844.5
AHQ-4-2, 2414 - 2415	K.NKHEAMITDLEER.L	1586.75247	2	7.05E-09	0.95	3.91	-	1385.0
AHQ-4-3, 2391	K.NKHEAMITDLEER.L	1586.75247	2	1.09E-07	0.95	4.04	-	1348.3
AHQ-4-4, 2382 - 2383	K.NKHEAMITDLEER.L	1586.75247	2	1.41E-07	0.94	4.11	-	1298.1
AHQ-4-6, 5542	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.82E-04	0.91	3.24	-	803.6
AHQ-4-13-, 5570	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.66E-07	0.88	3.66	-	626.2
AHQ-4-3, 5259	K.NLPIYSEEIVEM*YK.G	1744.98660	2	3.09E-05	0.82	3.65	-	375.4
AHQ-4-1, 5293 - 5357	K.NLPIYSEEIVEM*YK.G	1744.98660	2	3.65E-04	0.96	4.21	-	1305.1
AHQ-4-11, 4858	K.NLPIYSEEIVEM*YK.G	1744.98660	2	9.91E-05	0.87	3.48	-	654.0
AHQ-4-2, 5874 - 5942	K.NLPIYSEEIVEMYK.G	1728.98720	2	5.59E-07	0.93	4.06	-	656.1
AHQ-4-5, 5015	K.NLPIYSEEIVEM*YK.G	1744.98660	2	4.31E-04	0.95	4.37	-	1086.3
AHQ-4-2, 5262 - 5282	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.96E-04	0.92	4.06	-	715.9
AHQ-4-3, 5872	K.NLPIYSEEIVEMYK.G	1728.98720	2	4.12E-04	0.69	2.53	-	545.4
AHQ-4-10, 5056 - 5064	K.NLPIYSEEIVEMYK.G	1728.98720	2	5.52E-04	0.93	4.15	-	784.0
AHQ-4-1, 5157	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	6.73E-09	0.86	3.50	-	807.8
AHQ-4-2, 5716	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	8.97E-07	0.95	4.64	-	756.9
AHQ-4-2, 5123	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	1.47E-05	0.90	4.42	-	1073.3
AHQ-4-6, 5260	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	2.66E-06	0.87	4.18	-	495.2
AHQ-4-4, 5546	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	2.75E-08	0.94	4.64	-	897.6
AHQ-4-2, 5578	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	3	3.84E-07	0.70	3.03	-	479.4
AHQ-4-5, 5483	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.65E-10	0.93	4.53	-	859.9
AHQ-4-1, 5690	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	8.52E-05	0.86	4.00	-	549.1
AHQ-4-5, 5319	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	4.24E-07	0.91	4.93	-	627.0
AHQ-4-2, 5207	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	8.48E-08	0.93	3.97	-	1022.9
AHQ-4-3, 5096	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	8.09E-04	0.78	3.24	-	849.7
AHQ-4-2, 5879	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.81E-04	0.92	4.42	-	802.9
AHQ-4-3, 5209	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	2.59E-04	0.83	3.35	-	659.7
AHQ-4-3, 5583	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	7.06E-04	0.73	3.32	-	484.3
AHQ-4-3, 5592	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	3	3.42E-04	0.60	3.02	-	302.5
AHQ-4-1, 7254	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	6.82E-07	0.98	6.03	-	1896.6
AHQ-4-6, 7275	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	2.00E-06	0.97	5.11	-	1478.0
AHQ-4-2, 7534	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	2.92E-07	0.98	6.10	-	2428.7
AHQ-4-3, 7543	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	5.04E-09	0.98	6.08	-	1998.7
AHQ-4-3, 3111	R.QAQQERDELADEIANSSGK.G	2090.15168	2	1.16E-04	0.94	4.63	-	803.6
AHQ-4-2, 3226	R.QAQQERDELADEIANSSGK.G	2090.15168	2	4.53E-07	0.93	4.45	-	1014.2
AHQ-4-1, 3283 - 3290	R.QAQQERDELADEIANSSGK.G	2090.15168	2	5.02E-05	0.89	4.27	-	480.4
AHQ-4-1, 2886	R.QAQQERDELADEIANSSGK.G	2090.15168	2	7.66E-06	0.84	3.75	-	582.9
AHQ-4-3, 2776 - 2784	R.QAQQERDELADEIANSSGK.G	2090.15168	2	2.07E-04	0.87	4.02	-	513.1
AHQ-4-2, 4620	K.QELEEICHDLEAR.V	1643.75744	2	2.90E-05	0.66	3.08	-	337.2
AHQ-4-1, 4669	K.QELEEICHDLEAR.V	1643.75744	2	5.92E-07	0.30	2.55	-	250.3
AHQ-4-2, 2172	K.QIATLHAQVADM*K.K	1442.66637	2	3.56E-04	0.75	3.11	-	449.3
AHQ-4-2, 1951	R.QLEEAEEEAQR.A	1332.35590	2	3.24E-05	0.78	3.50	-	494.9
AHQ-4-3, 1921	R.QLEEAEEEAQR.A	1332.35590	2	1.21E-04	0.83	3.30	-	732.4
AHQ-4-3, 3419 - 3431	R.RGDLPFVVPR.R	1156.36217	2	6.25E-04	0.95	3.90	-	1226.5
AHQ-4-10, 3152	R.RGDLPFVVPR.R	1156.36217	2	1.49E-04	0.91	3.44	-	976.6
AHQ-4-5, 3090 - 3161	R.RGDLPFVVPR.R	1156.36217	2	6.37E-05	0.88	3.57	-	834.7
AHQ-4-2, 3388 - 3460	R.RGDLPFVVPR.R	1156.36217	2	4.59E-05	0.94	3.74	-	1202.0
AHQ-4-1, 3646 - 3714	R.RGDLPFVVPR.R	1156.36217	2	2.05E-04	0.95	3.97	-	1315.5
AHQ-4-4, 3410	R.RGDLPFVVPR.R	1156.36217	2	9.99E-07	0.92	3.54	-	1142.1
AHQ-4-11, 3286	R.RGDLPFVVPR.R	1156.36217	2	5.26E-06	0.93	3.66	-	1102.1
AHQ-4-6, 3124	R.RGDLPFVVPR.R	1156.36217	2	4.22E-05	0.90	3.24	-	948.5
AHQ-4-2, 2847	K.RHEM*PPHIYAITDTAYR.S	2088.33519	3	4.64E-06	0.96	4.53	-	1680.8
AHQ-4-1, 6871 - 6875	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	2.59E-13	0.98	7.24	-	1922.2
AHQ-4-2, 6935 - 6983	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.06E-07	0.98	6.43	-	2068.5
AHQ-4-4, 6902	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	6.12E-09	0.97	6.39	-	1347.7
AHQ-4-3, 6915 - 6929	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	6.27E-10	0.97	6.74	-	1489.7
AHQ-4-3, 2816	K.RQAQQERDELADEIANSSGK.G	2246.33803	2	2.42E-05	0.82	3.63	-	438.0
AHQ-4-2, 1871 - 1883	K.RQLEEAEEEAQR.A	1488.54225	2	2.55E-08	0.98	5.28	-	3426.9
AHQ-4-2, 6294 - 6336	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.54E-04	0.97	5.93	-	1582.1
AHQ-4-10, 5592	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	6.38E-06	0.97	5.95	-	1613.1
AHQ-4-2, 6388 - 6412	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.43E-06	0.89	4.67	-	897.8
AHQ-4-1, 6341	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	5.98E-06	0.88	4.11	-	801.9
AHQ-4-5, 6842 - 6861	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	8.87E-06	0.94	3.98	-	1464.0
AHQ-4-3, 7016 - 7017	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	4.09E-08	0.98	6.15	-	1968.9
AHQ-4-1, 6907 - 6909	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.01E-07	0.98	6.40	-	1958.3
AHQ-4-1, 6906	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	3.20E-06	0.94	4.88	-	1433.2
AHQ-4-1, 5901 - 5946	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	9.56E-05	0.83	3.40	-	1144.0
AHQ-4-1, 4854	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.12E-09	0.98	5.89	-	2046.5

AHQ-4-2, 7048	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	9.91E-08	0.96	4.74	-	1349.5
AHQ-4-2, 7039	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	1.35E-09	0.97	5.45	-	2266.0
AHQ-4-1, 5677	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	1.20E-05	0.96	5.02	-	1929.4
AHQ-4-3, 7031	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	9.41E-06	0.93	3.99	-	1106.6
AHQ-4-2, 7027 - 7091	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	6.33E-08	0.96	5.70	-	1265.4
AHQ-4-1, 4939	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	8.24E-05	0.89	3.82	-	945.0
AHQ-4-4, 6972 - 7014	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.54E-04	0.96	5.02	-	1627.0
AHQ-4-3, 5765	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	3.69E-04	0.52	3.24	-	592.3
AHQ-4-2, 4848 - 4923	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.26E-10	0.97	5.21	-	1725.6
AHQ-4-2, 5847 - 5928	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	2.36E-04	0.90	4.43	-	1290.3
AHQ-4-3, 4825 - 4836	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	3.62E-09	0.98	5.76	-	1618.5
AHQ-4-2, 3524 - 3539	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	9.48E-06	0.97	5.94	-	1590.0
AHQ-4-10, 3155	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	1.92E-09	0.94	4.93	-	1004.3
AHQ-4-3, 3493	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	2.13E-04	0.96	5.08	-	1643.6
AHQ-4-4, 3471	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	2.72E-07	0.97	5.26	-	1902.0
AHQ-4-5, 2783	R.SM*MQDREDQSILCTGESGAGK.T	2318.50627	2	4.86E-04	0.89	4.34	-	486.3
AHQ-4-5, 3295	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	2.66E-04	0.93	4.66	-	1395.4
AHQ-4-2, 3515	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	3	4.04E-04	0.59	3.14	-	654.0
AHQ-4-7, 3314 - 3323	K.TDLLLEPYNK.Y	1206.36989	2	3.23E-06	0.84	2.88	-	1102.5
AHQ-4-5, 3441	K.TDLLLEPYNK.Y	1206.36989	2	3.42E-05	0.85	3.66	-	811.7
AHQ-4-6, 3374 - 3375	K.TDLLLEPYNK.Y	1206.36989	2	5.44E-06	0.85	3.20	-	1059.2
AHQ-4-3, 3676	K.TDLLLEPYNK.Y	1206.36989	2	1.87E-05	0.86	3.56	-	906.7
AHQ-4-4, 3660 - 3671	K.TDLLLEPYNK.Y	1206.36989	2	2.30E-05	0.89	3.50	-	991.9
AHQ-4-2, 3770	K.TDLLLEPYNK.Y	1206.36989	2	9.89E-06	0.89	3.25	-	1192.6
AHQ-4-1, 3817	K.TDLLLEPYNK.Y	1206.36989	2	1.26E-04	0.80	3.24	-	858.8
AHQ-4-2, 3687 - 3699	K.TDLLLEPYNK.Y	1206.36989	2	2.30E-05	0.95	4.39	-	1238.6
AHQ-4-7, 3347 - 3415	K.TDLLLEPYNK.Y	1206.36989	1	6.63E-05	0.15	2.01	-	325.5
AHQ-4-3, 3827	K.TDLLLEPYNKYR.F	1525.73037	2	3.93E-07	0.82	2.83	-	992.0
AHQ-4-3, 4452 - 4455	K.TELEDTLDSTAAQQELR.S	1921.00969	2	3.23E-05	0.95	4.97	-	1254.0
AHQ-4-1, 4453	K.TELEDTLDSTAAQQELR.S	1921.00969	2	2.82E-07	0.92	3.95	-	1082.9
AHQ-4-4, 4422	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.10E-09	0.96	4.64	-	1719.4
AHQ-4-5, 4294 - 4298	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.72E-07	0.97	4.65	-	2263.4
AHQ-4-2, 3103	R.TEMEDLMSSK.D	1171.32449	2	2.85E-06	0.91	3.38	-	859.4
AHQ-4-2, 3126	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.77E-05	0.96	4.40	-	1832.7
AHQ-4-3, 3337 - 3345	R.TEMEDLMSSKDDVGK.S	1685.85626	2	4.59E-08	0.78	3.22	-	719.3
AHQ-4-2, 3366	R.TEMEDLMSSKDDVGK.S	1685.85626	2	2.17E-06	0.94	4.03	-	1366.1
AHQ-4-2, 2444	R.TEMEDLM*SSKDDVGK.S	1701.85566	2	8.89E-05	0.81	3.34	-	704.9
AHQ-4-5, 3147	R.TEMEDLMSSKDDVGK.S	1685.85626	2	3.20E-06	0.92	3.81	-	1101.1
AHQ-4-2, 6532 - 6550	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	5.74E-07	0.98	6.04	-	2382.2
AHQ-4-2, 6527 - 6604	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	2.79E-10	0.97	5.77	-	1460.4
AHQ-4-9, 5599 - 5624	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	5.17E-05	0.98	5.20	-	1990.1
AHQ-4-3, 6575 - 6651	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.96E-04	0.98	5.63	-	1836.2
AHQ-4-2, 6730	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	5.58E-04	0.96	4.02	-	1533.2
AHQ-4-7, 6071	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	2.50E-05	0.75	2.92	-	910.7
AHQ-4-2, 1692 - 1762	K.VAAYDKLEK.T	1037.19123	2	9.36E-04	0.84	3.11	-	600.9
AHQ-4-5, 3021	K.VEAQLQELQVK.F	1285.47179	2	2.00E-05	0.92	3.46	-	1141.2
AHQ-4-3, 3224	K.VEAQLQELQVK.F	1285.47179	2	3.74E-05	0.96	4.31	-	1368.5
AHQ-4-2, 3238	K.VEAQLQELQVK.F	1285.47179	2	1.62E-07	0.96	4.51	-	1544.8
AHQ-4-4, 3206	K.VEAQLQELQVK.F	1285.47179	2	1.76E-05	0.95	4.08	-	1258.8
AHQ-4-2, 3240	K.VEAQLQELQVK.F	1285.47179	1	9.66E-04	0.67	3.24	-	576.9
AHQ-4-11, 5574	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.16E-05	0.70	3.33	-	383.8
AHQ-4-13-, 5152 - 5160	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	9.38E-09	0.95	5.54	-	1161.2
AHQ-4-4, 5344 - 5355	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	3.64E-06	0.95	4.75	-	943.6
AHQ-4-10, 5472	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.39E-10	0.84	3.92	-	542.4
AHQ-4-6, 5650 - 5727	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.81E-07	0.89	3.85	-	859.2
AHQ-4-5, 5729 - 5797	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	7.93E-04	0.90	4.45	-	690.7
AHQ-4-4, 6064	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.87E-07	0.93	4.96	-	655.6
AHQ-4-6, 5754	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	9.30E-09	0.86	4.01	-	590.3
AHQ-4-10, 5237 - 5259	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.35E-10	0.96	4.61	-	1507.6
AHQ-4-5, 5893	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	3.67E-06	0.81	3.33	-	598.5
AHQ-4-13, 5270	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.27E-04	0.93	4.51	-	886.0
AHQ-4-10, 4673	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.34E-08	0.91	3.88	-	1320.3
AHQ-4-1, 5482 - 5551	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	2.26E-06	0.90	4.04	-	712.4
AHQ-4-10, 4653	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.69E-05	0.82	3.90	-	516.7
AHQ-4-6, 5059	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	4.82E-04	0.38	2.84	-	420.9
AHQ-4-4, 6071 - 6079	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	3.43E-10	0.92	4.74	-	815.2
AHQ-4-5, 5743 - 5807	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.30E-08	0.95	4.75	-	958.9
AHQ-4-1, 6094	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	5.36E-06	0.70	3.39	-	352.7
AHQ-4-2, 6099 - 6102	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	3.96E-10	0.94	4.85	-	1017.3
AHQ-4-13-, 5144	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	2.21E-04	0.78	3.27	-	548.1
AHQ-4-3, 6109	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.01E-08	0.90	4.11	-	826.0
AHQ-4-3, 6103	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.25E-10	0.92	4.48	-	585.3
AHQ-4-3, 6047 - 6115	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.74E-11	0.92	4.19	-	835.6
AHQ-4-2, 6098 - 6136	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	3.10E-09	0.94	4.77	-	692.9
AHQ-4-11, 4961	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	5.78E-06	0.78	3.40	-	676.6
AHQ-4-9, 5293	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	3.10E-04	0.52	2.99	-	291.1
AHQ-4-7, 5693 - 5694	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	5.76E-07	0.84	3.88	-	458.4
AHQ-4-2, 5327 - 5403	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.18E-07	0.91	4.09	-	722.7
AHQ-4-2, 5375 - 5392	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	2.02E-12	0.97	6.27	-	1730.7
AHQ-4-7, 5795 - 5870	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	3.96E-05	0.84	3.89	-	558.0
AHQ-4-3, 5385 - 5404	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.58E-05	0.92	4.62	-	940.0
AHQ-4-6, 6051	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.65E-08	0.37	2.84	-	321.0
AHQ-4-9, 5192 - 5196	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.98E-06	0.85	3.80	-	656.7
AHQ-4-13, 5789	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	6.45E-08	0.79	4.00	-	587.3
AHQ-4-6, 5743	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.43E-09	0.93	4.56	-	728.7
AHQ-4-2, 1902 - 1974	R.VEEEEERCQHLQAEK.K	1916.01642	2	6.78E-04	0.92	4.27	-	1094.2
AHQ-4-2, 3919	K.VIQYLAYVASSHK.S	1479.70484	3	9.09E-05	0.86	3.43	-	696.7
AHQ-4-2, 3918 - 3922	K.VIQYLAYVASSHK.S	1479.70484	2	2.06E-06	0.95	4.36	-	1036.0
AHQ-4-1, 4093	K.VIQYLAYVASSHK.S	1479.70484	3	2.63E-05	0.67	3.45	-	445.5
AHQ-4-6, 3523 - 3535	K.VIQYLAYVASSHK.S	1479.70484	2	2.63E-05	0.93	3.92	-	1103.9
AHQ-4-4, 3867	K.VIQYLAYVASSHK.S	1479.70484	2	4.85E-05	0.94	3.97	-	1186.7
AHQ-4-5, 3541 - 3542	K.VIQYLAYVASSHK.S	1479.70484	2	8.41E-06	0.87	3.17	-	968.6
AHQ-4-2, 4002	K.VIQYLAYVASSHK.S	1479.70484	2	2.70E-05	0.89	3.03	-	1119.9
AHQ-4-10, 3495	K.VIQYLAYVASSHK.S	1479.70484	2	4.31E-05	0.86	3.23	-	853.0
AHQ-4-7, 3430	K.VIQYLAYVASSHK.S	1479.70484	2	1.06E-06	0.95	4.17	-	1316.3
AHQ-4-1, 4083	K.VIQYLAYVASSHK.S	1479.70484	2	2.42E-05	0.80	2.83	-	961.3
AHQ-4-1, 6605 - 6607	R.VISGVLQLGNIVFK.K	1487.81155	2	9.68E-04	0.84	2.94	-	890.8
AHQ-4-3, 6624 - 6695	R.VISGVLQLGNIVFK.K	1487.81155	2	5.67E-06	0.97	4.87	-	1936.8
AHQ-4-2, 6515	R.VISGVLQLGNIVFK.K	1487.81155	2	9.98E-10	0.96	5.05	-	1268.9
AHQ-4-5, 6541	R.VISGVLQLGNIVFK.K	1487.81155	1	1.11E-05	0.64	3.20	-	440.2
AHQ-4-4, 6618 - 6684	R.VISGVLQLGNIVFK.K	1487.81155	2	6.05E-05	0.96	3.98	-	1867.2
AHQ-4-7, 6209 - 6287	R.VISGVLQLGNIVFK.K	1487.81155	1	3.96E-04	0.05	1.94	-	124.6
AHQ-4-6, 6346	R.VISGVLQLGNIVFK.K	1487.81155	2	2.50E-08	0.97	4.79	-	2010.9
AHQ-4-5, 6409	R.VISGVLQLGNIVFK.K	1487.81155	2	6.31E-04	0.96	3.35	-	2022.1
AHQ-4-7, 6246 - 6274	R.VISGVLQLGNIVFK.K	1487.81155	2	1.69E-07	0.98	5.28	-	1893.0
AHQ-4-2, 6608 - 6674	R.VISGVLQLGNIVFK.K	1487.81155	2	7.63E-10	0.96	4.61	-	1551.1
AHQ-4-5, 6443	R.VISGVLQLGNIVFK.K	1487.81155	1	8.15E-07	0.32	2.63	-	314.6

AHQ-4-2, 6624	R.VISGVLQLGNIVFK.K	1487.81155	1	4.37E-07	0.63	3.28	-	421.3
AHQ-4-10, 5744	R.VISGVLQLGNIVFK.K	1487.81155	2	2.28E-05	0.87	3.24	-	813.7
AHQ-4-2, 6875	R.VISGVLQLGNIVFK.K	1487.81155	2	1.60E-06	0.97	4.82	-	1823.9
AHQ-4-2, 6748	R.VISGVLQLGNIVFK.K	1487.81155	2	2.09E-09	0.98	5.65	-	1785.6
AHQ-4-4, 6580 - 6654	R.VISGVLQLGNIVFK.K	1487.81155	1	2.85E-04	0.49	2.75	-	429.1
AHQ-4-1, 6022	R.VISGVLQLGNIVFKK.E	1615.98446	2	7.25E-06	0.87	3.64	-	980.9
AHQ-4-2, 4927 - 4999	K.VSHLLGINVTDFTR.G	1572.79026	2	1.54E-10	0.97	5.64	-	1539.7
AHQ-4-4, 4923 - 4950	K.VSHLLGINVTDFTR.G	1572.79026	2	1.52E-09	0.96	4.27	-	1495.2
AHQ-4-12, 4778	K.VSHLLGINVTDFTR.G	1572.79026	2	5.06E-05	0.93	3.66	-	1083.5
AHQ-4-2, 4983 - 4991	K.VSHLLGINVTDFTR.G	1572.79026	3	1.17E-04	0.88	4.19	-	976.8
AHQ-4-1, 5011 - 5069	K.VSHLLGINVTDFTR.G	1572.79026	2	6.30E-10	0.96	4.83	-	1272.3
AHQ-4-6, 4571	K.VSHLLGINVTDFTR.G	1572.79026	2	1.07E-12	0.96	4.94	-	1259.2
AHQ-4-2, 5264	K.VSHLLGINVTDFTR.G	1572.79026	2	7.25E-05	0.96	4.07	-	1709.7
AHQ-4-5, 4642	K.VSHLLGINVTDFTR.G	1572.79026	3	7.38E-06	0.86	4.04	-	1026.4
AHQ-4-3, 4955 - 5027	K.VSHLLGINVTDFTR.G	1572.79026	2	1.78E-07	0.96	4.49	-	1452.8
AHQ-4-5, 4626 - 4699	K.VSHLLGINVTDFTR.G	1572.79026	2	1.08E-09	0.97	5.06	-	1497.3
AHQ-4-1, 3257	R.VVFQEFR.Q	925.06580	2	2.75E-04	0.82	2.65	-	816.4
AHQ-4-2, 3024 - 3042	R.VVFQEFR.Q	925.06580	2	3.91E-05	0.80	2.67	-	469.4
AHQ-4-3, 4256	R.YEILTPNSIPK.G	1275.47536	2	1.48E-06	0.81	3.12	-	821.4
AHQ-4-3, 4257	R.YEILTPNSIPK.G	1275.47536	1	3.25E-05	0.23	2.03	-	435.2
AHQ-4-2, 4271	R.YEILTPNSIPK.G	1275.47536	2	7.00E-07	0.91	3.41	-	1117.2
AHQ-4-3, 4013 - 4023	R.YEILTPNSIPK.G	1275.47536	1	8.93E-04	0.30	2.28	-	350.4
AHQ-4-4, 3987 - 3992	R.YEILTPNSIPK.G	1275.47536	2	2.98E-05	0.94	3.34	-	1372.2
gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				1.72E-14	23.87	290.27	50.10	55901.8
AHQ-4-6, 2254	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.52E-08	0.94	4.10	-	968.4
AHQ-4-10, 2175 - 2248	K.AHYGGFTVQNEANK.Y	1536.63020	2	4.39E-04	0.88	3.44	-	824.2
AHQ-4-7, 2045 - 2122	K.AHYGGFTVQNEANK.Y	1536.63020	2	9.96E-05	0.91	3.63	-	958.2
AHQ-4-4, 2275	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.77E-05	0.85	3.13	-	893.7
AHQ-4-8, 1936	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.77E-08	0.87	3.50	-	726.1
AHQ-4-7, 2217	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.77E-07	0.92	3.64	-	950.2
AHQ-4-6, 2102	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.24E-06	0.93	4.07	-	955.1
AHQ-4-6, 6539	K.APDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	3961.41191	3	9.33E-04	0.89	4.62	-	589.1
AHQ-4-11, 3981 - 3998	K.DNENVVNEYSSELEK.H	1769.80167	2	5.17E-06	0.88	4.30	-	734.4
AHQ-4-12, 4122	K.DNENVVNEYSSELEK.H	1769.80167	2	2.53E-04	0.88	3.98	-	832.6
AHQ-4-9, 3687	K.DNENVVNEYSSELEK.H	1769.80167	2	4.99E-04	0.78	3.63	-	541.4
AHQ-4-7, 3349 - 3418	K.DNENVVNEYSSELEK.H	1769.80167	2	5.91E-12	0.89	3.96	-	754.5
AHQ-4-6, 4264 - 4330	K.DNENVVNEYSSELEK.H	1769.80167	2	9.43E-09	0.86	3.95	-	775.0
AHQ-4-6, 3996 - 4066	K.DNENVVNEYSSELEK.H	1769.80167	2	3.17E-09	0.91	4.03	-	766.8
AHQ-4-7, 4054 - 4075	K.DNENVVNEYSSELEK.H	1769.80167	2	5.13E-09	0.95	5.20	-	969.0
AHQ-4-4, 4276 - 4280	K.DNENVVNEYSSELEK.H	1769.80167	2	5.07E-04	0.86	3.80	-	722.1
AHQ-4-1, 4341	K.DNENVVNEYSSELEK.H	1769.80167	2	3.08E-04	0.75	3.10	-	523.6
AHQ-4-6, 3552	K.DNENVVNEYSSELEK.H	1769.80167	2	2.92E-04	0.93	4.22	-	857.3
AHQ-4-6, 3390	K.EDGGGWWYNR.C	1240.26508	2	9.45E-05	0.72	2.76	-	629.6
AHQ-4-6, 3134 - 3138	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	7.14E-07	0.47	3.37	-	229.9
AHQ-4-6, 3859 - 3926	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	8.38E-08	0.93	4.55	-	764.6
AHQ-4-6, 3854 - 3878	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	6.07E-08	0.86	4.16	-	794.6
AHQ-4-8, 3662	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	6.26E-06	0.84	4.13	-	782.2
AHQ-4-8, 3666	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	6.01E-05	0.81	3.53	-	548.4
AHQ-4-7, 3833 - 3850	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	1.95E-04	0.84	3.65	-	1122.9
AHQ-4-9, 3496	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	5.09E-06	0.84	3.92	-	473.0
AHQ-4-7, 3829	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	3.01E-04	0.81	3.55	-	587.3
AHQ-4-7, 3351 - 3355	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	6.38E-06	0.64	3.17	-	425.8
AHQ-4-8, 3661	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.62E-04	0.92	4.41	-	683.6
AHQ-4-4, 4176	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	7.14E-04	0.65	3.35	-	384.5
AHQ-4-3, 4237 - 4249	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.23E-04	0.69	3.52	-	493.0
AHQ-4-6, 3404	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	4.17E-06	0.77	3.40	-	378.3
AHQ-4-6, 3231 - 3232	K.HGTDDGVVWM*NWK.G	1561.70314	2	6.55E-05	0.96	4.38	-	1402.6
AHQ-4-8, 3743	K.HGTDDGVVWMNWK.G	1545.70374	2	2.44E-07	0.95	4.53	-	1019.3
AHQ-4-6, 3971 - 3972	K.HGTDDGVVWMNWK.G	1545.70374	2	3.75E-06	0.97	4.68	-	1274.5
AHQ-4-4, 3543	K.HGTDDGVVWM*NWK.G	1561.70314	2	3.70E-04	0.69	2.98	-	404.8
AHQ-4-11, 4009	K.HGTDDGVVWMNWK.G	1545.70374	2	2.52E-04	0.96	4.03	-	1305.0
AHQ-4-7, 3925 - 3927	K.HGTDDGVVWMNWK.G	1545.70374	2	1.54E-06	0.96	4.35	-	1413.3
AHQ-4-7, 3154	K.HGTDDGVVWM*NWK.G	1561.70314	2	2.34E-06	0.96	3.99	-	1283.1
AHQ-4-8, 6007	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	4089.58482	3	1.89E-05	0.81	4.16	-	330.9
AHQ-4-7, 6225 - 6294	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	4089.58482	3	6.64E-04	0.80	4.39	-	213.1
AHQ-4-8, 2986	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	4.44E-06	0.94	5.14	-	1038.6
AHQ-4-7, 3282 - 3325	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.99E-06	0.88	4.15	-	666.6
AHQ-4-6, 3376	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	1.22E-07	0.96	5.32	-	1151.0
AHQ-4-6, 2959	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	2	2.74E-04	0.67	2.87	-	395.6
AHQ-4-6, 3334 - 3386	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	2.93E-08	0.95	5.42	-	837.2
AHQ-4-9, 2961 - 3024	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	4.97E-04	0.82	4.10	-	636.1
AHQ-4-8, 2985	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	1.00E-04	0.95	5.08	-	1035.7
AHQ-4-6, 2438	K.LESDVSAQM*EYCR.T	1605.72945	2	2.67E-05	0.95	3.72	-	1363.4
AHQ-4-8, 6766	R.MGPTELLIEMEDWK.G	1692.97836	2	1.20E-07	0.89	3.72	-	838.7
AHQ-4-6, 6374	R.M*GPTELLIEMEDWK.G	1708.97776	2	9.84E-06	0.96	4.71	-	1429.5
AHQ-4-7, 6383 - 6387	R.M*GPTELLIEMEDWK.G	1708.97776	2	9.39E-05	0.95	4.19	-	1376.5
AHQ-4-11, 6525	R.MGPTELLIEMEDWK.G	1692.97836	2	1.44E-08	0.95	4.63	-	1031.6
AHQ-4-6, 6987	R.MGPTELLIEMEDWK.G	1692.97836	2	1.23E-04	0.90	3.74	-	895.9
AHQ-4-7, 4661 - 4734	R.M*GPTELLIEM*EDWK.G	1724.97716	2	6.09E-04	0.84	2.97	-	950.7
AHQ-4-9, 6328	R.MGPTELLIEMEDWK.G	1692.97836	2	1.42E-08	0.88	3.90	-	924.8
AHQ-4-10, 5779	R.M*GPTELLIEMEDWK.G	1708.97776	2	3.18E-08	0.87	3.47	-	829.6
AHQ-4-6, 6894 - 6895	R.MGPTELLIEMEDWK.G	1692.97836	2	2.88E-08	0.97	5.17	-	1391.1
AHQ-4-7, 7021	R.MGPTELLIEMEDWK.G	1692.97836	2	8.46E-06	0.95	4.41	-	1426.9
AHQ-4-6, 6291 - 6367	R.MGPTELLIEMEDWKGDK.V	1993.29069	2	5.12E-06	0.37	2.74	-	277.5
AHQ-4-6, 5640	R.M*GPTELLIEMEDWKGDK.V	2009.29009	3	9.70E-04	0.91	4.14	-	981.7
AHQ-4-7, 5381 - 5382	K.NYCGLPGEYWLGNDK.I	1787.92994	2	2.53E-07	0.95	4.89	-	700.2
AHQ-4-6, 5760	K.NYCGLPGEYWLGNDK.I	1787.92994	2	2.56E-08	0.88	3.99	-	367.8
AHQ-4-6, 5254 - 5322	K.NYCGLPGEYWLGNDK.I	1787.92994	2	2.71E-08	0.94	4.63	-	485.1
AHQ-4-7, 5953 - 5965	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	2	3.08E-05	0.74	3.46	-	341.0
AHQ-4-6, 3779	K.QVKDNENVVNEYSSELEK.H	2125.23593	2	1.66E-04	0.25	2.69	-	151.1
AHQ-4-7, 2718	K.REEAPSLRPAPPPISGGGYR.A	2108.34617	3	1.95E-04	0.96	4.68	-	1970.6
AHQ-4-6, 4698	R.TMTIHNGMFFSTYDR.D	1822.05792	2	8.74E-05	0.76	2.91	-	723.6
AHQ-4-7, 3657 - 3681	R.TPCTVSCNIPVVSGK.E	1621.85811	2	3.04E-06	0.88	3.68	-	693.2
AHQ-4-7, 4691	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	2.37E-04	0.86	3.64	-	1113.2
AHQ-4-1, 5159	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	3.66E-05	0.75	3.21	-	708.9
AHQ-4-6, 4840 - 4911	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.22E-05	0.78	3.58	-	338.6
AHQ-4-8, 4607	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	3.48E-07	0.97	5.03	-	2267.0
AHQ-4-6, 4834 - 4902	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	4.05E-11	0.95	5.12	-	1303.9
AHQ-4-9, 4407	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	4.90E-08	0.92	4.58	-	1186.4
AHQ-4-7, 4795 - 4867	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	4.45E-08	0.93	4.51	-	1292.4
AHQ-4-7, 4963	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	5.25E-05	0.92	3.99	-	1278.8
AHQ-4-9, 4089	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	4.14E-10	0.94	4.37	-	1122.9
AHQ-4-6, 4075	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	2.74E-05	0.92	4.36	-	855.2
AHQ-4-7, 3954 - 4033	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	3.50E-08	0.94	4.78	-	1035.2
AHQ-4-6, 3903 - 3983	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	2.22E-05	0.93	4.53	-	932.9
AHQ-4-7, 4483 - 4553	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	2.65E-08	0.94	4.40	-	904.3
AHQ-4-7, 4621 - 4689	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	2.39E-06	0.93	4.38	-	866.6

AHQ-4-7, 4742	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	4.77E-05	0.93	4.06	-	892.6
AHQ-4-6, 4470 - 4550	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.72E-14	0.96	4.91	-	1301.7
AHQ-4-11, 4860	R.YYWGGQYTWDMAK.H	1669.84009	2	1.22E-07	0.96	3.89	-	1519.6
AHQ-4-7, 4974	R.YYWGGQYTWDMAK.H	1669.84009	2	3.67E-06	0.82	2.62	-	862.5
AHQ-4-6, 4962 - 5042	R.YYWGGQYTWDMAK.H	1669.84009	2	1.87E-08	0.95	3.71	-	1252.9
AHQ-4-12, 5087 - 5154	R.YYWGGQYTWDMAK.H	1669.84009	2	4.46E-05	0.85	3.10	-	766.9
AHQ-4-14, 5624 - 5629	R.YYWGGQYTWDM*AK.H	1685.83949	2	4.90E-04	0.61	2.62	-	358.2
AHQ-4-14, 5732 - 5740	R.YYWGGQYTWDM*AK.H	1685.83949	2	1.48E-05	0.97	4.52	-	1254.7
AHQ-4-14, 6345	R.YYWGGQYTWDMAK.H	1669.84009	2	1.12E-04	0.89	3.13	-	873.9
AHQ-4-14-, 4426 - 4430	R.YYWGGQYTWDM*AK.H	1685.83949	2	9.77E-04	0.97	4.77	-	1672.5
AHQ-4-14-, 4975	R.YYWGGQYTWDMAK.H	1669.84009	2	3.36E-05	0.95	3.80	-	1257.0
gi|24431935|ref|NP_065393.1|	reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sap			2.00E-14	0.97	10.31	2.80	129930.3
AHQ-4-13-, 6080 - 6148	K.YQFVREPEDEEEEEEEEEDEDEDLEELEVLER.K	4189.14063	3	2.00E-14	0.97	6.18	-	1621.5
gi|28626504|ref|NP_113659.3|	UNC-112 related protein 2 [Homo sapiens]			2.78E-14	26.14	300.35	58.10	75429.7
AHQ-4-6, 2955	K.AGDALWLR.F	902.03223	2	3.34E-04	0.89	3.29	-	1245.3
AHQ-4-14-, 6381	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	1.02E-12	0.97	5.42	-	1660.9
AHQ-4-10, 6011	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	3.57E-06	0.81	2.97	-	706.8
AHQ-4-12, 6565 - 6635	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	4.60E-07	0.93	4.20	-	1090.8
AHQ-4-9, 6103 - 6167	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.81E-05	0.95	4.37	-	964.7
AHQ-4-1, 6926 - 6929	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.91E-07	0.94	4.19	-	929.1
AHQ-4-8, 6417	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.64E-04	0.70	2.57	-	605.4
AHQ-4-10, 6044	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.47E-04	0.92	3.97	-	796.2
AHQ-4-5, 6845	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.56E-07	0.94	4.58	-	681.2
AHQ-4-6, 6614 - 6678	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.10E-08	0.95	4.91	-	787.0
AHQ-4-2, 7040	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.08E-09	0.92	3.90	-	784.9
AHQ-4-12, 6629	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.76E-06	0.88	3.57	-	633.8
AHQ-4-9, 6347	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.71E-06	0.90	3.93	-	604.9
AHQ-4-6, 6922 - 6927	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.80E-10	0.93	4.59	-	686.5
AHQ-4-6, 6742 - 6759	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.41E-05	0.93	4.37	-	777.9
AHQ-4-6, 6671	R.ASFSQPLFQAVAAICR.L	1768.02967	3	2.48E-08	0.95	5.06	-	1365.3
AHQ-4-3, 7019	R.ASFSQPLFQAVAAICR.L	1768.02967	2	6.17E-06	0.94	4.34	-	839.6
AHQ-4-6, 3406	K.EKEPEEELYDLSK.V	1609.71294	2	7.19E-09	0.81	3.53	-	434.1
AHQ-4-9, 3048 - 3051	K.EKEPEEELYDLSK.V	1609.71294	2	9.16E-07	0.86	3.67	-	426.0
AHQ-4-6, 3279 - 3358	K.EKEPEEELYDLSK.V	1609.71294	2	9.74E-09	0.86	4.07	-	428.0
AHQ-4-9, 6607 - 6609	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	5.50E-05	0.91	4.81	-	432.3
AHQ-4-9, 6392	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	9.18E-05	0.92	4.79	-	507.4
AHQ-4-13, 6797	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	7.82E-04	0.77	3.56	-	356.9
AHQ-4-6, 7159 - 7166	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	3.84E-05	0.94	5.23	-	543.2
AHQ-4-6, 6974 - 6976	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	5.10E-04	0.95	5.18	-	596.9
AHQ-4-12, 6974	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	4.32E-06	0.92	4.57	-	551.1
AHQ-4-9, 2820	K.GCEVVPDVNVSGQK.F	1489.63335	1	1.60E-05	0.80	3.15	-	731.9
AHQ-4-6, 3064	K.GCEVVPDVNVSGQK.F	1489.63335	1	2.48E-07	0.91	3.90	-	903.2
AHQ-4-12, 3182 - 3194	K.GCEVVPDVNVSGQK.F	1489.63335	2	4.24E-05	0.83	3.28	-	631.4
AHQ-4-13, 6852	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	2.14E-08	0.91	4.04	-	913.2
AHQ-4-6, 7072 - 7143	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	1.77E-10	0.94	4.61	-	1039.1
AHQ-4-14-, 6649	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	1.28E-13	0.95	5.51	-	803.6
AHQ-4-6, 2835	R.GM*PAHFSDSAQTEACYHM*LSR.P	2430.63997	3	5.34E-07	0.94	4.45	-	1326.5
AHQ-4-6, 3758	R.GMPAHFSDSAQTEACYHMLSR.P	2398.64117	3	7.03E-09	0.93	4.10	-	1333.8
AHQ-4-9, 3325	R.IDLAVGDVVK.T	1029.21223	1	1.16E-05	0.72	3.00	-	578.8
AHQ-4-13-, 3849 - 3850	R.IDLAVGDVVK.T	1029.21223	1	7.66E-04	0.43	2.64	-	398.8
AHQ-4-13, 4018	R.IDLAVGDVVK.T	1029.21223	1	9.89E-04	0.81	3.19	-	739.3
AHQ-4-9, 3323 - 3548	R.IDLAVGDVVK.T	1029.21223	1	8.16E-04	0.33	2.17	-	430.0
AHQ-4-6, 3634 - 3702	R.IDLAVGDVVK.T	1029.21223	1	2.53E-04	0.18	2.05	-	344.3
AHQ-4-6, 4394	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	7.11E-08	0.98	5.86	-	1595.1
AHQ-4-13, 4530	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	8.25E-13	0.98	5.87	-	2189.7
AHQ-4-1, 4730 - 4741	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.45E-09	0.98	5.43	-	2103.7
AHQ-4-12, 4418	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.32E-09	0.98	6.17	-	2432.4
AHQ-4-7, 4193	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.08E-08	0.98	6.01	-	1686.8
AHQ-4-4, 4616	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.67E-11	0.97	5.69	-	1216.8
AHQ-4-11, 4256	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	4.40E-07	0.91	4.77	-	984.2
AHQ-4-11, 4254	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	3.45E-09	0.98	6.16	-	1917.2
AHQ-4-12, 4417	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	2.67E-07	0.93	4.97	-	1436.4
AHQ-4-6, 4258 - 4323	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.78E-14	0.98	6.56	-	1942.9
AHQ-4-5, 4349	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.15E-04	0.97	5.01	-	1705.6
AHQ-4-9, 3889	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.01E-07	0.98	5.95	-	1454.2
AHQ-4-6, 4487	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.06E-09	0.98	5.14	-	2187.9
AHQ-4-10, 4011	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	7.62E-06	0.98	7.09	-	2214.9
AHQ-4-3, 4657 - 4667	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.73E-13	0.98	5.81	-	1570.1
AHQ-4-6, 2330	R.KDEILGIANNR.L	1243.39499	1	1.09E-04	0.18	1.83	-	204.1
AHQ-4-13, 2785 - 2845	R.KDEILGIANNR.L	1243.39499	1	2.92E-05	0.63	2.44	-	451.9
AHQ-4-13-, 2669 - 2676	R.KDEILGIANNR.L	1243.39499	2	3.64E-06	0.96	4.03	-	1427.8
AHQ-4-12, 2541 - 2543	R.KDEILGIANNR.L	1243.39499	2	5.68E-05	0.90	3.34	-	1028.7
AHQ-4-6, 2331 - 2410	R.KDEILGIANNR.L	1243.39499	2	3.27E-06	0.96	4.39	-	1468.9
AHQ-4-9, 2243 - 2304	R.KDEILGIANNR.L	1243.39499	2	1.97E-05	0.95	4.12	-	1470.8
AHQ-4-6, 2564	R.KDEILGIANNR.L	1243.39499	1	1.32E-10	0.19	1.92	-	291.7
AHQ-4-9, 2236 - 2309	R.KDEILGIANNR.L	1243.39499	1	6.77E-06	0.17	2.13	-	246.5
AHQ-4-6, 3708	R.KQDWSDHAIWWEQK.R	1858.00504	3	7.09E-07	0.93	4.36	-	1210.1
AHQ-4-6, 6540	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.10E-05	0.63	3.01	-	546.2
AHQ-4-8, 6474	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.85E-05	0.92	4.37	-	763.6
AHQ-4-6, 6654 - 6722	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.49E-06	0.96	4.97	-	915.5
AHQ-4-3, 7011 - 7081	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.08E-05	0.83	3.85	-	461.5
AHQ-4-14-, 6358 - 6397	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.61E-04	0.86	3.91	-	497.3
AHQ-4-7, 6789	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.20E-04	0.80	3.74	-	434.5
AHQ-4-6, 6235 - 6238	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.09E-06	0.93	4.37	-	852.7
AHQ-4-6, 6370 - 6435	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.08E-04	0.84	3.72	-	514.9
AHQ-4-6, 5586 - 5599	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.37E-04	0.95	4.44	-	1259.9
AHQ-4-13-, 6529	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.98E-06	0.85	3.72	-	580.4
AHQ-4-9, 6127	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.17E-04	0.85	3.61	-	522.1
AHQ-4-5, 6846	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.57E-06	0.93	4.43	-	842.3
AHQ-4-6, 6326 - 6334	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	1.35E-11	0.82	4.27	-	551.0
AHQ-4-12, 5769 - 5773	K.LLVPSPEGMSEIYLR.C	1705.01201	2	1.34E-06	0.58	3.07	-	228.3
AHQ-4-6, 4662 - 4742	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	9.50E-06	0.32	2.83	-	136.3
AHQ-4-6, 5826	K.LLVPSPEGMSEIYLR.C	1705.01201	2	9.43E-07	0.72	2.78	-	392.8
AHQ-4-11, 5570 - 5586	K.LLVPSPEGMSEIYLR.C	1705.01201	2	1.11E-05	0.71	2.72	-	329.7
AHQ-4-1, 7045	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.13E-09	0.90	4.38	-	1025.8
AHQ-4-4, 7162 - 7178	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.26E-04	0.87	4.19	-	973.4
AHQ-4-6, 6867 - 6938	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	9.09E-13	0.96	5.86	-	1417.2
AHQ-4-7, 7037	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	7.49E-08	0.79	3.37	-	898.4
AHQ-4-3, 7205 - 7208	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.41E-06	0.87	3.63	-	1403.6
AHQ-4-6, 6322 - 6390	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	6.13E-04	0.63	3.21	-	592.1
AHQ-4-9, 2059	R.LTQLYEQAR.W	1122.25622	2	9.59E-04	0.91	3.81	-	1172.6
AHQ-4-7, 2086	R.LTQLYEQAR.W	1122.25622	2	2.42E-06	0.89	3.45	-	1066.5
AHQ-4-6, 2114 - 2131	R.LTQLYEQAR.W	1122.25622	2	4.92E-05	0.91	3.97	-	949.4
AHQ-4-6, 3938 - 3959	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.97E-09	0.91	4.53	-	505.9
AHQ-4-11, 3904 - 3916	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.72E-08	0.88	3.66	-	641.4
AHQ-4-12, 4041	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.53E-08	0.87	4.02	-	418.6
AHQ-4-6, 3798 - 3870	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	8.08E-06	0.92	4.51	-	576.2

AHQ-4-14-, 4231 - 4241	K.TASGDYIDSSWELR.V	1600.66783	2	2.61E-07	0.74	3.35	-	765.4
AHQ-4-9, 3841 - 3843	K.TASGDYIDSSWELR.V	1600.66783	2	6.75E-11	0.92	3.63	-	863.9
AHQ-4-6, 4303 - 4380	K.TASGDYIDSSWELR.V	1600.66783	2	1.02E-10	0.95	4.36	-	1009.1
AHQ-4-9, 3191 - 3251	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	7.39E-04	0.95	5.43	-	1048.1
AHQ-4-9, 3468	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.11E-04	0.43	2.52	-	312.4
AHQ-4-11, 3660	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	6.64E-05	0.94	4.77	-	846.6
AHQ-4-6, 3547 - 3618	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	4.59E-06	0.93	5.04	-	693.3
AHQ-4-1, 4127	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.14E-06	0.77	3.28	-	339.0
AHQ-4-7, 3522	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	9.23E-04	0.93	4.54	-	901.2
AHQ-4-9, 3239	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	1.25E-04	0.82	3.93	-	395.1
AHQ-4-5, 3631	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	4.30E-04	0.93	4.80	-	974.1
AHQ-4-10, 3531	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.20E-05	0.91	4.31	-	683.2
AHQ-4-4, 3898	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	7.47E-05	0.76	3.40	-	468.5
AHQ-4-6, 3544 - 3614	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	1.73E-10	0.97	6.20	-	1316.7
AHQ-4-6, 7283	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	3.32E-09	0.96	5.24	-	1641.9
AHQ-4-6, 7302	R.TMADSSYTSEVQAILAFLSLQR.T	2432.73531	3	6.07E-06	0.97	5.36	-	1897.9
AHQ-4-3, 4151	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.96E-09	0.96	5.02	-	1124.6
AHQ-4-10, 3689 - 3695	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.42E-06	0.94	4.63	-	1238.9
AHQ-4-14, 4877 - 4949	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.61E-06	0.96	4.40	-	1484.5
AHQ-4-2, 4170	R.VFVGEEDPEAESVTLR.V	1777.91007	2	7.63E-06	0.74	3.21	-	1003.0
AHQ-4-13-, 3972 - 4045	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.19E-08	0.95	4.54	-	1178.4
AHQ-4-5, 3945	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.89E-13	0.96	4.51	-	1650.1
AHQ-4-9, 3491 - 3536	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.51E-04	0.86	3.44	-	945.4
AHQ-4-11, 3860	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.75E-11	0.95	4.50	-	1377.2
AHQ-4-14-, 3833	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.03E-06	0.85	3.16	-	1037.4
AHQ-4-6, 3856 - 3930	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.66E-06	0.87	3.61	-	1094.7
AHQ-4-8, 3674 - 3677	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.70E-09	0.96	4.74	-	1447.6
AHQ-4-7, 3853	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.97E-06	0.90	4.09	-	1044.3
AHQ-4-1, 4203	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.38E-10	0.91	4.12	-	907.9
AHQ-4-3, 4075 - 4152	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.18E-07	0.92	4.23	-	1133.2
AHQ-4-12, 3979	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.03E-05	0.85	3.34	-	935.9
AHQ-4-6, 2483	R.VTGESHIGGVLLK.I	1310.52448	1	1.72E-09	0.82	3.11	-	695.5
AHQ-4-9, 2351 - 2353	R.VTGESHIGGVLLK.I	1310.52448	2	1.75E-06	0.95	4.22	-	1384.0
AHQ-4-6, 2475	R.VTGESHIGGVLLK.I	1310.52448	2	1.43E-06	0.97	4.57	-	1869.8
AHQ-4-9, 2352	R.VTGESHIGGVLLK.I	1310.52448	1	4.75E-09	0.84	3.34	-	728.7
AHQ-4-7, 2401	R.VTGESHIGGVLLK.I	1310.52448	2	4.15E-09	0.96	4.08	-	1869.9
AHQ-4-11, 2661 - 2726	R.VTGESHIGGVLLK.I	1310.52448	2	7.55E-08	0.94	3.82	-	1458.7
AHQ-4-14-, 2698	R.VTGESHIGGVLLK.I	1310.52448	2	3.08E-08	0.94	3.75	-	1369.3
AHQ-4-13-, 2852	R.VTGESHIGGVLLK.I	1310.52448	2	1.12E-08	0.96	4.24	-	1900.0
AHQ-4-1, 2946	R.VTGESHIGGVLLK.I	1310.52448	2	2.48E-06	0.94	3.71	-	1516.6
AHQ-4-13, 2971 - 2979	R.VTGESHIGGVLLK.I	1310.52448	2	1.62E-09	0.94	3.81	-	1635.8
AHQ-4-3, 5011	K.VVLAGGVAPALFR.G	1270.54832	2	5.58E-08	0.96	4.65	-	1764.4
AHQ-4-6, 4686	K.VVLAGGVAPALFR.G	1270.54832	2	3.33E-07	0.96	4.85	-	1392.2
AHQ-4-11, 4632 - 4640	K.VVLAGGVAPALFR.G	1270.54832	2	1.91E-09	0.97	4.15	-	1899.7
AHQ-4-6, 4610	K.VVLAGGVAPALFR.G	1270.54832	1	1.07E-06	0.20	2.19	-	65.7
AHQ-4-7, 4519 - 4522	K.VVLAGGVAPALFR.G	1270.54832	2	1.70E-06	0.97	5.04	-	1583.4
AHQ-4-9, 4139 - 4208	K.VVLAGGVAPALFR.G	1270.54832	2	4.47E-05	0.93	3.39	-	1466.0
AHQ-4-4, 4979	K.VVLAGGVAPALFR.G	1270.54832	2	1.08E-04	0.96	4.26	-	1916.2
AHQ-4-5, 4711	K.VVLAGGVAPALFR.G	1270.54832	2	5.66E-07	0.97	5.11	-	1892.2
AHQ-4-2, 5012	K.VVLAGGVAPALFR.G	1270.54832	2	9.85E-06	0.94	3.40	-	1792.7
AHQ-4-1, 5085	K.VVLAGGVAPALFR.G	1270.54832	2	1.75E-07	0.96	4.69	-	1596.3
AHQ-4-6, 4594 - 4618	K.VVLAGGVAPALFR.G	1270.54832	2	6.50E-08	0.97	4.97	-	1624.7
AHQ-4-6, 2296 - 2302	K.YGILADAR.L	878.99544	2	1.47E-04	0.94	3.21	-	1287.2
AHQ-4-7, 2274	K.YGILADAR.L	878.99544	2	1.50E-05	0.94	2.70	-	1737.3
AHQ-4-6, 5215 - 5219	K.YYSFFDLDPK.T	1295.42046	2	3.82E-06	0.93	3.81	-	844.5
AHQ-4-9, 4712 - 4727	K.YYSFFDLDPK.T	1295.42046	2	1.95E-04	0.92	3.75	-	806.2
AHQ-4-1, 5678	K.YYSFFDLDPK.T	1295.42046	2	6.06E-05	0.79	3.21	-	741.0
gi|4503571|ref|NP_001419.1| enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n				3.11E-14	11.92	140.29	36.40	47168.7
AHQ-4-14-, 5213 - 5225	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.63E-05	0.97	5.79	-	1101.0
AHQ-4-13, 5370 - 5425	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.28E-10	0.93	4.28	-	570.6
AHQ-4-7, 5167	R.AAVPSGASTGIYEALELR.D	1806.00979	2	5.13E-05	0.80	3.46	-	338.7
AHQ-4-7, 5259	R.AAVPSGASTGIYEALELR.D	1806.00979	2	4.80E-04	0.94	4.28	-	766.0
AHQ-4-12, 5291 - 5329	R.AAVPSGASTGIYEALELR.D	1806.00979	2	6.12E-08	0.91	4.19	-	606.1
AHQ-4-8, 4777 - 4817	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.93E-12	0.93	4.89	-	451.3
AHQ-4-7, 4514 - 4517	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	4.20E-07	0.94	5.21	-	705.5
AHQ-4-9, 4021 - 4091	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	1.36E-04	0.67	3.72	-	710.9
AHQ-4-10, 4148	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	2.03E-05	0.87	4.11	-	671.5
AHQ-4-8, 4345	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	2.04E-06	0.84	3.95	-	797.6
AHQ-4-8, 5813 - 5885	K.DATNVGDEGGFAPNILENKEGLELLK.T	2744.99178	3	6.10E-06	0.54	3.21	-	584.5
AHQ-4-11, 6592	K.DYPVVSIEDPFDQDDWGAWQK.F	2511.63977	2	1.89E-05	0.83	3.34	-	552.4
AHQ-4-10, 6276 - 6283	K.DYPVVSIEDPFDQDDWGAWQK.F	2511.63977	2	4.74E-04	0.50	3.00	-	441.4
AHQ-4-8, 3821	R.GNPTVEVDLFTSK.G	1407.55065	1	3.76E-09	0.72	3.68	-	553.1
AHQ-4-8, 5685 - 5757	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	8.39E-11	0.95	5.59	-	1160.9
AHQ-4-7, 5979	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	6.25E-07	0.83	4.41	-	645.3
AHQ-4-8, 5126	K.LAM*QEFM*ILPVGAANFR.E	1941.30692	2	5.90E-04	0.90	3.85	-	660.6
AHQ-4-8, 6026	K.LAMQEFM*ILPVGAANFR.E	1925.30752	2	1.67E-05	0.90	4.20	-	868.5
AHQ-4-8, 6673 - 6743	K.LAMQEFMILPVGAANFR.E	1909.30812	2	2.20E-05	0.93	4.57	-	677.4
AHQ-4-8, 5725	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	1.74E-08	0.95	5.84	-	1025.2
AHQ-4-8, 5671 - 5738	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	1.59E-04	0.49	2.86	-	389.6
AHQ-4-10, 6225	K.LAMQEFMILPVGAANFR.E	1909.30812	2	2.79E-05	0.82	3.62	-	578.3
AHQ-4-8, 6769	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	2	4.29E-06	0.74	3.49	-	768.3
AHQ-4-8, 6771	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	3	3.11E-14	0.97	5.84	-	1930.9
AHQ-4-8, 1951	K.TIAPALVSK.K	900.09769	1	1.70E-04	0.52	2.50	-	337.4
AHQ-4-13, 3917	K.VNQIGSVTESLQACK.L	1635.82159	2	1.43E-04	0.79	3.26	-	543.5
AHQ-4-8, 3610 - 3626	K.VNQIGSVTESLQACK.L	1635.82159	2	1.43E-04	0.86	3.73	-	646.5
AHQ-4-8, 3357	K.VNQIGSVTESLQACK.L	1635.82159	2	4.96E-05	0.89	3.48	-	863.4
AHQ-4-11, 4690 - 4706	R.YISPDQLADLYK.S	1426.59557	2	3.25E-07	0.87	3.30	-	739.3
AHQ-4-9, 4313	R.YISPDQLADLYK.S	1426.59557	1	2.09E-05	0.45	3.00	-	426.8
AHQ-4-9, 4312 - 4315	R.YISPDQLADLYK.S	1426.59557	2	1.15E-06	0.93	4.36	-	699.7
AHQ-4-8, 4483	R.YISPDQLADLYK.S	1426.59557	1	3.42E-06	0.83	2.95	-	863.2
AHQ-4-7, 4750	R.YISPDQLADLYK.S	1426.59557	2	2.12E-07	0.94	3.85	-	1148.7
AHQ-4-8, 4470 - 4471	R.YISPDQLADLYK.S	1426.59557	2	2.81E-06	0.93	4.26	-	725.3
AHQ-4-10, 4404 - 4408	R.YISPDQLADLYK.S	1426.59557	2	3.09E-07	0.94	4.05	-	805.9
gi|27498267|ref|XP_209737.1| similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,				4.00E-14	3.31	50.31	41.10	11063.6
AHQ-4-10, 5563	R.DICNDVLSLLEK.F	1420.61093	2	4.69E-07	0.95	3.24	-	1651.1
AHQ-4-11, 5852	R.DICNDVLSLLEK.F	1420.61093	1	2.19E-09	0.74	2.77	-	764.9
AHQ-4-10, 6412 - 6483	R.DICNDVLSLLEK.F	1420.61093	1	9.27E-08	0.82	3.64	-	643.7
AHQ-4-9, 5649 - 5651	R.DICNDVLSLLEK.F	1420.61093	1	1.58E-10	0.68	2.51	-	650.9
AHQ-4-9, 5657	R.DICNDVLSLLEK.F	1420.61093	2	2.21E-04	0.92	3.71	-	1160.5
AHQ-4-9, 6537 - 6616	R.DICNDVLSLLEK.F	1420.61093	1	3.02E-05	0.70	3.21	-	566.1
AHQ-4-9, 6619	R.DICNDVLSLLEK.F	1420.61093	2	1.07E-06	0.97	5.06	-	1688.0
AHQ-4-10, 6409 - 6424	R.DICNDVLSLLEK.F	1420.61093	2	6.03E-06	0.96	4.32	-	1748.4
AHQ-4-10, 5567	R.DICNDVLSLLEK.F	1420.61093	1	6.69E-06	0.64	2.93	-	595.8
AHQ-4-10, 5559	R.DICNDVLSLLEK.F	1420.61093	1	3.18E-10	0.64	2.39	-	734.9
AHQ-4-11, 5854	R.DICNDVLSLLEK.F	1420.61093	2	4.54E-06	0.89	3.36	-	883.4
AHQ-4-10, 1657 - 1775	R.EKIQTELR.D	1017.16155	1	3.05E-04	0.11	1.91	-	90.4
AHQ-4-10, 6531	R.EKIQTELRDICNDVLSLLEK.F	2418.74987	2	2.72E-05	0.58	3.80	-	363.7

AHQ-4-10, 4781 - 4853	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.06E-12	0.96	4.86	-	1429.1
AHQ-4-10, 4911 - 4973	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.00E-10	0.97	5.78	-	1424.1
AHQ-4-10, 5080 - 5140	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.30E-09	0.95	4.60	-	1294.0
AHQ-4-10, 4439	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.47E-08	0.96	4.83	-	1166.1
AHQ-4-10, 5269 - 5328	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.43E-10	0.98	5.46	-	1750.2
AHQ-4-10, 4720	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	3.46E-08	0.98	5.98	-	2687.4
AHQ-4-14-, 5041	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	6.21E-10	0.98	5.96	-	1549.3
AHQ-4-13-, 5100	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.40E-08	0.98	6.21	-	1673.6
AHQ-4-10, 5731 - 5787	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.97E-04	0.85	3.66	-	762.5
AHQ-4-10, 5851 - 5897	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	9.78E-07	0.94	4.77	-	975.7
AHQ-4-10, 5956 - 6033	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.35E-04	0.83	3.12	-	869.4
AHQ-4-10, 6313	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.63E-04	0.50	2.62	-	390.5
AHQ-4-10, 4343 - 4417	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.60E-10	0.98	5.65	-	1574.2
AHQ-4-9, 4707	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.62E-09	0.97	5.53	-	1549.0
AHQ-4-10, 4663 - 4723	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.78E-07	0.98	5.58	-	1796.4
AHQ-4-11, 4617	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.19E-08	0.94	4.37	-	1018.5
AHQ-4-11, 4996	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.81E-07	0.97	5.68	-	1201.0
AHQ-4-11, 5000	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.56E-08	0.98	5.49	-	2727.8
AHQ-4-9, 4392	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.25E-12	0.96	4.76	-	1235.9
AHQ-4-10, 5124 - 5205	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.92E-07	0.97	5.39	-	1353.6
AHQ-4-12, 5111 - 5190	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.04E-08	0.97	5.59	-	1187.9
AHQ-4-13, 5232	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	7.42E-09	0.97	5.45	-	1429.5
AHQ-4-14, 6190 - 6196	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.00E-14	0.98	6.20	-	1540.2
AHQ-4-9, 4061	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	4.40E-07	0.98	5.77	-	2420.1
AHQ-4-10, 4108 - 4175	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	4.29E-07	0.97	5.54	-	1295.1
gi|11321601|ref|NP_002618.1|	phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom			4.33E-14	4.65	50.30	11.50	85595.6
AHQ-4-5, 3519	K.AIGVLTSGGDAQGMNAAVR.A	1789.00750	2	4.33E-14	0.98	5.90	-	1826.4
AHQ-4-5, 3239 - 3249	R.DLQSNVEHLTEK.M	1413.51529	2	3.80E-04	0.88	3.42	-	997.5
AHQ-4-5, 6039 - 6094	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	7.51E-06	0.87	4.02	-	581.0
AHQ-4-5, 6529	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	1.19E-06	0.96	5.02	-	949.7
AHQ-4-5, 5347	R.IIEVVDAIMTTAQSHQR.T	1913.18853	2	4.58E-12	0.96	5.22	-	1285.5
gi|4507907|ref|NP_000543.1|	von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille			6.88E-14	31.74	370.40	18.90	309296.7
AHQ-4-1, 4006	K.AHLLSLVDVM*QR.E	1398.65673	2	6.84E-08	0.94	3.59	-	1550.3
AHQ-4-1, 5014	K.AHLLSLVDVMQR.E	1382.65733	2	9.05E-06	0.95	3.82	-	1641.1
AHQ-4-2, 4291	R.CLPTACTIQLR.G	1335.57568	2	5.27E-07	0.56	2.69	-	457.8
AHQ-4-3, 5164	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	6.93E-04	0.34	2.72	-	409.4
AHQ-4-1, 5173	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	1.82E-04	0.78	3.01	-	676.7
AHQ-4-1, 4853	R.EQAPNLVYM*VTGNPASDEIK.R	2193.42002	2	3.37E-06	0.79	3.51	-	347.0
AHQ-4-1, 4186 - 4265	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	4.19E-05	0.78	3.54	-	542.6
AHQ-4-1, 4498	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	2.88E-08	0.81	3.97	-	479.7
AHQ-4-1, 2414 - 2415	R.GLRPSCPNSQSPVK.V	1528.71594	2	7.27E-04	0.89	3.78	-	910.6
AHQ-4-3, 4919	K.GLWEQCQLLK.S	1276.48664	2	1.46E-04	0.50	3.22	-	370.7
AHQ-4-1, 3126 - 3193	R.HIVTFDGQNFK.L	1306.45124	2	2.86E-04	0.82	3.08	-	636.4
AHQ-4-2, 2980	R.HIVTFDGQNFK.L	1306.45124	2	4.06E-04	0.77	3.23	-	490.8
AHQ-4-1, 4002 - 4069	R.IALLLM*ASQEPQR.M	1486.76229	2	4.88E-05	0.92	3.59	-	1041.1
AHQ-4-1, 5197 - 5270	R.IEDLPTM*VTLGNSFLHK.L	1932.23019	2	4.52E-04	0.75	3.35	-	638.1
AHQ-4-1, 5409	R.IEDLPTM*VTLGNSFLHK.L	1932.23019	2	2.62E-04	0.85	3.37	-	854.7
AHQ-4-1, 6362 - 6367	R.IEDLPTMVTLGNSFLHK.L	1916.23079	2	1.11E-07	0.97	4.71	-	1583.8
AHQ-4-1, 5905	R.IEDLPTMVTLGNSFLHK.L	1916.23079	2	2.18E-05	0.90	3.68	-	789.8
AHQ-4-1, 7058	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	1.01E-08	0.93	4.76	-	804.2
AHQ-4-2, 7450	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	7.08E-07	0.94	4.46	-	872.4
AHQ-4-1, 7181	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	3.53E-07	0.94	4.89	-	659.4
AHQ-4-3, 7447	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	3.97E-07	0.92	4.44	-	625.4
AHQ-4-1, 2678 - 2679	R.ILAGPAGDSNVVK.L	1241.41901	2	9.86E-09	0.94	3.50	-	1264.9
AHQ-4-1, 2770	R.ILAGPAGDSNVVK.L	1241.41901	2	4.86E-07	0.69	2.90	-	650.9
AHQ-4-2, 2510	R.ILAGPAGDSNVVK.L	1241.41901	2	2.64E-06	0.92	3.74	-	1020.6
AHQ-4-3, 2509	R.ILAGPAGDSNVVK.L	1241.41901	2	2.35E-05	0.85	3.23	-	789.6
AHQ-4-4, 2500	R.ILAGPAGDSNVVK.L	1241.41901	2	1.11E-05	0.85	3.02	-	890.9
AHQ-4-1, 6446 - 6453	K.ILDELLQTCVDPEDCPVCEVAGR.R	2692.97859	2	4.50E-05	0.76	3.67	-	317.5
AHQ-4-1, 3841	R.ILTSDVFQDCNK.L	1441.58869	2	1.92E-04	0.87	3.28	-	837.7
AHQ-4-2, 3804	R.ILTSDVFQDCNK.L	1441.58869	2	9.42E-08	0.82	2.98	-	855.5
AHQ-4-1, 4298	R.LSEAEFEVLK.A	1165.31777	2	5.46E-07	0.92	3.86	-	1028.4
AHQ-4-1, 4261	K.LTGSCSYVLFQNK.E	1518.71629	2	1.03E-05	0.93	3.44	-	1341.8
AHQ-4-3, 5205 - 5277	R.NSQWICSNEECPGECLVTGQSHFK.S	2872.07402	3	1.60E-08	0.88	4.06	-	753.0
AHQ-4-1, 5593 - 5602	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	6.88E-14	0.98	8.03	-	2203.4
AHQ-4-2, 5539 - 5544	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	5.33E-10	0.98	7.06	-	2716.4
AHQ-4-2, 5747	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	3.21E-04	0.85	3.41	-	1200.1
AHQ-4-3, 5547	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	4.44E-05	0.89	4.32	-	1003.1
AHQ-4-1, 5186 - 5201	K.RPGDVWTLPDQCHTVTCQPDGQTLLK.S	3026.35060	3	4.77E-05	0.89	4.67	-	774.8
AHQ-4-3, 4189	R.SFSIIGDFQNGKR.V	1469.62690	2	6.48E-10	0.82	3.31	-	698.0
AHQ-4-1, 4035	R.SGFTYVLHEGECCGR.C	1774.91285	2	1.84E-08	0.89	3.58	-	880.6
AHQ-4-2, 3978	R.SGFTYVLHEGECCGR.C	1774.91285	2	2.43E-06	0.94	3.75	-	1301.8
AHQ-4-1, 3450	R.SKEFMEEVIQR.M	1396.59450	2	7.31E-07	0.91	3.49	-	983.0
AHQ-4-3, 5083	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	2.57E-06	0.86	3.99	-	465.3
AHQ-4-4, 5040	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	4.44E-04	0.77	3.54	-	324.8
AHQ-4-1, 4983 - 5055	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	1.12E-09	0.85	4.18	-	404.9
AHQ-4-2, 5103	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	4.95E-08	0.93	4.75	-	584.3
AHQ-4-1, 4990	R.TPDFCAMSCPPSLVYNHCEHGCPR.H	2898.20140	3	6.03E-07	0.78	3.76	-	565.1
AHQ-4-1, 6203	K.TYGLCGICDENGANDFMLR.D	2209.42291	2	1.49E-07	0.88	3.75	-	613.4
AHQ-4-1, 5654 - 5733	K.TYGLCGICDENGANDFM*LR.D	2225.42231	2	6.81E-07	0.86	3.29	-	698.0
AHQ-4-1, 5797 - 5871	K.TYGLCGICDENGANDFM*LR.D	2225.42231	2	1.12E-08	0.83	3.22	-	650.4
AHQ-4-1, 4581	K.VIVIPVGIGPHANLK.Q	1527.87891	2	2.21E-07	0.81	3.18	-	537.5
AHQ-4-2, 2294	R.VKEEVFIQQR.N	1276.46658	2	5.60E-04	0.78	3.11	-	469.3
AHQ-4-1, 4713	R.VTVFPIGIGDR.Y	1174.37426	2	6.58E-04	0.94	3.92	-	1074.3
AHQ-4-2, 4662	R.VTVFPIGIGDR.Y	1174.37426	2	2.91E-06	0.94	3.68	-	1117.4
AHQ-4-1, 3611	R.WTCPCVCTGSSTR.H	1575.72645	2	3.57E-06	0.82	2.98	-	635.4
AHQ-4-2, 2846	K.YAGSQVASTSEVLK.Y	1440.58064	2	5.28E-08	0.94	3.69	-	1127.9
AHQ-4-4, 2812	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.50E-05	0.94	4.13	-	1053.1
AHQ-4-1, 2997	K.YAGSQVASTSEVLK.Y	1440.58064	1	2.79E-04	0.11	2.28	-	237.6
AHQ-4-3, 2840	K.YAGSQVASTSEVLK.Y	1440.58064	2	5.65E-10	0.93	3.90	-	927.4
AHQ-4-3, 7437	R.YFTFSGICQYLLAR.D	1741.00269	2	1.36E-08	0.97	4.61	-	1340.4
AHQ-4-2, 6946	K.YLFPGECQYVLVQDYCGSNPGTFR.I	2874.15305	2	2.39E-06	0.80	3.02	-	827.0
AHQ-4-2, 3268	R.YLSDHSFLVSQGDR.E	1624.73576	2	1.32E-05	0.96	4.31	-	1741.4
AHQ-4-1, 3445	R.YLSDHSFLVSQGDR.E	1624.73576	2	8.26E-07	0.96	5.04	-	1444.7
AHQ-4-1, 6111	K.YTLFQIFSK.I	1147.34728	2	1.70E-07	0.94	3.04	-	1165.8
gi|11968039|ref|NP_071930.1|	hypothetical protein FLJ22405 [Homo sapiens]			7.22E-14	0.90	10.19	4.60	46880.2
AHQ-4-14-, 6531	R.AVAPSPSGAIGGLLEQFAR.G	1842.08850	2	7.22E-14	0.90	3.71	-	689.3
gi|21361399|ref|NP_055040.2|	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp			1.23E-13	2.80	30.33	10.50	65308.3
AHQ-4-6, 3578	R.AISHEHSPSDLEAHFVPLVK.R	2214.46551	3	2.72E-05	0.97	4.94	-	1786.8
AHQ-4-6, 7212	K.DNTIEHLLPLFLAQLKDECPEVR.L	2753.12348	3	1.23E-13	0.97	6.57	-	1717.7
AHQ-4-6, 5671 - 5739	K.SEIIPMFSNLASDEQDSVR.L	2139.32924	2	2.07E-05	0.85	3.84	-	711.0
gi|4501881|ref|NP_001091.1|	alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA			1.30E-13	15.57	220.28	44.60	42050.8
AHQ-4-8, 1438 - 1522	K.AGFAGDDAPR.A	977.01283	2	1.14E-05	0.87	2.71	-	1226.8
AHQ-4-13, 2038 - 2101	K.AGFAGDDAPR.A	977.01283	2	4.51E-04	0.86	3.15	-	1009.9
AHQ-4-8, 1716 - 1780	K.AGFAGDDAPR.A	977.01283	2	1.70E-04	0.91	3.05	-	1378.4
AHQ-4-6, 2859	R.AVFPSIVGRPR.H	1199.43018	2	6.56E-04	0.53	2.67	-	460.5
AHQ-4-8, 2699	R.AVFPSIVGRPR.H	1199.43018	2	1.17E-04	0.59	2.67	-	582.7

AHQ-4-13, 3233 - 3237	R.AVFPSIVGRPR.H	1199.43018	2	4.01E-04	0.76	2.59	-	641.8
AHQ-4-8, 2292 - 2363	R.AVFPSIVGRPR.H	1199.43018	2	5.39E-05	0.53	2.61	-	470.0
AHQ-4-10, 2855	R.AVFPSIVGRPR.H	1199.43018	2	1.27E-05	0.80	3.10	-	675.7
AHQ-4-13, 3889	R.DLTDYLM*K.I	1015.16266	2	4.49E-04	0.72	2.91	-	443.9
AHQ-4-10, 4352	R.DLTDYLMK.I	999.16326	1	9.28E-04	0.18	1.92	-	311.2
AHQ-4-11, 4264	R.DLTDYLMK.I	999.16326	1	1.60E-04	0.67	2.38	-	723.8
AHQ-4-9, 4293 - 4301	R.DLTDYLMK.I	999.16326	1	5.02E-05	0.17	1.81	-	318.5
AHQ-4-11, 4274	R.DLTDYLMK.I	999.16326	2	9.52E-04	0.86	3.16	-	463.0
AHQ-4-13, 3896	R.DLTDYLM*K.I	1015.16266	1	9.70E-05	0.31	2.41	-	166.4
AHQ-4-8, 6555	R.DLTDYLMKILTER.G	1611.88498	2	6.89E-07	0.95	3.92	-	1319.7
AHQ-4-14, 6130	K.DLYANNVMSGGTTMYPGIADR.M	2247.49444	2	5.33E-04	0.27	2.58	-	354.1
AHQ-4-8, 1591 - 1671	K.DSYVGDEAQSK.R	1199.20634	2	8.63E-05	0.87	3.01	-	634.4
AHQ-4-8, 1432 - 1484	K.DSYVGDEAQSK.R	1199.20634	1	3.08E-05	0.79	3.85	-	475.4
AHQ-4-12, 1653 - 1709	K.DSYVGDEAQSK.R	1199.20634	2	3.68E-06	0.79	3.50	-	701.8
AHQ-4-13, 1843	K.DSYVGDEAQSK.R	1199.20634	1	6.98E-06	0.47	2.49	-	407.9
AHQ-4-5, 2702	K.EITALAPSTMK.I	1162.38206	1	7.26E-04	0.47	2.38	-	363.2
AHQ-4-10, 2624 - 2689	K.EITALAPSTMK.I	1162.38206	2	1.87E-06	0.79	3.17	-	509.4
AHQ-4-4, 2319	K.EITALAPSTM*K.I	1178.38146	2	7.17E-05	0.55	2.67	-	561.5
AHQ-4-13, 3037 - 3062	K.EITALAPSTMK.I	1162.38206	2	6.06E-04	0.73	2.79	-	516.2
AHQ-4-8, 1961 - 2028	K.EITALAPSTM*K.I	1178.38146	1	3.72E-04	0.08	1.93	-	95.5
AHQ-4-14, 3109 - 3165	K.EITALAPSTM*K.I	1178.38146	2	2.72E-04	0.60	2.74	-	474.8
AHQ-4-14, 3757 - 3948	K.EITALAPSTMK.I	1162.38206	1	4.61E-04	0.41	2.41	-	244.6
AHQ-4-7, 2598	K.EITALAPSTMK.I	1162.38206	1	3.11E-04	0.21	2.18	-	288.5
AHQ-4-14, 3924	K.EITALAPSTMK.I	1162.38206	2	4.06E-04	0.64	2.52	-	431.5
AHQ-4-8, 2329 - 2529	K.EITALAPSTMK.I	1162.38206	1	1.49E-04	0.53	2.74	-	351.2
AHQ-4-8, 2327 - 2403	K.EITALAPSTMK.I	1162.38206	2	3.08E-04	0.81	3.02	-	587.7
AHQ-4-13-, 2301 - 2380	K.EITALAPSTM*K.I	1178.38146	2	2.65E-04	0.87	2.94	-	824.7
AHQ-4-14-, 2763 - 2841	K.EITALAPSTMK.I	1162.38206	1	4.49E-05	0.62	2.98	-	237.0
AHQ-4-11, 2737 - 2810	K.EITALAPSTMK.I	1162.38206	1	8.80E-09	0.46	2.61	-	346.6
AHQ-4-14-, 2837 - 2838	K.EITALAPSTMK.I	1162.38206	2	4.78E-04	0.80	3.34	-	441.6
AHQ-4-8, 1892 - 1956	K.EITALAPSTM*K.I	1178.38146	2	8.11E-04	0.78	2.93	-	650.7
AHQ-4-8, 2019 - 2083	K.EITALAPSTM*K.I	1178.38146	2	1.99E-04	0.84	3.26	-	701.2
AHQ-4-8, 7194 - 7267	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	2	4.81E-07	0.74	3.57	-	470.4
AHQ-4-8, 7059	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	3	1.87E-05	0.61	3.07	-	622.0
AHQ-4-9, 1529 - 1603	R.HQGVMVGMGQK.D	1172.40691	1	8.19E-04	0.69	2.32	-	699.7
AHQ-4-8, 2271 - 2307	R.HQGVMVGMGQKDSYVGDEAQSK.R	2352.59065	3	8.31E-05	0.92	3.82	-	1203.9
AHQ-4-8, 1960	K.IKIIAPPER.K	1037.28073	2	5.64E-04	0.59	2.56	-	509.6
AHQ-4-13, 3153	K.IWHHTFYNELR.V	1516.68695	2	2.69E-06	0.87	3.57	-	1052.5
AHQ-4-8, 2399 - 2459	K.IWHHTFYNELR.V	1516.68695	2	6.08E-05	0.86	3.32	-	1072.5
AHQ-4-8, 2426	K.IWHHTFYNELR.V	1516.68695	3	1.93E-06	0.95	4.89	-	1969.4
AHQ-4-8, 2665 - 2733	K.IWHHTFYNELR.V	1516.68695	2	1.36E-05	0.65	3.18	-	430.9
AHQ-4-3, 2905 - 2976	K.IWHHTFYNELR.V	1516.68695	2	2.55E-04	0.67	2.71	-	717.0
AHQ-4-13-, 3038 - 3041	K.IWHHTFYNELR.V	1516.68695	2	3.45E-06	0.81	3.27	-	826.4
AHQ-4-8, 2319 - 2389	K.IWHHTFYNELR.V	1516.68695	3	2.37E-07	0.95	4.73	-	1254.5
AHQ-4-12, 2850	K.IWHHTFYNELR.V	1516.68695	3	5.36E-05	0.92	4.84	-	1155.2
AHQ-4-12, 2849 - 2918	K.IWHHTFYNELR.V	1516.68695	2	1.87E-07	0.83	3.23	-	965.8
AHQ-4-11, 2806	K.IWHHTFYNELR.V	1516.68695	3	3.17E-04	0.95	4.48	-	1604.1
AHQ-4-6, 2666	K.IWHHTFYNELR.V	1516.68695	2	1.08E-08	0.81	3.10	-	947.2
AHQ-4-9, 2733 - 2741	K.IWHHTFYNELR.V	1516.68695	2	2.10E-04	0.86	3.01	-	929.4
AHQ-4-9, 2465	K.IWHHTFYNELR.V	1516.68695	3	1.05E-04	0.90	3.88	-	1392.9
AHQ-4-9, 2439 - 2495	K.IWHHTFYNELR.V	1516.68695	2	1.18E-05	0.88	3.23	-	702.4
AHQ-4-8, 2735	K.IWHHTFYNELR.V	1516.68695	3	4.56E-06	0.94	4.12	-	1681.8
AHQ-4-1, 3187	K.IWHHTFYNELR.V	1516.68695	2	4.69E-04	0.76	2.76	-	628.8
AHQ-4-10, 4777 - 4788	R.LDLAGRDLTDYLMK.I	1624.88375	2	5.55E-04	0.86	3.42	-	955.0
AHQ-4-8, 4453	R.LDLAGRDLTDYLM*K.I	1640.88315	2	9.99E-04	0.68	3.25	-	476.3
AHQ-4-8, 4798 - 4870	K.SYELPDGQVITIGNER.F	1791.93998	2	3.30E-07	0.96	4.93	-	1225.4
AHQ-4-8, 4937 - 5011	K.SYELPDGQVITIGNER.F	1791.93998	2	1.60E-06	0.96	4.55	-	1321.8
AHQ-4-13-, 4869 - 4870	K.SYELPDGQVITIGNER.F	1791.93998	2	5.67E-13	0.97	5.55	-	1014.3
AHQ-4-13-, 4577	K.SYELPDGQVITIGNER.F	1791.93998	2	9.66E-06	0.88	3.14	-	846.0
AHQ-4-6, 5127 - 5135	K.SYELPDGQVITIGNER.F	1791.93998	2	4.81E-05	0.88	3.69	-	884.3
AHQ-4-6, 4823 - 4846	K.SYELPDGQVITIGNER.F	1791.93998	2	2.10E-05	0.89	3.77	-	853.7
AHQ-4-6, 4450 - 4458	K.SYELPDGQVITIGNER.F	1791.93998	2	4.84E-08	0.92	3.63	-	814.0
AHQ-4-8, 4550 - 4567	K.SYELPDGQVITIGNER.F	1791.93998	3	5.07E-09	0.96	5.07	-	1528.0
AHQ-4-8, 4545 - 4609	K.SYELPDGQVITIGNER.F	1791.93998	2	5.15E-13	0.97	4.97	-	1196.9
AHQ-4-13-, 5010 - 5080	K.SYELPDGQVITIGNER.F	1791.93998	2	8.00E-13	0.97	5.17	-	1246.7
AHQ-4-8, 4407 - 4477	K.SYELPDGQVITIGNER.F	1791.93998	2	9.69E-08	0.96	4.78	-	1163.1
AHQ-4-1, 4667 - 4671	K.SYELPDGQVITIGNER.F	1791.93998	2	1.28E-05	0.80	3.57	-	540.5
AHQ-4-9, 3895 - 3959	K.SYELPDGQVITIGNER.F	1791.93998	2	1.79E-05	0.71	2.90	-	652.1
AHQ-4-9, 4224 - 4296	K.SYELPDGQVITIGNER.F	1791.93998	2	1.76E-04	0.78	2.71	-	877.7
AHQ-4-8, 4253 - 4337	K.SYELPDGQVITIGNER.F	1791.93998	2	6.37E-12	0.97	5.58	-	899.0
AHQ-4-7, 4807	K.SYELPDGQVITIGNER.F	1791.93998	2	1.28E-06	0.94	4.52	-	788.2
AHQ-4-9, 4539 - 4619	K.SYELPDGQVITIGNER.F	1791.93998	2	5.22E-04	0.82	3.20	-	648.1
AHQ-4-5, 4905	K.SYELPDGQVITIGNER.F	1791.93998	2	9.75E-11	0.94	4.91	-	837.5
AHQ-4-5, 4549 - 4551	K.SYELPDGQVITIGNER.F	1791.93998	2	1.37E-09	0.88	3.39	-	800.4
AHQ-4-10, 4027 - 4107	K.SYELPDGQVITIGNER.F	1791.93998	2	1.02E-09	0.93	4.15	-	820.0
AHQ-4-10, 4169 - 4240	K.SYELPDGQVITIGNER.F	1791.93998	2	2.92E-12	0.93	3.80	-	948.4
AHQ-4-4, 5404	K.SYELPDGQVITIGNER.F	1791.93998	2	4.57E-04	0.72	2.84	-	491.0
AHQ-4-10, 4427 - 4461	K.SYELPDGQVITIGNER.F	1791.93998	2	6.86E-08	0.95	4.70	-	930.8
AHQ-4-10, 4604 - 4668	K.SYELPDGQVITIGNER.F	1791.93998	2	2.03E-10	0.95	4.43	-	1049.9
AHQ-4-13-, 4469	K.SYELPDGQVITIGNER.F	1791.93998	2	1.30E-13	0.93	3.97	-	1112.5
AHQ-4-4, 5056	K.SYELPDGQVITIGNER.F	1791.93998	2	4.26E-04	0.45	2.52	-	472.5
AHQ-4-1, 4758	K.SYELPDGQVITIGNER.F	1791.93998	2	9.27E-09	0.90	3.92	-	593.4
AHQ-4-4, 4711	K.SYELPDGQVITIGNER.F	1791.93998	2	1.61E-08	0.89	3.78	-	761.7
AHQ-4-3, 5131	K.SYELPDGQVITIGNER.F	1791.93998	2	8.17E-05	0.95	4.64	-	911.1
AHQ-4-11, 4297 - 4374	K.SYELPDGQVITIGNER.F	1791.93998	2	1.88E-08	0.95	4.59	-	868.2
AHQ-4-11, 4524	K.SYELPDGQVITIGNER.F	1791.93998	2	1.05E-10	0.94	3.70	-	1100.0
AHQ-4-11, 4685 - 4748	K.SYELPDGQVITIGNER.F	1791.93998	2	9.22E-04	0.92	4.25	-	823.1
AHQ-4-11, 4836 - 4893	K.SYELPDGQVITIGNER.F	1791.93998	2	3.36E-05	0.95	3.82	-	1077.3
AHQ-4-11, 4952 - 4958	K.SYELPDGQVITIGNER.F	1791.93998	2	2.79E-10	0.95	4.83	-	917.6
AHQ-4-3, 4747	K.SYELPDGQVITIGNER.F	1791.93998	2	2.87E-05	0.87	3.47	-	646.1
AHQ-4-8, 4654 - 4729	K.SYELPDGQVITIGNER.F	1791.93998	2	6.35E-07	0.90	3.71	-	885.5
AHQ-4-8, 4114 - 4185	K.SYELPDGQVITIGNER.F	1791.93998	2	1.73E-11	0.86	3.73	-	677.6
AHQ-4-14, 6224	K.SYELPDGQVITIGNER.F	1791.93998	2	2.99E-04	0.85	3.02	-	791.6
AHQ-4-1, 4857	K.SYELPDGQVITIGNER.F	1791.93998	2	1.17E-07	0.94	3.63	-	1144.9
AHQ-4-14, 6096	K.SYELPDGQVITIGNER.F	1791.93998	2	7.73E-08	0.93	3.92	-	956.8
AHQ-4-14, 6045 - 6117	K.SYELPDGQVITIGNER.F	1791.93998	2	1.57E-05	0.81	3.50	-	843.6
AHQ-4-12, 4530 - 4537	K.SYELPDGQVITIGNER.F	1791.93998	2	1.15E-10	0.96	4.81	-	1136.0
AHQ-4-12, 4663	K.SYELPDGQVITIGNER.F	1791.93998	2	2.12E-05	0.81	3.29	-	616.5
AHQ-4-12, 4898 - 4965	K.SYELPDGQVITIGNER.F	1791.93998	2	6.08E-12	0.96	5.02	-	1250.7
AHQ-4-12, 5079 - 5143	K.SYELPDGQVITIGNER.F	1791.93998	2	1.78E-09	0.96	4.75	-	1127.2
AHQ-4-1, 5137	K.SYELPDGQVITIGNER.F	1791.93998	2	1.73E-06	0.91	3.65	-	867.0
AHQ-4-1, 5310 - 5374	K.SYELPDGQVITIGNER.F	1791.93998	2	1.39E-10	0.95	4.13	-	1377.6
AHQ-4-2, 5352	K.SYELPDGQVITIGNER.F	1791.93998	2	1.01E-04	0.56	2.94	-	283.7
AHQ-4-7, 4683	K.SYELPDGQVITIGNER.F	1791.93998	2	1.62E-09	0.91	3.64	-	777.2
AHQ-4-2, 5152	K.SYELPDGQVITIGNER.F	1791.93998	2	4.55E-08	0.89	3.67	-	666.9
AHQ-4-2, 4904	K.SYELPDGQVITIGNER.F	1791.93998	2	7.36E-06	0.76	2.91	-	496.5
AHQ-4-2, 4771	K.SYELPDGQVITIGNER.F	1791.93998	2	1.21E-10	0.94	4.11	-	1070.0

AHQ-4-13, 4594 - 4614	K.SYELPDGQVITIGNER.F	1791.93998	2	7.58E-11	0.93	3.72	-	1004.1
AHQ-4-13, 4710	K.SYELPDGQVITIGNER.F	1791.93998	2	4.34E-11	0.93	3.89	-	851.2
AHQ-4-13, 4988	K.SYELPDGQVITIGNER.F	1791.93998	2	3.32E-09	0.95	4.14	-	1250.4
AHQ-4-13, 5141 - 5204	K.SYELPDGQVITIGNER.F	1791.93998	2	3.76E-11	0.95	4.18	-	1119.8
AHQ-4-7, 3525	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	5.20E-05	0.85	3.36	-	856.6
AHQ-4-3, 3948	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	4.92E-04	0.77	3.60	-	397.4
AHQ-4-12, 3766	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	5.78E-05	0.92	4.12	-	740.4
AHQ-4-13-, 3920	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	2.41E-05	0.90	3.94	-	764.3
AHQ-4-12, 3970 - 4043	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	8.62E-06	0.76	3.29	-	461.3
AHQ-4-12, 4302 - 4369	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.23E-04	0.87	4.05	-	703.9
AHQ-4-12, 4489 - 4563	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.56E-04	0.89	4.27	-	621.4
AHQ-4-8, 4243	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.39E-04	0.71	3.30	-	458.1
AHQ-4-9, 4465	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.56E-06	0.86	3.79	-	686.4
AHQ-4-2, 4663	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.11E-04	0.84	3.59	-	657.5
AHQ-4-13-, 4380 - 4445	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.31E-05	0.83	3.56	-	711.1
AHQ-4-9, 3887	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.05E-04	0.88	3.78	-	798.0
AHQ-4-8, 4661 - 4662	K.YPIEHGIITNWDDMEK.I	1962.17174	2	6.02E-09	0.81	4.11	-	544.8
AHQ-4-8, 4670	K.YPIEHGIITNWDDMEK.I	1962.17174	3	8.41E-05	0.85	3.95	-	1308.9
AHQ-4-8, 4237 - 4309	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.36E-05	0.92	4.37	-	764.0
AHQ-4-8, 6437	K.YPIEHGIITNWDDMEKIWHHTFYNELR.V	3459.83609	3	5.56E-05	0.79	3.98	-	443.5
AHQ-4-8, 5094	K.YPIEHGIITNWDDM*EKIWHHTFYNELR.V	3475.83549	3	2.27E-04	0.91	5.29	-	695.8
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				1.98E-13	16.40	190.38	16.80	191612.6
AHQ-4-4, 7479	K.AFMTADLPNELIELLEK.I	1948.26956	2	6.13E-05	0.92	4.32	-	543.9
AHQ-4-1, 7217	K.AFM*TADLPNELIELLEK.I	1964.26896	2	2.75E-04	0.90	4.50	-	507.5
AHQ-4-3, 7539	K.AFMTADLPNELIELLEK.I	1948.26956	2	7.69E-04	0.92	4.60	-	513.3
AHQ-4-3, 7423 - 7495	K.AFM*TADLPNELIELLEK.I	1964.26896	2	2.21E-06	0.84	4.10	-	436.7
AHQ-4-3, 1692	R.AHIAQLCEK.A	1071.23250	1	1.89E-04	0.17	1.95	-	271.6
AHQ-4-4, 4448	R.ALEHFTDLYDIK.R	1465.63179	2	2.39E-04	0.81	2.58	-	994.3
AHQ-4-1, 7253 - 7333	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	2.36E-06	0.89	4.58	-	652.0
AHQ-4-3, 4944	R.GQFSTDELVAEVEK.R	1552.66462	2	3.24E-08	0.92	3.60	-	1180.3
AHQ-4-4, 4787	R.GQFSTDELVAEVEKR.N	1708.85097	2	7.22E-10	0.92	3.87	-	998.9
AHQ-4-5, 4523	R.GQFSTDELVAEVEKR.N	1708.85097	2	1.88E-07	0.93	3.44	-	1397.1
AHQ-4-3, 4808	R.GQFSTDELVAEVEKR.N	1708.85097	2	2.06E-10	0.83	3.69	-	659.6
AHQ-4-3, 2011	R.IHEGCEEPATHNALAK.I	1778.92458	2	3.10E-08	0.88	4.08	-	422.5
AHQ-4-3, 3569	K.IVLDNSVFSEHR.N	1416.56400	2	2.29E-06	0.94	3.49	-	1614.4
AHQ-4-3, 7231	R.KFDVNTSAVQVLIEHIGNLDR.A	2369.66218	3	1.98E-13	0.99	7.62	-	3337.8
AHQ-4-3, 3511	R.KFNALFAQGNYSEAAK.V	1759.94281	2	4.03E-05	0.98	5.61	-	1545.1
AHQ-4-1, 4655	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	2.12E-08	0.94	4.56	-	830.8
AHQ-4-3, 4556	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	2.30E-06	0.95	4.59	-	1041.9
AHQ-4-3, 7284	R.LPVVIGGLLDVDCSEDVIK.N	2043.36744	2	2.38E-04	0.72	3.15	-	728.7
AHQ-4-3, 6423	R.NLQNLLILTAIK.A	1354.66353	2	5.52E-05	0.97	5.12	-	1956.1
AHQ-4-3, 2360	K.RDPHLACVAYER.G	1488.65351	2	9.86E-04	0.92	3.80	-	878.1
AHQ-4-2, 7100	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	1.70E-04	0.94	4.88	-	1195.6
AHQ-4-3, 7060	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	1.31E-05	0.95	5.67	-	1104.9
AHQ-4-1, 5138	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	6.35E-06	0.96	4.15	-	1619.2
AHQ-4-5, 7017	K.VGYTPDWIFLLR.N	1480.73443	2	2.19E-09	0.81	3.26	-	394.8
AHQ-4-3, 7187	K.VGYTPDWIFLLR.N	1480.73443	2	2.39E-09	0.82	3.51	-	379.7
AHQ-4-3, 4997	K.WLKEDKLECSEELGDLVK.S	2193.45974	2	1.92E-05	0.96	4.88	-	1606.4
gi|13562114|ref|NP_110400.1| beta tubulin 1, class VI [Homo sapiens]				2.11E-13	20.76	230.39	50.60	50326.6
AHQ-4-1, 6570 - 6579	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.82E-06	0.96	5.13	-	1333.3
AHQ-4-14-, 6046 - 6109	R.ALSVAELTQQMFDAR.N	1680.90740	2	7.63E-04	0.84	3.79	-	803.6
AHQ-4-2, 6595	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.48E-04	0.85	2.91	-	1184.5
AHQ-4-13, 6258 - 6320	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.47E-04	0.91	3.50	-	1299.6
AHQ-4-11, 5992 - 6018	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.98E-06	0.96	5.02	-	1297.7
AHQ-4-10, 4229	R.ALSVAELTQQM*FDAR.N	1696.90680	2	1.52E-04	0.93	3.86	-	1327.2
AHQ-4-7, 6219	R.ALSVAELTQQMFDAR.N	1680.90740	2	3.25E-04	0.94	3.77	-	1472.0
AHQ-4-7, 6217 - 6289	R.ALSVAELTQQMFDAR.N	1680.90740	2	6.19E-04	0.97	4.75	-	2070.2
AHQ-4-7, 4777	R.AVLVDLEPGTMDSIR.S	1616.86162	2	1.72E-07	0.92	4.27	-	755.3
AHQ-4-14, 6136 - 6172	R.AVLVDLEPGTMDSIR.S	1616.86162	2	5.55E-04	0.90	4.33	-	508.3
AHQ-4-12, 4161 - 4237	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	6.35E-06	0.87	4.00	-	520.3
AHQ-4-7, 4674 - 4745	R.AVLVDLEPGTMDSIR.S	1616.86162	2	3.71E-07	0.90	3.90	-	638.5
AHQ-4-7, 3739 - 3819	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	1.97E-05	0.92	4.49	-	838.6
AHQ-4-7, 3565 - 3633	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	1.78E-12	0.94	4.90	-	745.8
AHQ-4-14-, 3709 - 3711	R.EIVHIQIGQCGNQIGAK.F	1867.11965	3	9.58E-04	0.89	3.40	-	1694.9
AHQ-4-14, 4962	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	4.93E-07	0.85	3.98	-	417.7
AHQ-4-7, 3835	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	3.29E-04	0.72	3.21	-	496.1
AHQ-4-13, 4086	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	2.10E-07	0.92	4.28	-	666.4
AHQ-4-7, 3002 - 3003	K.EVDQQLLSVQTR.N	1416.56231	2	1.81E-04	0.85	3.96	-	693.7
AHQ-4-7, 5139	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.59E-10	0.98	5.67	-	2183.6
AHQ-4-14, 5897 - 5902	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	5.70E-05	0.96	4.57	-	1108.7
AHQ-4-7, 5287 - 5342	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	4.85E-05	0.90	3.98	-	975.0
AHQ-4-14-, 5119	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	1.95E-09	0.95	4.34	-	1439.7
AHQ-4-12, 5231	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.11E-13	0.98	6.56	-	2135.2
AHQ-4-14-, 5111 - 5129	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	8.42E-09	0.99	6.99	-	2372.4
AHQ-4-13-, 5181	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.13E-08	0.97	5.51	-	1355.9
AHQ-4-13, 5292	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.27E-07	0.98	6.12	-	1649.1
AHQ-4-12, 2222	R.GASALQLER.I	945.05542	2	9.81E-04	0.89	2.98	-	1234.1
AHQ-4-7, 6861 - 6926	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.66E-09	0.99	7.40	-	2985.1
AHQ-4-7, 6875	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	3.10E-05	0.89	4.06	-	1631.3
AHQ-4-13, 6766	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	2.49E-05	0.90	4.55	-	1192.2
AHQ-4-13-, 6692	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.31E-11	0.99	7.18	-	2969.1
AHQ-4-12, 6737	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	8.71E-09	0.98	6.95	-	2457.5
AHQ-4-13, 6765	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.76E-09	0.98	6.44	-	2256.3
AHQ-4-11, 6474	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	2.32E-05	0.85	3.84	-	1425.1
AHQ-4-11, 6465	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.06E-06	0.98	6.76	-	2141.5
AHQ-4-4, 7114	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	9.93E-11	0.99	7.31	-	2508.3
AHQ-4-14-, 6557	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.06E-12	0.98	6.09	-	2434.2
AHQ-4-10, 6151 - 6163	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.41E-07	0.98	6.60	-	2674.7
AHQ-4-9, 6220 - 6235	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.95E-05	0.98	6.17	-	2090.7
AHQ-4-8, 6490	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.76E-08	0.99	7.76	-	3602.7
AHQ-4-7, 7346 - 7422	R.GLSMAATFIGNNTAIQEIFNR.V	2269.56611	2	2.56E-06	0.94	4.87	-	929.7
AHQ-4-7, 6551	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	4.61E-07	0.87	3.73	-	729.2
AHQ-4-7, 6709 - 6773	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.44E-08	0.92	4.74	-	665.6
AHQ-4-9, 6033 - 6096	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	5.05E-06	0.93	4.77	-	606.5
AHQ-4-14-, 6462	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	8.72E-08	0.79	3.55	-	553.8
AHQ-4-12, 6522	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.43E-06	0.76	3.02	-	626.2
AHQ-4-14-, 6239 - 6309	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	8.56E-10	0.96	5.65	-	858.0
AHQ-4-13-, 6434 - 6502	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.97E-07	0.91	4.58	-	774.0
AHQ-4-13-, 6466	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	3	3.51E-04	0.93	4.89	-	1246.8
AHQ-4-13, 6533 - 6556	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.19E-07	0.93	5.06	-	615.6
AHQ-4-13, 6546	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	3	2.48E-05	0.95	4.70	-	1717.2
AHQ-4-7, 3234 - 3246	R.IM*NSFSVMPSPK.V	1354.62100	2	5.21E-07	0.81	3.50	-	489.4
AHQ-4-8, 3643 - 3701	R.IMNSFSVMPSPK.V	1338.62160	2	3.97E-09	0.89	3.20	-	810.2
AHQ-4-7, 2747	R.IMNSFSVM*PSPK.V	1354.62100	2	2.56E-04	0.54	2.80	-	378.2
AHQ-4-7, 3763	R.IMNSFSVMPSPK.V	1338.62160	2	2.49E-07	0.93	3.94	-	859.7
AHQ-4-7, 3498 - 3537	R.IMNSFSVMPSPK.V	1338.62160	2	1.18E-04	0.91	3.17	-	1516.9
AHQ-4-7, 3769	R.IMNSFSVMPSPK.V	1338.62160	1	2.30E-06	0.61	2.24	-	663.8

AHQ-4-14-, 3019 - 3021	R.ISVYYNEAYGR.K	1335.44622	2	8.20E-05	0.95	3.62	-	1312.4
AHQ-4-14, 4038 - 4109	R.ISVYYNEAYGR.K	1335.44622	2	2.35E-06	0.89	3.29	-	784.3
AHQ-4-13, 3373	R.ISVYYNEAYGR.K	1335.44622	1	5.42E-05	0.48	2.39	-	199.6
AHQ-4-7, 2905	R.ISVYYNEAYGR.K	1335.44622	2	6.36E-07	0.94	3.44	-	1251.1
AHQ-4-11, 3020	R.ISVYYNEAYGR.K	1335.44622	2	3.38E-04	0.65	2.74	-	603.4
AHQ-4-7, 3077	R.ISVYYNEAYGR.K	1335.44622	2	8.37E-07	0.72	3.06	-	677.8
AHQ-4-7, 2923	R.ISVYYNEAYGR.K	1335.44622	1	5.42E-05	0.23	2.19	-	109.0
AHQ-4-14-, 3175	R.ISVYYNEAYGR.K	1335.44622	2	9.83E-08	0.96	3.79	-	1510.9
AHQ-4-13-, 5182	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	3.34E-12	0.88	3.96	-	830.1
AHQ-4-13, 5290	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	9.58E-09	0.61	3.37	-	552.0
AHQ-4-12, 5223	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	6.57E-06	0.76	3.62	-	605.6
AHQ-4-12, 5150 - 5229	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	7.10E-08	0.91	4.43	-	607.3
AHQ-4-13-, 4986	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	2.52E-05	0.84	3.82	-	722.9
AHQ-4-11, 5581	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	8.11E-05	0.97	5.82	-	933.1
AHQ-4-14-, 5046 - 5109	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	2.02E-05	0.94	4.29	-	2056.9
AHQ-4-8, 4498	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.07E-05	0.95	4.99	-	757.8
AHQ-4-8, 5179	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	4.57E-06	0.95	4.63	-	859.9
AHQ-4-9, 5051	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	8.91E-06	0.94	4.55	-	644.2
AHQ-4-9, 4451 - 4460	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.45E-05	0.96	5.56	-	733.5
AHQ-4-7, 5553 - 5622	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	4.05E-09	0.97	6.34	-	935.9
AHQ-4-4, 5308	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.26E-04	0.94	4.42	-	786.8
AHQ-4-7, 4833	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	5.40E-05	0.97	5.08	-	2570.5
AHQ-4-7, 7402 - 7405	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	9.62E-06	0.93	4.57	-	1350.0
AHQ-4-14-, 6507	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	3.03E-04	0.84	3.77	-	699.3
AHQ-4-13, 6685 - 6690	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	9.98E-06	0.93	4.95	-	949.2
AHQ-4-14-, 6469 - 6535	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	1.86E-04	0.94	4.60	-	1252.6
AHQ-4-7, 6929	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	2.89E-07	0.76	3.68	-	512.1
AHQ-4-7, 6930	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	8.80E-08	0.89	3.73	-	815.9
AHQ-4-7, 6938	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	5.00E-06	0.84	4.04	-	774.5
AHQ-4-11, 6774 - 6776	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.51E-09	0.95	4.89	-	974.4
AHQ-4-7, 7326 - 7403	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.58E-09	0.94	5.65	-	770.3
AHQ-4-8, 7173 - 7174	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	4.48E-11	0.94	4.97	-	1041.9
AHQ-4-9, 6193 - 6256	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	5.43E-05	0.91	4.85	-	856.1
AHQ-4-9, 6657	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	4.69E-09	0.91	4.57	-	1008.1
AHQ-4-1, 6986	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	4.00E-04	0.71	3.33	-	701.3
AHQ-4-9, 6652 - 6728	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	2.29E-10	0.93	4.84	-	652.2
AHQ-4-7, 6037	R.NSSCFVEWIPNNVK.V	1695.87718	2	3.84E-07	0.85	3.25	-	728.4
AHQ-4-7, 5198 - 5215	R.NSSCFVEWIPNNVK.V	1695.87718	2	2.58E-06	0.79	3.46	-	553.5
AHQ-4-12, 5289	R.YLTVACIFR.G	1144.36822	2	6.05E-07	0.94	3.22	-	1146.2
AHQ-4-11, 5048	R.YLTVACIFR.G	1144.36822	2	9.23E-05	0.91	2.81	-	973.4
gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]				2.45E-13	33.41	410.34	38.10	129351.8
AHQ-4-2, 4740	K.AGTLDLSLTVQGK.Q	1303.48711	2	4.41E-05	0.90	3.57	-	975.2
AHQ-4-2, 4284	K.AGTLDLSLTVQGK.Q	1303.48711	2	1.08E-04	0.92	3.17	-	1402.9
AHQ-4-7, 1927	R.AQGYSGLSVK.V	1010.12587	1	7.91E-05	0.05	2.19	-	106.5
AHQ-4-5, 2503	R.AQLYIDCEK.M	1141.27636	1	4.00E-04	0.23	1.92	-	502.7
AHQ-4-5, 2499	R.AQLYIDCEK.M	1141.27636	1	4.00E-04	0.43	2.89	-	192.2
AHQ-4-10, 2523	R.AQLYIDCEK.M	1141.27636	1	5.72E-05	0.22	2.68	-	227.7
AHQ-4-10, 5745	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	2	5.49E-04	0.89	4.00	-	764.0
AHQ-4-10, 5867	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	2	1.68E-05	0.84	3.95	-	501.7
AHQ-4-6, 6359 - 6368	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	3	2.18E-04	0.86	4.62	-	521.2
AHQ-4-3, 6653	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	3	5.89E-07	0.94	5.00	-	1067.9
AHQ-4-2, 6655	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	3	5.02E-06	0.94	5.00	-	1021.8
AHQ-4-3, 4040	R.CENTDPGYNCLPCPPR.F	1954.10800	2	5.66E-04	0.89	3.89	-	496.6
AHQ-4-3, 4147 - 4217	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.07E-05	0.74	2.73	-	625.3
AHQ-4-4, 4000	R.CENTDPGYNCLPCPPR.F	1954.10800	2	6.40E-06	0.88	3.89	-	538.5
AHQ-4-2, 3942 - 4011	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.61E-05	0.42	2.85	-	301.6
AHQ-4-5, 3894	R.CENTDPGYNCLPCPPR.F	1954.10800	2	3.13E-07	0.90	4.05	-	476.3
AHQ-4-1, 3894 - 3898	R.CENTDPGYNCLPCPPR.F	1954.10800	2	3.58E-10	0.91	3.93	-	631.9
AHQ-4-2, 4048	R.CENTDPGYNCLPCPPR.F	1954.10800	2	3.71E-05	0.71	2.81	-	424.1
AHQ-4-2, 3907	K.CNYLGHYSDPMYR.C	1677.84222	2	8.39E-06	0.87	3.37	-	629.4
AHQ-4-3, 3880 - 3889	K.CNYLGHYSDPMYR.C	1677.84222	2	3.77E-07	0.94	4.39	-	807.2
AHQ-4-5, 3661	K.CNYLGHYSDPMYR.C	1677.84222	2	4.73E-04	0.85	3.70	-	808.7
AHQ-4-1, 3451	K.CNYLGHYSDPM*YR.C	1693.84162	2	2.87E-05	0.77	2.89	-	602.1
AHQ-4-2, 3375	K.CNYLGHYSDPM*YR.C	1693.84162	2	4.08E-04	0.94	3.60	-	1093.0
AHQ-4-4, 3319	K.CNYLGHYSDPM*YR.C	1693.84162	2	5.37E-04	0.91	3.01	-	951.9
AHQ-4-1, 3983	K.CNYLGHYSDPMYR.C	1677.84222	2	6.40E-07	0.80	3.08	-	523.1
AHQ-4-2, 3470	K.DCVGDVTENQICNK.Q	1654.75869	2	2.05E-04	0.95	4.03	-	1225.4
AHQ-4-3, 3455 - 3529	K.DCVGDVTENQICNK.Q	1654.75869	2	3.68E-06	0.94	4.35	-	970.1
AHQ-4-10, 2535	K.DHSGQVFSVVSNGK.A	1461.56164	1	3.68E-08	0.37	2.22	-	449.2
AHQ-4-3, 2668	K.DHSGQVFSVVSNGK.A	1461.56164	2	9.50E-06	0.93	3.60	-	1020.4
AHQ-4-5, 2531	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.08E-06	0.95	3.96	-	1214.2
AHQ-4-2, 2694 - 2762	K.DHSGQVFSVVSNGK.A	1461.56164	2	5.92E-07	0.95	4.24	-	1174.4
AHQ-4-10, 2536	K.DHSGQVFSVVSNGK.A	1461.56164	2	4.35E-07	0.96	4.17	-	1377.2
AHQ-4-10, 2637	K.DHSGQVFSVVSNGK.A	1461.56164	1	5.93E-11	0.54	2.33	-	562.0
AHQ-4-4, 2650	K.DHSGQVFSVVSNGK.A	1461.56164	2	4.88E-09	0.95	4.01	-	1397.0
AHQ-4-6, 3218	R.DNCQYVYNVDQR.D	1575.64166	2	1.37E-04	0.67	2.90	-	741.9
AHQ-4-5, 2947 - 3025	R.DNCQYVYNVDQR.D	1575.64166	2	5.50E-05	0.73	2.63	-	737.6
AHQ-4-4, 3098	R.DNCQYVYNVDQR.D	1575.64166	2	1.12E-04	0.88	3.57	-	970.4
AHQ-4-7, 2986	R.DNCQYVYNVDQR.D	1575.64166	2	2.53E-04	0.87	3.52	-	1034.2
AHQ-4-1, 3177	R.DNCQYVYNVDQR.D	1575.64166	2	6.10E-06	0.83	2.93	-	909.2
AHQ-4-3, 3123	R.DNCQYVYNVDQR.D	1575.64166	2	9.17E-04	0.93	3.74	-	1166.7
AHQ-4-2, 3140	R.DNCQYVYNVDQR.D	1575.64166	2	8.87E-05	0.90	3.83	-	902.1
AHQ-4-1, 3338	R.DNCQYVYNVDQR.D	1575.64166	2	1.30E-05	0.85	3.47	-	872.7
AHQ-4-4, 3334	R.DNCQYVYNVDQR.D	1575.64166	2	2.67E-05	0.57	2.73	-	835.7
AHQ-4-2, 6146 - 6220	K.DSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFR.R	4418.43100	3	1.17E-08	0.95	5.79	-	975.3
AHQ-4-3, 6152 - 6227	K.DSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFR.R	4418.43100	3	1.02E-05	0.80	4.07	-	576.0
AHQ-4-4, 6128 - 6186	K.DSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFR.R	4418.43100	3	2.52E-04	0.72	3.72	-	485.2
AHQ-4-1, 4274	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	4.77E-06	0.89	4.56	-	495.9
AHQ-4-6, 3988	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.75E-04	0.92	4.88	-	704.2
AHQ-4-5, 3866	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.88E-05	0.81	3.78	-	621.0
AHQ-4-4, 3870	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.92E-06	0.82	3.26	-	902.8
AHQ-4-3, 3913 - 3940	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	4.71E-08	0.90	4.55	-	738.5
AHQ-4-5, 4254	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	7.56E-05	0.88	4.45	-	510.8
AHQ-4-3, 4308	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.13E-04	0.89	4.20	-	769.2
AHQ-4-6, 3742	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.96E-09	0.79	3.73	-	618.5
AHQ-4-4, 4144	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.41E-04	0.94	5.21	-	788.4
AHQ-4-2, 3928 - 4003	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.29E-11	0.93	4.85	-	829.4
AHQ-4-1, 3863	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	8.54E-05	0.83	3.97	-	703.5
AHQ-4-4, 4260 - 4294	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.99E-06	0.87	4.40	-	487.4
AHQ-4-2, 4290 - 4358	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.54E-12	0.95	5.13	-	1089.5
AHQ-4-2, 4115	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.37E-05	0.89	4.32	-	734.7
AHQ-4-2, 3639 - 3646	K.FQDLVDAVR.A	1063.18877	2	2.75E-06	0.93	3.89	-	1067.3
AHQ-4-2, 3638 - 3644	K.FQDLVDAVR.A	1063.18877	1	2.54E-04	0.49	2.44	-	414.6
AHQ-4-1, 3750	K.FQDLVDAVR.A	1063.18877	2	7.50E-06	0.84	2.88	-	870.2
AHQ-4-10, 3252	K.FQDLVDAVR.A	1063.18877	1	1.75E-04	0.25	2.18	-	154.0
AHQ-4-5, 2619	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.73E-05	0.75	3.06	-	479.1
AHQ-4-1, 3103	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.15E-09	0.91	3.99	-	591.2

AHQ-4-2, 2928 - 2971	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	9.77E-11	0.76	3.67	-	385.3
AHQ-4-9, 2397	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.81E-04	0.56	2.89	-	347.6
AHQ-4-2, 2842	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.63E-10	0.90	4.12	-	552.7
AHQ-4-1, 2970 - 2977	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	1.39E-04	0.79	3.67	-	488.5
AHQ-4-1, 2954	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	8.49E-09	0.93	4.70	-	672.4
AHQ-4-4, 2680 - 2750	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.43E-05	0.87	3.89	-	558.4
AHQ-4-3, 2845 - 2923	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.59E-09	0.91	4.39	-	510.4
AHQ-4-3, 2732 - 2753	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	3.01E-09	0.90	4.28	-	667.6
AHQ-4-4, 2950	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.16E-05	0.82	3.43	-	611.5
AHQ-4-4, 5612	R.FVFGTTPEDILR.N	1395.58470	1	5.11E-05	0.16	2.10	-	158.9
AHQ-4-4, 5619	R.FVFGTTPEDILR.N	1395.58470	1	1.28E-04	0.39	2.60	-	149.7
AHQ-4-12, 5438	R.FVFGTTPEDILR.N	1395.58470	2	2.95E-04	0.75	2.67	-	556.3
AHQ-4-5, 5417	R.FVFGTTPEDILR.N	1395.58470	1	1.94E-08	0.08	2.09	-	46.8
AHQ-4-3, 5637 - 5665	R.FVFGTTPEDILR.N	1395.58470	2	5.18E-04	0.69	2.80	-	488.7
AHQ-4-2, 5638	R.FVFGTTPEDILR.N	1395.58470	1	1.07E-05	0.31	2.65	-	142.8
AHQ-4-9, 4796	R.FVFGTTPEDILR.N	1395.58470	1	3.30E-05	0.35	2.78	-	156.1
AHQ-4-3, 5652	R.FVFGTTPEDILR.N	1395.58470	1	2.47E-04	0.23	2.49	-	129.1
AHQ-4-2, 5662	K.GFLLLASLR.Q	990.22407	2	1.84E-05	0.97	3.42	-	2202.4
AHQ-4-7, 4389	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.50E-09	0.90	3.73	-	910.8
AHQ-4-9, 3991 - 3999	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.53E-10	0.89	4.10	-	739.5
AHQ-4-7, 4121 - 4123	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.45E-05	0.84	3.52	-	763.4
AHQ-4-6, 4546	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.05E-05	0.78	3.41	-	603.2
AHQ-4-4, 4826 - 4828	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.81E-05	0.79	3.32	-	591.6
AHQ-4-8, 3874 - 3875	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.41E-06	0.93	4.63	-	883.9
AHQ-4-4, 4324	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.90E-04	0.86	4.10	-	622.3
AHQ-4-11, 4334	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.53E-05	0.64	3.33	-	515.2
AHQ-4-6, 4402 - 4471	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.32E-05	0.87	4.08	-	781.7
AHQ-4-6, 4182 - 4216	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.61E-07	0.88	4.38	-	803.0
AHQ-4-6, 4042	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.50E-06	0.51	2.74	-	513.6
AHQ-4-4, 4479 - 4506	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.70E-04	0.86	3.74	-	779.2
AHQ-4-5, 4142	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.13E-06	0.66	2.70	-	788.3
AHQ-4-1, 4879	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.82E-06	0.90	3.59	-	1096.3
AHQ-4-1, 4798	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.92E-06	0.68	3.22	-	598.1
AHQ-4-10, 3849 - 3851	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.21E-05	0.88	3.72	-	846.8
AHQ-4-10, 3943 - 4016	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.59E-05	0.90	3.97	-	825.0
AHQ-4-2, 4870 - 4876	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.43E-10	0.92	4.41	-	1005.7
AHQ-4-10, 4075 - 4135	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.63E-09	0.93	4.44	-	958.0
AHQ-4-2, 4656 - 4730	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.19E-10	0.95	4.79	-	1225.7
AHQ-4-5, 4269	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.06E-05	0.86	3.96	-	687.1
AHQ-4-5, 4493	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.31E-05	0.85	3.71	-	826.8
AHQ-4-3, 4381	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.22E-09	0.89	3.88	-	744.9
AHQ-4-10, 4213	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.70E-09	0.88	3.67	-	853.5
AHQ-4-3, 4532 - 4535	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.11E-07	0.90	4.20	-	765.5
AHQ-4-3, 4687 - 4761	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.61E-08	0.93	4.34	-	1010.4
AHQ-4-3, 4859	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.04E-05	0.90	4.01	-	797.2
AHQ-4-11, 4180 - 4190	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.29E-04	0.82	3.27	-	578.9
AHQ-4-2, 4407	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.39E-04	0.86	3.99	-	639.9
AHQ-4-8, 4202	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.09E-06	0.86	3.60	-	748.6
AHQ-4-2, 2078 - 2079	K.GPDPSSPAFR.I	1031.10364	2	2.49E-05	0.71	3.12	-	437.0
AHQ-4-5, 1886 - 1922	K.GPDPSSPAFR.I	1031.10364	2	4.62E-05	0.56	2.51	-	463.2
AHQ-4-3, 2057 - 2068	K.GPDPSSPAFR.I	1031.10364	2	3.64E-05	0.84	3.20	-	601.6
AHQ-4-1, 2255	K.GPDPSSPAFR.I	1031.10364	2	3.27E-04	0.79	2.97	-	502.6
AHQ-4-10, 2007	K.GPDPSSPAFR.I	1031.10364	2	1.17E-04	0.76	2.92	-	494.1
AHQ-4-4, 2067	K.GPDPSSPAFR.I	1031.10364	2	2.72E-05	0.50	3.02	-	359.3
AHQ-4-1, 3171	R.GTLLALER.K	873.03234	2	9.28E-04	0.88	3.23	-	1018.8
AHQ-4-3, 2932	R.GTLLALER.K	873.03234	2	2.84E-04	0.91	3.59	-	954.9
AHQ-4-2, 2559 - 2570	K.GTSQNDPNWVVR.H	1373.45608	2	5.22E-04	0.56	3.01	-	516.4
AHQ-4-1, 2765 - 2774	K.GTSQNDPNWVVR.H	1373.45608	2	1.63E-04	0.60	2.86	-	625.6
AHQ-4-14-, 6186 - 6253	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.73E-05	0.78	3.99	-	387.0
AHQ-4-7, 6593 - 6611	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.30E-04	0.67	3.29	-	342.8
AHQ-4-8, 6229	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.02E-05	0.78	3.59	-	237.8
AHQ-4-13-, 6308 - 6322	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.59E-06	0.82	3.69	-	324.5
AHQ-4-13-, 6300	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.64E-08	0.88	4.26	-	424.8
AHQ-4-3, 6748 - 6775	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.45E-13	0.82	3.76	-	461.4
AHQ-4-9, 5919 - 5992	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.76E-07	0.76	3.43	-	319.8
AHQ-4-3, 6747 - 6819	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.01E-04	0.55	2.91	-	209.9
AHQ-4-2, 6742 - 6818	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.12E-08	0.86	3.93	-	631.6
AHQ-4-13, 6392	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.38E-07	0.69	3.33	-	243.3
AHQ-4-13, 6350 - 6388	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	6.05E-07	0.87	3.90	-	547.0
AHQ-4-2, 6746 - 6819	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	7.42E-06	0.87	4.27	-	312.4
AHQ-4-12, 6545	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.60E-04	0.67	3.22	-	418.1
AHQ-4-3, 6935	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.97E-07	0.69	3.45	-	320.2
AHQ-4-9, 5925 - 5936	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.25E-05	0.83	3.79	-	399.5
AHQ-4-14-, 6317	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.06E-09	0.74	3.42	-	361.9
AHQ-4-2, 6863 - 6942	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.61E-05	0.77	3.22	-	413.3
AHQ-4-2, 6884 - 6943	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.60E-10	0.69	3.47	-	436.0
AHQ-4-1, 6797	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.23E-04	0.66	3.27	-	359.6
AHQ-4-11, 6254 - 6296	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	6.06E-06	0.69	3.05	-	390.9
AHQ-4-11, 6144	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.60E-08	0.84	3.45	-	337.2
AHQ-4-11, 6070 - 6145	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.37E-08	0.76	3.61	-	367.3
AHQ-4-1, 6657 - 6733	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.56E-10	0.81	4.10	-	427.4
AHQ-4-1, 6651 - 6731	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	8.71E-06	0.60	2.82	-	245.5
AHQ-4-6, 6554 - 6632	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.18E-05	0.69	3.32	-	399.9
AHQ-4-10, 5716	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.18E-04	0.63	2.72	-	291.6
AHQ-4-10, 5931 - 5989	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.01E-07	0.84	4.04	-	386.1
AHQ-4-4, 6675 - 6746	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.31E-07	0.70	3.51	-	227.9
AHQ-4-4, 6720	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.23E-06	0.39	2.99	-	230.1
AHQ-4-4, 6820 - 6886	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	6.08E-07	0.91	4.57	-	601.2
AHQ-4-12, 6385 - 6386	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	8.98E-07	0.81	3.83	-	260.9
AHQ-4-6, 6454 - 6470	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.60E-10	0.87	4.50	-	421.2
AHQ-4-10, 5920 - 5975	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.98E-07	0.67	3.31	-	242.5
AHQ-4-6, 2386	K.IMADSGPIYDK.T	1210.38204	2	1.64E-06	0.92	3.80	-	702.9
AHQ-4-7, 2343	K.IMADSGPIYDK.T	1210.38204	2	5.23E-04	0.84	3.21	-	603.1
AHQ-4-14-, 2234	K.IM*ADSGPIYDK.T	1226.38144	2	1.83E-05	0.85	3.36	-	535.7
AHQ-4-11, 2224 - 2237	K.IM*ADSGPIYDK.T	1226.38144	2	6.75E-05	0.72	2.73	-	611.5
AHQ-4-11, 2481 - 2485	K.IMADSGPIYDK.T	1210.38204	2	7.35E-05	0.91	3.67	-	703.7
AHQ-4-2, 2291 - 2295	K.IM*ADSGPIYDK.T	1226.38144	2	1.31E-05	0.88	3.71	-	562.5
AHQ-4-13-, 2625 - 2644	K.IMADSGPIYDK.T	1210.38204	2	9.20E-05	0.90	3.11	-	852.3
AHQ-4-2, 2543	K.IMADSGPIYDK.T	1210.38204	2	1.24E-06	0.94	4.18	-	813.4
AHQ-4-12, 2549	K.IMADSGPIYDK.T	1210.38204	2	1.75E-05	0.93	3.88	-	762.5
AHQ-4-12, 2279 - 2351	K.IM*ADSGPIYDK.T	1226.38144	2	4.92E-04	0.59	2.57	-	514.4
AHQ-4-9, 6377 - 6440	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.30E-05	0.91	4.38	-	642.1
AHQ-4-11, 6629 - 6638	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.85E-09	0.96	5.26	-	918.6
AHQ-4-9, 6216 - 6283	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.71E-08	0.97	5.47	-	1373.0
AHQ-4-2, 7167 - 7242	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	9.59E-10	0.97	5.79	-	1143.7
AHQ-4-2, 7306	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.01E-07	0.97	5.44	-	1157.7
AHQ-4-9, 6468	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.38E-09	0.93	3.92	-	1031.8

AHQ-4-13, 6762 - 6825	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.39E-10	0.97	6.00	-	1368.8
AHQ-4-1, 7013 - 7082	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.00E-13	0.98	6.37	-	1849.2
AHQ-4-1, 7035	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	4.16E-04	0.82	3.79	-	918.6
AHQ-4-13-, 6680	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.55E-10	0.97	5.82	-	1404.9
AHQ-4-11, 6485 - 6564	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.98E-13	0.96	5.23	-	914.6
AHQ-4-7, 6993 - 7047	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	9.11E-04	0.59	2.66	-	543.5
AHQ-4-10, 6304	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.32E-10	0.97	5.62	-	1094.9
AHQ-4-10, 6176 - 6248	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.25E-11	0.97	5.93	-	1519.9
AHQ-4-6, 6998	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.24E-05	0.82	3.82	-	497.3
AHQ-4-3, 7283 - 7291	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.40E-11	0.97	5.67	-	1217.5
AHQ-4-5, 6939 - 7009	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.59E-06	0.98	6.74	-	1546.2
AHQ-4-5, 7083 - 7150	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.20E-09	0.96	5.34	-	1174.9
AHQ-4-5, 7177	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.76E-11	0.96	5.44	-	1089.2
AHQ-4-3, 7155 - 7221	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.24E-08	0.96	5.22	-	1212.9
AHQ-4-12, 6855	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.35E-04	0.91	4.22	-	599.4
AHQ-4-4, 7122 - 7188	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.90E-10	0.96	5.65	-	934.5
AHQ-4-4, 7207 - 7254	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.29E-10	0.97	6.05	-	1179.9
AHQ-4-14-, 6537 - 6605	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.81E-13	0.98	6.57	-	1345.5
AHQ-4-3, 2193 - 2236	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.27E-07	0.88	4.01	-	707.4
AHQ-4-2, 2326	R.KDHSGQVFSVVSNGK.A	1589.73455	2	7.99E-10	0.81	3.25	-	805.7
AHQ-4-12, 2275	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.87E-08	0.60	3.11	-	454.1
AHQ-4-1, 2433	R.KDHSGQVFSVVSNGK.A	1589.73455	2	4.53E-09	0.86	3.29	-	961.8
AHQ-4-5, 2027 - 2098	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.29E-08	0.91	4.08	-	801.5
AHQ-4-13-, 2354	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.57E-08	0.91	3.06	-	1426.7
AHQ-4-2, 2235 - 2250	R.KDHSGQVFSVVSNGK.A	1589.73455	2	3.14E-08	0.94	4.01	-	1202.6
AHQ-4-3, 2276 - 2316	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.54E-07	0.92	3.85	-	941.2
AHQ-4-11, 2234	K.KIMADSGPIYDK.T	1338.55496	2	3.69E-04	0.82	3.13	-	803.6
AHQ-4-2, 2316	K.KIMADSGPIYDK.T	1338.55496	1	3.88E-06	0.80	2.97	-	662.8
AHQ-4-3, 2283	K.KIMADSGPIYDK.T	1338.55496	2	6.86E-04	0.89	3.26	-	788.7
AHQ-4-2, 2311	K.KIMADSGPIYDK.T	1338.55496	2	1.01E-06	0.89	3.92	-	635.8
AHQ-4-5, 2194 - 2195	R.KVTEENKELANELR.R	1673.84976	2	2.60E-07	0.96	4.83	-	1368.0
AHQ-4-6, 2062	R.KVTEENKELANELR.R	1673.84976	2	1.60E-08	0.93	4.82	-	1212.8
AHQ-4-5, 1991 - 2071	R.KVTEENKELANELR.R	1673.84976	3	3.46E-06	0.79	3.89	-	727.3
AHQ-4-2, 2268	R.KVTEENKELANELR.R	1673.84976	3	3.00E-04	0.92	4.18	-	1284.3
AHQ-4-2, 2364	R.KVTEENKELANELR.R	1673.84976	2	2.91E-11	0.95	4.52	-	1487.8
AHQ-4-7, 2005	R.KVTEENKELANELR.R	1673.84976	2	3.99E-10	0.93	4.39	-	1286.3
AHQ-4-1, 2389 - 2457	R.KVTEENKELANELR.R	1673.84976	2	1.72E-09	0.95	5.07	-	1421.7
AHQ-4-4, 2324 - 2328	R.KVTEENKELANELR.R	1673.84976	2	1.20E-10	0.96	5.45	-	1493.0
AHQ-4-4, 2239 - 2311	R.KVTEENKELANELR.R	1673.84976	3	1.40E-04	0.79	3.82	-	900.4
AHQ-4-4, 2230	R.KVTEENKELANELR.R	1673.84976	2	6.99E-09	0.91	4.64	-	912.4
AHQ-4-2, 2262 - 2267	R.KVTEENKELANELR.R	1673.84976	2	1.66E-06	0.93	4.80	-	1208.3
AHQ-4-4, 1987	R.KVTEENKELANELR.R	1673.84976	2	2.73E-10	0.93	4.55	-	1221.0
AHQ-4-3, 2225	R.KVTEENKELANELR.R	1673.84976	2	8.14E-11	0.94	4.57	-	1284.3
AHQ-4-9, 1997	R.KVTEENKELANELR.R	1673.84976	2	1.01E-08	0.92	4.77	-	1041.9
AHQ-4-8, 1903	R.KVTEENKELANELR.R	1673.84976	2	1.30E-09	0.93	4.16	-	1224.1
AHQ-4-3, 2344	R.KVTEENKELANELR.R	1673.84976	2	1.81E-09	0.95	4.89	-	1314.2
AHQ-4-5, 2447	R.LCNNPAPQFGGK.D	1304.45694	2	5.36E-04	0.73	3.34	-	391.3
AHQ-4-2, 4470	R.LCNNPAPQFGGKDCVGDVTENQICNK.Q	2940.19303	3	4.27E-04	0.80	3.66	-	653.7
AHQ-4-2, 4475	R.LCNNPAPQFGGKDCVGDVTENQICNK.Q	2940.19303	2	1.95E-05	0.75	3.40	-	421.2
AHQ-4-3, 2125 - 2131	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	9.74E-04	0.86	3.62	-	555.4
AHQ-4-4, 2468	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	3.95E-07	0.89	4.09	-	488.8
AHQ-4-3, 2129	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	3	4.13E-04	0.85	3.66	-	856.5
AHQ-4-3, 2495	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.78E-08	0.85	3.84	-	487.6
AHQ-4-2, 2504	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	2.64E-05	0.89	3.49	-	1222.2
AHQ-4-5, 2398	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.60E-06	0.80	4.01	-	414.3
AHQ-4-1, 2593	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.52E-07	0.91	4.61	-	441.8
AHQ-4-5, 2039	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	3.57E-07	0.87	3.67	-	594.0
AHQ-4-2, 2503	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	9.48E-06	0.74	3.71	-	335.5
AHQ-4-4, 5492	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	5.70E-08	0.89	3.76	-	668.1
AHQ-4-6, 5588 - 5608	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.91E-06	0.78	3.71	-	330.5
AHQ-4-2, 5774	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.50E-05	0.64	3.42	-	321.6
AHQ-4-6, 5447	K.MENAELDVPIQSVFTR.D	1850.08607	2	7.28E-05	0.89	3.91	-	499.8
AHQ-4-5, 5506 - 5509	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.15E-11	0.94	4.98	-	622.5
AHQ-4-6, 5206	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	3.67E-05	0.89	4.26	-	504.1
AHQ-4-5, 5302	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.43E-09	0.88	3.58	-	617.4
AHQ-4-4, 5719	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.93E-04	0.89	4.23	-	481.2
AHQ-4-1, 5581 - 5650	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	4.82E-06	0.87	3.55	-	713.0
AHQ-4-3, 5533	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	7.36E-07	0.90	4.11	-	538.6
AHQ-4-7, 5403	K.MENAELDVPIQSVFTR.D	1850.08607	2	4.44E-07	0.86	3.91	-	446.6
AHQ-4-3, 5783 - 5799	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.52E-12	0.92	4.65	-	590.4
AHQ-4-11, 5292	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.57E-04	0.85	3.71	-	459.5
AHQ-4-2, 5534	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	8.10E-12	0.93	4.28	-	651.3
AHQ-4-10, 4948	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.88E-04	0.87	3.92	-	540.5
AHQ-4-2, 5552 - 5560	K.QHVVSVEEALLATGQWK.S	1896.13616	2	4.68E-05	0.72	2.91	-	548.2
AHQ-4-4, 3038	K.QVTQSYWDTNPTR.A	1596.68241	2	4.44E-07	0.86	3.38	-	687.1
AHQ-4-3, 3063 - 3064	K.QVTQSYWDTNPTR.A	1596.68241	2	2.42E-07	0.93	4.06	-	733.6
AHQ-4-6, 2843 - 2866	K.QVTQSYWDTNPTR.A	1596.68241	2	2.30E-04	0.44	2.96	-	221.8
AHQ-4-2, 3083	K.QVTQSYWDTNPTR.A	1596.68241	2	4.73E-09	0.94	4.13	-	883.6
AHQ-4-7, 2799	K.QVTQSYWDTNPTR.A	1596.68241	2	4.28E-06	0.80	3.62	-	300.1
AHQ-4-11, 2920 - 2921	K.QVTQSYWDTNPTR.A	1596.68241	2	1.86E-05	0.88	3.55	-	737.8
AHQ-4-5, 2869	K.QVTQSYWDTNPTR.A	1596.68241	2	9.48E-05	0.63	2.59	-	412.9
AHQ-4-5, 2563	R.RPPLCYHNGVQYR.N	1661.86889	2	2.83E-06	0.91	3.71	-	809.9
AHQ-4-2, 2715 - 2787	R.RPPLCYHNGVQYR.N	1661.86889	2	7.21E-07	0.82	3.56	-	547.1
AHQ-4-4, 2670 - 2678	R.RPPLCYHNGVQYR.N	1661.86889	2	3.56E-05	0.88	3.60	-	723.6
AHQ-4-6, 2546	R.RPPLCYHNGVQYR.N	1661.86889	2	9.30E-06	0.89	3.35	-	784.3
AHQ-4-1, 2938 - 2939	R.RPPLCYHNGVQYR.N	1661.86889	2	3.17E-06	0.89	3.70	-	710.1
AHQ-4-3, 2705 - 2787	R.RPPLCYHNGVQYR.N	1661.86889	2	1.01E-08	0.93	4.09	-	790.4
AHQ-4-3, 2508	R.RPPLCYHNGVQYR.N	1661.86889	2	1.17E-05	0.91	3.63	-	906.4
AHQ-4-11, 3642	K.SITLFVQEDR.A	1208.34588	2	3.54E-06	0.87	3.21	-	998.8
AHQ-4-5, 3633	K.SITLFVQEDR.A	1208.34588	2	3.54E-06	0.90	3.04	-	1142.9
AHQ-4-2, 3887 - 3894	K.SITLFVQEDR.A	1208.34588	2	8.87E-07	0.93	3.33	-	1328.3
AHQ-4-6, 3548 - 3559	K.SITLFVQEDR.A	1208.34588	2	1.23E-06	0.92	3.40	-	1278.2
AHQ-4-3, 3843 - 3881	K.SITLFVQEDR.A	1208.34588	2	4.55E-06	0.92	3.44	-	1170.5
AHQ-4-4, 3812	K.SITLFVQEDR.A	1208.34588	2	3.19E-05	0.93	3.52	-	1261.2
AHQ-4-1, 3993	K.SITLFVQEDR.A	1208.34588	2	7.76E-06	0.95	3.82	-	1390.6
AHQ-4-10, 3448	K.SITLFVQEDR.A	1208.34588	2	8.26E-04	0.92	3.55	-	1131.5
AHQ-4-2, 3987	K.SITLFVQEDR.A	1208.34588	2	2.17E-06	0.93	3.36	-	1334.2
AHQ-4-12, 3745	K.SITLFVQEDR.A	1208.34588	2	3.96E-06	0.94	3.50	-	1496.7
AHQ-4-1, 4597 - 4613	R.TIVTTLQDSIR.K	1247.42355	2	8.61E-08	0.96	4.15	-	1540.0
AHQ-4-9, 3725	R.TIVTTLQDSIR.K	1247.42355	2	7.05E-04	0.93	3.39	-	1266.8
AHQ-4-7, 4061 - 4063	R.TIVTTLQDSIR.K	1247.42355	2	7.47E-07	0.97	4.25	-	1650.9
AHQ-4-3, 4467 - 4541	R.TIVTTLQDSIR.K	1247.42355	2	2.09E-06	0.97	4.13	-	1610.4
AHQ-4-4, 4420 - 4427	R.TIVTTLQDSIR.K	1247.42355	2	4.21E-05	0.96	3.78	-	1851.4
AHQ-4-10, 3941	R.TIVTTLQDSIR.K	1247.42355	2	2.82E-05	0.94	3.09	-	1481.7
AHQ-4-2, 4496 - 4568	R.TIVTTLQDSIR.K	1247.42355	2	5.00E-06	0.97	4.15	-	1693.9
AHQ-4-14, 5492	R.TIVTTLQDSIR.K	1247.42355	2	5.99E-08	0.95	3.55	-	1554.4
AHQ-4-6, 4106 - 4126	R.TIVTTLQDSIR.K	1247.42355	2	2.49E-07	0.97	4.01	-	1704.0

AHQ-4-8, 3831	R.TIVTTLQDSIR.K	1247.42355	2	4.51E-06	0.95	3.92	-	1366.9
AHQ-4-5, 4173 - 4178	R.TIVTTLQDSIR.K	1247.42355	2	1.28E-05	0.96	4.31	-	1593.8
AHQ-4-1, 6537	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	1.44E-07	0.91	3.99	-	1296.5
AHQ-4-5, 2235 - 2306	K.VTEENKELANELR.R	1545.67685	2	3.94E-10	0.95	4.47	-	1287.1
AHQ-4-6, 2300	K.VTEENKELANELR.R	1545.67685	2	3.09E-05	0.92	4.11	-	986.1
AHQ-4-1, 2659	K.VTEENKELANELR.R	1545.67685	2	1.58E-05	0.59	2.66	-	828.6
AHQ-4-7, 2249 - 2253	K.VTEENKELANELR.R	1545.67685	2	7.46E-05	0.92	4.09	-	1097.2
AHQ-4-4, 2430	K.VTEENKELANELR.R	1545.67685	2	2.65E-08	0.91	4.18	-	1054.6
gi|7661818|ref|NP_054900.1| HSPC159 protein [Homo sapiens]				2.56E-13	3.79	50.25	35.50	19011.6
AHQ-4-11, 6608	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	5.00E-06	0.85	4.14	-	266.7
AHQ-4-12, 6841	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	6.96E-06	0.82	3.39	-	412.2
AHQ-4-13-, 6720	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	5.34E-07	0.88	4.16	-	302.6
AHQ-4-14-, 6609	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	6.75E-06	0.73	3.06	-	341.1
AHQ-4-12, 2533	K.INGDLQITK.L	1002.14688	1	1.35E-04	0.29	2.08	-	327.0
AHQ-4-12, 2462 - 2538	K.INGDLQITK.L	1002.14688	2	6.27E-04	0.79	2.61	-	589.0
AHQ-4-13, 3849 - 3882	R.IQTLSAIDTIK.I	1203.41068	2	1.01E-05	0.80	2.91	-	705.2
AHQ-4-13-, 3728 - 3744	R.IQTLSAIDTIK.I	1203.41068	2	5.01E-05	0.83	3.28	-	666.3
AHQ-4-13-, 6562	R.NSCISGERGEEQSAIPYFPFIPDQPFR.V	3144.41922	3	9.70E-05	0.72	3.94	-	391.7
AHQ-4-13-, 6686	R.NSCISGERGEEQSAIPYFPFIPDQPFR.V	3144.41922	3	2.76E-04	0.84	3.55	-	691.0
AHQ-4-13, 6636	R.NSCISGERGEEQSAIPYFPFIPDQPFR.V	3144.41922	3	9.63E-06	0.85	3.90	-	835.8
AHQ-4-11, 4660 - 4668	R.VFVDGHQLFDFYHR.I	1780.96540	2	2.56E-13	0.97	4.99	-	1427.4
AHQ-4-12, 4886	R.VFVDGHQLFDFYHR.I	1780.96540	2	4.86E-08	0.96	4.22	-	1597.2
gi|4507877|ref|NP_003364.1| vinculin isoform VCL [Homo sapiens]				3.12E-13	43.85	550.29	47.90	116721.6
AHQ-4-5, 7302 - 7375	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.12E-12	0.97	5.38	-	1320.0
AHQ-4-4, 7482 - 7488	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	3	3.31E-04	0.94	4.67	-	1340.8
AHQ-4-14-, 6718 - 6785	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.25E-08	0.97	5.37	-	1182.3
AHQ-4-3, 7468 - 7548	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.29E-06	0.93	4.20	-	864.0
AHQ-4-9, 6733 - 6739	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	9.42E-09	0.96	5.38	-	960.4
AHQ-4-13-, 6889	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.44E-04	0.94	4.50	-	934.5
AHQ-4-12, 7093	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	6.33E-09	0.98	5.67	-	1487.5
AHQ-4-10, 6529	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.58E-06	0.96	5.06	-	1167.9
AHQ-4-8, 7247 - 7251	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.11E-07	0.96	5.17	-	1145.7
AHQ-4-6, 7276 - 7278	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.15E-10	0.97	5.11	-	1087.9
AHQ-4-5, 7461 - 7462	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	9.51E-07	0.97	5.34	-	1339.4
AHQ-4-1, 7190 - 7259	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.18E-08	0.96	4.74	-	1024.4
AHQ-4-11, 6765 - 6844	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	8.74E-04	0.89	3.37	-	945.1
AHQ-4-4, 7480 - 7560	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.82E-11	0.97	5.21	-	1335.5
AHQ-4-11, 6921	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.81E-07	0.96	5.14	-	968.0
AHQ-4-7, 7481 - 7487	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.53E-06	0.96	5.09	-	970.7
AHQ-4-7, 2997	R.ALASQLQDSLK.D	1174.32943	2	5.24E-04	0.89	3.58	-	949.5
AHQ-4-4, 3342	R.ALASQLQDSLK.D	1174.32943	2	6.63E-05	0.88	3.42	-	1013.1
AHQ-4-5, 3082 - 3094	R.ALASQLQDSLK.D	1174.32943	2	9.83E-04	0.93	3.82	-	1129.7
AHQ-4-8, 2826	R.ALASQLQDSLK.D	1174.32943	2	7.19E-05	0.81	2.84	-	830.0
AHQ-4-6, 3050	R.ALASQLQDSLK.D	1174.32943	2	1.02E-04	0.90	3.52	-	890.4
AHQ-4-3, 3305	R.ALASQLQDSLK.D	1174.32943	2	1.35E-04	0.67	2.92	-	495.4
AHQ-4-5, 3317 - 3341	K.AQQVSQGLDVLTAK.V	1458.64233	2	6.07E-09	0.96	4.58	-	1521.6
AHQ-4-3, 3589	K.AQQVSQGLDVLTAK.V	1458.64233	1	4.36E-05	0.67	3.33	-	364.6
AHQ-4-8, 2954 - 2959	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.15E-08	0.97	4.44	-	1495.7
AHQ-4-5, 3323 - 3325	K.AQQVSQGLDVLTAK.V	1458.64233	1	6.85E-05	0.82	4.04	-	478.9
AHQ-4-4, 3756	K.AQQVSQGLDVLTAK.V	1458.64233	1	1.96E-05	0.28	2.38	-	424.1
AHQ-4-1, 3737	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.60E-08	0.97	4.63	-	1698.1
AHQ-4-5, 3531	K.AQQVSQGLDVLTAK.V	1458.64233	1	2.54E-06	0.77	3.35	-	488.1
AHQ-4-4, 3539	K.AQQVSQGLDVLTAK.V	1458.64233	1	1.37E-05	0.72	3.22	-	434.1
AHQ-4-7, 3211	K.AQQVSQGLDVLTAK.V	1458.64233	2	6.74E-09	0.95	4.34	-	1097.6
AHQ-4-4, 3484 - 3554	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.55E-10	0.97	5.00	-	1434.7
AHQ-4-7, 3214	K.AQQVSQGLDVLTAK.V	1458.64233	1	7.01E-04	0.17	2.21	-	373.4
AHQ-4-1, 2575	K.AVAGNISDPGLQK.S	1270.41721	2	1.12E-04	0.90	3.62	-	904.2
AHQ-4-4, 2340 - 2410	K.AVAGNISDPGLQK.S	1270.41721	2	1.86E-05	0.81	3.50	-	552.7
AHQ-4-3, 2424	K.AVAGNISDPGLQK.S	1270.41721	2	1.05E-05	0.87	3.86	-	629.6
AHQ-4-2, 2379 - 2452	K.AVAGNISDPGLQK.S	1270.41721	2	5.94E-04	0.66	3.06	-	571.7
AHQ-4-6, 2274	K.AVAGNISDPGLQK.S	1270.41721	1	2.71E-04	0.44	2.81	-	248.9
AHQ-4-5, 2274 - 2289	K.AVAGNISDPGLQK.S	1270.41721	2	8.72E-06	0.82	3.18	-	662.3
AHQ-4-7, 2237	K.AVAGNISDPGLQK.S	1270.41721	2	5.35E-06	0.80	3.57	-	465.4
AHQ-4-6, 5854 - 5882	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	7.39E-09	0.96	4.12	-	1674.5
AHQ-4-6, 5863	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	3.83E-06	0.90	3.94	-	1351.0
AHQ-4-4, 6098	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	2.87E-06	0.78	3.22	-	797.6
AHQ-4-4, 6114	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	1.31E-06	0.90	4.54	-	992.8
AHQ-4-8, 5698	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	5.00E-06	0.90	3.55	-	1007.3
AHQ-4-5, 5966 - 5969	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	6.74E-11	0.95	4.00	-	1265.6
AHQ-4-5, 5973 - 5989	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	2.26E-04	0.85	4.00	-	1033.9
AHQ-4-7, 5889 - 5897	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	8.86E-08	0.84	3.08	-	879.4
AHQ-4-6, 2187	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.67E-04	0.94	4.08	-	959.6
AHQ-4-5, 2134 - 2205	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.72E-07	0.92	3.86	-	757.7
AHQ-4-4, 2274 - 2291	R.DPSASPGDAGEQAIR.Q	1471.51169	2	7.19E-09	0.90	4.02	-	670.1
AHQ-4-4, 2279	R.DPSASPGDAGEQAIR.Q	1471.51169	1	4.19E-05	0.37	2.20	-	207.0
AHQ-4-3, 2309	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.57E-09	0.90	3.92	-	755.6
AHQ-4-1, 2410	R.DPSASPGDAGEQAIR.Q	1471.51169	2	5.58E-05	0.83	2.82	-	711.5
AHQ-4-5, 5706	K.ELLPVLISAMK.I	1214.54325	2	9.53E-04	0.88	3.48	-	675.6
AHQ-4-4, 6002	K.ELLPVLISAMK.I	1214.54325	2	3.89E-04	0.83	3.03	-	624.9
AHQ-4-5, 4510	K.ELLPVLISAM*K.I	1230.54265	2	1.23E-05	0.72	2.95	-	559.9
AHQ-4-10, 2857	K.ETVQTTEDQILK.R	1405.53306	2	3.12E-04	0.61	2.66	-	557.1
AHQ-4-5, 2917	K.ETVQTTEDQILK.R	1405.53306	1	1.14E-04	0.09	2.55	-	88.4
AHQ-4-3, 2937	K.ETVQTTEDQILKR.D	1561.71942	2	2.37E-05	0.71	2.95	-	571.0
AHQ-4-6, 2730	K.ETVQTTEDQILKR.D	1561.71942	2	1.97E-05	0.69	2.84	-	511.5
AHQ-4-11, 2832	K.ETVQTTEDQILKR.D	1561.71942	2	1.39E-05	0.80	3.61	-	540.7
AHQ-4-1, 3109	K.ETVQTTEDQILKR.D	1561.71942	2	9.76E-05	0.69	2.94	-	729.8
AHQ-4-5, 2721	K.ETVQTTEDQILKR.D	1561.71942	2	4.10E-04	0.84	3.57	-	664.8
AHQ-4-10, 2711	K.ETVQTTEDQILKR.D	1561.71942	2	1.09E-07	0.80	3.39	-	660.1
AHQ-4-4, 2910 - 2923	K.ETVQTTEDQILKR.D	1561.71942	2	5.01E-04	0.79	3.16	-	667.5
AHQ-4-4, 7347	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.87E-07	0.93	4.54	-	1138.2
AHQ-4-4, 7056 - 7102	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.44E-05	0.81	3.99	-	489.3
AHQ-4-5, 7201 - 7266	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.04E-10	0.96	5.45	-	987.6
AHQ-4-3, 7313	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	8.28E-05	0.93	4.43	-	794.7
AHQ-4-4, 7264 - 7331	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	5.72E-08	0.97	5.74	-	1071.6
AHQ-4-1, 7107	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.28E-04	0.93	4.48	-	824.2
AHQ-4-4, 6752	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	3	4.44E-08	0.84	3.69	-	774.3
AHQ-4-4, 6747	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	1.96E-11	0.87	3.63	-	941.9
AHQ-4-6, 6476	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	2.14E-07	0.53	3.08	-	582.7
AHQ-4-4, 1928 - 2006	K.GNDIIAAAK.R	872.98920	1	2.47E-05	0.34	2.12	-	516.8
AHQ-4-5, 3345	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	1.24E-06	0.88	3.81	-	721.0
AHQ-4-4, 3540	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	1.14E-05	0.89	4.25	-	657.3
AHQ-4-5, 1969	K.IAELCDDPKER.D	1347.47690	2	6.02E-05	0.77	2.95	-	833.1
AHQ-4-4, 3455	K.IAELCDDPKERDDILR.S	1960.15548	3	1.01E-06	0.89	3.53	-	1381.8
AHQ-4-5, 3235	K.IAELCDDPKERDDILR.S	1960.15548	3	5.91E-04	0.86	3.17	-	1416.1
AHQ-4-4, 3018	R.IPTISTQLK.I	1001.20202	2	3.61E-04	0.74	2.70	-	488.2
AHQ-4-5, 2822	R.IPTISTQLK.I	1001.20202	2	1.02E-04	0.70	2.64	-	551.0
AHQ-4-12, 2977 - 2999	R.IPTISTQLK.I	1001.20202	2	2.48E-04	0.79	2.61	-	710.5

AHQ-4-4, 4383 - 4419	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	6.62E-07	0.94	5.22	-	1085.9
AHQ-4-4, 4442	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	9.99E-08	0.83	3.35	-	415.6
AHQ-4-5, 4195	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	3.45E-10	0.95	5.46	-	1267.5
AHQ-4-5, 2614	R.LANVM*MGPYR.Q	1168.41500	2	1.21E-05	0.81	3.30	-	862.3
AHQ-4-4, 3300 - 3304	R.LANVMMGPYR.Q	1152.41560	2	5.22E-04	0.81	2.89	-	694.0
AHQ-4-4, 2819	R.LANVM*MGPYR.Q	1168.41500	2	3.57E-06	0.75	3.58	-	677.6
AHQ-4-5, 3011 - 3014	K.LLAVAATAPPDAPNR.E	1477.69048	2	2.06E-05	0.93	4.30	-	673.4
AHQ-4-2, 4430	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	5.85E-04	0.75	3.25	-	543.4
AHQ-4-4, 4488	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	2	8.12E-05	0.65	3.11	-	285.5
AHQ-4-1, 4742	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	1.17E-06	0.73	3.62	-	477.3
AHQ-4-4, 4658 - 4731	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	3.19E-04	0.83	4.08	-	609.0
AHQ-4-3, 4660	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	5.33E-09	0.54	3.04	-	458.9
AHQ-4-6, 3508	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.46E-09	0.93	3.95	-	791.2
AHQ-4-4, 4675	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	2.12E-04	0.95	4.22	-	1782.9
AHQ-4-11, 3540	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.00E-04	0.93	4.11	-	788.3
AHQ-4-3, 3784 - 3807	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	3.27E-06	0.91	4.26	-	544.8
AHQ-4-2, 3818	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.76E-05	0.95	4.47	-	810.9
AHQ-4-4, 3742 - 3748	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	7.38E-05	0.91	4.16	-	756.8
AHQ-4-5, 4453	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	6.78E-04	0.88	3.91	-	470.7
AHQ-4-5, 3574 - 3579	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	4.30E-06	0.93	4.65	-	586.6
AHQ-4-4, 3784	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	3	7.08E-05	0.97	5.37	-	2345.7
AHQ-4-12, 4194	R.MALLMAEMSR.L	1153.46531	2	5.28E-04	0.96	4.47	-	1740.4
AHQ-4-6, 3939 - 3940	K.MLGQMTDQVADLR.A	1478.72055	2	1.93E-07	0.96	4.74	-	1584.1
AHQ-4-5, 3114 - 3118	K.MLGQM*TDQVADLR.A	1494.71995	2	2.47E-07	0.94	4.24	-	1361.3
AHQ-4-4, 2855	K.M*LGQM*TDQVADLR.A	1510.71935	2	3.88E-06	0.96	3.75	-	1776.4
AHQ-4-6, 3511	K.M*LGQMTDQVADLR.A	1494.71995	2	5.02E-06	0.88	2.89	-	1198.1
AHQ-4-6, 3072	K.MLGQM*TDQVADLR.A	1494.71995	2	1.31E-04	0.77	2.88	-	829.2
AHQ-4-8, 3723	K.MLGQMTDQVADLR.A	1478.72055	2	8.37E-06	0.96	4.63	-	1903.3
AHQ-4-4, 3255	K.MLGQM*TDQVADLR.A	1494.71995	2	2.59E-04	0.91	3.37	-	1473.9
AHQ-4-7, 3919	K.MLGQMTDQVADLR.A	1478.72055	2	1.14E-05	0.96	3.95	-	1791.6
AHQ-4-1, 3018	K.M*LGQM*TDQVADLR.A	1510.71935	2	3.33E-04	0.90	3.43	-	1117.0
AHQ-4-4, 4199	K.M*LGQM*TDQVADLR.A	1510.71935	2	7.47E-04	0.84	2.98	-	973.8
AHQ-4-5, 4014	K.M*LGQM*TDQVADLR.A	1510.71935	2	9.27E-05	0.94	3.59	-	1408.1
AHQ-4-4, 4186	K.MLGQMTDQVADLR.A	1478.72055	2	9.67E-08	0.96	4.20	-	1973.3
AHQ-4-4, 3751	K.M*LGQMTDQVADLR.A	1494.71995	2	1.83E-06	0.95	4.05	-	1572.7
AHQ-4-5, 2713 - 2729	K.M*LGQM*TDQVADLR.A	1510.71935	2	6.01E-05	0.94	3.50	-	1587.1
AHQ-4-4, 3092 - 3095	K.M*SAEINEIIR.V	1192.36823	2	1.06E-07	0.93	3.16	-	1206.8
AHQ-4-6, 3483	K.MSAEINEIIR.V	1176.36883	2	1.39E-05	0.95	3.23	-	1986.5
AHQ-4-5, 2889	K.M*SAEINEIIR.V	1192.36823	2	4.49E-08	0.90	3.12	-	1119.6
AHQ-4-5, 3538	K.MSAEINEIIR.V	1176.36883	2	3.22E-05	0.92	3.26	-	1580.6
AHQ-4-5, 2886 - 2914	K.M*TGLVDEAIDTK.S	1309.46876	2	2.08E-07	0.92	3.27	-	1121.1
AHQ-4-4, 3062 - 3068	K.M*TGLVDEAIDTK.S	1309.46876	2	9.87E-08	0.94	3.99	-	1158.9
AHQ-4-6, 2863	K.M*TGLVDEAIDTK.S	1309.46876	2	5.51E-09	0.93	3.20	-	1317.0
AHQ-4-4, 2870	R.NPGNQAAYEHFETMK.N	1737.87437	2	4.05E-05	0.83	3.00	-	687.1
AHQ-4-5, 2635	R.NPGNQAAYEHFETMK.N	1737.87437	2	1.23E-05	0.88	3.45	-	766.6
AHQ-4-4, 2854	K.NQWIDNVEK.M	1146.23464	1	1.01E-04	0.32	2.42	-	207.1
AHQ-4-7, 2631	K.NQWIDNVEK.M	1146.23464	1	1.21E-05	0.45	2.50	-	218.6
AHQ-4-5, 2695	K.NQWIDNVEK.M	1146.23464	1	1.80E-04	0.41	2.58	-	195.9
AHQ-4-4, 2835 - 2907	K.SFLDSGYR.I	945.01074	1	1.47E-04	0.33	2.07	-	241.8
AHQ-4-4, 3391	R.SLGEISALTSK.L	1106.25186	1	1.45E-04	0.38	2.56	-	216.9
AHQ-4-1, 3621	R.SLGEISALTSK.L	1106.25186	2	2.09E-06	0.93	3.69	-	973.5
AHQ-4-6, 3150 - 3170	R.SLGEISALTSK.L	1106.25186	2	3.84E-05	0.93	3.69	-	993.1
AHQ-4-6, 3154	R.SLGEISALTSK.L	1106.25186	1	9.49E-08	0.47	2.92	-	133.4
AHQ-4-4, 3028	R.SLGEISALTSK.L	1106.25186	1	7.24E-04	0.18	2.06	-	345.9
AHQ-4-4, 3258 - 3262	K.SLLDASEEAIKK.D	1304.47187	2	2.78E-06	0.80	2.92	-	797.0
AHQ-4-2, 3283 - 3304	K.SLLDASEEAIKK.D	1304.47187	2	3.34E-04	0.64	2.57	-	581.1
AHQ-4-8, 2803	K.SLLDASEEAIKK.D	1304.47187	2	5.81E-06	0.92	3.45	-	1250.1
AHQ-4-5, 3058 - 3081	K.SLLDASEEAIKK.D	1304.47187	2	7.74E-06	0.77	2.78	-	881.0
AHQ-4-1, 3473	K.SLLDASEEAIKK.D	1304.47187	2	2.06E-06	0.85	2.84	-	1060.3
AHQ-4-5, 2153	K.STVEGIQASVK.T	1119.25064	2	5.01E-08	0.89	2.83	-	885.9
AHQ-4-4, 2292	K.STVEGIQASVK.T	1119.25064	2	1.24E-06	0.90	3.31	-	850.3
AHQ-4-2, 2340	K.STVEGIQASVK.T	1119.25064	2	3.78E-07	0.83	3.08	-	741.5
AHQ-4-12, 2421	R.TDAGFTLR.W	880.96819	2	3.80E-05	0.78	2.57	-	913.5
AHQ-4-14-, 6722	R.TIESILEPVAQQISHLVIM*HEEGEVDGK.A	3119.49274	3	4.63E-04	0.66	3.45	-	283.7
AHQ-4-5, 7402 - 7403	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	7.96E-07	0.80	3.98	-	476.5
AHQ-4-11, 6796 - 6798	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	7.00E-06	0.89	4.57	-	572.4
AHQ-4-5, 7369	R.TIESILEPVAQQISHLVIM*HEEGEVDGK.A	3119.49274	3	4.97E-05	0.79	3.71	-	475.5
AHQ-4-10, 6344	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	6.89E-06	0.82	4.20	-	513.3
AHQ-4-14-, 6430 - 6437	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	3.42E-06	0.77	4.08	-	440.6
AHQ-4-2, 7363	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.41E-04	0.69	3.37	-	488.0
AHQ-4-4, 4848	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	2.21E-04	0.70	3.15	-	503.8
AHQ-4-6, 7052 - 7067	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	7.27E-04	0.71	3.52	-	437.3
AHQ-4-12, 4685	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	1.14E-08	0.69	3.37	-	441.6
AHQ-4-12, 6810 - 6877	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.72E-08	0.87	4.38	-	524.5
AHQ-4-12, 5483	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	1.49E-09	0.76	3.80	-	400.1
AHQ-4-12, 5498 - 5543	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	6.27E-08	0.91	4.57	-	753.7
AHQ-4-12, 5923	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	6.35E-08	0.79	3.43	-	651.1
AHQ-4-12, 5865 - 5930	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	6.34E-06	0.92	5.63	-	607.5
AHQ-4-4, 7226 - 7291	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	6.60E-10	0.93	5.18	-	691.6
AHQ-4-5, 7217	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.52E-04	0.92	4.84	-	703.0
AHQ-4-4, 6278	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	8.96E-06	0.73	3.89	-	532.5
AHQ-4-4, 6279 - 6335	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	5.78E-09	0.91	5.14	-	560.6
AHQ-4-4, 6966 - 7031	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	5.23E-06	0.93	5.58	-	895.4
AHQ-4-4, 3194	R.TNLLQVCER.I	1134.28859	2	2.11E-04	0.91	3.32	-	1163.5
AHQ-4-10, 2963	R.TNLLQVCER.I	1134.28859	1	2.40E-07	0.26	2.02	-	67.0
AHQ-4-7, 5850 - 5858	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	6.21E-06	0.85	3.79	-	539.0
AHQ-4-4, 5503	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	3.60E-06	0.95	4.52	-	2405.9
AHQ-4-4, 5030	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	2.24E-06	0.95	4.59	-	1974.2
AHQ-4-5, 4837	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	1.63E-04	0.89	4.38	-	617.1
AHQ-4-3, 5552	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	1.63E-04	0.92	4.51	-	786.6
AHQ-4-4, 5007	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	7.46E-06	0.82	3.77	-	475.9
AHQ-4-6, 5415	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	2	1.99E-04	0.87	4.10	-	448.2
AHQ-4-5, 4751 - 4826	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	6.03E-04	0.91	4.65	-	634.6
AHQ-4-4, 5130	R.VDQLTAQLADLAAR.G	1485.66778	2	6.74E-06	0.96	3.57	-	2347.4
AHQ-4-4, 5142	R.VDQLTAQLADLAAR.G	1485.66778	1	1.18E-04	0.43	2.62	-	205.7
AHQ-4-5, 4978	R.VDQLTAQLADLAAR.G	1485.66778	2	1.00E-05	0.96	2.87	-	2486.8
AHQ-4-3, 5584	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.71E-06	0.95	3.91	-	1375.1
AHQ-4-1, 5633	R.VLQLTSWDEDAWASK.D	1749.90156	2	4.76E-06	0.94	4.38	-	914.6
AHQ-4-5, 5301 - 5369	R.VLQLTSWDEDAWASK.D	1749.90156	2	3.12E-13	0.97	4.60	-	1409.6
AHQ-4-2, 5598	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.57E-06	0.93	3.38	-	1110.1
AHQ-4-4, 5455 - 5535	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.86E-10	0.96	4.70	-	1324.8
AHQ-4-7, 5261	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.98E-11	0.97	5.15	-	1227.6
AHQ-4-5, 3037	R.VMLVNSMNTVK.E	1236.53081	2	8.85E-06	0.89	3.41	-	917.3
AHQ-4-4, 3154	R.VMLVNSMNTVK.E	1236.53081	2	4.37E-06	0.89	3.23	-	968.3
AHQ-4-5, 2718 - 2719	R.WIDNPTVDDR.G	1231.29640	2	9.70E-04	0.95	3.92	-	1296.9
AHQ-4-1, 2991	R.WIDNPTVDDR.G	1231.29640	2	3.37E-04	0.92	3.23	-	1135.6
AHQ-4-5, 2733	R.WIDNPTVDDR.G	1231.29640	1	8.80E-05	0.23	2.49	-	266.4

AHQ-4-4, 2831 - 2843	R.WIDNPTVDDR.G	1231.29640	2	1.36E-04	0.94	3.57	-	1245.0
gi|4503631|ref|NP_000120.1| coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,				3.17E-13	18.44	210.28	34.00	83232.8
AHQ-4-5, 5477 - 5549	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	2.39E-04	0.73	2.98	-	195.6
AHQ-4-5, 4210	R.EIRPNSTVQWEEVCRPWVSGHR.K	2724.99524	3	5.99E-06	0.84	4.01	-	545.8
AHQ-4-6, 5668 - 5683	K.ETFDVTLEPLSFK.K	1526.71190	2	4.46E-07	0.61	2.57	-	540.2
AHQ-4-5, 6746	R.GTQVVGSDMTVTVQFTNPLK.E	2123.41609	2	2.38E-06	0.98	5.42	-	2530.0
AHQ-4-5, 5522 - 5593	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.42E-11	0.88	3.83	-	442.9
AHQ-4-12, 5606 - 5619	K.GTYIPVPIVSELQSGK.W	1688.94594	2	1.88E-05	0.46	2.67	-	329.5
AHQ-4-12, 6846	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	4.57E-07	0.96	4.91	-	1201.4
AHQ-4-5, 7053 - 7121	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	7.36E-09	0.97	5.05	-	1405.0
AHQ-4-5, 7057	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	3.07E-06	0.90	4.42	-	858.5
AHQ-4-5, 7254	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.08E-06	0.95	4.71	-	1197.7
AHQ-4-7, 7030 - 7045	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.67E-06	0.96	4.98	-	1289.8
AHQ-4-10, 6288	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.50E-07	0.92	4.34	-	960.6
AHQ-4-13-, 6728	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.53E-07	0.96	4.93	-	1055.7
AHQ-4-9, 6331	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.12E-06	0.91	3.85	-	995.3
AHQ-4-9, 6332	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.95E-07	0.96	5.19	-	1226.2
AHQ-4-11, 6537	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	5.46E-06	0.95	4.90	-	1009.0
AHQ-4-14-, 6615	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	7.54E-10	0.98	5.51	-	1733.3
AHQ-4-6, 6946	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.21E-07	0.95	4.88	-	1068.2
AHQ-4-7, 1881	K.KDGTHVVENVDATHIGK.L	1820.98455	2	1.29E-05	0.89	3.69	-	726.1
AHQ-4-5, 1946 - 1962	K.KDGTHVVENVDATHIGK.L	1820.98455	2	5.78E-10	0.95	4.17	-	1319.8
AHQ-4-6, 2144	K.KDGTHVVENVDATHIGK.L	1820.98455	2	6.87E-04	0.82	3.26	-	600.9
AHQ-4-5, 2133	K.KDGTHVVENVDATHIGK.L	1820.98455	2	1.22E-04	0.68	3.12	-	313.0
AHQ-4-5, 2129	K.KDGTHVVENVDATHIGK.L	1820.98455	3	1.67E-04	0.91	4.01	-	1075.3
AHQ-4-10, 4573	K.KETFDVTLEPLSFK.K	1654.88482	2	2.99E-07	0.94	3.81	-	1426.1
AHQ-4-7, 4810 - 4830	K.KETFDVTLEPLSFK.K	1654.88482	2	1.62E-06	0.84	3.17	-	779.6
AHQ-4-11, 4876	K.KETFDVTLEPLSFK.K	1654.88482	2	5.78E-05	0.90	3.21	-	1230.1
AHQ-4-5, 4965	K.KETFDVTLEPLSFK.K	1654.88482	2	5.68E-09	0.96	4.47	-	1464.4
AHQ-4-5, 2417	R.KLIASMSSDSLR.H	1308.53039	2	2.67E-05	0.90	3.97	-	825.2
AHQ-4-5, 1534	K.KPLNTEGVMK.S	1117.34452	2	6.05E-04	0.45	2.66	-	361.7
AHQ-4-5, 4566 - 4579	R.LALETALMYGAK.K	1281.54655	2	9.12E-05	0.97	4.53	-	1871.6
AHQ-4-5, 2013 - 2017	K.LIASM*SSDSLR.H	1196.35688	2	9.64E-04	0.88	3.09	-	773.9
AHQ-4-14-, 2183	K.LIASM*SSDSLR.H	1196.35688	2	7.96E-05	0.86	3.27	-	726.5
AHQ-4-11, 2878	K.LIASMSSDSLR.H	1180.35748	2	7.92E-05	0.91	3.34	-	1082.8
AHQ-4-5, 2793 - 2799	K.LIASMSSDSLR.H	1180.35748	2	9.69E-06	0.96	4.21	-	1222.4
AHQ-4-5, 5469	R.M*YVAVWTPYGVLR.T	1571.86734	2	1.22E-08	0.95	4.56	-	973.7
AHQ-4-6, 5460 - 5528	R.M*YVAVWTPYGVLR.T	1571.86734	2	4.32E-05	0.85	3.14	-	819.0
AHQ-4-9, 5480	R.MYVAVWTPYGVLR.T	1555.86794	2	2.41E-04	0.95	4.44	-	1160.3
AHQ-4-5, 6089	R.MYVAVWTPYGVLR.T	1555.86794	2	2.74E-06	0.95	4.72	-	914.2
AHQ-4-11, 5302 - 5365	R.M*YVAVWTPYGVLR.T	1571.86734	2	3.91E-04	0.80	2.94	-	619.4
AHQ-4-6, 6606	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	1.14E-06	0.95	5.04	-	1199.9
AHQ-4-5, 6753 - 6765	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	3.17E-13	0.95	5.53	-	1097.4
AHQ-4-5, 3362	R.NVWVHLDGPGVTRPMK.K	1807.11248	2	8.08E-07	0.91	4.46	-	602.8
AHQ-4-5, 2951	R.NVWVHLDGPGVTRPM*K.K	1823.11188	2	2.02E-04	0.95	4.33	-	983.2
AHQ-4-5, 4595	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.24E-07	0.97	4.69	-	1909.4
AHQ-4-5, 5363	R.SNVDMDFEVENAVLGK.D	1767.93869	2	5.58E-05	0.78	3.05	-	838.1
AHQ-4-6, 4532	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.49E-06	0.91	3.57	-	1293.1
AHQ-4-7, 5518 - 5521	K.STVLTIPEIIIK.V	1327.63485	2	1.36E-04	0.92	3.42	-	1462.9
AHQ-4-13-, 5672 - 5677	K.STVLTIPEIIIK.V	1327.63485	2	2.07E-05	0.92	3.54	-	1290.5
AHQ-4-11, 5493 - 5496	K.STVLTIPEIIIK.V	1327.63485	2	2.60E-05	0.92	3.42	-	1407.3
gi|7661678|ref|NP_056461.1| RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B				3.83E-13	6.81	80.29	33.70	20824.7
AHQ-4-11, 4826	K.DTDDVPMILVGNKCDLEDER.V	2336.53972	2	6.65E-07	0.76	2.88	-	643.8
AHQ-4-11, 5100	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	2.61E-09	0.97	5.79	-	1559.9
AHQ-4-11, 6390 - 6452	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	1.80E-08	0.93	4.41	-	1633.5
AHQ-4-14-, 6409 - 6485	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	2.32E-06	0.91	4.29	-	1251.8
AHQ-4-11, 6713	K.QVEVDAQQCMLEILDTAGTEQFTAM*R.D	3003.33257	3	1.05E-05	0.73	3.75	-	782.1
AHQ-4-11, 3840 - 3901	R.QWNNCAFLESSAK.S	1556.68148	2	2.80E-06	0.43	2.95	-	174.6
AHQ-4-11, 4149 - 4212	R.QWNNCAFLESSAK.S	1556.68148	2	1.44E-07	0.55	2.87	-	308.1
AHQ-4-14, 4844 - 4918	R.VKDTDDVPMILVGNK.C	1644.91497	2	1.44E-05	0.80	2.70	-	1189.9
AHQ-4-13-, 3852	R.VKDTDDVPMILVGNK.C	1644.91497	2	2.34E-07	0.98	4.78	-	2139.4
AHQ-4-11, 3790 - 3794	R.VKDTDDVPMILVGNK.C	1644.91497	2	2.25E-04	0.96	4.81	-	1521.6
AHQ-4-11, 3569 - 3616	R.VKDTDDVPMILVGNK.C	1644.91497	3	1.30E-05	0.91	4.06	-	1656.1
AHQ-4-11, 3545 - 3613	R.VKDTDDVPMILVGNK.C	1644.91497	2	1.38E-07	0.98	5.69	-	1874.8
AHQ-4-13, 3989 - 3990	R.VKDTDDVPMILVGNK.C	1644.91497	2	4.40E-09	0.97	4.84	-	1787.4
AHQ-4-11, 4513 - 4582	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	1.29E-12	0.89	4.18	-	995.7
AHQ-4-11, 4433 - 4505	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	1.66E-08	0.92	3.92	-	991.4
AHQ-4-11, 4333	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	1.63E-06	0.87	4.02	-	839.2
AHQ-4-11, 4265 - 4328	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	3.73E-05	0.92	4.29	-	833.4
AHQ-4-11, 4225 - 4292	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	1.81E-11	0.93	5.00	-	982.5
AHQ-4-11, 4074	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	1.13E-08	0.96	5.61	-	1450.0
AHQ-4-11, 3934 - 4014	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	2	3.47E-04	0.70	2.96	-	503.4
AHQ-4-11, 3930 - 3997	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	1.61E-05	0.87	4.18	-	800.1
AHQ-4-13-, 4114 - 4117	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	5.67E-05	0.90	4.63	-	794.8
AHQ-4-11, 4422 - 4438	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	3.83E-13	0.94	4.84	-	1013.3
gi|14149734|ref|NP_065174.1| coronin, actin binding protein, 1B [Homo sapiens]				6.97E-13	0.95	10.26	5.90	54234.4
AHQ-4-6, 6932	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	6.97E-13	0.95	5.29	-	1241.2
gi|4507855|ref|NP_003472.1| Ubiquitin isopeptidase T; Ubiquitin-specific protease-5 (ubiquitin isop				7.99E-13	1.89	20.30	5.40	93393.2
AHQ-4-5, 4135	K.IFQNAPTDPTQDFSTQVAK.L	2109.28133	2	8.07E-06	0.91	3.82	-	786.2
AHQ-4-5, 7159	R.IGEWELIQESGVPLKPLFGPGYTGIR.N	2858.28283	3	7.99E-13	0.98	5.95	-	2212.7
gi|4505839|ref|NP_002645.1| pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro				1.04E-12	14.56	160.33	44.30	57913.6
AHQ-4-7, 6157	R.AGKPVICATQMLESMIK.K	1879.29869	3	9.29E-06	0.95	4.34	-	1970.3
AHQ-4-7, 6141 - 6142	R.AGKPVICATQMLESMIK.K	1879.29869	2	1.73E-06	0.97	5.20	-	1195.9
AHQ-4-7, 5414	K.CDENILWLDYK.N	1470.62849	1	5.28E-05	0.81	3.59	-	465.9
AHQ-4-7, 5522	K.CDENILWLDYK.N	1470.62849	1	4.34E-04	0.19	2.23	-	243.9
AHQ-4-7, 5806	R.EAEAAIYHLQLFEELR.R	1933.15326	2	3.99E-08	0.95	4.77	-	976.2
AHQ-4-7, 7407	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	2.48E-08	0.97	5.54	-	1399.4
AHQ-4-8, 4357	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	6.18E-06	0.89	3.59	-	983.4
AHQ-4-7, 5105 - 5110	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.05E-07	0.97	5.49	-	1503.1
AHQ-4-7, 4850 - 4875	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.22E-09	0.96	4.78	-	1532.1
AHQ-4-7, 4606	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	3.12E-05	0.93	3.96	-	1255.8
AHQ-4-7, 4523 - 4531	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.38E-05	0.94	4.58	-	1135.0
AHQ-4-1, 4795 - 4809	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	9.65E-05	0.68	2.85	-	598.7
AHQ-4-14-, 6369 - 6442	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	6.68E-05	0.92	4.17	-	1248.9
AHQ-4-7, 6809 - 6877	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	1.66E-04	0.95	4.70	-	935.3
AHQ-4-7, 6813 - 6881	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	3.72E-11	0.97	6.26	-	1751.3
AHQ-4-13, 6644 - 6649	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.27E-07	0.96	5.27	-	1445.6
AHQ-4-11, 6365 - 6366	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	2.68E-12	0.97	6.02	-	1675.1
AHQ-4-11, 6380	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	3.18E-06	0.95	4.73	-	778.3
AHQ-4-7, 2914	K.ITLDNAYMEK.C	1198.37126	2	1.43E-05	0.81	2.98	-	558.1
AHQ-4-7, 3831 - 3837	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	4.42E-06	0.92	4.34	-	1088.1
AHQ-4-7, 3817	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	5.16E-04	0.96	4.96	-	981.3
AHQ-4-7, 5062 - 5070	K.KGVNLPGAAVDLPAVSEKDIQDLK.F	2478.82685	3	6.43E-07	0.98	6.67	-	1833.3
AHQ-4-7, 5735 - 5801	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.59E-08	0.97	5.75	-	1274.8
AHQ-4-9, 5300	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	3.21E-07	0.95	4.57	-	991.0
AHQ-4-7, 5839 - 5905	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	3.04E-08	0.97	5.60	-	1035.9
AHQ-4-7, 5973 - 6041	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.04E-12	0.96	4.96	-	1157.4

AHQ-4-11, 5580 - 5641	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.25E-05	0.95	4.56	-	1105.7
AHQ-4-7, 7165	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.03E-05	0.82	3.15	-	768.9
AHQ-4-7, 6950	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.59E-04	0.90	3.69	-	889.8
AHQ-4-7, 6205 - 6281	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	9.12E-07	0.97	5.60	-	1362.9
AHQ-4-7, 6439 - 6511	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.84E-04	0.93	4.15	-	979.5
AHQ-4-7, 6606 - 6683	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.01E-06	0.93	4.14	-	865.1
AHQ-4-12, 5774	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.73E-06	0.92	3.87	-	818.6
AHQ-4-7, 5379	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	9.17E-06	0.95	4.15	-	1048.8
AHQ-4-7, 6833	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.60E-04	0.95	4.13	-	1212.1
AHQ-4-7, 6109 - 6114	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.30E-06	0.96	5.27	-	1061.4
AHQ-4-6, 3243	R.LDIDSPPITAR.N	1198.35099	2	2.04E-04	0.91	3.10	-	1053.4
AHQ-4-7, 3142 - 3215	R.LDIDSPPITAR.N	1198.35099	2	6.61E-04	0.94	3.95	-	1123.0
AHQ-4-12, 3373	R.LDIDSPPITAR.N	1198.35099	2	3.72E-06	0.94	3.44	-	1184.2
AHQ-4-13-, 3432	R.LDIDSPPITAR.N	1198.35099	2	2.71E-04	0.93	3.53	-	1086.8
AHQ-4-7, 2070	R.LNFSHGTHEYHAETIK.N	1885.02879	2	1.59E-05	0.92	4.17	-	896.8
AHQ-4-13-, 3444	R.NTGIICTIGPASR.S	1361.54994	2	7.98E-06	0.92	3.77	-	1042.9
AHQ-4-7, 3943	R.NTGIICTIGPASR.S	1361.54994	2	9.38E-05	0.88	3.23	-	965.2
AHQ-4-7, 3145 - 3175	R.NTGIICTIGPASR.S	1361.54994	2	7.94E-06	0.93	4.04	-	974.3
AHQ-4-13, 3585	R.NTGIICTIGPASR.S	1361.54994	2	6.18E-05	0.93	4.14	-	1056.4
AHQ-4-7, 5179	R.RFDEILEASDGIMVAR.G	1823.06385	2	1.59E-08	0.94	4.55	-	851.3
AHQ-4-7, 5334 - 5406	R.RFDEILEASDGIMVAR.G	1823.06385	2	3.22E-04	0.84	3.43	-	767.7
AHQ-4-7, 3873	R.TATESFASDPILYR.P	1571.71277	2	5.85E-07	0.72	2.99	-	539.3
AHQ-4-11, 5478	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	1.07E-05	0.69	3.10	-	572.1
AHQ-4-7, 5465 - 5534	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	7.92E-06	0.87	4.41	-	347.9
AHQ-4-7, 5457 - 5529	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	2.99E-07	0.81	3.21	-	902.7
AHQ-4-13, 5693 - 5768	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	6.33E-04	0.86	3.67	-	892.1
gi|13124879|ref|NP_002465.1|	smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]			1.39E-12	8.68	110.38	5.30	227336.7
AHQ-4-3, 4907 - 4911	R.DLGEELEALK.T	1117.23151	1	7.15E-05	0.10	2.14	-	335.8
AHQ-4-1, 4926	R.DLGEELEALK.T	1117.23151	2	5.96E-05	0.90	3.61	-	794.6
AHQ-4-2, 4938	R.DLGEELEALK.T	1117.23151	2	1.53E-04	0.93	3.80	-	978.1
AHQ-4-1, 2821	R.EDQSILCTGESGAGK.T	1553.63107	2	3.15E-04	0.69	3.43	-	386.8
AHQ-4-2, 2755	R.EDQSILCTGESGAGK.T	1553.63107	2	2.94E-04	0.71	2.89	-	478.7
AHQ-4-3, 2799	K.FDQLLAEEK.N	1093.21165	2	1.89E-04	0.90	2.90	-	1465.7
AHQ-4-2, 2804	K.FDQLLAEEK.N	1093.21165	1	2.38E-07	0.75	2.66	-	895.5
AHQ-4-4, 2780	K.FDQLLAEEK.N	1093.21165	1	1.30E-05	0.50	2.34	-	555.0
AHQ-4-2, 2800	K.FDQLLAEEK.N	1093.21165	2	2.39E-05	0.94	3.30	-	1680.3
AHQ-4-1, 2974	K.FDQLLAEEK.N	1093.21165	2	1.79E-05	0.92	3.51	-	1354.8
AHQ-4-1, 2966	K.FDQLLAEEK.N	1093.21165	1	8.50E-05	0.49	2.13	-	840.2
AHQ-4-4, 2331	K.KEEELQAALAR.L	1258.40643	1	2.40E-04	0.22	2.28	-	286.0
AHQ-4-2, 2356	K.KEEELQAALAR.L	1258.40643	1	4.43E-06	0.22	2.01	-	472.0
AHQ-4-4, 2327	K.KEEELQAALAR.L	1258.40643	2	3.59E-04	0.91	3.17	-	1379.6
AHQ-4-1, 2882	R.KFDQLLAEEK.N	1221.38456	2	8.47E-05	0.82	3.13	-	905.8
AHQ-4-2, 2567 - 2635	R.KFDQLLAEEK.N	1221.38456	2	2.13E-05	0.86	3.11	-	968.9
AHQ-4-1, 6183 - 6197	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	4.30E-08	0.97	5.89	-	1690.4
AHQ-4-4, 5420 - 5424	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	5.43E-04	0.45	2.55	-	167.3
AHQ-4-3, 6156	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	2.17E-10	0.98	6.09	-	2793.9
AHQ-4-1, 5533	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.83E-07	0.97	5.26	-	1906.5
AHQ-4-1, 5422	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	6.12E-07	0.98	5.80	-	2313.1
AHQ-4-3, 5335	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	7.65E-11	0.98	6.02	-	3528.3
AHQ-4-2, 5342	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	2.57E-10	0.98	6.61	-	2125.8
AHQ-4-2, 5571	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.45E-09	0.98	6.47	-	1942.6
AHQ-4-2, 6144 - 6218	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	5.45E-11	0.98	7.55	-	2949.9
AHQ-4-2, 2574 - 2654	R.NCAAYLK.L	840.96726	1	6.26E-04	0.57	2.40	-	603.1
AHQ-4-2, 2327	R.NCAAYLK.L	840.96726	1	9.14E-05	0.71	2.18	-	824.0
AHQ-4-2, 4586	R.NWQWWR.L	976.07459	2	6.99E-04	0.62	2.51	-	515.0
AHQ-4-6, 6082 - 6086	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.86E-11	0.96	4.55	-	1308.9
AHQ-4-2, 6299 - 6371	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.00E-07	0.95	4.67	-	1002.0
AHQ-4-2, 6523 - 6534	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.50E-09	0.96	4.75	-	1267.0
AHQ-4-6, 6248	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.31E-07	0.87	3.12	-	738.2
AHQ-4-5, 6326 - 6399	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.16E-09	0.94	4.24	-	928.6
AHQ-4-5, 6127	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.94E-10	0.95	4.44	-	1094.3
AHQ-4-7, 6005	K.QLLQANPILEAFGNAK.T	1727.98540	2	8.77E-05	0.71	2.87	-	529.2
AHQ-4-4, 6354 - 6374	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.36E-06	0.96	4.91	-	981.9
AHQ-4-1, 6339 - 6410	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.24E-08	0.97	5.08	-	1217.4
AHQ-4-3, 6543	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.05E-08	0.93	4.78	-	672.6
AHQ-4-3, 6379 - 6381	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.39E-12	0.96	4.54	-	1117.0
AHQ-4-9, 5492	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.04E-07	0.93	4.04	-	781.9
AHQ-4-1, 6526	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.50E-07	0.96	4.70	-	1209.8
AHQ-4-3, 5883	K.TQLEELEDELQATEDAK.L	1963.04334	3	3.98E-05	0.94	5.23	-	1172.7
AHQ-4-1, 5886	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.58E-06	0.97	4.68	-	1630.8
AHQ-4-1, 5870	K.TQLEELEDELQATEDAK.L	1963.04334	3	3.07E-07	0.95	5.25	-	1117.8
AHQ-4-4, 5818	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.36E-05	0.97	5.20	-	1735.5
AHQ-4-3, 5851	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.12E-04	0.98	5.60	-	1947.0
AHQ-4-2, 4124	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.17E-04	0.92	4.12	-	998.3
AHQ-4-3, 4108	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.58E-08	0.94	4.59	-	1022.4
AHQ-4-6, 5550	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.30E-09	0.98	6.39	-	2090.4
AHQ-4-2, 6239	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.21E-04	0.36	2.85	-	273.8
AHQ-4-2, 5866 - 5940	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.92E-10	0.99	7.24	-	2350.0
AHQ-4-7, 5609	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.39E-08	0.98	6.54	-	2021.2
AHQ-4-2, 6035 - 6106	K.TQLEELEDELQATEDAK.L	1963.04334	2	6.69E-07	0.98	6.60	-	2216.0
AHQ-4-2, 5878	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.04E-08	0.94	5.26	-	887.2
gi|4505981|ref|NP_002695.1|	pro-platelet basic protein (includes platelet basic protein, bet; Pro-p			1.70E-12	8.29	100.32	51.60	13894.1
AHQ-4-14, 5848 - 5916	K.EESLDSDLYAELR.C	1540.61070	2	1.63E-08	0.95	4.64	-	1086.0
AHQ-4-14, 5960 - 6032	K.EESLDSDLYAELR.C	1540.61070	2	4.53E-08	0.71	3.29	-	700.9
AHQ-4-14-, 4310	K.EESLDSDLYAELR.C	1540.61070	2	9.05E-08	0.81	2.68	-	755.8
AHQ-4-14-, 4785	K.EESLDSDLYAELR.C	1540.61070	2	2.72E-07	0.94	4.37	-	1018.3
AHQ-4-14-, 4641 - 4725	K.EESLDSDLYAELR.C	1540.61070	2	7.34E-08	0.95	4.66	-	980.8
AHQ-4-14-, 4650	K.GKEESLDSDLYAELR.C	1725.83517	2	1.70E-09	0.97	4.85	-	2096.5
AHQ-4-14-, 4525	K.GKEESLDSDLYAELR.C	1725.83517	2	1.97E-10	0.98	5.66	-	2906.0
AHQ-4-13, 4100 - 4105	K.GKEESLDSDLYAELR.C	1725.83517	2	5.57E-04	0.97	4.83	-	1534.4
AHQ-4-13, 4308	K.GKEESLDSDLYAELR.C	1725.83517	2	5.87E-06	0.98	5.26	-	2425.4
AHQ-4-14-, 4395 - 4461	K.GKEESLDSDLYAELR.C	1725.83517	2	6.91E-11	0.98	5.62	-	2726.9
AHQ-4-12, 4137 - 4138	K.GKEESLDSDLYAELR.C	1725.83517	2	1.70E-12	0.98	5.43	-	2495.4
AHQ-4-14-, 4297 - 4362	K.GKEESLDSDLYAELR.C	1725.83517	2	1.20E-11	0.98	6.07	-	2593.5
AHQ-4-14-, 5223	K.GKEESLDSDLYAELR.C	1725.83517	2	2.51E-06	0.98	4.67	-	2577.6
AHQ-4-14-, 4049	K.GKEESLDSDLYAELR.C	1725.83517	2	1.86E-11	0.98	5.95	-	3053.9
AHQ-4-14-, 4033 - 4111	K.GKEESLDSDLYAELR.C	1725.83517	2	7.51E-11	0.98	5.46	-	2028.6
AHQ-4-14-, 3921 - 3989	K.GKEESLDSDLYAELR.C	1725.83517	2	6.14E-11	0.98	6.01	-	2483.8
AHQ-4-14-, 3774 - 3857	K.GKEESLDSDLYAELR.C	1725.83517	2	3.00E-11	0.98	6.21	-	2224.9
AHQ-4-14-, 3682	K.GKEESLDSDLYAELR.C	1725.83517	2	1.50E-04	0.98	5.49	-	2205.8
AHQ-4-13-, 4184 - 4185	K.GKEESLDSDLYAELR.C	1725.83517	3	3.88E-06	0.92	3.86	-	1505.7
AHQ-4-13-, 4180 - 4201	K.GKEESLDSDLYAELR.C	1725.83517	2	2.33E-11	0.98	5.26	-	3273.3
AHQ-4-14, 6488 - 6566	K.GKEESLDSDLYAELR.C	1725.83517	2	3.10E-07	0.99	6.39	-	2852.5
AHQ-4-14, 6322	K.GKEESLDSDLYAELR.C	1725.83517	2	4.00E-06	0.97	4.79	-	1667.1
AHQ-4-14, 6204 - 6257	K.GKEESLDSDLYAELR.C	1725.83517	2	5.16E-06	0.98	5.56	-	2484.9
AHQ-4-14, 6108 - 6137	K.GKEESLDSDLYAELR.C	1725.83517	2	1.21E-08	0.97	4.29	-	1946.4
AHQ-4-14-, 4161 - 4237	K.GKEESLDSDLYAELR.C	1725.83517	2	1.91E-10	0.99	6.28	-	2838.8

AHQ-4-14, 5946 - 6021	K.GKEESLDSDLYAELR.C	1725.83517	2	8.71E-09	0.97	4.86	-	1672.3
AHQ-4-14, 5862 - 5926	K.GKEESLDSDLYAELR.C	1725.83517	2	1.70E-11	0.98	5.71	-	2682.0
AHQ-4-10, 3813 - 3825	K.GKEESLDSDLYAELR.C	1725.83517	2	6.60E-07	0.98	5.46	-	2356.4
AHQ-4-14, 5728 - 5784	K.GKEESLDSDLYAELR.C	1725.83517	2	8.95E-09	0.98	4.87	-	2183.8
AHQ-4-14-, 6361	K.GKEESLDSDLYAELR.C	1725.83517	2	2.32E-05	0.82	3.00	-	1238.5
AHQ-4-14, 5600 - 5668	K.GKEESLDSDLYAELR.C	1725.83517	2	1.47E-10	0.98	5.08	-	2416.9
AHQ-4-14, 5528 - 5592	K.GKEESLDSDLYAELR.C	1725.83517	3	2.08E-05	0.91	4.12	-	1021.1
AHQ-4-14, 5476 - 5540	K.GKEESLDSDLYAELR.C	1725.83517	2	3.87E-10	0.98	5.86	-	2547.6
AHQ-4-14, 5408 - 5468	K.GKEESLDSDLYAELR.C	1725.83517	3	3.24E-05	0.87	4.09	-	834.9
AHQ-4-14, 5358 - 5416	K.GKEESLDSDLYAELR.C	1725.83517	2	1.91E-09	0.98	5.71	-	2826.9
AHQ-4-14, 5240 - 5316	K.GKEESLDSDLYAELR.C	1725.83517	2	2.70E-11	0.98	5.48	-	2743.2
AHQ-4-14, 4629 - 4706	K.GKEESLDSDLYAELR.C	1725.83517	2	1.27E-06	0.98	4.97	-	2096.2
AHQ-4-14, 5166 - 5232	K.GKEESLDSDLYAELR.C	1725.83517	3	1.25E-08	0.91	4.40	-	1051.8
AHQ-4-14, 5108 - 5178	K.GKEESLDSDLYAELR.C	1725.83517	2	5.19E-09	0.98	5.65	-	2602.9
AHQ-4-14, 5057 - 5124	K.GKEESLDSDLYAELR.C	1725.83517	3	2.90E-06	0.92	4.17	-	1171.7
AHQ-4-14, 4976 - 5041	K.GKEESLDSDLYAELR.C	1725.83517	2	6.52E-08	0.97	5.27	-	1947.7
AHQ-4-14, 4946 - 5026	K.GKEESLDSDLYAELR.C	1725.83517	3	6.11E-07	0.86	3.99	-	824.8
AHQ-4-14, 4860 - 4932	K.GKEESLDSDLYAELR.C	1725.83517	3	6.10E-07	0.80	3.38	-	966.0
AHQ-4-14, 4850 - 4916	K.GKEESLDSDLYAELR.C	1725.83517	2	5.88E-10	0.98	5.46	-	2666.6
AHQ-4-14, 6062	K.GKEESLDSDLYAELRCM*CIK.T	2436.72245	3	1.82E-06	0.79	3.57	-	520.1
AHQ-4-14, 4904 - 4964	K.GTHCNQVEVIATLK.D	1571.78073	2	3.38E-08	0.97	4.91	-	1672.6
AHQ-4-14, 4710 - 4777	K.GTHCNQVEVIATLK.D	1571.78073	2	5.75E-08	0.96	5.08	-	1267.1
AHQ-4-13, 3493 - 3567	K.GTHCNQVEVIATLK.D	1571.78073	2	1.38E-05	0.97	5.07	-	1640.4
AHQ-4-14, 5024 - 5089	K.GTHCNQVEVIATLK.D	1571.78073	2	5.43E-09	0.97	5.36	-	1644.6
AHQ-4-13, 3583 - 3650	K.GTHCNQVEVIATLK.D	1571.78073	2	8.73E-08	0.97	4.27	-	2003.5
AHQ-4-13, 3750	K.GTHCNQVEVIATLK.D	1571.78073	2	4.35E-07	0.93	3.81	-	1160.8
AHQ-4-14, 4644 - 4656	K.GTHCNQVEVIATLK.D	1571.78073	2	5.62E-08	0.98	5.58	-	1819.3
AHQ-4-14, 5168 - 5237	K.GTHCNQVEVIATLK.D	1571.78073	2	2.77E-09	0.94	4.28	-	1145.9
AHQ-4-14-, 4441 - 4505	K.GTHCNQVEVIATLK.D	1571.78073	2	1.27E-08	0.98	4.93	-	1993.9
AHQ-4-14, 5301 - 5365	K.GTHCNQVEVIATLK.D	1571.78073	2	2.62E-04	0.97	4.45	-	1872.2
AHQ-4-14-, 4334	K.GTHCNQVEVIATLK.D	1571.78073	2	8.96E-08	0.97	4.43	-	1760.2
AHQ-4-14, 4520 - 4588	K.GTHCNQVEVIATLK.D	1571.78073	2	5.11E-06	0.96	4.53	-	1481.1
AHQ-4-14, 5425 - 5485	K.GTHCNQVEVIATLK.D	1571.78073	2	2.02E-05	0.95	4.42	-	1169.6
AHQ-4-14-, 4186 - 4251	K.GTHCNQVEVIATLK.D	1571.78073	2	4.62E-06	0.96	4.50	-	1516.3
AHQ-4-14, 4436 - 4512	K.GTHCNQVEVIATLK.D	1571.78073	2	1.50E-06	0.97	4.81	-	1523.4
AHQ-4-14, 5561 - 5632	K.GTHCNQVEVIATLK.D	1571.78073	2	1.18E-06	0.94	4.45	-	1182.9
AHQ-4-14-, 4023 - 4082	K.GTHCNQVEVIATLK.D	1571.78073	2	7.75E-10	0.97	5.18	-	1659.6
AHQ-4-14, 4352 - 4373	K.GTHCNQVEVIATLK.D	1571.78073	2	2.74E-06	0.97	5.09	-	1567.1
AHQ-4-14, 4268 - 4332	K.GTHCNQVEVIATLK.D	1571.78073	2	4.91E-09	0.97	5.58	-	1542.0
AHQ-4-14, 5836	K.GTHCNQVEVIATLK.D	1571.78073	2	9.10E-06	0.90	3.72	-	837.0
AHQ-4-14-, 3937 - 3997	K.GTHCNQVEVIATLK.D	1571.78073	2	8.99E-10	0.98	5.41	-	2280.3
AHQ-4-14-, 3809 - 3873	K.GTHCNQVEVIATLK.D	1571.78073	2	1.88E-10	0.97	5.35	-	1511.6
AHQ-4-14, 4140 - 4204	K.GTHCNQVEVIATLK.D	1571.78073	2	3.43E-04	0.95	3.87	-	1432.1
AHQ-4-14-, 3681 - 3745	K.GTHCNQVEVIATLK.D	1571.78073	2	1.44E-08	0.98	5.06	-	1740.4
AHQ-4-14, 4776 - 4841	K.GTHCNQVEVIATLK.D	1571.78073	2	3.58E-10	0.98	5.40	-	2055.9
AHQ-4-14-, 3573 - 3638	K.GTHCNQVEVIATLK.D	1571.78073	2	5.87E-10	0.97	5.32	-	1559.3
AHQ-4-14-, 3446 - 3509	K.GTHCNQVEVIATLK.D	1571.78073	2	1.84E-07	0.97	4.92	-	1353.4
AHQ-4-14, 6213	K.GTHCNQVEVIATLK.D	1571.78073	2	6.23E-05	0.94	4.40	-	1135.1
AHQ-4-14, 6309 - 6364	K.GTHCNQVEVIATLK.D	1571.78073	2	1.40E-04	0.89	4.13	-	703.0
AHQ-4-14-, 3369 - 3429	K.GTHCNQVEVIATLK.D	1571.78073	2	1.83E-10	0.97	5.52	-	1618.2
AHQ-4-14-, 3305 - 3350	K.GTHCNQVEVIATLK.D	1571.78073	2	1.84E-07	0.97	4.84	-	1535.0
AHQ-4-14-, 3219 - 3281	K.GTHCNQVEVIATLK.D	1571.78073	2	1.47E-07	0.97	5.10	-	1574.1
AHQ-4-14, 5678 - 5753	K.GTHCNQVEVIATLK.D	1571.78073	2	1.52E-04	0.94	4.01	-	1414.7
AHQ-4-13-, 3280 - 3356	K.GTHCNQVEVIATLK.D	1571.78073	2	1.86E-04	0.87	3.52	-	715.4
AHQ-4-13-, 3648	K.GTHCNQVEVIATLK.D	1571.78073	2	5.24E-07	0.96	4.56	-	1521.6
AHQ-4-13-, 3392 - 3462	K.GTHCNQVEVIATLK.D	1571.78073	2	1.46E-04	0.94	3.86	-	1395.0
AHQ-4-14-, 3771	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	9.14E-05	0.79	3.43	-	674.2
AHQ-4-14, 4089 - 4121	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	9.51E-05	0.93	4.24	-	1195.8
AHQ-4-14, 4049 - 4112	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	1.91E-04	0.98	6.13	-	1820.7
AHQ-4-14-, 3465	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.98E-07	0.91	4.50	-	796.4
AHQ-4-14, 3985 - 3989	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.10E-10	0.94	4.59	-	1220.4
AHQ-4-14, 3916 - 3984	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	1.74E-05	0.98	5.54	-	1937.6
AHQ-4-14, 4594	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	6.62E-06	0.92	4.09	-	714.9
AHQ-4-14, 4658	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	4.30E-04	0.35	3.16	-	405.0
AHQ-4-14-, 2897 - 2977	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.46E-08	0.95	4.66	-	1213.6
AHQ-4-14-, 2907 - 2979	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	5.95E-06	0.96	5.26	-	865.2
AHQ-4-14, 4213 - 4282	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	4.68E-07	0.92	4.14	-	1031.4
AHQ-4-14, 3810	K.GTHCNQVEVIATLKDGRK.I	2028.27941	3	2.34E-08	0.81	3.76	-	581.4
AHQ-4-14, 3616	K.GTHCNQVEVIATLKDGRK.I	2028.27941	2	5.81E-05	0.97	5.35	-	1624.6
AHQ-4-14-, 2641 - 2715	K.GTHCNQVEVIATLKDGRK.I	2028.27941	2	4.37E-05	0.96	5.14	-	1030.9
AHQ-4-13-, 2880	K.ICLDPDAPR.I	1058.19059	2	1.20E-04	0.81	2.90	-	858.0
AHQ-4-14-, 2725 - 2789	K.ICLDPDAPR.I	1058.19059	2	9.12E-05	0.78	2.85	-	865.8
AHQ-4-13-, 2588	R.KICLDPDAPR.I	1186.36350	2	1.81E-04	0.84	2.97	-	826.1
AHQ-4-14, 3640 - 3701	R.KICLDPDAPR.I	1186.36350	2	8.03E-05	0.88	3.31	-	893.2
AHQ-4-14, 3089	R.KICLDPDAPR.I	1186.36350	2	1.18E-05	0.86	3.00	-	963.1
AHQ-4-14-, 2593	R.KICLDPDAPR.I	1186.36350	2	1.26E-05	0.70	2.94	-	616.7
AHQ-4-14-, 2458 - 2517	R.KICLDPDAPR.I	1186.36350	2	3.27E-05	0.91	3.20	-	1061.4
AHQ-4-14, 3837 - 3905	R.KICLDPDAPR.I	1186.36350	2	4.45E-04	0.70	2.72	-	691.4
AHQ-4-14-, 2389 - 2457	R.KICLDPDAPR.I	1186.36350	2	1.50E-04	0.89	3.64	-	778.7
AHQ-4-14, 3522 - 3580	R.KICLDPDAPR.I	1186.36350	2	1.84E-04	0.86	3.01	-	943.8
AHQ-4-14, 3193 - 3270	R.KICLDPDAPR.I	1186.36350	2	1.16E-04	0.74	3.00	-	692.6
AHQ-4-14, 3300 - 3365	R.KICLDPDAPR.I	1186.36350	2	1.12E-05	0.88	3.44	-	853.3
AHQ-4-12, 2509	R.KICLDPDAPR.I	1186.36350	2	9.08E-05	0.63	2.75	-	786.0
AHQ-4-14, 1849	K.KLAGDESAD	905.92969	1	5.81E-05	0.35	2.16	-	356.3
AHQ-4-14, 1930	K.KLAGDESAD	905.92969	1	3.08E-04	0.07	1.88	-	201.7
AHQ-4-14, 2345	K.KLAGDESAD	905.92969	1	5.90E-05	0.13	1.86	-	232.9
AHQ-4-14, 1606	K.KLAGDESAD	905.92969	1	4.07E-04	0.17	1.88	-	305.6
AHQ-4-14, 4477 - 4550	K.NIQSLEVIGK.G	1101.27845	2	5.38E-04	0.81	3.39	-	560.5
AHQ-4-14-, 4093	K.NIQSLEVIGK.G	1101.27845	1	5.34E-04	0.68	2.61	-	581.9
AHQ-4-14-, 3654	K.NIQSLEVIGK.G	1101.27845	2	8.36E-05	0.85	3.03	-	993.6
AHQ-4-14, 4161 - 4228	K.NIQSLEVIGK.G	1101.27845	2	3.47E-05	0.90	3.64	-	825.2
AHQ-4-14-, 3273 - 3333	K.NIQSLEVIGK.G	1101.27845	2	7.40E-06	0.86	3.30	-	757.2
AHQ-4-14, 4392 - 4420	K.NIQSLEVIGK.G	1101.27845	2	3.00E-06	0.85	3.55	-	589.1
AHQ-4-14, 4600 - 4621	K.NIQSLEVIGK.G	1101.27845	2	4.58E-06	0.80	2.81	-	800.0
AHQ-4-14-, 3146 - 3210	K.NIQSLEVIGK.G	1101.27845	2	4.95E-05	0.91	4.10	-	748.8
AHQ-4-14, 4685 - 4732	K.NIQSLEVIGK.G	1101.27845	2	3.52E-05	0.87	3.28	-	909.6
AHQ-4-13, 3538	K.NIQSLEVIGK.G	1101.27845	2	1.23E-05	0.85	3.13	-	725.7
AHQ-4-14, 4708	K.NIQSLEVIGK.G	1101.27845	1	1.51E-05	0.77	3.01	-	469.4
AHQ-4-14-, 3035 - 3114	K.NIQSLEVIGK.G	1101.27845	2	2.72E-07	0.83	3.20	-	674.5
AHQ-4-13-, 3324 - 3325	K.NIQSLEVIGK.G	1101.27845	2	3.24E-05	0.86	3.57	-	611.0
gi|17986260|ref|NP_524147.1|	smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo			1.91E-12	3.59	40.36	23.30	12969.7
AHQ-4-12, 5645 - 5713	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	5.28E-07	0.98	7.28	-	1699.5
AHQ-4-12, 5785 - 5849	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	2.57E-04	0.64	4.23	-	419.2
AHQ-4-12, 5909 - 5973	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	1.04E-04	0.84	5.14	-	631.3
AHQ-4-12, 6037 - 6113	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	1.22E-07	0.96	7.18	-	1542.1
AHQ-4-12, 6097	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	9.85E-06	0.95	5.00	-	1646.4
AHQ-4-12, 6174 - 6237	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	1.16E-09	0.82	4.36	-	792.1

AHQ-4-12, 6197 - 6277	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	4.55E-06	0.98	5.98	-	2162.9
AHQ-4-12, 6306 - 6339	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	1.97E-07	0.85	4.96	-	891.8
AHQ-4-12, 6342 - 6405	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	4.27E-05	0.96	5.14	-	1919.2
AHQ-4-12, 7111 - 7159	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	3.42E-07	0.86	4.65	-	723.7
AHQ-4-13, 5994	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	1.31E-04	0.32	3.30	-	299.0
AHQ-4-14-, 5494	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	9.89E-10	0.94	5.11	-	1346.1
AHQ-4-14-, 5877 - 5949	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	1.91E-12	0.85	4.58	-	1045.3
gi|5453595|ref|NP_006358.1| adenylyl cyclase-associated protein [Homo sapiens]				2.03E-12	10.13	130.27	32.80	51672.7
AHQ-4-13, 2930 - 2933	R.ALLVTASQCQQPAENK.L	1759.96271	2	9.97E-04	0.94	4.87	-	704.2
AHQ-4-8, 2482	R.ALLVTASQCQQPAENK.L	1759.96271	2	1.91E-05	0.95	4.74	-	987.0
AHQ-4-7, 6758 - 6837	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	3.86E-08	0.91	4.88	-	950.5
AHQ-4-7, 6667	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	1.87E-06	0.95	5.45	-	1403.3
AHQ-4-7, 2927	K.EPAVLELEGK.K	1085.23265	1	5.99E-04	0.20	2.00	-	306.0
AHQ-4-7, 2314	K.KEPAVLELEGK.K	1213.40557	2	3.50E-04	0.66	2.68	-	416.9
AHQ-4-7, 7581	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	1.73E-09	0.97	5.11	-	1594.1
AHQ-4-5, 5007	K.LSDLLAPISEQIK.E	1427.66814	1	9.17E-04	0.68	3.41	-	425.3
AHQ-4-7, 4834 - 4906	K.LSDLLAPISEQIK.E	1427.66814	2	4.45E-04	0.88	3.63	-	936.0
AHQ-4-9, 4428	K.LSDLLAPISEQIK.E	1427.66814	1	1.09E-05	0.68	3.23	-	479.2
AHQ-4-7, 4835	K.LSDLLAPISEQIK.E	1427.66814	1	3.02E-05	0.38	2.15	-	417.6
AHQ-4-13-, 5012	K.LSDLLAPISEQIK.E	1427.66814	2	7.43E-06	0.84	2.97	-	858.9
AHQ-4-12, 5054	K.LSDLLAPISEQIK.E	1427.66814	2	6.74E-06	0.81	3.09	-	816.2
AHQ-4-7, 2849	K.NSLDCEIVSAK.S	1237.36245	2	9.50E-06	0.92	3.19	-	1142.8
AHQ-4-7, 4557	R.SALFAQINQGESITHALK.H	1929.16615	2	1.86E-06	0.57	3.45	-	305.0
AHQ-4-7, 4417 - 4489	R.SALFAQINQGESITHALK.H	1929.16615	3	2.48E-06	0.71	3.41	-	777.1
AHQ-4-9, 4096	R.SALFAQINQGESITHALK.H	1929.16615	2	6.28E-05	0.94	4.79	-	911.7
AHQ-4-7, 4398 - 4474	R.SALFAQINQGESITHALK.H	1929.16615	2	2.92E-07	0.92	5.00	-	599.5
AHQ-4-8, 4199	R.SALFAQINQGESITHALK.H	1929.16615	3	4.07E-06	0.72	3.14	-	543.3
AHQ-4-7, 4690	R.SALFAQINQGESITHALK.H	1929.16615	2	2.03E-12	0.95	4.65	-	988.5
AHQ-4-8, 4195	R.SALFAQINQGESITHALK.H	1929.16615	2	1.17E-09	0.90	4.44	-	687.4
AHQ-4-7, 1861	R.SGPKPFSAPKPQTSPSPK.R	1839.08461	2	5.63E-07	0.89	4.02	-	813.2
AHQ-4-7, 1857	R.SGPKPFSAPKPQTSPSPK.R	1839.08461	3	8.44E-08	0.89	3.45	-	1245.2
AHQ-4-7, 6737 - 6810	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	5.56E-05	0.71	3.29	-	252.7
AHQ-4-13, 6276 - 6290	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	1.35E-06	0.80	3.70	-	221.5
AHQ-4-14-, 6297 - 6370	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	4.54E-06	0.81	3.89	-	250.9
AHQ-4-10, 6057	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.09E-05	0.53	3.02	-	184.2
AHQ-4-13, 6618 - 6629	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	6.16E-05	0.67	3.21	-	287.0
AHQ-4-14-, 5953 - 6029	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	1.67E-06	0.70	3.23	-	258.1
AHQ-4-11, 6298 - 6358	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	6.74E-04	0.58	2.75	-	298.5
AHQ-4-11, 6038 - 6042	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	6.31E-06	0.72	3.44	-	178.0
AHQ-4-11, 4862	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	3.16E-04	0.83	3.99	-	512.7
AHQ-4-12, 4765	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	9.24E-07	0.93	4.41	-	796.6
AHQ-4-11, 4526 - 4592	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.73E-07	0.89	4.21	-	667.6
AHQ-4-10, 4311	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	3.09E-06	0.92	4.20	-	888.9
AHQ-4-13, 4866	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.37E-09	0.89	4.01	-	688.0
AHQ-4-8, 4397	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.72E-08	0.93	4.67	-	802.0
AHQ-4-7, 4730 - 4809	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.79E-08	0.93	4.40	-	875.1
AHQ-4-14, 5954	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	8.02E-07	0.93	4.77	-	823.5
AHQ-4-7, 4239	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.19E-05	0.88	3.98	-	550.5
AHQ-4-13-, 4762	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.19E-05	0.59	2.98	-	752.3
AHQ-4-7, 4589 - 4658	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.33E-08	0.93	4.81	-	563.7
AHQ-4-14-, 4691	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.53E-04	0.91	4.13	-	660.5
AHQ-4-1, 4994 - 5009	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.27E-04	0.72	3.02	-	544.6
AHQ-4-13-, 2613	K.VPTISINK.T	872.04435	1	1.47E-04	0.37	2.42	-	258.3
gi|9507215|ref|NP_061816.1| tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]				2.13E-12	3.36	40.20	13.10	50093.2
AHQ-4-14-, 5209	R.AVMIDLEPTVVDEVR.A	1686.95185	2	2.43E-04	0.86	3.15	-	941.1
AHQ-4-7, 3271	K.DVNVAIAAIK.T	1014.20080	1	2.11E-04	0.70	3.22	-	394.9
AHQ-4-9, 4892	R.IHFPLVTYAPIISAEK.A	1800.13312	2	6.94E-05	0.82	3.03	-	537.5
AHQ-4-7, 5331 - 5365	R.IHFPLVTYAPIISAEK.A	1800.13312	2	1.64E-07	0.93	3.81	-	732.1
AHQ-4-14-, 5201	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	2.50E-09	0.81	3.57	-	602.8
AHQ-4-14, 6504 - 6512	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	9.17E-08	0.86	3.69	-	403.2
AHQ-4-13, 5413	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	2.13E-12	0.87	4.00	-	593.3
gi|13489087|ref|NP_109591.1| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member				2.47E-12	5.49	60.22	22.70	42741.5
AHQ-4-8, 3887	K.FAYGYIEDLK.C	1219.36713	2	3.88E-07	0.90	2.84	-	1100.3
AHQ-4-8, 3749	K.FAYGYIEDLKCR.V	1536.73331	2	1.34E-05	0.89	2.74	-	1174.8
AHQ-4-8, 4011	R.LGVQDLFNSSK.A	1208.34588	2	3.46E-05	0.84	2.71	-	868.9
AHQ-4-8, 4326	R.LGVQDLFNSSK.A	1208.34588	2	1.89E-06	0.94	3.40	-	1429.1
AHQ-4-8, 3675	K.TYGADLASVDFQHASEDAR.K	2054.11949	3	1.08E-09	0.87	3.84	-	554.8
AHQ-4-8, 3665	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	2.47E-12	0.94	4.08	-	1172.9
AHQ-4-13, 4172	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	2.46E-09	0.72	3.58	-	288.9
AHQ-4-13-, 4050	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	2.87E-05	0.65	2.70	-	445.1
AHQ-4-13, 6272	K.TYNFLPEFLVSTQK.T	1687.91650	2	5.07E-04	0.88	3.94	-	467.9
AHQ-4-8, 5922 - 5931	K.TYNFLPEFLVSTQK.T	1687.91650	2	2.44E-05	0.92	4.31	-	551.1
AHQ-4-8, 7157	R.VLELPYQGEELSMVILLPDDIEDESTGLKK.I	3375.82891	3	1.22E-08	0.90	4.31	-	590.9
gi|4507951|ref|NP_003396.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept				2.52E-12	5.02	60.24	34.10	28218.5
AHQ-4-13-, 2969	K.AVTELNEPLSNEDR.N	1587.67060	2	3.02E-04	0.87	3.32	-	774.9
AHQ-4-13, 3085	K.AVTELNEPLSNEDR.N	1587.67060	2	8.75E-07	0.83	3.63	-	658.2
AHQ-4-10, 2731 - 2733	K.AVTELNEPLSNEDR.N	1587.67060	2	2.52E-12	0.95	4.88	-	916.0
AHQ-4-10, 2821 - 2869	K.AVTELNEPLSNEDR.N	1587.67060	2	1.44E-05	0.83	3.56	-	588.2
AHQ-4-11, 6678	K.ELETVCNDVLSLLDK.F	1749.96137	2	8.26E-05	0.60	2.66	-	473.8
AHQ-4-14-, 6646	K.ELETVCNDVLSLLDK.F	1749.96137	2	2.07E-07	0.93	4.32	-	667.5
AHQ-4-10, 3833	K.FLIKNCNDFQYESK.V	1808.00430	2	8.46E-05	0.78	3.57	-	514.7
AHQ-4-10, 2401	K.NSVVEASEAAYK.E	1268.35495	2	1.59E-04	0.84	3.06	-	984.9
AHQ-4-10, 2771 - 2780	K.NSVVEASEAAYK.E	1268.35495	1	2.17E-05	0.60	2.82	-	448.3
AHQ-4-10, 5657	K.QAFDDAIAELDTLNEDSYK.D	2159.24915	2	2.23E-05	0.90	4.21	-	639.1
AHQ-4-10, 2027	R.YLAEVASGEK.K	1067.17419	1	2.11E-05	0.41	2.79	-	187.4
AHQ-4-10, 2017 - 2089	R.YLAEVASGEK.K	1067.17419	1	2.78E-05	0.40	2.22	-	571.0
AHQ-4-10, 2036	R.YLAEVASGEK.K	1067.17419	2	1.25E-05	0.87	3.24	-	781.8
gi|4758086|ref|NP_004069.1| cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain				2.61E-12	4.28	50.27	45.60	20567.3
AHQ-4-11, 4058 - 4129	K.GFGFGQGAGALVHSE	1434.53788	2	3.17E-08	0.92	3.92	-	849.2
AHQ-4-13, 4361	K.GFGFGQGAGALVHSE	1434.53788	2	4.77E-05	0.87	3.58	-	651.4
AHQ-4-11, 3201	K.GLESTTLADKDGEIYCK.G	1902.06957	3	4.25E-04	0.85	3.96	-	543.9
AHQ-4-11, 3306	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.16E-04	0.94	3.95	-	1081.2
AHQ-4-13-, 3353	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.19E-06	0.95	4.68	-	1192.4
AHQ-4-11, 3156 - 3224	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.90E-09	0.97	5.15	-	1539.4
AHQ-4-10, 3089	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.47E-05	0.85	3.86	-	622.7
AHQ-4-13, 3485	K.GLESTTLADKDGEIYCK.G	1902.06957	2	4.17E-07	0.90	4.10	-	764.2
AHQ-4-13-, 3626	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	6.85E-06	0.87	3.68	-	870.1
AHQ-4-10, 3288 - 3301	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	3.36E-04	0.39	2.76	-	114.1
AHQ-4-13, 3752	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	3.96E-09	0.89	4.51	-	552.3
AHQ-4-12, 3506	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	1.63E-08	0.94	4.63	-	950.8
AHQ-4-11, 3397 - 3424	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	2.61E-12	0.87	4.15	-	616.2
AHQ-4-11, 3525	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	7.69E-07	0.88	4.40	-	388.5
AHQ-4-11, 3381 - 3460	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	1.92E-09	0.97	5.11	-	1356.2
AHQ-4-11, 3372	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	6.00E-08	0.97	5.45	-	1216.0
AHQ-4-11, 4052	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	1.97E-05	0.93	4.48	-	757.0
AHQ-4-11, 4165 - 4169	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	2.45E-06	0.54	2.97	-	142.2
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				2.70E-12	12.19	140.29	47.10	49481.2

AHQ-4-7, 4393 - 4461	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	6.20E-08	0.92	4.89	-	694.8
AHQ-4-6, 4499	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	1.56E-04	0.64	3.25	-	420.7
AHQ-4-7, 4469 - 4541	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	6.52E-07	0.80	3.88	-	387.0
AHQ-4-7, 4609	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	4.08E-06	0.73	3.62	-	388.2
AHQ-4-5, 4558 - 4565	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	2.10E-05	0.76	3.49	-	528.9
AHQ-4-1, 4333 - 4405	K.AIQLTYNPDESSKPNM*IDAATLK.S	2537.82826	3	4.73E-04	0.73	3.56	-	445.5
AHQ-4-11, 4550	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	9.81E-04	0.55	2.85	-	282.8
AHQ-4-12, 4733 - 4734	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	4.23E-05	0.53	2.95	-	315.8
AHQ-4-7, 5849	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	8.87E-06	0.68	2.93	-	496.8
AHQ-4-5, 5561 - 5630	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	7.02E-08	0.79	3.45	-	469.9
AHQ-4-1, 5889	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	4.32E-06	0.73	3.04	-	532.7
AHQ-4-13, 5548 - 5560	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.53E-10	0.72	3.15	-	516.9
AHQ-4-14-, 5481 - 5551	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.68E-10	0.80	3.45	-	495.8
AHQ-4-7, 5637 - 5705	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.46E-08	0.83	3.57	-	578.3
AHQ-4-7, 5461 - 5494	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	3.29E-08	0.81	3.40	-	649.4
AHQ-4-13-, 5537 - 5585	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.30E-05	0.62	3.02	-	429.4
AHQ-4-4, 5710 - 5712	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	6.67E-06	0.60	3.16	-	396.5
AHQ-4-14-, 5341 - 5417	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	5.85E-06	0.70	3.09	-	444.2
AHQ-4-7, 2435 - 2509	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	2.75E-06	0.98	5.81	-	2455.4
AHQ-4-7, 2423 - 2499	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	8.49E-06	0.97	5.23	-	999.2
AHQ-4-13-, 2789	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.58E-08	0.96	4.70	-	1268.2
AHQ-4-13, 2925	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	1.94E-04	0.90	3.82	-	775.3
AHQ-4-3, 2695	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.83E-06	0.90	3.88	-	696.2
AHQ-4-1, 2831	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.18E-08	0.95	4.63	-	1078.3
AHQ-4-13, 2833 - 2838	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.71E-05	0.97	5.12	-	1164.9
AHQ-4-1, 3277	R.DNCCILDER.F	1197.27847	2	3.52E-04	0.88	3.18	-	864.6
AHQ-4-5, 3193	R.DNCCILDER.F	1197.27847	2	1.16E-05	0.83	2.70	-	944.9
AHQ-4-1, 5553	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	2.65E-06	0.94	4.57	-	1618.7
AHQ-4-5, 5151	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	2.35E-05	0.96	4.78	-	2098.7
AHQ-4-5, 5278	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.53E-04	0.76	3.19	-	471.7
AHQ-4-4, 5534	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.80E-06	0.71	3.14	-	525.4
AHQ-4-1, 5634	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.24E-04	0.67	3.29	-	529.3
AHQ-4-11, 4990 - 5046	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.42E-04	0.90	4.31	-	614.7
AHQ-4-10, 4613 - 4688	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	6.88E-05	0.88	4.46	-	436.1
AHQ-4-9, 4705	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.47E-07	0.89	3.89	-	774.5
AHQ-4-9, 4559 - 4629	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	7.66E-05	0.89	4.05	-	680.4
AHQ-4-8, 4727 - 4737	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.07E-04	0.96	4.99	-	917.9
AHQ-4-7, 5134 - 5210	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.26E-10	0.95	5.04	-	898.9
AHQ-4-7, 4986 - 5054	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	4.98E-04	0.92	4.32	-	691.9
AHQ-4-2, 5455	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.57E-07	0.93	4.29	-	753.1
AHQ-4-3, 5432 - 5448	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.15E-04	0.94	4.63	-	890.6
AHQ-4-14-, 6395	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.26E-04	0.47	2.75	-	421.4
AHQ-4-1, 6869 - 6870	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	1.17E-06	0.78	3.90	-	618.6
AHQ-4-7, 6790 - 6858	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.24E-05	0.89	4.51	-	439.9
AHQ-4-13, 6633 - 6634	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	6.83E-07	0.80	3.38	-	524.5
AHQ-4-11, 6362	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	2.37E-06	0.75	3.33	-	741.7
AHQ-4-9, 6137 - 6201	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	4.24E-07	0.79	3.42	-	463.1
AHQ-4-6, 4334	K.IHLISTQSAIPYALR.V	1683.97576	2	1.72E-09	0.92	4.00	-	946.8
AHQ-4-1, 4829 - 4873	K.IHLISTQSAIPYALR.V	1683.97576	2	7.45E-04	0.91	3.53	-	1033.2
AHQ-4-5, 4346 - 4351	K.IHLISTQSAIPYALR.V	1683.97576	2	2.26E-04	0.92	3.80	-	620.7
AHQ-4-4, 4687	K.IHLISTQSAIPYALR.V	1683.97576	2	5.00E-06	0.94	3.99	-	1146.7
AHQ-4-8, 3882	K.IHLISTQSAIPYALR.V	1683.97576	2	4.41E-08	0.96	5.01	-	1129.6
AHQ-4-8, 3893	K.IHLISTQSAIPYALR.V	1683.97576	3	7.18E-04	0.74	3.64	-	564.4
AHQ-4-3, 4740	K.IHLISTQSAIPYALR.V	1683.97576	2	7.95E-11	0.97	4.82	-	1499.5
AHQ-4-11, 4350	K.IHLISTQSAIPYALR.V	1683.97576	2	3.19E-07	0.91	3.11	-	1330.5
AHQ-4-7, 4145 - 4225	K.IHLISTQSAIPYALR.V	1683.97576	2	2.70E-12	0.97	5.29	-	1346.8
AHQ-4-9, 3839	K.IHLISTQSAIPYALR.V	1683.97576	2	7.81E-09	0.97	4.94	-	1349.4
AHQ-4-2, 4742 - 4750	K.IHLISTQSAIPYALR.V	1683.97576	2	5.87E-08	0.94	4.60	-	966.8
AHQ-4-7, 1791	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	4.90E-07	0.73	2.69	-	637.5
AHQ-4-7, 1875	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	5.49E-04	0.40	2.54	-	320.4
AHQ-4-14-, 2071	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.70E-11	0.91	3.42	-	1183.3
AHQ-4-13-, 2137 - 2144	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.41E-11	0.97	4.74	-	1711.7
AHQ-4-11, 1980	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	7.05E-07	0.92	3.80	-	1200.2
AHQ-4-4, 1978	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.27E-06	0.69	3.56	-	415.2
AHQ-4-13, 2257	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.34E-06	0.90	3.57	-	1191.1
AHQ-4-7, 1665 - 1725	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	2.50E-06	0.90	3.24	-	1097.7
AHQ-4-1, 4078 - 4087	K.QSGLYFIKPLK.A	1294.56665	2	1.01E-04	0.58	2.69	-	328.0
AHQ-4-1, 4125	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	1.59E-05	0.91	4.04	-	1032.1
AHQ-4-2, 4074	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	9.67E-05	0.89	4.05	-	608.8
AHQ-4-9, 3411	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	2	4.20E-04	0.61	3.04	-	329.4
AHQ-4-10, 3760	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	1.78E-07	0.91	4.37	-	1237.1
AHQ-4-1, 4351	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	8.64E-05	0.93	4.43	-	1303.6
AHQ-4-11, 2858	K.YEASILTHDSSIR.Y	1492.61564	2	2.88E-06	0.85	3.18	-	737.1
AHQ-4-5, 2726	K.YEASILTHDSSIR.Y	1492.61564	2	8.59E-08	0.91	3.69	-	875.3
AHQ-4-7, 2597 - 2674	K.YEASILTHDSSIR.Y	1492.61564	2	7.48E-10	0.93	3.97	-	877.3
AHQ-4-9, 2527 - 2533	K.YEASILTHDSSIR.Y	1492.61564	2	8.06E-05	0.88	3.43	-	713.6
AHQ-4-12, 2833 - 2913	K.YEASILTHDSSIR.Y	1492.61564	2	1.91E-05	0.52	2.77	-	376.9
AHQ-4-2, 2895 - 2967	K.YEASILTHDSSIR.Y	1492.61564	2	2.01E-07	0.65	2.88	-	453.8
AHQ-4-8, 2499	K.YEASILTHDSSIR.Y	1492.61564	2	2.75E-07	0.89	2.82	-	914.0
AHQ-4-1, 2887	R.YLQEIYNSNNQK.I	1514.62131	2	2.64E-04	0.83	3.51	-	722.1
AHQ-4-4, 2788	R.YLQEIYNSNNQK.I	1514.62131	2	1.26E-04	0.93	3.98	-	1208.0
AHQ-4-7, 2599	R.YLQEIYNSNNQK.I	1514.62131	2	3.60E-05	0.93	4.00	-	1128.9
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				2.93E-12	19.41	220.32	22.60	138070.8
AHQ-4-1, 2439	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	3.55E-05	0.92	4.49	-	1078.4
AHQ-4-3, 2249 - 2252	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	5.90E-09	0.93	4.27	-	722.0
AHQ-4-4, 2247 - 2251	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	4.95E-07	0.95	5.14	-	727.7
AHQ-4-5, 2109	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	2.30E-04	0.90	3.96	-	1152.5
AHQ-4-2, 2286	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	6.78E-09	0.88	4.18	-	429.9
AHQ-4-3, 2347	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	2.93E-12	0.91	4.43	-	771.9
AHQ-4-3, 7340	K.CTSDMETILTFIPQFHR.L	2098.38838	3	2.55E-07	0.95	4.69	-	1318.6
AHQ-4-4, 7292	K.CTSDMETILTFIPQFHR.L	2098.38838	2	1.99E-05	0.47	2.74	-	447.5
AHQ-4-3, 4116 - 4129	R.DQALQLQVLNSR.F	1385.55144	2	9.53E-08	0.96	4.90	-	1528.4
AHQ-4-2, 4144	R.DQALQLQVLNSR.F	1385.55144	2	8.83E-08	0.95	3.86	-	1596.1
AHQ-4-13, 6301	K.FPPVTTFSGYLLYR.T	1661.92388	2	3.09E-04	0.78	2.95	-	524.8
AHQ-4-14-, 6069 - 6130	K.FPPVTTFSGYLLYR.T	1661.92388	2	1.34E-06	0.93	3.82	-	758.0
AHQ-4-10, 5683 - 5700	K.FPPVTTFSGYLLYR.T	1661.92388	2	2.33E-04	0.89	3.48	-	723.7
AHQ-4-2, 5983	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	6.10E-09	0.83	3.51	-	795.4
AHQ-4-6, 5644	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	6.94E-04	0.42	2.87	-	302.4
AHQ-4-4, 5914	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	6.09E-04	0.73	3.64	-	369.9
AHQ-4-3, 5943 - 5959	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	3.50E-05	0.95	5.22	-	1066.2
AHQ-4-2, 6272	K.GLTEFVEPIIQIK.T	1487.76518	1	6.11E-04	0.17	2.32	-	398.4
AHQ-4-1, 6251 - 6253	K.GLTEFVEPIIQIK.T	1487.76518	2	1.30E-06	0.95	4.56	-	1104.6
AHQ-4-5, 6061 - 6062	K.GLTEFVEPIIQIK.T	1487.76518	2	4.29E-06	0.92	4.06	-	966.7
AHQ-4-6, 6002	K.GLTEFVEPIIQIK.T	1487.76518	2	2.12E-05	0.71	2.58	-	884.2
AHQ-4-3, 6260 - 6291	K.GLTEFVEPIIQIK.T	1487.76518	2	5.29E-06	0.71	2.88	-	746.2
AHQ-4-3, 2607	K.GPCGWTGGSCPQR.S	1422.52885	2	6.90E-04	0.86	3.33	-	739.5
AHQ-4-3, 4231	K.GSVVTNERDQALQLQVLNSR.F	2228.45212	2	2.61E-04	0.66	3.58	-	404.6

AHQ-4-2, 3815	K.HSLPDIQLLQK.G	1292.50915	2	4.18E-08	0.92	3.40	-	1011.2
AHQ-4-3, 3739	K.HSLPDIQLLQK.G	1292.50915	2	3.33E-07	0.94	4.01	-	957.8
AHQ-4-4, 3759	K.HSLPDIQLLQK.G	1292.50915	2	3.75E-06	0.88	3.45	-	772.3
AHQ-4-3, 6151	K.IENLTSAVNSLNFIIK.E	1777.05472	2	1.38E-07	0.87	4.19	-	597.0
AHQ-4-3, 5188	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.76E-04	0.96	4.79	-	1487.8
AHQ-4-1, 5258	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.03E-05	0.89	3.37	-	1093.5
AHQ-4-5, 6545 - 6550	K.IFQNDMQETVAQLFK.T	1813.06743	2	1.29E-08	0.98	4.94	-	2384.7
AHQ-4-1, 5459	K.IFQNDM*QETVAQLFK.T	1829.06683	2	2.42E-04	0.94	3.87	-	1361.8
AHQ-4-3, 5421 - 5437	K.IFQNDM*QETVAQLFK.T	1829.06683	2	4.64E-10	0.95	4.67	-	1012.1
AHQ-4-3, 6719 - 6795	K.IFQNDMQETVAQLFK.T	1813.06743	2	3.89E-07	0.97	4.90	-	1571.9
AHQ-4-3, 5564	K.KIENLTSAVNSLNFIIK.E	1905.22764	2	5.17E-08	0.96	4.70	-	1476.9
AHQ-4-3, 4920	R.KKIENLTSAVNSLNFIIK.E	2033.40055	2	3.31E-07	0.87	3.64	-	722.5
AHQ-4-10, 3715	K.LAFESENINSEIHCDR.V	1936.04933	2	6.68E-06	0.90	4.13	-	778.1
AHQ-4-10, 3493 - 3563	K.LAFESENINSEIHCDR.V	1936.04933	2	2.25E-09	0.90	4.28	-	689.6
AHQ-4-4, 2736	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	1.69E-05	0.94	4.39	-	1123.5
AHQ-4-5, 2547	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	4.69E-08	0.97	6.10	-	1381.7
AHQ-4-3, 2743	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	6.27E-06	0.98	6.20	-	1689.0
AHQ-4-10, 3391 - 3419	K.LVEENALAPDFSK.G	1433.58810	1	2.35E-07	0.58	2.32	-	773.3
AHQ-4-11, 3596	K.LVEENALAPDFSK.G	1433.58810	2	2.29E-06	0.88	3.13	-	864.0
AHQ-4-10, 3375 - 3436	K.LVEENALAPDFSK.G	1433.58810	2	1.38E-05	0.93	4.00	-	851.5
AHQ-4-3, 7511	K.M*SEQLNDLTYDMEILQPLLEQGASLR.Q	3025.40122	3	1.24E-06	0.96	6.34	-	1754.5
AHQ-4-1, 7225	K.M*SEQLNDLTYDMEILQPLLEQGASLR.Q	3025.40122	3	1.03E-06	0.93	5.77	-	971.5
AHQ-4-2, 3848	R.NTDNIIYPEEYSSCSR.H	1950.02964	2	8.70E-04	0.77	3.72	-	339.0
AHQ-4-3, 7419	K.TM*TIINNAIDFIQDNYALK.E	2215.51196	2	5.04E-08	0.96	5.08	-	1013.9
AHQ-4-4, 7424 - 7504	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	4.85E-08	0.89	3.98	-	607.5
AHQ-4-3, 7461 - 7483	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	2.43E-09	0.96	5.35	-	888.3
AHQ-4-3, 4016	R.YNFVLQVAK.T	1082.27683	2	4.96E-06	0.92	3.29	-	1083.0
AHQ-4-3, 3997 - 4067	R.YNFVLQVAK.T	1082.27683	1	9.69E-08	0.74	2.51	-	740.0
gi|16933542|ref|NP_002017.1| fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s				2.97E-12	6.04	70.23	5.30	259222.8
AHQ-4-1, 4682	R.ITYGETGGNSPVQEFTVPGSK.S	2169.33354	2	1.45E-04	0.85	3.83	-	449.9
AHQ-4-2, 6330	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	5.95E-06	0.91	4.12	-	680.3
AHQ-4-1, 6187 - 6255	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	2.88E-05	0.81	3.64	-	520.3
AHQ-4-3, 6323	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	1.38E-04	0.71	3.16	-	415.9
AHQ-4-1, 6741	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	3.70E-11	0.90	4.56	-	445.8
AHQ-4-1, 4479	R.TKTETITGFQVDAVPANGQTPIQR.T	2573.84359	2	1.18E-04	0.72	2.92	-	474.7
AHQ-4-1, 4074 - 4077	R.VDVIPVNLPGEHGQR.L	1630.82981	2	7.94E-09	0.90	3.55	-	851.7
AHQ-4-1, 3459 - 3482	R.VPGTSTSATLTGLTR.G	1462.63098	2	4.66E-07	0.90	3.34	-	767.6
AHQ-4-2, 7330	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	2.62E-05	0.76	3.13	-	370.3
AHQ-4-3, 7311	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	2.97E-12	0.85	3.70	-	456.7
AHQ-4-1, 7102	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	2.98E-05	0.82	3.11	-	535.9
AHQ-4-1, 3973	K.YSFCTDHTVLVQTR.G	1728.90717	2	9.15E-08	0.92	3.81	-	1172.2
gi|5031635|ref|NP_005498.1| cofilin 1 (non-muscle) [Homo sapiens]				3.18E-12	11.08	120.41	60.80	18502.4
AHQ-4-13, 3638	K.AVLFCLSEDKK.N	1311.52930	2	5.17E-04	0.70	2.74	-	633.0
AHQ-4-12, 3313 - 3383	K.AVLFCLSEDKK.N	1311.52930	2	3.73E-04	0.79	3.36	-	557.5
AHQ-4-13-, 3501	K.AVLFCLSEDKK.N	1311.52930	2	1.23E-07	0.82	2.73	-	835.5
AHQ-4-12, 6967	K.EDLVFIFWAPESAPLK.S	1863.14454	2	4.09E-09	0.98	5.23	-	1924.2
AHQ-4-12, 5549 - 5617	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	2.37E-06	0.97	5.60	-	1294.5
AHQ-4-12, 5434	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	9.92E-06	0.94	4.58	-	1078.6
AHQ-4-12, 5685 - 5749	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.16E-10	0.97	5.26	-	1529.8
AHQ-4-14-, 5582	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	7.94E-05	0.96	5.13	-	1058.1
AHQ-4-12, 5787 - 5857	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.32E-09	0.96	4.98	-	1238.0
AHQ-4-12, 5829	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.18E-12	0.97	5.37	-	1617.3
AHQ-4-13, 5658 - 5736	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.34E-07	0.97	5.66	-	1177.2
AHQ-4-13-, 5613 - 5616	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.72E-11	0.98	5.89	-	1506.8
AHQ-4-12, 6014 - 6093	K.ESKKEDLVFIFWAPESAPLK.S	2335.68256	2	8.06E-05	0.77	3.22	-	518.7
AHQ-4-12, 5966 - 6029	K.ESKKEDLVFIFWAPESAPLK.S	2335.68256	3	1.84E-07	0.91	4.71	-	725.8
AHQ-4-14-, 2399 - 2459	K.HELQANCYEEVKDR.C	1792.90812	3	3.61E-06	0.68	3.34	-	476.7
AHQ-4-12, 2491	K.HELQANCYEEVKDR.C	1792.90812	3	6.25E-06	0.90	3.70	-	1295.5
AHQ-4-12, 2309 - 2378	K.HELQANCYEEVKDR.C	1792.90812	2	6.47E-07	0.97	5.46	-	1155.6
AHQ-4-12, 2822	K.KAVLFCLSEDKK.N	1439.70221	3	8.16E-04	0.92	3.88	-	1504.9
AHQ-4-12, 2818	K.KAVLFCLSEDKK.N	1439.70221	2	2.46E-05	0.92	4.09	-	960.2
AHQ-4-12, 2821 - 2825	K.KAVLFCLSEDKK.N	1439.70221	1	1.20E-04	0.24	2.63	-	344.5
AHQ-4-12, 6519 - 6581	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.35E-05	0.97	5.02	-	1333.9
AHQ-4-13-, 6477	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	3.43E-04	0.96	5.60	-	1376.5
AHQ-4-12, 6421 - 6454	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	7.79E-07	0.97	5.59	-	1587.8
AHQ-4-14-, 6327 - 6329	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	8.17E-11	0.98	5.31	-	2044.1
AHQ-4-13-, 6464	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	3.10E-06	0.97	5.13	-	1107.6
AHQ-4-12, 6425 - 6491	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	1.64E-07	0.96	5.20	-	1501.5
AHQ-4-11, 6234	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.07E-05	0.96	4.72	-	1354.9
AHQ-4-12, 5810	K.KEDLVFIFWAPESAPLKSK.M	2206.56802	2	2.60E-05	0.94	4.53	-	914.3
AHQ-4-12, 6510 - 6575	K.KNIILEEGKEILVGDVGQTVDDPYATFVK.M	3192.60499	3	2.47E-07	0.97	6.22	-	1919.8
AHQ-4-12, 3998	K.LGGSAVISLEGKPL	1341.57848	2	3.98E-04	0.95	3.77	-	1831.2
AHQ-4-12, 5122	K.LGGSAVISLEGKPL	1341.57848	2	1.14E-04	0.88	3.33	-	964.8
AHQ-4-12, 5033	K.LGGSAVISLEGKPL	1341.57848	2	3.02E-04	0.88	3.42	-	1022.3
AHQ-4-12, 4258 - 4333	K.LGGSAVISLEGKPL	1341.57848	2	9.20E-05	0.93	3.85	-	1301.9
AHQ-4-12, 4361	K.LGGSAVISLEGKPL	1341.57848	1	4.19E-04	0.57	2.68	-	428.6
AHQ-4-12, 4793 - 4863	K.LGGSAVISLEGKPL	1341.57848	2	1.68E-06	0.96	4.68	-	1317.9
AHQ-4-12, 4373 - 4441	K.LGGSAVISLEGKPL	1341.57848	2	2.70E-08	0.95	4.62	-	1218.2
AHQ-4-12, 4457 - 4525	K.LGGSAVISLEGKPL	1341.57848	2	1.22E-04	0.96	4.80	-	1427.2
AHQ-4-12, 4599 - 4666	K.LGGSAVISLEGKPL	1341.57848	2	3.09E-06	0.93	4.36	-	942.3
AHQ-4-12, 4657 - 4729	K.LGGSAVISLEGKPL	1341.57848	2	4.01E-08	0.95	4.31	-	1106.3
AHQ-4-12, 6817 - 6837	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.18E-09	0.98	7.24	-	2018.2
AHQ-4-13, 6756	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.97E-11	0.98	7.69	-	2103.7
AHQ-4-11, 6520	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	5.99E-04	0.91	4.52	-	995.1
AHQ-4-12, 6481	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	9.30E-08	0.97	6.68	-	1553.6
AHQ-4-12, 7061 - 7127	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.24E-06	0.96	6.40	-	1208.5
AHQ-4-12, 6977 - 7045	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.06E-07	0.96	5.98	-	1382.5
AHQ-4-14-, 6554 - 6623	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	9.67E-05	0.57	3.53	-	490.8
AHQ-4-12, 6721 - 6758	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.19E-05	0.93	5.20	-	973.2
AHQ-4-13-, 6672 - 6673	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	6.66E-12	0.98	8.16	-	1670.9
AHQ-4-12, 3110 - 3178	R.YALYDATYETK.E	1338.44364	1	2.64E-08	0.70	2.93	-	384.1
AHQ-4-13-, 3260	R.YALYDATYETK.E	1338.44364	2	4.41E-07	0.95	3.68	-	1233.8
AHQ-4-13, 3358 - 3421	R.YALYDATYETK.E	1338.44364	2	8.52E-05	0.90	3.35	-	1172.4
AHQ-4-13-, 3262	R.YALYDATYETK.E	1338.44364	1	1.47E-04	0.41	2.55	-	315.8
gi|21361198|ref|NP_000286.2| serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei				3.29E-12	0.95	10.23	4.30	46722.2
AHQ-4-7, 4505 - 4582	K.VFSNGADLSGVTEEAPLK.L	1835.00476	2	3.29E-12	0.95	4.68	-	1139.9
gi|4501893|ref|NP_001094.1| actinin, alpha 2 [Homo sapiens]				3.45E-12	8.58	100.27	12.60	103853.1
AHQ-4-1, 5153	K.CQLEINFNTLQTK.L	1610.81373	2	2.38E-04	0.86	3.28	-	864.2
AHQ-4-5, 5129	K.CQLEINFNTLQTK.L	1610.81373	2	6.15E-05	0.96	4.52	-	1327.9
AHQ-4-5, 5295	K.CQLEINFNTLQTK.L	1610.81373	2	9.85E-05	0.86	3.97	-	669.5
AHQ-4-5, 5021 - 5089	K.CQLEINFNTLQTK.L	1610.81373	2	3.73E-05	0.94	4.55	-	932.2
AHQ-4-4, 5008	K.EGLLLWCQR.K	1176.37031	2	3.72E-04	0.84	3.14	-	670.7
AHQ-4-4, 4282	R.FAIQDISVEETSAK.E	1538.68108	2	4.52E-09	0.91	4.27	-	705.8
AHQ-4-6, 4015	R.FAIQDISVEETSAK.E	1538.68108	2	3.45E-12	0.97	5.08	-	1606.1
AHQ-4-11, 4016 - 4028	R.FAIQDISVEETSAK.E	1538.68108	2	1.03E-08	0.92	4.10	-	872.5
AHQ-4-1, 4409	R.FAIQDISVEETSAK.E	1538.68108	2	1.56E-05	0.81	3.15	-	650.6
AHQ-4-5, 4129 - 4202	R.FAIQDISVEETSAK.E	1538.68108	2	8.66E-05	0.60	2.69	-	358.0

AHQ-4-5, 4030 - 4101	R.FAIQDISVEETSAK.E	1538.68108	2	7.36E-10	0.95	4.33	-	1280.3
AHQ-4-12, 4159	R.FAIQDISVEETSAK.E	1538.68108	2	1.35E-07	0.86	3.03	-	936.2
AHQ-4-1, 6222	K.GYEEWLLNEIR.R	1422.56701	2	1.74E-06	0.94	3.92	-	1356.0
AHQ-4-7, 5961 - 5966	K.GYEEWLLNEIR.R	1422.56701	1	1.26E-04	0.06	2.10	-	139.5
AHQ-4-6, 5990	K.GYEEWLLNEIR.R	1422.56701	1	6.16E-06	0.42	2.61	-	165.8
AHQ-4-6, 5970 - 5991	K.GYEEWLLNEIR.R	1422.56701	2	2.99E-07	0.97	4.29	-	2043.3
AHQ-4-6, 5931 - 5994	K.GYEEWLLNEIR.R	1422.56701	1	1.45E-04	0.32	2.40	-	257.6
AHQ-4-5, 6226	K.GYEEWLLNEIR.R	1422.56701	1	9.04E-10	0.31	2.42	-	153.5
AHQ-4-5, 6218	K.GYEEWLLNEIR.R	1422.56701	2	6.80E-05	0.85	2.58	-	1221.5
AHQ-4-5, 6053	K.GYEEWLLNEIR.R	1422.56701	1	5.17E-06	0.34	2.42	-	146.9
AHQ-4-4, 6254	K.GYEEWLLNEIR.R	1422.56701	1	4.19E-05	0.38	2.23	-	359.5
AHQ-4-4, 6246	K.GYEEWLLNEIR.R	1422.56701	2	3.21E-06	0.96	4.09	-	1805.8
AHQ-4-5, 6049 - 6093	K.GYEEWLLNEIR.R	1422.56701	2	4.57E-07	0.98	5.15	-	2266.7
AHQ-4-5, 2011	K.HEAFESDLAAHQDR.V	1626.66861	2	7.59E-10	0.98	4.78	-	1849.3
AHQ-4-5, 1532	K.HTNYTMEHIR.V	1302.44449	3	5.85E-06	0.81	3.17	-	985.4
AHQ-4-5, 3618	R.KAGTQIENIEEDFR.N	1650.77152	2	5.52E-06	0.94	4.18	-	930.3
AHQ-4-3, 1913	R.KHEAFESDLAAHQDR.V	1754.84152	2	3.16E-08	0.92	3.91	-	834.5
AHQ-4-5, 1655	R.KHEAFESDLAAHQDR.V	1754.84152	2	6.31E-07	0.89	3.16	-	952.3
AHQ-4-5, 1671	R.KHEAFESDLAAHQDR.V	1754.84152	3	2.18E-08	0.92	5.02	-	964.8
AHQ-4-5, 1673	R.KHEAFESDLAAHQDR.V	1754.84152	2	7.26E-11	0.98	5.32	-	1684.0
AHQ-4-5, 2570	R.KTFTAWCNSHLR.K	1522.71309	2	9.53E-10	0.87	3.45	-	918.6
AHQ-4-5, 4791 - 4863	K.LVSIGAEEIVDGNVK.M	1543.74400	2	2.07E-04	0.93	4.08	-	1172.5
AHQ-4-5, 4662 - 4738	K.LVSIGAEEIVDGNVK.M	1543.74400	2	8.32E-07	0.96	4.29	-	1272.0
gi|5031987|ref|NP_005720.1| peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]				3.52E-12	4.23	50.29	41.50	22040.1
AHQ-4-12, 3722 - 3795	R.FPDENFTLK.H	1111.22866	2	1.01E-04	0.80	2.84	-	649.8
AHQ-4-12, 5169 - 5179	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	2	6.58E-09	0.73	3.03	-	426.1
AHQ-4-12, 5151 - 5213	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	6.98E-12	0.94	4.67	-	1333.7
AHQ-4-11, 4949	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	3.52E-12	0.91	4.25	-	987.1
AHQ-4-12, 5429 - 5469	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	3	6.89E-07	0.74	3.36	-	704.8
AHQ-4-12, 5894 - 5967	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	2	7.03E-07	0.97	5.69	-	1218.6
AHQ-4-14-, 5759	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	3	8.95E-05	0.87	4.23	-	838.3
AHQ-4-12, 4699	R.VIPSFMCQAGDFTNHNGTGGK.S	2240.46178	2	2.20E-04	0.82	3.42	-	660.0
gi|5453607|ref|NP_006420.1| chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co				4.12E-12	0.97	10.22	2.60	59366.3
AHQ-4-7, 4990 - 5001	K.LPIGDVATQYFADR.D	1566.73935	2	4.12E-12	0.97	4.32	-	1566.6
gi|5453549|ref|NP_006397.1| thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho				4.28E-12	2.85	30.25	18.50	30539.7
AHQ-4-10, 3452	K.DYGVYLEDSGHTLR.G	1625.72052	2	4.42E-10	0.91	3.32	-	1111.7
AHQ-4-10, 3815	K.HGEVCPAGWKPGSETIIPDPAGK.L	2405.67144	2	1.05E-07	0.96	4.91	-	1448.5
AHQ-4-10, 3809	K.HGEVCPAGWKPGSETIIPDPAGK.L	2405.67144	3	2.29E-05	0.71	3.30	-	748.4
AHQ-4-10, 4504	R.IPLLSDLTHQISK.D	1465.71961	2	4.28E-12	0.98	4.92	-	1938.6
gi|4507149|ref|NP_000445.1| superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult				4.52E-12	3.71	40.38	57.80	15935.7
AHQ-4-12, 5359 - 5363	K.AVCVLKGDGPVQGIINFEQK.E	2174.50602	2	3.22E-06	0.98	5.97	-	1439.2
AHQ-4-12, 4326 - 4339	K.GDGPVQGIINFEQK.E	1502.65366	2	1.30E-09	0.80	2.96	-	589.1
AHQ-4-12, 4870	K.GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR.K	3522.76733	3	1.19E-05	0.95	5.18	-	1291.3
AHQ-4-11, 4661	K.GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR.K	3522.76733	3	7.93E-06	0.96	5.99	-	1274.3
AHQ-4-12, 5939 - 5954	R.HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR.T	3724.02282	3	4.52E-12	0.98	7.58	-	2104.9
AHQ-4-11, 5756	R.HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR.T	3724.02282	3	4.92E-07	0.96	5.99	-	1053.8
gi|28269681|ref|NP_783313.1| NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]				4.85E-12	1.82	20.27	27.00	14852.0
AHQ-4-13-, 6568	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	4.85E-12	0.97	5.32	-	1741.6
AHQ-4-13, 6638 - 6654	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	2.48E-05	0.93	4.26	-	1584.9
AHQ-4-13-, 4908 - 4984	R.VTLNPPGTFLEGVAK.V	1543.78883	2	3.56E-06	0.86	3.15	-	578.3
gi|4557395|ref|NP_000058.1| carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase;				4.90E-12	4.02	50.24	21.50	29245.8
AHQ-4-10, 6383 - 6384	K.AVQQPDGLAVLGIFLK.V	1669.98899	2	3.18E-05	0.93	4.66	-	586.3
AHQ-4-10, 2968	K.EPISVSSEQVLK.F	1316.48265	1	1.75E-04	0.35	2.87	-	224.4
AHQ-4-10, 3800 - 3857	R.ILNNGHAFNVEFDDSQDK.A	2064.15751	2	4.51E-07	0.94	4.54	-	1032.8
AHQ-4-10, 3895 - 3956	R.ILNNGHAFNVEFDDSQDK.A	2064.15751	2	4.19E-09	0.97	4.76	-	1519.3
AHQ-4-10, 3475	K.VVDVLDSIK.T	988.16011	2	1.11E-05	0.80	3.10	-	531.6
AHQ-4-10, 3199 - 3280	K.YAAELHLVHWNTK.Y	1582.78684	2	4.90E-12	0.98	4.83	-	2271.5
gi|4502549|ref|NP_001734.1| calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta				5.17E-12	1.86	20.23	10.70	16837.5
AHQ-4-11, 3965	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	1.52E-06	0.94	4.19	-	1002.9
AHQ-4-11, 4068 - 4146	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	1.44E-04	0.71	2.88	-	614.8
AHQ-4-12, 4083 - 4149	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	7.11E-07	0.91	4.33	-	850.9
AHQ-4-12, 4217 - 4250	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	1.31E-05	0.85	3.94	-	640.1
AHQ-4-12, 3905 - 3974	R.VFDKDGNGYISAAELR.H	1755.90933	2	3.27E-10	0.93	4.58	-	1111.1
AHQ-4-12, 3874	R.VFDKDGNGYISAAELR.H	1755.90933	3	8.76E-04	0.87	3.44	-	1456.4
AHQ-4-12, 3775 - 3841	R.VFDKDGNGYISAAELR.H	1755.90933	2	3.60E-10	0.96	4.62	-	1442.4
AHQ-4-11, 3714 - 3785	R.VFDKDGNGYISAAELR.H	1755.90933	2	5.17E-12	0.95	4.59	-	1197.4
gi|4501891|ref|NP_001093.1| actinin, alpha 1 [Homo sapiens]				5.51E-12	37.60	430.33	52.10	103056.9
AHQ-4-5, 7458 - 7525	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	2.89E-06	0.89	4.85	-	626.2
AHQ-4-5, 7593	R.AAPFNNWMEGAMEDLQDTFIVHTIEEIQGLTTAHEQFK.A	4364.82022	3	6.42E-09	0.93	4.91	-	1087.0
AHQ-4-11, 5056	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.31E-05	0.71	3.83	-	667.6
AHQ-4-5, 5238	K.AGTQIENIEEDFRDGLK.L	1936.06918	3	1.61E-05	0.58	3.39	-	462.6
AHQ-4-5, 5234 - 5257	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	8.42E-05	0.70	4.13	-	616.8
AHQ-4-12, 5298	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.78E-05	0.65	3.94	-	507.4
AHQ-4-5, 4627	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	4.40E-06	0.82	4.37	-	805.3
AHQ-4-6, 5186	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	5.99E-05	0.79	4.18	-	669.0
AHQ-4-1, 5639	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	3.75E-05	0.63	3.91	-	536.8
AHQ-4-4, 5488	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	5.01E-05	0.85	4.54	-	832.2
AHQ-4-5, 6455 - 6461	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	1.73E-06	0.74	3.33	-	654.7
AHQ-4-5, 6438	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	2.87E-10	0.94	4.89	-	844.7
AHQ-4-5, 5397	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	2.09E-10	0.95	5.03	-	675.6
AHQ-4-6, 6383	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.60E-11	0.94	4.76	-	740.7
AHQ-4-5, 3029 - 3031	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	1.54E-04	0.96	4.15	-	1622.2
AHQ-4-5, 3023	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	2.25E-05	0.96	4.15	-	2490.4
AHQ-4-6, 1946	K.ASIHEAWTDGK.E	1215.29697	2	3.58E-07	0.86	2.68	-	973.1
AHQ-4-5, 1853 - 1930	K.ASIHEAWTDGK.E	1215.29697	2	3.99E-05	0.82	2.88	-	794.7
AHQ-4-6, 5626	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.71E-06	0.95	4.64	-	1183.7
AHQ-4-5, 5738 - 5813	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.14E-11	0.97	5.76	-	1276.0
AHQ-4-5, 5217	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	7.13E-08	0.85	3.64	-	630.3
AHQ-4-5, 6117	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	2.80E-08	0.93	3.95	-	973.7
AHQ-4-4, 5872	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.28E-05	0.97	4.67	-	1506.4
AHQ-4-1, 5881	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	4.60E-07	0.94	4.50	-	989.4
AHQ-4-5, 4783 - 4833	K.DGLGFCALIHR.H	1260.44730	2	2.03E-04	0.88	2.89	-	1078.6
AHQ-4-6, 2263	R.DHSGTLGPEEFK.A	1317.38606	2	1.60E-04	0.82	2.67	-	730.2
AHQ-4-5, 3655	K.DYETATLSEIK.A	1270.36761	2	2.01E-04	0.85	2.61	-	1245.7
AHQ-4-5, 3407 - 3477	R.ELPPDQAEYCIAR.M	1563.71392	2	5.35E-07	0.66	2.50	-	168.5
AHQ-4-5, 3315 - 3397	R.ELPPDQAEYCIAR.M	1563.71392	2	2.40E-06	0.66	2.53	-	231.3
AHQ-4-5, 4397	R.ETADTDTADQVMASFK.I	1730.83208	2	5.68E-07	0.96	4.90	-	1403.8
AHQ-4-4, 4558	R.ETADTDTADQVMASFK.I	1730.83208	2	2.84E-06	0.85	3.40	-	734.4
AHQ-4-5, 3790	R.ETADTDTADQVMASFK.I	1730.83208	2	5.17E-07	0.95	4.32	-	1386.3
AHQ-4-13-, 4350	R.ETADTDTADQVMASFK.I	1730.83208	2	2.41E-06	0.97	5.00	-	1520.3
AHQ-4-11, 4236 - 4300	R.ETADTDTADQVMASFK.I	1730.83208	2	5.69E-05	0.82	2.86	-	1022.6
AHQ-4-5, 4518	R.ETADTDTADQVMASFK.I	1730.83208	2	5.44E-04	0.80	2.79	-	895.3
AHQ-4-13, 3335	R.ETADTDTADQVM*ASFK.I	1746.83148	2	9.50E-07	0.93	3.77	-	1087.4
AHQ-4-13-, 3197	R.ETADTDTADQVM*ASFK.I	1746.83148	2	6.03E-06	0.71	3.17	-	447.7
AHQ-4-14-, 4278	R.ETADTDTADQVMASFK.I	1730.83208	2	4.04E-05	0.87	3.73	-	757.3
AHQ-4-1, 4635	R.ETADTDTADQVMASFK.I	1730.83208	2	4.74E-04	0.93	4.17	-	1030.5
AHQ-4-6, 4315 - 4320	R.ETADTDTADQVMASFK.I	1730.83208	2	6.06E-08	0.94	4.49	-	1081.6

AHQ-4-10, 4013	R.ETADTDTADQVMASFK.I	1730.83208	2	1.75E-05	0.86	3.50	-	762.1
AHQ-4-5, 2747 - 2750	K.GISQEQMNEFR.A	1339.45991	1	5.51E-07	0.43	2.93	-	120.4
AHQ-4-5, 2025	K.GISQEQM*NEFR.A	1355.45931	2	2.46E-05	0.69	2.79	-	637.2
AHQ-4-6, 2738	K.GISQEQMNEFR.A	1339.45991	2	1.37E-05	0.82	3.18	-	707.9
AHQ-4-5, 2723 - 2725	K.GISQEQMNEFR.A	1339.45991	2	5.28E-07	0.87	3.15	-	903.7
AHQ-4-4, 2030	R.HRPELIDYGK.L	1228.38202	2	1.69E-04	0.89	3.41	-	612.7
AHQ-4-5, 1790	R.HRPELIDYGK.L	1228.38202	3	7.36E-06	0.93	3.81	-	1138.5
AHQ-4-5, 1770 - 1813	R.HRPELIDYGK.L	1228.38202	2	1.72E-04	0.94	3.99	-	736.5
AHQ-4-2, 5147	K.ICDQWDNLGALTQK.R	1663.83349	2	1.73E-06	0.94	3.43	-	1962.3
AHQ-4-5, 4849 - 4921	K.ICDQWDNLGALTQK.R	1663.83349	2	5.93E-09	0.98	4.81	-	2535.0
AHQ-4-5, 4625	K.ICDQWDNLGALTQK.R	1663.83349	2	4.88E-09	0.96	4.45	-	1585.6
AHQ-4-6, 4830	K.ICDQWDNLGALTQK.R	1663.83349	2	5.12E-06	0.96	3.62	-	2067.8
AHQ-4-4, 5066	K.ICDQWDNLGALTQK.R	1663.83349	2	1.80E-05	0.95	3.95	-	1596.9
AHQ-4-7, 4857	K.ICDQWDNLGALTQK.R	1663.83349	2	7.41E-09	0.97	4.46	-	2341.4
AHQ-4-3, 5129	K.ICDQWDNLGALTQK.R	1663.83349	2	5.56E-07	0.97	4.68	-	2023.9
AHQ-4-5, 5802 - 5877	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	1.25E-07	0.98	6.69	-	1294.5
AHQ-4-10, 5248 - 5313	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	5.33E-05	0.91	3.77	-	918.8
AHQ-4-6, 5795 - 5868	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	1.89E-10	0.91	4.64	-	1223.2
AHQ-4-5, 3902 - 3973	K.ILAGDKNYITMDELR.R	1753.01353	2	5.51E-12	0.96	4.60	-	1222.7
AHQ-4-5, 4813 - 4886	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	2	7.52E-07	0.93	4.16	-	1040.3
AHQ-4-5, 4141	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	3	1.00E-03	0.96	4.36	-	1959.4
AHQ-4-5, 4786	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	3	4.28E-04	0.74	3.56	-	505.5
AHQ-4-5, 4578	R.KAGTQIENIEEDFRDGLK.L	2064.24210	3	8.88E-06	0.93	5.57	-	1357.5
AHQ-4-6, 4734	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	9.91E-08	0.97	4.88	-	1609.5
AHQ-4-1, 5093	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	2.11E-04	0.97	4.62	-	1462.1
AHQ-4-5, 4989	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.19E-07	0.94	4.70	-	854.5
AHQ-4-5, 4330 - 4333	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.22E-10	0.98	5.49	-	1785.9
AHQ-4-8, 4427	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	5.57E-06	0.93	4.13	-	883.9
AHQ-4-4, 4988	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	3.28E-04	0.86	3.85	-	538.0
AHQ-4-5, 4775 - 4801	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	7.63E-09	0.97	5.48	-	1058.9
AHQ-4-9, 3644	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	3.20E-04	0.91	4.27	-	806.7
AHQ-4-5, 4086	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	4.58E-06	0.93	4.32	-	880.7
AHQ-4-6, 2936 - 3018	R.LAILGIHNEVSK.I	1294.52505	2	2.21E-06	0.95	3.63	-	1288.2
AHQ-4-5, 3009	R.LAILGIHNEVSK.I	1294.52505	1	5.06E-05	0.70	2.22	-	566.4
AHQ-4-5, 3005 - 3006	R.LAILGIHNEVSK.I	1294.52505	2	1.20E-06	0.95	4.27	-	1096.4
AHQ-4-6, 3442 - 3514	R.LAILGIHNEVSK.I	1294.52505	2	2.80E-05	0.96	3.49	-	1722.7
AHQ-4-8, 2746	R.LAILGIHNEVSK.I	1294.52505	2	7.31E-08	0.89	2.90	-	941.6
AHQ-4-5, 5953 - 6017	K.LASDLLEWIR.R	1216.41115	2	1.20E-07	0.98	4.82	-	2107.2
AHQ-4-7, 5917	K.LASDLLEWIR.R	1216.41115	2	8.46E-06	0.91	2.89	-	1525.6
AHQ-4-5, 5957 - 6022	K.LASDLLEWIR.R	1216.41115	1	1.69E-04	0.69	2.81	-	477.9
AHQ-4-6, 5910	K.LASDLLEWIR.R	1216.41115	2	2.31E-06	0.95	3.44	-	1957.9
AHQ-4-1, 6282	K.LASDLLEWIR.R	1216.41115	2	2.99E-08	0.96	4.02	-	2003.6
AHQ-4-6, 5922	K.LASDLLEWIR.R	1216.41115	1	5.79E-06	0.27	2.34	-	257.6
AHQ-4-3, 6829	K.LLETIDQLYLEYAK.R	1712.96427	2	8.99E-04	0.91	3.31	-	1142.7
AHQ-4-4, 6786	K.LLETIDQLYLEYAK.R	1712.96427	2	8.29E-04	0.95	3.81	-	1518.5
AHQ-4-7, 6670	K.LLETIDQLYLEYAK.R	1712.96427	2	7.03E-07	0.96	4.35	-	1246.9
AHQ-4-5, 6878 - 6906	K.LLETIDQLYLEYAK.R	1712.96427	2	3.59E-07	0.97	4.43	-	1677.7
AHQ-4-5, 6649 - 6733	K.LLETIDQLYLEYAK.R	1712.96427	2	1.25E-07	0.97	5.36	-	1288.1
AHQ-4-6, 6515 - 6596	K.LLETIDQLYLEYAK.R	1712.96427	2	2.10E-08	0.97	5.66	-	1329.2
AHQ-4-6, 6463 - 6530	K.LLETIDQLYLEYAK.R	1712.96427	2	1.58E-08	0.97	5.38	-	1460.2
AHQ-4-2, 6831	K.LLETIDQLYLEYAK.R	1712.96427	2	6.78E-07	0.95	4.22	-	1258.8
AHQ-4-1, 6714	K.LLETIDQLYLEYAK.R	1712.96427	2	1.25E-05	0.97	4.32	-	1745.7
AHQ-4-5, 6981 - 7046	K.LLETIDQLYLEYAK.R	1712.96427	2	1.78E-04	0.79	2.70	-	645.7
AHQ-4-5, 6782 - 6801	K.LLETIDQLYLEYAK.R	1712.96427	2	7.82E-09	0.97	5.27	-	1460.1
AHQ-4-6, 2355	R.LSNRPAFMPSEGR.M	1462.65941	2	5.76E-05	0.81	3.39	-	638.2
AHQ-4-6, 3740 - 3750	K.MLDAEDIVGTARPDEK.A	1760.94769	2	3.84E-05	0.91	3.93	-	935.9
AHQ-4-4, 3583 - 3584	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	1.23E-04	0.91	3.66	-	951.0
AHQ-4-9, 3413	K.MLDAEDIVGTARPDEK.A	1760.94769	2	5.41E-05	0.85	3.98	-	589.2
AHQ-4-4, 3994	K.MLDAEDIVGTARPDEK.A	1760.94769	2	9.48E-05	0.84	3.57	-	832.9
AHQ-4-6, 3746	K.MLDAEDIVGTARPDEK.A	1760.94769	3	4.20E-07	0.79	3.79	-	544.8
AHQ-4-7, 3702 - 3714	K.MLDAEDIVGTARPDEK.A	1760.94769	2	3.67E-06	0.80	3.82	-	616.6
AHQ-4-8, 3606	K.MLDAEDIVGTARPDEK.A	1760.94769	3	3.42E-09	0.76	3.34	-	605.6
AHQ-4-8, 3597	K.MLDAEDIVGTARPDEK.A	1760.94769	2	3.02E-05	0.93	4.64	-	803.7
AHQ-4-5, 3381 - 3386	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	9.58E-07	0.94	4.39	-	830.5
AHQ-4-5, 3382	K.M*LDAEDIVGTARPDEK.A	1776.94709	3	2.01E-04	0.78	3.25	-	789.4
AHQ-4-1, 3686 - 3753	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	5.19E-04	0.82	3.64	-	447.4
AHQ-4-5, 3813	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	8.04E-05	0.63	3.28	-	443.2
AHQ-4-5, 3793	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.63E-06	0.91	4.35	-	784.8
AHQ-4-6, 5455 - 5526	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.90E-08	0.98	5.95	-	1634.0
AHQ-4-6, 5046 - 5051	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	2.42E-05	0.93	3.87	-	951.0
AHQ-4-6, 5311	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	6.13E-08	0.95	4.22	-	1311.9
AHQ-4-6, 5195 - 5248	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	8.58E-08	0.96	4.77	-	1155.6
AHQ-4-5, 5154	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	6.46E-08	0.96	4.87	-	1194.1
AHQ-4-5, 5250 - 5317	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	3.82E-05	0.82	3.90	-	654.2
AHQ-4-5, 6069 - 6129	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.94E-08	0.92	4.23	-	1125.8
AHQ-4-4, 5816	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	6.61E-04	0.70	3.37	-	499.0
AHQ-4-5, 5986 - 5993	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	3.13E-08	0.97	4.87	-	1558.5
AHQ-4-5, 5407	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.80E-10	0.94	4.45	-	840.5
AHQ-4-5, 5523 - 5554	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	5.74E-08	0.96	4.73	-	1395.8
AHQ-4-1, 5582	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.19E-09	0.84	3.72	-	504.8
AHQ-4-5, 5869 - 5945	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.44E-10	0.97	4.55	-	1707.1
AHQ-4-5, 5555 - 5583	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	8.13E-07	0.98	5.48	-	1832.5
AHQ-4-5, 5621	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	6.61E-06	0.97	5.01	-	1447.6
AHQ-4-5, 5122	K.NVNIQNFHISWK.D	1500.68583	2	2.29E-07	0.95	4.04	-	1250.7
AHQ-4-6, 4459	K.NVNIQNFHISWK.D	1500.68583	2	1.96E-06	0.76	2.71	-	725.4
AHQ-4-5, 4437 - 4513	K.NVNIQNFHISWK.D	1500.68583	2	1.38E-06	0.95	4.02	-	1450.8
AHQ-4-1, 4966	K.NVNIQNFHISWK.D	1500.68583	2	1.22E-06	0.94	4.02	-	1178.0
AHQ-4-5, 3495	K.NYITMDELR.R	1155.30648	2	1.34E-04	0.73	2.63	-	611.8
AHQ-4-5, 4975 - 4977	K.QFGAQANVIGPWIQTK.M	1759.00118	2	2.06E-04	0.65	3.12	-	605.4
AHQ-4-5, 2693	R.QKDYETATLSEIK.A	1526.67030	2	9.01E-05	0.39	2.77	-	201.9
AHQ-4-5, 2895 - 2941	R.TINEVENQILTR.D	1430.58898	2	6.26E-04	0.70	2.67	-	846.5
AHQ-4-4, 3950	R.TINEVENQILTR.D	1430.58898	2	5.10E-05	0.78	3.10	-	826.1
AHQ-4-5, 3509 - 3511	R.TINEVENQILTR.D	1430.58898	2	8.79E-04	0.56	2.72	-	342.0
AHQ-4-5, 3759 - 3839	R.TINEVENQILTR.D	1430.58898	2	8.27E-04	0.74	2.83	-	893.0
AHQ-4-6, 3718 - 3727	R.TINEVENQILTR.D	1430.58898	2	5.36E-08	0.90	3.91	-	858.2
AHQ-4-5, 3770	R.TINEVENQILTR.D	1430.58898	1	3.75E-04	0.27	2.39	-	112.1
AHQ-4-3, 4007	R.TINEVENQILTR.D	1430.58898	2	1.83E-07	0.82	3.51	-	683.2
AHQ-4-1, 4099 - 4102	R.TINEVENQILTR.D	1430.58898	2	5.30E-05	0.90	3.32	-	1074.6
AHQ-4-5, 3946	R.TINEVENQILTR.D	1430.58898	1	5.80E-06	0.27	2.39	-	273.8
AHQ-4-8, 3585 - 3654	R.TINEVENQILTR.D	1430.58898	2	2.09E-05	0.88	3.42	-	840.1
AHQ-4-5, 7026 - 7039	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.57E-04	0.83	3.51	-	1080.2
AHQ-4-3, 6891	R.VGWEQLLTTIAR.T	1387.60894	2	3.54E-04	0.95	4.15	-	1353.1
AHQ-4-6, 6562 - 6578	R.VGWEQLLTTIAR.T	1387.60894	2	2.71E-07	0.97	4.50	-	1919.9
AHQ-4-1, 6831	R.VGWEQLLTTIAR.T	1387.60894	2	3.18E-06	0.90	3.27	-	1099.0
AHQ-4-7, 6590	R.VGWEQLLTTIAR.T	1387.60894	2	8.14E-09	0.95	4.00	-	1395.2
AHQ-4-14-, 6365	R.VGWEQLLTTIAR.T	1387.60894	2	4.74E-08	0.94	3.98	-	1306.9
AHQ-4-9, 5976 - 5981	R.VGWEQLLTTIAR.T	1387.60894	2	4.82E-07	0.96	4.45	-	1616.3

AHQ-4-11, 6272 - 6273	R.VGWEQLLTTIAR.T	1387.60894	2	1.17E-06	0.93	3.65	-	1362.5
AHQ-4-2, 6923	R.VGWEQLLTTIAR.T	1387.60894	2	8.23E-11	0.94	4.07	-	1193.6
AHQ-4-5, 6621 - 6690	R.VGWEQLLTTIAR.T	1387.60894	2	8.46E-07	0.97	4.86	-	1902.2
AHQ-4-10, 5948	R.VGWEQLLTTIAR.T	1387.60894	2	9.36E-06	0.94	3.76	-	1366.5
AHQ-4-8, 6278	R.VGWEQLLTTIAR.T	1387.60894	2	2.93E-07	0.90	3.48	-	1064.4
AHQ-4-4, 6863 - 6890	R.VGWEQLLTTIAR.T	1387.60894	2	7.65E-09	0.94	3.81	-	1417.0
AHQ-4-8, 3817	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	9.12E-05	0.94	4.44	-	1001.8
AHQ-4-5, 3419 - 3491	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.56E-09	0.97	5.39	-	1447.0
AHQ-4-4, 3619 - 3655	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.58E-07	0.90	4.03	-	833.8
AHQ-4-5, 3591 - 3665	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.60E-10	0.96	5.17	-	1006.2
AHQ-4-7, 4058	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.13E-04	0.95	4.92	-	1106.0
AHQ-4-3, 4416	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.17E-04	0.60	3.05	-	537.3
AHQ-4-5, 4097 - 4165	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.19E-09	0.97	5.83	-	1593.5
AHQ-4-5, 4233 - 4307	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.01E-10	0.96	5.00	-	1205.3
AHQ-4-5, 4377 - 4449	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	9.18E-12	0.96	5.13	-	1274.6
AHQ-4-5, 4537	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.91E-08	0.96	4.79	-	1308.3
AHQ-4-5, 4622	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	6.35E-08	0.96	4.69	-	1401.7
AHQ-4-6, 3416	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.13E-07	0.95	4.32	-	1138.0
AHQ-4-1, 4473	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.92E-10	0.93	4.27	-	1187.1
AHQ-4-6, 4432 - 4512	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.83E-10	0.96	4.87	-	1026.4
AHQ-4-1, 3749	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	4.99E-04	0.94	4.46	-	1049.1
AHQ-4-6, 4078	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.37E-07	0.96	4.95	-	1131.6
gi|4758606|ref|NP_004508.1| integrin-linked kinase [Homo sapiens]				5.81E-12	8.51	110.28	28.50	51418.9
AHQ-4-10, 5184	R.EVPFADLSNMEIGMK.V	1681.95558	2	9.75E-04	0.57	3.03	-	260.7
AHQ-4-7, 5450	K.FDMIVPILEK.M	1205.49168	2	6.08E-06	0.84	3.25	-	638.0
AHQ-4-7, 5451	K.FDMIVPILEK.M	1205.49168	1	1.04E-04	0.64	2.70	-	572.2
AHQ-4-7, 4770 - 4842	R.GM*AFLHTLEPLIPR.H	1611.93301	2	3.41E-06	0.90	3.44	-	1037.7
AHQ-4-9, 5175	R.GMAFLHTLEPLIPR.H	1595.93361	2	1.49E-05	0.96	5.06	-	971.7
AHQ-4-10, 4620 - 4632	R.GM*AFLHTLEPLIPR.H	1611.93301	2	4.34E-05	0.87	3.82	-	627.6
AHQ-4-7, 2207 - 2210	K.LNENHSGELWK.G	1327.42732	2	7.78E-06	0.71	3.17	-	529.1
AHQ-4-7, 2205	K.LNENHSGELWK.G	1327.42732	1	2.41E-08	0.70	2.34	-	550.2
AHQ-4-7, 1985 - 1987	K.LNENHSGELWK.G	1327.42732	2	1.79E-05	0.82	3.71	-	647.3
AHQ-4-7, 6231	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	7.71E-10	0.94	4.91	-	1338.6
AHQ-4-7, 6014 - 6017	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	1.03E-11	0.97	5.66	-	1763.1
AHQ-4-13, 4382 - 4421	R.M*YAPAWVAPEALQK.K	1591.85542	2	4.91E-08	0.93	4.05	-	793.8
AHQ-4-10, 3856 - 3919	R.M*YAPAWVAPEALQK.K	1591.85542	2	6.48E-04	0.84	3.41	-	542.6
AHQ-4-11, 4569	R.MYAPAWVAPEALQK.K	1575.85602	2	1.15E-06	0.85	3.22	-	694.3
AHQ-4-7, 1549	K.SRDFNEECPR.L	1311.36321	2	6.37E-04	0.49	2.62	-	230.5
AHQ-4-7, 4253 - 4323	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	2	7.71E-04	0.95	5.07	-	732.4
AHQ-4-13, 4688	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	2	8.79E-05	0.87	3.55	-	595.4
AHQ-4-7, 4255 - 4270	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	3	5.81E-12	0.94	4.57	-	961.8
AHQ-4-7, 2662	R.WQGNDIVVK.V	1059.20012	1	8.85E-05	0.35	2.01	-	483.3
gi|4759212|ref|NP_004598.1| beta-tubulin cofactor A [Homo sapiens]				6.64E-12	2.86	30.31	26.90	12854.8
AHQ-4-13, 3651	R.ILENEKDLEEAEEYK.E	1852.97372	2	3.62E-04	0.95	4.06	-	1378.2
AHQ-4-13-, 3341	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	6.64E-12	0.97	6.24	-	1431.6
AHQ-4-13, 3481	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	6.38E-06	0.87	4.11	-	576.5
AHQ-4-13, 3478	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	1.26E-08	0.95	5.47	-	1228.9
AHQ-4-13, 3502	R.RLEAAYLDLQR.I	1348.53280	2	1.98E-07	0.94	4.12	-	872.6
gi|5031857|ref|NP_005557.1| lactate dehydrogenase A [Homo sapiens]				8.11E-12	5.77	70.29	23.80	36688.5
AHQ-4-9, 6667	K.DDVFLSVPCILGQNGISDLVK.V	2291.60655	2	1.81E-05	0.63	3.27	-	275.0
AHQ-4-9, 6419	K.DLADELALVDVIEDK.L	1658.82864	2	8.40E-07	0.91	3.77	-	1246.3
AHQ-4-13, 6788 - 6793	K.DLADELALVDVIEDK.L	1658.82864	2	2.96E-10	0.98	5.61	-	1674.2
AHQ-4-14-, 6579	K.DLADELALVDVIEDK.L	1658.82864	2	5.69E-05	0.94	4.10	-	1327.2
AHQ-4-13-, 6688 - 6693	K.DLADELALVDVIEDK.L	1658.82864	2	8.11E-12	0.98	5.89	-	1831.5
AHQ-4-9, 6629	K.DLADELALVDVIEDKLK.G	1900.15980	2	2.01E-09	0.96	5.17	-	1197.0
AHQ-4-9, 6656	K.GLYGIKDDVFLSVPCILGQNGISDLVK.V	2923.37318	2	6.62E-06	0.83	3.78	-	390.4
AHQ-4-13, 2923	K.LVIITAGAR.Q	914.12760	2	4.76E-04	0.90	3.25	-	925.5
AHQ-4-9, 2120	K.TLHPDLGTDKDKEQWK.E	1912.09245	2	3.83E-06	0.62	2.74	-	431.3
AHQ-4-11, 2028	K.VTLTSEEEAR.L	1135.20693	2	3.20E-04	0.85	2.51	-	1138.7
gi|4504745|ref|NP_000410.1| integrin alpha 2b precursor [Homo sapiens]				8.16E-12	31.60	380.33	40.70	113374.2
AHQ-4-4, 1662 - 1726	R.AEAQVELR.G	916.01408	2	6.38E-04	0.84	2.95	-	965.9
AHQ-4-4, 1642 - 1755	R.AEAQVELR.G	916.01408	1	2.36E-05	0.31	2.37	-	234.1
AHQ-4-7, 5107	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.56E-07	0.92	4.40	-	700.2
AHQ-4-10, 4713	R.AEGGQCPSLLFDLR.D	1564.74505	2	9.55E-07	0.94	4.23	-	1025.2
AHQ-4-11, 5006	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.84E-05	0.93	4.24	-	787.4
AHQ-4-5, 5150 - 5206	R.AEGGQCPSLLFDLR.D	1564.74505	2	9.13E-05	0.86	3.17	-	732.3
AHQ-4-3, 5433	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.83E-05	0.92	3.73	-	849.3
AHQ-4-4, 5570 - 5582	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.98E-08	0.95	4.04	-	1179.5
AHQ-4-4, 5356 - 5439	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.47E-10	0.95	4.93	-	938.8
AHQ-4-6, 5095 - 5123	R.AEGGQCPSLLFDLR.D	1564.74505	2	7.08E-05	0.91	3.43	-	901.3
AHQ-4-13-, 5198	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.33E-06	0.86	3.14	-	713.6
AHQ-4-4, 5006	R.AEGGQCPSLLFDLRDETR.N	2066.23814	2	7.49E-04	0.27	2.99	-	263.4
AHQ-4-4, 4892	R.AEGGQCPSLLFDLRDETR.N	2066.23814	3	4.97E-07	0.88	3.79	-	951.7
AHQ-4-4, 2707 - 2783	R.ALSNVEGFER.L	1122.21308	1	5.90E-07	0.06	2.03	-	59.8
AHQ-4-6, 2578	R.ALSNVEGFER.L	1122.21308	2	1.14E-05	0.86	2.87	-	854.2
AHQ-4-3, 2745	R.ALSNVEGFER.L	1122.21308	2	1.38E-06	0.87	3.04	-	897.9
AHQ-4-2, 2776	R.ALSNVEGFER.L	1122.21308	2	4.92E-05	0.86	3.47	-	760.2
AHQ-4-4, 3102	R.ALSNVEGFER.L	1122.21308	1	5.53E-05	0.27	2.51	-	206.0
AHQ-4-4, 2696 - 2738	R.ALSNVEGFER.L	1122.21308	2	8.60E-04	0.87	3.18	-	820.8
AHQ-4-5, 4917 - 4933	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	4.93E-06	0.90	3.82	-	1049.1
AHQ-4-5, 5019 - 5090	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	5.98E-04	0.72	3.05	-	724.7
AHQ-4-4, 5094 - 5163	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	4.10E-05	0.92	4.58	-	853.2
AHQ-4-4, 5234 - 5303	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	4.86E-06	0.93	4.29	-	898.0
AHQ-4-4, 5524 - 5530	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	4.03E-05	0.87	3.84	-	674.4
AHQ-4-4, 3431	R.DETRNVGSQTLQTFK.A	1724.85363	2	1.02E-07	0.56	2.76	-	426.7
AHQ-4-4, 2994	R.DETRNVGSQTLQTFK.A	1724.85363	2	2.47E-05	0.85	3.27	-	977.4
AHQ-4-3, 4028	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.42E-04	0.89	3.94	-	759.1
AHQ-4-4, 4151	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.35E-04	0.89	4.24	-	578.8
AHQ-4-2, 4046	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.01E-09	0.92	4.00	-	835.9
AHQ-4-4, 4547	R.FGSAIAPLGDLDR.D	1332.48700	1	1.17E-04	0.84	3.30	-	566.5
AHQ-4-4, 4538 - 4540	R.FGSAIAPLGDLDR.D	1332.48700	2	1.06E-07	0.90	3.77	-	904.0
AHQ-4-7, 5626 - 5698	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.14E-04	0.87	3.87	-	1022.5
AHQ-4-3, 6175 - 6245	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	8.07E-08	0.84	3.99	-	791.1
AHQ-4-5, 5790 - 5857	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	9.88E-08	0.91	4.92	-	737.1
AHQ-4-3, 5999 - 6069	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	3.72E-06	0.90	4.51	-	911.9
AHQ-4-5, 6001 - 6075	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.75E-06	0.72	3.21	-	622.9
AHQ-4-4, 5839 - 5907	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.41E-06	0.92	4.74	-	684.9
AHQ-4-4, 6174 - 6243	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	6.19E-05	0.78	3.50	-	945.1
AHQ-4-1, 5989 - 6069	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	6.40E-04	0.86	4.20	-	700.5
AHQ-4-4, 5974 - 6042	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.67E-08	0.84	4.23	-	730.1
AHQ-4-7, 5697 - 5775	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.11E-05	0.56	3.55	-	574.2
AHQ-4-4, 6999 - 7063	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	2.54E-08	0.89	4.49	-	883.9
AHQ-4-4, 7575 - 7634	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.78E-05	0.80	3.83	-	326.2
AHQ-4-4, 6930 - 6950	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.60E-06	0.92	4.68	-	473.6
AHQ-4-4, 7436 - 7508	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	7.93E-07	0.94	5.13	-	544.4
AHQ-4-4, 7351 - 7415	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	9.87E-07	0.92	4.68	-	512.8
AHQ-4-4, 7218 - 7283	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.78E-07	0.91	4.50	-	571.2

AHQ-4-4, 6795 - 6866	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	9.42E-05	0.93	4.27	-	781.2
AHQ-4-4, 6662 - 6726	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.29E-06	0.95	5.04	-	794.3
AHQ-4-4, 6376 - 6442	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.47E-07	0.91	4.21	-	572.5
AHQ-4-4, 7027 - 7092	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	9.27E-08	0.94	5.11	-	483.2
AHQ-4-4, 7130 - 7194	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.58E-06	0.96	5.35	-	835.9
AHQ-4-11, 4752	R.GEAQVWTQLLR.A	1301.47614	2	3.97E-07	0.94	4.23	-	1154.8
AHQ-4-1, 5286	R.GEAQVWTQLLR.A	1301.47614	2	6.65E-05	0.91	3.47	-	1136.8
AHQ-4-10, 4425 - 4451	R.GEAQVWTQLLR.A	1301.47614	2	9.56E-07	0.95	4.31	-	1168.0
AHQ-4-4, 5634 - 5706	R.GNSFPASLVVAAEEGER.E	1733.86053	2	6.76E-10	0.94	4.73	-	892.3
AHQ-4-4, 5490 - 5563	R.GNSFPASLVVAAEEGER.E	1733.86053	2	2.08E-09	0.92	4.44	-	645.8
AHQ-4-4, 5352 - 5423	R.GNSFPASLVVAAEEGER.E	1733.86053	2	7.90E-05	0.84	3.78	-	613.6
AHQ-4-11, 5304 - 5377	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.46E-09	0.76	2.97	-	721.6
AHQ-4-4, 5910	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.28E-11	0.95	4.14	-	1218.0
AHQ-4-4, 6859	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	2	2.02E-05	0.35	2.50	-	301.3
AHQ-4-4, 6835 - 6903	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	8.29E-09	0.78	4.11	-	401.6
AHQ-4-4, 6564 - 6643	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	2.74E-09	0.72	3.66	-	296.1
AHQ-4-4, 6696 - 6770	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	5.01E-05	0.92	5.12	-	510.4
AHQ-4-1, 5451	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	3.97E-04	0.92	3.78	-	1272.5
AHQ-4-5, 4957	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.03E-08	0.94	4.63	-	820.8
AHQ-4-4, 5047	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.28E-07	0.95	4.85	-	721.3
AHQ-4-6, 4918	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	8.58E-05	0.93	4.88	-	605.5
AHQ-4-1, 5445 - 5453	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	6.51E-07	0.97	5.81	-	908.5
AHQ-4-4, 5179 - 5224	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	1.65E-04	0.90	4.03	-	1256.1
AHQ-4-4, 5171 - 5242	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.92E-06	0.97	5.42	-	1024.1
AHQ-4-7, 4737	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	4.65E-06	0.93	4.28	-	937.5
AHQ-4-3, 5233 - 5304	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.11E-06	0.96	5.30	-	886.9
AHQ-4-4, 5070 - 5139	R.GQVLVFLGQSEGLR.S	1503.72793	2	2.18E-07	0.97	5.78	-	1312.4
AHQ-4-1, 5227	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.27E-08	0.96	4.94	-	1235.7
AHQ-4-4, 5180 - 5251	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.16E-08	0.97	5.05	-	1517.5
AHQ-4-3, 5151	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.21E-08	0.97	4.92	-	1394.3
AHQ-4-4, 5368 - 5440	R.GQVLVFLGQSEGLR.S	1503.72793	2	8.77E-05	0.88	3.03	-	1185.1
AHQ-4-3, 4473	R.HDLLVGAPLYMESR.A	1601.85188	2	1.69E-06	0.93	2.99	-	1404.7
AHQ-4-6, 4095	R.HDLLVGAPLYMESR.A	1601.85188	2	6.26E-06	0.91	3.52	-	934.1
AHQ-4-5, 4155	R.HDLLVGAPLYMESR.A	1601.85188	2	1.10E-07	0.96	4.35	-	1441.4
AHQ-4-4, 4382	R.HDLLVGAPLYMESR.A	1601.85188	2	5.17E-10	0.97	4.92	-	1539.8
AHQ-4-4, 3618 - 3630	K.HSPICHTTMAFLR.D	1572.83705	2	3.40E-09	0.76	2.93	-	370.1
AHQ-4-4, 2960 - 2995	K.HSPICHTTM*AFLR.D	1588.83645	2	2.99E-04	0.76	2.66	-	613.5
AHQ-4-3, 3668	K.HSPICHTTMAFLR.D	1572.83705	2	1.25E-09	0.68	2.70	-	399.5
AHQ-4-11, 4168	K.IVLLDVPVR.A	1024.28196	2	9.42E-04	0.90	3.87	-	742.5
AHQ-4-5, 4183	K.IVLLDVPVR.A	1024.28196	2	7.88E-04	0.87	3.50	-	743.7
AHQ-4-12, 4305	K.IVLLDVPVR.A	1024.28196	2	3.71E-05	0.92	3.37	-	1086.1
AHQ-4-3, 4501	K.IVLLDVPVR.A	1024.28196	2	1.74E-04	0.84	3.27	-	780.6
AHQ-4-6, 4111	K.IVLLDVPVR.A	1024.28196	2	4.82E-04	0.87	3.61	-	767.8
AHQ-4-4, 4390 - 4464	K.IVLLDVPVR.A	1024.28196	2	3.04E-05	0.94	3.58	-	1276.3
AHQ-4-4, 4499	R.IYVENDFSWDK.R	1416.51610	2	7.69E-08	0.89	3.34	-	848.8
AHQ-4-4, 4508 - 4512	R.IYVENDFSWDK.R	1416.51610	1	3.06E-06	0.33	2.12	-	315.6
AHQ-4-4, 4179 - 4183	R.IYVENDFSWDKR.Y	1572.70245	2	5.71E-10	0.90	3.95	-	1006.8
AHQ-4-4, 3962 - 4038	R.IYVENDFSWDKR.Y	1572.70245	2	1.99E-07	0.96	4.07	-	1456.6
AHQ-4-10, 5483 - 5489	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	1.11E-04	0.71	3.31	-	348.4
AHQ-4-10, 6351 - 6353	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	1.63E-05	0.56	2.92	-	230.3
AHQ-4-10, 6203	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	2.13E-04	0.68	3.03	-	273.8
AHQ-4-10, 6199 - 6261	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	7.80E-06	0.94	5.25	-	428.1
AHQ-4-4, 4862	K.LSLNAELQLDR.Q	1272.43310	2	4.60E-06	0.95	4.00	-	1509.1
AHQ-4-4, 4698	K.LSLNAELQLDR.Q	1272.43310	2	7.63E-08	0.92	3.92	-	982.8
AHQ-4-4, 4780	K.LSLNAELQLDR.Q	1272.43310	2	1.83E-07	0.90	3.64	-	1013.3
AHQ-4-4, 4563	K.LSLNAELQLDR.Q	1272.43310	2	3.99E-05	0.75	2.88	-	662.5
AHQ-4-12, 2763	R.NVGSQTLQTFK.A	1223.36055	2	2.88E-06	0.91	3.64	-	628.5
AHQ-4-5, 2537 - 2541	R.NVGSQTLQTFK.A	1223.36055	2	1.56E-09	0.90	3.69	-	522.7
AHQ-4-6, 2566 - 2567	R.NVGSQTLQTFK.A	1223.36055	2	3.88E-06	0.89	3.59	-	576.4
AHQ-4-4, 3230	R.NVGSQTLQTFK.A	1223.36055	1	4.12E-05	0.10	2.00	-	205.3
AHQ-4-4, 2686 - 2754	R.NVGSQTLQTFK.A	1223.36055	2	3.97E-05	0.91	3.63	-	565.5
AHQ-4-7, 2493	R.NVGSQTLQTFK.A	1223.36055	2	1.35E-04	0.89	3.53	-	612.0
AHQ-4-4, 6638 - 6702	R.PSQVLDSPFPTGSAFGFSLR.G	2111.34205	2	6.20E-07	0.95	4.92	-	968.5
AHQ-4-10, 4437	R.QIFLPEPEQPSR.L	1441.61346	1	1.59E-04	0.21	2.16	-	244.3
AHQ-4-4, 5842	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	9.51E-04	0.37	2.54	-	278.2
AHQ-4-13, 5996	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.98E-04	0.96	4.42	-	1996.0
AHQ-4-6, 5887 - 5950	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	6.72E-05	0.88	4.47	-	1015.4
AHQ-4-4, 6270 - 6351	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	4.75E-09	0.96	5.31	-	694.2
AHQ-4-5, 5921 - 5922	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.40E-10	0.97	6.60	-	1322.3
AHQ-4-4, 6138 - 6206	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.75E-09	0.96	6.46	-	1086.8
AHQ-4-4, 6135 - 6203	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	7.79E-04	0.90	4.46	-	505.6
AHQ-4-4, 6234 - 6255	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.32E-08	0.96	5.76	-	1470.2
AHQ-4-3, 6243	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.89E-11	0.96	6.18	-	1190.1
AHQ-4-1, 6257	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	4.49E-07	0.96	5.79	-	1368.9
AHQ-4-4, 6356	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.96E-07	0.95	5.40	-	1166.8
AHQ-4-4, 3627 - 3698	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	3.11E-05	0.88	4.02	-	477.4
AHQ-4-4, 3842	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	6.44E-05	0.76	3.09	-	422.0
AHQ-4-10, 3368 - 3369	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.80E-06	0.94	4.75	-	666.1
AHQ-4-7, 3411	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	6.42E-06	0.81	3.52	-	502.4
AHQ-4-11, 3518 - 3522	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	3.92E-06	0.92	4.19	-	742.8
AHQ-4-5, 3499	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	4.20E-07	0.91	4.29	-	534.6
AHQ-4-4, 3279 - 3352	K.TEEAEKTPVGSCFLAQPESGRR.A	2451.65537	3	7.58E-04	0.63	3.42	-	346.1
AHQ-4-13-, 5472 - 5536	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	6.21E-05	0.89	3.50	-	993.0
AHQ-4-6, 5474 - 5494	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.53E-05	0.95	4.32	-	1178.1
AHQ-4-7, 5446	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.33E-07	0.95	4.90	-	948.9
AHQ-4-3, 5753 - 5823	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.17E-05	0.96	5.01	-	1170.0
AHQ-4-11, 5250 - 5332	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.27E-06	0.93	4.42	-	1194.9
AHQ-4-4, 5690 - 5772	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.87E-06	0.97	5.56	-	1100.2
AHQ-4-12, 5533	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	5.97E-06	0.94	4.33	-	998.3
AHQ-4-4, 5838 - 5906	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.42E-07	0.87	3.87	-	834.7
AHQ-4-5, 5550	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.28E-06	0.95	4.83	-	969.5
AHQ-4-1, 5790 - 5854	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.50E-07	0.95	5.28	-	933.4
AHQ-4-10, 4919 - 4991	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.13E-06	0.93	4.56	-	909.1
AHQ-4-5, 3597	K.TPVGSCFLAQPESGR.R	1607.76993	2	5.96E-06	0.93	4.06	-	881.5
AHQ-4-7, 3510	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.36E-05	0.90	3.89	-	631.9
AHQ-4-4, 3746 - 3747	K.TPVGSCFLAQPESGR.R	1607.76993	2	6.07E-07	0.93	4.37	-	794.2
AHQ-4-3, 3793 - 3816	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.65E-05	0.95	4.28	-	1060.2
AHQ-4-4, 3932	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.94E-07	0.85	3.45	-	641.0
AHQ-4-6, 3518	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.54E-07	0.86	3.22	-	799.5
AHQ-4-2, 3843 - 3851	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.91E-06	0.93	3.97	-	844.7
AHQ-4-10, 3404	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.23E-07	0.83	3.24	-	616.0
AHQ-4-1, 3901	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.25E-06	0.93	3.98	-	1060.1
AHQ-4-12, 3673	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.62E-06	0.89	3.14	-	1004.8
AHQ-4-6, 4331	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	3.27E-06	0.88	3.69	-	1138.7
AHQ-4-4, 4874 - 4875	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	3.73E-06	0.75	3.59	-	559.5
AHQ-4-4, 4876	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	3.43E-06	0.96	5.60	-	1422.7
AHQ-4-4, 5074	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	4.67E-04	0.95	4.83	-	1192.8

AHQ-4-4, 5175 - 5254	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	2.49E-06	0.95	5.11	-	1481.9
AHQ-4-4, 5479	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.66E-04	0.94	4.93	-	1146.8
AHQ-4-4, 4690	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	8.16E-12	0.92	4.20	-	1385.8
AHQ-4-4, 4595 - 4615	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	1.90E-07	0.98	6.48	-	2968.5
AHQ-4-5, 2338	R.VAIVVGAPR.T	882.08560	2	1.41E-05	0.94	3.40	-	1356.8
AHQ-4-13, 2734	R.VAIVVGAPR.T	882.08560	2	1.01E-04	0.93	3.34	-	1278.9
AHQ-4-6, 2338	R.VAIVVGAPR.T	882.08560	2	1.55E-06	0.89	3.20	-	1019.2
AHQ-4-4, 2472	R.VAIVVGAPR.T	882.08560	2	1.36E-07	0.94	3.62	-	1367.3
AHQ-4-13-, 2629	R.VAIVVGAPR.T	882.08560	2	7.83E-07	0.93	3.04	-	1406.0
AHQ-4-12, 2531	R.VAIVVGAPR.T	882.08560	2	5.14E-05	0.92	3.36	-	1159.8
AHQ-4-4, 6894 - 6956	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.15E-07	0.97	5.79	-	1353.3
AHQ-4-4, 6764 - 6830	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.54E-08	0.97	5.38	-	1625.5
AHQ-4-4, 6534 - 6607	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.04E-05	0.96	5.36	-	1401.9
AHQ-4-4, 7028 - 7103	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.10E-11	0.97	5.73	-	1268.6
AHQ-4-4, 6058 - 6100	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.74E-05	0.93	4.99	-	854.5
AHQ-4-4, 5915 - 5987	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	3.51E-07	0.95	4.59	-	1205.2
AHQ-4-4, 5831 - 5899	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.07E-05	0.98	5.90	-	1920.3
AHQ-4-4, 7166 - 7230	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	8.90E-11	0.98	6.14	-	2203.3
AHQ-4-4, 7300 - 7380	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.66E-04	0.96	5.18	-	1269.1
AHQ-4-4, 7527 - 7590	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.15E-06	0.96	5.22	-	1268.5
AHQ-4-3, 6145	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.19E-04	0.89	4.09	-	719.6
AHQ-4-4, 6248 - 6314	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.99E-04	0.96	5.43	-	998.4
AHQ-4-4, 6960 - 7022	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	7.17E-11	0.98	6.64	-	2102.5
AHQ-4-4, 6155 - 6178	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.82E-07	0.98	6.47	-	1573.1
AHQ-4-6, 3894 - 3899	R.VVLCELGNPMK.K	1261.53692	2	3.73E-06	0.94	3.87	-	1185.0
AHQ-4-6, 3108	R.VVLCELGNPM*K.K	1277.53632	2	5.95E-04	0.77	2.62	-	968.1
AHQ-4-4, 4147	R.VVLCELGNPMK.K	1261.53692	1	3.66E-07	0.83	3.43	-	732.5
AHQ-4-4, 4135	R.VVLCELGNPMK.K	1261.53692	2	4.88E-05	0.95	4.11	-	1290.0
AHQ-4-4, 3316	R.VVLCELGNPM*K.K	1277.53632	2	1.57E-04	0.90	3.80	-	1005.3
AHQ-4-5, 3977 - 4001	R.VVLCELGNPMK.K	1261.53692	2	1.08E-04	0.95	3.84	-	1317.1
AHQ-4-5, 3154	R.VVLCELGNPM*K.K	1277.53632	2	4.87E-04	0.75	2.97	-	678.5
AHQ-4-4, 4150	R.VYLFLQPR.G	1036.25129	2	2.71E-06	0.96	4.01	-	1401.5
AHQ-4-3, 4241	R.VYLFLQPR.G	1036.25129	2	4.91E-06	0.94	3.60	-	1120.4
AHQ-4-6, 3876	R.VYLFLQPR.G	1036.25129	2	3.45E-05	0.94	3.54	-	1294.2
AHQ-4-5, 3911 - 3925	R.VYLFLQPR.G	1036.25129	2	3.79E-05	0.96	4.02	-	1206.2
gi|27498332|ref|XP_212565.1| similar to tubulin, beta 5 [Homo sapiens]				8.36E-12	4.64	50.25	9.90	49670.5
AHQ-4-8, 5187	R.ALTVPELTQQVFDAK.N	1660.89259	2	3.79E-09	0.86	3.46	-	389.8
AHQ-4-11, 5408 - 5470	R.ALTVPELTQQVFDAK.N	1660.89259	2	1.06E-05	0.72	3.01	-	377.8
AHQ-4-7, 3279 - 3286	R.IM*NTFSVVPSPK.V	1336.58217	2	1.23E-08	0.92	3.48	-	1036.3
AHQ-4-7, 3755	R.IMNTFSVVPSPK.V	1320.58277	2	2.04E-09	0.95	3.40	-	1433.7
AHQ-4-7, 3541 - 3573	R.IMNTFSVVPSPK.V	1320.58277	2	9.69E-05	0.97	4.21	-	1943.6
AHQ-4-7, 7121	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	2.84E-06	0.86	3.55	-	562.0
AHQ-4-7, 7206 - 7281	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	2.19E-10	0.95	4.87	-	952.2
AHQ-4-7, 6974 - 7054	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	3.17E-04	0.89	3.73	-	992.5
AHQ-4-9, 5849	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.51E-04	0.68	2.88	-	435.5
AHQ-4-7, 6918 - 6934	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	8.36E-12	0.97	4.79	-	1472.5
AHQ-4-12, 6702	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.79E-08	0.94	4.43	-	923.4
AHQ-4-13, 6410	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	7.90E-05	0.95	4.61	-	1191.6
AHQ-4-13, 6717 - 6722	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	6.62E-11	0.97	4.96	-	1222.3
AHQ-4-13-, 6318	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	4.38E-07	0.94	4.46	-	928.6
AHQ-4-13-, 6537 - 6608	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	9.93E-04	0.61	3.08	-	413.7
AHQ-4-14-, 6191 - 6205	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.02E-05	0.96	4.54	-	1090.2
AHQ-4-14-, 6386 - 6401	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.47E-04	0.91	4.40	-	729.2
AHQ-4-14-, 6487	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	6.84E-06	0.90	3.61	-	694.7
AHQ-4-14-, 6526	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	7.68E-04	0.88	3.74	-	719.2
gi|4507643|ref|NP_003279.1| tumor protein D52-like 2; hD54 [Homo sapiens]				8.41E-12	0.96	10.28	14.60	22209.6
AHQ-4-10, 6488	R.TPAVEGLTEAEEEELRAELTKVEEEIVTLR.Q	3385.71879	3	8.41E-12	0.96	5.66	-	1125.0
gi|27500274|ref|XP_113950.3| similar to Munc13-4 protein [Homo sapiens]				1.01E-11	5.98	70.28	10.80	123281.1
AHQ-4-5, 7541	K.AFGELCPNTAPLPQLVTEALQTGTTEWFHLK.Q	3472.91108	3	1.34E-05	0.75	3.51	-	474.5
AHQ-4-4, 6556	R.ALLYEDALYTVLHR.L	1677.92484	2	5.94E-10	0.96	4.77	-	1326.6
AHQ-4-4, 4928 - 4930	R.AVQM*DELVPLGELTK.H	1659.92638	2	5.79E-08	0.70	2.89	-	491.3
AHQ-4-4, 3974	R.CREDQWYPLEPR.T	1650.79650	2	5.68E-05	0.81	3.28	-	590.0
AHQ-4-6, 4351	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	3.23E-04	0.78	3.10	-	1054.4
AHQ-4-4, 4732	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	2.01E-10	0.98	5.60	-	2231.1
AHQ-4-5, 4399	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	1.01E-11	0.95	4.97	-	1501.4
AHQ-4-4, 5548 - 5558	K.LPAQLAWEALEQR.V	1525.73360	2	1.53E-11	0.97	5.03	-	1605.5
AHQ-4-4, 4130	R.SVFPLSVSDSPAR.L	1362.51311	2	1.75E-04	0.82	2.81	-	1142.5
gi|29568101|ref|NP_006467.3| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT				1.03E-11	3.24	40.22	35.90	11400.3
AHQ-4-14-, 4427	R.LATFWYYAK.V	1163.34840	2	1.84E-06	0.82	2.69	-	396.8
AHQ-4-14-, 3590 - 3593	K.TPALVNAAVTYSK.P	1335.53080	2	1.03E-11	0.97	4.49	-	1876.2
AHQ-4-14-, 3498 - 3566	K.TPALVNAAVTYSKPR.L	1588.83283	3	1.92E-08	0.91	3.37	-	1399.5
AHQ-4-14, 4510 - 4577	K.TPALVNAAVTYSKPR.L	1588.83283	3	8.11E-09	0.88	3.34	-	1021.5
AHQ-4-14, 5386 - 5420	K.VELVPPTPAEIPR.A	1418.66294	2	1.03E-04	0.57	2.84	-	375.6
gi|17921989|ref|NP_005991.1| tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain				1.07E-11	11.83	140.24	38.60	49924.1
AHQ-4-12, 4607 - 4679	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	6.26E-04	0.96	4.41	-	2078.6
AHQ-4-14-, 5917	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	7.06E-08	0.93	4.11	-	1137.7
AHQ-4-14-, 5147 - 5226	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	2.30E-08	0.92	4.00	-	1271.5
AHQ-4-13, 5577	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	8.95E-10	0.92	3.77	-	1089.1
AHQ-4-13, 5416	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	2.24E-04	0.84	3.47	-	622.1
AHQ-4-13, 5320	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	7.29E-06	0.97	4.86	-	1710.9
AHQ-4-7, 6889	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	7.91E-06	0.71	3.11	-	475.6
AHQ-4-12, 6033 - 6114	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	8.94E-08	0.94	3.93	-	1479.4
AHQ-4-10, 5565	R.AVFVDLEPTVIDEIR.N	1716.95615	2	7.33E-07	0.88	3.70	-	1173.5
AHQ-4-9, 5575	R.AVFVDLEPTVIDEIR.N	1716.95615	2	5.60E-06	0.84	3.45	-	1137.9
AHQ-4-12, 6066 - 6075	R.AVFVDLEPTVIDEIR.N	1716.95615	2	2.88E-07	0.77	3.04	-	967.5
AHQ-4-7, 6027 - 6099	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.49E-06	0.93	4.17	-	1298.2
AHQ-4-12, 3350	K.DVNAAIAAIK.T	986.14745	2	1.30E-04	0.95	3.62	-	1538.0
AHQ-4-12, 3343 - 3349	K.DVNAAIAAIK.T	986.14745	1	1.29E-04	0.71	2.65	-	820.3
AHQ-4-12, 3019	K.DVNAAIAAIK.T	986.14745	1	2.38E-04	0.76	2.35	-	976.1
AHQ-4-7, 2922	K.DVNAAIAAIK.T	986.14745	1	1.64E-04	0.68	2.47	-	728.9
AHQ-4-7, 3382	K.DVNAAIAAIK.T	986.14745	1	6.06E-07	0.72	2.57	-	740.1
AHQ-4-7, 3150 - 3153	K.DVNAAIAAIK.T	986.14745	1	3.71E-04	0.52	2.20	-	491.5
AHQ-4-11, 3276	K.DVNAAIAAIK.T	986.14745	1	2.29E-04	0.27	1.95	-	571.4
AHQ-4-7, 3038 - 3041	K.FDLMYAK.R	888.06574	1	2.69E-04	0.61	2.58	-	304.0
AHQ-4-7, 4587 - 4667	R.IHFPLATYAPVISAEK.A	1758.05310	2	9.92E-05	0.87	3.44	-	738.0
AHQ-4-7, 4685 - 4766	R.IHFPLATYAPVISAEK.A	1758.05310	2	6.58E-05	0.94	4.23	-	604.2
AHQ-4-10, 4564 - 4629	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.09E-04	0.96	4.40	-	993.1
AHQ-4-1, 5483	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.54E-04	0.92	3.88	-	648.7
AHQ-4-11, 4880 - 4942	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.47E-04	0.88	3.60	-	663.3
AHQ-4-9, 4424	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.01E-04	0.96	4.63	-	924.6
AHQ-4-8, 4433	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.61E-05	0.91	3.92	-	845.5
AHQ-4-8, 4414 - 4485	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.41E-04	0.81	3.08	-	575.9
AHQ-4-14-, 6546	R.LISQIVSSITASLR.F	1488.75471	2	2.43E-09	0.93	4.01	-	975.5
AHQ-4-7, 6945 - 7025	R.LISQIVSSITASLR.F	1488.75471	2	3.46E-10	0.97	4.74	-	1290.6
AHQ-4-7, 7078 - 7141	R.LISQIVSSITASLR.F	1488.75471	2	1.07E-11	0.97	4.70	-	1384.1
AHQ-4-7, 7203	R.LISQIVSSITASLR.F	1488.75471	2	9.16E-08	0.95	4.04	-	1263.0
AHQ-4-10, 6197	R.LISQIVSSITASLR.F	1488.75471	2	3.59E-04	0.50	2.55	-	476.6

AHQ-4-8, 2873	R.NLDIERPTYTNLNR.L	1719.88022	2	1.60E-04	0.44	2.74	-	283.8
AHQ-4-9, 2899	R.NLDIERPTYTNLNR.L	1719.88022	2	2.32E-05	0.73	3.22	-	499.2
AHQ-4-10, 3147	R.NLDIERPTYTNLNR.L	1719.88022	2	7.55E-06	0.40	2.70	-	296.6
AHQ-4-13-, 3440 - 3441	R.NLDIERPTYTNLNR.L	1719.88022	2	7.77E-09	0.70	3.26	-	327.5
AHQ-4-14, 4357	R.NLDIERPTYTNLNR.L	1719.88022	2	3.26E-07	0.42	2.63	-	279.2
AHQ-4-5, 3278	R.NLDIERPTYTNLNR.L	1719.88022	2	5.32E-07	0.42	2.77	-	282.4
AHQ-4-13, 3570	R.NLDIERPTYTNLNR.L	1719.88022	2	2.77E-05	0.67	3.03	-	470.2
AHQ-4-6, 3210	R.NLDIERPTYTNLNR.L	1719.88022	2	6.19E-06	0.66	3.22	-	394.2
AHQ-4-7, 3109 - 3185	R.NLDIERPTYTNLNR.L	1719.88022	2	1.39E-06	0.75	3.76	-	266.2
AHQ-4-12, 5705 - 5730	R.SIQFVDWCPTGFK.V	1586.79232	2	4.20E-08	0.95	3.86	-	1278.6
AHQ-4-13-, 5645 - 5646	R.SIQFVDWCPTGFK.V	1586.79232	2	1.99E-07	0.94	4.49	-	921.6
AHQ-4-3, 6033	R.SIQFVDWCPTGFK.V	1586.79232	2	1.11E-06	0.89	3.10	-	960.5
AHQ-4-13, 5784 - 5788	R.SIQFVDWCPTGFK.V	1586.79232	2	1.20E-05	0.94	4.04	-	947.0
AHQ-4-14-, 5613	R.SIQFVDWCPTGFK.V	1586.79232	2	2.19E-04	0.71	2.62	-	572.9
AHQ-4-7, 5641 - 5711	R.SIQFVDWCPTGFK.V	1586.79232	2	5.48E-06	0.92	3.55	-	957.3
AHQ-4-11, 5505	R.SIQFVDWCPTGFK.V	1586.79232	2	4.37E-04	0.86	2.97	-	877.5
AHQ-4-5, 5787	R.SIQFVDWCPTGFK.V	1586.79232	2	4.64E-04	0.88	3.11	-	994.8
AHQ-4-6, 5696	R.SIQFVDWCPTGFK.V	1586.79232	2	2.32E-04	0.92	3.79	-	781.2
AHQ-4-9, 5200 - 5207	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	9.52E-08	0.85	4.05	-	461.9
AHQ-4-7, 5738	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.60E-08	0.78	3.42	-	460.0
AHQ-4-13-, 5590	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	6.46E-09	0.72	3.18	-	460.0
AHQ-4-13, 5694 - 5734	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.14E-08	0.66	3.28	-	404.6
AHQ-4-12, 5673 - 5674	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.32E-07	0.89	3.91	-	652.6
AHQ-4-14-, 5550	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.43E-09	0.86	3.70	-	563.3
AHQ-4-4, 4691	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	8.72E-04	0.13	2.52	-	166.2
AHQ-4-8, 4034 - 4110	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.53E-04	0.42	2.56	-	314.2
AHQ-4-13, 4558 - 4582	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.46E-06	0.64	3.17	-	372.8
AHQ-4-13, 4441 - 4508	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	6.36E-06	0.62	3.21	-	285.2
AHQ-4-14, 5453 - 5513	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.20E-04	0.80	3.23	-	403.5
AHQ-4-7, 4485	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	5.59E-07	0.64	3.08	-	334.2
AHQ-4-13-, 4340 - 4357	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.61E-07	0.48	3.17	-	275.4
AHQ-4-13-, 4424	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.47E-06	0.70	2.94	-	432.9
AHQ-4-12, 4395 - 4466	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.49E-10	0.81	3.50	-	382.7
AHQ-4-7, 4215 - 4289	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.94E-07	0.77	3.29	-	340.3
AHQ-4-14-, 4277 - 4341	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.01E-06	0.67	3.14	-	315.6
AHQ-4-14-, 4331	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.96E-05	0.81	3.36	-	494.5
AHQ-4-4, 4543 - 4622	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	7.40E-05	0.68	3.51	-	254.7
AHQ-4-11, 4285 - 4353	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.40E-06	0.79	3.33	-	401.3
AHQ-4-12, 3942	K.YM*ACCLLYR.G	1268.50804	2	2.64E-04	0.76	2.57	-	552.7
AHQ-4-7, 4349	K.YMACCLLYR.G	1252.50864	2	3.68E-06	0.94	3.53	-	951.7
AHQ-4-12, 4446	K.YMACCLLYR.G	1252.50864	2	9.42E-06	0.93	2.93	-	1117.0
gi|13994151|ref|NP_066272.1|	PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H			1.23E-11	15.15	180.27	55.00	36071.5
AHQ-4-14-, 6618	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	4.17E-06	0.90	4.49	-	694.4
AHQ-4-14-, 6559 - 6621	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.70E-09	0.88	4.60	-	645.1
AHQ-4-14-, 6414 - 6494	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.09E-07	0.86	4.37	-	410.1
AHQ-4-14-, 5997 - 6021	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	3.42E-05	0.88	4.16	-	683.3
AHQ-4-13, 6680 - 6694	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	9.80E-05	0.78	3.50	-	510.9
AHQ-4-12, 6901	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.23E-11	0.91	5.17	-	572.5
AHQ-4-12, 6678 - 6690	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.19E-04	0.88	4.85	-	410.8
AHQ-4-13-, 6624	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.07E-05	0.83	4.22	-	732.7
AHQ-4-13-, 6742	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	6.64E-11	0.93	4.90	-	802.8
AHQ-4-13-, 3621 - 3646	K.DFEQPLAISR.V	1176.30388	2	1.45E-04	0.87	2.64	-	1048.2
AHQ-4-14, 4582 - 4602	K.DFEQPLAISR.V	1176.30388	2	2.36E-04	0.76	2.82	-	677.1
AHQ-4-13, 3781 - 3792	K.DFEQPLAISR.V	1176.30388	2	8.68E-06	0.90	3.24	-	958.4
AHQ-4-12, 3581	K.DFEQPLAISR.V	1176.30388	2	2.63E-04	0.94	3.43	-	1315.8
AHQ-4-14-, 3553 - 3561	K.DFEQPLAISR.V	1176.30388	2	4.31E-06	0.94	3.94	-	1093.5
AHQ-4-14-, 3557 - 3631	K.DFEQPLAISR.V	1176.30388	1	5.67E-06	0.62	2.47	-	370.0
AHQ-4-14-, 3301	K.GCTDNLTLTVAR.S	1322.47058	2	2.55E-05	0.87	3.72	-	831.2
AHQ-4-13-, 3370 - 3373	K.GCTDNLTLTVAR.S	1322.47058	2	6.09E-04	0.82	3.29	-	751.6
AHQ-4-13, 3518	K.GCTDNLTLTVAR.S	1322.47058	2	5.45E-05	0.74	3.20	-	647.3
AHQ-4-14-, 3861 - 3875	K.GHFFVEDQIYCEK.H	1673.82684	2	8.81E-04	0.96	4.01	-	1377.5
AHQ-4-13, 4144	K.GHFFVEDQIYCEK.H	1673.82684	2	3.64E-04	0.96	3.90	-	1589.0
AHQ-4-12, 3965 - 4037	K.GHFFVEDQIYCEK.H	1673.82684	2	9.31E-07	0.95	4.34	-	1080.7
AHQ-4-12, 3975	K.GHFFVEDQIYCEK.H	1673.82684	3	2.23E-04	0.87	3.89	-	940.1
AHQ-4-13-, 4001 - 4065	K.GHFFVEDQIYCEK.H	1673.82684	2	3.20E-04	0.97	4.77	-	1447.8
AHQ-4-12, 2562	R.HRHPECYVCTDCGTNLK.Q	2151.34648	2	5.56E-04	0.66	3.16	-	305.1
AHQ-4-13-, 2685	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	4.36E-08	0.97	5.46	-	1705.2
AHQ-4-13, 2794	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	7.69E-08	0.96	5.18	-	1346.8
AHQ-4-13, 3371	R.IKGCTDNLTLTVAR.S	1563.80174	2	4.42E-06	0.92	3.81	-	769.1
AHQ-4-14-, 2994	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.11E-10	0.95	4.13	-	1233.7
AHQ-4-13, 3218	R.IKGCTDNLTLTVAR.S	1563.80174	2	6.49E-10	0.92	4.22	-	727.9
AHQ-4-13-, 3242	R.IKGCTDNLTLTVAR.S	1563.80174	2	3.64E-07	0.95	4.19	-	1132.4
AHQ-4-11, 3006	R.IKGCTDNLTLTVAR.S	1563.80174	2	4.38E-09	0.93	3.72	-	1074.8
AHQ-4-12, 3059	R.IKGCTDNLTLTVAR.S	1563.80174	2	6.55E-10	0.94	4.25	-	960.5
AHQ-4-13-, 5214	K.LPMCDKCGTGIVGVFVK.L	1884.27358	3	2.55E-06	0.81	3.67	-	775.4
AHQ-4-12, 4722 - 4774	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	2	6.57E-04	0.89	3.37	-	839.8
AHQ-4-14, 4668 - 4741	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.48E-08	0.96	5.24	-	1166.9
AHQ-4-14-, 3649	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.10E-09	0.94	4.48	-	877.7
AHQ-4-13, 3914	R.LVGGKDFEQPLAISR.V	1630.86972	2	9.41E-10	0.96	5.01	-	1287.2
AHQ-4-13-, 3698 - 3704	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	1.65E-07	0.81	3.51	-	698.3
AHQ-4-13, 3655	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	3.83E-05	0.72	3.06	-	752.9
AHQ-4-13, 3833	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	5.84E-07	0.86	3.46	-	559.3
AHQ-4-12, 3991	K.MNLASEPQEVLHIGSAHNR.S	2104.33619	2	1.01E-05	0.88	4.00	-	559.3
AHQ-4-13-, 6629	K.QSTSFLVLQEILESEEK.G	1981.18977	2	9.32E-08	0.97	5.01	-	1905.1
AHQ-4-13, 6710	K.QSTSFLVLQEILESEEK.G	1981.18977	2	5.01E-10	0.94	4.25	-	1126.2
AHQ-4-12, 6689 - 6706	K.QSTSFLVLQEILESEEK.G	1981.18977	2	6.15E-09	0.95	4.28	-	1558.8
AHQ-4-12, 6101	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	8.66E-05	0.73	3.35	-	494.0
AHQ-4-13, 6222	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	5.47E-06	0.81	3.34	-	847.9
AHQ-4-13-, 2442 - 2456	R.SAM*PFTASPASSTTAR.V	1599.74799	2	2.70E-04	0.91	3.49	-	1068.3
AHQ-4-11, 2896	R.SAMPFTASPASSTTAR.V	1583.74859	2	1.39E-08	0.43	2.65	-	354.7
AHQ-4-13, 3125	R.SAMPFTASPASSTTAR.V	1583.74859	2	7.38E-06	0.46	2.77	-	391.7
AHQ-4-12, 2373	R.SAM*PFTASPASSTTAR.V	1599.74799	2	2.02E-04	0.89	3.42	-	865.2
AHQ-4-12, 2941	R.SAMPFTASPASSTTAR.V	1583.74859	2	3.04E-04	0.58	2.67	-	458.8
AHQ-4-13, 3679 - 3812	K.VWSPLVTEEGK.R	1245.40612	1	1.89E-05	0.37	2.33	-	573.9
AHQ-4-13, 3206	K.VWSPLVTEEGKR.H	1401.59247	2	9.21E-09	0.87	3.07	-	1050.7
AHQ-4-14-, 2943	K.VWSPLVTEEGKR.H	1401.59247	2	4.75E-08	0.85	2.62	-	1100.6
AHQ-4-12, 2982	K.VWSPLVTEEGKR.H	1401.59247	2	3.47E-07	0.88	2.68	-	952.1
gi|5729842|ref|NP_006699.1|	glyoxalase I; lactoyl glutathione lyase; lactoylglutathione lyase [Homo			1.31E-11	0.97	10.30	10.90	20719.6
AHQ-4-11, 6661 - 6724	K.GLAFIQDPDGYWIEILNPNK.M	2304.58542	2	1.31E-11	0.97	6.08	-	926.5
gi|4885609|ref|NP_005408.1|	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen			1.37E-11	3.57	40.35	13.20	59834.4
AHQ-4-7, 3593	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	3.06E-07	0.90	3.15	-	1343.7
AHQ-4-7, 7445	R.LPQLVDMAAQIASGMAYVER.M	2164.53485	2	1.37E-11	0.99	6.92	-	2894.9
AHQ-4-7, 5470	R.TLKPGTMSPEAFLQEAQVMK.K	2207.59964	2	2.55E-05	0.78	3.95	-	794.0
AHQ-4-7, 6314	R.TQFNSLQQLVAYYSK.H	1790.99681	2	3.45E-08	0.94	4.08	-	1229.7
AHQ-4-7, 6154	R.TQFNSLQQLVAYYSK.H	1790.99681	2	2.78E-11	0.91	4.06	-	746.1
gi|29741246|ref|XP_294070.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			1.41E-11	3.28	40.22	14.60	35032.0
AHQ-4-13-, 5296	K.AENGKLVINGNPITIFQER.D	2114.39062	2	4.71E-09	0.54	3.03	-	290.5

AHQ-4-9, 4685 - 4751	K.AENGKLVINGNPITIFQER.D	2114.39062	2	6.32E-09	0.85	3.89	-	652.3
AHQ-4-9, 4831	K.AENGKLVINGNPITIFQER.D	2114.39062	2	1.26E-04	0.85	3.79	-	641.5
AHQ-4-13, 5429	K.AENGKLVINGNPITIFQER.D	2114.39062	2	7.97E-08	0.42	3.02	-	344.3
AHQ-4-9, 4996 - 5071	K.LVINGNPITIFQER.D	1614.87029	2	7.59E-11	0.96	4.02	-	1565.8
AHQ-4-13-, 5576 - 5644	K.LVINGNPITIFQER.D	1614.87029	2	9.85E-10	0.85	3.69	-	672.6
AHQ-4-14-, 5537 - 5602	K.LVINGNPITIFQER.D	1614.87029	2	1.72E-10	0.94	3.76	-	1081.7
AHQ-4-11, 5520 - 5601	K.LVINGNPITIFQER.D	1614.87029	2	1.21E-04	0.85	2.77	-	1183.6
AHQ-4-12, 5655 - 5722	K.LVINGNPITIFQER.D	1614.87029	2	1.31E-08	0.89	3.86	-	762.4
AHQ-4-10, 5120 - 5127	K.LVINGNPITIFQER.D	1614.87029	2	1.41E-11	0.95	4.17	-	1091.8
AHQ-4-9, 5087 - 5163	K.LVINGNPITIFQER.D	1614.87029	2	1.74E-10	0.95	4.12	-	1192.2
AHQ-4-13, 5708 - 5776	K.LVINGNPITIFQER.D	1614.87029	2	1.18E-05	0.88	3.40	-	999.0
AHQ-4-11, 5384 - 5456	K.LVINGNPITIFQER.D	1614.87029	2	5.35E-04	0.82	2.52	-	931.6
AHQ-4-9, 4609 - 4675	K.LVINGNPITIFQERDPSK.I	2042.32440	2	5.31E-10	0.88	3.80	-	587.9
AHQ-4-10, 6397	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	2	1.09E-06	0.90	4.23	-	1181.5
gi|5802974|ref|NP_006784.1| peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide				1.57E-11	4.42	50.26	28.90	27692.5
AHQ-4-10, 4156	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	1.81E-05	0.94	5.19	-	888.6
AHQ-4-11, 4440	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	1.12E-05	0.95	5.25	-	999.5
AHQ-4-11, 5290	R.DYGVLLEGSGLALR.G	1463.66058	2	1.57E-11	0.97	5.24	-	1890.2
AHQ-4-10, 4984 - 5055	R.DYGVLLEGSGLALR.G	1463.66058	2	1.43E-04	0.88	3.52	-	707.7
AHQ-4-11, 5212	R.GLFIIDPNGVIK.H	1286.54452	2	4.76E-06	0.82	3.16	-	922.6
AHQ-4-11, 5476	R.GLFIIDPNGVIK.H	1286.54452	2	1.37E-04	0.85	3.44	-	846.6
AHQ-4-11, 5473	R.GLFIIDPNGVIK.H	1286.54452	1	6.16E-05	0.16	1.86	-	339.1
AHQ-4-11, 2877 - 2882	K.HLSVNDLPVGR.S	1207.36435	2	1.63E-04	0.92	3.43	-	752.6
AHQ-4-10, 4761 - 4820	R.KNGGLGHMNIALLSDLTK.Q	1883.20557	2	1.13E-06	0.76	3.42	-	445.8
gi|4503689|ref|NP_000499.1| fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M				1.63E-11	18.21	230.29	33.00	94972.5
AHQ-4-6, 5830 - 5842	K.DSDWPFCSDEDWNYK.C	1965.98609	2	3.60E-06	0.94	3.94	-	848.5
AHQ-4-9, 5359 - 5360	K.DSDWPFCSDEDWNYK.C	1965.98609	2	1.90E-04	0.87	3.44	-	578.8
AHQ-4-7, 5945	K.DSDWPFCSDEDWNYK.C	1965.98609	2	4.62E-05	0.96	4.55	-	865.1
AHQ-4-9, 5005 - 5015	K.DSHSLTTNIMEILR.G	1630.84839	2	2.13E-05	0.95	4.01	-	1214.2
AHQ-4-11, 5480 - 5486	K.DSHSLTTNIMEILR.G	1630.84839	2	3.59E-07	0.96	4.61	-	1196.9
AHQ-4-7, 4627	K.DSHSLTTNIM*EILR.G	1646.84779	2	5.64E-06	0.78	3.55	-	632.4
AHQ-4-10, 5131 - 5137	K.DSHSLTTNIMEILR.G	1630.84839	2	1.29E-04	0.94	3.78	-	1229.1
AHQ-4-4, 2203	K.ESSSHHPGIAEFPSR.G	1638.72252	2	2.76E-07	0.84	3.19	-	654.3
AHQ-4-6, 2011	K.ESSSHHPGIAEFPSR.G	1638.72252	2	9.91E-04	0.84	3.05	-	728.2
AHQ-4-8, 2235	R.EVDLKDYEDQQK.Q	1510.58460	2	1.35E-04	0.64	2.84	-	503.0
AHQ-4-13, 2742	R.EVDLKDYEDQQK.Q	1510.58460	2	1.33E-07	0.87	3.22	-	795.1
AHQ-4-9, 2279 - 2289	R.EVDLKDYEDQQK.Q	1510.58460	2	2.57E-08	0.86	3.45	-	689.8
AHQ-4-11, 2468	R.EVDLKDYEDQQK.Q	1510.58460	2	3.52E-08	0.62	2.59	-	554.0
AHQ-4-6, 2342 - 2379	R.EVDLKDYEDQQK.Q	1510.58460	2	5.48E-05	0.76	3.02	-	642.7
AHQ-4-3, 2515	R.EVDLKDYEDQQK.Q	1510.58460	2	8.97E-09	0.87	3.46	-	686.2
AHQ-4-1, 2687	R.EVDLKDYEDQQK.Q	1510.58460	2	4.30E-08	0.84	3.17	-	721.7
AHQ-4-4, 2511	R.EVDLKDYEDQQK.Q	1510.58460	2	1.13E-05	0.76	2.92	-	719.1
AHQ-4-13-, 2636 - 2637	R.EVDLKDYEDQQK.Q	1510.58460	2	7.57E-07	0.91	3.68	-	878.8
AHQ-4-14-, 2545	R.EVDLKDYEDQQK.Q	1510.58460	2	3.80E-09	0.83	2.67	-	913.1
AHQ-4-10, 2428 - 2431	R.EVDLKDYEDQQK.Q	1510.58460	2	1.50E-06	0.90	3.77	-	804.1
AHQ-4-13, 6017 - 6021	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	6.39E-05	0.96	5.66	-	1469.8
AHQ-4-7, 6955	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	1.00E-04	0.91	3.93	-	1267.4
AHQ-4-13-, 6102 - 6165	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	1.41E-04	0.93	4.80	-	1023.0
AHQ-4-13, 6420 - 6425	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	5.06E-10	0.78	3.61	-	1007.8
AHQ-4-13, 6509	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	6.54E-05	0.84	3.54	-	996.8
AHQ-4-13, 6602 - 6672	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	1.02E-04	0.58	3.44	-	545.6
AHQ-4-6, 6535	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	2.91E-04	0.88	4.20	-	845.3
AHQ-4-13-, 5896 - 5912	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	4.22E-05	0.97	5.66	-	1574.7
AHQ-4-13-, 6386	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	7.69E-07	0.86	3.82	-	962.0
AHQ-4-1, 6261	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	5.66E-05	0.88	4.38	-	689.7
AHQ-4-13-, 6560 - 6630	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	1.01E-07	0.95	5.24	-	1280.6
AHQ-4-8, 3979	K.GLIDEVNQDFTNR.I	1521.61384	2	7.34E-07	0.92	3.42	-	913.6
AHQ-4-2, 4963	K.GLIDEVNQDFTNR.I	1521.61384	2	1.01E-05	0.94	4.07	-	978.1
AHQ-4-13, 4805	K.GLIDEVNQDFTNR.I	1521.61384	2	7.08E-06	0.92	3.46	-	1133.8
AHQ-4-6, 4647	K.GLIDEVNQDFTNR.I	1521.61384	2	2.85E-05	0.84	2.94	-	822.7
AHQ-4-3, 4928	K.GLIDEVNQDFTNR.I	1521.61384	2	8.33E-07	0.87	3.31	-	857.5
AHQ-4-1, 4901	K.GLIDEVNQDFTNR.I	1521.61384	2	9.88E-10	0.97	4.92	-	1379.6
AHQ-4-7, 4615 - 4694	K.GLIDEVNQDFTNR.I	1521.61384	2	8.28E-08	0.94	4.16	-	1045.7
AHQ-4-9, 3696	K.GLIDEVNQDFTNR.I	1521.61384	2	5.62E-04	0.81	3.20	-	584.3
AHQ-4-5, 4765	K.GLIDEVNQDFTNR.I	1521.61384	2	2.07E-07	0.84	3.18	-	983.4
AHQ-4-10, 4291 - 4293	K.GLIDEVNQDFTNR.I	1521.61384	2	2.28E-05	0.92	4.02	-	976.5
AHQ-4-9, 4219	K.GLIDEVNQDFTNR.I	1521.61384	2	1.03E-07	0.93	3.78	-	1074.7
AHQ-4-12, 4701 - 4703	K.GLIDEVNQDFTNR.I	1521.61384	2	4.15E-08	0.95	4.46	-	1021.8
AHQ-4-13-, 4653	K.GLIDEVNQDFTNR.I	1521.61384	2	4.38E-08	0.87	3.15	-	992.5
AHQ-4-4, 4895 - 4910	K.GLIDEVNQDFTNR.I	1521.61384	2	6.68E-06	0.91	3.71	-	929.9
AHQ-4-1, 2329	R.GSESGIFTNTK.E	1141.21317	1	3.03E-04	0.20	2.12	-	408.4
AHQ-4-6, 1950	R.GSESGIFTNTK.E	1141.21317	1	8.68E-05	0.19	2.06	-	275.5
AHQ-4-13-, 2292 - 2293	R.GSESGIFTNTK.E	1141.21317	2	3.36E-04	0.68	2.64	-	768.2
AHQ-4-1, 2326	R.GSESGIFTNTK.E	1141.21317	2	3.65E-04	0.84	2.92	-	1078.7
AHQ-4-13-, 2276 - 2288	R.GSESGIFTNTK.E	1141.21317	1	7.97E-08	0.47	2.47	-	384.6
AHQ-4-13, 2413	R.GSESGIFTNTK.E	1141.21317	2	4.06E-04	0.81	2.59	-	996.4
AHQ-4-12, 3001	R.HPDEAAFFDTASTGK.T	1594.66329	2	1.59E-04	0.77	3.10	-	583.4
AHQ-4-13-, 3068	R.HPDEAAFFDTASTGK.T	1594.66329	2	2.47E-04	0.78	3.28	-	405.2
AHQ-4-13, 3193	R.HPDEAAFFDTASTGK.T	1594.66329	2	5.86E-05	0.78	3.18	-	575.0
AHQ-4-13-, 2617 - 2650	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	9.25E-04	0.94	4.37	-	1388.9
AHQ-4-3, 2417	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	8.08E-04	0.96	4.96	-	1170.0
AHQ-4-13, 2741	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	4.50E-06	0.97	5.05	-	1490.4
AHQ-4-6, 2184 - 2258	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	7.97E-05	0.94	4.27	-	1756.1
AHQ-4-5, 2250	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.13E-05	0.95	4.63	-	741.0
AHQ-4-7, 2201 - 2203	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	6.88E-06	0.95	4.40	-	984.0
AHQ-4-9, 2156 - 2157	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	6.70E-07	0.98	5.27	-	1904.4
AHQ-4-12, 2469	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.57E-06	0.98	5.73	-	1931.7
AHQ-4-13-, 2618 - 2624	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.54E-06	0.97	5.29	-	1417.8
AHQ-4-9, 2425	K.LKNSLFEYQK.N	1270.45881	2	1.48E-04	0.27	2.60	-	244.5
AHQ-4-6, 2380	R.MELERPGGNEITR.G	1502.67870	2	7.26E-04	0.82	3.42	-	712.8
AHQ-4-8, 2851 - 2855	K.M*KPVPDLVPGNFK.S	1458.75054	2	2.31E-04	0.80	3.34	-	449.8
AHQ-4-7, 3102	K.M*KPVPDLVPGNFK.S	1458.75054	2	3.49E-04	0.65	2.81	-	458.2
AHQ-4-10, 3188	K.M*KPVPDLVPGNFK.S	1458.75054	2	3.49E-04	0.77	3.11	-	372.5
AHQ-4-9, 4631	K.NNKDSHSLTTNIMEILR.G	1987.22751	2	9.25E-08	0.90	4.16	-	742.5
AHQ-4-7, 3067	R.NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPR.P	4123.15285	3	6.82E-05	0.72	3.29	-	565.9
AHQ-4-7, 1942	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	2.21E-06	0.27	2.67	-	162.3
AHQ-4-4, 2179	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	3.25E-05	0.87	3.70	-	422.7
AHQ-4-7, 2046	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	1.63E-11	0.93	4.41	-	701.0
AHQ-4-9, 1929	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	8.95E-09	0.94	4.54	-	783.6
AHQ-4-7, 3097	K.NSLFEYQK.N	1029.12765	1	1.29E-04	0.43	2.14	-	386.0
AHQ-4-1, 2897	K.NSLFEYQK.N	1029.12765	1	2.37E-04	0.29	2.31	-	250.3
AHQ-4-6, 1956	R.PGSTGTWNPGSSER.G	1433.46515	2	1.57E-05	0.82	3.52	-	584.0
AHQ-4-11, 2110	R.PGSTGTWNPGSSER.G	1433.46515	2	4.65E-06	0.70	2.71	-	712.5
AHQ-4-8, 1837	R.PGSTGTWNPGSSER.G	1433.46515	2	1.19E-05	0.91	3.66	-	740.6
AHQ-4-1, 2291	R.PGSTGTWNPGSSER.G	1433.46515	2	1.28E-04	0.74	3.23	-	442.0
AHQ-4-3, 4980	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	4.95E-07	0.76	3.44	-	360.2
AHQ-4-13-, 4710	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	6.60E-09	0.90	3.71	-	777.0

AHQ-4-11, 4588	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.59E-09	0.93	4.61	-	696.2
AHQ-4-7, 4670 - 4677	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	4.60E-08	0.97	5.26	-	1613.8
AHQ-4-9, 4241	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	5.96E-05	0.95	4.67	-	943.1
AHQ-4-6, 4680	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	2.64E-09	0.97	5.43	-	1085.2
AHQ-4-10, 6183	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	6.41E-04	0.76	3.49	-	270.6
AHQ-4-13-, 6668	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	8.15E-04	0.90	4.22	-	356.8
AHQ-4-9, 6663	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.91E-06	0.87	3.72	-	407.3
AHQ-4-12, 7025 - 7026	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	8.29E-08	0.90	4.19	-	484.1
AHQ-4-11, 6777	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.75E-07	0.82	3.49	-	357.0
AHQ-4-1, 7021	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.69E-04	0.69	2.87	-	328.7
AHQ-4-11, 6468	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.66E-04	0.51	2.78	-	168.3
AHQ-4-1, 7206	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.96E-05	0.85	3.85	-	315.9
AHQ-4-2, 7182 - 7186	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	5.02E-05	0.50	2.58	-	216.4
AHQ-4-2, 7484	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	7.01E-06	0.80	3.58	-	303.6
AHQ-4-10, 6467	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.22E-05	0.83	3.78	-	352.9
AHQ-4-13-, 6836 - 6900	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.73E-08	0.94	4.55	-	580.1
AHQ-4-14-, 6539	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	3.72E-05	0.44	2.69	-	141.6
AHQ-4-6, 6846 - 6854	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	8.90E-06	0.59	3.03	-	228.3
AHQ-4-9, 6264	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.01E-04	0.67	3.38	-	254.7
AHQ-4-6, 7210	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.95E-07	0.91	4.39	-	425.6
AHQ-4-3, 7484	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	6.14E-08	0.79	3.33	-	358.4
AHQ-4-5, 7390	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.98E-05	0.63	3.31	-	281.0
AHQ-4-6, 2030	K.VQHIQLLQK.N	1107.33106	1	3.82E-04	0.59	2.39	-	660.4
AHQ-4-4, 2246	K.VQHIQLLQK.N	1107.33106	1	7.07E-04	0.60	2.22	-	632.1
AHQ-4-13-, 2385	K.VQHIQLLQK.N	1107.33106	1	8.36E-04	0.42	2.31	-	533.4
AHQ-4-6, 2038	K.VQHIQLLQK.N	1107.33106	1	8.92E-04	0.37	2.33	-	310.5
AHQ-4-7, 1965	K.VQHIQLLQK.N	1107.33106	1	3.30E-04	0.29	2.50	-	207.4
AHQ-4-8, 1863 - 1865	K.VQHIQLLQK.N	1107.33106	2	6.90E-05	0.89	3.52	-	827.5
AHQ-4-8, 1871	K.VQHIQLLQK.N	1107.33106	1	5.77E-04	0.34	2.15	-	199.9
AHQ-4-9, 1971	K.VQHIQLLQK.N	1107.33106	2	9.64E-04	0.75	2.70	-	618.9
AHQ-4-13, 2509	K.VQHIQLLQK.N	1107.33106	1	3.82E-04	0.56	2.36	-	664.4
AHQ-4-10, 2123	K.VQHIQLLQK.N	1107.33106	1	1.50E-04	0.79	3.14	-	550.1
AHQ-4-11, 2204	K.VQHIQLLQK.N	1107.33106	1	3.82E-04	0.70	2.41	-	803.6
AHQ-4-1, 2490	K.VQHIQLLQK.N	1107.33106	2	1.72E-04	0.87	2.82	-	971.1
AHQ-4-11, 2217	K.VQHIQLLQK.N	1107.33106	1	1.39E-04	0.50	2.66	-	435.8
gi|4502051|ref|NP_000688.1|	arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]			1.78E-11	10.39	120.28	26.20	75721.8
AHQ-4-6, 4835 - 4850	R.AAAQLTYCSLCPPDDLADR.G	2140.33708	2	6.60E-08	0.83	3.74	-	419.5
AHQ-4-6, 2070	K.AVSTGGGGHVQLLR.R	1352.52468	2	2.90E-10	0.88	3.69	-	861.8
AHQ-4-6, 3524 - 3526	K.EGLPLTIAADR.K	1156.31411	2	3.26E-05	0.88	3.26	-	656.0
AHQ-4-6, 2998 - 2999	R.EITEVGLCQAQDR.G	1520.64745	2	8.99E-06	0.89	3.81	-	635.4
AHQ-4-6, 3254	K.GDPELQAWCR.E	1233.33558	2	9.77E-07	0.81	2.61	-	603.3
AHQ-4-6, 7127	R.GEEEEFDHDVAEDLGLLQFVR.L	2448.58352	2	1.78E-11	0.98	5.53	-	2237.5
AHQ-4-6, 5312	R.GLLGLPGALYAHDALR.L	1637.90708	3	3.66E-05	0.79	3.45	-	877.1
AHQ-4-6, 5298 - 5307	R.GLLGLPGALYAHDALR.L	1637.90708	2	1.60E-09	0.89	3.87	-	655.3
AHQ-4-6, 5122 - 5187	R.ITVQGPGACAEVAFPCYR.W	1999.25659	2	9.34E-06	0.86	3.56	-	1007.1
AHQ-4-6, 4454	R.LPGDNALDMFQK.H	1349.53784	2	2.35E-07	0.96	4.47	-	1294.6
AHQ-4-6, 3896	R.TQLISDGGIFDK.A	1294.43554	2	2.42E-05	0.92	3.40	-	1224.8
AHQ-4-10, 4539	R.WVQGEDILSLPEGTAR.L	1771.95190	2	6.65E-04	0.58	2.98	-	471.7
AHQ-4-6, 4760	R.YVEGIVHLFYQR.D	1524.74730	2	6.00E-05	0.90	2.80	-	1186.6
gi|12025678|ref|NP_004915.2|	actinin, alpha 4 [Homo sapiens]			1.93E-11	3.51	40.28	7.80	104853.3
AHQ-4-5, 2773 - 2795	K.GISQEQMQEFR.A	1353.48658	2	5.35E-07	0.77	3.00	-	1171.2
AHQ-4-5, 4709	K.ICDQWDALGSLTHSR.R	1760.90926	2	5.47E-07	0.94	4.05	-	1302.5
AHQ-4-5, 4098	R.MAPYQGPDAVPGALDYK.S	1794.02097	2	9.67E-07	0.85	3.42	-	893.7
AHQ-4-6, 7054	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	6.67E-08	0.87	4.74	-	647.0
AHQ-4-5, 7203 - 7247	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	1.93E-11	0.95	5.66	-	1053.8
gi|4502695|ref|NP_001779.1|	cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c			2.04E-11	2.68	30.26	13.60	48786.6
AHQ-4-8, 3617	K.IYEFPETDDEEENKLVK.K	2099.23685	2	1.92E-06	0.79	3.47	-	443.3
AHQ-4-13, 5528	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	4.15E-04	0.80	3.45	-	599.2
AHQ-4-14-, 5366 - 5415	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	2.04E-11	0.95	5.17	-	927.2
AHQ-4-8, 5119	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	1.15E-05	0.95	4.95	-	977.5
AHQ-4-14-, 6390	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	3.89E-11	0.93	5.18	-	471.7
AHQ-4-14-, 6177	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	2.21E-08	0.74	3.33	-	335.7
gi|21361657|ref|NP_005304.3|	glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom			2.30E-11	12.82	160.36	39.20	56782.0
AHQ-4-7, 2118	K.DPNIVIAK.M	870.02845	1	7.72E-04	0.17	1.85	-	299.5
AHQ-4-7, 5809	R.ELSDFISYLQR.E	1371.52000	2	1.15E-05	0.94	3.89	-	1213.3
AHQ-4-7, 6615 - 6681	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	2	3.51E-04	0.83	3.46	-	677.9
AHQ-4-7, 6395 - 6462	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	2	1.88E-05	0.90	4.31	-	603.9
AHQ-4-7, 5385	K.FIQENIFGICPHMTEDNKDLIQGK.D	2850.21952	3	1.01E-06	0.87	4.56	-	628.9
AHQ-4-7, 5394 - 5398	K.FIQENIFGICPHMTEDNKDLIQGK.D	2850.21952	2	4.05E-04	0.64	2.98	-	489.1
AHQ-4-7, 7249	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	2.30E-11	0.98	6.44	-	3110.4
AHQ-4-7, 4618	R.FLQDYFDGNLK.R	1360.49568	2	5.12E-04	0.85	3.19	-	960.3
AHQ-4-7, 2271	K.FVM*QEEFSR.D	1189.32290	2	7.10E-04	0.85	2.70	-	869.6
AHQ-4-7, 4325	R.GFPTIYFSPANK.K	1342.52349	1	5.78E-04	0.78	3.35	-	509.7
AHQ-4-7, 5610 - 5611	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	2	1.28E-09	0.97	5.61	-	1428.7
AHQ-4-7, 2075 - 2157	R.LAPEYEAAATR.L	1192.30331	2	4.01E-06	0.74	2.75	-	340.2
AHQ-4-7, 2378	K.LNFAVASR.K	878.01067	2	1.57E-04	0.76	2.54	-	709.8
AHQ-4-7, 2006	K.LSKDPNIVIAK.M	1198.43727	2	4.42E-06	0.84	3.13	-	798.6
AHQ-4-7, 3339	K.MDATANDVPSPYEVR.G	1665.80646	2	2.34E-05	0.87	3.79	-	551.2
AHQ-4-7, 3451	K.MDATANDVPSPYEVR.G	1665.80646	2	4.58E-05	0.79	3.43	-	524.0
AHQ-4-7, 1890	K.RLAPEYEAAATR.L	1348.48966	2	1.54E-08	0.95	4.22	-	887.6
AHQ-4-10, 5676	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	2	4.22E-06	0.86	3.49	-	621.8
AHQ-4-7, 6263 - 6265	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	2	1.80E-06	0.99	7.22	-	2262.2
AHQ-4-7, 2818	K.YGVSGYPTLK.I	1085.23435	1	4.23E-05	0.36	2.36	-	278.3
gi|7705296|ref|NP_057271.1|	bridging integrator 2; bridging integrator-2; breast cancer associated			2.38E-11	3.28	40.24	11.00	61746.8
AHQ-4-10, 5488 - 5551	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	6.33E-08	0.93	4.28	-	1000.0
AHQ-4-10, 5607 - 5671	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	2.38E-11	0.93	4.16	-	1050.1
AHQ-4-14-, 6438	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.51E-07	0.95	4.75	-	906.2
AHQ-4-11, 6381	R.IGCYVTIFQNISNLR.D	1800.07167	2	7.63E-07	0.85	3.84	-	610.4
AHQ-4-10, 5905	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.66E-04	0.45	2.60	-	396.3
AHQ-4-9, 6184 - 6187	R.IGCYVTIFQNISNLR.D	1800.07167	2	4.66E-04	0.94	4.69	-	892.6
AHQ-4-10, 2640	K.LNHNLYEVMSK.L	1348.55307	2	2.17E-05	0.94	3.85	-	1127.7
AHQ-4-10, 4505 - 4531	R.VSETLQEIYSSEWDGHEELK.A	2380.50595	2	8.33E-04	0.47	2.63	-	356.8
gi|4504183|ref|NP_000843.1|	glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s			2.45E-11	6.34	70.27	48.60	23355.7
AHQ-4-10, 4904	K.AFLASPEYVNLPINGNGKQ	2033.27283	2	7.12E-05	0.58	2.77	-	762.1
AHQ-4-11, 5144 - 5204	K.AFLASPEYVNLPINGNGKQ	2033.27283	2	1.06E-05	0.85	3.31	-	990.1
AHQ-4-13-, 5369	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	1.14E-05	0.89	3.76	-	528.7
AHQ-4-11, 5124	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	1.81E-05	0.93	4.28	-	546.1
AHQ-4-11, 5217 - 5230	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.47E-05	0.80	3.54	-	406.6
AHQ-4-11, 5129	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	7.66E-09	0.82	3.49	-	455.0
AHQ-4-11, 3073	K.ASCLYGQLPK.F	1138.31884	2	5.67E-06	0.79	2.82	-	651.6
AHQ-4-11, 3008 - 3076	K.ASCLYGQLPK.F	1138.31884	2	3.05E-06	0.86	3.27	-	786.5
AHQ-4-11, 5284 - 5288	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.83E-07	0.97	5.42	-	1550.9
AHQ-4-13, 6514	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.92E-04	0.84	3.22	-	881.9
AHQ-4-11, 5120 - 5122	K.DQQEAALVDM*VNDGVEDLR.C	2134.26783	2	2.12E-08	0.96	5.40	-	967.4
AHQ-4-14-, 6218 - 6291	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.32E-06	0.86	3.64	-	786.6
AHQ-4-11, 6244	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	9.48E-06	0.91	3.92	-	835.6
AHQ-4-11, 4402	K.DQQEAALVDM*VNDGVEDLR.C	2134.26783	2	2.98E-07	0.93	4.65	-	675.1

AHQ-4-11, 4910 - 4972	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.76E-10	0.96	5.29	-	1044.2
AHQ-4-11, 4828 - 4844	K.FQDGDLTLYQSNTILR.H	1885.06701	2	8.86E-09	0.95	4.82	-	1025.0
AHQ-4-11, 4700 - 4780	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.45E-11	0.95	4.96	-	968.5
AHQ-4-10, 4515	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.69E-06	0.95	4.09	-	1256.7
AHQ-4-13, 5036 - 5040	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.18E-04	0.72	3.49	-	380.8
AHQ-4-14, 6113	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.63E-06	0.87	3.94	-	785.3
AHQ-4-14-, 4881	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.73E-11	0.96	5.30	-	908.9
AHQ-4-11, 4506	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	1.03E-08	0.92	4.28	-	649.4
AHQ-4-11, 4369 - 4376	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	5.11E-06	0.84	3.69	-	494.5
AHQ-4-10, 4117 - 4159	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	7.35E-07	0.83	3.85	-	279.5
gi|4506413|ref|NP_002875.1| RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				2.51E-11	6.14	70.27	27.70	20987.1
AHQ-4-11, 2384	K.CDLEDERVVGK.E	1321.43945	2	4.10E-04	0.80	3.01	-	931.3
AHQ-4-11, 6536 - 6616	K.INVNEIFYDLVR.Q	1495.70427	2	6.68E-08	0.94	4.57	-	1038.0
AHQ-4-14-, 6629 - 6701	K.INVNEIFYDLVR.Q	1495.70427	2	1.58E-07	0.95	4.92	-	1076.4
AHQ-4-14-, 6478	K.INVNEIFYDLVR.Q	1495.70427	2	1.64E-09	0.94	4.17	-	1417.5
AHQ-4-14-, 5809	K.INVNEIFYDLVR.Q	1495.70427	2	1.55E-06	0.95	3.97	-	1384.2
AHQ-4-13-, 6744	K.INVNEIFYDLVR.Q	1495.70427	2	3.48E-08	0.89	3.34	-	931.8
AHQ-4-13, 6840	K.INVNEIFYDLVR.Q	1495.70427	2	4.49E-06	0.96	4.60	-	1155.4
AHQ-4-11, 6732	K.INVNEIFYDLVR.Q	1495.70427	1	1.13E-06	0.30	2.62	-	314.5
AHQ-4-11, 6709 - 6718	K.INVNEIFYDLVR.Q	1495.70427	2	1.87E-07	0.94	4.35	-	1306.4
AHQ-4-11, 6548 - 6609	K.INVNEIFYDLVR.Q	1495.70427	1	1.55E-04	0.47	3.14	-	213.6
AHQ-4-11, 5696 - 5760	K.INVNEIFYDLVR.Q	1495.70427	2	7.67E-07	0.89	3.96	-	924.7
AHQ-4-11, 5698	K.INVNEIFYDLVR.Q	1495.70427	1	2.80E-09	0.13	1.91	-	172.5
AHQ-4-11, 6545 - 6674	K.INVNEIFYDLVR.Q	1495.70427	1	8.29E-07	0.43	3.01	-	293.6
AHQ-4-14-, 6630 - 6631	K.INVNEIFYDLVR.Q	1495.70427	1	1.28E-06	0.51	3.16	-	175.6
AHQ-4-11, 6405	K.INVNEIFYDLVR.Q	1495.70427	1	8.69E-07	0.20	1.96	-	226.3
AHQ-4-11, 6400	K.INVNEIFYDLVR.Q	1495.70427	2	4.99E-07	0.87	3.07	-	983.4
AHQ-4-12, 2685	K.LVVLGSGGVGK.S	986.19059	2	6.35E-05	0.88	3.26	-	887.9
AHQ-4-11, 2656	K.LVVLGSGGVGK.S	986.19059	2	1.76E-06	0.92	3.64	-	1068.7
AHQ-4-13-, 2776	K.LVVLGSGGVGK.S	986.19059	1	2.07E-05	0.84	3.10	-	812.6
AHQ-4-11, 2536 - 2604	K.LVVLGSGGVGK.S	986.19059	2	7.25E-05	0.92	3.50	-	1118.0
AHQ-4-11, 2560 - 2770	K.LVVLGSGGVGK.S	986.19059	1	7.93E-04	0.72	3.04	-	582.0
AHQ-4-11, 6240 - 6312	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.13E-04	0.95	5.06	-	1093.4
AHQ-4-11, 6493 - 6572	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.69E-06	0.96	4.77	-	1761.6
AHQ-4-14-, 5951 - 6013	K.SALTVQFVQGIFVEK.Y	1666.94196	2	4.36E-04	0.93	3.24	-	1595.3
AHQ-4-11, 6120 - 6182	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.81E-04	0.96	5.10	-	1700.3
AHQ-4-11, 5646	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.62E-06	0.93	4.27	-	1151.5
AHQ-4-11, 6636 - 6642	K.SALTVQFVQGIFVEK.Y	1666.94196	2	8.46E-07	0.94	3.84	-	1521.6
AHQ-4-14-, 6037 - 6081	K.SALTVQFVQGIFVEK.Y	1666.94196	2	4.95E-04	0.93	3.85	-	1438.3
AHQ-4-11, 6360 - 6433	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.16E-07	0.97	5.43	-	1801.4
AHQ-4-11, 5945 - 5990	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.36E-05	0.87	3.68	-	966.0
AHQ-4-11, 6737 - 6813	K.SALTVQFVQGIFVEK.Y	1666.94196	2	4.27E-08	0.97	4.47	-	1920.3
AHQ-4-11, 6900	K.SALTVQFVQGIFVEK.Y	1666.94196	2	8.90E-07	0.96	5.06	-	1602.2
AHQ-4-11, 5245 - 5253	K.SKINVNEIFYDLVR.Q	1710.95483	2	3.80E-10	0.94	4.39	-	1018.7
AHQ-4-11, 6313	K.SKINVNEIFYDLVR.Q	1710.95483	2	4.25E-09	0.92	3.74	-	951.5
AHQ-4-11, 5068 - 5084	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.95E-08	0.86	3.73	-	602.6
AHQ-4-11, 5924	K.SKINVNEIFYDLVR.Q	1710.95483	2	8.09E-08	0.91	3.72	-	935.6
AHQ-4-14-, 6063	K.SKINVNEIFYDLVR.Q	1710.95483	3	3.11E-06	0.95	4.81	-	1638.7
AHQ-4-11, 5605	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.17E-09	0.73	3.01	-	687.4
AHQ-4-14-, 6057	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.31E-10	0.96	4.82	-	1169.7
AHQ-4-11, 5902	K.SKINVNEIFYDLVR.Q	1710.95483	3	2.52E-08	0.94	4.00	-	1534.5
AHQ-4-11, 5701	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.18E-05	0.94	4.45	-	956.3
AHQ-4-11, 5834 - 5896	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.51E-11	0.95	4.59	-	1132.7
AHQ-4-11, 2752	K.YDPTIEDSYR.K	1259.30338	2	1.16E-06	0.79	2.62	-	396.9
AHQ-4-13-, 2744 - 2821	K.YDPTIEDSYR.K	1259.30338	2	2.02E-07	0.81	2.76	-	479.0
AHQ-4-14-, 2697 - 2699	K.YDPTIEDSYR.K	1259.30338	2	2.46E-05	0.79	2.58	-	551.8
AHQ-4-13, 2550	K.YDPTIEDSYRK.Q	1387.47629	2	1.60E-06	0.74	2.81	-	395.7
AHQ-4-11, 2276 - 2308	K.YDPTIEDSYRK.Q	1387.47629	2	2.14E-05	0.83	2.66	-	544.0
AHQ-4-13-, 2432 - 2444	K.YDPTIEDSYRK.Q	1387.47629	2	5.02E-06	0.82	2.89	-	569.3
gi|4504391|ref|NP_000179.1| hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]				2.64E-11	7.34	80.25	11.80	102502.4
AHQ-4-4, 6324	R.AILQQLGLNSTCDDSILVK.T	2090.38419	2	6.86E-06	0.90	4.03	-	858.4
AHQ-4-4, 4484 - 4486	K.ATDCVGHDVVTLLR.D	1557.75406	2	2.64E-11	0.96	4.41	-	1174.3
AHQ-4-4, 5718	K.GDFIALDLGGSSFR.I	1455.59700	2	8.80E-07	0.97	4.49	-	1825.2
AHQ-4-4, 2478	R.GKFNTSDVSAIEK.N	1396.52786	2	1.38E-06	0.77	3.03	-	744.6
AHQ-4-4, 2147	R.HIDLVEGDEGR.M	1240.30483	2	7.06E-08	0.95	4.04	-	1090.6
AHQ-4-4, 5506 - 5508	K.KLPVGFTFSFPCQQSK.I	1873.16425	2	7.19E-06	0.96	4.96	-	1054.1
AHQ-4-4, 6094	K.LPVGFTFSFPCQQSK.I	1744.99134	2	5.39E-05	0.90	3.80	-	751.3
AHQ-4-4, 6408	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	1.42E-05	0.91	4.21	-	775.0
AHQ-4-4, 6291 - 6311	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	2.64E-06	0.94	4.35	-	942.9
gi|4507651|ref|NP_003281.1| tropomyosin 4 [Homo sapiens]				2.84E-11	2.81	30.29	14.50	28521.6
AHQ-4-9, 3517 - 3579	R.AEVSELKCGDLEEELK.N	1851.02256	2	2.58E-05	0.89	4.29	-	723.9
AHQ-4-9, 4600	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	1.12E-07	0.88	4.82	-	805.2
AHQ-4-9, 5413 - 5425	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	2.84E-11	0.96	5.88	-	1401.0
AHQ-4-9, 1907	K.YSEKEDKYEEEIK.L	1690.78605	3	8.24E-05	0.95	5.06	-	1383.9
AHQ-4-9, 1780	K.YSEKEDKYEEEIK.L	1690.78605	2	2.04E-04	0.76	3.32	-	696.4
gi|4502905|ref|NP_001822.1| clusterin; complement-associated protein SP-40 [Homo sapiens]				2.94E-11	2.45	30.31	12.50	52494.3
AHQ-4-8, 2723	R.EILSVDCSTNNPSQAK.L	1764.89299	2	1.17E-05	0.67	2.86	-	582.4
AHQ-4-11, 5282	K.LFDSDPITVTVPVEVSR.K	1875.11203	2	8.09E-05	0.81	3.42	-	596.0
AHQ-4-11, 3396 - 3401	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	2.94E-11	0.97	6.23	-	1255.8
AHQ-4-9, 2980 - 2984	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	2.87E-04	0.97	6.15	-	1197.1
gi|4826898|ref|NP_005013.1| profilin 1; profilin-1 [Homo sapiens]				2.97E-11	16.30	190.29	77.90	15054.2
AHQ-4-13, 5116 - 5138	K.CSVIRDSLLQDGEFSM*DLR.T	2259.50329	3	1.22E-06	0.96	5.70	-	1295.1
AHQ-4-12, 2334	K.CYEMASHLR.R	1168.32854	2	3.09E-07	0.94	3.09	-	1635.1
AHQ-4-13, 2431 - 2510	K.CYEMASHLR.R	1168.32854	2	4.33E-04	0.95	3.12	-	1832.3
AHQ-4-13, 2065 - 2122	K.CYEM*ASHLR.R	1184.32794	2	1.79E-05	0.93	2.64	-	1607.5
AHQ-4-13, 1949 - 2009	K.CYEM*ASHLR.R	1184.32794	2	3.54E-05	0.90	2.93	-	1229.7
AHQ-4-13-, 1673 - 1737	K.CYEM*ASHLR.R	1184.32794	2	3.47E-06	0.91	3.11	-	1273.2
AHQ-4-13-, 1742 - 1800	K.CYEM*ASHLR.R	1184.32794	2	3.02E-04	0.88	2.96	-	1262.0
AHQ-4-13-, 1873 - 1936	K.CYEM*ASHLR.R	1184.32794	2	3.25E-04	0.85	2.64	-	1133.8
AHQ-4-13-, 2404 - 2468	K.CYEMASHLR.R	1168.32854	2	5.49E-04	0.96	3.31	-	2136.3
AHQ-4-13-, 2314 - 2384	K.CYEMASHLR.R	1168.32854	2	5.50E-05	0.95	3.34	-	1842.3
AHQ-4-13-, 1920 - 2000	K.CYEM*ASHLR.R	1184.32794	2	2.85E-06	0.85	3.09	-	727.1
AHQ-4-13, 4206	K.DRSSFYVNGLTLGGQK.C	1742.91379	3	1.93E-07	0.82	3.81	-	756.4
AHQ-4-13-, 4193 - 4194	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	7.79E-08	0.94	4.54	-	923.3
AHQ-4-13, 4196 - 4274	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.59E-07	0.98	5.75	-	1692.1
AHQ-4-12, 4931 - 4942	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.28E-05	0.87	3.07	-	1256.6
AHQ-4-12, 5318 - 5389	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.72E-09	0.95	4.00	-	1482.6
AHQ-4-12, 5506 - 5570	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.26E-08	0.95	3.90	-	1545.5
AHQ-4-12, 5595 - 5667	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.56E-07	0.96	3.64	-	2044.1
AHQ-4-12, 5745	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.60E-07	0.94	3.53	-	1449.5
AHQ-4-13-, 5456 - 5520	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.82E-10	0.98	5.24	-	2075.9
AHQ-4-12, 5835 - 5907	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.02E-04	0.80	3.34	-	564.4
AHQ-4-13-, 5393 - 5469	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.05E-05	0.87	3.52	-	1118.1
AHQ-4-13-, 5584 - 5650	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.97E-11	0.98	4.86	-	2154.7
AHQ-4-13-, 5822 - 5904	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.03E-09	0.98	5.03	-	2852.4
AHQ-4-14-, 4582 - 4589	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.36E-08	0.96	4.69	-	1585.5
AHQ-4-14-, 5347 - 5369	R.DSLLQDGEFSMDLR.T	1626.77023	2	8.58E-10	0.97	4.68	-	1962.7

AHQ-4-12, 4687 - 4769	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.67E-09	0.95	3.48	-	1758.5
AHQ-4-14-, 4467 - 4470	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.73E-08	0.95	4.15	-	1194.2
AHQ-4-13-, 5352 - 5420	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.45E-09	0.98	5.32	-	1939.0
AHQ-4-13-, 5201 - 5276	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.80E-09	0.94	3.87	-	1536.2
AHQ-4-13-, 5102	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.79E-05	0.93	3.86	-	1212.8
AHQ-4-13-, 4913 - 4962	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.22E-09	0.96	4.16	-	1700.7
AHQ-4-13-, 4692 - 4756	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.29E-09	0.97	4.91	-	1745.6
AHQ-4-13-, 4661	R.DSLLQDGEFSM*DLR.T	1642.76963	3	3.17E-06	0.96	4.32	-	2474.3
AHQ-4-14, 5764 - 5825	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.11E-11	0.94	3.90	-	1570.7
AHQ-4-13, 6981	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.48E-07	0.95	3.82	-	1716.9
AHQ-4-12, 4550	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.51E-05	0.92	3.18	-	1392.9
AHQ-4-13, 6185 - 6249	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.00E-07	0.96	4.51	-	1754.2
AHQ-4-13, 5917 - 5981	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.44E-04	0.61	2.73	-	661.5
AHQ-4-13-, 4466 - 4532	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.85E-08	0.96	4.63	-	1255.5
AHQ-4-14-, 5435	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.39E-05	0.83	2.87	-	958.8
AHQ-4-13-, 6001	R.DSLLQDGEFSMDLR.T	1626.77023	2	9.31E-04	0.97	4.61	-	2015.4
AHQ-4-13, 5696 - 5765	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.41E-07	0.97	4.54	-	1779.6
AHQ-4-13-, 4556 - 4621	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.89E-09	0.97	5.01	-	1859.2
AHQ-4-13, 5444 - 5513	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.29E-08	0.97	4.50	-	1666.3
AHQ-4-13, 4517	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.18E-06	0.96	4.30	-	1417.9
AHQ-4-13, 5333 - 5396	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.38E-09	0.96	4.54	-	1464.9
AHQ-4-13, 4604 - 4672	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.17E-10	0.96	4.53	-	1456.5
AHQ-4-13, 4736 - 4812	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.27E-07	0.96	3.93	-	1745.5
AHQ-4-13, 4864	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.28E-10	0.97	4.78	-	2057.5
AHQ-4-13, 4878 - 4954	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.20E-04	0.93	4.02	-	1179.5
AHQ-4-13, 5104	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.66E-07	0.95	3.38	-	1774.9
AHQ-4-13-, 6953	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.02E-04	0.87	2.63	-	1619.4
AHQ-4-13, 5252	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.14E-04	0.95	4.11	-	1479.6
AHQ-4-13, 5297 - 5366	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.41E-04	0.86	3.09	-	1116.4
AHQ-4-13-, 3512 - 3641	K.DSPSVWAAVPGK.T	1214.35211	1	2.73E-04	0.21	2.42	-	387.8
AHQ-4-13-, 3640 - 3652	K.DSPSVWAAVPGK.T	1214.35211	2	1.61E-06	0.91	3.95	-	860.0
AHQ-4-12, 3545 - 3549	K.DSPSVWAAVPGK.T	1214.35211	2	1.31E-07	0.86	2.96	-	1171.2
AHQ-4-13, 3505	K.DSPSVWAAVPGK.T	1214.35211	1	1.98E-04	0.42	2.51	-	505.4
AHQ-4-13, 3669 - 3713	K.DSPSVWAAVPGK.T	1214.35211	2	5.35E-07	0.91	3.75	-	947.6
AHQ-4-13, 3764 - 3840	K.DSPSVWAAVPGK.T	1214.35211	2	5.44E-07	0.89	3.26	-	1017.6
AHQ-4-13, 3905 - 3972	K.DSPSVWAAVPGK.T	1214.35211	2	2.91E-05	0.87	3.13	-	1004.0
AHQ-4-13-, 3513 - 3588	K.DSPSVWAAVPGK.T	1214.35211	2	2.49E-05	0.90	3.84	-	965.3
AHQ-4-13-, 6498 - 6556	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	4.46E-08	0.93	4.66	-	1605.5
AHQ-4-13-, 6700	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	6.41E-05	0.89	4.05	-	1352.7
AHQ-4-13, 1851 - 1885	K.EGVHGGLINK.K	1024.15577	1	4.01E-04	0.32	2.17	-	215.3
AHQ-4-14-, 4213 - 4214	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.13E-07	0.61	2.76	-	376.2
AHQ-4-14-, 4423 - 4542	R.SSFYVNGLTLGGQK.C	1471.63957	1	7.25E-08	0.61	2.60	-	417.9
AHQ-4-13-, 4512 - 4549	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.87E-06	0.95	4.25	-	1278.9
AHQ-4-14, 5404 - 5432	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.11E-10	0.89	3.40	-	698.0
AHQ-4-14, 5545 - 5581	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.02E-04	0.92	3.98	-	946.2
AHQ-4-13, 4385 - 4712	R.SSFYVNGLTLGGQK.C	1471.63957	1	9.89E-08	0.72	2.88	-	567.6
AHQ-4-13-, 4244 - 4304	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.40E-10	0.96	4.75	-	1003.8
AHQ-4-13-, 4248 - 4601	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.29E-09	0.65	2.75	-	535.3
AHQ-4-12, 4514 - 4526	R.SSFYVNGLTLGGQK.C	1471.63957	2	7.61E-08	0.97	4.68	-	1442.4
AHQ-4-12, 4455 - 4529	R.SSFYVNGLTLGGQK.C	1471.63957	1	5.13E-06	0.64	2.90	-	427.4
AHQ-4-12, 4285	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.26E-09	0.58	2.64	-	417.8
AHQ-4-12, 4283	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.43E-05	0.94	4.27	-	785.8
AHQ-4-14-, 4210 - 4219	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.00E-07	0.94	4.17	-	847.7
AHQ-4-13, 4468 - 4532	R.SSFYVNGLTLGGQK.C	1471.63957	2	5.56E-09	0.94	4.14	-	907.5
AHQ-4-13, 4384 - 4444	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.48E-06	0.91	4.09	-	624.6
AHQ-4-13-, 4249 - 4592	R.SSFYVNGLTLGGQK.C	1471.63957	1	7.19E-04	0.37	2.91	-	265.1
AHQ-4-13, 4600 - 4676	R.SSFYVNGLTLGGQK.C	1471.63957	2	8.36E-07	0.96	5.05	-	1084.0
AHQ-4-13, 3447	K.STGGAPTFNVTVTK.T	1380.52843	1	3.43E-07	0.34	2.34	-	431.2
AHQ-4-13-, 3065 - 3128	K.STGGAPTFNVTVTK.T	1380.52843	2	4.88E-07	0.75	2.89	-	431.7
AHQ-4-13-, 3188 - 3254	K.STGGAPTFNVTVTK.T	1380.52843	2	2.85E-07	0.75	3.00	-	387.3
AHQ-4-13-, 3002	K.STGGAPTFNVTVTK.T	1380.52843	1	1.28E-07	0.57	2.35	-	451.3
AHQ-4-13-, 2948 - 3025	K.STGGAPTFNVTVTK.T	1380.52843	2	1.79E-07	0.89	3.83	-	546.8
AHQ-4-12, 3035	K.STGGAPTFNVTVTK.T	1380.52843	2	2.52E-04	0.81	3.22	-	441.9
AHQ-4-13, 3209 - 3337	K.STGGAPTFNVTVTK.T	1380.52843	1	5.23E-06	0.70	2.97	-	471.1
AHQ-4-14-, 2993	K.STGGAPTFNVTVTK.T	1380.52843	1	2.34E-06	0.79	3.67	-	420.7
AHQ-4-13, 3067 - 3130	K.STGGAPTFNVTVTK.T	1380.52843	2	3.49E-04	0.84	3.31	-	503.9
AHQ-4-14-, 2989	K.STGGAPTFNVTVTK.T	1380.52843	2	1.01E-08	0.82	3.17	-	476.7
AHQ-4-13, 3077 - 3474	K.STGGAPTFNVTVTK.T	1380.52843	1	8.43E-04	0.13	2.01	-	265.6
AHQ-4-13, 3201 - 3271	K.STGGAPTFNVTVTK.T	1380.52843	2	6.78E-07	0.86	3.23	-	534.2
AHQ-4-13-, 3034	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	2.67E-04	0.81	3.73	-	426.6
AHQ-4-13-, 2844	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	9.89E-06	0.60	2.71	-	451.4
AHQ-4-13, 2957	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	4.17E-04	0.88	3.70	-	609.0
AHQ-4-13-, 3542	K.TDKTLVLLMGK.E	1219.51989	3	6.23E-05	0.93	3.95	-	1665.7
AHQ-4-13-, 2868	K.TDKTLVLLM*GK.E	1235.51929	2	6.25E-05	0.93	3.66	-	1046.3
AHQ-4-12, 3439	K.TDKTLVLLMGK.E	1219.51989	2	9.45E-06	0.93	3.48	-	1240.1
AHQ-4-13, 5944 - 6013	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.48E-05	0.90	4.05	-	754.9
AHQ-4-13, 5836 - 5896	K.TFVNITPAEVGVLVGK.D	1644.93630	2	6.82E-04	0.91	4.43	-	602.7
AHQ-4-13, 5834	K.TFVNITPAEVGVLVGK.D	1644.93630	3	1.57E-09	0.98	5.82	-	2528.8
AHQ-4-12, 5971	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.96E-05	0.89	3.15	-	1125.3
AHQ-4-12, 5881 - 5951	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.23E-09	0.93	4.68	-	780.1
AHQ-4-12, 5777 - 5841	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.90E-09	0.93	4.86	-	698.3
AHQ-4-13-, 6546	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.01E-04	0.75	3.00	-	646.5
AHQ-4-13, 5918	K.TFVNITPAEVGVLVGK.D	1644.93630	3	2.12E-10	0.98	5.58	-	2583.1
AHQ-4-13-, 5706 - 5781	K.TFVNITPAEVGVLVGK.D	1644.93630	3	5.75E-09	0.97	5.89	-	1317.5
AHQ-4-13-, 5712 - 5768	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.66E-06	0.92	4.23	-	768.8
AHQ-4-13-, 5808 - 5872	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.21E-05	0.94	4.63	-	990.6
AHQ-4-13, 5566 - 5608	K.TFVNITPAEVGVLVGK.D	1644.93630	2	6.33E-04	0.84	3.75	-	510.1
AHQ-4-13-, 5988	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.08E-05	0.90	4.02	-	781.0
AHQ-4-6, 5866 - 5867	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.59E-04	0.93	4.08	-	1018.7
AHQ-4-14-, 5765	K.TFVNITPAEVGVLVGK.D	1644.93630	2	5.24E-06	0.86	3.87	-	703.5
AHQ-4-13-, 5373	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	9.42E-09	0.88	4.03	-	630.9
AHQ-4-13, 5476 - 5492	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	1.78E-07	0.77	3.53	-	798.5
AHQ-4-13, 5478	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	7.92E-07	0.90	3.89	-	789.3
AHQ-4-13, 6284	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	7.70E-04	0.60	3.10	-	624.2
AHQ-4-13-, 2769 - 2824	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	5.12E-05	0.93	3.96	-	1006.3
AHQ-4-12, 2669	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	7.00E-04	0.90	3.89	-	766.3
AHQ-4-13, 2867 - 2931	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	3.12E-04	0.90	3.85	-	598.8
AHQ-4-13-, 3732 - 3733	K.TLVLLMGK.E	875.15478	2	2.45E-05	0.84	3.08	-	565.8
AHQ-4-12, 2846	K.TLVLLM*GK.E	891.15418	1	7.22E-04	0.07	1.83	-	106.3
AHQ-4-12, 2845	K.TLVLLM*GK.E	891.15418	2	5.28E-04	0.79	2.55	-	712.4
AHQ-4-13-, 3605 - 3669	K.TLVLLMGK.E	875.15478	2	4.45E-05	0.83	3.28	-	486.3
AHQ-4-13, 3760 - 3826	K.TLVLLMGK.E	875.15478	2	2.48E-04	0.84	2.91	-	521.0
AHQ-4-13, 3758 - 3825	K.TLVLLMGK.E	875.15478	1	1.94E-04	0.24	2.46	-	265.9
gi|17986001|ref|NP_005505.2| major histocompatibility complex, class I, B; HLA class I histocompati				3.28E-11	0.95	10.23	3.90	40459.8
AHQ-4-14-, 4803 - 4873	R.APWIEQEGPEYWDR.N	1776.88556	2	6.74E-11	0.95	4.49	-	1194.9
AHQ-4-8, 4445	R.APWIEQEGPEYWDR.N	1776.88556	2	3.28E-11	0.95	4.59	-	1088.6
gi|4504523|ref|NP_002148.1| heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (				3.69E-11	1.87	20.20	25.50	10931.6

AHQ-4-14-, 2679	K.VLQATVVAVGSGSK.G	1316.52902	2	3.88E-07	0.96	3.93	-	1782.1
AHQ-4-14, 3705	K.VLQATVVAVGSGSK.G	1316.52902	2	7.55E-07	0.76	2.58	-	933.2
AHQ-4-14-, 4925	K.VVLDDKDYFLFR.D	1530.74861	2	3.69E-11	0.91	3.27	-	776.8
AHQ-4-14, 6344 - 6348	K.VVLDDKDYFLFR.D	1530.74861	2	2.54E-07	0.95	3.98	-	1320.3
gi|21956645|ref|NP_665807.1| myotrophin; granule cell differentiation protein [Homo sapiens]				3.72E-11	3.84	40.33	49.20	12894.7
AHQ-4-13-, 4358	K.GADINAPDKHHITPLLSAVYEGHVSCVK.L	3031.39193	3	9.20E-05	0.98	6.17	-	2012.0
AHQ-4-14, 5004 - 5044	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.17E-04	0.96	4.42	-	1346.5
AHQ-4-13-, 4132 - 4133	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.23E-10	0.97	5.66	-	1509.6
AHQ-4-13-, 3996 - 4069	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.94E-08	0.98	6.37	-	1526.9
AHQ-4-13, 4136 - 4213	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.72E-11	0.98	6.48	-	1994.3
AHQ-4-13, 4252	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.13E-07	0.95	4.79	-	1105.2
AHQ-4-14-, 3823 - 3869	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	6.19E-05	0.98	5.47	-	1882.0
AHQ-4-14, 4944 - 5000	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.05E-05	0.97	5.18	-	1706.7
AHQ-4-14, 4849 - 4925	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	5.40E-04	0.95	4.90	-	889.1
AHQ-4-13, 4118 - 4122	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	1.71E-08	0.98	6.56	-	2848.4
AHQ-4-13-, 3984	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	3.68E-06	0.98	5.63	-	2319.0
AHQ-4-13, 4116	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	2	5.31E-05	0.96	5.32	-	1213.7
AHQ-4-13-, 3696 - 3717	K.NGDLDEVKDYVAK.G	1466.57496	2	1.13E-09	0.93	3.78	-	1274.2
AHQ-4-13-, 3597	K.NGDLDEVKDYVAK.G	1466.57496	2	2.21E-08	0.90	3.52	-	996.8
AHQ-4-14, 4501	K.NGDLDEVKDYVAK.G	1466.57496	2	3.45E-08	0.91	3.57	-	1019.9
AHQ-4-14, 4610	K.NGDLDEVKDYVAK.G	1466.57496	2	1.64E-07	0.93	3.73	-	1204.6
AHQ-4-13, 3868	K.NGDLDEVKDYVAK.G	1466.57496	1	5.81E-09	0.72	3.35	-	435.9
AHQ-4-14-, 3517	K.NGDLDEVKDYVAK.G	1466.57496	1	1.52E-04	0.44	2.01	-	433.9
AHQ-4-14-, 3518	K.NGDLDEVKDYVAK.G	1466.57496	2	4.99E-08	0.94	3.84	-	1268.4
AHQ-4-14-, 3614	K.NGDLDEVKDYVAK.G	1466.57496	2	1.04E-09	0.90	3.39	-	829.4
AHQ-4-13, 3856 - 3858	K.NGDLDEVKDYVAK.G	1466.57496	2	8.40E-09	0.96	4.53	-	1629.0
gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]				4.24E-11	13.43	160.30	70.90	22391.3
AHQ-4-13, 5921 - 5992	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.09E-04	0.94	4.07	-	1218.1
AHQ-4-12, 5805 - 5882	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.02E-08	0.97	4.70	-	1538.5
AHQ-4-12, 5937 - 6013	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.27E-07	0.96	4.81	-	1309.0
AHQ-4-12, 6077	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.02E-06	0.96	4.74	-	1306.7
AHQ-4-12, 6161 - 6167	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.23E-04	0.93	3.90	-	1044.4
AHQ-4-11, 5808 - 5868	R.DDGLFSGDPNWFPK.K	1595.69288	2	3.65E-04	0.97	4.81	-	1366.5
AHQ-4-11, 5969	R.DDGLFSGDPNWFPK.K	1595.69288	2	4.41E-04	0.88	3.22	-	953.2
AHQ-4-11, 5656 - 5724	R.DDGLFSGDPNWFPK.K	1595.69288	2	6.88E-06	0.96	4.44	-	1315.0
AHQ-4-12, 5071	R.DDGLFSGDPNWFPKK.S	1723.86579	2	4.80E-04	0.69	2.92	-	612.5
AHQ-4-12, 6310	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.93E-06	0.83	3.82	-	490.2
AHQ-4-11, 6845 - 6852	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	3	5.20E-06	0.63	3.57	-	594.6
AHQ-4-14-, 6113 - 6174	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	5.24E-06	0.83	3.99	-	312.5
AHQ-4-13, 6562	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	3.24E-04	0.53	3.00	-	405.0
AHQ-4-13-, 6217	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	3.05E-04	0.93	4.36	-	830.5
AHQ-4-11, 6324	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	8.77E-09	0.93	4.09	-	983.3
AHQ-4-13, 6961	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	3.55E-04	0.62	3.23	-	584.1
AHQ-4-11, 6769	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.16E-04	0.32	2.63	-	368.1
AHQ-4-11, 6772	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	7.12E-08	0.88	4.28	-	716.0
AHQ-4-13, 6956	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	7.90E-10	0.93	4.95	-	839.3
AHQ-4-13-, 6834 - 6840	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.03E-08	0.91	4.55	-	825.1
AHQ-4-13-, 6838	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	5.73E-07	0.80	4.03	-	593.6
AHQ-4-11, 5798 - 5800	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.07E-05	0.81	3.60	-	535.9
AHQ-4-12, 7010 - 7017	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.86E-09	0.90	4.76	-	962.3
AHQ-4-14-, 6729	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	7.26E-08	0.84	4.07	-	744.3
AHQ-4-12, 5762	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.47E-09	0.87	3.99	-	895.7
AHQ-4-14-, 6731 - 6734	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.97E-07	0.90	4.72	-	670.5
AHQ-4-12, 5761	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	8.26E-08	0.74	3.53	-	387.9
AHQ-4-11, 2597 - 2598	R.GASQAGMTGYGMPR.Q	1384.56732	2	9.25E-06	0.79	2.97	-	758.1
AHQ-4-12, 1902 - 1961	R.GPAYGLSR.E	820.91599	2	4.01E-04	0.86	2.83	-	930.8
AHQ-4-11, 2410	K.IQASTMAFK.Q	997.19374	1	8.80E-05	0.72	2.74	-	601.3
AHQ-4-11, 2370	R.NFSDNQLQEGK.N	1280.32582	2	3.89E-06	0.92	3.07	-	1490.7
AHQ-4-13-, 2277	R.NFSDNQLQEGK.N	1280.32582	1	9.97E-05	0.57	2.82	-	334.1
AHQ-4-12, 2577	R.NFSDNQLQEGK.N	1280.32582	2	1.28E-04	0.93	3.52	-	1256.5
AHQ-4-12, 2414	R.NFSDNQLQEGK.N	1280.32582	2	8.31E-06	0.94	3.63	-	1341.1
AHQ-4-12, 2313	R.NFSDNQLQEGK.N	1280.32582	1	1.32E-06	0.25	2.32	-	214.6
AHQ-4-12, 2113 - 2193	R.NFSDNQLQEGK.N	1280.32582	1	1.30E-04	0.06	1.99	-	192.4
AHQ-4-11, 2236 - 2250	K.NVIGLQM*GTNR.G	1219.39691	2	1.83E-04	0.94	3.41	-	1097.2
AHQ-4-13-, 5414	K.QMEQISQFLQAAER.Y	1679.87950	2	2.70E-09	0.95	4.56	-	1164.1
AHQ-4-12, 5451 - 5461	K.QMEQISQFLQAAER.Y	1679.87950	2	6.52E-07	0.94	4.42	-	1049.1
AHQ-4-13, 5549	K.QMEQISQFLQAAER.Y	1679.87950	2	4.27E-05	0.93	3.97	-	1124.0
AHQ-4-12, 4697	K.QM*EQISQFLQAAER.Y	1695.87890	2	2.77E-05	0.83	3.47	-	662.2
AHQ-4-11, 5210 - 5218	K.QMEQISQFLQAAER.Y	1679.87950	2	1.35E-04	0.96	4.66	-	1287.8
AHQ-4-13-, 6008	K.QMEQISQFLQAAER.Y	1679.87950	2	6.98E-07	0.87	2.98	-	1538.7
AHQ-4-11, 3440 - 3456	R.TLM*NLGGLAVAR.D	1232.47872	2	3.74E-04	0.92	4.04	-	884.8
AHQ-4-12, 4790	R.TLMNLGGLAVAR.D	1216.47932	2	8.18E-07	0.93	3.89	-	1252.7
AHQ-4-12, 4413 - 4437	R.TLMNLGGLAVAR.D	1216.47932	2	1.08E-06	0.94	4.33	-	1296.9
AHQ-4-13, 4570	R.TLMNLGGLAVAR.D	1216.47932	2	1.14E-04	0.87	3.78	-	846.3
AHQ-4-12, 3993	R.TLM*NLGGLAVAR.D	1232.47872	2	2.20E-06	0.86	3.24	-	817.6
AHQ-4-11, 4280 - 4344	R.TLMNLGGLAVAR.D	1216.47932	2	7.87E-04	0.87	3.74	-	960.0
AHQ-4-12, 3525 - 3593	R.TLM*NLGGLAVAR.D	1232.47872	2	4.35E-06	0.94	4.40	-	937.8
AHQ-4-11, 3873	R.TLM*NLGGLAVAR.D	1232.47872	2	9.50E-05	0.91	3.23	-	1128.6
AHQ-4-13, 6869	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	4.24E-11	0.96	5.33	-	983.6
AHQ-4-11, 6217 - 6253	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.21E-06	0.91	4.25	-	926.8
AHQ-4-11, 6317	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.07E-08	0.90	4.29	-	589.7
AHQ-4-11, 6602 - 6681	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.63E-08	0.97	5.52	-	1513.7
AHQ-4-12, 6961 - 7034	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	6.75E-11	0.98	6.07	-	1427.0
AHQ-4-11, 6682	R.YGINTTDIFQTVDLWEGK.N	2101.30080	3	1.50E-06	0.83	3.59	-	670.5
AHQ-4-12, 6829 - 6893	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	7.01E-08	0.94	4.78	-	850.8
AHQ-4-13-, 6756 - 6757	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.95E-09	0.97	5.32	-	1033.0
AHQ-4-12, 6726 - 6770	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	4.51E-09	0.96	5.12	-	988.8
AHQ-4-14-, 6594 - 6657	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.35E-08	0.96	5.14	-	1139.0
AHQ-4-12, 6467 - 6539	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	8.55E-08	0.94	4.24	-	1131.2
AHQ-4-12, 7113 - 7175	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.85E-10	0.96	4.63	-	1019.5
AHQ-4-12, 6898	R.YGINTTDIFQTVDLWEGKNMACVQR.T	2962.30673	3	1.07E-10	0.94	4.89	-	1241.7
AHQ-4-12, 6693	R.YGINTTDIFQTVDLWEGKNM*ACVQR.T	2978.30613	3	7.11E-05	0.89	4.40	-	622.0
gi|4507677|ref|NP_003290.1| tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu				4.33E-11	7.18	90.31	15.30	92468.2
AHQ-4-5, 6389	R.EAVEKEFEPLLNWMK.D	1864.15434	2	5.20E-06	0.89	3.97	-	633.2
AHQ-4-5, 3695	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	1.04E-04	0.94	4.54	-	1041.9
AHQ-4-1, 4163	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	3.38E-04	0.73	3.12	-	578.9
AHQ-4-5, 3974	K.GVVDSDDLPLNVSR.E	1486.60940	1	2.21E-05	0.15	2.01	-	280.6
AHQ-4-5, 3970	K.GVVDSDDLPLNVSR.E	1486.60940	2	7.31E-05	0.61	2.82	-	639.2
AHQ-4-5, 6905 - 6907	K.GYEVIYLTEPVDEYCIQALPEFDGKR.F	3107.43557	3	4.45E-05	0.86	4.02	-	690.3
AHQ-4-5, 3458	K.IADDKYNDTFWK.E	1516.63566	2	4.33E-11	0.93	3.69	-	1178.2
AHQ-4-5, 6263	K.KYSQFINFPIYVWSSK.T	2008.30657	2	6.03E-09	0.96	4.71	-	1554.1
AHQ-4-5, 3301	R.LSLNIDPDAK.V	1086.22065	1	1.94E-05	0.59	2.39	-	818.1
AHQ-4-5, 3878	K.SILFVPTSAPR.G	1188.40094	2	2.53E-04	0.87	2.95	-	1111.5
AHQ-4-6, 6750 - 6812	K.YSQFINFPIYVWSSK.T	1880.13366	2	1.03E-04	0.86	3.58	-	679.4
AHQ-4-5, 6922 - 6927	K.YSQFINFPIYVWSSK.T	1880.13366	2	2.91E-08	0.98	6.22	-	1631.1
gi|4758638|ref|NP_004896.1| peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi				4.84E-11	6.92	90.33	43.80	25034.8
AHQ-4-10, 4149	K.DGDSVM*VLPTIPEEEAK.K	1847.03409	2	3.72E-05	0.49	2.57	-	361.7

AHQ-4-10, 4689 - 4725	R.ELAILLGM*LDPAEKDEK.G	1902.19916	2	6.30E-04	0.96	5.08	-	1107.3
AHQ-4-10, 5651	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	6.35E-05	0.95	4.68	-	1055.5
AHQ-4-10, 5839 - 5840	R.FHDFLGDSWGILFSHPR.D	2032.24831	3	6.97E-09	0.96	4.87	-	1365.7
AHQ-4-10, 5835 - 5865	R.FHDFLGDSWGILFSHPR.D	2032.24831	2	4.84E-11	0.99	6.64	-	2910.1
AHQ-4-14-, 6290	R.FHDFLGDSWGILFSHPR.D	2032.24831	3	3.67E-07	0.94	4.76	-	1017.5
AHQ-4-10, 5724	R.FHDFLGDSWGILFSHPR.D	2032.24831	2	3.97E-06	0.96	4.56	-	1329.9
AHQ-4-14-, 5854	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	2.71E-06	0.60	3.16	-	332.6
AHQ-4-10, 5441 - 5512	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	1.19E-10	0.97	5.09	-	1580.2
AHQ-4-14-, 5853	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	4.56E-08	0.98	5.96	-	1943.2
AHQ-4-10, 4112 - 4113	K.LPFPIIDDR.N	1086.26548	2	4.06E-06	0.91	3.88	-	724.3
AHQ-4-10, 4120	K.LPFPIIDDR.N	1086.26548	1	7.56E-07	0.32	2.20	-	227.4
AHQ-4-10, 3263	K.LSILYPATTGR.N	1192.38959	2	5.92E-06	0.77	2.94	-	625.4
AHQ-4-10, 3489	R.VVFVFGPDK.K	1008.19471	1	3.63E-04	0.62	1.95	-	1023.1
AHQ-4-10, 2777	R.VVFVFGPDKK.L	1136.36763	2	1.48E-04	0.85	2.97	-	956.4
gi|20270343|ref|NP_620150.1|	hypothetical protein BC015408 [Homo sapiens]			5.05E-11	3.49	40.28	29.00	21415.8
AHQ-4-11, 3884 - 3896	R.DLPGALDEKELIEK.M	1570.76622	2	6.00E-04	0.69	3.17	-	312.4
AHQ-4-11, 5262	R.GVSAIVYMVDAADQEK.I	1696.90360	2	8.72E-08	0.86	3.75	-	725.8
AHQ-4-11, 5833	K.NELHNLLDKPQLQGIPVLVLGNK.R	2553.98492	2	3.53E-07	0.96	5.27	-	1216.9
AHQ-4-11, 5474	K.NELHNLLDKPQLQGIPVLVLGNKR.D	2710.17128	3	5.05E-11	0.98	5.66	-	2088.2
gi|4505257|ref|NP_002435.1|	moesin [Homo sapiens]			5.19E-11	10.94	120.29	25.60	67819.5
AHQ-4-6, 2303	K.ALTSELANAR.D	1046.15975	2	4.71E-04	0.87	3.06	-	817.0
AHQ-4-6, 2095 - 2171	K.AQMVQEDLEK.T	1191.33713	2	2.84E-04	0.79	3.21	-	422.9
AHQ-4-6, 7182	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	3	2.77E-07	0.92	5.24	-	782.0
AHQ-4-6, 6187	R.EVWFFGLQYQDTK.G	1661.83760	2	2.05E-08	0.97	3.78	-	1885.4
AHQ-4-11, 6693	K.FYPEDVSEELIQDITQR.L	2083.24065	2	1.13E-07	0.92	3.92	-	897.9
AHQ-4-6, 7110	K.FYPEDVSEELIQDITQR.L	2083.24065	3	9.07E-06	0.96	4.80	-	1756.1
AHQ-4-6, 7102 - 7103	K.FYPEDVSEELIQDITQR.L	2083.24065	2	3.89E-10	0.96	5.31	-	1023.9
AHQ-4-13, 6861	K.FYPEDVSEELIQDITQR.L	2083.24065	2	5.26E-06	0.95	4.33	-	1138.8
AHQ-4-10, 6388	K.FYPEDVSEELIQDITQR.L	2083.24065	2	6.59E-04	0.60	3.36	-	461.1
AHQ-4-6, 6148	K.IAQDLEMYGVNYFSIK.N	1892.16455	2	2.61E-04	0.76	2.65	-	684.4
AHQ-4-6, 1634	R.IQVWHEEHR.G	1234.34835	2	2.84E-05	0.92	3.05	-	1359.4
AHQ-4-6, 4490	K.KTQEQLALEMAELTAR.I	1833.10018	2	2.78E-09	0.97	4.66	-	1759.9
AHQ-4-6, 3434	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	1.07E-09	0.95	5.44	-	1367.4
AHQ-4-6, 3298 - 3366	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	1.12E-07	0.94	4.60	-	1528.0
AHQ-4-6, 3079	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	5.19E-11	0.89	4.20	-	1031.9
AHQ-4-6, 5183	K.TQEQLALEMAELTAR.I	1704.92727	2	2.63E-08	0.98	5.85	-	1924.1
AHQ-4-6, 3796	K.TQEQLALEM*AELTAR.I	1720.92667	2	3.73E-05	0.96	4.73	-	1428.9
gi|4504515|ref|NP_002146.1|	heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B			5.23E-11	3.27	50.25	8.20	70853.4
AHQ-4-6, 4755	R.IINEPTAAAIAYGLDR.R	1688.90603	3	2.30E-05	0.92	3.81	-	1670.4
AHQ-4-6, 4743 - 4744	R.IINEPTAAAIAYGLDR.R	1688.90603	2	5.23E-11	0.97	5.00	-	1445.5
AHQ-4-7, 4687	R.IINEPTAAAIAYGLDR.R	1688.90603	2	1.58E-05	0.92	3.77	-	945.6
AHQ-4-6, 4248 - 4319	K.LLQDFFNGK.E	1082.23369	1	5.59E-04	0.18	2.07	-	226.0
AHQ-4-6, 4191 - 4202	K.LLQDFFNGKELNK.S	1566.78249	2	3.92E-04	0.92	4.03	-	1138.3
AHQ-4-6, 3199	R.TTPSYVAFTDTER.L	1488.58062	1	2.06E-04	0.12	2.30	-	118.2
AHQ-4-12, 3366	R.TTPSYVAFTDTER.L	1488.58062	2	1.95E-05	0.73	2.59	-	563.3
AHQ-4-6, 1866	R.VEILANDQGNR.T	1229.32518	1	3.72E-04	0.47	2.43	-	261.0
gi|4505733|ref|NP_002610.1|	platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4			5.24E-11	5.56	60.27	38.60	10844.9
AHQ-4-14, 5384 - 5454	K.AGPHCPTAQLIATLK.N	1579.84600	2	6.01E-09	0.92	4.20	-	772.9
AHQ-4-12, 4002 - 4079	K.AGPHCPTAQLIATLK.N	1579.84600	2	2.64E-04	0.88	3.59	-	703.7
AHQ-4-14-, 3897 - 3919	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.20E-07	0.95	4.08	-	1204.4
AHQ-4-14-, 3905 - 3915	K.AGPHCPTAQLIATLK.N	1579.84600	3	3.48E-04	0.91	4.24	-	1223.0
AHQ-4-14-, 4162 - 4226	K.AGPHCPTAQLIATLK.N	1579.84600	2	3.59E-04	0.72	3.11	-	476.2
AHQ-4-14-, 4055 - 4130	K.AGPHCPTAQLIATLK.N	1579.84600	3	7.39E-05	0.83	3.87	-	990.6
AHQ-4-14-, 4010 - 4090	K.AGPHCPTAQLIATLK.N	1579.84600	2	6.92E-07	0.92	3.71	-	949.0
AHQ-4-13-, 4136 - 4157	K.AGPHCPTAQLIATLK.N	1579.84600	3	3.85E-04	0.81	3.98	-	815.4
AHQ-4-13-, 4116 - 4140	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.07E-04	0.92	3.68	-	895.8
AHQ-4-14, 5481	K.AGPHCPTAQLIATLK.N	1579.84600	3	5.95E-04	0.87	3.67	-	1019.7
AHQ-4-14, 5288 - 5338	K.AGPHCPTAQLIATLK.N	1579.84600	3	1.75E-05	0.61	3.46	-	617.9
AHQ-4-14, 5249 - 5325	K.AGPHCPTAQLIATLK.N	1579.84600	2	6.28E-04	0.93	4.07	-	779.9
AHQ-4-14, 5122 - 5186	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.08E-06	0.90	3.56	-	690.2
AHQ-4-14, 5765	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.21E-05	0.87	3.73	-	600.9
AHQ-4-14, 4929	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	5.13E-08	0.97	4.91	-	2126.3
AHQ-4-14, 4948	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	1.34E-08	0.96	4.57	-	1180.8
AHQ-4-14, 5090	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	1.26E-10	0.95	4.32	-	1069.9
AHQ-4-14, 4812 - 4821	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	6.04E-10	0.97	5.41	-	1796.8
AHQ-4-14, 5214	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.25E-07	0.91	3.71	-	971.3
AHQ-4-14-, 3829 - 3854	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.55E-09	0.97	5.28	-	1991.0
AHQ-4-13-, 4036	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	5.24E-11	0.96	4.24	-	2053.0
AHQ-4-14-, 3847	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	9.20E-08	0.95	5.09	-	876.0
AHQ-4-13-, 4054	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	8.48E-07	0.94	3.94	-	1166.3
AHQ-4-13, 4160	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	5.51E-06	0.97	4.81	-	2519.1
AHQ-4-14-, 3741	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	4.16E-08	0.96	5.08	-	1806.7
AHQ-4-14, 4816	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	9.73E-05	0.94	4.49	-	948.2
AHQ-4-13-, 3904	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	2.56E-06	0.96	4.54	-	2091.7
AHQ-4-14, 4529 - 4532	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	7.43E-10	0.95	4.77	-	1433.7
AHQ-4-14-, 3599	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	6.76E-08	0.87	3.77	-	733.0
AHQ-4-14-, 2482 - 2541	R.HITSLEVIK.A	1040.23825	2	1.16E-05	0.90	3.23	-	644.4
AHQ-4-13-, 2569 - 2632	R.HITSLEVIK.A	1040.23825	2	2.15E-06	0.90	3.43	-	671.6
AHQ-4-14-, 2357 - 2421	R.HITSLEVIK.A	1040.23825	2	2.18E-08	0.92	3.90	-	607.1
AHQ-4-14, 3557 - 3620	R.HITSLEVIK.A	1040.23825	2	1.45E-06	0.87	3.07	-	546.1
AHQ-4-14, 3436 - 3496	R.HITSLEVIK.A	1040.23825	2	5.37E-06	0.81	3.04	-	488.7
AHQ-4-14, 3333 - 3400	R.HITSLEVIK.A	1040.23825	2	2.85E-04	0.79	3.06	-	528.8
AHQ-4-13, 2698 - 2725	R.HITSLEVIK.A	1040.23825	2	4.81E-05	0.86	2.96	-	590.3
AHQ-4-14-, 2358	R.HITSLEVIK.A	1040.23825	1	9.12E-05	0.36	2.20	-	389.0
AHQ-4-14-, 4845 - 4909	K.ICLDLQAPLYK.K	1335.59400	2	2.91E-07	0.98	4.54	-	2458.6
AHQ-4-13-, 4909	K.ICLDLQAPLYK.K	1335.59400	2	1.37E-04	0.96	4.17	-	1721.8
AHQ-4-13, 5037	K.ICLDLQAPLYK.K	1335.59400	2	2.58E-05	0.95	4.03	-	1549.6
AHQ-4-14, 6382	K.ICLDLQAPLYK.K	1335.59400	2	1.41E-04	0.95	4.10	-	1146.1
AHQ-4-14, 6165 - 6228	K.ICLDLQAPLYK.K	1335.59400	2	3.97E-06	0.97	4.23	-	2281.7
AHQ-4-13-, 4404 - 4405	R.KICLDLQAPLYK.K	1463.76691	2	4.50E-08	0.97	5.02	-	1606.2
AHQ-4-14, 6037	R.KICLDLQAPLYK.K	1463.76691	2	1.59E-07	0.95	4.29	-	1076.0
AHQ-4-14, 5790 - 5864	R.KICLDLQAPLYK.K	1463.76691	2	3.05E-05	0.96	4.15	-	1467.1
AHQ-4-14, 5686 - 5745	R.KICLDLQAPLYK.K	1463.76691	2	6.65E-04	0.87	3.88	-	544.1
AHQ-4-14, 5549 - 5612	R.KICLDLQAPLYK.K	1463.76691	2	4.72E-07	0.98	5.33	-	2156.1
AHQ-4-13, 4545	R.KICLDLQAPLYK.K	1463.76691	1	1.33E-05	0.84	3.21	-	807.2
AHQ-4-13, 4541	R.KICLDLQAPLYK.K	1463.76691	3	5.88E-06	0.93	4.29	-	1195.0
AHQ-4-13, 4533	R.KICLDLQAPLYK.K	1463.76691	2	2.66E-05	0.97	4.61	-	1543.8
AHQ-4-14-, 4218	R.KICLDLQAPLYK.K	1463.76691	2	1.15E-05	0.96	4.37	-	1433.0
AHQ-4-14-, 4349 - 4421	R.KICLDLQAPLYK.K	1463.76691	2	8.29E-08	0.97	4.56	-	1620.2
AHQ-4-14-, 4361 - 4439	R.KICLDLQAPLYK.K	1463.76691	3	1.94E-06	0.94	4.25	-	1572.2
AHQ-4-14-, 4446	R.KICLDLQAPLYK.K	1463.76691	1	4.15E-08	0.83	3.49	-	543.8
AHQ-4-14-, 4485 - 4558	R.KICLDLQAPLYK.K	1463.76691	2	2.99E-05	0.95	4.29	-	1297.8
AHQ-4-8, 3942	R.KICLDLQAPLYK.K	1463.76691	2	2.95E-04	0.85	2.72	-	962.3
gi|18104967|ref|NP_000953.2|	prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland			6.10E-11	6.00	70.27	24.40	68686.0
AHQ-4-6, 3726	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	2.28E-07	0.87	3.67	-	686.3
AHQ-4-6, 3730 - 3748	K.AEHPTWGDEQLFQTTR.L	1917.02765	3	9.96E-04	0.84	3.46	-	1227.7
AHQ-4-6, 3647 - 3728	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	3	7.84E-05	0.87	3.43	-	1195.7

AHQ-4-6, 3646	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	2	2.84E-04	0.97	5.13	-	1423.5
AHQ-4-6, 7303	K.EM*AAELEELYGDIDALEFYPGLLLEK.C	2989.33908	2	3.12E-06	0.68	3.18	-	347.8
AHQ-4-6, 4947	R.FGMKPYTSFQELVGEK.E	1862.13845	2	1.88E-07	0.94	4.24	-	767.1
AHQ-4-6, 6979 - 7012	K.GLLGNPICSPEYWKPSTFGGEVGFNIVK.T	3069.47853	3	1.49E-06	0.80	4.16	-	427.2
AHQ-4-6, 3591	R.NSLRPSPSFTHFLLTHGR.W	2068.32687	3	3.65E-04	0.90	3.80	-	1284.3
AHQ-4-6, 5800 - 5814	K.YQVLDGEMYPPSVEEAPVLMHYPR.G	2822.20799	3	6.10E-11	0.93	5.34	-	631.1
gi|4504349|ref|NP_000509.1| beta globin [Homo sapiens]				6.65E-11	8.07	100.29	73.50	15998.3
AHQ-4-14, 6240	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	5.00E-06	0.89	4.31	-	605.4
AHQ-4-14-, 4970 - 4973	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	2.03E-05	0.95	4.84	-	901.4
AHQ-4-13-, 5125 - 5137	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	6.17E-06	0.90	4.05	-	642.2
AHQ-4-13-, 5044	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.25E-04	0.57	2.83	-	390.5
AHQ-4-13-, 4954 - 5020	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.01E-05	0.90	4.36	-	532.7
AHQ-4-13-, 5553 - 5568	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	3.56E-06	0.96	4.86	-	1173.1
AHQ-4-13-, 5372	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	8.80E-05	0.90	4.04	-	624.9
AHQ-4-13, 5673 - 5740	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	4.10E-07	0.95	4.94	-	923.9
AHQ-4-13, 5030 - 5044	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	9.53E-06	0.89	4.02	-	649.3
AHQ-4-13, 5128 - 5192	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	3.60E-06	0.88	4.16	-	497.6
AHQ-4-13, 5140	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	1.83E-04	0.89	3.50	-	1386.9
AHQ-4-13-, 3500	K.GTFATLSELHCDK.L	1480.62492	2	2.00E-08	0.86	3.75	-	585.6
AHQ-4-13-, 4992 - 5000	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	1.02E-10	0.93	4.67	-	1077.4
AHQ-4-13, 4873	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	7.02E-06	0.96	5.24	-	1168.5
AHQ-4-13-, 4770	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	1.60E-09	0.97	5.90	-	1382.3
AHQ-4-13-, 6572	R.LLGNVLVCVLAHHFGK.E	1779.14197	3	9.25E-06	0.64	3.18	-	443.0
AHQ-4-13-, 3438 - 3442	K.SAVTALWGK.V	933.08624	2	5.37E-05	0.65	2.51	-	595.0
AHQ-4-13, 3577 - 3582	K.SAVTALWGK.V	933.08624	2	2.23E-06	0.80	2.55	-	823.6
AHQ-4-13-, 4941	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	3.96E-08	0.97	5.60	-	1404.4
AHQ-4-13, 5132 - 5212	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	6.65E-11	0.97	5.27	-	1431.8
AHQ-4-13-, 5109 - 5176	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	8.62E-08	0.97	4.99	-	1703.2
AHQ-4-13, 5216	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	8.61E-07	0.74	3.16	-	525.5
AHQ-4-14-, 5078	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	6.27E-09	0.97	4.32	-	1862.4
AHQ-4-13-, 3250	K.VNVDEVGGEALGR.L	1315.41484	1	4.43E-07	0.45	2.55	-	265.0
AHQ-4-13, 3378	K.VNVDEVGGEALGR.L	1315.41484	2	1.11E-04	0.97	4.86	-	1635.8
AHQ-4-13, 3503	K.VNVDEVGGEALGR.L	1315.41484	2	6.56E-05	0.97	4.35	-	2231.5
AHQ-4-14-, 3206	K.VNVDEVGGEALGR.L	1315.41484	2	1.46E-04	0.87	3.28	-	954.6
AHQ-4-13, 3381	K.VNVDEVGGEALGR.L	1315.41484	1	1.71E-06	0.52	2.75	-	373.8
AHQ-4-13-, 3253	K.VNVDEVGGEALGR.L	1315.41484	1	1.49E-05	0.74	3.38	-	325.3
AHQ-4-13-, 2177	K.VVAGVANALAHK.Y	1150.35593	2	2.87E-07	0.96	4.20	-	1522.1
AHQ-4-13, 2790	K.VVAGVANALAHK.Y	1150.35593	2	1.13E-07	0.96	3.83	-	1581.7
AHQ-4-13, 2467 - 2546	K.VVAGVANALAHK.Y	1150.35593	2	7.48E-04	0.82	3.21	-	721.5
AHQ-4-13, 2302	K.VVAGVANALAHK.Y	1150.35593	1	7.99E-08	0.61	2.56	-	576.6
AHQ-4-13-, 2684	K.VVAGVANALAHK.Y	1150.35593	2	1.27E-05	0.96	3.76	-	1531.9
gi|29732955|ref|XP_291603.1| similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA				6.68E-11	0.88	10.23	16.80	11173.0
AHQ-4-10, 3656 - 3713	K.NISNASCTTNCIAPLAK.M	1838.05353	2	5.70E-04	0.51	2.80	-	750.2
AHQ-4-10, 3899 - 3964	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.85E-04	0.73	2.90	-	940.7
AHQ-4-11, 3828 - 3881	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.99E-06	0.81	4.02	-	1010.9
AHQ-4-11, 4197	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.79E-05	0.91	3.57	-	985.5
AHQ-4-9, 3692 - 3707	K.NISNASCTTNCIAPLAK.M	1838.05353	2	6.68E-11	0.88	4.61	-	953.2
gi|4758504|ref|NP_004484.1| hydroxyacyl-Coenzyme A dehydrogenase, type II [Homo sapiens]				7.16E-11	1.83	20.22	18.80	26922.9
AHQ-4-10, 6516	R.LGDPAEYAHLVQAIIENPFLNGEVIR.L	2880.24689	2	7.16E-11	0.93	4.15	-	1039.7
AHQ-4-10, 4567 - 4640	R.LVGQGASAVLLDLPNSGGEAQAK.K	2196.44680	2	5.11E-09	0.90	4.44	-	553.4
gi|4557305|ref|NP_000025.1| aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho				7.81E-11	11.13	130.27	54.10	39419.7
AHQ-4-8, 1867 - 1945	R.ALANSLACQGK.Y	1134.28859	2	2.06E-05	0.74	2.82	-	747.9
AHQ-4-8, 4306	R.ALANSLACQGKYTPSGQAGAAASESLFVSNHAY	3344.61352	3	2.32E-10	0.59	3.22	-	503.7
AHQ-4-8, 3721	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	4.24E-06	0.95	5.43	-	1112.2
AHQ-4-8, 3822	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	1.94E-04	0.86	4.10	-	723.6
AHQ-4-8, 5802 - 5825	K.CPLLKPWALTFSYGR.A	1811.13929	2	2.86E-05	0.86	3.80	-	588.4
AHQ-4-8, 3813	K.FSHEEIAMATVTALR.R	1676.91875	2	7.46E-09	0.95	4.44	-	1355.3
AHQ-4-13, 3015	K.GILAADESTGSIAK.R	1333.47008	2	1.52E-10	0.97	4.39	-	1636.7
AHQ-4-8, 2537	K.GILAADESTGSIAK.R	1333.47008	1	9.71E-06	0.54	3.15	-	271.1
AHQ-4-8, 2534	K.GILAADESTGSIAK.R	1333.47008	2	5.73E-08	0.97	4.58	-	1584.3
AHQ-4-12, 2863	K.GILAADESTGSIAK.R	1333.47008	2	4.29E-04	0.87	3.41	-	861.0
AHQ-4-11, 2813	K.GILAADESTGSIAK.R	1333.47008	2	8.05E-07	0.96	4.16	-	1433.0
AHQ-4-13-, 2901	K.GILAADESTGSIAK.R	1333.47008	2	3.55E-09	0.96	4.13	-	1700.4
AHQ-4-1, 4839	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	6.14E-06	0.50	3.73	-	221.1
AHQ-4-10, 4224	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	6.05E-08	0.51	3.75	-	296.0
AHQ-4-8, 4058 - 4138	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	7.81E-11	0.88	5.16	-	750.7
AHQ-4-9, 4151	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	1.52E-07	0.79	4.80	-	443.5
AHQ-4-9, 4016 - 4080	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	5.64E-08	0.77	4.45	-	515.5
AHQ-4-9, 3897 - 3920	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	2.08E-07	0.91	4.31	-	681.2
AHQ-4-9, 4753	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	6.10E-04	0.93	4.61	-	749.5
AHQ-4-8, 4862 - 4869	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.33E-04	0.97	5.42	-	1228.5
AHQ-4-8, 3754	K.VDKGVVPLAGTNGETTTQGLDGLSER.C	2615.83564	3	7.51E-05	0.66	3.76	-	842.5
AHQ-4-8, 6039	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	7.87E-06	0.94	4.07	-	941.4
AHQ-4-8, 5837	R.YASICQQNGIVPIVEPEILPDGDHDLK.R	3023.36334	3	1.05E-04	0.91	5.28	-	614.1
AHQ-4-8, 5135	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	6.53E-05	0.81	3.97	-	558.0
AHQ-4-8, 4087 - 4169	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	3.02E-10	0.88	4.17	-	405.0
AHQ-4-8, 4306	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	2.34E-08	0.91	3.97	-	719.5
gi|4885063|ref|NP_005156.1| aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase				8.73E-11	1.75	20.27	7.10	39455.6
AHQ-4-8, 4211	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	4.42E-08	0.95	4.46	-	999.4
AHQ-4-8, 4317 - 4385	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.25E-09	0.85	5.31	-	535.4
AHQ-4-8, 3991 - 4059	K.VDKGVVPLAGTDGETTTQGLDGLSER.C	2616.82041	3	8.73E-11	0.90	5.14	-	1230.7
gi|4507109|ref|NP_000336.1| alpha-synuclein isoform NACP140; non A4 component of amyloid precursor				9.29E-11	3.61	50.28	37.90	14460.1
AHQ-4-12, 2142 - 2214	K.EGVVHGVATVAEK.T	1296.45466	2	4.86E-04	0.48	2.69	-	396.8
AHQ-4-13, 4724	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	9.29E-11	0.96	5.59	-	903.0
AHQ-4-13-, 4617	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	4.50E-04	0.91	4.32	-	650.0
AHQ-4-12, 4659	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.59E-04	0.95	4.68	-	1047.3
AHQ-4-12, 4681	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	3	4.84E-04	0.96	5.28	-	1637.7
AHQ-4-14, 5792	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	4.32E-05	0.91	4.07	-	830.7
AHQ-4-14-, 4575	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.15E-05	0.96	5.54	-	869.3
AHQ-4-12, 2033 - 2035	K.TKEGVVHGVATVAEK.T	1525.73191	2	1.81E-06	0.96	4.77	-	1388.3
AHQ-4-13, 4334	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	8.36E-05	0.84	3.47	-	1369.7
AHQ-4-13-, 4221	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	4.71E-07	0.97	5.64	-	1508.4
AHQ-4-14, 5504	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.88E-06	0.97	5.22	-	1255.6
AHQ-4-14-, 4137	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	5.43E-07	0.89	4.51	-	992.5
AHQ-4-14-, 4142	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	4.88E-07	0.97	5.64	-	1799.4
AHQ-4-13, 4338	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	7.98E-10	0.97	5.41	-	1415.8
AHQ-4-12, 4126	K.TVEGAGSIAAATGFVK.K	1479.66001	1	4.88E-06	0.25	2.28	-	357.2
gi|5803133|ref|NP_006825.1| RAB32, member RAS oncogene family [Homo sapiens]				9.75E-11	1.61	20.15	12.40	24997.1
AHQ-4-10, 4405	K.VHLPNGSPIPAVLLANK.C	1741.07044	2	9.75E-11	0.73	2.96	-	332.5
AHQ-4-10, 2281	R.YVHQLFSQHYR.A	1478.63872	2	6.69E-08	0.88	2.64	-	1106.1
gi|17986258|ref|NP_066299.2| smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo				1.05E-10	7.15	80.26	37.10	16930.0
AHQ-4-14, 5284 - 5321	K.DQGTYEDYVEGLR.V	1545.58904	2	7.74E-06	0.62	2.90	-	611.5
AHQ-4-12, 4273 - 4343	K.DQGTYEDYVEGLR.V	1545.58904	2	7.32E-08	0.96	4.13	-	1346.6
AHQ-4-12, 3843 - 3925	K.EAFQLFDR.T	1026.12699	1	9.28E-04	0.12	1.97	-	100.0
AHQ-4-12, 3847 - 3914	K.EAFQLFDR.T	1026.12699	2	4.83E-04	0.80	3.45	-	556.9
AHQ-4-12, 2237	R.HVLVTLGEK.M	996.18547	2	1.00E-05	0.87	3.48	-	488.4
AHQ-4-13-, 2284	R.HVLVTLGEK.M	996.18547	2	1.19E-06	0.89	3.27	-	678.2

AHQ-4-12, 2149 - 2209	R.HVLVTLGEK.M	996.18547	1	2.48E-05	0.78	3.51	-	570.1
AHQ-4-13, 2418	R.HVLVTLGEK.M	996.18547	1	7.26E-04	0.64	2.91	-	565.7
AHQ-4-12, 2145 - 2225	R.HVLVTLGEK.M	996.18547	1	6.49E-04	0.78	2.57	-	850.3
AHQ-4-13-, 2289	R.HVLVTLGEK.M	996.18547	1	5.06E-04	0.78	2.83	-	720.3
AHQ-4-13-, 2309	R.HVLVTLGEK.M	996.18547	1	7.83E-06	0.54	3.19	-	232.4
AHQ-4-13, 2409	R.HVLVTLGEK.M	996.18547	2	2.34E-06	0.90	3.53	-	620.1
AHQ-4-12, 2143 - 2210	R.HVLVTLGEK.M	996.18547	2	3.35E-06	0.93	3.83	-	935.7
AHQ-4-12, 4017	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.36E-09	0.94	4.31	-	1204.5
AHQ-4-14-, 3629	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.28E-05	0.92	3.69	-	1627.8
AHQ-4-13-, 4052	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.15E-07	0.80	3.09	-	764.5
AHQ-4-13-, 3752	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.07E-06	0.91	3.92	-	1017.2
AHQ-4-13-, 3737 - 3756	K.NKDQGTYEDYVEGLR.V	1787.86505	3	4.19E-04	0.64	3.07	-	606.9
AHQ-4-12, 3885 - 3889	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.10E-09	0.88	3.61	-	820.6
AHQ-4-12, 3719 - 3801	K.NKDQGTYEDYVEGLR.V	1787.86505	2	7.47E-04	0.88	3.74	-	830.4
AHQ-4-12, 3585 - 3661	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.39E-09	0.93	4.20	-	1034.3
AHQ-4-12, 3590 - 3605	K.NKDQGTYEDYVEGLR.V	1787.86505	3	9.54E-07	0.93	4.20	-	1253.9
AHQ-4-13, 3890 - 3892	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.05E-10	0.94	4.22	-	1162.6
AHQ-4-12, 3714	K.NKDQGTYEDYVEGLR.V	1787.86505	3	1.20E-04	0.91	4.08	-	1257.6
AHQ-4-14, 4654	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.00E-08	0.92	4.16	-	1029.5
AHQ-4-13, 3379 - 3455	R.VFDKEGNGTVMGAEIR.H	1723.93228	2	2.12E-07	0.92	3.96	-	1038.5
AHQ-4-13, 2783	R.VFDKEGNGTVM*GAEIR.H	1739.93168	2	2.09E-05	0.83	3.26	-	757.8
AHQ-4-12, 3169 - 3237	R.VFDKEGNGTVMGAEIR.H	1723.93228	2	8.79E-10	0.95	4.21	-	1240.3
AHQ-4-13, 6386 - 6401	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	8.22E-04	0.92	4.24	-	765.5
AHQ-4-12, 6874 - 6875	K.VLDFEHFLPMLQTVAK.N	1889.25017	3	7.46E-04	0.92	3.84	-	1646.2
AHQ-4-12, 6838 - 6897	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	6.29E-09	0.95	5.01	-	922.7
AHQ-4-12, 6289 - 6370	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	5.61E-06	0.84	3.43	-	752.8
AHQ-4-13-, 6326	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	4.26E-05	0.81	3.28	-	871.1
AHQ-4-13-, 6753	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	9.78E-07	0.95	4.98	-	769.0
AHQ-4-12, 6279 - 6341	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	1.67E-05	0.95	5.20	-	961.9
AHQ-4-14-, 6185	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	2.20E-05	0.89	4.05	-	747.8
AHQ-4-14-, 6189	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	1.96E-04	0.92	4.49	-	657.2
AHQ-4-14-, 6641 - 6645	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	1.13E-10	0.95	5.05	-	848.6
AHQ-4-14-, 6643	K.VLDFEHFLPMLQTVAK.N	1889.25017	3	2.78E-05	0.93	4.44	-	1211.1
gi|30159830|ref|XP_302246.1| similar to HSPC280 [Homo sapiens]				1.06E-10	1.91	20.27	3.90	45644.4
AHQ-4-13, 6948	K.CANLFEALVGTLK.A	1437.68632	2	8.75E-08	0.97	4.86	-	1448.9
AHQ-4-13-, 6828 - 6829	K.CANLFEALVGTLK.A	1437.68632	2	9.54E-07	0.97	5.40	-	1498.3
AHQ-4-14-, 6723	K.CANLFEALVGTLK.A	1437.68632	2	7.18E-08	0.95	4.31	-	1225.0
AHQ-4-14-, 6670	R.DDKCANLFEALVGTLK.A	1796.03496	2	1.06E-10	0.96	4.79	-	1364.8
AHQ-4-14-, 6673	R.DDKCANLFEALVGTLK.A	1796.03496	3	1.17E-04	0.97	4.81	-	2526.8
AHQ-4-13-, 6778	R.DDKCANLFEALVGTLK.A	1796.03496	2	1.42E-09	0.96	4.60	-	1615.4
AHQ-4-13, 6880	R.DDKCANLFEALVGTLK.A	1796.03496	2	2.08E-07	0.93	3.84	-	1182.8
gi|10863927|ref|NP_066953.1| peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]				1.15E-10	5.30	60.29	30.90	18012.4
AHQ-4-12, 3870 - 3946	K.FEDENFILK.H	1155.28144	2	2.56E-04	0.74	3.31	-	501.2
AHQ-4-12, 4013 - 4019	K.FEDENFILK.H	1155.28144	2	3.46E-04	0.84	3.49	-	585.1
AHQ-4-14-, 3282	K.KITIADCGQLE	1249.41637	2	6.51E-04	0.85	3.33	-	816.9
AHQ-4-12, 3361 - 3434	K.KITIADCGQLE	1249.41637	2	1.05E-06	0.92	3.91	-	824.9
AHQ-4-13-, 3361	K.KITIADCGQLE	1249.41637	2	2.06E-05	0.93	3.18	-	1262.7
AHQ-4-12, 4583 - 4650	K.SIYGEKFEDENFILK.H	1833.03047	2	8.18E-08	0.95	4.81	-	1124.1
AHQ-4-14, 6025 - 6084	K.SIYGEKFEDENFILK.H	1833.03047	2	2.65E-06	0.91	3.94	-	992.7
AHQ-4-14-, 4630	K.SIYGEKFEDENFILK.H	1833.03047	2	3.85E-09	0.96	4.70	-	1482.6
AHQ-4-12, 4641 - 4717	K.SIYGEKFEDENFILK.H	1833.03047	2	4.50E-10	0.97	5.48	-	1271.5
AHQ-4-13, 4748	K.SIYGEKFEDENFILK.H	1833.03047	2	1.15E-10	0.97	5.76	-	1333.1
AHQ-4-12, 3490	K.VKEGMNIVEAMER.F	1506.77390	2	1.14E-07	0.89	4.22	-	964.6
AHQ-4-12, 2830	K.VKEGM*NIVEAMER.F	1522.77330	2	1.86E-05	0.88	3.79	-	871.3
AHQ-4-12, 4290	R.VSFELFADKVPK.T	1380.61317	2	7.80E-08	0.89	3.58	-	1071.9
AHQ-4-12, 4501	R.VSFELFADKVPK.T	1380.61317	2	1.71E-05	0.78	3.24	-	732.5
gi|27478749|ref|XP_208411.1| similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit				1.22E-10	1.43	20.20	8.70	25628.5
AHQ-4-9, 4048	K.GEMMDLQHGSLFLR.T	1634.90537	2	1.22E-10	0.93	4.01	-	1180.8
AHQ-4-13, 2534 - 2537	R.NVNIFK.F	734.86623	1	7.96E-04	0.49	2.32	-	504.8
gi|4557731|ref|NP_000618.1| latent transforming growth factor beta binding protein 1 precursor [Hom				1.23E-10	8.04	90.26	8.90	152790.9
AHQ-4-3, 3696	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	4.94E-08	0.95	4.80	-	1381.6
AHQ-4-2, 3740	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	2.49E-05	0.96	4.87	-	1379.4
AHQ-4-1, 3761	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	4.15E-05	0.95	4.92	-	1164.9
AHQ-4-4, 3668	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	4.00E-04	0.94	4.33	-	1281.6
AHQ-4-1, 2641	R.CTCGQGYQLSAAK.D	1446.58862	2	9.57E-07	0.91	3.60	-	826.5
AHQ-4-1, 4230	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	2.25E-06	0.97	5.29	-	1379.8
AHQ-4-1, 3437	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	1.23E-10	0.90	4.02	-	654.0
AHQ-4-1, 3289	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	2.30E-04	0.70	3.08	-	333.2
AHQ-4-1, 2866 - 2869	K.GFVPAGESSSEAGGENYK.D	1786.83392	2	1.51E-06	0.95	4.42	-	1145.1
AHQ-4-1, 3102	K.LCQIPVHGASVPK.L	1407.66344	2	5.12E-05	0.74	2.82	-	450.9
AHQ-4-1, 2963	R.TSTDLDVDVDQPK.E	1433.50014	2	6.68E-06	0.85	3.45	-	788.8
AHQ-4-2, 2592 - 2596	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	8.52E-07	0.94	4.60	-	1170.5
AHQ-4-3, 2581	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	7.57E-05	0.91	3.61	-	1400.0
AHQ-4-1, 2739	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	7.40E-09	0.89	3.76	-	1093.3
AHQ-4-1, 3673	R.YTCICYEGYR.F	1387.51964	2	1.22E-04	0.87	2.83	-	676.4
gi|21464101|ref|NP_036611.2| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein				1.24E-10	4.60	50.27	30.80	28302.4
AHQ-4-10, 6597 - 6629	K.ELEAVCQDVLSLLDNYLIK.N	2237.55566	2	1.66E-06	0.96	4.93	-	1248.1
AHQ-4-10, 3868	R.NLLSVAYKNVVGAR.R	1504.75906	2	1.24E-10	0.92	3.72	-	1016.9
AHQ-4-14, 3940	K.NVTELNEPLSNEER.N	1644.72215	2	1.27E-04	0.78	2.91	-	607.8
AHQ-4-14-, 2921	K.NVTELNEPLSNEER.N	1644.72215	2	8.57E-09	0.90	3.35	-	980.7
AHQ-4-10, 5457	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	3.58E-04	0.69	3.21	-	505.3
AHQ-4-10, 6024 - 6095	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	5.46E-10	0.97	5.30	-	1226.8
AHQ-4-12, 6638	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	2.55E-05	0.81	3.32	-	762.7
AHQ-4-13, 6669	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	4.53E-09	0.94	4.63	-	1084.7
AHQ-4-9, 6219	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	1.40E-04	0.67	2.80	-	744.2
AHQ-4-10, 2115	R.YLAEVATGEK.R	1081.20087	1	6.24E-04	0.49	2.29	-	751.6
AHQ-4-10, 2128	R.YLAEVATGEK.R	1081.20087	2	2.37E-06	0.84	2.99	-	859.5
AHQ-4-10, 2132	R.YLAEVATGEK.R	1081.20087	1	1.32E-05	0.50	2.79	-	270.2
gi|10835187|ref|NP_000627.1| superoxide dismutase 2, mitochondrial [Homo sapiens]				1.28E-10	5.44	60.26	56.80	24733.0
AHQ-4-14-, 6045	K.AIWNVINWENVTER.Y	1744.93137	2	7.44E-08	0.95	4.57	-	1101.0
AHQ-4-13, 6256 - 6274	K.AIWNVINWENVTER.Y	1744.93137	2	7.21E-07	0.95	4.53	-	1228.7
AHQ-4-11, 6261	K.AIWNVINWENVTER.Y	1744.93137	2	5.33E-06	0.90	3.45	-	1111.7
AHQ-4-13-, 6172	K.AIWNVINWENVTER.Y	1744.93137	2	6.18E-06	0.92	3.51	-	1230.6
AHQ-4-11, 5964	K.AIWNVINWENVTER.Y	1744.93137	3	5.94E-06	0.93	4.30	-	1121.9
AHQ-4-11, 5920 - 5980	K.AIWNVINWENVTER.Y	1744.93137	2	1.28E-10	0.97	5.28	-	1288.5
AHQ-4-11, 5640	K.AIWNVINWENVTER.Y	1744.93137	2	5.71E-05	0.61	2.66	-	598.2
AHQ-4-12, 6179	K.AIWNVINWENVTER.Y	1744.93137	2	8.00E-05	0.94	4.19	-	1098.4
AHQ-4-11, 4378	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	2	5.56E-07	0.90	4.19	-	680.0
AHQ-4-11, 3745 - 3808	K.GDVTAQIALQPALK.F	1425.65548	1	2.70E-06	0.84	3.78	-	791.6
AHQ-4-11, 3726 - 3788	K.GDVTAQIALQPALK.F	1425.65548	1	7.32E-05	0.64	2.55	-	917.4
AHQ-4-11, 3937	K.GDVTAQIALQPALK.F	1425.65548	2	1.16E-06	0.91	3.42	-	1165.6
AHQ-4-11, 6830	R.GHLQIAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYK.N	4296.85327	3	1.46E-05	0.80	3.86	-	693.0
AHQ-4-11, 2264 - 2338	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	1.27E-09	0.91	3.60	-	1018.7
AHQ-4-11, 2172	K.HHAAYVNNLNVTEEK.Y	1739.86999	3	4.69E-04	0.96	4.82	-	1745.2
AHQ-4-11, 6086	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	1.07E-05	0.90	3.56	-	1055.9
AHQ-4-11, 5993	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	5.38E-05	0.82	3.72	-	540.7
AHQ-4-11, 6577 - 6644	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	1.58E-07	0.95	4.92	-	1103.8

gi|7657313|ref|NP_055277.1| Lsm1 protein [Homo sapiens]				1.32E-10	0.93	10.22	12.00	15179.3
AHQ-4-12, 5902	R.SIDQFANLVLHQTVER.I	1871.08670	2	1.32E-10	0.93	4.41	-	860.4
gi|4502303|ref|NP_001688.1| mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m				1.38E-10	3.74	40.25	30.00	23277.2
AHQ-4-11, 6632 - 6652	R.FSPLTTNLINLLAENGR.L	1874.13050	2	1.38E-10	0.91	3.96	-	1131.5
AHQ-4-11, 5405 - 5460	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	1.66E-06	0.92	4.57	-	784.3
AHQ-4-11, 5468	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	7.27E-09	0.96	5.10	-	1264.9
AHQ-4-13, 5714	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	7.09E-04	0.85	3.91	-	654.7
AHQ-4-14-, 5539	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	2.65E-05	0.94	4.44	-	1278.3
AHQ-4-11, 3502 - 3509	K.LVRPPVQVYGIEGR.Y	1583.85942	2	2.70E-04	0.96	4.53	-	1020.1
AHQ-4-11, 3133 - 3158	K.VAASVLNPYVK.R	1161.37549	2	2.05E-07	0.91	3.21	-	905.5
gi|14210536|ref|NP_115914.1| similar to chicken tubulin beta 5 [Homo sapiens]				1.41E-10	1.51	20.23	3.80	49856.8
AHQ-4-7, 6910	K.MASTFIGNSTAIQELFK.R	1859.13610	2	1.41E-10	0.65	3.99	-	512.5
AHQ-4-13-, 6061	K.M*ASTFIGNSTAIQELFK.R	1875.13550	2	3.63E-04	0.40	2.70	-	623.6
AHQ-4-7, 6015	K.M*ASTFIGNSTAIQELFK.R	1875.13550	2	9.92E-06	0.86	4.56	-	912.0
gi|4758950|ref|NP_000933.1| peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]				1.80E-10	7.99	90.25	34.70	23742.4
AHQ-4-12, 4186	K.DFMIQGGDFTR.G	1287.42660	2	1.87E-06	0.90	3.37	-	1135.2
AHQ-4-11, 2825	R.DKPLKDVIIADCGK.I	1573.83653	3	6.05E-05	0.93	4.55	-	1117.7
AHQ-4-11, 2816 - 2821	R.DKPLKDVIIADCGK.I	1573.83653	2	4.49E-09	0.96	4.56	-	1276.6
AHQ-4-11, 4192 - 4270	K.DTNGSQFFITTVK.T	1458.59766	2	8.19E-07	0.96	4.44	-	1533.2
AHQ-4-13, 4509	K.DTNGSQFFITTVK.T	1458.59766	1	6.99E-06	0.04	1.86	-	170.3
AHQ-4-11, 4245	K.DTNGSQFFITTVK.T	1458.59766	1	3.97E-06	0.06	1.83	-	216.8
AHQ-4-12, 4314 - 4386	K.DTNGSQFFITTVK.T	1458.59766	1	3.18E-06	0.29	2.12	-	423.9
AHQ-4-12, 4358	K.DTNGSQFFITTVK.T	1458.59766	2	5.53E-09	0.88	3.53	-	788.9
AHQ-4-11, 2369	K.DVIIADCGK.I	992.12891	1	1.55E-07	0.56	2.29	-	498.6
AHQ-4-12, 2419	K.DVIIADCGK.I	992.12891	1	7.79E-07	0.61	2.12	-	622.7
AHQ-4-12, 3007	K.HYGPGWVSMANAGK.D	1475.65664	2	1.80E-10	0.97	4.97	-	1317.1
AHQ-4-12, 3053	K.IEVEKPFAIAK.E	1245.49240	2	1.85E-04	0.93	3.64	-	1398.9
AHQ-4-14-, 4301	K.TVDNFVALATGEK.G	1365.51377	2	3.75E-05	0.94	3.88	-	1170.6
AHQ-4-12, 4337 - 4347	K.TVDNFVALATGEK.G	1365.51377	2	1.97E-06	0.93	4.30	-	867.5
AHQ-4-12, 4351	K.TVDNFVALATGEK.G	1365.51377	1	2.50E-04	0.35	2.82	-	265.8
AHQ-4-11, 4213 - 4224	K.TVDNFVALATGEK.G	1365.51377	2	7.44E-06	0.90	3.86	-	827.0
AHQ-4-12, 4135	R.VIKDFMIQGGDFTR.G	1627.88933	2	1.67E-06	0.94	3.95	-	1095.5
AHQ-4-12, 2895 - 2967	K.VLEGMEVVR.K	1032.23962	2	5.56E-06	0.93	3.75	-	1039.0
AHQ-4-12, 2970	K.VLEGMEVVR.K	1032.23962	1	2.07E-04	0.14	2.15	-	133.7
gi|27764873|ref|NP_057070.2| cytokine receptor-like factor 3; cytokine receptor-like molecule 9; cy				1.88E-10	0.94	10.18	3.20	49737.6
AHQ-4-7, 3090	K.LIEHGVNTAEDLVR.E	1566.74089	2	1.88E-10	0.94	3.65	-	1454.7
gi|4505763|ref|NP_000282.1| phosphoglycerate kinase 1 [Homo sapiens]				1.88E-10	3.87	50.29	19.20	44614.4
AHQ-4-10, 5292 - 5361	K.ACANPAAGSVILLENLR.F	1771.03187	2	1.01E-04	0.81	4.04	-	420.8
AHQ-4-8, 5467 - 5486	K.ACANPAAGSVILLENLR.F	1771.03187	2	6.89E-04	0.94	4.66	-	1101.8
AHQ-4-8, 2081	R.AHSSMVGVNLPQK.A	1368.58752	1	7.89E-06	0.28	2.10	-	400.9
AHQ-4-8, 4825 - 4826	K.ALESPERPFLAILGGAK.V	1770.06542	2	4.95E-09	0.96	5.74	-	1083.7
AHQ-4-8, 4371 - 4406	K.DVLFLKDCVGPEVEK.A	1750.00620	2	1.88E-10	0.96	4.33	-	1535.0
AHQ-4-11, 5181	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	7.01E-09	0.86	3.68	-	581.1
gi|5453740|ref|NP_006462.1| myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat				1.93E-10	5.45	60.32	27.50	19794.0
AHQ-4-11, 6088	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	2.98E-05	0.95	4.60	-	1313.5
AHQ-4-14-, 5365 - 5367	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.64E-07	0.97	5.42	-	1585.4
AHQ-4-13, 5537	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	4.62E-09	0.96	4.92	-	1386.7
AHQ-4-12, 6185 - 6186	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	3.54E-06	0.96	4.81	-	1613.3
AHQ-4-11, 5196 - 5260	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.30E-08	0.98	5.82	-	1618.3
AHQ-4-11, 5358	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	3.95E-08	0.94	4.48	-	1033.2
AHQ-4-11, 5556	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.47E-04	0.57	3.15	-	385.8
AHQ-4-12, 5474	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	5.24E-07	0.94	3.87	-	1192.8
AHQ-4-14-, 6043 - 6062	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	7.32E-07	0.97	4.87	-	2027.8
AHQ-4-11, 5961	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	5.84E-07	0.89	3.63	-	887.6
AHQ-4-11, 5790	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	2.85E-04	0.70	2.85	-	897.5
AHQ-4-11, 5664 - 5726	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.93E-10	0.94	4.62	-	1143.1
AHQ-4-14-, 5814	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.76E-09	0.97	4.95	-	1267.4
AHQ-4-12, 4686	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	4.65E-04	0.41	2.58	-	214.7
AHQ-4-11, 5654 - 5717	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	2.87E-09	0.98	6.36	-	1619.0
AHQ-4-12, 5913 - 5934	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	3.81E-07	0.97	5.12	-	1606.5
AHQ-4-12, 5926	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.64E-07	0.94	4.21	-	1409.5
AHQ-4-11, 4540	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	3	2.92E-04	0.78	3.09	-	922.2
AHQ-4-11, 4388 - 4392	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	1.01E-06	0.95	4.49	-	1236.2
AHQ-4-14-, 4513	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	3	3.12E-06	0.85	3.37	-	1059.6
AHQ-4-12, 4150	K.GNFNYIEFTR.I	1261.36733	2	1.19E-04	0.89	3.59	-	969.0
AHQ-4-11, 4229	K.GNFNYIEFTR.I	1261.36733	2	1.15E-05	0.78	3.35	-	800.6
AHQ-4-11, 3345	K.KGNFNYIEFTR.I	1389.54025	2	3.64E-04	0.93	2.80	-	1362.9
gi|4557677|ref|NP_000203.1| integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu				1.95E-10	18.42	230.31	33.60	87185.6
AHQ-4-3, 2864 - 2868	R.AKWDTANNPLYK.E	1421.58225	2	4.56E-06	0.90	3.18	-	810.1
AHQ-4-1, 3090	R.AKWDTANNPLYK.E	1421.58225	2	1.34E-04	0.87	3.33	-	773.6
AHQ-4-6, 5275	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	5.21E-09	0.97	6.20	-	1695.1
AHQ-4-3, 5441 - 5511	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	2.15E-05	0.92	4.45	-	1165.5
AHQ-4-4, 5467	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	3.45E-05	0.95	5.14	-	1302.8
AHQ-4-3, 5499 - 5567	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	2	3.59E-06	0.85	4.20	-	510.7
AHQ-4-4, 5572	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	2.10E-04	0.90	4.76	-	743.9
AHQ-4-6, 4266	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	3.16E-06	0.84	4.11	-	429.0
AHQ-4-4, 4459	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.68E-05	0.88	4.77	-	474.7
AHQ-4-5, 4381	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	6.76E-07	0.86	4.06	-	609.1
AHQ-4-2, 4524 - 4536	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	1.60E-06	0.77	3.66	-	514.9
AHQ-4-3, 4548	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.02E-07	0.77	3.58	-	528.3
AHQ-4-1, 5979 - 6045	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	4.01E-04	0.89	3.70	-	872.8
AHQ-4-3, 4621 - 4692	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	4.03E-07	0.90	3.78	-	760.0
AHQ-4-3, 6113 - 6187	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	4.25E-07	0.85	3.76	-	578.1
AHQ-4-3, 6780	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	7.43E-04	0.67	2.85	-	582.8
AHQ-4-1, 4587 - 4609	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	2.23E-04	0.92	4.02	-	707.8
AHQ-4-3, 6583 - 6655	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.10E-07	0.91	4.14	-	787.1
AHQ-4-3, 6351 - 6419	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	4.56E-04	0.81	3.16	-	677.9
AHQ-4-3, 6256 - 6284	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	4.67E-09	0.92	4.36	-	737.2
AHQ-4-4, 5035	K.DDLWSIQNLGTK.L	1390.52332	1	7.03E-08	0.42	2.65	-	321.3
AHQ-4-5, 4898 - 4901	K.DDLWSIQNLGTK.L	1390.52332	1	1.92E-04	0.20	1.98	-	272.7
AHQ-4-4, 5027	K.DDLWSIQNLGTK.L	1390.52332	2	3.52E-04	0.79	2.71	-	962.4
AHQ-4-3, 5017 - 5088	K.DDLWSIQNLGTK.L	1390.52332	1	1.97E-07	0.29	2.10	-	297.9
AHQ-4-1, 5067	K.DDLWSIQNLGTK.L	1390.52332	2	6.18E-04	0.72	3.05	-	591.7
AHQ-4-3, 4757 - 4769	K.DNCAPESIEFPVSEAR.V	1822.93099	2	2.90E-07	0.79	2.71	-	1046.2
AHQ-4-8, 4165 - 4166	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.72E-04	0.58	2.69	-	716.0
AHQ-4-11, 4222	K.DNCAPESIEFPVSEAR.V	1822.93099	2	2.16E-04	0.81	2.98	-	683.0
AHQ-4-3, 3325	K.EATSTFTNITYR.G	1404.50685	2	5.50E-06	0.82	3.27	-	640.7
AHQ-4-4, 3247 - 3327	K.EATSTFTNITYR.G	1404.50685	2	1.38E-04	0.62	2.80	-	558.2
AHQ-4-1, 3447	K.EATSTFTNITYR.G	1404.50685	2	5.84E-05	0.68	2.78	-	476.1
AHQ-4-1, 3717 - 3797	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.78E-07	0.94	4.09	-	1285.4
AHQ-4-6, 3443	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	4.09E-07	0.85	3.55	-	859.5
AHQ-4-2, 3720	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	3.26E-06	0.89	3.74	-	946.8
AHQ-4-4, 3646	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	2.86E-04	0.76	3.42	-	705.1
AHQ-4-4, 3631 - 3708	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	5.93E-04	0.94	3.89	-	1441.6
AHQ-4-5, 3523	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	8.61E-05	0.93	3.89	-	1159.0
AHQ-4-1, 3718	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	3.44E-05	0.67	3.29	-	445.5
AHQ-4-4, 4768	R.GKCECGSCVCIQPGSYGDTCEKCPTCPDACTFK.K	3900.25293	3	7.53E-05	0.75	3.94	-	437.2

AHQ-4-3, 1928 - 1999	K.GSGDSSQVTQVSPQR.I	1533.58302	2	3.61E-05	0.93	3.85	-	1229.2
AHQ-4-3, 2433	K.HVLTLTDQVTR.F	1283.45912	2	8.54E-07	0.90	3.29	-	805.5
AHQ-4-8, 2244	K.HVLTLTDQVTR.F	1283.45912	1	4.70E-06	0.13	1.84	-	161.3
AHQ-4-3, 2544 - 2615	K.HVLTLTDQVTR.F	1283.45912	2	6.80E-08	0.94	3.87	-	857.3
AHQ-4-8, 2241	K.HVLTLTDQVTR.F	1283.45912	2	1.84E-07	0.81	3.06	-	459.6
AHQ-4-7, 2361	K.HVLTLTDQVTR.F	1283.45912	2	1.72E-04	0.93	3.42	-	851.4
AHQ-4-4, 2560	K.HVLTLTDQVTR.F	1283.45912	2	2.67E-05	0.93	3.91	-	717.0
AHQ-4-4, 2576	K.HVLTLTDQVTR.F	1283.45912	1	4.29E-04	0.64	3.15	-	319.6
AHQ-4-6, 2399 - 2406	K.HVLTLTDQVTR.F	1283.45912	2	9.45E-06	0.85	3.06	-	589.8
AHQ-4-1, 2790	K.HVLTLTDQVTR.F	1283.45912	2	5.11E-06	0.89	3.34	-	575.5
AHQ-4-5, 2411 - 2433	K.HVLTLTDQVTR.F	1283.45912	2	9.03E-08	0.91	3.52	-	681.4
AHQ-4-4, 4991	K.IGDTVSFSIEAK.V	1267.41009	2	1.90E-04	0.66	2.81	-	609.9
AHQ-4-2, 3902	R.NDASHLLVFTTDAK.T	1532.67977	2	1.23E-08	0.94	4.19	-	1102.2
AHQ-4-4, 3807 - 3820	R.NDASHLLVFTTDAK.T	1532.67977	2	1.47E-09	0.94	4.42	-	1044.9
AHQ-4-4, 4379	R.NDASHLLVFTTDAK.T	1532.67977	2	1.17E-07	0.92	3.91	-	954.4
AHQ-4-6, 3515	R.NDASHLLVFTTDAK.T	1532.67977	2	1.02E-07	0.97	5.40	-	1322.1
AHQ-4-6, 4130	R.NDASHLLVFTTDAK.T	1532.67977	2	8.06E-06	0.79	3.08	-	862.3
AHQ-4-3, 4435	R.NDASHLLVFTTDAK.T	1532.67977	2	2.26E-07	0.82	3.02	-	818.1
AHQ-4-7, 3447 - 3459	R.NDASHLLVFTTDAK.T	1532.67977	2	1.84E-08	0.96	4.40	-	1175.1
AHQ-4-6, 3444 - 3522	R.NDASHLLVFTTDAK.T	1532.67977	2	2.52E-05	0.93	3.91	-	875.3
AHQ-4-1, 4527	R.NDASHLLVFTTDAK.T	1532.67977	2	2.21E-08	0.94	4.16	-	1042.5
AHQ-4-1, 4023	R.NDASHLLVFTTDAK.T	1532.67977	2	9.27E-04	0.70	2.62	-	777.3
AHQ-4-3, 3836 - 3888	R.NDASHLLVFTTDAK.T	1532.67977	2	4.75E-08	0.97	4.41	-	1588.6
AHQ-4-5, 2949	K.SFTIKPVGFK.D	1124.35685	2	1.14E-05	0.73	2.88	-	753.2
AHQ-4-3, 3228	K.SFTIKPVGFK.D	1124.35685	2	7.80E-06	0.75	2.61	-	850.2
AHQ-4-3, 4491 - 4508	K.SILYVVEEPECPK.G	1564.78173	2	1.42E-04	0.79	3.04	-	834.7
AHQ-4-1, 2875	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	6.98E-08	0.91	3.46	-	1324.8
AHQ-4-3, 3048	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	7.77E-07	0.87	3.14	-	993.8
AHQ-4-3, 2955 - 3035	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.95E-10	0.90	3.27	-	1065.0
AHQ-4-4, 2940	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.55E-07	0.88	2.89	-	1174.9
AHQ-4-3, 3684 - 3719	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.94E-07	0.88	3.20	-	1012.3
AHQ-4-3, 1469 - 1537	K.THIALDGR.L	882.98732	1	9.75E-04	0.13	1.98	-	146.0
AHQ-4-1, 2045	R.VLEDRPLSDK.G	1172.31354	2	1.24E-05	0.85	3.51	-	775.5
AHQ-4-3, 1684 - 1751	R.VLEDRPLSDK.G	1172.31354	2	2.07E-05	0.90	3.85	-	790.1
AHQ-4-6, 2558	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	7.72E-08	0.96	5.00	-	1861.3
AHQ-4-3, 2747	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	3.14E-07	0.94	4.63	-	1290.1
AHQ-4-3, 3268 - 3269	K.WDTANNPLYK.E	1222.33111	2	1.41E-07	0.56	2.67	-	423.7
AHQ-4-4, 3260	K.WDTANNPLYK.E	1222.33111	2	5.21E-05	0.67	2.92	-	583.4
AHQ-4-6, 3582 - 3584	K.YCECDDFSCVR.Y	1514.59674	2	3.12E-06	0.95	4.12	-	1030.4
AHQ-4-4, 3722	K.YCECDDFSCVR.Y	1514.59674	2	2.53E-06	0.92	3.38	-	1146.7
AHQ-4-1, 3745 - 3746	K.YCECDDFSCVR.Y	1514.59674	2	4.36E-09	0.97	4.29	-	1353.0
AHQ-4-5, 3670 - 3673	K.YCECDDFSCVR.Y	1514.59674	2	4.11E-09	0.94	3.84	-	1048.0
AHQ-4-3, 3749 - 3776	K.YCECDDFSCVR.Y	1514.59674	2	7.35E-07	0.93	3.52	-	1038.0
AHQ-4-2, 3788	K.YCECDDFSCVR.Y	1514.59674	2	4.45E-07	0.89	3.34	-	802.4
gi|13518026|ref|NP_004978.2| LIM and senescent cell antigen-like domains 1 [Homo sapiens]				2.03E-10	3.42	40.26	13.80	37251.2
AHQ-4-8, 4081	K.CHAIIDEQPLIFK.N	1585.84900	3	9.40E-07	0.95	4.88	-	1426.5
AHQ-4-8, 4065 - 4073	K.CHAIIDEQPLIFK.N	1585.84900	2	7.12E-04	0.96	4.81	-	1538.8
AHQ-4-9, 3936 - 3939	K.CHAIIDEQPLIFK.N	1585.84900	2	2.61E-04	0.96	4.84	-	1348.7
AHQ-4-14-, 3898	K.CYEKFPLELK.K	1328.55832	2	3.16E-04	0.72	2.66	-	751.2
AHQ-4-8, 2798	K.MGVPICGACR.R	1123.35250	2	6.94E-05	0.80	2.91	-	482.8
AHQ-4-11, 3380 - 3382	R.VIEGDVVSALNK.A	1244.41966	2	3.82E-08	0.97	5.14	-	1225.2
AHQ-4-14, 4502	R.VIEGDVVSALNK.A	1244.41966	2	5.45E-08	0.90	2.98	-	974.7
AHQ-4-14-, 3469	R.VIEGDVVSALNK.A	1244.41966	2	2.45E-09	0.97	4.73	-	1556.2
AHQ-4-8, 3014	R.VIEGDVVSALNK.A	1244.41966	2	2.03E-10	0.96	4.39	-	1251.9
AHQ-4-9, 3015	R.VIEGDVVSALNK.A	1244.41966	2	2.70E-05	0.90	3.47	-	1014.4
gi|14251209|ref|NP_001279.2| chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo				2.04E-10	7.63	90.29	47.30	26922.5
AHQ-4-9, 5805 - 5868	K.FLDGNELTLADCNLLPK.L	1935.18752	2	1.08E-05	0.87	3.94	-	1132.9
AHQ-4-9, 2875	K.GVTFNVTTVDTK.R	1282.42476	2	5.65E-08	0.88	3.52	-	830.9
AHQ-4-13, 3545	K.GVTFNVTTVDTK.R	1282.42476	2	6.58E-06	0.93	3.62	-	1111.9
AHQ-4-13, 2586 - 2593	K.IGNCPFSQR.L	1080.19948	2	8.41E-05	0.75	2.56	-	681.1
AHQ-4-12, 5687	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	9.99E-05	0.61	3.75	-	554.0
AHQ-4-9, 5367	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	2.74E-04	0.82	4.61	-	656.6
AHQ-4-9, 5129 - 5203	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	1.74E-06	0.94	5.39	-	1304.9
AHQ-4-13, 5440	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.05E-05	0.97	5.36	-	1007.5
AHQ-4-9, 4983	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	5.67E-08	0.94	4.52	-	749.1
AHQ-4-9, 4836 - 4907	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	4.82E-07	0.92	4.40	-	611.3
AHQ-4-13-, 5316 - 5324	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	4.52E-04	0.96	5.18	-	1072.6
AHQ-4-9, 4752 - 4759	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	8.55E-06	0.96	5.07	-	965.6
AHQ-4-11, 5165 - 5168	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.26E-07	0.97	5.72	-	909.7
AHQ-4-13-, 5460	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.30E-09	0.96	5.27	-	880.4
AHQ-4-12, 5399	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	4.10E-04	0.95	5.00	-	889.8
AHQ-4-9, 5139 - 5140	K.LCPGGQLPFLLYGTEVHTDTNK.I	2462.76290	2	3.31E-05	0.75	4.11	-	457.1
AHQ-4-13-, 5685	R.LFM*VLWLK.G	1066.38391	2	8.36E-04	0.92	2.85	-	1239.5
AHQ-4-12, 2667	K.LHIVQVVCK.K	1097.35623	1	2.64E-05	0.75	2.23	-	858.5
AHQ-4-9, 2319	K.LHIVQVVCK.K	1097.35623	1	1.40E-05	0.64	2.54	-	512.6
AHQ-4-9, 4829 - 4875	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	9.08E-04	0.89	4.32	-	457.0
AHQ-4-10, 4829	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	2.04E-10	0.91	4.79	-	374.1
AHQ-4-12, 5297	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	1.02E-06	0.85	4.03	-	450.8
gi|4504077|ref|NP_000165.1| glycoprotein IX (platelet) [Homo sapiens]				2.14E-10	4.43	50.21	27.10	19046.0
AHQ-4-11, 4881	R.ALETMGLWVDCR.G	1452.68135	2	4.42E-08	0.87	3.17	-	966.3
AHQ-4-11, 4072	R.ALETM*GLWVDCR.G	1468.68075	2	4.09E-05	0.91	2.98	-	1249.8
AHQ-4-12, 2605 - 2645	R.CASPSLAAHGPLGR.L	1395.56962	2	2.14E-10	0.93	4.22	-	918.0
AHQ-4-14, 3578 - 3605	R.CASPSLAAHGPLGR.L	1395.56962	2	1.42E-04	0.88	3.05	-	868.7
AHQ-4-11, 2582	R.CASPSLAAHGPLGR.L	1395.56962	1	4.72E-05	0.78	3.26	-	351.6
AHQ-4-11, 2556 - 2602	R.CASPSLAAHGPLGR.L	1395.56962	2	1.56E-08	0.91	3.49	-	1051.6
AHQ-4-11, 3192 - 3264	R.GHGLTALPALPAR.T	1274.49706	2	8.24E-05	0.93	3.84	-	940.9
AHQ-4-12, 3278	R.GHGLTALPALPAR.T	1274.49706	1	1.83E-05	0.72	2.96	-	327.1
AHQ-4-12, 3229 - 3297	R.GHGLTALPALPAR.T	1274.49706	2	9.11E-05	0.91	3.55	-	761.2
AHQ-4-11, 3222	R.GHGLTALPALPAR.T	1274.49706	1	1.48E-05	0.83	3.35	-	355.8
AHQ-4-11, 2973 - 3040	R.TPEALLQVR.C	1027.19957	2	1.91E-04	0.88	3.33	-	922.2
AHQ-4-14, 4145	R.TPEALLQVR.C	1027.19957	2	3.83E-06	0.89	2.53	-	1307.0
AHQ-4-14-, 3025	R.TPEALLQVR.C	1027.19957	2	1.83E-05	0.92	3.20	-	1377.5
AHQ-4-12, 3031 - 3089	R.TPEALLQVR.C	1027.19957	2	6.07E-05	0.87	3.13	-	858.0
gi|29730023|ref|XP_291482.1| similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno				2.22E-10	5.88	70.22	14.10	63563.0
AHQ-4-6, 4348	K.ELEEIVQPIISK.L	1398.62680	1	1.20E-07	0.69	2.94	-	299.0
AHQ-4-5, 4675	R.IINKPTAAAIAYGLDK.R	1659.95097	2	1.16E-09	0.84	4.12	-	805.7
AHQ-4-6, 4184	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	2.41E-08	0.76	3.99	-	751.1
AHQ-4-10, 3980	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	2.36E-04	0.33	2.64	-	493.1
AHQ-4-5, 3289	K.KKELEEIVQPIISK.L	1654.97263	2	3.63E-05	0.92	4.20	-	1040.5
AHQ-4-5, 3439	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	1.40E-09	0.90	4.41	-	594.0
AHQ-4-7, 3373	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	1.72E-04	0.55	3.08	-	213.6
AHQ-4-6, 3364 - 3440	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	8.96E-05	0.87	4.35	-	434.2
AHQ-4-5, 3331	K.NQLTSNPKNTVFDAK.R	1677.84011	2	3.55E-09	0.86	4.32	-	815.3
AHQ-4-6, 5534	K.TFAPKEISAMVLTK.M	1536.86124	2	2.22E-10	0.91	3.61	-	1424.8
AHQ-4-5, 5586	K.TFAPKEISAMVLTK.M	1536.86124	2	4.64E-09	0.90	4.06	-	1262.5
gi|4507645|ref|NP_000356.1| triosephosphate isomerase 1 [Homo sapiens]				2.33E-10	4.29	50.32	38.60	26669.3
AHQ-4-10, 3551 - 3617	K.DCGATWVVLGHSER.R	1588.72671	2	2.47E-06	0.92	3.75	-	1033.8

AHQ-4-10, 6311	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	7.03E-05	0.67	3.42	-	252.3
AHQ-4-14-, 6603	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	2.86E-10	0.49	3.29	-	174.4
AHQ-4-10, 6059 - 6124	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	9.30E-05	0.78	4.08	-	214.7
AHQ-4-10, 6205 - 6256	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	3.53E-04	0.72	3.95	-	229.1
AHQ-4-10, 3743	R.KQSLGELIGTLNAAK.V	1543.79037	2	2.41E-04	0.91	3.62	-	1104.0
AHQ-4-10, 4889 - 4901	K.VAHALAEGLGVIACIGEK.L	1810.10800	2	2.33E-10	0.99	6.47	-	2674.7
AHQ-4-10, 5039 - 5059	K.VPADTEVVCAPPTAYIDFAR.Q	2194.44943	2	8.34E-06	0.98	6.29	-	1098.3
gi|29742410|ref|XP_291183.1| similar to TREM-like transcript 1 [Homo sapiens]				2.37E-10	0.92	10.21	5.10	32678.3
AHQ-4-13-, 4168 - 4192	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.51E-08	0.76	3.37	-	372.6
AHQ-4-13-, 4260 - 4324	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	2.37E-10	0.92	4.13	-	699.1
AHQ-4-11, 4204	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.30E-07	0.81	3.25	-	431.2
gi|13129150|ref|NP_005339.1| heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H				2.45E-10	2.66	30.25	5.20	84659.1
AHQ-4-5, 2759	K.ELHINLIPNKQDR.T	1590.80882	2	3.70E-06	0.81	3.46	-	525.8
AHQ-4-5, 4009 - 4033	R.NPDDITNEEYGEFYK.S	1834.87381	2	2.45E-10	0.96	4.99	-	1139.7
AHQ-4-5, 3810 - 3817	R.RAPFDLFENR.K	1265.40235	2	9.80E-06	0.89	3.60	-	662.6
gi|20070125|ref|NP_000909.2| prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke				2.58E-10	3.59	60.24	17.50	57115.9
AHQ-4-7, 4831	K.HNQLPLVIEFTEQTAPK.I	1966.22639	2	3.30E-04	0.94	4.51	-	741.7
AHQ-4-12, 5814	K.QPVKVLVGK.N	968.21840	1	2.13E-04	0.25	2.03	-	422.3
AHQ-4-7, 7521	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	3	2.58E-10	0.94	4.72	-	1446.4
AHQ-4-7, 3625	K.THILLFLPK.S	1082.36310	1	3.41E-04	0.26	2.06	-	302.0
AHQ-4-7, 1943	K.YKPESEELTAER.I	1452.54828	1	5.24E-07	0.31	2.64	-	201.5
AHQ-4-7, 1933 - 1941	K.YKPESEELTAER.I	1452.54828	2	9.75E-05	0.65	2.61	-	293.7
AHQ-4-7, 3770	K.YQLDKDGVVLFK.K	1425.65394	2	4.53E-05	0.91	3.86	-	1056.8
gi|12408656|ref|NP_005177.2| calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ				2.61E-10	10.24	130.34	19.00	81889.4
AHQ-4-6, 5018	K.APSDLYQIILK.A	1261.49183	2	3.96E-09	0.97	3.92	-	1954.5
AHQ-4-6, 6306 - 6310	R.DM*ETIGFAVYEVPPELVGQPAVHLK.R	2757.15391	3	8.37E-09	0.81	3.54	-	816.3
AHQ-4-6, 6684 - 6686	R.DMETIGFAVYEVPPELVGQPAVHLK.R	2741.15451	3	5.80E-09	0.93	4.13	-	1470.4
AHQ-4-6, 6023	R.FRLPPGEYVVVPSTFEPNKEGDFVLR.F	2994.39160	3	3.89E-08	0.97	6.89	-	1513.4
AHQ-4-6, 4104 - 4108	R.KAPSDLYQIILK.A	1389.66474	2	2.88E-07	0.94	4.43	-	960.6
AHQ-4-6, 4802 - 4863	R.LEICNLTPDALK.S	1388.61207	2	2.32E-04	0.83	3.18	-	989.1
AHQ-4-6, 4684 - 4748	R.LPPGEYVVVPSTFEPNK.E	1874.12573	2	7.07E-04	0.66	3.06	-	518.6
AHQ-4-6, 5659 - 5662	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	1.32E-09	0.91	4.41	-	743.9
AHQ-4-5, 5733	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	2.61E-10	0.70	3.21	-	522.6
AHQ-4-6, 6355 - 6418	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	2	1.16E-05	0.93	4.37	-	883.3
AHQ-4-6, 5054	R.NYPATFWVNPQFK.I	1612.81141	2	2.50E-04	0.90	3.02	-	1043.1
AHQ-4-6, 2858	R.SEQFINLR.E	1007.12521	1	6.48E-06	0.16	1.83	-	250.2
AHQ-4-6, 2862 - 2867	R.SEQFINLR.E	1007.12521	2	2.11E-04	0.92	3.32	-	1185.4
AHQ-4-6, 4158	K.WNTTLYEGTWR.R	1427.54534	2	1.97E-05	0.75	2.57	-	655.0
AHQ-4-6, 3071 - 3122	K.YLGQDYEQLR.V	1285.38720	2	8.36E-07	0.69	2.83	-	427.1
gi|21361621|ref|NP_002624.2| phosphoglucomutase 1 [Homo sapiens]				2.79E-10	3.04	40.20	12.10	61448.7
AHQ-4-6, 3690	K.ADNFEYSDPVDGSISR.N	1772.80725	2	2.05E-06	0.69	2.75	-	660.5
AHQ-4-6, 3607	K.FNISNGGPAPEAITDK.I	1631.76820	2	2.79E-10	0.95	4.07	-	1421.4
AHQ-4-6, 3842 - 3844	K.IALYETPTGWK.F	1279.46570	2	3.59E-05	0.64	2.79	-	649.3
AHQ-4-6, 7324	K.VFQSSANYAENFIQSIISTVEPAQR.Q	2801.06026	3	1.21E-04	0.75	3.14	-	782.0
gi|10834976|ref|NP_000572.1| glutathione peroxidase 1 [Homo sapiens]				2.91E-10	7.45	100.27	59.70	21909.0
AHQ-4-11, 5232	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	2.91E-10	0.94	4.12	-	1046.1
AHQ-4-11, 2728 - 2793	R.DYTQMNELQR.R	1298.40778	2	6.92E-04	0.84	3.05	-	783.4
AHQ-4-11, 4234	K.FLVGPDGVPLR.R	1170.38561	2	6.24E-06	0.94	3.35	-	1283.1
AHQ-4-11, 3964	K.FLVGPDGVPLR.R	1170.38561	2	3.81E-05	0.85	2.63	-	903.9
AHQ-4-11, 4812	R.GLVVLGFPCNQFGHQENAK.N	2117.37312	2	1.47E-04	0.55	2.96	-	356.1
AHQ-4-11, 4966	R.GLVVLGFPCNQFGHQENAK.N	2117.37312	2	1.58E-05	0.30	2.57	-	218.5
AHQ-4-11, 3774 - 3802	R.LAAAAAQSVYAFSAR.P	1497.68025	2	1.97E-04	0.92	3.66	-	1334.8
AHQ-4-11, 3128	R.NDVAWNFEK.F	1123.19953	1	2.03E-04	0.26	1.93	-	262.2
AHQ-4-11, 3221	K.NEEILNSLK.Y	1060.18319	1	1.64E-04	0.38	2.29	-	271.1
AHQ-4-11, 5453	R.PGGGFEPNFMLFEK.C	1570.79310	2	9.28E-05	0.97	4.94	-	1130.1
AHQ-4-13-, 3948	R.PLAGGEPVSLGSLR.G	1353.54935	2	1.83E-04	0.88	3.11	-	789.7
AHQ-4-14-, 3734 - 3797	R.PLAGGEPVSLGSLR.G	1353.54935	2	1.02E-09	0.94	3.75	-	1120.7
AHQ-4-11, 3649 - 3725	R.PLAGGEPVSLGSLR.G	1353.54935	2	1.50E-07	0.95	4.94	-	957.5
AHQ-4-11, 3789	R.PLAGGEPVSLGSLR.G	1353.54935	2	4.51E-08	0.95	4.10	-	1397.1
AHQ-4-11, 3476	R.PLAGGEPVSLGSLR.G	1353.54935	2	1.16E-06	0.94	3.97	-	1134.8
AHQ-4-13, 4090	R.PLAGGEPVSLGSLR.G	1353.54935	2	8.79E-05	0.87	3.35	-	774.0
AHQ-4-14, 4880 - 4898	R.PLAGGEPVSLGSLR.G	1353.54935	2	6.09E-06	0.91	3.76	-	737.6
AHQ-4-11, 5102	K.YVRPGGGFEPNFMLFEK.C	1989.28515	3	2.30E-06	0.96	5.46	-	1368.0
AHQ-4-11, 5096	K.YVRPGGGFEPNFMLFEK.C	1989.28515	2	1.37E-05	0.96	4.90	-	1202.9
gi|4557597|ref|NP_001449.1| gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);				3.18E-10	2.01	30.26	1.70	288897.4
AHQ-4-1, 4793	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.35E-05	0.91	4.55	-	482.2
AHQ-4-1, 4794 - 4813	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.36E-07	0.86	4.33	-	450.2
AHQ-4-7, 4053 - 4066	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.08E-06	0.93	5.19	-	386.5
AHQ-4-7, 4017 - 4057	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	3.18E-10	0.90	4.37	-	880.0
AHQ-4-6, 4166	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	2.12E-04	0.87	3.95	-	476.7
AHQ-4-2, 4690	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	7.36E-06	0.93	4.70	-	763.1
AHQ-4-3, 4663	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	1.40E-05	0.90	4.73	-	569.6
AHQ-4-4, 4587	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	4.69E-08	0.88	4.24	-	540.6
AHQ-4-5, 4201	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	5.86E-04	0.89	4.39	-	411.5
AHQ-4-9, 3753	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	4.57E-05	0.93	4.71	-	484.9
AHQ-4-2, 1747 - 1792	K.IECDDKGDGSCDVR.Y	1628.67809	2	1.08E-05	0.83	2.89	-	854.2
AHQ-4-2, 1864	K.IECDDKGDGSCDVR.Y	1628.67809	2	2.17E-04	0.87	2.87	-	1042.3
AHQ-4-2, 2023	K.NDNDTFTVK.Y	1054.09237	1	6.71E-06	0.28	1.83	-	347.3
gi|5803225|ref|NP_006752.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon poly				3.21E-10	2.93	50.27	27.10	29173.7
AHQ-4-13-, 6677	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	1.07E-08	0.97	5.43	-	1477.5
AHQ-4-13, 6772	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	1.57E-04	0.97	5.26	-	1280.5
AHQ-4-9, 6343	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	2.58E-07	0.86	2.99	-	1072.3
AHQ-4-10, 6237 - 6239	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	4.03E-05	0.63	3.19	-	480.8
AHQ-4-14-, 6563	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	3.21E-10	0.96	4.73	-	1081.2
AHQ-4-9, 6875 - 6877	K.AAFDDAIAELDTLSEESYKDSTLIMQLLR.D	3260.61486	3	5.76E-07	0.54	3.09	-	608.0
AHQ-4-9, 3137	K.AASDIAMTELPPTHPIR.L	1821.09110	2	7.75E-04	0.30	2.74	-	215.6
AHQ-4-9, 2241	K.EAAENSLVAYK.A	1195.30397	2	9.62E-06	0.61	2.95	-	578.1
AHQ-4-9, 1551 - 1553	K.HLIPAANTGESK.V	1238.37521	1	3.75E-05	0.53	2.39	-	558.4
gi|4503327|ref|NP_000389.1| cytochrome b5 reductase membrane-bound isoform; diaphorase (NADH) [Homo				3.29E-10	6.35	80.35	36.20	34234.6
AHQ-4-9, 4188 - 4199	K.DILLRPELEELR.N	1496.73370	2	3.46E-05	0.88	3.43	-	872.8
AHQ-4-9, 5507 - 5571	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	2	1.65E-06	0.94	4.67	-	703.5
AHQ-4-9, 5508	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	3	1.66E-09	0.95	4.90	-	1327.2
AHQ-4-9, 2543	R.GPSGLLVYQGK.G	1119.29547	1	4.04E-05	0.77	3.16	-	439.9
AHQ-4-9, 5388 - 5463	R.IDGNLVVRPYTPISSDDDKGFVDLVIK.V	2977.35765	3	3.23E-07	0.98	7.03	-	1782.2
AHQ-4-9, 4699	R.PYTPISSDDDKGFVDLVIK.V	2110.34914	2	3.18E-04	0.93	4.38	-	1048.7
AHQ-4-9, 3148	R.STPAITLESPDIK.Y	1372.54621	1	3.08E-05	0.61	3.33	-	400.5
AHQ-4-9, 4035 - 4051	R.STPAITLESPDIKYPLR.L	1902.18061	2	3.29E-10	0.92	4.35	-	648.0
AHQ-4-9, 4515	K.SVGMIAGGTGITPM*LQVIR.A	1918.31483	2	1.23E-05	0.31	2.78	-	334.7
gi|5031593|ref|NP_005708.1| actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub				3.65E-10	5.53	60.26	53.60	16320.3
AHQ-4-12, 2914 - 2935	K.ALAAGGVGSIVR.V	1071.25558	2	1.70E-05	0.98	4.62	-	2493.0
AHQ-4-14-, 2902	K.ALAAGGVGSIVR.V	1071.25558	2	4.20E-06	0.97	3.98	-	2367.9
AHQ-4-12, 3467	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	1.19E-05	0.85	3.61	-	629.7
AHQ-4-12, 4030 - 4098	K.AVQSLDKNGVDLLMK.Y	1631.91943	2	2.61E-08	0.96	5.15	-	1377.7
AHQ-4-12, 4243 - 4254	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	3.63E-08	0.91	3.94	-	668.7
AHQ-4-12, 4573 - 4574	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	3.65E-10	0.95	4.76	-	1051.6
AHQ-4-12, 4753	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	1.33E-05	0.81	3.56	-	525.4
AHQ-4-12, 4141	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	1.20E-06	0.86	3.47	-	798.5

AHQ-4-12, 4391 - 4462	R.KVDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR.Q	3890.92031	3	3.46E-05	0.89	4.92	-	628.4
gi|30159310|ref|XP_301899.1| similar to beta-actin [Homo sapiens]				3.71E-10	1.53	20.18	9.20	32376.4
AHQ-4-5, 1496	K.DSYVGNEAQSK.R	1198.22158	1	5.82E-04	0.49	2.25	-	338.0
AHQ-4-8, 1419 - 1792	K.DSYVGNEAQSK.R	1198.22158	1	3.71E-10	0.65	2.87	-	376.8
AHQ-4-8, 1451 - 1526	K.DSYVGNEAQSK.R	1198.22158	2	7.19E-05	0.58	2.55	-	620.9
AHQ-4-12, 1871	K.DSYVGNEAQSK.R	1198.22158	1	1.26E-04	0.14	1.89	-	210.4
AHQ-4-9, 1499	K.DSYVGNEAQSK.R	1198.22158	1	3.65E-05	0.45	2.37	-	329.3
AHQ-4-13, 1775 - 1899	K.DSYVGNEAQSK.R	1198.22158	1	1.54E-09	0.43	2.20	-	377.1
AHQ-4-12, 1631 - 1766	K.DSYVGNEAQSK.R	1198.22158	1	2.41E-07	0.71	2.74	-	531.3
AHQ-4-12, 4905 - 4939	K.SYKLLDGQVITIGNER.F	1807.04092	2	4.54E-04	0.60	2.88	-	354.7
AHQ-4-10, 4125 - 4127	K.SYKLLDGQVITIGNER.F	1807.04092	2	2.64E-05	0.72	2.90	-	522.0
AHQ-4-8, 4519 - 4597	K.SYKLLDGQVITIGNER.F	1807.04092	2	1.94E-05	0.88	3.55	-	770.4
gi|4504345|ref|NP_000508.1| alpha 2 globin [Homo sapiens]				3.94E-10	3.79	40.32	50.70	15257.4
AHQ-4-13, 4372	K.FLASVSTVLTSK.Y	1253.46970	2	2.05E-04	0.80	2.70	-	899.4
AHQ-4-13-, 4240 - 4246	K.FLASVSTVLTSK.Y	1253.46970	2	4.41E-09	0.93	3.87	-	1296.5
AHQ-4-13, 4125	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	5.19E-06	0.90	4.06	-	975.8
AHQ-4-13-, 4002	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	1.87E-09	0.91	3.65	-	977.4
AHQ-4-13-, 4005 - 4008	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	3.94E-10	0.95	4.33	-	1097.1
AHQ-4-13, 4124	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	2.18E-07	0.90	3.74	-	695.4
AHQ-4-13-, 5532	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	5.93E-05	0.96	5.88	-	1391.6
AHQ-4-13-, 2549	K.VGAHAGEYGAEALER.M	1530.62397	2	7.87E-10	0.95	4.20	-	1229.4
AHQ-4-13, 2669	K.VGAHAGEYGAEALER.M	1530.62397	3	7.66E-06	0.98	6.34	-	2321.7
AHQ-4-13, 2653	K.VGAHAGEYGAEALER.M	1530.62397	2	1.97E-08	0.97	4.25	-	1588.7
gi|7705855|ref|NP_057226.1| steroid dehydrogenase homolog; likely ortholog of mouse Kik1 steroid de				4.00E-10	0.97	10.21	4.80	34323.9
AHQ-4-9, 5680	K.TFVDFFSQCLHEEYR.S	1980.14540	2	4.00E-10	0.97	4.26	-	1709.3
gi|5174731|ref|NP_005990.1| translin-associated factor X; translin-like protein [Homo sapiens] [MAS				4.19E-10	0.95	10.23	6.60	33112.2
AHQ-4-9, 6844	R.VTPVDYLLGVADLTGELMR.M	2063.40379	2	4.19E-10	0.95	4.62	-	966.3
gi|14211923|ref|NP_115982.1| PKCI-1-related HIT protein [Homo sapiens]				4.24E-10	2.25	30.29	32.50	17161.6
AHQ-4-13, 3406	K.AQQATPGGAAPTIFSR.I	1573.73512	2	1.43E-09	0.83	3.65	-	401.1
AHQ-4-13, 6252	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	4.15E-08	0.85	3.78	-	756.0
AHQ-4-13, 6253 - 6257	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	4.33E-08	0.96	5.56	-	1032.6
AHQ-4-13-, 6196	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	4.24E-10	0.79	3.22	-	868.0
AHQ-4-13-, 6209	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	1.29E-07	0.96	5.70	-	1147.7
AHQ-4-13-, 6184 - 6198	K.SLPADILYEDQQCLVFR.D	2069.32354	2	5.29E-04	0.83	3.36	-	616.5
AHQ-4-13, 6213 - 6278	K.SLPADILYEDQQCLVFR.D	2069.32354	2	7.53E-05	0.63	3.05	-	162.8
gi|4502295|ref|NP_001677.1| ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti				4.56E-10	10.74	130.27	31.20	57955.2
AHQ-4-7, 5538 - 5561	R.AIAELGIYPAVDPLDSTSR.I	1989.21513	2	2.46E-04	0.58	2.95	-	361.9
AHQ-4-7, 6047	R.FLSQPFQVAEVFTGHMGK.L	2024.33104	3	6.37E-05	0.83	4.04	-	423.9
AHQ-4-7, 4258 - 4281	R.FTQAGSEVSALLGR.I	1436.59522	2	3.15E-07	0.96	4.66	-	1393.7
AHQ-4-7, 7278	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	4.56E-10	0.95	4.82	-	1313.3
AHQ-4-7, 7414	K.GFQQILAGEYDHLPEQAFYMVGPIEEAVAK.A	3352.76051	3	2.82E-09	0.94	5.47	-	863.8
AHQ-4-7, 3379	R.IMDPNIVGSEHYDVAR.G	1817.01617	2	5.60E-07	0.87	3.82	-	639.5
AHQ-4-7, 3578	R.IMNVIGEPIDER.G	1386.59962	2	1.83E-04	0.91	3.40	-	1070.2
AHQ-4-7, 2635	K.IPVGPETLGR.I	1039.21035	2	2.87E-04	0.87	2.86	-	736.5
AHQ-4-7, 2639	K.IPVGPETLGR.I	1039.21035	1	1.04E-05	0.36	2.02	-	229.4
AHQ-4-7, 3941	R.LVLEVAQHLGESTVR.T	1651.88893	2	1.49E-08	0.97	4.71	-	1452.7
AHQ-4-7, 3223	K.VALVYGQMNQPPGAR.A	1601.85511	2	2.21E-07	0.91	3.79	-	836.5
AHQ-4-7, 2651	K.VALVYGQM*NQPPGAR.A	1617.85451	2	5.92E-04	0.77	3.09	-	609.5
AHQ-4-7, 4494	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	1.34E-06	0.88	4.28	-	385.7
AHQ-4-7, 3734	K.VVDLLAPYAK.G	1089.30927	2	7.05E-04	0.81	2.64	-	867.6
gi|29739414|ref|XP_294015.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				4.80E-10	2.57	30.24	17.70	26916.7
AHQ-4-12, 4001	K.IISNASCTTNCLAPLAK.V	1837.10868	2	8.61E-07	0.56	3.29	-	711.3
AHQ-4-9, 3465 - 3507	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.24E-06	0.91	4.28	-	1380.4
AHQ-4-9, 3568 - 3639	K.IISNASCTTNCLAPLAK.V	1837.10868	2	8.70E-09	0.82	3.90	-	1081.1
AHQ-4-9, 3788 - 3856	K.IISNASCTTNCLAPLAK.V	1837.10868	2	5.58E-06	0.90	3.61	-	1303.3
AHQ-4-9, 3899 - 3969	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.27E-06	0.89	4.15	-	1334.9
AHQ-4-11, 4050	K.IISNASCTTNCLAPLAK.V	1837.10868	2	4.97E-06	0.80	3.49	-	1090.9
AHQ-4-9, 4732	K.LISWYDNEFGYSNR.V	1764.87478	2	7.63E-04	0.65	2.96	-	429.3
AHQ-4-14-, 4929	K.LISWYDNEFGYSNR.V	1764.87478	2	2.06E-08	0.97	4.73	-	1743.3
AHQ-4-9, 4445 - 4507	K.LISWYDNEFGYSNR.V	1764.87478	2	2.09E-09	0.94	4.38	-	938.6
AHQ-4-9, 4635	K.LISWYDNEFGYSNR.V	1764.87478	2	4.22E-08	0.93	4.18	-	814.1
AHQ-4-11, 4742 - 4804	K.LISWYDNEFGYSNR.V	1764.87478	2	5.17E-07	0.84	3.28	-	852.6
AHQ-4-11, 4878 - 4950	K.LISWYDNEFGYSNR.V	1764.87478	2	3.42E-07	0.95	4.21	-	949.6
AHQ-4-10, 4548	K.LISWYDNEFGYSNR.V	1764.87478	2	4.62E-08	0.96	4.44	-	1396.9
AHQ-4-13, 5102	K.LISWYDNEFGYSNR.V	1764.87478	2	5.14E-08	0.96	4.46	-	1323.5
AHQ-4-14, 6296 - 6297	K.LISWYDNEFGYSNR.V	1764.87478	2	4.80E-10	0.96	4.62	-	1150.1
AHQ-4-13-, 4980	K.LISWYDNEFGYSNR.V	1764.87478	2	7.23E-09	0.96	4.43	-	1337.6
AHQ-4-9, 1941	R.VVDLMAHM*ASKE	1347.58686	1	1.75E-05	0.78	3.11	-	352.6
gi|7656991|ref|NP_055140.1| coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;				4.83E-10	7.23	90.27	25.70	53248.7
AHQ-4-6, 5823 - 5862	R.AIFLADGNVFTTGFSR.M	1716.91793	2	1.79E-05	0.96	4.64	-	1281.7
AHQ-4-6, 5980 - 5986	R.AIFLADGNVFTTGFSR.M	1716.91793	2	4.65E-06	0.97	4.63	-	1775.2
AHQ-4-6, 3688	K.CDLISIPK.K	947.13128	2	6.58E-05	0.80	2.82	-	700.0
AHQ-4-6, 2908	R.HVFGQAVKNDQCYDDIR.V	2067.22783	2	5.12E-09	0.95	5.21	-	880.1
AHQ-4-6, 3019	R.KCEPIIMTVPR.K	1345.65706	2	1.57E-04	0.81	2.83	-	587.9
AHQ-4-7, 2926	R.KCEPIIMTVPR.K	1345.65706	2	1.95E-04	0.71	2.67	-	629.1
AHQ-4-6, 7122	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	4.83E-10	0.95	5.36	-	1114.3
AHQ-4-7, 7313	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	2.36E-09	0.95	5.32	-	1165.6
AHQ-4-6, 3714	K.NADPILISLK.H	1084.29103	1	2.01E-04	0.11	2.09	-	233.8
AHQ-4-6, 2120	K.NDQCYDDIR.V	1200.21762	2	1.11E-04	0.89	3.20	-	1177.7
AHQ-4-6, 2660	R.VGIVAWHPTAR.N	1207.40918	3	2.83E-04	0.82	3.52	-	719.6
AHQ-4-7, 6010	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	4.85E-08	0.92	4.34	-	801.2
AHQ-4-7, 5997 - 6001	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	4.74E-04	0.74	2.81	-	729.1
AHQ-4-10, 5497 - 5501	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	3.67E-06	0.79	3.73	-	688.8
AHQ-4-6, 6060 - 6064	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	1.63E-07	0.94	4.83	-	786.3
gi|4507521|ref|NP_001055.1| transketolase [Homo sapiens]				4.87E-10	0.90	10.19	3.00	67877.3
AHQ-4-6, 4574	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	4.87E-10	0.90	3.83	-	613.8
gi|30148492|ref|XP_293610.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				4.89E-10	1.76	20.23	2.60	72113.4
AHQ-4-6, 4598 - 4606	R.IINEPTAAAIAYGLDK.K	1660.89259	2	4.85E-07	0.88	4.29	-	917.9
AHQ-4-7, 4554	R.IINEPTAAAIAYGLDK.K	1660.89259	2	4.89E-10	0.95	4.66	-	816.6
AHQ-4-6, 4026	R.IINEPTAAAIAYGLDKK.V	1789.06550	3	9.27E-09	0.81	3.53	-	449.7
gi|4505735|ref|NP_002611.1| platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H				4.93E-10	0.97	10.25	14.40	11552.6
AHQ-4-14, 4801 - 4881	R.AEAEEDGDLQCLCVK.T	1739.86036	2	1.00E-09	0.94	4.28	-	1194.2
AHQ-4-14-, 3685 - 3762	R.AEAEEDGDLQCLCVK.T	1739.86036	2	4.93E-10	0.97	4.94	-	1372.0
AHQ-4-14, 4693 - 4697	R.AEAEEDGDLQCLCVK.T	1739.86036	2	2.11E-06	0.93	4.09	-	851.3
gi|4502969|ref|NP_000745.1| catechol-O-methyltransferase isoform MB-COMT [Homo sapiens]				4.94E-10	0.94	10.21	5.50	30036.9
AHQ-4-10, 6065 - 6072	R.YLPDTLLLEECGLLR.K	1807.10089	2	4.94E-10	0.94	4.14	-	1234.2
gi|6857820|ref|NP_005019.2| phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl				5.51E-10	1.93	20.28	7.60	46224.3
AHQ-4-7, 4546 - 4547	R.FGIDDQDFQNSLTR.S	1656.73462	2	5.51E-10	0.95	4.83	-	1390.4
AHQ-4-7, 2469 - 2471	K.HGAGAEISTVNPEQYSK.R	1788.89618	2	2.79E-07	0.98	5.53	-	2044.8
gi|11559923|ref|NP_071496.1| eukaryotic translation initiation factor 4H isoform 1 [Homo sapiens] [				5.83E-10	0.93	10.26	11.70	27384.8
AHQ-4-11, 6832	K.ELPTEPPYTAYVGNLPFNTVQGDIDAIFK.D	3211.56532	3	5.83E-10	0.93	5.23	-	841.9
gi|5729997|ref|NP_004154.2| RAB27B, member RAS oncogene family [Homo sapiens]				5.94E-10	6.11	70.24	34.90	24607.7
AHQ-4-11, 6500	K.AVETLLDLIMK.R	1246.54211	2	3.68E-05	0.88	3.73	-	719.4
AHQ-4-11, 5588	K.AVETLLDLIM*K.R	1262.54151	2	1.64E-05	0.87	2.91	-	1150.6
AHQ-4-10, 5229	K.AVETLLDLIM*K.R	1262.54151	2	1.44E-05	0.84	3.23	-	669.8
AHQ-4-10, 6167	K.AVETLLDLIMK.R	1246.54211	2	1.50E-06	0.86	3.80	-	561.2
AHQ-4-13, 3159	K.LLALGDSGVGK.T	1030.20023	1	1.45E-04	0.76	2.58	-	746.4

AHQ-4-10, 5928 - 5929	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	4.05E-07	0.86	3.95	-	565.4
AHQ-4-10, 5215	R.NWM*SQLQANAYCENPDIVLIGNK.A	2696.99712	2	3.41E-06	0.87	3.59	-	688.8
AHQ-4-11, 6226	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	2.61E-04	0.78	3.15	-	767.4
AHQ-4-10, 5743	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	8.24E-05	0.89	4.08	-	641.1
AHQ-4-11, 3461	K.VHLQLWDTAGQER.F	1553.70390	2	8.83E-07	0.96	4.16	-	1524.5
AHQ-4-10, 3303	K.VHLQLWDTAGQER.F	1553.70390	2	1.27E-08	0.96	4.41	-	1535.0
AHQ-4-10, 4056 - 4088	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	3.10E-05	0.76	2.66	-	783.9
AHQ-4-12, 4495 - 4561	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	3.76E-04	0.55	2.61	-	661.2
AHQ-4-10, 4147 - 4225	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	5.94E-10	0.95	4.80	-	718.8
AHQ-4-11, 4389	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	1.21E-09	0.95	4.30	-	1285.2
gi|4503747|ref|NP_001448.1| filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a				6.01E-10	3.91	50.25	1.40	278191.4
AHQ-4-1, 3630 - 3715	K.DLAEDAPWK.K	1045.12708	1	2.46E-06	0.34	1.97	-	495.3
AHQ-4-1, 3731	K.DLAEDAPWK.K	1045.12708	2	1.49E-04	0.86	2.96	-	894.0
AHQ-4-4, 3603	K.DLAEDAPWK.K	1045.12708	1	1.47E-06	0.36	1.83	-	677.7
AHQ-4-3, 3635	K.DLAEDAPWK.K	1045.12708	1	4.88E-06	0.45	2.18	-	523.7
AHQ-4-2, 3656	K.DLAEDAPWK.K	1045.12708	1	6.50E-06	0.33	2.08	-	499.8
AHQ-4-2, 3674	K.DLAEDAPWK.K	1045.12708	1	5.69E-06	0.65	2.69	-	630.5
AHQ-4-5, 3459 - 3466	K.DLAEDAPWK.K	1045.12708	1	5.74E-06	0.38	2.33	-	543.2
AHQ-4-1, 3083	K.DLAEDAPWKK.I	1173.29999	2	1.66E-04	0.76	2.76	-	876.8
AHQ-4-6, 6290	R.LIALLEVLSQK.R	1227.51852	2	7.56E-08	0.96	4.30	-	1093.2
AHQ-4-3, 6585 - 6616	R.LIALLEVLSQK.R	1227.51852	2	1.94E-07	0.97	5.02	-	1226.9
AHQ-4-1, 6598	R.LIALLEVLSQK.R	1227.51852	2	1.26E-08	0.97	4.50	-	1455.5
AHQ-4-4, 6570	R.LIALLEVLSQK.R	1227.51852	2	4.39E-07	0.97	4.99	-	1405.1
AHQ-4-2, 6648	R.LIALLEVLSQK.R	1227.51852	2	6.01E-10	0.97	4.98	-	1378.8
AHQ-4-11, 6000	R.LIALLEVLSQK.R	1227.51852	2	1.62E-08	0.96	4.38	-	1233.5
AHQ-4-5, 6298 - 6363	R.LIALLEVLSQK.R	1227.51852	2	5.58E-07	0.97	4.70	-	1339.3
AHQ-4-2, 6675 - 6743	R.QM*QLENVSVALEFLDR.E	1909.15348	2	8.58E-06	0.88	4.35	-	652.4
AHQ-4-1, 7162 - 7167	R.QMQLENVSVALEFLDR.E	1893.15408	2	7.39E-04	0.94	4.59	-	866.0
gi|13775198|ref|NP_112576.1| SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr				6.03E-10	4.24	50.29	32.30	10437.7
AHQ-4-14-, 4638	R.IQYQLVDISQDNALR.D	1776.97168	2	6.03E-10	0.96	4.72	-	1822.8
AHQ-4-13-, 4684 - 4697	R.IQYQLVDISQDNALR.D	1776.97168	2	9.40E-09	0.97	5.73	-	1525.9
AHQ-4-13-, 4766 - 4833	R.IQYQLVDISQDNALR.D	1776.97168	2	8.97E-08	0.95	4.69	-	1415.7
AHQ-4-14, 5876 - 5942	R.IQYQLVDISQDNALR.D	1776.97168	2	4.26E-04	0.95	3.80	-	1856.8
AHQ-4-13, 4729 - 4808	R.IQYQLVDISQDNALR.D	1776.97168	2	1.92E-05	0.97	4.78	-	1659.7
AHQ-4-13-, 4704	R.IQYQLVDISQDNALR.D	1776.97168	3	1.35E-07	0.97	5.55	-	2047.2
AHQ-4-13, 5049 - 5113	R.IQYQLVDISQDNALRDEMR.A	2308.55751	2	8.28E-04	0.91	4.47	-	692.2
AHQ-4-13, 5177 - 5248	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.54E-06	0.80	3.91	-	498.7
AHQ-4-14, 5602 - 5680	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.50E-06	0.77	3.46	-	520.9
AHQ-4-14, 5690 - 5770	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	4.93E-07	0.75	3.47	-	541.6
AHQ-4-13, 4605	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.74E-07	0.72	3.19	-	514.1
AHQ-4-13-, 5028 - 5096	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	6.90E-06	0.76	3.40	-	635.5
AHQ-4-13-, 4898 - 4964	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.22E-04	0.73	3.23	-	528.1
AHQ-4-14-, 4917 - 4977	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.02E-06	0.74	3.62	-	378.6
AHQ-4-13-, 5088 - 5122	R.IQYQLVDISQDNALRDEMR.A	2308.55751	2	2.26E-04	0.90	4.34	-	580.9
AHQ-4-13-, 4208	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	5.91E-06	0.76	3.13	-	733.2
AHQ-4-13-, 4305 - 4384	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	9.55E-04	0.72	3.04	-	343.6
AHQ-4-13-, 4397 - 4460	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.75E-05	0.77	3.10	-	619.5
AHQ-4-13-, 4537	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.09E-06	0.70	3.05	-	653.1
AHQ-4-14-, 4463	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.91E-05	0.72	3.29	-	372.0
AHQ-4-13, 4692	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	6.17E-08	0.67	3.27	-	372.9
AHQ-4-13, 4373	K.RIQYQLVDISQDNALR.D	1933.15803	2	1.04E-05	0.94	4.84	-	864.8
AHQ-4-13-, 1608 - 1672	R.VYSTSVTGSR.E	1057.13940	2	2.02E-07	0.91	3.63	-	879.2
AHQ-4-13-, 1732 - 1797	R.VYSTSVTGSR.E	1057.13940	2	8.15E-08	0.93	3.46	-	1151.1
AHQ-4-13, 2074 - 2137	R.VYSTSVTGSR.E	1057.13940	2	1.21E-05	0.89	2.93	-	1056.6
AHQ-4-13-, 1856 - 1861	R.VYSTSVTGSR.E	1057.13940	2	9.88E-07	0.92	3.30	-	984.0
AHQ-4-13-, 1944 - 2004	R.VYSTSVTGSR.E	1057.13940	2	1.46E-06	0.85	2.72	-	922.1
AHQ-4-13, 1933 - 1998	R.VYSTSVTGSR.E	1057.13940	2	4.22E-05	0.85	2.98	-	780.7
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				6.44E-10	2.64	30.33	7.40	32164.8
AHQ-4-1, 5017	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.89E-09	0.94	4.80	-	863.4
AHQ-4-1, 5165	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.23E-06	0.93	4.66	-	839.7
AHQ-4-1, 5523	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.48E-04	0.83	3.80	-	513.2
AHQ-4-2, 5250 - 5251	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.18E-04	0.92	4.69	-	717.5
AHQ-4-2, 5763	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.48E-06	0.92	4.36	-	705.9
AHQ-4-3, 5095	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.83E-05	0.93	4.39	-	888.5
AHQ-4-3, 5229 - 5231	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.93E-05	0.93	4.75	-	717.9
AHQ-4-3, 5576	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.64E-09	0.92	4.86	-	529.5
AHQ-4-4, 5054	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.84E-07	0.93	4.73	-	632.4
AHQ-4-4, 5183 - 5188	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.22E-04	0.94	5.44	-	608.5
AHQ-4-4, 5267	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.78E-05	0.80	3.47	-	585.7
AHQ-4-4, 5531 - 5556	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.96E-07	0.78	3.49	-	562.3
AHQ-4-5, 5011 - 5086	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.05E-06	0.93	4.43	-	828.2
AHQ-4-6, 4974	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.20E-06	0.90	4.21	-	653.4
AHQ-4-7, 4930	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.07E-04	0.86	4.31	-	470.7
AHQ-4-14-, 5349 - 5413	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.24E-04	0.86	3.85	-	742.5
AHQ-4-8, 4774 - 4853	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.19E-06	0.96	5.22	-	1079.8
AHQ-4-8, 4921 - 4985	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.02E-07	0.95	5.14	-	781.3
AHQ-4-8, 5025 - 5097	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.78E-06	0.96	5.48	-	1073.2
AHQ-4-14-, 5235 - 5250	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.66E-06	0.95	5.15	-	906.5
AHQ-4-8, 5098 - 5169	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.47E-07	0.98	6.56	-	1347.0
AHQ-4-8, 5446 - 5525	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.05E-04	0.97	6.19	-	1034.7
AHQ-4-8, 5589 - 5654	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.76E-04	0.97	5.54	-	1059.9
AHQ-4-8, 5717 - 5786	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.62E-06	0.96	5.76	-	824.9
AHQ-4-8, 5853 - 5917	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.09E-04	0.96	5.34	-	1096.2
AHQ-4-8, 5985 - 6054	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.09E-05	0.97	6.28	-	1011.0
AHQ-4-8, 6117 - 6181	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.86E-06	0.95	5.42	-	914.1
AHQ-4-8, 6254 - 6321	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.99E-04	0.94	4.82	-	963.0
AHQ-4-8, 6385 - 6454	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.22E-06	0.95	4.97	-	871.9
AHQ-4-8, 6469 - 6533	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.45E-04	0.92	3.98	-	1018.6
AHQ-4-8, 6557 - 6622	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.25E-05	0.95	5.19	-	987.1
AHQ-4-8, 6687 - 6757	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.44E-06	0.95	5.25	-	834.1
AHQ-4-8, 7071 - 7142	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.21E-04	0.90	4.50	-	608.6
AHQ-4-8, 7213 - 7289	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.44E-04	0.95	4.71	-	928.4
AHQ-4-8, 7355 - 7373	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.20E-06	0.94	5.16	-	618.3
AHQ-4-9, 4427 - 4505	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.55E-06	0.92	4.46	-	817.9
AHQ-4-9, 4833 - 4844	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.65E-04	0.93	4.90	-	737.3
AHQ-4-10, 4421 - 4500	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.44E-10	0.94	4.64	-	998.0
AHQ-4-10, 4491 - 4547	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.84E-06	0.95	5.03	-	1069.7
AHQ-4-10, 4603 - 4605	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.05E-05	0.96	4.79	-	1240.3
AHQ-4-10, 4695 - 4756	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.52E-04	0.91	3.96	-	828.6
AHQ-4-10, 4796 - 4801	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.23E-07	0.93	4.35	-	804.6
AHQ-4-10, 4943 - 5007	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.10E-06	0.96	5.50	-	849.0
AHQ-4-10, 5068 - 5128	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.01E-06	0.81	3.56	-	697.5
AHQ-4-10, 5412 - 5413	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.00E-06	0.85	4.34	-	508.5
AHQ-4-11, 4693	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.24E-07	0.89	4.01	-	660.4
AHQ-4-11, 4808 - 4824	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.23E-04	0.95	5.29	-	779.9
AHQ-4-11, 5104	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.83E-07	0.94	4.81	-	882.5
AHQ-4-11, 5258 - 5334	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.81E-04	0.93	4.75	-	751.2

AHQ-4-12, 4861 - 4934	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.27E-09	0.94	4.62	-	929.2
AHQ-4-12, 4990 - 4997	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.07E-05	0.92	4.28	-	967.1
AHQ-4-12, 5295	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.87E-08	0.95	5.07	-	1149.0
AHQ-4-12, 5441 - 5442	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.40E-07	0.91	4.57	-	696.1
AHQ-4-13, 4841	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.06E-06	0.90	4.48	-	536.6
AHQ-4-13, 4936 - 5004	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.66E-04	0.94	4.73	-	854.3
AHQ-4-13, 5028 - 5093	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.80E-04	0.95	4.95	-	1175.5
AHQ-4-13, 5157 - 5225	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.54E-04	0.92	4.02	-	975.2
AHQ-4-13, 5165	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.30E-06	0.97	5.77	-	1097.7
AHQ-4-13, 5321 - 5322	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.83E-04	0.90	4.12	-	891.4
AHQ-4-13, 5653 - 5689	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.80E-07	0.97	6.17	-	918.4
AHQ-4-14, 5758 - 5817	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.93E-10	0.95	4.89	-	1023.1
AHQ-4-14, 5888 - 5948	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.09E-04	0.91	4.24	-	713.3
AHQ-4-14, 6016	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.64E-04	0.97	5.73	-	1064.9
AHQ-4-14, 6086 - 6144	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.43E-06	0.91	4.05	-	811.0
AHQ-4-14, 6208 - 6278	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.55E-04	0.89	4.11	-	616.4
AHQ-4-14, 6253 - 6326	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.36E-05	0.95	4.87	-	1171.6
AHQ-4-14, 6384 - 6456	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.63E-04	0.97	6.13	-	975.6
AHQ-4-14, 6457 - 6536	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.47E-04	0.91	4.32	-	671.5
AHQ-4-14, 6505 - 6581	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.49E-04	0.95	5.30	-	904.1
AHQ-4-13-, 4725 - 4805	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.55E-06	0.96	5.28	-	1087.6
AHQ-4-13-, 4873 - 4936	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.76E-05	0.96	5.78	-	995.3
AHQ-4-13-, 5084	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.00E-04	0.95	4.78	-	1080.5
AHQ-4-13-, 5140 - 5205	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.72E-05	0.96	4.82	-	1231.3
AHQ-4-13-, 5173 - 5178	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.90E-06	0.77	3.72	-	448.2
AHQ-4-13-, 5293 - 5362	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.71E-04	0.95	5.05	-	828.3
AHQ-4-13-, 5421 - 5433	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.24E-06	0.96	5.93	-	779.0
AHQ-4-13-, 5504 - 5569	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.98E-04	0.94	4.57	-	1001.7
AHQ-4-14-, 4671	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.08E-08	0.95	4.64	-	950.4
AHQ-4-14-, 4763 - 4825	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.12E-05	0.94	4.98	-	826.6
AHQ-4-14-, 4886 - 4955	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.92E-05	0.96	4.99	-	1040.4
AHQ-4-14-, 5017	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.45E-08	0.97	5.88	-	1138.8
AHQ-4-14-, 5083 - 5162	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.86E-06	0.97	6.11	-	1124.7
AHQ-4-14-, 5115 - 5141	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.39E-08	0.93	4.64	-	768.3
AHQ-4-14-, 5477 - 5541	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.36E-04	0.90	4.48	-	600.3
AHQ-4-8, 3993 - 4066	K.YPIEHSIITNWDDMEK.I	1992.19784	2	9.01E-04	0.28	2.71	-	358.7
AHQ-4-8, 5046	K.YPIEHSIITNWDDMEK.I	1992.19784	2	6.92E-05	0.77	3.64	-	527.8
gi|5902128|ref|NP_008880.1| syntaxin binding protein 2; Hunc18b [Homo sapiens]				6.77E-10	9.42	100.31	26.10	66438.1
AHQ-4-6, 6286	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	2	6.54E-08	0.97	6.15	-	1234.9
AHQ-4-6, 6574	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	1.36E-04	0.87	3.90	-	676.3
AHQ-4-6, 2930	R.KGPEDTAQLAHAVLAK.L	1649.87303	3	6.77E-10	0.97	5.29	-	1743.7
AHQ-4-6, 2919 - 2932	R.KGPEDTAQLAHAVLAK.L	1649.87303	2	1.36E-05	0.93	4.44	-	955.8
AHQ-4-6, 2150	K.LIQHANVQAHSSLIR.N	1687.92773	2	1.42E-05	0.97	4.27	-	1831.1
AHQ-4-6, 6342 - 6362	K.LIVPVLLDAAVPAYDK.I	1698.03911	2	2.03E-08	0.97	4.34	-	1974.1
AHQ-4-6, 3058	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	4.00E-09	0.95	4.95	-	923.8
AHQ-4-6, 5344 - 5378	R.NLWPFVSDPAPTASSQAAVSAR.F	2273.48981	2	1.44E-05	0.94	4.53	-	839.3
AHQ-4-6, 5879	R.REPIPSLEAIYLLSPTEK.S	2057.37574	3	1.13E-04	0.84	3.68	-	999.3
AHQ-4-6, 5871	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	5.23E-06	0.96	5.25	-	1345.5
AHQ-4-6, 4611	K.WEVLIGSSHILTPTR.F	1709.97007	2	9.84E-07	0.94	3.95	-	1085.1
AHQ-4-6, 2552	K.YSTHLHLADDCMK.H	1592.77877	3	2.14E-04	0.88	3.35	-	1164.5
gi|4506925|ref|NP_003013.1| SH3 domain binding glutamic acid-rich protein like; SH3-binding domain				7.60E-10	3.62	40.35	50.00	12774.2
AHQ-4-13-, 6268 - 6330	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.86E-04	0.80	3.57	-	643.4
AHQ-4-13-, 5980 - 6049	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	6.96E-05	0.92	4.53	-	653.7
AHQ-4-13-, 6068 - 6144	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	8.40E-05	0.93	3.57	-	1264.9
AHQ-4-13, 6080 - 6144	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	3.96E-06	0.82	3.76	-	448.9
AHQ-4-13, 5080 - 5144	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.78E-08	0.97	6.94	-	1257.2
AHQ-4-13, 4966 - 5032	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	5.77E-08	0.90	4.60	-	679.2
AHQ-4-13-, 4896 - 4976	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	7.60E-10	0.96	6.08	-	1157.0
AHQ-4-13-, 5040 - 5104	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.24E-09	0.96	6.42	-	1063.4
AHQ-4-13-, 5133	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.12E-08	0.95	5.51	-	965.5
AHQ-4-13, 5173	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	5.65E-04	0.84	3.52	-	805.3
AHQ-4-13, 4210 - 4272	R.GDYDAFFEAR.E	1191.23073	2	2.37E-04	0.87	3.06	-	927.3
AHQ-4-13-, 2364 - 2434	R.VYIASSSGSTAIK.K	1284.44065	2	6.95E-04	0.88	3.64	-	1101.3
AHQ-4-13, 2479 - 2487	R.VYIASSSGSTAIK.K	1284.44065	2	2.73E-04	0.97	4.33	-	2389.0
gi|27478053|ref|XP_015334.4| similar to heat shock 70kD protein binding protein; progesterone recep				7.68E-10	0.98	10.28	11.60	16603.8
AHQ-4-7, 4697	R.LLGHWEEAAHDLALACK.L	1936.18044	2	7.68E-10	0.98	5.61	-	2239.1
gi|22043610|ref|XP_171081.1| similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1; rh				7.80E-10	3.38	50.25	28.60	21543.1
AHQ-4-11, 2541	R.AVLCPPPVK.K	982.22199	1	5.56E-05	0.12	2.02	-	167.4
AHQ-4-11, 2657 - 2660	R.HHCPNTPIILVGTK.L	1588.85612	2	7.67E-04	0.82	3.25	-	581.0
AHQ-4-11, 3730 - 3800	K.KLTPITYPQGLAMAK.E	1632.99216	2	1.15E-04	0.83	4.15	-	371.5
AHQ-4-11, 4196	K.LTPITYPQGLAMAK.E	1504.81924	2	7.53E-04	0.63	2.98	-	321.2
AHQ-4-11, 4688	K.PVNLGLWDTAGQEDYDR.L	1950.05441	2	7.80E-10	0.98	4.91	-	2030.1
gi|4502011|ref|NP_000467.1| adenylate kinase 1 [Homo sapiens]				7.81E-10	6.08	70.24	42.30	21634.7
AHQ-4-11, 6824	K.GQLVPLETVLDMLR.D	1584.90590	2	7.81E-10	0.94	4.62	-	616.8
AHQ-4-11, 5137	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	2	9.03E-06	0.75	3.23	-	602.6
AHQ-4-11, 5648	R.IGQPTLLLYVDAGPETMTQR.L	2204.53234	2	7.57E-07	0.95	4.80	-	938.1
AHQ-4-11, 3342	K.IIFVVGGPGSGK.G	1131.34939	1	2.91E-04	0.77	2.27	-	1121.0
AHQ-4-11, 6178	R.KVNAEGSVDSVFSQVCTHLDALK	2506.77407	3	3.96E-07	0.97	4.75	-	2422.9
AHQ-4-11, 6320 - 6354	K.VNAEGSVDSVFSQVCTHLDALK	2378.60116	2	3.08E-06	0.78	3.18	-	583.6
AHQ-4-11, 3624	K.YGYTHLSTGDLLR.S	1496.64912	2	1.77E-06	0.93	3.51	-	1071.5
gi|4504111|ref|NP_002077.1| growth factor receptor-bound protein 2 [Homo sapiens]				8.01E-10	1.27	20.16	11.10	25206.2
AHQ-4-10, 3639 - 3705	K.FNSLNELVDYHR.S	1507.63200	2	2.11E-04	0.40	2.54	-	452.7
AHQ-4-10, 3233	K.VLNEECDQNWYK.A	1599.70313	2	8.01E-10	0.86	3.28	-	778.0
gi|4758988|ref|NP_004152.1| RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho				8.11E-10	3.57	40.26	25.40	22677.6
AHQ-4-11, 6096 - 6158	K.EFADSLGIPFLETSAK.N	1725.91990	2	5.58E-05	0.70	3.13	-	467.6
AHQ-4-13, 6338 - 6413	K.EFADSLGIPFLETSAK.N	1725.91990	2	1.38E-04	0.73	3.53	-	414.1
AHQ-4-12, 6266	K.EFADSLGIPFLETSAK.N	1725.91990	2	2.62E-05	0.60	3.12	-	517.6
AHQ-4-11, 5977 - 6037	K.EFADSLGIPFLETSAK.N	1725.91990	2	1.25E-07	0.91	4.59	-	611.3
AHQ-4-11, 5981 - 6061	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.23E-08	0.97	5.16	-	1234.3
AHQ-4-11, 5554	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.60E-05	0.74	3.04	-	738.8
AHQ-4-14-, 5835 - 5902	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.47E-06	0.95	4.05	-	1315.2
AHQ-4-11, 6185 - 6264	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.10E-06	0.96	4.45	-	1228.1
AHQ-4-11, 6810	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.60E-05	0.85	3.50	-	607.6
AHQ-4-11, 6905	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.68E-06	0.92	3.95	-	912.0
AHQ-4-11, 6122 - 6197	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	8.11E-10	0.94	4.01	-	1262.7
AHQ-4-11, 5848 - 5916	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	5.72E-08	0.95	4.40	-	1100.5
AHQ-4-11, 3953	K.NATNVEQSFM*TM*AAEIK.K	1918.13902	2	2.06E-04	0.92	4.06	-	1060.7
AHQ-4-11, 4750	K.NATNVEQSFMTM*AAEIK.K	1902.13962	2	2.63E-04	0.79	3.91	-	968.5
gi|5729877|ref|NP_006588.1| heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD				8.22E-10	10.40	120.27	22.30	70897.6
AHQ-4-6, 4107 - 4134	R.ARFEELNADLFR.G	1481.63768	2	2.28E-06	0.89	3.58	-	746.3
AHQ-4-6, 4244	R.ARFEELNADLFR.G	1481.63768	2	1.81E-08	0.94	3.84	-	1076.7
AHQ-4-6, 4551	R.FEELNADLFR.G	1254.37310	2	6.57E-05	0.93	3.64	-	1350.4
AHQ-4-6, 4552	R.FEELNADLFR.G	1254.37310	1	6.44E-07	0.26	2.02	-	361.3
AHQ-4-14-, 5165	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	1.80E-07	0.86	3.88	-	688.3
AHQ-4-6, 5178	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	8.22E-10	0.93	4.92	-	893.0
AHQ-4-6, 5182 - 5198	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	2	1.85E-08	0.97	5.40	-	1334.3
AHQ-4-6, 5263	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	1.05E-04	0.68	3.20	-	585.0

AHQ-4-6, 3282	K.LDKSQIHDIVLVGGSTR.I	1839.08615	2	3.88E-06	0.90	3.92	-	755.5
AHQ-4-6, 2627 - 2628	K.MKEIAEAYLGK.T	1253.49320	1	1.35E-05	0.52	2.28	-	485.5
AHQ-4-6, 2630	K.MKEIAEAYLGK.T	1253.49320	2	6.63E-07	0.91	3.68	-	965.7
AHQ-4-6, 2235	K.M*KEIAEAYLGK.T	1269.49260	2	1.08E-06	0.91	3.73	-	1041.2
AHQ-4-6, 3712	K.NQVAMNPTNTVFDAK.R	1650.83816	2	1.44E-05	0.90	3.68	-	799.0
AHQ-4-6, 2434	R.RFDDAVVQSDMK.H	1411.56603	2	5.95E-06	0.96	4.40	-	1568.5
AHQ-4-6, 5062 - 5130	K.SFYPEEVSSMVLTK.M	1617.84485	2	2.25E-09	0.89	3.66	-	492.5
AHQ-4-7, 6957	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	7.08E-06	0.94	4.71	-	1020.9
AHQ-4-6, 6798 - 6800	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	7.35E-09	0.95	4.60	-	995.4
AHQ-4-6, 6806 - 6818	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	3	2.47E-07	0.95	5.47	-	1340.9
AHQ-4-6, 7056	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	3.19E-06	0.87	4.15	-	483.1
AHQ-4-6, 2780	K.SQIHDIVLVGGSTR.I	1482.66712	2	9.72E-07	0.97	4.29	-	2059.5
AHQ-4-7, 2691	K.SQIHDIVLVGGSTR.I	1482.66712	2	3.28E-06	0.96	4.42	-	1435.2
AHQ-4-6, 4623 - 4691	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	3.33E-05	0.87	3.83	-	497.1
gi|5031599|ref|NP_005722.1| actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub				8.33E-10	1.88	30.29	19.00	34332.8
AHQ-4-9, 3389 - 3391	R.DNTINLIHTFR.D	1344.50101	1	9.74E-05	0.08	1.87	-	227.2
AHQ-4-10, 3660	R.DNTINLIHTFR.D	1344.50101	2	1.55E-04	0.90	3.22	-	1003.4
AHQ-4-9, 2332	K.ELQAHGADELLK.R	1324.46487	2	1.93E-04	0.84	3.31	-	865.8
AHQ-4-14-, 6598	K.FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK.T	3638.89648	3	8.33E-10	0.96	5.70	-	1279.6
gi|29568111|ref|NP_006088.2| myosin, light polypeptide 9, regulatory; myosin regulatory light chain				8.35E-10	1.89	30.17	12.20	19827.1
AHQ-4-11, 3336	R.FTDEEVDEMYR.E	1434.51009	1	5.06E-06	0.27	2.02	-	449.4
AHQ-4-11, 3348	R.FTDEEVDEMYR.E	1434.51009	1	8.35E-10	0.60	2.65	-	320.7
AHQ-4-13, 3610	R.FTDEEVDEMYR.E	1434.51009	2	1.58E-07	0.93	3.32	-	1256.5
AHQ-4-11, 2640	R.FTDEEVDEM*YR.E	1450.50949	2	6.01E-06	0.94	3.31	-	1317.2
AHQ-4-13, 4054 - 4065	K.GNFNYVEFTR.I	1247.34066	2	5.09E-06	0.79	2.67	-	764.4
AHQ-4-11, 3918	K.GNFNYVEFTR.I	1247.34066	1	2.42E-08	0.36	2.01	-	462.0
gi|4758442|ref|NP_004115.1| glia maturation factor, beta [Homo sapiens]				9.24E-10	1.46	20.19	19.00	16713.1
AHQ-4-12, 6570	R.VSYPLCFIFSSPVGCKPEQQM*MYAGSK.N	3131.61197	3	6.29E-05	0.64	3.84	-	588.5
AHQ-4-12, 6781 - 6859	R.VSYPLCFIFSSPVGCKPEQQMMYAGSK.N	3115.61257	3	9.24E-10	0.82	3.68	-	513.2
AHQ-4-12, 6423 - 6499	R.VSYPLCFIFSSPVGCKPEQQM*MYAGSK.N	3131.61197	3	8.67E-05	0.42	3.01	-	423.5
gi|5729887|ref|NP_006624.1| IQ motif containing GTPase activating protein 2 [Homo sapiens]				9.68E-10	4.75	50.27	4.80	180611.0
AHQ-4-5, 3481	K.AWVNQLETQTGEASK.L	1662.78230	2	7.97E-06	0.97	5.34	-	1650.5
AHQ-4-13, 5613	K.GVLLDIDDLQTNQFK.N	1719.91690	2	5.61E-04	0.69	2.73	-	738.8
AHQ-4-13-, 5484 - 5494	K.GVLLDIDDLQTNQFK.N	1719.91690	2	2.71E-05	0.96	4.12	-	1732.5
AHQ-4-3, 5951	K.LGIAPQIQDLLGK.V	1366.63117	2	4.53E-06	0.87	3.23	-	588.4
AHQ-4-4, 4940	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	3.77E-06	0.96	4.34	-	1408.8
AHQ-4-3, 4967	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	9.68E-10	0.97	5.25	-	1751.9
AHQ-4-4, 4258	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	6.65E-06	0.93	3.89	-	1235.7
AHQ-4-3, 4303	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	1.91E-08	0.97	5.40	-	1470.8
gi|4507725|ref|NP_000362.1| transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum				9.78E-10	4.69	50.30	53.10	15886.9
AHQ-4-13, 3962	K.AADDTWEPFASGK.T	1395.45529	2	2.76E-06	0.86	3.71	-	534.4
AHQ-4-13-, 3816	K.AADDTWEPFASGK.T	1395.45529	2	2.66E-07	0.96	4.45	-	1155.2
AHQ-4-12, 3717	K.AADDTWEPFASGK.T	1395.45529	2	7.47E-06	0.91	3.78	-	832.9
AHQ-4-13, 4137	R.GSPAINVAVHVFR.K	1367.58095	2	7.46E-09	0.92	4.04	-	948.2
AHQ-4-13-, 4012 - 4013	R.GSPAINVAVHVFR.K	1367.58095	2	1.90E-08	0.94	4.26	-	1115.9
AHQ-4-12, 5919	R.RYTIAALLSPYSYSTTAVVTNPKE	2646.97608	2	1.20E-04	0.96	4.79	-	1474.0
AHQ-4-12, 5557	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	2.47E-05	0.95	5.02	-	1401.1
AHQ-4-12, 5547	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	9.78E-10	0.97	5.61	-	1395.9
AHQ-4-13-, 5509 - 5510	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	5.45E-07	0.97	5.97	-	1693.2
AHQ-4-13, 5612	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	3.17E-06	0.88	3.67	-	923.4
AHQ-4-13-, 6465	K.TSESGELHGLTTEEEFVEGIYKVEIDTK.S	3142.37019	3	3.30E-08	0.88	4.48	-	652.8
gi|25188179|ref|NP_005653.3| voltage-dependent anion channel 3 [Homo sapiens]				9.92E-10	3.53	60.21	20.50	30658.4
AHQ-4-10, 3008 - 3176	K.LSQNNFALGYK.A	1255.40424	1	6.23E-05	0.22	2.07	-	283.6
AHQ-4-10, 4535	K.LTLDTIFVPNTGK.K	1419.64771	1	7.82E-06	0.33	2.56	-	360.2
AHQ-4-10, 3965	K.LTLDTIFVPNTGKK.S	1547.82062	2	3.92E-05	0.82	3.39	-	758.0
AHQ-4-9, 3651 - 3713	K.LTLDTIFVPNTGKK.S	1547.82062	2	3.75E-04	0.67	3.15	-	488.4
AHQ-4-10, 3381	K.VCNYGLTFTQK.W	1332.50706	1	4.19E-04	0.42	2.92	-	236.4
AHQ-4-9, 4213	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	6.65E-08	0.73	3.59	-	378.3
AHQ-4-9, 3769	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.12E-08	0.90	4.13	-	523.0
AHQ-4-9, 4032	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.77E-09	0.62	3.18	-	451.4
AHQ-4-10, 3991	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	9.92E-10	0.80	3.64	-	496.0
AHQ-4-10, 3995	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	3	5.38E-07	0.79	3.23	-	759.2
AHQ-4-10, 4165	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	4.09E-05	0.84	3.55	-	574.6
AHQ-4-10, 4331 - 4335	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	5.89E-09	0.84	3.96	-	574.5
AHQ-4-14, 5769	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	1.27E-06	0.84	3.99	-	561.7
AHQ-4-10, 3555 - 3616	K.YKVCNYGLTFTQK.W	1623.85410	2	4.26E-08	0.93	3.46	-	1231.8
gi|4507953|ref|NP_003397.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep				1.10E-09	9.07	120.32	50.60	27744.9
AHQ-4-10, 1693 - 1711	R.EKIETELR.D	1018.14631	2	1.83E-05	0.53	2.56	-	579.5
AHQ-4-10, 6533	R.EKIETELRDICNDVLSLLEK.F	2419.73463	3	1.11E-07	0.86	3.74	-	903.9
AHQ-4-10, 5629	R.EKIETELRDICNDVLSLLEK.F	2419.73463	2	2.52E-06	0.62	3.03	-	465.5
AHQ-4-11, 3388	K.FLIPNASQAESK.V	1305.46156	1	1.50E-06	0.35	2.06	-	443.5
AHQ-4-10, 2945 - 3337	K.FLIPNASQAESK.V	1305.46156	1	4.97E-06	0.65	2.79	-	481.9
AHQ-4-9, 2989 - 3053	K.FLIPNASQAESK.V	1305.46156	1	9.58E-08	0.30	2.02	-	584.9
AHQ-4-10, 2981 - 3043	K.FLIPNASQAESK.V	1305.46156	2	6.50E-05	0.79	3.18	-	471.4
AHQ-4-10, 2943 - 3003	K.FLIPNASQAESK.V	1305.46156	2	1.91E-05	0.65	2.73	-	367.0
AHQ-4-9, 6695	K.IETELRDICNDVLSLLEK.F	2162.44718	2	3.78E-05	0.89	4.73	-	1086.4
AHQ-4-9, 5757	K.IETELRDICNDVLSLLEK.F	2162.44718	2	1.16E-08	0.96	4.71	-	1538.0
AHQ-4-10, 5695	K.IETELRDICNDVLSLLEK.F	2162.44718	2	1.62E-07	0.93	4.83	-	1091.9
AHQ-4-10, 6505	R.LGLALNFSVFYYEILNSPEK.A	2318.65200	2	2.83E-06	0.86	4.43	-	325.5
AHQ-4-14-, 2163 - 2231	K.SVTEQGAELSNEER.N	1549.57922	2	4.61E-05	0.95	4.62	-	1327.2
AHQ-4-13-, 2328 - 2340	K.SVTEQGAELSNEER.N	1549.57922	2	3.27E-06	0.87	3.22	-	1263.7
AHQ-4-10, 2191 - 2251	K.SVTEQGAELSNEER.N	1549.57922	2	5.44E-09	0.92	3.45	-	1283.3
AHQ-4-1, 2427	K.SVTEQGAELSNEER.N	1549.57922	2	6.18E-07	0.62	2.95	-	612.5
AHQ-4-10, 4657 - 4669	K.SVTEQGAELSNEERNLLSVAYK.N	2438.63331	2	1.65E-04	0.74	3.17	-	406.0
AHQ-4-10, 6356 - 6415	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	6.14E-08	0.98	6.05	-	1627.0
AHQ-4-9, 6517 - 6595	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	7.28E-08	0.96	5.42	-	1112.0
AHQ-4-13, 6890	K.TAFDEAIAELDTLSEESYK.D	2133.25160	3	2.99E-05	0.92	4.24	-	1181.7
AHQ-4-13, 6888	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	5.19E-09	0.97	5.62	-	1456.9
AHQ-4-13-, 6776 - 6777	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.50E-08	0.98	6.36	-	1832.3
AHQ-4-12, 6957 - 6959	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	5.37E-07	0.97	5.34	-	1293.9
AHQ-4-10, 5688	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.72E-04	0.67	3.10	-	564.3
AHQ-4-11, 6721	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.88E-08	0.97	5.40	-	1456.9
AHQ-4-14-, 6677 - 6747	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.72E-06	0.96	4.90	-	1195.7
AHQ-4-10, 6527 - 6568	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	5.87E-06	0.65	3.69	-	668.2
AHQ-4-10, 6525 - 6600	K.TAFDEAIAELDTLSEESYKDSTLIMQLLR.D	3304.66764	3	5.06E-07	0.94	5.20	-	1258.8
AHQ-4-9, 6761 - 6839	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	1.10E-09	0.92	4.56	-	1104.8
AHQ-4-10, 2399 - 2459	R.YDDMAACMK.S	1106.27579	1	6.22E-08	0.11	1.80	-	295.5
AHQ-4-10, 1801 - 1883	R.YLAEVAAGDDKK.G	1280.40887	2	2.83E-05	0.96	3.83	-	1776.2
AHQ-4-13-, 2068	R.YLAEVAAGDDKK.G	1280.40887	2	9.74E-07	0.95	3.46	-	1700.6
AHQ-4-13, 2170 - 2209	R.YLAEVAAGDDKK.G	1280.40887	2	9.44E-07	0.95	3.37	-	1826.6
AHQ-4-11, 1889 - 1918	R.YLAEVAAGDDKK.G	1280.40887	2	1.63E-05	0.93	2.91	-	1447.4
gi|4557801|ref|NP_000261.1| purine nucleoside phosphorylase [Homo sapiens]				1.12E-09	7.29	80.29	41.20	32147.7
AHQ-4-9, 3837 - 3907	R.DHINLPGFSGQNPLR.G	1665.83425	2	2.28E-04	0.88	4.20	-	462.7
AHQ-4-9, 3915	R.FHMYEGYPLWK.V	1471.70636	1	1.15E-07	0.91	3.69	-	922.7
AHQ-4-13-, 4009	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	3	1.12E-09	0.98	5.44	-	3989.6
AHQ-4-13, 7024	K.LEQFVSILMASIPLPDK.A	1902.28716	2	5.39E-04	0.79	3.31	-	615.3
AHQ-4-9, 6720	K.LEQFVSILMASIPLPDK.A	1902.28716	2	5.69E-04	0.96	5.08	-	1056.5

AHQ-4-13-, 6877	K.LEQFVSILMASIPLPDK.A	1902.28716	2	1.34E-05	0.97	5.70	-	1234.9
AHQ-4-13, 4317	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	2.33E-05	0.92	4.22	-	710.3
AHQ-4-13-, 4188	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	1.62E-04	0.92	4.71	-	563.4
AHQ-4-9, 4423	K.LGADAVGMSTVPEVIVAR.H	1786.08666	2	5.52E-06	0.88	3.36	-	808.3
AHQ-4-9, 3720	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	5.78E-04	0.95	4.25	-	1310.2
AHQ-4-13-, 5865	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	6.63E-06	0.80	3.60	-	472.3
AHQ-4-13, 5972	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	4.35E-04	0.90	3.82	-	642.2
AHQ-4-9, 5371 - 5433	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	1.20E-06	0.97	5.53	-	1310.6
AHQ-4-9, 5573	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	2.87E-07	0.95	4.82	-	1199.2
gi|4505989|ref|NP_000299.1| protective protein for beta-galactosidase; Protective protein for beta-				1.17E-09	1.89	20.23	6.90	54495.8
AHQ-4-10, 4927 - 4929	K.CNFYDNKDLECVTNLQEVAR.I	2491.69642	2	2.48E-06	0.91	4.29	-	762.3
AHQ-4-12, 3473	K.YGDSGEQIAGFVK.E	1371.47686	2	1.17E-09	0.98	4.49	-	2559.8
AHQ-4-11, 3392	K.YGDSGEQIAGFVK.E	1371.47686	2	8.19E-08	0.97	4.53	-	2133.0
gi|6005846|ref|NP_009215.1| PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro				1.20E-09	6.53	70.32	40.40	39547.7
AHQ-4-13-, 6532 - 6541	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	3.49E-07	0.97	6.25	-	922.8
AHQ-4-12, 6610	R.AVLPLLDAQQPCYLLYR.L	2035.39506	3	1.20E-09	0.93	4.78	-	1251.4
AHQ-4-12, 6597 - 6598	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	1.03E-08	0.97	6.44	-	952.0
AHQ-4-12, 6515	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	4.98E-06	0.85	3.52	-	451.5
AHQ-4-14-, 6394 - 6405	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	4.84E-08	0.96	5.20	-	858.5
AHQ-4-12, 5931	K.EFGGGHIKDELFGTVKDDLSFAGYQK.H	2860.12617	3	1.68E-04	0.94	4.45	-	1485.8
AHQ-4-11, 4029 - 4102	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	8.88E-06	0.91	4.11	-	809.4
AHQ-4-10, 3824	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	1.12E-04	0.76	3.80	-	548.2
AHQ-4-11, 4188	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	2.02E-09	0.96	4.93	-	1174.6
AHQ-4-11, 5533	K.HTHEGDPLESVVFIYSMPGYK.C	2407.68601	2	5.84E-07	0.85	3.39	-	595.5
AHQ-4-11, 6338	K.KIEIGDGAELTAEFLYDEVHPK.Q	2475.73515	3	1.70E-04	0.97	5.45	-	1857.5
AHQ-4-11, 6136	K.KIEIGDGAELTAEFLYDEVHPK.Q	2475.73515	3	2.22E-06	0.96	5.24	-	1638.3
AHQ-4-13-, 4685	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	1.80E-08	0.97	4.28	-	2052.5
AHQ-4-12, 4759	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	3	4.64E-06	0.97	5.24	-	2333.8
AHQ-4-12, 4743	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	2.65E-05	0.95	3.76	-	1871.5
AHQ-4-13, 4822	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	3.36E-05	0.84	3.03	-	1119.5
gi|4759082|ref|NP_004648.1| serum deprivation response protein; serum deprivation response; phospha				1.23E-09	2.67	30.30	11.10	47172.9
AHQ-4-10, 5817 - 5821	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	6.06E-06	0.96	4.53	-	1598.1
AHQ-4-11, 6165	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.05E-04	0.95	3.75	-	1554.1
AHQ-4-12, 6343 - 6409	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.41E-05	0.97	4.86	-	1827.5
AHQ-4-9, 6059	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	8.78E-06	0.97	4.79	-	1949.9
AHQ-4-9, 5887 - 5947	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.23E-09	0.97	4.94	-	1444.1
AHQ-4-11, 3394	K.LVNMLDAVQENQHK.M	1639.85851	2	1.03E-06	0.75	3.43	-	610.8
AHQ-4-12, 3454 - 3523	K.LVNMLDAVQENQHK.M	1639.85851	2	3.70E-04	0.90	4.06	-	962.9
AHQ-4-9, 5587 - 5655	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.09E-06	0.95	4.85	-	1108.0
AHQ-4-9, 5716 - 5783	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.26E-05	0.84	3.74	-	582.9
AHQ-4-11, 5876 - 5904	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.81E-07	0.92	4.65	-	666.3
AHQ-4-11, 6053	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.61E-06	0.91	4.28	-	712.5
AHQ-4-8, 5950	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.64E-05	0.96	5.25	-	1025.2
AHQ-4-6, 6202	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	7.52E-04	0.93	3.98	-	964.4
AHQ-4-10, 5595	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.96E-04	0.95	5.00	-	935.8
AHQ-4-12, 6085 - 6153	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	9.75E-08	0.96	5.20	-	971.1
AHQ-4-9, 5869 - 5877	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	9.68E-06	0.96	4.86	-	1098.0
AHQ-4-13-, 6093	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.50E-09	0.96	4.89	-	986.5
AHQ-4-14-, 5973 - 5977	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.71E-06	0.97	5.91	-	1052.6
gi|5031573|ref|NP_005712.1| ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye				1.30E-09	5.90	70.27	36.10	47370.9
AHQ-4-7, 7478 - 7479	R.DITYFIQQLLR.D	1410.64250	2	1.09E-06	0.97	4.95	-	1688.4
AHQ-4-7, 7477	R.DITYFIQQLLR.D	1410.64250	1	2.47E-04	0.22	2.32	-	222.5
AHQ-4-7, 7553 - 7557	R.FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR.R	4319.79733	3	6.04E-08	0.91	5.39	-	793.9
AHQ-4-7, 5791	K.GVDDLDFFIGDEAIEKPTYATK.W	2445.66268	3	4.11E-07	0.70	3.24	-	501.3
AHQ-4-9, 5656	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	2.00E-04	0.35	3.00	-	355.3
AHQ-4-7, 6378	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	4.16E-06	0.78	3.65	-	479.2
AHQ-4-7, 6498 - 6501	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	1.08E-06	0.74	3.74	-	463.2
AHQ-4-7, 2522	R.LKPKPIDVQVITHHMQR.Y	2041.45264	3	1.30E-09	0.77	3.79	-	439.8
AHQ-4-7, 3545	R.LPACVVDCGTGYTK.L	1543.74421	2	7.62E-04	0.89	3.76	-	750.7
AHQ-4-1, 6746	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	5.40E-04	0.85	3.87	-	742.6
AHQ-4-7, 6769	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	3.18E-06	0.93	5.47	-	741.1
AHQ-4-9, 5995 - 6060	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	1.56E-04	0.91	4.56	-	866.1
gi|9910542|ref|NP_064535.1| SAR1a gene homolog 1; SAR1 protein [Homo sapiens]				1.36E-09	3.79	40.27	46.00	22366.6
AHQ-4-11, 6054 - 6082	R.LGQHVPTLHPTSEELTIAGMTFTTFDLGGHEQAR.R	3694.08659	3	4.00E-05	0.93	5.35	-	850.1
AHQ-4-11, 3652	K.LREIFGLYGQTTGK.G	1583.81305	2	3.89E-04	0.97	4.53	-	1728.3
AHQ-4-11, 6780	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	1.36E-09	0.97	4.62	-	1632.6
AHQ-4-11, 6414	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	6.99E-07	0.80	3.36	-	649.9
AHQ-4-11, 6549	K.VELNALM*TDETISNVPILILGNK.I	2514.92088	2	6.41E-05	0.92	4.13	-	800.4
gi|4504071|ref|NP_000164.1| platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA				1.43E-09	5.21	60.23	9.40	68955.0
AHQ-4-4, 5032	R.GLGELQELYLK.G	1263.46458	2	1.57E-04	0.95	3.80	-	1408.5
AHQ-4-1, 5142	R.GLGELQELYLK.G	1263.46458	2	2.55E-05	0.94	4.07	-	1153.5
AHQ-4-3, 5069	R.GLGELQELYLK.G	1263.46458	2	2.00E-05	0.93	3.88	-	1168.7
AHQ-4-12, 4018 - 4046	R.GQDLLSTVSIR.Y	1189.34410	2	1.50E-06	0.95	3.67	-	1365.1
AHQ-4-13-, 4078 - 4086	R.GQDLLSTVSIR.Y	1189.34410	2	2.17E-06	0.96	3.96	-	1561.3
AHQ-4-1, 4287 - 4290	R.GQDLLSTVSIR.Y	1189.34410	2	3.46E-07	0.95	4.22	-	1143.4
AHQ-4-14-, 3899	R.GQDLLSTVSIR.Y	1189.34410	2	4.11E-05	0.91	2.66	-	1404.1
AHQ-4-3, 4175	R.GQDLLSTVSIR.Y	1189.34410	2	4.42E-04	0.94	3.83	-	1204.7
AHQ-4-13, 4212 - 4216	R.GQDLLSTVSIR.Y	1189.34410	2	7.88E-07	0.90	3.56	-	909.5
AHQ-4-4, 1974	R.GVLQGHLESSR.N	1183.29965	1	3.36E-04	0.30	2.12	-	424.1
AHQ-4-4, 1983	R.GVLQGHLESSR.N	1183.29965	2	7.83E-04	0.78	3.05	-	611.4
AHQ-4-5, 1754	R.GVLQGHLESSR.N	1183.29965	2	3.43E-04	0.88	3.16	-	929.4
AHQ-4-3, 1944 - 1969	R.GVLQGHLESSR.N	1183.29965	2	3.77E-05	0.87	3.33	-	862.0
AHQ-4-3, 2512	R.LTQLNLDR.C	973.10877	2	1.86E-04	0.68	2.51	-	797.1
AHQ-4-4, 3592 - 3596	R.LTQLNLDRCELTK.L	1605.83862	2	8.64E-05	0.80	3.90	-	564.4
AHQ-4-1, 3785	R.LTQLNLDRCELTK.L	1605.83862	2	9.33E-04	0.63	3.14	-	669.1
AHQ-4-3, 3607 - 3628	R.LTQLNLDRCELTK.L	1605.83862	2	2.42E-04	0.80	3.38	-	665.7
AHQ-4-3, 5328	R.WLQDNAENVYVWK.Q	1665.82948	2	1.43E-09	0.97	4.54	-	2187.4
AHQ-4-1, 5053 - 5057	R.WLQDNAENVYVWK.Q	1665.82948	2	2.16E-04	0.93	4.14	-	1277.4
gi|4503477|ref|NP_001950.1| eukaryotic translation elongation factor 1 beta 2; eukaryotic translati				1.44E-09	0.90	10.22	6.70	24763.6
AHQ-4-9, 4049	K.SPAGLQVLNDYLADK.S	1604.78589	2	1.44E-09	0.90	3.66	-	648.3
gi|16507237|ref|NP_005338.1| heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he				1.46E-09	8.04	90.30	19.10	72332.5
AHQ-4-6, 4775	R.AKFEELNMDLFR.S	1513.74309	2	8.54E-05	0.92	3.28	-	1102.6
AHQ-4-5, 3971	R.AKFEELNM*DLFR.S	1529.74249	2	5.52E-04	0.89	2.82	-	1278.9
AHQ-4-6, 5508	K.DNHLLGTFDLTGIPPAPR.G	1935.17239	2	2.62E-07	0.90	3.79	-	735.1
AHQ-4-6, 6062	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	2.86E-05	0.92	4.17	-	787.1
AHQ-4-6, 4614	K.IEWLESHQDADIEDFK.A	1976.08864	2	1.49E-07	0.98	5.95	-	2102.4
AHQ-4-5, 4681 - 4690	K.IEWLESHQDADIEDFK.A	1976.08864	2	6.76E-09	0.98	5.67	-	1763.7
AHQ-4-5, 3713	R.ITPSYVAFTPEGER.L	1567.72412	2	8.96E-06	0.70	2.99	-	488.2
AHQ-4-6, 3491	K.KSDIDEIVLVGGSTR.I	1589.77277	2	1.46E-09	0.97	4.96	-	2095.1
AHQ-4-5, 3638	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	3.53E-05	0.94	4.33	-	1137.2
AHQ-4-6, 3656	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	2.78E-07	0.91	3.91	-	905.5
AHQ-4-6, 2712	K.TKPYIQVDIGGGQTK.T	1605.81703	2	8.71E-07	0.85	2.99	-	913.2
gi|30150022|ref|XP_300862.1| similar to beta-tubulin 4Q [Homo sapiens]				1.47E-09	7.06	80.23	24.80	33545.2
AHQ-4-7, 6309 - 6375	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	1.34E-07	0.88	3.78	-	1113.5
AHQ-4-7, 6445 - 6521	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	2.91E-05	0.78	3.45	-	703.0
AHQ-4-7, 3161 - 3231	R.FPGQLNADLR.K	1131.26634	2	5.41E-05	0.87	3.34	-	741.7
AHQ-4-8, 2842	R.FPGQLNADLR.K	1131.26634	2	9.12E-05	0.77	2.51	-	854.6

AHQ-4-7, 3017 - 3093	R.FPGQLNADLR.K	1131.26634	2	3.29E-05	0.90	3.06	-	926.2
AHQ-4-9, 2873	R.FPGQLNADLR.K	1131.26634	2	9.55E-06	0.83	2.93	-	687.7
AHQ-4-7, 2703	R.FPGQLNADLRK.L	1259.43925	2	1.07E-04	0.74	2.69	-	859.1
AHQ-4-7, 1458	K.IREEYPDR.I	1078.16030	2	8.37E-04	0.87	3.18	-	829.7
AHQ-4-7, 3482 - 3503	R.KLAVNMVPFPR.L	1272.58771	2	1.05E-08	0.96	4.53	-	1361.6
AHQ-4-7, 3486 - 3567	K.LAVNM*VPFPR.L	1160.41420	2	5.32E-06	0.94	3.76	-	1021.9
AHQ-4-8, 3903	K.LAVNMVPFPR.L	1144.41480	2	5.35E-04	0.88	2.95	-	788.2
AHQ-4-7, 4158 - 4166	K.LAVNMVPFPR.L	1144.41480	2	1.91E-05	0.91	4.09	-	659.5
AHQ-4-9, 3849	K.LAVNMVPFPR.L	1144.41480	2	3.30E-04	0.84	2.86	-	833.3
AHQ-4-7, 5445	R.LHFFMPGFAPLTSR.G	1621.92962	2	8.95E-07	0.94	3.97	-	819.6
AHQ-4-9, 4991 - 4993	R.LHFFMPGFAPLTSR.G	1621.92962	2	1.47E-09	0.94	3.83	-	836.1
gi|4505667|ref|NP_001074.1|	phosphodiesterase 5A isoform 1; cGMP-binding cGMP-specific 3',5'-cyclic			1.52E-09	0.94	10.23	1.90	100012.4
AHQ-4-5, 4145 - 4151	R.FPWTTENTGNVNQQCIR.S	2067.22783	2	1.52E-09	0.94	4.61	-	1058.6
gi|6912638|ref|NP_036557.1|	ras suppressor protein 1 [Homo sapiens]			1.56E-09	6.57	80.26	41.50	31540.1
AHQ-4-10, 6495 - 6500	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	1.12E-05	0.69	3.38	-	463.8
AHQ-4-12, 7065	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	4.70E-06	0.88	4.30	-	523.8
AHQ-4-10, 5644 - 5703	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	5.34E-05	0.92	4.41	-	543.0
AHQ-4-10, 3640	R.DNDLISLPK.E	1015.14242	2	4.89E-04	0.86	3.16	-	1012.8
AHQ-4-10, 3399 - 3459	R.DNDLISLPK.E	1015.14242	2	9.67E-04	0.84	3.11	-	940.6
AHQ-4-10, 6477	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	3	6.92E-08	0.87	4.50	-	624.2
AHQ-4-10, 6472	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	2	7.89E-04	0.68	3.66	-	182.8
AHQ-4-10, 6420	R.GISNM*LDVNGLFTLSHITQLVLSHNK.L	2869.28903	3	1.27E-05	0.74	3.41	-	609.6
AHQ-4-10, 5275	K.LQILSLRDNDLISLPK.E	1839.16919	2	8.99E-08	0.96	5.23	-	1788.4
AHQ-4-10, 5359 - 5417	K.LQILSLRDNDLISLPK.E	1839.16919	2	2.41E-08	0.92	4.47	-	1263.2
AHQ-4-10, 4267	K.LTMVPPNIAELK.N	1326.63045	1	5.32E-05	0.46	2.77	-	416.7
AHQ-4-11, 5702 - 5768	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	1.56E-09	0.90	3.69	-	673.6
AHQ-4-10, 5375 - 5400	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	5.38E-05	0.84	3.75	-	448.8
AHQ-4-10, 5431 - 5459	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	2.86E-08	0.95	5.07	-	594.4
AHQ-4-13-, 5873 - 5898	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	1.34E-04	0.89	3.87	-	563.1
gi|4758970|ref|NP_004150.1|	proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be			1.59E-09	0.83	10.14	5.10	29769.4
AHQ-4-11, 3933 - 4008	K.VESTDVSDLLHQYR.E	1662.78230	2	1.59E-09	0.83	2.86	-	954.3
gi|6996010|ref|NP_002038.1|	glycyl-tRNA synthetase; GlyRS; glycine tRNA ligase [Homo sapiens]			1.61E-09	0.89	10.14	1.90	77530.3
AHQ-4-5, 4509	K.LPFAAAQIGNSFR.N	1392.58727	2	1.61E-09	0.89	2.86	-	1237.9
gi|4507171|ref|NP_003109.1|	secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec			1.63E-09	3.19	40.21	13.20	34632.0
AHQ-4-8, 2695	R.LEAGDHPVELLAR.D	1420.59579	2	4.89E-09	0.96	4.27	-	1404.0
AHQ-4-8, 2818	K.LHLDYIGPCK.Y	1217.41920	2	1.65E-05	0.81	2.95	-	612.6
AHQ-4-8, 2301	K.RLEAGDHPVELLAR.D	1576.78214	2	1.35E-04	0.85	3.59	-	518.7
AHQ-4-8, 2296	K.RLEAGDHPVELLAR.D	1576.78214	3	1.63E-09	0.89	3.24	-	1258.7
AHQ-4-9, 5923 - 5924	K.YIPPCLDSELTEFPLR.M	1952.21655	2	2.55E-07	0.52	2.55	-	210.8
AHQ-4-10, 5841	K.YIPPCLDSELTEFPLR.M	1952.21655	2	5.30E-05	0.37	2.61	-	125.4
AHQ-4-8, 6237 - 6239	K.YIPPCLDSELTEFPLR.M	1952.21655	2	2.22E-06	0.53	2.61	-	222.3
gi|4557419|ref|NP_000063.1|	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36			1.68E-09	2.76	30.24	10.20	53052.1
AHQ-4-1, 4902	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	3.35E-07	0.83	3.13	-	635.5
AHQ-4-6, 5438	K.SQVLQFFSSDICR.S	1588.76661	2	1.54E-04	0.95	4.19	-	1172.3
AHQ-4-5, 5482 - 5489	K.SQVLQFFSSDICR.S	1588.76661	2	1.68E-09	0.97	4.89	-	1325.7
AHQ-4-5, 7225 - 7253	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.01E-07	0.97	4.74	-	1367.2
gi|6005942|ref|NP_009057.1|	valosin-containing protein; yeast Cdc48p homolog; transitional endoplas			1.68E-09	7.49	90.26	13.60	89321.3
AHQ-4-5, 3617	K.GVLFYGPPGCGK.T	1253.45154	2	6.03E-05	0.53	2.74	-	757.3
AHQ-4-5, 2566	R.KYEM*FAQTLQQSR.G	1646.84948	2	1.60E-05	0.92	3.63	-	947.2
AHQ-4-5, 3045	R.KYEMFAQTLQQSR.G	1630.85008	2	3.26E-08	0.97	4.94	-	1669.4
AHQ-4-5, 5675	R.LDQLIYIPLPDEK.S	1557.81228	2	3.86E-06	0.94	4.39	-	915.5
AHQ-4-5, 2782	R.LEILQIHTK.N	1095.31705	1	6.44E-06	0.42	2.09	-	460.7
AHQ-4-5, 5227	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	1.87E-04	0.83	3.77	-	410.8
AHQ-4-5, 7393 - 7399	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	1.68E-09	0.97	5.24	-	1579.0
AHQ-4-5, 6255	R.RIVSQLLTLMDGLK.Q	1587.95293	2	2.08E-04	0.95	4.64	-	1080.6
AHQ-4-5, 3291	R.WALSQSNPSALR.E	1330.47434	2	2.02E-07	0.94	4.00	-	1297.5
gi|24797067|ref|NP_002107.3|	major histocompatibility complex, class I, A precursor; HLA-A1 class I			1.69E-09	2.82	30.28	11.50	40840.5
AHQ-4-14-, 4913 - 4914	R.FIAVGYVDDTQFVR.F	1630.82504	2	4.64E-09	0.98	5.52	-	2078.9
AHQ-4-14, 6152 - 6226	R.FIAVGYVDDTQFVR.F	1630.82504	2	4.27E-05	0.92	3.74	-	916.3
AHQ-4-8, 1836	R.YLENGKETLQR.T	1351.49032	2	2.68E-04	0.90	2.97	-	1286.2
AHQ-4-8, 2713	R.YTCHVQHEGLPKPLTLR.W	2051.35781	3	2.95E-05	0.96	5.01	-	2342.3
AHQ-4-8, 2711 - 2717	R.YTCHVQHEGLPKPLTLR.W	2051.35781	2	1.69E-09	0.94	5.06	-	1061.6
gi|24119203|ref|NP_705935.1|	tropomyosin 3 [Homo sapiens]			1.73E-09	5.42	60.26	16.10	29032.5
AHQ-4-9, 3103	R.IQLVEEELDR.A	1244.37653	2	4.54E-06	0.89	3.63	-	847.8
AHQ-4-10, 3356	R.IQLVEEELDR.A	1244.37653	1	3.64E-04	0.26	2.43	-	453.0
AHQ-4-10, 3360	R.IQLVEEELDR.A	1244.37653	2	8.24E-07	0.91	3.28	-	1069.7
AHQ-4-9, 2457 - 2463	K.IQVLQQQADDAEER.A	1643.73738	2	1.73E-09	0.97	4.64	-	1682.0
AHQ-4-9, 2137 - 2207	R.KIQVLQQQADDAEER.A	1771.91030	2	3.84E-04	0.98	5.23	-	1752.7
AHQ-4-9, 2224	R.KIQVLQQQADDAEER.A	1771.91030	3	5.59E-09	0.86	3.26	-	1437.7
AHQ-4-9, 2739 - 2761	R.RIQLVEEELDR.A	1400.56288	2	2.88E-08	0.97	5.06	-	1707.6
AHQ-4-9, 3128 - 3136	R.RIQLVEEELDRAQER.L	1885.07177	3	2.63E-04	0.93	4.39	-	1232.7
AHQ-4-9, 2668	K.TIDDLEDKLK.C	1190.32563	2	6.16E-06	0.79	3.24	-	543.8
gi|4885387|ref|NP_005318.1|	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain; L-3-hydroxyacyl-			1.73E-09	0.93	10.24	9.60	34286.3
AHQ-4-9, 6799	K.TLSTIATSTDAASVVHSTDLVVEAIVENLK.V	3086.43759	3	1.73E-09	0.93	4.75	-	1028.9
gi|4507869|ref|NP_003361.1|	vasodilator-stimulated phosphoprotein [Homo sapiens]			1.74E-09	3.61	40.29	14.50	39829.4
AHQ-4-7, 3461	R.KMQPDQQVVINCAIVR.G	1901.24418	2	4.49E-04	0.96	4.85	-	1110.9
AHQ-4-7, 6019 - 6025	K.VKEEIIEAFVQELR.K	1703.96061	2	1.74E-09	0.98	5.85	-	1646.0
AHQ-4-7, 6030	K.VKEEIIEAFVQELR.K	1703.96061	2	7.88E-06	0.94	3.06	-	2121.6
AHQ-4-13-, 2832 - 2906	R.VQIYHNPTANSFR.V	1547.69936	2	7.57E-07	0.54	2.51	-	465.7
AHQ-4-7, 2531	R.VQIYHNPTANSFR.V	1547.69936	2	2.16E-07	0.92	3.61	-	1177.4
AHQ-4-14, 3692 - 3714	R.VQIYHNPTANSFR.V	1547.69936	2	2.35E-04	0.56	2.90	-	294.4
AHQ-4-7, 2439	R.VQIYHNPTANSFR.V	1547.69936	2	3.48E-04	0.69	2.86	-	584.4
AHQ-4-7, 2591	K.YNQATPNFHQWR.D	1562.67258	2	4.72E-05	0.76	2.86	-	530.9
gi|4885281|ref|NP_005262.1|	glutamate dehydrogenase 1 [Homo sapiens]			1.87E-09	0.88	10.19	2.90	61397.5
AHQ-4-7, 3603 - 3611	K.HGGTIPIVPTAEFQDR.I	1738.92514	2	1.87E-09	0.88	3.72	-	560.0
gi|13569962|ref|NP_112243.1|	RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap			1.87E-09	3.63	40.31	26.40	22171.0
AHQ-4-11, 4341 - 4405	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	6.67E-08	0.98	5.93	-	1689.8
AHQ-4-11, 4626 - 4677	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	4.99E-08	0.97	5.38	-	1846.6
AHQ-4-11, 2024	R.M*GPGAASGGERPNLK.I	1458.62590	2	1.34E-05	0.75	3.24	-	537.1
AHQ-4-11, 2014 - 2016	R.MGPGAASGGERPNLK.I	1442.62650	2	1.87E-09	0.93	3.97	-	1213.5
AHQ-4-11, 1678	R.M*GPGAASGGERPNLK.I	1458.62590	2	1.02E-04	0.48	2.84	-	424.9
AHQ-4-11, 6524	K.NATNVEQAFMTMAAEIK.K	1870.14079	2	1.49E-07	0.98	6.16	-	1643.7
gi|4757812|ref|NP_004880.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso			2.09E-09	2.74	30.22	25.50	10917.8
AHQ-4-13, 6098	R.DFSPSGIFGAFQR.G	1429.56124	2	3.05E-07	0.89	3.34	-	917.5
AHQ-4-13-, 5996 - 6009	R.DFSPSGIFGAFQR.G	1429.56124	2	2.09E-09	0.95	4.34	-	1142.2
AHQ-4-14-, 5885	R.DFSPSGIFGAFQR.G	1429.56124	2	1.26E-06	0.84	2.91	-	890.6
AHQ-4-14-, 5457	K.LGELPSWILM*R.D	1331.60876	2	1.71E-06	0.95	4.00	-	829.7
AHQ-4-13-, 5513	K.LGELPSWILM*R.D	1331.60876	2	8.18E-07	0.92	3.81	-	576.5
AHQ-4-14-, 5907	K.LGELPSWILMR.D	1315.60936	2	1.08E-06	0.93	3.97	-	796.8
AHQ-4-13, 5634	K.LGELPSWILM*R.D	1331.60876	2	1.87E-07	0.86	2.88	-	565.8
gi|4507745|ref|NP_003320.1|	thioredoxin [Homo sapiens]			2.14E-09	2.18	30.19	22.90	11693.3
AHQ-4-13-, 3908	K.EKLEATINELV	1259.43110	2	4.60E-05	0.92	2.82	-	1560.9
AHQ-4-13-, 4177	K.LEATINELV	1002.14365	1	2.58E-04	0.34	1.84	-	392.8
AHQ-4-13, 4010	K.TAFQEALDAAGDK.L	1337.41728	1	5.45E-07	0.76	3.17	-	705.6
AHQ-4-14, 4828 - 4846	K.TAFQEALDAAGDK.L	1337.41728	2	1.84E-06	0.88	3.34	-	1187.4
AHQ-4-13, 3934 - 3996	K.TAFQEALDAAGDK.L	1337.41728	2	2.72E-07	0.92	3.37	-	1304.0
AHQ-4-13-, 3844 - 3845	K.TAFQEALDAAGDK.L	1337.41728	2	1.21E-07	0.90	3.39	-	1279.4

AHQ-4-13-, 3861	K.TAFQEALDAAGDK.L	1337.41728	1	3.48E-04	0.67	2.96	-	669.9
AHQ-4-13-, 3880	K.TAFQEALDAAGDK.L	1337.41728	2	2.98E-08	0.92	3.10	-	1523.2
AHQ-4-13-, 2808	K.TAFQEALDAAGDK.L	1337.41728	2	1.51E-07	0.87	3.41	-	1127.2
AHQ-4-13, 3992 - 4066	K.TAFQEALDAAGDK.L	1337.41728	2	2.14E-09	0.92	3.63	-	1218.7
AHQ-4-13, 2937	K.TAFQEALDAAGDK.L	1337.41728	2	3.57E-05	0.67	2.58	-	856.7
AHQ-4-14-, 3735	K.TAFQEALDAAGDK.L	1337.41728	2	1.42E-08	0.95	3.85	-	1609.2
gi|23110944|ref|NP_002782.1| proteasome alpha 6 subunit; prosomal P27K protein; proteasome subunit				2.31E-09	1.59	20.16	8.90	27399.3
AHQ-4-10, 2529	R.HITIFSPEGR.L	1157.30379	2	9.48E-04	0.81	2.78	-	618.4
AHQ-4-10, 3999	K.LLDSSTVTHLFK.I	1361.56825	2	2.31E-09	0.79	3.10	-	602.7
gi|10716563|ref|NP_001737.1| calnexin [Homo sapiens]				2.43E-09	2.51	30.21	5.20	67567.8
AHQ-4-5, 4907	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.43E-09	0.91	3.49	-	1276.2
AHQ-4-5, 4866 - 4889	K.APVPTGEVYFADSFDR.G	1771.90722	2	5.06E-05	0.94	3.96	-	1056.8
AHQ-4-1, 5154	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.65E-05	0.94	4.14	-	1177.0
AHQ-4-5, 6875	K.IPNPDFFEDLEPFR.M	1736.90447	2	1.97E-05	0.78	3.26	-	478.5
AHQ-4-1, 6923	K.IPNPDFFEDLEPFR.M	1736.90447	2	3.01E-06	0.83	3.21	-	656.3
AHQ-4-9, 5568	R.KIPNPDFFEDLEPFR.M	1865.07739	2	3.39E-04	0.77	3.41	-	487.9
AHQ-4-5, 6250	R.KIPNPDFFEDLEPFR.M	1865.07739	2	6.66E-04	0.93	3.83	-	989.2
gi|4504973|ref|NP_002292.1| lactate dehydrogenase C [Homo sapiens]				2.44E-09	0.94	10.20	3.60	36311.0
AHQ-4-11, 2353	R.VIGSGCNLDSAR.F	1250.36445	2	8.02E-08	0.86	3.34	-	695.8
AHQ-4-9, 2193	R.VIGSGCNLDSAR.F	1250.36445	2	2.44E-09	0.94	3.91	-	815.7
gi|21314617|ref|NP_000433.2| platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e				2.48E-09	4.56	60.27	12.30	82449.6
AHQ-4-5, 5901 - 5911	R.CESISGTLPISYQLLK.T	1811.08954	2	2.74E-05	0.66	3.09	-	316.8
AHQ-4-4, 6626	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	1.75E-06	0.96	5.30	-	925.9
AHQ-4-1, 6606	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	8.66E-07	0.84	3.56	-	818.5
AHQ-4-3, 6676	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	7.19E-07	0.96	5.24	-	988.3
AHQ-4-8, 6111	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	3.07E-04	0.89	3.82	-	817.6
AHQ-4-1, 6358	R.DQNFVILEFPVEEQDR.V	1979.13566	2	2.42E-06	0.88	4.35	-	777.3
AHQ-4-5, 6306	R.DQNFVILEFPVEEQDR.V	1979.13566	2	3.00E-04	0.81	3.82	-	618.8
AHQ-4-4, 6406	R.DQNFVILEFPVEEQDR.V	1979.13566	2	1.65E-04	0.53	3.62	-	437.7
AHQ-4-4, 3598	K.EQEGEYYCTAFNR.A	1668.72232	2	2.03E-05	0.87	3.11	-	723.3
AHQ-4-4, 4102	K.STESYFIPEVR.I	1328.45199	2	7.28E-04	0.88	3.37	-	820.0
AHQ-4-4, 4107	K.STESYFIPEVR.I	1328.45199	1	1.70E-05	0.32	2.51	-	178.6
AHQ-4-1, 5723	K.VIAPVDEVQISILSSK.V	1698.98227	2	1.04E-05	0.70	2.61	-	483.0
AHQ-4-4, 5606 - 5608	K.VIAPVDEVQISILSSK.V	1698.98227	2	2.48E-09	0.87	3.42	-	543.3
gi|21361478|ref|NP_055944.2| septin 6 isoform B; septin 2 [Homo sapiens]				2.49E-09	3.47	40.29	18.00	49716.3
AHQ-4-7, 3787 - 3789	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L	3147.31508	3	2.49E-09	0.97	5.80	-	1629.1
AHQ-4-7, 3450	K.SLDDEVNAFK.Q	1138.20928	1	7.34E-04	0.57	2.26	-	618.8
AHQ-4-7, 2897	K.TAAELLQSQGSQAGGSQTLK.R	1976.13485	2	8.80E-07	0.96	4.49	-	1858.0
AHQ-4-7, 4889	R.TVPLAGHVGFDSLPDQLVNK.S	2108.38284	2	4.47E-08	0.96	5.06	-	1050.9
gi|4503725|ref|NP_000792.1| FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei				2.57E-09	2.76	30.25	29.60	11950.6
AHQ-4-13, 4044 - 4068	R.GWEEGVAQMSVGQR.A	1534.67926	2	3.00E-04	0.91	3.70	-	1364.7
AHQ-4-13-, 3892 - 3893	R.GWEEGVAQMSVGQR.A	1534.67926	2	9.38E-09	0.95	4.07	-	1292.5
AHQ-4-13-, 2980 - 2981	R.GWEEGVAQM*SVGQR.A	1550.67866	2	2.57E-09	0.97	5.02	-	1282.8
AHQ-4-13, 3105 - 3177	R.GWEEGVAQM*SVGQR.A	1550.67866	2	7.60E-04	0.95	4.11	-	1241.6
AHQ-4-13-, 2622	K.RGQTCVVHYTGM*LEDGKK.F	2097.36199	3	1.66E-04	0.85	3.85	-	654.2
gi|4508047|ref|NP_003452.1| zyxin [Homo sapiens]				2.61E-09	1.67	20.20	8.00	61277.0
AHQ-4-8, 7129	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	2	4.40E-07	0.77	3.43	-	419.5
AHQ-4-9, 6611	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	2	1.36E-05	0.69	2.76	-	545.3
AHQ-4-8, 3577	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	2	2.61E-09	0.90	4.03	-	655.7
gi|4759140|ref|NP_004243.1| solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulato				2.67E-09	0.89	10.20	3.90	38868.2
AHQ-4-13-, 3806	R.LLVVDPETDEQLQK.L	1627.81777	2	2.67E-09	0.89	3.56	-	665.6
AHQ-4-13, 3949 - 3950	R.LLVVDPETDEQLQK.L	1627.81777	2	7.04E-07	0.92	4.06	-	733.2
gi|18860900|ref|NP_002834.2| protein tyrosine phosphatase, receptor type, J precursor; protein tyro				2.69E-09	7.73	90.20	10.00	145926.2
AHQ-4-1, 4447	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	3	2.17E-08	0.93	3.78	-	1308.2
AHQ-4-1, 4605	K.DFIATQGPLPNTLK.D	1515.73548	2	5.93E-04	0.79	3.13	-	779.7
AHQ-4-1, 2814	K.FSGFEASHGPIK.A	1277.40990	2	2.07E-06	0.89	3.08	-	947.2
AHQ-4-1, 5309	K.GLIDGAESYVSFSR.Y	1501.62253	2	2.69E-09	0.95	3.84	-	1572.2
AHQ-4-1, 5825 - 5845	K.SFCTDPASMASFDCEVVPK.E	2151.38014	2	3.82E-04	0.91	3.97	-	813.6
AHQ-4-1, 5407 - 5477	K.SPDGASEYVYHLVIESK.H	1895.05866	2	2.79E-08	0.90	3.99	-	790.9
AHQ-4-1, 4545	R.VENFEAYFK.K	1147.26100	2	4.08E-06	0.86	3.61	-	563.2
AHQ-4-1, 4353	K.VITEPIPVSDLR.V	1339.56259	2	2.09E-04	0.71	2.59	-	576.4
AHQ-4-1, 3869 - 3897	R.VLLESIGSHEELTQDSR.L	1914.06352	2	1.29E-05	0.91	3.68	-	922.5
AHQ-4-1, 3903	R.VLLESIGSHEELTQDSR.L	1914.06352	3	2.32E-08	0.80	3.19	-	826.5
gi|5803227|ref|NP_006817.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype				2.82E-09	2.82	30.26	20.40	27764.1
AHQ-4-10, 3353	R.KQTIDNSQGAYQEAFDISK.K	2144.28408	2	2.81E-05	0.97	5.21	-	1361.1
AHQ-4-13-, 6642	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	3.14E-06	0.92	4.08	-	936.8
AHQ-4-14-, 6514 - 6515	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	4.22E-08	0.96	5.23	-	1208.4
AHQ-4-11, 2542	K.YLIANATNPESK.V	1321.46099	2	4.81E-05	0.74	2.89	-	635.3
AHQ-4-10, 2597	K.YLIANATNPESK.V	1321.46099	1	5.44E-08	0.44	2.41	-	503.9
AHQ-4-10, 2485	K.YLIANATNPESK.V	1321.46099	1	2.82E-09	0.89	4.17	-	586.4
AHQ-4-10, 2484	K.YLIANATNPESK.V	1321.46099	2	6.90E-05	0.93	3.40	-	1488.2
gi|29727565|ref|XP_291384.1| similar to Cytochrome c, somatic [Homo sapiens]				3.21E-09	0.98	10.28	16.20	11621.4
AHQ-4-13-, 6394 - 6400	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	3.21E-09	0.98	5.70	-	1873.0
AHQ-4-13, 6485	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	2.93E-04	0.96	4.78	-	1219.7
gi|23200010|ref|NP_112585.2| Williams Beuren syndrome chromosome region 21 isoform 4 [Homo sapiens]				3.21E-09	0.71	10.16	20.80	10639.1
AHQ-4-10, 6532	R.LLDGEAALPAVVFLHGLFGSK.T	2155.52425	2	3.21E-09	0.71	3.18	-	278.4
gi|4827050|ref|NP_005142.1| ubiquitin specific protease 14 [Homo sapiens]				3.38E-09	0.96	10.21	2.60	56068.8
AHQ-4-13-, 4257	K.AQLFALTGVQPAR.Q	1372.59750	2	3.38E-09	0.96	4.13	-	1760.5
gi|6005749|ref|NP_009193.1| RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA				3.38E-09	1.97	30.18	20.60	19846.9
AHQ-4-10, 2413 - 2492	K.DGLILTSR.G	875.00510	1	2.72E-04	0.28	2.64	-	130.2
AHQ-4-10, 3192	R.DVVICPDASLEDAKK.E	1661.85581	2	2.81E-04	0.71	3.12	-	525.4
AHQ-4-11, 3321	R.DVVICPDASLEDAKK.E	1661.85581	2	4.99E-05	0.86	3.67	-	596.3
AHQ-4-10, 2953	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	3.38E-09	0.82	3.27	-	548.2
gi|21361122|ref|NP_001440.2| four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap				4.40E-09	3.10	50.27	21.80	31894.7
AHQ-4-9, 2205	K.AIVAGDQNVEYK.G	1307.43431	1	1.10E-05	0.31	2.58	-	488.8
AHQ-4-11, 2378	K.AIVAGDQNVEYK.G	1307.43431	2	8.64E-05	0.89	3.87	-	620.0
AHQ-4-9, 2813	K.CLHPLANETFVAK.D	1501.73210	2	5.54E-04	0.65	2.77	-	319.4
AHQ-4-12, 3287	K.CLHPLANETFVAK.D	1501.73210	2	4.32E-08	0.80	2.89	-	517.9
AHQ-4-13-, 3810	R.FVFHQEQVYCPDCAK.K	1931.13758	2	4.40E-09	0.98	5.41	-	1818.6
AHQ-4-9, 2699 - 2712	K.GEDFYCVTCHETK.F	1648.75260	2	2.64E-04	0.88	3.28	-	876.1
AHQ-4-9, 2043	K.NPITGFGK.G	833.95467	1	3.90E-04	0.13	1.88	-	144.8
gi|29729616|ref|XP_292963.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				4.43E-09	1.70	20.30	16.40	18025.4
AHQ-4-12, 4865 - 4929	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	8.98E-04	0.63	2.71	-	516.1
AHQ-4-12, 4877 - 4949	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.84E-06	0.95	6.02	-	1180.2
AHQ-4-12, 5002 - 5066	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	9.38E-05	0.89	4.27	-	592.6
AHQ-4-12, 5162	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	1.65E-05	0.57	2.70	-	333.4
AHQ-4-12, 5459 - 5522	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	8.30E-06	0.78	4.09	-	796.5
AHQ-4-12, 5517 - 5593	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	7.20E-06	0.89	4.52	-	512.2
AHQ-4-12, 5657	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	2.80E-05	0.83	3.97	-	612.6
AHQ-4-13, 5088	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	4.43E-09	0.81	3.79	-	796.7
AHQ-4-13, 5586	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	2.71E-05	0.78	3.74	-	892.2
AHQ-4-13-, 4852	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	2.45E-07	0.94	4.81	-	1284.0
AHQ-4-13-, 5476	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	2.91E-05	0.77	3.65	-	791.9
AHQ-4-14-, 4813	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.75E-04	0.93	5.44	-	948.0
gi|5031677|ref|NP_005681.1| dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [				4.53E-09	8.56	100.26	19.00	78060.6
AHQ-4-14, 6125 - 6133	K.ALQGASQIIAEIR.E	1370.57991	2	1.60E-08	0.95	3.73	-	1916.9
AHQ-4-13-, 4745	K.ALQGASQIIAEIR.E	1370.57991	2	2.42E-08	0.90	3.41	-	1434.9

AHQ-4-13-, 4378	K.GHAVNLLDVPVPVAR.K	1557.82197	2	1.06E-05	0.95	4.14	-	1180.5
AHQ-4-5, 7059 - 7062	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	1.03E-08	0.97	5.10	-	1449.0
AHQ-4-11, 6529	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	1.42E-06	0.79	3.04	-	688.6
AHQ-4-6, 6843 - 6914	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	1.01E-04	0.85	3.14	-	940.2
AHQ-4-5, 6495	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	1.48E-05	0.65	2.97	-	637.7
AHQ-4-6, 6376	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	2.86E-05	0.85	3.67	-	703.9
AHQ-4-5, 3054	R.IIQHCSNYSTQELLR.F	1864.07262	2	1.94E-05	0.95	4.70	-	1104.2
AHQ-4-7, 6150	K.LYTDFDEIRQEIENETER.I	2301.40883	2	2.82E-05	0.50	2.71	-	363.5
AHQ-4-6, 6131	K.LYTDFDEIRQEIENETER.I	2301.40883	2	3.47E-04	0.24	2.70	-	203.9
AHQ-4-14-, 6093 - 6103	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	6.39E-09	0.94	4.56	-	1150.5
AHQ-4-14-, 6689	K.SSLLDDLLTESEDMAQR.R	1924.07698	2	3.38E-05	0.97	4.96	-	1443.1
AHQ-4-13-, 6250	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	4.53E-09	0.86	3.46	-	886.3
AHQ-4-13, 6318 - 6322	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	4.49E-04	0.97	4.62	-	1693.4
AHQ-4-6, 4639	K.SVTDSIRDEYAFLQK.K	1772.93666	2	1.00E-05	0.82	3.53	-	759.7
AHQ-4-7, 4594	K.SVTDSIRDEYAFLQK.K	1772.93666	2	9.04E-05	0.92	4.15	-	1007.6
AHQ-4-6, 7202 - 7203	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	1.00E-06	0.96	4.55	-	1252.0
gi|15723376|ref|NP_277050.1| MacGAP protein [Homo sapiens]				4.60E-09	0.95	10.18	2.10	70163.1
AHQ-4-5, 3070	R.FLSQESGVAQTLK.K	1408.58178	2	4.60E-09	0.95	3.51	-	1763.3
gi|5453555|ref|NP_006316.1| ras-related nuclear protein [Homo sapiens]				4.68E-09	1.78	20.22	14.40	24422.9
AHQ-4-10, 5175 - 5176	K.SNYNFEKPFLWLAR.K	1786.02509	2	4.68E-09	0.90	4.35	-	526.5
AHQ-4-10, 5637	K.SNYNFEKPFLWLAR.K	1786.02509	2	1.83E-07	0.52	2.84	-	275.4
AHQ-4-10, 4568	R.VCENIPIVLCGNKVDIK.D	1974.33162	2	2.72E-04	0.87	4.06	-	489.6
gi|5031601|ref|NP_005711.1| actin related protein 2/3 complex subunit 1B; ARP2/3 protein complex su				4.73E-09	0.84	10.16	3.80	40949.5
AHQ-4-8, 2104	K.EVEERPAPTPWGSK.M	1583.72678	2	4.73E-09	0.84	3.15	-	613.5
gi|4759270|ref|NP_004613.1| translin; recombination hotspot associated factor; recombination hotspo				4.87E-09	0.96	10.24	7.00	26182.8
AHQ-4-10, 5884	R.PLHISTFINELDSGFR.L	1847.06360	2	4.87E-09	0.96	4.71	-	1429.3
gi|5729875|ref|NP_006658.1| progesterone receptor membrane component 1; progesterone binding protei				4.98E-09	2.60	30.21	17.90	21671.0
AHQ-4-10, 4171	K.FYGPEGPYGVFAGR.D	1517.66849	2	4.03E-05	0.91	3.36	-	971.8
AHQ-4-11, 4414 - 4430	K.FYGPEGPYGVFAGR.D	1517.66849	2	9.08E-04	0.87	3.36	-	645.9
AHQ-4-11, 2850	R.GDQPAASGDSDDDEPPPLPR.L	2037.04410	2	4.98E-09	0.88	3.61	-	772.5
AHQ-4-11, 3906	R.KFYGPEGPYGVFAGR.D	1645.84140	2	4.71E-04	0.94	4.13	-	1032.0
AHQ-4-10, 3745	R.KFYGPEGPYGVFAGR.D	1645.84140	2	4.23E-04	0.82	3.13	-	601.7
gi|22042381|ref|XP_065237.3| similar to FKSG30 [Homo sapiens]				5.00E-09	1.41	20.18	8.30	42016.0
AHQ-4-5, 2827	K.QEYDESGPSIVHR.K	1517.58206	2	3.54E-04	0.46	2.54	-	465.9
AHQ-4-8, 2015 - 2059	K.QEYDESGPSIVHR.K	1517.58206	2	2.98E-07	0.63	2.80	-	333.7
AHQ-4-13-, 2396 - 2420	K.QEYDESGPSIVHR.K	1517.58206	2	6.61E-07	0.79	2.96	-	415.9
AHQ-4-13, 2513 - 2517	K.QEYDESGPSIVHR.K	1517.58206	2	5.00E-09	0.72	3.13	-	414.3
AHQ-4-14-, 2265 - 2275	K.QEYDESGPSIVHR.K	1517.58206	2	2.35E-07	0.65	2.82	-	388.6
AHQ-4-8, 3298 - 3370	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	3.20E-05	0.45	2.79	-	244.8
AHQ-4-8, 3161 - 3230	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	2.71E-04	0.26	2.67	-	208.3
AHQ-4-10, 3477 - 3541	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	7.84E-05	0.68	3.19	-	372.3
AHQ-4-12, 3763 - 3787	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	3.09E-07	0.69	3.61	-	310.5
gi|6041669|ref|NP_004538.2| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd				5.12E-09	0.88	10.19	14.00	15208.5
AHQ-4-13-, 4804	R.TLPETLDPAEYNISPETR.R	2047.20831	2	5.12E-09	0.88	3.79	-	639.6
AHQ-4-13, 4929	R.TLPETLDPAEYNISPETR.R	2047.20831	2	4.54E-05	0.77	2.78	-	656.6
gi|4507789|ref|NP_003338.1| ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]				5.26E-09	0.92	10.21	9.70	17861.5
AHQ-4-12, 5265	R.IEINFPAEYPFKPPK.I	1791.08155	3	5.26E-09	0.92	4.26	-	1092.1
AHQ-4-13, 5362	R.IEINFPAEYPFKPPK.I	1791.08155	2	2.09E-04	0.60	2.97	-	560.4
AHQ-4-12, 5219 - 5281	R.IEINFPAEYPFKPPK.I	1791.08155	2	9.73E-09	0.91	4.03	-	982.0
gi|29742827|ref|XP_294099.1| similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]				5.33E-09	2.50	30.23	14.20	17094.0
AHQ-4-11, 2844	K.EAFNMIDQNR.D	1238.35558	2	4.08E-06	0.83	3.42	-	714.1
AHQ-4-11, 2197 - 2206	K.EAFNM*IDQNR.D	1254.35498	2	2.51E-04	0.70	3.26	-	458.0
AHQ-4-11, 3633 - 3696	R.FTDEEVDELYR.E	1416.47127	2	3.40E-08	0.96	4.19	-	1674.2
AHQ-4-11, 3700 - 3764	R.FTDEEVDELYR.E	1416.47127	1	2.12E-07	0.31	1.80	-	457.7
AHQ-4-11, 3708 - 3772	R.FTDEEVDELYR.E	1416.47127	1	4.52E-08	0.70	2.72	-	524.4
AHQ-4-12, 3821	R.FTDEEVDELYR.E	1416.47127	2	4.61E-08	0.97	4.37	-	1860.3
AHQ-4-12, 3831	R.FTDEEVDELYR.E	1416.47127	1	9.01E-07	0.56	2.65	-	422.8
AHQ-4-13, 3937 - 4016	R.FTDEEVDELYR.E	1416.47127	2	4.48E-05	0.87	3.25	-	1198.4
AHQ-4-13, 4020 - 4093	R.FTDEEVDELYR.E	1416.47127	2	5.57E-09	0.90	3.02	-	1085.6
AHQ-4-14, 4805	R.FTDEEVDELYR.E	1416.47127	2	5.33E-09	0.96	3.91	-	1827.2
AHQ-4-13-, 3869 - 3873	R.FTDEEVDELYR.E	1416.47127	2	6.03E-09	0.97	4.62	-	1853.3
AHQ-4-14-, 3763	R.FTDEEVDELYR.E	1416.47127	2	1.15E-08	0.97	4.15	-	1787.2
gi|7706497|ref|NP_057392.1| UMP-CMP kinase [Homo sapiens]				5.40E-09	6.21	70.28	32.90	25854.7
AHQ-4-11, 5928	R.IQTYLQSTKPIIDLYEEMGK.V	2371.73502	2	2.59E-05	0.90	4.29	-	576.8
AHQ-4-11, 5041 - 5049	R.IQTYLQSTKPIIDLYEEM*GK.V	2387.73442	2	4.22E-04	0.88	4.00	-	403.6
AHQ-4-11, 5890	K.IVPVEITISLLK.R	1325.66210	2	9.44E-05	0.67	2.81	-	203.9
AHQ-4-11, 2476	R.KNPDSQYGELIEK.Y	1521.65375	2	2.66E-08	0.87	3.52	-	715.9
AHQ-4-11, 6834	K.SVDEVFDEVVQIFDK.E	1769.92954	2	4.82E-07	0.97	5.56	-	1364.1
AHQ-4-11, 6841 - 6842	K.SVDEVFDEVVQIFDKEG	1956.09563	2	1.18E-05	0.95	4.85	-	1169.6
AHQ-4-11, 3644	K.YGYTHLSAGELLR.D	1480.64969	2	5.40E-09	0.96	4.23	-	1502.6
gi|10346135|ref|NP_055083.1| microtubule-associated protein, RP/EB family, member 2; T-cell activat				5.56E-09	1.92	20.26	9.80	37031.1
AHQ-4-9, 6385	R.FQDNLDFIQWFK.K	1601.78539	2	1.54E-06	0.93	3.72	-	1018.8
AHQ-4-12, 6849 - 6857	R.FQDNLDFIQWFK.K	1601.78539	2	5.56E-09	0.97	5.15	-	1253.9
AHQ-4-12, 4911	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	3.27E-04	0.94	4.83	-	1324.6
AHQ-4-9, 4227	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	2	5.95E-06	0.95	5.14	-	791.0
gi|16933567|ref|NP_005361.2| mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]				5.84E-09	0.93	10.21	6.80	23668.1
AHQ-4-11, 5892	K.ANINVENAFFTLAR.D	1580.76926	2	1.75E-08	0.92	4.07	-	745.9
AHQ-4-14-, 5839	K.ANINVENAFFTLAR.D	1580.76926	2	4.32E-05	0.86	3.30	-	753.8
AHQ-4-11, 5034	K.ANINVENAFFTLAR.D	1580.76926	2	5.84E-09	0.93	4.19	-	937.2
gi|21735621|ref|NP_005909.2| mitochondrial malate dehydrogenase precursor [Homo sapiens]				5.89E-09	4.44	50.26	29.00	35503.0
AHQ-4-14-, 6033	K.GYLGPEQLPDCLKGCDVVVIPAGVPR.K	2813.24211	3	6.87E-05	0.65	3.46	-	490.0
AHQ-4-9, 5016	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	3	6.45E-06	0.96	5.07	-	1505.3
AHQ-4-11, 5372 - 5382	K.SQETECTYFSTPLLLGK.K	1976.19328	2	5.89E-09	0.97	5.11	-	1369.1
AHQ-4-9, 4976	K.SQETECTYFSTPLLLGK.K	1976.19328	2	5.28E-08	0.96	4.57	-	1328.6
AHQ-4-9, 6068	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	4.36E-05	0.97	4.84	-	1657.7
AHQ-4-11, 4792 - 4793	K.VDFPQDQLTALTGR.I	1561.72111	2	1.63E-04	0.73	2.81	-	619.5
AHQ-4-9, 4464 - 4469	K.VDFPQDQLTALTGR.I	1561.72111	2	1.04E-07	0.90	3.97	-	826.8
gi|5902134|ref|NP_009005.1| coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin				5.93E-09	4.03	50.23	18.70	51026.0
AHQ-4-7, 4150	R.DAGPLLISLK.D	1027.23948	1	2.99E-04	0.59	2.89	-	383.3
AHQ-4-7, 1946 - 1959	R.KLQATVQELQK.R	1286.50292	2	4.38E-05	0.96	4.22	-	1638.8
AHQ-4-6, 6947 - 6959	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	5.93E-09	0.90	4.46	-	682.4
AHQ-4-7, 7062	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	1.42E-05	0.91	4.69	-	535.4
AHQ-4-7, 4005	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	4.28E-06	0.87	3.73	-	752.8
AHQ-4-13-, 4161	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	2.52E-07	0.80	3.24	-	633.0
AHQ-4-6, 4014	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	3.02E-05	0.91	4.23	-	678.0
AHQ-4-7, 7389	R.YFEITSEAPFLHYLSMFSSK.E	2398.71748	2	3.96E-04	0.78	3.09	-	443.9
gi|4507143|ref|NP_003786.1| sorting nexin 3 isoform a; sorting nexin 3A [Homo sapiens]				6.09E-09	0.93	10.18	8.60	18762.2
AHQ-4-12, 5061	R.GDDGIFDDNFIEER.K	1642.66158	2	6.09E-09	0.93	3.69	-	1086.6
gi|4759300|ref|NP_004772.1| vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated				6.20E-09	2.90	30.29	33.00	11309.0
AHQ-4-14-, 3493	R.ADALQAGASQFETSAAK.L	1666.77095	2	4.41E-06	0.94	4.38	-	944.8
AHQ-4-14, 4489 - 4493	R.ADALQAGASQFETSAAK.L	1666.77095	2	5.50E-04	0.74	3.47	-	548.9
AHQ-4-13-, 3564	R.ADALQAGASQFETSAAK.L	1666.77095	2	6.71E-09	0.92	4.35	-	920.3
AHQ-4-13, 3717 - 3728	R.ADALQAGASQFETSAAK.L	1666.77095	2	6.20E-09	0.96	5.12	-	987.1
AHQ-4-13-, 3720 - 3721	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	4.75E-06	0.97	5.79	-	1282.2
AHQ-4-13, 4985	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	2.06E-05	0.98	5.21	-	1971.3
gi|10835002|ref|NP_001166.1| Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]				6.65E-09	6.02	70.24	42.30	22987.8
AHQ-4-10, 2344	K.APEPHVEEDDDDELDSK.L	1940.90995	3	1.33E-06	0.96	4.87	-	1560.4

AHQ-4-10, 2277 - 2339	K.APEPHVEEDDDDELDSK.L	1940.90995	2	2.00E-04	0.93	4.55	-	897.2
AHQ-4-13-, 5552	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	6.33E-05	0.87	3.69	-	944.7
AHQ-4-12, 5618	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.66E-04	0.85	4.19	-	723.0
AHQ-4-10, 5255 - 5315	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	2	6.25E-05	0.91	4.35	-	694.5
AHQ-4-10, 5291	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	2	6.70E-05	0.89	4.27	-	600.9
AHQ-4-14-, 5505	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	2.91E-04	0.86	3.66	-	780.0
AHQ-4-11, 5616	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	2.94E-04	0.82	3.92	-	493.9
AHQ-4-10, 2919 - 2921	K.ELQEMDKDDESLIK.Y	1693.85489	2	3.59E-04	0.89	3.97	-	776.4
AHQ-4-10, 5845 - 5903	R.LTLVCESAPGPITM*DLTGDLEALKK.E	2691.11214	3	1.74E-06	0.64	3.38	-	317.0
AHQ-4-10, 6123 - 6157	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	6.65E-09	0.86	3.76	-	800.6
AHQ-4-10, 3629	K.SLKELQEMDKDDESLIK.Y	2022.26370	2	3.10E-04	0.90	3.82	-	1006.0
gi|7657431|ref|NP_055205.1| EBNA-2 co-activator (100kD) [Homo sapiens]				7.85E-09	1.81	20.20	3.80	99689.7
AHQ-4-4, 6640	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	7.85E-09	0.88	3.93	-	415.2
AHQ-4-5, 6518 - 6525	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	6.51E-05	0.90	4.06	-	450.7
AHQ-4-6, 6391	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	3.65E-05	0.77	3.38	-	371.5
AHQ-4-4, 3042	R.SSHYDELLAAEAR.A	1462.54640	2	1.23E-08	0.93	2.93	-	2193.3
gi|4503785|ref|NP_000135.1| frataxin; Friedreich ataxia (frataxin) [Homo sapiens]				8.47E-09	0.94	10.21	5.70	23218.1
AHQ-4-13-, 3761	K.LGGDLGTYVINK.Q	1250.42590	2	8.47E-09	0.94	4.15	-	959.3
gi|4503821|ref|NP_001456.1| FYN binding protein (FYB-120/130); FYN-binding protein (FYB-120/130) [H				8.79E-09	0.93	10.27	2.60	85450.5
AHQ-4-12, 4153	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	1.32E-07	0.93	4.47	-	719.4
AHQ-4-13, 4269	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	1.08E-06	0.96	5.34	-	749.9
AHQ-4-10, 3823	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	8.79E-09	0.93	4.52	-	498.4
gi|29737978|ref|XP_290747.1| similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy				9.47E-09	3.65	40.26	1.50	191380.7
AHQ-4-6, 3658	K.ADFCIIHYAGK.V	1296.47641	2	1.41E-07	0.96	3.82	-	1390.4
AHQ-4-5, 3730	K.ADFCIIHYAGK.V	1296.47641	1	5.26E-06	0.62	2.77	-	485.1
AHQ-4-5, 3714 - 3751	K.ADFCIIHYAGK.V	1296.47641	2	2.80E-07	0.91	3.23	-	1057.6
AHQ-4-2, 4006	K.ADFCIIHYAGK.V	1296.47641	1	8.24E-05	0.88	3.47	-	662.0
AHQ-4-2, 3994 - 3999	K.ADFCIIHYAGK.V	1296.47641	2	8.89E-07	0.97	4.31	-	2181.8
AHQ-4-4, 3924	K.ADFCIIHYAGK.V	1296.47641	2	4.53E-04	0.80	2.97	-	1012.8
AHQ-4-3, 3963	K.ADFCIIHYAGK.V	1296.47641	2	3.53E-06	0.89	3.16	-	937.3
AHQ-4-2, 2798	R.AGVLAHLEEER.D	1224.34854	1	2.57E-04	0.58	2.83	-	624.8
AHQ-4-2, 2728 - 2795	R.AGVLAHLEEER.D	1224.34854	2	4.79E-08	0.96	4.24	-	1590.9
AHQ-4-3, 2739 - 2807	R.AGVLAHLEEER.D	1224.34854	2	2.24E-06	0.95	4.17	-	1454.1
AHQ-4-4, 2822	R.AGVLAHLEEER.D	1224.34854	2	3.32E-06	0.94	3.55	-	1437.7
AHQ-4-2, 2866	R.AGVLAHLEEER.D	1224.34854	2	5.40E-07	0.96	4.28	-	1741.7
AHQ-4-1, 2983 - 3061	R.AGVLAHLEEER.D	1224.34854	2	3.75E-08	0.97	4.42	-	1987.2
AHQ-4-1, 3853	K.DKADFCIIHYAGK.V	1539.73719	2	9.47E-09	0.96	4.54	-	1551.1
AHQ-4-2, 3758	K.DKADFCIIHYAGK.V	1539.73719	3	4.97E-06	0.89	4.15	-	946.9
AHQ-4-4, 3679	K.DKADFCIIHYAGK.V	1539.73719	2	1.02E-08	0.97	4.74	-	1620.0
AHQ-4-2, 3751	K.DKADFCIIHYAGK.V	1539.73719	2	3.44E-06	0.96	4.58	-	1328.1
AHQ-4-1, 3854	K.DKADFCIIHYAGK.V	1539.73719	3	2.65E-07	0.86	3.79	-	897.2
AHQ-4-3, 3695	K.DKADFCIIHYAGK.V	1539.73719	2	5.24E-08	0.98	5.19	-	1976.5
AHQ-4-5, 4530	K.LDPHLVLDQLR.C	1319.53460	3	1.90E-06	0.76	3.22	-	611.0
AHQ-4-3, 4775	K.LDPHLVLDQLR.C	1319.53460	2	2.33E-05	0.82	2.61	-	766.0
gi|21624607|ref|NP_066972.1| coactosin-like 1 [Homo sapiens]				9.61E-09	2.70	40.31	21.80	15944.9
AHQ-4-12, 2138	R.AAYNLVR.D	806.93245	2	4.76E-04	0.92	2.74	-	1067.9
AHQ-4-13-, 2092 - 2182	K.EVVQNFAK.E	935.05900	1	1.94E-04	0.25	2.65	-	109.7
AHQ-4-13-, 6772 - 6774	K.FALITWIGENVSGLQR.A	1805.06986	2	1.53E-04	0.98	6.22	-	2427.0
AHQ-4-13, 6882 - 6884	K.FALITWIGENVSGLQR.A	1805.06986	2	3.82E-05	0.98	6.01	-	2317.1
AHQ-4-12, 6937 - 6939	K.FALITWIGENVSGLQR.A	1805.06986	2	9.61E-09	0.97	5.54	-	1754.7
AHQ-4-13, 2945	R.KELEEDFIK.S	1151.29110	1	1.29E-04	0.56	2.80	-	541.1
AHQ-4-13, 2942	R.KELEEDFIK.S	1151.29110	2	6.52E-04	0.74	2.90	-	684.2
gi|7657176|ref|NP_055070.1| transmembrane protein 4 [Homo sapiens]				9.62E-09	0.87	10.18	8.80	20652.1
AHQ-4-11, 3529 - 3536	R.INPDGSQSVVEVPYAR.S	1731.88777	2	9.62E-09	0.87	3.66	-	660.0
gi|4758208|ref|NP_004081.1| dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;				9.70E-09	2.70	30.24	24.30	20478.2
AHQ-4-11, 5933 - 6005	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	7.31E-05	0.94	4.85	-	931.9
AHQ-4-14-, 5987	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	2.60E-06	0.92	3.67	-	1376.3
AHQ-4-11, 4048	R.IYVGNASVAQDIPK.L	1475.67136	2	9.70E-09	0.89	3.63	-	880.6
AHQ-4-11, 2929	K.LGITHVLNAAEGR.S	1351.53669	2	6.26E-05	0.88	3.15	-	975.3
gi|4506877|ref|NP_002996.1| selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;				9.74E-09	6.58	80.27	21.80	90844.7
AHQ-4-3, 4903	K.AVQCQHLEAPSEGTM*DCVHPLTAFAYGSSCK.F	3472.80519	3	4.43E-04	0.83	3.96	-	542.1
AHQ-4-2, 6883	R.CDNLGQWTAPAPVCQALQCQDLPVPNEAR.V	3313.64431	3	3.02E-05	0.75	4.04	-	366.0
AHQ-4-3, 6083	R.CIDSGHWSAPLPTCEAISCEPLESPVHGSM*DCSPSLR.A	4162.54346	3	2.79E-04	0.95	5.43	-	1152.1
AHQ-4-3, 6281 - 6360	K.LECLASGIWTNKPPQCLAAQCPPLKIPER.G	3352.89300	3	5.04E-08	0.50	3.16	-	587.7
AHQ-4-3, 3067 - 3076	R.PSGQWTAVTPACR.A	1432.58672	2	4.65E-07	0.95	3.98	-	1210.1
AHQ-4-3, 5049 - 5067	K.STCQFICDEGYSLSGPER.L	2109.23671	2	9.74E-09	0.94	4.74	-	930.0
AHQ-4-1, 5013 - 5027	K.STCQFICDEGYSLSGPER.L	2109.23671	2	2.86E-05	0.77	3.13	-	712.1
AHQ-4-2, 5074 - 5080	K.STCQFICDEGYSLSGPER.L	2109.23671	2	7.52E-08	0.95	4.66	-	917.8
AHQ-4-4, 5015	K.STCQFICDEGYSLSGPER.L	2109.23671	2	1.02E-07	0.95	4.81	-	967.6
AHQ-4-3, 6475 - 6485	K.VLPYYSSYYWIGIR.K	1781.04522	2	3.83E-08	0.94	4.49	-	765.3
AHQ-4-3, 2812	R.YTDLVAIQNK.N	1165.32100	1	4.53E-04	0.72	2.78	-	628.4
gi|5174727|ref|NP_005989.1| chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring				9.87E-09	4.41	50.20	11.40	60330.4
AHQ-4-6, 3558	R.AVAQALEVIPR.T	1167.38326	2	9.28E-05	0.94	3.53	-	1774.1
AHQ-4-6, 4419 - 4488	K.GISDLAQHYLMR.A	1404.61986	2	1.01E-08	0.84	2.82	-	1186.9
AHQ-4-6, 4338	K.IPGGIIEDSCVLR.G	1430.65218	2	3.91E-05	0.90	3.72	-	998.0
AHQ-4-6, 2658	R.TLIQNCGASTIR.L	1335.51249	2	8.16E-04	0.78	2.70	-	769.7
AHQ-4-6, 5396	R.WSSLACNIALDAVK.M	1549.77353	2	9.87E-09	0.94	4.06	-	1286.5
gi|5453605|ref|NP_006421.1| chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-				1.01E-08	1.84	20.23	4.80	57838.8
AHQ-4-7, 6530	R.DALSDLALHFLNK.M	1457.65603	2	1.01E-08	0.97	4.63	-	1782.0
AHQ-4-7, 3369	K.VIDPATATSVDLR.D	1358.52277	2	8.12E-04	0.87	3.27	-	859.2
gi|30160191|ref|XP_294035.2| similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme				1.08E-08	0.96	10.20	2.80	50222.2
AHQ-4-7, 5071 - 5143	K.IYVDDGLISLQVK.Q	1463.70048	2	1.08E-08	0.96	3.96	-	1713.3
gi|4758304|ref|NP_004902.1| protein disulfide isomerase related protein (calcium-binding protein, i				1.09E-08	6.64	80.21	13.00	72931.9
AHQ-4-6, 6044 - 6046	R.EVSQPDWTPPPEVTLVLTK.E	2137.41772	2	2.69E-04	0.70	3.55	-	261.2
AHQ-4-6, 3699	K.FAM*EPEEFDSDTLR.E	1703.80830	2	4.93E-06	0.80	3.18	-	506.6
AHQ-4-6, 4547	K.FAMEPEEFDSDTLR.E	1687.80890	2	1.09E-08	0.84	3.37	-	502.5
AHQ-4-6, 3482	R.FDVSGYPTIK.I	1127.27123	2	4.38E-07	0.91	2.90	-	1310.0
AHQ-4-6, 2752	K.IDATSASVLASR.F	1191.31686	2	5.62E-08	0.90	3.39	-	1293.0
AHQ-4-6, 2739	K.VSQGQLVVMQPEK.F	1443.69431	2	7.48E-07	0.95	3.86	-	1681.8
AHQ-4-6, 2262	K.VSQGQLVVM*QPEK.F	1459.69371	2	4.85E-07	0.78	3.24	-	705.4
AHQ-4-6, 2744	K.VSQGQLVVMQPEK.F	1443.69431	1	2.50E-07	0.76	3.12	-	705.2
AHQ-4-6, 5078	K.YGIVDYMIEQSGPPSK.E	1785.01085	2	7.52E-06	0.95	4.15	-	1336.8
gi|4502201|ref|NP_001649.1| ADP-ribosylation factor 1 [Homo sapiens]				1.11E-08	8.53	100.30	58.60	20696.6
AHQ-4-12, 4603 - 4827	R.DAVLLVFANK.Q	1090.29726	1	2.50E-05	0.82	2.79	-	933.8
AHQ-4-12, 4655 - 4725	R.DAVLLVFANK.Q	1090.29726	2	2.16E-05	0.97	4.26	-	2192.9
AHQ-4-12, 5201	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	7.41E-07	0.97	5.50	-	1443.2
AHQ-4-12, 5097	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	2.61E-04	0.98	5.97	-	1965.6
AHQ-4-12, 5545	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.26E-06	0.69	2.89	-	168.9
AHQ-4-12, 5305	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.08E-06	0.97	4.95	-	1782.6
AHQ-4-12, 5446	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	9.30E-06	0.98	5.28	-	1972.4
AHQ-4-12, 4715	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	4.40E-05	0.59	3.08	-	343.3
AHQ-4-12, 3645 - 3715	R.ILMVGLDAAGK.T	1088.34632	2	5.95E-06	0.94	4.27	-	1074.9
AHQ-4-11, 3045	R.ILM*VGLDAAGK.T	1104.34572	2	7.03E-05	0.95	3.12	-	1993.9
AHQ-4-12, 3086 - 3091	R.ILM*VGLDAAGK.T	1104.34572	2	1.63E-06	0.95	3.79	-	1520.3
AHQ-4-13, 6469 - 6478	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	8.21E-04	0.73	3.97	-	224.1
AHQ-4-14-, 6245 - 6246	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	7.13E-04	0.53	2.93	-	176.2
AHQ-4-11, 6221 - 6289	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	6.72E-05	0.80	4.08	-	224.2

AHQ-4-12, 6643 - 6719	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	5.70E-05	0.53	2.90	-	209.1
AHQ-4-12, 2109	K.LGLHSLR.H	795.95280	2	6.52E-04	0.85	2.93	-	864.3
AHQ-4-12, 6942	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	2	2.63E-05	0.88	4.01	-	628.0
AHQ-4-14-, 6679	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	2	4.89E-04	0.65	2.80	-	545.5
AHQ-4-12, 5101 - 5173	K.NISFTVWDVGGQDK.I	1566.69621	2	1.41E-04	0.94	4.28	-	998.9
AHQ-4-13, 5189 - 5196	K.NISFTVWDVGGQDK.I	1566.69621	2	3.33E-05	0.92	4.13	-	725.8
AHQ-4-11, 4902	K.NISFTVWDVGGQDK.I	1566.69621	2	1.68E-04	0.95	3.96	-	1251.4
AHQ-4-13-, 5072	K.NISFTVWDVGGQDK.I	1566.69621	2	5.20E-06	0.86	3.18	-	780.1
AHQ-4-14-, 5018 - 5085	K.NISFTVWDVGGQDK.I	1566.69621	2	4.71E-08	0.91	3.76	-	765.2
AHQ-4-12, 5017 - 5089	K.NISFTVWDVGGQDK.I	1566.69621	2	2.92E-05	0.89	3.97	-	678.1
AHQ-4-12, 3653 - 3733	K.QDLPNAMNAAEITDK.L	1631.79001	2	1.11E-08	0.93	4.09	-	839.5
AHQ-4-12, 3891 - 3958	K.QDLPNAMNAAEITDK.L	1631.79001	2	9.50E-05	0.89	4.00	-	727.6
gi|4758018|ref|NP_004359.1| calponin 2; Calonin 2 [Homo sapiens]				1.17E-08	2.71	30.28	12.60	33696.9
AHQ-4-12, 5105	K.DGTILCTLMNK.L	1267.49833	2	2.24E-06	0.90	3.33	-	1008.2
AHQ-4-12, 2797 - 2798	K.GLQSGVDIGVK.Y	1073.22510	2	1.23E-05	0.92	3.65	-	1199.7
AHQ-4-13, 2999	K.GLQSGVDIGVK.Y	1073.22510	2	2.16E-05	0.92	3.09	-	1377.1
AHQ-4-13-, 2877	K.GLQSGVDIGVK.Y	1073.22510	2	1.23E-06	0.88	3.04	-	1089.7
AHQ-4-12, 6530	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	4.89E-05	0.95	4.39	-	1174.5
AHQ-4-12, 6391 - 6453	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.32E-08	0.97	4.53	-	1879.1
AHQ-4-11, 6186 - 6189	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	9.06E-07	0.97	4.86	-	2020.6
AHQ-4-13, 6393 - 6456	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	5.78E-07	0.94	4.33	-	967.9
AHQ-4-10, 5872 - 5873	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.78E-05	0.97	5.38	-	1275.6
AHQ-4-13-, 6360	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	9.81E-08	0.97	5.67	-	1164.8
AHQ-4-14-, 6235	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.17E-08	0.93	3.82	-	1092.5
gi|21361322|ref|NP_006078.2| tubulin, beta, 5 [Homo sapiens]				1.18E-08	1.85	20.23	9.90	49585.5
AHQ-4-7, 2821	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	1.18E-08	0.93	4.01	-	1069.0
AHQ-4-12, 2899	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	3.95E-05	0.83	3.42	-	596.9
AHQ-4-7, 2677	R.EIVHLQAGQCGNQIGAK.F	1825.03962	3	5.12E-04	0.89	3.50	-	1583.1
AHQ-4-7, 5291	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	6.56E-05	0.92	4.64	-	974.2
gi|30150448|ref|XP_293066.2| similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose				1.18E-08	0.95	10.22	2.90	58788.2
AHQ-4-6, 4492	R.VINEPTAAALAYGLDK.S	1646.86592	2	1.18E-08	0.95	4.49	-	929.7
gi|9966867|ref|NP_065123.1| eIF-5A2 protein; eIF5AII [Homo sapiens]				1.19E-08	3.56	40.30	19.60	16793.1
AHQ-4-12, 3617	K.KYEDICPSTHNMDVPNIK.R	2163.41723	2	4.03E-05	0.78	3.42	-	422.2
AHQ-4-12, 3610 - 3619	K.KYEDICPSTHNMDVPNIK.R	2163.41723	3	2.10E-06	0.96	5.37	-	1459.1
AHQ-4-12, 2983	K.KYEDICPSTHNM*DVPNIK.R	2179.41663	3	1.61E-04	0.97	5.95	-	1715.5
AHQ-4-12, 4797	K.VHLVGIDIFTGK.K	1299.54329	2	1.19E-08	0.94	3.70	-	1100.3
AHQ-4-12, 4799 - 4802	K.VHLVGIDIFTGK.K	1299.54329	1	1.00E-07	0.85	3.13	-	931.6
AHQ-4-12, 3301	K.YEDICPSTHNM*DVPNIK.R	2051.24372	2	4.04E-04	0.69	2.90	-	671.7
gi|18201905|ref|NP_000166.2| glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras				1.20E-08	2.66	30.22	7.90	63146.7
AHQ-4-7, 6698	K.ILLANFLAQTEALM*R.G	1721.05778	2	5.65E-05	0.79	3.51	-	368.4
AHQ-4-7, 2754 - 2757	K.TFTTQETITNAETAK.E	1656.77283	2	1.20E-08	0.95	4.33	-	1360.2
AHQ-4-7, 3561	R.VWYVSNIDGTHIAK.T	1603.80282	2	5.06E-07	0.92	3.52	-	945.7
gi|20357552|ref|NP_005222.2| cortactin isoform a; oncogene EMS1 [Homo sapiens]				1.28E-08	0.89	10.18	2.20	61585.7
AHQ-4-13, 5456 - 5466	R.YGLFPANYVELR.Q	1442.64306	2	3.39E-06	0.84	3.25	-	514.7
AHQ-4-12, 5357 - 5366	R.YGLFPANYVELR.Q	1442.64306	2	1.28E-08	0.89	3.51	-	630.9
gi|4507231|ref|NP_003134.1| single-stranded DNA binding protein; single-stranded DNA-binding protei				1.31E-08	3.15	40.22	25.70	17259.5
AHQ-4-13, 2559	R.DVAYQYVK.K	986.10277	1	1.29E-04	0.36	2.28	-	398.1
AHQ-4-13, 6066 - 6137	K.NPVTIFSLATNEM*WR.S	1796.04007	2	1.13E-04	0.94	4.19	-	1179.7
AHQ-4-13, 6778	K.NPVTIFSLATNEMWR.S	1780.04067	2	1.31E-08	0.91	3.31	-	978.4
AHQ-4-13-, 3208 - 3221	R.SGDSEVYQLGDVSQK.T	1612.67692	2	7.85E-08	0.93	4.12	-	1022.9
AHQ-4-13, 3331 - 3334	R.SGDSEVYQLGDVSQK.T	1612.67692	2	7.39E-06	0.95	4.34	-	1320.3
gi|5031597|ref|NP_005710.1| actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub				1.42E-08	4.31	50.29	32.60	20546.5
AHQ-4-11, 6373	K.DTDIVDEAIYYFK.A	1592.72721	2	3.11E-08	0.89	3.62	-	867.4
AHQ-4-13, 6673	K.DTDIVDEAIYYFK.A	1592.72721	2	4.68E-07	0.90	3.77	-	970.1
AHQ-4-12, 6630 - 6637	K.DTDIVDEAIYYFK.A	1592.72721	2	1.42E-08	0.97	5.75	-	1550.2
AHQ-4-14-, 6421	K.DTDIVDEAIYYFK.A	1592.72721	2	1.06E-04	0.95	4.04	-	1648.3
AHQ-4-12, 6981 - 6982	K.EM*YTLGITNFPIPGEPGFPLNAIYAK.P	2871.29861	2	2.87E-05	0.83	3.78	-	382.2
AHQ-4-11, 6745 - 6790	K.EM*YTLGITNFPIPGEPGFPLNAIYAK.P	2871.29861	2	4.80E-05	0.89	4.15	-	455.9
AHQ-4-11, 5806	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	8.23E-08	0.72	3.15	-	718.1
AHQ-4-12, 4193	K.LIGNM*ALLPIR.S	1227.54522	2	7.88E-05	0.89	3.75	-	988.4
AHQ-4-11, 6664	K.SQGEKEM*YTLGITNFPIPGEPGFPLNAIYAK.P	3400.84505	3	7.18E-04	0.89	4.90	-	420.4
gi|4507949|ref|NP_003395.1| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,				1.43E-08	4.35	50.27	33.30	28082.2
AHQ-4-10, 1644 - 1703	K.AVTEQGHELSNEER.N	1599.64147	2	7.88E-06	0.81	3.92	-	491.3
AHQ-4-10, 6580	K.IEAELQDICNDVLELLDK.Y	2132.37471	2	1.43E-08	0.97	5.41	-	1280.1
AHQ-4-10, 3752 - 3757	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	4.92E-04	0.77	3.75	-	367.1
AHQ-4-14-, 6522 - 6601	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	5.21E-04	0.89	3.82	-	473.4
AHQ-4-10, 6447 - 6517	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	6.47E-04	0.51	3.18	-	328.5
AHQ-4-10, 6195	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	6.65E-06	0.95	4.82	-	1284.6
AHQ-4-14-, 6762 - 6765	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	2.92E-04	0.47	3.11	-	298.5
AHQ-4-10, 2667	K.YLIPNATQPESK.V	1361.52512	1	6.97E-04	0.21	2.22	-	422.3
AHQ-4-10, 2687 - 2688	K.YLIPNATQPESK.V	1361.52512	2	4.23E-04	0.85	3.04	-	757.0
AHQ-4-10, 2853	K.YLIPNATQPESK.V	1361.52512	1	2.09E-05	0.77	2.22	-	1045.0
AHQ-4-10, 2753 - 2763	K.YLIPNATQPESK.V	1361.52512	1	1.31E-06	0.86	3.06	-	816.3
gi|27480104|ref|XP_208215.1| similar to triosephosphate isomerase 1 [Homo sapiens]				1.45E-08	5.00	60.24	26.10	26942.6
AHQ-4-10, 2725	R.HVFGESDELIGQK.V	1459.58565	1	4.47E-06	0.86	3.78	-	785.8
AHQ-4-12, 2937	R.HVFGESDELIGQK.V	1459.58565	2	1.45E-08	0.93	3.74	-	721.8
AHQ-4-10, 2063 - 2200	K.IAVAAQNCYK.V	1139.30684	1	3.26E-07	0.39	2.86	-	172.3
AHQ-4-10, 2560	R.IIYGGSVTGATCK.E	1328.51672	1	2.89E-05	0.70	3.15	-	359.5
AHQ-4-10, 2556	R.IIYGGSVTGATCK.E	1328.51672	2	8.10E-07	0.88	3.28	-	691.9
AHQ-4-10, 2443	R.RHVFGESDELIGQK.V	1615.77200	2	1.29E-04	0.96	4.89	-	1294.8
AHQ-4-10, 1976	K.SNVSDAVAQSTR.I	1235.28659	2	1.22E-07	0.94	3.75	-	1399.0
AHQ-4-10, 3480 - 3485	K.VTNGAFTGEISPGM*IK.D	1638.86726	2	3.76E-04	0.91	3.43	-	1076.6
gi|4506505|ref|NP_002916.1| regulator of G-protein signaling 10 [Homo sapiens]				1.49E-08	4.13	50.20	32.90	19607.9
AHQ-4-11, 3452 - 3532	K.ILEEPHPLMFQK.L	1482.77213	2	3.71E-06	0.92	3.97	-	845.5
AHQ-4-11, 4613	K.LQDQIFNLMK.Y	1250.49254	2	6.31E-05	0.84	3.49	-	586.2
AHQ-4-11, 2486	R.TEEEEEDLPDAQTAAK.R	1776.79097	2	1.49E-08	0.81	3.58	-	506.1
AHQ-4-11, 5845	K.WAASLENLLEDPEGVK.R	1771.94867	2	4.07E-05	0.77	3.15	-	897.1
AHQ-4-11, 5276	K.WAASLENLLEDPEGVKR.F	1928.13502	2	1.05E-07	0.79	4.05	-	386.4
gi|4505813|ref|NP_003737.1| cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain				1.54E-08	1.63	20.19	24.70	10365.8
AHQ-4-14-, 2245	R.NFGSYVTHETK.H	1283.37131	2	1.54E-08	0.85	3.25	-	724.3
AHQ-4-13-, 3504	K.YNPTWHCIVGR.N	1404.57820	2	4.90E-05	0.76	3.19	-	369.3
AHQ-4-14-, 3501 - 3514	K.YNPTWHCIVGR.N	1404.57820	2	1.34E-07	0.78	2.87	-	467.4
AHQ-4-13, 3649	K.YNPTWHCIVGR.N	1404.57820	2	1.28E-04	0.71	2.63	-	549.8
gi|14249348|ref|NP_116120.1| hypothetical protein MGC14353 [Homo sapiens]				1.61E-08	0.89	10.17	11.40	13940.7
AHQ-4-13-, 4080	K.SWCPDCVQAEPVVR.E	1705.89366	2	1.61E-08	0.89	3.41	-	882.3
AHQ-4-13, 4193 - 4224	K.SWCPDCVQAEPVVR.E	1705.89366	2	1.61E-08	0.89	3.27	-	1027.6
gi|27597085|ref|NP_000357.3| tropomyosin 1 (alpha) [Homo sapiens]				1.83E-08	1.92	20.25	9.50	32865.7
AHQ-4-9, 2656	R.AQKDEEKMEIQEIQLK.E	1961.22673	2	3.15E-05	0.96	5.08	-	1451.3
AHQ-4-9, 2759	R.KLVIIESDLER.A	1315.54103	2	1.83E-08	0.95	4.16	-	1389.8
AHQ-4-9, 2748	R.KLVIIESDLER.A	1315.54103	1	4.01E-05	0.39	1.90	-	486.3
gi|4502285|ref|NP_001672.1| ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 2; ATP				1.88E-08	2.07	30.21	5.10	109690.3
AHQ-4-1, 6639	K.DIVPGDIVEIAVGDKVPADIR.L	2192.49806	2	7.85E-04	0.62	2.69	-	640.9
AHQ-4-1, 4526	R.VDQSILTGESVSVIK.H	1575.78600	2	5.02E-05	0.50	2.65	-	642.1
AHQ-4-1, 4830 - 4835	K.VGEATETALTCLVEK.M	1622.81958	2	1.88E-08	0.95	4.16	-	1416.1
gi|4557235|ref|NP_000009.1| acyl-Coenzyme A dehydrogenase, very long chain precursor [Homo sapiens]				1.94E-08	1.67	20.21	4.70	70389.7
AHQ-4-6, 5174	R.AGLGSGLSLSGLVHPELSR.S	1851.09693	2	1.94E-08	0.73	3.22	-	560.4
AHQ-4-6, 3814	R.ALEQFATVVEAK.L	1306.48946	2	1.28E-05	0.94	4.29	-	1247.9

gi|4506185|ref|NP_002780.1| proteasome alpha 4 subunit; proteasome component C9; proteasome subunit				1.95E-08	1.51	20.17	17.60	29483.6
AHQ-4-10, 6136	K.LNEDMACSVAGITSDANVLTNELR.L	2595.84629	2	1.95E-08	0.77	3.26	-	437.9
AHQ-4-10, 6392 - 6457	R.YLLQYQEPIPCEQLVTALCDIK.Q	2698.10465	2	1.66E-04	0.74	3.31	-	413.2
gi|29747201|ref|XP_290702.1| similar to My016 protein [Homo sapiens]				1.95E-08	0.96	10.25	10.50	16932.3
AHQ-4-14-, 3447	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	8.27E-06	0.94	4.52	-	1023.0
AHQ-4-14, 4382	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	1.95E-08	0.96	5.04	-	1090.9
gi|4503545|ref|NP_001961.1| eukaryotic translation initiation factor 5A; eIF5AI; eIF5A [Homo sapien				1.99E-08	1.74	20.24	26.00	16832.2
AHQ-4-12, 3963	R.EDLRLPEGDLGKEIEQK.Y	1970.17021	2	7.48E-05	0.79	3.83	-	327.0
AHQ-4-12, 6958	R.NDFQLIGIQDGYLSLLQDSGEVR.E	2581.81935	2	1.99E-08	0.95	4.74	-	1024.8
gi|14149680|ref|NP_056107.1| KIAA0747 protein [Homo sapiens]				2.03E-08	3.63	40.23	5.70	122855.6
AHQ-4-12, 5558	R.FEWELPLDEAQR.R	1533.66622	2	6.87E-07	0.82	3.16	-	616.6
AHQ-4-6, 6975	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	2.03E-08	0.88	3.95	-	535.3
AHQ-4-4, 7231	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	1.28E-07	0.91	3.89	-	654.4
AHQ-4-12, 3999	R.LTHVDSPLEAPAGPLGQVK.L	1930.19405	2	1.27E-04	0.96	4.58	-	1240.3
AHQ-4-12, 4494	K.VQLDLAETDLSQGVAR.W	1715.88665	2	5.97E-08	0.96	4.25	-	1896.2
gi|4502107|ref|NP_001145.1| annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoag				2.05E-08	1.82	20.22	9.10	35936.5
AHQ-4-9, 6008	R.DLLDDLKSELTGK.F	1447.61309	2	2.48E-08	0.96	4.48	-	1429.8
AHQ-4-9, 6300	K.GLGTDEESILTLLTSR.S	1705.88853	2	2.05E-08	0.86	3.47	-	889.9
gi|5031973|ref|NP_005733.1| protein disulfide isomerase-related protein [Homo sapiens]				2.11E-08	2.73	40.24	13.20	48121.0
AHQ-4-7, 4619	K.GSFSEQGINEFLR.E	1484.59520	1	3.25E-07	0.44	2.75	-	123.1
AHQ-4-12, 4015	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	2.52E-06	0.86	3.40	-	879.4
AHQ-4-7, 3782	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	2.11E-08	0.87	3.39	-	839.9
AHQ-4-7, 4110	K.NLEPEWAAAASEVK.E	1515.64921	2	2.48E-05	0.45	2.77	-	235.1
AHQ-4-7, 6146	R.TGEAIVDAALSALR.Q	1387.56411	1	5.59E-06	0.17	1.80	-	203.3
AHQ-4-7, 6137 - 6138	R.TGEAIVDAALSALR.Q	1387.56411	2	2.75E-08	0.97	4.82	-	1958.6
gi|21361670|ref|NP_054782.2| src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo				2.12E-08	0.84	10.19	4.20	48294.0
AHQ-4-12, 5622	K.SPTDWALFTYEGNSNDIR.V	2087.19108	2	2.12E-08	0.84	3.78	-	598.4
gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre				2.20E-08	5.98	70.25	25.70	48141.1
AHQ-4-7, 5742	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	2.24E-06	0.95	5.08	-	1181.1
AHQ-4-7, 5351 - 5427	R.FYALSASFEPFSNK.G	1608.77470	2	2.20E-08	0.96	3.80	-	1566.7
AHQ-4-7, 5187	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	3.16E-07	0.64	3.06	-	618.3
AHQ-4-7, 5075 - 5117	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	6.72E-08	0.89	4.12	-	991.0
AHQ-4-7, 2234	K.IKDPDASKPEDWDER.A	1801.89173	2	2.57E-05	0.95	4.35	-	989.3
AHQ-4-7, 4811	K.KPEDWDEEM*DGEWEPPVIQNPEYK.G	2978.14866	3	1.69E-05	0.87	4.38	-	779.7
AHQ-4-7, 1973	K.KVHVIFNYK.G	1148.38164	1	1.84E-06	0.75	2.72	-	458.4
AHQ-4-7, 2349	K.VHVIFNYK.G	1020.20872	1	1.90E-04	0.61	2.38	-	553.6
gi|4757810|ref|NP_004037.1| ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,				2.70E-08	6.55	80.18	21.20	59750.3
AHQ-4-7, 3562 - 3577	R.EAYPGDVFYLHSR.L	1554.68713	2	1.45E-07	0.78	2.90	-	654.1
AHQ-4-7, 5378	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	3	9.71E-07	0.82	3.60	-	901.6
AHQ-4-7, 6130	K.GMSLNLEPDNVGVVVFGNDK.L	2105.35763	2	1.31E-04	0.84	3.65	-	448.1
AHQ-4-7, 3139 - 3179	K.HALIIYDDLSK.Q	1288.47413	2	2.70E-08	0.94	3.00	-	1392.8
AHQ-4-7, 3669 - 3742	R.ILGADTSVDLEETGR.V	1576.68772	2	2.47E-04	0.61	3.04	-	653.5
AHQ-4-14-, 6254 - 6266	K.LKEIVTNFLAGFEA	1552.79572	2	2.90E-04	0.92	3.04	-	1248.2
AHQ-4-7, 3523	K.TGTAEMSSILEER.I	1424.55988	2	6.84E-05	0.88	3.19	-	1100.7
AHQ-4-7, 2838	R.VLSIGDGIAR.V	1001.16212	2	4.45E-06	0.76	2.72	-	707.0
gi|17986283|ref|NP_006000.2| tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu				2.86E-08	1.83	20.27	10.40	50135.3
AHQ-4-1, 6021	R.AVFVDLEPTVIDEVR.T	1702.92947	2	7.84E-05	0.61	2.81	-	497.5
AHQ-4-2, 6015	R.AVFVDLEPTVIDEVR.T	1702.92947	2	5.89E-05	0.92	4.28	-	844.7
AHQ-4-3, 6015	R.AVFVDLEPTVIDEVR.T	1702.92947	2	6.40E-08	0.94	4.90	-	802.8
AHQ-4-4, 5967 - 5970	R.AVFVDLEPTVIDEVR.T	1702.92947	2	4.40E-07	0.96	4.97	-	1242.0
AHQ-4-7, 5563 - 5634	R.AVFVDLEPTVIDEVR.T	1702.92947	2	2.23E-07	0.96	5.42	-	1115.4
AHQ-4-7, 5701 - 5777	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.83E-04	0.92	4.34	-	755.8
AHQ-4-13-, 5620 - 5628	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.46E-06	0.94	4.99	-	935.7
AHQ-4-12, 5631 - 5698	R.AVFVDLEPTVIDEVR.T	1702.92947	2	8.99E-06	0.92	4.21	-	785.1
AHQ-4-13, 5753 - 5754	R.AVFVDLEPTVIDEVR.T	1702.92947	2	2.86E-08	0.95	4.85	-	1048.8
AHQ-4-14-, 5573 - 5585	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.26E-05	0.93	4.00	-	1172.0
AHQ-4-7, 7411	K.LADQCTGLQGFLVFHSFGGGTGSGFTSLLMER.L	3393.79432	3	1.46E-05	0.88	3.90	-	1056.1
gi|5031595|ref|NP_005709.1| actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub				2.95E-08	3.75	50.30	33.90	19666.9
AHQ-4-12, 4318	R.AENFFILR.R	1010.17070	2	3.25E-04	0.95	3.55	-	1578.1
AHQ-4-11, 6274	R.ATLQAALCLENFSSQVVER.H	2138.38741	2	5.24E-05	0.91	4.08	-	950.0
AHQ-4-11, 4114 - 4116	K.ELLLQPVTISR.N	1269.51549	1	1.72E-04	0.17	2.55	-	100.4
AHQ-4-12, 3403	R.IVAEEFLK.N	949.12558	2	3.08E-04	0.77	2.96	-	380.7
AHQ-4-12, 3106 - 3114	K.VLIEGSINSVR.V	1187.37134	2	2.95E-08	0.95	4.00	-	1301.5
AHQ-4-13, 3403	K.VLIEGSINSVR.V	1187.37134	2	1.57E-04	0.92	3.42	-	1100.8
AHQ-4-11, 3057	K.VLIEGSINSVR.V	1187.37134	2	8.80E-07	0.96	3.67	-	1625.8
gi|4504073|ref|NP_000398.1| glycoprotein Ib beta polypeptide precursor [Homo sapiens]				2.95E-08	1.74	20.20	10.70	21717.6
AHQ-4-1, 4929	R.LLPYLAEDELR.A	1332.52691	2	1.14E-04	0.80	3.02	-	445.1
AHQ-4-3, 4884	R.LLPYLAEDELR.A	1332.52691	2	3.00E-05	0.74	2.90	-	496.2
AHQ-4-7, 4442	R.LLPYLAEDELR.A	1332.52691	2	3.39E-06	0.77	3.11	-	349.5
AHQ-4-8, 4215	R.LLPYLAEDELR.A	1332.52691	2	1.43E-06	0.78	2.81	-	520.7
AHQ-4-10, 4176	R.LLPYLAEDELR.A	1332.52691	2	1.38E-06	0.86	3.14	-	465.6
AHQ-4-13, 4758	R.LLPYLAEDELR.A	1332.52691	2	2.95E-08	0.79	2.84	-	516.7
AHQ-4-11, 4456 - 4521	R.LLPYLAEDELR.A	1332.52691	2	2.10E-04	0.80	3.01	-	429.7
AHQ-4-13-, 4636	R.LLPYLAEDELR.A	1332.52691	2	1.23E-06	0.78	2.51	-	679.4
AHQ-4-11, 4124	R.LSLTDPLVAER.A	1214.39356	2	2.90E-05	0.96	4.00	-	1399.8
gi|29150259|ref|NP_803875.1| fibrocystin L; polycystic kidney and hepatic disease-like 1 [Homo sapi				3.01E-08	1.72	20.24	0.80	465745.4
AHQ-4-1, 6615 - 6695	R.DAFSYNCLQTPIITDFSPK.V	2219.45575	2	3.01E-08	0.90	4.71	-	611.2
AHQ-4-1, 3443	K.SPPEEGSLVVITK.G	1356.54678	2	7.46E-05	0.82	2.85	-	662.6
gi|5031691|ref|NP_004640.1| chromosome 21 open reading frame 33; human HES1 protein, homolog to E.c				3.14E-08	0.63	10.15	9.30	28142.2
AHQ-4-11, 5285 - 5342	K.ITDLANLSAANHDAAIFPGGFGAAK.N	2443.69961	3	3.14E-08	0.63	3.06	-	774.0
gi|20127528|ref|NP_037459.2| parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]				3.14E-08	5.91	70.26	22.00	41714.0
AHQ-4-9, 2883 - 2888	K.ARPEDVVNLDLK.S	1369.54878	2	1.98E-04	0.96	4.92	-	1122.4
AHQ-4-9, 2891	K.ARPEDVVNLDLK.S	1369.54878	1	2.13E-06	0.77	3.56	-	323.4
AHQ-4-13-, 3472	K.ARPEDVVNLDLK.S	1369.54878	2	9.13E-05	0.91	4.20	-	815.0
AHQ-4-14, 4410	K.ARPEDVVNLDLK.S	1369.54878	2	1.20E-06	0.83	3.40	-	706.2
AHQ-4-13, 3601	K.ARPEDVVNLDLK.S	1369.54878	2	2.44E-05	0.89	3.68	-	792.2
AHQ-4-10, 3165	K.ARPEDVVNLDLK.S	1369.54878	2	7.71E-05	0.79	3.37	-	684.4
AHQ-4-14-, 3418	K.ARPEDVVNLDLK.S	1369.54878	2	2.44E-04	0.82	3.67	-	548.2
AHQ-4-9, 4779 - 4805	R.DAFDTLFDHAPDKLSVVK.K	2019.24293	2	1.50E-04	0.89	3.95	-	584.9
AHQ-4-9, 2259	K.KSLITFVNK.H	1050.27627	1	5.60E-04	0.56	2.15	-	564.1
AHQ-4-9, 3180	K.LNVAEVTQSEIGQK.Q	1516.67865	2	1.65E-06	0.95	4.54	-	969.6
AHQ-4-9, 3277	R.LPEHVTVQVVVVR.K	1475.76086	2	3.14E-08	0.84	3.22	-	859.6
AHQ-4-9, 3264	R.LPEHVTVQVVVVR.K	1475.76086	1	8.94E-04	0.15	1.89	-	284.7
AHQ-4-9, 3372	K.QLEEDLYDGQVLQK.L	1678.82164	2	7.22E-04	0.78	3.04	-	737.4
AHQ-4-9, 3556	K.QLEEDLYDGQVLQK.L	1678.82164	2	8.56E-06	0.87	3.11	-	1168.6
AHQ-4-9, 6600	K.VLLDWINDVLVEER.I	1713.95549	2	3.19E-07	0.97	5.15	-	1634.7
AHQ-4-9, 5764 - 5836	K.VLLDWINDVLVEER.I	1713.95549	2	4.29E-04	0.95	4.03	-	1356.6
gi|10190678|ref|NP_065691.1| RP42 homolog; squamous cell carcinoma-related oncogene [Homo sapiens]				3.25E-08	0.88	10.18	6.60	30124.1
AHQ-4-10, 5677 - 5721	K.LDVATDNFFQNPELYIR.E	2056.26326	2	3.25E-08	0.88	3.63	-	885.3
gi|4758756|ref|NP_004528.1| nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr				3.30E-08	3.35	40.26	14.60	45373.8
AHQ-4-7, 7267	K.GIPEFWLTVFK.N	1337.58999	2	1.43E-06	0.65	2.78	-	205.9
AHQ-4-7, 5483	R.LDGLVETPTGYIESLPR.V	1861.08535	2	4.72E-04	0.90	4.02	-	803.8
AHQ-4-7, 5582	R.LDGLVETPTGYIESLPR.V	1861.08535	2	1.15E-06	0.93	3.91	-	937.0
AHQ-4-7, 5346	K.NVDLLSDMVQEHDEPILK.H	2096.34751	2	3.30E-08	0.97	5.11	-	1346.9
AHQ-4-7, 4607 - 4611	K.YAVLYQPLFDK.R	1357.57807	1	3.26E-04	0.80	2.68	-	805.6
gi|4557032|ref|NP_002291.1| lactate dehydrogenase B [Homo sapiens]				3.52E-08	7.10	90.29	33.80	36638.3
AHQ-4-13-, 4501	K.FIIPQIVK.Y	958.22198	2	9.54E-04	0.76	2.89	-	615.0

AHQ-4-9, 6648 - 6719	K.GM*YGIENEVFLSLPCILNAR.G	2314.66682	2	1.44E-06	0.96	5.86	-	761.6
AHQ-4-13-, 2165	K.IVADKDYSVTANSK.I	1511.65887	2	7.81E-06	0.94	3.64	-	1369.4
AHQ-4-9, 1915	K.IVADKDYSVTANSK.I	1511.65887	2	8.99E-07	0.88	3.58	-	743.4
AHQ-4-13, 2274 - 2278	K.IVADKDYSVTANSK.I	1511.65887	2	1.50E-05	0.94	4.00	-	1161.7
AHQ-4-9, 2999 - 3004	K.LIAPVAEEEATVPNNK.I	1695.89534	2	7.78E-04	0.45	2.53	-	686.7
AHQ-4-9, 1865	K.LKDDEVAQLK.K	1159.31477	2	3.28E-05	0.63	2.83	-	555.7
AHQ-4-9, 1857	K.LKDDEVAQLK.K	1159.31477	1	1.27E-04	0.16	2.42	-	324.9
AHQ-4-9, 3476	K.LKGEM*MDLQHGSLFLQTPK.I	2190.57228	2	5.98E-04	0.53	2.68	-	626.6
AHQ-4-9, 3336 - 3343	K.MVVESAYEVIK.L	1268.50463	2	3.52E-08	0.96	4.46	-	1184.2
AHQ-4-13, 6754	K.SLADELALVDVLEDK.L	1630.81843	2	2.06E-06	0.97	5.39	-	1660.0
AHQ-4-9, 6291 - 6301	K.SLADELALVDVLEDK.L	1630.81843	2	2.69E-04	0.95	4.36	-	1380.9
AHQ-4-13-, 6656	K.SLADELALVDVLEDK.L	1630.81843	2	3.06E-05	0.97	4.76	-	1674.4
AHQ-4-14-, 6534 - 6543	K.SLADELALVDVLEDK.L	1630.81843	2	9.23E-04	0.95	3.98	-	1407.8
AHQ-4-14-, 6669	K.SLADELALVDVLEDKLK.G	1872.14959	2	1.37E-04	0.97	4.70	-	1681.9
AHQ-4-9, 6527 - 6567	K.SLADELALVDVLEDKLK.G	1872.14959	2	5.83E-05	0.96	4.25	-	1686.2
gi|4757766|ref|NP_004299.1| Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa				3.55E-08	2.20	30.26	8.70	50435.4
AHQ-4-7, 6206	K.FLLDHQGELFPSPDPSGL	1970.17037	2	1.12E-05	0.55	2.92	-	409.3
AHQ-4-11, 5870 - 5874	K.FLLDHQGELFPSPDPSGL	1970.17037	2	3.99E-05	0.33	2.66	-	390.1
AHQ-4-11, 5917	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	5.35E-07	0.94	4.81	-	720.3
AHQ-4-8, 5958	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	1.54E-05	0.92	4.16	-	811.4
AHQ-4-7, 6185 - 6190	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	3	3.80E-04	0.82	3.96	-	657.0
AHQ-4-7, 6166 - 6178	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	2.84E-05	0.96	5.23	-	869.2
AHQ-4-7, 7241	K.YNMGLPVDFDQYNELHLPAVILK.T	2691.09719	2	3.55E-08	0.71	3.22	-	427.9
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				3.55E-08	5.85	70.24	56.50	22006.2
AHQ-4-10, 6519 - 6521	K.DQFPEVYVPTVFENYIADIEVDGK.Q	2789.04149	2	3.55E-08	0.86	3.87	-	418.6
AHQ-4-10, 4372	K.HFCPNVPIILVGNK.K	1609.91693	2	5.05E-07	0.94	4.04	-	1188.1
AHQ-4-11, 4553 - 4560	K.HFCPNVPIILVGNK.K	1609.91693	2	7.64E-04	0.97	3.84	-	2034.5
AHQ-4-10, 4201	K.HFCPNVPIILVGNK.K	1609.91693	2	1.38E-07	0.97	4.47	-	1750.0
AHQ-4-10, 3875 - 3929	K.HFCPNVPIILVGNKK.D	1738.08985	2	5.21E-08	0.88	3.37	-	973.8
AHQ-4-10, 4012	R.ISAFGYLECSAK.T	1347.51850	2	4.19E-06	0.94	3.53	-	1032.0
AHQ-4-10, 6331	R.LRPLSYPDTDVILM*CFSIDSPDSLENIPEK.W	3483.90759	3	2.01E-04	0.94	4.90	-	1179.3
AHQ-4-10, 2532	K.LVIVGDGACGK.T	1090.27572	1	7.84E-04	0.44	1.92	-	683.3
AHQ-4-10, 4596	K.QVELALWDTAGQEDYDR.L	2010.10662	2	7.03E-05	0.81	3.46	-	742.9
gi|4506005|ref|NP_002700.1| protein phosphatase 1, catalytic subunit, beta isoform [Homo sapiens] [				3.70E-08	3.80	40.26	20.80	37186.6
AHQ-4-9, 3396	R.AHQVVEDGYEFFAK.R	1640.77679	2	1.72E-04	0.94	3.46	-	1243.4
AHQ-4-14-, 6714	R.EIFLSQPILLELEAPLK.I	1954.33857	2	5.19E-05	0.94	4.46	-	903.5
AHQ-4-9, 6628	R.EIFLSQPILLELEAPLK.I	1954.33857	2	9.70E-08	0.94	4.89	-	699.2
AHQ-4-9, 4681	K.IFCCHGGLSPDLQSMEQIR.R	2251.54930	2	1.10E-05	0.96	4.82	-	1672.4
AHQ-4-9, 6564 - 6568	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	2.38E-06	0.96	5.20	-	901.7
AHQ-4-9, 6384	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	3.70E-08	0.96	4.99	-	945.8
gi|4505621|ref|NP_002558.1| prostatic binding protein; phosphatidylethanolamine binding protein [Ho				3.96E-08	2.87	30.26	37.40	21056.6
AHQ-4-11, 4889 - 4894	R.APVAGTCYQAEWDDYVPK.L	2072.23961	2	5.02E-05	0.98	5.29	-	1885.7
AHQ-4-11, 4502	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	2.40E-07	0.97	5.27	-	1464.1
AHQ-4-11, 4193 - 4257	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	3.96E-08	0.96	4.21	-	1528.0
AHQ-4-11, 5280 - 5340	K.WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK.V	3473.79274	3	7.16E-05	0.94	4.95	-	1315.0
gi|10863977|ref|NP_067000.1| LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-				3.98E-08	1.90	20.26	40.00	10834.5
AHQ-4-14-, 6565	K.NDLSICGTLHSVDQYLNIK.L	2192.43507	2	2.98E-07	0.93	4.59	-	983.7
AHQ-4-14-, 5329	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	3.98E-08	0.96	5.23	-	1229.1
gi|4507793|ref|NP_003339.1| ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast); ubiquitin-conj				4.47E-08	4.14	50.27	36.80	17137.7
AHQ-4-12, 5809	K.LELFLPEEYPMAAPK.V	1749.06325	2	4.47E-08	0.86	4.30	-	533.8
AHQ-4-13, 5400	K.LELFLPEEYPM*AAPK.V	1765.06265	2	4.95E-04	0.84	3.91	-	444.0
AHQ-4-12, 5327	K.LELFLPEEYPM*AAPK.V	1765.06265	2	1.78E-05	0.74	3.23	-	433.6
AHQ-4-12, 3258	R.LLAEPVPGIK.A	1037.27750	2	9.84E-05	0.70	2.79	-	541.9
AHQ-4-12, 3247	R.LLAEPVPGIK.A	1037.27750	1	7.34E-04	0.69	2.36	-	708.5
AHQ-4-12, 2163	K.TNEAQAIETAR.A	1204.27249	2	2.76E-04	0.80	3.11	-	992.4
AHQ-4-13, 2350 - 2351	K.TNEAQAIETAR.A	1204.27249	2	2.66E-04	0.91	3.47	-	1341.5
AHQ-4-13-, 2244	K.TNEAQAIETAR.A	1204.27249	2	9.78E-05	0.88	3.13	-	1312.4
AHQ-4-12, 5267	R.YFHVVIAGPQDSPFEGGTFK.L	2197.43341	2	1.85E-04	0.96	4.98	-	1007.0
AHQ-4-13, 5269 - 5337	R.YFHVVIAGPQDSPFEGGTFK.L	2197.43341	2	1.91E-04	0.93	4.40	-	930.0
AHQ-4-12, 5274	R.YFHVVIAGPQDSPFEGGTFK.L	2197.43341	3	1.67E-05	0.96	5.44	-	1587.3
gi|5031931|ref|NP_005585.1| nascent-polypeptide-associated complex alpha polypeptide [Homo sapiens]				4.72E-08	0.96	10.21	6.50	23383.7
AHQ-4-13, 4162	K.SPASDTYIVFGEAK.I	1485.61987	2	4.72E-08	0.96	4.14	-	1504.7
gi|10864055|ref|NP_067069.1| megakaryocyte-enhanced gene transcript 1 protein; lymphocyte antigen-6				4.73E-08	1.69	20.25	8.90	40891.9
AHQ-4-9, 4859	R.AADGSPCNVLLCSVVPSR.R	1905.14311	2	8.34E-05	0.73	2.94	-	644.5
AHQ-4-1, 5653	R.AADGSPCNVLLCSVVPSR.R	1905.14311	2	2.89E-04	0.77	3.29	-	647.4
AHQ-4-9, 3661	R.YWCAVLGQHHNYQNWR.V	2134.32402	2	4.73E-08	0.96	4.95	-	1260.3
gi|20535366|ref|XP_053177.4| similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap				4.79E-08	2.08	30.23	7.30	49858.2
AHQ-4-7, 3061	K.DVNAAIATIK.T	1016.17355	1	2.86E-05	0.31	2.16	-	302.9
AHQ-4-7, 2857	K.DVNAAIATIK.T	1016.17355	1	2.32E-04	0.18	2.24	-	149.0
AHQ-4-7, 2750	K.DVNAAIATIK.T	1016.17355	1	1.29E-05	0.34	2.18	-	396.9
AHQ-4-11, 2985	K.DVNAAIATIK.T	1016.17355	1	6.03E-05	0.10	2.06	-	198.4
AHQ-4-6, 5159	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	8.67E-08	0.86	3.69	-	652.5
AHQ-4-4, 5419	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.50E-07	0.45	2.96	-	361.3
AHQ-4-2, 5459	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.13E-05	0.49	2.71	-	433.1
AHQ-4-7, 4815	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.97E-08	0.78	3.58	-	354.4
AHQ-4-7, 4975	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	6.53E-06	0.54	2.94	-	363.8
AHQ-4-7, 5137 - 5209	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.38E-06	0.95	4.51	-	1178.9
AHQ-4-7, 5234 - 5305	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.25E-07	0.93	4.31	-	1004.4
AHQ-4-7, 5375 - 5415	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.29E-04	0.45	2.91	-	248.0
AHQ-4-1, 5463	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.28E-06	0.71	2.98	-	564.3
AHQ-4-11, 4985 - 5024	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.55E-08	0.89	4.21	-	609.4
AHQ-4-12, 5197 - 5271	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	6.45E-05	0.54	2.91	-	479.1
AHQ-4-14-, 5069 - 5133	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.79E-08	0.92	4.52	-	568.0
AHQ-4-14-, 4967	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.60E-07	0.84	3.89	-	490.3
AHQ-4-14, 5937	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.79E-07	0.73	3.19	-	466.8
AHQ-4-14, 6289 - 6349	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.83E-07	0.89	3.70	-	820.2
AHQ-4-14, 6404 - 6485	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	8.96E-07	0.95	4.00	-	1174.2
AHQ-4-13-, 5156	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.62E-05	0.37	2.77	-	323.6
AHQ-4-12, 5683 - 5758	R.TIQFVDWCPTGFK.V	1600.81899	2	5.44E-05	0.73	3.27	-	535.1
AHQ-4-14-, 5625 - 5703	R.TIQFVDWCPTGFK.V	1600.81899	2	3.15E-05	0.82	2.90	-	678.0
AHQ-4-13, 5797 - 5817	R.TIQFVDWCPTGFK.V	1600.81899	2	7.01E-04	0.70	2.81	-	615.1
gi|4506365|ref|NP_002856.1| RAB2, member RAS oncogene family [Homo sapiens]				4.85E-08	1.88	20.20	12.70	23545.4
AHQ-4-11, 5352 - 5381	R.DTFNHLTTWLEDAR.Q	1719.83554	2	4.85E-08	0.92	4.09	-	955.6
AHQ-4-11, 4273	K.LQIWDTAGQESFR.S	1551.68478	2	1.25E-05	0.95	3.99	-	1550.9
gi|5453832|ref|NP_006380.1| oxygen regulated protein precursor; oxygen regulated protein (150kD) [H				4.85E-08	1.56	20.21	4.90	111334.8
AHQ-4-3, 6691	K.VLQLINDNTATALSYGVFR.R	2096.37206	2	1.46E-04	0.71	3.03	-	732.3
AHQ-4-3, 7703	R.VPGPVQQALQSAEM*SLDEIEQVILVGGATR.V	3153.55387	3	4.85E-08	0.85	4.21	-	497.0
gi|5454090|ref|NP_006271.1| signal sequence receptor, delta; translocon-associated protein delta [H				5.06E-08	0.89	10.17	6.40	18998.5
AHQ-4-12, 4869	R.FFDEESYSLLR.K	1406.52121	2	5.06E-08	0.89	3.44	-	878.5
gi|21389549|ref|NP_653263.1| hypothetical protein MGC26605 [Homo sapiens]				5.10E-08	1.71	20.19	14.90	26927.8
AHQ-4-10, 5115	R.AITVFSPDGHLFQVEYAQEAVK.K	2450.73052	2	5.72E-05	0.86	3.77	-	698.2
AHQ-4-10, 4273	K.LTVEDPVTVEYITR.F	1635.83990	2	5.10E-08	0.86	3.82	-	520.5
gi|5803181|ref|NP_006810.1| stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo				5.32E-08	0.94	10.26	3.50	62638.9
AHQ-4-13, 6421 - 6430	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	8.97E-08	0.95	4.64	-	1127.8
AHQ-4-6, 6466	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	5.32E-08	0.94	5.10	-	675.7
gi|4504557|ref|NP_000864.1| intercellular adhesion molecule 2 precursor [Homo sapiens]				5.37E-08	0.93	10.23	5.80	30653.1
AHQ-4-6, 7300	R.VPTVEPLDSLTLFLFR.G	1848.17455	2	5.37E-08	0.93	4.53	-	567.4

gi|28373103|ref|NP_005164.2| sarco/endoplasmic reticulum Ca2+ -ATPase isoform a; ATPase, Ca(2+)-tra				5.58E-08	1.90	20.22	3.80	109255.5
AHQ-4-1, 6737	K.CSEDNPLFAGIDCEVFESR.F	2248.38927	2	1.58E-04	0.93	4.43	-	749.5
AHQ-4-1, 3905	R.HFSVTAEGGLSPAQVTGAR.E	1886.05823	2	5.58E-08	0.97	4.43	-	2006.9
gi|5803201|ref|NP_006818.1| transmembrane trafficking protein [Homo sapiens]				5.62E-08	0.96	10.20	5.00	24975.8
AHQ-4-11, 4896	R.IPDQLVILDMK.H	1285.57833	2	5.62E-08	0.96	3.91	-	1573.3
gi|5803009|ref|NP_006786.1| EH-domain containing 1; homolog of Drosophila past; EH domain containin				6.08E-08	1.88	20.31	5.10	60844.7
AHQ-4-7, 7459	R.FMCAQLPNPVLDSISIIDTPGILSGEK.Q	2918.37521	2	6.08E-08	0.96	6.12	-	959.5
AHQ-4-7, 7429 - 7486	R.FM*CAQLPNPVLDSISIIDTPGILSGEK.Q	2934.37461	2	5.01E-06	0.91	4.60	-	739.8
gi|21361070|ref|NP_002617.2| phosphofructokinase, liver; Phosphofructokinase, liver type; human liv				6.10E-08	0.95	10.22	2.10	90202.5
AHQ-4-5, 5361	K.GQVQEVGWHDVAGWLGR.G	1895.07004	2	6.10E-08	0.95	4.47	-	1164.5
gi|4557703|ref|NP_000414.1| keratin 2a [Homo sapiens]				6.64E-08	2.79	30.24	5.60	65864.9
AHQ-4-4, 3016	R.FLEQQNQVLQTK.W	1476.65935	2	1.63E-05	0.95	3.76	-	2017.4
AHQ-4-13-, 2984	R.FLEQQNQVLQTK.W	1476.65935	2	5.44E-06	0.97	4.75	-	2058.9
AHQ-4-1, 3118 - 3198	R.FLEQQNQVLQTK.W	1476.65935	2	6.64E-08	0.97	4.66	-	2325.9
AHQ-4-1, 4379	K.LNDLEEALQQAK.E	1372.50630	2	1.71E-05	0.94	4.32	-	1274.0
AHQ-4-1, 6225	K.VDLLNQEIEFLK.V	1461.68459	2	1.04E-06	0.88	3.72	-	792.1
gi|27482573|ref|XP_208709.1| similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro				6.65E-08	2.18	30.26	31.80	17875.4
AHQ-4-12, 4893	K.GQVCLPVISAENWKPATK.T	2000.30757	2	2.34E-05	0.96	5.19	-	1036.9
AHQ-4-12, 2117	K.IYHPNIDEK.G	1129.24722	1	1.51E-04	0.37	1.99	-	576.4
AHQ-4-12, 6798	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	7.26E-07	0.96	4.60	-	1809.0
AHQ-4-12, 6797	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	2	6.65E-08	0.85	3.95	-	504.0
gi|5453726|ref|NP_006300.1| leucine rich repeat (in FLII) interacting protein 2 [Homo sapiens] [MAS				6.86E-08	0.92	10.18	1.90	82170.9
AHQ-4-12, 4182	K.AEQDITTLEQSISR.L	1591.70238	2	6.86E-08	0.92	3.57	-	1106.3
gi|29740995|ref|XP_291768.1| similar to Proteasome activator complex subunit 2 (Proteasome activato				6.94E-08	0.97	10.23	9.60	19192.6
AHQ-4-10, 6279	R.AFYAELYHIISSNLEK.T	1899.13528	2	6.94E-08	0.97	4.56	-	1830.6
gi|4758984|ref|NP_004654.1| RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho				7.07E-08	5.96	70.30	31.90	24393.3
AHQ-4-11, 2624 - 2678	K.AQIWDTAGQER.Y	1275.35241	2	3.48E-06	0.96	4.44	-	1666.0
AHQ-4-13-, 2826	K.AQIWDTAGQER.Y	1275.35241	2	1.94E-04	0.93	3.23	-	1258.0
AHQ-4-11, 4286 - 4293	R.DDEYDYLFK.V	1208.25483	1	4.66E-06	0.58	2.83	-	540.1
AHQ-4-11, 4678 - 4740	R.DHADSNIVIMLVGNK.S	1626.85974	2	1.80E-07	0.98	5.35	-	1771.0
AHQ-4-11, 4065	R.DHADSNIVIM*LVGNK.S	1642.85914	2	1.20E-04	0.97	4.56	-	2030.5
AHQ-4-11, 4888 - 4948	R.GAVGALLVYDIAK.H	1290.53317	2	7.07E-08	0.98	6.03	-	2840.2
AHQ-4-11, 2964 - 2969	K.STIGVEFATR.S	1081.20410	2	5.65E-05	0.91	3.30	-	970.4
AHQ-4-11, 2708	K.VVLIGDSGVGK.S	1044.22690	1	4.40E-04	0.54	2.52	-	738.9
AHQ-4-11, 2712	K.VVLIGDSGVGK.S	1044.22690	1	1.88E-04	0.58	2.95	-	596.7
gi|4505759|ref|NP_002622.1| phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo				7.12E-08	1.76	20.27	8.50	53151.7
AHQ-4-8, 6337 - 6415	K.IKDAFDRNPELQNLLLDDFFK.S	2552.86598	2	8.24E-05	0.79	3.57	-	495.1
AHQ-4-8, 6238	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	1.99E-07	0.92	3.96	-	909.5
AHQ-4-7, 6283	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	7.12E-08	0.97	5.31	-	1734.1
gi|19913424|ref|NP_001681.2| ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT				7.24E-08	1.69	20.22	5.50	68303.7
AHQ-4-6, 4998	R.ALDEYYDKHFTEFVPLR.T	2144.37051	2	4.95E-04	0.75	3.37	-	435.0
AHQ-4-6, 4135	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	7.24E-08	0.95	4.36	-	938.7
gi|8922673|ref|NP_060692.1| parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]				7.50E-08	1.14	20.23	5.60	42243.4
AHQ-4-9, 4071 - 4105	R.DAFDTLFDHAPDK.L	1492.57096	2	7.50E-08	0.96	4.52	-	1506.2
AHQ-4-9, 4079	R.DAFDTLFDHAPDK.L	1492.57096	1	1.06E-06	0.80	3.39	-	579.9
AHQ-4-9, 3488 - 3564	R.VLYNLFTK.Y	998.19983	1	2.75E-04	0.17	1.94	-	273.2
gi|4826657|ref|NP_004333.1| caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]				8.22E-08	2.76	30.22	9.30	62662.9
AHQ-4-12, 4959	K.EFDPTITDASLSLPSR.R	1749.89986	2	1.64E-04	0.89	3.93	-	680.9
AHQ-4-13, 2633 - 2706	K.GNVFSSPTAAGTPNK.E	1448.56286	2	3.30E-04	0.86	3.41	-	856.2
AHQ-4-13-, 2604	K.GNVFSSPTAAGTPNK.E	1448.56286	2	1.87E-05	0.91	3.39	-	1184.0
AHQ-4-12, 3701	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	8.22E-08	0.96	4.30	-	1453.5
AHQ-4-11, 3601	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	1.78E-07	0.58	2.84	-	557.7
AHQ-4-10, 3471 - 3472	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	2.03E-04	0.83	3.37	-	685.0
AHQ-4-6, 3616	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	1.43E-04	0.93	4.15	-	1106.1
gi|20539300|ref|XP_088391.4| similar to tropomyosin 4 [Homo sapiens]				8.51E-08	0.96	10.23	6.90	18592.1
AHQ-4-9, 2959	R.KLVILEGELER.A	1299.54160	2	8.51E-08	0.96	4.64	-	1381.4
gi|23110925|ref|NP_002789.1| proteasome beta 6 subunit; proteasome subunit Y; proteasome subunit be				8.59E-08	1.84	20.26	20.90	25357.6
AHQ-4-11, 2361	R.LAAIAESGVER.Q	1116.24998	2	8.59E-08	0.95	3.68	-	1454.0
AHQ-4-11, 6744	R.SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK.E	4058.45788	3	3.02E-04	0.90	5.11	-	634.8
gi|4507207|ref|NP_003121.1| sorcin; Sorcin (class 4 gene) [Homo sapiens]				8.73E-08	0.93	10.22	10.10	21676.3
AHQ-4-11, 4490 - 4564	R.CLTQSGIAGGYKPFNLETCR.L	2275.54736	2	8.73E-08	0.93	4.34	-	871.3
gi|4557361|ref|NP_001187.1| BH3 interacting domain death agonist; BH3-interacting domain death agon				9.02E-08	3.72	40.23	36.40	21994.6
AHQ-4-11, 6848	R.DLATALEQLLQAYPR.D	1702.93270	2	3.13E-07	0.92	4.43	-	801.4
AHQ-4-11, 6016	R.DVFHTTVNFINQNLR.T	1819.01348	2	6.44E-04	0.91	3.62	-	1038.0
AHQ-4-11, 6101 - 6164	R.ELDALGHELPVLAPQWEGYDELQTDGNR.S	3167.38790	3	9.59E-06	0.93	4.69	-	888.5
AHQ-4-11, 2680	R.IEADSESQEDIIR.N	1505.56635	2	9.02E-08	0.96	3.52	-	2293.6
gi|5730031|ref|NP_005688.2| secretory carrier membrane protein 2 [Homo sapiens]				9.49E-08	0.91	10.21	6.10	36648.6
AHQ-4-1, 5899	R.TGASFQQAQEEFSQGIFSSR.T	2206.31396	2	9.49E-08	0.91	4.14	-	776.3
gi|14165439|ref|NP_002131.2| heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch bindin				9.54E-08	0.79	10.15	4.10	51027.9
AHQ-4-6, 5072	R.GSYGDLGGPIITTQVTIPK.D	1918.18004	2	9.54E-08	0.79	3.05	-	719.4
gi|17149842|ref|NP_004461.2| FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep				1.03E-07	0.69	10.16	8.50	15649.2
AHQ-4-13-, 4172 - 4182	K.LVIPSELGYGER.G	1333.51491	2	1.03E-07	0.69	2.54	-	440.3
gi|10835242|ref|NP_006249.1| protein kinase, cGMP-dependent, type I; Protein kinase, cGMP-dependent				1.05E-07	0.96	10.22	2.50	77803.3
AHQ-4-6, 6771	K.LSDFNIIDTLGVGGFGR.V	1781.98992	2	1.05E-07	0.96	4.44	-	1311.7
gi|27477800|ref|XP_208313.1| similar to tropomyosin 4 [Homo sapiens]				1.07E-07	0.91	10.24	10.10	18426.7
AHQ-4-9, 4612 - 4679	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.80E-06	0.93	3.50	-	1552.1
AHQ-4-9, 4615	K.CGDLEEELKNVTNNLK.S	1878.05124	2	5.14E-04	0.88	3.71	-	711.4
AHQ-4-9, 5019 - 5099	K.CGDLEEELKNVTNNLK.S	1878.05124	2	2.95E-06	0.53	2.83	-	723.5
AHQ-4-9, 5255 - 5315	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.07E-07	0.91	4.02	-	1127.2
AHQ-4-9, 4131	K.CGDLEEELKNVTNNLK.S	1878.05124	2	3.06E-07	0.95	4.78	-	1123.4
gi|7330335|ref|NP_039234.1| chloride intracellular channel 4; chloride intracellular channel 4 like				1.14E-07	0.88	10.20	6.30	28771.9
AHQ-4-10, 2865	K.AGSDGESIGNCPFSQR.L	1683.73852	2	1.14E-07	0.88	4.00	-	550.7
gi|22748619|ref|NP_689476.1| tropomyosin 3 [Homo sapiens]				1.22E-07	0.52	10.25	4.50	28222.6
AHQ-4-9, 2787	R.KLVIIEGDLER.T	1285.51492	1	1.22E-07	0.52	3.05	-	329.6
AHQ-4-9, 2772 - 2836	R.KLVIIEGDLER.T	1285.51492	2	4.75E-04	0.89	3.44	-	1061.9
gi|4505303|ref|NP_002466.1| myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m				1.23E-07	2.76	30.23	11.50	22763.8
AHQ-4-12, 2522	R.ALGQNPTNAEVLK.V	1355.52211	2	6.68E-04	0.84	3.48	-	688.3
AHQ-4-13-, 2728 - 2732	R.ALGQNPTNAEVLK.V	1355.52211	2	1.96E-06	0.83	3.91	-	397.7
AHQ-4-12, 2609 - 2673	R.ALGQNPTNAEVLK.V	1355.52211	2	5.53E-06	0.76	3.83	-	339.7
AHQ-4-12, 2610 - 2810	R.ALGQNPTNAEVLK.V	1355.52211	1	2.60E-04	0.30	2.49	-	391.0
AHQ-4-12, 2614 - 2741	R.ALGQNPTNAEVLK.V	1355.52211	1	2.33E-05	0.36	2.83	-	330.4
AHQ-4-12, 2717 - 2787	R.ALGQNPTNAEVLK.V	1355.52211	2	1.23E-07	0.92	4.54	-	620.6
AHQ-4-12, 2969	R.ALGQNPTNAEVLK.V	1355.52211	1	8.31E-06	0.09	2.14	-	246.3
AHQ-4-13, 2837 - 2842	R.ALGQNPTNAEVLK.V	1355.52211	2	6.90E-05	0.73	3.56	-	388.5
AHQ-4-13, 3367 - 3443	K.ILYSQCGDVMR.A	1343.55489	2	4.86E-04	0.81	2.65	-	882.8
AHQ-4-13-, 2672 - 2681	K.ILYSQCGDVM*R.A	1359.55429	2	4.15E-07	0.93	3.48	-	1200.0
AHQ-4-12, 2589 - 2653	K.ILYSQCGDVM*R.A	1359.55429	2	4.52E-07	0.91	3.26	-	964.1
AHQ-4-14-, 2594	K.ILYSQCGDVM*R.A	1359.55429	2	1.52E-07	0.91	3.11	-	1123.4
AHQ-4-12, 3259	K.ILYSQCGDVMR.A	1343.55489	2	5.44E-07	0.93	3.46	-	1172.3
gi|4503447|ref|NP_001389.1| peroxisomal enoyl-coenzyme A hydratase-like protein; delta3,5-delta2,4-				1.23E-07	0.68	10.15	3.40	35994.1
AHQ-4-9, 3744	R.YCAQDAFFQVK.E	1378.53429	1	1.23E-07	0.68	2.93	-	362.7
gi|4885153|ref|NP_005198.1| v-crk sarcoma virus CT10 oncogene homolog (avian)-like; v-crk avian sar				1.25E-07	4.58	60.25	30.40	33776.7
AHQ-4-10, 5805 - 5883	K.IGDQEFDHLPALLEFYK.I	2036.27195	2	3.12E-05	0.95	5.09	-	904.2
AHQ-4-10, 5899	K.IGDQEFDHLPALLEFYK.I	2036.27195	2	8.35E-07	0.95	4.56	-	995.9
AHQ-4-9, 5964 - 6000	K.IGDQEFDHLPALLEFYK.I	2036.27195	2	4.50E-05	0.93	4.71	-	943.6
AHQ-4-13-, 4120	K.IHYLDTTTLIEPAPR.Y	1740.98094	2	1.10E-04	0.66	2.76	-	553.7
AHQ-4-10, 5092	K.KGEILVIIEKPEEQWWSAR.N	2312.65223	2	1.25E-07	0.86	3.83	-	634.6

AHQ-4-10, 5015	R.TLYDFPGNDAEDLPFK.K	1842.98222	2	1.97E-04	0.78	3.27	-	371.5
AHQ-4-10, 4899	R.YPSPPMGSVSAPNLPTAEDNLEYVR.T	2705.98075	2	1.69E-05	0.60	2.99	-	336.8
AHQ-4-10, 4553 - 4556	R.YPSPPM*GSVSAPNLPTAEDNLEYVR.T	2721.98015	2	1.62E-05	0.74	3.38	-	567.1
gi|12545410|ref|NP_031394.1| RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,				1.28E-07	1.74	20.21	5.80	95912.5
AHQ-4-5, 5109	R.APSDSAPGCSPCTGGLPANIQLDIDGDRETER.I	3360.54658	3	6.83E-06	0.80	3.86	-	509.9
AHQ-4-5, 6421 - 6422	K.SLCPFYGEDFYCEIPR.S	2056.26024	2	1.28E-07	0.93	4.26	-	732.4
gi|7705704|ref|NP_057001.1| glutathione S-transferase subunit 13 homolog [Homo sapiens]				1.29E-07	2.81	30.28	19.90	25496.7
AHQ-4-11, 3324	K.AGMSAEQAQGLLEK.I	1433.61314	2	6.06E-07	0.94	3.89	-	1499.2
AHQ-4-11, 4417 - 4420	R.FLTAVNLEHPEMLEK.A	1772.05845	2	1.29E-07	0.98	5.57	-	1731.7
AHQ-4-11, 4476	R.NEDITEPQSILAAAEK.A	1729.86695	2	5.36E-04	0.89	4.15	-	545.7
gi|7661922|ref|NP_055814.1| RAB21, member RAS oncogene family [Homo sapiens]				1.42E-07	0.98	10.31	7.60	24347.4
AHQ-4-10, 3921 - 3924	R.HVSIQEAESYAESVGAK.H	1805.92351	2	1.42E-07	0.98	6.23	-	1456.6
gi|30147105|ref|XP_210550.2| similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48				1.59E-07	0.95	10.22	2.20	61339.9
AHQ-4-5, 4061	K.ADLINNLGTIAK.S	1243.43490	2	1.59E-07	0.95	4.45	-	1079.4
gi|7662338|ref|NP_054735.1| suppressor of actin 1 [Homo sapiens]				1.61E-07	1.68	20.19	6.80	66966.5
AHQ-4-1, 4278	R.GIDSEGHAANFVETEQIVHYNGSK.A	2603.74197	3	1.61E-07	0.86	3.72	-	1009.8
AHQ-4-1, 4331	R.LSNTSPEFQEM*SLLER.A	1898.08433	2	6.65E-05	0.82	3.45	-	530.0
gi|4507487|ref|NP_003238.1| thrombospondin 2 [Homo sapiens]				1.61E-07	1.78	20.22	2.60	129954.5
AHQ-4-1, 5350 - 5358	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.61E-07	0.95	4.46	-	1152.6
AHQ-4-1, 3037	R.NALWHTGNTPGQVR.T	1551.69124	2	1.07E-04	0.91	3.73	-	884.6
AHQ-4-2, 2520	R.NALWHTGNTPGQVR.T	1551.69124	2	2.85E-04	0.85	3.10	-	868.2
AHQ-4-2, 3084	R.NALWHTGNTPGQVR.T	1551.69124	2	8.56E-04	0.68	3.01	-	614.5
AHQ-4-4, 2824	R.NALWHTGNTPGQVR.T	1551.69124	2	6.02E-06	0.92	3.85	-	961.6
AHQ-4-6, 2842	R.NALWHTGNTPGQVR.T	1551.69124	2	6.47E-06	0.78	2.69	-	871.9
AHQ-4-7, 2554	R.NALWHTGNTPGQVR.T	1551.69124	2	9.85E-05	0.88	3.78	-	680.9
AHQ-4-8, 2147	R.NALWHTGNTPGQVR.T	1551.69124	2	7.24E-07	0.81	3.25	-	826.4
AHQ-4-11, 2744	R.NALWHTGNTPGQVR.T	1551.69124	2	5.61E-06	0.68	2.76	-	801.3
AHQ-4-13-, 2708	R.NALWHTGNTPGQVR.T	1551.69124	2	4.56E-07	0.83	3.17	-	887.2
gi|4502021|ref|NP_003680.1| aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase);				1.62E-07	1.65	20.23	10.30	36648.3
AHQ-4-9, 3360	K.ALQAAYGASAPSVTSAALR.W	1806.01302	2	1.65E-04	0.69	3.01	-	435.0
AHQ-4-9, 4955 - 4956	R.FYAYNPLAGGLLTGK.Y	1585.82741	2	1.62E-07	0.96	4.69	-	1237.9
gi|19923483|ref|NP_057406.2| GTPase Rab14 [Homo sapiens]				1.62E-07	5.89	80.21	50.20	23896.8
AHQ-4-11, 4202	R.GAAGALMVYDITR.R	1338.55819	2	1.22E-04	0.90	3.18	-	1273.1
AHQ-4-10, 3583	K.IYQNIQDGSLDLNAAESGVQHKPSAPQGGR.L	3152.38123	3	1.09E-06	0.84	4.03	-	819.4
AHQ-4-10, 4592	R.NLTNPNTVIILIGNK.A	1624.90662	2	3.58E-04	0.87	3.48	-	562.2
AHQ-4-11, 4884	R.NLTNPNTVIILIGNK.A	1624.90662	2	1.20E-05	0.70	2.93	-	620.2
AHQ-4-11, 3084	K.SCLLHQFTEK.K	1264.43272	2	3.18E-05	0.93	3.48	-	1085.1
AHQ-4-10, 2985	K.SCLLHQFTEK.K	1264.43272	2	7.58E-06	0.90	3.48	-	772.9
AHQ-4-10, 3880	R.STYNHLSSWLTDAR.N	1651.76121	2	9.59E-04	0.86	2.90	-	903.7
AHQ-4-11, 4390 - 4393	K.TGENVEDAFLEAAK.K	1494.58517	2	1.62E-07	0.93	4.27	-	828.2
AHQ-4-10, 4137	K.TGENVEDAFLEAAK.K	1494.58517	2	4.56E-07	0.84	3.52	-	583.6
AHQ-4-10, 3784	K.TGENVEDAFLEAAKK.I	1622.75808	2	2.45E-05	0.27	2.62	-	234.3
AHQ-4-10, 3915	K.YIIIGDMGVGK.S	1166.41554	1	7.37E-04	0.50	2.01	-	1012.7
gi|5802966|ref|NP_006861.1| destrin (actin depolymerizing factor); destrin [Homo sapiens]				1.64E-07	0.64	10.15	6.70	18505.6
AHQ-4-12, 3726	R.YALYDASFETK.E	1308.41754	1	1.64E-07	0.64	2.97	-	387.3
gi|5902016|ref|NP_008939.1| reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sapi				1.64E-07	1.59	20.23	14.10	22395.3
AHQ-4-1, 3158 - 3226	R.HQAQIDHYLGLANK.N	1608.78270	2	9.95E-06	0.93	3.56	-	1304.9
AHQ-4-12, 2931	R.HQAQIDHYLGLANK.N	1608.78270	2	1.46E-05	0.92	3.90	-	908.0
AHQ-4-1, 3005	K.YSNSALGHVNCTIK.E	1565.73305	2	1.64E-07	0.65	2.53	-	812.3
gi|7657007|ref|NP_055210.1| dual adaptor of phosphotyrosine and 3-phosphoinositides [Homo sapiens]				1.76E-07	2.71	30.20	15.70	32044.2
AHQ-4-13-, 3874 - 3876	R.DSNETTGLYSLSVR.A	1542.62982	2	1.98E-04	0.58	3.15	-	555.5
AHQ-4-13, 4036	R.DSNETTGLYSLSVR.A	1542.62982	2	3.18E-06	0.87	3.56	-	898.1
AHQ-4-13-, 5994	R.SDGEAELLQDLGWYHGNLTR.H	2275.41943	2	1.76E-07	0.90	4.10	-	873.8
AHQ-4-13-, 3420	K.TGVEADEWIK.I	1148.24730	2	2.22E-06	0.93	2.98	-	1625.7
gi|18104989|ref|NP_002822.2| protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t				1.78E-07	2.20	30.16	7.70	67560.7
AHQ-4-6, 4956	R.DLSGLDAETLLK.G	1275.43053	2	1.35E-06	0.86	2.91	-	1154.4
AHQ-4-6, 6695 - 6718	R.ESLSQPGDFVLSVLSDQPK.A	2047.25144	2	3.09E-05	0.77	3.29	-	342.4
AHQ-4-6, 3927	R.IQNSGDFYDLYGGEK.F	1706.79040	2	1.78E-07	0.57	2.88	-	548.4
gi|4557871|ref|NP_001054.1| transferrin [Homo sapiens]				1.79E-07	0.94	10.23	2.70	77049.5
AHQ-4-5, 7330	R.SAGWNIPIGLLYCDLPEPR.K	2173.47658	2	1.79E-07	0.94	4.64	-	756.0
gi|7657649|ref|NP_055362.1| tropomodulin 3 (ubiquitous) [Homo sapiens]				1.81E-07	0.96	10.24	5.40	39594.5
AHQ-4-11, 5038	K.YKDLDEDELLGNLSETELK.Q	2225.39217	2	1.81E-07	0.96	4.73	-	1330.8
gi|4507295|ref|NP_003560.1| syntaxin 7 [Homo sapiens]				1.81E-07	1.76	20.20	9.60	29845.3
AHQ-4-13-, 2529 - 2533	K.ITQCSVEIQR.T	1235.39292	2	1.94E-04	0.83	3.32	-	1038.6
AHQ-4-13, 3489	R.TLNQLGTPQDSPELR.Q	1669.81798	2	3.73E-05	0.76	3.23	-	411.9
AHQ-4-13-, 3360	R.TLNQLGTPQDSPELR.Q	1669.81798	2	6.65E-06	0.77	3.04	-	464.5
AHQ-4-10, 3095 - 3096	R.TLNQLGTPQDSPELR.Q	1669.81798	2	1.81E-07	0.93	4.10	-	849.0
gi|4826848|ref|NP_004991.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5; NADH dehydrogena				1.84E-07	0.98	10.37	22.40	13458.6
AHQ-4-13, 6908	K.KLEDQLQGGQLEEVILQAEHELNLAR.K	2975.30339	3	1.84E-07	0.98	7.45	-	2068.1
gi|5453603|ref|NP_006422.1| chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c				1.85E-07	2.74	30.21	7.90	57487.9
AHQ-4-7, 2874	R.EALLSSAVDHGSDEVK.F	1657.76083	2	1.85E-07	0.93	3.95	-	1380.3
AHQ-4-7, 2934	R.GATQQILDEAER.S	1331.41427	2	8.65E-06	0.87	3.45	-	840.8
AHQ-4-7, 5490	R.SLHDALCVLAQTVK.D	1556.80920	2	5.85E-04	0.95	3.03	-	1967.2
gi|5123454|ref|NP_005336.2| heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind				1.86E-07	5.43	60.23	16.40	70037.7
AHQ-4-6, 2942	K.AQIHDLVLVGGSTR.I	1466.66769	2	1.89E-07	0.95	3.68	-	1661.8
AHQ-4-6, 4732	K.DAGVIAGLNVLR.I	1198.39736	2	1.47E-06	0.97	3.46	-	2494.4
AHQ-4-6, 6210 - 6222	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G	3058.37100	3	3.41E-04	0.93	4.62	-	1551.5
AHQ-4-6, 3004	R.LVNHFVEEFK.R	1262.43837	2	1.86E-07	0.73	2.50	-	627.1
AHQ-4-6, 3516	K.NQVALNPQNTVFDAK.R	1659.82478	2	8.86E-04	0.94	4.38	-	775.7
AHQ-4-6, 6792	K.SINPDEAVAYGAAVQAAILM*GDK.S	2321.59293	2	4.19E-04	0.92	3.81	-	1204.0
gi|20149594|ref|NP_031381.2| heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea				1.86E-07	5.66	60.24	9.40	83263.6
AHQ-4-5, 2989 - 2990	R.ELISNASDALDK.I	1276.37539	2	1.86E-07	0.91	4.01	-	809.1
AHQ-4-5, 5418	K.HSQFIGYPITLYLEK.E	1810.08487	2	2.08E-06	0.96	4.65	-	1108.4
AHQ-4-5, 4106 - 4118	R.NPDDITQEEYGEFYK.S	1848.90048	2	4.00E-06	0.95	4.72	-	1124.6
AHQ-4-5, 3771	K.SLTNDWEDHLAVK.H	1528.64798	2	8.32E-07	0.92	4.17	-	917.6
AHQ-4-5, 4138	R.TLTLVDTGIGMTK.A	1350.60718	2	1.45E-06	0.95	3.63	-	1297.1
AHQ-4-5, 3473	R.TLTLVDTGIGM*TK.A	1366.60658	2	9.97E-05	0.96	3.59	-	1528.4
gi|21361370|ref|NP_002853.2| phosphorylase, glycogen; brain [Homo sapiens]				1.87E-07	4.37	50.28	8.90	96695.3
AHQ-4-5, 3598	R.GLAGLGDVAEVR.K	1157.30210	2	9.26E-05	0.97	4.09	-	2022.1
AHQ-4-6, 3330	R.HLDHVAALFPGDVDR.L	1662.83036	2	1.19E-06	0.85	3.01	-	869.6
AHQ-4-7, 3265 - 3266	R.HLDHVAALFPGDVDR.L	1662.83036	2	7.31E-04	0.89	3.90	-	738.9
AHQ-4-5, 5761 - 5791	K.LLPLVSDEVFIR.D	1401.67552	2	1.87E-07	0.64	2.53	-	450.0
AHQ-4-5, 6613	K.WLDTQVVLAMPYDTPVPGYK.N	2294.65394	2	1.64E-05	0.94	4.82	-	707.6
AHQ-4-5, 6659	R.WLLLCNPGLADTIVEK.I	1844.16436	2	1.88E-04	0.97	5.53	-	1577.9
gi|7657056|ref|NP_055415.1| EH-domain containing 3; EH domain containing 3 [Homo sapiens]				2.05E-07	3.11	40.24	14.40	60886.7
AHQ-4-7, 3293	R.EHQISPGDFPNLK.R	1482.62245	2	5.04E-05	0.41	2.69	-	555.1
AHQ-4-7, 5519	R.FHEFHSPALEDADFDNKPMVLLVGQYSTGK.T	3394.75749	3	4.61E-05	0.92	4.88	-	742.1
AHQ-4-13-, 5326	K.LADIDKDGM*LDDDEFALANHLIK.V	2589.86003	3	2.05E-07	0.90	3.96	-	1361.7
AHQ-4-8, 4394	R.YLLEQDFPGMR.I	1369.57075	2	6.86E-05	0.88	3.49	-	1019.8
gi|4758158|ref|NP_004395.1| neural precursor cell expressed, developmentally down-regulated 5 [Homo				2.06E-07	0.94	10.26	6.40	41487.2
AHQ-4-8, 5806	R.TMLITHMQDLQEVTQDLHYENFR.S	2864.20650	3	2.06E-07	0.94	5.26	-	992.1
gi|21618359|ref|NP_004095.3| fatty acid synthase [Homo sapiens]				2.07E-07	1.91	20.27	1.70	273262.0
AHQ-4-1, 6166 - 6169	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	7.36E-06	0.93	5.10	-	774.8
AHQ-4-3, 7045 - 7127	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	1.48E-05	0.69	2.85	-	633.2
AHQ-4-1, 6957 - 6973	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	2.07E-07	0.98	5.39	-	2083.8
gi|8393638|ref|NP_058642.1| F11 receptor isoform a precursor; platelet F11 receptor; platelet adhes				2.11E-07	0.80	10.16	7.70	32582.9
AHQ-4-8, 4449	K.LIVLVPPSKPTVNIPSSATIGNR.A	2374.80814	2	2.11E-07	0.80	3.00	-	453.9

gi|18570595|ref|XP_095590.1| similar to myosin regulatory light chain [Homo sapiens]				2.15E-07	0.95	10.19	8.90	13951.5
AHQ-4-11, 3033 - 3100	K.LNGTDPEDVIR.H	1229.32195	2	2.15E-07	0.95	3.71	-	1369.3
AHQ-4-12, 3129 - 3195	K.LNGTDPEDVIR.H	1229.32195	2	7.84E-05	0.82	3.36	-	739.6
AHQ-4-13, 3318	K.LNGTDPEDVIR.H	1229.32195	2	4.60E-05	0.93	3.39	-	1310.5
AHQ-4-11, 2936 - 2937	K.LNGTDPEDVIR.H	1229.32195	2	4.59E-07	0.91	3.36	-	1039.2
gi|5032161|ref|NP_005639.1| elongin C; transcription elongation factor B (SIII), polypeptide 1 (15k				2.24E-07	2.77	30.25	30.40	12473.1
AHQ-4-13, 4865 - 4944	K.AMLSGPGQFAENETNEVNFR.E	2212.38515	2	1.28E-06	0.92	5.05	-	1257.1
AHQ-4-13, 4948	K.AMLSGPGQFAENETNEVNFR.E	2212.38515	2	3.64E-07	0.92	3.91	-	1001.6
AHQ-4-13-, 4481	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	5.60E-07	0.93	4.29	-	981.9
AHQ-4-13-, 4829	K.AMLSGPGQFAENETNEVNFR.E	2212.38515	2	2.24E-07	0.93	4.53	-	1013.6
AHQ-4-13-, 2714	K.TYGGCEGPDAM*YVK.L	1565.70692	2	2.59E-04	0.89	3.93	-	521.3
AHQ-4-13, 2830	K.TYGGCEGPDAM*YVK.L	1565.70692	2	3.81E-07	0.90	3.59	-	808.0
gi|4757826|ref|NP_004039.1| beta-2-microglobulin [Homo sapiens]				2.26E-07	2.47	30.24	35.30	13714.5
AHQ-4-14-, 6577 - 6650	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	3	4.86E-06	0.87	4.61	-	558.5
AHQ-4-14-, 2034	K.VEHSDLSFSK.D	1149.23530	1	2.26E-07	0.72	2.97	-	437.6
AHQ-4-14-, 1886	R.VNHVTLSQPK.I	1123.28735	1	1.44E-05	0.41	2.33	-	296.9
AHQ-4-14-, 1805	R.VNHVTLSQPK.I	1123.28735	1	1.79E-04	0.55	2.62	-	223.5
AHQ-4-14-, 1757	R.VNHVTLSQPK.I	1123.28735	2	9.66E-07	0.88	2.74	-	947.4
AHQ-4-14-, 1709	R.VNHVTLSQPK.I	1123.28735	1	1.68E-05	0.56	2.52	-	377.2
gi|17318569|ref|NP_006112.2| keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]				2.28E-07	4.63	50.22	9.50	66066.3
AHQ-4-1, 4090	K.LNDLEDALQQAK.E	1358.47963	2	8.85E-07	0.95	4.37	-	1609.1
AHQ-4-1, 3861	K.QISNLQQSISDAEQR.G	1717.81950	2	2.28E-07	0.91	3.96	-	722.7
AHQ-4-1, 6385	R.SLDLDSIIAEVK.A	1303.48388	2	1.55E-06	0.93	3.72	-	1247.4
AHQ-4-1, 4734	K.WELLQQVDTSTR.T	1476.61621	2	1.52E-05	0.90	3.43	-	1128.6
AHQ-4-1, 3093	K.YEELQITAGR.H	1180.29253	2	5.04E-06	0.95	3.68	-	1771.5
gi|20127517|ref|NP_009148.2| programmed cell death 10; apoptosis-related protein 15 [Homo sapiens]				2.36E-07	1.59	20.16	17.50	24701.4
AHQ-4-10, 3835	R.LIHQTNLILQTFK.T	1569.87265	2	5.73E-05	0.84	3.04	-	682.5
AHQ-4-10, 4985	R.MAADDVEEYMIERPEPEFQDLNEK.A	2900.14441	2	2.36E-07	0.75	3.16	-	509.3
gi|6680033|ref|NP_031379.1| guanine nucleotide binding protein (G protein) alpha 12 [Homo sapiens]				2.39E-07	0.74	10.14	2.90	44250.9
AHQ-4-8, 2757	K.ILLLGAGESGK.S	1058.25357	1	2.39E-07	0.74	2.52	-	784.9
gi|7705849|ref|NP_057215.1| ras-related GTP-binding protein RAB10; ras-related GTP-binding protein				2.39E-07	2.52	30.22	21.00	22540.8
AHQ-4-11, 6202 - 6214	K.AFLTLAEDILR.K	1262.47982	2	5.09E-07	0.96	4.42	-	1520.4
AHQ-4-11, 6966	R.FSDDAFNTTFISTIGIDFK.I	2140.33380	2	2.39E-07	0.67	3.93	-	621.3
AHQ-4-11, 1753	R.NIDEHANEDVER.M	1441.44245	2	4.04E-05	0.90	3.62	-	827.0
gi|5032007|ref|NP_005850.1| purine-rich element binding protein A; purine-rich single-stranded DNA-				2.42E-07	0.86	10.17	8.10	34910.5
AHQ-4-8, 4419	K.LIDDYGVEEEPAELPEGTSLTVDNKR.F	2891.09052	3	2.42E-07	0.86	3.48	-	987.4
gi|4504743|ref|NP_002194.1| integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o				2.46E-07	2.57	30.22	5.90	129294.4
AHQ-4-3, 4839 - 4915	K.KGILGQHQFLEGPEGIENTR.F	2224.46193	2	3.53E-05	0.91	4.46	-	677.7
AHQ-4-3, 7001	R.STNINFYEISSDGNVPSIVHSFEDVGPK.F	3054.26956	3	9.84E-04	0.81	3.85	-	1021.7
AHQ-4-3, 5263	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	2.46E-07	0.85	3.46	-	719.7
AHQ-4-4, 5226	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	1.73E-06	0.89	3.73	-	739.1
AHQ-4-5, 5093	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	4.46E-04	0.80	3.12	-	717.1
AHQ-4-1, 5190 - 5261	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	2.41E-05	0.90	3.94	-	764.5
gi|4885417|ref|NP_005330.1| huntingtin interacting protein 2; ubiquitin-conjugating enzyme E2-25 KD				2.54E-07	2.54	30.18	19.00	22406.5
AHQ-4-11, 2769 - 2780	R.GEIAGPPDTPYEGGR.Y	1516.59406	2	2.54E-07	0.81	3.45	-	568.1
AHQ-4-11, 3449	K.IPETYPFNPPK.V	1303.48726	2	7.77E-04	0.81	2.95	-	770.9
AHQ-4-11, 4600 - 4608	K.VDLVDENFTELR.G	1450.57553	2	3.69E-06	0.92	3.65	-	869.3
gi|4506405|ref|NP_002872.1| v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP				2.69E-07	1.89	20.27	15.50	23408.4
AHQ-4-10, 3328	R.SKAEEWGVQYVETSAK.T	1812.95765	2	2.69E-07	0.97	5.49	-	1466.8
AHQ-4-10, 3197	R.VKAEEDKIPLLVVGNK.S	1753.07630	2	2.21E-05	0.92	4.21	-	938.5
gi|4757768|ref|NP_004300.1| Rho GDP dissociation inhibitor (GDI) alpha [Homo sapiens]				2.75E-07	1.82	20.26	8.30	23206.9
AHQ-4-10, 3536 - 3539	K.SIQEIQELDKDDESLR.K	1919.03693	2	2.75E-07	0.96	5.11	-	950.2
AHQ-4-10, 3128 - 3131	K.SIQEIQELDKDDESLRK.Y	2047.20984	3	7.50E-04	0.72	3.65	-	577.4
AHQ-4-10, 3120	K.SIQEIQELDKDDESLRK.Y	2047.20984	2	7.48E-05	0.86	4.16	-	710.7
gi|4502985|ref|NP_001854.1| cytochrome c oxidase subunit VIb; human cytochrome oxidase subunit VIb				2.77E-07	0.97	10.28	20.90	10192.3
AHQ-4-14-, 6098	R.VYQSLCPTSWVTDWDEQR.A	2272.43560	2	2.77E-07	0.97	5.62	-	1191.2
AHQ-4-14-, 6026 - 6095	R.VYQSLCPTSWVTDWDEQR.A	2272.43560	2	1.04E-04	0.71	3.07	-	410.5
gi|20532885|ref|XP_086931.2| similar to epsilon isoform of 14-3-3 protein [Homo sapiens]				2.79E-07	0.97	10.25	4.70	29380.0
AHQ-4-9, 6357	K.LICCDILDVLDK.H	1479.74157	1	5.43E-05	0.84	4.22	-	548.8
AHQ-4-10, 6243 - 6251	K.LICCDILDVLDK.H	1479.74157	2	6.30E-05	0.92	3.91	-	700.3
AHQ-4-9, 6348 - 6353	K.LICCDILDVLDK.H	1479.74157	2	2.79E-07	0.97	5.06	-	1061.3
gi|20127454|ref|NP_004035.2| 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cy				2.88E-07	0.97	10.23	3.20	64615.5
AHQ-4-6, 3092	K.HVSPAGAAVGIPLSEDEAK.V	1849.03467	2	2.88E-07	0.97	4.60	-	1983.3
gi|4507767|ref|NP_003326.1| ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi				2.93E-07	3.26	40.22	7.40	111719.5
AHQ-4-5, 7285 - 7290	R.GLNPDLQVIPLTYPLDPTTEHIYGDNFFSR.V	3434.79811	3	9.20E-06	0.71	3.85	-	305.0
AHQ-4-4, 4296	R.HSYLHLAENYLIR.Y	1629.84351	2	3.59E-06	0.86	2.99	-	1001.6
AHQ-4-4, 4278	R.VTELVQQLTGQAPAPGQR.V	1894.12181	2	5.34E-04	0.91	4.22	-	796.8
AHQ-4-4, 4040 - 4098	R.YFPSTAEHTLQWAR.H	1707.86959	2	2.93E-07	0.78	3.42	-	464.7
gi|4502099|ref|NP_001143.1| solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra				2.95E-07	0.95	10.22	5.00	32895.0
AHQ-4-10, 4080	R.KGTDIMYTGTLDCWR.K	1819.05212	2	2.95E-07	0.95	4.45	-	1121.2
gi|22267436|ref|NP_056284.1| DKFZp564D177 protein [Homo sapiens]				2.95E-07	1.83	20.22	13.00	28466.4
AHQ-4-11, 6337	K.DKEWQEQFLIPNLALIDK.Q	2201.50664	2	2.95E-07	0.94	4.48	-	879.9
AHQ-4-10, 5992 - 6016	K.DKEWQEQFLIPNLALIDK.Q	2201.50664	2	9.55E-04	0.87	4.18	-	504.4
AHQ-4-11, 3608	K.LVGVFHTEYGALNR.V	1576.78061	2	2.82E-04	0.89	3.44	-	809.4
gi|5729808|ref|NP_006557.1| adhesion glycoprotein; platelet and T cell activation antigen 1; DNAX a				3.05E-07	0.96	10.23	6.00	38583.7
AHQ-4-6, 4794	K.IGTQQDSIAIFSPTHGMVIR.K	2172.49357	3	3.05E-07	0.96	4.55	-	1921.5
gi|6598323|ref|NP_001485.2| GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom				3.07E-07	2.63	30.31	12.80	50662.9
AHQ-4-6, 7208	K.FDLGQDVIDFTGHALALYR.T	2152.39418	2	7.16E-04	0.70	2.91	-	743.5
AHQ-4-7, 5271	R.NPYYGGESASITPLEDLYK.R	2118.28499	2	2.15E-06	0.96	4.66	-	1562.4
AHQ-4-6, 6822 - 6826	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	3.07E-07	0.97	5.69	-	1027.3
AHQ-4-7, 6911 - 6925	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.77E-05	0.96	5.07	-	927.9
AHQ-4-8, 6606 - 6613	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.02E-04	0.98	6.13	-	1147.4
AHQ-4-9, 6245	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	2.78E-04	0.94	4.28	-	906.2
AHQ-4-3, 7153	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.01E-04	0.87	3.76	-	562.7
gi|15147250|ref|NP_150281.1| protein phosphatase 1, regulatory (inhibitor) subunit 14A; 17-kDa PKC-				3.15E-07	0.88	10.22	10.90	16692.9
AHQ-4-12, 6826	K.SCGKPVEDFIQELLAK.L	1836.09909	2	3.15E-07	0.88	4.32	-	493.9
gi|4505753|ref|NP_002620.1| phosphoglycerate mutase 1 (brain); Phosphoglycerate mutase A, nonmuscle				3.16E-07	3.11	40.22	30.70	28803.7
AHQ-4-10, 3675 - 3685	R.FSGWYDADLSPAGHEEAK.R	1981.06697	2	1.75E-04	0.82	3.38	-	669.6
AHQ-4-10, 3859	K.NLKPIKPMQFLGDEETVR.K	2116.46992	2	7.17E-04	0.83	4.13	-	408.5
AHQ-4-10, 4068 - 4072	R.SYDVPPPPMEPDHPFYSNISK.D	2418.66566	2	3.32E-04	0.56	2.95	-	248.4
AHQ-4-10, 4525 - 4591	R.YADLTEDQLPSCESLKDTIAR.A	2427.62735	2	3.16E-07	0.90	4.45	-	449.3
gi|6912494|ref|NP_036457.1| microtubule-associated protein, RP/EB family, member 1; ADENOMATOUS POL				3.50E-07	3.68	40.29	21.60	29998.9
AHQ-4-12, 3954	K.FFDANYDGKDYDPVAAR.Q	1965.06754	2	3.64E-07	0.89	3.92	-	620.3
AHQ-4-12, 6599	K.FQDNFEFVQWFK.K	1635.80184	2	3.02E-05	0.96	4.19	-	1525.9
AHQ-4-12, 2578	K.LEHEYIQNFK.I	1321.46268	2	3.50E-07	0.84	3.31	-	901.7
AHQ-4-13-, 4561	R.NIELICQENEGENDPVLQR.I	2272.43545	2	1.27E-06	0.98	5.89	-	1724.6
AHQ-4-13, 4553	R.NIELICQENEGENDPVLQR.I	2272.43545	2	3.22E-05	0.96	4.82	-	1429.7
gi|4503423|ref|NP_001939.1| dUTP pyrophosphatase [Homo sapiens]				3.64E-07	0.95	10.21	10.40	17748.0
AHQ-4-11, 5448 - 5454	R.IFYPEIEEVQALDDTER.G	2068.22598	2	3.64E-07	0.95	4.22	-	1372.8
gi|4503643|ref|NP_000121.1| coagulation factor V precursor; labile factor; factor V Leiden [Homo sa				3.64E-07	0.93	10.19	0.70	251716.5
AHQ-4-1, 5117 - 5189	R.GEYEEHLGILGPIIR.A	1696.92816	2	3.64E-07	0.93	3.83	-	1243.9
gi|13786129|ref|NP_112586.1| RAB33B, member RAS oncogene family; likely ortholog of mouse RAB33b [H				3.76E-07	0.82	10.15	4.80	25717.4
AHQ-4-13, 3614	K.IQLWDTAGQER.F	1317.43243	1	3.60E-04	0.06	1.85	-	234.8
AHQ-4-13-, 3481	K.IQLWDTAGQER.F	1317.43243	2	3.76E-07	0.82	3.06	-	749.1
AHQ-4-10, 3172	K.IQLWDTAGQER.F	1317.43243	1	4.06E-04	0.40	2.90	-	289.6
gi|4758038|ref|NP_004246.1| cytochrome c oxidase subunit Va precursor; cytochrome c oxidase polypep				3.81E-07	0.97	10.21	10.00	16774.1
AHQ-4-13-, 4769 - 4836	K.GINTLVTYDMVPEPK.I	1677.94342	2	4.99E-04	0.65	2.72	-	769.3

AHQ-4-13, 4886 - 4956	K.GINTLVTYDMVPEPK.I	1677.94342	2	3.81E-07	0.97	4.23	-	1744.5
gi|5174539|ref|NP_005908.1|	cytosolic malate dehydrogenase; soluble malate dehydrogenase [Homo sapi			3.86E-07	1.50	20.16	8.40	36425.9
AHQ-4-13, 3134	K.DVIATDKEDVAFK.D	1451.60343	2	1.81E-05	0.78	2.71	-	841.4
AHQ-4-9, 4637	K.EVGVYEALKDDSWLK.G	1752.94535	2	3.86E-07	0.73	3.07	-	800.2
gi|22059949|ref|XP_114617.2|	similar to tubulin, beta 5 [Homo sapiens]			3.86E-07	1.38	20.31	13.00	22810.8
AHQ-4-7, 5317	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	2.40E-05	0.95	5.65	-	1172.6
AHQ-4-13-, 5233	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	7.62E-05	0.78	3.78	-	677.3
AHQ-4-12, 5342 - 5354	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	2.85E-05	0.95	5.36	-	1428.9
AHQ-4-13, 5390	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	6.06E-04	0.91	4.50	-	1019.3
AHQ-4-14-, 5194	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	4.94E-06	0.97	6.18	-	1552.0
AHQ-4-13, 2862	R.ISVYYNEATGGK.Y	1302.41453	1	3.86E-07	0.41	2.50	-	256.4
AHQ-4-12, 2703	R.ISVYYNEATGGK.Y	1302.41453	2	3.22E-04	0.78	2.71	-	762.8
AHQ-4-7, 2453	R.ISVYYNEATGGK.Y	1302.41453	2	1.22E-06	0.84	2.53	-	845.8
gi|16950601|ref|NP_005956.2|	myosin light chain kinase isoform 6; myosin light chain kinase [Homo s			4.09E-07	1.21	20.19	2.60	110074.8
AHQ-4-6, 4856	R.STSFNVQDLLPDHEYK.F	1894.03076	2	1.79E-06	0.32	2.59	-	336.0
AHQ-4-6, 3316	K.VSDFYDIEER.L	1273.33005	2	4.09E-07	0.89	2.62	-	1061.8
gi|4504521|ref|NP_002147.1|	heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P			4.10E-07	0.93	10.20	4.90	61024.2
AHQ-4-14-, 6833	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D	2870.28530	3	4.10E-07	0.93	3.97	-	1467.3
gi|18765729|ref|NP_003816.2|	synaptosomal-associated protein 23 isoform SNAP23A; synaptosomal-assoc			4.17E-07	0.95	10.18	6.60	23353.9
AHQ-4-12, 4459	R.ILGLAIESQDAGIK.T	1428.65614	2	4.17E-07	0.95	3.63	-	1451.2
gi|4502013|ref|NP_001616.1|	adenylate kinase 2 isoform a; adenylate kinase, mitochondrial; adenylat			4.37E-07	2.01	30.19	21.80	26477.6
AHQ-4-10, 6127	K.EKLDSVIEFSIPDSLLIR.R	2075.39107	2	1.08E-04	0.85	3.79	-	707.1
AHQ-4-10, 3623 - 3680	R.LQAYHTQTTPLIEYYR.K	1998.22695	2	1.59E-05	0.88	3.77	-	829.4
AHQ-4-10, 5519	K.NLETPLCKNGFLLDGFPR.T	2093.39146	2	4.37E-07	0.28	2.65	-	354.4
gi|19923262|ref|NP_004153.2|	RAB5A, member RAS oncogene family; RAS-associated protein RAB5A [Homo			4.38E-07	0.92	10.21	5.10	23658.5
AHQ-4-10, 3239 - 3241	K.LVLLGESAVGK.S	1086.30692	2	4.38E-07	0.92	4.25	-	1052.3
gi|4507747|ref|NP_003321.1|	thioredoxin reductase 1 [Homo sapiens]			4.48E-07	0.95	10.27	7.20	54419.1
AHQ-4-7, 7421 - 7423	K.IPVTDEEQTNVPYIYAIGDILEDKVELTPVAIQAGR.L	3972.44634	3	4.48E-07	0.95	5.47	-	1019.1
gi|4505409|ref|NP_002503.1|	non-metastatic cells 2, protein (NM23B) expressed in; Non-metastatic ce			4.66E-07	1.77	20.20	12.50	17297.9
AHQ-4-12, 6071 - 6149	K.EISLWFKPEELVDYK.S	1897.15929	2	5.20E-04	0.92	4.04	-	842.0
AHQ-4-12, 6166 - 6238	K.EISLWFKPEELVDYK.S	1897.15929	2	4.66E-07	0.90	3.70	-	747.3
AHQ-4-12, 5794	K.SAEKEISLWFKPEELVDYK.S	2312.60263	3	7.16E-04	0.86	3.85	-	620.3
gi|4506417|ref|NP_002877.1|	RAP2B, member of RAS oncogene family [Homo sapiens]			4.73E-07	5.18	60.23	39.90	20494.2
AHQ-4-11, 5026 - 5028	K.ALAEEWSCPFMETSAK.N	1859.06988	2	8.37E-05	0.95	4.52	-	969.8
AHQ-4-11, 6033	K.ASVDELFAEIVR.Q	1349.51434	2	2.19E-06	0.93	3.54	-	1435.9
AHQ-4-11, 2633	K.VDLEGEREVSYGEGK.A	1667.75571	2	2.95E-04	0.92	3.79	-	984.5
AHQ-4-11, 3022	R.VPMILVGNK.V	971.24256	2	2.18E-05	0.87	2.66	-	791.2
AHQ-4-11, 2285	K.VVVLGSGGVGK.S	972.16391	2	1.18E-05	0.77	2.97	-	767.9
AHQ-4-11, 4122	K.YDPTIEDFYR.K	1319.40042	2	4.73E-07	0.75	2.61	-	421.3
gi|5453714|ref|NP_006448.1|	LIM protein (similar to rat protein kinase C-binding enigma) [Homo sapi			5.16E-07	0.65	10.17	2.50	64027.9
AHQ-4-13-, 2846	K.EVVKPVPITSPAVSK.V	1551.85241	2	7.35E-05	0.82	3.32	-	366.2
AHQ-4-13, 2961	K.EVVKPVPITSPAVSK.V	1551.85241	2	5.16E-07	0.65	2.81	-	274.8
gi|4885183|ref|NP_005210.1|	diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS			5.17E-07	3.64	50.24	5.90	138977.7
AHQ-4-3, 5348	K.LVAEDLSQDCFWTK.V	1713.88927	2	2.09E-06	0.82	3.28	-	613.1
AHQ-4-3, 7607	R.M*EMDDFNEVFQILLNTVK.D	2203.52145	2	9.18E-06	0.85	4.58	-	912.0
AHQ-4-3, 6037	K.TAQNLSIFLGSFR.M	1454.65537	2	2.35E-05	0.62	2.76	-	467.6
AHQ-4-3, 7540	K.VGCLQLINALITPAEELDFR.V	2274.62236	2	5.17E-07	0.95	4.82	-	768.3
AHQ-4-3, 7540	K.VGCLQLINALITPAEELDFRVHIRSELM*R.L	3412.97170	3	6.27E-04	0.40	3.03	-	178.9
gi|4505585|ref|NP_002563.1|	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30			5.19E-07	0.96	10.23	8.70	25569.1
AHQ-4-10, 6355	K.ICKPLHELIMQLLEETPEEK.Q	2452.87287	2	5.19E-07	0.96	4.65	-	1475.1
gi|30151001|ref|XP_170195.2|	similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl			5.56E-07	0.72	10.14	2.60	46759.8
AHQ-4-10, 3429	R.AAYFGIYDTAK.G	1220.35512	2	1.22E-06	0.91	2.68	-	1118.4
AHQ-4-10, 3393 - 3423	R.AAYFGIYDTAK.G	1220.35512	1	5.56E-07	0.72	2.75	-	487.9
gi|18201911|ref|NP_000629.2|	vitronectin precursor; serum spreading factor; somatomedin B; compleme			5.57E-07	0.93	10.22	3.10	54335.4
AHQ-4-13, 5769 - 5838	R.SIAQYWLGCPAPGHL	1671.90045	2	5.57E-07	0.93	4.42	-	651.9
gi|7705501|ref|NP_057546.1|	hypothetical protein HSPC194 [Homo sapiens]			5.69E-07	2.64	30.21	41.10	11564.5
AHQ-4-14-, 6807	K.AGSVPSLAAGLLFGSLAGLGAYQLSQDPR.N	2818.17710	2	5.69E-07	0.71	3.37	-	514.9
AHQ-4-14-, 6273 - 6293	K.FMPAGLIAGASLLM*VAK.V	1707.13765	2	9.65E-06	0.95	4.00	-	1269.4
AHQ-4-14-, 5857	K.FM*PAGLIAGASLLM*VAK.V	1723.13705	2	4.32E-06	0.98	4.25	-	2460.7
gi|5031571|ref|NP_005713.1|	actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog			5.86E-07	7.05	80.27	29.90	44760.5
AHQ-4-8, 5522	K.CGYAGSNFPEHIFPALVGRPIIR.S	2573.95654	3	1.56E-05	0.83	3.89	-	939.2
AHQ-4-8, 3481 - 3549	K.DLMVGDEASELR.S	1335.46633	2	2.76E-05	0.91	3.35	-	1095.9
AHQ-4-8, 2794	R.GYAFNHSADFETVR.M	1614.69943	2	5.86E-07	0.90	3.72	-	983.7
AHQ-4-10, 3080	R.GYAFNHSADFETVR.M	1614.69943	2	1.63E-04	0.87	3.65	-	734.6
AHQ-4-8, 3418	K.HIVLSGGSTMYPGLPSR.L	1773.04967	2	1.76E-05	0.98	5.33	-	2102.8
AHQ-4-8, 3706	K.HLWDYTFGPEK.L	1393.52736	2	3.84E-06	0.90	3.35	-	697.4
AHQ-4-8, 2497	R.KVVVCDNGTGFVK.C	1424.64764	2	3.79E-05	0.93	3.95	-	1036.2
AHQ-4-8, 3550 - 3557	K.LCYVGYNIEQEQK.L	1645.81494	2	1.33E-06	0.96	4.23	-	1315.3
AHQ-4-8, 4069 - 4147	R.SM*LEVNYPMENGIVR.N	1769.03643	2	1.32E-05	0.65	3.41	-	489.8
gi|5453970|ref|NP_006245.1|	protein kinase C, delta [Homo sapiens]			6.33E-07	0.64	10.15	1.80	77476.6
AHQ-4-6, 3895	K.LLAEALNQVTQR.A	1356.55324	2	6.33E-07	0.64	2.62	-	833.4
gi|5453760|ref|NP_006147.1|	neural precursor cell expressed, developmentally down-regulated 8 [Homo			6.57E-07	0.77	10.17	17.30	9071.5
AHQ-4-14-, 3609	K.EIEIDIEPTDKVER.I	1686.84208	2	6.57E-07	0.77	3.48	-	345.5
gi|7705266|ref|NP_057537.1|	SH3 protein interacting with Nck, 90 kDa; SH3 protein; SH3 protein inte			6.67E-07	0.97	10.26	2.80	78959.8
AHQ-4-13-, 6821	R.SAEPNALAFAAGETFLVLER.S	2107.35171	2	6.67E-07	0.97	5.26	-	1674.7
gi|21614499|ref|NP_003370.2|	villin 2; Villin-2; cytovillin [Homo sapiens]			6.85E-07	2.65	30.21	3.40	69412.3
AHQ-4-6, 4138	K.APDFVFYAPR.L	1183.33971	2	1.33E-06	0.98	4.26	-	2025.8
AHQ-4-6, 4946 - 4971	K.IGFPWSEIR.N	1105.27049	2	1.05E-04	0.90	2.90	-	972.4
AHQ-4-6, 3460	K.KAPDFVFYAPR.L	1311.51262	2	6.85E-07	0.77	2.86	-	594.4
gi|17450333|ref|XP_060887.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			6.87E-07	0.97	10.24	11.00	17503.9
AHQ-4-12, 6701	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	6.87E-07	0.97	4.84	-	1655.1
AHQ-4-14-, 6278	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	8.95E-04	0.74	3.01	-	551.0
AHQ-4-12, 6477 - 6497	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	4.35E-06	0.81	3.44	-	560.6
gi|4503481|ref|NP_001395.1|	eukaryotic translation elongation factor 1 gamma; elongation factor 1-g			6.92E-07	0.91	10.19	3.20	50118.5
AHQ-4-12, 2582	R.KLDPGSEETQTLVR.E	1573.73020	2	1.21E-06	0.71	3.39	-	380.0
AHQ-4-8, 2249	R.KLDPGSEETQTLVR.E	1573.73020	2	6.92E-07	0.91	3.78	-	630.4
gi|4557385|ref|NP_000055.1|	complement component 3 precursor; acylation-stimulating protein cleavag			6.98E-07	0.80	10.19	1.00	187162.3
AHQ-4-6, 4716	R.SGIPIVTSPYQIHFTK.T	1789.06720	2	6.98E-07	0.80	3.23	-	522.4
gi|7706314|ref|NP_057107.1|	CGI-77 protein [Homo sapiens]			7.17E-07	0.85	10.21	9.70	33425.0
AHQ-4-11, 6668	R.ALSHILQTPIEIIQADSPPIIVGEEYSK.K	3063.49045	3	7.17E-07	0.85	4.28	-	815.9
gi|20551618|ref|XP_167021.1|	similar to calponin 2; Calonin 2 [Homo sapiens]			7.24E-07	1.87	20.26	3.70	47327.9
AHQ-4-12, 5649 - 5650	R.SMQNWHQLENLSNFIK.A	1990.23155	2	8.96E-06	0.96	5.25	-	1093.9
AHQ-4-12, 5306 - 5385	R.SM*QNWHQLENLSNFIK.A	2006.23095	2	7.24E-07	0.91	3.98	-	786.1
gi|14765644|ref|XP_037574.1|	similar to PTPL1-associated RhoGAP 1 [Homo sapiens]			7.29E-07	0.91	10.22	2.90	124613.7
AHQ-4-13-, 6896	R.SPLTAASPGELPTEGAGPDVVEDISHLLADVAR.F	3286.59214	3	7.29E-07	0.91	4.35	-	828.5
gi|4502097|ref|NP_001142.1|	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra			7.48E-07	2.29	30.15	16.80	33148.4
AHQ-4-10, 3103	R.AAYFGVYDTAK.G	1206.32845	2	2.83E-06	0.75	2.71	-	577.2
AHQ-4-10, 6431	R.YFAGNLASGGAAGATSLCFVYPLDFAR.T	2799.10926	2	2.84E-05	0.69	3.10	-	444.7
AHQ-4-14-, 5679	R.YFPTQALNFAFK.D	1447.66130	2	2.67E-05	0.86	2.90	-	681.0
AHQ-4-10, 5172 - 5191	R.YFPTQALNFAFK.D	1447.66130	2	7.48E-07	0.85	3.06	-	614.4
gi|5453710|ref|NP_006139.1|	LIM and SH3 protein 1; Lasp-1 [Homo sapiens]			7.56E-07	0.88	10.17	5.00	29717.0
AHQ-4-13, 4094	K.GFSVVADTPELQR.I	1419.56466	1	4.15E-04	0.07	2.11	-	172.7
AHQ-4-13, 4084	K.GFSVVADTPELQR.I	1419.56466	2	7.56E-07	0.88	3.31	-	954.9
gi|4758076|ref|NP_004068.1|	citrate synthase precursor; Citrate synthase, mitochondrial [Homo sapie			7.66E-07	1.67	20.16	5.80	51706.2
AHQ-4-8, 4378	K.GLVYETSVLDPDEGIR.F	1763.92654	2	3.45E-06	0.82	3.27	-	628.8
AHQ-4-8, 2997	K.IVPNVLLEQGK.A	1210.44805	2	7.66E-07	0.85	2.73	-	476.3
gi|20270259|ref|NP_620061.1|	phosphoglycerate kinase 2; phosphoglycerate kinase 1, pseudogene 2 [Ho			7.89E-07	0.90	10.19	3.60	44895.0

AHQ-4-8, 3191 - 3234	K.LGDVYVNDAFGTAHR.A	1635.76178	2	7.89E-07	0.90	3.78	-	821.5
gi|28827809|ref|NP_789797.1| nucleoside diphosphate kinase B-like [Homo sapiens]				8.04E-07	3.14	50.19	29.20	15529.0
AHQ-4-12, 3339	R.GDFCIQVGR.N	1053.17404	2	6.90E-05	0.92	3.64	-	1046.3
AHQ-4-12, 3355	R.GDFCIQVGR.N	1053.17404	1	7.33E-06	0.26	1.99	-	271.9
AHQ-4-12, 1651	R.NIIHGSDSVK.S	1070.18131	1	8.29E-04	0.40	1.99	-	340.5
AHQ-4-12, 2090	R.NIIHGSDSVKSAEK.E	1485.62464	2	9.27E-07	0.83	3.70	-	828.8
AHQ-4-12, 2089	R.NIIHGSDSVKSAEK.E	1485.62464	1	1.24E-04	0.66	3.43	-	470.8
AHQ-4-12, 2758 - 2837	R.VMLGETNPADSKPGTIR.G	1787.03151	2	2.76E-05	0.79	3.88	-	455.3
AHQ-4-12, 2573	R.VM*LGETNPADSKPGTIR.G	1803.03091	3	8.04E-07	0.86	3.67	-	681.2
AHQ-4-12, 2571	R.VM*LGETNPADSKPGTIR.G	1803.03091	2	1.40E-04	0.51	2.83	-	515.9
gi|4506765|ref|NP_002952.1| S100 calcium-binding protein A4; 18A2; 42A; S100 calcium-binding protei				8.04E-07	1.92	20.19	10.90	11728.5
AHQ-4-14-, 3371	K.ALDVMVSTFHK.Y	1248.47665	2	2.58E-05	0.96	3.88	-	1657.9
AHQ-4-14-, 2757 - 2769	K.ALDVM*VSTFHK.Y	1264.47605	2	8.04E-07	0.96	3.81	-	1535.0
gi|4826659|ref|NP_004921.1| F-actin capping protein beta subunit; Cap Z [Homo sapiens]				8.23E-07	1.84	20.20	10.30	30628.5
AHQ-4-9, 3587	K.GCWDSIHVVEVQEK.S	1687.85505	2	8.23E-07	0.93	3.97	-	1387.4
AHQ-4-10, 3148	R.KLEVEANNAFDQYR.D	1697.82988	2	3.81E-05	0.91	3.26	-	1178.6
gi|4502693|ref|NP_001760.1| CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen				8.28E-07	1.73	20.30	10.10	25415.9
AHQ-4-6, 3035 - 3080	K.KDVLETFTVK.S	1180.37558	2	7.70E-04	0.59	2.64	-	661.0
AHQ-4-10, 3016	K.KDVLETFTVK.S	1180.37558	2	3.62E-05	0.84	3.00	-	863.1
AHQ-4-11, 3134	K.KDVLETFTVK.S	1180.37558	2	7.61E-05	0.85	3.23	-	904.5
AHQ-4-12, 3215	K.KDVLETFTVK.S	1180.37558	2	8.28E-07	0.86	2.97	-	912.0
AHQ-4-13-, 3396	K.KDVLETFTVK.S	1180.37558	2	2.30E-04	0.76	2.54	-	814.6
AHQ-4-13, 3527	K.KDVLETFTVK.S	1180.37558	2	4.60E-04	0.89	2.95	-	1078.9
AHQ-4-1, 3529	K.KDVLETFTVK.S	1180.37558	2	1.24E-05	0.75	2.75	-	791.5
AHQ-4-12, 3755	K.SCPDAIKEVFDNK.F	1524.67770	2	3.94E-04	0.87	3.46	-	773.6
gi|22538465|ref|NP_002786.2| proteasome beta 3 subunit; proteasome theta chain; proteasome chain 13				8.32E-07	1.80	20.24	16.60	22948.8
AHQ-4-10, 4728 - 4735	R.FGPYYTEPVIAGLDPK.T	1768.00162	2	8.32E-07	0.84	3.08	-	859.6
AHQ-4-10, 5783	R.LYIGLAGLATDVQTVAQR.L	1890.17306	2	8.56E-05	0.96	4.80	-	1731.9
gi|4557327|ref|NP_000033.1| beta-2-glycoprotein I precursor [Homo sapiens]				8.33E-07	0.76	10.18	7.20	38312.0
AHQ-4-7, 7379 - 7383	K.WSPELPVCAPIICPPPSIPTFATLR.V	2823.32174	2	8.33E-07	0.76	3.64	-	387.7
gi|6912238|ref|NP_036226.1| peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]				8.42E-07	4.22	50.25	16.80	22026.2
AHQ-4-12, 3875	R.FSMVVQDGIVK.A	1223.46709	2	8.42E-07	0.96	3.75	-	1502.4
AHQ-4-12, 5307 - 5369	K.GVLFGVPGAFTPGCSK.T	1595.84389	2	3.35E-04	0.65	2.72	-	453.7
AHQ-4-12, 4667	K.KGVLFGVPGAFTPGCSK.T	1724.01680	2	4.71E-04	0.95	5.00	-	779.8
AHQ-4-12, 3399	R.LLADPTGAFGK.E	1090.25413	2	1.38E-05	0.79	3.25	-	466.9
AHQ-4-12, 4749	K.VNLAELFK.G	934.11414	2	5.35E-05	0.86	2.91	-	849.7
gi|10880136|ref|NP_004032.2| arrestin beta 1 isoform A [Homo sapiens]				8.42E-07	1.87	20.24	10.50	47065.3
AHQ-4-7, 4391	K.CPVAMEEADDTVAPSSTFCK.V	2218.42489	2	4.68E-06	0.93	4.79	-	839.6
AHQ-4-7, 7255 - 7333	R.DFVDHIDLVDPVDGVVLVDPEYLK.E	2713.03129	2	8.42E-07	0.95	4.47	-	1004.8
gi|4504483|ref|NP_000185.1| hypoxanthine phosphoribosyltransferase 1 [Homo sapiens]				8.48E-07	3.58	40.30	33.00	24579.2
AHQ-4-10, 4997	K.NVLIVEDIIDTGK.T	1429.64090	1	3.11E-04	0.83	3.43	-	717.7
AHQ-4-10, 6359	R.SPGVVISDDEPGYDLDLFCIPNHYAEDLER.V	3438.67572	3	8.48E-07	0.95	6.07	-	797.3
AHQ-4-10, 4355	R.SVGYKPDFVGFEIPDK.F	1799.01571	2	5.55E-06	0.93	4.30	-	790.4
AHQ-4-10, 3417	K.VIGGDDLSTLTGK.N	1276.41852	2	7.32E-05	0.86	3.16	-	602.3
gi|7706675|ref|NP_057661.1| RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M				8.78E-07	4.13	50.23	23.60	23461.5
AHQ-4-11, 4577	R.GSDVIIMLVGNK.T	1246.50220	2	7.37E-05	0.94	3.84	-	1407.4
AHQ-4-11, 3241 - 3300	R.LQLWDTAGQER.F	1317.43243	2	1.33E-06	0.93	3.68	-	988.2
AHQ-4-11, 3488 - 3516	K.LVFLGEQSVGK.T	1177.37492	2	8.78E-07	0.86	2.98	-	876.8
AHQ-4-11, 2673	R.RVASALPGMENVQEK.S	1629.86363	2	1.19E-05	0.95	4.63	-	1030.1
AHQ-4-11, 2984	R.VASALPGMENVQEK.S	1473.67727	2	5.69E-06	0.46	2.62	-	212.1
gi|22749499|ref|NP_689979.1| hypothetical protein MGC40107 [Homo sapiens]				9.05E-07	0.97	10.30	24.80	11741.6
AHQ-4-14-, 5595	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	2	1.64E-04	0.95	4.52	-	1501.5
AHQ-4-14-, 5581 - 5594	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	9.05E-07	0.97	5.94	-	1438.7
gi|5803135|ref|NP_006852.1| RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind				9.40E-07	0.94	10.19	5.50	23025.1
AHQ-4-11, 3658	K.LLIIGDSGVGK.S	1072.28025	2	3.18E-04	0.92	3.37	-	1092.8
AHQ-4-13, 3921	K.LLIIGDSGVGK.S	1072.28025	2	1.66E-04	0.81	3.14	-	664.5
AHQ-4-13-, 3788	K.LLIIGDSGVGK.S	1072.28025	2	9.40E-07	0.94	3.74	-	1335.4
AHQ-4-11, 3556 - 3584	K.LLIIGDSGVGK.S	1072.28025	2	7.34E-05	0.94	3.79	-	1223.4
gi|4758484|ref|NP_004823.1| glutathione-S-transferase like; glutathione transferase omega [Homo sap				9.42E-07	1.03	20.18	3.70	27565.7
AHQ-4-9, 2239	K.GSAPPGPVPEGSIR.I	1321.46422	1	1.37E-04	0.12	2.15	-	158.6
AHQ-4-10, 2551	R.HEVININLK.N	1080.26247	2	9.42E-07	0.91	3.50	-	788.0
gi|4502297|ref|NP_001678.1| ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit				9.54E-07	1.72	20.23	13.70	17489.8
AHQ-4-13-, 2525 - 2528	K.AQAELVGTADEATR.A	1432.51860	2	1.13E-06	0.95	4.63	-	1142.0
AHQ-4-13, 2639 - 2641	K.AQAELVGTADEATR.A	1432.51860	1	3.42E-05	0.49	2.91	-	193.6
AHQ-4-12, 2479	K.AQAELVGTADEATR.A	1432.51860	2	9.54E-07	0.91	4.00	-	627.9
AHQ-4-13, 2429	R.IEANEALVK.A	987.13221	2	2.54E-04	0.81	3.23	-	573.3
gi|30158489|ref|XP_301421.1| similar to Chloride intracellular channel protein 1 (Nuclear chloride				9.73E-07	0.76	10.19	6.60	28267.5
AHQ-4-12, 6107 - 6111	K.FLNGNELTLADCNLLPK.L	1934.20276	2	9.73E-07	0.76	3.57	-	603.1
AHQ-4-9, 5663 - 5732	K.FLNGNELTLADCNLLPK.L	1934.20276	2	1.37E-05	0.90	3.73	-	1336.9
gi|18105037|ref|NP_004709.2| cytochrome c oxidase subunit VIIa polypeptide 2 like; estrogen recepto				1.03E-06	0.92	10.26	28.90	12614.6
AHQ-4-13-, 6134	K.LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK.L	3399.87995	3	1.03E-06	0.92	4.83	-	792.7
AHQ-4-14-, 6007	K.LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK.L	3399.87995	3	6.55E-04	0.83	4.14	-	657.5
AHQ-4-13, 6212	K.LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK.L	3399.87995	3	7.49E-05	0.93	5.23	-	574.4
gi|5453597|ref|NP_006126.1| F-actin capping protein alpha-1 subunit; Cap Z [Homo sapiens]				1.08E-06	2.23	30.19	19.90	32922.5
AHQ-4-9, 3737 - 3796	R.EGAAHAFAQYNMDQFTPVK.I	2126.33709	2	5.46E-05	0.72	3.10	-	393.1
AHQ-4-9, 4275 - 4279	K.FITHAPPGEFNEVFNDVR.L	2090.28294	2	3.23E-05	0.67	3.13	-	283.4
AHQ-4-10, 4949	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	5.19E-05	0.69	3.08	-	379.4
AHQ-4-9, 4860 - 4932	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	1.08E-06	0.84	3.82	-	469.0
gi|21361547|ref|NP_002930.2| ribonuclease/angiogenin inhibitor; Placental ribonuclease inhibitor [H				1.10E-06	0.90	10.19	3.30	49973.3
AHQ-4-14-, 6366	R.WAELLPLLQQCQVVR.L	1855.19360	2	1.10E-06	0.90	3.79	-	733.7
gi|10835035|ref|NP_003157.1| sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3; t				1.14E-06	2.48	30.21	22.70	34196.0
AHQ-4-9, 5093 - 5132	K.SHLPLALLPQTLLDQK.V	1788.12388	2	2.81E-04	0.83	3.54	-	652.9
AHQ-4-9, 4592	R.VPFLEVNDPGEPSGLETLKDTPPPR.L	2706.00039	3	2.78E-06	0.79	3.75	-	528.8
AHQ-4-9, 6037 - 6116	K.YFAEALGPLQSFQARPDDLLINTYPK.S	2969.33891	3	1.14E-06	0.85	4.07	-	547.1
gi|19923457|ref|NP_057447.2| glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M				1.23E-06	0.96	10.25	3.20	67308.6
AHQ-4-7, 5387	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	2	5.32E-05	0.92	4.30	-	775.2
AHQ-4-7, 5383	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	1.23E-06	0.96	5.01	-	1552.0
gi|4557797|ref|NP_000260.1| non-metastatic cells 1 protein [Homo sapiens]				1.24E-06	3.23	40.20	21.70	17148.6
AHQ-4-12, 4006	K.DRPFFAGLVK.Y	1150.35439	2	2.60E-05	0.77	2.80	-	851.3
AHQ-4-12, 3181	R.GLVGEIIK.R	829.01947	2	6.04E-04	0.72	3.06	-	510.4
AHQ-4-12, 2802	R.GLVGEIIKR.F	985.20582	2	3.71E-05	0.85	2.72	-	771.4
AHQ-4-12, 2025 - 2091	R.NIIHGSDSVESAEK.E	1486.56627	1	1.24E-06	0.88	4.02	-	505.2
gi|21361565|ref|NP_001679.2| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, is				1.25E-06	1.83	20.22	9.00	28908.4
AHQ-4-11, 2804	R.HYLFDVQR.N	1078.20513	2	1.25E-06	0.92	2.91	-	1260.4
AHQ-4-11, 6858	R.YGLIPEEFFQFLYPK.T	1892.18434	2	1.02E-05	0.91	4.32	-	462.9
gi|10880989|ref|NP_067075.1| RAB18, member RAS oncogene family; RAB18 small GTPase [Homo sapiens] [				1.27E-06	1.71	20.24	14.10	22976.9
AHQ-4-11, 3628	K.IIQTPGLWESENQNK.G	1757.92522	2	4.29E-05	0.77	2.89	-	531.0
AHQ-4-11, 6141	K.LDNWLNELETYCTR.N	1828.98037	2	1.27E-06	0.94	4.88	-	655.7
gi|4506063|ref|NP_002725.1| protein kinase, cAMP-dependent, regulatory, type I, alpha; tissue-speci				1.30E-06	2.37	30.21	10.80	42981.4
AHQ-4-7, 5077 - 5085	R.LTVADALEPVQFEDGQK.I	1861.04222	2	1.73E-05	0.91	4.17	-	568.5
AHQ-4-7, 2859 - 2883	K.NVLFSHLDDNER.S	1459.54574	2	4.86E-05	0.73	2.78	-	610.8
AHQ-4-7, 4922 - 4993	K.VSILESLDKWER.L	1475.67136	2	1.30E-06	0.73	2.74	-	627.5
gi|11496885|ref|NP_005442.2| enigma protein; LIM domain protein [Homo sapiens]				1.32E-06	1.82	20.18	7.20	49844.4
AHQ-4-11, 4644	K.VVLEGPAPWGFR.L	1328.54318	2	1.94E-06	0.92	3.26	-	1065.8
AHQ-4-13-, 4828 - 4830	K.VVLEGPAPWGFR.L	1328.54318	2	1.32E-06	0.92	3.37	-	985.0
AHQ-4-14-, 4787	K.VVLEGPAPWGFR.L	1328.54318	2	2.65E-06	0.75	2.62	-	818.6
AHQ-4-10, 4160	R.YLVALGHAYHPEEFVCSQCGK.V	2468.74928	2	1.65E-06	0.89	3.67	-	721.3

gi|5729804|ref|NP_006694.1| nudix (nucleoside diphosphate linked moiety X)-type motif 3; diphosphoi				1.33E-06	0.86	10.21	9.90	19470.8
AHQ-4-11, 3632	K.VLQYHKPVQASYFETLR.Q	2080.37433	2	1.33E-06	0.86	4.13	-	374.9
gi|19743813|ref|NP_002202.2| integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib				1.38E-06	1.14	20.24	3.10	88414.9
AHQ-4-5, 5118	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	1.38E-06	0.95	4.82	-	1034.6
AHQ-4-3, 5343 - 5416	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	7.65E-04	0.85	3.88	-	596.4
AHQ-4-4, 2348	K.NVLSLTNK.G	889.03177	1	1.84E-04	0.19	2.06	-	218.9
gi|30154095|ref|XP_293967.2| similar to gamma actin-like protein [Homo sapiens]				1.40E-06	1.41	20.19	12.20	19259.0
AHQ-4-8, 4695 - 4773	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.65E-06	0.56	3.01	-	374.2
AHQ-4-8, 4930	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.33E-05	0.30	2.53	-	369.4
AHQ-4-8, 6189 - 6206	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	7.33E-05	0.34	2.86	-	476.9
AHQ-4-13, 4877	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.74E-06	0.56	3.37	-	385.4
AHQ-4-13, 5317	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	2.92E-06	0.82	3.75	-	635.5
AHQ-4-14, 5797	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.40E-06	0.58	3.15	-	425.6
AHQ-4-14, 5908 - 5972	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.15E-05	0.38	2.96	-	336.6
AHQ-4-14, 6097 - 6156	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.68E-06	0.63	3.06	-	613.5
AHQ-4-13-, 4868 - 4872	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.93E-05	0.46	2.71	-	405.8
AHQ-4-14-, 4690 - 4771	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	8.62E-04	0.71	3.40	-	365.5
AHQ-4-14-, 4833 - 4885	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	8.53E-04	0.58	3.07	-	466.2
AHQ-4-14-, 5007 - 5013	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.68E-05	0.72	3.25	-	578.3
gi|19923437|ref|NP_057366.2| adenylate kinase 3 alpha like [Homo sapiens]				1.47E-06	1.85	20.23	12.80	25565.2
AHQ-4-10, 6031	K.NLTQYSWLLDGFPR.T	1710.91339	2	1.47E-06	0.96	4.69	-	1434.1
AHQ-4-10, 4363	K.TVGIDDLTGEPLIQR.E	1627.82100	2	3.17E-04	0.89	3.73	-	788.3
gi|29736622|ref|XP_293924.1| similar to cytoplasmic beta-actin [Homo sapiens]				1.51E-06	3.49	40.26	21.50	42002.9
AHQ-4-8, 6982	R.FRCPEAIFQPSFLGIESSGIHETTFNSIMK.C	3446.89713	3	1.05E-05	0.93	4.84	-	1164.5
AHQ-4-8, 6081 - 6122	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	4.00E-05	0.94	5.18	-	1286.2
AHQ-4-8, 6242 - 6315	R.TTGIVMDSGDGVTHIVPIYEGYALPHAILR.L	3197.65320	3	1.51E-06	0.83	3.99	-	807.0
AHQ-4-8, 5946 - 6015	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	4.52E-04	0.80	4.17	-	723.4
AHQ-4-8, 3669	R.VAPDEHPILLTEAPLNPKINR.E	2338.69122	3	2.75E-04	0.78	3.69	-	817.0
gi|19913373|ref|NP_079536.2| G6B protein isoform G6b-A precursor; G6B protein; immunoglobulin recep				1.52E-06	1.82	20.17	8.40	25002.6
AHQ-4-11, 2336	R.TVLHVLGDR.T	1010.17224	2	1.52E-06	0.95	3.19	-	1690.6
AHQ-4-12, 2422	R.TVLHVLGDR.T	1010.17224	2	5.15E-04	0.85	2.76	-	998.6
AHQ-4-9, 2089	R.TVLHVLGDR.T	1010.17224	1	1.56E-05	0.28	1.93	-	377.7
AHQ-4-11, 5132 - 5138	R.WVWAPSFPACK.G	1350.56891	2	9.28E-05	0.86	3.30	-	749.1
gi|5901944|ref|NP_008977.1| elastin microfibril interface located protein; TNF? elastin microfibril				1.52E-06	3.49	40.22	6.90	106694.7
AHQ-4-4, 3535	R.APAPASAPPGPSEELLR.Q	1660.85268	2	7.47E-06	0.83	3.65	-	336.8
AHQ-4-5, 2879	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	4.17E-06	0.84	3.57	-	606.0
AHQ-4-3, 3012 - 3036	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	9.96E-06	0.87	3.46	-	840.8
AHQ-4-4, 3003	R.GTELGGAAGQGGHPPGYTSLASR.L	2142.27464	2	3.18E-05	0.89	4.47	-	314.0
AHQ-4-3, 3611	R.LDTVAGGLQGLR.E	1200.37012	2	1.52E-06	0.93	3.56	-	1192.1
gi|23510338|ref|NP_003325.2| ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity				1.55E-06	3.83	50.23	6.80	117848.1
AHQ-4-4, 4771 - 4774	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	2.12E-05	0.93	4.59	-	565.5
AHQ-4-4, 4638	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	5.24E-04	0.94	4.46	-	585.4
AHQ-4-4, 3638 - 3643	K.DNPGVVTCLDEAR.H	1447.55333	2	1.23E-05	0.89	3.43	-	776.8
AHQ-4-4, 4086	R.FEVQGLQPNGEEM*TLK.Q	1837.04413	2	6.44E-06	0.39	3.10	-	214.2
AHQ-4-4, 5436	R.LAGTQPLEVLEAVQR.S	1624.86348	2	4.33E-05	0.87	4.02	-	438.2
AHQ-4-4, 3680	R.LQTSSVLVSGLR.G	1260.46546	2	1.55E-06	0.75	2.82	-	611.0
gi|18543899|ref|XP_086916.1| similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic				1.64E-06	1.65	20.20	19.80	21265.8
AHQ-4-11, 3204	K.NRPTSISWDGLDSGK.L	1633.74419	2	1.64E-06	0.94	4.07	-	912.4
AHQ-4-11, 5118	R.YVWLVYEQDRPLKCDEPILSNR.S	2796.15005	2	5.71E-05	0.71	3.28	-	305.2
AHQ-4-11, 5076 - 5117	R.YVWLVYEQDRPLKCDEPILSNR.S	2796.15005	3	9.08E-05	0.85	3.96	-	681.5
gi|4504085|ref|NP_000399.1| glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA				1.67E-06	3.13	40.21	8.90	80814.1
AHQ-4-6, 5878	R.LAFLNVQAAEEALPR.I	1642.88050	2	8.93E-04	0.71	2.53	-	905.3
AHQ-4-6, 5519	R.LVQDYGLESEVAQHLAATYGDK.A	2408.60567	3	2.78E-04	0.85	3.57	-	865.5
AHQ-4-6, 2328	R.SM*AEDTINAAVK.T	1266.40397	2	3.20E-04	0.65	2.61	-	948.1
AHQ-4-6, 6166	R.YGAATANYMEVVSLLK.K	1731.00632	2	1.67E-06	0.93	3.75	-	1056.1
gi|29743626|ref|XP_297123.1| hypothetical protein XP_297123 [Homo sapiens]				1.73E-06	0.89	10.20	13.80	13908.9
AHQ-4-13, 6940	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	1.76E-04	0.73	3.15	-	1023.6
AHQ-4-13-, 6817 - 6818	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	3.84E-04	0.64	3.18	-	649.0
AHQ-4-12, 7009	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	1.73E-06	0.89	4.00	-	1175.1
gi|9257257|ref|NP_059830.1| WD repeat-containing protein 1 isoform 1 [Homo sapiens]				1.77E-06	0.85	10.18	3.80	66193.1
AHQ-4-6, 4807 - 4887	K.VVTVFSVADGYSENNVFYGHHAK.I	2541.75861	3	1.77E-06	0.85	3.67	-	629.3
gi|22027655|ref|NP_003907.3| adaptor-related protein complex 1 sigma 2 subunit; clathrin adaptor co				1.83E-06	0.96	10.27	10.20	18614.6
AHQ-4-12, 3934	K.AIEQADLLQEEAETPR.S	1813.94395	2	1.83E-06	0.96	5.32	-	1221.3
gi|4757952|ref|NP_001782.1| cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p				1.88E-06	3.33	40.29	26.70	21258.5
AHQ-4-11, 2201 - 2268	K.CVVVGDGAVGK.T	1062.22237	1	3.42E-04	0.54	2.02	-	807.6
AHQ-4-11, 6544 - 6618	K.NVFDEAILAALEPPEPK.K	1854.09282	3	1.88E-06	0.96	5.89	-	1076.5
AHQ-4-11, 5692	K.TPFLLVGTQIDLR.D	1473.74174	2	9.64E-06	0.95	3.87	-	1496.5
AHQ-4-11, 2456	K.YVECSALTQK.G	1200.34381	2	5.69E-06	0.88	3.01	-	684.9
gi|30147623|ref|XP_293669.2| similar to actinin, alpha 4 [Homo sapiens]				1.96E-06	0.96	10.27	3.50	57794.4
AHQ-4-5, 3926 - 4003	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	1.96E-06	0.96	5.35	-	972.2
gi|4503573|ref|NP_001967.1| enolase 3; enolase-3, beta, muscle; muscle specific enolase; beta enola				1.98E-06	0.88	10.18	3.50	46958.5
AHQ-4-14, 4664 - 4665	K.VNQIGSVTESIQACK.L	1635.82159	2	1.98E-06	0.88	3.63	-	678.9
gi|4503971|ref|NP_001484.1| GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r				2.05E-06	4.49	50.25	14.50	50582.4
AHQ-4-6, 4219	R.FQLLEGPPESMGR.G	1461.66818	2	2.18E-04	0.92	4.44	-	866.1
AHQ-4-6, 5202	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	4.94E-05	0.96	4.98	-	1128.3
AHQ-4-6, 4763	R.NPYYGGESSSITPLEELYKR.F	2304.49745	2	3.38E-06	0.85	3.72	-	530.5
AHQ-4-6, 2838	K.TFEGVDPQTTSMR.D	1469.60235	2	2.05E-06	0.91	3.52	-	916.8
AHQ-4-7, 7227	K.VPSTETEALASNLMGMFEK.R	2056.34679	2	8.26E-06	0.85	4.15	-	519.1
gi|27480842|ref|XP_208238.1| similar to bA92K2.2 (similar to ubiquitin) [Homo sapiens]				2.14E-06	0.77	10.13	0.00	17966.9
AHQ-4-14-, 2806	K.ESTLHLVLR.L	1068.25169	2	2.14E-06	0.77	2.65	-	382.2
gi|17986273|ref|NP_524144.1| fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2				2.19E-06	1.64	20.20	8.20	21145.0
AHQ-4-12, 3175 - 3245	R.VFDKEGNGTVMGAELR.H	1723.93228	3	1.63E-04	0.82	3.33	-	1074.6
AHQ-4-14, 3494	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	2.19E-06	0.83	3.00	-	767.7
AHQ-4-12, 2602 - 2666	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	5.90E-06	0.88	3.93	-	663.2
gi|30148988|ref|XP_301130.1| similar to Zinc finger protein 132 [Homo sapiens]				2.21E-06	0.69	10.16	3.90	49370.7
AHQ-4-7, 5487	R.EISALCLLLEQVELWNR.H	2088.41313	2	2.21E-06	0.69	3.11	-	744.1
gi|4503823|ref|NP_002028.1| protein-tyrosine kinase fyn isoform a; proto-oncogene tyrosine-protein				2.24E-06	0.81	10.16	2.00	60761.5
AHQ-4-7, 3454 - 3458	K.WTAPEAALYGR.F	1235.37302	2	2.24E-06	0.81	3.25	-	556.2
gi|4506381|ref|NP_002863.1| ras-related C3 botulinum toxin substrate 2; Ras-related C3 botulinum to				2.28E-06	0.82	10.20	7.30	21428.7
AHQ-4-11, 4412 - 4424	K.LAPITYPQGLALAK.E	1456.75431	2	2.28E-06	0.82	2.71	-	673.2
gi|4557471|ref|NP_001274.1| adaptor-related protein complex 1, sigma 1 subunit isoform 1; clathrin-				2.32E-06	0.97	10.25	10.10	18732.9
AHQ-4-12, 3567	K.AIEQADLLQEEDESPR.S	1843.92692	2	2.32E-06	0.97	4.99	-	1637.8
gi|4503141|ref|NP_001805.1| cathepsin C isoform a preproprotein; dipeptidyl-peptidase I; dipeptidyl				2.37E-06	0.95	10.24	4.10	51841.5
AHQ-4-14-, 5385 - 5406	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	2.37E-06	0.95	4.83	-	1011.8
gi|20070156|ref|NP_003565.2| vessicle-associated membrane protein (VAMP)-associated protein of 33 k				2.62E-06	0.94	10.19	5.00	27317.4
AHQ-4-12, 4073	K.GPFTDVVTTNLK.L	1292.46278	2	2.62E-06	0.94	3.85	-	1384.8
gi|23110942|ref|NP_002781.2| proteasome alpha 5 subunit; proteasome component 5; macropain subunit				2.63E-06	0.84	10.20	7.90	26410.9
AHQ-4-10, 2965 - 2977	R.AIGSASEGAQSSLQEVYHK.S	1963.09463	2	2.63E-06	0.84	3.96	-	624.6
gi|30153515|ref|XP_293925.2| similar to phosphoglycerate mutase (EC 5.4.2.1) B chain - rat [Homo sa				2.68E-06	0.86	10.17	2.70	57163.7
AHQ-4-10, 5639 - 5647	R.ALPFWNEEIVPQIK.E	1684.95898	2	2.68E-06	0.86	3.34	-	675.7
gi|30149013|ref|XP_302138.1| similar to alpha tubulin [Homo sapiens]				2.75E-06	0.61	10.16	4.60	22444.5
AHQ-4-13, 5096	R.EIINLVLDR.I	1085.27902	2	1.03E-04	0.80	3.25	-	799.8
AHQ-4-13-, 4973	R.EIINLVLDR.I	1085.27902	2	5.86E-04	0.81	3.05	-	854.4
AHQ-4-7, 4905	R.EIINLVLDR.I	1085.27902	1	2.75E-06	0.61	2.69	-	236.2
gi|4506407|ref|NP_002873.1| RAN binding protein 1 [Homo sapiens]				2.81E-06	0.82	10.17	5.50	23310.0
AHQ-4-10, 4081	K.TLEEDEEELFK.M	1382.45159	2	2.81E-06	0.82	3.38	-	492.7
gi|20428652|ref|NP_005347.2| lymphocyte-specific protein tyrosine kinase; oncogene LCK; membrane as				2.82E-06	0.91	10.18	2.00	57969.3

AHQ-4-7, 2150 - 2155	R.LIEDNEYTAR.E	1224.30217	2	2.82E-06	0.91	3.70	-	799.0
gi|5174393|ref|NP_006001.1| arginine-rich, mutated in early stage tumors; arginine-rich protein [Ho				2.85E-06	2.76	30.25	20.50	26906.2
AHQ-4-12, 5597 - 5669	K.DRDVTFSPATIENELIK.F	1949.15100	2	2.85E-06	0.96	5.02	-	1398.9
AHQ-4-12, 2791	K.IINEVSKPLAHHIPVEK.I	1925.26378	2	4.02E-05	0.84	3.60	-	756.0
AHQ-4-12, 3671 - 3746	R.LCYYIGATDDAATK.I	1563.71069	2	3.34E-04	0.95	4.28	-	1105.8
gi|11321581|ref|NP_003840.1| succinate-CoA ligase, GDP-forming, alpha subunit [Homo sapiens]				2.93E-06	0.88	10.19	4.80	35059.2
AHQ-4-8, 3603	R.LIGPNCPGVINPGECK.I	1727.98391	2	2.93E-06	0.88	3.80	-	547.9
gi|20547107|ref|XP_114482.1| similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN				3.03E-06	1.41	20.20	3.90	94330.3
AHQ-4-4, 6991 - 7000	R.EFSITDVVPYPISLR.W	1736.98906	2	5.80E-05	0.52	2.94	-	265.8
AHQ-4-4, 6766	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	3.03E-06	0.89	4.08	-	604.4
gi|6679056|ref|NP_031387.1| nidogen 2 (osteonidogen); nidogen 2 [Homo sapiens]				3.04E-06	0.82	10.21	2.10	151153.0
AHQ-4-2, 7082	R.AGLELGAEPETIVNSGLISPEGLAIDHIR.R	2973.32740	3	3.04E-06	0.82	4.12	-	572.0
gi|5174613|ref|NP_005960.1| nucleosome assembly protein 1-like 4; nucleosome assembly protein 2 [Ho				3.07E-06	0.38	10.17	2.70	42823.1
AHQ-4-7, 2650 - 2661	K.FYEEVHDLER.K	1337.41897	1	3.07E-06	0.38	1.84	-	354.0
AHQ-4-7, 2637	K.FYEEVHDLER.K	1337.41897	2	4.79E-05	0.93	3.38	-	1671.7
gi|21361619|ref|NP_061882.2| TOLLIP protein; Toll-interacting protein [Homo sapiens]				3.14E-06	0.96	10.26	5.10	30281.6
AHQ-4-11, 5628	R.GPVYIGELPQDFLR.I	1604.83072	2	3.14E-06	0.96	5.12	-	1112.7
gi|28077085|ref|NP_004559.3| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member				3.38E-06	0.94	10.24	5.30	42586.7
AHQ-4-8, 4354	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	2	3.38E-06	0.94	4.80	-	932.7
gi|4505775|ref|NP_002626.1| phosphate carrier precursor isoform 1b; phosphate carrier, mitochondria				3.46E-06	1.16	20.15	11.90	39958.5
AHQ-4-9, 5901	K.GWAPTFLGYSMQGLCK.F	1818.10896	2	3.46E-06	0.78	3.05	-	514.3
AHQ-4-9, 6644	K.YYALCGFGGVLSCGLTHTAVVPLDLVK.C	2914.38804	2	1.91E-04	0.38	2.57	-	298.6
gi|5901922|ref|NP_008996.1| CDC37 homolog [Homo sapiens]				3.66E-06	0.94	10.23	5.60	44468.0
AHQ-4-7, 6805	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	3.66E-06	0.94	4.57	-	691.8
gi|4506713|ref|NP_002945.1| ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte				3.66E-06	0.51	10.22	10.30	17964.8
AHQ-4-14-, 4293 - 4315	K.TITLEVEPSDTIENVK.A	1788.97431	2	8.94E-04	0.83	3.93	-	684.7
AHQ-4-14-, 4453 - 4487	K.TITLEVEPSDTIENVK.A	1788.97431	2	3.66E-06	0.51	2.72	-	405.9
AHQ-4-14-, 4201	K.TITLEVEPSDTIENVK.A	1788.97431	2	1.20E-04	0.75	4.25	-	476.7
gi|18426915|ref|NP_004386.2| drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [				3.69E-06	1.84	20.25	2.30	71438.9
AHQ-4-8, 3611	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	1.94E-05	0.96	5.05	-	1009.8
AHQ-4-13-, 5557	K.YVLINWVGEDVPDAR.K	1746.94404	2	9.11E-04	0.88	3.53	-	871.6
AHQ-4-13, 5665	K.YVLINWVGEDVPDAR.K	1746.94404	2	3.69E-06	0.89	3.48	-	1086.3
gi|4502219|ref|NP_001656.1| ras homolog gene family, member G (rho G); RhoG [Homo sapiens]				3.72E-06	1.82	20.21	16.80	21338.4
AHQ-4-11, 4852 - 4918	K.EYIPTVFDNYSAQSAVDGR.T	2133.25975	2	3.90E-06	0.93	4.14	-	852.9
AHQ-4-11, 3369	R.YLECSALQQDGVK.E	1512.66692	2	3.72E-06	0.89	2.99	-	1194.5
gi|30148978|ref|XP_291520.2| similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK				3.97E-06	0.79	10.18	2.20	68413.1
AHQ-4-12, 4889 - 4891	R.DWSHYFKTIKDLR.A	1709.92863	2	6.33E-04	0.57	2.80	-	627.6
AHQ-4-13-, 4864 - 4865	R.DWSHYFKTIKDLR.A	1709.92863	2	4.46E-06	0.61	3.13	-	536.3
AHQ-4-11, 4798 - 4868	R.DWSHYFKTIKDLR.A	1709.92863	2	3.97E-06	0.79	3.51	-	745.6
gi|6715607|ref|NP_000175.1| G-gamma globin [Homo sapiens]				4.09E-06	0.93	10.17	6.80	16126.3
AHQ-4-13-, 4844	R.LLVVYPWTQR.F	1275.52342	2	4.09E-06	0.93	3.48	-	1142.3
AHQ-4-14-, 4814	R.LLVVYPWTQR.F	1275.52342	2	6.65E-04	0.83	2.62	-	936.8
AHQ-4-13, 4932	R.LLVVYPWTQR.F	1275.52342	2	9.76E-05	0.86	3.17	-	765.3
gi|20127408|ref|NP_000173.2| hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub				4.21E-06	1.74	20.23	6.20	82999.1
AHQ-4-6, 6460	R.DSIFSNLTGQLDYQGFEK.A	2063.20943	2	4.21E-06	0.89	4.22	-	650.6
AHQ-4-6, 6602	K.EVEAVIPDHCIFASNTSALPISEIAAVSK.R	3071.44790	3	5.09E-05	0.86	4.55	-	431.0
gi|8393147|ref|NP_058625.1| chloride intracellular channel 5 [Homo sapiens]				4.36E-06	0.83	10.18	6.80	28109.7
AHQ-4-9, 5600 - 5679	K.FLDGDELTLADCNLLPK.L	1936.17229	2	4.36E-06	0.83	3.51	-	607.4
gi|4505591|ref|NP_002565.1| peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc				4.46E-06	2.48	40.19	18.10	22110.2
AHQ-4-11, 2840	K.DISLSDYK.G	941.01717	1	1.56E-04	0.37	2.07	-	516.4
AHQ-4-10, 3621 - 3701	R.GLFIIDDK.G	921.07223	1	5.65E-04	0.72	3.08	-	714.2
AHQ-4-11, 3490	R.LVQAFQFTDK.H	1197.36469	2	5.15E-05	0.94	3.86	-	1196.0
AHQ-4-11, 3492	R.LVQAFQFTDK.H	1197.36469	1	4.46E-06	0.60	2.08	-	700.1
AHQ-4-11, 2996 - 2997	R.TIAQDYGVLK.A	1108.26945	2	1.30E-05	0.79	2.99	-	542.8
gi|5032041|ref|NP_005605.1| Ras homolog enriched in brain 2 [Homo sapiens]				4.62E-06	1.71	20.22	14.10	20497.4
AHQ-4-12, 4981 - 5058	K.ALAESWNAAFLESSAK.E	1695.85389	2	4.62E-06	0.95	4.50	-	1169.8
AHQ-4-12, 2806 - 2807	K.ENQTAVDVFR.R	1179.26463	2	1.27E-04	0.76	3.02	-	568.8
gi|23111030|ref|NP_037478.2| sorting nexin 12 [Homo sapiens]				4.67E-06	0.96	10.21	8.60	18884.4
AHQ-4-12, 5091	R.GDEGIFEESFIEER.R	1657.71615	2	4.67E-06	0.96	4.20	-	1440.3
gi|4757818|ref|NP_004879.1| ATPase, H+ transporting, lysosomal, V1 subunit G isoform 1; vacuolar H(				4.69E-06	0.77	10.15	9.30	13757.4
AHQ-4-13-, 2790	K.EEAQAEIEQYR.L	1366.41548	2	4.69E-06	0.77	3.06	-	496.8
gi|8923221|ref|NP_060193.1| hypothetical protein FLJ20245 [Homo sapiens]				4.69E-06	0.94	10.19	3.30	46941.8
AHQ-4-8, 3021	R.PLLLALHGPSGVGK.S	1359.64187	2	4.69E-06	0.94	3.72	-	1448.7
gi|4505145|ref|NP_002387.1| malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochon				4.79E-06	1.75	20.23	4.80	65443.3
AHQ-4-6, 2799	K.IETQDIQALR.F	1187.32821	2	4.79E-06	0.86	3.10	-	1056.3
AHQ-4-6, 6720	R.ILGLGDLGVYGMGIPVGK.L	1760.13394	2	3.39E-05	0.88	3.53	-	1031.6
gi|13489091|ref|NP_066949.1| 3-mercaptopyruvate sulfurtransferase [Homo sapiens]				4.86E-06	1.44	20.22	10.80	33178.2
AHQ-4-9, 6044	R.AGQPLQLLDASWYLPK.L	1801.07798	2	4.86E-06	0.97	4.46	-	1679.5
AHQ-4-9, 4200	R.HIPGAAFFDIDQCSDR.T	1850.98926	2	3.49E-04	0.47	2.66	-	318.5
gi|29729345|ref|XP_290995.1| similar to speckle-type POZ protein [Homo sapiens]				5.05E-06	1.27	20.20	10.90	18703.4
AHQ-4-3, 6205 - 6208	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	5.12E-05	0.76	3.95	-	762.0
AHQ-4-4, 6162	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	3.44E-04	0.42	3.19	-	431.9
AHQ-4-2, 6195	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	5.05E-06	0.51	3.12	-	578.4
gi|7662651|ref|NP_054778.1| RGC32 protein [Homo sapiens]				5.05E-06	0.88	10.22	17.10	12924.1
AHQ-4-12, 4277	K.LNSPTDSTPALLSATVTPQK.A	2042.27634	2	5.05E-06	0.88	4.37	-	395.4
gi|4557697|ref|NP_000412.1| keratin 10; Keratin-10 [Homo sapiens]				5.19E-06	2.12	30.19	10.00	57247.1
AHQ-4-1, 2826	R.ALEESNYELEGK.I	1382.45482	2	2.14E-05	0.74	2.85	-	720.0
AHQ-4-1, 5649	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.36E-05	0.59	3.01	-	465.9
AHQ-4-1, 6873	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	5.19E-06	0.79	3.75	-	531.2
gi|25306267|ref|NP_001700.2| brain-derived neurotrophic factor isoform a preproprotein [Homo sapien				5.23E-06	0.94	10.18	6.10	27817.8
AHQ-4-13-, 3686	K.TAVDMSGGTVTVLEK.V	1508.71993	2	4.02E-05	0.86	3.21	-	769.0
AHQ-4-13, 3838	K.TAVDMSGGTVTVLEK.V	1508.71993	2	5.23E-06	0.94	3.68	-	1413.2
gi|5031569|ref|NP_005727.1| ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r				5.46E-06	2.84	30.30	15.20	42613.4
AHQ-4-8, 3598	R.ACYLSINPQKDETLETEK.A	2141.34169	2	7.95E-06	0.94	4.43	-	805.3
AHQ-4-8, 5029	K.AQYYLPDGSTIEIGPSR.F	1868.03645	2	2.57E-04	0.94	4.95	-	562.2
AHQ-4-8, 4950	K.DQLQTFSEEHPVLLTEAPLNPR.K	2535.79382	2	5.46E-06	0.96	5.93	-	766.0
gi|4759044|ref|NP_004841.1| Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]				5.48E-06	0.91	10.20	1.20	160883.4
AHQ-4-3, 6901 - 6949	K.AFVGNQLPFIGFTYYR.E	1894.16356	2	5.48E-06	0.91	4.08	-	683.1
gi|4557014|ref|NP_001743.1| catalase [Homo sapiens]				5.66E-06	1.96	40.20	8.70	59755.8
AHQ-4-7, 2369	K.DAQIFIQK.K	963.11234	1	4.80E-04	0.16	1.92	-	508.5
AHQ-4-7, 4001 - 4015	R.DLFNAIATGK.Y	1050.19000	1	2.53E-04	0.23	2.12	-	330.9
AHQ-4-7, 4678	R.DPILFPSFIHSQK.R	1529.76385	2	5.66E-06	0.65	2.93	-	401.9
AHQ-4-7, 4366	R.LGPNYLHIPVNCPYR.A	1815.08803	2	1.97E-05	0.73	2.54	-	445.0
AHQ-4-7, 4362	R.LGPNYLHIPVNCPYR.A	1815.08803	2	1.52E-05	0.91	4.01	-	712.0
gi|9845511|ref|NP_008839.2| ras-related C3 botulinum toxin substrate 1 isoform Rac1; rho family, sm				5.78E-06	0.88	10.16	5.20	21450.0
AHQ-4-11, 2968 - 3032	K.YLECSALTQR.G	1242.38392	2	5.78E-06	0.88	3.12	-	1008.4
gi|22538814|ref|NP_002976.2| small inducible cytokine A5 precursor; T-cell specific protein p288; T				5.91E-06	0.82	10.16	12.10	9989.6
AHQ-4-14, 4814 - 4825	K.CSNPAVVFVTR.K	1251.43718	2	5.91E-06	0.82	3.14	-	624.3
gi|10337595|ref|NP_066283.1| protein phosphatase 1A isoform 1; protein phosphatase 2C alpha isoform				6.16E-06	0.81	10.19	4.70	42447.5
AHQ-4-7, 3402	K.GPTEQLVSPEPEVHDIER.S	2033.18486	2	6.16E-06	0.81	3.72	-	423.8
gi|30148346|ref|XP_302059.1| similar to MLRQ subunit of the NADH: ubiquinone oxidoreductase complex				6.27E-06	0.34	10.11	6.60	17253.8
AHQ-4-14-, 3302	K.FYSVNVDYSK.L	1222.32788	1	6.27E-06	0.34	1.98	-	191.4
gi|11321585|ref|NP_002065.1| guanine nucleotide-binding protein, beta-1 subunit; G protein, beta-1				6.84E-06	0.63	10.16	5.90	37376.8
AHQ-4-9, 4412	R.KACADATLSQITNNIDPVGR.I	2146.36794	2	6.84E-06	0.63	3.15	-	266.7
gi|29731325|ref|XP_293023.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				6.94E-06	0.69	10.18	6.00	28867.8
AHQ-4-14, 5038 - 5053	K.AGPNTNGSQFFICTAK.T	1714.88050	2	6.94E-06	0.69	3.60	-	282.5
gi|30148500|ref|XP_302052.1| similar to cytoplasmic actin [Homo sapiens]				7.09E-06	0.70	10.14	3.70	33098.0

AHQ-4-8, 2381 - 2400	K.EITALAPSSM*K.I	1164.35479	1	7.09E-06	0.70	2.79	-	364.4
gi|10863873|ref|NP_000651.1|	transforming growth factor, beta 1 (Camurati-Engelmann disease); trans			7.16E-06	3.53	40.20	11.80	44422.0
AHQ-4-13-, 3330	R.ALDTNYCFSSTEK.N	1537.63010	2	7.16E-06	0.87	3.24	-	680.5
AHQ-4-13, 3473	R.ALDTNYCFSSTEK.N	1537.63010	2	7.70E-05	0.88	3.61	-	645.0
AHQ-4-13-, 6512 - 6577	K.GYHANFCLGPCPYIWSLDTQYSK.V	2781.07085	3	2.74E-04	0.86	3.83	-	993.2
AHQ-4-13-, 3488	K.VEQLSNMIVR.S	1189.41074	2	1.84E-05	0.95	4.02	-	1547.1
AHQ-4-13-, 2653 - 2702	K.VEQLSNM*IVR.S	1205.41014	2	3.38E-04	0.84	3.32	-	710.2
AHQ-4-13, 3621 - 3635	K.VEQLSNMIVR.S	1189.41074	2	4.66E-04	0.92	3.51	-	1440.4
gi|18375652|ref|NP_002826.2|	protein tyrosine phosphatase, non-receptor type 12; protein-tyrosine p			7.38E-06	0.93	10.20	2.10	88119.9
AHQ-4-7, 7163 - 7166	R.YWPLYGEDPITFAPFK.I	1945.20411	2	7.38E-06	0.93	3.98	-	818.7
gi|4557241|ref|NP_001095.1|	skeletal muscle specific actinin, alpha 3 [Homo sapiens]			7.42E-06	0.90	10.16	0.90	103293.7
AHQ-4-9, 2480	K.ALDFIASK.G	865.00867	1	2.75E-04	0.51	2.31	-	435.5
AHQ-4-10, 2669	K.ALDFIASK.G	865.00867	1	1.75E-04	0.50	2.36	-	425.2
AHQ-4-5, 2638	K.ALDFIASK.G	865.00867	2	7.42E-06	0.90	3.21	-	761.0
gi|27481323|ref|XP_208234.1|	similar to unactive progesterone receptor, 23 kD; likely ortholog of m			7.43E-06	0.71	10.14	8.10	18694.3
AHQ-4-11, 4380 - 4425	K.LTFSCLGGSDNFK.H	1447.59493	2	7.43E-06	0.71	2.76	-	597.3
gi|4504107|ref|NP_002076.1|	glutathione peroxidase 4; phospholipid hydroperoxidase; sperm nucleus g			7.51E-06	0.90	10.19	7.10	22137.7
AHQ-4-12, 4074 - 4077	K.TEVNYTQLVDLHAR.Y	1659.82478	2	7.51E-06	0.90	3.75	-	1009.2
gi|4505185|ref|NP_002406.1|	macrophage migration inhibitory factor (glycosylation-inhibiting factor			7.85E-06	0.96	10.21	7.80	12476.2
AHQ-4-13-, 4529	K.LLCGLLAER.L	1046.26608	2	4.13E-05	0.93	3.50	-	1059.1
AHQ-4-14-, 4489 - 4498	K.LLCGLLAER.L	1046.26608	2	4.51E-05	0.94	3.56	-	1128.8
AHQ-4-14, 5700	K.LLCGLLAER.L	1046.26608	2	7.85E-06	0.96	4.15	-	1168.5
gi|5730118|ref|NP_006514.1|	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble; X-prolyl aminope			7.95E-06	0.92	10.20	2.60	69858.4
AHQ-4-6, 6195 - 6264	R.GSLTFEPLTLVPIQTK.M	1745.05263	2	7.95E-06	0.92	3.94	-	730.5
gi|6005786|ref|NP_009214.1|	monoglyceride lipase; lysophospholipase-like [Homo sapiens]			8.07E-06	2.30	30.24	14.40	34292.3
AHQ-4-14-, 5985 - 6001	K.LTVPFLLLQGSADR.L	1530.79329	2	4.27E-04	0.67	2.63	-	546.2
AHQ-4-9, 5743	R.TPQSIPYQDLPHLVNADGQYLFCR.Y	2835.14314	3	2.24E-04	0.69	3.94	-	390.4
AHQ-4-9, 6591	K.VLNLVLPNLSLGPIDSSVLSR.N	2207.59900	2	2.58E-05	0.93	4.71	-	854.7
AHQ-4-9, 6583	K.VLNLVLPNLSLGPIDSSVLSR.N	2207.59900	2	8.07E-06	0.94	4.68	-	685.9
gi|20483052|ref|XP_166241.1|	similar to PTD015 protein [Homo sapiens]			8.38E-06	0.76	10.13	8.20	13332.1
AHQ-4-13-, 2738	K.VPSSTVEYLK.K	1123.28089	2	8.38E-06	0.76	2.51	-	739.7
gi|4507879|ref|NP_003365.1|	voltage-dependent anion channel 1 [Homo sapiens]			9.15E-06	0.61	10.15	3.90	30772.3
AHQ-4-9, 3916	R.WTEYGLTFTEK.W	1375.50711	1	9.15E-06	0.61	3.08	-	297.3
gi|23957682|ref|NP_705840.1|	heparan sulfate 3-OST-5 [Homo sapiens]			9.28E-06	0.01	10.13	6.90	20812.0
AHQ-4-14, 6369 - 6386	K.FYQITGRTLNWP	1496.69395	1	9.28E-06	0.01	1.85	-	73.7
gi|4506045|ref|NP_002718.1|	proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p			9.61E-06	0.85	10.16	8.20	17623.6
AHQ-4-1, 4181	K.GPM*FELLPGESNK.I	1435.62747	2	9.61E-06	0.85	3.20	-	632.3
gi|28178832|ref|NP_002159.2|	isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat			9.85E-06	3.47	40.23	11.50	50909.0
AHQ-4-8, 3614 - 3685	K.DLAGCIHGLSNVK.L	1385.57150	2	2.00E-04	0.90	3.41	-	933.5
AHQ-4-8, 3686	K.DLAGCIHGLSNVK.L	1385.57150	1	2.19E-04	0.49	2.47	-	366.1
AHQ-4-8, 3699	R.LIDDM*VAQVLK.S	1261.51361	2	8.50E-04	0.89	3.76	-	798.0
AHQ-4-8, 4382 - 4383	R.NILGGTVFREPIICK.N	1719.04170	2	1.56E-05	0.92	4.26	-	804.5
AHQ-4-8, 1600 - 1639	K.TIEAEAAHGTVTR.H	1356.46696	2	9.85E-06	0.76	2.94	-	635.5
gi|14780596|ref|XP_033004.1|	hypothetical protein BC005107 [Homo sapiens]			1.00E-05	0.30	10.13	5.00	18127.9
AHQ-4-2, 2012	R.EQIIAKAK.A	901.08569	1	2.31E-04	0.42	2.27	-	360.6
AHQ-4-3, 1663 - 1871	R.EQIIAKAK.A	901.08569	1	1.79E-04	0.25	2.41	-	248.2
AHQ-4-5, 1611	R.EQIIAKAK.A	901.08569	1	1.00E-05	0.30	2.41	-	294.5
AHQ-4-2, 1710 - 1848	R.EQIIAKAK.A	901.08569	1	1.18E-04	0.34	2.68	-	248.8
gi|15011904|ref|NP_036222.2|	microfilament and actin filament cross-linker protein isoform a; 620 k			1.05E-05	0.73	10.15	0.40	620320.6
AHQ-4-1, 4833 - 4834	K.IGQSLSSLTSPAEQGVLSEK.I	2032.23832	2	1.05E-05	0.73	3.01	-	623.8
gi|7705819|ref|NP_057181.1|	HSPC039 protein [Homo sapiens]			1.06E-05	0.96	10.22	24.40	8968.7
AHQ-4-14-, 5027	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	1.06E-05	0.96	4.48	-	1583.5
gi|21361388|ref|NP_008868.2|	SMT3 suppressor of mif two 3 homolog 2; SMT3 (suppressor of mif two 3,			1.08E-05	0.82	10.16	12.60	10870.2
AHQ-4-12, 2567	K.VAGQDGSVVQFK.I	1235.37133	2	1.08E-05	0.82	3.12	-	722.7
gi|4506363|ref|NP_002861.1|	RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s			1.11E-05	0.76	10.17	5.40	22774.0
AHQ-4-11, 2901	K.LQVWDTAGQER.F	1303.40576	2	1.11E-05	0.76	2.98	-	872.7
gi|5902726|ref|NP_005800.1|	peroxiredoxin 2; thioredoxin-dependent peroxide reductase 1 (thiol-spec			1.12E-05	1.69	20.24	9.10	21856.8
AHQ-4-11, 6538	K.EGGLGPLNIPLLADVTR.R	1736.00583	2	7.51E-04	0.75	3.33	-	341.7
AHQ-4-11, 5972	R.KEGGLGPLNIPLLADVTR.R	1864.17875	2	1.12E-05	0.94	4.75	-	719.1
gi|15306356|ref|XP_035638.2|	similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan			1.13E-05	1.65	20.18	6.90	18795.1
AHQ-4-13-, 3464	R.ESDVPLKTEEFEVTK.T	1751.91253	2	4.17E-04	0.86	3.45	-	543.6
AHQ-4-12, 3374	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.13E-05	0.87	3.68	-	583.7
AHQ-4-13, 3627	R.GAEIEYAMAYSK.A	1333.49204	2	9.16E-05	0.78	2.82	-	960.5
gi|4885539|ref|NP_005380.1|	protein-L-isoaspartate (D-aspartate) O-methyltransferase [Homo sapiens]			1.23E-05	1.26	20.18	15.90	24636.2
AHQ-4-11, 5089 - 5154	K.ALDVGSGSGILTACFAR.M	1696.90662	2	1.23E-05	0.63	3.22	-	747.6
AHQ-4-11, 4525	R.LILPVGPAGGNQM*LEQYDK.L	2060.35997	2	2.98E-04	0.63	3.33	-	161.7
gi|20127486|ref|NP_005808.2|	cargo selection protein (mannose 6 phosphate receptor binding pr [Homo			1.23E-05	0.76	10.18	3.90	47046.6
AHQ-4-10, 4067	R.IATSLDGFDVASVQQQR.Q	1835.99599	2	1.23E-05	0.76	3.66	-	611.7
gi|30157216|ref|XP_292133.2|	similar to genethonin 1 [Homo sapiens]			1.34E-05	0.73	10.20	4.50	39693.8
AHQ-4-3, 4643 - 4655	K.TITLEVKPSDTIENVK.A	1788.03268	2	9.07E-04	0.42	3.89	-	246.3
AHQ-4-14, 5448 - 5514	K.TITLEVKPSDTIENVK.A	1788.03268	2	6.70E-04	0.63	3.97	-	406.9
AHQ-4-14-, 4379	K.TITLEVKPSDTIENVK.A	1788.03268	2	1.34E-05	0.73	3.42	-	556.2
AHQ-4-2, 4652	K.TITLEVKPSDTIENVK.A	1788.03268	2	2.19E-04	0.51	3.08	-	398.8
gi|4758440|ref|NP_004868.1|	glia maturation factor, gamma [Homo sapiens]			1.38E-05	1.87	20.25	12.70	16801.2
AHQ-4-12, 6039	R.QMVVLEEEFQNISPEELK.M	2163.43385	2	1.38E-05	0.97	5.06	-	1824.7
AHQ-4-12, 5609 - 5614	R.QM*VVLEEEFQNISPEELK.M	2179.43325	2	1.29E-04	0.91	4.23	-	849.5
gi|4505329|ref|NP_003818.1|	N-ethylmaleimide-sensitive factor attachment protein, alpha; alpha-SNAP			1.39E-05	0.97	10.23	4.40	33246.6
AHQ-4-9, 3983	K.VAGYAALLEQYQK.A	1454.65214	2	1.39E-05	0.97	4.67	-	1578.5
gi|14249382|ref|NP_116139.1|	hypothetical protein MGC15429 [Homo sapiens]			1.47E-05	0.96	10.19	4.80	22345.5
AHQ-4-11, 4233	R.FSVLLLHGIR.F	1155.41731	2	1.47E-05	0.96	3.65	-	1559.9
gi|5453998|ref|NP_006382.1|	importin 7; RAN-binding protein 7 [Homo sapiens]			1.48E-05	0.89	10.19	1.40	119515.7
AHQ-4-4, 6854	R.ENIVEAIIHSPELIR.V	1733.98994	2	1.48E-05	0.89	3.80	-	737.1
gi|19923233|ref|NP_002970.2|	sterol carrier protein 2 [Homo sapiens]			1.49E-05	1.76	20.18	4.20	58993.3
AHQ-4-13, 2667	K.KLEEEGEQFVK.K	1336.47242	2	4.73E-04	0.89	3.35	-	834.2
AHQ-4-13-, 2688	K.LQNLQLQPGNAK.L	1324.51124	2	1.49E-05	0.87	3.69	-	788.0
gi|22748683|ref|NP_689522.1|	hypothetical protein FLJ35564 [Homo sapiens]			1.50E-05	0.04	10.11	1.80	70407.8
AHQ-4-7, 2117	K.HGHYPNTIAEK.H	1267.37511	1	1.50E-05	0.04	1.95	-	125.7
gi|5453892|ref|NP_006209.1|	phosphoinositide-3-kinase, catalytic, alpha polypeptide; phosphatidylin			1.57E-05	0.75	10.16	1.50	124411.5
AHQ-4-9, 5809 - 5864	R.QVEAMEKLINLTDILK.Q	1859.22068	2	1.57E-05	0.75	3.14	-	912.1
gi|30153966|ref|XP_293932.2|	similar to hypothetical protein BC013073 [Homo sapiens]			1.59E-05	0.76	10.21	9.00	21711.3
AHQ-4-1, 4254 - 4257	R.MIFTLFTINVSKDIRHH	2073.44997	3	1.59E-05	0.76	3.48	-	871.7
AHQ-4-2, 3746 - 3747	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.23E-04	0.39	2.89	-	317.7
AHQ-4-2, 4031	R.MIFTLFTINVSKDIRHH	2073.44997	2	4.53E-04	0.30	2.97	-	376.1
AHQ-4-5, 4021 - 4022	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.31E-05	0.57	2.92	-	593.8
AHQ-4-5, 4123	R.MIFTLFTINVSKDIRHH	2073.44997	2	6.94E-04	0.74	3.61	-	474.5
AHQ-4-6, 3942	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.28E-05	0.76	3.72	-	522.3
AHQ-4-8, 3755	R.MIFTLFTINVSKDIRHH	2073.44997	2	4.79E-05	0.46	2.92	-	463.5
AHQ-4-1, 4245 - 4313	R.MIFTLFTINVSKDIRHH	2073.44997	2	5.17E-04	0.47	3.11	-	435.9
gi|4501865|ref|NP_001087.1|	ATP citrate lyase [Homo sapiens]			1.63E-05	0.98	10.33	2.00	121419.0
AHQ-4-4, 6327	R.LLQDHPWLLSQNLVVKPDQLIK.R	2599.06730	3	1.63E-05	0.98	6.58	-	1789.6
gi|14589893|ref|NP_001785.2|	cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-			1.72E-05	0.21	10.14	2.00	100279.9
AHQ-4-3, 4872	K.VENPIDLYIYVIDM*NDNR.P	2213.45293	2	1.72E-05	0.21	2.74	-	288.3
gi|30158852|ref|XP_301583.1|	similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa			1.74E-05	0.79	10.17	6.50	19197.0
AHQ-4-8, 2253 - 2332	K.IWHHTFYNKLR.V	1515.74533	2	1.74E-05	0.79	3.49	-	834.6
gi|5902090|ref|NP_008862.1|	solute carrier family 2 (facilitated glucose transporter), member 3; GL			1.74E-05	0.85	10.19	3.00	53924.0
AHQ-4-1, 5291	R.LWGTQDVSQDIQEMK.D	1778.96471	2	1.74E-05	0.85	3.82	-	524.8
gi|27479531|ref|XP_208746.1|	similar to golgi complex associated protein 1; golgi resident protein			1.76E-05	0.95	10.24	5.50	35740.3

AHQ-4-10, 3892 - 3960	R.DVQAGSHDYPGEGIYLLK.F	1963.13623	2	1.76E-05	0.95	4.71	-	955.3
gi|6912586|ref|NP_036220.1|	6-phosphogluconolactonase [Homo sapiens]			1.80E-05	2.36	30.26	24.00	27546.7
AHQ-4-10, 3883	R.ILEDQEENPLPAALVQPHTGK.L	2300.55348	2	9.11E-05	0.67	3.59	-	336.5
AHQ-4-10, 2424	K.IVAPISDSPKPPPQR.V	1602.85951	2	2.88E-05	0.79	3.25	-	547.6
AHQ-4-10, 6085	R.LPIPESQVITINPELPVEEAAEDYAK.K	2867.19683	2	1.80E-05	0.90	5.21	-	369.4
gi|6005902|ref|NP_009043.1|	thrombospondin 3 [Homo sapiens]			1.87E-05	1.51	20.14	0.70	104200.6
AHQ-4-2, 4092	R.FYVVM*WK.Q	989.21487	2	4.65E-04	0.78	2.63	-	580.2
AHQ-4-2, 4695 - 4768	R.FYVVMWK.Q	973.21547	1	7.70E-04	0.62	2.06	-	862.6
AHQ-4-3, 4669 - 4749	R.FYVVMWK.Q	973.21547	1	7.25E-04	0.84	2.54	-	944.0
AHQ-4-4, 4627	R.FYVVMWK.Q	973.21547	1	1.23E-04	0.75	2.43	-	758.1
AHQ-4-6, 4262	R.FYVVMWK.Q	973.21547	1	2.28E-04	0.68	2.15	-	795.4
AHQ-4-7, 4107 - 4177	R.FYVVMWK.Q	973.21547	1	1.55E-04	0.83	2.14	-	1061.3
AHQ-4-9, 3812	R.FYVVMWK.Q	973.21547	1	3.46E-04	0.73	2.19	-	942.2
AHQ-4-9, 3816	R.FYVVMWK.Q	973.21547	1	6.00E-04	0.56	2.58	-	355.3
AHQ-4-11, 4289	R.FYVVMWK.Q	973.21547	1	4.59E-04	0.80	2.26	-	1028.2
AHQ-4-11, 4301	R.FYVVMWK.Q	973.21547	2	1.86E-04	0.79	2.54	-	604.4
AHQ-4-11, 4306	R.FYVVMWK.Q	973.21547	1	1.87E-05	0.73	2.34	-	743.0
gi|5803217|ref|NP_006821.1|	ubiquinol-cytochrome c reductase (6.4kD) subunit [Homo sapiens]			1.89E-05	0.86	10.17	21.40	6569.6
AHQ-4-14-, 6182	R.LILDWVPYINGK.F	1431.70332	2	1.89E-05	0.86	3.42	-	711.3
gi|4507509|ref|NP_003245.1|	tissue inhibitor of metalloproteinase 1 precursor; Erythroid-potentiati			1.90E-05	1.83	20.26	21.30	23170.8
AHQ-4-9, 6501 - 6503	K.LQDGLLHITTCSFVAPWNSLSLAQR.R	2830.21117	2	3.47E-05	0.87	3.92	-	694.4
AHQ-4-9, 4027	K.LQSGTHCLWTDQLLQGSEK.G	2203.41795	2	1.90E-05	0.96	5.25	-	1301.7
gi|24497612|ref|NP_116262.2|	nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr			1.91E-05	2.81	40.23	9.40	72695.6
AHQ-4-6, 4080	R.EYVLYLRPTGPLAQK.L	1749.04621	2	4.66E-04	0.96	4.51	-	1249.7
AHQ-4-6, 6634	K.LGCDWVATIFSR.D	1426.62208	2	1.91E-05	0.89	2.73	-	1001.1
AHQ-4-6, 3011	K.LSDFWQQSK.Q	1139.24210	1	4.03E-04	0.19	2.19	-	284.4
AHQ-4-6, 6080	R.RPYEDQGLGETTPLTIICQPMQPLR.V	2916.32264	3	3.57E-04	0.77	3.37	-	671.0
gi|4506077|ref|NP_002734.1|	protein kinase C substrate 80K-H; glucosidase II, beta subunit; AGE-bin			2.00E-05	0.89	10.16	1.90	59296.0
AHQ-4-5, 3205	K.LWEEQLAAAK.A	1159.31646	2	2.00E-05	0.89	3.30	-	811.1
gi|7657647|ref|NP_055363.1|	tropomodulin 2 (neuronal) [Homo sapiens]			2.01E-05	0.82	10.14	3.10	39594.8
AHQ-4-11, 3154	K.FGYQFTKQGPR.T	1329.48804	2	2.01E-05	0.82	2.77	-	709.8
gi|29736026|ref|XP_085123.3|	similar to Ras-related protein Rab-15 [Homo sapiens]			2.02E-05	0.92	10.19	5.30	23517.8
AHQ-4-14-, 3414	R.IQIWDTAGQER.Y	1317.43243	2	2.02E-05	0.92	3.73	-	954.7
gi|7705767|ref|NP_057086.1|	CGI-49 protein [Homo sapiens]			2.04E-05	0.87	10.24	6.80	46920.8
AHQ-4-1, 7255	K.GPEAGYVATPIAM*VQAAMTLLSDASHLPK.A	2957.41485	3	2.04E-05	0.87	4.87	-	722.3
gi|4507383|ref|NP_001052.1|	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil			2.13E-05	1.92	20.23	5.80	60675.3
AHQ-4-12, 4359	R.FQACPETQVPLQLESK.S	1877.10807	2	4.95E-04	0.95	4.28	-	1265.4
AHQ-4-7, 4221 - 4277	R.FQACPETQVPLQLESK.S	1877.10807	2	4.60E-05	0.96	4.22	-	1384.0
AHQ-4-1, 4633	R.FQACPETQVPLQLESK.S	1877.10807	2	5.32E-05	0.89	3.25	-	1006.8
AHQ-4-7, 3698	R.HSASPMGVQDFDIVR.D	1659.84828	2	2.13E-05	0.96	4.60	-	1292.3
gi|5453599|ref|NP_006127.1|	capping protein (actin filament) muscle Z-line, alpha 2; F-actin cappin			2.21E-05	1.50	20.24	11.90	32948.9
AHQ-4-9, 4176 - 4179	R.EGAAHAFAQYNLDQFTPVK.I	2108.29826	2	1.14E-04	0.96	4.76	-	1237.5
AHQ-4-9, 4664	K.FTITPSTTQVVGILK.I	1605.90007	2	2.21E-05	0.55	3.02	-	212.3
gi|4507649|ref|NP_003280.1|	tropomyosin 2 (beta) [Homo sapiens]			2.33E-05	0.91	10.18	4.60	32989.6
AHQ-4-9, 2403	K.ATDAEADVASLNR.R	1333.38703	2	2.33E-05	0.91	3.07	-	1236.6
gi|4503291|ref|NP_001346.1|	D-dopachrome tautomerase [Homo sapiens]			2.34E-05	0.90	10.17	9.30	12711.7
AHQ-4-14-, 5538	R.FFPLESWQIGK.I	1352.56151	2	2.34E-05	0.90	3.41	-	666.9
AHQ-4-13, 5728	R.FFPLESWQIGK.I	1352.56151	2	3.09E-05	0.79	2.71	-	768.5
gi|23065552|ref|NP_000840.2|	glutathione S-transferase M3; glutathione S-transferase, Mu-3; brain G			2.38E-05	0.82	10.17	6.20	26559.4
AHQ-4-10, 3848	K.LKPQYLEELPGQLK.Q	1656.94708	2	2.38E-05	0.82	3.12	-	580.8
AHQ-4-10, 3765 - 3839	K.LKPQYLEELPGQLK.Q	1656.94708	2	2.73E-04	0.83	3.30	-	576.3
gi|8922804|ref|NP_060760.1|	hypothetical protein FLJ10983 [Homo sapiens]			2.39E-05	0.90	10.17	1.60	68268.9
AHQ-4-6, 3260	R.LDQETAQWLR.W	1260.38088	2	2.39E-05	0.90	3.34	-	1104.3
gi|4506193|ref|NP_002784.1|	proteasome beta 1 subunit; proteasome subunit HC5; proteasome component			2.41E-05	2.71	30.33	22.00	26489.2
AHQ-4-11, 5572	K.AGGSASAMLQPLLDNQVGFK.N	2005.28443	2	3.34E-04	0.87	4.23	-	337.1
AHQ-4-11, 2922 - 2924	K.NM*QNVEHVPLSLDR.A	1668.85668	2	2.41E-05	0.86	3.69	-	872.8
AHQ-4-11, 6550	R.RFFPYYVYNIIGGLDEEGK.G	2281.55031	2	4.83E-05	0.98	6.66	-	1891.9
gi|9966825|ref|NP_065089.1|	HEF like Protein [Homo sapiens]			2.44E-05	0.97	10.26	2.80	86696.2
AHQ-4-13, 4301	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	2.44E-05	0.97	5.23	-	1417.3
gi|4502565|ref|NP_001740.1|	calpain, small subunit 1; calpain, small polypeptide; calcium-dependent			2.44E-05	1.44	20.22	7.10	28315.5
AHQ-4-11, 6437 - 6496	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	2.44E-05	0.52	3.06	-	210.2
AHQ-4-12, 6941	R.YSDESGNMDFDNFISCLVR.L	2271.42628	2	3.75E-05	0.92	4.37	-	993.5
AHQ-4-10, 6152	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	3.72E-04	0.87	3.89	-	584.8
gi|16904381|ref|NP_006717.1|	LPS-responsive vesicle trafficking, beach and anchor containing; vesic			2.48E-05	0.72	10.21	0.50	319158.3
AHQ-4-4, 3796	R.VGVGTSFGLPQTR.R	1319.49146	2	2.48E-05	0.72	2.79	-	744.7
gi|4502861|ref|NP_001275.1|	adaptor-related protein complex 3, sigma 1 subunit; clathrin-associated			2.58E-05	0.87	10.17	7.80	21732.0
AHQ-4-12, 3895	K.FYQPYSEDTQQQIIR.E	1917.06756	2	2.58E-05	0.87	3.39	-	785.1
gi|5803013|ref|NP_006808.1|	endoplasmic reticulum protein 29 precursor; endoplasmic reticulum lumen			2.59E-05	1.35	20.17	11.50	28993.2
AHQ-4-10, 3628	R.DGDFENPVPYTGAVK.V	1609.71786	2	3.75E-05	0.62	3.34	-	346.5
AHQ-4-10, 3691	K.ILDQGEDFPASEMTR.I	1709.85924	2	2.59E-05	0.74	2.83	-	572.0
gi|8923812|ref|NP_060943.1|	uncharacterized hypothalamus protein HT012 [Homo sapiens]			2.67E-05	0.92	10.17	8.60	14960.4
AHQ-4-13, 4181 - 4246	K.TLAFTSVDLTNK.A	1310.47811	2	2.67E-05	0.92	3.39	-	1286.5
gi|27499559|ref|XP_062669.7|	similar to lactate dehydrogenase A -like [Homo sapiens]			2.81E-05	0.91	10.25	5.60	33375.6
AHQ-4-9, 6707	K.LIIVSNPVDILTYVAWK.L	1945.33337	2	2.81E-05	0.91	4.91	-	704.2
gi|21624643|ref|NP_660202.1|	similar to CG3714 gene product [Homo sapiens]			2.83E-05	0.62	10.13	9.00	14620.8
AHQ-4-7, 2971	R.SPAQYQVVLSER.L	1377.52778	2	2.83E-05	0.62	2.52	-	558.9
gi|6005854|ref|NP_009204.1|	repressor of estrogen receptor activity; B-cell associated protein [Hom			2.86E-05	1.78	20.19	10.70	33296.1
AHQ-4-9, 6439	R.IPWFQYPIIYDIR.A	1725.02480	2	4.78E-05	0.91	3.41	-	1125.2
AHQ-4-9, 6035	R.IYLTADNLVLNLQDESFTR.G	2226.47137	2	2.86E-05	0.87	3.90	-	680.1
gi|4759086|ref|NP_004883.1|	vesicle trafficking protein sec22b [Homo sapiens]			2.97E-05	0.74	10.17	6.50	24740.4
AHQ-4-12, 3939	R.NLGSINTELQDVQR.I	1587.71696	2	2.97E-05	0.74	3.31	-	682.3
gi|21361456|ref|NP_055425.2|	alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph			3.01E-05	1.51	20.20	3.30	109437.2
AHQ-4-5, 4311	R.LSFQHDPETSVLVLR.K	1741.96893	2	3.01E-05	0.90	4.05	-	702.6
AHQ-4-5, 3571	R.VVIIGAGKPAAVVLQTK.G	1665.05702	2	1.05E-04	0.61	2.65	-	673.2
gi|11993943|ref|NP_055419.1|	Tax interaction protein 1 [Homo sapiens]			3.04E-05	0.89	10.18	13.70	13734.6
AHQ-4-13-, 4110	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	1.04E-04	0.92	3.59	-	1164.1
AHQ-4-13, 4241	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	3.04E-05	0.89	3.69	-	872.1
gi|15718761|ref|NP_004976.2|	c-K-ras2 protein isoform b; Kirsten rat sarcoma-2 viral (v-Ki-ras2) on			3.19E-05	0.86	10.21	8.00	21424.4
AHQ-4-11, 3582	R.VKDSEDVPM*VLVGNK.C	1646.88770	2	3.19E-05	0.86	4.17	-	675.5
gi|4504041|ref|NP_002061.1|	guanine nucleotide binding protein (G protein), alpha inhibiting activi			3.39E-05	0.72	10.16	4.20	40450.7
AHQ-4-10, 3721	R.IAQSDYIPTQQDVLR.T	1747.93034	2	1.61E-04	0.64	3.00	-	373.3
AHQ-4-8, 3689	R.IAQSDYIPTQQDVLR.T	1747.93034	2	3.39E-05	0.72	3.28	-	281.4
gi|4504061|ref|NP_002067.1|	glucosamine (N-acetyl)-6-sulfatase precursor; N-acetylglucosamine-6-sul			3.40E-05	0.41	10.15	3.30	62081.8
AHQ-4-4, 5383	K.RWQTLLSVDDLVEKLVKR.L	2199.58179	2	8.62E-05	0.10	2.58	-	181.9
AHQ-4-5, 5385	K.RWQTLLSVDDLVEKLVKR.L	2199.58179	2	3.40E-05	0.41	3.05	-	236.3
AHQ-4-3, 5420 - 5473	K.RWQTLLSVDDLVEKLVKR.L	2199.58179	2	6.00E-05	0.38	2.60	-	277.5
gi|21389337|ref|NP_653164.1|	ribose 5-phosphate isomerase A (ribose 5-phosphate epimerase); RIBOSE			3.41E-05	0.95	10.25	8.00	26090.9
AHQ-4-10, 3696	R.NNQVLGIGSGSTIVHAVQR.I	1951.17659	2	3.41E-05	0.95	4.91	-	890.5
gi|4506427|ref|NP_002880.1|	retinoic acid receptor responder (tazarotene induced) 2 [Homo sapiens]			3.58E-05	0.87	10.17	6.70	18617.5
AHQ-4-12, 3638	R.GLQVALEEFHK.H	1271.44680	2	3.58E-05	0.87	3.32	-	1110.0
gi|21264318|ref|NP_004028.3|	adenosine monophosphate deaminase 2 (isoform L) [Homo sapiens]			3.62E-05	0.76	10.14	2.00	100687.2
AHQ-4-5, 5519	R.SAPYEFPEESPIEQLEER.R	2151.27185	2	3.62E-05	0.76	2.88	-	563.5
gi|5453559|ref|NP_006347.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; ATP			3.62E-05	1.57	20.20	18.60	18491.1
AHQ-4-11, 4105 - 4184	K.KYPYWPHQPIENL	1685.90553	2	3.62E-05	0.67	3.16	-	401.6
AHQ-4-11, 5402	R.LAALPENPPAIDWAYYK.A	1933.19486	2	1.83E-04	0.91	4.05	-	533.8
gi|29732725|ref|XP_291587.1|	similar to Endoplasmin precursor (94 kDa glucose-regulated protein) (G			3.69E-05	0.59	10.14	2.70	37967.5
AHQ-4-5, 3066	R.GLFDEYGSK.K	1016.08574	1	3.69E-05	0.59	2.74	-	348.2

gi|4758790|ref|NP_004543.1| NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q				3.75E-05	0.92	10.19	11.30	12517.4
AHQ-4-13-, 6601	K.IEYDDFVECLLR.Q	1573.74872	2	3.75E-05	0.92	3.88	-	751.8
gi|20543399|ref|XP_116396.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				3.84E-05	0.83	10.17	5.00	19852.7
AHQ-4-13, 4546	R.VSFKLFADK.F	1055.25138	1	3.55E-04	0.53	2.41	-	701.0
AHQ-4-12, 4370 - 4443	R.VSFKLFADK.F	1055.25138	2	3.84E-05	0.83	3.48	-	826.3
gi|30148456|ref|XP_293602.2| similar to glutathione-S-transferase like; glutathione transferase ome				4.01E-05	0.78	10.17	3.90	29139.6
AHQ-4-11, 4432	K.VPSLVGSFLR.T	1075.28583	2	3.34E-04	0.92	3.36	-	1008.8
AHQ-4-10, 4131	K.VPSLVGSFLR.T	1075.28583	2	4.01E-05	0.78	2.95	-	723.0
gi|4501841|ref|NP_001596.1| alanyl-tRNA synthetase [Homo sapiens]				4.07E-05	1.18	20.15	3.40	106800.7
AHQ-4-4, 7316	R.EIADLGEALATAVIPQWQK.D	2054.33195	2	2.75E-04	0.52	2.86	-	492.7
AHQ-4-4, 3422	K.ITCLCQVPQNAANR.G	1647.85889	2	4.07E-05	0.66	3.02	-	348.9
gi|4557581|ref|NP_001435.1| fatty acid binding protein 5 (psoriasis-associated); E-FABP [Homo sapie				4.10E-05	0.85	10.17	10.40	15164.4
AHQ-4-12, 3463	K.LVVECVM*NNVTCTR.I	1713.97902	2	4.10E-05	0.85	3.43	-	553.1
gi|11496277|ref|NP_068805.1| mitogen-activated protein kinase kinase 1 interacting protein 1; MEK p				4.11E-05	0.94	10.22	12.90	13622.6
AHQ-4-14-, 5411	K.SIICYYNTYQVVQFNR.L	2070.31322	2	4.11E-05	0.94	4.45	-	1032.7
gi|29727317|ref|XP_298144.1| hypothetical protein XP_298144 [Homo sapiens]				4.14E-05	0.60	10.14	8.00	22108.6
AHQ-4-3, 6640	K.GEYNLTLDTALTSNLK.T	1753.93165	2	4.14E-05	0.60	2.53	-	860.7
gi|14745898|ref|XP_016144.2| similar to tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat				4.18E-05	0.96	10.21	7.50	18201.0
AHQ-4-11, 6517	K.LLCCDILDVLDK.N	1479.74157	2	4.18E-05	0.96	4.16	-	1195.5
gi|30147468|ref|XP_208318.2| similar to hypothetical protein [Homo sapiens]				4.27E-05	0.24	10.11	6.30	21576.5
AHQ-4-9, 2421	K.SHGLLVQQALPK.A	1291.52439	1	4.27E-05	0.24	1.85	-	315.1
gi|29029559|ref|NP_001307.2| CSE1 chromosome segregation 1-like protein isoform a; cellular apoptos				4.34E-05	0.96	10.22	1.80	110415.8
AHQ-4-1, 6694	K.LLQTDDEEEAGLLELLK.S	1930.14276	2	4.34E-05	0.96	4.41	-	1660.8
gi|4503117|ref|NP_000091.1| cystatin B; stefin B; liver thiol proteinase inhibitor; CPI-B [Homo sap				4.47E-05	1.83	20.19	33.70	11139.5
AHQ-4-13, 3675	K.SQVVAGTNYFIK.V	1327.51036	2	4.47E-05	0.90	3.39	-	1134.7
AHQ-4-13, 3828	R.VFQSLPHENKPLTLSNYQTNK.A	2459.74218	3	1.53E-04	0.93	3.80	-	1440.4
gi|5031985|ref|NP_005787.1| nuclear transport factor 2; placental protein 15 [Homo sapiens]				4.63E-05	3.37	40.22	63.00	14478.4
AHQ-4-14-, 5697	K.ADEDPIM*GFHQMFLLK.N	1909.21859	2	2.44E-04	0.76	3.22	-	574.0
AHQ-4-14-, 5982 - 5989	K.IQHSITAQDHQPTPDSCIISMVVGQLK.A	3006.40418	3	8.27E-05	0.90	4.48	-	1047.4
AHQ-4-14-, 4450	K.NINDAWVCTNDM*FR.L	1773.92828	2	7.91E-05	0.78	3.43	-	593.8
AHQ-4-14-, 6287	R.TQLGAIYIDASCLTWEGQQFQGK.A	2616.88699	2	4.63E-05	0.93	4.33	-	994.7
gi|24234688|ref|NP_004125.3| heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre				4.75E-05	0.79	10.17	2.80	73680.1
AHQ-4-6, 6003	K.STNGDTFLGGEDFDQALLR.H	2057.16328	2	4.75E-05	0.79	3.47	-	558.5
gi|21359867|ref|NP_001907.2| cytochrome c-1 [Homo sapiens]				4.77E-05	0.95	10.20	7.40	35389.7
AHQ-4-10, 6116	R.HGGEDYVFSLLTGYCEPPTGVSLR.E	2656.90798	2	4.77E-05	0.95	3.91	-	1646.2
gi|21359837|ref|NP_003312.2| Tu translation elongation factor, mitochondrial [Homo sapiens]				4.91E-05	1.54	20.18	8.20	49541.2
AHQ-4-8, 6010	R.DLEKPFLLPVEAVYSVPGR.G	2130.47156	2	1.11E-04	0.85	3.61	-	662.9
AHQ-4-8, 4771	R.TIGTGLVTNTLAMTEEEK.N	1909.14859	2	4.91E-05	0.69	3.27	-	452.4
gi|20149635|ref|NP_057227.2| p47 protein [Homo sapiens]				5.05E-05	0.69	10.16	5.10	40572.5
AHQ-4-13, 4618	K.ASSSILIDESEPTTNIQIR.L	2075.26319	2	5.05E-05	0.69	3.24	-	496.8
gi|18640750|ref|NP_570138.1| regulator of G-protein signalling 18; regulator of G-protein signaling				5.06E-05	0.79	10.18	8.90	27582.0
AHQ-4-10, 3889	K.EVITNSITQPTLHSFDAAQSR.V	2316.51300	2	5.06E-05	0.79	3.53	-	338.4
gi|13385594|ref|NP_085056.1| cytochrome b5 outer mitochondrial membrane precursor; type 2 cyt-b5 [H				5.13E-05	0.94	10.25	23.30	16332.0
AHQ-4-11, 5901	R.FLNEHPGGEEVLLEQAGVDASESFEDVGHSSDAR.E	3629.75848	3	5.13E-05	0.94	5.03	-	1149.7
gi|21614520|ref|NP_000393.2| glucose-6-phosphate dehydrogenase [Homo sapiens]				5.23E-05	0.84	10.13	1.90	59257.4
AHQ-4-7, 2898	K.GYLDDPTVPR.G	1133.23587	2	5.23E-05	0.84	2.62	-	737.9
gi|4506189|ref|NP_002783.1| proteasome alpha 7 subunit isoform 1; proteasome subunit RC6-1; proteas				5.30E-05	0.61	10.14	4.40	27886.7
AHQ-4-10, 2781	K.ALLEVVQSGGK.N	1101.27845	1	5.30E-05	0.61	2.80	-	519.2
gi|22060072|ref|XP_088293.2| similar to cytochrome c [Homo sapiens]				5.35E-05	2.18	30.16	24.80	11887.8
AHQ-4-13-, 4213	R.ADLIAYLK.K	907.08869	2	5.35E-05	0.91	3.18	-	968.7
AHQ-4-13, 4354	R.ADLIAYLK.K	907.08869	2	5.39E-05	0.90	3.28	-	1009.5
AHQ-4-13, 3042	K.M*IFVGIK.K	824.06630	1	8.00E-05	0.44	2.07	-	257.0
AHQ-4-13, 3657	K.TGPNLHGLFGR.K	1169.31780	2	9.89E-04	0.82	2.64	-	614.4
gi|5803187|ref|NP_006746.1| transaldolase 1; dihydroxyacetone transferase; glycerone transferase [H				5.48E-05	0.30	10.13	3.30	37539.9
AHQ-4-9, 3324	K.LLGELLQDNAK.L	1214.39356	1	5.48E-05	0.30	1.84	-	574.1
gi|4502211|ref|NP_001654.1| ADP-ribosylation factor 6 [Homo sapiens]				5.72E-05	1.38	20.16	18.30	20082.0
AHQ-4-12, 4038	K.FNVWDVGGQDK.I	1265.35598	2	5.72E-05	0.89	3.12	-	1126.5
AHQ-4-12, 5538	K.LGQSVTTIPTVGFNVETVTYK.N	2255.55261	2	1.66E-04	0.49	2.92	-	147.4
gi|22041780|ref|XP_059066.2| similar to 14-3-3 protein sigma (Stratifin) (Epithelial cell marker pr				6.20E-05	0.13	10.18	4.00	27773.9
AHQ-4-11, 5704	K.DSTLIMQLLR.D	1190.43864	1	6.20E-05	0.13	2.09	-	233.6
gi|5454152|ref|NP_006285.1| ubiquinol-cytochrome c reductase binding protein [Homo sapiens]				6.53E-05	0.96	10.21	11.70	13530.4
AHQ-4-13-, 5184	K.YEEENFYLEPYLK.E	1737.88601	2	6.53E-05	0.96	4.20	-	1819.5
AHQ-4-13, 5300	K.YEEENFYLEPYLK.E	1737.88601	2	2.52E-04	0.95	3.80	-	1660.1
gi|30158950|ref|XP_301585.1| similar to natural killer cell transcript 4 [Homo sapiens]				6.66E-05	0.57	10.17	15.40	18547.1
AHQ-4-12, 4881	R.EPTVNKDIHQRTCDLSKTIEAPAER.Q	2911.19785	3	6.66E-05	0.57	3.38	-	337.9
gi|4557038|ref|NP_002467.1| atrial/embryonic alkali myosin light chain; myosin, atrial/fetal muscle				6.68E-05	0.52	10.15	9.60	21564.5
AHQ-4-12, 4958	R.ALGQNPTNAEVLRVLGKPK.P	2006.33843	2	6.68E-05	0.52	3.02	-	299.5
gi|8923579|ref|NP_060377.1| hypothetical protein FLJ20625 [Homo sapiens]				6.71E-05	0.89	10.30	18.60	17744.7
AHQ-4-14-, 6167 - 6219	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	6.71E-05	0.89	4.63	-	660.7
gi|4758784|ref|NP_004540.1| NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa; NADH				6.78E-05	0.86	10.16	7.60	14187.4
AHQ-4-13, 2851	K.REDYLYAVR.D	1185.31400	2	6.78E-05	0.86	3.13	-	946.6
gi|10835189|ref|NP_000628.1| glutathione reductase [Homo sapiens]				6.87E-05	0.93	10.22	3.80	51700.3
AHQ-4-7, 2279	R.GHAAFTSDPKPTIEVSGK.K	1843.03012	2	6.87E-05	0.93	4.16	-	589.8
gi|19923750|ref|NP_002858.2| RAB3B, member RAS oncogene family; Brain antigen RAB3B [Homo sapiens]				6.95E-05	0.93	10.19	5.00	24757.7
AHQ-4-13-, 3390 - 3468	K.LQIWDTAGQER.Y	1317.43243	2	6.95E-05	0.93	3.84	-	1159.9
gi|19923142|ref|NP_002256.2| karyopherin beta 1; nuclear factor p97; importin 90; importin beta-1 s				6.99E-05	0.73	10.17	1.70	97169.7
AHQ-4-14-, 6463	R.AAVENLPTFLVELSR.V	1659.90783	2	6.99E-05	0.73	3.38	-	383.4
gi|9845297|ref|NP_063940.1| second mitochondria-derived activator of caspase isoform Smac-alpha, pr				7.11E-05	0.94	10.19	4.20	27130.6
AHQ-4-11, 3089	K.LAEAQIEELR.Q	1172.31354	2	7.11E-05	0.94	3.83	-	1539.7
gi|30147857|ref|XP_293007.2| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				7.14E-05	0.56	10.16	5.90	20789.8
AHQ-4-12, 3529	K.KITIADCGQLQ	1248.43160	2	7.14E-05	0.56	2.62	-	831.6
gi|29734623|ref|XP_299768.1| hypothetical protein XP_299768 [Homo sapiens]				7.68E-05	0.10	10.11	7.50	14905.7
AHQ-4-9, 3208 - 3397	K.RMVPVKEIDR.L	1243.50477	1	7.12E-04	0.24	2.28	-	373.8
AHQ-4-11, 3510	K.RMVPVKEIDR.L	1243.50477	1	7.68E-05	0.10	1.90	-	344.1
AHQ-4-6, 3455	K.RMVPVKEIDR.L	1243.50477	1	3.48E-04	0.13	1.88	-	262.1
gi|6005717|ref|NP_009031.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e; ATP				8.03E-05	0.19	20.12	29.00	7933.1
AHQ-4-14-, 2878	R.ELAEDDSILK	1133.23094	1	2.52E-04	0.04	2.02	-	81.6
AHQ-4-5, 2182	K.KQDELKRIAR.E	1257.46804	1	8.03E-05	0.14	2.02	-	250.7
gi|30149221|ref|XP_291446.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				9.10E-05	0.95	10.19	3.90	45688.5
AHQ-4-6, 2159 - 2230	R.STAGDTHLGGEDFDNR.M	1692.68222	2	9.10E-05	0.95	3.83	-	1551.2
gi|7657124|ref|NP_055165.1| TNF-induced protein [Homo sapiens]				9.34E-05	0.96	10.23	10.50	22047.4
AHQ-4-12, 7053 - 7123	K.SIATTLIDDTSSEVLDELYR.V	2242.42274	2	9.34E-05	0.96	4.55	-	1289.0
gi|30149460|ref|XP_210540.2| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				9.46E-05	0.90	10.18	4.00	29287.8
AHQ-4-5, 2038 - 2114	K.HIYYITGETK.D	1225.37490	2	9.46E-05	0.90	3.28	-	712.0
gi|22538467|ref|NP_002787.2| proteasome beta 4 subunit; proteasome subunit, beta type, 4; proteasom				9.73E-05	0.33	10.10	3.40	29204.0
AHQ-4-10, 2631	R.FQIATVTEK.G	1037.19123	1	9.73E-05	0.33	2.06	-	270.2
gi|4504045|ref|NP_002063.1| guanine nucleotide binding protein (G protein), q polypeptide [Homo sap				9.92E-05	1.76	20.20	8.90	42142.8
AHQ-4-9, 6632	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	2.08E-04	0.84	3.63	-	552.6
AHQ-4-10, 6444	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	5.13E-04	0.45	2.70	-	381.0
AHQ-4-8, 4149	K.VSAFENPYVDAIK.S	1453.62101	2	9.92E-05	0.92	4.00	-	860.4
gi|30148125|ref|XP_303117.1| hypothetical protein XP_303117 [Homo sapiens]				9.93E-05	0.24	10.13	9.40	15235.5
AHQ-4-2, 2464	K.DKVIFIKELATLR.K	1546.87899	2	9.93E-05	0.24	2.62	-	308.4
gi|4502167|ref|NP_000475.1| amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disea				1.01E-04	0.86	10.18	2.30	86942.8
AHQ-4-4, 6978	R.CLVGEFVSDALLVPDKCK.F	2053.38561	2	1.01E-04	0.86	3.70	-	830.2
gi|5453722|ref|NP_006321.1| lysophospholipase I; lysophospholipase 1; lysophospholipid-specific lys				1.06E-04	0.93	10.19	6.10	24669.5
AHQ-4-11, 6416	K.LAGVTALSCWLPLR.A	1558.86992	2	1.06E-04	0.93	3.77	-	1091.6
gi|12707570|ref|NP_004083.2| mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor [Homo				1.08E-04	1.50	20.17	13.40	31371.2

AHQ-4-10, 4891	K.AQFAQPEILIGTIPGAGGTQR.L	2126.40140	2	1.08E-04	0.70	3.00	-	651.1
AHQ-4-10, 4585 - 4644	K.IFEEDPAVGAIVLTGGDK.A	1832.04401	2	4.63E-04	0.80	3.38	-	721.8
gi|8923114|ref|NP_060140.1|	ubiquitin-specific protease otubain 1 [Homo sapiens]			1.12E-04	0.91	10.20	5.50	31311.8
AHQ-4-10, 3712	R.IQQEIAVQNPLVSER.L	1724.93991	2	1.12E-04	0.91	4.01	-	1017.6
gi|29736201|ref|XP_292230.1|	similar to DnaJ homolog subfamily C member 8 (Splicing protein spf31)			1.13E-04	0.17	10.09	4.10	28482.2
AHQ-4-14, 6176 - 6237	K.MKLFAQLEIK.R	1221.53748	1	1.13E-04	0.17	1.88	-	422.0
gi|4759302|ref|NP_004729.1|	VAMP (vesicle-associated membrane protein)-associated protein B and C;			1.14E-04	0.81	10.16	5.80	27228.2
AHQ-4-12, 4274	K.FRGPFTDVVTTNLK.L	1595.82383	2	1.14E-04	0.81	3.18	-	820.9
gi|10047092|ref|NP_037391.1|	neuronal protein [Homo sapiens]			1.17E-04	0.84	10.15	5.00	31454.0
AHQ-4-12, 6078	R.TTDIFQTVDLWEGK.D	1653.81378	2	1.17E-04	0.84	3.08	-	799.6
gi|7705827|ref|NP_057187.1|	GTP-binding protein Sara [Homo sapiens]			1.18E-04	0.32	10.18	5.60	22409.7
AHQ-4-11, 4136	K.LVFLGLDNAGK.T	1147.34882	1	1.18E-04	0.32	2.09	-	521.4
AHQ-4-11, 4132 - 4210	K.LVFLGLDNAGK.T	1147.34882	2	9.81E-04	0.94	3.59	-	1268.7
gi|4557773|ref|NP_000248.1|	myosin, heavy polypeptide 7, cardiac muscle, beta [Homo sapiens]			1.18E-04	1.26	20.17	1.20	223110.8
AHQ-4-3, 3481	R.CNGVLEGIR.I	1019.15759	2	1.49E-04	0.84	3.01	-	793.3
AHQ-4-2, 3492	R.CNGVLEGIR.I	1019.15759	2	1.18E-04	0.83	3.07	-	646.7
AHQ-4-2, 4240	R.IEELEEELESERTAR.A	1833.93203	2	2.95E-04	0.43	3.13	-	548.2
gi|22065448|ref|XP_084610.2|	similar to tubulin alpha-1 chain - Chinese hamster [Homo sapiens] [MAS			1.24E-04	0.84	10.18	2.40	41009.4
AHQ-4-11, 4805	K.EIIDLVLDR.I	1086.26378	2	1.24E-04	0.84	3.12	-	1179.5
gi|20070158|ref|NP_003567.2|	serine/threonine kinase 24 (STE20 homolog, yeast); STE20-like kinase 3			1.26E-04	0.94	10.23	4.30	49307.6
AHQ-4-7, 7327 - 7381	K.RPFSQCLSTIISPLFAELK.E	2209.59351	2	1.26E-04	0.94	4.55	-	1001.2
gi|21361794|ref|NP_060918.2|	TIP120 protein [Homo sapiens]			1.28E-04	1.47	20.18	3.20	136374.7
AHQ-4-4, 4879	K.TVIGELPPASSGSALAANVCK.K	2044.31552	2	4.66E-04	0.59	3.10	-	276.6
AHQ-4-4, 4580	K.VIRPLDQPSSFDATPYIK.D	2048.32741	2	1.28E-04	0.88	3.59	-	774.2
gi|30149555|ref|XP_301154.1|	similar to heat shock protein 86 [Homo sapiens]			1.31E-04	0.93	10.20	10.60	15781.6
AHQ-4-5, 5601	K.HSQFIGYPITLFVEK.E	1780.05877	2	1.31E-04	0.93	4.01	-	911.3
gi|7656952|ref|NP_055227.1|	calcyclin binding protein [Homo sapiens]			1.39E-04	1.38	20.24	17.50	26209.8
AHQ-4-10, 3887	K.KAELLDNEKPAAVVAPITTGYTVK.I	2529.91377	2	1.39E-04	0.95	4.85	-	923.7
AHQ-4-10, 2348	K.KIYEDGDDDMKRTINK.A	1942.14037	2	8.89E-04	0.43	2.74	-	439.3
gi|22749247|ref|NP_689822.1|	hypothetical protein FLJ32001 [Homo sapiens]			1.42E-04	0.91	10.18	2.90	79570.3
AHQ-4-14-, 6258	R.ALPLCLHQIAESYFQEEDYEK.A	2585.82652	2	1.42E-04	0.91	3.52	-	1555.1
gi|20535081|ref|XP_067504.4|	similar to Cop-coated vesicle membrane protein p24 precursor (p24A) [H			1.44E-04	0.89	10.19	4.60	29313.6
AHQ-4-12, 4515 - 4585	R.VSFELFADEVPK.T	1381.55480	2	1.44E-04	0.89	3.72	-	759.6
gi|18572267|ref|XP_088476.1|	similar to thioredoxin domain containing 4; endoplasmic reticulum resi			1.48E-04	0.88	10.15	3.40	46970.9
AHQ-4-7, 4839	K.TPADCPVIAIDSFR.H	1563.75706	2	1.48E-04	0.88	3.03	-	925.8
gi|11128019|ref|NP_061820.1|	cytochrome c [Homo sapiens]			1.49E-04	0.82	10.18	13.30	11748.7
AHQ-4-13, 2286	K.TGQAPGYSYTAANK.N	1429.51641	2	1.49E-04	0.82	3.53	-	429.4
gi|20070272|ref|NP_057110.2|	androgen-regulated short-chain dehydrogenase/reductase 1; prostate sho			1.49E-04	0.72	10.17	6.30	35414.1
AHQ-4-9, 3016	K.GSGVTTYSVHPGTVQSELVR.H	2075.26811	2	1.49E-04	0.72	3.38	-	376.7
gi|18491024|ref|NP_005691.2|	dipeptidylpeptidase III isoform 1; dipeptidylpeptidase III [Homo sapie			1.54E-04	0.68	10.18	2.40	82588.6
AHQ-4-6, 4088	R.LASVLGSEPSLDSEVTSK.L	1819.98840	2	1.54E-04	0.68	2.86	-	382.9
gi|27413156|ref|NP_000338.2|	spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)			1.60E-04	0.93	10.19	0.70	246320.0
AHQ-4-2, 5026	R.FQIQDIVVQTQEGR.E	1661.84068	2	1.60E-04	0.93	3.54	-	1569.5
gi|30147562|ref|XP_304825.1|	hypothetical protein XP_304825 [Homo sapiens]			1.67E-04	0.11	10.15	14.10	21498.6
AHQ-4-13-, 4744	R.VYGSEELVTVKSCGM*IPGKEIYMCLM*CK.L	3319.92038	3	1.67E-04	0.11	3.00	-	170.6
gi|21361553|ref|NP_003168.2|	spleen tyrosine kinase [Homo sapiens]			1.70E-04	1.64	20.18	4.70	72065.7
AHQ-4-13, 5781	R.EEAEDYLVQGGM*SDGLYLLR.Q	2275.47789	2	1.73E-04	0.88	3.69	-	796.3
AHQ-4-6, 2510	K.YLEESNFVHR.D	1294.39732	2	1.70E-04	0.76	2.89	-	719.5
gi|4503445|ref|NP_001944.1|	endothelial cell growth factor 1 (platelet-derived); thymidine phosphor			1.74E-04	0.61	10.17	3.90	49955.2
AHQ-4-7, 7373	R.DVTATVDSLPLITASILSK.K	1945.24371	2	1.74E-04	0.61	3.43	-	255.5
gi|5031957|ref|NP_005701.1|	polyglutamine binding protein 1; nuclear protein containing WW domain 3			1.86E-04	0.46	10.14	7.20	30472.0
AHQ-4-9, 4587	R.NEAKTGADTTAAGPLFQQR.P	1977.12453	2	1.86E-04	0.46	2.72	-	424.2
gi|4557377|ref|NP_000052.1|	Bruton agammaglobulinemia tyrosine kinase [Homo sapiens]			1.89E-04	0.94	10.22	2.60	76280.8
AHQ-4-6, 3410	R.HYVVCSTPQSQYYLAEK.H	2075.28663	2	1.89E-04	0.94	4.44	-	768.2
gi|30152949|ref|XP_301425.1|	similar to Heat shock protein HSP 90-beta (HSP 84) (HSP 90) [Homo sapi			2.00E-04	0.44	10.17	2.50	42437.9
AHQ-4-5, 2021 - 2046	K.YINQEELNK.I	1151.25119	1	2.00E-04	0.44	3.32	-	274.1
gi|29727204|ref|XP_290872.1|	similar to Pyruvate kinase, M2 isozyme [Homo sapiens]			2.10E-04	0.93	10.16	5.40	16297.7
AHQ-4-7, 2053	R.APIIAVTR.N	841.03348	2	2.10E-04	0.93	3.09	-	1166.2
gi|8923582|ref|NP_060378.1|	hypothetical protein FLJ20626 [Homo sapiens]			2.16E-04	0.52	10.14	2.70	48956.7
AHQ-4-6, 2770	R.AFDWKSQLVIHR.K	1500.72897	2	2.16E-04	0.52	2.56	-	544.8
gi|28178825|ref|NP_005887.2|	isocitrate dehydrogenase 1 (NADP+), soluble; oxalosuccinate decarboxyl			2.24E-04	0.82	10.18	4.10	46659.0
AHQ-4-8, 6511 - 6591	K.GQETSTNPIASIFAWTR.G	1880.05046	2	2.24E-04	0.82	3.51	-	544.0
gi|30153852|ref|XP_171113.3|	similar to Moesin (Membrane-organizing extension spike protein) [Homo			2.25E-04	0.97	10.23	9.30	15601.7
AHQ-4-6, 1667 - 1675	R.RKPDTIEVQQMK.A	1473.72364	2	2.25E-04	0.97	4.65	-	1610.6
gi|7705300|ref|NP_057701.1|	hypothetical protein BM-002 [Homo sapiens]			2.26E-04	0.81	10.21	17.60	9117.5
AHQ-4-14-, 5313 - 5315	K.VLSVPESTPFTAVLK.F	1588.86951	2	2.26E-04	0.81	3.30	-	342.8
gi|29743324|ref|XP_293276.1|	similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote			2.33E-04	1.83	20.34	16.00	21244.7
AHQ-4-13, 5644 - 5725	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPMPK.L	3228.70228	3	4.18E-04	0.93	5.89	-	1442.7
AHQ-4-13-, 5086 - 5153	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	5.75E-04	0.81	4.75	-	659.0
AHQ-4-14-, 5493	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPMPK.L	3228.70228	3	2.33E-04	0.88	5.29	-	1076.9
AHQ-4-13, 5368 - 5432	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	4.12E-04	0.94	6.82	-	1158.1
gi|4557321|ref|NP_000030.1|	apolipoprotein A-I precursor [Homo sapiens]			2.37E-04	0.78	10.15	4.50	30777.6
AHQ-4-14-, 6114	K.VSFLSALEEYTK.K	1387.55934	2	2.37E-04	0.78	2.54	-	967.3
gi|20149570|ref|NP_005816.2|	RAS guanyl releasing protein 2 isoform 1; calcium and diacylglycerol-r			2.51E-04	0.95	10.21	1.80	75547.0
AHQ-4-6, 3006	K.LDQALVVEHIEK.M	1394.59824	2	2.51E-04	0.95	4.23	-	1389.4
gi|29739720|ref|XP_291724.1|	similar to 60S RIBOSOMAL PROTEIN L26 [Homo sapiens]			2.52E-04	0.25	10.17	11.10	39345.5
AHQ-4-8, 7243 - 7321	R.GSSSSLQKRRLNTHLDSQAMPLIPAGALDPLYSGAVLSER.K	4238.77865	3	2.52E-04	0.25	3.48	-	106.5
gi|11072091|ref|NP_057736.2|	Crn, crooked neck-like 1; CGI-201 protein; crooked neck protein (crn);			2.53E-04	0.16	10.11	1.10	99200.7
AHQ-4-4, 3127	R.FVLVHPDVK.N	1054.26662	1	2.53E-04	0.16	1.93	-	414.1
gi|28376664|ref|NP_777550.1|	hypothetical protein LOC93550 [Homo sapiens]			2.53E-04	0.51	10.12	1.20	80359.5
AHQ-4-12, 2290	K.M*KLLKAKMK.N	1107.50252	1	2.53E-04	0.51	2.22	-	791.3
gi|5031855|ref|NP_005556.1|	lymphocyte cytosolic protein 2; SH2 domain-containing leukocyte protein			2.53E-04	0.79	10.15	2.30	60187.8
AHQ-4-12, 4130 - 4143	K.ESQVYLLGTGLR.G	1336.51879	2	2.53E-04	0.79	3.10	-	996.7
gi|4505395|ref|NP_002499.1|	nidogen (enactin); Nidogen; nidogen (entactin) [Homo sapiens]			2.54E-04	0.52	10.17	0.60	136488.3
AHQ-4-2, 4503	K.NLYFTDWK.M	1087.20879	1	2.54E-04	0.52	2.37	-	479.2
gi|24308400|ref|NP_612366.1|	hypothetical protein BC010682 [Homo sapiens]			2.54E-04	0.57	10.14	4.80	39866.6
AHQ-4-9, 5968	R.CQFTLKPISDSVGVFLR.Q	1969.29348	2	2.54E-04	0.57	2.75	-	371.9
gi|4505877|ref|NP_000436.1|	plectin 1, intermediate filament binding protein 500kDa; plectin 1, int			2.54E-04	0.77	10.17	0.30	518488.0
AHQ-4-1, 5285	K.VQSGSESVIQEYVDLR.T	1809.95530	2	2.54E-04	0.77	3.46	-	592.8
gi|20357529|ref|NP_005264.2|	guanine nucleotide-binding protein, beta-2 subunit; G protein, beta-2			2.54E-04	0.92	10.21	5.90	37330.8
AHQ-4-9, 4395 - 4413	R.KACGDSTLTQITAGLDPVGR.I	2062.29094	2	2.54E-04	0.92	4.24	-	783.6
gi|29745994|ref|XP_290546.1|	similar to KIAA0830 protein [Homo sapiens]			2.54E-04	0.86	10.16	2.60	55016.4
AHQ-4-1, 4431	K.ILEVVNQIQDEER.M	1585.74098	2	2.54E-04	0.86	3.27	-	1060.1
gi|12548785|ref|NP_068711.1|	gamma-aminobutyric acid (GABA) A receptor, beta 2 isoform 1 [Homo sapi			2.60E-04	0.82	10.17	2.30	59150.1
AHQ-4-11, 5997	R.LDVNKIFYKDIK.Q	1496.77530	2	2.60E-04	0.82	3.44	-	804.5
gi|29727249|ref|XP_298422.1|	hypothetical protein XP_298422 [Homo sapiens]			2.65E-04	0.46	10.15	7.40	21396.6
AHQ-4-3, 3509 - 3581	K.GKAGIQTQICLTLK.P	1532.83078	2	2.65E-04	0.46	3.04	-	381.0
gi|28461290|ref|NP_443728.2|	TRALPUSH; no opposite paired repeat protein [Homo sapiens]			2.66E-04	0.49	10.14	0.40	240073.5
AHQ-4-4, 3716	K.KKPQVNAK.D	913.09970	1	2.81E-04	0.20	2.11	-	384.0
AHQ-4-10, 3343	K.KKPQVNAK.D	913.09970	1	2.66E-04	0.49	2.81	-	375.6
AHQ-4-11, 3517	K.KKPQVNAK.D	913.09970	1	3.16E-04	0.63	2.63	-	577.7
AHQ-4-3, 3728	K.KKPQVNAK.D	913.09970	1	3.78E-04	0.24	2.18	-	354.1
gi|4502475|ref|NP_001723.1|	butyrophilin, subfamily 1, member A1 [Homo sapiens]			2.71E-04	0.41	10.10	1.70	59003.9
AHQ-4-12, 2986	R.LLEELKWKK.A	1187.45608	1	2.71E-04	0.41	2.08	-	595.6
gi|14249526|ref|NP_116214.1|	zinc finger protein 382; multiple-zinc-finger-Kruppel-associated box p			2.80E-04	0.28	10.14	2.60	63794.0
AHQ-4-13, 5480	R.PLIFINHKKLIKER.S	1750.16684	2	2.80E-04	0.28	2.60	-	424.1
gi|4502459|ref|NP_001719.1|	basigin; OK blood group; emmprin; collagenase stimulatory factor; M6 an			2.82E-04	0.21	10.13	6.70	29220.7

AHQ-4-7, 4006	R.SELHIENLNMEADPGQYR.C	2117.28536	2	2.82E-04	0.21	2.54	-	185.6
gi|4557469|ref|NP_001273.1|	adaptor-related protein complex 2, beta 1 subunit; adaptin, beta 2 (bet			2.85E-04	0.91	10.28	1.30	104551.9
AHQ-4-6, 6119	R.CVSTLLDLIQTK.V	1392.64385	2	2.85E-04	0.91	3.42	-	1120.5
gi|5031611|ref|NP_005859.1|	BET1 homolog; Golgi vesicular membrane trafficking protein p18; Bet1p h			2.92E-04	0.75	10.18	15.30	13289.4
AHQ-4-13-, 4733	K.LLAEM*DSQFDSTTGFLGK.T	1977.18145	2	2.92E-04	0.75	3.67	-	154.3
gi|9257195|ref|NP_004733.1|	BAI1-associated protein 1; WW domain-containing protein 3; atrophin-1 i			2.92E-04	0.62	10.17	1.30	136980.0
AHQ-4-12, 7145 - 7146	R.CRGLKEGDLIVEVNKK.N	1860.16856	2	2.92E-04	0.62	3.33	-	473.7
gi|16418461|ref|NP_443195.1|	mitochondrial topoisomerase I [Homo sapiens]			2.96E-04	0.29	10.16	2.20	69871.5
AHQ-4-14, 5788	R.WEKEKHEDGVKWR.Q	1727.90404	2	2.96E-04	0.29	2.66	-	320.0
AHQ-4-14-, 4537	R.WEKEKHEDGVKWR.Q	1727.90404	2	4.47E-04	0.41	3.13	-	488.4
AHQ-4-14, 5533 - 5598	R.WEKEKHEDGVKWR.Q	1727.90404	2	5.00E-04	0.58	3.21	-	341.7
gi|24111250|ref|NP_006563.2|	guanine nucleotide binding protein (G protein), alpha 13 [Homo sapiens			2.97E-04	0.29	10.14	4.50	44049.3
AHQ-4-8, 4801	K.LGEPDYIPSQQDILLAR.R	1929.16292	2	2.97E-04	0.29	2.81	-	189.2
gi|4757886|ref|NP_004330.1|	pituitary tumor-transforming protein 1-interacting protein precursor; c			3.02E-04	0.95	10.20	10.00	20323.7
AHQ-4-10, 5185 - 5243	K.ACLDYPVTSVLPPASLCK.L	1994.31817	2	3.02E-04	0.95	4.05	-	1178.3
gi|8922712|ref|NP_060713.1|	hypothetical protein FLJ10849 [Homo sapiens]			3.06E-04	0.63	10.18	4.20	49397.9
AHQ-4-7, 3389	K.DTDPDSKPFSLQETYEAK.R	2072.17149	2	3.06E-04	0.63	3.18	-	265.1
gi|13899297|ref|NP_113646.1|	B aggressive lymphoma gene [Homo sapiens]			3.07E-04	0.26	10.12	1.30	96282.7
AHQ-4-5, 2589	K.SILQQAGVEMK.S	1204.42218	1	9.66E-04	0.03	1.87	-	340.0
AHQ-4-3, 2777	K.SILQQAGVEMK.S	1204.42218	1	3.07E-04	0.26	2.34	-	608.6
gi|4502599|ref|NP_001748.1|	carbonyl reductase 1; carbonyl reductase (NADPH); carbonyl reductase (N			3.11E-04	0.68	10.15	5.40	30374.7
AHQ-4-9, 4961	R.DVCTELLPLIKPQGR.V	1741.04567	2	3.11E-04	0.68	3.01	-	437.9
gi|20540302|ref|XP_166540.1|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			3.19E-04	0.22	10.09	6.10	12714.2
AHQ-4-6, 1568	K.DNNLLGK.F	773.85763	1	3.19E-04	0.22	1.82	-	319.8
gi|27500008|ref|XP_208872.1|	similar to tropomyosin 3 [Homo sapiens]			3.20E-04	0.81	10.19	6.50	28954.4
AHQ-4-9, 3013	R.ALKDEEKM*ELQELQLK.E	1962.25460	2	3.20E-04	0.81	3.79	-	460.8
gi|5729873|ref|NP_006656.1|	heparanase; heparanase-1 [Homo sapiens]			3.22E-04	1.47	20.21	3.30	61176.4
AHQ-4-14-, 4351	R.FLILLGSPK.L	988.24808	1	6.65E-04	0.64	2.48	-	257.9
AHQ-4-14-, 4894	K.TDFLIFDPK.K	1096.25713	1	5.11E-04	0.47	2.06	-	538.7
AHQ-4-14-, 4889	K.TDFLIFDPK.K	1096.25713	2	3.22E-04	0.83	2.74	-	1035.9
gi|5453854|ref|NP_006187.1|	poly(rC) binding protein 1; heterogenous nuclear ribonucleoprotein X; p			3.26E-04	0.93	10.22	5.90	37525.7
AHQ-4-14-, 6315	R.QVTITGSAASISLAQYLINAR.L	2178.47461	2	3.26E-04	0.93	4.38	-	719.1
gi|4502501|ref|NP_000583.1|	complement component 4B proprotein [Homo sapiens]			3.28E-04	0.05	10.12	0.50	192795.6
AHQ-4-6, 4806 - 4866	K.SCGLHQLLR.G	1085.26240	1	3.28E-04	0.05	2.03	-	98.0
gi|8922416|ref|NP_060560.1|	hypothetical protein FLJ10420 [Homo sapiens]			3.29E-04	0.90	10.19	10.30	28338.6
AHQ-4-10, 5344	R.TSGELFAQAPVDQFPGTAVESVTDSSR.Y	2797.96841	2	3.29E-04	0.90	3.90	-	609.5
gi|23097308|ref|NP_149062.1|	nesprin 1 isoform longest; synaptic nuclei expressed gene 1; nesprin 1			3.37E-04	0.41	10.15	0.20	1005196.0
AHQ-4-13, 2674	K.GHSLLKSAREKGER.A	1568.76324	2	3.37E-04	0.41	2.95	-	366.3
gi|13376181|ref|NP_079079.1|	hypothetical protein FLJ21665 [Homo sapiens]			3.45E-04	0.78	10.15	3.80	49908.5
AHQ-4-7, 5207	R.SFGGGTGSGFTSLLMER.L	1704.88582	2	3.45E-04	0.78	3.00	-	812.2
gi|30156394|ref|XP_062437.6|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			3.46E-04	0.14	10.13	3.30	44396.0
AHQ-4-11, 4653 - 4664	R.DWSHYFKIIDDLR.A	1708.89749	2	3.46E-04	0.14	2.53	-	304.0
gi|7019375|ref|NP_037373.1|	formin homology 2 domain containing 1; FH1/FH2 domain-containing protei			3.51E-04	0.91	10.24	2.10	126496.5
AHQ-4-7, 3766	K.FSGVAGEAPSNPSVPVAVSSGPGR.G	2227.41945	2	3.51E-04	0.91	4.78	-	501.6
gi|4502205|ref|NP_001651.1|	ADP-ribosylation factor 4 [Homo sapiens]			3.54E-04	0.81	10.16	5.60	20510.6
AHQ-4-11, 2414	R.IQEVADELQK.M	1173.29830	2	3.54E-04	0.81	3.27	-	700.4
gi|4505369|ref|NP_002486.1|	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q			3.66E-04	0.81	10.16	8.60	20107.8
AHQ-4-12, 4615	K.LDITTLTGVPEEHIK.T	1666.89713	2	3.66E-04	0.81	3.16	-	767.0
gi|21361427|ref|NP_055182.2|	hypothetical protein, estradiol-induced [Homo sapiens]			3.69E-04	0.38	10.13	8.90	21551.0
AHQ-4-13, 5786	K.EDEIPETVSLEMLDAAK.N	1891.08690	2	3.69E-04	0.38	2.67	-	257.0
gi|24430151|ref|NP_002793.2|	proteasome 26S ATPase subunit 1; proteasome 26S subunit, ATPase, 1; 26			3.70E-04	0.82	10.19	4.50	49184.2
AHQ-4-7, 4962	K.APQETYADIGGLDNQIQEIK.E	2204.37942	2	3.70E-04	0.82	3.89	-	459.0
gi|24307917|ref|NP_006819.1|	RNA helicase family [Homo sapiens]			3.71E-04	0.44	10.16	0.90	251471.2
AHQ-4-11, 6409	K.QVKAGHQVMVFVHARNATVR.T	2249.63086	3	3.71E-04	0.44	3.14	-	353.1
gi|29725607|ref|NP_061141.2|	smooth muscle cell associated protein-1 [Homo sapiens]			3.83E-04	0.85	10.16	1.70	103076.3
AHQ-4-5, 4906	R.ALIPLALEGTDVGQTK.A	1626.87614	2	3.83E-04	0.85	3.23	-	696.9
gi|17448269|ref|XP_069750.1|	similar to GDP dissociation inhibitor isoform 2; GDI-2 [Homo sapiens]			3.86E-04	0.92	10.19	4.20	32024.9
AHQ-4-13, 4353	K.DLGTESQIFISR.A	1366.50176	2	3.86E-04	0.92	3.74	-	1099.9
gi|29729329|ref|XP_291459.1|	similar to Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18) [			3.93E-04	1.20	20.17	18.30	17172.9
AHQ-4-12, 5699	K.EILVGDVGQTVNNLYATFVK.M	2181.47373	2	6.44E-04	0.84	3.45	-	794.3
AHQ-4-12, 2281 - 2355	K.NIILEEGK.E	916.05399	1	3.93E-04	0.36	2.11	-	488.6
gi|14161692|ref|NP_115706.1|	calpain small subunit 2 [Homo sapiens]			3.94E-04	0.80	10.14	2.80	27660.1
AHQ-4-12, 3305	K.LGFEEFK.Y	869.98378	2	3.94E-04	0.80	2.82	-	651.7
gi|15451916|ref|NP_001195.2|	bone morphogenetic protein receptor, type II isoform 1 precursor; type			4.05E-04	0.26	10.15	2.60	115200.7
AHQ-4-9, 5695	K.SVSPTVNPM*STAMQNERNLSHNRRVPK.I	3068.44225	3	4.05E-04	0.26	3.02	-	280.0
gi|6912516|ref|NP_036463.1|	methionine sulfoxide reductase A; peptide met (O) reductase [Homo sapie			4.13E-04	0.58	10.14	8.50	26132.3
AHQ-4-10, 3677	K.GVYSTQVGFAGGYTSNPTYK.E	2098.25701	2	4.13E-04	0.58	2.83	-	439.9
gi|27500115|ref|XP_208901.1|	similar to ubiquitin-conjugating enzyme E2M; UBC12 homolog, yeast [Hom			4.25E-04	0.83	10.16	8.70	20964.0
AHQ-4-11, 5949 - 6020	K.TCDISFSDPDDLLNFK.L	1889.02935	2	4.25E-04	0.83	3.23	-	792.1
gi|7706563|ref|NP_057614.1|	RAB-8b protein [Homo sapiens]			4.28E-04	0.72	10.15	7.20	23584.0
AHQ-4-11, 4842	R.GAM*GIM*LVYDITNEK.S	1687.96006	2	4.28E-04	0.72	3.06	-	594.2
gi|23397516|ref|NP_694968.1|	immune associated nucleotide protein [Homo sapiens]			4.28E-04	0.52	10.18	7.70	34508.4
AHQ-4-8, 5425	K.MVQCNEGAYFSDDIYKDTEERLK.Q	2814.05454	3	4.28E-04	0.52	3.56	-	382.2
gi|20546215|ref|XP_115639.1|	similar to leukocyte immunoglobulin-like receptor, subfamily B (with T			4.31E-04	0.56	10.15	4.70	42748.2
AHQ-4-13, 4796	R.CSREVNSREDNVLYRVVK.P	2225.47152	2	4.31E-04	0.56	3.01	-	646.9
gi|13376719|ref|NP_079413.1|	hypothetical protein FLJ21439 [Homo sapiens]			4.42E-04	0.83	10.14	2.40	48893.8
AHQ-4-11, 4449	K.GDFNYLEEFK.Q	1262.34887	2	4.42E-04	0.83	2.85	-	813.4
gi|4503609|ref|NP_001976.1|	electron-transfer-flavoprotein, beta polypeptide; electron-transferring			4.50E-04	0.80	10.15	4.70	27843.4
AHQ-4-10, 3073	K.LSVISVEDPPQR.T	1340.50744	2	4.50E-04	0.80	3.05	-	935.3
gi|4502849|ref|NP_001272.1|	cytoskeleton-associated protein 1 [Homo sapiens]			4.52E-04	0.71	10.17	10.20	27394.4
AHQ-4-9, 6123 - 6140	K.YGAFVKPAVVTVGDFPEEDYGLDEI	2731.98993	2	4.52E-04	0.71	3.44	-	460.8
gi|29734552|ref|XP_291269.1|	similar to KIAA1875 protein [Homo sapiens]			4.53E-04	0.73	10.17	1.70	93320.7
AHQ-4-13-, 4649	R.M*LAPKRSWGTPQLR.L	1657.96500	2	4.53E-04	0.73	3.36	-	692.7
gi|21702742|ref|NP_055309.1|	trinucleotide repeat containing 6; EDIE; GW182 autoantigen [Homo sapie			4.55E-04	0.45	10.16	1.60	182051.8
AHQ-4-4, 5831 - 5899	K.PALRWGDSKGSNCQGGWEDDSAATGM*VK.S	2999.19916	3	4.55E-04	0.45	3.02	-	271.5
gi|4504213|ref|NP_000847.1|	guanylate cyclase 1, soluble, alpha 3 [Homo sapiens]			4.65E-04	0.50	10.13	2.00	81377.2
AHQ-4-6, 4567	R.GLYLSDIPIHNALR.D	1582.82829	2	4.65E-04	0.50	2.60	-	409.8
gi|4507303|ref|NP_001045.1|	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 2; th			4.71E-04	0.31	10.14	8.80	34310.4
AHQ-4-9, 6148 - 6164	K.YFAEALGPLQSFQARPDDLLISTYPK.S	2942.31346	2	4.71E-04	0.31	2.71	-	216.2
gi|29788766|ref|NP_064424.2|	tubulin, beta polypeptide 4, member Q [Homo sapiens]			4.74E-04	0.69	10.18	3.50	48377.2
AHQ-4-13, 4060	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	4.74E-04	0.69	3.53	-	279.0
gi|29735989|ref|XP_299876.1|	hypothetical protein XP_299876 [Homo sapiens]			4.76E-04	0.21	10.13	5.80	31166.3
AHQ-4-6, 4539	K.SLEKVFADLIRGSKDK.K	1807.08406	2	4.76E-04	0.21	2.67	-	342.5
gi|4507287|ref|NP_003755.1|	syntaxin 11 [Homo sapiens]			4.84E-04	1.38	20.21	8.40	32955.3
AHQ-4-9, 4211	K.EVSGDQIEDMFEQGK.W	1712.81676	2	8.21E-04	0.87	4.30	-	674.5
AHQ-4-9, 3455	R.LAELLDLSK.Q	1002.18679	1	4.84E-04	0.51	2.74	-	399.6
gi|30155919|ref|XP_292814.2|	similar to zinc finger protein 433 [Homo sapiens]			4.84E-04	0.53	10.16	1.60	108732.0
AHQ-4-14-, 4870	K.CKQCGKGFNLPSSIR.Y	1755.01259	2	4.84E-04	0.53	3.28	-	392.5
gi|5902124|ref|NP_008878.1|	signal recognition particle 72kDa; signal recognition particle 72kD [Ho			4.88E-04	0.40	10.14	2.40	74605.7
AHQ-4-9, 3597	R.LERYDECLAVYRDLVR.N	2072.33065	2	4.88E-04	0.40	2.72	-	527.9
gi|30152324|ref|XP_305530.1|	hypothetical protein XP_305530 [Homo sapiens]			4.99E-04	0.65	10.16	3.80	40332.7
AHQ-4-10, 4220	R.SGLWNASLCIEGRR.E	1620.81507	2	4.99E-04	0.65	3.13	-	541.5
gi|30148924|ref|XP_292989.2|	similar to SOCS box protein ASB-18 [Homo sapiens]			5.00E-04	0.62	10.15	2.60	79848.7
AHQ-4-12, 6123	R.TRGACPPRPAQASGTRAPR.G	2009.24265	3	5.00E-04	0.62	3.08	-	772.3
gi|27482697|ref|XP_166112.3|	similar to KIAA1217 protein [Homo sapiens]			5.28E-04	0.08	10.15	0.60	146877.8
AHQ-4-3, 1620 - 1648	R.EAFLEHLK.Q	987.13390	1	5.28E-04	0.08	1.93	-	229.9
gi|10835121|ref|NP_000289.1|	pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H			5.29E-04	0.62	10.14	1.90	61829.8

AHQ-4-7, 3414	R.GDLGIEIPAEK.V	1142.28420	1	5.29E-04	0.62	2.76	-	504.5
gi|19923231|ref|NP_002860.2| RAB6A, member RAS oncogene family; Oncogene RAB6; RAB6, member RAS onc				5.41E-04	0.83	10.15	6.70	23548.6
AHQ-4-11, 2849	R.VAAALPGMESTQDR.S	1446.61192	2	5.41E-04	0.83	3.07	-	593.8
gi|4505941|ref|NP_000929.1| DNA directed RNA polymerase II polypeptide B; polymerase (RNA) II (DNA				5.42E-04	0.33	10.13	1.40	133895.7
AHQ-4-11, 5161 - 5172	K.FIDRGKDFNLELAIKTR.I	2037.35099	2	5.42E-04	0.33	2.68	-	453.0
gi|19913441|ref|NP_002140.2| hippocalcin-like 1; visinin-like protein 3; calcium-binding protein BD				5.46E-04	0.89	10.18	7.80	22313.1
AHQ-4-11, 4161	R.ENTEFTDHELQEWYK.G	1970.04095	2	5.46E-04	0.89	3.52	-	947.1
gi|27544939|ref|NP_060932.2| uncharacterized hematopoietic stem/progenitor cells protein MDS027 [Ho				5.68E-04	1.60	20.15	32.00	8744.9
AHQ-4-14, 6017	R.EYIEIITSSIK.K	1296.49134	2	5.68E-04	0.78	2.83	-	941.5
AHQ-4-14-, 5031	K.IADFLNSFDM*SCR.S	1593.76350	2	7.74E-04	0.82	2.92	-	801.7
gi|28557683|ref|NP_787068.1| hypothetical protein FLJ38451 [Homo sapiens]				5.87E-04	0.05	10.09	7.20	19531.9
AHQ-4-9, 4920	K.FFNQSSSLNNHR.R	1451.52853	1	5.87E-04	0.05	1.89	-	258.2
gi|7669501|ref|NP_005552.2| lysosomal-associated membrane protein 1 [Homo sapiens]				5.93E-04	0.94	10.23	3.80	44772.8
AHQ-4-4, 7198	R.FFLQGIQLNTILPDAR.D	1847.14988	2	5.93E-04	0.94	4.52	-	1002.8
gi|28557709|ref|NP_787082.1| hypothetical protein LOC221823 [Homo sapiens]				6.15E-04	0.92	10.21	5.30	34839.1
AHQ-4-9, 4348 - 4352	R.VYAILTHGIFSGPAISR.I	1803.09710	2	6.15E-04	0.92	4.23	-	703.7
gi|22907039|ref|NP_055323.2| apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3C [H				6.46E-04	0.59	10.15	7.40	22825.7
AHQ-4-11, 4997 - 5061	R.LYYFQYPCYQEGLR.S	1902.11778	2	6.46E-04	0.59	3.07	-	431.6
gi|4885263|ref|NP_005252.1| GTP binding protein overexpressed in skeletal muscle; GTP-binding prote				6.67E-04	0.47	10.14	3.40	33949.3
AHQ-4-13, 4145	R.ASFEKASELR.I	1138.25565	2	6.67E-04	0.47	2.72	-	502.3
gi|20536114|ref|XP_031223.2| similar to Hypothetical protein KIAA1034 [Homo sapiens]				6.85E-04	0.09	10.10	1.40	82555.0
AHQ-4-12, 3515 - 3639	R.YHVKHHGKLK.E	1247.47653	1	6.85E-04	0.09	1.92	-	275.9
gi|4759316|ref|NP_004175.1| tryptophanyl-tRNA synthetase; interferon-induced protein 53 [Homo sapie				6.93E-04	0.54	10.13	3.40	53087.0
AHQ-4-7, 5190	K.ALIEVLQPLIAEHQAR.R	1802.11065	2	6.93E-04	0.54	2.64	-	395.3
gi|4505705|ref|NP_003759.1| phosphoprotein enriched in astrocytes 15; Phosphoprotein enriched in as				7.04E-04	0.88	10.19	13.10	15040.0
AHQ-4-12, 6095	K.LDKDNLSYIEHIFEISR.R	2093.32504	2	7.04E-04	0.88	3.84	-	655.4
gi|21361409|ref|NP_036515.2| osteoclast stimulating factor 1 [Homo sapiens]				7.41E-04	0.68	10.16	11.50	24063.9
AHQ-4-10, 4957	R.TGLIPSNYVAEQAESIDNPLHEAAK.R	2668.89701	2	7.41E-04	0.68	3.27	-	319.1
gi|29732170|ref|XP_291550.1| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				7.45E-04	0.96	10.24	12.70	13262.9
AHQ-4-5, 3875	K.HLEINPDHSIIETLR.Q	1787.99770	3	7.45E-04	0.96	4.71	-	1839.6
gi|22538387|ref|NP_005742.4| A kinase anchor protein 9 isoform 2; yotiao; A-kinase anchoring protei				7.70E-04	0.37	20.15	0.80	452984.5
AHQ-4-10, 4740	K.DNLITKQNQLILEISK.L	1871.16805	2	8.10E-04	0.18	2.61	-	239.1
AHQ-4-14-, 5053 - 5061	R.GEESESATDSFPKKIK.G	1753.88851	2	7.70E-04	0.19	3.05	-	317.8
gi|4505301|ref|NP_002463.1| myosin, heavy polypeptide 8, skeletal muscle, perinatal [Homo sapiens]				7.75E-04	0.57	10.17	1.40	222660.8
AHQ-4-5, 3591 - 3665	K.AGLLGLLEEM*RDEKLAQIITRTQAVCR.G	3103.60765	3	7.75E-04	0.57	3.32	-	360.1
gi|6912240|ref|NP_036227.1| adaptor-related protein complex 3, mu 1 subunit; mu-adaptin 3A; AP-3 ad				7.82E-04	0.61	10.16	5.50	46938.9
AHQ-4-10, 4357	K.GLVNLQSGAPKPEENPSLNIQFK.I	2481.78929	2	7.82E-04	0.61	3.23	-	257.1
gi|27479431|ref|XP_050793.2| similar to KIAA1393 protein [Homo sapiens]				7.89E-04	0.26	10.12	1.60	58245.9
AHQ-4-5, 4705	-.M*VLWILWR.P	1133.43358	1	7.89E-04	0.26	1.87	-	524.5
gi|4758032|ref|NP_004757.1| coatomer protein complex, subunit beta 2 (beta prime); coatomer binding				8.17E-04	0.67	10.15	2.10	102486.5
AHQ-4-5, 6453	K.AAESLADPTEYENLFPGLK.E	2066.25322	2	8.17E-04	0.67	3.01	-	416.4
gi|7770075|ref|NP_054702.1| tachykinin 1 isoform alpha precursor; neurokinin A; neurokinin alpha; t				8.18E-04	0.41	10.13	12.60	13035.8
AHQ-4-1, 6245 - 6318	K.MAYERSAM*QNYERR.R	1822.01952	2	8.18E-04	0.41	2.53	-	433.2
gi|4507795|ref|NP_003340.1| ubiquitin-conjugating enzyme E2 variant 1 isoform b; DNA-binding protei				8.24E-04	0.77	10.16	4.10	25796.6
AHQ-4-12, 3358	K.YPEAPPFVR.F	1076.22914	2	8.24E-04	0.77	3.18	-	481.1
gi|8922297|ref|NP_060502.1| LUC7-like; sarcoplasmic reticulum protein LUC7B1 [Homo sapiens]				8.27E-04	0.08	10.10	2.20	38405.1
AHQ-4-9, 2935	R.EKLDQLR.K	902.03054	1	8.27E-04	0.08	2.02	-	320.8
gi|22129786|ref|NP_059980.1| gp25L2 protein [Homo sapiens]				8.35E-04	0.64	10.20	5.10	25104.5
AHQ-4-10, 2901	R.QLVEQVEQIQK.E	1342.52334	2	8.35E-04	0.64	3.16	-	454.4
gi|4505273|ref|NP_002442.1| 5'-methylthioadenosine phosphorylase [Homo sapiens]				8.39E-04	0.91	10.17	6.40	31249.9
AHQ-4-9, 5035	K.IGIIGGTGLDDPEILEGR.T	1826.04101	2	8.39E-04	0.91	3.44	-	1068.8
gi|29725611|ref|NP_066954.2| regulatory subunit PR 53 of protein phosphatase 2A isoform b; phosphot				8.40E-04	0.90	10.23	9.00	36775.0
AHQ-4-8, 7143	K.LDEEAENLVATVVPTHLAAAVPEVAVYLK.E	3063.49045	3	8.40E-04	0.90	4.63	-	960.2
gi|24119274|ref|NP_443099.1| voltage gated channel like 1; four repeat voltage-gated ion channel [H				8.51E-04	0.18	10.14	0.50	200329.3
AHQ-4-14-, 3707	K.FPNRPQMVK.I	1117.34944	1	8.51E-04	0.18	2.09	-	208.4
gi|4502989|ref|NP_001856.1| cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor; hepa				8.58E-04	0.80	10.14	15.70	9395.9
AHQ-4-14-, 5233	K.LFQEDDEIPLYLK.G	1623.82758	2	8.58E-04	0.80	2.85	-	1188.5
gi|30147267|ref|XP_304295.1| hypothetical protein XP_304295 [Homo sapiens]				8.58E-04	0.49	10.13	0.00	38558.9
AHQ-4-13-, 5956 - 5957	K.PLGWIGQMQGEK.A	1344.56442	2	8.58E-04	0.49	2.51	-	561.2
gi|21361290|ref|NP_005596.2| protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform				8.67E-04	0.31	10.13	3.10	58129.1
AHQ-4-12, 6537	-.M*SGRRFHLSTTDRVIK.A	1921.21709	2	8.67E-04	0.31	2.56	-	359.4
gi|7656894|ref|NP_055093.1| heat shock protein (hsp110 family) [Homo sapiens]				8.68E-04	0.88	10.16	1.70	94504.9
AHQ-4-4, 5590 - 5591	R.GCALQCAILSPAFK.V	1538.81393	2	8.68E-04	0.88	3.29	-	1175.8
gi|4506675|ref|NP_002941.1| ribophorin I [Homo sapiens]				8.70E-04	0.63	10.21	1.50	68569.0
AHQ-4-1, 2301	R.LAHLGVQVK.G	965.17461	1	8.70E-04	0.63	2.41	-	610.3
gi|21361470|ref|NP_056286.2| DKFZP566O1646 protein [Homo sapiens]				8.85E-04	0.87	10.23	6.00	32129.7
AHQ-4-13-, 6696 - 6701	K.ILECVIKTIKAKQEILK.Q	2029.51654	3	8.85E-04	0.87	4.70	-	1175.1
gi|30155210|ref|XP_305433.1| hypothetical protein XP_305433 [Homo sapiens]				9.00E-04	0.13	10.14	6.80	31248.6
AHQ-4-11, 6634 - 6692	K.VGPPPTTYPNEASQFLTKR.N	2104.35106	2	9.00E-04	0.13	2.81	-	195.0
gi|13699868|ref|NP_005947.2| methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methenyltet				9.28E-04	0.05	10.12	0.90	101530.5
AHQ-4-4, 4127 - 4139	K.ATHIKLPR.T	936.13649	1	9.28E-04	0.05	2.02	-	89.8
gi|4506677|ref|NP_002942.1| ribophorin II [Homo sapiens]				9.43E-04	0.74	10.21	2.90	69301.6
AHQ-4-1, 6705 - 6771	K.TSFTPVGDVFELNFM*NVK.F	2062.33118	2	9.43E-04	0.74	3.38	-	503.5
gi|27481006|ref|XP_117198.2| hypothetical protein XP_117198 [Homo sapiens]				9.60E-04	0.14	10.12	0.40	251738.6
AHQ-4-3, 3219 - 3220	K.EDELQEM*M*VK.D	1284.43954	1	9.60E-04	0.14	2.42	-	354.6
gi|9055270|ref|NP_061027.1| low density lipoprotein-related protein 1B (deleted in tumors); low den				9.71E-04	0.37	10.17	0.60	515514.6
AHQ-4-2, 4479	R.QPDVSKHLCMINNGGCSHLCLLAPGK.T	2911.35097	3	9.71E-04	0.37	3.07	-	311.2
gi|4885057|ref|NP_005152.1| angiotensin II receptor-like 1; angiotensin receptor-like 1 [Homo sapie				9.97E-04	0.16	10.11	2.10	42660.3
AHQ-4-2, 4388	R.KERIEGLR.K	1001.16535	1	9.97E-04	0.16	2.06	-	211.0

Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|4501885|ref|NP_001092.1| beta actin; beta cytoskeletal actin [Homo sapiens]				1.00E-30	14.86	160.41	33.30	41736.5
AHQ-5-14-, 6527	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	2.57E-04	0.65	3.65	-	421.1
AHQ-5-14-, 6346 - 6405	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	7.72E-05	0.87	4.48	-	886.2
AHQ-5-14-, 5934	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.30E-04	0.92	4.73	-	601.5
AHQ-5-13-, 6608	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.99E-08	0.66	3.71	-	630.8
AHQ-5-13-, 6527	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	3.09E-04	0.62	3.65	-	391.7
AHQ-5-13-, 6428 - 6491	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	7.01E-07	0.87	5.41	-	517.1
AHQ-5-13-, 6332 - 6344	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	4.81E-06	0.82	3.74	-	442.6
AHQ-5-13-, 6156	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.05E-09	0.86	4.15	-	485.1
AHQ-5-2, 7261 - 7294	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.13E-06	0.86	3.82	-	536.3
AHQ-5-13-, 6011 - 6071	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	6.29E-04	0.88	4.13	-	669.2
AHQ-5-13, 6404 - 6409	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	8.12E-09	0.93	4.87	-	786.8
AHQ-5-13, 6140 - 6168	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	3.13E-05	0.92	4.95	-	560.9
AHQ-5-8, 6417 - 6485	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	9.72E-06	0.57	3.55	-	299.3
AHQ-5-8, 6552 - 6620	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.20E-05	0.80	4.17	-	626.8
AHQ-5-3, 7238 - 7306	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.26E-05	0.77	3.77	-	536.1
AHQ-5-8, 6636 - 6702	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	9.79E-05	0.68	3.68	-	482.0
AHQ-5-10, 6328 - 6395	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	7.85E-09	0.94	5.19	-	841.4
AHQ-5-9, 6386	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.56E-08	0.94	5.15	-	725.7
AHQ-5-8, 6774 - 6846	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	9.22E-05	0.91	4.68	-	757.7
AHQ-5-4, 7256 - 7326	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.85E-04	0.93	4.60	-	1003.8
AHQ-5-8, 6882 - 6948	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.98E-06	0.95	5.44	-	870.7
AHQ-5-9, 6239 - 6318	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	8.93E-10	0.92	4.41	-	990.4
AHQ-5-7, 7119 - 7123	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.36E-07	0.93	4.99	-	792.8
AHQ-5-8, 6030	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.96E-04	0.83	3.79	-	571.1
AHQ-5-8, 7296 - 7365	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.38E-10	0.94	5.55	-	613.3
AHQ-5-5, 7159	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.68E-06	0.85	4.00	-	574.6
AHQ-5-5, 7249	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.37E-08	0.90	4.55	-	704.6
AHQ-5-8, 7012 - 7081	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	1.99E-09	0.95	5.35	-	946.2
AHQ-5-8, 7148 - 7225	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.62E-10	0.96	5.44	-	1046.8
AHQ-5-8, 7204 - 7273	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	3.08E-07	0.84	3.68	-	661.2
AHQ-5-8, 7161 - 7184	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.05E-07	0.89	4.63	-	1033.7
AHQ-5-8, 7260 - 7330	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	8.64E-10	0.95	5.63	-	1173.1
AHQ-5-8, 7054 - 7136	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.01E-06	0.91	4.53	-	701.8
AHQ-5-8, 7038 - 7109	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.99E-07	0.84	4.10	-	730.2
AHQ-5-8, 7290 - 7344	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	4.50E-07	0.93	5.09	-	902.1
AHQ-5-8, 6941 - 7008	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	2.86E-06	0.94	5.61	-	1115.5
AHQ-5-8, 6934 - 6998	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.46E-06	0.80	3.44	-	661.7
AHQ-5-8, 7401 - 7404	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	9.70E-06	0.93	5.37	-	778.8
AHQ-5-4, 7340 - 7345	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	6.95E-05	0.89	4.63	-	1024.4
AHQ-5-9, 6342 - 6402	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	4.76E-08	0.93	4.45	-	946.6
AHQ-5-10, 6384 - 6426	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.00E-05	0.81	3.14	-	822.3
AHQ-5-8, 6580	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	7.96E-05	0.81	3.76	-	865.7
AHQ-5-10, 6418 - 6420	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	2.16E-04	0.85	4.25	-	839.9
AHQ-5-8, 6541 - 6609	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.61E-04	0.62	3.13	-	421.5
AHQ-5-11, 6692	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	6.65E-05	0.87	3.37	-	915.8
AHQ-5-8, 7345 - 7416	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.09E-07	0.92	4.38	-	791.7
AHQ-5-8, 5388 - 5457	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.20E-07	0.86	3.70	-	1203.1
AHQ-5-8, 5242 - 5312	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.18E-04	0.85	4.04	-	878.1
AHQ-5-8, 6166 - 6252	R.FRCPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3555.03753	3	8.83E-04	0.84	4.76	-	657.2
AHQ-5-8, 7185 - 7258	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	7.09E-10	0.98	6.50	-	2081.7
AHQ-5-8, 6824 - 6897	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	1.33E-09	0.96	6.80	-	845.4
AHQ-5-8, 6692 - 6757	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	2.24E-13	0.98	7.40	-	1408.2
AHQ-5-9, 5892 - 5959	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	3.83E-06	0.85	4.38	-	569.1
AHQ-5-9, 6314	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	4.26E-07	0.95	5.55	-	1023.2
AHQ-5-8, 6554 - 6629	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	4.81E-04	0.96	5.23	-	1514.4
AHQ-5-8, 6320 - 6398	R.FRCPEALFQPSFLGMESCGIHETTFNSIM*K.C	3555.03753	3	4.63E-07	0.96	6.14	-	864.7
AHQ-5-8, 6960 - 7024	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	1.53E-13	0.98	8.20	-	2127.8
AHQ-5-1, 2613	R.GYSFTTTAER.E	1133.19273	2	1.33E-04	0.95	3.36	-	1200.9
AHQ-5-8, 2172 - 2240	R.GYSFTTTAER.E	1133.19273	2	2.77E-05	0.89	2.71	-	1123.8
AHQ-5-13, 2711	R.GYSFTTTAER.E	1133.19273	2	4.73E-04	0.88	2.72	-	1096.2
AHQ-5-12, 2448	R.GYSFTTTAER.E	1133.19273	2	2.25E-04	0.92	3.16	-	1009.8
AHQ-5-4, 2412	R.GYSFTTTAER.E	1133.19273	2	1.52E-05	0.83	2.87	-	879.2
AHQ-5-14-, 2423	R.GYSFTTTAER.E	1133.19273	2	1.04E-04	0.91	3.06	-	867.5
AHQ-5-6, 2270	R.GYSFTTTAER.E	1133.19273	2	1.66E-04	0.88	2.83	-	983.4
AHQ-5-2, 2397	R.GYSFTTTAER.E	1133.19273	2	9.57E-06	0.94	3.21	-	1196.8
AHQ-5-3, 2449 - 2454	R.GYSFTTTAER.E	1133.19273	2	8.28E-04	0.93	3.40	-	1129.5
AHQ-5-7, 2248	R.GYSFTTTAER.E	1133.19273	2	4.94E-04	0.86	2.96	-	843.1
AHQ-5-13-, 4219 - 4279	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	4.70E-05	0.84	3.69	-	566.3
AHQ-5-8, 4348 - 4357	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	1.37E-04	0.93	4.88	-	1302.0
AHQ-5-10, 3874 - 3875	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	1.09E-04	0.95	4.43	-	1206.1
AHQ-5-10, 4242	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	4.52E-06	0.82	3.11	-	564.0
AHQ-5-8, 3825 - 3826	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	1.76E-06	0.97	6.33	-	1220.7
AHQ-5-14, 5712	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	2.96E-04	0.82	2.91	-	706.2
AHQ-5-13, 4781 - 4784	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.44E-06	0.96	4.72	-	1293.4
AHQ-5-14-, 4611 - 4661	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.66E-08	0.95	4.24	-	1259.4
AHQ-5-8, 4668 - 4669	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	3.45E-06	0.90	4.01	-	1079.8
AHQ-5-14, 5518 - 5576	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	4.20E-04	0.92	4.14	-	827.5
AHQ-5-9, 6398 - 6463	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	1.13E-05	0.94	4.58	-	1127.4
AHQ-5-8, 7408	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	7.48E-09	0.98	6.39	-	2212.7
AHQ-5-7, 5690	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.59E-07	0.94	5.05	-	1096.3
AHQ-5-6, 5864 - 5905	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.01E-06	0.90	4.58	-	669.8
AHQ-5-6, 5690	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.40E-12	0.97	5.91	-	1943.4
AHQ-5-7, 5774	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.32E-07	0.94	5.08	-	1194.3
AHQ-5-7, 5190	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.78E-07	0.94	4.93	-	1333.1
AHQ-5-14-, 5615 - 5697	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.22E-16	0.98	6.46	-	2070.2
AHQ-5-14-, 5439	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.36E-06	0.97	6.17	-	1682.3
AHQ-5-5, 5919	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.35E-11	0.97	6.00	-	1768.7
AHQ-5-5, 5717 - 5797	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.42E-09	0.97	6.21	-	1310.2
AHQ-5-5, 5515	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.95E-07	0.95	5.60	-	1217.9
AHQ-5-6, 5385 - 5388	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.94E-06	0.95	5.70	-	1003.9
AHQ-5-14-, 5357	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.20E-06	0.97	6.24	-	1276.3
AHQ-5-8, 4829 - 4900	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.52E-08	0.96	5.67	-	1423.2
AHQ-5-9, 4643 - 4714	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.57E-05	0.72	3.47	-	578.6
AHQ-5-9, 4788 - 4820	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.14E-06	0.96	5.75	-	1202.7
AHQ-5-9, 4998 - 5078	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.29E-07	0.97	6.08	-	1663.8
AHQ-5-9, 5128 - 5150	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.38E-04	0.42	3.21	-	431.6
AHQ-5-9, 5134 - 5190	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.67E-15	0.98	6.87	-	1674.3
AHQ-5-9, 5246 - 5323	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.01E-09	0.96	5.62	-	1451.1
AHQ-5-8, 4969 - 5041	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.19E-06	0.96	5.42	-	1655.8
AHQ-5-5, 5390	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.12E-06	0.91	4.55	-	937.8
AHQ-5-1, 5827	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.31E-06	0.93	4.84	-	951.3
AHQ-5-4, 6170 - 6185	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.00E-30	0.97	6.05	-	1366.8
AHQ-5-4, 5944 - 6012	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.31E-06	0.97	5.59	-	1768.4
AHQ-5-1, 5908	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.47E-06	0.90	4.91	-	839.0

AHQ-5-1, 6191 - 6200	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.20E-07	0.96	5.96	-	1390.3
AHQ-5-8, 5072 - 5138	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	9.28E-08	0.96	5.62	-	1239.3
AHQ-5-8, 5116 - 5194	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.99E-11	0.96	5.91	-	1290.8
AHQ-5-10, 4786 - 4854	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.39E-05	0.97	5.68	-	1680.8
AHQ-5-10, 4923 - 4992	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.82E-08	0.96	5.53	-	1709.6
AHQ-5-10, 5135 - 5202	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.28E-14	0.98	7.05	-	1767.9
AHQ-5-10, 5262 - 5323	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.55E-16	0.98	7.14	-	1722.1
AHQ-5-10, 5386	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.22E-14	0.97	6.25	-	1802.0
AHQ-5-10, 5519	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.85E-04	0.88	3.96	-	1067.0
AHQ-5-4, 5646	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.19E-07	0.95	5.37	-	1182.4
AHQ-5-13-, 5753 - 5760	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.03E-11	0.98	7.05	-	2086.6
AHQ-5-3, 6195 - 6213	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.55E-15	0.97	6.43	-	1726.1
AHQ-5-13-, 5657	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.39E-07	0.97	5.51	-	1691.8
AHQ-5-11, 5363	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.77E-06	0.92	4.85	-	1239.8
AHQ-5-11, 5538 - 5618	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.60E-07	0.96	5.47	-	1750.0
AHQ-5-11, 5690	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.23E-09	0.95	4.88	-	1600.9
AHQ-5-3, 6089 - 6125	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.77E-11	0.97	5.80	-	1665.0
AHQ-5-8, 5753 - 5824	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.94E-14	0.97	6.12	-	1523.9
AHQ-5-13-, 5455	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.48E-08	0.94	4.96	-	1201.2
AHQ-5-12, 5438	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.05E-05	0.95	5.29	-	1283.4
AHQ-5-12, 5522	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.69E-06	0.89	4.31	-	815.8
AHQ-5-12, 5740 - 5813	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.16E-08	0.97	5.80	-	1526.3
AHQ-5-8, 5616 - 5685	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.67E-15	0.97	5.90	-	1610.1
AHQ-5-13-, 5371	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.66E-05	0.93	5.00	-	983.9
AHQ-5-8, 5532 - 5596	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.00E-30	0.98	6.63	-	1739.1
AHQ-5-13, 5438	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.10E-09	0.95	5.36	-	1145.1
AHQ-5-13, 5713	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.02E-10	0.96	6.21	-	1266.5
AHQ-5-13, 5810	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.76E-06	0.90	4.48	-	676.6
AHQ-5-3, 5675 - 5746	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.66E-05	0.96	5.96	-	1164.7
AHQ-5-8, 5260 - 5328	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.25E-11	0.98	6.92	-	1830.1
AHQ-5-8, 5425 - 5458	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.85E-04	0.90	4.50	-	830.1
AHQ-5-8, 5400 - 5468	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.39E-11	0.97	6.11	-	1611.2
AHQ-5-14, 6040 - 6110	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.27E-08	0.96	5.90	-	1123.7
AHQ-5-14, 6292 - 6304	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.61E-05	0.96	5.69	-	1321.8
AHQ-5-14, 6374	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.09E-05	0.80	3.76	-	772.0
AHQ-5-7, 5480 - 5484	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.05E-12	0.97	5.96	-	1498.2
AHQ-5-3, 3927 - 3998	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.43E-04	0.90	4.41	-	625.4
AHQ-5-13, 3996 - 3997	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.77E-04	0.87	4.27	-	570.8
AHQ-5-12, 3740 - 3808	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.25E-05	0.93	4.80	-	990.0
AHQ-5-11, 3686	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.18E-04	0.94	4.67	-	1002.9
AHQ-5-8, 3592	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.49E-04	0.83	3.55	-	720.7
AHQ-5-8, 3452 - 3525	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.07E-06	0.86	3.90	-	569.9
AHQ-5-2, 3866 - 3931	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	9.42E-04	0.68	3.29	-	762.0
AHQ-5-8, 3340 - 3406	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	3.02E-06	0.73	4.17	-	491.0
AHQ-5-10, 3471 - 3526	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.89E-05	0.92	4.70	-	853.9
AHQ-5-8, 3322 - 3388	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.90E-04	0.93	4.85	-	783.5
AHQ-5-8, 3224 - 3273	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	2.05E-04	0.80	4.41	-	754.1
AHQ-5-8, 3096 - 3142	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.90E-06	0.89	4.27	-	730.7
AHQ-5-9, 3330	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.73E-07	0.90	4.30	-	725.6
AHQ-5-9, 3214 - 3274	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.36E-05	0.96	5.51	-	1019.3
AHQ-5-8, 3033 - 3061	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	8.09E-04	0.51	3.38	-	453.6
AHQ-5-6, 3569	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.76E-05	0.86	4.03	-	591.1
AHQ-5-1, 4081	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.25E-04	0.82	4.29	-	386.3
AHQ-5-1, 4033 - 4099	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.85E-05	0.90	3.83	-	880.6
AHQ-5-13-, 3923 - 3949	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.43E-06	0.89	4.18	-	755.0
gi|4504517|ref|NP_001531.1| heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M				1.00E-30	5.73	70.37	43.90	22782.3
AHQ-5-11, 2159	K.DGVVEITGK.H	918.02674	1	3.96E-04	0.11	1.82	-	321.1
AHQ-5-14, 5650	K.LATQSNEITIPVTFESR.A	1907.11412	2	2.30E-04	0.49	2.82	-	294.7
AHQ-5-10, 4480	K.LATQSNEITIPVTFESR.A	1907.11412	2	7.43E-07	0.67	3.62	-	285.8
AHQ-5-13, 4944	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.40E-04	0.72	3.27	-	417.6
AHQ-5-11, 4782 - 4799	K.LATQSNEITIPVTFESR.A	1907.11412	2	6.51E-10	0.92	4.70	-	403.0
AHQ-5-13-, 4785 - 4857	K.LATQSNEITIPVTFESR.A	1907.11412	2	6.66E-10	0.87	3.89	-	385.5
AHQ-5-11, 4654 - 4675	K.LATQSNEITIPVTFESR.A	1907.11412	2	3.84E-06	0.53	2.80	-	239.1
AHQ-5-10, 4187	R.LFDQAFGLPR.L	1164.33793	2	3.56E-05	0.96	4.15	-	1436.0
AHQ-5-11, 4496	R.LFDQAFGLPR.L	1164.33793	2	6.44E-07	0.96	4.47	-	1518.9
AHQ-5-11, 6504 - 6512	R.LPEEWSQWLGGSSWPGYVR.P	2235.44173	2	6.38E-07	0.95	4.64	-	1100.3
AHQ-5-10, 6231	R.LPEEWSQWLGGSSWPGYVR.P	2235.44173	2	3.06E-08	0.95	4.84	-	1074.9
AHQ-5-10, 6430	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	3.33E-15	0.98	7.34	-	1369.2
AHQ-5-11, 6706	R.LPEEWSQWLGGSSWPGYVRPLPPAAIESPAVAAPAYSR.A	4095.56787	3	1.00E-30	0.97	6.55	-	1472.2
AHQ-5-11, 4036	R.PLPPAAIESPAVAAPAYSR.A	1879.14874	2	5.48E-09	0.84	3.22	-	469.7
AHQ-5-13, 4677	R.VSLDVNHFAPDELTVK.T	1784.99058	2	2.97E-07	0.93	4.69	-	905.3
AHQ-5-11, 4700	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.21E-08	0.93	4.27	-	1090.6
AHQ-5-11, 4520 - 4546	R.VSLDVNHFAPDELTVK.T	1784.99058	2	3.63E-10	0.95	4.54	-	1158.7
AHQ-5-14, 5388 - 5450	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.40E-08	0.96	5.25	-	1247.7
AHQ-5-10, 4346	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.50E-04	0.75	3.10	-	535.3
AHQ-5-10, 4190 - 4192	R.VSLDVNHFAPDELTVK.T	1784.99058	2	9.61E-08	0.92	4.26	-	837.3
AHQ-5-13-, 4845	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.26E-10	0.97	5.21	-	1807.0
gi|4504345|ref|NP_000508.1| alpha 2 globin [Homo sapiens]				1.00E-30	4.78	50.35	50.70	15257.4
AHQ-5-13-, 4223	K.FLASVSTVLTSK.Y	1253.46970	2	3.11E-07	0.91	3.35	-	1019.8
AHQ-5-13, 4085 - 4092	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	8.46E-09	0.96	4.60	-	1133.7
AHQ-5-13, 4097 - 4109	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	4.10E-08	0.81	3.41	-	595.3
AHQ-5-13-, 4012	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	2.88E-09	0.91	3.90	-	798.5
AHQ-5-14, 4788	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	6.55E-04	0.88	3.41	-	983.1
AHQ-5-14-, 3865 - 3866	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	2.71E-09	0.84	3.69	-	653.9
AHQ-5-14-, 3863 - 3877	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	4.20E-10	0.95	4.45	-	992.3
AHQ-5-14-, 5951 - 5999	K.VADALTNAVAHVDDMPNALSALSDLHAHK.L	2998.32055	3	4.11E-13	0.96	6.18	-	1240.0
AHQ-5-14-, 6202 - 6283	K.VADALTNAVAHVDDMPNALSALSDLHAHK.L	2998.32055	3	1.00E-30	0.98	6.94	-	2108.3
AHQ-5-13-, 6317	K.VADALTNAVAHVDDMPNALSALSDLHAHK.L	2998.32055	3	9.24E-08	0.97	6.02	-	1453.4
AHQ-5-14-, 5490	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	7.22E-07	0.97	6.24	-	1525.4
AHQ-5-14, 6138 - 6200	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	2.47E-05	0.97	5.83	-	1600.4
AHQ-5-14-, 2478	K.VGAHAGEYGAEALER.M	1530.62397	2	5.32E-10	0.97	4.42	-	2077.1
AHQ-5-13-, 2560	K.VGAHAGEYGAEALER.M	1530.62397	3	2.17E-04	0.96	5.45	-	1945.9
AHQ-5-13-, 2559 - 2561	K.VGAHAGEYGAEALER.M	1530.62397	2	3.97E-12	0.97	4.14	-	1853.5
AHQ-5-14, 3253	K.VGAHAGEYGAEALER.M	1530.62397	2	1.27E-04	0.89	3.16	-	989.2
AHQ-5-13, 2701	K.VGAHAGEYGAEALER.M	1530.62397	2	2.00E-11	0.97	4.46	-	1896.8
AHQ-5-14-, 2483	K.VGAHAGEYGAEALER.M	1530.62397	3	6.30E-04	0.98	5.50	-	2819.1
gi|4885387|ref|NP_005318.1| L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain; L-3-hydroxyacyl-				2.22E-16	0.95	10.28	9.60	34286.3
AHQ-5-12, 7156 - 7158	K.TLSTIATSTDAASVVHSTDLVVEAIVENLK.V	3086.43759	3	5.10E-08	0.94	4.90	-	1226.9
AHQ-5-9, 6598 - 6599	K.TLSTIATSTDAASVVHSTDLVVEAIVENLK.V	3086.43759	3	2.22E-16	0.95	5.60	-	1038.5
gi|16753233|ref|NP_006280.2| talin 1 [Homo sapiens]				5.55E-16	114.11	1300.40	56.20	269665.3
AHQ-5-1, 3239	K.AAAFEEQENETVVVK.E	1664.79496	2	2.13E-04	0.85	3.81	-	854.0
AHQ-5-2, 3410	K.AAAFEEQENETVVVK.E	1664.79496	2	2.17E-04	0.95	4.27	-	1429.6
AHQ-5-2, 3158	K.AAAFEEQENETVVVK.E	1664.79496	2	1.97E-06	0.93	4.27	-	1280.7
AHQ-5-4, 3338 - 3350	K.AAAFEEQENETVVVK.E	1664.79496	2	2.69E-07	0.95	4.68	-	1236.3
AHQ-5-3, 3211	K.AAAFEEQENETVVVK.E	1664.79496	2	8.37E-04	0.91	4.26	-	853.2
AHQ-5-5, 2929	R.AAMEPIVISAK.T	1130.38320	1	2.40E-04	0.15	1.87	-	488.8
AHQ-5-2, 2430	R.AAM*EPIVISAK.T	1146.38260	1	1.73E-04	0.49	2.68	-	203.3

AHQ-5-2, 2433	R.AAM*EPIVISAK.T	1146.38260	2	3.83E-06	0.75	2.79	-	589.8
AHQ-5-4, 3120 - 3145	R.AAMEPIVISAK.T	1130.38320	2	1.42E-06	0.80	2.79	-	642.0
AHQ-5-4, 2460 - 2465	R.AAM*EPIVISAK.T	1146.38260	2	9.73E-06	0.74	2.65	-	864.8
AHQ-5-1, 3315	R.AAMEPIVISAK.T	1130.38320	2	1.44E-05	0.74	2.54	-	735.1
AHQ-5-3, 2489 - 2495	R.AAM*EPIVISAK.T	1146.38260	2	1.40E-07	0.83	2.61	-	946.9
AHQ-5-3, 2486	R.AAM*EPIVISAK.T	1146.38260	1	3.88E-04	0.69	2.87	-	286.7
AHQ-5-6, 2920	R.AAMEPIVISAK.T	1130.38320	1	1.90E-04	0.19	2.11	-	544.6
AHQ-5-3, 3149 - 3150	R.AAMEPIVISAK.T	1130.38320	2	1.08E-05	0.77	2.91	-	484.9
AHQ-5-4, 1833 - 1838	K.ADAEGESDLENSR.K	1393.35296	2	1.65E-04	0.87	3.07	-	998.1
AHQ-5-5, 1718	K.ADAEGESDLENSR.K	1393.35296	2	1.18E-05	0.86	2.71	-	1065.6
AHQ-5-2, 1830	K.ADAEGESDLENSR.K	1393.35296	2	3.85E-06	0.93	3.60	-	1191.3
AHQ-5-5, 2458	K.AGALQCSPSDAYTK.K	1470.58689	1	4.64E-09	0.79	3.54	-	510.2
AHQ-5-3, 2591	K.AGALQCSPSDAYTK.K	1470.58689	1	5.41E-08	0.83	3.43	-	682.8
AHQ-5-2, 2525	K.AGALQCSPSDAYTK.K	1470.58689	2	5.64E-04	0.94	3.96	-	1021.5
AHQ-5-2, 2533	K.AGALQCSPSDAYTK.K	1470.58689	1	6.15E-07	0.89	3.95	-	748.3
AHQ-5-1, 2720	K.AGALQCSPSDAYTK.K	1470.58689	2	9.87E-04	0.89	3.60	-	756.5
AHQ-5-4, 2545 - 2550	K.AGALQCSPSDAYTK.K	1470.58689	2	2.28E-05	0.91	3.98	-	848.1
AHQ-5-4, 2564	K.AGALQCSPSDAYTK.K	1470.58689	1	1.61E-06	0.79	3.04	-	684.6
AHQ-5-2, 2523	K.AGALQCSPSDAYTK.K	1470.58689	1	3.53E-04	0.40	2.46	-	507.2
AHQ-5-3, 2301	K.AGALQCSPSDAYTKK.E	1598.75981	2	6.55E-04	0.79	3.15	-	701.6
AHQ-5-8, 5830 - 5848	K.AGFLDLKDFLPK.E	1364.61374	2	3.49E-04	0.90	3.53	-	1027.4
AHQ-5-1, 4204	K.AIAVTVQEMVTK.S	1290.55498	2	9.13E-09	0.94	4.18	-	1214.6
AHQ-5-3, 4145	K.AIAVTVQEMVTK.S	1290.55498	2	1.50E-05	0.95	4.27	-	1253.4
AHQ-5-3, 4025	K.AIAVTVQEMVTK.S	1290.55498	2	1.91E-04	0.95	4.36	-	1113.2
AHQ-5-4, 3968 - 3980	K.AIAVTVQEMVTK.S	1290.55498	2	2.69E-08	0.96	4.85	-	1131.8
AHQ-5-2, 2406	K.ALDGAFTEENR.A	1223.27427	2	2.17E-06	0.94	3.64	-	1498.4
AHQ-5-4, 2414	K.ALDGAFTEENR.A	1223.27427	2	5.30E-07	0.90	3.10	-	1312.5
AHQ-5-3, 2443 - 2450	K.ALDGAFTEENR.A	1223.27427	2	5.14E-07	0.95	3.80	-	1554.4
AHQ-5-1, 2729	K.ALDGAFTEENR.A	1223.27427	2	5.80E-05	0.97	4.39	-	1816.0
AHQ-5-2, 2522 - 2546	K.ALDGAFTEENR.A	1223.27427	2	1.13E-04	0.96	4.27	-	1651.3
AHQ-5-7, 3555	K.ALDYYMLR.N	1045.23686	2	4.21E-06	0.94	3.29	-	954.4
AHQ-5-13-, 3947	K.ALDYYMLR.N	1045.23686	2	1.40E-04	0.93	2.86	-	1041.2
AHQ-5-13, 3433	K.ALDYYM*LR.N	1061.23626	2	1.91E-05	0.91	3.14	-	890.6
AHQ-5-7, 2944	K.ALDYYM*LR.N	1061.23626	2	6.52E-05	0.90	2.68	-	1001.1
AHQ-5-13, 4049	K.ALDYYMLR.N	1045.23686	2	7.97E-07	0.93	3.57	-	761.6
AHQ-5-2, 1743 - 1782	R.ALEATTEHIR.Q	1141.25953	2	6.35E-07	0.90	3.35	-	1219.5
AHQ-5-5, 1634 - 1655	R.ALEATTEHIR.Q	1141.25953	1	7.68E-05	0.20	2.02	-	235.3
AHQ-5-5, 1631	R.ALEATTEHIR.Q	1141.25953	2	3.04E-04	0.86	2.87	-	1206.9
AHQ-5-4, 1786 - 1849	R.ALEATTEHIR.Q	1141.25953	2	1.21E-04	0.85	3.06	-	1025.9
AHQ-5-3, 3445	K.ALGDLISATK.A	989.14811	2	4.91E-06	0.94	3.65	-	909.1
AHQ-5-5, 3245	K.ALGDLISATK.A	989.14811	2	2.44E-06	0.94	3.94	-	900.7
AHQ-5-4, 3408 - 3478	K.ALGDLISATK.A	989.14811	2	1.58E-04	0.94	3.95	-	864.9
AHQ-5-2, 3362 - 3439	K.ALGDLISATK.A	989.14811	2	9.93E-06	0.92	3.83	-	753.3
AHQ-5-6, 3197 - 3213	K.ALGDLISATK.A	989.14811	2	9.29E-05	0.93	3.59	-	842.3
AHQ-5-3, 3442	K.ALGDLISATK.A	989.14811	1	4.89E-05	0.52	2.40	-	578.8
AHQ-5-1, 3532	K.ALGDLISATK.A	989.14811	2	3.77E-06	0.94	3.81	-	907.6
AHQ-5-5, 2426	K.ALSTDPAAPNLK.S	1198.35099	2	2.24E-07	0.67	2.88	-	585.6
AHQ-5-2, 2489	K.ALSTDPAAPNLK.S	1198.35099	2	1.03E-07	0.84	3.05	-	803.6
AHQ-5-4, 2538 - 2573	K.ALSTDPAAPNLK.S	1198.35099	2	2.28E-06	0.57	2.84	-	658.1
AHQ-5-3, 2559	K.ALSTDPAAPNLK.S	1198.35099	2	8.69E-04	0.82	3.05	-	664.4
AHQ-5-1, 2716	K.ALSTDPAAPNLK.S	1198.35099	2	2.34E-05	0.74	2.83	-	583.7
AHQ-5-5, 2427 - 2429	K.ALSTDPAAPNLK.S	1198.35099	1	2.94E-06	0.06	1.98	-	239.2
AHQ-5-2, 2498	K.ALSTDPAAPNLK.S	1198.35099	1	9.74E-06	0.18	2.19	-	347.7
AHQ-5-3, 3570	K.ALSTDPAAPNLKSQLAAAAR.A	1967.21592	2	3.58E-04	0.59	2.79	-	339.8
AHQ-5-2, 6809 - 6886	R.ANQAIQMACQSLGEPGCTQAQVLSAATIVAK.H	3220.64522	3	3.27E-06	0.95	5.54	-	982.8
AHQ-5-2, 5713	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.01E-10	0.97	5.45	-	1655.8
AHQ-5-1, 6423	K.APGQLECETAIAALNSCLR.D	2077.32566	2	8.61E-06	0.97	5.14	-	1218.1
AHQ-5-2, 6387	K.APGQLECETAIAALNSCLR.D	2077.32566	2	8.42E-06	0.97	5.28	-	1275.7
AHQ-5-3, 5749	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.16E-08	0.94	4.38	-	1026.5
AHQ-5-2, 6699	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.78E-11	0.94	4.29	-	1003.0
AHQ-5-4, 6436	K.APGQLECETAIAALNSCLR.D	2077.32566	2	7.25E-07	0.97	4.93	-	1414.6
AHQ-5-5, 6913 - 6914	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.44E-06	0.97	5.43	-	2080.0
AHQ-5-3, 7085	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	6.09E-04	0.48	3.16	-	497.5
AHQ-5-4, 7040 - 7044	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.15E-05	0.97	5.09	-	2200.3
AHQ-5-2, 7045 - 7046	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.41E-05	0.95	4.65	-	1871.5
AHQ-5-1, 7007	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	5.27E-07	0.97	5.80	-	1674.6
AHQ-5-2, 2773 - 2841	K.ASAGPQPLLVQSCK.A	1457.67763	2	6.42E-08	0.70	2.91	-	370.6
AHQ-5-5, 2630 - 2653	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.72E-09	0.85	3.53	-	521.6
AHQ-5-5, 2670	K.ASAGPQPLLVQSCK.A	1457.67763	1	2.07E-08	0.68	3.34	-	346.8
AHQ-5-1, 3040	K.ASAGPQPLLVQSCK.A	1457.67763	1	6.93E-07	0.71	3.26	-	446.5
AHQ-5-6, 2702	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.96E-08	0.58	3.18	-	336.9
AHQ-5-2, 2747 - 2822	K.ASAGPQPLLVQSCK.A	1457.67763	1	8.09E-08	0.73	3.38	-	499.9
AHQ-5-3, 2873	K.ASAGPQPLLVQSCK.A	1457.67763	1	6.78E-07	0.66	3.60	-	310.3
AHQ-5-3, 2862 - 2893	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.81E-06	0.84	3.43	-	480.9
AHQ-5-4, 2845	K.ASAGPQPLLVQSCK.A	1457.67763	1	2.24E-08	0.49	3.12	-	279.3
AHQ-5-4, 2808 - 2878	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.72E-06	0.83	3.67	-	376.0
AHQ-5-4, 4302 - 4372	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.12E-04	0.90	4.24	-	510.7
AHQ-5-3, 4370 - 4441	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.82E-13	0.94	4.56	-	815.2
AHQ-5-2, 3546	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	7.41E-04	0.73	3.04	-	521.7
AHQ-5-1, 3840	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.53E-04	0.82	3.50	-	573.3
AHQ-5-6, 4110	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.63E-06	0.83	4.08	-	420.5
AHQ-5-3, 3785	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.87E-05	0.88	3.95	-	470.9
AHQ-5-2, 4019	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	9.61E-04	0.44	2.68	-	332.9
AHQ-5-2, 3734 - 3737	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.38E-08	0.90	4.20	-	635.5
AHQ-5-7, 4012	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.29E-05	0.86	3.99	-	433.9
AHQ-5-2, 4306 - 4377	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.75E-08	0.95	5.04	-	831.4
AHQ-5-4, 3746	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.48E-04	0.83	3.46	-	535.8
AHQ-5-2, 4451 - 4522	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.81E-05	0.83	3.87	-	405.5
AHQ-5-5, 4190 - 4195	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	9.08E-07	0.94	4.98	-	627.7
AHQ-5-5, 3593 - 3595	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.96E-06	0.89	4.33	-	490.9
AHQ-5-1, 4427 - 4500	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.08E-07	0.94	4.53	-	817.7
AHQ-5-4, 4453	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.47E-06	0.82	3.98	-	423.4
AHQ-5-3, 5082	K.AVAEQIPLLVQGVR.G	1493.77619	1	2.37E-05	0.41	3.07	-	165.8
AHQ-5-3, 5057 - 5129	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.23E-06	0.92	4.04	-	638.4
AHQ-5-6, 4746 - 4760	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.71E-05	0.84	3.59	-	489.6
AHQ-5-2, 5027	K.AVAEQIPLLVQGVR.G	1493.77619	3	8.30E-05	0.96	4.76	-	1973.2
AHQ-5-2, 5005	K.AVAEQIPLLVQGVR.G	1493.77619	1	5.40E-06	0.79	3.77	-	300.6
AHQ-5-1, 5107 - 5177	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.59E-05	0.92	4.30	-	642.3
AHQ-5-1, 5128	K.AVAEQIPLLVQGVR.G	1493.77619	1	6.90E-06	0.79	3.49	-	464.6
AHQ-5-2, 4969 - 5038	K.AVAEQIPLLVQGVR.G	1493.77619	2	7.00E-06	0.96	5.18	-	904.2
AHQ-5-5, 4786 - 4794	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.74E-06	0.88	4.02	-	557.0
AHQ-5-4, 5028 - 5030	K.AVAEQIPLLVQGVR.G	1493.77619	1	9.91E-05	0.30	2.95	-	273.8
AHQ-5-5, 4814	K.AVAEQIPLLVQGVR.G	1493.77619	1	1.19E-09	0.29	2.54	-	108.7
AHQ-5-4, 3797	K.AVASAAAALVLK.A	1085.32216	2	9.85E-06	0.94	3.32	-	1628.7
AHQ-5-4, 3880	K.AVASAAAALVLK.A	1085.32216	2	4.18E-05	0.96	3.97	-	1649.6
AHQ-5-2, 4047	K.AVASAAAALVLK.A	1085.32216	2	8.39E-05	0.94	3.62	-	1424.1
AHQ-5-1, 4003	K.AVASAAAALVLK.A	1085.32216	2	1.10E-05	0.96	4.24	-	1474.3

AHQ-5-2, 3810	K.AVASAAAALVLK.A	1085.32216	2	3.55E-06	0.96	4.02	-	1555.3
AHQ-5-1, 4184 - 4256	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	8.20E-06	0.85	4.06	-	695.2
AHQ-5-3, 4158 - 4177	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.61E-08	0.94	4.34	-	1282.3
AHQ-5-2, 4125 - 4202	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.17E-06	0.74	3.13	-	853.4
AHQ-5-2, 4893	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.69E-04	0.63	2.90	-	797.0
AHQ-5-4, 4269	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.34E-08	0.86	3.83	-	999.7
AHQ-5-1, 3899 - 3973	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	8.74E-05	0.97	5.22	-	2073.6
AHQ-5-3, 4246 - 4317	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.03E-05	0.77	3.31	-	676.9
AHQ-5-2, 4362 - 4441	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.75E-04	0.90	3.97	-	689.2
AHQ-5-1, 4541	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.50E-06	0.53	3.02	-	503.7
AHQ-5-2, 3873	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.18E-06	0.96	4.58	-	1387.2
AHQ-5-2, 4719 - 4743	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.08E-05	0.84	3.81	-	901.0
AHQ-5-1, 4339 - 4411	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.01E-07	0.96	4.91	-	1498.1
AHQ-5-2, 4277 - 4286	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.23E-07	0.97	4.85	-	2247.5
AHQ-5-2, 5689	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.93E-04	0.74	3.70	-	852.9
AHQ-5-3, 7406	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.41E-09	0.96	5.29	-	1746.8
AHQ-5-6, 7209	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	2.11E-07	0.97	5.85	-	1726.0
AHQ-5-2, 4869	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	2.69E-08	0.91	4.23	-	652.5
AHQ-5-3, 5865	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	3.49E-04	0.69	3.13	-	578.1
AHQ-5-1, 5879 - 5880	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	2.63E-08	0.86	4.07	-	515.4
AHQ-5-2, 5741 - 5810	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	3.50E-06	0.77	3.62	-	414.0
AHQ-5-4, 4873	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	5.68E-07	0.87	4.37	-	389.4
AHQ-5-5, 6127	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.49E-06	0.85	4.06	-	521.0
AHQ-5-2, 6253 - 6323	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.18E-06	0.89	4.04	-	1082.9
AHQ-5-2, 5867 - 5933	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	3.91E-11	0.92	4.62	-	1026.7
AHQ-5-3, 6033	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.19E-06	0.93	4.78	-	1157.5
AHQ-5-1, 5995	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	4.86E-05	0.93	4.59	-	1257.9
AHQ-5-4, 6270 - 6337	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.80E-11	0.94	5.41	-	778.7
AHQ-5-3, 6337 - 6413	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.32E-11	0.89	4.36	-	951.2
AHQ-5-1, 6263 - 6299	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.98E-13	0.89	4.42	-	983.2
AHQ-5-5, 6181	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.24E-11	0.93	4.87	-	1384.6
AHQ-5-4, 7241 - 7317	R.AVTDSINQLITMCTQQAPGQKECDNALRELETVR.E	3894.32086	3	2.02E-06	0.77	3.81	-	677.7
AHQ-5-1, 2533	R.CVSCLPGQR.D	1079.23309	1	6.60E-04	0.28	1.93	-	170.3
AHQ-5-7, 3216 - 3286	R.DDILNGSHPVSFDK.A	1544.64741	2	3.75E-09	0.92	3.88	-	852.5
AHQ-5-8, 3337 - 3417	R.DDILNGSHPVSFDK.A	1544.64741	2	1.05E-08	0.94	3.77	-	1294.8
AHQ-5-10, 3363	R.DDILNGSHPVSFDK.A	1544.64741	2	5.27E-05	0.78	3.23	-	707.7
AHQ-5-4, 3553	R.DDILNGSHPVSFDK.A	1544.64741	2	2.49E-07	0.87	3.57	-	721.1
AHQ-5-8, 3152	R.DDILNGSHPVSFDK.A	1544.64741	2	9.74E-07	0.96	3.91	-	1484.6
AHQ-5-7, 3444 - 3516	R.DDILNGSHPVSFDK.A	1544.64741	2	3.85E-08	0.92	4.39	-	828.9
AHQ-5-7, 4659	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	3.06E-07	0.97	5.46	-	1507.2
AHQ-5-3, 5414 - 5486	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.35E-11	0.88	3.58	-	727.6
AHQ-5-5, 6026 - 6094	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.10E-10	0.95	4.64	-	993.2
AHQ-5-1, 5449 - 5480	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	8.66E-13	0.96	4.80	-	1295.9
AHQ-5-5, 6070	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.26E-08	0.93	4.32	-	885.5
AHQ-5-6, 5982	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.60E-09	0.94	4.58	-	941.4
AHQ-5-2, 6185 - 6261	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.58E-09	0.97	5.07	-	1441.4
AHQ-5-7, 5834	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	7.74E-10	0.93	4.40	-	824.0
AHQ-5-4, 6217 - 6233	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.14E-13	0.97	4.86	-	1461.9
AHQ-5-3, 6491	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	9.15E-09	0.88	3.49	-	845.5
AHQ-5-4, 6393 - 6470	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	8.93E-07	0.95	5.12	-	912.5
AHQ-5-3, 6335 - 6415	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.59E-08	0.93	4.11	-	1059.5
AHQ-5-4, 6476	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.27E-11	0.95	4.32	-	1103.9
AHQ-5-3, 6245 - 6265	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	1.09E-07	0.94	5.22	-	1115.5
AHQ-5-2, 5919	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.99E-07	0.78	3.54	-	566.9
AHQ-5-10, 5430	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.77E-10	0.91	3.88	-	866.8
AHQ-5-1, 6227	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	7.33E-10	0.96	5.08	-	1270.5
AHQ-5-2, 5361 - 5442	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	9.14E-12	0.95	4.51	-	1136.6
AHQ-5-2, 6354	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.33E-07	0.95	4.72	-	1026.4
AHQ-5-9, 5291 - 5294	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.40E-07	0.93	4.48	-	871.9
AHQ-5-3, 6242 - 6254	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.92E-09	0.96	5.19	-	1134.2
AHQ-5-11, 5704	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.91E-10	0.94	4.26	-	1076.2
AHQ-5-4, 5416 - 5490	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.14E-12	0.90	4.15	-	803.2
AHQ-5-3, 5806 - 5873	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	9.15E-07	0.56	3.26	-	546.0
AHQ-5-2, 5413 - 5482	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.63E-07	0.97	4.55	-	1750.3
AHQ-5-4, 5428 - 5501	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.71E-10	0.93	4.33	-	972.1
AHQ-5-4, 5445 - 5456	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.89E-08	0.96	4.55	-	2122.1
AHQ-5-1, 5436	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.52E-05	0.87	3.61	-	656.2
AHQ-5-2, 5426 - 5454	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	1.49E-04	0.92	4.15	-	1775.1
AHQ-5-3, 5475 - 5483	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.60E-05	0.94	4.89	-	1556.9
AHQ-5-3, 5454 - 5530	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.50E-04	0.88	3.86	-	648.2
AHQ-5-1, 3684 - 3685	R.DPPSWSVLAGHSR.T	1409.53156	2	5.24E-10	0.93	4.11	-	751.7
AHQ-5-4, 3520	R.DPPSWSVLAGHSR.T	1409.53156	3	1.29E-06	0.87	3.98	-	588.3
AHQ-5-4, 3496 - 3509	R.DPPSWSVLAGHSR.T	1409.53156	2	6.53E-10	0.87	3.49	-	533.7
AHQ-5-2, 3471	R.DPPSWSVLAGHSR.T	1409.53156	3	1.46E-08	0.92	4.45	-	759.4
AHQ-5-2, 3449 - 3497	R.DPPSWSVLAGHSR.T	1409.53156	2	1.66E-09	0.96	4.28	-	850.1
AHQ-5-3, 3530 - 3539	R.DPPSWSVLAGHSR.T	1409.53156	2	2.19E-09	0.92	3.69	-	576.1
AHQ-5-10, 4667	R.DPVQLNLLYVQAR.D	1529.76539	2	1.26E-06	0.97	4.67	-	1631.2
AHQ-5-7, 5024 - 5083	R.DPVQLNLLYVQAR.D	1529.76539	2	5.77E-08	0.93	4.06	-	885.4
AHQ-5-3, 2391	K.EAAYHPEVAPDVR.L	1454.56910	1	8.80E-06	0.77	2.62	-	524.3
AHQ-5-6, 2206	K.EAAYHPEVAPDVR.L	1454.56910	2	3.31E-06	0.75	3.12	-	600.6
AHQ-5-2, 2326	K.EAAYHPEVAPDVR.L	1454.56910	1	2.75E-08	0.73	3.13	-	335.2
AHQ-5-5, 2242	K.EAAYHPEVAPDVR.L	1454.56910	1	4.63E-06	0.61	2.61	-	338.6
AHQ-5-5, 2229 - 2239	K.EAAYHPEVAPDVR.L	1454.56910	2	6.75E-06	0.82	2.80	-	867.1
AHQ-5-4, 2353	K.EAAYHPEVAPDVR.L	1454.56910	1	7.44E-10	0.86	3.13	-	547.2
AHQ-5-5, 6011 - 6085	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.74E-06	0.96	5.26	-	1392.9
AHQ-5-1, 6113 - 6168	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.33E-05	0.89	4.14	-	827.0
AHQ-5-5, 6153	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.45E-06	0.86	3.88	-	876.3
AHQ-5-4, 5920 - 5926	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.12E-07	0.87	3.53	-	871.8
AHQ-5-4, 6137 - 6208	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.39E-05	0.92	4.47	-	1084.8
AHQ-5-2, 7338	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.89E-04	0.61	3.04	-	705.9
AHQ-5-4, 6248 - 6317	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.77E-05	0.92	3.96	-	1121.8
AHQ-5-8, 5849	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.11E-06	0.83	3.29	-	866.4
AHQ-5-4, 6333 - 6386	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.11E-06	0.97	5.75	-	1822.0
AHQ-5-4, 6512	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.10E-05	0.61	3.06	-	843.7
AHQ-5-4, 6657	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.01E-05	0.40	2.70	-	366.3
AHQ-5-2, 6614 - 6686	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.73E-05	0.96	4.63	-	1909.2
AHQ-5-1, 6235 - 6315	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.98E-07	0.96	5.03	-	1352.4
AHQ-5-3, 6443	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.03E-08	0.87	3.56	-	813.1
AHQ-5-2, 6355	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.81E-05	0.89	3.49	-	1205.2
AHQ-5-3, 6301 - 6369	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.91E-08	0.96	4.98	-	1382.8
AHQ-5-3, 6198 - 6273	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.53E-06	0.94	4.51	-	1302.6
AHQ-5-6, 5952 - 5953	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.76E-06	0.95	5.02	-	1276.7
AHQ-5-9, 5279	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.56E-04	0.86	3.54	-	999.0
AHQ-5-10, 5358 - 5418	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.10E-06	0.73	3.70	-	594.2
AHQ-5-2, 6213 - 6282	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.95E-09	0.96	4.94	-	1395.1
AHQ-5-6, 6072 - 6148	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.91E-06	0.90	3.91	-	1268.6
AHQ-5-2, 6066 - 6146	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.18E-07	0.94	4.64	-	1063.4

AHQ-5-11, 5655	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.91E-05	0.70	3.14	-	548.7
AHQ-5-3, 7518	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	1.43E-04	0.95	5.34	-	1227.1
AHQ-5-1, 7339	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	8.24E-07	0.95	5.52	-	1265.4
AHQ-5-9, 6491 - 6503	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	2	2.71E-04	0.66	3.04	-	482.3
AHQ-5-4, 7469 - 7470	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	9.21E-14	0.95	5.90	-	1051.1
AHQ-5-5, 7413	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	4.55E-06	0.88	4.13	-	862.4
AHQ-5-2, 7501 - 7503	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	5.22E-14	0.96	6.19	-	1310.8
AHQ-5-2, 7483 - 7554	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.15E-10	0.98	6.46	-	2112.7
AHQ-5-5, 7337	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.52E-04	0.88	4.29	-	832.3
AHQ-5-10, 6606	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.84E-09	0.96	5.87	-	1542.3
AHQ-5-3, 7598	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	9.42E-04	0.85	3.78	-	913.9
AHQ-5-8, 7284	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	9.44E-09	0.97	6.14	-	2011.4
AHQ-5-3, 7514	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	5.98E-04	0.77	3.53	-	599.4
AHQ-5-4, 7502 - 7529	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	6.79E-12	0.97	6.46	-	1428.1
AHQ-5-7, 7370	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.93E-08	0.97	6.55	-	1687.3
AHQ-5-6, 7356	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	8.93E-10	0.95	5.54	-	1157.5
AHQ-5-4, 7372	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	6.33E-04	0.94	5.26	-	975.1
AHQ-5-5, 7449 - 7470	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	2.00E-12	0.97	6.46	-	1293.6
AHQ-5-4, 7225 - 7226	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	2.37E-08	0.79	4.41	-	378.6
AHQ-5-2, 6973 - 7037	R.ELLENPVQPINDMSYFGCLDSVM*ENSK.V	3148.48814	3	7.26E-04	0.95	5.47	-	1080.3
AHQ-5-1, 7259	R.ELLENPVQPINDMSYFGCLDSVMENSK.V	3132.48874	3	3.27E-04	0.95	5.62	-	885.4
AHQ-5-1, 7033	R.ELLENPVQPINDMSYFGCLDSVM*ENSK.V	3148.48814	3	5.78E-07	0.75	3.63	-	448.7
AHQ-5-8, 2566 - 2636	R.EQGVEEHETLLLR.R	1553.69898	2	8.24E-10	0.87	3.67	-	441.1
AHQ-5-14, 6177 - 6178	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	7.78E-04	0.91	4.41	-	991.9
AHQ-5-7, 5322 - 5338	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	9.13E-08	0.97	6.26	-	1869.7
AHQ-5-14-, 5441	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	4.86E-04	0.97	5.79	-	2067.0
AHQ-5-13, 5553	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	8.44E-07	0.97	5.89	-	1319.1
AHQ-5-13-, 5479	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	5.00E-15	0.98	6.53	-	2553.9
AHQ-5-8, 5106	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	7.96E-10	0.97	5.89	-	1656.2
AHQ-5-14, 5936	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.46E-06	0.98	6.55	-	2035.7
AHQ-5-13, 5206	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	4.85E-12	0.98	6.79	-	1858.9
AHQ-5-14-, 5071	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	5.36E-07	0.98	8.05	-	2362.5
AHQ-5-13-, 5063 - 5136	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	2.42E-09	0.98	6.57	-	2856.2
AHQ-5-7, 4844 - 4858	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.96E-08	0.98	7.17	-	1501.1
AHQ-5-11, 4972	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	2.51E-05	0.93	4.48	-	1256.1
AHQ-5-4, 2260	K.EVANSTANLVK.T	1146.27608	2	4.36E-05	0.86	2.81	-	938.5
AHQ-5-3, 2061 - 2143	K.EVANSTANLVK.T	1146.27608	1	3.66E-04	0.20	2.42	-	140.8
AHQ-5-4, 2046 - 2064	K.EVANSTANLVK.T	1146.27608	2	5.61E-04	0.91	3.28	-	1131.3
AHQ-5-2, 2115 - 2257	K.EVANSTANLVK.T	1146.27608	1	2.79E-04	0.13	2.12	-	135.2
AHQ-5-8, 4216	K.EVIQEWNLTNIK.R	1487.68214	2	2.63E-07	0.94	4.43	-	1105.1
AHQ-5-13-, 4663 - 4735	K.EVIQEWNLTNIK.R	1487.68214	2	8.38E-04	0.59	2.51	-	714.8
AHQ-5-12, 4617 - 4697	K.EVIQEWNLTNIK.R	1487.68214	2	2.84E-04	0.88	3.71	-	927.7
AHQ-5-8, 3656	K.EVIQEWNLTNIKR.W	1643.86849	2	5.43E-07	0.18	2.55	-	284.3
AHQ-5-8, 2696	K.FFYSDQNVDSR.D	1378.42795	2	7.42E-06	0.84	2.98	-	770.6
AHQ-5-7, 2755	K.FFYSDQNVDSR.D	1378.42795	2	6.32E-06	0.92	3.46	-	1149.6
AHQ-5-7, 5842	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	5.55E-16	0.98	6.90	-	2215.1
AHQ-5-8, 5796	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	5.09E-11	0.97	5.74	-	2179.7
AHQ-5-7, 5964	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	2.24E-04	0.67	3.43	-	628.7
AHQ-5-2, 7385	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	5.95E-04	0.77	3.60	-	510.7
AHQ-5-3, 6567 - 6638	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	3.96E-07	0.93	4.16	-	1197.4
AHQ-5-1, 6504 - 6571	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	3.53E-13	0.95	5.10	-	1173.2
AHQ-5-3, 6581 - 6653	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	3.83E-08	0.88	4.67	-	584.0
AHQ-5-1, 7191	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	1.44E-08	0.90	4.54	-	679.3
AHQ-5-3, 7638 - 7698	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	3.56E-05	0.81	3.40	-	798.9
AHQ-5-2, 6585 - 6653	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	7.90E-05	0.83	3.93	-	618.2
AHQ-5-3, 7402	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	1.66E-04	0.86	3.53	-	928.3
AHQ-5-2, 7462	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	2.67E-05	0.94	4.83	-	933.0
AHQ-5-4, 7333	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	1.27E-04	0.78	3.55	-	480.3
AHQ-5-2, 7642 - 7705	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	2.73E-11	0.93	5.21	-	650.9
AHQ-5-4, 2629	K.FLPSELRDEH	1243.35032	2	3.17E-06	0.62	2.84	-	290.3
AHQ-5-7, 4674	K.GLAGAVSELLR.S	1086.26701	2	6.10E-07	0.97	5.13	-	1901.5
AHQ-5-2, 5155 - 5193	K.GLAGAVSELLR.S	1086.26701	2	2.18E-06	0.98	4.86	-	2269.4
AHQ-5-5, 4949 - 4962	K.GLAGAVSELLR.S	1086.26701	2	1.73E-07	0.97	4.96	-	1826.9
AHQ-5-1, 5292	K.GLAGAVSELLR.S	1086.26701	2	1.17E-07	0.97	4.41	-	1957.8
AHQ-5-4, 5156	K.GLAGAVSELLR.S	1086.26701	2	1.92E-06	0.98	5.23	-	2451.5
AHQ-5-3, 5238	K.GLAGAVSELLR.S	1086.26701	2	3.95E-07	0.98	4.91	-	2083.5
AHQ-5-8, 4494	K.GLAGAVSELLR.S	1086.26701	2	5.66E-07	0.97	5.06	-	1835.2
AHQ-5-6, 4901	K.GLAGAVSELLR.S	1086.26701	2	2.31E-05	0.97	4.19	-	1855.0
AHQ-5-5, 6662 - 6727	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	5.42E-05	0.93	5.13	-	649.4
AHQ-5-2, 6789 - 6865	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	5.74E-07	0.95	5.64	-	1399.7
AHQ-5-1, 6773 - 6843	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.04E-05	0.94	5.40	-	971.4
AHQ-5-9, 5856	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.91E-06	0.53	2.87	-	306.7
AHQ-5-5, 6665 - 6689	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	4.04E-07	0.94	5.48	-	883.1
AHQ-5-3, 6865 - 6933	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.56E-05	0.82	3.99	-	756.2
AHQ-5-1, 6752 - 6812	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	6.81E-04	0.72	3.27	-	413.1
AHQ-5-2, 6793 - 6861	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	6.48E-04	0.93	4.69	-	936.4
AHQ-5-4, 6966	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	8.86E-04	0.67	3.35	-	717.0
AHQ-5-4, 6824 - 6892	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	5.09E-07	0.95	4.96	-	1046.3
AHQ-5-6, 6592 - 6612	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	6.38E-04	0.87	4.63	-	738.2
AHQ-5-6, 6594	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.27E-04	0.82	3.75	-	533.9
AHQ-5-2, 6934	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.82E-04	0.71	3.29	-	412.1
AHQ-5-13-, 6883	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	2.63E-06	0.93	4.91	-	1297.8
AHQ-5-7, 7402 - 7406	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	4.17E-12	0.97	6.72	-	1758.1
AHQ-5-4, 7480 - 7557	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	6.18E-09	0.98	7.01	-	1538.1
AHQ-5-6, 7408 - 7410	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	6.92E-11	0.97	6.01	-	1709.9
AHQ-5-5, 7463 - 7505	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	5.98E-11	0.96	5.91	-	1316.6
AHQ-5-9, 6586 - 6587	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	2.70E-09	0.96	5.72	-	1668.4
AHQ-5-2, 7522 - 7601	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.61E-14	0.96	5.92	-	1319.3
AHQ-5-3, 7461 - 7462	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	2.11E-13	0.99	7.92	-	3489.9
AHQ-5-1, 7284 - 7285	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	4.22E-06	0.98	7.37	-	2577.6
AHQ-5-2, 7453 - 7454	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	3.94E-11	0.98	7.43	-	2015.2
AHQ-5-5, 7353 - 7354	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	3.24E-04	0.97	6.20	-	1807.5
AHQ-5-4, 7413 - 7416	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	9.36E-08	0.99	7.73	-	2835.8
AHQ-5-9, 6439 - 6440	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	9.04E-04	0.58	3.25	-	184.0
AHQ-5-5, 7410	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.40E-07	0.92	4.52	-	893.3
AHQ-5-3, 7521 - 7526	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.81E-07	0.95	5.13	-	1248.3
AHQ-5-3, 7522 - 7523	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.50E-09	0.96	5.66	-	1334.8
AHQ-5-6, 5549	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.42E-12	0.89	4.12	-	727.2
AHQ-5-1, 7344	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.28E-04	0.89	3.79	-	1012.6
AHQ-5-2, 7505	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.04E-08	0.94	4.28	-	1342.6
AHQ-5-4, 5832	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.24E-10	0.95	5.38	-	919.2
AHQ-5-1, 7343 - 7347	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.04E-06	0.96	5.63	-	946.2
AHQ-5-5, 7409	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.29E-10	0.95	5.38	-	913.6
AHQ-5-4, 7472 - 7473	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.23E-06	0.93	4.74	-	1210.4
AHQ-5-6, 7324	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.53E-07	0.83	3.52	-	938.4
AHQ-5-4, 7476	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.06E-09	0.93	5.06	-	721.5
AHQ-5-8, 7226	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.48E-05	0.85	4.02	-	904.3

AHQ-5-7, 7310 - 7311	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.18E-06	0.94	5.21	-	929.3
AHQ-5-8, 7224 - 7229	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.35E-07	0.96	5.49	-	1066.3
AHQ-5-2, 5790	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.37E-07	0.92	4.67	-	936.5
AHQ-5-3, 5893	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.69E-11	0.95	5.18	-	894.3
AHQ-5-2, 7506 - 7526	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.43E-06	0.93	4.81	-	731.7
AHQ-5-5, 5550	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.05E-07	0.96	5.18	-	1102.7
AHQ-5-9, 6494	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.94E-06	0.94	5.17	-	766.6
AHQ-5-2, 5791	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.00E-06	0.95	4.83	-	1103.3
AHQ-5-6, 7325 - 7326	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.78E-07	0.95	5.14	-	1104.6
AHQ-5-11, 3166	R.IGITNHDEYSLVR.E	1517.66833	2	7.99E-06	0.87	3.37	-	1011.2
AHQ-5-8, 3225 - 3304	R.IGITNHDEYSLVR.E	1517.66833	2	1.28E-04	0.96	4.41	-	1365.1
AHQ-5-13, 3780 - 3798	R.IGITNHDEYSLVR.E	1517.66833	2	5.39E-07	0.90	3.59	-	1008.5
AHQ-5-13-, 3328	R.IGITNHDEYSLVR.E	1517.66833	3	1.27E-10	0.94	4.47	-	1029.1
AHQ-5-7, 3063	R.IGITNHDEYSLVR.E	1517.66833	2	1.89E-05	0.82	2.99	-	934.9
AHQ-5-7, 3238 - 3314	R.IGITNHDEYSLVR.E	1517.66833	2	2.54E-10	0.94	3.89	-	1377.3
AHQ-5-10, 3020	R.IGITNHDEYSLVR.E	1517.66833	2	1.83E-05	0.92	3.84	-	1013.6
AHQ-5-7, 2904	R.IGITNHDEYSLVR.E	1517.66833	2	7.66E-09	0.94	3.91	-	1358.8
AHQ-5-7, 3439	R.IGITNHDEYSLVR.E	1517.66833	2	5.33E-11	0.93	3.66	-	1191.5
AHQ-5-13-, 3700	R.IGITNHDEYSLVR.E	1517.66833	2	6.26E-09	0.95	4.15	-	1223.9
AHQ-5-13-, 3327	R.IGITNHDEYSLVR.E	1517.66833	2	3.04E-11	0.93	3.84	-	1079.3
AHQ-5-8, 4493 - 4498	R.ILAQATSDLVNAIK.A	1457.69748	2	7.83E-10	0.97	5.11	-	1870.1
AHQ-5-4, 4166	R.ILAQATSDLVNAIK.A	1457.69748	2	1.92E-05	0.96	4.33	-	1767.1
AHQ-5-4, 4178	R.ILAQATSDLVNAIK.A	1457.69748	1	2.29E-04	0.42	2.44	-	407.9
AHQ-5-2, 5118	R.ILAQATSDLVNAIK.A	1457.69748	1	2.83E-06	0.69	3.56	-	424.9
AHQ-5-4, 4454	R.ILAQATSDLVNAIK.A	1457.69748	2	4.24E-07	0.96	4.08	-	1640.3
AHQ-5-5, 4922	R.ILAQATSDLVNAIK.A	1457.69748	2	3.01E-08	0.96	4.31	-	1991.2
AHQ-5-6, 4872 - 4888	R.ILAQATSDLVNAIK.A	1457.69748	2	8.42E-08	0.97	4.63	-	1704.4
AHQ-5-7, 4706 - 4715	R.ILAQATSDLVNAIK.A	1457.69748	2	4.42E-07	0.97	4.85	-	1974.7
AHQ-5-2, 5109 - 5110	R.ILAQATSDLVNAIK.A	1457.69748	2	5.80E-09	0.98	5.62	-	1881.5
AHQ-5-7, 4716 - 4719	R.ILAQATSDLVNAIK.A	1457.69748	1	7.18E-04	0.42	2.66	-	433.4
AHQ-5-4, 5120	R.ILAQATSDLVNAIK.A	1457.69748	1	6.11E-07	0.59	2.94	-	535.7
AHQ-5-2, 4630	R.ILAQATSDLVNAIK.A	1457.69748	2	4.16E-07	0.98	5.16	-	2285.9
AHQ-5-2, 4434	R.ILAQATSDLVNAIK.A	1457.69748	2	2.38E-09	0.98	5.37	-	1951.4
AHQ-5-3, 5197	R.ILAQATSDLVNAIK.A	1457.69748	1	9.55E-05	0.89	3.92	-	729.0
AHQ-5-3, 5177	R.ILAQATSDLVNAIK.A	1457.69748	2	1.71E-09	0.98	4.85	-	2173.2
AHQ-5-1, 5199	R.ILAQATSDLVNAIK.A	1457.69748	2	4.53E-09	0.98	5.70	-	2888.5
AHQ-5-2, 4149	R.ILAQATSDLVNAIK.A	1457.69748	2	2.11E-08	0.98	4.64	-	2155.4
AHQ-5-1, 4303 - 4305	R.ILAQATSDLVNAIK.A	1457.69748	2	4.70E-06	0.96	3.93	-	1745.1
AHQ-5-3, 4234	R.ILAQATSDLVNAIK.A	1457.69748	2	5.70E-07	0.97	4.49	-	2006.9
AHQ-5-7, 5832 - 5903	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	6.40E-06	0.97	5.07	-	1421.3
AHQ-5-13, 5900 - 5924	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.95E-05	0.97	5.68	-	1267.0
AHQ-5-8, 5754	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	5.02E-04	0.91	4.01	-	816.2
AHQ-5-13-, 5812 - 5860	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	4.91E-04	0.96	5.28	-	1078.2
AHQ-5-13-, 5340 - 5373	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	8.54E-07	0.94	4.40	-	1533.7
AHQ-5-12, 5425 - 5468	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.52E-04	0.81	3.87	-	1050.7
AHQ-5-14, 6057 - 6094	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.63E-06	0.92	4.03	-	1367.3
AHQ-5-8, 4972 - 5040	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	7.89E-06	0.96	4.55	-	2116.8
AHQ-5-8, 4885 - 4953	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	5.62E-06	0.87	3.82	-	945.1
AHQ-5-11, 5224 - 5302	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.69E-08	0.90	4.30	-	1072.8
AHQ-5-13, 2974	K.ISIGNVVK.T	830.00746	2	1.70E-04	0.70	2.54	-	503.9
AHQ-5-7, 1494 - 1554	K.KEEITGTLR.K	1047.18765	1	3.48E-04	0.42	2.37	-	329.9
AHQ-5-7, 2352	R.KFFYSDQNVDSR.D	1506.60087	2	5.94E-05	0.66	3.08	-	521.2
AHQ-5-8, 2222	R.KFFYSDQNVDSR.D	1506.60087	2	4.96E-05	0.88	3.35	-	758.8
AHQ-5-13, 2717	K.KGIWLEAGK.A	1002.19171	2	2.34E-04	0.92	3.24	-	1055.4
AHQ-5-7, 2078	K.KGIWLEAGK.A	1002.19171	1	2.88E-04	0.07	2.01	-	249.5
AHQ-5-7, 2403 - 2483	K.LAQAAQSSVATITR.L	1417.59344	2	2.97E-04	0.96	4.21	-	1548.1
AHQ-5-13-, 2715 - 2716	K.LAQAAQSSVATITR.L	1417.59344	2	5.47E-05	0.86	3.70	-	1216.5
AHQ-5-3, 2473	K.LAQAAQSSVATITR.L	1417.59344	2	2.30E-08	0.94	3.68	-	1270.7
AHQ-5-13, 2849	K.LAQAAQSSVATITR.L	1417.59344	2	1.00E-04	0.77	2.76	-	1024.0
AHQ-5-6, 2472 - 2550	K.LAQAAQSSVATITR.L	1417.59344	2	1.83E-11	0.97	4.18	-	1738.4
AHQ-5-5, 2465	K.LAQAAQSSVATITR.L	1417.59344	2	1.94E-09	0.97	4.68	-	1899.4
AHQ-5-4, 2445	K.LAQAAQSSVATITR.L	1417.59344	2	1.70E-06	0.92	3.26	-	1236.3
AHQ-5-2, 2630 - 2659	K.LAQAAQSSVATITR.L	1417.59344	2	1.92E-04	0.91	3.67	-	1091.1
AHQ-5-1, 2649 - 2656	K.LAQAAQSSVATITR.L	1417.59344	2	7.64E-06	0.96	3.80	-	1786.7
AHQ-5-1, 2787 - 2812	K.LAQAAQSSVATITR.L	1417.59344	2	1.58E-11	0.97	4.72	-	2015.4
AHQ-5-3, 2634 - 2670	K.LAQAAQSSVATITR.L	1417.59344	2	8.14E-11	0.97	4.72	-	1462.3
AHQ-5-2, 2347 - 2425	K.LAQAAQSSVATITR.L	1417.59344	2	2.68E-10	0.96	5.14	-	1332.0
AHQ-5-2, 2519 - 2593	K.LAQAAQSSVATITR.L	1417.59344	2	6.21E-10	0.98	5.71	-	2185.5
AHQ-5-4, 2592 - 2628	K.LAQAAQSSVATITR.L	1417.59344	2	4.00E-10	0.97	5.04	-	1678.2
AHQ-5-5, 2330	K.LAQAAQSSVATITR.L	1417.59344	2	8.08E-11	0.96	4.56	-	1499.7
AHQ-5-14-, 2654 - 2655	K.LAQAAQSSVATITR.L	1417.59344	2	4.22E-09	0.95	4.30	-	1493.6
AHQ-5-10, 2472	K.LAQAAQSSVATITR.L	1417.59344	2	7.70E-06	0.78	2.58	-	703.9
AHQ-5-3, 2927	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	7.42E-05	0.96	5.05	-	1049.9
AHQ-5-4, 3101	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	4.30E-06	0.97	5.75	-	1964.2
AHQ-5-6, 2902	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.01E-09	0.96	5.16	-	766.9
AHQ-5-3, 3137 - 3143	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.84E-05	0.91	4.92	-	480.3
AHQ-5-4, 3105 - 3121	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.23E-06	0.97	5.84	-	1091.6
AHQ-5-2, 2862	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	3.06E-11	0.94	4.36	-	1014.7
AHQ-5-5, 2909	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	9.48E-08	0.92	4.60	-	586.1
AHQ-5-2, 3053	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.65E-06	0.96	5.44	-	733.4
AHQ-5-6, 2732	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	7.27E-07	0.82	3.41	-	1218.0
AHQ-5-1, 3303	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.74E-07	0.97	5.30	-	2162.9
AHQ-5-3, 3458	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.55E-10	0.94	4.17	-	885.5
AHQ-5-5, 2902	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.64E-07	0.97	5.51	-	1969.9
AHQ-5-1, 3307	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.75E-06	0.95	5.34	-	698.4
AHQ-5-6, 2840 - 2908	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.88E-10	0.97	5.84	-	2088.2
AHQ-5-1, 5643	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.69E-06	0.92	3.72	-	1613.5
AHQ-5-1, 5357 - 5424	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.32E-10	0.95	4.62	-	1073.0
AHQ-5-2, 5505 - 5507	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.37E-04	0.96	5.37	-	933.4
AHQ-5-1, 5491	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.93E-07	0.82	3.83	-	563.6
AHQ-5-3, 5609 - 5621	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	7.78E-07	0.98	5.71	-	2425.0
AHQ-5-13-, 5268	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.45E-06	0.98	5.74	-	1661.2
AHQ-5-4, 5357 - 5432	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.69E-11	0.96	5.21	-	1180.5
AHQ-5-2, 5358 - 5433	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.12E-07	0.96	5.14	-	994.5
AHQ-5-4, 5468 - 5542	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.31E-07	0.96	5.04	-	1169.1
AHQ-5-14-, 5222	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.29E-05	0.95	4.70	-	972.8
AHQ-5-4, 5576	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.70E-04	0.81	3.30	-	1039.5
AHQ-5-2, 5638 - 5706	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.47E-05	0.97	5.84	-	983.9
AHQ-5-5, 5217 - 5218	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.21E-12	0.95	4.97	-	997.0
AHQ-5-6, 5500	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.09E-07	0.92	4.48	-	722.7
AHQ-5-13-, 5259	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.56E-04	0.80	3.04	-	686.5
AHQ-5-2, 5757	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.48E-09	0.93	4.52	-	725.4
AHQ-5-7, 5115 - 5186	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.11E-05	0.92	4.15	-	873.8
AHQ-5-14-, 5035 - 5047	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.47E-07	0.91	4.80	-	570.4
AHQ-5-6, 5260 - 5333	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.52E-10	0.97	5.49	-	1330.6
AHQ-5-1, 5641	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.02E-05	0.97	5.20	-	1477.0
AHQ-5-7, 5016 - 5018	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.17E-08	0.96	4.50	-	1450.3

AHQ-5-6, 5148	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.22E-04	0.91	3.74	-	1001.2
AHQ-5-5, 5547 - 5567	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.73E-11	0.96	5.40	-	921.9
AHQ-5-4, 5612 - 5680	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.66E-06	0.97	5.30	-	1443.6
AHQ-5-5, 5385 - 5398	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.07E-07	0.98	5.84	-	2604.0
AHQ-5-1, 5773 - 5851	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.78E-07	0.95	5.04	-	865.1
AHQ-5-4, 5749	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.05E-04	0.94	4.78	-	938.5
AHQ-5-5, 5373	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.50E-06	0.96	4.96	-	1232.9
AHQ-5-8, 3484	K.LHTDDELNWLDHGR.T	1721.81153	2	5.02E-06	0.64	3.13	-	136.3
AHQ-5-9, 3143	K.LHTDDELNWLDHGR.T	1721.81153	2	3.08E-05	0.98	5.01	-	2461.7
AHQ-5-10, 3292 - 3371	K.LHTDDELNWLDHGR.T	1721.81153	2	1.65E-09	0.97	4.87	-	1844.0
AHQ-5-8, 3028	K.LHTDDELNWLDHGR.T	1721.81153	2	3.55E-07	0.97	4.83	-	1778.1
AHQ-5-7, 3343 - 3358	K.LHTDDELNWLDHGR.T	1721.81153	3	1.86E-07	0.92	4.59	-	988.2
AHQ-5-5, 5070	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.63E-09	0.97	5.87	-	1485.7
AHQ-5-8, 4490 - 4516	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	9.38E-10	0.96	5.60	-	1276.8
AHQ-5-2, 5269 - 5270	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.41E-05	0.97	5.51	-	1880.8
AHQ-5-6, 5042 - 5052	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.20E-09	0.98	6.82	-	1297.4
AHQ-5-12, 5173	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.20E-12	0.98	5.94	-	1926.8
AHQ-5-12, 5164	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	9.70E-08	0.95	4.84	-	1342.9
AHQ-5-5, 5065 - 5133	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	6.23E-07	0.96	5.31	-	1497.2
AHQ-5-9, 4466	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.07E-12	0.98	6.19	-	1597.8
AHQ-5-4, 5313	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.09E-10	0.98	6.37	-	1579.7
AHQ-5-3, 5365 - 5393	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.35E-09	0.98	6.61	-	1534.4
AHQ-5-2, 5265	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.87E-07	0.97	6.25	-	1208.3
AHQ-5-4, 5312 - 5317	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	7.06E-10	0.97	5.75	-	1427.0
AHQ-5-8, 4508	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	9.94E-08	0.95	5.05	-	1233.2
AHQ-5-3, 5367	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	6.61E-08	0.96	5.27	-	1457.6
AHQ-5-11, 4979	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	5.89E-08	0.97	5.64	-	1975.9
AHQ-5-7, 4828	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.83E-06	0.98	6.21	-	1736.4
AHQ-5-7, 4827 - 4851	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	5.97E-06	0.97	5.86	-	1572.9
AHQ-5-6, 5045	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.81E-06	0.84	3.71	-	880.0
AHQ-5-1, 5411	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	8.21E-12	0.98	6.74	-	1932.9
AHQ-5-9, 4472	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.53E-09	0.91	4.18	-	915.2
AHQ-5-1, 5412	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.24E-06	0.96	5.26	-	1594.7
AHQ-5-1, 5420	K.LLAALLEDEGGSGRPLLQAAKGLAGAVSELLR.S	3190.68337	3	8.30E-04	0.63	3.88	-	552.3
AHQ-5-2, 4481 - 4559	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.64E-05	0.84	3.62	-	408.6
AHQ-5-1, 4467 - 4535	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.59E-05	0.62	2.96	-	231.2
AHQ-5-2, 4341 - 4410	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.94E-11	0.93	4.59	-	406.0
AHQ-5-1, 4331 - 4399	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.42E-06	0.86	3.81	-	378.5
AHQ-5-3, 4462 - 4533	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.92E-04	0.70	3.09	-	241.4
AHQ-5-4, 4428 - 4430	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	7.24E-04	0.82	3.68	-	333.0
AHQ-5-5, 4085 - 4165	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.53E-05	0.85	3.87	-	409.2
AHQ-5-2, 4201 - 4270	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	4.36E-10	0.88	3.98	-	416.7
AHQ-5-4, 4288 - 4360	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.42E-05	0.90	4.00	-	518.9
AHQ-5-1, 4232 - 4308	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.77E-04	0.83	3.85	-	293.7
AHQ-5-4, 4152 - 4220	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.62E-07	0.76	3.39	-	291.6
AHQ-5-3, 4193 - 4262	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.17E-06	0.92	4.32	-	461.9
AHQ-5-3, 4333 - 4413	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.99E-06	0.94	5.01	-	461.2
AHQ-5-5, 4238	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	5.55E-04	0.59	3.07	-	216.3
AHQ-5-3, 6086	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.95E-06	0.95	5.03	-	1447.5
AHQ-5-5, 4362	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.51E-07	0.96	5.08	-	1006.9
AHQ-5-2, 5409	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.91E-08	0.97	5.82	-	1589.6
AHQ-5-6, 5812	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.72E-08	0.88	3.64	-	690.0
AHQ-5-3, 4530 - 4541	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.05E-14	0.97	5.33	-	1234.1
AHQ-5-8, 5028 - 5029	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.37E-08	0.98	5.84	-	1886.8
AHQ-5-2, 4471 - 4501	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.70E-09	0.93	4.79	-	671.9
AHQ-5-4, 5628 - 5677	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.70E-09	0.97	5.47	-	1432.3
AHQ-5-4, 5636	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	5.52E-04	0.96	4.71	-	2090.7
AHQ-5-1, 5761	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	5.73E-04	0.97	5.82	-	1879.2
AHQ-5-3, 6069 - 6083	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.25E-12	0.98	5.40	-	2101.5
AHQ-5-3, 5685	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.25E-09	0.98	6.12	-	1764.3
AHQ-5-4, 5868	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.60E-12	0.97	5.01	-	1513.7
AHQ-5-5, 5410	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.35E-04	0.94	4.36	-	1241.6
AHQ-5-9, 4768	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.26E-05	0.93	3.92	-	1179.0
AHQ-5-2, 5575 - 5627	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	3.93E-04	0.97	5.93	-	1986.8
AHQ-5-4, 6004	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.08E-10	0.97	5.27	-	1401.9
AHQ-5-3, 5470	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.10E-08	0.93	4.52	-	816.7
AHQ-5-4, 6010	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.10E-05	0.94	4.64	-	1223.2
AHQ-5-5, 5609 - 5622	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.64E-04	0.79	3.23	-	729.1
AHQ-5-1, 4575 - 4652	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.14E-07	0.92	4.26	-	765.6
AHQ-5-6, 5400	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.12E-10	0.97	5.27	-	1540.1
AHQ-5-4, 4508	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.04E-08	0.95	5.34	-	799.9
AHQ-5-3, 5595 - 5665	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.84E-13	0.98	5.81	-	1853.5
AHQ-5-2, 5535 - 5605	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.98E-12	0.98	5.79	-	2026.5
AHQ-5-5, 5817 - 5890	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.15E-11	0.98	5.79	-	1989.8
AHQ-5-2, 5763 - 5793	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.76E-13	0.98	5.91	-	1755.8
AHQ-5-1, 5748 - 5816	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.61E-12	0.96	4.74	-	1466.8
AHQ-5-1, 6044	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.92E-08	0.94	3.96	-	1138.3
AHQ-5-7, 5218	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.77E-08	0.95	4.69	-	1246.5
AHQ-5-3, 5925	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.96E-08	0.97	5.14	-	1331.5
AHQ-5-2, 1834 - 1867	R.MATNAAAQNAIK.K	1204.38227	2	3.73E-05	0.86	3.79	-	676.8
AHQ-5-1, 4145 - 4217	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	4.78E-09	0.94	5.29	-	1049.3
AHQ-5-1, 4404	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	5.95E-05	0.82	3.61	-	870.1
AHQ-5-5, 3898	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.76E-08	0.94	5.34	-	953.8
AHQ-5-4, 3872	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	6.69E-08	0.92	4.56	-	1185.7
AHQ-5-7, 3923	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.02E-04	0.76	3.01	-	748.3
AHQ-5-2, 4357	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	2	4.22E-11	0.93	4.68	-	736.8
AHQ-5-4, 4061	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	5.69E-09	0.91	4.10	-	1027.1
AHQ-5-3, 4339	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	7.00E-09	0.90	4.26	-	780.6
AHQ-5-2, 4271 - 4343	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	3.77E-07	0.95	5.12	-	1307.8
AHQ-5-8, 3754 - 3757	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.98E-07	0.96	5.42	-	1275.2
AHQ-5-2, 4097	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	6.02E-10	0.94	5.49	-	969.1
AHQ-5-10, 3788 - 3842	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.65E-05	0.90	4.43	-	815.5
AHQ-5-2, 4082	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	2	2.13E-04	0.67	2.82	-	519.9
AHQ-5-4, 4694	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	2.20E-04	0.87	3.73	-	853.0
AHQ-5-2, 4558	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	9.17E-07	0.96	5.07	-	1610.8
AHQ-5-4, 7130	K.MVGGIAQIIAAQEEMLR.K	1831.19407	3	8.53E-10	0.98	6.86	-	2937.7
AHQ-5-10, 5948	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	3.51E-04	0.95	4.99	-	949.6
AHQ-5-4, 7116 - 7128	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	3.29E-08	0.97	5.60	-	1532.9
AHQ-5-4, 6825	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	4.33E-07	0.98	5.67	-	1656.5
AHQ-5-2, 6430	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	6.32E-10	0.98	5.41	-	1866.8
AHQ-5-8, 6610	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	6.22E-04	0.93	3.59	-	1421.7
AHQ-5-4, 6433 - 6513	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	2	2.19E-09	0.97	5.68	-	1367.6
AHQ-5-7, 6810	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	4.33E-08	0.94	4.62	-	1274.8
AHQ-5-2, 6790	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.43E-06	0.96	4.53	-	1484.4
AHQ-5-3, 7161 - 7178	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	2.80E-07	0.97	5.31	-	1806.9
AHQ-5-2, 7109 - 7174	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	9.55E-14	0.98	6.12	-	2194.3
AHQ-5-9, 6096	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	3.00E-06	0.96	4.96	-	1505.0

AHQ-5-2, 7130	K.MVGGIAQIIAAQEEMLR.K	1831.19407	3	3.07E-10	0.98	6.89	-	2776.3
AHQ-5-2, 7270	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	4.17E-06	0.95	4.18	-	1481.8
AHQ-5-6, 6881	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	3.18E-06	0.98	5.61	-	1702.7
AHQ-5-6, 6586	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	2.45E-07	0.97	5.78	-	1553.8
AHQ-5-5, 6967 - 6970	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	8.74E-10	0.97	5.37	-	1783.7
AHQ-5-1, 7105	K.MVGGIAQIIAAQEEMLR.K	1831.19407	2	5.04E-07	0.97	5.61	-	1449.8
AHQ-5-13, 6474	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	5.00E-05	0.90	4.00	-	969.4
AHQ-5-2, 6094	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	2.85E-06	0.97	5.56	-	1616.0
AHQ-5-8, 2028	K.NCGQMSEIEAK.V	1268.40005	2	1.20E-05	0.79	2.79	-	1048.0
AHQ-5-3, 4777 - 4779	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.39E-07	0.93	4.53	-	632.5
AHQ-5-1, 4564 - 4580	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.11E-05	0.82	3.56	-	426.1
AHQ-5-1, 4729 - 4801	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.13E-04	0.57	2.65	-	394.4
AHQ-5-6, 4577 - 4578	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.40E-06	0.83	3.47	-	492.2
AHQ-5-4, 4073 - 4076	K.NLGTALAELR.T	1058.21367	2	7.09E-05	0.91	3.50	-	1022.4
AHQ-5-1, 4289 - 4293	K.NLGTALAELR.T	1058.21367	2	8.40E-05	0.88	3.52	-	849.5
AHQ-5-5, 3853	K.NLGTALAELR.T	1058.21367	2	3.48E-04	0.91	3.64	-	1041.7
AHQ-5-2, 4041 - 4057	K.NLGTALAELR.T	1058.21367	2	1.90E-04	0.90	3.67	-	884.9
AHQ-5-4, 2577 - 2578	K.PAAVAAENEEIGSHIK.H	1636.78798	2	8.44E-10	0.98	5.69	-	2560.3
AHQ-5-1, 2789	K.PAAVAAENEEIGSHIK.H	1636.78798	2	2.10E-05	0.97	5.08	-	1557.5
AHQ-5-5, 2433	K.PAAVAAENEEIGSHIK.H	1636.78798	3	5.96E-11	0.97	5.52	-	1561.1
AHQ-5-4, 2576	K.PAAVAAENEEIGSHIK.H	1636.78798	3	6.51E-09	0.98	5.61	-	2388.4
AHQ-5-6, 2416	K.PAAVAAENEEIGSHIK.H	1636.78798	2	7.47E-05	0.97	5.27	-	1506.3
AHQ-5-6, 2420 - 2421	K.PAAVAAENEEIGSHIK.H	1636.78798	3	4.55E-11	0.98	6.12	-	2236.1
AHQ-5-2, 2518	K.PAAVAAENEEIGSHIK.H	1636.78798	2	7.27E-09	0.98	5.59	-	2033.0
AHQ-5-2, 2521	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.84E-10	0.98	6.05	-	1915.8
AHQ-5-3, 2621	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.30E-09	0.96	5.19	-	1492.3
AHQ-5-3, 2617	K.PAAVAAENEEIGSHIK.H	1636.78798	2	8.25E-08	0.98	6.08	-	2275.6
AHQ-5-5, 2435	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.23E-06	0.98	6.09	-	2052.0
AHQ-5-7, 2831	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.54E-04	0.68	3.38	-	312.1
AHQ-5-4, 3162	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	6.09E-06	0.86	4.01	-	499.5
AHQ-5-1, 3348	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	6.36E-06	0.95	4.88	-	933.1
AHQ-5-5, 2945 - 2946	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.97E-05	0.93	4.60	-	735.8
AHQ-5-6, 2936 - 2942	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.76E-06	0.94	4.79	-	760.2
AHQ-5-2, 3113	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	5.79E-04	0.87	3.92	-	667.2
AHQ-5-3, 3198 - 3199	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.92E-07	0.93	4.75	-	793.0
AHQ-5-4, 3161	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	4.05E-04	0.78	3.18	-	763.3
AHQ-5-5, 3857	R.QELAVFCSPEPPAK.T	1574.77985	2	4.32E-05	0.76	2.64	-	747.6
AHQ-5-2, 3994 - 3998	R.QELAVFCSPEPPAK.T	1574.77985	2	5.93E-07	0.94	4.06	-	1151.3
AHQ-5-1, 4149 - 4152	R.QELAVFCSPEPPAK.T	1574.77985	2	2.29E-07	0.94	3.96	-	1117.8
AHQ-5-8, 3638	R.QELAVFCSPEPPAK.T	1574.77985	2	2.47E-05	0.75	2.70	-	674.5
AHQ-5-2, 7493 - 7541	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	1.08E-05	0.89	5.02	-	529.0
AHQ-5-3, 7505 - 7549	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	2.67E-09	0.95	5.79	-	1009.2
AHQ-5-5, 7401 - 7445	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	4.44E-15	0.96	6.08	-	950.9
AHQ-5-2, 7473	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	2.13E-07	0.91	5.01	-	902.0
AHQ-5-6, 7308 - 7348	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	3.69E-08	0.94	5.83	-	695.8
AHQ-5-9, 6478	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	1.12E-04	0.96	5.75	-	1132.9
AHQ-5-7, 7295 - 7343	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALMQLAK.A	4138.52644	3	3.17E-12	0.96	5.72	-	962.8
AHQ-5-2, 3765	K.QVAASTAQLLVACK.V	1461.70942	2	8.15E-08	0.90	3.09	-	739.7
AHQ-5-3, 3814	K.QVAASTAQLLVACK.V	1461.70942	2	8.65E-11	0.89	3.65	-	577.5
AHQ-5-1, 3933 - 3935	K.QVAASTAQLLVACK.V	1461.70942	2	3.05E-06	0.95	4.13	-	826.2
AHQ-5-8, 5094	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	2.40E-06	0.95	4.73	-	892.4
AHQ-5-1, 6119	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	1.56E-05	0.96	4.73	-	1471.9
AHQ-5-4, 5921	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	7.90E-06	0.98	6.03	-	1572.1
AHQ-5-2, 4846	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	1.29E-04	0.84	3.99	-	399.3
AHQ-5-3, 5991	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	1.36E-05	0.98	6.51	-	2296.2
AHQ-5-2, 4929	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	9.20E-05	0.88	3.80	-	455.1
AHQ-5-5, 5610	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	1.88E-05	0.98	5.53	-	2243.3
AHQ-5-2, 5874 - 5883	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	2.49E-06	0.98	6.24	-	1978.3
AHQ-5-1, 3084	K.SIAAATSALVK.A	1032.21612	2	3.27E-05	0.89	3.09	-	924.5
AHQ-5-4, 2852	K.SIAAATSALVK.A	1032.21612	2	6.56E-04	0.77	3.07	-	602.8
AHQ-5-2, 2809	K.SIAAATSALVK.A	1032.21612	2	5.65E-05	0.87	3.25	-	869.8
AHQ-5-7, 3999	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	9.30E-06	0.94	4.25	-	1177.9
AHQ-5-8, 3822 - 3828	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	9.30E-10	0.96	4.57	-	1641.9
AHQ-5-7, 3938 - 4008	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	8.32E-07	0.90	4.10	-	1252.3
AHQ-5-9, 3748	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	1.08E-05	0.88	3.25	-	1018.5
AHQ-5-8, 3810	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	7.77E-05	0.86	3.41	-	1138.8
AHQ-5-6, 5100 - 5129	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.49E-06	0.91	4.21	-	636.8
AHQ-5-2, 5125	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.23E-08	0.89	4.34	-	484.4
AHQ-5-4, 5584	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.54E-08	0.82	3.45	-	416.6
AHQ-5-5, 5335 - 5341	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.69E-07	0.89	4.25	-	470.5
AHQ-5-1, 4768	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.55E-08	0.84	3.75	-	457.4
AHQ-5-5, 4582	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.32E-09	0.87	4.04	-	468.4
AHQ-5-4, 4729	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.22E-09	0.86	4.09	-	446.8
AHQ-5-4, 5484 - 5513	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.25E-06	0.83	3.79	-	466.0
AHQ-5-7, 4971	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.10E-06	0.77	3.14	-	442.5
AHQ-5-2, 4718 - 4721	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.37E-09	0.93	4.40	-	672.8
AHQ-5-4, 5308 - 5377	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.35E-05	0.87	3.79	-	446.7
AHQ-5-2, 5431 - 5503	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.39E-08	0.84	3.90	-	421.3
AHQ-5-1, 5355 - 5423	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.88E-06	0.74	3.49	-	346.0
AHQ-5-5, 5151 - 5169	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.05E-07	0.89	3.90	-	528.3
AHQ-5-1, 5492 - 5549	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.56E-04	0.36	2.87	-	166.7
AHQ-5-3, 5613	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.82E-05	0.77	3.55	-	340.3
AHQ-5-1, 5581 - 5623	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.34E-07	0.89	4.25	-	493.5
AHQ-5-3, 5513 - 5541	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.75E-06	0.90	4.15	-	592.6
AHQ-5-2, 5559 - 5633	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.79E-06	0.90	3.92	-	604.2
AHQ-5-3, 5433	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.82E-05	0.78	3.45	-	380.7
AHQ-5-2, 5273 - 5341	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.61E-06	0.77	3.37	-	375.3
AHQ-5-4, 5137	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.47E-06	0.79	3.06	-	629.6
AHQ-5-3, 5337 - 5409	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.09E-06	0.87	4.23	-	427.6
AHQ-5-3, 5199	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.54E-05	0.85	3.66	-	504.9
AHQ-5-5, 5478 - 5553	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.29E-11	0.91	4.00	-	650.1
AHQ-5-2, 4949	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.88E-09	0.85	3.81	-	445.7
AHQ-5-2, 7439 - 7447	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.44E-12	0.98	6.59	-	2260.6
AHQ-5-6, 7238	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	3.30E-11	0.97	6.13	-	1766.1
AHQ-5-13, 6816	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.69E-05	0.96	5.17	-	1738.5
AHQ-5-3, 7446	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.85E-13	0.97	6.43	-	1683.9
AHQ-5-7, 7226	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.06E-07	0.96	5.03	-	1690.6
AHQ-5-1, 7471 - 7505	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	6.65E-04	0.66	3.21	-	645.1
AHQ-5-4, 7620 - 7665	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	6.13E-04	0.77	3.39	-	1037.8
AHQ-5-2, 7665 - 7671	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.36E-05	0.97	5.99	-	1453.4
AHQ-5-1, 7204 - 7271	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.89E-08	0.96	5.66	-	1488.3
AHQ-5-13-, 4229	K.TKEVIQEWNLTNIK.R	1716.95938	2	8.67E-06	0.97	5.02	-	1612.9
AHQ-5-10, 3838	K.TKEVIQEWNLTNIK.R	1716.95938	2	2.95E-05	0.97	5.03	-	1775.4
AHQ-5-7, 3868	K.TKEVIQEWNLTNIK.R	1716.95938	3	2.85E-05	0.89	4.34	-	1201.9
AHQ-5-7, 3878	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.30E-07	0.98	5.47	-	1927.0
AHQ-5-12, 4214 - 4216	K.TKEVIQEWNLTNIK.R	1716.95938	2	6.63E-07	0.91	4.19	-	1008.9
AHQ-5-11, 4095	K.TKEVIQEWNLTNIK.R	1716.95938	2	2.61E-06	0.97	4.88	-	1972.2

AHQ-5-8, 3708	K.TKEVIQEWNLTNIK.R	1716.95938	2	5.54E-08	0.97	4.69	-	1862.3
AHQ-5-5, 6461 - 6493	K.TLAESALQLLYTAK.E	1522.76793	2	5.82E-06	0.90	3.14	-	960.0
AHQ-5-2, 6541 - 6610	K.TLAESALQLLYTAK.E	1522.76793	2	1.13E-08	0.97	5.45	-	1284.1
AHQ-5-1, 6621 - 6653	K.TLAESALQLLYTAK.E	1522.76793	2	1.81E-07	0.97	5.19	-	1373.9
AHQ-5-11, 6082	K.TLAESALQLLYTAK.E	1522.76793	2	2.13E-06	0.94	4.24	-	849.5
AHQ-5-2, 6681	K.TLAESALQLLYTAK.E	1522.76793	2	5.24E-08	0.90	2.69	-	1176.5
AHQ-5-4, 6612 - 6680	K.TLAESALQLLYTAK.E	1522.76793	2	9.89E-09	0.97	5.55	-	1373.6
AHQ-5-3, 6782	K.TLAESALQLLYTAK.E	1522.76793	2	2.38E-04	0.80	2.83	-	825.5
AHQ-5-3, 6637 - 6709	K.TLAESALQLLYTAK.E	1522.76793	2	2.97E-07	0.97	5.31	-	1222.0
AHQ-5-1, 3304 - 3308	K.TLSHPQQMALLDQTK.T	1711.96464	3	7.20E-06	0.93	4.37	-	1157.9
AHQ-5-4, 3102 - 3106	K.TLSHPQQMALLDQTK.T	1711.96464	3	6.32E-05	0.95	5.15	-	1435.2
AHQ-5-4, 3096	K.TLSHPQQMALLDQTK.T	1711.96464	2	3.23E-05	0.95	4.55	-	907.4
AHQ-5-1, 3292	K.TLSHPQQMALLDQTK.T	1711.96464	2	7.37E-05	0.96	5.31	-	808.4
AHQ-5-9, 2715	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.12E-05	0.96	5.47	-	839.0
AHQ-5-2, 3017 - 3085	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.59E-08	0.95	5.09	-	885.7
AHQ-5-6, 2889 - 2890	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.32E-04	0.96	5.22	-	870.8
AHQ-5-3, 3050 - 3125	K.TLSHPQQMALLDQTK.T	1711.96464	2	9.59E-04	0.90	3.91	-	608.9
AHQ-5-2, 3099	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.80E-04	0.90	3.87	-	635.8
AHQ-5-2, 3051	K.TLSHPQQMALLDQTK.T	1711.96464	3	1.20E-05	0.94	4.73	-	1271.5
AHQ-5-3, 3146	K.TLSHPQQMALLDQTK.T	1711.96464	3	1.56E-05	0.95	4.98	-	1377.6
AHQ-5-8, 2638	K.TLSHPQQMALLDQTK.T	1711.96464	2	7.68E-08	0.95	4.49	-	913.4
AHQ-5-1, 3591	K.TM*LESAGGLIQTAR.A	1464.67035	2	4.59E-07	0.96	4.54	-	1493.7
AHQ-5-6, 4068 - 4069	K.TMLESAGGLIQTAR.A	1448.67095	2	1.43E-04	0.80	2.75	-	1223.4
AHQ-5-1, 4459	K.TMLESAGGLIQTAR.A	1448.67095	2	2.14E-10	0.94	3.90	-	1770.9
AHQ-5-5, 4138	K.TMLESAGGLIQTAR.A	1448.67095	2	1.28E-09	0.93	4.55	-	1262.9
AHQ-5-4, 3460 - 3477	K.TM*LESAGGLIQTAR.A	1464.67035	2	2.50E-06	0.96	4.27	-	1665.7
AHQ-5-4, 4308 - 4334	K.TMLESAGGLIQTAR.A	1448.67095	2	2.97E-06	0.94	3.41	-	1880.3
AHQ-5-2, 4325 - 4394	K.TMLESAGGLIQTAR.A	1448.67095	2	9.72E-05	0.84	3.03	-	1322.8
AHQ-5-2, 3429	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.16E-10	0.97	4.42	-	1988.6
AHQ-5-3, 4381 - 4394	K.TMLESAGGLIQTAR.A	1448.67095	2	6.14E-09	0.96	5.04	-	1745.4
AHQ-5-3, 4381 - 4394	K.TMLESAGGLIQTARALAVNPR.D	2170.52235	3	5.59E-04	0.43	3.06	-	401.5
AHQ-5-13-, 4775	K.TMQFEPSTMVYDACR.I	1838.07571	2	5.14E-04	0.87	3.68	-	600.5
AHQ-5-13, 4861	K.TMQFEPSTMVYDACR.I	1838.07571	2	2.04E-04	0.91	4.65	-	512.9
AHQ-5-14-, 4211	K.TM*QFEPSTMVYDACR.I	1854.07511	2	2.11E-04	0.93	4.52	-	640.6
AHQ-5-14-, 4733	K.TMQFEPSTMVYDACR.I	1838.07571	2	4.18E-04	0.75	3.46	-	432.7
AHQ-5-13, 4300	K.TM*QFEPSTMVYDACR.I	1854.07511	2	6.35E-05	0.90	4.12	-	621.6
AHQ-5-7, 4050	K.TM*QFEPSTMVYDACR.I	1854.07511	2	3.71E-04	0.81	3.31	-	552.2
AHQ-5-13-, 4203	K.TM*QFEPSTMVYDACR.I	1854.07511	2	2.21E-06	0.92	3.87	-	698.4
AHQ-5-2, 2939	K.TSTPEDFIR.M	1066.14629	1	1.34E-04	0.10	1.84	-	169.7
AHQ-5-13, 4305	K.TVTDM*LMTICAR.I	1429.70947	2	2.57E-05	0.71	3.15	-	817.4
AHQ-5-13, 3774 - 3844	K.TVTDM*LM*TICAR.I	1445.70887	2	3.00E-07	0.82	3.21	-	623.9
AHQ-5-13-, 5345	K.TVTDMLMTICAR.I	1413.71007	2	2.21E-06	0.81	2.74	-	889.2
AHQ-5-8, 4601	K.TVTDMLM*TICAR.I	1429.70947	2	9.19E-04	0.80	3.06	-	989.6
AHQ-5-8, 4582 - 4592	K.TYGVSFFLVK.E	1161.37395	2	5.97E-04	0.91	3.56	-	742.5
AHQ-5-11, 5048	K.TYGVSFFLVK.E	1161.37395	2	7.87E-05	0.79	3.18	-	492.0
AHQ-5-1, 5529	K.TYGVSFFLVK.E	1161.37395	2	4.48E-04	0.90	3.49	-	701.8
AHQ-5-7, 4867	K.TYGVSFFLVK.E	1161.37395	2	1.74E-04	0.89	3.52	-	719.2
AHQ-5-1, 5487 - 5555	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	8.64E-07	0.95	4.54	-	1165.2
AHQ-5-4, 5405	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	1.47E-04	0.75	2.69	-	885.4
AHQ-5-10, 5691 - 5708	R.VAGSVTELIQAAEAMK.G	1618.87752	2	4.36E-07	0.95	4.31	-	1377.0
AHQ-5-6, 6281	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.44E-05	0.95	3.89	-	1489.7
AHQ-5-3, 6506 - 6578	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.77E-13	0.97	5.46	-	1509.1
AHQ-5-9, 5518	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.69E-08	0.97	5.47	-	1508.4
AHQ-5-3, 5459 - 5482	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	8.74E-06	0.94	4.39	-	1057.4
AHQ-5-1, 6533 - 6559	R.VAGSVTELIQAAEAMK.G	1618.87752	2	7.86E-08	0.97	5.12	-	1388.3
AHQ-5-2, 6407 - 6486	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.41E-11	0.98	5.78	-	1711.0
AHQ-5-2, 5351 - 5421	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	2.01E-06	0.96	4.95	-	1218.7
AHQ-5-8, 5969	R.VAGSVTELIQAAEAMK.G	1618.87752	2	8.50E-07	0.97	4.38	-	1993.9
AHQ-5-4, 6525 - 6532	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.11E-08	0.98	5.66	-	2068.0
AHQ-5-6, 5833 - 5902	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.69E-07	0.90	4.29	-	504.5
AHQ-5-10, 5080 - 5107	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.73E-05	0.44	3.38	-	447.6
AHQ-5-6, 5658	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.87E-07	0.95	4.73	-	861.6
AHQ-5-5, 6115 - 6142	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.22E-11	0.98	5.65	-	1537.3
AHQ-5-5, 5854 - 5934	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.47E-12	0.95	5.29	-	616.8
AHQ-5-7, 5726 - 5758	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.89E-11	0.96	4.62	-	1159.8
AHQ-5-8, 5549 - 5621	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.90E-09	0.96	5.41	-	913.0
AHQ-5-8, 5397	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.59E-09	0.94	4.53	-	1032.5
AHQ-5-9, 5027	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.16E-05	0.88	3.79	-	661.4
AHQ-5-9, 5174	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.24E-11	0.93	4.10	-	709.4
AHQ-5-4, 5836 - 5908	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.92E-09	0.95	5.31	-	742.3
AHQ-5-3, 6082 - 6162	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.39E-09	0.96	5.66	-	951.1
AHQ-5-2, 6174 - 6242	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.32E-09	0.82	3.86	-	487.9
AHQ-5-4, 6006 - 6072	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.08E-07	0.88	4.12	-	396.8
AHQ-5-2, 6037 - 6107	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.71E-10	0.92	4.59	-	601.0
AHQ-5-2, 6010 - 6079	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	6.69E-09	0.96	5.20	-	1958.4
AHQ-5-2, 5901 - 5971	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.56E-08	0.96	5.05	-	909.6
AHQ-5-3, 5895 - 5973	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.38E-06	0.97	5.46	-	1123.2
AHQ-5-2, 5818 - 5834	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.70E-06	0.92	4.70	-	565.2
AHQ-5-2, 5721	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.15E-05	0.37	2.72	-	347.2
AHQ-5-12, 5796	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.97E-06	0.91	4.84	-	665.3
AHQ-5-1, 5860 - 5912	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.30E-07	0.90	4.17	-	537.5
AHQ-5-1, 5928	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.02E-04	0.73	3.49	-	354.9
AHQ-5-1, 6051	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.87E-05	0.92	4.45	-	671.0
AHQ-5-10, 5254 - 5316	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.61E-10	0.87	4.00	-	427.0
AHQ-5-11, 5610	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.57E-09	0.96	5.06	-	1113.7
AHQ-5-1, 6135 - 6203	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.34E-13	0.96	5.04	-	1185.2
AHQ-5-4, 6140 - 6141	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.00E-06	0.96	5.43	-	909.2
AHQ-5-7, 5546 - 5550	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.80E-07	0.95	4.99	-	978.5
AHQ-5-1, 6060 - 6141	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	2.14E-07	0.96	5.52	-	1618.9
AHQ-5-4, 3772	K.VGDDPAVWQLK.N	1228.37879	1	9.53E-04	0.61	2.43	-	640.4
AHQ-5-2, 3751	K.VGDDPAVWQLK.N	1228.37879	2	3.17E-08	0.91	3.63	-	980.5
AHQ-5-6, 3504	K.VGDDPAVWQLK.N	1228.37879	2	1.98E-09	0.93	4.02	-	886.2
AHQ-5-3, 3810	K.VGDDPAVWQLK.N	1228.37879	2	1.92E-06	0.89	3.62	-	655.9
AHQ-5-2, 3733 - 3801	K.VGDDPAVWQLK.N	1228.37879	2	7.75E-09	0.86	3.29	-	731.5
AHQ-5-1, 3936	K.VGDDPAVWQLK.N	1228.37879	2	8.17E-08	0.93	3.77	-	875.7
AHQ-5-4, 3760 - 3785	K.VGDDPAVWQLK.N	1228.37879	2	1.01E-08	0.94	4.14	-	865.1
AHQ-5-5, 3546	K.VGDDPAVWQLK.N	1228.37879	2	1.75E-08	0.94	4.02	-	937.0
AHQ-5-2, 3117	K.VGDDPAVWQLKNSAK.V	1628.81068	2	1.85E-07	0.89	3.70	-	762.4
AHQ-5-4, 3154	K.VGDDPAVWQLKNSAK.V	1628.81068	2	4.18E-11	0.88	3.60	-	786.3
AHQ-5-3, 3187	K.VGDDPAVWQLKNSAK.V	1628.81068	2	3.38E-06	0.78	3.27	-	542.3
AHQ-5-2, 2275 - 2278	K.VLGEAM*TGISQNAK.N	1435.62901	1	5.76E-04	0.10	1.84	-	67.9
AHQ-5-2, 2270 - 2342	K.VLGEAM*TGISQNAK.N	1435.62901	2	8.76E-04	0.97	4.84	-	1518.4
AHQ-5-1, 3219	K.VLGEAMTGISQNAK.N	1419.62961	2	1.37E-05	0.96	4.27	-	1685.8
AHQ-5-6, 2882	K.VLGEAMTGISQNAK.N	1419.62961	2	3.48E-04	0.84	3.12	-	1026.5
AHQ-5-3, 3094	K.VLGEAMTGISQNAK.N	1419.62961	1	3.33E-08	0.85	3.80	-	432.3
AHQ-5-3, 3083 - 3153	K.VLGEAMTGISQNAK.N	1419.62961	1	3.30E-04	0.26	1.90	-	372.4
AHQ-5-6, 2172	K.VLGEAM*TGISQNAK.N	1435.62901	2	8.51E-04	0.95	3.78	-	1568.4

AHQ-5-2, 3005	K.VLGEAMTGISQNAK.N	1419.62961	2	6.41E-08	0.77	2.85	-	1151.2
AHQ-5-3, 3081 - 3159	K.VLGEAMTGISQNAK.N	1419.62961	2	2.43E-13	0.98	5.39	-	2007.3
AHQ-5-2, 3031	K.VLGEAMTGISQNAK.N	1419.62961	1	6.26E-05	0.73	3.50	-	328.3
AHQ-5-2, 3115	K.VLGEAMTGISQNAK.N	1419.62961	1	9.40E-04	0.23	1.93	-	316.5
AHQ-5-3, 3275	K.VLGEAMTGISQNAK.N	1419.62961	2	1.64E-07	0.93	3.27	-	1426.9
AHQ-5-1, 3244	K.VLGEAMTGISQNAK.N	1419.62961	1	1.45E-04	0.35	2.64	-	299.6
AHQ-5-4, 3064	K.VLGEAMTGISQNAK.N	1419.62961	1	8.84E-09	0.76	3.39	-	333.4
AHQ-5-4, 3053 - 3126	K.VLGEAMTGISQNAK.N	1419.62961	2	3.26E-12	0.98	5.39	-	2107.0
AHQ-5-5, 2894	K.VLGEAMTGISQNAK.N	1419.62961	2	3.60E-09	0.98	4.76	-	2155.0
AHQ-5-1, 2581	K.VLGEAM*TGISQNAK.N	1435.62901	2	2.99E-04	0.65	2.63	-	627.6
AHQ-5-2, 3195	K.VLGEAMTGISQNAK.N	1419.62961	2	5.12E-07	0.89	2.82	-	1121.8
AHQ-5-4, 2280 - 2297	K.VLGEAM*TGISQNAK.N	1435.62901	2	5.70E-05	0.95	4.30	-	1175.9
AHQ-5-4, 3238	K.VLGEAMTGISQNAK.N	1419.62961	2	2.20E-08	0.97	3.93	-	2326.2
AHQ-5-2, 5446 - 5526	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	1.14E-08	0.94	5.77	-	648.8
AHQ-5-1, 5496 - 5565	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	4.40E-06	0.85	4.18	-	634.1
AHQ-5-1, 4944 - 5021	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	2.15E-07	0.93	5.25	-	602.3
AHQ-5-4, 5465 - 5544	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	4.97E-10	0.92	5.43	-	485.1
AHQ-5-2, 1689	K.VLVQNAAGSQEK.L	1244.37976	2	2.37E-05	0.83	3.29	-	640.2
AHQ-5-2, 1794	K.VLVQNAAGSQEK.L	1244.37976	2	2.96E-04	0.88	2.98	-	1016.8
AHQ-5-4, 1720 - 1790	K.VLVQNAAGSQEK.L	1244.37976	2	1.76E-07	0.93	3.83	-	998.1
AHQ-5-4, 1780	K.VLVQNAAGSQEK.L	1244.37976	1	1.76E-06	0.65	2.19	-	620.0
AHQ-5-1, 1881	K.VLVQNAAGSQEK.L	1244.37976	2	1.58E-06	0.92	3.67	-	1039.1
AHQ-5-4, 1618 - 1624	K.VLVQNAAGSQEK.L	1244.37976	2	8.68E-05	0.79	3.25	-	610.5
AHQ-5-3, 1547 - 1611	K.VLVQNAAGSQEK.L	1244.37976	2	9.66E-04	0.90	3.63	-	902.4
AHQ-5-3, 1670	K.VLVQNAAGSQEK.L	1244.37976	1	2.99E-10	0.45	2.35	-	350.5
AHQ-5-2, 1546 - 1613	K.VLVQNAAGSQEK.L	1244.37976	2	6.34E-06	0.94	3.72	-	1075.7
AHQ-5-4, 1534 - 1557	K.VLVQNAAGSQEK.L	1244.37976	2	4.63E-09	0.91	3.60	-	833.5
AHQ-5-2, 4666	K.VMVTNVTSLLK.T	1205.49322	2	5.72E-06	0.88	3.73	-	736.6
AHQ-5-2, 4281 - 4299	K.VM*VTNVTSLLK.T	1221.49262	2	2.58E-06	0.90	3.70	-	776.0
AHQ-5-4, 4693 - 4697	K.VMVTNVTSLLK.T	1205.49322	2	4.96E-06	0.95	4.14	-	990.2
AHQ-5-3, 4389	K.VM*VTNVTSLLK.T	1221.49262	2	2.18E-04	0.86	3.21	-	794.9
AHQ-5-6, 4370 - 4378	K.VMVTNVTSLLK.T	1205.49322	2	9.53E-05	0.90	4.08	-	695.3
AHQ-5-8, 3921	K.VMVTNVTSLLK.T	1205.49322	2	8.91E-06	0.88	3.38	-	916.4
AHQ-5-4, 4310	K.VM*VTNVTSLLK.T	1221.49262	2	6.44E-05	0.84	3.12	-	919.7
AHQ-5-3, 4769	K.VMVTNVTSLLK.T	1205.49322	2	3.30E-06	0.95	4.42	-	960.8
AHQ-5-1, 4481	K.VM*VTNVTSLLK.T	1221.49262	2	4.40E-04	0.89	3.49	-	774.7
AHQ-5-7, 4172	K.VMVTNVTSLLK.T	1205.49322	2	2.87E-06	0.91	4.03	-	836.1
AHQ-5-1, 4852	K.VMVTNVTSLLK.T	1205.49322	2	6.88E-05	0.90	4.00	-	853.2
AHQ-5-5, 4427	K.VMVTNVTSLLK.T	1205.49322	2	3.71E-04	0.92	3.84	-	874.6
AHQ-5-4, 2721	R.VQELGHGCAALVTK.A	1484.70307	2	6.18E-05	0.87	3.11	-	898.1
AHQ-5-2, 2617	R.VQELGHGCAALVTK.A	1484.70307	2	3.48E-04	0.93	3.81	-	1133.8
AHQ-5-2, 2633	R.VQELGHGCAALVTK.A	1484.70307	1	2.19E-06	0.84	3.56	-	569.9
AHQ-5-1, 2873	R.VQELGHGCAALVTK.A	1484.70307	2	1.00E-08	0.98	5.11	-	1759.3
AHQ-5-6, 2524 - 2541	R.VQELGHGCAALVTK.A	1484.70307	2	4.12E-04	0.97	4.40	-	1827.1
AHQ-5-6, 2521	R.VQELGHGCAALVTK.A	1484.70307	1	3.17E-08	0.93	3.68	-	955.1
AHQ-5-3, 2694	R.VQELGHGCAALVTK.A	1484.70307	2	3.91E-04	0.96	4.33	-	1530.4
AHQ-5-4, 2658	R.VQELGHGCAALVTK.A	1484.70307	1	1.06E-06	0.84	3.38	-	596.6
AHQ-5-5, 2454 - 2521	R.VQELGHGCAALVTK.A	1484.70307	2	5.47E-10	0.98	4.71	-	2082.5
AHQ-5-5, 2511	R.VQELGHGCAALVTK.A	1484.70307	1	2.72E-05	0.82	2.84	-	826.3
AHQ-5-4, 2566 - 2648	R.VQELGHGCAALVTK.A	1484.70307	2	2.69E-09	0.97	5.03	-	1641.6
AHQ-5-4, 2526	K.VSHVLAALQAGNR.G	1336.52525	1	1.96E-07	0.72	3.27	-	209.6
AHQ-5-3, 2534 - 2593	K.VSHVLAALQAGNR.G	1336.52525	2	1.11E-04	0.96	4.12	-	1656.4
AHQ-5-3, 2542	K.VSHVLAALQAGNR.G	1336.52525	1	3.44E-06	0.72	3.10	-	284.3
AHQ-5-3, 2679	K.VSHVLAALQAGNR.G	1336.52525	1	5.11E-06	0.65	2.61	-	433.1
AHQ-5-5, 2362	K.VSHVLAALQAGNR.G	1336.52525	1	1.08E-04	0.48	2.38	-	157.3
AHQ-5-5, 2357	K.VSHVLAALQAGNR.G	1336.52525	2	3.18E-10	0.98	5.07	-	2071.8
AHQ-5-1, 2791	K.VSHVLAALQAGNR.G	1336.52525	2	1.55E-08	0.98	4.67	-	2078.2
AHQ-5-5, 2355	K.VSHVLAALQAGNR.G	1336.52525	1	8.15E-06	0.87	3.31	-	466.5
AHQ-5-6, 2357	K.VSHVLAALQAGNR.G	1336.52525	1	4.87E-04	0.59	2.40	-	362.4
AHQ-5-7, 2311	K.VSHVLAALQAGNR.G	1336.52525	2	2.62E-08	0.96	4.12	-	1676.6
AHQ-5-4, 2520	K.VSHVLAALQAGNR.G	1336.52525	1	5.41E-07	0.86	3.48	-	410.7
AHQ-5-7, 2306	K.VSHVLAALQAGNR.G	1336.52525	1	3.42E-04	0.85	3.05	-	520.9
AHQ-5-2, 2455 - 2527	K.VSHVLAALQAGNR.G	1336.52525	2	5.35E-09	0.97	4.31	-	1977.5
AHQ-5-2, 2454 - 2530	K.VSHVLAALQAGNR.G	1336.52525	1	2.81E-04	0.70	3.12	-	314.4
AHQ-5-6, 2360	K.VSHVLAALQAGNR.G	1336.52525	1	6.89E-07	0.65	2.60	-	289.6
AHQ-5-1, 2783	K.VSHVLAALQAGNR.G	1336.52525	1	2.52E-05	0.86	3.28	-	632.7
AHQ-5-1, 6111 - 6112	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.90E-06	0.96	5.31	-	970.2
AHQ-5-6, 5729	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.38E-07	0.97	5.37	-	1093.4
AHQ-5-9, 5938 - 5942	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.68E-06	0.95	5.26	-	852.6
AHQ-5-4, 6837 - 6917	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	7.86E-07	0.98	6.57	-	1360.3
AHQ-5-1, 6864 - 6928	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.26E-05	0.95	4.71	-	1061.2
AHQ-5-4, 6918 - 6938	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	8.32E-08	0.94	4.89	-	1409.3
AHQ-5-3, 6966 - 7033	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.98E-08	0.97	6.27	-	943.3
AHQ-5-3, 6866 - 6945	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.82E-06	0.97	5.81	-	1137.8
AHQ-5-3, 6065 - 6066	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	6.97E-05	0.96	4.84	-	1319.9
AHQ-5-4, 6980	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.04E-05	0.97	5.90	-	798.4
AHQ-5-7, 5539	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	7.98E-05	0.93	4.25	-	997.0
AHQ-5-7, 6622 - 6630	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.22E-05	0.97	5.84	-	962.3
AHQ-5-11, 6358	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.29E-05	0.92	4.78	-	698.2
AHQ-5-8, 6402	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.31E-07	0.96	5.46	-	990.0
AHQ-5-5, 6781 - 6785	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.60E-06	0.97	5.62	-	1147.6
AHQ-5-5, 5753 - 5787	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.34E-05	0.90	3.95	-	911.5
AHQ-5-14, 6441	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.45E-04	0.50	3.14	-	182.3
AHQ-5-1, 6115	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	4.30E-07	0.94	4.72	-	1766.2
AHQ-5-2, 6899 - 6903	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	5.00E-09	0.97	5.75	-	1534.1
AHQ-5-2, 6797 - 6863	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.70E-05	0.96	5.14	-	1088.0
AHQ-5-2, 5970 - 5973	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	2.61E-06	0.94	5.08	-	1364.1
AHQ-5-2, 5962 - 6030	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.49E-07	0.96	4.88	-	1132.9
AHQ-5-4, 5993 - 6066	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.21E-07	0.96	5.60	-	1003.0
AHQ-5-1, 6908	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	4.54E-06	0.96	5.37	-	1406.2
AHQ-5-14-, 6399	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.74E-08	0.97	6.09	-	1351.0
AHQ-5-2, 4727 - 4797	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	9.09E-06	0.96	5.26	-	923.7
AHQ-5-2, 4601	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.52E-05	0.77	3.64	-	235.1
AHQ-5-2, 4922	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.83E-05	0.76	3.74	-	271.5
AHQ-5-3, 4666	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.45E-08	0.93	4.85	-	460.3
AHQ-5-3, 4786 - 4822	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.00E-07	0.95	5.06	-	629.9
AHQ-5-4, 4616	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.12E-06	0.95	4.73	-	667.3
AHQ-5-4, 4757	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.33E-08	0.95	4.83	-	814.2
AHQ-5-12, 4562	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.99E-05	0.89	3.64	-	747.5
AHQ-5-5, 4478	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.45E-05	0.93	4.27	-	702.0
AHQ-5-5, 4585 - 4653	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.70E-11	0.97	6.02	-	897.2
AHQ-5-6, 4413	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.00E-05	0.83	4.08	-	275.8
AHQ-5-6, 4516 - 4517	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.29E-05	0.95	5.11	-	777.2
AHQ-5-14-, 4402 - 4471	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.63E-05	0.93	4.51	-	705.8
AHQ-5-1, 4800	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.65E-06	0.88	3.58	-	590.1
AHQ-5-7, 4378 - 4442	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.39E-06	0.72	3.31	-	446.5
AHQ-5-8, 4312	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.93E-09	0.97	5.07	-	1261.5

AHQ-5-8, 4328 - 4332	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	4.03E-06	0.89	4.36	-	1040.2
AHQ-5-9, 4058 - 4066	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.02E-06	0.95	5.22	-	834.8
AHQ-5-13-, 4521	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.59E-06	0.59	2.93	-	304.2
gi|4503571|ref|NP_001419.1| enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n				5.55E-16	12.28	150.37	44.70	47168.7
AHQ-5-14-, 5202	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.10E-04	0.73	2.80	-	382.5
AHQ-5-13-, 5249 - 5280	R.AAVPSGASTGIYEALELR.D	1806.00979	2	4.20E-04	0.95	5.19	-	580.9
AHQ-5-12, 5308	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.05E-12	0.95	5.02	-	498.2
AHQ-5-13, 5353 - 5417	R.AAVPSGASTGIYEALELR.D	1806.00979	2	9.57E-12	0.97	5.60	-	663.2
AHQ-5-11, 5104	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.04E-04	0.68	2.93	-	332.0
AHQ-5-8, 4938 - 5010	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.76E-05	0.92	4.40	-	498.2
AHQ-5-14, 5996 - 6004	R.AAVPSGASTGIYEALELR.D	1806.00979	2	5.21E-04	0.95	4.77	-	738.5
AHQ-5-8, 4774 - 4841	R.AAVPSGASTGIYEALELR.D	1806.00979	2	8.77E-14	0.97	5.69	-	841.2
AHQ-5-8, 4292 - 4360	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	1.30E-08	0.94	5.01	-	872.6
AHQ-5-8, 5856 - 5889	K.DATNVGDEGGFAPNILENKEGLELLK.T	2744.99178	3	5.55E-16	0.86	4.30	-	1127.4
AHQ-5-8, 5838 - 5918	K.DATNVGDEGGFAPNILENKEGLELLK.T	2744.99178	2	2.23E-09	0.58	3.78	-	399.7
AHQ-5-9, 6242	K.DYPVVSIEDPFDQDDWGAWQK.F	2511.63977	2	5.34E-06	0.45	2.67	-	423.8
AHQ-5-8, 4389	K.FTASAGIQVVGDDLTVTNPK.R	2034.25590	2	3.98E-06	0.87	3.83	-	745.8
AHQ-5-13, 4313	R.GNPTVEVDLFTSK.G	1407.55065	2	1.09E-06	0.85	3.25	-	834.8
AHQ-5-8, 3813	R.GNPTVEVDLFTSK.G	1407.55065	1	5.06E-09	0.73	3.53	-	610.1
AHQ-5-13-, 4213	R.GNPTVEVDLFTSK.G	1407.55065	1	4.23E-04	0.31	1.92	-	571.1
AHQ-5-8, 5668 - 5740	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	6.16E-08	0.91	4.76	-	893.4
AHQ-5-8, 5120	K.LAM*QEFM*ILPVGAANFR.E	1941.30692	2	1.19E-05	0.93	3.93	-	1030.5
AHQ-5-10, 6263	K.LAMQEFMILPVGAANFR.E	1909.30812	2	1.18E-04	0.87	3.92	-	626.1
AHQ-5-8, 6690 - 6752	K.LAMQEFMILPVGAANFR.E	1909.30812	2	4.81E-05	0.96	4.84	-	1090.2
AHQ-5-8, 5728 - 5749	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	3.05E-05	0.89	4.22	-	957.5
AHQ-5-8, 6768 - 6769	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	3	3.25E-09	0.98	7.42	-	2642.5
AHQ-5-8, 6766 - 6780	K.SFIKDYPVVSIEDPFDQDDWGAWQK.F	2987.22328	2	1.71E-04	0.81	3.91	-	521.3
AHQ-5-8, 2090	R.SGKYDLDFK.S	1073.18043	2	1.44E-05	0.72	2.53	-	701.4
AHQ-5-8, 1949	K.TIAPALVSK.K	900.09769	1	6.53E-04	0.24	2.03	-	256.0
AHQ-5-8, 3364 - 3429	K.VNQIGSVTESLQACK.L	1635.82159	2	1.25E-05	0.89	3.66	-	965.9
AHQ-5-14, 4504 - 4568	K.VNQIGSVTESLQACK.L	1635.82159	2	2.40E-06	0.90	4.28	-	644.8
AHQ-5-8, 4474 - 4480	R.YISPDQLADLYK.S	1426.59557	2	3.48E-09	0.95	4.98	-	839.0
AHQ-5-9, 4296	R.YISPDQLADLYK.S	1426.59557	2	4.14E-06	0.87	3.45	-	634.7
gi|4505879|ref|NP_002655.1| pleckstrin; p47 [Homo sapiens]				5.55E-16	11.13	130.43	52.00	40082.5
AHQ-5-1, 6053	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.69E-05	0.87	4.09	-	709.9
AHQ-5-10, 5126	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	5.69E-09	0.95	5.87	-	902.2
AHQ-5-12, 5664 - 5680	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.39E-06	0.95	5.60	-	1075.2
AHQ-5-13, 5661	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.49E-04	0.94	5.39	-	1012.2
AHQ-5-13-, 5585	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	2.60E-05	0.65	2.73	-	474.4
AHQ-5-13-, 5573 - 5584	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	7.83E-10	0.97	6.37	-	1639.9
AHQ-5-14, 6204	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.33E-08	0.94	5.17	-	1238.3
AHQ-5-14, 6210	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	2.90E-05	0.67	3.12	-	185.8
AHQ-5-8, 5305	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.97E-07	0.97	6.17	-	1709.2
AHQ-5-8, 5308	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	1.82E-07	0.68	2.88	-	368.5
AHQ-5-8, 2269	R.GCVVTSVESNSNGR.K	1467.54464	2	8.78E-08	0.91	3.44	-	1053.5
AHQ-5-13-, 2507	R.GCVVTSVESNSNGR.K	1467.54464	2	1.60E-07	0.84	3.25	-	724.2
AHQ-5-8, 2818	K.GSTLTSPCQDFGK.R	1399.50867	1	3.58E-05	0.23	2.18	-	267.2
AHQ-5-8, 2276	K.GSTLTSPCQDFGKR.M	1555.69502	2	7.56E-06	0.62	2.82	-	507.3
AHQ-5-13-, 2881	K.GSTLTSPCQDFGKR.M	1555.69502	2	8.40E-08	0.68	3.04	-	448.3
AHQ-5-8, 7338 - 7342	K.GSVFNTWKPMWVVLLEDGIEFYK.K	2760.20112	2	1.12E-05	0.82	3.73	-	342.1
AHQ-5-9, 6351 - 6418	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	5.02E-06	0.94	4.28	-	1298.2
AHQ-5-10, 6342	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	4.45E-09	0.98	5.74	-	1508.8
AHQ-5-8, 7104 - 7178	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	1.44E-13	0.98	6.63	-	1569.1
AHQ-5-8, 7021 - 7034	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	7.69E-09	0.97	5.10	-	1390.7
AHQ-5-11, 6851	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.82E-08	0.98	7.64	-	2764.5
AHQ-5-8, 7146	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.12E-07	0.97	6.68	-	1972.3
AHQ-5-8, 7252 - 7320	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.11E-07	0.98	7.09	-	1998.7
AHQ-5-14-, 6797 - 6798	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	5.55E-16	0.98	8.13	-	2445.9
AHQ-5-12, 7080 - 7084	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	8.02E-13	0.99	8.55	-	3524.3
AHQ-5-8, 7389	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	2.79E-11	0.99	8.56	-	3796.7
AHQ-5-13-, 6847 - 6921	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	8.55E-12	0.99	7.74	-	2869.4
AHQ-5-9, 6519	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	6.19E-07	0.98	6.71	-	2342.7
AHQ-5-10, 6567	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	6.50E-12	0.98	7.21	-	1837.4
AHQ-5-9, 5886	R.LPETIDLGALYLSMK.D	1664.98779	2	2.97E-04	0.98	4.54	-	2109.7
AHQ-5-8, 6366 - 6432	R.LPETIDLGALYLSMK.D	1664.98779	2	3.33E-07	0.97	4.23	-	2052.1
AHQ-5-12, 6474 - 6480	R.LPETIDLGALYLSMK.D	1664.98779	2	2.76E-08	0.98	5.02	-	1994.7
AHQ-5-12, 5752 - 5761	R.LPETIDLGALYLSM*K.D	1680.98719	2	5.55E-07	0.97	5.08	-	1341.1
AHQ-5-10, 5982 - 5987	R.LPETIDLGALYLSMK.D	1664.98779	2	3.40E-06	0.98	4.92	-	2018.5
AHQ-5-8, 6526 - 6593	R.LPETIDLGALYLSMK.D	1664.98779	2	9.64E-06	0.97	4.63	-	2079.5
AHQ-5-9, 5991	R.LPETIDLGALYLSMK.D	1664.98779	2	8.53E-04	0.76	2.77	-	918.1
AHQ-5-8, 5413	R.LPETIDLGALYLSM*K.D	1680.98719	2	2.49E-04	0.94	4.10	-	1229.1
AHQ-5-8, 4822 - 4893	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	2	3.73E-04	0.91	3.98	-	868.9
AHQ-5-8, 4828	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	3	4.62E-10	0.93	4.82	-	825.4
AHQ-5-12, 5309	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	3	1.83E-04	0.93	4.73	-	1135.0
AHQ-5-8, 5908 - 5977	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	3	1.87E-04	0.90	4.34	-	928.0
AHQ-5-8, 5773 - 5844	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	3	4.30E-05	0.89	4.17	-	748.3
AHQ-5-8, 5814 - 5894	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	5.03E-05	0.98	6.20	-	1610.8
AHQ-5-10, 5556 - 5558	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	1.28E-06	0.98	6.01	-	1539.3
AHQ-5-8, 5917 - 5984	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	2.29E-04	0.98	6.14	-	1784.1
AHQ-5-8, 6200 - 6220	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	5.80E-05	0.97	5.34	-	1497.7
AHQ-5-9, 5402 - 5410	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	1.95E-05	0.97	5.68	-	1229.2
AHQ-5-8, 5722 - 5744	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	6.30E-08	0.96	5.54	-	692.0
AHQ-5-8, 4118 - 4128	K.QQDHFFQAAFLEER.D	1766.89390	2	9.41E-06	0.41	2.53	-	115.5
AHQ-5-12, 4510	K.QQDHFFQAAFLEER.D	1766.89390	2	5.97E-10	0.78	3.20	-	269.7
AHQ-5-8, 3890	K.QQDHFFQAAFLEER.D	1766.89390	2	6.22E-08	0.84	3.60	-	170.0
AHQ-5-10, 6631 - 6699	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	3.63E-10	0.89	4.52	-	682.6
AHQ-5-9, 6582	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	6.62E-10	0.93	5.03	-	925.7
AHQ-5-12, 7144	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	1.57E-08	0.82	4.28	-	407.9
AHQ-5-12, 7140 - 7141	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	3.87E-08	0.92	4.69	-	1028.1
AHQ-5-10, 6630	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	7.30E-06	0.31	2.77	-	415.1
AHQ-5-13-, 6891 - 6892	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	4.06E-07	0.79	3.52	-	586.4
AHQ-5-8, 7321 - 7337	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	5.77E-08	0.92	4.90	-	944.5
AHQ-5-14-, 6837	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	3.89E-12	0.94	5.08	-	980.1
gi|4507953|ref|NP_003397.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep				5.55E-16	7.95	100.29	46.50	27744.9
AHQ-5-9, 2830	K.FLIPNASQAESK.V	1305.46156	1	2.66E-06	0.64	2.81	-	467.8
AHQ-5-10, 3183 - 3230	K.FLIPNASQAESK.V	1305.46156	1	6.26E-04	0.28	2.54	-	432.6
AHQ-5-10, 3171 - 3315	K.FLIPNASQAESK.V	1305.46156	1	2.18E-06	0.44	2.22	-	433.3
AHQ-5-10, 3010	K.FLIPNASQAESK.V	1305.46156	2	2.09E-07	0.83	2.83	-	684.7
AHQ-5-11, 3119	K.FLIPNASQAESK.V	1305.46156	2	2.84E-04	0.52	2.58	-	346.2
AHQ-5-10, 2944 - 3007	K.FLIPNASQAESK.V	1305.46156	1	8.71E-04	0.18	2.32	-	347.9
AHQ-5-10, 6507 - 6574	K.IETELRDICNDVLSLLEK.F	2162.44718	2	3.58E-04	0.97	5.48	-	1540.9
AHQ-5-10, 5734	K.IETELRDICNDVLSLLEK.F	2162.44718	2	5.74E-08	0.95	5.16	-	1349.6
AHQ-5-10, 6564 - 6579	R.LGLALNFSVFYYEILNSPEK.A	2318.65200	2	4.11E-06	0.88	4.44	-	538.1
AHQ-5-13-, 2321	K.SVTEQGAELSNEER.N	1549.57922	2	2.66E-05	0.91	3.83	-	1059.1
AHQ-5-14-, 2206 - 2275	K.SVTEQGAELSNEER.N	1549.57922	2	2.38E-10	0.95	4.46	-	1420.0
AHQ-5-9, 2171	K.SVTEQGAELSNEER.N	1549.57922	2	3.70E-04	0.93	3.70	-	991.1
AHQ-5-13, 2479	K.SVTEQGAELSNEER.N	1549.57922	2	8.44E-07	0.93	3.74	-	1381.9

AHQ-5-10, 2159 - 2238	K.SVTEQGAELSNEER.N	1549.57922	2	3.89E-06	0.95	4.56	-	1217.6
AHQ-5-10, 4656	K.SVTEQGAELSNEERNLLSVAYK.N	2438.63331	2	8.25E-05	0.59	3.18	-	317.9
AHQ-5-10, 5727	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.93E-05	0.82	3.47	-	547.7
AHQ-5-10, 6406 - 6470	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	4.43E-09	0.98	5.90	-	1444.1
AHQ-5-9, 6414	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	6.54E-07	0.96	4.89	-	1347.1
AHQ-5-13-, 6744 - 6747	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	6.84E-09	0.97	5.33	-	1473.4
AHQ-5-13, 6812 - 6838	K.TAFDEAIAELDTLSEESYK.D	2133.25160	3	3.02E-05	0.90	4.21	-	763.9
AHQ-5-13, 6809 - 6868	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.02E-09	0.97	5.47	-	1430.9
AHQ-5-12, 6960	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.54E-08	0.96	5.29	-	1163.0
AHQ-5-14-, 6701	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.05E-11	0.97	5.59	-	1160.2
AHQ-5-11, 6742	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	5.54E-09	0.96	4.89	-	1279.1
AHQ-5-10, 6686	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	5.55E-16	0.93	4.94	-	1070.4
AHQ-5-9, 6568 - 6639	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	9.44E-08	0.92	4.77	-	773.1
AHQ-5-10, 6583 - 6586	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	2.60E-10	0.87	4.52	-	688.9
AHQ-5-10, 2370 - 2430	R.YDDMAACMK.S	1106.27579	1	5.75E-05	0.36	2.30	-	318.1
AHQ-5-10, 4124	R.YDDMAACMKSVTEQGAELSNEER.N	2636.83241	2	7.81E-04	0.54	2.95	-	237.1
AHQ-5-13-, 2049	R.YLAEVAAGDDKK.G	1280.40887	2	7.62E-05	0.89	3.11	-	1248.7
AHQ-5-13, 2225	R.YLAEVAAGDDKK.G	1280.40887	2	8.11E-04	0.89	3.33	-	990.7
AHQ-5-11, 1907 - 1914	R.YLAEVAAGDDKK.G	1280.40887	2	1.47E-05	0.96	3.69	-	1932.3
AHQ-5-10, 1807 - 1867	R.YLAEVAAGDDKK.G	1280.40887	1	2.23E-04	0.88	3.59	-	903.1
AHQ-5-10, 1800 - 1852	R.YLAEVAAGDDKK.G	1280.40887	2	1.08E-05	0.96	3.71	-	1814.9
AHQ-5-12, 1970	R.YLAEVAAGDDKK.G	1280.40887	2	1.36E-07	0.95	3.35	-	1816.7
gi|21361755|ref|NP_004090.3| stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie				5.55E-16	7.46	80.33	39.20	31708.5
AHQ-5-9, 4103 - 4104	K.EASMVITESPAALQLR.Y	1716.98119	2	9.42E-04	0.47	2.89	-	462.9
AHQ-5-13, 4180	K.EASM*VITESPAALQLR.Y	1732.98059	2	4.79E-04	0.81	3.56	-	662.0
AHQ-5-1, 4341	K.EASM*VITESPAALQLR.Y	1732.98059	2	3.66E-06	0.93	4.04	-	1097.1
AHQ-5-14-, 4581 - 4583	K.EASMVITESPAALQLR.Y	1716.98119	2	3.75E-06	0.94	4.62	-	1173.5
AHQ-5-1, 4856 - 4927	K.EASMVITESPAALQLR.Y	1716.98119	2	7.78E-06	0.92	3.93	-	1201.7
AHQ-5-10, 6511	K.GPGLFFILPCTDSFIK.V	1814.13672	2	1.65E-04	0.95	4.33	-	944.6
AHQ-5-1, 7307 - 7309	K.GPGLFFILPCTDSFIK.V	1814.13672	2	1.23E-04	0.94	4.63	-	791.6
AHQ-5-9, 6451 - 6454	K.GPGLFFILPCTDSFIK.V	1814.13672	2	2.49E-07	0.95	5.22	-	719.4
AHQ-5-13, 6880	K.GPGLFFILPCTDSFIK.V	1814.13672	2	3.90E-04	0.88	3.84	-	538.9
AHQ-5-3, 7489	K.GPGLFFILPCTDSFIK.V	1814.13672	2	7.77E-06	0.93	4.67	-	711.5
AHQ-5-4, 7441	K.GPGLFFILPCTDSFIK.V	1814.13672	2	4.54E-04	0.92	3.93	-	838.9
AHQ-5-1, 6265	K.NLSQILSDREEIAHNM*QSTLDDATDAWGIK.V	3389.65279	3	6.39E-05	0.93	4.54	-	1525.0
AHQ-5-1, 7235	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	2.51E-05	0.97	6.60	-	1369.5
AHQ-5-9, 6379	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	1.15E-07	0.97	6.39	-	1727.6
AHQ-5-10, 6354 - 6434	K.NLSQILSDREEIAHNMQSTLDDATDAWGIK.V	3373.65339	3	1.30E-10	0.97	6.68	-	1440.4
AHQ-5-9, 6590 - 6592	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	6.67E-05	0.83	3.75	-	420.6
AHQ-5-1, 7419	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	5.49E-04	0.92	4.26	-	582.3
AHQ-5-10, 3608	R.VQNATLAVANITNADSATR.L	1931.09731	2	7.78E-10	0.90	3.98	-	853.9
AHQ-5-1, 4699	R.VQNATLAVANITNADSATR.L	1931.09731	2	9.07E-08	0.94	4.46	-	1039.0
AHQ-5-1, 4196	R.VQNATLAVANITNADSATR.L	1931.09731	2	5.78E-05	0.95	4.59	-	1128.1
AHQ-5-2, 3894	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.16E-04	0.88	3.60	-	748.5
AHQ-5-1, 3949 - 4024	R.VQNATLAVANITNADSATR.L	1931.09731	2	5.55E-16	0.97	6.36	-	1150.0
AHQ-5-10, 4075	R.VQNATLAVANITNADSATR.L	1931.09731	2	3.29E-08	0.81	3.51	-	563.5
AHQ-5-14-, 3741	R.YLQTLTTIAAEK.N	1352.55813	2	1.79E-06	0.94	4.15	-	1097.4
AHQ-5-13-, 3843	R.YLQTLTTIAAEK.N	1352.55813	2	2.02E-04	0.95	3.79	-	1378.5
gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]				1.67E-15	33.02	400.32	38.40	129351.8
AHQ-5-4, 4258	K.AGTLDLSLTVQGK.Q	1303.48711	2	1.95E-05	0.80	2.63	-	901.4
AHQ-5-2, 4206	K.AGTLDLSLTVQGK.Q	1303.48711	2	4.51E-09	0.89	3.15	-	1415.7
AHQ-5-11, 3846	K.AGTLDLSLTVQGK.Q	1303.48711	2	2.37E-07	0.90	3.65	-	1124.5
AHQ-5-4, 2152	R.AQGYSGLSVK.V	1010.12587	1	1.86E-05	0.16	2.38	-	226.5
AHQ-5-6, 2508	R.AQLYIDCEK.M	1141.27636	1	3.07E-05	0.12	1.86	-	394.1
AHQ-5-3, 2657	R.AQLYIDCEK.M	1141.27636	1	9.46E-04	0.16	1.81	-	553.1
AHQ-5-9, 5682	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	2	1.68E-07	0.83	3.48	-	571.4
AHQ-5-10, 5900	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	2	1.38E-04	0.74	2.97	-	574.6
AHQ-5-3, 6806 - 6819	R.AQLYIDCEKMENAELDVPIQSVFTR.D	2972.33983	2	1.04E-04	0.84	3.39	-	752.1
AHQ-5-2, 6230	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	5.26E-07	0.94	5.27	-	921.3
AHQ-5-3, 4049	R.CENTDPGYNCLPCPPR.F	1954.10800	2	8.68E-05	0.88	3.79	-	576.1
AHQ-5-1, 3931	R.CENTDPGYNCLPCPPR.F	1954.10800	2	9.57E-07	0.87	3.77	-	505.9
AHQ-5-2, 3867 - 3938	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.44E-04	0.64	3.13	-	659.6
AHQ-5-3, 4070 - 4146	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.02E-13	0.90	3.85	-	605.2
AHQ-5-4, 4148 - 4202	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.10E-04	0.74	3.05	-	351.8
AHQ-5-3, 4217	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.83E-06	0.75	3.29	-	389.9
AHQ-5-5, 3873 - 3954	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.72E-05	0.85	3.35	-	524.9
AHQ-5-4, 4029	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.35E-07	0.94	4.50	-	719.0
AHQ-5-2, 4669	K.CGACPPGYSGNGIQCTDVDECKEVPDACFNHNGEHR.C	4115.32052	3	5.92E-04	0.72	3.50	-	454.5
AHQ-5-4, 3844 - 3848	K.CNYLGHYSDPMYR.C	1677.84222	2	2.44E-09	0.94	4.11	-	819.6
AHQ-5-4, 4074	K.CNYLGHYSDPMYR.C	1677.84222	2	8.09E-08	0.80	2.90	-	670.2
AHQ-5-2, 3831 - 3857	K.CNYLGHYSDPMYR.C	1677.84222	2	8.57E-08	0.95	4.29	-	1057.2
AHQ-5-1, 3985 - 3991	K.CNYLGHYSDPMYR.C	1677.84222	2	3.27E-08	0.95	4.30	-	871.4
AHQ-5-4, 3364 - 3434	K.DCVGDVTENQICNK.Q	1654.75869	2	8.69E-05	0.88	3.31	-	977.0
AHQ-5-3, 3462	K.DCVGDVTENQICNK.Q	1654.75869	2	5.63E-05	0.92	3.98	-	870.0
AHQ-5-2, 3467	K.DCVGDVTENQICNK.Q	1654.75869	2	3.86E-06	0.94	4.30	-	1074.0
AHQ-5-6, 6310	K.DDFDHDSVPDIDDICPENVDISETDFR.R	3183.22991	3	2.11E-04	0.94	4.58	-	1237.8
AHQ-5-5, 2631 - 2703	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.86E-05	0.83	2.72	-	794.6
AHQ-5-6, 2536 - 2614	K.DHSGQVFSVVSNGK.A	1461.56164	2	1.08E-07	0.92	3.82	-	887.3
AHQ-5-3, 2687	K.DHSGQVFSVVSNGK.A	1461.56164	2	5.65E-08	0.90	3.87	-	858.3
AHQ-5-13-, 2740	K.DHSGQVFSVVSNGK.A	1461.56164	2	5.16E-08	0.91	3.65	-	921.3
AHQ-5-2, 3371 - 3385	R.DNCQYVYNVDQR.D	1575.64166	2	4.46E-07	0.94	3.88	-	1218.7
AHQ-5-3, 3121	R.DNCQYVYNVDQR.D	1575.64166	2	6.11E-05	0.94	4.25	-	1132.4
AHQ-5-4, 3104	R.DNCQYVYNVDQR.D	1575.64166	2	1.38E-04	0.90	3.94	-	821.4
AHQ-5-5, 3030 - 3031	R.DNCQYVYNVDQR.D	1575.64166	2	1.54E-07	0.95	4.68	-	1125.6
AHQ-5-1, 3180	R.DNCQYVYNVDQR.D	1575.64166	2	1.43E-05	0.65	2.83	-	553.3
AHQ-5-2, 3106	R.DNCQYVYNVDQR.D	1575.64166	2	9.59E-05	0.88	3.67	-	884.0
AHQ-5-4, 6145 - 6206	K.DSGDGDRGDACKDDFDHDSVPDIDDICPENVDISETDFR.R	4418.43100	3	1.78E-05	0.72	3.78	-	412.2
AHQ-5-5, 4151	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	8.29E-05	0.82	3.76	-	451.2
AHQ-5-4, 3894 - 3922	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	6.98E-10	0.91	4.84	-	616.6
AHQ-5-1, 4284 - 4301	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	9.37E-09	0.95	5.71	-	616.8
AHQ-5-4, 4172	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.65E-05	0.90	4.57	-	594.7
AHQ-5-2, 4279 - 4353	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	7.43E-06	0.94	5.23	-	901.3
AHQ-5-4, 4261	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.51E-09	0.89	4.32	-	523.6
AHQ-5-5, 4255 - 4271	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	2.80E-04	0.87	4.53	-	408.2
AHQ-5-3, 4271 - 4349	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.67E-15	0.94	5.64	-	632.5
AHQ-5-2, 3913 - 3987	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	5.13E-08	0.89	4.28	-	736.2
AHQ-5-1, 3896	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.85E-07	0.88	4.56	-	640.2
AHQ-5-2, 4194	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	3.10E-08	0.92	4.73	-	921.0
AHQ-5-5, 3865 - 3867	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	9.71E-07	0.77	3.44	-	532.1
AHQ-5-3, 3915 - 3926	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.31E-10	0.89	4.27	-	790.7
AHQ-5-2, 3577	K.FQDLVDAVR.A	1063.18877	2	8.96E-08	0.90	3.15	-	1076.5
AHQ-5-4, 3598	K.FQDLVDAVR.A	1063.18877	1	8.31E-05	0.12	1.97	-	234.2
AHQ-5-10, 3215	K.FQDLVDAVR.A	1063.18877	1	1.51E-05	0.21	2.17	-	283.6
AHQ-5-2, 4185	R.FQMIPLDPK.G	1089.33277	2	4.58E-06	0.83	3.61	-	677.8
AHQ-5-4, 4221	R.FQMIPLDPK.G	1089.33277	2	1.74E-05	0.76	2.82	-	765.9
AHQ-5-4, 2848	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.14E-06	0.89	4.14	-	468.5
AHQ-5-1, 2916 - 2927	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.02E-06	0.88	4.28	-	515.7

AHQ-5-3, 2817 - 2886	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.30E-09	0.96	5.53	-	704.6
AHQ-5-5, 2621	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	6.72E-10	0.93	4.18	-	798.1
AHQ-5-2, 2647 - 2649	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	5.66E-04	0.84	3.99	-	393.2
AHQ-5-6, 2552	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.52E-07	0.86	4.11	-	436.3
AHQ-5-2, 2654 - 2657	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	9.13E-06	0.67	3.44	-	435.3
AHQ-5-2, 2761	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.07E-09	0.85	3.83	-	489.4
AHQ-5-9, 2466	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	7.25E-04	0.66	2.90	-	437.6
AHQ-5-10, 4838	R.FVFGTTPEDILR.N	1395.58470	1	5.47E-04	0.40	2.49	-	243.9
AHQ-5-10, 4852	R.FVFGTTPEDILR.N	1395.58470	1	6.33E-07	0.13	2.44	-	74.5
AHQ-5-2, 5574	R.FVFGTTPEDILR.N	1395.58470	1	2.67E-04	0.20	2.41	-	117.7
AHQ-5-9, 4736	R.FVFGTTPEDILR.N	1395.58470	1	3.03E-06	0.33	2.62	-	174.6
AHQ-5-3, 5654 - 5678	R.FVFGTTPEDILR.N	1395.58470	2	7.56E-04	0.83	2.79	-	870.3
AHQ-5-5, 5414	R.FVFGTTPEDILR.N	1395.58470	1	1.06E-04	0.08	2.21	-	127.2
AHQ-5-4, 5645	R.FVFGTTPEDILR.N	1395.58470	1	1.59E-07	0.33	2.55	-	131.8
AHQ-5-6, 5384	R.FVFGTTPEDILR.N	1395.58470	1	8.88E-06	0.27	2.69	-	76.6
AHQ-5-3, 5659	R.FVFGTTPEDILR.N	1395.58470	1	2.02E-07	0.28	2.63	-	105.8
AHQ-5-7, 4062 - 4063	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.71E-05	0.91	4.43	-	643.2
AHQ-5-10, 3923 - 3991	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.42E-06	0.83	3.39	-	783.3
AHQ-5-5, 4505 - 4517	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.74E-05	0.94	4.42	-	1085.1
AHQ-5-10, 4220	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.42E-07	0.85	3.48	-	828.8
AHQ-5-10, 4326 - 4364	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.96E-06	0.54	2.78	-	553.4
AHQ-5-6, 4597	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.29E-05	0.92	3.97	-	946.6
AHQ-5-6, 4394 - 4460	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.64E-08	0.92	4.30	-	967.0
AHQ-5-9, 3794	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.32E-04	0.70	3.27	-	506.7
AHQ-5-4, 4566 - 4648	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.21E-07	0.90	3.78	-	963.0
AHQ-5-6, 4212 - 4214	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.26E-05	0.92	4.92	-	775.1
AHQ-5-4, 4482 - 4545	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.38E-05	0.77	3.60	-	543.3
AHQ-5-2, 4725	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.01E-04	0.94	4.22	-	1257.0
AHQ-5-5, 4162	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.86E-06	0.56	2.78	-	571.5
AHQ-5-1, 4723	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.69E-06	0.91	4.04	-	783.9
AHQ-5-2, 4586 - 4657	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.11E-10	0.95	4.85	-	1097.0
AHQ-5-3, 4537	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.10E-05	0.87	3.65	-	759.6
AHQ-5-3, 4701 - 4781	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.85E-06	0.92	4.11	-	1035.1
AHQ-5-2, 4487	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.57E-04	0.91	4.47	-	749.1
AHQ-5-10, 3832 - 3836	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.58E-05	0.84	3.09	-	1041.2
AHQ-5-9, 3999 - 4006	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.72E-09	0.91	3.78	-	1014.6
AHQ-5-1, 4617	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.08E-06	0.76	3.37	-	584.4
AHQ-5-7, 4307 - 4322	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.92E-08	0.80	3.72	-	619.5
AHQ-5-5, 4282 - 4294	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.80E-04	0.84	3.67	-	753.2
AHQ-5-5, 1922	K.GPDPSSPAFR.I	1031.10364	2	1.76E-04	0.67	2.68	-	465.3
AHQ-5-3, 2075	K.GPDPSSPAFR.I	1031.10364	2	4.57E-04	0.70	2.76	-	444.4
AHQ-5-1, 2289	K.GPDPSSPAFR.I	1031.10364	2	2.02E-04	0.65	2.51	-	456.1
AHQ-5-2, 2042	K.GPDPSSPAFR.I	1031.10364	2	7.85E-05	0.81	2.82	-	673.1
AHQ-5-2, 2834	R.GTLLALER.K	873.03234	2	1.54E-04	0.93	3.55	-	1210.9
AHQ-5-5, 2695	R.GTLLALER.K	873.03234	2	3.77E-04	0.87	3.30	-	943.1
AHQ-5-4, 2905	R.GTLLALER.K	873.03234	2	2.13E-04	0.92	3.65	-	983.6
AHQ-5-4, 2536 - 2544	K.GTSQNDPNWVVR.H	1373.45608	2	1.81E-04	0.76	2.98	-	1046.6
AHQ-5-3, 2561 - 2563	K.GTSQNDPNWVVR.H	1373.45608	2	5.43E-04	0.68	2.94	-	608.3
AHQ-5-14-, 6209	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.78E-06	0.69	3.14	-	238.1
AHQ-5-14-, 6335 - 6385	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.38E-04	0.83	4.26	-	272.6
AHQ-5-7, 6478 - 6502	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	9.36E-09	0.76	3.65	-	472.5
AHQ-5-3, 6777	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.13E-07	0.80	3.56	-	343.1
AHQ-5-3, 6974	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.07E-06	0.74	3.25	-	388.5
AHQ-5-3, 6773	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.65E-04	0.84	3.57	-	502.7
AHQ-5-3, 6762 - 6829	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.92E-08	0.66	2.89	-	376.1
AHQ-5-9, 5775 - 5828	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.48E-05	0.49	2.82	-	220.3
AHQ-5-5, 6586	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.83E-07	0.85	3.85	-	271.6
AHQ-5-13-, 6283	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	6.86E-06	0.78	3.44	-	263.1
AHQ-5-8, 6253 - 6254	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.37E-06	0.80	3.86	-	260.1
AHQ-5-1, 6725 - 6803	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.93E-05	0.82	3.99	-	459.3
AHQ-5-1, 6728 - 6807	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.89E-06	0.47	2.90	-	193.5
AHQ-5-13, 6348	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.50E-04	0.77	3.28	-	276.2
AHQ-5-2, 6878 - 6941	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	6.37E-07	0.75	3.78	-	413.7
AHQ-5-2, 6713 - 6783	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.99E-10	0.90	4.50	-	489.9
AHQ-5-10, 5828 - 5886	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.15E-10	0.70	3.46	-	293.2
AHQ-5-10, 5850 - 5910	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.63E-04	0.71	3.47	-	291.4
AHQ-5-10, 5950 - 6026	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	6.69E-08	0.83	3.67	-	356.5
AHQ-5-13, 6337 - 6340	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.48E-08	0.77	3.59	-	437.3
AHQ-5-10, 6022	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.32E-05	0.82	3.79	-	313.7
AHQ-5-14-, 6201 - 6266	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.43E-06	0.78	3.79	-	371.0
AHQ-5-4, 6692 - 6760	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.47E-05	0.76	3.56	-	265.2
AHQ-5-12, 6373 - 6377	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	8.99E-14	0.85	4.41	-	383.7
AHQ-5-11, 6180 - 6188	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.78E-08	0.73	3.55	-	264.1
AHQ-5-6, 6433 - 6510	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.37E-04	0.83	3.81	-	418.1
AHQ-5-5, 6801 - 6869	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.86E-05	0.59	3.16	-	408.9
AHQ-5-4, 6736	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.41E-10	0.64	3.44	-	336.2
AHQ-5-4, 6754	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.77E-08	0.74	3.46	-	271.1
AHQ-5-4, 6850 - 6921	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.13E-06	0.82	3.73	-	485.8
AHQ-5-6, 6606 - 6685	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.27E-05	0.84	4.08	-	490.7
AHQ-5-6, 2384	K.IMADSGPIYDK.T	1210.38204	2	5.33E-07	0.89	3.32	-	717.6
AHQ-5-2, 2478	K.IMADSGPIYDK.T	1210.38204	2	3.27E-05	0.90	3.52	-	734.5
AHQ-5-14-, 2277	K.IM*ADSGPIYDK.T	1226.38144	2	5.04E-05	0.85	3.22	-	586.8
AHQ-5-2, 2254 - 2331	K.IM*ADSGPIYDK.T	1226.38144	2	1.42E-04	0.86	3.04	-	723.9
AHQ-5-7, 2344	K.IMADSGPIYDK.T	1210.38204	2	6.98E-06	0.89	3.29	-	871.2
AHQ-5-11, 2490 - 2499	K.IMADSGPIYDK.T	1210.38204	2	2.15E-06	0.93	3.74	-	808.2
AHQ-5-6, 6872 - 6936	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.00E-10	0.97	5.85	-	1305.2
AHQ-5-11, 6511 - 6586	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.00E-14	0.98	6.20	-	1509.9
AHQ-5-10, 6366 - 6374	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.71E-08	0.97	6.30	-	1223.9
AHQ-5-10, 6239 - 6316	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.81E-12	0.97	5.68	-	1174.5
AHQ-5-4, 7152 - 7220	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.68E-09	0.97	5.29	-	1151.2
AHQ-5-12, 6754	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.26E-10	0.96	4.74	-	1397.0
AHQ-5-14-, 6558 - 6625	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.34E-11	0.98	6.01	-	1578.6
AHQ-5-2, 7147 - 7215	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.39E-10	0.97	5.79	-	1200.5
AHQ-5-13, 6629 - 6698	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.41E-11	0.98	6.03	-	1433.3
AHQ-5-1, 7100 - 7177	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.11E-14	0.97	5.26	-	1465.8
AHQ-5-2, 7281	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.67E-10	0.97	5.80	-	1305.2
AHQ-5-2, 7310 - 7373	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.07E-11	0.98	6.26	-	1481.1
AHQ-5-9, 6231 - 6287	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.21E-07	0.95	4.87	-	888.4
AHQ-5-13-, 6648	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.05E-06	0.95	4.89	-	985.6
AHQ-5-10, 6226 - 6306	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.90E-07	0.98	6.26	-	1426.9
AHQ-5-9, 6118	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.54E-07	0.95	4.69	-	948.2
AHQ-5-7, 6862	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.88E-09	0.93	4.76	-	709.2
AHQ-5-7, 7043	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.16E-08	0.93	4.11	-	1047.4
AHQ-5-4, 7288	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.29E-11	0.96	5.38	-	835.8
AHQ-5-3, 7189 - 7262	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.79E-06	0.95	4.97	-	883.7
AHQ-5-3, 7329	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.23E-09	0.97	5.76	-	1235.3
AHQ-5-5, 7011 - 7021	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.36E-12	0.96	5.20	-	1121.6

AHQ-5-10, 2087 - 2128	R.KDHSGQVFSVVSNGK.A	1589.73455	2	7.05E-07	0.83	3.44	-	533.4
AHQ-5-4, 2209	R.KDHSGQVFSVVSNGK.A	1589.73455	2	4.20E-07	0.82	3.56	-	648.8
AHQ-5-6, 2101 - 2102	R.KDHSGQVFSVVSNGK.A	1589.73455	2	6.77E-09	0.77	3.33	-	533.4
AHQ-5-5, 2059	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.31E-07	0.89	3.81	-	816.0
AHQ-5-3, 2219 - 2294	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.49E-11	0.72	3.05	-	630.0
AHQ-5-5, 2151	R.KDHSGQVFSVVSNGK.A	1589.73455	2	3.98E-11	0.84	3.20	-	710.9
AHQ-5-13-, 2347	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.69E-12	0.88	3.68	-	803.2
AHQ-5-2, 2187 - 2197	R.KDHSGQVFSVVSNGK.A	1589.73455	2	8.10E-10	0.90	3.72	-	797.9
AHQ-5-2, 2273	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.78E-10	0.93	3.60	-	1384.1
AHQ-5-13, 2513	R.KDHSGQVFSVVSNGK.A	1589.73455	2	7.22E-07	0.87	3.46	-	827.3
AHQ-5-4, 2265	K.KIMADSGPIYDK.T	1338.55496	1	6.24E-05	0.73	2.84	-	584.0
AHQ-5-2, 2263	K.KIMADSGPIYDK.T	1338.55496	2	3.09E-06	0.95	3.98	-	1097.5
AHQ-5-2, 2226	R.KVTEENKELANELR.R	1673.84976	3	3.65E-08	0.84	3.95	-	692.8
AHQ-5-2, 2214	R.KVTEENKELANELR.R	1673.84976	2	6.95E-08	0.96	5.19	-	1669.7
AHQ-5-9, 2100 - 2102	R.KVTEENKELANELR.R	1673.84976	2	4.21E-08	0.94	4.85	-	1282.9
AHQ-5-5, 2206	R.KVTEENKELANELR.R	1673.84976	2	6.43E-09	0.92	4.17	-	876.6
AHQ-5-4, 2318	R.KVTEENKELANELR.R	1673.84976	2	1.86E-10	0.96	4.99	-	1504.3
AHQ-5-6, 1818	R.KVTEENKELANELR.R	1673.84976	2	2.80E-05	0.89	3.92	-	881.8
AHQ-5-2, 1971	R.KVTEENKELANELR.R	1673.84976	2	4.81E-05	0.96	4.52	-	1777.4
AHQ-5-5, 2082 - 2089	R.KVTEENKELANELR.R	1673.84976	2	7.27E-04	0.95	5.09	-	1137.4
AHQ-5-1, 2468	R.KVTEENKELANELR.R	1673.84976	2	2.19E-10	0.93	4.07	-	1158.7
AHQ-5-4, 2225	R.KVTEENKELANELR.R	1673.84976	2	2.03E-11	0.94	4.44	-	1268.7
AHQ-5-3, 2250 - 2318	R.KVTEENKELANELR.R	1673.84976	2	5.85E-11	0.93	4.27	-	1214.0
AHQ-5-7, 2022	R.KVTEENKELANELR.R	1673.84976	2	3.25E-10	0.95	4.91	-	1341.6
AHQ-5-3, 2365	R.KVTEENKELANELR.R	1673.84976	2	1.50E-07	0.94	5.06	-	1200.3
AHQ-5-6, 2065	R.KVTEENKELANELR.R	1673.84976	2	5.68E-06	0.94	4.64	-	1450.0
AHQ-5-2, 2310	R.KVTEENKELANELR.R	1673.84976	2	2.65E-09	0.96	5.07	-	1439.1
AHQ-5-3, 2497	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.76E-09	0.87	3.74	-	563.6
AHQ-5-5, 2046	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	2.14E-05	0.82	3.74	-	585.5
AHQ-5-5, 2397	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	2.13E-06	0.87	4.25	-	442.7
AHQ-5-4, 2476 - 2477	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.69E-09	0.86	4.10	-	483.6
AHQ-5-6, 2378	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.25E-09	0.89	4.03	-	524.9
AHQ-5-2, 2466	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	5.20E-05	0.66	3.58	-	356.7
AHQ-5-3, 2613	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.94E-05	0.51	2.93	-	343.1
AHQ-5-5, 5506	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.27E-05	0.83	3.74	-	433.2
AHQ-5-7, 5299 - 5310	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.69E-06	0.92	4.53	-	496.3
AHQ-5-1, 5596 - 5601	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	3.53E-10	0.92	4.15	-	677.4
AHQ-5-10, 4954 - 4955	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.74E-06	0.92	4.16	-	663.2
AHQ-5-3, 5797 - 5805	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.42E-05	0.92	4.38	-	548.2
AHQ-5-1, 5847	K.MENAELDVPIQSVFTR.D	1850.08607	2	9.19E-06	0.87	3.63	-	582.4
AHQ-5-6, 5477	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.39E-04	0.71	3.11	-	554.0
AHQ-5-2, 5709	K.MENAELDVPIQSVFTR.D	1850.08607	2	4.04E-04	0.63	2.73	-	509.2
AHQ-5-2, 5471 - 5487	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.02E-07	0.95	4.83	-	808.4
AHQ-5-5, 5667	K.MENAELDVPIQSVFTR.D	1850.08607	2	7.16E-05	0.52	2.71	-	280.8
AHQ-5-10, 5071	K.MENAELDVPIQSVFTR.D	1850.08607	2	5.61E-04	0.58	2.53	-	363.4
AHQ-5-4, 5732	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.50E-04	0.88	4.05	-	397.9
AHQ-5-2, 5841 - 5909	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.62E-08	0.84	3.71	-	397.1
AHQ-5-11, 5327 - 5387	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.37E-04	0.57	2.77	-	500.1
AHQ-5-4, 5881	K.MENAELDVPIQSVFTR.D	1850.08607	2	7.86E-05	0.82	3.15	-	527.9
AHQ-5-6, 5618	K.MENAELDVPIQSVFTR.D	1850.08607	2	1.20E-05	0.82	3.50	-	545.5
AHQ-5-3, 3062	K.QVTQSYWDTNPTR.A	1596.68241	2	8.72E-05	0.71	2.78	-	609.6
AHQ-5-4, 2958 - 3028	K.QVTQSYWDTNPTR.A	1596.68241	2	3.41E-07	0.76	2.87	-	706.9
AHQ-5-5, 2873 - 2878	K.QVTQSYWDTNPTR.A	1596.68241	2	1.09E-05	0.53	2.85	-	280.9
AHQ-5-2, 3001	K.QVTQSYWDTNPTR.A	1596.68241	2	4.03E-07	0.89	3.48	-	759.5
AHQ-5-2, 2459	R.RPPLCYHNGVQYR.N	1661.86889	2	2.04E-09	0.94	3.69	-	977.3
AHQ-5-6, 2356	R.RPPLCYHNGVQYR.N	1661.86889	2	7.72E-05	0.81	2.97	-	566.7
AHQ-5-2, 2635 - 2710	R.RPPLCYHNGVQYR.N	1661.86889	2	4.19E-07	0.92	3.98	-	739.9
AHQ-5-4, 2660 - 2736	R.RPPLCYHNGVQYR.N	1661.86889	2	2.18E-07	0.91	3.79	-	752.5
AHQ-5-3, 2718 - 2791	R.RPPLCYHNGVQYR.N	1661.86889	2	2.13E-07	0.91	3.74	-	742.7
AHQ-5-2, 2231	R.SCDSLNNRCEGSSVQTR.T	1973.04966	2	2.09E-07	0.53	2.89	-	287.7
AHQ-5-4, 3818	K.SITLFVQEDR.A	1208.34588	2	3.97E-07	0.92	3.38	-	1188.6
AHQ-5-5, 3635	K.SITLFVQEDR.A	1208.34588	2	1.06E-06	0.91	3.21	-	1255.6
AHQ-5-1, 3992	K.SITLFVQEDR.A	1208.34588	2	7.39E-07	0.95	3.74	-	1490.1
AHQ-5-2, 3822	K.SITLFVQEDR.A	1208.34588	2	3.59E-06	0.96	3.91	-	1513.5
AHQ-5-13, 3954	K.SITLFVQEDR.A	1208.34588	2	2.69E-06	0.94	3.31	-	1449.7
AHQ-5-3, 3858 - 3866	K.SITLFVQEDR.A	1208.34588	2	7.38E-06	0.92	3.65	-	1071.1
AHQ-5-12, 3730	K.SITLFVQEDR.A	1208.34588	2	1.43E-06	0.92	3.56	-	1245.3
AHQ-5-6, 4156	R.TIVTTLQDSIR.K	1247.42355	1	5.74E-05	0.04	1.87	-	85.6
AHQ-5-12, 4292	R.TIVTTLQDSIR.K	1247.42355	2	1.37E-05	0.94	3.95	-	1101.0
AHQ-5-9, 3759 - 3780	R.TIVTTLQDSIR.K	1247.42355	2	1.07E-04	0.92	3.68	-	1023.3
AHQ-5-1, 4589 - 4592	R.TIVTTLQDSIR.K	1247.42355	2	2.03E-06	0.96	3.81	-	1570.1
AHQ-5-6, 3108	R.TIVTTLQDSIR.K	1247.42355	2	1.02E-04	0.95	3.40	-	1557.6
AHQ-5-2, 3263	R.TIVTTLQDSIR.K	1247.42355	2	9.83E-08	0.96	3.28	-	1915.6
AHQ-5-13, 4358	R.TIVTTLQDSIR.K	1247.42355	2	2.90E-05	0.96	3.72	-	1752.6
AHQ-5-2, 4545	R.TIVTTLQDSIR.K	1247.42355	2	1.06E-04	0.96	3.75	-	1695.4
AHQ-5-5, 4202 - 4227	R.TIVTTLQDSIR.K	1247.42355	2	1.26E-06	0.97	4.43	-	1677.1
AHQ-5-7, 4004 - 4015	R.TIVTTLQDSIR.K	1247.42355	2	1.71E-05	0.96	3.84	-	1475.5
AHQ-5-2, 4402 - 4473	R.TIVTTLQDSIR.K	1247.42355	2	5.93E-06	0.97	4.02	-	2028.2
AHQ-5-6, 4136	R.TIVTTLQDSIR.K	1247.42355	2	8.28E-07	0.96	4.05	-	1534.7
AHQ-5-3, 4481 - 4518	R.TIVTTLQDSIR.K	1247.42355	2	5.13E-06	0.97	3.84	-	1729.3
AHQ-5-4, 4404 - 4484	R.TIVTTLQDSIR.K	1247.42355	2	3.63E-04	0.97	3.92	-	2069.0
AHQ-5-2, 2393	K.VTEENKELANELR.R	1545.67685	2	1.03E-07	0.92	3.76	-	1116.3
AHQ-5-1, 2648	K.VTEENKELANELR.R	1545.67685	2	1.31E-04	0.62	2.82	-	695.9
AHQ-5-6, 2288 - 2297	K.VTEENKELANELR.R	1545.67685	2	1.58E-05	0.91	3.85	-	1044.8
AHQ-5-7, 2258	K.VTEENKELANELR.R	1545.67685	2	9.63E-05	0.80	3.36	-	785.8
AHQ-5-3, 2457	K.VTEENKELANELR.R	1545.67685	2	3.78E-08	0.86	3.86	-	764.7
gi|4502295|ref|NP_001677.1| ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti				2.22E-15	13.82	160.28	42.70	57955.2
AHQ-5-7, 7410	R.DQEGQDVLLFIDNIFR.F	1923.11524	2	4.06E-12	0.96	5.18	-	1099.8
AHQ-5-7, 5958	R.FLSQPFQVAEVFTGHMGK.L	2024.33104	3	1.68E-09	0.86	4.28	-	387.7
AHQ-5-7, 4194	R.FTQAGSEVSALLGR.I	1436.59522	1	1.92E-04	0.52	2.96	-	108.6
AHQ-5-7, 4183	R.FTQAGSEVSALLGR.I	1436.59522	2	1.48E-11	0.94	4.02	-	1249.4
AHQ-5-7, 7280	K.GFQQILAGEYDHLPEQAFYMVGPIEEAVAK.A	3352.76051	3	3.30E-09	0.73	3.53	-	488.7
AHQ-5-7, 7162	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	2.22E-15	0.96	5.53	-	1192.0
AHQ-5-7, 3347	R.IMDPNIVGSEHYDVAR.G	1817.01617	2	6.77E-12	0.94	3.94	-	929.1
AHQ-5-7, 3535 - 3606	R.IMNVIGEPIDER.G	1386.59962	2	1.34E-05	0.90	3.80	-	929.2
AHQ-5-7, 4416 - 4491	R.IPSAVGYQPTLATDMGTMQER.I	2267.56880	2	4.98E-06	0.92	4.40	-	439.8
AHQ-5-7, 3799	R.IPSAVGYQPTLATDM*GTMQER.I	2283.56820	2	1.65E-05	0.66	4.37	-	370.1
AHQ-5-7, 2611	K.IPVGPETLGR.I	1039.21035	2	4.33E-05	0.90	2.75	-	944.2
AHQ-5-7, 3890	R.LVLEVAQHLGESTVR.T	1651.88893	2	2.27E-08	0.97	4.79	-	1820.3
AHQ-5-7, 7298	K.SLQDIIAILGMDELSEEDKLTVSR.A	2677.02230	2	3.18E-06	0.88	4.31	-	438.6
AHQ-5-7, 4920	R.TREGNDLYHEMIESGVINLK.D	2319.58030	3	1.18E-05	0.95	4.38	-	1901.3
AHQ-5-7, 3199	K.VALVYGQMNQPPGAR.A	1601.85511	2	3.67E-09	0.90	3.91	-	672.1
AHQ-5-7, 4427 - 4463	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	3.90E-05	0.61	3.33	-	241.6
AHQ-5-7, 3695	K.VVDLLAPYAK.G	1089.30927	1	2.69E-05	0.74	2.59	-	900.8
gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act				2.78E-15	96.94	1150.36	54.50	280757.4
AHQ-5-4, 5353 - 5426	R.AEAGVPAEFSIWTR.E	1534.69735	2	3.70E-05	0.83	3.78	-	490.7
AHQ-5-7, 4935 - 4942	R.AEAGVPAEFSIWTR.E	1534.69735	2	1.70E-04	0.78	3.39	-	353.5

AHQ-5-2, 2174 - 2178	R.AEFTVETR.S	953.03118	2	8.16E-04	0.88	2.78	-	985.5
AHQ-5-2, 2129	R.AEFTVETR.S	953.03118	1	7.82E-04	0.14	1.93	-	253.6
AHQ-5-2, 2469 - 2470	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	9.40E-08	0.97	4.40	-	1970.3
AHQ-5-4, 2516	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	7.10E-09	0.95	4.27	-	1136.9
AHQ-5-3, 2735	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.52E-06	0.88	3.43	-	908.4
AHQ-5-1, 2699 - 2769	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.11E-08	0.93	3.55	-	1238.4
AHQ-5-6, 2385	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.12E-06	0.88	3.25	-	1032.1
AHQ-5-3, 2562	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	5.02E-06	0.27	2.71	-	140.8
AHQ-5-3, 2537 - 2610	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.67E-08	0.94	3.73	-	1302.2
AHQ-5-2, 2474	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	1.08E-06	0.28	2.59	-	189.2
AHQ-5-2, 2686	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.52E-04	0.64	3.08	-	830.2
AHQ-5-14, 4333	K.AGNNMLLVGVHGPR.T	1435.68033	2	1.12E-04	0.70	2.86	-	590.2
AHQ-5-14, 4206 - 4276	K.AGNNMLLVGVHGPR.T	1435.68033	2	9.20E-07	0.78	3.27	-	793.4
AHQ-5-14-, 3335 - 3399	K.AGNNMLLVGVHGPR.T	1435.68033	3	8.09E-05	0.88	3.87	-	1006.5
AHQ-5-14, 3626 - 3688	K.AGNNM*LLVGVHGPR.T	1451.67973	2	4.02E-08	0.80	2.94	-	710.3
AHQ-5-14-, 3067	K.AGNNMLLVGVHGPR.T	1435.68033	1	1.48E-04	0.19	2.24	-	167.9
AHQ-5-14-, 3405	K.AGNNMLLVGVHGPR.T	1435.68033	2	1.72E-08	0.87	3.24	-	819.3
AHQ-5-14-, 2934	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.28E-06	0.66	2.53	-	735.8
AHQ-5-14-, 2753	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.31E-05	0.89	3.29	-	841.7
AHQ-5-14-, 2665 - 2743	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.50E-05	0.84	3.15	-	770.6
AHQ-5-14-, 3061	K.AGNNMLLVGVHGPR.T	1435.68033	2	4.36E-05	0.79	3.14	-	734.6
AHQ-5-11, 3016	K.AGNNMLLVGVHGPR.T	1435.68033	3	3.53E-06	0.88	3.38	-	1442.5
AHQ-5-14-, 2666 - 2739	K.AGNNM*LLVGVHGPR.T	1451.67973	3	1.93E-05	0.89	4.04	-	845.5
AHQ-5-14, 3469 - 3546	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.60E-05	0.87	3.62	-	760.8
AHQ-5-14-, 3058 - 3065	K.AGNNMLLVGVHGPR.T	1435.68033	3	2.17E-05	0.91	3.88	-	1451.5
AHQ-5-2, 1549	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	8.15E-04	0.75	3.05	-	554.4
AHQ-5-2, 2125	K.AGVAPLQVK.V	883.07036	2	7.50E-05	0.79	2.54	-	636.1
AHQ-5-3, 2187	K.AGVAPLQVK.V	883.07036	2	3.77E-05	0.76	2.71	-	565.0
AHQ-5-1, 2400	K.AGVAPLQVK.V	883.07036	2	2.88E-05	0.81	2.76	-	600.9
AHQ-5-4, 2178	K.AGVAPLQVK.V	883.07036	2	7.16E-06	0.85	2.80	-	722.8
AHQ-5-1, 7416 - 7439	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	2	4.59E-05	0.70	3.22	-	595.4
AHQ-5-1, 7421 - 7485	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	2.91E-06	0.96	5.96	-	1465.2
AHQ-5-2, 7679 - 7691	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	1.78E-06	0.96	5.58	-	1516.6
AHQ-5-1, 7508	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	1.03E-04	0.91	4.08	-	1100.1
AHQ-5-3, 7670	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	1.09E-04	0.84	3.93	-	936.8
AHQ-5-3, 2517	K.AHVVPCFDASK.V	1232.39073	2	1.59E-06	0.79	2.69	-	651.9
AHQ-5-4, 2500	K.AHVVPCFDASK.V	1232.39073	2	4.06E-05	0.79	2.63	-	679.8
AHQ-5-4, 6300 - 6372	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.84E-05	0.91	4.94	-	707.0
AHQ-5-2, 6345 - 6414	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.57E-13	0.95	5.56	-	859.7
AHQ-5-1, 6408 - 6477	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.06E-09	0.93	5.00	-	678.2
AHQ-5-2, 6489 - 6557	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.70E-09	0.95	5.96	-	823.2
AHQ-5-4, 6389 - 6460	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.22E-11	0.93	4.96	-	867.1
AHQ-5-2, 6621 - 6695	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.40E-12	0.93	5.54	-	716.4
AHQ-5-4, 6542	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.50E-07	0.82	4.31	-	352.6
AHQ-5-9, 5498	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.42E-08	0.93	5.07	-	740.8
AHQ-5-10, 5634	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.82E-06	0.76	3.60	-	612.1
AHQ-5-1, 6232 - 6281	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.61E-08	0.84	4.11	-	588.4
AHQ-5-3, 6493 - 6574	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.04E-08	0.93	5.02	-	907.4
AHQ-5-8, 6004 - 6005	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.08E-10	0.89	4.46	-	556.5
AHQ-5-6, 6109 - 6180	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.11E-07	0.92	5.33	-	529.2
AHQ-5-5, 6453	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.89E-14	0.80	3.79	-	533.8
AHQ-5-8, 6146	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	8.16E-08	0.70	3.73	-	400.1
AHQ-5-5, 6341 - 6407	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.53E-08	0.89	4.61	-	662.5
AHQ-5-6, 6244 - 6246	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.29E-09	0.94	5.71	-	600.4
AHQ-5-7, 6110	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.99E-14	0.94	5.65	-	657.3
AHQ-5-3, 6409 - 6435	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.24E-13	0.85	3.68	-	701.6
AHQ-5-3, 6589 - 6657	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.82E-12	0.91	4.96	-	736.8
AHQ-5-9, 5640 - 5642	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.03E-10	0.94	5.42	-	907.2
AHQ-5-5, 6207 - 6274	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.40E-08	0.91	4.60	-	704.9
AHQ-5-1, 6539 - 6613	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.58E-13	0.95	5.80	-	629.3
AHQ-5-7, 6271 - 6342	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.16E-08	0.89	4.65	-	490.2
AHQ-5-6, 3060 - 3133	R.ANLPQSFQVDTSK.A	1435.56409	2	3.23E-09	0.85	3.63	-	523.1
AHQ-5-4, 3288	R.ANLPQSFQVDTSK.A	1435.56409	1	6.60E-08	0.52	2.95	-	331.5
AHQ-5-2, 3186 - 3206	R.ANLPQSFQVDTSK.A	1435.56409	2	6.20E-09	0.84	3.32	-	502.4
AHQ-5-3, 3285	R.ANLPQSFQVDTSK.A	1435.56409	1	3.86E-08	0.76	3.18	-	517.0
AHQ-5-3, 3279	R.ANLPQSFQVDTSK.A	1435.56409	1	4.26E-05	0.24	2.27	-	399.9
AHQ-5-8, 2836	R.ANLPQSFQVDTSK.A	1435.56409	2	6.52E-08	0.88	3.37	-	565.8
AHQ-5-3, 3277	R.ANLPQSFQVDTSK.A	1435.56409	2	1.80E-05	0.82	3.09	-	619.8
AHQ-5-1, 3395 - 3397	R.ANLPQSFQVDTSK.A	1435.56409	2	3.38E-09	0.93	3.70	-	807.8
AHQ-5-1, 3387	R.ANLPQSFQVDTSK.A	1435.56409	1	2.82E-05	0.37	2.62	-	284.9
AHQ-5-5, 3038 - 3111	R.ANLPQSFQVDTSK.A	1435.56409	2	6.16E-09	0.90	3.76	-	658.8
AHQ-5-5, 3091 - 3095	R.ANLPQSFQVDTSK.A	1435.56409	1	7.10E-04	0.73	2.74	-	502.0
AHQ-5-2, 3193	R.ANLPQSFQVDTSK.A	1435.56409	1	2.49E-08	0.60	2.92	-	371.1
AHQ-5-4, 3256	R.ANLPQSFQVDTSK.A	1435.56409	2	1.44E-05	0.69	2.79	-	410.0
AHQ-5-2, 4591	R.ANLPQSFQVDTSKAGVAPLQVK.V	2299.61185	2	5.22E-07	0.92	4.45	-	949.7
AHQ-5-3, 4675	R.ANLPQSFQVDTSKAGVAPLQVK.V	2299.61185	2	3.67E-05	0.94	4.87	-	937.5
AHQ-5-1, 3527	R.APSVANVGSHCDLSLK.I	1656.84249	2	4.78E-05	0.93	4.53	-	681.3
AHQ-5-5, 3150 - 3154	R.APSVANVGSHCDLSLK.I	1656.84249	2	2.10E-09	0.95	4.86	-	637.7
AHQ-5-3, 1643	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	4.75E-04	0.91	3.94	-	657.9
AHQ-5-5, 1526	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	5.00E-08	0.94	4.13	-	896.8
AHQ-5-4, 1653	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	3.67E-05	0.90	4.04	-	703.0
AHQ-5-3, 3637 - 3638	R.AWGPGLEGGVVGK.S	1227.39403	2	3.17E-08	0.95	4.26	-	942.3
AHQ-5-6, 3356 - 3364	R.AWGPGLEGGVVGK.S	1227.39403	2	5.43E-07	0.91	3.76	-	771.3
AHQ-5-5, 3406 - 3425	R.AWGPGLEGGVVGK.S	1227.39403	2	1.91E-07	0.92	3.50	-	972.8
AHQ-5-4, 3622	R.AWGPGLEGGVVGK.S	1227.39403	2	5.06E-06	0.92	3.74	-	990.1
AHQ-5-7, 3260	R.AWGPGLEGGVVGK.S	1227.39403	2	5.02E-05	0.87	3.23	-	899.3
AHQ-5-2, 3578 - 3661	R.AWGPGLEGGVVGK.S	1227.39403	2	8.95E-08	0.89	3.49	-	941.5
AHQ-5-1, 3756 - 3829	R.AWGPGLEGGVVGK.S	1227.39403	2	7.13E-06	0.91	3.51	-	781.8
AHQ-5-4, 3082 - 3156	R.AYGPGIEPTGNMVK.K	1434.64274	1	4.32E-04	0.44	2.79	-	280.9
AHQ-5-3, 3179	R.AYGPGIEPTGNMVK.K	1434.64274	1	1.65E-04	0.56	2.78	-	416.9
AHQ-5-2, 2465	R.AYGPGIEPTGNM*VK.K	1450.64214	2	4.61E-04	0.67	2.63	-	450.7
AHQ-5-2, 3299 - 3313	R.AYGPGIEPTGNMVK.K	1434.64274	2	5.34E-04	0.56	2.95	-	547.7
AHQ-5-5, 2887 - 2957	R.AYGPGIEPTGNMVK.K	1434.64274	2	1.96E-04	0.74	2.99	-	555.0
AHQ-5-5, 2954	R.AYGPGIEPTGNMVK.K	1434.64274	2	3.17E-05	0.88	4.24	-	457.2
AHQ-5-3, 3375 - 3454	R.AYGPGIEPTGNMVK.K	1434.64274	2	7.79E-04	0.81	3.07	-	646.4
AHQ-5-3, 3383 - 3453	R.AYGPGIEPTGNMVK.K	1434.64274	1	1.77E-04	0.72	2.98	-	542.3
AHQ-5-7, 2846	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.10E-06	0.79	3.10	-	627.6
AHQ-5-2, 3398 - 3399	R.AYGPGIEPTGNMVK.K	1434.64274	2	9.97E-04	0.92	4.18	-	741.4
AHQ-5-1, 3283 - 3325	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.18E-05	0.52	2.69	-	448.0
AHQ-5-2, 3403	R.AYGPGIEPTGNMVK.K	1434.64274	1	4.86E-04	0.54	2.61	-	509.8
AHQ-5-2, 6409	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	4.76E-08	0.94	4.35	-	684.4
AHQ-5-2, 6534	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.42E-05	0.62	2.66	-	410.1
AHQ-5-1, 6340	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	3.78E-12	0.96	4.97	-	1736.4
AHQ-5-1, 6325 - 6401	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	5.18E-07	0.94	5.13	-	479.6
AHQ-5-6, 6190	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	6.01E-05	0.77	3.31	-	467.0
AHQ-5-2, 6346 - 6374	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	8.11E-12	0.97	5.86	-	1957.2
AHQ-5-3, 6389 - 6465	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	5.65E-09	0.96	4.94	-	948.8

AHQ-5-2, 6283 - 6341	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.43E-11	0.95	4.92	-	733.6
AHQ-5-2, 6162 - 6175	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.18E-10	0.94	4.35	-	976.2
AHQ-5-5, 6290	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	4.07E-04	0.86	3.57	-	504.5
AHQ-5-4, 6373 - 6452	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.30E-06	0.92	4.13	-	751.9
AHQ-5-3, 6227	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.08E-07	0.88	4.07	-	554.5
AHQ-5-4, 6605	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	6.78E-04	0.82	3.91	-	331.4
AHQ-5-2, 6959 - 7035	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	8.98E-07	0.62	3.17	-	508.3
AHQ-5-2, 7209 - 7277	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	5.76E-05	0.83	4.23	-	503.8
AHQ-5-3, 6702 - 6731	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	1.68E-05	0.55	3.41	-	395.1
AHQ-5-1, 6657 - 6721	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	1.04E-05	0.55	3.28	-	433.0
AHQ-5-2, 6705 - 6742	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	1.70E-09	0.70	3.60	-	377.9
AHQ-5-3, 6619 - 6633	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	1.49E-06	0.80	4.01	-	362.1
AHQ-5-3, 2937 - 2949	K.CSGPGLSPGMVR.A	1219.41699	2	2.56E-06	0.71	2.96	-	490.4
AHQ-5-2, 2858 - 2881	K.CSGPGLSPGMVR.A	1219.41699	2	3.57E-05	0.85	3.24	-	647.7
AHQ-5-3, 2947	K.CSGPGLSPGMVR.A	1219.41699	1	9.20E-05	0.57	2.85	-	216.3
AHQ-5-4, 2917	K.CSGPGLSPGMVR.A	1219.41699	2	3.25E-06	0.67	2.79	-	501.7
AHQ-5-5, 5239	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	3.87E-09	0.95	4.27	-	1170.4
AHQ-5-2, 5415 - 5466	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	9.90E-11	0.96	5.26	-	989.7
AHQ-5-1, 5563 - 5583	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	1.08E-10	0.93	4.78	-	682.9
AHQ-5-1, 5564 - 5576	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	1.99E-09	0.97	5.65	-	1188.7
AHQ-5-2, 5411 - 5485	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	9.27E-09	0.92	4.67	-	704.2
AHQ-5-3, 5497 - 5499	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	1.39E-11	0.95	4.77	-	981.2
AHQ-5-1, 5047 - 5061	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	1.39E-07	0.89	4.07	-	716.8
AHQ-5-2, 4938	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	2.44E-05	0.88	4.23	-	597.3
AHQ-5-5, 4759 - 4766	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	3.82E-04	0.80	4.10	-	473.3
AHQ-5-3, 5025 - 5026	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	1.75E-05	0.89	4.48	-	419.1
AHQ-5-4, 5480	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	3.44E-14	0.95	5.22	-	862.8
AHQ-5-1, 5053	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	2	9.82E-04	0.91	4.01	-	828.6
AHQ-5-5, 5227 - 5246	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	2.47E-04	0.75	3.21	-	494.1
AHQ-5-4, 5476	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	1.38E-08	0.96	4.47	-	1213.2
AHQ-5-2, 3977	R.DAEM*PATEKDLAEDAPWK.K	2034.18987	2	8.23E-04	0.80	3.39	-	545.3
AHQ-5-2, 4599	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	2.69E-05	0.89	3.65	-	915.5
AHQ-5-1, 4688	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	4.65E-04	0.88	3.68	-	877.6
AHQ-5-5, 4457	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	1.40E-04	0.84	3.66	-	578.0
AHQ-5-1, 4116	R.DAEM*PATEKDLAEDAPWK.K	2034.18987	2	4.74E-04	0.68	3.28	-	365.8
AHQ-5-2, 4079	R.DAEMPATEKDLAEDAPWKK.I	2146.36338	3	1.64E-06	0.85	4.01	-	519.0
AHQ-5-5, 3925 - 3993	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	6.18E-04	0.90	3.75	-	1220.4
AHQ-5-3, 4089 - 4159	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.20E-04	0.86	3.96	-	941.0
AHQ-5-1, 4361	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.49E-07	0.89	4.33	-	611.7
AHQ-5-1, 4103 - 4173	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	7.50E-06	0.95	4.69	-	1258.7
AHQ-5-4, 4041 - 4101	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.34E-04	0.86	3.44	-	1041.3
AHQ-5-2, 4389 - 4457	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	6.56E-08	0.91	4.62	-	977.6
AHQ-5-3, 4465 - 4539	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	3.05E-07	0.82	3.49	-	946.8
AHQ-5-8, 3820	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	7.33E-08	0.91	4.23	-	1013.2
AHQ-5-10, 3866 - 3867	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.91E-04	0.93	3.98	-	1218.9
AHQ-5-1, 4524 - 4596	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	5.97E-09	0.94	4.03	-	1376.2
AHQ-5-1, 4587 - 4656	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.70E-06	0.95	4.53	-	1329.1
AHQ-5-2, 4517 - 4590	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.09E-06	0.91	4.28	-	934.4
AHQ-5-3, 4449 - 4529	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	7.88E-08	0.93	4.20	-	1173.8
AHQ-5-3, 4611	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.65E-07	0.89	3.73	-	953.7
AHQ-5-6, 4113 - 4133	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.25E-05	0.82	3.68	-	908.3
AHQ-5-4, 4461	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.14E-05	0.96	5.28	-	1284.9
AHQ-5-5, 4281	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.13E-09	0.95	4.53	-	1342.7
AHQ-5-9, 3746 - 3747	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.50E-05	0.93	4.60	-	1044.6
AHQ-5-1, 4488 - 4555	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.03E-08	0.93	4.63	-	993.0
AHQ-5-4, 4376 - 4380	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.42E-07	0.95	4.74	-	1286.8
AHQ-5-4, 4389	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	4.74E-07	0.80	3.20	-	923.9
AHQ-5-2, 4746	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.06E-04	0.92	4.39	-	886.5
AHQ-5-7, 3918 - 3998	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	7.44E-04	0.84	3.77	-	706.3
AHQ-5-5, 4145 - 4201	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.64E-07	0.93	3.98	-	1171.8
AHQ-5-1, 4753	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.62E-06	0.94	4.29	-	1229.6
AHQ-5-2, 4379 - 4449	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.62E-06	0.89	3.98	-	946.3
AHQ-5-2, 4661	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.91E-07	0.93	4.15	-	1100.9
AHQ-5-1, 4685	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	9.06E-11	0.91	4.08	-	969.4
AHQ-5-4, 4646 - 4716	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.34E-06	0.86	3.21	-	1119.7
AHQ-5-5, 4537 - 4609	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.79E-05	0.83	2.96	-	1129.1
AHQ-5-5, 4683 - 4755	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	3.37E-09	0.88	3.73	-	985.9
AHQ-5-2, 4717	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.79E-05	0.70	2.82	-	870.9
AHQ-5-2, 1694 - 1766	R.DAPQDFHPDR.V	1198.22650	2	3.10E-05	0.61	3.04	-	386.8
AHQ-5-1, 2060	R.DAPQDFHPDR.V	1198.22650	2	4.76E-06	0.77	3.14	-	545.7
AHQ-5-6, 4837 - 4912	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	3.20E-06	0.91	4.54	-	582.7
AHQ-5-5, 4915 - 4929	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.74E-04	0.90	4.39	-	721.8
AHQ-5-4, 5228	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.07E-06	0.67	3.15	-	396.6
AHQ-5-3, 5022 - 5029	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	8.27E-05	0.82	4.14	-	514.7
AHQ-5-8, 4690	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	6.21E-04	0.47	2.57	-	313.7
AHQ-5-4, 5056 - 5125	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.02E-04	0.91	4.44	-	645.7
AHQ-5-4, 4954 - 4986	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.99E-05	0.90	4.12	-	725.6
AHQ-5-5, 5173 - 5177	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.38E-04	0.87	4.39	-	540.3
AHQ-5-2, 5001	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.64E-05	0.75	3.46	-	544.8
AHQ-5-1, 4971 - 5049	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.49E-06	0.87	4.02	-	646.1
AHQ-5-5, 4998	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	3.02E-06	0.84	4.08	-	531.3
AHQ-5-14-, 2363	K.DKGEYTLVVK.W	1152.32223	1	4.80E-04	0.28	2.10	-	468.2
AHQ-5-14, 3233	K.DKGEYTLVVK.W	1152.32223	1	1.80E-04	0.10	2.00	-	356.1
AHQ-5-14-, 2353 - 2359	K.DKGEYTLVVK.W	1152.32223	2	2.70E-07	0.82	3.06	-	655.8
AHQ-5-5, 2195	K.DKGEYTLVVK.W	1152.32223	1	2.80E-05	0.26	2.28	-	444.3
AHQ-5-4, 2977 - 2980	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	2.72E-04	0.53	3.06	-	405.6
AHQ-5-3, 3258	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	3.14E-05	0.88	3.73	-	763.3
AHQ-5-3, 2942 - 3013	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.23E-05	0.86	3.28	-	767.6
AHQ-5-2, 3089	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	4.72E-07	0.92	3.84	-	962.0
AHQ-5-2, 2889 - 2958	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.31E-08	0.95	4.14	-	1182.7
AHQ-5-2, 3197 - 3271	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	9.84E-05	0.95	4.38	-	1181.4
AHQ-5-1, 3065 - 3137	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.38E-06	0.93	4.16	-	1024.3
AHQ-5-1, 3164	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	3.61E-05	0.87	3.76	-	651.1
AHQ-5-1, 3203	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.04E-07	0.93	3.88	-	1057.4
AHQ-5-3, 3118	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.32E-11	0.94	4.13	-	1073.6
AHQ-5-1, 3331	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	4.13E-05	0.87	3.49	-	786.1
AHQ-5-4, 2966 - 3046	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	7.70E-09	0.96	4.57	-	1428.5
AHQ-5-7, 3054	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	1.26E-09	0.86	3.71	-	436.2
AHQ-5-1, 3485 - 3555	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.21E-06	0.97	5.29	-	1427.2
AHQ-5-1, 3507	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	7.06E-06	0.59	3.38	-	301.9
AHQ-5-5, 5231	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	2.83E-04	0.37	2.36	-	309.6
AHQ-5-6, 3165	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	1.39E-06	0.51	2.89	-	290.6
AHQ-5-7, 3140	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	2.63E-04	0.08	1.96	-	217.2
AHQ-5-5, 3199	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	3.79E-06	0.65	3.57	-	286.8
AHQ-5-13, 3491	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	2.85E-04	0.90	3.36	-	1246.1
AHQ-5-1, 2687 - 2688	R.EATTEFSVDAR.A	1226.27493	2	5.73E-05	0.85	3.10	-	759.3
AHQ-5-2, 2598 - 2599	R.EATTEFSVDAR.A	1226.27493	2	4.67E-06	0.85	2.97	-	846.4

AHQ-5-2, 6525 - 6594	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	5.68E-08	0.94	5.81	-	653.8
AHQ-5-4, 6456 - 6526	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.07E-06	0.95	5.66	-	1079.3
AHQ-5-5, 6351 - 6433	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.48E-08	0.94	5.95	-	626.1
AHQ-5-1, 6425 - 6507	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.55E-07	0.93	5.12	-	640.2
AHQ-5-4, 6540 - 6604	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.72E-07	0.92	5.24	-	684.2
AHQ-5-2, 6389 - 6457	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.79E-12	0.91	4.63	-	850.1
AHQ-5-6, 6264 - 6340	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.07E-05	0.94	5.41	-	905.7
AHQ-5-3, 6471 - 6545	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.06E-10	0.95	5.85	-	784.7
AHQ-5-2, 6661	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.30E-10	0.86	4.37	-	461.8
AHQ-5-3, 6575 - 6641	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.05E-08	0.91	4.87	-	650.8
AHQ-5-1, 6555 - 6583	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	6.39E-09	0.94	5.63	-	669.5
AHQ-5-10, 4540	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.49E-05	0.82	3.45	-	1034.5
AHQ-5-2, 4887 - 4889	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.35E-04	0.71	3.47	-	621.3
AHQ-5-5, 5021 - 5050	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.39E-07	0.90	4.09	-	613.4
AHQ-5-4, 5188 - 5261	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	6.78E-06	0.47	2.69	-	570.5
AHQ-5-1, 5260	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	3.34E-09	0.97	5.27	-	1671.1
AHQ-5-3, 5255	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	4.21E-07	0.97	5.39	-	1941.4
AHQ-5-1, 5191 - 5259	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.10E-07	0.92	4.37	-	993.7
AHQ-5-6, 4981 - 4985	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.22E-07	0.92	3.97	-	842.3
AHQ-5-8, 4662 - 4732	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.33E-08	0.92	4.13	-	889.2
AHQ-5-2, 5233	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	6.04E-09	0.94	4.62	-	1116.6
AHQ-5-3, 5221 - 5289	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.19E-07	0.93	4.42	-	1006.1
AHQ-5-2, 5147 - 5217	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.51E-11	0.96	4.62	-	1307.6
AHQ-5-1, 4889 - 4959	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.57E-04	0.32	2.55	-	374.8
AHQ-5-1, 4056	R.ENGVYLIDVK.F	1150.30633	1	4.24E-04	0.04	1.84	-	258.8
AHQ-5-5, 3970	R.ENGVYLIDVK.F	1150.30633	1	1.90E-05	0.17	1.99	-	274.5
AHQ-5-6, 3792	R.ENGVYLIDVK.F	1150.30633	1	9.64E-04	0.21	2.26	-	270.2
AHQ-5-8, 2846	K.FADQHVPGSPFSVK.V	1516.68203	2	1.22E-04	0.74	3.05	-	447.6
AHQ-5-2, 3377	K.FADQHVPGSPFSVK.V	1516.68203	2	6.52E-07	0.72	2.78	-	409.0
AHQ-5-4, 3420	K.FADQHVPGSPFSVK.V	1516.68203	3	1.97E-04	0.94	4.03	-	1350.5
AHQ-5-12, 3316	K.FADQHVPGSPFSVK.V	1516.68203	2	2.52E-06	0.78	3.38	-	364.3
AHQ-5-3, 3450	K.FADQHVPGSPFSVK.V	1516.68203	2	3.36E-08	0.79	3.05	-	476.4
AHQ-5-5, 3177	K.FADQHVPGSPFSVK.V	1516.68203	3	2.58E-04	0.94	4.25	-	1542.0
AHQ-5-1, 3567	K.FADQHVPGSPFSVK.V	1516.68203	2	7.26E-10	0.85	3.26	-	573.9
AHQ-5-5, 3162 - 3233	K.FADQHVPGSPFSVK.V	1516.68203	2	4.29E-07	0.78	3.93	-	405.9
AHQ-5-1, 3585	K.FADQHVPGSPFSVK.V	1516.68203	3	1.52E-07	0.93	4.31	-	940.0
AHQ-5-13-, 3417	K.FADQHVPGSPFSVK.V	1516.68203	2	6.46E-08	0.76	2.99	-	420.0
AHQ-5-1, 3599 - 3651	K.FADQHVPGSPFSVK.V	1516.68203	2	1.75E-06	0.86	3.55	-	541.8
AHQ-5-13, 3523 - 3530	K.FADQHVPGSPFSVK.V	1516.68203	2	2.89E-05	0.91	4.09	-	619.2
AHQ-5-4, 5696	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	7.31E-09	0.88	4.24	-	935.3
AHQ-5-4, 5618 - 5693	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.26E-08	0.97	5.96	-	882.7
AHQ-5-6, 5364	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.75E-05	0.91	4.45	-	908.9
AHQ-5-8, 4981	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.50E-04	0.86	3.67	-	580.6
AHQ-5-1, 5819	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	6.24E-07	0.95	4.92	-	1010.5
AHQ-5-7, 5198 - 5204	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.11E-06	0.97	5.49	-	1309.6
AHQ-5-4, 5596 - 5676	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.24E-06	0.92	4.72	-	869.9
AHQ-5-3, 5714 - 5715	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	7.98E-08	0.98	6.77	-	1036.6
AHQ-5-10, 4888	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.20E-05	0.89	3.63	-	845.7
AHQ-5-8, 4989 - 4996	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.93E-07	0.86	4.41	-	555.1
AHQ-5-9, 4762	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.14E-05	0.96	5.29	-	1208.7
AHQ-5-1, 5807 - 5875	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.49E-08	0.92	5.02	-	783.7
AHQ-5-13, 5381 - 5412	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.37E-06	0.90	4.50	-	698.3
AHQ-5-11, 5223 - 5250	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.58E-05	0.91	4.66	-	854.8
AHQ-5-2, 5657 - 5726	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.50E-08	0.93	5.11	-	1049.8
AHQ-5-3, 5566 - 5645	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.31E-05	0.96	5.44	-	1145.5
AHQ-5-5, 5393	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	7.10E-05	0.94	4.81	-	801.1
AHQ-5-13-, 5313 - 5315	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	7.11E-04	0.94	4.90	-	1009.0
AHQ-5-6, 5373 - 5432	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	3.59E-06	0.93	3.73	-	1484.9
AHQ-5-2, 5531 - 5603	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	7.87E-08	0.97	5.94	-	1227.8
AHQ-5-5, 5389 - 5415	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.22E-06	0.93	4.65	-	1126.7
AHQ-5-1, 5679 - 5743	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.58E-06	0.92	4.88	-	792.6
AHQ-5-9, 4742	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.40E-04	0.93	4.29	-	956.7
AHQ-5-12, 5408	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.52E-07	0.95	5.05	-	1041.4
AHQ-5-3, 5638 - 5710	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	8.33E-08	0.96	5.71	-	1262.3
AHQ-5-2, 5458 - 5538	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	6.91E-06	0.92	4.93	-	712.3
AHQ-5-1, 5680 - 5756	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.82E-07	0.96	5.45	-	995.1
AHQ-5-5, 4987 - 5057	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	6.04E-06	0.91	4.38	-	600.6
AHQ-5-1, 5324	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	1.08E-06	0.87	3.61	-	623.0
AHQ-5-7, 4806	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	2.24E-05	0.90	4.38	-	637.3
AHQ-5-5, 3534	K.FNGTHIPGSPFK.I	1302.46259	2	2.00E-05	0.86	3.52	-	598.7
AHQ-5-3, 3818	K.FNGTHIPGSPFK.I	1302.46259	2	1.64E-05	0.66	2.77	-	540.8
AHQ-5-4, 3765	K.FNGTHIPGSPFK.I	1302.46259	1	3.07E-04	0.57	2.17	-	507.0
AHQ-5-1, 3923	K.FNGTHIPGSPFK.I	1302.46259	2	9.42E-06	0.76	3.23	-	596.9
AHQ-5-4, 3764	K.FNGTHIPGSPFK.I	1302.46259	2	9.11E-08	0.65	3.14	-	423.3
AHQ-5-7, 3408	K.FNGTHIPGSPFK.I	1302.46259	1	7.99E-04	0.10	1.82	-	250.7
AHQ-5-7, 3587	K.FNGTHIPGSPFK.I	1302.46259	2	7.10E-06	0.57	2.53	-	543.8
AHQ-5-1, 3831	K.FNGTHIPGSPFK.I	1302.46259	2	6.41E-07	0.80	2.58	-	731.7
AHQ-5-5, 2671 - 2675	R.FVPAEMGTHTVSVK.Y	1503.74821	2	6.87E-11	0.89	3.72	-	570.4
AHQ-5-3, 2930	R.FVPAEMGTHTVSVK.Y	1503.74821	2	5.73E-06	0.79	3.12	-	431.7
AHQ-5-4, 2885	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.61E-06	0.94	4.24	-	719.6
AHQ-5-4, 6909 - 6974	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	3.38E-05	0.85	4.14	-	650.8
AHQ-5-3, 6229 - 6297	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	4.61E-04	0.84	4.29	-	659.3
AHQ-5-2, 3238 - 3309	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	5.26E-06	0.93	4.74	-	724.9
AHQ-5-4, 3316 - 3332	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.58E-06	0.91	4.00	-	778.3
AHQ-5-1, 3617 - 3623	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	9.54E-06	0.80	3.24	-	698.9
AHQ-5-2, 3329 - 3397	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.84E-05	0.85	3.19	-	882.1
AHQ-5-3, 3341 - 3413	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.56E-05	0.93	4.18	-	870.0
AHQ-5-2, 3659	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	5.11E-07	0.87	3.26	-	921.3
AHQ-5-2, 3509	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.67E-05	0.74	2.92	-	616.1
AHQ-5-1, 3431 - 3500	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.70E-05	0.87	4.10	-	564.4
AHQ-5-8, 2844 - 2853	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.46E-05	0.72	3.35	-	676.3
AHQ-5-6, 3096	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.60E-06	0.86	3.45	-	795.4
AHQ-5-3, 3331 - 3407	K.GKLDVQFSGLTK.G	1293.49392	2	5.57E-07	0.89	3.97	-	714.1
AHQ-5-1, 3493	K.GKLDVQFSGLTK.G	1293.49392	2	8.28E-05	0.91	3.67	-	1052.9
AHQ-5-2, 3419	K.GKLDVQFSGLTK.G	1293.49392	2	2.37E-06	0.87	3.44	-	869.3
AHQ-5-2, 3209	K.GKLDVQFSGLTK.G	1293.49392	2	4.91E-06	0.92	3.73	-	998.3
AHQ-5-3, 3330	K.GKLDVQFSGLTK.G	1293.49392	1	1.47E-04	0.31	2.02	-	383.9
AHQ-5-9, 4396	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	8.56E-05	0.74	3.24	-	560.3
AHQ-5-1, 5227 - 5295	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	4.19E-07	0.97	6.07	-	1544.5
AHQ-5-2, 5157 - 5225	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	3	9.11E-10	0.94	5.25	-	1120.1
AHQ-5-2, 5153 - 5222	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.02E-07	0.96	5.79	-	1024.4
AHQ-5-3, 5186 - 5334	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	6.11E-15	0.98	6.98	-	1686.2
AHQ-5-1, 5087 - 5159	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	9.37E-12	0.98	6.55	-	1560.5
AHQ-5-2, 2078	K.GTVEPQLEAR.G	1100.20741	2	2.74E-06	0.84	3.30	-	582.5
AHQ-5-4, 2121	K.GTVEPQLEAR.G	1100.20741	2	1.57E-06	0.89	3.67	-	624.2
AHQ-5-6, 1960	K.GTVEPQLEAR.G	1100.20741	2	8.66E-05	0.67	2.87	-	420.6
AHQ-5-3, 2129 - 2131	K.GTVEPQLEAR.G	1100.20741	2	2.19E-05	0.82	3.05	-	517.4

AHQ-5-1, 2332	K.GTVEPQLEAR.G	1100.20741	2	3.46E-04	0.74	2.92	-	440.5
AHQ-5-3, 5531 - 5601	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	3.15E-05	0.97	5.06	-	1287.5
AHQ-5-2, 5135	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	1.37E-06	0.74	3.67	-	651.7
AHQ-5-3, 5798 - 5814	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	1.87E-06	0.93	4.12	-	878.8
AHQ-5-1, 5323	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.98E-04	0.96	4.70	-	1337.2
AHQ-5-2, 5123 - 5202	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.85E-04	0.95	4.67	-	1067.2
AHQ-5-3, 5225 - 5294	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.41E-04	0.95	4.77	-	972.1
AHQ-5-2, 5514 - 5525	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	2.24E-10	0.98	6.35	-	1336.7
AHQ-5-4, 5141	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	7.71E-06	0.93	4.41	-	923.4
AHQ-5-4, 5564 - 5565	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	1.15E-04	0.98	5.68	-	1342.9
AHQ-5-5, 5330	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	5.72E-07	0.97	5.42	-	1305.1
AHQ-5-4, 3858 - 3866	R.IANLQTDLSDGLR.L	1416.56231	2	1.17E-07	0.87	3.63	-	772.6
AHQ-5-5, 3706	R.IANLQTDLSDGLR.L	1416.56231	2	8.84E-08	0.92	3.53	-	1057.7
AHQ-5-3, 3889	R.IANLQTDLSDGLR.L	1416.56231	2	7.46E-05	0.89	3.46	-	875.7
AHQ-5-1, 4584	R.IANLQTDLSDGLR.L	1416.56231	2	2.40E-05	0.89	3.63	-	899.2
AHQ-5-11, 3983	R.IANLQTDLSDGLR.L	1416.56231	2	1.04E-04	0.94	3.98	-	1021.8
AHQ-5-12, 4093	R.IANLQTDLSDGLR.L	1416.56231	2	3.79E-05	0.95	4.49	-	1004.1
AHQ-5-4, 4249	R.IANLQTDLSDGLR.L	1416.56231	2	1.62E-04	0.88	3.52	-	801.6
AHQ-5-1, 4363 - 4431	R.IANLQTDLSDGLR.L	1416.56231	2	1.08E-04	0.93	3.91	-	1174.7
AHQ-5-3, 4301 - 4377	R.IANLQTDLSDGLR.L	1416.56231	2	5.25E-06	0.94	4.31	-	1051.9
AHQ-5-2, 3833 - 3914	R.IANLQTDLSDGLR.L	1416.56231	2	1.41E-07	0.92	3.95	-	915.5
AHQ-5-1, 3971	R.IANLQTDLSDGLR.L	1416.56231	2	3.52E-07	0.96	4.57	-	1341.3
AHQ-5-5, 4053	R.IANLQTDLSDGLR.L	1416.56231	2	1.56E-05	0.94	3.89	-	1142.9
AHQ-5-7, 3876	R.IANLQTDLSDGLR.L	1416.56231	2	1.77E-07	0.84	3.00	-	920.1
AHQ-5-6, 3609 - 3682	R.IANLQTDLSDGLR.L	1416.56231	2	3.33E-04	0.55	2.65	-	474.3
AHQ-5-5, 4057 - 4058	R.IANLQTDLSDGLR.L	1416.56231	1	8.99E-04	0.63	2.98	-	311.5
AHQ-5-2, 4217 - 4289	R.IANLQTDLSDGLR.L	1416.56231	2	5.86E-04	0.86	3.76	-	739.6
AHQ-5-1, 4264	R.IANLQTDLSDGLR.L	1416.56231	2	2.94E-06	0.95	4.29	-	987.7
AHQ-5-2, 4229	R.IANLQTDLSDGLR.L	1416.56231	1	8.05E-04	0.41	2.54	-	284.7
AHQ-5-8, 3738	R.IANLQTDLSDGLR.L	1416.56231	2	3.03E-08	0.95	3.95	-	1206.5
AHQ-5-2, 4399 - 4479	R.IANLQTDLSDGLR.L	1416.56231	2	5.01E-07	0.87	3.74	-	718.0
AHQ-5-9, 3643	R.IANLQTDLSDGLR.L	1416.56231	2	1.59E-06	0.88	2.95	-	1008.6
AHQ-5-5, 5439 - 5457	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	3.98E-08	0.96	5.67	-	1167.9
AHQ-5-4, 5616 - 5617	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	7.66E-11	0.98	5.63	-	1807.0
AHQ-5-5, 5418 - 5498	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.74E-08	0.97	4.83	-	1658.6
AHQ-5-6, 5378	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	6.93E-09	0.98	5.29	-	1581.3
AHQ-5-5, 5017	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.48E-05	0.90	4.53	-	554.3
AHQ-5-7, 3864	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	9.23E-05	0.94	4.18	-	1291.4
AHQ-5-1, 5712	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	9.06E-07	0.88	4.30	-	771.6
AHQ-5-3, 5649	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.76E-07	0.97	5.35	-	1537.9
AHQ-5-11, 5156 - 5215	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.62E-07	0.94	4.51	-	1014.3
AHQ-5-5, 4021 - 4069	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	5.31E-07	0.98	5.37	-	2091.0
AHQ-5-1, 4253 - 4323	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	3.26E-05	0.97	5.18	-	1370.7
AHQ-5-6, 3966 - 3993	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.08E-05	0.97	5.00	-	1583.9
AHQ-5-8, 5060	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.95E-09	0.98	5.70	-	1527.1
AHQ-5-4, 4177 - 4188	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.21E-04	0.97	5.02	-	2028.6
AHQ-5-1, 5691	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.14E-09	0.97	5.01	-	1510.2
AHQ-5-3, 2477	K.IVGPSGAAVPCK.V	1157.36530	2	2.86E-06	0.90	3.19	-	1012.3
AHQ-5-1, 2636	K.IVGPSGAAVPCK.V	1157.36530	2	8.49E-09	0.94	3.98	-	1108.9
AHQ-5-4, 2456	K.IVGPSGAAVPCK.V	1157.36530	2	2.07E-08	0.77	2.90	-	635.2
AHQ-5-5, 4034	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	8.31E-10	0.96	5.14	-	1534.0
AHQ-5-1, 4292 - 4372	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	3.74E-05	0.92	4.74	-	422.0
AHQ-5-2, 4174 - 4189	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.02E-06	0.92	4.72	-	1062.8
AHQ-5-1, 4383 - 4451	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	6.03E-09	0.95	5.11	-	721.3
AHQ-5-3, 4253 - 4322	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	7.67E-09	0.95	5.41	-	1223.1
AHQ-5-3, 4257 - 4329	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	7.76E-06	0.94	5.62	-	415.9
AHQ-5-1, 4295 - 4364	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	9.58E-11	0.92	4.75	-	969.2
AHQ-5-2, 4258 - 4330	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	6.70E-11	0.88	4.04	-	1129.4
AHQ-5-4, 4217 - 4293	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	2.19E-06	0.87	4.13	-	418.5
AHQ-5-2, 4178 - 4249	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.99E-04	0.90	4.17	-	426.8
AHQ-5-4, 4214 - 4289	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.55E-07	0.75	3.51	-	564.3
AHQ-5-2, 4318	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	4.76E-05	0.84	3.56	-	442.4
AHQ-5-6, 3972	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	4.90E-06	0.92	4.80	-	958.3
AHQ-5-3, 4361	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	5.25E-09	0.74	3.37	-	675.3
AHQ-5-5, 4277 - 4301	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	4.40E-04	0.88	3.95	-	1278.9
AHQ-5-1, 4501	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.93E-04	0.72	3.35	-	315.0
AHQ-5-6, 3952 - 4029	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.29E-06	0.91	4.31	-	538.5
AHQ-5-4, 4248 - 4330	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.33E-09	0.97	6.04	-	1892.2
AHQ-5-5, 3955	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	2.23E-04	0.82	3.22	-	532.4
AHQ-5-3, 4357 - 4429	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	5.12E-11	0.97	5.81	-	2143.0
AHQ-5-6, 3958 - 4024	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	7.61E-07	0.94	4.96	-	1531.3
AHQ-5-7, 3846 - 3914	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.22E-05	0.61	2.88	-	307.9
AHQ-5-5, 3998 - 4070	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.74E-09	0.97	5.93	-	2236.7
AHQ-5-8, 3736	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.58E-05	0.89	3.94	-	540.1
AHQ-5-4, 4254 - 4324	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.05E-05	0.84	3.89	-	457.4
AHQ-5-2, 4294	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	7.94E-09	0.96	5.10	-	1687.5
AHQ-5-1, 3475 - 3501	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	5.01E-05	0.92	4.09	-	1168.1
AHQ-5-1, 3503	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	1.90E-06	0.96	5.51	-	911.2
AHQ-5-6, 3025	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.33E-09	0.94	4.04	-	1494.1
AHQ-5-1, 3604 - 3681	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	2.58E-04	0.93	4.77	-	973.9
AHQ-5-1, 3635 - 3707	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	1.63E-06	0.94	4.66	-	836.6
AHQ-5-4, 3474	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.58E-07	0.89	3.93	-	926.5
AHQ-5-4, 3472	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	2.02E-04	0.86	3.57	-	534.2
AHQ-5-3, 3287 - 3357	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	8.38E-04	0.90	4.37	-	423.4
AHQ-5-3, 3397 - 3471	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	2.38E-04	0.93	4.41	-	1058.4
AHQ-5-5, 3061	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.35E-09	0.93	4.23	-	1279.7
AHQ-5-3, 3425 - 3503	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	4.21E-09	0.94	4.71	-	743.2
AHQ-5-2, 3407 - 3433	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	6.41E-04	0.72	3.35	-	259.3
AHQ-5-2, 3305 - 3378	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	2.85E-06	0.95	5.11	-	1240.4
AHQ-5-3, 3557	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	9.47E-04	0.79	3.10	-	1002.1
AHQ-5-3, 3578	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	1.44E-06	0.88	3.53	-	769.1
AHQ-5-2, 3167 - 3230	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	3.55E-06	0.94	4.91	-	922.4
AHQ-5-4, 3912	K.LDVQFSGLTK.G	1108.26945	1	3.27E-04	0.16	2.05	-	253.8
AHQ-5-3, 3949	K.LDVQFSGLTK.G	1108.26945	2	2.46E-04	0.92	3.84	-	912.9
AHQ-5-3, 3953	K.LDVQFSGLTK.G	1108.26945	1	1.28E-04	0.36	2.30	-	272.2
AHQ-5-4, 3926	K.LDVQFSGLTK.G	1108.26945	2	3.11E-06	0.83	2.99	-	712.9
AHQ-5-1, 4051	K.LDVQFSGLTK.G	1108.26945	2	3.35E-06	0.93	3.66	-	1129.3
AHQ-5-2, 3909	K.LDVQFSGLTK.G	1108.26945	1	1.70E-04	0.54	2.63	-	347.0
AHQ-5-2, 3897	K.LDVQFSGLTK.G	1108.26945	2	1.58E-04	0.94	3.84	-	926.3
AHQ-5-2, 7018	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	2	2.05E-05	0.90	4.88	-	464.7
AHQ-5-2, 7023	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	3.79E-05	0.93	4.91	-	1150.5
AHQ-5-1, 5016	K.LPQLPITNFSR.D	1286.50461	1	6.68E-04	0.56	2.21	-	339.4
AHQ-5-1, 5003 - 5027	K.LPQLPITNFSR.D	1286.50461	2	1.68E-05	0.85	2.63	-	717.6
AHQ-5-4, 4924	K.LPQLPITNFSR.D	1286.50461	2	3.01E-04	0.79	2.77	-	634.1
AHQ-5-2, 5106 - 5119	K.LPQLPITNFSR.D	1286.50461	2	1.91E-04	0.66	2.76	-	476.6
AHQ-5-2, 4841 - 4917	K.LPQLPITNFSR.D	1286.50461	2	1.05E-05	0.92	3.20	-	864.8
AHQ-5-3, 5271	K.LPQLPITNFSR.D	1286.50461	2	4.18E-06	0.70	2.89	-	368.7

AHQ-5-5, 5058	K.LPQLPITNFSR.D	1286.50461	2	1.10E-04	0.75	2.61	-	506.0
AHQ-5-2, 4847 - 4918	K.LPQLPITNFSR.D	1286.50461	1	3.45E-05	0.59	2.49	-	270.7
AHQ-5-3, 4962	K.LPQLPITNFSR.D	1286.50461	2	1.18E-04	0.82	3.02	-	516.1
AHQ-5-9, 4136	K.LPQLPITNFSR.D	1286.50461	2	3.20E-04	0.86	2.87	-	665.5
AHQ-5-2, 5189	K.LPQLPITNFSR.D	1286.50461	2	1.38E-04	0.84	2.94	-	616.3
AHQ-5-1, 5687	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.44E-08	0.91	3.86	-	786.5
AHQ-5-1, 5599 - 5667	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	1.55E-12	0.98	7.22	-	2650.9
AHQ-5-4, 5574 - 5644	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.55E-07	0.93	4.34	-	766.5
AHQ-5-2, 5665 - 5737	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.51E-10	0.97	6.28	-	808.2
AHQ-5-9, 4787	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.32E-04	0.82	3.50	-	524.0
AHQ-5-3, 5582 - 5663	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.99E-09	0.93	4.46	-	803.4
AHQ-5-12, 5358	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	7.84E-06	0.95	4.98	-	963.4
AHQ-5-2, 5581 - 5649	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.82E-07	0.97	5.77	-	1533.4
AHQ-5-1, 5589 - 5659	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.37E-08	0.95	5.56	-	723.5
AHQ-5-2, 5529 - 5601	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.76E-08	0.97	6.12	-	901.5
AHQ-5-6, 5386 - 5402	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.13E-06	0.88	3.72	-	661.4
AHQ-5-1, 2976	R.LRNGHVGISFVPK.E	1424.67564	2	1.11E-04	0.82	2.84	-	630.5
AHQ-5-4, 2976	R.LRNGHVGISFVPK.E	1424.67564	2	4.82E-06	0.75	2.92	-	586.1
AHQ-5-5, 2613 - 2619	R.LRNGHVGISFVPK.E	1424.67564	2	1.12E-04	0.64	2.61	-	493.3
AHQ-5-3, 3010 - 3086	R.LRNGHVGISFVPK.E	1424.67564	2	2.12E-04	0.71	2.84	-	612.7
AHQ-5-5, 2726 - 2727	R.LRNGHVGISFVPK.E	1424.67564	2	1.48E-04	0.76	2.90	-	581.9
AHQ-5-5, 2505	R.LRNGHVGISFVPK.E	1424.67564	2	8.57E-04	0.78	2.83	-	507.0
AHQ-5-1, 4143	R.LSPFMADIR.D	1050.25664	2	4.91E-05	0.71	2.55	-	556.2
AHQ-5-5, 3115 - 3169	R.LTVSSLQESGLK.V	1262.43499	2	3.73E-05	0.74	2.61	-	514.9
AHQ-5-3, 3422	R.LTVSSLQESGLK.V	1262.43499	2	9.11E-05	0.91	3.13	-	1055.9
AHQ-5-6, 3126 - 3132	R.LTVSSLQESGLK.V	1262.43499	2	9.04E-07	0.88	3.29	-	891.1
AHQ-5-14, 5202	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.56E-05	0.70	3.37	-	287.4
AHQ-5-2, 4087	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.20E-04	0.92	4.09	-	918.0
AHQ-5-7, 3664	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	3.09E-05	0.97	5.09	-	1889.2
AHQ-5-1, 4619 - 4625	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.45E-08	0.95	5.23	-	1088.1
AHQ-5-5, 4159 - 4231	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.48E-08	0.94	4.24	-	1300.3
AHQ-5-5, 4157 - 4230	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.10E-08	0.97	5.14	-	1307.6
AHQ-5-12, 4010	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.14E-05	0.90	4.18	-	620.3
AHQ-5-3, 4174	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.58E-05	0.97	5.94	-	1180.5
AHQ-5-1, 4601 - 4608	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.29E-10	0.97	5.32	-	1531.6
AHQ-5-1, 4309	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	4.05E-06	0.97	5.79	-	1841.7
AHQ-5-5, 3841 - 3915	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.83E-05	0.95	4.54	-	1398.9
AHQ-5-8, 3609	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.60E-05	0.90	4.07	-	972.1
AHQ-5-11, 4171	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	3.38E-04	0.89	3.89	-	928.1
AHQ-5-4, 4429	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.55E-10	0.96	5.70	-	858.6
AHQ-5-8, 3612	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.46E-10	0.98	6.12	-	1668.2
AHQ-5-13-, 4072	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.47E-07	0.96	5.24	-	1059.8
AHQ-5-11, 4164	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.87E-10	0.95	4.47	-	1100.1
AHQ-5-6, 4137	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.58E-04	0.88	3.30	-	654.1
AHQ-5-5, 3702	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	9.42E-05	0.87	3.76	-	601.4
AHQ-5-3, 4525	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.11E-06	0.91	4.14	-	879.5
AHQ-5-7, 3656	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.29E-05	0.92	4.40	-	880.0
AHQ-5-1, 4424	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	4.57E-05	0.88	3.54	-	965.9
AHQ-5-5, 3821 - 3897	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.85E-07	0.98	6.30	-	1463.3
AHQ-5-7, 3980	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.71E-06	0.95	5.00	-	824.3
AHQ-5-1, 4421	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.02E-08	0.93	4.08	-	1189.1
AHQ-5-14, 4829	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.88E-05	0.93	4.71	-	812.7
AHQ-5-4, 4081 - 4149	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.78E-08	0.97	5.28	-	1266.2
AHQ-5-13, 4156 - 4161	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	4.47E-13	0.98	6.11	-	1725.7
AHQ-5-6, 3796	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.01E-06	0.97	5.30	-	1337.9
AHQ-5-4, 4066	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	4.48E-09	0.97	5.45	-	1579.6
AHQ-5-1, 4280	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	7.46E-06	0.97	5.62	-	1057.3
AHQ-5-13, 4157	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.22E-09	0.97	5.36	-	1472.4
AHQ-5-4, 4065	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.66E-08	0.96	5.32	-	1068.0
AHQ-5-5, 3967	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	6.27E-06	0.69	3.47	-	364.5
AHQ-5-11, 3887 - 3888	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.34E-05	0.96	5.24	-	865.1
AHQ-5-5, 2378	K.MDCQECPEGYR.V	1447.55375	2	6.98E-08	0.91	3.37	-	871.6
AHQ-5-4, 2438 - 2509	K.MDCQECPEGYR.V	1447.55375	2	9.80E-06	0.89	3.61	-	701.9
AHQ-5-5, 2383	K.MDCQECPEGYR.V	1447.55375	1	1.23E-06	0.34	2.33	-	158.5
AHQ-5-4, 2981	R.NGHVGISFVPK.E	1155.33104	1	6.23E-07	0.39	2.17	-	473.1
AHQ-5-4, 3201	R.NGHVGISFVPK.E	1155.33104	2	9.39E-05	0.75	2.84	-	711.6
AHQ-5-5, 2762	R.NGHVGISFVPK.E	1155.33104	1	3.36E-07	0.61	2.54	-	436.8
AHQ-5-4, 3188	R.NGHVGISFVPK.E	1155.33104	1	1.38E-06	0.40	2.31	-	291.2
AHQ-5-5, 2981 - 2982	R.NGHVGISFVPK.E	1155.33104	1	5.62E-05	0.21	2.08	-	271.1
AHQ-5-1, 5037	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	1.06E-05	0.55	2.54	-	393.6
AHQ-5-4, 4846	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	1.28E-04	0.93	4.21	-	1819.0
AHQ-5-1, 4901	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	3.74E-06	0.95	4.26	-	1123.9
AHQ-5-2, 1799	K.RAEFTVETR.S	1109.21754	2	1.08E-05	0.89	3.38	-	703.7
AHQ-5-1, 2157	K.RAEFTVETR.S	1109.21754	2	1.27E-05	0.94	3.70	-	1025.3
AHQ-5-5, 2682 - 2755	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	6.22E-04	0.93	4.10	-	1459.7
AHQ-5-1, 3940	K.RIANLQTDLSDGLR.L	1572.74866	2	1.02E-06	0.94	4.14	-	1136.3
AHQ-5-2, 3710 - 3773	K.RIANLQTDLSDGLR.L	1572.74866	2	5.95E-09	0.88	4.10	-	472.7
AHQ-5-4, 2798 - 2809	R.RLTVSSLQESGLK.V	1418.62134	2	4.29E-04	0.96	4.48	-	1284.1
AHQ-5-2, 2853	R.RLTVSSLQESGLK.V	1418.62134	2	5.92E-05	0.97	4.87	-	2089.0
AHQ-5-7, 2567 - 2570	R.RLTVSSLQESGLK.V	1418.62134	2	5.48E-05	0.98	4.57	-	2363.0
AHQ-5-1, 3095	R.RLTVSSLQESGLK.V	1418.62134	2	3.42E-04	0.97	4.51	-	2238.5
AHQ-5-4, 2898	R.RLTVSSLQESGLK.V	1418.62134	2	6.72E-06	0.98	4.57	-	2833.1
AHQ-5-1, 7460 - 7468	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	1.19E-05	0.95	5.45	-	1341.7
AHQ-5-3, 7622 - 7687	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	4.42E-07	0.78	3.85	-	709.0
AHQ-5-1, 7317 - 7397	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	2.58E-08	0.87	4.34	-	815.8
AHQ-5-2, 3829 - 3901	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.73E-10	0.97	5.31	-	1974.3
AHQ-5-3, 3898 - 3969	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.48E-05	0.88	3.99	-	583.2
AHQ-5-2, 3823 - 3893	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.33E-06	0.94	4.89	-	729.6
AHQ-5-5, 3753	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.96E-06	0.78	3.52	-	469.9
AHQ-5-3, 4170	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	6.31E-07	0.85	3.86	-	631.3
AHQ-5-1, 4015 - 4083	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	6.78E-07	0.88	4.24	-	624.3
AHQ-5-2, 4051	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.79E-06	0.86	3.54	-	967.3
AHQ-5-5, 3733	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.22E-08	0.93	4.21	-	1147.7
AHQ-5-9, 3340	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.28E-04	0.63	2.94	-	439.5
AHQ-5-3, 3907	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.10E-06	0.96	4.59	-	1690.6
AHQ-5-2, 4043 - 4118	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	9.10E-06	0.95	5.29	-	631.9
AHQ-5-1, 4151 - 4220	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.21E-05	0.89	4.30	-	611.0
AHQ-5-4, 3868 - 3937	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.30E-08	0.92	4.47	-	677.8
AHQ-5-3, 3990	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	9.62E-07	0.84	3.60	-	754.5
AHQ-5-2, 4218	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.74E-07	0.78	3.73	-	445.0
AHQ-5-1, 4017 - 4087	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	5.13E-06	0.96	5.41	-	1489.6
AHQ-5-3, 4053	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.60E-05	0.85	3.48	-	644.3
AHQ-5-5, 3582 - 3654	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.29E-09	0.89	3.58	-	1202.6
AHQ-5-8, 3441	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.37E-07	0.90	4.09	-	639.7
AHQ-5-2, 4037	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.23E-07	0.93	5.10	-	606.4
AHQ-5-2, 3961	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	6.53E-07	0.91	4.79	-	620.0
AHQ-5-5, 3661	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.23E-07	0.94	5.30	-	630.3

AHQ-5-4, 3869 - 3948	R.SAGQGEVLVYYVEDPAGHQEEAK.V	2314.45074	3	6.18E-09	0.92	4.27	-	1129.9
AHQ-5-6, 3128	K.SPFEVYVDK.S	1084.20321	1	2.39E-05	0.80	3.20	-	583.5
AHQ-5-7, 2995	K.SPFEVYVDK.S	1084.20321	1	2.49E-04	0.11	1.82	-	250.8
AHQ-5-5, 3157	K.SPFEVYVDK.S	1084.20321	2	1.38E-05	0.86	2.84	-	1075.9
AHQ-5-5, 3149 - 3173	K.SPFEVYVDK.S	1084.20321	1	1.27E-04	0.60	1.88	-	1007.7
AHQ-5-4, 3341	K.SPFEVYVDK.S	1084.20321	1	8.55E-05	0.82	2.99	-	778.8
AHQ-5-2, 3255 - 3326	K.SPFEVYVDK.S	1084.20321	1	4.04E-06	0.87	3.44	-	829.0
AHQ-5-4, 3342	K.SPFEVYVDK.S	1084.20321	2	1.46E-05	0.89	3.23	-	835.2
AHQ-5-3, 3358	K.SPFEVYVDK.S	1084.20321	2	4.31E-06	0.92	3.29	-	1132.6
AHQ-5-2, 3247 - 3317	K.SPFEVYVDK.S	1084.20321	1	3.32E-04	0.69	2.41	-	960.6
AHQ-5-2, 3254 - 3325	K.SPFEVYVDK.S	1084.20321	2	5.45E-06	0.93	3.34	-	1086.8
AHQ-5-1, 3435 - 3492	K.SPFEVYVDK.S	1084.20321	2	9.89E-06	0.94	3.51	-	1167.0
AHQ-5-3, 3346	K.SPFEVYVDK.S	1084.20321	1	7.92E-04	0.72	2.99	-	666.6
AHQ-5-4, 3329	K.SPFEVYVDK.S	1084.20321	1	3.75E-06	0.69	2.37	-	882.0
AHQ-5-1, 3105	K.SPFEVYVDKSQGDASK.V	1757.87886	2	1.29E-04	0.96	4.37	-	1539.5
AHQ-5-3, 2977	K.SPFEVYVDKSQGDASK.V	1757.87886	2	4.19E-04	0.80	3.26	-	639.9
AHQ-5-3, 5077 - 5157	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.26E-07	0.93	4.65	-	751.5
AHQ-5-3, 4933	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.38E-04	0.73	3.52	-	517.6
AHQ-5-4, 5029 - 5102	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.25E-07	0.93	4.23	-	1002.4
AHQ-5-2, 4873	K.SPFSVAVSPSLDLSK.I	1534.73557	2	8.58E-05	0.87	3.76	-	697.8
AHQ-5-2, 5010 - 5077	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.31E-06	0.95	3.96	-	1271.7
AHQ-5-4, 3448 - 3468	R.SPYTVTVGQACNPSACR.A	1871.04208	2	8.95E-06	0.93	4.35	-	580.4
AHQ-5-6, 3252	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.15E-06	0.93	4.48	-	611.1
AHQ-5-1, 3504 - 3579	R.SPYTVTVGQACNPSACR.A	1871.04208	2	6.47E-04	0.91	4.31	-	552.4
AHQ-5-2, 3501	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.41E-06	0.94	4.76	-	772.5
AHQ-5-5, 3247 - 3321	R.SPYTVTVGQACNPSACR.A	1871.04208	2	8.45E-06	0.92	4.26	-	535.6
AHQ-5-3, 3427 - 3481	R.SPYTVTVGQACNPSACR.A	1871.04208	2	7.30E-06	0.93	4.32	-	695.7
AHQ-5-1, 2891	K.SQGDASKVTAQGPGLEPSGNIANK.T	2327.49419	2	3.89E-07	0.38	2.56	-	196.0
AHQ-5-14-, 2107 - 2187	K.SSFTVDCSK.A	1032.10676	1	9.54E-05	0.35	2.41	-	169.6
AHQ-5-14, 2930	K.SSFTVDCSK.A	1032.10676	1	4.19E-04	0.30	1.92	-	331.6
AHQ-5-6, 4732	R.TFSVWYVPEVTGTHK.V	1751.96228	3	6.50E-06	0.76	3.40	-	451.4
AHQ-5-2, 4963	R.TFSVWYVPEVTGTHK.V	1751.96228	3	3.83E-05	0.73	3.51	-	523.3
AHQ-5-4, 5018	R.TFSVWYVPEVTGTHK.V	1751.96228	3	1.29E-05	0.76	3.48	-	468.4
AHQ-5-5, 2769	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	7.04E-06	0.80	3.17	-	772.1
AHQ-5-2, 2863 - 2899	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	4.31E-09	0.92	4.16	-	954.9
AHQ-5-3, 2965	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	3.32E-09	0.93	3.97	-	991.5
AHQ-5-1, 3257	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	5.92E-04	0.26	2.69	-	277.1
AHQ-5-4, 2945	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	5.41E-08	0.84	3.68	-	564.7
AHQ-5-3, 2929 - 2954	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	4.57E-04	0.86	3.63	-	667.1
AHQ-5-1, 2892	R.TGVELGKPTHFTVNAK.A	1699.93205	2	1.48E-04	0.91	4.18	-	609.5
AHQ-5-3, 2703	R.TGVELGKPTHFTVNAK.A	1699.93205	3	2.83E-06	0.42	3.20	-	533.5
AHQ-5-1, 3001 - 3077	R.TGVELGKPTHFTVNAK.A	1699.93205	2	2.54E-04	0.76	3.25	-	526.4
AHQ-5-2, 2825	R.TGVELGKPTHFTVNAK.A	1699.93205	2	5.17E-06	0.83	3.49	-	616.4
AHQ-5-2, 2571	R.TGVELGKPTHFTVNAK.A	1699.93205	2	2.20E-05	0.92	4.26	-	634.4
AHQ-5-4, 2657	R.TGVELGKPTHFTVNAK.A	1699.93205	3	1.29E-04	0.81	3.54	-	777.1
AHQ-5-5, 2766 - 2838	K.THEAEIVEGENHTYCIR.F	2060.19046	2	3.44E-07	0.98	6.41	-	1760.8
AHQ-5-4, 3000 - 3012	K.THEAEIVEGENHTYCIR.F	2060.19046	2	4.56E-11	0.98	5.68	-	1887.0
AHQ-5-3, 3045	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.10E-10	0.97	4.70	-	2135.5
AHQ-5-1, 3129	K.THEAEIVEGENHTYCIR.F	2060.19046	2	6.57E-09	0.97	5.08	-	1668.7
AHQ-5-6, 2756 - 2834	K.THEAEIVEGENHTYCIR.F	2060.19046	3	9.77E-12	0.94	4.76	-	1037.7
AHQ-5-1, 3135 - 3140	K.THEAEIVEGENHTYCIR.F	2060.19046	3	8.66E-05	0.91	3.99	-	934.1
AHQ-5-2, 2974	K.THEAEIVEGENHTYCIR.F	2060.19046	2	5.25E-07	0.92	4.24	-	905.1
AHQ-5-1, 3260	K.THEAEIVEGENHTYCIR.F	2060.19046	2	6.77E-12	0.98	5.54	-	2257.0
AHQ-5-7, 2760	K.THEAEIVEGENHTYCIR.F	2060.19046	2	1.38E-06	0.95	4.46	-	923.3
AHQ-5-7, 2671 - 2744	K.THEAEIVEGENHTYCIR.F	2060.19046	2	7.45E-06	0.98	5.84	-	1500.4
AHQ-5-4, 2938 - 3017	K.THEAEIVEGENHTYCIR.F	2060.19046	3	6.85E-13	0.94	4.63	-	1176.8
AHQ-5-6, 2833 - 2848	K.THEAEIVEGENHTYCIR.F	2060.19046	2	4.86E-07	0.97	5.26	-	1549.1
AHQ-5-1, 3924	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	3	2.11E-04	0.82	3.62	-	559.4
AHQ-5-13-, 3043	R.TPCEEILVK.H	1090.27249	2	6.17E-06	0.89	3.19	-	1018.5
AHQ-5-5, 2907	R.TPCEEILVK.H	1090.27249	1	8.50E-04	0.74	3.22	-	528.3
AHQ-5-13, 3173 - 3175	R.TPCEEILVK.H	1090.27249	2	5.35E-06	0.87	3.53	-	772.5
AHQ-5-7, 2806	R.TPCEEILVK.H	1090.27249	2	6.35E-04	0.70	2.84	-	563.7
AHQ-5-2, 3041	R.TPCEEILVK.H	1090.27249	2	1.05E-04	0.71	2.62	-	630.1
AHQ-5-14-, 2981 - 2995	R.TPCEEILVK.H	1090.27249	2	5.04E-05	0.92	3.25	-	1025.5
AHQ-5-14, 3849 - 3904	R.TPCEEILVK.H	1090.27249	1	5.46E-06	0.44	2.51	-	372.5
AHQ-5-14, 3840 - 3896	R.TPCEEILVK.H	1090.27249	2	3.17E-06	0.84	3.32	-	606.2
AHQ-5-1, 3216 - 3217	R.TPCEEILVK.H	1090.27249	2	2.75E-04	0.88	3.22	-	858.3
AHQ-5-4, 3058	R.TPCEEILVK.H	1090.27249	2	2.25E-06	0.86	2.99	-	843.5
AHQ-5-4, 3061	R.TPCEEILVK.H	1090.27249	1	1.23E-05	0.38	2.57	-	418.4
AHQ-5-6, 2892	R.TPCEEILVK.H	1090.27249	2	2.19E-05	0.76	2.95	-	633.4
AHQ-5-2, 3026	R.TPCEEILVK.H	1090.27249	1	1.03E-05	0.26	2.25	-	390.2
AHQ-5-3, 3241 - 3309	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.93E-09	0.95	4.76	-	1036.7
AHQ-5-2, 3175 - 3245	R.VANPSGNLTETYVQDR.G	1764.87462	2	9.43E-11	0.91	3.70	-	658.9
AHQ-5-2, 3023 - 3093	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.04E-10	0.95	4.40	-	1100.3
AHQ-5-4, 3462 - 3470	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.26E-12	0.94	4.30	-	866.5
AHQ-5-5, 3109	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.96E-13	0.96	4.92	-	969.2
AHQ-5-2, 3541	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.03E-12	0.87	3.52	-	608.5
AHQ-5-4, 3277	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.04E-11	0.94	4.25	-	1002.7
AHQ-5-2, 3401 - 3469	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.60E-12	0.94	4.26	-	979.8
AHQ-5-3, 3426 - 3501	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.15E-11	0.94	4.39	-	981.1
AHQ-5-6, 3045	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.91E-08	0.93	4.01	-	890.8
AHQ-5-1, 3519 - 3589	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.43E-09	0.96	4.76	-	1266.8
AHQ-5-2, 3315 - 3330	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.62E-09	0.95	4.44	-	1058.6
AHQ-5-3, 3577	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.39E-06	0.89	3.65	-	732.2
AHQ-5-1, 3345 - 3415	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.12E-12	0.94	4.52	-	786.5
AHQ-5-1, 3221	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.68E-09	0.93	4.19	-	831.6
AHQ-5-4, 2738 - 2741	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.68E-08	0.90	3.85	-	739.6
AHQ-5-13-, 2625	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	8.50E-05	0.77	3.31	-	515.1
AHQ-5-5, 2401	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.48E-07	0.87	3.86	-	476.8
AHQ-5-2, 2731	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.63E-07	0.86	3.87	-	456.3
AHQ-5-1, 2899	K.VAQPTITDNKDGTVTVR.Y	1816.00621	3	4.68E-04	0.72	3.14	-	431.8
AHQ-5-5, 2567	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.29E-07	0.87	3.85	-	599.9
AHQ-5-1, 2893 - 2900	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.81E-07	0.91	4.33	-	613.2
AHQ-5-10, 2399	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.21E-04	0.85	3.64	-	564.0
AHQ-5-10, 2556 - 2559	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.04E-10	0.87	3.85	-	635.0
AHQ-5-4, 2514	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.82E-06	0.87	4.08	-	585.5
AHQ-5-12, 2738	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.95E-05	0.73	3.04	-	495.6
AHQ-5-3, 2794	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.96E-05	0.87	3.87	-	616.4
AHQ-5-8, 2230	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.02E-04	0.75	3.00	-	527.3
AHQ-5-11, 2676 - 2688	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	8.83E-04	0.82	3.63	-	435.4
AHQ-5-1, 3823	K.VDINTEDLEDGTCR.V	1638.69283	2	3.03E-07	0.89	3.14	-	980.2
AHQ-5-8, 3386 - 3396	K.VDINTEDLEDGTCR.V	1638.69283	2	1.44E-04	0.90	3.70	-	1062.5
AHQ-5-2, 3423	K.VDINTEDLEDGTCR.V	1638.69283	2	1.75E-04	0.89	3.90	-	765.4
AHQ-5-1, 3717	K.VDINTEDLEDGTCR.V	1638.69283	2	1.56E-06	0.96	4.82	-	1138.7
AHQ-5-7, 3434 - 3435	K.VDINTEDLEDGTCR.V	1638.69283	2	8.85E-07	0.92	3.78	-	1013.7
AHQ-5-5, 3422	K.VDINTEDLEDGTCR.V	1638.69283	2	2.56E-05	0.88	3.34	-	869.9
AHQ-5-4, 3644	K.VDINTEDLEDGTCR.V	1638.69283	2	9.28E-05	0.91	4.03	-	893.2

AHQ-5-1, 3439	K.VDINTEDLEDGTCR.V	1638.69283	2	1.95E-06	0.95	4.35	-	1195.6
AHQ-5-6, 3492	K.VDINTEDLEDGTCR.V	1638.69283	2	8.56E-07	0.94	4.00	-	1180.0
AHQ-5-5, 3545	K.VDINTEDLEDGTCR.V	1638.69283	2	7.25E-08	0.94	4.25	-	1104.4
AHQ-5-5, 3646 - 3721	K.VDINTEDLEDGTCR.V	1638.69283	2	1.36E-08	0.92	3.61	-	990.6
AHQ-5-3, 3670	K.VDINTEDLEDGTCR.V	1638.69283	2	7.88E-07	0.89	3.30	-	817.8
AHQ-5-4, 3788 - 3789	K.VDINTEDLEDGTCR.V	1638.69283	2	2.55E-09	0.93	3.89	-	1171.1
AHQ-5-3, 2463	K.VDVGKDQEFTVK.S	1365.51377	1	5.36E-04	0.50	3.21	-	319.7
AHQ-5-4, 2436	K.VDVGKDQEFTVK.S	1365.51377	2	1.36E-06	0.91	3.72	-	762.1
AHQ-5-2, 2413	K.VDVGKDQEFTVK.S	1365.51377	3	1.55E-04	0.62	3.07	-	425.0
AHQ-5-2, 2410	K.VDVGKDQEFTVK.S	1365.51377	1	6.60E-06	0.24	2.66	-	261.7
AHQ-5-2, 2401	K.VDVGKDQEFTVK.S	1365.51377	2	3.77E-08	0.91	3.99	-	678.2
AHQ-5-5, 2322	K.VDVGKDQEFTVK.S	1365.51377	2	9.82E-09	0.81	3.34	-	539.9
AHQ-5-6, 2312	K.VDVGKDQEFTVK.S	1365.51377	2	1.66E-09	0.87	3.72	-	576.3
AHQ-5-1, 2639	K.VDVGKDQEFTVK.S	1365.51377	2	8.74E-07	0.87	3.36	-	606.3
AHQ-5-4, 2442	K.VDVGKDQEFTVK.S	1365.51377	1	1.27E-06	0.49	3.06	-	327.8
AHQ-5-3, 2650 - 2674	K.VEPGLGADNSVVR.F	1313.44209	2	3.86E-09	0.75	2.65	-	245.3
AHQ-5-1, 2831	K.VEPGLGADNSVVR.F	1313.44209	1	8.26E-05	0.06	1.90	-	160.1
AHQ-5-2, 2577 - 2646	K.VEPGLGADNSVVR.F	1313.44209	2	2.94E-05	0.65	2.53	-	226.1
AHQ-5-1, 2792 - 2864	K.VEPGLGADNSVVR.F	1313.44209	2	4.27E-04	0.65	3.24	-	237.7
AHQ-5-3, 2646 - 2721	K.VEPGLGADNSVVR.F	1313.44209	1	7.33E-04	0.13	1.89	-	250.6
AHQ-5-2, 2587	K.VEPGLGADNSVVR.F	1313.44209	1	5.59E-05	0.47	2.38	-	254.7
AHQ-5-3, 6473 - 6541	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	6.50E-07	0.95	5.56	-	1060.7
AHQ-5-4, 6517	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	1.15E-05	0.93	5.42	-	681.2
AHQ-5-4, 6381 - 6448	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.94E-04	0.85	4.68	-	649.6
AHQ-5-2, 6381 - 6449	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.64E-06	0.96	6.16	-	1069.2
AHQ-5-7, 7266 - 7271	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	8.34E-06	0.92	4.62	-	634.3
AHQ-5-1, 7260 - 7327	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	3.03E-06	0.90	3.82	-	1007.6
AHQ-5-5, 7269	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	9.54E-05	0.44	2.52	-	304.0
AHQ-5-5, 7365	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	9.61E-04	0.83	4.07	-	519.4
AHQ-5-4, 7428	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	8.71E-05	0.64	2.74	-	540.4
AHQ-5-8, 7182	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	2.23E-04	0.63	3.01	-	316.6
AHQ-5-8, 7118 - 7193	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	3.71E-07	0.94	5.14	-	768.5
AHQ-5-6, 4161	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	7.73E-11	0.97	5.33	-	1588.4
AHQ-5-4, 4433 - 4440	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	2.99E-09	0.96	5.52	-	1216.1
AHQ-5-7, 4022	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	2.34E-06	0.96	4.78	-	1548.6
AHQ-5-5, 4209 - 4278	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.85E-07	0.97	5.41	-	1512.3
AHQ-5-1, 4567	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	1.88E-07	0.95	4.93	-	1789.3
AHQ-5-7, 4295	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	6.04E-08	0.94	4.24	-	1133.9
AHQ-5-3, 4838 - 4850	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	6.92E-06	0.93	4.90	-	799.3
AHQ-5-8, 4150	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	5.11E-04	0.89	3.24	-	1061.1
AHQ-5-8, 4144	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.78E-15	0.91	4.59	-	657.4
AHQ-5-1, 4880	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.64E-07	0.93	4.34	-	1167.6
AHQ-5-5, 4513 - 4591	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	6.98E-10	0.92	5.01	-	625.7
AHQ-5-5, 4518	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	4.25E-06	0.86	3.38	-	985.5
AHQ-5-7, 4294	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.06E-09	0.90	4.61	-	504.5
AHQ-5-4, 4794 - 4805	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	3.67E-13	0.94	4.27	-	1299.6
AHQ-5-6, 4485	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	2.33E-07	0.73	3.22	-	589.2
AHQ-5-6, 4472	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	4.90E-09	0.86	4.13	-	511.9
AHQ-5-9, 4020	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	2.89E-08	0.83	3.64	-	723.6
AHQ-5-4, 4772	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.94E-10	0.88	4.35	-	481.2
AHQ-5-5, 3701	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.06E-06	0.93	4.35	-	604.3
AHQ-5-1, 3997	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.53E-06	0.84	3.25	-	573.5
AHQ-5-1, 3852 - 3929	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.11E-09	0.89	4.27	-	481.6
AHQ-5-8, 3418 - 3420	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.76E-06	0.81	3.53	-	360.9
AHQ-5-4, 3816 - 3884	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.17E-08	0.88	3.76	-	644.4
AHQ-5-6, 3568	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.21E-07	0.88	3.52	-	634.1
AHQ-5-7, 3398	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.33E-07	0.89	3.66	-	639.0
AHQ-5-3, 3845 - 3925	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.85E-07	0.87	3.71	-	532.6
AHQ-5-8, 3289	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.06E-08	0.86	3.67	-	465.7
AHQ-5-2, 3731 - 3805	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.41E-08	0.87	3.32	-	613.6
AHQ-5-2, 1494	K.VPVHDVTDASK.V	1168.28175	2	2.72E-06	0.94	2.99	-	1447.1
AHQ-5-5, 1466	K.VPVHDVTDASK.V	1168.28175	2	3.81E-09	0.84	2.81	-	829.4
AHQ-5-2, 4293	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.12E-07	0.87	4.32	-	746.1
AHQ-5-1, 4248 - 4321	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.97E-06	0.97	5.05	-	1682.8
AHQ-5-2, 4121 - 4126	R.VQVQDNEGCPVEALVK.D	1786.98493	2	7.27E-06	0.96	5.37	-	1043.9
AHQ-5-3, 4354	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.52E-07	0.92	4.44	-	872.3
AHQ-5-5, 3982	R.VQVQDNEGCPVEALVK.D	1786.98493	2	5.10E-06	0.96	4.98	-	1124.6
AHQ-5-3, 4189 - 4197	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.60E-07	0.96	5.11	-	1066.8
AHQ-5-1, 4391 - 4436	R.VQVQDNEGCPVEALVK.D	1786.98493	2	2.03E-10	0.97	4.89	-	1528.7
AHQ-5-4, 4133	R.VQVQDNEGCPVEALVK.D	1786.98493	2	5.81E-06	0.93	4.66	-	790.5
AHQ-5-4, 4234 - 4305	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.25E-09	0.91	4.24	-	874.6
AHQ-5-2, 5461	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.76E-06	0.87	3.65	-	1088.2
AHQ-5-1, 5367 - 5435	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	5.43E-09	0.95	4.79	-	1919.9
AHQ-5-1, 4913 - 4923	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.99E-10	0.97	6.03	-	1564.6
AHQ-5-2, 4698 - 4759	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	7.04E-08	0.96	5.77	-	1311.7
AHQ-5-3, 4845	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	7.59E-04	0.82	3.09	-	692.3
AHQ-5-4, 4748 - 4820	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	8.47E-05	0.92	4.42	-	704.8
AHQ-5-4, 4720 - 4788	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.94E-07	0.94	5.18	-	969.7
AHQ-5-3, 4851	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.64E-06	0.93	5.07	-	945.7
AHQ-5-6, 4417 - 4465	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	6.86E-05	0.94	4.76	-	1076.6
AHQ-5-12, 4620	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	2.90E-04	0.87	3.95	-	615.2
AHQ-5-5, 4423 - 4494	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	3.09E-10	0.98	6.91	-	1079.2
AHQ-5-8, 3873	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	3.25E-07	0.93	4.76	-	1023.9
AHQ-5-9, 3951	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.65E-04	0.92	4.43	-	859.7
AHQ-5-5, 4405 - 4477	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	5.09E-06	0.93	4.86	-	957.9
AHQ-5-1, 4915	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	7.43E-07	0.94	4.50	-	955.1
AHQ-5-7, 2402	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.08E-04	0.37	2.60	-	297.5
AHQ-5-2, 2538 - 2569	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.11E-05	0.86	3.69	-	593.5
AHQ-5-6, 2592	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.68E-04	0.52	2.76	-	379.3
AHQ-5-3, 2810	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	6.30E-07	0.75	3.26	-	588.4
AHQ-5-2, 2713 - 2786	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.39E-04	0.91	4.36	-	617.1
AHQ-5-5, 2469 - 2473	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.25E-04	0.77	3.69	-	467.8
AHQ-5-13-, 2701	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	9.09E-04	0.65	2.73	-	641.2
AHQ-5-5, 2607 - 2610	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.29E-07	0.81	4.01	-	468.8
AHQ-5-1, 2767 - 2912	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	9.37E-06	0.90	4.36	-	571.7
AHQ-5-4, 2728	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.24E-09	0.70	3.15	-	347.1
AHQ-5-1, 3272	K.VTVLFAGQHIAK.S	1284.53185	1	1.75E-04	0.66	2.84	-	475.7
AHQ-5-2, 2911	K.VTVLFAGQHIAK.S	1284.53185	1	6.89E-04	0.65	3.11	-	469.9
AHQ-5-4, 3020	K.VTVLFAGQHIAK.S	1284.53185	2	2.16E-04	0.82	3.12	-	660.4
AHQ-5-2, 2905 - 2981	K.VTVLFAGQHIAK.S	1284.53185	2	2.57E-06	0.94	4.05	-	1104.8
AHQ-5-5, 2773 - 2794	K.VTVLFAGQHIAK.S	1284.53185	2	7.97E-06	0.94	3.98	-	1091.3
AHQ-5-6, 2817 - 2829	K.VTVLFAGQHIAK.S	1284.53185	1	7.67E-04	0.45	2.55	-	452.1
AHQ-5-6, 2810	K.VTVLFAGQHIAK.S	1284.53185	2	5.50E-06	0.89	3.54	-	799.7
AHQ-5-7, 2647 - 2652	K.VTVLFAGQHIAK.S	1284.53185	1	1.43E-04	0.58	2.66	-	459.2
AHQ-5-1, 3252	K.VTVLFAGQHIAK.S	1284.53185	2	3.54E-07	0.93	3.91	-	891.3
AHQ-5-5, 5166	R.VTYCPTEPGNYIINIK.F	1884.14221	2	8.19E-11	0.89	4.04	-	493.4
AHQ-5-3, 5090	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.85E-05	0.88	3.42	-	614.9

AHQ-5-5, 4842 - 4913	R.VTYCPTEPGNYIINIK.F	1884.14221	2	9.53E-07	0.83	3.45	-	421.7
AHQ-5-4, 5136 - 5142	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.49E-04	0.93	4.65	-	452.0
AHQ-5-3, 5203	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.76E-05	0.77	3.30	-	301.2
AHQ-5-4, 5340	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.49E-06	0.74	3.04	-	368.0
AHQ-5-1, 5204 - 5284	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.26E-06	0.90	3.99	-	530.7
AHQ-5-2, 5134	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.88E-05	0.76	3.31	-	350.7
AHQ-5-5, 4981	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.77E-05	0.94	4.24	-	691.6
AHQ-5-8, 4606 - 4673	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.06E-04	0.92	4.23	-	499.4
AHQ-5-1, 5052	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.25E-04	0.53	2.96	-	221.3
AHQ-5-4, 5064	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	2.15E-04	0.85	3.03	-	671.8
AHQ-5-3, 5629	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.10E-04	0.77	3.10	-	655.1
AHQ-5-14, 6084	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	9.14E-05	0.76	3.25	-	450.5
AHQ-5-4, 5586 - 5592	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.89E-05	0.87	3.64	-	606.0
AHQ-5-13, 5433 - 5436	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.52E-05	0.90	3.44	-	939.4
AHQ-5-13-, 5343	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.90E-07	0.80	3.27	-	529.1
AHQ-5-1, 5703 - 5705	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.02E-04	0.89	3.47	-	693.8
AHQ-5-5, 5310 - 5349	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.23E-04	0.94	3.81	-	1118.9
AHQ-5-8, 4881	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.98E-04	0.84	3.56	-	602.9
AHQ-5-9, 4614 - 4695	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.54E-04	0.52	2.67	-	427.7
AHQ-5-2, 5549	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.48E-04	0.81	3.46	-	452.0
AHQ-5-10, 4812	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	9.63E-05	0.78	3.19	-	468.9
AHQ-5-6, 5320 - 5332	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.37E-04	0.81	3.16	-	630.1
AHQ-5-7, 5138 - 5139	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.30E-05	0.59	2.79	-	341.0
AHQ-5-14-, 4829 - 4831	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	3.06E-04	0.80	3.37	-	450.3
AHQ-5-13, 3465	R.YAPSEAGLHEMDIR.Y	1589.75482	2	4.83E-04	0.87	2.81	-	1018.0
AHQ-5-10, 3022	R.YAPSEAGLHEMDIR.Y	1589.75482	2	3.19E-05	0.88	3.11	-	887.1
AHQ-5-5, 3047 - 3117	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.19E-05	0.91	4.04	-	664.7
AHQ-5-11, 3190	R.YAPSEAGLHEMDIR.Y	1589.75482	2	3.45E-04	0.88	3.11	-	1034.0
AHQ-5-4, 2529 - 2530	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	5.04E-04	0.79	2.54	-	901.2
AHQ-5-1, 2739	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	1.34E-04	0.77	2.71	-	731.9
AHQ-5-4, 3306 - 3349	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.12E-06	0.94	3.67	-	1183.3
AHQ-5-7, 2946	R.YAPSEAGLHEMDIR.Y	1589.75482	2	6.47E-04	0.64	2.70	-	611.7
AHQ-5-1, 4392 - 4463	K.YGGDEIPFSPYR.V	1401.50466	2	7.19E-05	0.80	3.24	-	562.0
AHQ-5-2, 4274	K.YGGDEIPFSPYR.V	1401.50466	1	2.48E-06	0.46	2.62	-	422.9
AHQ-5-2, 4259 - 4329	K.YGGDEIPFSPYR.V	1401.50466	2	1.79E-04	0.84	3.78	-	583.5
AHQ-5-3, 4353	K.YGGDEIPFSPYR.V	1401.50466	1	3.93E-06	0.17	2.34	-	344.6
AHQ-5-1, 4397 - 4401	K.YGGDEIPFSPYR.V	1401.50466	1	4.28E-04	0.29	2.40	-	440.5
AHQ-5-4, 3225 - 3228	K.YGGPYHIGGSPFK.A	1380.53182	1	1.92E-04	0.78	2.88	-	531.0
AHQ-5-3, 3263	K.YGGPYHIGGSPFK.A	1380.53182	2	1.75E-10	0.97	4.41	-	1909.2
AHQ-5-4, 3240	K.YGGPYHIGGSPFK.A	1380.53182	3	1.14E-05	0.86	3.64	-	664.9
AHQ-5-5, 3062	K.YGGPYHIGGSPFK.A	1380.53182	2	7.56E-09	0.96	4.53	-	1469.2
AHQ-5-2, 3178	K.YGGPYHIGGSPFK.A	1380.53182	2	4.95E-05	0.94	4.04	-	1047.0
AHQ-5-8, 2724 - 2746	K.YGGPYHIGGSPFK.A	1380.53182	1	1.51E-04	0.70	2.65	-	464.7
AHQ-5-9, 2796	K.YGGPYHIGGSPFK.A	1380.53182	2	1.14E-07	0.94	3.87	-	1217.5
AHQ-5-5, 3023	K.YGGPYHIGGSPFK.A	1380.53182	3	2.09E-07	0.87	3.85	-	678.0
AHQ-5-5, 3006	K.YGGPYHIGGSPFK.A	1380.53182	1	7.46E-09	0.88	4.05	-	430.8
AHQ-5-5, 2927 - 2993	K.YGGPYHIGGSPFK.A	1380.53182	2	1.49E-08	0.96	3.75	-	1785.3
AHQ-5-1, 3388	K.YGGPYHIGGSPFK.A	1380.53182	2	5.00E-08	0.96	3.76	-	1864.9
AHQ-5-11, 3120	K.YGGPYHIGGSPFK.A	1380.53182	2	4.35E-09	0.97	4.16	-	2358.7
AHQ-5-7, 2874	K.YGGPYHIGGSPFK.A	1380.53182	1	2.48E-06	0.77	3.26	-	408.2
AHQ-5-4, 3221 - 3229	K.YGGPYHIGGSPFK.A	1380.53182	2	1.65E-12	0.97	4.40	-	2017.2
AHQ-5-1, 3256	K.YGGQPVPNFPSK.L	1291.43658	2	5.02E-04	0.78	3.11	-	404.0
AHQ-5-1, 3096 - 3163	K.YGGQPVPNFPSK.L	1291.43658	2	5.84E-05	0.91	3.18	-	702.2
AHQ-5-6, 2776 - 2802	K.YGGQPVPNFPSK.L	1291.43658	2	1.81E-04	0.83	2.64	-	568.1
AHQ-5-2, 2918 - 2989	K.YGGQPVPNFPSK.L	1291.43658	2	2.00E-04	0.87	3.29	-	431.9
AHQ-5-4, 2961	K.YGGQPVPNFPSK.L	1291.43658	2	9.84E-05	0.92	3.51	-	546.5
AHQ-5-2, 2922	K.YGGQPVPNFPSK.L	1291.43658	2	2.41E-07	0.90	3.63	-	515.3
AHQ-5-3, 2991 - 2993	K.YGGQPVPNFPSK.L	1291.43658	2	7.72E-05	0.92	3.71	-	598.9
AHQ-5-6, 3848	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	4.06E-05	0.76	3.25	-	700.7
AHQ-5-3, 4319	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.70E-07	0.88	4.34	-	715.9
AHQ-5-4, 4182	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.34E-07	0.88	4.15	-	797.6
AHQ-5-1, 4440 - 4507	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.27E-04	0.79	3.80	-	476.5
AHQ-5-5, 3910 - 3913	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	4.01E-06	0.84	4.32	-	584.3
AHQ-5-7, 3639 - 3718	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.84E-04	0.79	3.44	-	787.8
AHQ-5-1, 4456	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	2	1.70E-04	0.84	3.78	-	415.0
AHQ-5-8, 2260	K.YNEQHVPGSPFTAR.V	1603.71978	2	9.22E-05	0.78	3.32	-	312.2
AHQ-5-13-, 2845	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.10E-06	0.46	2.57	-	327.4
AHQ-5-2, 2986 - 2995	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.40E-05	0.84	3.45	-	432.6
AHQ-5-1, 2908	K.YNEQHVPGSPFTAR.V	1603.71978	3	2.40E-06	0.90	4.18	-	1019.0
AHQ-5-4, 2677 - 2692	K.YNEQHVPGSPFTAR.V	1603.71978	2	3.25E-07	0.87	3.34	-	583.7
AHQ-5-7, 2479	K.YNEQHVPGSPFTAR.V	1603.71978	2	8.32E-05	0.65	3.10	-	390.0
AHQ-5-1, 2896 - 2897	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.43E-08	0.88	3.51	-	484.0
AHQ-5-3, 2729 - 2730	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.89E-07	0.67	2.73	-	428.3
AHQ-5-1, 3173 - 3175	K.YNEQHVPGSPFTAR.V	1603.71978	2	4.75E-06	0.93	3.61	-	716.0
AHQ-5-5, 2522 - 2537	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.07E-05	0.88	3.51	-	599.1
AHQ-5-5, 2531	K.YNEQHVPGSPFTAR.V	1603.71978	3	3.78E-07	0.94	4.24	-	1391.7
AHQ-5-10, 2538 - 2540	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.61E-05	0.85	3.10	-	601.9
AHQ-5-2, 2655 - 2666	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.70E-07	0.90	3.73	-	600.8
AHQ-5-6, 2556	K.YNEQHVPGSPFTAR.V	1603.71978	2	8.68E-08	0.92	4.64	-	513.3
AHQ-5-2, 4638 - 4689	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.37E-06	0.92	4.59	-	656.6
AHQ-5-2, 4577 - 4621	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.42E-06	0.88	4.14	-	535.7
AHQ-5-2, 4426 - 4437	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.19E-08	0.90	4.23	-	703.5
AHQ-5-2, 4781 - 4794	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.71E-10	0.95	4.60	-	1028.0
AHQ-5-6, 4418 - 4424	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.74E-06	0.93	4.15	-	863.1
AHQ-5-4, 4633 - 4710	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.14E-05	0.95	4.96	-	769.0
AHQ-5-3, 4774 - 4847	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.32E-10	0.96	5.01	-	1095.4
AHQ-5-9, 3971	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.83E-04	0.85	3.72	-	582.5
AHQ-5-3, 4485	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	9.98E-05	0.88	3.85	-	705.2
AHQ-5-7, 4270	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.01E-07	0.94	4.45	-	846.5
AHQ-5-5, 4475 - 4487	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.01E-05	0.90	4.43	-	614.2
AHQ-5-3, 4635 - 4706	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.59E-06	0.94	4.69	-	891.4
AHQ-5-8, 4141 - 4142	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.12E-07	0.92	4.62	-	607.1
AHQ-5-1, 4655 - 4719	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.90E-06	0.89	3.99	-	709.2
AHQ-5-1, 4829 - 4899	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.14E-10	0.94	4.82	-	814.1
AHQ-5-1, 6499 - 6579	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.50E-09	0.92	4.34	-	863.9
AHQ-5-1, 6715	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	1.71E-09	0.70	3.06	-	440.1
AHQ-5-1, 6844 - 6907	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	4.61E-05	0.93	3.95	-	947.7
AHQ-5-2, 6441 - 6469	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	4.12E-09	0.87	2.71	-	1204.5
AHQ-5-2, 6711	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.03E-05	0.87	3.61	-	811.6
AHQ-5-2, 6751 - 6829	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.17E-09	0.94	4.32	-	866.1
AHQ-5-2, 6819 - 6885	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	3.21E-09	0.68	3.01	-	402.8
AHQ-5-2, 6898	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.78E-10	0.95	5.09	-	829.7
AHQ-5-3, 6533 - 6550	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.31E-10	0.91	3.81	-	971.2
AHQ-5-3, 6901 - 6975	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	4.86E-11	0.73	3.26	-	475.0
AHQ-5-4, 6536	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.91E-04	0.84	3.46	-	809.8
AHQ-5-4, 6861 - 6889	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	2.37E-06	0.95	4.60	-	966.2
AHQ-5-3, 6889 - 6958	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	2.88E-04	0.64	3.22	-	413.1

gi|13124879|ref|NP_002465.1| smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]				5.55E-15	7.72	100.35	5.10	227336.7
AHQ-5-2, 4897	R.DLGEELEALK.T	1117.23151	2	8.67E-07	0.93	3.65	-	981.8
AHQ-5-1, 4952	R.DLGEELEALK.T	1117.23151	2	1.43E-04	0.84	3.19	-	683.7
AHQ-5-3, 4951	R.DLGEELEALK.T	1117.23151	1	1.00E-04	0.31	2.72	-	358.0
AHQ-5-6, 2622 - 2626	R.EDQSILCTGESGAGK.T	1553.63107	2	6.07E-04	0.84	3.58	-	499.5
AHQ-5-1, 2955	K.FDQLLAEEK.N	1093.21165	2	3.79E-05	0.91	3.11	-	1399.8
AHQ-5-2, 2737	K.FDQLLAEEK.N	1093.21165	1	2.04E-06	0.57	2.40	-	761.9
AHQ-5-2, 2734 - 2755	K.FDQLLAEEK.N	1093.21165	2	2.63E-05	0.89	3.23	-	1273.1
AHQ-5-2, 2729	K.FDQLLAEEK.N	1093.21165	1	4.74E-04	0.79	2.54	-	1129.2
AHQ-5-1, 2924 - 2951	K.FDQLLAEEK.N	1093.21165	1	2.11E-05	0.64	2.07	-	985.5
AHQ-5-4, 2609	R.KFDQLLAEEK.N	1221.38456	2	4.28E-04	0.90	3.32	-	1138.1
AHQ-5-6, 2464	R.KFDQLLAEEK.N	1221.38456	1	6.94E-06	0.55	1.97	-	767.1
AHQ-5-1, 6208	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.38E-07	0.98	6.24	-	2982.7
AHQ-5-1, 6215	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	1.81E-08	0.97	5.15	-	1740.1
AHQ-5-5, 6202 - 6266	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	6.43E-05	0.72	2.85	-	709.8
AHQ-5-3, 6179	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	2.32E-04	0.81	3.64	-	924.4
AHQ-5-1, 5523	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	7.61E-06	0.88	2.77	-	1213.7
AHQ-5-2, 5267	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	2.04E-07	0.99	6.79	-	3673.5
AHQ-5-2, 5406 - 5407	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	9.01E-07	0.89	3.78	-	882.5
AHQ-5-4, 6126	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	3.07E-07	0.90	2.87	-	1183.5
AHQ-5-2, 6397	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	5.74E-12	0.98	5.93	-	2777.0
AHQ-5-2, 6395 - 6471	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	4.24E-11	0.98	5.49	-	2214.2
AHQ-5-2, 6054 - 6134	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	2.30E-07	0.97	4.92	-	1872.0
AHQ-5-2, 6057 - 6126	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	6.97E-08	0.98	6.70	-	3099.8
AHQ-5-2, 6161 - 6206	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	6.68E-09	0.95	4.54	-	1381.9
AHQ-5-2, 6171	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	5.55E-15	0.98	6.48	-	2500.6
AHQ-5-2, 6263	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	2.99E-11	0.99	6.91	-	3477.8
AHQ-5-2, 2535	R.NCAAYLK.L	840.96726	1	2.86E-04	0.56	1.96	-	739.6
AHQ-5-3, 4555	R.NWQWWR.L	976.07459	1	1.95E-04	0.35	2.09	-	191.4
AHQ-5-2, 6458 - 6461	K.QLLQANPILEAFGNAK.T	1727.98540	2	7.80E-07	0.95	4.29	-	1140.3
AHQ-5-6, 6288	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.15E-05	0.90	4.15	-	675.0
AHQ-5-7, 5926 - 5935	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.67E-06	0.94	4.46	-	921.8
AHQ-5-9, 5371	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.78E-04	0.81	3.43	-	573.6
AHQ-5-6, 6112 - 6114	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.91E-09	0.94	4.16	-	839.3
AHQ-5-1, 6393 - 6463	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.63E-10	0.96	4.74	-	948.9
AHQ-5-5, 6139 - 6201	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.48E-04	0.96	4.53	-	1211.5
AHQ-5-4, 6376 - 6396	K.QLLQANPILEAFGNAK.T	1727.98540	2	6.32E-12	0.97	5.35	-	1063.5
AHQ-5-3, 6410 - 6429	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.30E-08	0.96	4.54	-	1150.2
AHQ-5-2, 6235 - 6317	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.96E-10	0.96	4.93	-	1136.1
AHQ-5-1, 6557	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.79E-04	0.81	3.04	-	690.8
AHQ-5-10, 5520 - 5538	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.83E-05	0.97	4.67	-	1536.5
AHQ-5-4, 5825 - 5829	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.53E-06	0.98	6.12	-	1567.6
AHQ-5-2, 4077	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.88E-10	0.96	5.41	-	1247.3
AHQ-5-5, 5619 - 5689	K.TQLEELEDELQATEDAK.L	1963.04334	2	7.37E-08	0.98	6.86	-	2062.3
AHQ-5-3, 5897	K.TQLEELEDELQATEDAK.L	1963.04334	3	3.74E-05	0.95	4.94	-	1165.1
AHQ-5-3, 5877 - 5901	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.85E-06	0.98	6.16	-	1992.5
AHQ-5-1, 5925	K.TQLEELEDELQATEDAK.L	1963.04334	3	2.20E-09	0.96	5.23	-	1340.6
AHQ-5-1, 5915 - 5919	K.TQLEELEDELQATEDAK.L	1963.04334	2	3.66E-06	0.98	6.33	-	2813.6
AHQ-5-6, 5602	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.27E-11	0.98	6.56	-	2295.0
AHQ-5-2, 5797 - 5878	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.88E-04	0.98	6.15	-	2456.3
AHQ-5-3, 4110	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.39E-04	0.84	3.77	-	644.6
AHQ-5-2, 5826	K.TQLEELEDELQATEDAK.L	1963.04334	3	8.24E-09	0.94	5.00	-	996.4
AHQ-5-2, 5887 - 5953	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.56E-04	0.92	3.85	-	1208.4
AHQ-5-4, 5861	K.TQLEELEDELQATEDAK.L	1963.04334	3	4.42E-04	0.93	4.83	-	1209.3
gi|4826898|ref|NP_005013.1| profilin 1; profilin-1 [Homo sapiens]				7.22E-15	17.77	210.32	71.40	15054.2
AHQ-5-13-, 4899	K.CSVIRDSLLQDGEFSM*DLR.T	2259.50329	3	3.22E-07	0.96	5.79	-	1516.7
AHQ-5-13-, 5528 - 5588	K.CSVIRDSLLQDGEFSMDLR.T	2243.50389	3	4.21E-05	0.95	4.50	-	1706.0
AHQ-5-13-, 4991	K.CSVIRDSLLQDGEFSM*DLR.T	2259.50329	3	4.63E-04	0.82	3.67	-	869.2
AHQ-5-13-, 1653 - 1711	K.CYEM*ASHLR.R	1184.32794	2	6.68E-05	0.86	2.53	-	1278.8
AHQ-5-13-, 1687 - 1767	K.CYEM*ASHLR.R	1184.32794	2	3.05E-06	0.93	3.59	-	1063.4
AHQ-5-13-, 1823 - 1892	K.CYEM*ASHLR.R	1184.32794	2	2.34E-05	0.94	3.83	-	1124.4
AHQ-5-13-, 2039	K.CYEM*ASHLR.R	1184.32794	2	4.18E-05	0.86	2.94	-	1031.5
AHQ-5-13-, 2295 - 2371	K.CYEMASHLR.R	1168.32854	2	4.75E-05	0.96	3.97	-	1969.9
AHQ-5-13-, 2379 - 2500	K.CYEMASHLR.R	1168.32854	1	2.10E-06	0.53	2.98	-	237.9
AHQ-5-13-, 2383 - 2443	K.CYEMASHLR.R	1168.32854	2	5.16E-04	0.95	3.26	-	1855.2
AHQ-5-13-, 2467 - 2533	K.CYEMASHLR.R	1168.32854	2	2.69E-04	0.93	2.54	-	1870.8
AHQ-5-14-, 2341	K.CYEMASHLR.R	1168.32854	2	3.15E-05	0.95	3.31	-	1742.6
AHQ-5-13, 2057 - 2118	K.CYEM*ASHLR.R	1184.32794	2	2.50E-05	0.91	3.26	-	1370.7
AHQ-5-13, 2601 - 2617	K.CYEMASHLR.R	1168.32854	2	2.87E-06	0.97	3.80	-	2092.3
AHQ-5-13-, 4183	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	4.29E-06	0.96	5.00	-	1157.4
AHQ-5-13, 4148 - 4150	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.31E-10	0.97	5.29	-	1293.3
AHQ-5-13-, 4055 - 4119	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	2.16E-10	0.97	5.62	-	1151.8
AHQ-5-12, 4049	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	7.22E-15	0.97	4.86	-	1295.6
AHQ-5-13, 4281	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.09E-09	0.96	5.86	-	859.1
AHQ-5-12, 5666 - 5689	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.96E-04	0.88	3.72	-	622.4
AHQ-5-12, 5782 - 5860	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.15E-11	0.90	3.73	-	1034.7
AHQ-5-13-, 4827 - 4903	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.03E-10	0.97	4.66	-	1919.0
AHQ-5-13-, 4691 - 4755	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.42E-08	0.97	4.82	-	2103.5
AHQ-5-13-, 4636	R.DSLLQDGEFSM*DLR.T	1642.76963	3	4.29E-07	0.96	4.93	-	1899.0
AHQ-5-13-, 4563 - 4628	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.33E-07	0.95	4.02	-	1766.3
AHQ-5-12, 5576 - 5613	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.62E-07	0.95	4.31	-	1360.1
AHQ-5-13-, 4449 - 4515	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.94E-11	0.96	4.68	-	1260.7
AHQ-5-12, 5448 - 5524	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.47E-04	0.88	3.98	-	753.9
AHQ-5-13-, 4343	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.21E-07	0.93	3.77	-	1074.8
AHQ-5-12, 5306 - 5385	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.83E-09	0.96	4.48	-	1548.5
AHQ-5-12, 4690 - 4725	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.06E-08	0.95	3.73	-	1719.4
AHQ-5-13-, 5791 - 5872	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.42E-05	0.94	3.17	-	1699.3
AHQ-5-12, 4581 - 4582	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.77E-07	0.93	4.06	-	1020.4
AHQ-5-13-, 5091 - 5092	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.44E-09	0.96	4.62	-	1450.2
AHQ-5-13-, 5189 - 5271	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.99E-10	0.94	4.12	-	1387.1
AHQ-5-13-, 5205 - 5287	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.86E-09	0.91	3.59	-	1029.4
AHQ-5-13-, 5381 - 5443	R.DSLLQDGEFSMDLR.T	1626.77023	2	6.98E-06	0.98	5.25	-	2043.5
AHQ-5-13-, 5387 - 5456	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.93E-04	0.95	3.88	-	1899.7
AHQ-5-13-, 5393	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.92E-06	0.97	4.11	-	2274.8
AHQ-5-13-, 5473 - 5539	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.72E-05	0.93	3.07	-	1631.1
AHQ-5-14-, 4578 - 4595	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.69E-07	0.96	4.69	-	1567.3
AHQ-5-14, 5417	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.72E-05	0.95	3.73	-	1575.5
AHQ-5-13, 6906	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.10E-05	0.94	3.59	-	1478.0
AHQ-5-13, 6658	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.46E-10	0.92	3.75	-	1155.5
AHQ-5-13, 6502 - 6562	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.70E-06	0.95	4.30	-	1596.5
AHQ-5-13, 6209 - 6282	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.69E-09	0.95	3.80	-	2004.3
AHQ-5-13, 6053 - 6129	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.15E-04	0.93	3.11	-	1588.9
AHQ-5-13-, 6120	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.93E-05	0.96	4.06	-	1675.0
AHQ-5-14-, 5333 - 5413	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.23E-09	0.97	3.99	-	2064.9
AHQ-5-13, 5462 - 5541	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.60E-07	0.94	3.32	-	1906.5
AHQ-5-13, 5932 - 5992	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.81E-05	0.93	3.32	-	1783.1
AHQ-5-13, 5676 - 5744	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.20E-09	0.97	4.61	-	1771.3

AHQ-5-13, 5548 - 5613	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.75E-10	0.98	4.67	-	2609.7
AHQ-5-13-, 5571 - 5607	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.90E-09	0.98	5.38	-	1805.4
AHQ-5-13, 4549 - 4613	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.41E-08	0.95	4.07	-	1230.7
AHQ-5-13, 5448 - 5486	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.90E-11	0.97	5.30	-	1704.7
AHQ-5-13, 4676 - 4740	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.85E-09	0.96	4.00	-	1888.3
AHQ-5-13, 4780 - 4844	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.71E-07	0.95	4.00	-	1692.5
AHQ-5-13, 4929 - 4982	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.84E-08	0.96	5.03	-	1588.2
AHQ-5-13, 5329 - 5393	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.12E-04	0.84	3.15	-	1166.8
AHQ-5-13, 5050 - 5120	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.08E-05	0.95	4.43	-	1552.0
AHQ-5-13, 5146 - 5210	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.03E-06	0.94	4.09	-	1354.8
AHQ-5-13, 5249 - 5324	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.75E-10	0.97	4.84	-	1589.4
AHQ-5-13, 5310 - 5384	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.09E-10	0.97	4.75	-	1701.5
AHQ-5-13-, 4217	R.DSLLQDGEFSM*DLRTK.S	1872.04688	2	8.56E-04	0.71	3.19	-	340.2
AHQ-5-13, 3615 - 3689	K.DSPSVWAAVPGK.T	1214.35211	2	1.21E-07	0.92	3.78	-	978.8
AHQ-5-13-, 3663 - 3741	K.DSPSVWAAVPGK.T	1214.35211	2	1.05E-05	0.89	3.50	-	924.3
AHQ-5-13, 3932 - 3993	K.DSPSVWAAVPGK.T	1214.35211	2	1.40E-05	0.80	2.75	-	943.3
AHQ-5-13, 3735 - 3796	K.DSPSVWAAVPGK.T	1214.35211	2	8.46E-04	0.90	3.32	-	1051.5
AHQ-5-13, 3469	K.DSPSVWAAVPGK.T	1214.35211	2	2.20E-05	0.87	3.11	-	923.6
AHQ-5-13-, 3495 - 3620	K.DSPSVWAAVPGK.T	1214.35211	1	6.69E-04	0.27	2.54	-	297.3
AHQ-5-12, 3545 - 3578	K.DSPSVWAAVPGK.T	1214.35211	2	8.61E-08	0.93	3.15	-	1390.7
AHQ-5-13-, 3491 - 3555	K.DSPSVWAAVPGK.T	1214.35211	2	6.39E-05	0.90	3.73	-	885.3
AHQ-5-13, 2355	K.KCYEMASHLR.R	1296.50145	2	2.93E-04	0.80	2.56	-	1097.6
AHQ-5-13, 4322 - 4384	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.03E-08	0.94	4.11	-	790.0
AHQ-5-13, 4324 - 4388	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.68E-06	0.69	2.89	-	449.3
AHQ-5-13, 4432 - 4506	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.68E-08	0.96	4.24	-	1276.1
AHQ-5-13, 4476 - 4673	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.53E-05	0.48	2.51	-	382.8
AHQ-5-14-, 4473	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.15E-07	0.95	3.33	-	1442.2
AHQ-5-12, 4289	R.SSFYVNGLTLGGQK.C	1471.63957	1	6.20E-11	0.44	2.14	-	397.6
AHQ-5-12, 4461 - 4528	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.46E-08	0.77	3.02	-	637.8
AHQ-5-13, 4660 - 4724	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.05E-05	0.68	2.57	-	599.3
AHQ-5-14-, 4423 - 4554	R.SSFYVNGLTLGGQK.C	1471.63957	1	4.48E-06	0.51	2.55	-	416.8
AHQ-5-13-, 4225 - 4701	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.10E-07	0.68	2.94	-	425.2
AHQ-5-14, 5113 - 5126	R.SSFYVNGLTLGGQK.C	1471.63957	2	5.28E-04	0.91	3.78	-	757.3
AHQ-5-14, 5128	R.SSFYVNGLTLGGQK.C	1471.63957	1	7.09E-08	0.50	2.04	-	512.1
AHQ-5-14, 5282 - 5362	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.31E-06	0.70	2.68	-	499.7
AHQ-5-13-, 4439 - 4511	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.49E-06	0.97	4.78	-	1440.4
AHQ-5-13-, 4220 - 4293	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.01E-08	0.96	4.56	-	1201.3
AHQ-5-14-, 4238	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.72E-10	0.75	2.71	-	548.1
AHQ-5-13-, 4347 - 4415	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.49E-05	0.93	3.79	-	957.2
AHQ-5-14-, 4237 - 4257	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.83E-08	0.95	4.22	-	1154.5
AHQ-5-13-, 4852	R.SSFYVNGLTLGGQKCSVIR.D	2088.37322	2	6.57E-04	0.23	2.82	-	204.6
AHQ-5-13, 4937 - 5014	R.SSFYVNGLTLGGQKCSVIR.D	2088.37322	2	5.29E-04	0.75	3.72	-	414.5
AHQ-5-13, 3066 - 3125	K.STGGAPTFNVTVTK.T	1380.52843	2	2.63E-07	0.87	3.54	-	516.8
AHQ-5-13, 3098	K.STGGAPTFNVTVTK.T	1380.52843	1	3.10E-05	0.50	2.61	-	441.6
AHQ-5-13, 3189 - 3399	K.STGGAPTFNVTVTK.T	1380.52843	1	9.89E-04	0.63	2.75	-	418.9
AHQ-5-13, 3278 - 3341	K.STGGAPTFNVTVTK.T	1380.52843	2	2.47E-07	0.65	2.70	-	461.6
AHQ-5-13, 3401 - 3473	K.STGGAPTFNVTVTK.T	1380.52843	2	2.98E-09	0.79	3.05	-	399.8
AHQ-5-14, 3912	K.STGGAPTFNVTVTK.T	1380.52843	1	1.14E-04	0.20	2.39	-	332.6
AHQ-5-13-, 2948 - 3013	K.STGGAPTFNVTVTK.T	1380.52843	2	4.75E-09	0.91	4.38	-	501.2
AHQ-5-13-, 2952 - 3380	K.STGGAPTFNVTVTK.T	1380.52843	1	4.00E-04	0.31	2.52	-	276.9
AHQ-5-13-, 3080	K.STGGAPTFNVTVTK.T	1380.52843	2	1.85E-05	0.74	3.04	-	405.4
AHQ-5-13-, 3179 - 3245	K.STGGAPTFNVTVTK.T	1380.52843	2	5.39E-09	0.81	3.12	-	480.0
AHQ-5-13-, 3307 - 3384	K.STGGAPTFNVTVTK.T	1380.52843	2	2.05E-09	0.77	3.33	-	309.8
AHQ-5-12, 3052	K.STGGAPTFNVTVTK.T	1380.52843	2	3.10E-07	0.87	3.38	-	449.4
AHQ-5-12, 3048	K.STGGAPTFNVTVTK.T	1380.52843	1	4.77E-05	0.39	2.45	-	422.7
AHQ-5-12, 3046 - 3126	K.STGGAPTFNVTVTK.T	1380.52843	2	4.01E-05	0.68	2.80	-	354.2
AHQ-5-12, 2978 - 3029	K.STGGAPTFNVTVTK.T	1380.52843	1	5.97E-04	0.57	2.46	-	513.0
AHQ-5-12, 2913 - 2982	K.STGGAPTFNVTVTK.T	1380.52843	2	2.09E-05	0.81	3.09	-	485.6
AHQ-5-13, 3537	K.STGGAPTFNVTVTK.T	1380.52843	2	6.25E-06	0.67	2.87	-	401.6
AHQ-5-14-, 3042	K.STGGAPTFNVTVTK.T	1380.52843	1	3.28E-04	0.51	2.91	-	481.7
AHQ-5-13, 3129	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	1.02E-04	0.92	3.98	-	712.6
AHQ-5-13, 2981	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	5.21E-05	0.84	3.52	-	497.9
AHQ-5-13-, 2859 - 2863	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	4.23E-04	0.89	3.92	-	620.1
AHQ-5-13-, 2875 - 2887	K.TDKTLVLLM*GK.E	1235.51929	2	1.23E-04	0.93	3.79	-	1029.0
AHQ-5-13-, 3449 - 3515	K.TDKTLVLLMGK.E	1219.51989	2	5.00E-09	0.95	4.31	-	1243.3
AHQ-5-13, 3567 - 3645	K.TDKTLVLLMGK.E	1219.51989	2	1.03E-08	0.96	4.41	-	1309.4
AHQ-5-13, 2931 - 3007	K.TDKTLVLLM*GK.E	1235.51929	2	6.46E-04	0.91	3.49	-	927.2
AHQ-5-13-, 5763 - 5823	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.10E-05	0.93	4.08	-	1035.8
AHQ-5-12, 5892 - 5964	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.18E-07	0.91	4.17	-	750.2
AHQ-5-12, 5837	K.TFVNITPAEVGVLVGK.D	1644.93630	3	7.51E-07	0.97	5.40	-	1544.8
AHQ-5-12, 5790 - 5856	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.56E-08	0.96	5.07	-	1079.4
AHQ-5-13-, 5664 - 5681	K.TFVNITPAEVGVLVGK.D	1644.93630	3	8.51E-08	0.98	6.34	-	1918.2
AHQ-5-12, 6005	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.13E-04	0.80	3.07	-	879.5
AHQ-5-13-, 5751 - 5816	K.TFVNITPAEVGVLVGK.D	1644.93630	3	9.76E-10	0.96	5.55	-	1272.9
AHQ-5-13, 6588	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.44E-04	0.71	3.59	-	333.1
AHQ-5-13-, 6524 - 6529	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.71E-06	0.90	4.24	-	808.7
AHQ-5-14-, 5726 - 5753	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.37E-04	0.93	4.58	-	877.5
AHQ-5-13, 5956 - 6024	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.04E-06	0.94	4.82	-	923.2
AHQ-5-13-, 5648 - 5707	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.27E-06	0.83	3.74	-	791.2
AHQ-5-13, 5820 - 5898	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.14E-08	0.93	4.40	-	906.0
AHQ-5-13, 5788 - 5853	K.TFVNITPAEVGVLVGK.D	1644.93630	3	2.60E-08	0.96	5.05	-	1615.8
AHQ-5-13, 5604 - 5672	K.TFVNITPAEVGVLVGK.D	1644.93630	2	8.54E-05	0.81	3.44	-	653.0
AHQ-5-13-, 5867 - 5929	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.11E-08	0.93	4.57	-	781.3
AHQ-5-13-, 5991 - 6051	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.34E-06	0.91	4.08	-	872.0
AHQ-5-4, 6162	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.83E-04	0.57	2.97	-	386.3
AHQ-5-13-, 5357 - 5431	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	2.51E-04	0.88	3.89	-	602.5
AHQ-5-12, 5433 - 5442	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	1.28E-07	0.80	3.69	-	551.1
AHQ-5-13, 6238	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	1.70E-04	0.77	3.10	-	763.0
AHQ-5-13, 5444	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	9.39E-05	0.60	3.06	-	518.4
AHQ-5-13, 5454 - 5522	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	5.97E-06	0.89	3.70	-	783.9
AHQ-5-13-, 2719 - 2795	R.TKSTGGAPTFNVTVTK.T	1609.80568	3	1.06E-06	0.90	4.41	-	740.6
AHQ-5-13-, 2783 - 2784	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	5.46E-06	0.89	4.11	-	617.0
AHQ-5-12, 2656	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	1.62E-05	0.94	4.27	-	850.8
AHQ-5-13, 2817 - 2890	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	1.74E-04	0.94	4.34	-	876.5
AHQ-5-13, 2923 - 2943	R.TKSTGGAPTFNVTVTK.T	1609.80568	3	9.05E-05	0.67	3.48	-	633.5
AHQ-5-14-, 2715	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	7.67E-07	0.97	5.08	-	1299.5
AHQ-5-13, 2926	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	2.29E-04	0.89	3.36	-	839.1
AHQ-5-13, 3701 - 3772	K.TLVLLMGK.E	875.15478	2	9.45E-05	0.77	2.53	-	519.0
AHQ-5-13-, 3699 - 3763	K.TLVLLMGK.E	875.15478	2	3.71E-06	0.81	3.12	-	445.1
AHQ-5-12, 3568 - 3569	K.TLVLLMGK.E	875.15478	2	5.72E-04	0.84	3.12	-	624.7
AHQ-5-12, 2841	K.TLVLLM*GK.E	891.15418	2	6.94E-04	0.76	2.85	-	520.1
AHQ-5-13, 3982	K.TLVLLMGK.E	875.15478	2	9.58E-06	0.77	3.05	-	482.6
AHQ-5-13, 3062 - 3123	K.TLVLLM*GK.E	891.15418	2	1.27E-04	0.84	2.83	-	862.2
AHQ-5-13-, 3572 - 3636	K.TLVLLMGK.E	875.15478	2	2.24E-05	0.80	3.20	-	425.2
gi|7661678|ref|NP_056461.1| RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B				9.44E-15	10.89	120.30	35.90	20824.7
AHQ-5-11, 4270	K.DTDDVPMILVGNK.C	1417.61048	2	1.63E-08	0.89	3.10	-	970.9
AHQ-5-11, 6523	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	5.85E-05	0.94	4.74	-	1282.4

AHQ-5-11, 6439 - 6462	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	8.25E-08	0.97	5.53	-	2262.9
AHQ-5-11, 5127	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	1.14E-10	0.95	5.52	-	1377.7
AHQ-5-13-, 6540 - 6611	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	7.39E-04	0.90	4.38	-	1245.4
AHQ-5-11, 6694 - 6695	R.KQVEVDAQQCMLEILDTAGTEQFTAMR.D	3115.50608	3	2.42E-09	0.95	5.57	-	1052.2
AHQ-5-11, 6719	K.QVEVDAQQCMLEILDTAGTEQFTAM*R.D	3003.33257	3	3.15E-04	0.77	3.38	-	750.2
AHQ-5-11, 6778 - 6780	K.QVEVDAQQCMLEILDTAGTEQFTAMR.D	2987.33317	2	2.05E-08	0.87	4.12	-	658.6
AHQ-5-11, 3859 - 3920	R.QWNNCAFLESSAK.S	1556.68148	2	1.10E-06	0.68	3.51	-	180.8
AHQ-5-11, 4106 - 4175	R.QWNNCAFLESSAK.S	1556.68148	2	7.09E-08	0.77	3.48	-	377.3
AHQ-5-13-, 3869	R.VKDTDDVPMILVGNK.C	1644.91497	2	1.13E-06	0.98	5.82	-	1921.6
AHQ-5-13, 3950 - 3952	R.VKDTDDVPMILVGNK.C	1644.91497	2	4.25E-06	0.96	4.55	-	1406.7
AHQ-5-13, 3966	R.VKDTDDVPMILVGNK.C	1644.91497	3	1.15E-04	0.92	3.83	-	1473.2
AHQ-5-11, 3159 - 3226	R.VKDTDDVPM*ILVGNK.C	1660.91437	2	8.70E-04	0.95	4.14	-	1299.1
AHQ-5-11, 3794	R.VKDTDDVPMILVGNK.C	1644.91497	2	1.76E-08	0.96	4.35	-	1457.8
AHQ-5-11, 3591 - 3654	R.VKDTDDVPMILVGNK.C	1644.91497	3	1.85E-06	0.94	4.66	-	1438.7
AHQ-5-11, 3586 - 3650	R.VKDTDDVPMILVGNK.C	1644.91497	2	2.77E-10	0.98	6.07	-	1894.1
AHQ-5-13-, 3885	R.VKDTDDVPMILVGNK.C	1644.91497	3	1.43E-06	0.91	3.75	-	1429.0
AHQ-5-13, 4522	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	3.01E-07	0.84	4.06	-	677.3
AHQ-5-11, 4396 - 4459	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	9.44E-15	0.94	4.15	-	1243.3
AHQ-5-11, 4314 - 4395	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	5.11E-10	0.93	4.93	-	1009.2
AHQ-5-11, 4252 - 4323	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	5.06E-08	0.94	4.55	-	900.6
AHQ-5-11, 4474 - 4540	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	4.12E-12	0.95	5.23	-	1265.6
AHQ-5-11, 4179 - 4244	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	7.93E-07	0.70	3.35	-	694.9
AHQ-5-11, 4090	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	8.40E-09	0.96	5.55	-	1566.2
AHQ-5-13-, 4459	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	1.88E-07	0.91	4.30	-	1115.9
AHQ-5-11, 4462	R.VKDTDDVPMILVGNKCDLEDERVVGK.E	2947.33182	3	1.78E-04	0.90	4.59	-	1036.6
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				9.99E-15	103.21	1170.39	47.70	226529.8
AHQ-5-2, 1815 - 1886	R.ALEEAMEQK.A	1049.18068	2	8.52E-05	0.87	3.49	-	760.0
AHQ-5-3, 1833 - 1897	R.ALEEAMEQK.A	1049.18068	1	8.13E-04	0.32	2.37	-	520.5
AHQ-5-2, 3839	K.ALELDSNLYR.I	1194.31920	2	2.20E-06	0.90	3.47	-	936.9
AHQ-5-4, 3721 - 3722	K.ALELDSNLYR.I	1194.31920	2	2.14E-06	0.95	4.21	-	1246.3
AHQ-5-5, 3525	K.ALELDSNLYR.I	1194.31920	2	1.95E-06	0.91	3.67	-	966.6
AHQ-5-2, 3713 - 3727	K.ALELDSNLYR.I	1194.31920	2	1.38E-06	0.95	3.93	-	1395.2
AHQ-5-3, 3750	K.ALELDSNLYR.I	1194.31920	2	6.41E-08	0.95	4.24	-	1326.4
AHQ-5-3, 3755 - 3811	K.ALELDSNLYR.I	1194.31920	1	2.85E-06	0.42	2.54	-	247.9
AHQ-5-1, 3876 - 3883	K.ALELDSNLYR.I	1194.31920	2	5.52E-06	0.94	3.87	-	1217.8
AHQ-5-3, 2785 - 2799	R.ALEQQVEEMK.T	1205.36380	2	3.68E-05	0.93	4.29	-	1186.2
AHQ-5-5, 2589	R.ALEQQVEEMK.T	1205.36380	2	1.63E-04	0.89	3.59	-	1168.4
AHQ-5-2, 2717	R.ALEQQVEEMK.T	1205.36380	2	1.51E-05	0.92	4.02	-	1088.0
AHQ-5-1, 2939	R.ALEQQVEEMK.T	1205.36380	2	9.47E-05	0.89	3.59	-	1011.6
AHQ-5-3, 2039	R.ALEQQVEEM*K.T	1221.36320	2	4.00E-05	0.58	2.79	-	603.1
AHQ-5-6, 2609	R.ALEQQVEEMK.T	1205.36380	2	1.57E-04	0.84	3.09	-	1014.0
AHQ-5-5, 6523	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	4.05E-04	0.96	4.88	-	1823.2
AHQ-5-3, 6694	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.54E-10	0.98	6.94	-	1718.9
AHQ-5-6, 7273	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	4.49E-04	0.95	5.29	-	1302.5
AHQ-5-2, 7431	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	3.44E-07	0.96	6.03	-	1213.8
AHQ-5-2, 6654	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	3.33E-12	0.97	6.16	-	1758.8
AHQ-5-6, 6476	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.09E-08	0.97	6.72	-	1324.3
AHQ-5-1, 6648 - 6663	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.45E-04	0.98	7.13	-	1845.1
AHQ-5-4, 7424 - 7425	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	3.09E-07	0.97	6.53	-	1531.4
AHQ-5-6, 4968 - 4976	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.09E-08	0.96	5.02	-	1235.3
AHQ-5-1, 5229 - 5307	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.98E-06	0.97	5.64	-	1361.2
AHQ-5-2, 5294	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.80E-09	0.97	5.91	-	1349.1
AHQ-5-9, 4431 - 4435	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.49E-07	0.96	5.05	-	1315.6
AHQ-5-2, 5150 - 5223	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.45E-08	0.98	6.15	-	1594.8
AHQ-5-2, 4985	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.26E-07	0.94	4.56	-	839.9
AHQ-5-1, 5484	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.41E-10	0.98	6.45	-	1248.3
AHQ-5-2, 5382 - 5459	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.84E-08	0.97	5.39	-	1569.9
AHQ-5-3, 5030	K.ANLQIDQINTDLNLER.S	1871.04187	2	7.32E-05	0.91	4.42	-	673.4
AHQ-5-5, 5030 - 5045	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.62E-08	0.97	5.31	-	1518.3
AHQ-5-3, 5315	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.79E-10	0.97	5.49	-	1134.8
AHQ-5-3, 5479	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.68E-07	0.94	4.84	-	764.3
AHQ-5-4, 2233	K.ASITALEAK.I	904.04321	2	1.51E-05	0.93	3.12	-	1210.6
AHQ-5-1, 2469	K.ASITALEAK.I	904.04321	2	6.93E-06	0.95	3.43	-	1565.5
AHQ-5-3, 2246	K.ASITALEAK.I	904.04321	2	2.61E-04	0.92	3.35	-	1060.7
AHQ-5-2, 2194	K.ASITALEAK.I	904.04321	2	6.70E-06	0.94	3.41	-	1432.7
AHQ-5-2, 1859	R.ASREEILAQAK.E	1216.36955	2	3.68E-05	0.92	3.46	-	1491.8
AHQ-5-3, 1906	R.ASREEILAQAK.E	1216.36955	2	5.61E-07	0.94	3.37	-	1739.7
AHQ-5-4, 1921	R.ASREEILAQAK.E	1216.36955	2	1.29E-05	0.95	3.69	-	1817.9
AHQ-5-2, 3379	R.DELADEIANSSGK.G	1349.38323	1	9.49E-07	0.75	2.81	-	511.8
AHQ-5-3, 3217 - 3222	R.DELADEIANSSGK.G	1349.38323	1	1.21E-06	0.65	2.71	-	465.8
AHQ-5-2, 2879	R.DELADEIANSSGK.G	1349.38323	1	2.66E-09	0.72	2.48	-	581.4
AHQ-5-1, 3268	R.DELADEIANSSGK.G	1349.38323	2	6.42E-04	0.92	3.79	-	1078.6
AHQ-5-2, 3198 - 3205	R.DELADEIANSSGK.G	1349.38323	2	2.87E-08	0.94	3.91	-	1281.9
AHQ-5-2, 3191	R.DELADEIANSSGK.G	1349.38323	1	1.54E-04	0.25	2.08	-	570.4
AHQ-5-2, 3203	R.DELADEIANSSGK.G	1349.38323	1	2.96E-06	0.70	2.89	-	391.5
AHQ-5-1, 7140 - 7141	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	3.26E-07	0.97	5.77	-	2034.9
AHQ-5-2, 7081 - 7145	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	4.63E-10	0.98	6.71	-	1701.5
AHQ-5-3, 7270	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.50E-06	0.93	4.11	-	1641.1
AHQ-5-1, 6999 - 7000	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.47E-11	0.98	7.08	-	2368.4
AHQ-5-4, 7070	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.74E-10	0.97	6.25	-	1590.6
AHQ-5-6, 6880	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	4.17E-05	0.95	5.30	-	1374.3
AHQ-5-3, 7109 - 7121	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.25E-09	0.97	6.12	-	1632.6
AHQ-5-2, 6649	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	2	3.22E-13	0.85	3.62	-	610.6
AHQ-5-3, 6682	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	2	4.93E-11	0.67	2.93	-	397.3
AHQ-5-2, 6645	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	3.87E-10	0.85	3.89	-	646.4
AHQ-5-4, 2032	K.DLEAHIDSANK.N	1213.27938	2	1.48E-05	0.98	4.17	-	2957.3
AHQ-5-2, 1998 - 2029	K.DLEAHIDSANK.N	1213.27938	2	1.91E-07	0.98	4.29	-	2588.8
AHQ-5-3, 2037	K.DLEAHIDSANK.N	1213.27938	2	2.70E-07	0.98	4.17	-	2739.5
AHQ-5-1, 2272	K.DLEAHIDSANK.N	1213.27938	2	2.67E-06	0.98	4.49	-	2815.6
AHQ-5-2, 1949 - 2013	K.DLEAHIDSANK.N	1213.27938	1	5.61E-04	0.59	1.87	-	756.1
AHQ-5-2, 2379	K.DLEAHIDSANKNRDEAIK.Q	2040.18063	2	3.44E-05	0.91	4.09	-	877.6
AHQ-5-5, 7473 - 7474	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	3.60E-08	0.97	6.18	-	1797.2
AHQ-5-2, 7529	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	2.78E-09	0.96	5.45	-	1393.6
AHQ-5-7, 7371	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.44E-08	0.94	4.32	-	1876.7
AHQ-5-1, 7351	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	2.40E-07	0.95	5.19	-	1503.2
AHQ-5-2, 7641	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	7.69E-10	0.96	5.06	-	1573.3
AHQ-5-10, 6603	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.02E-05	0.79	3.69	-	844.6
AHQ-5-4, 7526	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	6.60E-10	0.97	5.61	-	1873.2
AHQ-5-2, 3386	K.DVLLQVDDER.R	1202.29650	1	5.39E-08	0.24	2.34	-	176.7
AHQ-5-2, 3381	K.DVLLQVDDER.R	1202.29650	2	1.87E-07	0.95	3.54	-	1666.0
AHQ-5-1, 2971 - 2972	K.DVLLQVDDERR.N	1358.48286	2	9.77E-05	0.82	3.43	-	790.5
AHQ-5-1, 2044	R.EEILAQAK.E	902.02731	1	5.79E-05	0.14	2.19	-	269.6
AHQ-5-4, 2833 - 2914	R.ELEDATETADAMNR.E	1566.63006	2	3.07E-10	0.95	4.94	-	1018.7
AHQ-5-5, 2753	R.ELEDATETADAMNR.E	1566.63006	2	6.67E-07	0.85	3.50	-	853.0
AHQ-5-6, 2725	R.ELEDATETADAMNR.E	1566.63006	2	1.12E-06	0.88	3.15	-	1180.5
AHQ-5-1, 2928	R.ELEDATETADAMNR.E	1566.63006	2	2.67E-04	0.89	3.44	-	991.0
AHQ-5-3, 2850	R.ELEDATETADAMNR.E	1566.63006	2	8.25E-09	0.93	3.93	-	1206.4

AHQ-5-2, 2815	R.ELEDATETADAMNR.E	1566.63006	2	4.34E-08	0.94	4.26	-	1058.6
AHQ-5-3, 3798	R.ELEDATETADAMNREVSSLK.N	2210.36264	2	6.49E-07	0.70	3.01	-	353.9
AHQ-5-3, 5970 - 6042	R.ELESQISELQEDLESER.A	2035.10956	3	1.24E-05	0.98	5.61	-	2717.7
AHQ-5-2, 6319	R.ELESQISELQEDLESER.A	2035.10956	2	1.07E-08	0.94	4.17	-	1218.3
AHQ-5-1, 6043	R.ELESQISELQEDLESER.A	2035.10956	2	1.82E-09	0.94	4.44	-	1003.6
AHQ-5-2, 4681	R.ELESQISELQEDLESER.A	2035.10956	2	5.46E-06	0.92	3.91	-	923.8
AHQ-5-2, 5949 - 5981	R.ELESQISELQEDLESER.A	2035.10956	2	6.47E-11	0.97	5.52	-	1252.5
AHQ-5-4, 5956	R.ELESQISELQEDLESER.A	2035.10956	2	1.52E-07	0.96	5.25	-	1122.4
AHQ-5-1, 5959 - 6027	R.ELESQISELQEDLESER.A	2035.10956	2	3.92E-05	0.91	4.44	-	933.1
AHQ-5-1, 6040	R.ELESQISELQEDLESER.A	2035.10956	3	6.40E-06	0.98	5.62	-	2641.5
AHQ-5-2, 5966 - 5969	R.ELESQISELQEDLESER.A	2035.10956	3	3.13E-09	0.98	5.98	-	2626.4
AHQ-5-2, 5506 - 5582	R.ELESQISELQEDLESER.A	2035.10956	2	2.45E-07	0.93	4.38	-	797.3
AHQ-5-3, 6029	R.ELESQISELQEDLESER.A	2035.10956	2	4.01E-10	0.96	5.15	-	1171.4
AHQ-5-5, 5833 - 5841	R.ELESQISELQEDLESER.A	2035.10956	2	3.35E-07	0.93	4.47	-	855.5
AHQ-5-2, 2070	R.EMEAELEDERK.Q	1379.47597	1	7.07E-04	0.24	2.36	-	177.3
AHQ-5-1, 2308	R.EMEAELEDERK.Q	1379.47597	2	4.36E-06	0.92	3.42	-	1288.4
AHQ-5-4, 2093	R.EMEAELEDERK.Q	1379.47597	2	2.01E-05	0.86	3.11	-	927.3
AHQ-5-3, 2101	R.EMEAELEDERK.Q	1379.47597	2	1.47E-05	0.93	3.25	-	1474.5
AHQ-5-2, 2063	R.EMEAELEDERK.Q	1379.47597	2	1.39E-05	0.91	3.24	-	1183.1
AHQ-5-2, 4453 - 4525	K.EQADFAIEALAK.A	1306.44632	2	9.40E-04	0.80	2.78	-	583.9
AHQ-5-1, 4552 - 4623	K.EQADFAIEALAK.A	1306.44632	2	4.92E-04	0.62	2.58	-	605.2
AHQ-5-1, 2499	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.75E-07	0.86	3.98	-	540.1
AHQ-5-6, 2169	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	5.98E-04	0.83	3.83	-	700.1
AHQ-5-4, 2276	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.78E-06	0.87	4.19	-	527.2
AHQ-5-3, 2310	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	3.47E-04	0.89	3.92	-	832.8
AHQ-5-2, 2261	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.06E-04	0.89	4.14	-	706.9
AHQ-5-3, 3465	R.FLSNGHVTIPGQQDK.D	1641.80946	2	3.14E-06	0.93	4.00	-	788.4
AHQ-5-2, 5927 - 6009	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	1.06E-05	0.95	5.60	-	886.5
AHQ-5-2, 5198 - 5238	R.FLSNGHVTIPGQQDKDMFQETMEAM*R.I	3028.39040	3	4.19E-05	0.90	5.65	-	909.0
AHQ-5-4, 6101	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	7.95E-07	0.88	4.62	-	719.2
AHQ-5-9, 5136	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	1.39E-05	0.71	3.34	-	624.3
AHQ-5-2, 5374	R.FLSNGHVTIPGQQDKDM*FQETMEAMR.I	3028.39040	3	2.35E-04	0.87	5.22	-	795.5
AHQ-5-3, 6059 - 6130	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	5.79E-06	0.91	5.02	-	585.4
AHQ-5-5, 5873	R.FLSNGHVTIPGQQDKDMFQETMEAMR.I	3012.39100	3	3.82E-04	0.91	4.55	-	723.1
AHQ-5-3, 3623	K.FVSELWK.D	909.06314	1	3.08E-04	0.56	2.43	-	791.8
AHQ-5-4, 2673	K.HEAMITDLEER.L	1344.47646	2	1.22E-05	0.97	4.33	-	1392.3
AHQ-5-2, 2594 - 2665	K.HEAMITDLEER.L	1344.47646	2	2.62E-07	0.97	4.43	-	1315.2
AHQ-5-3, 2741	K.HEAMITDLEER.L	1344.47646	2	8.03E-05	0.97	4.08	-	1551.2
AHQ-5-2, 2662	K.HEAMITDLEER.L	1344.47646	1	1.28E-04	0.84	3.47	-	638.0
AHQ-5-1, 2925	K.HEAMITDLEER.L	1344.47646	2	7.97E-06	0.97	4.30	-	1635.6
AHQ-5-2, 2658	K.HEAMITDLEER.L	1344.47646	1	8.01E-05	0.50	2.27	-	700.8
AHQ-5-2, 3413 - 3481	R.HEMPPHIYAITDTAYR.S	1916.14944	2	1.57E-06	0.89	3.38	-	887.9
AHQ-5-2, 3595	R.HEMPPHIYAITDTAYR.S	1916.14944	3	1.63E-08	0.97	4.63	-	2366.9
AHQ-5-10, 3115	R.HEMPPHIYAITDTAYR.S	1916.14944	2	4.98E-04	0.91	3.50	-	834.6
AHQ-5-5, 3223 - 3295	R.HEMPPHIYAITDTAYR.S	1916.14944	2	4.25E-05	0.90	3.97	-	805.3
AHQ-5-4, 3508	R.HEMPPHIYAITDTAYR.S	1916.14944	2	5.10E-05	0.89	3.37	-	832.6
AHQ-5-3, 3185	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	2.45E-04	0.81	2.95	-	667.7
AHQ-5-1, 3352	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	3.54E-05	0.89	3.00	-	859.9
AHQ-5-2, 3506	R.HEMPPHIYAITDTAYR.S	1916.14944	3	1.94E-09	0.98	4.93	-	3262.8
AHQ-5-4, 3158	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	1.31E-04	0.80	2.60	-	774.8
AHQ-5-2, 3663	R.HEMPPHIYAITDTAYR.S	1916.14944	2	6.90E-04	0.86	3.02	-	935.6
AHQ-5-2, 3549	R.HEMPPHIYAITDTAYR.S	1916.14944	2	7.48E-06	0.92	3.42	-	889.6
AHQ-5-1, 3749	R.HEMPPHIYAITDTAYR.S	1916.14944	2	2.10E-06	0.93	4.10	-	616.0
AHQ-5-3, 4553	K.HSQAVEELAEQLEQTK.R	1840.96940	3	2.77E-07	0.97	5.56	-	2158.7
AHQ-5-4, 4485	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.08E-13	0.98	5.77	-	2353.3
AHQ-5-2, 4469 - 4541	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.57E-12	0.98	5.99	-	2443.5
AHQ-5-1, 4676 - 4693	K.HSQAVEELAEQLEQTK.R	1840.96940	3	4.28E-07	0.97	5.12	-	2124.0
AHQ-5-3, 4545 - 4618	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.06E-10	0.98	6.44	-	2217.1
AHQ-5-2, 4477	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.90E-08	0.97	5.50	-	2015.4
AHQ-5-4, 4497	K.HSQAVEELAEQLEQTK.R	1840.96940	3	4.19E-06	0.97	5.36	-	2086.2
AHQ-5-1, 4667 - 4671	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.93E-06	0.97	5.50	-	1795.0
AHQ-5-1, 4240 - 4249	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	8.37E-11	0.98	5.91	-	2078.0
AHQ-5-2, 3959 - 4009	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	3.96E-07	0.98	7.29	-	2419.8
AHQ-5-3, 4063 - 4097	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	2.99E-09	0.98	6.09	-	2481.4
AHQ-5-5, 3791	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.19E-09	0.98	6.07	-	2176.3
AHQ-5-4, 4028	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	8.76E-06	0.98	6.62	-	1730.9
AHQ-5-2, 3958 - 3997	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.80E-09	0.98	5.80	-	2142.4
AHQ-5-5, 3782	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	5.25E-09	0.94	5.11	-	1001.8
AHQ-5-1, 4239 - 4263	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.83E-06	0.97	5.51	-	1645.9
AHQ-5-4, 4032	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.73E-07	0.98	5.98	-	2145.5
AHQ-5-3, 4062	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.14E-05	0.97	6.32	-	1516.1
AHQ-5-5, 3537 - 3539	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.24E-09	0.91	3.76	-	1402.9
AHQ-5-2, 4003 - 4005	R.IAEFTTNLTEEEEK.S	1654.75371	2	7.67E-08	0.98	4.97	-	2556.3
AHQ-5-2, 4491	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.08E-05	0.92	3.77	-	1569.2
AHQ-5-2, 4403	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.80E-06	0.88	3.04	-	1334.8
AHQ-5-2, 3853 - 3927	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.63E-09	0.96	4.35	-	2014.2
AHQ-5-2, 4089 - 4158	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.43E-06	0.95	4.11	-	1470.3
AHQ-5-4, 3670 - 3741	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.56E-07	0.97	5.15	-	1818.5
AHQ-5-1, 3847 - 3915	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.13E-07	0.90	3.82	-	1471.1
AHQ-5-1, 3984	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.09E-09	0.92	3.59	-	1488.9
AHQ-5-6, 3476	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.86E-09	0.97	4.57	-	1975.2
AHQ-5-4, 3813	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.85E-07	0.93	3.67	-	1661.4
AHQ-5-3, 3734 - 3805	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.15E-10	0.98	5.38	-	1827.8
AHQ-5-1, 4068	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.55E-07	0.95	4.73	-	1155.5
AHQ-5-4, 3978 - 4056	R.IAEFTTNLTEEEEK.S	1654.75371	2	6.85E-08	0.97	4.34	-	2002.1
AHQ-5-3, 3865 - 3933	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.59E-08	0.96	4.44	-	1559.9
AHQ-5-3, 3985 - 4002	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.15E-10	0.97	4.69	-	1815.5
AHQ-5-2, 3711 - 3785	R.IAEFTTNLTEEEEK.S	1654.75371	2	7.72E-12	0.98	5.06	-	2163.0
AHQ-5-2, 3227	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	9.93E-06	0.85	3.59	-	654.0
AHQ-5-3, 3326	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	8.19E-10	0.87	3.75	-	770.3
AHQ-5-2, 3569	R.IAEFTTNLTEEEEKSKSLAK.L	2269.49132	2	4.30E-04	0.81	3.73	-	697.7
AHQ-5-5, 3175 - 3205	K.IAQLEEQLDNETK.E	1531.64695	2	4.43E-05	0.92	4.01	-	1066.6
AHQ-5-2, 3775	K.IAQLEEQLDNETK.E	1531.64695	2	1.07E-05	0.89	3.17	-	1074.2
AHQ-5-2, 3319 - 3389	K.IAQLEEQLDNETK.E	1531.64695	2	3.10E-05	0.93	3.83	-	1081.3
AHQ-5-3, 2914	K.IAQLEEQLDNETK.E	1531.64695	2	6.50E-04	0.87	2.86	-	1008.0
AHQ-5-1, 3601	K.IAQLEEQLDNETK.E	1531.64695	2	1.78E-05	0.84	3.29	-	819.3
AHQ-5-5, 3041	K.IAQLEEQLDNETK.E	1531.64695	2	6.36E-06	0.76	3.12	-	615.0
AHQ-5-9, 2928 - 2935	K.IAQLEEQLDNETK.E	1531.64695	2	4.44E-05	0.93	4.19	-	925.7
AHQ-5-2, 3466	K.IAQLEEQLDNETK.E	1531.64695	2	1.31E-07	0.95	4.20	-	1439.8
AHQ-5-2, 3098	K.IAQLEEQLDNETK.E	1531.64695	2	1.57E-06	0.91	3.91	-	1030.1
AHQ-5-3, 3474	K.IAQLEEQLDNETK.E	1531.64695	2	3.27E-04	0.77	2.97	-	761.0
AHQ-5-1, 3233 - 3235	K.IAQLEEQLDNETK.E	1531.64695	2	4.16E-09	0.97	4.99	-	1713.8
AHQ-5-2, 2867	K.IAQLEEQLDNETK.E	1531.64695	2	8.37E-05	0.95	4.21	-	1194.2
AHQ-5-7, 3048	K.IAQLEEQLDNETK.E	1531.64695	2	5.78E-06	0.92	3.83	-	1042.0
AHQ-5-6, 3125 - 3144	K.IAQLEEQLDNETK.E	1531.64695	2	8.97E-10	0.97	5.29	-	1440.3
AHQ-5-11, 3192	K.IAQLEEQLDNETK.E	1531.64695	2	8.89E-09	0.96	4.03	-	1625.3
AHQ-5-10, 3046 - 3048	K.IAQLEEQLDNETK.E	1531.64695	2	1.63E-05	0.92	3.48	-	1263.6

AHQ-5-1, 3445	K.IAQLEEQLDNETK.E	1531.64695	2	1.44E-06	0.93	3.52	-	1284.8
AHQ-5-3, 3161	K.IAQLEEQLDNETK.E	1531.64695	2	6.20E-08	0.95	4.71	-	1370.7
AHQ-5-6, 3000	K.IAQLEEQLDNETK.E	1531.64695	2	5.44E-05	0.82	3.33	-	515.4
AHQ-5-2, 2997	K.IAQLEEQLDNETKER.Q	1816.94784	3	2.97E-08	0.82	3.54	-	877.1
AHQ-5-2, 3418 - 3493	K.IAQLEEQLDNETKER.Q	1816.94784	2	9.77E-09	0.95	4.51	-	1321.8
AHQ-5-2, 2977	K.IAQLEEQLDNETKER.Q	1816.94784	2	9.17E-04	0.62	2.81	-	683.5
AHQ-5-2, 6739 - 6806	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	2.42E-04	0.94	5.31	-	995.8
AHQ-5-2, 6665 - 6733	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.44E-07	0.98	6.15	-	1562.3
AHQ-5-2, 6019 - 6085	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.58E-06	0.97	5.22	-	1437.0
AHQ-5-1, 5895 - 5963	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	3	2.32E-04	0.85	4.17	-	801.1
AHQ-5-13, 6361	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.35E-05	0.94	4.28	-	1140.8
AHQ-5-14-, 6213	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.74E-06	0.92	3.55	-	1122.4
AHQ-5-2, 6801 - 6879	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.40E-06	0.95	4.82	-	1230.3
AHQ-5-7, 6508 - 6522	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.71E-06	0.96	4.55	-	1296.6
AHQ-5-2, 5853 - 5913	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.02E-05	0.96	5.12	-	965.0
AHQ-5-14, 6108 - 6182	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	4.15E-04	0.86	3.45	-	640.4
AHQ-5-1, 6127	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.49E-06	0.88	3.84	-	854.5
AHQ-5-4, 6748 - 6780	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	6.10E-05	0.96	5.12	-	919.4
AHQ-5-4, 6766 - 6768	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	4.56E-04	0.96	5.78	-	1325.5
AHQ-5-6, 6544	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.97E-06	0.95	4.56	-	1060.5
AHQ-5-6, 6466 - 6537	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	7.32E-06	0.96	5.33	-	1102.1
AHQ-5-2, 5397 - 5405	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	3.01E-05	0.94	4.93	-	738.0
AHQ-5-3, 6785 - 6853	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.62E-05	0.96	5.30	-	1042.1
AHQ-5-3, 6795 - 6797	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	1.87E-08	0.95	5.62	-	1155.1
AHQ-5-5, 6617	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.32E-06	0.96	4.89	-	1143.9
AHQ-5-1, 6731	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	6.64E-04	0.96	5.05	-	1453.4
AHQ-5-8, 6312	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.51E-06	0.97	5.68	-	1404.4
AHQ-5-1, 5440	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	7.61E-04	0.82	3.63	-	501.3
AHQ-5-8, 4789	R.IMGIPEEEQMGLLR.V	1616.92826	2	7.08E-05	0.69	2.81	-	432.4
AHQ-5-4, 5372	R.IMGIPEEEQMGLLR.V	1616.92826	2	6.73E-07	0.90	3.69	-	517.0
AHQ-5-5, 5189	R.IMGIPEEEQMGLLR.V	1616.92826	2	2.02E-04	0.73	3.07	-	325.6
AHQ-5-1, 4101	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	2.27E-04	0.71	2.65	-	547.2
AHQ-5-2, 5317 - 5319	R.IMGIPEEEQMGLLR.V	1616.92826	2	5.18E-09	0.93	4.37	-	699.7
AHQ-5-3, 5401 - 5410	R.IMGIPEEEQMGLLR.V	1616.92826	2	5.03E-10	0.90	3.78	-	529.9
AHQ-5-2, 4750	R.IM*GIPEEEQMGLLR.V	1632.92766	2	1.60E-05	0.93	4.07	-	780.2
AHQ-5-1, 6033 - 6052	K.IRELESQISELQEDLESER.A	2304.45416	3	3.31E-09	0.98	6.78	-	2649.8
AHQ-5-2, 5886 - 5905	K.IRELESQISELQEDLESER.A	2304.45416	3	4.45E-10	0.98	7.84	-	2304.0
AHQ-5-4, 5913 - 5914	K.IRELESQISELQEDLESER.A	2304.45416	3	1.27E-09	0.98	6.32	-	2448.2
AHQ-5-2, 6219 - 6225	K.IRELESQISELQEDLESER.A	2304.45416	2	5.92E-04	0.89	3.27	-	870.5
AHQ-5-3, 5974 - 5993	K.IRELESQISELQEDLESER.A	2304.45416	3	3.03E-06	0.97	5.82	-	2073.0
AHQ-5-5, 5706 - 5775	K.IRELESQISELQEDLESER.A	2304.45416	2	1.04E-10	0.98	6.65	-	1402.1
AHQ-5-6, 5582 - 5644	K.IRELESQISELQEDLESER.A	2304.45416	2	2.60E-04	0.98	6.31	-	1408.0
AHQ-5-2, 5831 - 5897	K.IRELESQISELQEDLESER.A	2304.45416	2	2.43E-04	0.99	7.12	-	2035.5
AHQ-5-4, 5909	K.IRELESQISELQEDLESER.A	2304.45416	2	3.88E-08	0.97	6.16	-	1000.9
AHQ-5-3, 4453	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.24E-11	0.97	5.61	-	1107.3
AHQ-5-5, 4333	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.10E-05	0.95	4.51	-	1575.9
AHQ-5-6, 4250	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.33E-08	0.97	6.40	-	1344.6
AHQ-5-2, 4381	K.KANLQIDQINTDLNLER.S	1999.21478	2	5.65E-11	0.96	5.48	-	1018.2
AHQ-5-2, 4834	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.31E-06	0.96	5.13	-	1180.8
AHQ-5-2, 4997	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.07E-04	0.94	4.59	-	1048.1
AHQ-5-1, 4537	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.83E-06	0.83	4.03	-	609.1
AHQ-5-4, 4570 - 4600	K.KANLQIDQINTDLNLER.S	1999.21478	2	9.45E-05	0.97	5.66	-	1565.1
AHQ-5-2, 4557	K.KANLQIDQINTDLNLER.S	1999.21478	3	3.11E-06	0.87	4.34	-	864.2
AHQ-5-3, 2414 - 2490	R.KKVEAQLQELQVK.F	1541.81761	2	1.20E-06	0.97	5.12	-	1697.0
AHQ-5-4, 2385 - 2396	R.KKVEAQLQELQVK.F	1541.81761	2	1.64E-08	0.98	5.50	-	1896.3
AHQ-5-1, 2628 - 2631	R.KKVEAQLQELQVK.F	1541.81761	2	4.30E-08	0.97	5.20	-	1772.7
AHQ-5-2, 2338 - 2345	R.KKVEAQLQELQVK.F	1541.81761	2	2.41E-08	0.98	5.52	-	2167.3
AHQ-5-5, 2249	R.KKVEAQLQELQVK.F	1541.81761	2	6.63E-06	0.96	4.46	-	1460.5
AHQ-5-1, 3548	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.12E-09	0.98	5.70	-	1646.4
AHQ-5-2, 3675	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.18E-05	0.98	5.49	-	2189.2
AHQ-5-3, 3525	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.52E-10	0.98	5.95	-	1645.8
AHQ-5-3, 3958	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.66E-04	0.88	3.65	-	710.0
AHQ-5-3, 3369 - 3438	K.KLEEEQIILEDQNCK.L	1891.08992	2	9.95E-06	0.98	5.85	-	1760.8
AHQ-5-1, 3649 - 3660	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.11E-06	0.98	5.47	-	1935.4
AHQ-5-3, 3730	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.69E-07	0.98	5.50	-	2185.6
AHQ-5-2, 3342 - 3390	K.KLEEEQIILEDQNCK.L	1891.08992	3	1.39E-10	0.89	4.17	-	1073.1
AHQ-5-4, 3393	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.71E-05	0.98	5.67	-	2154.2
AHQ-5-2, 3582	K.KLEEEQIILEDQNCK.L	1891.08992	2	4.08E-10	0.98	5.52	-	1981.2
AHQ-5-2, 3373 - 3445	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.54E-07	0.97	5.19	-	1573.4
AHQ-5-2, 3483 - 3513	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.74E-05	0.98	5.89	-	1728.2
AHQ-5-3, 3643	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.29E-09	0.93	4.30	-	752.5
AHQ-5-2, 3558 - 3587	K.KLEEEQIILEDQNCK.L	1891.08992	3	7.93E-04	0.67	3.12	-	867.5
AHQ-5-4, 3500	K.KLEEEQIILEDQNCK.L	1891.08992	2	4.04E-11	0.98	6.32	-	2215.7
AHQ-5-5, 7209 - 7211	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	5.62E-09	0.93	5.64	-	784.4
AHQ-5-3, 7334 - 7338	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	6.32E-07	0.97	6.15	-	1173.6
AHQ-5-1, 7195	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	4.85E-07	0.92	5.39	-	842.8
AHQ-5-2, 7309 - 7377	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	9.16E-06	0.94	5.26	-	1100.6
AHQ-5-2, 7279 - 7345	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	6.27E-07	0.97	6.29	-	1363.7
AHQ-5-5, 7206	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	8.74E-11	0.97	5.75	-	1505.0
AHQ-5-3, 7337 - 7349	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	1.18E-08	0.91	5.13	-	798.5
AHQ-5-1, 7196 - 7408	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.07E-06	0.98	7.24	-	1470.7
AHQ-5-7, 7066	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	7.06E-04	0.86	3.82	-	680.0
AHQ-5-4, 7297	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	6.54E-07	0.91	5.02	-	943.5
AHQ-5-3, 6390	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	5.77E-05	0.68	3.51	-	741.9
AHQ-5-2, 2495	K.KLVWVPSDK.S	1072.28194	1	1.88E-04	0.40	2.33	-	515.0
AHQ-5-13-, 2812	K.KLVWVPSDK.S	1072.28194	1	1.97E-04	0.64	2.52	-	399.3
AHQ-5-2, 2501	K.KLVWVPSDK.S	1072.28194	2	1.54E-05	0.87	3.17	-	959.6
AHQ-5-6, 2397	K.KLVWVPSDK.S	1072.28194	1	6.72E-05	0.46	2.07	-	543.2
AHQ-5-2, 3565	K.KMEDSVGCLETAEEVK.R	1827.02450	2	2.75E-05	0.95	4.71	-	1181.0
AHQ-5-3, 3593	K.KMEDSVGCLETAEEVK.R	1827.02450	2	7.63E-04	0.93	4.05	-	1274.7
AHQ-5-2, 3042	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	3.43E-06	0.89	3.74	-	732.1
AHQ-5-3, 2814	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	1.37E-04	0.86	3.80	-	592.4
AHQ-5-3, 2818 - 2819	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	3.37E-06	0.94	5.20	-	899.8
AHQ-5-2, 2722	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	2.68E-07	0.88	4.41	-	816.2
AHQ-5-1, 3343	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	5.18E-09	0.95	4.16	-	1294.3
AHQ-5-4, 3196	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	2.11E-07	0.93	4.88	-	974.3
AHQ-5-1, 3337	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	2.06E-12	0.96	5.51	-	1626.9
AHQ-5-2, 3135 - 3141	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	2.31E-08	0.97	5.14	-	1331.0
AHQ-5-2, 2726 - 2727	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	2.34E-05	0.78	3.54	-	448.7
AHQ-5-4, 3190	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	8.72E-10	0.95	4.38	-	1331.8
AHQ-5-3, 3205	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	5.33E-10	0.97	5.77	-	1546.7
AHQ-5-3, 3206	K.KMEDSVGCLETAEEVKR.K	1983.21085	2	4.21E-11	0.97	5.15	-	1437.5
AHQ-5-3, 4930	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	8.41E-05	0.93	4.41	-	1564.5
AHQ-5-2, 4861	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	2.79E-05	0.75	3.12	-	474.5
AHQ-5-4, 5373	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	1.53E-06	0.82	3.56	-	616.3
AHQ-5-1, 4981	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	7.03E-04	0.93	4.39	-	1521.3
AHQ-5-2, 5310 - 5347	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	4.40E-08	0.98	6.16	-	1521.9

AHQ-5-1, 4144 - 4215	K.KQELEEICHDLEAR.V	1771.93036	2	9.54E-07	0.97	5.04	-	1782.2
AHQ-5-5, 3825	K.KQELEEICHDLEAR.V	1771.93036	2	4.40E-05	0.97	4.99	-	1829.8
AHQ-5-4, 4022	K.KQELEEICHDLEAR.V	1771.93036	2	3.38E-07	0.97	4.87	-	1808.0
AHQ-5-5, 3818 - 3831	K.KQELEEICHDLEAR.V	1771.93036	3	4.15E-04	0.95	4.73	-	1690.8
AHQ-5-6, 3786	K.KQELEEICHDLEAR.V	1771.93036	2	1.07E-04	0.96	4.44	-	1655.0
AHQ-5-1, 4211	K.KQELEEICHDLEAR.V	1771.93036	3	1.25E-04	0.96	5.44	-	1727.5
AHQ-5-2, 4013 - 4073	K.KQELEEICHDLEAR.V	1771.93036	2	3.34E-04	0.96	4.95	-	1651.5
AHQ-5-2, 4010 - 4081	K.KQELEEICHDLEAR.V	1771.93036	3	4.23E-04	0.97	5.71	-	1949.4
AHQ-5-4, 2725	K.KVEAQLQELQVK.F	1413.64470	2	3.60E-06	0.97	4.77	-	1703.0
AHQ-5-1, 2984 - 2985	K.KVEAQLQELQVK.F	1413.64470	1	1.44E-06	0.16	2.39	-	321.4
AHQ-5-2, 2673	K.KVEAQLQELQVK.F	1413.64470	2	2.36E-05	0.97	5.20	-	1694.6
AHQ-5-1, 2983	K.KVEAQLQELQVK.F	1413.64470	2	2.31E-06	0.96	4.72	-	1586.2
AHQ-5-3, 2759 - 2766	K.KVEAQLQELQVK.F	1413.64470	2	6.08E-04	0.97	4.93	-	1861.0
AHQ-5-3, 2767 - 2769	K.KVEAQLQELQVK.F	1413.64470	1	1.71E-05	0.32	2.53	-	380.2
AHQ-5-2, 2681	K.KVEAQLQELQVK.F	1413.64470	1	1.76E-05	0.75	3.37	-	523.7
AHQ-5-5, 2541	K.KVEAQLQELQVK.F	1413.64470	2	1.11E-06	0.97	5.37	-	1510.0
AHQ-5-2, 3803 - 3813	K.LEEEQIILEDQNCK.L	1762.91700	2	2.83E-08	0.96	5.20	-	1095.9
AHQ-5-4, 3977	K.LEEEQIILEDQNCK.L	1762.91700	2	2.57E-05	0.94	4.20	-	1175.5
AHQ-5-3, 4005	K.LEEEQIILEDQNCK.L	1762.91700	2	7.02E-10	0.97	5.47	-	1611.9
AHQ-5-3, 3861 - 3935	K.LEEEQIILEDQNCK.L	1762.91700	2	3.71E-08	0.97	5.73	-	1321.8
AHQ-5-4, 3824 - 3829	K.LEEEQIILEDQNCK.L	1762.91700	2	4.38E-08	0.96	5.20	-	1057.1
AHQ-5-2, 3906 - 3982	K.LEEEQIILEDQNCK.L	1762.91700	2	3.09E-09	0.96	4.96	-	1168.0
AHQ-5-1, 4005	K.LEEEQIILEDQNCK.L	1762.91700	2	8.49E-10	0.88	3.96	-	684.0
AHQ-5-4, 7400	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	4.87E-09	0.96	5.26	-	1028.1
AHQ-5-2, 7437 - 7438	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	1.22E-08	0.97	5.89	-	1115.2
AHQ-5-1, 7268	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	3.30E-07	0.94	5.36	-	1268.0
AHQ-5-3, 3463	R.LEVNLQAMK.A	1046.26630	2	5.62E-06	0.81	3.16	-	574.1
AHQ-5-1, 3600	R.LEVNLQAMK.A	1046.26630	2	3.16E-05	0.83	3.25	-	615.9
AHQ-5-2, 3361	R.LEVNLQAMK.A	1046.26630	2	3.16E-05	0.92	3.73	-	779.1
AHQ-5-2, 3707	R.LEVNLQAMK.A	1046.26630	1	4.94E-05	0.28	2.76	-	318.4
AHQ-5-1, 3543	K.LKDVLLQVDDER.R	1443.62767	2	8.10E-09	0.97	4.27	-	1942.0
AHQ-5-2, 3294	K.LKDVLLQVDDER.R	1443.62767	2	6.84E-08	0.95	4.13	-	1366.3
AHQ-5-2, 3257	K.LKDVLLQVDDER.R	1443.62767	1	3.89E-05	0.21	2.14	-	347.3
AHQ-5-4, 3376 - 3378	K.LKDVLLQVDDER.R	1443.62767	2	5.75E-09	0.96	4.05	-	1737.4
AHQ-5-3, 2923	K.LKDVLLQVDDERR.N	1599.81402	2	2.66E-04	0.86	3.53	-	1037.9
AHQ-5-11, 2852	K.LKDVLLQVDDERR.N	1599.81402	2	1.02E-04	0.82	2.98	-	1067.1
AHQ-5-5, 2649	K.LKDVLLQVDDERR.N	1599.81402	2	2.16E-05	0.91	3.89	-	1181.2
AHQ-5-2, 2814 - 2850	K.LKDVLLQVDDERR.N	1599.81402	2	2.59E-05	0.86	3.54	-	970.2
AHQ-5-1, 3088	K.LKDVLLQVDDERR.N	1599.81402	2	3.67E-04	0.95	3.78	-	1585.9
AHQ-5-3, 2691	K.LKNKHEAMITDLEER.L	1828.08363	2	1.58E-10	0.91	3.60	-	921.1
AHQ-5-3, 7699	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	3	1.69E-06	0.87	3.89	-	1128.1
AHQ-5-2, 7651	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	3	1.06E-05	0.92	4.13	-	1455.2
AHQ-5-2, 6063 - 6133	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.06E-09	0.97	5.14	-	1663.4
AHQ-5-10, 5416	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.30E-05	0.88	3.70	-	1023.7
AHQ-5-2, 5009	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	7.96E-07	0.70	3.37	-	637.8
AHQ-5-6, 5934	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.69E-04	0.88	3.99	-	800.0
AHQ-5-2, 6098 - 6169	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.49E-05	0.93	4.83	-	856.4
AHQ-5-3, 5677	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.60E-04	0.91	3.82	-	800.5
AHQ-5-1, 6259	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.90E-09	0.97	5.14	-	1643.5
AHQ-5-6, 5933	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.76E-10	0.97	5.49	-	1784.7
AHQ-5-1, 6260	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	7.62E-04	0.90	4.26	-	778.7
AHQ-5-4, 6161	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	8.89E-08	0.91	4.38	-	882.1
AHQ-5-7, 5822	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.10E-10	0.95	4.41	-	1191.7
AHQ-5-2, 5011	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.60E-09	0.95	4.61	-	1210.9
AHQ-5-3, 6233 - 6259	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	6.87E-07	0.94	5.15	-	943.4
AHQ-5-2, 6165	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.10E-10	0.97	5.02	-	1709.4
AHQ-5-3, 6231 - 6303	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.44E-11	0.96	4.90	-	1323.9
AHQ-5-5, 5978 - 6049	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.69E-05	0.91	4.50	-	791.6
AHQ-5-2, 5587	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.46E-08	0.85	3.26	-	744.5
AHQ-5-4, 6160 - 6165	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.66E-11	0.96	4.68	-	1417.1
AHQ-5-5, 6038 - 6039	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.02E-11	0.97	5.69	-	1396.7
AHQ-5-3, 6090 - 6157	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.99E-15	0.98	6.40	-	1513.9
AHQ-5-2, 5869 - 5938	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	7.56E-12	0.98	6.73	-	1757.0
AHQ-5-2, 6005 - 6073	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.20E-11	0.98	6.14	-	1383.5
AHQ-5-3, 6225	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.80E-09	0.97	5.29	-	1392.9
AHQ-5-2, 6141 - 6205	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.11E-07	0.97	6.02	-	1307.6
AHQ-5-1, 5951 - 6019	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	7.55E-14	0.98	7.00	-	1613.6
AHQ-5-3, 6307 - 6379	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.51E-11	0.97	6.25	-	1124.3
AHQ-5-5, 5782 - 5827	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.96E-06	0.97	5.11	-	1267.6
AHQ-5-2, 6226 - 6302	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.21E-08	0.97	5.39	-	1299.5
AHQ-5-3, 6017 - 6085	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.00E-10	0.98	6.71	-	1930.8
AHQ-5-3, 7030	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	7.21E-06	0.87	3.74	-	883.4
AHQ-5-5, 5901 - 5971	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.73E-04	0.94	4.53	-	1226.8
AHQ-5-2, 6454 - 6533	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.02E-07	0.98	6.15	-	1792.2
AHQ-5-1, 6088	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.53E-09	0.97	6.02	-	983.7
AHQ-5-2, 7225	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.40E-05	0.93	4.51	-	717.1
AHQ-5-4, 5893 - 5965	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.26E-08	0.98	5.60	-	1737.6
AHQ-5-2, 6602 - 6683	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.67E-09	0.98	6.08	-	1355.9
AHQ-5-3, 5919 - 5989	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.74E-13	0.98	6.16	-	1423.7
AHQ-5-1, 6173	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.14E-10	0.97	5.36	-	1611.3
AHQ-5-2, 4107	K.LRLEVNLQAMK.A	1315.61090	2	2.87E-05	0.94	3.74	-	1312.5
AHQ-5-4, 4042	K.LRLEVNLQAMK.A	1315.61090	2	5.16E-04	0.92	3.55	-	1086.3
AHQ-5-1, 3697	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	3.54E-04	0.67	3.35	-	606.3
AHQ-5-3, 5305 - 5313	R.LTEMETLQSQLMAEK.L	1753.03211	2	6.02E-08	0.92	3.86	-	1251.1
AHQ-5-3, 5193	R.LTEMETLQSQLMAEK.L	1753.03211	2	1.22E-04	0.97	5.10	-	1758.5
AHQ-5-2, 4571 - 4589	R.LTEMETLQSQLM*AEK.L	1769.03151	2	5.82E-04	0.96	5.32	-	1222.0
AHQ-5-2, 5237 - 5250	R.LTEMETLQSQLMAEK.L	1753.03211	2	2.36E-04	0.89	3.59	-	1128.6
AHQ-5-4, 4581	R.LTEMETLQSQLM*AEK.L	1769.03151	2	2.38E-04	0.89	3.80	-	957.5
AHQ-5-2, 3451 - 3530	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	1.02E-04	0.94	4.30	-	1110.2
AHQ-5-2, 5121 - 5137	R.LTEMETLQSQLMAEK.L	1753.03211	2	8.51E-10	0.98	5.86	-	1675.1
AHQ-5-4, 5128	R.LTEMETLQSQLMAEK.L	1753.03211	2	1.19E-04	0.97	4.89	-	1767.6
AHQ-5-3, 3982	K.MEDSVGCLETAEEVK.R	1698.85159	2	4.56E-07	0.91	4.24	-	646.5
AHQ-5-2, 3934	K.MEDSVGCLETAEEVK.R	1698.85159	2	2.07E-06	0.66	2.94	-	599.7
AHQ-5-4, 3504	K.MEDSVGCLETAEEVKR.K	1855.03794	2	3.04E-09	0.88	3.76	-	577.1
AHQ-5-3, 3191	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	7.92E-07	0.87	3.47	-	596.9
AHQ-5-2, 3137	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	1.00E-05	0.93	3.86	-	881.2
AHQ-5-3, 3538	K.MEDSVGCLETAEEVKR.K	1855.03794	2	3.00E-08	0.76	3.01	-	548.9
AHQ-5-2, 3510	K.MEDSVGCLETAEEVKR.K	1855.03794	3	1.28E-07	0.69	3.18	-	574.0
AHQ-5-2, 5626 - 5645	K.MQQNIQELEEQLEEEESAR.Q	2334.46063	3	9.54E-12	0.97	6.95	-	1672.5
AHQ-5-13-, 5148 - 5167	K.NFINNPLAQADWAAK.K	1673.85315	2	2.54E-08	0.96	5.44	-	1076.0
AHQ-5-7, 4954	K.NFINNPLAQADWAAK.K	1673.85315	2	3.79E-04	0.96	4.94	-	1128.2
AHQ-5-5, 5178 - 5201	K.NFINNPLAQADWAAK.K	1673.85315	2	7.72E-10	0.96	4.70	-	1186.0
AHQ-5-2, 5321 - 5393	K.NFINNPLAQADWAAK.K	1673.85315	2	5.47E-11	0.95	4.83	-	948.9
AHQ-5-13, 5252 - 5253	K.NFINNPLAQADWAAK.K	1673.85315	2	3.68E-09	0.96	4.79	-	1236.1
AHQ-5-1, 5452 - 5461	K.NFINNPLAQADWAAK.K	1673.85315	2	3.32E-06	0.92	4.21	-	940.2
AHQ-5-3, 6127	K.NFINNPLAQADWAAK.K	1673.85315	2	1.11E-05	0.91	3.95	-	790.1
AHQ-5-9, 4544	K.NFINNPLAQADWAAK.K	1673.85315	2	6.19E-05	0.72	3.02	-	600.2

AHQ-5-4, 6086	K.NFINNPLAQADWAAK.K	1673.85315	2	8.18E-09	0.92	4.24	-	779.5
AHQ-5-12, 5209	K.NFINNPLAQADWAAK.K	1673.85315	2	2.90E-04	0.66	2.59	-	760.1
AHQ-5-2, 5498	K.NFINNPLAQADWAAK.K	1673.85315	2	1.11E-08	0.87	3.80	-	648.7
AHQ-5-2, 6045	K.NFINNPLAQADWAAK.K	1673.85315	2	2.71E-08	0.91	4.03	-	853.0
AHQ-5-1, 6085 - 6100	K.NFINNPLAQADWAAK.K	1673.85315	2	7.07E-06	0.94	4.38	-	948.4
AHQ-5-10, 5298	K.NFINNPLAQADWAAK.K	1673.85315	2	3.40E-05	0.80	3.58	-	641.9
AHQ-5-3, 5413	K.NFINNPLAQADWAAK.K	1673.85315	2	1.85E-05	0.96	4.89	-	1227.4
AHQ-5-2, 5746	K.NFINNPLAQADWAAK.K	1673.85315	2	5.38E-08	0.95	4.27	-	1284.3
AHQ-5-14-, 5115	K.NFINNPLAQADWAAK.K	1673.85315	2	2.74E-08	0.93	4.14	-	1081.9
AHQ-5-6, 5120	K.NFINNPLAQADWAAK.K	1673.85315	2	6.56E-07	0.94	4.53	-	1038.1
AHQ-5-4, 5382	K.NFINNPLAQADWAAK.K	1673.85315	2	3.73E-11	0.96	5.14	-	1173.4
AHQ-5-4, 2370	K.NKHEAMITDLEER.L	1586.75247	2	3.77E-08	0.91	3.08	-	1322.2
AHQ-5-5, 2250	K.NKHEAMITDLEER.L	1586.75247	2	8.63E-08	0.89	3.68	-	781.9
AHQ-5-3, 2405	K.NKHEAMITDLEER.L	1586.75247	2	3.41E-09	0.91	3.41	-	1083.8
AHQ-5-1, 2627	K.NKHEAMITDLEER.L	1586.75247	2	1.26E-05	0.88	3.09	-	911.0
AHQ-5-2, 2337 - 2349	K.NKHEAMITDLEER.L	1586.75247	2	2.92E-06	0.93	3.73	-	1248.4
AHQ-5-2, 5177 - 5181	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.88E-05	0.96	4.73	-	1169.7
AHQ-5-1, 5311	K.NLPIYSEEIVEM*YK.G	1744.98660	2	6.05E-06	0.92	3.96	-	817.1
AHQ-5-6, 5573 - 5597	K.NLPIYSEEIVEMYK.G	1728.98720	2	6.05E-04	0.90	3.78	-	622.9
AHQ-5-1, 5967	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.64E-04	0.90	3.54	-	766.9
AHQ-5-13, 5662	K.NLPIYSEEIVEMYK.G	1728.98720	2	4.15E-05	0.95	4.25	-	950.2
AHQ-5-4, 5225 - 5300	K.NLPIYSEEIVEM*YK.G	1744.98660	2	9.51E-05	0.94	4.65	-	797.0
AHQ-5-12, 5626	K.NLPIYSEEIVEMYK.G	1728.98720	2	6.36E-05	0.70	2.97	-	475.9
AHQ-5-3, 5898 - 5909	K.NLPIYSEEIVEMYK.G	1728.98720	2	8.92E-05	0.91	3.88	-	760.4
AHQ-5-13-, 5561	K.NLPIYSEEIVEMYK.G	1728.98720	2	8.04E-05	0.88	3.14	-	726.8
AHQ-5-11, 5435 - 5442	K.NLPIYSEEIVEMYK.G	1728.98720	2	7.84E-06	0.93	4.27	-	711.4
AHQ-5-10, 5056	K.NLPIYSEEIVEMYK.G	1728.98720	2	7.02E-05	0.77	3.23	-	524.5
AHQ-5-7, 5374 - 5384	K.NLPIYSEEIVEMYK.G	1728.98720	2	9.84E-04	0.86	3.75	-	465.3
AHQ-5-3, 6207	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	3.82E-05	0.65	2.94	-	497.1
AHQ-5-2, 5795	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.36E-07	0.96	5.06	-	1038.4
AHQ-5-4, 5548	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	8.73E-05	0.94	4.77	-	915.4
AHQ-5-2, 5630	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	4.11E-08	0.95	4.13	-	1048.5
AHQ-5-2, 5509	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	3	5.47E-05	0.69	3.22	-	355.2
AHQ-5-3, 5889 - 5962	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	7.82E-10	0.92	3.85	-	841.9
AHQ-5-3, 5727	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.33E-05	0.90	4.15	-	584.8
AHQ-5-5, 5321	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	3.39E-05	0.82	3.65	-	672.1
AHQ-5-3, 5589 - 5607	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	2.40E-04	0.88	4.07	-	622.3
AHQ-5-6, 5242 - 5296	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	7.04E-07	0.81	3.63	-	590.6
AHQ-5-3, 5227	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	3.81E-05	0.80	3.65	-	677.3
AHQ-5-3, 5131	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	5.19E-07	0.85	3.34	-	921.1
AHQ-5-1, 5597 - 5676	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	2.21E-04	0.94	4.49	-	825.9
AHQ-5-2, 5034	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	4.01E-08	0.93	4.27	-	831.3
AHQ-5-1, 5777	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	4.67E-05	0.91	3.97	-	700.6
AHQ-5-2, 5490 - 5558	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.63E-05	0.90	3.80	-	898.5
AHQ-5-1, 5183	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	1.20E-07	0.87	3.63	-	848.2
AHQ-5-2, 5041 - 5051	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	9.30E-09	0.91	4.11	-	1053.2
AHQ-5-1, 5176	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	1.11E-04	0.88	3.50	-	867.6
AHQ-5-3, 7558	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	3.85E-06	0.98	5.56	-	2053.6
AHQ-5-6, 7361	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	2.51E-04	0.97	5.96	-	1364.9
AHQ-5-2, 7545	K.PAGPPGILALLDEECWFPK.A	2112.43315	2	8.33E-08	0.98	5.94	-	2019.3
AHQ-5-2, 3066	R.QAQQERDELADEIANSSGK.G	2090.15168	2	5.04E-04	0.89	3.72	-	612.8
AHQ-5-3, 2782	R.QAQQERDELADEIANSSGK.G	2090.15168	2	4.98E-04	0.78	3.57	-	536.5
AHQ-5-3, 3109 - 3115	R.QAQQERDELADEIANSSGK.G	2090.15168	2	2.84E-06	0.85	3.78	-	504.8
AHQ-5-1, 3259	R.QAQQERDELADEIANSSGK.G	2090.15168	3	1.97E-05	0.93	4.27	-	1208.8
AHQ-5-2, 4546	K.QELEEICHDLEAR.V	1643.75744	2	9.33E-06	0.92	3.95	-	831.6
AHQ-5-2, 1927	R.QLEEAEEEAQR.A	1332.35590	2	3.62E-06	0.80	3.20	-	577.8
AHQ-5-2, 2782	K.QTLENERGELANEVK.V	1730.85818	3	1.71E-04	0.53	3.01	-	322.2
AHQ-5-10, 3111	R.RGDLPFVVPR.R	1156.36217	2	6.65E-05	0.94	3.83	-	1049.3
AHQ-5-6, 3142 - 3148	R.RGDLPFVVPR.R	1156.36217	2	1.20E-04	0.92	3.60	-	967.1
AHQ-5-2, 3266 - 3337	R.RGDLPFVVPR.R	1156.36217	2	3.19E-06	0.94	3.94	-	1093.3
AHQ-5-11, 3304	R.RGDLPFVVPR.R	1156.36217	2	3.64E-06	0.94	3.87	-	1244.5
AHQ-5-4, 3397 - 3406	R.RGDLPFVVPR.R	1156.36217	2	2.17E-05	0.96	3.92	-	1577.4
AHQ-5-1, 3636 - 3643	R.RGDLPFVVPR.R	1156.36217	2	2.65E-06	0.97	4.18	-	1553.5
AHQ-5-3, 3433 - 3443	R.RGDLPFVVPR.R	1156.36217	2	5.33E-04	0.91	3.51	-	1014.0
AHQ-5-2, 2701	K.RHEM*PPHIYAITDTAYR.S	2088.33519	3	1.65E-05	0.95	4.30	-	1631.0
AHQ-5-1, 6924	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	2.17E-10	0.96	5.85	-	1375.4
AHQ-5-2, 6887 - 6954	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.86E-11	0.96	6.06	-	1327.3
AHQ-5-4, 6932	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	3.52E-06	0.95	5.33	-	1571.2
AHQ-5-2, 2758	K.RQAQQERDELADEIANSSGK.G	2246.33803	2	8.35E-04	0.41	2.76	-	266.3
AHQ-5-3, 1871	K.RQLEEAEEEAQR.A	1488.54225	2	2.14E-04	0.97	4.88	-	1838.8
AHQ-5-2, 1837	K.RQLEEAEEEAQR.A	1488.54225	2	1.24E-05	0.98	5.35	-	2926.1
AHQ-5-3, 6469	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.10E-07	0.92	4.78	-	855.3
AHQ-5-4, 6345	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.00E-07	0.76	3.55	-	537.2
AHQ-5-2, 6459 - 6531	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.79E-08	0.96	6.05	-	1089.1
AHQ-5-13-, 6021 - 6089	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.13E-06	0.86	4.13	-	698.3
AHQ-5-13-, 5903	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	9.70E-09	0.96	5.58	-	1496.3
AHQ-5-2, 6221 - 6301	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.15E-09	0.94	5.24	-	927.6
AHQ-5-5, 6218 - 6293	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	4.79E-09	0.92	4.77	-	1005.1
AHQ-5-1, 6449	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	7.78E-08	0.95	5.16	-	1429.6
AHQ-5-1, 6303 - 6365	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	7.43E-05	0.97	5.73	-	2149.2
AHQ-5-2, 6679	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.37E-08	0.94	5.26	-	1000.4
AHQ-5-10, 5562	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.12E-08	0.93	4.45	-	999.0
AHQ-5-3, 6373	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	6.77E-10	0.93	4.81	-	1073.5
AHQ-5-13, 6170	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.73E-04	0.87	4.13	-	807.5
AHQ-5-2, 6370	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	9.01E-09	0.83	3.68	-	739.8
AHQ-5-4, 6970 - 7042	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	2.93E-04	0.91	3.88	-	1152.4
AHQ-5-1, 6009	K.SM*EAEMIQLQEELAAAER.A	2066.30004	3	5.28E-04	0.86	4.30	-	1253.6
AHQ-5-2, 4817	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	5.95E-07	0.97	5.28	-	1534.4
AHQ-5-4, 5901 - 5974	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	1.19E-05	0.88	4.64	-	923.9
AHQ-5-7, 6710	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	5.56E-09	0.96	5.07	-	1181.6
AHQ-5-3, 7065	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	8.12E-04	0.89	3.70	-	999.9
AHQ-5-2, 7005 - 7077	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	2.42E-04	0.97	5.64	-	1841.2
AHQ-5-3, 7055	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	1.92E-05	0.96	4.44	-	2062.5
AHQ-5-2, 7014 - 7015	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.65E-08	0.95	5.08	-	1224.1
AHQ-5-3, 7045	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	4.41E-06	0.96	4.86	-	1630.7
AHQ-5-5, 6877 - 6951	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.83E-04	0.97	5.62	-	1481.8
AHQ-5-1, 6984	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	9.68E-11	0.97	4.89	-	2697.0
AHQ-5-3, 4870	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.32E-08	0.97	5.08	-	1645.7
AHQ-5-1, 5689	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	2.90E-07	0.92	4.37	-	1412.4
AHQ-5-2, 7143 - 7217	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.64E-05	0.96	4.58	-	1839.1
AHQ-5-3, 7041 - 7110	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	6.64E-04	0.97	5.55	-	1980.4
AHQ-5-1, 4872	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.50E-08	0.98	5.38	-	1837.1
AHQ-5-3, 5949 - 6027	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	5.43E-08	0.94	4.87	-	1716.3
AHQ-5-1, 3607	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	3.70E-05	0.98	5.85	-	1548.8
AHQ-5-3, 3495	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	3.92E-09	0.96	5.10	-	1694.0
AHQ-5-6, 3248	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	6.33E-07	0.96	5.89	-	1381.3
AHQ-5-4, 3458	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	2.20E-06	0.95	4.98	-	1494.6

AHQ-5-2, 3437	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	1.44E-06	0.97	6.11	-	1264.7
AHQ-5-5, 3293	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	2.15E-04	0.97	5.67	-	1508.5
AHQ-5-1, 3807 - 3816	K.TDLLLEPYNK.Y	1206.36989	2	1.28E-04	0.90	3.92	-	958.1
AHQ-5-7, 3291 - 3292	K.TDLLLEPYNK.Y	1206.36989	2	1.70E-04	0.79	2.84	-	963.6
AHQ-5-4, 3677	K.TDLLLEPYNK.Y	1206.36989	1	8.27E-04	0.05	1.87	-	231.1
AHQ-5-4, 3669	K.TDLLLEPYNK.Y	1206.36989	2	1.43E-06	0.88	3.57	-	916.3
AHQ-5-3, 3693 - 3694	K.TDLLLEPYNK.Y	1206.36989	2	7.76E-05	0.92	4.01	-	992.1
AHQ-5-5, 3461	K.TDLLLEPYNK.Y	1206.36989	2	5.38E-06	0.95	3.67	-	1520.1
AHQ-5-6, 3397	K.TDLLLEPYNK.Y	1206.36989	2	5.46E-07	0.94	4.20	-	1096.2
AHQ-5-2, 3615 - 3697	K.TDLLLEPYNK.Y	1206.36989	2	2.30E-05	0.94	4.12	-	1202.1
AHQ-5-2, 3795 - 3799	K.TDLLLEPYNKYR.F	1525.73037	2	8.29E-07	0.92	4.14	-	905.9
AHQ-5-2, 3943	K.TDLLLEPYNKYR.F	1525.73037	2	1.84E-06	0.63	2.65	-	669.3
AHQ-5-4, 4438	K.TELEDTLDSTAAQQELR.S	1921.00969	2	4.95E-06	0.95	4.51	-	1278.6
AHQ-5-1, 4432 - 4480	K.TELEDTLDSTAAQQELR.S	1921.00969	2	7.83E-07	0.96	4.79	-	1224.4
AHQ-5-3, 4457 - 4470	K.TELEDTLDSTAAQQELR.S	1921.00969	2	2.91E-08	0.94	4.43	-	1173.0
AHQ-5-5, 4302	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.78E-06	0.96	4.55	-	1645.8
AHQ-5-2, 3029	R.TEMEDLMSSK.D	1171.32449	2	6.12E-05	0.92	3.35	-	1002.8
AHQ-5-1, 3184 - 3185	R.TEMEDLMSSK.D	1171.32449	2	2.15E-04	0.87	3.06	-	782.7
AHQ-5-4, 3050	R.TEMEDLMSSK.D	1171.32449	2	1.02E-05	0.87	2.82	-	971.6
AHQ-5-4, 3325 - 3358	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.64E-07	0.90	3.97	-	1009.1
AHQ-5-3, 3343	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.05E-04	0.92	3.53	-	1170.0
AHQ-5-5, 3151	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.76E-07	0.91	3.89	-	1067.4
AHQ-5-2, 3297	R.TEMEDLMSSKDDVGK.S	1685.85626	2	4.86E-09	0.95	4.43	-	1168.2
AHQ-5-1, 3240	R.TEMEDLMSSKDDVGK.S	1685.85626	2	5.25E-06	0.86	3.43	-	983.0
AHQ-5-6, 3106	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.19E-06	0.69	2.82	-	828.7
AHQ-5-2, 6709	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.01E-06	0.98	5.50	-	1747.4
AHQ-5-7, 5924 - 5966	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	2.01E-05	0.81	3.36	-	834.2
AHQ-5-6, 6286	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	6.31E-05	0.97	4.81	-	1938.4
AHQ-5-3, 6605	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.54E-07	0.98	5.63	-	1887.0
AHQ-5-2, 6438 - 6478	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.62E-07	0.96	5.48	-	1230.6
AHQ-5-4, 6585	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	3.68E-07	0.96	4.99	-	1360.9
AHQ-5-2, 6433 - 6479	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	1.69E-04	0.98	5.41	-	1779.7
AHQ-5-6, 6290	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	3.12E-08	0.96	4.90	-	1354.0
AHQ-5-4, 1750	K.VAAYDKLEK.T	1037.19123	2	3.03E-05	0.68	2.56	-	551.9
AHQ-5-2, 3149	K.VEAQLQELQVK.F	1285.47179	2	1.32E-06	0.92	3.66	-	1195.1
AHQ-5-4, 3202	K.VEAQLQELQVK.F	1285.47179	2	1.13E-05	0.95	3.86	-	1499.2
AHQ-5-3, 3227 - 3233	K.VEAQLQELQVK.F	1285.47179	2	2.59E-06	0.96	4.11	-	1605.4
AHQ-5-5, 3034	K.VEAQLQELQVK.F	1285.47179	2	9.45E-06	0.92	3.44	-	1250.9
AHQ-5-1, 3365 - 3368	K.VEAQLQELQVK.F	1285.47179	2	9.49E-07	0.96	4.17	-	1321.8
AHQ-5-10, 4658	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	6.14E-06	0.90	4.25	-	645.4
AHQ-5-2, 6014	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	7.58E-13	0.94	5.17	-	599.2
AHQ-5-6, 5106 - 5109	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.12E-05	0.93	4.19	-	1166.9
AHQ-5-6, 5108	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	5.17E-05	0.85	3.61	-	763.5
AHQ-5-13-, 5144 - 5145	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.58E-09	0.95	4.78	-	1547.7
AHQ-5-10, 5246	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	5.41E-08	0.92	4.42	-	795.7
AHQ-5-11, 5599 - 5612	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	7.99E-08	0.89	4.20	-	723.5
AHQ-5-2, 6013 - 6018	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.72E-08	0.95	5.24	-	857.2
AHQ-5-6, 5689 - 5761	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.19E-11	0.93	4.39	-	985.0
AHQ-5-6, 5700 - 5777	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	6.44E-08	0.81	3.56	-	612.8
AHQ-5-6, 5782 - 5861	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.92E-09	0.91	4.26	-	776.0
AHQ-5-2, 6289	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.67E-08	0.85	4.28	-	537.0
AHQ-5-2, 6294	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	6.08E-10	0.88	3.96	-	1044.2
AHQ-5-1, 6124 - 6144	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.60E-08	0.90	3.74	-	688.0
AHQ-5-4, 6064 - 6076	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.77E-09	0.95	4.90	-	862.6
AHQ-5-4, 6077	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.06E-07	0.86	3.45	-	1043.9
AHQ-5-2, 5283 - 5306	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.45E-09	0.88	4.02	-	567.6
AHQ-5-2, 5985 - 6053	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.00E-11	0.97	5.55	-	1048.5
AHQ-5-3, 6138	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.33E-08	0.89	4.31	-	701.0
AHQ-5-3, 6133	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.16E-09	0.95	4.69	-	1063.4
AHQ-5-1, 6143	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.93E-04	0.75	3.07	-	759.4
AHQ-5-13, 5746	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.35E-09	0.92	4.33	-	756.6
AHQ-5-1, 5443 - 5512	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.70E-04	0.77	3.78	-	427.3
AHQ-5-9, 5106 - 5107	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.52E-12	0.96	4.75	-	1432.1
AHQ-5-5, 5159	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	8.87E-04	0.31	2.96	-	306.9
AHQ-5-13, 5229	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	9.29E-05	0.68	3.25	-	379.0
AHQ-5-5, 5757 - 5825	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	3.34E-10	0.94	5.02	-	729.0
AHQ-5-5, 5915	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.49E-09	0.92	4.54	-	687.7
AHQ-5-2, 5309 - 5311	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	4.94E-09	0.96	5.63	-	1083.6
AHQ-5-7, 5631	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.00E-05	0.69	3.02	-	489.1
AHQ-5-7, 5623	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.82E-09	0.89	3.88	-	705.8
AHQ-5-2, 1910	R.VEEEAAQKNMALK.K	1461.66649	1	5.96E-04	0.24	1.87	-	433.1
AHQ-5-4, 1900	R.VEEEEEERCQHLQAEK.K	1916.01642	2	9.28E-05	0.70	3.18	-	741.4
AHQ-5-2, 1858	R.VEEEEEERCQHLQAEK.K	1916.01642	2	4.56E-05	0.85	3.57	-	843.3
AHQ-5-10, 3438	K.VIQYLAYVASSHK.S	1479.70484	2	1.97E-05	0.86	3.43	-	841.6
AHQ-5-7, 3404	K.VIQYLAYVASSHK.S	1479.70484	2	5.24E-06	0.93	3.36	-	1254.8
AHQ-5-2, 3821	K.VIQYLAYVASSHK.S	1479.70484	3	8.57E-05	0.81	3.70	-	519.8
AHQ-5-4, 3873 - 3878	K.VIQYLAYVASSHK.S	1479.70484	2	5.97E-04	0.96	4.19	-	1604.7
AHQ-5-6, 3520	K.VIQYLAYVASSHK.S	1479.70484	2	3.11E-04	0.96	3.98	-	1708.6
AHQ-5-3, 3903 - 3914	K.VIQYLAYVASSHK.S	1479.70484	2	8.36E-07	0.96	4.29	-	1388.7
AHQ-5-1, 4053 - 4128	K.VIQYLAYVASSHK.S	1479.70484	2	4.47E-05	0.92	3.74	-	1208.6
AHQ-5-2, 3818	K.VIQYLAYVASSHK.S	1479.70484	2	4.61E-07	0.96	3.88	-	1617.3
AHQ-5-2, 6543 - 6590	R.VISGVLQLGNIVFK.K	1487.81155	1	4.46E-06	0.46	3.20	-	343.2
AHQ-5-6, 6393 - 6461	R.VISGVLQLGNIVFK.K	1487.81155	2	9.06E-10	0.98	4.83	-	2086.4
AHQ-5-3, 6655 - 6730	R.VISGVLQLGNIVFK.K	1487.81155	2	6.43E-09	0.97	5.59	-	1449.8
AHQ-5-3, 6754	R.VISGVLQLGNIVFK.K	1487.81155	2	7.84E-05	0.92	2.95	-	1608.1
AHQ-5-2, 6551 - 6633	R.VISGVLQLGNIVFK.K	1487.81155	2	6.77E-09	0.97	5.39	-	1814.5
AHQ-5-2, 6677	R.VISGVLQLGNIVFK.K	1487.81155	1	2.93E-07	0.61	2.93	-	440.1
AHQ-5-13, 6330	R.VISGVLQLGNIVFK.K	1487.81155	2	1.19E-04	0.96	4.64	-	1288.9
AHQ-5-2, 6701	R.VISGVLQLGNIVFK.K	1487.81155	2	5.38E-05	0.97	3.65	-	2173.4
AHQ-5-5, 6465 - 6541	R.VISGVLQLGNIVFK.K	1487.81155	2	1.62E-04	0.97	4.50	-	1642.0
AHQ-5-7, 6150 - 6167	R.VISGVLQLGNIVFK.K	1487.81155	2	2.94E-07	0.96	4.51	-	1454.0
AHQ-5-2, 6443	R.VISGVLQLGNIVFK.K	1487.81155	2	1.10E-09	0.97	5.39	-	1281.9
AHQ-5-1, 6647 - 6667	R.VISGVLQLGNIVFK.K	1487.81155	2	5.03E-04	0.90	3.38	-	1049.2
AHQ-5-5, 6490	R.VISGVLQLGNIVFK.K	1487.81155	1	4.31E-04	0.60	3.34	-	249.8
AHQ-5-6, 6404 - 6410	R.VISGVLQLGNIVFK.K	1487.81155	1	2.92E-04	0.48	2.94	-	612.3
AHQ-5-1, 6047	R.VISGVLQLGNIVFKK.E	1615.98446	2	7.83E-08	0.90	3.64	-	955.2
AHQ-5-3, 2191 - 2205	K.VKPLLQVSR.Q	1040.28462	2	1.35E-05	0.48	2.52	-	305.1
AHQ-5-5, 4657 - 4659	K.VSHLLGINVTDFTR.G	1572.79026	2	4.11E-09	0.93	4.28	-	1153.5
AHQ-5-4, 4932 - 4940	K.VSHLLGINVTDFTR.G	1572.79026	2	2.63E-10	0.97	5.32	-	1617.2
AHQ-5-2, 4842 - 4913	K.VSHLLGINVTDFTR.G	1572.79026	2	2.60E-10	0.96	4.54	-	1453.6
AHQ-5-5, 4671	K.VSHLLGINVTDFTR.G	1572.79026	3	8.96E-05	0.88	3.78	-	1217.6
AHQ-5-1, 5069 - 5071	K.VSHLLGINVTDFTR.G	1572.79026	3	1.17E-04	0.87	3.73	-	989.6
AHQ-5-1, 5055	K.VSHLLGINVTDFTR.G	1572.79026	2	3.02E-11	0.97	5.21	-	1604.4
AHQ-5-2, 5111	K.VSHLLGINVTDFTR.G	1572.79026	2	2.29E-04	0.94	4.16	-	1157.2
AHQ-5-6, 4596	K.VSHLLGINVTDFTR.G	1572.79026	2	7.42E-11	0.97	4.49	-	1663.4
AHQ-5-3, 4985 - 4991	K.VSHLLGINVTDFTR.G	1572.79026	2	6.10E-11	0.97	5.02	-	1530.6
AHQ-5-3, 5011	K.VSHLLGINVTDFTR.G	1572.79026	3	6.34E-04	0.92	4.14	-	1210.1

AHQ-5-6, 4601	K.VSHLLGINVTDFTR.G	1572.79026	3	3.52E-05	0.80	3.64	-	906.6
AHQ-5-2, 2929 - 3002	R.VVFQEFR.Q	925.06580	2	2.69E-04	0.84	2.52	-	677.6
AHQ-5-2, 3946	R.YEILTPNSIPK.G	1275.47536	2	1.30E-07	0.91	3.78	-	1013.4
AHQ-5-4, 3996 - 4012	R.YEILTPNSIPK.G	1275.47536	2	2.15E-06	0.92	3.49	-	1134.4
AHQ-5-4, 4001 - 4004	R.YEILTPNSIPK.G	1275.47536	1	3.34E-05	0.39	2.64	-	386.6
AHQ-5-2, 4091	R.YEILTPNSIPK.G	1275.47536	2	1.34E-04	0.83	2.90	-	907.2
AHQ-5-5, 3802 - 3819	R.YEILTPNSIPK.G	1275.47536	2	7.73E-05	0.90	3.37	-	1058.6
AHQ-5-3, 4026 - 4027	R.YEILTPNSIPK.G	1275.47536	2	1.55E-05	0.89	3.32	-	1182.6
AHQ-5-2, 6245	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	3	5.62E-09	0.96	5.00	-	1786.9
AHQ-5-10, 5451	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	2	6.62E-09	0.92	4.05	-	795.8
AHQ-5-1, 6293	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	3	8.85E-09	0.94	4.92	-	1087.0
gi|4506877|ref|NP_002996.1| selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;				1.44E-14	8.85	100.30	24.00	90844.7
AHQ-5-2, 5377 - 5394	K.AVQCQHLEAPSEGTMDCVHPLTAFAYGSSCK.F	3456.80579	3	8.46E-04	0.83	4.18	-	519.9
AHQ-5-3, 4926 - 4931	K.AVQCQHLEAPSEGTM*DCVHPLTAFAYGSSCK.F	3472.80519	3	2.65E-05	0.91	4.68	-	752.3
AHQ-5-4, 6860	R.CDNLGQWTAPAPVCQALQCQDLPVPNEAR.V	3313.64431	3	5.41E-06	0.87	4.61	-	722.1
AHQ-5-2, 6273	R.CIDSGHWSAPLPTCEAISCEPLESPVHGSMDCSPSLR.A	4146.54406	3	6.07E-06	0.97	6.07	-	1429.8
AHQ-5-3, 6329	R.CIDSGHWSAPLPTCEAISCEPLESPVHGSMDCSPSLR.A	4146.54406	3	1.75E-04	0.95	4.89	-	1526.9
AHQ-5-3, 4749 - 4751	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	1.18E-05	0.93	4.31	-	598.0
AHQ-5-2, 4726	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	1.26E-04	0.91	4.03	-	751.8
AHQ-5-3, 6298	K.LECLASGIWTNKPPQCLAAQCPPLKIPER.G	3352.89300	3	1.44E-14	0.93	4.54	-	1105.0
AHQ-5-3, 3066	R.PSGQWTAVTPACR.A	1432.58672	2	1.74E-05	0.83	3.03	-	788.9
AHQ-5-2, 3007	R.PSGQWTAVTPACR.A	1432.58672	2	3.44E-05	0.86	3.06	-	765.7
AHQ-5-2, 5039	K.STCQFICDEGYSLSGPER.L	2109.23671	2	2.71E-09	0.95	4.47	-	1039.1
AHQ-5-1, 5044 - 5051	K.STCQFICDEGYSLSGPER.L	2109.23671	2	5.44E-12	0.95	4.41	-	1162.3
AHQ-5-4, 5033	K.STCQFICDEGYSLSGPER.L	2109.23671	2	1.37E-07	0.94	4.43	-	931.1
AHQ-5-3, 5058 - 5069	K.STCQFICDEGYSLSGPER.L	2109.23671	2	4.02E-08	0.94	4.13	-	1030.7
AHQ-5-3, 6517	K.VLPYYSSYYWIGIR.K	1781.04522	2	8.13E-12	0.95	4.69	-	865.5
AHQ-5-2, 2738	R.YTDLVAIQNK.N	1165.32100	1	1.76E-04	0.68	2.68	-	632.9
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				1.44E-14	2.40	30.31	13.10	32164.8
AHQ-5-1, 5064	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.47E-08	0.96	5.24	-	980.7
AHQ-5-1, 5208 - 5280	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.59E-06	0.91	4.19	-	763.1
AHQ-5-1, 5544 - 5556	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.42E-04	0.96	5.44	-	1055.2
AHQ-5-1, 5760 - 5795	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.07E-05	0.93	5.05	-	701.3
AHQ-5-2, 5209 - 5213	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.31E-06	0.96	5.46	-	752.3
AHQ-5-2, 5733	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.73E-04	0.80	3.59	-	567.3
AHQ-5-3, 5241 - 5242	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.33E-05	0.86	3.86	-	625.9
AHQ-5-3, 5577	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.96E-06	0.95	5.37	-	860.2
AHQ-5-3, 5773 - 5842	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.07E-04	0.74	3.30	-	551.4
AHQ-5-4, 5088	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.92E-07	0.95	5.13	-	895.2
AHQ-5-4, 5205	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.33E-05	0.72	3.14	-	633.6
AHQ-5-4, 5217	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.28E-07	0.93	5.19	-	667.0
AHQ-5-4, 5552	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.97E-06	0.95	4.79	-	1180.2
AHQ-5-4, 5708 - 5729	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.89E-04	0.94	4.63	-	1001.1
AHQ-5-5, 5025 - 5105	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.97E-05	0.94	5.15	-	748.2
AHQ-5-5, 5455	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.81E-09	0.97	5.66	-	1300.9
AHQ-5-6, 5024	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.43E-07	0.94	4.83	-	885.4
AHQ-5-6, 5369 - 5392	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.72E-08	0.95	5.15	-	1038.9
AHQ-5-6, 5510 - 5530	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.57E-04	0.90	4.20	-	941.2
AHQ-5-14-, 5473 - 5489	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.25E-13	0.94	5.59	-	633.0
AHQ-5-8, 4588	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.83E-04	0.80	3.79	-	348.8
AHQ-5-8, 4701 - 4772	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.68E-05	0.97	6.13	-	1153.1
AHQ-5-8, 4730 - 4798	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.36E-05	0.95	5.01	-	1013.4
AHQ-5-8, 4868 - 4940	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.06E-05	0.95	4.75	-	933.7
AHQ-5-8, 5008 - 5078	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.22E-06	0.92	4.18	-	806.3
AHQ-5-8, 5104 - 5145	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.96E-05	0.92	4.68	-	618.5
AHQ-5-8, 5221 - 5253	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.38E-07	0.97	6.12	-	1376.9
AHQ-5-8, 5230 - 5245	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.45E-05	0.85	3.95	-	636.3
AHQ-5-8, 5320 - 5385	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.49E-06	0.97	5.57	-	1108.5
AHQ-5-8, 5452 - 5520	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.94E-05	0.96	5.25	-	1042.3
AHQ-5-8, 5552 - 5617	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.30E-06	0.95	4.72	-	1113.4
AHQ-5-8, 5681 - 5752	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.38E-06	0.97	5.71	-	1085.8
AHQ-5-8, 5768 - 5836	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.87E-06	0.96	5.33	-	977.5
AHQ-5-8, 5900 - 5966	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.47E-04	0.94	5.47	-	646.4
AHQ-5-8, 6032 - 6096	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.23E-05	0.96	5.09	-	1081.8
AHQ-5-8, 6161 - 6240	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.29E-07	0.97	5.93	-	967.2
AHQ-5-8, 6309 - 6376	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.29E-05	0.96	5.36	-	838.1
AHQ-5-8, 6430 - 6504	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.66E-06	0.86	3.47	-	812.6
AHQ-5-8, 6568 - 6632	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.44E-04	0.84	3.71	-	603.5
AHQ-5-8, 6696 - 6765	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.49E-06	0.92	4.44	-	785.9
AHQ-5-8, 6801 - 6864	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.40E-05	0.84	3.15	-	894.4
AHQ-5-8, 7334 - 7405	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.25E-04	0.93	4.76	-	920.9
AHQ-5-9, 4398 - 4470	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.36E-08	0.96	5.31	-	899.8
AHQ-5-10, 4434 - 4484	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.21E-06	0.95	5.08	-	726.2
AHQ-5-10, 4538 - 4599	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.99E-06	0.96	5.45	-	948.8
AHQ-5-10, 4704	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.43E-04	0.92	4.34	-	734.0
AHQ-5-10, 4951 - 5026	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.79E-05	0.94	4.85	-	793.9
AHQ-5-10, 5487 - 5550	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.73E-04	0.88	3.92	-	704.3
AHQ-5-11, 4718	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.18E-06	0.92	4.62	-	735.0
AHQ-5-11, 5126	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.32E-07	0.98	5.82	-	1980.4
AHQ-5-12, 4862 - 4929	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.69E-10	0.93	4.56	-	777.0
AHQ-5-12, 4992 - 5000	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.43E-04	0.94	4.73	-	879.1
AHQ-5-12, 5286	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.44E-14	0.97	5.40	-	1884.4
AHQ-5-12, 5428 - 5496	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.16E-05	0.84	3.88	-	617.3
AHQ-5-13, 4820 - 4889	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.19E-08	0.97	5.18	-	1305.4
AHQ-5-13, 5046 - 5121	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.20E-04	0.52	2.52	-	522.5
AHQ-5-13, 5172 - 5180	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.75E-07	0.96	5.62	-	1069.5
AHQ-5-13, 5236 - 5309	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.61E-06	0.95	5.29	-	914.4
AHQ-5-13, 5270 - 5277	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.86E-06	0.91	4.18	-	920.9
AHQ-5-13, 5320 - 5394	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.11E-06	0.91	4.27	-	690.1
AHQ-5-13, 5460 - 5524	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.36E-04	0.94	5.02	-	692.8
AHQ-5-13, 5588 - 5660	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.92E-04	0.93	4.70	-	742.4
AHQ-5-14, 5440	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.83E-09	0.96	5.14	-	1031.9
AHQ-5-14, 5533 - 5581	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.07E-05	0.95	5.09	-	849.3
AHQ-5-14, 5640 - 5696	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.72E-05	0.90	4.11	-	776.9
AHQ-5-14, 5722 - 5754	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.97E-05	0.96	5.61	-	965.6
AHQ-5-14, 5808 - 5885	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.01E-07	0.96	4.99	-	1244.3
AHQ-5-14, 5944 - 6006	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.25E-04	0.93	4.48	-	1099.7
AHQ-5-14, 6082 - 6141	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.64E-04	0.84	3.87	-	541.7
AHQ-5-13-, 4692 - 4739	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.58E-07	0.96	4.68	-	1267.8
AHQ-5-13-, 4803 - 4872	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.55E-06	0.97	5.55	-	1269.9
AHQ-5-13-, 4935	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.72E-05	0.91	3.96	-	804.5
AHQ-5-13-, 5047	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.10E-09	0.94	4.82	-	852.9
AHQ-5-13-, 5140	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.06E-09	0.97	5.42	-	1283.0
AHQ-5-13-, 5277 - 5339	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.06E-06	0.95	5.34	-	769.1
AHQ-5-13-, 5375 - 5435	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.41E-05	0.94	4.75	-	930.1
AHQ-5-14-, 4662 - 4725	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.12E-07	0.97	5.76	-	1235.6
AHQ-5-14-, 4763 - 4825	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.07E-04	0.97	5.88	-	1339.5

AHQ-5-14-, 4890	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.34E-06	0.96	5.50	-	1023.2
AHQ-5-14-, 4993 - 5053	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.91E-05	0.94	4.80	-	886.0
AHQ-5-14-, 5063 - 5129	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.79E-07	0.97	5.86	-	1332.2
AHQ-5-14-, 5117 - 5118	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.98E-08	0.95	4.81	-	1124.8
AHQ-5-14-, 5153 - 5221	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.55E-04	0.94	4.98	-	874.4
AHQ-5-14-, 5269	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.69E-04	0.90	4.42	-	506.8
AHQ-5-14-, 5297 - 5361	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.96E-05	0.92	4.79	-	670.5
AHQ-5-14-, 5345 - 5425	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.41E-05	0.96	5.66	-	804.2
AHQ-5-14-, 5497 - 5571	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.66E-06	0.96	4.97	-	1036.6
AHQ-5-8, 3176	K.YPIEHSIITNWDDMEK.I	1992.19784	2	6.30E-04	0.50	2.91	-	526.2
gi|4504165|ref|NP_000168.1| gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]				2.00E-14	20.36	230.39	38.60	85696.9
AHQ-5-5, 3610 - 3686	K.AGALNSNDAFVLK.T	1320.47622	2	9.69E-08	0.91	4.24	-	731.9
AHQ-5-5, 3682 - 3754	K.AGALNSNDAFVLK.T	1320.47622	1	3.07E-06	0.30	2.07	-	394.6
AHQ-5-5, 3699	K.AGALNSNDAFVLK.T	1320.47622	1	2.29E-04	0.44	2.58	-	385.4
AHQ-5-7, 3259	K.AGALNSNDAFVLK.T	1320.47622	2	4.68E-04	0.85	3.79	-	490.9
AHQ-5-5, 3607	K.AGALNSNDAFVLK.T	1320.47622	1	2.41E-07	0.44	2.66	-	358.1
AHQ-5-6, 3660	K.AGALNSNDAFVLK.T	1320.47622	2	4.35E-04	0.89	3.77	-	596.6
AHQ-5-6, 3298 - 3368	K.AGALNSNDAFVLK.T	1320.47622	2	3.24E-08	0.89	3.87	-	732.9
AHQ-5-4, 5942	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.64E-05	0.87	3.56	-	596.9
AHQ-5-5, 5573	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.97E-06	0.95	5.75	-	617.6
AHQ-5-3, 6022	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.79E-06	0.96	5.60	-	721.4
AHQ-5-5, 5718 - 5742	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.13E-10	0.97	5.72	-	888.0
AHQ-5-5, 5809	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	9.79E-08	0.95	5.60	-	713.7
AHQ-5-2, 5954	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.41E-05	0.93	4.60	-	682.5
AHQ-5-7, 5563	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.10E-06	0.87	4.27	-	474.8
AHQ-5-1, 6057 - 6069	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.52E-04	0.93	4.55	-	737.3
AHQ-5-10, 5004	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	8.18E-06	0.86	4.38	-	376.9
AHQ-5-1, 5865	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.59E-04	0.86	3.99	-	440.4
AHQ-5-9, 5024 - 5034	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.10E-06	0.95	5.45	-	597.1
AHQ-5-8, 5380 - 5382	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	8.98E-07	0.95	5.17	-	743.9
AHQ-5-8, 5209	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	7.87E-04	0.55	2.92	-	282.7
AHQ-5-5, 5899 - 5909	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.03E-06	0.92	4.85	-	560.8
AHQ-5-6, 5524	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	9.06E-05	0.92	4.62	-	486.3
AHQ-5-5, 5893	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	4.47E-05	0.83	3.25	-	1204.6
AHQ-5-6, 5596	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	5.21E-08	0.91	4.36	-	993.1
AHQ-5-5, 5629 - 5645	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	6.48E-09	0.96	4.81	-	1588.6
AHQ-5-13, 2389	K.DSQEEEKTEALTSAK.R	1666.72289	3	1.64E-07	0.97	4.18	-	2591.6
AHQ-5-13, 2385	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.48E-07	0.90	3.57	-	1078.7
AHQ-5-5, 2097	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.21E-06	0.92	3.91	-	1128.5
AHQ-5-10, 2048	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.15E-06	0.86	3.55	-	879.0
AHQ-5-5, 1997 - 2007	K.DSQEEEKTEALTSAK.R	1666.72289	3	7.79E-07	0.97	5.28	-	1988.6
AHQ-5-5, 1993 - 2029	K.DSQEEEKTEALTSAK.R	1666.72289	2	5.17E-07	0.92	3.59	-	1294.9
AHQ-5-6, 1992	K.DSQEEEKTEALTSAK.R	1666.72289	3	1.46E-05	0.90	3.73	-	1416.3
AHQ-5-6, 1980	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.51E-07	0.93	4.14	-	1220.4
AHQ-5-1, 2336	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.41E-06	0.80	3.14	-	1093.0
AHQ-5-3, 2145 - 2149	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.14E-07	0.88	3.30	-	1175.7
AHQ-5-8, 1884 - 1885	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.66E-06	0.93	3.65	-	1513.9
AHQ-5-13-, 2227 - 2228	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.58E-06	0.95	4.22	-	1341.0
AHQ-5-5, 5098	K.EPAHLMSLFGGKPMIIYK.G	2033.48916	2	1.16E-04	0.89	4.02	-	652.5
AHQ-5-5, 6902	R.EVQGFESATFLGYFK.S	1723.90570	2	2.13E-05	0.82	2.52	-	1018.7
AHQ-5-13-, 6104	R.EVQGFESATFLGYFK.S	1723.90570	2	7.30E-06	0.96	4.39	-	1463.8
AHQ-5-5, 6391 - 6466	R.EVQGFESATFLGYFK.S	1723.90570	2	1.21E-06	0.96	4.58	-	1283.3
AHQ-5-13, 6180 - 6244	R.EVQGFESATFLGYFK.S	1723.90570	2	1.18E-05	0.91	3.48	-	1201.4
AHQ-5-5, 7163	R.EVQGFESATFLGYFK.S	1723.90570	2	1.30E-04	0.77	2.59	-	837.6
AHQ-5-14-, 5991 - 6001	R.EVQGFESATFLGYFK.S	1723.90570	2	9.39E-05	0.96	4.60	-	1548.0
AHQ-5-9, 6540 - 6566	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	2	2.16E-05	0.68	2.80	-	443.4
AHQ-5-5, 7438 - 7511	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	2	2.00E-04	0.93	4.25	-	732.0
AHQ-5-12, 2242	K.HVVPNEVVVQR.L	1276.46981	2	5.31E-06	0.93	3.33	-	695.4
AHQ-5-5, 2275	K.HVVPNEVVVQR.L	1276.46981	1	1.34E-05	0.44	1.85	-	415.9
AHQ-5-6, 2054	K.HVVPNEVVVQR.L	1276.46981	2	5.21E-06	0.74	2.87	-	364.3
AHQ-5-8, 1904	K.HVVPNEVVVQR.L	1276.46981	2	1.39E-05	0.89	2.76	-	801.1
AHQ-5-7, 2014 - 2016	K.HVVPNEVVVQR.L	1276.46981	2	4.97E-09	0.90	3.60	-	519.4
AHQ-5-5, 2073	K.HVVPNEVVVQR.L	1276.46981	1	3.56E-06	0.25	2.61	-	165.1
AHQ-5-11, 2186	K.HVVPNEVVVQR.L	1276.46981	2	8.50E-09	0.90	3.44	-	573.7
AHQ-5-5, 2018 - 2090	K.HVVPNEVVVQR.L	1276.46981	1	3.45E-07	0.28	2.17	-	342.4
AHQ-5-5, 2061	K.HVVPNEVVVQR.L	1276.46981	2	4.66E-06	0.91	3.32	-	640.0
AHQ-5-5, 6835 - 6883	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	7.99E-08	0.89	3.68	-	1139.2
AHQ-5-5, 6462	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	7.39E-08	0.96	5.34	-	1500.8
AHQ-5-5, 6310 - 6381	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	3.92E-07	0.96	4.75	-	1702.4
AHQ-5-5, 6182	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	2.96E-13	0.95	5.44	-	1124.9
AHQ-5-6, 5476 - 5484	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.13E-09	0.98	7.44	-	1978.7
AHQ-5-3, 5769 - 5837	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	2.07E-05	0.79	3.67	-	577.2
AHQ-5-5, 5475 - 5545	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	2.00E-14	0.98	6.98	-	2033.2
AHQ-5-7, 5252	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.54E-06	0.95	5.35	-	1210.8
AHQ-5-5, 5215	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	4.49E-05	0.95	4.98	-	1330.2
AHQ-5-5, 5561 - 5631	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	3.32E-04	0.94	4.74	-	1087.8
AHQ-5-5, 2297	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	7.34E-06	0.89	4.06	-	598.6
AHQ-5-6, 2285	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	2.10E-04	0.76	3.50	-	300.4
AHQ-5-5, 2106	K.PALPAGTEDTAKEDAANRK.L	1956.10363	2	3.64E-05	0.62	2.81	-	414.9
AHQ-5-6, 2769	K.SEDCFILDHGK.D	1322.42590	2	1.12E-06	0.91	3.76	-	905.0
AHQ-5-5, 2754 - 2757	K.SEDCFILDHGK.D	1322.42590	2	1.84E-06	0.95	3.81	-	1190.5
AHQ-5-8, 1846	K.TGAQELLR.V	888.00387	2	8.66E-06	0.73	2.72	-	703.1
AHQ-5-5, 1926 - 1937	K.TGAQELLR.V	888.00387	2	7.25E-05	0.93	3.18	-	1285.1
AHQ-5-5, 4602	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	7.77E-05	0.96	4.94	-	1266.9
AHQ-5-5, 4450 - 4527	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	4.04E-05	0.94	3.87	-	1196.7
AHQ-5-5, 4313 - 4381	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	6.25E-05	0.96	4.81	-	1036.8
AHQ-5-5, 4198	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	9.42E-04	0.93	4.17	-	1089.3
AHQ-5-5, 4818	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	1.28E-07	0.96	5.32	-	1033.8
AHQ-5-6, 4761	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	4.65E-05	0.97	5.12	-	1201.4
AHQ-5-6, 5044	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	4.32E-10	0.94	5.30	-	904.3
AHQ-5-5, 4178 - 4182	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	6.06E-07	0.95	5.72	-	826.5
AHQ-5-5, 5078 - 5087	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	1.71E-12	0.95	5.61	-	996.2
AHQ-5-5, 3385 - 3457	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	2.09E-04	0.93	5.67	-	1274.1
AHQ-5-5, 3469	R.VPFDAATLHTSTAM*AAQHGMDDDGTGQK.Q	2891.10081	3	2.81E-06	0.94	5.56	-	1690.4
AHQ-5-5, 3845 - 3846	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	9.22E-12	0.99	7.81	-	2750.1
AHQ-5-5, 3863	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	2	1.23E-05	0.92	4.28	-	728.8
AHQ-5-5, 6765 - 6838	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	3	5.63E-04	0.83	4.15	-	646.1
AHQ-5-5, 7170 - 7250	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	2	1.99E-04	0.53	2.54	-	470.9
AHQ-5-5, 6161 - 6242	K.VSNGAGTMSVSLVADENPFAQGALK.S	2464.73740	3	7.52E-09	0.97	6.67	-	1868.2
AHQ-5-5, 6305 - 6375	K.VSNGAGTMSVSLVADENPFAQGALK.S	2464.73740	2	1.20E-05	0.36	2.81	-	268.0
gi|4504745|ref|NP_000410.1| integrin alpha 2b precursor [Homo sapiens]				2.39E-14	32.84	380.34	42.30	113374.2
AHQ-5-4, 1636 - 1937	R.AEAQVELR.G	916.01408	1	8.69E-04	0.30	2.00	-	345.2
AHQ-5-1, 5416 - 5479	R.AEGGQCPSLLFDLR.D	1564.74505	2	9.44E-05	0.93	3.87	-	898.9
AHQ-5-4, 5082	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.02E-04	0.88	3.14	-	1105.5
AHQ-5-13, 5293	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.88E-05	0.88	3.46	-	853.6
AHQ-5-10, 4702	R.AEGGQCPSLLFDLR.D	1564.74505	2	9.31E-07	0.90	3.70	-	921.4
AHQ-5-4, 5368 - 5440	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.34E-07	0.95	4.19	-	973.4

AHQ-5-12, 5158 - 5220	R.AEGGQCPSLLFDLR.D	1564.74505	2	8.43E-05	0.89	3.57	-	736.9
AHQ-5-7, 5014	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.48E-04	0.86	3.42	-	757.3
AHQ-5-4, 5464	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.85E-05	0.91	3.69	-	848.3
AHQ-5-5, 5221	R.AEGGQCPSLLFDLR.D	1564.74505	2	6.04E-06	0.94	3.54	-	1208.2
AHQ-5-3, 5446	R.AEGGQCPSLLFDLR.D	1564.74505	2	9.72E-06	0.93	3.84	-	1035.2
AHQ-5-4, 2773	R.ALSNVEGFER.L	1122.21308	2	2.53E-05	0.87	2.93	-	913.2
AHQ-5-4, 2688 - 2756	R.ALSNVEGFER.L	1122.21308	2	7.52E-07	0.87	3.19	-	837.4
AHQ-5-3, 2761 - 2762	R.ALSNVEGFER.L	1122.21308	2	2.59E-06	0.86	3.31	-	833.8
AHQ-5-5, 2561	R.ALSNVEGFER.L	1122.21308	2	1.66E-04	0.86	2.92	-	1008.0
AHQ-5-4, 5104 - 5172	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	4.40E-04	0.91	4.50	-	667.3
AHQ-5-5, 4930 - 4939	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	9.97E-05	0.77	3.28	-	574.3
AHQ-5-4, 5361 - 5378	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	1.63E-04	0.94	4.76	-	930.4
AHQ-5-4, 5212 - 5288	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	1.28E-06	0.92	4.47	-	670.6
AHQ-5-4, 2982	R.DETRNVGSQTLQTFK.A	1724.85363	2	9.11E-06	0.90	4.12	-	882.0
AHQ-5-4, 3122 - 3200	R.DETRNVGSQTLQTFK.A	1724.85363	2	3.67E-06	0.78	3.15	-	530.8
AHQ-5-5, 3885 - 3886	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.32E-08	0.94	4.84	-	737.8
AHQ-5-4, 4174	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.88E-04	0.88	3.35	-	899.4
AHQ-5-4, 3982	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	5.56E-05	0.72	3.23	-	573.3
AHQ-5-4, 3021 - 3024	R.EQNSLDSWGPK.V	1261.32250	1	9.54E-06	0.10	1.94	-	196.6
AHQ-5-4, 4532 - 4537	R.FGSAIAPLGDLDR.D	1332.48700	2	1.16E-08	0.95	4.09	-	1130.7
AHQ-5-4, 4390	R.FGSAIAPLGDLDR.D	1332.48700	2	3.05E-04	0.69	2.87	-	781.5
AHQ-5-4, 4557	R.FGSAIAPLGDLDR.D	1332.48700	1	3.29E-08	0.80	3.25	-	512.3
AHQ-5-5, 5813 - 5882	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.96E-08	0.94	5.47	-	1030.6
AHQ-5-3, 6053 - 6109	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.06E-09	0.91	4.92	-	944.2
AHQ-5-6, 5737 - 5802	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.50E-06	0.79	4.01	-	817.9
AHQ-5-4, 6016 - 6080	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.31E-09	0.93	5.40	-	797.7
AHQ-5-5, 5949 - 6025	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.55E-04	0.86	4.27	-	852.9
AHQ-5-4, 5878 - 5948	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.12E-08	0.91	5.18	-	578.6
AHQ-5-4, 7212 - 7280	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.00E-06	0.95	5.04	-	699.3
AHQ-5-4, 6420 - 6488	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.47E-07	0.95	5.29	-	680.8
AHQ-5-4, 6901 - 6965	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	8.33E-07	0.90	4.67	-	1265.0
AHQ-5-4, 6874 - 6933	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.84E-10	0.97	5.93	-	967.5
AHQ-5-4, 6553 - 6622	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.41E-06	0.89	4.04	-	526.5
AHQ-5-4, 6945 - 7016	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.26E-05	0.96	5.03	-	1038.7
AHQ-5-5, 6921 - 7001	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.29E-04	0.79	3.43	-	460.7
AHQ-5-4, 6668 - 6732	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	3.63E-04	0.74	3.50	-	327.9
AHQ-5-4, 6800 - 6868	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.73E-06	0.91	4.04	-	647.2
AHQ-5-4, 7080 - 7145	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.17E-08	0.95	5.15	-	590.1
AHQ-5-10, 4411 - 4436	R.GEAQVWTQLLR.A	1301.47614	2	7.93E-07	0.95	4.19	-	1141.4
AHQ-5-11, 4787 - 4850	R.GEAQVWTQLLR.A	1301.47614	2	5.34E-05	0.84	3.50	-	646.7
AHQ-5-4, 5960	R.GNSFPASLVVAAEEGER.E	1733.86053	2	7.93E-09	0.87	3.74	-	894.6
AHQ-5-4, 5332 - 5404	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.68E-11	0.86	3.91	-	699.9
AHQ-5-4, 5806 - 5872	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.03E-07	0.67	2.99	-	560.9
AHQ-5-4, 5630 - 5710	R.GNSFPASLVVAAEEGER.E	1733.86053	2	4.55E-09	0.94	4.37	-	841.8
AHQ-5-4, 5545 - 5560	R.GNSFPASLVVAAEEGER.E	1733.86053	2	2.67E-04	0.91	4.19	-	732.7
AHQ-5-4, 5448 - 5492	R.GNSFPASLVVAAEEGER.E	1733.86053	2	9.44E-06	0.81	3.74	-	563.6
AHQ-5-4, 6905 - 6969	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	1.40E-08	0.79	4.26	-	427.6
AHQ-5-4, 6841 - 6912	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	2	1.22E-07	0.55	3.28	-	214.9
AHQ-5-4, 6716 - 6785	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	5.98E-07	0.87	4.57	-	445.1
AHQ-5-4, 5065	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	9.78E-06	0.85	3.72	-	499.1
AHQ-5-5, 4974 - 4997	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	4.19E-07	0.97	5.50	-	1310.8
AHQ-5-4, 5185 - 5252	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.86E-06	0.97	6.05	-	998.4
AHQ-5-3, 5317 - 5341	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.13E-04	0.97	5.73	-	1148.7
AHQ-5-4, 5265 - 5320	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.39E-14	0.98	5.82	-	1312.8
AHQ-5-4, 5284	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	6.29E-05	0.90	3.84	-	1129.1
AHQ-5-6, 4948	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.77E-08	0.98	5.98	-	1232.0
AHQ-5-3, 5319 - 5322	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	6.67E-04	0.88	3.88	-	919.1
AHQ-5-4, 5080 - 5152	R.GQVLVFLGQSEGLR.S	1503.72793	2	7.21E-08	0.98	5.29	-	1897.8
AHQ-5-4, 5168 - 5238	R.GQVLVFLGQSEGLR.S	1503.72793	2	2.43E-08	0.96	4.33	-	1285.5
AHQ-5-3, 5195	R.GQVLVFLGQSEGLR.S	1503.72793	2	4.09E-07	0.95	3.84	-	1257.6
AHQ-5-4, 4377 - 4448	R.HDLLVGAPLYMESR.A	1601.85188	2	5.01E-06	0.97	4.32	-	1738.3
AHQ-5-3, 4487	R.HDLLVGAPLYMESR.A	1601.85188	2	2.06E-08	0.96	4.35	-	1436.1
AHQ-5-5, 4179	R.HDLLVGAPLYMESR.A	1601.85188	2	9.02E-08	0.94	3.26	-	1478.2
AHQ-5-4, 4385	R.HDLLVGAPLYMESR.A	1601.85188	3	1.79E-06	0.94	4.04	-	1328.0
AHQ-5-4, 3604 - 3676	K.HSPICHTTMAFLR.D	1572.83705	2	3.34E-08	0.81	3.02	-	477.0
AHQ-5-2, 4439	K.IVLLDVPVR.A	1024.28196	2	1.43E-04	0.92	3.37	-	1229.4
AHQ-5-5, 4211 - 4229	K.IVLLDVPVR.A	1024.28196	2	8.25E-04	0.92	3.78	-	939.8
AHQ-5-11, 4195	K.IVLLDVPVR.A	1024.28196	2	2.66E-05	0.93	3.44	-	1268.1
AHQ-5-6, 4142	K.IVLLDVPVR.A	1024.28196	2	1.52E-05	0.93	3.63	-	1060.3
AHQ-5-12, 4313	K.IVLLDVPVR.A	1024.28196	2	6.53E-04	0.91	3.48	-	982.4
AHQ-5-4, 4388 - 4456	K.IVLLDVPVR.A	1024.28196	2	6.92E-04	0.93	3.94	-	960.2
AHQ-5-4, 4525	R.IYVENDFSWDK.R	1416.51610	1	3.36E-08	0.33	2.13	-	377.9
AHQ-5-4, 4516 - 4518	R.IYVENDFSWDK.R	1416.51610	2	2.49E-06	0.86	3.38	-	549.8
AHQ-5-4, 3921	R.IYVENDFSWDKR.Y	1572.70245	3	9.65E-05	0.68	3.24	-	468.7
AHQ-5-4, 3885 - 3965	R.IYVENDFSWDKR.Y	1572.70245	2	9.89E-07	0.94	4.04	-	1253.4
AHQ-5-11, 6502 - 6560	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	1.61E-04	0.73	3.32	-	298.1
AHQ-5-10, 6404	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	4.56E-04	0.81	3.58	-	291.9
AHQ-5-10, 6238 - 6299	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	1.73E-08	0.90	4.23	-	396.4
AHQ-5-10, 6114 - 6179	R.LQDPVLVSCDSAPCTVVQCDLQEMAR.G	2996.36144	2	9.09E-06	0.67	2.76	-	428.2
AHQ-5-4, 4878	K.LSLNAELQLDR.Q	1272.43310	2	6.39E-08	0.92	3.84	-	1131.5
AHQ-5-4, 4730 - 4809	K.LSLNAELQLDR.Q	1272.43310	2	5.86E-06	0.94	3.77	-	1484.1
AHQ-5-11, 2068	R.NRPPLEEDDEEGE	1529.50164	2	2.39E-05	0.92	3.12	-	1380.9
AHQ-5-7, 2490	R.NVGSQTLQTFK.A	1223.36055	2	7.10E-04	0.86	3.32	-	491.4
AHQ-5-6, 2565	R.NVGSQTLQTFK.A	1223.36055	2	2.76E-07	0.92	3.52	-	796.4
AHQ-5-4, 2625 - 2696	R.NVGSQTLQTFK.A	1223.36055	2	1.14E-05	0.95	4.10	-	816.8
AHQ-5-12, 2761	R.NVGSQTLQTFK.A	1223.36055	2	4.77E-07	0.80	3.00	-	510.8
AHQ-5-4, 6664 - 6728	R.PSQVLDSPFPTGSAFGFSLR.G	2111.34205	2	1.21E-06	0.95	5.07	-	975.0
AHQ-5-4, 7570 - 7645	R.QGLGASVVSWSDVIVACAPWQHWNVLEK.T	3139.53208	3	3.64E-07	0.93	5.54	-	763.5
AHQ-5-4, 7397 - 7468	R.QGLGASVVSWSDVIVACAPWQHWNVLEK.T	3139.53208	3	3.48E-10	0.95	5.75	-	916.0
AHQ-5-4, 6244 - 6313	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.12E-05	0.97	6.57	-	1599.4
AHQ-5-4, 6284 - 6285	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	1.93E-09	0.97	6.28	-	842.0
AHQ-5-4, 6148 - 6216	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	1.07E-10	0.96	5.31	-	746.7
AHQ-5-3, 6263 - 6295	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	3.79E-04	0.91	4.85	-	1430.8
AHQ-5-4, 6001 - 6070	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.97E-04	0.79	3.35	-	1294.0
AHQ-5-4, 6149 - 6220	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.04E-12	0.98	6.69	-	2245.7
AHQ-5-6, 5914 - 5929	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.74E-08	0.97	6.42	-	1482.8
AHQ-5-14-, 5806	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	8.72E-06	0.92	4.78	-	1111.9
AHQ-5-5, 5947 - 5986	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.56E-10	0.98	6.69	-	1870.6
AHQ-5-1, 6287	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	3.51E-08	0.94	4.99	-	1020.1
AHQ-5-7, 5779	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	4.37E-04	0.93	4.31	-	1366.5
AHQ-5-7, 3367	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	4.77E-04	0.89	3.85	-	590.4
AHQ-5-3, 3745	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.28E-04	0.84	3.60	-	490.8
AHQ-5-6, 3452	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	6.18E-07	0.92	4.08	-	636.6
AHQ-5-4, 3640 - 3714	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	3.25E-07	0.96	5.39	-	866.8
AHQ-5-11, 3538	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.47E-04	0.87	4.02	-	413.1
AHQ-5-10, 3336	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.50E-04	0.92	3.98	-	743.2
AHQ-5-5, 3502	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.87E-05	0.94	4.56	-	653.3

AHQ-5-4, 5702 - 5773	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	5.08E-07	0.97	5.37	-	1378.2
AHQ-5-6, 5513	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.92E-04	0.85	3.27	-	759.9
AHQ-5-4, 5670 - 5748	R.TLGPSQEETGGVFLCPWR.A	2036.25364	3	2.75E-07	0.92	4.33	-	1379.4
AHQ-5-1, 5825 - 5891	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	9.76E-08	0.91	4.60	-	730.9
AHQ-5-11, 5343 - 5362	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.01E-09	0.96	5.24	-	1132.0
AHQ-5-10, 4919 - 4994	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.41E-04	0.95	4.91	-	1159.4
AHQ-5-13-, 5459	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	6.46E-06	0.93	4.68	-	828.6
AHQ-5-13, 5550 - 5564	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.96E-07	0.95	4.66	-	1028.6
AHQ-5-5, 5557 - 5558	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.10E-08	0.97	4.94	-	1405.5
AHQ-5-9, 4862 - 4876	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	5.04E-05	0.89	4.25	-	719.7
AHQ-5-3, 5822 - 5890	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	5.85E-09	0.96	5.16	-	1118.0
AHQ-5-7, 5342	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.28E-07	0.94	4.58	-	1052.4
AHQ-5-12, 5520	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	6.62E-08	0.94	4.42	-	1033.4
AHQ-5-7, 3462 - 3531	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.37E-05	0.88	3.51	-	754.4
AHQ-5-6, 3536 - 3540	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.04E-09	0.90	3.89	-	697.9
AHQ-5-1, 3901	K.TPVGSCFLAQPESGR.R	1607.76993	2	9.70E-08	0.87	3.43	-	823.6
AHQ-5-5, 3609	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.12E-07	0.95	4.35	-	1023.5
AHQ-5-2, 3789	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.29E-07	0.84	3.01	-	664.7
AHQ-5-11, 3572	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.37E-07	0.92	3.95	-	774.7
AHQ-5-4, 3752 - 3820	K.TPVGSCFLAQPESGR.R	1607.76993	2	5.49E-08	0.93	4.14	-	747.2
AHQ-5-3, 3807	K.TPVGSCFLAQPESGR.R	1607.76993	2	4.44E-06	0.89	3.66	-	840.6
AHQ-5-5, 4395	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	3.65E-09	0.90	3.97	-	1122.3
AHQ-5-3, 4679 - 4683	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	4.21E-07	0.82	3.51	-	906.5
AHQ-5-4, 4588	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	1.34E-08	0.96	5.16	-	1760.0
AHQ-5-4, 5069 - 5118	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	3.98E-07	0.94	5.14	-	1185.7
AHQ-5-4, 5336 - 5406	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	9.42E-06	0.94	4.62	-	1560.6
AHQ-5-4, 5493	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	2.23E-04	0.94	4.68	-	1209.1
AHQ-5-4, 5688	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	3.11E-04	0.93	4.62	-	1257.8
AHQ-5-4, 5833 - 5904	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	2	6.70E-04	0.35	2.60	-	311.3
AHQ-5-4, 5856 - 5929	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.02E-08	0.96	5.20	-	1490.3
AHQ-5-4, 6273	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.29E-05	0.89	4.38	-	798.2
AHQ-5-4, 5945	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	9.81E-07	0.95	4.62	-	1532.0
AHQ-5-4, 7061	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.58E-06	0.96	5.33	-	1575.2
AHQ-5-4, 6032	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	9.05E-10	0.97	5.85	-	1902.2
AHQ-5-4, 6465	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.46E-06	0.96	4.79	-	1970.2
AHQ-5-12, 2534	R.VAIVVGAPR.T	882.08560	2	7.93E-06	0.92	3.16	-	1364.9
AHQ-5-3, 2514	R.VAIVVGAPR.T	882.08560	2	8.22E-05	0.94	3.27	-	1425.5
AHQ-5-13-, 2631	R.VAIVVGAPR.T	882.08560	2	1.38E-05	0.93	3.34	-	1248.0
AHQ-5-5, 2345	R.VAIVVGAPR.T	882.08560	2	5.71E-06	0.94	3.30	-	1437.5
AHQ-5-11, 2478	R.VAIVVGAPR.T	882.08560	2	3.37E-04	0.78	2.65	-	880.1
AHQ-5-13, 2778	R.VAIVVGAPR.T	882.08560	2	2.60E-06	0.89	2.93	-	1037.3
AHQ-5-4, 7081 - 7161	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	7.34E-07	0.98	6.77	-	2344.6
AHQ-5-6, 6837	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.39E-04	0.89	3.61	-	1023.4
AHQ-5-4, 6020 - 6089	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.85E-10	0.98	6.51	-	1704.5
AHQ-5-4, 7536 - 7613	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.21E-13	0.98	6.50	-	2118.1
AHQ-5-4, 7664	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.64E-07	0.97	6.23	-	1126.7
AHQ-5-4, 6952 - 7017	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	8.59E-07	0.97	5.90	-	1511.4
AHQ-5-4, 6157 - 6229	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.02E-09	0.98	5.88	-	1752.3
AHQ-5-4, 6296 - 6370	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	7.85E-07	0.97	5.81	-	1509.5
AHQ-5-4, 5912 - 5953	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.21E-06	0.96	5.85	-	804.0
AHQ-5-4, 6838 - 6906	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.33E-08	0.98	6.30	-	1676.4
AHQ-5-4, 7230 - 7261	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.40E-06	0.98	6.52	-	1470.9
AHQ-5-4, 6684 - 6749	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.36E-07	0.95	5.24	-	1208.2
AHQ-5-4, 4144 - 4213	R.VVLCELGNPMK.K	1261.53692	2	4.41E-06	0.96	4.18	-	1338.0
AHQ-5-2, 4177	R.VVLCELGNPMK.K	1261.53692	2	1.62E-04	0.91	3.19	-	1025.6
AHQ-5-3, 4239	R.VVLCELGNPMK.K	1261.53692	2	6.49E-06	0.94	4.01	-	1044.8
AHQ-5-4, 3308	R.VVLCELGNPM*K.K	1277.53632	2	1.87E-04	0.78	2.92	-	681.4
AHQ-5-5, 3997 - 4013	R.VVLCELGNPMK.K	1261.53692	2	8.88E-08	0.96	3.93	-	1674.2
AHQ-5-4, 4150	R.VVLCELGNPMK.K	1261.53692	1	3.09E-04	0.88	3.53	-	998.6
AHQ-5-6, 3928 - 3930	R.VVLCELGNPMK.K	1261.53692	2	1.29E-05	0.91	3.83	-	910.1
AHQ-5-5, 3331	R.VVLCELGNPMKK.N	1389.70984	2	1.46E-04	0.90	3.02	-	1099.1
AHQ-5-4, 3544 - 3573	R.VVLCELGNPMKK.N	1389.70984	2	9.53E-08	0.85	2.90	-	1048.7
AHQ-5-4, 4132 - 4210	R.VYLFLQPR.G	1036.25129	2	6.49E-06	0.95	3.65	-	1426.1
AHQ-5-6, 3893	R.VYLFLQPR.G	1036.25129	2	4.19E-05	0.96	4.19	-	1355.7
gi|5902128|ref|NP_008880.1| syntaxin binding protein 2; Hunc18b [Homo sapiens]				2.72E-14	6.73	80.29	21.40	66438.1
AHQ-5-6, 6348	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	2	2.72E-14	0.97	5.88	-	1254.7
AHQ-5-6, 6624	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	3.44E-05	0.71	3.19	-	523.5
AHQ-5-6, 2938	R.KGPEDTAQLAHAVLAK.L	1649.87303	3	4.08E-07	0.97	5.48	-	1855.1
AHQ-5-6, 2929	R.KGPEDTAQLAHAVLAK.L	1649.87303	2	3.63E-08	0.80	2.86	-	906.0
AHQ-5-6, 6394	K.LIVPVLLDAAVPAYDK.I	1698.03911	2	2.80E-05	0.96	3.67	-	1721.9
AHQ-5-6, 3072	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	1.66E-06	0.85	3.89	-	488.7
AHQ-5-6, 5348 - 5416	R.NLWPFVSDPAPTASSQAAVSAR.F	2273.48981	2	9.10E-05	0.76	3.20	-	635.6
AHQ-5-6, 5904	R.REPIPSLEAIYLLSPTEK.S	2057.37574	3	2.34E-07	0.74	3.08	-	800.6
AHQ-5-6, 4642	K.WEVLIGSSHILTPTR.F	1709.97007	2	4.21E-08	0.93	3.93	-	1105.4
gi|9507215|ref|NP_061816.1| tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]				3.16E-14	2.36	30.22	9.80	50093.2
AHQ-5-7, 3236	K.DVNVAIAAIK.T	1014.20080	1	2.22E-05	0.49	2.64	-	332.0
AHQ-5-9, 4836	R.IHFPLVTYAPIISAEK.A	1800.13312	2	6.08E-05	0.80	3.28	-	484.0
AHQ-5-7, 5248 - 5278	R.IHFPLVTYAPIISAEK.A	1800.13312	2	1.12E-07	0.94	4.44	-	616.9
AHQ-5-14-, 5211	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	3.16E-14	0.93	4.22	-	861.2
AHQ-5-14-, 5435	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	3.62E-10	0.77	3.56	-	286.1
AHQ-5-13, 5402	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	7.49E-12	0.85	3.75	-	561.3
gi|21361657|ref|NP_005304.3| glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom				3.50E-14	8.76	110.35	28.50	56782.0
AHQ-5-7, 2120	K.DPNIVIAK.M	870.02845	1	2.75E-04	0.30	1.92	-	352.1
AHQ-5-7, 5720 - 5730	R.ELSDFISYLQR.E	1371.52000	2	5.72E-06	0.96	4.26	-	1507.0
AHQ-5-7, 6346	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	2	3.94E-06	0.95	5.04	-	844.8
AHQ-5-7, 7136 - 7139	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	3.50E-14	0.98	7.10	-	2224.2
AHQ-5-7, 7138	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	2	2.78E-09	0.95	4.03	-	1480.1
AHQ-5-9, 6348	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	3.31E-05	0.82	4.03	-	891.5
AHQ-5-7, 4526	R.FLQDYFDGNLK.R	1360.49568	1	2.29E-04	0.10	1.80	-	361.8
AHQ-5-7, 4520	R.FLQDYFDGNLK.R	1360.49568	2	7.06E-05	0.93	3.56	-	1454.5
AHQ-5-7, 5510	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	2	4.92E-05	0.96	4.86	-	1322.2
AHQ-5-7, 2384	K.LNFAVASR.K	878.01067	2	9.28E-04	0.79	2.63	-	794.0
AHQ-5-7, 2027 - 2100	K.LSKDPNIVIAK.M	1198.43727	2	2.68E-06	0.70	2.69	-	734.6
AHQ-5-7, 3222 - 3296	K.MDATANDVPSPYEVR.G	1665.80646	2	7.47E-05	0.73	3.63	-	388.8
AHQ-5-7, 2162	K.SEPIPESNDGPVK.V	1369.45928	1	3.92E-04	0.32	2.26	-	372.2
AHQ-5-7, 2312	K.SEPIPESNDGPVK.V	1369.45928	1	1.77E-04	0.48	1.95	-	569.7
AHQ-5-9, 5546 - 5554	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	2	8.05E-07	0.98	5.37	-	2375.6
AHQ-5-7, 6156 - 6162	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	3	5.29E-06	0.89	4.57	-	568.2
gi|5031987|ref|NP_005720.1| peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]				4.94E-14	3.91	50.26	41.50	22040.1
AHQ-5-12, 3714 - 3786	R.FPDENFTLK.H	1111.22866	2	2.27E-04	0.61	2.55	-	549.0
AHQ-5-12, 3993	R.FPDENFTLK.H	1111.22866	2	5.29E-04	0.85	2.88	-	705.0
AHQ-5-11, 5050	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	1.09E-11	0.87	4.27	-	802.3
AHQ-5-12, 5194 - 5234	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	4.94E-14	0.84	3.95	-	746.7
AHQ-5-12, 5049 - 5128	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	1.00E-06	0.83	3.48	-	994.2
AHQ-5-12, 5154 - 5222	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	2	2.47E-06	0.64	2.92	-	278.8
AHQ-5-12, 5297 - 5360	K.HVGPGVLSM*ANAGPNTNGSQFFICTIK.T	2836.19605	2	4.69E-04	0.72	3.48	-	238.7
AHQ-5-12, 5844 - 5904	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	2	1.62E-06	0.89	3.86	-	659.7

AHQ-5-12, 5850 - 5913	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	3	2.01E-06	0.95	5.25	-	1435.9
AHQ-5-12, 5969	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	2	7.20E-06	0.77	3.21	-	527.9
AHQ-5-14-, 5843 - 5874	K.HVGPGVLSMANAGPNTNGSQFFICTIK.T	2820.19665	3	1.04E-04	0.90	4.46	-	1108.7
AHQ-5-12, 4616 - 4688	R.VIPSFMCQAGDFTNHNGTGGK.S	2240.46178	2	1.12E-06	0.84	3.39	-	719.2
gi|13562114|ref|NP_110400.1|	beta tubulin 1, class VI [Homo sapiens]			5.88E-14	18.43	210.37	59.20	50326.6
AHQ-5-7, 7246	K.AFVHWYTSEGMDINEFGEAENNIHDLVSEYQQFQDAK.A	4364.62586	3	1.22E-04	0.97	6.72	-	1086.2
AHQ-5-13, 6272 - 6278	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.55E-05	0.95	4.52	-	1456.7
AHQ-5-3, 6618	R.ALSVAELTQQMFDAR.N	1680.90740	2	4.47E-06	0.96	4.57	-	1517.9
AHQ-5-9, 5551 - 5564	R.ALSVAELTQQMFDAR.N	1680.90740	2	4.34E-07	0.97	5.27	-	1439.1
AHQ-5-7, 6111 - 6186	R.ALSVAELTQQMFDAR.N	1680.90740	2	3.74E-07	0.98	5.69	-	1812.8
AHQ-5-14-, 6097 - 6099	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.56E-06	0.96	5.09	-	1371.3
AHQ-5-4, 6588	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.98E-04	0.30	2.69	-	494.6
AHQ-5-11, 6018 - 6035	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.17E-04	0.91	3.73	-	1241.8
AHQ-5-10, 5747	R.ALSVAELTQQMFDAR.N	1680.90740	2	3.00E-05	0.87	3.61	-	1019.7
AHQ-5-5, 6447	R.ALSVAELTQQMFDAR.N	1680.90740	2	8.47E-04	0.93	3.99	-	1256.2
AHQ-5-2, 6538	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.61E-05	0.95	4.57	-	1413.3
AHQ-5-13-, 4127 - 4128	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	8.16E-04	0.72	3.27	-	510.2
AHQ-5-3, 5155	R.AVLVDLEPGTMDSIR.S	1616.86162	2	2.80E-04	0.76	2.96	-	489.0
AHQ-5-7, 4584 - 4656	R.AVLVDLEPGTMDSIR.S	1616.86162	2	1.83E-05	0.88	3.89	-	651.9
AHQ-5-7, 3503 - 3574	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	5.28E-04	0.92	4.33	-	835.1
AHQ-5-8, 3449	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	5.18E-05	0.90	3.91	-	760.2
AHQ-5-7, 3678 - 3747	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	3.67E-08	0.94	4.24	-	1061.3
AHQ-5-9, 2870	K.EVDQQLLSVQTR.N	1416.56231	2	2.07E-05	0.90	3.77	-	892.2
AHQ-5-8, 2857 - 2858	K.EVDQQLLSVQTR.N	1416.56231	2	3.95E-08	0.76	3.56	-	521.9
AHQ-5-7, 2964 - 2983	K.EVDQQLLSVQTR.N	1416.56231	2	5.57E-06	0.78	3.25	-	706.9
AHQ-5-13, 5266	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	1.19E-06	0.92	4.25	-	1403.3
AHQ-5-14-, 5105 - 5106	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	6.77E-14	0.99	6.47	-	2411.1
AHQ-5-14, 5472 - 5546	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	7.75E-04	0.91	4.07	-	779.5
AHQ-5-14, 5940 - 5942	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	3.12E-12	0.99	6.24	-	3147.7
AHQ-5-13-, 5169 - 5171	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	5.88E-14	0.98	6.21	-	2289.4
AHQ-5-13, 5221 - 5289	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	6.51E-05	0.95	4.62	-	1236.0
AHQ-5-7, 5028 - 5071	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	7.97E-09	0.98	6.01	-	1657.3
AHQ-5-7, 5146 - 5148	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.23E-07	0.97	5.03	-	1661.0
AHQ-5-7, 5330	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	3.16E-07	0.94	4.55	-	1013.9
AHQ-5-14-, 4567	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	1.11E-04	0.96	4.78	-	1194.3
AHQ-5-12, 5204 - 5269	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.88E-05	0.93	4.37	-	674.0
AHQ-5-13-, 5173	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	1.11E-08	0.95	4.46	-	1473.7
AHQ-5-10, 4698 - 4736	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	9.62E-08	0.97	5.18	-	1800.5
AHQ-5-7, 6726 - 6794	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	8.88E-09	0.99	7.30	-	2791.4
AHQ-5-7, 6734 - 6804	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	3.87E-06	0.90	4.45	-	1618.0
AHQ-5-11, 6506	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.28E-04	0.71	3.35	-	995.6
AHQ-5-11, 6499	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.88E-11	0.98	6.53	-	2484.0
AHQ-5-7, 6890	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.89E-08	0.98	5.90	-	2108.8
AHQ-5-7, 7075	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.44E-06	0.95	5.30	-	1072.3
AHQ-5-13-, 6668	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.96E-08	0.99	7.21	-	2719.5
AHQ-5-10, 6196	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.98E-06	0.98	6.24	-	1921.4
AHQ-5-12, 6724	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	7.58E-04	0.89	4.13	-	1503.4
AHQ-5-13, 6705	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.13E-08	0.98	7.25	-	2212.3
AHQ-5-12, 6716 - 6720	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.37E-09	0.98	6.95	-	2172.5
AHQ-5-9, 6078	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.05E-08	0.98	6.65	-	2720.8
AHQ-5-4, 7149	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	8.00E-13	0.99	7.05	-	2876.3
AHQ-5-14-, 6569	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	2.53E-05	0.95	4.51	-	1767.9
AHQ-5-3, 7186	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.75E-06	0.98	5.99	-	2388.7
AHQ-5-13, 6709	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.11E-04	0.90	3.94	-	1749.8
AHQ-5-8, 6521 - 6584	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.11E-06	0.97	4.63	-	1999.4
AHQ-5-8, 6545	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	3.69E-04	0.81	3.62	-	1251.7
AHQ-5-14-, 6570	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.90E-10	0.98	6.68	-	2358.7
AHQ-5-13-, 6448	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	5.08E-07	0.79	3.20	-	771.4
AHQ-5-7, 7140 - 7211	R.GLSMAATFIGNNTAIQEIFNR.V	2269.56611	2	5.79E-08	0.94	5.09	-	773.3
AHQ-5-14-, 6319 - 6321	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	8.09E-09	0.91	4.64	-	705.2
AHQ-5-13, 6500	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.45E-07	0.91	4.66	-	691.0
AHQ-5-9, 5910	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.74E-04	0.66	3.28	-	379.7
AHQ-5-7, 6602 - 6672	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.44E-08	0.91	4.57	-	609.6
AHQ-5-8, 3650	R.IMNSFSVMPSPK.V	1338.62160	2	1.94E-06	0.93	3.53	-	999.9
AHQ-5-7, 3692	R.IMNSFSVMPSPK.V	1338.62160	2	1.77E-06	0.92	3.54	-	873.6
AHQ-5-7, 3428 - 3515	R.IMNSFSVMPSPK.V	1338.62160	1	1.47E-05	0.37	2.76	-	229.6
AHQ-5-7, 3852	R.IMNSFSVMPSPK.V	1338.62160	2	4.55E-06	0.94	3.67	-	1320.5
AHQ-5-7, 2752	R.IMNSFSVM*PSPK.V	1354.62100	2	2.85E-05	0.75	2.88	-	683.0
AHQ-5-7, 3842	R.IMNSFSVMPSPK.V	1338.62160	1	8.17E-05	0.13	1.83	-	308.7
AHQ-5-7, 3490 - 3502	R.IMNSFSVMPSPK.V	1338.62160	2	3.53E-05	0.94	3.85	-	1285.7
AHQ-5-7, 2895	R.ISVYYNEAYGR.K	1335.44622	1	5.80E-09	0.29	2.09	-	135.4
AHQ-5-14-, 3049	R.ISVYYNEAYGR.K	1335.44622	2	4.76E-08	0.93	3.01	-	1340.1
AHQ-5-13-, 3229	R.ISVYYNEAYGR.K	1335.44622	2	8.23E-08	0.93	3.60	-	1105.7
AHQ-5-7, 2883 - 2899	R.ISVYYNEAYGR.K	1335.44622	2	6.98E-07	0.93	3.66	-	1036.6
AHQ-5-8, 2788	R.ISVYYNEAYGR.K	1335.44622	2	3.44E-06	0.89	2.81	-	1160.2
AHQ-5-7, 4840	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	3.54E-07	0.90	4.31	-	904.8
AHQ-5-12, 5208	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	7.39E-04	0.60	3.04	-	596.3
AHQ-5-12, 5142	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	9.02E-04	0.64	2.77	-	642.3
AHQ-5-7, 4642 - 4643	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	3.04E-09	0.90	4.54	-	701.8
AHQ-5-11, 5611	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	8.50E-05	0.96	5.16	-	814.3
AHQ-5-10, 5219	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	1.98E-05	0.96	4.68	-	986.1
AHQ-5-14-, 5734	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	4.15E-08	0.87	3.48	-	1252.0
AHQ-5-9, 4954 - 4956	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	5.26E-09	0.97	5.74	-	907.3
AHQ-5-9, 4426 - 4428	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.93E-05	0.97	5.28	-	1020.7
AHQ-5-8, 5152	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	1.34E-07	0.97	5.48	-	757.1
AHQ-5-12, 5805	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	3.44E-08	0.97	5.76	-	937.4
AHQ-5-7, 5459 - 5530	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	1.42E-04	0.98	6.08	-	2181.9
AHQ-5-7, 5455 - 5527	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	1.46E-04	0.96	5.44	-	777.2
AHQ-5-6, 5744	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	2.54E-07	0.95	4.79	-	816.6
AHQ-5-5, 5762	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	5.92E-04	0.93	4.57	-	719.6
AHQ-5-11, 4970	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	3.78E-05	0.96	5.33	-	1605.7
AHQ-5-8, 7189 - 7197	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	6.64E-07	0.94	5.06	-	730.6
AHQ-5-7, 6819	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	1.04E-07	0.88	4.21	-	869.5
AHQ-5-7, 6839	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	6.20E-05	0.90	4.50	-	890.0
AHQ-5-14-, 6475 - 6554	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	9.29E-06	0.92	4.71	-	924.8
AHQ-5-3, 7475 - 7493	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.41E-06	0.92	5.19	-	598.8
AHQ-5-10, 6518	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	6.67E-06	0.91	4.35	-	716.8
AHQ-5-7, 7203 - 7247	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	2.93E-05	0.93	5.08	-	712.0
AHQ-5-7, 7270 - 7272	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	5.81E-07	0.93	4.86	-	1184.3
AHQ-5-7, 7326	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	7.33E-05	0.85	3.54	-	703.7
AHQ-5-9, 6460	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	2.18E-07	0.85	4.59	-	767.5
AHQ-5-9, 6436 - 6486	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	2.87E-09	0.95	5.08	-	837.0
AHQ-5-9, 6074	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	1.12E-07	0.90	4.15	-	928.9
AHQ-5-8, 7192	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	3.12E-07	0.79	3.84	-	815.0
AHQ-5-8, 6660	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	1.02E-08	0.87	4.17	-	800.9
AHQ-5-8, 6661 - 6662	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	2.69E-09	0.95	5.01	-	1043.8
AHQ-5-3, 7494	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	1.52E-05	0.88	4.41	-	823.1

AHQ-5-11, 5720	R.NSSCFVEWIPNNVK.V	1695.87718	2	1.98E-08	0.82	3.07	-	802.3
AHQ-5-11, 5207	R.NSSCFVEWIPNNVK.V	1695.87718	2	1.86E-05	0.33	2.53	-	309.7
AHQ-5-12, 5314	R.NSSCFVEWIPNNVK.V	1695.87718	2	1.50E-04	0.73	3.05	-	487.4
AHQ-5-7, 5010 - 5031	R.YLTVACIFR.G	1144.36822	2	1.11E-06	0.92	3.57	-	844.9
gi|4502549|ref|NP_001734.1| calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta				6.27E-14	4.02	50.23	47.00	16837.5
AHQ-5-12, 3493 - 3497	K.DTDSEEEIREAFR.V	1597.62234	2	5.95E-04	0.47	2.54	-	447.4
AHQ-5-12, 5920 - 5938	R.EADIDGDGQVNYEEFVQM*MTAK	2507.69302	3	9.52E-06	0.91	4.32	-	1937.5
AHQ-5-12, 4088 - 4156	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	4.91E-05	0.93	4.11	-	997.2
AHQ-5-11, 3984 - 3990	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	4.53E-06	0.95	4.55	-	1241.4
AHQ-5-12, 3192	K.MKDTDSEEEIREAFR.V	1856.99233	2	1.49E-10	0.72	3.25	-	463.3
AHQ-5-12, 3892 - 3969	R.VFDKDGNGYISAAELR.H	1755.90933	2	3.15E-11	0.96	4.61	-	1481.0
AHQ-5-12, 3905	R.VFDKDGNGYISAAELR.H	1755.90933	3	3.18E-05	0.95	3.89	-	2135.2
AHQ-5-12, 3760 - 3824	R.VFDKDGNGYISAAELR.H	1755.90933	2	6.27E-14	0.96	4.62	-	1257.9
AHQ-5-12, 3886	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.25E-08	0.93	3.38	-	1266.5
AHQ-5-11, 3731 - 3756	R.VFDKDGNGYISAAELR.H	1755.90933	2	6.88E-12	0.94	4.09	-	1150.9
AHQ-5-13, 3946	R.VFDKDGNGYISAAELR.H	1755.90933	2	4.28E-08	0.95	4.43	-	1203.4
AHQ-5-14, 4608	R.VFDKDGNGYISAAELR.H	1755.90933	2	2.80E-09	0.93	3.52	-	1174.1
AHQ-5-13-, 3852	R.VFDKDGNGYISAAELR.H	1755.90933	2	6.32E-11	0.95	4.30	-	1379.1
gi|4501881|ref|NP_001091.1| alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA				6.88E-14	15.49	200.30	44.30	42050.8
AHQ-5-4, 1772	K.AGFAGDDAPR.A	977.01283	2	9.67E-06	0.87	3.05	-	943.0
AHQ-5-12, 1904 - 1977	K.AGFAGDDAPR.A	977.01283	2	2.01E-04	0.68	2.71	-	838.5
AHQ-5-8, 1589 - 1652	K.AGFAGDDAPR.A	977.01283	2	9.88E-04	0.90	2.80	-	1444.7
AHQ-5-8, 1712 - 1773	K.AGFAGDDAPR.A	977.01283	2	6.90E-05	0.88	2.73	-	1050.5
AHQ-5-13, 2095 - 2154	K.AGFAGDDAPR.A	977.01283	2	5.48E-05	0.88	3.31	-	1001.3
AHQ-5-8, 2908 - 2986	R.AVFPSIVGR.P	946.12815	2	9.50E-04	0.78	2.51	-	711.8
AHQ-5-11, 3022 - 3096	R.AVFPSIVGRPR.H	1199.43018	2	1.77E-04	0.39	2.53	-	387.4
AHQ-5-8, 2572	R.AVFPSIVGRPR.H	1199.43018	2	5.96E-05	0.86	3.01	-	810.7
AHQ-5-9, 2646 - 2702	R.AVFPSIVGRPR.H	1199.43018	2	1.06E-05	0.79	3.01	-	751.3
AHQ-5-10, 4016	R.DLTDYLMK.I	999.16326	2	1.51E-04	0.81	3.06	-	458.6
AHQ-5-10, 4336 - 4344	R.DLTDYLMK.I	999.16326	1	7.02E-04	0.30	2.12	-	348.2
AHQ-5-7, 4323	R.DLTDYLMK.I	999.16326	1	9.28E-04	0.21	2.45	-	218.0
AHQ-5-1, 3904	R.DLTDYLM*K.I	1015.16266	2	2.14E-04	0.79	2.56	-	644.4
AHQ-5-8, 3508 - 3576	R.DLTDYLM*K.I	1015.16266	1	3.68E-04	0.27	1.81	-	123.9
AHQ-5-14-, 4290	R.DLTDYLMK.I	999.16326	1	5.23E-04	0.26	1.91	-	511.3
AHQ-5-14, 5217	R.DLTDYLMK.I	999.16326	1	6.38E-04	0.21	2.37	-	221.9
AHQ-5-12, 3693	R.DLTDYLM*K.I	1015.16266	1	8.37E-04	0.23	2.16	-	132.4
AHQ-5-13, 4444	R.DLTDYLMK.I	999.16326	1	4.37E-04	0.46	2.10	-	604.5
AHQ-5-5, 4481	R.DLTDYLMK.I	999.16326	1	1.62E-05	0.47	2.22	-	653.0
AHQ-5-14-, 4833 - 4838	K.DLYANNVMSGGTTM*YPGIADR.M	2263.49384	2	2.38E-04	0.56	3.15	-	527.7
AHQ-5-12, 1552 - 1608	K.DSYVGDEAQSK.R	1199.20634	2	8.93E-05	0.79	3.01	-	446.9
AHQ-5-8, 1430	K.DSYVGDEAQSKR.G	1355.39270	2	4.43E-09	0.79	2.90	-	669.1
AHQ-5-14-, 2770 - 2897	K.EITALAPSTMK.I	1162.38206	1	1.80E-05	0.55	2.70	-	281.9
AHQ-5-14, 3621 - 3792	K.EITALAPSTMK.I	1162.38206	1	6.54E-04	0.64	3.22	-	259.0
AHQ-5-14-, 2765 - 2837	K.EITALAPSTMK.I	1162.38206	2	4.70E-04	0.84	3.59	-	468.1
AHQ-5-13, 2526 - 2589	K.EITALAPSTM*K.I	1178.38146	2	3.93E-05	0.84	2.88	-	778.1
AHQ-5-8, 1962 - 2037	K.EITALAPSTM*K.I	1178.38146	2	2.43E-04	0.80	3.00	-	694.7
AHQ-5-14-, 2301 - 2374	K.EITALAPSTM*K.I	1178.38146	2	1.12E-04	0.86	3.23	-	705.7
AHQ-5-13-, 2355 - 2432	K.EITALAPSTM*K.I	1178.38146	2	4.03E-04	0.87	3.69	-	636.8
AHQ-5-13-, 2868 - 2932	K.EITALAPSTMK.I	1162.38206	2	2.13E-04	0.86	3.44	-	594.0
AHQ-5-8, 2308 - 2377	K.EITALAPSTMK.I	1162.38206	2	3.87E-05	0.79	2.96	-	538.1
AHQ-5-13, 3034 - 3038	K.EITALAPSTMK.I	1162.38206	2	3.34E-04	0.78	2.89	-	596.3
AHQ-5-13-, 2911 - 2913	K.EITALAPSTMK.I	1162.38206	1	2.21E-08	0.62	2.70	-	362.1
AHQ-5-2, 2835	K.EITALAPSTMK.I	1162.38206	1	9.04E-05	0.31	1.87	-	346.2
AHQ-5-6, 2741	K.EITALAPSTMK.I	1162.38206	1	2.19E-04	0.74	3.21	-	324.0
AHQ-5-13-, 2921 - 2929	K.EITALAPSTM*K.I	1178.38146	2	4.97E-04	0.59	3.00	-	392.1
AHQ-5-9, 2570	K.EITALAPSTMK.I	1162.38206	1	1.02E-06	0.60	2.90	-	331.5
AHQ-5-8, 7076	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	3	9.44E-07	0.78	3.62	-	709.9
AHQ-5-8, 7394 - 7414	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	2	4.42E-05	0.79	3.59	-	401.7
AHQ-5-1, 7225	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	3	1.42E-06	0.79	3.41	-	832.9
AHQ-5-6, 2653 - 2664	K.IWHHTFYNELR.V	1516.68695	2	4.14E-06	0.74	3.33	-	771.4
AHQ-5-9, 2502 - 2558	K.IWHHTFYNELR.V	1516.68695	2	8.44E-06	0.85	3.58	-	972.1
AHQ-5-3, 2901 - 2969	K.IWHHTFYNELR.V	1516.68695	2	1.19E-05	0.70	3.20	-	700.6
AHQ-5-9, 2511 - 2519	K.IWHHTFYNELR.V	1516.68695	3	2.20E-05	0.93	4.31	-	1783.4
AHQ-5-12, 2849 - 2920	K.IWHHTFYNELR.V	1516.68695	2	2.70E-07	0.90	3.72	-	1110.1
AHQ-5-12, 2852 - 2869	K.IWHHTFYNELR.V	1516.68695	3	6.02E-05	0.96	4.69	-	1410.0
AHQ-5-10, 2568 - 2618	K.IWHHTFYNELR.V	1516.68695	2	3.27E-04	0.81	3.05	-	611.5
AHQ-5-5, 2617 - 2625	K.IWHHTFYNELR.V	1516.68695	2	3.52E-08	0.80	3.26	-	832.9
AHQ-5-8, 2388 - 2468	K.IWHHTFYNELR.V	1516.68695	2	7.45E-04	0.86	2.99	-	864.8
AHQ-5-8, 2389 - 2457	K.IWHHTFYNELR.V	1516.68695	3	1.54E-05	0.95	4.49	-	2105.3
AHQ-5-12, 3013	K.IWHHTFYNELR.V	1516.68695	2	6.03E-08	0.93	3.79	-	1057.7
AHQ-5-8, 2580 - 2582	K.IWHHTFYNELR.V	1516.68695	3	3.38E-04	0.95	4.18	-	1789.3
AHQ-5-8, 2749 - 2829	K.IWHHTFYNELR.V	1516.68695	2	3.70E-07	0.91	3.37	-	883.3
AHQ-5-13, 3162	K.IWHHTFYNELR.V	1516.68695	3	3.94E-05	0.94	4.57	-	1879.3
AHQ-5-1, 3297	K.IWHHTFYNELR.V	1516.68695	2	1.40E-06	0.72	2.78	-	653.7
AHQ-5-8, 2252 - 2330	K.IWHHTFYNELR.V	1516.68695	2	2.63E-06	0.73	3.28	-	702.2
AHQ-5-13-, 3024 - 3029	K.IWHHTFYNELR.V	1516.68695	2	1.90E-08	0.77	3.29	-	792.9
AHQ-5-1, 3085	K.IWHHTFYNELR.V	1516.68695	2	1.47E-06	0.66	2.83	-	591.5
AHQ-5-8, 4929 - 4966	R.LDLAGRDLTDYLMK.I	1624.88375	2	3.26E-04	0.76	3.33	-	696.4
AHQ-5-8, 4802 - 4873	R.LDLAGRDLTDYLMK.I	1624.88375	2	4.13E-06	0.72	3.58	-	367.4
AHQ-5-1, 4791	K.SYELPDGQVITIGNER.F	1791.93998	2	8.46E-09	0.90	3.43	-	907.4
AHQ-5-8, 4252 - 4333	K.SYELPDGQVITIGNER.F	1791.93998	2	1.85E-13	0.97	5.30	-	1281.7
AHQ-5-8, 4396 - 4468	K.SYELPDGQVITIGNER.F	1791.93998	2	1.11E-12	0.96	5.34	-	891.7
AHQ-5-8, 4412 - 4481	K.SYELPDGQVITIGNER.F	1791.93998	2	6.88E-14	0.95	4.41	-	1041.0
AHQ-5-8, 4148 - 4222	K.SYELPDGQVITIGNER.F	1791.93998	2	1.36E-10	0.97	5.39	-	1360.5
AHQ-5-8, 4548 - 4624	K.SYELPDGQVITIGNER.F	1791.93998	2	7.81E-11	0.96	4.71	-	1233.1
AHQ-5-1, 4883 - 4955	K.SYELPDGQVITIGNER.F	1791.93998	2	1.77E-11	0.95	4.60	-	978.6
AHQ-5-8, 4670 - 4744	K.SYELPDGQVITIGNER.F	1791.93998	2	1.41E-08	0.96	4.72	-	1164.7
AHQ-5-1, 5160 - 5175	K.SYELPDGQVITIGNER.F	1791.93998	2	1.69E-10	0.95	4.68	-	1024.0
AHQ-5-1, 5335 - 5404	K.SYELPDGQVITIGNER.F	1791.93998	2	3.26E-08	0.96	4.82	-	1037.3
AHQ-5-8, 4545 - 4613	K.SYELPDGQVITIGNER.F	1791.93998	3	3.07E-08	0.94	4.33	-	1459.6
AHQ-5-8, 4808 - 4884	K.SYELPDGQVITIGNER.F	1791.93998	2	8.87E-13	0.95	4.69	-	977.1
AHQ-5-13-, 4997 - 5059	K.SYELPDGQVITIGNER.F	1791.93998	2	5.76E-13	0.96	4.84	-	1033.4
AHQ-5-8, 4998	K.SYELPDGQVITIGNER.F	1791.93998	3	3.64E-09	0.92	4.31	-	1448.4
AHQ-5-13-, 4835 - 4873	K.SYELPDGQVITIGNER.F	1791.93998	2	1.56E-11	0.96	5.04	-	1155.4
AHQ-5-13-, 4568	K.SYELPDGQVITIGNER.F	1791.93998	2	9.57E-06	0.90	3.71	-	861.1
AHQ-5-13-, 4453	K.SYELPDGQVITIGNER.F	1791.93998	2	8.27E-08	0.92	3.99	-	805.5
AHQ-5-2, 4729	K.SYELPDGQVITIGNER.F	1791.93998	2	1.50E-11	0.94	4.37	-	917.3
AHQ-5-7, 4722	K.SYELPDGQVITIGNER.F	1791.93998	2	2.46E-07	0.96	4.84	-	905.2
AHQ-5-6, 5160	K.SYELPDGQVITIGNER.F	1791.93998	2	1.55E-07	0.84	3.14	-	691.1
AHQ-5-6, 5076	K.SYELPDGQVITIGNER.F	1791.93998	2	3.83E-06	0.93	4.14	-	793.4
AHQ-5-6, 4862	K.SYELPDGQVITIGNER.F	1791.93998	2	2.56E-07	0.90	3.88	-	803.6
AHQ-5-2, 5089	K.SYELPDGQVITIGNER.F	1791.93998	2	5.89E-06	0.87	3.68	-	757.3
AHQ-5-2, 5295	K.SYELPDGQVITIGNER.F	1791.93998	2	2.94E-07	0.93	3.87	-	934.6
AHQ-5-9, 3958 - 4027	K.SYELPDGQVITIGNER.F	1791.93998	2	1.22E-11	0.94	4.55	-	1046.6
AHQ-5-3, 4761 - 4765	K.SYELPDGQVITIGNER.F	1791.93998	2	5.35E-07	0.93	4.05	-	847.9
AHQ-5-9, 4191	K.SYELPDGQVITIGNER.F	1791.93998	2	9.12E-10	0.93	3.94	-	1046.7
AHQ-5-9, 4300 - 4358	K.SYELPDGQVITIGNER.F	1791.93998	2	1.00E-11	0.95	4.91	-	880.7

AHQ-5-3, 4909	K.SYELPDGQVITIGNER.F	1791.93998	2	1.83E-06	0.92	3.39	-	1107.8
AHQ-5-9, 4498 - 4574	K.SYELPDGQVITIGNER.F	1791.93998	2	5.22E-07	0.94	4.16	-	951.0
AHQ-5-6, 4500	K.SYELPDGQVITIGNER.F	1791.93998	2	4.62E-08	0.90	3.58	-	770.7
AHQ-5-13, 5186	K.SYELPDGQVITIGNER.F	1791.93998	2	4.74E-06	0.90	3.27	-	1121.4
AHQ-5-10, 4094 - 4171	K.SYELPDGQVITIGNER.F	1791.93998	2	5.00E-13	0.92	3.97	-	852.2
AHQ-5-10, 4230 - 4266	K.SYELPDGQVITIGNER.F	1791.93998	2	9.07E-11	0.93	3.91	-	917.8
AHQ-5-5, 5227 - 5246	K.SYELPDGQVITIGNER.F	1791.93998	2	9.72E-04	0.65	2.63	-	361.0
AHQ-5-10, 4354 - 4416	K.SYELPDGQVITIGNER.F	1791.93998	2	4.66E-11	0.96	4.61	-	1293.1
AHQ-5-10, 4460 - 4519	K.SYELPDGQVITIGNER.F	1791.93998	2	3.29E-05	0.82	3.30	-	660.3
AHQ-5-10, 4603 - 4666	K.SYELPDGQVITIGNER.F	1791.93998	2	1.76E-11	0.97	4.80	-	1946.4
AHQ-5-5, 4897 - 4965	K.SYELPDGQVITIGNER.F	1791.93998	2	2.26E-08	0.94	4.20	-	1089.2
AHQ-5-11, 4315	K.SYELPDGQVITIGNER.F	1791.93998	2	2.84E-04	0.86	3.49	-	581.7
AHQ-5-11, 4399 - 4402	K.SYELPDGQVITIGNER.F	1791.93998	2	8.74E-13	0.97	5.22	-	1163.5
AHQ-5-11, 4538	K.SYELPDGQVITIGNER.F	1791.93998	2	3.47E-07	0.83	3.14	-	602.5
AHQ-5-11, 4916 - 4978	K.SYELPDGQVITIGNER.F	1791.93998	2	6.39E-08	0.95	4.13	-	1105.2
AHQ-5-5, 4565	K.SYELPDGQVITIGNER.F	1791.93998	2	1.57E-11	0.90	3.46	-	840.5
AHQ-5-5, 4482	K.SYELPDGQVITIGNER.F	1791.93998	2	1.67E-05	0.80	3.13	-	586.2
AHQ-5-13, 5101 - 5164	K.SYELPDGQVITIGNER.F	1791.93998	2	3.17E-13	0.96	4.79	-	1098.7
AHQ-5-13, 4932 - 4996	K.SYELPDGQVITIGNER.F	1791.93998	2	2.28E-07	0.96	5.06	-	983.3
AHQ-5-4, 5354 - 5369	K.SYELPDGQVITIGNER.F	1791.93998	2	2.60E-11	0.96	4.80	-	1094.4
AHQ-5-13, 4657	K.SYELPDGQVITIGNER.F	1791.93998	2	2.18E-06	0.76	2.95	-	528.7
AHQ-5-13, 4546	K.SYELPDGQVITIGNER.F	1791.93998	2	2.52E-07	0.92	3.56	-	825.9
AHQ-5-3, 5147	K.SYELPDGQVITIGNER.F	1791.93998	2	3.93E-06	0.80	2.97	-	649.7
AHQ-5-12, 4537	K.SYELPDGQVITIGNER.F	1791.93998	2	2.54E-12	0.94	4.28	-	827.0
AHQ-5-3, 5330 - 5397	K.SYELPDGQVITIGNER.F	1791.93998	2	2.63E-06	0.88	3.62	-	633.1
AHQ-5-4, 4617	K.SYELPDGQVITIGNER.F	1791.93998	2	1.84E-08	0.80	3.07	-	845.3
AHQ-5-12, 4909 - 4940	K.SYELPDGQVITIGNER.F	1791.93998	2	1.34E-05	0.93	3.92	-	881.2
AHQ-5-4, 4728	K.SYELPDGQVITIGNER.F	1791.93998	2	4.73E-10	0.94	4.06	-	914.6
AHQ-5-12, 5085 - 5148	K.SYELPDGQVITIGNER.F	1791.93998	2	5.73E-05	0.86	3.66	-	762.9
AHQ-5-8, 4733	K.SYELPDGQVITIGNERFR.C	2095.30102	2	4.46E-05	0.76	3.79	-	277.5
AHQ-5-5, 3653	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	8.87E-04	0.81	3.39	-	500.3
AHQ-5-3, 3942 - 3945	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	3	2.73E-04	0.61	3.17	-	747.6
AHQ-5-12, 4566	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.32E-08	0.86	3.90	-	656.0
AHQ-5-12, 4412	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.85E-06	0.87	3.99	-	772.6
AHQ-5-13, 4474	K.YPIEHGIITNWDDMEK.I	1962.17174	3	8.75E-04	0.87	3.81	-	1128.2
AHQ-5-12, 3973 - 4053	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	6.26E-04	0.86	4.09	-	611.5
AHQ-5-13, 4649	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.06E-06	0.83	3.20	-	597.8
AHQ-5-4, 4577	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.82E-05	0.83	3.63	-	713.9
AHQ-5-12, 4701	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.90E-04	0.62	2.84	-	706.9
AHQ-5-5, 4347	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.42E-04	0.86	4.21	-	639.8
AHQ-5-6, 4261	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.40E-05	0.85	3.58	-	708.7
AHQ-5-9, 4439	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.06E-08	0.85	3.82	-	554.9
AHQ-5-9, 4026 - 4099	K.YPIEHGIITNWDDMEK.I	1962.17174	2	8.91E-06	0.86	4.25	-	565.0
AHQ-5-3, 4649 - 4651	K.YPIEHGIITNWDDMEK.I	1962.17174	2	7.67E-04	0.85	3.97	-	690.9
AHQ-5-4, 4768	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.38E-04	0.79	3.79	-	644.0
AHQ-5-9, 3818 - 3887	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.67E-04	0.93	4.55	-	766.2
AHQ-5-9, 3632	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.69E-04	0.79	3.62	-	669.4
AHQ-5-8, 3814 - 3885	K.YPIEHGIITNWDDMEK.I	1962.17174	3	9.77E-04	0.80	4.09	-	712.8
AHQ-5-8, 3956 - 4032	K.YPIEHGIITNWDDMEK.I	1962.17174	3	8.62E-06	0.87	4.01	-	1108.4
AHQ-5-8, 4188 - 4192	K.YPIEHGIITNWDDMEK.I	1962.17174	2	6.32E-06	0.82	3.97	-	447.3
AHQ-5-8, 4590	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.42E-05	0.80	3.64	-	654.1
AHQ-5-8, 4052 - 4121	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.83E-04	0.86	3.99	-	832.4
AHQ-5-12, 5050	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.53E-08	0.83	3.90	-	533.8
AHQ-5-8, 4676 - 4677	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.45E-08	0.84	3.95	-	565.4
AHQ-5-8, 4069 - 4136	K.YPIEHGIITNWDDMEK.I	1962.17174	3	4.84E-04	0.73	3.59	-	731.0
AHQ-5-8, 6440 - 6508	K.YPIEHGIITNWDDMEKIWHHTFYNELR.V	3459.83609	3	4.33E-09	0.92	5.36	-	721.1
AHQ-5-8, 5077	K.YPIEHGIITNWDDM*EKIWHHTFYNELR.V	3475.83549	3	7.01E-07	0.95	5.98	-	1030.1
gi|10834976|ref|NP_000572.1| glutathione peroxidase 1 [Homo sapiens]				7.83E-14	9.09	110.26	59.20	21909.0
AHQ-5-11, 5364	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	7.83E-14	0.94	3.62	-	1528.5
AHQ-5-11, 5292	K.CEVNGAGAHPLFAFLR.E	1760.99723	3	2.02E-07	0.70	3.03	-	644.3
AHQ-5-11, 5259 - 5303	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	5.56E-10	0.92	3.87	-	953.5
AHQ-5-11, 4246	K.FLVGPDGVPLR.R	1170.38561	2	3.71E-07	0.91	3.41	-	939.2
AHQ-5-11, 3951 - 3994	K.FLVGPDGVPLR.R	1170.38561	2	7.15E-04	0.89	3.08	-	1191.3
AHQ-5-11, 5035	R.GLVVLGFPCNQFGHQENAK.N	2117.37312	2	2.58E-06	0.66	3.46	-	280.2
AHQ-5-11, 4868 - 4936	R.GLVVLGFPCNQFGHQENAK.N	2117.37312	2	7.75E-05	0.93	4.86	-	602.7
AHQ-5-11, 5935	R.GLVVLGFPCNQFGHQENAKNEEILNSLK.Y	3158.53371	3	3.06E-07	0.74	3.58	-	249.7
AHQ-5-11, 3838	R.LAAAAAQSVYAFSAR.P	1497.68025	2	1.93E-05	0.97	4.27	-	1817.8
AHQ-5-11, 3759 - 3780	K.LITWSPVCR.N	1133.34543	2	5.20E-04	0.74	2.51	-	714.7
AHQ-5-11, 5495	K.LITWSPVCRNDVAWNFEK.F	2237.52236	2	2.78E-05	0.95	4.64	-	1018.5
AHQ-5-11, 3144	R.NDVAWNFEK.F	1123.19953	1	4.53E-04	0.36	2.10	-	400.8
AHQ-5-11, 5491 - 5496	R.PGGGFEPNFMLFEK.C	1570.79310	2	1.41E-06	0.96	4.74	-	851.1
AHQ-5-11, 3740 - 3803	R.PLAGGEPVSLGSLR.G	1353.54935	2	3.76E-06	0.96	4.78	-	1113.7
AHQ-5-14-, 3831 - 3834	R.PLAGGEPVSLGSLR.G	1353.54935	2	7.43E-08	0.95	3.91	-	1412.5
AHQ-5-14, 4720	R.PLAGGEPVSLGSLR.G	1353.54935	2	2.75E-08	0.93	4.16	-	867.4
AHQ-5-11, 5131 - 5146	K.YVRPGGGFEPNFMLFEK.C	1989.28515	2	2.75E-04	0.97	5.28	-	1802.4
AHQ-5-11, 5138	K.YVRPGGGFEPNFMLFEK.C	1989.28515	3	1.81E-07	0.94	4.38	-	1345.5
AHQ-5-10, 4759 - 4776	K.YVRPGGGFEPNFMLFEK.C	1989.28515	2	8.07E-04	0.86	3.86	-	685.0
gi|4503631|ref|NP_000120.1| coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,				1.14E-13	21.49	240.29	36.90	83232.8
AHQ-5-5, 5353 - 5429	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	3.51E-06	0.78	3.85	-	233.5
AHQ-5-11, 5202 - 5268	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	4.64E-05	0.58	3.10	-	181.2
AHQ-5-13, 5370	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	9.91E-10	0.60	2.71	-	239.7
AHQ-5-5, 5489 - 5565	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	5.34E-05	0.76	4.24	-	189.5
AHQ-5-5, 2339	K.DGTHVVENVDATHIGK.L	1692.81163	3	2.56E-05	0.94	4.70	-	1176.7
AHQ-5-6, 2325	K.DGTHVVENVDATHIGK.L	1692.81163	2	2.63E-06	0.94	4.16	-	1022.6
AHQ-5-11, 5460 - 5522	K.ETFDVTLEPLSFK.K	1526.71190	2	4.35E-05	0.42	2.54	-	527.1
AHQ-5-5, 5738 - 5805	K.ETFDVTLEPLSFK.K	1526.71190	2	1.10E-06	0.93	4.16	-	1118.2
AHQ-5-5, 4861 - 4881	K.ETFDVTLEPLSFKK.E	1654.88482	2	1.08E-08	0.80	3.22	-	560.1
AHQ-5-5, 6857	R.GTQVVGSDMTVTVQFTNPLK.E	2123.41609	2	4.13E-10	0.95	4.42	-	1241.9
AHQ-5-5, 7175 - 7199	R.GTQVVGSDMTVTVQFTNPLK.E	2123.41609	2	1.18E-13	0.98	5.55	-	2000.9
AHQ-5-5, 6961 - 7031	R.GTQVVGSDMTVTVQFTNPLK.E	2123.41609	2	1.67E-12	0.98	5.47	-	2874.9
AHQ-5-8, 5097	K.GTYIPVPIVSELQSGK.W	1688.94594	2	9.24E-04	0.67	2.62	-	419.2
AHQ-5-5, 5521 - 5593	K.GTYIPVPIVSELQSGK.W	1688.94594	2	9.31E-07	0.80	3.20	-	421.0
AHQ-5-10, 5018	K.GTYIPVPIVSELQSGK.W	1688.94594	2	1.18E-06	0.45	2.72	-	209.8
AHQ-5-6, 6996 - 7006	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.02E-08	0.94	4.42	-	1017.8
AHQ-5-6, 7089	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	4.95E-04	0.68	2.98	-	554.5
AHQ-5-10, 6335 - 6336	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.58E-04	0.96	4.51	-	1347.6
AHQ-5-9, 6176 - 6190	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.05E-07	0.94	4.78	-	890.2
AHQ-5-5, 7169 - 7235	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	8.04E-07	0.96	4.88	-	1362.7
AHQ-5-11, 6572	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	4.67E-07	0.77	3.45	-	747.1
AHQ-5-5, 7074 - 7147	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	2.45E-09	0.90	4.81	-	814.1
AHQ-5-12, 6777 - 6842	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.61E-07	0.96	4.89	-	1463.2
AHQ-5-11, 6567	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.19E-10	0.97	5.02	-	1434.7
AHQ-5-5, 7073 - 7145	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	4.28E-07	0.97	5.79	-	1405.7
AHQ-5-13, 6744 - 6745	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.91E-07	0.95	4.62	-	1251.7
AHQ-5-7, 6915 - 6926	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.68E-05	0.96	5.10	-	1084.3
AHQ-5-1, 7193 - 7199	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.52E-04	0.84	3.60	-	655.0
AHQ-5-14-, 6634	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.75E-08	0.96	4.97	-	1256.6

AHQ-5-5, 5258	R.HVYGELDVQIQR.R	1457.61612	2	1.39E-04	0.68	2.62	-	525.0
AHQ-5-5, 3399 - 3470	R.HVYGELDVQIQR.R	1457.61612	2	1.88E-07	0.89	3.01	-	868.9
AHQ-5-5, 7141 - 7215	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	1.40E-07	0.94	5.37	-	972.6
AHQ-5-5, 7462	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	9.56E-05	0.85	4.36	-	650.3
AHQ-5-5, 7323	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	5.79E-06	0.94	5.08	-	1141.0
AHQ-5-7, 1907	K.KDGTHVVENVDATHIGK.L	1820.98455	2	5.50E-05	0.95	4.14	-	1325.2
AHQ-5-5, 1966	K.KDGTHVVENVDATHIGK.L	1820.98455	2	9.92E-07	0.95	4.08	-	1192.3
AHQ-5-6, 1961 - 1965	K.KDGTHVVENVDATHIGK.L	1820.98455	2	3.76E-08	0.96	4.72	-	1342.0
AHQ-5-11, 4910	K.KETFDVTLEPLSFK.K	1654.88482	2	1.43E-07	0.97	4.90	-	1659.1
AHQ-5-5, 4978 - 4985	K.KETFDVTLEPLSFK.K	1654.88482	2	1.96E-04	0.97	4.64	-	2033.4
AHQ-5-5, 2423 - 2493	R.KLIASMSSDSLR.H	1308.53039	2	3.80E-04	0.87	3.72	-	924.1
AHQ-5-5, 1742	K.KPLNTEGVMK.S	1117.34452	1	2.81E-04	0.44	2.55	-	213.7
AHQ-5-5, 1528	K.KPLNTEGVMK.S	1117.34452	1	8.04E-05	0.54	2.44	-	385.6
AHQ-5-5, 4741	R.LALETALMYGAK.K	1281.54655	2	9.50E-08	0.95	3.71	-	1679.4
AHQ-5-5, 4587 - 4666	R.LALETALMYGAK.K	1281.54655	2	7.99E-08	0.96	4.29	-	1497.9
AHQ-5-5, 4826	R.LALETALMYGAK.K	1281.54655	2	2.83E-06	0.96	3.71	-	1763.6
AHQ-5-6, 4544 - 4622	R.LALETALMYGAK.K	1281.54655	2	2.48E-05	0.96	3.66	-	1733.1
AHQ-5-5, 2031 - 2037	K.LIASM*SSDSLR.H	1196.35688	2	5.36E-05	0.95	3.78	-	1194.5
AHQ-5-14-, 2219	K.LIASM*SSDSLR.H	1196.35688	2	7.17E-05	0.87	2.72	-	829.4
AHQ-5-7, 2699	K.LIASMSSDSLR.H	1180.35748	2	6.63E-05	0.91	2.92	-	1041.6
AHQ-5-11, 2886 - 2887	K.LIASMSSDSLR.H	1180.35748	2	6.22E-05	0.89	3.17	-	936.6
AHQ-5-5, 2785 - 2806	K.LIASMSSDSLR.H	1180.35748	2	7.11E-06	0.95	3.76	-	1387.0
AHQ-5-5, 6105 - 6137	R.MYVAVWTPYGVLR.T	1555.86794	2	1.32E-06	0.95	4.76	-	981.3
AHQ-5-6, 5478	R.M*YVAVWTPYGVLR.T	1571.86734	2	6.80E-06	0.93	3.54	-	1218.9
AHQ-5-6, 6073	R.MYVAVWTPYGVLR.T	1555.86794	2	2.65E-05	0.94	3.77	-	993.4
AHQ-5-9, 5367 - 5378	R.MYVAVWTPYGVLR.T	1555.86794	2	1.49E-05	0.94	4.26	-	991.6
AHQ-5-5, 6214 - 6283	R.MYVAVWTPYGVLR.T	1555.86794	2	4.44E-07	0.95	4.24	-	992.4
AHQ-5-5, 5477 - 5502	R.M*YVAVWTPYGVLR.T	1571.86734	2	1.84E-06	0.95	4.20	-	984.5
AHQ-5-11, 5346 - 5399	R.M*YVAVWTPYGVLR.T	1571.86734	2	3.66E-04	0.87	3.33	-	589.8
AHQ-5-5, 6754	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	4.69E-11	0.91	4.03	-	1290.0
AHQ-5-5, 6859	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	1.25E-07	0.92	4.51	-	1017.8
AHQ-5-7, 6626	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	1.14E-13	0.88	4.05	-	981.3
AHQ-5-6, 6660	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	4.85E-08	0.95	5.30	-	1082.4
AHQ-5-5, 3387	R.NVWVHLDGPGVTR.P	1450.62682	2	5.20E-07	0.94	3.70	-	1269.6
AHQ-5-11, 3370 - 3450	R.NVWVHLDGPGVTR.P	1450.62682	2	9.79E-05	0.76	2.83	-	783.5
AHQ-5-5, 3370	R.NVWVHLDGPGVTRPMK.K	1807.11248	3	3.38E-06	0.83	3.76	-	779.0
AHQ-5-8, 2904	R.NVWVHLDGPGVTRPMK.K	1807.11248	2	2.65E-04	0.77	2.82	-	594.9
AHQ-5-6, 3272 - 3326	R.NVWVHLDGPGVTRPMK.K	1807.11248	2	1.09E-04	0.94	3.77	-	1013.5
AHQ-5-5, 3369	R.NVWVHLDGPGVTRPMK.K	1807.11248	2	1.36E-05	0.93	3.78	-	941.6
AHQ-5-5, 5338 - 5382	R.SNVDMDFEVENAVLGK.D	1767.93869	2	7.62E-10	0.98	5.78	-	2489.7
AHQ-5-5, 4622	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.46E-08	0.97	4.99	-	1915.3
AHQ-5-5, 5638 - 5713	K.STVLTIPEIIIK.V	1327.63485	2	1.21E-07	0.95	3.78	-	1643.3
gi|29742410|ref|XP_291183.1| similar to TREM-like transcript 1 [Homo sapiens]				1.31E-13	2.69	30.30	21.20	32678.3
AHQ-5-13-, 4157 - 4159	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	2.34E-05	0.93	4.23	-	633.0
AHQ-5-10, 3946 - 3962	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	6.15E-04	0.76	2.95	-	409.8
AHQ-5-11, 4218	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.35E-06	0.68	3.20	-	294.1
AHQ-5-13-, 4189 - 4319	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.31E-13	0.82	3.34	-	519.2
AHQ-5-9, 4475	K.VLVCSKPVTYATVIFPGGNK.G	2152.54196	2	7.47E-04	0.89	4.52	-	477.6
AHQ-5-9, 4471	R.VSGMNPSSVVHHVSDSGPAAELPLDVPHIR.L	3106.46224	3	3.86E-08	0.97	6.10	-	1411.1
gi|4827056|ref|NP_005103.1| WD repeat-containing protein 1 isoform 2 [Homo sapiens]				1.88E-13	10.91	130.33	46.40	58001.9
AHQ-5-7, 4650	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	1.17E-04	0.93	4.78	-	671.1
AHQ-5-9, 4275	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	3.35E-08	0.94	4.72	-	914.3
AHQ-5-6, 5890 - 5962	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	5.73E-05	0.76	3.96	-	561.4
AHQ-5-10, 5140	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	6.98E-13	0.93	4.76	-	952.6
AHQ-5-6, 5753 - 5820	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.88E-13	0.96	5.70	-	1253.2
AHQ-5-9, 5043	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	3.16E-10	0.91	4.46	-	666.7
AHQ-5-1, 5952	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.65E-10	0.90	4.32	-	931.5
AHQ-5-6, 5656 - 5676	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	4.46E-13	0.95	5.37	-	894.7
AHQ-5-7, 5570 - 5600	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.43E-08	0.90	4.79	-	653.0
AHQ-5-6, 5562	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	2	1.94E-05	0.87	3.49	-	818.5
AHQ-5-6, 5525	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	3	5.93E-04	0.91	5.01	-	879.9
AHQ-5-6, 4740	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	5.36E-06	0.94	4.38	-	1195.2
AHQ-5-10, 4226	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	1.62E-07	0.96	4.69	-	1367.6
AHQ-5-9, 4114	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	8.45E-05	0.95	4.87	-	1068.6
AHQ-5-6, 4589 - 4662	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	7.91E-08	0.96	4.55	-	1389.5
AHQ-5-6, 2032	K.IKDIAWTEDSKR.I	1462.63267	2	6.34E-07	0.92	4.08	-	963.4
AHQ-5-6, 2030	K.IKDIAWTEDSKR.I	1462.63267	3	1.21E-05	0.87	3.86	-	838.0
AHQ-5-6, 5708 - 5724	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	4.30E-07	0.69	3.82	-	446.5
AHQ-5-6, 5532 - 5598	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	2.93E-09	0.83	3.35	-	958.6
AHQ-5-6, 5433 - 5509	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.36E-07	0.95	5.33	-	997.3
AHQ-5-11, 5330	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	3.84E-04	0.86	3.65	-	787.7
AHQ-5-13, 4106	R.LYSILGTTLKDEGK.L	1538.76736	2	1.31E-04	0.89	3.40	-	912.2
AHQ-5-10, 3578	R.LYSILGTTLKDEGK.L	1538.76736	2	3.82E-05	0.93	3.89	-	1186.0
AHQ-5-6, 3648	R.LYSILGTTLKDEGK.L	1538.76736	2	2.18E-04	0.92	4.05	-	979.4
AHQ-5-6, 5005 - 5016	R.MTVDESGQLISCSMDDTVR.Y	2146.36365	2	2.08E-05	0.82	3.80	-	518.6
AHQ-5-10, 3860	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	7.46E-05	0.85	3.55	-	842.2
AHQ-5-6, 4060	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	2.96E-06	0.84	3.55	-	821.3
AHQ-5-6, 4141	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	2.95E-08	0.97	6.60	-	862.5
AHQ-5-6, 2109	K.VINSVDIK.Q	888.04378	1	3.61E-04	0.26	2.31	-	391.8
AHQ-5-1, 4133	K.YAPSGFYIASGDVSGK.L	1619.75589	2	5.76E-08	0.81	3.48	-	555.5
AHQ-5-6, 3700 - 3770	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.16E-09	0.93	4.00	-	806.8
AHQ-5-12, 3900	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.35E-09	0.92	3.70	-	739.6
AHQ-5-14-, 3817	K.YAPSGFYIASGDVSGK.L	1619.75589	2	3.42E-05	0.94	4.15	-	829.9
AHQ-5-6, 2589	K.YEYQPFAGK.I	1103.20822	2	7.20E-04	0.68	2.59	-	504.2
gi|4504349|ref|NP_000509.1| beta globin [Homo sapiens]				3.01E-13	10.22	120.30	70.70	15998.3
AHQ-5-14-, 3027 - 3033	K.EFTPPVQAAYQK.V	1379.54213	2	1.57E-04	0.84	3.10	-	817.6
AHQ-5-14-, 4958 - 5037	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	2.64E-06	0.89	4.25	-	586.1
AHQ-5-14-, 5537	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	3.01E-13	0.98	5.95	-	1817.1
AHQ-5-13-, 5688	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	4.00E-04	0.93	4.63	-	870.0
AHQ-5-13, 5766	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	2.93E-06	0.93	4.46	-	818.6
AHQ-5-13, 5677	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	6.46E-04	0.36	2.59	-	472.3
AHQ-5-13, 5634 - 5700	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	8.52E-07	0.94	4.50	-	882.7
AHQ-5-13-, 5544 - 5555	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	4.12E-05	0.94	4.43	-	797.1
AHQ-5-13-, 4995 - 5068	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	6.99E-05	0.91	4.29	-	566.3
AHQ-5-13, 5464	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	6.58E-07	0.94	4.58	-	720.5
AHQ-5-13, 5090 - 5156	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	2.13E-04	0.92	4.23	-	675.9
AHQ-5-13, 5100	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	2.22E-04	0.89	3.71	-	1022.0
AHQ-5-14, 6196	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.06E-07	0.93	4.49	-	727.8
AHQ-5-13, 3601	K.GTFATLSELHCDK.L	1480.62492	2	8.23E-07	0.41	2.78	-	377.6
AHQ-5-13-, 3475 - 3479	K.GTFATLSELHCDK.L	1480.62492	2	6.83E-07	0.92	4.10	-	646.9
AHQ-5-13, 5068 - 5133	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	2.92E-08	0.91	4.42	-	856.0
AHQ-5-13-, 4984	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	4.97E-10	0.92	4.38	-	1141.7
AHQ-5-13-, 4773	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	2.21E-10	0.97	5.98	-	1705.9
AHQ-5-13-, 4776	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	7.90E-09	0.97	5.42	-	1716.4
AHQ-5-13, 4860	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	1.92E-08	0.97	5.78	-	1302.0
AHQ-5-13, 4862	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	1.54E-07	0.96	5.08	-	1547.0
AHQ-5-13-, 2793	K.LHVDPENFR.L	1127.23455	1	2.27E-04	0.22	1.88	-	329.9

AHQ-5-13-, 2775	K.LHVDPENFR.L	1127.23455	2	2.14E-04	0.82	2.93	-	877.5
AHQ-5-13, 6593	R.LLGNVLVCVLAHHFGK.E	1779.14197	2	1.24E-04	0.89	3.58	-	970.5
AHQ-5-13, 3551	K.SAVTALWGK.V	933.08624	2	1.10E-04	0.81	2.51	-	736.6
AHQ-5-13-, 3427 - 3452	K.SAVTALWGK.V	933.08624	2	9.77E-06	0.76	2.63	-	663.4
AHQ-5-13-, 3432	K.SAVTALWGK.V	933.08624	1	1.35E-04	0.06	2.10	-	122.5
AHQ-5-13-, 5104 - 5123	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	2.55E-07	0.83	3.63	-	599.3
AHQ-5-13, 4965 - 5028	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	5.13E-11	0.97	5.66	-	1248.1
AHQ-5-14, 5874 - 5937	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	5.85E-13	0.95	4.77	-	1238.0
AHQ-5-13-, 4941	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	2.51E-10	0.82	3.68	-	497.0
AHQ-5-13, 5217	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.32E-11	0.96	4.57	-	1314.1
AHQ-5-13, 5189	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	5.91E-09	0.84	3.43	-	605.4
AHQ-5-13-, 4936 - 5008	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	6.71E-11	0.96	4.89	-	1473.9
AHQ-5-14-, 5069	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	8.79E-05	0.97	5.14	-	1471.7
AHQ-5-13, 5116 - 5184	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	8.02E-11	0.98	5.54	-	2050.1
AHQ-5-13, 5029	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	3.77E-07	0.78	3.31	-	474.8
AHQ-5-13-, 5103 - 5107	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	9.61E-12	0.98	6.04	-	1993.3
AHQ-5-13-, 3247	K.VNVDEVGGEALGR.L	1315.41484	1	2.45E-08	0.44	2.39	-	312.3
AHQ-5-13-, 3244 - 3249	K.VNVDEVGGEALGR.L	1315.41484	2	3.70E-06	0.97	4.79	-	1791.5
AHQ-5-13, 3351 - 3354	K.VNVDEVGGEALGR.L	1315.41484	2	3.29E-06	0.97	4.88	-	1983.2
AHQ-5-14-, 3175	K.VNVDEVGGEALGR.L	1315.41484	2	1.01E-05	0.94	3.82	-	1480.4
AHQ-5-13-, 3256	K.VNVDEVGGEALGR.L	1315.41484	1	1.61E-06	0.62	2.97	-	254.9
AHQ-5-13-, 2671	K.VVAGVANALAHK.Y	1150.35593	2	2.73E-06	0.94	3.52	-	1369.4
AHQ-5-13, 2813	K.VVAGVANALAHK.Y	1150.35593	2	9.72E-05	0.96	3.95	-	1848.1
AHQ-5-13, 2343	K.VVAGVANALAHK.Y	1150.35593	1	9.05E-07	0.83	2.80	-	810.6
gi|17986273|ref|NP_524144.1| fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2				3.31E-13	0.95	10.21	8.20	21145.0
AHQ-5-12, 3160 - 3184	R.VFDKEGNGTVMGAELR.H	1723.93228	3	3.52E-04	0.90	3.71	-	1317.4
AHQ-5-12, 3282 - 3350	R.VFDKEGNGTVMGAELR.H	1723.93228	2	3.31E-13	0.95	3.94	-	1342.3
AHQ-5-13, 3430	R.VFDKEGNGTVMGAELR.H	1723.93228	2	1.19E-10	0.93	3.49	-	1095.3
AHQ-5-13-, 3312	R.VFDKEGNGTVMGAELR.H	1723.93228	2	8.63E-12	0.94	4.12	-	1187.0
AHQ-5-12, 3157 - 3226	R.VFDKEGNGTVMGAELR.H	1723.93228	2	2.29E-11	0.96	4.18	-	1388.7
gi|4757826|ref|NP_004039.1| beta-2-microglobulin [Homo sapiens]				3.99E-13	2.45	30.23	30.30	13714.5
AHQ-5-14-, 6389	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	2	7.54E-06	0.84	3.70	-	527.4
AHQ-5-14-, 6601	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	3	3.16E-06	0.87	4.53	-	456.6
AHQ-5-14-, 6333	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	7.63E-09	0.85	4.15	-	1017.1
AHQ-5-14-, 6563	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	3.99E-13	0.89	4.31	-	854.2
AHQ-5-14-, 1887 - 1951	R.VNHVTLSQPK.I	1123.28735	2	6.55E-05	0.74	2.59	-	563.5
AHQ-5-14-, 1821 - 1970	R.VNHVTLSQPK.I	1123.28735	1	5.43E-07	0.68	3.23	-	295.2
AHQ-5-14, 2449	R.VNHVTLSQPK.I	1123.28735	1	6.56E-04	0.13	1.93	-	275.5
gi|6005846|ref|NP_009215.1| PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro				4.54E-13	6.53	70.31	38.70	39547.7
AHQ-5-14-, 6410 - 6418	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	1.28E-08	0.97	6.02	-	987.1
AHQ-5-9, 5986	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	2.93E-05	0.95	4.59	-	904.6
AHQ-5-12, 6504	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	3.55E-05	0.81	3.81	-	355.0
AHQ-5-13-, 6520	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	6.37E-11	0.97	5.52	-	1010.5
AHQ-5-12, 6588	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	2.85E-09	0.95	5.19	-	707.8
AHQ-5-13, 6569 - 6580	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	2.01E-09	0.96	5.18	-	956.2
AHQ-5-12, 6604	R.AVLPLLDAQQPCYLLYR.L	2035.39506	3	2.27E-09	0.96	5.14	-	1544.6
AHQ-5-12, 5930	K.EFGGGHIKDELFGTVKDDLSFAGYQK.H	2860.12617	3	1.54E-05	0.92	4.72	-	864.6
AHQ-5-10, 3802	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	3.28E-06	0.93	4.40	-	757.9
AHQ-5-11, 4048	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	5.91E-06	0.93	4.67	-	782.2
AHQ-5-9, 3687	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	7.39E-05	0.90	4.29	-	799.8
AHQ-5-11, 4224	K.HQTLQGLAFPLQPEAQR.A	1935.17562	3	4.21E-05	0.83	3.19	-	1080.3
AHQ-5-11, 4202	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	2.14E-11	0.98	5.49	-	1913.8
AHQ-5-10, 3928	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	4.54E-13	0.96	5.02	-	1040.2
AHQ-5-11, 6183	K.KIEIGDGAELTAEFLYDEVHPK.Q	2475.73515	3	5.28E-11	0.98	6.23	-	2347.6
AHQ-5-11, 5120	R.LLDSVEQDFHLEIAK.K	1757.96513	2	1.60E-06	0.84	3.42	-	666.3
AHQ-5-13-, 4684	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	2.73E-10	0.94	3.56	-	1822.2
AHQ-5-13, 4777	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	6.16E-05	0.96	4.35	-	1775.2
AHQ-5-12, 4736	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	4.62E-09	0.97	4.68	-	1945.3
AHQ-5-12, 4749	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	3	5.59E-04	0.96	4.58	-	2122.5
gi|4507729|ref|NP_001060.1| tubulin, beta polypeptide [Homo sapiens]				4.62E-13	7.39	90.36	31.20	49906.7
AHQ-5-7, 2788 - 2790	R.EIVHIQAGQCGNQIGAK.F	1825.03962	2	6.09E-07	0.96	4.68	-	1443.9
AHQ-5-7, 2816	K.EVDEQMLNVQNK.N	1447.59668	1	1.18E-04	0.26	2.36	-	260.9
AHQ-5-7, 2683	K.EVDEQMLNVQNK.N	1447.59668	1	1.07E-08	0.49	3.11	-	229.7
AHQ-5-8, 6053	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.87E-09	0.98	5.92	-	2316.0
AHQ-5-14-, 6159	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.31E-06	0.99	6.95	-	3047.4
AHQ-5-13-, 6284	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	2.92E-04	0.71	3.10	-	930.9
AHQ-5-13-, 6271 - 6277	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.38E-12	0.99	7.24	-	3060.8
AHQ-5-10, 5770	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.63E-08	0.98	6.06	-	2147.9
AHQ-5-13, 6324	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.71E-08	0.98	5.88	-	2427.4
AHQ-5-11, 5995 - 6064	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.20E-08	0.99	7.16	-	3141.8
AHQ-5-7, 6056 - 6122	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.67E-07	0.99	7.17	-	2574.2
AHQ-5-13, 6320 - 6338	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	4.12E-06	0.92	5.08	-	1077.8
AHQ-5-7, 6087 - 6164	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	2.99E-05	0.80	4.41	-	754.3
AHQ-5-7, 6190	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	7.37E-06	0.98	6.30	-	2664.3
AHQ-5-9, 5526 - 5562	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.53E-06	0.98	5.12	-	2256.0
AHQ-5-12, 6225	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	5.14E-07	0.99	6.57	-	2827.8
AHQ-5-12, 6237	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	8.80E-05	0.82	3.74	-	819.3
AHQ-5-13-, 4399	R.ISEQFTAMFR.R	1230.41818	2	8.40E-06	0.89	3.79	-	932.9
AHQ-5-7, 4296 - 4312	R.ISEQFTAMFR.R	1230.41818	2	1.16E-06	0.95	3.41	-	1774.4
AHQ-5-10, 6435	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	2.39E-06	0.89	4.13	-	688.2
AHQ-5-9, 6374	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	2.08E-04	0.87	4.04	-	930.8
AHQ-5-7, 7115 - 7166	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	3.95E-10	0.95	5.22	-	794.2
AHQ-5-7, 6034	K.LTTPTYGDLNHLVSATM*SGVTTCLR.F	2727.06467	3	1.29E-06	0.69	3.32	-	587.1
AHQ-5-7, 6196	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	4.58E-04	0.74	3.29	-	753.6
AHQ-5-9, 5555	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	1.79E-10	0.94	4.50	-	956.1
AHQ-5-8, 7073	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	1.22E-05	0.63	3.19	-	800.3
AHQ-5-8, 7077	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	9.43E-08	0.95	5.42	-	695.8
AHQ-5-7, 6191	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	1.55E-06	0.89	3.74	-	753.0
AHQ-5-7, 5940	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	1.64E-07	0.90	4.31	-	1195.4
AHQ-5-7, 6528	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	7.93E-09	0.84	3.95	-	945.0
AHQ-5-7, 5900	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.08E-04	0.69	3.08	-	617.1
AHQ-5-7, 5376	K.NSSYFVEWIPNNVK.T	1697.87148	2	4.84E-06	0.83	2.97	-	855.9
AHQ-5-7, 5294	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.71E-04	0.93	4.09	-	887.0
AHQ-5-12, 5429 - 5434	K.NSSYFVEWIPNNVK.T	1697.87148	2	4.05E-04	0.88	3.78	-	705.4
AHQ-5-7, 6059 - 6132	K.NSSYFVEWIPNNVK.T	1697.87148	2	9.79E-07	0.57	2.99	-	516.8
AHQ-5-7, 5127 - 5202	K.NSSYFVEWIPNNVK.T	1697.87148	2	2.53E-05	0.88	3.98	-	634.0
AHQ-5-7, 6431 - 6504	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	2.11E-10	0.97	5.60	-	1136.8
AHQ-5-11, 6080	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	8.34E-07	0.94	4.81	-	800.7
AHQ-5-11, 6091 - 6152	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	7.59E-10	0.97	5.70	-	1849.1
AHQ-5-11, 6166	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	6.38E-12	0.96	5.36	-	892.0
AHQ-5-7, 6442 - 6506	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	5.69E-12	0.97	6.11	-	1903.2
AHQ-5-12, 6217 - 6228	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.09E-07	0.97	6.27	-	1888.9
AHQ-5-7, 6354 - 6418	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	1.24E-06	0.96	5.70	-	963.2
AHQ-5-7, 6214 - 6287	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	2.73E-05	0.95	4.98	-	849.2
AHQ-5-12, 6348	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	1.45E-07	0.96	5.46	-	828.1
AHQ-5-10, 5772 - 5852	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.33E-09	0.97	6.27	-	1509.0
AHQ-5-7, 6572	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	1.86E-05	0.95	5.16	-	986.7

AHQ-5-9, 5763 - 5779	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	9.01E-08	0.94	4.91	-	844.1
AHQ-5-9, 5720 - 5727	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	2.13E-09	0.97	5.40	-	1967.5
AHQ-5-9, 5680 - 5719	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	5.81E-05	0.83	3.21	-	637.2
AHQ-5-14-, 6106 - 6185	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.62E-13	0.97	7.03	-	1472.2
AHQ-5-8, 6241	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	2.92E-06	0.84	3.50	-	543.9
AHQ-5-14-, 6277	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	6.06E-09	0.94	5.08	-	1260.4
gi|4758606|ref|NP_004508.1| integrin-linked kinase [Homo sapiens]				4.75E-13	13.32	150.29	29.40	51418.9
AHQ-5-13, 5244	R.EVPFADLSNMEIGM*K.V	1697.95498	2	8.08E-06	0.92	3.55	-	1145.9
AHQ-5-13-, 5612	R.EVPFADLSNMEIGMK.V	1681.95558	2	1.19E-04	0.83	2.69	-	526.5
AHQ-5-7, 4091	R.EVPFADLSNM*EIGM*K.V	1713.95438	2	7.29E-05	0.81	2.90	-	602.3
AHQ-5-7, 5347	K.FDMIVPILEK.M	1205.49168	2	2.33E-06	0.85	3.14	-	694.5
AHQ-5-7, 4179 - 4208	K.FDM*IVPILEK.M	1221.49108	2	1.28E-06	0.83	2.92	-	703.1
AHQ-5-12, 2062	R.GDDTPLHLAASHGHR.D	1584.67809	2	1.69E-11	0.96	4.44	-	1377.8
AHQ-5-11, 4984	R.GM*AFLHTLEPLIPR.H	1611.93301	2	1.29E-04	0.88	2.98	-	976.1
AHQ-5-10, 4616	R.GM*AFLHTLEPLIPR.H	1611.93301	2	1.35E-06	0.83	3.32	-	616.2
AHQ-5-5, 5925	R.GMAFLHTLEPLIPR.H	1595.93361	2	1.44E-07	0.87	3.57	-	762.9
AHQ-5-7, 5552 - 5630	R.GMAFLHTLEPLIPR.H	1595.93361	2	4.44E-10	0.97	4.71	-	1471.6
AHQ-5-7, 5491 - 5558	R.GMAFLHTLEPLIPR.H	1595.93361	2	1.13E-04	0.75	2.98	-	529.6
AHQ-5-7, 5568	R.GMAFLHTLEPLIPR.H	1595.93361	3	1.12E-07	0.88	3.87	-	1061.2
AHQ-5-7, 2003	K.LNENHSGELWK.G	1327.42732	2	1.21E-04	0.90	3.71	-	996.7
AHQ-5-7, 5914 - 5990	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	4.75E-13	0.96	5.74	-	1247.8
AHQ-5-7, 6102	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	1.13E-08	0.94	5.09	-	938.1
AHQ-5-14-, 5850	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	6.00E-09	0.94	5.17	-	1127.3
AHQ-5-10, 4252	R.MYAPAWVAPEALQK.K	1575.85602	2	2.56E-06	0.87	3.29	-	879.2
AHQ-5-7, 4414	R.MYAPAWVAPEALQK.K	1575.85602	2	4.78E-11	0.96	4.43	-	1077.9
AHQ-5-11, 4596	R.MYAPAWVAPEALQK.K	1575.85602	2	1.15E-06	0.97	4.22	-	1575.5
AHQ-5-7, 3963 - 4014	R.M*YAPAWVAPEALQK.K	1591.85542	2	1.19E-06	0.95	4.33	-	1018.4
AHQ-5-13, 4793	R.MYAPAWVAPEALQK.K	1575.85602	2	6.34E-04	0.65	2.63	-	804.1
AHQ-5-13, 4253 - 4321	R.M*YAPAWVAPEALQK.K	1591.85542	2	5.93E-04	0.95	3.97	-	1007.8
AHQ-5-7, 4367	R.SAVVEMLIMR.G	1149.45316	2	5.89E-08	0.92	3.65	-	1211.6
AHQ-5-7, 4180 - 4258	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	3	7.44E-10	0.89	3.50	-	1227.3
AHQ-5-9, 3963	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	2	8.34E-04	0.91	4.32	-	559.2
AHQ-5-13, 4653	K.VALEGLRPTIPPGISPHVCK.L	2143.53829	3	3.09E-07	0.83	3.60	-	657.7
AHQ-5-7, 2682	R.WQGNDIVVK.V	1059.20012	1	1.61E-05	0.74	2.30	-	854.1
gi|4758970|ref|NP_004150.1| proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be				5.63E-13	2.69	30.24	14.70	29769.4
AHQ-5-11, 2383	K.FQHGVIAAVDSR.A	1300.44824	2	1.92E-05	0.78	2.58	-	837.0
AHQ-5-11, 2280	K.KGPGLYYVDEHGTR.L	1592.73690	2	4.63E-10	0.97	4.79	-	1330.8
AHQ-5-11, 4042	K.VESTDVSDLLHQYR.E	1662.78230	2	5.63E-13	0.95	4.11	-	1255.3
AHQ-5-11, 3959 - 4022	K.VESTDVSDLLHQYR.E	1662.78230	2	1.88E-08	0.93	3.96	-	1053.5
gi|5729877|ref|NP_006588.1| heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD				5.99E-13	12.89	140.33	24.60	70897.6
AHQ-5-6, 4584	R.FEELNADLFR.G	1254.37310	2	4.39E-05	0.91	4.00	-	1052.0
AHQ-5-6, 5481	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	2	1.07E-05	0.71	3.73	-	766.7
AHQ-5-6, 5213 - 5280	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	6.37E-12	0.96	6.60	-	819.4
AHQ-5-6, 5201 - 5268	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	2	1.05E-06	0.96	5.04	-	970.9
AHQ-5-14-, 5155	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	1.01E-07	0.82	3.84	-	418.5
AHQ-5-6, 3644	K.HWPFMVVNDAGRPK.V	1654.91970	2	8.49E-04	0.92	3.32	-	1002.7
AHQ-5-6, 5566	K.ILDKCNEIINWLDK.N	1776.04688	2	7.47E-10	0.94	4.92	-	1140.7
AHQ-5-6, 3250 - 3277	K.LDKSQIHDIVLVGGSTR.I	1839.08615	2	2.85E-06	0.92	4.03	-	808.4
AHQ-5-6, 3734	K.NQVAMNPTNTVFDAK.R	1650.83816	2	8.63E-05	0.70	2.61	-	689.8
AHQ-5-6, 3328 - 3365	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	8.69E-06	0.90	3.66	-	921.8
AHQ-5-6, 3309 - 3317	K.NQVAMNPTNTVFDAK.R	1650.83816	2	1.92E-08	0.85	3.51	-	570.1
AHQ-5-6, 4004	K.NQVAMNPTNTVFDAK.R	1650.83816	2	8.65E-10	0.93	4.48	-	781.8
AHQ-5-6, 2781 - 2793	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	1.51E-04	0.93	3.96	-	868.7
AHQ-5-6, 4652	K.NSLESYAFNMK.A	1304.45393	1	8.42E-04	0.31	2.16	-	303.3
AHQ-5-6, 3837 - 3885	K.NSLESYAFNMK.A	1304.45393	2	7.31E-05	0.86	3.20	-	876.1
AHQ-5-6, 1932 - 1934	R.RFDDAVVQSDM*K.H	1427.56543	2	4.37E-04	0.93	3.32	-	940.8
AHQ-5-6, 2428 - 2430	R.RFDDAVVQSDMK.H	1411.56603	2	1.12E-06	0.95	4.34	-	1314.4
AHQ-5-6, 5102 - 5168	K.SFYPEEVSSMVLTK.M	1617.84485	2	1.08E-11	0.91	3.87	-	616.6
AHQ-5-6, 7125	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	5.99E-13	0.94	5.03	-	783.5
AHQ-5-6, 6864 - 6930	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	3.46E-08	0.97	5.53	-	1139.3
AHQ-5-7, 6838	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	1.81E-05	0.92	4.49	-	706.5
AHQ-5-7, 2691 - 2700	K.SQIHDIVLVGGSTR.I	1482.66712	2	1.54E-07	0.95	3.75	-	1525.2
AHQ-5-6, 2788	K.SQIHDIVLVGGSTR.I	1482.66712	1	2.25E-07	0.84	3.73	-	433.1
AHQ-5-6, 2780	K.SQIHDIVLVGGSTR.I	1482.66712	2	2.81E-06	0.96	4.18	-	1652.9
AHQ-5-6, 4666 - 4736	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	1.97E-07	0.87	3.79	-	503.9
gi|9966764|ref|NP_009191.1| lysophospholipase II; acyl-protein thioesterase [Homo sapiens]				6.94E-13	0.97	10.26	11.30	24736.8
AHQ-5-10, 6436	R.ETAAVIFLHGLGDTGHSWADALSTIR.L	2740.02329	3	6.94E-13	0.97	5.15	-	2459.3
gi|7669492|ref|NP_002037.2| glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]				7.03E-13	8.68	100.34	39.70	36053.0
AHQ-5-10, 3298	R.GALQNIIPASTGAAK.A	1412.61680	1	7.43E-06	0.48	3.05	-	243.8
AHQ-5-9, 3079 - 3138	R.GALQNIIPASTGAAK.A	1412.61680	1	2.16E-05	0.78	3.71	-	407.6
AHQ-5-9, 3083 - 3142	R.GALQNIIPASTGAAK.A	1412.61680	2	3.28E-04	0.73	3.45	-	432.7
AHQ-5-11, 3503	R.GALQNIIPASTGAAK.A	1412.61680	1	3.38E-09	0.80	3.41	-	519.4
AHQ-5-9, 5466 - 5530	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	1.18E-06	0.95	5.94	-	1177.1
AHQ-5-9, 5239	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	1.61E-12	0.87	4.58	-	599.6
AHQ-5-9, 5699 - 5758	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	1.88E-04	0.96	5.90	-	1056.6
AHQ-5-9, 6286 - 6358	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	2.96E-08	0.97	6.19	-	1719.2
AHQ-5-9, 6168 - 6226	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	1.86E-05	0.90	4.95	-	707.4
AHQ-5-9, 5899 - 5956	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	1.68E-04	0.72	3.87	-	501.5
AHQ-5-9, 5572 - 5632	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L	4039.28524	3	7.03E-13	0.96	6.02	-	1195.7
AHQ-5-9, 5651 - 5728	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	2.19E-11	0.97	6.50	-	2272.6
AHQ-5-11, 6722	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	8.68E-10	0.95	6.06	-	1671.8
AHQ-5-10, 6450	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	1.15E-11	0.95	6.77	-	1441.2
AHQ-5-11, 6726	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	8.69E-09	0.96	6.36	-	1319.0
AHQ-5-9, 6322 - 6378	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	2.54E-07	0.97	6.82	-	1811.7
AHQ-5-10, 6452	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	2	1.73E-10	0.98	6.85	-	1648.2
AHQ-5-9, 4284 - 4288	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	1.09E-04	0.83	3.66	-	469.8
AHQ-5-9, 4106	R.VIISAPSADAPM*FVMGVNHEK.Y	2230.59327	2	1.58E-07	0.64	3.11	-	628.4
AHQ-5-10, 4675	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	2.99E-08	0.70	3.09	-	364.9
AHQ-5-9, 4022	R.VIISAPSADAPMFVM*GVNHEK.Y	2230.59327	2	2.34E-07	0.70	3.55	-	730.4
AHQ-5-12, 5040 - 5045	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	3	8.51E-07	0.54	3.07	-	311.3
AHQ-5-9, 3944 - 4023	R.VIISAPSADAPM*FVMGVNHEK.Y	2230.59327	2	6.57E-04	0.31	3.07	-	305.8
AHQ-5-10, 3992	R.VIISAPSADAPMFVM*GVNHEK.Y	2230.59327	2	3.21E-04	0.44	3.21	-	357.2
AHQ-5-10, 4466	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	4.68E-05	0.82	3.44	-	586.7
AHQ-5-9, 4507	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	7.05E-09	0.91	3.97	-	654.0
AHQ-5-4, 4270	R.VPTANVSVVDLTCR.L	1532.74450	2	1.82E-08	0.91	3.53	-	891.3
AHQ-5-11, 3982 - 4046	R.VPTANVSVVDLTCR.L	1532.74450	2	1.19E-08	0.90	3.83	-	756.9
AHQ-5-11, 3792	R.VPTANVSVVDLTCR.L	1532.74450	2	5.81E-05	0.89	3.06	-	940.0
AHQ-5-12, 4117 - 4148	R.VPTANVSVVDLTCR.L	1532.74450	2	2.74E-10	0.95	4.21	-	1254.3
AHQ-5-14, 4845 - 4846	R.VPTANVSVVDLTCR.L	1532.74450	2	5.47E-10	0.93	4.00	-	961.6
AHQ-5-9, 4004	R.VPTANVSVVDLTCR.L	1532.74450	2	1.70E-07	0.90	3.82	-	900.8
AHQ-5-9, 3902	R.VPTANVSVVDLTCR.L	1532.74450	2	5.92E-06	0.89	3.39	-	833.6
AHQ-5-9, 3734 - 3815	R.VPTANVSVVDLTCR.L	1532.74450	2	3.25E-09	0.94	4.17	-	1006.1
AHQ-5-9, 3619	R.VPTANVSVVDLTCR.L	1532.74450	2	3.25E-06	0.87	3.12	-	941.2
AHQ-5-10, 3760 - 3824	R.VPTANVSVVDLTCR.L	1532.74450	2	8.16E-05	0.83	2.96	-	817.2
AHQ-5-9, 3618 - 3678	R.VPTANVSVVDLTCR.L	1532.74450	2	5.85E-09	0.96	4.69	-	1174.0
AHQ-5-9, 3487	R.VPTANVSVVDLTCR.L	1532.74450	2	7.06E-09	0.94	3.98	-	1152.6
AHQ-5-13, 4188	R.VPTANVSVVDLTCR.L	1532.74450	2	1.28E-07	0.93	3.71	-	1037.8

AHQ-5-13-, 4099	R.VPTANVSVVDLTCR.L	1532.74450	2	2.07E-09	0.95	4.27	-	1079.9
AHQ-5-9, 6646	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	3.13E-06	0.86	3.78	-	635.5
AHQ-5-9, 6539 - 6610	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	3.23E-06	0.94	4.45	-	918.0
AHQ-5-9, 6403 - 6470	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.30E-05	0.94	4.50	-	952.6
AHQ-5-9, 6260	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	5.45E-04	0.65	3.44	-	380.4
AHQ-5-9, 6251 - 6315	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	7.66E-06	0.89	4.18	-	557.9
AHQ-5-9, 6120 - 6192	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	2.13E-07	0.94	4.18	-	1049.8
AHQ-5-9, 5992 - 6059	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.56E-05	0.90	3.61	-	1001.2
AHQ-5-9, 5870 - 5934	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.87E-07	0.95	4.38	-	1122.5
AHQ-5-9, 5752 - 5814	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	9.97E-08	0.95	4.62	-	1057.4
AHQ-5-9, 5672 - 5744	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	4.18E-04	0.84	3.49	-	738.7
AHQ-5-13, 6208 - 6281	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	9.04E-07	0.93	4.19	-	938.8
AHQ-5-9, 5667 - 5691	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.23E-07	0.91	4.02	-	825.3
AHQ-5-10, 5832	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	3.37E-04	0.82	3.79	-	507.3
AHQ-5-13-, 6015 - 6091	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.83E-07	0.95	5.25	-	829.0
AHQ-5-13-, 6111 - 6172	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	9.34E-07	0.96	5.23	-	1189.1
AHQ-5-13-, 6241	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	4.14E-06	0.87	3.89	-	564.1
gi|29739414|ref|XP_294015.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				7.10E-13	3.25	40.24	17.70	26916.7
AHQ-5-11, 3971	K.IISNASCTTNCLAPLAK.V	1837.10868	2	5.55E-07	0.73	3.51	-	1026.7
AHQ-5-10, 3638 - 3700	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.14E-07	0.90	4.15	-	1390.4
AHQ-5-9, 3514 - 3578	K.IISNASCTTNCLAPLAK.V	1837.10868	2	7.10E-13	0.91	4.83	-	1282.5
AHQ-5-9, 3635 - 3696	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.42E-09	0.88	4.11	-	1335.5
AHQ-5-10, 3844 - 3900	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.85E-06	0.30	2.62	-	499.3
AHQ-5-9, 4671	K.LISWYDNEFGYSNR.V	1764.87478	2	1.76E-06	0.85	3.76	-	671.8
AHQ-5-9, 4826	K.LISWYDNEFGYSNR.V	1764.87478	2	8.85E-06	0.84	3.52	-	806.7
AHQ-5-13-, 4971	K.LISWYDNEFGYSNR.V	1764.87478	2	7.73E-06	0.89	3.30	-	895.8
AHQ-5-9, 4542 - 4604	K.LISWYDNEFGYSNR.V	1764.87478	2	7.92E-06	0.94	4.40	-	771.8
AHQ-5-9, 4430 - 4486	K.LISWYDNEFGYSNR.V	1764.87478	2	9.64E-08	0.96	4.41	-	1184.5
AHQ-5-14-, 4923 - 4931	K.LISWYDNEFGYSNR.V	1764.87478	2	1.70E-10	0.96	4.87	-	1303.1
AHQ-5-14, 5829 - 5832	K.LISWYDNEFGYSNR.V	1764.87478	2	1.53E-08	0.93	4.08	-	1011.6
AHQ-5-10, 4550 - 4592	K.LISWYDNEFGYSNR.V	1764.87478	2	3.97E-09	0.90	3.48	-	992.3
AHQ-5-11, 4819 - 4879	K.LISWYDNEFGYSNR.V	1764.87478	2	2.59E-07	0.93	4.06	-	805.9
AHQ-5-11, 4952	K.LISWYDNEFGYSNR.V	1764.87478	2	5.95E-06	0.90	3.54	-	883.9
AHQ-5-12, 5022 - 5077	K.LISWYDNEFGYSNR.V	1764.87478	2	2.51E-08	0.96	4.36	-	1339.4
AHQ-5-13, 5076	K.LISWYDNEFGYSNR.V	1764.87478	2	8.07E-08	0.89	3.49	-	720.1
AHQ-5-9, 2492	R.VVDLMAHMASK.E	1202.47292	2	6.08E-04	0.93	3.15	-	1237.9
AHQ-5-11, 2786	R.VVDLMAHMASK.E	1202.47292	2	1.80E-07	0.96	3.93	-	1439.2
AHQ-5-9, 2598 - 2676	R.VVDLMAHMASKE	1331.58746	1	7.08E-04	0.42	2.60	-	297.1
gi|30159830|ref|XP_302246.1| similar to HSPC280 [Homo sapiens]				8.45E-13	1.93	20.25	3.90	45644.4
AHQ-5-14-, 6745	K.CANLFEALVGTLK.A	1437.68632	2	4.40E-06	0.97	4.91	-	1491.8
AHQ-5-14-, 6725	R.DDKCANLFEALVGTLK.A	1796.03496	2	8.45E-13	0.96	4.92	-	1618.7
AHQ-5-14-, 6693 - 6694	R.DDKCANLFEALVGTLK.A	1796.03496	3	1.00E-05	0.94	4.64	-	1720.5
AHQ-5-14-, 6643	R.DDKCANLFEALVGTLK.A	1796.03496	2	8.16E-09	0.93	3.82	-	1155.5
gi|4507645|ref|NP_000356.1| triosephosphate isomerase 1 [Homo sapiens]				8.60E-13	5.43	60.33	38.60	26669.3
AHQ-5-10, 3522 - 3580	K.DCGATWVVLGHSER.R	1588.72671	2	7.92E-06	0.93	3.97	-	1117.3
AHQ-5-10, 6222 - 6278	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	8.32E-05	0.79	3.99	-	262.2
AHQ-5-10, 6079 - 6086	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	3.96E-07	0.81	4.28	-	214.1
AHQ-5-10, 6338 - 6412	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	6.75E-08	0.71	3.86	-	242.3
AHQ-5-10, 3714	R.KQSLGELIGTLNAAK.V	1543.79037	2	4.92E-06	0.96	4.49	-	1342.9
AHQ-5-10, 3931 - 3939	R.KQSLGELIGTLNAAK.V	1543.79037	2	8.26E-04	0.93	3.71	-	1350.0
AHQ-5-10, 4748	K.QSLGELIGTLNAAK.V	1415.61746	2	1.41E-06	0.90	3.27	-	918.8
AHQ-5-10, 4882 - 4950	K.VAHALAEGLGVIACIGEK.L	1810.10800	2	8.60E-13	0.99	6.54	-	3019.7
AHQ-5-10, 5046 - 5110	K.VPADTEVVCAPPTAYIDFAR.Q	2194.44943	2	5.72E-04	0.94	4.68	-	801.8
AHQ-5-14-, 5470	K.VPADTEVVCAPPTAYIDFAR.Q	2194.44943	2	5.57E-04	0.94	4.76	-	751.2
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				1.14E-12	24.28	280.34	55.80	75429.7
AHQ-5-6, 2957 - 2958	K.AGDALWLR.F	902.03223	2	1.30E-04	0.93	3.98	-	1225.9
AHQ-5-14-, 6387 - 6394	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	1.76E-08	0.97	5.22	-	1410.8
AHQ-5-10, 5978 - 6056	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	1.30E-05	0.61	2.57	-	769.8
AHQ-5-6, 6752 - 6821	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.65E-10	0.95	4.61	-	926.3
AHQ-5-6, 6668 - 6732	R.ASFSQPLFQAVAAICR.L	1768.02967	2	7.36E-09	0.96	5.07	-	1038.4
AHQ-5-7, 6667 - 6695	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.12E-05	0.91	3.95	-	824.3
AHQ-5-1, 6987 - 6991	R.ASFSQPLFQAVAAICR.L	1768.02967	2	7.12E-07	0.95	4.22	-	1171.3
AHQ-5-12, 6630	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.29E-05	0.89	3.45	-	787.6
AHQ-5-4, 7013	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.00E-05	0.95	4.51	-	983.3
AHQ-5-9, 5966 - 6027	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.84E-04	0.94	4.36	-	699.4
AHQ-5-11, 6400 - 6478	R.ASFSQPLFQAVAAICR.L	1768.02967	2	7.75E-04	0.79	3.35	-	524.1
AHQ-5-3, 7046	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.04E-10	0.96	4.94	-	909.1
AHQ-5-5, 6867 - 6870	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.01E-09	0.96	5.07	-	1035.4
AHQ-5-6, 6984 - 7062	R.ASFSQPLFQAVAAICR.L	1768.02967	2	7.73E-04	0.91	4.00	-	700.1
AHQ-5-10, 6091	R.ASFSQPLFQAVAAICR.L	1768.02967	2	9.58E-06	0.90	3.73	-	890.6
AHQ-5-6, 6713	R.ASFSQPLFQAVAAICR.L	1768.02967	3	1.61E-05	0.92	4.38	-	1017.0
AHQ-5-11, 3451 - 3474	K.EKEPEEELYDLSK.V	1609.71294	2	3.93E-05	0.79	3.48	-	392.8
AHQ-5-9, 3107	K.EKEPEEELYDLSK.V	1609.71294	2	1.60E-07	0.92	4.06	-	595.4
AHQ-5-6, 3273 - 3344	K.EKEPEEELYDLSK.V	1609.71294	2	1.00E-05	0.76	3.21	-	457.6
AHQ-5-3, 7317	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	1.92E-04	0.95	5.13	-	547.3
AHQ-5-1, 7185	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	4.62E-04	0.63	3.18	-	209.4
AHQ-5-12, 6824 - 6832	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	7.73E-05	0.95	5.13	-	664.6
AHQ-5-13, 6724	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	1.92E-05	0.85	4.10	-	428.6
AHQ-5-11, 6628	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	7.67E-04	0.78	3.54	-	331.4
AHQ-5-9, 6422 - 6423	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	2.18E-05	0.94	5.34	-	439.7
AHQ-5-10, 6346	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	6.50E-04	0.87	4.28	-	320.5
AHQ-5-6, 7058 - 7076	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	3	2.67E-04	0.95	4.76	-	1565.4
AHQ-5-6, 7240	R.FIQAWQSLPDFGISYVMVR.F	2258.62653	2	4.46E-06	0.95	5.05	-	765.3
AHQ-5-9, 2890	K.GCEVVPDVNVSGQK.F	1489.63335	1	5.16E-07	0.88	3.74	-	849.4
AHQ-5-11, 3139	K.GCEVVPDVNVSGQK.F	1489.63335	1	2.44E-04	0.76	2.33	-	1105.6
AHQ-5-13, 3358 - 3417	K.GCEVVPDVNVSGQK.F	1489.63335	2	9.15E-04	0.66	2.52	-	603.9
AHQ-5-6, 3086	K.GCEVVPDVNVSGQK.F	1489.63335	1	1.77E-06	0.82	3.08	-	840.9
AHQ-5-13, 6776	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	8.41E-05	0.82	3.81	-	676.6
AHQ-5-14-, 6669	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	7.47E-07	0.95	4.91	-	1000.3
AHQ-5-6, 7180 - 7249	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	1.76E-07	0.89	4.44	-	453.9
AHQ-5-6, 3788 - 3797	R.GMPAHFSDSAQTEACYHMLSR.P	2398.64117	3	1.14E-12	0.94	5.25	-	904.5
AHQ-5-3, 3957	R.IDLAVGDVVK.T	1029.21223	1	4.17E-05	0.24	1.93	-	404.0
AHQ-5-6, 3641 - 3712	R.IDLAVGDVVK.T	1029.21223	1	3.58E-05	0.30	2.10	-	439.7
AHQ-5-6, 3638 - 3708	R.IDLAVGDVVK.T	1029.21223	2	5.63E-06	0.92	3.33	-	1248.4
AHQ-5-9, 3382	R.IDLAVGDVVK.T	1029.21223	1	3.62E-05	0.54	2.47	-	452.4
AHQ-5-14, 4654	R.IDLAVGDVVK.T	1029.21223	1	1.76E-04	0.42	2.10	-	520.8
AHQ-5-4, 4618	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.74E-05	0.98	6.41	-	2100.9
AHQ-5-12, 4426	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	5.65E-06	0.92	4.79	-	1358.6
AHQ-5-11, 4271	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	3.30E-04	0.98	6.53	-	2067.8
AHQ-5-9, 3811 - 3870	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	7.43E-06	0.91	4.33	-	826.9
AHQ-5-11, 4267	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	6.96E-06	0.95	5.42	-	1144.7
AHQ-5-1, 4727	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.12E-11	0.98	6.18	-	2234.1
AHQ-5-7, 4107	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.97E-07	0.97	5.57	-	1443.7
AHQ-5-13-, 4448	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.40E-12	0.98	6.55	-	2181.5
AHQ-5-3, 4677	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.16E-06	0.98	6.77	-	2005.8
AHQ-5-4, 4609	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	3.56E-04	0.70	3.77	-	880.2
AHQ-5-12, 4425	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	8.37E-11	0.98	5.86	-	2046.0

AHQ-5-6, 4410 - 4477	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	9.07E-07	0.98	6.10	-	1814.2
AHQ-5-6, 4270 - 4340	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	3.45E-12	0.98	6.13	-	1971.5
AHQ-5-6, 1550	K.IVEQINR.K	872.00444	2	9.81E-04	0.73	2.52	-	675.8
AHQ-5-12, 2537	R.KDEILGIANNR.L	1243.39499	1	1.05E-05	0.25	1.94	-	333.6
AHQ-5-12, 2532 - 2541	R.KDEILGIANNR.L	1243.39499	2	5.09E-05	0.90	3.38	-	1010.7
AHQ-5-11, 2484	R.KDEILGIANNR.L	1243.39499	2	2.75E-04	0.85	2.98	-	899.2
AHQ-5-6, 2324 - 2329	R.KDEILGIANNR.L	1243.39499	2	1.32E-04	0.95	3.65	-	1465.2
AHQ-5-6, 2500 - 2568	R.KDEILGIANNR.L	1243.39499	2	2.21E-04	0.83	3.35	-	1042.6
AHQ-5-6, 2413 - 2414	R.KDEILGIANNR.L	1243.39499	1	2.73E-08	0.46	1.90	-	420.6
AHQ-5-6, 2408 - 2412	R.KDEILGIANNR.L	1243.39499	2	3.09E-05	0.91	3.86	-	1101.7
AHQ-5-6, 2326	R.KDEILGIANNR.L	1243.39499	1	4.52E-05	0.33	2.31	-	239.0
AHQ-5-13, 2814 - 2875	R.KDEILGIANNR.L	1243.39499	2	1.64E-05	0.92	3.69	-	1125.5
AHQ-5-9, 2322	R.KDEILGIANNR.L	1243.39499	2	3.91E-06	0.92	3.21	-	1248.9
AHQ-5-7, 3615	R.KQDWSDHAIWWEQK.R	1858.00504	2	6.73E-05	0.85	3.72	-	591.9
AHQ-5-6, 6600 - 6653	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.56E-06	0.91	4.19	-	648.3
AHQ-5-7, 6671 - 6694	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	7.51E-05	0.96	5.64	-	899.0
AHQ-5-6, 6704 - 6768	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.87E-05	0.94	4.82	-	716.2
AHQ-5-5, 6853 - 6855	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.30E-05	0.83	4.02	-	446.2
AHQ-5-9, 5983	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	7.77E-04	0.94	4.94	-	670.7
AHQ-5-6, 6792 - 6854	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.13E-06	0.92	4.34	-	709.7
AHQ-5-6, 5616	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.50E-08	0.92	4.25	-	811.1
AHQ-5-14-, 6415 - 6462	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.51E-04	0.79	3.75	-	370.2
AHQ-5-6, 6436 - 6509	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.67E-06	0.89	3.82	-	684.0
AHQ-5-3, 5939	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.22E-04	0.45	3.03	-	290.5
AHQ-5-8, 6492 - 6500	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	7.10E-05	0.94	4.43	-	825.6
AHQ-5-6, 6385	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	9.47E-08	0.79	3.45	-	457.1
AHQ-5-14-, 5677 - 5702	K.LLVPSPEGMSEIYLR.C	1705.01201	2	6.04E-06	0.70	2.76	-	363.0
AHQ-5-9, 5122	K.LLVPSPEGMSEIYLR.C	1705.01201	2	5.03E-06	0.71	2.88	-	267.4
AHQ-5-12, 5780 - 5789	K.LLVPSPEGMSEIYLR.C	1705.01201	2	3.13E-06	0.64	2.69	-	267.4
AHQ-5-6, 5696 - 5769	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.51E-09	0.64	2.76	-	389.4
AHQ-5-1, 6159	K.LLVPSPEGMSEIYLR.C	1705.01201	2	1.78E-05	0.66	2.56	-	275.7
AHQ-5-6, 5836 - 5840	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.74E-09	0.77	3.18	-	386.9
AHQ-5-6, 4694 - 4765	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	2.56E-05	0.62	2.82	-	307.3
AHQ-5-11, 5598 - 5615	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.76E-05	0.70	2.97	-	417.9
AHQ-5-3, 6145	K.LLVPSPEGMSEIYLR.C	1705.01201	2	5.49E-07	0.72	3.02	-	354.2
AHQ-5-1, 7139	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	3.31E-08	0.94	5.00	-	1172.7
AHQ-5-8, 6772	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	5.38E-06	0.89	4.19	-	1210.4
AHQ-5-6, 7020	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.18E-05	0.94	4.31	-	1646.3
AHQ-5-6, 6928 - 6957	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.80E-11	0.91	4.75	-	968.9
AHQ-5-9, 2144	R.LTQLYEQAR.W	1122.25622	2	3.91E-05	0.91	3.41	-	1027.4
AHQ-5-7, 2095 - 2108	R.LTQLYEQAR.W	1122.25622	2	5.13E-06	0.88	3.25	-	1130.8
AHQ-5-6, 2117 - 2124	R.LTQLYEQAR.W	1122.25622	2	2.18E-05	0.91	3.86	-	1013.5
AHQ-5-13, 2535	R.LTQLYEQAR.W	1122.25622	2	5.47E-04	0.80	2.71	-	783.4
AHQ-5-11, 3934	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	3.87E-09	0.88	3.87	-	570.1
AHQ-5-12, 4042 - 4048	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	3.12E-08	0.88	4.30	-	426.0
AHQ-5-4, 4173	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	5.82E-04	0.82	3.54	-	432.2
AHQ-5-13-, 4060 - 4124	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	6.71E-08	0.92	4.33	-	623.2
AHQ-5-6, 3877 - 3957	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	8.43E-10	0.93	4.43	-	588.5
AHQ-5-6, 4104 - 4178	K.TASGDYIDSSWELR.V	1600.66783	2	2.39E-09	0.89	3.58	-	746.3
AHQ-5-9, 3864 - 3872	K.TASGDYIDSSWELR.V	1600.66783	2	4.30E-07	0.94	3.89	-	985.5
AHQ-5-6, 4248 - 4316	K.TASGDYIDSSWELR.V	1600.66783	2	1.61E-09	0.95	4.27	-	1000.2
AHQ-5-6, 4468 - 4549	K.TASGDYIDSSWELR.V	1600.66783	2	6.88E-05	0.87	3.15	-	901.5
AHQ-5-8, 4105	K.TASGDYIDSSWELR.V	1600.66783	2	1.20E-05	0.84	3.28	-	757.6
AHQ-5-14-, 4253	K.TASGDYIDSSWELR.V	1600.66783	2	9.32E-08	0.95	3.92	-	1326.8
AHQ-5-7, 4135	K.TASGDYIDSSWELR.V	1600.66783	2	7.40E-05	0.82	3.31	-	623.8
AHQ-5-4, 3893	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	3.41E-06	0.97	6.13	-	1444.8
AHQ-5-10, 3487	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.10E-05	0.87	3.87	-	542.7
AHQ-5-6, 3546 - 3617	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	3.55E-04	0.95	5.31	-	739.0
AHQ-5-3, 3941 - 3946	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	1.94E-04	0.93	5.46	-	829.1
AHQ-5-5, 3657	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	8.17E-04	0.88	4.54	-	407.5
AHQ-5-6, 3612 - 3692	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	4.05E-07	0.94	5.63	-	985.0
AHQ-5-1, 4084	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.00E-07	0.90	4.15	-	648.4
AHQ-5-9, 3310	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.62E-04	0.95	5.21	-	718.6
AHQ-5-1, 4076	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	7.73E-06	0.95	5.40	-	1082.7
AHQ-5-11, 3672	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	1.72E-04	0.92	4.66	-	591.0
AHQ-5-5, 3649	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	7.90E-04	0.89	4.65	-	1005.3
AHQ-5-11, 3668	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	5.02E-04	0.96	5.60	-	1275.9
AHQ-5-3, 4157	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.11E-06	0.84	3.15	-	892.3
AHQ-5-11, 3882	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.94E-05	0.93	4.31	-	1033.0
AHQ-5-6, 3873 - 3940	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.75E-10	0.93	4.26	-	1080.5
AHQ-5-6, 4010	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.03E-06	0.97	4.67	-	2131.8
AHQ-5-14-, 3861	R.VFVGEEDPEAESVTLR.V	1777.91007	2	7.34E-09	0.95	4.53	-	1269.7
AHQ-5-13-, 3969	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.55E-07	0.97	4.67	-	1428.0
AHQ-5-4, 4104 - 4180	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.48E-05	0.96	4.36	-	1620.9
AHQ-5-1, 4199	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.28E-05	0.91	4.28	-	908.2
AHQ-5-2, 4106	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.59E-08	0.95	4.47	-	1228.8
AHQ-5-9, 3538 - 3595	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.75E-05	0.91	4.14	-	999.9
AHQ-5-13, 4064	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.66E-06	0.97	4.99	-	1549.0
AHQ-5-12, 3981	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.08E-07	0.94	4.55	-	935.4
AHQ-5-8, 3680	R.VFVGEEDPEAESVTLR.V	1777.91007	2	7.39E-08	0.95	4.42	-	1288.3
AHQ-5-5, 3961	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.80E-07	0.94	4.30	-	1542.8
AHQ-5-7, 3788	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.44E-05	0.89	3.76	-	1028.2
AHQ-5-9, 2430	R.VTGESHIGGVLLK.I	1310.52448	1	1.49E-09	0.81	3.31	-	818.9
AHQ-5-7, 2406	R.VTGESHIGGVLLK.I	1310.52448	2	1.17E-08	0.98	4.89	-	2764.8
AHQ-5-11, 2674 - 2736	R.VTGESHIGGVLLK.I	1310.52448	2	2.13E-06	0.88	3.61	-	960.8
AHQ-5-8, 2249	R.VTGESHIGGVLLK.I	1310.52448	2	1.23E-07	0.94	3.67	-	1474.9
AHQ-5-14-, 2745	R.VTGESHIGGVLLK.I	1310.52448	2	1.98E-09	0.97	4.51	-	2295.6
AHQ-5-13, 2982	R.VTGESHIGGVLLK.I	1310.52448	2	2.58E-09	0.92	3.69	-	1262.7
AHQ-5-11, 2680	R.VTGESHIGGVLLK.I	1310.52448	1	2.63E-04	0.80	2.56	-	961.9
AHQ-5-9, 2379 - 2434	R.VTGESHIGGVLLK.I	1310.52448	2	1.27E-09	0.93	3.60	-	1381.7
AHQ-5-6, 2462	R.VTGESHIGGVLLK.I	1310.52448	2	1.54E-07	0.91	3.45	-	1365.0
AHQ-5-1, 5083	K.VVLAGGVAPALFR.G	1270.54832	2	7.10E-08	0.98	5.07	-	2181.6
AHQ-5-6, 4625	K.VVLAGGVAPALFR.G	1270.54832	1	2.63E-04	0.24	2.25	-	146.0
AHQ-5-11, 4659 - 4664	K.VVLAGGVAPALFR.G	1270.54832	2	7.14E-07	0.96	4.39	-	1409.3
AHQ-5-6, 4617 - 4688	K.VVLAGGVAPALFR.G	1270.54832	1	9.79E-04	0.70	2.79	-	222.0
AHQ-5-6, 4612 - 4685	K.VVLAGGVAPALFR.G	1270.54832	2	1.33E-07	0.96	5.09	-	1385.9
AHQ-5-5, 4726	K.VVLAGGVAPALFR.G	1270.54832	2	1.21E-08	0.97	5.00	-	1786.0
AHQ-5-10, 4304	K.VVLAGGVAPALFR.G	1270.54832	2	7.26E-08	0.92	3.59	-	1402.2
AHQ-5-4, 4969 - 5001	K.VVLAGGVAPALFR.G	1270.54832	2	3.18E-06	0.95	3.91	-	1500.0
AHQ-5-9, 4056 - 4135	K.VVLAGGVAPALFR.G	1270.54832	2	5.60E-06	0.87	3.13	-	1208.7
AHQ-5-7, 4458 - 4472	K.VVLAGGVAPALFR.G	1270.54832	2	4.53E-08	0.96	4.33	-	1791.1
AHQ-5-6, 2300	K.YGILADAR.L	878.99544	2	8.39E-05	0.94	3.20	-	1327.8
AHQ-5-6, 5245	K.YYSFFDLDPK.T	1295.42046	2	2.33E-04	0.76	3.22	-	667.2
gi|4505839|ref|NP_002645.1| pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro				1.37E-12	15.51	170.31	41.40	57913.6
AHQ-5-7, 6038 - 6040	R.AGKPVICATQMLESMIK.K	1879.29869	2	8.83E-06	0.96	4.48	-	1188.3
AHQ-5-7, 5291	K.CDENILWLDYK.N	1470.62849	1	1.03E-07	0.83	3.65	-	466.7
AHQ-5-7, 5679 - 5751	R.EAEAAIYHLQLFEELR.R	1933.15326	2	1.68E-04	0.96	4.48	-	1134.1

AHQ-5-7, 5038 - 5068	R.EAEAAIYHLQLFEELRR.L	2089.33962	2	6.52E-06	0.85	4.14	-	313.2
AHQ-5-7, 7344	K.FGVEQDVDMVFASFIR.K	1861.11055	2	4.96E-08	0.97	5.09	-	1557.5
AHQ-5-7, 7442	K.FGVEQDVDMVFASFIR.K	1861.11055	2	7.27E-12	0.96	5.01	-	1211.9
AHQ-5-7, 7276	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	2.34E-08	0.97	4.96	-	1450.2
AHQ-5-7, 4747 - 4816	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	3.50E-06	0.95	4.76	-	1134.3
AHQ-5-7, 4952 - 5011	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	4.68E-05	0.95	4.42	-	1373.8
AHQ-5-7, 4536 - 4607	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	5.33E-05	0.84	3.89	-	734.9
AHQ-5-7, 4419 - 4492	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	6.70E-04	0.63	3.23	-	478.9
AHQ-5-11, 6398	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	3.67E-04	0.75	3.12	-	618.3
AHQ-5-7, 6798	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	2.32E-04	0.96	4.85	-	2079.4
AHQ-5-8, 6576 - 6641	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	5.65E-08	0.91	4.11	-	773.0
AHQ-5-9, 6018	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.15E-04	0.91	4.10	-	1325.6
AHQ-5-7, 6639 - 6706	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	1.28E-09	0.97	5.99	-	894.9
AHQ-5-13, 6608	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	2.48E-07	0.96	4.87	-	1636.6
AHQ-5-7, 6690 - 6735	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.32E-10	0.97	5.22	-	2415.3
AHQ-5-14-, 6382 - 6453	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.37E-12	0.97	6.00	-	2132.3
AHQ-5-13-, 6552	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	7.56E-09	0.94	4.85	-	1281.5
AHQ-5-7, 6770	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	2	2.68E-04	0.85	3.35	-	690.7
AHQ-5-1, 6995	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	7.93E-08	0.95	5.02	-	1410.4
AHQ-5-7, 4355 - 4426	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	4.56E-06	0.89	3.56	-	629.6
AHQ-5-7, 2887 - 2948	K.ITLDNAYMEK.C	1198.37126	2	4.28E-06	0.74	2.86	-	542.2
AHQ-5-7, 3782 - 3787	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	8.17E-04	0.97	5.67	-	1027.3
AHQ-5-7, 3803	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	5.16E-06	0.95	5.07	-	1379.4
AHQ-5-7, 4979 - 4980	K.KGVNLPGAAVDLPAVSEKDIQDLK.F	2478.82685	3	9.63E-08	0.97	6.17	-	1760.9
AHQ-5-7, 6140	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	3.72E-06	0.96	5.25	-	1023.9
AHQ-5-7, 5850 - 5918	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.20E-08	0.96	5.09	-	1158.9
AHQ-5-7, 5282	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.78E-07	0.96	4.59	-	1141.1
AHQ-5-7, 5986	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	4.38E-05	0.94	4.29	-	964.6
AHQ-5-7, 6075 - 6147	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	7.33E-06	0.86	3.31	-	837.9
AHQ-5-12, 5785	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.32E-07	0.96	4.26	-	1120.5
AHQ-5-7, 6780 - 6820	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.61E-05	0.88	4.05	-	563.1
AHQ-5-7, 5714 - 5782	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	7.67E-09	0.97	5.04	-	1351.2
AHQ-5-7, 6239 - 6250	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.80E-05	0.94	4.80	-	891.3
AHQ-5-10, 5328	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.57E-07	0.94	4.28	-	960.1
AHQ-5-12, 3381	R.LDIDSPPITAR.N	1198.35099	2	6.76E-05	0.86	2.98	-	864.0
AHQ-5-13, 3527 - 3534	R.LDIDSPPITAR.N	1198.35099	2	7.28E-04	0.86	3.47	-	764.5
AHQ-5-6, 3282	R.LDIDSPPITAR.N	1198.35099	2	5.32E-05	0.84	2.64	-	991.7
AHQ-5-7, 3167	R.LDIDSPPITAR.N	1198.35099	1	6.96E-04	0.14	2.12	-	210.6
AHQ-5-11, 3334	R.LDIDSPPITAR.N	1198.35099	2	6.99E-06	0.91	3.70	-	920.9
AHQ-5-7, 2092	R.LNFSHGTHEYHAETIK.N	1885.02879	3	2.59E-04	0.95	4.65	-	1425.0
AHQ-5-7, 2083 - 2086	R.LNFSHGTHEYHAETIK.N	1885.02879	2	1.86E-04	0.92	4.28	-	825.9
AHQ-5-7, 3114 - 3188	R.NTGIICTIGPASR.S	1361.54994	2	1.35E-04	0.89	3.58	-	875.1
AHQ-5-7, 3123 - 3200	R.NTGIICTIGPASR.S	1361.54994	1	1.00E-04	0.65	2.97	-	160.8
AHQ-5-7, 3862 - 3867	R.NTGIICTIGPASR.S	1361.54994	2	2.11E-04	0.75	2.96	-	747.6
AHQ-5-14-, 3407	R.NTGIICTIGPASR.S	1361.54994	2	6.32E-05	0.87	3.40	-	1003.2
AHQ-5-13, 3550	R.NTGIICTIGPASR.S	1361.54994	2	4.20E-06	0.94	4.04	-	1079.0
AHQ-5-13-, 3431	R.NTGIICTIGPASR.S	1361.54994	2	1.04E-04	0.92	3.88	-	1057.4
AHQ-5-11, 3331	R.NTGIICTIGPASR.S	1361.54994	2	1.74E-04	0.84	3.44	-	885.7
AHQ-5-12, 5710	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	3.20E-05	0.57	3.14	-	166.8
AHQ-5-7, 5392 - 5463	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	1.06E-05	0.93	4.82	-	1037.0
AHQ-5-7, 5430	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	6.71E-06	0.77	3.91	-	229.1
AHQ-5-13, 5729	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	1.10E-04	0.63	2.92	-	429.6
gi|4504351|ref|NP_000510.1| delta globin [Homo sapiens]				1.44E-12	0.95	10.23	12.90	16055.4
AHQ-5-13-, 5513	R.FFESFGDLSSPDAVMGNPK.V	2046.24551	2	5.11E-08	0.93	4.31	-	1144.4
AHQ-5-13, 5624	R.FFESFGDLSSPDAVMGNPK.V	2046.24551	2	1.44E-12	0.95	4.68	-	1201.8
gi|5453595|ref|NP_006358.1| adenylyl cyclase-associated protein [Homo sapiens]				1.52E-12	9.40	110.30	31.20	51672.7
AHQ-5-8, 2480	R.ALLVTASQCQQPAENK.L	1759.96271	2	1.76E-07	0.94	4.49	-	851.7
AHQ-5-13-, 2807 - 2811	R.ALLVTASQCQQPAENK.L	1759.96271	2	1.32E-08	0.97	5.01	-	1298.0
AHQ-5-7, 2530	R.ALLVTASQCQQPAENK.L	1759.96271	2	2.99E-06	0.95	5.14	-	819.0
AHQ-5-13, 2946	R.ALLVTASQCQQPAENK.L	1759.96271	2	2.47E-04	0.93	4.01	-	1039.1
AHQ-5-7, 6558	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	4.63E-07	0.93	4.75	-	1273.0
AHQ-5-7, 2627	K.EFHTTGLAWSK.T	1277.40990	1	6.64E-04	0.76	3.39	-	455.9
AHQ-5-7, 2323 - 2330	K.KEPAVLELEGK.K	1213.40557	2	6.08E-07	0.85	3.00	-	491.5
AHQ-5-7, 7432 - 7499	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	1.52E-12	0.98	5.99	-	1519.7
AHQ-5-12, 5052	K.LSDLLAPISEQIK.E	1427.66814	2	9.27E-05	0.93	4.15	-	1130.0
AHQ-5-7, 4758	K.LSDLLAPISEQIK.E	1427.66814	2	1.93E-04	0.73	2.97	-	560.7
AHQ-5-13, 5089	K.LSDLLAPISEQIK.E	1427.66814	2	6.29E-05	0.87	2.76	-	1045.5
AHQ-5-14-, 4966	K.LSDLLAPISEQIK.E	1427.66814	2	3.95E-04	0.84	3.07	-	797.0
AHQ-5-7, 4767	K.LSDLLAPISEQIK.E	1427.66814	1	1.48E-05	0.67	3.01	-	498.9
AHQ-5-7, 4614	R.SALFAQINQGESITHALK.H	1929.16615	2	1.13E-09	0.89	4.22	-	587.4
AHQ-5-7, 4480	R.SALFAQINQGESITHALK.H	1929.16615	2	1.06E-06	0.84	3.88	-	469.7
AHQ-5-9, 4035 - 4107	R.SALFAQINQGESITHALK.H	1929.16615	2	4.90E-05	0.91	4.50	-	515.2
AHQ-5-8, 4196	R.SALFAQINQGESITHALK.H	1929.16615	2	1.78E-04	0.77	4.00	-	326.3
AHQ-5-7, 4330 - 4398	R.SALFAQINQGESITHALK.H	1929.16615	2	3.28E-08	0.92	5.31	-	521.3
AHQ-5-7, 4332 - 4354	R.SALFAQINQGESITHALK.H	1929.16615	3	5.69E-05	0.84	3.96	-	660.9
AHQ-5-7, 1874 - 1875	R.SGPKPFSAPKPQTSPSPK.R	1839.08461	2	8.12E-06	0.94	4.29	-	1066.6
AHQ-5-7, 1871 - 1880	R.SGPKPFSAPKPQTSPSPK.R	1839.08461	3	1.40E-05	0.93	4.14	-	1369.4
AHQ-5-8, 6596	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	2.10E-05	0.75	3.56	-	273.2
AHQ-5-13, 6577	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.87E-04	0.32	2.54	-	152.0
AHQ-5-14-, 6314 - 6386	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	2.56E-06	0.80	3.46	-	380.7
AHQ-5-14-, 5969	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	5.82E-05	0.71	3.40	-	230.8
AHQ-5-10, 6102 - 6123	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	4.15E-05	0.41	2.79	-	167.3
AHQ-5-11, 6316 - 6386	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	5.86E-04	0.83	3.79	-	273.5
AHQ-5-14-, 6067 - 6070	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	9.02E-07	0.70	3.58	-	158.6
AHQ-5-12, 6624 - 6626	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	5.34E-04	0.48	2.77	-	208.9
AHQ-5-7, 6614 - 6687	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	1.75E-04	0.43	2.59	-	222.7
AHQ-5-13, 4836	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.11E-04	0.88	4.51	-	515.6
AHQ-5-10, 4300 - 4303	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.44E-07	0.93	4.53	-	755.1
AHQ-5-8, 4404	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.28E-07	0.91	4.50	-	581.9
AHQ-5-7, 4850 - 4918	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	8.46E-08	0.92	4.40	-	641.8
AHQ-5-13-, 4760	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.95E-05	0.96	4.93	-	1148.2
AHQ-5-7, 4728	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.86E-08	0.92	4.25	-	802.9
AHQ-5-7, 4638	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.23E-05	0.90	3.78	-	881.3
AHQ-5-7, 4510 - 4582	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.73E-06	0.93	4.56	-	759.4
AHQ-5-4, 4929 - 4956	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.51E-04	0.63	3.00	-	422.8
gi|21361785|ref|NP_543010.2| histidyl-tRNA synthetase 2; histidyl-tRNA synthetase; bA379J5.3; chrom				1.59E-12	0.98	10.34	12.70	24013.4
AHQ-5-10, 6423	K.GNKPDFHLAMPTEQAEGFYNSFLEQLR.K	3141.46192	3	1.59E-12	0.98	6.71	-	2351.8
gi|13994151|ref|NP_066272.1| PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H				1.64E-12	16.59	200.33	64.10	36071.5
AHQ-5-14-, 6642	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.70E-10	0.85	4.27	-	536.4
AHQ-5-12, 6672 - 6677	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.28E-05	0.79	3.87	-	404.8
AHQ-5-9, 6335	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	2.65E-07	0.69	3.87	-	387.5
AHQ-5-14-, 6545 - 6618	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.15E-07	0.89	5.06	-	362.8
AHQ-5-13, 6761	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.64E-12	0.93	4.97	-	815.4
AHQ-5-13, 6641	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	2.47E-06	0.89	4.60	-	517.6
AHQ-5-14-, 6435 - 6485	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	6.50E-06	0.79	3.60	-	402.8
AHQ-5-11, 6686	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.16E-10	0.91	4.63	-	646.2
AHQ-5-14-, 6263 - 6339	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.02E-11	0.93	4.79	-	1068.2

AHQ-5-12, 6901	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	6.65E-10	0.89	4.39	-	574.4
AHQ-5-13-, 6711 - 6712	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	7.59E-10	0.97	6.65	-	1362.7
AHQ-5-13-, 6348	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	2.14E-05	0.86	4.07	-	701.1
AHQ-5-12, 4462	K.CGTGIVGVFVK.L	1138.36198	2	5.14E-05	0.91	2.71	-	1329.8
AHQ-5-13, 4520	K.CGTGIVGVFVK.L	1138.36198	2	8.28E-04	0.87	2.77	-	1101.5
AHQ-5-13-, 3611 - 3643	K.DFEQPLAISR.V	1176.30388	2	1.00E-03	0.87	3.03	-	1037.2
AHQ-5-13, 3731	K.DFEQPLAISR.V	1176.30388	2	1.45E-05	0.95	3.76	-	1199.5
AHQ-5-12, 3585 - 3588	K.DFEQPLAISR.V	1176.30388	2	4.75E-06	0.93	4.02	-	903.6
AHQ-5-12, 3584	K.DFEQPLAISR.V	1176.30388	1	3.21E-05	0.47	1.90	-	326.2
AHQ-5-13, 3485	K.GCTDNLTLTVAR.S	1322.47058	2	6.58E-07	0.78	2.94	-	757.8
AHQ-5-13-, 3363	K.GCTDNLTLTVAR.S	1322.47058	2	3.66E-07	0.73	3.36	-	594.0
AHQ-5-13, 4104	K.GHFFVEDQIYCEK.H	1673.82684	2	3.62E-04	0.94	4.02	-	1015.0
AHQ-5-12, 3962 - 4028	K.GHFFVEDQIYCEK.H	1673.82684	2	1.34E-04	0.96	4.37	-	1373.5
AHQ-5-13-, 3996 - 4059	K.GHFFVEDQIYCEK.H	1673.82684	2	4.19E-06	0.96	3.86	-	1467.9
AHQ-5-13, 4212	K.GHFFVEDQIYCEK.H	1673.82684	2	2.11E-05	0.92	3.08	-	1163.6
AHQ-5-12, 2960	R.HPECYVCTDCGTNLK.Q	1858.02023	2	1.54E-05	0.72	2.87	-	430.5
AHQ-5-13-, 2676 - 2696	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	1.31E-06	0.97	5.44	-	1369.9
AHQ-5-13, 2819 - 2829	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	4.58E-07	0.93	4.40	-	1239.7
AHQ-5-12, 2561	R.HRHPECYVCTDCGTNLK.Q	2151.34648	2	1.26E-04	0.72	3.21	-	397.2
AHQ-5-13-, 2687	R.HRHPECYVCTDCGTNLK.Q	2151.34648	2	9.29E-04	0.84	3.43	-	541.2
AHQ-5-11, 3027	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.36E-08	0.94	4.11	-	986.2
AHQ-5-14, 3869 - 3944	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.86E-10	0.91	3.77	-	888.5
AHQ-5-12, 3069	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.06E-08	0.92	3.57	-	1054.7
AHQ-5-14-, 3050	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.75E-10	0.95	4.38	-	1026.2
AHQ-5-13, 3190	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.10E-09	0.93	3.92	-	1009.4
AHQ-5-13, 4849	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	3	5.75E-04	0.90	4.14	-	1076.8
AHQ-5-14, 4490 - 4532	R.LVGGKDFEQPLAISR.V	1630.86972	2	2.91E-07	0.93	4.20	-	1109.1
AHQ-5-13, 3868 - 3876	R.LVGGKDFEQPLAISR.V	1630.86972	2	5.16E-09	0.96	4.92	-	1314.4
AHQ-5-13, 3790	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	3.25E-05	0.92	3.93	-	708.9
AHQ-5-13, 3786	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	8.06E-05	0.77	3.09	-	758.4
AHQ-5-13-, 3723	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	4.67E-05	0.91	4.17	-	568.6
AHQ-5-11, 3424	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	2.08E-06	0.85	3.59	-	450.2
AHQ-5-9, 3442	K.MNLASEPQEVLHIGSAHNR.S	2104.33619	2	8.85E-08	0.85	4.28	-	465.1
AHQ-5-12, 3994	K.MNLASEPQEVLHIGSAHNR.S	2104.33619	2	1.72E-06	0.87	4.24	-	559.1
AHQ-5-13, 4162	K.MNLASEPQEVLHIGSAHNR.S	2104.33619	2	6.82E-11	0.96	4.79	-	1234.7
AHQ-5-13-, 4097	K.MNLASEPQEVLHIGSAHNR.S	2104.33619	2	1.16E-05	0.95	4.93	-	784.5
AHQ-5-12, 6676	K.QSTSFLVLQEILESEEK.G	1981.18977	2	1.14E-08	0.97	4.73	-	1701.1
AHQ-5-13, 6653	K.QSTSFLVLQEILESEEK.G	1981.18977	2	3.39E-08	0.96	4.15	-	1708.2
AHQ-5-13-, 6597	K.QSTSFLVLQEILESEEK.G	1981.18977	2	7.58E-06	0.97	5.34	-	1502.9
AHQ-5-12, 6096	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	9.01E-04	0.83	3.88	-	717.9
AHQ-5-13, 2593 - 2595	R.SAM*PFTASPASSTTAR.V	1599.74799	2	4.05E-05	0.81	3.21	-	720.5
AHQ-5-9, 2634	R.SAMPFTASPASSTTAR.V	1583.74859	2	2.61E-04	0.53	2.76	-	395.2
AHQ-5-12, 2361 - 2374	R.SAM*PFTASPASSTTAR.V	1599.74799	2	1.91E-04	0.89	3.41	-	989.3
AHQ-5-13-, 2448 - 2451	R.SAM*PFTASPASSTTAR.V	1599.74799	2	6.56E-07	0.92	3.62	-	1162.2
AHQ-5-10, 3668 - 3688	K.TAASGVEANSRPLDHAQPPSSLVIDKESEVYK.M	3397.69458	3	2.01E-04	0.91	5.02	-	664.4
AHQ-5-11, 3928	K.TAASGVEANSRPLDHAQPPSSLVIDKESEVYK.M	3397.69458	3	7.04E-04	0.90	4.56	-	791.8
AHQ-5-13, 1666	K.VAASIGNAQK.L	959.08209	1	5.42E-04	0.15	2.21	-	183.6
AHQ-5-13-, 3063	K.VWSPLVTEEGKR.H	1401.59247	2	4.85E-06	0.58	2.64	-	514.4
AHQ-5-13, 3185	K.VWSPLVTEEGKR.H	1401.59247	2	1.69E-07	0.66	2.73	-	555.5
gi|29740995|ref|XP_291768.1|	similar to Proteasome activator complex subunit 2 (Proteasome activato			1.82E-12	0.98	10.28	9.60	19192.6
AHQ-5-10, 6323	R.AFYAELYHIISSNLEK.T	1899.13528	2	1.82E-12	0.98	5.64	-	1786.0
gi|13775198|ref|NP_112576.1|	SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr			1.95E-12	4.75	60.32	35.50	10437.7
AHQ-5-14, 5545 - 5550	R.IQYQLVDISQDNALR.D	1776.97168	2	1.72E-04	0.78	3.33	-	846.9
AHQ-5-13-, 4768 - 4833	R.IQYQLVDISQDNALR.D	1776.97168	2	1.14E-10	0.98	6.19	-	2067.4
AHQ-5-13-, 4683 - 4708	R.IQYQLVDISQDNALR.D	1776.97168	2	1.95E-12	0.98	5.33	-	2210.9
AHQ-5-14-, 4779 - 4790	R.IQYQLVDISQDNALR.D	1776.97168	2	7.79E-05	0.90	3.75	-	1182.4
AHQ-5-13-, 4535	R.IQYQLVDISQDNALR.D	1776.97168	2	3.00E-07	0.97	4.88	-	2003.1
AHQ-5-13, 4776 - 4837	R.IQYQLVDISQDNALR.D	1776.97168	2	5.74E-11	0.98	6.39	-	1822.2
AHQ-5-13, 4790	R.IQYQLVDISQDNALR.D	1776.97168	3	5.37E-08	0.95	5.05	-	1677.3
AHQ-5-13, 4917	R.IQYQLVDISQDNALR.D	1776.97168	2	3.81E-09	0.97	5.50	-	1539.5
AHQ-5-14, 5458 - 5464	R.IQYQLVDISQDNALR.D	1776.97168	2	5.87E-07	0.97	4.78	-	2087.5
AHQ-5-14-, 4630 - 4691	R.IQYQLVDISQDNALR.D	1776.97168	2	6.21E-10	0.95	3.90	-	1800.1
AHQ-5-14-, 4903 - 4985	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.99E-06	0.89	4.79	-	591.4
AHQ-5-13-, 4517	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	4.16E-04	0.60	3.08	-	355.3
AHQ-5-13-, 4193	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	8.45E-06	0.84	3.88	-	504.7
AHQ-5-13, 4928 - 4933	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.60E-07	0.78	3.60	-	517.8
AHQ-5-13, 5113 - 5173	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.26E-11	0.83	3.66	-	702.0
AHQ-5-13-, 4909 - 4979	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.52E-07	0.84	3.36	-	569.6
AHQ-5-13, 4197	K.RIQYQLVDISQDNALRDEM*R.A	2480.74326	3	4.06E-04	0.79	3.46	-	547.9
AHQ-5-13-, 1685 - 1763	R.VYSTSVTGSR.E	1057.13940	2	2.58E-06	0.89	3.03	-	963.7
AHQ-5-13-, 1783 - 1843	R.VYSTSVTGSR.E	1057.13940	2	5.39E-06	0.88	2.79	-	1016.6
AHQ-5-13, 2105 - 2183	R.VYSTSVTGSR.E	1057.13940	2	1.92E-06	0.89	2.75	-	1066.7
AHQ-5-13, 1986 - 2045	R.VYSTSVTGSR.E	1057.13940	2	9.16E-07	0.70	2.55	-	555.9
AHQ-5-13-, 1903 - 1968	R.VYSTSVTGSR.E	1057.13940	2	4.38E-06	0.85	2.85	-	934.8
AHQ-5-13-, 2073	R.VYSTSVTGSR.E	1057.13940	2	1.21E-05	0.82	2.52	-	710.2
AHQ-5-13, 1847 - 1927	R.VYSTSVTGSR.E	1057.13940	2	9.73E-04	0.81	2.62	-	964.0
AHQ-5-13, 2409	R.VYSTSVTGSREIK.S	1427.58510	2	2.41E-04	0.54	2.94	-	468.9
AHQ-5-13-, 2256	R.VYSTSVTGSREIK.S	1427.58510	2	1.68E-05	0.62	2.80	-	566.8
gi|4507907|ref|NP_000543.1|	von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille			2.01E-12	29.36	330.30	17.00	309296.7
AHQ-5-1, 5059	K.AFVLSSVDELEQQR.D	1621.77332	2	4.58E-06	0.94	3.50	-	1612.2
AHQ-5-3, 4038	R.CLPSACEVVTGSPR.G	1535.72531	2	6.59E-06	0.88	3.66	-	869.9
AHQ-5-1, 4311	R.CLPTACTIQLR.G	1335.57568	2	7.18E-04	0.61	2.87	-	475.1
AHQ-5-1, 5196 - 5203	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	7.42E-06	0.72	3.38	-	490.6
AHQ-5-3, 5187	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	6.00E-06	0.61	3.03	-	511.0
AHQ-5-3, 5810	R.EQAPNLVYMVTGNPASDEIK.R	2177.42062	2	3.51E-07	0.74	3.11	-	479.5
AHQ-5-1, 5787 - 5852	R.EQAPNLVYMVTGNPASDEIK.R	2177.42062	2	3.93E-06	0.80	3.22	-	624.9
AHQ-5-1, 5871	R.EQAPNLVYMVTGNPASDEIK.R	2177.42062	2	9.69E-06	0.90	3.89	-	729.4
AHQ-5-2, 5735	R.EQAPNLVYMVTGNPASDEIK.R	2177.42062	2	2.92E-05	0.65	3.27	-	271.2
AHQ-5-1, 4869	R.EQAPNLVYM*VTGNPASDEIK.R	2193.42002	2	1.82E-07	0.91	4.35	-	508.3
AHQ-5-1, 4180 - 4188	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	2.09E-10	0.92	3.99	-	903.1
AHQ-5-1, 4487 - 4556	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	6.33E-08	0.78	3.75	-	531.7
AHQ-5-1, 6417	R.IEDLPTMVTLGNSFLHK.L	1916.23079	3	1.12E-05	0.85	3.70	-	684.7
AHQ-5-1, 5955	R.IEDLPTMVTLGNSFLHK.L	1916.23079	2	2.01E-12	0.96	5.07	-	1182.4
AHQ-5-1, 5209	R.IEDLPTM*VTLGNSFLHK.L	1932.23019	2	7.93E-08	0.90	4.66	-	820.0
AHQ-5-1, 7291 - 7292	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	1.48E-08	0.96	5.51	-	834.0
AHQ-5-2, 7457 - 7458	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	4.50E-09	0.95	4.89	-	815.4
AHQ-5-1, 7296	R.IGWPNAPILIQDFETLPR.E	2081.40223	3	7.62E-07	0.94	5.02	-	1042.5
AHQ-5-3, 7394 - 7467	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	5.31E-04	0.70	2.81	-	409.8
AHQ-5-1, 7161	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	2.62E-04	0.83	3.08	-	840.0
AHQ-5-1, 2679	R.ILAGPAGDSNVVK.L	1241.41901	2	8.31E-07	0.95	3.89	-	1290.7
AHQ-5-3, 2522	R.ILAGPAGDSNVVK.L	1241.41901	2	6.84E-04	0.75	2.96	-	570.4
AHQ-5-1, 3848	R.ILTSDVFQDCNK.L	1441.58869	2	3.84E-09	0.94	4.30	-	913.5
AHQ-5-1, 4312	R.LSEAEFEVLK.A	1165.31777	2	5.95E-07	0.93	3.58	-	1254.5
AHQ-5-1, 4268 - 4281	K.LTGSCSYVLFQNK.E	1518.71629	2	1.26E-07	0.94	4.61	-	1015.4
AHQ-5-4, 5166 - 5177	R.NSQWICSNEECPGECLVTGQSHFK.S	2872.07402	3	4.02E-06	0.83	3.92	-	595.1
AHQ-5-2, 5494	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	7.10E-07	0.98	5.61	-	2222.1
AHQ-5-1, 5580 - 5605	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	2	5.57E-05	0.97	5.67	-	1076.0

AHQ-5-3, 4214	R.SFSIIGDFQNGKR.V	1469.62690	2	1.82E-06	0.90	3.15	-	1136.6
AHQ-5-1, 4000 - 4055	R.SGFTYVLHEGECCGR.C	1774.91285	2	8.48E-07	0.92	3.33	-	1319.2
AHQ-5-1, 3392 - 3401	R.SKEFMEEVIQR.M	1396.59450	2	1.49E-04	0.86	3.37	-	747.5
AHQ-5-4, 5050	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	1.44E-04	0.55	2.85	-	248.0
AHQ-5-3, 5102 - 5105	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	9.40E-06	0.85	4.21	-	340.1
AHQ-5-1, 4999 - 5076	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	6.34E-07	0.89	4.25	-	539.7
AHQ-5-2, 5055	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	1.48E-06	0.83	3.94	-	489.0
AHQ-5-4, 5698	K.TCGLCGNYNGNQGDDFLTPSGLAEPR.V	2816.97516	2	6.24E-04	0.70	2.92	-	514.6
AHQ-5-1, 5004	R.TPDFCAMSCPPSLVYNHCEHGCPR.H	2898.20140	3	1.14E-07	0.91	4.38	-	818.2
AHQ-5-1, 5800 - 5868	K.TYGLCGICDENGANDFM*LR.D	2225.42231	2	8.06E-11	0.92	4.41	-	605.3
AHQ-5-2, 6298	K.TYGLCGICDENGANDFMLR.D	2209.42291	2	3.74E-06	0.88	4.16	-	547.1
AHQ-5-1, 6136 - 6207	K.TYGLCGICDENGANDFMLR.D	2209.42291	2	5.42E-04	0.46	2.68	-	531.9
AHQ-5-1, 6251	K.TYGLCGICDENGANDFMLR.D	2209.42291	2	5.14E-07	0.90	4.22	-	644.3
AHQ-5-1, 3605	R.VAVVEYHDGSHAYIGLK.D	1859.07438	2	6.46E-04	0.95	4.13	-	1397.7
AHQ-5-1, 2475 - 2481	R.VKEEVFIQQR.N	1276.46658	2	5.18E-07	0.83	3.26	-	677.7
AHQ-5-1, 4720	R.VTVFPIGIGDR.Y	1174.37426	2	2.51E-06	0.94	3.85	-	1134.6
AHQ-5-1, 3615	R.WTCPCVCTGSSTR.H	1575.72645	2	2.66E-07	0.91	3.30	-	888.5
AHQ-5-3, 2839	K.YAGSQVASTSEVLK.Y	1440.58064	2	2.61E-06	0.94	3.57	-	1305.8
AHQ-5-2, 2775	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.41E-05	0.93	4.03	-	918.2
AHQ-5-1, 2964	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.45E-08	0.96	4.26	-	1417.3
AHQ-5-3, 7458	R.YFTFSGICQYLLAR.D	1741.00269	2	6.87E-06	0.92	3.56	-	979.6
AHQ-5-1, 6847	K.YLFPGECQYVLVQDYCGSNPGTFR.I	2874.15305	3	6.77E-07	0.92	3.90	-	1563.0
AHQ-5-1, 3400	R.YLSDHSFLVSQGDR.E	1624.73576	2	1.55E-07	0.96	4.34	-	1605.9
AHQ-5-2, 3183	R.YLSDHSFLVSQGDR.E	1624.73576	2	1.57E-05	0.92	3.67	-	1190.3
AHQ-5-1, 6145	K.YTLFQIFSK.I	1147.34728	2	6.67E-06	0.95	3.21	-	1400.7
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				2.04E-12	21.22	240.40	21.90	191612.6
AHQ-5-3, 7554	K.AFMTADLPNELIELLEK.I	1948.26956	2	2.06E-10	0.94	4.63	-	757.1
AHQ-5-3, 7513 - 7515	K.AFM*TADLPNELIELLEK.I	1964.26896	2	6.15E-05	0.93	4.68	-	650.5
AHQ-5-3, 4494	R.ALEHFTDLYDIK.R	1465.63179	2	1.15E-04	0.94	3.64	-	1125.4
AHQ-5-1, 4604	R.ALEHFTDLYDIK.R	1465.63179	2	6.98E-05	0.80	2.79	-	837.6
AHQ-5-5, 4171	R.CNEPAVWSQLAK.A	1404.57328	1	1.44E-04	0.70	3.17	-	334.5
AHQ-5-3, 7555	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	1.60E-05	0.95	5.41	-	1135.1
AHQ-5-4, 7505	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	4.50E-07	0.94	5.02	-	1195.0
AHQ-5-1, 7367	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	8.31E-12	0.94	4.67	-	1305.1
AHQ-5-3, 4957	R.GQFSTDELVAEVEK.R	1552.66462	2	1.61E-07	0.93	3.78	-	1204.7
AHQ-5-4, 4930	R.GQFSTDELVAEVEK.R	1552.66462	2	4.24E-04	0.69	2.88	-	947.5
AHQ-5-3, 4821 - 4899	R.GQFSTDELVAEVEKR.N	1708.85097	2	2.11E-09	0.92	3.83	-	1182.3
AHQ-5-4, 4778 - 4796	R.GQFSTDELVAEVEKR.N	1708.85097	2	1.75E-09	0.94	4.34	-	1050.9
AHQ-5-3, 3219	K.HDVVFLITK.Y	1072.28194	2	1.24E-07	0.96	3.85	-	1339.6
AHQ-5-3, 3406	R.HSSLAGCQIINYR.T	1520.69551	2	9.98E-04	0.96	3.96	-	1343.7
AHQ-5-4, 3529	K.IVLDNSVFSEHR.N	1416.56400	2	9.24E-09	0.92	3.06	-	1469.6
AHQ-5-3, 3519 - 3574	K.IVLDNSVFSEHR.N	1416.56400	2	3.84E-08	0.85	2.82	-	940.1
AHQ-5-3, 6459	K.KAVDVFFPPEAQNDFPVAMQISEK.H	2709.06938	3	2.21E-05	0.95	4.60	-	1582.4
AHQ-5-3, 7293 - 7295	R.KFDVNTSAVQVLIEHIGNLDR.A	2369.66218	3	5.76E-11	0.98	6.32	-	2244.6
AHQ-5-3, 3521 - 3523	R.KFNALFAQGNYSEAAK.V	1759.94281	2	2.04E-12	0.97	5.07	-	1556.2
AHQ-5-3, 4559 - 4573	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	1.02E-04	0.94	4.49	-	976.0
AHQ-5-1, 4669 - 4691	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	3.37E-05	0.93	3.78	-	1283.8
AHQ-5-3, 4583	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	3	1.35E-07	0.80	3.36	-	999.2
AHQ-5-3, 4386 - 4458	K.LHIIEVGTPPTGNQPFPK.K	1946.23831	2	1.27E-05	0.92	4.47	-	486.3
AHQ-5-3, 7381	R.LLEMNLMHAPQVADAILGNQMFTHYDR.A	3130.61385	3	5.90E-09	0.98	7.95	-	2103.3
AHQ-5-3, 3887	K.LLYNNVSNFGR.L	1297.44435	2	2.45E-05	0.86	2.87	-	770.8
AHQ-5-3, 6466	R.NLQNLLILTAIK.A	1354.66353	2	1.53E-04	0.97	5.16	-	1596.0
AHQ-5-5, 2375	R.RPISADSAIMNPASK.V	1558.78540	2	3.98E-06	0.93	4.07	-	993.4
AHQ-5-3, 2513	R.RPISADSAIMNPASK.V	1558.78540	2	2.23E-07	0.92	4.03	-	1078.0
AHQ-5-3, 7082 - 7111	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	2	7.38E-04	0.91	4.29	-	401.3
AHQ-5-4, 7066	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	7.09E-06	0.96	5.99	-	1318.0
AHQ-5-3, 5161	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	7.86E-12	0.97	5.51	-	1741.8
AHQ-5-3, 4894	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	9.84E-04	0.71	2.79	-	629.8
AHQ-5-4, 5109	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	3.29E-07	0.92	3.97	-	945.9
AHQ-5-4, 7205	K.VGYTPDWIFLLR.N	1480.73443	2	1.24E-05	0.77	3.21	-	430.1
AHQ-5-3, 7235	K.VGYTPDWIFLLR.N	1480.73443	2	2.11E-10	0.92	4.01	-	676.4
AHQ-5-1, 7163	K.VGYTPDWIFLLR.N	1480.73443	2	1.73E-10	0.77	3.32	-	380.7
AHQ-5-3, 3093	K.VIQCFAETGQVQK.I	1509.70940	2	1.29E-07	0.97	4.31	-	2265.2
AHQ-5-3, 3505 - 3506	K.VSQPIEGHAASFAQFK.M	1717.90593	2	3.71E-04	0.17	2.51	-	352.8
gi|4505981|ref|NP_002695.1| pro-platelet basic protein (includes platelet basic protein, bet; Pro-p				2.18E-12	8.36	100.31	53.90	13894.1
AHQ-5-14-, 4767	K.EESLDSDLYAELR.C	1540.61070	2	5.32E-04	0.90	3.69	-	703.6
AHQ-5-14, 5481 - 5552	K.EESLDSDLYAELR.C	1540.61070	2	7.33E-05	0.92	3.89	-	978.3
AHQ-5-14, 5162	K.EESLDSDLYAELR.C	1540.61070	2	2.09E-04	0.48	2.56	-	400.7
AHQ-5-14-, 4434	K.EESLDSDLYAELR.C	1540.61070	2	5.94E-05	0.88	3.00	-	1120.3
AHQ-5-14-, 4641 - 4701	K.EESLDSDLYAELR.C	1540.61070	2	1.61E-05	0.97	4.59	-	1519.7
AHQ-5-14-, 4610	K.GKEESLDSDLYAELR.C	1725.83517	2	1.52E-06	0.98	4.41	-	2889.8
AHQ-5-14-, 3698	K.GKEESLDSDLYAELR.C	1725.83517	2	1.69E-07	0.98	5.34	-	2264.3
AHQ-5-14-, 4443 - 4513	K.GKEESLDSDLYAELR.C	1725.83517	2	9.21E-10	0.98	5.71	-	2851.5
AHQ-5-13, 4276	K.GKEESLDSDLYAELR.C	1725.83517	3	7.44E-05	0.76	3.21	-	961.4
AHQ-5-14, 5896	K.GKEESLDSDLYAELR.C	1725.83517	2	2.04E-05	0.97	4.72	-	2133.2
AHQ-5-14-, 4291 - 4357	K.GKEESLDSDLYAELR.C	1725.83517	2	7.13E-09	0.98	5.18	-	2782.7
AHQ-5-14-, 4169 - 4229	K.GKEESLDSDLYAELR.C	1725.83517	2	1.11E-09	0.98	5.48	-	2635.4
AHQ-5-13, 4272 - 4273	K.GKEESLDSDLYAELR.C	1725.83517	2	6.91E-11	0.98	5.40	-	2839.5
AHQ-5-14-, 4129 - 4197	K.GKEESLDSDLYAELR.C	1725.83517	3	1.90E-06	0.81	3.61	-	854.2
AHQ-5-14, 5528	K.GKEESLDSDLYAELR.C	1725.83517	2	4.58E-07	0.97	4.53	-	2237.7
AHQ-5-14-, 4073 - 4141	K.GKEESLDSDLYAELR.C	1725.83517	2	7.35E-11	0.98	6.28	-	2675.0
AHQ-5-12, 4145	K.GKEESLDSDLYAELR.C	1725.83517	2	3.12E-07	0.97	5.17	-	1874.8
AHQ-5-14-, 3973 - 4049	K.GKEESLDSDLYAELR.C	1725.83517	3	2.00E-06	0.89	4.03	-	1161.6
AHQ-5-14, 5385 - 5456	K.GKEESLDSDLYAELR.C	1725.83517	2	1.78E-08	0.98	5.72	-	2580.8
AHQ-5-14-, 3950 - 4018	K.GKEESLDSDLYAELR.C	1725.83517	2	2.18E-12	0.98	6.03	-	2261.2
AHQ-5-14, 5337 - 5397	K.GKEESLDSDLYAELR.C	1725.83517	2	1.49E-06	0.97	4.75	-	2182.0
AHQ-5-14, 5241 - 5305	K.GKEESLDSDLYAELR.C	1725.83517	2	4.53E-08	0.98	5.62	-	2680.0
AHQ-5-14-, 3823 - 3901	K.GKEESLDSDLYAELR.C	1725.83517	3	3.90E-04	0.80	3.64	-	885.0
AHQ-5-14, 5637 - 5702	K.GKEESLDSDLYAELR.C	1725.83517	2	9.35E-05	0.97	4.61	-	1721.7
AHQ-5-14-, 3821 - 3886	K.GKEESLDSDLYAELR.C	1725.83517	2	7.50E-12	0.98	5.92	-	2149.1
AHQ-5-14, 5124 - 5182	K.GKEESLDSDLYAELR.C	1725.83517	2	2.14E-09	0.98	5.41	-	2533.2
AHQ-5-14, 5008 - 5069	K.GKEESLDSDLYAELR.C	1725.83517	2	5.46E-08	0.98	5.62	-	2869.9
AHQ-5-14, 4690 - 4752	K.GKEESLDSDLYAELR.C	1725.83517	2	1.20E-11	0.98	5.20	-	2502.3
AHQ-5-14, 4812 - 4873	K.GKEESLDSDLYAELR.C	1725.83517	2	4.52E-11	0.98	6.08	-	2344.2
AHQ-5-14, 4920 - 4980	K.GKEESLDSDLYAELR.C	1725.83517	2	1.47E-07	0.98	5.06	-	2664.7
AHQ-5-13-, 4171	K.GKEESLDSDLYAELR.C	1725.83517	2	5.03E-10	0.98	6.07	-	2517.1
AHQ-5-14-, 3737 - 3805	K.GTHCNQVEVIATLK.D	1571.78073	2	2.43E-11	0.98	5.35	-	2018.9
AHQ-5-14, 4672 - 4746	K.GTHCNQVEVIATLK.D	1571.78073	2	7.07E-05	0.98	4.72	-	2254.3
AHQ-5-14, 5021 - 5089	K.GTHCNQVEVIATLK.D	1571.78073	2	1.27E-05	0.96	4.41	-	1402.2
AHQ-5-14, 4560 - 4616	K.GTHCNQVEVIATLK.D	1571.78073	2	2.57E-07	0.97	4.87	-	1732.3
AHQ-5-14, 4445 - 4500	K.GTHCNQVEVIATLK.D	1571.78073	2	6.12E-07	0.96	4.47	-	1467.5
AHQ-5-14, 4348 - 4408	K.GTHCNQVEVIATLK.D	1571.78073	2	4.83E-10	0.97	5.09	-	1842.8
AHQ-5-14, 5272	K.GTHCNQVEVIATLK.D	1571.78073	2	2.02E-04	0.87	3.61	-	672.1
AHQ-5-14-, 3869 - 3935	K.GTHCNQVEVIATLK.D	1571.78073	2	7.48E-11	0.97	5.12	-	1541.4
AHQ-5-14, 4224 - 4297	K.GTHCNQVEVIATLK.D	1571.78073	2	3.44E-05	0.97	4.94	-	1789.0
AHQ-5-14, 4100 - 4166	K.GTHCNQVEVIATLK.D	1571.78073	2	1.96E-06	0.97	4.77	-	1649.7
AHQ-5-14, 4012	K.GTHCNQVEVIATLK.D	1571.78073	2	4.52E-07	0.95	4.07	-	1243.4

AHQ-5-14-, 4133 - 4194	K.GTHCNQVEVIATLK.D	1571.78073	2	9.23E-09	0.98	4.58	-	2293.2
AHQ-5-14, 5642	K.GTHCNQVEVIATLK.D	1571.78073	2	2.57E-04	0.56	2.64	-	483.9
AHQ-5-14, 5802	K.GTHCNQVEVIATLK.D	1571.78073	2	1.34E-04	0.89	3.49	-	881.8
AHQ-5-14-, 4342	K.GTHCNQVEVIATLK.D	1571.78073	2	2.14E-04	0.94	3.81	-	1291.3
AHQ-5-13-, 3293 - 3367	K.GTHCNQVEVIATLK.D	1571.78073	2	1.70E-06	0.96	4.24	-	1761.2
AHQ-5-14-, 4475	K.GTHCNQVEVIATLK.D	1571.78073	2	9.78E-06	0.95	3.82	-	1392.6
AHQ-5-14, 4830	K.GTHCNQVEVIATLK.D	1571.78073	2	2.66E-07	0.96	4.32	-	1645.5
AHQ-5-14-, 3605 - 3670	K.GTHCNQVEVIATLK.D	1571.78073	2	6.68E-12	0.98	5.25	-	1748.6
AHQ-5-14-, 3513 - 3585	K.GTHCNQVEVIATLK.D	1571.78073	2	6.14E-09	0.98	5.53	-	2045.1
AHQ-5-14-, 3429 - 3477	K.GTHCNQVEVIATLK.D	1571.78073	2	1.62E-04	0.98	5.47	-	1907.2
AHQ-5-14-, 3365 - 3395	K.GTHCNQVEVIATLK.D	1571.78073	2	1.05E-09	0.97	5.51	-	1561.6
AHQ-5-14-, 3251 - 3302	K.GTHCNQVEVIATLK.D	1571.78073	2	2.59E-06	0.97	4.29	-	1706.6
AHQ-5-14, 3930 - 3988	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	2.44E-06	0.98	5.71	-	2094.7
AHQ-5-14-, 2945	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	9.65E-07	0.97	4.87	-	1215.8
AHQ-5-14-, 2947 - 3025	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.38E-09	0.95	4.78	-	1300.1
AHQ-5-14, 3804 - 3860	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	3.95E-06	0.98	5.42	-	1839.0
AHQ-5-14-, 3235 - 3305	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.91E-06	0.89	4.41	-	678.9
AHQ-5-14, 4334 - 4394	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	3.39E-04	0.93	4.66	-	500.6
AHQ-5-14-, 3486 - 3499	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	3.24E-05	0.94	4.65	-	506.7
AHQ-5-14-, 3367	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.99E-06	0.92	4.71	-	877.2
AHQ-5-14-, 3454	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.74E-07	0.95	4.92	-	1188.5
AHQ-5-14-, 2670 - 2679	K.GTHCNQVEVIATLKDGRK.I	2028.27941	3	1.25E-06	0.93	4.06	-	1382.4
AHQ-5-14-, 2677	K.GTHCNQVEVIATLKDGRK.I	2028.27941	2	4.61E-05	0.96	5.50	-	1016.3
AHQ-5-14, 3538 - 3596	K.GTHCNQVEVIATLKDGRK.I	2028.27941	2	2.76E-07	0.94	4.42	-	1012.4
AHQ-5-14, 3524 - 3602	K.GTHCNQVEVIATLKDGRK.I	2028.27941	3	2.45E-04	0.81	3.72	-	510.9
AHQ-5-14-, 2766 - 2841	K.ICLDPDAPR.I	1058.19059	2	1.95E-04	0.89	3.68	-	918.0
AHQ-5-14, 3636 - 3698	K.ICLDPDAPR.I	1058.19059	2	2.54E-05	0.77	3.09	-	839.7
AHQ-5-14-, 2457 - 2517	R.KICLDPDAPR.I	1186.36350	1	3.46E-05	0.20	2.28	-	164.2
AHQ-5-14, 3198 - 3273	R.KICLDPDAPR.I	1186.36350	2	5.52E-05	0.80	2.97	-	769.7
AHQ-5-14, 3030 - 3093	R.KICLDPDAPR.I	1186.36350	2	6.60E-04	0.20	2.63	-	327.1
AHQ-5-14-, 2445 - 2505	R.KICLDPDAPR.I	1186.36350	2	7.11E-05	0.92	3.70	-	1010.7
AHQ-5-14-, 2529 - 2589	R.KICLDPDAPR.I	1186.36350	2	7.81E-05	0.88	3.28	-	1003.2
AHQ-5-14, 3492 - 3552	R.KICLDPDAPR.I	1186.36350	2	3.14E-05	0.59	3.09	-	474.2
AHQ-5-14, 1932	K.KLAGDESAD	905.92969	1	2.51E-04	0.41	2.10	-	332.3
AHQ-5-14, 1398 - 1453	K.KLAGDESAD	905.92969	1	2.32E-04	0.44	2.07	-	444.0
AHQ-5-14-, 4114	K.NIQSLEVIGK.G	1101.27845	1	5.45E-04	0.34	2.30	-	420.3
AHQ-5-14, 4065 - 4136	K.NIQSLEVIGK.G	1101.27845	2	3.20E-05	0.78	2.97	-	621.5
AHQ-5-14, 4180 - 4240	K.NIQSLEVIGK.G	1101.27845	2	1.84E-06	0.85	3.40	-	597.6
AHQ-5-14, 4296 - 4362	K.NIQSLEVIGK.G	1101.27845	2	4.59E-04	0.71	2.82	-	549.2
AHQ-5-12, 3218	K.NIQSLEVIGK.G	1101.27845	2	1.38E-06	0.92	3.65	-	1066.9
AHQ-5-14, 4958	K.NIQSLEVIGK.G	1101.27845	1	5.00E-05	0.56	2.83	-	502.2
AHQ-5-13-, 3331	K.NIQSLEVIGK.G	1101.27845	2	3.94E-05	0.82	2.97	-	713.7
AHQ-5-14-, 3665	K.NIQSLEVIGK.G	1101.27845	1	1.78E-04	0.48	2.53	-	304.4
AHQ-5-14-, 3102 - 3179	K.NIQSLEVIGK.G	1101.27845	2	2.80E-04	0.88	3.36	-	761.8
AHQ-5-14, 4465	K.NIQSLEVIGK.G	1101.27845	1	7.41E-04	0.51	2.94	-	196.2
AHQ-5-14, 4409	K.TTSGIHPKNIQSLEVIGK.G	1923.20305	2	5.66E-05	0.82	4.08	-	277.9
gi|4506413|ref|NP_002875.1| RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				2.19E-12	5.94	70.26	33.20	20987.1
AHQ-5-11, 2390 - 2455	K.CDLEDERVVGK.E	1321.43945	2	1.70E-05	0.77	2.71	-	903.3
AHQ-5-14-, 6645 - 6721	K.INVNEIFYDLVR.Q	1495.70427	2	7.15E-10	0.96	5.07	-	1087.7
AHQ-5-14-, 6483 - 6491	K.INVNEIFYDLVR.Q	1495.70427	2	2.94E-04	0.79	2.98	-	654.6
AHQ-5-10, 6396	K.INVNEIFYDLVR.Q	1495.70427	2	3.77E-08	0.94	4.27	-	1098.5
AHQ-5-10, 6392 - 6400	K.INVNEIFYDLVR.Q	1495.70427	1	8.86E-05	0.20	2.55	-	220.4
AHQ-5-14-, 5813	K.INVNEIFYDLVR.Q	1495.70427	2	1.15E-07	0.91	3.61	-	985.3
AHQ-5-13-, 6721	K.INVNEIFYDLVR.Q	1495.70427	2	1.45E-07	0.95	4.28	-	1150.0
AHQ-5-13, 6774	K.INVNEIFYDLVR.Q	1495.70427	2	8.00E-07	0.96	5.14	-	1188.5
AHQ-5-12, 6876	K.INVNEIFYDLVR.Q	1495.70427	1	3.50E-09	0.38	3.36	-	174.5
AHQ-5-12, 6874	K.INVNEIFYDLVR.Q	1495.70427	2	2.52E-07	0.94	4.72	-	1063.1
AHQ-5-11, 6618 - 6750	K.INVNEIFYDLVR.Q	1495.70427	1	2.83E-04	0.25	3.04	-	196.6
AHQ-5-11, 5726 - 5727	K.INVNEIFYDLVR.Q	1495.70427	1	5.24E-06	0.13	2.16	-	182.8
AHQ-5-11, 6568 - 6639	K.INVNEIFYDLVR.Q	1495.70427	2	2.48E-07	0.96	4.76	-	1191.7
AHQ-5-11, 6431 - 6434	K.INVNEIFYDLVR.Q	1495.70427	1	1.76E-06	0.14	2.33	-	149.2
AHQ-5-11, 6428	K.INVNEIFYDLVR.Q	1495.70427	2	7.65E-08	0.89	3.66	-	868.0
AHQ-5-14-, 6649	K.INVNEIFYDLVR.Q	1495.70427	1	5.20E-06	0.45	2.92	-	245.3
AHQ-5-12, 2685	K.LVVLGSGGVGK.S	986.19059	2	6.20E-05	0.91	3.53	-	1137.3
AHQ-5-13, 2907	K.LVVLGSGGVGK.S	986.19059	2	3.48E-07	0.89	3.52	-	956.9
AHQ-5-11, 2574 - 2643	K.LVVLGSGGVGK.S	986.19059	2	7.13E-05	0.92	3.56	-	1210.5
AHQ-5-11, 5974 - 6054	K.SALTVQFVQGIFVEK.Y	1666.94196	2	6.86E-05	0.96	4.58	-	1525.8
AHQ-5-14-, 6017 - 6095	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.40E-04	0.96	4.55	-	1777.4
AHQ-5-11, 6495 - 6559	K.SALTVQFVQGIFVEK.Y	1666.94196	2	9.00E-04	0.96	4.90	-	1509.0
AHQ-5-11, 6354 - 6415	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.35E-04	0.96	4.73	-	1601.1
AHQ-5-11, 5684	K.SALTVQFVQGIFVEK.Y	1666.94196	2	6.25E-06	0.95	4.67	-	1171.5
AHQ-5-11, 6624 - 6691	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.91E-04	0.97	4.74	-	2118.6
AHQ-5-11, 6880	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.14E-06	0.95	4.64	-	1410.5
AHQ-5-11, 6964	K.SALTVQFVQGIFVEK.Y	1666.94196	2	4.42E-07	0.95	4.60	-	1386.4
AHQ-5-11, 6258 - 6334	K.SALTVQFVQGIFVEK.Y	1666.94196	2	7.82E-04	0.96	5.11	-	1461.2
AHQ-5-13, 6256 - 6322	K.SALTVQFVQGIFVEK.Y	1666.94196	2	4.07E-04	0.91	3.95	-	1159.3
AHQ-5-13-, 6184	K.SALTVQFVQGIFVEK.Y	1666.94196	2	5.22E-04	0.94	3.92	-	1422.5
AHQ-5-11, 6118 - 6196	K.SALTVQFVQGIFVEK.Y	1666.94196	2	7.79E-08	0.97	5.21	-	1510.3
AHQ-5-11, 5283 - 5290	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.76E-10	0.93	4.23	-	859.4
AHQ-5-14-, 6055 - 6061	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.19E-12	0.96	5.06	-	1212.2
AHQ-5-14-, 6053	K.SKINVNEIFYDLVR.Q	1710.95483	3	1.72E-06	0.93	4.32	-	1397.2
AHQ-5-11, 6355	K.SKINVNEIFYDLVR.Q	1710.95483	2	4.77E-12	0.95	4.36	-	1225.4
AHQ-5-11, 5094 - 5106	K.SKINVNEIFYDLVR.Q	1710.95483	2	3.91E-09	0.89	3.96	-	666.1
AHQ-5-11, 5931	K.SKINVNEIFYDLVR.Q	1710.95483	2	6.66E-11	0.92	4.28	-	818.4
AHQ-5-11, 5934	K.SKINVNEIFYDLVR.Q	1710.95483	3	1.20E-09	0.96	4.79	-	1539.0
AHQ-5-11, 2510	K.YDPTIEDSYR.K	1259.30338	2	5.65E-09	0.76	2.66	-	421.1
AHQ-5-14-, 2729 - 2741	K.YDPTIEDSYR.K	1259.30338	2	3.69E-07	0.81	2.95	-	409.3
AHQ-5-11, 2698 - 2762	K.YDPTIEDSYR.K	1259.30338	2	8.61E-05	0.75	2.65	-	356.5
AHQ-5-12, 2768 - 2770	K.YDPTIEDSYR.K	1259.30338	2	1.82E-05	0.71	2.68	-	376.4
AHQ-5-13-, 2813	K.YDPTIEDSYR.K	1259.30338	2	1.12E-06	0.85	2.93	-	477.8
AHQ-5-11, 2187	K.YDPTIEDSYRK.Q	1387.47629	2	1.70E-05	0.63	2.51	-	454.9
AHQ-5-11, 2268 - 2332	K.YDPTIEDSYRK.Q	1387.47629	2	2.60E-05	0.57	2.65	-	307.6
AHQ-5-13-, 2441	K.YDPTIEDSYRK.Q	1387.47629	2	8.46E-05	0.70	2.52	-	447.0
gi|24431935|ref|NP_065393.1| reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sap				2.19E-12	0.97	10.33	2.80	129930.3
AHQ-5-14-, 5961	K.YQFVREPEDEEEEEEEEEDEDEDLEELEVLER.K	4189.14063	3	2.19E-12	0.97	6.57	-	1574.4
AHQ-5-13, 6128	K.YQFVREPEDEEEEEEEEEDEDEDLEELEVLER.K	4189.14063	3	1.81E-09	0.97	6.05	-	1782.5
gi|4501891|ref|NP_001093.1| actinin, alpha 1 [Homo sapiens]				2.36E-12	40.28	460.31	52.00	103056.9
AHQ-5-5, 7439 - 7510	R.AAPFNNWMEGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4380.81962	3	5.82E-06	0.74	4.05	-	937.5
AHQ-5-6, 7358	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	8.51E-04	0.82	3.98	-	772.8
AHQ-5-5, 7451	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	1.83E-09	0.92	4.44	-	1074.5
AHQ-5-5, 7583	R.AAPFNNWMEGAMEDLQDTFIVHTIEEIQGLTTAHEQFK.A	4364.82022	3	2.21E-04	0.95	5.68	-	992.5
AHQ-5-9, 4600	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	4.95E-04	0.22	2.92	-	184.0
AHQ-5-1, 5624	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.82E-07	0.86	4.45	-	891.3
AHQ-5-3, 5546	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.61E-05	0.77	4.13	-	759.0
AHQ-5-5, 4674 - 4678	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.06E-07	0.87	4.84	-	778.2
AHQ-5-6, 5208	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.15E-04	0.84	4.35	-	468.6
AHQ-5-5, 5241 - 5261	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.19E-05	0.84	4.58	-	943.4

AHQ-5-4, 5500	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	8.81E-05	0.89	4.97	-	927.4
AHQ-5-5, 5614	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.86E-08	0.75	3.80	-	469.6
AHQ-5-5, 5411	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	3	4.92E-04	0.76	3.28	-	932.1
AHQ-5-5, 5405 - 5473	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	1.56E-06	0.87	4.09	-	493.0
AHQ-5-6, 6437	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.30E-09	0.87	4.02	-	629.2
AHQ-5-4, 6690 - 6701	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	8.04E-09	0.94	4.66	-	797.5
AHQ-5-5, 6497 - 6561	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.23E-07	0.93	4.68	-	768.9
AHQ-5-5, 3289 - 3357	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	6.29E-05	0.91	3.62	-	919.1
AHQ-5-5, 3043	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	6.91E-07	0.96	4.35	-	2258.3
AHQ-5-5, 1886 - 1953	K.ASIHEAWTDGK.E	1215.29697	2	4.28E-07	0.82	2.68	-	1001.8
AHQ-5-5, 4963	R.CQKICDQWDNLGALTQK.R	2081.31600	2	4.60E-09	0.93	4.57	-	839.4
AHQ-5-1, 5936 - 5997	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	5.79E-07	0.95	5.07	-	1052.9
AHQ-5-3, 5954	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.34E-09	0.95	5.34	-	889.7
AHQ-5-6, 5678 - 5684	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	8.89E-09	0.96	5.07	-	1086.6
AHQ-5-4, 5890 - 5892	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	2.35E-09	0.96	4.62	-	1539.9
AHQ-5-5, 5229	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	7.58E-09	0.95	4.34	-	1294.7
AHQ-5-5, 5741 - 5807	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	2.21E-09	0.97	5.77	-	1280.5
AHQ-5-6, 4793	K.DGLGFCALIHR.H	1260.44730	2	3.47E-06	0.91	3.04	-	1326.9
AHQ-5-5, 5079	K.DGLGFCALIHR.H	1260.44730	2	7.20E-07	0.89	2.93	-	1423.5
AHQ-5-4, 5014 - 5017	K.DGLGFCALIHR.H	1260.44730	2	1.84E-05	0.92	3.02	-	1267.6
AHQ-5-5, 2279	R.DHSGTLGPEEFK.A	1317.38606	1	3.08E-07	0.62	3.26	-	251.5
AHQ-5-5, 2273 - 2274	R.DHSGTLGPEEFK.A	1317.38606	2	6.89E-07	0.88	3.63	-	624.3
AHQ-5-6, 2273	R.DHSGTLGPEEFK.A	1317.38606	2	5.11E-04	0.79	3.04	-	551.1
AHQ-5-4, 3837	K.DYETATLSEIK.A	1270.36761	2	1.00E-04	0.91	3.35	-	1277.0
AHQ-5-10, 3996	R.ETADTDTADQVMASFK.I	1730.83208	2	1.05E-06	0.94	4.31	-	1089.1
AHQ-5-9, 3927	R.ETADTDTADQVMASFK.I	1730.83208	2	3.25E-04	0.58	2.55	-	694.2
AHQ-5-4, 3232	R.ETADTDTADQVM*ASFK.I	1746.83148	2	1.46E-05	0.92	4.19	-	834.4
AHQ-5-2, 4579	R.ETADTDTADQVMASFK.I	1730.83208	2	2.92E-05	0.74	2.67	-	812.9
AHQ-5-1, 4651	R.ETADTDTADQVMASFK.I	1730.83208	2	2.11E-06	0.94	4.17	-	1223.1
AHQ-5-13-, 4335	R.ETADTDTADQVMASFK.I	1730.83208	2	5.44E-09	0.98	5.57	-	1918.2
AHQ-5-4, 4565	R.ETADTDTADQVMASFK.I	1730.83208	2	5.28E-07	0.95	3.96	-	1106.9
AHQ-5-11, 4238	R.ETADTDTADQVMASFK.I	1730.83208	2	2.65E-08	0.81	2.95	-	966.8
AHQ-5-6, 4364	R.ETADTDTADQVMASFK.I	1730.83208	2	4.17E-06	0.95	3.69	-	1633.7
AHQ-5-5, 4397 - 4426	R.ETADTDTADQVMASFK.I	1730.83208	2	2.35E-10	0.94	3.94	-	1295.1
AHQ-5-13, 3310	R.ETADTDTADQVM*ASFK.I	1746.83148	2	3.59E-08	0.95	4.66	-	1102.0
AHQ-5-3, 4615	R.ETADTDTADQVMASFK.I	1730.83208	2	2.56E-07	0.86	3.48	-	913.5
AHQ-5-5, 2749	K.GISQEQM*NEFR.A	1355.45931	2	2.05E-05	0.87	3.11	-	863.1
AHQ-5-6, 2740	K.GISQEQMNEFR.A	1339.45991	2	1.00E-04	0.89	3.42	-	906.9
AHQ-5-5, 2039	K.GISQEQM*NEFR.A	1355.45931	2	4.92E-04	0.80	3.09	-	704.5
AHQ-5-4, 2884 - 2896	K.GISQEQMNEFR.A	1339.45991	2	3.29E-08	0.90	3.20	-	973.9
AHQ-5-5, 2486 - 2495	K.GISQEQMNEFR.A	1339.45991	2	6.44E-06	0.64	2.67	-	589.8
AHQ-5-5, 2721 - 2786	K.GISQEQMNEFR.A	1339.45991	2	3.76E-05	0.88	3.24	-	879.3
AHQ-5-4, 2025	R.HRPELIDYGK.L	1228.38202	2	2.61E-04	0.89	3.69	-	581.2
AHQ-5-5, 1811	R.HRPELIDYGK.L	1228.38202	1	1.22E-04	0.16	1.84	-	203.3
AHQ-5-5, 4937	K.ICDQWDNLGALTQK.R	1663.83349	2	5.17E-06	0.98	5.07	-	2261.9
AHQ-5-6, 4869	K.ICDQWDNLGALTQK.R	1663.83349	2	7.29E-07	0.97	4.31	-	2104.6
AHQ-5-4, 5078	K.ICDQWDNLGALTQK.R	1663.83349	2	1.12E-04	0.95	3.37	-	1955.9
AHQ-5-6, 4797 - 4873	K.ICDQWDNLGALTQK.R	1663.83349	2	8.60E-05	0.88	3.63	-	1122.6
AHQ-5-3, 5142	K.ICDQWDNLGALTQK.R	1663.83349	2	7.21E-08	0.97	4.48	-	1833.5
AHQ-5-5, 5838 - 5905	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	4.79E-07	0.87	3.59	-	870.5
AHQ-5-5, 5965 - 6033	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	7.34E-07	0.94	4.90	-	1184.2
AHQ-5-9, 5142 - 5212	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	1.87E-06	0.93	4.57	-	941.1
AHQ-5-6, 5828	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	5.44E-06	0.88	3.25	-	1398.9
AHQ-5-5, 4181	K.ILAGDKNYITMDELR.R	1753.01353	2	1.77E-08	0.96	4.81	-	1086.0
AHQ-5-5, 3999	K.ILAGDKNYITMDELR.R	1753.01353	3	3.90E-07	0.93	4.73	-	976.4
AHQ-5-5, 3986	K.ILAGDKNYITMDELR.R	1753.01353	2	1.42E-05	0.91	4.14	-	703.1
AHQ-5-5, 2597	R.IMSIVDPNR.L	1045.23840	2	1.53E-05	0.85	3.01	-	774.4
AHQ-5-5, 4161 - 4169	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	2	2.28E-05	0.93	4.38	-	716.7
AHQ-5-5, 6199	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	2	2.39E-07	0.78	3.27	-	516.8
AHQ-5-5, 4838	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	3	2.91E-10	0.96	5.35	-	1680.3
AHQ-5-5, 4833 - 4905	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	2	1.04E-04	0.89	3.70	-	968.7
AHQ-5-5, 4163	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	3	1.54E-05	0.94	5.24	-	1150.1
AHQ-5-5, 4557 - 4637	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	3	6.35E-04	0.59	3.55	-	332.8
AHQ-5-5, 4562 - 4613	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	1.93E-07	0.93	4.68	-	786.7
AHQ-5-6, 4505	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	3	4.27E-04	0.71	3.56	-	343.2
AHQ-5-4, 4812	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	4.99E-06	0.93	4.55	-	865.0
AHQ-5-5, 4695	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	8.31E-06	0.89	3.85	-	792.4
AHQ-5-5, 4242	K.IVQTYHVNM*AGTNPYTTITPQEINGK.W	2908.23575	2	6.87E-04	0.46	2.62	-	234.0
AHQ-5-5, 4615 - 4638	R.KAGTQIENIEEDFRDGLK.L	2064.24210	3	1.33E-04	0.95	6.24	-	1385.3
AHQ-5-5, 5106	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.09E-10	0.98	5.80	-	1792.4
AHQ-5-9, 4228	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	3.13E-07	0.96	4.79	-	1110.6
AHQ-5-6, 4768 - 4769	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	6.36E-09	0.97	4.99	-	1447.7
AHQ-5-2, 5013	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	6.16E-05	0.96	5.08	-	1154.5
AHQ-5-1, 5100	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	4.38E-04	0.97	5.08	-	1366.1
AHQ-5-5, 4802 - 4803	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.19E-05	0.97	5.45	-	1247.3
AHQ-5-5, 4337	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	7.58E-08	0.97	5.33	-	1602.4
AHQ-5-4, 5000	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	4.40E-06	0.96	5.24	-	1121.3
AHQ-5-5, 4067 - 4142	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	4.14E-04	0.96	4.55	-	1505.0
AHQ-5-5, 2995 - 3077	R.LAILGIHNEVSK.I	1294.52505	2	1.66E-08	0.95	3.75	-	1560.7
AHQ-5-5, 3017	R.LAILGIHNEVSK.I	1294.52505	1	8.72E-04	0.45	1.98	-	429.8
AHQ-5-5, 3598	R.LAILGIHNEVSK.I	1294.52505	2	5.49E-07	0.82	2.69	-	896.3
AHQ-5-6, 3024	R.LAILGIHNEVSK.I	1294.52505	2	2.32E-07	0.96	3.85	-	1329.0
AHQ-5-4, 3268 - 3270	R.LAILGIHNEVSK.I	1294.52505	1	3.95E-06	0.23	2.30	-	308.7
AHQ-5-4, 3265 - 3300	R.LAILGIHNEVSK.I	1294.52505	2	3.30E-05	0.82	3.34	-	806.8
AHQ-5-5, 3035	R.LAILGIHNEVSK.I	1294.52505	1	4.69E-05	0.75	3.07	-	366.9
AHQ-5-5, 3555 - 3562	R.LAILGIHNEVSK.I	1294.52505	2	2.26E-04	0.88	2.83	-	878.2
AHQ-5-5, 3499 - 3571	R.LAILGIHNEVSK.I	1294.52505	1	2.93E-04	0.32	2.14	-	475.9
AHQ-5-1, 6323	K.LASDLLEWIR.R	1216.41115	2	4.55E-08	0.96	3.92	-	1671.3
AHQ-5-4, 6222	K.LASDLLEWIR.R	1216.41115	2	8.24E-08	0.97	4.02	-	2031.9
AHQ-5-6, 5950 - 5956	K.LASDLLEWIR.R	1216.41115	2	2.16E-07	0.97	4.41	-	2251.3
AHQ-5-5, 5969 - 6037	K.LASDLLEWIR.R	1216.41115	2	7.87E-08	0.96	4.25	-	1771.0
AHQ-5-3, 6311	K.LASDLLEWIR.R	1216.41115	2	1.39E-06	0.96	4.29	-	1629.2
AHQ-5-5, 6582 - 6657	K.LLETIDQLYLEYAK.R	1712.96427	2	1.21E-08	0.97	5.43	-	1305.9
AHQ-5-5, 6709 - 6773	K.LLETIDQLYLEYAK.R	1712.96427	2	1.57E-07	0.97	5.36	-	1356.8
AHQ-5-3, 6854	K.LLETIDQLYLEYAK.R	1712.96427	2	4.55E-07	0.96	4.04	-	1508.2
AHQ-5-5, 6919 - 6993	K.LLETIDQLYLEYAK.R	1712.96427	2	1.37E-04	0.95	4.36	-	1169.6
AHQ-5-5, 7061	K.LLETIDQLYLEYAK.R	1712.96427	2	5.66E-07	0.95	4.43	-	1160.8
AHQ-5-7, 6579	K.LLETIDQLYLEYAK.R	1712.96427	2	2.22E-06	0.93	3.69	-	1028.4
AHQ-5-1, 6784 - 6787	K.LLETIDQLYLEYAK.R	1712.96427	2	1.16E-08	0.98	5.56	-	1493.5
AHQ-5-14-, 6267	K.LLETIDQLYLEYAK.R	1712.96427	2	7.95E-06	0.81	2.99	-	827.8
AHQ-5-4, 6793 - 6866	K.LLETIDQLYLEYAK.R	1712.96427	2	2.36E-08	0.95	4.51	-	1089.8
AHQ-5-5, 6837 - 6839	K.LLETIDQLYLEYAK.R	1712.96427	2	2.29E-08	0.96	4.42	-	1555.4
AHQ-5-6, 6580 - 6648	K.LLETIDQLYLEYAK.R	1712.96427	2	9.43E-09	0.98	5.62	-	1629.1
AHQ-5-6, 2341	R.LSNRPAFMPSEGR.M	1462.65941	2	1.85E-04	0.72	3.10	-	689.9
AHQ-5-4, 2505	R.LSNRPAFMPSEGR.M	1462.65941	2	4.08E-04	0.84	3.36	-	701.3
AHQ-5-5, 2341	R.LSNRPAFMPSEGR.M	1462.65941	2	3.48E-04	0.73	3.15	-	506.3
AHQ-5-9, 3458	K.MLDAEDIVGTARPDEK.A	1760.94769	2	8.76E-07	0.73	3.57	-	543.0

AHQ-5-5, 3806	K.MLDAEDIVGTARPDEK.A	1760.94769	3	6.28E-05	0.79	3.47	-	502.0
AHQ-5-5, 3809 - 3810	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.72E-05	0.89	4.44	-	834.1
AHQ-5-4, 3992	K.MLDAEDIVGTARPDEK.A	1760.94769	2	9.75E-05	0.83	3.45	-	832.5
AHQ-5-4, 3990 - 3997	K.MLDAEDIVGTARPDEK.A	1760.94769	3	6.14E-08	0.80	3.83	-	524.9
AHQ-5-6, 3738 - 3777	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.52E-09	0.83	3.79	-	703.3
AHQ-5-8, 3610 - 3621	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.07E-09	0.94	4.52	-	1084.1
AHQ-5-5, 3403	K.M*LDAEDIVGTARPDEK.A	1776.94709	3	2.49E-04	0.84	3.49	-	764.3
AHQ-5-7, 3659 - 3660	K.MLDAEDIVGTARPDEK.A	1760.94769	2	8.40E-09	0.91	4.54	-	650.9
AHQ-5-5, 3395 - 3401	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	6.10E-06	0.92	3.75	-	1027.9
AHQ-5-1, 4157	K.MLDAEDIVGTARPDEK.A	1760.94769	2	1.51E-05	0.90	3.89	-	950.3
AHQ-5-6, 3769	K.MLDAEDIVGTARPDEK.A	1760.94769	3	5.06E-05	0.69	3.71	-	506.8
AHQ-5-4, 3592	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	6.20E-07	0.91	3.78	-	951.8
AHQ-5-6, 3337	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	3.33E-04	0.83	2.96	-	770.3
AHQ-5-5, 5889	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	3.94E-07	0.96	4.61	-	1328.9
AHQ-5-4, 5570	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	3.92E-07	0.94	4.13	-	1243.4
AHQ-5-5, 5711	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	4.31E-04	0.74	3.08	-	660.4
AHQ-5-5, 5983	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	7.43E-10	0.94	4.08	-	1113.0
AHQ-5-5, 6134 - 6147	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.53E-10	0.94	4.24	-	1505.7
AHQ-5-4, 5816 - 5821	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	3.71E-04	0.85	3.58	-	655.1
AHQ-5-6, 5824 - 5897	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	5.51E-08	0.96	4.73	-	1301.5
AHQ-5-5, 5566 - 5637	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.15E-05	0.98	5.30	-	1862.3
AHQ-5-6, 5508 - 5576	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.99E-04	0.98	5.39	-	1579.3
AHQ-5-5, 5562 - 5574	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	4.21E-10	0.96	5.14	-	1121.9
AHQ-5-6, 5356	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	6.93E-08	0.97	5.36	-	1285.4
AHQ-5-7, 5440	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	2.99E-05	0.94	4.35	-	917.7
AHQ-5-5, 5255 - 5329	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	9.57E-07	0.96	4.61	-	1097.3
AHQ-5-6, 5286	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	3.35E-09	0.94	4.99	-	771.0
AHQ-5-5, 5157 - 5187	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	7.08E-05	0.91	4.17	-	722.0
AHQ-5-4, 5446	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	7.15E-07	0.91	3.84	-	1088.5
AHQ-5-4, 5730	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	5.97E-04	0.81	3.07	-	768.9
AHQ-5-5, 4463 - 4491	K.NVNIQNFHISWK.D	1500.68583	2	2.44E-06	0.94	3.48	-	1342.8
AHQ-5-5, 4570	K.NVNIQNFHISWK.D	1500.68583	2	4.22E-07	0.83	2.75	-	966.0
AHQ-5-1, 4953	K.NVNIQNFHISWK.D	1500.68583	2	9.47E-07	0.97	4.52	-	2004.2
AHQ-5-5, 5135	K.NVNIQNFHISWK.D	1500.68583	2	3.79E-07	0.93	3.73	-	1095.7
AHQ-5-10, 4144	K.NVNIQNFHISWK.D	1500.68583	2	3.19E-04	0.84	3.37	-	812.9
AHQ-5-3, 4879	K.NVNIQNFHISWK.D	1500.68583	2	3.45E-05	0.91	3.28	-	1139.6
AHQ-5-4, 3702	K.NYITMDELR.R	1155.30648	2	2.49E-05	0.64	2.60	-	505.3
AHQ-5-5, 3501 - 3515	K.NYITMDELR.R	1155.30648	2	1.52E-05	0.84	2.92	-	686.6
AHQ-5-5, 5005	K.QFGAQANVIGPWIQTK.M	1759.00118	2	5.00E-05	0.89	4.69	-	535.2
AHQ-5-5, 2691	R.QKDYETATLSEIK.A	1526.67030	2	1.42E-05	0.61	3.02	-	347.6
AHQ-5-3, 4013	R.TINEVENQILTR.D	1430.58898	2	3.84E-04	0.85	3.22	-	931.4
AHQ-5-1, 4109	R.TINEVENQILTR.D	1430.58898	2	4.08E-07	0.89	3.89	-	827.0
AHQ-5-2, 3949	R.TINEVENQILTR.D	1430.58898	2	1.39E-07	0.85	3.79	-	794.8
AHQ-5-5, 3966 - 4038	R.TINEVENQILTR.D	1430.58898	2	1.34E-05	0.88	3.83	-	815.0
AHQ-5-4, 3961	R.TINEVENQILTR.D	1430.58898	2	7.91E-05	0.89	3.63	-	892.5
AHQ-5-5, 2937	R.TINEVENQILTR.D	1430.58898	1	7.51E-05	0.29	2.42	-	242.5
AHQ-5-5, 3421	R.TINEVENQILTR.D	1430.58898	2	8.18E-07	0.61	2.73	-	415.9
AHQ-5-5, 3973 - 4041	R.TINEVENQILTR.D	1430.58898	1	1.86E-05	0.17	2.04	-	283.7
AHQ-5-8, 3590	R.TINEVENQILTR.D	1430.58898	2	5.46E-06	0.93	3.68	-	1049.3
AHQ-5-5, 7133 - 7203	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.78E-04	0.85	3.49	-	1149.9
AHQ-5-5, 7085 - 7149	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	6.44E-07	0.90	3.79	-	804.6
AHQ-5-5, 7038 - 7106	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	6.89E-04	0.92	4.61	-	956.6
AHQ-5-5, 6983 - 7049	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	9.76E-06	0.91	4.61	-	754.3
AHQ-5-1, 7137	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	2.11E-08	0.94	5.18	-	1119.2
AHQ-5-4, 7193 - 7197	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	2.55E-05	0.96	5.51	-	1375.5
AHQ-5-14-, 6373	R.VGWEQLLTTIAR.T	1387.60894	2	3.33E-09	0.95	4.16	-	1457.8
AHQ-5-9, 5836	R.VGWEQLLTTIAR.T	1387.60894	2	1.79E-04	0.89	3.61	-	910.4
AHQ-5-10, 5995	R.VGWEQLLTTIAR.T	1387.60894	2	1.98E-07	0.97	5.31	-	1729.1
AHQ-5-5, 6653 - 6673	R.VGWEQLLTTIAR.T	1387.60894	2	1.44E-07	0.97	4.96	-	2070.6
AHQ-5-4, 6869 - 6896	R.VGWEQLLTTIAR.T	1387.60894	2	1.59E-08	0.97	4.97	-	1487.5
AHQ-5-11, 6310	R.VGWEQLLTTIAR.T	1387.60894	2	4.22E-08	0.93	3.73	-	1194.6
AHQ-5-6, 6621 - 6644	R.VGWEQLLTTIAR.T	1387.60894	2	3.36E-08	0.96	4.03	-	1658.6
AHQ-5-3, 6927	R.VGWEQLLTTIAR.T	1387.60894	2	1.66E-08	0.94	3.73	-	1389.3
AHQ-5-2, 6862	R.VGWEQLLTTIAR.T	1387.60894	2	4.31E-06	0.91	3.71	-	1036.7
AHQ-5-5, 6737	R.VGWEQLLTTIAR.T	1387.60894	2	1.55E-06	0.94	3.98	-	1323.0
AHQ-5-7, 6510 - 6515	R.VGWEQLLTTIAR.T	1387.60894	2	6.58E-08	0.96	4.81	-	1400.4
AHQ-5-1, 6892 - 6900	R.VGWEQLLTTIAR.T	1387.60894	2	3.29E-06	0.97	4.88	-	2080.7
AHQ-5-8, 6313	R.VGWEQLLTTIAR.T	1387.60894	2	1.11E-09	0.97	4.79	-	1700.1
AHQ-5-6, 4484	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.89E-11	0.91	4.13	-	661.9
AHQ-5-8, 3812	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.86E-07	0.96	4.97	-	1400.4
AHQ-5-6, 4390	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	8.36E-08	0.89	3.89	-	552.4
AHQ-5-6, 4108 - 4176	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.55E-06	0.95	4.95	-	1052.1
AHQ-5-6, 3408 - 3440	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.53E-07	0.96	5.44	-	1098.5
AHQ-5-5, 4682	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.78E-05	0.86	4.04	-	628.1
AHQ-5-5, 4379 - 4451	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.36E-12	0.97	5.08	-	1394.1
AHQ-5-5, 4217 - 4286	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.48E-07	0.97	4.72	-	1670.9
AHQ-5-5, 4114 - 4185	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.10E-05	0.97	5.46	-	1494.7
AHQ-5-5, 3677	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.54E-10	0.96	5.05	-	939.1
AHQ-5-5, 3585	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.37E-05	0.92	4.33	-	881.9
AHQ-5-5, 3445 - 3498	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	5.50E-06	0.95	4.83	-	1199.7
AHQ-5-4, 4706	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.33E-05	0.93	3.94	-	1070.5
AHQ-5-4, 3654	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.44E-06	0.88	3.76	-	1093.3
AHQ-5-3, 4423	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.05E-06	0.92	3.97	-	1126.9
AHQ-5-2, 4711	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.59E-05	0.90	3.81	-	665.4
AHQ-5-1, 4472	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.44E-08	0.95	5.23	-	968.2
AHQ-5-5, 4546 - 4603	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.08E-11	0.97	5.09	-	1261.4
gi|5031635|ref|NP_005498.1| cofilin 1 (non-muscle) [Homo sapiens]				2.69E-12	10.24	110.35	59.00	18502.4
AHQ-5-12, 4158	K.AVLFCLSEDK.K	1183.35638	2	1.07E-06	0.91	3.37	-	857.7
AHQ-5-13-, 3480	K.AVLFCLSEDKK.N	1311.52930	2	3.86E-06	0.89	3.15	-	930.2
AHQ-5-12, 3289 - 3368	K.AVLFCLSEDKK.N	1311.52930	2	1.29E-04	0.90	3.29	-	953.4
AHQ-5-12, 6968	K.EDLVFIFWAPESAPLK.S	1863.14454	2	7.18E-06	0.96	4.11	-	1717.0
AHQ-5-12, 5696 - 5760	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	5.02E-07	0.97	5.50	-	1505.2
AHQ-5-12, 5558 - 5628	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	9.56E-10	0.97	5.41	-	1435.3
AHQ-5-12, 5830 - 5909	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	6.69E-10	0.96	4.81	-	1344.1
AHQ-5-14, 6205	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	6.40E-08	0.96	4.30	-	1492.4
AHQ-5-13, 5688	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.39E-07	0.94	4.03	-	996.1
AHQ-5-13-, 5597	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.66E-08	0.97	5.11	-	1642.4
AHQ-5-14-, 5583 - 5589	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	2.59E-08	0.98	5.76	-	2232.7
AHQ-5-11, 5551	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	9.94E-07	0.95	4.35	-	1220.5
AHQ-5-12, 5440	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.75E-06	0.96	4.45	-	1463.1
AHQ-5-5, 5902	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.95E-06	0.73	3.06	-	660.6
AHQ-5-12, 2285 - 2336	K.HELQANCYEEVKDR.C	1792.90812	2	2.96E-05	0.97	4.95	-	1585.8
AHQ-5-12, 2301 - 2372	K.HELQANCYEEVKDR.C	1792.90812	3	4.53E-09	0.98	6.09	-	2218.4
AHQ-5-12, 2444 - 2514	K.HELQANCYEEVKDR.C	1792.90812	2	1.92E-07	0.96	4.34	-	1409.5
AHQ-5-13-, 2405	K.HELQANCYEEVKDR.C	1792.90812	3	8.40E-06	0.80	3.61	-	705.0
AHQ-5-13-, 2573	K.HELQANCYEEVKDR.C	1792.90812	3	9.65E-05	0.72	3.43	-	569.6
AHQ-5-12, 2817	K.KAVLFCLSEDKK.N	1439.70221	3	1.20E-05	0.94	4.38	-	1297.8

AHQ-5-12, 2816	K.KAVLFCLSEDKK.N	1439.70221	2	9.02E-05	0.94	3.87	-	1262.0
AHQ-5-12, 2820	K.KAVLFCLSEDKK.N	1439.70221	1	5.91E-05	0.37	2.41	-	451.7
AHQ-5-14-, 6337	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	2.13E-05	0.97	6.44	-	1491.6
AHQ-5-13-, 6449	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	8.96E-09	0.97	5.12	-	1481.7
AHQ-5-13, 6494	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	1.18E-04	0.96	4.82	-	1190.7
AHQ-5-13-, 6452	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	2.17E-04	0.95	4.67	-	1512.1
AHQ-5-12, 6396 - 6464	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	1.70E-05	0.98	5.81	-	2070.8
AHQ-5-12, 6397 - 6469	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	1.18E-10	0.96	5.58	-	1312.7
AHQ-5-13, 6490	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	6.84E-05	0.96	4.87	-	1641.2
AHQ-5-12, 6524 - 6585	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.04E-07	0.97	5.36	-	1293.9
AHQ-5-11, 6278	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.06E-06	0.96	4.55	-	1180.4
AHQ-5-14-, 6330	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.95E-04	0.96	5.08	-	1058.3
AHQ-5-12, 5829	K.KEDLVFIFWAPESAPLKSK.M	2206.56802	2	7.65E-05	0.96	4.77	-	1185.4
AHQ-5-13-, 4372	K.LGGSAVISLEGKPL	1341.57848	2	1.31E-04	0.90	3.81	-	949.5
AHQ-5-12, 4350 - 4420	K.LGGSAVISLEGKPL	1341.57848	2	1.03E-04	0.94	4.26	-	1234.4
AHQ-5-12, 4646 - 4726	K.LGGSAVISLEGKPL	1341.57848	2	1.83E-04	0.96	4.61	-	1184.2
AHQ-5-12, 4460 - 4500	K.LGGSAVISLEGKPL	1341.57848	2	1.17E-08	0.96	4.40	-	1232.9
AHQ-5-12, 4788 - 4853	K.LGGSAVISLEGKPL	1341.57848	2	9.09E-08	0.96	4.40	-	1297.9
AHQ-5-12, 4564 - 4588	K.LGGSAVISLEGKPL	1341.57848	2	2.74E-07	0.96	4.66	-	1267.5
AHQ-5-12, 4989	K.LGGSAVISLEGKPL	1341.57848	2	4.77E-05	0.96	4.33	-	1398.0
AHQ-5-12, 4478 - 4609	K.LGGSAVISLEGKPL	1341.57848	1	9.90E-04	0.53	2.85	-	336.1
AHQ-5-12, 4905	K.LGGSAVISLEGKPL	1341.57848	2	1.31E-04	0.93	3.60	-	1092.6
AHQ-5-14-, 6573 - 6641	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.55E-06	0.96	5.51	-	1559.5
AHQ-5-12, 6708 - 6772	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	4.85E-07	0.98	6.74	-	1836.6
AHQ-5-13-, 6639 - 6651	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	3.98E-08	0.98	7.05	-	2374.1
AHQ-5-12, 7196	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.90E-07	0.96	6.01	-	1204.0
AHQ-5-12, 7110 - 7136	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	2.69E-12	0.97	6.27	-	1744.1
AHQ-5-12, 6820 - 6888	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	6.86E-09	0.97	7.10	-	1462.9
AHQ-5-12, 6477 - 6554	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.29E-05	0.97	6.59	-	1417.1
AHQ-5-13, 3374	R.YALYDATYETK.E	1338.44364	1	1.42E-07	0.76	3.19	-	452.2
AHQ-5-13, 3331 - 3393	R.YALYDATYETK.E	1338.44364	2	6.84E-07	0.93	3.81	-	875.2
AHQ-5-12, 3106 - 3173	R.YALYDATYETK.E	1338.44364	1	1.22E-09	0.75	3.10	-	516.8
AHQ-5-12, 3076 - 3148	R.YALYDATYETK.E	1338.44364	2	1.42E-08	0.95	3.97	-	1197.2
AHQ-5-13-, 3228 - 3292	R.YALYDATYETK.E	1338.44364	2	1.88E-05	0.91	3.24	-	948.8
AHQ-5-13-, 3297	R.YALYDATYETK.E	1338.44364	1	1.41E-04	0.24	2.52	-	295.2
gi|29732955|ref|XP_291603.1| similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA				2.78E-12	0.94	10.21	16.80	11173.0
AHQ-5-9, 3862 - 3919	K.NISNASCTTNCIAPLAK.M	1838.05353	2	7.55E-11	0.87	4.16	-	1163.1
AHQ-5-9, 3980	K.NISNASCTTNCIAPLAK.M	1838.05353	2	6.98E-09	0.86	3.75	-	1141.4
AHQ-5-10, 3759	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.95E-10	0.67	3.74	-	777.9
AHQ-5-11, 3843 - 3908	K.NISNASCTTNCIAPLAK.M	1838.05353	2	8.61E-10	0.95	4.29	-	1589.2
AHQ-5-11, 4072 - 4074	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.78E-12	0.94	4.21	-	1123.7
AHQ-5-11, 4200	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.49E-06	0.75	3.34	-	1055.4
AHQ-5-9, 3768 - 3802	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.54E-08	0.78	3.79	-	1043.7
gi|29741246|ref|XP_294070.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				3.18E-12	4.08	50.39	14.60	35032.0
AHQ-5-9, 4636 - 4694	K.AENGKLVINGNPITIFQER.D	2114.39062	2	1.08E-07	0.79	3.46	-	773.6
AHQ-5-13, 5390	K.AENGKLVINGNPITIFQER.D	2114.39062	2	5.85E-05	0.64	3.16	-	395.4
AHQ-5-14-, 5259	K.AENGKLVINGNPITIFQER.D	2114.39062	2	6.17E-06	0.63	2.86	-	401.8
AHQ-5-13-, 5285	K.AENGKLVINGNPITIFQER.D	2114.39062	2	1.58E-04	0.44	2.72	-	345.7
AHQ-5-13-, 5563 - 5632	K.LVINGNPITIFQER.D	1614.87029	2	6.39E-07	0.84	3.15	-	641.2
AHQ-5-14-, 5542 - 5609	K.LVINGNPITIFQER.D	1614.87029	2	1.78E-09	0.93	3.52	-	1180.2
AHQ-5-9, 5038 - 5094	K.LVINGNPITIFQER.D	1614.87029	2	2.89E-09	0.93	4.10	-	1056.9
AHQ-5-9, 4911 - 4990	K.LVINGNPITIFQER.D	1614.87029	2	1.16E-10	0.92	4.05	-	1013.1
AHQ-5-12, 5665 - 5738	K.LVINGNPITIFQER.D	1614.87029	2	7.88E-08	0.88	3.32	-	729.3
AHQ-5-13, 5668 - 5736	K.LVINGNPITIFQER.D	1614.87029	2	1.78E-08	0.92	3.81	-	963.9
AHQ-5-13-, 5191	K.LVINGNPITIFQERDPSK.I	2042.32440	2	1.04E-07	0.45	2.79	-	303.6
AHQ-5-9, 4562 - 4632	K.LVINGNPITIFQERDPSK.I	2042.32440	2	1.75E-05	0.83	3.37	-	591.5
AHQ-5-9, 6434	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	2	2.73E-06	0.97	5.64	-	2101.5
AHQ-5-9, 6366 - 6435	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	3.18E-12	0.98	7.75	-	2502.4
AHQ-5-9, 5639 - 5711	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	2	3.37E-05	0.94	5.53	-	1303.0
AHQ-5-11, 6154	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	1.18E-05	0.95	5.81	-	1739.7
AHQ-5-10, 6455	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	2	1.39E-04	0.92	3.43	-	1435.6
gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]				3.52E-12	16.69	210.30	88.40	22391.3
AHQ-5-12, 5848 - 5888	R.DDGLFSGDPNWFPK.K	1595.69288	2	6.42E-09	0.93	3.99	-	966.7
AHQ-5-11, 5627 - 5674	R.DDGLFSGDPNWFPK.K	1595.69288	2	9.96E-08	0.96	3.91	-	1458.4
AHQ-5-11, 5739 - 5802	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.67E-07	0.96	4.82	-	1246.6
AHQ-5-11, 5823 - 5883	R.DDGLFSGDPNWFPK.K	1595.69288	2	8.06E-07	0.96	4.22	-	1334.2
AHQ-5-14-, 5774 - 5842	R.DDGLFSGDPNWFPK.K	1595.69288	2	4.73E-06	0.95	4.51	-	1176.7
AHQ-5-12, 6060	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.67E-04	0.92	3.18	-	1260.3
AHQ-5-12, 6305	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.58E-06	0.96	4.96	-	1018.5
AHQ-5-13-, 6851	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	3	1.37E-04	0.81	4.20	-	624.4
AHQ-5-13, 6288	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.33E-07	0.92	4.67	-	698.9
AHQ-5-12, 7094	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	4.35E-05	0.94	5.11	-	673.2
AHQ-5-12, 7074 - 7076	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	9.36E-05	0.86	4.61	-	438.0
AHQ-5-11, 6338	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	4.04E-04	0.75	3.55	-	364.1
AHQ-5-13-, 6195	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.62E-07	0.91	4.09	-	732.8
AHQ-5-13-, 6843 - 6845	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.68E-05	0.91	4.62	-	483.9
AHQ-5-14-, 6117 - 6173	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	9.01E-06	0.73	3.40	-	333.0
AHQ-5-11, 6868	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	3	4.66E-08	0.90	4.79	-	780.0
AHQ-5-11, 6856	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	9.02E-04	0.78	3.86	-	477.5
AHQ-5-13-, 6800 - 6869	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.96E-07	0.82	3.57	-	884.7
AHQ-5-11, 6794 - 6796	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.57E-09	0.91	4.07	-	1075.9
AHQ-5-13, 6888	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	3.45E-08	0.90	4.62	-	634.5
AHQ-5-12, 5773	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	2.37E-08	0.87	3.50	-	749.2
AHQ-5-11, 5822 - 5848	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	4.60E-05	0.71	3.53	-	414.8
AHQ-5-12, 5777	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.16E-09	0.85	3.71	-	1019.2
AHQ-5-11, 5826	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.74E-06	0.91	4.46	-	862.5
AHQ-5-13, 6884 - 6886	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.80E-08	0.94	5.17	-	1054.4
AHQ-5-12, 7012 - 7017	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	9.12E-04	0.57	2.57	-	608.3
AHQ-5-14-, 6749 - 6759	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.66E-08	0.83	3.48	-	981.3
AHQ-5-13-, 6804	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.84E-05	0.81	3.23	-	779.5
AHQ-5-11, 6790 - 6792	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	8.02E-10	0.90	4.75	-	614.0
AHQ-5-12, 7013 - 7025	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.76E-09	0.93	5.03	-	792.3
AHQ-5-12, 7132	R.ENFQNWLKDGTVLCELINALYPEGQAPVK.K	3349.75795	3	2.21E-04	0.54	3.25	-	351.3
AHQ-5-11, 2366	K.ENPRNFSDNQLQEGK.N	1776.84549	2	1.87E-04	0.76	3.34	-	572.3
AHQ-5-11, 2599 - 2626	R.GASQAGMTGYGMPR.Q	1384.56732	2	4.02E-04	0.85	3.24	-	778.9
AHQ-5-11, 2056 - 2060	R.GPAYGLSREVQQK.I	1433.59456	2	1.18E-05	0.91	4.31	-	935.0
AHQ-5-11, 2410	K.IQASTMAFK.Q	997.19374	1	7.25E-05	0.68	2.14	-	864.1
AHQ-5-12, 2465	K.IQASTMAFK.Q	997.19374	2	1.54E-06	0.49	2.70	-	224.6
AHQ-5-12, 2040	K.IQASTM*AFK.Q	1013.19314	1	7.58E-04	0.21	2.06	-	65.9
AHQ-5-11, 2114 - 2119	K.KIQASTMAFK.Q	1125.36665	2	5.93E-04	0.85	3.30	-	931.7
AHQ-5-12, 2406	R.NFSDNQLQEGK.N	1280.32582	2	1.82E-04	0.90	3.34	-	1041.4
AHQ-5-12, 2405	R.NFSDNQLQEGK.N	1280.32582	1	8.04E-06	0.56	3.03	-	327.0
AHQ-5-12, 2562	R.NFSDNQLQEGK.N	1280.32582	1	1.54E-05	0.24	1.89	-	404.6
AHQ-5-11, 2158 - 2224	R.NFSDNQLQEGK.N	1280.32582	2	8.17E-04	0.80	2.90	-	754.5
AHQ-5-13, 2429	R.NFSDNQLQEGK.N	1280.32582	2	8.92E-05	0.85	3.45	-	618.9
AHQ-5-13-, 2272	R.NFSDNQLQEGK.N	1280.32582	1	2.26E-04	0.44	2.39	-	263.0
AHQ-5-11, 2275 - 2363	R.NFSDNQLQEGK.N	1280.32582	1	1.37E-08	0.43	2.79	-	271.1

AHQ-5-11, 2364	R.NFSDNQLQEGK.N	1280.32582	2	9.62E-06	0.92	3.56	-	1020.7
AHQ-5-12, 2290	R.NFSDNQLQEGK.N	1280.32582	1	1.84E-04	0.15	2.12	-	267.7
AHQ-5-12, 2088	R.NFSDNQLQEGK.N	1280.32582	2	7.40E-05	0.83	3.20	-	809.4
AHQ-5-11, 2542	R.NFSDNQLQEGK.N	1280.32582	1	5.37E-05	0.18	2.02	-	321.1
AHQ-5-11, 3200	K.NVIGLQMGTNR.G	1203.39751	2	1.41E-07	0.91	3.10	-	1563.6
AHQ-5-11, 2234 - 2235	K.NVIGLQM*GTNR.G	1219.39691	2	4.57E-06	0.96	4.28	-	1284.1
AHQ-5-11, 2966	K.NVIGLQMGTNR.G	1203.39751	2	2.37E-05	0.94	3.88	-	1341.6
AHQ-5-11, 2975	K.NVIGLQM*GTNR.G	1219.39691	2	2.40E-04	0.88	2.85	-	973.0
AHQ-5-13-, 4716 - 4717	K.QM*EQISQFLQAAER.Y	1695.87890	2	2.22E-05	0.84	3.69	-	517.5
AHQ-5-14-, 4670	K.QM*EQISQFLQAAER.Y	1695.87890	2	5.99E-04	0.93	3.74	-	874.8
AHQ-5-13-, 5400 - 5408	K.QMEQISQFLQAAER.Y	1679.87950	2	1.14E-04	0.95	4.62	-	1065.5
AHQ-5-12, 5456	K.QMEQISQFLQAAER.Y	1679.87950	3	9.72E-07	0.96	4.56	-	2021.4
AHQ-5-14-, 5346 - 5363	K.QMEQISQFLQAAER.Y	1679.87950	2	3.91E-04	0.96	4.60	-	1200.0
AHQ-5-12, 4704	K.QM*EQISQFLQAAER.Y	1695.87890	2	2.61E-04	0.94	4.16	-	963.8
AHQ-5-11, 5234 - 5266	K.QMEQISQFLQAAER.Y	1679.87950	2	2.05E-04	0.96	4.94	-	1334.3
AHQ-5-12, 7116	K.QYDADLEQILIQWITTQCR.K	2396.66131	3	6.73E-08	0.95	4.97	-	1574.7
AHQ-5-13-, 6867	K.QYDADLEQILIQWITTQCR.K	2396.66131	3	1.12E-08	0.95	4.69	-	1683.2
AHQ-5-11, 4647	R.TLMNLGGLAVAR.D	1216.47932	2	1.63E-06	0.92	3.73	-	1310.3
AHQ-5-11, 4286 - 4355	R.TLMNLGGLAVAR.D	1216.47932	2	7.53E-07	0.93	4.47	-	977.8
AHQ-5-12, 3989	R.TLM*NLGGLAVAR.D	1232.47872	2	3.91E-04	0.76	2.90	-	718.9
AHQ-5-11, 3459 - 3462	R.TLM*NLGGLAVAR.D	1232.47872	2	3.94E-07	0.94	4.39	-	953.2
AHQ-5-13, 4528 - 4545	R.TLMNLGGLAVAR.D	1216.47932	2	3.45E-07	0.93	4.15	-	1196.0
AHQ-5-12, 4421 - 4489	R.TLMNLGGLAVAR.D	1216.47932	2	6.27E-07	0.91	4.21	-	938.0
AHQ-5-13-, 4436 - 4452	R.TLMNLGGLAVAR.D	1216.47932	2	8.47E-06	0.94	4.26	-	1253.8
AHQ-5-12, 4786	R.TLMNLGGLAVAR.D	1216.47932	1	2.78E-04	0.12	1.99	-	256.4
AHQ-5-12, 4590	R.TLMNLGGLAVAR.D	1216.47932	2	2.17E-05	0.87	3.24	-	997.4
AHQ-5-13-, 3509	R.TLM*NLGGLAVAR.D	1232.47872	2	7.39E-04	0.76	3.04	-	846.4
AHQ-5-11, 3902	R.TLM*NLGGLAVAR.D	1232.47872	2	9.22E-08	0.84	3.21	-	872.4
AHQ-5-12, 6674 - 6736	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	9.85E-08	0.94	4.73	-	1034.6
AHQ-5-12, 6912 - 7058	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.59E-09	0.96	5.26	-	1239.2
AHQ-5-11, 6927	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.40E-08	0.95	4.87	-	823.0
AHQ-5-13-, 6723	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	8.20E-08	0.97	5.48	-	1372.5
AHQ-5-11, 6840	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.82E-05	0.91	4.08	-	923.6
AHQ-5-11, 6698 - 6756	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	6.28E-08	0.97	5.29	-	1221.2
AHQ-5-11, 6490	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.52E-12	0.96	4.59	-	1251.2
AHQ-5-11, 6270 - 6279	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.03E-08	0.97	5.22	-	1258.3
AHQ-5-12, 7146 - 7160	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.16E-08	0.93	4.12	-	845.5
AHQ-5-12, 6829 - 6897	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.44E-10	0.98	5.12	-	1754.9
AHQ-5-14-, 6595 - 6674	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	5.09E-09	0.97	5.90	-	1335.5
AHQ-5-12, 6568 - 6632	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	5.59E-05	0.64	2.87	-	542.1
AHQ-5-1, 7241	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.96E-05	0.92	4.39	-	795.7
AHQ-5-12, 6902	R.YGINTTDIFQTVDLWEGKNMACVQR.T	2962.30673	3	8.45E-10	0.92	4.94	-	936.0
AHQ-5-12, 6680 - 6684	R.YGINTTDIFQTVDLWEGKNM*ACVQR.T	2978.30613	3	9.16E-07	0.64	3.72	-	403.2
gi|17986260|ref|NP_524147.1|	smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo			3.68E-12	3.25	40.31	23.30	12969.7
AHQ-5-12, 5868 - 5933	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	1.09E-04	0.83	4.70	-	779.3
AHQ-5-12, 5974 - 6037	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	5.41E-07	0.97	5.96	-	1802.1
AHQ-5-12, 6080 - 6145	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	3.27E-09	0.92	5.54	-	1501.9
AHQ-5-12, 6100 - 6169	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	1.02E-05	0.97	5.36	-	2003.6
AHQ-5-12, 6208 - 6270	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	9.82E-07	0.84	4.74	-	602.0
AHQ-5-12, 6233 - 6297	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	9.77E-09	0.98	6.07	-	2254.4
AHQ-5-12, 6362	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	1.48E-04	0.95	5.33	-	1613.9
AHQ-5-12, 6701	K.MTEEEVEMLVAGHEDSNGCINYEELVR.M	3156.42556	3	2.50E-04	0.96	5.52	-	2259.9
AHQ-5-12, 6712	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	4.55E-10	0.37	3.23	-	401.2
AHQ-5-12, 7121	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	2.99E-06	0.78	3.99	-	394.2
AHQ-5-14, 6073	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	3.10E-06	0.95	5.00	-	1309.2
AHQ-5-14-, 5785	K.M*TEEEVEMLVAGHEDSNGCINYEELVR.M	3172.42496	3	1.05E-06	0.61	3.36	-	530.6
AHQ-5-14-, 5881 - 5894	K.MTEEEVEM*LVAGHEDSNGCINYEELVR.M	3172.42496	3	3.68E-12	0.96	6.26	-	1905.6
gi|4557677|ref|NP_000203.1|	integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu			3.84E-12	20.20	250.27	39.10	87185.6
AHQ-5-6, 2662	R.AKWDTANNPLYK.E	1421.58225	2	1.38E-08	0.81	3.18	-	580.6
AHQ-5-3, 2875	R.AKWDTANNPLYK.E	1421.58225	1	1.31E-06	0.73	3.10	-	421.6
AHQ-5-3, 2869	R.AKWDTANNPLYK.E	1421.58225	2	2.18E-05	0.91	3.32	-	817.7
AHQ-5-3, 5458 - 5529	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	6.16E-06	0.95	5.41	-	1249.5
AHQ-5-3, 5553 - 5614	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	2	9.79E-09	0.93	4.71	-	655.5
AHQ-5-3, 5457 - 5525	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	2	5.66E-05	0.77	3.61	-	457.6
AHQ-5-1, 4503	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.99E-06	0.83	3.67	-	573.7
AHQ-5-4, 4406 - 4476	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	5.88E-05	0.65	3.40	-	491.0
AHQ-5-3, 4534 - 4607	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.66E-06	0.66	3.28	-	479.1
AHQ-5-5, 4378	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	9.71E-05	0.72	3.16	-	483.2
AHQ-5-6, 4304	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.36E-04	0.64	3.40	-	395.6
AHQ-5-2, 4497 - 4519	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	3.65E-06	0.81	3.89	-	548.6
AHQ-5-3, 4447 - 4517	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	8.63E-05	0.53	3.06	-	343.0
AHQ-5-3, 7714	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.34E-07	0.78	3.39	-	437.3
AHQ-5-3, 6998 - 7079	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	7.93E-04	0.91	3.86	-	757.0
AHQ-5-3, 6670 - 6739	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.67E-06	0.90	3.44	-	769.4
AHQ-5-1, 6061	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	4.29E-08	0.88	3.65	-	580.8
AHQ-5-3, 6526 - 6602	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	3.77E-06	0.83	3.59	-	555.9
AHQ-5-3, 6367 - 6439	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	5.43E-04	0.94	4.50	-	900.1
AHQ-5-3, 6281 - 6350	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	7.48E-06	0.96	5.19	-	1032.5
AHQ-5-3, 6131 - 6210	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	6.29E-07	0.96	4.98	-	993.5
AHQ-5-1, 4624	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.21E-05	0.91	3.88	-	817.3
AHQ-5-4, 4644	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	3.05E-06	0.86	3.48	-	545.2
AHQ-5-1, 6240	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.11E-04	0.87	3.38	-	637.9
AHQ-5-3, 4626 - 4627	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.44E-05	0.93	4.03	-	796.7
AHQ-5-9, 4326	K.DDLWSIQNLGTK.L	1390.52332	1	1.99E-05	0.49	2.32	-	373.6
AHQ-5-1, 5089	K.DDLWSIQNLGTK.L	1390.52332	2	1.41E-06	0.93	4.03	-	962.5
AHQ-5-6, 4849 - 4853	K.DDLWSIQNLGTK.L	1390.52332	2	1.71E-04	0.88	3.16	-	983.9
AHQ-5-6, 4861	K.DDLWSIQNLGTK.L	1390.52332	1	1.11E-04	0.47	2.36	-	444.7
AHQ-5-3, 5073	K.DDLWSIQNLGTK.L	1390.52332	2	6.85E-07	0.94	4.11	-	931.9
AHQ-5-3, 5075	K.DDLWSIQNLGTK.L	1390.52332	1	2.59E-09	0.36	2.51	-	273.0
AHQ-5-3, 4763	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.01E-04	0.91	3.60	-	1257.8
AHQ-5-5, 4425 - 4438	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.60E-04	0.77	3.29	-	711.5
AHQ-5-3, 3323	K.EATSTFTNITYR.G	1404.50685	2	8.25E-06	0.70	3.21	-	507.9
AHQ-5-1, 3432	K.EATSTFTNITYR.G	1404.50685	2	4.68E-05	0.84	2.95	-	704.4
AHQ-5-3, 3255 - 3327	K.EATSTFTNITYR.G	1404.50685	2	1.06E-07	0.60	2.69	-	496.0
AHQ-5-3, 2258	R.FQYYEDSSGK.S	1224.25749	1	2.96E-05	0.65	2.56	-	516.9
AHQ-5-3, 2253 - 2281	R.FQYYEDSSGK.S	1224.25749	2	4.44E-04	0.58	2.92	-	384.1
AHQ-5-1, 3731 - 3733	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.50E-05	0.97	4.51	-	1993.2
AHQ-5-6, 3473	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.24E-04	0.82	3.35	-	908.9
AHQ-5-3, 3598 - 3677	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.11E-06	0.96	4.56	-	1759.3
AHQ-5-3, 3663 - 3743	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.61E-08	0.74	2.96	-	663.6
AHQ-5-2, 3669	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	3.44E-07	0.86	3.92	-	730.2
AHQ-5-3, 3831 - 3839	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.65E-05	0.92	4.06	-	966.6
AHQ-5-3, 3674	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	1.79E-06	0.88	3.83	-	843.0
AHQ-5-5, 3518	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	9.45E-06	0.90	3.39	-	1249.7
AHQ-5-4, 3638	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.61E-06	0.85	3.72	-	668.3
AHQ-5-4, 3646	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	9.04E-05	0.68	3.14	-	562.7
AHQ-5-3, 4798 - 4805	R.GKCECGSCVCIQPGSYGDTCEKCPTCPDACTFK.K	3900.25293	3	4.77E-06	0.92	5.02	-	756.6

AHQ-5-3, 4399 - 4405	R.GKCECGSCVCIQPGSYGDTCEKCPTCPDACTFKK.E	4028.42584	3	1.99E-04	0.87	4.46	-	769.6
AHQ-5-3, 1974 - 2043	K.GSGDSSQVTQVSPQR.I	1533.58302	2	8.68E-04	0.52	2.53	-	634.7
AHQ-5-3, 1765 - 1775	K.GSGDSSQVTQVSPQR.I	1533.58302	2	6.98E-05	0.65	2.95	-	759.5
AHQ-5-6, 1634	K.GSGDSSQVTQVSPQR.I	1533.58302	2	2.10E-04	0.71	3.02	-	701.7
AHQ-5-5, 1642	K.GSGDSSQVTQVSPQR.I	1533.58302	2	2.29E-04	0.78	3.04	-	798.8
AHQ-5-3, 2567	K.HVLTLTDQVTR.F	1283.45912	1	8.95E-06	0.76	3.43	-	334.9
AHQ-5-1, 2777	K.HVLTLTDQVTR.F	1283.45912	2	1.10E-04	0.85	3.26	-	546.1
AHQ-5-3, 2558 - 2629	K.HVLTLTDQVTR.F	1283.45912	2	7.05E-06	0.91	3.43	-	704.7
AHQ-5-3, 2447	K.HVLTLTDQVTR.F	1283.45912	2	6.72E-05	0.90	3.32	-	829.0
AHQ-5-4, 2553 - 2557	K.HVLTLTDQVTR.F	1283.45912	2	8.21E-06	0.95	3.95	-	890.4
AHQ-5-6, 2396 - 2400	K.HVLTLTDQVTR.F	1283.45912	2	3.45E-07	0.87	3.26	-	567.4
AHQ-5-6, 2405	K.HVLTLTDQVTR.F	1283.45912	1	2.01E-04	0.20	2.04	-	264.1
AHQ-5-7, 2356 - 2367	K.HVLTLTDQVTR.F	1283.45912	2	3.78E-04	0.90	3.30	-	743.5
AHQ-5-5, 2417	K.HVLTLTDQVTR.F	1283.45912	2	1.05E-05	0.88	3.26	-	605.3
AHQ-5-3, 5127	K.IGDTVSFSIEAK.V	1267.41009	2	9.80E-06	0.82	2.92	-	668.7
AHQ-5-3, 3657	K.ITGKYCECDDFSCVR.Y	1914.08378	2	1.46E-04	0.69	3.04	-	564.7
AHQ-5-3, 5517 - 5586	R.LAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEK.L	3997.35517	3	4.24E-04	0.92	5.30	-	574.6
AHQ-5-3, 3562	R.NDASHLLVFTTDAK.T	1532.67977	2	1.17E-05	0.92	3.75	-	961.1
AHQ-5-7, 3372 - 3442	R.NDASHLLVFTTDAK.T	1532.67977	2	2.89E-05	0.90	3.94	-	893.7
AHQ-5-5, 3506 - 3579	R.NDASHLLVFTTDAK.T	1532.67977	2	4.63E-09	0.95	3.90	-	1391.2
AHQ-5-6, 3458 - 3528	R.NDASHLLVFTTDAK.T	1532.67977	2	4.97E-10	0.95	4.03	-	1414.5
AHQ-5-3, 3782 - 3854	R.NDASHLLVFTTDAK.T	1532.67977	2	3.66E-07	0.96	4.59	-	1296.1
AHQ-5-3, 3873	R.NDASHLLVFTTDAK.T	1532.67977	3	3.99E-07	0.95	4.75	-	1166.7
AHQ-5-3, 4281 - 4351	R.NDASHLLVFTTDAK.T	1532.67977	2	2.03E-04	0.92	3.75	-	889.8
AHQ-5-1, 4019	R.NDASHLLVFTTDAK.T	1532.67977	2	1.10E-09	0.95	4.52	-	973.9
AHQ-5-1, 4525	R.NDASHLLVFTTDAK.T	1532.67977	2	1.26E-10	0.94	3.87	-	1222.4
AHQ-5-4, 3821 - 3828	R.NDASHLLVFTTDAK.T	1532.67977	2	3.41E-09	0.95	4.58	-	998.8
AHQ-5-4, 4401	R.NDASHLLVFTTDAK.T	1532.67977	2	4.17E-10	0.93	3.95	-	1033.2
AHQ-5-3, 4450	R.NDASHLLVFTTDAK.T	1532.67977	2	5.85E-06	0.94	4.17	-	1167.0
AHQ-5-2, 3161	K.SFTIKPVGFK.D	1124.35685	2	8.08E-04	0.79	2.61	-	1100.0
AHQ-5-5, 2961 - 2974	K.SFTIKPVGFK.D	1124.35685	2	3.52E-05	0.80	2.67	-	944.3
AHQ-5-3, 3231 - 3242	K.SFTIKPVGFK.D	1124.35685	2	4.59E-05	0.90	2.92	-	1367.6
AHQ-5-6, 3406 - 3456	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.94E-11	0.89	3.33	-	938.4
AHQ-5-4, 3682	R.TDTCMSSNGLLCSGR.G	1661.81786	2	5.76E-07	0.85	3.23	-	1418.4
AHQ-5-3, 2957 - 2967	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.32E-07	0.86	3.04	-	1032.5
AHQ-5-1, 3625	R.TDTCMSSNGLLCSGR.G	1661.81786	2	7.76E-09	0.94	3.80	-	1080.3
AHQ-5-1, 3723	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.54E-10	0.96	4.09	-	1569.0
AHQ-5-3, 2853 - 2854	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.50E-07	0.91	3.75	-	1026.9
AHQ-5-3, 3806	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.32E-08	0.68	2.71	-	772.1
AHQ-5-4, 3569 - 3580	R.TDTCMSSNGLLCSGR.G	1661.81786	2	4.42E-07	0.91	3.68	-	975.3
AHQ-5-4, 2854	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.34E-07	0.89	3.25	-	1037.4
AHQ-5-3, 3690 - 3766	R.TDTCMSSNGLLCSGR.G	1661.81786	2	3.84E-12	0.96	4.52	-	1444.8
AHQ-5-4, 2946	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.00E-06	0.72	2.66	-	590.2
AHQ-5-3, 1714 - 1783	R.VLEDRPLSDK.G	1172.31354	2	1.81E-05	0.92	3.58	-	962.1
AHQ-5-3, 2742	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	5.73E-08	0.93	4.30	-	1473.6
AHQ-5-3, 3265	K.WDTANNPLYK.E	1222.33111	2	4.25E-04	0.50	2.83	-	394.6
AHQ-5-5, 3669	K.YCECDDFSCVR.Y	1514.59674	2	2.63E-06	0.95	3.51	-	1383.1
AHQ-5-1, 3785	K.YCECDDFSCVR.Y	1514.59674	2	9.79E-06	0.87	3.01	-	847.2
AHQ-5-6, 3624	K.YCECDDFSCVR.Y	1514.59674	2	5.51E-05	0.91	3.38	-	986.7
AHQ-5-2, 3769	K.YCECDDFSCVR.Y	1514.59674	2	3.85E-06	0.95	3.57	-	1359.7
AHQ-5-4, 3732 - 3733	K.YCECDDFSCVR.Y	1514.59674	2	3.11E-05	0.89	3.06	-	1047.3
AHQ-5-3, 3749 - 3827	K.YCECDDFSCVR.Y	1514.59674	2	1.02E-07	0.95	4.05	-	1122.7
gi|10863927|ref|NP_066953.1| peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]				4.24E-12	6.48	80.27	30.90	18012.4
AHQ-5-12, 3108 - 3117	K.EGM*NIVEAMER.F	1295.46882	2	1.13E-04	0.66	2.85	-	397.8
AHQ-5-12, 4094 - 4096	K.EGMNIVEAMER.F	1279.46942	2	3.85E-05	0.85	3.58	-	569.1
AHQ-5-13, 4096	K.FEDENFILK.H	1155.28144	2	3.73E-04	0.71	2.95	-	526.2
AHQ-5-12, 3865 - 3929	K.FEDENFILK.H	1155.28144	2	1.15E-04	0.85	3.77	-	595.6
AHQ-5-12, 4005	K.FEDENFILK.H	1155.28144	2	3.34E-05	0.88	3.42	-	740.3
AHQ-5-13, 3478 - 3479	K.KITIADCGQLE	1249.41637	2	3.23E-04	0.74	3.19	-	822.2
AHQ-5-12, 3649	K.KITIADCGQLE	1249.41637	2	3.07E-04	0.80	3.46	-	952.1
AHQ-5-12, 3354	K.KITIADCGQLE	1249.41637	2	1.50E-04	0.63	3.14	-	709.4
AHQ-5-12, 4586 - 4660	K.SIYGEKFEDENFILK.H	1833.03047	2	2.10E-09	0.96	5.44	-	1177.6
AHQ-5-14-, 4618	K.SIYGEKFEDENFILK.H	1833.03047	2	8.72E-10	0.95	5.01	-	1008.2
AHQ-5-14, 5509 - 5578	K.SIYGEKFEDENFILK.H	1833.03047	2	2.17E-05	0.96	4.78	-	1265.7
AHQ-5-12, 4577 - 4648	K.SIYGEKFEDENFILK.H	1833.03047	2	5.46E-11	0.95	5.09	-	986.0
AHQ-5-12, 4712 - 4754	K.SIYGEKFEDENFILK.H	1833.03047	2	4.24E-12	0.93	3.61	-	1364.6
AHQ-5-12, 2830	K.VKEGM*NIVEAMER.F	1522.77330	2	1.59E-04	0.79	3.44	-	780.7
AHQ-5-12, 4366	R.VSFELFADK.V	1056.19300	1	1.63E-04	0.68	2.50	-	633.7
AHQ-5-12, 4457	R.VSFELFADK.V	1056.19300	2	4.87E-06	0.87	3.36	-	1007.7
AHQ-5-12, 4297	R.VSFELFADKVPK.T	1380.61317	2	3.23E-07	0.87	3.59	-	884.1
AHQ-5-12, 4508	R.VSFELFADKVPK.T	1380.61317	2	8.97E-07	0.78	3.09	-	619.0
AHQ-5-12, 4593	R.VSFELFADKVPK.T	1380.61317	2	6.83E-06	0.88	3.42	-	887.1
gi|4504391|ref|NP_000179.1| hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]				5.30E-12	9.37	110.26	15.50	102502.4
AHQ-5-4, 6348	R.AILQQLGLNSTCDDSILVK.T	2090.38419	2	3.02E-04	0.82	3.65	-	493.6
AHQ-5-4, 4480	K.ATDCVGHDVVTLLR.D	1557.75406	2	9.80E-11	0.95	4.49	-	1132.5
AHQ-5-5, 4270	K.ATDCVGHDVVTLLR.D	1557.75406	2	2.93E-10	0.84	2.99	-	807.3
AHQ-5-4, 2654	K.FLSQIESDR.L	1095.18763	1	8.09E-05	0.19	2.15	-	210.2
AHQ-5-4, 3182	K.GAALITAVGVR.L	1028.23070	2	3.91E-05	0.97	3.98	-	2304.5
AHQ-5-4, 5665 - 5734	K.GDFIALDLGGSSFR.I	1455.59700	1	2.65E-05	0.44	2.04	-	372.0
AHQ-5-4, 5733	K.GDFIALDLGGSSFR.I	1455.59700	2	1.01E-09	0.98	5.26	-	2163.5
AHQ-5-4, 2142 - 2222	R.HIDLVEGDEGR.M	1240.30483	2	2.21E-08	0.94	4.03	-	992.3
AHQ-5-4, 5512	K.KLPVGFTFSFPCQQSK.I	1873.16425	2	5.46E-04	0.94	4.54	-	893.5
AHQ-5-4, 6100	K.LPVGFTFSFPCQQSK.I	1744.99134	2	1.15E-06	0.96	4.42	-	1131.2
AHQ-5-4, 5928	R.LSDETLIDIMTR.F	1407.61560	2	7.51E-06	0.81	2.59	-	1195.8
AHQ-5-4, 7377	R.SANLVAATLGAILNR.L	1484.72615	2	3.37E-04	0.88	3.27	-	1091.4
AHQ-5-4, 6316 - 6380	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	5.30E-12	0.94	4.37	-	925.6
gi|17921989|ref|NP_005991.1| tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain				5.96E-12	13.18	160.26	42.90	49924.1
AHQ-5-13-, 5135 - 5143	R.AFVHWYVGEGMEEGEFSEAR.E	2331.50495	3	6.39E-04	0.94	4.66	-	1308.2
AHQ-5-7, 5892 - 5967	R.AFVHWYVGEGMEEGEFSEAR.E	2331.50495	2	5.44E-04	0.85	2.86	-	909.1
AHQ-5-12, 5165	R.AFVHWYVGEGMEEGEFSEAR.E	2331.50495	2	3.95E-05	0.91	3.65	-	1027.6
AHQ-5-13-, 5183 - 5188	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	9.37E-08	0.96	4.70	-	1534.6
AHQ-5-13-, 6009 - 6076	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.16E-08	0.94	4.51	-	1185.1
AHQ-5-7, 6054 - 6128	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.61E-05	0.83	3.39	-	785.3
AHQ-5-14-, 5142	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	3.53E-08	0.92	3.96	-	1293.1
AHQ-5-7, 6712 - 6778	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	7.65E-05	0.37	2.67	-	511.5
AHQ-5-13, 6194 - 6266	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	6.74E-04	0.94	4.47	-	1122.7
AHQ-5-13, 6113	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	6.56E-06	0.93	3.94	-	1240.7
AHQ-5-7, 6847 - 6884	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.02E-06	0.67	3.67	-	189.9
AHQ-5-13, 5537	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	5.96E-12	0.95	4.00	-	1391.9
AHQ-5-13, 5222 - 5296	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.07E-05	0.94	3.98	-	1368.7
AHQ-5-7, 5078 - 5151	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.50E-04	0.96	4.06	-	1700.3
AHQ-5-12, 5786	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.39E-04	0.45	2.67	-	396.6
AHQ-5-12, 5466 - 5532	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	7.77E-05	0.68	2.98	-	521.3
AHQ-5-7, 6198 - 6267	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.46E-04	0.92	4.28	-	1201.4
AHQ-5-12, 6032 - 6102	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	2.44E-07	0.92	4.66	-	1091.8
AHQ-5-14-, 5937	R.AVFVDLEPTVIDEIR.N	1716.95615	2	9.29E-06	0.85	2.82	-	1530.2
AHQ-5-13-, 6028 - 6037	R.AVFVDLEPTVIDEIR.N	1716.95615	2	7.06E-11	0.93	3.84	-	1587.1

AHQ-5-12, 6064	R.AVFVDLEPTVIDEIR.N	1716.95615	2	2.12E-05	0.90	2.93	-	1802.6
AHQ-5-7, 5995 - 6070	R.AVFVDLEPTVIDEIR.N	1716.95615	2	7.96E-09	0.95	4.47	-	1643.1
AHQ-5-6, 6205	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.55E-05	0.86	3.25	-	1367.8
AHQ-5-3, 6483	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.21E-06	0.75	3.04	-	987.3
AHQ-5-11, 5891	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.00E-05	0.82	3.18	-	968.6
AHQ-5-10, 5583 - 5591	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.46E-06	0.84	3.39	-	1061.4
AHQ-5-7, 4972	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	4.97E-06	0.92	4.28	-	778.7
AHQ-5-7, 5888	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	8.04E-06	0.95	4.50	-	1068.2
AHQ-5-7, 6552 - 6624	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	5.98E-04	0.76	3.31	-	677.9
AHQ-5-7, 5152 - 5168	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	8.96E-06	0.92	3.61	-	1323.7
AHQ-5-12, 3012	K.DVNAAIAAIK.T	986.14745	1	3.79E-06	0.80	2.66	-	1019.9
AHQ-5-7, 2886	K.DVNAAIAAIK.T	986.14745	1	2.70E-06	0.79	2.57	-	909.2
AHQ-5-8, 2970	K.DVNAAIAAIK.T	986.14745	1	4.91E-04	0.29	2.00	-	249.4
AHQ-5-5, 3282	K.DVNAAIAAIK.T	986.14745	1	5.36E-04	0.08	1.93	-	329.4
AHQ-5-12, 3348	K.DVNAAIAAIK.T	986.14745	2	1.50E-04	0.93	3.71	-	1092.8
AHQ-5-7, 3335	K.DVNAAIAAIK.T	986.14745	1	3.92E-05	0.80	2.91	-	757.0
AHQ-5-12, 3338 - 3349	K.DVNAAIAAIK.T	986.14745	1	4.00E-05	0.84	2.83	-	1003.8
AHQ-5-7, 3226 - 3248	K.EIIDPVLDR.I	1070.22122	2	1.74E-04	0.68	2.62	-	438.7
AHQ-5-9, 2916 - 2983	K.FDLMYAK.R	888.06574	1	9.39E-04	0.25	1.85	-	445.0
AHQ-5-13, 3514	K.FDLMYAK.R	888.06574	2	7.74E-04	0.79	2.90	-	813.6
AHQ-5-13-, 3404	K.FDLMYAK.R	888.06574	2	6.24E-04	0.80	2.66	-	833.8
AHQ-5-1, 5417	R.IHFPLATYAPVISAEK.A	1758.05310	2	2.75E-05	0.91	3.81	-	597.3
AHQ-5-6, 5017	R.IHFPLATYAPVISAEK.A	1758.05310	2	2.81E-04	0.90	3.40	-	852.5
AHQ-5-4, 5262	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.15E-06	0.91	3.99	-	583.6
AHQ-5-7, 4595 - 4670	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.19E-08	0.96	5.03	-	801.1
AHQ-5-7, 4708 - 4778	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.96E-04	0.94	4.12	-	754.9
AHQ-5-11, 4891 - 4956	R.IHFPLATYAPVISAEK.A	1758.05310	2	8.70E-05	0.90	3.61	-	631.3
AHQ-5-3, 5293 - 5314	R.IHFPLATYAPVISAEK.A	1758.05310	2	8.95E-05	0.93	4.00	-	653.3
AHQ-5-10, 4547 - 4608	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.69E-05	0.94	4.17	-	750.4
AHQ-5-9, 4423 - 4496	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.29E-08	0.88	3.98	-	508.8
AHQ-5-9, 4390	R.IHFPLATYAPVISAEK.A	1758.05310	2	6.92E-06	0.87	3.42	-	583.6
AHQ-5-6, 4934 - 5004	R.IHFPLATYAPVISAEK.A	1758.05310	2	5.35E-04	0.90	3.99	-	607.0
AHQ-5-8, 6701	R.LISQIVSSITASLR.F	1488.75471	2	2.50E-07	0.92	3.51	-	977.9
AHQ-5-7, 5786	R.LISQIVSSITASLR.F	1488.75471	2	3.61E-07	0.87	2.98	-	976.2
AHQ-5-7, 6818 - 6883	R.LISQIVSSITASLR.F	1488.75471	2	8.91E-09	0.97	5.19	-	1386.7
AHQ-5-7, 6947 - 7012	R.LISQIVSSITASLR.F	1488.75471	2	1.04E-08	0.94	4.60	-	908.7
AHQ-5-10, 6248	R.LISQIVSSITASLR.F	1488.75471	2	1.26E-04	0.90	3.33	-	1098.1
AHQ-5-7, 7164	R.LISQIVSSITASLR.F	1488.75471	2	2.67E-05	0.96	4.63	-	1260.7
AHQ-5-7, 7074	R.LISQIVSSITASLR.F	1488.75471	2	1.87E-07	0.94	3.76	-	1359.1
AHQ-5-9, 6114 - 6172	R.LISQIVSSITASLR.F	1488.75471	2	1.15E-06	0.94	3.76	-	1146.7
AHQ-5-5, 3271	R.NLDIERPTYTNLNR.L	1719.88022	2	5.37E-07	0.78	2.92	-	674.6
AHQ-5-7, 3098 - 3166	R.NLDIERPTYTNLNR.L	1719.88022	2	2.59E-06	0.42	2.95	-	267.8
AHQ-5-9, 2959 - 2966	R.NLDIERPTYTNLNR.L	1719.88022	2	1.22E-07	0.59	3.39	-	354.7
AHQ-5-8, 2892	R.NLDIERPTYTNLNR.L	1719.88022	2	5.16E-06	0.51	3.14	-	355.6
AHQ-5-13, 3545 - 3547	R.NLDIERPTYTNLNR.L	1719.88022	2	2.21E-04	0.68	2.93	-	460.1
AHQ-5-14, 4253	R.NLDIERPTYTNLNR.L	1719.88022	2	3.77E-05	0.67	3.30	-	269.0
AHQ-5-13, 5741	R.SIQFVDWCPTGFK.V	1586.79232	2	8.13E-04	0.77	2.60	-	850.0
AHQ-5-12, 5713	R.SIQFVDWCPTGFK.V	1586.79232	2	5.31E-04	0.93	4.12	-	878.1
AHQ-5-13-, 5629 - 5631	R.SIQFVDWCPTGFK.V	1586.79232	2	2.29E-08	0.95	4.27	-	1094.8
AHQ-5-4, 5992	R.SIQFVDWCPTGFK.V	1586.79232	2	2.18E-04	0.93	3.84	-	1002.6
AHQ-5-7, 5534 - 5603	R.SIQFVDWCPTGFK.V	1586.79232	2	3.08E-06	0.96	4.87	-	972.2
AHQ-5-3, 6057	R.SIQFVDWCPTGFK.V	1586.79232	2	2.42E-04	0.89	3.68	-	778.1
AHQ-5-7, 5818 - 5898	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.10E-08	0.87	3.94	-	530.2
AHQ-5-14, 6268	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	5.60E-08	0.61	2.85	-	448.0
AHQ-5-7, 6068	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.85E-06	0.61	2.96	-	363.6
AHQ-5-13-, 5543 - 5577	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	8.51E-07	0.59	3.03	-	376.2
AHQ-5-12, 5681	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	7.78E-09	0.90	4.02	-	751.7
AHQ-5-12, 5688	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.58E-06	0.81	3.42	-	592.4
AHQ-5-3, 6005	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	6.40E-08	0.83	3.73	-	480.9
AHQ-5-7, 5734	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	7.44E-08	0.74	3.38	-	378.9
AHQ-5-1, 6028 - 6029	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	6.86E-08	0.81	3.73	-	480.4
AHQ-5-9, 5100 - 5170	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.27E-05	0.64	2.93	-	393.2
AHQ-5-6, 5720 - 5765	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.36E-09	0.86	3.74	-	556.1
AHQ-5-14-, 5549	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	6.09E-09	0.77	3.52	-	486.0
AHQ-5-7, 5596 - 5666	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.96E-09	0.84	3.71	-	513.4
AHQ-5-13, 5621 - 5696	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	4.83E-07	0.83	3.66	-	528.1
AHQ-5-7, 6371	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	9.57E-06	0.50	2.96	-	268.8
AHQ-5-7, 5724 - 5802	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.42E-08	0.94	4.69	-	796.0
AHQ-5-13, 4488 - 4562	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	7.32E-07	0.78	3.72	-	316.2
AHQ-5-13, 4404 - 4420	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.98E-04	0.45	2.72	-	276.1
AHQ-5-9, 4064	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.52E-04	0.54	2.86	-	195.9
AHQ-5-7, 4140 - 4210	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	5.31E-06	0.72	3.18	-	320.4
AHQ-5-7, 4238 - 4306	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	5.11E-06	0.43	2.81	-	285.2
AHQ-5-12, 4532	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.64E-05	0.63	2.81	-	406.6
AHQ-5-10, 3959 - 4026	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.27E-05	0.88	4.22	-	398.6
AHQ-5-13-, 4321 - 4387	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.44E-04	0.83	3.62	-	458.1
AHQ-5-13-, 4408	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.27E-05	0.57	2.72	-	354.6
AHQ-5-4, 4553 - 4625	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	6.60E-05	0.79	4.02	-	287.2
AHQ-5-12, 4397 - 4464	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	9.78E-07	0.50	2.55	-	303.9
AHQ-5-14-, 4333	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.32E-05	0.57	2.62	-	351.5
AHQ-5-11, 4236 - 4316	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	5.35E-06	0.61	3.10	-	336.6
AHQ-5-7, 4374 - 4375	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.70E-07	0.76	3.25	-	384.0
AHQ-5-12, 3945	K.YM*ACCLLYR.G	1268.50804	2	1.03E-05	0.81	2.55	-	592.8
AHQ-5-12, 4433	K.YMACCLLYR.G	1252.50864	2	8.31E-06	0.95	3.59	-	1194.5
AHQ-5-7, 3746 - 3748	K.YM*ACCLLYR.G	1268.50804	2	1.18E-06	0.74	2.95	-	472.3
AHQ-5-7, 4254	K.YMACCLLYR.G	1252.50864	2	3.38E-05	0.96	3.70	-	1335.7
AHQ-5-7, 4256	K.YMACCLLYR.G	1252.50864	1	2.46E-06	0.43	2.67	-	177.2
gi|4503327|ref|NP_000389.1| cytochrome b5 reductase membrane-bound isoform; diaphorase (NADH) [Homo				6.03E-12	7.91	100.30	49.50	34234.6
AHQ-5-9, 3924	R.AIMKDPDDHTVCHLLFANQTEK.D	2585.89793	3	2.46E-07	0.92	4.36	-	1114.6
AHQ-5-9, 4999 - 5067	R.APEAWDYGQGFVNEEMIR.D	2113.29517	2	5.71E-04	0.93	4.39	-	848.7
AHQ-5-9, 4182 - 4194	K.DILLRPELEELR.N	1496.73370	2	1.68E-08	0.77	3.27	-	659.3
AHQ-5-11, 4668	K.DILLRPELEELR.N	1496.73370	2	1.43E-05	0.77	3.07	-	819.7
AHQ-5-9, 5380	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	2	8.26E-07	0.87	3.60	-	813.6
AHQ-5-9, 5383 - 5386	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	3	6.03E-12	0.96	6.04	-	1083.9
AHQ-5-9, 2616	R.GPSGLLVYQGK.G	1119.29547	2	2.87E-05	0.94	3.69	-	1186.7
AHQ-5-9, 2619	R.GPSGLLVYQGK.G	1119.29547	1	3.19E-07	0.62	3.04	-	385.9
AHQ-5-9, 5284 - 5354	R.IDGNLVVRPYTPISSDDDKGFVDLVIK.V	2977.35765	3	7.91E-07	0.91	4.97	-	1093.2
AHQ-5-9, 3203	R.STPAITLESPDIK.Y	1372.54621	1	1.82E-05	0.51	2.80	-	378.8
AHQ-5-9, 4044	R.STPAITLESPDIKYPLR.L	1902.18061	2	8.24E-09	0.83	3.85	-	455.3
AHQ-5-9, 4467 - 4492	K.SVGMIAGGTGITPM*LQVIR.A	1918.31483	2	2.14E-05	0.77	3.59	-	492.6
AHQ-5-9, 5238	K.SVGMIAGGTGITPMLQVIR.A	1902.31543	2	3.79E-04	0.68	3.45	-	446.9
gi|4505257|ref|NP_002435.1| moesin [Homo sapiens]				6.53E-12	9.00	100.27	24.80	67819.5
AHQ-5-6, 2304	K.ALTSELANAR.D	1046.15975	2	4.21E-05	0.90	3.86	-	756.8
AHQ-5-6, 2186	K.ALTSELANARDESK.K	1505.61272	2	1.62E-07	0.93	3.92	-	1097.7
AHQ-5-6, 2100	K.AQMVQEDLEK.T	1191.33713	2	1.71E-05	0.76	2.94	-	622.5
AHQ-5-13, 6840	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	3	8.55E-07	0.75	3.49	-	799.5
AHQ-5-14-, 5867 - 5906	R.EVWFFGLQYQDTK.G	1661.83760	2	1.03E-05	0.96	4.31	-	1198.2

AHQ-5-13-, 6733	K.FYPEDVSEELIQDITQR.L	2083.24065	2	8.87E-04	0.91	3.80	-	704.5
AHQ-5-9, 6384	K.FYPEDVSEELIQDITQR.L	2083.24065	2	7.38E-06	0.85	3.19	-	984.2
AHQ-5-6, 7184	K.FYPEDVSEELIQDITQR.L	2083.24065	2	4.10E-08	0.95	4.56	-	1026.6
AHQ-5-6, 7193	K.FYPEDVSEELIQDITQR.L	2083.24065	3	5.95E-09	0.89	4.39	-	791.5
AHQ-5-7, 7179	K.FYPEDVSEELIQDITQR.L	2083.24065	2	3.50E-06	0.95	4.52	-	1101.6
AHQ-5-6, 5517 - 5518	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	5.57E-07	0.97	5.02	-	1726.5
AHQ-5-6, 4521	K.KTQEQLALEMAELTAR.I	1833.10018	2	1.86E-05	0.97	5.09	-	1650.5
AHQ-5-6, 3308 - 3377	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	6.53E-12	0.89	4.77	-	1071.0
AHQ-5-6, 3446 - 3518	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	4.51E-08	0.95	5.41	-	1485.2
AHQ-5-6, 5212	K.TQEQLALEMAELTAR.I	1704.92727	2	8.60E-08	0.98	5.10	-	2109.8
gi|4507521|ref|NP_001055.1| transketolase [Homo sapiens]				6.89E-12	1.76	20.24	5.90	67877.3
AHQ-5-6, 4608	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	6.89E-12	0.93	4.45	-	510.9
AHQ-5-6, 4630	K.ILATPPQEDAPSVDIANIR.M	2021.26036	3	4.74E-04	0.95	4.85	-	1428.5
AHQ-5-6, 3304	R.LGQSDPAPLQHQMDIYQK.R	2070.31497	2	2.81E-04	0.83	3.40	-	655.0
gi|5901944|ref|NP_008977.1| elastin microfibril interface located protein; TNF? elastin microfibril				7.40E-12	5.48	60.24	11.20	106694.7
AHQ-5-3, 3559 - 3561	R.APAPASAPPGPSEELLR.Q	1660.85268	2	2.85E-06	0.86	3.83	-	426.8
AHQ-5-4, 2985	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	7.16E-04	0.89	3.87	-	900.7
AHQ-5-3, 3029 - 3030	R.GTELGGAAGQGGHPPGYTSLASR.L	2142.27464	2	2.95E-07	0.91	4.86	-	447.6
AHQ-5-3, 3622	R.LDTVAGGLQGLR.E	1200.37012	2	8.17E-07	0.96	3.96	-	1518.0
AHQ-5-3, 2763	R.LVGSGLHTVEAAGEAR.Q	1567.72888	2	7.40E-12	0.96	4.21	-	1474.1
AHQ-5-3, 3705	R.PARPNLSGSSAGSPLSGLGGEGPGESEK.V	2596.74928	3	3.91E-06	0.91	4.56	-	862.7
gi|4506925|ref|NP_003013.1| SH3 domain binding glutamic acid-rich protein like; SH3-binding domain				7.51E-12	3.81	40.32	58.80	12774.2
AHQ-5-14-, 5898	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.07E-06	0.76	3.64	-	554.3
AHQ-5-13-, 5967 - 6031	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.45E-07	0.96	4.87	-	955.3
AHQ-5-13, 6293 - 6352	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	7.35E-07	0.82	3.20	-	802.5
AHQ-5-13, 6132 - 6204	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.65E-05	0.85	3.54	-	667.3
AHQ-5-13, 6048 - 6116	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	9.81E-06	0.87	4.08	-	502.5
AHQ-5-13-, 6219 - 6265	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.24E-05	0.92	4.05	-	869.8
AHQ-5-13, 4978 - 5048	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.23E-08	0.94	5.29	-	1090.6
AHQ-5-13-, 4904 - 4927	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.30E-05	0.96	5.63	-	1475.3
AHQ-5-13-, 4983 - 5056	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	7.51E-12	0.97	6.47	-	1372.2
AHQ-5-13-, 5119	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.44E-06	0.92	5.14	-	863.6
AHQ-5-13, 5074 - 5148	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	4.42E-07	0.93	4.75	-	1054.2
AHQ-5-13, 4204 - 4224	R.GDYDAFFEAR.E	1191.23073	2	4.43E-06	0.93	3.67	-	1071.9
AHQ-5-13-, 2352	R.VYIASSSGSTAIK.K	1284.44065	2	1.98E-05	0.95	3.77	-	1958.1
AHQ-5-13, 2515	R.VYIASSSGSTAIK.K	1284.44065	2	8.48E-05	0.93	3.24	-	1739.2
gi|5803149|ref|NP_006806.1| coated vesicle membrane protein [Homo sapiens]				7.70E-12	0.96	10.29	13.90	22761.1
AHQ-5-11, 6806	K.GQDMETEAHQNKLEEMINELAVAMTAVK.H	3132.53686	3	7.70E-12	0.96	5.72	-	1296.5
gi|21361456|ref|NP_055425.2| alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph				7.77E-12	3.63	40.24	6.80	109437.2
AHQ-5-5, 4742	R.FGAVWTGDNTAEWDHLK.I	1948.08335	2	1.76E-05	0.86	3.75	-	616.4
AHQ-5-5, 4335 - 4339	R.LSFQHDPETSVLVLR.K	1741.96893	2	1.35E-08	0.87	4.15	-	625.0
AHQ-5-4, 3810	K.MMDYLQGSGETPQTDVR.W	1929.12196	2	7.72E-06	0.95	4.85	-	1065.2
AHQ-5-4, 3889 - 3892	R.VVIIGAGKPAAVVLQTK.G	1665.05702	2	7.77E-12	0.95	4.89	-	834.6
gi|27500274|ref|XP_113950.3| similar to Munc13-4 protein [Homo sapiens]				8.47E-12	10.78	120.30	20.00	123281.1
AHQ-5-5, 7534 - 7535	K.AFGELCPNTAPLPQLVTEALQTGTTEWFHLK.Q	3472.91108	3	9.44E-06	0.90	4.62	-	549.5
AHQ-5-4, 7580	K.AFGELCPNTAPLPQLVTEALQTGTTEWFHLK.Q	3472.91108	3	3.62E-11	0.77	3.68	-	435.4
AHQ-5-4, 7380	K.ALLGLVQDVIGDLHQCQR.T	2037.32944	3	1.96E-06	0.94	4.14	-	1451.7
AHQ-5-4, 6566	R.ALLYEDALYTVLHR.L	1677.92484	2	5.04E-11	0.96	4.13	-	1562.2
AHQ-5-4, 4698	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	7.71E-10	0.97	5.91	-	1806.4
AHQ-5-4, 3498	K.LGELTDLHGLR.R	1224.39168	2	6.08E-04	0.85	3.32	-	1018.9
AHQ-5-4, 3052	R.LGHPEPNHVTEASELLR.Y	1900.08490	2	1.68E-04	0.80	3.46	-	615.6
AHQ-5-4, 5568	K.LPAQLAWEALEQR.V	1525.73360	2	8.47E-12	0.98	5.03	-	1641.8
AHQ-5-6, 5290	K.LPAQLAWEALEQR.V	1525.73360	2	4.23E-04	0.85	3.12	-	713.5
AHQ-5-4, 7426 - 7444	R.LPLTYPAPNGDPILQLLEGR.K	2178.51621	2	1.58E-05	0.87	4.19	-	537.7
AHQ-5-4, 4126	R.SVFPLSVSDSPAR.L	1362.51311	2	9.69E-08	0.88	3.13	-	925.5
AHQ-5-4, 7293	R.VGAVLEQGQLQNTLHAQLQSALAGLGHEIR.T	3153.54178	3	3.07E-06	0.96	5.80	-	1738.5
AHQ-5-4, 6384	R.WFQPAIPSWLQK.T	1501.75533	2	1.80E-07	0.83	3.17	-	505.1
AHQ-5-4, 3401 - 3424	R.YLQEAFHVEPEEHQQTLQR.V	2383.56113	3	2.47E-08	0.97	5.80	-	1823.5
gi|7706497|ref|NP_057392.1| UMP-CMP kinase [Homo sapiens]				1.05E-11	3.98	50.22	26.80	25854.7
AHQ-5-11, 5955 - 5980	R.IQTYLQSTKPIIDLYEEMGK.V	2371.73502	2	2.48E-06	0.91	4.29	-	645.1
AHQ-5-11, 5062	R.IQTYLQSTKPIIDLYEEM*GK.V	2387.73442	2	9.10E-04	0.35	2.54	-	224.1
AHQ-5-11, 2496	R.KNPDSQYGELIEK.Y	1521.65375	2	1.42E-04	0.93	4.09	-	814.1
AHQ-5-14-, 6794	K.SVDEVFDEVVQIFDK.E	1769.92954	2	1.35E-04	0.83	3.50	-	652.6
AHQ-5-11, 3660	K.YGYTHLSAGELLR.D	1480.64969	2	1.05E-11	0.96	4.42	-	1248.7
gi|4759082|ref|NP_004648.1| serum deprivation response protein; serum deprivation response; phospha				1.25E-11	4.12	60.26	24.20	47172.9
AHQ-5-9, 5798 - 5855	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	7.58E-04	0.94	4.31	-	1346.6
AHQ-5-11, 6162 - 6168	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	9.70E-10	0.96	4.74	-	1355.4
AHQ-5-13, 6369	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	7.70E-07	0.97	4.81	-	1623.7
AHQ-5-6, 6524 - 6532	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	3.77E-04	0.91	3.67	-	1018.8
AHQ-5-7, 6416	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	8.80E-06	0.94	3.53	-	1327.5
AHQ-5-12, 6344 - 6356	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.46E-04	0.95	4.39	-	1261.8
AHQ-5-10, 5868	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.82E-07	0.96	4.38	-	1478.7
AHQ-5-9, 5683 - 5742	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	3.60E-06	0.95	3.66	-	1468.6
AHQ-5-11, 1895	R.LENNHAQLLR.R	1208.35234	1	4.66E-08	0.10	2.22	-	153.0
AHQ-5-12, 3470	K.LVNMLDAVQENQHK.M	1639.85851	2	3.91E-08	0.49	2.89	-	369.9
AHQ-5-9, 3767	R.QEKPSSPSPMPSSTPSPSLNLGNTEEAIR.D	3040.30937	3	6.54E-05	0.89	4.24	-	1127.0
AHQ-5-13-, 3355	R.SDGDPVQPAVLQVHQTS	1778.90130	2	1.84E-04	0.63	2.71	-	541.9
AHQ-5-6, 3221	R.SDGDPVQPAVLQVHQTS	1778.90130	2	1.13E-07	0.73	3.18	-	676.1
AHQ-5-11, 5876 - 5922	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.60E-09	0.96	5.28	-	1059.5
AHQ-5-9, 5706 - 5766	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.23E-04	0.90	4.00	-	739.8
AHQ-5-9, 5463 - 5522	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.25E-11	0.96	5.22	-	1103.5
AHQ-5-8, 5968 - 5970	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.25E-06	0.96	5.15	-	1028.6
AHQ-5-13, 6126 - 6130	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.18E-04	0.94	4.78	-	818.9
AHQ-5-6, 6248	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.55E-06	0.95	4.59	-	993.6
AHQ-5-4, 6510	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.33E-05	0.76	2.91	-	771.2
AHQ-5-10, 5618 - 5619	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.89E-04	0.93	4.30	-	712.2
AHQ-5-14-, 5977	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.86E-04	0.92	4.30	-	766.8
gi|30159310|ref|XP_301899.1| similar to beta-actin [Homo sapiens]				1.27E-11	1.45	20.17	9.20	32376.4
AHQ-5-5, 1498	K.DSYVGNEAQSK.R	1198.22158	1	1.11E-05	0.41	2.20	-	330.1
AHQ-5-8, 1418 - 1882	K.DSYVGNEAQSK.R	1198.22158	1	1.07E-09	0.65	2.69	-	374.0
AHQ-5-8, 1453 - 1522	K.DSYVGNEAQSK.R	1198.22158	2	4.67E-05	0.80	3.15	-	731.9
AHQ-5-8, 1593 - 1658	K.DSYVGNEAQSK.R	1198.22158	2	5.12E-05	0.76	3.38	-	577.3
AHQ-5-8, 1736 - 1789	K.DSYVGNEAQSK.R	1198.22158	2	3.28E-05	0.80	2.99	-	730.6
AHQ-5-12, 1866	K.DSYVGNEAQSK.R	1198.22158	1	1.27E-05	0.32	2.17	-	407.9
AHQ-5-13, 1917	K.DSYVGNEAQSK.R	1198.22158	1	1.27E-11	0.58	2.51	-	371.7
AHQ-5-12, 1669	K.DSYVGNEAQSK.R	1198.22158	2	5.75E-06	0.83	3.19	-	960.9
AHQ-5-12, 1596 - 1652	K.DSYVGNEAQSK.R	1198.22158	1	4.18E-07	0.50	2.43	-	373.2
AHQ-5-8, 4160 - 4169	K.SYKLLDGQVITIGNER.F	1807.04092	2	4.49E-05	0.56	2.61	-	396.0
AHQ-5-8, 4414	K.SYKLLDGQVITIGNER.F	1807.04092	2	2.25E-09	0.87	3.45	-	936.7
AHQ-5-8, 4504 - 4580	K.SYKLLDGQVITIGNER.F	1807.04092	2	9.31E-04	0.77	3.13	-	674.0
gi|4505763|ref|NP_000282.1| phosphoglycerate kinase 1 [Homo sapiens]				1.28E-11	5.95	70.28	29.70	44614.4
AHQ-5-8, 5461	K.ACANPAAGSVILLENLR.F	1771.03187	2	3.36E-05	0.92	4.26	-	830.7
AHQ-5-9, 5196	K.ACANPAAGSVILLENLR.F	1771.03187	2	2.53E-06	0.91	4.32	-	770.0
AHQ-5-11, 5656	K.ACANPAAGSVILLENLR.F	1771.03187	2	1.55E-06	0.96	4.68	-	1542.6
AHQ-5-8, 2086	R.AHSSMVGVNLPQK.A	1368.58752	2	9.77E-08	0.95	4.20	-	1388.4
AHQ-5-8, 2085	R.AHSSMVGVNLPQK.A	1368.58752	1	1.23E-05	0.61	2.24	-	611.8
AHQ-5-8, 4842	K.ALESPERPFLAILGGAK.V	1770.06542	2	1.30E-07	0.97	5.53	-	1398.5

AHQ-5-10, 4863	K.ALESPERPFLAILGGAK.V	1770.06542	2	1.28E-11	0.94	4.97	-	922.5
AHQ-5-9, 4691 - 4700	K.ALESPERPFLAILGGAK.V	1770.06542	2	1.90E-04	0.97	5.59	-	1795.3
AHQ-5-10, 4279	K.DVLFLKDCVGPEVEK.A	1750.00620	2	4.95E-04	0.85	4.01	-	577.0
AHQ-5-8, 4382 - 4390	K.DVLFLKDCVGPEVEK.A	1750.00620	2	1.69E-04	0.91	3.87	-	1066.8
AHQ-5-8, 5114	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	3.32E-08	0.65	3.09	-	414.7
AHQ-5-11, 5218	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	1.21E-06	0.71	3.50	-	387.0
AHQ-5-8, 4448	K.TGQATVASGIPAGWMGLDCGPESSKK.Y	2607.90190	2	9.88E-08	0.85	4.21	-	247.0
AHQ-5-8, 4453	K.TGQATVASGIPAGWMGLDCGPESSKK.Y	2607.90190	3	5.51E-05	0.85	3.69	-	739.0
AHQ-5-8, 4853	K.VLNNMEIGTSLFDEEGAK.I	1968.17459	2	9.04E-04	0.89	3.89	-	657.1
AHQ-5-8, 5105	K.VLNNMEIGTSLFDEEGAK.I	1968.17459	2	6.12E-07	0.70	2.83	-	470.1
gi|10880136|ref|NP_004032.2| arrestin beta 1 isoform A [Homo sapiens]				1.29E-11	2.61	30.25	13.40	47065.3
AHQ-5-7, 7194 - 7206	R.DFVDHIDLVDPVDGVVLVDPEYLK.E	2713.03129	2	3.39E-05	0.94	4.99	-	791.4
AHQ-5-7, 2178	K.VQYAPERPGPQPTAETTR.Q	1999.17334	2	5.44E-04	0.72	3.22	-	372.5
AHQ-5-7, 5124	R.YGREDLDVLGLTFR.K	1654.84814	2	1.29E-11	0.95	4.35	-	1541.7
gi|14149734|ref|NP_065174.1| coronin, actin binding protein, 1B [Homo sapiens]				1.55E-11	1.71	20.24	8.20	54234.4
AHQ-5-6, 2838	R.KCEPIVMTVPR.K	1331.63039	2	7.42E-06	0.76	2.71	-	628.1
AHQ-5-6, 7010 - 7088	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	1.55E-11	0.95	4.76	-	1344.2
gi|4507877|ref|NP_003364.1| vinculin isoform VCL [Homo sapiens]				1.69E-11	50.38	600.33	48.30	116721.6
AHQ-5-14-, 6807	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.30E-10	0.96	5.28	-	960.1
AHQ-5-4, 7508 - 7509	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.36E-09	0.97	5.52	-	1179.8
AHQ-5-13-, 6856	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.69E-11	0.97	5.35	-	1072.4
AHQ-5-5, 7302 - 7377	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.19E-05	0.87	3.39	-	669.1
AHQ-5-12, 7100	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.23E-07	0.96	5.10	-	1025.1
AHQ-5-5, 7453	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.36E-07	0.97	5.34	-	1206.0
AHQ-5-11, 6864	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.52E-07	0.97	5.36	-	1198.1
AHQ-5-10, 6587	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.40E-07	0.96	4.91	-	1040.0
AHQ-5-9, 6538	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.08E-05	0.96	4.85	-	1123.3
AHQ-5-8, 7268	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.29E-05	0.97	5.41	-	1375.4
AHQ-5-3, 7487 - 7562	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.50E-08	0.96	5.21	-	1020.2
AHQ-5-6, 7365 - 7369	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.11E-06	0.97	5.71	-	970.3
AHQ-5-7, 7350	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	9.39E-11	0.96	5.35	-	1015.6
AHQ-5-1, 7375	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.55E-09	0.95	4.53	-	941.5
AHQ-5-4, 3298	R.ALASQLQDSLK.D	1174.32943	2	1.11E-05	0.94	3.88	-	1257.7
AHQ-5-1, 3419	R.ALASQLQDSLK.D	1174.32943	2	5.94E-04	0.89	3.16	-	1086.4
AHQ-5-4, 3337	R.ALASQLQDSLK.D	1174.32943	2	9.36E-05	0.92	3.68	-	1111.6
AHQ-5-6, 2990 - 3061	R.ALASQLQDSLK.D	1174.32943	2	1.33E-05	0.88	3.02	-	1048.7
AHQ-5-2, 3231	R.ALASQLQDSLK.D	1174.32943	2	3.15E-04	0.93	3.85	-	1000.5
AHQ-5-4, 3484 - 3552	K.AQQVSQGLDVLTAK.V	1458.64233	1	7.31E-04	0.69	3.12	-	458.1
AHQ-5-7, 3194	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.60E-10	0.97	4.41	-	1464.7
AHQ-5-4, 3533	K.AQQVSQGLDVLTAK.V	1458.64233	1	2.70E-04	0.69	3.52	-	369.1
AHQ-5-5, 3335	K.AQQVSQGLDVLTAK.V	1458.64233	1	2.66E-07	0.48	3.36	-	209.8
AHQ-5-8, 2964	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.68E-04	0.91	3.15	-	1124.8
AHQ-5-1, 3725	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.08E-08	0.96	3.96	-	1462.8
AHQ-5-4, 3485 - 3557	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.84E-09	0.97	4.58	-	1615.5
AHQ-5-2, 3489 - 3562	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.72E-09	0.96	4.66	-	1387.0
AHQ-5-6, 3292 - 3296	K.AQQVSQGLDVLTAK.V	1458.64233	2	6.13E-08	0.95	4.61	-	1307.5
AHQ-5-5, 2282 - 2310	K.AVAGNISDPGLQK.S	1270.41721	2	4.68E-05	0.92	3.73	-	937.3
AHQ-5-6, 2272	K.AVAGNISDPGLQK.S	1270.41721	1	4.00E-06	0.47	2.45	-	401.4
AHQ-5-2, 2386	K.AVAGNISDPGLQK.S	1270.41721	2	6.83E-04	0.87	3.39	-	773.0
AHQ-5-6, 2269	K.AVAGNISDPGLQK.S	1270.41721	2	2.27E-06	0.79	3.38	-	591.8
AHQ-5-7, 2236	K.AVAGNISDPGLQK.S	1270.41721	2	4.06E-06	0.74	3.07	-	473.7
AHQ-5-3, 2437	K.AVAGNISDPGLQK.S	1270.41721	2	2.29E-06	0.93	3.83	-	869.6
AHQ-5-1, 2584	K.AVAGNISDPGLQK.S	1270.41721	2	1.07E-05	0.63	2.93	-	439.4
AHQ-5-4, 2388 - 2400	K.AVAGNISDPGLQK.S	1270.41721	2	1.32E-05	0.82	3.10	-	714.0
AHQ-5-8, 2126	K.AVAGNISDPGLQK.S	1270.41721	2	7.52E-05	0.60	2.51	-	547.0
AHQ-5-4, 6122	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	1.33E-05	0.93	4.24	-	1608.4
AHQ-5-8, 5729 - 5736	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	3.20E-05	0.93	3.92	-	1200.1
AHQ-5-5, 5962 - 6017	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	4.59E-05	0.95	3.77	-	1555.0
AHQ-5-1, 6171	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	3.85E-05	0.94	4.09	-	1319.4
AHQ-5-1, 6161	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	6.01E-05	0.63	3.12	-	904.0
AHQ-5-4, 6120 - 6121	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	6.75E-05	0.95	3.83	-	1620.8
AHQ-5-5, 5981	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	8.96E-06	0.93	4.53	-	1319.9
AHQ-5-6, 5920	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	3.67E-08	0.87	4.09	-	1208.8
AHQ-5-5, 2226	R.DPSASPGDAGEQAIR.Q	1471.51169	1	4.49E-07	0.27	2.31	-	168.2
AHQ-5-4, 2214 - 2284	R.DPSASPGDAGEQAIR.Q	1471.51169	2	3.48E-08	0.92	3.72	-	917.5
AHQ-5-3, 2323	R.DPSASPGDAGEQAIR.Q	1471.51169	2	6.83E-07	0.89	3.91	-	501.7
AHQ-5-2, 2298	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.62E-07	0.84	3.69	-	482.5
AHQ-5-4, 2286	R.DPSASPGDAGEQAIR.Q	1471.51169	1	1.57E-09	0.40	2.32	-	192.0
AHQ-5-5, 2143 - 2215	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.41E-06	0.91	3.70	-	845.8
AHQ-5-1, 2453	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.49E-04	0.69	2.69	-	515.0
AHQ-5-4, 2484	R.DYLIDGSR.G	939.00451	1	6.31E-05	0.18	2.08	-	223.4
AHQ-5-4, 2504	R.DYLIDGSR.G	939.00451	1	1.50E-05	0.54	2.82	-	294.6
AHQ-5-4, 5990 - 6013	K.ELLPVLISAMK.I	1214.54325	2	2.25E-05	0.87	3.24	-	779.3
AHQ-5-5, 5709	K.ELLPVLISAMK.I	1214.54325	2	2.03E-05	0.84	3.23	-	633.0
AHQ-5-11, 5591	K.ELLPVLISAMK.I	1214.54325	2	3.38E-06	0.62	2.93	-	432.6
AHQ-5-1, 6183	K.ELLPVLISAMK.I	1214.54325	2	8.29E-05	0.71	2.75	-	495.8
AHQ-5-4, 2596	R.ELTPQVVSAAR.I	1171.32878	2	8.18E-04	0.93	3.31	-	1404.7
AHQ-5-5, 2915	K.ETVQTTEDQILK.R	1405.53306	1	1.20E-05	0.12	2.28	-	110.3
AHQ-5-6, 2744 - 2752	K.ETVQTTEDQILKR.D	1561.71942	2	9.46E-06	0.88	3.37	-	921.6
AHQ-5-5, 2719	K.ETVQTTEDQILKR.D	1561.71942	2	3.46E-06	0.71	2.98	-	500.4
AHQ-5-4, 2897	K.ETVQTTEDQILKR.D	1561.71942	2	1.29E-07	0.76	3.19	-	639.0
AHQ-5-4, 7105	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	6.63E-05	0.89	4.35	-	493.8
AHQ-5-6, 7145	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.67E-04	0.82	3.52	-	660.2
AHQ-5-5, 7225 - 7298	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.37E-09	0.96	5.38	-	1130.6
AHQ-5-11, 6675	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.07E-08	0.93	4.89	-	715.1
AHQ-5-5, 7574	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	8.91E-04	0.26	2.95	-	245.7
AHQ-5-4, 7620 - 7665	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.87E-04	0.88	4.10	-	599.3
AHQ-5-4, 6756	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	1.97E-09	0.94	4.25	-	1146.4
AHQ-5-4, 2000	K.GNDIIAAAK.R	872.98920	1	2.49E-05	0.26	2.11	-	542.6
AHQ-5-5, 3354 - 3355	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	4.67E-08	0.94	4.53	-	991.2
AHQ-5-5, 1991	K.IAELCDDPKER.D	1347.47690	2	3.90E-04	0.83	3.03	-	863.1
AHQ-5-4, 2118 - 2154	K.IAELCDDPKER.D	1347.47690	2	2.98E-05	0.84	3.10	-	776.2
AHQ-5-5, 3238	K.IAELCDDPKERDDILR.S	1960.15548	2	8.05E-04	0.54	3.01	-	350.2
AHQ-5-5, 3250	K.IAELCDDPKERDDILR.S	1960.15548	3	2.37E-07	0.89	3.83	-	1246.1
AHQ-5-4, 3446 - 3514	K.IAELCDDPKERDDILR.S	1960.15548	3	5.94E-05	0.79	3.02	-	1384.6
AHQ-5-6, 2846	R.IPTISTQLK.I	1001.20202	2	2.92E-04	0.78	2.66	-	738.5
AHQ-5-4, 3001 - 3002	R.IPTISTQLK.I	1001.20202	2	1.57E-06	0.87	2.57	-	1020.5
AHQ-5-12, 2990	R.IPTISTQLK.I	1001.20202	1	1.52E-05	0.41	2.57	-	349.5
AHQ-5-4, 2024	R.KIAELCDDPKER.D	1475.64981	3	4.08E-08	0.87	3.65	-	1182.9
AHQ-5-4, 4381 - 4420	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	3.71E-10	0.97	6.59	-	1440.3
AHQ-5-5, 4205 - 4273	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.20E-08	0.91	4.48	-	708.9
AHQ-5-5, 4183 - 4259	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	3.73E-07	0.97	5.82	-	1752.8
AHQ-5-5, 2583 - 2602	R.LANVMM*GPYR.Q	1168.41500	2	1.44E-04	0.80	2.83	-	816.4
AHQ-5-6, 2636	R.LANVM*MGPYR.Q	1168.41500	2	6.76E-05	0.88	3.70	-	917.3
AHQ-5-4, 2153	R.LANVM*M*GPYR.Q	1184.41440	2	1.78E-05	0.88	3.40	-	756.8
AHQ-5-4, 3282	R.LANVMMGPYR.Q	1152.41560	2	6.04E-04	0.86	3.33	-	660.3
AHQ-5-4, 2776	R.LANVMM*GPYR.Q	1168.41500	2	3.92E-05	0.79	3.44	-	677.1

AHQ-5-5, 3013 - 3014	K.LLAVAATAPPDAPNR.E	1477.69048	2	3.64E-05	0.92	4.52	-	501.5
AHQ-5-3, 4409	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	9.65E-05	0.87	3.81	-	868.3
AHQ-5-6, 4100	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	1.47E-06	0.68	3.26	-	632.4
AHQ-5-2, 4342	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	4.12E-05	0.84	3.65	-	674.1
AHQ-5-4, 4276 - 4345	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	2.71E-05	0.78	3.89	-	625.5
AHQ-5-1, 4471	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	8.79E-06	0.84	3.56	-	702.8
AHQ-5-4, 4561 - 4632	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	8.98E-07	0.84	4.26	-	466.8
AHQ-5-4, 4701 - 4702	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	9.80E-08	0.88	4.43	-	722.6
AHQ-5-3, 4694 - 4770	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	2.51E-05	0.81	3.79	-	533.6
AHQ-5-1, 4757	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	5.92E-04	0.77	2.98	-	485.5
AHQ-5-4, 3792	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	3	2.44E-07	0.97	5.23	-	1963.7
AHQ-5-8, 4140	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	2.77E-05	0.92	4.31	-	712.6
AHQ-5-4, 3753	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	5.37E-07	0.88	4.05	-	588.4
AHQ-5-6, 3532	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	2.89E-09	0.94	4.66	-	719.8
AHQ-5-11, 4359	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	9.45E-08	0.91	4.10	-	1101.6
AHQ-5-11, 3554 - 3627	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	7.51E-04	0.75	2.86	-	671.0
AHQ-5-4, 4645	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	3.14E-06	0.95	4.97	-	1480.1
AHQ-5-4, 4317	R.MALLMAEMSR.L	1153.46531	2	1.32E-07	0.95	4.21	-	1502.1
AHQ-5-12, 3146	R.MALLMAEM*SR.L	1169.46471	2	5.43E-06	0.94	3.58	-	1336.0
AHQ-5-12, 4192	R.MALLMAEMSR.L	1153.46531	2	3.87E-04	0.95	3.95	-	1520.9
AHQ-5-2, 4205	K.MLGQMTDQVADLR.A	1478.72055	2	3.98E-10	0.95	4.63	-	1398.7
AHQ-5-5, 4017 - 4027	K.MLGQMTDQVADLR.A	1478.72055	2	5.07E-07	0.95	4.47	-	1284.6
AHQ-5-4, 4209	K.MLGQMTDQVADLR.A	1478.72055	1	2.54E-05	0.58	2.81	-	392.3
AHQ-5-9, 3620	K.MLGQMTDQVADLR.A	1478.72055	2	4.09E-05	0.86	3.15	-	1122.7
AHQ-5-5, 4031 - 4109	K.M*LGQM*TDQVADLR.A	1510.71935	2	9.33E-05	0.95	3.74	-	1539.7
AHQ-5-7, 3850 - 3860	K.MLGQMTDQVADLR.A	1478.72055	2	2.14E-06	0.95	4.27	-	1563.1
AHQ-5-4, 3756	K.M*LGQMTDQVADLR.A	1494.71995	2	1.15E-06	0.97	4.25	-	2091.8
AHQ-5-8, 3721	K.MLGQMTDQVADLR.A	1478.72055	2	1.19E-07	0.92	3.29	-	1454.7
AHQ-5-1, 4325	K.MLGQMTDQVADLR.A	1478.72055	2	2.61E-06	0.96	4.27	-	1816.0
AHQ-5-4, 4189	K.MLGQMTDQVADLR.A	1478.72055	2	2.51E-06	0.95	4.13	-	1664.1
AHQ-5-4, 3260	K.MLGQM*TDQVADLR.A	1494.71995	2	2.08E-07	0.94	4.06	-	1572.8
AHQ-5-6, 3969	K.MLGQMTDQVADLR.A	1478.72055	2	4.49E-06	0.91	3.94	-	1190.3
AHQ-5-5, 3126 - 3130	K.MLGQM*TDQVADLR.A	1494.71995	2	4.21E-05	0.97	4.32	-	2194.0
AHQ-5-4, 2842	K.M*LGQM*TDQVADLR.A	1510.71935	2	2.02E-04	0.96	3.89	-	1995.7
AHQ-5-3, 4258	K.MLGQMTDQVADLR.A	1478.72055	2	6.44E-04	0.93	3.62	-	1529.0
AHQ-5-5, 2898	K.M*SAEINEIIR.V	1192.36823	2	8.61E-08	0.90	2.91	-	1108.8
AHQ-5-4, 3072	K.M*SAEINEIIR.V	1192.36823	2	6.31E-07	0.94	3.10	-	1514.4
AHQ-5-5, 2893	K.M*TGLVDEAIDTK.S	1309.46876	2	6.95E-07	0.95	4.11	-	1329.8
AHQ-5-6, 3329	K.MTGLVDEAIDTK.S	1293.46936	2	4.35E-04	0.96	3.30	-	1703.5
AHQ-5-4, 3560 - 3637	K.MTGLVDEAIDTK.S	1293.46936	2	2.78E-04	0.97	4.25	-	1877.7
AHQ-5-4, 3048	K.M*TGLVDEAIDTK.S	1309.46876	2	1.32E-07	0.94	3.62	-	1231.8
AHQ-5-4, 2849 - 2857	R.NPGNQAAYEHFETMK.N	1737.87437	2	8.53E-09	0.91	3.90	-	890.4
AHQ-5-4, 2865	R.NPGNQAAYEHFETMK.N	1737.87437	3	3.33E-05	0.68	3.37	-	469.8
AHQ-5-5, 2639 - 2645	R.NPGNQAAYEHFETMK.N	1737.87437	2	5.23E-05	0.92	3.68	-	1080.8
AHQ-5-4, 2364	R.NPGNQAAYEHFETM*K.N	1753.87377	2	9.46E-04	0.91	3.92	-	689.2
AHQ-5-6, 2668 - 2669	R.NPGNQAAYEHFETMK.N	1737.87437	2	8.48E-07	0.81	3.82	-	417.6
AHQ-5-4, 2829	K.NQWIDNVEK.M	1146.23464	2	1.03E-04	0.61	2.70	-	451.4
AHQ-5-4, 2834	K.NQWIDNVEK.M	1146.23464	1	5.23E-05	0.33	2.34	-	190.8
AHQ-5-5, 2694	K.NQWIDNVEK.M	1146.23464	1	1.17E-04	0.74	2.72	-	332.6
AHQ-5-5, 3010	K.NQWIDNVEK.M	1146.23464	1	5.88E-05	0.13	1.95	-	272.1
AHQ-5-4, 2749	K.QVATALQNLQTK.T	1315.50112	2	2.93E-04	0.88	3.70	-	583.8
AHQ-5-4, 2706 - 2785	K.QVATALQNLQTK.T	1315.50112	2	5.82E-04	0.90	3.47	-	724.7
AHQ-5-6, 3170	R.SLGEISALTSK.L	1106.25186	1	2.22E-04	0.17	2.23	-	102.7
AHQ-5-5, 3191	R.SLGEISALTSK.L	1106.25186	1	4.65E-04	0.47	2.82	-	132.9
AHQ-5-5, 3193	R.SLGEISALTSK.L	1106.25186	2	2.96E-05	0.93	3.76	-	847.6
AHQ-5-1, 3580	R.SLGEISALTSK.L	1106.25186	1	2.72E-04	0.20	2.03	-	368.3
AHQ-5-4, 3388	R.SLGEISALTSK.L	1106.25186	1	6.19E-06	0.52	2.87	-	180.7
AHQ-5-7, 3059	R.SLGEISALTSK.L	1106.25186	1	3.12E-05	0.29	2.34	-	92.5
AHQ-5-6, 3049	K.SLLDASEEAIKK.D	1304.47187	2	3.09E-05	0.66	2.63	-	625.1
AHQ-5-4, 3262	K.SLLDASEEAIKK.D	1304.47187	1	3.71E-04	0.10	2.10	-	357.3
AHQ-5-4, 3248 - 3296	K.SLLDASEEAIKK.D	1304.47187	2	1.76E-06	0.84	2.95	-	920.2
AHQ-5-5, 3070 - 3086	K.SLLDASEEAIKK.D	1304.47187	2	1.29E-04	0.82	2.77	-	822.9
AHQ-5-4, 2228 - 2296	K.STVEGIQASVK.T	1119.25064	2	4.85E-06	0.90	3.05	-	886.1
AHQ-5-6, 2160	K.STVEGIQASVK.T	1119.25064	2	1.04E-05	0.81	2.61	-	789.9
AHQ-5-5, 2166	K.STVEGIQASVK.T	1119.25064	2	6.02E-07	0.89	2.95	-	1012.3
AHQ-5-5, 7398	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	9.76E-04	0.71	3.46	-	547.6
AHQ-5-3, 7378	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.03E-05	0.81	3.80	-	507.4
AHQ-5-14-, 6582 - 6653	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	7.23E-05	0.91	4.93	-	552.7
AHQ-5-14-, 6442	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	4.04E-07	0.58	3.26	-	526.1
AHQ-5-5, 7233 - 7234	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.55E-10	0.93	5.36	-	622.6
AHQ-5-13-, 6705	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	3.72E-11	0.91	5.26	-	419.4
AHQ-5-13-, 6496 - 6573	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	1.94E-04	0.65	3.30	-	524.2
AHQ-5-12, 6581 - 6644	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	6.00E-07	0.77	4.05	-	623.2
AHQ-5-12, 6384	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	1.65E-04	0.77	4.05	-	620.6
AHQ-5-12, 5869 - 5932	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	2.76E-05	0.74	3.91	-	458.9
AHQ-5-12, 5542	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	2.45E-06	0.72	3.48	-	556.5
AHQ-5-12, 5416 - 5497	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	6.29E-06	0.88	4.57	-	372.8
AHQ-5-11, 6680 - 6712	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.72E-06	0.91	4.73	-	693.5
AHQ-5-6, 6100	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.94E-10	0.88	4.07	-	592.5
AHQ-5-4, 6301 - 6308	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	1.88E-06	0.88	5.12	-	480.5
AHQ-5-4, 6306	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	5.67E-05	0.79	4.19	-	434.9
AHQ-5-2, 7366	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	6.69E-07	0.86	4.37	-	508.6
AHQ-5-4, 6989 - 7052	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	8.52E-08	0.77	4.78	-	484.3
AHQ-5-10, 6403	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.04E-05	0.87	4.12	-	777.7
AHQ-5-10, 5475	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	6.88E-05	0.61	3.53	-	428.2
AHQ-5-4, 7129 - 7141	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	3.19E-05	0.56	3.32	-	386.3
AHQ-5-4, 7249 - 7268	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.05E-06	0.89	4.83	-	598.3
AHQ-5-1, 7215 - 7216	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.14E-06	0.84	4.18	-	502.3
AHQ-5-4, 7337	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	9.76E-05	0.87	4.56	-	508.8
AHQ-5-12, 3102	R.TNLLQVCER.I	1134.28859	2	4.74E-06	0.95	3.88	-	1460.2
AHQ-5-14-, 3095	R.TNLLQVCER.I	1134.28859	2	4.55E-05	0.86	3.25	-	896.6
AHQ-5-4, 3141 - 3212	R.TNLLQVCER.I	1134.28859	2	2.90E-04	0.78	2.78	-	730.5
AHQ-5-5, 5953 - 5987	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	3.29E-04	0.92	4.40	-	665.0
AHQ-5-5, 5958	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	3	3.54E-06	0.93	4.38	-	1330.9
AHQ-5-5, 5453	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	2	1.90E-04	0.92	4.47	-	691.3
AHQ-5-5, 5313	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	4.31E-07	0.94	4.78	-	1873.0
AHQ-5-5, 4845	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	1.28E-06	0.95	4.85	-	860.5
AHQ-5-4, 5701	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	3	2.58E-07	0.95	5.35	-	1671.8
AHQ-5-7, 5776 - 5787	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	6.51E-05	0.76	3.50	-	658.8
AHQ-5-1, 5612	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	1.05E-06	0.96	5.19	-	1007.8
AHQ-5-4, 6156	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	3	6.14E-09	0.96	4.65	-	2092.0
AHQ-5-4, 5025	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	3.84E-05	0.94	4.64	-	834.2
AHQ-5-5, 5290 - 5294	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	2.46E-05	0.79	3.43	-	796.2
AHQ-5-4, 5517	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	9.24E-11	0.95	4.98	-	1855.6
AHQ-5-5, 4993	R.VDQLTAQLADLAAR.G	1485.66778	2	2.26E-10	0.98	5.02	-	2865.8
AHQ-5-4, 5140	R.VDQLTAQLADLAAR.G	1485.66778	2	5.84E-06	0.98	5.00	-	2469.6
AHQ-5-4, 5540 - 5613	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.77E-06	0.98	5.03	-	1919.2

AHQ-5-4, 5681	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.45E-05	0.94	4.39	-	906.5
AHQ-5-6, 5304	R.VLQLTSWDEDAWASK.D	1749.90156	2	6.80E-07	0.96	4.38	-	1214.3
AHQ-5-5, 5295 - 5365	R.VLQLTSWDEDAWASK.D	1749.90156	2	7.64E-06	0.97	5.51	-	1363.9
AHQ-5-3, 5594	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.20E-06	0.94	3.95	-	1223.8
AHQ-5-5, 5443	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.19E-04	0.88	3.16	-	1042.3
AHQ-5-1, 5644	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.20E-07	0.96	4.79	-	1020.6
AHQ-5-4, 5458	R.VLQLTSWDEDAWASK.D	1749.90156	2	4.34E-06	0.88	3.67	-	707.2
AHQ-5-4, 2357 - 2360	R.VMLVNSM*NTVK.E	1252.53021	2	2.88E-06	0.94	3.67	-	1227.9
AHQ-5-5, 2926	R.VMLVNSMNTVK.E	1236.53081	2	7.23E-07	0.95	3.62	-	1534.5
AHQ-5-4, 3116 - 3192	R.VMLVNSMNTVK.E	1236.53081	2	5.03E-05	0.94	3.93	-	1115.7
AHQ-5-4, 3205	R.VMLVNSMNTVK.E	1236.53081	2	3.04E-04	0.91	3.14	-	1049.9
AHQ-5-5, 3045	R.VMLVNSMNTVK.E	1236.53081	2	5.84E-07	0.83	3.02	-	798.5
AHQ-5-4, 2813 - 2828	R.WIDNPTVDDR.G	1231.29640	2	2.27E-04	0.94	3.55	-	1138.8
AHQ-5-1, 2992	R.WIDNPTVDDR.G	1231.29640	2	1.05E-04	0.95	3.62	-	1675.2
gi|5032161|ref|NP_005639.1| elongin C; transcription elongation factor B (SIII), polypeptide 1 (15k				1.78E-11	3.79	40.29	41.10	12473.1
AHQ-5-13, 4293	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	1.04E-09	0.95	4.53	-	1387.3
AHQ-5-13, 4548	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	7.05E-07	0.96	5.00	-	1435.7
AHQ-5-13, 4640	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	7.87E-05	0.94	4.51	-	915.8
AHQ-5-13, 4909	K.AMLSGPGQFAENETNEVNFR.E	2212.38515	2	1.78E-11	0.98	5.84	-	1874.9
AHQ-5-13-, 4553	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	1.59E-04	0.92	4.28	-	856.5
AHQ-5-13-, 3045	K.LISSDGHEFIVK.R	1345.52569	2	4.34E-07	0.89	3.65	-	891.7
AHQ-5-13, 3161	K.LISSDGHEFIVK.R	1345.52569	2	1.43E-08	0.92	3.78	-	922.8
AHQ-5-13-, 2708	K.TYGGCEGPDAM*YVK.L	1565.70692	2	3.27E-06	0.93	4.34	-	756.6
gi|6005942|ref|NP_009057.1| valosin-containing protein; yeast Cdc48p homolog; transitional endoplas				1.79E-11	9.57	120.35	23.60	89321.3
AHQ-5-5, 3561	R.ELQELVQYPVEHPDK.F	1825.01157	2	5.06E-04	0.69	2.77	-	510.4
AHQ-5-5, 6257	R.ETVVEVPQVTWEDIGGLEDVKR.E	2499.75825	3	1.74E-05	0.75	3.48	-	571.8
AHQ-5-5, 3631	K.GVLFYGPPGCGK.T	1253.45154	2	8.15E-06	0.83	3.07	-	834.9
AHQ-5-5, 6821 - 6822	R.IVSQLLTLMDGLK.Q	1431.76657	2	1.59E-06	0.97	4.94	-	1414.6
AHQ-5-5, 3058	R.KYEMFAQTLQQSR.G	1630.85008	2	6.91E-09	0.97	4.58	-	1875.7
AHQ-5-5, 5682 - 5759	R.LDQLIYIPLPDEK.S	1557.81228	2	3.00E-06	0.96	5.19	-	980.6
AHQ-5-5, 2793	R.LEILQIHTK.N	1095.31705	1	2.11E-04	0.54	2.43	-	340.9
AHQ-5-5, 5074 - 5099	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	1.34E-07	0.99	6.91	-	2257.9
AHQ-5-5, 7390	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	1.79E-11	0.96	4.71	-	1210.9
AHQ-5-5, 7414	R.QAAPCVLFFDELDSIAK.A	1926.17909	2	8.30E-04	0.31	2.61	-	215.4
AHQ-5-5, 4894	K.VVETDPSPYCIVAPDTVIHCEGEPIKR.E	3085.45473	3	3.61E-05	0.68	3.71	-	382.9
AHQ-5-5, 3298 - 3305	R.WALSQSNPSALR.E	1330.47434	2	5.49E-07	0.93	3.66	-	1318.5
gi|4505733|ref|NP_002610.1| platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4				2.06E-11	5.58	60.26	38.60	10844.9
AHQ-5-13-, 4140 - 4151	K.AGPHCPTAQLIATLK.N	1579.84600	2	8.68E-04	0.94	4.14	-	845.8
AHQ-5-12, 4081	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.39E-05	0.90	3.86	-	712.4
AHQ-5-14, 5090 - 5164	K.AGPHCPTAQLIATLK.N	1579.84600	2	4.03E-04	0.87	3.76	-	682.1
AHQ-5-14-, 4035 - 4098	K.AGPHCPTAQLIATLK.N	1579.84600	2	5.34E-06	0.92	4.05	-	772.9
AHQ-5-14-, 3953 - 4034	K.AGPHCPTAQLIATLK.N	1579.84600	3	2.36E-04	0.79	3.70	-	909.1
AHQ-5-14-, 3949 - 3967	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.86E-07	0.91	3.89	-	857.2
AHQ-5-14, 4960 - 5032	K.AGPHCPTAQLIATLK.N	1579.84600	2	8.06E-08	0.94	3.99	-	950.5
AHQ-5-14-, 3786 - 3795	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.10E-05	0.96	4.89	-	1081.6
AHQ-5-13-, 3901	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	4.56E-07	0.90	3.74	-	1656.9
AHQ-5-14, 4689	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.07E-07	0.90	4.05	-	768.6
AHQ-5-14, 4801 - 4860	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	1.08E-04	0.95	4.50	-	991.4
AHQ-5-14, 4809	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	2.06E-11	0.96	5.05	-	1717.5
AHQ-5-14-, 3873 - 3914	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.76E-10	0.97	5.17	-	2387.9
AHQ-5-14-, 3891	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.07E-10	0.95	4.64	-	861.4
AHQ-5-14, 4548	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	2.07E-04	0.83	4.09	-	696.8
AHQ-5-14, 4436	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	2	6.21E-08	0.96	4.83	-	1314.0
AHQ-5-14-, 3443 - 3498	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	1.45E-06	0.94	4.45	-	1415.2
AHQ-5-14, 4552	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	2	2.94E-05	0.96	5.16	-	968.8
AHQ-5-14, 3245 - 3320	R.HITSLEVIK.A	1040.23825	2	2.73E-04	0.71	2.95	-	385.1
AHQ-5-14, 3376 - 3432	R.HITSLEVIK.A	1040.23825	2	8.22E-07	0.82	3.17	-	466.2
AHQ-5-14, 3488 - 3554	R.HITSLEVIK.A	1040.23825	2	1.56E-04	0.86	3.49	-	471.8
AHQ-5-13-, 2593 - 2665	R.HITSLEVIK.A	1040.23825	2	1.78E-05	0.90	3.67	-	583.9
AHQ-5-13, 2753	R.HITSLEVIK.A	1040.23825	2	3.17E-04	0.81	3.08	-	458.0
AHQ-5-12, 2453	R.HITSLEVIK.A	1040.23825	2	3.29E-04	0.81	2.86	-	493.7
AHQ-5-14-, 2545	R.HITSLEVIK.A	1040.23825	1	2.91E-04	0.42	2.18	-	455.7
AHQ-5-14-, 2417 - 2481	R.HITSLEVIK.A	1040.23825	2	2.19E-06	0.90	3.69	-	567.2
AHQ-5-14-, 2527 - 2590	R.HITSLEVIK.A	1040.23825	2	5.76E-06	0.75	2.75	-	500.5
AHQ-5-13-, 4915 - 4916	K.ICLDLQAPLYK.K	1335.59400	2	2.56E-05	0.97	4.19	-	2105.9
AHQ-5-14, 5732	K.ICLDLQAPLYK.K	1335.59400	1	1.62E-05	0.66	2.94	-	536.5
AHQ-5-14, 5700 - 5761	K.ICLDLQAPLYK.K	1335.59400	2	3.91E-05	0.95	4.17	-	1537.4
AHQ-5-14-, 4739	K.ICLDLQAPLYK.K	1335.59400	2	2.00E-05	0.92	3.56	-	1173.4
AHQ-5-14-, 4846 - 4869	K.ICLDLQAPLYK.K	1335.59400	2	2.59E-06	0.96	4.53	-	1713.0
AHQ-5-14, 5288 - 5350	R.KICLDLQAPLYK.K	1463.76691	1	3.94E-04	0.78	3.18	-	714.1
AHQ-5-14, 5281 - 5344	R.KICLDLQAPLYK.K	1463.76691	2	8.89E-06	0.97	4.96	-	1490.0
AHQ-5-14, 5312	R.KICLDLQAPLYK.K	1463.76691	1	5.38E-06	0.93	4.08	-	980.3
AHQ-5-14-, 4365 - 4397	R.KICLDLQAPLYK.K	1463.76691	2	1.45E-04	0.98	4.72	-	1914.4
AHQ-5-14-, 4374 - 4437	R.KICLDLQAPLYK.K	1463.76691	1	1.56E-04	0.79	2.94	-	841.1
AHQ-5-14-, 4378 - 4445	R.KICLDLQAPLYK.K	1463.76691	3	2.48E-05	0.94	4.49	-	1320.4
AHQ-5-14-, 4382 - 4447	R.KICLDLQAPLYK.K	1463.76691	1	1.03E-07	0.93	4.42	-	680.1
AHQ-5-14-, 4457	R.KICLDLQAPLYK.K	1463.76691	2	2.59E-07	0.96	4.11	-	1561.3
AHQ-5-14, 5404	R.KICLDLQAPLYK.K	1463.76691	2	1.21E-04	0.94	4.21	-	1247.7
AHQ-5-13, 4494	R.KICLDLQAPLYK.K	1463.76691	2	2.67E-05	0.94	4.44	-	1037.0
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				2.21E-11	20.18	240.31	24.80	138070.8
AHQ-5-3, 2273	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	9.02E-04	0.91	4.45	-	1022.8
AHQ-5-3, 2362	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	6.49E-10	0.90	4.69	-	667.8
AHQ-5-2, 2233	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	1.65E-06	0.93	4.69	-	679.8
AHQ-5-3, 2266	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	5.56E-05	0.94	4.94	-	688.1
AHQ-5-3, 7369	K.CTSDMETILTFIPQFHR.L	2098.38838	3	6.61E-06	0.85	3.64	-	747.1
AHQ-5-3, 7365 - 7367	K.CTSDMETILTFIPQFHR.L	2098.38838	2	9.37E-06	0.85	3.75	-	652.4
AHQ-5-3, 6562	K.CTSDM*ETILTFIPQFHR.L	2114.38778	2	7.60E-06	0.73	3.42	-	462.9
AHQ-5-3, 4115 - 4119	R.DQALQLQVLNSR.F	1385.55144	2	6.20E-07	0.97	4.49	-	1882.8
AHQ-5-3, 1878 - 1889	K.ETLSTIKDNSEIHHK.C	1752.90698	2	6.54E-06	0.42	2.71	-	285.1
AHQ-5-3, 2725	K.EVHEQLLSTEQVSDQK.N	1870.99550	2	3.43E-04	0.94	4.00	-	1165.7
AHQ-5-13, 6246 - 6261	K.FPPVTTFSGYLLYR.T	1661.92388	2	6.18E-04	0.85	3.16	-	667.3
AHQ-5-10, 5723 - 5739	K.FPPVTTFSGYLLYR.T	1661.92388	2	5.55E-06	0.93	3.63	-	896.4
AHQ-5-14-, 6079 - 6098	K.FPPVTTFSGYLLYR.T	1661.92388	2	5.31E-06	0.96	4.31	-	995.4
AHQ-5-3, 5981 - 6055	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	3.76E-05	0.86	4.25	-	484.9
AHQ-5-3, 5985	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.46E-08	0.96	5.56	-	1271.2
AHQ-5-4, 5938	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	3.65E-05	0.95	4.37	-	1278.7
AHQ-5-3, 6289 - 6313	K.GLTEFVEPIIQIK.T	1487.76518	2	7.46E-05	0.91	3.83	-	878.2
AHQ-5-1, 6295 - 6297	K.GLTEFVEPIIQIK.T	1487.76518	2	2.38E-04	0.91	4.02	-	858.8
AHQ-5-4, 6269	K.GLTEFVEPIIQIK.T	1487.76518	1	1.83E-04	0.14	1.99	-	358.5
AHQ-5-3, 2627 - 2645	K.GPCGWTGGSCPQR.S	1422.52885	2	1.42E-05	0.92	3.52	-	1042.3
AHQ-5-3, 4245 - 4255	K.GSVVTNERDQALQLQVLNSR.F	2228.45212	2	4.46E-06	0.90	4.36	-	826.6
AHQ-5-3, 2049	R.GVAEQQQQQGCGDPEVM*QK.M	2135.27911	2	3.67E-04	0.91	4.03	-	777.8
AHQ-5-4, 3750 - 3825	K.HSLPDIQLLQK.G	1292.50915	2	1.75E-04	0.64	2.78	-	442.6
AHQ-5-3, 3757	K.HSLPDIQLLQK.G	1292.50915	2	1.39E-06	0.93	3.47	-	1071.8
AHQ-5-1, 3965 - 3976	K.HSLPDIQLLQK.G	1292.50915	2	9.49E-07	0.84	3.13	-	709.9
AHQ-5-1, 6656 - 6735	K.IFQNDMQETVAQLFK.T	1813.06743	2	2.60E-04	0.94	4.29	-	1237.3
AHQ-5-4, 6729 - 6773	K.IFQNDMQETVAQLFK.T	1813.06743	2	2.04E-04	0.96	4.50	-	1407.5

AHQ-5-3, 6743 - 6769	K.IFQNDMQETVAQLFK.T	1813.06743	2	1.04E-06	0.97	4.97	-	1853.7
AHQ-5-3, 5583	K.KIENLTSAVNSLNFIIK.E	1905.22764	2	5.39E-11	0.97	5.03	-	1977.5
AHQ-5-3, 4966	R.KKIENLTSAVNSLNFIIK.E	2033.40055	2	2.21E-11	0.94	4.24	-	1174.8
AHQ-5-3, 2683 - 2757	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	3.51E-06	0.98	6.14	-	1353.8
AHQ-5-2, 2674	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	4.30E-04	0.95	4.84	-	1120.9
AHQ-5-10, 3406	K.LVEENALAPDFSK.G	1433.58810	1	2.45E-06	0.74	3.70	-	403.9
AHQ-5-3, 7533 - 7534	K.MSEQLNDLTYDMEILQPLLEQGASLR.Q	3009.40182	3	2.99E-04	0.77	3.66	-	778.1
AHQ-5-3, 2633	R.QEMTLTCEKPIK.E	1479.74501	2	1.81E-05	0.64	3.13	-	319.7
AHQ-5-3, 7501 - 7502	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	1.56E-06	0.95	5.51	-	698.5
AHQ-5-3, 7438	K.TM*TIINNAIDFIQDNYALK.E	2215.51196	2	3.20E-09	0.95	4.80	-	1013.4
AHQ-5-3, 7199 - 7265	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	3.72E-09	0.94	5.11	-	901.7
AHQ-5-3, 3405 - 3423	K.TVSSLSEDLESTR.Q	1424.49324	1	8.73E-04	0.14	1.90	-	165.7
AHQ-5-3, 4034	R.YNFVLQVAK.T	1082.27683	2	5.07E-06	0.93	3.32	-	993.5
gi|4502051|ref|NP_000688.1| arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]				2.47E-11	4.35	50.26	10.90	75721.8
AHQ-5-6, 3542	K.EGLPLTIAADR.K	1156.31411	2	8.95E-04	0.81	2.98	-	644.8
AHQ-5-6, 7212	R.GEEEEFDHDVAEDLGLLQFVR.L	2448.58352	2	2.47E-11	0.97	5.00	-	2023.8
AHQ-5-6, 5324	R.GLLGLPGALYAHDALR.L	1637.90708	2	3.69E-10	0.87	3.65	-	554.9
AHQ-5-6, 4496	R.LPGDNALDMFQK.H	1349.53784	2	1.48E-05	0.90	4.08	-	807.9
AHQ-5-6, 3920	R.TQLISDGGIFDK.A	1294.43554	2	1.58E-05	0.80	3.05	-	739.9
gi|4757810|ref|NP_004037.1| ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,				2.69E-11	5.47	60.29	15.70	59750.3
AHQ-5-7, 3530 - 3554	R.EAYPGDVFYLHSR.L	1554.68713	2	7.51E-07	0.74	2.98	-	428.2
AHQ-5-7, 5290	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	3	2.69E-11	0.96	5.75	-	1611.2
AHQ-5-7, 3103 - 3106	K.HALIIYDDLSK.Q	1288.47413	2	2.96E-09	0.95	3.71	-	1320.8
AHQ-5-7, 3611 - 3632	R.ILGADTSVDLEETGR.V	1576.68772	2	6.41E-10	0.93	3.75	-	1156.5
AHQ-5-14-, 6259 - 6275	K.LKEIVTNFLAGFEA	1552.79572	2	1.58E-06	0.92	3.22	-	1085.7
AHQ-5-7, 3478	K.TGTAEMSSILEER.I	1424.55988	2	3.64E-06	0.97	4.41	-	2076.9
gi|4501893|ref|NP_001094.1| actinin, alpha 2 [Homo sapiens]				2.70E-11	9.96	110.26	12.60	103853.1
AHQ-5-5, 4359	K.AGTQIENIEEDFR.N	1522.59861	2	2.10E-06	0.82	3.39	-	801.2
AHQ-5-5, 5022 - 5093	K.CQLEINFNTLQTK.L	1610.81373	2	2.10E-04	0.95	4.32	-	1167.2
AHQ-5-5, 5163 - 5234	K.CQLEINFNTLQTK.L	1610.81373	2	5.67E-10	0.96	4.20	-	1686.8
AHQ-5-5, 5303	K.CQLEINFNTLQTK.L	1610.81373	2	9.37E-04	0.84	3.34	-	618.3
AHQ-5-4, 5133 - 5206	K.CQLEINFNTLQTK.L	1610.81373	2	5.15E-08	0.87	3.92	-	596.2
AHQ-5-5, 4846	R.DLLLDPAWEK.Q	1200.36535	2	7.17E-04	0.66	2.67	-	741.4
AHQ-5-5, 4805 - 4849	K.EGLLLWCQR.K	1176.37031	2	2.24E-05	0.93	3.65	-	937.3
AHQ-5-4, 5005 - 5021	K.EGLLLWCQR.K	1176.37031	2	2.00E-04	0.92	3.11	-	971.7
AHQ-5-11, 4038	R.FAIQDISVEETSAK.E	1538.68108	2	1.26E-04	0.81	2.91	-	938.0
AHQ-5-4, 4285 - 4304	R.FAIQDISVEETSAK.E	1538.68108	2	2.70E-11	0.94	4.13	-	1143.9
AHQ-5-6, 3973 - 4045	R.FAIQDISVEETSAK.E	1538.68108	2	2.21E-09	0.88	3.59	-	841.6
AHQ-5-5, 3995 - 4030	R.FAIQDISVEETSAK.E	1538.68108	2	2.47E-04	0.89	3.24	-	1195.8
AHQ-5-5, 4106 - 4177	R.FAIQDISVEETSAK.E	1538.68108	2	1.45E-07	0.95	4.23	-	1195.3
AHQ-5-1, 4400 - 4405	R.FAIQDISVEETSAK.E	1538.68108	2	9.12E-09	0.94	4.12	-	1095.3
AHQ-5-8, 3788	R.FAIQDISVEETSAK.E	1538.68108	2	2.04E-04	0.62	3.25	-	397.8
AHQ-5-12, 4162 - 4186	R.FAIQDISVEETSAK.E	1538.68108	2	6.89E-07	0.94	3.71	-	1168.4
AHQ-5-5, 6058 - 6125	K.GYEEWLLNEIR.R	1422.56701	1	5.71E-04	0.61	2.82	-	373.3
AHQ-5-6, 6005	K.GYEEWLLNEIR.R	1422.56701	1	5.84E-07	0.27	2.50	-	126.6
AHQ-5-6, 6004	K.GYEEWLLNEIR.R	1422.56701	1	6.06E-04	0.38	2.39	-	331.4
AHQ-5-6, 5397 - 5409	K.GYEEWLLNEIR.R	1422.56701	1	3.43E-07	0.26	2.02	-	230.0
AHQ-5-4, 6265 - 6276	K.GYEEWLLNEIR.R	1422.56701	2	2.04E-07	0.97	5.13	-	1666.9
AHQ-5-1, 6272 - 6273	K.GYEEWLLNEIR.R	1422.56701	2	7.66E-06	0.92	3.88	-	920.0
AHQ-5-5, 2033	K.HEAFESDLAAHQDR.V	1626.66861	2	6.80E-08	0.97	4.61	-	1451.4
AHQ-5-5, 3641	R.KAGTQIENIEEDFR.N	1650.77152	2	1.55E-06	0.96	5.19	-	1086.0
AHQ-5-4, 1933	R.KHEAFESDLAAHQDR.V	1754.84152	2	9.93E-09	0.95	3.95	-	1416.2
AHQ-5-5, 1709	R.KHEAFESDLAAHQDR.V	1754.84152	2	3.01E-08	0.97	4.81	-	1380.0
AHQ-5-6, 1760	R.KHEAFESDLAAHQDR.V	1754.84152	2	2.74E-09	0.92	4.01	-	870.2
AHQ-5-5, 2571	R.KTFTAWCNSHLR.K	1522.71309	2	1.20E-09	0.90	3.38	-	921.7
AHQ-5-5, 2798	R.KTFTAWCNSHLR.K	1522.71309	2	1.02E-05	0.91	3.78	-	938.3
AHQ-5-5, 5199	K.LVSIGAEEIVDGNVK.M	1543.74400	2	8.20E-06	0.93	4.28	-	1068.7
AHQ-5-5, 4489 - 4559	K.LVSIGAEEIVDGNVK.M	1543.74400	2	4.76E-05	0.86	3.00	-	979.0
AHQ-5-5, 4633	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.11E-06	0.93	3.48	-	1333.2
gi|13489087|ref|NP_109591.1| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member				2.94E-11	5.46	60.30	29.00	42741.5
AHQ-5-9, 4520	K.IPELLASGMVDNMTK.L	1619.92892	2	3.17E-04	0.89	3.27	-	1153.8
AHQ-5-8, 4020	R.LGVQDLFNSSK.A	1208.34588	2	5.93E-07	0.89	3.01	-	1065.3
AHQ-5-9, 4906	K.LHEWTKPENLDFIEVNVSLPR.F	2537.85454	2	6.70E-06	0.93	4.21	-	655.0
AHQ-5-13, 4118	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	8.05E-07	0.79	3.55	-	435.9
AHQ-5-8, 3678 - 3753	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	2.94E-11	0.96	4.97	-	1151.2
AHQ-5-8, 3677	K.TYGADLASVDFQHASEDAR.K	2054.11949	3	4.20E-08	0.75	3.64	-	476.8
AHQ-5-13-, 6169	K.TYNFLPEFLVSTQK.T	1687.91650	2	1.11E-04	0.84	3.49	-	483.4
AHQ-5-8, 7173 - 7174	R.VLELPYQGEELSMVILLPDDIEDESTGLKK.I	3375.82891	3	3.51E-06	0.95	5.99	-	628.3
gi|14149680|ref|NP_056107.1| KIAA0747 protein [Homo sapiens]				3.09E-11	3.62	40.25	5.70	122855.6
AHQ-5-12, 5538	R.FEWELPLDEAQR.R	1533.66622	2	1.36E-07	0.84	3.20	-	645.8
AHQ-5-4, 7269 - 7276	R.LLVPLVPDLQDVAQLR.S	1790.13977	2	1.23E-05	0.84	3.31	-	609.4
AHQ-5-12, 3988	R.LTHVDSPLEAPAGPLGQVK.L	1930.19405	2	6.35E-07	0.97	4.97	-	1463.4
AHQ-5-12, 4498 - 4514	K.VQLDLAETDLSQGVAR.W	1715.88665	2	3.09E-11	0.97	4.95	-	2066.5
gi|4505759|ref|NP_002622.1| phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo				3.37E-11	3.76	40.28	12.80	53151.7
AHQ-5-8, 7100 - 7106	K.DAFDRNPELQNLLLDDFFK.S	2311.53482	2	2.27E-06	0.98	5.38	-	1804.2
AHQ-5-8, 6453	K.IKDAFDRNPELQNLLLDDFFK.S	2552.86598	3	3.37E-11	0.94	5.05	-	1399.1
AHQ-5-8, 6048	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	3.24E-08	0.97	5.53	-	1450.6
AHQ-5-8, 4108 - 4110	K.VGTGEPCCDWVGDEGAGHFVK.M	2280.43619	2	3.56E-07	0.87	4.03	-	552.4
gi|5453898|ref|NP_006212.1| protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1; dod;				3.42E-11	1.68	20.21	21.50	18243.2
AHQ-5-12, 5453	K.SGEEDFESLASQFSDCSSAK.A	2183.20603	2	2.15E-04	0.73	2.84	-	586.8
AHQ-5-12, 4061	R.TKEEALELINGYIQK.I	1749.98614	2	3.42E-11	0.95	4.18	-	1420.0
gi|5031857|ref|NP_005557.1| lactate dehydrogenase A [Homo sapiens]				3.45E-11	4.20	60.30	22.00	36688.5
AHQ-5-9, 6468	K.DDVFLSVPCILGQNGISDLVK.V	2291.60655	2	8.35E-04	0.24	2.59	-	224.2
AHQ-5-13-, 6656 - 6659	K.DLADELALVDVIEDK.L	1658.82864	2	3.45E-11	0.98	5.76	-	1811.5
AHQ-5-14-, 6593	K.DLADELALVDVIEDK.L	1658.82864	2	2.06E-10	0.98	5.40	-	2029.7
AHQ-5-13, 6714 - 6716	K.DLADELALVDVIEDK.L	1658.82864	2	1.70E-09	0.98	5.96	-	1974.9
AHQ-5-9, 6438	K.DLADELALVDVIEDKLK.G	1900.15980	2	1.42E-10	0.96	5.20	-	1482.3
AHQ-5-13, 5150	K.DQLIYNLLK.E	1120.32337	2	5.42E-04	0.70	2.61	-	754.7
AHQ-5-9, 6464	K.GLYGIKDDVFLSVPCILGQNGISDLVK.V	2923.37318	2	1.28E-06	0.86	4.11	-	397.8
AHQ-5-9, 6604	K.GYTSWAIGLSVADLAESIMK.N	2113.41967	2	4.30E-05	0.46	3.11	-	369.8
gi|4507793|ref|NP_003339.1| ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast); ubiquitin-conj				3.46E-11	3.83	50.24	36.80	17137.7
AHQ-5-12, 5266 - 5317	K.LELFLPEEYPM*AAPK.V	1765.06265	2	3.48E-05	0.85	3.91	-	420.0
AHQ-5-13, 5369 - 5376	K.LELFLPEEYPM*AAPK.V	1765.06265	2	1.18E-07	0.86	3.88	-	519.2
AHQ-5-12, 5812 - 5814	K.LELFLPEEYPMAAPK.V	1749.06325	2	5.54E-06	0.75	4.11	-	413.1
AHQ-5-13, 5772	K.LELFLPEEYPMAAPK.V	1749.06325	2	2.79E-07	0.83	3.69	-	566.8
AHQ-5-12, 3232	R.LLAEPVPGIK.A	1037.27750	1	1.18E-04	0.30	2.14	-	437.0
AHQ-5-12, 3222	R.LLAEPVPGIK.A	1037.27750	2	1.67E-04	0.65	2.90	-	455.1
AHQ-5-13, 2393 - 2394	K.TNEAQAIETAR.A	1204.27249	2	6.87E-05	0.90	3.35	-	1259.1
AHQ-5-12, 2130	K.TNEAQAIETAR.A	1204.27249	2	3.46E-05	0.88	3.50	-	1016.1
AHQ-5-12, 5245 - 5248	R.YFHVVIAGPQDSPFEGGTFK.L	2197.43341	3	3.46E-11	0.95	4.81	-	1481.0
gi|5729997|ref|NP_004154.2| RAB27B, member RAS oncogene family [Homo sapiens]				3.74E-11	4.98	60.24	40.80	24607.7
AHQ-5-10, 5243	K.AVETLLDLIM*K.R	1262.54151	2	3.77E-05	0.89	3.42	-	904.3
AHQ-5-11, 5620	K.AVETLLDLIM*K.R	1262.54151	2	1.16E-04	0.88	3.71	-	621.7
AHQ-5-10, 6212	K.AVETLLDLIMK.R	1246.54211	2	1.09E-07	0.87	3.76	-	564.8
AHQ-5-10, 5786	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	1.09E-05	0.84	3.20	-	662.3
AHQ-5-11, 6252	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	7.64E-09	0.91	4.59	-	586.2
AHQ-5-10, 5906 - 5966	R.NWMSQLQANAYCENPDIVLIGNK.A	2680.99772	2	2.83E-06	0.91	4.10	-	836.0

AHQ-5-10, 2466 - 2543	K.TQIPDTVNGGNSGNLDGEKPPEKK.C	2496.67285	2	9.61E-04	0.65	3.18	-	422.7
AHQ-5-10, 3268	K.VHLQLWDTAGQER.F	1553.70390	2	3.74E-11	0.98	4.90	-	1918.8
AHQ-5-13-, 4564	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	1.04E-07	0.68	2.79	-	550.4
AHQ-5-10, 4106	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	1.51E-07	0.96	4.79	-	1115.8
gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				3.77E-11	24.18	290.27	51.90	55901.8
AHQ-5-7, 2058	K.AHYGGFTVQNEANK.Y	1536.63020	2	3.93E-09	0.93	3.97	-	971.3
AHQ-5-6, 2256	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.08E-07	0.94	3.86	-	1297.5
AHQ-5-6, 2097	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.67E-06	0.94	3.98	-	1255.4
AHQ-5-11, 2238	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.66E-09	0.93	3.93	-	1026.2
AHQ-5-7, 2227 - 2228	K.AHYGGFTVQNEANK.Y	1536.63020	2	3.69E-05	0.95	4.25	-	1186.4
AHQ-5-7, 3458	K.AHYGGFTVQNEANKYQISVNK.Y	2369.57759	2	4.06E-05	0.84	3.39	-	656.5
AHQ-5-10, 3748 - 3803	K.DNENVVNEYSSELEK.H	1769.80167	2	1.34E-07	0.85	3.68	-	654.3
AHQ-5-9, 3722 - 3727	K.DNENVVNEYSSELEK.H	1769.80167	2	1.48E-05	0.86	3.93	-	741.5
AHQ-5-7, 3978 - 3979	K.DNENVVNEYSSELEK.H	1769.80167	2	1.11E-06	0.93	4.29	-	921.7
AHQ-5-12, 4133	K.DNENVVNEYSSELEK.H	1769.80167	2	6.01E-04	0.50	2.77	-	413.0
AHQ-5-4, 4296	K.DNENVVNEYSSELEK.H	1769.80167	2	1.47E-06	0.87	3.70	-	771.3
AHQ-5-7, 3328	K.DNENVVNEYSSELEK.H	1769.80167	2	5.30E-05	0.78	3.20	-	532.9
AHQ-5-11, 4020 - 4030	K.DNENVVNEYSSELEK.H	1769.80167	2	6.07E-07	0.91	4.13	-	882.4
AHQ-5-6, 3384	K.DNENVVNEYSSELEK.H	1769.80167	2	2.56E-05	0.85	3.52	-	635.1
AHQ-5-2, 4310 - 4331	K.DNENVVNEYSSELEK.H	1769.80167	2	1.42E-04	0.33	2.58	-	362.0
AHQ-5-6, 4365 - 4384	K.DNENVVNEYSSELEK.H	1769.80167	2	8.39E-08	0.92	4.14	-	911.1
AHQ-5-6, 4021 - 4092	K.DNENVVNEYSSELEK.H	1769.80167	2	7.88E-10	0.93	4.49	-	851.3
AHQ-5-12, 3533	K.EDGGGWWYNR.C	1240.26508	2	1.43E-04	0.75	2.74	-	590.0
AHQ-5-6, 3424	K.EDGGGWWYNR.C	1240.26508	2	4.36E-05	0.76	3.05	-	553.3
AHQ-5-7, 3039	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	3	3.76E-04	0.79	3.69	-	720.8
AHQ-5-6, 3157 - 3172	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	3.95E-09	0.54	3.22	-	306.7
AHQ-5-6, 3953	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	8.32E-07	0.69	3.11	-	1049.0
AHQ-5-6, 3425	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	9.26E-05	0.64	3.55	-	324.3
AHQ-5-8, 3672	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	6.22E-05	0.80	3.41	-	1060.4
AHQ-5-7, 3778	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	3.59E-07	0.77	3.56	-	519.5
AHQ-5-9, 3543	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.60E-05	0.89	3.87	-	655.0
AHQ-5-8, 3669	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.10E-06	0.80	3.67	-	468.8
AHQ-5-6, 3884 - 3956	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	2.62E-05	0.93	4.86	-	625.4
AHQ-5-6, 3242 - 3312	K.HGTDDGVVWM*NWK.G	1561.70314	2	1.19E-05	0.96	3.75	-	1571.2
AHQ-5-11, 4067	K.HGTDDGVVWMNWK.G	1545.70374	2	9.36E-09	0.94	3.76	-	1200.7
AHQ-5-6, 4000 - 4002	K.HGTDDGVVWMNWK.G	1545.70374	2	6.81E-09	0.98	5.04	-	1709.2
AHQ-5-7, 3863	K.HGTDDGVVWMNWK.G	1545.70374	2	1.47E-08	0.96	4.92	-	1188.5
AHQ-5-7, 6298 - 6332	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQER.P	3723.12454	3	1.33E-08	0.84	4.29	-	529.3
AHQ-5-11, 6004	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	4089.58482	3	1.21E-05	0.49	3.19	-	261.1
AHQ-5-6, 3376	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	2.83E-09	0.82	3.94	-	494.4
AHQ-5-7, 3266	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.16E-04	0.91	4.78	-	713.9
AHQ-5-7, 3254 - 3322	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	3.37E-05	0.95	5.05	-	973.0
AHQ-5-9, 3088	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	2.38E-06	0.91	4.30	-	727.3
AHQ-5-8, 2997	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	6.68E-04	0.94	4.48	-	1088.5
AHQ-5-8, 2982	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	2.13E-05	0.86	4.63	-	571.4
AHQ-5-6, 3380 - 3389	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	4.22E-05	0.94	5.22	-	839.7
AHQ-5-7, 2862	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	2	6.08E-05	0.79	3.44	-	371.8
AHQ-5-6, 2980	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	2	6.09E-04	0.67	2.79	-	484.8
AHQ-5-6, 2513	K.KREEAPSLRPAPPPISGGGYR.A	2236.51908	3	4.85E-06	0.90	3.94	-	1103.0
AHQ-5-6, 6442 - 6460	R.M*GPTELLIEMEDWK.G	1708.97776	2	9.76E-10	0.96	4.79	-	1455.5
AHQ-5-8, 6786	R.MGPTELLIEMEDWK.G	1692.97836	2	9.04E-05	0.89	3.76	-	781.0
AHQ-5-9, 6179	R.MGPTELLIEMEDWK.G	1692.97836	2	3.66E-08	0.85	3.23	-	970.1
AHQ-5-11, 6548	R.MGPTELLIEMEDWK.G	1692.97836	2	1.95E-06	0.95	4.28	-	1256.5
AHQ-5-6, 6952 - 7016	R.MGPTELLIEMEDWK.G	1692.97836	2	4.40E-07	0.95	4.53	-	1123.3
AHQ-5-6, 5214 - 5282	R.MGPTELLIEM*EDWK.G	1708.97776	2	3.01E-04	0.90	3.79	-	739.6
AHQ-5-10, 6294	R.MGPTELLIEMEDWK.G	1692.97836	2	1.95E-04	0.89	3.66	-	805.2
AHQ-5-7, 6988	R.MGPTELLIEMEDWK.G	1692.97836	2	6.18E-05	0.95	3.98	-	1529.3
AHQ-5-10, 5819	R.M*GPTELLIEMEDWK.G	1708.97776	2	7.46E-07	0.94	4.21	-	1176.4
AHQ-5-11, 4686 - 4719	R.M*GPTELLIEM*EDWK.G	1724.97716	2	2.04E-05	0.88	3.56	-	840.3
AHQ-5-7, 6902 - 6967	R.MGPTELLIEMEDWK.G	1692.97836	2	1.05E-09	0.97	5.37	-	1297.1
AHQ-5-7, 6294 - 6302	R.M*GPTELLIEMEDWK.G	1708.97776	2	2.55E-07	0.96	4.84	-	1409.5
AHQ-5-8, 6021	R.MGPTELLIEMEDWKGDK.V	1993.29069	3	4.09E-06	0.87	4.01	-	621.3
AHQ-5-7, 6080 - 6160	R.MGPTELLIEMEDWKGDK.V	1993.29069	2	7.71E-05	0.82	3.52	-	497.7
AHQ-5-6, 5830	K.NYCGLPGEYWLGNDK.I	1787.92994	2	1.95E-07	0.89	3.89	-	390.4
AHQ-5-6, 5162 - 5173	K.NYCGLPGEYWLGNDK.I	1787.92994	2	3.73E-04	0.92	4.18	-	470.0
AHQ-5-6, 5293 - 5360	K.NYCGLPGEYWLGNDK.I	1787.92994	2	3.77E-11	0.95	4.91	-	606.3
AHQ-5-7, 5859	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	2	2.73E-07	0.84	3.43	-	531.2
AHQ-5-6, 5750 - 5817	R.TMTIHNGMFFSTYDRDNDGWLTSDPR.K	3079.32935	3	8.33E-04	0.72	4.11	-	226.3
AHQ-5-8, 3577 - 3581	R.TPCTVSCNIPVVSGK.E	1621.85811	2	6.24E-06	0.89	3.61	-	777.4
AHQ-5-6, 3710 - 3784	R.TPCTVSCNIPVVSGK.E	1621.85811	2	3.25E-05	0.92	3.90	-	713.5
AHQ-5-7, 3610 - 3647	R.TPCTVSCNIPVVSGK.E	1621.85811	2	8.19E-05	0.83	3.59	-	490.5
AHQ-5-8, 4622 - 4628	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	2.63E-09	0.94	4.38	-	1450.4
AHQ-5-7, 4786	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	5.94E-07	0.90	3.79	-	1272.9
AHQ-5-6, 5036	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	2.76E-05	0.73	3.54	-	593.4
AHQ-5-3, 5179 - 5198	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	8.33E-04	0.87	3.82	-	931.3
AHQ-5-6, 4876 - 4950	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	3.26E-08	0.95	4.89	-	1347.9
AHQ-5-6, 4881 - 4952	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.47E-08	0.71	3.25	-	289.8
AHQ-5-4, 5121	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	2.18E-06	0.90	4.50	-	1040.9
AHQ-5-9, 4370	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	9.15E-05	0.86	3.47	-	955.4
AHQ-5-9, 4088	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	5.10E-09	0.94	4.55	-	1153.0
AHQ-5-8, 4354	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.41E-08	0.93	4.54	-	707.2
AHQ-5-7, 4560 - 4636	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	4.60E-07	0.91	4.56	-	518.2
AHQ-5-7, 4415 - 4495	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.53E-08	0.96	4.67	-	1363.7
AHQ-5-7, 3951	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	3.65E-06	0.91	3.74	-	889.2
AHQ-5-6, 4522 - 4540	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.94E-06	0.93	4.15	-	890.6
AHQ-5-6, 4649	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.80E-07	0.83	3.25	-	770.8
AHQ-5-6, 4033	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	4.47E-06	0.94	4.04	-	1008.7
AHQ-5-7, 1775	K.YQISVNK.Y	851.96999	1	6.15E-05	0.36	2.49	-	296.4
AHQ-5-6, 1814 - 1820	K.YQISVNK.Y	851.96999	1	7.62E-04	0.44	2.14	-	488.2
AHQ-5-11, 4890	R.YYWGGQYTWDMAK.H	1669.84009	2	6.54E-04	0.92	3.13	-	1192.0
AHQ-5-6, 4350 - 4420	R.YYWGGQYTWDM*AK.H	1685.83949	2	2.82E-05	0.88	3.30	-	815.1
AHQ-5-6, 5028	R.YYWGGQYTWDMAK.H	1669.84009	2	8.93E-05	0.96	4.36	-	1253.6
AHQ-5-6, 4998 - 5068	R.YYWGGQYTWDMAK.H	1669.84009	2	1.75E-05	0.94	3.92	-	947.9
AHQ-5-12, 5065 - 5130	R.YYWGGQYTWDMAK.H	1669.84009	2	2.16E-04	0.93	3.88	-	924.8
AHQ-5-14-, 4427 - 4497	R.YYWGGQYTWDM*AK.H	1685.83949	2	9.66E-07	0.91	2.98	-	1048.0
AHQ-5-14-, 4971	R.YYWGGQYTWDMAK.H	1669.84009	2	7.13E-06	0.96	3.49	-	1572.2
gi|4504183|ref|NP_000843.1| glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s				3.93E-11	4.63	50.30	39.50	23355.7
AHQ-5-11, 5256 - 5286	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	1.06E-05	0.86	3.99	-	468.5
AHQ-5-10, 4788	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.18E-05	0.85	3.54	-	441.6
AHQ-5-11, 5162 - 5211	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.78E-08	0.92	4.19	-	490.9
AHQ-5-12, 5398	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	1.55E-05	0.59	3.14	-	296.0
AHQ-5-11, 5164 - 5168	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	3	6.46E-06	0.60	3.44	-	710.2
AHQ-5-11, 3098	K.ASCLYGQLPK.F	1138.31884	2	3.23E-06	0.91	3.30	-	917.2
AHQ-5-11, 3030 - 3099	K.ASCLYGQLPK.F	1138.31884	2	1.10E-06	0.87	2.97	-	930.4
AHQ-5-13, 6476	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	2.69E-07	0.91	4.05	-	855.5
AHQ-5-11, 6227 - 6290	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.84E-08	0.95	4.35	-	1224.9
AHQ-5-14-, 6294 - 6305	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.38E-06	0.96	5.12	-	1040.2

AHQ-5-10, 5999 - 6002	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	8.82E-06	0.97	5.92	-	1213.6
AHQ-5-11, 6275 - 6276	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	3	2.59E-06	0.97	5.22	-	2002.5
AHQ-5-11, 6455	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.83E-06	0.90	3.71	-	858.9
AHQ-5-11, 4947	K.FQDGDLTLYQSNTILR.H	1885.06701	2	7.55E-08	0.93	4.49	-	787.5
AHQ-5-11, 4858	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.18E-08	0.93	4.44	-	872.0
AHQ-5-11, 4731 - 4795	K.FQDGDLTLYQSNTILR.H	1885.06701	2	3.18E-10	0.96	4.87	-	1026.3
AHQ-5-14-, 4881	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.27E-06	0.95	4.93	-	982.3
AHQ-5-13-, 4919	K.FQDGDLTLYQSNTILR.H	1885.06701	2	2.61E-05	0.91	4.74	-	531.6
AHQ-5-14, 5721	K.FQDGDLTLYQSNTILR.H	1885.06701	2	5.04E-06	0.95	3.95	-	1276.9
AHQ-5-13, 5005 - 5009	K.FQDGDLTLYQSNTILR.H	1885.06701	2	6.81E-04	0.72	3.28	-	484.2
AHQ-5-10, 4502	K.FQDGDLTLYQSNTILR.H	1885.06701	2	6.54E-06	0.95	4.88	-	935.1
AHQ-5-13-, 4589	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	3.93E-11	0.93	4.67	-	597.1
AHQ-5-11, 4512	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	1.49E-07	0.93	4.49	-	786.9
AHQ-5-11, 4620	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	9.58E-05	0.93	4.70	-	685.7
AHQ-5-13, 4669	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	2.53E-09	0.95	4.51	-	960.9
AHQ-5-11, 4392 - 4403	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	8.17E-07	0.83	3.84	-	434.7
gi|27498267|ref|XP_209737.1| similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,				3.93E-11	3.28	40.33	33.70	11063.6
AHQ-5-14-, 6702 - 6714	R.DICNDVLSLLEK.F	1420.61093	2	1.13E-06	0.97	5.00	-	1770.1
AHQ-5-10, 6464 - 6479	R.DICNDVLSLLEK.F	1420.61093	2	1.43E-06	0.97	4.97	-	2248.9
AHQ-5-10, 6463 - 6527	R.DICNDVLSLLEK.F	1420.61093	1	3.75E-04	0.79	3.05	-	701.0
AHQ-5-9, 5511	R.DICNDVLSLLEK.F	1420.61093	1	6.45E-09	0.24	2.12	-	558.2
AHQ-5-9, 6431 - 6432	R.DICNDVLSLLEK.F	1420.61093	2	2.28E-07	0.96	4.61	-	1495.4
AHQ-5-9, 6475	R.DICNDVLSLLEK.F	1420.61093	1	3.35E-04	0.63	2.78	-	591.0
AHQ-5-10, 5587	R.DICNDVLSLLEK.F	1420.61093	1	9.71E-09	0.37	2.59	-	531.0
AHQ-5-10, 5586 - 5594	R.DICNDVLSLLEK.F	1420.61093	2	7.98E-07	0.95	4.40	-	1279.7
AHQ-5-10, 5582	R.DICNDVLSLLEK.F	1420.61093	1	7.55E-10	0.44	2.27	-	630.4
AHQ-5-11, 5875	R.DICNDVLSLLEK.F	1420.61093	2	7.20E-05	0.97	3.99	-	1933.4
AHQ-5-10, 4664 - 4722	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.16E-08	0.98	5.69	-	1488.5
AHQ-5-10, 4710	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.01E-09	0.98	5.52	-	2436.9
AHQ-5-10, 4754 - 4814	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.85E-10	0.97	5.40	-	1384.4
AHQ-5-10, 4878 - 4938	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.32E-10	0.97	5.58	-	1472.3
AHQ-5-10, 4998 - 5058	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.16E-07	0.96	5.01	-	1207.6
AHQ-5-10, 5134 - 5210	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.29E-06	0.97	5.13	-	1531.0
AHQ-5-10, 4431 - 4494	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.51E-10	0.97	5.39	-	1569.3
AHQ-5-10, 5458 - 5463	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	9.60E-07	0.97	4.64	-	1607.0
AHQ-5-10, 5564 - 5627	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.27E-08	0.97	5.28	-	1189.7
AHQ-5-10, 5566	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.19E-06	0.84	3.76	-	624.0
AHQ-5-10, 4272 - 4332	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.73E-10	0.96	5.11	-	1299.2
AHQ-5-13-, 5079 - 5083	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.23E-06	0.97	5.44	-	1555.6
AHQ-5-14-, 5033	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.33E-09	0.97	5.60	-	1207.1
AHQ-5-10, 5830 - 5896	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.14E-04	0.88	3.84	-	953.9
AHQ-5-10, 5958 - 6028	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.58E-06	0.88	3.64	-	980.4
AHQ-5-10, 6266 - 6331	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.44E-06	0.94	4.11	-	1133.0
AHQ-5-10, 6388	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.14E-04	0.78	3.43	-	395.3
AHQ-5-9, 4674	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.61E-08	0.96	4.63	-	1337.0
AHQ-5-6, 5238 - 5241	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	6.87E-08	0.97	5.31	-	1652.5
AHQ-5-11, 4732	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.70E-07	0.93	4.29	-	822.5
AHQ-5-11, 5014 - 5015	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.93E-11	0.97	5.00	-	1463.4
AHQ-5-11, 5031	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	9.02E-10	0.98	6.61	-	2590.7
AHQ-5-10, 5367 - 5395	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.03E-10	0.97	5.75	-	1188.6
AHQ-5-12, 5180 - 5246	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.87E-09	0.96	4.62	-	1341.4
AHQ-5-13, 5200	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.60E-09	0.97	5.46	-	1164.9
AHQ-5-5, 5311	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.06E-09	0.94	4.84	-	747.7
AHQ-5-10, 4268 - 4271	K.GIVDQSQQAYQEAFEISKK.E	2170.36467	2	1.29E-05	0.90	3.88	-	1049.7
AHQ-5-10, 4080 - 4151	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	6.88E-06	0.95	5.05	-	815.9
AHQ-5-13-, 4581	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	2.56E-06	0.97	5.31	-	1477.8
gi|4758208|ref|NP_004081.1| dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;				4.15E-11	5.12	60.23	45.90	20478.2
AHQ-5-11, 4096 - 4166	R.AADFIDQALAQK.N	1291.43488	1	6.59E-07	0.45	2.69	-	588.4
AHQ-5-11, 5359 - 5390	K.ANDTQEFNLSAYFER.A	1805.88207	2	7.12E-09	0.94	4.09	-	1248.7
AHQ-5-11, 6103 - 6119	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	4.15E-11	0.93	4.59	-	866.8
AHQ-5-11, 5958 - 6023	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	9.53E-06	0.94	4.45	-	1006.4
AHQ-5-11, 3638	R.IYVGNASVAQDIPK.L	1475.67136	2	4.08E-04	0.94	3.79	-	1095.1
AHQ-5-11, 3271 - 3275	K.LGITHVLNAAEGR.S	1351.53669	2	4.58E-08	0.93	3.73	-	1177.3
AHQ-5-11, 2938	K.LGITHVLNAAEGR.S	1351.53669	2	2.04E-05	0.84	2.82	-	944.1
AHQ-5-11, 3498	R.SFMHVNTNANFYK.D	1573.75708	2	2.66E-05	0.93	3.40	-	1213.8
gi|7661818|ref|NP_054900.1| HSPC159 protein [Homo sapiens]				4.50E-11	4.75	60.33	50.00	19011.6
AHQ-5-14-, 6631	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.20E-05	0.82	3.99	-	255.6
AHQ-5-13-, 6628 - 6691	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.84E-08	0.88	3.97	-	397.0
AHQ-5-13, 6736	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	2.02E-07	0.86	3.78	-	382.4
AHQ-5-12, 6773 - 6836	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.52E-04	0.29	2.59	-	209.0
AHQ-5-11, 6623 - 6630	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	1.41E-06	0.87	3.76	-	437.3
AHQ-5-14-, 6633	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	4.97E-06	0.91	4.19	-	491.5
AHQ-5-12, 2522	K.INGDLQITK.L	1002.14688	1	2.24E-05	0.54	2.13	-	491.6
AHQ-5-13, 3793	R.IQTLSAIDTIK.I	1203.41068	2	6.21E-04	0.69	2.80	-	502.0
AHQ-5-11, 4759	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	2	6.64E-07	0.97	5.69	-	1186.9
AHQ-5-11, 4903 - 4971	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	2	2.94E-10	0.98	6.69	-	1861.1
AHQ-5-8, 5952	R.VEILCEYPRFRVFVDGHQLFDFYHR.I	3245.65958	3	6.81E-04	0.70	3.23	-	734.0
AHQ-5-11, 4694	R.VFVDGHQLFDFYHR.I	1780.96540	3	8.89E-10	0.87	4.02	-	551.8
AHQ-5-11, 4687 - 4696	R.VFVDGHQLFDFYHR.I	1780.96540	2	4.50E-11	0.96	4.55	-	1405.0
AHQ-5-11, 4796	R.VFVDGHQLFDFYHR.I	1780.96540	2	6.81E-04	0.93	3.94	-	943.9
AHQ-5-12, 4873	R.VFVDGHQLFDFYHR.I	1780.96540	2	1.14E-10	0.94	3.75	-	1535.3
gi|5729887|ref|NP_006624.1| IQ motif containing GTPase activating protein 2 [Homo sapiens]				4.51E-11	6.98	80.25	9.30	180611.0
AHQ-5-5, 3485	K.AWVNQLETQTGEASK.L	1662.78230	2	1.03E-07	0.91	4.08	-	858.3
AHQ-5-3, 5869	K.GVLLDIDDLQTNQFK.N	1719.91690	2	1.85E-06	0.96	4.86	-	1379.1
AHQ-5-6, 7436	K.IGGILANELSVDEAALHAAVIAINEAVEK.G	2932.31842	3	1.25E-09	0.92	4.90	-	1000.2
AHQ-5-3, 5998	K.LGIAPQIQDLLGK.V	1366.63117	2	2.67E-05	0.84	3.50	-	497.6
AHQ-5-3, 4989	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	4.55E-08	0.95	4.56	-	1280.6
AHQ-5-2, 4942 - 4951	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	4.51E-11	0.94	4.46	-	1091.0
AHQ-5-4, 4952	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	6.52E-09	0.97	5.07	-	1763.1
AHQ-5-5, 6943	R.NQPGNTLTEILETPATAQQEVDHATDMVSR.A	3268.51558	3	2.03E-06	0.84	3.93	-	465.8
AHQ-5-3, 7115	R.NQPGNTLTEILETPATAQQEVDHATDMVSR.A	3268.51558	3	3.54E-08	0.89	4.26	-	597.4
AHQ-5-3, 3022	R.SPAIGLNNLDK.A	1142.28743	1	2.33E-04	0.56	2.66	-	423.8
AHQ-5-4, 4264	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	2.40E-07	0.95	4.94	-	1228.4
gi|29730023|ref|XP_291482.1| similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno				4.55E-11	5.19	60.23	14.10	63563.0
AHQ-5-8, 4376	R.IINKPTAAAIAYGLDK.R	1659.95097	2	4.69E-06	0.80	3.15	-	890.2
AHQ-5-7, 4476 - 4487	R.IINKPTAAAIAYGLDK.R	1659.95097	2	4.81E-05	0.84	3.47	-	829.0
AHQ-5-6, 4198 - 4209	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	8.50E-07	0.88	4.64	-	1036.5
AHQ-5-6, 3228	K.KKELEEIVQPIISK.L	1654.97263	2	1.91E-06	0.88	4.39	-	567.9
AHQ-5-5, 3451 - 3481	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	5.87E-06	0.90	4.47	-	660.7
AHQ-5-7, 3210	K.NQLTSNPKNTVFDAK.R	1677.84011	2	1.10E-05	0.52	3.50	-	256.5
AHQ-5-5, 3345	K.NQLTSNPKNTVFDAK.R	1677.84011	2	4.75E-11	0.86	3.88	-	918.9
AHQ-5-6, 5560 - 5572	K.TFAPKEISAMVLTK.M	1536.86124	2	4.55E-11	0.87	3.23	-	1104.0
gi|4507677|ref|NP_003290.1| tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu				4.75E-11	8.50	100.28	18.10	92468.2
AHQ-5-5, 6454	R.EAVEKEFEPLLNWMK.D	1864.15434	2	1.38E-05	0.92	4.13	-	722.7
AHQ-5-5, 4461	K.EEASDYLELDTIK.N	1526.62393	2	1.07E-04	0.58	2.79	-	584.8
AHQ-5-5, 3711 - 3713	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	8.52E-06	0.96	5.23	-	1142.6
AHQ-5-1, 4135	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	2.67E-04	0.77	3.46	-	488.2

AHQ-5-5, 3985 - 3989	K.GVVDSDDLPLNVSR.E	1486.60940	1	8.63E-04	0.55	2.83	-	381.1
AHQ-5-5, 6917	K.GYEVIYLTEPVDEYCIQALPEFDGKR.F	3107.43557	3	9.08E-09	0.81	3.96	-	498.4
AHQ-5-5, 3475	K.IADDKYNDTFWK.E	1516.63566	2	5.23E-07	0.92	3.60	-	958.5
AHQ-5-5, 6321	K.KYSQFINFPIYVWSSK.T	2008.30657	2	8.31E-09	0.97	4.46	-	1790.3
AHQ-5-5, 5269	R.LISLTDENALSGNEELTVK.I	2047.24975	2	4.75E-11	0.94	4.51	-	1034.3
AHQ-5-5, 3889 - 3901	K.SILFVPTSAPR.G	1188.40094	2	5.10E-05	0.88	3.40	-	1088.6
AHQ-5-5, 6941 - 6945	K.YSQFINFPIYVWSSK.T	1880.13366	2	1.58E-07	0.97	5.60	-	1337.5
gi|4885413|ref|NP_005331.1| histidine triad nucleotide binding protein 1; Histidine triad nucleotid				4.89E-11	3.68	40.30	47.60	13801.8
AHQ-5-13-, 2345	K.CAADLGLNK.G	963.09080	2	5.48E-05	0.82	2.86	-	785.2
AHQ-5-13-, 5515 - 5549	R.CLAFHDISPQAPTHFLVIPK.K	2293.67220	3	2.07E-07	0.97	5.34	-	1810.5
AHQ-5-13-, 6072	K.IIFEDDRCLAFHDISPQAPTHFLVIPK.K	3182.64001	3	5.16E-06	0.96	5.90	-	1291.7
AHQ-5-13, 6136	K.IIFEDDRCLAFHDISPQAPTHFLVIPK.K	3182.64001	3	1.21E-05	0.96	5.47	-	1331.8
AHQ-5-13-, 3865	R.MVVNEGSDGGQSVYHVHLHVLGGR.Q	2548.82255	3	4.89E-11	0.94	4.58	-	1382.0
gi|7657007|ref|NP_055210.1| dual adaptor of phosphotyrosine and 3-phosphoinositides [Homo sapiens]				4.93E-11	1.63	20.20	11.80	32044.2
AHQ-5-13-, 3876 - 3881	R.DSNETTGLYSLSVR.A	1542.62982	2	1.36E-05	0.71	2.95	-	574.2
AHQ-5-12, 5113	R.HAAEALLLSNGCDGSYLLR.D	2062.29263	2	4.93E-11	0.93	3.93	-	1134.9
gi|4557419|ref|NP_000063.1| CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36				4.96E-11	3.59	40.25	12.70	53052.1
AHQ-5-5, 4709 - 4747	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.07E-06	0.91	3.91	-	755.7
AHQ-5-4, 4872	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	2.45E-04	0.71	3.45	-	362.5
AHQ-5-3, 4917	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.55E-07	0.76	3.30	-	483.0
AHQ-5-1, 4919 - 4929	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	3.99E-05	0.84	3.57	-	645.8
AHQ-5-5, 2994 - 2998	R.LQVNLLVKPSEK.I	1368.64707	2	3.37E-05	0.90	3.35	-	1313.7
AHQ-5-4, 5728 - 5738	K.SQVLQFFSSDICR.S	1588.76661	2	1.45E-08	0.95	3.94	-	1182.2
AHQ-5-5, 5481 - 5487	K.SQVLQFFSSDICR.S	1588.76661	2	2.79E-08	0.96	4.62	-	1340.5
AHQ-5-1, 5843	K.SQVLQFFSSDICR.S	1588.76661	2	2.85E-04	0.75	2.59	-	695.6
AHQ-5-6, 5473	K.SQVLQFFSSDICR.S	1588.76661	2	3.82E-09	0.96	4.42	-	1442.3
AHQ-5-5, 7255 - 7265	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	4.96E-11	0.96	4.92	-	1323.2
AHQ-5-1, 7223	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.77E-10	0.97	4.86	-	1484.6
gi|5453607|ref|NP_006420.1| chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co				5.00E-11	1.64	20.23	6.60	59366.3
AHQ-5-7, 4903 - 4906	K.LPIGDVATQYFADR.D	1566.73935	2	5.00E-11	0.96	4.64	-	1313.8
AHQ-5-7, 7023 - 7096	K.SQDAEVGDGTTSVTLLAAEFLK.Q	2253.44875	2	3.16E-04	0.68	3.12	-	494.2
gi|10346135|ref|NP_055083.1| microtubule-associated protein, RP/EB family, member 2; T-cell activat				5.73E-11	1.90	20.32	9.80	37031.1
AHQ-5-9, 6219	R.FQDNLDFIQWFK.K	1601.78539	2	1.33E-06	0.96	4.20	-	1426.4
AHQ-5-12, 6846 - 6853	R.FQDNLDFIQWFK.K	1601.78539	2	2.42E-08	0.96	4.71	-	1220.1
AHQ-5-14-, 6639	R.FQDNLDFIQWFK.K	1601.78539	2	1.48E-09	0.92	3.50	-	1121.4
AHQ-5-12, 4914	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	2	3.42E-08	0.94	4.46	-	1082.7
AHQ-5-12, 4900	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	2.58E-07	0.79	3.76	-	772.2
AHQ-5-9, 4212 - 4214	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	2	5.73E-11	0.98	6.34	-	1261.3
gi|4758304|ref|NP_004902.1| protein disulfide isomerase related protein (calcium-binding protein, i				5.90E-11	5.04	60.25	12.20	72931.9
AHQ-5-6, 4620	K.DLGLSESGEDVNAAILDESGKK.F	2248.38737	2	5.90E-11	0.96	5.09	-	1315.1
AHQ-5-6, 3742	K.FAM*EPEEFDSDTLR.E	1703.80830	2	1.31E-04	0.85	3.26	-	612.8
AHQ-5-6, 4585	K.FAMEPEEFDSDTLR.E	1687.80890	2	8.01E-08	0.82	3.92	-	522.3
AHQ-5-6, 3845	K.GESDPAYQQYQDAANNLR.E	2041.08081	2	9.52E-11	0.89	4.26	-	623.8
AHQ-5-6, 2768	K.IDATSASVLASR.F	1191.31686	2	3.10E-06	0.94	3.71	-	1375.2
AHQ-5-6, 2746	K.VSQGQLVVMQPEK.F	1443.69431	1	2.52E-06	0.58	2.84	-	519.1
gi|7705296|ref|NP_057271.1| bridging integrator 2; bridging integrator-2; breast cancer associated				6.06E-11	4.69	60.26	18.10	61746.8
AHQ-5-7, 6135	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	2.38E-07	0.90	3.69	-	1004.0
AHQ-5-10, 5567 - 5643	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	6.06E-11	0.90	3.76	-	914.6
AHQ-5-7, 7378 - 7383	K.AQTVFEDLNQELLEELPILYNSR.I	2736.02649	2	1.20E-07	0.82	3.75	-	480.2
AHQ-5-10, 2544	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	8.56E-06	0.83	3.37	-	492.9
AHQ-5-6, 6812	R.IGCYVTIFQNISNLR.D	1800.07167	2	1.08E-04	0.93	3.99	-	1045.0
AHQ-5-9, 5963 - 6035	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.27E-07	0.94	4.43	-	1007.8
AHQ-5-10, 6067 - 6130	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.62E-08	0.95	5.21	-	811.0
AHQ-5-10, 2598	K.LNHNLYEVMSK.L	1348.55307	2	6.78E-05	0.71	2.77	-	694.5
AHQ-5-10, 4496 - 4555	R.VSETLQEIYSSEWDGHEELK.A	2380.50595	2	8.82E-06	0.49	2.80	-	318.0
gi|5803227|ref|NP_006817.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype				6.23E-11	4.59	60.29	33.10	27764.1
AHQ-5-10, 1522	K.EMQPTHPIR.L	1109.28418	1	1.59E-05	0.09	1.89	-	71.7
AHQ-5-10, 3536	R.KQTIDNSQGAYQEAFDISK.K	2144.28408	2	5.37E-04	0.88	3.91	-	566.4
AHQ-5-10, 6451	R.SICTTVLELLDK.Y	1393.62862	2	9.89E-05	0.89	3.61	-	870.5
AHQ-5-13-, 6615 - 6621	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	3.44E-09	0.97	5.48	-	1214.0
AHQ-5-13, 6677	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	1.48E-06	0.96	4.63	-	1294.5
AHQ-5-14-, 6521	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	1.34E-07	0.98	5.87	-	1702.1
AHQ-5-10, 6548 - 6622	K.TAFDEAIAELDTLNEDSYKDSTLIM*QLLR.D	3333.66581	3	6.23E-11	0.95	5.59	-	1078.2
AHQ-5-10, 2458	K.YLIANATNPESK.V	1321.46099	2	4.62E-05	0.96	4.03	-	1560.0
AHQ-5-10, 2459	K.YLIANATNPESK.V	1321.46099	1	8.48E-07	0.91	4.26	-	724.8
AHQ-5-10, 2572 - 2574	K.YLIANATNPESK.V	1321.46099	1	1.48E-07	0.82	3.00	-	769.5
gi|4503445|ref|NP_001944.1| endothelial cell growth factor 1 (platelet-derived); thymidine phosphor				6.36E-11	3.37	40.28	14.30	49955.2
AHQ-5-7, 6503	R.ALPLALVLHELGAGR.S	1530.83966	2	6.36E-11	0.98	5.69	-	1511.0
AHQ-5-7, 7399	R.DLVTTLGGALLWLSGHAGTQAQGAAR.V	2565.86952	3	1.24E-04	0.92	4.04	-	1205.9
AHQ-5-7, 7318 - 7398	R.DLVTTLGGALLWLSGHAGTQAQGAAR.V	2565.86952	2	1.90E-05	0.80	3.07	-	681.1
AHQ-5-7, 2826	K.FGGAAVFPNQEQAR.E	1492.62056	2	1.77E-04	0.67	2.68	-	754.1
AHQ-5-7, 2840	R.VAAALTAMDKPLGR.C	1414.69933	2	6.79E-05	0.93	3.32	-	1285.5
gi|12025678|ref|NP_004915.2| actinin, alpha 4 [Homo sapiens]				7.56E-11	5.62	70.25	14.30	104853.3
AHQ-5-5, 4401	K.AGTQIENIDEDFRDGLK.L	1922.04251	2	1.15E-06	0.93	4.67	-	1018.4
AHQ-5-4, 4856	R.ETTDTDTADQVIASFK.V	1742.81936	2	2.29E-06	0.90	3.63	-	1020.8
AHQ-5-5, 2778 - 2782	K.GISQEQMQEFR.A	1353.48658	2	1.04E-07	0.73	3.14	-	978.1
AHQ-5-5, 4051	K.MLDAEDIVNTARPDEK.A	1817.99924	3	7.56E-11	0.88	4.06	-	595.2
AHQ-5-5, 4046	K.MLDAEDIVNTARPDEK.A	1817.99924	2	6.53E-06	0.90	4.08	-	753.1
AHQ-5-5, 3937 - 3962	K.MVSDINNGWQHLEQAEK.G	2000.18160	2	5.26E-09	0.37	2.52	-	370.6
AHQ-5-5, 7221	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	3.49E-07	0.89	4.57	-	834.7
AHQ-5-6, 7129	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	7.17E-06	0.90	4.93	-	743.3
AHQ-5-7, 7082	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	6.54E-05	0.78	4.23	-	508.2
AHQ-5-5, 6513 - 6594	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	1.23E-08	0.92	4.98	-	720.6
gi|4503821|ref|NP_001456.1| FYN binding protein (FYB-120/130); FYN-binding protein (FYB-120/130) [H				7.63E-11	0.93	10.24	2.60	85450.5
AHQ-5-12, 4157	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	7.63E-11	0.93	4.84	-	537.4
AHQ-5-10, 3806	R.DLQVKPGESLEVIQTTDDTK.V	2217.41641	2	5.39E-06	0.83	3.68	-	396.3
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				8.16E-11	12.32	160.34	51.90	49481.2
AHQ-5-8, 4177 - 4178	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	4.96E-04	0.88	4.21	-	452.4
AHQ-5-9, 4040	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	2.21E-05	0.55	3.19	-	236.0
AHQ-5-7, 4308 - 4390	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	2.19E-05	0.89	4.45	-	532.5
AHQ-5-1, 4332	K.AIQLTYNPDESSKPNM*IDAATLK.S	2537.82826	3	9.22E-04	0.59	3.00	-	371.6
AHQ-5-7, 4543 - 4623	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	2.87E-04	0.73	3.54	-	391.0
AHQ-5-11, 4590	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	3.87E-05	0.53	2.78	-	258.2
AHQ-5-5, 4581	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	5.74E-09	0.84	3.87	-	465.1
AHQ-5-5, 4578	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	2.95E-07	0.87	4.05	-	606.6
AHQ-5-7, 4402 - 4474	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	6.47E-05	0.84	3.98	-	406.7
AHQ-5-3, 4866	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	3.69E-04	0.57	3.03	-	402.3
AHQ-5-7, 6908 - 6976	K.ANQQFLVYCEIDGSGNGWTVFQK.R	2663.90221	2	1.39E-08	0.45	2.80	-	276.2
AHQ-5-7, 7039 - 7106	K.ANQQFLVYCEIDGSGNGWTVFQK.R	2663.90221	2	1.74E-06	0.81	3.82	-	487.3
AHQ-5-7, 5422 - 5490	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	4.41E-10	0.75	3.05	-	606.7
AHQ-5-13, 5493 - 5562	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	5.94E-08	0.39	2.53	-	442.3
AHQ-5-14-, 5327 - 5393	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	5.99E-06	0.80	3.21	-	679.1
AHQ-5-7, 5559 - 5636	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	6.36E-07	0.81	3.24	-	534.2
AHQ-5-4, 5894	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	4.68E-06	0.71	3.09	-	329.6
AHQ-5-4, 5720	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	9.23E-08	0.84	3.41	-	700.0
AHQ-5-14, 6124 - 6136	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.68E-05	0.63	3.12	-	324.9
AHQ-5-5, 2499	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	1.14E-07	0.94	4.46	-	968.9

AHQ-5-13, 2861	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.27E-06	0.93	4.75	-	732.9
AHQ-5-13, 2865 - 2941	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	1.40E-05	0.96	4.23	-	2118.5
AHQ-5-7, 2422 - 2495	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	7.51E-07	0.97	5.38	-	1397.6
AHQ-5-14-, 2661	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	7.66E-07	0.95	4.23	-	1274.6
AHQ-5-13-, 2724	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	3.95E-07	0.97	5.08	-	2414.3
AHQ-5-13-, 2728 - 2799	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.37E-10	0.97	5.43	-	1099.7
AHQ-5-4, 5422	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	5.13E-04	0.92	4.21	-	1545.9
AHQ-5-5, 5326 - 5339	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.38E-05	0.89	3.94	-	900.0
AHQ-5-4, 5424	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.43E-04	0.87	3.90	-	595.6
AHQ-5-1, 5527	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	3.03E-05	0.87	3.57	-	1365.3
AHQ-5-12, 5214	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	6.14E-05	0.92	4.13	-	1542.6
AHQ-5-3, 5453	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	9.56E-05	0.93	4.70	-	536.9
AHQ-5-10, 4682	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	4.12E-05	0.86	3.67	-	589.9
AHQ-5-9, 4667	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.37E-07	0.71	3.50	-	454.6
AHQ-5-7, 5051 - 5126	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.51E-08	0.96	5.21	-	1019.6
AHQ-5-8, 4749 - 4750	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.28E-04	0.91	4.19	-	684.8
AHQ-5-6, 5116	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.98E-05	0.92	4.35	-	681.7
AHQ-5-7, 4910 - 4978	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.09E-04	0.94	4.68	-	698.0
AHQ-5-11, 6378 - 6379	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.87E-07	0.73	3.00	-	481.3
AHQ-5-12, 6609	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	5.95E-06	0.82	4.18	-	439.5
AHQ-5-14-, 6406 - 6409	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	4.69E-05	0.88	3.78	-	658.1
AHQ-5-12, 6612	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	9.65E-07	0.85	4.02	-	504.9
AHQ-5-13, 6597 - 6601	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	8.87E-04	0.82	3.54	-	535.8
AHQ-5-1, 6959 - 6960	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	8.21E-05	0.60	3.43	-	576.4
AHQ-5-13-, 6503	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	2.45E-05	0.92	3.60	-	1030.9
AHQ-5-10, 6066 - 6128	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	7.19E-05	0.86	4.16	-	667.9
AHQ-5-5, 4402	K.IHLISTQSAIPYALR.V	1683.97576	2	1.87E-07	0.91	3.55	-	985.8
AHQ-5-8, 3857 - 3858	K.IHLISTQSAIPYALR.V	1683.97576	2	8.16E-11	0.97	4.97	-	1334.4
AHQ-5-7, 4080 - 4159	K.IHLISTQSAIPYALR.V	1683.97576	2	1.12E-09	0.97	5.29	-	1287.4
AHQ-5-4, 4610 - 4684	K.IHLISTQSAIPYALR.V	1683.97576	2	4.39E-04	0.96	4.82	-	1216.8
AHQ-5-2, 4649	K.IHLISTQSAIPYALR.V	1683.97576	2	5.17E-09	0.96	4.84	-	1335.4
AHQ-5-4, 4680	K.IHLISTQSAIPYALR.V	1683.97576	2	2.62E-09	0.96	4.90	-	1323.5
AHQ-5-3, 4753	K.IHLISTQSAIPYALR.V	1683.97576	2	8.41E-08	0.94	4.44	-	910.0
AHQ-5-9, 3787 - 3846	K.IHLISTQSAIPYALR.V	1683.97576	2	1.50E-06	0.94	4.40	-	1085.4
AHQ-5-9, 3878	K.IHLISTQSAIPYALR.V	1683.97576	2	6.41E-05	0.95	4.04	-	1233.7
AHQ-5-7, 1671	R.LDGSVDFKK.N	1009.13788	2	3.63E-05	0.41	2.64	-	437.4
AHQ-5-4, 1973	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	9.04E-09	0.88	3.53	-	861.7
AHQ-5-7, 1768 - 1836	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	8.81E-04	0.82	3.62	-	478.4
AHQ-5-11, 1975	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	8.96E-06	0.87	3.55	-	799.3
AHQ-5-14-, 2101	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.34E-04	0.96	4.53	-	1224.8
AHQ-5-13-, 2139	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.63E-06	0.93	4.00	-	1066.0
AHQ-5-13, 2303	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.67E-08	0.95	4.48	-	1351.5
AHQ-5-9, 2632	R.TSTADYAMFK.V	1135.27203	1	7.10E-04	0.17	2.15	-	161.9
AHQ-5-7, 3662	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	5.97E-07	0.81	3.89	-	638.0
AHQ-5-1, 4129	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	5.33E-07	0.92	4.70	-	848.4
AHQ-5-5, 3843	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	1.19E-04	0.94	4.78	-	1020.7
AHQ-5-5, 4065	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	5.77E-05	0.95	5.65	-	1395.4
AHQ-5-7, 3832 - 3902	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	2.91E-05	0.97	6.70	-	1202.8
AHQ-5-1, 4355 - 4365	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	2.81E-09	0.96	5.76	-	1335.2
AHQ-5-9, 3639	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	4.92E-07	0.98	6.77	-	1943.9
AHQ-5-8, 3729	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	7.46E-08	0.96	6.13	-	1308.7
AHQ-5-5, 3135	R.VELEDWNGR.T	1118.18129	2	1.06E-06	0.91	2.87	-	1310.3
AHQ-5-11, 2882	K.YEASILTHDSSIR.Y	1492.61564	2	3.43E-07	0.74	3.19	-	474.0
AHQ-5-3, 2961	K.YEASILTHDSSIR.Y	1492.61564	2	1.38E-07	0.83	2.99	-	597.9
AHQ-5-9, 2592 - 2599	K.YEASILTHDSSIR.Y	1492.61564	2	2.05E-04	0.85	3.04	-	788.2
AHQ-5-12, 2917	K.YEASILTHDSSIR.Y	1492.61564	2	3.78E-07	0.90	3.88	-	695.3
AHQ-5-5, 2722 - 2751	K.YEASILTHDSSIR.Y	1492.61564	2	4.66E-07	0.86	3.04	-	795.1
AHQ-5-7, 2610 - 2612	K.YEASILTHDSSIR.Y	1492.61564	1	9.31E-04	0.42	2.26	-	360.7
AHQ-5-7, 2596 - 2667	K.YEASILTHDSSIR.Y	1492.61564	2	1.23E-08	0.93	3.92	-	898.7
AHQ-5-1, 3099	K.YEASILTHDSSIR.Y	1492.61564	2	3.33E-08	0.86	3.23	-	698.4
AHQ-5-1, 2889	R.YLQEIYNSNNQK.I	1514.62131	2	8.34E-06	0.90	3.93	-	1007.4
gi|9966867|ref|NP_065123.1| eIF-5A2 protein; eIF5AII [Homo sapiens]				8.51E-11	3.75	40.31	19.60	16793.1
AHQ-5-11, 3534	K.KYEDICPSTHNMDVPNIK.R	2163.41723	3	1.53E-07	0.97	5.75	-	2118.7
AHQ-5-12, 3612 - 3613	K.KYEDICPSTHNMDVPNIK.R	2163.41723	2	2.10E-04	0.92	4.16	-	876.6
AHQ-5-12, 2992	K.KYEDICPSTHNM*DVPNIK.R	2179.41663	3	1.38E-06	0.95	4.66	-	1546.4
AHQ-5-12, 3609	K.KYEDICPSTHNMDVPNIK.R	2163.41723	3	8.51E-11	0.98	6.17	-	2507.0
AHQ-5-12, 4818	K.VHLVGIDIFTGK.K	1299.54329	1	2.35E-08	0.96	4.11	-	1380.4
AHQ-5-12, 4796 - 4798	K.VHLVGIDIFTGK.K	1299.54329	2	1.13E-07	0.96	4.52	-	1306.1
AHQ-5-12, 4797	K.VHLVGIDIFTGK.K	1299.54329	1	2.16E-06	0.65	1.82	-	1092.7
AHQ-5-11, 4680	K.VHLVGIDIFTGK.K	1299.54329	2	1.97E-09	0.91	3.14	-	1100.5
AHQ-5-12, 3937	K.YEDICPSTHNMDVPNIK.R	2035.24432	2	6.47E-07	0.91	4.21	-	691.2
gi|21735621|ref|NP_005909.2| mitochondrial malate dehydrogenase precursor [Homo sapiens]				8.90E-11	4.16	50.31	29.00	35503.0
AHQ-5-9, 5619	K.GYLGPEQLPDCLKGCDVVVIPAGVPR.K	2813.24211	3	5.48E-04	0.64	3.36	-	420.6
AHQ-5-9, 4916 - 4919	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	2	3.93E-08	0.91	4.59	-	597.5
AHQ-5-9, 4932	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	3	1.49E-06	0.97	6.20	-	1600.4
AHQ-5-9, 4890	K.SQETECTYFSTPLLLGK.K	1976.19328	2	1.40E-08	0.96	4.33	-	1436.3
AHQ-5-11, 5402	K.SQETECTYFSTPLLLGK.K	1976.19328	2	8.90E-11	0.95	4.52	-	1159.0
AHQ-5-9, 5922 - 5926	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	5.07E-07	0.98	5.65	-	1423.5
AHQ-5-13, 6482 - 6561	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	5.20E-05	0.93	4.17	-	1126.1
AHQ-5-9, 4450	K.VDFPQDQLTALTGR.I	1561.72111	2	3.10E-06	0.68	3.02	-	812.5
gi|17986001|ref|NP_005505.2| major histocompatibility complex, class I, B; HLA class I histocompati				9.19E-11	1.92	20.28	7.70	40459.8
AHQ-5-8, 4456	R.APWIEQEGPEYWDR.N	1776.88556	2	9.19E-11	0.98	5.51	-	1580.3
AHQ-5-8, 4678	R.FISVGYVDDTQFVR.F	1646.82447	2	1.59E-06	0.95	3.92	-	1416.3
gi|21956645|ref|NP_665807.1| myotrophin; granule cell differentiation protein [Homo sapiens]				9.66E-11	4.74	50.37	66.90	12894.7
AHQ-5-14, 5354 - 5364	K.GADINAPDKHHITPLLSAVYEGHVSCVK.L	3031.39193	3	1.30E-05	0.98	7.46	-	2147.5
AHQ-5-14-, 3819 - 3889	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	9.91E-11	0.98	6.36	-	1629.6
AHQ-5-14, 4760 - 4836	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.98E-04	0.97	5.53	-	1499.1
AHQ-5-14-, 3905 - 3974	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.72E-06	0.97	4.89	-	1537.4
AHQ-5-13, 4136 - 4206	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	6.26E-08	0.96	4.56	-	1334.1
AHQ-5-13-, 3952 - 4015	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.10E-09	0.98	6.28	-	1714.7
AHQ-5-13-, 4075	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	6.69E-05	0.95	4.30	-	1073.9
AHQ-5-13-, 3995	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	5.53E-07	0.97	5.18	-	2101.3
AHQ-5-14-, 6718 - 6723	R.KPLHYAADCGQLEILEFLLLK.G	2473.91510	3	2.16E-08	0.96	5.46	-	1399.1
AHQ-5-14-, 3617	K.NGDLDEVKDYVAK.G	1466.57496	2	3.13E-08	0.92	3.49	-	1090.0
AHQ-5-14, 4452	K.NGDLDEVKDYVAK.G	1466.57496	1	3.81E-04	0.61	2.67	-	403.0
AHQ-5-14, 4440 - 4450	K.NGDLDEVKDYVAK.G	1466.57496	2	3.04E-08	0.97	4.25	-	1750.4
AHQ-5-14-, 3526 - 3595	K.NGDLDEVKDYVAK.G	1466.57496	1	9.66E-11	0.85	3.52	-	489.0
AHQ-5-14-, 3518 - 3599	K.NGDLDEVKDYVAK.G	1466.57496	2	3.13E-08	0.94	3.70	-	1364.7
gi|10863977|ref|NP_067000.1| LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-				1.07E-10	1.91	20.24	40.00	10834.5
AHQ-5-14-, 6585	K.NDLSICGTLHSVDQYLNIK.L	2192.43507	2	1.50E-06	0.95	4.72	-	1255.7
AHQ-5-14-, 6591	K.NDLSICGTLHSVDQYLNIK.L	2192.43507	3	1.91E-05	0.88	3.78	-	709.7
AHQ-5-14-, 5241 - 5321	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	1.07E-10	0.96	4.41	-	1401.3
AHQ-5-14, 6029 - 6064	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	1.95E-10	0.95	4.72	-	1116.8
gi|5453722|ref|NP_006321.1| lysophospholipase I; lysophospholipase 1; lysophospholipid-specific lys				1.07E-10	1.91	20.22	12.60	24669.5
AHQ-5-11, 2943	K.ALIDQEVKNGIPSNR.I	1654.84968	2	1.07E-10	0.95	4.32	-	1124.4
AHQ-5-11, 6454	K.LAGVTALSCWLPLR.A	1558.86992	2	5.59E-05	0.96	4.43	-	1374.7
gi|7706244|ref|NP_057005.1| divalent cation tolerant protein CUTA [Homo sapiens]				1.11E-10	2.35	30.36	37.80	16832.5

AHQ-5-13, 4257	K.GKIEEDSEVLM*MIK.T	1638.92898	2	2.48E-05	0.43	2.66	-	524.5
AHQ-5-13-, 6749	R.LAACVNLIPQITSIYEWK.G	2121.48472	2	1.11E-10	0.94	4.64	-	579.7
AHQ-5-13, 6849 - 6850	R.SVHPYEVAEVIALPVEQGNFPYLQWVR.Q	3142.55428	3	7.05E-09	0.98	7.16	-	2180.0
AHQ-5-12, 6989	R.SVHPYEVAEVIALPVEQGNFPYLQWVR.Q	3142.55428	3	2.34E-06	0.95	5.11	-	1693.0
gi|21361621|ref|NP_002624.2| phosphoglucomutase 1 [Homo sapiens]				1.14E-10	2.77	30.23	10.70	61448.7
AHQ-5-6, 3636 - 3640	K.FNISNGGPAPEAITDK.I	1631.76820	2	1.14E-10	0.97	4.59	-	1886.7
AHQ-5-6, 6457	R.LVIGQNGILSTPAVSCIIR.K	2013.39093	2	4.34E-10	0.91	4.31	-	710.4
AHQ-5-14-, 6841	K.VFQSSANYAENFIQSIISTVEPAQR.Q	2801.06026	3	9.75E-05	0.90	4.10	-	813.4
gi|4502027|ref|NP_000468.1| albumin precursor; PRO0883 protein [Homo sapiens]				1.17E-10	27.25	330.34	57.00	69366.4
AHQ-5-6, 2344 - 2345	K.AAFTECCQAADK.A	1374.47927	2	6.48E-07	0.90	3.57	-	847.2
AHQ-5-6, 1617 - 1684	K.AEFAEVSK.L	880.96496	1	7.05E-04	0.09	1.97	-	358.2
AHQ-5-1, 5781	K.AVMDDFAAFVEK.C	1343.53006	2	3.57E-06	0.83	2.98	-	841.8
AHQ-5-5, 5518	K.AVMDDFAAFVEK.C	1343.53006	1	2.89E-07	0.86	3.74	-	824.1
AHQ-5-13, 5505	K.AVMDDFAAFVEK.C	1343.53006	2	1.57E-05	0.93	3.98	-	983.6
AHQ-5-12, 5469	K.AVMDDFAAFVEK.C	1343.53006	2	4.61E-06	0.90	3.28	-	1159.0
AHQ-5-5, 5503	K.AVMDDFAAFVEK.C	1343.53006	2	6.22E-09	0.94	3.64	-	1229.4
AHQ-5-14-, 5335	K.AVMDDFAAFVEK.C	1343.53006	2	2.84E-09	0.95	3.87	-	1380.7
AHQ-5-6, 5474	K.AVMDDFAAFVEK.C	1343.53006	1	1.40E-06	0.88	4.06	-	801.0
AHQ-5-6, 5462	K.AVMDDFAAFVEK.C	1343.53006	2	1.70E-08	0.95	3.85	-	1439.0
AHQ-5-6, 4409	K.AVM*DDFAAFVEK.C	1359.52946	1	4.41E-04	0.42	2.48	-	285.0
AHQ-5-5, 4462	K.AVM*DDFAAFVEK.C	1359.52946	2	3.97E-07	0.94	3.38	-	1223.9
AHQ-5-5, 2026 - 2030	K.CCAAADPHECYAK.V	1556.67999	2	2.72E-07	0.77	3.24	-	611.4
AHQ-5-6, 2313	K.CCTESLVNR.R	1141.25805	2	3.84E-06	0.88	2.84	-	1058.4
AHQ-5-6, 6165	K.EFNAETFTFHADICTLSEK.E	2262.43749	2	3.74E-06	0.84	4.11	-	381.0
AHQ-5-5, 6729	K.EFNAETFTFHADICTLSEK.E	2262.43749	2	5.97E-10	0.77	3.48	-	470.1
AHQ-5-5, 6254	K.EFNAETFTFHADICTLSEK.E	2262.43749	2	7.91E-05	0.59	2.84	-	337.7
AHQ-5-5, 6845	K.EFNAETFTFHADICTLSEK.E	2262.43749	2	3.79E-04	0.80	3.46	-	516.7
AHQ-5-6, 2542	R.ETYGEMADCCAK.Q	1437.55563	1	3.05E-04	0.42	2.86	-	143.6
AHQ-5-5, 3842	R.ETYGEMADCCAKQEPERNECFLQHK.D	3135.38952	3	7.91E-04	0.72	3.45	-	583.7
AHQ-5-6, 2373	R.FKDLGEENFK.A	1227.34766	2	2.16E-06	0.79	2.84	-	679.5
AHQ-5-13, 2858 - 2859	R.FKDLGEENFK.A	1227.34766	1	7.99E-05	0.45	2.33	-	421.4
AHQ-5-14-, 2650	R.FKDLGEENFK.A	1227.34766	2	1.26E-04	0.83	3.15	-	714.1
AHQ-5-13, 2853	R.FKDLGEENFK.A	1227.34766	2	2.74E-04	0.72	2.87	-	543.9
AHQ-5-5, 2390	R.FKDLGEENFK.A	1227.34766	2	6.34E-06	0.85	3.31	-	667.0
AHQ-5-6, 2682	K.FQNALLVR.Y	961.14282	2	7.02E-04	0.90	3.23	-	957.8
AHQ-5-6, 6565	R.HPYFYAPELLFFAK.R	1744.02658	3	2.48E-08	0.97	5.39	-	1476.4
AHQ-5-5, 2317	K.KQTALVELVK.H	1129.37494	1	5.32E-04	0.09	1.87	-	281.8
AHQ-5-5, 2319	K.KQTALVELVK.H	1129.37494	2	5.72E-06	0.84	3.29	-	759.2
AHQ-5-8, 2886 - 2888	K.KVPQVSTPTLVEVSR.N	1640.90605	2	7.57E-06	0.92	3.79	-	842.4
AHQ-5-5, 3279	K.KVPQVSTPTLVEVSR.N	1640.90605	3	8.90E-07	0.92	4.44	-	1103.5
AHQ-5-6, 3217 - 3288	K.KVPQVSTPTLVEVSR.N	1640.90605	2	8.97E-06	0.91	3.70	-	838.7
AHQ-5-9, 2978 - 3059	K.KVPQVSTPTLVEVSR.N	1640.90605	2	5.20E-04	0.54	3.16	-	506.4
AHQ-5-4, 3536	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.35E-08	0.92	3.89	-	754.6
AHQ-5-7, 3087	K.KVPQVSTPTLVEVSR.N	1640.90605	2	8.57E-06	0.79	3.28	-	453.4
AHQ-5-5, 3267 - 3327	K.KVPQVSTPTLVEVSR.N	1640.90605	2	7.29E-05	0.86	2.83	-	879.5
AHQ-5-2, 3505	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.87E-08	0.91	3.53	-	907.2
AHQ-5-11, 3372 - 3440	K.KVPQVSTPTLVEVSR.N	1640.90605	2	4.50E-05	0.43	2.82	-	415.2
AHQ-5-3, 3569 - 3581	K.KVPQVSTPTLVEVSR.N	1640.90605	2	9.73E-08	0.93	3.76	-	859.7
AHQ-5-10, 3155	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.06E-08	0.90	3.91	-	617.6
AHQ-5-1, 3727	K.KVPQVSTPTLVEVSR.N	1640.90605	2	4.78E-05	0.68	3.18	-	567.9
AHQ-5-13, 3405	K.LVNEVTEFAK.T	1150.30633	2	5.44E-05	0.83	3.04	-	656.5
AHQ-5-5, 3029 - 3105	K.LVNEVTEFAK.T	1150.30633	2	6.01E-06	0.80	3.13	-	547.7
AHQ-5-6, 3016 - 3085	K.LVNEVTEFAK.T	1150.30633	2	8.26E-07	0.88	2.80	-	896.8
AHQ-5-6, 5632 - 5649	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	8.63E-06	0.98	6.54	-	3067.7
AHQ-5-4, 5937	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	3.85E-05	0.96	5.28	-	1751.5
AHQ-5-6, 5224	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	1.61E-06	0.98	6.80	-	1795.5
AHQ-5-5, 7419	R.MPCAEDYLSVVLNQLCVLHEK.T	2521.91535	3	1.93E-06	0.95	4.54	-	1319.3
AHQ-5-6, 4989 - 4996	K.QNCELFEQLGEYK.F	1659.79847	2	2.18E-05	0.92	3.81	-	817.1
AHQ-5-6, 3649	R.RHPDYSVVLLLR.L	1468.72842	3	6.93E-05	0.95	4.61	-	1754.0
AHQ-5-5, 3722	R.RHPDYSVVLLLR.L	1468.72842	3	2.67E-06	0.97	4.88	-	2575.9
AHQ-5-6, 3652	R.RHPDYSVVLLLR.L	1468.72842	2	6.13E-06	0.88	3.38	-	764.1
AHQ-5-10, 5311	R.RHPYFYAPELLFFAK.R	1900.21293	2	2.61E-04	0.96	4.89	-	1539.9
AHQ-5-6, 5752	R.RHPYFYAPELLFFAK.R	1900.21293	2	1.17E-10	0.98	5.01	-	2492.2
AHQ-5-6, 5756	R.RHPYFYAPELLFFAK.R	1900.21293	3	8.86E-08	0.96	4.87	-	1784.2
AHQ-5-5, 5699 - 5777	R.RHPYFYAPELLFFAK.R	1900.21293	2	1.61E-10	0.98	5.57	-	2812.8
AHQ-5-5, 7361	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	2.94E-04	0.95	5.22	-	1339.9
AHQ-5-5, 7330	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	4.03E-06	0.92	5.12	-	861.4
AHQ-5-6, 7272	K.RMPCAEDYLSVVLNQLCVLHEK.T	2678.10170	3	1.22E-04	0.94	5.41	-	1071.8
AHQ-5-6, 7228 - 7234	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	6.26E-08	0.96	5.88	-	1411.9
AHQ-5-12, 4686 - 4694	R.RPCFSALEVDETYVPK.E	1913.14041	2	7.70E-04	0.83	3.62	-	542.0
AHQ-5-13-, 4685	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.00E-04	0.88	3.71	-	581.0
AHQ-5-13-, 4688	R.RPCFSALEVDETYVPK.E	1913.14041	3	1.10E-04	0.86	3.87	-	784.6
AHQ-5-10, 4243	R.RPCFSALEVDETYVPK.E	1913.14041	2	4.00E-05	0.90	3.78	-	579.5
AHQ-5-5, 4661 - 4737	R.RPCFSALEVDETYVPK.E	1913.14041	2	3.33E-04	0.94	4.25	-	951.7
AHQ-5-13, 4773	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.68E-04	0.84	3.86	-	493.5
AHQ-5-9, 4123	R.RPCFSALEVDETYVPK.E	1913.14041	2	5.14E-05	0.88	3.81	-	500.0
AHQ-5-1, 4980	R.RPCFSALEVDETYVPK.E	1913.14041	2	6.26E-06	0.91	4.15	-	729.0
AHQ-5-4, 4888	R.RPCFSALEVDETYVPK.E	1913.14041	2	6.59E-05	0.78	3.85	-	354.9
AHQ-5-7, 4456	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.96E-07	0.88	3.86	-	660.8
AHQ-5-5, 6474 - 6477	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	2.02E-05	0.93	5.31	-	730.7
AHQ-5-6, 6892 - 6938	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	8.51E-08	0.96	5.79	-	1342.7
AHQ-5-6, 6897 - 6960	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	6.48E-09	0.96	4.66	-	1187.7
AHQ-5-5, 6973 - 7037	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	1.03E-08	0.94	5.58	-	854.4
AHQ-5-7, 6307	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	7.41E-04	0.86	4.40	-	445.0
AHQ-5-3, 7170 - 7245	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	6.56E-05	0.92	4.18	-	703.3
AHQ-5-7, 6871	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	1.19E-07	0.85	4.13	-	322.5
AHQ-5-3, 7175 - 7237	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	6.11E-05	0.94	5.47	-	766.8
AHQ-5-5, 2314	K.SLHTLFGDK.L	1018.14800	1	1.56E-04	0.32	2.64	-	269.6
AHQ-5-5, 4914	K.SLHTLFGDKLCTVATLR.E	1934.24913	3	5.58E-05	0.80	3.36	-	713.0
AHQ-5-14, 5914	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	1.79E-04	0.94	4.20	-	866.9
AHQ-5-5, 5011	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	2.17E-04	0.52	2.83	-	296.1
AHQ-5-6, 5792	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.51E-04	0.89	4.22	-	393.3
AHQ-5-5, 5618	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.96E-06	0.83	4.05	-	397.1
AHQ-5-9, 5098	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.15E-05	0.88	4.19	-	367.7
AHQ-5-5, 5803 - 5870	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.26E-04	0.90	4.02	-	452.8
AHQ-5-3, 6102	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.46E-04	0.92	4.24	-	553.0
AHQ-5-10, 5215	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	4.16E-04	0.69	3.26	-	318.9
AHQ-5-5, 5810 - 5867	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.77E-07	0.95	4.44	-	1360.9
AHQ-5-1, 6103	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.45E-04	0.90	4.55	-	416.7
AHQ-5-6, 5892	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.18E-04	0.87	4.13	-	435.7
AHQ-5-7, 5607 - 5608	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	8.86E-05	0.93	4.79	-	458.2
AHQ-5-6, 5732 - 5801	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.53E-06	0.97	5.21	-	1711.9
AHQ-5-6, 2901 - 2953	K.VHTECCHGDLLECADDR.A	2091.20307	2	2.43E-05	0.91	3.63	-	1213.9
AHQ-5-5, 2919 - 2969	K.VHTECCHGDLLECADDR.A	2091.20307	2	7.32E-06	0.93	4.46	-	1152.2
AHQ-5-7, 3438 - 3440	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	2.48E-05	0.51	2.66	-	547.7
AHQ-5-1, 3912	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	2.98E-05	0.77	3.74	-	514.2
AHQ-5-6, 3737	K.VPQVSTPTLVEVSR.N	1512.73313	2	7.87E-07	0.91	2.96	-	1044.6

AHQ-5-6, 2196	K.YICENQDSISSK.L	1445.53420	2	2.43E-05	0.82	3.05	-	515.6
AHQ-5-6, 2402	K.YICENQDSISSK.L	1445.53420	1	2.28E-04	0.39	1.95	-	457.9
AHQ-5-5, 2221	K.YICENQDSISSK.L	1445.53420	1	2.88E-07	0.63	2.99	-	360.7
AHQ-5-6, 2200	K.YICENQDSISSK.L	1445.53420	1	8.36E-06	0.49	2.57	-	337.3
gi|4885063|ref|NP_005156.1| aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase				1.24E-10	1.85	20.29	7.10	39455.6
AHQ-5-9, 4072 - 4150	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.24E-10	0.97	5.75	-	820.7
AHQ-5-8, 4325 - 4393	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	5.03E-08	0.89	5.27	-	778.1
AHQ-5-12, 4638	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.68E-09	0.94	5.09	-	521.2
AHQ-5-8, 4058	K.VDKGVVPLAGTDGETTTQGLDGLSER.C	2616.82041	3	5.71E-10	0.89	5.03	-	1024.5
AHQ-5-8, 4057	K.VDKGVVPLAGTDGETTTQGLDGLSER.C	2616.82041	2	4.60E-04	0.62	3.28	-	175.7
gi|18201905|ref|NP_000166.2| glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras				1.32E-10	5.52	70.29	24.20	63146.7
AHQ-5-7, 1754	K.HFVALSTNTTK.V	1219.37190	1	1.25E-05	0.31	1.94	-	355.6
AHQ-5-7, 7312	K.ILLANFLAQTEALMR.G	1705.05838	2	2.71E-10	0.97	5.43	-	1375.0
AHQ-5-7, 7252	K.TITDVINIGIGGSDLGPLMVTEALKPYSSGGPR.V	3330.79783	3	1.32E-10	0.93	5.22	-	668.2
AHQ-5-7, 5936 - 5946	K.TLAQLNPESSLFIIASK.T	1833.11828	2	4.45E-04	0.84	4.22	-	328.8
AHQ-5-7, 5312	R.VDHQTGPIVWGEPGTNGQHAFYQLIHQGTK.M	3317.61777	3	9.43E-04	0.89	5.70	-	844.5
AHQ-5-7, 2951	K.VFEGNRPTNSIVFTK.L	1709.92693	2	5.89E-04	0.65	3.22	-	516.7
AHQ-5-7, 3538	R.VWYVSNIDGTHIAK.T	1603.80282	2	8.84E-09	0.93	3.68	-	1137.0
gi|4557305|ref|NP_000025.1| aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho				1.32E-10	8.42	100.28	39.60	39419.7
AHQ-5-8, 1888	R.ALANSLACQGK.Y	1134.28859	2	1.12E-04	0.82	3.21	-	808.5
AHQ-5-13, 2441	R.ALANSLACQGK.Y	1134.28859	2	2.77E-07	0.79	3.02	-	812.7
AHQ-5-8, 5610 - 5682	R.ALANSLACQGKYTPSGQAGAAASESLFVSNHAY	3344.61352	3	6.52E-06	0.49	3.06	-	415.6
AHQ-5-8, 5973	R.ALANSLACQGKYTPSGQAGAAASESLFVSNHAY	3344.61352	3	7.14E-07	0.33	3.21	-	265.9
AHQ-5-8, 3716	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	2.03E-08	0.96	5.69	-	1055.3
AHQ-5-8, 5826 - 5893	K.CPLLKPWALTFSYGR.A	1811.13929	2	4.45E-05	0.68	2.85	-	393.1
AHQ-5-8, 5862	K.CPLLKPWALTFSYGR.A	1811.13929	3	1.03E-06	0.96	5.14	-	1444.3
AHQ-5-9, 5364	K.CPLLKPWALTFSYGR.A	1811.13929	2	2.58E-04	0.83	3.58	-	483.2
AHQ-5-8, 3748 - 3817	K.FSHEEIAMATVTALR.R	1676.91875	2	2.13E-06	0.90	3.48	-	1220.3
AHQ-5-8, 3980	K.FSHEEIAMATVTALR.R	1676.91875	2	2.75E-05	0.58	2.56	-	630.9
AHQ-5-8, 2542	K.GILAADESTGSIAK.R	1333.47008	2	1.54E-09	0.98	4.67	-	1818.1
AHQ-5-12, 2862	K.GILAADESTGSIAK.R	1333.47008	2	1.37E-07	0.97	4.16	-	2000.1
AHQ-5-9, 2607	K.GILAADESTGSIAK.R	1333.47008	1	3.15E-04	0.35	2.69	-	323.2
AHQ-5-8, 2541	K.GILAADESTGSIAK.R	1333.47008	1	1.79E-05	0.68	2.97	-	383.8
AHQ-5-8, 4046 - 4054	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	1.03E-06	0.84	4.97	-	594.0
AHQ-5-10, 4214 - 4216	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	1.44E-10	0.83	4.80	-	568.1
AHQ-5-8, 4138	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	1.76E-09	0.92	5.20	-	1150.7
AHQ-5-9, 4014 - 4078	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	5.58E-08	0.78	4.54	-	607.8
AHQ-5-9, 3920	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	2.18E-08	0.63	3.72	-	399.2
AHQ-5-8, 4565	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.32E-10	0.96	5.16	-	1051.2
AHQ-5-9, 4698	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.90E-05	0.88	4.35	-	474.7
AHQ-5-8, 4872	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.05E-08	0.97	5.51	-	1027.4
AHQ-5-10, 4836	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	5.61E-04	0.94	4.87	-	754.2
AHQ-5-9, 4444	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	6.49E-10	0.93	4.14	-	925.5
AHQ-5-8, 6056	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	1.22E-04	0.93	3.83	-	969.8
AHQ-5-8, 6265	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	3.32E-05	0.89	3.49	-	904.6
AHQ-5-8, 4104 - 4172	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	2.47E-05	0.82	3.72	-	236.5
gi|14765644|ref|XP_037574.1| similar to PTPL1-associated RhoGAP 1 [Homo sapiens]				1.48E-10	0.74	10.17	2.90	124613.7
AHQ-5-7, 7367	R.SPLTAASPGELPTEGAGPDVVEDISHLLADVAR.F	3286.59214	3	1.48E-10	0.74	3.40	-	374.6
gi|27498332|ref|XP_212565.1| similar to tubulin, beta 5 [Homo sapiens]				1.49E-10	2.87	30.28	6.50	49670.5
AHQ-5-7, 3599	R.IMNTFSVVPSPK.V	1320.58277	2	2.05E-04	0.60	2.80	-	560.3
AHQ-5-7, 3691	R.IMNTFSVVPSPK.V	1320.58277	2	2.57E-06	0.93	3.68	-	988.6
AHQ-5-7, 3708	R.IMNTFSVVPSPK.V	1320.58277	1	3.46E-06	0.17	1.96	-	348.0
AHQ-5-7, 3498 - 3572	R.IMNTFSVVPSPK.V	1320.58277	2	4.87E-04	0.95	3.87	-	1544.8
AHQ-5-7, 6814	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	8.31E-06	0.97	4.92	-	1131.3
AHQ-5-7, 6858 - 6928	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	4.30E-08	0.97	5.55	-	1345.0
AHQ-5-7, 7159	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	6.19E-07	0.95	4.54	-	1071.9
AHQ-5-12, 6694 - 6698	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.11E-04	0.94	4.00	-	980.9
AHQ-5-13, 6374 - 6392	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.84E-05	0.96	4.78	-	975.5
AHQ-5-13, 6660	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.49E-10	0.97	5.06	-	989.0
AHQ-5-14-, 6505	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.61E-06	0.75	2.72	-	728.6
gi|13899317|ref|NP_113657.1| SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M				1.63E-10	5.45	60.30	72.00	12326.0
AHQ-5-14-, 5319 - 5389	K.ESNTVFSFLGLKPR.L	1595.82383	2	2.64E-08	0.74	3.46	-	428.9
AHQ-5-14-, 5671 - 5678	K.ESNTVFSFLGLKPR.L	1595.82383	3	5.78E-05	0.83	3.59	-	657.6
AHQ-5-14, 5877	K.ESNTVFSFLGLKPR.L	1595.82383	2	1.36E-05	0.59	2.92	-	405.4
AHQ-5-14, 6242 - 6276	K.ESNTVFSFLGLKPR.L	1595.82383	2	1.41E-09	0.76	3.47	-	453.6
AHQ-5-14-, 5365	K.ESNTVFSFLGLKPR.L	1595.82383	2	1.01E-08	0.82	3.63	-	424.5
AHQ-5-14, 6333	K.ESNTVFSFLGLKPR.L	1595.82383	2	5.65E-08	0.67	3.10	-	440.9
AHQ-5-14-, 4889 - 4901	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	1.63E-10	0.97	6.05	-	1753.0
AHQ-5-14-, 4893 - 4899	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	2	1.58E-04	0.92	4.57	-	831.1
AHQ-5-14-, 4977 - 4998	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	2.60E-07	0.98	5.71	-	2287.0
AHQ-5-14-, 4191	K.IEFEEVDITM*SEEQR.Q	1872.00051	2	6.76E-06	0.94	3.83	-	1222.6
AHQ-5-14, 4636	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	9.14E-05	0.60	2.93	-	464.6
AHQ-5-14-, 3643	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	2.46E-04	0.81	3.19	-	843.4
AHQ-5-14, 4520 - 4566	K.KPTQGNPLPPQIFNGDR.Y	1880.09682	2	1.07E-07	0.89	3.53	-	952.8
AHQ-5-14, 6288 - 6358	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	3.90E-05	0.91	4.83	-	893.0
AHQ-5-14, 6428	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	6.12E-04	0.85	4.46	-	536.7
AHQ-5-14-, 5781 - 5854	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	5.18E-04	0.87	4.32	-	650.8
AHQ-5-14, 5430	R.VFIASSSGFVAIK.K	1326.56551	1	5.98E-05	0.48	2.59	-	491.1
AHQ-5-14-, 4285	R.VFIASSSGFVAIK.K	1326.56551	2	1.38E-06	0.96	3.43	-	2135.4
AHQ-5-14-, 4619	R.VFIASSSGFVAIK.K	1326.56551	2	5.19E-08	0.98	4.05	-	3290.5
gi|21624607|ref|NP_066972.1| coactosin-like 1 [Homo sapiens]				1.65E-10	4.37	60.30	50.00	15944.9
AHQ-5-13, 2421 - 2422	R.AAYNLVR.D	806.93245	2	1.63E-04	0.88	3.04	-	843.4
AHQ-5-13-, 2240	R.AAYNLVR.D	806.93245	2	1.74E-05	0.92	2.58	-	1326.8
AHQ-5-12, 2108	R.AAYNLVR.D	806.93245	2	3.67E-04	0.92	2.71	-	1142.9
AHQ-5-13-, 5292	R.DDGSAVIWVTFK.Y	1338.49001	2	2.95E-08	0.96	4.71	-	1361.9
AHQ-5-13, 2306	K.EVVQNFAK.E	935.05900	1	8.26E-04	0.09	2.00	-	149.3
AHQ-5-12, 6936 - 6937	K.FALITWIGENVSGLQR.A	1805.06986	2	8.11E-08	0.98	5.92	-	1786.7
AHQ-5-13, 6808	K.FALITWIGENVSGLQR.A	1805.06986	2	1.03E-07	0.97	5.48	-	1528.7
AHQ-5-13-, 6743	K.FALITWIGENVSGLQR.A	1805.06986	2	1.29E-04	0.98	5.42	-	2090.1
AHQ-5-13, 2967	R.KELEEDFIK.S	1151.29110	2	2.65E-04	0.85	3.20	-	881.0
AHQ-5-12, 2689 - 2722	R.KELEEDFIK.S	1151.29110	2	4.49E-04	0.76	2.74	-	728.3
AHQ-5-13-, 2827 - 2829	R.KELEEDFIK.S	1151.29110	2	1.73E-04	0.71	2.62	-	707.7
AHQ-5-13-, 2840	R.KELEEDFIK.S	1151.29110	1	5.77E-04	0.35	2.55	-	352.3
AHQ-5-13, 2970 - 2971	R.KELEEDFIK.S	1151.29110	1	8.36E-04	0.45	2.62	-	420.6
AHQ-5-12, 5368	K.YDGSTIVPGEQGAEYQHFIQQCTDDVR.L	3116.27790	3	1.38E-07	0.81	3.90	-	392.6
AHQ-5-13, 5344 - 5413	K.YDGSTIVPGEQGAEYQHFIQQCTDDVR.L	3116.27790	3	1.65E-10	0.71	3.50	-	365.6
gi|7657486|ref|NP_055217.1| low molecular mass ubiquinone-binding protein [Homo sapiens]				1.67E-10	0.96	10.25	14.00	11316.3
AHQ-5-14-, 3818	R.HVISYSLSPFEQR.A	1563.73870	2	1.67E-10	0.96	4.90	-	1044.5
AHQ-5-14, 4744 - 4753	R.HVISYSLSPFEQR.A	1563.73870	2	7.78E-08	0.95	4.39	-	1179.6
gi|4758460|ref|NP_004479.1| glycoprotein V (platelet) [Homo sapiens]				1.72E-10	5.45	60.29	22.30	60958.9
AHQ-5-6, 5453	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	3.68E-04	0.76	3.42	-	834.6
AHQ-5-5, 5469	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	1.02E-07	0.83	4.22	-	589.0
AHQ-5-6, 5449	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	2	2.58E-05	0.87	3.60	-	756.8
AHQ-5-5, 4630 - 4702	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	2.44E-07	0.94	3.77	-	1462.5
AHQ-5-5, 5725	R.LMISDSHISAVAPGTFSDLIK.L	2203.54435	2	7.73E-04	0.95	4.73	-	1026.9
AHQ-5-5, 4530	R.LPNLSSLTLSR.N	1201.39802	2	8.28E-07	0.95	3.59	-	1671.2
AHQ-5-6, 7381 - 7417	K.LVNLQELALNQNQLDFLPASLFTNLENLK.L	3314.77659	3	2.29E-05	0.96	5.78	-	1080.8

AHQ-5-5, 7374	R.LVSLDSGLLNSLGALTELQFHR.N	2384.71675	3	1.72E-10	0.83	4.00	-	671.1
gi|7656991|ref|NP_055140.1| coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;				1.76E-10	5.48	70.34	27.80	53248.7
AHQ-5-6, 5984 - 6050	R.AIFLADGNVFTTGFSR.M	1716.91793	2	1.54E-05	0.96	4.97	-	1411.6
AHQ-5-7, 5819 - 5895	R.AIFLADGNVFTTGFSR.M	1716.91793	2	9.80E-08	0.95	3.73	-	1489.5
AHQ-5-6, 5900 - 5980	R.AIFLADGNVFTTGFSR.M	1716.91793	2	2.37E-10	0.97	5.25	-	1347.3
AHQ-5-6, 3037 - 3040	R.KCEPIIMTVPR.K	1345.65706	2	3.31E-06	0.87	3.11	-	807.2
AHQ-5-6, 7200	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	1.76E-10	0.98	6.77	-	2058.0
AHQ-5-6, 3724	K.NADPILISLK.H	1084.29103	1	1.31E-04	0.32	2.21	-	273.7
AHQ-5-6, 7253 - 7256	K.NMQEPIALHEMDTSNGVLLPFYDPDTSIIYLCGK.G	3885.39261	3	6.90E-06	0.60	3.24	-	349.7
AHQ-5-6, 2213	K.SIKDTICNQDER.I	1480.58332	2	1.56E-06	0.84	2.77	-	1164.7
AHQ-5-6, 6116 - 6129	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	2.04E-06	0.91	4.51	-	707.5
AHQ-5-7, 5906	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	2.55E-05	0.88	3.44	-	1044.0
gi|17986258|ref|NP_066299.2| smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo				1.85E-10	6.78	80.26	42.40	16930.0
AHQ-5-13, 4326 - 4380	K.DQGTYEDYVEGLR.V	1545.58904	2	1.87E-08	0.81	2.95	-	752.4
AHQ-5-12, 4290	K.DQGTYEDYVEGLR.V	1545.58904	2	8.14E-05	0.84	2.75	-	1025.5
AHQ-5-12, 4193 - 4264	K.DQGTYEDYVEGLR.V	1545.58904	2	3.42E-09	0.92	3.66	-	1031.6
AHQ-5-13-, 4201	K.DQGTYEDYVEGLR.V	1545.58904	2	2.31E-04	0.89	3.59	-	926.4
AHQ-5-12, 3840 - 3916	K.EAFQLFDR.T	1026.12699	2	1.28E-04	0.63	2.57	-	508.8
AHQ-5-12, 3946	K.EAFQLFDR.T	1026.12699	2	5.53E-04	0.63	2.50	-	510.7
AHQ-5-12, 2121 - 2176	R.HVLVTLGEK.M	996.18547	1	8.81E-04	0.67	3.19	-	447.2
AHQ-5-13-, 2279 - 2305	R.HVLVTLGEK.M	996.18547	2	7.06E-04	0.87	3.01	-	664.0
AHQ-5-12, 2224	R.HVLVTLGEK.M	996.18547	2	6.54E-05	0.82	2.96	-	475.9
AHQ-5-14-, 2238	R.HVLVTLGEK.M	996.18547	2	2.00E-07	0.84	2.73	-	586.7
AHQ-5-12, 2116 - 2180	R.HVLVTLGEK.M	996.18547	2	6.47E-06	0.91	3.62	-	705.1
AHQ-5-13, 2462	R.HVLVTLGEK.M	996.18547	2	9.08E-05	0.93	3.40	-	909.5
AHQ-5-12, 3882	K.NKDQGTYEDYVEGLR.V	1787.86505	2	9.42E-10	0.92	4.19	-	1215.1
AHQ-5-12, 3586 - 3652	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.50E-08	0.95	5.19	-	1175.6
AHQ-5-13-, 3717 - 3779	K.NKDQGTYEDYVEGLR.V	1787.86505	3	1.65E-05	0.89	3.29	-	1291.3
AHQ-5-12, 3576 - 3640	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.96E-09	0.90	3.80	-	784.1
AHQ-5-14, 4516	K.NKDQGTYEDYVEGLR.V	1787.86505	2	8.22E-07	0.95	4.33	-	1155.8
AHQ-5-14-, 3649	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.20E-07	0.92	4.45	-	830.9
AHQ-5-13-, 3755	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.62E-10	0.93	4.18	-	1087.0
AHQ-5-12, 3986 - 4056	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.85E-10	0.90	3.86	-	879.0
AHQ-5-13, 3860	K.NKDQGTYEDYVEGLR.V	1787.86505	2	4.90E-07	0.92	3.97	-	1005.1
AHQ-5-12, 3284	R.VFDKEGNGTVMGAEIR.H	1723.93228	3	2.80E-07	0.88	3.73	-	1205.9
AHQ-5-12, 2581 - 2649	R.VFDKEGNGTVM*GAEIR.H	1739.93168	2	4.50E-05	0.70	3.12	-	468.9
AHQ-5-12, 3180	R.VFDKEGNGTVM*GAEIR.H	1739.93168	2	2.58E-04	0.77	3.11	-	767.9
AHQ-5-14-, 2617	R.VFDKEGNGTVM*GAEIR.H	1739.93168	2	8.12E-06	0.80	3.60	-	610.6
AHQ-5-12, 6193 - 6272	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	6.49E-05	0.89	3.92	-	766.0
AHQ-5-12, 6336	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	2.01E-05	0.91	4.26	-	546.9
AHQ-5-13, 6765	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	1.45E-05	0.95	4.77	-	884.0
AHQ-5-13-, 6316	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	3.79E-05	0.89	3.58	-	965.8
AHQ-5-13-, 6716 - 6717	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	3.32E-10	0.97	5.13	-	1352.9
AHQ-5-13, 6376	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	3.80E-06	0.84	3.30	-	819.7
AHQ-5-12, 6869	K.VLDFEHFLPMLQTVAK.N	1889.25017	3	6.19E-05	0.84	3.46	-	1348.4
AHQ-5-12, 6273 - 6352	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	2.72E-05	0.81	3.04	-	770.2
AHQ-5-12, 6868 - 6881	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	1.63E-07	0.96	4.91	-	1128.5
AHQ-5-14-, 6199	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	3.86E-04	0.82	3.40	-	603.2
AHQ-5-14-, 6203	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	1.80E-04	0.87	3.71	-	909.7
AHQ-5-14-, 6661	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	1.83E-07	0.96	5.14	-	1067.4
gi|5453740|ref|NP_006462.1| myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat				1.91E-10	6.53	80.32	38.60	19794.0
AHQ-5-12, 5465 - 5470	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	4.30E-08	0.95	4.62	-	1113.4
AHQ-5-11, 5878	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	5.21E-04	0.62	2.94	-	393.1
AHQ-5-14-, 5367	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	4.19E-08	0.96	4.84	-	1150.7
AHQ-5-11, 5275	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	5.78E-05	0.90	3.59	-	975.6
AHQ-5-14, 6061	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.51E-08	0.88	4.03	-	430.7
AHQ-5-12, 6094 - 6172	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	2.99E-06	0.90	4.14	-	790.0
AHQ-5-11, 5990 - 6058	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.12E-05	0.98	5.41	-	1757.6
AHQ-5-11, 5695 - 5734	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.66E-08	0.95	4.56	-	1589.2
AHQ-5-11, 5824 - 5834	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	5.50E-07	0.98	6.31	-	1740.7
AHQ-5-11, 5832 - 5844	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	4.99E-06	0.96	4.64	-	1715.6
AHQ-5-14-, 5801	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.98E-10	0.91	4.01	-	1136.5
AHQ-5-11, 5688 - 5750	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.03E-08	0.97	5.54	-	1631.3
AHQ-5-13-, 5900	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	2.80E-09	0.94	4.10	-	1720.4
AHQ-5-12, 4569	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	1.66E-04	0.90	4.37	-	618.0
AHQ-5-12, 5917	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.91E-10	0.97	5.11	-	1700.4
AHQ-5-12, 5922	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	2.04E-08	0.93	4.15	-	1405.4
AHQ-5-14-, 5802	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	3.22E-09	0.95	4.78	-	923.3
AHQ-5-11, 6142 - 6215	K.EAFNMIDQNRDGFIDKEDLHDMLASLGK.N	3224.57104	3	4.20E-05	0.95	5.15	-	1310.2
AHQ-5-11, 6243	K.EAFNMIDQNRDGFIDKEDLHDMLASLGK.N	3224.57104	3	6.34E-06	0.96	5.63	-	1648.2
AHQ-5-12, 2605	R.ELLTTMGDR.F	1036.18513	1	6.99E-04	0.23	1.81	-	130.1
AHQ-5-11, 2539	R.ELLTTMGDR.F	1036.18513	1	8.24E-05	0.24	1.97	-	73.9
AHQ-5-11, 4243	K.GNFNYIEFTR.I	1261.36733	1	2.06E-04	0.37	2.06	-	391.6
AHQ-5-11, 4239	K.GNFNYIEFTR.I	1261.36733	2	6.72E-05	0.70	3.15	-	674.6
AHQ-5-13-, 4196	K.GNFNYIEFTR.I	1261.36733	2	1.79E-05	0.77	2.79	-	754.2
AHQ-5-11, 4107	K.GNFNYIEFTR.I	1261.36733	1	3.18E-04	0.34	2.24	-	263.6
AHQ-5-11, 4002 - 4070	K.GNFNYIEFTR.I	1261.36733	2	5.47E-05	0.79	3.06	-	720.8
AHQ-5-12, 4152	K.GNFNYIEFTR.I	1261.36733	2	3.98E-04	0.82	2.96	-	918.0
AHQ-5-11, 3380	K.KGNFNYIEFTR.I	1389.54025	2	3.99E-07	0.92	2.97	-	1034.6
gi|4502219|ref|NP_001656.1| ras homolog gene family, member G (rho G); RhoG [Homo sapiens]				1.94E-10	1.67	20.20	18.80	21338.4
AHQ-5-11, 4878 - 4895	K.EYIPTVFDNYSAQSAVDGR.T	2133.25975	2	7.74E-04	0.75	3.41	-	381.2
AHQ-5-11, 4826	R.TVNLNLWDTAGQEEYDR.L	2025.12129	2	1.94E-10	0.92	3.99	-	1157.1
gi|6912638|ref|NP_036557.1| ras suppressor protein 1 [Homo sapiens]				1.99E-10	5.39	60.27	45.80	31540.1
AHQ-5-10, 6492 - 6562	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	1.02E-09	0.77	3.79	-	560.6
AHQ-5-12, 7068 - 7069	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	3.57E-05	0.80	4.02	-	416.5
AHQ-5-10, 5694 - 5754	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	2.30E-04	0.85	3.83	-	431.5
AHQ-5-10, 5814 - 5879	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	1.99E-10	0.92	4.52	-	494.3
AHQ-5-13-, 6119 - 6181	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	4.28E-04	0.70	2.86	-	402.8
AHQ-5-11, 6024 - 6086	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	9.27E-04	0.49	3.03	-	308.2
AHQ-5-12, 6282	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	4.91E-06	0.77	3.44	-	362.5
AHQ-5-10, 6530 - 6532	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	2	1.72E-05	0.82	4.10	-	295.7
AHQ-5-10, 6531	R.GISNMLDVNGLFTLSHITQLVLSHNK.L	2853.28963	3	3.61E-09	0.86	4.30	-	698.0
AHQ-5-10, 5379 - 5438	K.LQILSLRDNDLISLPK.E	1839.16919	2	1.88E-05	0.91	4.31	-	1270.5
AHQ-5-10, 5290	K.LQILSLRDNDLISLPK.E	1839.16919	2	1.19E-06	0.93	4.85	-	1185.7
AHQ-5-10, 5431	R.LTVLPPELGNLDLTGQK.Q	1809.09672	3	3.20E-07	0.97	5.40	-	2076.9
AHQ-5-11, 5798	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	4.49E-06	0.81	3.59	-	420.1
AHQ-5-11, 5676 - 5738	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	5.27E-05	0.79	3.48	-	408.1
AHQ-5-13-, 5859 - 5887	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	9.87E-05	0.94	4.83	-	626.5
AHQ-5-10, 6432 - 6498	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	2	6.83E-06	0.94	5.28	-	680.0
AHQ-5-14-, 6757 - 6829	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	3	6.49E-04	0.90	4.45	-	741.3
AHQ-5-13, 6822 - 6892	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	3	1.05E-04	0.93	5.37	-	656.5
gi|27482573|ref|XP_208709.1| similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro				2.22E-10	2.04	30.27	31.80	17875.4
AHQ-5-12, 4880 - 4892	K.GQVCLPVISAENWKPATK.T	2000.30757	2	2.22E-10	0.96	5.41	-	775.1
AHQ-5-12, 4897	K.GQVCLPVISAENWKPATK.T	2000.30757	3	1.05E-06	0.55	3.22	-	267.7
AHQ-5-12, 2092	K.IYHPNIDEK.G	1129.24722	1	2.75E-04	0.15	1.97	-	346.1
AHQ-5-12, 6781	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	3.74E-10	0.93	4.79	-	1036.2
AHQ-5-12, 6780	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	2	2.14E-04	0.69	3.27	-	452.1

gi|4507149|ref|NP_000445.1| superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult				2.25E-10	3.43	40.32	57.80	15935.7
AHQ-5-12, 5346	K.AVCVLKGDGPVQGIINFEQK.E	2174.50602	2	4.30E-06	0.95	5.23	-	820.7
AHQ-5-11, 5151	K.AVCVLKGDGPVQGIINFEQK.E	2174.50602	3	4.21E-08	0.86	3.37	-	1228.8
AHQ-5-12, 4546	K.GDGPVQGIINFEQK.E	1502.65366	2	5.10E-09	0.65	2.98	-	443.8
AHQ-5-12, 4952	K.GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR.K	3522.76733	3	5.53E-05	0.93	4.96	-	930.0
AHQ-5-12, 4852	K.GLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSR.K	3522.76733	3	2.25E-10	0.97	6.45	-	1686.4
AHQ-5-12, 5937 - 6004	R.HVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGR.T	3724.02282	3	3.23E-04	0.95	4.79	-	1399.5
gi|23510338|ref|NP_003325.2| ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity				2.30E-10	6.70	80.26	11.20	117848.1
AHQ-5-4, 6594 - 6600	R.AAVATFLQSVQVPEFTPK.S	1934.22430	2	6.45E-07	0.89	4.34	-	683.6
AHQ-5-4, 4641	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	8.16E-10	0.92	3.98	-	672.2
AHQ-5-4, 3648 - 3649	K.DNPGVVTCLDEAR.H	1447.55333	2	2.30E-10	0.96	4.44	-	1016.2
AHQ-5-4, 4569	R.HQYYNQEWTLWDR.F	1839.94657	2	3.67E-04	0.70	3.21	-	792.3
AHQ-5-4, 2292	R.KPLLESGTLGTK.G	1244.46280	2	1.16E-05	0.76	2.92	-	702.1
AHQ-5-4, 5441	R.LAGTQPLEVLEAVQR.S	1624.86348	2	3.54E-07	0.79	3.57	-	342.7
AHQ-5-6, 5164	R.LAGTQPLEVLEAVQR.S	1624.86348	2	1.07E-04	0.51	2.82	-	326.7
AHQ-5-4, 5090 - 5161	K.NFPNAIEHTLQWAR.D	1697.87794	2	3.05E-06	0.76	3.17	-	585.3
AHQ-5-5, 6598	K.SLVASLAEPDFVVTDFAK.F	1910.15638	2	6.85E-05	0.93	4.88	-	581.8
AHQ-5-4, 6742 - 6758	K.SLVASLAEPDFVVTDFAK.F	1910.15638	2	3.44E-04	0.94	5.19	-	722.4
gi|5031597|ref|NP_005710.1| actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub				2.47E-10	3.64	40.26	29.80	20546.5
AHQ-5-11, 6394 - 6395	K.DTDIVDEAIYYFK.A	1592.72721	2	1.95E-08	0.97	5.18	-	1485.5
AHQ-5-14-, 6429	K.DTDIVDEAIYYFK.A	1592.72721	2	4.25E-07	0.96	4.63	-	1426.3
AHQ-5-12, 6620 - 6629	K.DTDIVDEAIYYFK.A	1592.72721	2	5.56E-09	0.96	4.71	-	1370.5
AHQ-5-11, 6767 - 6771	K.EM*YTLGITNFPIPGEPGFPLNAIYAK.P	2871.29861	2	2.38E-04	0.76	3.46	-	267.1
AHQ-5-12, 6022	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	2.47E-10	0.94	4.47	-	1139.2
AHQ-5-11, 5838	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	1.36E-05	0.90	3.97	-	809.7
AHQ-5-12, 5138	K.LIGNMALLPIR.S	1211.54582	2	4.11E-04	0.97	3.98	-	2306.0
gi|21361322|ref|NP_006078.2| tubulin, beta, 5 [Homo sapiens]				2.53E-10	2.38	30.27	13.70	49585.5
AHQ-5-7, 2655	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	2.02E-04	0.88	3.69	-	872.5
AHQ-5-11, 2856	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	1.48E-04	0.96	4.20	-	1734.1
AHQ-5-9, 2614	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	9.70E-05	0.69	2.95	-	595.6
AHQ-5-13, 3054 - 3119	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	1.79E-04	0.92	3.87	-	1221.0
AHQ-5-7, 5283	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	9.26E-05	0.87	4.44	-	613.5
AHQ-5-7, 5191	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	1.82E-05	0.94	5.34	-	950.5
AHQ-5-7, 6380	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	8.56E-04	0.19	2.53	-	365.3
AHQ-5-12, 6686	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	3.07E-07	0.80	4.11	-	761.1
AHQ-5-7, 6784 - 6852	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	2.53E-10	0.75	3.94	-	648.9
AHQ-5-7, 6539	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	6.50E-04	0.25	2.62	-	394.7
gi|20535366|ref|XP_053177.4| similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap				2.60E-10	2.15	30.25	9.60	49858.2
AHQ-5-12, 3028	K.DVNAAIATIK.T	1016.17355	2	8.71E-05	0.85	3.10	-	862.8
AHQ-5-12, 2873	K.DVNAAIATIK.T	1016.17355	1	7.93E-05	0.57	2.50	-	496.5
AHQ-5-7, 3026	K.DVNAAIATIK.T	1016.17355	1	8.26E-05	0.46	2.29	-	420.3
AHQ-5-7, 2730	K.DVNAAIATIK.T	1016.17355	1	2.79E-05	0.53	2.40	-	494.2
AHQ-5-6, 5180	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.10E-06	0.44	2.80	-	271.5
AHQ-5-4, 5430 - 5509	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.72E-09	0.91	4.29	-	651.4
AHQ-5-7, 4856 - 4907	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.30E-07	0.87	4.26	-	497.5
AHQ-5-3, 5455 - 5478	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.76E-08	0.90	3.62	-	981.9
AHQ-5-7, 5174 - 5243	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.46E-05	0.78	3.34	-	502.2
AHQ-5-14-, 4718	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	8.50E-07	0.63	2.92	-	335.6
AHQ-5-8, 4876	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.99E-09	0.85	3.38	-	681.8
AHQ-5-9, 4588 - 4590	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	8.32E-08	0.94	4.60	-	893.6
AHQ-5-11, 5008 - 5051	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.29E-06	0.48	2.68	-	462.1
AHQ-5-11, 5012 - 5086	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.69E-10	0.95	4.91	-	930.6
AHQ-5-7, 5035 - 5106	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	9.55E-09	0.96	4.96	-	1201.0
AHQ-5-1, 5464	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.68E-06	0.81	3.65	-	483.9
AHQ-5-13-, 5152	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.69E-08	0.86	3.90	-	567.0
AHQ-5-14, 5856 - 5912	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.60E-10	0.94	5.03	-	819.4
AHQ-5-14-, 5074	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.37E-07	0.82	3.33	-	678.9
AHQ-5-7, 5691	R.TIQFVDWCPTGFK.V	1600.81899	2	5.98E-06	0.69	2.68	-	555.8
AHQ-5-12, 5765 - 5772	R.TIQFVDWCPTGFK.V	1600.81899	2	4.99E-05	0.85	3.55	-	592.9
gi|4507869|ref|NP_003361.1| vasodilator-stimulated phosphoprotein [Homo sapiens]				2.75E-10	4.01	50.27	14.20	39829.4
AHQ-5-13-, 2343	R.ATVMLYDDGNKR.W	1383.55582	2	1.38E-06	0.62	3.06	-	467.3
AHQ-5-8, 3821	K.MQPDQQVVINCAIVR.G	1773.07126	2	7.46E-04	0.76	3.04	-	512.5
AHQ-5-13, 4056 - 4130	K.M*QPDQQVVINCAIVR.G	1789.07066	2	1.14E-04	0.73	3.42	-	671.8
AHQ-5-7, 5938 - 5939	K.VKEEIIEAFVQELR.K	1703.96061	2	2.75E-10	0.97	5.31	-	1827.1
AHQ-5-7, 2524 - 2535	R.VQIYHNPTANSFR.V	1547.69936	2	5.09E-06	0.93	3.65	-	1027.5
AHQ-5-7, 2439	R.VQIYHNPTANSFR.V	1547.69936	2	7.41E-05	0.85	3.51	-	734.4
gi|8922673|ref|NP_060692.1| parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]				2.81E-10	0.97	10.25	3.50	42243.4
AHQ-5-9, 4070 - 4082	R.DAFDTLFDHAPDK.L	1492.57096	2	2.81E-10	0.97	4.94	-	1715.1
AHQ-5-9, 4083	R.DAFDTLFDHAPDK.L	1492.57096	1	4.38E-08	0.88	3.76	-	639.1
AHQ-5-1, 4912	R.DAFDTLFDHAPDK.L	1492.57096	2	5.74E-08	0.97	4.39	-	1683.2
gi|4507725|ref|NP_000362.1| transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum				2.90E-10	6.04	70.34	53.70	15886.9
AHQ-5-13, 3936 - 3937	K.AADDTWEPFASGK.T	1395.45529	1	1.49E-05	0.31	2.13	-	395.2
AHQ-5-13, 4100	R.GSPAINVAVHVFR.K	1367.58095	2	1.07E-08	0.93	3.86	-	1059.5
AHQ-5-13-, 4016	R.GSPAINVAVHVFR.K	1367.58095	2	2.90E-10	0.94	3.94	-	1170.6
AHQ-5-13, 3238	R.KAADDTWEPFASGK.T	1523.62820	2	3.84E-05	0.97	4.84	-	1424.9
AHQ-5-13, 5942	R.RYTIAALLSPYSYSTTAVVTNPK.E	2517.86154	2	3.11E-04	0.91	3.91	-	980.0
AHQ-5-13, 5965	R.RYTIAALLSPYSYSTTAVVTNPKE	2646.97608	2	1.46E-04	0.98	6.85	-	2248.8
AHQ-5-12, 5546	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	1.51E-05	0.96	4.60	-	1319.4
AHQ-5-13, 5590 - 5633	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	9.59E-05	0.97	5.66	-	1539.1
AHQ-5-13, 5593 - 5596	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	1.35E-07	0.96	5.01	-	1076.3
AHQ-5-13-, 5492	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	2.89E-06	0.94	4.89	-	1203.5
AHQ-5-13-, 5493 - 5516	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	7.25E-04	0.96	5.76	-	786.5
AHQ-5-13-, 6447	K.TSESGELHGLTTEEEFVEGIYKVEIDTK.S	3142.37019	3	1.77E-08	0.96	5.68	-	1267.3
gi|4759300|ref|NP_004772.1| vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated				3.18E-10	3.79	40.30	40.00	11309.0
AHQ-5-14-, 3514	R.ADALQAGASQFETSAAK.L	1666.77095	2	1.02E-09	0.92	3.74	-	990.2
AHQ-5-13-, 3587	R.ADALQAGASQFETSAAK.L	1666.77095	2	8.64E-09	0.96	5.06	-	996.9
AHQ-5-13, 3662	R.ADALQAGASQFETSAAK.L	1666.77095	2	5.62E-06	0.96	5.58	-	944.3
AHQ-5-13, 4950	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	5.07E-08	0.98	5.70	-	1994.7
AHQ-5-13-, 3731	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	2.20E-05	0.97	5.53	-	1650.4
AHQ-5-13, 4838	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	3.06E-06	0.97	4.37	-	1531.9
AHQ-5-13, 3832	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	8.05E-07	0.98	5.57	-	2057.0
AHQ-5-13-, 4865	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	3.18E-10	0.98	6.01	-	1606.1
AHQ-5-14-, 4502	K.LSELDDRADALQAGASQFETSAAK.L	2495.64172	3	2.95E-04	0.81	3.71	-	1251.8
AHQ-5-13-, 4551 - 4565	K.LSELDDRADALQAGASQFETSAAK.L	2495.64172	3	1.56E-04	0.92	5.23	-	979.1
gi|21464101|ref|NP_036611.2| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein				3.38E-10	6.05	80.29	49.00	28302.4
AHQ-5-10, 1507	K.AYSEAHEISK.E	1135.20862	1	1.47E-04	0.58	2.28	-	654.7
AHQ-5-10, 6612	K.ELEAVCQDVLSLLDNYLIK.N	2237.55566	2	1.07E-04	0.97	5.41	-	1387.6
AHQ-5-10, 6446	R.LGLALNYSVFYYEIQNAPEQACHLAK.T	3015.38773	3	3.38E-10	0.96	5.73	-	1052.8
AHQ-5-10, 3772 - 3826	R.NLLSVAYKNVVGAR.R	1504.75906	2	4.49E-06	0.96	3.71	-	1944.8
AHQ-5-11, 2940 - 2944	K.NVTELNEPLSNEER.N	1644.72215	2	2.65E-04	0.95	4.43	-	1075.9
AHQ-5-10, 2787	K.NVTELNEPLSNEER.N	1644.72215	2	2.69E-06	0.77	3.23	-	642.0
AHQ-5-10, 5479	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	4.06E-04	0.64	3.61	-	329.7
AHQ-5-10, 5864 - 5936	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	4.58E-08	0.92	4.20	-	1057.8
AHQ-5-10, 6107 - 6134	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	5.74E-06	0.94	5.46	-	1080.4
AHQ-5-9, 6070	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	9.72E-04	0.86	3.54	-	739.7
AHQ-5-10, 2156	R.YDDMAAAMK.N	1016.17419	1	5.83E-05	0.17	1.94	-	291.4
AHQ-5-10, 2107	R.YLAEVATGEK.R	1081.20087	1	3.79E-08	0.72	3.06	-	351.3

AHQ-5-10, 2115	R.YLAEVATGEK.R	1081.20087	2	1.08E-06	0.88	3.14	-	960.6
gi|4503689|ref|NP_000499.1| fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M				3.56E-10	17.51	220.29	28.80	94972.5
AHQ-5-6, 5885	K.DSDWPFCSDEDWNYK.C	1965.98609	2	2.98E-06	0.90	3.56	-	652.1
AHQ-5-7, 5839 - 5848	K.DSDWPFCSDEDWNYK.C	1965.98609	2	4.72E-05	0.80	3.13	-	462.6
AHQ-5-1, 6075	K.DSDWPFCSDEDWNYK.C	1965.98609	2	1.60E-07	0.85	3.34	-	466.7
AHQ-5-6, 5901 - 5973	K.DSDWPFCSDEDWNYK.C	1965.98609	2	4.68E-06	0.94	4.22	-	697.0
AHQ-5-10, 5131 - 5151	K.DSHSLTTNIMEILR.G	1630.84839	2	5.03E-04	0.96	4.37	-	1474.7
AHQ-5-9, 4915	K.DSHSLTTNIMEILR.G	1630.84839	2	3.38E-06	0.94	3.98	-	1024.6
AHQ-5-8, 5153	K.DSHSLTTNIMEILR.G	1630.84839	2	2.92E-04	0.96	4.60	-	1166.3
AHQ-5-10, 4371	K.DSHSLTTNIM*EILR.G	1646.84779	2	1.09E-04	0.91	3.73	-	1047.7
AHQ-5-6, 5628	K.DSHSLTTNIMEILR.G	1630.84839	2	2.15E-06	0.96	4.02	-	1675.5
AHQ-5-11, 2167 - 2172	K.ESSSHHPGIAEFPSR.G	1638.72252	2	1.26E-07	0.86	3.01	-	761.4
AHQ-5-12, 2234	K.ESSSHHPGIAEFPSR.G	1638.72252	2	7.11E-05	0.76	2.66	-	663.2
AHQ-5-8, 2226	R.EVDLKDYEDQQK.Q	1510.58460	2	1.43E-07	0.80	3.12	-	574.3
AHQ-5-4, 2497	R.EVDLKDYEDQQK.Q	1510.58460	2	8.63E-06	0.87	3.38	-	710.9
AHQ-5-13-, 2633 - 2640	R.EVDLKDYEDQQK.Q	1510.58460	2	7.31E-08	0.88	3.56	-	664.0
AHQ-5-7, 2339 - 2343	R.EVDLKDYEDQQK.Q	1510.58460	2	3.02E-04	0.85	3.24	-	732.4
AHQ-5-9, 2355	R.EVDLKDYEDQQK.Q	1510.58460	2	4.63E-06	0.86	3.02	-	805.9
AHQ-5-3, 2529	R.EVDLKDYEDQQK.Q	1510.58460	2	1.59E-05	0.70	2.87	-	500.1
AHQ-5-14-, 2587	R.EVDLKDYEDQQK.Q	1510.58460	2	2.67E-09	0.90	3.84	-	619.6
AHQ-5-6, 2376	R.EVDLKDYEDQQK.Q	1510.58460	2	1.25E-07	0.66	2.62	-	544.3
AHQ-5-13, 2774	R.EVDLKDYEDQQK.Q	1510.58460	2	1.25E-04	0.70	2.72	-	707.8
AHQ-5-6, 6598 - 6622	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	3.13E-08	0.95	5.41	-	1040.9
AHQ-5-6, 6852 - 6917	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	1.14E-06	0.96	5.30	-	1674.2
AHQ-5-1, 6757 - 6800	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	1.53E-07	0.76	3.44	-	885.4
AHQ-5-13-, 6275	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	3.85E-06	0.94	5.16	-	977.5
AHQ-5-13, 6232 - 6234	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	1.14E-06	0.88	4.70	-	819.4
AHQ-5-6, 1549	R.GGSTSYGTGSETESPR.N	1573.55765	2	9.06E-06	0.62	3.14	-	466.7
AHQ-5-10, 4296	K.GLIDEVNQDFTNR.I	1521.61384	2	1.60E-06	0.83	3.71	-	760.3
AHQ-5-3, 4949	K.GLIDEVNQDFTNR.I	1521.61384	2	1.22E-04	0.91	3.91	-	949.5
AHQ-5-6, 4580	K.GLIDEVNQDFTNR.I	1521.61384	2	5.12E-05	0.48	2.59	-	532.5
AHQ-5-9, 4216	K.GLIDEVNQDFTNR.I	1521.61384	2	1.45E-04	0.83	2.77	-	1125.8
AHQ-5-6, 4676 - 4700	K.GLIDEVNQDFTNR.I	1521.61384	2	2.42E-07	0.92	3.81	-	875.0
AHQ-5-1, 4939	K.GLIDEVNQDFTNR.I	1521.61384	2	1.43E-07	0.89	3.67	-	782.0
AHQ-5-5, 4795	K.GLIDEVNQDFTNR.I	1521.61384	2	4.03E-10	0.96	4.86	-	1330.2
AHQ-5-2, 4921	K.GLIDEVNQDFTNR.I	1521.61384	2	6.66E-07	0.92	3.65	-	949.0
AHQ-5-13, 4734	K.GLIDEVNQDFTNR.I	1521.61384	2	9.55E-05	0.90	3.28	-	1103.8
AHQ-5-7, 4512 - 4587	K.GLIDEVNQDFTNR.I	1521.61384	2	2.38E-07	0.92	3.74	-	1026.1
AHQ-5-12, 4696	K.GLIDEVNQDFTNR.I	1521.61384	2	2.68E-06	0.93	3.43	-	1229.8
AHQ-5-4, 4909	K.GLIDEVNQDFTNR.I	1521.61384	2	2.77E-06	0.92	3.38	-	1159.5
AHQ-5-8, 4454	K.GLIDEVNQDFTNR.I	1521.61384	2	4.93E-10	0.94	3.91	-	1032.3
AHQ-5-8, 3966	K.GLIDEVNQDFTNR.I	1521.61384	2	1.12E-05	0.84	3.33	-	676.8
AHQ-5-13-, 4635 - 4664	K.GLIDEVNQDFTNR.I	1521.61384	2	1.12E-06	0.91	3.80	-	997.8
AHQ-5-4, 2141	R.GSESGIFTNTK.E	1141.21317	1	3.13E-04	0.11	1.80	-	221.5
AHQ-5-6, 1998	R.GSESGIFTNTK.E	1141.21317	1	1.20E-04	0.25	2.21	-	217.1
AHQ-5-13-, 2296	R.GSESGIFTNTK.E	1141.21317	2	4.83E-04	0.90	3.48	-	1202.1
AHQ-5-6, 2089	R.GSESGIFTNTK.E	1141.21317	1	3.79E-04	0.29	2.19	-	399.9
AHQ-5-13, 2467	R.GSESGIFTNTK.E	1141.21317	2	6.53E-05	0.69	2.62	-	1001.1
AHQ-5-12, 3006	R.HPDEAAFFDTASTGK.T	1594.66329	2	2.27E-05	0.69	3.10	-	422.2
AHQ-5-13-, 3052	R.HPDEAAFFDTASTGK.T	1594.66329	2	3.56E-10	0.81	3.51	-	300.3
AHQ-5-9, 4180	R.HQSACKDSDWPFCSDEDWNYK.C	2678.76438	2	1.46E-06	0.62	2.56	-	516.1
AHQ-5-10, 2308	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	2.51E-06	0.97	5.26	-	1297.8
AHQ-5-7, 2216	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	5.62E-06	0.93	4.21	-	839.1
AHQ-5-13, 2791 - 2797	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	6.58E-09	0.97	5.33	-	1367.7
AHQ-5-12, 2462	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.21E-06	0.98	5.74	-	1734.8
AHQ-5-11, 2408	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	4.65E-07	0.97	5.36	-	1849.9
AHQ-5-11, 2396	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	3.94E-08	0.96	5.26	-	1010.5
AHQ-5-13-, 2641	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	2.85E-08	0.97	4.83	-	1330.2
AHQ-5-9, 2238	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.97E-04	0.95	4.36	-	1063.9
AHQ-5-6, 2237	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	8.72E-04	0.97	4.95	-	1663.8
AHQ-5-7, 2315	R.MELERPGGNEITR.G	1502.67870	2	5.86E-04	0.67	3.07	-	462.4
AHQ-5-9, 2950 - 2951	K.M*KPVPDLVPGNFK.S	1458.75054	2	1.75E-05	0.86	3.27	-	598.2
AHQ-5-6, 3200	K.M*KPVPDLVPGNFK.S	1458.75054	2	3.39E-04	0.33	2.56	-	223.7
AHQ-5-9, 4582	K.NNKDSHSLTTNIMEILR.G	1987.22751	2	1.31E-05	0.87	3.56	-	929.3
AHQ-5-1, 2367	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	3.85E-07	0.80	3.30	-	480.8
AHQ-5-7, 2051 - 2054	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	9.28E-08	0.89	3.86	-	670.0
AHQ-5-7, 1936	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	4.93E-07	0.88	3.89	-	669.5
AHQ-5-6, 1953	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	2.70E-05	0.88	3.93	-	614.3
AHQ-5-7, 3058	K.NSLFEYQK.N	1029.12765	1	8.71E-05	0.14	1.89	-	202.1
AHQ-5-8, 2954	K.NSLFEYQK.N	1029.12765	1	1.04E-04	0.13	1.80	-	184.0
AHQ-5-9, 4224	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.73E-06	0.94	4.51	-	979.4
AHQ-5-10, 4306	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	3.38E-07	0.96	4.85	-	1093.8
AHQ-5-11, 4603	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	7.81E-06	0.95	4.62	-	1121.3
AHQ-5-12, 4768	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	4.16E-09	0.95	4.78	-	952.7
AHQ-5-6, 4644 - 4724	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.76E-07	0.95	4.19	-	1274.6
AHQ-5-3, 7503	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.14E-05	0.83	3.51	-	322.4
AHQ-5-7, 7223 - 7278	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.41E-06	0.21	2.55	-	250.5
AHQ-5-1, 7319 - 7392	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.00E-05	0.82	3.69	-	304.3
AHQ-5-13-, 6803 - 6868	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	9.53E-07	0.88	4.04	-	537.0
AHQ-5-11, 6498	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	8.08E-04	0.66	3.22	-	191.6
AHQ-5-11, 6739 - 6799	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.36E-08	0.92	4.21	-	534.7
AHQ-5-4, 7452	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.60E-06	0.82	3.63	-	312.1
AHQ-5-13, 6897	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.36E-05	0.84	3.89	-	279.4
AHQ-5-6, 7292	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	4.21E-07	0.87	3.73	-	550.2
AHQ-5-6, 6908	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	7.23E-05	0.73	3.64	-	145.9
AHQ-5-9, 6462	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.28E-06	0.85	3.34	-	559.7
AHQ-5-12, 6733	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	6.52E-04	0.54	2.68	-	226.3
AHQ-5-12, 7028	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	9.40E-06	0.90	3.94	-	499.7
AHQ-5-2, 7179	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.15E-04	0.76	3.02	-	312.7
AHQ-5-13, 6693	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	3.87E-04	0.83	3.66	-	330.0
AHQ-5-5, 7389 - 7391	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.16E-07	0.86	3.64	-	466.9
AHQ-5-6, 1990 - 2033	K.VQHIQLLQK.N	1107.33106	2	1.23E-04	0.65	2.66	-	565.9
AHQ-5-6, 2029	K.VQHIQLLQK.N	1107.33106	1	6.19E-04	0.41	2.41	-	565.5
AHQ-5-6, 2040	K.VQHIQLLQK.N	1107.33106	1	6.95E-04	0.61	2.75	-	521.0
AHQ-5-7, 1986	K.VQHIQLLQK.N	1107.33106	2	8.75E-05	0.70	2.83	-	572.8
AHQ-5-7, 1987	K.VQHIQLLQK.N	1107.33106	1	1.89E-04	0.35	2.71	-	223.8
AHQ-5-8, 1876	K.VQHIQLLQK.N	1107.33106	2	3.23E-05	0.73	2.69	-	608.9
AHQ-5-3, 2251	K.VQHIQLLQK.N	1107.33106	1	2.27E-04	0.49	2.36	-	625.1
AHQ-5-9, 2062	K.VQHIQLLQK.N	1107.33106	1	1.29E-04	0.72	2.70	-	724.8
AHQ-5-9, 2068 - 2074	K.VQHIQLLQK.N	1107.33106	2	7.18E-05	0.80	3.03	-	689.6
AHQ-5-1, 2495	K.VQHIQLLQK.N	1107.33106	1	3.23E-05	0.49	2.58	-	624.1
AHQ-5-10, 2098	K.VQHIQLLQK.N	1107.33106	1	3.23E-04	0.78	3.13	-	539.1
AHQ-5-8, 1880	K.VQHIQLLQK.N	1107.33106	1	5.28E-04	0.52	2.67	-	204.0
gi|7705767|ref|NP_057086.1| CGI-49 protein [Homo sapiens]				4.26E-10	0.67	10.19	6.80	46920.8
AHQ-5-1, 7429	K.GPEAGYVATPIAMVQAAM*TLLSDASHLPK.A	2957.41485	3	4.26E-10	0.67	3.89	-	569.9
gi|4502565|ref|NP_001740.1| calpain, small subunit 1; calpain, small polypeptide; calcium-dependent				4.37E-10	3.75	40.22	17.50	28315.5
AHQ-5-11, 2694	R.SMVAVMDSDTTGK.L	1342.52228	2	5.66E-08	0.95	4.08	-	1134.4

AHQ-5-12, 2734 - 2742	R.SMVAVMDSDTTGK.L	1342.52228	2	6.08E-06	0.93	3.47	-	1183.0
AHQ-5-11, 2223	R.THYSNIEANESEEVR.Q	1778.81502	3	4.68E-07	0.95	4.22	-	1632.8
AHQ-5-12, 6650 - 6685	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	3.20E-09	0.92	4.14	-	882.9
AHQ-5-12, 6945	R.YSDESGNMDFDNFISCLVR.L	2271.42628	2	6.95E-10	0.92	4.42	-	775.1
AHQ-5-14-, 6514	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	4.37E-10	0.93	4.42	-	1093.9
AHQ-5-11, 6451 - 6464	R.YSDESGNM*DFDNFISCLVR.L	2287.42568	2	1.77E-08	0.94	3.81	-	1347.4
gi|28373103|ref|NP_005164.2| sarco/endoplasmic reticulum Ca2+ -ATPase isoform a; ATPase, Ca(2+)-tra				4.41E-10	0.96	10.23	1.90	109255.5
AHQ-5-1, 3909	R.HFSVTAEGGLSPAQVTGAR.E	1886.05823	2	4.41E-10	0.96	4.66	-	1549.5
gi|10835187|ref|NP_000627.1| superoxide dismutase 2, mitochondrial [Homo sapiens]				4.55E-10	5.63	60.28	56.80	24733.0
AHQ-5-11, 5894 - 5967	K.AIWNVINWENVTER.Y	1744.93137	2	2.05E-07	0.93	3.92	-	903.3
AHQ-5-13-, 6165	K.AIWNVINWENVTER.Y	1744.93137	2	1.09E-04	0.93	3.95	-	1120.5
AHQ-5-12, 6174	K.AIWNVINWENVTER.Y	1744.93137	2	1.50E-06	0.92	3.88	-	896.3
AHQ-5-11, 6116 - 6194	K.AIWNVINWENVTER.Y	1744.93137	2	4.32E-09	0.96	4.28	-	1549.6
AHQ-5-11, 6027	K.AIWNVINWENVTER.Y	1744.93137	2	1.30E-09	0.94	3.92	-	1280.3
AHQ-5-14-, 6042 - 6110	K.AIWNVINWENVTER.Y	1744.93137	2	1.89E-06	0.96	4.50	-	1338.9
AHQ-5-11, 4407	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	2	7.47E-08	0.92	4.45	-	880.0
AHQ-5-11, 4502 - 4527	K.FNGGGHINHSIFWTNLSPNGGGEPK.G	2638.83761	2	2.75E-04	0.87	4.22	-	634.1
AHQ-5-11, 3739 - 3874	K.GDVTAQIALQPALK.F	1425.65548	1	1.76E-04	0.52	2.45	-	775.6
AHQ-5-11, 3736 - 3799	K.GDVTAQIALQPALK.F	1425.65548	2	2.44E-07	0.91	4.13	-	808.1
AHQ-5-11, 3750 - 3810	K.GDVTAQIALQPALK.F	1425.65548	1	2.57E-04	0.72	3.10	-	768.5
AHQ-5-11, 6824 - 6854	R.GHLQIAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYK.N	4296.85327	3	4.55E-10	0.97	5.68	-	1857.4
AHQ-5-11, 2274 - 2354	K.HHAAYVNNLNVTEEK.Y	1739.86999	3	3.78E-05	0.89	4.18	-	1127.6
AHQ-5-11, 2174	K.HHAAYVNNLNVTEEK.Y	1739.86999	3	2.43E-04	0.89	4.23	-	1128.5
AHQ-5-11, 2270 - 2335	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	4.35E-09	0.97	4.32	-	1814.6
AHQ-5-11, 2170	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	6.25E-07	0.97	4.52	-	1907.8
AHQ-5-11, 6028 - 6056	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	4.96E-06	0.96	5.04	-	990.0
AHQ-5-11, 6895 - 6971	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	2.95E-08	0.92	4.58	-	628.3
gi|4506193|ref|NP_002784.1| proteasome beta 1 subunit; proteasome subunit HC5; proteasome component				4.55E-10	4.39	50.29	19.50	26489.2
AHQ-5-11, 6774	R.FFPYYVYNIIGGLDEEGK.G	2125.36396	2	4.55E-10	0.93	4.19	-	765.2
AHQ-5-11, 3935	K.GAVYSFDPVGSYQR.D	1546.66500	2	3.70E-05	0.88	3.50	-	949.9
AHQ-5-11, 3408	K.NMQNVEHVPLSLDR.A	1652.85728	2	6.25E-06	0.88	4.07	-	612.6
AHQ-5-11, 2942	K.NM*QNVEHVPLSLDR.A	1668.85668	2	2.90E-04	0.72	2.77	-	745.6
AHQ-5-11, 6591	R.RFFPYYVYNIIGGLDEEGK.G	2281.55031	2	6.61E-08	0.98	5.88	-	1710.0
gi|5031677|ref|NP_005681.1| dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [				4.59E-10	8.41	100.27	22.70	78060.6
AHQ-5-13-, 4745	K.ALQGASQIIAEIR.E	1370.57991	2	4.27E-04	0.90	3.76	-	1189.8
AHQ-5-13, 4832 - 4834	K.ALQGASQIIAEIR.E	1370.57991	2	1.81E-04	0.89	3.65	-	1326.8
AHQ-5-13, 5269 - 5280	K.DTLQSELVGQLYK.S	1494.67144	2	3.74E-06	0.87	3.10	-	986.0
AHQ-5-13, 4398 - 4460	K.GHAVNLLDVPVPVAR.K	1557.82197	2	1.91E-06	0.75	2.86	-	678.8
AHQ-5-5, 7070	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	1.73E-06	0.94	4.59	-	980.7
AHQ-5-6, 6962	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	3.71E-05	0.90	3.48	-	1006.9
AHQ-5-6, 3032	R.IIQHCSNYSTQELLR.F	1864.07262	2	1.46E-04	0.94	4.64	-	779.2
AHQ-5-6, 7312 - 7314	K.LQDVFNTVGADIIQLPQIVVVGTQSSGK.S	2928.32977	2	9.76E-07	0.81	4.10	-	366.8
AHQ-5-6, 6204	K.LYTDFDEIRQEIENETER.I	2301.40883	2	3.00E-04	0.40	2.61	-	297.0
AHQ-5-13, 6826 - 6889	K.SSLLDDLLTESEDMAQR.R	1924.07698	2	3.69E-06	0.88	3.88	-	700.4
AHQ-5-13, 6285	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	1.08E-07	0.92	3.94	-	947.7
AHQ-5-14-, 6094	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	2.14E-06	0.97	4.84	-	2042.9
AHQ-5-14-, 6709 - 6779	K.SSLLDDLLTESEDMAQR.R	1924.07698	2	1.04E-09	0.93	4.32	-	947.1
AHQ-5-6, 7284	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	4.59E-10	0.97	5.31	-	1364.3
gi|4758638|ref|NP_004896.1| peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi				5.01E-10	7.67	90.33	42.40	25034.8
AHQ-5-10, 4595 - 4668	R.ELAILLGM*LDPAEKDEK.G	1902.19916	2	6.13E-04	0.94	4.31	-	911.4
AHQ-5-10, 5628 - 5686	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	7.29E-06	0.96	5.03	-	1100.3
AHQ-5-10, 5878 - 5890	R.FHDFLGDSWGILFSHPR.D	2032.24831	3	3.21E-09	0.95	5.08	-	1077.6
AHQ-5-10, 5894	R.FHDFLGDSWGILFSHPR.D	2032.24831	2	9.33E-07	0.98	5.96	-	2152.4
AHQ-5-10, 5806 - 5870	R.FHDFLGDSWGILFSHPR.D	2032.24831	2	2.44E-07	0.98	6.51	-	2334.7
AHQ-5-10, 5456 - 5530	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	5.01E-10	0.97	5.17	-	1525.9
AHQ-5-14-, 5858	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	2.25E-04	0.61	3.88	-	296.5
AHQ-5-10, 5588 - 5647	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	8.56E-08	0.94	4.51	-	1003.6
AHQ-5-10, 5498	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	4.05E-06	0.77	4.18	-	382.9
AHQ-5-14-, 5857	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	3.34E-06	0.96	4.42	-	1581.0
AHQ-5-10, 4082	K.LPFPIIDDR.N	1086.26548	2	1.79E-05	0.93	3.28	-	1238.0
AHQ-5-10, 2476	R.VATPVDWK.D	916.05568	1	3.82E-04	0.47	2.34	-	401.5
AHQ-5-10, 5102 - 5170	R.VATPVDWKDGDSVMVLPTIPEEEAK.K	2728.06777	2	3.80E-06	0.92	4.50	-	687.9
AHQ-5-10, 3455	R.VVFVFGPDK.K	1008.19471	1	2.39E-04	0.68	2.22	-	1202.2
AHQ-5-10, 2728	R.VVFVFGPDKK.L	1136.36763	2	1.79E-06	0.85	3.02	-	759.5
gi|4759096|ref|NP_004252.1| 15 kDa selenoprotein [Homo sapiens]				5.04E-10	0.94	10.19	9.90	17640.3
AHQ-5-12, 6118	K.LLDDNGNIAEELSILK.W	1757.96344	2	5.04E-10	0.94	3.86	-	1138.6
gi|22749499|ref|NP_689979.1| hypothetical protein MGC40107 [Homo sapiens]				5.07E-10	0.98	10.33	24.80	11741.6
AHQ-5-14-, 5494	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	2.03E-05	0.96	5.27	-	1840.1
AHQ-5-14-, 5581 - 5582	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	5.07E-10	0.98	6.62	-	1989.5
AHQ-5-14, 6253	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	1.84E-05	0.84	3.93	-	745.4
gi|4503423|ref|NP_001939.1| dUTP pyrophosphatase [Homo sapiens]				5.39E-10	0.97	10.24	10.40	17748.0
AHQ-5-11, 5475 - 5480	R.IFYPEIEEVQALDDTER.G	2068.22598	2	5.39E-10	0.97	4.73	-	1517.2
gi|29742827|ref|XP_294099.1| similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]				5.39E-10	1.43	30.23	14.20	17094.0
AHQ-5-11, 2731 - 2811	K.EAFNMIDQNR.D	1238.35558	2	4.36E-05	0.73	2.82	-	525.3
AHQ-5-11, 2802 - 2858	K.EAFNMIDQNR.D	1238.35558	1	4.16E-06	0.19	1.91	-	230.8
AHQ-5-11, 2198 - 2243	K.EAFNM*IDQNR.D	1254.35498	2	1.03E-04	0.64	2.68	-	537.4
AHQ-5-11, 3126 - 3128	R.FTDEEVDELYR.E	1416.47127	2	9.18E-10	0.96	4.46	-	1468.8
AHQ-5-11, 3651 - 3718	R.FTDEEVDELYR.E	1416.47127	2	4.77E-07	0.95	3.80	-	1439.6
AHQ-5-11, 3710 - 3774	R.FTDEEVDELYR.E	1416.47127	1	2.16E-06	0.40	1.85	-	475.3
AHQ-5-11, 3715 - 3778	R.FTDEEVDELYR.E	1416.47127	1	5.39E-10	0.60	2.63	-	464.5
AHQ-5-11, 3783	R.FTDEEVDELYR.E	1416.47127	2	2.94E-08	0.97	4.59	-	1655.8
AHQ-5-12, 3812 - 3825	R.FTDEEVDELYR.E	1416.47127	2	1.38E-07	0.97	4.67	-	1504.2
AHQ-5-12, 3813	R.FTDEEVDELYR.E	1416.47127	1	6.89E-06	0.14	1.83	-	363.3
AHQ-5-13, 3980	R.FTDEEVDELYR.E	1416.47127	2	7.06E-07	0.94	3.48	-	1353.0
AHQ-5-14, 4632 - 4633	R.FTDEEVDELYR.E	1416.47127	2	7.81E-08	0.90	3.46	-	1102.1
AHQ-5-13-, 3868	R.FTDEEVDELYR.E	1416.47127	2	6.17E-07	0.96	4.62	-	1203.5
AHQ-5-14-, 3774	R.FTDEEVDELYR.E	1416.47127	2	1.05E-08	0.97	4.20	-	1706.5
gi|4503725|ref|NP_000792.1| FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei				5.40E-10	1.88	20.24	13.00	11950.6
AHQ-5-13, 4013	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.92E-06	0.95	4.21	-	1275.8
AHQ-5-14, 4661 - 4673	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.02E-04	0.88	3.82	-	904.4
AHQ-5-13-, 2977	R.GWEEGVAQM*SVGQR.A	1550.67866	2	1.69E-08	0.96	4.79	-	1234.2
AHQ-5-13-, 3891	R.GWEEGVAQMSVGQR.A	1534.67926	2	2.65E-05	0.87	3.19	-	1193.6
AHQ-5-14-, 3790 - 3798	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.79E-05	0.94	3.87	-	1532.3
AHQ-5-13, 3110	R.GWEEGVAQM*SVGQR.A	1550.67866	2	5.40E-10	0.93	3.63	-	1182.1
gi|9910542|ref|NP_064535.1| SAR1a gene homolog 1; SAR1 protein [Homo sapiens]				6.26E-10	3.46	40.25	34.30	22366.6
AHQ-5-11, 3614	R.EIFGLYGQTTGK.G	1314.46845	1	3.71E-05	0.68	3.45	-	233.2
AHQ-5-11, 3599 - 3611	R.EIFGLYGQTTGK.G	1314.46845	2	9.44E-04	0.92	3.56	-	937.7
AHQ-5-11, 6084	R.LGQHVPTLHPTSEELTIAGMTFTTFDLGGHEQAR.R	3694.08659	3	6.01E-04	0.88	4.74	-	677.3
AHQ-5-11, 3671	K.LREIFGLYGQTTGK.G	1583.81305	2	6.26E-10	0.98	5.03	-	2861.9
AHQ-5-11, 6803	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	2.23E-07	0.90	3.56	-	1056.7
AHQ-5-11, 6423 - 6430	K.NYLPAINGIVFLVDCADHSR.L	2276.55690	2	1.91E-06	0.93	4.25	-	734.3
gi|4557731|ref|NP_000618.1| latent transforming growth factor beta binding protein 1 precursor [Hom				6.32E-10	10.99	130.30	13.90	152790.9
AHQ-5-3, 3726	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	9.31E-05	0.96	4.96	-	1189.9
AHQ-5-1, 3775	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	2.06E-07	0.95	5.18	-	1088.8
AHQ-5-1, 6719 - 6732	K.CLCLPGYVPSDKPNYCTPLNTALNLEK.D	3142.56947	3	4.85E-08	0.87	4.28	-	654.6
AHQ-5-1, 2592 - 2663	R.CTCGQGYQLSAAK.D	1446.58862	2	5.93E-05	0.86	3.80	-	543.3
AHQ-5-1, 4241 - 4260	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	6.32E-10	0.98	6.09	-	1386.7

AHQ-5-2, 4203	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	9.02E-04	0.85	3.83	-	396.3
AHQ-5-3, 4219	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	5.45E-08	0.92	4.47	-	690.6
AHQ-5-1, 2232	K.DQCEDIDECQHR.H	1607.61898	2	4.34E-05	0.77	3.17	-	642.2
AHQ-5-1, 3263 - 3276	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	5.14E-05	0.89	3.80	-	527.1
AHQ-5-1, 3433	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	1.03E-06	0.95	4.38	-	943.6
AHQ-5-1, 4020	K.EEPVEALTFSR.E	1278.39297	2	7.97E-04	0.82	2.86	-	660.1
AHQ-5-1, 2257	K.HPPEASVQIHQVSR.I	1585.74913	2	1.51E-08	0.57	2.73	-	324.7
AHQ-5-1, 6128	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	6.23E-05	0.89	4.19	-	729.8
AHQ-5-2, 6121	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	8.85E-06	0.92	5.06	-	877.2
AHQ-5-3, 6183	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	1.81E-04	0.94	4.71	-	1285.4
AHQ-5-1, 3357	K.TQTIHSTYSHQQVIPHVYPVAAK.T	2606.92010	3	2.22E-05	0.93	4.79	-	1090.4
AHQ-5-1, 2969	R.TSTDLDVDVDQPK.E	1433.50014	2	1.14E-06	0.79	3.24	-	855.2
AHQ-5-1, 2755	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.73E-06	0.86	3.66	-	1057.2
AHQ-5-3, 2594	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	7.19E-07	0.86	3.65	-	1081.6
AHQ-5-4, 2561	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	2.19E-07	0.77	3.39	-	847.9
AHQ-5-1, 3683	R.YTCICYEGYR.F	1387.51964	2	2.91E-04	0.79	2.77	-	517.5
gi|4507109|ref|NP_000336.1| alpha-synuclein isoform NACP140; non A4 component of amyloid precursor				6.50E-10	5.57	60.32	45.70	14460.1
AHQ-5-12, 2149	K.EGVVHGVATVAEK.T	1296.45466	1	1.96E-07	0.85	3.53	-	455.7
AHQ-5-13-, 2179 - 2239	K.EGVVHGVATVAEK.T	1296.45466	2	4.88E-05	0.69	2.81	-	483.9
AHQ-5-13-, 4633	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	3.58E-06	0.94	4.78	-	776.2
AHQ-5-12, 4765	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	6.41E-08	0.94	4.95	-	681.7
AHQ-5-14-, 4577 - 4582	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.63E-08	0.98	6.44	-	1389.8
AHQ-5-14, 5390	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	2.61E-05	0.89	4.17	-	606.1
AHQ-5-13, 4698	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	3	2.85E-04	0.96	5.52	-	1542.4
AHQ-5-12, 4654	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	5.22E-06	0.95	4.61	-	1017.2
AHQ-5-12, 4673	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	3	8.78E-05	0.98	5.91	-	2448.9
AHQ-5-13, 4686	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	2.64E-07	0.95	5.15	-	925.1
AHQ-5-12, 2012	K.TKEGVLYVGSK.T	1181.36357	2	1.42E-06	0.86	2.82	-	811.6
AHQ-5-12, 2004	K.TKEGVVHGVATVAEK.T	1525.73191	2	6.50E-10	0.97	5.38	-	1551.8
AHQ-5-13, 4280 - 4288	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	3.21E-04	0.95	5.61	-	1513.8
AHQ-5-13, 4284	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	2.18E-08	0.96	5.65	-	1116.2
AHQ-5-13, 4205 - 4282	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.35E-07	0.95	4.78	-	934.2
AHQ-5-12, 4204 - 4210	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	6.20E-08	0.93	4.80	-	1622.4
AHQ-5-14, 5029	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	5.09E-06	0.96	4.95	-	1345.2
AHQ-5-12, 4196 - 4228	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	2.62E-07	0.98	5.54	-	1758.1
AHQ-5-14-, 4179 - 4193	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	8.17E-09	0.98	6.22	-	1878.6
AHQ-5-13-, 4195	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	4.46E-06	0.95	4.92	-	1594.0
AHQ-5-13-, 4199 - 4204	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.55E-08	0.98	5.73	-	1803.0
AHQ-5-14-, 4177	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	1.33E-05	0.93	4.68	-	1611.5
AHQ-5-12, 4136	K.TVEGAGSIAAATGFVK.K	1479.66001	1	8.03E-07	0.58	2.99	-	369.4
AHQ-5-12, 4122 - 4140	K.TVEGAGSIAAATGFVK.K	1479.66001	2	1.98E-05	0.93	3.59	-	1335.8
AHQ-5-13, 4232 - 4310	K.TVEGAGSIAAATGFVK.K	1479.66001	2	3.10E-09	0.92	4.22	-	938.0
gi|5803225|ref|NP_006752.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon poly				6.56E-10	1.91	20.29	11.40	29173.7
AHQ-5-13, 6620 - 6700	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	9.97E-07	0.96	5.76	-	804.9
AHQ-5-10, 6286 - 6288	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	1.41E-05	0.95	4.48	-	1263.4
AHQ-5-9, 6178 - 6183	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	6.56E-10	0.96	4.95	-	1145.3
AHQ-5-9, 6670 - 6671	K.AAFDDAIAELDTLSEESYKDSTLIMQLLR.D	3260.61486	3	3.06E-06	0.95	5.48	-	1197.6
gi|25306267|ref|NP_001700.2| brain-derived neurotrophic factor isoform a preproprotein [Homo sapien				6.76E-10	0.98	10.29	6.10	27817.8
AHQ-5-13-, 3692 - 3695	K.TAVDMSGGTVTVLEK.V	1508.71993	2	6.76E-10	0.98	5.85	-	1901.7
AHQ-5-13, 3784	K.TAVDMSGGTVTVLEK.V	1508.71993	2	3.89E-05	0.88	3.08	-	1075.0
gi|4505989|ref|NP_000299.1| protective protein for beta-galactosidase; Protective protein for beta-				7.30E-10	0.98	10.23	2.70	54495.8
AHQ-5-12, 3481	K.YGDSGEQIAGFVK.E	1371.47686	2	7.30E-10	0.98	4.51	-	2464.3
gi|27478749|ref|XP_208411.1| similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit				7.34E-10	1.90	20.27	13.40	25628.5
AHQ-5-9, 4047	K.GEMMDLQHGSLFLR.T	1634.90537	2	7.34E-10	0.97	4.85	-	1467.8
AHQ-5-11, 6846	K.LLIVSNPVDILTYVAWK.I	1945.33337	2	7.39E-06	0.94	5.37	-	814.5
gi|4757812|ref|NP_004880.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso				8.32E-10	2.84	30.23	25.50	10917.8
AHQ-5-14-, 5899	R.DFSPSGIFGAFQR.G	1429.56124	1	3.18E-06	0.10	2.02	-	178.6
AHQ-5-14-, 5885 - 5897	R.DFSPSGIFGAFQR.G	1429.56124	2	8.58E-08	0.94	4.34	-	1043.3
AHQ-5-13, 6076	R.DFSPSGIFGAFQR.G	1429.56124	2	8.32E-10	0.96	4.69	-	1198.5
AHQ-5-14-, 5905	K.LGELPSWILMR.D	1315.60936	2	7.82E-08	0.94	4.47	-	865.1
AHQ-5-14-, 5455	K.LGELPSWILM*R.D	1331.60876	2	7.38E-06	0.94	4.07	-	675.9
gi|16933542|ref|NP_002017.1| fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s				9.19E-10	3.03	40.21	3.40	259222.8
AHQ-5-1, 4991	K.GLKPGVVYEGQLISIQQYGHQEVTR.F	2801.14977	3	1.90E-05	0.87	4.26	-	621.9
AHQ-5-1, 4583	R.ITYGETGGNSPVQEFTVPGSK.S	2169.33354	2	1.33E-05	0.48	2.63	-	378.8
AHQ-5-1, 5017 - 5096	R.NLQPASEYTVSLVAIK.G	1733.98671	2	2.72E-04	0.80	3.08	-	491.1
AHQ-5-2, 7321	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	9.19E-10	0.88	3.71	-	522.9
AHQ-5-1, 7205	R.VTWAPPPSIDLTNFLVR.Y	1927.23500	2	4.94E-08	0.81	3.33	-	479.8
gi|29568111|ref|NP_006088.2| myosin, light polypeptide 9, regulatory; myosin regulatory light chain				9.67E-10	2.90	40.25	23.80	19827.1
AHQ-5-11, 3366	R.FTDEEVDEMYR.E	1434.51009	1	3.32E-06	0.64	2.68	-	426.7
AHQ-5-11, 2651	R.FTDEEVDEM*YR.E	1450.50949	2	3.89E-06	0.95	3.47	-	1366.5
AHQ-5-11, 3952	K.GNFNYVEFTR.I	1247.34066	1	7.60E-06	0.37	2.19	-	264.4
AHQ-5-11, 3942 - 3964	K.GNFNYVEFTR.I	1247.34066	2	1.07E-04	0.84	3.31	-	777.4
AHQ-5-11, 5774 - 5840	R.NAFACFDEEASGFIHEDHLR.E	2367.49548	2	9.67E-10	0.94	4.93	-	726.0
gi|4505753|ref|NP_002620.1| phosphoglycerate mutase 1 (brain); Phosphoglycerate mutase A, nonmuscle				9.91E-10	5.57	70.21	38.20	28803.7
AHQ-5-10, 3650	R.FSGWYDADLSPAGHEEAK.R	1981.06697	2	3.98E-06	0.92	4.06	-	883.9
AHQ-5-10, 3296	R.FSGWYDADLSPAGHEEAKR.G	2137.25332	2	3.12E-07	0.85	3.76	-	610.8
AHQ-5-10, 3818	K.NLKPIKPMQFLGDEETVR.K	2116.46992	2	2.09E-06	0.93	4.14	-	778.5
AHQ-5-10, 4046	R.SYDVPPPPMEPDHPFYSNISK.D	2418.66566	2	9.91E-10	0.55	2.72	-	275.5
AHQ-5-10, 3731	R.SYDVPPPPM*EPDHPFYSNISK.D	2434.66506	2	6.09E-05	0.64	2.87	-	277.8
AHQ-5-10, 6660	R.TLWTVLDAIDQM*WLPVVR.T	2173.56304	2	1.32E-04	0.76	3.41	-	500.6
AHQ-5-10, 4572 - 4590	R.YADLTEDQLPSCESLKDTIAR.A	2427.62735	3	2.66E-06	0.92	3.98	-	1299.2
gi|4502201|ref|NP_001649.1| ADP-ribosylation factor 1 [Homo sapiens]				1.01E-09	10.53	120.31	47.00	20696.6
AHQ-5-12, 4662 - 4730	R.DAVLLVFANK.Q	1090.29726	2	1.12E-07	0.97	4.44	-	2180.5
AHQ-5-12, 4605 - 4869	R.DAVLLVFANK.Q	1090.29726	1	5.44E-04	0.76	2.87	-	777.6
AHQ-5-12, 5545 - 5624	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.77E-04	0.95	4.97	-	687.1
AHQ-5-12, 5402	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.32E-07	0.97	5.66	-	1545.5
AHQ-5-12, 5278	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	2.39E-09	0.98	6.26	-	2518.7
AHQ-5-12, 5174	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	5.72E-07	0.98	6.04	-	2433.1
AHQ-5-12, 5757	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	6.17E-04	0.93	3.99	-	1058.4
AHQ-5-12, 4894 - 4965	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.32E-04	0.98	5.66	-	2059.0
AHQ-5-12, 5032 - 5101	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	1.10E-06	0.98	6.27	-	2300.8
AHQ-5-12, 5016 - 5086	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	2.53E-09	0.93	4.58	-	1131.2
AHQ-5-12, 4676 - 4741	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	1.64E-05	0.90	3.83	-	1041.3
AHQ-5-12, 4540 - 4608	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	3.63E-09	0.95	5.35	-	1038.7
AHQ-5-12, 3645 - 3708	R.ILMVGLDAAGK.T	1088.34632	1	9.40E-04	0.77	2.33	-	1388.8
AHQ-5-12, 3088	R.ILM*VGLDAAGK.T	1104.34572	1	2.57E-04	0.58	2.65	-	194.1
AHQ-5-12, 3084	R.ILM*VGLDAAGK.T	1104.34572	2	2.41E-05	0.91	2.98	-	1113.0
AHQ-5-11, 3568	R.ILMVGLDAAGK.T	1088.34632	1	7.15E-04	0.86	2.85	-	1171.9
AHQ-5-11, 3567	R.ILMVGLDAAGK.T	1088.34632	2	7.07E-05	0.92	3.65	-	1024.2
AHQ-5-12, 3642 - 3660	R.ILMVGLDAAGK.T	1088.34632	2	1.17E-07	0.95	4.26	-	1228.2
AHQ-5-12, 3669	R.ILMVGLDAAGK.T	1088.34632	1	7.21E-05	0.87	3.80	-	597.8
AHQ-5-12, 6448 - 6522	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	3	1.23E-04	0.96	5.49	-	1127.2
AHQ-5-12, 6382 - 6437	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	2.25E-05	0.69	3.58	-	216.6
AHQ-5-11, 6248 - 6306	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	3.83E-04	0.81	3.79	-	231.6
AHQ-5-12, 6500 - 6560	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	5.65E-05	0.86	3.89	-	317.0
AHQ-5-12, 2077	K.LGLHSLR.H	795.95280	2	3.94E-04	0.84	2.76	-	853.5
AHQ-5-12, 2544 - 2545	R.MLAEDELR.D	977.11769	2	2.53E-04	0.87	2.93	-	994.4

AHQ-5-14-, 6699 - 6733	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	2	1.22E-04	0.78	3.26	-	527.0
AHQ-5-11, 4892 - 4955	K.NISFTVWDVGGQDK.I	1566.69621	2	7.67E-04	0.85	3.73	-	626.1
AHQ-5-12, 5068 - 5133	K.NISFTVWDVGGQDK.I	1566.69621	2	1.01E-09	0.93	4.09	-	951.3
AHQ-5-14-, 5017	K.NISFTVWDVGGQDK.I	1566.69621	2	4.65E-04	0.90	3.67	-	687.4
AHQ-5-13-, 5067 - 5073	K.NISFTVWDVGGQDK.I	1566.69621	2	3.45E-07	0.96	4.35	-	1203.1
AHQ-5-12, 5196 - 5197	K.NISFTVWDVGGQDK.I	1566.69621	2	2.22E-08	0.93	4.13	-	844.3
AHQ-5-14, 5929	K.NISFTVWDVGGQDK.I	1566.69621	2	3.61E-04	0.55	2.82	-	456.4
AHQ-5-12, 3648 - 3720	K.QDLPNAMNAAEITDK.L	1631.79001	2	2.07E-08	0.94	4.60	-	885.4
AHQ-5-12, 3896 - 3964	K.QDLPNAMNAAEITDK.L	1631.79001	2	9.74E-05	0.94	4.25	-	1060.0
AHQ-5-12, 3064	K.QDLPNAM*NAAEITDK.L	1647.78941	2	3.21E-04	0.73	3.12	-	530.2
gi|4557597|ref|NP_001449.1| gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);				1.04E-09	1.75	30.28	1.70	288897.4
AHQ-5-4, 4568	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.11E-05	0.94	4.83	-	642.7
AHQ-5-1, 4751 - 4776	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	4.24E-09	0.91	4.94	-	591.4
AHQ-5-1, 4765 - 4767	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	8.34E-09	0.95	5.60	-	493.4
AHQ-5-7, 4035	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.04E-09	0.93	5.03	-	535.0
AHQ-5-7, 3955 - 4028	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	9.21E-04	0.93	4.37	-	811.1
AHQ-5-3, 4678	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	5.82E-04	0.51	3.09	-	285.1
AHQ-5-6, 4193	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.01E-07	0.95	5.36	-	561.6
AHQ-5-8, 3798	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.43E-05	0.96	5.39	-	969.6
AHQ-5-4, 4612	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	4.16E-06	0.79	4.06	-	374.5
AHQ-5-5, 4214 - 4285	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	6.13E-05	0.87	4.31	-	461.8
AHQ-5-5, 4241 - 4310	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	2.25E-04	0.95	5.17	-	627.5
AHQ-5-2, 1718 - 1781	K.IECDDKGDGSCDVR.Y	1628.67809	2	7.97E-04	0.80	2.99	-	680.0
AHQ-5-4, 1793	K.IECDDKGDGSCDVR.Y	1628.67809	2	1.01E-04	0.50	2.58	-	381.2
AHQ-5-1, 2561	K.NDNDTFTVK.Y	1054.09237	1	8.60E-04	0.04	1.81	-	161.6
AHQ-5-2, 1803 - 1997	K.NDNDTFTVK.Y	1054.09237	1	2.15E-05	0.33	2.23	-	227.8
gi|16507237|ref|NP_005338.1| heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he				1.07E-09	10.93	120.27	25.40	72332.5
AHQ-5-6, 4809 - 4820	R.AKFEELNMDLFR.S	1513.74309	2	1.74E-09	0.94	4.13	-	1264.1
AHQ-5-6, 3808	K.DAGTIAGLNVMR.I	1218.40894	2	4.40E-04	0.94	3.74	-	1066.0
AHQ-5-6, 5468 - 5545	K.DNHLLGTFDLTGIPPAPR.G	1935.17239	2	1.73E-06	0.92	4.44	-	697.3
AHQ-5-6, 6117	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	4.09E-08	0.93	4.51	-	878.3
AHQ-5-6, 4641	K.IEWLESHQDADIEDFK.A	1976.08864	2	3.05E-07	0.97	5.30	-	1704.2
AHQ-5-6, 3669 - 3716	R.ITPSYVAFTPEGER.L	1567.72412	2	6.37E-08	0.68	2.94	-	492.5
AHQ-5-6, 3490	K.KSDIDEIVLVGGSTR.I	1589.77277	2	1.07E-09	0.96	4.86	-	1564.8
AHQ-5-6, 3026	K.KSQIFSTASDNQPTVTIK.V	1966.18156	2	1.20E-05	0.97	5.03	-	1362.1
AHQ-5-6, 3020	K.KSQIFSTASDNQPTVTIK.V	1966.18156	3	1.88E-04	0.79	3.45	-	772.7
AHQ-5-6, 2092	K.MKETAEAYLGK.K	1241.43928	2	4.39E-05	0.87	3.19	-	729.3
AHQ-5-5, 3645	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	8.48E-04	0.95	4.51	-	1109.2
AHQ-5-6, 2700	K.TKPYIQVDIGGGQTK.T	1605.81703	2	2.74E-06	0.90	3.49	-	956.9
AHQ-5-5, 3766	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	8.76E-06	0.68	3.06	-	323.2
AHQ-5-6, 3622	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	3	5.10E-06	0.90	4.41	-	783.4
AHQ-5-6, 3832	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	2.70E-05	0.84	3.68	-	446.6
gi|20357552|ref|NP_005222.2| cortactin isoform a; oncogene EMS1 [Homo sapiens]				1.08E-09	2.65	30.23	7.80	61585.7
AHQ-5-12, 3968	R.LPSSPVYEDAASFK.A	1511.65733	2	1.87E-05	0.91	2.96	-	1035.6
AHQ-5-13-, 3993	R.LPSSPVYEDAASFK.A	1511.65733	2	2.16E-05	0.88	3.57	-	633.8
AHQ-5-11, 3868 - 3930	R.LPSSPVYEDAASFK.A	1511.65733	2	1.97E-05	0.69	2.58	-	613.1
AHQ-5-13, 4021	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	4.16E-04	0.82	3.10	-	868.2
AHQ-5-12, 5349 - 5356	R.YGLFPANYVELR.Q	1442.64306	1	4.05E-04	0.31	2.91	-	141.7
AHQ-5-12, 5333 - 5344	R.YGLFPANYVELR.Q	1442.64306	2	1.08E-09	0.92	3.99	-	587.8
gi|4502011|ref|NP_000467.1| adenylate kinase 1 [Homo sapiens]				1.08E-09	4.71	50.29	42.30	21634.7
AHQ-5-11, 6842 - 6843	K.GQLVPLETVLDMLR.D	1584.90590	2	1.08E-09	0.97	5.71	-	669.5
AHQ-5-11, 5660	R.IGQPTLLLYVDAGPETMTQR.L	2204.53234	2	2.33E-05	0.91	4.27	-	697.2
AHQ-5-11, 3362	K.IIFVVGGPGSGK.G	1131.34939	2	2.07E-04	0.96	3.82	-	1875.9
AHQ-5-11, 5924	R.KVNAEGSVDSVFSQVCTHLDALK	2506.77407	3	9.30E-06	0.97	5.83	-	1933.9
AHQ-5-11, 3646	K.YGYTHLSTGDLLR.S	1496.64912	1	6.98E-06	0.79	3.03	-	402.8
AHQ-5-11, 3639	K.YGYTHLSTGDLLR.S	1496.64912	2	2.97E-08	0.91	3.38	-	926.6
gi|20547107|ref|XP_114482.1| similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN				1.11E-09	0.95	10.25	2.10	94330.3
AHQ-5-4, 6777 - 6786	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	1.11E-09	0.95	5.09	-	885.9
gi|4507171|ref|NP_003109.1| secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec				1.24E-09	3.25	40.32	24.10	34632.0
AHQ-5-9, 2751	R.LEAGDHPVELLAR.D	1420.59579	2	1.24E-09	0.96	4.37	-	1426.9
AHQ-5-8, 2713	R.LEAGDHPVELLAR.D	1420.59579	2	6.52E-08	0.93	3.83	-	1067.5
AHQ-5-9, 2875 - 2876	K.LHLDYIGPCK.Y	1217.41920	1	1.48E-04	0.81	2.42	-	1149.9
AHQ-5-8, 2770 - 2845	K.LHLDYIGPCK.Y	1217.41920	2	7.02E-04	0.80	3.16	-	617.5
AHQ-5-9, 6336 - 6338	K.NYNMYIFPVHWQFGQLDQHPIDGYLSHTELAPLR.A	4102.58560	3	4.84E-05	0.96	6.41	-	1020.8
AHQ-5-10, 5880	K.YIPPCLDSELTEFPLR.M	1952.21655	2	3.16E-04	0.42	2.56	-	112.7
AHQ-5-9, 5770 - 5840	K.YIPPCLDSELTEFPLR.M	1952.21655	2	1.01E-04	0.52	2.81	-	106.5
gi|5031571|ref|NP_005713.1| actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog				1.29E-09	6.49	70.26	26.60	44760.5
AHQ-5-8, 5514	K.CGYAGSNFPEHIFPALVGRPIIR.S	2573.95654	3	6.77E-05	0.90	4.16	-	1014.5
AHQ-5-8, 3476 - 3544	K.DLMVGDEASELR.S	1335.46633	2	7.69E-05	0.93	3.81	-	1084.9
AHQ-5-8, 3541 - 3546	K.DLMVGDEASELR.S	1335.46633	1	7.25E-04	0.11	2.01	-	231.2
AHQ-5-8, 2824	R.GYAFNHSADFETVR.M	1614.69943	2	3.58E-05	0.92	3.47	-	1185.6
AHQ-5-8, 3445	K.HIVLSGGSTMYPGLPSR.L	1773.04967	2	7.43E-05	0.98	5.28	-	1635.1
AHQ-5-8, 3730 - 3732	K.HLWDYTFGPEK.L	1393.52736	1	5.41E-05	0.81	3.18	-	608.7
AHQ-5-8, 3720	K.HLWDYTFGPEK.L	1393.52736	2	7.13E-08	0.89	3.85	-	473.6
AHQ-5-8, 3568	K.LCYVGYNIEQEQK.L	1645.81494	2	6.43E-07	0.96	4.34	-	1650.2
AHQ-5-8, 4689	R.SMLEVNYPMENGIVR.N	1753.03703	2	1.29E-09	0.91	3.98	-	833.3
gi|21361370|ref|NP_002853.2| phosphorylase, glycogen; brain [Homo sapiens]				1.38E-09	1.93	20.28	3.30	96695.3
AHQ-5-5, 3402	R.HLDHVAALFPGDVDR.L	1662.83036	2	1.38E-09	0.97	5.28	-	1670.5
AHQ-5-5, 6217	K.IGEEFLTDLSQLK.K	1493.68345	2	1.21E-04	0.96	4.03	-	1696.2
gi|20149570|ref|NP_005816.2| RAS guanyl releasing protein 2 isoform 1; calcium and diacylglycerol-r				1.43E-09	1.73	20.21	5.20	75547.0
AHQ-5-6, 5270	K.ILFQDYHSFVTHGCTVDNPVLER.F	2750.03824	3	1.43E-09	0.91	4.30	-	901.4
AHQ-5-6, 3002 - 3028	K.LDQALVVEHIEK.M	1394.59824	2	8.20E-09	0.83	3.51	-	685.1
gi|21361399|ref|NP_055040.2| protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp				1.44E-09	1.88	20.32	7.10	65308.3
AHQ-5-6, 7294	K.DNTIEHLLPLFLAQLKDECPEVR.L	2753.12348	3	1.44E-09	0.99	6.49	-	3657.5
AHQ-5-6, 5772 - 5784	K.SEIIPMFSNLASDEQDSVR.L	2139.32924	2	5.11E-08	0.90	4.03	-	607.3
gi|14251209|ref|NP_001279.2| chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo				1.55E-09	5.11	70.29	44.00	26922.5
AHQ-5-9, 5274 - 5335	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	2	8.04E-06	0.71	3.44	-	247.7
AHQ-5-14-, 5651	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	2	4.08E-07	0.37	2.53	-	273.5
AHQ-5-9, 5739	K.FLDGNELTLADCNLLPK.L	1935.18752	2	2.09E-05	0.35	2.89	-	482.0
AHQ-5-14-, 3353	K.GVTFNVTTVDTK.R	1282.42476	2	1.53E-06	0.94	4.07	-	1143.2
AHQ-5-13, 3521 - 3525	K.GVTFNVTTVDTK.R	1282.42476	2	4.04E-08	0.96	4.29	-	1499.3
AHQ-5-13-, 3403	K.GVTFNVTTVDTK.R	1282.42476	2	7.89E-07	0.89	3.37	-	856.3
AHQ-5-9, 5023 - 5096	R.KFLDGNELTLADCNLLPK.L	2063.36044	2	2.91E-06	0.91	4.98	-	1128.0
AHQ-5-10, 4779 - 4819	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	5.03E-04	0.93	4.74	-	727.5
AHQ-5-10, 5028	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.63E-07	0.87	3.49	-	633.5
AHQ-5-14-, 5275	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	8.97E-06	0.95	4.95	-	651.3
AHQ-5-11, 5194 - 5196	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.20E-06	0.94	4.92	-	587.0
AHQ-5-14-, 5418	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.67E-05	0.95	4.66	-	811.3
AHQ-5-13-, 5447	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.31E-06	0.94	4.50	-	783.9
AHQ-5-13-, 5311 - 5331	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	5.59E-04	0.94	4.90	-	727.1
AHQ-5-12, 5386	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.51E-06	0.95	4.62	-	799.3
AHQ-5-9, 4696 - 4699	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.55E-09	0.96	5.38	-	758.5
AHQ-5-13, 5400 - 5406	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	4.12E-07	0.97	5.71	-	1040.6
AHQ-5-13, 5533	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	5.56E-07	0.94	4.25	-	945.3
AHQ-5-14, 6041 - 6122	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.47E-05	0.94	4.54	-	813.7
AHQ-5-9, 2391 - 2412	K.LHIVQVVCK.K	1097.35623	1	1.68E-04	0.52	2.30	-	428.2
AHQ-5-12, 2674	K.LHIVQVVCK.K	1097.35623	2	3.27E-05	0.76	2.95	-	517.4

AHQ-5-12, 2673	K.LHIVQVVCK.K	1097.35623	1	4.15E-06	0.78	2.51	-	931.7
AHQ-5-9, 2399	K.LHIVQVVCK.K	1097.35623	1	7.47E-05	0.70	2.95	-	393.7
AHQ-5-9, 4786 - 4854	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	7.43E-09	0.84	3.81	-	433.6
AHQ-5-12, 5261 - 5289	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	1.59E-04	0.69	3.06	-	354.8
AHQ-5-11, 5148	K.VLDNYLTSPLPEEVDETSAEDEGVSQR.K	2994.12446	2	3.37E-09	0.79	3.65	-	369.2
gi|5729875|ref|NP_006658.1| progesterone receptor membrane component 1; progesterone binding protei				1.56E-09	2.81	30.24	17.90	21671.0
AHQ-5-10, 4147	K.FYGPEGPYGVFAGR.D	1517.66849	2	3.93E-04	0.87	3.10	-	686.1
AHQ-5-11, 4468	K.FYGPEGPYGVFAGR.D	1517.66849	2	1.56E-09	0.92	3.75	-	1022.9
AHQ-5-11, 2862	R.GDQPAASGDSDDDEPPPLPR.L	2037.04410	2	2.75E-08	0.92	4.18	-	752.1
AHQ-5-11, 3947	R.KFYGPEGPYGVFAGR.D	1645.84140	2	6.10E-06	0.96	4.68	-	1336.0
AHQ-5-10, 3702	R.KFYGPEGPYGVFAGR.D	1645.84140	2	1.80E-09	0.96	4.79	-	1207.1
gi|18860900|ref|NP_002834.2| protein tyrosine phosphatase, receptor type, J precursor; protein tyro				1.59E-09	9.20	100.25	12.90	145926.2
AHQ-5-1, 3469 - 3473	R.AGSPTAPVHDESLVGPVDPSSGQQSR.D	2576.71806	2	8.62E-06	0.93	4.46	-	659.4
AHQ-5-1, 3488	R.AGSPTAPVHDESLVGPVDPSSGQQSR.D	2576.71806	3	2.56E-04	0.86	4.07	-	737.9
AHQ-5-1, 5948	K.AVSISPTNVILTWK.S	1529.80530	2	4.97E-09	0.83	3.08	-	614.5
AHQ-5-1, 4443	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	3	1.59E-09	0.96	5.08	-	1611.6
AHQ-5-1, 5348	K.GLIDGAESYVSFSR.Y	1501.62253	2	2.99E-08	0.96	4.68	-	1424.1
AHQ-5-1, 3937	K.KDFIATQGPLPNTLK.D	1643.90840	2	2.64E-05	0.97	5.04	-	1636.8
AHQ-5-1, 5835 - 5899	K.SFCTDPASMASFDCEVVPK.E	2151.38014	2	2.94E-05	0.88	3.53	-	829.4
AHQ-5-1, 5349 - 5371	K.SPDGASEYVYHLVIESK.H	1895.05866	2	1.07E-07	0.94	4.90	-	1086.7
AHQ-5-1, 2741	K.TKGDPLGTEGGLDASNTER.S	1918.99702	2	1.02E-05	0.92	4.16	-	969.5
AHQ-5-1, 4344 - 4347	K.VITEPIPVSDLR.V	1339.56259	2	5.32E-06	0.91	3.50	-	865.2
AHQ-5-1, 3841 - 3889	R.VLLESIGSHEELTQDSR.L	1914.06352	2	3.31E-07	0.90	4.00	-	878.8
gi|28077085|ref|NP_004559.3| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member				1.61E-09	0.92	10.22	5.30	42586.7
AHQ-5-9, 4158	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	2	4.43E-05	0.87	4.18	-	725.3
AHQ-5-8, 4370 - 4378	K.SGGGGDIHQGFQSLLTEVNK.T	2045.19887	2	1.61E-09	0.92	4.46	-	795.2
gi|4758790|ref|NP_004543.1| NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q				1.74E-09	0.94	10.19	11.30	12517.4
AHQ-5-13, 6652	K.IEYDDFVECLLR.Q	1573.74872	2	1.74E-09	0.94	3.75	-	1138.1
gi|4885609|ref|NP_005408.1| v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen				1.78E-09	4.02	50.23	15.90	59834.4
AHQ-5-7, 6835 - 6903	R.AGPLAGGVTTFVALYDYESR.T	2088.30526	2	2.43E-04	0.89	3.80	-	923.8
AHQ-5-7, 2378	R.GPSAAFAPAAAEPK.L	1285.43034	1	2.99E-04	0.47	2.35	-	487.0
AHQ-5-7, 3808 - 3874	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	3.80E-08	0.78	3.19	-	736.0
AHQ-5-7, 3542	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	6.22E-06	0.87	3.25	-	892.1
AHQ-5-13, 4062	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	4.56E-04	0.33	2.54	-	436.5
AHQ-5-7, 5336 - 5406	K.TLKPGTMSPEAFLQEAQVMK.K	2207.59964	2	1.81E-04	0.93	4.16	-	851.9
AHQ-5-7, 5399	K.TLKPGTMSPEAFLQEAQVMK.K	2207.59964	3	4.05E-04	0.63	3.39	-	718.0
AHQ-5-7, 6202	R.TQFNSLQQLVAYYSK.H	1790.99681	2	1.78E-09	0.94	3.86	-	1348.9
AHQ-5-7, 6042	R.TQFNSLQQLVAYYSK.H	1790.99681	2	3.80E-08	0.76	2.71	-	801.5
gi|21361478|ref|NP_055944.2| septin 6 isoform B; septin 2 [Homo sapiens]				1.79E-09	2.84	30.25	15.90	49716.3
AHQ-5-7, 3726 - 3800	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L	3147.31508	3	1.47E-06	0.93	4.72	-	942.4
AHQ-5-7, 2694	R.KTAAELLQSQGSQAGGSQTLK.R	2104.30776	2	1.08E-04	0.96	4.88	-	1127.6
AHQ-5-10, 4591	R.TVPLAGHVGFDSLPDQLVNK.S	2108.38284	2	1.58E-05	0.88	4.03	-	576.0
AHQ-5-7, 4815	R.TVPLAGHVGFDSLPDQLVNK.S	2108.38284	2	1.79E-09	0.95	4.92	-	981.9
gi|29568101|ref|NP_006467.3| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT				1.82E-09	1.89	20.24	14.60	11400.3
AHQ-5-14-, 3613	K.TPALVNAAVTYSK.P	1335.53080	2	1.80E-06	0.94	3.62	-	1168.5
AHQ-5-14-, 3541 - 3597	K.TPALVNAAVTYSKPR.L	1588.83283	3	1.82E-09	0.95	4.88	-	1135.3
AHQ-5-14-, 3537	K.TPALVNAAVTYSKPR.L	1588.83283	2	1.77E-04	0.95	4.31	-	1342.7
AHQ-5-14, 4444	K.TPALVNAAVTYSKPR.L	1588.83283	2	3.45E-08	0.96	4.47	-	1286.3
gi|4508047|ref|NP_003452.1| zyxin [Homo sapiens]				1.88E-09	3.45	40.26	16.80	61277.0
AHQ-5-9, 6426 - 6488	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	2	3.49E-04	0.55	2.61	-	354.4
AHQ-5-8, 7144	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	3	1.88E-09	0.79	3.59	-	816.3
AHQ-5-8, 7145	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	2	2.33E-08	0.96	5.12	-	875.4
AHQ-5-9, 6427	K.EVEELEQLTQQLMQDMEHPQR.Q	2612.87876	3	1.56E-04	0.85	3.56	-	740.2
AHQ-5-12, 3877	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	1.86E-04	0.89	4.73	-	807.5
AHQ-5-8, 3584 - 3642	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	2	5.44E-05	0.94	4.66	-	767.9
AHQ-5-6, 3748	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	1.43E-05	0.79	3.82	-	680.7
AHQ-5-10, 3575	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	2	4.58E-05	0.91	4.56	-	684.1
AHQ-5-11, 3796	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	5.74E-07	0.88	4.40	-	715.9
AHQ-5-13-, 3889	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	9.26E-05	0.94	4.64	-	1230.4
AHQ-5-9, 3491	K.SPSSSQPLPQVPAPAQSQTQFHVQPQPQPK.P	3223.54419	3	1.02E-05	0.85	4.37	-	506.6
AHQ-5-10, 6628	K.VSSIDLEIDSLSSLLDDMTK.N	2182.43225	2	1.47E-07	0.94	4.87	-	725.9
gi|5802974|ref|NP_006784.1| peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide				2.38E-09	2.63	30.27	20.70	27692.5
AHQ-5-10, 4138	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	9.32E-09	0.95	5.41	-	1161.7
AHQ-5-11, 4475	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	2.38E-09	0.91	4.85	-	826.0
AHQ-5-11, 3948	K.DLSLDDFK.G	953.02795	1	3.98E-05	0.37	2.15	-	454.7
AHQ-5-10, 3732	K.DLSLDDFK.G	953.02795	1	4.94E-07	0.74	2.85	-	485.7
AHQ-5-11, 5312	R.DYGVLLEGSGLALR.G	1463.66058	2	4.70E-07	0.98	4.64	-	2134.5
gi|4504523|ref|NP_002148.1| heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (				2.76E-09	1.18	20.17	11.80	10931.6
AHQ-5-14-, 2971	K.VLLPEYGGTK.V	1077.25535	1	3.97E-04	0.26	2.01	-	223.3
AHQ-5-14-, 4929 - 4937	K.VVLDDKDYFLFR.D	1530.74861	3	1.16E-07	0.88	3.03	-	772.2
AHQ-5-14, 5866	K.VVLDDKDYFLFR.D	1530.74861	2	2.76E-09	0.92	3.35	-	1129.9
gi|13385594|ref|NP_085056.1| cytochrome b5 outer mitochondrial membrane precursor; type 2 cyt-b5 [H				2.82E-09	0.93	10.23	23.30	16332.0
AHQ-5-11, 5942	R.FLNEHPGGEEVLLEQAGVDASESFEDVGHSSDAR.E	3629.75848	3	2.82E-09	0.93	4.66	-	1014.7
gi|22538814|ref|NP_002976.2| small inducible cytokine A5 precursor; T-cell specific protein p288; T				2.94E-09	0.88	10.15	12.10	9989.6
AHQ-5-14-, 3719	K.CSNPAVVFVTR.K	1251.43718	2	2.94E-09	0.88	3.07	-	846.2
gi|4557871|ref|NP_001054.1| transferrin [Homo sapiens]				2.95E-09	0.96	10.26	2.70	77049.5
AHQ-5-5, 7325	R.SAGWNIPIGLLYCDLPEPR.K	2173.47658	2	2.95E-09	0.96	5.14	-	831.8
gi|5453714|ref|NP_006448.1| LIM protein (similar to rat protein kinase C-binding enigma) [Homo sapi				2.96E-09	1.73	20.21	4.90	64027.9
AHQ-5-13-, 2011	R.ASAAPKPEPVPVQK.G	1419.65094	2	6.45E-04	0.81	2.83	-	755.6
AHQ-5-13-, 2844 - 2848	K.EVVKPVPITSPAVSK.V	1551.85241	2	2.96E-09	0.92	4.15	-	485.3
gi|4758086|ref|NP_004069.1| cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain				3.11E-09	6.44	70.26	46.10	20567.3
AHQ-5-11, 4082	K.GFGFGQGAGALVHSE	1434.53788	1	3.10E-06	0.30	2.43	-	459.7
AHQ-5-13, 4304	K.GFGFGQGAGALVHSE	1434.53788	2	4.48E-06	0.95	4.22	-	1083.3
AHQ-5-13-, 4209	K.GFGFGQGAGALVHSE	1434.53788	2	1.16E-07	0.92	3.59	-	1099.4
AHQ-5-12, 3290 - 3298	K.GLESTTLADKDGEIYCK.G	1902.06957	2	3.28E-07	0.88	4.25	-	642.2
AHQ-5-10, 3063	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.97E-07	0.91	4.37	-	667.7
AHQ-5-11, 2475	K.GYGYGQGAGTLSTDK.G	1475.54194	2	3.87E-08	0.95	3.90	-	1347.9
AHQ-5-10, 3259	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	6.09E-05	0.35	2.66	-	172.1
AHQ-5-13, 3721	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	3.11E-09	0.91	4.45	-	671.1
AHQ-5-11, 3548	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	7.14E-07	0.87	3.88	-	534.0
AHQ-5-11, 3427	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	3.35E-06	0.86	3.86	-	708.7
AHQ-5-13-, 3637	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	2.06E-05	0.83	4.14	-	506.4
AHQ-5-12, 3505	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	5.33E-07	0.75	3.81	-	342.0
AHQ-5-11, 2922	K.KNLDSTTVAVHGEEIYCK.S	2066.27805	2	9.86E-06	0.89	3.96	-	494.0
AHQ-5-14, 4316	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	1.26E-07	0.91	4.25	-	715.8
AHQ-5-11, 3390 - 3464	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	2.36E-05	0.97	4.59	-	1375.2
AHQ-5-11, 3891	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	1.96E-07	0.95	4.57	-	928.2
AHQ-5-11, 4172	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	9.43E-06	0.94	4.70	-	798.7
AHQ-5-11, 4071	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	5.06E-06	0.82	3.72	-	500.5
gi|18543899|ref|XP_086916.1| similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic				3.17E-09	1.85	20.21	19.80	21265.8
AHQ-5-11, 3230	K.NRPTSISWDGLDSGK.L	1633.74419	2	3.06E-04	0.94	4.25	-	988.1
AHQ-5-11, 5142 - 5212	R.YVWLVYEQDRPLKCDEPILSNR.S	2796.15005	3	3.17E-09	0.91	4.14	-	864.1
gi|27480104|ref|XP_208215.1| similar to triosephosphate isomerase 1 [Homo sapiens]				3.22E-09	5.53	70.25	26.90	26942.6
AHQ-5-10, 2692	R.HVFGESDELIGQK.V	1459.58565	1	3.22E-09	0.85	3.80	-	662.5
AHQ-5-10, 2687	R.HVFGESDELIGQK.V	1459.58565	2	1.11E-04	0.97	4.78	-	1124.0
AHQ-5-10, 2044 - 2108	K.IAVAAQNCYK.V	1139.30684	1	9.05E-04	0.14	2.28	-	98.9
AHQ-5-10, 2412 - 2416	R.RHVFGESDELIGQK.V	1615.77200	2	8.19E-09	0.97	4.97	-	1566.4

AHQ-5-10, 1958 - 1960	K.SNVSDAVAQSTR.I	1235.28659	1	7.54E-04	0.18	2.37	-	258.8
AHQ-5-10, 1976 - 1988	K.SNVSDAVAQSTR.I	1235.28659	2	4.18E-05	0.95	3.78	-	1891.1
AHQ-5-10, 4059	K.VTNGAFTGEISPGMIK.D	1622.86786	2	6.13E-04	0.92	4.35	-	910.0
AHQ-5-10, 3466	K.VTNGAFTGEISPGM*IK.D	1638.86726	2	7.75E-04	0.89	3.22	-	1060.7
AHQ-5-10, 4914 - 4946	K.VVLAYEPVWAIGTGK.T	1603.88587	2	4.24E-05	0.80	3.11	-	781.3
gi|13518026|ref|NP_004978.2| LIM and senescent cell antigen-like domains 1 [Homo sapiens]				3.23E-09	4.23	50.24	22.50	37251.2
AHQ-5-8, 4060 - 4065	K.CHAIIDEQPLIFK.N	1585.84900	2	1.23E-07	0.95	4.84	-	1256.0
AHQ-5-11, 4380	K.CHAIIDEQPLIFK.N	1585.84900	2	3.26E-04	0.95	4.48	-	1230.6
AHQ-5-9, 3942 - 3946	K.CHAIIDEQPLIFK.N	1585.84900	2	3.74E-04	0.96	4.81	-	1472.3
AHQ-5-9, 2895	R.ELKGELYCLPCHDK.M	1765.00101	2	6.29E-07	0.82	3.02	-	893.7
AHQ-5-13, 3926 - 3930	K.FVEFDMKPVCK.K	1401.67594	2	4.05E-04	0.86	3.61	-	1045.3
AHQ-5-9, 4454	R.KGLAYCETHYNQLFGDVCFHCNR.V	2894.17088	3	7.17E-05	0.65	3.12	-	335.9
AHQ-5-11, 3399	R.VIEGDVVSALNK.A	1244.41966	2	3.23E-09	0.95	4.11	-	1247.9
AHQ-5-9, 3060 - 3064	R.VIEGDVVSALNK.A	1244.41966	1	2.12E-04	0.45	2.16	-	688.2
AHQ-5-8, 3022	R.VIEGDVVSALNK.A	1244.41966	2	1.46E-06	0.94	3.87	-	1075.3
AHQ-5-9, 3070 - 3072	R.VIEGDVVSALNK.A	1244.41966	2	4.56E-07	0.96	4.46	-	1132.1
AHQ-5-13-, 3467 - 3543	R.VIEGDVVSALNK.A	1244.41966	2	7.10E-09	0.96	4.59	-	1306.8
AHQ-5-14-, 3478	R.VIEGDVVSALNK.A	1244.41966	2	6.48E-08	0.97	4.54	-	1423.6
gi|4507295|ref|NP_003560.1| syntaxin 7 [Homo sapiens]				3.34E-09	0.88	10.18	5.70	29845.3
AHQ-5-13-, 3352	R.TLNQLGTPQDSPELR.Q	1669.81798	2	4.41E-04	0.76	3.09	-	519.2
AHQ-5-13, 3467	R.TLNQLGTPQDSPELR.Q	1669.81798	2	3.34E-09	0.88	3.52	-	745.1
gi|10716563|ref|NP_001737.1| calnexin [Homo sapiens]				3.46E-09	4.39	50.22	10.10	67567.8
AHQ-5-12, 4928	K.APVPTGEVYFADSFDR.G	1771.90722	2	7.59E-05	0.82	3.04	-	661.9
AHQ-5-5, 4901 - 4970	K.APVPTGEVYFADSFDR.G	1771.90722	2	3.46E-09	0.96	4.39	-	1738.6
AHQ-5-6, 4877 - 4956	K.APVPTGEVYFADSFDR.G	1771.90722	2	9.35E-05	0.75	3.32	-	857.6
AHQ-5-5, 4213	R.GTLSGWILSK.A	1062.24392	2	1.33E-06	0.89	3.24	-	831.5
AHQ-5-5, 3887	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	2	2.50E-04	0.83	3.57	-	541.7
AHQ-5-5, 6887	K.IPNPDFFEDLEPFR.M	1736.90447	2	2.03E-06	0.79	3.10	-	566.3
AHQ-5-5, 6285 - 6355	R.KIPNPDFFEDLEPFR.M	1865.07739	2	1.16E-07	0.91	3.84	-	768.5
gi|4557801|ref|NP_000261.1| purine nucleoside phosphorylase [Homo sapiens]				3.47E-09	7.16	80.33	41.20	32147.7
AHQ-5-9, 3910 - 3922	R.DHINLPGFSGQNPLR.G	1665.83425	2	4.13E-09	0.92	4.65	-	540.0
AHQ-5-10, 4008	R.DHINLPGFSGQNPLR.G	1665.83425	2	7.69E-04	0.83	3.20	-	687.7
AHQ-5-9, 3912	R.FHMYEGYPLWK.V	1471.70636	1	1.44E-04	0.77	2.36	-	991.2
AHQ-5-13-, 4017	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	2	2.80E-06	0.96	5.08	-	1055.4
AHQ-5-14, 4792	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	2	9.45E-06	0.94	4.51	-	756.5
AHQ-5-13-, 4023	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	3	3.47E-09	0.97	4.83	-	2556.9
AHQ-5-13, 4098	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	3	1.62E-05	0.97	5.15	-	2562.4
AHQ-5-9, 6522 - 6523	K.LEQFVSILMASIPLPDK.A	1902.28716	2	3.59E-06	0.93	4.38	-	710.0
AHQ-5-13-, 6780 - 6844	K.LEQFVSILMASIPLPDK.A	1902.28716	2	1.19E-04	0.94	4.75	-	801.9
AHQ-5-11, 4803	K.LGADAVGMSTVPEVIVAR.H	1786.08666	2	2.38E-05	0.74	2.82	-	731.9
AHQ-5-13, 4250 - 4256	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	1.17E-05	0.92	4.04	-	905.7
AHQ-5-13-, 4179	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	1.81E-04	0.93	4.48	-	849.3
AHQ-5-9, 3750	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	7.73E-04	0.90	3.75	-	768.6
AHQ-5-13-, 5848	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	2.81E-04	0.88	4.16	-	515.1
AHQ-5-13, 5912 - 5937	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	1.51E-05	0.92	4.35	-	603.0
AHQ-5-9, 5302	K.LTQAQIFDYSEIPNFPR.S	2040.26383	2	1.53E-05	0.92	4.30	-	724.0
AHQ-5-9, 5259 - 5272	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	5.86E-05	0.98	5.93	-	2383.0
AHQ-5-9, 5343	R.VFHLLGVDTLVVTNAAGGLNPK.F	2236.59890	2	4.13E-08	0.98	6.61	-	2386.5
gi|4505877|ref|NP_000436.1| plectin 1, intermediate filament binding protein 500kDa; plectin 1, int				3.52E-09	5.53	60.24	2.30	518488.0
AHQ-5-1, 2776	R.AALAHSEEVTASQVAATK.T	1784.94898	2	1.95E-08	0.96	4.75	-	1187.2
AHQ-5-3, 3813	K.AGVVGPELHEQLLSAEK.A	1777.99958	2	4.61E-04	0.93	3.95	-	1268.2
AHQ-5-3, 5211	R.APVPASELLASGVLSR.A	1567.81193	2	4.13E-06	0.96	4.37	-	1203.6
AHQ-5-1, 5855	R.ESADPLGAWLQDAR.R	1529.63597	2	3.48E-04	0.79	2.90	-	746.8
AHQ-5-1, 6873 - 6953	K.SEEM*QTVQQEQLLQETQALQQSFLSEK.D	3198.46199	3	1.05E-06	0.92	4.18	-	1241.6
AHQ-5-1, 2993	R.SLQEEHVAVAQLR.E	1480.65123	2	3.52E-09	0.97	4.83	-	1850.2
gi|6005749|ref|NP_009193.1| RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA				3.61E-09	2.37	30.19	24.30	19846.9
AHQ-5-10, 3166 - 3167	R.DVVICPDASLEDAKK.E	1661.85581	2	1.03E-04	0.84	2.98	-	867.3
AHQ-5-11, 3346 - 3347	R.DVVICPDASLEDAKK.E	1661.85581	2	9.14E-04	0.91	3.70	-	905.8
AHQ-5-11, 3446	K.GAEEM*ETVIPVDVM*R.R	1708.93613	2	9.25E-05	0.64	2.90	-	405.6
AHQ-5-11, 3074	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	4.97E-07	0.78	3.33	-	580.1
AHQ-5-10, 2916 - 2920	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	3.61E-09	0.90	3.61	-	743.2
gi|25188179|ref|NP_005653.3| voltage-dependent anion channel 3 [Homo sapiens]				3.72E-09	2.68	40.22	20.10	30658.4
AHQ-5-10, 3072 - 3151	K.LSQNNFALGYK.A	1255.40424	1	1.30E-06	0.51	2.59	-	328.8
AHQ-5-10, 4544	K.LTLDTIFVPNTGK.K	1419.64771	1	3.35E-07	0.78	2.95	-	635.4
AHQ-5-11, 4882 - 4887	K.LTLDTIFVPNTGK.K	1419.64771	2	1.61E-04	0.85	3.21	-	711.9
AHQ-5-9, 4192 - 4203	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	7.08E-07	0.78	3.67	-	485.8
AHQ-5-10, 3970	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	3	6.27E-04	0.80	3.52	-	738.0
AHQ-5-10, 4142	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.06E-06	0.88	3.94	-	719.0
AHQ-5-10, 4314	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.94E-07	0.82	3.86	-	511.5
AHQ-5-10, 3963	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	8.76E-06	0.80	3.63	-	405.0
AHQ-5-14, 5280	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	3.74E-06	0.50	2.78	-	384.1
AHQ-5-9, 3798	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	3.80E-07	0.84	3.63	-	517.8
AHQ-5-14, 5670	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	3.72E-09	0.43	2.87	-	430.9
AHQ-5-10, 3523	K.YKVCNYGLTFTQK.W	1623.85410	2	3.83E-09	0.96	4.39	-	1211.3
gi|4759212|ref|NP_004598.1| beta-tubulin cofactor A [Homo sapiens]				3.79E-09	2.88	30.37	26.90	12854.8
AHQ-5-13, 3470	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	3.79E-09	0.98	7.34	-	2471.6
AHQ-5-13-, 3349	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	1.05E-07	0.97	5.13	-	1491.9
AHQ-5-13-, 3351	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	1.68E-07	0.95	5.14	-	1165.9
AHQ-5-13, 3857 - 3862	R.LEAAYLDLQR.I	1192.34645	1	2.00E-04	0.35	2.63	-	375.7
AHQ-5-13, 3841 - 3848	R.LEAAYLDLQR.I	1192.34645	2	5.42E-06	0.97	4.00	-	1794.2
AHQ-5-13-, 3369	R.RLEAAYLDLQR.I	1348.53280	2	3.31E-06	0.91	3.65	-	724.1
AHQ-5-13, 3458	R.RLEAAYLDLQR.I	1348.53280	2	2.77E-07	0.93	4.14	-	691.0
gi|30150271|ref|XP_292964.2| similar to Heat shock protein HSP 90-beta (HSP 84) (Tumor specific tra				3.81E-09	0.82	10.19	4.10	47348.8
AHQ-5-5, 4717	K.CLELFSELAEDKKNYKK.F	2117.40810	2	3.81E-09	0.82	3.77	-	828.6
gi|28827809|ref|NP_789797.1| nucleoside diphosphate kinase B-like [Homo sapiens]				4.40E-09	4.82	60.25	43.10	15529.0
AHQ-5-12, 3328	R.GDFCIQVGR.N	1053.17404	1	2.52E-05	0.37	2.22	-	239.9
AHQ-5-12, 3337	R.GDFCIQVGR.N	1053.17404	1	8.60E-05	0.36	2.44	-	231.1
AHQ-5-12, 3336	R.GDFCIQVGR.N	1053.17404	2	1.62E-06	0.93	3.39	-	1414.6
AHQ-5-12, 1609	R.NIIHGSDSVK.S	1070.18131	1	3.45E-06	0.59	2.41	-	478.9
AHQ-5-12, 2064	R.NIIHGSDSVKSAEK.E	1485.62464	1	1.86E-05	0.69	3.30	-	415.8
AHQ-5-12, 2756 - 2826	R.VMLGETNPADSKPGTIR.G	1787.03151	2	3.71E-06	0.74	3.49	-	564.0
AHQ-5-12, 2752 - 2753	R.VMLGETNPADSKPGTIR.G	1787.03151	3	4.40E-09	0.86	3.55	-	819.7
AHQ-5-12, 2568 - 2569	R.VM*LGETNPADSKPGTIR.G	1803.03091	2	1.48E-05	0.83	3.30	-	713.9
AHQ-5-12, 6924 - 6994	K.YM*NSGPVVAMVWEGLNVVK.T	2110.48562	2	3.92E-07	0.93	5.00	-	627.2
gi|14211923|ref|NP_115982.1| PKCI-1-related HIT protein [Homo sapiens]				4.81E-09	3.04	40.31	41.70	17161.6
AHQ-5-13, 3377 - 3386	K.AQQATPGGAAPTIFSR.I	1573.73512	2	2.07E-06	0.89	3.86	-	476.1
AHQ-5-13-, 3272 - 3279	K.AQQATPGGAAPTIFSR.I	1573.73512	2	2.83E-06	0.87	4.05	-	395.2
AHQ-5-13-, 4757 - 4763	R.DVAPQAPVHFLVIPK.K	1631.94245	2	6.64E-04	0.59	3.16	-	373.9
AHQ-5-13-, 6177 - 6187	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	3.93E-08	0.97	6.15	-	1469.4
AHQ-5-13, 6229	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	1.96E-05	0.96	5.01	-	1631.7
AHQ-5-13-, 6175	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	4.81E-09	0.87	3.84	-	816.2
AHQ-5-13, 6225	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	2.43E-07	0.77	3.12	-	809.7
AHQ-5-13-, 6155 - 6215	K.SLPADILYEDQQCLVFR.D	2069.32354	2	2.71E-04	0.94	4.15	-	1173.1
AHQ-5-13, 6166 - 6240	K.SLPADILYEDQQCLVFR.D	2069.32354	2	2.54E-04	0.70	3.17	-	283.8
gi|4502695|ref|NP_001779.1| cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c				4.81E-09	2.15	30.24	13.60	48786.6
AHQ-5-8, 3632	K.IYEFPETDDEEENKLVK.K	2099.23685	3	1.37E-04	0.57	3.04	-	380.5
AHQ-5-8, 3628	K.IYEFPETDDEEENKLVK.K	2099.23685	2	4.71E-04	0.60	3.04	-	341.9

AHQ-5-13, 5485	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	1.94E-05	0.73	3.53	-	445.5
AHQ-5-14-, 5359	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	9.83E-05	0.93	4.60	-	850.2
AHQ-5-8, 5098	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	2.11E-04	0.94	4.76	-	978.0
AHQ-5-14-, 6401	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	4.81E-09	0.85	4.14	-	484.1
gi|4502205|ref|NP_001651.1| ADP-ribosylation factor 4 [Homo sapiens]				4.85E-09	1.79	20.22	13.30	20510.6
AHQ-5-11, 2426	R.IQEVADELQK.M	1173.29830	2	6.97E-04	0.85	3.54	-	624.8
AHQ-5-12, 5518	K.NICFTVWDVGGQDR.I	1668.81182	2	4.85E-09	0.94	4.48	-	774.7
AHQ-5-11, 5335	K.NICFTVWDVGGQDR.I	1668.81182	2	9.89E-07	0.89	3.37	-	898.5
gi|4503747|ref|NP_001448.1| filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a				4.92E-09	4.12	50.26	1.40	278191.4
AHQ-5-3, 3634	K.DLAEDAPWK.K	1045.12708	1	4.15E-05	0.41	1.98	-	605.7
AHQ-5-2, 3545 - 3617	K.DLAEDAPWK.K	1045.12708	1	2.70E-06	0.36	1.88	-	627.3
AHQ-5-5, 3467	K.DLAEDAPWK.K	1045.12708	1	2.17E-04	0.33	1.99	-	526.7
AHQ-5-1, 3037	K.DLAEDAPWKK.I	1173.29999	2	7.09E-05	0.89	3.11	-	1099.3
AHQ-5-13, 6312	R.LIALLEVLSQK.R	1227.51852	2	1.89E-04	0.96	4.13	-	1439.8
AHQ-5-1, 6623	R.LIALLEVLSQK.R	1227.51852	2	3.55E-07	0.96	4.34	-	1393.7
AHQ-5-3, 6614	R.LIALLEVLSQK.R	1227.51852	2	4.11E-08	0.95	4.07	-	1112.1
AHQ-5-4, 6581	R.LIALLEVLSQK.R	1227.51852	2	1.64E-05	0.97	5.07	-	1295.9
AHQ-5-11, 6036	R.LIALLEVLSQK.R	1227.51852	2	6.50E-08	0.96	4.21	-	1415.9
AHQ-5-2, 6473 - 6514	R.LIALLEVLSQK.R	1227.51852	2	1.94E-08	0.97	4.78	-	1452.3
AHQ-5-5, 6349 - 6358	R.LIALLEVLSQK.R	1227.51852	2	3.24E-08	0.98	5.10	-	1568.8
AHQ-5-6, 6329	R.LIALLEVLSQK.R	1227.51852	2	4.92E-09	0.97	4.86	-	1501.8
AHQ-5-7, 6079	R.LIALLEVLSQK.R	1227.51852	2	6.10E-07	0.96	4.11	-	1486.8
AHQ-5-14-, 6157	R.LIALLEVLSQK.R	1227.51852	2	2.10E-04	0.92	3.27	-	1260.0
AHQ-5-1, 7155 - 7156	R.QMQLENVSVALEFLDR.E	1893.15408	2	3.54E-05	0.94	4.09	-	1267.8
AHQ-5-2, 6646 - 6718	R.QM*QLENVSVALEFLDR.E	1909.15348	2	5.04E-07	0.95	4.55	-	1147.9
gi|22043610|ref|XP_171081.1| similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1; rh				5.02E-09	2.70	30.26	24.00	21543.1
AHQ-5-11, 2678 - 2687	R.HHCPNTPIILVGTK.L	1588.85612	3	9.28E-06	0.79	3.15	-	1004.6
AHQ-5-11, 3356 - 3363	K.KLTPITYPQGLAM*AK.E	1648.99156	2	7.71E-05	0.93	3.90	-	985.1
AHQ-5-11, 4711	K.PVNLGLWDTAGQEDYDR.L	1950.05441	2	5.02E-09	0.98	5.18	-	2364.7
gi|27477800|ref|XP_208313.1| similar to tropomyosin 4 [Homo sapiens]				5.10E-09	0.94	10.26	10.10	18426.7
AHQ-5-9, 4572 - 4631	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.33E-07	0.97	5.27	-	1520.3
AHQ-5-9, 4942 - 5011	K.CGDLEEELKNVTNNLK.S	1878.05124	2	9.35E-05	0.97	4.91	-	1694.5
AHQ-5-9, 5175 - 5234	K.CGDLEEELKNVTNNLK.S	1878.05124	2	5.10E-09	0.94	4.40	-	1206.6
AHQ-5-9, 4126 - 4127	K.CGDLEEELKNVTNNLK.S	1878.05124	2	2.04E-06	0.95	4.50	-	1342.2
gi|12545410|ref|NP_031394.1| RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,				5.45E-09	1.68	20.24	4.30	95912.5
AHQ-5-5, 5153	K.SADVEPVSASAAHILGEVCR.E	2070.26993	2	5.45E-09	0.95	4.81	-	960.9
AHQ-5-5, 6417	K.SLCPFYGEDFYCEIPR.S	2056.26024	2	3.37E-04	0.73	2.64	-	573.5
gi|10835002|ref|NP_001166.1| Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]				5.51E-09	5.96	70.27	47.30	22987.8
AHQ-5-10, 2315	K.APEPHVEEDDDDELDSK.L	1940.90995	2	5.51E-09	0.97	5.43	-	1419.5
AHQ-5-13, 5632	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.10E-04	0.83	3.96	-	869.5
AHQ-5-12, 5822	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	2	2.60E-04	0.76	3.37	-	362.2
AHQ-5-12, 5821	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	1.22E-04	0.86	4.06	-	652.6
AHQ-5-10, 5074	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	8.38E-07	0.88	3.97	-	815.8
AHQ-5-10, 5279 - 5338	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	2	6.26E-04	0.91	4.53	-	619.4
AHQ-5-10, 5284 - 5350	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	1.06E-04	0.89	4.69	-	634.4
AHQ-5-12, 5629	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.42E-08	0.83	4.02	-	671.5
AHQ-5-11, 5647 - 5650	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	1.12E-04	0.87	4.45	-	587.0
AHQ-5-14-, 5513 - 5514	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	7.97E-08	0.96	5.27	-	1331.8
AHQ-5-10, 2894 - 2895	K.ELQEMDKDDESLIK.Y	1693.85489	2	1.34E-06	0.92	4.25	-	759.6
AHQ-5-10, 2903	K.ELQEMDKDDESLIK.Y	1693.85489	2	5.04E-04	0.81	3.33	-	785.1
AHQ-5-10, 6166 - 6186	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	8.49E-08	0.87	4.21	-	581.2
AHQ-5-12, 6436	R.LTLVCESAPGPITM*DLTGDLEALKK.E	2691.11214	3	2.14E-04	0.77	3.35	-	621.9
AHQ-5-12, 6692 - 6700	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	7.52E-09	0.86	4.38	-	579.1
AHQ-5-11, 6484 - 6488	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	3	7.50E-09	0.66	3.36	-	604.7
AHQ-5-10, 6178	R.LTLVCESAPGPITMDLTGDLEALKK.E	2675.11274	2	9.11E-07	0.84	3.83	-	366.5
AHQ-5-10, 3024 - 3086	K.TLLGDGPVVTDPK.A	1312.49400	2	7.78E-08	0.92	3.46	-	1034.7
gi|4507777|ref|NP_003331.1| ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast); UbcH5C; ubi				5.69E-09	0.93	10.21	12.20	16687.1
AHQ-5-13, 5404	R.IYHPNINSNGSICLDILR.S	2101.37199	2	5.69E-09	0.93	4.27	-	780.4
gi|30148492|ref|XP_293610.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				5.82E-09	2.70	30.22	4.30	72113.4
AHQ-5-6, 2774	R.FDDAVVQSDMK.H	1255.37968	2	5.82E-09	0.92	3.32	-	1071.1
AHQ-5-6, 4632 - 4701	R.IINEPTAAAIAYGLDK.K	1660.89259	2	9.07E-07	0.88	4.40	-	934.1
AHQ-5-10, 4286 - 4288	R.IINEPTAAAIAYGLDK.K	1660.89259	2	1.47E-06	0.89	4.33	-	979.6
AHQ-5-7, 3944	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	8.18E-06	0.69	3.01	-	442.7
AHQ-5-6, 4052	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	2.12E-06	0.90	4.11	-	584.4
AHQ-5-6, 4049	R.IINEPTAAAIAYGLDKK.V	1789.06550	3	3.03E-04	0.76	3.33	-	413.4
gi|4507383|ref|NP_001052.1| thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil				6.25E-09	5.41	60.24	12.70	60675.3
AHQ-5-7, 4139 - 4218	R.FQACPETQVPLQLESK.S	1877.10807	2	4.19E-05	0.96	4.54	-	1099.3
AHQ-5-1, 4636	R.FQACPETQVPLQLESK.S	1877.10807	2	5.64E-08	0.93	4.13	-	992.9
AHQ-5-7, 3668	R.HSASPMGVQDFDIVR.D	1659.84828	2	3.93E-08	0.97	4.80	-	1443.8
AHQ-5-7, 4195	R.KLYGPLCGYYLGR.R	1561.82914	2	6.66E-04	0.78	2.93	-	815.1
AHQ-5-7, 4924	K.LYGPLCGYYLGR.R	1433.65622	2	1.16E-06	0.91	2.97	-	1035.9
AHQ-5-7, 5838	K.PSPFIGNLTFFR.Q	1396.61752	2	6.25E-09	0.86	2.81	-	816.4
AHQ-5-7, 2815	R.YAESGDAFDIQR.C	1372.42172	2	2.20E-07	0.96	4.23	-	1722.5
gi|29732170|ref|XP_291550.1| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				6.26E-09	0.96	10.23	12.70	13262.9
AHQ-5-6, 3830	K.HLEINPDHSIIETLR.Q	1787.99770	2	2.30E-04	0.77	3.66	-	478.3
AHQ-5-5, 3877	K.HLEINPDHSIIETLR.Q	1787.99770	2	6.26E-09	0.96	4.66	-	1100.4
gi|21614520|ref|NP_000393.2| glucose-6-phosphate dehydrogenase [Homo sapiens]				6.32E-09	0.87	10.23	2.90	59257.4
AHQ-5-14-, 5545	R.DGLLPENTFIVGYAR.S	1665.87093	2	6.32E-09	0.87	3.87	-	498.6
gi|4505621|ref|NP_002558.1| prostatic binding protein; phosphatidylethanolamine binding protein [Ho				6.41E-09	2.90	30.29	37.40	21056.6
AHQ-5-11, 4926 - 5006	R.APVAGTCYQAEWDDYVPK.L	2072.23961	2	6.41E-09	0.98	5.86	-	1717.5
AHQ-5-11, 4530	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	1.54E-08	0.97	5.08	-	1401.1
AHQ-5-11, 4259 - 4264	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	4.49E-04	0.93	4.44	-	1063.5
AHQ-5-11, 5310 - 5370	K.WSGPLSLQEVDEQPQHPLHVTYAGAAVDELGK.V	3473.79274	3	1.88E-08	0.95	5.32	-	1280.2
gi|4504505|ref|NP_000405.1| hydroxysteroid (17-beta) dehydrogenase 4 [Homo sapiens]				6.48E-09	0.90	10.23	3.70	79685.9
AHQ-5-6, 5436	K.VAVAIPNRPPDAVLTDTTSLNQAALYR.L	2868.23765	3	6.48E-09	0.90	4.62	-	761.2
gi|4507949|ref|NP_003395.1| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,				7.14E-09	4.10	50.31	33.30	28082.2
AHQ-5-10, 1716	K.AVTEQGHELSNEER.N	1599.64147	2	2.98E-05	0.85	3.76	-	492.2
AHQ-5-10, 6634 - 6635	K.IEAELQDICNDVLELLDK.Y	2132.37471	2	2.88E-06	0.97	6.20	-	1155.0
AHQ-5-10, 3734	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	1.34E-04	0.87	4.27	-	408.9
AHQ-5-10, 3974	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	7.14E-09	0.93	4.86	-	676.4
AHQ-5-10, 6230 - 6235	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	3.09E-05	0.93	4.04	-	1447.4
AHQ-5-10, 2822	K.YLIPNATQPESK.V	1361.52512	1	1.07E-05	0.42	2.03	-	602.1
AHQ-5-10, 2726	K.YLIPNATQPESK.V	1361.52512	1	2.89E-05	0.53	2.12	-	657.0
gi|20127528|ref|NP_037459.2| parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]				7.87E-09	6.64	80.25	32.10	41714.0
AHQ-5-13, 3573 - 3579	K.ARPEDVVNLDLK.S	1369.54878	2	1.71E-05	0.93	4.50	-	842.2
AHQ-5-9, 2946 - 2970	K.ARPEDVVNLDLK.S	1369.54878	2	8.54E-06	0.96	5.07	-	1051.8
AHQ-5-9, 2960	K.ARPEDVVNLDLK.S	1369.54878	1	2.15E-05	0.51	2.96	-	233.5
AHQ-5-10, 3126	K.ARPEDVVNLDLK.S	1369.54878	2	1.87E-04	0.93	4.57	-	840.8
AHQ-5-14-, 3431	K.ARPEDVVNLDLK.S	1369.54878	2	8.68E-04	0.89	3.85	-	588.4
AHQ-5-9, 4726	R.DAFDTLFDHAPDKLSVVK.K	2019.24293	2	9.53E-08	0.93	4.67	-	756.7
AHQ-5-9, 5064 - 5135	R.EGLLHSSHISEELTTTTEMMMGR.F	2591.92450	2	6.57E-04	0.79	3.64	-	446.3
AHQ-5-9, 5194	R.EGLLHSSHISEELTTTTEMMMGR.F	2591.92450	2	2.27E-04	0.61	3.38	-	222.0
AHQ-5-9, 4946	R.EGLLHSSHISEELTTTTEMMMGR.F	2591.92450	2	2.29E-04	0.74	3.86	-	259.9
AHQ-5-9, 2350	K.KSLITFVNK.H	1050.27627	1	9.00E-04	0.48	2.59	-	375.6
AHQ-5-1, 3964	K.LNVAEVTQSEIGQK.Q	1516.67865	2	7.87E-09	0.92	3.78	-	1255.7
AHQ-5-13, 3877	K.LNVAEVTQSEIGQK.Q	1516.67865	2	3.29E-05	0.97	4.56	-	1538.6
AHQ-5-9, 3218 - 3236	K.LNVAEVTQSEIGQK.Q	1516.67865	2	3.18E-06	0.90	4.04	-	766.5

AHQ-5-9, 3318	R.LPEHVTVQVVVVR.K	1475.76086	2	1.19E-08	0.88	3.61	-	908.9
AHQ-5-9, 3602	K.QLEEDLYDGQVLQK.L	1678.82164	2	6.00E-05	0.93	4.19	-	1077.9
AHQ-5-9, 6415	K.VLLDWINDVLVEER.I	1713.95549	2	1.86E-05	0.96	4.62	-	1598.2
AHQ-5-9, 5610 - 5666	K.VLLDWINDVLVEER.I	1713.95549	2	8.03E-06	0.91	3.69	-	975.4
gi|4758040|ref|NP_004365.1| cytochrome c oxidase subunit VIc proprotein; cytochrome c oxidase subun				7.91E-09	0.91	10.17	16.00	8781.4
AHQ-5-14-, 4646	R.NYDVMKDFEEMR.K	1577.76431	2	7.91E-09	0.91	3.49	-	781.6
gi|4502107|ref|NP_001145.1| annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoag				8.04E-09	3.57	40.23	21.60	35936.5
AHQ-5-9, 5859	R.DLLDDLKSELTGK.F	1447.61309	2	8.04E-09	0.97	4.70	-	1751.7
AHQ-5-9, 5858 - 5863	R.DLLDDLKSELTGK.F	1447.61309	1	4.21E-04	0.40	2.45	-	339.1
AHQ-5-9, 6352	R.DPDAGIDEAQVEQDAQALFQAGELK.W	2659.80061	2	1.45E-08	0.78	3.39	-	380.5
AHQ-5-9, 6362	R.ETSGNLEQLLLAVVK.S	1614.86536	2	6.68E-05	0.87	3.76	-	683.0
AHQ-5-9, 6138 - 6144	K.GLGTDEESILTLLTSR.S	1705.88853	2	1.35E-08	0.95	4.62	-	1192.2
gi|5803181|ref|NP_006810.1| stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo				8.91E-09	0.93	10.24	3.50	62638.9
AHQ-5-13, 6378	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	8.57E-05	0.39	2.68	-	380.6
AHQ-5-6, 6528	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	8.91E-09	0.93	4.78	-	592.0
gi|30150022|ref|XP_300862.1| similar to beta-tubulin 4Q [Homo sapiens]				8.96E-09	4.46	50.28	17.50	33545.2
AHQ-5-12, 6140	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	9.23E-06	0.88	4.21	-	972.2
AHQ-5-7, 3074 - 3142	R.FPGQLNADLR.K	1131.26634	2	8.29E-06	0.89	3.24	-	876.6
AHQ-5-7, 3214 - 3290	R.FPGQLNADLR.K	1131.26634	2	1.05E-04	0.88	3.38	-	637.8
AHQ-5-8, 2854	R.FPGQLNADLR.K	1131.26634	2	4.45E-06	0.78	2.86	-	553.4
AHQ-5-7, 2990 - 3062	R.FPGQLNADLR.K	1131.26634	2	4.82E-04	0.89	3.43	-	675.2
AHQ-5-7, 3467	R.KLAVNMVPFPR.L	1272.58771	2	9.98E-07	0.96	4.03	-	1631.3
AHQ-5-7, 3466 - 3470	K.LAVNM*VPFPR.L	1160.41420	2	3.38E-04	0.96	3.94	-	1327.7
AHQ-5-8, 3804 - 3877	K.LAVNMVPFPR.L	1144.41480	2	1.25E-06	0.85	3.11	-	623.2
AHQ-5-9, 3851	K.LAVNMVPFPR.L	1144.41480	2	8.49E-05	0.45	2.60	-	461.3
AHQ-5-4, 4654	K.LAVNMVPFPR.L	1144.41480	2	8.96E-09	0.89	3.16	-	764.0
AHQ-5-7, 4094	K.LAVNMVPFPR.L	1144.41480	2	4.70E-06	0.90	3.25	-	748.7
gi|4505735|ref|NP_002611.1| platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H				8.99E-09	1.92	20.25	26.00	11552.6
AHQ-5-14-, 3773 - 3842	R.AEAEEDGDLQCLCVK.T	1739.86036	2	8.99E-09	0.96	4.68	-	1307.8
AHQ-5-14-, 3682	R.AEAEEDGDLQCLCVK.T	1739.86036	2	3.90E-07	0.95	4.68	-	870.9
AHQ-5-14-, 5750 - 5758	R.KICLDLQALLYK.K	1479.80948	2	5.42E-05	0.96	4.94	-	1091.5
gi|4506365|ref|NP_002856.1| RAB2, member RAS oncogene family [Homo sapiens]				9.04E-09	2.96	40.21	23.10	23545.4
AHQ-5-11, 5382 - 5410	R.DTFNHLTTWLEDAR.Q	1719.83554	2	4.03E-06	0.89	3.81	-	952.0
AHQ-5-11, 4308	K.LQIWDTAGQESFR.S	1551.68478	2	9.04E-09	0.97	4.10	-	2115.6
AHQ-5-11, 4188	K.SCLLLQFTDKR.F	1382.61075	2	6.70E-04	0.85	2.86	-	1056.6
AHQ-5-11, 3404 - 3410	K.YIIIGDTGVGK.S	1136.32280	2	9.00E-04	0.91	4.03	-	1088.1
AHQ-5-11, 3398	K.YIIIGDTGVGK.S	1136.32280	1	3.93E-05	0.25	2.02	-	553.6
gi|7661728|ref|NP_054736.1| HSPC003 protein [Homo sapiens]				9.19E-09	0.75	10.17	21.60	13507.4
AHQ-5-14-, 5501	R.VTAAIASNIWAAYDRNGNQAFNEDNLK.F	2968.18636	3	9.19E-09	0.75	3.35	-	571.6
gi|4758950|ref|NP_000933.1| peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]				9.38E-09	8.54	110.24	39.40	23742.4
AHQ-5-11, 3675	K.DFM*IQGGDFTR.G	1303.42600	2	2.45E-04	0.85	3.34	-	838.0
AHQ-5-12, 4188 - 4194	K.DFMIQGGDFTR.G	1287.42660	1	4.01E-04	0.47	2.61	-	224.6
AHQ-5-12, 4184	K.DFMIQGGDFTR.G	1287.42660	2	2.03E-04	0.89	3.04	-	1180.9
AHQ-5-11, 2836	R.DKPLKDVIIADCGK.I	1573.83653	3	2.21E-06	0.94	4.46	-	1526.8
AHQ-5-11, 2826	R.DKPLKDVIIADCGK.I	1573.83653	2	1.13E-08	0.93	3.36	-	1368.1
AHQ-5-12, 2889	R.DKPLKDVIIADCGK.I	1573.83653	3	5.08E-05	0.86	3.70	-	915.1
AHQ-5-12, 2872	R.DKPLKDVIIADCGK.I	1573.83653	2	9.38E-09	0.91	3.46	-	987.5
AHQ-5-12, 4368 - 4408	K.DTNGSQFFITTVK.T	1458.59766	2	6.37E-06	0.91	3.67	-	1191.0
AHQ-5-11, 4207 - 4280	K.DTNGSQFFITTVK.T	1458.59766	1	6.96E-05	0.37	2.50	-	417.2
AHQ-5-11, 4203 - 4275	K.DTNGSQFFITTVK.T	1458.59766	2	5.29E-04	0.93	3.69	-	1419.9
AHQ-5-12, 4394	K.DTNGSQFFITTVK.T	1458.59766	1	5.81E-06	0.26	2.26	-	322.5
AHQ-5-11, 2371	K.DVIIADCGK.I	992.12891	1	3.53E-06	0.67	2.14	-	608.2
AHQ-5-12, 2397	K.DVIIADCGK.I	992.12891	1	3.99E-05	0.70	2.20	-	669.0
AHQ-5-11, 2915 - 2991	K.HYGPGWVSMANAGK.D	1475.65664	2	1.15E-04	0.95	3.93	-	1173.8
AHQ-5-12, 3008	K.HYGPGWVSMANAGK.D	1475.65664	2	1.20E-05	0.97	4.70	-	1272.9
AHQ-5-14-, 4318	K.TVDNFVALATGEK.G	1365.51377	2	9.86E-06	0.92	3.89	-	924.1
AHQ-5-11, 4222 - 4227	K.TVDNFVALATGEK.G	1365.51377	2	7.19E-07	0.87	3.42	-	836.8
AHQ-5-12, 4340 - 4356	K.TVDNFVALATGEK.G	1365.51377	2	3.20E-06	0.90	3.85	-	835.9
AHQ-5-12, 4342	K.TVDNFVALATGEK.G	1365.51377	1	2.42E-04	0.17	1.83	-	325.6
AHQ-5-12, 4349	K.TVDNFVALATGEK.G	1365.51377	1	1.14E-04	0.51	2.94	-	323.6
AHQ-5-12, 4805 - 4809	R.VIFGLFGK.T	881.09607	2	9.42E-04	0.84	2.58	-	535.8
AHQ-5-12, 4810	R.VIFGLFGK.T	881.09607	1	2.01E-04	0.52	2.58	-	619.4
AHQ-5-12, 3686 - 3737	R.VIKDFM*IQGGDFTR.G	1643.88873	2	4.34E-04	0.74	2.91	-	565.8
AHQ-5-12, 4138	R.VIKDFMIQGGDFTR.G	1627.88933	2	3.21E-06	0.95	4.60	-	1318.6
AHQ-5-12, 2961 - 2964	K.VLEGMEVVR.K	1032.23962	2	2.05E-06	0.91	3.84	-	824.9
gi|5174389|ref|NP_005882.1| acetyl-Coenzyme A acetyltransferase 2; acetoacetyl Coenzyme A thiolase				9.65E-09	0.63	10.16	6.80	41295.5
AHQ-5-14-, 6495	R.ATVAPEDVSEVIFGHVLAAGCGQNPVR.Q	2796.10845	3	9.65E-09	0.63	3.20	-	345.4
gi|4758756|ref|NP_004528.1| nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr				1.04E-08	1.62	20.30	7.40	45373.8
AHQ-5-7, 7158	K.GIPEFWLTVFK.N	1337.58999	2	1.04E-08	0.65	2.80	-	228.4
AHQ-5-9, 4804	K.NVDLLSDMVQEHDEPILK.H	2096.34751	2	1.42E-06	0.89	4.00	-	792.0
AHQ-5-7, 5247	K.NVDLLSDMVQEHDEPILK.H	2096.34751	2	7.50E-08	0.97	5.94	-	1267.3
gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre				1.11E-08	8.20	100.29	39.60	48141.1
AHQ-5-7, 3160	R.AKIDDPTDSKPEDWDKPEHIPDPDAK.K	2961.14253	2	7.91E-06	0.69	3.17	-	392.5
AHQ-5-7, 5811	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	2	2.93E-04	0.58	2.74	-	373.6
AHQ-5-7, 5664	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	2	2.37E-04	0.94	4.33	-	1070.5
AHQ-5-7, 5814	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	2.09E-05	0.91	3.96	-	1394.2
AHQ-5-7, 5662 - 5702	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	1.87E-07	0.95	5.77	-	835.8
AHQ-5-7, 3710 - 3716	K.EQFLDGDGWTSR.W	1411.45795	2	1.54E-04	0.89	3.02	-	1073.1
AHQ-5-7, 5176 - 5254	R.FYALSASFEPFSNK.G	1608.77470	2	2.41E-04	0.95	3.57	-	1788.0
AHQ-5-14-, 5287 - 5354	R.FYALSASFEPFSNK.G	1608.77470	2	1.44E-08	0.96	4.19	-	1549.0
AHQ-5-7, 1903	K.HEQNIDCGGGYVK.L	1478.56912	1	1.11E-08	0.87	3.96	-	648.9
AHQ-5-13, 2381	K.HEQNIDCGGGYVK.L	1478.56912	2	9.33E-04	0.95	4.09	-	1267.3
AHQ-5-7, 5103	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	2.70E-07	0.85	3.92	-	681.9
AHQ-5-7, 2232	K.IKDPDASKPEDWDER.A	1801.89173	2	8.50E-05	0.93	4.02	-	947.8
AHQ-5-7, 1988	K.KVHVIFNYK.G	1148.38164	1	5.07E-07	0.78	2.69	-	561.3
AHQ-5-13, 5994	K.LFPNSLDQTDM*HGDSEYNIMFGPDICGPGTK.K	3475.78447	3	1.48E-07	0.78	4.01	-	801.0
AHQ-5-7, 2354	K.VHVIFNYK.G	1020.20872	1	5.61E-04	0.49	2.19	-	574.2
gi|4507789|ref|NP_003338.1| ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]				1.12E-08	0.96	10.25	9.70	17861.5
AHQ-5-12, 5249	R.IEINFPAEYPFKPPK.I	1791.08155	3	1.12E-08	0.96	4.99	-	1502.1
AHQ-5-12, 5205 - 5276	R.IEINFPAEYPFKPPK.I	1791.08155	2	2.14E-08	0.91	3.87	-	979.1
gi|4758018|ref|NP_004359.1| calponin 2; Calonin 2 [Homo sapiens]				1.20E-08	1.89	20.26	9.10	33696.9
AHQ-5-12, 2789	K.GLQSGVDIGVK.Y	1073.22510	2	6.51E-06	0.89	3.12	-	1044.6
AHQ-5-13-, 2872	K.GLQSGVDIGVK.Y	1073.22510	2	3.71E-06	0.92	3.21	-	1333.1
AHQ-5-12, 6498	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.55E-04	0.93	3.48	-	1282.3
AHQ-5-13, 6365 - 6424	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	5.76E-07	0.96	4.65	-	1249.7
AHQ-5-12, 6365 - 6429	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.20E-08	0.97	5.19	-	1581.7
AHQ-5-14-, 6233 - 6250	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.12E-05	0.90	3.29	-	1298.0
AHQ-5-9, 5827 - 5890	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	4.68E-04	0.86	3.36	-	1093.3
gi|4759086|ref|NP_004883.1| vesicle trafficking protein sec22b [Homo sapiens]				1.22E-08	0.90	10.19	6.50	24740.4
AHQ-5-12, 3941	R.NLGSINTELQDVQR.I	1587.71696	2	1.22E-08	0.90	3.75	-	1129.4
gi|4502491|ref|NP_001203.1| complement component 1, q subcomponent binding protein precursor; hyalu				1.26E-08	0.71	10.19	10.60	31362.0
AHQ-5-9, 6630 - 6675	R.GVDNTFADELVELSTALEHQEYITFLEDLK.S	3441.73936	3	1.26E-08	0.71	3.81	-	464.0
gi|4557297|ref|NP_000022.1| delta-aminolevulinic acid dehydratase; porphobilinogen synthase; aminol				1.26E-08	0.94	10.20	5.80	36294.7
AHQ-5-9, 4348 - 4375	R.GSAADSEESPAIEAIHLLR.K	1967.12642	2	1.26E-08	0.94	4.09	-	1115.5
gi|4507651|ref|NP_003281.1| tropomyosin 4 [Homo sapiens]				1.27E-08	2.89	40.26	15.30	28521.6
AHQ-5-9, 5298 - 5299	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	2	9.95E-04	0.79	3.36	-	820.1
AHQ-5-9, 4478 - 4555	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	3.42E-07	0.72	3.65	-	817.0

AHQ-5-9, 4543	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	2	4.66E-04	0.28	2.69	-	210.5
AHQ-5-9, 5295	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	2.52E-07	0.90	4.73	-	993.8
AHQ-5-9, 1716	R.EKAEGDVAALNR.R	1273.37796	1	2.56E-04	0.05	1.87	-	75.2
AHQ-5-13-, 2637	K.IQALQQQADEAEDR.A	1615.68404	2	6.85E-06	0.97	4.77	-	1709.3
AHQ-5-11, 2504 - 2508	K.IQALQQQADEAEDR.A	1615.68404	2	1.23E-05	0.94	3.95	-	1320.5
AHQ-5-9, 2382	K.IQALQQQADEAEDR.A	1615.68404	2	8.58E-07	0.97	4.87	-	1860.8
AHQ-5-10, 2226	R.KIQALQQQADEAEDR.A	1743.85695	2	1.27E-08	0.97	5.22	-	1873.0
gi|4502303|ref|NP_001688.1| mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m				1.28E-08	2.75	30.25	24.90	23277.2
AHQ-5-11, 6659 - 6663	R.FSPLTTNLINLLAENGR.L	1874.13050	2	6.35E-07	0.93	4.25	-	1269.3
AHQ-5-13, 5666	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	3.18E-08	0.95	4.92	-	914.8
AHQ-5-14, 6118 - 6168	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	1.28E-08	0.94	4.71	-	855.1
AHQ-5-14-, 5530	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	1.13E-05	0.95	5.00	-	817.6
AHQ-5-11, 3507	K.LVRPPVQVYGIEGR.Y	1583.85942	2	9.29E-04	0.88	3.46	-	782.3
gi|4502905|ref|NP_001822.1| clusterin; complement-associated protein SP-40 [Homo sapiens]				1.34E-08	1.27	20.27	7.80	52494.3
AHQ-5-9, 5191	R.ASSIIDELFQDR.F	1394.51197	1	1.44E-07	0.32	2.80	-	223.7
AHQ-5-11, 3411	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	1.34E-08	0.95	5.36	-	783.1
gi|13489091|ref|NP_066949.1| 3-mercaptopyruvate sulfurtransferase [Homo sapiens]				1.34E-08	1.69	20.24	14.50	33178.2
AHQ-5-9, 5846 - 5902	R.AGQPLQLLDASWYLPK.L	1801.07798	2	1.34E-08	0.97	4.87	-	1690.9
AHQ-5-9, 6354 - 6355	R.DGIEPGHIPGTVNIPFTDFLSQEGLEK.S	2912.19939	2	9.52E-05	0.72	3.43	-	320.5
gi|7657431|ref|NP_055205.1| EBNA-2 co-activator (100kD) [Homo sapiens]				1.36E-08	0.93	10.25	2.40	99689.7
AHQ-5-5, 6530 - 6543	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	5.98E-07	0.86	3.71	-	387.2
AHQ-5-6, 6446	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	1.47E-04	0.83	3.59	-	425.5
AHQ-5-4, 6653	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	1.36E-08	0.93	5.06	-	557.8
gi|12408656|ref|NP_005177.2| calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ				1.37E-08	8.14	110.30	21.40	81889.4
AHQ-5-6, 5048	K.APSDLYQIILK.A	1261.49183	2	1.37E-08	0.90	3.72	-	910.8
AHQ-5-6, 3453	R.DFFLANASR.A	1041.14166	1	2.78E-04	0.18	2.14	-	194.8
AHQ-5-6, 3460	R.DFFLANASR.A	1041.14166	2	3.62E-05	0.91	2.83	-	1278.7
AHQ-5-6, 6212 - 6289	K.IRLDETDDPDDYGDRESGCSFVLALMQK.H	3248.50119	3	1.91E-05	0.52	3.06	-	519.6
AHQ-5-6, 4128 - 4148	R.KAPSDLYQIILK.A	1389.66474	2	3.27E-04	0.93	3.75	-	1015.1
AHQ-5-6, 4848 - 4926	R.LEICNLTPDALK.S	1388.61207	1	9.61E-04	0.21	2.58	-	265.2
AHQ-5-6, 5673 - 5712	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	2	5.30E-05	0.76	3.56	-	297.7
AHQ-5-6, 5960 - 5966	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	5.45E-06	0.61	3.25	-	337.6
AHQ-5-6, 6482	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	2	8.40E-04	0.98	5.53	-	2003.0
AHQ-5-6, 6478 - 6498	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	3	3.04E-05	0.90	3.98	-	950.2
AHQ-5-6, 5085 - 5165	R.NYPATFWVNPQFK.I	1612.81141	2	6.78E-08	0.97	4.67	-	1500.9
AHQ-5-6, 4072	K.RPTELLSNPQFIVDGATR.T	2015.25904	2	9.33E-05	0.91	4.74	-	407.7
AHQ-5-6, 4356	K.RPTELLSNPQFIVDGATR.T	2015.25904	3	3.20E-06	0.95	5.00	-	1344.2
AHQ-5-6, 2861	R.SEQFINLR.E	1007.12521	1	2.66E-05	0.36	2.23	-	321.0
AHQ-5-6, 3136 - 3210	K.YLGQDYEQLR.V	1285.38720	2	7.24E-08	0.88	3.28	-	641.7
AHQ-5-6, 3141	K.YLGQDYEQLR.V	1285.38720	1	6.51E-04	0.06	1.81	-	201.2
gi|21361122|ref|NP_001440.2| four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap				1.39E-08	3.53	40.29	18.90	31894.7
AHQ-5-12, 2430	K.AIVAGDQNVEYK.G	1307.43431	2	6.95E-04	0.80	2.92	-	905.2
AHQ-5-9, 2808 - 2883	K.CLHPLANETFVAK.D	1501.73210	2	1.85E-07	0.94	3.69	-	764.5
AHQ-5-13-, 3395	K.CLHPLANETFVAK.D	1501.73210	2	9.28E-07	0.78	2.73	-	487.2
AHQ-5-13-, 3821	R.FVFHQEQVYCPDCAK.K	1931.13758	2	4.61E-07	0.98	5.65	-	2126.0
AHQ-5-13, 3913	R.FVFHQEQVYCPDCAK.K	1931.13758	2	1.27E-07	0.97	4.93	-	1744.0
AHQ-5-14, 4533	R.FVFHQEQVYCPDCAK.K	1931.13758	2	1.39E-08	0.96	4.30	-	1692.9
AHQ-5-9, 3347 - 3355	R.FVFHQEQVYCPDCAK.K	1931.13758	2	3.37E-08	0.98	5.77	-	1708.5
AHQ-5-12, 3718	R.FVFHQEQVYCPDCAK.K	1931.13758	2	2.86E-08	0.97	4.46	-	1819.1
AHQ-5-9, 2772 - 2783	K.GEDFYCVTCHETK.F	1648.75260	2	1.25E-05	0.83	3.62	-	519.7
gi|5123454|ref|NP_005336.2| heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind				1.41E-08	4.95	60.33	17.50	70037.7
AHQ-5-6, 5346	K.AAAIGIDLGTTYSCVGVFQHGK.V	2267.54677	2	4.41E-05	0.29	2.97	-	382.9
AHQ-5-6, 2885 - 2965	K.AQIHDLVLVGGSTR.I	1466.66769	2	6.60E-07	0.83	2.86	-	1216.4
AHQ-5-6, 4762	K.DAGVIAGLNVLR.I	1198.39736	2	1.14E-05	0.96	3.25	-	2011.7
AHQ-5-6, 6278	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G	3058.37100	3	1.41E-08	0.98	6.70	-	2390.3
AHQ-5-6, 3010	R.LVNHFVEEFK.R	1262.43837	2	1.03E-05	0.94	3.17	-	1563.3
AHQ-5-6, 6853	K.SINPDEAVAYGAAVQAAILM*GDK.S	2321.59293	2	1.10E-05	0.94	4.47	-	955.8
gi|15306356|ref|XP_035638.2| similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan				1.45E-08	1.81	20.21	15.60	18795.1
AHQ-5-13, 3558	R.ESDVPLKTEEFEVTK.T	1751.91253	2	5.90E-05	0.68	2.74	-	421.1
AHQ-5-13-, 3443 - 3451	R.ESDVPLKTEEFEVTK.T	1751.91253	2	4.05E-04	0.88	3.45	-	728.0
AHQ-5-12, 3377 - 3382	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.45E-08	0.86	3.96	-	470.6
AHQ-5-13-, 3456	R.GAEIEYAMAYSK.A	1333.49204	2	3.30E-06	0.95	4.13	-	1377.6
gi|4557032|ref|NP_002291.1| lactate dehydrogenase B [Homo sapiens]				1.50E-08	9.20	110.28	30.50	36638.3
AHQ-5-9, 3830	K.FIIPQIVK.Y	958.22198	1	4.35E-04	0.34	2.44	-	416.4
AHQ-5-9, 3739	K.GEM*MDLQHGSLFLQTPK.I	1949.24111	2	3.27E-04	0.68	3.86	-	702.7
AHQ-5-9, 4184 - 4190	K.GEMMDLQHGSLFLQTPK.I	1933.24171	2	6.31E-05	0.93	4.41	-	957.7
AHQ-5-13, 2317 - 2362	K.IVADKDYSVTANSK.I	1511.65887	2	1.50E-08	0.94	3.69	-	1190.7
AHQ-5-13, 2747	K.IVVVTAGVR.Q	914.12760	2	3.21E-04	0.88	3.13	-	923.6
AHQ-5-13, 3585	K.LIAPVAEEEATVPNNK.I	1695.89534	2	2.50E-05	0.84	3.28	-	594.6
AHQ-5-14-, 3466	K.LIAPVAEEEATVPNNK.I	1695.89534	2	4.99E-05	0.89	3.57	-	769.8
AHQ-5-13, 3493	K.LIAPVAEEEATVPNNK.I	1695.89534	2	5.47E-04	0.73	3.07	-	606.1
AHQ-5-9, 1963 - 1964	K.LKDDEVAQLK.K	1159.31477	2	4.84E-05	0.75	2.86	-	632.3
AHQ-5-9, 3935	K.LKGEMMDLQHGSLFLQTPK.I	2174.57288	2	1.58E-07	0.96	5.21	-	1366.2
AHQ-5-9, 3387 - 3394	K.MVVESAYEVIK.L	1268.50463	2	4.19E-08	0.95	4.32	-	980.6
AHQ-5-14-, 3799 - 3802	K.MVVESAYEVIK.L	1268.50463	2	1.17E-07	0.93	3.87	-	953.0
AHQ-5-13-, 3912	K.MVVESAYEVIK.L	1268.50463	2	4.88E-07	0.91	3.17	-	1147.9
AHQ-5-13-, 6631 - 6632	K.SLADELALVDVLEDK.L	1630.81843	2	3.96E-08	0.96	5.35	-	1137.2
AHQ-5-13, 6690	K.SLADELALVDVLEDK.L	1630.81843	2	1.13E-05	0.98	5.57	-	1758.6
AHQ-5-14-, 6493 - 6557	K.SLADELALVDVLEDK.L	1630.81843	2	3.09E-05	0.97	4.70	-	2079.4
AHQ-5-13, 6798	K.SLADELALVDVLEDKLK.G	1872.14959	2	9.87E-05	0.94	4.07	-	1208.8
AHQ-5-9, 6346 - 6382	K.SLADELALVDVLEDKLK.G	1872.14959	2	1.84E-04	0.92	3.60	-	1182.4
AHQ-5-14-, 6619 - 6691	K.SLADELALVDVLEDKLK.G	1872.14959	2	3.72E-05	0.96	4.62	-	1578.0
gi|24431969|ref|NP_037473.2| hypothetical protein PTD004; homologous yeast-44.2 protein [Homo sapie				1.50E-08	0.96	10.24	3.80	44683.2
AHQ-5-8, 7129	K.IPAFLNVVDIAGLVK.G	1569.91256	2	1.50E-08	0.96	4.90	-	1502.1
gi|19923483|ref|NP_057406.2| GTPase Rab14 [Homo sapiens]				1.52E-08	4.04	50.21	38.60	23896.8
AHQ-5-10, 3548	K.IYQNIQDGSLDLNAAESGVQHKPSAPQGGR.L	3152.38123	3	1.17E-06	0.78	3.57	-	606.4
AHQ-5-10, 4516 - 4574	R.NLTNPNTVIILIGNK.A	1624.90662	2	2.64E-04	0.79	2.87	-	624.5
AHQ-5-10, 2952	K.SCLLHQFTEK.K	1264.43272	2	3.57E-06	0.91	3.65	-	789.2
AHQ-5-10, 3854	R.STYNHLSSWLTDAR.N	1651.76121	2	2.01E-06	0.94	3.93	-	1101.3
AHQ-5-10, 3766	R.STYNHLSSWLTDAR.N	1651.76121	2	1.51E-04	0.95	4.12	-	1373.6
AHQ-5-10, 4119	K.TGENVEDAFLEAAK.K	1494.58517	1	1.52E-08	0.62	3.01	-	532.7
gi|20270343|ref|NP_620150.1| hypothetical protein BC015408 [Homo sapiens]				1.68E-08	1.73	20.30	19.90	21415.8
AHQ-5-11, 3932 - 3936	R.DLPGALDEKELIEK.M	1570.76622	2	2.99E-08	0.77	3.33	-	456.5
AHQ-5-11, 5862 - 5863	K.NELHNLLDKPQLQGIPVLVLGNK.R	2553.98492	2	5.61E-05	0.96	5.57	-	1031.3
AHQ-5-11, 5860 - 5912	K.NELHNLLDKPQLQGIPVLVLGNK.R	2553.98492	3	1.68E-08	0.96	5.97	-	910.4
gi|4759140|ref|NP_004243.1| solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulato				1.71E-08	0.89	10.18	3.90	38868.2
AHQ-5-13-, 3812	R.LLVVDPETDEQLQK.L	1627.81777	2	1.71E-08	0.89	3.59	-	612.7
AHQ-5-13, 3908	R.LLVVDPETDEQLQK.L	1627.81777	2	6.46E-04	0.91	3.70	-	653.8
gi|4507855|ref|NP_003472.1| Ubiquitin isopeptidase T; Ubiquitin-specific protease-5 (ubiquitin isop				1.72E-08	0.93	10.22	3.10	93393.2
AHQ-5-5, 7186	R.IGEWELIQESGVPLKPLFGPGYTGIR.N	2858.28283	3	1.72E-08	0.93	4.31	-	1497.4
gi|14249348|ref|NP_116120.1| hypothetical protein MGC14353 [Homo sapiens]				1.80E-08	0.91	10.16	11.40	13940.7
AHQ-5-13-, 4065	K.SWCPDCVQAEPVVR.E	1705.89366	2	1.80E-08	0.91	3.07	-	1054.2
AHQ-5-13, 4166	K.SWCPDCVQAEPVVR.E	1705.89366	2	1.54E-04	0.90	3.11	-	1219.0
gi|4885417|ref|NP_005330.1| huntingtin interacting protein 2; ubiquitin-conjugating enzyme E2-25 KD				1.98E-08	0.92	10.19	6.00	22406.5
AHQ-5-11, 4619	K.VDLVDENFTELR.G	1450.57553	2	1.98E-08	0.92	3.46	-	1017.8
gi|29737978|ref|XP_290747.1| similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy				1.98E-08	3.37	40.23	1.50	191380.7
AHQ-5-6, 3668 - 3680	K.ADFCIIHYAGK.V	1296.47641	2	2.56E-05	0.89	3.02	-	1010.5

AHQ-5-4, 3949 - 3950	K.ADFCIIHYAGK.V	1296.47641	1	4.23E-04	0.72	2.58	-	685.2
AHQ-5-1, 4091	K.ADFCIIHYAGK.V	1296.47641	2	4.06E-06	0.95	3.65	-	1282.9
AHQ-5-2, 3905 - 3917	K.ADFCIIHYAGK.V	1296.47641	2	2.16E-05	0.96	3.78	-	1621.3
AHQ-5-3, 3970 - 3993	K.ADFCIIHYAGK.V	1296.47641	2	6.08E-07	0.96	3.94	-	1741.5
AHQ-5-2, 3918	K.ADFCIIHYAGK.V	1296.47641	1	9.98E-08	0.72	3.16	-	512.6
AHQ-5-4, 2690 - 2761	R.AGVLAHLEEER.D	1224.34854	1	6.86E-04	0.12	2.08	-	271.4
AHQ-5-3, 2750 - 2821	R.AGVLAHLEEER.D	1224.34854	2	1.74E-06	0.94	3.89	-	1398.1
AHQ-5-4, 2764	R.AGVLAHLEEER.D	1224.34854	2	1.98E-08	0.92	4.01	-	1093.2
AHQ-5-2, 2690 - 2762	R.AGVLAHLEEER.D	1224.34854	2	1.74E-06	0.96	4.27	-	1738.4
AHQ-5-2, 2693	R.AGVLAHLEEER.D	1224.34854	1	3.48E-05	0.48	2.56	-	507.6
AHQ-5-1, 2944 - 3011	R.AGVLAHLEEER.D	1224.34854	2	7.50E-07	0.93	3.76	-	1186.1
AHQ-5-3, 3701	K.DKADFCIIHYAGK.V	1539.73719	2	1.24E-05	0.97	4.58	-	1606.6
AHQ-5-2, 3662	K.DKADFCIIHYAGK.V	1539.73719	2	1.19E-06	0.97	4.60	-	1708.0
AHQ-5-5, 3447	K.DKADFCIIHYAGK.V	1539.73719	2	1.89E-07	0.95	4.15	-	1437.2
AHQ-5-1, 3856	K.DKADFCIIHYAGK.V	1539.73719	2	4.68E-07	0.96	4.42	-	1690.7
AHQ-5-2, 3671	K.DKADFCIIHYAGK.V	1539.73719	3	6.78E-05	0.94	4.41	-	1304.5
AHQ-5-4, 4744	K.LDPHLVLDQLR.C	1319.53460	2	2.13E-05	0.75	2.63	-	631.9
AHQ-5-3, 4797	K.LDPHLVLDQLR.C	1319.53460	2	2.06E-07	0.78	2.73	-	649.4
AHQ-5-5, 4538	K.LDPHLVLDQLR.C	1319.53460	2	5.19E-07	0.82	2.85	-	537.2
AHQ-5-5, 4554	K.LDPHLVLDQLR.C	1319.53460	3	1.17E-06	0.92	3.75	-	1135.8
AHQ-5-1, 4888	K.LDPHLVLDQLR.C	1319.53460	3	1.60E-04	0.87	3.45	-	795.9
AHQ-5-1, 4875 - 4876	K.LDPHLVLDQLR.C	1319.53460	2	6.36E-07	0.71	2.62	-	590.4
gi|4503785|ref|NP_000135.1| frataxin; Friedreich ataxia (frataxin) [Homo sapiens]				2.03E-08	0.95	10.22	5.70	23218.1
AHQ-5-13-, 3767 - 3771	K.LGGDLGTYVINK.Q	1250.42590	2	2.30E-08	0.95	4.41	-	1054.1
AHQ-5-13, 3864 - 3866	K.LGGDLGTYVINK.Q	1250.42590	2	2.03E-08	0.95	4.48	-	1117.2
gi|4506713|ref|NP_002945.1| ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte				2.03E-08	0.79	10.19	10.30	17964.8
AHQ-5-14-, 4490	K.TITLEVEPSDTIENVK.A	1788.97431	2	4.31E-06	0.86	3.38	-	631.3
AHQ-5-14-, 4230 - 4305	K.TITLEVEPSDTIENVK.A	1788.97431	2	2.03E-08	0.79	3.83	-	628.2
gi|4507951|ref|NP_003396.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept				2.07E-08	3.66	40.23	20.70	28218.5
AHQ-5-14-, 2909 - 2974	K.AVTELNEPLSNEDR.N	1587.67060	2	1.20E-04	0.77	3.36	-	530.7
AHQ-5-10, 2838	K.AVTELNEPLSNEDR.N	1587.67060	2	2.07E-08	0.90	4.23	-	664.6
AHQ-5-10, 2696	K.AVTELNEPLSNEDR.N	1587.67060	2	7.02E-08	0.88	3.94	-	519.2
AHQ-5-14-, 6665 - 6666	K.ELETVCNDVLSLLDK.F	1749.96137	2	5.67E-07	0.92	4.31	-	788.5
AHQ-5-10, 2483 - 2551	K.NSVVEASEAAYK.E	1268.35495	1	5.16E-04	0.31	2.17	-	300.6
AHQ-5-10, 2755 - 2758	K.NSVVEASEAAYK.E	1268.35495	1	1.59E-04	0.83	3.46	-	589.7
AHQ-5-10, 2371	K.NSVVEASEAAYK.E	1268.35495	2	2.05E-04	0.82	3.27	-	627.9
AHQ-5-13-, 2592	K.NSVVEASEAAYK.E	1268.35495	2	3.72E-08	0.94	3.61	-	1129.7
AHQ-5-10, 2020	R.YLAEVASGEK.K	1067.17419	2	6.36E-07	0.89	3.01	-	944.3
AHQ-5-10, 2010	R.YLAEVASGEK.K	1067.17419	1	2.30E-05	0.49	2.86	-	205.8
AHQ-5-10, 2003	R.YLAEVASGEK.K	1067.17419	1	1.42E-04	0.39	2.09	-	622.4
AHQ-5-13, 2391	R.YLAEVASGEK.K	1067.17419	1	4.40E-05	0.15	2.06	-	385.4
gi|4506505|ref|NP_002916.1| regulator of G-protein signaling 10 [Homo sapiens]				2.13E-08	1.71	20.22	16.20	19607.9
AHQ-5-11, 4639 - 4650	K.LQDQIFNLMK.Y	1250.49254	2	2.82E-04	0.85	3.71	-	561.5
AHQ-5-11, 5306 - 5326	K.WAASLENLLEDPEGVKR.F	1928.13502	2	2.13E-08	0.86	4.33	-	423.6
gi|4557395|ref|NP_000058.1| carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase;				2.28E-08	6.07	70.25	30.40	29245.8
AHQ-5-10, 6442	K.AVQQPDGLAVLGIFLK.V	1669.98899	2	1.39E-05	0.94	5.05	-	568.3
AHQ-5-10, 2956	K.EPISVSSEQVLK.F	1316.48265	1	2.07E-06	0.60	2.87	-	241.4
AHQ-5-10, 3780 - 3843	R.ILNNGHAFNVEFDDSQDK.A	2064.15751	2	4.27E-06	0.93	4.59	-	950.1
AHQ-5-10, 3899	R.ILNNGHAFNVEFDDSQDK.A	2064.15751	2	1.38E-07	0.93	3.93	-	1283.4
AHQ-5-10, 2803	K.KYAAELHLVHWNTK.Y	1710.95976	2	2.09E-05	0.97	3.75	-	2285.7
AHQ-5-10, 3062	K.SADFTNFDPR.G	1170.21306	2	2.20E-05	0.88	3.22	-	906.6
AHQ-5-10, 3440 - 3450	K.VVDVLDSIK.T	988.16011	2	1.51E-04	0.79	2.91	-	436.6
AHQ-5-10, 3160	K.YAAELHLVHWNTK.Y	1582.78684	2	2.28E-08	0.96	3.90	-	1786.8
gi|30150448|ref|XP_293066.2| similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose				2.36E-08	0.92	10.21	2.90	58788.2
AHQ-5-6, 4530	R.VINEPTAAALAYGLDK.S	1646.86592	2	2.36E-08	0.92	4.21	-	630.4
gi|4506005|ref|NP_002700.1| protein phosphatase 1, catalytic subunit, beta isoform [Homo sapiens] [				2.46E-08	3.81	40.25	20.80	37186.6
AHQ-5-9, 3434	R.AHQVVEDGYEFFAK.R	1640.77679	2	1.20E-04	0.97	4.32	-	1527.6
AHQ-5-14-, 6737	R.EIFLSQPILLELEAPLK.I	1954.33857	2	3.20E-06	0.92	4.33	-	576.2
AHQ-5-9, 6442 - 6444	R.EIFLSQPILLELEAPLK.I	1954.33857	2	2.46E-08	0.95	4.92	-	656.1
AHQ-5-9, 4627	K.IFCCHGGLSPDLQSMEQIR.R	2251.54930	2	1.95E-06	0.95	4.43	-	1316.5
AHQ-5-9, 6387	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	2.96E-05	0.94	4.30	-	862.0
AHQ-5-9, 6212	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	2.25E-05	0.95	3.97	-	1269.2
gi|14042953|ref|NP_114420.1| FKSG17 [Homo sapiens]				2.47E-08	0.92	10.17	6.10	23305.9
AHQ-5-11, 4587	K.NILFVITKPDVYK.S	1550.86611	2	2.47E-08	0.92	3.48	-	1136.7
gi|4557471|ref|NP_001274.1| adaptor-related protein complex 1, sigma 1 subunit isoform 1; clathrin-				2.48E-08	0.98	10.29	10.10	18732.9
AHQ-5-12, 3566	K.AIEQADLLQEEDESPR.S	1843.92692	2	2.48E-08	0.98	5.78	-	1739.5
gi|4557377|ref|NP_000052.1| Bruton agammaglobulinemia tyrosine kinase [Homo sapiens]				2.54E-08	1.81	20.23	6.20	76280.8
AHQ-5-6, 7332	R.FPYPFQVVYDEGPLYVFSPTEELR.K	2894.22412	2	2.46E-06	0.84	3.81	-	663.2
AHQ-5-6, 3426	R.HYVVCSTPQSQYYLAEK.H	2075.28663	2	2.54E-08	0.97	4.68	-	1325.5
gi|28178832|ref|NP_002159.2| isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat				2.60E-08	4.65	50.24	14.80	50909.0
AHQ-5-8, 3624 - 3692	K.DLAGCIHGLSNVK.L	1385.57150	2	9.51E-08	0.97	4.63	-	2005.3
AHQ-5-13-, 3688 - 3751	R.DQTDDQVTIDSALATQK.Y	1849.93146	2	3.02E-04	0.86	3.33	-	915.5
AHQ-5-8, 1817 - 1890	R.GKLDGNQDLIR.F	1229.36832	2	7.57E-07	0.89	3.06	-	1057.5
AHQ-5-8, 4985	R.LIDDMVAQVLK.S	1245.51421	2	4.99E-06	0.96	4.79	-	1233.7
AHQ-5-8, 4402	R.NILGGTVFREPIICK.N	1719.04170	2	2.60E-08	0.96	4.71	-	1188.4
gi|24119203|ref|NP_705935.1| tropomyosin 3 [Homo sapiens]				2.74E-08	4.35	50.24	14.50	29032.5
AHQ-5-6, 3474	R.IQLVEEELDR.A	1244.37653	2	5.25E-06	0.88	2.85	-	1120.2
AHQ-5-10, 3332 - 3334	R.IQLVEEELDR.A	1244.37653	2	1.27E-07	0.87	3.53	-	748.5
AHQ-5-11, 3523	R.IQLVEEELDR.A	1244.37653	2	1.84E-05	0.89	3.45	-	839.9
AHQ-5-9, 3159	R.IQLVEEELDR.A	1244.37653	2	2.68E-06	0.89	3.53	-	842.8
AHQ-5-10, 2583	K.IQVLQQQADDAEER.A	1643.73738	2	2.29E-07	0.84	3.07	-	878.5
AHQ-5-9, 2526	K.IQVLQQQADDAEER.A	1643.73738	2	8.95E-08	0.79	2.93	-	761.1
AHQ-5-10, 2327 - 2334	R.KIQVLQQQADDAEER.A	1771.91030	2	9.05E-04	0.94	4.45	-	715.1
AHQ-5-11, 2420	R.KIQVLQQQADDAEER.A	1771.91030	2	6.82E-05	0.91	4.21	-	545.5
AHQ-5-10, 2998 - 3000	R.RIQLVEEELDR.A	1400.56288	2	2.74E-08	0.97	4.78	-	1603.5
AHQ-5-9, 2806 - 2814	R.RIQLVEEELDR.A	1400.56288	2	1.19E-07	0.96	4.18	-	1547.0
AHQ-5-9, 2688 - 2747	K.TIDDLEDKLK.C	1190.32563	2	2.40E-06	0.81	3.15	-	610.7
gi|4504077|ref|NP_000165.1| glycoprotein IX (platelet) [Homo sapiens]				2.76E-08	3.64	40.23	19.80	19046.0
AHQ-5-11, 4898	R.ALETMGLWVDCR.G	1452.68135	2	1.55E-06	0.94	3.13	-	1504.7
AHQ-5-11, 2586	R.CASPSLAAHGPLGR.L	1395.56962	1	7.59E-04	0.70	2.71	-	380.9
AHQ-5-12, 2600	R.CASPSLAAHGPLGR.L	1395.56962	2	5.20E-06	0.86	3.32	-	801.4
AHQ-5-11, 2570	R.CASPSLAAHGPLGR.L	1395.56962	2	2.76E-08	0.91	3.40	-	1071.7
AHQ-5-11, 3262	R.GHGLTALPALPAR.T	1274.49706	1	2.35E-04	0.69	3.12	-	396.4
AHQ-5-11, 3214 - 3279	R.GHGLTALPALPAR.T	1274.49706	2	1.88E-04	0.92	4.03	-	758.4
AHQ-5-12, 3220 - 3288	R.GHGLTALPALPAR.T	1274.49706	2	1.59E-04	0.95	4.56	-	816.4
AHQ-5-11, 3219 - 3294	R.GHGLTALPALPAR.T	1274.49706	1	6.84E-05	0.85	3.60	-	449.5
AHQ-5-12, 3081	R.TPEALLQVR.C	1027.19957	2	8.94E-06	0.94	3.01	-	1412.7
AHQ-5-14-, 3089	R.TPEALLQVR.C	1027.19957	2	9.59E-04	0.86	3.03	-	816.1
AHQ-5-14-, 3094	R.TPEALLQVR.C	1027.19957	1	1.69E-04	0.57	2.10	-	207.3
AHQ-5-11, 3056	R.TPEALLQVR.C	1027.19957	2	1.09E-04	0.95	3.58	-	1539.4
gi|6598323|ref|NP_001485.2| GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom				2.82E-08	3.54	40.32	15.10	50662.9
AHQ-5-6, 3360	K.MLLYTEVTR.Y	1126.35141	2	9.28E-06	0.81	2.62	-	813.5
AHQ-5-8, 4465	R.NPYYGGESASITPLEDLYKR.F	2274.47135	2	2.82E-08	0.77	3.63	-	345.6
AHQ-5-7, 6800	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.80E-06	0.95	4.75	-	939.9
AHQ-5-8, 6642	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	3.99E-06	0.95	4.95	-	796.0
AHQ-5-9, 6090 - 6091	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	5.07E-05	0.96	5.18	-	906.0
AHQ-5-6, 6888 - 6896	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	7.57E-07	0.98	6.37	-	1163.9

AHQ-5-8, 7257	K.VPSTEAEALASSLMGLFEK.R	1981.25641	2	4.45E-06	0.98	6.43	-	1837.5
gi|4757952|ref|NP_001782.1| cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p				2.88E-08	4.44	50.28	32.50	21258.5
AHQ-5-11, 2242	K.CVVVGDGAVGK.T	1062.22237	2	1.70E-04	0.75	2.60	-	922.8
AHQ-5-11, 6575 - 6644	K.NVFDEAILAALEPPEPK.K	1854.09282	3	1.46E-05	0.96	5.62	-	1338.3
AHQ-5-11, 3835 - 3842	K.TCLLISYTTNK.F	1315.51795	2	9.75E-04	0.93	3.72	-	1376.1
AHQ-5-11, 5784	K.TPFLLVGTQIDLR.D	1473.74174	2	5.58E-04	0.98	4.87	-	2135.8
AHQ-5-11, 5646 - 5708	K.TPFLLVGTQIDLR.D	1473.74174	2	8.43E-07	0.94	4.09	-	1228.3
AHQ-5-11, 2470	K.YVECSALTQK.G	1200.34381	2	2.88E-08	0.86	2.96	-	700.5
gi|29729616|ref|XP_292963.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				2.95E-08	1.84	20.35	16.40	18025.4
AHQ-5-12, 4874 - 4954	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.58E-07	0.95	5.72	-	1113.4
AHQ-5-12, 5018 - 5080	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	2.22E-04	0.91	4.08	-	689.0
AHQ-5-12, 5485 - 5548	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	1.45E-05	0.86	3.79	-	498.8
AHQ-5-12, 5612 - 5676	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	2	3.13E-07	0.89	4.45	-	618.5
AHQ-5-13, 4936	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.09E-05	0.95	5.54	-	1222.1
AHQ-5-13, 4949	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	4.27E-05	0.82	3.83	-	477.2
AHQ-5-13, 5538 - 5565	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	7.57E-04	0.91	5.40	-	958.5
AHQ-5-13-, 5467 - 5532	K.HTGPGILSMANAGPNTNGSQFFICTAK.S	2794.11605	3	2.95E-08	0.95	6.98	-	1065.1
AHQ-5-14-, 4945	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.05E-07	0.89	4.87	-	766.7
gi|18640750|ref|NP_570138.1| regulator of G-protein signalling 18; regulator of G-protein signaling				2.96E-08	0.71	10.18	8.90	27582.0
AHQ-5-11, 4128	K.EVITNSITQPTLHSFDAAQSR.V	2316.51300	2	2.96E-08	0.71	3.51	-	351.3
AHQ-5-10, 3831	K.EVITNSITQPTLHSFDAAQSR.V	2316.51300	2	2.87E-04	0.63	3.12	-	381.5
gi|5174613|ref|NP_005960.1| nucleosome assembly protein 1-like 4; nucleosome assembly protein 2 [Ho				2.98E-08	1.90	20.30	7.50	42823.1
AHQ-5-7, 2630	K.FYEEVHDLER.K	1337.41897	2	2.63E-06	0.93	3.16	-	1405.8
AHQ-5-7, 7176 - 7180	R.NVDMLSELVQEYDEPILK.H	2136.40840	2	2.98E-08	0.98	6.04	-	1498.8
gi|21389549|ref|NP_653263.1| hypothetical protein MGC26605 [Homo sapiens]				3.22E-08	1.83	20.25	14.90	26927.8
AHQ-5-10, 5112 - 5118	R.AITVFSPDGHLFQVEYAQEAVK.K	2450.73052	2	5.35E-07	0.96	5.06	-	1186.4
AHQ-5-10, 4262	K.LTVEDPVTVEYITR.F	1635.83990	2	3.22E-08	0.88	3.78	-	598.2
gi|4758038|ref|NP_004246.1| cytochrome c oxidase subunit Va precursor; cytochrome c oxidase polypep				3.35E-08	2.48	30.26	40.70	16774.1
AHQ-5-13, 6806 - 6885	K.EIYPYVIQELRPTLNELGISTPEELGLDKV	3430.88913	3	5.85E-06	0.92	5.29	-	554.0
AHQ-5-13-, 4779 - 4844	K.GINTLVTYDMVPEPK.I	1677.94342	2	2.82E-04	0.93	3.57	-	1238.2
AHQ-5-13, 4856 - 4924	K.GINTLVTYDMVPEPK.I	1677.94342	2	2.69E-04	0.62	2.87	-	497.6
AHQ-5-14-, 5729	R.WVTYFNKPDIDAWELR.K	2054.29220	2	3.35E-08	0.94	4.54	-	786.6
gi|24497612|ref|NP_116262.2| nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr				3.38E-08	2.61	30.18	7.90	72695.6
AHQ-5-6, 4096	R.EYVLYLRPTGPLAQK.L	1749.04621	2	7.10E-04	0.89	3.69	-	533.7
AHQ-5-6, 6692	K.LGCDWVATIFSR.D	1426.62208	2	3.38E-08	0.91	3.28	-	1094.1
AHQ-5-6, 7276	R.SVQAACDWLFSHVGDPFLDDPLPR.E	2745.01846	2	3.28E-05	0.80	3.12	-	478.5
gi|30158489|ref|XP_301421.1| similar to Chloride intracellular channel protein 1 (Nuclear chloride				3.39E-08	1.78	30.21	11.60	28267.5
AHQ-5-9, 5479 - 5550	K.FLNGNELTLADCNLLPK.L	1934.20276	2	2.31E-06	0.86	4.23	-	974.4
AHQ-5-12, 6112 - 6121	K.FLNGNELTLADCNLLPK.L	1934.20276	2	3.39E-08	0.82	3.82	-	961.2
AHQ-5-10, 5223	R.KFLNGNELTLADCNLLPK.L	2062.37568	2	2.75E-05	0.77	3.61	-	866.6
AHQ-5-10, 2423	K.NSNPALNDNLQK.G	1328.41362	1	2.28E-04	0.02	2.19	-	101.4
AHQ-5-9, 2080	K.NSNPALNDNLQK.G	1328.41362	1	1.59E-04	0.19	2.19	-	198.5
gi|10835035|ref|NP_003157.1| sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3; t				3.57E-08	0.88	10.25	8.80	34196.0
AHQ-5-9, 5972	K.YFAEALGPLQSFQARPDDLLINTYPK.S	2969.33891	3	3.57E-08	0.88	4.30	-	607.0
gi|4826659|ref|NP_004921.1| F-actin capping protein beta subunit; Cap Z [Homo sapiens]				3.88E-08	3.16	40.24	25.00	30628.5
AHQ-5-10, 3752	K.GCWDSIHVVEVQEK.S	1687.85505	2	5.41E-04	0.87	3.22	-	1224.1
AHQ-5-9, 3630	K.GCWDSIHVVEVQEK.S	1687.85505	2	3.88E-08	0.90	3.79	-	1224.0
AHQ-5-9, 2939 - 2962	R.KLEVEANNAFDQYR.D	1697.82988	2	1.23E-06	0.96	4.75	-	1555.2
AHQ-5-9, 2911	R.QMEKDETVSDCSPHIANIGR.L	2289.48951	2	3.55E-04	0.53	2.84	-	304.1
AHQ-5-9, 3599	R.SPWSNKYDPPLEDGAMPSAR.L	2219.41928	2	5.85E-06	0.76	3.52	-	403.3
gi|19923457|ref|NP_057447.2| glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M				4.01E-08	0.96	10.24	3.20	67308.6
AHQ-5-7, 5295	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	2	4.31E-06	0.90	4.35	-	490.1
AHQ-5-7, 5292	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	4.01E-08	0.96	4.81	-	1653.1
gi|5031593|ref|NP_005708.1| actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub				4.03E-08	5.20	60.26	39.10	16320.3
AHQ-5-12, 2912	K.ALAAGGVGSIVR.V	1071.25558	2	3.36E-05	0.97	4.14	-	1849.5
AHQ-5-12, 4032 - 4101	K.AVQSLDKNGVDLLMK.Y	1631.91943	2	2.06E-07	0.96	4.86	-	1373.5
AHQ-5-12, 3520 - 3590	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	2.53E-07	0.87	3.77	-	600.2
AHQ-5-12, 4570 - 4584	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	4.03E-08	0.97	5.14	-	1435.1
AHQ-5-12, 4249	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	1.18E-07	0.85	3.73	-	494.2
AHQ-5-12, 4160	K.GFESPSDNSSAM*LLQWHEK.A	2180.33989	2	7.18E-08	0.78	3.32	-	504.0
AHQ-5-12, 4164	R.QGNMTAALQAALK.N	1317.54052	2	3.38E-06	0.65	2.89	-	437.0
gi|29788766|ref|NP_064424.2| tubulin, beta polypeptide 4, member Q [Homo sapiens]				4.05E-08	0.96	10.28	7.40	48377.2
AHQ-5-8, 6072	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	2.93E-05	0.91	4.25	-	991.2
AHQ-5-11, 5975 - 5984	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	4.05E-08	0.96	5.59	-	1516.7
AHQ-5-7, 6146 - 6206	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	2.26E-07	0.86	3.67	-	1217.0
gi|4501993|ref|NP_003650.1| alkylglycerone phosphate synthase precursor [Homo sapiens]				4.08E-08	0.86	10.17	2.60	72911.4
AHQ-5-6, 6017	R.GISDPLTVFEQTEAAAR.E	1805.96665	2	4.08E-08	0.86	3.46	-	813.5
gi|30147857|ref|XP_293007.2| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				4.13E-08	0.60	10.15	5.90	20789.8
AHQ-5-12, 3266 - 3281	K.KITIADCGQLQ	1248.43160	2	4.13E-08	0.60	3.05	-	691.6
gi|4507745|ref|NP_003320.1| thioredoxin [Homo sapiens]				4.34E-08	1.89	20.19	22.90	11693.3
AHQ-5-13, 5052	K.EKLEATINELV	1259.43110	2	1.10E-05	0.96	3.58	-	2081.1
AHQ-5-14, 4656	K.TAFQEALDAAGDK.L	1337.41728	2	3.47E-05	0.91	3.11	-	1313.8
AHQ-5-13-, 3851	K.TAFQEALDAAGDK.L	1337.41728	2	1.22E-06	0.94	3.73	-	1462.9
AHQ-5-14-, 3745 - 3746	K.TAFQEALDAAGDK.L	1337.41728	2	4.34E-08	0.93	3.48	-	1435.9
AHQ-5-13, 3968 - 3986	K.TAFQEALDAAGDK.L	1337.41728	2	1.71E-06	0.93	3.56	-	1362.0
gi|21361670|ref|NP_054782.2| src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo				4.40E-08	0.65	10.17	4.60	48294.0
AHQ-5-10, 5244	R.VAGTGEGGLEEMVEELNSGK.V	2007.16599	2	4.40E-08	0.65	3.43	-	246.4
gi|28269681|ref|NP_783313.1| NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]				4.41E-08	1.72	20.27	27.00	14852.0
AHQ-5-14-, 6434 - 6438	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	4.41E-08	0.95	5.37	-	1229.7
AHQ-5-13, 4988 - 5064	R.VTLNPPGTFLEGVAK.V	1543.78883	2	5.95E-04	0.78	2.93	-	438.3
gi|9845511|ref|NP_008839.2| ras-related C3 botulinum toxin substrate 1 isoform Rac1; rho family, sm				4.62E-08	0.97	10.19	5.20	21450.0
AHQ-5-11, 3083	K.YLECSALTQR.G	1242.38392	2	4.62E-08	0.97	3.72	-	1866.2
AHQ-5-11, 2979 - 3046	K.YLECSALTQR.G	1242.38392	2	1.13E-06	0.91	3.35	-	1025.8
gi|4758988|ref|NP_004152.1| RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho				4.71E-08	2.61	30.27	17.60	22677.6
AHQ-5-11, 5923	K.EFADSLGIPFLETSAK.N	1725.91990	2	9.70E-04	0.73	3.22	-	440.3
AHQ-5-11, 5847 - 5911	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	5.71E-06	0.91	3.88	-	886.1
AHQ-5-11, 5542 - 5607	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.11E-05	0.95	4.33	-	1390.9
AHQ-5-11, 5970 - 6042	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.30E-07	0.98	4.85	-	1935.9
AHQ-5-14-, 5607	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.18E-05	0.88	3.66	-	960.4
AHQ-5-11, 6107 - 6171	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.15E-06	0.97	5.04	-	1426.1
AHQ-5-11, 6110	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.51E-06	0.77	3.27	-	538.9
AHQ-5-11, 6234 - 6302	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.58E-04	0.95	4.14	-	1238.4
AHQ-5-11, 6830 - 6903	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	7.88E-04	0.76	3.05	-	562.6
AHQ-5-11, 6967 - 6978	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.00E-04	0.96	4.92	-	1194.2
AHQ-5-14-, 5845 - 5909	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	4.71E-08	0.97	5.43	-	1544.2
AHQ-5-11, 6030	K.NATNVEQSFMTMAAEIK.K	1886.14022	2	4.80E-06	0.91	4.23	-	1325.2
gi|5174393|ref|NP_006001.1| arginine-rich, mutated in early stage tumors; arginine-rich protein [Ho				4.72E-08	2.40	30.27	13.70	26906.2
AHQ-5-12, 4626	K.DRDVTFSPATIENELIK.F	1949.15100	2	9.06E-07	0.97	5.35	-	1453.8
AHQ-5-12, 5601 - 5677	K.DRDVTFSPATIENELIK.F	1949.15100	2	6.11E-04	0.94	4.72	-	1076.0
AHQ-5-12, 5156	R.DVTFSPATIENELIK.F	1677.87678	2	4.72E-08	0.62	2.64	-	477.1
AHQ-5-12, 6184	R.DVTFSPATIENELIK.F	1677.87678	2	4.64E-06	0.70	3.31	-	445.5
AHQ-5-12, 3144 - 3217	K.ILDDWGETCKGCAEK.S	1784.94596	2	1.26E-06	0.82	3.29	-	518.0
gi|4504743|ref|NP_002194.1| integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o				5.05E-08	2.56	30.25	4.60	129294.4
AHQ-5-3, 4641	K.GILGQHQFLEGPEGIENTR.F	2096.28902	2	2.01E-04	0.94	4.94	-	878.0
AHQ-5-3, 3317	K.TQVGLIQYANNPR.V	1474.64668	2	5.05E-08	0.82	2.96	-	1160.4
AHQ-5-2, 5241	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	4.56E-04	0.42	2.52	-	398.9
AHQ-5-3, 5277 - 5302	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	5.51E-04	0.91	3.99	-	636.3

AHQ-5-4, 5254	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	1.60E-05	0.85	3.76	-	603.2
AHQ-5-1, 5291	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	3.13E-07	0.80	3.57	-	568.4
gi|4502171|ref|NP_000476.1| adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho				5.16E-08	2.61	30.21	22.80	19607.6
AHQ-5-11, 4998	R.GKLPGPTLWASYSLEYGK.A	1968.24075	2	4.96E-05	0.79	3.40	-	523.5
AHQ-5-11, 3495	R.IDYIAGLDSR.G	1123.24098	2	5.16E-08	0.96	4.27	-	1677.6
AHQ-5-11, 5584 - 5602	R.SFPDFPTPGVVFR.D	1466.66462	1	6.78E-04	0.06	1.82	-	136.3
AHQ-5-11, 5575 - 5583	R.SFPDFPTPGVVFR.D	1466.66462	2	2.78E-04	0.86	2.90	-	726.8
gi|18104967|ref|NP_000953.2| prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland				5.27E-08	8.19	90.27	23.20	68686.0
AHQ-5-6, 3753 - 3826	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	2.28E-04	0.92	3.76	-	846.3
AHQ-5-6, 3674 - 3754	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	2	8.72E-04	0.86	3.76	-	639.2
AHQ-5-7, 3579	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	2	5.89E-06	0.96	4.76	-	1298.3
AHQ-5-6, 4973	R.FGMKPYTSFQELVGEK.E	1862.13845	2	5.27E-08	0.94	4.56	-	570.3
AHQ-5-6, 4234	R.FGM*KPYTSFQELVGEK.E	1878.13785	2	2.35E-05	0.88	3.56	-	561.5
AHQ-5-6, 7050	K.GLLGNPICSPEYWKPSTFGGEVGFNIVK.T	3069.47853	3	9.59E-05	0.88	4.64	-	480.0
AHQ-5-6, 3585	R.NSLRPSPSFTHFLLTHGR.W	2068.32687	3	1.62E-04	0.89	4.18	-	860.0
AHQ-5-6, 3244 - 3313	R.VPDASQDDGPAVERPSTEL	1984.06747	2	6.21E-07	0.96	5.38	-	962.5
AHQ-5-6, 5832	K.YQVLDGEMYPPSVEEAPVLMHYPR.G	2822.20799	3	3.91E-05	0.93	4.80	-	795.3
AHQ-5-6, 5312	K.YQVLDGEMYPPSVEEAPVLM*HYPR.G	2838.20739	3	3.92E-06	0.84	4.10	-	750.2
gi|4507231|ref|NP_003134.1| single-stranded DNA binding protein; single-stranded DNA-binding protei				5.41E-08	4.17	50.27	37.80	17259.5
AHQ-5-13, 2597	R.DVAYQYVK.K	986.10277	1	1.72E-05	0.35	1.96	-	634.7
AHQ-5-13, 5969 - 6040	K.NPVTIFSLATNEM*WR.S	1796.04007	2	2.35E-06	0.97	5.16	-	1119.0
AHQ-5-13-, 6672 - 6673	K.NPVTIFSLATNEMWR.S	1780.04067	2	7.36E-06	0.98	5.35	-	2074.1
AHQ-5-13-, 6053	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	2.08E-06	0.94	4.22	-	892.1
AHQ-5-13, 6133	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	1.11E-06	0.96	5.42	-	1078.9
AHQ-5-13-, 3191	R.SGDSEVYQLGDVSQK.T	1612.67692	2	2.79E-07	0.93	4.01	-	1092.1
AHQ-5-13, 3293	R.SGDSEVYQLGDVSQK.T	1612.67692	2	5.41E-08	0.91	4.16	-	889.4
gi|4503971|ref|NP_001484.1| GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r				5.57E-08	1.88	20.28	8.50	50582.4
AHQ-5-7, 5088	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	1.95E-04	0.89	3.36	-	885.7
AHQ-5-6, 5198 - 5248	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	1.35E-07	0.91	4.13	-	750.6
AHQ-5-7, 7118 - 7122	K.VPSTETEALASNLMGMFEK.R	2056.34679	2	5.57E-08	0.97	5.24	-	1490.3
AHQ-5-6, 7160	K.VPSTETEALASNLMGMFEK.R	2056.34679	2	5.81E-06	0.98	5.69	-	1668.3
gi|7657124|ref|NP_055165.1| TNF-induced protein [Homo sapiens]				5.62E-08	0.96	10.26	10.50	22047.4
AHQ-5-12, 7056 - 7120	K.SIATTLIDDTSSEVLDELYR.V	2242.42274	2	5.62E-08	0.96	5.20	-	1124.1
gi|4502687|ref|NP_003865.1| CD84 antigen (leukocyte antigen); leukocyte antigen CD84 [Homo sapiens]				5.67E-08	0.96	10.22	4.90	36870.6
AHQ-5-7, 4570	R.IHALGPNYNLVISDLR.M	1796.06296	2	5.67E-08	0.96	4.33	-	1320.5
gi|4505329|ref|NP_003818.1| N-ethylmaleimide-sensitive factor attachment protein, alpha; alpha-SNAP				5.73E-08	2.16	30.27	14.20	33246.6
AHQ-5-9, 4583	K.AALCHFCIDMLNAK.L	1666.96721	2	7.65E-08	0.96	4.91	-	1267.8
AHQ-5-9, 3631	K.HDAATCFVDAGNAFK.K	1625.74381	2	5.73E-08	0.98	5.36	-	3250.7
AHQ-5-9, 3984	K.VAGYAALLEQYQK.A	1454.65214	1	7.86E-05	0.22	2.20	-	600.4
gi|4506285|ref|NP_003470.1| protein tyrosine phosphatase type IVA, member 2 isoform 1; protein tyro				5.76E-08	0.88	10.16	8.40	19127.1
AHQ-5-11, 2854 - 2906	R.FLITHNPTNATLNK.F	1584.80104	2	5.76E-08	0.88	3.23	-	1150.8
gi|5729873|ref|NP_006656.1| heparanase; heparanase-1 [Homo sapiens]				5.83E-08	3.52	40.22	8.30	61176.4
AHQ-5-8, 7254	R.EDFLNPDVLDIFISSVQK.V	2080.32304	2	8.44E-05	0.93	4.33	-	744.7
AHQ-5-7, 7339 - 7340	R.EDFLNPDVLDIFISSVQK.V	2080.32304	2	4.38E-05	0.91	4.12	-	533.8
AHQ-5-9, 6520	R.EDFLNPDVLDIFISSVQK.V	2080.32304	2	1.07E-05	0.90	4.33	-	607.1
AHQ-5-7, 7244	R.TATREDFLNPDVLDIFISSVQK.V	2509.79627	2	2.90E-05	0.83	3.11	-	630.4
AHQ-5-14-, 4897	K.TDFLIFDPK.K	1096.25713	1	1.49E-04	0.35	2.31	-	374.9
AHQ-5-14-, 4910	K.TDFLIFDPK.K	1096.25713	2	7.85E-06	0.85	2.53	-	1129.5
AHQ-5-7, 3363	K.YLLRPLGPHGLLSK.S	1564.89924	2	5.83E-08	0.94	3.60	-	1263.7
gi|5031573|ref|NP_005712.1| ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye				5.85E-08	7.87	90.26	33.50	47370.9
AHQ-5-9, 4411	R.AEPEDHYFLLTEPPLNTPENR.E	2483.67423	2	1.62E-04	0.66	3.37	-	494.0
AHQ-5-7, 4731	R.AEPEDHYFLLTEPPLNTPENR.E	2483.67423	2	6.50E-05	0.81	3.57	-	447.7
AHQ-5-8, 7266	R.DITYFIQQLLR.D	1410.64250	2	1.26E-05	0.93	3.97	-	1145.8
AHQ-5-9, 6531	R.DITYFIQQLLR.D	1410.64250	1	3.48E-04	0.07	2.01	-	182.2
AHQ-5-8, 2700	R.DREVGIPPEQSLETAK.A	1769.93431	2	4.77E-04	0.95	4.97	-	954.7
AHQ-5-8, 6228 - 6296	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	1.85E-05	0.92	4.74	-	698.6
AHQ-5-10, 5684	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	5.53E-05	0.86	4.09	-	447.2
AHQ-5-9, 5523	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	1.67E-04	0.47	3.10	-	267.3
AHQ-5-12, 6156	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	4.60E-04	0.59	3.02	-	322.9
AHQ-5-7, 6127 - 6136	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	3.79E-04	0.85	4.26	-	460.6
AHQ-5-8, 2272	R.LKPKPIDVQVITHHMQR.Y	2041.45264	2	1.03E-05	0.94	4.30	-	1056.0
AHQ-5-13-, 3677	R.LPACVVDCGTGYTK.L	1543.74421	2	1.88E-07	0.93	3.93	-	1004.9
AHQ-5-13-, 4047	K.NIVLSGGSTMFR.D	1282.49463	2	5.85E-08	0.89	3.09	-	1199.4
AHQ-5-8, 6341 - 6360	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	2.65E-04	0.94	5.28	-	784.2
AHQ-5-7, 6518 - 6563	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	2.82E-05	0.92	4.61	-	1025.6
AHQ-5-9, 5860	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	3.74E-05	0.90	4.53	-	792.4
AHQ-5-9, 3363	R.YSYVCPDLVK.E	1245.42618	1	1.13E-06	0.57	2.55	-	601.4
gi|11321601|ref|NP_002618.1| phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom				5.91E-08	5.74	60.33	13.40	85595.6
AHQ-5-5, 3521	K.AIGVLTSGGDAQGMNAAVR.A	1789.00750	2	5.91E-08	0.98	6.58	-	2211.7
AHQ-5-6, 3193	R.DLQSNVEHLTEK.M	1413.51529	2	4.20E-06	0.89	3.93	-	877.3
AHQ-5-5, 3249	R.DLQSNVEHLTEK.M	1413.51529	2	3.67E-06	0.91	3.38	-	1131.7
AHQ-5-5, 6109	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	7.57E-06	0.96	4.80	-	1255.1
AHQ-5-6, 6021 - 6025	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	1.18E-05	0.89	4.17	-	553.3
AHQ-5-7, 5894 - 5932	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	3.45E-05	0.71	3.34	-	466.9
AHQ-5-5, 6529	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	1.78E-07	0.95	5.11	-	806.9
AHQ-5-13, 6270	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	7.79E-06	0.92	4.36	-	718.3
AHQ-5-5, 4902	R.LPLMECVQMTQDVQK.A	1822.16087	2	8.71E-06	0.97	4.68	-	2211.1
AHQ-5-5, 3313	K.NVLGHMQQGGAPSPFDR.N	1812.00285	2	1.66E-06	0.95	4.03	-	1644.3
gi|4502985|ref|NP_001854.1| cytochrome c oxidase subunit VIb; human cytochrome oxidase subunit VIb				5.92E-08	0.97	10.25	20.90	10192.3
AHQ-5-14-, 6107	R.VYQSLCPTSWVTDWDEQR.A	2272.43560	2	5.92E-08	0.97	5.03	-	1493.6
gi|17986283|ref|NP_006000.2| tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu				6.10E-08	0.95	10.26	3.30	50135.3
AHQ-5-2, 5959	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.12E-04	0.83	3.56	-	736.9
AHQ-5-3, 6047	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.27E-06	0.93	4.72	-	755.1
AHQ-5-4, 5980	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.67E-04	0.89	4.22	-	668.7
AHQ-5-7, 5524 - 5594	R.AVFVDLEPTVIDEVR.T	1702.92947	2	6.10E-08	0.95	5.14	-	1066.7
AHQ-5-11, 5523 - 5535	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.33E-06	0.83	4.36	-	466.6
AHQ-5-12, 5705	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.37E-04	0.89	4.16	-	701.2
AHQ-5-13, 5708	R.AVFVDLEPTVIDEVR.T	1702.92947	2	2.38E-05	0.90	4.55	-	561.6
AHQ-5-13-, 5603	R.AVFVDLEPTVIDEVR.T	1702.92947	2	5.07E-05	0.93	4.04	-	1012.0
AHQ-5-14-, 5585 - 5590	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.48E-05	0.94	4.68	-	987.6
gi|7706675|ref|NP_057661.1| RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M				6.21E-08	2.76	30.26	16.30	23461.5
AHQ-5-11, 4612	R.GSDVIIMLVGNK.T	1246.50220	2	3.09E-07	0.94	3.99	-	1522.3
AHQ-5-14-, 3421	R.LQLWDTAGQER.F	1317.43243	2	6.21E-08	0.89	3.41	-	846.9
AHQ-5-11, 3310	R.LQLWDTAGQER.F	1317.43243	1	7.37E-04	0.13	2.20	-	233.6
AHQ-5-12, 3318 - 3390	R.LQLWDTAGQER.F	1317.43243	2	1.37E-05	0.78	2.78	-	720.5
AHQ-5-13-, 3377 - 3453	R.LQLWDTAGQER.F	1317.43243	2	4.40E-05	0.89	3.31	-	883.6
AHQ-5-14-, 3349 - 3425	R.LQLWDTAGQER.F	1317.43243	2	1.21E-04	0.86	3.26	-	857.4
AHQ-5-10, 3088 - 3148	R.LQLWDTAGQER.F	1317.43243	2	3.55E-06	0.89	3.23	-	906.5
AHQ-5-11, 3504 - 3526	K.LVFLGEQSVGK.T	1177.37492	2	2.45E-06	0.93	3.54	-	1363.6
gi|4557361|ref|NP_001187.1| BH3 interacting domain death agonist; BH3-interacting domain death agon				6.34E-08	1.88	20.24	21.00	21994.6
AHQ-5-11, 6138 - 6174	R.ELDALGHELPVLAPQWEGYDELQTDGNR.S	3167.38790	3	6.34E-08	0.94	4.88	-	1109.1
AHQ-5-11, 2682	R.IEADSESQEDIIR.N	1505.56635	2	2.13E-04	0.95	3.19	-	2147.4
gi|12408675|ref|NP_036526.2| prefoldin 2 [Homo sapiens]				6.38E-08	0.83	10.17	7.80	16647.7
AHQ-5-12, 3702	K.IIETLTQQLQAK.G	1386.61925	2	6.38E-08	0.83	3.31	-	848.7
gi|6912238|ref|NP_036226.1| peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]				6.38E-08	6.32	70.22	44.90	22026.2
AHQ-5-12, 6948 - 7033	K.ETDLLLDDSLVSIFGNR.R	1908.09888	2	1.05E-04	0.91	3.89	-	855.3
AHQ-5-12, 3861 - 3938	R.FSMVVQDGIVK.A	1223.46709	2	1.07E-06	0.96	4.10	-	1562.6

AHQ-5-12, 4666 - 4680	K.KGVLFGVPGAFTPGCSK.T	1724.01680	2	5.74E-07	0.94	4.44	-	842.4
AHQ-5-12, 3406	R.LLADPTGAFGK.E	1090.25413	1	9.46E-04	0.08	1.85	-	181.5
AHQ-5-12, 3402 - 3422	R.LLADPTGAFGK.E	1090.25413	2	1.47E-05	0.89	3.72	-	606.8
AHQ-5-12, 4177 - 4232	K.THLPGFVEQAEALK.A	1540.74504	2	6.38E-08	0.93	4.08	-	494.4
AHQ-5-12, 4908 - 4982	K.VGDAIPAVEVFEGEPGNK.V	1829.00022	2	7.36E-05	0.91	4.15	-	517.7
AHQ-5-12, 4777 - 4844	K.VGDAIPAVEVFEGEPGNK.V	1829.00022	2	1.01E-06	0.86	4.20	-	369.6
AHQ-5-12, 6909	K.VGDAIPAVEVFEGEPGNKVNLAELFK.G	2744.09176	2	1.09E-07	0.84	3.27	-	508.5
gi|9966825|ref|NP_065089.1| HEF like Protein [Homo sapiens]				6.39E-08	1.87	20.31	4.30	86696.2
AHQ-5-13, 4241	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	3	2.06E-04	0.91	4.26	-	999.7
AHQ-5-13, 4245	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	2.60E-04	0.98	6.20	-	1669.3
AHQ-5-13-, 4165	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	7.46E-04	0.97	5.71	-	1469.8
AHQ-5-13-, 3428	K.LVDTLCMETQER.D	1496.68930	2	6.39E-08	0.96	4.64	-	1148.9
AHQ-5-13, 3559 - 3571	K.LVDTLCMETQER.D	1496.68930	2	2.92E-05	0.89	2.66	-	923.8
gi|4757768|ref|NP_004300.1| Rho GDP dissociation inhibitor (GDI) alpha [Homo sapiens]				6.59E-08	2.75	30.23	15.70	23206.9
AHQ-5-12, 4632	R.AEEYEFLTPVEEAPK.G	1752.89898	2	1.42E-05	0.85	3.34	-	805.5
AHQ-5-10, 4170	R.AEEYEFLTPVEEAPK.G	1752.89898	2	1.01E-06	0.91	3.88	-	813.3
AHQ-5-14-, 4586	R.AEEYEFLTPVEEAPK.G	1752.89898	2	6.59E-08	0.88	3.99	-	744.3
AHQ-5-10, 3503	K.SIQEIQELDKDDESLR.K	1919.03693	2	4.56E-06	0.94	3.87	-	1223.9
AHQ-5-10, 3476 - 3534	K.SIQEIQELDKDDESLR.K	1919.03693	2	1.10E-05	0.95	4.42	-	1445.8
AHQ-5-10, 3090	K.SIQEIQELDKDDESLRK.Y	2047.20984	2	1.58E-05	0.93	4.65	-	810.2
gi|4757786|ref|NP_004306.1| N-acylsphingosine amidohydrolase (acid ceramidase) 1; N-acylsphingosine				6.62E-08	2.17	30.24	14.20	44649.3
AHQ-5-14-, 6234 - 6295	R.GAVPWYTINLDLPPYK.R	1848.13310	2	8.28E-04	0.73	3.38	-	475.7
AHQ-5-14-, 6407 - 6422	K.LPGLLGNFPGPFEEEMK.G	1876.16512	2	6.62E-08	0.96	4.78	-	1273.5
AHQ-5-9, 5674	R.TSQENISFETMYDVLSTKPVLNK.L	2645.96676	2	4.67E-05	0.48	2.90	-	368.0
gi|4503477|ref|NP_001950.1| eukaryotic translation elongation factor 1 beta 2; eukaryotic translati				6.73E-08	1.73	20.22	14.70	24763.6
AHQ-5-9, 4732	K.SPAGLQVLNDYLADK.S	1604.78589	2	6.61E-07	0.92	4.40	-	762.5
AHQ-5-9, 4050	K.SPAGLQVLNDYLADK.S	1604.78589	2	6.45E-06	0.74	3.33	-	375.5
AHQ-5-9, 4484	K.SSILLDVKPWDDETDMAK.L	2064.30228	2	6.73E-08	0.81	3.62	-	427.0
gi|4504515|ref|NP_002146.1| heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B				7.01E-08	5.85	70.23	12.60	70853.4
AHQ-5-6, 4884 - 4890	R.ARFEELCSDLFR.S	1544.71384	2	5.85E-07	0.95	4.14	-	1160.7
AHQ-5-6, 2244 - 2246	K.ATAGDTHLGGEDFDNR.L	1676.68279	2	8.68E-07	0.97	4.66	-	1499.6
AHQ-5-6, 4778	R.IINEPTAAAIAYGLDR.R	1688.90603	2	1.82E-07	0.91	3.87	-	967.5
AHQ-5-6, 4284 - 4393	K.LLQDFFNGK.E	1082.23369	1	5.17E-04	0.28	2.38	-	310.0
AHQ-5-6, 4236 - 4309	K.LLQDFFNGKELNK.S	1566.78249	2	8.79E-08	0.94	4.24	-	1352.2
AHQ-5-13-, 3435 - 3436	R.TTPSYVAFTDTER.L	1488.58062	2	7.01E-08	0.90	2.94	-	1133.8
AHQ-5-6, 2050	R.VEILANDQGNR.T	1229.32518	2	2.34E-06	0.90	3.32	-	1157.7
AHQ-5-6, 2021 - 2088	R.VEILANDQGNR.T	1229.32518	1	3.70E-04	0.37	2.05	-	358.3
gi|24234688|ref|NP_004125.3| heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre				7.06E-08	2.58	30.19	6.20	73680.1
AHQ-5-6, 5586	R.AQFEGIVTDLIR.R	1362.55625	2	9.34E-08	0.95	3.74	-	1577.1
AHQ-5-6, 6037	K.STNGDTFLGGEDFDQALLR.H	2057.16328	2	7.06E-08	0.79	3.40	-	450.4
AHQ-5-6, 3497	K.VQQTVQDLFGR.A	1291.43811	2	1.95E-04	0.84	3.12	-	1042.6
gi|5729980|ref|NP_006547.1| phosphomevalonate kinase [Homo sapiens]				7.28E-08	1.81	20.20	15.10	21994.8
AHQ-5-11, 5282	K.IVEGISQPIWLVSDTR.R	1814.07506	2	7.28E-08	0.91	3.97	-	650.9
AHQ-5-11, 6632	R.LEEQLENLIEFIR.S	1646.86592	2	4.21E-05	0.90	3.81	-	1051.6
gi|24308263|ref|NP_067045.1| TcD37 homolog; prune [Homo sapiens]				7.55E-08	0.96	10.24	3.80	50199.3
AHQ-5-7, 7458	K.LLPLLQEALSAYFDSMK.I	1940.29226	2	7.55E-08	0.96	4.78	-	1243.9
gi|4507143|ref|NP_003786.1| sorting nexin 3 isoform a; sorting nexin 3A [Homo sapiens]				7.68E-08	0.96	10.22	8.60	18762.2
AHQ-5-12, 5057 - 5058	R.GDDGIFDDNFIEER.K	1642.66158	2	7.68E-08	0.96	4.35	-	1159.0
gi|4506417|ref|NP_002877.1| RAP2B, member of RAS oncogene family [Homo sapiens]				7.87E-08	3.31	40.19	23.00	20494.2
AHQ-5-11, 6070	K.ASVDELFAEIVR.Q	1349.51434	2	2.03E-04	0.91	3.73	-	1207.6
AHQ-5-11, 3051	R.VPMILVGNK.V	971.24256	2	5.01E-06	0.89	2.83	-	873.8
AHQ-5-11, 2291	K.VVVLGSGGVGK.S	972.16391	2	4.64E-04	0.86	3.23	-	890.5
AHQ-5-11, 2286	K.VVVLGSGGVGK.S	972.16391	1	3.02E-04	0.73	2.39	-	803.2
AHQ-5-11, 4140	K.YDPTIEDFYR.K	1319.40042	2	7.87E-08	0.78	2.88	-	335.8
gi|4504073|ref|NP_000398.1| glycoprotein Ib beta polypeptide precursor [Homo sapiens]				8.32E-08	2.68	30.20	15.50	21717.6
AHQ-5-1, 4932	R.LLPYLAEDELR.A	1332.52691	2	3.11E-06	0.82	3.10	-	482.1
AHQ-5-3, 4901 - 4913	R.LLPYLAEDELR.A	1332.52691	2	8.32E-08	0.83	2.82	-	578.0
AHQ-5-6, 4565	R.LLPYLAEDELR.A	1332.52691	2	6.47E-07	0.78	2.62	-	542.4
AHQ-5-7, 4366	R.LLPYLAEDELR.A	1332.52691	2	1.78E-04	0.82	2.99	-	471.6
AHQ-5-8, 4213	R.LLPYLAEDELR.A	1332.52691	2	3.82E-04	0.82	3.21	-	360.8
AHQ-5-13, 4721	R.LLPYLAEDELR.A	1332.52691	2	5.88E-06	0.84	3.22	-	612.8
AHQ-5-11, 4479 - 4499	R.LLPYLAEDELR.A	1332.52691	2	4.18E-06	0.84	2.91	-	479.1
AHQ-5-10, 4150 - 4210	R.LLPYLAEDELR.A	1332.52691	2	2.34E-05	0.75	3.12	-	388.8
AHQ-5-10, 4159	R.LLPYLAEDELR.A	1332.52691	1	9.82E-06	0.47	2.77	-	235.8
AHQ-5-13-, 4631 - 4632	R.LLPYLAEDELR.A	1332.52691	2	2.52E-07	0.90	3.48	-	735.2
AHQ-5-10, 3882 - 3883	R.LSLTDPLVAER.A	1214.39356	2	1.05E-06	0.92	3.81	-	1057.4
AHQ-5-11, 4142 - 4156	R.LSLTDPLVAER.A	1214.39356	2	2.77E-06	0.96	3.94	-	1389.3
AHQ-5-10, 2103	R.TAHLGANPWR.C	1123.24913	2	9.42E-04	0.78	3.07	-	476.4
AHQ-5-11, 2207	R.TAHLGANPWR.C	1123.24913	2	7.33E-07	0.92	3.55	-	946.2
gi|4758984|ref|NP_004654.1| RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho				8.36E-08	5.32	60.30	22.70	24393.3
AHQ-5-11, 2686 - 2767	K.AQIWDTAGQER.Y	1275.35241	2	4.88E-04	0.94	3.38	-	1403.2
AHQ-5-12, 2741	K.AQIWDTAGQER.Y	1275.35241	2	1.11E-06	0.95	3.95	-	1423.4
AHQ-5-11, 4092 - 4115	R.DHADSNIVIM*LVGNK.S	1642.85914	2	3.11E-04	0.98	4.90	-	2391.6
AHQ-5-11, 4715 - 4778	R.DHADSNIVIMLVGNK.S	1626.85974	2	1.09E-06	0.97	4.51	-	1944.6
AHQ-5-11, 4922 - 4982	R.GAVGALLVYDIAK.H	1290.53317	2	8.36E-08	0.98	6.00	-	2197.5
AHQ-5-13-, 5112	R.GAVGALLVYDIAK.H	1290.53317	2	8.97E-08	0.89	2.93	-	1209.9
AHQ-5-11, 1934	K.HLTYENVER.W	1161.24931	1	7.69E-04	0.55	2.16	-	531.4
AHQ-5-11, 2984	K.STIGVEFATR.S	1081.20410	2	4.80E-06	0.88	2.72	-	832.6
gi|4885281|ref|NP_005262.1| glutamate dehydrogenase 1 [Homo sapiens]				8.55E-08	1.36	20.21	6.60	61397.5
AHQ-5-7, 3596 - 3598	K.HGGTIPIVPTAEFQDR.I	1738.92514	2	8.55E-08	0.92	4.23	-	550.2
AHQ-5-7, 4156	K.IIAEGANGPTTPEADKIFLER.N	2243.50193	2	3.53E-04	0.44	2.76	-	339.4
gi|29729950|ref|XP_293759.1| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				8.66E-08	0.94	10.21	5.00	39776.4
AHQ-5-5, 4887	K.CLELFTELAEDKENYKK.F	2132.37640	2	8.66E-08	0.94	4.28	-	1135.5
gi|5031985|ref|NP_005787.1| nuclear transport factor 2; placental protein 15 [Homo sapiens]				8.89E-08	4.49	50.28	63.00	14478.4
AHQ-5-14-, 5689	K.ADEDPIM*GFHQMFLLK.N	1909.21859	2	6.70E-04	0.75	3.58	-	453.1
AHQ-5-14-, 5421	K.IQHSITAQDHQPTPDSCIISM*VVGQLK.A	3022.40358	3	5.85E-04	0.95	5.42	-	1284.8
AHQ-5-14-, 5981 - 5997	K.IQHSITAQDHQPTPDSCIISMVVGQLK.A	3006.40418	3	8.56E-07	0.96	5.25	-	1740.9
AHQ-5-14, 6140 - 6197	K.IQHSITAQDHQPTPDSCIISM*VVGQLK.A	3022.40358	3	8.89E-08	0.96	5.50	-	1652.6
AHQ-5-14-, 5278	K.NINDAWVCTNDMFR.L	1757.92888	2	1.42E-04	0.93	4.13	-	885.7
AHQ-5-14-, 6309	R.TQLGAIYIDASCLTWEGQQFQGK.A	2616.88699	2	7.93E-06	0.88	3.51	-	1011.3
gi|4557703|ref|NP_000414.1| keratin 2a [Homo sapiens]				9.38E-08	3.69	40.28	12.40	65864.9
AHQ-5-1, 7081 - 7084	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	6.47E-05	0.94	5.56	-	1131.5
AHQ-5-14-, 2937	R.FLEQQNQVLQTK.W	1476.65935	2	9.08E-05	0.97	4.51	-	2202.7
AHQ-5-4, 2998	R.FLEQQNQVLQTK.W	1476.65935	2	7.24E-05	0.94	3.94	-	1428.0
AHQ-5-6, 2825	R.FLEQQNQVLQTK.W	1476.65935	2	9.38E-08	0.92	3.94	-	903.7
AHQ-5-1, 3073 - 3148	R.FLEQQNQVLQTK.W	1476.65935	2	9.23E-07	0.97	3.99	-	2433.1
AHQ-5-14-, 5939	R.NLDLDSIIAEVK.A	1330.50933	2	9.15E-06	0.95	3.82	-	1302.8
AHQ-5-1, 6264	K.VDLLNQEIEFLK.V	1461.68459	2	6.54E-07	0.89	3.77	-	861.8
gi|4826848|ref|NP_004991.1| NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5; NADH dehydrogena				9.69E-08	0.98	10.39	22.40	13458.6
AHQ-5-14-, 6713	K.KLEDQLQGGQLEEVILQAEHELNLAR.K	2975.30339	3	9.69E-08	0.98	7.76	-	2745.8
gi|6912494|ref|NP_036457.1| microtubule-associated protein, RP/EB family, member 1; ADENOMATOUS POL				9.99E-08	3.80	40.27	21.60	29998.9
AHQ-5-12, 3980	K.FFDANYDGKDYDPVAAR.Q	1965.06754	2	9.99E-08	0.92	4.53	-	527.1
AHQ-5-12, 6592	K.FQDNFEFVQWFK.K	1635.80184	2	1.53E-05	0.97	4.98	-	1368.2
AHQ-5-13-, 3260	K.LTVEDLEKER.D	1232.36575	2	1.01E-06	0.95	3.76	-	1375.5
AHQ-5-13-, 4428	R.NIELICQENEGENDPVLQR.I	2272.43545	2	2.97E-05	0.97	5.34	-	1361.2
AHQ-5-13, 4509	R.NIELICQENEGENDPVLQR.I	2272.43545	2	3.24E-04	0.97	5.33	-	1600.9
gi|4502643|ref|NP_001753.1| chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing				1.02E-07	1.83	20.26	7.00	58023.9

AHQ-5-6, 4718	K.DGNVLLHEMQIQHPTASLIAK.V	2316.66592	3	1.02E-07	0.95	5.29	-	966.0
AHQ-5-6, 4582	K.VLAQNSGFDLQETLVK.I	1762.98491	2	2.39E-06	0.88	3.63	-	804.7
gi|11496885|ref|NP_005442.2| enigma protein; LIM domain protein [Homo sapiens]				1.02E-07	1.54	20.21	9.40	49844.4
AHQ-5-14-, 6135	K.AAQAGVAVGDWVLSIDGENAGSLTHIEAQNK.I	3123.37980	3	7.66E-04	0.65	3.14	-	454.3
AHQ-5-13-, 4824	K.VVLEGPAPWGFR.L	1328.54318	2	1.19E-06	0.89	3.55	-	790.7
AHQ-5-13, 4910	K.VVLEGPAPWGFR.L	1328.54318	2	1.02E-07	0.89	3.57	-	845.3
AHQ-5-11, 4622 - 4684	K.VVLEGPAPWGFR.L	1328.54318	2	7.22E-04	0.81	3.13	-	644.5
gi|5453549|ref|NP_006397.1| thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho				1.06E-07	1.88	20.22	13.70	30539.7
AHQ-5-10, 3423	K.DYGVYLEDSGHTLR.G	1625.72052	2	1.06E-07	0.95	3.99	-	1113.7
AHQ-5-10, 3790	K.HGEVCPAGWKPGSETIIPDPAGK.L	2405.67144	3	2.88E-05	0.93	4.38	-	1267.4
gi|6857820|ref|NP_005019.2| phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl				1.07E-07	2.78	30.24	11.30	46224.3
AHQ-5-7, 4462	R.FGIDDQDFQNSLTR.S	1656.73462	2	3.07E-07	0.87	3.69	-	932.6
AHQ-5-7, 4311	R.FGIDDQDFQNSLTR.S	1656.73462	2	5.38E-07	0.66	3.04	-	666.2
AHQ-5-7, 2470	K.HGAGAEISTVNPEQYSK.R	1788.89618	2	1.07E-07	0.96	4.88	-	1434.0
AHQ-5-7, 3930	K.TITSEDVAEMHNILK.K	1701.92338	2	4.86E-07	0.95	4.42	-	1202.8
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				1.10E-07	2.44	30.23	25.40	22006.2
AHQ-5-10, 6575 - 6578	K.DQFPEVYVPTVFENYIADIEVDGK.Q	2789.04149	2	2.09E-06	0.91	4.57	-	436.7
AHQ-5-10, 4163	K.HFCPNVPIILVGNK.K	1609.91693	2	1.10E-07	0.97	4.53	-	1712.8
AHQ-5-10, 2508 - 2510	K.LVIVGDGACGK.T	1090.27572	1	6.33E-05	0.55	2.21	-	578.4
gi|4502297|ref|NP_001678.1| ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit				1.12E-07	1.44	20.18	13.70	17489.8
AHQ-5-13, 2679	K.AQAELVGTADEATR.A	1432.51860	2	1.36E-06	0.92	3.68	-	941.5
AHQ-5-13, 2683	K.AQAELVGTADEATR.A	1432.51860	1	3.84E-04	0.16	2.29	-	217.4
AHQ-5-13, 2691	K.AQAELVGTADEATR.A	1432.51860	1	1.20E-06	0.52	3.00	-	168.5
AHQ-5-13-, 2548	K.AQAELVGTADEATR.A	1432.51860	1	1.12E-07	0.71	3.28	-	244.3
AHQ-5-13, 2471	R.IEANEALVK.A	987.13221	2	2.99E-04	0.74	2.83	-	563.8
gi|4506025|ref|NP_000936.1| protein phosphatase 3, regulatory subunit B, alpha isoform 1; protein p				1.17E-07	0.81	10.15	9.40	19299.8
AHQ-5-12, 5534	R.VIDIFDTDGNGEVDFK.E	1784.90107	2	1.17E-07	0.81	2.96	-	612.8
gi|4557469|ref|NP_001273.1| adaptor-related protein complex 2, beta 1 subunit; adaptin, beta 2 (bet				1.21E-07	1.81	20.24	4.10	104551.9
AHQ-5-6, 6161	R.CVSTLLDLIQTK.V	1392.64385	2	7.71E-04	0.86	2.68	-	1290.3
AHQ-5-6, 7182	K.KPSETQELVQQVLSLATQDSDNPDLR.D	2913.14409	3	1.21E-07	0.95	4.72	-	1662.7
gi|22027651|ref|NP_001118.2| adaptor-related protein complex 1 beta 1 subunit isoform a; beta-adapt				1.21E-07	0.95	10.28	2.70	104636.1
AHQ-5-6, 7189	K.KPTETQELVQQVLSLATQDSDNPDLR.D	2927.17076	2	6.05E-04	0.90	3.37	-	1084.2
AHQ-5-6, 7188	K.KPTETQELVQQVLSLATQDSDNPDLR.D	2927.17076	3	1.21E-07	0.95	5.62	-	979.1
gi|4503545|ref|NP_001961.1| eukaryotic translation initiation factor 5A; eIF5AI; eIF5A [Homo sapien				1.22E-07	1.75	20.20	26.00	16832.2
AHQ-5-12, 3966	R.EDLRLPEGDLGKEIEQK.Y	1970.17021	2	1.89E-05	0.82	4.10	-	343.9
AHQ-5-12, 6965	R.NDFQLIGIQDGYLSLLQDSGEVR.E	2581.81935	2	1.22E-07	0.93	4.08	-	1209.9
gi|29727565|ref|XP_291384.1| similar to Cytochrome c, somatic [Homo sapiens]				1.25E-07	0.97	10.25	16.20	11621.4
AHQ-5-14-, 6282	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	1.87E-04	0.96	4.98	-	1316.7
AHQ-5-13, 6454 - 6533	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	1.25E-07	0.97	4.84	-	1794.6
gi|22059949|ref|XP_114617.2| similar to tubulin, beta 5 [Homo sapiens]				1.30E-07	1.87	20.32	18.80	22810.8
AHQ-5-11, 5134 - 5139	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	2.06E-05	0.95	6.04	-	1082.9
AHQ-5-13-, 5265	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	4.44E-05	0.95	5.89	-	966.2
AHQ-5-7, 5363	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	5.30E-04	0.88	4.49	-	880.2
AHQ-5-14-, 5186 - 5253	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	7.97E-07	0.97	6.31	-	1381.6
AHQ-5-12, 2700	R.ISVYYNEATGGK.Y	1302.41453	2	1.99E-05	0.68	2.60	-	545.9
AHQ-5-13, 2886	R.ISVYYNEATGGK.Y	1302.41453	2	7.26E-06	0.64	2.77	-	493.6
AHQ-5-7, 2454	R.ISVYYNEATGGK.Y	1302.41453	1	2.07E-05	0.67	3.05	-	397.4
AHQ-5-7, 2447	R.ISVYYNEATGGK.Y	1302.41453	2	1.30E-07	0.90	2.83	-	1147.0
AHQ-5-11, 2644 - 2652	R.ISVYYNEATGGK.Y	1302.41453	1	3.00E-04	0.14	2.00	-	275.2
gi|7705849|ref|NP_057215.1| ras-related GTP-binding protein RAB10; ras-related GTP-binding protein				1.32E-07	1.80	20.23	15.00	22540.8
AHQ-5-11, 6236 - 6239	K.AFLTLAEDILR.K	1262.47982	1	4.54E-04	0.11	2.14	-	232.6
AHQ-5-14-, 6318	K.AFLTLAEDILR.K	1262.47982	2	1.32E-07	0.95	4.29	-	1691.7
AHQ-5-13, 6513	K.AFLTLAEDILR.K	1262.47982	2	1.36E-06	0.94	4.03	-	1303.1
AHQ-5-11, 6235 - 6259	K.AFLTLAEDILR.K	1262.47982	2	4.58E-07	0.96	4.62	-	1447.3
AHQ-5-11, 6931	R.FSDDAFNTTFISTIGIDFK.I	2140.33380	2	1.66E-05	0.85	3.76	-	951.6
gi|20149594|ref|NP_031381.2| heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea				1.45E-07	5.20	60.22	11.00	83263.6
AHQ-5-5, 2353	K.EDQTEYLEER.R	1312.32145	2	4.42E-04	0.66	2.60	-	417.3
AHQ-5-5, 2978	R.ELISNASDALDK.I	1276.37539	2	1.32E-06	0.87	3.48	-	788.2
AHQ-5-5, 3414 - 3418	K.HLEINPDHPIVETLR.Q	1784.00905	3	2.53E-05	0.93	3.79	-	1337.1
AHQ-5-5, 5447	K.HSQFIGYPITLYLEK.E	1810.08487	2	2.86E-04	0.91	3.94	-	752.7
AHQ-5-5, 4105	R.NPDDITQEEYGEFYK.S	1848.90048	2	3.60E-05	0.95	4.43	-	1161.5
AHQ-5-5, 3778 - 3794	K.SLTNDWEDHLAVK.H	1528.64798	2	1.45E-07	0.88	3.12	-	1229.2
gi|18570595|ref|XP_095590.1| similar to myosin regulatory light chain [Homo sapiens]				1.49E-07	0.94	10.19	8.90	13951.5
AHQ-5-11, 3044 - 3110	K.LNGTDPEDVIR.H	1229.32195	2	1.54E-05	0.90	3.64	-	859.7
AHQ-5-12, 3125	K.LNGTDPEDVIR.H	1229.32195	2	1.49E-07	0.94	3.51	-	1321.0
AHQ-5-11, 2946	K.LNGTDPEDVIR.H	1229.32195	2	7.92E-05	0.93	3.72	-	1071.0
gi|6041669|ref|NP_004538.2| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd				1.56E-07	0.88	10.18	14.00	15208.5
AHQ-5-13-, 4791	R.TLPETLDPAEYNISPETR.R	2047.20831	2	1.56E-07	0.88	3.57	-	604.9
AHQ-5-13, 4877	R.TLPETLDPAEYNISPETR.R	2047.20831	2	4.69E-06	0.83	3.45	-	515.4
gi|17450333|ref|XP_060887.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				1.74E-07	0.87	10.21	11.00	17503.9
AHQ-5-12, 6688 - 6717	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	4.30E-07	0.95	4.28	-	1331.5
AHQ-5-13-, 6616	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	7.86E-05	0.90	3.94	-	917.4
AHQ-5-12, 6473 - 6552	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	1.74E-07	0.87	3.26	-	869.6
gi|20127517|ref|NP_009148.2| programmed cell death 10; apoptosis-related protein 15 [Homo sapiens]				1.87E-07	0.71	10.17	11.30	24701.4
AHQ-5-10, 4988	R.MAADDVEEYMIERPEPEFQDLNEK.A	2900.14441	2	1.87E-07	0.71	3.42	-	375.4
gi|7656952|ref|NP_055227.1| calcyclin binding protein [Homo sapiens]				1.88E-07	1.82	20.24	19.30	26209.8
AHQ-5-10, 3862	K.KAELLDNEKPAAVVAPITTGYTVK.I	2529.91377	3	3.33E-04	0.95	4.70	-	1569.9
AHQ-5-10, 5518 - 5522	K.SYSMIVNNLLKPISVEGSSK.K	2167.51201	2	7.56E-05	0.77	3.63	-	340.7
AHQ-5-10, 4654	K.SYSMIVNNLLKPISVEGSSK.K	2167.51201	2	1.88E-07	0.87	3.48	-	620.6
gi|5453597|ref|NP_006126.1| F-actin capping protein alpha-1 subunit; Cap Z [Homo sapiens]				1.89E-07	1.82	20.25	12.60	32922.5
AHQ-5-13-, 2823	K.DVQDSLTVSNEAQTAK.E	1706.79025	2	1.33E-06	0.97	4.94	-	1158.2
AHQ-5-9, 4790 - 4855	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	1.89E-07	0.86	4.16	-	549.0
gi|13128974|ref|NP_076933.1| hypothetical protein MGC3265 [Homo sapiens]				1.90E-07	0.96	10.23	4.50	46867.3
AHQ-5-7, 2712	K.ANVIHATVTSVTLHSTEGK.A	1966.18479	2	1.90E-07	0.96	4.69	-	1266.0
gi|9910280|ref|NP_064505.1| UDP-glucose ceramide glucosyltransferase-like 1; UDP-glucose:glycoprote				1.93E-07	1.72	20.23	2.60	177187.7
AHQ-5-3, 7039	R.AVYLGELPHDQDVVEYIMNQPNVVPR.I	2997.37416	2	1.93E-07	0.94	4.68	-	1006.9
AHQ-5-3, 4630	K.LNIQPSEADYAVDIR.S	1704.86232	2	1.78E-04	0.78	3.43	-	402.7
gi|5031973|ref|NP_005733.1| protein disulfide isomerase-related protein [Homo sapiens]				2.02E-07	3.68	50.25	18.90	48121.0
AHQ-5-7, 7319 - 7320	R.ALDLFSDNAPPPELLEIINEDIAK.R	2638.95072	2	7.74E-06	0.86	3.96	-	342.3
AHQ-5-7, 4538	K.GSFSEQGINEFLR.E	1484.59520	1	4.14E-07	0.02	2.17	-	57.3
AHQ-5-7, 4522	K.GSFSEQGINEFLR.E	1484.59520	2	8.25E-04	0.86	3.26	-	911.1
AHQ-5-12, 3942 - 4021	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	8.18E-04	0.69	2.61	-	706.5
AHQ-5-7, 3738 - 3739	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	5.86E-04	0.86	3.83	-	663.3
AHQ-5-7, 4568 - 4574	K.LAAVDATVNQVLASR.Y	1528.73579	2	5.73E-06	0.97	4.98	-	1710.5
AHQ-5-7, 6035	R.TGEAIVDAALSALR.Q	1387.56411	2	2.02E-07	0.97	4.45	-	2182.9
gi|4504071|ref|NP_000164.1| platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA				2.02E-07	4.50	50.23	9.40	68955.0
AHQ-5-3, 5087 - 5107	R.GLGELQELYLK.G	1263.46458	2	4.48E-05	0.96	4.70	-	1481.9
AHQ-5-12, 4013 - 4016	R.GQDLLSTVSIR.Y	1189.34410	2	3.21E-07	0.95	3.82	-	1367.3
AHQ-5-3, 4182	R.GQDLLSTVSIR.Y	1189.34410	2	1.40E-05	0.96	4.24	-	1343.6
AHQ-5-13-, 4076	R.GQDLLSTVSIR.Y	1189.34410	2	2.77E-05	0.91	3.85	-	906.4
AHQ-5-1, 4275	R.GQDLLSTVSIR.Y	1189.34410	2	1.62E-05	0.95	4.01	-	1395.0
AHQ-5-4, 4124 - 4134	R.GQDLLSTVSIR.Y	1189.34410	2	5.07E-06	0.96	4.23	-	1390.9
AHQ-5-14-, 3945	R.GQDLLSTVSIR.Y	1189.34410	2	2.02E-07	0.95	3.35	-	1670.5
AHQ-5-3, 1957 - 1962	R.GVLQGHLESSR.N	1183.29965	2	1.69E-05	0.87	3.18	-	815.9
AHQ-5-4, 1970	R.GVLQGHLESSR.N	1183.29965	2	1.85E-06	0.90	3.28	-	1102.5
AHQ-5-3, 3617	R.LTQLNLDRCELTK.L	1605.83862	2	2.66E-05	0.81	3.30	-	813.4
AHQ-5-4, 3606 - 3609	R.LTQLNLDRCELTK.L	1605.83862	2	9.27E-04	0.92	3.92	-	980.4

AHQ-5-4, 4974	R.WLQDNAENVYVWK.Q	1665.82948	2	3.49E-05	0.88	3.20	-	1279.5
gi|16950601|ref|NP_005956.2| myosin light chain kinase isoform 6; myosin light chain kinase [Homo s				2.05E-07	3.04	40.18	5.70	110074.8
AHQ-5-5, 5606	K.IEGYPDPEVVWFK.D	1579.77650	2	5.84E-05	0.86	2.59	-	651.4
AHQ-5-6, 3448	K.LVQCVDAFEEK.A	1339.49637	2	3.22E-05	0.93	3.22	-	1234.2
AHQ-5-5, 3519	K.SSLPPVLGTESDATVK.K	1601.78032	2	5.78E-07	0.47	2.68	-	241.1
AHQ-5-5, 4919 - 4935	R.STSFNVQDLLPDHEYK.F	1894.03076	2	2.05E-07	0.79	3.55	-	484.8
gi|5453605|ref|NP_006421.1| chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-				2.08E-07	1.90	20.24	4.80	57838.8
AHQ-5-7, 6438	R.DALSDLALHFLNK.M	1457.65603	2	2.52E-07	0.97	4.82	-	2135.5
AHQ-5-7, 3334	K.VIDPATATSVDLR.D	1358.52277	2	2.08E-07	0.92	3.56	-	985.5
gi|22042381|ref|XP_065237.3| similar to FKSG30 [Homo sapiens]				2.19E-07	1.37	20.18	0.00	42016.0
AHQ-5-14-, 2825 - 2889	K.QEYDESGPSIVHR.K	1517.58206	2	2.48E-05	0.57	2.99	-	697.7
AHQ-5-14-, 2333	K.QEYDESGPSIVHR.K	1517.58206	2	2.37E-07	0.74	2.93	-	398.0
AHQ-5-13, 2550	K.QEYDESGPSIVHR.K	1517.58206	2	2.19E-07	0.64	2.74	-	333.0
AHQ-5-13-, 2389 - 2411	K.QEYDESGPSIVHR.K	1517.58206	2	6.22E-06	0.83	3.57	-	439.1
AHQ-5-8, 2024 - 2088	K.QEYDESGPSIVHR.K	1517.58206	2	4.05E-04	0.53	2.80	-	273.0
AHQ-5-9, 3231 - 3291	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	1.61E-05	0.72	3.35	-	454.7
AHQ-5-8, 3112 - 3181	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	4.22E-04	0.72	3.69	-	282.0
gi|5453710|ref|NP_006139.1| LIM and SH3 protein 1; Lasp-1 [Homo sapiens]				2.23E-07	0.91	10.18	5.00	29717.0
AHQ-5-13-, 3951	K.GFSVVADTPELQR.I	1419.56466	2	4.66E-04	0.76	2.77	-	650.1
AHQ-5-12, 3913	K.GFSVVADTPELQR.I	1419.56466	2	2.23E-07	0.91	3.53	-	1238.2
gi|14043026|ref|NP_003752.2| vesicle-associated membrane protein 8; endobrevin [Homo sapiens]				2.30E-07	1.74	20.23	24.00	11438.2
AHQ-5-13-, 2491	R.NKTEDLEATSEHFK.T	1649.74039	3	2.30E-07	0.96	4.63	-	1868.7
AHQ-5-13-, 2493	R.NKTEDLEATSEHFK.T	1649.74039	2	4.31E-05	0.91	3.41	-	1122.6
AHQ-5-13, 2985 - 2990	R.NLQSEVEGVK.N	1103.20807	2	5.08E-04	0.78	2.91	-	846.9
gi|4502167|ref|NP_000475.1| amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disea				2.38E-07	0.92	10.20	2.10	86942.8
AHQ-5-4, 2316	K.YLETPGDENEHAHFQK.A	1915.99652	2	2.38E-07	0.92	3.96	-	739.6
gi|5032041|ref|NP_005605.1| Ras homolog enriched in brain 2 [Homo sapiens]				2.42E-07	0.82	10.23	8.70	20497.4
AHQ-5-12, 5225	K.ALAESWNAAFLESSAK.E	1695.85389	2	2.42E-07	0.82	3.44	-	470.6
AHQ-5-12, 4984 - 5010	K.ALAESWNAAFLESSAK.E	1695.85389	2	2.87E-06	0.96	4.62	-	1236.4
gi|4506183|ref|NP_002779.1| proteasome alpha 3 subunit isoform 1; proteasome subunit C8; macropain				2.43E-07	0.69	10.13	3.90	28433.1
AHQ-5-10, 2552	K.IIYIVHDEVK.D	1229.44983	1	2.43E-07	0.69	2.57	-	567.2
gi|10880989|ref|NP_067075.1| RAB18, member RAS oncogene family; RAB18 small GTPase [Homo sapiens] [				2.49E-07	3.20	40.22	26.70	22976.9
AHQ-5-11, 3634	K.IIQTPGLWESENQNK.G	1757.92522	2	3.74E-06	0.73	3.14	-	396.8
AHQ-5-11, 3419	K.LAIWDTAGQER.F	1260.38088	2	3.76E-05	0.83	2.87	-	862.2
AHQ-5-11, 6170	K.LDNWLNELETYCTR.N	1828.98037	2	2.49E-07	0.95	4.34	-	1033.6
AHQ-5-11, 5782 - 5795	K.TCDGVQCAFEELVEK.I	1787.94661	2	3.09E-04	0.69	3.35	-	534.8
gi|30147623|ref|XP_293669.2| similar to actinin, alpha 4 [Homo sapiens]				2.49E-07	0.88	10.21	3.50	57794.4
AHQ-5-5, 3935 - 4005	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	2.49E-07	0.88	4.13	-	625.1
gi|27597085|ref|NP_000357.3| tropomyosin 1 (alpha) [Homo sapiens]				2.51E-07	1.92	20.27	9.50	32865.7
AHQ-5-9, 2722 - 2723	R.AQKDEEKMEIQEIQLK.E	1961.22673	2	2.51E-07	0.96	5.30	-	1419.1
AHQ-5-9, 2832	R.KLVIIESDLER.A	1315.54103	2	8.05E-07	0.96	4.61	-	1310.3
AHQ-5-9, 2815 - 2819	R.KLVIIESDLER.A	1315.54103	1	3.83E-05	0.73	3.10	-	436.3
gi|7657313|ref|NP_055277.1| Lsm1 protein [Homo sapiens]				2.64E-07	1.62	20.19	26.30	15179.3
AHQ-5-12, 6021	K.ESDTPLQQVSIEEILEEQR.V	2244.39872	2	2.64E-07	0.92	3.73	-	932.5
AHQ-5-12, 5914	R.SIDQFANLVLHQTVER.I	1871.08670	2	1.80E-04	0.70	3.20	-	441.4
gi|20551618|ref|XP_167021.1| similar to calponin 2; Calonin 2 [Homo sapiens]				2.74E-07	1.83	20.28	3.70	47327.9
AHQ-5-11, 5470	R.SMQNWHQLENLSNFIK.A	1990.23155	2	1.17E-04	0.95	4.61	-	1187.6
AHQ-5-12, 5288 - 5290	R.SM*QNWHQLENLSNFIK.A	2006.23095	2	2.74E-07	0.92	4.18	-	771.5
AHQ-5-12, 5406	R.SMQNWHQLENLSNFIK.A	1990.23155	2	2.91E-05	0.94	4.18	-	1190.9
AHQ-5-12, 5648 - 5661	R.SMQNWHQLENLSNFIK.A	1990.23155	2	1.32E-06	0.97	5.55	-	1565.0
AHQ-5-12, 5654	R.SMQNWHQLENLSNFIK.A	1990.23155	3	3.35E-04	0.90	4.26	-	1008.8
AHQ-5-10, 5066 - 5067	R.SMQNWHQLENLSNFIK.A	1990.23155	2	7.62E-07	0.91	4.12	-	747.2
gi|21614499|ref|NP_003370.2| villin 2; Villin-2; cytovillin [Homo sapiens]				2.80E-07	2.60	30.21	3.40	69412.3
AHQ-5-6, 4165	K.APDFVFYAPR.L	1183.33971	2	2.80E-07	0.97	4.15	-	1686.2
AHQ-5-6, 4984	K.IGFPWSEIR.N	1105.27049	2	8.53E-06	0.90	2.73	-	982.0
AHQ-5-7, 4770	K.IGFPWSEIR.N	1105.27049	2	2.10E-06	0.83	2.83	-	732.2
AHQ-5-6, 3468	K.KAPDFVFYAPR.L	1311.51262	2	1.35E-06	0.80	3.07	-	625.3
gi|4757766|ref|NP_004299.1| Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa				2.96E-07	3.52	40.24	16.60	50435.4
AHQ-5-14-, 5923	K.FLLDHQGELFPSPDPSGL	1970.17037	2	2.26E-06	0.80	3.12	-	709.1
AHQ-5-8, 3702	K.NPEQEPIPIVLR.E	1405.62426	2	1.84E-04	0.86	3.39	-	720.9
AHQ-5-7, 3823	K.NPEQEPIPIVLR.E	1405.62426	2	9.16E-05	0.89	3.80	-	940.3
AHQ-5-8, 5980 - 5994	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	5.50E-06	0.88	4.30	-	461.6
AHQ-5-11, 5956	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	2.96E-07	0.95	4.79	-	855.2
AHQ-5-7, 7128	K.YNMGLPVDFDQYNELHLPAVILK.T	2691.09719	3	1.82E-05	0.61	3.25	-	235.9
AHQ-5-7, 7120 - 7127	K.YNMGLPVDFDQYNELHLPAVILK.T	2691.09719	2	8.67E-06	0.88	3.61	-	822.6
gi|4506405|ref|NP_002872.1| v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP				2.98E-07	1.93	20.26	15.50	23408.4
AHQ-5-10, 3290	R.SKAEEWGVQYVETSAK.T	1812.95765	2	2.98E-07	0.97	4.72	-	1523.6
AHQ-5-10, 3124 - 3182	R.VKAEEDKIPLLVVGNK.S	1753.07630	2	1.15E-04	0.96	5.21	-	1189.7
gi|13569962|ref|NP_112243.1| RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap				3.03E-07	3.43	40.33	26.40	22171.0
AHQ-5-11, 4387 - 4451	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	3.03E-07	0.98	6.54	-	2369.8
AHQ-5-11, 4551	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	3	5.40E-05	0.77	3.40	-	846.1
AHQ-5-11, 4714	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	8.04E-06	0.96	5.09	-	1117.7
AHQ-5-11, 2008 - 2028	R.MGPGAASGGERPNLK.I	1442.62650	3	2.50E-06	0.81	3.24	-	822.9
AHQ-5-11, 6396 - 6466	K.NATNVEQAFMTM*AAEIK.K	1886.14019	2	3.79E-04	0.68	3.65	-	617.0
AHQ-5-11, 6551	K.NATNVEQAFMTMAAEIK.K	1870.14079	2	8.97E-07	0.95	4.45	-	1167.6
AHQ-5-11, 6558	K.NATNVEQAFMTMAAEIK.K	1870.14079	3	2.84E-06	0.95	5.69	-	1184.5
AHQ-5-11, 5071 - 5143	K.NATNVEQAFMTM*AAEIK.K	1886.14019	2	4.53E-04	0.79	3.58	-	853.2
gi|30158852|ref|XP_301583.1| similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa				3.08E-07	0.90	10.17	6.50	19197.0
AHQ-5-4, 2768 - 2841	K.IWHHTFYNKLR.V	1515.74533	2	5.70E-06	0.71	3.16	-	602.0
AHQ-5-8, 2401	K.IWHHTFYNKLR.V	1515.74533	2	3.08E-07	0.90	3.23	-	912.5
AHQ-5-11, 2778 - 2859	K.IWHHTFYNKLR.V	1515.74533	2	1.16E-05	0.44	2.60	-	482.9
AHQ-5-13, 3153	K.IWHHTFYNKLR.V	1515.74533	2	5.00E-06	0.67	3.02	-	683.6
AHQ-5-2, 2798	K.IWHHTFYNKLR.V	1515.74533	2	2.13E-05	0.73	3.36	-	752.4
gi|5031569|ref|NP_005727.1| ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r				3.09E-07	2.54	30.22	15.20	42613.4
AHQ-5-8, 3608	R.ACYLSINPQKDETLETEK.A	2141.34169	2	4.71E-05	0.75	3.27	-	415.4
AHQ-5-8, 5044 - 5061	K.AQYYLPDGSTIEIGPSR.F	1868.03645	2	3.66E-04	0.92	4.50	-	545.2
AHQ-5-8, 4934	K.DQLQTFSEEHPVLLTEAPLNPR.K	2535.79382	2	3.09E-07	0.87	3.63	-	601.6
gi|20539300|ref|XP_088391.4| similar to tropomyosin 4 [Homo sapiens]				3.21E-07	1.91	30.24	16.90	18592.1
AHQ-5-9, 2868	R.AMKDEEKMEIQEMQLK.E	1982.33285	2	2.88E-06	0.96	4.87	-	1261.8
AHQ-5-9, 3030	R.KLVILEGELER.A	1299.54160	1	9.70E-04	0.21	2.50	-	253.2
AHQ-5-9, 3120	R.KLVILEGELER.A	1299.54160	2	3.25E-04	0.80	2.89	-	884.1
AHQ-5-11, 3487	R.KLVILEGELER.A	1299.54160	2	3.21E-07	0.85	3.40	-	932.7
AHQ-5-9, 3007 - 3124	R.KLVILEGELER.A	1299.54160	1	2.85E-04	0.58	2.57	-	510.8
AHQ-5-9, 3700 - 3708	K.LVILEGELER.A	1171.36868	1	7.72E-05	0.10	1.84	-	210.7
gi|4506671|ref|NP_000995.1| ribosomal protein P2; 60S acidic ribosomal protein P2; acidic ribosomal				3.37E-07	0.88	10.23	28.70	11664.9
AHQ-5-13-, 3744	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK.K	2776.05225	2	3.96E-06	0.86	4.19	-	461.4
AHQ-5-13, 3830	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK.K	2776.05225	2	3.37E-07	0.88	4.63	-	354.4
gi|4503743|ref|NP_002009.1| flightless I homolog [Homo sapiens]				3.64E-07	3.36	40.25	5.70	144750.1
AHQ-5-3, 3177 - 3181	K.AVQGAQQPSLYQIR.T	1559.75158	2	3.64E-07	0.86	3.44	-	653.3
AHQ-5-3, 6547	R.TGLCYLPEELAALQK.L	1707.96931	2	2.57E-04	0.85	3.63	-	426.9
AHQ-5-3, 7294	R.TQSNLPTSLEGLSNLADVDLSCNDLTR.V	2936.15611	2	1.85E-06	0.70	3.08	-	676.8
AHQ-5-4, 6810	K.VGLGLGYLELPQINYK.L	1778.08432	2	1.98E-04	0.95	4.35	-	993.3
gi|27480842|ref|XP_208238.1| similar to bA92K2.2 (similar to ubiquitin) [Homo sapiens]				3.78E-07	0.74	10.13	5.80	17966.9
AHQ-5-14-, 2774 - 2850	K.ESTLHLVLR.L	1068.25169	2	2.69E-06	0.80	2.68	-	443.3
AHQ-5-14, 3872	K.ESTLHLVLR.L	1068.25169	2	3.78E-07	0.74	2.60	-	447.9
gi|17318569|ref|NP_006112.2| keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]				3.78E-07	1.85	20.23	4.30	66066.3
AHQ-5-14-, 5943	R.SLDLDSIIAEVK.A	1303.48388	2	2.25E-06	0.94	4.33	-	1191.7

AHQ-5-1, 6439	R.SLDLDSIIAEVK.A	1303.48388	2	7.82E-07	0.95	4.52	-	1373.0
AHQ-5-14-, 6303	R.THNLEPYFESFINNLR.R	1995.18315	3	3.78E-07	0.90	4.33	-	1240.4
gi|10835189|ref|NP_000628.1| glutathione reductase [Homo sapiens]				3.89E-07	2.46	30.22	10.90	51700.3
AHQ-5-7, 4547 - 4550	K.ADFDNTVAIHPTSSEELVTLR	2316.50977	2	3.89E-07	0.86	4.23	-	365.8
AHQ-5-7, 2272	R.GHAAFTSDPKPTIEVSGK.K	1843.03012	2	5.39E-06	0.92	4.41	-	486.8
AHQ-5-7, 3132 - 3203	K.LGGTCVNVGCVPK.K	1363.58589	2	6.99E-04	0.68	2.69	-	947.0
gi|18104989|ref|NP_002822.2| protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t				4.14E-07	0.89	10.17	2.00	67560.7
AHQ-5-6, 5000 - 5010	R.DLSGLDAETLLK.G	1275.43053	2	4.14E-07	0.89	3.19	-	1276.2
gi|4505813|ref|NP_003737.1| cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain				4.15E-07	2.24	30.19	49.40	10365.8
AHQ-5-14, 4802 - 4805	K.NADMSEEM*QQDSVECATQALEK.Y	2532.67934	2	4.43E-06	0.64	3.80	-	578.9
AHQ-5-14-, 2289	R.NFGSYVTHETK.H	1283.37131	2	2.51E-06	0.93	3.48	-	1033.3
AHQ-5-14-, 3510	K.YNPTWHCIVGR.N	1404.57820	2	5.12E-05	0.74	3.00	-	378.9
AHQ-5-14, 4416 - 4430	K.YNPTWHCIVGR.N	1404.57820	2	4.15E-07	0.68	2.55	-	474.5
gi|4502861|ref|NP_001275.1| adaptor-related protein complex 3, sigma 1 subunit; clathrin-associated				4.19E-07	0.91	10.18	7.80	21732.0
AHQ-5-11, 3807	K.FYQPYSEDTQQQIIR.E	1917.06756	2	4.19E-07	0.91	3.53	-	761.6
gi|10863873|ref|NP_000651.1| transforming growth factor, beta 1 (Camurati-Engelmann disease); trans				4.23E-07	2.68	30.21	5.90	44422.0
AHQ-5-13, 3446	R.ALDTNYCFSSTEK.N	1537.63010	2	4.23E-07	0.88	3.54	-	740.7
AHQ-5-13-, 3319	R.ALDTNYCFSSTEK.N	1537.63010	2	2.40E-06	0.90	3.35	-	804.0
AHQ-5-13-, 2653	K.VEQLSNM*IVR.S	1205.41014	2	3.49E-04	0.82	3.15	-	872.2
AHQ-5-13, 3590 - 3591	K.VEQLSNMIVR.S	1189.41074	2	1.65E-05	0.95	4.12	-	1463.4
AHQ-5-13-, 3468 - 3472	K.VEQLSNMIVR.S	1189.41074	2	9.61E-06	0.92	3.71	-	1203.2
AHQ-5-13, 2714 - 2793	K.VEQLSNM*IVR.S	1205.41014	2	1.62E-04	0.87	3.54	-	852.3
gi|6005826|ref|NP_009160.1| protein kinase C and casein kinase substrate in neurons 2; pacsin 2 [Ho				4.66E-07	1.56	20.18	4.50	55904.6
AHQ-5-6, 2946	K.AIYHDLEQSIR.A	1345.48578	2	1.50E-04	0.61	2.55	-	591.8
AHQ-5-6, 3785	K.AYAQQLTEWAR.R	1337.46534	2	4.66E-07	0.95	3.53	-	1820.4
gi|28178825|ref|NP_005887.2| isocitrate dehydrogenase 1 (NADP+), soluble; oxalosuccinate decarboxyl				4.87E-07	0.89	10.20	4.10	46659.0
AHQ-5-8, 6481 - 6560	K.GQETSTNPIASIFAWTR.G	1880.05046	2	4.87E-07	0.89	4.06	-	610.4
gi|17149842|ref|NP_004461.2| FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep				4.87E-07	2.37	30.20	18.30	15649.2
AHQ-5-13, 5038	K.GWDQGLLGMCEGEK.R	1581.75275	2	6.90E-04	0.75	3.03	-	721.3
AHQ-5-13-, 4144	K.GWDQGLLGM*CEGEK.R	1597.75215	2	5.33E-04	0.76	2.68	-	812.4
AHQ-5-13-, 4937 - 4940	K.GWDQGLLGMCEGEK.R	1581.75275	2	1.99E-04	0.94	3.90	-	1110.1
AHQ-5-13, 4172 - 4252	K.GWDQGLLGM*CEGEK.R	1597.75215	2	2.06E-06	0.56	2.56	-	612.9
AHQ-5-13-, 4163	K.LVIPSELGYGER.G	1333.51491	2	4.87E-07	0.88	3.26	-	537.5
gi|4502211|ref|NP_001654.1| ADP-ribosylation factor 6 [Homo sapiens]				4.88E-07	0.98	20.19	18.30	20082.0
AHQ-5-12, 4036	K.FNVWDVGGQDK.I	1265.35598	1	4.88E-07	0.15	2.06	-	556.2
AHQ-5-12, 4033	K.FNVWDVGGQDK.I	1265.35598	2	4.02E-06	0.94	3.73	-	1215.8
AHQ-5-12, 5544 - 5609	K.LGQSVTTIPTVGFNVETVTYK.N	2255.55261	2	3.61E-04	0.83	3.82	-	216.7
gi|21264318|ref|NP_004028.3| adenosine monophosphate deaminase 2 (isoform L) [Homo sapiens]				4.98E-07	1.71	20.23	3.50	100687.2
AHQ-5-5, 6057 - 6063	K.CGVPFTDLLDAAK.S	1408.60184	2	5.74E-07	0.78	2.71	-	562.0
AHQ-5-5, 5513 - 5530	R.SAPYEFPEESPIEQLEER.R	2151.27185	2	4.98E-07	0.93	4.51	-	759.9
gi|24111250|ref|NP_006563.2| guanine nucleotide binding protein (G protein), alpha 13 [Homo sapiens				5.08E-07	0.80	10.19	4.50	44049.3
AHQ-5-8, 4816	K.LGEPDYIPSQQDILLAR.R	1929.16292	2	5.08E-07	0.80	3.84	-	390.8
gi|5729804|ref|NP_006694.1| nudix (nucleoside diphosphate linked moiety X)-type motif 3; diphosphoi				5.08E-07	2.40	30.25	21.50	19470.8
AHQ-5-11, 3648	K.VLQYHKPVQASYFETLR.Q	2080.37433	2	5.08E-07	0.94	4.90	-	513.1
AHQ-5-11, 4808 - 4811	R.WIVPGGGMEPEEEPSVAAVR.E	2111.36386	2	3.90E-06	0.84	3.50	-	479.0
AHQ-5-11, 4368	R.WIVPGGGM*EPEEEPSVAAVR.E	2127.36326	2	6.90E-05	0.62	2.94	-	338.9
gi|20070156|ref|NP_003565.2| vessicle-associated membrane protein (VAMP)-associated protein of 33 k				5.55E-07	0.95	10.18	5.00	27317.4
AHQ-5-12, 4076	K.GPFTDVVTTNLK.L	1292.46278	2	5.55E-07	0.95	3.53	-	1604.0
gi|4758442|ref|NP_004115.1| glia maturation factor, beta [Homo sapiens]				5.66E-07	1.06	20.21	19.00	16713.1
AHQ-5-12, 6562	R.VSYPLCFIFSSPVGCKPEQQMM*YAGSK.N	3131.61197	3	2.50E-04	0.37	3.10	-	312.6
AHQ-5-12, 6430 - 6494	R.VSYPLCFIFSSPVGCKPEQQM*MYAGSK.N	3131.61197	3	5.66E-07	0.69	4.16	-	538.3
gi|4826665|ref|NP_005116.1| copper chaperone for superoxide dismutase [Homo sapiens]				5.71E-07	0.90	10.21	10.20	29040.4
AHQ-5-9, 5882 - 5883	K.GMGSGQLQNLGAAVAILGGPGTVQGVVR.F	2609.00248	2	5.71E-07	0.90	4.26	-	707.7
gi|5031595|ref|NP_005709.1| actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub				5.88E-07	7.21	80.35	59.50	19666.9
AHQ-5-11, 4198	R.AENFFILR.R	1010.17070	2	4.72E-04	0.96	3.57	-	1943.1
AHQ-5-12, 4322	R.AENFFILR.R	1010.17070	2	1.19E-04	0.95	3.84	-	1652.9
AHQ-5-11, 6160 - 6219	R.ATLQAALCLENFSSQVVER.H	2138.38741	2	3.31E-06	0.91	4.12	-	861.6
AHQ-5-11, 4134	K.ELLLQPVTISR.N	1269.51549	2	2.71E-04	0.87	3.25	-	736.3
AHQ-5-12, 3408 - 3416	R.IVAEEFLK.N	949.12558	2	3.34E-04	0.68	2.78	-	380.4
AHQ-5-11, 5871 - 5887	R.KPVEGYDISFLITNFHTEQMYK.H	2662.01271	3	6.29E-06	0.97	6.97	-	1285.1
AHQ-5-12, 7126	K.LVDFVIHFMEEIDKEISEM*K.L	2469.85893	3	5.88E-07	0.94	5.26	-	919.4
AHQ-5-11, 5499 - 5503	R.RKPVEGYDISFLITNFHTEQMYK.H	2818.19906	3	4.63E-06	0.98	6.92	-	2070.0
AHQ-5-12, 3101	K.VLIEGSINSVR.V	1187.37134	2	3.23E-04	0.92	3.46	-	1089.6
AHQ-5-12, 3189	K.VLIEGSINSVR.V	1187.37134	2	9.84E-06	0.91	3.68	-	830.9
gi|18426915|ref|NP_004386.2| drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [				5.90E-07	3.02	40.23	11.40	71438.9
AHQ-5-8, 3625	K.KSESEVEEAAAIIAQRPDNPR.E	2311.49476	3	1.08E-06	0.70	3.22	-	460.3
AHQ-5-13, 4060 - 4120	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	2.50E-05	0.73	3.26	-	559.1
AHQ-5-13, 4129	K.LAASGEGGLQELSGHFENQK.V	2073.20908	3	2.10E-05	0.60	3.07	-	558.9
AHQ-5-13-, 4028 - 4041	K.LAASGEGGLQELSGHFENQK.V	2073.20908	3	2.70E-04	0.78	3.95	-	409.0
AHQ-5-13-, 3975 - 4039	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	3.09E-04	0.85	4.04	-	640.8
AHQ-5-8, 2481	R.SPSDSSTASTPVAEQIER.A	1862.93023	2	1.18E-05	0.74	3.27	-	436.7
AHQ-5-13-, 5524	K.YVLINWVGEDVPDAR.K	1746.94404	2	1.06E-04	0.95	4.65	-	1249.8
AHQ-5-13, 5628	K.YVLINWVGEDVPDAR.K	1746.94404	2	5.90E-07	0.97	4.57	-	1984.5
gi|4826657|ref|NP_004333.1| caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]				6.06E-07	5.38	60.24	18.80	62662.9
AHQ-5-6, 4961	K.EFDPTITDASLSLPSR.R	1749.89986	2	1.11E-04	0.85	3.50	-	745.2
AHQ-5-13-, 2605	K.GNVFSSPTAAGTPNK.E	1448.56286	2	6.06E-07	0.92	4.01	-	918.0
AHQ-5-13-, 4575 - 4656	K.KGFTEVKSQNGEFMTHKLK.H	2210.54181	3	4.08E-06	0.83	4.18	-	1113.8
AHQ-5-13, 2947	R.LEQYTSAIEGTK.S	1340.46107	2	6.42E-06	0.90	3.04	-	1218.7
AHQ-5-13, 2897 - 2898	K.SAKPTKPAASDLPVPAEGVR.N	1992.26539	2	1.09E-05	0.95	4.88	-	758.8
AHQ-5-6, 3633	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	2.76E-06	0.93	4.31	-	976.6
gi|4885183|ref|NP_005210.1| diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS				6.20E-07	4.65	50.26	7.10	138977.7
AHQ-5-3, 3207 - 3210	R.DVQNFPAATDEKDKFVEK.M	2082.25588	2	7.72E-04	0.87	3.94	-	567.0
AHQ-5-3, 2267	K.LQDLQGEKDALHSEK.Q	1711.85486	2	6.25E-07	0.93	4.18	-	1089.1
AHQ-5-3, 6726	K.LQFSEQVENIKPEIVSVTAACEELR.K	2892.23121	3	6.20E-07	0.94	5.19	-	1246.5
AHQ-5-4, 5341	K.LVAEDLSQDCFWTK.V	1713.88927	2	4.18E-04	0.61	2.54	-	573.5
AHQ-5-3, 5361 - 5366	K.LVAEDLSQDCFWTK.V	1713.88927	2	3.70E-06	0.96	4.83	-	1103.1
AHQ-5-3, 5959	K.QDLEAEVSQLTGEVAK.L	1717.85617	2	5.18E-06	0.95	5.01	-	1007.3
gi|23110925|ref|NP_002789.1| proteasome beta 6 subunit; proteasome subunit Y; proteasome subunit be				6.48E-07	0.97	10.21	4.60	25357.6
AHQ-5-11, 2362	R.LAAIAESGVER.Q	1116.24998	2	6.48E-07	0.97	4.29	-	1725.2
gi|29731325|ref|XP_293023.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				7.04E-07	0.66	10.15	6.00	28867.8
AHQ-5-13, 4201	K.AGPNTNGSQFFICTAK.T	1714.88050	2	3.82E-06	0.71	2.86	-	559.7
AHQ-5-12, 4116	K.AGPNTNGSQFFICTAK.T	1714.88050	2	7.04E-07	0.66	2.73	-	582.3
gi|6912586|ref|NP_036220.1| 6-phosphogluconolactonase [Homo sapiens]				7.13E-07	1.43	20.20	14.00	27546.7
AHQ-5-10, 3859	R.ILEDQEENPLPAALVQPHTGK.L	2300.55348	2	7.13E-07	0.88	4.01	-	614.3
AHQ-5-10, 3846	R.LVPFDHAESTYGLYR.T	1768.94970	2	2.31E-06	0.55	2.54	-	253.0
gi|4506045|ref|NP_002718.1| proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p				7.35E-07	1.53	20.19	17.10	17623.6
AHQ-5-1, 2452	R.CNPDSNSANCLEEK.G	1640.68887	2	1.97E-06	0.67	2.95	-	423.4
AHQ-5-1, 4176 - 4195	K.GPM*FELLPGESNK.I	1435.62747	2	7.35E-07	0.86	3.88	-	630.3
gi|8922835|ref|NP_060776.1| hypothetical protein FLJ11036 [Homo sapiens]				7.37E-07	0.94	10.21	6.90	22353.4
AHQ-5-13, 6068 - 6134	R.IHSVLQGFIPLFQK.F	1627.95380	2	7.37E-07	0.94	4.23	-	963.8
gi|7657056|ref|NP_055415.1| EH-domain containing 3; EH domain containing 3 [Homo sapiens]				7.51E-07	3.34	40.24	12.90	60886.7
AHQ-5-7, 5411	R.FHEFHSPALEDADFDNKPMVLLVGQYSTGK.T	3394.75749	3	2.84E-06	0.91	4.56	-	876.1
AHQ-5-7, 4754	K.LFEAEEQDLFR.D	1397.51432	2	7.51E-07	0.96	3.37	-	2328.3
AHQ-5-7, 5866	R.VYIGSFWSHPLLIPDNR.K	2015.30234	2	2.59E-06	0.92	4.80	-	559.0
AHQ-5-10, 5507	R.VYIGSFWSHPLLIPDNR.K	2015.30234	2	2.20E-06	0.59	2.84	-	513.2
AHQ-5-7, 4516	R.YLLEQDFPGMR.I	1369.57075	2	4.84E-05	0.87	2.94	-	1221.6
gi|4557675|ref|NP_000201.1| integrin alpha chain, alpha 6 [Homo sapiens]				7.78E-07	2.61	30.26	4.50	119509.5

AHQ-5-6, 3208 - 3222	K.FGSCQQGVAATFTK.D	1503.66172	2	4.46E-04	0.66	2.75	-	538.4
AHQ-5-4, 3432	K.FGSCQQGVAATFTK.D	1503.66172	2	7.78E-07	0.84	3.26	-	706.4
AHQ-5-3, 3467	K.FGSCQQGVAATFTK.D	1503.66172	2	2.95E-04	0.71	2.62	-	707.1
AHQ-5-4, 2877	K.LETTSNQDNLAPITAK.A	1716.87141	2	3.10E-05	0.80	3.46	-	566.8
AHQ-5-4, 4272 - 4280	K.LRPIPITASVEIQEPSSR.R	1994.28128	2	1.00E-05	0.97	5.28	-	1345.1
AHQ-5-3, 4343 - 4410	K.LRPIPITASVEIQEPSSR.R	1994.28128	2	6.74E-05	0.87	4.04	-	655.0
gi|19923437|ref|NP_057366.2|	adenylate kinase 3 alpha like [Homo sapiens]			7.80E-07	0.94	10.21	6.20	25565.2
AHQ-5-10, 6074	K.NLTQYSWLLDGFPR.T	1710.91339	2	7.80E-07	0.94	4.17	-	1326.2
gi|5902726|ref|NP_005800.1|	peroxiredoxin 2; thioredoxin-dependent peroxide reductase 1 (thiol-spec			7.82E-07	1.77	20.23	9.10	21856.8
AHQ-5-11, 6570	K.EGGLGPLNIPLLADVTR.R	1736.00583	2	7.82E-07	0.84	3.26	-	580.6
AHQ-5-11, 6007	R.KEGGLGPLNIPLLADVTR.R	1864.17875	2	6.71E-05	0.93	4.57	-	635.1
gi|18491024|ref|NP_005691.2|	dipeptidylpeptidase III isoform 1; dipeptidylpeptidase III [Homo sapie			7.86E-07	1.63	20.17	5.16	82588.6
AHQ-5-6, 7286 - 7357	R.FPEDGPELEEILTQLATADAR.F	2316.50654	2	3.39E-04	0.72	3.28	-	466.5
AHQ-5-6, 4581	K.LAQDFLDSQNLSAYNTR.L	1957.09009	2	7.86E-07	0.91	3.35	-	1093.1
gi|4502013|ref|NP_001616.1|	adenylate kinase 2 isoform a; adenylate kinase, mitochondrial; adenylat			7.86E-07	1.60	20.26	14.23	26477.6
AHQ-5-10, 3583	R.LQAYHTQTTPLIEYYR.K	1998.22695	2	2.63E-06	0.96	5.29	-	1176.2
AHQ-5-10, 5532	K.NLETPLCKNGFLLDGFPR.T	2093.39146	2	7.86E-07	0.64	3.13	-	336.4
gi|21361388|ref|NP_008868.2|	SMT3 suppressor of mif two 3 homolog 2; SMT3 (suppressor of mif two 3,			8.06E-07	0.76	10.15	12.63	10870.2
AHQ-5-12, 2552	K.VAGQDGSVVQFK.I	1235.37133	2	8.06E-07	0.76	3.05	-	758.7
gi|5803013|ref|NP_006808.1|	endoplasmic reticulum protein 29 precursor; endoplasmic reticulum lumen			8.07E-07	2.60	30.21	14.94	28993.2
AHQ-5-10, 6486	K.GQGVYLGM*PGCLPVYDALAGEFIR.A	2601.98207	2	8.07E-07	0.89	4.21	-	544.4
AHQ-5-10, 6538	K.GQGVYLGMPGCLPVYDALAGEFIR.A	2585.98267	2	5.75E-04	0.82	4.00	-	350.7
AHQ-5-10, 3660	K.ILDQGEDFPASEMTR.I	1709.85924	2	3.50E-04	0.89	3.53	-	796.1
gi|4758484|ref|NP_004823.1|	glutathione-S-transferase like; glutathione transferase omega [Homo sap			8.17E-07	2.80	50.17	34.02	27565.7
AHQ-5-10, 3635	K.EDPTVSALLTSEK.D	1390.51840	1	4.75E-05	0.31	2.32	-	253.5
AHQ-5-10, 2352	K.GSAPPGPVPEGSIR.I	1321.46422	1	3.52E-04	0.77	3.49	-	334.4
AHQ-5-10, 2502	R.HEVININLK.N	1080.26247	1	1.29E-04	0.71	2.82	-	532.5
AHQ-5-10, 2506	R.HEVININLK.N	1080.26247	2	8.17E-07	0.94	3.47	-	1152.3
AHQ-5-10, 2514	R.HEVININLK.N	1080.26247	1	1.16E-04	0.71	3.28	-	330.6
AHQ-5-9, 2416	R.HEVININLK.N	1080.26247	1	1.16E-04	0.66	3.20	-	314.6
AHQ-5-10, 6443	K.KNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKK.L	4074.56041	3	1.51E-04	0.65	3.49	-	374.2
AHQ-5-9, 3950	K.VPSLVGSFIR.S	1075.28583	1	6.60E-04	0.13	2.04	-	130.9
gi|4506243|ref|NP_002810.1|	polypyrimidine tract-binding protein 1 isoform a; RNA-binding protein;			8.19E-07	0.92	10.22	3.59	59632.7
AHQ-5-9, 5964	R.KLPIDVTEGEVISLGLPFGK.V	2113.48244	2	8.19E-07	0.92	4.42	-	812.4
gi|4503141|ref|NP_001805.1|	cathepsin C isoform a preproprotein; dipeptidyl-peptidase I; dipeptidyl			8.24E-07	0.97	10.23	4.10	51841.5
AHQ-5-14-, 5385 - 5387	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	8.24E-07	0.97	4.64	-	1635.7
AHQ-5-14, 6066 - 6068	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	7.53E-04	0.82	3.45	-	773.3
gi|11496277|ref|NP_068805.1|	mitogen-activated protein kinase kinase 1 interacting protein 1; MEK p			8.40E-07	1.76	20.24	35.48	13622.6
AHQ-5-14-, 5405	K.SIICYYNTYQVVQFNR.L	2070.31322	2	1.20E-05	0.91	3.65	-	1230.7
AHQ-5-14-, 5098 - 5162	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	1.88E-04	0.92	4.87	-	710.1
AHQ-5-14, 6144	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	8.40E-07	0.85	4.07	-	722.3
AHQ-5-14, 6026	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	1.36E-05	0.90	4.23	-	871.2
gi|29747201|ref|XP_290702.1|	similar to My016 protein [Homo sapiens]			8.81E-07	1.84	20.23	23.03	16932.3
AHQ-5-14-, 3445	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	5.11E-04	0.96	4.62	-	1281.9
AHQ-5-14, 4248	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	7.24E-05	0.94	3.44	-	1392.5
AHQ-5-14-, 5058 - 5133	R.LVNACLAEELPHIHAFEQK.T	2221.52124	3	8.81E-07	0.90	3.90	-	1083.4
gi|7705819|ref|NP_057181.1|	HSPC039 protein [Homo sapiens]			8.84E-07	0.92	10.18	24.39	8968.7
AHQ-5-14, 5840	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	8.84E-07	0.92	3.63	-	1116.1
gi|5174727|ref|NP_005989.1|	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring			8.91E-07	5.19	60.23	15.63	60330.4
AHQ-5-6, 3557	R.AVAQALEVIPR.T	1167.38326	2	4.79E-06	0.95	4.10	-	1638.4
AHQ-5-6, 3560	R.AVAQALEVIPR.T	1167.38326	1	3.39E-05	0.10	1.97	-	120.8
AHQ-5-6, 5117	K.ELGIWEPLAVK.L	1255.48728	2	3.25E-05	0.84	3.51	-	509.1
AHQ-5-6, 4373	K.IPGGIIEDSCVLR.G	1430.65218	2	8.91E-07	0.90	3.36	-	1105.8
AHQ-5-6, 2945	R.NLQDAMQVCR.N	1236.40442	2	2.79E-04	0.88	3.13	-	929.7
AHQ-5-6, 6245 - 6316	R.NVLLDPQLVPGGGASEMAVAHALTEK.S	2618.99091	3	1.36E-06	0.76	3.75	-	556.2
AHQ-5-6, 5425	R.WSSLACNIALDAVK.M	1549.77353	2	9.49E-05	0.86	3.31	-	894.2
gi|4502693|ref|NP_001760.1|	CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen			9.24E-07	2.54	30.25	21.05	25415.9
AHQ-5-11, 6807	K.AIHYALNCCGLAGGVEQFISDICPK.K	2798.16446	3	9.24E-07	0.74	3.74	-	527.3
AHQ-5-11, 6808	K.AIHYALNCCGLAGGVEQFISDICPK.K	2798.16446	2	1.71E-04	0.96	4.92	-	1344.1
AHQ-5-14-, 3127	K.KDVLETFTVK.S	1180.37558	2	3.16E-04	0.82	3.34	-	664.2
AHQ-5-11, 3146 - 3207	K.KDVLETFTVK.S	1180.37558	2	4.36E-04	0.91	3.10	-	1196.3
AHQ-5-10, 2979	K.KDVLETFTVK.S	1180.37558	2	1.80E-04	0.81	2.81	-	850.5
AHQ-5-12, 3208	K.KDVLETFTVK.S	1180.37558	2	9.86E-05	0.87	3.19	-	863.1
AHQ-5-8, 2765	K.KDVLETFTVK.S	1180.37558	2	7.00E-04	0.92	3.53	-	948.1
AHQ-5-11, 3678	K.SCPDAIKEVFDNK.F	1524.67770	2	4.86E-05	0.93	3.92	-	1101.5
gi|21536449|ref|NP_002613.2|	prefoldin 1; prefoldin subunit 1 [Homo sapiens]			9.29E-07	0.96	10.21	9.02	14210.4
AHQ-5-13-, 3803 - 3813	K.LADIQIEQLNR.T	1313.48523	2	9.29E-07	0.96	4.12	-	2132.0
AHQ-5-13, 3896	K.LADIQIEQLNR.T	1313.48523	2	7.54E-04	0.94	3.76	-	1607.7
gi|27478053|ref|XP_015334.4|	similar to heat shock 70kD protein binding protein; progesterone recep			9.32E-07	0.97	10.28	11.64	16603.8
AHQ-5-7, 4611	R.LLGHWEEAAHDLALACK.L	1936.18044	2	9.32E-07	0.97	5.61	-	1503.1
gi|11559923|ref|NP_071496.1|	eukaryotic translation initiation factor 4H isoform 1 [Homo sapiens] [			9.51E-07	0.76	10.18	8.47	27384.8
AHQ-5-10, 4375	R.TVATPLNQVANPNSAIFGGAR.P	2099.33604	2	9.51E-07	0.76	3.60	-	410.9
gi|30147105|ref|XP_210550.2|	similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48			9.81E-07	0.93	10.20	2.21	61339.9
AHQ-5-5, 4610	K.ADLINNLGTIAK.S	1243.43490	2	3.98E-04	0.87	3.27	-	679.0
AHQ-5-5, 4074 - 4083	K.ADLINNLGTIAK.S	1243.43490	2	9.81E-07	0.93	4.01	-	892.3
gi|14745898|ref|XP_016144.2|	similar to tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat			9.89E-07	0.91	10.20	7.55	18201.0
AHQ-5-11, 6546	K.LLCCDILDVLDK.N	1479.74157	2	3.57E-05	0.95	4.09	-	1088.0
AHQ-5-9, 6196	K.LLCCDILDVLDK.N	1479.74157	1	9.89E-07	0.91	3.97	-	854.4
gi|5453916|ref|NP_006311.1|	progesterone membrane binding protein [Homo sapiens]			1.04E-06	0.90	10.16	6.28	23818.3
AHQ-5-10, 4514	K.FYGPAGPYGIFAGR.D	1473.65885	2	1.04E-06	0.90	3.14	-	941.2
gi|4507487|ref|NP_003238.1|	thrombospondin 2 [Homo sapiens]			1.06E-06	0.86	10.20	1.19	129954.5
AHQ-5-2, 2449	R.NALWHTGNTPGQVR.T	1551.69124	2	4.46E-04	0.93	3.92	-	1047.6
AHQ-5-4, 2949 - 3025	R.NALWHTGNTPGQVR.T	1551.69124	2	1.54E-05	0.72	2.77	-	556.2
AHQ-5-5, 2346	R.NALWHTGNTPGQVR.T	1551.69124	2	7.73E-04	0.87	3.70	-	883.1
AHQ-5-5, 2627	R.NALWHTGNTPGQVR.T	1551.69124	2	6.66E-05	0.89	3.48	-	929.2
AHQ-5-8, 2144	R.NALWHTGNTPGQVR.T	1551.69124	2	1.06E-06	0.86	3.58	-	780.9
AHQ-5-14-, 2642	R.NALWHTGNTPGQVR.T	1551.69124	2	2.07E-06	0.80	3.28	-	623.2
AHQ-5-1, 3005	R.NALWHTGNTPGQVR.T	1551.69124	2	1.26E-04	0.75	3.33	-	586.3
gi|30149327|ref|XP_293672.2|	similar to ebiP7687 [Homo sapiens]			1.08E-06	0.65	10.13	1.92	59404.3
AHQ-5-5, 2591	K.SIYYITGESK.E	1161.28598	1	1.08E-06	0.65	2.65	-	610.1
gi|4506765|ref|NP_002952.1|	S100 calcium-binding protein A4; 18A2; 42A; S100 calcium-binding protei			1.09E-06	0.93	10.18	10.89	11728.5
AHQ-5-14-, 3390	K.ALDVMVSTFHK.Y	1248.47665	2	1.09E-06	0.93	3.69	-	1092.8
gi|17017988|ref|NP_001853.2|	cytochrome c oxidase subunit Vb precursor; cytochrome c oxidase polype			1.12E-06	0.87	10.17	9.30	13695.6
AHQ-5-13-, 3487	K.KGLDPYNVLAPK.G	1315.54272	2	1.12E-06	0.87	3.43	-	729.9
gi|4504973|ref|NP_002292.1|	lactate dehydrogenase C [Homo sapiens]			1.14E-06	0.89	10.20	3.61	36311.0
AHQ-5-9, 2274 - 2275	R.VIGSGCNLDSAR.F	1250.36445	2	1.14E-06	0.89	4.05	-	624.8
gi|13129150|ref|NP_005339.1|	heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H			1.14E-06	1.84	20.28	3.42	84659.1
AHQ-5-5, 4022 - 4023	R.NPDDITNEEYGEFYK.S	1834.87381	2	1.14E-06	0.97	5.70	-	1164.4
AHQ-5-5, 3835	R.RAPFDLFENR.K	1265.40235	2	3.03E-06	0.87	3.43	-	711.9
gi|5454090|ref|NP_006271.1|	signal sequence receptor, delta; translocon-associated protein delta [H			1.14E-06	1.57	20.16	17.34	18998.5
AHQ-5-12, 4865	R.FFDEESYSLLR.K	1406.52121	2	1.14E-06	0.83	3.12	-	699.6
AHQ-5-12, 6178	R.NNEDISIIPPLFTVSVDHR.G	2167.40715	3	5.92E-06	0.74	3.30	-	718.0
gi|4503481|ref|NP_001395.1|	eukaryotic translation elongation factor 1 gamma; elongation factor 1-g			1.17E-06	0.90	10.20	3.20	50118.5
AHQ-5-8, 2236 - 2238	R.KLDPGSEETQTLVR.E	1573.73020	2	1.17E-06	0.90	4.02	-	496.1
gi|22748619|ref|NP_689476.1|	tropomyosin 3 [Homo sapiens]			1.18E-06	2.84	30.24	16.46	28222.6
AHQ-5-9, 3362 - 3375	R.ALKDEEKMELQEIQLK.E	1946.25520	2	1.34E-04	0.95	4.74	-	1481.8
AHQ-5-9, 2843 - 2854	R.KLVIIEGDLER.T	1285.51492	2	1.18E-06	0.95	4.49	-	1396.2

AHQ-5-9, 1980 - 1990	K.YSQKEDKYEEEIK.I	1689.80129	2	6.58E-04	0.93	4.54	-	1581.2
gi|4505273|ref|NP_002442.1| 5'-methylthioadenosine phosphorylase [Homo sapiens]				1.20E-06	0.90	10.22	6.01	31249.9
AHQ-5-9, 4147	K.YVDTPFGKPSDALILGK.I	1822.09396	2	1.20E-06	0.90	4.35	-	666.5
gi|4504041|ref|NP_002061.1| guanine nucleotide binding protein (G protein), alpha inhibiting activi				1.26E-06	0.79	10.17	4.23	40450.7
AHQ-5-8, 3697	R.IAQSDYIPTQQDVLR.T	1747.93034	2	1.26E-06	0.79	3.42	-	365.4
gi|7661922|ref|NP_055814.1| RAB21, member RAS oncogene family [Homo sapiens]				1.31E-06	0.95	10.21	7.56	24347.4
AHQ-5-10, 3895 - 3955	R.HVSIQEAESYAESVGAK.H	1805.92351	2	1.31E-06	0.95	4.25	-	1246.6
gi|4758076|ref|NP_004068.1| citrate synthase precursor; Citrate synthase, mitochondrial [Homo sapie				1.36E-06	1.64	20.18	5.79	51706.2
AHQ-5-8, 4388	K.GLVYETSVLDPDEGIR.F	1763.92654	2	1.36E-06	0.84	3.55	-	568.1
AHQ-5-8, 3000	K.IVPNVLLEQGK.A	1210.44805	2	4.45E-05	0.80	2.69	-	451.2
gi|30154095|ref|XP_293967.2| similar to gamma actin-like protein [Homo sapiens]				1.38E-06	1.21	20.20	12.21	19259.0
AHQ-5-3, 5111	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	9.28E-04	0.31	2.76	-	342.7
AHQ-5-10, 4450	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.03E-04	0.40	2.68	-	405.2
AHQ-5-10, 4824 - 4903	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	3.56E-04	0.62	2.82	-	543.9
AHQ-5-13, 4826	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	4.88E-06	0.72	3.58	-	451.6
AHQ-5-13, 4952 - 4956	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.38E-06	0.36	2.73	-	398.1
AHQ-5-14, 5596 - 5661	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	7.63E-06	0.57	3.44	-	367.1
AHQ-5-13-, 4729	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.06E-05	0.67	3.03	-	582.5
AHQ-5-13-, 5156	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	1.87E-06	0.86	4.06	-	496.8
AHQ-5-14-, 4697	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	6.69E-06	0.88	4.02	-	614.1
AHQ-5-14-, 4793 - 4853	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	4.64E-06	0.67	3.17	-	532.8
AHQ-5-14-, 5001	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.10E-05	0.72	3.14	-	682.7
gi|12707570|ref|NP_004083.2| mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor [Homo				1.39E-06	0.94	10.17	5.86	31371.2
AHQ-5-10, 6560	K.ICPVETLVEEAIQCAEK.I	1992.25744	2	1.39E-06	0.94	3.42	-	1407.3
gi|29743324|ref|XP_293276.1| similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote				1.40E-06	1.87	20.32	15.98	21244.7
AHQ-5-13, 5317 - 5380	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	4.56E-04	0.94	6.12	-	1463.5
AHQ-5-13-, 5215 - 5279	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	4.31E-05	0.89	5.65	-	966.0
AHQ-5-13-, 5523 - 5599	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPMPK.L	3228.70228	3	2.63E-05	0.96	6.21	-	1131.4
AHQ-5-14-, 5210	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	1.40E-06	0.91	6.13	-	947.5
AHQ-5-11, 5488 - 5506	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPMPK.L	3228.70228	3	8.88E-04	0.94	6.39	-	1267.6
gi|5729808|ref|NP_006557.1| adhesion glycoprotein; platelet and T cell activation antigen 1; DNAX a				1.43E-06	1.70	20.22	11.31	38583.7
AHQ-5-6, 4824	K.IGTQQDSIAIFSPTHGMVIR.K	2172.49357	2	1.43E-06	0.94	4.35	-	1049.4
AHQ-5-6, 4822	K.IGTQQDSIAIFSPTHGMVIR.K	2172.49357	3	1.34E-05	0.97	4.41	-	2598.3
AHQ-5-6, 6670	R.WSVIVIPDVTVSDSGLYR.C	2007.27528	2	9.79E-04	0.76	3.05	-	376.6
gi|19913424|ref|NP_001681.2| ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT				1.47E-06	3.60	40.23	10.53	68303.7
AHQ-5-6, 4164	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	1.47E-06	0.92	3.75	-	961.3
AHQ-5-6, 1993	K.LPANHPLLTGQR.V	1317.52194	2	8.31E-05	0.83	3.20	-	639.2
AHQ-5-6, 2905	R.TALVANTSNMPVAAR.E	1516.74852	2	2.34E-06	0.92	3.85	-	1164.2
AHQ-5-6, 5237 - 5310	R.VGSHITGGDIYGIVSENSLIK.H	2160.41292	2	3.45E-05	0.93	4.54	-	873.8
gi|4505303|ref|NP_002466.1| myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m				1.50E-06	2.58	30.19	11.54	22763.8
AHQ-5-12, 2608 - 2736	R.ALGQNPTNAEVLK.V	1355.52211	1	6.40E-04	0.26	2.75	-	230.5
AHQ-5-12, 2612 - 2676	R.ALGQNPTNAEVLK.V	1355.52211	2	1.50E-06	0.77	3.46	-	549.2
AHQ-5-12, 2617 - 2680	R.ALGQNPTNAEVLK.V	1355.52211	1	3.35E-04	0.13	2.79	-	222.4
AHQ-5-12, 2776 - 2844	R.ALGQNPTNAEVLK.V	1355.52211	2	2.59E-04	0.75	3.45	-	439.7
AHQ-5-13-, 2679 - 2752	R.ALGQNPTNAEVLK.V	1355.52211	2	7.66E-05	0.84	3.89	-	400.7
AHQ-5-12, 2965 - 2966	R.ALGQNPTNAEVLK.V	1355.52211	2	1.06E-05	0.78	3.30	-	401.4
AHQ-5-12, 3264 - 3294	K.ILYSQCGDVMR.A	1343.55489	2	7.26E-04	0.85	2.99	-	867.4
AHQ-5-12, 2578 - 2644	K.ILYSQCGDVM*R.A	1359.55429	2	7.04E-05	0.79	2.96	-	761.4
AHQ-5-14-, 2621	K.ILYSQCGDVM*R.A	1359.55429	2	2.49E-06	0.91	2.82	-	1098.6
AHQ-5-14-, 3227	K.ILYSQCGDVMR.A	1343.55489	2	2.46E-06	0.91	3.15	-	1041.1
gi|7705704|ref|NP_057001.1| glutathione S-transferase subunit 13 homolog [Homo sapiens]				1.55E-06	4.62	50.22	24.78	25496.7
AHQ-5-11, 3343 - 3378	K.AGMSAEQAQGLLEK.I	1433.61314	2	3.94E-06	0.90	3.82	-	1313.4
AHQ-5-11, 2558 - 2560	K.AGM*SAEQAQGLLEK.I	1449.61254	2	1.70E-05	0.94	3.99	-	1405.4
AHQ-5-11, 4442	R.FLTAVNLEHPEMLEK.A	1772.05845	2	4.03E-05	0.94	4.40	-	1196.7
AHQ-5-11, 3108	R.HHLQIPIHFPK.D	1367.62578	2	4.05E-05	0.94	3.52	-	1320.2
AHQ-5-11, 4500	R.NEDITEPQSILAAAEK.A	1729.86695	2	1.55E-06	0.90	4.12	-	726.2
gi|11321640|ref|NP_066301.1| basic beta 1 syntrophin; 59-DAP; syntrophin, beta 1; syntrophin, beta				1.61E-06	0.65	10.15	3.35	58060.8
AHQ-5-6, 4634	R.TAFTDLPEQVPESISNQK.R	2005.17142	2	1.61E-06	0.65	2.95	-	508.5
gi|4885539|ref|NP_005380.1| protein-L-isoaspartate (D-aspartate) O-methyltransferase [Homo sapiens]				1.64E-06	1.36	20.28	14.54	24636.2
AHQ-5-11, 5203	R.LILPVGPAGGNQMLEQYDK.L	2044.36057	2	7.78E-06	0.41	2.64	-	231.6
AHQ-5-10, 1936	K.SGGASHSELIHNLR.K	1478.59543	2	1.64E-06	0.94	4.07	-	1181.7
gi|29727204|ref|XP_290872.1| similar to Pyruvate kinase, M2 isozyme [Homo sapiens]				1.74E-06	1.62	20.19	20.13	16297.7
AHQ-5-9, 2143	R.APIIAVTR.N	841.03348	1	1.77E-04	0.28	2.19	-	216.1
AHQ-5-7, 2067	R.APIIAVTR.N	841.03348	2	3.06E-05	0.94	3.09	-	1232.4
AHQ-5-7, 4884 - 4928	K.KGDVVIVLTGWRPGSGFTNTMR.V	2392.76561	3	1.74E-06	0.69	3.23	-	658.9
gi|4507767|ref|NP_003326.1| ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi				1.76E-06	4.00	50.19	6.53	111719.5
AHQ-5-4, 4994	K.FQHLHGRPPQPWDPVDAETVVGLAR.D	2824.14835	3	1.76E-06	0.87	3.74	-	964.6
AHQ-5-4, 7356	R.GLNPDLQVIPLTYPLDPTTEHIYGDNFFSR.V	3434.79811	3	3.87E-04	0.67	3.35	-	406.3
AHQ-5-4, 3361	K.LLDEELYSR.Q	1138.25242	2	4.24E-05	0.83	3.09	-	619.6
AHQ-5-4, 4282	R.VTELVQQLTGQAPAPGQR.V	1894.12181	2	4.91E-04	0.82	3.16	-	870.3
AHQ-5-4, 4025 - 4098	R.YFPSTAEHTLQWAR.H	1707.86959	2	2.04E-04	0.82	3.54	-	424.5
gi|5453603|ref|NP_006422.1| chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c				1.80E-06	2.71	30.20	9.72	57487.9
AHQ-5-7, 2838	R.EALLSSAVDHGSDEVK.F	1657.76083	2	1.80E-06	0.91	4.01	-	1176.2
AHQ-5-7, 5386	R.SLHDALCVLAQTVK.D	1556.80920	2	3.99E-04	0.94	3.54	-	1359.6
AHQ-5-7, 6994	R.VQDDEVGDGTTSVTVLAAELLR.E	2289.48263	2	1.48E-05	0.87	3.83	-	862.1
gi|18201911|ref|NP_000629.2| vitronectin precursor; serum spreading factor; somatomedin B; compleme				1.92E-06	0.90	10.21	3.14	54335.4
AHQ-5-13-, 5611 - 5689	R.SIAQYWLGCPAPGHL	1671.90045	2	1.92E-06	0.90	3.74	-	747.8
AHQ-5-13, 5728	R.SIAQYWLGCPAPGHL	1671.90045	2	7.72E-05	0.93	4.25	-	746.6
gi|20127408|ref|NP_000173.2| hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub				1.93E-06	1.87	20.25	5.90	82999.1
AHQ-5-6, 7220	K.KLDSLTTSFGFPVGAATLVDEVGVDVAK.H	2838.20186	3	1.47E-05	0.94	5.09	-	1184.6
AHQ-5-6, 2989	K.TGIEQGSDAGYLCESQK.F	1844.93497	2	1.93E-06	0.93	4.46	-	860.6
gi|5453990|ref|NP_006254.1| proteasome (prosome, macropain) activator subunit 1 (PA28 alpha); Prote				1.96E-06	1.81	20.26	9.24	28722.9
AHQ-5-10, 5675	K.ISELDAFLKEPALNEANLSNLK.A	2430.73906	2	1.96E-06	0.94	5.28	-	666.7
AHQ-5-10, 5251 - 5256	K.KISELDAFLKEPALNEANLSNLK.A	2558.91197	3	6.25E-04	0.87	4.21	-	744.3
gi|21618359|ref|NP_004095.3| fatty acid synthase [Homo sapiens]				2.02E-06	1.90	20.28	1.67	273262.0
AHQ-5-1, 6209	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	2.77E-06	0.93	5.57	-	530.7
AHQ-5-1, 7024	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	2.02E-06	0.96	4.40	-	1322.6
gi|20070125|ref|NP_000909.2| prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke				2.09E-06	3.63	40.33	14.37	57115.9
AHQ-5-7, 2380	K.LGETYKDHENIVIAK.M	1730.94291	2	1.38E-04	0.83	3.52	-	718.5
AHQ-5-7, 7394	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	3	2.09E-06	0.97	6.51	-	1811.3
AHQ-5-7, 7392	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	2	3.82E-06	0.93	4.35	-	1244.4
AHQ-5-7, 3650 - 3651	K.VDATEESDLAQQYGVR.G	1781.85882	2	9.56E-06	0.98	5.07	-	2123.6
AHQ-5-7, 3715 - 3730	K.YQLDKDGVVLFK.K	1425.65394	2	1.50E-05	0.85	3.59	-	865.0
gi|8922712|ref|NP_060713.1| hypothetical protein FLJ10849 [Homo sapiens]				2.10E-06	2.25	30.25	11.42	49397.9
AHQ-5-7, 2336	K.AAAQLLQSQAQQSGAQQTK.K	1958.12276	2	1.66E-05	0.97	5.04	-	1422.1
AHQ-5-7, 5087	R.NLSLSGHVGFDSLPDQLVNK.S	2141.36970	2	2.10E-06	0.32	2.66	-	288.8
AHQ-5-7, 2487	K.RNEFLGELQK.K	1234.38656	2	3.90E-04	0.95	3.85	-	1734.1
gi|5031611|ref|NP_005859.1| BET1 homolog; Golgi vesicular membrane trafficking protein p18; Bet1p h				2.15E-06	1.80	20.24	15.25	13289.4
AHQ-5-14, 6042 - 6121	K.LLAEMDSQFDSTTGFLGK.T	1961.18205	2	1.74E-05	0.85	3.76	-	505.7
AHQ-5-14-, 4693	K.LLAEM*DSQFDSTTGFLGK.T	1977.18145	2	7.87E-06	0.95	4.84	-	1084.3
AHQ-5-14-, 5445	K.LLAEMDSQFDSTTGFLGK.T	1961.18205	2	3.06E-05	0.87	3.64	-	685.5
AHQ-5-13, 4824	K.LLAEM*DSQFDSTTGFLGK.T	1977.18145	2	2.15E-06	0.95	4.38	-	1175.7
gi|4503607|ref|NP_000117.1| electron transfer flavoprotein, alpha polypeptide; electron-transferrin				2.15E-06	0.81	10.19	8.11	35079.3
AHQ-5-9, 6474	K.TIVAINKDPEAPIFQVADYGIVADLFK.V	2949.38904	2	2.15E-06	0.81	3.78	-	363.5
gi|4501841|ref|NP_001596.1| alanyl-tRNA synthetase [Homo sapiens]				2.17E-06	1.77	20.22	3.41	106800.7
AHQ-5-4, 7353	R.EIADLGEALATAVIPQWQK.D	2054.33195	2	2.17E-06	0.91	4.34	-	1052.6
AHQ-5-4, 3454	K.VGAEDADGIDMAYR.V	1483.58588	2	1.08E-04	0.85	3.08	-	1049.1

gi|21314617|ref|NP_000433.2| platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e				2.19E-06	7.70	90.28	17.48	82449.6
AHQ-5-4, 6057 - 6058	R.CESISGTLPISYQLLK.T	1811.08954	2	4.85E-04	0.83	3.64	-	356.8
AHQ-5-5, 5918	R.CESISGTLPISYQLLK.T	1811.08954	2	4.32E-04	0.91	4.56	-	371.7
AHQ-5-4, 6644 - 6717	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	1.15E-04	0.97	5.64	-	1373.9
AHQ-5-5, 6505 - 6550	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	2	2.19E-06	0.96	5.33	-	1148.0
AHQ-5-4, 6429 - 6440	R.DQNFVILEFPVEEQDR.V	1979.13566	2	6.80E-05	0.80	3.82	-	660.0
AHQ-5-5, 6325	R.DQNFVILEFPVEEQDR.V	1979.13566	2	8.16E-04	0.81	4.18	-	510.9
AHQ-5-3, 6481	R.DQNFVILEFPVEEQDR.V	1979.13566	2	2.51E-04	0.86	4.25	-	661.6
AHQ-5-1, 6429	R.DQNFVILEFPVEEQDR.V	1979.13566	2	3.67E-05	0.87	3.51	-	884.2
AHQ-5-4, 3456	K.EDTIVSQTQDFTK.I	1512.60049	2	2.91E-04	0.93	4.12	-	764.7
AHQ-5-4, 3600	K.EQEGEYYCTAFNR.A	1668.72232	2	3.56E-05	0.86	3.16	-	629.6
AHQ-5-4, 2348	R.IISGIHMQTSESTK.S	1532.74472	2	1.69E-05	0.96	3.97	-	1220.8
AHQ-5-4, 4225	R.ISYDAQFEVIK.G	1313.48046	2	1.19E-05	0.85	3.13	-	858.6
AHQ-5-4, 4053 - 4130	K.STESYFIPEVR.I	1328.45199	2	4.02E-05	0.84	2.72	-	733.1
AHQ-5-4, 4114	K.STESYFIPEVR.I	1328.45199	2	7.44E-05	0.82	3.14	-	569.9
AHQ-5-4, 4653 - 4660	K.TTAEYQVLVEGVPSPR.V	1746.94234	2	9.91E-04	0.55	2.70	-	534.4
gi|22538465|ref|NP_002786.2| proteasome beta 3 subunit; proteasome theta chain; proteasome chain 13				2.20E-06	1.86	20.27	16.59	22948.8
AHQ-5-11, 5088	R.FGPYYTEPVIAGLDPK.T	1768.00162	2	2.40E-06	0.88	3.55	-	871.9
AHQ-5-10, 5848	R.LYIGLAGLATDVQTVAQR.L	1890.17306	2	2.20E-06	0.97	5.33	-	2172.5
gi|4506195|ref|NP_002785.1| proteasome beta 2 subunit; proteasome subunit, beta type, 2; macropain				2.34E-06	0.68	10.18	4.98	22836.1
AHQ-5-11, 2463 - 2536	R.VAASNIVQMK.D	1061.28096	2	2.34E-06	0.68	2.79	-	479.4
gi|4758648|ref|NP_004512.1| kinesin family member 5B; kinesin 1 (110-120kD) [Homo sapiens]				2.43E-06	1.61	20.19	4.15	109684.2
AHQ-5-4, 7449	K.SLSALGNVISALAEGSTYVPYR.D	2269.53938	2	2.43E-06	0.81	3.71	-	572.1
AHQ-5-4, 3934	R.TTIVICCSPSSYNESETK.S	2079.24882	2	1.98E-05	0.80	3.44	-	475.2
gi|21361427|ref|NP_055182.2| hypothetical protein, estradiol-induced [Homo sapiens]				2.43E-06	0.95	10.23	8.95	21551.0
AHQ-5-13-, 5628	K.EDEIPETVSLEMLDAAK.N	1891.08690	2	2.43E-06	0.95	4.57	-	661.3
gi|5031599|ref|NP_005722.1| actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub				2.46E-06	2.59	40.19	23.33	34332.8
AHQ-5-9, 2054	R.ASHTAPQVLFSHR.E	1451.61481	1	4.45E-05	0.34	2.36	-	425.2
AHQ-5-9, 2368	K.DSIVHQAGMLK.R	1199.40563	2	2.46E-06	0.92	3.16	-	1303.3
AHQ-5-9, 2419	K.ELQAHGADELLK.R	1324.46487	1	2.40E-05	0.52	2.44	-	325.6
AHQ-5-9, 2418	K.ELQAHGADELLK.R	1324.46487	2	3.66E-05	0.93	3.65	-	1396.9
AHQ-5-9, 6243	K.FENAAAGNKPEAVEVTFADFDGVLYHISNPNGDK.T	3638.89648	3	1.31E-05	0.80	3.77	-	757.6
gi|5453555|ref|NP_006316.1| ras-related nuclear protein [Homo sapiens]				2.46E-06	1.84	20.22	14.81	24422.9
AHQ-5-10, 5172	K.SNYNFEKPFLWLAR.K	1786.02509	2	2.46E-06	0.91	3.82	-	666.5
AHQ-5-10, 3927	K.YVATLGVEVHPLVFHTNR.G	2053.35211	2	4.56E-06	0.93	4.45	-	751.8
gi|20070158|ref|NP_003567.2| serine/threonine kinase 24 (STE20 homolog, yeast); STE20-like kinase 3				2.47E-06	0.84	10.24	3.39	49307.6
AHQ-5-7, 3602	K.SQACGGNLGSIEELR.G	1592.71366	2	2.47E-06	0.84	2.80	-	1524.9
gi|4758182|ref|NP_004399.1| dynamin 1; dynamin; dynamin1; Dynamin-1 [Homo sapiens]				2.47E-06	0.90	10.18	1.74	97406.7
AHQ-5-5, 4601	K.VPVGDQPPDIEFQIR.D	1710.91170	2	2.47E-06	0.90	3.64	-	657.9
gi|7657649|ref|NP_055362.1| tropomodulin 3 (ubiquitous) [Homo sapiens]				2.60E-06	0.73	10.13	3.13	39594.5
AHQ-5-11, 3168	K.FGYQFTQQGPR.T	1329.44490	2	2.60E-06	0.73	2.68	-	708.3
gi|21361565|ref|NP_001679.2| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, is				2.64E-06	2.59	30.21	15.23	28908.4
AHQ-5-11, 2816	R.HYLFDVQR.N	1078.20513	2	2.64E-06	0.89	2.92	-	978.9
AHQ-5-14-, 6822	R.YGLIPEEFFQFLYPK.T	1892.18434	2	2.33E-04	0.79	3.15	-	394.4
AHQ-5-11, 6878	R.YGLIPEEFFQFLYPK.T	1892.18434	2	7.92E-04	0.93	4.04	-	503.6
AHQ-5-10, 6607	R.YGLIPEEFFQFLYPK.T	1892.18434	2	4.84E-04	0.43	2.76	-	249.7
AHQ-5-11, 4648	K.YGPFVADFADKLNEQK.L	1843.02858	2	3.39E-05	0.91	3.93	-	959.2
gi|24797067|ref|NP_002107.3| major histocompatibility complex, class I, A precursor; HLA-A1 class I				2.71E-06	3.36	40.22	15.89	40840.5
AHQ-5-8, 4713	R.APWIEQEGPEYWDQETR.N	2135.23420	2	2.71E-06	0.89	3.57	-	707.8
AHQ-5-11, 3251	K.WAAVVVPSGEEQR.Y	1428.57478	2	3.37E-05	0.72	2.81	-	595.0
AHQ-5-8, 2789 - 2872	K.WAAVVVPSGEEQR.Y	1428.57478	2	7.99E-05	0.93	3.66	-	1183.8
AHQ-5-8, 1881	R.YLENGKETLQR.T	1351.49032	2	1.21E-04	0.87	2.79	-	1118.0
AHQ-5-8, 2729	R.YTCHVQHEGLPKPLTLR.W	2051.35781	3	2.95E-04	0.87	4.42	-	1253.5
AHQ-5-8, 2717	R.YTCHVQHEGLPKPLTLR.W	2051.35781	2	9.99E-05	0.88	4.03	-	796.0
gi|11321585|ref|NP_002065.1| guanine nucleotide-binding protein, beta-1 subunit; G protein, beta-1				2.76E-06	0.64	10.16	5.29	37376.8
AHQ-5-9, 6404	R.LLLAGYDDFNCNVWDALK.A	2129.37744	2	2.76E-06	0.64	3.17	-	447.1
gi|4557697|ref|NP_000412.1| keratin 10; Keratin-10 [Homo sapiens]				2.76E-06	0.83	10.21	4.81	57247.1
AHQ-5-1, 6961	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	2.76E-06	0.83	4.14	-	670.6
gi|19913441|ref|NP_002140.2| hippocalcin-like 1; visinin-like protein 3; calcium-binding protein BD				2.90E-06	0.94	10.21	7.77	22313.1
AHQ-5-11, 4176	R.ENTEFTDHELQEWYK.G	1970.04095	2	2.90E-06	0.94	4.19	-	1154.5
gi|4504483|ref|NP_000185.1| hypoxanthine phosphoribosyltransferase 1 [Homo sapiens]				2.95E-06	0.93	10.23	7.34	24579.2
AHQ-5-10, 4338 - 4342	R.SVGYKPDFVGFEIPDK.F	1799.01571	2	2.95E-06	0.93	4.62	-	692.9
gi|5803201|ref|NP_006818.1| transmembrane trafficking protein [Homo sapiens]				2.98E-06	0.95	10.20	5.02	24975.8
AHQ-5-11, 4931	R.IPDQLVILDMK.H	1285.57833	2	2.98E-06	0.95	4.05	-	1119.2
gi|5454152|ref|NP_006285.1| ubiquinol-cytochrome c reductase binding protein [Homo sapiens]				3.05E-06	0.97	10.24	11.71	13530.4
AHQ-5-13-, 5176 - 5187	K.YEEENFYLEPYLK.E	1737.88601	2	3.05E-06	0.97	4.75	-	1752.2
gi|22027655|ref|NP_003907.3| adaptor-related protein complex 1 sigma 2 subunit; clathrin adaptor co				3.08E-06	0.94	10.24	10.19	18614.6
AHQ-5-12, 3934	K.AIEQADLLQEEAETPR.S	1813.94395	2	3.08E-06	0.94	4.72	-	1125.6
gi|29729345|ref|XP_290995.1| similar to speckle-type POZ protein [Homo sapiens]				3.14E-06	1.00	20.16	10.91	18703.4
AHQ-5-3, 6235	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	3.14E-06	0.54	3.17	-	624.7
AHQ-5-4, 6168	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	8.03E-04	0.46	2.94	-	514.9
AHQ-5-1, 6261	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	2.44E-04	0.61	3.05	-	759.7
gi|4502099|ref|NP_001143.1| solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra				3.36E-06	0.96	10.23	5.03	32895.0
AHQ-5-10, 4054	R.KGTDIMYTGTLDCWR.K	1819.05212	2	3.36E-06	0.96	4.63	-	1401.4
gi|27363461|ref|NP_057153.8| mitochondria-associated GM-CSF signaling molecule [Homo sapiens]				3.46E-06	0.95	10.22	18.40	13824.6
AHQ-5-13, 6218	R.SAAASNLSGLSLQEAQQILNVSK.L	2330.58112	2	3.46E-06	0.95	4.50	-	1463.3
gi|4557619|ref|NP_000149.1| glucan (1,4-alpha-), branching enzyme 1 (glycogen branching enzyme); Gl				3.46E-06	0.63	10.15	2.42	80443.3
AHQ-5-6, 5865	R.LLEIDPYLKPYAVDFQR.R	2081.39900	2	3.46E-06	0.63	3.04	-	305.3
gi|5174745|ref|NP_005995.1| ubiquinol-cytochrome c reductase hinge protein [Homo sapiens]				3.57E-06	0.82	10.20	19.78	10754.7
AHQ-5-13, 5770	R.SHTEEDCTEELFDFLHAR.D	2238.33288	3	3.57E-06	0.82	3.99	-	683.4
gi|17464200|ref|XP_059776.1| similar to FK506-binding protein 1A; FK506-binding protein 1; FK506-bi				3.58E-06	0.86	10.20	29.63	12178.9
AHQ-5-14-, 6517	K.LTISPDYAYGATGHPGIIPPHATLVFDVELLK.L	3407.90208	3	3.58E-06	0.86	3.94	-	1028.6
gi|22749247|ref|NP_689822.1| hypothetical protein FLJ32001 [Homo sapiens]				3.67E-06	0.95	10.25	2.48	79570.3
AHQ-5-12, 6224 - 6229	K.RIEIAEVVPTEGLVSILK.K	1967.33888	2	3.67E-06	0.95	5.01	-	1059.0
gi|4758504|ref|NP_004484.1| hydroxyacyl-Coenzyme A dehydrogenase, type II [Homo sapiens]				3.76E-06	1.78	20.22	16.48	26922.9
AHQ-5-10, 4564 - 4636	R.LVGQGASAVLLDLPNSGGEAQAK.K	2196.44680	2	3.52E-04	0.38	2.69	-	210.3
AHQ-5-10, 4372	R.LVGQGASAVLLDLPNSGGEAQAK.K	2196.44680	2	3.76E-06	0.88	4.28	-	677.3
AHQ-5-10, 5932	R.VM*TIAPGLFGTPLLTSLPEK.V	2102.52303	2	3.27E-05	0.90	4.37	-	507.2
gi|8923812|ref|NP_060943.1| uncharacterized hypothalamus protein HT012 [Homo sapiens]				3.77E-06	1.77	20.17	15.71	14960.4
AHQ-5-13-, 2520	K.ITLVSAAPGK.V	957.14925	2	2.22E-04	0.90	2.60	-	1239.0
AHQ-5-13-, 4073 - 4100	K.TLAFTSVDLTNK.A	1310.47811	2	3.77E-06	0.87	2.51	-	967.4
AHQ-5-13, 4186	K.TLAFTSVDLTNK.A	1310.47811	2	9.78E-05	0.91	3.38	-	911.3
gi|4759044|ref|NP_004841.1| Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]				3.81E-06	0.82	10.18	0.86	160883.4
AHQ-5-3, 2446	R.LKDEEISAAAIK.A	1288.47244	2	3.81E-06	0.82	3.63	-	563.3
gi|5453629|ref|NP_006391.1| dynactin 2; dynactin complex 50 kD subunit; dynamitin; 50 kD dynein-ass				4.11E-06	0.91	10.20	4.68	44819.3
AHQ-5-8, 4898	K.LLGPDAAINLTDPDGALAK.R	1866.10514	2	4.11E-06	0.91	4.10	-	817.4
gi|29736622|ref|XP_293924.1| similar to cytoplasmic beta-actin [Homo sapiens]				4.25E-06	1.89	30.22	21.54	42002.9
AHQ-5-9, 4779	K.DLYANTVLSGGSTM*YPGIADR.M	2218.42957	2	3.23E-05	0.46	3.26	-	408.9
AHQ-5-8, 6633 - 6644	R.FRCPEAIFQPSFLGIESSGIHETTFNSIMK.C	3446.89713	3	4.25E-06	0.86	4.41	-	492.9
AHQ-5-8, 6817	R.FRCPEAIFQPSFLGIESSGIHETTFNSIMK.C	3446.89713	3	5.91E-05	0.62	3.01	-	629.1
AHQ-5-8, 6237	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	1.31E-04	0.76	3.47	-	681.8
AHQ-5-8, 5982	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	3.19E-05	0.57	3.23	-	648.3
gi|6005886|ref|NP_009200.1| syntaxin binding protein 3; syntaxin 4 binding protein [Homo sapiens] [				4.43E-06	0.92	10.18	2.87	67573.7
AHQ-5-6, 7114	K.AAYIYFTDFCPDNLFNK.I	2101.32255	2	4.43E-06	0.92	3.70	-	1148.4
gi|8922601|ref|NP_060654.1| hypothetical protein FLJ10702 [Homo sapiens]				4.48E-06	0.87	10.17	8.60	21538.9
AHQ-5-11, 5436	R.GVNAIVYMIDAADREK.I	1766.01230	2	4.48E-06	0.87	3.48	-	911.1
gi|11496891|ref|NP_000662.2| class III alcohol dehydrogenase 5 chi subunit; Alcohol dehydrogenase (				4.75E-06	0.95	10.25	5.88	39738.1

AHQ-5-8, 4809	K.AAVAWEAGKPLSIEEIEVAPPK.A	2306.64276	2	4.75E-06	0.95	5.09	-	930.2
gi|4503291|ref|NP_001346.1| D-dopachrome tautomerase [Homo sapiens]				5.09E-06	1.92	20.24	19.49	12711.7
AHQ-5-14-, 3709	R.LCAAAASILGK.P	1076.29219	2	1.14E-04	0.95	3.19	-	1717.5
AHQ-5-14-, 3838	R.SHSAHFFEFLTK.E	1451.61004	2	5.09E-06	0.98	4.89	-	1709.7
AHQ-5-14, 4870	R.SHSAHFFEFLTK.E	1451.61004	1	8.25E-06	0.61	2.63	-	520.2
gi|4505585|ref|NP_002563.1| platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30				5.11E-06	1.76	20.19	17.03	25569.1
AHQ-5-10, 5482 - 5551	R.ELFSPLHALNFGIGGDTTR.H	2046.27160	2	5.11E-06	0.83	3.74	-	646.5
AHQ-5-10, 6408	K.ICKPLHELIMQLLEETPEEK.Q	2452.87287	2	6.83E-04	0.93	3.53	-	1199.0
gi|4505591|ref|NP_002565.1| peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc				5.14E-06	2.44	30.26	15.58	22110.2
AHQ-5-11, 2566	K.ATAVMPDGQFK.D	1165.34450	2	6.24E-04	0.66	2.88	-	418.4
AHQ-5-11, 3515	R.LVQAFQFTDK.H	1197.36469	2	5.14E-06	0.92	3.73	-	939.0
AHQ-5-11, 3012 - 3020	R.TIAQDYGVLK.A	1108.26945	2	6.57E-04	0.85	3.27	-	657.9
gi|4504085|ref|NP_000399.1| glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA				5.22E-06	1.54	20.19	3.44	80814.1
AHQ-5-6, 6105	R.VIFFLPWQK.M	1178.44934	2	1.43E-04	0.66	2.83	-	492.4
AHQ-5-6, 6206	R.YGAATANYMEVVSLLK.K	1731.00632	2	5.22E-06	0.87	3.62	-	695.1
gi|30148644|ref|XP_293716.2| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				5.38E-06	0.95	10.17	1.23	105150.3
AHQ-5-5, 4146	R.TLTIVDTGIGMTK.A	1350.60718	2	5.38E-06	0.95	3.38	-	1417.3
gi|4504937|ref|NP_003928.1| kynureninase (L-kynurenine hydrolase); l-kynurenine hydrolase [Homo sap				5.57E-06	0.64	10.17	4.73	52351.3
AHQ-5-11, 4514	R.MIKPREGEETLRIEDILEVIEK.E	2642.06592	3	5.57E-06	0.64	3.31	-	425.5
gi|4503643|ref|NP_000121.1| coagulation factor V precursor; labile factor; factor V Leiden [Homo sa				6.20E-06	1.64	20.18	1.39	251716.5
AHQ-5-4, 4996	R.GEYEEHLGILGPIIR.A	1696.92816	2	5.19E-04	0.84	3.39	-	955.3
AHQ-5-3, 3714 - 3793	K.LSEGASYLDHTFPAEK.M	1765.90099	2	6.20E-06	0.80	3.54	-	702.1
gi|4885153|ref|NP_005198.1| v-crk sarcoma virus CT10 oncogene homolog (avian)-like; v-crk avian sar				6.26E-06	1.71	20.23	10.89	33776.7
AHQ-5-10, 5931 - 5954	K.IGDQEFDHLPALLEFYK.I	2036.27195	2	5.31E-05	0.94	4.50	-	776.3
AHQ-5-9, 5808	K.IGDQEFDHLPALLEFYK.I	2036.27195	2	6.26E-06	0.93	4.39	-	890.4
AHQ-5-10, 5012	R.TLYDFPGNDAEDLPFK.K	1842.98222	2	2.27E-05	0.78	3.55	-	391.2
gi|21361070|ref|NP_002617.2| phosphofructokinase, liver; Phosphofructokinase, liver type; human liv				6.29E-06	0.93	10.21	2.06	90202.5
AHQ-5-5, 5375	K.GQVQEVGWHDVAGWLGR.G	1895.07004	2	6.29E-06	0.93	4.30	-	801.0
gi|5803135|ref|NP_006852.1| RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind				6.33E-06	0.85	10.17	5.47	23025.1
AHQ-5-14-, 3707	K.LLIIGDSGVGK.S	1072.28025	2	6.33E-06	0.85	3.00	-	997.1
AHQ-5-11, 3574 - 3596	K.LLIIGDSGVGK.S	1072.28025	2	5.14E-04	0.91	3.38	-	1043.3
gi|20127454|ref|NP_004035.2| 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cy				6.35E-06	0.93	10.20	2.87	64615.5
AHQ-5-6, 4705	K.AFTHTAQYDEAISDYFR.K	2036.14577	2	6.35E-06	0.93	4.09	-	1133.6
gi|30160191|ref|XP_294035.2| similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme				6.44E-06	0.97	10.23	2.83	50222.2
AHQ-5-7, 4999 - 5030	K.IYVDDGLISLQVK.Q	1463.70048	1	3.92E-04	0.64	2.90	-	643.6
AHQ-5-7, 4959 - 5026	K.IYVDDGLISLQVK.Q	1463.70048	2	6.44E-06	0.97	4.69	-	1759.6
gi|4557894|ref|NP_000230.1| lysozyme precursor [Homo sapiens]				6.46E-06	0.90	10.23	18.92	16537.0
AHQ-5-13, 5989	K.TPGAVNACHLSCSALLQDNIADAVACAK.R	2932.25718	3	6.46E-06	0.90	4.67	-	951.5
gi|5902134|ref|NP_009005.1| coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin				6.50E-06	4.39	50.23	14.32	51026.0
AHQ-5-7, 3220	R.CEPIAMTVPR.K	1175.40412	2	4.08E-05	0.87	2.94	-	998.5
AHQ-5-7, 1964	R.KLQATVQELQK.R	1286.50292	2	9.52E-04	0.95	4.59	-	1399.7
AHQ-5-6, 7028	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	8.49E-06	0.83	3.91	-	385.1
AHQ-5-4, 7246	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	3.18E-05	0.85	4.36	-	502.9
AHQ-5-7, 7042	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	5.62E-04	0.76	3.57	-	472.6
AHQ-5-3, 7297	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	6.50E-06	0.87	4.12	-	511.8
AHQ-5-1, 7172	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	1.31E-05	0.86	4.14	-	625.7
AHQ-5-7, 6955	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	1.70E-05	0.89	4.54	-	459.1
AHQ-5-7, 2222	K.LQATVQELQK.R	1158.33000	2	3.10E-04	0.81	2.91	-	667.3
AHQ-5-7, 3942 - 3962	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	3.73E-05	0.88	3.88	-	602.7
gi|4506363|ref|NP_002861.1| RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s				6.55E-06	1.56	20.17	10.84	22774.0
AHQ-5-11, 3670	K.LLLIGDSGVGK.T	1072.28025	2	1.11E-05	0.89	3.26	-	1000.3
AHQ-5-13, 3865	K.LLLIGDSGVGK.T	1072.28025	2	1.55E-04	0.82	3.33	-	786.2
AHQ-5-13-, 3776	K.LLLIGDSGVGK.T	1072.28025	2	1.62E-05	0.93	3.42	-	1301.6
AHQ-5-11, 2919	K.LQVWDTAGQER.F	1303.40576	2	6.55E-06	0.67	2.68	-	722.5
gi|5901922|ref|NP_008996.1| CDC37 homolog [Homo sapiens]				7.41E-06	0.89	10.22	5.56	44468.0
AHQ-5-8, 6532	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	7.41E-06	0.89	3.91	-	519.9
AHQ-5-7, 6686	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	1.98E-04	0.93	4.32	-	630.0
gi|30149555|ref|XP_301154.1| similar to heat shock protein 86 [Homo sapiens]				7.47E-06	0.93	10.19	10.56	15781.6
AHQ-5-5, 5615	K.HSQFIGYPITLFVEK.E	1780.05877	2	7.47E-06	0.93	3.85	-	1115.8
gi|13654272|ref|NP_112484.1| hypothetical protein HT036 [Homo sapiens]				7.62E-06	0.67	10.18	9.80	22615.6
AHQ-5-10, 5599	R.ITDPQYFLDTPQQAAAILQK.V	2262.54684	2	7.62E-06	0.67	3.61	-	182.3
gi|4504111|ref|NP_002077.1| growth factor receptor-bound protein 2 [Homo sapiens]				7.64E-06	1.69	20.17	11.06	25206.2
AHQ-5-10, 3616 - 3678	K.FNSLNELVDYHR.S	1507.63200	2	7.64E-06	0.85	3.32	-	882.7
AHQ-5-10, 3211	K.VLNEECDQNWYK.A	1599.70313	2	4.11E-04	0.84	3.28	-	559.0
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				9.17E-06	0.94	10.23	4.66	61986.9
AHQ-5-14-, 6081 - 6087	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	9.17E-06	0.94	4.40	-	1569.6
gi|18152767|ref|NP_542775.1| synaptotagmin-like 4 (granuphilin-a) [Homo sapiens]				9.18E-06	0.49	10.15	2.98	76009.1
AHQ-5-9, 4775	R.ETVGQSLLHQTQMGDIWPGR.K	2254.51154	2	9.18E-06	0.49	3.01	-	354.8
gi|27501260|ref|XP_210460.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				9.54E-06	0.63	10.13	6.77	26988.2
AHQ-5-9, 3675	K.IISNASCTTSCLTPLAK.N	1840.10934	2	9.54E-06	0.63	2.66	-	726.4
gi|30157216|ref|XP_292133.2| similar to genethonin 1 [Homo sapiens]				9.58E-06	0.41	10.17	4.51	39693.8
AHQ-5-4, 4601	K.TITLEVKPSDTIENVK.A	1788.03268	2	3.98E-04	0.58	3.32	-	488.6
AHQ-5-8, 4114 - 4116	K.TITLEVKPSDTIENVK.A	1788.03268	2	3.20E-04	0.18	2.64	-	261.2
AHQ-5-13, 4385 - 4448	K.TITLEVKPSDTIENVK.A	1788.03268	2	9.58E-06	0.41	2.83	-	326.9
AHQ-5-14, 5122 - 5181	K.TITLEVKPSDTIENVK.A	1788.03268	2	2.26E-04	0.49	3.46	-	276.8
AHQ-5-14-, 4390	K.TITLEVKPSDTIENVK.A	1788.03268	2	1.48E-05	0.68	3.13	-	502.4
AHQ-5-3, 4655 - 4658	K.TITLEVKPSDTIENVK.A	1788.03268	2	4.23E-05	0.57	3.40	-	405.5
gi|4885235|ref|NP_005239.1| Gardner-Rasheed feline sarcoma viral (v-fgr) oncogene homolog; Gardner-				9.61E-06	0.89	10.24	3.78	59478.3
AHQ-5-7, 5387	K.TLKPGTMSPKAFLEEAQVMK.L	2207.64277	2	9.61E-06	0.89	4.75	-	979.4
gi|4507509|ref|NP_003245.1| tissue inhibitor of metalloproteinase 1 precursor; Erythroid-potentiati				9.69E-06	1.90	20.26	21.26	23170.8
AHQ-5-10, 6407	K.LQDGLLHITTCSFVAPWNSLSLAQR.R	2830.21117	2	9.69E-06	0.94	4.64	-	904.4
AHQ-5-9, 6330	K.LQDGLLHITTCSFVAPWNSLSLAQR.R	2830.21117	2	1.14E-04	0.94	4.59	-	901.3
AHQ-5-10, 4139	K.LQSGTHCLWTDQLLQGSEK.G	2203.41795	2	4.64E-05	0.96	5.26	-	1130.8
gi|19743813|ref|NP_002202.2| integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib				1.00E-05	0.91	10.27	2.13	88414.9
AHQ-5-1, 5384	K.LKPEDITQIQPQQLVLR.L	2020.36187	3	2.56E-05	0.83	3.57	-	967.4
AHQ-5-3, 5354	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	2.37E-05	0.93	4.73	-	788.7
AHQ-5-4, 5328	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	1.00E-05	0.91	4.16	-	912.6
AHQ-5-5, 5143	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	2.19E-04	0.97	5.40	-	1377.6
AHQ-5-6, 5082	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	2.71E-04	0.88	4.40	-	553.4
AHQ-5-10, 4630	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	4.72E-05	0.88	3.84	-	778.1
AHQ-5-1, 5381 - 5400	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	4.09E-04	0.91	4.27	-	741.2
gi|4557797|ref|NP_000260.1| non-metastatic cells 1 protein [Homo sapiens]				1.01E-05	5.28	70.22	40.79	17148.6
AHQ-5-12, 4008	K.DRPFFAGLVK.Y	1150.35439	2	5.48E-05	0.92	3.19	-	1339.2
AHQ-5-12, 3542	K.FMQASEDLLK.E	1182.37183	1	3.03E-04	0.16	1.82	-	602.6
AHQ-5-12, 3177	R.GLVGEIIK.R	829.01947	2	2.10E-04	0.74	2.68	-	607.6
AHQ-5-12, 2800	R.GLVGEIIKR.F	985.20582	2	6.14E-04	0.85	2.86	-	873.2
AHQ-5-12, 2066	R.NIIHGSDSVESAEK.E	1486.56627	1	1.01E-05	0.88	4.33	-	567.6
AHQ-5-12, 2886 - 2954	R.TFIAIKPDGVQR.G	1345.57205	2	2.78E-05	0.89	3.53	-	833.7
AHQ-5-12, 6110 - 6180	K.YM*HSGPVVAMVWEGLNVVK.T	2133.52242	2	4.92E-04	0.83	3.34	-	606.6
gi|15626999|ref|NP_258412.1| inosine triphosphatase; Inosine triphosphatase-A [Homo sapiens]				1.01E-05	1.71	20.24	19.59	21445.5
AHQ-5-10, 4270	K.IDLPEYQGEPDEISIQK.C	1975.14209	2	1.01E-05	0.79	3.70	-	601.0
AHQ-5-10, 5568	K.KLEEVVQILGDKFPCTLVAQK.I	2417.84985	2	5.42E-04	0.92	4.84	-	785.3
gi|30147721|ref|XP_060104.2| similar to RIKEN cDNA 5430400H23 [Homo sapiens]				1.03E-05	0.38	10.15	1.13	146351.4
AHQ-5-12, 6261	K.YQELQGLSKSKDAEK.G	1724.89354	2	1.03E-05	0.38	3.03	-	363.4
gi|6005786|ref|NP_009214.1| monoglyceride lipase; lysophospholipase-like [Homo sapiens]				1.03E-05	3.49	40.26	23.96	34292.3
AHQ-5-14-, 5998	K.LTVPFLLLQGSADR.L	1530.79329	2	3.85E-04	0.72	2.93	-	654.5
AHQ-5-9, 3532	R.NKTEVDIYNSDPLICR.A	1939.13627	2	8.68E-05	0.95	4.25	-	1236.6

AHQ-5-9, 5519 - 5600	R.TPQSIPYQDLPHLVNADGQYLFCR.Y	2835.14314	2	1.03E-05	0.86	3.39	-	725.4
AHQ-5-9, 6411	K.VLNLVLPNLSLGPIDSSVLSR.N	2207.59900	2	1.40E-05	0.96	5.24	-	915.2
gi|15723376|ref|NP_277050.1| MacGAP protein [Homo sapiens]				1.09E-05	0.92	10.18	2.10	70163.1
AHQ-5-5, 3085	R.FLSQESGVAQTLK.K	1408.58178	2	1.09E-05	0.92	3.55	-	1248.7
gi|5031601|ref|NP_005711.1| actin related protein 2/3 complex subunit 1B; ARP2/3 protein complex su				1.09E-05	1.56	20.24	10.75	40949.5
AHQ-5-9, 5948	R.STVLSLDWHPNNVLLAAGSCDFK.C	2546.83989	2	1.09E-05	0.60	2.68	-	428.7
AHQ-5-8, 2900	R.TQIAICPNNHEVHIYEK.S	2068.29887	2	1.84E-05	0.96	4.82	-	1181.0
gi|5729842|ref|NP_006699.1| glyoxalase I; lactoyl glutathione lyase; lactoylglutathione lyase [Homo				1.11E-05	0.97	10.28	10.87	20719.6
AHQ-5-11, 6743 - 6819	K.GLAFIQDPDGYWIEILNPNK.M	2304.58542	2	1.11E-05	0.97	5.60	-	1166.8
gi|7657176|ref|NP_055070.1| transmembrane protein 4 [Homo sapiens]				1.11E-05	0.81	10.19	8.79	20652.1
AHQ-5-11, 3543	R.INPDGSQSVVEVPYAR.S	1731.88777	2	1.11E-05	0.81	3.28	-	709.0
gi|4506381|ref|NP_002863.1| ras-related C3 botulinum toxin substrate 2; Ras-related C3 botulinum to				1.15E-05	0.89	10.18	7.81	21428.7
AHQ-5-11, 3912 - 3986	K.KLAPITYPQGLALAK.E	1584.92723	2	1.15E-05	0.89	3.54	-	705.7
gi|21361619|ref|NP_061882.2| TOLLIP protein; Toll-interacting protein [Homo sapiens]				1.22E-05	0.88	10.18	4.74	30281.6
AHQ-5-11, 4767	R.IAWTHITIPESLR.Q	1537.78752	2	1.22E-05	0.88	3.38	-	991.3
gi|22060072|ref|XP_088293.2| similar to cytochrome c [Homo sapiens]				1.32E-05	0.87	10.16	7.62	11887.8
AHQ-5-13-, 4212	R.ADLIAYLK.K	907.08869	2	1.32E-05	0.87	2.78	-	942.2
AHQ-5-13, 4314	R.ADLIAYLK.K	907.08869	2	5.97E-05	0.92	3.16	-	1056.3
gi|14780596|ref|XP_033004.1| hypothetical protein BC005107 [Homo sapiens]				1.38E-05	0.41	10.14	5.00	18127.9
AHQ-5-3, 2003	R.EQIIAKAK.A	901.08569	1	1.38E-05	0.41	2.22	-	307.0
AHQ-5-4, 1758 - 1825	R.EQIIAKAK.A	901.08569	1	5.70E-04	0.19	2.29	-	200.7
AHQ-5-5, 1674	R.EQIIAKAK.A	901.08569	1	9.09E-05	0.49	2.45	-	415.5
AHQ-5-3, 1707 - 1849	R.EQIIAKAK.A	901.08569	1	1.41E-04	0.33	2.53	-	301.6
gi|6715607|ref|NP_000175.1| G-gamma globin [Homo sapiens]				1.40E-05	0.91	10.18	6.80	16126.3
AHQ-5-14-, 4817 - 4818	R.LLVVYPWTQR.F	1275.52342	2	1.50E-05	0.93	3.55	-	1053.1
AHQ-5-13-, 4823 - 4829	R.LLVVYPWTQR.F	1275.52342	2	1.40E-05	0.91	3.46	-	1039.2
gi|4758476|ref|NP_004801.1| GRB2-related adaptor protein 2; growth factor receptor-bound protein 2-				1.41E-05	0.73	10.16	3.64	37908.9
AHQ-5-11, 2500	K.AELGSQEGYVPK.N	1278.39297	2	1.41E-05	0.73	3.17	-	580.7
gi|4885287|ref|NP_005265.1| guanine nucleotide binding protein (G protein), gamma 5 [Homo sapiens]				1.46E-05	0.69	10.17	39.71	7318.4
AHQ-5-14-, 5177	K.QFCLQNAQHDPLLTGVSSSTNPFRPQK.V	3073.38890	3	1.46E-05	0.69	3.34	-	354.9
gi|29740132|ref|XP_299177.1| hypothetical protein XP_299177 [Homo sapiens]				1.48E-05	0.78	10.20	2.67	114488.9
AHQ-5-5, 5143	R.RCHEEKLPLSAGTASHKGQASAQPITPR.Q	3030.36879	3	1.48E-05	0.78	4.04	-	534.1
gi|29727317|ref|XP_298144.1| hypothetical protein XP_298144 [Homo sapiens]				1.51E-05	0.55	10.15	7.96	22108.6
AHQ-5-3, 6673	K.GEYNLTLDTALTSNLK.T	1753.93165	2	1.51E-05	0.55	3.00	-	617.1
gi|5174539|ref|NP_005908.1| cytosolic malate dehydrogenase; soluble malate dehydrogenase [Homo sapi				1.62E-05	1.32	20.18	8.08	36425.9
AHQ-5-9, 4584	K.EVGVYEALKDDSWLK.G	1752.94535	2	3.23E-05	0.90	3.62	-	1090.1
AHQ-5-9, 4156	K.FVEGLPINDFSR.E	1394.55680	1	1.62E-05	0.42	2.68	-	236.2
gi|29729329|ref|XP_291459.1| similar to Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18) [				1.68E-05	1.33	20.21	18.30	17172.9
AHQ-5-12, 5720 - 5725	K.EILVGDVGQTVNNLYATFVK.M	2181.47373	2	1.68E-05	0.89	4.13	-	623.1
AHQ-5-13, 2545	K.NIILEEGK.E	916.05399	1	1.02E-04	0.44	2.25	-	521.0
gi|29731000|ref|XP_291064.1| similar to KIAA0540 protein [Homo sapiens]				1.71E-05	0.64	10.21	0.93	224374.8
AHQ-5-1, 5317	R.CPSLSEPFSSCCIGSAGYR.T	2139.32924	2	1.71E-05	0.64	3.70	-	224.5
gi|8393147|ref|NP_058625.1| chloride intracellular channel 5 [Homo sapiens]				1.73E-05	0.75	10.20	7.17	28109.7
AHQ-5-9, 5286 - 5360	R.KFLDGDELTLADCNLLPK.L	2064.34520	2	1.73E-05	0.75	4.09	-	695.0
gi|4505775|ref|NP_002626.1| phosphate carrier precursor isoform 1b; phosphate carrier, mitochondria				1.79E-05	0.63	10.20	7.48	39958.5
AHQ-5-9, 6450	K.YYALCGFGGVLSCGLTHTAVVPLDLVK.C	2914.38804	2	1.79E-05	0.63	2.83	-	557.4
gi|23065552|ref|NP_000840.2| glutathione S-transferase M3; glutathione S-transferase, Mu-3; brain G				1.80E-05	0.90	10.19	6.22	26559.4
AHQ-5-10, 3812	K.LKPQYLEELPGQLK.Q	1656.94708	2	1.80E-05	0.90	3.77	-	875.3
gi|8922416|ref|NP_060560.1| hypothetical protein FLJ10420 [Homo sapiens]				1.82E-05	0.62	10.14	10.27	28338.6
AHQ-5-11, 5663	R.TSGELFAQAPVDQFPGTAVESVTDSSR.Y	2797.96841	2	1.82E-05	0.62	2.77	-	362.5
gi|8393638|ref|NP_058642.1| F11 receptor isoform a precursor; platelet F11 receptor; platelet adhes				1.83E-05	0.58	10.14	7.69	32582.9
AHQ-5-8, 4469	K.LIVLVPPSKPTVNIPSSATIGNR.A	2374.80814	2	1.83E-05	0.58	2.78	-	316.4
gi|4505881|ref|NP_000292.1| plasminogen [Homo sapiens]				1.83E-05	0.82	10.18	1.98	90568.6
AHQ-5-4, 4925 - 4941	K.VIPACLPSPNYVVADR.T	1773.04622	2	1.83E-05	0.82	3.54	-	546.6
gi|5453832|ref|NP_006380.1| oxygen regulated protein precursor; oxygen regulated protein (150kD) [H				1.85E-05	0.97	10.27	1.90	111334.8
AHQ-5-3, 6691 - 6749	K.VLQLINDNTATALSYGVFR.R	2096.37206	2	1.85E-05	0.97	5.34	-	1348.6
gi|7662651|ref|NP_054778.1| RGC32 protein [Homo sapiens]				1.90E-05	1.41	20.21	26.50	12924.1
AHQ-5-12, 5298 - 5301	K.ELEAFIADLDK.T	1264.40621	1	4.27E-04	0.53	2.74	-	295.1
AHQ-5-12, 5304	K.ELEAFIADLDK.T	1264.40621	2	4.28E-04	0.94	3.21	-	1566.2
AHQ-5-12, 4280	K.LNSPTDSTPALLSATVTPQK.A	2042.27634	2	1.90E-05	0.89	4.28	-	448.0
gi|7705827|ref|NP_057187.1| GTP-binding protein Sara [Homo sapiens]				1.91E-05	1.88	20.20	11.11	22409.7
AHQ-5-11, 4158	K.LVFLGLDNAGK.T	1147.34882	2	8.52E-05	0.95	4.08	-	1222.4
AHQ-5-11, 2876	K.TTLLHMLKDDR.L	1343.57797	2	1.91E-05	0.93	2.96	-	1650.6
gi|30149221|ref|XP_291446.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				1.94E-05	0.96	10.20	3.86	45688.5
AHQ-5-6, 2218 - 2220	R.STAGDTHLGGEDFDNR.M	1692.68222	2	1.94E-05	0.96	4.09	-	1508.5
gi|10190678|ref|NP_065691.1| RP42 homolog; squamous cell carcinoma-related oncogene [Homo sapiens]				1.96E-05	0.86	10.20	6.56	30124.1
AHQ-5-10, 5760	K.LDVATDNFFQNPELYIR.E	2056.26326	2	1.96E-05	0.86	3.99	-	563.2
gi|9845522|ref|NP_000365.2| uroporphyrinogen decarboxylase; uroporphyrinogen III decarboxylase [Hom				1.96E-05	0.74	10.16	6.81	40802.7
AHQ-5-9, 6363	K.TVTLQGNLDPCALYASEEEIGQLVK.Q	2751.05952	2	1.96E-05	0.74	3.30	-	455.8
gi|5453892|ref|NP_006209.1| phosphoinositide-3-kinase, catalytic, alpha polypeptide; phosphatidylin				1.98E-05	0.67	10.16	1.50	124411.5
AHQ-5-9, 5712 - 5723	R.QVEAMEKLINLTDILK.Q	1859.22068	2	1.98E-05	0.67	3.14	-	721.6
gi|30148500|ref|XP_302052.1| similar to cytoplasmic actin [Homo sapiens]				2.05E-05	0.11	10.14	3.70	33098.0
AHQ-5-13-, 2923	K.EITALAPSSM*K.I	1164.35479	1	2.05E-05	0.11	2.49	-	147.8
AHQ-5-10, 2646	K.EITALAPSSM*K.I	1164.35479	2	6.98E-04	0.52	2.84	-	298.0
gi|19923993|ref|NP_612469.1| chemokine-like factor super family 5 [Homo sapiens]				2.09E-05	0.97	10.26	12.18	17444.2
AHQ-5-12, 4906	R.DRHPEEGVVAELQGFAVDK.A	2097.27378	2	2.09E-05	0.97	5.10	-	1540.1
gi|4506205|ref|NP_002791.1| proteasome beta 9 subunit isoform 1 proprotein; proteasome subunit, bet				2.13E-05	0.90	10.16	5.48	23264.2
AHQ-5-11, 4434	R.FTTDAIALAMSR.D	1297.50607	2	2.13E-05	0.90	3.24	-	1401.9
gi|30148978|ref|XP_291520.2| similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK				2.14E-05	0.80	10.18	2.15	68413.1
AHQ-5-11, 4828 - 4894	R.DWSHYFKTIKDLR.A	1709.92863	2	2.14E-05	0.80	3.47	-	852.9
AHQ-5-12, 4884	R.DWSHYFKTIKDLR.A	1709.92863	2	1.01E-04	0.35	2.55	-	536.1
AHQ-5-13, 4942	R.DWSHYFKTIKDLR.A	1709.92863	2	1.07E-04	0.59	3.07	-	575.0
AHQ-5-13-, 4860	R.DWSHYFKTIKDLR.A	1709.92863	2	6.72E-04	0.82	3.63	-	732.6
AHQ-5-11, 4644 - 4706	R.DWSHYFKTIKDLR.A	1709.92863	2	2.53E-04	0.52	3.07	-	478.0
gi|4506677|ref|NP_002942.1| ribophorin II [Homo sapiens]				2.15E-05	0.94	10.21	2.69	69301.6
AHQ-5-1, 5093	R.LQVTNVLSQPLTQATVK.L	1841.14195	2	2.15E-05	0.94	4.27	-	908.2
gi|4758128|ref|NP_004725.1| doublecortin and CaM kinase-like 1; doublecortin-like kinase [Homo sapi				2.18E-05	0.43	10.12	1.23	81099.6
AHQ-5-7, 1979	R.EYALKIIKK.S	1106.38297	1	2.18E-05	0.43	2.36	-	635.9
gi|5803011|ref|NP_001966.1| enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron				2.26E-05	0.93	10.24	3.69	47268.3
AHQ-5-8, 6369	R.YITGDQLGALYQDFVR.D	1860.05915	2	2.26E-05	0.93	4.87	-	680.5
gi|27483766|ref|XP_208162.1| similar to PTK9 protein tyrosine kinase 9; protein tyrosine kinase 9 [				2.26E-05	0.82	10.18	6.04	30488.3
AHQ-5-12, 4044	K.EFGGGHIKDEIFGTVK.E	1734.93326	2	2.26E-05	0.82	3.59	-	509.6
gi|4505667|ref|NP_001074.1| phosphodiesterase 5A isoform 1; cGMP-binding cGMP-specific 3',5'-cyclic				2.39E-05	1.85	20.22	2.97	100012.4
AHQ-5-5, 4150	R.FPWTTENTGNVNQQCIR.S	2067.22783	2	1.01E-04	0.92	4.34	-	921.2
AHQ-5-5, 3859	R.RGEFFELIR.K	1167.34182	2	2.39E-05	0.92	3.64	-	1068.6
gi|4557321|ref|NP_000030.1| apolipoprotein A-I precursor [Homo sapiens]				2.58E-05	1.79	20.18	9.74	30777.6
AHQ-5-14-, 5151	K.LLDNWDSVTSTFSK.L	1613.74965	2	7.08E-05	0.87	3.31	-	873.2
AHQ-5-11, 5082 - 5090	K.LLDNWDSVTSTFSK.L	1613.74965	2	3.65E-04	0.90	3.67	-	890.3
AHQ-5-14-, 6101 - 6111	K.VSFLSALEEYTK.K	1387.55934	2	2.58E-05	0.92	3.21	-	1177.8
gi|15149476|ref|NP_002878.2| arginyl-tRNA synthetase [Homo sapiens]				2.58E-05	0.45	10.14	3.03	75378.5
AHQ-5-6, 4925	K.AAYPDLENPPLLVTPSQQAK.F	2153.42038	2	2.58E-05	0.45	2.71	-	437.0
gi|6005731|ref|NP_009167.1| calcium binding protein P22; SLC9A1 binding protein; calcineurin homolo				2.69E-05	0.85	10.15	6.15	22456.0
AHQ-5-11, 4600	R.IPELAINPLGDR.I	1308.50858	2	2.69E-05	0.85	2.73	-	1302.0
gi|17999541|ref|NP_060676.2| vacuolar protein sorting 35; maternal-embryonic 3 [Homo sapiens]				2.71E-05	0.81	20.15	3.64	91706.5
AHQ-5-11, 6587 - 6594	R.ERQELRILVGTNLVR.L	1797.09563	2	5.07E-05	0.12	2.61	-	306.4
AHQ-5-5, 2953	K.LNLEHIATSSAVSK.E	1470.65311	2	2.71E-05	0.69	3.06	-	686.7
gi|4505903|ref|NP_002666.1| promyelocytic leukemia protein isoform 6; promyelocytic leukemia, induc				2.77E-05	0.40	10.16	3.95	70023.2

AHQ-5-3, 4959 - 4978	R.M*KCYASDQEVLDMHGFLRQALCRLR.Q	3117.59653	3	2.77E-05	0.40	3.17	-	231.7
gi|6005745|ref|NP_009165.1| dynactin 3 isoform 1; dynactin light chain [Homo sapiens]				2.82E-05	0.88	10.16	5.91	21119.3
AHQ-5-11, 2764	K.VQVALGNISSK.R	1116.29312	2	2.82E-05	0.88	3.23	-	850.0
gi|10864055|ref|NP_067069.1| megakaryocyte-enhanced gene transcript 1 protein; lymphocyte antigen-6				2.98E-05	0.82	10.17	4.71	40891.9
AHQ-5-9, 4792	R.AADGSPCNVLLCSVVPSR.R	1905.14311	2	2.98E-05	0.82	3.39	-	758.4
gi|4505061|ref|NP_002346.1| cation-dependent mannose-6-phosphate receptor precursor; Mr 46,000 Man6				3.04E-05	0.75	10.16	5.05	30993.1
AHQ-5-8, 2838	R.HTLADNFNPVSEER.G	1629.71240	2	3.04E-05	0.75	3.20	-	493.1
gi|21361547|ref|NP_002930.2| ribonuclease/angiogenin inhibitor; Placental ribonuclease inhibitor [H				3.08E-05	0.82	10.19	3.25	49973.3
AHQ-5-14-, 6383	R.WAELLPLLQQCQVVR.L	1855.19360	2	3.08E-05	0.82	3.35	-	542.2
AHQ-5-7, 6615	R.WAELLPLLQQCQVVR.L	1855.19360	2	5.23E-05	0.89	3.89	-	605.5
gi|5802966|ref|NP_006861.1| destrin (actin depolymerizing factor); destrin [Homo sapiens]				3.15E-05	0.98	10.27	10.30	18505.6
AHQ-5-12, 6864	R.KEELM*FFLWAPELAPLK.S	2079.48962	2	3.15E-05	0.98	5.46	-	2301.4
gi|4502923|ref|NP_001830.1| calponin 3; calponin, acidic [Homo sapiens]				3.17E-05	0.90	10.17	3.34	36413.4
AHQ-5-13-, 2692	K.GPSYGLSAEVK.N	1108.22631	2	5.46E-04	0.92	2.85	-	1424.7
AHQ-5-12, 2572	K.GPSYGLSAEVK.N	1108.22631	2	3.17E-05	0.90	3.34	-	935.2
gi|4557241|ref|NP_001095.1| skeletal muscle specific actinin, alpha 3 [Homo sapiens]				3.18E-05	0.84	10.15	0.89	103293.7
AHQ-5-11, 2815	K.ALDFIASK.G	865.00867	1	2.75E-04	0.58	2.38	-	683.5
AHQ-5-5, 2642	K.ALDFIASK.G	865.00867	2	3.18E-05	0.84	3.08	-	608.5
gi|20543399|ref|XP_116396.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				3.21E-05	0.87	10.16	5.00	19852.7
AHQ-5-12, 4364	R.VSFKLFADK.F	1055.25138	2	3.21E-05	0.87	3.27	-	1020.9
AHQ-5-13-, 4405	R.VSFKLFADK.F	1055.25138	1	3.96E-05	0.30	2.71	-	315.8
AHQ-5-12, 4360 - 4568	R.VSFKLFADK.F	1055.25138	1	6.58E-04	0.58	2.14	-	909.4
gi|4505145|ref|NP_002387.1| malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochon				3.35E-05	1.63	20.18	8.56	65443.3
AHQ-5-6, 7250 - 7270	K.IDSYQEPFTHSAPESIPDTFEDAVNILKPSTIIGVAGAGR.L	4245.65187	3	1.68E-04	0.72	3.61	-	437.4
AHQ-5-6, 2812	K.IETQDIQALR.F	1187.32821	2	3.35E-05	0.91	3.14	-	1282.4
gi|29732725|ref|XP_291587.1| similar to Endoplasmin precursor (94 kDa glucose-regulated protein) (G				3.35E-05	0.47	10.13	2.74	37967.5
AHQ-5-5, 3079	R.GLFDEYGSK.K	1016.08574	1	3.35E-05	0.47	2.61	-	225.9
gi|7706371|ref|NP_057190.1| vesicle transport-related protein [Homo sapiens]				3.35E-05	0.79	10.17	2.97	72479.5
AHQ-5-6, 6625 - 6688	K.GSPFPEVAESVQQELESYR.A	2153.29097	2	3.35E-05	0.79	3.49	-	633.0
gi|4507649|ref|NP_003280.1| tropomyosin 2 (beta) [Homo sapiens]				3.48E-05	0.79	10.16	4.58	32989.6
AHQ-5-9, 2472 - 2548	K.ATDAEADVASLNR.R	1333.38703	2	3.48E-05	0.79	2.53	-	1190.5
gi|8923932|ref|NP_060935.1| uncharacterized hematopoietic stem/progenitor cells protein MDS030 [Hom				3.51E-05	0.87	10.17	8.84	17229.3
AHQ-5-12, 2725	R.MKGEAEDILETEK.S	1493.66212	2	3.51E-05	0.87	3.34	-	871.5
gi|4502021|ref|NP_003680.1| aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase);				3.68E-05	0.91	10.18	4.55	36648.3
AHQ-5-9, 4879 - 4952	R.FYAYNPLAGGLLTGK.Y	1585.82741	2	3.68E-05	0.91	3.66	-	990.7
gi|17402865|ref|NP_003303.2| thiosulfate sulfurtransferase; rhodanese [Homo sapiens]				3.68E-05	0.94	20.15	10.77	33428.7
AHQ-5-9, 3586 - 3651	R.FLGTEPEPDAVGLDSGHIR.G	2011.18089	2	3.68E-05	0.19	2.52	-	225.8
AHQ-5-9, 3792	K.TYEQVLENLESKR.F	1609.76254	2	6.60E-05	0.75	3.02	-	426.5
gi|10835121|ref|NP_000289.1| pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H				3.69E-05	0.94	10.18	1.92	61829.8
AHQ-5-7, 3370	R.GDLGIEIPAEK.V	1142.28420	1	2.95E-04	0.26	2.36	-	377.6
AHQ-5-7, 3368 - 3399	R.GDLGIEIPAEK.V	1142.28420	2	3.69E-05	0.94	3.53	-	1204.6
gi|5902016|ref|NP_008939.1| reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sapi				3.76E-05	0.96	10.22	7.04	22395.3
AHQ-5-12, 2941	R.HQAQIDHYLGLANK.N	1608.78270	2	6.07E-04	0.96	4.44	-	1101.8
AHQ-5-14, 3778 - 3858	R.HQAQIDHYLGLANK.N	1608.78270	2	7.67E-04	0.62	2.73	-	573.8
AHQ-5-1, 3104	R.HQAQIDHYLGLANK.N	1608.78270	2	3.76E-05	0.96	4.04	-	1336.8
gi|21618338|ref|NP_003141.2| signal transducer and activator of transcription 3 isoform 2; acute-ph				3.85E-05	0.81	10.18	3.38	87980.2
AHQ-5-6, 2866 - 2868	R.LLQTAATAAQQGGQANHPTAAVVTEK.Q	2577.83547	3	3.33E-04	0.71	3.34	-	677.7
AHQ-5-5, 2871 - 2883	R.LLQTAATAAQQGGQANHPTAAVVTEK.Q	2577.83547	3	3.85E-05	0.81	3.53	-	757.1
gi|4501865|ref|NP_001087.1| ATP citrate lyase [Homo sapiens]				3.87E-05	0.97	10.32	1.99	121419.0
AHQ-5-4, 6358	R.LLQDHPWLLSQNLVVKPDQLIK.R	2599.06730	3	3.87E-05	0.97	6.37	-	1670.2
gi|4507795|ref|NP_003340.1| ubiquitin-conjugating enzyme E2 variant 1 isoform b; DNA-binding protei				3.89E-05	0.86	10.14	4.07	25796.6
AHQ-5-12, 3365	K.YPEAPPFVR.F	1076.22914	2	3.89E-05	0.86	2.84	-	785.8
gi|5803217|ref|NP_006821.1| ubiquinol-cytochrome c reductase (6.4kD) subunit [Homo sapiens]				3.94E-05	0.83	10.13	21.43	6569.6
AHQ-5-14-, 6171	R.LILDWVPYINGK.F	1431.70332	2	3.94E-05	0.83	2.59	-	775.8
gi|7019485|ref|NP_037364.1| programmed cell death 6; apoptosis-linked gene 2 [Homo sapiens]				3.96E-05	0.82	10.15	6.81	21868.3
AHQ-5-11, 5438	K.AGVNFSEFTGVWK.Y	1442.59992	2	3.96E-05	0.82	3.04	-	784.0
gi|30149460|ref|XP_210540.2| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				4.09E-05	0.94	10.16	3.95	29287.8
AHQ-5-5, 2049 - 2062	K.HIYYITGETK.D	1225.37490	2	4.09E-05	0.94	3.12	-	1059.1
gi|22045787|ref|XP_166506.2| similar to Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation fact				4.24E-05	0.88	10.22	10.30	24824.7
AHQ-5-7, 5270	R.VETGVLKPGMVVTFAPVNVTTEVK.S	2516.98163	2	4.24E-05	0.88	4.43	-	424.3
gi|27499559|ref|XP_062669.7| similar to lactate dehydrogenase A -like [Homo sapiens]				4.26E-05	0.95	10.27	5.63	33375.6
AHQ-5-9, 6510	K.LIIVSNPVDILTYVAWK.L	1945.33337	2	4.26E-05	0.95	5.34	-	1053.6
gi|4502249|ref|NP_003878.1| development- and differentiation-enhancing factor 2; PYK2 C terminus-as				4.37E-05	0.71	10.14	1.69	111649.9
AHQ-5-7, 3588	R.LKHEHCEELLTQALSGR.F	2023.25963	2	4.37E-05	0.71	2.88	-	746.8
gi|24158492|ref|NP_699179.1| F-box only protein 29; F-box protein Fbx29 [Homo sapiens]				4.45E-05	0.46	10.14	2.51	67296.3
AHQ-5-13-, 5044	R.RRWQEELAQAQAPKK.R	1840.07906	2	4.45E-05	0.46	2.73	-	432.4
AHQ-5-8, 5625	R.RRWQEELAQAQAPKK.R	1840.07906	2	4.60E-04	0.33	2.87	-	361.6
gi|5453599|ref|NP_006127.1| capping protein (actin filament) muscle Z-line, alpha 2; F-actin cappin				4.55E-05	1.72	20.25	12.24	32948.9
AHQ-5-9, 4615	K.FTITPSTTQVVGILK.I	1605.90007	2	4.55E-05	0.77	3.38	-	336.9
AHQ-5-9, 4215	K.KIDGQQTIIACIESHQFQAK.N	2317.60733	2	5.65E-05	0.95	4.56	-	966.1
gi|18104998|ref|NP_001119.2| adaptor-related protein complex 1, gamma 1 subunit; gamma adaptin; cla				4.55E-05	0.97	10.30	3.27	91679.3
AHQ-5-13-, 6755	K.TFQLQLLSPSSSIVPAFNTGTITQVIK.V	2892.33903	3	4.55E-05	0.97	6.01	-	1658.7
gi|7662502|ref|NP_054779.1| MCT-1 protein [Homo sapiens]				4.65E-05	0.96	10.28	10.50	20555.2
AHQ-5-11, 5186	K.FVLSGANIMCPGLTSPGAK.L	1922.25862	2	4.65E-05	0.96	5.55	-	983.0
gi|4507195|ref|NP_003119.1| spectrin, beta, non-erythrocytic 1; Spectrin, beta, nonerythrocytic-1 (				4.74E-05	0.53	10.15	0.51	274628.5
AHQ-5-3, 5543	R.LAEISDVWEEMK.T	1450.63894	1	4.74E-05	0.53	2.91	-	547.2
gi|30153966|ref|XP_293932.2| similar to hypothetical protein BC013073 [Homo sapiens]				4.79E-05	0.31	10.21	9.04	21711.3
AHQ-5-1, 4075	R.MIFTLFTINVSKDIRHH	2073.44997	2	1.61E-04	0.56	3.21	-	320.2
AHQ-5-1, 4247 - 4320	R.MIFTLFTINVSKDIRHH	2073.44997	2	2.13E-04	0.66	3.32	-	562.2
AHQ-5-2, 3919 - 3990	R.MIFTLFTINVSKDIRHH	2073.44997	2	9.46E-04	0.31	2.80	-	347.1
AHQ-5-2, 4182 - 4257	R.MIFTLFTINVSKDIRHH	2073.44997	2	7.16E-04	0.53	3.35	-	359.8
AHQ-5-3, 4009	R.MIFTLFTINVSKDIRHH	2073.44997	2	4.79E-05	0.31	2.85	-	385.5
AHQ-5-4, 4186	R.MIFTLFTINVSKDIRHH	2073.44997	3	1.96E-04	0.86	3.71	-	1280.5
AHQ-5-5, 4037	R.MIFTLFTINVSKDIRHH	2073.44997	2	1.12E-04	0.20	2.77	-	248.8
AHQ-5-5, 4050 - 4130	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.06E-04	0.54	3.11	-	432.8
AHQ-5-6, 3662	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.98E-04	0.31	2.80	-	326.7
gi|20547663|ref|XP_166266.1| similar to Esterase D [Homo sapiens]				4.87E-05	1.48	20.18	14.54	31462.6
AHQ-5-9, 6252 - 6326	R.MYSYVTEELPQLINANFPVDPQR.M	2726.05680	2	3.38E-04	0.64	3.20	-	356.2
AHQ-5-9, 5678 - 5679	K.SVSAFAPICNPVLCPWGK.K	2006.33387	2	4.87E-05	0.84	3.69	-	405.8
gi|21389505|ref|NP_653321.1| hypothetical protein FLJ31564 [Homo sapiens]				4.96E-05	0.37	10.15		73208.7
AHQ-5-14, 4812 - 4873	R.DSICCKLSNGADILFEPKLKFM	2590.03282	3	4.96E-05	0.37	3.07	-	288.1
gi|4505185|ref|NP_002406.1| macrophage migration inhibitory factor (glycosylation-inhibiting factor				5.00E-05	0.52	10.17	7.83	12476.2
AHQ-5-14-, 4489 - 4501	K.LLCGLLAER.L	1046.26608	2	7.45E-05	0.94	3.49	-	1170.3
AHQ-5-14, 5412	K.LLCGLLAER.L	1046.26608	1	5.00E-05	0.52	2.66	-	189.6
gi|24308035|ref|NP_056034.1| KIAA1067 protein [Homo sapiens]				5.05E-05	0.92	10.20	2.14	74668.5
AHQ-5-6, 6534	R.HDFSTVLTVFPILR.H	1645.92598	2	5.05E-05	0.92	3.99	-	1093.7
gi|29740794|ref|XP_294045.1| similar to Translationally controlled tumor protein (TCTP) (p23) (Hist				5.05E-05	0.76	10.16	6.84	21098.5
AHQ-5-11, 2724 - 2726	R.VKPFMTGAAEQIK.H	1420.70234	2	5.05E-05	0.76	3.25	-	513.0
gi|14165439|ref|NP_002131.2| heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch bindin				5.30E-05	0.47	10.14	4.09	51027.9
AHQ-5-6, 5110	R.GSYGDLGGPIITTQVTIPK.D	1918.18004	2	5.30E-05	0.47	2.87	-	464.7
gi|4758440|ref|NP_004868.1| glia maturation factor, gamma [Homo sapiens]				5.52E-05	0.81	10.21	9.15	16801.2
AHQ-5-12, 4274 - 4345	R.TTDDLTEAWLQEK.L	1550.64872	2	5.52E-05	0.81	2.95	-	1282.0
gi|11386183|ref|NP_008921.1| WAS protein family, member 2; suppressor of cyclic-AMP receptor (WASP-				5.55E-05	0.57	10.14	3.21	54283.7
AHQ-5-14-, 6051	R.SELECVTNITLANVIR.Q	1834.08473	2	5.55E-05	0.57	2.82	-	405.1
gi|30149013|ref|XP_302138.1| similar to alpha tubulin [Homo sapiens]				5.92E-05	0.88	10.15	4.62	22444.5
AHQ-5-13, 5069	R.EIINLVLDR.I	1085.27902	2	5.92E-05	0.88	3.09	-	986.3
AHQ-5-13-, 4964	R.EIINLVLDR.I	1085.27902	2	6.37E-04	0.67	2.64	-	702.0

AHQ-5-12, 5021	R.EIINLVLDR.I	1085.27902	2	1.83E-04	0.66	3.02	-	624.3
gi|13786129|ref|NP_112586.1|	RAB33B, member RAS oncogene family; likely ortholog of mouse RAB33b [H			6.08E-05	0.16	10.15	4.80	25717.4
AHQ-5-11, 3435	K.IQLWDTAGQER.F	1317.43243	1	3.60E-04	0.40	3.00	-	245.6
AHQ-5-10, 3138	K.IQLWDTAGQER.F	1317.43243	1	6.08E-05	0.16	2.14	-	264.6
gi|7705855|ref|NP_057226.1|	steroid dehydrogenase homolog; likely ortholog of mouse Kik1 steroid de			6.18E-05	0.93	10.20	4.81	34323.9
AHQ-5-9, 5535	K.TFVDFFSQCLHEEYR.S	1980.14540	2	6.18E-05	0.93	3.96	-	1209.4
gi|14749486|ref|XP_051854.1|	similar to Mesoderm development candidate 2 [Homo sapiens]			6.30E-05	0.66	10.15	8.55	26076.5
AHQ-5-10, 3775	R.LLEQWEKDDDIEEGDLPEHK.R	2439.57340	2	6.30E-05	0.66	2.94	-	575.1
gi|4504045|ref|NP_002063.1|	guanine nucleotide binding protein (G protein), q polypeptide [Homo sap			6.30E-05	0.96	10.26	5.29	42142.8
AHQ-5-9, 6443	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	4.11E-04	0.78	3.59	-	528.8
AHQ-5-10, 6502 - 6503	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	2.96E-04	0.90	4.03	-	700.5
AHQ-5-8, 7162	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	6.30E-05	0.96	5.29	-	976.5
gi|6005854|ref|NP_009204.1|	repressor of estrogen receptor activity; B-cell associated protein [Hom			6.40E-05	1.68	20.23	10.70	33296.1
AHQ-5-9, 6282	R.IPWFQYPIIYDIR.A	1725.02480	2	6.40E-05	0.96	4.53	-	1365.2
AHQ-5-9, 5830 - 5906	R.IYLTADNLVLNLQDESFTR.G	2226.47137	2	1.04E-04	0.72	3.11	-	543.3
gi|29738504|ref|XP_292188.1|	similar to ribosomal protein L31 [Homo sapiens]			6.45E-05	0.70	10.17	6.25	23740.3
AHQ-5-4, 5058	R.GITSTVICRSQDR.K	1494.65636	3	6.45E-05	0.70	3.39	-	684.4
gi|20532885|ref|XP_086931.2|	similar to epsilon isoform of 14-3-3 protein [Homo sapiens]			6.54E-05	1.87	20.24	10.98	29380.0
AHQ-5-9, 3535 - 3603	K.LAEQAERYDEMVESMK.K	1930.14986	2	7.38E-04	0.91	4.20	-	821.6
AHQ-5-10, 6282	K.LICCDILDVLDK.H	1479.74157	2	9.14E-04	0.95	4.27	-	995.2
AHQ-5-9, 6194 - 6195	K.LICCDILDVLDK.H	1479.74157	2	6.54E-05	0.95	4.78	-	789.1
gi|4758784|ref|NP_004540.1|	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2, 14.5kDa; NADH			6.57E-05	0.88	10.16	7.56	14187.4
AHQ-5-13-, 2737	K.REDYLYAVR.D	1185.31400	2	6.57E-05	0.88	3.11	-	865.8
gi|8922754|ref|NP_060735.1|	hypothetical protein FLJ10901 [Homo sapiens]			6.92E-05	0.59	10.16	4.52	72890.9
AHQ-5-14-, 5642 - 5721	R.LPTQPGPGWSRCPPSLLCALSFQKSTM*ESK.D	3380.86025	3	6.92E-05	0.59	3.13	-	550.5
gi|5453559|ref|NP_006347.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; ATP			6.98E-05	1.87	20.24	17.39	18491.1
AHQ-5-11, 6435 - 6442	K.TIDWVAFAEIIPQNQK.A	1874.12896	2	1.32E-04	0.95	4.74	-	876.5
AHQ-5-11, 4838	K.YPYWPHQPIENL	1557.73261	2	6.98E-05	0.92	3.40	-	1173.1
gi|16933540|ref|NP_004451.2|	fibroblast activation protein, alpha subunit; integral membrane serine			7.09E-05	0.30	10.10	1.32	87711.9
AHQ-5-10, 6131 - 6210	K.FIEM*GFIDEK.R	1245.42636	1	7.09E-05	0.30	1.94	-	691.8
gi|4503377|ref|NP_001377.1|	dihydropyrimidinase-like 2; collapsin response mediator protein hCRMP-2			7.40E-05	2.35	30.21	10.84	62293.3
AHQ-5-7, 3988 - 4068	R.AITIANQTNCPLYITK.V	1823.10355	2	7.40E-05	0.63	3.16	-	223.1
AHQ-5-7, 5372	R.FQMPDQGMTSADDFFQGTK.A	2152.34998	2	1.21E-04	0.82	3.18	-	787.9
AHQ-5-7, 4940	R.ILDLGITGPEGHVLSRPEEVEAEAVNR.A	2902.20927	3	3.72E-04	0.90	4.18	-	813.5
gi|20428652|ref|NP_005347.2|	lymphocyte-specific protein tyrosine kinase; oncogene LCK; membrane as			7.48E-05	0.81	10.18	1.96	57969.3
AHQ-5-7, 2166 - 2174	R.LIEDNEYTAR.E	1224.30217	2	7.48E-05	0.81	3.52	-	566.5
gi|4503013|ref|NP_003906.1|	copine I [Homo sapiens]			7.51E-05	0.93	10.24	3.72	59058.5
AHQ-5-6, 7328	R.EALAQTVLAEVPTQLVSYFR.A	2236.55253	2	7.51E-05	0.93	4.86	-	687.8
gi|27481323|ref|XP_208234.1|	similar to unactive progesterone receptor, 23 kD; likely ortholog of m			7.64E-05	0.73	10.13		18694.3
AHQ-5-11, 4406	K.LTFSCLGGSDNFK.H	1447.59493	2	7.64E-05	0.73	2.61	-	825.3
gi|30156575|ref|XP_301313.1|	similar to caspase 1 isoform alpha precursor; interleukin 1-beta conve			7.68E-05	0.22	10.11	7.14	16555.1
AHQ-5-14, 4761	K.YLALIISNTK.F	1136.36594	1	7.68E-05	0.22	2.27	-	294.4
gi|5174737|ref|NP_006077.1|	tubulin, beta, 4 [Homo sapiens]			7.78E-05	0.29	10.14	3.78	50517.5
AHQ-5-14-, 6182 - 6218	K.M*SSTFIGNSTAIQELFK.R	1891.13493	2	7.78E-05	0.29	2.81	-	194.4
gi|14249382|ref|NP_116139.1|	hypothetical protein MGC15429 [Homo sapiens]			7.92E-05	2.51	30.26	17.14	22345.5
AHQ-5-11, 4258	R.FSVLLLHGIR.F	1155.41731	2	1.26E-04	0.91	2.99	-	1128.0
AHQ-5-11, 6734	K.GAGHPCYLDKPEEWHTGLLDFLQGLQ	2984.29058	3	7.92E-05	0.77	4.54	-	363.5
AHQ-5-11, 4899 - 4938	K.TPALIVYGDQDPMGQTSFEHLK.Q	2448.73644	3	2.00E-04	0.82	3.72	-	747.9
gi|4503573|ref|NP_001967.1|	enolase 3; enolase-3, beta, muscle; muscle specific enolase; beta enola			8.26E-05	0.85	10.19	3.46	46958.5
AHQ-5-14-, 3671 - 3681	K.VNQIGSVTESIQACK.L	1635.82159	2	8.26E-05	0.85	3.15	-	862.3
AHQ-5-8, 2946	K.VNQIGSVTESIQACK.L	1635.82159	2	8.88E-05	0.87	3.77	-	654.6
gi|4507287|ref|NP_003755.1|	syntaxin 11 [Homo sapiens]			8.39E-05	2.14	30.23	14.29	32955.3
AHQ-5-9, 4124	R.DIRDIQDENQLLVADVK.R	1985.18488	2	8.39E-05	0.97	4.53	-	1717.9
AHQ-5-9, 4202	K.EVSGDQIEDMFEQGK.W	1712.81676	2	1.26E-04	0.59	2.89	-	578.0
AHQ-5-9, 3499	R.LAELLDLSK.Q	1002.18679	1	6.27E-04	0.69	3.06	-	399.8
AHQ-5-9, 3498	R.LAELLDLSK.Q	1002.18679	1	3.03E-04	0.58	2.56	-	821.2
gi|29725611|ref|NP_066954.2|	regulatory subunit PR 53 of protein phosphatase 2A isoform b; phosphot			8.66E-05	0.64	10.13	6.81	36775.0
AHQ-5-9, 4878	K.TGPFAEHSNQLWNISAVPSWSK.V	2457.68484	2	8.66E-05	0.64	2.64	-	444.7
gi|4502989|ref|NP_001856.1|	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor; hepa			8.95E-05	0.83	10.15	15.66	9395.9
AHQ-5-14-, 5225 - 5257	K.LFQEDDEIPLYLK.G	1623.82758	2	8.95E-05	0.83	3.09	-	834.3
AHQ-5-14, 6020	K.LFQEDDEIPLYLK.G	1623.82758	2	9.71E-04	0.91	2.97	-	1499.8
gi|28376635|ref|NP_783865.1|	Rab37-like [Homo sapiens]			8.96E-05	0.87	10.18	5.56	24169.2
AHQ-5-10, 3712	R.AWLTEIHEYAQR.D	1517.67002	2	8.96E-05	0.87	3.50	-	735.7
gi|21450665|ref|NP_659415.1|	hypothetical protein FLJ32745 [Homo sapiens]			8.97E-05	0.31	10.13	2.11	76218.1
AHQ-5-12, 6436	K.KQETEEELIENDYR.V	1796.87025	2	8.97E-05	0.31	2.51	-	131.1
gi|19923750|ref|NP_002858.2|	RAB3B, member RAS oncogene family; Brain antigen RAB3B [Homo sapiens]			9.07E-05	0.92	10.17	5.02	24757.7
AHQ-5-11, 3302 - 3355	K.LQIWDTAGQER.Y	1317.43243	2	9.07E-05	0.92	3.32	-	979.0
gi|14161692|ref|NP_115706.1|	calpain small subunit 2 [Homo sapiens]			9.14E-05	0.99	20.14	5.65	27660.1
AHQ-5-12, 3285	K.LGFEEFK.Y	869.98378	2	9.14E-05	0.78	2.55	-	690.3
AHQ-5-10, 3267	K.YLWNNIK.K	951.10326	1	3.55E-04	0.22	2.01	-	298.6
gi|7330335|ref|NP_039234.1|	chloride intracellular channel 4; chloride intracellular channel 4 like			9.53E-05	0.78	10.17	8.70	28771.9
AHQ-5-10, 5158	K.LDEYLNSPLPDEIDENSMEDIK.F	2580.76043	2	9.53E-05	0.78	3.35	-	539.2
gi|11993943|ref|NP_055419.1|	Tax interaction protein 1 [Homo sapiens]			9.80E-05	0.90	10.19	13.71	13734.6
AHQ-5-13-, 4113	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	9.80E-05	0.90	3.18	-	1243.3
AHQ-5-13, 4190 - 4216	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	4.74E-04	0.88	3.80	-	938.3
gi|5803009|ref|NP_006786.1|	EH-domain containing 1; homolog of Drosophila past; EH domain containin			9.91E-05	0.78	10.20	2.81	60844.7
AHQ-5-7, 3578	R.KKEPELFQTVAEGLR.Q	1746.00072	2	9.91E-05	0.78	3.49	-	509.0
gi|30157049|ref|XP_301676.1|	similar to G1/S-specific cyclin D3 [Homo sapiens]			9.93E-05	0.52	10.16	7.83	36968.4
AHQ-5-9, 6332	K.AGDELTELLAGVTWVTEVGCLQAAAPR.L	2830.16311	3	9.93E-05	0.52	3.10	-	579.2
gi|4503179|ref|NP_003602.1|	oral-facial-digital syndrome 1; chromosome X open reading frame 5; oral			1.06E-04	0.08	10.14	0.99	116670.5
AHQ-5-5, 5975	K.KEELNQSVNR.V	1217.31440	1	1.06E-04	0.08	2.38	-	201.4
gi|8923733|ref|NP_060055.1|	sugar transporter (SLC2A6 gene) [Homo sapiens]			1.10E-04	0.51	10.16	6.11	54569.1
AHQ-5-8, 6638	R.KLSIM*FSAVPSAAGYALMAGAHGLWM*LLLGR.T	3266.93502	3	1.10E-04	0.51	3.11	-	384.4
gi|4759302|ref|NP_004729.1|	VAMP (vesicle-associated membrane protein)-associated protein B and C;			1.11E-04	1.31	20.14	11.52	27228.2
AHQ-5-12, 4281	K.FRGPFTDVVTTNLK.L	1595.82383	2	1.11E-04	0.89	2.65	-	1860.8
AHQ-5-12, 3418	K.VEQVLSLEPQHELK.F	1649.86980	2	8.32E-04	0.43	2.73	-	397.3
gi|4506057|ref|NP_002722.1|	protein kinase, cAMP-dependent, catalytic, beta [Homo sapiens]			1.13E-04	0.14	10.13	2.56	40622.4
AHQ-5-8, 3137	R.NLLQVDLTK.R	1044.22690	1	1.13E-04	0.14	1.88	-	193.2
gi|29731460|ref|XP_293027.1|	similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl			1.16E-04	0.39	10.14	4.69	23572.2
AHQ-5-10, 2042 - 2066	K.LLLQVQHASK.Q	1137.35716	1	1.16E-04	0.39	2.19	-	369.7
gi|23110942|ref|NP_002781.2|	proteasome alpha 5 subunit; proteasome component 5; macropain subunit			1.22E-04	0.93	10.21	7.88	26410.9
AHQ-5-10, 4290	K.GPQLFHMDPSGTFVQCDAR.A	2165.39491	2	1.22E-04	0.93	4.15	-	945.8
gi|4557251|ref|NP_001101.1|	a disintegrin and metalloprotease domain 10 [Homo sapiens]			1.24E-04	0.84	10.22	1.87	84141.7
AHQ-5-5, 3978	R.TITLQPGSPCNDFR.G	1607.76993	2	1.24E-04	0.84	3.45	-	412.3
gi|11863152|ref|NP_004964.2|	jumonji; jumonji (mouse) homolog [Homo sapiens]			1.24E-04	0.42	10.13	1.04	138733.5
AHQ-5-13-, 4523	K.KWNKLADM*LRIPR.T	1658.00814	2	1.24E-04	0.42	2.58	-	617.7
gi|19923142|ref|NP_002256.2|	karyopherin beta 1; nuclear factor p97; importin 90; importin beta-1 s			1.26E-04	0.91	10.19	1.60	97169.7
AHQ-5-5, 2577	K.TVSPDRLELEAAQK.F	1557.73077	2	1.26E-04	0.91	3.79	-	1214.1
gi|15553127|ref|NP_000180.2|	hexokinase 2; hexokinase-2, muscle [Homo sapiens]			1.27E-04	1.38	20.16	2.07	102379.3
AHQ-5-4, 2269	K.GAAM*VTAVAYR.L	1126.31148	2	1.27E-04	0.92	3.23	-	1294.2
AHQ-5-4, 4312	R.NILIDFTK.R	964.14024	1	1.33E-04	0.46	2.23	-	333.6
gi|5802978|ref|NP_006780.1|	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 2; apo			1.31E-04	0.53	10.16	12.50	25703.0
AHQ-5-1, 5397 - 5419	K.LKELIELPPFEIVTGERLPANFFKFQFR.N	3380.96783	3	1.31E-04	0.53	3.27	-	261.7
gi|6005717|ref|NP_009031.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e; ATP			1.32E-04	0.16	10.12	14.49	7933.1
AHQ-5-4, 2320	K.KQDELKRIAR.E	1257.46804	1	1.32E-04	0.16	2.32	-	260.8
gi|5803121|ref|NP_006801.1|	for protein disulfide isomerase-related [Homo sapiens]			1.33E-04	1.77	20.16	4.24	59594.0
AHQ-5-7, 3720	R.FHISEFPTLK.Y	1219.41350	2	1.33E-04	0.87	2.68	-	995.4

AHQ-5-7, 2860	K.GPPLWEEDPGAK.D	1296.40999	2	4.66E-04	0.90	3.28	-	927.4
gi|17473323|ref|XP_061930.1| similar to Homeobox protein DBX1 [Homo sapiens]				1.34E-04	0.17	10.11	2.62	37282.8
AHQ-5-11, 2814 - 2824	R.RAVFSDVQR.K	1078.20667	1	1.34E-04	0.17	2.16	-	244.3
gi|4503609|ref|NP_001976.1| electron-transfer-flavoprotein, beta polypeptide; electron-transferring				1.34E-04	0.95	10.23	6.27	27843.4
AHQ-5-10, 4678	K.HSMNPFCEIAVEEAVR.L	1891.11834	2	1.34E-04	0.95	4.58	-	1012.0
gi|30148456|ref|XP_293602.2| similar to glutathione-S-transferase like; glutathione transferase ome				1.35E-04	0.88	10.16	3.88	29139.6
AHQ-5-10, 4090	K.VPSLVGSFLR.T	1075.28583	2	2.11E-04	0.89	3.13	-	1034.4
AHQ-5-11, 4443	K.VPSLVGSFLR.T	1075.28583	2	1.66E-04	0.86	3.02	-	821.4
AHQ-5-9, 3955	K.VPSLVGSFLR.T	1075.28583	2	1.35E-04	0.88	2.88	-	918.9
gi|29741138|ref|XP_291762.1| similar to hypothetical protein MGC33214 [Homo sapiens]				1.35E-04	0.53	10.17	3.01	56604.2
AHQ-5-13-, 4700	K.NSSVPCASLRRVCLR.E	1778.05092	3	1.35E-04	0.53	3.31	-	668.1
gi|4504521|ref|NP_002147.1| heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P				1.35E-04	1.62	20.20	3.84	61024.2
AHQ-5-7, 5523	K.TLNDELEIIEGMK.F	1505.71604	2	1.35E-04	0.67	2.79	-	634.7
AHQ-5-7, 2516	K.VGLQVVAVK.A	913.13961	2	2.11E-04	0.95	3.13	-	1806.4
gi|4557014|ref|NP_001743.1| catalase [Homo sapiens]				1.37E-04	0.75	20.19	3.42	59755.8
AHQ-5-7, 2362	K.DAQIFIQK.K	963.11234	1	1.37E-04	0.39	2.10	-	604.7
AHQ-5-7, 3946	R.DLFNAIATGK.Y	1050.19000	1	9.36E-04	0.36	1.92	-	552.0
gi|6005735|ref|NP_009194.1| coatomer protein complex, subunit epsilon [Homo sapiens]				1.39E-04	0.91	10.22	6.82	34493.9
AHQ-5-9, 4095	R.KFGVVLDEIKPSSAPELQAVR.M	2284.64032	2	1.39E-04	0.91	4.33	-	594.1
gi|24307939|ref|NP_036205.1| chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]				1.42E-04	0.92	10.17	3.14	59670.7
AHQ-5-7, 7087	R.WVGGPEIELIAIATGGR.I	1739.99618	2	1.42E-04	0.92	3.40	-	1396.7
gi|4502097|ref|NP_001142.1| solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra				1.44E-04	1.12	20.18	13.13	33148.4
AHQ-5-10, 6476 - 6543	R.YFAGNLASGGAAGATSLCFVYPLDFAR.T	2799.10926	2	2.71E-04	0.83	3.67	-	649.6
AHQ-5-10, 5171 - 5174	R.YFPTQALNFAFK.D	1447.66130	1	1.44E-04	0.29	2.26	-	453.1
gi|29732043|ref|XP_294519.1| similar to chromosome 15 open reading frame 2 [Homo sapiens]				1.45E-04	0.46	10.16	2.70	121243.9
AHQ-5-7, 7150 - 7151	R.QLAAISATSVINITGRSLIIEWGVWDSVMK.K	3260.79557	3	1.45E-04	0.46	3.14	-	481.1
gi|22065448|ref|XP_084610.2| similar to tubulin alpha-1 chain - Chinese hamster [Homo sapiens] [MAS				1.46E-04	0.88	10.18	2.41	41009.4
AHQ-5-7, 4818 - 4834	K.EIIDLVLDR.I	1086.26378	2	1.46E-04	0.88	3.56	-	860.2
gi|20149621|ref|NP_056348.2| DKFZP586B1621 protein [Homo sapiens]				1.52E-04	0.74	10.19	3.65	58946.8
AHQ-5-7, 1999	R.VAPAEPQEAPDSTAAGGSASK.R	1942.03059	2	1.52E-04	0.74	3.71	-	322.5
gi|4506063|ref|NP_002725.1| protein kinase, cAMP-dependent, regulatory, type I, alpha; tissue-speci				1.54E-04	0.85	10.20	4.46	42981.4
AHQ-5-8, 4817	R.LTVADALEPVQFEDGQK.I	1861.04222	2	8.36E-04	0.52	2.87	-	253.9
AHQ-5-7, 4986	R.LTVADALEPVQFEDGQK.I	1861.04222	2	1.54E-04	0.85	4.00	-	452.9
gi|5453998|ref|NP_006382.1| importin 7; RAN-binding protein 7 [Homo sapiens]				1.57E-04	0.75	10.16	1.64	119515.7
AHQ-5-4, 5286	R.NPVWYQALTHGLNEEQR.K	2056.22658	2	1.57E-04	0.75	3.29	-	497.5
gi|20149635|ref|NP_057227.2| p47 protein [Homo sapiens]				1.58E-04	0.54	10.13	6.22	40572.5
AHQ-5-8, 3345	K.LGSTAPQVLSTSSPAQQAENEAK.A	2315.48018	2	1.58E-04	0.54	2.70	-	363.5
gi|22748857|ref|NP_689616.1| hypothetical protein FLJ39155 [Homo sapiens]				1.59E-04	0.62	10.14	1.99	43814.7
AHQ-5-12, 2337	K.KMSISNPK.T	905.09784	2	1.59E-04	0.62	2.74	-	501.2
gi|10864021|ref|NP_067033.1| MUM2 protein [Homo sapiens]				1.60E-04	0.87	10.17	11.03	16831.5
AHQ-5-13, 6072 - 6141	K.NPLCPLGQTVQSELFR.S	1861.11187	2	1.60E-04	0.87	3.46	-	546.0
gi|4885079|ref|NP_005165.1| ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypept				1.61E-04	0.67	10.13	3.37	32880.7
AHQ-5-9, 2967	K.EVMLVGIGDK.I	1061.27773	1	1.61E-04	0.67	2.63	-	474.4
gi|23308567|ref|NP_079356.2| asparaginase-like 1 protein [Homo sapiens]				1.66E-04	0.90	10.23	10.06	32084.3
AHQ-5-12, 4722	R.VGDSPCLGAGGYADNDIGAVSTTGHGESILK.V	3021.21957	3	1.66E-04	0.90	4.66	-	866.6
gi|16306548|ref|NP_006504.2| seryl-tRNA synthetase; serine-tRNA ligase [Homo sapiens]				1.70E-04	0.59	10.16	3.50	58776.9
AHQ-5-7, 6315	K.EVMQEVAQLSQFDEELYK.V	2187.41227	2	1.70E-04	0.59	3.14	-	484.6
gi|7657585|ref|NP_055067.1| solute carrier family 25 (mitochondrial carrier; ornithine transporter)				1.75E-04	0.86	10.18	5.32	32736.1
AHQ-5-10, 5152	K.DGPLGFYHGLSSTLLR.E	1733.94849	2	1.75E-04	0.86	3.56	-	895.8
gi|22748799|ref|NP_689584.1| hypothetical protein MGC26818 [Homo sapiens]				1.75E-04	0.82	10.14	5.56	21222.4
AHQ-5-11, 1996	K.HAVTGEAVELR.S	1182.31165	2	1.75E-04	0.82	2.78	-	767.3
gi|8923579|ref|NP_060377.1| hypothetical protein FLJ20625 [Homo sapiens]				1.79E-04	0.91	10.28	8.07	17744.7
AHQ-5-12, 5401	R.TDEQALLSSILAK.T	1389.57677	2	1.79E-04	0.91	3.30	-	1049.9
gi|4506181|ref|NP_002778.1| proteasome alpha 2 subunit; proteasome subunit HC3; proteasome componen				1.79E-04	0.95	10.22	5.98	25898.4
AHQ-5-10, 3272 - 3280	K.HIGLVYSGMGPDYR.V	1565.77809	2	1.79E-04	0.95	4.32	-	1132.6
gi|29736026|ref|XP_085123.3| similar to Ras-related protein Rab-15 [Homo sapiens]				1.84E-04	0.74	10.14	5.29	23517.8
AHQ-5-13, 3577	R.IQIWDTAGQER.Y	1317.43243	2	1.84E-04	0.74	2.90	-	660.2
gi|30154099|ref|XP_299053.2| similar to High mobility group protein 1 (HMG-1) (Amphoterin) (Heparin				1.85E-04	0.27	10.10	1.34	83174.7
AHQ-5-2, 3465	R.FGALGDRAER.S	1092.19020	1	1.85E-04	0.27	1.95	-	304.4
gi|6005902|ref|NP_009043.1| thrombospondin 3 [Homo sapiens]				1.87E-04	0.55	10.15		104200.6
AHQ-5-1, 4796	R.FYVVMWK.Q	973.21547	1	4.49E-04	0.74	2.12	-	1038.0
AHQ-5-2, 4603	R.FYVVMWK.Q	973.21547	2	2.57E-04	0.90	2.99	-	861.0
AHQ-5-4, 4606	R.FYVVMWK.Q	973.21547	1	1.87E-04	0.55	1.85	-	672.3
AHQ-5-6, 4288	R.FYVVMWK.Q	973.21547	1	2.82E-04	0.74	2.18	-	821.7
AHQ-5-7, 4047 - 4118	R.FYVVMWK.Q	973.21547	1	3.86E-04	0.58	1.91	-	804.3
AHQ-5-9, 3832	R.FYVVMWK.Q	973.21547	1	8.92E-04	0.74	2.72	-	575.0
AHQ-5-9, 3835	R.FYVVMWK.Q	973.21547	1	2.59E-04	0.80	2.34	-	922.7
AHQ-5-10, 4028	R.FYVVMWK.Q	973.21547	1	5.76E-04	0.52	2.24	-	400.6
AHQ-5-11, 4306 - 4331	R.FYVVMWK.Q	973.21547	1	3.54E-04	0.78	2.32	-	981.1
gi|14141168|ref|NP_005007.2| poly(rC)-binding protein 2 isoform a; poly(rC)-binding protein 2; alph				2.00E-04	0.80	10.16	3.55	38650.9
AHQ-5-11, 4772	R.IITLAGPTNAIFK.A	1359.63864	2	2.00E-04	0.80	3.24	-	497.0
gi|6005978|ref|NP_009098.1| zinc finger protein 258 [Homo sapiens]				2.02E-04	0.48	10.16	3.73	79098.7
AHQ-5-5, 5621	R.DFGERWGNYCKM*CSYCSQTSPNLVENR.L	3379.63995	3	2.02E-04	0.48	3.14	-	194.0
gi|5453760|ref|NP_006147.1| neural precursor cell expressed, developmentally down-regulated 8 [Homo				2.02E-04	0.25	10.15	17.28	9071.5
AHQ-5-14, 4481 - 4510	K.EIEIDIEPTDKVER.I	1686.84208	2	2.02E-04	0.25	2.57	-	291.6
gi|7669501|ref|NP_005552.2| lysosomal-associated membrane protein 1 [Homo sapiens]				2.05E-04	0.92	10.20	3.85	44772.8
AHQ-5-4, 7237	R.FFLQGIQLNTILPDAR.D	1847.14988	2	2.05E-04	0.92	4.03	-	964.1
gi|18087855|ref|NP_542408.1| dynein light chain 2 [Homo sapiens]				2.05E-04	0.63	10.12	7.87	10349.8
AHQ-5-14, 3890 - 3952	K.DIAAYIK.K	793.93045	1	2.05E-04	0.63	2.20	-	591.1
gi|21359837|ref|NP_003312.2| Tu translation elongation factor, mitochondrial [Homo sapiens]				2.16E-04	0.83	10.19	4.20	49541.2
AHQ-5-8, 6025 - 6037	R.DLEKPFLLPVEAVYSVPGR.G	2130.47156	2	2.16E-04	0.83	3.89	-	499.4
gi|29734623|ref|XP_299768.1| hypothetical protein XP_299768 [Homo sapiens]				2.19E-04	0.48	10.12	7.46	14905.7
AHQ-5-10, 3323	K.RMVPVKEIDR.L	1243.50477	1	2.19E-04	0.48	2.31	-	608.9
gi|19913373|ref|NP_079536.2| G6B protein isoform G6b-A precursor; G6B protein; immunoglobulin recep				2.23E-04	1.60	20.17	16.46	25002.6
AHQ-5-9, 3350	R.GPGPGTEPALCGSGPSSPQQAPPAVHSGPC	2858.07042	2	2.23E-04	0.65	2.95	-	438.3
AHQ-5-12, 2402	R.TVLHVLGDR.T	1010.17224	2	2.60E-04	0.95	3.08	-	1654.1
AHQ-5-11, 2304 - 2336	R.TVLHVLGDR.T	1010.17224	2	3.21E-04	0.85	2.66	-	1152.2
gi|7705501|ref|NP_057546.1| hypothetical protein HSPC194 [Homo sapiens]				2.25E-04	0.95	10.19	15.18	11564.5
AHQ-5-14-, 6290	K.FMPAGLIAGASLLM*VAK.V	1707.13765	2	2.25E-04	0.95	3.69	-	1475.9
gi|4758158|ref|NP_004395.1| neural precursor cell expressed, developmentally down-regulated 5 [Homo				2.26E-04	1.66	20.18	9.70	41487.2
AHQ-5-8, 5605	R.LYPWGVVEVENPEHNDFLK.L	2286.52696	2	3.52E-04	0.75	3.03	-	484.7
AHQ-5-14-, 6586	K.STLINSLFLTDLYPER.V	1883.13416	2	2.26E-04	0.90	3.70	-	901.3
gi|4557385|ref|NP_000055.1| complement component 3 precursor; acylation-stimulating protein cleavag				2.26E-04	0.94	10.20	1.32	187162.3
AHQ-5-6, 4532	R.VPVAVQGEDTVQSLTQGDGVAK.L	2199.40432	2	2.26E-04	0.94	4.01	-	930.9
gi|24430132|ref|NP_036610.2| WW domain binding protein 2 [Homo sapiens]				2.27E-04	0.64	10.17	5.75	28086.8
AHQ-5-13, 4254	K.DCEIKQPVFGANYIK.G	1784.02587	2	2.27E-04	0.64	2.98	-	320.9
gi|16160851|ref|XP_035527.2| similar to KIAA1370 protein [Homo sapiens]				2.30E-04	0.36	10.13	1.39	121668.8
AHQ-5-13, 4709 - 4714	R.TLKSFSMVDSSISNR.Q	1672.88527	2	2.30E-04	0.36	2.68	-	447.3
gi|10092691|ref|NP_055243.1| tight junction protein 3 (zona occludens 3) [Homo sapiens]				2.33E-04	0.46	10.15	2.10	104827.2
AHQ-5-7, 7423	R.RSPGGGSEANGLALVSGFKR.L	1961.17147	2	2.33E-04	0.46	3.04	-	450.5
gi|22748879|ref|NP_689628.1| hypothetical protein FLJ32642 [Homo sapiens]				2.49E-04	0.30	10.13	5.04	44342.1
AHQ-5-13-, 2700 - 2763	K.SASSSAAGSPGGLTSLQQQK.Q	1862.97660	2	2.49E-04	0.30	2.67	-	301.3
gi|22048785|ref|XP_047659.6| similar to KIAA0532 protein [Homo sapiens]				2.58E-04	0.29	10.15	1.24	188838.7
AHQ-5-5, 3485	K.QKLPSYILENNELTELCVKAK.G	2492.87358	3	2.58E-04	0.29	3.04	-	255.5
gi|4759274|ref|NP_004777.1| thioredoxin-like, 32kDa; thioredoxin-related 32 kDa protein; thioredoxi				2.65E-04	0.45	10.14	7.96	32251.1
AHQ-5-9, 5262	R.SEPTQALELTEDDIKEDGIVPLR.Y	2569.80365	2	2.65E-04	0.45	2.78	-	426.9
gi|29743626|ref|XP_297123.1| hypothetical protein XP_297123 [Homo sapiens]				2.68E-04	0.75	10.15	13.79	13908.9

AHQ-5-13-, 6783	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	2.68E-04	0.75	2.92	-	922.2
gi|23308579|ref|NP_006592.3|	unactive progesterone receptor, 23 kD; likely ortholog of mouse telome			2.82E-04	0.94	10.23	10.63	18697.3
AHQ-5-11, 4695	K.HLNEIDLFHCIDPNDSK.H	2069.24049	2	2.82E-04	0.94	4.59	-	617.9
gi|22267436|ref|NP_056284.1|	DKFZp564D177 protein [Homo sapiens]			2.86E-04	0.57	10.15	7.29	28466.4
AHQ-5-10, 6054	K.DKEWQEQFLIPNLALIDK.Q	2201.50664	2	2.86E-04	0.57	2.93	-	426.6
gi|12707562|ref|NP_073728.1|	period 2 isoform 2; period, Drosophila, homolog of, 2; period circadia			2.97E-04	0.89	10.17	0.88	136578.7
AHQ-5-4, 4154 - 4181	R.AEICKNGNKTK.N	1264.43426	2	2.97E-04	0.89	3.45	-	861.2
gi|22035665|ref|NP_055874.1|	talin 2 [Homo sapiens]			2.98E-04	0.41	10.14	0.43	271552.5
AHQ-5-7, 2138	K.NCGEMSEIEAK.V	1269.38481	1	2.98E-04	0.41	2.80	-	289.5
gi|18375655|ref|NP_055184.2|	protein tyrosine phosphatase, non-receptor type 18; brain-derived phos			3.01E-04	0.86	10.21	6.52	50482.1
AHQ-5-13, 5093	R.VPADQSPAGSGAYEDVAGGAQTGGLGFNLR.I	2864.03331	3	3.01E-04	0.86	4.27	-	925.2
gi|29739581|ref|XP_084467.3|	similar to eukaryotic initiation factor 5A [Homo sapiens]			3.03E-04	0.94	10.20	8.44	16773.1
AHQ-5-12, 2922	R.LPEGDLGKEIEQK.Y	1456.62321	2	3.03E-04	0.94	4.09	-	1318.0
gi|27262622|ref|NP_065176.2|	neuron navigator 1; neuron navigator-1; pore membrane and/or filament			3.10E-04	0.37	10.15	1.76	202078.2
AHQ-5-11, 4903 - 4971	K.LSHISRLELVESLDSDEVDLKSGYMSDSDLMGK.T	3671.06345	3	3.10E-04	0.37	3.04	-	324.8
gi|22129786|ref|NP_059980.1|	gp25L2 protein [Homo sapiens]			3.13E-04	0.91	10.22	7.94	25104.5
AHQ-5-10, 5758 - 5759	K.CFIEEIPDETMVIGNYR.T	2088.34713	2	3.13E-04	0.91	4.34	-	535.3
gi|4757712|ref|NP_004026.1|	acyl-Coenzyme A oxidase isoform a; acyl-coenzyme A oxidase 1 [Homo sapi			3.20E-04	0.93	10.26	4.24	74745.4
AHQ-5-6, 6861	R.GRPEPLDLHLGMFLPTLLHQATAEQQER.F	3199.63241	3	3.20E-04	0.93	5.11	-	962.9
gi|7019375|ref|NP_037373.1|	formin homology 2 domain containing 1; FH1/FH2 domain-containing protei			3.21E-04	0.87	10.20	2.06	126496.5
AHQ-5-7, 3712	K.FSGVAGEAPSNPSVPVAVSSGPGR.G	2227.41945	2	3.21E-04	0.87	4.05	-	485.2
gi|13259508|ref|NP_075408.1|	dynactin 1 isoform 2; dynactin 1 (p150, Glued (Drosophila) homolog); p			3.21E-04	0.21	10.13	1.22	127403.0
AHQ-5-11, 3851	-.M*M*RQAPTARKTTTR.R	1681.96674	2	3.21E-04	0.21	2.62	-	321.2
gi|4506807|ref|NP_000325.1|	sodium channel, voltage-gated, type IV, alpha; hyperkalemic periodic pa			3.24E-04	0.53	10.16	1.63	208061.0
AHQ-5-11, 6524 - 6603	K.PNKIKLITLDLPMVPGDKIHCLDILFALTK.E	3420.17196	3	3.24E-04	0.53	3.15	-	391.0
gi|14149817|ref|NP_115523.1|	hypothetical protein DKFZp434D0127 [Homo sapiens]			3.37E-04	0.32	10.10	0.98	81154.7
AHQ-5-14-, 3667	R.RRILMGK.I	874.13334	1	3.37E-04	0.32	1.99	-	296.6
gi|7706563|ref|NP_057614.1|	RAB-8b protein [Homo sapiens]			3.55E-04	0.30	10.14	3.86	23584.0
AHQ-5-11, 3191	K.LAIDYGIK.F	893.06202	1	3.55E-04	0.30	1.90	-	513.4
gi|29789112|ref|NP_065765.1|	KIAA1198 protein [Homo sapiens]			3.56E-04	0.51	10.13	2.08	61340.2
AHQ-5-12, 3662 - 3676	K.THTGEKPFVCR.E	1333.49829	2	3.56E-04	0.51	2.56	-	615.6
gi|30156276|ref|XP_304146.1|	hypothetical protein XP_304146 [Homo sapiens]			3.72E-04	0.70	10.17	6.88	28134.9
AHQ-5-7, 6024 - 6098	-.M*AGALKAQGRNDLEKWR.E	1961.23808	2	3.72E-04	0.70	3.36	-	952.6
gi|23397534|ref|NP_694978.1|	hypothetical protein MGC45491 [Homo sapiens]			3.76E-04	0.25	10.15	7.62	24260.8
AHQ-5-14-, 4643	R.KNSTSKDLVTLGASSLR.E	1778.00112	2	3.76E-04	0.25	3.04	-	313.6
gi|30156349|ref|XP_301652.1|	similar to Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) [			3.83E-04	0.23	10.15	9.33	21450.7
AHQ-5-8, 4044 - 4066	K.M*HAADLTVSALRGDM*DEK.E	1993.20912	2	3.83E-04	0.23	2.75	-	321.8
gi|4505359|ref|NP_002481.1|	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6, 14kDa; NADH dehy			3.94E-04	0.92	10.17	8.59	15136.5
AHQ-5-13, 2299	R.FFHETEAPRPK.D	1359.51414	2	3.94E-04	0.92	3.44	-	1074.3
gi|27479210|ref|XP_212118.1|	hypothetical protein XP_212118 [Homo sapiens]			3.97E-04	0.14	10.10	6.48	12593.6
AHQ-5-3, 2206 - 2242	R.LCNWPLK.L	932.12153	1	3.97E-04	0.14	2.06	-	308.0
gi|17482508|ref|XP_058957.1|	similar to QIL1 [Homo sapiens]			4.18E-04	0.78	10.26	16.95	13087.2
AHQ-5-14-, 6663	R.DSWNAGIM*TVMSALSVAPSK.A	2082.38744	2	4.18E-04	0.78	4.04	-	666.3
gi|4507955|ref|NP_003394.1|	YY1 transcription factor [Homo sapiens]			4.33E-04	0.27	10.10	2.17	44712.3
AHQ-5-13-, 2736	K.KFAQSTNLK.S	1037.19446	1	4.33E-04	0.27	2.00	-	222.0
gi|10864011|ref|NP_067022.1|	sulfide dehydrogenase like; sulfide dehydrogenase like (yeast) [Homo s			4.54E-04	0.08	10.09	1.33	49960.4
AHQ-5-4, 1976	K.NLIEVR.A	743.87466	1	4.54E-04	0.08	1.89	-	213.9
gi|27477134|ref|NP_079199.2|	nucleoporin 210; nuclear pore membrane glycoprotein 210; gp210 [Homo s			4.63E-04	0.21	10.15	0.95	205108.8
AHQ-5-2, 4169	R.CDAIVDLIHDIQIVSTTR.E	2071.34097	2	4.63E-04	0.21	2.70	-	277.9
gi|4506407|ref|NP_002873.1|	RAN binding protein 1 [Homo sapiens]			4.70E-04	0.86	10.16	5.47	23310.0
AHQ-5-10, 4064	K.TLEEDEEELFK.M	1382.45159	2	4.70E-04	0.86	3.26	-	622.8
gi|6912340|ref|NP_036277.1|	deoxythymidylate kinase (thymidylate kinase); thymidylate kinase [Homo			4.75E-04	0.63	10.13	5.69	23827.2
AHQ-5-11, 3828	R.YAFSGVAFTGAK.E	1219.37036	2	4.75E-04	0.63	2.50	-	743.0
gi|20270303|ref|NP_620124.1|	mitochondrial Rho 2 [Homo sapiens]			4.80E-04	0.61	10.15	3.24	68117.5
AHQ-5-5, 5789	R.LSDQDLDQALSDEELNAFQK.S	2280.38792	2	4.80E-04	0.61	3.03	-	359.3
gi|4506467|ref|NP_002897.1|	radixin [Homo sapiens]			5.16E-04	0.87	10.17	2.40	68563.4
AHQ-5-6, 4016	R.ILALCM*GNHELYMR.R	1739.07675	2	5.16E-04	0.87	3.32	-	639.9
gi|21362062|ref|NP_115744.2|	leucine zipper and CTNNBIP1 domain containing [Homo sapiens]			5.21E-04	0.54	10.14	7.89	21494.4
AHQ-5-11, 4035	K.ETLEQLSEFNDSLKK.I	1781.94186	2	5.21E-04	0.54	2.68	-	344.9
gi|20553919|ref|XP_033811.2|	similar to hypothetical protein FLJ14775 [Homo sapiens]			5.24E-04	0.46	10.14		17460.4
AHQ-5-13, 6097 - 6104	R.NGSKEGNHHSTQPKR.N	1677.76352	2	5.24E-04	0.46	2.86	-	525.2
gi|7657548|ref|NP_055378.1|	spondyloepiphyseal dysplasia, late; sedlin [Homo sapiens]			5.28E-04	0.53	10.14	10.00	16444.6
AHQ-5-13, 5160 - 5170	K.FSMNPFYEPNSPIR.S	1699.91087	2	5.28E-04	0.53	2.68	-	384.7
gi|21361794|ref|NP_060918.2|	TIP120 protein [Homo sapiens]			5.32E-04	0.91	10.19	1.06	136374.7
AHQ-5-4, 4501	R.AVAALLTIPEAEK.S	1326.56381	2	5.32E-04	0.91	3.73	-	1028.0
gi|25121940|ref|NP_004482.2|	glucocorticoid receptor DNA binding factor 1 isoform b [Homo sapiens]			5.40E-04	0.34	10.11	0.66	172174.1
AHQ-5-7, 3151 - 3192	R.EDTSLPSLSK.D	1077.16739	1	5.40E-04	0.34	2.24	-	456.9
gi|29737976|ref|XP_290742.1|	similar to Phosphoribosylformylglycinamidine synthase (FGAM synthase)			5.40E-04	0.81	10.19	2.09	144733.3
AHQ-5-3, 7241 - 7303	R.LGGTALAQCFSQLGEHPPDLDLPENLVR.A	3050.39201	3	5.40E-04	0.81	3.76	-	662.2
gi|19923233|ref|NP_002970.2|	sterol carrier protein 2 [Homo sapiens]			5.43E-04	0.90	10.17	2.01	58993.3
AHQ-5-13, 2710	K.KLEEEGEQFVK.K	1336.47242	2	5.43E-04	0.90	3.44	-	884.0
gi|4506185|ref|NP_002780.1|	proteasome alpha 4 subunit; proteasome component C9; proteasome subunit			5.52E-04	0.77	10.17	9.20	29483.6
AHQ-5-10, 6180 - 6195	K.LNEDMACSVAGITSDANVLTNELR.L	2595.84629	2	5.52E-04	0.77	3.37	-	405.0
gi|4502125|ref|NP_001152.1|	nudix-type motif 2; diadenosine 5',5''-P1,P4-tetraphosphate pyrophospho			5.85E-04	0.92	10.22	9.52	16829.1
AHQ-5-12, 6294	R.WLGLEEACQLAQFK.E	1694.93232	2	5.85E-04	0.92	4.34	-	731.3
gi|6912714|ref|NP_036592.1|	translocase of inner mitochondrial membrane 9 homolog; translocase of i			5.85E-04	0.34	10.15	17.98	10377.9
AHQ-5-14-, 6145	K.LTETCFLDCVKDFTTR.E	2009.24656	3	5.85E-04	0.34	3.03	-	327.9
gi|4504051|ref|NP_002064.1|	guanine nucleotide binding protein, alpha z polypeptide; transducin alp			5.92E-04	0.66	10.14	4.51	40923.5
AHQ-5-9, 5467 - 5472	K.EYKPLIIYNAIDSLTR.I	1910.20274	2	5.92E-04	0.66	2.72	-	417.6
gi|21361827|ref|NP_062826.2|	putative methyltransferase M6A; putative methyltransferase [Homo sapie			5.97E-04	0.64	10.15	3.10	64473.6
AHQ-5-3, 4237	K.YVHYEIDACMDSEAPGSK.D	2074.23418	3	5.97E-04	0.64	3.10	-	962.6
gi|7705638|ref|NP_057158.1|	CGI-143 protein [Homo sapiens]			5.97E-04	0.70	10.17	10.95	14289.3
AHQ-5-14-, 3978 - 4037	R.TKLEEALSPEVLELR.N	1727.98047	2	5.97E-04	0.70	3.35	-	856.4
gi|30148290|ref|XP_302053.1|	similar to transrationally controlled tumor protein [Homo sapiens] [MA			6.04E-04	0.16	10.11	6.09	13275.9
AHQ-5-11, 1990 - 1995	K.HILANFK.N	843.00793	1	6.04E-04	0.16	2.24	-	211.0
gi|17440554|ref|XP_067503.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			6.05E-04	0.37	10.18	7.93	18110.6
AHQ-5-12, 3532	R.VKEGM*DIVEAM*ER.F	1539.75747	2	6.05E-04	0.37	2.53	-	250.0
gi|7662518|ref|NP_054756.1|	NTT5 protein [Homo sapiens]			6.06E-04	0.07	10.10	1.36	82226.5
AHQ-5-14-, 3677	K.FGLQQLVVAK.I	1103.33918	1	6.06E-04	0.07	2.05	-	134.4
gi|5803133|ref|NP_006825.1|	RAB32, member RAS oncogene family [Homo sapiens]			6.13E-04	0.26	10.13	4.44	24997.1
AHQ-5-10, 2426	K.DNINIEEAAR.F	1145.20505	1	6.13E-04	0.26	2.33	-	228.3
gi|4503539|ref|NP_001409.1|	eukaryotic translation initiation factor 4 gamma, 2; Eukaryotic transla			6.13E-04	0.86	10.18	1.65	102361.2
AHQ-5-8, 5108	K.LQDREWLTELFQQSK.V	1922.13048	2	6.13E-04	0.86	3.62	-	629.1
gi|5032137|ref|NP_005629.1|	synaptobrevin-like 1 [Homo sapiens]			6.14E-04	1.32	20.15	13.18	24934.9
AHQ-5-13-, 4607 - 4672	K.LTYSHGNYLFHYICQDR.I	2189.39466	2	6.14E-04	0.50	2.83	-	236.8
AHQ-5-13, 2889	K.VMETQAQVDELK.G	1391.57303	2	8.79E-04	0.82	3.10	-	912.9
gi|28557709|ref|NP_787082.1|	hypothetical protein LOC221823 [Homo sapiens]			6.15E-04	0.80	10.17	5.35	34839.1
AHQ-5-9, 4338 - 4351	R.VYAILTHGIFSGPAISR.I	1803.09710	2	6.15E-04	0.80	3.39	-	636.3
gi|30158216|ref|XP_210184.2|	similar to hypothetical protein BC015353 [Homo sapiens]			6.21E-04	0.32	10.15	1.97	85272.8
AHQ-5-2, 2193 - 2269	R.PCLCLCSEEGRAPM*R.C	1856.11562	3	6.21E-04	0.32	3.02	-	299.2
gi|4504175|ref|NP_000839.1|	glutathione S-transferase M2; glutathione S-transferase 4; GST, muscle;			6.21E-04	0.83	10.17	7.80	25744.5
AHQ-5-10, 5924	K.LGLDFPNLPYLIDGTHK.I	1914.19309	2	6.21E-04	0.83	3.32	-	754.7
gi|5032007|ref|NP_005850.1|	purine-rich element binding protein A; purine-rich single-stranded DNA-			6.23E-04	0.79	10.18	8.07	34910.5
AHQ-5-8, 4417	K.LIDDYGVEEEPAELPEGTSLTVDNKR.F	2891.09052	3	6.23E-04	0.79	3.69	-	576.8
gi|8922648|ref|NP_060677.1|	hypothetical protein FLJ10759 [Homo sapiens]			6.28E-04	0.60	10.16	3.16	54190.3
AHQ-5-8, 4472 - 4550	R.TTIGEAFERLHRLLR.E	1813.09675	2	6.28E-04	0.60	3.16	-	292.4
gi|4507797|ref|NP_003341.1|	ubiquitin-conjugating enzyme E2 variant 2; 1 alpha,25-dihydroxyvitamin			6.29E-04	0.85	10.19	6.90	16362.7

AHQ-5-12, 2976 - 2977	R.LLEELEEGQK.G	1188.30974	2	6.29E-04	0.85	3.74	-	837.2
gi|20373153|ref|NP_115997.4| myosin XVIIIB; myosin 18B [Homo sapiens]				6.31E-04	0.91	10.21	0.70	285231.7
AHQ-5-8, 6557	R.ITAAQLQTMLLEKSRVAR.Q	2030.42494	2	6.31E-04	0.91	4.27	-	1368.9
gi|22041780|ref|XP_059066.2| similar to 14-3-3 protein sigma (Stratifin) (Epithelial cell marker pr				6.50E-04	0.93	10.19		27773.9
AHQ-5-10, 5344 - 5414	K.DSTLIMQLLR.D	1190.43864	2	6.50E-04	0.93	3.83	-	1353.6
gi|4506569|ref|NP_002932.1| roundabout 1 isoform a; roundabout 1; axon guidance receptor [Homo sapi				6.79E-04	0.62	10.16	1.88	180928.0
AHQ-5-1, 7383	K.GLKPNAIYLFLVRAANAYGISDPSQISDPVK.T	3319.79806	3	6.79E-04	0.62	3.12	-	699.6
gi|4507783|ref|NP_003335.1| ubiquitin-conjugating enzyme E2H (UBC8 homolog, yeast); ubiquitin-conju				6.87E-04	0.58	10.14	8.20	20655.0
AHQ-5-11, 4064	K.FYGPQGTPYEGGVWK.V	1686.84715	2	6.87E-04	0.58	2.83	-	355.6
gi|30158950|ref|XP_301585.1| similar to natural killer cell transcript 4 [Homo sapiens]				7.26E-04	0.41	10.16	15.43	18547.1
AHQ-5-14-, 4770 - 4849	R.EPTVNKDIHQRTCDLSKTIEAPAER.Q	2911.19785	3	7.26E-04	0.41	3.22	-	320.5
gi|17452829|ref|XP_071133.1| similar to ATP synthase, H+ transporting, mitochondrial F0 complex, su				7.38E-04	0.45	10.15	6.25	16522.7
AHQ-5-11, 3011	K.AGLVDDFEK.K	994.08007	1	7.38E-04	0.45	2.20	-	681.8
gi|30157691|ref|XP_293394.2| similar to Nucleolar phosphoprotein p130 (Nucleolar 130 kDa protein) (				7.64E-04	0.09	10.10	1.61	59387.8
AHQ-5-2, 1642	R.KADSNSSEK.E	965.98512	1	7.64E-04	0.09	1.80	-	200.2
gi|11545777|ref|NP_071349.1| likely ortholog of mouse ubiquitin-conjugating enzyme E2-230K [Homo sa				7.75E-04	0.37	10.16	4.04	81876.4
AHQ-5-11, 4512	R.TTDIVIRIGNTEDGAPHKEDEQPSVGQVAR.V	3234.48055	3	7.75E-04	0.37	3.16	-	233.8
gi|29745994|ref|XP_290546.1| similar to KIAA0830 protein [Homo sapiens]				7.76E-04	0.86	10.16	2.00	55016.4
AHQ-5-9, 2888	R.DRIPVYSAFR.A	1224.39337	2	7.76E-04	0.86	3.24	-	690.5
gi|9257195|ref|NP_004733.1| BAI1-associated protein 1; WW domain-containing protein 3; atrophin-1 i				7.77E-04	0.43	10.13	1.27	136980.0
AHQ-5-12, 7152 - 7154	R.CRGLKEGDLIVEVNKK.N	1860.16856	2	7.77E-04	0.43	2.66	-	483.6
gi|5031855|ref|NP_005556.1| lymphocyte cytosolic protein 2; SH2 domain-containing leukocyte protein				7.84E-04	0.92	10.18	3.00	60187.8
AHQ-5-10, 6379	R.SEVLGWDPDSLADYFK.K	1842.98222	2	7.84E-04	0.92	3.58	-	1309.2
gi|29729857|ref|XP_293567.1| similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60)				7.93E-04	0.90	10.16	3.38	38427.8
AHQ-5-14-, 3473	R.TVIIEQSWGSPK.V	1345.52569	2	7.93E-04	0.90	3.24	-	1122.9
gi|29739273|ref|XP_291710.1| similar to Ras suppressor protein 1 (Rsu-1) (RSP-1) [Homo sapiens] [MA				8.01E-04	0.86	10.18	5.39	18917.8
AHQ-5-11, 3566	R.DNNLISLPK.E	1014.15766	2	8.01E-04	0.86	2.98	-	1115.9
gi|30147267|ref|XP_304295.1| hypothetical protein XP_304295 [Homo sapiens]				8.03E-04	0.70	10.14		38558.9
AHQ-5-13-, 5939 - 5941	K.PLGWIGQMQGEK.A	1344.56442	2	8.03E-04	0.70	2.90	-	660.0
gi|4757818|ref|NP_004879.1| ATPase, H+ transporting, lysosomal, V1 subunit G isoform 1; vacuolar H(				8.31E-04	0.74	10.17	9.32	13757.4
AHQ-5-13-, 2764	K.EEAQAEIEQYR.L	1366.41548	2	8.31E-04	0.74	3.33	-	662.6
gi|4506427|ref|NP_002880.1| retinoic acid receptor responder (tazarotene induced) 2 [Homo sapiens]				8.32E-04	0.82	10.15	6.75	18617.5
AHQ-5-12, 3646	R.GLQVALEEFHK.H	1271.44680	2	8.32E-04	0.82	3.04	-	1009.7
gi|4502501|ref|NP_000583.1| complement component 4B proprotein [Homo sapiens]				8.43E-04	0.08	10.14	0.52	192795.6
AHQ-5-8, 4492 - 4496	K.SCGLHQLLR.G	1085.26240	1	8.43E-04	0.08	2.11	-	63.5
gi|29741003|ref|XP_295854.1| hypothetical protein XP_295854 [Homo sapiens]				8.46E-04	0.50	10.15	25.93	11483.2
AHQ-5-7, 7350	-.MKFLRQGIPECPSTANPLLLASPSILKK.L	3112.74244	3	8.46E-04	0.50	3.02	-	211.7
gi|18551340|ref|XP_087062.1| similar to 60S acidic ribosomal protein P1 [Homo sapiens]				8.48E-04	0.31	10.14	16.67	10090.5
AHQ-5-12, 6308	K.AAGVNVEPFWPGLFAK.A	1703.96399	2	8.48E-04	0.31	2.87	-	389.3
gi|14150122|ref|NP_115712.1| hypothetical protein MGC14799 [Homo sapiens]				8.52E-04	0.25	10.14	6.28	26046.7
AHQ-5-4, 4038	R.LM*KIEKFFPHVLEK.E	1776.17817	2	8.52E-04	0.25	2.71	-	372.5
gi|16950611|ref|NP_444253.1| myosin light chain kinase isoform 1; myosin light chain kinase [Homo s				8.61E-04	0.78	10.18	1.46	210771.9
AHQ-5-5, 6194	K.LESEEDVSQAFLEAVAEEKPHVKPYFSK.T	3208.51984	3	8.61E-04	0.78	3.61	-	632.7
gi|23110944|ref|NP_002782.1| proteasome alpha 6 subunit; prosomal P27K protein; proteasome subunit				8.66E-04	0.73	10.14	3.66	27399.3
AHQ-5-10, 3470	R.LYQVEYAFK.A	1161.33081	1	8.66E-04	0.73	2.37	-	913.0
gi|6005727|ref|NP_006576.1| chaperonin containing TCP1, subunit 8 (theta); T-complex protein 1, the				8.68E-04	0.46	10.21	2.19	59662.4
AHQ-5-7, 3562	R.GSTDNLMDDIER.V	1366.43729	2	8.68E-04	0.46	2.58	-	540.2
gi|8923582|ref|NP_060378.1| hypothetical protein FLJ20626 [Homo sapiens]				8.72E-04	0.58	10.15	2.67	48956.7
AHQ-5-14-, 2811 - 2887	R.AFDWKSQLVIHR.K	1500.72897	2	8.72E-04	0.58	2.74	-	633.1
gi|23097308|ref|NP_149062.1| nesprin 1 isoform longest; synaptic nuclei expressed gene 1; nesprin 1				8.75E-04	0.31	10.15	0.23	########
AHQ-5-9, 6123	K.ELNALETSSSAMDMQISQIK.V	2197.47364	2	8.75E-04	0.31	2.77	-	246.4
gi|20070272|ref|NP_057110.2| androgen-regulated short-chain dehydrogenase/reductase 1; prostate sho				8.79E-04	0.87	10.18	3.77	35414.1
AHQ-5-13, 5054	K.LANILFTQELAR.R	1389.62483	2	8.79E-04	0.87	3.70	-	809.4
gi|5453974|ref|NP_006247.1| protein kinase C-like 2 [Homo sapiens]				9.10E-04	0.05	10.13	1.83	112033.9
AHQ-5-8, 4641 - 4710	K.LDFSDTMVQQKLDDIKDR.I	2168.41372	2	9.10E-04	0.05	2.64	-	159.6
gi|4503529|ref|NP_001407.1| eukaryotic translation initiation factor 4A, isoform 1 [Homo sapiens] [				9.23E-04	0.89	10.19	3.69	46153.7
AHQ-5-8, 3490	K.LQMEAPHIIVGTPGR.V	1619.91357	2	9.23E-04	0.89	3.77	-	925.2
gi|4503301|ref|NP_001350.1| 2,4-dienoyl CoA reductase 1 precursor; 4-enoyl-CoA reductase [Homo sapi				9.24E-04	0.46	10.14	6.87	36067.5
AHQ-5-9, 4823	K.VHAIQCDVRDPDMVQNTVSELIK.V	2670.01637	2	9.24E-04	0.46	2.78	-	233.0
gi|10800412|ref|NP_036458.2| microtubule-associated protein, RP/EB family, member 3; APC binding pr				9.40E-04	0.64	10.13	3.56	31982.0
AHQ-5-9, 1999	K.LEHEYIHNFK.V	1330.47280	1	9.40E-04	0.64	2.58	-	616.2
gi|4505237|ref|NP_002427.1| palmitoylated membrane protein 1; membrane protein, palmitoylated 1 (55				9.46E-04	0.52	10.14	3.86	52296.2
AHQ-5-9, 5328	K.HSSIFDQLDVVSYEEVVR.L	2123.30800	2	9.46E-04	0.52	2.82	-	433.4
gi|5453854|ref|NP_006187.1| poly(rC) binding protein 1; heterogenous nuclear ribonucleoprotein X; p				9.47E-04	0.75	10.19	3.93	37525.7
AHQ-5-11, 3907	R.LVVPATQCGSLIGK.G	1444.72199	2	9.47E-04	0.75	3.35	-	459.4
gi|4885583|ref|NP_005397.1| Rho-associated, coiled-coil containing protein kinase 1; p160ROCK; p160				9.98E-04	0.56	10.16	1.18	158173.3
AHQ-5-13-, 3359	R.LEEANSMLTKDIEILR.R	1876.16497	3	9.98E-04	0.56	3.13	-	535.7

Reference File, Scan(s)	Peptide	MH+	z	P (pro) P (pep)	Sf Sf	Score XC	Coverage	MW Sp
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				1.00E-30	8.98	100.35	26.80	61986.9
AHQ-6-6, 5863 - 5879	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.72E-11	0.96	5.47	-	1488.3
AHQ-6-11, 5677 - 5691	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	8.67E-09	0.92	4.80	-	951.8
AHQ-6-1, 6010 - 6018	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.43E-11	0.98	6.15	-	2062.3
AHQ-6-10, 5292	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.03E-07	0.85	4.01	-	830.1
AHQ-6-7, 5722	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.11E-10	0.95	5.07	-	1274.8
AHQ-6-14-, 5834 - 5835	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.00E-30	0.98	6.69	-	1978.3
AHQ-6-2, 5983	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	5.68E-11	0.97	5.84	-	2004.4
AHQ-6-4, 5940 - 6007	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.06E-05	0.96	5.75	-	1318.4
AHQ-6-3, 5940 - 5941	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.68E-11	0.97	6.34	-	1955.6
AHQ-6-3, 4473	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	1.27E-04	0.85	3.76	-	1172.8
AHQ-6-14-, 4392	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	9.43E-04	0.87	3.68	-	1055.3
AHQ-6-4, 4475	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	4.32E-08	0.97	5.84	-	2065.3
AHQ-6-4, 4485	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	8.46E-04	0.74	3.18	-	637.4
AHQ-6-10, 4188 - 4194	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	2.43E-04	0.87	4.08	-	608.9
AHQ-6-10, 4148 - 4207	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	1.03E-07	0.96	6.50	-	1320.3
AHQ-6-1, 4615	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	1.96E-04	0.77	3.02	-	1092.4
AHQ-6-7, 4214	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	2.62E-05	0.81	3.82	-	493.6
AHQ-6-5, 4337 - 4405	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	6.47E-06	0.92	4.30	-	1374.8
AHQ-6-2, 4514	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	4.13E-05	0.93	4.79	-	1352.6
AHQ-6-6, 4360	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	2.76E-05	0.91	4.69	-	1062.6
AHQ-6-10, 4611 - 4614	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	1.77E-05	0.92	4.58	-	722.5
AHQ-6-4, 4956	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	7.51E-04	0.55	2.50	-	536.9
AHQ-6-14-, 4823	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	3.53E-05	0.91	3.89	-	828.7
AHQ-6-14-, 4983	R.HGVQELEIELQSQLSK.K	1839.03978	2	1.14E-04	0.76	2.77	-	517.1
AHQ-6-1, 5166	R.HGVQELEIELQSQLSK.K	1839.03978	3	1.19E-04	0.88	4.15	-	1184.8
AHQ-6-10, 4716 - 4788	R.HGVQELEIELQSQLSK.K	1839.03978	2	8.75E-12	0.98	6.92	-	2163.9
AHQ-6-10, 5194	R.KDIENQYETQITQIEHEVSSSGQEVQSSAK.E	3394.55959	3	3.19E-06	0.85	3.95	-	925.4
AHQ-6-10, 6094	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	4.52E-05	0.74	3.33	-	410.8
AHQ-6-1, 6427 - 6466	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	6.80E-12	0.79	3.75	-	440.5
AHQ-6-13-, 6198	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	2.04E-04	0.86	3.53	-	964.0
AHQ-6-7, 6031 - 6096	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	2.55E-07	0.94	4.46	-	1113.8
AHQ-6-4, 6392 - 6448	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	8.34E-07	0.74	3.07	-	548.7
AHQ-6-13, 6232	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	1.13E-05	0.76	3.48	-	712.9
AHQ-6-5, 5848	K.SDLEM*QYETLQEELM*ALKK.N	2332.63427	3	6.04E-04	0.69	3.17	-	595.8
AHQ-6-7, 3027 - 3031	K.TLLDIDNTR.M	1061.17119	2	7.03E-06	0.91	3.27	-	922.0
AHQ-6-12, 3181	K.TLLDIDNTR.M	1061.17119	2	2.39E-04	0.84	2.71	-	730.7
AHQ-6-2, 3075 - 3083	K.VQALEEANNDLENK.I	1587.67060	2	5.12E-04	0.96	4.48	-	1563.6
AHQ-6-3, 3054 - 3068	K.VQALEEANNDLENK.I	1587.67060	2	7.13E-05	0.92	3.63	-	1046.7
AHQ-6-4, 3032	K.VQALEEANNDLENK.I	1587.67060	2	6.30E-05	0.95	3.81	-	1486.7
AHQ-6-7, 2894 - 2895	K.VQALEEANNDLENK.I	1587.67060	2	7.18E-07	0.97	4.83	-	1657.8
AHQ-6-5, 2981	K.VQALEEANNDLENK.I	1587.67060	2	5.63E-08	0.98	5.37	-	2101.1
AHQ-6-12, 3012 - 3020	K.VQALEEANNDLENK.I	1587.67060	2	4.50E-09	0.96	4.82	-	1428.1
AHQ-6-6, 2982	K.VQALEEANNDLENK.I	1587.67060	2	4.89E-07	0.97	4.38	-	1832.7
gi|4507729|ref|NP_001060.1| tubulin, beta polypeptide [Homo sapiens]				5.55E-16	6.17	70.34	21.80	49906.7
AHQ-6-13-, 2377 - 2378	K.EVDEQM*LNVQNK.N	1463.59608	2	2.24E-04	0.83	3.41	-	905.8
AHQ-6-8, 5850 - 5913	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.43E-11	0.98	5.68	-	2771.1
AHQ-6-13-, 5958	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.40E-05	0.98	6.66	-	2432.1
AHQ-6-14-, 5935 - 5995	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	5.66E-14	0.99	6.72	-	2914.6
AHQ-6-13, 6017	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.38E-05	0.97	5.52	-	1585.4
AHQ-6-7, 5802	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.44E-14	0.98	6.22	-	2449.3
AHQ-6-13, 6007	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	2.06E-05	0.77	4.08	-	708.0
AHQ-6-8, 5904	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.68E-06	0.98	6.37	-	2926.2
AHQ-6-7, 3456 - 3474	R.ISEQFTAM*FR.R	1246.41758	2	4.13E-04	0.84	3.05	-	836.5
AHQ-6-13-, 4430	R.ISEQFTAMFR.R	1230.41818	2	8.61E-06	0.94	3.80	-	1295.8
AHQ-6-11, 4296	R.ISEQFTAMFR.R	1230.41818	2	2.18E-04	0.85	2.69	-	916.4
AHQ-6-14-, 5727	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	2.80E-06	0.77	4.14	-	696.3
AHQ-6-13-, 5962 - 6034	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	4.50E-05	0.64	3.50	-	553.0
AHQ-6-7, 5602	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	9.47E-04	0.65	3.37	-	616.9
AHQ-6-7, 5086 - 5146	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.78E-06	0.84	3.55	-	629.2
AHQ-6-13-, 5297	K.NSSYFVEWIPNNVK.T	1697.87148	2	6.10E-04	0.88	3.52	-	856.6
AHQ-6-8, 5173	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.22E-04	0.41	2.50	-	474.8
AHQ-6-7, 5495	K.NSSYFVEWIPNNVK.T	1697.87148	2	3.06E-04	0.46	2.62	-	447.2
AHQ-6-13, 5388	K.NSSYFVEWIPNNVK.T	1697.87148	2	9.74E-04	0.77	2.85	-	685.2
AHQ-6-13-, 5894 - 5956	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	5.55E-16	0.98	6.33	-	2149.7
AHQ-6-7, 5755 - 5810	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.06E-06	0.96	5.89	-	1327.5
AHQ-6-8, 5872 - 5928	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	2.72E-12	0.97	5.57	-	2229.6
AHQ-6-12, 5815 - 5836	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.47E-05	0.74	3.34	-	722.7
AHQ-6-14-, 5902 - 5960	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.08E-05	0.95	5.60	-	1290.9
AHQ-6-10, 5698 - 5751	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	8.00E-06	0.93	5.12	-	1163.6
AHQ-6-13, 6044 - 6115	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.69E-05	0.84	4.32	-	825.4
gi|16753233|ref|NP_006280.2| talin 1 [Homo sapiens]				2.78E-15	105.41	1190.37	53.60	269665.3
AHQ-6-3, 3206 - 3280	K.AAAFEEQENETVVVK.E	1664.79496	2	2.26E-05	0.95	5.11	-	1316.6
AHQ-6-2, 3420 - 3491	K.AAAFEEQENETVVVK.E	1664.79496	2	2.68E-07	0.92	4.26	-	1139.1
AHQ-6-2, 3222 - 3280	K.AAAFEEQENETVVVK.E	1664.79496	2	7.93E-07	0.94	4.62	-	1241.1
AHQ-6-5, 3131 - 3200	K.AAAFEEQENETVVVK.E	1664.79496	2	6.66E-08	0.89	4.16	-	999.0
AHQ-6-1, 3387 - 3456	K.AAAFEEQENETVVVK.E	1664.79496	2	7.31E-07	0.89	4.26	-	872.6
AHQ-6-2, 3286 - 3356	K.AAAFEEQENETVVVK.E	1664.79496	2	6.27E-06	0.90	4.11	-	1048.9
AHQ-6-4, 3175 - 3225	K.AAAFEEQENETVVVK.E	1664.79496	2	1.61E-05	0.95	4.62	-	1146.2
AHQ-6-3, 2697	R.AAM*EPIVISAK.T	1146.38260	2	4.79E-06	0.78	2.53	-	821.0
AHQ-6-2, 2699	R.AAM*EPIVISAK.T	1146.38260	1	5.66E-04	0.53	2.93	-	195.2
AHQ-6-2, 3322	R.AAMEPIVISAK.T	1130.38320	2	8.45E-06	0.77	2.67	-	601.8
AHQ-6-4, 2660	R.AAM*EPIVISAK.T	1146.38260	1	3.72E-05	0.30	2.00	-	205.7
AHQ-6-3, 2696	R.AAM*EPIVISAK.T	1146.38260	1	5.61E-05	0.15	1.89	-	173.0
AHQ-6-3, 3312 - 3320	R.AAMEPIVISAK.T	1130.38320	2	1.32E-04	0.79	3.13	-	510.4
AHQ-6-6, 1986	K.ADAEGESDLENSR.K	1393.35296	2	6.04E-04	0.81	2.63	-	880.9
AHQ-6-5, 1988	K.ADAEGESDLENSR.K	1393.35296	2	1.48E-08	0.95	4.02	-	1341.8
AHQ-6-2, 2036	K.ADAEGESDLENSR.K	1393.35296	2	7.52E-08	0.85	3.03	-	734.3
AHQ-6-3, 2678 - 2740	K.AGALQCSPSDAYTK.K	1470.58689	2	9.62E-04	0.50	2.61	-	406.4
AHQ-6-4, 2643	K.AGALQCSPSDAYTK.K	1470.58689	2	4.06E-04	0.89	3.52	-	820.1
AHQ-6-2, 2668 - 2670	K.AGALQCSPSDAYTK.K	1470.58689	2	1.25E-06	0.93	3.98	-	1085.0
AHQ-6-5, 2619	K.AGALQCSPSDAYTK.K	1470.58689	2	1.78E-05	0.87	3.84	-	619.7
AHQ-6-2, 2451 - 2456	K.AGALQCSPSDAYTKK.E	1598.75981	2	5.69E-04	0.85	3.75	-	509.9
AHQ-6-4, 2948	K.AIAVTVQEM*VTK.S	1306.55438	2	4.82E-04	0.93	3.78	-	965.5
AHQ-6-2, 3000 - 3071	K.AIAVTVQEM*VTK.S	1306.55438	2	2.41E-04	0.94	3.85	-	1095.7
AHQ-6-2, 3987 - 3991	K.AIAVTVQEMVTK.S	1290.55498	2	5.99E-05	0.97	4.93	-	1655.7
AHQ-6-1, 3180	K.AIAVTVQEM*VTK.S	1306.55438	2	5.71E-08	0.96	4.57	-	1024.7
AHQ-6-3, 3966 - 3980	K.AIAVTVQEMVTK.S	1290.55498	2	2.07E-06	0.96	4.55	-	1471.1
AHQ-6-5, 3893 - 3905	K.AIAVTVQEMVTK.S	1290.55498	2	3.14E-04	0.95	4.20	-	1294.8
AHQ-6-4, 3939	K.AIAVTVQEMVTK.S	1290.55498	2	8.63E-04	0.92	4.01	-	917.5
AHQ-6-6, 2666	K.ALDGAFTEENR.A	1223.27427	2	7.88E-05	0.93	3.24	-	1420.1
AHQ-6-4, 2704 - 2776	K.ALDGAFTEENR.A	1223.27427	2	5.94E-06	0.88	3.04	-	1330.1
AHQ-6-2, 2546	K.ALDGAFTEENR.A	1223.27427	2	2.86E-06	0.92	3.32	-	1301.9
AHQ-6-4, 2508 - 2515	K.ALDGAFTEENR.A	1223.27427	2	6.60E-06	0.90	3.46	-	1112.5
AHQ-6-3, 2540	K.ALDGAFTEENR.A	1223.27427	2	9.21E-08	0.94	3.68	-	1364.9

AHQ-6-1, 2956	K.ALDGAFTEENR.A	1223.27427	2	1.19E-05	0.97	3.98	-	1970.8
AHQ-6-8, 3597	K.ALDYYMLR.N	1045.23686	2	1.56E-04	0.91	3.15	-	862.8
AHQ-6-5, 2032	R.ALEATTEHIR.Q	1141.25953	2	6.51E-05	0.82	3.19	-	919.9
AHQ-6-7, 2007	R.ALEATTEHIR.Q	1141.25953	2	1.77E-05	0.84	2.92	-	1092.3
AHQ-6-3, 2114	R.ALEATTEHIR.Q	1141.25953	2	2.09E-04	0.83	3.26	-	954.5
AHQ-6-6, 2042	R.ALEATTEHIR.Q	1141.25953	2	1.49E-04	0.64	2.86	-	885.6
AHQ-6-4, 2059	R.ALEATTEHIR.Q	1141.25953	2	2.11E-04	0.88	2.79	-	1348.1
AHQ-6-2, 2086 - 2159	R.ALEATTEHIR.Q	1141.25953	2	7.24E-05	0.93	2.95	-	1716.0
AHQ-6-4, 3416	K.ALGDLISATK.A	989.14811	2	3.60E-05	0.88	3.34	-	746.5
AHQ-6-2, 3456 - 3520	K.ALGDLISATK.A	989.14811	2	2.53E-05	0.89	3.16	-	948.0
AHQ-6-3, 3450	K.ALGDLISATK.A	989.14811	2	7.85E-06	0.84	3.05	-	679.4
AHQ-6-5, 3365	K.ALGDLISATK.A	989.14811	2	1.87E-06	0.90	3.22	-	879.8
AHQ-6-6, 2654	K.ALSTDPAAPNLK.S	1198.35099	2	8.04E-06	0.78	2.84	-	675.7
AHQ-6-4, 2501	K.ALSTDPAAPNLK.S	1198.35099	2	4.22E-04	0.61	2.70	-	558.8
AHQ-6-3, 2712	K.ALSTDPAAPNLK.S	1198.35099	2	7.23E-04	0.68	2.74	-	512.4
AHQ-6-4, 2648 - 2712	K.ALSTDPAAPNLK.S	1198.35099	2	5.21E-06	0.65	2.73	-	561.0
AHQ-6-2, 2704 - 2706	K.ALSTDPAAPNLK.S	1198.35099	2	5.86E-04	0.76	3.07	-	611.4
AHQ-6-4, 5689 - 5763	R.ANQAIQM*ACQSLGEPGCTQAQVLSAATIVAK.H	3236.64462	3	7.22E-04	0.74	3.95	-	503.9
AHQ-6-3, 5788 - 5794	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.08E-11	0.97	5.39	-	1516.7
AHQ-6-3, 5173 - 5229	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.46E-10	0.96	5.15	-	1300.0
AHQ-6-2, 5824 - 5900	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.34E-05	0.93	3.94	-	1062.6
AHQ-6-4, 5864	K.APGQLECETAIAALNSCLR.D	2077.32566	2	8.47E-07	0.95	4.39	-	1279.3
AHQ-6-5, 6271	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	1.30E-04	0.54	3.00	-	637.2
AHQ-6-2, 6310	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	2.87E-07	0.96	4.35	-	2040.1
AHQ-6-4, 5636 - 5639	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	2	1.28E-05	0.95	4.56	-	1476.1
AHQ-6-6, 2927 - 2934	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.21E-04	0.42	2.93	-	317.7
AHQ-6-2, 3030 - 3031	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.44E-04	0.38	2.94	-	306.6
AHQ-6-4, 3001 - 3009	K.ASAGPQPLLVQSCK.A	1457.67763	1	7.72E-04	0.44	2.51	-	493.9
AHQ-6-1, 3244	K.ASAGPQPLLVQSCK.A	1457.67763	2	4.92E-06	0.72	2.83	-	434.5
AHQ-6-5, 3136	K.ASAGPQPLLVQSCK.A	1457.67763	2	9.35E-05	0.60	2.58	-	442.7
AHQ-6-3, 2997 - 3056	K.ASAGPQPLLVQSCK.A	1457.67763	2	3.58E-05	0.79	3.36	-	434.7
AHQ-6-7, 2851 - 2852	K.ASAGPQPLLVQSCK.A	1457.67763	2	4.86E-04	0.80	3.70	-	386.9
AHQ-6-3, 4137	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.46E-04	0.71	3.11	-	500.1
AHQ-6-5, 3577	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	9.84E-08	0.88	3.51	-	722.7
AHQ-6-5, 4071	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	4.01E-06	0.78	3.38	-	508.4
AHQ-6-1, 3803	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	4.54E-06	0.91	4.27	-	597.9
AHQ-6-6, 3554	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	4.65E-06	0.86	3.83	-	578.5
AHQ-6-4, 4155 - 4156	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	4.81E-07	0.93	4.50	-	601.6
AHQ-6-6, 4046 - 4048	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.93E-05	0.89	4.12	-	499.8
AHQ-6-5, 4780 - 4781	K.AVAEQIPLLVQGVR.G	1493.77619	2	6.56E-07	0.95	4.81	-	925.9
AHQ-6-4, 4851	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.77E-06	0.82	3.08	-	713.6
AHQ-6-1, 4948 - 4960	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.08E-07	0.90	4.08	-	650.8
AHQ-6-6, 4742	K.AVAEQIPLLVQGVR.G	1493.77619	2	7.00E-08	0.87	3.73	-	617.6
AHQ-6-2, 4835 - 4895	K.AVAEQIPLLVQGVR.G	1493.77619	2	3.38E-06	0.85	3.45	-	680.7
AHQ-6-2, 4858	K.AVAEQIPLLVQGVR.G	1493.77619	3	6.35E-04	0.97	5.01	-	2378.2
AHQ-6-3, 4830	K.AVAEQIPLLVQGVR.G	1493.77619	2	6.31E-06	0.63	2.73	-	407.9
AHQ-6-4, 3856 - 3859	K.AVASAAAALVLK.A	1085.32216	2	3.87E-06	0.97	4.64	-	1569.5
AHQ-6-5, 3791 - 3869	K.AVASAAAALVLK.A	1085.32216	2	5.40E-06	0.96	4.20	-	1492.8
AHQ-6-2, 3596	K.AVASAAAALVLK.A	1085.32216	2	5.71E-07	0.92	2.84	-	1419.0
AHQ-6-1, 4028	K.AVASAAAALVLK.A	1085.32216	2	6.22E-05	0.95	3.86	-	1353.4
AHQ-6-2, 3842 - 3902	K.AVASAAAALVLK.A	1085.32216	2	5.65E-06	0.95	4.01	-	1401.4
AHQ-6-2, 3968	K.AVASAAAALVLK.A	1085.32216	2	3.37E-06	0.94	3.65	-	1198.4
AHQ-6-3, 3757	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.72E-04	0.89	3.60	-	974.3
AHQ-6-5, 3921 - 3987	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.82E-06	0.94	4.23	-	1298.5
AHQ-6-4, 3968 - 4041	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.30E-05	0.88	4.33	-	456.8
AHQ-6-2, 4216	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.51E-06	0.87	3.58	-	979.4
AHQ-6-2, 3735 - 3802	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.31E-05	0.92	4.06	-	1147.3
AHQ-6-2, 3975 - 4027	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.15E-07	0.90	3.93	-	1132.7
AHQ-6-2, 4091 - 4152	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.92E-04	0.74	3.67	-	667.9
AHQ-6-3, 3985 - 3986	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.02E-07	0.95	4.32	-	1447.5
AHQ-6-6, 6370	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	4.50E-05	0.90	3.98	-	1331.8
AHQ-6-2, 6474 - 6475	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	5.55E-15	0.97	6.15	-	1286.5
AHQ-6-3, 6422 - 6436	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	3.36E-07	0.95	5.20	-	1353.7
AHQ-6-1, 6471	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	3.37E-06	0.91	3.81	-	1467.3
AHQ-6-2, 5354	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	3.23E-06	0.69	3.67	-	347.1
AHQ-6-2, 5346	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	3	3.85E-04	0.85	4.10	-	633.7
AHQ-6-3, 5610	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.40E-04	0.81	3.54	-	519.5
AHQ-6-2, 4559	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	5.20E-06	0.67	3.42	-	321.7
AHQ-6-3, 5309	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	7.68E-06	0.44	2.51	-	281.3
AHQ-6-3, 5433 - 5436	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.26E-05	0.94	5.41	-	894.8
AHQ-6-1, 5523	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	8.19E-04	0.93	4.79	-	1119.4
AHQ-6-3, 5678 - 5756	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	4.76E-06	0.64	3.60	-	513.0
AHQ-6-5, 5419 - 5481	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.42E-04	0.91	4.57	-	801.3
AHQ-6-2, 5471	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	3.70E-06	0.83	3.94	-	640.1
AHQ-6-4, 5504	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	2.69E-09	0.91	4.88	-	801.6
AHQ-6-7, 3311	R.DDILNGSHPVSFDK.A	1544.64741	2	5.95E-10	0.90	3.39	-	1024.3
AHQ-6-10, 3322 - 3323	R.DDILNGSHPVSFDK.A	1544.64741	2	4.20E-07	0.91	3.55	-	1066.5
AHQ-6-7, 3406	R.DDILNGSHPVSFDK.A	1544.64741	2	1.89E-08	0.90	3.62	-	889.3
AHQ-6-8, 4432	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	1.47E-07	0.98	5.91	-	2549.4
AHQ-6-2, 5680	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.23E-06	0.92	4.31	-	718.4
AHQ-6-4, 5703	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.04E-11	0.93	4.08	-	1030.8
AHQ-6-2, 5058	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.35E-11	0.96	4.59	-	1347.7
AHQ-6-5, 5631	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	4.12E-05	0.72	3.77	-	579.7
AHQ-6-4, 5073	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.82E-09	0.89	4.18	-	719.6
AHQ-6-3, 5636	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.76E-04	0.85	3.42	-	740.7
AHQ-6-5, 5639 - 5641	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.45E-05	0.88	4.08	-	617.8
AHQ-6-1, 5087	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	5.07E-07	0.96	5.02	-	1713.9
AHQ-6-3, 4986	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.13E-06	0.97	5.40	-	2167.1
AHQ-6-5, 4956	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.52E-07	0.94	4.25	-	1279.7
AHQ-6-4, 4471	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.16E-04	0.88	3.40	-	1200.9
AHQ-6-5, 4971 - 4984	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.55E-05	0.95	4.63	-	1611.0
AHQ-6-4, 5031	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.12E-04	0.89	3.90	-	769.0
AHQ-6-3, 4940 - 4996	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.52E-04	0.82	3.56	-	626.6
AHQ-6-2, 5012	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	7.08E-05	0.95	4.30	-	1877.5
AHQ-6-4, 3567	R.DPPSWSVLAGHSR.T	1409.53156	2	4.25E-10	0.89	3.09	-	601.5
AHQ-6-4, 3577	R.DPPSWSVLAGHSR.T	1409.53156	3	3.89E-07	0.90	4.29	-	727.9
AHQ-6-2, 3618	R.DPPSWSVLAGHSR.T	1409.53156	2	1.84E-10	0.83	2.86	-	485.1
AHQ-6-2, 3628	R.DPPSWSVLAGHSR.T	1409.53156	3	1.77E-05	0.87	4.43	-	488.3
AHQ-6-1, 3792	R.DPPSWSVLAGHSR.T	1409.53156	2	4.09E-05	0.58	2.60	-	312.2
AHQ-6-3, 3596 - 3597	R.DPPSWSVLAGHSR.T	1409.53156	2	2.40E-09	0.91	3.45	-	620.5
AHQ-6-3, 3601	R.DPPSWSVLAGHSR.T	1409.53156	3	2.31E-07	0.89	4.03	-	660.4
AHQ-6-10, 4679	R.DPVQLNLLYVQAR.D	1529.76539	2	2.32E-04	0.94	3.90	-	1222.8
AHQ-6-8, 4737	R.DPVQLNLLYVQAR.D	1529.76539	2	2.14E-06	0.96	4.33	-	1624.7
AHQ-6-7, 4746	R.DPVQLNLLYVQAR.D	1529.76539	2	9.90E-08	0.95	4.48	-	1386.5
AHQ-6-4, 2499	K.EAAYHPEVAPDVR.L	1454.56910	2	2.81E-04	0.73	2.54	-	652.1
AHQ-6-3, 2546	K.EAAYHPEVAPDVR.L	1454.56910	2	1.98E-07	0.81	2.63	-	863.3
AHQ-6-8, 5448 - 5514	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.63E-06	0.86	3.98	-	725.7

AHQ-6-4, 5617 - 5675	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.29E-09	0.97	5.51	-	1854.0
AHQ-6-1, 5727	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.85E-07	0.90	3.46	-	1201.1
AHQ-6-1, 5588 - 5664	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.64E-05	0.93	4.11	-	1218.9
AHQ-6-7, 5370	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.84E-06	0.94	4.49	-	1237.0
AHQ-6-2, 5658 - 5714	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.73E-07	0.97	5.14	-	1604.5
AHQ-6-6, 5518 - 5583	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.09E-08	0.96	5.03	-	1148.1
AHQ-6-6, 5323	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.46E-08	0.81	3.43	-	624.3
AHQ-6-5, 5572 - 5644	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.83E-07	0.95	4.98	-	1049.7
AHQ-6-4, 5461 - 5531	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.20E-06	0.51	2.67	-	475.5
AHQ-6-2, 5776 - 5836	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.82E-04	0.93	4.24	-	1255.3
AHQ-6-3, 5700 - 5762	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.61E-05	0.70	3.39	-	525.0
AHQ-6-3, 5589 - 5645	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.75E-09	0.97	5.23	-	1634.4
AHQ-6-14-, 5506	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.95E-07	0.97	4.58	-	2016.6
AHQ-6-10, 5290 - 5291	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.32E-09	0.96	4.84	-	1719.4
AHQ-6-2, 5572 - 5639	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.99E-09	0.96	5.12	-	1435.2
AHQ-6-3, 5392	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.55E-07	0.83	3.39	-	779.0
AHQ-6-4, 5716	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.45E-06	0.91	3.75	-	1229.9
AHQ-6-2, 6542	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	1.18E-08	0.94	5.10	-	1224.0
AHQ-6-5, 6468	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	3.50E-09	0.94	5.06	-	900.4
AHQ-6-4, 6555	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	2.04E-04	0.94	5.00	-	1077.8
AHQ-6-2, 6534 - 6604	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	4.99E-04	0.67	3.55	-	465.7
AHQ-6-6, 6394	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	2.36E-06	0.85	4.17	-	646.3
AHQ-6-3, 6434 - 6456	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	2.55E-04	0.95	5.92	-	1265.8
AHQ-6-1, 6512	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	5.86E-05	0.91	4.25	-	1266.8
AHQ-6-4, 6595 - 6665	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	4.87E-05	0.81	3.96	-	675.5
AHQ-6-2, 6472 - 6494	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	5.65E-05	0.95	5.32	-	1168.9
AHQ-6-3, 5793 - 5814	R.ELLENPVQPINDM*SYFGCLDSVM*ENSK.V	3164.48754	3	3.44E-06	0.95	5.53	-	817.9
AHQ-6-4, 5871 - 5941	R.ELLENPVQPINDM*SYFGCLDSVM*ENSK.V	3164.48754	3	5.02E-05	0.72	3.60	-	336.0
AHQ-6-2, 6246 - 6304	R.ELLENPVQPINDMSYFGCLDSVM*ENSK.V	3148.48814	3	2.12E-06	0.79	3.90	-	373.6
AHQ-6-8, 5200	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	2.52E-12	0.97	6.01	-	1869.4
AHQ-6-7, 5087 - 5166	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	1.75E-06	0.94	4.68	-	1349.5
AHQ-6-13, 5372	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	2.78E-06	0.97	5.58	-	2164.8
AHQ-6-13-, 5288 - 5290	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	1.33E-04	0.97	6.05	-	1399.4
AHQ-6-14-, 5298	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	1.99E-10	0.98	6.66	-	2280.7
AHQ-6-8, 4754 - 4812	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.91E-07	0.97	5.89	-	1860.3
AHQ-6-7, 4847	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	4.50E-05	0.92	4.28	-	1340.2
AHQ-6-14-, 5007	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.26E-04	0.98	6.39	-	2614.1
AHQ-6-7, 4402	K.EVIQEWNLTNIK.R	1487.68214	2	9.53E-05	0.86	3.87	-	574.5
AHQ-6-8, 4409	K.EVIQEWNLTNIK.R	1487.68214	2	7.34E-05	0.92	3.94	-	1205.0
AHQ-6-7, 2902 - 2903	K.FFYSDQNVDSR.D	1378.42795	2	1.09E-07	0.94	3.62	-	1283.9
AHQ-6-8, 2861 - 2862	K.FFYSDQNVDSR.D	1378.42795	2	1.38E-08	0.92	3.74	-	930.4
AHQ-6-8, 5540	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	1.09E-09	0.98	7.28	-	2241.9
AHQ-6-10, 5366	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	1.41E-04	0.68	3.07	-	582.3
AHQ-6-1, 5912	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	1.57E-06	0.73	3.41	-	455.9
AHQ-6-3, 6382	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	7.97E-05	0.83	3.24	-	1128.0
AHQ-6-2, 6614 - 6676	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	3.14E-06	0.91	5.24	-	830.2
AHQ-6-2, 6143 - 6203	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	4.86E-05	0.81	4.10	-	486.0
AHQ-6-5, 6388	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	2	1.53E-04	0.87	3.14	-	1107.2
AHQ-6-3, 5844	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	6.13E-05	0.85	3.40	-	796.2
AHQ-6-1, 6435 - 6440	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	4.49E-05	0.88	4.37	-	673.1
AHQ-6-4, 6471	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	1.93E-08	0.77	3.46	-	662.2
AHQ-6-2, 5918 - 5975	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	5.30E-10	0.96	5.69	-	1196.6
AHQ-6-3, 6378 - 6384	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	8.00E-12	0.92	4.67	-	705.4
AHQ-6-4, 5919 - 5951	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	3.79E-07	0.72	3.38	-	618.3
AHQ-6-2, 5882 - 5911	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	1.94E-06	0.92	3.87	-	1099.0
AHQ-6-4, 2851 - 2920	K.FLPSELRDEH	1243.35032	2	2.90E-05	0.58	2.53	-	291.5
AHQ-6-2, 5019 - 5022	K.GLAGAVSELLR.S	1086.26701	2	8.98E-07	0.97	4.88	-	2039.1
AHQ-6-4, 5015	K.GLAGAVSELLR.S	1086.26701	2	2.70E-07	0.98	4.80	-	2114.6
AHQ-6-3, 5002	K.GLAGAVSELLR.S	1086.26701	2	1.81E-06	0.97	4.80	-	2075.3
AHQ-6-5, 4952	K.GLAGAVSELLR.S	1086.26701	2	6.84E-07	0.96	4.07	-	1619.9
AHQ-6-1, 5122	K.GLAGAVSELLR.S	1086.26701	2	1.11E-06	0.97	4.55	-	1975.6
AHQ-6-2, 6010 - 6076	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.59E-10	0.92	4.94	-	1028.7
AHQ-6-2, 6132 - 6202	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.02E-04	0.89	4.64	-	804.7
AHQ-6-4, 6243 - 6324	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	9.35E-08	0.88	4.28	-	1022.7
AHQ-6-6, 6060	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	5.27E-05	0.88	4.10	-	679.6
AHQ-6-4, 6201	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	4.27E-05	0.95	5.15	-	949.1
AHQ-6-5, 6125	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	3.43E-05	0.95	5.44	-	821.8
AHQ-6-1, 6602	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	5.41E-07	0.97	6.24	-	1618.8
AHQ-6-9, 6207	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	6.12E-07	0.95	5.36	-	1244.2
AHQ-6-4, 6657 - 6659	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	4.56E-10	0.92	4.66	-	1467.4
AHQ-6-6, 6502 - 6503	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	8.16E-11	0.96	6.26	-	1405.7
AHQ-6-7, 6362	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	3.98E-07	0.94	4.96	-	1415.5
AHQ-6-10, 6239	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	3.30E-05	0.91	3.71	-	1583.1
AHQ-6-2, 6570 - 6640	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.05E-05	0.84	4.24	-	803.5
AHQ-6-5, 6581	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.31E-10	0.97	6.42	-	1616.9
AHQ-6-5, 6472	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	2.44E-05	0.97	5.63	-	1752.7
AHQ-6-4, 6560	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	3.39E-07	0.98	6.99	-	1928.6
AHQ-6-1, 6506	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	4.42E-07	0.98	6.10	-	2221.2
AHQ-6-2, 6500	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	5.24E-07	0.98	6.99	-	2438.6
AHQ-6-6, 6450	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.65E-09	0.79	3.86	-	795.5
AHQ-6-3, 6512	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.35E-05	0.92	4.55	-	822.8
AHQ-6-2, 5516	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.84E-07	0.92	4.20	-	1108.4
AHQ-6-2, 5527	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.51E-07	0.76	3.57	-	398.9
AHQ-6-4, 6611 - 6612	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.48E-08	0.93	4.60	-	1157.7
AHQ-6-3, 6513	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	6.40E-08	0.92	4.66	-	715.0
AHQ-6-5, 6527	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	8.18E-04	0.87	3.69	-	959.5
AHQ-6-2, 6551	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.52E-08	0.92	4.26	-	989.5
AHQ-6-6, 6451	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.12E-07	0.94	4.88	-	742.2
AHQ-6-2, 6552	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.46E-07	0.94	5.22	-	870.1
AHQ-6-4, 5544	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.27E-06	0.93	4.49	-	1106.9
AHQ-6-11, 3301	R.IGITNHDEYSLVR.E	1517.66833	2	2.33E-07	0.73	2.84	-	629.2
AHQ-6-13-, 3422	R.IGITNHDEYSLVR.E	1517.66833	3	6.03E-06	0.89	3.58	-	769.6
AHQ-6-8, 3153 - 3214	R.IGITNHDEYSLVR.E	1517.66833	2	1.58E-04	0.63	2.68	-	970.6
AHQ-6-13-, 3425	R.IGITNHDEYSLVR.E	1517.66833	2	2.08E-07	0.92	3.83	-	1075.7
AHQ-6-13-, 3666 - 3674	R.IGITNHDEYSLVR.E	1517.66833	2	9.56E-06	0.94	3.89	-	1112.1
AHQ-6-8, 3404 - 3472	R.IGITNHDEYSLVR.E	1517.66833	2	3.56E-08	0.90	3.37	-	986.2
AHQ-6-7, 3134 - 3194	R.IGITNHDEYSLVR.E	1517.66833	2	1.97E-05	0.92	3.73	-	1008.3
AHQ-6-3, 4060	R.ILAQATSDLVNAIK.A	1457.69748	2	1.24E-07	0.97	4.07	-	2025.9
AHQ-6-2, 4260	R.ILAQATSDLVNAIK.A	1457.69748	2	2.25E-09	0.97	5.07	-	1496.6
AHQ-6-4, 4068 - 4077	R.ILAQATSDLVNAIK.A	1457.69748	2	4.21E-10	0.97	4.72	-	2125.5
AHQ-6-7, 4638	R.ILAQATSDLVNAIK.A	1457.69748	2	1.68E-07	0.98	4.90	-	2175.8
AHQ-6-5, 3995 - 4060	R.ILAQATSDLVNAIK.A	1457.69748	2	6.96E-07	0.96	4.27	-	1526.9
AHQ-6-5, 4815	R.ILAQATSDLVNAIK.A	1457.69748	2	6.01E-07	0.96	4.47	-	1743.4
AHQ-6-11, 4643	R.ILAQATSDLVNAIK.A	1457.69748	2	3.26E-04	0.72	2.74	-	722.7
AHQ-6-2, 4579	R.ILAQATSDLVNAIK.A	1457.69748	2	4.19E-06	0.96	3.21	-	1974.0
AHQ-6-1, 4982 - 4983	R.ILAQATSDLVNAIK.A	1457.69748	2	1.52E-09	0.98	5.57	-	1874.7
AHQ-6-6, 4786	R.ILAQATSDLVNAIK.A	1457.69748	2	9.01E-09	0.97	4.93	-	1893.1

AHQ-6-2, 4087	R.ILAQATSDLVNAIK.A	1457.69748	2	6.82E-08	0.98	4.88	-	2961.0
AHQ-6-6, 3962	R.ILAQATSDLVNAIK.A	1457.69748	2	8.77E-07	0.97	4.13	-	1700.0
AHQ-6-2, 4468 - 4483	R.ILAQATSDLVNAIK.A	1457.69748	2	1.99E-06	0.92	3.97	-	1013.6
AHQ-6-3, 4864	R.ILAQATSDLVNAIK.A	1457.69748	2	3.83E-09	0.98	4.70	-	2072.1
AHQ-6-1, 4219	R.ILAQATSDLVNAIK.A	1457.69748	2	5.40E-07	0.96	3.61	-	1755.8
AHQ-6-4, 4889	R.ILAQATSDLVNAIK.A	1457.69748	2	4.21E-04	0.97	4.41	-	2185.2
AHQ-6-13-, 5529	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	8.74E-09	0.93	3.94	-	1071.8
AHQ-6-14-, 5531	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	2.55E-05	0.64	3.20	-	366.9
AHQ-6-8, 4985 - 5050	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.00E-08	0.97	4.94	-	1859.3
AHQ-6-14-, 5172 - 5206	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.63E-11	0.94	4.37	-	1338.4
AHQ-6-14, 5802 - 5841	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	5.22E-06	0.89	3.32	-	1431.6
AHQ-6-10, 4987	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.11E-10	0.92	3.95	-	1246.6
AHQ-6-8, 4993 - 5053	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	2	1.77E-05	0.92	3.91	-	901.1
AHQ-6-8, 1767	K.KEEITGTLR.K	1047.18765	1	2.18E-06	0.34	2.12	-	344.2
AHQ-6-8, 2588 - 2590	R.KFFYSDQNVDSR.D	1506.60087	2	2.90E-04	0.93	3.62	-	1205.9
AHQ-6-8, 2387	K.KGIWLEAGK.A	1002.19171	2	7.86E-05	0.88	3.21	-	799.1
AHQ-6-5, 2576	K.LAQAAQSSVATITR.L	1417.59344	2	1.96E-10	0.97	5.22	-	1759.9
AHQ-6-8, 2601	K.LAQAAQSSVATITR.L	1417.59344	2	3.82E-07	0.90	2.95	-	1162.2
AHQ-6-4, 2603	K.LAQAAQSSVATITR.L	1417.59344	2	6.14E-10	0.96	4.02	-	1794.1
AHQ-6-7, 2647	K.LAQAAQSSVATITR.L	1417.59344	2	1.94E-06	0.86	3.53	-	590.4
AHQ-6-4, 2757 - 2768	K.LAQAAQSSVATITR.L	1417.59344	2	1.31E-09	0.96	3.81	-	1630.7
AHQ-6-3, 2800	K.LAQAAQSSVATITR.L	1417.59344	2	8.03E-10	0.97	4.49	-	1748.6
AHQ-6-3, 2633	K.LAQAAQSSVATITR.L	1417.59344	2	3.57E-06	0.86	2.87	-	954.6
AHQ-6-4, 2773	K.LAQAAQSSVATITR.L	1417.59344	1	1.06E-04	0.12	2.25	-	99.0
AHQ-6-10, 2691	K.LAQAAQSSVATITR.L	1417.59344	2	4.16E-05	0.73	2.53	-	818.4
AHQ-6-1, 3022	K.LAQAAQSSVATITR.L	1417.59344	2	4.22E-09	0.96	4.24	-	1434.2
AHQ-6-2, 2626	K.LAQAAQSSVATITR.L	1417.59344	2	9.42E-08	0.96	4.03	-	1882.5
AHQ-6-6, 2723	K.LAQAAQSSVATITR.L	1417.59344	2	5.63E-10	0.96	4.32	-	1458.4
AHQ-6-6, 2584	K.LAQAAQSSVATITR.L	1417.59344	2	1.27E-05	0.90	3.67	-	865.5
AHQ-6-5, 2719	K.LAQAAQSSVATITR.L	1417.59344	2	2.05E-09	0.96	4.33	-	1403.4
AHQ-6-14-, 2784	K.LAQAAQSSVATITR.L	1417.59344	2	1.19E-06	0.92	3.42	-	1091.7
AHQ-6-4, 2772	K.LAQAAQSSVATITR.L	1417.59344	1	3.02E-04	0.65	3.02	-	244.6
AHQ-6-1, 3514 - 3530	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.35E-10	0.98	5.90	-	2343.0
AHQ-6-3, 3305 - 3306	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	6.65E-08	0.93	5.00	-	592.5
AHQ-6-5, 3203	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	7.33E-06	0.93	4.68	-	1216.7
AHQ-6-4, 3264	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.02E-06	0.95	5.17	-	728.0
AHQ-6-2, 3319	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.13E-05	0.93	4.86	-	622.9
AHQ-6-2, 3288 - 3351	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	9.74E-07	0.97	4.99	-	2229.6
AHQ-6-2, 3559	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.11E-14	0.97	5.73	-	1781.7
AHQ-6-4, 5065	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.56E-06	0.88	3.48	-	1481.6
AHQ-6-2, 5216 - 5226	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	4.20E-05	0.93	4.06	-	1564.3
AHQ-6-5, 5296 - 5335	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.44E-08	0.92	4.56	-	696.6
AHQ-6-2, 5192 - 5250	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.12E-07	0.96	5.44	-	932.6
AHQ-6-5, 4928 - 4987	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.19E-06	0.82	3.82	-	587.3
AHQ-6-2, 5034	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	2.22E-06	0.97	4.50	-	2590.8
AHQ-6-6, 5250	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.82E-07	0.87	4.00	-	532.8
AHQ-6-3, 5320 - 5324	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.15E-10	0.93	4.84	-	737.3
AHQ-6-5, 5163 - 5164	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.80E-06	0.97	5.89	-	1404.4
AHQ-6-2, 4996 - 5064	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.73E-07	0.95	5.07	-	953.2
AHQ-6-4, 5383	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.56E-07	0.96	4.56	-	1324.4
AHQ-6-3, 5200	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	3.77E-09	0.98	6.17	-	2452.2
AHQ-6-14-, 5096 - 5100	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.00E-07	0.94	4.81	-	917.8
AHQ-6-3, 5169 - 5225	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.54E-07	0.95	4.63	-	1081.8
AHQ-6-4, 5057	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.86E-07	0.96	4.90	-	1220.7
AHQ-6-6, 4898 - 4938	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.56E-07	0.94	4.82	-	780.9
AHQ-6-7, 4775	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.03E-07	0.91	4.14	-	807.8
AHQ-6-6, 5123	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.17E-08	0.96	5.16	-	1061.3
AHQ-6-1, 5298	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	4.04E-07	0.97	5.19	-	2211.1
AHQ-6-4, 5248 - 5313	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.41E-04	0.95	5.02	-	973.2
AHQ-6-1, 5292 - 5296	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.24E-05	0.96	5.03	-	1254.4
AHQ-6-1, 5118	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.59E-06	0.84	3.79	-	561.2
AHQ-6-1, 5411	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.05E-05	0.72	3.56	-	533.0
AHQ-6-3, 4964 - 5010	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.87E-08	0.96	4.96	-	1091.5
AHQ-6-7, 4962	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.62E-06	0.93	4.22	-	1025.2
AHQ-6-7, 3618 - 3622	K.LHTDDELNWLDHGR.T	1721.81153	2	7.59E-05	0.95	4.38	-	1317.7
AHQ-6-8, 3428 - 3496	K.LHTDDELNWLDHGR.T	1721.81153	3	4.66E-09	0.92	4.54	-	916.9
AHQ-6-8, 3492	K.LHTDDELNWLDHGR.T	1721.81153	2	1.63E-06	0.96	4.74	-	1359.7
AHQ-6-6, 4163	K.LLAALLEDEGGSGR.P	1401.54764	2	5.98E-05	0.87	2.62	-	1096.2
AHQ-6-4, 4267	K.LLAALLEDEGGSGR.P	1401.54764	2	4.15E-06	0.93	2.68	-	1728.9
AHQ-6-3, 5097	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.32E-08	0.98	6.62	-	1395.4
AHQ-6-7, 4787 - 4854	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.96E-10	0.97	5.39	-	1439.7
AHQ-6-1, 5243	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.86E-05	0.97	5.91	-	1437.8
AHQ-6-8, 4814	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.81E-06	0.96	5.35	-	1512.0
AHQ-6-8, 4810	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.50E-06	0.97	6.12	-	1172.3
AHQ-6-10, 4767	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	6.43E-06	0.83	3.53	-	913.2
AHQ-6-10, 4770	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.41E-06	0.94	4.69	-	969.3
AHQ-6-1, 5232	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.12E-06	0.91	4.17	-	1253.2
AHQ-6-6, 5026	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	9.02E-09	0.97	5.83	-	1302.4
AHQ-6-6, 5018	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.42E-10	0.96	5.02	-	1671.5
AHQ-6-7, 4855 - 4859	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.20E-06	0.96	4.51	-	1559.3
AHQ-6-4, 5131 - 5135	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.08E-11	0.98	6.51	-	2028.3
AHQ-6-3, 5096	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.23E-08	0.94	4.87	-	1211.1
AHQ-6-4, 5129	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.76E-10	0.98	6.92	-	1686.6
AHQ-6-12, 4925	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.73E-04	0.92	4.33	-	891.7
AHQ-6-12, 4924	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.56E-05	0.82	3.48	-	769.1
AHQ-6-2, 5086 - 5146	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.84E-04	0.97	5.59	-	1374.7
AHQ-6-11, 4883	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.12E-06	0.86	3.62	-	759.7
AHQ-6-5, 5061	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.66E-14	0.98	6.59	-	1931.0
AHQ-6-2, 5114	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	5.65E-08	0.95	4.73	-	1446.3
AHQ-6-5, 5057	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.29E-08	0.95	4.75	-	1802.9
AHQ-6-5, 3943 - 4003	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.06E-07	0.68	3.19	-	228.9
AHQ-6-4, 3987 - 4051	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.41E-06	0.70	3.36	-	380.5
AHQ-6-4, 4115 - 4176	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.11E-05	0.84	3.91	-	309.2
AHQ-6-3, 3976 - 4036	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.82E-05	0.78	3.39	-	302.5
AHQ-6-1, 4211	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.53E-09	0.83	3.50	-	401.1
AHQ-6-2, 4050 - 4115	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.95E-05	0.93	4.97	-	433.0
AHQ-6-3, 4096 - 4157	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.64E-05	0.84	4.07	-	284.5
AHQ-6-4, 4240 - 4252	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	9.13E-07	0.83	3.91	-	287.0
AHQ-6-1, 4082 - 4152	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.43E-04	0.44	2.64	-	219.0
AHQ-6-2, 5322 - 5378	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.31E-12	0.98	5.51	-	1952.4
AHQ-6-4, 4280	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.75E-10	0.95	4.43	-	1093.9
AHQ-6-1, 5394	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.53E-10	0.98	6.10	-	2008.8
AHQ-6-2, 5486 - 5495	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.18E-05	0.96	4.86	-	1055.3
AHQ-6-5, 5267	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	4.71E-06	0.96	5.21	-	1626.2
AHQ-6-4, 5249	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.54E-05	0.91	3.84	-	828.7
AHQ-6-4, 5343 - 5404	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.35E-10	0.98	6.11	-	2086.2
AHQ-6-5, 5263 - 5324	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.77E-09	0.97	5.38	-	1291.1

AHQ-6-6, 5234	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	7.60E-05	0.97	5.42	-	1778.1
AHQ-6-6, 4162 - 4178	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.19E-06	0.78	3.56	-	441.6
AHQ-6-3, 5293 - 5349	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.02E-04	0.97	5.87	-	1914.8
AHQ-6-2, 4288 - 4356	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.30E-08	0.89	4.26	-	600.1
AHQ-6-2, 5599	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.78E-15	0.98	5.59	-	2017.5
AHQ-6-3, 4256	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.50E-07	0.77	3.38	-	499.5
AHQ-6-6, 5215	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.69E-08	0.94	4.64	-	1032.4
AHQ-6-5, 4204	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.14E-07	0.94	4.62	-	827.6
AHQ-6-3, 5265 - 5348	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.93E-12	0.97	5.20	-	1788.1
AHQ-6-3, 5558	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.05E-14	0.97	5.28	-	1428.2
AHQ-6-6, 5392	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.76E-07	0.88	3.51	-	941.2
AHQ-6-1, 5387	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.27E-12	0.97	5.91	-	1510.2
AHQ-6-2, 4954	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.53E-06	0.95	4.65	-	1257.9
AHQ-6-7, 5066 - 5067	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.04E-06	0.97	5.80	-	1414.0
AHQ-6-4, 5347	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.09E-09	0.98	6.03	-	2296.9
AHQ-6-11, 5051	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.14E-06	0.91	4.00	-	929.0
AHQ-6-2, 5164	R.LNEAAAGLNQAATELVQASRGTPQDLAR.A	2867.12501	3	2.85E-09	0.68	3.14	-	475.6
AHQ-6-4, 5176	R.LNEAAAGLNQAATELVQASRGTPQDLAR.A	2867.12501	3	6.29E-04	0.68	3.50	-	476.7
AHQ-6-2, 2131	R.MATNAAAQNAIK.K	1204.38227	2	4.38E-05	0.88	3.79	-	633.8
AHQ-6-6, 3166	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	2.09E-06	0.83	3.55	-	1030.7
AHQ-6-4, 4025	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.97E-07	0.87	4.06	-	803.1
AHQ-6-2, 4071	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.62E-07	0.98	5.65	-	2498.4
AHQ-6-3, 4025	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.42E-07	0.85	3.74	-	993.1
AHQ-6-2, 4159 - 4228	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.83E-04	0.89	4.70	-	807.7
AHQ-6-6, 3943	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.18E-06	0.82	3.70	-	804.5
AHQ-6-4, 3931 - 3937	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	5.01E-09	0.96	5.44	-	1175.5
AHQ-6-3, 3934	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.15E-06	0.81	3.38	-	766.0
AHQ-6-2, 4064	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	7.97E-11	0.89	4.36	-	1161.4
AHQ-6-13-, 6064	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.23E-07	0.91	3.94	-	1009.6
AHQ-6-2, 5647 - 5718	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	4.65E-08	0.96	4.59	-	1458.2
AHQ-6-14-, 6044 - 6059	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	5.20E-05	0.97	5.08	-	1521.5
AHQ-6-1, 5687	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	1.17E-04	0.90	3.74	-	1665.2
AHQ-6-5, 5679	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	5.51E-05	0.91	3.65	-	1099.3
AHQ-6-2, 5724	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	9.18E-06	0.98	6.29	-	2267.4
AHQ-6-1, 5758	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	5.90E-04	0.93	4.10	-	1098.5
AHQ-6-14-, 5576 - 5587	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.68E-07	0.97	5.00	-	1503.1
AHQ-6-4, 5672 - 5744	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.96E-09	0.98	5.66	-	1725.4
AHQ-6-14-, 5508 - 5574	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	2.08E-05	0.93	4.50	-	1400.5
AHQ-6-8, 2258	K.NCGQMSEIEAK.V	1268.40005	2	7.10E-07	0.91	3.23	-	1319.3
AHQ-6-4, 4381 - 4460	K.NGNLPEFGDAISTASK.A	1621.73018	2	7.27E-05	0.83	3.37	-	583.1
AHQ-6-6, 4304	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.15E-08	0.89	3.41	-	839.8
AHQ-6-3, 4230	K.NGNLPEFGDAISTASK.A	1621.73018	2	9.84E-04	0.78	3.51	-	420.0
AHQ-6-1, 4506	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.65E-05	0.83	3.12	-	532.9
AHQ-6-2, 4232 - 4294	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.09E-05	0.82	3.59	-	505.9
AHQ-6-5, 4343	K.NGNLPEFGDAISTASK.A	1621.73018	2	4.61E-05	0.83	3.30	-	508.4
AHQ-6-6, 4030	K.NLGTALAELR.T	1058.21367	2	8.56E-04	0.91	3.09	-	1023.6
AHQ-6-1, 4318	K.NLGTALAELR.T	1058.21367	2	2.72E-04	0.86	3.42	-	786.9
AHQ-6-5, 4073	K.NLGTALAELR.T	1058.21367	2	7.11E-04	0.83	3.17	-	845.0
AHQ-6-2, 5230	K.NLGTALAELR.T	1058.21367	2	4.20E-04	0.90	3.35	-	1119.5
AHQ-6-3, 2848	K.PAAVAAENEEIGSHIK.H	1636.78798	2	3.04E-06	0.97	4.96	-	1629.7
AHQ-6-4, 2805 - 2825	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.01E-09	0.97	5.47	-	2003.0
AHQ-6-6, 2776	K.PAAVAAENEEIGSHIK.H	1636.78798	2	7.53E-05	0.98	4.74	-	2205.4
AHQ-6-4, 2803	K.PAAVAAENEEIGSHIK.H	1636.78798	2	3.10E-06	0.96	4.47	-	1470.2
AHQ-6-5, 2771	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.93E-10	0.97	4.86	-	1849.7
AHQ-6-5, 2765 - 2776	K.PAAVAAENEEIGSHIK.H	1636.78798	3	7.62E-07	0.98	5.43	-	2310.2
AHQ-6-2, 2851	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.08E-09	0.98	5.65	-	2337.0
AHQ-6-2, 2848	K.PAAVAAENEEIGSHIK.H	1636.78798	2	2.20E-04	0.97	5.16	-	1854.5
AHQ-6-6, 2772	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.72E-10	0.96	4.99	-	1879.6
AHQ-6-3, 2850	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.48E-09	0.97	5.46	-	1818.1
AHQ-6-5, 3261	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	6.13E-05	0.87	4.36	-	418.1
AHQ-6-2, 3367 - 3376	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.96E-06	0.89	4.27	-	590.6
AHQ-6-3, 3348 - 3349	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.28E-04	0.91	4.58	-	559.8
AHQ-6-3, 3345	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	7.80E-05	0.76	3.24	-	749.3
AHQ-6-6, 3243	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	7.60E-06	0.83	3.73	-	493.3
AHQ-6-6, 3242	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	1.49E-08	0.75	3.19	-	748.8
AHQ-6-4, 3311	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.50E-04	0.85	4.07	-	479.7
AHQ-6-1, 3544	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	8.90E-06	0.71	3.22	-	642.5
AHQ-6-5, 3808 - 3880	R.QELAVFCSPEPPAK.T	1574.77985	2	6.06E-06	0.84	3.06	-	857.8
AHQ-6-6, 3847 - 3850	R.QELAVFCSPEPPAK.T	1574.77985	2	4.56E-06	0.90	3.52	-	994.3
AHQ-6-2, 3962 - 3964	R.QELAVFCSPEPPAK.T	1574.77985	2	5.49E-07	0.92	3.84	-	1007.3
AHQ-6-6, 3658	K.QVAASTAQLLVACK.V	1461.70942	2	8.11E-06	0.74	3.13	-	511.4
AHQ-6-2, 3795	K.QVAASTAQLLVACK.V	1461.70942	2	6.80E-04	0.86	3.50	-	534.7
AHQ-6-13-, 3748	K.QVAASTAQLLVACK.V	1461.70942	2	1.57E-06	0.85	3.26	-	690.3
AHQ-6-5, 3696 - 3773	K.QVAASTAQLLVACK.V	1461.70942	2	1.13E-04	0.85	3.14	-	622.1
AHQ-6-4, 3755	K.QVAASTAQLLVACK.V	1461.70942	2	1.37E-04	0.78	3.14	-	463.5
AHQ-6-4, 4793 - 4871	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	5.60E-04	0.77	3.75	-	381.3
AHQ-6-4, 5655	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	1.20E-04	0.96	4.85	-	1345.6
AHQ-6-2, 5650	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	1.47E-04	0.97	4.72	-	1737.6
AHQ-6-2, 3587	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	3.01E-04	0.59	3.43	-	447.3
AHQ-6-3, 3569	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	9.66E-07	0.61	3.28	-	647.7
AHQ-6-2, 3298	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	6.75E-04	0.94	4.95	-	1071.0
AHQ-6-2, 3780	R.SGASGPENFQVGSMPPAQQQITSGQM*HR.G	2945.19807	3	6.31E-05	0.55	3.18	-	308.9
AHQ-6-3, 3124	K.SIAAATSALVK.A	1032.21612	2	3.48E-04	0.89	2.95	-	970.6
AHQ-6-13-, 3774 - 3850	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	9.06E-06	0.96	4.95	-	1884.4
AHQ-6-8, 4014	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	4.54E-09	0.92	3.93	-	998.0
AHQ-6-8, 4013	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	1.31E-05	0.95	4.73	-	1509.7
AHQ-6-8, 3678	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	6.69E-07	0.96	5.27	-	1628.4
AHQ-6-5, 5081 - 5099	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.74E-06	0.90	4.19	-	488.4
AHQ-6-2, 4947 - 5018	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.23E-06	0.89	3.83	-	501.5
AHQ-6-2, 5170	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.80E-06	0.86	3.82	-	481.5
AHQ-6-2, 4444	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.14E-09	0.88	4.25	-	437.7
AHQ-6-4, 4451	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	8.14E-08	0.90	4.14	-	625.3
AHQ-6-3, 5113 - 5140	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.95E-07	0.87	4.51	-	367.0
AHQ-6-4, 5012 - 5071	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.23E-05	0.69	3.34	-	301.2
AHQ-6-3, 4425	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.22E-07	0.72	3.20	-	358.0
AHQ-6-6, 5082	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.95E-05	0.77	3.37	-	353.9
AHQ-6-4, 5164 - 5225	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.20E-07	0.85	3.76	-	600.3
AHQ-6-1, 5230	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.10E-06	0.64	3.07	-	389.5
AHQ-6-2, 4567	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.11E-04	0.74	3.83	-	330.2
AHQ-6-3, 4909 - 4978	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.88E-08	0.86	3.72	-	471.2
AHQ-6-3, 5020	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.93E-05	0.78	3.62	-	309.8
AHQ-6-2, 5071 - 5147	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.04E-07	0.93	4.95	-	583.5
AHQ-6-1, 4555	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.50E-06	0.84	3.66	-	581.3
AHQ-6-6, 4907 - 4962	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.38E-06	0.82	3.72	-	449.7
AHQ-6-5, 4893 - 4968	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.52E-05	0.93	4.48	-	615.4
AHQ-6-1, 5048 - 5119	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.08E-06	0.90	4.08	-	588.0
AHQ-6-2, 5258	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.95E-04	0.53	3.32	-	214.7

AHQ-6-3, 4540	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	8.69E-04	0.43	2.71	-	327.3
AHQ-6-5, 4365	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.59E-11	0.74	3.71	-	384.8
AHQ-6-7, 4786	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.58E-05	0.71	3.34	-	311.5
AHQ-6-2, 6438 - 6515	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	3.55E-05	0.59	3.23	-	480.1
AHQ-6-8, 6352 - 6354	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.40E-08	0.92	4.93	-	1071.8
AHQ-6-2, 6698	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	3.09E-10	0.95	5.18	-	1385.9
AHQ-6-1, 6486	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	6.49E-11	0.98	7.37	-	2108.7
AHQ-6-8, 4025 - 4101	K.TKEVIQEWNLTNIK.R	1716.95938	2	6.61E-06	0.94	3.92	-	1414.5
AHQ-6-7, 4096	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.67E-06	0.94	3.88	-	1235.8
AHQ-6-10, 5700 - 5710	K.TLAESALQLLYTAK.E	1522.76793	2	1.20E-05	0.84	3.00	-	796.0
AHQ-6-8, 5892	K.TLAESALQLLYTAK.E	1522.76793	2	2.11E-07	0.93	4.01	-	889.3
AHQ-6-14-, 5910 - 5911	K.TLAESALQLLYTAK.E	1522.76793	2	1.26E-07	0.94	3.60	-	1100.7
AHQ-6-3, 5998	K.TLAESALQLLYTAK.E	1522.76793	3	1.43E-04	0.95	4.58	-	1617.9
AHQ-6-6, 5927 - 5928	K.TLAESALQLLYTAK.E	1522.76793	2	2.27E-04	0.95	4.30	-	1068.3
AHQ-6-5, 6004	K.TLAESALQLLYTAK.E	1522.76793	3	6.25E-06	0.96	4.75	-	1830.0
AHQ-6-5, 5991	K.TLAESALQLLYTAK.E	1522.76793	2	8.50E-05	0.96	3.94	-	1272.5
AHQ-6-3, 5992 - 5993	K.TLAESALQLLYTAK.E	1522.76793	2	3.74E-07	0.96	4.91	-	902.2
AHQ-6-7, 5778 - 5782	K.TLAESALQLLYTAK.E	1522.76793	2	1.46E-04	0.94	3.84	-	1353.1
AHQ-6-11, 5764 - 5768	K.TLAESALQLLYTAK.E	1522.76793	2	3.82E-04	0.93	3.32	-	1172.9
AHQ-6-2, 6026 - 6047	K.TLAESALQLLYTAK.E	1522.76793	2	3.11E-06	0.94	4.30	-	950.9
AHQ-6-4, 6059 - 6080	K.TLAESALQLLYTAK.E	1522.76793	2	1.35E-06	0.92	3.38	-	1076.3
AHQ-6-4, 6071	K.TLAESALQLLYTAK.E	1522.76793	3	1.39E-07	0.96	4.60	-	1718.0
AHQ-6-1, 6082 - 6083	K.TLAESALQLLYTAK.E	1522.76793	2	8.87E-06	0.96	4.72	-	1178.6
AHQ-6-4, 3285 - 3297	K.TLSHPQQMALLDQTK.T	1711.96464	3	6.13E-05	0.95	4.92	-	1367.1
AHQ-6-4, 3193 - 3271	K.TLSHPQQMALLDQTK.T	1711.96464	2	5.40E-04	0.76	3.46	-	443.6
AHQ-6-2, 3330	K.TLSHPQQMALLDQTK.T	1711.96464	3	2.69E-06	0.93	4.85	-	1076.2
AHQ-6-5, 3224 - 3231	K.TLSHPQQMALLDQTK.T	1711.96464	2	4.21E-05	0.95	4.95	-	691.9
AHQ-6-6, 4056 - 4115	K.TMLESAGGLIQTAR.A	1448.67095	2	1.50E-09	0.90	3.39	-	1585.9
AHQ-6-3, 4172 - 4204	K.TMLESAGGLIQTAR.A	1448.67095	2	1.37E-07	0.94	3.67	-	1621.4
AHQ-6-2, 4186 - 4242	K.TMLESAGGLIQTAR.A	1448.67095	2	2.24E-08	0.95	4.15	-	1637.0
AHQ-6-1, 3660	K.TM*LESAGGLIQTAR.A	1464.67035	2	2.80E-07	0.92	3.35	-	1189.6
AHQ-6-2, 3486 - 3547	K.TM*LESAGGLIQTAR.A	1464.67035	2	5.22E-04	0.68	2.63	-	985.2
AHQ-6-5, 4147	K.TMLESAGGLIQTAR.A	1448.67095	2	1.75E-07	0.96	3.68	-	2326.5
AHQ-6-2, 3488 - 3546	K.TM*LESAGGLIQTAR.A	1464.67035	2	8.40E-09	0.96	4.93	-	1425.8
AHQ-6-4, 4209	K.TMLESAGGLIQTAR.A	1448.67095	2	9.38E-07	0.90	3.50	-	1562.0
AHQ-6-13, 4344	K.TM*QFEPSTMVYDACR.I	1854.07511	2	1.48E-06	0.86	3.94	-	492.0
AHQ-6-8, 4009	K.TM*QFEPSTMVYDACR.I	1854.07511	2	8.54E-05	0.93	4.51	-	671.2
AHQ-6-8, 4454 - 4456	K.TMQFEPSTMVYDACR.I	1838.07571	2	3.02E-05	0.89	4.02	-	479.6
AHQ-6-8, 5014	K.TVTDMLMTICAR.I	1413.71007	2	1.77E-05	0.85	2.69	-	935.3
AHQ-6-8, 4026	K.TVTDM*LMTICAR.I	1429.70947	2	4.87E-04	0.58	2.58	-	738.2
AHQ-6-7, 4911	K.TYGVSFFLVK.E	1161.37395	2	2.01E-07	0.87	3.26	-	707.3
AHQ-6-8, 4886	K.TYGVSFFLVK.E	1161.37395	2	1.26E-05	0.82	3.38	-	535.6
AHQ-6-1, 5222	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	1.29E-05	0.83	2.95	-	920.7
AHQ-6-5, 5075 - 5144	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.21E-05	0.75	2.81	-	890.6
AHQ-6-5, 5877 - 5935	R.VAGSVTELIQAAEAMK.G	1618.87752	2	4.85E-09	0.95	4.41	-	1191.5
AHQ-6-4, 5147 - 5148	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	3.25E-05	0.96	4.64	-	1638.1
AHQ-6-6, 5042	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	3.18E-08	0.94	4.43	-	1095.7
AHQ-6-7, 5720	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.96E-05	0.87	3.45	-	837.0
AHQ-6-3, 5104	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	1.40E-06	0.95	3.93	-	1520.7
AHQ-6-4, 5980 - 5993	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.91E-09	0.94	3.81	-	1239.0
AHQ-6-2, 5080 - 5142	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.38E-06	0.95	4.08	-	1359.2
AHQ-6-2, 5956	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.63E-09	0.96	4.43	-	1236.4
AHQ-6-1, 6019	R.VAGSVTELIQAAEAMK.G	1618.87752	2	5.54E-06	0.94	4.43	-	1057.8
AHQ-6-2, 5130	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	3.56E-05	0.91	4.29	-	802.5
AHQ-6-7, 4883 - 4896	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.45E-04	0.85	3.85	-	782.0
AHQ-6-8, 5802	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.53E-06	0.95	4.29	-	1187.8
AHQ-6-3, 5921	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.46E-05	0.92	3.46	-	1321.7
AHQ-6-6, 5850	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.20E-07	0.95	4.21	-	1163.7
AHQ-6-6, 5490	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	4.10E-05	0.90	4.13	-	1174.6
AHQ-6-6, 5415 - 5487	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.60E-07	0.92	4.26	-	769.0
AHQ-6-6, 5331	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.10E-05	0.84	3.85	-	463.8
AHQ-6-3, 5414 - 5481	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	4.80E-08	0.85	3.29	-	1284.3
AHQ-6-3, 5478	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.27E-08	0.92	4.60	-	487.8
AHQ-6-3, 5512 - 5568	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	2.32E-04	0.92	4.79	-	1318.6
AHQ-6-9, 5182	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.33E-08	0.76	3.24	-	631.5
AHQ-6-7, 5251	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.63E-05	0.53	2.74	-	230.8
AHQ-6-2, 5543 - 5598	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	2.83E-08	0.96	4.83	-	2049.8
AHQ-6-10, 5255	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.74E-04	0.70	3.03	-	449.2
AHQ-6-7, 5339	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.48E-09	0.94	4.72	-	877.7
AHQ-6-2, 5442 - 5514	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	5.43E-08	0.92	4.55	-	1385.2
AHQ-6-5, 5551	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	7.69E-07	0.92	4.21	-	1308.0
AHQ-6-5, 5547	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.03E-09	0.95	5.02	-	686.5
AHQ-6-5, 5380 - 5459	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.98E-06	0.96	5.14	-	859.1
AHQ-6-4, 5468 - 5545	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.78E-09	0.94	4.68	-	853.1
AHQ-6-4, 5469 - 5549	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	3.38E-05	0.94	4.66	-	1533.4
AHQ-6-2, 5447 - 5504	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.00E-08	0.85	3.81	-	523.1
AHQ-6-4, 5627 - 5697	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.00E-08	0.95	4.53	-	1061.3
AHQ-6-4, 5628 - 5629	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	1.35E-04	0.94	5.05	-	1063.7
AHQ-6-2, 5538 - 5595	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.21E-10	0.97	5.83	-	1097.3
AHQ-6-1, 5642 - 5698	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.40E-06	0.90	4.17	-	589.5
AHQ-6-2, 5362 - 5434	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.66E-06	0.92	4.21	-	804.8
AHQ-6-1, 3962	K.VGDDPAVWQLK.N	1228.37879	2	1.58E-07	0.94	4.16	-	954.1
AHQ-6-7, 3574 - 3599	K.VGDDPAVWQLK.N	1228.37879	2	7.99E-06	0.86	3.26	-	820.9
AHQ-6-3, 3785	K.VGDDPAVWQLK.N	1228.37879	2	9.42E-07	0.89	3.68	-	660.3
AHQ-6-5, 3704 - 3711	K.VGDDPAVWQLK.N	1228.37879	2	4.77E-09	0.93	3.69	-	947.1
AHQ-6-6, 3672	K.VGDDPAVWQLK.N	1228.37879	2	4.87E-06	0.81	2.97	-	723.1
AHQ-6-2, 3822	K.VGDDPAVWQLK.N	1228.37879	2	2.04E-08	0.93	4.00	-	865.2
AHQ-6-2, 3763 - 3834	K.VGDDPAVWQLK.N	1228.37879	2	7.07E-08	0.90	3.65	-	742.0
AHQ-6-4, 3767 - 3768	K.VGDDPAVWQLK.N	1228.37879	2	5.85E-10	0.94	4.15	-	949.4
AHQ-6-4, 3268	K.VGDDPAVWQLKNSAK.V	1628.81068	2	9.99E-10	0.79	3.09	-	689.7
AHQ-6-6, 3200	K.VGDDPAVWQLKNSAK.V	1628.81068	2	8.60E-04	0.86	3.02	-	896.6
AHQ-6-2, 2532	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.47E-06	0.94	3.74	-	1352.0
AHQ-6-5, 2389	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.73E-06	0.95	4.13	-	1354.1
AHQ-6-2, 2442 - 2447	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.04E-04	0.89	3.48	-	872.6
AHQ-6-3, 2537	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.44E-05	0.94	3.79	-	1302.0
AHQ-6-2, 3156	K.VLGEAMTGISQNAK.N	1419.62961	2	8.60E-06	0.97	4.34	-	1864.0
AHQ-6-3, 4617 - 4676	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	3.16E-09	0.91	4.33	-	886.8
AHQ-6-4, 5171 - 5184	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	7.47E-05	0.84	4.15	-	725.6
AHQ-6-3, 5109	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	3.29E-07	0.90	4.77	-	754.9
AHQ-6-2, 4630 - 4694	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	2.27E-11	0.92	5.30	-	501.5
AHQ-6-2, 4750	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	6.69E-11	0.90	4.88	-	616.1
AHQ-6-3, 1953 - 1993	K.VLVQNAAGSQEK.L	1244.37976	2	1.61E-05	0.53	2.53	-	461.5
AHQ-6-5, 1856	K.VLVQNAAGSQEK.L	1244.37976	2	5.09E-06	0.71	2.84	-	447.7
AHQ-6-3, 1854	K.VLVQNAAGSQEK.L	1244.37976	2	1.86E-05	0.80	2.93	-	648.9
AHQ-6-4, 1781 - 1835	K.VLVQNAAGSQEK.L	1244.37976	2	3.91E-08	0.94	3.70	-	1122.7
AHQ-6-6, 1752 - 1810	K.VLVQNAAGSQEK.L	1244.37976	2	2.14E-04	0.90	3.37	-	936.1
AHQ-6-6, 1878	K.VLVQNAAGSQEK.L	1244.37976	2	2.03E-05	0.80	3.12	-	553.2

AHQ-6-5, 1729 - 1788	K.VLVQNAAGSQEK.L	1244.37976	2	1.55E-04	0.93	3.58	-	1182.4
AHQ-6-2, 1839 - 1894	K.VLVQNAAGSQEK.L	1244.37976	2	6.80E-09	0.92	3.82	-	840.1
AHQ-6-4, 1893 - 1917	K.VLVQNAAGSQEK.L	1244.37976	2	7.05E-11	0.90	3.44	-	887.1
AHQ-6-4, 4272 - 4291	K.VM*VTNVTSLLK.T	1221.49262	2	5.59E-06	0.90	3.47	-	998.7
AHQ-6-5, 4195	K.VM*VTNVTSLLK.T	1221.49262	2	9.36E-06	0.85	2.81	-	962.3
AHQ-6-4, 4600	K.VMVTNVTSLLK.T	1205.49322	2	6.14E-06	0.87	3.49	-	939.8
AHQ-6-3, 4602 - 4608	K.VMVTNVTSLLK.T	1205.49322	2	4.75E-06	0.90	4.06	-	772.7
AHQ-6-2, 4283	K.VM*VTNVTSLLK.T	1221.49262	2	2.11E-05	0.84	3.29	-	639.5
AHQ-6-5, 4513	K.VMVTNVTSLLK.T	1205.49322	2	3.18E-07	0.90	3.74	-	801.3
AHQ-6-6, 4159	K.VM*VTNVTSLLK.T	1221.49262	2	3.31E-04	0.80	2.72	-	648.7
AHQ-6-3, 4268	K.VM*VTNVTSLLK.T	1221.49262	2	1.43E-05	0.81	3.12	-	611.2
AHQ-6-2, 4615	K.VMVTNVTSLLK.T	1205.49322	2	2.82E-06	0.83	3.54	-	713.5
AHQ-6-6, 4466	K.VMVTNVTSLLK.T	1205.49322	2	8.72E-04	0.92	4.08	-	872.3
AHQ-6-7, 2742	R.VQELGHGCAALVTK.A	1484.70307	2	1.54E-04	0.97	4.86	-	1772.0
AHQ-6-3, 2904	R.VQELGHGCAALVTK.A	1484.70307	2	8.26E-05	0.98	5.21	-	1923.0
AHQ-6-2, 2904	R.VQELGHGCAALVTK.A	1484.70307	2	8.08E-05	0.97	5.02	-	1717.2
AHQ-6-4, 2855	R.VQELGHGCAALVTK.A	1484.70307	2	2.16E-05	0.95	4.24	-	1300.0
AHQ-6-5, 2823	R.VQELGHGCAALVTK.A	1484.70307	2	1.05E-09	0.97	5.06	-	1300.9
AHQ-6-6, 2823	R.VQELGHGCAALVTK.A	1484.70307	2	1.80E-05	0.97	4.70	-	1477.9
AHQ-6-4, 2837	K.VSHVLAALQAGNR.G	1336.52525	1	6.97E-04	0.56	2.23	-	456.7
AHQ-6-5, 2788	K.VSHVLAALQAGNR.G	1336.52525	2	4.07E-08	0.97	4.19	-	1791.8
AHQ-6-3, 2880 - 2882	K.VSHVLAALQAGNR.G	1336.52525	2	3.52E-08	0.98	4.75	-	2078.0
AHQ-6-2, 2887	K.VSHVLAALQAGNR.G	1336.52525	1	3.80E-05	0.41	2.42	-	278.7
AHQ-6-4, 2827	K.VSHVLAALQAGNR.G	1336.52525	2	3.75E-10	0.97	4.70	-	1811.0
AHQ-6-2, 2874	K.VSHVLAALQAGNR.G	1336.52525	2	8.83E-10	0.97	4.05	-	2056.1
AHQ-6-6, 2791	K.VSHVLAALQAGNR.G	1336.52525	2	2.14E-08	0.97	4.24	-	1599.8
AHQ-6-3, 6218 - 6221	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	1.27E-05	0.91	4.15	-	1151.2
AHQ-6-3, 6216	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.67E-06	0.90	4.08	-	673.9
AHQ-6-4, 6249 - 6307	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.40E-07	0.96	5.51	-	1104.8
AHQ-6-3, 5554 - 5560	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.03E-05	0.93	4.52	-	912.5
AHQ-6-4, 6296 - 6320	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	3.24E-10	0.93	4.28	-	1264.9
AHQ-6-1, 6298	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.94E-05	0.79	3.68	-	404.6
AHQ-6-6, 5482	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.39E-06	0.96	4.59	-	1297.6
AHQ-6-6, 5488	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	7.34E-08	0.95	4.83	-	1500.7
AHQ-6-4, 5624	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.22E-06	0.93	3.57	-	1656.5
AHQ-6-5, 6212 - 6215	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.63E-05	0.96	5.40	-	908.7
AHQ-6-5, 5535	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.61E-08	0.92	3.86	-	1407.2
AHQ-6-5, 5532	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	8.08E-07	0.92	4.15	-	828.2
AHQ-6-1, 5640	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	6.42E-06	0.95	4.57	-	988.2
AHQ-6-6, 6139	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.67E-05	0.83	3.79	-	499.6
AHQ-6-4, 5623 - 5625	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.05E-07	0.97	5.60	-	1106.7
AHQ-6-1, 5639	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.60E-09	0.92	3.68	-	1415.8
AHQ-6-2, 6210 - 6266	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.84E-07	0.97	5.82	-	1001.5
AHQ-6-7, 5328	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.27E-04	0.86	3.98	-	631.2
AHQ-6-2, 5707 - 5766	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.77E-04	0.86	3.80	-	485.5
AHQ-6-2, 5592	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.16E-06	0.94	4.16	-	1515.0
AHQ-6-2, 5574 - 5627	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.06E-05	0.91	4.11	-	1039.2
AHQ-6-5, 4407	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	9.17E-06	0.89	3.80	-	1016.3
AHQ-6-5, 4392	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.62E-10	0.95	4.82	-	944.3
AHQ-6-4, 4484	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.23E-05	0.95	5.15	-	654.1
AHQ-6-4, 4391	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.04E-04	0.74	3.42	-	368.1
AHQ-6-11, 4276	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.72E-04	0.81	3.16	-	621.4
AHQ-6-2, 4378	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.88E-07	0.95	4.74	-	620.1
AHQ-6-14-, 4376	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.61E-07	0.89	3.97	-	575.5
AHQ-6-6, 4362	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.42E-08	0.92	4.22	-	794.6
AHQ-6-2, 4482	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.16E-07	0.92	4.61	-	583.2
AHQ-6-2, 4490 - 4492	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	1.27E-09	0.91	4.24	-	1102.2
AHQ-6-3, 4469	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	3.16E-04	0.85	3.39	-	987.6
AHQ-6-3, 4454 - 4488	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.55E-07	0.95	4.58	-	888.4
AHQ-6-3, 4370	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.00E-06	0.42	3.00	-	157.6
AHQ-6-8, 4248 - 4249	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.10E-06	0.96	5.54	-	722.3
AHQ-6-1, 4582	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.75E-06	0.93	4.34	-	715.3
AHQ-6-7, 4211 - 4218	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.62E-07	0.90	4.45	-	506.9
AHQ-6-4, 4489 - 4507	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	7.00E-05	0.82	3.27	-	1035.5
gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act				2.78E-15	95.35	1110.38	56.10	280757.4
AHQ-6-7, 4848	R.AEAGVPAEFSIWTR.E	1534.69735	2	1.56E-04	0.40	2.58	-	245.5
AHQ-6-4, 5103 - 5165	R.AEAGVPAEFSIWTR.E	1534.69735	2	2.64E-05	0.75	3.10	-	427.0
AHQ-6-4, 2559	K.AEISFEDR.K	967.01472	2	5.35E-05	0.93	3.10	-	1235.4
AHQ-6-4, 2172	K.AEISFEDRK.D	1095.18763	2	5.01E-04	0.79	2.75	-	842.6
AHQ-6-5, 2123	K.AEISFEDRK.D	1095.18763	2	2.48E-04	0.82	2.86	-	936.7
AHQ-6-4, 2701	K.AFGPGLQGGSAGSPAR.F	1430.55077	1	1.65E-04	0.26	2.51	-	133.7
AHQ-6-3, 2748	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.37E-08	0.86	2.81	-	1075.0
AHQ-6-7, 2582	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.48E-05	0.94	3.03	-	1704.5
AHQ-6-1, 2936	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.12E-10	0.94	3.21	-	1730.3
AHQ-6-4, 2683	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.09E-08	0.95	3.58	-	1754.5
AHQ-6-3, 2637 - 2709	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	5.64E-10	0.94	3.64	-	1428.1
AHQ-6-5, 2644	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	3.95E-09	0.91	3.13	-	1350.5
AHQ-6-14-, 2791 - 2846	K.AGNNM*LLVGVHGPR.T	1451.67973	2	6.34E-08	0.71	2.84	-	596.8
AHQ-6-14, 3608 - 3666	K.AGNNM*LLVGVHGPR.T	1451.67973	2	2.84E-05	0.75	3.19	-	531.1
AHQ-6-14-, 2844 - 2847	K.AGNNM*LLVGVHGPR.T	1451.67973	3	1.28E-07	0.87	4.17	-	869.5
AHQ-6-14, 4160 - 4162	K.AGNNMLLVGVHGPR.T	1435.68033	2	4.92E-04	0.86	3.42	-	743.3
AHQ-6-14-, 2970	K.AGNNM*LLVGVHGPR.T	1451.67973	2	5.14E-06	0.54	2.51	-	389.9
AHQ-6-5, 2920	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.69E-04	0.82	2.94	-	759.0
AHQ-6-14-, 3451 - 3467	K.AGNNMLLVGVHGPR.T	1435.68033	2	4.80E-08	0.91	3.61	-	912.5
AHQ-6-4, 2975 - 2976	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.43E-04	0.87	3.61	-	668.6
AHQ-6-14, 3733 - 3793	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.48E-04	0.80	3.01	-	699.0
AHQ-6-4, 1840	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	6.75E-05	0.65	2.74	-	558.3
AHQ-6-2, 1843 - 1880	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	2.40E-07	0.87	4.04	-	624.3
AHQ-6-2, 2414	K.AGVAPLQVK.V	883.07036	2	1.85E-05	0.80	2.69	-	656.8
AHQ-6-3, 2425	K.AGVAPLQVK.V	883.07036	2	1.67E-04	0.80	2.85	-	563.2
AHQ-6-4, 2384	K.AGVAPLQVK.V	883.07036	2	1.36E-05	0.83	2.82	-	723.0
AHQ-6-1, 2659	K.AGVAPLQVK.V	883.07036	2	5.98E-06	0.75	2.66	-	577.1
AHQ-6-2, 6659	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	2	6.15E-04	0.57	2.59	-	576.4
AHQ-6-3, 6614	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	3.12E-04	0.77	3.26	-	827.6
AHQ-6-4, 2724	K.AHVVPCFDASK.V	1232.39073	1	1.03E-04	0.68	2.73	-	520.4
AHQ-6-1, 3000	K.AHVVPCFDASK.V	1232.39073	2	2.17E-04	0.75	2.53	-	694.5
AHQ-6-1, 5955	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.51E-08	0.90	4.33	-	891.2
AHQ-6-5, 5804 - 5867	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.46E-11	0.96	6.08	-	1079.2
AHQ-6-6, 5752 - 5811	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.36E-05	0.90	4.70	-	540.3
AHQ-6-7, 5599 - 5658	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	8.43E-10	0.87	4.65	-	586.7
AHQ-6-5, 5648	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.89E-05	0.73	3.03	-	656.3
AHQ-6-3, 5822 - 5876	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.69E-10	0.94	5.14	-	885.5
AHQ-6-2, 5756 - 5830	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.12E-08	0.91	4.51	-	714.1
AHQ-6-2, 5852 - 5922	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.14E-07	0.93	5.31	-	838.9
AHQ-6-2, 1691	R.ALTQTGGPHVK.A	1109.26067	2	6.63E-05	0.74	2.70	-	746.5
AHQ-6-2, 3414 - 3478	R.ANLPQSFQVDTSK.A	1435.56409	2	5.62E-10	0.89	3.56	-	658.7
AHQ-6-8, 3141	R.ANLPQSFQVDTSK.A	1435.56409	1	1.27E-05	0.67	2.64	-	470.0

AHQ-6-5, 3172 - 3248	R.ANLPQSFQVDTSK.A	1435.56409	2	3.11E-08	0.89	3.73	-	720.6
AHQ-6-2, 3348	R.ANLPQSFQVDTSK.A	1435.56409	1	2.44E-06	0.48	2.70	-	360.7
AHQ-6-8, 3132	R.ANLPQSFQVDTSK.A	1435.56409	2	5.20E-07	0.83	3.43	-	413.5
AHQ-6-4, 3413	R.APSVANVGSHCDLSLK.I	1656.84249	2	6.14E-05	0.90	4.51	-	625.8
AHQ-6-1, 5598 - 5675	K.ASGPGLNTTGVPASLPVEFTIDAK.D	2343.61826	3	1.33E-04	0.73	3.84	-	618.8
AHQ-6-4, 1935	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	8.19E-05	0.93	3.76	-	978.6
AHQ-6-7, 1891	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	1.10E-04	0.91	3.93	-	864.0
AHQ-6-5, 3553	R.AWGPGLEGGVVGK.S	1227.39403	2	1.18E-08	0.88	3.67	-	811.0
AHQ-6-3, 3648	R.AWGPGLEGGVVGK.S	1227.39403	2	1.23E-06	0.88	3.45	-	857.3
AHQ-6-7, 3448	R.AWGPGLEGGVVGK.S	1227.39403	2	6.14E-06	0.85	3.17	-	906.1
AHQ-6-4, 3565 - 3632	R.AWGPGLEGGVVGK.S	1227.39403	2	3.93E-04	0.89	3.23	-	867.4
AHQ-6-1, 3819	R.AWGPGLEGGVVGK.S	1227.39403	2	6.12E-05	0.85	3.20	-	743.0
AHQ-6-2, 3663	R.AWGPGLEGGVVGK.S	1227.39403	2	3.24E-06	0.83	3.51	-	598.1
AHQ-6-2, 2818	R.AYGPGIEPTGNM*VK.K	1450.64214	2	3.04E-06	0.71	3.13	-	371.9
AHQ-6-6, 2643	R.AYGPGIEPTGNM*VK.K	1450.64214	2	3.32E-04	0.74	3.08	-	392.4
AHQ-6-3, 5688 - 5754	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	6.32E-05	0.80	3.28	-	551.8
AHQ-6-2, 5726 - 5790	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	4.53E-04	0.90	3.99	-	701.4
AHQ-6-4, 5789	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	3.61E-06	0.85	3.85	-	557.0
AHQ-6-1, 5759	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.19E-06	0.95	4.60	-	1442.2
AHQ-6-1, 5754	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.78E-04	0.68	3.23	-	353.1
AHQ-6-3, 5697	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	6.49E-10	0.94	4.14	-	1662.0
AHQ-6-2, 5968 - 5991	K.CAPGVVGPAEADIDFDIIRNDNDTFTVK.Y	3052.31840	3	2.25E-05	0.84	4.32	-	537.0
AHQ-6-3, 3006	K.CSGPGLSPGMVR.A	1219.41699	2	1.82E-06	0.81	2.86	-	863.1
AHQ-6-3, 3002	K.CSGPGLSPGMVR.A	1219.41699	2	7.75E-08	0.76	2.85	-	851.3
AHQ-6-2, 4812	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	6.56E-06	0.92	4.25	-	670.8
AHQ-6-3, 4788	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	1.91E-04	0.77	3.56	-	504.7
AHQ-6-4, 4812	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	3.08E-05	0.86	4.17	-	421.8
AHQ-6-2, 4439	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	5.23E-07	0.95	4.37	-	1248.5
AHQ-6-2, 3911	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.83E-08	0.89	3.62	-	946.1
AHQ-6-11, 3748	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	7.65E-04	0.84	3.29	-	836.1
AHQ-6-5, 3820 - 3879	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	6.30E-04	0.84	3.52	-	1017.9
AHQ-6-8, 3689	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.63E-06	0.90	3.86	-	961.9
AHQ-6-13, 3989	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	6.51E-05	0.51	2.65	-	741.3
AHQ-6-5, 3872	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	5.50E-07	0.97	5.06	-	1731.0
AHQ-6-1, 4015	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	7.11E-06	0.95	4.34	-	1524.6
AHQ-6-13-, 3836	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	4.07E-04	0.71	2.82	-	656.7
AHQ-6-4, 3932 - 3988	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	2.39E-04	0.96	4.75	-	1415.6
AHQ-6-1, 4768	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	1.06E-08	0.93	3.53	-	1485.8
AHQ-6-3, 4657	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	7.35E-08	0.95	4.18	-	1556.8
AHQ-6-2, 4700 - 4770	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	3.50E-06	0.88	3.97	-	884.9
AHQ-6-2, 4680	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	1.60E-08	0.94	4.29	-	1325.3
AHQ-6-10, 4030	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	7.01E-07	0.87	3.95	-	826.3
AHQ-6-2, 4291	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	3.34E-09	0.96	4.59	-	1818.3
AHQ-6-5, 4191	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.42E-09	0.92	3.98	-	1200.4
AHQ-6-4, 4279 - 4283	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	1.30E-07	0.91	3.64	-	1258.1
AHQ-6-4, 4189 - 4271	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.90E-04	0.88	3.79	-	859.7
AHQ-6-11, 4092	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.28E-07	0.94	4.23	-	1229.6
AHQ-6-2, 4290 - 4352	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.28E-05	0.94	4.43	-	1332.6
AHQ-6-1, 4423	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	2.19E-07	0.89	3.44	-	1165.7
AHQ-6-1, 4411	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.10E-09	0.95	4.91	-	1120.2
AHQ-6-6, 4164	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	1.95E-05	0.86	3.12	-	1235.5
AHQ-6-6, 4158	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.29E-09	0.94	4.38	-	1147.9
AHQ-6-3, 4261 - 4332	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.94E-06	0.90	3.63	-	1113.4
AHQ-6-3, 4465	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.44E-07	0.93	4.01	-	1167.6
AHQ-6-3, 4265 - 4293	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	8.52E-08	0.84	3.36	-	910.4
AHQ-6-7, 4031	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.46E-04	0.90	3.86	-	1105.7
AHQ-6-8, 4008	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.38E-06	0.94	4.49	-	1169.2
AHQ-6-1, 4470 - 4471	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	2.59E-07	0.96	4.78	-	1383.0
AHQ-6-2, 4394 - 4395	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	6.18E-09	0.92	4.04	-	1269.2
AHQ-6-6, 4266	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	9.26E-10	0.86	3.50	-	990.8
AHQ-6-3, 4362	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	3.53E-05	0.93	3.94	-	1226.9
AHQ-6-5, 4223 - 4299	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	5.68E-08	0.97	5.00	-	1702.9
AHQ-6-4, 4192	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.73E-06	0.49	2.88	-	420.5
AHQ-6-7, 4132	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	5.45E-09	0.89	3.59	-	942.0
AHQ-6-4, 4325 - 4380	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	2.42E-04	0.82	3.42	-	893.2
AHQ-6-2, 2028	R.DAPQDFHPDR.V	1198.22650	2	3.52E-07	0.78	2.99	-	593.5
AHQ-6-3, 2044	R.DAPQDFHPDR.V	1198.22650	2	9.34E-05	0.69	2.75	-	641.3
AHQ-6-4, 4593 - 4655	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	4.55E-07	0.93	4.90	-	682.4
AHQ-6-6, 4479 - 4518	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.15E-05	0.86	4.15	-	583.2
AHQ-6-5, 4704	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	6.33E-04	0.51	3.08	-	360.4
AHQ-6-5, 4541 - 4609	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.75E-07	0.90	4.57	-	626.7
AHQ-6-8, 4364 - 4426	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	6.25E-04	0.58	3.19	-	315.1
AHQ-6-1, 4646 - 4723	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.59E-06	0.91	4.27	-	809.5
AHQ-6-14, 3329	K.DKGEYTLVVK.W	1152.32223	1	5.92E-05	0.26	2.05	-	497.0
AHQ-6-4, 2543	K.DKGEYTLVVK.W	1152.32223	1	3.53E-05	0.10	1.94	-	334.0
AHQ-6-6, 2522 - 2526	K.DKGEYTLVVK.W	1152.32223	2	8.08E-04	0.73	2.80	-	482.0
AHQ-6-5, 2519	K.DKGEYTLVVK.W	1152.32223	2	5.19E-05	0.76	2.77	-	583.2
AHQ-6-3, 2597	K.DKGEYTLVVK.W	1152.32223	2	6.62E-05	0.56	2.71	-	401.4
AHQ-6-5, 3132	K.DNGNGTYSCSYVPR.K	1591.64109	2	5.30E-07	0.88	3.07	-	1036.0
AHQ-6-1, 3315	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	4.07E-05	0.94	3.97	-	1190.3
AHQ-6-3, 3069 - 3132	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.18E-06	0.95	4.37	-	1383.3
AHQ-6-2, 3063 - 3130	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.22E-05	0.93	3.76	-	1012.6
AHQ-6-2, 3227 - 3302	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.20E-07	0.85	3.71	-	521.6
AHQ-6-3, 3222 - 3300	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	5.89E-04	0.63	3.15	-	244.0
AHQ-6-4, 3192	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.88E-04	0.22	2.63	-	174.4
AHQ-6-1, 3579	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	5.89E-06	0.93	4.07	-	1106.9
AHQ-6-5, 3312 - 3377	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.09E-06	0.95	4.28	-	1435.6
AHQ-6-4, 3369 - 3372	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.46E-06	0.97	5.17	-	1298.7
AHQ-6-7, 3199	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	5.03E-05	0.84	3.24	-	951.2
AHQ-6-4, 3379	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	9.48E-04	0.23	2.48	-	312.1
AHQ-6-5, 3441 - 3511	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	5.62E-04	0.91	2.94	-	1499.1
AHQ-6-2, 2600 - 2676	R.EATTEFSVDAR.A	1226.27493	2	4.58E-04	0.73	2.79	-	635.9
AHQ-6-6, 2628 - 2648	R.EATTEFSVDAR.A	1226.27493	2	1.61E-04	0.84	3.16	-	706.1
AHQ-6-2, 2683 - 2747	R.EATTEFSVDAR.A	1226.27493	2	1.65E-04	0.89	3.38	-	732.2
AHQ-6-1, 2900	R.EATTEFSVDAR.A	1226.27493	2	1.26E-04	0.89	3.17	-	800.8
AHQ-6-1, 5868 - 5922	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.02E-05	0.91	4.77	-	703.7
AHQ-6-3, 5868 - 5924	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	6.38E-09	0.94	5.69	-	676.4
AHQ-6-5, 5840 - 5899	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.49E-06	0.94	5.76	-	636.1
AHQ-6-4, 5911 - 5987	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.20E-05	0.89	4.98	-	520.7
AHQ-6-2, 5834 - 5890	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	7.55E-08	0.93	5.16	-	702.9
AHQ-6-3, 5758 - 5812	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.18E-10	0.82	3.96	-	564.5
AHQ-6-3, 5920 - 5984	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.40E-09	0.93	5.13	-	892.4
AHQ-6-2, 5947 - 6003	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.49E-09	0.94	5.45	-	767.8
AHQ-6-1, 5978 - 6035	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.37E-10	0.95	5.94	-	781.7
AHQ-6-4, 4836 - 4908	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.50E-05	0.91	3.88	-	920.6
AHQ-6-8, 4637	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.12E-06	0.87	3.41	-	869.2
AHQ-6-10, 4574	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.96E-06	0.93	4.06	-	821.5

AHQ-6-9, 4514	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.54E-05	0.65	2.98	-	562.6
AHQ-6-4, 4923	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.01E-07	0.92	4.38	-	880.1
AHQ-6-6, 4799	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	6.29E-06	0.84	3.61	-	774.2
AHQ-6-3, 4816 - 4876	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.56E-08	0.92	4.45	-	922.5
AHQ-6-5, 4821 - 4832	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.34E-05	0.63	2.50	-	776.3
AHQ-6-3, 4888	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	4.61E-05	0.96	5.27	-	1479.9
AHQ-6-2, 4907	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	2.80E-04	0.94	4.49	-	1162.8
AHQ-6-2, 4635	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.98E-06	0.84	3.48	-	669.5
AHQ-6-2, 4838 - 4912	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.87E-06	0.93	3.95	-	1264.4
AHQ-6-7, 3295	K.FADQHVPGSPFSVK.V	1516.68203	2	8.32E-05	0.65	3.24	-	288.5
AHQ-6-6, 3383 - 3384	K.FADQHVPGSPFSVK.V	1516.68203	2	3.00E-05	0.91	3.94	-	597.6
AHQ-6-5, 3409	K.FADQHVPGSPFSVK.V	1516.68203	3	7.61E-08	0.92	3.95	-	1156.0
AHQ-6-4, 3476	K.FADQHVPGSPFSVK.V	1516.68203	3	1.74E-06	0.95	4.14	-	1410.2
AHQ-6-4, 3468 - 3548	K.FADQHVPGSPFSVK.V	1516.68203	2	7.98E-07	0.81	3.46	-	472.0
AHQ-6-1, 3684 - 3699	K.FADQHVPGSPFSVK.V	1516.68203	2	2.39E-08	0.88	3.43	-	565.4
AHQ-6-1, 3690	K.FADQHVPGSPFSVK.V	1516.68203	3	1.95E-08	0.94	4.07	-	1388.4
AHQ-6-6, 3386	K.FADQHVPGSPFSVK.V	1516.68203	3	2.97E-05	0.88	3.75	-	960.1
AHQ-6-3, 5270	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.32E-04	0.87	3.55	-	581.1
AHQ-6-6, 5174 - 5186	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	9.46E-04	0.72	3.39	-	567.2
AHQ-6-2, 5154 - 5223	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.06E-05	0.88	4.72	-	562.7
AHQ-6-3, 5364	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.88E-07	0.89	4.01	-	977.7
AHQ-6-2, 5278 - 5323	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.12E-11	0.93	5.06	-	822.1
AHQ-6-2, 5303	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	5.68E-06	0.94	5.05	-	731.3
AHQ-6-2, 5382 - 5439	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	6.37E-06	0.88	4.38	-	762.5
AHQ-6-5, 5204 - 5241	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	9.07E-06	0.92	4.59	-	889.4
AHQ-6-1, 5320 - 5379	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.42E-11	0.95	5.48	-	1129.0
AHQ-6-13, 5229	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.30E-05	0.86	4.45	-	677.4
AHQ-6-4, 5296 - 5355	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.71E-09	0.94	5.49	-	874.3
AHQ-6-5, 5023 - 5085	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	3	3.07E-06	0.91	4.18	-	1204.2
AHQ-6-5, 4920	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	7.11E-06	0.89	4.39	-	442.6
AHQ-6-5, 5019	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	4.58E-04	0.71	3.07	-	440.8
AHQ-6-4, 5003	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	1.59E-06	0.89	3.88	-	552.8
AHQ-6-3, 4976	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	1.28E-05	0.85	3.04	-	713.2
AHQ-6-4, 5113	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	3.21E-08	0.92	4.31	-	752.8
AHQ-6-1, 5160 - 5220	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	3	6.44E-04	0.88	4.48	-	704.2
AHQ-6-1, 5082	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	4.10E-04	0.71	2.72	-	593.7
AHQ-6-5, 3691	K.FNGTHIPGSPFK.I	1302.46259	3	3.98E-05	0.84	3.44	-	991.8
AHQ-6-3, 3130	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.98E-04	0.78	2.94	-	543.6
AHQ-6-5, 2961 - 3012	R.FVPAEMGTHTVSVK.Y	1503.74821	2	4.21E-09	0.74	2.72	-	404.4
AHQ-6-6, 2408 - 2472	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	3.92E-04	0.86	3.51	-	330.6
AHQ-6-6, 3014	R.FVPAEMGTHTVSVK.Y	1503.74821	2	7.38E-08	0.79	2.87	-	509.1
AHQ-6-2, 5656	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	6.60E-04	0.38	2.60	-	298.1
AHQ-6-1, 6258	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	2.90E-05	0.57	3.01	-	385.9
AHQ-6-2, 5654	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	7.52E-04	0.50	2.95	-	392.6
AHQ-6-1, 3566	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.65E-05	0.87	3.13	-	943.5
AHQ-6-2, 3359 - 3418	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	4.65E-05	0.76	2.94	-	666.8
AHQ-6-4, 3355	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	5.32E-05	0.86	3.35	-	817.5
AHQ-6-6, 3282	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.08E-07	0.68	3.15	-	503.9
AHQ-6-8, 3152	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.66E-06	0.90	3.42	-	892.5
AHQ-6-7, 3151 - 3190	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.61E-04	0.58	2.69	-	467.3
AHQ-6-5, 3299	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.22E-06	0.91	4.13	-	750.7
AHQ-6-1, 3714	K.GKLDVQFSGLTK.G	1293.49392	2	9.77E-05	0.92	3.52	-	1172.0
AHQ-6-3, 4696 - 4764	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.57E-04	0.95	4.84	-	1018.5
AHQ-6-2, 4938	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.31E-04	0.91	3.48	-	1008.5
AHQ-6-2, 4799 - 4876	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	6.02E-12	0.98	6.48	-	1545.5
AHQ-6-1, 4836 - 4864	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	7.89E-07	0.93	4.47	-	809.0
AHQ-6-2, 4798 - 4875	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	3	4.89E-04	0.79	3.68	-	522.0
AHQ-6-5, 4707 - 4743	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.39E-06	0.85	3.46	-	702.5
AHQ-6-3, 4573 - 4636	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	4.49E-07	0.92	4.44	-	795.1
AHQ-6-2, 4667 - 4739	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	6.71E-07	0.97	6.05	-	1324.1
AHQ-6-3, 4920	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.47E-06	0.93	3.97	-	800.8
AHQ-6-4, 4749 - 4816	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.66E-07	0.97	5.27	-	1533.2
AHQ-6-1, 4686 - 4756	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	3.24E-05	0.92	4.12	-	823.7
AHQ-6-2, 2315 - 2316	K.GTVEPQLEAR.G	1100.20741	2	1.54E-05	0.87	3.48	-	585.2
AHQ-6-3, 4977 - 5056	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	7.59E-07	0.82	3.81	-	523.7
AHQ-6-3, 4980	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	2.63E-04	0.73	3.81	-	712.3
AHQ-6-2, 5008	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	3.87E-04	0.91	4.46	-	1076.0
AHQ-6-4, 5017	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.56E-06	0.96	4.91	-	1365.8
AHQ-6-2, 5007 - 5020	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.65E-06	0.96	5.12	-	1100.0
AHQ-6-6, 4050 - 4128	R.IANLQTDLSDGLR.L	1416.56231	2	4.22E-05	0.91	3.38	-	1072.6
AHQ-6-5, 3712	R.IANLQTDLSDGLR.L	1416.56231	2	2.21E-05	0.87	2.87	-	1032.5
AHQ-6-12, 4036	R.IANLQTDLSDGLR.L	1416.56231	2	1.42E-07	0.93	3.94	-	975.1
AHQ-6-2, 3806	R.IANLQTDLSDGLR.L	1416.56231	2	4.26E-08	0.96	4.42	-	1148.7
AHQ-6-10, 3926 - 3927	R.IANLQTDLSDGLR.L	1416.56231	2	3.50E-05	0.90	3.77	-	862.9
AHQ-6-1, 3934	R.IANLQTDLSDGLR.L	1416.56231	2	3.96E-05	0.92	3.92	-	1117.8
AHQ-6-7, 3922	R.IANLQTDLSDGLR.L	1416.56231	2	2.20E-05	0.84	3.28	-	889.8
AHQ-6-4, 4151	R.IANLQTDLSDGLR.L	1416.56231	2	1.25E-06	0.89	3.33	-	897.3
AHQ-6-5, 4075 - 4077	R.IANLQTDLSDGLR.L	1416.56231	2	8.19E-08	0.95	4.63	-	1107.6
AHQ-6-3, 3774	R.IANLQTDLSDGLR.L	1416.56231	2	2.00E-07	0.86	3.47	-	743.5
AHQ-6-1, 4292	R.IANLQTDLSDGLR.L	1416.56231	2	6.50E-05	0.95	4.34	-	1108.3
AHQ-6-4, 3784	R.IANLQTDLSDGLR.L	1416.56231	2	5.90E-08	0.94	4.46	-	1077.0
AHQ-6-11, 3981 - 3983	R.IANLQTDLSDGLR.L	1416.56231	2	4.47E-07	0.93	4.02	-	871.2
AHQ-6-14-, 4060	R.IANLQTDLSDGLR.L	1416.56231	2	2.42E-05	0.88	3.24	-	956.7
AHQ-6-13, 4236	R.IANLQTDLSDGLR.L	1416.56231	2	9.47E-06	0.88	3.49	-	772.8
AHQ-6-3, 4144	R.IANLQTDLSDGLR.L	1416.56231	2	1.30E-05	0.96	4.55	-	1138.8
AHQ-6-6, 3919	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.59E-08	0.98	5.50	-	1836.1
AHQ-6-8, 4966	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	6.09E-09	0.96	4.47	-	1447.2
AHQ-6-4, 4004 - 4067	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	5.28E-08	0.97	5.06	-	1660.0
AHQ-6-3, 4001	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	6.99E-05	0.93	3.69	-	1250.2
AHQ-6-1, 5330	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	2.34E-07	0.91	4.14	-	930.9
AHQ-6-1, 5326 - 5327	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.63E-10	0.98	6.64	-	1770.0
AHQ-6-5, 5187	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.66E-08	0.96	4.61	-	1310.1
AHQ-6-5, 5201	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	6.71E-06	0.87	3.95	-	929.7
AHQ-6-2, 4067	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	5.35E-05	0.91	4.27	-	680.9
AHQ-6-7, 3803	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.63E-07	0.95	4.59	-	1034.4
AHQ-6-4, 5283	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.26E-09	0.97	4.76	-	1507.6
AHQ-6-4, 5287 - 5289	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	2.42E-07	0.89	4.49	-	726.4
AHQ-6-2, 5264	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.53E-07	0.96	4.60	-	1489.0
AHQ-6-5, 3939 - 4001	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.71E-06	0.98	5.69	-	1583.2
AHQ-6-6, 5159	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.83E-12	0.96	5.45	-	1044.0
AHQ-6-1, 4146	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.37E-05	0.98	5.23	-	2043.5
AHQ-6-5, 3972	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	3	6.41E-04	0.84	3.84	-	710.5
AHQ-6-3, 2608	K.IVGPSGAAVPCK.V	1157.36530	2	1.76E-06	0.84	3.25	-	716.3
AHQ-6-2, 2599 - 2604	K.IVGPSGAAVPCK.V	1157.36530	2	4.11E-09	0.94	4.11	-	844.9
AHQ-6-6, 3984	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.01E-05	0.91	4.57	-	971.0
AHQ-6-3, 4065 - 4126	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	9.37E-10	0.94	5.32	-	853.2
AHQ-6-1, 4218	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	3.32E-05	0.89	4.37	-	325.3

AHQ-6-4, 4087	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.31E-05	0.81	3.71	-	402.3
AHQ-6-1, 4303	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.83E-07	0.91	4.21	-	1160.4
AHQ-6-2, 4090	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.42E-08	0.93	4.89	-	1217.0
AHQ-6-2, 4192	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.78E-10	0.92	4.53	-	1146.9
AHQ-6-5, 4011	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.54E-06	0.91	4.62	-	951.7
AHQ-6-3, 4069	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	5.89E-06	0.86	3.72	-	445.5
AHQ-6-4, 4081	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.98E-05	0.88	3.95	-	1123.6
AHQ-6-1, 4210	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	8.85E-04	0.88	4.14	-	785.0
AHQ-6-1, 4438	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	1.81E-06	0.83	4.41	-	712.2
AHQ-6-5, 4235	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	5.13E-08	0.89	4.61	-	832.3
AHQ-6-4, 4256 - 4319	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	9.08E-05	0.82	3.70	-	606.1
AHQ-6-5, 4115 - 4187	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.52E-09	0.98	6.05	-	2227.5
AHQ-6-5, 4188	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	9.68E-05	0.77	3.36	-	448.3
AHQ-6-4, 4237 - 4299	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	7.18E-12	0.97	6.02	-	1967.4
AHQ-6-1, 4435	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.29E-11	0.98	6.03	-	2376.9
AHQ-6-6, 4171	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.22E-05	0.62	2.89	-	357.3
AHQ-6-4, 4284	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	9.45E-06	0.91	4.10	-	648.4
AHQ-6-3, 4225 - 4294	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.12E-06	0.97	5.82	-	1761.0
AHQ-6-5, 4199	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.91E-09	0.95	4.59	-	1603.3
AHQ-6-4, 3419	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	8.78E-06	0.92	3.91	-	1457.2
AHQ-6-1, 3751	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	3.20E-05	0.89	3.85	-	892.8
AHQ-6-4, 3531	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	9.72E-04	0.89	4.31	-	908.3
AHQ-6-3, 3562	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.86E-05	0.88	3.39	-	1334.6
AHQ-6-2, 3460 - 3526	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.43E-05	0.96	5.09	-	1410.7
AHQ-6-3, 3456	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	5.02E-09	0.95	4.87	-	1204.9
AHQ-6-3, 3881	K.LDVQFSGLTK.G	1108.26945	2	1.38E-06	0.93	3.06	-	1648.2
AHQ-6-4, 3888	K.LDVQFSGLTK.G	1108.26945	2	7.95E-07	0.89	3.40	-	752.1
AHQ-6-2, 3914	K.LDVQFSGLTK.G	1108.26945	2	1.99E-06	0.92	3.44	-	1239.1
AHQ-6-1, 4044	K.LDVQFSGLTK.G	1108.26945	2	7.78E-07	0.92	3.28	-	1105.8
AHQ-6-2, 6318	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	2.78E-06	0.93	4.94	-	855.7
AHQ-6-3, 4720	K.LPQLPITNFSR.D	1286.50461	2	1.66E-04	0.86	3.18	-	680.9
AHQ-6-5, 4641 - 4708	K.LPQLPITNFSR.D	1286.50461	2	6.58E-04	0.84	3.07	-	693.5
AHQ-6-4, 4747	K.LPQLPITNFSR.D	1286.50461	2	4.48E-06	0.90	3.08	-	815.0
AHQ-6-1, 4990 - 4992	K.LPQLPITNFSR.D	1286.50461	2	4.89E-06	0.84	3.13	-	727.3
AHQ-6-2, 4890	K.LPQLPITNFSR.D	1286.50461	2	1.12E-05	0.84	2.78	-	793.7
AHQ-6-2, 4730 - 4786	K.LPQLPITNFSR.D	1286.50461	2	6.80E-04	0.83	2.87	-	640.8
AHQ-6-6, 5090	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.62E-07	0.94	4.80	-	787.6
AHQ-6-5, 5135	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.10E-08	0.96	5.85	-	761.8
AHQ-6-4, 5212 - 5216	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.40E-06	0.96	6.05	-	814.1
AHQ-6-2, 5144 - 5203	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	9.47E-05	0.79	3.51	-	382.8
AHQ-6-4, 5179 - 5235	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	4.73E-04	0.91	4.49	-	834.8
AHQ-6-1, 5258 - 5331	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.75E-13	0.97	6.52	-	1654.3
AHQ-6-5, 5119	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.13E-08	0.94	4.64	-	873.0
AHQ-6-2, 5143 - 5202	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	2.78E-15	0.99	7.62	-	2817.5
AHQ-6-5, 5071 - 5127	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	9.87E-05	0.85	4.18	-	851.9
AHQ-6-5, 3156	R.LRNGHVGISFVPK.E	1424.67564	3	2.97E-04	0.87	3.35	-	1348.4
AHQ-6-1, 3480	R.LRNGHVGISFVPK.E	1424.67564	3	1.35E-05	0.91	3.69	-	1473.0
AHQ-6-5, 2973 - 3053	R.LRNGHVGISFVPK.E	1424.67564	2	3.08E-04	0.78	2.81	-	621.7
AHQ-6-2, 4039	R.LSPFMADIR.D	1050.25664	2	2.58E-05	0.76	2.85	-	401.6
AHQ-6-5, 3941	R.LSPFMADIR.D	1050.25664	2	1.63E-05	0.70	2.59	-	446.0
AHQ-6-5, 3389	R.LTVSSLQESGLK.V	1262.43499	2	1.69E-07	0.92	3.34	-	1116.2
AHQ-6-1, 3639	R.LTVSSLQESGLK.V	1262.43499	2	1.38E-05	0.87	2.94	-	949.2
AHQ-6-8, 3212 - 3217	R.LTVSSLQESGLK.V	1262.43499	2	1.86E-07	0.87	3.12	-	932.4
AHQ-6-13-, 4092	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	3.07E-05	0.97	5.73	-	1914.5
AHQ-6-1, 4544	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.99E-07	0.95	4.69	-	1137.3
AHQ-6-5, 4032 - 4092	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.02E-04	0.92	4.30	-	1025.4
AHQ-6-13, 4249	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.40E-05	0.93	4.12	-	1182.1
AHQ-6-6, 4020	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.91E-06	0.94	4.70	-	852.5
AHQ-6-4, 4107 - 4108	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.65E-04	0.97	5.70	-	1321.9
AHQ-6-1, 4296	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.25E-05	0.95	5.11	-	1240.6
AHQ-6-4, 4103	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	7.88E-11	0.96	5.59	-	1264.8
AHQ-6-5, 4288	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.97E-08	0.96	5.22	-	1427.5
AHQ-6-6, 4019 - 4091	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.64E-05	0.86	3.30	-	1018.5
AHQ-6-4, 4373	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.25E-06	0.94	4.39	-	1079.3
AHQ-6-4, 4361 - 4424	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.84E-11	0.95	4.78	-	973.4
AHQ-6-5, 3775	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	4.54E-04	0.89	3.70	-	1022.0
AHQ-6-5, 4295	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.38E-08	0.95	4.60	-	1096.0
AHQ-6-5, 4033	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.33E-07	0.95	4.55	-	1196.0
AHQ-6-4, 2487	K.MDCQECPEGYR.V	1447.55375	2	1.47E-04	0.68	2.79	-	612.6
AHQ-6-5, 2216 - 2277	K.M*DCQECPEGYR.V	1463.55315	2	2.15E-06	0.75	2.69	-	1094.9
AHQ-6-1, 4710	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	8.07E-07	0.88	3.69	-	1255.6
AHQ-6-5, 4508	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	7.05E-09	0.95	4.81	-	991.2
AHQ-6-4, 4609	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	1.23E-09	0.97	4.97	-	1714.8
AHQ-6-1, 4826	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	1.75E-04	0.88	3.80	-	1176.3
AHQ-6-3, 4593	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	3.13E-10	0.86	4.11	-	1252.6
AHQ-6-2, 2163 - 2180	K.RAEFTVETR.S	1109.21754	2	1.79E-04	0.95	3.83	-	1012.0
AHQ-6-3, 2176	K.RAEFTVETR.S	1109.21754	2	1.01E-05	0.92	3.15	-	907.2
AHQ-6-6, 2096 - 2106	K.RAEFTVETR.S	1109.21754	2	1.59E-06	0.79	2.81	-	531.7
AHQ-6-4, 2124	K.RAEFTVETR.S	1109.21754	2	1.34E-06	0.92	3.34	-	1029.2
AHQ-6-5, 2080	K.RAEFTVETR.S	1109.21754	2	1.49E-05	0.90	3.04	-	847.9
AHQ-6-1, 3372	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	8.17E-06	0.97	5.27	-	1859.3
AHQ-6-3, 3166	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	1.87E-05	0.97	5.01	-	2230.3
AHQ-6-5, 3056	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	6.39E-04	0.98	5.65	-	3248.6
AHQ-6-2, 3188	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	3.45E-04	0.97	5.12	-	1984.4
AHQ-6-2, 3848	K.RIANLQTDLSDGLR.L	1572.74866	2	1.85E-07	0.82	3.60	-	533.2
AHQ-6-5, 3069	R.RLTVSSLQESGLK.V	1418.62134	2	1.44E-06	0.96	4.40	-	1590.7
AHQ-6-2, 6560 - 6620	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	5.79E-09	0.95	4.10	-	1491.1
AHQ-6-1, 6590 - 6647	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	5.02E-06	0.95	4.86	-	1551.1
AHQ-6-2, 6496 - 6563	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	1.82E-05	0.97	5.88	-	1870.8
AHQ-6-1, 6599 - 6638	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	1.27E-05	0.88	3.20	-	1099.0
AHQ-6-2, 6699	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	5.15E-04	0.94	4.49	-	1026.9
AHQ-6-2, 6622 - 6702	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	9.07E-12	0.97	6.16	-	2152.7
AHQ-6-1, 4039	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.13E-07	0.88	3.91	-	603.6
AHQ-6-6, 3771	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.06E-07	0.93	4.48	-	991.5
AHQ-6-4, 3863	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.35E-08	0.94	4.91	-	812.7
AHQ-6-4, 3864	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.93E-07	0.89	3.89	-	997.9
AHQ-6-7, 3656	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.36E-06	0.80	3.76	-	424.4
AHQ-6-7, 3662	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.60E-07	0.94	4.00	-	1415.7
AHQ-6-2, 4051	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.30E-06	0.64	3.08	-	328.3
AHQ-6-6, 3770	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.13E-06	0.91	4.47	-	588.2
AHQ-6-3, 3877 - 3884	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.39E-07	0.93	4.39	-	784.8
AHQ-6-1, 4038	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.11E-09	0.90	3.78	-	1413.2
AHQ-6-2, 4004	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.04E-05	0.85	3.43	-	1296.1
AHQ-6-5, 3804 - 3835	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.44E-09	0.94	4.56	-	1124.6
AHQ-6-3, 3876	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.52E-08	0.90	4.27	-	988.2
AHQ-6-2, 3895 - 3922	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	5.81E-09	0.95	4.30	-	1681.4
AHQ-6-5, 3803	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.99E-05	0.96	5.35	-	989.6

AHQ-6-2, 3896 - 3954	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.21E-05	0.94	4.76	-	788.9
AHQ-6-5, 3345	K.SPFEVYVDK.S	1084.20321	1	2.77E-04	0.57	1.99	-	879.5
AHQ-6-5, 3343	K.SPFEVYVDK.S	1084.20321	2	2.11E-06	0.94	3.30	-	1237.1
AHQ-6-3, 3425	K.SPFEVYVDK.S	1084.20321	1	2.68E-07	0.78	2.55	-	1058.2
AHQ-6-2, 3442	K.SPFEVYVDK.S	1084.20321	1	3.91E-05	0.81	2.89	-	807.0
AHQ-6-7, 3240	K.SPFEVYVDK.S	1084.20321	1	1.38E-04	0.80	3.18	-	657.4
AHQ-6-1, 3615	K.SPFEVYVDK.S	1084.20321	2	1.15E-05	0.85	2.93	-	902.1
AHQ-6-3, 3424	K.SPFEVYVDK.S	1084.20321	2	1.21E-05	0.95	3.39	-	1268.9
AHQ-6-2, 3434	K.SPFEVYVDK.S	1084.20321	2	4.71E-06	0.94	3.42	-	1280.5
AHQ-6-4, 3396	K.SPFEVYVDK.S	1084.20321	2	9.88E-07	0.92	3.45	-	915.5
AHQ-6-5, 4732	K.SPFSVAVSPSLDLSK.I	1534.73557	2	8.18E-05	0.78	3.24	-	680.5
AHQ-6-3, 4561 - 4620	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.44E-04	0.85	3.36	-	635.6
AHQ-6-3, 4716 - 4772	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.74E-05	0.86	3.69	-	780.4
AHQ-6-4, 4799 - 4859	K.SPFSVAVSPSLDLSK.I	1534.73557	2	8.44E-06	0.65	2.99	-	509.3
AHQ-6-7, 4546	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.43E-04	0.73	3.09	-	632.3
AHQ-6-2, 4740 - 4802	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.51E-04	0.85	3.39	-	733.0
AHQ-6-1, 3578	R.SPYTVTVGQACNPSACR.A	1871.04208	2	6.65E-06	0.90	4.03	-	430.8
AHQ-6-2, 3431	R.SPYTVTVGQACNPSACR.A	1871.04208	3	2.07E-04	0.89	3.93	-	1015.3
AHQ-6-7, 3226	R.SPYTVTVGQACNPSACR.A	1871.04208	2	5.47E-04	0.57	2.84	-	275.9
AHQ-6-2, 3388 - 3450	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.70E-05	0.90	4.16	-	513.4
AHQ-6-6, 3259 - 3322	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.51E-05	0.85	3.64	-	475.2
AHQ-6-5, 3327	R.SPYTVTVGQACNPSACR.A	1871.04208	2	7.40E-05	0.88	3.61	-	562.9
AHQ-6-4, 3388	R.SPYTVTVGQACNPSACR.A	1871.04208	2	3.63E-05	0.90	4.26	-	386.4
AHQ-6-3, 3352 - 3412	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.06E-06	0.89	3.73	-	536.7
AHQ-6-6, 4807 - 4872	R.TFSVWYVPEVTGTHK.V	1751.96228	2	1.48E-04	0.45	2.64	-	217.7
AHQ-6-6, 4820	R.TFSVWYVPEVTGTHK.V	1751.96228	3	3.40E-07	0.67	3.37	-	360.8
AHQ-6-1, 5020	R.TFSVWYVPEVTGTHK.V	1751.96228	3	1.71E-08	0.82	3.37	-	578.0
AHQ-6-2, 4918	R.TFSVWYVPEVTGTHK.V	1751.96228	3	1.25E-04	0.77	3.40	-	508.6
AHQ-6-3, 4908	R.TFSVWYVPEVTGTHK.V	1751.96228	3	6.35E-07	0.66	3.01	-	433.4
AHQ-6-6, 3040	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	1.76E-05	0.87	3.52	-	777.2
AHQ-6-3, 3138	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.03E-05	0.83	3.13	-	806.6
AHQ-6-2, 3135	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	3.38E-10	0.93	3.81	-	1310.0
AHQ-6-4, 3109	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	7.77E-07	0.85	3.36	-	768.9
AHQ-6-5, 3041	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.07E-06	0.93	4.38	-	778.2
AHQ-6-2, 2987 - 3066	R.TGVELGKPTHFTVNAK.A	1699.93205	3	7.61E-06	0.68	3.26	-	752.7
AHQ-6-5, 2905	R.TGVELGKPTHFTVNAK.A	1699.93205	2	7.81E-04	0.84	3.30	-	584.9
AHQ-6-3, 3128	R.TGVELGKPTHFTVNAK.A	1699.93205	2	2.17E-06	0.76	3.21	-	468.7
AHQ-6-5, 3176	K.THEAEIVEGENHTYCIR.F	2060.19046	2	4.51E-12	0.97	5.39	-	1670.2
AHQ-6-4, 3213	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.81E-11	0.86	3.69	-	969.6
AHQ-6-1, 3356	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.67E-08	0.95	4.76	-	1221.5
AHQ-6-5, 3043	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.16E-11	0.96	5.07	-	1418.0
AHQ-6-6, 3034	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.39E-07	0.92	4.13	-	1077.3
AHQ-6-4, 3093 - 3103	K.THEAEIVEGENHTYCIR.F	2060.19046	3	3.39E-11	0.94	4.57	-	1150.5
AHQ-6-4, 3088	K.THEAEIVEGENHTYCIR.F	2060.19046	2	5.02E-05	0.94	3.84	-	1212.6
AHQ-6-3, 3792	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	3	8.49E-04	0.78	3.26	-	744.3
AHQ-6-2, 3731	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	2	2.31E-07	0.96	4.35	-	1525.8
AHQ-6-2, 3823	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	3	1.32E-04	0.87	3.96	-	696.3
AHQ-6-11, 3095 - 3101	R.TPCEEILVK.H	1090.27249	2	1.53E-04	0.77	3.01	-	765.8
AHQ-6-12, 3133	R.TPCEEILVK.H	1090.27249	2	4.66E-04	0.88	2.68	-	888.9
AHQ-6-1, 3379	R.TPCEEILVK.H	1090.27249	2	3.59E-05	0.76	2.77	-	715.7
AHQ-6-13-, 3200 - 3201	R.TPCEEILVK.H	1090.27249	2	1.24E-05	0.71	2.67	-	692.4
AHQ-6-2, 3196	R.TPCEEILVK.H	1090.27249	2	2.54E-05	0.81	3.04	-	698.2
AHQ-6-4, 3137	R.TPCEEILVK.H	1090.27249	2	1.96E-05	0.88	2.85	-	894.2
AHQ-6-6, 3092 - 3094	R.TPCEEILVK.H	1090.27249	2	6.06E-06	0.75	2.68	-	610.8
AHQ-6-5, 3089	R.TPCEEILVK.H	1090.27249	2	4.03E-04	0.60	2.63	-	626.9
AHQ-6-3, 3368 - 3446	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.04E-11	0.96	4.79	-	1071.5
AHQ-6-6, 3287	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.36E-08	0.89	3.90	-	700.0
AHQ-6-6, 3199	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.11E-10	0.90	3.80	-	624.8
AHQ-6-2, 3218 - 3283	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.03E-12	0.95	4.50	-	1293.8
AHQ-6-5, 3307 - 3385	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.22E-13	0.93	4.10	-	753.4
AHQ-6-4, 3433	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.88E-14	0.89	4.19	-	553.2
AHQ-6-5, 3209 - 3243	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.28E-11	0.92	4.05	-	803.3
AHQ-6-3, 3152	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.40E-09	0.78	3.31	-	594.4
AHQ-6-1, 3622	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.80E-09	0.88	4.08	-	632.9
AHQ-6-4, 3257 - 3275	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.80E-09	0.87	3.58	-	645.0
AHQ-6-1, 3474 - 3540	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.02E-12	0.96	4.93	-	1098.7
AHQ-6-2, 3396 - 3474	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.70E-13	0.95	4.49	-	1051.5
AHQ-6-7, 3119	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.16E-09	0.93	4.46	-	935.7
AHQ-6-3, 3278 - 3288	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.18E-10	0.93	4.30	-	735.0
AHQ-6-2, 3346 - 3410	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.60E-10	0.97	4.95	-	1316.3
AHQ-6-4, 2653	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.12E-04	0.85	3.65	-	652.0
AHQ-6-8, 2633	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.72E-05	0.67	2.65	-	420.0
AHQ-6-6, 2822	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.11E-04	0.66	3.23	-	411.4
AHQ-6-4, 2760 - 2835	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	9.05E-06	0.89	4.04	-	629.9
AHQ-6-8, 2530	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.76E-04	0.77	3.11	-	548.2
AHQ-6-1, 3108 - 3112	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.02E-09	0.90	4.06	-	588.8
AHQ-6-5, 2717 - 2791	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.41E-04	0.82	3.95	-	424.2
AHQ-6-3, 2901	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.89E-04	0.70	3.00	-	397.4
AHQ-6-13-, 3492	K.VDINTEDLEDGTCR.V	1638.69283	2	6.09E-04	0.74	2.71	-	777.8
AHQ-6-4, 3248	K.VDINTEDLEDGTCR.V	1638.69283	2	2.41E-06	0.83	3.13	-	758.2
AHQ-6-4, 3331 - 3336	K.VDINTEDLEDGTCR.V	1638.69283	2	7.90E-06	0.93	3.70	-	1188.0
AHQ-6-2, 3551	K.VDINTEDLEDGTCR.V	1638.69283	2	3.89E-05	0.90	2.96	-	1195.5
AHQ-6-1, 3676	K.VDINTEDLEDGTCR.V	1638.69283	2	4.19E-06	0.95	4.42	-	1236.4
AHQ-6-8, 3105	K.VDINTEDLEDGTCR.V	1638.69283	2	1.93E-05	0.77	3.26	-	624.5
AHQ-6-4, 3511	K.VDINTEDLEDGTCR.V	1638.69283	2	1.45E-07	0.95	4.45	-	1379.8
AHQ-6-3, 3269	K.VDINTEDLEDGTCR.V	1638.69283	2	2.13E-04	0.61	2.78	-	506.6
AHQ-6-1, 3439 - 3486	K.VDINTEDLEDGTCR.V	1638.69283	2	1.72E-05	0.92	3.41	-	1305.9
AHQ-6-8, 3292	K.VDINTEDLEDGTCR.V	1638.69283	2	1.29E-04	0.93	3.74	-	1162.5
AHQ-6-13, 3648	K.VDINTEDLEDGTCR.V	1638.69283	2	1.60E-05	0.79	2.83	-	699.2
AHQ-6-6, 2602	K.VDVGKDQEFTVK.S	1365.51377	2	2.45E-06	0.85	3.17	-	590.6
AHQ-6-4, 2623 - 2624	K.VDVGKDQEFTVK.S	1365.51377	2	8.24E-07	0.84	3.11	-	731.0
AHQ-6-1, 2887	K.VDVGKDQEFTVK.S	1365.51377	2	5.93E-07	0.88	3.48	-	737.2
AHQ-6-3, 2652 - 2674	K.VDVGKDQEFTVK.S	1365.51377	2	5.05E-06	0.87	3.52	-	694.5
AHQ-6-2, 2650	K.VDVGKDQEFTVK.S	1365.51377	2	6.50E-06	0.90	3.92	-	738.2
AHQ-6-3, 2784 - 2845	K.VEPGLGADNSVVR.F	1313.44209	2	1.37E-04	0.68	2.55	-	202.9
AHQ-6-5, 2720 - 2728	K.VEPGLGADNSVVR.F	1313.44209	2	2.05E-05	0.60	2.56	-	272.1
AHQ-6-2, 2768 - 2839	K.VEPGLGADNSVVR.F	1313.44209	2	1.37E-06	0.59	2.87	-	207.8
AHQ-6-2, 5842 - 5910	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.72E-05	0.95	5.89	-	739.8
AHQ-6-5, 5764 - 5823	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	1.35E-05	0.94	5.41	-	947.2
AHQ-6-1, 5831 - 5886	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	5.31E-06	0.92	5.36	-	682.7
AHQ-6-3, 5765 - 5820	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	7.85E-07	0.90	4.88	-	612.2
AHQ-6-2, 6510	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	7.94E-04	0.88	4.59	-	690.1
AHQ-6-8, 6394	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	2.94E-05	0.90	4.47	-	600.8
AHQ-6-4, 6571	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.76E-04	0.80	3.27	-	679.1
AHQ-6-6, 6406 - 6408	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	5.96E-04	0.84	4.65	-	503.4
AHQ-6-8, 6393	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	9.90E-04	0.93	4.67	-	1073.1
AHQ-6-5, 6477 - 6479	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.24E-07	0.93	4.84	-	584.6

AHQ-6-5, 4211 - 4231	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	5.23E-09	0.98	6.12	-	2083.3
AHQ-6-6, 4184	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	2.46E-08	0.95	4.93	-	1111.1
AHQ-6-6, 4107 - 4182	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	1.11E-06	0.94	4.71	-	1492.1
AHQ-6-1, 4464	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.13E-06	0.77	3.42	-	597.1
AHQ-6-5, 4216	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	6.93E-08	0.95	5.33	-	860.6
AHQ-6-4, 4292	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	3.77E-09	0.95	4.58	-	1747.9
AHQ-6-4, 4297 - 4315	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.10E-06	0.97	5.45	-	1662.2
AHQ-6-7, 4058	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	6.73E-05	0.94	4.49	-	1010.1
AHQ-6-7, 4359 - 4360	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	2.71E-04	0.79	3.53	-	548.8
AHQ-6-1, 4758	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.39E-10	0.92	5.03	-	578.1
AHQ-6-3, 4626	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.25E-09	0.88	4.37	-	563.2
AHQ-6-7, 4362	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.29E-05	0.88	4.32	-	474.3
AHQ-6-5, 4545	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.31E-12	0.93	4.96	-	726.1
AHQ-6-2, 4670	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.61E-11	0.89	4.34	-	551.3
AHQ-6-8, 4344	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.33E-05	0.92	4.64	-	687.7
AHQ-6-6, 4516	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.45E-07	0.87	4.35	-	522.9
AHQ-6-5, 4576	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.28E-11	0.94	4.33	-	1333.7
AHQ-6-4, 4621 - 4647	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.90E-13	0.95	5.66	-	809.4
AHQ-6-5, 3739 - 3805	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.36E-07	0.88	3.83	-	464.7
AHQ-6-7, 3487	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.09E-09	0.87	3.67	-	562.4
AHQ-6-6, 3580 - 3642	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.70E-05	0.93	4.20	-	778.6
AHQ-6-6, 3695 - 3763	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.08E-06	0.87	3.77	-	445.7
AHQ-6-1, 3851 - 3904	K.VNQPASFAVSLNGAK.G	1503.68480	2	6.06E-09	0.96	4.44	-	940.4
AHQ-6-4, 3672 - 3736	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.83E-09	0.87	3.86	-	533.4
AHQ-6-4, 3811 - 3871	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.74E-08	0.79	3.37	-	411.7
AHQ-6-2, 3728	K.VNQPASFAVSLNGAK.G	1503.68480	2	6.37E-06	0.83	3.45	-	671.7
AHQ-6-3, 3694 - 3758	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.67E-10	0.90	4.06	-	565.2
AHQ-6-5, 3608 - 3671	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.63E-08	0.91	4.07	-	682.5
AHQ-6-1, 4026	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.88E-07	0.85	3.07	-	682.7
AHQ-6-5, 1728	K.VPVHDVTDASK.V	1168.28175	2	8.00E-05	0.65	2.72	-	451.8
AHQ-6-2, 1699 - 1754	K.VPVHDVTDASK.V	1168.28175	2	2.69E-07	0.91	3.30	-	897.0
AHQ-6-2, 1840	K.VPVHDVTDASK.V	1168.28175	2	7.55E-07	0.87	3.11	-	850.3
AHQ-6-3, 4162	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.78E-06	0.82	3.41	-	580.7
AHQ-6-1, 4191 - 4264	R.VQVQDNEGCPVEALVK.D	1786.98493	2	2.03E-07	0.95	4.66	-	1089.0
AHQ-6-4, 4033	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.19E-05	0.96	4.05	-	1650.0
AHQ-6-3, 4030 - 4101	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.36E-06	0.96	5.05	-	1257.0
AHQ-6-3, 3968 - 4032	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.48E-05	0.90	3.93	-	945.4
AHQ-6-1, 4134 - 4202	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.08E-05	0.97	4.99	-	1571.4
AHQ-6-2, 4055 - 4123	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.36E-05	0.97	5.11	-	1751.6
AHQ-6-3, 5028	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.04E-07	0.88	3.99	-	960.0
AHQ-6-1, 4998 - 5054	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	2.44E-11	0.87	4.17	-	1006.3
AHQ-6-2, 5043 - 5104	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.15E-08	0.84	3.87	-	1253.8
AHQ-6-2, 4926 - 4982	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	9.43E-10	0.85	3.71	-	1136.0
AHQ-6-2, 4831	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	7.00E-08	0.94	4.63	-	1452.0
AHQ-6-3, 4808 - 4826	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	5.04E-08	0.89	4.00	-	1307.4
AHQ-6-5, 4591 - 4651	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	9.21E-07	0.95	5.31	-	1338.6
AHQ-6-5, 4444	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.28E-04	0.83	3.52	-	839.4
AHQ-6-4, 4699 - 4759	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	6.97E-08	0.96	5.27	-	1435.3
AHQ-6-8, 4404 - 4406	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	5.42E-04	0.95	5.08	-	912.9
AHQ-6-6, 4582 - 4587	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	3.59E-06	0.96	5.09	-	956.9
AHQ-6-2, 4756	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.37E-05	0.97	5.80	-	1582.5
AHQ-6-1, 4850	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.94E-07	0.94	4.83	-	1079.5
AHQ-6-6, 4500 - 4571	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.76E-08	0.95	5.23	-	1328.8
AHQ-6-7, 4414	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	6.14E-07	0.96	4.65	-	1560.1
AHQ-6-3, 4718	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	7.67E-08	0.96	5.81	-	1392.3
AHQ-6-8, 4405	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.60E-07	0.95	5.12	-	1154.5
AHQ-6-3, 2750 - 2826	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.51E-05	0.92	4.61	-	579.1
AHQ-6-1, 3083	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	6.83E-06	0.87	3.86	-	483.2
AHQ-6-2, 2880 - 2882	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	9.54E-09	0.92	4.63	-	654.5
AHQ-6-7, 2614 - 2674	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	8.57E-04	0.69	3.00	-	568.8
AHQ-6-2, 2742 - 2820	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	6.62E-05	0.93	4.96	-	563.8
AHQ-6-4, 2848	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.44E-06	0.58	2.74	-	402.8
AHQ-6-1, 2982	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	5.68E-06	0.83	3.63	-	631.3
AHQ-6-6, 2698	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	6.22E-05	0.83	3.82	-	559.5
AHQ-6-5, 2672 - 2707	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.92E-06	0.85	3.39	-	741.1
AHQ-6-4, 3279	K.VTVLFAGQHIAK.S	1284.53185	2	4.32E-07	0.92	3.58	-	1003.4
AHQ-6-5, 3217	K.VTVLFAGQHIAK.S	1284.53185	2	4.35E-10	0.94	3.94	-	1083.3
AHQ-6-7, 3099	K.VTVLFAGQHIAK.S	1284.53185	2	5.01E-06	0.76	3.13	-	507.0
AHQ-6-2, 3318	K.VTVLFAGQHIAK.S	1284.53185	2	3.80E-06	0.92	3.91	-	938.7
AHQ-6-4, 3289	K.VTVLFAGQHIAK.S	1284.53185	1	6.13E-04	0.57	2.49	-	542.1
AHQ-6-3, 3316	K.VTVLFAGQHIAK.S	1284.53185	2	3.28E-06	0.92	3.91	-	828.0
AHQ-6-2, 3327	K.VTVLFAGQHIAK.S	1284.53185	3	1.06E-04	0.72	3.27	-	537.8
AHQ-6-8, 2968	K.VTVLFAGQHIAK.S	1284.53185	2	7.90E-06	0.86	3.33	-	851.8
AHQ-6-6, 4646	R.VTYCPTEPGNYIINIK.F	1884.14221	2	5.38E-06	0.67	2.79	-	302.5
AHQ-6-1, 4963	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.50E-05	0.84	3.43	-	446.6
AHQ-6-4, 4844 - 4903	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.52E-05	0.90	4.07	-	491.7
AHQ-6-4, 4912	R.VTYCPTEPGNYIINIK.F	1884.14221	3	9.11E-05	0.90	4.42	-	783.2
AHQ-6-3, 4722	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.89E-06	0.80	3.35	-	404.4
AHQ-6-3, 4857	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.44E-04	0.80	3.26	-	448.1
AHQ-6-5, 4675	R.VTYCPTEPGNYIINIK.F	1884.14221	2	4.69E-06	0.84	3.76	-	381.0
AHQ-6-5, 4768 - 4835	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.77E-05	0.89	3.98	-	501.4
AHQ-6-5, 4820	R.VTYCPTEPGNYIINIK.F	1884.14221	3	6.24E-05	0.92	4.54	-	901.2
AHQ-6-1, 4822	R.VTYCPTEPGNYIINIK.F	1884.14221	2	7.90E-13	0.89	3.49	-	687.0
AHQ-6-14-, 4762 - 4763	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	9.41E-04	0.90	3.51	-	852.9
AHQ-6-7, 4610	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	1.89E-06	0.76	3.20	-	365.2
AHQ-6-13, 5272 - 5281	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.08E-05	0.88	3.32	-	795.0
AHQ-6-8, 3184 - 3185	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.42E-04	0.91	3.76	-	1002.1
AHQ-6-4, 2695	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	1.96E-06	0.73	2.85	-	631.5
AHQ-6-4, 3387	R.YAPSEAGLHEMDIR.Y	1589.75482	2	7.16E-06	0.87	3.09	-	976.1
AHQ-6-7, 3947	K.YGGDEIPFSPYR.V	1401.50466	2	6.26E-06	0.49	2.73	-	342.6
AHQ-6-2, 4199 - 4208	K.YGGDEIPFSPYR.V	1401.50466	1	1.17E-04	0.36	2.52	-	421.3
AHQ-6-4, 4168	K.YGGDEIPFSPYR.V	1401.50466	2	1.88E-06	0.71	2.67	-	514.9
AHQ-6-3, 4160 - 4169	K.YGGDEIPFSPYR.V	1401.50466	2	3.61E-07	0.85	3.43	-	686.3
AHQ-6-8, 3188 - 3192	K.YGGPYHIGGSPFK.A	1380.53182	2	1.02E-08	0.97	4.67	-	1923.3
AHQ-6-4, 3395	K.YGGPYHIGGSPFK.A	1380.53182	2	1.77E-08	0.98	4.91	-	2151.2
AHQ-6-6, 3335	K.YGGPYHIGGSPFK.A	1380.53182	2	1.44E-09	0.98	4.80	-	2036.1
AHQ-6-4, 3407	K.YGGPYHIGGSPFK.A	1380.53182	3	7.29E-07	0.89	3.99	-	622.6
AHQ-6-7, 3223	K.YGGPYHIGGSPFK.A	1380.53182	2	4.30E-04	0.96	4.16	-	1672.9
AHQ-6-5, 3351	K.YGGPYHIGGSPFK.A	1380.53182	3	1.41E-04	0.92	4.60	-	674.9
AHQ-6-13-, 3472	K.YGGPYHIGGSPFK.A	1380.53182	2	1.09E-08	0.96	3.95	-	1843.7
AHQ-6-1, 3640	K.YGGPYHIGGSPFK.A	1380.53182	2	2.23E-06	0.98	4.44	-	2385.0
AHQ-6-3, 3440	K.YGGPYHIGGSPFK.A	1380.53182	2	9.86E-09	0.92	3.64	-	1075.8
AHQ-6-5, 3341	K.YGGPYHIGGSPFK.A	1380.53182	2	1.63E-09	0.98	4.35	-	2394.5
AHQ-6-3, 3104	K.YGGQPVPNFPSK.L	1291.43658	1	1.10E-04	0.39	2.64	-	266.9
AHQ-6-3, 3092	K.YGGQPVPNFPSK.L	1291.43658	2	3.36E-05	0.84	3.23	-	428.9
AHQ-6-2, 3090	K.YGGQPVPNFPSK.L	1291.43658	2	8.76E-06	0.92	3.42	-	638.7
AHQ-6-5, 3000	K.YGGQPVPNFPSK.L	1291.43658	2	1.45E-04	0.88	3.14	-	557.3

AHQ-6-1, 3291	K.YGGQPVPNFPSK.L	1291.43658	2	3.94E-04	0.90	2.98	-	713.1
AHQ-6-4, 2992 - 3055	K.YGGQPVPNFPSK.L	1291.43658	2	3.38E-04	0.74	2.90	-	337.0
AHQ-6-5, 4196	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	6.94E-06	0.81	3.61	-	675.8
AHQ-6-7, 4035 - 4078	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.50E-06	0.89	4.01	-	833.0
AHQ-6-3, 2949	K.YNEQHVPGSPFTAR.V	1603.71978	2	5.90E-04	0.92	3.83	-	711.6
AHQ-6-4, 2892	K.YNEQHVPGSPFTAR.V	1603.71978	2	3.96E-07	0.88	3.89	-	566.0
AHQ-6-2, 2952 - 2959	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.02E-08	0.82	3.20	-	461.4
AHQ-6-5, 2816 - 2881	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.35E-06	0.90	3.54	-	577.0
AHQ-6-8, 2602 - 2660	K.YNEQHVPGSPFTAR.V	1603.71978	2	3.49E-05	0.78	3.18	-	483.2
AHQ-6-1, 4463 - 4518	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	8.51E-05	0.94	4.26	-	869.2
AHQ-6-1, 4606	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	9.09E-07	0.87	3.59	-	570.6
AHQ-6-7, 4158	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.13E-06	0.85	3.44	-	560.8
AHQ-6-3, 4334 - 4401	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.29E-07	0.95	5.23	-	670.8
AHQ-6-6, 4290	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.20E-04	0.84	3.60	-	551.7
AHQ-6-8, 4161	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.71E-06	0.90	3.83	-	703.3
AHQ-6-5, 4332	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.32E-04	0.89	4.19	-	615.9
AHQ-6-2, 4254	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.27E-06	0.92	3.91	-	790.9
AHQ-6-4, 4420	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.63E-05	0.94	4.71	-	719.9
AHQ-6-4, 4528	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.31E-06	0.88	3.69	-	617.5
AHQ-6-2, 4354 - 4414	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.97E-07	0.91	4.22	-	698.6
AHQ-6-2, 4518 - 4574	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.05E-09	0.92	4.46	-	638.9
AHQ-6-3, 4498	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.35E-09	0.93	4.42	-	723.3
AHQ-6-2, 6208 - 6219	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	9.11E-06	0.88	3.65	-	622.6
AHQ-6-3, 6197 - 6208	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	2.37E-07	0.78	2.92	-	666.8
AHQ-6-2, 6183 - 6238	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	4.55E-06	0.71	3.07	-	476.9
AHQ-6-2, 5876 - 5936	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.56E-07	0.85	2.99	-	902.8
gi|4504165|ref|NP_000168.1| gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]				3.89E-15	22.16	250.37	43.50	85696.9
AHQ-6-7, 3555 - 3632	K.AGALNSNDAFVLK.T	1320.47622	2	7.84E-04	0.80	3.35	-	770.5
AHQ-6-5, 3207	K.AGKEPGLQIWR.V	1255.45060	3	2.48E-07	0.88	3.99	-	1105.2
AHQ-6-5, 3201	K.AGKEPGLQIWR.V	1255.45060	2	2.35E-04	0.61	2.55	-	471.8
AHQ-6-10, 5171	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.74E-04	0.82	3.83	-	381.9
AHQ-6-5, 5449 - 5513	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.92E-07	0.97	5.86	-	933.7
AHQ-6-6, 5406	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.05E-05	0.94	4.87	-	639.0
AHQ-6-5, 5287 - 5289	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.48E-04	0.95	5.19	-	747.1
AHQ-6-5, 6483	R.ATEVPVSWESFNNGDCFILDLGNNIHQWCGSNSNR.Y	4042.29257	3	3.89E-15	0.90	4.21	-	916.3
AHQ-6-6, 5338	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.67E-09	0.93	4.29	-	1288.1
AHQ-6-5, 5323 - 5385	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.15E-11	0.95	4.63	-	1527.3
AHQ-6-5, 2227 - 2299	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.64E-06	0.93	3.84	-	1374.3
AHQ-6-13-, 2329	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.87E-06	0.88	3.23	-	1132.8
AHQ-6-6, 2255	K.DSQEEEKTEALTSAK.R	1666.72289	3	8.90E-05	0.94	4.07	-	1595.5
AHQ-6-5, 2181 - 2239	K.DSQEEEKTEALTSAK.R	1666.72289	3	9.33E-07	0.95	4.01	-	1929.7
AHQ-6-13, 2508	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.29E-06	0.83	3.00	-	1083.9
AHQ-6-6, 2246	K.DSQEEEKTEALTSAK.R	1666.72289	2	5.97E-07	0.95	4.07	-	1374.2
AHQ-6-7, 2194	K.DSQEEEKTEALTSAK.R	1666.72289	2	6.10E-08	0.93	4.02	-	1284.2
AHQ-6-6, 5826	R.EVQGFESATFLGYFK.S	1723.90570	2	2.89E-08	0.87	3.49	-	896.8
AHQ-6-5, 5832 - 5887	R.EVQGFESATFLGYFK.S	1723.90570	2	5.65E-10	0.97	4.99	-	1791.2
AHQ-6-13-, 5788 - 5790	R.EVQGFESATFLGYFK.S	1723.90570	2	4.53E-11	0.96	5.46	-	972.2
AHQ-6-5, 6217 - 6281	R.EVQGFESATFLGYFK.S	1723.90570	2	7.08E-06	0.88	3.59	-	845.7
AHQ-6-5, 6617 - 6679	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	2	1.91E-07	0.77	3.37	-	283.3
AHQ-6-6, 6460	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	2	3.12E-04	0.81	3.16	-	454.1
AHQ-6-6, 6458	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	3	1.14E-08	0.91	4.32	-	957.5
AHQ-6-5, 6535	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	3	7.99E-14	0.96	5.88	-	1209.4
AHQ-6-11, 2391	K.HVVPNEVVVQR.L	1276.46981	2	2.14E-04	0.85	2.89	-	529.3
AHQ-6-5, 5865 - 5923	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	1.17E-07	0.96	5.68	-	1393.2
AHQ-6-5, 5835	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	6.83E-08	0.86	4.12	-	895.2
AHQ-6-5, 5107	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.38E-09	0.97	5.94	-	1502.5
AHQ-6-5, 5367 - 5387	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	5.00E-15	0.98	7.45	-	1816.5
AHQ-6-6, 5335	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	7.09E-08	0.97	6.36	-	1565.6
AHQ-6-5, 2117 - 2121	K.PALPAGTEDTAK.E	1171.28241	2	5.78E-07	0.88	3.07	-	534.7
AHQ-6-5, 2497	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	1.63E-07	0.90	3.97	-	555.7
AHQ-6-7, 4443 - 4448	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	2.03E-04	0.30	2.68	-	261.5
AHQ-6-6, 3062	K.SEDCFILDHGK.D	1322.42590	2	2.56E-04	0.95	3.80	-	1355.2
AHQ-6-5, 3045	K.SEDCFILDHGK.D	1322.42590	2	3.29E-05	0.93	3.22	-	1547.9
AHQ-6-5, 2245	K.TGAQELLR.V	888.00387	2	9.79E-05	0.86	2.92	-	1001.1
AHQ-6-5, 4200	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	9.57E-05	0.92	3.81	-	1230.9
AHQ-6-5, 4307 - 4367	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	2.97E-06	0.97	4.69	-	1677.2
AHQ-6-5, 4427	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	7.77E-05	0.73	2.98	-	740.9
AHQ-6-10, 4130 - 4138	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	2.72E-04	0.72	2.91	-	747.5
AHQ-6-5, 4788 - 4799	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	8.90E-09	0.97	5.58	-	1179.7
AHQ-6-5, 3649 - 3721	R.VHVSEEGTEPEAM*LQVLGPK.P	2167.42570	2	7.59E-05	0.91	4.48	-	542.3
AHQ-6-5, 4197	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	1.84E-06	0.93	5.09	-	964.7
AHQ-6-6, 4172	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	1.18E-04	0.86	4.49	-	474.2
AHQ-6-5, 4980 - 5043	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	1.82E-04	0.86	4.12	-	765.1
AHQ-6-5, 3912	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	2.61E-08	0.97	6.06	-	1653.8
AHQ-6-5, 3520 - 3580	R.VPFDAATLHTSTAM*AAQHGMDDDGTGQK.Q	2891.10081	3	4.03E-05	0.87	5.26	-	1087.8
AHQ-6-5, 6060 - 6079	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	2	1.24E-04	0.84	3.70	-	638.8
AHQ-6-5, 5985 - 6055	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	3	1.19E-04	0.88	3.25	-	1272.0
AHQ-6-5, 5149 - 5224	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	2.56E-04	0.67	2.97	-	477.3
AHQ-6-5, 5183 - 5207	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	3	6.25E-05	0.86	4.53	-	1119.6
AHQ-6-6, 5140	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	4.16E-09	0.88	3.76	-	823.7
AHQ-6-6, 5142	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	3	2.20E-05	0.77	3.39	-	1255.8
gi|4505257|ref|NP_002435.1| moesin [Homo sapiens]				5.00E-15	12.09	130.28	25.50	67819.5
AHQ-6-6, 2608 - 2615	K.ALTSELANAR.D	1046.15975	2	1.85E-04	0.89	3.25	-	818.8
AHQ-6-6, 6391	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	3	9.51E-08	0.85	4.19	-	635.3
AHQ-6-6, 5662 - 5718	R.EVWFFGLQYQDTK.G	1661.83760	2	1.22E-05	0.91	3.43	-	953.5
AHQ-6-6, 6355 - 6360	K.FYPEDVSEELIQDITQR.L	2083.24065	2	3.64E-11	0.95	4.78	-	1044.5
AHQ-6-6, 6362	K.FYPEDVSEELIQDITQR.L	2083.24065	3	2.07E-04	0.88	3.91	-	969.7
AHQ-6-6, 5258	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	1.39E-05	0.95	4.56	-	938.0
AHQ-6-6, 5546 - 5619	K.IAQDLEMYGVNYFSIK.N	1892.16455	2	2.93E-05	0.91	3.90	-	776.3
AHQ-6-6, 2070	R.IQVWHEEHR.G	1234.34835	2	1.10E-06	0.91	3.11	-	1202.1
AHQ-6-6, 4579	K.KTQEQLALEMAELTAR.I	1833.10018	2	1.78E-06	0.96	4.82	-	1614.4
AHQ-6-6, 3618	K.KTQEQLALEM*AELTAR.I	1849.09958	3	4.57E-05	0.94	4.52	-	1369.2
AHQ-6-6, 3596	K.KTQEQLALEM*AELTAR.I	1849.09958	2	3.69E-04	0.92	3.90	-	909.3
AHQ-6-6, 2048	R.RALELEQER.K	1144.26342	2	1.96E-04	0.91	3.52	-	1313.9
AHQ-6-6, 3155 - 3226	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	9.28E-10	0.97	5.51	-	1788.6
AHQ-6-6, 3023 - 3087	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	2.55E-09	0.96	5.67	-	1619.4
AHQ-6-6, 3338 - 3399	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	5.00E-15	0.96	5.41	-	1696.4
AHQ-6-6, 5104	K.TQEQLALEMAELTAR.I	1704.92727	2	3.79E-04	0.96	4.52	-	1420.9
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				6.11E-15	90.72	1060.36	44.00	226529.8
AHQ-6-3, 2146	R.ALEEAMEQK.A	1049.18068	2	2.53E-04	0.84	3.15	-	921.3
AHQ-6-3, 3722 - 3742	K.ALELDSNLYR.I	1194.31920	2	1.17E-06	0.95	3.90	-	1146.4
AHQ-6-2, 3646	K.ALELDSNLYR.I	1194.31920	2	4.45E-05	0.94	3.50	-	1497.8
AHQ-6-2, 3888	K.ALELDSNLYR.I	1194.31920	2	1.84E-07	0.93	3.46	-	1123.8
AHQ-6-2, 3747	K.ALELDSNLYR.I	1194.31920	2	1.72E-06	0.93	3.46	-	1226.7
AHQ-6-4, 3713	K.ALELDSNLYR.I	1194.31920	2	8.34E-08	0.94	3.94	-	1128.5
AHQ-6-1, 3894	K.ALELDSNLYR.I	1194.31920	2	1.43E-06	0.96	4.13	-	1471.5
AHQ-6-6, 3626	K.ALELDSNLYR.I	1194.31920	2	1.79E-06	0.90	3.46	-	1018.6

AHQ-6-5, 3596 - 3659	K.ALELDSNLYR.I	1194.31920	2	1.84E-06	0.91	3.19	-	1164.8
AHQ-6-4, 2176	R.ALEQQVEEM*K.T	1221.36320	2	3.32E-05	0.82	3.31	-	845.0
AHQ-6-6, 2862	R.ALEQQVEEMK.T	1205.36380	2	5.48E-05	0.85	3.27	-	948.1
AHQ-6-3, 2889 - 2941	R.ALEQQVEEMK.T	1205.36380	2	4.78E-05	0.79	2.91	-	915.0
AHQ-6-2, 2950	R.ALEQQVEEMK.T	1205.36380	2	2.98E-05	0.91	3.81	-	1064.5
AHQ-6-2, 2204	R.ALEQQVEEM*K.T	1221.36320	2	8.73E-05	0.81	3.31	-	826.4
AHQ-6-5, 2863 - 2864	R.ALEQQVEEMK.T	1205.36380	2	6.18E-06	0.91	4.11	-	929.2
AHQ-6-5, 5975 - 5976	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	4.10E-11	0.97	6.57	-	1721.0
AHQ-6-1, 6051	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	2.05E-12	0.96	5.70	-	1717.0
AHQ-6-6, 5836 - 5904	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	9.37E-07	0.88	4.49	-	1088.1
AHQ-6-3, 5976	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	5.32E-10	0.97	6.66	-	1755.7
AHQ-6-2, 6011 - 6066	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	2.11E-14	0.97	6.35	-	1770.4
AHQ-6-1, 5108	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.26E-04	0.94	4.54	-	1108.0
AHQ-6-1, 4959	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.10E-09	0.98	5.27	-	1750.9
AHQ-6-5, 4631 - 4701	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.86E-04	0.90	4.50	-	664.5
AHQ-6-3, 4664	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.41E-05	0.94	4.64	-	730.8
AHQ-6-7, 4634	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.11E-04	0.94	4.68	-	1093.3
AHQ-6-2, 4972 - 5035	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.16E-08	0.98	5.82	-	1721.0
AHQ-6-4, 4905 - 4972	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.12E-05	0.72	3.21	-	744.9
AHQ-6-3, 4794 - 4862	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.73E-07	0.97	5.88	-	1282.1
AHQ-6-2, 4806 - 4874	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.86E-04	0.96	4.21	-	1568.1
AHQ-6-10, 4564	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.58E-06	0.96	4.46	-	1421.5
AHQ-6-2, 4612 - 4690	K.ANLQIDQINTDLNLER.S	1871.04187	2	8.30E-08	0.95	4.80	-	958.1
AHQ-6-9, 4495	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.49E-04	0.80	3.15	-	729.2
AHQ-6-2, 4764	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.27E-05	0.91	4.12	-	767.7
AHQ-6-3, 5014	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.95E-08	0.94	4.67	-	1299.3
AHQ-6-6, 4788	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.76E-08	0.98	5.59	-	1712.7
AHQ-6-8, 4630	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.19E-06	0.90	3.88	-	706.7
AHQ-6-3, 2468	K.ASITALEAK.I	904.04321	2	3.83E-06	0.93	3.49	-	1112.4
AHQ-6-6, 2396	K.ASITALEAK.I	904.04321	2	6.73E-04	0.83	2.94	-	696.9
AHQ-6-5, 2387	K.ASITALEAK.I	904.04321	2	2.65E-06	0.91	2.68	-	1042.1
AHQ-6-4, 2423	K.ASITALEAK.I	904.04321	2	4.01E-04	0.92	3.16	-	1086.6
AHQ-6-2, 2464 - 2466	K.ASITALEAK.I	904.04321	2	8.20E-07	0.94	3.48	-	1153.5
AHQ-6-3, 2106 - 2178	R.ASREEILAQAK.E	1216.36955	2	9.81E-06	0.93	3.69	-	1383.0
AHQ-6-4, 2093 - 2136	R.ASREEILAQAK.E	1216.36955	2	4.06E-06	0.92	3.41	-	1329.6
AHQ-6-2, 2170	R.ASREEILAQAK.E	1216.36955	2	6.57E-04	0.91	3.24	-	1422.6
AHQ-6-6, 3076	R.DELADEIANSSGK.G	1349.38323	2	1.21E-05	0.96	3.99	-	1647.2
AHQ-6-2, 2783	R.DELADEIANSSGK.G	1349.38323	2	3.55E-06	0.91	3.31	-	1158.6
AHQ-6-2, 3159	R.DELADEIANSSGK.G	1349.38323	2	9.27E-08	0.95	4.04	-	1376.1
AHQ-6-1, 6307	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.62E-05	0.94	4.53	-	1290.7
AHQ-6-3, 6244 - 6245	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	2	1.26E-06	0.56	2.57	-	652.3
AHQ-6-4, 5972 - 6032	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	1.38E-06	0.87	3.93	-	842.8
AHQ-6-2, 2236 - 2252	K.DLEAHIDSANK.N	1213.27938	2	6.60E-08	0.97	4.27	-	2106.6
AHQ-6-3, 2236	K.DLEAHIDSANK.N	1213.27938	2	3.04E-06	0.97	4.04	-	2159.9
AHQ-6-4, 2191	K.DLEAHIDSANK.N	1213.27938	2	7.82E-08	0.98	4.49	-	2726.8
AHQ-6-5, 2168	K.DLEAHIDSANK.N	1213.27938	2	7.85E-08	0.96	3.89	-	1569.4
AHQ-6-3, 6536	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	2.13E-08	0.97	5.39	-	2239.0
AHQ-6-2, 6578 - 6643	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	8.84E-09	0.97	5.26	-	2050.5
AHQ-6-1, 6582	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	3.77E-09	0.97	6.11	-	1783.0
AHQ-6-6, 6479	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	3.08E-06	0.91	3.69	-	1546.1
AHQ-6-4, 6639	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	1.78E-05	0.91	4.33	-	1381.4
AHQ-6-5, 2889	K.DVLLQVDDERR.N	1358.48286	2	5.20E-04	0.74	3.07	-	657.0
AHQ-6-2, 2972	K.DVLLQVDDERR.N	1358.48286	2	3.46E-04	0.74	3.00	-	778.8
AHQ-6-11, 2237	R.ELEDATETADAM*NR.E	1582.62946	2	4.18E-04	0.69	2.55	-	713.7
AHQ-6-4, 2823	R.ELEDATETADAMNR.E	1566.63006	2	1.33E-07	0.92	3.80	-	1100.5
AHQ-6-11, 2785	R.ELEDATETADAMNR.E	1566.63006	2	2.22E-05	0.95	3.60	-	1896.0
AHQ-6-2, 2832 - 2854	R.ELEDATETADAMNR.E	1566.63006	2	5.76E-08	0.90	3.43	-	916.1
AHQ-6-12, 2831 - 2835	R.ELEDATETADAMNR.E	1566.63006	2	6.74E-06	0.85	2.97	-	821.0
AHQ-6-5, 2787	R.ELEDATETADAMNR.E	1566.63006	2	4.46E-07	0.85	3.21	-	792.9
AHQ-6-6, 5390	R.ELESQISELQEDLESER.A	2035.10956	2	2.56E-06	0.94	4.29	-	982.4
AHQ-6-1, 5467 - 5535	R.ELESQISELQEDLESER.A	2035.10956	2	1.42E-06	0.91	4.21	-	857.9
AHQ-6-4, 5183	R.ELESQISELQEDLESER.A	2035.10956	2	1.44E-04	0.80	3.51	-	621.6
AHQ-6-2, 5172	R.ELESQISELQEDLESER.A	2035.10956	2	4.67E-11	0.94	4.34	-	846.6
AHQ-6-4, 5467 - 5527	R.ELESQISELQEDLESER.A	2035.10956	2	8.03E-09	0.95	4.74	-	1235.2
AHQ-6-5, 5447	R.ELESQISELQEDLESER.A	2035.10956	2	1.74E-09	0.90	3.94	-	843.5
AHQ-6-7, 5242	R.ELESQISELQEDLESER.A	2035.10956	2	2.87E-05	0.88	3.90	-	723.3
AHQ-6-3, 5476	R.ELESQISELQEDLESER.A	2035.10956	2	6.47E-05	0.94	4.55	-	818.2
AHQ-6-3, 5460	R.ELESQISELQEDLESER.A	2035.10956	3	3.88E-09	0.98	6.02	-	2284.3
AHQ-6-4, 5532	R.ELESQISELQEDLESER.A	2035.10956	3	2.13E-08	0.98	6.32	-	2082.7
AHQ-6-2, 5491	R.ELESQISELQEDLESER.A	2035.10956	2	1.43E-06	0.96	5.32	-	1037.9
AHQ-6-3, 5021	R.ELESQISELQEDLESER.A	2035.10956	2	6.89E-07	0.90	3.97	-	871.4
AHQ-6-4, 2251 - 2253	R.EMEAELEDERK.Q	1379.47597	2	1.45E-06	0.92	3.25	-	1300.2
AHQ-6-2, 4346	K.EQADFAIEALAK.A	1306.44632	1	5.66E-04	0.35	2.82	-	272.9
AHQ-6-2, 4336 - 4398	K.EQADFAIEALAK.A	1306.44632	2	1.70E-04	0.75	2.67	-	546.7
AHQ-6-3, 2564	R.EQEVNILK.K	973.10554	1	1.25E-04	0.10	1.91	-	145.4
AHQ-6-2, 2416 - 2483	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	9.44E-06	0.90	3.98	-	820.0
AHQ-6-3, 2492	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	9.84E-06	0.89	4.05	-	722.3
AHQ-6-5, 2428	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.06E-05	0.86	4.09	-	631.9
AHQ-6-4, 2451	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	4.40E-07	0.84	3.72	-	669.2
AHQ-6-2, 3408 - 3471	R.FLSNGHVTIPGQQDK.D	1641.80946	2	2.02E-05	0.95	4.56	-	1071.6
AHQ-6-2, 2994	K.HEAMITDLEER.L	1344.47646	2	2.88E-06	0.96	3.70	-	1379.2
AHQ-6-4, 2483	K.HEAM*ITDLEER.L	1360.47586	2	8.46E-04	0.96	3.78	-	1580.3
AHQ-6-2, 2526	K.HEAM*ITDLEER.L	1360.47586	2	1.14E-04	0.96	4.11	-	1574.4
AHQ-6-6, 2907	K.HEAMITDLEER.L	1344.47646	2	1.69E-05	0.90	2.84	-	1122.5
AHQ-6-3, 2993	K.HEAMITDLEER.L	1344.47646	2	4.00E-07	0.96	3.83	-	1347.8
AHQ-6-3, 2521	K.HEAM*ITDLEER.L	1360.47586	2	7.42E-05	0.97	4.07	-	2081.7
AHQ-6-2, 3655	R.HEMPPHIYAITDTAYR.S	1916.14944	3	2.09E-08	0.98	4.85	-	2605.0
AHQ-6-2, 3399	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	3.07E-05	0.75	2.65	-	588.6
AHQ-6-1, 3595	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	4.71E-07	0.96	4.74	-	1659.6
AHQ-6-5, 3289	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	4.23E-04	0.96	4.10	-	1984.2
AHQ-6-2, 3651	R.HEMPPHIYAITDTAYR.S	1916.14944	2	8.49E-08	0.89	3.60	-	761.0
AHQ-6-2, 3326 - 3404	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	8.36E-04	0.75	3.07	-	865.9
AHQ-6-2, 4467	K.HSQAVEELAEQLEQTK.R	1840.96940	3	2.97E-07	0.96	5.33	-	1784.2
AHQ-6-1, 4595 - 4654	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.10E-04	0.97	4.43	-	1922.4
AHQ-6-1, 4602	K.HSQAVEELAEQLEQTK.R	1840.96940	3	4.21E-06	0.97	5.25	-	2046.0
AHQ-6-2, 4466	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.39E-11	0.98	6.42	-	2199.3
AHQ-6-3, 4444 - 4446	K.HSQAVEELAEQLEQTK.R	1840.96940	3	2.56E-06	0.97	6.07	-	2033.3
AHQ-6-4, 4453	K.HSQAVEELAEQLEQTK.R	1840.96940	3	4.20E-05	0.89	3.91	-	1291.2
AHQ-6-3, 4440 - 4504	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.94E-08	0.98	5.80	-	1755.0
AHQ-6-4, 4439	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.46E-08	0.98	5.65	-	1922.3
AHQ-6-2, 4150	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	3.19E-11	0.98	5.61	-	2050.8
AHQ-6-2, 4147	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.30E-09	0.98	6.10	-	1846.7
AHQ-6-3, 4121	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	2.52E-08	0.99	6.61	-	3036.7
AHQ-6-3, 4120	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	4.13E-11	0.98	6.55	-	1561.4
AHQ-6-6, 4022	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.23E-05	0.97	6.17	-	1248.6
AHQ-6-4, 4117	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.80E-12	0.98	6.06	-	2421.3
AHQ-6-1, 4299	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	4.77E-08	0.97	6.15	-	1461.0

AHQ-6-4, 4111	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.02E-06	0.97	6.11	-	1253.8
AHQ-6-5, 4047	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	4.50E-12	0.96	5.39	-	1423.5
AHQ-6-3, 3681 - 3705	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.38E-07	0.88	3.47	-	1091.3
AHQ-6-2, 3682 - 3746	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.07E-09	0.97	5.23	-	2077.0
AHQ-6-13-, 3672	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.83E-08	0.93	3.55	-	1397.7
AHQ-6-4, 3740 - 3748	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.97E-06	0.97	4.66	-	2487.4
AHQ-6-1, 3847	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.67E-05	0.97	4.47	-	2132.2
AHQ-6-4, 3653 - 3671	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.84E-05	0.96	4.27	-	1881.6
AHQ-6-2, 3794 - 3850	R.IAEFTTNLTEEEEK.S	1654.75371	2	8.79E-09	0.91	3.64	-	1294.4
AHQ-6-6, 3582 - 3640	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.22E-06	0.94	4.05	-	1340.3
AHQ-6-2, 3562 - 3622	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.22E-05	0.77	2.81	-	815.4
AHQ-6-3, 3594 - 3652	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.07E-07	0.96	4.18	-	1663.5
AHQ-6-2, 3910	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.82E-07	0.95	4.11	-	1593.4
AHQ-6-5, 3619 - 3621	R.IAEFTTNLTEEEEK.S	1654.75371	2	7.94E-09	0.96	4.84	-	1891.0
AHQ-6-3, 3770	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.58E-06	0.82	3.31	-	864.2
AHQ-6-3, 3882 - 3893	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.32E-09	0.97	4.67	-	2023.3
AHQ-6-7, 3494	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.38E-04	0.80	2.87	-	1049.9
AHQ-6-3, 4944	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	3.04E-04	0.54	3.17	-	569.0
AHQ-6-2, 5242	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	1.48E-04	0.91	4.54	-	776.9
AHQ-6-1, 3552	K.IAQLEEQLDNETK.E	1531.64695	2	4.93E-09	0.96	4.48	-	1517.3
AHQ-6-4, 3335 - 3404	K.IAQLEEQLDNETK.E	1531.64695	2	1.51E-04	0.94	3.46	-	1585.9
AHQ-6-2, 3748	K.IAQLEEQLDNETK.E	1531.64695	2	1.05E-07	0.92	3.99	-	966.5
AHQ-6-2, 2963	K.IAQLEEQLDNETK.E	1531.64695	2	9.39E-04	0.96	4.50	-	1393.1
AHQ-6-5, 3284	K.IAQLEEQLDNETK.E	1531.64695	2	1.32E-07	0.97	4.67	-	1638.2
AHQ-6-3, 3718	K.IAQLEEQLDNETK.E	1531.64695	2	3.27E-05	0.83	3.29	-	834.2
AHQ-6-6, 3051	K.IAQLEEQLDNETK.E	1531.64695	2	1.93E-06	0.95	3.90	-	1564.3
AHQ-6-11, 3259	K.IAQLEEQLDNETK.E	1531.64695	2	1.72E-05	0.82	2.59	-	972.1
AHQ-6-2, 3127	K.IAQLEEQLDNETK.E	1531.64695	2	2.53E-07	0.90	3.77	-	977.1
AHQ-6-7, 3195	K.IAQLEEQLDNETK.E	1531.64695	2	1.88E-04	0.89	3.83	-	848.7
AHQ-6-12, 3316	K.IAQLEEQLDNETK.E	1531.64695	2	1.47E-06	0.94	3.40	-	1374.3
AHQ-6-2, 3480	K.IAQLEEQLDNETK.E	1531.64695	2	3.89E-10	0.93	3.83	-	1206.8
AHQ-6-2, 3378 - 3382	K.IAQLEEQLDNETK.E	1531.64695	2	2.17E-07	0.97	4.41	-	1693.9
AHQ-6-3, 3465	K.IAQLEEQLDNETK.E	1531.64695	2	1.84E-07	0.96	4.53	-	1412.5
AHQ-6-3, 3360	K.IAQLEEQLDNETK.E	1531.64695	2	7.50E-08	0.96	4.14	-	1570.6
AHQ-6-3, 3136	K.IAQLEEQLDNETK.E	1531.64695	2	1.94E-07	0.97	4.81	-	1689.5
AHQ-6-6, 3268	K.IAQLEEQLDNETK.E	1531.64695	2	1.59E-08	0.95	3.97	-	1370.3
AHQ-6-2, 3136	K.IAQLEEQLDNETKER.Q	1816.94784	2	2.79E-05	0.76	3.46	-	594.1
AHQ-6-2, 3514 - 3584	K.IAQLEEQLDNETKER.Q	1816.94784	2	2.04E-06	0.86	3.67	-	963.3
AHQ-6-3, 3493	K.IAQLEEQLDNETKER.Q	1816.94784	2	8.05E-07	0.84	3.76	-	655.5
AHQ-6-14-, 5930	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.74E-04	0.85	3.33	-	697.7
AHQ-6-3, 5753	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.61E-04	0.54	2.77	-	467.0
AHQ-6-6, 5895 - 5958	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.77E-04	0.91	4.22	-	823.8
AHQ-6-2, 5566	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	6.78E-05	0.96	5.13	-	1168.2
AHQ-6-5, 5948 - 6027	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.51E-07	0.96	5.31	-	1063.0
AHQ-6-4, 6115	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	2.90E-04	0.96	5.04	-	1117.2
AHQ-6-2, 6004 - 6062	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.15E-05	0.83	3.82	-	541.3
AHQ-6-2, 5028	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	9.12E-06	0.95	4.78	-	1036.2
AHQ-6-3, 5341 - 5397	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	3	1.60E-04	0.84	3.92	-	886.2
AHQ-6-6, 4423	R.IM*GIPEEEQMGLLR.V	1632.92766	2	6.40E-05	0.86	3.38	-	590.9
AHQ-6-2, 4480 - 4543	R.IMGIPEEEQM*GLLR.V	1632.92766	2	7.74E-04	0.72	3.46	-	539.6
AHQ-6-5, 4408 - 4467	R.IMGIPEEEQM*GLLR.V	1632.92766	2	8.01E-04	0.54	2.76	-	383.2
AHQ-6-2, 3899 - 3918	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	4.34E-04	0.89	3.73	-	662.4
AHQ-6-5, 3832	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	6.20E-05	0.86	3.45	-	539.4
AHQ-6-2, 5060 - 5066	R.IMGIPEEEQMGLLR.V	1616.92826	2	3.31E-05	0.67	3.12	-	375.3
AHQ-6-5, 4996	R.IMGIPEEEQMGLLR.V	1616.92826	2	3.60E-07	0.58	2.80	-	336.3
AHQ-6-6, 3799 - 3800	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	7.60E-04	0.94	4.13	-	885.8
AHQ-6-2, 6538	R.INFDVNGYIVGANIETYLLEK.S	2386.68474	3	6.31E-04	0.94	4.07	-	1955.4
AHQ-6-3, 5500	K.IRELESQISELQEDLESER.A	2304.45416	3	5.75E-09	0.98	6.21	-	2043.2
AHQ-6-2, 5542	K.IRELESQISELQEDLESER.A	2304.45416	2	2.53E-06	0.97	6.00	-	1035.0
AHQ-6-1, 5594 - 5600	K.IRELESQISELQEDLESER.A	2304.45416	2	1.50E-05	0.98	6.74	-	1314.1
AHQ-6-4, 5557 - 5567	K.IRELESQISELQEDLESER.A	2304.45416	2	8.75E-07	0.98	7.11	-	1975.4
AHQ-6-1, 5536 - 5591	K.IRELESQISELQEDLESER.A	2304.45416	3	3.87E-07	0.95	4.61	-	1643.0
AHQ-6-3, 5501	K.IRELESQISELQEDLESER.A	2304.45416	2	3.97E-07	0.98	6.37	-	1319.0
AHQ-6-4, 5563	K.IRELESQISELQEDLESER.A	2304.45416	3	1.73E-04	0.97	5.58	-	1623.6
AHQ-6-2, 4948	K.ITDVIIGFQACCR.G	1555.80136	2	6.75E-04	0.79	2.77	-	772.9
AHQ-6-2, 5266 - 5288	K.ITDVIIGFQACCR.G	1555.80136	2	6.40E-04	0.73	3.12	-	802.3
AHQ-6-2, 4458	K.KANLQIDQINTDLNLER.S	1999.21478	3	7.64E-04	0.89	4.36	-	851.4
AHQ-6-4, 4463	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.80E-05	0.88	3.81	-	747.2
AHQ-6-6, 4319	K.KANLQIDQINTDLNLER.S	1999.21478	2	5.98E-05	0.93	4.98	-	932.4
AHQ-6-3, 4262	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.96E-09	0.97	4.84	-	1468.9
AHQ-6-2, 4642 - 4691	K.KANLQIDQINTDLNLER.S	1999.21478	3	2.14E-05	0.88	4.19	-	759.7
AHQ-6-6, 2652	R.KKVEAQLQELQVK.F	1541.81761	2	1.08E-07	0.97	4.63	-	2130.9
AHQ-6-5, 2651 - 2656	R.KKVEAQLQELQVK.F	1541.81761	2	6.83E-08	0.97	5.12	-	1689.5
AHQ-6-3, 2716 - 2781	R.KKVEAQLQELQVK.F	1541.81761	2	1.27E-06	0.98	5.50	-	2076.4
AHQ-6-4, 2679	R.KKVEAQLQELQVK.F	1541.81761	2	3.64E-06	0.96	4.72	-	1367.3
AHQ-6-4, 3513	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.63E-12	0.98	5.65	-	1589.1
AHQ-6-3, 3542	K.KLEEEQIILEDQNCK.L	1891.08992	3	7.97E-06	0.90	4.42	-	1176.6
AHQ-6-2, 3479 - 3560	K.KLEEEQIILEDQNCK.L	1891.08992	3	3.88E-08	0.93	4.86	-	1277.7
AHQ-6-2, 3558	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.07E-06	0.98	6.08	-	2397.2
AHQ-6-2, 3440 - 3496	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.79E-10	0.98	5.49	-	1884.0
AHQ-6-3, 3457 - 3525	K.KLEEEQIILEDQNCK.L	1891.08992	2	3.33E-10	0.98	5.97	-	2157.1
AHQ-6-2, 5771	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.05E-07	0.92	4.69	-	1398.6
AHQ-6-3, 5736	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.60E-06	0.93	4.73	-	1387.0
AHQ-6-1, 6446	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	9.10E-12	0.96	6.14	-	1106.8
AHQ-6-1, 6447	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.12E-05	0.73	2.77	-	875.6
AHQ-6-4, 6487	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	5.16E-08	0.88	4.54	-	878.2
AHQ-6-2, 2926	K.KLVWVPSDK.S	1072.28194	2	1.50E-05	0.92	3.48	-	1055.1
AHQ-6-2, 3235	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	1.29E-05	0.92	3.82	-	972.7
AHQ-6-2, 3343	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.70E-04	0.94	4.87	-	1458.0
AHQ-6-2, 2990	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	7.50E-08	0.96	4.84	-	1685.7
AHQ-6-2, 2992	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	7.22E-06	0.60	3.02	-	449.6
AHQ-6-3, 2986	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	3.05E-07	0.71	3.33	-	498.8
AHQ-6-5, 3233	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	3.39E-08	0.92	4.66	-	992.6
AHQ-6-2, 4726	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	1.75E-07	0.56	3.02	-	257.4
AHQ-6-2, 4712	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	5.42E-04	0.75	3.50	-	767.9
AHQ-6-4, 4715	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	2.62E-06	0.78	3.82	-	923.5
AHQ-6-2, 4086	K.KQELEEICHDLEAR.V	1771.93036	3	2.75E-06	0.97	5.47	-	2076.2
AHQ-6-1, 4240	K.KQELEEICHDLEAR.V	1771.93036	3	9.14E-06	0.95	4.91	-	1657.8
AHQ-6-1, 4238 - 4314	K.KQELEEICHDLEAR.V	1771.93036	2	8.50E-09	0.97	5.33	-	2032.4
AHQ-6-5, 4009	K.KQELEEICHDLEAR.V	1771.93036	3	6.74E-04	0.96	5.39	-	1358.2
AHQ-6-2, 4082 - 4084	K.KQELEEICHDLEAR.V	1771.93036	2	7.09E-04	0.97	4.97	-	1925.2
AHQ-6-2, 3051	K.KVEAQLQELQVK.F	1413.64470	3	3.11E-04	0.90	4.16	-	1284.6
AHQ-6-4, 2995	K.KVEAQLQELQVK.F	1413.64470	2	7.07E-07	0.94	4.55	-	1112.4
AHQ-6-5, 2936 - 2955	K.KVEAQLQELQVK.F	1413.64470	2	4.27E-06	0.94	4.05	-	1337.3
AHQ-6-2, 3028	K.KVEAQLQELQVK.F	1413.64470	2	6.95E-07	0.94	4.53	-	1052.2
AHQ-6-1, 3891	K.LEEEQIILEDQNCK.L	1762.91700	2	2.04E-08	0.94	3.93	-	1206.0
AHQ-6-4, 3732 - 3797	K.LEEEQIILEDQNCK.L	1762.91700	2	3.34E-05	0.95	4.57	-	1031.2

AHQ-6-2, 3814	K.LEEEQIILEDQNCK.L	1762.91700	2	1.34E-08	0.98	5.68	-	1597.9
AHQ-6-5, 3725	K.LEEEQIILEDQNCK.L	1762.91700	2	1.77E-12	0.92	3.87	-	903.7
AHQ-6-4, 2641 - 2645	R.LEVNLQAM*K.A	1062.26570	2	3.25E-04	0.88	3.60	-	722.2
AHQ-6-3, 3545	R.LEVNLQAMK.A	1046.26630	2	4.89E-04	0.86	3.29	-	735.9
AHQ-6-2, 2674 - 2678	R.LEVNLQAM*K.A	1062.26570	2	2.08E-04	0.93	3.72	-	895.7
AHQ-6-3, 2685	R.LEVNLQAM*K.A	1062.26570	2	4.72E-05	0.87	3.27	-	745.8
AHQ-6-2, 3468 - 3527	K.LKDVLLQVDDER.R	1443.62767	2	6.63E-07	0.93	3.80	-	1210.8
AHQ-6-3, 3510	K.LKDVLLQVDDER.R	1443.62767	2	2.14E-07	0.92	3.94	-	1069.8
AHQ-6-4, 3136	K.LKDVLLQVDDERR.N	1599.81402	2	1.78E-04	0.85	3.58	-	783.1
AHQ-6-6, 3099	K.LKDVLLQVDDERR.N	1599.81402	2	2.37E-06	0.68	2.79	-	810.0
AHQ-6-3, 3140 - 3200	K.LKDVLLQVDDERR.N	1599.81402	2	4.17E-05	0.72	3.27	-	599.7
AHQ-6-11, 3107	K.LKDVLLQVDDERR.N	1599.81402	3	4.07E-04	0.90	3.25	-	1064.1
AHQ-6-11, 3100 - 3180	K.LKDVLLQVDDERR.N	1599.81402	2	3.68E-04	0.76	3.02	-	840.0
AHQ-6-3, 6580 - 6656	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	3	1.70E-04	0.89	3.62	-	1533.7
AHQ-6-2, 6556 - 6615	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	2.80E-04	0.92	4.49	-	719.3
AHQ-6-2, 6128 - 6198	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	3.65E-06	0.57	2.53	-	409.6
AHQ-6-2, 6670	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	3.33E-06	0.96	4.68	-	1389.3
AHQ-6-6, 5642 - 5646	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.19E-08	0.97	5.04	-	1702.3
AHQ-6-1, 5795 - 5827	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.07E-09	0.97	5.21	-	1427.0
AHQ-6-5, 5703	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	8.36E-10	0.96	4.94	-	1384.4
AHQ-6-2, 5703 - 5768	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.72E-07	0.97	5.24	-	1469.2
AHQ-6-7, 5498	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.25E-10	0.92	4.01	-	1040.7
AHQ-6-5, 5699	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	4.67E-04	0.84	3.65	-	813.7
AHQ-6-2, 5374	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.94E-06	0.93	4.13	-	944.2
AHQ-6-2, 5363	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.51E-07	0.95	5.11	-	1328.3
AHQ-6-3, 5713	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	7.24E-10	0.97	5.29	-	1863.0
AHQ-6-4, 5776 - 5779	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.16E-10	0.97	5.60	-	1332.0
AHQ-6-3, 4805	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.31E-06	0.87	3.47	-	824.1
AHQ-6-2, 5662 - 5719	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.46E-11	0.97	5.34	-	1572.4
AHQ-6-5, 5111	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.54E-07	0.96	4.89	-	993.9
AHQ-6-1, 5515	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	4.27E-10	0.98	6.48	-	2387.1
AHQ-6-1, 5472 - 5531	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.19E-08	0.98	6.27	-	1773.8
AHQ-6-5, 5383 - 5457	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.29E-07	0.98	6.24	-	1606.4
AHQ-6-4, 5464 - 5480	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.79E-07	0.94	4.54	-	851.6
AHQ-6-7, 5179	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.38E-05	0.87	3.45	-	877.6
AHQ-6-1, 5176 - 5238	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.70E-07	0.92	4.54	-	673.8
AHQ-6-2, 5140 - 5159	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.02E-04	0.94	4.63	-	727.4
AHQ-6-3, 5614 - 5674	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.96E-07	0.96	5.03	-	1228.1
AHQ-6-3, 5502 - 5562	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.12E-07	0.96	5.39	-	1207.6
AHQ-6-6, 5350	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.21E-07	0.95	5.04	-	952.9
AHQ-6-4, 5509	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	5.94E-05	0.96	4.76	-	1794.1
AHQ-6-2, 5380 - 5462	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.23E-06	0.98	6.46	-	1759.3
AHQ-6-2, 5459	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	4.51E-10	0.98	6.06	-	1949.4
AHQ-6-4, 5203 - 5269	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.96E-05	0.88	4.17	-	755.8
AHQ-6-1, 5702	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.21E-07	0.88	3.82	-	724.4
AHQ-6-4, 5583	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.98E-07	0.88	4.40	-	674.6
AHQ-6-3, 5389 - 5448	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.11E-15	0.98	6.64	-	1593.5
AHQ-6-3, 5141	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.32E-07	0.97	5.21	-	1361.1
AHQ-6-3, 5424	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	7.43E-05	0.95	5.59	-	1191.8
AHQ-6-14, 5924	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.07E-04	0.86	3.26	-	888.9
AHQ-6-2, 6102	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.92E-05	0.81	3.17	-	695.2
AHQ-6-2, 5518 - 5578	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.64E-11	0.97	5.37	-	1484.3
AHQ-6-2, 5108 - 5167	K.LQVELDNVTGLLSQSDSKSSK.L	2249.46164	3	1.94E-05	0.64	3.50	-	493.1
AHQ-6-1, 4092	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	4.89E-04	0.96	4.00	-	1927.3
AHQ-6-2, 4830 - 4903	R.LTEMETLQSQLMAEK.L	1753.03211	2	1.70E-05	0.94	4.62	-	1058.3
AHQ-6-2, 3506 - 3566	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	3.65E-05	0.94	3.95	-	1339.2
AHQ-6-4, 3519	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	6.70E-05	0.88	3.60	-	1066.1
AHQ-6-3, 3932 - 3996	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	4.01E-04	0.94	3.81	-	1836.1
AHQ-6-3, 4386 - 4456	R.LTEMETLQSQLM*AEK.L	1769.03151	2	3.12E-04	0.93	4.26	-	1138.3
AHQ-6-1, 3694	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	5.79E-05	0.95	4.53	-	1109.7
AHQ-6-4, 3985	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	3.69E-06	0.83	3.16	-	773.8
AHQ-6-2, 3960 - 4022	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	1.52E-07	0.97	4.51	-	1662.7
AHQ-6-3, 3476 - 3549	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	3.77E-04	0.94	4.39	-	1131.4
AHQ-6-4, 3827	K.MEDSVGCLETAEEVK.R	1698.85159	2	3.71E-05	0.92	4.51	-	636.1
AHQ-6-2, 3556	K.MEDSVGCLETAEEVKR.K	1855.03794	2	6.12E-08	0.65	2.88	-	379.3
AHQ-6-3, 3256 - 3257	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	3.88E-07	0.91	3.59	-	806.3
AHQ-6-3, 3261	K.M*EDSVGCLETAEEVKR.K	1871.03734	3	8.32E-04	0.83	3.70	-	817.9
AHQ-6-2, 3220 - 3267	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	2.85E-06	0.82	3.54	-	503.1
AHQ-6-2, 4976 - 5038	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	2.51E-05	0.90	4.41	-	934.1
AHQ-6-4, 5063 - 5123	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	3.73E-10	0.97	6.03	-	1494.5
AHQ-6-2, 5515 - 5519	K.NFINNPLAQADWAAK.K	1673.85315	2	4.86E-10	0.95	4.77	-	968.5
AHQ-6-2, 5103	K.NFINNPLAQADWAAK.K	1673.85315	2	1.84E-05	0.96	4.92	-	1315.2
AHQ-6-6, 5411	K.NFINNPLAQADWAAK.K	1673.85315	2	7.57E-13	0.88	4.02	-	789.6
AHQ-6-1, 5195	K.NFINNPLAQADWAAK.K	1673.85315	2	4.60E-06	0.95	4.59	-	1008.9
AHQ-6-11, 4857	K.NFINNPLAQADWAAK.K	1673.85315	2	5.41E-05	0.86	3.59	-	814.1
AHQ-6-4, 5121	K.NFINNPLAQADWAAK.K	1673.85315	2	2.01E-06	0.94	4.21	-	1193.8
AHQ-6-5, 4981 - 5041	K.NFINNPLAQADWAAK.K	1673.85315	2	4.98E-08	0.95	4.83	-	1066.1
AHQ-6-1, 5564	K.NFINNPLAQADWAAK.K	1673.85315	2	6.65E-06	0.73	2.62	-	653.9
AHQ-6-2, 5262 - 5331	K.NFINNPLAQADWAAK.K	1673.85315	2	3.73E-09	0.96	4.80	-	1469.2
AHQ-6-10, 5179	K.NFINNPLAQADWAAK.K	1673.85315	2	5.83E-04	0.82	3.45	-	517.5
AHQ-6-6, 4999	K.NFINNPLAQADWAAK.K	1673.85315	2	1.89E-09	0.94	4.57	-	976.0
AHQ-6-5, 5467	K.NFINNPLAQADWAAK.K	1673.85315	2	2.24E-08	0.95	4.60	-	1046.3
AHQ-6-3, 5058 - 5077	K.NFINNPLAQADWAAK.K	1673.85315	2	3.91E-05	0.96	4.63	-	1333.9
AHQ-6-7, 4846	K.NFINNPLAQADWAAK.K	1673.85315	2	9.93E-08	0.92	4.19	-	928.6
AHQ-6-2, 2726 - 2728	K.NKHEAMITDLEER.L	1586.75247	2	6.01E-05	0.93	3.63	-	1188.4
AHQ-6-3, 2734	K.NKHEAMITDLEER.L	1586.75247	2	2.26E-05	0.89	3.47	-	1062.0
AHQ-6-4, 2689	K.NKHEAMITDLEER.L	1586.75247	2	1.10E-05	0.90	3.43	-	1148.4
AHQ-6-5, 5417 - 5427	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.11E-05	0.90	3.57	-	636.4
AHQ-6-3, 4942 - 4948	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.14E-08	0.97	4.81	-	1342.8
AHQ-6-2, 4970 - 4971	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.65E-07	0.95	5.05	-	838.2
AHQ-6-1, 5546	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.11E-04	0.92	3.60	-	883.4
AHQ-6-6, 4866	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.24E-04	0.88	3.71	-	590.0
AHQ-6-4, 4981 - 4988	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.26E-06	0.95	4.44	-	1046.7
AHQ-6-2, 5296 - 5300	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	4.55E-06	0.93	4.43	-	856.7
AHQ-6-2, 5122	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	1.98E-05	0.73	3.14	-	709.3
AHQ-6-2, 5294	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	7.46E-09	0.84	3.81	-	687.8
AHQ-6-2, 4886	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	8.15E-06	0.80	3.71	-	620.4
AHQ-6-2, 4848 - 4884	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	1.09E-08	0.93	3.76	-	1094.3
AHQ-6-4, 4893	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	2.21E-04	0.56	2.68	-	469.0
AHQ-6-3, 2485	K.PLLQVSR.Q	812.98013	1	9.86E-04	0.20	1.96	-	237.0
AHQ-6-2, 2386	K.QIATLHAQVADM*K.K	1442.66637	2	3.59E-04	0.62	2.66	-	324.3
AHQ-6-2, 2106	R.QLEEAEEEAQR.A	1332.35590	2	7.18E-04	0.86	3.06	-	1015.0
AHQ-6-4, 2079	R.QLEEAEEEAQR.A	1332.35590	2	5.59E-07	0.72	3.06	-	496.3
AHQ-6-6, 2060	R.QLEEAEEEAQR.A	1332.35590	2	4.82E-05	0.53	2.99	-	351.6
AHQ-6-3, 2973 - 3004	K.QTLENERGELANEVK.V	1730.85818	2	1.65E-04	0.64	3.31	-	376.9
AHQ-6-11, 3507	R.RGDLPFVVPR.R	1156.36217	2	7.14E-05	0.85	2.71	-	892.4
AHQ-6-2, 3635	R.RGDLPFVVPR.R	1156.36217	2	5.79E-06	0.93	3.60	-	1109.9

AHQ-6-10, 3431 - 3432	R.RGDLPFVVPR.R	1156.36217	2	8.95E-06	0.86	3.27	-	707.3
AHQ-6-12, 3568	R.RGDLPFVVPR.R	1156.36217	2	2.13E-05	0.93	3.28	-	1269.8
AHQ-6-8, 3320	R.RGDLPFVVPR.R	1156.36217	2	1.61E-04	0.90	3.50	-	795.6
AHQ-6-4, 3597	R.RGDLPFVVPR.R	1156.36217	2	5.10E-06	0.93	3.67	-	1235.7
AHQ-6-5, 3535	R.RGDLPFVVPR.R	1156.36217	2	4.28E-06	0.94	4.02	-	1066.5
AHQ-6-1, 3830	R.RGDLPFVVPR.R	1156.36217	2	1.75E-06	0.93	3.46	-	1315.5
AHQ-6-3, 3628	R.RGDLPFVVPR.R	1156.36217	2	5.23E-05	0.95	3.62	-	1489.3
AHQ-6-6, 3506	R.RGDLPFVVPR.R	1156.36217	2	7.77E-06	0.94	4.03	-	1122.8
AHQ-6-3, 6254	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	2.85E-08	0.96	6.20	-	1419.6
AHQ-6-4, 6323	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.96E-05	0.92	4.63	-	1178.5
AHQ-6-2, 6286	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.73E-09	0.97	6.32	-	1409.6
AHQ-6-13-, 5604	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	4.77E-07	0.94	4.81	-	1249.2
AHQ-6-6, 5787	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.15E-08	0.92	4.66	-	891.9
AHQ-6-2, 5743 - 5803	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	7.63E-08	0.94	5.33	-	1125.4
AHQ-6-4, 5944	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	4.97E-04	0.76	3.18	-	1016.5
AHQ-6-5, 5853	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.07E-07	0.88	4.21	-	933.4
AHQ-6-2, 5868 - 5932	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	3.31E-08	0.96	5.74	-	1471.5
AHQ-6-2, 5240 - 5263	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	6.82E-06	0.89	4.04	-	1133.3
AHQ-6-2, 4584	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	3.81E-08	0.96	4.37	-	1515.9
AHQ-6-1, 5480 - 5534	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	5.14E-04	0.50	3.04	-	564.6
AHQ-6-2, 5436 - 5510	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	5.17E-07	0.95	5.14	-	1663.3
AHQ-6-3, 4554	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	4.91E-08	0.97	5.01	-	1770.9
AHQ-6-4, 5517 - 5576	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	5.96E-05	0.73	3.88	-	442.8
AHQ-6-5, 4492	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.52E-08	0.97	5.57	-	1533.2
AHQ-6-1, 4676 - 4683	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.90E-11	0.98	5.88	-	1816.4
AHQ-6-4, 4504 - 4579	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	3.83E-08	0.97	5.25	-	1668.3
AHQ-6-6, 4447	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	8.00E-09	0.96	4.66	-	1790.1
AHQ-6-2, 4723	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.11E-08	0.97	5.51	-	1640.3
AHQ-6-4, 3683	K.TDLLLEPYNK.Y	1206.36989	2	9.63E-06	0.90	3.61	-	1131.1
AHQ-6-2, 3648 - 3710	K.TDLLLEPYNK.Y	1206.36989	2	1.09E-05	0.83	3.33	-	877.1
AHQ-6-3, 3638 - 3700	K.TDLLLEPYNK.Y	1206.36989	2	5.06E-04	0.90	3.30	-	1117.8
AHQ-6-7, 3483	K.TDLLLEPYNK.Y	1206.36989	2	7.15E-07	0.91	3.94	-	1022.8
AHQ-6-5, 3603	K.TDLLLEPYNK.Y	1206.36989	2	4.58E-05	0.86	3.46	-	964.9
AHQ-6-1, 3868	K.TDLLLEPYNK.Y	1206.36989	2	3.88E-07	0.90	3.63	-	1062.9
AHQ-6-6, 3588 - 3598	K.TDLLLEPYNK.Y	1206.36989	2	3.29E-04	0.92	4.23	-	904.2
AHQ-6-2, 3862	K.TDLLLEPYNKYR.F	1525.73037	2	1.57E-06	0.82	3.29	-	815.3
AHQ-6-1, 4236 - 4306	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.11E-11	0.98	5.37	-	2390.2
AHQ-6-3, 4184	K.TELEDTLDSTAAQQELR.S	1921.00969	3	1.94E-07	0.97	5.37	-	2248.0
AHQ-6-2, 4202 - 4267	K.TELEDTLDSTAAQQELR.S	1921.00969	2	8.89E-09	0.96	4.94	-	1416.4
AHQ-6-3, 4114 - 4182	K.TELEDTLDSTAAQQELR.S	1921.00969	2	4.43E-11	0.98	5.67	-	2121.1
AHQ-6-4, 4137 - 4191	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.24E-05	0.94	4.09	-	1438.1
AHQ-6-2, 3744	K.TELEDTLDSTAAQQELR.S	1921.00969	2	2.09E-05	0.59	3.05	-	563.1
AHQ-6-2, 3934	K.TELEDTLDSTAAQQELR.S	1921.00969	2	3.90E-04	0.75	2.74	-	873.4
AHQ-6-2, 3380	R.TEMEDLMSSKDDVGK.S	1685.85626	2	2.96E-05	0.89	3.64	-	961.2
AHQ-6-2, 2048	R.TEM*EDLM*SSKDDVGK.S	1717.85506	2	4.85E-04	0.65	2.91	-	450.9
AHQ-6-2, 2571	R.TEMEDLM*SSKDDVGK.S	1701.85566	2	2.61E-05	0.90	3.79	-	1028.7
AHQ-6-2, 6135 - 6136	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	8.74E-05	0.96	4.96	-	1211.7
AHQ-6-6, 6031 - 6087	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	3.64E-05	0.91	4.70	-	1027.1
AHQ-6-2, 6118 - 6179	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.66E-08	0.97	5.76	-	1653.0
AHQ-6-5, 6097 - 6167	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.36E-04	0.96	4.95	-	1711.0
AHQ-6-2, 1952 - 1971	K.THEAQIQEMR.Q	1243.37536	2	8.29E-05	0.71	2.55	-	925.0
AHQ-6-3, 2080	K.VAAYDKLEK.T	1037.19123	2	3.52E-04	0.88	3.12	-	929.9
AHQ-6-2, 3352	K.VEAQLQELQVK.F	1285.47179	1	7.76E-05	0.07	2.47	-	290.7
AHQ-6-2, 5638	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	3.02E-07	0.90	4.84	-	677.0
AHQ-6-5, 5589 - 5652	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.41E-06	0.49	3.01	-	283.6
AHQ-6-13-, 5485	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	1.53E-08	0.79	3.69	-	449.8
AHQ-6-3, 5089	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	7.44E-08	0.88	4.00	-	728.5
AHQ-6-10, 4756 - 4772	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	1.08E-07	0.88	4.00	-	713.9
AHQ-6-2, 5106 - 5132	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	2.33E-07	0.95	4.84	-	1350.5
AHQ-6-2, 5640	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	9.61E-10	0.93	4.61	-	707.4
AHQ-6-5, 5505 - 5581	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	3.76E-07	0.81	3.32	-	868.5
AHQ-6-2, 2116	R.VEEEEERCQHLQAEK.K	1916.01642	3	4.88E-05	0.93	4.85	-	859.3
AHQ-6-5, 3881	K.VIQYLAYVASSHK.S	1479.70484	2	9.13E-04	0.94	4.02	-	1183.1
AHQ-6-2, 3947 - 3974	K.VIQYLAYVASSHK.S	1479.70484	2	7.43E-08	0.95	3.91	-	1378.8
AHQ-6-4, 3940	K.VIQYLAYVASSHK.S	1479.70484	2	1.58E-04	0.88	3.21	-	942.9
AHQ-6-10, 3739	K.VIQYLAYVASSHK.S	1479.70484	2	2.54E-04	0.90	3.52	-	889.1
AHQ-6-6, 3842	K.VIQYLAYVASSHK.S	1479.70484	2	2.00E-08	0.95	3.80	-	1222.4
AHQ-6-5, 3877	K.VIQYLAYVASSHK.S	1479.70484	3	2.65E-04	0.80	3.41	-	591.4
AHQ-6-4, 3945	K.VIQYLAYVASSHK.S	1479.70484	2	9.48E-10	0.96	4.37	-	1401.3
AHQ-6-2, 3982 - 3992	K.VIQYLAYVASSHK.S	1479.70484	3	1.71E-05	0.92	4.02	-	942.9
AHQ-6-3, 3960	K.VIQYLAYVASSHK.S	1479.70484	2	9.63E-07	0.93	3.95	-	960.2
AHQ-6-7, 3731 - 3791	K.VIQYLAYVASSHK.S	1479.70484	2	1.44E-04	0.79	2.81	-	847.0
AHQ-6-1, 4135	K.VIQYLAYVASSHK.S	1479.70484	2	3.40E-04	0.90	3.12	-	1131.0
AHQ-6-8, 5905	R.VISGVLQLGNIVFK.K	1487.81155	2	1.60E-06	0.97	4.52	-	1720.8
AHQ-6-6, 5946	R.VISGVLQLGNIVFK.K	1487.81155	2	1.62E-06	0.97	4.38	-	1810.1
AHQ-6-14-, 5928	R.VISGVLQLGNIVFK.K	1487.81155	2	5.36E-06	0.96	3.87	-	1581.6
AHQ-6-7, 5786	R.VISGVLQLGNIVFK.K	1487.81155	2	1.11E-06	0.98	5.37	-	1753.2
AHQ-6-13, 6005	R.VISGVLQLGNIVFK.K	1487.81155	2	3.74E-05	0.96	3.79	-	1526.3
AHQ-6-2, 5967 - 6044	R.VISGVLQLGNIVFK.K	1487.81155	2	2.68E-06	0.95	4.49	-	1102.7
AHQ-6-5, 6012 - 6015	R.VISGVLQLGNIVFK.K	1487.81155	2	4.43E-07	0.94	3.51	-	1310.2
AHQ-6-1, 5646	R.VISGVLQLGNIVFKK.E	1615.98446	2	3.56E-04	0.92	3.58	-	1276.3
AHQ-6-2, 5582	R.VISGVLQLGNIVFKK.E	1615.98446	2	5.25E-06	0.91	3.99	-	941.7
AHQ-6-5, 5516	R.VISGVLQLGNIVFKK.E	1615.98446	2	1.20E-09	0.96	4.82	-	1146.7
AHQ-6-3, 5490 - 5552	R.VISGVLQLGNIVFKK.E	1615.98446	2	1.03E-07	0.90	3.53	-	941.0
AHQ-6-1, 4930	K.VSHLLGINVTDFTR.G	1572.79026	3	2.02E-05	0.91	4.50	-	752.8
AHQ-6-2, 4867	K.VSHLLGINVTDFTR.G	1572.79026	2	1.54E-06	0.87	3.32	-	953.3
AHQ-6-9, 4395	K.VSHLLGINVTDFTR.G	1572.79026	2	1.81E-04	0.82	2.90	-	803.1
AHQ-6-3, 4734 - 4792	K.VSHLLGINVTDFTR.G	1572.79026	2	3.12E-07	0.90	3.61	-	1053.3
AHQ-6-2, 4811	K.VSHLLGINVTDFTR.G	1572.79026	3	1.27E-06	0.92	3.58	-	1539.4
AHQ-6-5, 4747	K.VSHLLGINVTDFTR.G	1572.79026	2	4.99E-08	0.94	3.75	-	1243.0
AHQ-6-7, 4547	K.VSHLLGINVTDFTR.G	1572.79026	2	7.94E-12	0.94	4.25	-	1166.0
AHQ-6-4, 4819 - 4891	K.VSHLLGINVTDFTR.G	1572.79026	2	1.88E-08	0.96	4.45	-	1661.4
AHQ-6-2, 4746 - 4804	K.VSHLLGINVTDFTR.G	1572.79026	2	1.72E-08	0.93	4.10	-	1015.9
AHQ-6-1, 3463	R.VVFQEFR.Q	925.06580	2	4.29E-04	0.82	2.70	-	587.8
AHQ-6-2, 3950 - 3999	R.YEILTPNSIPK.G	1275.47536	2	5.12E-05	0.93	3.70	-	1135.2
AHQ-6-3, 4102	R.YEILTPNSIPK.G	1275.47536	2	2.54E-04	0.85	3.16	-	819.0
AHQ-6-4, 3921 - 3991	R.YEILTPNSIPK.G	1275.47536	2	9.67E-05	0.84	3.38	-	732.3
AHQ-6-4, 4113	R.YEILTPNSIPK.G	1275.47536	2	3.36E-06	0.91	2.96	-	1034.7
AHQ-6-10, 2218	K.YLYVDK.N	800.92145	1	2.46E-04	0.30	2.17	-	426.4
gi|4504745|ref|NP_000410.1|	integrin alpha 2b precursor [Homo sapiens]			1.83E-14	28.76	330.33	38.50	113374.2
AHQ-6-14-, 4978 - 5048	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.17E-05	0.82	2.84	-	940.4
AHQ-6-13-, 5048 - 5073	R.AEGGQCPSLLFDLR.D	1564.74505	2	6.09E-04	0.80	2.92	-	684.1
AHQ-6-4, 5112	R.AEGGQCPSLLFDLR.D	1564.74505	2	7.00E-06	0.95	3.98	-	1073.1
AHQ-6-11, 4884 - 4889	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.07E-06	0.85	3.42	-	783.9
AHQ-6-5, 5072	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.34E-06	0.95	4.19	-	1021.5
AHQ-6-7, 4811 - 4874	R.AEGGQCPSLLFDLR.D	1564.74505	2	4.57E-04	0.86	3.12	-	700.2
AHQ-6-10, 4782	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.33E-04	0.40	2.70	-	419.0

AHQ-6-6, 4942 - 5020	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.85E-05	0.86	3.45	-	812.0
AHQ-6-3, 5102	R.AEGGQCPSLLFDLR.D	1564.74505	2	6.08E-07	0.87	3.18	-	791.1
AHQ-6-7, 4862	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.63E-07	0.92	4.07	-	774.7
AHQ-6-4, 4692	R.AEGGQCPSLLFDLRDETR.N	2066.23814	3	3.76E-07	0.66	3.67	-	489.9
AHQ-6-6, 2846	R.ALSNVEGFER.L	1122.21308	2	7.72E-04	0.53	2.58	-	548.9
AHQ-6-4, 2879	R.ALSNVEGFER.L	1122.21308	2	6.07E-07	0.84	3.12	-	794.1
AHQ-6-7, 2782	R.ALSNVEGFER.L	1122.21308	2	1.80E-05	0.86	2.82	-	783.0
AHQ-6-3, 2944	R.ALSNVEGFER.L	1122.21308	2	6.04E-04	0.81	2.91	-	667.3
AHQ-6-5, 2856	R.ALSNVEGFER.L	1122.21308	2	3.93E-05	0.90	3.13	-	1042.3
AHQ-6-4, 4927 - 4987	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	5.08E-04	0.94	5.04	-	899.9
AHQ-6-4, 3073	R.DETRNVGSQTLQTFK.A	1724.85363	2	1.94E-05	0.83	3.08	-	1044.6
AHQ-6-4, 3975	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	9.19E-04	0.91	4.04	-	735.9
AHQ-6-6, 3691 - 3723	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	4.64E-05	0.84	3.78	-	544.0
AHQ-6-5, 3716 - 3741	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.05E-09	0.91	4.34	-	835.9
AHQ-6-4, 3875	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	6.77E-05	0.87	3.76	-	598.5
AHQ-6-4, 3775 - 3777	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.16E-10	0.95	4.81	-	874.5
AHQ-6-3, 3777	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	7.41E-05	0.85	3.72	-	706.6
AHQ-6-5, 5428 - 5487	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.64E-09	0.86	4.28	-	656.5
AHQ-6-5, 5523	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.89E-04	0.88	4.10	-	972.8
AHQ-6-5, 5604	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.71E-07	0.70	3.35	-	620.0
AHQ-6-3, 5542	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.50E-04	0.83	3.72	-	790.0
AHQ-6-4, 5607 - 5668	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	8.10E-04	0.93	5.09	-	820.2
AHQ-6-4, 5492 - 5551	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.32E-04	0.94	5.34	-	840.7
AHQ-6-4, 5935 - 5991	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	3.50E-04	0.82	4.12	-	771.5
AHQ-6-4, 6291 - 6353	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	4.37E-04	0.85	4.01	-	769.5
AHQ-6-4, 5891	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	2.39E-04	0.85	3.88	-	398.7
AHQ-6-3, 5686 - 5761	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	7.29E-05	0.67	3.49	-	466.9
AHQ-6-11, 4739	R.GEAQVWTQLLR.A	1301.47614	2	2.02E-04	0.76	3.26	-	546.4
AHQ-6-10, 4634 - 4650	R.GEAQVWTQLLR.A	1301.47614	2	1.42E-06	0.83	3.30	-	833.3
AHQ-6-1, 5115	R.GEAQVWTQLLR.A	1301.47614	2	1.12E-06	0.92	3.87	-	1043.7
AHQ-6-4, 5605	R.GNSFPASLVVAAEEGER.E	1733.86053	2	7.04E-07	0.26	2.54	-	444.0
AHQ-6-4, 5221 - 5279	R.GNSFPASLVVAAEEGER.E	1733.86053	2	6.09E-11	0.94	4.23	-	913.8
AHQ-6-4, 5399 - 5465	R.GNSFPASLVVAAEEGER.E	1733.86053	2	2.14E-11	0.92	4.14	-	981.9
AHQ-6-6, 5119	R.GNSFPASLVVAAEEGER.E	1733.86053	2	3.49E-04	0.38	2.68	-	413.4
AHQ-6-4, 5271 - 5339	R.GNSFPASLVVAAEEGER.E	1733.86053	2	8.17E-09	0.90	4.31	-	629.2
AHQ-6-4, 5109 - 5189	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.68E-05	0.89	3.74	-	781.4
AHQ-6-4, 6048 - 6107	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	3.82E-06	0.81	3.90	-	434.6
AHQ-6-4, 5920 - 5992	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	4.14E-05	0.67	3.36	-	389.1
AHQ-6-4, 5075 - 5137	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	7.46E-05	0.76	3.21	-	804.7
AHQ-6-4, 5080 - 5081	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	8.87E-09	0.98	6.21	-	1342.3
AHQ-6-3, 5080	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.43E-04	0.96	5.16	-	1188.2
AHQ-6-7, 4818	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.07E-06	0.94	4.67	-	732.8
AHQ-6-6, 4990 - 5000	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	5.27E-06	0.98	6.25	-	1214.6
AHQ-6-5, 5020	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	4.41E-04	0.85	3.33	-	981.0
AHQ-6-5, 5029	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.33E-10	0.97	5.64	-	1007.4
AHQ-6-7, 4812	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	7.35E-05	0.77	3.41	-	752.4
AHQ-6-3, 4900	R.GQVLVFLGQSEGLR.S	1503.72793	2	9.77E-04	0.94	4.11	-	1182.6
AHQ-6-6, 4806	R.GQVLVFLGQSEGLR.S	1503.72793	2	3.74E-07	0.96	4.39	-	1495.9
AHQ-6-4, 4989 - 5032	R.GQVLVFLGQSEGLR.S	1503.72793	2	4.24E-06	0.88	3.15	-	1191.3
AHQ-6-5, 4840	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.41E-07	0.96	4.66	-	1327.9
AHQ-6-4, 4907 - 4931	R.GQVLVFLGQSEGLR.S	1503.72793	2	5.21E-09	0.98	5.55	-	1651.7
AHQ-6-5, 3792	R.HDLLVGAPLYM*ESR.A	1617.85128	2	9.42E-05	0.90	3.69	-	825.2
AHQ-6-4, 3855	R.HDLLVGAPLYM*ESR.A	1617.85128	3	9.26E-05	0.82	3.45	-	995.6
AHQ-6-11, 4213 - 4216	K.IVLLDVPVR.A	1024.28196	2	9.98E-05	0.89	3.98	-	715.3
AHQ-6-4, 4377 - 4384	K.IVLLDVPVR.A	1024.28196	2	4.00E-04	0.91	3.40	-	982.6
AHQ-6-4, 4287	R.IYVENDFSWDK.R	1416.51610	2	8.24E-09	0.90	3.55	-	836.9
AHQ-6-4, 4124	R.IYVENDFSWDKR.Y	1572.70245	2	7.32E-10	0.88	3.34	-	1161.2
AHQ-6-4, 3920	R.IYVENDFSWDKR.Y	1572.70245	3	1.20E-05	0.80	3.06	-	682.0
AHQ-6-4, 3897 - 3959	R.IYVENDFSWDKR.Y	1572.70245	2	5.95E-06	0.90	3.46	-	990.7
AHQ-6-4, 4027	R.IYVENDFSWDKR.Y	1572.70245	2	3.13E-07	0.94	3.96	-	1219.6
AHQ-6-4, 4329	K.LSLNAELQLDR.Q	1272.43310	1	2.11E-04	0.40	1.99	-	580.9
AHQ-6-4, 4289 - 4357	K.LSLNAELQLDR.Q	1272.43310	2	3.68E-05	0.87	3.41	-	970.8
AHQ-6-4, 4483	K.LSLNAELQLDR.Q	1272.43310	2	1.83E-07	0.93	3.58	-	1158.2
AHQ-6-11, 2896	R.NVGSQTLQTFK.A	1223.36055	2	2.51E-04	0.84	3.08	-	498.3
AHQ-6-4, 6591 - 6653	R.QGLGASVVSWSDVIVACAPWQHWNVLEK.T	3139.53208	3	1.26E-08	0.93	5.49	-	592.7
AHQ-6-5, 6508	R.QGLGASVVSWSDVIVACAPWQHWNVLEK.T	3139.53208	3	2.92E-05	0.93	5.27	-	656.1
AHQ-6-4, 2104 - 2111	K.SCVLPQTK.T	934.09260	2	7.57E-04	0.56	2.64	-	521.8
AHQ-6-3, 5718	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	8.97E-05	0.97	6.40	-	1761.7
AHQ-6-4, 5561 - 5633	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.83E-14	0.97	6.36	-	1592.5
AHQ-6-7, 5482	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.05E-11	0.97	6.50	-	1708.0
AHQ-6-4, 5771	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	5.23E-04	0.82	3.65	-	381.5
AHQ-6-4, 5759 - 5819	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	8.49E-11	0.96	6.28	-	1227.3
AHQ-6-5, 5691	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	9.51E-09	0.93	5.28	-	938.0
AHQ-6-1, 5800	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	7.19E-04	0.83	3.49	-	1150.1
AHQ-6-5, 5669 - 5704	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	4.83E-05	0.52	2.86	-	311.5
AHQ-6-4, 3625 - 3703	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	3	2.03E-04	0.69	3.71	-	478.4
AHQ-6-6, 3619 - 3623	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	3	6.02E-04	0.70	3.56	-	651.1
AHQ-6-3, 3730	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	8.21E-04	0.89	4.06	-	502.5
AHQ-6-5, 3647	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	3	1.06E-04	0.84	3.45	-	1063.4
AHQ-6-4, 3645 - 3707	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.40E-09	0.90	4.27	-	484.1
AHQ-6-4, 3400 - 3401	K.TEEAEKTPVGSCFLAQPESGRR.A	2451.65537	3	1.05E-04	0.71	3.58	-	444.2
AHQ-6-11, 5121 - 5123	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.88E-06	0.89	3.85	-	905.4
AHQ-6-4, 5368 - 5447	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	7.69E-05	0.96	5.28	-	1128.5
AHQ-6-12, 5164	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.38E-06	0.91	3.75	-	937.3
AHQ-6-13-, 5266 - 5278	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.94E-06	0.82	3.79	-	680.6
AHQ-6-7, 5126	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.92E-06	0.89	4.08	-	683.3
AHQ-6-3, 5305 - 5361	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.00E-06	0.90	3.98	-	863.5
AHQ-6-11, 3584	K.TPVGSCFLAQPESGR.R	1607.76993	2	9.17E-04	0.62	2.68	-	468.1
AHQ-6-7, 3518	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.76E-06	0.84	3.74	-	496.8
AHQ-6-4, 3695 - 3760	K.TPVGSCFLAQPESGR.R	1607.76993	2	8.13E-04	0.95	3.89	-	1303.1
AHQ-6-12, 3639	K.TPVGSCFLAQPESGR.R	1607.76993	2	5.91E-04	0.79	3.11	-	749.8
AHQ-6-10, 3526	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.75E-04	0.76	3.25	-	454.3
AHQ-6-5, 3644 - 3651	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.18E-05	0.89	3.62	-	749.7
AHQ-6-3, 4430 - 4460	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	2.77E-04	0.78	3.36	-	822.7
AHQ-6-4, 4847 - 4917	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	3.03E-06	0.92	4.73	-	743.6
AHQ-6-5, 4360	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	1.73E-05	0.95	4.53	-	1460.1
AHQ-6-4, 4445	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	2	5.51E-04	0.77	3.06	-	719.2
AHQ-6-4, 4433	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	3.03E-05	0.92	3.74	-	1503.3
AHQ-6-4, 4524	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	9.18E-10	0.85	3.93	-	1012.7
AHQ-6-4, 2661	R.VAIVVGAPR.T	882.08560	2	3.35E-06	0.94	3.25	-	1242.6
AHQ-6-5, 2633	R.VAIVVGAPR.T	882.08560	2	1.49E-06	0.93	3.20	-	1330.6
AHQ-6-7, 2559	R.VAIVVGAPR.T	882.08560	2	8.33E-06	0.91	2.93	-	1132.5
AHQ-6-4, 5813 - 5839	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.04E-09	0.97	5.57	-	1292.1
AHQ-6-4, 5548 - 5611	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.51E-06	0.90	4.79	-	795.2
AHQ-6-4, 6668 - 6727	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	7.22E-08	0.98	5.85	-	2052.5
AHQ-6-4, 5681 - 5720	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.34E-04	0.96	5.57	-	1177.0
AHQ-6-5, 4000	R.VVLCELGNPMK.K	1261.53692	2	2.52E-05	0.88	3.39	-	940.9

AHQ-6-4, 3327	R.VVLCELGNPM*K.K	1277.53632	2	3.01E-05	0.89	3.28	-	1061.0
AHQ-6-4, 4063 - 4064	R.VVLCELGNPMK.K	1261.53692	2	2.66E-06	0.96	4.24	-	1484.7
AHQ-6-4, 4212	R.VYLFLQPR.G	1036.25129	2	9.00E-06	0.93	3.26	-	1189.9
gi|4506413|ref|NP_002875.1|	RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s			2.11E-14	8.00	90.34	49.50	20987.1
AHQ-6-11, 2512	K.CDLEDERVVGK.E	1321.43945	2	2.09E-05	0.90	3.27	-	1167.1
AHQ-6-11, 6329	R.DLYM*KNGQGFALVYSITAQSTFNDLQDLR.E	3326.68143	3	2.02E-08	0.89	4.48	-	1135.6
AHQ-6-11, 6188 - 6269	R.DLYM*KNGQGFALVYSITAQSTFNDLQDLR.E	3326.68143	3	2.11E-14	0.98	6.87	-	1714.8
AHQ-6-13, 6320	K.INVNEIFYDLVR.Q	1495.70427	2	4.38E-09	0.96	4.67	-	1490.5
AHQ-6-11, 6037	K.INVNEIFYDLVR.Q	1495.70427	2	1.75E-06	0.86	3.20	-	964.9
AHQ-6-11, 5140	K.INVNEIFYDLVR.Q	1495.70427	2	3.68E-04	0.88	3.24	-	1180.1
AHQ-6-11, 6148	K.INVNEIFYDLVR.Q	1495.70427	1	1.01E-04	0.40	2.60	-	190.2
AHQ-6-11, 6143	K.INVNEIFYDLVR.Q	1495.70427	1	8.31E-04	0.46	3.14	-	264.4
AHQ-6-11, 5441 - 5452	K.INVNEIFYDLVR.Q	1495.70427	2	1.18E-07	0.93	3.61	-	1336.1
AHQ-6-11, 6132 - 6195	K.INVNEIFYDLVR.Q	1495.70427	2	1.71E-08	0.96	5.06	-	1276.6
AHQ-6-14-, 5588	K.INVNEIFYDLVR.Q	1495.70427	2	4.89E-05	0.73	2.52	-	752.1
AHQ-6-12, 2863	K.LVVLGSGGVGK.S	986.19059	2	3.22E-04	0.56	2.74	-	460.0
AHQ-6-11, 2787 - 2844	K.LVVLGSGGVGK.S	986.19059	2	1.01E-05	0.92	3.83	-	973.7
AHQ-6-11, 6364 - 6373	K.NGQGFALVYSITAQSTFNDLQDLR.E	2659.89181	2	1.59E-05	0.95	4.56	-	1367.4
AHQ-6-11, 6227 - 6291	K.NGQGFALVYSITAQSTFNDLQDLR.E	2659.89181	2	4.25E-06	0.97	5.04	-	1655.0
AHQ-6-11, 5675 - 5743	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.72E-06	0.95	4.33	-	1291.5
AHQ-6-11, 5631	K.SALTVQFVQGIFVEK.Y	1666.94196	3	1.34E-04	0.94	3.60	-	1844.2
AHQ-6-11, 5431 - 5440	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.05E-05	0.82	3.45	-	713.9
AHQ-6-14-, 5762	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.31E-06	0.96	3.79	-	1770.5
AHQ-6-11, 5800 - 5871	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.53E-05	0.96	4.11	-	1940.8
AHQ-6-13-, 5798 - 5870	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.41E-04	0.96	4.87	-	1577.7
AHQ-6-11, 5927 - 5989	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.45E-05	0.94	4.68	-	1170.7
AHQ-6-11, 6328	K.SALTVQFVQGIFVEK.Y	1666.94196	2	4.68E-05	0.94	3.95	-	1241.2
AHQ-6-14-, 5863	K.SKINVNEIFYDLVR.Q	1710.95483	3	4.22E-05	0.90	3.57	-	1365.6
AHQ-6-11, 5696	K.SKINVNEIFYDLVR.Q	1710.95483	3	9.35E-05	0.78	3.43	-	852.3
AHQ-6-11, 5200	K.SKINVNEIFYDLVR.Q	1710.95483	2	5.48E-08	0.83	3.51	-	612.8
AHQ-6-11, 5011	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.15E-07	0.92	3.64	-	851.3
AHQ-6-11, 5692 - 5773	K.SKINVNEIFYDLVR.Q	1710.95483	2	3.47E-06	0.67	3.01	-	759.4
AHQ-6-11, 5827 - 5884	K.SKINVNEIFYDLVR.Q	1710.95483	2	7.00E-06	0.62	2.86	-	466.7
AHQ-6-14-, 5163	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.42E-04	0.63	3.06	-	562.5
AHQ-6-14-, 2842	K.YDPTIEDSYR.K	1259.30338	2	1.99E-05	0.80	2.59	-	396.7
AHQ-6-11, 2360 - 2361	K.YDPTIEDSYRK.Q	1387.47629	2	1.60E-05	0.69	2.77	-	451.3
AHQ-6-11, 2451	K.YDPTIEDSYRK.Q	1387.47629	2	1.95E-05	0.63	2.69	-	304.3
gi|4507485|ref|NP_003237.1|	thrombospondin 1 [Homo sapiens]			2.66E-14	35.28	410.33	33.80	129351.8
AHQ-6-2, 3994 - 4054	K.AGTLDLSLTVQGK.Q	1303.48711	2	1.58E-04	0.95	3.82	-	1404.1
AHQ-6-2, 4127	K.AGTLDLSLTVQGK.Q	1303.48711	2	4.09E-05	0.92	3.95	-	999.3
AHQ-6-4, 4021	K.AGTLDLSLTVQGK.Q	1303.48711	2	1.71E-06	0.94	3.86	-	1502.8
AHQ-6-6, 3903 - 3980	K.AGTLDLSLTVQGK.Q	1303.48711	2	1.46E-04	0.86	3.44	-	896.0
AHQ-6-3, 4092	K.AGTLDLSLTVQGK.Q	1303.48711	2	5.41E-04	0.96	3.79	-	1826.2
AHQ-6-2, 2814	R.AQLYIDCEK.M	1141.27636	2	8.47E-04	0.81	3.02	-	580.5
AHQ-6-6, 2736	R.AQLYIDCEK.M	1141.27636	2	5.11E-04	0.77	2.62	-	695.1
AHQ-6-2, 5663 - 5742	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	2.67E-08	0.96	6.05	-	1098.0
AHQ-6-5, 5620 - 5680	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	2.05E-06	0.95	6.03	-	947.0
AHQ-6-6, 3702 - 3707	R.CENTDPGYNCLPCPPR.F	1954.10800	2	3.41E-06	0.91	4.37	-	534.7
AHQ-6-5, 3601	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.57E-06	0.88	4.17	-	473.6
AHQ-6-3, 3776 - 3837	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.69E-05	0.83	3.41	-	520.9
AHQ-6-2, 3683	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.67E-08	0.91	3.81	-	659.3
AHQ-6-5, 3729	R.CENTDPGYNCLPCPPR.F	1954.10800	2	7.78E-06	0.90	3.34	-	829.4
AHQ-6-4, 3787	R.CENTDPGYNCLPCPPR.F	1954.10800	2	9.79E-04	0.81	3.37	-	496.4
AHQ-6-3, 3356 - 3364	K.CNYLGHYSDPM*YR.C	1693.84162	2	5.48E-04	0.89	3.67	-	630.2
AHQ-6-4, 3807	K.CNYLGHYSDPMYR.C	1677.84222	2	6.17E-04	0.94	3.99	-	890.5
AHQ-6-2, 3847 - 3855	K.CNYLGHYSDPMYR.C	1677.84222	2	1.98E-07	0.95	4.16	-	958.1
AHQ-6-3, 3805	K.CNYLGHYSDPMYR.C	1677.84222	2	5.79E-05	0.90	3.10	-	1093.2
AHQ-6-5, 3179	K.DCVGDVTENQICNK.Q	1654.75869	2	1.37E-04	0.93	3.98	-	1071.4
AHQ-6-3, 3240 - 3241	K.DCVGDVTENQICNK.Q	1654.75869	2	2.18E-06	0.96	4.47	-	1218.5
AHQ-6-6, 3178	K.DCVGDVTENQICNK.Q	1654.75869	2	2.51E-04	0.89	3.71	-	803.1
AHQ-6-2, 2826 - 2896	K.DHSGQVFSVVSNGK.A	1461.56164	2	4.89E-06	0.95	3.96	-	1429.6
AHQ-6-5, 2911 - 2943	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.51E-08	0.84	3.12	-	756.9
AHQ-6-6, 2916	K.DHSGQVFSVVSNGK.A	1461.56164	2	8.49E-06	0.95	3.93	-	1155.6
AHQ-6-2, 3002 - 3034	K.DHSGQVFSVVSNGK.A	1461.56164	2	6.43E-05	0.80	3.26	-	639.2
AHQ-6-3, 3000	K.DHSGQVFSVVSNGK.A	1461.56164	2	1.75E-06	0.92	3.40	-	1009.8
AHQ-6-6, 2807	K.DHSGQVFSVVSNGK.A	1461.56164	2	4.51E-05	0.96	3.50	-	1658.7
AHQ-6-3, 2832 - 2896	K.DHSGQVFSVVSNGK.A	1461.56164	2	1.36E-05	0.96	4.55	-	1489.9
AHQ-6-2, 6539	K.DLQAICGISCDELSSMVLELR.G	2412.74406	3	2.82E-10	0.97	5.10	-	1770.7
AHQ-6-3, 3172	R.DNCQYVYNVDQR.D	1575.64166	2	6.21E-07	0.86	3.36	-	929.2
AHQ-6-7, 2908	R.DNCQYVYNVDQR.D	1575.64166	2	4.86E-06	0.91	3.86	-	1008.9
AHQ-6-4, 3167	R.DNCQYVYNVDQR.D	1575.64166	2	2.50E-06	0.94	4.06	-	1576.1
AHQ-6-6, 2974	R.DNCQYVYNVDQR.D	1575.64166	2	9.17E-04	0.73	3.04	-	667.6
AHQ-6-2, 3155 - 3195	R.DNCQYVYNVDQR.D	1575.64166	2	9.12E-05	0.66	2.72	-	731.1
AHQ-6-2, 3059	R.DNCQYVYNVDQR.D	1575.64166	2	2.65E-05	0.69	2.84	-	867.9
AHQ-6-6, 3107 - 3131	R.DNCQYVYNVDQR.D	1575.64166	2	2.92E-05	0.93	3.66	-	1354.7
AHQ-6-3, 3048	R.DNCQYVYNVDQR.D	1575.64166	2	6.68E-06	0.93	4.01	-	992.6
AHQ-6-3, 3589 - 3649	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	8.94E-08	0.93	4.81	-	950.0
AHQ-6-3, 3680 - 3753	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.30E-13	0.92	4.94	-	784.9
AHQ-6-5, 3571 - 3631	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.41E-09	0.94	5.37	-	770.6
AHQ-6-6, 3570	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.66E-14	0.94	4.97	-	1151.1
AHQ-6-4, 3644	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.33E-10	0.92	4.84	-	790.6
AHQ-6-2, 4019	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.12E-05	0.95	5.46	-	748.5
AHQ-6-2, 3591 - 3654	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	6.14E-07	0.88	4.00	-	813.3
AHQ-6-2, 3714 - 3784	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.67E-09	0.94	5.40	-	878.4
AHQ-6-4, 3995	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.58E-05	0.94	5.22	-	803.6
AHQ-6-6, 3907	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.91E-07	0.93	5.13	-	824.4
AHQ-6-3, 3604	K.FQDLVDAVR.A	1063.18877	2	8.25E-06	0.88	3.06	-	975.7
AHQ-6-10, 3419 - 3424	K.FQDLVDAVR.A	1063.18877	2	1.95E-05	0.83	2.64	-	920.8
AHQ-6-2, 3626	K.FQDLVDAVR.A	1063.18877	2	2.46E-06	0.81	2.74	-	863.1
AHQ-6-3, 4192	R.FQMIPLDPK.G	1089.33277	2	1.82E-04	0.79	2.70	-	753.4
AHQ-6-5, 2803 - 2879	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.93E-09	0.70	3.19	-	304.0
AHQ-6-4, 3007	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	6.37E-07	0.78	3.67	-	327.3
AHQ-6-5, 2872	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.42E-06	0.93	4.38	-	668.9
AHQ-6-8, 2668	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.67E-04	0.85	3.89	-	594.7
AHQ-6-1, 3188	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.47E-04	0.79	3.44	-	536.8
AHQ-6-3, 3049	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	5.99E-05	0.62	3.22	-	280.2
AHQ-6-6, 2874 - 2876	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.52E-05	0.88	3.94	-	601.5
AHQ-6-2, 2976 - 3050	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.97E-07	0.89	4.31	-	506.9
AHQ-6-3, 2885 - 2960	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	9.48E-04	0.91	4.44	-	526.9
AHQ-6-4, 2911	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.94E-05	0.91	4.38	-	488.5
AHQ-6-11, 5047 - 5048	R.FVFGTTPEDILR.N	1395.58470	2	4.32E-05	0.64	3.06	-	427.0
AHQ-6-1, 5382	R.FVFGTTPEDILR.N	1395.58470	2	5.36E-04	0.74	2.57	-	681.4
AHQ-6-4, 5340	R.FVFGTTPEDILR.N	1395.58470	1	3.80E-04	0.10	2.01	-	175.2
AHQ-6-3, 5268	R.FVFGTTPEDILR.N	1395.58470	2	5.27E-04	0.78	2.63	-	804.8
AHQ-6-11, 5160	K.GFLLLASLR.Q	990.22407	2	3.87E-04	0.93	2.88	-	1516.5
AHQ-6-13, 5425	K.GFLLLASLR.Q	990.22407	2	6.22E-04	0.85	2.58	-	1004.8
AHQ-6-4, 5433	K.GFLLLASLR.Q	990.22407	2	4.26E-04	0.97	3.56	-	2266.4

AHQ-6-1, 5520	K.GFLLLASLR.Q	990.22407	2	8.29E-05	0.96	3.71	-	1936.0
AHQ-6-3, 5393	K.GFLLLASLR.Q	990.22407	2	2.00E-04	0.96	3.75	-	1951.3
AHQ-6-5, 5351	K.GFLLLASLR.Q	990.22407	2	3.30E-04	0.95	2.88	-	1885.5
AHQ-6-2, 5430 - 5444	K.GFLLLASLR.Q	990.22407	2	3.67E-05	0.97	4.03	-	2100.7
AHQ-6-7, 4266 - 4324	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.17E-04	0.85	3.37	-	983.3
AHQ-6-11, 4223	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.19E-04	0.65	2.91	-	483.0
AHQ-6-5, 4035 - 4105	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.19E-07	0.92	4.22	-	909.0
AHQ-6-6, 4402 - 4463	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.95E-05	0.90	4.32	-	746.6
AHQ-6-6, 4306	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.41E-07	0.89	3.62	-	918.3
AHQ-6-6, 4224	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.44E-07	0.85	4.05	-	582.6
AHQ-6-3, 4344 - 4409	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.98E-04	0.91	4.40	-	879.4
AHQ-6-10, 4091 - 4166	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.35E-04	0.90	4.06	-	923.8
AHQ-6-3, 4516	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.81E-06	0.79	3.54	-	661.7
AHQ-6-3, 4638	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.56E-06	0.75	3.37	-	622.2
AHQ-6-6, 4084 - 4152	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.75E-04	0.90	4.07	-	920.1
AHQ-6-4, 4523 - 4587	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.48E-04	0.75	3.20	-	603.2
AHQ-6-4, 4435 - 4459	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.17E-05	0.76	3.19	-	491.3
AHQ-6-4, 4337	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.63E-05	0.87	3.94	-	564.0
AHQ-6-2, 4663	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.11E-07	0.75	2.80	-	677.1
AHQ-6-5, 4272 - 4347	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.77E-05	0.90	3.55	-	918.2
AHQ-6-5, 4440 - 4501	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.34E-05	0.87	4.00	-	692.2
AHQ-6-2, 4380 - 4442	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.31E-08	0.91	4.52	-	805.1
AHQ-6-1, 4491 - 4548	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.96E-07	0.91	4.33	-	787.5
AHQ-6-7, 4102 - 4167	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.86E-05	0.77	3.66	-	560.7
AHQ-6-2, 2246	K.GPDPSSPAFR.I	1031.10364	2	5.57E-05	0.72	3.04	-	488.1
AHQ-6-3, 2246 - 2270	K.GPDPSSPAFR.I	1031.10364	2	4.82E-05	0.64	2.87	-	440.4
AHQ-6-5, 3075	R.GTLLALER.K	873.03234	2	2.31E-04	0.91	3.14	-	1191.1
AHQ-6-2, 3180	R.GTLLALER.K	873.03234	2	6.35E-04	0.91	3.27	-	1215.8
AHQ-6-10, 3020	R.GTLLALER.K	873.03234	2	7.34E-04	0.85	2.90	-	859.3
AHQ-6-4, 3147	R.GTLLALER.K	873.03234	2	3.16E-04	0.85	2.85	-	1038.4
AHQ-6-12, 3148	R.GTLLALER.K	873.03234	2	4.67E-04	0.79	2.98	-	782.2
AHQ-6-3, 2778	K.GTSQNDPNWVVR.H	1373.45608	2	2.98E-04	0.50	2.75	-	646.8
AHQ-6-4, 6128	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	4.43E-08	0.76	3.50	-	336.7
AHQ-6-8, 5922	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.32E-08	0.62	3.18	-	363.3
AHQ-6-3, 6036 - 6097	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.02E-13	0.82	3.86	-	390.9
AHQ-6-6, 5956 - 6022	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.11E-08	0.79	3.75	-	391.9
AHQ-6-13-, 5925	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.99E-04	0.67	3.18	-	349.1
AHQ-6-6, 6078	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.41E-04	0.72	3.29	-	373.7
AHQ-6-2, 6068 - 6126	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.51E-08	0.91	4.94	-	450.9
AHQ-6-7, 5814 - 5870	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	8.29E-08	0.86	4.36	-	391.8
AHQ-6-14-, 5922 - 5987	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.47E-06	0.81	3.71	-	380.1
AHQ-6-3, 6049 - 6108	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.35E-04	0.41	2.53	-	237.0
AHQ-6-3, 6152 - 6160	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.51E-04	0.77	3.48	-	491.7
AHQ-6-2, 2384 - 2431	K.IM*ADSGPIYDK.T	1226.38144	2	3.66E-05	0.75	3.23	-	485.2
AHQ-6-11, 2657	K.IMADSGPIYDK.T	1210.38204	2	6.13E-04	0.64	2.71	-	582.8
AHQ-6-12, 2413 - 2420	K.IM*ADSGPIYDK.T	1226.38144	2	4.60E-04	0.85	2.84	-	1032.0
AHQ-6-2, 2698	K.IMADSGPIYDK.T	1210.38204	2	5.13E-05	0.77	2.96	-	496.6
AHQ-6-6, 2638 - 2646	K.IMADSGPIYDK.T	1210.38204	2	1.32E-07	0.94	3.69	-	1025.3
AHQ-6-8, 2552	K.IMADSGPIYDK.T	1210.38204	2	7.08E-06	0.83	3.25	-	530.7
AHQ-6-3, 2708	K.IMADSGPIYDK.T	1210.38204	2	3.41E-05	0.94	3.49	-	1038.1
AHQ-6-12, 2700	K.IMADSGPIYDK.T	1210.38204	2	8.92E-05	0.81	3.27	-	545.6
AHQ-6-2, 6378 - 6435	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.70E-09	0.97	5.73	-	1245.7
AHQ-6-3, 6352 - 6353	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.86E-10	0.97	6.55	-	775.6
AHQ-6-13-, 6228	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.30E-09	0.96	5.48	-	874.0
AHQ-6-6, 6266 - 6327	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.58E-12	0.93	4.54	-	792.0
AHQ-6-1, 6407	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.94E-05	0.88	4.20	-	567.2
AHQ-6-10, 5986 - 6030	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.59E-04	0.64	3.34	-	315.1
AHQ-6-11, 6093	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.93E-04	0.61	2.88	-	417.2
AHQ-6-14-, 6242	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.62E-08	0.94	5.45	-	631.9
AHQ-6-5, 6305 - 6363	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	6.96E-10	0.98	5.96	-	1524.9
AHQ-6-5, 6348	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.70E-10	0.98	6.39	-	1326.4
AHQ-6-4, 6435	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.30E-11	0.96	5.20	-	1087.8
AHQ-6-7, 6130	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.31E-08	0.95	4.84	-	946.9
AHQ-6-3, 2490 - 2548	R.KDHSGQVFSVVSNGK.A	1589.73455	2	4.50E-05	0.78	3.14	-	503.0
AHQ-6-3, 2470	R.KDHSGQVFSVVSNGK.A	1589.73455	3	1.07E-04	0.92	4.21	-	1236.3
AHQ-6-3, 2406 - 2469	R.KDHSGQVFSVVSNGK.A	1589.73455	2	7.44E-07	0.84	3.24	-	788.8
AHQ-6-4, 2416 - 2479	R.KDHSGQVFSVVSNGK.A	1589.73455	2	4.03E-11	0.94	3.72	-	1316.7
AHQ-6-2, 2472	R.KDHSGQVFSVVSNGK.A	1589.73455	3	5.83E-06	0.87	3.61	-	1212.5
AHQ-6-5, 2384 - 2456	R.KDHSGQVFSVVSNGK.A	1589.73455	3	2.04E-05	0.88	3.62	-	1326.8
AHQ-6-2, 2478 - 2480	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.72E-07	0.87	3.84	-	691.7
AHQ-6-5, 2381 - 2447	R.KDHSGQVFSVVSNGK.A	1589.73455	2	2.35E-07	0.76	3.44	-	619.5
AHQ-6-2, 2574	R.KDHSGQVFSVVSNGK.A	1589.73455	2	7.00E-10	0.91	3.73	-	997.5
AHQ-6-6, 2395 - 2468	R.KDHSGQVFSVVSNGK.A	1589.73455	3	1.47E-05	0.90	3.48	-	1522.4
AHQ-6-6, 2391 - 2459	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.16E-06	0.44	2.74	-	336.8
AHQ-6-12, 2509 - 2552	K.KIMADSGPIYDK.T	1338.55496	2	5.08E-05	0.63	2.59	-	559.4
AHQ-6-2, 2482	R.KVTEENKELANELR.R	1673.84976	2	9.39E-11	0.94	4.27	-	1373.9
AHQ-6-3, 2218	R.KVTEENKELANELR.R	1673.84976	2	8.50E-09	0.94	4.20	-	1327.1
AHQ-6-2, 2214	R.KVTEENKELANELR.R	1673.84976	2	2.02E-09	0.96	4.87	-	1588.5
AHQ-6-4, 2431 - 2475	R.KVTEENKELANELR.R	1673.84976	2	1.67E-08	0.94	4.72	-	1340.0
AHQ-6-5, 2403 - 2461	R.KVTEENKELANELR.R	1673.84976	2	2.52E-06	0.93	4.90	-	747.1
AHQ-6-3, 2488	R.KVTEENKELANELR.R	1673.84976	3	1.30E-07	0.69	3.37	-	573.7
AHQ-6-8, 2267	R.KVTEENKELANELR.R	1673.84976	2	9.09E-08	0.93	4.63	-	1067.4
AHQ-6-3, 2484	R.KVTEENKELANELR.R	1673.84976	2	8.11E-11	0.90	4.62	-	889.0
AHQ-6-6, 2160	R.KVTEENKELANELR.R	1673.84976	2	1.82E-06	0.53	2.85	-	480.3
AHQ-6-4, 2552	R.KVTEENKELANELR.R	1673.84976	2	1.11E-09	0.96	5.10	-	1592.3
AHQ-6-9, 2343	R.KVTEENKELANELR.R	1673.84976	2	2.17E-04	0.80	2.99	-	732.6
AHQ-6-6, 2418	R.KVTEENKELANELR.R	1673.84976	3	3.82E-05	0.66	3.29	-	502.6
AHQ-6-6, 2406	R.KVTEENKELANELR.R	1673.84976	2	6.15E-04	0.74	3.65	-	489.1
AHQ-6-2, 2688	R.LCNNPAPQFGGK.D	1304.45694	2	2.69E-04	0.83	3.32	-	627.1
AHQ-6-5, 2629 - 2632	R.LCNNPAPQFGGK.D	1304.45694	2	2.43E-04	0.88	3.97	-	595.2
AHQ-6-4, 2669	R.LCNNPAPQFGGK.D	1304.45694	2	4.85E-06	0.85	3.88	-	531.6
AHQ-6-3, 2692	R.LCNNPAPQFGGK.D	1304.45694	2	2.37E-04	0.91	3.63	-	813.1
AHQ-6-2, 4194	R.LCNNPAPQFGGKDCVGDVTENQICNK.Q	2940.19303	3	6.29E-08	0.89	4.57	-	570.9
AHQ-6-3, 4161 - 4164	R.LCNNPAPQFGGKDCVGDVTENQICNK.Q	2940.19303	3	7.11E-07	0.89	5.03	-	554.7
AHQ-6-3, 2225	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	3	5.30E-04	0.87	3.93	-	813.1
AHQ-6-2, 2568	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	2.67E-08	0.92	4.29	-	641.9
AHQ-6-3, 2565 - 2568	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.09E-08	0.86	4.34	-	424.2
AHQ-6-6, 2192	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	5.68E-04	0.80	3.54	-	331.7
AHQ-6-3, 2222	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	3.68E-05	0.81	3.08	-	561.3
AHQ-6-4, 2537	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.68E-06	0.82	3.90	-	514.5
AHQ-6-6, 2519	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.52E-06	0.85	3.98	-	331.2
AHQ-6-2, 2231	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	2.31E-04	0.82	3.37	-	553.6
AHQ-6-4, 2188	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	1.85E-04	0.86	3.72	-	500.3
AHQ-6-5, 2508	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	8.02E-08	0.90	3.85	-	576.8
AHQ-6-4, 2192	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	3	2.32E-08	0.85	4.09	-	796.3
AHQ-6-5, 2169 - 2171	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	1.40E-05	0.89	4.19	-	583.0
AHQ-6-2, 6458 - 6536	R.LGLFVFSQEM*VFFSDLK.Y	2024.36769	2	5.10E-05	0.75	3.77	-	624.4

AHQ-6-6, 5078 - 5079	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	3.18E-10	0.88	4.29	-	572.3
AHQ-6-5, 5117 - 5128	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.21E-09	0.96	4.95	-	841.3
AHQ-6-3, 5149	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.37E-04	0.81	3.55	-	519.2
AHQ-6-4, 5211 - 5240	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	4.33E-11	0.96	5.22	-	827.4
AHQ-6-2, 5163 - 5219	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.79E-07	0.93	4.27	-	692.4
AHQ-6-6, 3054	K.QVTQSYWDTNPTR.A	1596.68241	2	2.04E-07	0.73	2.86	-	505.6
AHQ-6-5, 3055	K.QVTQSYWDTNPTR.A	1596.68241	2	6.45E-07	0.83	3.08	-	607.4
AHQ-6-8, 2928	K.QVTQSYWDTNPTR.A	1596.68241	2	3.47E-06	0.57	2.89	-	374.0
AHQ-6-7, 2971	K.QVTQSYWDTNPTR.A	1596.68241	2	1.25E-07	0.80	3.35	-	426.9
AHQ-6-6, 2828	R.RPPLCYHNGVQYR.N	1661.86889	2	2.81E-04	0.90	3.43	-	665.1
AHQ-6-3, 2786	R.RPPLCYHNGVQYR.N	1661.86889	2	1.78E-04	0.50	2.61	-	300.7
AHQ-6-4, 2737	R.RPPLCYHNGVQYR.N	1661.86889	2	1.10E-04	0.76	3.03	-	475.5
AHQ-6-4, 2856	R.RPPLCYHNGVQYR.N	1661.86889	2	8.14E-06	0.87	3.63	-	561.6
AHQ-6-4, 2859	R.RPPLCYHNGVQYR.N	1661.86889	3	3.60E-06	0.95	4.38	-	1435.4
AHQ-6-5, 2847	R.RPPLCYHNGVQYR.N	1661.86889	2	7.15E-05	0.77	3.17	-	525.2
AHQ-6-2, 2939 - 2942	R.RPPLCYHNGVQYR.N	1661.86889	2	4.48E-05	0.88	3.61	-	642.0
AHQ-6-5, 3751 - 3755	K.SITLFVQEDR.A	1208.34588	2	2.09E-06	0.93	3.58	-	1230.2
AHQ-6-3, 3832	K.SITLFVQEDR.A	1208.34588	2	1.20E-06	0.91	3.25	-	1069.3
AHQ-6-11, 3691	K.SITLFVQEDR.A	1208.34588	2	7.04E-06	0.87	3.25	-	845.6
AHQ-6-2, 3858	K.SITLFVQEDR.A	1208.34588	2	1.64E-06	0.94	3.87	-	1264.3
AHQ-6-6, 3708 - 3722	K.SITLFVQEDR.A	1208.34588	2	1.58E-06	0.95	3.73	-	1406.2
AHQ-6-10, 3618	K.SITLFVQEDR.A	1208.34588	2	1.51E-05	0.92	3.11	-	1573.4
AHQ-6-13, 3981	K.SITLFVQEDR.A	1208.34588	2	2.04E-04	0.90	3.17	-	1159.1
AHQ-6-4, 3813 - 3873	K.SITLFVQEDR.A	1208.34588	2	4.30E-06	0.92	3.52	-	1198.3
AHQ-6-5, 4267	R.TIVTTLQDSIR.K	1247.42355	2	5.67E-07	0.95	3.46	-	1383.4
AHQ-6-5, 3277	R.TIVTTLQDSIR.K	1247.42355	2	5.45E-05	0.97	3.48	-	2448.4
AHQ-6-6, 4223	R.TIVTTLQDSIR.K	1247.42355	2	1.04E-06	0.97	4.09	-	1806.4
AHQ-6-1, 4515	R.TIVTTLQDSIR.K	1247.42355	2	7.70E-07	0.97	3.95	-	1905.1
AHQ-6-2, 4382 - 4402	R.TIVTTLQDSIR.K	1247.42355	2	2.74E-06	0.96	4.12	-	1609.6
AHQ-6-4, 3348	R.TIVTTLQDSIR.K	1247.42355	2	4.57E-05	0.94	3.11	-	1750.6
AHQ-6-3, 4345 - 4368	R.TIVTTLQDSIR.K	1247.42355	2	6.21E-08	0.97	4.62	-	1540.5
AHQ-6-4, 4339 - 4353	R.TIVTTLQDSIR.K	1247.42355	2	5.05E-08	0.96	4.25	-	1584.6
AHQ-6-7, 4110	R.TIVTTLQDSIR.K	1247.42355	2	1.57E-07	0.95	3.83	-	1303.1
AHQ-6-2, 5958	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	4.87E-08	0.86	3.84	-	1038.7
AHQ-6-5, 5900	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	1.60E-07	0.95	4.91	-	1625.7
AHQ-6-2, 6454	K.TKDLQAICGISCDELSSMVLELR.G	2642.02130	3	3.07E-06	0.94	4.62	-	1835.2
AHQ-6-5, 6427 - 6428	K.TKDLQAICGISCDELSSMVLELR.G	2642.02130	3	5.09E-07	0.98	5.77	-	2296.9
AHQ-6-4, 2615 - 2651	K.VTEENKELANELR.R	1545.67685	2	3.42E-07	0.90	3.86	-	1076.1
AHQ-6-6, 2623	K.VTEENKELANELR.R	1545.67685	2	3.53E-09	0.87	3.63	-	842.1
AHQ-6-7, 2550 - 2551	K.VTEENKELANELR.R	1545.67685	2	3.48E-07	0.75	3.26	-	511.1
AHQ-6-3, 2688	K.VTEENKELANELR.R	1545.67685	2	4.10E-09	0.86	3.36	-	927.5
AHQ-6-5, 2624	K.VTEENKELANELR.R	1545.67685	2	1.32E-09	0.92	4.26	-	903.6
AHQ-6-4, 2807	K.VTEENKELANELR.R	1545.67685	2	1.18E-04	0.56	2.72	-	598.4
gi|9257257|ref|NP_059830.1|	WD repeat-containing protein 1 isoform 1 [Homo sapiens]			3.05E-14	1.81	20.22	7.90	66193.1
AHQ-6-6, 4196	R.LHHVSSLAWLDEHTLVTTSHDASVK.E	2785.06406	3	3.05E-14	0.92	4.41	-	953.1
AHQ-6-6, 4927	K.VVTVFSVADGYSENNVFYGHHAK.I	2541.75861	3	1.51E-07	0.89	4.38	-	521.7
gi|18104967|ref|NP_000953.2|	prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland			4.05E-14	4.64	50.36	16.20	68686.0
AHQ-6-6, 3923	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	2.41E-06	0.95	4.08	-	1013.6
AHQ-6-6, 3843 - 3854	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	3	1.95E-04	0.78	3.48	-	793.4
AHQ-6-6, 6487 - 6488	K.EM*AAELEELYGDIDALEFYPGLLLEK.C	2989.33908	3	5.07E-06	0.97	5.93	-	1564.5
AHQ-6-6, 6484	K.IVIEEYVQQLSGYFLQLK.F	2171.52045	3	4.05E-14	0.98	7.23	-	1981.8
AHQ-6-6, 3235 - 3294	R.VPDASQDDGPAVERPSTEL	1984.06747	2	1.21E-08	0.97	5.42	-	1074.5
gi|13562114|ref|NP_110400.1|	beta tubulin 1, class VI [Homo sapiens]			4.22E-14	15.48	180.37	53.90	50326.6
AHQ-6-7, 6254	K.AFVHWYTSEGMDINEFGEAENNIHDLVSEYQQFQDAK.A	4364.62586	3	1.59E-04	0.89	4.22	-	774.7
AHQ-6-14-, 5867	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.61E-04	0.95	4.47	-	1298.7
AHQ-6-13-, 4526	R.ALSVAELTQQM*FDAR.N	1696.90680	2	1.67E-04	0.90	3.52	-	1218.6
AHQ-6-14-, 4528	R.ALSVAELTQQM*FDAR.N	1696.90680	2	3.66E-05	0.91	3.73	-	872.6
AHQ-6-8, 4377 - 4378	R.ALSVAELTQQM*FDAR.N	1696.90680	2	1.46E-04	0.94	4.28	-	1365.9
AHQ-6-8, 5832	R.ALSVAELTQQMFDAR.N	1680.90740	2	5.77E-05	0.96	4.67	-	1596.4
AHQ-6-13, 3668	K.AVLEEDEEVTEEAEM*EPEDKGH	2532.58787	3	3.47E-05	0.77	3.48	-	604.9
AHQ-6-14-, 4667 - 4726	R.AVLVDLEPGTMDSIR.S	1616.86162	2	6.66E-08	0.95	4.45	-	914.5
AHQ-6-14-, 4046 - 4047	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	6.87E-06	0.91	4.14	-	676.1
AHQ-6-13-, 4062 - 4121	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	5.88E-08	0.90	3.99	-	695.3
AHQ-6-8, 4494	R.AVLVDLEPGTMDSIR.S	1616.86162	2	1.85E-05	0.91	3.97	-	739.0
AHQ-6-12, 4657	R.AVLVDLEPGTMDSIR.S	1616.86162	2	5.79E-08	0.86	3.19	-	665.5
AHQ-6-14, 4552 - 4617	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	8.81E-04	0.81	3.30	-	700.4
AHQ-6-12, 3739	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	6.21E-05	0.80	3.37	-	608.2
AHQ-6-14-, 3899	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	2.48E-08	0.96	4.78	-	1198.8
AHQ-6-9, 3515 - 3516	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	8.91E-06	0.71	3.11	-	564.0
AHQ-6-14-, 3792	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	2.24E-05	0.88	3.76	-	836.9
AHQ-6-8, 3097 - 3106	K.EVDQQLLSVQTR.N	1416.56231	2	3.90E-04	0.67	2.90	-	588.5
AHQ-6-14-, 5014	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	7.05E-07	0.87	3.12	-	1385.0
AHQ-6-14-, 5010	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	1.15E-05	0.96	4.79	-	1090.7
AHQ-6-9, 6026	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	7.80E-07	0.63	2.57	-	866.1
AHQ-6-13-, 6248	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	5.30E-06	0.94	4.96	-	1910.7
AHQ-6-14-, 6266	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	2.63E-04	0.84	4.03	-	1209.0
AHQ-6-13-, 6249 - 6250	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.22E-14	0.99	7.25	-	2530.8
AHQ-6-7, 6163	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	3.12E-11	0.98	6.50	-	2556.1
AHQ-6-13, 6288	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.17E-12	0.99	7.35	-	2687.7
AHQ-6-11, 6115	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.36E-04	0.80	3.49	-	1143.7
AHQ-6-14-, 6267 - 6268	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.84E-08	0.98	6.40	-	2561.7
AHQ-6-8, 6261	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.94E-07	0.98	6.59	-	2685.1
AHQ-6-7, 6167	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.81E-04	0.93	4.52	-	1782.7
AHQ-6-13-, 6038 - 6069	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	4.43E-07	0.93	4.61	-	863.6
AHQ-6-7, 5922	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	2.66E-04	0.62	2.97	-	427.9
AHQ-6-13, 6139	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	3	1.11E-04	0.69	3.03	-	784.8
AHQ-6-14-, 6192	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	2.41E-05	0.62	2.86	-	440.1
AHQ-6-14-, 5974 - 6030	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.17E-07	0.90	4.60	-	754.9
AHQ-6-14-, 6070	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	7.63E-06	0.86	3.97	-	715.1
AHQ-6-13-, 5921	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	4.54E-04	0.75	3.29	-	551.8
AHQ-6-11, 3169	R.ISVYYNEAYGR.K	1335.44622	2	6.09E-06	0.93	3.38	-	1078.9
AHQ-6-14, 4001 - 4072	R.ISVYYNEAYGR.K	1335.44622	2	2.03E-07	0.93	3.40	-	1031.2
AHQ-6-12, 3160 - 3203	R.ISVYYNEAYGR.K	1335.44622	2	4.36E-07	0.96	3.62	-	1684.3
AHQ-6-8, 3070 - 3090	R.ISVYYNEAYGR.K	1335.44622	2	4.37E-04	0.85	3.20	-	746.7
AHQ-6-13-, 3262 - 3321	R.ISVYYNEAYGR.K	1335.44622	2	1.79E-07	0.92	3.27	-	1390.2
AHQ-6-13-, 3388	R.ISVYYNEAYGR.K	1335.44622	2	8.07E-04	0.82	3.06	-	688.2
AHQ-6-14-, 3190	R.ISVYYNEAYGR.K	1335.44622	2	2.38E-07	0.94	3.82	-	1137.5
AHQ-6-14-, 3279	R.ISVYYNEAYGR.K	1335.44622	2	6.87E-06	0.79	2.65	-	795.7
AHQ-6-7, 3074 - 3078	R.ISVYYNEAYGR.K	1335.44622	2	1.99E-08	0.95	3.64	-	1222.8
AHQ-6-13-, 4878 - 4941	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	2.71E-08	0.84	3.97	-	874.9
AHQ-6-7, 4867	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	6.73E-07	0.90	3.75	-	716.3
AHQ-6-10, 4768	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	1.49E-05	0.81	3.14	-	635.4
AHQ-6-11, 5432	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	3.42E-05	0.85	3.50	-	1088.2
AHQ-6-8, 5461	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	2.21E-04	0.95	4.62	-	826.7
AHQ-6-8, 5460	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	2.44E-04	0.94	4.18	-	1641.8
AHQ-6-10, 5347 - 5354	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	3.85E-04	0.80	3.44	-	816.9
AHQ-6-13-, 5024 - 5029	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	1.49E-04	0.95	4.59	-	1831.5

AHQ-6-7, 5442 - 5443	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	7.63E-04	0.96	5.30	-	1677.0
AHQ-6-9, 5281	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	1.28E-04	0.75	3.27	-	428.8
AHQ-6-8, 6181 - 6236	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	1.25E-04	0.91	4.18	-	1087.4
AHQ-6-14-, 6195	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	6.79E-04	0.83	3.44	-	1108.2
AHQ-6-7, 6039 - 6094	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	3.94E-06	0.73	3.20	-	865.6
AHQ-6-8, 4925 - 4997	R.NSSCFVEWIPNNVK.V	1695.87718	2	3.58E-04	0.50	2.78	-	606.6
AHQ-6-12, 5008	R.NSSCFVEWIPNNVK.V	1695.87718	2	2.95E-04	0.73	2.84	-	587.5
AHQ-6-10, 4880 - 4935	R.NSSCFVEWIPNNVK.V	1695.87718	2	1.64E-05	0.62	2.91	-	501.1
AHQ-6-14-, 3228	R.VSEHFSAMFK.R	1183.36152	2	6.80E-07	0.91	2.94	-	1329.3
gi|4826898|ref|NP_005013.1| profilin 1; profilin-1 [Homo sapiens]				5.33E-14	12.86	140.29	67.10	15054.2
AHQ-6-13, 2240 - 2315	K.CYEM*ASHLR.R	1184.32794	2	1.25E-04	0.89	3.06	-	1110.4
AHQ-6-13-, 2533 - 2588	K.CYEMASHLR.R	1168.32854	2	3.46E-04	0.96	3.39	-	2018.3
AHQ-6-13-, 1886 - 1958	K.CYEM*ASHLR.R	1184.32794	2	7.50E-04	0.87	2.85	-	1189.7
AHQ-6-13-, 2000 - 2056	K.CYEM*ASHLR.R	1184.32794	2	5.40E-04	0.90	2.70	-	1360.7
AHQ-6-13, 2116 - 2196	K.CYEM*ASHLR.R	1184.32794	2	2.21E-04	0.88	3.30	-	870.1
AHQ-6-13-, 4162 - 4221	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	8.18E-13	0.98	5.68	-	1482.7
AHQ-6-13, 4149	K.DRSSFYVNGLTLGGQK.C	1742.91379	3	1.36E-05	0.93	4.38	-	1330.2
AHQ-6-13, 4152	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	5.33E-14	0.97	5.24	-	1314.2
AHQ-6-13, 4285	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	3.20E-07	0.94	4.46	-	845.7
AHQ-6-12, 4853 - 4933	R.DSLLQDGEFSMDLR.T	1626.77023	2	8.50E-07	0.93	3.56	-	1257.3
AHQ-6-12, 5005	R.DSLLQDGEFSMDLR.T	1626.77023	2	6.81E-06	0.70	2.71	-	613.2
AHQ-6-13-, 4994 - 5052	R.DSLLQDGEFSMDLR.T	1626.77023	2	6.45E-07	0.96	3.94	-	1580.4
AHQ-6-13-, 4892	R.DSLLQDGEFSMDLR.T	1626.77023	2	6.07E-05	0.94	3.88	-	1304.3
AHQ-6-13-, 4813 - 4890	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.95E-05	0.88	3.65	-	996.8
AHQ-6-13-, 4653	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.33E-04	0.94	4.15	-	1327.3
AHQ-6-12, 4432 - 4448	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.06E-05	0.90	3.45	-	1078.0
AHQ-6-12, 4305	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.57E-06	0.85	2.79	-	1225.6
AHQ-6-13-, 4572	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.65E-10	0.97	4.54	-	1693.6
AHQ-6-13-, 4445 - 4500	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.90E-08	0.96	4.54	-	1697.1
AHQ-6-13-, 4324 - 4384	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.87E-07	0.96	4.38	-	1577.3
AHQ-6-13-, 5002 - 5081	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.86E-06	0.64	3.09	-	571.2
AHQ-6-13-, 5108 - 5164	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.87E-09	0.97	4.85	-	1964.0
AHQ-6-13-, 5168 - 5170	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.03E-04	0.92	3.27	-	1648.8
AHQ-6-13-, 5220 - 5276	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.72E-05	0.97	4.40	-	1940.1
AHQ-6-14, 5238	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.34E-05	0.95	3.82	-	1817.3
AHQ-6-13, 5705	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.22E-05	0.71	2.84	-	769.2
AHQ-6-14-, 4459 - 4518	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.16E-11	0.97	4.57	-	1815.8
AHQ-6-13, 5331 - 5392	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.09E-07	0.94	3.30	-	1512.2
AHQ-6-13-, 5334	R.DSLLQDGEFSMDLR.T	1626.77023	2	9.32E-06	0.97	3.76	-	2301.1
AHQ-6-14-, 4374	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.44E-08	0.92	3.92	-	855.7
AHQ-6-13, 5449	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.98E-08	0.97	3.62	-	2358.3
AHQ-6-13, 5235 - 5291	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.05E-09	0.97	4.42	-	1809.2
AHQ-6-13, 5129	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.46E-06	0.92	4.19	-	908.5
AHQ-6-13, 5119 - 5181	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.57E-04	0.95	4.49	-	1193.2
AHQ-6-13, 4460 - 4519	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.53E-08	0.96	4.14	-	1726.1
AHQ-6-13, 5019	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.27E-05	0.89	3.54	-	941.8
AHQ-6-13, 4905	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.13E-04	0.60	2.62	-	732.3
AHQ-6-13, 4577 - 4647	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.76E-10	0.96	4.02	-	1746.6
AHQ-6-13, 4633	R.DSLLQDGEFSM*DLR.T	1642.76963	3	5.59E-04	0.94	4.01	-	2008.6
AHQ-6-13, 4703 - 4773	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.12E-07	0.96	4.16	-	2120.8
AHQ-6-13-, 3568 - 3628	K.DSPSVWAAVPGK.T	1214.35211	2	1.30E-07	0.86	3.57	-	819.6
AHQ-6-13, 3727 - 3783	K.DSPSVWAAVPGK.T	1214.35211	2	3.84E-05	0.86	2.96	-	1055.9
AHQ-6-12, 3551 - 3555	K.DSPSVWAAVPGK.T	1214.35211	2	1.43E-06	0.86	3.22	-	803.1
AHQ-6-13, 3861 - 3915	K.DSPSVWAAVPGK.T	1214.35211	2	5.44E-06	0.63	2.56	-	726.9
AHQ-6-13, 3531	K.DSPSVWAAVPGK.T	1214.35211	2	8.90E-04	0.81	2.88	-	843.5
AHQ-6-14-, 4375 - 4439	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.39E-09	0.95	4.12	-	1298.8
AHQ-6-14-, 4250	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.62E-07	0.95	3.89	-	1032.1
AHQ-6-13, 4355	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.34E-07	0.39	2.38	-	341.0
AHQ-6-13, 4432 - 4513	R.SSFYVNGLTLGGQK.C	1471.63957	2	5.74E-09	0.96	4.49	-	1206.1
AHQ-6-12, 4185 - 4207	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.22E-10	0.96	4.57	-	949.7
AHQ-6-12, 4201	R.SSFYVNGLTLGGQK.C	1471.63957	1	4.55E-08	0.44	2.19	-	421.4
AHQ-6-13, 4496 - 4559	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.89E-08	0.62	2.99	-	488.7
AHQ-6-13-, 4378 - 4440	R.SSFYVNGLTLGGQK.C	1471.63957	2	5.98E-10	0.96	4.59	-	1331.0
AHQ-6-14, 4990	R.SSFYVNGLTLGGQK.C	1471.63957	2	9.90E-05	0.71	2.91	-	420.1
AHQ-6-14, 5106 - 5164	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.23E-04	0.89	3.55	-	890.6
AHQ-6-13, 4347 - 4371	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.03E-06	0.92	3.93	-	714.1
AHQ-6-13-, 4360 - 4420	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.61E-08	0.80	3.30	-	554.4
AHQ-6-13-, 4241 - 4308	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.00E-08	0.90	3.71	-	804.3
AHQ-6-13-, 4224	R.SSFYVNGLTLGGQK.C	1471.63957	1	9.19E-08	0.71	2.93	-	635.7
AHQ-6-13, 4571 - 4639	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.58E-09	0.97	4.75	-	1636.7
AHQ-6-13, 3319 - 3391	K.STGGAPTFNVTVTK.T	1380.52843	2	2.48E-11	0.78	3.02	-	482.3
AHQ-6-12, 3188	K.STGGAPTFNVTVTK.T	1380.52843	1	8.51E-04	0.22	2.14	-	365.5
AHQ-6-13, 3447 - 3503	K.STGGAPTFNVTVTK.T	1380.52843	2	5.40E-04	0.75	3.04	-	299.0
AHQ-6-13-, 3062 - 3120	K.STGGAPTFNVTVTK.T	1380.52843	2	2.55E-04	0.87	3.49	-	511.9
AHQ-6-13-, 3118	K.STGGAPTFNVTVTK.T	1380.52843	1	2.61E-04	0.53	2.39	-	501.5
AHQ-6-13-, 3210	K.STGGAPTFNVTVTK.T	1380.52843	1	9.01E-05	0.46	2.81	-	407.6
AHQ-6-13-, 3260 - 3320	K.STGGAPTFNVTVTK.T	1380.52843	2	3.10E-06	0.85	3.18	-	456.0
AHQ-6-13, 3184 - 3260	K.STGGAPTFNVTVTK.T	1380.52843	2	3.82E-06	0.89	3.69	-	543.9
AHQ-6-13, 3269	K.STGGAPTFNVTVTK.T	1380.52843	1	1.73E-07	0.59	2.58	-	604.7
AHQ-6-12, 3169 - 3207	K.STGGAPTFNVTVTK.T	1380.52843	2	1.94E-08	0.88	3.81	-	458.1
AHQ-6-13-, 3040 - 3094	K.TDKTLVLLM*GK.E	1235.51929	2	4.92E-04	0.92	3.65	-	1014.0
AHQ-6-12, 3671	K.TDKTLVLLMGK.E	1219.51989	2	2.17E-04	0.82	2.89	-	1036.5
AHQ-6-13, 3183 - 3199	K.TDKTLVLLM*GK.E	1235.51929	2	9.77E-07	0.92	3.57	-	966.4
AHQ-6-13-, 3729	K.TDKTLVLLMGK.E	1219.51989	3	9.25E-05	0.93	3.72	-	1839.9
AHQ-6-14, 6249 - 6257	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.48E-04	0.87	3.78	-	894.0
AHQ-6-13-, 5506 - 5518	K.TFVNITPAEVGVLVGK.D	1644.93630	3	2.28E-04	0.92	4.22	-	1230.3
AHQ-6-13, 5365 - 5444	K.TFVNITPAEVGVLVGK.D	1644.93630	2	5.90E-04	0.66	3.21	-	397.2
AHQ-6-13-, 5274 - 5358	K.TFVNITPAEVGVLVGK.D	1644.93630	2	5.65E-05	0.83	4.05	-	547.9
AHQ-6-12, 5579	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.16E-05	0.90	3.69	-	873.1
AHQ-6-12, 5465	K.TFVNITPAEVGVLVGK.D	1644.93630	3	1.25E-07	0.93	3.86	-	1399.9
AHQ-6-12, 5445 - 5499	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.59E-05	0.88	3.62	-	644.4
AHQ-6-13, 5511 - 5571	K.TFVNITPAEVGVLVGK.D	1644.93630	2	6.57E-06	0.92	4.24	-	813.1
AHQ-6-13, 5627 - 5707	K.TFVNITPAEVGVLVGK.D	1644.93630	2	6.92E-06	0.93	4.23	-	984.8
AHQ-6-13, 5589 - 5608	K.TFVNITPAEVGVLVGK.D	1644.93630	3	1.00E-09	0.97	5.83	-	1563.4
AHQ-6-13-, 5440 - 5504	K.TFVNITPAEVGVLVGK.D	1644.93630	2	9.22E-05	0.92	3.74	-	974.8
AHQ-6-12, 5187	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	8.19E-06	0.55	3.12	-	526.4
AHQ-6-13, 5921	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	2.18E-06	0.87	3.63	-	675.9
AHQ-6-13-, 5205 - 5273	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	1.81E-07	0.90	4.12	-	633.2
AHQ-6-13, 3501	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	4.92E-04	0.43	2.61	-	281.2
AHQ-6-13-, 2948	R.TKSTGGAPTFNVTVTK.T	1609.80568	3	1.64E-04	0.87	3.91	-	1080.2
AHQ-6-13-, 2858 - 2933	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	1.33E-07	0.96	4.79	-	1006.7
AHQ-6-13, 3073 - 3100	R.TKSTGGAPTFNVTVTK.T	1609.80568	3	1.06E-04	0.78	3.54	-	773.8
AHQ-6-12, 2903	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	4.49E-06	0.90	3.77	-	743.0
AHQ-6-13, 3943 - 4003	K.TLVLLMGK.E	875.15478	2	1.18E-05	0.84	2.70	-	745.4
AHQ-6-13-, 3801 - 3860	K.TLVLLMGK.E	875.15478	2	1.42E-04	0.83	2.80	-	678.8
gi|4501881|ref|NP_001091.1| alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA				7.94E-14	9.57	130.27	28.40	42050.8
AHQ-6-8, 1882 - 1948	K.AGFAGDDAPR.A	977.01283	2	7.22E-04	0.75	2.63	-	1041.4

AHQ-6-8, 1998 - 2064	K.AGFAGDDAPR.A	977.01283	2	1.26E-04	0.89	3.35	-	995.6
AHQ-6-14, 4166	R.AVFPSIVGRPR.H	1199.43018	2	9.90E-04	0.14	2.53	-	248.5
AHQ-6-8, 3437	R.DLTDYLM*K.I	1015.16266	2	9.03E-04	0.69	2.76	-	391.7
AHQ-6-9, 3402	R.DLTDYLM*K.I	1015.16266	1	4.53E-04	0.35	2.51	-	136.1
AHQ-6-8, 3406 - 3464	R.DLTDYLM*K.I	1015.16266	1	5.86E-04	0.20	1.97	-	101.6
AHQ-6-12, 3601	R.DLTDYLM*K.I	1015.16266	2	7.85E-04	0.66	2.57	-	426.5
AHQ-6-8, 4413	R.DLTDYLMK.I	999.16326	1	4.26E-04	0.39	1.94	-	481.8
AHQ-6-8, 4049 - 4085	R.DLTDYLMK.I	999.16326	2	4.06E-05	0.86	3.21	-	430.7
AHQ-6-8, 1638 - 1694	K.DSYVGDEAQSK.R	1199.20634	2	3.83E-05	0.77	3.06	-	882.2
AHQ-6-8, 1588 - 1726	K.DSYVGDEAQSK.R	1199.20634	1	1.64E-04	0.80	3.28	-	465.3
AHQ-6-8, 1544 - 1582	K.DSYVGDEAQSK.R	1199.20634	2	8.46E-06	0.85	3.57	-	983.6
AHQ-6-13, 3211	K.EITALAPSTMK.I	1162.38206	1	2.81E-04	0.14	2.04	-	224.5
AHQ-6-10, 2890 - 2907	K.EITALAPSTMK.I	1162.38206	2	6.90E-05	0.73	2.84	-	568.9
AHQ-6-14, 3212 - 3284	K.EITALAPSTM*K.I	1178.38146	2	6.69E-05	0.61	2.68	-	585.8
AHQ-6-14-, 3022	K.EITALAPSTMK.I	1162.38206	1	3.71E-05	0.48	2.22	-	299.1
AHQ-6-13, 2615 - 2675	K.EITALAPSTM*K.I	1178.38146	2	9.29E-04	0.56	2.67	-	435.3
AHQ-6-13-, 2472 - 2532	K.EITALAPSTM*K.I	1178.38146	2	2.93E-05	0.86	3.32	-	744.8
AHQ-6-8, 2270 - 2330	K.EITALAPSTM*K.I	1178.38146	2	1.94E-05	0.85	3.46	-	610.2
AHQ-6-8, 2878	K.EITALAPSTMK.I	1162.38206	1	4.47E-04	0.21	2.01	-	265.3
AHQ-6-8, 2745 - 2804	K.IWHHTFYNELR.V	1516.68695	3	8.20E-05	0.95	5.22	-	1604.8
AHQ-6-8, 2848 - 2920	K.IWHHTFYNELR.V	1516.68695	2	4.02E-07	0.92	3.54	-	880.4
AHQ-6-8, 2728 - 2805	K.IWHHTFYNELR.V	1516.68695	2	7.60E-04	0.74	3.14	-	772.0
AHQ-6-8, 3066 - 3124	K.IWHHTFYNELR.V	1516.68695	2	8.04E-08	0.91	3.46	-	1056.1
AHQ-6-9, 3066 - 3142	K.IWHHTFYNELR.V	1516.68695	2	1.34E-07	0.77	2.71	-	710.1
AHQ-6-12, 3201	K.IWHHTFYNELR.V	1516.68695	3	1.49E-05	0.86	4.11	-	1057.7
AHQ-6-8, 4933 - 4984	R.LDLAGRDLTDYLMK.I	1624.88375	2	5.19E-07	0.86	3.59	-	742.0
AHQ-6-6, 4858	K.SYELPDGQVITIGNER.F	1791.93998	2	6.62E-07	0.80	2.92	-	784.8
AHQ-6-13-, 4844 - 4906	K.SYELPDGQVITIGNER.F	1791.93998	2	4.60E-10	0.96	4.53	-	1190.4
AHQ-6-6, 4736 - 4774	K.SYELPDGQVITIGNER.F	1791.93998	2	6.58E-04	0.88	3.55	-	791.5
AHQ-6-8, 4076 - 4124	K.SYELPDGQVITIGNER.F	1791.93998	2	7.22E-07	0.93	3.59	-	1050.2
AHQ-6-13-, 4701 - 4756	K.SYELPDGQVITIGNER.F	1791.93998	2	4.50E-09	0.88	3.52	-	798.7
AHQ-6-13-, 4369	K.SYELPDGQVITIGNER.F	1791.93998	2	2.81E-07	0.92	3.89	-	763.9
AHQ-6-8, 4208 - 4268	K.SYELPDGQVITIGNER.F	1791.93998	2	4.13E-09	0.95	4.59	-	1008.3
AHQ-6-8, 4233	K.SYELPDGQVITIGNER.F	1791.93998	3	1.81E-08	0.95	4.62	-	1501.6
AHQ-6-8, 4324 - 4325	K.SYELPDGQVITIGNER.F	1791.93998	2	1.09E-11	0.96	4.72	-	1223.1
AHQ-6-5, 4896 - 4899	K.SYELPDGQVITIGNER.F	1791.93998	2	6.80E-09	0.94	4.14	-	957.1
AHQ-6-5, 4767	K.SYELPDGQVITIGNER.F	1791.93998	2	2.19E-08	0.96	4.63	-	1302.4
AHQ-6-8, 4448 - 4514	K.SYELPDGQVITIGNER.F	1791.93998	2	9.95E-07	0.96	4.78	-	968.1
AHQ-6-8, 4517	K.SYELPDGQVITIGNER.F	1791.93998	3	1.58E-07	0.94	4.37	-	1220.2
AHQ-6-8, 4572 - 4650	K.SYELPDGQVITIGNER.F	1791.93998	2	1.15E-12	0.97	5.37	-	1167.4
AHQ-6-4, 4487	K.SYELPDGQVITIGNER.F	1791.93998	2	6.93E-05	0.92	3.98	-	875.6
AHQ-6-7, 4215	K.SYELPDGQVITIGNER.F	1791.93998	2	2.01E-06	0.87	3.29	-	734.0
AHQ-6-8, 4768 - 4828	K.SYELPDGQVITIGNER.F	1791.93998	2	6.61E-11	0.96	4.63	-	1232.9
AHQ-6-14-, 4734	K.SYELPDGQVITIGNER.F	1791.93998	2	1.07E-10	0.95	4.26	-	1343.3
AHQ-6-7, 4586	K.SYELPDGQVITIGNER.F	1791.93998	2	5.22E-06	0.90	3.56	-	863.0
AHQ-6-3, 4952	K.SYELPDGQVITIGNER.F	1791.93998	2	3.78E-08	0.85	3.62	-	584.5
AHQ-6-2, 4990	K.SYELPDGQVITIGNER.F	1791.93998	2	1.41E-04	0.91	3.81	-	840.5
AHQ-6-9, 4019 - 4096	K.SYELPDGQVITIGNER.F	1791.93998	2	4.63E-09	0.95	4.91	-	846.6
AHQ-6-9, 4110 - 4190	K.SYELPDGQVITIGNER.F	1791.93998	2	2.50E-08	0.94	4.25	-	959.2
AHQ-6-9, 4380 - 4450	K.SYELPDGQVITIGNER.F	1791.93998	2	7.27E-13	0.96	5.04	-	1083.5
AHQ-6-9, 4528 - 4582	K.SYELPDGQVITIGNER.F	1791.93998	2	2.99E-10	0.92	4.08	-	790.1
AHQ-6-9, 4638 - 4639	K.SYELPDGQVITIGNER.F	1791.93998	2	2.44E-04	0.92	4.38	-	931.5
AHQ-6-2, 4832 - 4839	K.SYELPDGQVITIGNER.F	1791.93998	2	4.31E-07	0.85	3.23	-	834.2
AHQ-6-10, 4099 - 4154	K.SYELPDGQVITIGNER.F	1791.93998	2	8.94E-05	0.71	3.15	-	409.0
AHQ-6-10, 4242	K.SYELPDGQVITIGNER.F	1791.93998	2	1.13E-06	0.90	3.29	-	887.5
AHQ-6-10, 4448 - 4526	K.SYELPDGQVITIGNER.F	1791.93998	2	7.94E-14	0.97	4.86	-	1357.6
AHQ-6-10, 4508	K.SYELPDGQVITIGNER.F	1791.93998	3	9.50E-07	0.96	4.80	-	1811.0
AHQ-6-10, 4610 - 4667	K.SYELPDGQVITIGNER.F	1791.93998	2	1.21E-11	0.96	4.57	-	1168.2
AHQ-6-11, 4200 - 4259	K.SYELPDGQVITIGNER.F	1791.93998	2	5.61E-04	0.43	2.68	-	536.5
AHQ-6-11, 4255	K.SYELPDGQVITIGNER.F	1791.93998	2	1.60E-08	0.92	3.91	-	767.8
AHQ-6-11, 4547 - 4621	K.SYELPDGQVITIGNER.F	1791.93998	2	4.14E-09	0.90	3.43	-	832.6
AHQ-6-11, 4589	K.SYELPDGQVITIGNER.F	1791.93998	3	4.64E-10	0.95	4.31	-	1427.5
AHQ-6-11, 4700	K.SYELPDGQVITIGNER.F	1791.93998	2	2.13E-06	0.92	3.79	-	902.2
AHQ-6-8, 4713 - 4772	K.SYELPDGQVITIGNER.F	1791.93998	2	6.69E-11	0.95	4.24	-	1149.9
AHQ-6-1, 5043	K.SYELPDGQVITIGNER.F	1791.93998	2	2.41E-06	0.92	3.62	-	1006.6
AHQ-6-12, 4229	K.SYELPDGQVITIGNER.F	1791.93998	2	4.34E-08	0.94	3.94	-	1066.9
AHQ-6-12, 4321 - 4385	K.SYELPDGQVITIGNER.F	1791.93998	2	1.78E-09	0.93	4.31	-	779.6
AHQ-6-12, 4635	K.SYELPDGQVITIGNER.F	1791.93998	2	1.56E-08	0.92	4.06	-	804.1
AHQ-6-12, 4757 - 4836	K.SYELPDGQVITIGNER.F	1791.93998	2	1.49E-09	0.94	4.55	-	829.4
AHQ-6-1, 4916	K.SYELPDGQVITIGNER.F	1791.93998	2	2.68E-07	0.93	4.10	-	923.7
AHQ-6-1, 4587 - 4663	K.SYELPDGQVITIGNER.F	1791.93998	2	8.04E-04	0.77	2.99	-	540.1
AHQ-6-13, 4484	K.SYELPDGQVITIGNER.F	1791.93998	2	3.12E-09	0.95	4.04	-	1117.2
AHQ-6-13, 4836	K.SYELPDGQVITIGNER.F	1791.93998	2	3.32E-06	0.91	4.03	-	723.3
AHQ-6-13, 4964 - 4988	K.SYELPDGQVITIGNER.F	1791.93998	2	1.16E-09	0.95	4.23	-	1191.0
AHQ-6-14-, 4875	K.SYELPDGQVITIGNER.F	1791.93998	2	4.00E-05	0.94	3.78	-	1237.4
AHQ-6-9, 3559 - 3616	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	7.07E-04	0.68	3.18	-	480.7
AHQ-6-8, 4106 - 4168	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.40E-05	0.88	3.85	-	788.9
AHQ-6-8, 4678	K.YPIEHGIITNWDDMEK.I	1962.17174	2	9.50E-07	0.89	4.11	-	669.9
AHQ-6-8, 3912 - 3992	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.76E-06	0.91	3.96	-	1123.8
AHQ-6-8, 3822 - 3880	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	2.27E-04	0.82	3.41	-	704.0
AHQ-6-8, 3793 - 3820	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	1.86E-04	0.85	3.70	-	668.1
AHQ-6-8, 4100 - 4160	K.YPIEHGIITNWDDMEK.I	1962.17174	3	3.25E-05	0.87	3.98	-	1224.4
AHQ-6-8, 4346 - 4408	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.77E-05	0.91	4.02	-	892.0
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				9.44E-14	21.28	240.33	55.10	75429.7
AHQ-6-6, 3306	K.AGDALWLR.F	902.03223	2	1.00E-04	0.93	3.94	-	1280.9
AHQ-6-5, 6287 - 6289	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.24E-07	0.95	4.93	-	814.9
AHQ-6-3, 6294	R.ASFSQPLFQAVAAICR.L	1768.02967	2	7.10E-04	0.61	2.62	-	424.2
AHQ-6-11, 6031	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.66E-05	0.70	2.63	-	466.2
AHQ-6-7, 6050	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.32E-04	0.95	4.42	-	1011.3
AHQ-6-6, 6130 - 6200	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.73E-05	0.96	5.03	-	902.5
AHQ-6-6, 3118	K.DEILGIANNR.L	1115.22208	2	6.80E-05	0.87	2.64	-	1391.4
AHQ-6-7, 3468	K.EKEPEEELYDLSK.V	1609.71294	2	9.19E-08	0.88	3.72	-	481.7
AHQ-6-6, 3515 - 3586	K.EKEPEEELYDLSK.V	1609.71294	2	1.23E-07	0.79	3.54	-	476.7
AHQ-6-6, 6247 - 6311	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	1.70E-04	0.92	4.55	-	576.1
AHQ-6-12, 6173	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	5.74E-05	0.81	3.50	-	271.1
AHQ-6-6, 6314	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	3	9.74E-04	0.85	3.77	-	642.6
AHQ-6-6, 3176	K.GCEVVPDVNVSGQK.F	1489.63335	1	4.64E-05	0.90	3.09	-	1147.7
AHQ-6-6, 3135 - 3194	K.GCEVVPDVNVSGQK.F	1489.63335	2	1.53E-04	0.74	2.84	-	672.3
AHQ-6-12, 6204	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	2.08E-05	0.93	4.16	-	1229.0
AHQ-6-6, 6346 - 6347	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	2.61E-09	0.94	4.60	-	1170.9
AHQ-6-14-, 6294	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	3.20E-05	0.88	4.13	-	778.6
AHQ-6-6, 3115	R.GM*PAHFSDSAQTEACYHM*LSR.P	2430.63997	3	3.45E-07	0.92	4.17	-	1284.2
AHQ-6-9, 3551	R.IDLAVGDVVK.T	1029.21223	1	9.32E-05	0.67	2.63	-	540.0
AHQ-6-6, 3755	R.IDLAVGDVVK.T	1029.21223	1	4.29E-04	0.83	2.98	-	669.7
AHQ-6-9, 4086	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	3.48E-04	0.96	4.80	-	1516.7
AHQ-6-6, 4331 - 4404	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	7.00E-06	0.80	4.09	-	600.9
AHQ-6-12, 4327 - 4336	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	9.44E-14	0.98	6.68	-	1701.5

AHQ-6-6, 4334 - 4395	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	1.79E-13	0.98	6.36	-	2329.7
AHQ-6-6, 2730	R.KDEILGIANNR.L	1243.39499	2	9.37E-06	0.92	3.68	-	1344.9
AHQ-6-12, 2743	R.KDEILGIANNR.L	1243.39499	2	2.52E-04	0.90	3.35	-	911.0
AHQ-6-9, 2585 - 2589	R.KDEILGIANNR.L	1243.39499	2	3.88E-05	0.83	3.16	-	786.8
AHQ-6-6, 2591 - 2670	R.KDEILGIANNR.L	1243.39499	2	1.39E-05	0.91	3.34	-	1128.4
AHQ-6-6, 3966	R.KQDWSDHAIWWEQK.R	1858.00504	3	6.72E-07	0.96	5.03	-	1495.0
AHQ-6-8, 6094	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.03E-05	0.78	3.49	-	511.8
AHQ-6-4, 6317	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	6.19E-05	0.61	3.10	-	346.2
AHQ-6-7, 5983 - 5986	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.13E-07	0.93	4.67	-	693.9
AHQ-6-6, 5310	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	6.73E-04	0.93	4.48	-	763.6
AHQ-6-1, 6300	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.79E-04	0.51	3.06	-	380.8
AHQ-6-5, 6239	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.86E-07	0.91	3.98	-	722.7
AHQ-6-6, 5770 - 5835	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.67E-07	0.90	3.97	-	826.7
AHQ-6-6, 6134 - 6190	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.75E-04	0.88	3.89	-	621.5
AHQ-6-6, 6034 - 6047	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.03E-06	0.85	3.83	-	581.2
AHQ-6-6, 5930	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	6.82E-07	0.73	3.29	-	370.1
AHQ-6-6, 5763	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	2.82E-06	0.62	3.09	-	331.4
AHQ-6-6, 5452 - 5510	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.86E-08	0.86	2.89	-	818.0
AHQ-6-5, 6367	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.63E-06	0.93	4.67	-	1000.3
AHQ-6-7, 6146	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	8.42E-09	0.83	4.14	-	907.5
AHQ-6-8, 6256	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.88E-08	0.92	4.70	-	976.1
AHQ-6-1, 6418	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.11E-06	0.73	3.05	-	1006.5
AHQ-6-6, 6283	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.42E-06	0.94	5.34	-	1173.0
AHQ-6-7, 2355 - 2358	R.LTQLYEQAR.W	1122.25622	2	1.59E-07	0.91	3.80	-	1102.5
AHQ-6-6, 2404 - 2442	R.LTQLYEQAR.W	1122.25622	2	1.56E-04	0.86	2.81	-	974.6
AHQ-6-8, 3857 - 3860	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	4.16E-04	0.85	3.97	-	412.9
AHQ-6-5, 4005	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.57E-04	0.67	2.82	-	413.2
AHQ-6-13-, 3972 - 4030	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	7.69E-08	0.74	3.47	-	551.7
AHQ-6-6, 3904 - 3963	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	3.47E-06	0.92	4.40	-	595.4
AHQ-6-7, 4088	K.TASGDYIDSSWELR.V	1600.66783	2	6.54E-08	0.85	3.39	-	773.7
AHQ-6-13-, 4277	K.TASGDYIDSSWELR.V	1600.66783	2	1.83E-04	0.84	3.31	-	919.4
AHQ-6-6, 4094 - 4100	K.TASGDYIDSSWELR.V	1600.66783	2	5.10E-06	0.76	3.06	-	458.2
AHQ-6-6, 4190	K.TASGDYIDSSWELR.V	1600.66783	2	1.44E-10	0.91	3.60	-	999.6
AHQ-6-13, 4403	K.TASGDYIDSSWELR.V	1600.66783	2	2.14E-05	0.82	3.06	-	972.9
AHQ-6-7, 3723	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	2.62E-05	0.80	3.45	-	540.6
AHQ-6-9, 6179	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	4.93E-04	0.91	4.32	-	1077.8
AHQ-6-7, 6335	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	7.93E-07	0.95	4.88	-	1526.0
AHQ-6-6, 6474	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	4.54E-06	0.97	5.83	-	1821.6
AHQ-6-5, 3865 - 3923	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.75E-05	0.93	4.23	-	1095.6
AHQ-6-13-, 3862 - 3930	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.84E-06	0.86	4.17	-	626.4
AHQ-6-7, 3770	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.20E-05	0.88	3.73	-	1043.8
AHQ-6-6, 3882	R.VFVGEEDPEAESVTLR.V	1777.91007	3	5.14E-04	0.94	4.14	-	1737.0
AHQ-6-8, 3792	R.VFVGEEDPEAESVTLR.V	1777.91007	2	8.57E-04	0.81	3.60	-	808.1
AHQ-6-10, 3767 - 3770	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.87E-05	0.90	3.59	-	1258.7
AHQ-6-14, 4636 - 4697	R.VFVGEEDPEAESVTLR.V	1777.91007	2	7.16E-05	0.93	3.86	-	1146.5
AHQ-6-11, 3832	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.02E-08	0.94	3.97	-	1180.2
AHQ-6-9, 3671 - 3676	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.79E-04	0.61	3.06	-	693.8
AHQ-6-6, 3852 - 3911	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.07E-11	0.95	4.42	-	1269.7
AHQ-6-13, 4055 - 4113	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.89E-05	0.96	4.46	-	1620.7
AHQ-6-3, 3918 - 3984	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.64E-05	0.88	3.21	-	1142.0
AHQ-6-12, 3881	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.10E-05	0.78	2.96	-	851.2
AHQ-6-14-, 3910	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.30E-11	0.96	4.40	-	1585.8
AHQ-6-12, 2973	R.VTGESHIGGVLLK.I	1310.52448	2	1.02E-05	0.85	2.98	-	1201.4
AHQ-6-7, 2724 - 2794	R.VTGESHIGGVLLK.I	1310.52448	2	9.44E-05	0.87	3.24	-	1154.4
AHQ-6-6, 2866 - 2926	R.VTGESHIGGVLLK.I	1310.52448	2	8.27E-08	0.97	4.06	-	1986.8
AHQ-6-14-, 2980	R.VTGESHIGGVLLK.I	1310.52448	2	9.35E-06	0.96	3.87	-	1752.3
AHQ-6-6, 2872	R.VTGESHIGGVLLK.I	1310.52448	1	7.80E-04	0.49	2.03	-	733.6
AHQ-6-7, 2791	R.VTGESHIGGVLLK.I	1310.52448	2	5.53E-05	0.91	3.52	-	1123.0
AHQ-6-5, 2896	R.VTGESHIGGVLLK.I	1310.52448	2	1.22E-05	0.91	3.11	-	1300.5
AHQ-6-11, 4509 - 4577	K.VVLAGGVAPALFR.G	1270.54832	2	5.01E-04	0.91	3.35	-	1081.3
AHQ-6-10, 4479 - 4483	K.VVLAGGVAPALFR.G	1270.54832	2	1.25E-06	0.97	4.13	-	1923.4
AHQ-6-6, 4663 - 4687	K.VVLAGGVAPALFR.G	1270.54832	2	1.33E-11	0.97	5.04	-	1878.8
AHQ-6-7, 4538	K.VVLAGGVAPALFR.G	1270.54832	2	2.41E-10	0.97	4.51	-	1863.4
gi|13124879|ref|NP_002465.1|	smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]			1.29E-13	6.46	80.36	4.20	227336.7
AHQ-6-2, 4636	R.DLGEELEALK.T	1117.23151	2	1.07E-05	0.90	3.53	-	766.9
AHQ-6-5, 2887	K.FDQLLAEEK.N	1093.21165	2	5.29E-06	0.89	2.59	-	1465.0
AHQ-6-2, 2966	K.FDQLLAEEK.N	1093.21165	2	1.33E-05	0.90	3.08	-	1372.2
AHQ-6-3, 2964	K.FDQLLAEEK.N	1093.21165	1	4.71E-04	0.75	2.39	-	1057.0
AHQ-6-3, 2970	K.FDQLLAEEK.N	1093.21165	2	1.73E-04	0.91	3.05	-	1426.7
AHQ-6-2, 2555 - 2579	K.KEEELQAALAR.L	1258.40643	1	6.62E-06	0.52	2.28	-	557.7
AHQ-6-4, 2531	K.KEEELQAALAR.L	1258.40643	2	3.46E-05	0.92	3.61	-	1320.3
AHQ-6-5, 2827 - 2851	R.KFDQLLAEEK.N	1221.38456	2	1.96E-04	0.90	3.34	-	1206.1
AHQ-6-4, 2880	R.KFDQLLAEEK.N	1221.38456	1	3.90E-04	0.71	2.74	-	692.7
AHQ-6-3, 2926	R.KFDQLLAEEK.N	1221.38456	1	3.18E-05	0.26	2.33	-	453.3
AHQ-6-6, 2818 - 2834	R.KFDQLLAEEK.N	1221.38456	2	5.25E-05	0.83	3.25	-	1018.1
AHQ-6-2, 2876 - 2916	R.KFDQLLAEEK.N	1221.38456	2	2.60E-04	0.92	3.63	-	1159.2
AHQ-6-2, 2920 - 2922	R.KFDQLLAEEK.N	1221.38456	1	6.01E-04	0.58	2.78	-	783.1
AHQ-6-3, 2920 - 2921	R.KFDQLLAEEK.N	1221.38456	2	1.98E-04	0.88	3.44	-	992.8
AHQ-6-3, 5685	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.24E-05	0.89	3.29	-	1497.1
AHQ-6-2, 5666 - 5723	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.52E-10	0.99	6.64	-	3760.4
AHQ-6-3, 5064 - 5069	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.10E-05	0.98	7.27	-	2641.6
AHQ-6-2, 5090 - 5162	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.29E-13	0.98	6.68	-	2359.8
AHQ-6-4, 5728	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	5.07E-04	0.89	3.16	-	1550.6
AHQ-6-2, 5116	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	2	8.35E-06	0.73	2.80	-	538.6
AHQ-6-2, 5283	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.96E-05	0.92	4.17	-	1553.7
AHQ-6-1, 5198	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.55E-07	0.98	6.65	-	2329.2
AHQ-6-2, 5966	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.25E-07	0.92	4.27	-	553.3
AHQ-6-2, 5870 - 5878	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.62E-08	0.95	4.23	-	1052.2
AHQ-6-2, 5758 - 5814	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.21E-09	0.95	4.36	-	870.0
AHQ-6-7, 5604 - 5606	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.64E-05	0.89	4.36	-	400.5
AHQ-6-6, 5864 - 5936	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.53E-07	0.82	3.20	-	636.0
AHQ-6-6, 5698 - 5759	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.75E-09	0.96	4.95	-	1132.7
AHQ-6-3, 5770 - 5836	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.15E-08	0.96	4.64	-	1242.8
AHQ-6-3, 5936	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.15E-05	0.90	3.63	-	624.8
AHQ-6-5, 5820 - 5885	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.59E-04	0.93	4.31	-	899.3
AHQ-6-5, 5707 - 5767	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.10E-07	0.84	3.85	-	509.6
AHQ-6-1, 5830 - 5910	K.QLLQANPILEAFGNAK.T	1727.98540	2	8.66E-04	0.90	3.54	-	792.0
AHQ-6-1, 6026	K.QLLQANPILEAFGNAK.T	1727.98540	2	8.47E-06	0.87	3.68	-	520.6
AHQ-6-4, 5848 - 5903	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.01E-11	0.93	4.41	-	780.3
AHQ-6-4, 6015	K.QLLQANPILEAFGNAK.T	1727.98540	2	8.38E-06	0.92	3.76	-	859.8
AHQ-6-10, 5468 - 5508	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.62E-04	0.82	3.62	-	525.9
AHQ-6-1, 5471	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.44E-08	0.96	5.99	-	1309.6
AHQ-6-5, 5316 - 5359	K.TQLEELEDELQATEDAK.L	1963.04334	2	3.44E-06	0.98	5.58	-	2089.0
AHQ-6-2, 3930 - 4008	K.TQLEELEDELQATEDAK.L	1963.04334	2	9.28E-07	0.97	5.38	-	1591.3
AHQ-6-2, 5410 - 5484	K.TQLEELEDELQATEDAK.L	1963.04334	2	8.91E-06	0.97	4.63	-	1820.1
AHQ-6-1, 5466	K.TQLEELEDELQATEDAK.L	1963.04334	2	5.44E-05	0.95	4.49	-	1279.1
AHQ-6-6, 5298 - 5304	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.30E-07	0.98	6.04	-	1765.3

AHQ-6-2, 5414	K.TQLEELEDELQATEDAK.L	1963.04334	3	3.34E-05	0.94	5.01	-	974.3
AHQ-6-3, 5377	K.TQLEELEDELQATEDAK.L	1963.04334	3	5.75E-06	0.95	5.01	-	1163.1
AHQ-6-7, 5128 - 5158	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.99E-05	0.96	4.73	-	1489.4
AHQ-6-3, 5370	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.64E-04	0.97	5.94	-	1327.9
AHQ-6-4, 5432 - 5436	K.TQLEELEDELQATEDAK.L	1963.04334	2	7.64E-09	0.98	5.96	-	2641.4
gi|13994151|ref|NP_066272.1|	PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H			1.50E-13	11.43	140.30	50.80	36071.5
AHQ-6-14-, 5672 - 5732	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.15E-05	0.94	5.52	-	719.5
AHQ-6-14-, 6160 - 6218	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.50E-13	0.95	6.00	-	690.1
AHQ-6-13, 4535 - 4536	K.CGTGIVGVFVK.L	1138.36198	2	3.08E-04	0.93	3.23	-	1334.7
AHQ-6-11, 3505	K.DFEQPLAISR.V	1176.30388	2	8.23E-06	0.93	3.78	-	1051.0
AHQ-6-13, 3745	K.DFEQPLAISR.V	1176.30388	2	1.09E-06	0.88	3.17	-	881.2
AHQ-6-12, 3563	K.DFEQPLAISR.V	1176.30388	2	1.88E-05	0.88	3.38	-	879.3
AHQ-6-14-, 3575	K.DFEQPLAISR.V	1176.30388	2	1.06E-05	0.96	4.06	-	1449.2
AHQ-6-13-, 3586 - 3609	K.DFEQPLAISR.V	1176.30388	2	3.24E-06	0.73	2.75	-	631.2
AHQ-6-13, 3543 - 3544	K.GCTDNLTLTVAR.S	1322.47058	2	3.28E-04	0.76	2.94	-	703.3
AHQ-6-13, 4127	K.GHFFVEDQIYCEK.H	1673.82684	2	7.56E-04	0.90	3.44	-	832.2
AHQ-6-13-, 3990 - 4004	K.GHFFVEDQIYCEK.H	1673.82684	2	2.87E-04	0.96	4.59	-	1367.7
AHQ-6-12, 3920	K.GHFFVEDQIYCEK.H	1673.82684	2	9.98E-05	0.95	4.06	-	1240.3
AHQ-6-14-, 3963 - 3972	K.GHFFVEDQIYCEK.H	1673.82684	2	4.72E-06	0.96	4.08	-	1681.4
AHQ-6-13, 4093 - 4155	K.GHFFVEDQIYCEK.H	1673.82684	2	4.52E-04	0.87	3.25	-	621.3
AHQ-6-11, 3875	K.GHFFVEDQIYCEK.H	1673.82684	2	8.94E-04	0.89	3.43	-	768.0
AHQ-6-12, 3220	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.84E-08	0.90	3.77	-	848.7
AHQ-6-13, 3419	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.14E-11	0.87	3.40	-	628.2
AHQ-6-14, 4050 - 4106	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.25E-06	0.80	3.16	-	688.1
AHQ-6-13-, 3292	R.IKGCTDNLTLTVAR.S	1563.80174	2	7.51E-11	0.96	4.35	-	1250.3
AHQ-6-14-, 3218	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.08E-08	0.94	3.88	-	1106.7
AHQ-6-12, 4575	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	3	1.43E-05	0.58	3.60	-	559.1
AHQ-6-13, 4753	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	3	5.92E-05	0.91	3.90	-	1270.5
AHQ-6-13, 3895	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.32E-08	0.92	4.77	-	683.5
AHQ-6-13-, 3772	R.LVGGKDFEQPLAISR.V	1630.86972	2	7.69E-07	0.97	5.12	-	1412.7
AHQ-6-14-, 3747 - 3748	R.LVGGKDFEQPLAISR.V	1630.86972	2	2.73E-08	0.98	5.72	-	2159.3
AHQ-6-13-, 3717	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	6.94E-06	0.92	4.32	-	609.2
AHQ-6-13-, 3709 - 3724	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	8.60E-04	0.73	3.18	-	558.8
AHQ-6-13-, 6197 - 6200	K.QSTSFLVLQEILESEEK.G	1981.18977	2	1.19E-07	0.97	5.28	-	1470.8
AHQ-6-13, 6239	K.QSTSFLVLQEILESEEK.G	1981.18977	2	9.79E-07	0.95	4.06	-	1414.5
AHQ-6-13-, 5840	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	4.31E-06	0.70	3.04	-	497.5
AHQ-6-13, 2705	R.SAM*PFTASPASSTTAR.V	1599.74799	2	3.85E-05	0.75	2.84	-	720.1
AHQ-6-12, 2517 - 2523	R.SAM*PFTASPASSTTAR.V	1599.74799	2	2.55E-07	0.92	3.61	-	1022.8
AHQ-6-13-, 2530	R.SAM*PFTASPASSTTAR.V	1599.74799	2	3.48E-05	0.95	3.89	-	1487.5
AHQ-6-12, 3063	R.SAMPFTASPASSTTAR.V	1583.74859	2	2.08E-04	0.60	2.73	-	541.8
AHQ-6-11, 2479 - 2487	R.SAM*PFTASPASSTTAR.V	1599.74799	2	7.20E-07	0.84	3.14	-	872.8
AHQ-6-13, 4744 - 4747	R.VTPPEGYEVVTVFPK	1662.90695	2	2.61E-07	0.47	2.59	-	115.1
gi|4502549|ref|NP_001734.1|	calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta			2.15E-13	1.90	20.23	22.10	16837.5
AHQ-6-12, 3828 - 3833	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	2.02E-06	0.75	3.35	-	576.7
AHQ-6-12, 4043 - 4100	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	7.23E-07	0.94	4.24	-	1051.1
AHQ-6-13-, 3817	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.44E-06	0.70	2.90	-	346.4
AHQ-6-12, 3736 - 3792	R.VFDKDGNGYISAAELR.H	1755.90933	2	2.15E-13	0.96	4.56	-	1549.9
gi|4501885|ref|NP_001092.1|	beta actin; beta cytoskeletal actin [Homo sapiens]			2.55E-13	13.55	150.35	36.00	41736.5
AHQ-6-8, 5653 - 5728	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	4.15E-05	0.91	4.92	-	479.2
AHQ-6-8, 6148 - 6221	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.08E-05	0.79	4.77	-	372.3
AHQ-6-8, 5756 - 5813	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	9.84E-04	0.88	4.50	-	555.0
AHQ-6-13-, 6118	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	3.64E-04	0.75	3.83	-	366.7
AHQ-6-8, 6022 - 6096	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	3.43E-06	0.73	3.75	-	605.8
AHQ-6-13-, 5680 - 5740	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	8.70E-06	0.90	4.47	-	563.7
AHQ-6-8, 6544	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.11E-07	0.90	4.45	-	745.9
AHQ-6-8, 6510	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	2.00E-06	0.67	3.07	-	622.5
AHQ-6-2, 6446 - 6447	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	4.64E-04	0.79	4.00	-	701.3
AHQ-6-8, 6449 - 6516	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.28E-06	0.93	4.97	-	1254.5
AHQ-6-8, 6422	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	2.17E-05	0.77	3.66	-	640.5
AHQ-6-8, 6408 - 6472	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	4.67E-06	0.92	4.16	-	834.5
AHQ-6-9, 6049	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	4.49E-05	0.84	3.27	-	795.4
AHQ-6-8, 6316 - 6382	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.25E-10	0.95	5.30	-	1384.6
AHQ-6-10, 6056 - 6086	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.35E-05	0.60	3.10	-	573.1
AHQ-6-8, 6576	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	4.91E-05	0.87	3.79	-	1116.3
AHQ-6-8, 6280 - 6341	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	8.14E-06	0.91	4.14	-	837.6
AHQ-6-8, 6284 - 6292	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	9.86E-07	0.97	6.73	-	1473.3
AHQ-6-8, 5661 - 5721	R.FRCPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3571.03693	3	2.33E-09	0.97	6.85	-	826.8
AHQ-6-8, 5876 - 5950	R.FRCPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3555.03753	3	4.62E-07	0.92	5.73	-	906.8
AHQ-6-8, 6168 - 6225	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	4.72E-08	0.97	6.49	-	1393.4
AHQ-6-8, 2355 - 2416	R.GYSFTTTAER.E	1133.19273	2	3.40E-04	0.92	3.29	-	1040.5
AHQ-6-10, 2510 - 2572	R.GYSFTTTAER.E	1133.19273	2	1.66E-04	0.93	3.19	-	1216.7
AHQ-6-4, 2593 - 2596	R.GYSFTTTAER.E	1133.19273	2	2.04E-05	0.90	3.19	-	861.2
AHQ-6-8, 2562	R.GYSFTTTAER.E	1133.19273	2	9.43E-05	0.86	2.75	-	901.3
AHQ-6-8, 2442 - 2504	R.GYSFTTTAER.E	1133.19273	2	1.61E-04	0.92	3.32	-	1197.7
AHQ-6-11, 2576 - 2577	R.GYSFTTTAER.E	1133.19273	2	2.21E-04	0.95	3.48	-	1330.0
AHQ-6-8, 4321 - 4368	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.11E-05	0.92	4.17	-	896.3
AHQ-6-8, 4340 - 4366	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	7.09E-04	0.87	4.29	-	1063.5
AHQ-6-8, 4430	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	1.92E-04	0.84	3.95	-	808.2
AHQ-6-8, 4557 - 4616	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.44E-08	0.97	5.13	-	1319.6
AHQ-6-10, 4018	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	1.87E-04	0.85	3.60	-	887.2
AHQ-6-8, 3981 - 4017	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	5.88E-06	0.82	4.15	-	910.4
AHQ-6-14-, 4386	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	3.56E-04	0.80	3.26	-	830.8
AHQ-6-14-, 4276	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	1.19E-05	0.55	3.01	-	590.8
AHQ-6-13-, 4149 - 4205	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	1.55E-05	0.97	5.38	-	1708.5
AHQ-6-14-, 4174	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	9.56E-04	0.93	4.30	-	1071.6
AHQ-6-8, 6396 - 6466	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	8.87E-10	0.98	7.06	-	2775.2
AHQ-6-8, 5577 - 5645	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	4.61E-06	0.94	4.04	-	1463.1
AHQ-6-8, 6366 - 6436	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	4.36E-05	0.86	3.46	-	1019.3
AHQ-6-8, 6348 - 6416	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	4.61E-04	0.96	4.68	-	1316.8
AHQ-6-8, 6552 - 6569	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	2.10E-11	0.98	6.62	-	1944.7
AHQ-6-9, 6148 - 6217	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	6.07E-05	0.66	2.81	-	650.8
AHQ-6-8, 6328 - 6424	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	3.64E-10	0.98	6.69	-	2039.0
AHQ-6-8, 5385	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	1.41E-04	0.78	3.03	-	713.2
AHQ-6-8, 6112 - 6173	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	2.94E-05	0.98	5.65	-	2042.2
AHQ-6-7, 5095	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.61E-05	0.89	4.69	-	840.7
AHQ-6-6, 5423 - 5500	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.79E-06	0.94	5.14	-	1207.0
AHQ-6-14-, 5447	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.42E-07	0.93	4.90	-	964.1
AHQ-6-6, 5271	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.29E-05	0.97	6.05	-	1770.3
AHQ-6-5, 5552	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.18E-07	0.96	5.89	-	1240.9
AHQ-6-13-, 5425 - 5488	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.32E-10	0.96	5.38	-	1435.6
AHQ-6-13-, 5214	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.21E-06	0.91	4.25	-	1125.0
AHQ-6-14, 5808 - 5880	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.13E-06	0.95	5.23	-	1341.0
AHQ-6-8, 5641	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.77E-04	0.89	4.39	-	874.5
AHQ-6-8, 5500 - 5557	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.69E-09	0.96	5.91	-	1472.0
AHQ-6-4, 5637	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.75E-10	0.97	5.61	-	1687.0
AHQ-6-4, 5401	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.22E-09	0.97	6.22	-	1301.6
AHQ-6-8, 5369 - 5440	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.55E-13	0.97	5.78	-	1688.8

AHQ-6-3, 5574 - 5633	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.27E-04	0.94	5.16	-	1125.6
AHQ-6-3, 5344 - 5405	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.41E-05	0.94	5.70	-	979.2
AHQ-6-8, 5289 - 5364	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.16E-04	0.71	3.47	-	829.9
AHQ-6-8, 5244 - 5305	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	6.58E-07	0.97	6.61	-	1562.9
AHQ-6-13, 5508	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.41E-05	0.93	4.86	-	1148.9
AHQ-6-13, 5285	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.48E-04	0.75	3.69	-	503.3
AHQ-6-9, 5146 - 5202	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.27E-05	0.93	4.82	-	1034.0
AHQ-6-8, 5188 - 5222	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.04E-11	0.96	6.00	-	1097.0
AHQ-6-8, 5100 - 5160	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.62E-07	0.97	5.81	-	2138.1
AHQ-6-1, 5452	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.50E-04	0.92	4.52	-	1277.2
AHQ-6-12, 5141 - 5195	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	9.99E-05	0.94	5.42	-	936.4
AHQ-6-8, 4961 - 5040	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.99E-06	0.95	5.77	-	971.4
AHQ-6-10, 4996 - 5070	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.71E-09	0.98	6.86	-	1590.4
AHQ-6-10, 5226 - 5282	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.35E-11	0.95	5.69	-	1243.8
AHQ-6-14-, 5227 - 5292	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.46E-08	0.94	5.02	-	1099.6
AHQ-6-5, 5311	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.25E-07	0.96	5.77	-	1238.2
AHQ-6-11, 5285 - 5324	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.29E-05	0.91	4.15	-	1108.9
AHQ-6-11, 5100 - 5156	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.80E-08	0.94	5.65	-	1082.6
AHQ-6-11, 3803	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.55E-07	0.93	4.31	-	1027.0
AHQ-6-12, 3843 - 3900	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.06E-05	0.91	4.00	-	785.7
AHQ-6-10, 3715 - 3738	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.26E-05	0.92	4.73	-	751.7
AHQ-6-13, 4039	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.22E-06	0.90	4.25	-	742.1
AHQ-6-9, 3642 - 3654	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.80E-05	0.89	4.14	-	580.1
AHQ-6-9, 3532 - 3599	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.49E-06	0.94	4.99	-	891.9
AHQ-6-14, 4674	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.67E-06	0.91	3.85	-	999.3
AHQ-6-8, 3686 - 3744	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.37E-11	0.92	4.79	-	775.2
AHQ-6-13-, 3908	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.95E-05	0.86	3.68	-	596.3
AHQ-6-8, 3580 - 3640	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.28E-05	0.93	4.57	-	903.1
AHQ-6-8, 3493 - 3557	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	4.05E-04	0.80	4.33	-	836.1
AHQ-6-8, 3488 - 3564	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.11E-05	0.89	4.40	-	661.2
AHQ-6-6, 3831	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.61E-04	0.84	3.96	-	496.8
AHQ-6-5, 3861 - 3871	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.38E-05	0.78	3.11	-	576.5
AHQ-6-14-, 3904	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.69E-11	0.92	4.24	-	876.8
AHQ-6-4, 3911 - 3973	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.59E-05	0.90	4.03	-	628.0
AHQ-6-3, 3897 - 3962	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.02E-04	0.87	4.23	-	564.1
AHQ-6-2, 3995	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.38E-04	0.77	3.79	-	466.1
AHQ-6-1, 4127	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.24E-05	0.87	4.09	-	637.1
AHQ-6-1, 4123	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	5.24E-04	0.85	4.00	-	1137.2
gi|7656991|ref|NP_055140.1|	coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;			3.11E-13	6.31	70.32	23.60	53248.7
AHQ-6-6, 5598 - 5654	R.AIFLADGNVFTTGFSR.M	1716.91793	2	1.79E-06	0.97	5.66	-	1673.8
AHQ-6-6, 5506 - 5562	R.AIFLADGNVFTTGFSR.M	1716.91793	2	3.11E-13	0.97	5.55	-	1683.2
AHQ-6-7, 5374 - 5430	R.AIFLADGNVFTTGFSR.M	1716.91793	2	2.10E-04	0.96	4.56	-	1368.4
AHQ-6-6, 3368	R.KCEPIIMTVPR.K	1345.65706	2	6.43E-04	0.77	2.61	-	774.8
AHQ-6-6, 6354	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	6.44E-09	0.98	6.30	-	1935.4
AHQ-6-6, 2336	K.SIKDTICNQDER.I	1480.58332	2	2.89E-07	0.88	2.93	-	1121.9
AHQ-6-6, 2422	K.SIKDTICNQDER.I	1480.58332	2	6.27E-06	0.91	3.55	-	1149.1
AHQ-6-7, 2963	R.VGIVAWHPTAR.N	1207.40918	2	7.78E-04	0.81	2.83	-	901.3
AHQ-6-6, 4194	R.VTWDSSFCAVNPR.F	1540.68205	2	2.91E-09	0.94	3.82	-	1320.2
AHQ-6-6, 5590 - 5667	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	1.52E-07	0.77	3.31	-	665.7
AHQ-6-6, 5674	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	4.81E-09	0.96	5.32	-	833.6
gi|4557435|ref|NP_001242.1|	CD68 antigen; Macrophage antigen CD68 (microsialin); macrosialin; scave			3.31E-13	0.85	10.20	6.20	37408.0
AHQ-6-5, 4500	R.LQAAQLPHTGVFGQSFSCPSDR.S	2405.63153	3	1.23E-07	0.87	4.04	-	720.1
AHQ-6-3, 4586	R.LQAAQLPHTGVFGQSFSCPSDR.S	2405.63153	3	3.31E-13	0.85	3.76	-	907.0
gi|5803011|ref|NP_001966.1|	enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron			6.73E-13	0.97	10.24	3.70	47268.3
AHQ-6-8, 6024	R.YITGDQLGALYQDFVR.D	1860.05915	2	6.73E-13	0.97	4.87	-	1462.7
gi|4501891|ref|NP_001093.1|	actinin, alpha 1 [Homo sapiens]			7.52E-13	34.48	390.30	49.30	103056.9
AHQ-6-5, 6540 - 6545	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	1.91E-10	0.95	6.07	-	903.6
AHQ-6-6, 5080 - 5144	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	8.93E-05	0.84	4.29	-	805.5
AHQ-6-4, 4708	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.18E-05	0.62	3.53	-	566.1
AHQ-6-5, 6059 - 6075	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	2.65E-05	0.67	3.06	-	560.9
AHQ-6-4, 6133 - 6140	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	2.65E-06	0.82	3.81	-	659.6
AHQ-6-4, 5460 - 5520	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	7.62E-07	0.95	4.65	-	945.7
AHQ-6-5, 6063	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	4.08E-08	0.92	4.54	-	604.4
AHQ-6-4, 6131	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	7.00E-08	0.93	4.55	-	700.5
AHQ-6-4, 2316	K.ASIHEAWTDGK.E	1215.29697	2	2.69E-04	0.81	3.01	-	761.4
AHQ-6-5, 5344	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.65E-07	0.93	3.87	-	890.3
AHQ-6-7, 5152	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.58E-05	0.86	3.89	-	685.8
AHQ-6-4, 5371 - 5431	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.79E-06	0.96	4.89	-	1129.9
AHQ-6-4, 4924	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	7.52E-13	0.95	4.20	-	1088.9
AHQ-6-4, 4796	K.DGLGFCALIHR.H	1260.44730	2	5.93E-07	0.91	2.64	-	1570.8
AHQ-6-5, 4728	K.DGLGFCALIHR.H	1260.44730	2	6.38E-08	0.90	2.97	-	1218.9
AHQ-6-4, 2597	R.DHSGTLGPEEFK.A	1317.38606	2	4.59E-05	0.95	3.61	-	1200.8
AHQ-6-6, 2582	R.DHSGTLGPEEFK.A	1317.38606	2	9.51E-06	0.80	2.91	-	662.1
AHQ-6-4, 3715	K.DYETATLSEIK.A	1270.36761	2	1.68E-05	0.92	3.66	-	1147.1
AHQ-6-4, 4101	R.ETADTDTADQVMASFK.I	1730.83208	2	3.24E-05	0.87	3.58	-	657.0
AHQ-6-5, 4277	R.ETADTDTADQVMASFK.I	1730.83208	2	5.44E-05	0.95	4.00	-	1423.8
AHQ-6-4, 4269 - 4331	R.ETADTDTADQVMASFK.I	1730.83208	2	4.11E-08	0.96	4.53	-	1294.3
AHQ-6-5, 3140	R.ETADTDTADQVM*ASFK.I	1746.83148	2	3.35E-08	0.96	5.09	-	1112.0
AHQ-6-11, 4143	R.ETADTDTADQVMASFK.I	1730.83208	2	2.95E-04	0.59	2.83	-	457.5
AHQ-6-4, 2853	R.ETADTDTADQVM*ASFK.I	1746.83148	2	7.29E-04	0.63	2.57	-	810.4
AHQ-6-4, 3187 - 3191	R.ETADTDTADQVM*ASFK.I	1746.83148	2	2.73E-07	0.96	4.60	-	1213.2
AHQ-6-5, 2293	K.GISQEQM*NEFR.A	1355.45931	2	4.76E-04	0.70	2.92	-	608.1
AHQ-6-4, 3016	K.GISQEQMNEFR.A	1339.45991	2	1.01E-05	0.88	3.24	-	844.9
AHQ-6-4, 2409	K.GISQEQM*NEFR.A	1355.45931	2	1.10E-07	0.86	2.99	-	899.3
AHQ-6-4, 2311	K.GISQEQM*NEFR.A	1355.45931	2	5.99E-06	0.79	3.39	-	652.9
AHQ-6-6, 2970 - 3004	K.GISQEQMNEFR.A	1339.45991	2	1.70E-05	0.83	3.01	-	778.2
AHQ-6-4, 2720	K.GISQEQMNEFR.A	1339.45991	2	4.12E-05	0.61	2.57	-	555.9
AHQ-6-5, 2971	K.GISQEQMNEFR.A	1339.45991	2	3.41E-05	0.83	2.95	-	823.3
AHQ-6-4, 2235 - 2304	R.HRPELIDYGK.L	1228.38202	2	3.42E-04	0.92	3.44	-	766.4
AHQ-6-4, 2236	R.HRPELIDYGK.L	1228.38202	3	1.15E-05	0.89	3.39	-	1209.7
AHQ-6-5, 2224	R.HRPELIDYGK.L	1228.38202	2	5.87E-04	0.93	3.79	-	702.0
AHQ-6-3, 4704 - 4761	K.ICDQWDNLGALTQK.R	1663.83349	2	5.15E-04	0.64	2.81	-	601.2
AHQ-6-5, 4723	K.ICDQWDNLGALTQK.R	1663.83349	2	7.59E-05	0.96	3.94	-	1937.4
AHQ-6-4, 4781 - 4848	K.ICDQWDNLGALTQK.R	1663.83349	2	3.50E-07	0.95	3.78	-	1535.5
AHQ-6-6, 4682 - 4747	K.ICDQWDNLGALTQK.R	1663.83349	2	3.67E-04	0.93	3.86	-	1456.2
AHQ-6-4, 4665 - 4737	K.ICDQWDNLGALTQK.R	1663.83349	2	3.37E-06	0.41	2.79	-	585.9
AHQ-6-4, 5644 - 5724	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	6.25E-10	0.96	5.91	-	1352.9
AHQ-6-4, 5587 - 5645	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	1.52E-06	0.94	4.40	-	1257.9
AHQ-6-10, 5274	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	1.94E-04	0.90	3.44	-	1332.4
AHQ-6-4, 5525	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	4.98E-08	0.95	5.09	-	1175.3
AHQ-6-6, 5522	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	2.07E-04	0.73	3.20	-	979.3
AHQ-6-4, 5741	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	4.85E-05	0.84	3.31	-	1450.2
AHQ-6-7, 5386 - 5387	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	4.39E-06	0.88	3.52	-	625.3
AHQ-6-4, 4123 - 4193	K.ILAGDKNYITMDELR.R	1753.01353	2	3.59E-05	0.94	4.26	-	990.9
AHQ-6-6, 4134	K.ILAGDKNYITMDELR.R	1753.01353	2	1.68E-04	0.63	2.97	-	427.7
AHQ-6-4, 2365	R.IM*SIVDPNR.L	1061.23780	2	2.06E-06	0.73	2.68	-	653.5
AHQ-6-5, 4876	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	3	2.12E-09	0.92	4.55	-	1213.1

AHQ-6-4, 4173	K.IVQTYHVNM*AGTNPYTTITPQEINGK.W	2908.23575	2	3.66E-07	0.47	2.76	-	433.8
AHQ-6-4, 4545	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	1.29E-05	0.88	4.06	-	537.3
AHQ-6-4, 4817	R.KAGTQIENIEEDFRDGLK.L	2064.24210	3	9.07E-10	0.94	5.21	-	966.3
AHQ-6-5, 4760 - 4837	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	7.58E-08	0.97	4.92	-	1511.9
AHQ-6-4, 4811 - 4884	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	5.33E-05	0.97	5.24	-	1475.6
AHQ-6-7, 4563 - 4580	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	3.87E-04	0.92	4.16	-	908.5
AHQ-6-4, 4348	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	2.71E-05	0.94	4.28	-	956.7
AHQ-6-4, 4363	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	1.10E-05	0.96	4.77	-	1495.9
AHQ-6-5, 4304	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	3.52E-05	0.97	4.68	-	1590.8
AHQ-6-4, 3803 - 3837	R.LAILGIHNEVSK.I	1294.52505	2	1.31E-05	0.94	3.40	-	1383.8
AHQ-6-6, 3382	R.LAILGIHNEVSK.I	1294.52505	2	3.16E-08	0.90	3.57	-	784.7
AHQ-6-5, 3397	R.LAILGIHNEVSK.I	1294.52505	2	2.07E-08	0.93	3.42	-	1059.9
AHQ-6-4, 3447 - 3495	R.LAILGIHNEVSK.I	1294.52505	2	5.60E-07	0.90	3.43	-	866.3
AHQ-6-7, 3275	R.LAILGIHNEVSK.I	1294.52505	2	2.05E-04	0.79	2.93	-	905.2
AHQ-6-4, 5791	K.LASDLLEWIR.R	1216.41115	2	2.83E-07	0.97	4.38	-	1748.4
AHQ-6-6, 5659 - 5660	K.LASDLLEWIR.R	1216.41115	2	2.25E-08	0.96	4.04	-	1849.5
AHQ-6-4, 5799	K.LASDLLEWIR.R	1216.41115	1	5.66E-06	0.57	2.32	-	517.1
AHQ-6-5, 5715 - 5723	K.LASDLLEWIR.R	1216.41115	2	1.05E-07	0.97	4.66	-	2137.2
AHQ-6-4, 6159	K.LLETIDQLYLEYAK.R	1712.96427	3	4.35E-07	0.97	5.32	-	1856.8
AHQ-6-4, 5217	K.LLETIDQLYLEYAK.R	1712.96427	2	5.69E-06	0.91	3.70	-	803.2
AHQ-6-5, 6048 - 6103	K.LLETIDQLYLEYAK.R	1712.96427	2	2.59E-07	0.97	5.26	-	1242.1
AHQ-6-4, 2743 - 2747	R.LSNRPAFMPSEGR.M	1462.65941	2	2.54E-04	0.85	3.44	-	677.1
AHQ-6-6, 2718	R.LSNRPAFMPSEGR.M	1462.65941	2	6.46E-04	0.83	3.51	-	700.3
AHQ-6-4, 2263	R.LSNRPAFM*PSEGR.M	1478.65881	3	6.41E-06	0.82	3.41	-	1068.9
AHQ-6-5, 3539	K.M*LDAEDIVGTARPDEK.A	1776.94709	3	8.66E-04	0.79	3.26	-	710.1
AHQ-6-6, 3499	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	2.53E-04	0.80	2.90	-	741.8
AHQ-6-5, 3891	K.MLDAEDIVGTARPDEK.A	1760.94769	2	8.87E-06	0.85	4.04	-	640.9
AHQ-6-4, 3943 - 3947	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.26E-08	0.94	4.33	-	1112.7
AHQ-6-5, 3517	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	2.23E-05	0.85	3.65	-	658.0
AHQ-6-4, 3948	K.MLDAEDIVGTARPDEK.A	1760.94769	3	7.81E-06	0.84	3.78	-	596.9
AHQ-6-4, 3572	K.M*LDAEDIVGTARPDEK.A	1776.94709	3	8.43E-07	0.87	3.76	-	806.5
AHQ-6-6, 5066 - 5070	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	9.53E-08	0.97	5.24	-	1241.3
AHQ-6-4, 5039	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	6.04E-08	0.96	4.59	-	1324.2
AHQ-6-4, 5197	R.M*VSDINNAWGCLEQVEK.G	2011.22273	3	3.88E-09	0.97	5.81	-	1713.4
AHQ-6-5, 5105	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.58E-07	0.96	4.55	-	1262.0
AHQ-6-5, 4885 - 4945	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	4.24E-06	0.86	3.84	-	540.4
AHQ-6-4, 5356 - 5364	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.49E-10	0.97	5.23	-	1232.8
AHQ-6-5, 4625	K.NVNIQNFHISWK.D	1500.68583	2	3.17E-04	0.76	2.95	-	692.1
AHQ-6-7, 4418	K.NVNIQNFHISWK.D	1500.68583	2	9.59E-05	0.65	3.38	-	425.6
AHQ-6-4, 4695	K.NVNIQNFHISWK.D	1500.68583	2	2.52E-06	0.87	3.16	-	1016.9
AHQ-6-4, 4980	K.QFGAQANVIGPWIQTK.M	1759.00118	2	1.84E-05	0.82	3.42	-	746.6
AHQ-6-6, 3427	R.TINEVENQILTR.D	1430.58898	2	1.01E-05	0.58	2.54	-	498.6
AHQ-6-4, 4037	R.TINEVENQILTR.D	1430.58898	2	2.64E-04	0.93	4.21	-	1139.3
AHQ-6-4, 3115 - 3116	R.TINEVENQILTR.D	1430.58898	2	1.89E-05	0.88	3.62	-	869.3
AHQ-6-7, 3715 - 3719	R.TINEVENQILTR.D	1430.58898	2	4.94E-05	0.75	3.12	-	881.0
AHQ-6-4, 3507	R.TINEVENQILTR.D	1430.58898	2	1.14E-05	0.76	3.10	-	434.8
AHQ-6-6, 3815	R.TINEVENQILTR.D	1430.58898	2	2.02E-06	0.91	3.65	-	1148.0
AHQ-6-4, 4055	R.TINEVENQILTR.D	1430.58898	1	1.86E-04	0.06	1.99	-	174.2
AHQ-6-5, 3851	R.TINEVENQILTR.D	1430.58898	2	5.07E-07	0.88	3.79	-	866.8
AHQ-6-5, 3981	R.TINEVENQILTR.D	1430.58898	2	8.01E-04	0.87	3.23	-	913.6
AHQ-6-5, 3073	R.TINEVENQILTR.D	1430.58898	2	5.99E-04	0.46	2.57	-	465.7
AHQ-6-5, 6351	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	3.41E-07	0.66	2.87	-	576.7
AHQ-6-6, 6288	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	1.52E-04	0.81	3.16	-	561.8
AHQ-6-6, 6126	R.VGWEQLLTTIAR.T	1387.60894	2	1.24E-05	0.84	3.19	-	771.8
AHQ-6-3, 6212	R.VGWEQLLTTIAR.T	1387.60894	2	1.77E-05	0.91	3.39	-	1121.4
AHQ-6-2, 6274	R.VGWEQLLTTIAR.T	1387.60894	2	4.10E-05	0.91	3.59	-	1035.3
AHQ-6-10, 5891 - 5894	R.VGWEQLLTTIAR.T	1387.60894	2	8.43E-06	0.91	3.81	-	1212.3
AHQ-6-7, 5972 - 5978	R.VGWEQLLTTIAR.T	1387.60894	2	2.12E-07	0.94	3.87	-	1185.2
AHQ-6-5, 6195 - 6196	R.VGWEQLLTTIAR.T	1387.60894	2	4.28E-10	0.96	4.32	-	1560.6
AHQ-6-8, 6081	R.VGWEQLLTTIAR.T	1387.60894	2	9.45E-07	0.94	3.86	-	1330.2
AHQ-6-4, 6259 - 6328	R.VGWEQLLTTIAR.T	1387.60894	2	1.94E-06	0.96	3.93	-	1575.8
AHQ-6-11, 5952	R.VGWEQLLTTIAR.T	1387.60894	2	2.18E-06	0.86	3.07	-	899.0
AHQ-6-6, 3483 - 3490	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.71E-06	0.95	4.61	-	1323.3
AHQ-6-5, 4085 - 4143	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.15E-06	0.94	4.82	-	907.0
AHQ-6-5, 3509 - 3572	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.16E-06	0.86	4.12	-	788.8
AHQ-6-4, 4588	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.20E-06	0.96	4.46	-	1378.4
AHQ-6-4, 4336 - 4407	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.65E-05	0.96	4.75	-	1091.8
AHQ-6-4, 4207	K.VLAVNQENEQLMEDYEK.L	2053.23635	3	1.01E-12	0.95	4.92	-	1115.9
AHQ-6-4, 4159	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.05E-08	0.95	4.87	-	1066.6
AHQ-6-4, 4119 - 4199	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	8.23E-07	0.92	4.05	-	1017.3
AHQ-6-8, 3961	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.37E-06	0.80	3.19	-	644.9
AHQ-6-4, 3880	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	8.82E-06	0.95	4.94	-	1054.9
AHQ-6-4, 3729	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.16E-09	0.97	5.46	-	1773.2
AHQ-6-4, 3563 - 3623	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	4.26E-10	0.97	5.00	-	1362.5
AHQ-6-4, 3441	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.31E-08	0.85	3.38	-	709.6
AHQ-6-6, 4042 - 4099	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.61E-08	0.89	4.20	-	822.2
gi|4505879|ref|NP_002655.1|	pleckstrin; p47 [Homo sapiens]			7.73E-13	8.50	100.39	37.40	40082.5
AHQ-6-13-, 5372	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.62E-05	0.98	6.82	-	1859.9
AHQ-6-11, 5252 - 5303	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	3.21E-05	0.92	4.30	-	1246.3
AHQ-6-9, 5110	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	4.67E-06	0.81	3.43	-	560.5
AHQ-6-8, 5284	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	2.72E-07	0.80	3.20	-	644.0
AHQ-6-13, 5452	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	7.96E-11	0.91	4.57	-	1004.8
AHQ-6-12, 5303	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	7.14E-10	0.96	5.44	-	1526.8
AHQ-6-10, 5174	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.11E-06	0.75	3.43	-	666.5
AHQ-6-13, 2681 - 2755	R.GCVVTSVESNSNGR.K	1467.54464	2	5.24E-04	0.79	3.10	-	711.5
AHQ-6-8, 2335 - 2411	R.GCVVTSVESNSNGR.K	1467.54464	2	4.91E-06	0.91	3.46	-	1247.7
AHQ-6-8, 2348 - 2429	R.GCVVTSVESNSNGR.K	1467.54464	1	1.55E-05	0.22	2.45	-	132.8
AHQ-6-13, 3172	K.GSTLTSPCQDFGKR.M	1555.69502	2	2.01E-04	0.61	2.80	-	440.9
AHQ-6-8, 6324	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	3	7.19E-06	0.96	4.54	-	2137.1
AHQ-6-9, 6127 - 6167	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	8.12E-10	0.99	7.10	-	3359.4
AHQ-6-11, 6259 - 6333	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	7.73E-13	0.99	7.85	-	3107.1
AHQ-6-3, 6520	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.66E-08	0.97	6.88	-	1671.1
AHQ-6-8, 6438 - 6518	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	6.69E-10	0.99	7.35	-	3420.4
AHQ-6-8, 6525	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.16E-05	0.98	7.59	-	2200.7
AHQ-6-8, 5344	R.LPETIDLGALYLSM*K.D	1680.98719	2	9.35E-05	0.96	4.50	-	1326.8
AHQ-6-13, 5467 - 5527	R.LPETIDLGALYLSM*K.D	1680.98719	2	4.05E-05	0.89	3.59	-	945.0
AHQ-6-12, 5036 - 5037	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	3	2.75E-05	0.87	4.14	-	750.5
AHQ-6-12, 5035 - 5039	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	2	2.69E-04	0.92	4.32	-	872.3
AHQ-6-8, 5690	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	1.80E-04	0.98	5.00	-	2164.4
AHQ-6-8, 5726 - 5806	R.QEGLMIASSLLNEGYLQPAGDM*SK.S	2569.89376	3	4.19E-05	0.50	3.35	-	269.5
AHQ-6-8, 6477 - 6517	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.81E-10	0.96	5.69	-	1356.9
AHQ-6-12, 6363 - 6364	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	2.40E-09	0.95	5.30	-	1173.4
AHQ-6-9, 6201	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	9.33E-12	0.88	4.03	-	989.6
AHQ-6-8, 6492 - 6560	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	5.51E-05	0.79	3.92	-	441.8
AHQ-6-11, 6299	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	7.96E-11	0.92	4.59	-	1081.4
AHQ-6-10, 6234	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	2.84E-06	0.55	3.37	-	456.8
AHQ-6-10, 6228	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	3.18E-06	0.87	3.84	-	837.1

AHQ-6-9, 6203 - 6277	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	3.76E-06	0.74	3.88	-	437.4
gi|9910280|ref|NP_064505.1|	UDP-glucose ceramide glucosyltransferase-like 1; UDP-glucose:glycoprote			9.33E-13	0.94	10.23	1.60	177187.7
AHQ-6-3, 6524	R.IIGPLEDSELFNQDDFHLLENIILK.T	2927.29710	3	9.33E-13	0.94	4.67	-	1120.4
gi|17921989|ref|NP_005991.1|	tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain			1.52E-12	12.47	150.34	46.90	49924.1
AHQ-6-13-, 4540 - 4610	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	3.52E-04	0.94	4.64	-	1477.8
AHQ-6-13, 4804	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	2.78E-05	0.83	3.26	-	1156.2
AHQ-6-14-, 4506 - 4582	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	6.25E-04	0.86	3.37	-	908.8
AHQ-6-12, 4509 - 4591	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	3.80E-05	0.70	3.13	-	812.8
AHQ-6-13-, 5188 - 5244	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.10E-05	0.91	3.93	-	946.9
AHQ-6-13-, 4964 - 5020	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	2.47E-05	0.94	4.54	-	987.0
AHQ-6-7, 4880	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	8.18E-07	0.94	4.12	-	1181.4
AHQ-6-13-, 5696 - 5744	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	7.66E-05	0.96	5.13	-	1237.1
AHQ-6-13, 5309 - 5317	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.62E-04	0.92	4.10	-	1071.8
AHQ-6-7, 5551 - 5556	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	3.80E-05	0.96	5.07	-	1427.4
AHQ-6-13, 5120 - 5140	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.05E-05	0.97	4.79	-	1761.6
AHQ-6-14-, 5026	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	2.35E-06	0.96	4.36	-	1503.6
AHQ-6-14-, 5208	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.52E-12	0.79	3.08	-	733.3
AHQ-6-14-, 5687 - 5690	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.09E-04	0.91	4.10	-	1064.1
AHQ-6-12, 5116	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	4.89E-04	0.91	3.44	-	1128.1
AHQ-6-11, 5525 - 5567	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.69E-08	0.76	2.74	-	904.0
AHQ-6-14-, 5688 - 5702	R.AVFVDLEPTVIDEIR.N	1716.95615	2	3.50E-09	0.93	3.29	-	1628.7
AHQ-6-13, 5779	R.AVFVDLEPTVIDEIR.N	1716.95615	2	3.89E-08	0.82	3.20	-	1033.6
AHQ-6-13-, 5702	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.83E-06	0.91	3.66	-	1254.9
AHQ-6-12, 3379	K.DVNAAIAAIK.T	986.14745	2	2.80E-05	0.94	3.88	-	1338.6
AHQ-6-7, 2924	K.DVNAAIAAIK.T	986.14745	1	6.14E-05	0.62	1.96	-	921.4
AHQ-6-10, 4708 - 4764	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.78E-04	0.93	4.45	-	567.9
AHQ-6-7, 4767 - 4826	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.06E-04	0.94	4.19	-	735.9
AHQ-6-8, 4738 - 4797	R.IHFPLATYAPVISAEK.A	1758.05310	2	6.70E-06	0.94	4.49	-	748.7
AHQ-6-13-, 5004	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.24E-04	0.79	3.48	-	441.5
AHQ-6-13-, 6242	R.LISQIVSSITASLR.F	1488.75471	2	3.93E-10	0.96	4.21	-	1341.4
AHQ-6-7, 6126 - 6150	R.LISQIVSSITASLR.F	1488.75471	2	9.04E-07	0.88	3.58	-	702.0
AHQ-6-14-, 6255 - 6258	R.LISQIVSSITASLR.F	1488.75471	2	4.53E-08	0.96	4.81	-	1395.4
AHQ-6-7, 6246	K.LSDQCTGLQGFLVFHSFGGGTGSGFTSLLM*ER.L	3425.79315	3	3.23E-07	0.97	6.76	-	1320.4
AHQ-6-8, 3246	R.NLDIERPTYTNLNR.L	1719.88022	2	3.92E-04	0.70	2.92	-	596.3
AHQ-6-12, 3403 - 3459	R.NLDIERPTYTNLNR.L	1719.88022	2	5.78E-04	0.73	3.46	-	459.9
AHQ-6-14-, 3478	R.NLDIERPTYTNLNR.L	1719.88022	2	1.84E-04	0.50	2.97	-	277.8
AHQ-6-14, 4248	R.NLDIERPTYTNLNR.L	1719.88022	2	7.96E-04	0.78	3.03	-	596.8
AHQ-6-13-, 3513	R.NLDIERPTYTNLNR.L	1719.88022	2	6.92E-09	0.50	2.98	-	251.3
AHQ-6-7, 3846	R.QLFHPEQLITGK.E	1411.63050	2	3.17E-05	0.56	3.16	-	169.2
AHQ-6-7, 5294	R.SIQFVDWCPTGFK.V	1586.79232	2	2.57E-04	0.87	3.45	-	843.5
AHQ-6-11, 5283 - 5291	R.SIQFVDWCPTGFK.V	1586.79232	2	5.74E-07	0.85	3.39	-	879.5
AHQ-6-14-, 5434	R.SIQFVDWCPTGFK.V	1586.79232	2	1.42E-05	0.90	3.36	-	883.7
AHQ-6-13, 5528	R.SIQFVDWCPTGFK.V	1586.79232	2	1.08E-05	0.90	3.14	-	1050.5
AHQ-6-12, 5335 - 5343	R.SIQFVDWCPTGFK.V	1586.79232	2	4.20E-04	0.90	3.45	-	870.9
AHQ-6-7, 5178 - 5234	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.56E-08	0.90	4.17	-	644.7
AHQ-6-9, 5024 - 5094	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.49E-04	0.72	3.41	-	395.1
AHQ-6-14, 5950 - 6012	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.60E-11	0.94	4.23	-	993.6
AHQ-6-13, 5471	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	5.74E-08	0.86	3.84	-	532.1
AHQ-6-13-, 5362	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.22E-06	0.91	4.27	-	565.3
AHQ-6-10, 5092 - 5148	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	6.02E-05	0.57	3.19	-	244.2
AHQ-6-8, 5300	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	7.79E-09	0.79	3.63	-	464.9
AHQ-6-14-, 5364	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.73E-09	0.94	4.37	-	848.7
AHQ-6-12, 4312 - 4368	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	6.03E-07	0.61	3.44	-	186.4
AHQ-6-7, 4100 - 4162	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.82E-04	0.59	2.62	-	353.9
AHQ-6-13-, 4262 - 4320	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.39E-04	0.54	2.89	-	353.3
AHQ-6-13, 4381 - 4440	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	7.61E-04	0.68	3.19	-	310.1
AHQ-6-12, 4192 - 4251	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	5.02E-05	0.32	2.51	-	232.8
AHQ-6-3, 4414	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.46E-04	0.16	2.52	-	198.1
AHQ-6-8, 4152	K.YMACCLLYR.G	1252.50864	1	1.65E-05	0.17	2.28	-	133.6
AHQ-6-7, 4116 - 4186	K.YMACCLLYR.G	1252.50864	2	8.92E-05	0.91	2.83	-	954.0
AHQ-6-13, 4071 - 4081	K.YM*ACCLLYR.G	1268.50804	2	2.75E-04	0.74	2.69	-	530.5
AHQ-6-14-, 4363	K.YMACCLLYR.G	1252.50864	2	8.90E-07	0.95	3.60	-	1222.0
gi|4557419|ref|NP_000063.1|	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36			2.14E-12	3.77	40.24	12.90	53052.1
AHQ-6-1, 4628 - 4694	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.98E-04	0.50	2.92	-	318.1
AHQ-6-6, 4454	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	7.49E-05	0.76	3.14	-	504.3
AHQ-6-5, 4487 - 4488	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	7.36E-10	0.93	4.12	-	772.3
AHQ-6-4, 4584	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	2.63E-04	0.67	2.99	-	469.3
AHQ-6-5, 3092	K.RLQVNLLVKPSEK.I	1524.83342	3	4.25E-06	0.95	3.65	-	2244.2
AHQ-6-5, 5312	K.SQVLQFFSSDICR.S	1588.76661	2	5.88E-05	0.93	3.82	-	1245.8
AHQ-6-1, 5442	K.SQVLQFFSSDICR.S	1588.76661	2	9.21E-08	0.94	3.76	-	1404.6
AHQ-6-6, 5275	K.SQVLQFFSSDICR.S	1588.76661	2	1.14E-06	0.92	3.69	-	1333.8
AHQ-6-5, 6415 - 6416	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.61E-11	0.96	4.88	-	1278.8
AHQ-6-1, 6462	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	2.14E-12	0.95	3.94	-	1120.0
gi|4503571|ref|NP_001419.1|	enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n			2.27E-12	8.51	100.25	25.60	47168.7
AHQ-6-14-, 5102	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.22E-08	0.94	4.78	-	595.2
AHQ-6-13-, 5102	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.40E-11	0.93	4.14	-	616.0
AHQ-6-14, 5760	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.03E-12	0.94	4.92	-	477.7
AHQ-6-13, 5192	R.AAVPSGASTGIYEALELR.D	1806.00979	2	7.35E-05	0.94	4.57	-	583.0
AHQ-6-11, 4960	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.44E-05	0.89	3.65	-	493.3
AHQ-6-8, 4806	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.84E-05	0.83	3.64	-	442.9
AHQ-6-8, 4909 - 4916	R.AAVPSGASTGIYEALELR.D	1806.00979	2	9.26E-04	0.83	3.60	-	380.7
AHQ-6-10, 4114 - 4170	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	4.63E-04	0.73	3.55	-	506.3
AHQ-6-8, 5593 - 5602	K.DATNVGDEGGFAPNILENKEGLELLK.T	2744.99178	3	2.27E-12	0.79	4.17	-	642.9
AHQ-6-8, 4000	R.GNPTVEVDLFTSK.G	1407.55065	1	4.82E-04	0.27	2.45	-	511.5
AHQ-6-8, 4006	R.GNPTVEVDLFTSK.G	1407.55065	1	7.50E-09	0.73	3.62	-	703.4
AHQ-6-8, 2259 - 2268	R.IGAEVYHNLK.N	1144.30502	2	2.09E-04	0.90	3.45	-	1196.0
AHQ-6-8, 6262	K.LAMQEFMILPVGAANFR.E	1909.30812	2	3.87E-05	0.95	4.78	-	962.8
AHQ-6-8, 5628	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	1.67E-04	0.65	3.26	-	595.9
AHQ-6-8, 3629 - 3690	K.VNQIGSVTESLQACK.L	1635.82159	2	4.11E-05	0.95	4.06	-	1376.1
AHQ-6-10, 3567	K.VNQIGSVTESLQACK.L	1635.82159	2	4.48E-05	0.56	2.77	-	518.0
AHQ-6-8, 4730	K.VVIGM*DVAASEFFR.S	1557.79584	2	5.97E-05	0.95	3.72	-	1549.9
AHQ-6-8, 4485	R.YISPDQLADLYK.S	1426.59557	2	3.84E-08	0.91	4.10	-	723.1
AHQ-6-8, 4490	R.YISPDQLADLYK.S	1426.59557	1	2.75E-05	0.77	3.57	-	564.3
gi|4507357|ref|NP_003555.1|	transgelin 2; SM22-alpha homolog [Homo sapiens]			2.38E-12	12.41	140.28	62.80	22391.3
AHQ-6-13-, 5430 - 5484	R.DDGLFSGDPNWFPK.K	1595.69288	2	3.79E-04	0.92	3.47	-	1222.1
AHQ-6-12, 5561 - 5623	R.DDGLFSGDPNWFPK.K	1595.69288	2	4.46E-04	0.80	3.01	-	763.9
AHQ-6-11, 5379 - 5439	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.15E-04	0.96	4.27	-	1373.0
AHQ-6-12, 5415 - 5495	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.13E-07	0.98	5.07	-	1798.0
AHQ-6-11, 5469 - 5549	R.DDGLFSGDPNWFPK.K	1595.69288	2	5.11E-04	0.88	3.51	-	862.2
AHQ-6-12, 4921	R.DDGLFSGDPNWFPKK.S	1723.86579	2	3.07E-06	0.89	3.40	-	927.4
AHQ-6-13-, 6393 - 6394	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	6.11E-05	0.69	3.21	-	467.5
AHQ-6-14-, 5847 - 5900	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	3.96E-04	0.17	2.53	-	230.1
AHQ-6-11, 6217 - 6225	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	9.10E-04	0.57	2.93	-	521.3
AHQ-6-11, 5483	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.67E-08	0.85	3.87	-	888.8
AHQ-6-11, 6219	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.90E-09	0.90	4.25	-	979.4
AHQ-6-12, 6276 - 6283	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	3.73E-07	0.81	3.74	-	566.2
AHQ-6-13-, 6349	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.15E-08	0.85	3.97	-	706.8

AHQ-6-11, 2756	R.GASQAGMTGYGMPR.Q	1384.56732	2	6.12E-05	0.73	2.72	-	779.8
AHQ-6-12, 2085 - 2115	R.GPAYGLSR.E	820.91599	2	6.66E-04	0.87	2.71	-	953.2
AHQ-6-12, 2491	R.NFSDNQLQEGK.N	1280.32582	2	8.33E-05	0.91	3.71	-	1018.2
AHQ-6-12, 2637 - 2701	R.NFSDNQLQEGK.N	1280.32582	2	2.27E-04	0.87	3.47	-	833.8
AHQ-6-12, 2243 - 2300	R.NFSDNQLQEGK.N	1280.32582	2	1.23E-06	0.79	3.11	-	652.0
AHQ-6-11, 2516 - 2583	R.NFSDNQLQEGK.N	1280.32582	2	3.63E-04	0.91	3.21	-	1156.3
AHQ-6-11, 2395	R.NFSDNQLQEGK.N	1280.32582	2	1.51E-05	0.85	3.66	-	697.6
AHQ-6-11, 3131	K.NVIGLQMGTNR.G	1203.39751	2	7.49E-07	0.93	3.70	-	1215.9
AHQ-6-11, 2423 - 2503	K.NVIGLQM*GTNR.G	1219.39691	2	1.19E-04	0.95	3.86	-	1207.5
AHQ-6-12, 4547	K.QM*EQISQFLQAAER.Y	1695.87890	3	2.97E-07	0.93	3.51	-	1958.2
AHQ-6-12, 4455 - 4535	K.QM*EQISQFLQAAER.Y	1695.87890	2	8.28E-04	0.83	3.56	-	654.8
AHQ-6-12, 5131 - 5139	K.QMEQISQFLQAAER.Y	1679.87950	2	1.69E-08	0.96	4.36	-	1420.9
AHQ-6-11, 4472	K.QM*EQISQFLQAAER.Y	1695.87890	3	3.39E-07	0.96	4.92	-	1730.8
AHQ-6-14-, 5254	K.QMEQISQFLQAAER.Y	1679.87950	2	5.54E-06	0.80	3.11	-	707.1
AHQ-6-11, 3835 - 3844	R.TLM*NLGGLAVAR.D	1232.47872	2	7.81E-05	0.87	3.21	-	1022.4
AHQ-6-12, 3619 - 3647	R.TLM*NLGGLAVAR.D	1232.47872	2	2.29E-07	0.92	4.07	-	957.4
AHQ-6-12, 4375	R.TLMNLGGLAVAR.D	1216.47932	2	1.11E-04	0.86	3.76	-	844.3
AHQ-6-12, 3825 - 3889	R.TLM*NLGGLAVAR.D	1232.47872	2	8.54E-06	0.84	2.86	-	1042.3
AHQ-6-11, 4307 - 4331	R.TLMNLGGLAVAR.D	1216.47932	2	9.88E-07	0.93	4.26	-	1197.4
AHQ-6-13, 6319	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.38E-12	0.94	4.41	-	847.5
AHQ-6-12, 6207	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	8.64E-10	0.96	5.40	-	980.2
AHQ-6-11, 6075 - 6153	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.72E-09	0.97	5.20	-	1500.2
AHQ-6-14-, 6298 - 6300	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	5.89E-10	0.97	5.62	-	1277.8
AHQ-6-13-, 6284	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	4.00E-08	0.96	4.77	-	1173.7
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				2.70E-12	1.89	20.30	7.40	32164.8
AHQ-6-2, 4808	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.16E-05	0.93	4.46	-	848.6
AHQ-6-3, 4786	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.41E-04	0.88	4.14	-	573.5
AHQ-6-4, 4832	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.18E-04	0.79	3.69	-	501.7
AHQ-6-4, 5297	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.89E-04	0.90	4.07	-	665.4
AHQ-6-5, 4620	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.01E-09	0.92	4.71	-	675.6
AHQ-6-5, 4751	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.35E-05	0.95	4.96	-	758.3
AHQ-6-6, 4722	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.26E-05	0.88	4.03	-	665.1
AHQ-6-8, 4392 - 4462	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.73E-04	0.73	3.25	-	469.9
AHQ-6-8, 4478 - 4540	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.26E-08	0.95	5.43	-	857.9
AHQ-6-8, 4578 - 4638	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.57E-04	0.96	5.36	-	1076.4
AHQ-6-8, 4697 - 4757	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.06E-09	0.97	5.93	-	1035.8
AHQ-6-8, 4798 - 4868	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.70E-12	0.97	5.81	-	1227.1
AHQ-6-8, 4816 - 4896	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.11E-04	0.90	4.35	-	513.4
AHQ-6-8, 4953 - 5012	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.68E-06	0.96	5.32	-	941.9
AHQ-6-8, 5072 - 5132	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.97E-07	0.97	5.69	-	1226.8
AHQ-6-8, 5994 - 6070	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.41E-06	0.83	3.91	-	610.4
AHQ-6-9, 4251 - 4307	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.99E-06	0.79	3.11	-	698.0
AHQ-6-9, 4398 - 4455	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.99E-05	0.95	5.73	-	757.4
AHQ-6-9, 4494	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.30E-04	0.37	2.58	-	280.4
AHQ-6-10, 4314 - 4374	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.61E-07	0.87	4.41	-	418.2
AHQ-6-10, 4443 - 4498	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.29E-04	0.94	5.02	-	891.6
AHQ-6-10, 4542	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.55E-05	0.78	3.73	-	421.4
AHQ-6-10, 4659	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.50E-05	0.89	4.18	-	363.7
AHQ-6-10, 4751 - 4806	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.46E-04	0.93	4.53	-	1047.0
AHQ-6-11, 4564	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.17E-05	0.96	5.25	-	1100.4
AHQ-6-12, 4465 - 4520	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.68E-06	0.89	4.11	-	711.2
AHQ-6-12, 4588 - 4644	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.58E-04	0.95	4.95	-	908.4
AHQ-6-12, 4896	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.02E-04	0.74	3.10	-	553.8
AHQ-6-13, 4651 - 4675	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.70E-10	0.96	5.23	-	959.3
AHQ-6-13, 4749 - 4807	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.77E-07	0.96	5.41	-	1062.8
AHQ-6-13, 4868 - 4869	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.76E-04	0.93	4.79	-	798.5
AHQ-6-13, 4972 - 5029	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.24E-04	0.90	4.00	-	760.6
AHQ-6-13, 5071 - 5128	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.47E-09	0.95	5.26	-	928.8
AHQ-6-13, 5207 - 5264	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.46E-04	0.93	4.58	-	785.1
AHQ-6-14, 5320 - 5380	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.70E-06	0.94	4.84	-	931.4
AHQ-6-14, 5437 - 5516	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.27E-05	0.92	4.63	-	893.0
AHQ-6-14, 5733 - 5789	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.04E-04	0.93	4.69	-	838.7
AHQ-6-13-, 4618 - 4676	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.27E-07	0.95	5.04	-	928.6
AHQ-6-13-, 4733 - 4741	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.66E-05	0.94	4.30	-	970.5
AHQ-6-13-, 4840	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.17E-07	0.91	4.37	-	670.3
AHQ-6-13-, 4940 - 5010	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.33E-04	0.95	5.32	-	916.9
AHQ-6-13-, 5092	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.20E-04	0.94	5.21	-	658.8
AHQ-6-13-, 5254	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.27E-04	0.89	4.20	-	722.0
AHQ-6-14-, 4511 - 4559	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.04E-12	0.92	4.49	-	782.5
AHQ-6-14-, 4636 - 4707	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.58E-04	0.97	5.68	-	1148.9
AHQ-6-14-, 4808 - 4862	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.56E-08	0.97	5.90	-	1141.1
AHQ-6-14-, 4939 - 5016	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.12E-04	0.93	4.70	-	980.9
AHQ-6-14-, 5075 - 5130	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.94E-05	0.97	6.01	-	967.6
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				2.83E-12	12.19	150.25	46.00	49481.2
AHQ-6-8, 4336	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	4.52E-05	0.71	3.34	-	379.0
AHQ-6-7, 4315 - 4392	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	5.14E-07	0.80	3.54	-	468.3
AHQ-6-7, 4300	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	2.82E-04	0.38	3.04	-	268.8
AHQ-6-9, 4199	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	6.45E-05	0.61	3.23	-	279.7
AHQ-6-14-, 5203 - 5214	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.34E-11	0.86	3.56	-	623.3
AHQ-6-7, 5058 - 5114	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.83E-12	0.87	3.64	-	662.7
AHQ-6-13-, 5336 - 5393	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	4.85E-10	0.49	2.82	-	357.1
AHQ-6-7, 5163 - 5218	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	4.64E-07	0.63	2.81	-	492.8
AHQ-6-13-, 5185 - 5240	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	3.78E-06	0.78	3.03	-	729.2
AHQ-6-7, 2663 - 2738	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	7.91E-05	0.96	4.73	-	1706.9
AHQ-6-7, 2658 - 2720	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.17E-07	0.96	4.99	-	1131.1
AHQ-6-8, 2641	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	5.17E-08	0.94	4.29	-	878.3
AHQ-6-11, 3075 - 3081	R.DNCCILDER.F	1197.27847	2	4.37E-04	0.90	3.13	-	1049.9
AHQ-6-12, 3117	R.DNCCILDER.F	1197.27847	2	1.04E-04	0.84	3.06	-	811.2
AHQ-6-5, 5115	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	1.47E-04	0.72	3.29	-	960.0
AHQ-6-10, 4832	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	5.89E-04	0.70	2.82	-	671.4
AHQ-6-4, 5196	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.15E-05	0.69	3.42	-	321.6
AHQ-6-7, 4886 - 4947	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.89E-07	0.90	4.14	-	660.4
AHQ-6-7, 5990 - 6056	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	2.66E-05	0.87	4.00	-	581.2
AHQ-6-7, 4262 - 4294	K.IHLISTQSAIPYALR.V	1683.97576	2	4.64E-07	0.93	3.78	-	1119.3
AHQ-6-9, 4182 - 4198	K.IHLISTQSAIPYALR.V	1683.97576	2	1.60E-10	0.97	4.72	-	1485.5
AHQ-6-7, 4370 - 4432	K.IHLISTQSAIPYALR.V	1683.97576	2	1.58E-04	0.68	3.13	-	488.1
AHQ-6-11, 4364	K.IHLISTQSAIPYALR.V	1683.97576	2	6.62E-08	0.95	4.21	-	1053.8
AHQ-6-7, 2051	R.LDGSVDFKK.N	1009.13788	2	4.48E-06	0.65	2.54	-	617.5
AHQ-6-13-, 2260	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.81E-06	0.83	2.75	-	992.5
AHQ-6-14-, 2207 - 2214	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	4.38E-09	0.92	3.87	-	1112.2
AHQ-6-12, 2241	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	2.20E-04	0.41	2.55	-	322.6
AHQ-6-8, 2082 - 2083	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	4.76E-08	0.92	3.80	-	1125.3
AHQ-6-7, 2078 - 2134	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.21E-07	0.95	3.78	-	1674.3
AHQ-6-7, 3703 - 3706	K.QSGLYFIKPLK.A	1294.56665	2	4.80E-06	0.79	3.07	-	475.2
AHQ-6-7, 2950	R.TSTADYAMFK.V	1135.27203	1	4.07E-04	0.13	2.01	-	95.0
AHQ-6-7, 3702	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	5.41E-06	0.90	4.36	-	857.9
AHQ-6-8, 3732	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	3.04E-04	0.75	3.10	-	584.6

AHQ-6-7, 3858	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	3.39E-05	0.94	5.04	-	929.9
AHQ-6-7, 3131	R.VELEDWNGR.T	1118.18129	2	7.45E-04	0.87	2.68	-	1216.0
AHQ-6-7, 3048	R.VELEDWNGR.T	1118.18129	2	1.46E-06	0.90	2.98	-	1187.7
AHQ-6-11, 3059	K.YEASILTHDSSIR.Y	1492.61564	2	4.26E-07	0.92	3.96	-	848.3
AHQ-6-10, 2939 - 2994	K.YEASILTHDSSIR.Y	1492.61564	2	4.82E-06	0.92	3.59	-	1054.1
AHQ-6-7, 2922 - 2923	K.YEASILTHDSSIR.Y	1492.61564	2	4.07E-07	0.92	3.73	-	838.6
AHQ-6-3, 3158	K.YEASILTHDSSIR.Y	1492.61564	2	3.77E-09	0.78	2.53	-	788.0
AHQ-6-12, 3089	K.YEASILTHDSSIR.Y	1492.61564	2	3.18E-06	0.72	2.87	-	456.7
gi|13775198|ref|NP_112576.1|	SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr			3.10E-12	4.01	50.26	34.40	10437.7
AHQ-6-14, 5288	R.IQYQLVDISQDNALR.D	1776.97168	2	3.89E-05	0.92	3.80	-	1371.1
AHQ-6-13-, 4625 - 4686	R.IQYQLVDISQDNALR.D	1776.97168	2	6.19E-10	0.95	4.53	-	1282.1
AHQ-6-13-, 4552	R.IQYQLVDISQDNALR.D	1776.97168	3	9.71E-06	0.96	4.82	-	2252.3
AHQ-6-13-, 4544	R.IQYQLVDISQDNALR.D	1776.97168	2	3.10E-12	0.96	4.32	-	1851.1
AHQ-6-13, 4671 - 4732	R.IQYQLVDISQDNALR.D	1776.97168	2	1.63E-05	0.95	4.15	-	1606.0
AHQ-6-13, 4681	R.IQYQLVDISQDNALR.D	1776.97168	3	2.09E-06	0.96	5.05	-	2105.7
AHQ-6-13, 4803	R.IQYQLVDISQDNALR.D	1776.97168	2	1.27E-04	0.89	3.57	-	992.1
AHQ-6-14-, 4555 - 4616	R.IQYQLVDISQDNALR.D	1776.97168	2	5.49E-11	0.97	5.13	-	1724.6
AHQ-6-13, 4924	R.IQYQLVDISQDNALRDEMR.A	2308.55751	2	2.45E-04	0.80	3.74	-	425.4
AHQ-6-13, 5024 - 5068	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	2.06E-06	0.56	3.02	-	460.5
AHQ-6-14, 5053 - 5132	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.50E-05	0.92	4.57	-	740.1
AHQ-6-13, 4907 - 4963	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	3.91E-06	0.55	3.04	-	384.6
AHQ-6-14-, 4430	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	4.05E-07	0.73	3.19	-	379.2
AHQ-6-14-, 4339	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	6.08E-04	0.72	3.11	-	635.0
AHQ-6-13-, 4404 - 4473	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.30E-06	0.72	3.70	-	484.1
AHQ-6-13, 4387 - 4447	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.32E-05	0.73	3.25	-	502.8
AHQ-6-13, 4287	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	4.65E-07	0.80	3.09	-	723.1
AHQ-6-13-, 4860	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	2.02E-07	0.65	3.06	-	394.1
AHQ-6-13-, 4726 - 4800	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	5.07E-04	0.88	3.75	-	866.1
AHQ-6-13-, 1946	R.VYSTSVTGSR.E	1057.13940	2	1.53E-04	0.83	2.72	-	853.7
AHQ-6-13-, 1828 - 1889	R.VYSTSVTGSR.E	1057.13940	2	3.85E-04	0.79	2.79	-	593.9
AHQ-6-13, 2151 - 2227	R.VYSTSVTGSR.E	1057.13940	2	1.32E-06	0.88	3.23	-	865.2
AHQ-6-13, 2547	R.VYSTSVTGSREIK.S	1427.58510	2	9.99E-04	0.78	2.79	-	842.5
gi|4759212|ref|NP_004598.1|	beta-tubulin cofactor A [Homo sapiens]			3.21E-12	2.90	30.31	25.90	12854.8
AHQ-6-13-, 3561	R.ILENEKDLEEAEEYK.E	1852.97372	2	9.32E-12	0.97	5.39	-	1516.8
AHQ-6-13-, 3402	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	3.21E-12	0.97	5.59	-	1602.4
AHQ-6-13-, 3413	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	1.50E-06	0.97	6.15	-	1237.8
AHQ-6-13, 3539	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	3.45E-12	0.97	6.09	-	1328.6
AHQ-6-13, 3849 - 3859	R.LEAAYLDLQR.I	1192.34645	2	5.36E-06	0.96	3.86	-	1558.5
gi|4557677|ref|NP_000203.1|	integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu			3.74E-12	20.08	240.30	35.50	87185.6
AHQ-6-4, 3064	R.AKWDTANNPLYK.E	1421.58225	2	2.06E-07	0.56	3.06	-	319.5
AHQ-6-3, 3097 - 3160	R.AKWDTANNPLYK.E	1421.58225	2	2.48E-07	0.80	3.31	-	801.9
AHQ-6-12, 3041 - 3049	R.AKWDTANNPLYK.E	1421.58225	2	3.96E-04	0.72	2.85	-	556.8
AHQ-6-3, 5116	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	2.54E-05	0.85	3.85	-	766.1
AHQ-6-3, 5201	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	2.59E-05	0.93	4.72	-	1061.3
AHQ-6-3, 4180 - 4242	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	3.99E-05	0.83	4.15	-	451.0
AHQ-6-5, 4123	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	8.54E-08	0.71	3.77	-	521.9
AHQ-6-1, 5459 - 5532	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	3.61E-05	0.93	3.90	-	942.7
AHQ-6-3, 5432 - 5488	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.27E-08	0.92	3.86	-	793.9
AHQ-6-3, 5545	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.00E-05	0.92	4.08	-	751.5
AHQ-6-1, 4388	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.73E-07	0.95	4.50	-	1009.5
AHQ-6-6, 4183	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.23E-05	0.89	3.23	-	916.8
AHQ-6-4, 4295	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	4.01E-04	0.56	2.77	-	393.9
AHQ-6-3, 4346	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	7.27E-04	0.66	3.12	-	629.8
AHQ-6-3, 4222 - 4280	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	6.41E-08	0.93	4.05	-	960.4
AHQ-6-5, 5484	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	3.69E-07	0.92	3.98	-	868.7
AHQ-6-4, 4760	K.DDLWSIQNLGTK.L	1390.52332	2	5.35E-05	0.74	3.01	-	610.4
AHQ-6-6, 4154 - 4156	K.DNCAPESIEFPVSEAR.V	1822.93099	2	3.12E-06	0.74	2.98	-	582.1
AHQ-6-2, 4282	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.60E-04	0.78	3.11	-	842.4
AHQ-6-8, 4022	K.DNCAPESIEFPVSEAR.V	1822.93099	2	5.24E-07	0.57	2.82	-	479.1
AHQ-6-3, 4237	K.DNCAPESIEFPVSEAR.V	1822.93099	2	3.49E-06	0.89	3.44	-	970.8
AHQ-6-4, 3345	K.EATSTFTNITYR.G	1404.50685	2	9.02E-06	0.82	3.07	-	670.1
AHQ-6-3, 3372 - 3378	K.EATSTFTNITYR.G	1404.50685	2	2.48E-05	0.87	3.13	-	905.3
AHQ-6-5, 3300	K.EATSTFTNITYR.G	1404.50685	2	3.77E-08	0.87	2.91	-	903.3
AHQ-6-4, 2376 - 2377	R.FQYYEDSSGK.S	1224.25749	1	5.96E-04	0.41	2.28	-	440.4
AHQ-6-3, 2412	R.FQYYEDSSGK.S	1224.25749	1	2.18E-04	0.58	2.70	-	463.3
AHQ-6-6, 3450	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.39E-05	0.92	3.93	-	1277.5
AHQ-6-1, 3711	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	4.32E-04	0.70	2.91	-	584.8
AHQ-6-4, 3527	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	9.89E-06	0.96	4.34	-	1834.3
AHQ-6-3, 3536 - 3614	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	5.71E-07	0.92	3.78	-	1353.3
AHQ-6-5, 3471	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.35E-05	0.96	4.44	-	1581.7
AHQ-6-3, 4437	R.GKCECGSCVCIQPGSYGDTCEKCPTCPDACTFK.K	3900.25293	3	3.37E-05	0.84	4.11	-	556.4
AHQ-6-3, 1970 - 2028	K.GSGDSSQVTQVSPQR.I	1533.58302	2	9.63E-04	0.66	3.12	-	665.1
AHQ-6-8, 2616	K.HVLTLTDQVTR.F	1283.45912	2	7.18E-06	0.87	3.39	-	555.6
AHQ-6-4, 2781	K.HVLTLTDQVTR.F	1283.45912	2	5.59E-07	0.92	3.52	-	754.1
AHQ-6-3, 2758 - 2833	K.HVLTLTDQVTR.F	1283.45912	2	2.82E-09	0.94	3.78	-	795.2
AHQ-6-1, 3063	K.HVLTLTDQVTR.F	1283.45912	2	7.58E-07	0.93	3.48	-	814.4
AHQ-6-6, 2743	K.HVLTLTDQVTR.F	1283.45912	2	2.09E-04	0.71	2.99	-	414.9
AHQ-6-5, 2744	K.HVLTLTDQVTR.F	1283.45912	2	2.52E-05	0.92	3.23	-	818.7
AHQ-6-2, 2840	K.HVLTLTDQVTR.F	1283.45912	2	1.87E-08	0.91	3.40	-	723.9
AHQ-6-4, 4060	K.IGDTVSFSIEAK.V	1267.41009	2	1.62E-05	0.70	2.54	-	810.9
AHQ-6-3, 4229	K.IGDTVSFSIEAK.V	1267.41009	2	4.36E-05	0.89	3.11	-	870.2
AHQ-6-3, 4104	K.IGDTVSFSIEAK.V	1267.41009	2	1.24E-04	0.86	2.98	-	897.7
AHQ-6-3, 3588	K.IGDTVSFSIEAK.V	1267.41009	2	2.86E-08	0.88	3.29	-	960.8
AHQ-6-3, 3537 - 3600	K.ITGKYCECDDFSCVR.Y	1914.08378	2	1.15E-04	0.83	3.48	-	724.2
AHQ-6-4, 3823 - 3887	R.NDASHLLVFTTDAK.T	1532.67977	2	1.23E-09	0.98	5.94	-	1698.9
AHQ-6-9, 3552	R.NDASHLLVFTTDAK.T	1532.67977	2	3.86E-06	0.77	2.99	-	611.2
AHQ-6-4, 4120	R.NDASHLLVFTTDAK.T	1532.67977	2	3.91E-06	0.80	3.31	-	752.5
AHQ-6-4, 4275	R.NDASHLLVFTTDAK.T	1532.67977	2	3.54E-11	0.96	4.64	-	1260.9
AHQ-6-3, 3821 - 3880	R.NDASHLLVFTTDAK.T	1532.67977	2	4.11E-09	0.96	4.59	-	1307.0
AHQ-6-6, 3764	R.NDASHLLVFTTDAK.T	1532.67977	2	1.10E-07	0.94	4.07	-	1150.7
AHQ-6-7, 3651	R.NDASHLLVFTTDAK.T	1532.67977	2	5.42E-06	0.94	3.96	-	1169.7
AHQ-6-5, 3815	R.NDASHLLVFTTDAK.T	1532.67977	3	1.03E-06	0.86	4.01	-	924.8
AHQ-6-3, 3894	R.NDASHLLVFTTDAK.T	1532.67977	3	5.34E-05	0.95	4.38	-	1396.9
AHQ-6-4, 3465	K.SFTIKPVGFK.D	1124.35685	2	1.17E-05	0.88	2.84	-	1113.4
AHQ-6-6, 3398	K.SFTIKPVGFK.D	1124.35685	2	8.12E-05	0.77	2.68	-	792.2
AHQ-6-3, 2961	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.79E-11	0.94	3.55	-	1444.2
AHQ-6-4, 2789	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.97E-08	0.93	3.77	-	1321.2
AHQ-6-4, 3493	R.TDTCMSSNGLLCSGR.G	1661.81786	2	9.00E-05	0.81	3.21	-	776.5
AHQ-6-5, 3429 - 3504	R.TDTCMSSNGLLCSGR.G	1661.81786	2	4.54E-05	0.37	2.57	-	561.1
AHQ-6-4, 3399	R.TDTCMSSNGLLCSGR.G	1661.81786	2	3.06E-09	0.95	4.04	-	1226.8
AHQ-6-3, 2796 - 2868	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.74E-12	0.95	3.91	-	1656.1
AHQ-6-5, 2015	R.VLEDRPLSDK.G	1172.31354	2	1.87E-06	0.94	3.60	-	1081.6
AHQ-6-3, 2062 - 2134	R.VLEDRPLSDK.G	1172.31354	2	1.68E-04	0.92	3.66	-	997.0
AHQ-6-4, 2035	R.VLEDRPLSDK.G	1172.31354	2	1.68E-05	0.91	3.19	-	1122.1
AHQ-6-6, 2034	R.VLEDRPLSDK.G	1172.31354	2	6.19E-05	0.85	3.12	-	894.1
AHQ-6-3, 2836	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	1.75E-09	0.95	4.79	-	1535.2
AHQ-6-7, 2690	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	8.03E-08	0.90	4.27	-	967.6

AHQ-6-5, 2763	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	2.80E-07	0.90	3.86	-	1004.1
AHQ-6-4, 2811	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	1.97E-06	0.93	4.86	-	1104.0
AHQ-6-4, 3313	K.WDTANNPLYK.E	1222.33111	2	8.63E-05	0.79	2.82	-	788.0
AHQ-6-3, 3504 - 3552	K.YCECDDFSCVR.Y	1514.59674	2	2.63E-06	0.96	3.88	-	1437.6
AHQ-6-6, 3468 - 3470	K.YCECDDFSCVR.Y	1514.59674	2	3.21E-04	0.95	3.61	-	1408.5
AHQ-6-3, 2373	R.YCRDEIESVK.E	1300.42023	2	4.65E-06	0.92	3.60	-	1175.0
gi|4501893|ref|NP_001094.1|	actinin, alpha 2 [Homo sapiens]			4.76E-12	10.66	120.26	13.30	103853.1
AHQ-6-4, 4432	K.AGTQIENIEEDFR.N	1522.59861	2	6.43E-05	0.88	3.65	-	878.4
AHQ-6-4, 5181 - 5244	K.AGTQIENIEEDFRNGLK.L	1935.08442	2	1.35E-07	0.58	3.76	-	613.1
AHQ-6-4, 4933	K.AGTQIENIEEDFRNGLK.L	1935.08442	2	5.30E-04	0.41	3.20	-	363.2
AHQ-6-6, 4726	K.CQLEINFNTLQTK.L	1610.81373	2	1.08E-06	0.94	4.28	-	1039.6
AHQ-6-4, 4673	K.CQLEINFNTLQTK.L	1610.81373	2	7.56E-07	0.95	4.35	-	1103.5
AHQ-6-5, 4753	K.CQLEINFNTLQTK.L	1610.81373	2	5.26E-07	0.93	3.93	-	954.3
AHQ-6-4, 4827 - 4828	K.CQLEINFNTLQTK.L	1610.81373	2	6.89E-10	0.95	4.27	-	1375.1
AHQ-6-4, 4783	K.EGLLLWCQR.K	1176.37031	2	9.56E-04	0.82	2.76	-	709.6
AHQ-6-6, 4058 - 4136	R.FAIQDISVEETSAK.E	1538.68108	2	3.82E-08	0.93	3.82	-	1243.1
AHQ-6-7, 3950	R.FAIQDISVEETSAK.E	1538.68108	2	6.38E-07	0.90	3.47	-	1087.3
AHQ-6-2, 4211	R.FAIQDISVEETSAK.E	1538.68108	2	2.68E-05	0.60	2.58	-	583.3
AHQ-6-3, 4166	R.FAIQDISVEETSAK.E	1538.68108	2	1.55E-10	0.94	3.98	-	1164.6
AHQ-6-4, 4152 - 4165	R.FAIQDISVEETSAK.E	1538.68108	2	6.30E-10	0.94	4.25	-	1086.3
AHQ-6-5, 4091	R.FAIQDISVEETSAK.E	1538.68108	2	2.28E-07	0.92	3.69	-	1134.8
AHQ-6-4, 4031	R.FAIQDISVEETSAK.E	1538.68108	2	1.80E-05	0.93	4.05	-	1065.8
AHQ-6-10, 3931	R.FAIQDISVEETSAK.E	1538.68108	2	3.39E-04	0.51	2.52	-	589.4
AHQ-6-6, 5606 - 5623	K.GYEEWLLNEIR.R	1422.56701	2	5.91E-07	0.94	3.87	-	1399.1
AHQ-6-4, 5291 - 5300	K.GYEEWLLNEIR.R	1422.56701	2	1.72E-06	0.94	3.68	-	1315.9
AHQ-6-4, 5736	K.GYEEWLLNEIR.R	1422.56701	2	2.10E-07	0.96	4.00	-	1692.9
AHQ-6-4, 5851	K.GYEEWLLNEIR.R	1422.56701	2	1.18E-04	0.87	3.16	-	1070.2
AHQ-6-5, 5667	K.GYEEWLLNEIR.R	1422.56701	2	1.56E-07	0.81	2.99	-	952.0
AHQ-6-4, 2364	K.HEAFESDLAAHQDR.V	1626.66861	2	6.12E-12	0.97	5.15	-	1502.3
AHQ-6-4, 3900 - 3961	R.KAGTQIENIEEDFR.N	1650.77152	2	1.86E-04	0.89	3.34	-	812.8
AHQ-6-6, 2151 - 2226	R.KHEAFESDLAAHQDR.V	1754.84152	2	2.13E-09	0.95	4.44	-	1199.7
AHQ-6-4, 2143	R.KHEAFESDLAAHQDR.V	1754.84152	2	4.76E-12	0.97	5.10	-	1391.8
AHQ-6-4, 3205	R.KTFTAWCNSHLR.K	1522.71309	2	8.35E-10	0.90	3.27	-	1136.1
AHQ-6-5, 5775	K.LM*LLLEVISGER.L	1389.68652	2	9.41E-07	0.98	4.96	-	2131.7
AHQ-6-4, 4300 - 4307	K.LVSIGAEEIVDGNVK.M	1543.74400	2	9.84E-07	0.96	4.54	-	1364.1
AHQ-6-4, 4039 - 4099	K.LVSIGAEEIVDGNVK.M	1543.74400	2	5.30E-09	0.97	4.84	-	1559.5
AHQ-6-5, 4247 - 4313	K.LVSIGAEEIVDGNVK.M	1543.74400	2	3.04E-06	0.54	2.50	-	922.8
AHQ-6-4, 4657	K.LVSIGAEEIVDGNVK.M	1543.74400	2	3.59E-05	0.93	4.39	-	852.3
gi|4505733|ref|NP_002610.1|	platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4			4.90E-12	6.42	70.29	39.60	10844.9
AHQ-6-14-, 4382	K.AGPHCPTAQLIATLK.N	1579.84600	2	3.62E-07	0.79	3.08	-	573.0
AHQ-6-13, 4275 - 4348	K.AGPHCPTAQLIATLK.N	1579.84600	2	5.44E-06	0.89	3.53	-	702.1
AHQ-6-14-, 4140	K.AGPHCPTAQLIATLK.N	1579.84600	2	2.77E-06	0.90	3.96	-	729.1
AHQ-6-14-, 4055 - 4056	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.06E-05	0.95	4.05	-	1055.3
AHQ-6-14, 4824 - 4893	K.AGPHCPTAQLIATLK.N	1579.84600	2	7.24E-08	0.94	4.36	-	889.9
AHQ-6-13-, 4150 - 4226	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.46E-04	0.93	3.59	-	983.1
AHQ-6-14, 4758 - 4762	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	1.70E-10	0.97	5.19	-	1513.7
AHQ-6-14, 4760	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	6.60E-09	0.97	5.06	-	2068.9
AHQ-6-14-, 3982 - 4034	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.66E-10	0.98	5.42	-	3240.0
AHQ-6-14-, 3988	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	4.90E-12	0.95	4.54	-	1027.1
AHQ-6-14-, 3872	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	2.31E-07	0.96	4.77	-	1105.0
AHQ-6-14, 4649 - 4668	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	2.79E-07	0.97	5.25	-	1946.6
AHQ-6-14, 4646 - 4677	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	2.76E-06	0.92	4.11	-	850.3
AHQ-6-14-, 3819 - 3878	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	3.19E-10	0.98	5.87	-	3207.8
AHQ-6-14-, 3627	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	2	3.38E-06	0.89	4.34	-	569.5
AHQ-6-14-, 3754	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	1.75E-09	0.96	5.20	-	1619.6
AHQ-6-14-, 2610 - 2682	R.HITSLEVIK.A	1040.23825	2	1.33E-06	0.91	3.87	-	531.9
AHQ-6-14, 3572 - 3636	R.HITSLEVIK.A	1040.23825	2	8.15E-07	0.87	3.22	-	631.0
AHQ-6-14, 3458 - 3520	R.HITSLEVIK.A	1040.23825	2	1.42E-05	0.76	3.30	-	400.1
AHQ-6-14-, 4764	K.ICLDLQAPLYK.K	1335.59400	1	2.83E-05	0.69	3.23	-	525.8
AHQ-6-14-, 4746 - 4748	K.ICLDLQAPLYK.K	1335.59400	2	1.64E-07	0.98	4.94	-	2389.5
AHQ-6-13-, 4760	K.ICLDLQAPLYK.K	1335.59400	2	7.00E-06	0.97	3.97	-	2042.1
AHQ-6-14-, 4944	K.ICLDLQAPLYK.K	1335.59400	2	3.80E-05	0.91	3.61	-	1090.0
AHQ-6-13, 4883	K.ICLDLQAPLYK.K	1335.59400	2	1.00E-05	0.96	3.63	-	1927.3
AHQ-6-14, 5488	K.ICLDLQAPLYK.K	1335.59400	2	6.86E-05	0.97	4.72	-	1979.5
AHQ-6-14-, 4614	K.ICLDLQAPLYK.K	1335.59400	2	4.55E-04	0.92	3.21	-	1358.4
AHQ-6-14-, 4407	R.KICLDLQAPLYK.K	1463.76691	1	5.59E-04	0.81	2.92	-	882.4
AHQ-6-14-, 4423	R.KICLDLQAPLYK.K	1463.76691	1	2.46E-07	0.88	3.67	-	860.0
AHQ-6-14-, 4402 - 4462	R.KICLDLQAPLYK.K	1463.76691	2	3.34E-06	0.97	5.12	-	1484.2
AHQ-6-14, 5189 - 5248	R.KICLDLQAPLYK.K	1463.76691	2	4.40E-06	0.95	4.14	-	1246.0
AHQ-6-12, 4377	R.KICLDLQAPLYK.K	1463.76691	2	4.59E-06	0.83	3.03	-	982.5
AHQ-6-14-, 4404 - 4470	R.KICLDLQAPLYK.K	1463.76691	3	1.89E-06	0.94	4.23	-	1579.5
AHQ-6-14, 4772	R.KICLDLQAPLYKK.I	1591.93982	2	5.30E-05	0.84	3.53	-	920.3
gi|4758086|ref|NP_004069.1|	cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain			5.14E-12	6.20	70.23	50.30	20567.3
AHQ-6-13, 4324	K.GFGFGQGAGALVHSE	1434.53788	2	3.97E-04	0.60	2.77	-	460.1
AHQ-6-11, 4005 - 4063	K.GFGFGQGAGALVHSE	1434.53788	2	1.14E-05	0.93	3.86	-	877.1
AHQ-6-11, 3232 - 3287	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.62E-06	0.95	4.49	-	1262.9
AHQ-6-11, 3229 - 3296	K.GLESTTLADKDGEIYCK.G	1902.06957	3	2.94E-08	0.91	4.44	-	696.0
AHQ-6-11, 2608	K.GYGYGQGAGTLSTDK.G	1475.54194	2	4.69E-05	0.85	3.00	-	789.2
AHQ-6-11, 3493 - 3511	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	4.04E-09	0.81	3.54	-	662.4
AHQ-6-13-, 3620	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	7.12E-10	0.85	3.59	-	636.9
AHQ-6-13-, 3625	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	2.69E-08	0.81	4.09	-	554.9
AHQ-6-11, 3496	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	7.50E-11	0.93	4.65	-	762.3
AHQ-6-13-, 3566	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	2.56E-06	0.92	4.19	-	723.9
AHQ-6-11, 3449 - 3456	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	8.25E-08	0.91	4.43	-	737.4
AHQ-6-14-, 3534	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	5.14E-12	0.84	3.44	-	695.2
AHQ-6-11, 4585	K.SCFLCMVCK.K	1208.47423	2	4.91E-04	0.91	3.17	-	840.8
AHQ-6-11, 4053	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	2.87E-05	0.83	3.96	-	583.1
gi|4504521|ref|NP_002147.1|	heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P			5.41E-12	2.32	30.27	11.70	61024.2
AHQ-6-14-, 6303	R.ALM*LQGVDLLADAVAVTM*GPK.G	2146.55768	3	8.79E-10	0.97	5.12	-	2469.1
AHQ-6-7, 5076	K.ISSIQSIVPALEIANAHR.K	1920.20240	2	2.17E-04	0.40	2.95	-	290.0
AHQ-6-7, 6374	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D	2870.28530	3	5.41E-12	0.95	5.34	-	1263.7
gi|5031635|ref|NP_005498.1|	cofilin 1 (non-muscle) [Homo sapiens]			6.15E-12	9.33	100.34	62.70	18502.4
AHQ-6-13-, 3610	K.AVLFCLSEDKK.N	1311.52930	2	2.76E-05	0.81	2.63	-	774.3
AHQ-6-12, 3515 - 3571	K.AVLFCLSEDKK.N	1311.52930	2	5.02E-05	0.75	2.95	-	789.0
AHQ-6-14-, 5382	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	7.90E-07	0.97	5.03	-	1490.9
AHQ-6-14, 5961 - 5965	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.67E-07	0.96	4.78	-	1371.3
AHQ-6-13-, 5364 - 5438	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.20E-09	0.98	5.88	-	1801.5
AHQ-6-12, 5296	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	2.82E-10	0.94	4.42	-	944.2
AHQ-6-13, 5448 - 5455	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.34E-09	0.98	5.74	-	1705.5
AHQ-6-12, 2507 - 2567	K.HELQANCYEEVKDR.C	1792.90812	3	6.15E-12	0.98	6.09	-	2356.6
AHQ-6-12, 2628 - 2687	K.HELQANCYEEVKDR.C	1792.90812	2	2.51E-08	0.96	4.38	-	1162.6
AHQ-6-13-, 2518 - 2589	K.HELQANCYEEVKDR.C	1792.90812	3	1.35E-05	0.91	4.00	-	1089.0
AHQ-6-12, 2483 - 2543	K.HELQANCYEEVKDR.C	1792.90812	2	2.12E-07	0.97	4.78	-	1724.2
AHQ-6-12, 3116	K.KAVLFCLSEDKK.N	1439.70221	3	2.36E-06	0.88	3.93	-	896.3
AHQ-6-13-, 6112	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	1.29E-04	0.97	5.01	-	1687.2
AHQ-6-12, 3972 - 3975	K.LGGSAVISLEGKPL	1341.57848	2	2.36E-04	0.93	4.17	-	1097.6
AHQ-6-14-, 4338	K.LGGSAVISLEGKPL	1341.57848	2	2.11E-05	0.79	3.14	-	639.0

AHQ-6-12, 4267 - 4332	K.LGGSAVISLEGKPL	1341.57848	2	2.44E-05	0.97	4.93	-	1311.1
AHQ-6-12, 4387	K.LGGSAVISLEGKPL	1341.57848	2	8.77E-05	0.93	4.28	-	933.6
AHQ-6-13-, 4345 - 4346	K.LGGSAVISLEGKPL	1341.57848	2	6.74E-06	0.96	4.72	-	1356.1
AHQ-6-12, 3052 - 3121	K.LTGIKHELQANCYEEVKDR.C	2305.55341	3	7.56E-10	0.98	6.34	-	1766.6
AHQ-6-12, 6039 - 6120	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	6.79E-06	0.95	5.40	-	1273.2
AHQ-6-12, 6167 - 6175	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	3.72E-07	0.98	6.77	-	2134.9
AHQ-6-14-, 6184 - 6239	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.88E-05	0.92	5.04	-	904.9
AHQ-6-12, 3231 - 3261	R.YALYDATYETK.E	1338.44364	2	3.98E-09	0.94	3.78	-	1060.9
AHQ-6-12, 3245	R.YALYDATYETK.E	1338.44364	1	4.21E-08	0.68	3.09	-	425.5
AHQ-6-13, 3417 - 3485	R.YALYDATYETK.E	1338.44364	2	5.89E-04	0.83	3.62	-	848.3
AHQ-6-12, 2964	R.YALYDATYETKESK.K	1682.80875	2	8.24E-05	0.89	3.17	-	1157.9
gi|5032161|ref|NP_005639.1|	elongin C; transcription elongation factor B (SIII), polypeptide 1 (15k			6.87E-12	1.86	20.27	30.40	12473.1
AHQ-6-13, 4487 - 4548	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	1.86E-07	0.92	4.20	-	890.0
AHQ-6-13-, 4390	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	6.87E-12	0.97	5.41	-	1791.9
AHQ-6-13, 4269	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	1.04E-10	0.74	2.72	-	685.9
AHQ-6-13-, 2797 - 2866	K.TYGGCEGPDAM*YVK.L	1565.70692	2	6.72E-07	0.89	3.56	-	792.9
gi|4505981|ref|NP_002695.1|	pro-platelet basic protein (includes platelet basic protein, bet; Pro-p			7.07E-12	8.23	90.30	46.90	13894.1
AHQ-6-14, 5304 - 5360	K.EESLDSDLYAELR.C	1540.61070	2	1.09E-06	0.85	3.29	-	800.2
AHQ-6-14-, 4295 - 4358	K.EESLDSDLYAELR.C	1540.61070	2	1.16E-06	0.88	3.51	-	593.6
AHQ-6-14-, 4560 - 4640	K.EESLDSDLYAELR.C	1540.61070	2	2.31E-08	0.94	4.38	-	906.4
AHQ-6-13-, 4581	K.EESLDSDLYAELR.C	1540.61070	2	1.15E-05	0.90	3.55	-	917.8
AHQ-6-13, 4072	K.GKEESLDSDLYAELR.C	1725.83517	2	4.58E-05	0.85	3.10	-	759.8
AHQ-6-13, 4295	K.GKEESLDSDLYAELR.C	1725.83517	2	9.75E-10	0.98	5.24	-	2037.7
AHQ-6-13, 4296 - 4307	K.GKEESLDSDLYAELR.C	1725.83517	3	9.20E-04	0.85	4.10	-	780.4
AHQ-6-14-, 4355	K.GKEESLDSDLYAELR.C	1725.83517	2	1.10E-09	0.98	5.07	-	2226.7
AHQ-6-12, 4091	K.GKEESLDSDLYAELR.C	1725.83517	2	8.91E-08	0.98	5.19	-	1899.8
AHQ-6-14-, 4266	K.GKEESLDSDLYAELR.C	1725.83517	2	5.65E-09	0.98	5.22	-	2458.9
AHQ-6-14-, 4147 - 4207	K.GKEESLDSDLYAELR.C	1725.83517	2	1.49E-09	0.98	6.00	-	2692.0
AHQ-6-14-, 4110 - 4186	K.GKEESLDSDLYAELR.C	1725.83517	3	1.05E-04	0.91	4.42	-	1118.3
AHQ-6-14-, 4026 - 4086	K.GKEESLDSDLYAELR.C	1725.83517	2	1.16E-08	0.98	5.49	-	2691.1
AHQ-6-14-, 3986 - 4048	K.GKEESLDSDLYAELR.C	1725.83517	3	4.12E-06	0.89	3.98	-	1191.8
AHQ-6-14-, 3898 - 3966	K.GKEESLDSDLYAELR.C	1725.83517	2	2.16E-11	0.98	5.60	-	2019.0
AHQ-6-14-, 3755	K.GKEESLDSDLYAELR.C	1725.83517	2	9.72E-09	0.97	5.01	-	1805.8
AHQ-6-14-, 4527	K.GKEESLDSDLYAELR.C	1725.83517	2	1.05E-10	0.98	5.09	-	2214.0
AHQ-6-14, 5914	K.GKEESLDSDLYAELR.C	1725.83517	2	3.92E-06	0.93	3.30	-	1720.7
AHQ-6-14, 5570 - 5625	K.GKEESLDSDLYAELR.C	1725.83517	2	9.59E-08	0.97	4.56	-	1949.2
AHQ-6-14, 4632 - 4689	K.GKEESLDSDLYAELR.C	1725.83517	2	8.76E-04	0.96	4.69	-	1260.6
AHQ-6-14, 4657 - 4713	K.GKEESLDSDLYAELR.C	1725.83517	3	1.58E-05	0.88	4.35	-	990.6
AHQ-6-14, 5309 - 5364	K.GKEESLDSDLYAELR.C	1725.83517	2	1.20E-07	0.96	4.63	-	1706.6
AHQ-6-14, 4744 - 4800	K.GKEESLDSDLYAELR.C	1725.83517	2	6.63E-10	0.98	5.31	-	2114.7
AHQ-6-6, 4122	K.GKEESLDSDLYAELR.C	1725.83517	2	1.80E-06	0.98	4.82	-	2365.9
AHQ-6-14, 4825 - 4888	K.GKEESLDSDLYAELR.C	1725.83517	3	1.72E-05	0.83	4.23	-	784.3
AHQ-6-14, 5221 - 5276	K.GKEESLDSDLYAELR.C	1725.83517	2	6.75E-06	0.98	5.61	-	2130.5
AHQ-6-14, 4860 - 4937	K.GKEESLDSDLYAELR.C	1725.83517	2	2.05E-09	0.98	5.62	-	2717.8
AHQ-6-14, 5088 - 5144	K.GKEESLDSDLYAELR.C	1725.83517	2	5.86E-06	0.98	5.36	-	1925.3
AHQ-6-14, 4932 - 4988	K.GKEESLDSDLYAELR.C	1725.83517	3	5.49E-06	0.94	4.70	-	1412.4
AHQ-6-14, 4984 - 5000	K.GKEESLDSDLYAELR.C	1725.83517	2	1.44E-06	0.98	5.38	-	2637.1
AHQ-6-14-, 4779	K.GKEESLDSDLYAELR.C	1725.83517	2	7.47E-04	0.96	4.60	-	1322.4
AHQ-6-14, 4906 - 4980	K.GTHCNQVEVIATLK.D	1571.78073	2	1.40E-06	0.91	3.88	-	916.3
AHQ-6-14, 4165 - 4224	K.GTHCNQVEVIATLK.D	1571.78073	2	3.75E-04	0.93	3.68	-	1345.0
AHQ-6-14, 4764	K.GTHCNQVEVIATLK.D	1571.78073	2	1.75E-04	0.97	4.46	-	2218.8
AHQ-6-14, 4670 - 4694	K.GTHCNQVEVIATLK.D	1571.78073	2	1.17E-04	0.95	4.45	-	1372.3
AHQ-6-14, 4550 - 4628	K.GTHCNQVEVIATLK.D	1571.78073	2	1.06E-05	0.97	4.90	-	1428.6
AHQ-6-14, 4428 - 4484	K.GTHCNQVEVIATLK.D	1571.78073	2	6.38E-09	0.97	5.31	-	1830.8
AHQ-6-14-, 3854	K.GTHCNQVEVIATLK.D	1571.78073	2	6.05E-04	0.96	4.02	-	1503.7
AHQ-6-13-, 3493 - 3565	K.GTHCNQVEVIATLK.D	1571.78073	2	2.31E-09	0.94	4.18	-	949.6
AHQ-6-14, 4260 - 4336	K.GTHCNQVEVIATLK.D	1571.78073	2	1.63E-08	0.97	4.80	-	2020.0
AHQ-6-14-, 3706 - 3784	K.GTHCNQVEVIATLK.D	1571.78073	2	4.34E-09	0.97	5.28	-	1708.0
AHQ-6-14-, 3574 - 3648	K.GTHCNQVEVIATLK.D	1571.78073	2	2.17E-06	0.96	4.75	-	1376.4
AHQ-6-14-, 3524 - 3590	K.GTHCNQVEVIATLK.D	1571.78073	2	1.08E-08	0.96	4.68	-	1415.3
AHQ-6-14, 5034 - 5105	K.GTHCNQVEVIATLK.D	1571.78073	2	2.45E-05	0.95	3.59	-	1609.3
AHQ-6-14-, 3262 - 3332	K.GTHCNQVEVIATLK.D	1571.78073	2	2.38E-05	0.93	3.82	-	1038.6
AHQ-6-14-, 3115 - 3187	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	9.77E-08	0.98	5.39	-	1863.5
AHQ-6-14-, 3258	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	7.07E-12	0.98	5.83	-	2069.0
AHQ-6-14-, 3107 - 3134	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	2.08E-08	0.95	4.20	-	1546.1
AHQ-6-14, 3965 - 4034	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	3.76E-06	0.97	5.47	-	1489.6
AHQ-6-14, 3957 - 4026	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	4.10E-06	0.94	4.42	-	1416.7
AHQ-6-14, 4080 - 4141	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	7.46E-07	0.94	4.82	-	1116.0
AHQ-6-14-, 2810 - 2875	K.GTHCNQVEVIATLKDGRK.I	2028.27941	3	3.53E-04	0.84	3.49	-	931.8
AHQ-6-14-, 2839 - 2912	K.ICLDPDAPR.I	1058.19059	2	3.36E-05	0.90	3.26	-	1176.0
AHQ-6-13, 3133	K.ICLDPDAPR.I	1058.19059	2	5.52E-04	0.90	3.40	-	1180.5
AHQ-6-14-, 2590 - 2650	R.KICLDPDAPR.I	1186.36350	2	2.29E-04	0.89	3.43	-	917.4
AHQ-6-14, 3468 - 3524	R.KICLDPDAPR.I	1186.36350	2	4.71E-04	0.83	3.19	-	726.7
AHQ-6-13-, 2704 - 2716	R.KICLDPDAPR.I	1186.36350	2	4.61E-06	0.86	3.11	-	920.6
AHQ-6-14, 3356 - 3414	R.KICLDPDAPR.I	1186.36350	2	2.71E-06	0.92	3.41	-	1093.4
AHQ-6-14-, 2678 - 2742	R.KICLDPDAPR.I	1186.36350	2	8.96E-05	0.91	3.40	-	1045.3
AHQ-6-13, 2815 - 2895	R.KICLDPDAPR.I	1186.36350	2	8.30E-05	0.39	2.59	-	403.0
AHQ-6-14, 3232 - 3300	R.KICLDPDAPR.I	1186.36350	2	1.03E-05	0.74	2.79	-	617.5
AHQ-6-14-, 4071	K.NIQSLEVIGK.G	1101.27845	2	2.72E-04	0.93	3.04	-	1528.9
AHQ-6-14, 4149 - 4229	K.NIQSLEVIGK.G	1101.27845	2	9.18E-05	0.88	3.80	-	661.2
AHQ-6-14, 4854	K.NIQSLEVIGK.G	1101.27845	2	2.94E-04	0.80	2.54	-	1031.4
AHQ-6-14, 4244 - 4300	K.NIQSLEVIGK.G	1101.27845	2	7.83E-05	0.90	3.70	-	790.0
AHQ-6-14-, 3672 - 3696	K.NIQSLEVIGK.G	1101.27845	2	9.20E-04	0.88	2.52	-	1178.1
AHQ-6-14-, 3290 - 3331	K.NIQSLEVIGK.G	1101.27845	2	3.77E-04	0.88	2.81	-	1091.5
AHQ-6-14-, 3394 - 3472	K.NIQSLEVIGK.G	1101.27845	2	1.84E-06	0.88	3.41	-	793.2
AHQ-6-14-, 3511 - 3579	K.NIQSLEVIGK.G	1101.27845	2	4.88E-04	0.83	2.97	-	832.9
AHQ-6-14-, 3622	K.TTSGIHPKNIQSLEVIGK.G	1923.20305	3	1.58E-07	0.86	3.52	-	810.3
gi|4503631|ref|NP_000120.1|	coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,			7.19E-12	18.63	220.31	41.80	83232.8
AHQ-6-5, 4977 - 5044	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	8.97E-04	0.50	3.20	-	124.8
AHQ-6-5, 5103 - 5159	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	2.63E-05	0.68	3.42	-	191.6
AHQ-6-5, 2336	R.CGPASVQAIK.H	1032.19627	2	2.78E-04	0.71	2.56	-	837.6
AHQ-6-5, 2601	K.DGTHVVENVDATHIGK.L	1692.81163	2	2.16E-06	0.92	3.58	-	1150.9
AHQ-6-5, 2599	K.DGTHVVENVDATHIGK.L	1692.81163	3	3.67E-07	0.95	4.47	-	1385.9
AHQ-6-7, 2532	K.DGTHVVENVDATHIGK.L	1692.81163	2	2.01E-04	0.95	4.47	-	1353.1
AHQ-6-5, 6568 - 6639	K.EAVLIQAGEYM*GQLLEQASLHFFVTAR.I	3039.45415	3	2.03E-06	0.89	5.03	-	517.6
AHQ-6-5, 4833	R.GTQVVGSDM*TVTVQFTNPLK.E	2139.41549	2	4.00E-11	0.92	3.94	-	800.0
AHQ-6-5, 5393	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.74E-04	0.46	2.51	-	353.7
AHQ-6-7, 5186 - 5206	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.17E-05	0.69	3.12	-	304.7
AHQ-6-8, 5225 - 5233	K.GTYIPVPIVSELQSGK.W	1688.94594	2	7.91E-04	0.68	3.43	-	316.1
AHQ-6-5, 5480	K.GTYIPVPIVSELQSGK.W	1688.94594	2	9.30E-05	0.25	2.57	-	141.7
AHQ-6-9, 5983 - 6044	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.00E-04	0.83	2.67	-	1011.6
AHQ-6-5, 6404	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.50E-08	0.98	5.82	-	1733.5
AHQ-6-5, 6403	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	8.61E-07	0.83	4.14	-	437.2
AHQ-6-13, 6299	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.05E-05	0.73	3.06	-	797.1
AHQ-6-7, 6190 - 6258	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.81E-06	0.95	4.73	-	915.2
AHQ-6-13-, 6201 - 6268	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.46E-04	0.93	4.23	-	1065.1
AHQ-6-5, 3403 - 3465	R.HVYGELDVQIQR.R	1457.61612	2	2.69E-05	0.92	3.70	-	1073.1

AHQ-6-5, 6161 - 6228	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	4.77E-04	0.95	5.08	-	1616.1
AHQ-6-5, 6592 - 6667	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	1.86E-05	0.94	5.66	-	832.8
AHQ-6-5, 6283 - 6353	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	2.07E-10	0.95	5.47	-	1107.1
AHQ-6-5, 6051 - 6105	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	5.58E-06	0.96	6.14	-	1005.5
AHQ-6-5, 5852 - 5920	R.IVTNYFSAHDNDANLQMDIFLEEDGNVNSK.L	3415.64559	3	2.15E-05	0.94	5.64	-	1336.6
AHQ-6-5, 2284 - 2343	K.KDGTHVVENVDATHIGK.L	1820.98455	2	1.31E-04	0.96	4.71	-	1452.4
AHQ-6-5, 2459	K.KDGTHVVENVDATHIGK.L	1820.98455	3	2.85E-06	0.93	4.36	-	1428.1
AHQ-6-5, 2287	K.KDGTHVVENVDATHIGK.L	1820.98455	3	5.32E-09	0.98	6.15	-	3406.3
AHQ-6-5, 4923 - 4999	K.KETFDVTLEPLSFK.K	1654.88482	2	3.19E-10	0.94	3.71	-	1362.0
AHQ-6-10, 4714	K.KETFDVTLEPLSFK.K	1654.88482	2	2.03E-05	0.93	3.65	-	1268.2
AHQ-6-5, 2797	R.KLIASMSSDSLR.H	1308.53039	2	3.26E-08	0.90	3.63	-	1008.2
AHQ-6-10, 2747	R.KLIASMSSDSLR.H	1308.53039	2	1.47E-05	0.84	2.97	-	952.0
AHQ-6-5, 1971	K.KPLNTEGVMK.S	1117.34452	2	1.11E-04	0.42	2.69	-	325.4
AHQ-6-6, 4124 - 4142	R.LALETALM*YGAK.K	1297.54595	2	8.81E-04	0.94	4.08	-	1070.6
AHQ-6-7, 5156	R.M*YVAVWTPYGVLR.T	1571.86734	2	6.19E-04	0.69	3.08	-	455.7
AHQ-6-5, 6175 - 6192	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	4.35E-05	0.90	5.16	-	781.5
AHQ-6-5, 3639	R.NVWVHLDGPGVTR.P	1450.62682	2	2.24E-07	0.92	3.52	-	1266.9
AHQ-6-10, 3531	R.NVWVHLDGPGVTR.P	1450.62682	2	2.74E-05	0.64	2.58	-	675.3
AHQ-6-5, 2833	K.QIGGDGM*M*DITDTYK.F	1677.83576	2	2.99E-04	0.48	2.61	-	411.4
AHQ-6-5, 5205	R.SNVDMDFEVENAVLGK.D	1767.93869	2	7.19E-12	0.95	4.75	-	1133.5
AHQ-6-5, 4423 - 4483	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	7.31E-08	0.96	4.27	-	1585.9
AHQ-6-5, 4232	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.47E-05	0.83	3.40	-	729.9
AHQ-6-6, 5050	R.SNVDMDFEVENAVLGK.D	1767.93869	2	5.59E-06	0.91	3.55	-	931.3
AHQ-6-5, 4864	R.SNVDMDFEVENAVLGK.D	1767.93869	2	1.45E-05	0.78	2.87	-	714.1
AHQ-6-5, 5077	R.SNVDMDFEVENAVLGK.D	1767.93869	2	7.58E-08	0.94	3.54	-	1848.0
AHQ-6-6, 4436	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	2.66E-09	0.92	4.00	-	1108.4
AHQ-6-10, 4210 - 4270	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	2.14E-06	0.87	3.50	-	1039.3
AHQ-6-10, 5234 - 5240	K.STVLTIPEIIIK.V	1327.63485	2	4.55E-06	0.92	3.62	-	1080.9
AHQ-6-7, 5324	K.STVLTIPEIIIK.V	1327.63485	2	8.93E-04	0.82	2.99	-	975.9
AHQ-6-13-, 5468	K.STVLTIPEIIIK.V	1327.63485	2	6.59E-04	0.74	2.66	-	1009.4
AHQ-6-5, 5521 - 5548	K.STVLTIPEIIIK.V	1327.63485	2	9.07E-04	0.93	3.12	-	1567.6
AHQ-6-5, 6552 - 6625	R.YGQCWVFAGVFNTFLR.C	1967.23783	2	9.40E-11	0.97	5.23	-	1100.8
gi|4504349|ref|NP_000509.1|	beta globin [Homo sapiens]			8.13E-12	8.76	100.31	70.70	15998.3
AHQ-6-14-, 3167 - 3175	K.EFTPPVQAAYQK.V	1379.54213	2	6.56E-06	0.74	2.99	-	500.3
AHQ-6-14-, 5352	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	2.44E-06	0.95	4.05	-	1131.8
AHQ-6-13-, 5426	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	7.20E-07	0.85	3.35	-	666.0
AHQ-6-13-, 5332	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.50E-07	0.97	5.42	-	968.7
AHQ-6-13, 5515 - 5524	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	7.06E-08	0.95	4.50	-	1018.3
AHQ-6-13-, 4942 - 4944	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	5.94E-08	0.93	4.32	-	870.0
AHQ-6-13, 4864 - 4912	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	5.23E-08	0.88	3.89	-	583.4
AHQ-6-13, 4892 - 4955	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	5.65E-05	0.90	4.16	-	1206.2
AHQ-6-13-, 4848	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.05E-06	0.94	4.38	-	923.0
AHQ-6-13-, 4834	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	3.97E-07	0.95	4.29	-	1787.8
AHQ-6-13, 4947 - 5027	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.63E-05	0.94	4.95	-	695.2
AHQ-6-13-, 4736 - 4792	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	3.00E-06	0.89	3.86	-	598.9
AHQ-6-13, 5423	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	2.26E-07	0.93	4.77	-	575.8
AHQ-6-13, 3765 - 3779	K.GTFATLSELHCDK.L	1480.62492	2	4.49E-05	0.80	3.27	-	529.9
AHQ-6-13-, 3630	K.GTFATLSELHCDK.L	1480.62492	2	1.59E-07	0.88	3.69	-	714.4
AHQ-6-13-, 4873	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	2	2.36E-09	0.87	4.15	-	375.1
AHQ-6-13, 5003	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	3.17E-08	0.93	4.55	-	1066.2
AHQ-6-13-, 4856	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	8.13E-12	0.95	5.20	-	1275.6
AHQ-6-13-, 4696	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	6.65E-09	0.97	6.15	-	1423.5
AHQ-6-13-, 4490	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	7.73E-10	0.98	5.99	-	2268.1
AHQ-6-13, 4837	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	2.97E-07	0.95	5.45	-	1343.7
AHQ-6-13-, 4700 - 4740	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	4.10E-06	0.97	5.69	-	1305.1
AHQ-6-13-, 3541 - 3545	K.SAVTALWGK.V	933.08624	2	6.96E-07	0.88	3.04	-	831.6
AHQ-6-14-, 4996	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.32E-09	0.97	5.34	-	1897.8
AHQ-6-13-, 5148 - 5150	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	3.92E-10	0.82	3.85	-	662.0
AHQ-6-13, 5055 - 5111	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.38E-11	0.96	4.61	-	1637.3
AHQ-6-13-, 4982 - 5040	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.57E-05	0.97	5.24	-	1813.9
AHQ-6-14, 5685	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	5.01E-07	0.87	3.68	-	756.2
AHQ-6-13-, 4808	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	1.97E-07	0.89	4.04	-	587.4
AHQ-6-13-, 4809 - 4882	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	4.59E-11	0.98	5.94	-	1640.3
AHQ-6-13, 4929 - 5007	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.58E-05	0.97	5.05	-	1983.5
AHQ-6-13, 4923 - 4931	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	1.84E-08	0.85	4.05	-	467.8
AHQ-6-13-, 4577	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.02E-10	0.97	5.24	-	1746.7
AHQ-6-13, 5083 - 5087	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	3.51E-08	0.84	3.67	-	567.3
AHQ-6-13-, 3284	K.VNVDEVGGEALGR.L	1315.41484	2	5.85E-05	0.96	4.90	-	1319.2
AHQ-6-14-, 3230	K.VNVDEVGGEALGR.L	1315.41484	2	1.22E-06	0.97	4.87	-	1962.5
AHQ-6-13, 3431 - 3432	K.VNVDEVGGEALGR.L	1315.41484	1	5.07E-08	0.59	2.59	-	356.7
AHQ-6-13, 3423 - 3496	K.VNVDEVGGEALGR.L	1315.41484	2	2.73E-05	0.98	4.71	-	2260.6
AHQ-6-13, 3352 - 3425	K.VNVDEVGGEALGR.L	1315.41484	2	7.36E-07	0.94	4.25	-	1192.3
AHQ-6-13-, 3372	K.VNVDEVGGEALGR.L	1315.41484	2	2.67E-04	0.96	4.12	-	1624.8
AHQ-6-14-, 2479 - 2542	K.VVAGVANALAHK.Y	1150.35593	2	5.82E-04	0.84	2.64	-	1152.9
AHQ-6-13-, 2592 - 2604	K.VVAGVANALAHK.Y	1150.35593	2	9.43E-07	0.97	3.78	-	2114.7
AHQ-6-13-, 2212 - 2282	K.VVAGVANALAHK.Y	1150.35593	2	4.88E-04	0.95	3.67	-	1723.2
AHQ-6-13, 2768 - 2831	K.VVAGVANALAHK.Y	1150.35593	2	5.65E-07	0.94	3.64	-	1524.8
gi|9507215|ref|NP_061816.1|	tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]			8.38E-12	3.45	40.26	13.10	50093.2
AHQ-6-14, 5452 - 5453	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	6.74E-05	0.94	4.00	-	1422.7
AHQ-6-13-, 4737	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	1.55E-06	0.94	4.52	-	1069.7
AHQ-6-14-, 4664 - 4742	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	3.14E-07	0.97	5.12	-	1404.1
AHQ-6-13, 4791 - 4851	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	6.44E-04	0.54	2.52	-	868.0
AHQ-6-12, 3496	K.DVNVAIAAIK.T	1014.20080	2	1.55E-05	0.92	3.41	-	1181.5
AHQ-6-7, 5227	R.IHFPLVTYAPIISAEK.A	1800.13312	2	7.50E-05	0.66	3.10	-	357.1
AHQ-6-14, 5697 - 5756	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	5.37E-09	0.64	3.26	-	469.4
AHQ-6-13-, 5201	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	1.06E-07	0.90	3.99	-	735.4
AHQ-6-7, 4928 - 4972	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	2.59E-04	0.53	3.18	-	486.1
AHQ-6-13, 5179	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	5.05E-09	0.79	3.34	-	517.7
AHQ-6-14-, 5066	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	8.38E-12	0.91	4.26	-	721.5
gi|4502027|ref|NP_000468.1|	albumin precursor; PRO0883 protein [Homo sapiens]			1.32E-11	35.67	410.40	64.70	69366.4
AHQ-6-5, 2529	K.AAFTECCQAADK.A	1374.47927	1	4.32E-04	0.55	2.91	-	425.0
AHQ-6-5, 2071	K.ADDKETCFAEEGK.K	1501.55462	2	4.09E-08	0.65	2.55	-	767.6
AHQ-6-5, 1855	K.ADDKETCFAEEGKK.L	1629.72754	2	9.56E-06	0.80	3.24	-	768.1
AHQ-6-5, 1951 - 2007	K.AEFAEVSK.L	880.96496	2	8.62E-04	0.60	2.53	-	398.6
AHQ-6-6, 5164	K.AEFAEVSKLVTDLTK.V	1651.88247	2	9.90E-05	0.76	3.65	-	567.6
AHQ-6-5, 6491	K.ALVLIAFAQYLQQCPFEDHVK.L	2492.87697	3	1.32E-11	0.97	5.79	-	1240.3
AHQ-6-5, 4391	K.AVM*DDFAAFVEK.C	1359.52946	2	1.58E-04	0.95	3.94	-	1277.9
AHQ-6-5, 5239 - 5255	K.AVMDDFAAFVEK.C	1343.53006	2	5.97E-08	0.96	4.29	-	1568.4
AHQ-6-14-, 5210	K.AVMDDFAAFVEK.C	1343.53006	2	2.73E-08	0.96	4.30	-	1689.8
AHQ-6-6, 5208	K.AVMDDFAAFVEK.C	1343.53006	2	1.13E-07	0.97	3.91	-	2297.5
AHQ-6-6, 2186	K.CCAAADPHECYAK.V	1556.67999	2	6.43E-07	0.83	3.23	-	582.7
AHQ-6-5, 2285	K.CCKADDKETCFAEEGK.K	1952.08719	2	1.84E-04	0.89	3.64	-	767.1
AHQ-6-5, 2391	K.CCTESLVNR.R	1141.25805	2	7.63E-06	0.89	3.19	-	1008.3
AHQ-6-4, 2429	K.CCTESLVNR.R	1141.25805	2	4.62E-05	0.75	2.61	-	746.9
AHQ-6-5, 6296 - 6307	K.DVFLGM*FLYEYAR.R	1640.88331	2	3.67E-06	0.96	4.36	-	1492.4
AHQ-6-6, 6226	K.DVFLGM*FLYEYAR.R	1640.88331	2	1.16E-04	0.95	3.90	-	1330.5
AHQ-6-1, 6367	K.DVFLGM*FLYEYAR.R	1640.88331	2	7.13E-05	0.90	3.24	-	930.4

AHQ-6-5, 2711 - 2779	R.FKDLGEENFK.A	1227.34766	2	5.78E-06	0.90	3.81	-	803.1
AHQ-6-10, 2700	R.FKDLGEENFK.A	1227.34766	2	8.18E-04	0.82	2.72	-	858.9
AHQ-6-6, 2715	R.FKDLGEENFK.A	1227.34766	2	5.50E-07	0.83	3.55	-	595.6
AHQ-6-13, 2931 - 3007	R.FKDLGEENFK.A	1227.34766	2	1.01E-06	0.62	2.91	-	401.7
AHQ-6-6, 3042	K.FQNALLVR.Y	961.14282	2	5.28E-04	0.82	2.82	-	796.8
AHQ-6-5, 6187	R.HPYFYAPELLFFAK.R	1744.02658	3	6.60E-07	0.93	4.62	-	1144.2
AHQ-6-6, 6118	R.HPYFYAPELLFFAK.R	1744.02658	3	4.42E-06	0.92	4.40	-	972.4
AHQ-6-7, 3346 - 3402	K.KVPQVSTPTLVEVSR.N	1640.90605	2	7.22E-05	0.91	3.35	-	817.9
AHQ-6-1, 3732 - 3812	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.63E-06	0.83	2.83	-	723.5
AHQ-6-3, 3625	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.78E-04	0.86	3.18	-	707.9
AHQ-6-6, 3478	K.KVPQVSTPTLVEVSR.N	1640.90605	3	1.88E-08	0.91	4.11	-	1160.9
AHQ-6-5, 3276	K.KVPQVSTPTLVEVSR.N	1640.90605	2	4.20E-08	0.84	3.36	-	626.1
AHQ-6-5, 3456 - 3523	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.33E-07	0.94	4.35	-	878.8
AHQ-6-6, 3426 - 3482	K.KVPQVSTPTLVEVSR.N	1640.90605	2	6.29E-10	0.80	3.14	-	601.1
AHQ-6-5, 3563 - 3637	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.19E-07	0.88	3.25	-	775.1
AHQ-6-5, 3507 - 3568	K.KVPQVSTPTLVEVSR.N	1640.90605	3	4.97E-09	0.95	5.24	-	1290.8
AHQ-6-5, 3927	K.KVPQVSTPTLVEVSRNLGK.V	2053.39186	3	6.12E-08	0.68	3.27	-	624.9
AHQ-6-5, 2733	K.KYLYEIAR.R	1056.23937	2	3.87E-05	0.74	2.64	-	612.7
AHQ-6-5, 1572 - 1624	K.LDELRDEGK.A	1075.15472	2	9.31E-04	0.54	2.53	-	588.0
AHQ-6-6, 1591 - 1662	K.LDELRDEGK.A	1075.15472	2	2.98E-04	0.58	2.56	-	501.5
AHQ-6-7, 2395	K.LKECCEKPLLEK.S	1549.83503	2	2.28E-04	0.92	3.92	-	1196.2
AHQ-6-5, 2444	K.LKECCEKPLLEK.S	1549.83503	2	8.88E-04	0.95	4.24	-	1538.2
AHQ-6-5, 2443	K.LKECCEKPLLEK.S	1549.83503	3	4.04E-04	0.82	4.34	-	677.9
AHQ-6-5, 4031	K.LVAASQAALGL	1014.20080	2	1.19E-06	0.93	3.53	-	1086.3
AHQ-6-6, 3999	K.LVAASQAALGL	1014.20080	2	9.33E-07	0.90	3.23	-	972.8
AHQ-6-5, 3476 - 3488	K.LVNEVTEFAK.T	1150.30633	2	5.17E-06	0.80	3.09	-	447.8
AHQ-6-6, 3266	K.LVNEVTEFAK.T	1150.30633	2	9.27E-07	0.86	3.22	-	712.7
AHQ-6-5, 3149 - 3151	K.LVNEVTEFAK.T	1150.30633	1	6.61E-07	0.64	2.65	-	570.3
AHQ-6-6, 3459 - 3522	K.LVNEVTEFAK.T	1150.30633	2	5.58E-07	0.92	3.29	-	955.3
AHQ-6-10, 3198 - 3207	K.LVNEVTEFAK.T	1150.30633	2	2.05E-04	0.90	3.19	-	1002.1
AHQ-6-5, 3249 - 3315	K.LVNEVTEFAK.T	1150.30633	2	2.11E-06	0.90	3.66	-	656.4
AHQ-6-7, 3178	K.LVNEVTEFAK.T	1150.30633	2	1.83E-04	0.83	2.75	-	820.7
AHQ-6-14-, 3286 - 3343	K.LVNEVTEFAK.T	1150.30633	2	4.12E-06	0.64	2.85	-	432.9
AHQ-6-5, 3480	K.LVNEVTEFAK.T	1150.30633	1	9.14E-07	0.68	2.43	-	762.1
AHQ-6-5, 4709	R.LVRPEVDVM*CTAFHDNEETFLK.K	2668.98368	3	7.42E-07	0.96	5.22	-	1195.3
AHQ-6-6, 4679	R.LVRPEVDVM*CTAFHDNEETFLK.K	2668.98368	3	5.27E-04	0.92	4.54	-	1114.9
AHQ-6-5, 5504	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	5.75E-06	0.98	7.96	-	2169.5
AHQ-6-6, 5451	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	1.00E-04	0.98	6.77	-	1912.8
AHQ-6-6, 5214	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	8.06E-06	0.97	6.62	-	1531.3
AHQ-6-6, 4330	R.LVRPEVDVM*CTAFHDNEETFLKK.Y	2797.15659	3	1.28E-05	0.94	5.22	-	822.1
AHQ-6-7, 3939	R.RHPDYSVVLLLR.L	1468.72842	2	1.58E-04	0.90	3.32	-	982.8
AHQ-6-5, 4093 - 4163	R.RHPDYSVVLLLR.L	1468.72842	3	2.62E-05	0.95	4.52	-	1795.5
AHQ-6-6, 5727	R.RHPYFYAPELLFFAK.R	1900.21293	2	8.82E-07	0.98	5.22	-	2477.6
AHQ-6-6, 5722	R.RHPYFYAPELLFFAK.R	1900.21293	3	5.76E-09	0.97	5.43	-	1751.6
AHQ-6-5, 5728 - 5811	R.RHPYFYAPELLFFAK.R	1900.21293	2	3.80E-05	0.98	4.87	-	2016.2
AHQ-6-5, 5781	R.RHPYFYAPELLFFAK.R	1900.21293	2	1.71E-10	0.98	5.50	-	2472.4
AHQ-6-5, 5780 - 5845	R.RHPYFYAPELLFFAK.R	1900.21293	3	1.55E-08	0.97	5.36	-	1953.2
AHQ-6-5, 6455	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	2.49E-05	0.93	5.40	-	1031.7
AHQ-6-6, 6324 - 6382	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	1.23E-04	0.92	5.26	-	761.7
AHQ-6-5, 4461	R.RPCFSALEVDETYVPK.E	1913.14041	3	1.58E-06	0.95	4.93	-	1442.2
AHQ-6-6, 4519 - 4578	R.RPCFSALEVDETYVPK.E	1913.14041	3	2.76E-04	0.84	4.03	-	649.7
AHQ-6-5, 4548 - 4608	R.RPCFSALEVDETYVPK.E	1913.14041	2	4.38E-05	0.97	5.31	-	968.3
AHQ-6-5, 4551 - 4611	R.RPCFSALEVDETYVPK.E	1913.14041	3	1.25E-05	0.95	5.46	-	1179.7
AHQ-6-5, 4449	R.RPCFSALEVDETYVPK.E	1913.14041	2	9.38E-07	0.86	3.77	-	629.9
AHQ-6-8, 4390 - 4461	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.61E-04	0.63	2.96	-	326.1
AHQ-6-5, 5939	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	2	1.41E-04	0.94	4.99	-	796.6
AHQ-6-6, 5852 - 5922	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	1.47E-07	0.96	6.36	-	974.3
AHQ-6-5, 6272 - 6339	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	7.19E-06	0.92	4.80	-	686.8
AHQ-6-6, 6275	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	6.26E-04	0.83	4.00	-	605.5
AHQ-6-7, 5714 - 5726	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	5.29E-05	0.94	5.45	-	692.9
AHQ-6-5, 4965	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	6.83E-06	0.95	4.32	-	1218.5
AHQ-6-5, 4955	K.SLHTLFGDKLCTVATLR.E	1934.24913	3	7.39E-04	0.84	3.79	-	623.2
AHQ-6-6, 1918	K.TCVADESAENCDK.S	1501.53308	2	4.17E-04	0.94	3.85	-	1429.3
AHQ-6-5, 1880 - 1937	K.TCVADESAENCDK.S	1501.53308	2	1.26E-09	0.97	4.52	-	1991.2
AHQ-6-5, 4363	K.TCVADESAENCDKSLHTLFGDK.L	2500.65848	3	9.33E-05	0.88	4.32	-	719.6
AHQ-6-5, 3745 - 3747	K.TYETTLEKCCAAADPHECYAK.V	2522.72734	3	2.89E-09	0.95	4.93	-	1072.7
AHQ-6-5, 5392	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.94E-04	0.94	4.40	-	730.2
AHQ-6-5, 5384	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	6.07E-07	0.93	4.53	-	1090.6
AHQ-6-4, 5616	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.42E-08	0.96	5.42	-	1162.1
AHQ-6-1, 5628	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.35E-04	0.88	4.32	-	362.2
AHQ-6-6, 5254	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	8.94E-04	0.79	3.30	-	1153.0
AHQ-6-5, 5495	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	4.57E-04	0.47	3.03	-	251.2
AHQ-6-6, 5462 - 5535	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.78E-07	0.96	5.65	-	608.5
AHQ-6-5, 5499 - 5503	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.47E-06	0.97	5.36	-	1581.9
AHQ-6-6, 5478	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.94E-06	0.90	4.43	-	389.2
AHQ-6-10, 5223	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	3.77E-04	0.92	4.00	-	1145.4
AHQ-6-1, 5624	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	5.22E-04	0.94	3.96	-	1404.1
AHQ-6-7, 5296	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.72E-06	0.89	4.22	-	441.8
AHQ-6-3, 5548	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.50E-05	0.90	4.17	-	504.3
AHQ-6-3, 5546	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.27E-05	0.93	4.58	-	1017.6
AHQ-6-7, 5303	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.74E-07	0.95	4.83	-	1169.2
AHQ-6-5, 5591	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.31E-08	0.94	4.49	-	1346.9
AHQ-6-5, 5592	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	4.88E-07	0.92	4.61	-	489.4
AHQ-6-9, 5154	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.59E-05	0.49	2.56	-	218.0
AHQ-6-2, 5584 - 5587	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.82E-04	0.93	4.64	-	504.0
AHQ-6-6, 5470 - 5471	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	3.74E-05	0.97	5.26	-	1837.4
AHQ-6-6, 3082	K.VHTECCHGDLLECADDR.A	2091.20307	2	1.37E-07	0.95	4.44	-	1277.9
AHQ-6-5, 3084 - 3093	K.VHTECCHGDLLECADDR.A	2091.20307	2	4.10E-08	0.97	5.54	-	1531.6
AHQ-6-6, 3635	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	2.51E-05	0.80	3.31	-	757.9
AHQ-6-6, 3652	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	6.02E-04	0.85	3.38	-	775.2
AHQ-6-7, 3547	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	7.58E-05	0.92	4.62	-	946.7
AHQ-6-10, 3686	K.VPQVSTPTLVEVSR.N	1512.73313	2	6.05E-05	0.72	3.07	-	454.8
AHQ-6-5, 3827	K.VPQVSTPTLVEVSR.N	1512.73313	2	1.68E-07	0.89	2.94	-	829.7
AHQ-6-6, 3790	K.VPQVSTPTLVEVSR.N	1512.73313	2	6.62E-06	0.76	2.65	-	704.3
AHQ-6-6, 2470	K.YICENQDSISSK.L	1445.53420	2	2.14E-05	0.83	3.43	-	550.0
AHQ-6-6, 2283 - 2358	K.YICENQDSISSK.L	1445.53420	2	1.33E-05	0.91	3.94	-	694.5
AHQ-6-5, 2361	K.YICENQDSISSK.L	1445.53420	1	1.27E-05	0.64	3.12	-	275.6
AHQ-6-5, 2453	K.YICENQDSISSK.L	1445.53420	2	3.62E-07	0.90	3.46	-	854.5
AHQ-6-5, 2268 - 2347	K.YICENQDSISSK.L	1445.53420	2	2.08E-04	0.93	4.25	-	764.9
gi|21361755|ref|NP_004090.3| stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie				1.40E-11	4.49	50.27	24.70	31708.5
AHQ-6-10, 3867 - 3884	K.EASM*VITESPAALQLR.Y	1732.98059	2	3.36E-04	0.61	2.99	-	589.4
AHQ-6-1, 4246	K.EASM*VITESPAALQLR.Y	1732.98059	2	1.32E-04	0.93	3.82	-	1152.5
AHQ-6-1, 4671 - 4743	K.EASMVITESPAALQLR.Y	1716.98119	2	5.31E-06	0.84	3.45	-	936.7
AHQ-6-13-, 6348	K.GPGLFFILPCTDSFIK.V	1814.13672	2	6.10E-04	0.89	3.83	-	636.8
AHQ-6-1, 6530	K.GPGLFFILPCTDSFIK.V	1814.13672	2	7.31E-05	0.95	4.66	-	818.5
AHQ-6-1, 6507	K.NSTIVFPLPIDM*LQGIIGAK.H	2144.56315	2	1.47E-04	0.81	3.87	-	341.9
AHQ-6-2, 3886	R.VQNATLAVANITNADSATR.L	1931.09731	2	3.06E-07	0.94	4.16	-	930.2

AHQ-6-10, 3638	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.95E-08	0.92	3.65	-	1226.8
AHQ-6-1, 4007 - 4010	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.40E-11	0.97	5.45	-	1350.2
AHQ-6-10, 4118	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.09E-04	0.87	3.60	-	626.1
AHQ-6-1, 3896	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.68E-06	0.74	3.52	-	498.9
AHQ-6-1, 4486	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.90E-11	0.94	4.14	-	977.2
gi|29568101|ref|NP_006467.3| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT				1.70E-11	0.92	10.21	14.60	11400.3
AHQ-6-14-, 3635	K.TPALVNAAVTYSKPR.L	1588.83283	3	1.70E-11	0.92	4.15	-	1033.4
AHQ-6-14-, 3588 - 3631	K.TPALVNAAVTYSKPR.L	1588.83283	2	1.52E-04	0.95	3.88	-	1349.0
gi|4504345|ref|NP_000508.1| alpha 2 globin [Homo sapiens]				2.03E-11	3.82	40.32	50.70	15257.4
AHQ-6-13, 4349	K.FLASVSTVLTSK.Y	1253.46970	2	9.43E-04	0.92	3.52	-	1144.1
AHQ-6-13, 4144 - 4199	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	2.72E-06	0.83	3.87	-	447.0
AHQ-6-13, 4147 - 4217	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	7.40E-06	0.90	3.62	-	823.7
AHQ-6-13-, 4005 - 4064	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	6.49E-10	0.88	4.06	-	617.6
AHQ-6-13-, 4014 - 4077	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	6.42E-10	0.96	4.10	-	1547.8
AHQ-6-14-, 3996	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	3.84E-07	0.89	3.51	-	645.5
AHQ-6-14-, 5326 - 5384	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	6.34E-07	0.97	6.42	-	1398.6
AHQ-6-13-, 5405	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	5.38E-06	0.97	5.49	-	2213.3
AHQ-6-13, 2845 - 2904	K.VGAHAGEYGAEALER.M	1530.62397	3	1.89E-05	0.96	5.50	-	1839.7
AHQ-6-13-, 2664 - 2724	K.VGAHAGEYGAEALER.M	1530.62397	3	1.04E-05	0.97	5.73	-	2205.7
AHQ-6-13-, 2669 - 2728	K.VGAHAGEYGAEALER.M	1530.62397	2	2.03E-11	0.97	4.89	-	1804.7
AHQ-6-13, 2844 - 2903	K.VGAHAGEYGAEALER.M	1530.62397	2	5.18E-09	0.97	4.37	-	1599.5
gi|21956645|ref|NP_665807.1| myotrophin; granule cell differentiation protein [Homo sapiens]				2.20E-11	1.92	20.30	25.40	12894.7
AHQ-6-13-, 3956 - 4017	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.33E-08	0.97	5.18	-	1523.0
AHQ-6-14-, 3958	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.18E-07	0.95	4.82	-	927.4
AHQ-6-13, 4143 - 4207	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.68E-06	0.97	5.86	-	1356.0
AHQ-6-14, 4606 - 4684	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.97E-05	0.92	4.17	-	956.3
AHQ-6-14, 4672 - 4741	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.81E-06	0.98	6.06	-	1943.3
AHQ-6-14-, 3930 - 3934	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.60E-10	0.98	5.91	-	1699.5
AHQ-6-14-, 3812 - 3876	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.84E-05	0.96	4.72	-	1056.8
AHQ-6-14-, 4043 - 4095	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.42E-06	0.88	3.68	-	759.6
AHQ-6-13-, 4080	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.20E-11	0.96	4.86	-	1289.9
AHQ-6-14-, 3628	K.NGDLDEVKDYVAK.G	1466.57496	2	9.12E-10	0.95	4.01	-	1507.5
AHQ-6-13-, 3662	K.NGDLDEVKDYVAK.G	1466.57496	2	2.27E-08	0.90	3.33	-	1078.4
AHQ-6-13-, 3570	K.NGDLDEVKDYVAK.G	1466.57496	2	2.31E-09	0.96	4.16	-	1725.4
AHQ-6-13, 3807	K.NGDLDEVKDYVAK.G	1466.57496	2	1.13E-06	0.90	3.16	-	1167.6
AHQ-6-13, 3715	K.NGDLDEVKDYVAK.G	1466.57496	2	2.79E-09	0.90	3.40	-	1241.2
AHQ-6-14-, 3536	K.NGDLDEVKDYVAK.G	1466.57496	2	3.53E-07	0.92	3.69	-	1149.2
gi|27498267|ref|XP_209737.1| similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,				2.33E-11	3.52	40.29	33.70	11063.6
AHQ-6-10, 6118 - 6130	R.DICNDVLSLLEK.F	1420.61093	2	5.31E-05	0.94	3.66	-	1598.2
AHQ-6-10, 5406 - 5411	R.DICNDVLSLLEK.F	1420.61093	2	1.44E-07	0.89	3.02	-	1077.5
AHQ-6-14, 5552 - 5562	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.38E-05	0.94	4.90	-	826.1
AHQ-6-10, 4288 - 4368	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.75E-05	0.97	5.31	-	1396.5
AHQ-6-13, 5023 - 5025	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	6.77E-08	0.98	5.65	-	1586.8
AHQ-6-13-, 4888	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.31E-08	0.97	5.76	-	1347.1
AHQ-6-10, 4678 - 4734	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.28E-09	0.98	5.77	-	1835.7
AHQ-6-10, 4682 - 4748	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	2.26E-06	0.95	5.18	-	1507.4
AHQ-6-10, 4790 - 4840	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.51E-07	0.96	4.93	-	1332.2
AHQ-6-10, 4876 - 4907	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.84E-08	0.95	4.63	-	1018.8
AHQ-6-10, 4460	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.84E-11	0.96	4.55	-	1377.2
AHQ-6-9, 4634 - 4642	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.69E-09	0.96	4.88	-	1211.5
AHQ-6-10, 6256	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.03E-05	0.91	3.60	-	810.5
AHQ-6-11, 4755 - 4756	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.44E-08	0.97	5.65	-	1384.4
AHQ-6-11, 4761 - 4824	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.73E-05	0.92	4.01	-	1237.4
AHQ-6-14-, 4908 - 4918	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.33E-11	0.96	5.07	-	1402.8
AHQ-6-10, 4362	K.GIVDQSQQAYQEAFEISKK.E	2170.36467	2	2.47E-04	0.71	3.20	-	660.8
AHQ-6-10, 4266	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	8.05E-06	0.96	5.27	-	1340.0
AHQ-6-10, 4271	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	3	9.64E-04	0.83	3.91	-	1048.7
gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				2.64E-11	17.77	220.25	46.00	55901.8
AHQ-6-11, 2452	K.AHYGGFTVQNEANK.Y	1536.63020	2	3.10E-07	0.92	3.53	-	985.0
AHQ-6-10, 2412	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.27E-06	0.91	3.08	-	1120.9
AHQ-6-7, 2475 - 2535	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.64E-11	0.94	3.92	-	1155.1
AHQ-6-7, 3660	K.AHYGGFTVQNEANKYQISVNK.Y	2369.57759	2	1.20E-04	0.91	3.82	-	823.2
AHQ-6-6, 3130	R.DNDGWLTSDPR.K	1276.29403	2	1.68E-06	0.82	2.96	-	862.6
AHQ-6-6, 3272	K.DNENVVNEYSSELEK.H	1769.80167	2	7.70E-06	0.86	3.51	-	623.3
AHQ-6-11, 3904	K.DNENVVNEYSSELEK.H	1769.80167	2	5.20E-06	0.49	3.31	-	454.2
AHQ-6-11, 4028	K.DNENVVNEYSSELEK.H	1769.80167	2	1.60E-05	0.48	2.66	-	484.1
AHQ-6-7, 4063	K.DNENVVNEYSSELEK.H	1769.80167	2	3.73E-06	0.91	3.70	-	807.2
AHQ-6-7, 3927 - 3998	K.DNENVVNEYSSELEK.H	1769.80167	2	9.57E-05	0.91	4.21	-	584.0
AHQ-6-7, 3798 - 3860	K.DNENVVNEYSSELEK.H	1769.80167	2	7.71E-05	0.84	3.32	-	989.8
AHQ-6-6, 4111 - 4179	K.DNENVVNEYSSELEK.H	1769.80167	2	9.78E-06	0.95	5.05	-	806.9
AHQ-6-5, 4025	K.DNENVVNEYSSELEK.H	1769.80167	2	2.28E-04	0.76	3.60	-	646.6
AHQ-6-7, 3442 - 3451	K.DNENVVNEYSSELEK.H	1769.80167	2	8.02E-09	0.93	4.82	-	791.7
AHQ-6-8, 3805 - 3876	K.DNENVVNEYSSELEK.H	1769.80167	2	6.83E-04	0.85	3.49	-	707.6
AHQ-6-8, 3210	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	7.00E-04	0.44	2.66	-	299.6
AHQ-6-7, 3866	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.89E-05	0.79	3.90	-	449.6
AHQ-6-9, 3780	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.68E-04	0.51	3.10	-	349.2
AHQ-6-6, 4002	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	9.56E-06	0.92	4.38	-	713.8
AHQ-6-8, 3877	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	2.93E-04	0.74	3.44	-	486.6
AHQ-6-6, 4003	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	2.43E-08	0.89	3.72	-	1318.8
AHQ-6-6, 3574	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	3	7.91E-05	0.79	3.49	-	779.1
AHQ-6-7, 3428 - 3486	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	8.88E-06	0.82	3.37	-	696.9
AHQ-6-7, 5683	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	4089.58482	3	5.77E-06	0.60	3.30	-	276.2
AHQ-6-7, 3175	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	2	2.71E-05	0.68	2.63	-	582.2
AHQ-6-7, 3176 - 3186	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	1.21E-07	0.83	4.03	-	556.0
AHQ-6-7, 3551 - 3559	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.07E-04	0.89	4.63	-	552.6
AHQ-6-7, 3556	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	8.30E-04	0.78	3.67	-	593.6
AHQ-6-6, 3612 - 3670	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.26E-05	0.82	3.95	-	691.3
AHQ-6-8, 3465	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.80E-05	0.83	4.52	-	525.7
AHQ-6-6, 3288	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	1.68E-08	0.66	3.75	-	427.0
AHQ-6-8, 3148	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	5.81E-05	0.78	3.83	-	730.1
AHQ-6-6, 2575	K.LESDVSAQM*EYCR.T	1605.72945	2	2.26E-06	0.88	3.43	-	776.1
AHQ-6-7, 2506 - 2528	K.LESDVSAQM*EYCR.T	1605.72945	2	1.70E-07	0.94	4.05	-	1021.4
AHQ-6-7, 5787	R.M*GPTELLIEMEDWK.G	1708.97776	2	4.11E-05	0.96	4.55	-	1449.4
AHQ-6-6, 4624 - 4684	R.M*GPTELLIEM*EDWK.G	1724.97716	2	9.86E-05	0.81	2.67	-	1097.6
AHQ-6-7, 5404	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	2	8.53E-06	0.57	2.51	-	292.3
AHQ-6-7, 2964 - 3030	K.REEAPSLRPAPPPISGGGYR.A	2108.34617	3	1.17E-09	0.94	4.62	-	1272.8
AHQ-6-6, 3687 - 3760	R.TPCTVSCNIPVVSGK.E	1621.85811	2	1.55E-05	0.43	2.78	-	325.5
AHQ-6-8, 3565	R.TPCTVSCNIPVVSGK.E	1621.85811	2	5.92E-06	0.73	3.16	-	430.6
AHQ-6-7, 3583 - 3586	R.TPCTVSCNIPVVSGK.E	1621.85811	2	1.25E-06	0.80	3.32	-	460.6
AHQ-6-6, 4662 - 4738	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	2.81E-09	0.91	4.35	-	1016.4
AHQ-6-7, 4468 - 4535	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	9.26E-06	0.94	4.64	-	1299.1
AHQ-6-7, 4590	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	7.06E-10	0.94	4.80	-	1176.7
AHQ-6-6, 4739 - 4740	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.57E-07	0.90	4.50	-	395.1
AHQ-6-7, 3726 - 3783	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	6.95E-08	0.93	4.46	-	789.4
AHQ-6-8, 3762	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	1.30E-04	0.92	4.31	-	784.7
AHQ-6-6, 4303 - 4371	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	3.12E-06	0.88	3.85	-	727.4
AHQ-6-7, 4174 - 4175	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	8.52E-08	0.95	4.34	-	1217.0

AHQ-6-6, 3839 - 3898	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	4.92E-08	0.92	4.24	-	854.0
AHQ-6-8, 4201 - 4202	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	3.15E-10	0.95	4.67	-	883.8
AHQ-6-7, 2106	K.YQISVNK.Y	851.96999	1	2.65E-04	0.23	2.42	-	214.6
AHQ-6-6, 4350	R.YYWGGQYTWDM*AK.H	1685.83949	2	9.81E-04	0.92	3.43	-	1005.2
AHQ-6-7, 4171 - 4210	R.YYWGGQYTWDM*AK.H	1685.83949	2	1.09E-05	0.92	3.41	-	1011.1
AHQ-6-6, 4891 - 4894	R.YYWGGQYTWDMAK.H	1669.84009	2	3.00E-11	0.94	3.65	-	1196.0
AHQ-6-12, 4320 - 4339	R.YYWGGQYTWDM*AK.H	1685.83949	2	7.80E-04	0.74	2.75	-	603.2
AHQ-6-14-, 4395 - 4416	R.YYWGGQYTWDM*AK.H	1685.83949	2	1.34E-04	0.96	4.26	-	1203.3
AHQ-6-7, 4732 - 4742	R.YYWGGQYTWDMAK.H	1669.84009	2	6.78E-07	0.93	3.46	-	1125.7
gi|4507877|ref|NP_003364.1| vinculin isoform VCL [Homo sapiens]				2.73E-11	42.36	480.31	44.90	116721.6
AHQ-6-14-, 6407	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.13E-07	0.96	5.06	-	961.7
AHQ-6-1, 6579	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.59E-05	0.75	2.85	-	435.5
AHQ-6-11, 6271	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.12E-10	0.97	5.20	-	1041.2
AHQ-6-10, 6211	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.07E-09	0.94	4.46	-	866.0
AHQ-6-7, 6334	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.87E-07	0.96	4.66	-	1036.3
AHQ-6-4, 6569 - 6635	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.53E-08	0.98	6.17	-	1113.6
AHQ-6-4, 6631	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	3	7.44E-04	0.96	5.03	-	1702.1
AHQ-6-3, 6533	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	6.43E-05	0.92	3.64	-	881.3
AHQ-6-5, 6547	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.97E-07	0.97	5.24	-	1252.3
AHQ-6-1, 3600	R.ALASQLQDSLK.D	1174.32943	2	1.14E-04	0.89	3.15	-	924.3
AHQ-6-6, 3299	R.ALASQLQDSLK.D	1174.32943	2	1.61E-06	0.87	2.94	-	1036.3
AHQ-6-7, 3211 - 3214	R.ALASQLQDSLK.D	1174.32943	1	2.62E-04	0.32	2.77	-	265.1
AHQ-6-3, 3408	R.ALASQLQDSLK.D	1174.32943	2	2.35E-04	0.88	3.23	-	995.1
AHQ-6-5, 3317	R.ALASQLQDSLK.D	1174.32943	2	1.54E-04	0.84	3.23	-	895.4
AHQ-6-6, 3435 - 3494	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.23E-08	0.97	4.95	-	1684.6
AHQ-6-4, 3504 - 3585	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.00E-06	0.97	4.56	-	1667.1
AHQ-6-4, 3588	K.AQQVSQGLDVLTAK.V	1458.64233	1	2.92E-06	0.68	3.66	-	347.2
AHQ-6-8, 3313	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.51E-04	0.95	4.30	-	1280.4
AHQ-6-5, 3527 - 3528	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.16E-09	0.97	5.16	-	1540.2
AHQ-6-5, 3524 - 3531	K.AQQVSQGLDVLTAK.V	1458.64233	1	3.51E-05	0.61	3.07	-	434.8
AHQ-6-2, 3642	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.56E-07	0.97	4.16	-	1731.8
AHQ-6-4, 2511	K.AVAGNISDPGLQK.S	1270.41721	2	3.98E-04	0.76	3.04	-	558.7
AHQ-6-5, 2496	K.AVAGNISDPGLQK.S	1270.41721	2	1.16E-04	0.88	3.47	-	734.6
AHQ-6-8, 2356	K.AVAGNISDPGLQK.S	1270.41721	2	1.62E-04	0.64	2.94	-	526.9
AHQ-6-7, 2439	K.AVAGNISDPGLQK.S	1270.41721	2	2.41E-04	0.90	3.55	-	805.1
AHQ-6-5, 5563 - 5569	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	8.74E-06	0.94	4.89	-	1385.7
AHQ-6-4, 5641	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	2.79E-06	0.94	4.67	-	1435.4
AHQ-6-4, 5643	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	3.26E-04	0.93	4.13	-	1126.4
AHQ-6-5, 5567	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	3.55E-05	0.91	3.63	-	927.9
AHQ-6-7, 2271	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.43E-06	0.80	3.27	-	533.9
AHQ-6-5, 2311 - 2312	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.15E-06	0.92	3.91	-	834.2
AHQ-6-4, 2343	R.DPSASPGDAGEQAIR.Q	1471.51169	1	1.32E-04	0.17	2.05	-	150.2
AHQ-6-4, 2349	R.DPSASPGDAGEQAIR.Q	1471.51169	1	8.39E-04	0.19	2.03	-	156.9
AHQ-6-4, 2272 - 2335	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.96E-07	0.87	3.60	-	605.6
AHQ-6-3, 2381	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.42E-05	0.77	3.13	-	536.0
AHQ-6-5, 5315 - 5372	R.EAFQPQEPDFPPPPPDLEQLR.L	2448.67149	2	5.91E-05	0.80	3.22	-	581.4
AHQ-6-6, 3002 - 3012	K.ETVQTTEDQILKR.D	1561.71942	2	6.39E-04	0.79	2.72	-	865.6
AHQ-6-5, 3001	K.ETVQTTEDQILKR.D	1561.71942	2	6.37E-07	0.80	3.14	-	736.1
AHQ-6-10, 2954 - 2956	K.ETVQTTEDQILKR.D	1561.71942	2	6.10E-04	0.69	2.83	-	576.0
AHQ-6-4, 6637	K.GILEYLTVAEVVETM*EDLVTYTK.N	2633.99263	3	3.77E-05	0.96	5.09	-	1757.1
AHQ-6-6, 6334	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	6.61E-09	0.97	5.00	-	1235.3
AHQ-6-7, 6191	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	8.17E-05	0.92	4.43	-	686.7
AHQ-6-3, 6401	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	3.12E-06	0.95	5.08	-	735.1
AHQ-6-14-, 6284	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	3.71E-04	0.65	2.86	-	658.6
AHQ-6-2, 6438 - 6515	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	6.63E-07	0.94	4.77	-	951.4
AHQ-6-4, 6489	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.43E-04	0.97	5.72	-	1073.5
AHQ-6-4, 6357 - 6407	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.04E-05	0.91	3.90	-	858.9
AHQ-6-11, 6060 - 6137	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.33E-05	0.93	4.48	-	804.2
AHQ-6-5, 6399	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.73E-11	0.96	5.14	-	1162.2
AHQ-6-4, 6193	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	5.76E-08	0.90	4.25	-	695.6
AHQ-6-4, 3549	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	1.07E-05	0.94	4.56	-	821.5
AHQ-6-4, 3492 - 3551	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	3	7.42E-07	0.86	3.91	-	737.2
AHQ-6-5, 3497	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	3	1.98E-04	0.89	3.54	-	1251.6
AHQ-6-4, 2269	K.IAELCDDPKER.D	1347.47690	2	1.20E-04	0.54	2.53	-	522.8
AHQ-6-4, 2189	R.KIAELCDDPKER.D	1475.64981	2	1.49E-06	0.83	3.19	-	937.4
AHQ-6-4, 3303	R.KIAELCDDPKERDDILR.S	2088.32839	2	9.96E-05	0.89	3.73	-	872.6
AHQ-6-5, 4224	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	2.71E-04	0.73	3.57	-	285.3
AHQ-6-4, 4153 - 4215	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	2.41E-06	0.94	5.04	-	1103.2
AHQ-6-4, 4203 - 4281	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	3.73E-07	0.66	3.22	-	275.5
AHQ-6-4, 4285	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	1.67E-07	0.95	5.33	-	1409.3
AHQ-6-6, 4176	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.02E-06	0.63	2.63	-	360.7
AHQ-6-5, 4208	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	7.31E-06	0.85	3.80	-	1110.6
AHQ-6-5, 3380	R.LANVMMGPYR.Q	1152.41560	2	7.21E-05	0.94	3.54	-	1102.6
AHQ-6-4, 3417	R.LANVMMGPYR.Q	1152.41560	2	6.24E-04	0.92	3.36	-	946.6
AHQ-6-4, 4177 - 4243	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	2.03E-05	0.63	3.04	-	644.6
AHQ-6-6, 3579 - 3590	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	4.22E-06	0.90	4.05	-	740.2
AHQ-6-11, 3547	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	3.63E-05	0.89	3.43	-	794.0
AHQ-6-5, 3611	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	5.07E-06	0.87	3.16	-	817.3
AHQ-6-4, 3692	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	3	4.19E-07	0.97	5.08	-	2469.6
AHQ-6-4, 3668	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	7.44E-05	0.87	3.87	-	527.1
AHQ-6-4, 4465	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	2.47E-05	0.90	4.38	-	901.9
AHQ-6-4, 3721 - 3727	K.M*LGQMTDQVADLR.A	1494.71995	2	4.08E-04	0.98	4.95	-	2782.1
AHQ-6-4, 4084	K.MLGQMTDQVADLR.A	1478.72055	2	6.62E-08	0.96	4.84	-	1393.1
AHQ-6-4, 3291	K.MLGQM*TDQVADLR.A	1494.71995	2	1.08E-07	0.92	4.28	-	1265.8
AHQ-6-6, 2906	K.M*LGQM*TDQVADLR.A	1510.71935	2	8.97E-07	0.96	3.83	-	1996.9
AHQ-6-5, 2888	K.M*LGQM*TDQVADLR.A	1510.71935	2	3.09E-05	0.92	3.43	-	1392.8
AHQ-6-5, 4013 - 4081	K.MLGQMTDQVADLR.A	1478.72055	2	3.93E-07	0.94	3.40	-	1897.8
AHQ-6-4, 2931	K.M*LGQM*TDQVADLR.A	1510.71935	2	2.93E-05	0.97	4.25	-	2176.0
AHQ-6-5, 3664	K.M*LGQMTDQVADLR.A	1494.71995	2	6.24E-05	0.96	3.98	-	1868.4
AHQ-6-6, 3630	K.M*LGQMTDQVADLR.A	1494.71995	2	2.42E-05	0.97	3.97	-	2450.2
AHQ-6-5, 3235	K.MLGQM*TDQVADLR.A	1494.71995	2	8.17E-06	0.96	4.56	-	2011.9
AHQ-6-6, 3170 - 3231	K.MLGQM*TDQVADLR.A	1494.71995	2	8.25E-05	0.63	2.67	-	857.4
AHQ-6-4, 5417 - 5456	R.MQEAMTQEVSDVFSDTTTPIK.L	2359.61664	2	1.77E-04	0.84	3.47	-	1034.8
AHQ-6-6, 3162	K.M*SAEINEIIR.V	1192.36823	2	9.40E-06	0.86	3.21	-	828.6
AHQ-6-4, 3229	K.M*SAEINEIIR.V	1192.36823	2	1.34E-06	0.93	3.57	-	1269.1
AHQ-6-5, 3168	K.M*SAEINEIIR.V	1192.36823	2	4.83E-07	0.95	3.76	-	1517.9
AHQ-6-6, 3474	K.MTGLVDEAIDTK.S	1293.46936	2	2.21E-04	0.90	3.04	-	1119.1
AHQ-6-4, 3555	K.MTGLVDEAIDTK.S	1293.46936	2	5.72E-07	0.97	4.51	-	1773.8
AHQ-6-4, 3059 - 3128	K.M*TGLVDEAIDTK.S	1309.46876	2	1.37E-06	0.93	2.98	-	1375.2
AHQ-6-5, 3072	K.M*TGLVDEAIDTK.S	1309.46876	2	1.60E-06	0.92	3.18	-	1318.9
AHQ-6-4, 3127	K.M*TGLVDEAIDTK.S	1309.46876	2	1.64E-09	0.93	3.61	-	1180.4
AHQ-6-5, 3496	K.MTGLVDEAIDTK.S	1293.46936	2	2.17E-07	0.96	3.88	-	1650.4
AHQ-6-6, 3028	R.NPGNQAAYEHFETMK.N	1737.87437	2	9.29E-04	0.39	2.63	-	429.2
AHQ-6-4, 2561	R.NPGNQAAYEHFETM*K.N	1753.87377	2	1.22E-04	0.93	3.98	-	948.1
AHQ-6-4, 3060	R.NPGNQAAYEHFETMK.N	1737.87437	2	1.03E-06	0.94	4.11	-	1077.6
AHQ-6-5, 2923 - 2925	K.SFLDSGYR.I	945.01074	2	5.22E-04	0.84	3.20	-	543.4
AHQ-6-4, 2960	K.SFLDSGYR.I	945.01074	2	3.19E-04	0.87	2.62	-	827.7

AHQ-6-6, 3406	R.SLGEISALTSK.L	1106.25186	2	1.38E-05	0.93	3.47	-	934.3
AHQ-6-4, 3471	R.SLGEISALTSK.L	1106.25186	2	6.00E-06	0.91	3.28	-	973.8
AHQ-6-4, 3483	R.SLGEISALTSK.L	1106.25186	1	1.59E-05	0.37	2.83	-	174.0
AHQ-6-4, 3633	R.SLGEISALTSK.L	1106.25186	2	6.24E-06	0.94	3.56	-	1096.6
AHQ-6-7, 3307	R.SLGEISALTSK.L	1106.25186	2	9.05E-04	0.84	3.03	-	702.4
AHQ-6-5, 3335	K.SLLDASEEAIKK.D	1304.47187	2	1.20E-05	0.81	2.93	-	791.2
AHQ-6-4, 3375	K.SLLDASEEAIKK.D	1304.47187	2	1.29E-08	0.83	2.66	-	892.2
AHQ-6-3, 3437	K.SLLDASEEAIKK.D	1304.47187	2	2.24E-08	0.80	2.80	-	839.9
AHQ-6-6, 3334 - 3355	K.SLLDASEEAIKK.D	1304.47187	2	9.16E-04	0.83	2.97	-	1009.2
AHQ-6-5, 2375 - 2416	K.STVEGIQASVK.T	1119.25064	2	1.45E-04	0.81	2.61	-	848.7
AHQ-6-7, 2363	K.STVEGIQASVK.T	1119.25064	2	6.88E-06	0.89	3.18	-	903.1
AHQ-6-4, 2443	K.STVEGIQASVK.T	1119.25064	2	2.94E-07	0.93	3.17	-	1066.5
AHQ-6-3, 2504	K.STVEGIQASVK.T	1119.25064	2	4.52E-06	0.87	3.04	-	866.0
AHQ-6-4, 2568 - 2580	R.TDAGFTLR.W	880.96819	2	3.30E-04	0.91	2.79	-	1118.9
AHQ-6-5, 2544	R.TDAGFTLR.W	880.96819	2	5.13E-04	0.86	2.72	-	903.6
AHQ-6-11, 6216	R.TIESILEPVAQQISHLVIM*HEEGEVDGK.A	3119.49274	3	4.24E-04	0.44	3.01	-	213.9
AHQ-6-4, 6351 - 6412	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	1.00E-06	0.79	4.39	-	506.7
AHQ-6-4, 5707 - 5787	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	7.89E-07	0.77	3.78	-	758.1
AHQ-6-12, 5105 - 5163	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	1.13E-04	0.79	3.84	-	515.8
AHQ-6-3, 6285 - 6286	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	8.14E-04	0.51	3.05	-	453.0
AHQ-6-14-, 5606	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	1.67E-05	0.75	4.47	-	604.8
AHQ-6-4, 6499	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	6.80E-04	0.84	3.85	-	559.9
AHQ-6-5, 3247	R.TNLLQVCER.I	1134.28859	2	5.67E-05	0.87	3.02	-	1050.1
AHQ-6-6, 3239	R.TNLLQVCER.I	1134.28859	2	4.76E-04	0.92	2.97	-	1500.1
AHQ-6-12, 3264	R.TNLLQVCER.I	1134.28859	2	4.74E-06	0.88	3.09	-	978.4
AHQ-6-6, 5102	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	5.23E-07	0.89	3.88	-	868.2
AHQ-6-4, 4745 - 4805	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	7.16E-08	0.95	5.10	-	782.2
AHQ-6-4, 4815	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	2.60E-05	0.97	5.39	-	1876.8
AHQ-6-5, 5612	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	2	1.89E-04	0.46	3.48	-	242.8
AHQ-6-5, 5140	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	1.20E-06	0.91	3.95	-	1813.9
AHQ-6-5, 5133	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	6.16E-06	0.97	5.84	-	1247.5
AHQ-6-4, 5723 - 5729	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	3	1.04E-06	0.95	5.03	-	1571.4
AHQ-6-4, 5365	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	3	1.20E-04	0.87	4.57	-	1000.7
AHQ-6-3, 5184	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	8.73E-06	0.69	3.29	-	541.1
AHQ-6-5, 4740	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	2.66E-05	0.97	5.54	-	2264.6
AHQ-6-5, 4727	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	3.80E-04	0.53	2.94	-	467.4
AHQ-6-4, 5229	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	8.34E-09	0.95	4.74	-	2209.9
AHQ-6-5, 4831	R.VDQLTAQLADLAAR.G	1485.66778	2	3.70E-07	0.98	4.73	-	3306.4
AHQ-6-6, 4796 - 4798	R.VDQLTAQLADLAAR.G	1485.66778	2	8.98E-08	0.98	4.53	-	2866.1
AHQ-6-4, 4904 - 4968	R.VDQLTAQLADLAAR.G	1485.66778	2	4.50E-09	0.98	5.23	-	2704.2
AHQ-6-3, 5209	R.VLQLTSWDEDAWASK.D	1749.90156	2	6.78E-06	0.94	4.18	-	982.8
AHQ-6-5, 5097 - 5161	R.VLQLTSWDEDAWASK.D	1749.90156	2	3.43E-06	0.96	4.79	-	1229.1
AHQ-6-6, 5122	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.51E-04	0.93	4.08	-	876.5
AHQ-6-2, 5244	R.VLQLTSWDEDAWASK.D	1749.90156	2	4.68E-10	0.96	4.64	-	1353.4
AHQ-6-10, 4852 - 4906	R.VLQLTSWDEDAWASK.D	1749.90156	2	3.83E-05	0.53	2.83	-	467.4
AHQ-6-4, 5236 - 5276	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.30E-09	0.97	5.16	-	1629.3
AHQ-6-4, 5133	R.VLQLTSWDEDAWASK.D	1749.90156	2	9.03E-09	0.95	4.20	-	1155.5
AHQ-6-4, 3293	R.VMLVNSMNTVK.E	1236.53081	2	2.40E-05	0.94	3.58	-	1325.2
gi|21361657|ref|NP_005304.3|	glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom			2.75E-11	5.25	60.30	19.60	56782.0
AHQ-6-13-, 5429	R.ELSDFISYLQR.E	1371.52000	2	2.64E-04	0.95	4.14	-	1378.9
AHQ-6-13, 5531	R.ELSDFISYLQR.E	1371.52000	2	1.33E-04	0.88	3.03	-	982.8
AHQ-6-7, 6211	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	2.75E-11	0.98	5.97	-	2589.7
AHQ-6-7, 4331	R.GFPTIYFSPANK.K	1342.52349	2	2.15E-05	0.74	2.84	-	616.8
AHQ-6-7, 5344	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	3	1.53E-07	0.91	3.68	-	1383.5
AHQ-6-7, 2991 - 3040	K.M*DATANDVPSPYEVR.G	1681.80586	2	1.57E-05	0.82	3.88	-	353.0
AHQ-6-7, 3047	K.YGVSGYPTLK.I	1085.23435	2	4.32E-05	0.92	3.19	-	974.7
gi|4507953|ref|NP_003397.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep			4.15E-11	5.38	60.29	29.80	27744.9
AHQ-6-10, 5622	K.IETELRDICNDVLSLLEK.F	2162.44718	3	6.38E-07	0.85	3.87	-	569.5
AHQ-6-14-, 2376	K.SVTEQGAELSNEER.N	1549.57922	2	2.21E-08	0.92	3.54	-	1262.6
AHQ-6-10, 2154 - 2230	K.SVTEQGAELSNEER.N	1549.57922	2	3.00E-07	0.89	3.65	-	1065.6
AHQ-6-10, 2318 - 2379	K.SVTEQGAELSNEER.N	1549.57922	2	9.35E-08	0.96	5.09	-	1381.1
AHQ-6-13-, 2412 - 2442	K.SVTEQGAELSNEER.N	1549.57922	2	2.21E-07	0.88	3.73	-	1156.7
AHQ-6-12, 2403 - 2404	K.SVTEQGAELSNEER.N	1549.57922	2	4.79E-08	0.94	3.99	-	1363.0
AHQ-6-13, 2600	K.SVTEQGAELSNEER.N	1549.57922	2	2.40E-06	0.90	3.60	-	1130.3
AHQ-6-13-, 6296	K.TAFDEAIAELDTLSEESYK.D	2133.25160	3	9.12E-06	0.91	4.50	-	967.0
AHQ-6-14-, 6254 - 6314	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.15E-06	0.92	3.74	-	1132.1
AHQ-6-13-, 6233 - 6297	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.31E-04	0.96	4.65	-	1388.9
AHQ-6-10, 6114 - 6116	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	4.15E-11	0.97	5.75	-	1478.4
AHQ-6-13, 6343	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.00E-05	0.96	4.92	-	1166.1
AHQ-6-10, 6202 - 6282	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	1.04E-10	0.88	4.32	-	801.6
AHQ-6-10, 2327	R.YLAEVAAGDDK.K	1152.23595	1	2.86E-05	0.80	2.42	-	1452.5
AHQ-6-12, 2156	R.YLAEVAAGDDKK.G	1280.40887	2	2.65E-04	0.90	3.15	-	1294.9
AHQ-6-10, 2082	R.YLAEVAAGDDKK.G	1280.40887	1	5.05E-05	0.87	3.49	-	759.9
AHQ-6-10, 2056 - 2110	R.YLAEVAAGDDKK.G	1280.40887	2	1.70E-05	0.95	3.61	-	1635.8
AHQ-6-13-, 2136 - 2193	R.YLAEVAAGDDKK.G	1280.40887	2	1.30E-04	0.89	3.12	-	1438.5
gi|5729877|ref|NP_006588.1|	heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD			4.69E-11	13.42	150.24	22.90	70897.6
AHQ-6-6, 4295	R.ARFEELNADLFR.G	1481.63768	2	3.50E-06	0.97	4.70	-	1245.4
AHQ-6-6, 4510	R.ARFEELNADLFR.G	1481.63768	2	2.66E-05	0.88	3.39	-	811.6
AHQ-6-6, 4523	R.FEELNADLFR.G	1254.37310	2	1.36E-05	0.93	3.69	-	1367.4
AHQ-6-6, 5072	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	4.69E-11	0.88	4.17	-	814.4
AHQ-6-6, 5366	K.ILDKCNEIINWLDK.N	1776.04688	2	4.28E-05	0.95	4.75	-	1340.6
AHQ-6-6, 5379	K.ILDKCNEIINWLDK.N	1776.04688	3	1.69E-04	0.86	4.59	-	711.7
AHQ-6-6, 2587	K.M*KEIAEAYLGK.T	1269.49260	2	1.23E-04	0.84	3.02	-	926.8
AHQ-6-6, 2536 - 2595	K.M*KEIAEAYLGK.T	1269.49260	3	4.35E-04	0.79	3.20	-	993.1
AHQ-6-6, 2742 - 2798	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	1.93E-05	0.92	3.93	-	829.9
AHQ-6-6, 3310	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	2.82E-04	0.93	4.39	-	781.9
AHQ-6-6, 3888	K.NQVAMNPTNTVFDAK.R	1650.83816	2	6.97E-05	0.92	3.76	-	746.2
AHQ-6-6, 3514	K.NQVAMNPTNTVFDAK.R	1650.83816	2	9.44E-06	0.93	3.85	-	936.4
AHQ-6-6, 4440	K.NSLESYAFNMK.A	1304.45393	2	3.99E-05	0.86	3.19	-	800.1
AHQ-6-6, 3318	K.NSLESYAFNM*K.A	1320.45333	2	4.02E-05	0.87	3.35	-	839.2
AHQ-6-6, 2724	R.RFDDAVVQSDMK.H	1411.56603	2	4.94E-08	0.94	4.13	-	1155.2
AHQ-6-13-, 2840	R.RFDDAVVQSDMK.H	1411.56603	2	2.45E-05	0.87	2.85	-	1338.0
AHQ-6-6, 4299 - 4370	K.SFYPEEVSSM*VLTK.M	1633.84425	2	3.58E-05	0.82	3.36	-	688.6
AHQ-6-6, 5010	K.SFYPEEVSSMVLTK.M	1617.84485	2	4.47E-06	0.86	3.17	-	555.3
AHQ-6-6, 6234 - 6246	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	2.09E-05	0.94	4.46	-	877.4
AHQ-6-6, 6243	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	3	5.78E-04	0.55	3.03	-	529.8
AHQ-6-6, 3111	K.SQIHDIVLVGGSTR.I	1482.66712	2	3.35E-08	0.97	3.98	-	2104.8
AHQ-6-6, 4432 - 4442	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	3	1.98E-04	0.74	3.75	-	678.3
gi|4503545|ref|NP_001961.1|	eukaryotic translation initiation factor 5A; eIF5AI; eIF5A [Homo sapien			4.81E-11	1.88	20.28	15.60	16832.2
AHQ-6-12, 6227	R.NDFQLIGIQDGYLSLLQDSGEVR.E	2581.81935	2	4.81E-11	0.97	5.54	-	985.0
AHQ-6-12, 6161	K.RNDFQLIGIQDGYLSLLQDSGEVR.E	2738.00571	3	1.79E-09	0.92	4.75	-	1113.9
gi|5031857|ref|NP_005557.1|	lactate dehydrogenase A [Homo sapiens]			5.17E-11	2.78	30.27	13.60	36688.5
AHQ-6-14-, 6246	K.DLADELALVDVIEDK.L	1658.82864	2	8.53E-11	0.97	4.54	-	1685.5
AHQ-6-13, 6272	K.DLADELALVDVIEDK.L	1658.82864	2	1.95E-08	0.93	3.72	-	1257.6
AHQ-6-13-, 6229 - 6230	K.DLADELALVDVIEDK.L	1658.82864	2	5.17E-11	0.97	5.44	-	1609.6
AHQ-6-9, 6213	K.GYTSWAIGLSVADLAESIMK.N	2113.41967	2	1.88E-06	0.93	4.33	-	1010.8
AHQ-6-11, 2136 - 2201	K.VTLTSEEEAR.L	1135.20693	2	5.74E-04	0.88	2.94	-	1139.3

gi|17318569|ref|NP_006112.2| keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]				6.56E-11	17.11	210.25	38.80	66066.3
AHQ-6-7, 2012	K.AQYEDIAQK.S	1066.14629	2	5.55E-05	0.46	2.52	-	416.9
AHQ-6-10, 2856	R.DYQELMNTK.L	1142.26457	1	5.86E-04	0.51	2.69	-	271.1
AHQ-6-10, 2846	R.DYQELMNTK.L	1142.26457	1	4.82E-04	0.65	2.67	-	420.5
AHQ-6-6, 2218	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	1.69E-06	0.91	4.80	-	612.8
AHQ-6-3, 2264	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	3.92E-05	0.74	3.74	-	404.0
AHQ-6-14-, 2243	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	4.66E-05	0.62	2.87	-	417.4
AHQ-6-4, 2217	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	2.56E-04	0.77	4.00	-	287.1
AHQ-6-2, 2270	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	1.47E-04	0.36	2.81	-	242.2
AHQ-6-12, 2263	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	4.86E-04	0.69	2.77	-	440.8
AHQ-6-10, 2507	R.GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR.G	3314.18235	3	4.46E-05	0.75	3.48	-	927.1
AHQ-6-13-, 2616	R.GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR.G	3314.18235	3	8.77E-06	0.83	4.43	-	812.1
AHQ-6-1, 5123	K.LALDLEIATYR.T	1278.47925	2	3.40E-06	0.96	4.32	-	2328.0
AHQ-6-2, 3940	K.LNDLEDALQQAK.E	1358.47963	2	1.24E-06	0.96	4.00	-	1819.4
AHQ-6-13-, 3893	K.LNDLEDALQQAK.E	1358.47963	2	8.39E-08	0.98	5.06	-	2136.2
AHQ-6-8, 3657 - 3660	K.LNDLEDALQQAK.E	1358.47963	2	2.56E-06	0.97	4.63	-	2240.5
AHQ-6-10, 3644 - 3698	K.LNDLEDALQQAK.E	1358.47963	2	5.69E-07	0.97	4.76	-	1992.1
AHQ-6-1, 4066	K.LNDLEDALQQAK.E	1358.47963	2	1.31E-04	0.97	4.81	-	1858.5
AHQ-6-12, 3809	K.LNDLEDALQQAK.E	1358.47963	2	3.29E-06	0.94	4.07	-	1377.8
AHQ-6-5, 3845	K.LNDLEDALQQAK.E	1358.47963	2	1.26E-04	0.96	4.59	-	1529.1
AHQ-6-3, 3913	K.LNDLEDALQQAK.E	1358.47963	2	7.32E-08	0.97	4.89	-	1877.1
AHQ-6-6, 3808	K.LNDLEDALQQAK.E	1358.47963	2	1.56E-05	0.97	4.64	-	2201.6
AHQ-6-10, 3784	K.LNDLEDALQQAK.E	1358.47963	2	4.21E-08	0.85	3.41	-	1168.3
AHQ-6-7, 3692	K.LNDLEDALQQAK.E	1358.47963	2	6.94E-04	0.93	3.95	-	1486.1
AHQ-6-14-, 3864 - 3879	K.LNDLEDALQQAK.E	1358.47963	2	2.86E-06	0.96	4.52	-	1751.4
AHQ-6-13, 4027	K.LNDLEDALQQAK.E	1358.47963	2	5.51E-06	0.97	4.65	-	2150.8
AHQ-6-4, 3904	K.LNDLEDALQQAK.E	1358.47963	2	2.68E-04	0.96	4.36	-	1626.5
AHQ-6-11, 4147	K.NKLNDLEDALQQAK.E	1600.75564	2	1.34E-04	0.87	3.29	-	894.4
AHQ-6-10, 3558	K.NKLNDLEDALQQAK.E	1600.75564	2	8.52E-05	0.93	3.82	-	1168.7
AHQ-6-10, 4092	K.NKLNDLEDALQQAK.E	1600.75564	3	8.60E-05	0.92	4.15	-	1525.2
AHQ-6-1, 4488 - 4562	K.NKLNDLEDALQQAK.E	1600.75564	2	1.52E-04	0.95	3.84	-	1697.1
AHQ-6-10, 2743 - 2798	K.NMQDM*VEDYR.N	1317.43134	2	1.20E-04	0.81	3.05	-	815.5
AHQ-6-10, 3368 - 3374	K.NMQDMVEDYR.N	1301.43194	2	5.38E-05	0.75	3.10	-	795.4
AHQ-6-12, 3617	K.QISNLQQSISDAEQR.G	1717.81950	2	1.34E-04	0.77	3.05	-	594.9
AHQ-6-13-, 3689 - 3692	K.QISNLQQSISDAEQR.G	1717.81950	2	5.61E-08	0.89	4.11	-	562.8
AHQ-6-5, 3632	K.QISNLQQSISDAEQR.G	1717.81950	2	6.56E-11	0.90	4.20	-	684.6
AHQ-6-6, 3595	K.QISNLQQSISDAEQR.G	1717.81950	2	4.95E-07	0.84	3.29	-	710.6
AHQ-6-13, 3764 - 3825	K.QISNLQQSISDAEQR.G	1717.81950	2	7.55E-07	0.82	3.37	-	668.9
AHQ-6-7, 3499 - 3558	K.QISNLQQSISDAEQR.G	1717.81950	2	9.12E-06	0.82	3.35	-	692.0
AHQ-6-14-, 3666	K.QISNLQQSISDAEQR.G	1717.81950	2	4.99E-07	0.90	4.04	-	594.6
AHQ-6-11, 3501 - 3553	K.QISNLQQSISDAEQR.G	1717.81950	2	4.04E-04	0.60	3.02	-	389.1
AHQ-6-14-, 3587 - 3667	K.QISNLQQSISDAEQR.G	1717.81950	2	3.48E-04	0.76	3.05	-	492.3
AHQ-6-10, 3502	K.QISNLQQSISDAEQR.G	1717.81950	2	4.82E-05	0.94	4.20	-	1108.1
AHQ-6-1, 3860	K.QISNLQQSISDAEQR.G	1717.81950	2	1.70E-06	0.91	4.05	-	820.6
AHQ-6-4, 3679	K.QISNLQQSISDAEQR.G	1717.81950	2	1.17E-07	0.88	3.57	-	818.9
AHQ-6-10, 3302 - 3359	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	5.71E-05	0.91	3.28	-	1367.3
AHQ-6-4, 3529	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	5.99E-06	0.87	3.10	-	1172.0
AHQ-6-11, 3421 - 3477	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	1.89E-04	0.65	2.64	-	698.4
AHQ-6-6, 3436	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	2.30E-06	0.90	3.21	-	1345.1
AHQ-6-6, 1955	K.SKAEAESLYQSK.Y	1341.44907	2	6.48E-09	0.89	3.49	-	773.6
AHQ-6-4, 4029	K.SKAEAESLYQSKYEELQITAGR.H	2502.71900	2	1.38E-06	0.83	2.94	-	979.6
AHQ-6-5, 5803	R.SLDLDSIIAEVK.A	1303.48388	2	7.69E-07	0.96	3.94	-	1580.9
AHQ-6-11, 5547 - 5548	R.SLDLDSIIAEVK.A	1303.48388	2	1.30E-06	0.95	4.25	-	1429.7
AHQ-6-6, 5723	R.SLDLDSIIAEVK.A	1303.48388	2	6.36E-05	0.90	3.44	-	1243.4
AHQ-6-3, 5802	R.SLDLDSIIAEVK.A	1303.48388	2	1.08E-06	0.95	4.27	-	1368.2
AHQ-6-13, 5788 - 5799	R.SLDLDSIIAEVK.A	1303.48388	2	1.90E-06	0.96	4.70	-	1358.8
AHQ-6-2, 5838	R.SLDLDSIIAEVK.A	1303.48388	2	6.28E-05	0.94	3.63	-	1284.3
AHQ-6-1, 5802 - 5871	R.SLDLDSIIAEVK.A	1303.48388	2	2.77E-08	0.95	4.58	-	1149.3
AHQ-6-10, 5487	R.SLDLDSIIAEVK.A	1303.48388	1	3.63E-04	0.63	2.63	-	606.8
AHQ-6-10, 5474 - 5475	R.SLDLDSIIAEVK.A	1303.48388	2	8.44E-07	0.96	4.99	-	1208.6
AHQ-6-4, 5875	R.SLDLDSIIAEVK.A	1303.48388	2	6.56E-06	0.94	4.04	-	1096.8
AHQ-6-10, 4316	K.SLNNQFASFIDK.V	1384.51877	1	5.23E-05	0.63	3.16	-	417.5
AHQ-6-1, 4724	K.SLNNQFASFIDK.V	1384.51877	2	1.67E-07	0.83	3.44	-	519.3
AHQ-6-1, 4950	K.SLNNQFASFIDK.V	1384.51877	2	1.76E-05	0.88	3.54	-	862.0
AHQ-6-3, 4616	K.SLNNQFASFIDK.V	1384.51877	2	3.02E-08	0.94	3.95	-	967.8
AHQ-6-7, 4328	K.SLNNQFASFIDK.V	1384.51877	2	4.00E-07	0.94	4.33	-	978.0
AHQ-6-10, 4306	K.SLNNQFASFIDK.V	1384.51877	2	1.33E-06	0.90	3.48	-	823.5
AHQ-6-12, 2524 - 2529	R.SLVNLGGSK.S	875.00510	1	3.21E-04	0.07	1.81	-	141.2
AHQ-6-6, 6028 - 6096	R.THNLEPYFESFINNLR.R	1995.18315	2	1.47E-04	0.64	3.11	-	258.4
AHQ-6-10, 5854 - 5878	R.THNLEPYFESFINNLR.R	1995.18315	2	8.31E-05	0.91	4.04	-	534.4
AHQ-6-1, 6282	R.THNLEPYFESFINNLR.R	1995.18315	3	9.98E-06	0.92	4.17	-	1203.8
AHQ-6-7, 5192 - 5212	R.THNLEPYFESFINNLR.R	1995.18315	2	1.25E-04	0.90	3.75	-	729.1
AHQ-6-7, 5938	R.THNLEPYFESFINNLR.R	1995.18315	3	1.07E-05	0.96	4.79	-	2141.0
AHQ-6-5, 6164 - 6179	R.THNLEPYFESFINNLR.R	1995.18315	2	1.79E-05	0.61	2.94	-	438.1
AHQ-6-11, 5908 - 5916	R.THNLEPYFESFINNLR.R	1995.18315	3	3.88E-04	0.91	4.43	-	1300.2
AHQ-6-7, 5939	R.THNLEPYFESFINNLR.R	1995.18315	2	4.52E-05	0.89	3.29	-	794.7
AHQ-6-10, 5112 - 5166	R.THNLEPYFESFINNLR.R	1995.18315	2	9.16E-04	0.59	2.90	-	444.3
AHQ-6-13, 3357	R.TNAENEFVTIK.K	1266.38219	2	1.25E-05	0.84	3.17	-	672.5
AHQ-6-3, 3201	R.TNAENEFVTIK.K	1266.38219	2	5.90E-05	0.84	3.20	-	650.3
AHQ-6-1, 3407	R.TNAENEFVTIK.K	1266.38219	2	2.72E-04	0.93	3.66	-	1146.2
AHQ-6-2, 3208	R.TNAENEFVTIK.K	1266.38219	2	7.20E-06	0.89	3.70	-	761.2
AHQ-6-6, 3103	R.TNAENEFVTIK.K	1266.38219	2	1.41E-06	0.91	3.48	-	903.8
AHQ-6-7, 2999 - 3003	R.TNAENEFVTIK.K	1266.38219	2	7.86E-06	0.90	3.40	-	861.8
AHQ-6-12, 3101 - 3159	R.TNAENEFVTIK.K	1266.38219	2	1.42E-05	0.83	2.73	-	950.8
AHQ-6-5, 3099	R.TNAENEFVTIK.K	1266.38219	2	2.74E-04	0.78	2.92	-	689.2
AHQ-6-12, 2705 - 2769	R.TNAENEFVTIKK.D	1394.55511	2	9.04E-05	0.80	2.90	-	851.8
AHQ-6-5, 2645	R.TNAENEFVTIKK.D	1394.55511	2	1.79E-05	0.75	2.77	-	774.6
AHQ-6-10, 2602	R.TNAENEFVTIKK.D	1394.55511	2	3.54E-05	0.86	3.04	-	987.2
AHQ-6-13-, 2756	R.TNAENEFVTIKK.D	1394.55511	2	2.77E-04	0.92	3.55	-	1269.5
AHQ-6-11, 4251 - 4275	K.WELLQQVDTSTR.T	1476.61621	2	1.37E-05	0.91	3.42	-	1397.5
AHQ-6-6, 4338 - 4375	K.WELLQQVDTSTR.T	1476.61621	2	2.19E-07	0.83	3.11	-	884.3
AHQ-6-10, 4147 - 4202	K.WELLQQVDTSTR.T	1476.61621	2	4.12E-07	0.94	4.02	-	1451.4
AHQ-6-10, 4175	K.WELLQQVDTSTR.T	1476.61621	2	8.06E-09	0.96	4.21	-	1546.1
AHQ-6-12, 4308 - 4365	K.WELLQQVDTSTR.T	1476.61621	2	1.83E-06	0.94	4.07	-	1294.3
AHQ-6-3, 4448 - 4508	K.WELLQQVDTSTR.T	1476.61621	2	3.58E-04	0.72	2.71	-	1119.1
AHQ-6-5, 4384	K.WELLQQVDTSTR.T	1476.61621	2	1.50E-06	0.93	3.72	-	1243.9
AHQ-6-2, 4486	K.WELLQQVDTSTR.T	1476.61621	2	1.08E-07	0.95	3.79	-	1670.4
AHQ-6-4, 4469	K.WELLQQVDTSTR.T	1476.61621	2	1.21E-05	0.94	3.85	-	1712.0
AHQ-6-4, 3019	K.YEELQITAGR.H	1180.29253	2	6.20E-05	0.94	3.74	-	1465.3
AHQ-6-13, 3215 - 3221	K.YEELQITAGR.H	1180.29253	2	2.57E-05	0.95	3.55	-	1848.5
AHQ-6-5, 2967	K.YEELQITAGR.H	1180.29253	2	6.02E-04	0.94	3.80	-	1503.5
AHQ-6-12, 2963 - 3021	K.YEELQITAGR.H	1180.29253	2	6.62E-05	0.97	4.27	-	2295.8
AHQ-6-13-, 3069 - 3076	K.YEELQITAGR.H	1180.29253	2	2.35E-04	0.94	3.43	-	1604.0
AHQ-6-3, 3052	K.YEELQITAGR.H	1180.29253	2	1.41E-05	0.95	3.97	-	1635.0
AHQ-6-6, 2956	K.YEELQITAGR.H	1180.29253	2	5.89E-04	0.93	3.37	-	1462.0
AHQ-6-11, 2975 - 2992	K.YEELQITAGR.H	1180.29253	2	5.20E-04	0.94	3.53	-	1618.3
AHQ-6-2, 3064	K.YEELQITAGR.H	1180.29253	2	4.07E-06	0.94	4.05	-	1608.0

AHQ-6-10, 2892 - 2895	K.YEELQITAGR.H	1180.29253	2	3.76E-05	0.96	4.39	-	1622.6
AHQ-6-1, 3256	K.YEELQITAGR.H	1180.29253	2	1.89E-05	0.94	3.90	-	1558.1
gi|4557697|ref|NP_000412.1|	keratin 10; Keratin-10 [Homo sapiens]			7.14E-11	9.05	110.25	19.10	57247.1
AHQ-6-1, 3019	R.ALEESNYELEGK.I	1382.45482	2	3.16E-05	0.95	3.88	-	1362.7
AHQ-6-14-, 2775	R.ALEESNYELEGK.I	1382.45482	2	4.12E-06	0.91	3.47	-	1086.6
AHQ-6-12, 2713 - 2779	R.ALEESNYELEGK.I	1382.45482	2	9.18E-07	0.87	3.47	-	693.5
AHQ-6-11, 2733	R.ALEESNYELEGK.I	1382.45482	2	3.80E-09	0.91	3.30	-	1199.7
AHQ-6-10, 2690	R.ALEESNYELEGK.I	1382.45482	2	1.77E-06	0.88	3.56	-	920.1
AHQ-6-2, 2803	R.ALEESNYELEGK.I	1382.45482	2	6.36E-06	0.86	3.74	-	854.5
AHQ-6-8, 2612	R.ALEESNYELEGK.I	1382.45482	2	3.86E-07	0.87	3.31	-	926.1
AHQ-6-7, 2650	R.ALEESNYELEGK.I	1382.45482	2	3.70E-06	0.90	3.46	-	998.4
AHQ-6-6, 2734	R.ALEESNYELEGK.I	1382.45482	2	5.53E-07	0.90	3.79	-	846.5
AHQ-6-5, 2732	R.ALEESNYELEGK.I	1382.45482	2	4.75E-07	0.84	3.19	-	859.8
AHQ-6-3, 2798	R.ALEESNYELEGK.I	1382.45482	2	8.52E-07	0.88	3.59	-	856.3
AHQ-6-4, 2763 - 2765	R.ALEESNYELEGK.I	1382.45482	2	3.16E-08	0.93	3.76	-	1062.9
AHQ-6-3, 3492	K.DAEAWFNEK.S	1110.15762	2	7.07E-04	0.69	2.91	-	565.1
AHQ-6-3, 4420	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	6.56E-07	0.76	3.26	-	556.4
AHQ-6-11, 4953	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	9.92E-06	0.76	3.33	-	574.5
AHQ-6-3, 5124 - 5181	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	5.53E-04	0.68	2.75	-	571.8
AHQ-6-10, 4151 - 4160	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	5.05E-07	0.90	4.09	-	775.0
AHQ-6-14-, 4340	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.57E-04	0.56	2.85	-	328.6
AHQ-6-10, 4894	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.44E-07	0.85	3.66	-	659.5
AHQ-6-13-, 5096	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.39E-05	0.85	4.02	-	539.1
AHQ-6-13-, 4329	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	8.11E-07	0.71	3.39	-	521.5
AHQ-6-1, 4542 - 4547	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	5.80E-09	0.90	3.92	-	657.6
AHQ-6-1, 5282	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.35E-05	0.86	3.78	-	761.8
AHQ-6-6, 5127 - 5130	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.81E-06	0.79	3.30	-	640.1
AHQ-6-11, 4221 - 4229	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.14E-08	0.86	3.64	-	622.9
AHQ-6-2, 5238 - 5299	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.05E-04	0.82	3.65	-	533.9
AHQ-6-13, 4211	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	4.53E-06	0.90	4.16	-	704.0
AHQ-6-2, 4167	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.06E-09	0.85	3.64	-	575.5
AHQ-6-12, 4011	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	5.96E-07	0.94	4.33	-	1044.0
AHQ-6-6, 4028	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	3.00E-08	0.85	3.41	-	715.1
AHQ-6-13-, 4084	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	3.45E-08	0.92	4.20	-	860.5
AHQ-6-10, 3899 - 3956	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	3.08E-05	0.83	3.89	-	510.2
AHQ-6-1, 4263	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.29E-09	0.93	4.02	-	952.8
AHQ-6-3, 4042 - 4117	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	4.03E-08	0.83	3.66	-	619.2
AHQ-6-14-, 4032	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	4.88E-05	0.80	3.40	-	622.3
AHQ-6-14, 4769 - 4770	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.94E-08	0.89	3.88	-	830.6
AHQ-6-11, 3951	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	8.96E-07	0.88	3.73	-	859.8
AHQ-6-13-, 3324	K.IRLENEIQTYR.S	1435.61046	2	8.47E-07	0.95	3.93	-	1596.7
AHQ-6-10, 3071 - 3130	K.IRLENEIQTYR.S	1435.61046	2	7.39E-04	0.81	3.25	-	930.1
AHQ-6-13, 3468	K.IRLENEIQTYR.S	1435.61046	2	3.22E-07	0.95	3.89	-	1704.9
AHQ-6-3, 2550	R.LENEIQTYR.S	1166.26586	2	6.38E-05	0.88	3.42	-	1149.6
AHQ-6-7, 2423	R.LENEIQTYR.S	1166.26586	2	3.79E-04	0.88	3.55	-	999.9
AHQ-6-4, 2504	R.LENEIQTYR.S	1166.26586	2	2.08E-05	0.91	3.57	-	1364.9
AHQ-6-10, 2668 - 2678	R.LKYENEVALR.Q	1235.41446	2	2.75E-06	0.57	2.85	-	375.0
AHQ-6-11, 2717	R.LKYENEVALR.Q	1235.41446	2	3.72E-07	0.71	2.89	-	397.2
AHQ-6-14-, 5343	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	7.40E-04	0.93	5.02	-	919.8
AHQ-6-4, 6312	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	1.70E-04	0.89	4.11	-	1096.2
AHQ-6-13-, 5330	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	2.51E-04	0.87	4.07	-	861.8
AHQ-6-14-, 6115	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	6.24E-05	0.85	3.66	-	953.6
AHQ-6-7, 5224	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	2.22E-04	0.86	3.94	-	920.2
AHQ-6-3, 4106	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	5.04E-05	0.88	4.12	-	716.1
AHQ-6-1, 4976 - 5052	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	7.14E-11	0.93	4.20	-	1107.4
AHQ-6-3, 4873 - 4932	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	3.34E-05	0.83	3.58	-	819.3
AHQ-6-3, 2165	R.SLLEGEGSSGGGGR.G	1263.29680	2	2.91E-04	0.49	2.64	-	678.1
gi|4507109|ref|NP_000336.1|	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor			7.81E-11	2.85	30.28	27.10	14460.1
AHQ-6-12, 4440	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.41E-04	0.96	5.10	-	1028.0
AHQ-6-1, 4448	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	2.81E-04	0.90	3.82	-	1661.2
AHQ-6-12, 4157	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	6.11E-07	0.97	5.50	-	1176.4
AHQ-6-13, 4252 - 4319	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	4.19E-04	0.92	4.27	-	1641.7
AHQ-6-13, 4191 - 4247	K.TVEGAGSIAAATGFVK.K	1479.66001	2	2.16E-10	0.94	3.75	-	1414.2
AHQ-6-12, 4059 - 4069	K.TVEGAGSIAAATGFVK.K	1479.66001	2	7.42E-10	0.93	3.84	-	1008.0
AHQ-6-13-, 4124	K.TVEGAGSIAAATGFVK.K	1479.66001	2	7.81E-11	0.93	3.79	-	1146.1
AHQ-6-1, 4311	K.TVEGAGSIAAATGFVK.K	1479.66001	2	4.84E-08	0.95	3.81	-	1649.1
gi|4504183|ref|NP_000843.1|	glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s			1.05E-10	5.10	60.23	39.50	23355.7
AHQ-6-11, 5056 - 5119	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	3	1.20E-07	0.80	3.82	-	924.6
AHQ-6-11, 5060	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	6.52E-04	0.79	3.45	-	368.7
AHQ-6-11, 3213	K.ASCLYGQLPK.F	1138.31884	2	2.53E-06	0.85	2.91	-	803.4
AHQ-6-11, 4879	K.DQQEAALVDM*VNDGVEDLR.C	2134.26783	2	2.72E-07	0.93	4.50	-	854.0
AHQ-6-11, 5840 - 5921	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	1.94E-04	0.73	3.65	-	347.8
AHQ-6-11, 4744	K.FQDGDLTLYQSNTILR.H	1885.06701	2	5.03E-05	0.79	3.52	-	660.3
AHQ-6-11, 4647 - 4648	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.09E-04	0.93	4.08	-	754.2
AHQ-6-11, 4535 - 4591	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.05E-10	0.85	3.90	-	579.8
AHQ-6-10, 4548 - 4550	K.FQDGDLTLYQSNTILR.H	1885.06701	2	5.03E-05	0.92	4.61	-	659.9
AHQ-6-14-, 4714 - 4786	K.FQDGDLTLYQSNTILR.H	1885.06701	2	4.71E-06	0.87	4.00	-	757.9
AHQ-6-11, 4352	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	8.87E-08	0.93	4.69	-	742.2
gi|4502491|ref|NP_001203.1|	complement component 1, q subcomponent binding protein precursor; hyalu			1.28E-10	0.93	10.28	10.60	31362.0
AHQ-6-9, 6240	R.GVDNTFADELVELSTALEHQEYITFLEDLK.S	3441.73936	3	1.28E-10	0.93	5.54	-	634.7
gi|4502295|ref|NP_001677.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti			1.52E-10	5.72	70.24	21.70	57955.2
AHQ-6-7, 5150	R.AIAELGIYPAVDPLDSTSR.I	1989.21513	2	2.94E-05	0.79	2.96	-	496.7
AHQ-6-7, 6302 - 6370	R.DQEGQDVLLFIDNIFR.F	1923.11524	2	6.19E-05	0.66	3.08	-	405.2
AHQ-6-7, 4235 - 4238	R.FTQAGSEVSALLGR.I	1436.59522	2	1.52E-10	0.97	4.85	-	1344.5
AHQ-6-7, 3148	R.IM*DPNIVGSEHYDVAR.G	1833.01557	2	5.25E-04	0.64	2.71	-	534.5
AHQ-6-7, 4002	R.LVLEVAQHLGESTVR.T	1651.88893	2	9.06E-05	0.96	4.29	-	1727.0
AHQ-6-7, 6262	K.SLQDIIAILGM*DELSEEDKLTVSR.A	2693.02170	3	1.28E-08	0.88	4.30	-	580.6
AHQ-6-7, 5323	R.VALTGLTVAEYFR.D	1440.66861	2	9.34E-07	0.81	3.22	-	811.4
gi|20535366|ref|XP_053177.4|	similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap			1.53E-10	1.81	30.24	9.60	49858.2
AHQ-6-7, 2787	K.DVNAAIATIK.T	1016.17355	1	3.98E-06	0.24	1.98	-	391.8
AHQ-6-7, 2990	K.DVNAAIATIK.T	1016.17355	2	4.03E-04	0.81	2.98	-	865.7
AHQ-6-12, 3265	K.DVNAAIATIK.T	1016.17355	1	5.27E-06	0.72	2.41	-	563.1
AHQ-6-12, 3123	K.DVNAAIATIK.T	1016.17355	2	4.14E-04	0.91	3.49	-	1032.0
AHQ-6-11, 3092	K.DVNAAIATIK.T	1016.17355	2	6.67E-05	0.85	3.06	-	972.2
AHQ-6-13-, 3173	K.DVNAAIATIK.T	1016.17355	2	3.89E-04	0.77	2.91	-	712.1
AHQ-6-7, 4834 - 4875	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.10E-07	0.93	4.58	-	664.7
AHQ-6-11, 4812	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.79E-04	0.59	2.96	-	331.0
AHQ-6-7, 4788 - 4816	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.26E-05	0.86	3.68	-	634.0
AHQ-6-7, 4430	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	4.31E-06	0.85	3.96	-	439.6
AHQ-6-13, 4733	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	6.32E-07	0.83	3.74	-	372.6
AHQ-6-14-, 5148	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.46E-09	0.93	4.33	-	812.9
AHQ-6-14, 5329	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.18E-08	0.91	4.14	-	539.2
AHQ-6-14, 5580 - 5636	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.86E-07	0.94	4.79	-	740.1
AHQ-6-14, 5692 - 5702	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.28E-04	0.79	3.66	-	406.7
AHQ-6-7, 5014	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.53E-10	0.87	3.76	-	647.1
AHQ-6-13-, 4972	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	9.75E-07	0.68	3.38	-	445.1
AHQ-6-14-, 4942 - 4998	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.20E-09	0.94	4.45	-	957.6

AHQ-6-14-, 4594	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.92E-10	0.92	4.39	-	559.0
AHQ-6-14-, 4847 - 4874	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.92E-08	0.83	3.58	-	518.5
AHQ-6-13, 5501 - 5565	R.TIQFVDWCPTGFK.V	1600.81899	2	7.27E-05	0.81	3.36	-	558.4
AHQ-6-13-, 5464 - 5477	R.TIQFVDWCPTGFK.V	1600.81899	2	2.67E-04	0.83	3.16	-	709.5
AHQ-6-14-, 5419 - 5466	R.TIQFVDWCPTGFK.V	1600.81899	2	1.43E-05	0.70	3.06	-	705.4
gi|29568111|ref|NP_006088.2|	myosin, light polypeptide 9, regulatory; myosin regulatory light chain			1.60E-10	2.72	30.21	12.20	19827.1
AHQ-6-12, 3451	R.FTDEEVDEMYR.E	1434.51009	2	1.60E-10	0.94	4.13	-	945.3
AHQ-6-12, 2797	R.FTDEEVDEM*YR.E	1450.50949	2	8.02E-04	0.90	2.99	-	956.4
AHQ-6-13-, 2838	R.FTDEEVDEM*YR.E	1450.50949	2	9.43E-04	0.92	2.68	-	1537.5
AHQ-6-12, 3815	K.GNFNYVEFTR.I	1247.34066	2	1.16E-05	0.88	3.41	-	730.0
AHQ-6-11, 3915	K.GNFNYVEFTR.I	1247.34066	2	5.85E-04	0.78	2.87	-	670.9
AHQ-6-11, 3755 - 3757	K.GNFNYVEFTR.I	1247.34066	2	7.27E-05	0.87	3.41	-	691.4
gi|4506925|ref|NP_003013.1|	SH3 domain binding glutamic acid-rich protein like; SH3-binding domain			2.08E-10	2.73	30.34	50.00	12774.2
AHQ-6-13-, 5622 - 5676	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	1.28E-04	0.85	4.16	-	459.5
AHQ-6-13, 5755 - 5811	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	6.40E-04	0.96	4.78	-	1053.4
AHQ-6-13-, 5724 - 5780	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	6.50E-04	0.87	3.20	-	818.0
AHQ-6-13, 4999 - 5048	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.08E-10	0.94	5.46	-	826.1
AHQ-6-13-, 4781 - 4841	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	8.34E-09	0.97	6.31	-	999.8
AHQ-6-13-, 4900 - 4960	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.17E-08	0.96	5.90	-	1067.7
AHQ-6-13, 4889 - 4944	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	4.60E-10	0.97	6.72	-	1238.4
AHQ-6-13-, 2498 - 2561	R.VYIASSSGSTAIK.K	1284.44065	2	4.46E-05	0.96	4.37	-	1784.2
AHQ-6-13, 2673 - 2732	R.VYIASSSGSTAIK.K	1284.44065	2	2.72E-05	0.95	3.68	-	1989.3
gi|5031597|ref|NP_005710.1|	actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub			2.16E-10	1.74	20.22	9.00	20546.5
AHQ-6-12, 6047 - 6048	K.DTDIVDEAIYYFK.A	1592.72721	2	2.38E-05	0.94	3.59	-	1112.8
AHQ-6-13-, 6152	K.DTDIVDEAIYYFK.A	1592.72721	2	4.30E-09	0.96	3.98	-	1523.5
AHQ-6-14-, 6143	K.DTDIVDEAIYYFK.A	1592.72721	2	2.16E-10	0.93	4.05	-	1150.8
AHQ-6-12, 5537 - 5609	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	6.32E-05	0.81	3.47	-	693.8
gi|29741246|ref|XP_294070.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			2.28E-10	3.12	40.22	13.00	35032.0
AHQ-6-12, 5221 - 5287	K.LVINGNPITIFQER.D	1614.87029	2	9.46E-09	0.88	3.05	-	902.8
AHQ-6-9, 5066 - 5122	K.LVINGNPITIFQER.D	1614.87029	2	3.62E-05	0.90	3.40	-	916.7
AHQ-6-13-, 5354 - 5414	K.LVINGNPITIFQER.D	1614.87029	2	2.28E-10	0.96	4.27	-	1469.7
AHQ-6-14, 6013	K.LVINGNPITIFQER.D	1614.87029	2	6.82E-07	0.86	3.07	-	733.9
AHQ-6-10, 5099 - 5154	K.LVINGNPITIFQER.D	1614.87029	2	9.29E-08	0.86	2.73	-	767.6
AHQ-6-11, 5232 - 5311	K.LVINGNPITIFQER.D	1614.87029	2	1.37E-04	0.91	3.20	-	1041.3
AHQ-6-14-, 5374	K.LVINGNPITIFQER.D	1614.87029	2	3.27E-10	0.92	3.55	-	1109.5
AHQ-6-13, 5447 - 5503	K.LVINGNPITIFQER.D	1614.87029	2	3.51E-10	0.94	3.83	-	1021.5
AHQ-6-13, 5559 - 5560	K.LVINGNPITIFQER.D	1614.87029	2	8.55E-08	0.95	3.82	-	1282.4
AHQ-6-9, 4731 - 4802	K.LVINGNPITIFQERDPSK.I	2042.32440	2	7.73E-07	0.52	3.03	-	243.5
AHQ-6-9, 5703 - 5747	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	4.16E-08	0.86	4.48	-	940.3
AHQ-6-9, 6091	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	5.09E-04	0.78	3.98	-	1052.6
gi|4757810|ref|NP_004037.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,			2.50E-10	6.18	70.23	15.70	59750.3
AHQ-6-7, 3738	R.EAYPGDVFYLHSR.L	1554.68713	2	2.42E-08	0.89	2.78	-	1043.2
AHQ-6-7, 5543	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	3	6.66E-06	0.97	4.65	-	2353.6
AHQ-6-7, 3420	K.HALIIYDDLSK.Q	1288.47413	2	8.65E-08	0.95	3.85	-	1201.7
AHQ-6-7, 3543	R.ILGADTSVDLEETGR.V	1576.68772	2	2.60E-08	0.93	4.04	-	1061.6
AHQ-6-14-, 3684	R.ILGADTSVDLEETGR.V	1576.68772	2	2.50E-10	0.95	4.33	-	1176.6
AHQ-6-7, 5874 - 5946	K.LKEIVTNFLAGFEA	1552.79572	2	7.61E-05	0.86	3.13	-	871.5
AHQ-6-7, 3634	K.TGTAEMSSILEER.I	1424.55988	2	3.32E-07	0.82	2.95	-	1137.5
AHQ-6-7, 2588	K.TGTAEM*SSILEER.I	1440.55928	2	3.65E-06	0.74	2.97	-	808.5
gi|4503689|ref|NP_000499.1|	fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M			2.52E-10	12.12	160.26	20.10	94972.5
AHQ-6-8, 5318	K.DSDWPFCSDEDWNYK.C	1965.98609	2	3.19E-05	0.95	4.03	-	843.0
AHQ-6-7, 4626 - 4628	K.DSHSLTTNIM*EILR.G	1646.84779	2	2.51E-05	0.95	4.09	-	1406.6
AHQ-6-6, 4779	K.DSHSLTTNIM*EILR.G	1646.84779	2	9.02E-06	0.93	3.60	-	1320.1
AHQ-6-10, 4538 - 4555	K.DSHSLTTNIM*EILR.G	1646.84779	2	1.27E-04	0.93	3.54	-	1310.9
AHQ-6-8, 2537	R.EVDLKDYEDQQK.Q	1510.58460	2	4.32E-08	0.87	3.07	-	958.9
AHQ-6-9, 2537 - 2563	R.EVDLKDYEDQQK.Q	1510.58460	2	1.65E-06	0.83	3.44	-	578.1
AHQ-6-10, 2599 - 2600	R.EVDLKDYEDQQK.Q	1510.58460	2	9.13E-09	0.92	3.82	-	951.4
AHQ-6-6, 2626	R.EVDLKDYEDQQK.Q	1510.58460	2	1.47E-05	0.74	2.90	-	630.1
AHQ-6-13-, 2729	R.EVDLKDYEDQQK.Q	1510.58460	2	1.35E-05	0.65	2.55	-	559.3
AHQ-6-7, 1799 - 1854	R.GGSTSYGTGSETESPR.N	1573.55765	2	1.07E-06	0.84	3.29	-	723.2
AHQ-6-6, 1842 - 1898	R.GGSTSYGTGSETESPR.N	1573.55765	2	1.20E-06	0.52	2.92	-	397.7
AHQ-6-12, 4427	K.GLIDEVNQDFTNR.I	1521.61384	2	5.86E-06	0.84	3.22	-	769.7
AHQ-6-9, 4224	K.GLIDEVNQDFTNR.I	1521.61384	2	8.97E-08	0.93	3.62	-	1105.8
AHQ-6-6, 4467 - 4526	K.GLIDEVNQDFTNR.I	1521.61384	2	3.86E-04	0.73	3.23	-	732.1
AHQ-6-13, 4648 - 4720	K.GLIDEVNQDFTNR.I	1521.61384	2	4.84E-05	0.93	3.81	-	961.0
AHQ-6-5, 4517 - 4553	K.GLIDEVNQDFTNR.I	1521.61384	2	8.35E-09	0.94	3.42	-	1318.4
AHQ-6-4, 4597	K.GLIDEVNQDFTNR.I	1521.61384	2	1.45E-05	0.91	3.71	-	887.8
AHQ-6-11, 4309 - 4365	K.GLIDEVNQDFTNR.I	1521.61384	2	1.14E-05	0.77	3.02	-	680.1
AHQ-6-10, 4310	K.GLIDEVNQDFTNR.I	1521.61384	2	1.71E-06	0.94	4.07	-	1175.5
AHQ-6-8, 4365 - 4376	K.GLIDEVNQDFTNR.I	1521.61384	2	6.98E-05	0.90	3.54	-	826.5
AHQ-6-8, 3832 - 3834	K.GLIDEVNQDFTNR.I	1521.61384	2	2.52E-10	0.91	4.01	-	722.5
AHQ-6-7, 3806	K.GLIDEVNQDFTNR.I	1521.61384	2	3.02E-04	0.86	3.55	-	661.0
AHQ-6-7, 4336	K.GLIDEVNQDFTNR.I	1521.61384	2	3.71E-04	0.81	3.43	-	559.0
AHQ-6-3, 4576	K.GLIDEVNQDFTNR.I	1521.61384	2	1.24E-05	0.81	2.92	-	854.3
AHQ-6-14-, 2352	R.GSESGIFTNTK.E	1141.21317	2	4.88E-04	0.79	2.95	-	904.2
AHQ-6-6, 2304	R.GSESGIFTNTK.E	1141.21317	1	5.10E-04	0.28	2.08	-	314.4
AHQ-6-6, 3147	R.HPDEAAFFDTASTGK.T	1594.66329	2	1.91E-04	0.81	3.27	-	501.4
AHQ-6-10, 3072	R.HPDEAAFFDTASTGK.T	1594.66329	2	6.52E-04	0.26	2.53	-	278.5
AHQ-6-12, 3175	R.HPDEAAFFDTASTGK.T	1594.66329	2	6.37E-06	0.66	3.19	-	331.3
AHQ-6-6, 2664	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	1.40E-07	0.97	5.12	-	2147.0
AHQ-6-10, 2646	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.59E-05	0.88	3.45	-	782.9
AHQ-6-6, 2659	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	5.26E-07	0.95	4.60	-	956.3
AHQ-6-7, 2574	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	9.91E-07	0.96	4.63	-	1181.3
AHQ-6-11, 2691	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	4.09E-04	0.96	4.80	-	1341.3
AHQ-6-12, 2768 - 2844	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	1.40E-07	0.98	5.08	-	2440.8
AHQ-6-9, 2815 - 2816	K.LKNSLFEYQK.N	1270.45881	1	1.66E-04	0.15	1.80	-	314.8
AHQ-6-6, 2668	R.MELERPGGNEITR.G	1502.67870	2	5.73E-04	0.71	2.59	-	695.2
AHQ-6-6, 2216	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	1.64E-05	0.91	4.03	-	882.5
AHQ-6-7, 2156 - 2216	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	8.54E-05	0.91	3.97	-	751.1
AHQ-6-8, 2120	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	9.27E-10	0.94	4.82	-	895.8
AHQ-6-6, 2319	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	2.56E-07	0.90	4.40	-	347.0
AHQ-6-6, 2832 - 2843	K.NSLFEYQK.N	1029.12765	1	8.12E-04	0.12	2.07	-	160.1
AHQ-6-8, 2168	R.PGSTGTWNPGSSER.G	1433.46515	2	2.95E-05	0.82	3.09	-	596.0
AHQ-6-11, 2285 - 2296	R.PGSTGTWNPGSSER.G	1433.46515	2	1.62E-04	0.73	3.34	-	451.2
AHQ-6-6, 6278	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.12E-04	0.76	3.36	-	311.1
AHQ-6-6, 6424 - 6426	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	1.54E-04	0.90	4.03	-	587.6
AHQ-6-6, 2450 - 2462	K.VQHIQLLQK.N	1107.33106	2	3.66E-04	0.86	3.24	-	739.0
AHQ-6-10, 2414 - 2434	K.VQHIQLLQK.N	1107.33106	2	7.69E-05	0.75	2.69	-	750.0
gi|4758606|ref|NP_004508.1|	integrin-linked kinase [Homo sapiens]			3.06E-10	5.61	70.21	17.50	51418.9
AHQ-6-7, 4038 - 4040	R.EVPFADLSNM*EIGM*K.V	1713.95438	2	9.15E-05	0.72	3.30	-	470.2
AHQ-6-13, 5075	R.EVPFADLSNMEIGM*K.V	1697.95498	2	8.34E-04	0.58	2.67	-	364.8
AHQ-6-7, 4236	K.FDM*IVPILEK.M	1221.49108	2	5.41E-05	0.89	3.16	-	1033.6
AHQ-6-7, 2151	R.GDDTPLHLAASHGHR.D	1584.67809	3	3.06E-10	0.88	3.17	-	1743.6
AHQ-6-7, 4866 - 4915	R.GM*AFLHTLEPLIPR.H	1611.93301	2	3.05E-06	0.90	3.33	-	973.2
AHQ-6-7, 2343	K.LNENHSGELWK.G	1327.42732	2	2.23E-05	0.71	3.02	-	757.6
AHQ-6-7, 4054 - 4062	R.M*YAPAWVAPEALQK.K	1591.85542	2	3.79E-04	0.93	4.10	-	688.6
gi|6005942|ref|NP_009057.1|	valosin-containing protein; yeast Cdc48p homolog; transitional endoplas			3.08E-10	11.99	140.27	25.20	89321.3

AHQ-6-5, 4471	K.DVDLEFLAK.M	1050.18677	1	4.40E-05	0.60	2.22	-	1006.0
AHQ-6-5, 3715	R.ELQELVQYPVEHPDK.F	1825.01157	2	4.74E-04	0.89	3.37	-	1025.8
AHQ-6-5, 3499	R.EVDIGIPDATGR.L	1243.34863	2	9.15E-04	0.76	2.74	-	441.3
AHQ-6-5, 3731	K.GVLFYGPPGCGK.T	1253.45154	2	9.68E-06	0.83	3.16	-	840.3
AHQ-6-5, 6257 - 6261	R.IVSQLLTLMDGLK.Q	1431.76657	2	2.35E-09	0.95	4.40	-	1172.3
AHQ-6-5, 3359	R.KYEMFAQTLQQSR.G	1630.85008	2	8.69E-07	0.96	4.13	-	1786.9
AHQ-6-5, 5440	R.LDQLIYIPLPDEK.S	1557.81228	2	3.68E-06	0.92	3.63	-	1064.6
AHQ-6-5, 3237	R.LEILQIHTK.N	1095.31705	2	4.69E-04	0.83	2.51	-	1106.3
AHQ-6-5, 4801	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	2.21E-05	0.98	5.35	-	1957.9
AHQ-6-5, 3817	K.M*DELQLFR.G	1068.22879	2	3.14E-04	0.86	2.79	-	1137.1
AHQ-6-5, 6503	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	2.67E-04	0.94	4.25	-	1095.0
AHQ-6-5, 5491	K.NVFIIGATNRPDIIDPAILRPGR.L	2519.93026	3	8.77E-05	0.72	3.86	-	504.8
AHQ-6-5, 4791	K.VVETDPSPYCIVAPDTVIHCEGEPIKR.E	3085.45473	3	3.08E-10	0.83	3.85	-	443.5
AHQ-6-5, 3495 - 3500	R.WALSQSNPSALR.E	1330.47434	2	1.93E-05	0.90	3.85	-	942.9
gi|29739414|ref|XP_294015.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			3.22E-10	1.69	20.23	12.80	26916.7
AHQ-6-9, 3719 - 3776	K.IISNASCTTNCLAPLAK.V	1837.10868	2	3.17E-05	0.85	3.96	-	1203.4
AHQ-6-11, 3833	K.IISNASCTTNCLAPLAK.V	1837.10868	2	5.86E-04	0.85	2.57	-	1652.3
AHQ-6-11, 3749	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.01E-09	0.79	3.10	-	1298.0
AHQ-6-10, 3687 - 3766	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.02E-07	0.85	3.70	-	1418.1
AHQ-6-10, 3978	K.IISNASCTTNCLAPLAK.V	1837.10868	2	1.25E-08	0.62	3.17	-	854.1
AHQ-6-10, 4602	K.LISWYDNEFGYSNR.V	1764.87478	2	7.10E-06	0.95	4.50	-	935.9
AHQ-6-9, 4615 - 4671	K.LISWYDNEFGYSNR.V	1764.87478	2	1.25E-04	0.77	3.32	-	677.5
AHQ-6-9, 4490 - 4546	K.LISWYDNEFGYSNR.V	1764.87478	2	1.58E-07	0.93	4.32	-	1004.3
AHQ-6-11, 4613 - 4671	K.LISWYDNEFGYSNR.V	1764.87478	2	5.88E-06	0.91	4.21	-	808.5
AHQ-6-11, 4781	K.LISWYDNEFGYSNR.V	1764.87478	2	1.28E-06	0.63	2.71	-	534.3
AHQ-6-13, 4968	K.LISWYDNEFGYSNR.V	1764.87478	2	1.35E-09	0.94	3.90	-	1156.7
AHQ-6-13-, 4852	K.LISWYDNEFGYSNR.V	1764.87478	2	3.22E-10	0.91	3.68	-	848.4
AHQ-6-14-, 4774 - 4838	K.LISWYDNEFGYSNR.V	1764.87478	2	9.52E-06	0.90	4.17	-	432.0
AHQ-6-14-, 4904	K.LISWYDNEFGYSNR.V	1764.87478	2	2.24E-05	0.87	3.65	-	636.9
gi|4827056|ref|NP_005103.1|	WD repeat-containing protein 1 isoform 2 [Homo sapiens]			3.24E-10	10.03	110.31	35.40	58001.9
AHQ-6-6, 4836	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	6.20E-08	0.91	4.32	-	637.2
AHQ-6-6, 4835 - 4903	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	3.24E-10	0.97	5.72	-	1688.4
AHQ-6-6, 3864	R.FATASADGQIYIYDGK.T	1720.86021	2	1.85E-05	0.83	3.38	-	1121.1
AHQ-6-6, 3740 - 3802	R.FATASADGQIYIYDGK.T	1720.86021	2	1.58E-08	0.90	3.52	-	871.4
AHQ-6-6, 5407	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	3	2.92E-06	0.87	4.26	-	790.1
AHQ-6-6, 5418	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	2	2.20E-05	0.89	3.96	-	674.6
AHQ-6-6, 4455 - 4514	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	2.80E-09	0.97	5.39	-	1603.9
AHQ-6-6, 5303 - 5358	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	6.25E-10	0.91	4.22	-	898.8
AHQ-6-6, 5347 - 5420	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	2.08E-08	0.83	3.95	-	451.5
AHQ-6-6, 5190 - 5246	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.59E-06	0.94	4.64	-	1022.6
AHQ-6-7, 3815	R.LYSILGTTLKDEGK.L	1538.76736	2	5.39E-04	0.86	3.23	-	880.2
AHQ-6-12, 3940	R.LYSILGTTLKDEGK.L	1538.76736	2	8.02E-05	0.90	3.67	-	901.2
AHQ-6-6, 3926 - 3927	R.LYSILGTTLKDEGK.L	1538.76736	2	6.55E-06	0.94	4.20	-	1112.8
AHQ-6-6, 4167	R.M*TVDESGQLISCSMDDTVR.Y	2162.36305	2	1.65E-04	0.90	3.82	-	844.1
AHQ-6-6, 4203	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	3.62E-05	0.83	3.16	-	762.9
AHQ-6-6, 4070	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	4.02E-06	0.98	6.27	-	2699.8
AHQ-6-6, 4168	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	4.18E-08	0.97	5.71	-	1776.3
AHQ-6-12, 3831	K.YAPSGFYIASGDVSGK.L	1619.75589	2	3.22E-04	0.66	2.84	-	558.9
AHQ-6-6, 3768 - 3830	K.YAPSGFYIASGDVSGK.L	1619.75589	2	7.73E-10	0.92	3.81	-	970.7
AHQ-6-6, 2851 - 2867	K.YEYQPFAGK.I	1103.20822	2	5.00E-06	0.84	2.87	-	589.4
gi|7669492|ref|NP_002037.2|	glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]			3.93E-10	1.87	20.28	11.30	36053.0
AHQ-6-11, 5839 - 5912	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	8.10E-06	0.93	5.60	-	1491.4
AHQ-6-11, 3943	R.VPTANVSVVDLTCR.L	1532.74450	2	1.88E-09	0.96	4.59	-	1102.4
AHQ-6-9, 3750 - 3786	R.VPTANVSVVDLTCR.L	1532.74450	2	8.54E-09	0.94	3.82	-	1049.3
AHQ-6-5, 4039 - 4119	R.VPTANVSVVDLTCR.L	1532.74450	2	2.69E-05	0.83	2.76	-	881.0
AHQ-6-12, 4007 - 4064	R.VPTANVSVVDLTCR.L	1532.74450	2	1.75E-09	0.94	4.16	-	919.5
AHQ-6-13, 4175	R.VPTANVSVVDLTCR.L	1532.74450	2	3.62E-08	0.95	4.06	-	1120.1
AHQ-6-14, 4768	R.VPTANVSVVDLTCR.L	1532.74450	2	1.73E-06	0.89	3.57	-	631.4
AHQ-6-13-, 4052	R.VPTANVSVVDLTCR.L	1532.74450	2	3.13E-09	0.89	3.89	-	800.7
AHQ-6-14-, 4031	R.VPTANVSVVDLTCR.L	1532.74450	2	3.93E-10	0.94	4.48	-	1013.8
gi|30150448|ref|XP_293066.2|	similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose			4.07E-10	0.95	10.23	2.90	58788.2
AHQ-6-6, 4474 - 4483	R.VINEPTAAALAYGLDK.S	1646.86592	2	4.07E-10	0.95	4.65	-	874.2
gi|4502051|ref|NP_000688.1|	arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]			4.12E-10	8.91	110.22	22.60	75721.8
AHQ-6-6, 4654	R.AAAQLTYCSLCPPDDLADR.G	2140.33708	2	5.63E-06	0.90	3.80	-	528.3
AHQ-6-6, 2456	K.AVSTGGGGHVQLLR.R	1352.52468	2	1.06E-05	0.75	3.37	-	493.0
AHQ-6-6, 3106 - 3179	R.EITEVGLCQAQDR.G	1520.64745	2	1.93E-05	0.85	3.32	-	777.5
AHQ-6-6, 6467	K.ELQNGSLFEADFILLDGIPANVIR.G	2645.99132	2	1.14E-04	0.84	3.37	-	708.6
AHQ-6-6, 3419	K.GDPELQAWCR.E	1233.33558	2	1.00E-06	0.73	2.67	-	435.8
AHQ-6-6, 5283	R.GLLGLPGALYAHDALR.L	1637.90708	2	4.12E-10	0.90	3.47	-	680.4
AHQ-6-6, 3660	R.LPGDNALDM*FQK.H	1365.53724	2	1.70E-04	0.60	2.89	-	585.2
AHQ-6-6, 4410	R.LPGDNALDMFQK.H	1349.53784	2	4.51E-04	0.85	3.05	-	881.0
AHQ-6-6, 3964	R.TQLISDGGIFDK.A	1294.43554	2	7.95E-04	0.84	2.95	-	866.9
AHQ-6-6, 4524 - 4559	R.VATGAWLFSGSYNR.V	1529.68080	2	1.62E-04	0.76	3.22	-	583.6
AHQ-6-6, 4756 - 4822	R.WVQGEDILSLPEGTAR.L	1771.95190	2	1.70E-04	0.89	4.50	-	652.1
gi|5031677|ref|NP_005681.1|	dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [			5.59E-10	4.27	50.22	8.90	78060.6
AHQ-6-13-, 4648 - 4649	K.ALQGASQIIAEIR.E	1370.57991	2	1.30E-08	0.95	3.92	-	1661.7
AHQ-6-13, 4780	K.ALQGASQIIAEIR.E	1370.57991	2	8.19E-06	0.93	3.78	-	1531.1
AHQ-6-13-, 4969	K.DTLQSELVGQLYK.S	1494.67144	2	3.38E-04	0.85	3.16	-	1044.8
AHQ-6-6, 6308	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	3.41E-09	0.62	2.89	-	697.1
AHQ-6-6, 5908	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	8.12E-05	0.90	3.77	-	904.9
AHQ-6-5, 5979	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	2.18E-07	0.90	3.98	-	952.4
AHQ-6-13-, 5866	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	5.59E-10	0.95	4.35	-	1279.5
gi|27500274|ref|XP_113950.3|	similar to Munc13-4 protein [Homo sapiens]			5.70E-10	8.46	100.24	12.50	123281.1
AHQ-6-4, 6684	K.AFGELCPNTAPLPQLVTEALQTGTTEWFHLK.Q	3472.91108	3	8.33E-09	0.81	3.97	-	481.0
AHQ-6-4, 6027 - 6063	R.ALLYEDALYTVLHR.L	1677.92484	2	5.70E-10	0.92	3.42	-	1156.9
AHQ-6-4, 4735	R.AVQM*DELVPLGELTK.H	1659.92638	2	3.45E-07	0.63	2.79	-	511.1
AHQ-6-4, 5577	R.AVQMDELVPLGELTK.H	1643.92698	2	7.14E-04	0.81	3.17	-	626.0
AHQ-6-4, 2496	R.DLELQAASSR.E	1090.16939	2	9.72E-05	0.95	3.66	-	1573.3
AHQ-6-4, 3480	R.IQQQAETTSEELGAVTVK.A	1933.10674	2	3.19E-06	0.96	4.64	-	1270.9
AHQ-6-4, 5088	R.LALVYCSLIK.A	1181.46990	2	2.86E-07	0.89	3.51	-	830.9
AHQ-6-4, 5311 - 5319	K.LPAQLAWEALEQR.V	1525.73360	2	3.21E-09	0.96	4.76	-	1339.4
AHQ-6-5, 5232	K.LPAQLAWEALEQR.V	1525.73360	2	2.37E-06	0.92	3.68	-	1153.9
AHQ-6-4, 4076	R.SVFPLSVSDSPAR.L	1362.51311	2	1.37E-05	0.83	3.07	-	867.1
AHQ-6-4, 5876	R.WFQPAIPSWLQK.T	1501.75533	2	8.85E-05	0.70	2.99	-	371.1
gi|4504523|ref|NP_002148.1|	heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (			6.75E-10	1.75	20.24	25.50	10931.6
AHQ-6-14-, 2815 - 2874	K.VLQATVVAVGSGSK.G	1316.52902	2	6.75E-10	0.97	4.81	-	1462.3
AHQ-6-14-, 4783 - 4863	K.VVLDDKDYFLFR.D	1530.74861	2	4.37E-07	0.78	2.93	-	856.6
AHQ-6-14-, 4864	K.VVLDDKDYFLFR.D	1530.74861	3	1.33E-05	0.87	3.30	-	709.4
AHQ-6-14, 5534 - 5600	K.VVLDDKDYFLFR.D	1530.74861	2	6.37E-06	0.86	3.23	-	741.1
gi|29737978|ref|XP_290747.1|	similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy			7.24E-10	3.60	40.24	1.50	191380.7
AHQ-6-3, 3864 - 3941	K.ADFCIIHYAGK.V	1296.47641	2	3.72E-05	0.86	2.90	-	1232.8
AHQ-6-5, 3867	K.ADFCIIHYAGK.V	1296.47641	2	7.24E-10	0.96	4.10	-	1238.5
AHQ-6-1, 4112	K.ADFCIIHYAGK.V	1296.47641	2	1.43E-07	0.91	3.47	-	1010.4
AHQ-6-4, 3924 - 3953	K.ADFCIIHYAGK.V	1296.47641	2	4.00E-07	0.92	3.18	-	1328.1
AHQ-6-6, 3838	K.ADFCIIHYAGK.V	1296.47641	2	7.59E-07	0.94	3.72	-	1130.1
AHQ-6-2, 3972	K.ADFCIIHYAGK.V	1296.47641	1	3.60E-05	0.67	2.56	-	600.3
AHQ-6-2, 3958 - 3966	K.ADFCIIHYAGK.V	1296.47641	2	1.12E-06	0.96	3.85	-	1656.0

AHQ-6-1, 3320	R.AGVLAHLEEER.D	1224.34854	2	2.04E-06	0.96	4.14	-	1755.9
AHQ-6-2, 3086	R.AGVLAHLEEER.D	1224.34854	2	1.19E-07	0.96	4.14	-	1665.6
AHQ-6-3, 3082	R.AGVLAHLEEER.D	1224.34854	2	1.27E-08	0.95	4.42	-	1280.3
AHQ-6-4, 3044	R.AGVLAHLEEER.D	1224.34854	2	1.44E-06	0.96	4.28	-	1449.1
AHQ-6-6, 2919 - 2999	R.AGVLAHLEEER.D	1224.34854	2	1.73E-06	0.95	3.81	-	1758.6
AHQ-6-5, 2992	R.AGVLAHLEEER.D	1224.34854	2	9.20E-08	0.96	4.36	-	1594.6
AHQ-6-6, 3608	K.DKADFCIIHYAGK.V	1539.73719	2	3.69E-06	0.91	3.41	-	1286.2
AHQ-6-2, 3766	K.DKADFCIIHYAGK.V	1539.73719	3	4.95E-08	0.95	4.36	-	1812.1
AHQ-6-3, 3738	K.DKADFCIIHYAGK.V	1539.73719	2	1.20E-04	0.95	4.12	-	1330.6
AHQ-6-2, 3751	K.DKADFCIIHYAGK.V	1539.73719	2	4.10E-06	0.96	4.82	-	1509.4
AHQ-6-5, 3645	K.DKADFCIIHYAGK.V	1539.73719	2	1.33E-08	0.96	4.10	-	1722.5
AHQ-6-1, 3910	K.DKADFCIIHYAGK.V	1539.73719	2	3.47E-05	0.89	3.77	-	777.9
AHQ-6-3, 4597 - 4598	K.LDPHLVLDQLR.C	1319.53460	2	2.32E-06	0.73	2.86	-	614.9
AHQ-6-2, 4624	K.LDPHLVLDQLR.C	1319.53460	3	1.24E-04	0.90	3.31	-	1101.3
AHQ-6-4, 4603	K.LDPHLVLDQLR.C	1319.53460	2	2.39E-05	0.64	2.52	-	418.8
AHQ-6-5, 4521	K.LDPHLVLDQLR.C	1319.53460	3	2.76E-05	0.91	3.65	-	952.1
gi|5453898|ref|NP_006212.1|	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1; dod;			7.30E-10	0.97	10.24	9.20	18243.2
AHQ-6-12, 4013	R.TKEEALELINGYIQK.I	1749.98614	2	7.30E-10	0.97	4.78	-	1455.4
gi|4758950|ref|NP_000933.1|	peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]			7.65E-10	5.49	60.22	31.50	23742.4
AHQ-6-12, 3065 - 3068	R.DKPLKDVIIADCGK.I	1573.83653	3	4.22E-06	0.91	4.42	-	938.0
AHQ-6-14-, 3079	R.DKPLKDVIIADCGK.I	1573.83653	2	7.15E-04	0.74	2.70	-	717.6
AHQ-6-12, 3061	R.DKPLKDVIIADCGK.I	1573.83653	2	7.65E-10	0.91	3.70	-	1117.1
AHQ-6-12, 4131 - 4187	K.DTNGSQFFITTVK.T	1458.59766	2	3.07E-07	0.93	3.84	-	1126.4
AHQ-6-12, 3228	K.HYGPGWVSMANAGK.D	1475.65664	2	6.12E-04	0.95	4.10	-	1198.6
AHQ-6-12, 4227 - 4288	K.TVDNFVALATGEK.G	1365.51377	2	8.07E-05	0.92	3.56	-	981.8
AHQ-6-12, 4473 - 4553	K.TVDNFVALATGEK.G	1365.51377	2	1.56E-06	0.91	3.65	-	881.4
AHQ-6-14-, 4366	K.TVDNFVALATGEK.G	1365.51377	2	1.65E-05	0.93	3.58	-	1131.1
AHQ-6-12, 3731 - 3800	R.VIKDFM*IQGGDFTR.G	1643.88873	2	2.60E-05	0.84	3.42	-	891.9
AHQ-6-12, 4105 - 4109	R.VIKDFMIQGGDFTR.G	1627.88933	2	7.79E-06	0.94	3.95	-	1310.4
gi|5902128|ref|NP_008880.1|	syntaxin binding protein 2; Hunc18b [Homo sapiens]			7.96E-10	9.91	110.28	33.40	66438.1
AHQ-6-6, 6490	R.AADPVSPLLHELTFQAMAYDLLDIEQDTYR.Y	3437.82058	3	9.35E-08	0.94	5.40	-	841.4
AHQ-6-6, 5874	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	3	3.06E-06	0.92	4.68	-	951.9
AHQ-6-6, 6074 - 6079	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	4.87E-05	0.94	3.92	-	1014.4
AHQ-6-7, 5927	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	3.71E-04	0.49	2.75	-	469.3
AHQ-6-6, 3312	R.KGPEDTAQLAHAVLAK.L	1649.87303	3	1.52E-09	0.96	5.31	-	1260.0
AHQ-6-6, 3587	K.LCSVEQDLAM*GSDAEGEK.I	1957.08386	2	5.52E-05	0.82	3.28	-	839.2
AHQ-6-6, 5944	K.LIVPVLLDAAVPAYDK.I	1698.03911	3	1.56E-06	0.98	5.64	-	2477.0
AHQ-6-6, 3218 - 3219	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	1.87E-08	0.93	4.79	-	607.3
AHQ-6-6, 5227	R.NLWPFVSDPAPTASSQAAVSAR.F	2273.48981	2	5.27E-05	0.88	4.01	-	543.5
AHQ-6-6, 6462	R.QLEVLAQQIATLCATLQEYPAIR.Y	2632.02938	3	1.12E-04	0.84	3.56	-	1093.8
AHQ-6-6, 5671 - 5672	R.REPIPSLEAIYLLSPTEK.S	2057.37574	3	1.41E-06	0.78	3.37	-	931.8
AHQ-6-6, 5670	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	1.26E-04	0.97	5.26	-	1273.4
AHQ-6-6, 4706	K.WEVLIGSSHILTPTR.F	1709.97007	2	7.96E-10	0.93	3.65	-	1110.1
gi|20357552|ref|NP_005222.2|	cortactin isoform a; oncogene EMS1 [Homo sapiens]			8.52E-10	4.82	60.26	15.80	61585.7
AHQ-6-14-, 4532 - 4547	K.ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK.E	3334.37643	3	8.82E-04	0.76	3.70	-	515.1
AHQ-6-14-, 4659 - 4730	K.ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK.E	3334.37643	3	3.93E-04	0.88	4.83	-	463.9
AHQ-6-14-, 4807	K.ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK.E	3334.37643	3	5.06E-05	0.75	3.22	-	759.1
AHQ-6-12, 3895 - 3908	R.LPSSPVYEDAASFK.A	1511.65733	2	1.76E-04	0.76	3.01	-	681.4
AHQ-6-13, 4007	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	3.13E-06	0.92	3.78	-	1006.0
AHQ-6-14, 4576	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	2.49E-04	0.91	3.55	-	962.1
AHQ-6-12, 3803	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	2.56E-07	0.87	3.09	-	959.6
AHQ-6-13-, 3870	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	8.52E-10	0.97	5.27	-	1282.1
AHQ-6-14-, 3852 - 3916	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	1.37E-09	0.93	3.89	-	1055.4
AHQ-6-13, 3139 - 3140	K.VDKSAVGFEYQGK.T	1428.57155	2	1.16E-06	0.85	3.59	-	511.0
AHQ-6-13-, 2980	R.VDQSAVGFEYQGK.T	1428.52841	2	1.51E-08	0.77	2.76	-	798.0
AHQ-6-12, 5071	R.YGLFPANYVELR.Q	1442.64306	2	1.17E-05	0.73	2.67	-	458.6
gi|6005749|ref|NP_009193.1|	RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA			8.64E-10	2.64	30.23	22.20	19846.9
AHQ-6-10, 6242	R.GPGTSFEFALAIVEALNGK.E	1922.17039	2	8.64E-10	0.90	3.86	-	1044.4
AHQ-6-10, 6183	R.GPGTSFEFALAIVEALNGKEVAAQVK.A	2648.00721	3	1.64E-05	0.91	4.61	-	873.2
AHQ-6-11, 3193	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	1.22E-09	0.83	3.28	-	636.9
gi|13129150|ref|NP_005339.1|	heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H			8.79E-10	2.46	30.23	4.40	84659.1
AHQ-6-5, 2512	K.FYEQFSK.N	949.04099	1	8.22E-05	0.69	2.14	-	762.7
AHQ-6-5, 3919	R.NPDDITNEEYGEFYK.S	1834.87381	2	2.77E-09	0.96	4.65	-	1190.5
AHQ-6-6, 3895	R.NPDDITNEEYGEFYK.S	1834.87381	2	1.90E-09	0.90	3.89	-	857.9
AHQ-6-5, 3833	R.NPDDITNEEYGEFYK.S	1834.87381	2	8.79E-10	0.96	4.62	-	1250.4
AHQ-6-5, 4083	R.RAPFDLFENR.K	1265.40235	2	1.08E-06	0.81	3.32	-	536.8
gi|4557305|ref|NP_000025.1|	aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho			9.77E-10	6.90	90.23	36.50	39419.7
AHQ-6-8, 2123 - 2194	R.ALANSLACQGK.Y	1134.28859	2	4.17E-05	0.80	3.29	-	653.4
AHQ-6-8, 4273 - 4338	R.ALANSLACQGKYTPSGQAGAAASESLFVSNHAY	3344.61352	3	2.05E-05	0.53	3.03	-	417.9
AHQ-6-9, 4039 - 4044	K.FSHEEIAMATVTALR.R	1676.91875	2	1.01E-05	0.93	3.55	-	1253.9
AHQ-6-11, 2944	K.GILAADESTGSIAK.R	1333.47008	2	1.32E-08	0.94	3.69	-	1460.7
AHQ-6-12, 2977 - 2980	K.GILAADESTGSIAK.R	1333.47008	2	8.43E-08	0.95	3.94	-	1377.4
AHQ-6-8, 2696	K.GILAADESTGSIAK.R	1333.47008	2	9.77E-10	0.96	4.28	-	1154.6
AHQ-6-13, 3161	K.GILAADESTGSIAK.R	1333.47008	2	1.12E-07	0.93	3.67	-	1105.7
AHQ-6-9, 2787	K.GILAADESTGSIAK.R	1333.47008	2	1.97E-04	0.84	2.75	-	825.8
AHQ-6-9, 4174	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	5.65E-06	0.72	3.95	-	601.6
AHQ-6-8, 3976	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	2.12E-04	0.79	4.53	-	643.8
AHQ-6-9, 4595 - 4620	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.16E-04	0.77	2.97	-	571.7
AHQ-6-9, 4962	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.51E-04	0.90	3.99	-	616.7
AHQ-6-9, 3816	K.IGEHTPSALAIM*ENANVLAR.Y	2124.40728	2	2.95E-04	0.40	2.55	-	394.5
AHQ-6-8, 4706	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	8.51E-08	0.92	4.40	-	656.0
AHQ-6-8, 5236	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	2.01E-05	0.88	4.56	-	642.3
AHQ-6-8, 4273 - 4338	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	8.87E-07	0.78	3.63	-	335.7
gi|21361198|ref|NP_000286.2|	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei			1.05E-09	0.86	10.24	4.30	46722.2
AHQ-6-14-, 4380	K.VFSNGADLSGVTEEAPLK.L	1835.00476	2	1.05E-09	0.86	3.38	-	772.4
AHQ-6-7, 4156 - 4234	K.VFSNGADLSGVTEEAPLK.L	1835.00476	2	2.40E-06	0.94	4.83	-	887.0
gi|4507231|ref|NP_003134.1|	single-stranded DNA binding protein; single-stranded DNA-binding protei			1.13E-09	2.51	30.22	32.40	17259.5
AHQ-6-13-, 5689	K.NPVTIFSLATNEM*WR.S	1796.04007	2	1.29E-07	0.83	3.12	-	974.2
AHQ-6-13-, 5745	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	3.79E-06	0.77	3.41	-	606.0
AHQ-6-13-, 3261	R.SGDSEVYQLGDVSQK.T	1612.67692	2	1.68E-09	0.94	4.48	-	1022.0
AHQ-6-13, 3408	R.SGDSEVYQLGDVSQK.T	1612.67692	2	1.13E-09	0.91	3.55	-	1255.5
gi|10835187|ref|NP_000627.1|	superoxide dismutase 2, mitochondrial [Homo sapiens]			1.15E-09	3.52	40.25	28.40	24733.0
AHQ-6-13-, 5848	K.AIWNVINWENVTER.Y	1744.93137	2	1.85E-07	0.91	3.47	-	1114.2
AHQ-6-13, 5912	K.AIWNVINWENVTER.Y	1744.93137	2	8.30E-06	0.54	2.62	-	519.5
AHQ-6-11, 5623 - 5679	K.AIWNVINWENVTER.Y	1744.93137	2	2.32E-09	0.90	3.50	-	977.2
AHQ-6-14-, 5826	K.AIWNVINWENVTER.Y	1744.93137	2	3.61E-04	0.83	3.19	-	807.8
AHQ-6-14-, 3859 - 3863	K.GDVTAQIALQPALK.F	1425.65548	2	2.43E-06	0.83	3.83	-	730.0
AHQ-6-11, 3777	K.GDVTAQIALQPALK.F	1425.65548	1	3.60E-05	0.49	2.83	-	523.1
AHQ-6-11, 3717 - 3771	K.GDVTAQIALQPALK.F	1425.65548	2	3.72E-07	0.90	4.19	-	824.9
AHQ-6-13-, 3857	K.GDVTAQIALQPALK.F	1425.65548	2	8.06E-05	0.75	3.03	-	751.4
AHQ-6-11, 2416 - 2488	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	1.15E-09	0.96	5.08	-	1186.2
AHQ-6-11, 2595	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	1.29E-08	0.91	3.45	-	946.1
AHQ-6-11, 5857 - 5936	K.LTAASVGVQGSGWGWLGFNK.E	2036.27841	2	8.62E-06	0.76	2.88	-	594.4
gi|20149545|ref|NP_002717.2|	prolyl endopeptidase [Homo sapiens]			1.26E-09	0.75	10.13	2.40	80733.0
AHQ-6-6, 5578	R.VFLDPNILSDDGTVALR.G	1846.07392	2	1.26E-09	0.75	2.69	-	805.9
gi|4759300|ref|NP_004772.1|	vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated			1.28E-09	2.81	30.26	33.00	11309.0
AHQ-6-13-, 3584	R.ADALQAGASQFETSAAK.L	1666.77095	2	1.28E-09	0.90	3.93	-	892.1

AHQ-6-13, 4852	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	2.34E-09	0.94	4.48	-	1095.6
AHQ-6-13-, 3688	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	2.57E-08	0.97	5.16	-	1564.0
AHQ-6-13, 3827	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	1.75E-06	0.95	4.47	-	1137.1
gi|4507725|ref|NP_000362.1|	transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum			1.35E-09	2.77	30.24	32.70	15886.9
AHQ-6-13, 3951	K.AADDTWEPFASGK.T	1395.45529	2	4.55E-06	0.86	3.43	-	570.7
AHQ-6-13-, 4034	R.GSPAINVAVHVFR.K	1367.58095	2	6.37E-08	0.94	4.07	-	1150.4
AHQ-6-13, 4159 - 4193	R.GSPAINVAVHVFR.K	1367.58095	2	1.35E-09	0.94	3.97	-	1121.3
AHQ-6-13-, 5304	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	1.33E-04	0.94	4.65	-	1658.6
AHQ-6-13-, 5313 - 5316	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	6.63E-08	0.96	4.84	-	1465.9
AHQ-6-13, 5387	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	1.40E-04	0.72	2.58	-	725.4
gi|30148492|ref|XP_293610.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			1.36E-09	3.23	40.19	4.30	72113.4
AHQ-6-6, 2930	R.FDDAVVQSDMK.H	1255.37968	2	1.36E-09	0.92	3.54	-	816.0
AHQ-6-6, 2306 - 2334	R.FDDAVVQSDM*K.H	1271.37908	2	2.80E-07	0.91	3.15	-	1073.9
AHQ-6-7, 4426	R.IINEPTAAAIAYGLDK.K	1660.89259	2	6.18E-06	0.69	3.55	-	700.2
AHQ-6-6, 4215 - 4222	R.IINEPTAAAIAYGLDKK.V	1789.06550	3	5.65E-07	0.71	3.49	-	280.4
AHQ-6-6, 4135 - 4214	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	1.51E-06	0.89	3.86	-	615.3
gi|24119203|ref|NP_705935.1|	tropomyosin 3 [Homo sapiens]			1.38E-09	4.67	50.28	14.50	29032.5
AHQ-6-12, 3628	R.IQLVEEELDR.A	1244.37653	2	9.92E-08	0.87	2.78	-	1026.8
AHQ-6-10, 3504	R.IQLVEEELDR.A	1244.37653	2	6.73E-05	0.87	3.21	-	946.7
AHQ-6-10, 2767	K.IQVLQQQADDAEER.A	1643.73738	2	1.38E-09	0.95	3.84	-	1493.9
AHQ-6-10, 2562	R.KIQVLQQQADDAEER.A	1771.91030	2	1.49E-06	0.98	5.22	-	2174.7
AHQ-6-9, 2483 - 2509	R.KIQVLQQQADDAEER.A	1771.91030	2	3.79E-06	0.97	5.03	-	1857.3
AHQ-6-9, 3140	R.RIQLVEEELDR.A	1400.56288	2	1.81E-07	0.97	4.53	-	1566.7
AHQ-6-9, 2990 - 3008	K.TIDDLEDKLK.C	1190.32563	2	4.13E-05	0.91	3.58	-	819.5
gi|4557871|ref|NP_001054.1|	transferrin [Homo sapiens]			1.39E-09	6.14	70.29	14.50	77049.5
AHQ-6-5, 4868 - 4872	K.EDPQTFYYAVAVVK.K	1630.82181	2	5.87E-05	0.70	2.81	-	556.7
AHQ-6-5, 3561	K.EGYYGYTGAFR.C	1284.35776	2	2.67E-05	0.85	3.07	-	776.2
AHQ-6-5, 4007	R.FDEFFSEGCAPGSK.K	1579.66868	2	5.05E-05	0.95	3.88	-	1408.7
AHQ-6-5, 3329	K.IECVSAETTEDCIAK.I	1728.87748	2	1.97E-05	0.93	3.65	-	1300.7
AHQ-6-5, 3085	R.KPVDEYKDCHLAQVPSHTVVAR.S	2551.86290	3	1.59E-05	0.95	5.71	-	759.9
AHQ-6-5, 3164	R.LKCDEWSVNSVGK.I	1523.69293	2	1.39E-09	0.86	3.28	-	789.9
AHQ-6-5, 4489	K.M*YLGYEYVTAIR.N	1495.72451	2	2.58E-06	0.90	3.03	-	1093.5
gi|4885609|ref|NP_005408.1|	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen			1.48E-09	3.65	40.26	15.70	59834.4
AHQ-6-7, 6099	R.AGPLAGGVTTFVALYDYESR.T	2088.30526	2	1.74E-06	0.96	5.25	-	1266.2
AHQ-6-7, 6316	R.KEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL	3998.26826	3	1.48E-09	0.86	4.39	-	349.0
AHQ-6-7, 6339	K.SDVWSFGILLTELTTK.G	1811.06794	2	1.47E-05	0.96	4.74	-	1277.9
AHQ-6-7, 5931	R.TQFNSLQQLVAYYSK.H	1790.99681	2	1.63E-06	0.87	2.91	-	1009.7
AHQ-6-7, 5771 - 5850	R.TQFNSLQQLVAYYSK.H	1790.99681	2	1.63E-05	0.81	3.26	-	1060.0
AHQ-6-7, 5598 - 5630	R.TQFNSLQQLVAYYSK.H	1790.99681	2	5.91E-04	0.68	2.83	-	677.0
gi|4503747|ref|NP_001448.1|	filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a			1.52E-09	3.04	40.25	1.40	278191.4
AHQ-6-3, 3057	K.DLAEDAPWKK.I	1173.29999	2	6.57E-04	0.44	2.72	-	547.4
AHQ-6-2, 6046	R.LIALLEVLSQK.R	1227.51852	2	1.17E-06	0.96	4.08	-	1419.3
AHQ-6-13, 6008	R.LIALLEVLSQK.R	1227.51852	2	3.11E-05	0.94	3.88	-	926.3
AHQ-6-1, 6098	R.LIALLEVLSQK.R	1227.51852	2	1.52E-09	0.96	4.36	-	1300.7
AHQ-6-4, 6087	R.LIALLEVLSQK.R	1227.51852	2	5.34E-07	0.96	4.28	-	1393.7
AHQ-6-3, 6016	R.LIALLEVLSQK.R	1227.51852	2	1.59E-07	0.96	4.45	-	1443.2
AHQ-6-11, 5767 - 5771	R.LIALLEVLSQK.R	1227.51852	2	4.12E-07	0.97	4.59	-	1484.6
AHQ-6-13-, 5953	R.LIALLEVLSQK.R	1227.51852	2	1.68E-05	0.90	3.28	-	819.5
AHQ-6-5, 6007	R.LIALLEVLSQK.R	1227.51852	2	6.56E-07	0.97	5.06	-	1365.0
AHQ-6-6, 5943	R.LIALLEVLSQK.R	1227.51852	2	6.45E-09	0.94	3.64	-	1117.9
AHQ-6-7, 5790	R.LIALLEVLSQK.R	1227.51852	2	2.92E-07	0.97	4.61	-	1434.1
AHQ-6-10, 5706	R.LIALLEVLSQK.R	1227.51852	2	1.13E-05	0.95	3.75	-	1280.2
AHQ-6-2, 6330 - 6402	R.QMQLENVSVALEFLDR.E	1893.15408	2	1.00E-06	0.83	3.56	-	529.7
AHQ-6-1, 6067	R.QM*QLENVSVALEFLDR.E	1909.15348	2	2.87E-07	0.81	3.86	-	564.7
AHQ-6-3, 6448 - 6449	R.QMQLENVSVALEFLDR.E	1893.15408	2	2.83E-04	0.94	3.91	-	1211.9
gi|4505839|ref|NP_002645.1|	pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro			1.55E-09	12.90	150.25	37.50	57913.6
AHQ-6-7, 5776	R.AGKPVICATQMLESMIK.K	1879.29869	3	7.27E-04	0.66	3.20	-	682.5
AHQ-6-7, 5098	R.EAEAAIYHLQLFEELRR.L	2089.33962	2	3.15E-04	0.23	2.65	-	171.1
AHQ-6-7, 6282	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	3.44E-07	0.96	4.60	-	1487.4
AHQ-6-7, 6322	K.FGVEQDVDMVFASFIR.K	1861.11055	2	1.55E-09	0.96	4.57	-	1622.0
AHQ-6-7, 4194 - 4250	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	8.83E-08	0.95	4.55	-	1487.6
AHQ-6-7, 4747 - 4790	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.91E-04	0.96	4.49	-	1490.6
AHQ-6-7, 4554	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	4.64E-05	0.97	4.59	-	1996.6
AHQ-6-8, 4292	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.03E-04	0.80	3.09	-	832.4
AHQ-6-7, 6030 - 6036	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	1.36E-05	0.97	4.96	-	2051.9
AHQ-6-7, 4302	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	9.92E-04	0.82	3.10	-	637.9
AHQ-6-8, 4342	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	5.52E-04	0.93	4.70	-	619.3
AHQ-6-7, 5288	K.GVNLPGAAVDLPAVSEKDIQDLK.F	2350.65394	2	5.48E-05	0.92	3.81	-	742.2
AHQ-6-7, 5290	K.GVNLPGAAVDLPAVSEKDIQDLK.F	2350.65394	3	7.12E-07	0.84	3.66	-	488.7
AHQ-6-7, 3930	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	2.76E-06	0.88	4.26	-	869.8
AHQ-6-7, 5030 - 5107	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.49E-08	0.97	5.08	-	1225.9
AHQ-6-2, 5580	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.60E-04	0.56	2.95	-	501.7
AHQ-6-7, 5254 - 5310	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	7.83E-07	0.97	4.85	-	1383.6
AHQ-6-7, 5304	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	3	1.52E-04	0.89	4.45	-	932.0
AHQ-6-3, 5553	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	3.48E-05	0.93	4.00	-	1091.8
AHQ-6-11, 5297	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.90E-06	0.91	3.76	-	837.9
AHQ-6-7, 5367 - 5432	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.14E-07	0.92	4.01	-	884.8
AHQ-6-7, 3263	R.LDIDSPPITAR.N	1198.35099	2	2.11E-06	0.96	3.76	-	1565.8
AHQ-6-7, 2402	R.LNFSHGTHEYHAETIK.N	1885.02879	3	7.47E-06	0.91	3.96	-	1130.7
AHQ-6-7, 2398	R.LNFSHGTHEYHAETIK.N	1885.02879	2	1.54E-05	0.89	3.69	-	680.0
AHQ-6-7, 2698	R.LNFSHGTHEYHAETIK.N	1885.02879	2	7.33E-04	0.63	2.87	-	391.8
AHQ-6-13-, 3484	R.NTGIICTIGPASR.S	1361.54994	2	6.86E-04	0.84	3.60	-	797.7
AHQ-6-7, 3272	R.NTGIICTIGPASR.S	1361.54994	2	1.35E-07	0.94	3.94	-	977.1
AHQ-6-7, 3674 - 3676	R.NTGIICTIGPASR.S	1361.54994	2	4.68E-05	0.89	3.50	-	1011.4
AHQ-6-13, 3627	R.NTGIICTIGPASR.S	1361.54994	2	7.88E-05	0.82	2.99	-	907.4
AHQ-6-6, 3392	R.NTGIICTIGPASR.S	1361.54994	2	1.75E-04	0.85	3.37	-	777.7
AHQ-6-7, 3902	R.TATESFASDPILYR.P	1571.71277	2	5.57E-07	0.87	3.47	-	725.1
AHQ-6-7, 5279 - 5338	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	1.60E-05	0.87	3.87	-	1095.2
gi|4557731|ref|NP_000618.1|	latent transforming growth factor beta binding protein 1 precursor [Hom			1.65E-09	6.03	70.23	8.00	152790.9
AHQ-6-2, 3627	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	8.59E-04	0.95	4.69	-	1159.1
AHQ-6-2, 2608	R.CTCGQGYQLSAAK.D	1446.58862	2	1.97E-04	0.74	2.66	-	497.7
AHQ-6-3, 3989	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	1.65E-09	0.91	4.30	-	771.2
AHQ-6-1, 3396	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	5.27E-04	0.75	3.08	-	480.2
AHQ-6-1, 5626 - 5688	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	2.27E-04	0.82	3.85	-	369.4
AHQ-6-2, 5586	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	8.49E-05	0.89	4.24	-	769.9
AHQ-6-4, 2881	R.TSTDLDVDVDQPK.E	1433.50014	2	1.32E-07	0.93	4.06	-	1172.8
AHQ-6-5, 2837	R.TSTDLDVDVDQPK.E	1433.50014	2	2.86E-05	0.75	2.84	-	770.2
AHQ-6-4, 2703	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.18E-07	0.88	3.62	-	1146.3
AHQ-6-2, 2740	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.47E-07	0.89	3.78	-	999.3
AHQ-6-3, 2741	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.19E-06	0.85	3.29	-	1038.4
AHQ-6-6, 2675	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	3.18E-05	0.82	3.35	-	758.8
gi|18543899|ref|XP_086916.1|	similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic			1.70E-09	1.76	20.26	15.50	21265.8
AHQ-6-11, 4159 - 4208	K.LYTLVLTDPDAPSR.K	1561.76102	2	3.98E-04	0.80	3.36	-	763.1
AHQ-6-11, 3383 - 3392	K.NRPTSISWDGLDSGK.L	1633.74419	2	1.70E-09	0.97	5.16	-	1332.3
gi|7661818|ref|NP_054900.1|	HSPC159 protein [Homo sapiens]			1.71E-09	4.12	50.21	41.90	19011.6
AHQ-6-13-, 6256 - 6257	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	6.37E-08	0.91	4.30	-	442.4
AHQ-6-13, 6291 - 6363	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	5.43E-05	0.84	4.10	-	260.5

AHQ-6-11, 6127	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.08E-06	0.84	3.71	-	333.2
AHQ-6-14-, 6274	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	7.35E-08	0.82	3.40	-	371.7
AHQ-6-11, 2591 - 2647	K.INGDLQITK.L	1002.14688	2	3.70E-05	0.85	3.17	-	725.1
AHQ-6-11, 4588 - 4649	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	3	1.24E-04	0.87	3.80	-	1102.6
AHQ-6-13-, 6174	R.NSCISGERGEEQSAIPYFPFIPDQPFR.V	3144.41922	3	6.44E-06	0.63	3.25	-	381.2
AHQ-6-12, 4693	R.VFVDGHQLFDFYHR.I	1780.96540	3	1.71E-09	0.86	3.53	-	642.3
AHQ-6-11, 4627 - 4631	R.VFVDGHQLFDFYHR.I	1780.96540	2	2.60E-06	0.93	4.22	-	882.9
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				1.72E-09	18.04	210.30	23.70	138070.8
AHQ-6-3, 2453	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	6.94E-07	0.94	4.63	-	826.8
AHQ-6-3, 2450 - 2520	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	3.31E-05	0.97	5.30	-	1959.7
AHQ-6-4, 2408	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	4.30E-07	0.93	4.64	-	754.0
AHQ-6-4, 2413	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	1.92E-04	0.83	4.01	-	753.7
AHQ-6-3, 5870 - 5904	K.CTSDM*ETILTFIPQFHR.L	2114.38778	3	1.36E-05	0.90	4.24	-	784.9
AHQ-6-3, 5901	K.CTSDM*ETILTFIPQFHR.L	2114.38778	2	1.12E-06	0.48	3.03	-	371.3
AHQ-6-2, 3980 - 4048	R.DQALQLQVLNSR.F	1385.55144	2	4.84E-05	0.88	3.22	-	904.9
AHQ-6-5, 3836	R.DQALQLQVLNSR.F	1385.55144	2	1.67E-06	0.93	3.44	-	1152.6
AHQ-6-2, 4136	R.DQALQLQVLNSR.F	1385.55144	2	2.24E-06	0.95	3.36	-	1698.6
AHQ-6-3, 3896 - 3953	R.DQALQLQVLNSR.F	1385.55144	2	2.28E-07	0.97	4.51	-	2037.1
AHQ-6-3, 3253	K.ESLRGECEDMLSK.C	1555.71360	2	1.77E-04	0.68	3.10	-	558.5
AHQ-6-3, 2888	K.EVHEQLLSTEQVSDQK.N	1870.99550	3	3.17E-04	0.93	3.95	-	1746.2
AHQ-6-2, 2900	K.EVHEQLLSTEQVSDQK.N	1870.99550	2	4.56E-05	0.96	4.64	-	1253.2
AHQ-6-3, 2884	K.EVHEQLLSTEQVSDQK.N	1870.99550	2	5.75E-04	0.95	4.39	-	1300.1
AHQ-6-10, 5632	K.FPPVTTFSGYLLYR.T	1661.92388	2	5.23E-06	0.83	2.87	-	580.4
AHQ-6-2, 5984 - 5987	K.FPPVTTFSGYLLYR.T	1661.92388	2	1.31E-06	0.90	4.30	-	703.6
AHQ-6-2, 5559 - 5567	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	3.98E-08	0.92	4.38	-	1033.6
AHQ-6-3, 5524 - 5540	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	8.15E-06	0.97	5.50	-	1830.1
AHQ-6-3, 5528	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	3.74E-04	0.72	3.90	-	352.0
AHQ-6-1, 5796	K.GLTEFVEPIIQIK.T	1487.76518	2	1.20E-07	0.83	3.54	-	699.3
AHQ-6-2, 5751	K.GLTEFVEPIIQIK.T	1487.76518	2	2.71E-06	0.90	3.98	-	830.0
AHQ-6-3, 5709	K.GLTEFVEPIIQIK.T	1487.76518	2	5.88E-05	0.90	3.71	-	735.8
AHQ-6-3, 2694	K.GPCGWTGGSCPQR.S	1422.52885	2	5.11E-04	0.77	2.85	-	676.1
AHQ-6-3, 2156 - 2157	R.GVAEQQQQQGCGDPEVM*QK.M	2135.27911	2	1.48E-04	0.95	4.40	-	977.9
AHQ-6-3, 3848	K.HSLPDIQLLQK.G	1292.50915	2	1.72E-09	0.93	3.79	-	1033.8
AHQ-6-3, 5597	K.IENLTSAVNSLNFIIK.E	1777.05472	2	3.34E-04	0.70	3.11	-	491.1
AHQ-6-2, 5070	K.IFQNDM*QETVAQLFK.T	1829.06683	2	2.45E-04	0.87	3.38	-	912.9
AHQ-6-2, 4950	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.70E-05	0.95	4.25	-	1240.7
AHQ-6-3, 4905 - 4916	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.15E-05	0.96	4.82	-	1390.4
AHQ-6-10, 5026	R.IPYLGVYVFK.Y	1199.46532	2	4.50E-04	0.89	2.97	-	1127.8
AHQ-6-3, 5781	K.KIENLTSAVNSLNFIIK.E	1905.22764	3	6.41E-04	0.94	4.46	-	1596.5
AHQ-6-3, 2954	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	2.86E-08	0.98	6.09	-	1718.4
AHQ-6-3, 2952	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	3	2.03E-05	0.96	4.81	-	2091.3
AHQ-6-2, 3786	K.LVEENALAPDFSK.G	1433.58810	2	7.03E-04	0.81	2.90	-	633.7
AHQ-6-2, 3694	K.LVEENALAPDFSK.G	1433.58810	1	5.59E-04	0.16	1.82	-	309.0
AHQ-6-10, 3468 - 3536	K.LVEENALAPDFSK.G	1433.58810	2	4.82E-05	0.68	3.01	-	657.5
AHQ-6-3, 3764	K.LVEENALAPDFSK.G	1433.58810	2	1.84E-04	0.68	2.79	-	676.9
AHQ-6-11, 3613 - 3615	K.LVEENALAPDFSK.G	1433.58810	2	2.43E-06	0.59	3.06	-	526.6
AHQ-6-3, 6412 - 6414	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	9.38E-08	0.94	5.30	-	1502.1
AHQ-6-1, 6470	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	8.91E-07	0.84	3.69	-	958.4
AHQ-6-3, 5877	K.TM*TIINNAIDFIQDNYALK.E	2215.51196	2	3.10E-07	0.95	4.56	-	1189.4
AHQ-6-4, 3432	K.TVSSLSEDLESTR.Q	1424.49324	2	1.99E-07	0.81	2.94	-	678.2
AHQ-6-3, 4017	R.YNFVLQVAK.T	1082.27683	2	1.24E-06	0.94	3.85	-	947.9
gi|20149594|ref|NP_031381.2| heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea				1.80E-09	4.62	50.24	9.40	83263.6
AHQ-6-4, 3161	R.ELISNASDALDK.I	1276.37539	2	3.28E-07	0.85	3.29	-	776.6
AHQ-6-5, 5435	K.HSQFIGYPITLYLEK.E	1810.08487	2	1.68E-04	0.96	4.55	-	1165.9
AHQ-6-5, 3932 - 3988	R.NPDDITQEEYGEFYK.S	1848.90048	2	1.80E-09	0.97	4.73	-	1707.4
AHQ-6-5, 3945	K.SLTNDWEDHLAVK.H	1528.64798	2	5.60E-06	0.92	3.97	-	887.7
AHQ-6-5, 3695	R.TLTLVDTGIGM*TK.A	1366.60658	2	7.40E-07	0.92	3.77	-	966.6
gi|16507237|ref|NP_005338.1| heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he				1.83E-09	8.84	100.26	23.50	72332.5
AHQ-6-6, 4867	R.AKFEELNMDLFR.S	1513.74309	2	6.18E-05	0.93	3.81	-	1051.3
AHQ-6-6, 5496 - 5554	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	1.83E-09	0.94	4.42	-	1037.2
AHQ-6-6, 5531	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	1.82E-06	0.97	4.85	-	1768.1
AHQ-6-6, 4332	R.IINEPTAAAIAYGLDKR.E	1817.07894	3	2.75E-08	0.70	3.21	-	438.8
AHQ-6-6, 3786	R.ITPSYVAFTPEGER.L	1567.72412	2	4.89E-05	0.59	2.57	-	604.9
AHQ-6-5, 3823	R.ITPSYVAFTPEGER.L	1567.72412	2	3.82E-07	0.91	3.62	-	754.1
AHQ-6-6, 3727	K.KSDIDEIVLVGGSTR.I	1589.77277	2	6.14E-08	0.95	4.00	-	1736.3
AHQ-6-6, 3538 - 3599	K.NQLTSNPENTVFDAK.R	1678.78173	2	7.12E-04	0.81	3.35	-	476.1
AHQ-6-5, 3192	K.NQLTSNPENTVFDAK.R	1678.78173	2	2.38E-09	0.75	3.08	-	644.1
AHQ-6-5, 3705 - 3707	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	3.95E-04	0.96	4.84	-	1204.9
AHQ-6-6, 3664	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	1.68E-08	0.94	4.66	-	929.9
AHQ-6-6, 4614 - 4686	K.TFAPEEISAM*VLTK.M	1553.80227	2	5.65E-07	0.91	4.25	-	1386.5
AHQ-6-6, 3058	K.TKPYIQVDIGGGQTK.T	1605.81703	2	5.37E-06	0.86	3.18	-	755.7
AHQ-6-6, 3059	K.TKPYIQVDIGGGQTK.T	1605.81703	3	4.05E-04	0.85	3.74	-	1097.3
AHQ-6-6, 3816 - 3875	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	7.77E-05	0.95	4.97	-	641.8
gi|30159310|ref|XP_301899.1| similar to beta-actin [Homo sapiens]				1.89E-09	1.68	30.18	9.60	32376.4
AHQ-6-8, 1511 - 1876	K.DSYVGNEAQSK.R	1198.22158	1	1.58E-08	0.43	3.14	-	332.4
AHQ-6-8, 2072	K.DSYVGNEAQSK.R	1198.22158	2	9.92E-04	0.77	2.81	-	796.1
AHQ-6-8, 1750 - 1828	K.DSYVGNEAQSK.R	1198.22158	2	1.77E-05	0.84	3.19	-	859.2
AHQ-6-8, 1955 - 2014	K.DSYVGNEAQSK.R	1198.22158	2	5.25E-05	0.67	2.78	-	603.1
AHQ-6-8, 1976 - 2046	K.DSYVGNEAQSK.R	1198.22158	1	7.68E-04	0.25	2.29	-	378.4
AHQ-6-13, 2044 - 2092	K.DSYVGNEAQSK.R	1198.22158	2	7.64E-04	0.74	2.83	-	844.5
AHQ-6-8, 1559 - 1622	K.DSYVGNEAQSKR.G	1354.40793	2	4.99E-07	0.41	2.56	-	421.4
AHQ-6-8, 4492 - 4561	K.SYKLLDGQVITIGNER.F	1807.04092	2	8.97E-04	0.59	2.59	-	374.8
AHQ-6-8, 4693 - 4722	K.SYKLLDGQVITIGNER.F	1807.04092	2	1.89E-09	0.84	3.58	-	693.4
AHQ-6-8, 4301 - 4308	K.SYKLLDGQVITIGNER.F	1807.04092	2	1.08E-06	0.87	3.32	-	821.0
AHQ-6-8, 4110	K.SYKLLDGQVITIGNER.F	1807.04092	2	1.50E-04	0.74	2.80	-	528.3
gi|5453740|ref|NP_006462.1| myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat				1.90E-09	5.53	60.24	27.50	19794.0
AHQ-6-14-, 5814 - 5819	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	9.86E-07	0.96	4.60	-	1403.0
AHQ-6-14-, 5188 - 5252	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	4.76E-06	0.96	4.88	-	1449.9
AHQ-6-13, 5308	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.36E-04	0.94	4.03	-	1288.3
AHQ-6-13-, 5224	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.60E-05	0.95	4.24	-	1323.9
AHQ-6-11, 4995 - 5059	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.90E-09	0.96	4.60	-	1686.7
AHQ-6-11, 5115	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	3.30E-08	0.91	4.30	-	719.7
AHQ-6-11, 5201 - 5255	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.67E-04	0.87	4.05	-	526.2
AHQ-6-12, 5051 - 5111	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	8.66E-05	0.95	4.66	-	1305.0
AHQ-6-13-, 5837	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	2.61E-06	0.96	4.22	-	1560.9
AHQ-6-11, 5580 - 5647	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.77E-04	0.95	4.73	-	991.3
AHQ-6-14, 5801 - 5840	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	6.11E-06	0.84	3.40	-	774.7
AHQ-6-12, 4396 - 4397	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	3	7.01E-04	0.80	3.37	-	717.3
AHQ-6-11, 5447 - 5524	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.16E-07	0.95	4.88	-	1313.8
AHQ-6-12, 5515	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	5.80E-07	0.96	4.90	-	1161.5
AHQ-6-11, 4325	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	1.87E-05	0.90	4.27	-	610.4
AHQ-6-11, 4323	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	3	1.16E-04	0.93	3.86	-	1781.9
AHQ-6-12, 4391	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	1.25E-05	0.89	3.88	-	630.1
AHQ-6-11, 5451 - 5528	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	7.01E-06	0.91	3.77	-	1162.3
AHQ-6-12, 4088	K.GNFNYIEFTR.I	1261.36733	2	5.75E-04	0.74	3.11	-	691.1
AHQ-6-11, 4021 - 4051	K.GNFNYIEFTR.I	1261.36733	2	2.68E-05	0.84	3.73	-	705.4
AHQ-6-13, 4323	K.GNFNYIEFTR.I	1261.36733	2	5.38E-04	0.62	2.70	-	608.4

AHQ-6-11, 3556	K.KGNFNYIEFTR.I	1389.54025	2	1.60E-06	0.93	3.15	-	1200.4
gi|21314617|ref|NP_000433.2|	platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e			2.10E-09	5.44	70.23	13.40	82449.6
AHQ-6-4, 5591	R.CESISGTLPISYQLLK.T	1811.08954	2	6.06E-06	0.66	2.93	-	301.1
AHQ-6-1, 5844	R.DQNFVILEFPVEEQDR.V	1979.13566	2	3.92E-05	0.63	2.81	-	729.9
AHQ-6-4, 5844 - 5865	R.DQNFVILEFPVEEQDR.V	1979.13566	2	3.68E-04	0.78	3.67	-	738.8
AHQ-6-5, 5755	R.DQNFVILEFPVEEQDR.V	1979.13566	2	1.30E-04	0.92	4.60	-	740.0
AHQ-6-3, 3430 - 3432	K.EDTIVSQTQDFTK.I	1512.60049	2	4.92E-05	0.81	3.22	-	593.9
AHQ-6-4, 3411	K.EDTIVSQTQDFTK.I	1512.60049	2	7.87E-06	0.74	3.31	-	455.4
AHQ-6-5, 3361	K.EDTIVSQTQDFTK.I	1512.60049	2	3.14E-04	0.80	3.29	-	516.8
AHQ-6-4, 4104	R.ISYDAQFEVIK.G	1313.48046	2	4.47E-09	0.87	3.43	-	784.3
AHQ-6-3, 4112	R.ISYDAQFEVIK.G	1313.48046	2	1.71E-05	0.85	3.00	-	855.6
AHQ-6-4, 4079	K.STESYFIPEVR.I	1328.45199	2	2.77E-06	0.89	3.27	-	852.7
AHQ-6-5, 4023	K.STESYFIPEVR.I	1328.45199	2	6.48E-04	0.80	2.75	-	629.6
AHQ-6-3, 4474	K.TTAEYQVLVEGVPSPR.V	1746.94234	2	7.77E-05	0.75	2.77	-	660.3
AHQ-6-3, 5269 - 5274	K.VIAPVDEVQISILSSK.V	1698.98227	2	2.10E-09	0.90	3.97	-	633.0
AHQ-6-1, 5362 - 5427	K.VIAPVDEVQISILSSK.V	1698.98227	2	1.64E-06	0.90	3.89	-	609.2
AHQ-6-4, 5320 - 5336	K.VIAPVDEVQISILSSK.V	1698.98227	2	2.62E-04	0.85	2.98	-	745.6
gi|5031593|ref|NP_005708.1|	actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub			2.20E-09	3.73	40.29	41.10	16320.3
AHQ-6-12, 3092 - 3093	K.ALAAGGVGSIVR.V	1071.25558	2	8.46E-05	0.98	4.73	-	2180.6
AHQ-6-12, 3659 - 3664	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	2.20E-09	0.92	4.45	-	667.1
AHQ-6-12, 3989 - 4060	K.AVQSLDKNGVDLLMK.Y	1631.91943	2	6.48E-05	0.88	4.31	-	481.3
AHQ-6-12, 3527	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	2.19E-06	0.93	4.19	-	738.8
AHQ-6-12, 4152 - 4208	R.KVDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR.Q	3890.92031	3	3.18E-05	0.96	5.74	-	1268.5
gi|4557703|ref|NP_000414.1|	keratin 2a [Homo sapiens]			2.39E-09	8.45	100.26	19.20	65864.9
AHQ-6-1, 3275	R.FLEQQNQVLQTK.W	1476.65935	2	8.10E-08	0.97	5.03	-	1992.8
AHQ-6-8, 2842 - 2850	R.FLEQQNQVLQTK.W	1476.65935	2	8.03E-05	0.96	4.26	-	1771.3
AHQ-6-10, 3075	R.FLEQQNQVLQTK.W	1476.65935	2	6.05E-05	0.95	4.42	-	1730.7
AHQ-6-2, 3074 - 3082	R.FLEQQNQVLQTK.W	1476.65935	2	3.20E-08	0.98	5.21	-	2393.5
AHQ-6-7, 2896	R.FLEQQNQVLQTK.W	1476.65935	2	4.01E-08	0.97	4.90	-	2005.7
AHQ-6-6, 2983	R.FLEQQNQVLQTK.W	1476.65935	2	3.02E-09	0.95	4.34	-	1302.0
AHQ-6-3, 3037 - 3076	R.FLEQQNQVLQTK.W	1476.65935	2	6.23E-07	0.95	4.32	-	1550.7
AHQ-6-13-, 3077	R.FLEQQNQVLQTK.W	1476.65935	2	4.55E-07	0.97	5.02	-	2051.3
AHQ-6-12, 3027	R.FLEQQNQVLQTK.W	1476.65935	2	6.69E-06	0.95	4.25	-	1488.1
AHQ-6-4, 3039	R.FLEQQNQVLQTK.W	1476.65935	2	4.01E-08	0.97	4.74	-	1995.8
AHQ-6-10, 2919 - 2944	R.FLEQQNQVLQTK.W	1476.65935	2	6.18E-08	0.97	4.35	-	2222.4
AHQ-6-5, 2987 - 3063	R.FLEQQNQVLQTK.W	1476.65935	2	7.52E-08	0.97	4.69	-	1924.6
AHQ-6-13-, 2301 - 2341	R.GFSSGSAVVSGGSR.R	1255.31950	2	3.34E-05	0.91	3.59	-	1228.6
AHQ-6-10, 2799	K.IEISELNR.V	974.09353	2	8.28E-04	0.91	3.26	-	1063.4
AHQ-6-10, 2806	K.IEISELNR.V	974.09353	1	2.98E-04	0.24	2.29	-	171.7
AHQ-6-12, 2911	K.IEISELNR.V	974.09353	2	7.36E-04	0.80	2.70	-	794.2
AHQ-6-1, 4307	K.LNDLEEALQQAK.E	1372.50630	2	3.80E-05	0.95	4.26	-	1514.5
AHQ-6-2, 5839	R.NLDLDSIIAEVK.A	1330.50933	2	7.13E-07	0.95	4.28	-	1072.1
AHQ-6-3, 5801 - 5806	R.NLDLDSIIAEVK.A	1330.50933	2	4.63E-07	0.96	4.92	-	1252.9
AHQ-6-13, 5791 - 5792	R.NLDLDSIIAEVK.A	1330.50933	2	1.93E-06	0.97	5.10	-	1260.7
AHQ-6-6, 5730	R.NLDLDSIIAEVK.A	1330.50933	2	2.25E-06	0.96	4.57	-	1283.6
AHQ-6-13-, 5709	R.NLDLDSIIAEVK.A	1330.50933	2	2.76E-07	0.95	4.06	-	1209.5
AHQ-6-1, 5870	R.NLDLDSIIAEVK.A	1330.50933	2	3.65E-06	0.95	4.28	-	1232.1
AHQ-6-7, 5575	R.NLDLDSIIAEVK.A	1330.50933	2	4.94E-05	0.96	4.56	-	1187.0
AHQ-6-5, 5791	R.NLDLDSIIAEVK.A	1330.50933	2	1.20E-07	0.96	4.51	-	1184.4
AHQ-6-10, 5470 - 5480	R.NLDLDSIIAEVK.A	1330.50933	2	1.75E-06	0.97	4.79	-	1467.2
AHQ-6-4, 5880	R.NLDLDSIIAEVK.A	1330.50933	2	2.04E-06	0.96	4.78	-	1114.6
AHQ-6-12, 5620	R.NLDLDSIIAEVK.A	1330.50933	2	1.60E-06	0.93	4.01	-	1030.3
AHQ-6-14-, 5694 - 5716	R.NLDLDSIIAEVK.A	1330.50933	2	2.39E-09	0.96	4.95	-	1150.0
AHQ-6-4, 3188	K.NVQDAIADAEQR.G	1330.38637	2	7.48E-06	0.90	3.25	-	1125.3
AHQ-6-5, 3129	K.NVQDAIADAEQR.G	1330.38637	2	1.36E-08	0.88	3.06	-	1028.6
AHQ-6-6, 3119	K.NVQDAIADAEQR.G	1330.38637	2	7.02E-07	0.84	3.46	-	730.0
AHQ-6-14-, 4503	R.TSQNSELNNMQDLVEDYKK.K	2257.42100	3	3.30E-05	0.84	3.70	-	774.8
AHQ-6-12, 5480	K.VDLLNQEIEFLK.V	1461.68459	2	1.89E-06	0.48	2.77	-	431.2
AHQ-6-6, 5607	K.VDLLNQEIEFLK.V	1461.68459	2	3.19E-07	0.90	4.03	-	795.1
AHQ-6-13, 5651	K.VDLLNQEIEFLK.V	1461.68459	2	4.72E-07	0.92	4.03	-	879.3
AHQ-6-4, 5743 - 5753	K.VDLLNQEIEFLK.V	1461.68459	2	4.96E-07	0.91	4.11	-	906.4
AHQ-6-10, 5359	K.VDLLNQEIEFLK.V	1461.68459	2	4.51E-05	0.78	3.40	-	552.7
AHQ-6-3, 5684 - 5716	K.VDLLNQEIEFLK.V	1461.68459	2	4.75E-07	0.95	4.23	-	1252.6
AHQ-6-7, 5391 - 5450	K.VDLLNQEIEFLK.V	1461.68459	2	4.36E-05	0.82	3.33	-	777.5
AHQ-6-14-, 5570 - 5579	K.VDLLNQEIEFLK.V	1461.68459	2	1.51E-08	0.94	4.44	-	1026.5
AHQ-6-2, 5722	K.VDLLNQEIEFLK.V	1461.68459	2	1.55E-05	0.92	4.13	-	1033.1
AHQ-6-5, 5663	K.VDLLNQEIEFLK.V	1461.68459	2	8.06E-07	0.90	3.71	-	900.2
AHQ-6-13-, 5384	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	1.29E-06	0.83	3.41	-	773.2
AHQ-6-14-, 5386 - 5394	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	2.84E-04	0.94	4.75	-	1360.0
AHQ-6-13-, 3178	K.YEELQVTVGR.H	1194.31920	2	1.26E-04	0.95	3.02	-	2081.1
gi|13899317|ref|NP_113657.1|	SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M			2.51E-09	4.53	50.28	72.90	12326.0
AHQ-6-14, 5976 - 5984	K.ESNTVFSFLGLKPR.L	1595.82383	2	2.51E-09	0.81	3.65	-	491.0
AHQ-6-14-, 5310	K.ESNTVFSFLGLKPR.L	1595.82383	2	6.58E-09	0.76	3.54	-	369.9
AHQ-6-13, 5404	K.ESNTVFSFLGLKPR.L	1595.82383	2	2.80E-04	0.50	2.62	-	390.8
AHQ-6-14-, 4798 - 4856	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	5.95E-09	0.96	5.62	-	1754.1
AHQ-6-14-, 5484	K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E	3380.64432	3	2.73E-04	0.81	4.10	-	449.8
AHQ-6-14-, 4319	R.VFIASSSGFVAIK.K	1326.56551	2	2.71E-08	0.98	5.06	-	2958.1
AHQ-6-14-, 3756	R.VFIASSSGFVAIKK.K	1454.73842	2	5.78E-05	0.95	4.29	-	1390.7
gi|20070125|ref|NP_000909.2|	prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke			2.66E-09	3.26	50.28	15.90	57115.9
AHQ-6-7, 4827	K.ILFIFIDSDHTDNQR.I	1835.00968	2	9.43E-07	0.84	3.23	-	1032.0
AHQ-6-7, 2692	K.LGETYKDHENIVIAK.M	1730.94291	2	8.53E-05	0.50	2.92	-	350.9
AHQ-6-12, 5451 - 5525	K.QPVKVLVGK.N	968.21840	1	3.92E-04	0.19	1.96	-	344.9
AHQ-6-14, 6272	K.QPVKVLVGK.N	968.21840	1	3.25E-04	0.36	2.18	-	446.9
AHQ-6-10, 6231	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	3	2.66E-09	0.95	5.05	-	1421.2
AHQ-6-7, 6350	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	3	2.23E-06	0.97	5.69	-	1740.0
AHQ-6-7, 2214 - 2219	K.YKPESEELTAER.I	1452.54828	2	4.88E-06	0.62	2.95	-	271.0
gi|18860900|ref|NP_002834.2|	protein tyrosine phosphatase, receptor type, J precursor; protein tyro			2.74E-09	6.97	80.28	10.20	145926.2
AHQ-6-1, 3534	R.AGSPTAPVHDESLVGPVDPSSGQQSR.D	2576.71806	3	4.52E-04	0.91	4.27	-	1238.9
AHQ-6-1, 4352	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	2	1.63E-06	0.97	4.94	-	1988.5
AHQ-6-1, 4356	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	3	3.26E-07	0.97	5.51	-	1774.9
AHQ-6-1, 4846 - 4848	R.DTEVLLVGLEPGTR.Y	1499.69122	2	3.74E-07	0.93	3.45	-	1519.8
AHQ-6-1, 4999 - 5004	K.GLIDGAESYVSFSR.Y	1501.62253	2	2.74E-09	0.94	4.11	-	1212.5
AHQ-6-1, 4763 - 4823	K.SFCTDPASM*ASFDCEVVPK.E	2167.37954	2	7.27E-04	0.73	3.15	-	631.9
AHQ-6-1, 5163	K.SPDGASEYVYHLVIESK.H	1895.05866	2	8.13E-04	0.91	4.02	-	934.9
AHQ-6-1, 5172	K.SPDGASEYVYHLVIESK.H	1895.05866	3	3.87E-07	0.78	3.36	-	686.2
AHQ-6-1, 3798	K.TPSSTGPSPVFDIK.A	1433.58810	2	4.21E-05	0.80	3.13	-	724.3
AHQ-6-1, 4271	K.VITEPIPVSDLR.V	1339.56259	2	3.39E-07	0.91	3.40	-	837.6
gi|7661678|ref|NP_056461.1|	RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B			3.16E-09	5.12	60.26	33.70	20824.7
AHQ-6-11, 6039 - 6097	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	1.21E-05	0.83	3.74	-	851.0
AHQ-6-11, 6349	R.KQVEVDAQQCMLEILDTAGTEQFTAM*R.D	3131.50548	3	6.53E-04	0.91	3.94	-	1127.4
AHQ-6-11, 4029 - 4099	R.QWNNCAFLESSAK.S	1556.68148	2	3.21E-06	0.53	2.74	-	230.3
AHQ-6-11, 3743	R.VKDTDDVPM*ILVGNK.C	1660.91437	2	3.07E-04	0.93	3.70	-	1243.5
AHQ-6-11, 3292 - 3347	R.VKDTDDVPM*ILVGNK.C	1660.91437	2	2.86E-04	0.97	5.02	-	1836.6
AHQ-6-11, 3725	R.VKDTDDVPMILVGNK.C	1644.91497	3	1.63E-04	0.95	4.62	-	1670.2
AHQ-6-11, 3709	R.VKDTDDVPMILVGNK.C	1644.91497	2	4.91E-04	0.89	2.85	-	1335.0
AHQ-6-13-, 3890	R.VKDTDDVPMILVGNK.C	1644.91497	2	6.19E-08	0.97	4.62	-	1828.5
AHQ-6-13, 4203	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	2.27E-04	0.90	3.92	-	1124.0

AHQ-6-11, 3997 - 4059	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	6.85E-06	0.96	5.26	-	1569.7
AHQ-6-11, 4211 - 4267	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	3.16E-09	0.86	4.64	-	816.5
gi|29730023|ref|XP_291482.1| similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno				3.63E-09	4.87	60.24	13.60	63563.0
AHQ-6-6, 4575	R.IINKPTAAAIAYGLDK.R	1659.95097	2	5.10E-07	0.82	4.02	-	709.9
AHQ-6-5, 4639	R.IINKPTAAAIAYGLDK.R	1659.95097	2	1.18E-07	0.87	4.07	-	1050.4
AHQ-6-6, 4335	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	3.63E-09	0.93	4.88	-	1211.3
AHQ-6-7, 4196 - 4200	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	6.07E-06	0.70	3.79	-	505.1
AHQ-6-6, 3434 - 3510	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	4.79E-06	0.91	4.41	-	589.5
AHQ-6-5, 3999	R.NELESYAYSLK.N	1317.42597	2	3.50E-04	0.81	2.62	-	1018.7
AHQ-6-5, 3468 - 3536	K.NQLTSNPKNTVFDAK.R	1677.84011	2	1.45E-05	0.69	3.03	-	515.0
AHQ-6-6, 5382	K.TFAPKEISAMVLTK.M	1536.86124	2	1.12E-06	0.67	2.95	-	755.0
AHQ-6-5, 5444	K.TFAPKEISAMVLTK.M	1536.86124	2	2.84E-06	0.83	2.99	-	878.1
gi|27480104|ref|XP_208215.1| similar to triosephosphate isomerase 1 [Homo sapiens]				3.93E-09	3.38	40.21	22.90	26942.6
AHQ-6-10, 2883 - 2958	R.HVFGESDELIGQK.V	1459.58565	2	9.68E-04	0.88	3.13	-	637.5
AHQ-6-10, 2710 - 2714	R.IIYGGSVTGATCK.E	1328.51672	2	9.58E-05	0.69	2.84	-	430.6
AHQ-6-10, 4004 - 4038	K.VTNGAFTGEISPGMIK.D	1622.86786	2	3.93E-09	0.94	4.23	-	1213.0
AHQ-6-11, 5103	K.VVLAYEPVWAIGTGK.T	1603.88587	2	6.10E-05	0.87	3.72	-	764.6
gi|5453832|ref|NP_006380.1| oxygen regulated protein precursor; oxygen regulated protein (150kD) [H				4.25E-09	2.35	30.22	4.40	111334.8
AHQ-6-3, 2317 - 2321	K.AEAGPEGVAPAPEGEK.K	1509.59983	2	3.22E-07	0.91	4.32	-	671.1
AHQ-6-3, 3266	K.LYQPEYQEVSTEEQR.E	1899.99217	2	1.96E-04	0.57	3.01	-	402.4
AHQ-6-3, 6076	R.VEFEELCADLFER.V	1658.81048	2	4.25E-09	0.87	3.16	-	880.3
gi|4758460|ref|NP_004479.1| glycoprotein V (platelet) [Homo sapiens]				4.42E-09	8.15	90.27	29.30	60958.9
AHQ-6-5, 5288	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	3.96E-04	0.81	3.52	-	696.6
AHQ-6-6, 4434 - 4503	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	2.87E-06	0.84	3.02	-	1221.7
AHQ-6-5, 3819	R.GVLQSQSFSGM*TVLQR.L	1754.98948	2	4.61E-06	0.93	4.04	-	1121.7
AHQ-6-5, 4537 - 4539	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	4.42E-09	0.97	5.10	-	1904.4
AHQ-6-1, 3992 - 4040	R.GVLQSQSFSGM*TVLQR.L	1754.98948	2	9.65E-04	0.88	3.37	-	1055.0
AHQ-6-5, 5331	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	3	3.11E-06	0.95	5.08	-	1282.8
AHQ-6-5, 5347	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	2	4.36E-05	0.89	3.62	-	917.5
AHQ-6-6, 4476	R.LPNLSSLTLSR.N	1201.39802	2	5.96E-05	0.78	3.07	-	970.6
AHQ-6-5, 4504	R.LPNLSSLTLSR.N	1201.39802	2	1.34E-04	0.93	3.32	-	1383.0
AHQ-6-6, 6435	R.LSALPQGAFQGLGELQVLALHSNGLTALPDGLLR.G	3471.99408	3	1.73E-07	0.93	5.18	-	800.6
AHQ-6-4, 6597	R.LSALPQGAFQGLGELQVLALHSNGLTALPDGLLR.G	3471.99408	3	3.81E-07	0.74	3.33	-	491.1
AHQ-6-5, 3709	R.LTEVLLGHNSWR.C	1425.61726	2	7.36E-05	0.91	3.39	-	1111.4
AHQ-6-5, 6588	K.LVNLQELALNQNQLDFLPASLFTNLENLK.L	3314.77659	3	5.25E-08	0.94	5.40	-	974.4
AHQ-6-6, 6506	K.LVNLQELALNQNQLDFLPASLFTNLENLK.L	3314.77659	3	2.21E-06	0.92	5.17	-	676.1
AHQ-6-5, 5833	K.M*VLLEQLFLDHNALR.G	1829.15633	2	6.31E-07	0.92	4.19	-	862.2
gi|4757766|ref|NP_004299.1| Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa				4.44E-09	1.29	20.17	8.70	50435.4
AHQ-6-8, 5649	K.FLLDHQGELFPSPDPSGL	1970.17037	2	1.35E-04	0.65	3.03	-	376.6
AHQ-6-7, 5554 - 5631	K.FLLDHQGELFPSPDPSGL	1970.17037	2	4.44E-09	0.76	3.36	-	519.6
AHQ-6-7, 5618	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	1.06E-04	0.53	2.94	-	369.9
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				4.53E-09	3.73	40.21	22.80	22006.2
AHQ-6-10, 4391	K.HFCPNVPIILVGNK.K	1609.91693	2	2.75E-07	0.96	4.17	-	1408.7
AHQ-6-10, 4003	K.HFCPNVPIILVGNKK.D	1738.08985	3	5.09E-04	0.91	3.15	-	1979.7
AHQ-6-10, 4167 - 4168	R.ISAFGYLECSAK.T	1347.51850	2	8.97E-08	0.90	3.11	-	920.6
AHQ-6-10, 4628 - 4639	K.QVELALWDTAGQEDYDR.L	2010.10662	2	4.53E-09	0.96	4.15	-	1528.7
gi|4508047|ref|NP_003452.1| zyxin [Homo sapiens]				4.56E-09	0.94	10.25	4.40	61277.0
AHQ-6-8, 3729 - 3733	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	4.56E-09	0.94	5.00	-	1072.4
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				4.64E-09	9.19	110.24	9.70	191612.6
AHQ-6-3, 4357	R.ALEHFTDLYDIK.R	1465.63179	2	6.23E-05	0.83	3.41	-	733.7
AHQ-6-3, 5734 - 5800	R.GQCDLELINVCNENSLFK.S	2156.37965	2	8.37E-05	0.37	2.88	-	243.8
AHQ-6-3, 4642	R.GQFSTDELVAEVEK.R	1552.66462	2	1.53E-06	0.93	3.49	-	1303.6
AHQ-6-4, 4660	R.GQFSTDELVAEVEK.R	1552.66462	2	6.38E-05	0.72	3.20	-	573.7
AHQ-6-3, 5092	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	4.64E-09	0.86	4.10	-	847.7
AHQ-6-3, 4266 - 4284	K.LHIIEVGTPPTGNQPFPK.K	1946.23831	2	4.86E-04	0.82	3.55	-	517.1
AHQ-6-3, 5704	K.LLLPWLEAR.I	1111.36131	2	2.43E-05	0.74	2.70	-	596.7
AHQ-6-3, 6165 - 6209	R.LPVVIGGLLDVDCSEDVIK.N	2043.36744	2	2.77E-05	0.94	4.44	-	980.4
AHQ-6-3, 5888 - 5894	R.NLQNLLILTAIK.A	1354.66353	2	6.78E-06	0.97	4.76	-	1704.4
AHQ-6-3, 4244 - 4289	R.NNLAGAEELFAR.K	1305.42165	2	8.84E-04	0.83	3.05	-	835.3
AHQ-6-3, 3145	K.VIQCFAETGQVQK.I	1509.70940	2	5.60E-07	0.96	3.83	-	1863.3
AHQ-6-5, 3065	K.VIQCFAETGQVQK.I	1509.70940	2	3.57E-06	0.96	4.12	-	1878.8
AHQ-6-3, 4985 - 5057	K.WLLLTGISAQQNR.V	1500.72728	2	2.90E-05	0.96	4.00	-	1756.4
gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre				5.08E-09	5.90	70.27	32.90	48141.1
AHQ-6-7, 3348	R.AKIDDPTDSKPEDWDKPEHIPDPDAK.K	2961.14253	3	1.25E-04	0.63	3.16	-	383.6
AHQ-6-7, 5431 - 5458	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	5.08E-09	0.93	5.03	-	820.7
AHQ-6-7, 2170 - 2190	K.HEQNIDCGGGYVK.L	1478.56912	2	3.10E-05	0.90	4.18	-	754.3
AHQ-6-7, 3462	K.IDDPTDSKPEDWDKPEHIPDPDAK.K	2761.89139	3	1.80E-07	0.86	4.33	-	542.0
AHQ-6-7, 4882 - 4958	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	1.01E-08	0.89	4.34	-	883.9
AHQ-6-7, 4570	K.KPEDWDEEM*DGEWEPPVIQNPEYK.G	2978.14866	3	2.02E-04	0.94	5.33	-	754.2
AHQ-6-7, 6218 - 6284	K.SGTIFDNFLITNDEAYAEEFGNETWGVTK.A	3270.46022	3	2.60E-07	0.75	3.60	-	786.1
gi|4557323|ref|NP_000031.1| apolipoprotein C-III precursor [Homo sapiens]				5.14E-09	0.94	10.18	16.20	10852.2
AHQ-6-14-, 3164	K.DALSSVQESQVAQQAR.G	1717.81950	2	5.14E-09	0.94	3.58	-	1556.9
gi|30160191|ref|XP_294035.2| similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme				5.17E-09	0.97	10.22	2.80	50222.2
AHQ-6-11, 4793	K.IYVDDGLISLQVK.Q	1463.70048	2	1.28E-04	0.93	3.29	-	1477.0
AHQ-6-7, 4762	K.IYVDDGLISLQVK.Q	1463.70048	2	5.17E-09	0.97	4.37	-	2167.6
gi|22059949|ref|XP_114617.2| similar to tubulin, beta 5 [Homo sapiens]				5.22E-09	0.96	10.28	13.00	22810.8
AHQ-6-7, 4966	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	5.22E-09	0.96	5.68	-	1547.8
gi|21624607|ref|NP_066972.1| coactosin-like 1 [Homo sapiens]				5.79E-09	2.80	30.28	24.60	15944.9
AHQ-6-12, 2347	R.AAYNLVR.D	806.93245	2	2.38E-04	0.91	2.57	-	1361.1
AHQ-6-13-, 5028	R.DDGSAVIWVTFK.Y	1338.49001	2	3.07E-05	0.92	3.35	-	1127.4
AHQ-6-13-, 6300	K.FALITWIGENVSGLQR.A	1805.06986	2	1.47E-06	0.98	5.33	-	2215.9
AHQ-6-13-, 6301	K.FALITWIGENVSGLQR.A	1805.06986	3	5.79E-09	0.97	5.33	-	2112.6
AHQ-6-13, 6351 - 6355	K.FALITWIGENVSGLQR.A	1805.06986	2	5.11E-04	0.97	5.58	-	1614.4
gi|4758018|ref|NP_004359.1| calponin 2; Calonin 2 [Homo sapiens]				5.79E-09	1.83	20.20	9.10	33696.9
AHQ-6-12, 2949 - 3025	K.GLQSGVDIGVK.Y	1073.22510	2	3.86E-06	0.92	3.45	-	1298.6
AHQ-6-12, 5888 - 5899	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	5.79E-09	0.91	4.02	-	928.2
AHQ-6-13, 6012 - 6055	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.86E-06	0.84	3.10	-	864.6
AHQ-6-14-, 5979	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	4.29E-05	0.94	3.97	-	1134.1
AHQ-6-11, 5825	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.22E-05	0.92	3.63	-	1136.8
gi|6005846|ref|NP_009215.1| PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro				5.83E-09	4.89	60.23	31.50	39547.7
AHQ-6-14-, 6142	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	3.18E-06	0.90	4.62	-	539.7
AHQ-6-13-, 6153	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	8.45E-05	0.66	2.96	-	451.8
AHQ-6-9, 3847 - 3848	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	6.78E-04	0.49	3.07	-	463.8
AHQ-6-12, 2741	K.HLSSCAAPAPLTSAER.E	1669.84126	3	4.47E-04	0.83	3.74	-	689.5
AHQ-6-11, 4263	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	5.83E-09	0.96	4.61	-	1017.2
AHQ-6-11, 5867 - 5925	K.KIEIGDGAELTAEFLYDEVHPK.Q	2475.73515	3	1.71E-04	0.81	3.65	-	1026.9
AHQ-6-12, 4479	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	3.50E-04	0.90	3.20	-	1436.2
gi|4507907|ref|NP_000543.1| von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille				6.14E-09	13.79	160.39	7.60	309296.7
AHQ-6-2, 3836	R.CLPSACEVVTGSPR.G	1535.72531	2	1.35E-04	0.67	3.36	-	460.9
AHQ-6-1, 3947	R.CLPSACEVVTGSPR.G	1535.72531	2	1.69E-04	0.82	3.56	-	633.2
AHQ-6-1, 4055 - 4063	R.IALLLM*ASQEPQR.M	1486.76229	2	1.74E-04	0.94	3.83	-	1363.2
AHQ-6-1, 6515	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	7.69E-09	0.90	3.75	-	679.7
AHQ-6-2, 2684	R.ILAGPAGDSNVVK.L	1241.41901	2	8.44E-07	0.80	2.78	-	843.5
AHQ-6-1, 2908	R.ILAGPAGDSNVVK.L	1241.41901	2	2.36E-06	0.94	3.73	-	1303.9
AHQ-6-1, 3843	R.ILTSDVFQDCNK.L	1441.58869	2	3.36E-06	0.93	3.69	-	1077.2
AHQ-6-1, 6395	R.LLDLVFLLDGSSR.L	1448.68905	2	8.28E-06	0.86	3.00	-	947.7
AHQ-6-1, 5507	R.LPGDIQVVPIGVGPNANVQELER.I	2415.73085	2	7.49E-07	0.54	2.65	-	374.5

AHQ-6-2, 5463	R.LPGDIQVVPIGVGPNANVQELER.I	2415.73085	2	9.51E-05	0.55	2.78	-	254.6
AHQ-6-1, 4258	R.LSEAEFEVLK.A	1165.31777	2	7.79E-06	0.87	3.47	-	917.7
AHQ-6-1, 4206	K.LTGSCSYVLFQNK.E	1518.71629	2	2.91E-06	0.90	4.02	-	850.9
AHQ-6-1, 5278 - 5358	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	6.14E-09	0.98	7.86	-	2212.3
AHQ-6-2, 5218	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	3.24E-07	0.98	6.99	-	2863.6
AHQ-6-1, 4843	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	6.53E-09	0.89	3.81	-	519.6
AHQ-6-1, 5302 - 5364	K.TYGLCGICDENGANDFM*LR.D	2225.42231	2	6.92E-07	0.87	4.15	-	574.2
AHQ-6-2, 2508	R.VKEEVFIQQR.N	1276.46658	2	4.09E-06	0.87	3.49	-	789.8
AHQ-6-2, 4496	R.VTVFPIGIGDR.Y	1174.37426	2	5.53E-06	0.93	3.27	-	1220.6
AHQ-6-1, 4592	R.VTVFPIGIGDR.Y	1174.37426	2	3.94E-07	0.91	3.46	-	979.3
AHQ-6-1, 3163	K.YAGSQVASTSEVLK.Y	1440.58064	2	3.29E-07	0.90	3.40	-	940.2
AHQ-6-2, 2948 - 2954	K.YAGSQVASTSEVLK.Y	1440.58064	2	7.93E-05	0.94	4.29	-	837.7
AHQ-6-1, 5726	K.YTLFQIFSK.I	1147.34728	2	2.78E-06	0.95	3.41	-	1204.4
gi|4502201|ref|NP_001649.1|	ADP-ribosylation factor 1 [Homo sapiens]			7.09E-09	4.48	50.20	27.60	20696.6
AHQ-6-12, 4428	R.DAVLLVFANK.Q	1090.29726	1	8.95E-05	0.82	2.37	-	1090.8
AHQ-6-12, 3699 - 3701	R.ILMVGLDAAGK.T	1088.34632	2	1.42E-05	0.94	4.00	-	1126.4
AHQ-6-12, 3219	R.ILM*VGLDAAGK.T	1104.34572	2	1.07E-05	0.95	3.41	-	1671.2
AHQ-6-12, 4812 - 4868	K.NISFTVWDVGGQDK.I	1566.69621	2	7.23E-05	0.77	3.05	-	734.5
AHQ-6-13, 5043	K.NISFTVWDVGGQDK.I	1566.69621	2	1.17E-05	0.77	2.67	-	766.4
AHQ-6-13-, 4928 - 4938	K.NISFTVWDVGGQDK.I	1566.69621	2	7.09E-09	0.92	4.09	-	764.6
AHQ-6-12, 3124	K.QDLPNAM*NAAEITDK.L	1647.78941	2	3.70E-04	0.85	3.32	-	571.7
gi|4758304|ref|NP_004902.1|	protein disulfide isomerase related protein (calcium-binding protein, i			7.13E-09	5.40	60.24	13.80	72931.9
AHQ-6-6, 4451	K.DLGLSESGEDVNAAILDESGKK.F	2248.38737	2	2.27E-07	0.96	4.89	-	1292.4
AHQ-6-6, 3712	K.FAM*EPEEFDSDTLR.E	1703.80830	2	1.16E-04	0.85	3.27	-	688.4
AHQ-6-6, 3607	R.FDVSGYPTIK.I	1127.27123	2	9.30E-05	0.91	2.80	-	1382.2
AHQ-6-6, 3823	K.GESDPAYQQYQDAANNLR.E	2041.08081	2	1.61E-07	0.87	4.19	-	692.0
AHQ-6-6, 2898	K.IDATSASVLASR.F	1191.31686	2	7.13E-09	0.95	3.58	-	1700.9
AHQ-6-6, 2495	K.VSQGQLVVM*QPEK.F	1459.69371	2	1.08E-05	0.86	3.27	-	1062.3
gi|5031973|ref|NP_005733.1|	protein disulfide isomerase-related protein [Homo sapiens]			7.29E-09	2.51	30.23	10.20	48121.0
AHQ-6-7, 4527 - 4534	K.GSFSEQGINEFLR.E	1484.59520	2	8.13E-06	0.75	3.14	-	577.4
AHQ-6-8, 3852	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	3.40E-07	0.93	3.77	-	1439.7
AHQ-6-7, 3826	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	4.38E-08	0.81	3.17	-	697.5
AHQ-6-7, 4494	K.LAAVDATVNQVLASR.Y	1528.73579	2	7.29E-09	0.96	4.51	-	1362.7
gi|4504391|ref|NP_000179.1|	hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]			8.23E-09	4.31	50.21	8.60	102502.4
AHQ-6-4, 4389 - 4396	K.ATDCVGHDVVTLLR.D	1557.75406	2	8.23E-09	0.90	3.70	-	814.7
AHQ-6-4, 5391	K.GDFIALDLGGSSFR.I	1455.59700	2	5.68E-04	0.95	3.77	-	1544.2
AHQ-6-4, 5669	K.LPVGFTFSFPCQQSK.I	1744.99134	2	5.18E-05	0.78	3.18	-	529.4
AHQ-6-4, 6548	R.SANLVAATLGAILNR.L	1484.72615	2	4.91E-04	0.94	4.24	-	1365.6
AHQ-6-4, 5740	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	1.19E-06	0.74	3.14	-	556.7
gi|4557361|ref|NP_001187.1|	BH3 interacting domain death agonist; BH3-interacting domain death agon			8.76E-09	0.95	10.19	6.70	21994.6
AHQ-6-11, 2783 - 2784	R.IEADSESQEDIIR.N	1505.56635	2	8.76E-09	0.95	3.81	-	1925.8
gi|29731460|ref|XP_293027.1|	similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl			8.78E-09	0.97	10.20	6.10	23572.2
AHQ-6-10, 4275	K.DFLAGGVAAAISK.M	1220.39980	2	8.78E-09	0.97	3.99	-	2721.5
gi|13259510|ref|NP_004073.2|	dynactin 1 isoform 1; dynactin 1 (p150, Glued (Drosophila) homolog); p			9.01E-09	1.75	20.22	3.00	141693.7
AHQ-6-3, 4286	R.AESLQQEVEALK.E	1345.48086	2	9.22E-05	0.85	3.14	-	1309.3
AHQ-6-4, 6687	R.GAAGEQLSFAAGLVYSLSLLQATLHR.Y	2675.03589	3	9.01E-09	0.90	4.49	-	825.1
gi|17986283|ref|NP_006000.2|	tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu			9.14E-09	0.91	10.30	3.30	50135.3
AHQ-6-10, 5186	R.AVFVDLEPTVIDEVR.T	1702.92947	2	2.65E-04	0.57	2.81	-	506.2
AHQ-6-12, 5327	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.54E-05	0.85	3.52	-	683.5
AHQ-6-13-, 5388	R.AVFVDLEPTVIDEVR.T	1702.92947	2	5.44E-08	0.90	4.18	-	843.0
AHQ-6-14-, 5136	R.AVFVDLEPTVIDEVR.T	1702.92947	2	4.29E-05	0.88	4.08	-	501.0
AHQ-6-14-, 5390 - 5391	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.41E-06	0.96	5.52	-	899.2
AHQ-6-7, 5200 - 5270	R.AVFVDLEPTVIDEVR.T	1702.92947	2	9.14E-09	0.91	4.39	-	655.0
gi|21361370|ref|NP_002853.2|	phosphorylase, glycogen; brain [Homo sapiens]			1.05E-08	0.88	10.14	1.40	96695.3
AHQ-6-5, 5584	K.LLPLVSDEVFIR.D	1401.67552	2	1.05E-08	0.88	2.83	-	811.1
gi|30154095|ref|XP_293967.2|	similar to gamma actin-like protein [Homo sapiens]			1.06E-08	1.43	30.18	28.50	19259.0
AHQ-6-8, 4424	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.90E-05	0.78	3.42	-	545.9
AHQ-6-8, 4524 - 4600	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	4.83E-07	0.52	2.74	-	427.9
AHQ-6-14-, 4571 - 4650	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	4.64E-04	0.52	3.18	-	453.8
AHQ-6-10, 4386	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.24E-07	0.71	3.54	-	409.8
AHQ-6-10, 4660	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	9.78E-04	0.32	2.57	-	482.3
AHQ-6-12, 4640	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	6.59E-04	0.45	3.01	-	415.9
AHQ-6-14, 5330 - 5392	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.45E-06	0.62	3.27	-	381.9
AHQ-6-13-, 4672	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.59E-06	0.51	2.85	-	401.9
AHQ-6-13-, 5104	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	3.08E-05	0.10	2.63	-	191.8
AHQ-6-14-, 4872	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	4.16E-06	0.81	3.51	-	766.2
AHQ-6-8, 6440	R.NIKEKLCYLVLDFEQEM*ATAASSSSLEK.S	3223.61779	3	1.06E-08	0.62	3.39	-	646.2
gi|5453595|ref|NP_006358.1|	adenylyl cyclase-associated protein [Homo sapiens]			1.06E-08	7.20	90.31	27.60	51672.7
AHQ-6-7, 2859	R.ALLVTASQCQQPAENK.L	1759.96271	2	8.30E-05	0.37	2.54	-	246.2
AHQ-6-7, 2730 - 2743	R.ALLVTASQCQQPAENK.L	1759.96271	2	5.89E-06	0.96	5.23	-	1058.0
AHQ-6-8, 2656	R.ALLVTASQCQQPAENK.L	1759.96271	2	7.81E-06	0.94	4.40	-	909.6
AHQ-6-7, 2731	K.KEPAVLELEGK.K	1213.40557	2	9.43E-08	0.86	3.22	-	512.8
AHQ-6-7, 6303 - 6383	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	8.21E-08	0.98	6.28	-	1533.0
AHQ-6-7, 6390 - 6455	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	3.05E-06	0.97	5.45	-	1666.8
AHQ-6-7, 4712	K.LSDLLAPISEQIK.E	1427.66814	1	1.20E-07	0.70	3.04	-	564.0
AHQ-6-7, 4694 - 4768	K.LSDLLAPISEQIK.E	1427.66814	2	3.02E-04	0.71	2.97	-	686.1
AHQ-6-7, 3287	K.NSLDCEIVSAK.S	1237.36245	2	1.59E-06	0.95	3.79	-	1532.5
AHQ-6-7, 2974 - 3023	K.NSLDCEIVSAK.S	1237.36245	2	1.19E-05	0.93	3.46	-	1058.9
AHQ-6-14-, 3056 - 3120	K.NSLDCEIVSAK.S	1237.36245	2	1.37E-04	0.84	2.82	-	884.8
AHQ-6-7, 3290	K.NSLDCEIVSAK.S	1237.36245	1	2.29E-04	0.31	2.16	-	439.9
AHQ-6-8, 4452	R.SALFAQINQGESITHALK.H	1929.16615	2	1.06E-08	0.94	4.58	-	971.3
AHQ-6-7, 4643 - 4699	R.SALFAQINQGESITHALK.H	1929.16615	2	9.57E-04	0.52	2.85	-	407.2
AHQ-6-7, 4498	R.SALFAQINQGESITHALK.H	1929.16615	2	3.70E-06	0.85	3.76	-	593.5
AHQ-6-7, 4439 - 4514	R.SALFAQINQGESITHALK.H	1929.16615	3	1.17E-05	0.81	3.85	-	651.7
AHQ-6-7, 2199	R.SGPKPFSAPKPQTSPSPK.R	1839.08461	2	2.75E-05	0.68	3.05	-	649.6
AHQ-6-7, 4536 - 4614	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.90E-08	0.94	4.40	-	952.8
AHQ-6-7, 4423 - 4478	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.89E-04	0.89	4.43	-	681.6
AHQ-6-7, 4260	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.98E-05	0.88	3.83	-	874.7
AHQ-6-7, 3980 - 3987	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.25E-07	0.75	3.47	-	204.6
AHQ-6-8, 4445	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.49E-07	0.90	4.03	-	659.9
AHQ-6-7, 4670 - 4720	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	7.40E-04	0.80	2.93	-	789.4
AHQ-6-10, 4396	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	3.20E-04	0.92	4.01	-	870.2
AHQ-6-11, 4467	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.55E-07	0.89	4.09	-	565.1
AHQ-6-12, 4533	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.88E-05	0.65	3.13	-	463.8
AHQ-6-13-, 4614	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.68E-04	0.81	3.07	-	669.1
AHQ-6-7, 2564	K.VPTISINK.T	872.04435	1	3.87E-05	0.20	2.06	-	259.0
gi|4758756|ref|NP_004528.1|	nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr			1.09E-08	1.78	20.23	7.20	45373.8
AHQ-6-7, 6242 - 6243	K.GIPEFWLTVFK.N	1337.58999	2	1.09E-08	0.84	3.42	-	274.1
AHQ-6-7, 5142 - 5143	R.LDGLVETPTGYIESLPR.V	1861.08535	2	6.78E-05	0.94	4.56	-	827.8
gi|5729997|ref|NP_004154.2|	RAB27B, member RAS oncogene family [Homo sapiens]			1.15E-08	2.78	30.24	19.30	24607.7
AHQ-6-11, 5381 - 5383	K.AVETLLDLIM*K.R	1262.54151	2	9.22E-05	0.87	3.50	-	717.5
AHQ-6-10, 5294 - 5323	K.AVETLLDLIM*K.R	1262.54151	2	9.01E-06	0.87	3.46	-	727.6
AHQ-6-11, 3635 - 3636	K.VHLQLWDTAGQER.F	1553.70390	2	1.15E-08	0.96	4.21	-	1375.2
AHQ-6-10, 3562	K.VHLQLWDTAGQER.F	1553.70390	2	8.48E-08	0.93	3.41	-	1216.8
AHQ-6-11, 4240 - 4299	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	3.42E-06	0.57	3.04	-	649.0
AHQ-6-12, 4372	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	3.15E-05	0.73	2.90	-	551.8
AHQ-6-13-, 4458	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	1.73E-04	0.36	2.53	-	221.0

AHQ-6-10, 4174 - 4230	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	1.20E-07	0.96	4.77	-	1149.3
gi|4506877|ref|NP_002996.1|	selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;			1.16E-08	5.87	70.22	14.30	90844.7
AHQ-6-3, 4646	K.AVQCQHLEAPSEGTM*DCVHPLTAFAYGSSCK.F	3472.80519	3	6.75E-05	0.85	4.38	-	486.5
AHQ-6-3, 4361	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	6.99E-05	0.92	4.21	-	659.3
AHQ-6-3, 5497	K.LECLASGIWTNKPPQCLAAQCPPLK.I	2857.31818	3	2.10E-06	0.89	3.64	-	1488.7
AHQ-6-3, 5601 - 5672	K.LECLASGIWTNKPPQCLAAQCPPLKIPER.G	3352.89300	3	9.35E-06	0.48	3.21	-	572.4
AHQ-6-3, 3154	R.PSGQWTAVTPACR.A	1432.58672	2	3.61E-05	0.93	3.64	-	904.1
AHQ-6-4, 4720	K.STCQFICDEGYSLSGPER.L	2109.23671	2	3.85E-06	0.90	3.44	-	778.9
AHQ-6-2, 4703	K.STCQFICDEGYSLSGPER.L	2109.23671	2	1.16E-08	0.94	4.36	-	844.3
AHQ-6-2, 2991	R.YTDLVAIQNK.N	1165.32100	2	1.53E-06	0.86	2.70	-	883.3
AHQ-6-3, 2984	R.YTDLVAIQNK.N	1165.32100	2	2.62E-04	0.93	3.55	-	1125.9
gi|4504517|ref|NP_001531.1|	heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M			1.19E-08	2.42	30.26	21.00	22782.3
AHQ-6-11, 4499 - 4580	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.08E-05	0.87	3.79	-	538.2
AHQ-6-14-, 4635 - 4711	K.LATQSNEITIPVTFESR.A	1907.11412	2	7.23E-06	0.75	3.82	-	243.4
AHQ-6-10, 4326	R.LFDQAFGLPR.L	1164.33793	2	4.52E-07	0.96	4.19	-	1494.8
AHQ-6-11, 4395 - 4400	R.LFDQAFGLPR.L	1164.33793	2	1.52E-07	0.96	4.34	-	1481.1
AHQ-6-10, 4478	R.VSLDVNHFAPDELTVK.T	1784.99058	2	4.84E-05	0.93	3.99	-	1290.5
AHQ-6-10, 4330	R.VSLDVNHFAPDELTVK.T	1784.99058	2	6.26E-08	0.92	4.40	-	860.5
AHQ-6-11, 4501 - 4560	R.VSLDVNHFAPDELTVK.T	1784.99058	2	9.29E-07	0.86	3.76	-	767.8
AHQ-6-13-, 4537	R.VSLDVNHFAPDELTVK.T	1784.99058	2	2.88E-08	0.96	5.14	-	1114.4
AHQ-6-13-, 4538	R.VSLDVNHFAPDELTVK.T	1784.99058	3	1.43E-06	0.84	3.90	-	530.4
AHQ-6-11, 4405	R.VSLDVNHFAPDELTVK.T	1784.99058	3	1.19E-08	0.70	3.30	-	321.6
AHQ-6-11, 4369 - 4407	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.68E-08	0.96	4.94	-	1325.4
gi|4757768|ref|NP_004300.1|	Rho GDP dissociation inhibitor (GDI) alpha [Homo sapiens]			1.26E-08	3.46	40.23	22.50	23206.9
AHQ-6-10, 4298	R.AEEYEFLTPVEEAPK.G	1752.89898	2	6.58E-05	0.86	3.03	-	1087.5
AHQ-6-10, 3031	K.IDKTDYMVGSYGPR.A	1602.79350	2	3.00E-05	0.90	3.00	-	1305.2
AHQ-6-10, 3674	K.SIQEIQELDKDDESLR.K	1919.03693	2	1.26E-08	0.87	3.75	-	992.8
AHQ-6-10, 3352	K.SIQEIQELDKDDESLRK.Y	2047.20984	2	5.40E-04	0.83	3.67	-	605.6
gi|4505303|ref|NP_002466.1|	myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m			1.37E-08	1.63	20.20	11.50	22763.8
AHQ-6-12, 2787 - 2853	R.ALGQNPTNAEVLK.V	1355.52211	2	1.37E-08	0.81	3.87	-	364.6
AHQ-6-12, 2801	R.ALGQNPTNAEVLK.V	1355.52211	1	1.84E-05	0.19	2.66	-	332.7
AHQ-6-13-, 2753	K.ILYSQCGDVM*R.A	1359.55429	2	2.10E-07	0.82	2.71	-	949.8
AHQ-6-14-, 2708	K.ILYSQCGDVM*R.A	1359.55429	2	1.21E-04	0.72	2.74	-	528.6
AHQ-6-12, 2707 - 2708	K.ILYSQCGDVM*R.A	1359.55429	2	1.46E-06	0.89	2.80	-	1157.3
gi|30159830|ref|XP_302246.1|	similar to HSPC280 [Homo sapiens]			1.40E-08	1.92	20.23	3.90	45644.4
AHQ-6-14-, 6358	K.CANLFEALVGTLK.A	1437.68632	2	1.40E-08	0.96	4.69	-	1238.2
AHQ-6-14-, 6315	R.DDKCANLFEALVGTLK.A	1796.03496	3	4.31E-07	0.96	4.53	-	2399.8
gi|4502695|ref|NP_001779.1|	cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c			1.41E-08	0.60	10.15	5.50	48786.6
AHQ-6-8, 6060 - 6109	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	2	1.41E-08	0.60	2.92	-	364.1
gi|10716563|ref|NP_001737.1|	calnexin [Homo sapiens]			1.48E-08	4.47	50.28	10.10	67567.8
AHQ-6-5, 4775	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.48E-08	0.95	4.20	-	1212.4
AHQ-6-7, 4618	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.47E-06	0.58	2.67	-	535.5
AHQ-6-5, 4353	R.GTLSGWILSK.A	1062.24392	2	1.04E-05	0.87	2.85	-	824.0
AHQ-6-5, 3863	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	3	1.24E-04	0.83	3.53	-	796.6
AHQ-6-5, 6277	K.IPNPDFFEDLEPFR.M	1736.90447	2	1.57E-06	0.92	3.67	-	853.1
AHQ-6-5, 5884	R.KIPNPDFFEDLEPFR.M	1865.07739	3	1.44E-05	0.97	5.62	-	2561.0
AHQ-6-5, 5876	R.KIPNPDFFEDLEPFR.M	1865.07739	2	1.71E-07	0.90	3.70	-	749.6
gi|4503445|ref|NP_001944.1|	endothelial cell growth factor 1 (platelet-derived); thymidine phosphor			1.69E-08	0.93	10.19	3.10	49955.2
AHQ-6-7, 6067	R.ALPLALVLHELGAGR.S	1530.83966	2	1.69E-08	0.93	3.74	-	1309.4
gi|27477800|ref|XP_208313.1|	similar to tropomyosin 4 [Homo sapiens]			1.88E-08	0.89	10.23	10.10	18426.7
AHQ-6-9, 5082	K.CGDLEEELKNVTNNLK.S	1878.05124	2	5.06E-04	0.95	4.54	-	1210.9
AHQ-6-9, 4211 - 4214	K.CGDLEEELKNVTNNLK.S	1878.05124	3	1.88E-08	0.89	3.80	-	1123.9
gi|4507521|ref|NP_001055.1|	transketolase [Homo sapiens]			2.10E-08	2.64	30.25	9.10	67877.3
AHQ-6-6, 4456	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	2.10E-08	0.74	3.16	-	348.3
AHQ-6-6, 5570	K.LDNLVAILDINR.L	1369.59192	2	2.83E-08	0.96	3.94	-	1534.1
AHQ-6-6, 6326	K.SKDDQVTVIGAGVTLHEALAAAELLK.K	2651.00941	3	8.34E-05	0.93	5.07	-	796.8
gi|4507487|ref|NP_003238.1|	thrombospondin 2 [Homo sapiens]			2.13E-08	1.68	20.21	2.60	129954.5
AHQ-6-1, 5008	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	6.39E-08	0.94	3.63	-	1278.8
AHQ-6-2, 4966 - 5030	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	2.13E-08	0.96	4.15	-	1549.8
AHQ-6-4, 4965	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	5.80E-08	0.94	3.84	-	1273.6
AHQ-6-3, 4850 - 4930	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	3.78E-04	0.46	2.71	-	508.1
AHQ-6-3, 3018	R.NALWHTGNTPGQVR.T	1551.69124	2	5.33E-04	0.87	3.38	-	881.6
AHQ-6-4, 2985	R.NALWHTGNTPGQVR.T	1551.69124	2	4.18E-04	0.91	3.29	-	1133.9
AHQ-6-3, 2822	R.NALWHTGNTPGQVR.T	1551.69124	2	7.68E-06	0.85	3.28	-	896.8
AHQ-6-6, 2711 - 2738	R.NALWHTGNTPGQVR.T	1551.69124	2	4.30E-04	0.89	3.57	-	950.7
AHQ-6-7, 2838	R.NALWHTGNTPGQVR.T	1551.69124	2	1.61E-05	0.92	3.58	-	1196.0
AHQ-6-11, 2755	R.NALWHTGNTPGQVR.T	1551.69124	2	5.06E-04	0.65	2.77	-	662.5
AHQ-6-11, 2951	R.NALWHTGNTPGQVR.T	1551.69124	2	1.87E-04	0.84	2.93	-	845.2
AHQ-6-11, 3085	R.NALWHTGNTPGQVR.T	1551.69124	2	2.92E-07	0.72	2.74	-	762.4
AHQ-6-14-, 2802	R.NALWHTGNTPGQVR.T	1551.69124	2	6.46E-06	0.77	2.91	-	710.8
gi|4507745|ref|NP_003320.1|	thioredoxin [Homo sapiens]			2.14E-08	1.72	20.18	22.90	11693.3
AHQ-6-13-, 3878	K.EKLEATINELV	1259.43110	2	1.84E-05	0.81	2.69	-	831.3
AHQ-6-13-, 3852 - 3853	K.TAFQEALDAAGDK.L	1337.41728	2	2.14E-08	0.92	3.51	-	1319.4
AHQ-6-14-, 3823 - 3830	K.TAFQEALDAAGDK.L	1337.41728	2	5.36E-07	0.91	2.81	-	1682.0
AHQ-6-13, 3991	K.TAFQEALDAAGDK.L	1337.41728	2	2.24E-07	0.91	3.28	-	1280.0
gi|11321601|ref|NP_002618.1|	phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom			2.19E-08	2.45	30.22	7.80	85595.6
AHQ-6-5, 4796	K.ASYDVSDSGQLEHVQPWSV	2105.20640	2	3.29E-04	0.56	2.90	-	357.6
AHQ-6-5, 5615 - 5616	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	9.66E-06	0.95	4.46	-	1282.2
AHQ-6-5, 5947	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	2.19E-08	0.93	4.47	-	824.3
gi|4507677|ref|NP_003290.1|	tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu			2.23E-08	6.18	70.28	12.80	92468.2
AHQ-6-4, 2485 - 2491	K.DISTNYYASQK.K	1290.36061	2	5.39E-05	0.82	3.03	-	625.7
AHQ-6-5, 3185	K.FAFQAEVNR.M	1082.19378	2	3.32E-05	0.86	2.62	-	1190.8
AHQ-6-4, 3239	K.FAFQAEVNR.M	1082.19378	2	3.31E-05	0.90	2.84	-	1164.5
AHQ-6-6, 3866	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	1.10E-05	0.95	4.38	-	1613.2
AHQ-6-4, 3976	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	6.01E-05	0.97	5.14	-	2452.5
AHQ-6-5, 3895	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	2.23E-08	0.98	5.54	-	2710.5
AHQ-6-5, 3916	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	1.31E-04	0.84	3.73	-	492.0
AHQ-6-6, 3876	K.GVVDSDDLPLNVSR.E	1486.60940	2	6.96E-07	0.91	4.32	-	730.2
AHQ-6-5, 6575	R.IKEDEDDKTVLDLAVVLFETATLR.S	2735.07994	3	3.02E-08	0.89	4.17	-	986.4
AHQ-6-6, 4000	K.SILFVPTSAPR.G	1188.40094	2	2.71E-04	0.86	2.61	-	1137.4
AHQ-6-4, 6427 - 6463	K.YSQFINFPIYVWSSK.T	1880.13366	2	9.90E-06	0.82	3.74	-	633.3
AHQ-6-6, 6271	K.YSQFINFPIYVWSSK.T	1880.13366	2	2.13E-05	0.62	2.85	-	381.3
AHQ-6-5, 6344	K.YSQFINFPIYVWSSK.T	1880.13366	2	1.35E-05	0.94	4.26	-	812.3
gi|11993943|ref|NP_055419.1|	Tax interaction protein 1 [Homo sapiens]			2.24E-08	0.87	10.20	13.70	13734.6
AHQ-6-13-, 4057 - 4074	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	5.20E-07	0.93	4.08	-	1101.4
AHQ-6-13, 4180	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	2.24E-08	0.87	3.64	-	854.4
gi|29742827|ref|XP_294099.1|	similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]			2.29E-08	0.96	10.23	7.40	17094.0
AHQ-6-12, 3755 - 3756	R.FTDEEVDELYR.E	1416.47127	2	3.75E-08	0.97	4.64	-	1551.0
AHQ-6-12, 3763 - 3765	R.FTDEEVDELYR.E	1416.47127	1	1.09E-04	0.32	1.99	-	330.0
AHQ-6-14, 4580	R.FTDEEVDELYR.E	1416.47127	2	6.72E-07	0.88	3.00	-	1093.6
AHQ-6-14-, 3822 - 3839	R.FTDEEVDELYR.E	1416.47127	2	2.29E-08	0.96	4.25	-	1391.5
AHQ-6-11, 3695	R.FTDEEVDELYR.E	1416.47127	2	5.07E-08	0.96	3.90	-	1723.6
gi|4504077|ref|NP_000165.1|	glycoprotein IX (platelet) [Homo sapiens]			2.31E-08	2.76	30.21	20.30	19046.0
AHQ-6-14-, 2803	R.CASPSLAAHGPLGR.L	1395.56962	2	7.20E-06	0.73	2.66	-	664.0
AHQ-6-11, 2751	R.CASPSLAAHGPLGR.L	1395.56962	2	2.31E-08	0.86	3.02	-	797.5
AHQ-6-11, 3453	R.GHGLTALPALPAR.T	1274.49706	3	7.44E-05	0.88	3.33	-	1101.7
AHQ-6-12, 3500 - 3580	R.GHGLTALPALPAR.T	1274.49706	2	8.25E-05	0.83	2.92	-	701.8

AHQ-6-11, 3447 - 3465	R.GHGLTALPALPAR.T	1274.49706	2	5.09E-05	0.95	4.15	-	1018.1
AHQ-6-11, 3235 - 3241	R.TPEALLQVR.C	1027.19957	2	3.41E-05	0.94	3.56	-	1347.2
gi|5901944|ref|NP_008977.1|	elastin microfibril interface located protein; TNF? elastin microfibril			2.59E-08	4.70	50.28	9.60	106694.7
AHQ-6-3, 2996	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	2.73E-07	0.93	4.49	-	810.6
AHQ-6-3, 3617	R.LDTVAGGLQGLR.E	1200.37012	2	7.38E-06	0.95	3.92	-	1549.1
AHQ-6-3, 2942	R.LVGSGLHTVEAAGEAR.Q	1567.72888	2	4.06E-06	0.96	4.20	-	1429.3
AHQ-6-3, 3709	R.PARPNLSGSSAGSPLSGLGGEGPGESEK.V	2596.74928	3	2.59E-08	0.95	5.51	-	1111.6
AHQ-6-3, 2893	R.RGTELGGAAGQGGHPPGYTSLASR.L	2298.46100	3	8.77E-06	0.91	4.39	-	958.5
gi|17986258|ref|NP_066299.2|	smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo			2.63E-08	4.47	50.24	26.50	16930.0
AHQ-6-12, 4032 - 4087	K.DQGTYEDYVEGLR.V	1545.58904	2	1.14E-06	0.92	3.98	-	1038.4
AHQ-6-13, 4293 - 4304	K.DQGTYEDYVEGLR.V	1545.58904	2	4.67E-04	0.89	3.66	-	1003.4
AHQ-6-12, 2396 - 2473	R.HVLVTLGEK.M	996.18547	2	2.86E-07	0.86	3.20	-	624.3
AHQ-6-13-, 2432 - 2456	R.HVLVTLGEK.M	996.18547	2	2.24E-05	0.82	3.28	-	493.2
AHQ-6-12, 3916	K.NKDQGTYEDYVEGLR.V	1787.86505	2	4.24E-06	0.84	3.69	-	722.5
AHQ-6-12, 3743 - 3813	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.56E-05	0.89	3.75	-	1066.9
AHQ-6-14-, 3695 - 3723	K.NKDQGTYEDYVEGLR.V	1787.86505	3	5.49E-04	0.87	3.73	-	937.0
AHQ-6-13-, 3768	K.NKDQGTYEDYVEGLR.V	1787.86505	3	3.98E-04	0.89	3.86	-	1062.3
AHQ-6-13-, 3758 - 3766	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.63E-08	0.91	3.86	-	1018.4
AHQ-6-12, 3651 - 3653	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.57E-05	0.93	4.90	-	1033.5
AHQ-6-12, 3648	K.NKDQGTYEDYVEGLR.V	1787.86505	2	8.41E-05	0.86	4.02	-	634.3
AHQ-6-14, 4494	K.NKDQGTYEDYVEGLR.V	1787.86505	2	6.65E-07	0.83	3.71	-	830.3
AHQ-6-14-, 3964	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.33E-05	0.58	3.13	-	392.8
AHQ-6-12, 5865 - 5907	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	5.32E-04	0.83	3.65	-	793.0
AHQ-6-13-, 5964	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	3.34E-06	0.85	3.47	-	733.9
AHQ-6-13-, 5965	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	1.53E-05	0.85	3.91	-	419.2
AHQ-6-12, 5863 - 5931	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	6.15E-06	0.86	4.06	-	569.1
AHQ-6-12, 6208	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	3.31E-04	0.92	4.34	-	714.3
AHQ-6-13, 6016	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	5.91E-05	0.81	3.30	-	850.7
AHQ-6-14-, 5946 - 5966	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	1.55E-05	0.89	4.11	-	801.1
AHQ-6-14-, 5950	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	1.09E-04	0.90	4.06	-	838.6
gi|4506365|ref|NP_002856.1|	RAB2, member RAS oncogene family [Homo sapiens]			2.78E-08	1.82	20.18	13.70	23545.4
AHQ-6-11, 4076	K.IQEGVFDINNEANGIK.I	1761.91387	2	8.53E-05	0.87	3.53	-	650.4
AHQ-6-11, 4231	K.LQIWDTAGQESFR.S	1551.68478	2	2.78E-08	0.95	3.66	-	1517.1
gi|4505763|ref|NP_000282.1|	phosphoglycerate kinase 1 [Homo sapiens]			2.85E-08	5.04	60.27	23.00	44614.4
AHQ-6-8, 5425	K.ACANPAAGSVILLENLR.F	1771.03187	2	7.66E-06	0.92	3.89	-	1134.3
AHQ-6-8, 5149	K.ALESPERPFLAILGGAK.V	1770.06542	2	2.85E-08	0.96	5.38	-	1320.0
AHQ-6-10, 5080	K.ALESPERPFLAILGGAK.V	1770.06542	2	4.46E-04	0.73	3.29	-	636.7
AHQ-6-8, 4402	K.DVLFLKDCVGPEVEK.A	1750.00620	2	4.88E-07	0.92	4.35	-	877.1
AHQ-6-8, 5013	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	3.45E-06	0.90	3.80	-	753.4
AHQ-6-8, 6381 - 6386	K.QIVWNGPVGVFEWEAFAR.G	2106.37033	2	1.84E-04	0.45	2.55	-	245.5
AHQ-6-8, 4020	K.YSLEPVAVELK.S	1248.44991	2	2.21E-06	0.89	3.01	-	952.1
gi|5729887|ref|NP_006624.1|	IQ motif containing GTPase activating protein 2 [Homo sapiens]			2.94E-08	3.59	40.26	3.90	180611.0
AHQ-6-3, 5386	K.GVLLDIDDLQTNQFK.N	1719.91690	2	2.15E-07	0.97	5.21	-	1802.1
AHQ-6-3, 4645	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	2.94E-08	0.98	5.04	-	1959.1
AHQ-6-4, 4687 - 4763	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	3.78E-05	0.90	3.50	-	947.5
AHQ-6-3, 4064	K.TLVGSENPPLTVIR.K	1496.73370	2	8.68E-04	0.78	3.08	-	692.9
AHQ-6-5, 4027	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	1.90E-07	0.86	3.35	-	945.5
gi|7657431|ref|NP_055205.1|	EBNA-2 co-activator (100kD) [Homo sapiens]			3.01E-08	1.83	20.25	4.50	99689.7
AHQ-6-4, 5933 - 5943	K.DTNGENIAESLVAEGLATR.R	1961.07704	2	3.01E-08	0.96	5.09	-	1779.8
AHQ-6-4, 6035 - 6047	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	7.80E-06	0.87	4.10	-	349.1
gi|30147105|ref|XP_210550.2|	similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48			3.09E-08	0.92	10.19	2.20	61339.9
AHQ-6-5, 4497	K.ADLINNLGTIAK.S	1243.43490	2	4.81E-05	0.90	3.65	-	679.9
AHQ-6-5, 4120	K.ADLINNLGTIAK.S	1243.43490	2	3.09E-08	0.92	3.77	-	985.6
gi|14249348|ref|NP_116120.1|	hypothetical protein MGC14353 [Homo sapiens]			3.25E-08	2.52	30.19	30.90	13940.7
AHQ-6-13-, 4010	K.SWCPDCVQAEPVVR.E	1705.89366	2	1.18E-05	0.87	3.17	-	826.2
AHQ-6-13-, 4668	K.TIFAYFTGSK.D	1135.29336	2	5.82E-05	0.75	3.06	-	434.2
AHQ-6-13-, 4142	R.YEEVSVSGFEEFHR.A	1715.80053	2	3.25E-08	0.90	3.72	-	798.2
gi|4758984|ref|NP_004654.1|	RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho			3.61E-08	3.49	40.26	17.10	24393.3
AHQ-6-12, 2868	K.AQIWDTAGQER.Y	1275.35241	2	9.28E-05	0.93	2.92	-	1589.9
AHQ-6-11, 4083	R.DHADSNIVIM*LVGNK.S	1642.85914	2	3.61E-08	0.98	5.11	-	1974.5
AHQ-6-11, 4823	R.GAVGALLVYDIAK.H	1290.53317	2	9.73E-04	0.93	3.74	-	1299.0
AHQ-6-11, 2875	K.VVLIGDSGVGK.S	1044.22690	2	5.61E-05	0.65	2.89	-	921.6
gi|10863977|ref|NP_067000.1|	LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-			3.67E-08	0.96	10.24	20.00	10834.5
AHQ-6-14-, 5192	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	3.67E-08	0.96	4.88	-	1385.1
AHQ-6-14, 5796	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	1.22E-05	0.93	4.09	-	994.2
gi|14210536|ref|NP_115914.1|	similar to chicken tubulin beta 5 [Homo sapiens]			3.78E-08	0.58	10.15	3.80	49856.8
AHQ-6-14-, 5963	K.M*ASTFIGNSTAIQELFK.R	1875.13550	2	5.10E-06	0.46	3.03	-	551.6
AHQ-6-7, 5834	K.M*ASTFIGNSTAIQELFK.R	1875.13550	2	3.78E-08	0.58	2.96	-	711.1
gi|4507171|ref|NP_003109.1|	secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec			3.91E-08	1.51	20.19	9.60	34632.0
AHQ-6-8, 3045 - 3104	R.LEAGDHPVELLAR.D	1420.59579	2	3.91E-08	0.93	3.88	-	927.3
AHQ-6-8, 5916 - 5920	K.YIPPCLDSELTEFPLR.M	1952.21655	2	3.08E-07	0.58	2.96	-	276.6
gi|5729770|ref|NP_000382.3|	ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky			3.97E-08	0.92	10.17	2.50	61247.6
AHQ-6-8, 3284	R.LYQQHGAGLFDVTR.G	1605.77881	2	3.97E-08	0.92	3.42	-	1307.8
gi|17986260|ref|NP_524147.1|	smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo			4.03E-08	0.95	10.28	23.30	12969.7
AHQ-6-14-, 5314	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	4.03E-08	0.95	5.30	-	1284.0
AHQ-6-13-, 5296	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	6.26E-06	0.95	5.51	-	1254.0
gi|4885183|ref|NP_005210.1|	diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS			4.15E-08	5.10	60.25	7.00	138977.7
AHQ-6-3, 4525	R.LGLHQVLQDLR.E	1292.51238	2	3.03E-05	0.76	2.94	-	675.5
AHQ-6-3, 2449	K.LQDLQGEKDALHSEK.Q	1711.85486	2	2.22E-05	0.74	3.00	-	711.5
AHQ-6-3, 4949 - 4950	K.LVAEDLSQDCFWTK.V	1713.88927	2	4.15E-08	0.95	5.10	-	807.8
AHQ-6-3, 5438	K.QDLEAEVSQLTGEVAK.L	1717.85617	2	4.21E-04	0.79	2.97	-	908.9
AHQ-6-3, 5617	K.TAQNLSIFLGSFR.M	1454.65537	2	6.44E-04	0.89	2.95	-	1159.7
AHQ-6-3, 4750	R.VQLNVFDEQGEEDSYDLK.G	2129.22304	2	3.32E-05	0.96	4.62	-	1351.1
gi|12408656|ref|NP_005177.2|	calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ			4.34E-08	10.05	110.27	20.60	81889.4
AHQ-6-6, 4955	K.APSDLYQIILK.A	1261.49183	2	7.84E-08	0.94	3.67	-	1111.5
AHQ-6-6, 2931	K.IRLDETDDPDDYGDR.E	1795.79921	2	2.55E-06	0.82	3.48	-	619.2
AHQ-6-6, 6180	K.LGLVEFNILWNR.I	1474.73142	2	7.37E-06	0.89	3.32	-	1066.8
AHQ-6-6, 4611	R.LPPGEYVVVPSTFEPNK.E	1874.12573	2	1.61E-06	0.92	4.11	-	766.4
AHQ-6-6, 5558	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	5.07E-06	0.79	3.34	-	639.2
AHQ-6-6, 5446	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	3.21E-07	0.90	4.25	-	712.5
AHQ-6-6, 5986	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	3	3.57E-04	0.60	3.73	-	428.2
AHQ-6-6, 5994	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	2	1.41E-06	0.91	4.73	-	554.4
AHQ-6-6, 3902 - 3906	K.LYELIITR.Y	1021.23493	2	5.25E-04	0.97	3.86	-	2079.8
AHQ-6-6, 5015 - 5016	R.NYPATFWVNPQFK.I	1612.81141	2	2.79E-07	0.95	3.89	-	1348.8
AHQ-6-6, 4422	K.RPTELLSNPQFIVDGATR.T	2015.25904	3	4.45E-04	0.93	5.05	-	944.6
AHQ-6-6, 4414	K.RPTELLSNPQFIVDGATR.T	2015.25904	2	3.64E-05	0.91	4.67	-	393.4
AHQ-6-6, 3196	R.SEQFINLR.E	1007.12521	1	3.88E-04	0.28	2.16	-	252.1
AHQ-6-6, 3191	R.SEQFINLR.E	1007.12521	2	1.04E-04	0.92	3.38	-	1115.3
AHQ-6-6, 6486	R.YSEPDLAVDFDNFVCCLVR.L	2322.55612	2	4.34E-08	0.94	4.61	-	686.5
gi|4885079|ref|NP_005165.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypept			4.52E-08	0.94	10.24	10.40	32880.7
AHQ-6-9, 6159	R.KPPTFGDASVIALELLNSGYEFDEGSIIFNK.F	3373.75299	3	4.52E-08	0.94	4.86	-	1331.4
gi|4507789|ref|NP_003338.1|	ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]			4.52E-08	1.69	20.22	26.00	17861.5
AHQ-6-12, 5007	R.IEINFPAEYPFKPPK.I	1791.08155	3	4.52E-08	0.93	4.34	-	1246.0
AHQ-6-12, 4995 - 5004	R.IEINFPAEYPFKPPK.I	1791.08155	2	1.52E-07	0.94	4.46	-	1179.6
AHQ-6-12, 6184	R.NIQVDEANLLTWQGLIVPDNPPYDK.G	2854.16307	2	4.16E-05	0.76	3.40	-	321.2
gi|8393159|ref|NP_059118.1|	calmodulin-like skin protein [Homo sapiens]			4.58E-08	0.77	10.23	15.80	15920.4
AHQ-6-14-, 4940	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	8.24E-07	0.93	4.65	-	823.4

AHQ-6-10, 4722	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	4.58E-08	0.77	3.70	-	422.1
gi|4504981|ref|NP_002296.1|	beta-galactosidase binding lectin precursor; Lectin, galactose-binding,			4.75E-08	0.95	10.23	11.90	14715.6
AHQ-6-13-, 4738	R.LNLEAINYM*AADGDFK.I	1801.99824	2	4.75E-08	0.95	4.64	-	957.5
AHQ-6-13, 4861	R.LNLEAINYM*AADGDFK.I	1801.99824	2	9.34E-06	0.84	3.38	-	704.4
gi|5031595|ref|NP_005709.1|	actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub			5.05E-08	1.87	20.20	11.30	19666.9
AHQ-6-12, 4328	R.AENFFILR.R	1010.17070	2	2.05E-04	0.96	3.93	-	1672.9
AHQ-6-12, 3211 - 3272	K.VLIEGSINSVR.V	1187.37134	2	5.05E-08	0.92	3.85	-	1003.0
gi|7705501|ref|NP_057546.1|	hypothetical protein HSPC194 [Homo sapiens]			5.57E-08	0.94	10.19	15.20	11564.5
AHQ-6-14-, 5635 - 5638	K.FM*PAGLIAGASLLM*VAK.V	1723.13705	2	5.57E-08	0.94	3.78	-	1338.9
gi|4507669|ref|NP_003286.1|	tumor protein, translationally-controlled 1; fortilin; histamine-releas			5.61E-08	0.89	10.16	8.10	19595.2
AHQ-6-11, 4607	R.DLISHDEMFSDIYK.I	1713.88949	2	5.61E-08	0.89	3.28	-	881.7
gi|30148644|ref|XP_293716.2|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			5.74E-08	0.93	10.18	1.20	105150.3
AHQ-6-5, 4159 - 4167	R.TLTIVDTGIGMTK.A	1350.60718	2	5.74E-08	0.93	3.61	-	1132.7
gi|15431310|ref|NP_000517.2|	keratin 14; cytokeratin 14 [Homo sapiens]			5.81E-08	4.46	50.22	17.20	51621.2
AHQ-6-10, 2731 - 2808	R.ALEEANADLEVK.I	1302.41284	2	7.96E-07	0.94	4.04	-	1300.9
AHQ-6-10, 2550	R.APSTYGGGLSVSSSR.F	1426.51406	2	5.81E-08	0.80	2.86	-	621.3
AHQ-6-10, 2666 - 2692	K.ASLENSLEETK.G	1221.29659	2	1.41E-06	0.87	3.28	-	1084.9
AHQ-6-1, 3915	R.GQVGGDVNVEM*DAAPGVDLSR.I	2103.25697	2	1.06E-05	0.92	4.03	-	714.5
AHQ-6-10, 3135	R.LLEGEDAHLSSSQFSSGSQSSR.D	2310.37735	2	1.54E-07	0.92	4.31	-	667.0
AHQ-6-8, 3102	R.LLEGEDAHLSSSQFSSGSQSSR.D	2310.37735	2	3.63E-05	0.70	3.73	-	379.5
gi|22027538|ref|NP_037506.2|	programmed cell death 6 interacting protein; ALG-2 interacting protein			5.87E-08	1.73	20.18	3.90	96022.6
AHQ-6-5, 3199	K.FIQQTYPSGGEEQAQYCR.A	2164.29714	2	2.74E-04	0.85	3.63	-	402.1
AHQ-6-5, 5031	R.SVIEQGGIQTVDQLIK.E	1728.96847	2	5.87E-08	0.87	3.63	-	1072.7
gi|12025678|ref|NP_004915.2|	actinin, alpha 4 [Homo sapiens]			5.91E-08	7.74	90.25	12.70	104853.3
AHQ-6-4, 3539 - 3541	R.DYETATLSDIK.A	1256.34094	2	8.95E-04	0.96	3.58	-	1754.5
AHQ-6-4, 4583 - 4595	R.ETTDTDTADQVIASFK.V	1742.81936	2	3.70E-07	0.96	4.42	-	1463.1
AHQ-6-4, 2317	K.GISQEQM*QEFR.A	1369.48598	2	1.42E-06	0.68	3.08	-	861.5
AHQ-6-4, 4321	R.KDDPVTNLNNAFEVAEK.Y	1905.05509	2	5.91E-08	0.96	5.09	-	980.8
AHQ-6-4, 3779	R.KDDPVTNLNNAFEVAEK.Y	1905.05509	2	7.39E-07	0.95	4.41	-	1267.8
AHQ-6-4, 3816 - 3885	R.M*APYQGPDAVPGALDYK.S	1810.02037	2	2.88E-06	0.93	3.80	-	1332.7
AHQ-6-4, 4121	K.MLDAEDIVNTARPDEK.A	1817.99924	2	2.25E-06	0.73	3.33	-	630.1
AHQ-6-4, 3769	K.M*LDAEDIVNTARPDEK.A	1833.99864	2	8.16E-05	0.85	3.99	-	491.3
AHQ-6-4, 6488	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	1.60E-04	0.85	3.69	-	952.5
AHQ-6-4, 6152	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	2.91E-06	0.82	3.89	-	604.0
gi|20127408|ref|NP_000173.2|	hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub			6.14E-08	3.47	40.22	7.90	82999.1
AHQ-6-6, 2676 - 2678	K.DTSASAVAVGLK.Q	1119.25064	2	7.94E-05	0.92	3.08	-	1307.0
AHQ-6-6, 3464 - 3539	K.GFYIYQEGVK.R	1204.35569	2	1.66E-05	0.81	2.64	-	736.0
AHQ-6-6, 3086	K.TGIEQGSDAGYLCESQK.F	1844.93497	2	6.14E-08	0.93	4.34	-	825.9
AHQ-6-6, 5666	K.TVLGTPEVLLGALPGAGGTQR.L	2008.30795	2	4.93E-04	0.82	3.53	-	521.3
gi|21614499|ref|NP_003370.2|	villin 2; Villin-2; cytovillin [Homo sapiens]			6.18E-08	1.81	20.23	1.90	69412.3
AHQ-6-6, 4280 - 4282	K.APDFVFYAPR.L	1183.33971	2	6.18E-08	0.97	4.54	-	1531.7
AHQ-6-6, 3795	K.KAPDFVFYAPR.L	1311.51262	2	9.49E-07	0.84	3.11	-	713.1
gi|5453603|ref|NP_006422.1|	chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c			6.27E-08	4.45	50.24	15.30	57487.9
AHQ-6-7, 3067	R.EALLSSAVDHGSDEVK.F	1657.76083	2	6.27E-08	0.93	4.17	-	1070.7
AHQ-6-7, 3034 - 3111	R.GATQQILDEAER.S	1331.41427	2	3.47E-04	0.77	2.78	-	941.6
AHQ-6-7, 5600 - 5611	K.LGGSLADSYLDEGFLLDK.K	1914.10189	2	5.06E-04	0.93	4.17	-	997.9
AHQ-6-7, 5246	R.SLHDALCVLAQTVK.D	1556.80920	2	1.61E-04	0.87	3.42	-	885.3
AHQ-6-7, 6170	R.VQDDEVGDGTTSVTVLAAELLR.E	2289.48263	2	1.88E-06	0.95	4.76	-	980.8
gi|21464101|ref|NP_036611.2|	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein			6.68E-08	0.92	10.23	5.70	28302.4
AHQ-6-14-, 3096	K.NVTELNEPLSNEER.N	1644.72215	2	1.18E-05	0.95	4.50	-	973.6
AHQ-6-10, 2982	K.NVTELNEPLSNEER.N	1644.72215	2	6.68E-08	0.92	3.86	-	797.5
gi|14251209|ref|NP_001279.2|	chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo			7.00E-08	2.96	40.27	25.30	26922.5
AHQ-6-14-, 5443 - 5448	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	2	2.38E-07	0.79	3.41	-	382.8
AHQ-6-13-, 3464 - 3465	K.GVTFNVTTVDTK.R	1282.42476	2	1.88E-06	0.92	3.84	-	964.7
AHQ-6-13, 3611	K.GVTFNVTTVDTK.R	1282.42476	2	1.44E-07	0.95	4.05	-	1186.7
AHQ-6-13, 5232	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	4.18E-05	0.94	4.36	-	894.8
AHQ-6-10, 5032	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.32E-07	0.84	3.78	-	448.0
AHQ-6-13-, 5137	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.27E-06	0.89	4.06	-	568.3
AHQ-6-13-, 5230	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	7.00E-08	0.94	4.10	-	941.8
AHQ-6-14-, 5160 - 5218	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	7.35E-04	0.92	4.12	-	748.9
AHQ-6-11, 5023 - 5024	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	7.45E-04	0.96	5.46	-	778.9
AHQ-6-9, 2736	K.LHIVQVVCK.K	1097.35623	1	9.95E-05	0.28	2.09	-	356.2
gi|4502303|ref|NP_001688.1|	mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m			7.02E-08	4.51	50.22	35.70	23277.2
AHQ-6-11, 6139	R.FSPLTTNLINLLAENGR.L	1874.13050	2	4.02E-06	0.87	3.18	-	1087.7
AHQ-6-11, 5208 - 5211	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	1.65E-04	0.91	4.24	-	656.2
AHQ-6-11, 3627	K.LVRPPVQVYGIEGR.Y	1583.85942	3	3.52E-05	0.95	4.34	-	1709.7
AHQ-6-11, 3576 - 3577	K.TDPSILGGM*IVR.I	1275.50037	2	3.60E-05	0.86	2.97	-	864.2
AHQ-6-11, 3311 - 3312	K.VAASVLNPYVK.R	1161.37549	2	7.02E-08	0.92	3.81	-	701.6
gi|6857820|ref|NP_005019.2|	phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl			7.08E-08	0.98	10.25	4.20	46224.3
AHQ-6-7, 2759	K.HGAGAEISTVNPEQYSK.R	1788.89618	2	7.08E-08	0.98	4.93	-	2201.6
gi|13518026|ref|NP_004978.2|	LIM and senescent cell antigen-like domains 1 [Homo sapiens]			7.42E-08	1.77	20.18	7.70	37251.2
AHQ-6-11, 4336	K.CHAIIDEQPLIFK.N	1585.84900	2	4.96E-04	0.83	3.38	-	825.2
AHQ-6-9, 3282	R.VIEGDVVSALNK.A	1244.41966	2	2.93E-04	0.87	3.01	-	1022.4
AHQ-6-12, 3507	R.VIEGDVVSALNK.A	1244.41966	2	1.00E-06	0.93	3.28	-	1041.9
AHQ-6-8, 3304	R.VIEGDVVSALNK.A	1244.41966	2	7.42E-08	0.94	3.55	-	1092.7
gi|6912638|ref|NP_036557.1|	ras suppressor protein 1 [Homo sapiens]			7.98E-08	4.15	50.25	30.70	31540.1
AHQ-6-10, 6182 - 6190	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	2.67E-04	0.53	3.19	-	542.1
AHQ-6-12, 6311 - 6312	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	1.18E-04	0.57	3.20	-	306.9
AHQ-6-10, 5571 - 5639	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	8.38E-04	0.90	4.34	-	397.4
AHQ-6-10, 6134 - 6135	R.GISNM*LDVNGLFTLSHITQLVLSHNK.L	2869.28903	3	7.98E-08	0.92	4.51	-	960.8
AHQ-6-10, 5299	K.LQILSLRDNDLISLPK.E	1839.16919	2	5.75E-04	0.80	3.66	-	930.7
AHQ-6-10, 5208 - 5264	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	7.79E-04	0.50	2.78	-	401.1
AHQ-6-10, 5352 - 5370	R.LTVLPPELGNLDLTGQK.Q	1809.09672	3	9.74E-05	0.96	4.98	-	1354.5
AHQ-6-10, 5318 - 5374	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	6.61E-04	0.84	3.32	-	586.1
AHQ-6-13-, 5569 - 5637	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	2.72E-04	0.76	2.96	-	344.8
gi|5453605|ref|NP_006421.1|	chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-			8.09E-08	1.66	20.25	5.90	57838.8
AHQ-6-7, 5879	R.DALSDLALHFLNK.M	1457.65603	2	8.09E-08	0.98	4.91	-	2448.4
AHQ-6-7, 5675	K.LGGTIDDCELVEGLVLTQK.V	2062.32762	2	7.83E-05	0.68	3.39	-	499.8
gi|4557321|ref|NP_000030.1|	apolipoprotein A-I precursor [Homo sapiens]			8.36E-08	2.70	30.18	15.70	30777.6
AHQ-6-11, 5508 - 5511	R.EQLGPVTQEFWDNLEK.E	1934.09489	2	2.04E-06	0.86	3.69	-	511.4
AHQ-6-13-, 5033	K.LLDNWDSVTSTFSK.L	1613.74965	2	3.42E-05	0.83	3.30	-	621.4
AHQ-6-14-, 5030 - 5036	K.LLDNWDSVTSTFSK.L	1613.74965	2	5.55E-06	0.89	3.62	-	857.4
AHQ-6-11, 5711	K.VSFLSALEEYTK.K	1387.55934	2	8.36E-08	0.95	3.68	-	1289.5
AHQ-6-10, 5662	K.VSFLSALEEYTK.K	1387.55934	2	4.93E-06	0.93	3.59	-	977.4
gi|4505877|ref|NP_000436.1|	plectin 1, intermediate filament binding protein 500kDa; plectin 1, int			8.39E-08	3.51	40.23	1.30	518488.0
AHQ-6-3, 4924 - 5001	R.APVPASELLASGVLSR.A	1567.81193	2	2.06E-04	0.91	3.78	-	914.1
AHQ-6-3, 3228	K.AYSDPSTGEPATYGELQQR.C	2071.14682	2	1.03E-06	0.93	4.67	-	595.6
AHQ-6-1, 4280	R.SIQEELQQLR.Q	1244.37976	2	5.21E-06	0.81	3.12	-	1153.0
AHQ-6-2, 4983	K.VQSGSESVIQEYVDLR.T	1809.95530	2	8.39E-08	0.87	3.31	-	894.0
gi|4503971|ref|NP_001484.1|	GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r			8.61E-08	2.75	30.25	14.50	50582.4
AHQ-6-7, 4935	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	3.35E-07	0.96	4.95	-	960.8
AHQ-6-7, 3991	R.TDDYLDQPCLETVNR.I	1840.94632	2	5.20E-06	0.90	3.64	-	685.6
AHQ-6-6, 6296	K.YIAIASTTVETTDPEKEVEPALELLEPIDQK.F	3444.82460	3	8.61E-08	0.90	4.00	-	898.3
gi|4557597|ref|NP_001449.1|	gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);			8.82E-08	2.14	30.27	1.70	288897.4
AHQ-6-5, 4453 - 4479	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	8.49E-05	0.90	4.84	-	714.2
AHQ-6-6, 4419	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.57E-06	0.94	5.33	-	838.5
AHQ-6-6, 4418	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.55E-05	0.91	4.63	-	314.3

AHQ-6-4, 4549	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.30E-05	0.78	4.17	-	390.0
AHQ-6-4, 4556 - 4565	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	2.10E-05	0.94	5.32	-	426.9
AHQ-6-7, 4263	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.83E-05	0.67	3.08	-	449.6
AHQ-6-5, 4463	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	8.82E-08	0.92	4.53	-	487.8
AHQ-6-3, 2030	K.IECDDKGDGSCDVR.Y	1628.67809	2	7.57E-06	0.84	3.44	-	734.2
AHQ-6-2, 1931 - 2006	K.IECDDKGDGSCDVR.Y	1628.67809	2	7.88E-05	0.43	2.65	-	350.9
AHQ-6-3, 2121 - 2198	K.NDNDTFTVK.Y	1054.09237	1	1.20E-04	0.38	2.11	-	300.2
gi|27498332|ref|XP_212565.1|	similar to tubulin, beta 5 [Homo sapiens]			9.03E-08	3.32	40.26	8.60	49670.5
AHQ-6-7, 3258	R.IM*NTFSVVPSPK.V	1336.58217	2	2.76E-05	0.85	3.26	-	742.1
AHQ-6-7, 5826 - 5838	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.89E-06	0.90	4.10	-	739.7
AHQ-6-7, 6040 - 6074	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.53E-04	0.91	3.57	-	728.6
AHQ-6-7, 6131 - 6136	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	2.06E-05	0.74	3.28	-	718.4
AHQ-6-14-, 5956 - 5968	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.40E-06	0.95	4.26	-	1290.0
AHQ-6-11, 5979 - 6044	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.75E-05	0.63	3.21	-	385.8
AHQ-6-13, 6047	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	9.03E-08	0.96	5.20	-	1076.5
AHQ-6-13, 6205 - 6220	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.70E-05	0.86	4.07	-	549.8
AHQ-6-13-, 5905 - 5982	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.00E-04	0.94	4.63	-	937.5
AHQ-6-13-, 6128 - 6189	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	3.60E-04	0.94	4.21	-	924.2
AHQ-6-13-, 6160	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	9.86E-05	0.95	3.99	-	1312.0
AHQ-6-14-, 6140 - 6198	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	7.15E-07	0.95	5.21	-	738.5
AHQ-6-11, 4287	R.YLTVAAVFR.G	1040.23994	2	2.83E-05	0.77	2.62	-	627.2
gi|4503725|ref|NP_000792.1|	FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei			9.26E-08	1.83	20.25	13.00	11950.6
AHQ-6-13-, 3084	R.GWEEGVAQM*SVGQR.A	1550.67866	2	2.20E-05	0.92	3.66	-	962.6
AHQ-6-13-, 3868 - 3869	R.GWEEGVAQMSVGQR.A	1534.67926	2	9.26E-08	0.89	3.57	-	1249.1
AHQ-6-14-, 3034	R.GWEEGVAQM*SVGQR.A	1550.67866	2	1.07E-06	0.94	3.96	-	1078.6
AHQ-6-14-, 3844 - 3846	R.GWEEGVAQMSVGQR.A	1534.67926	2	5.12E-05	0.96	4.99	-	1222.3
AHQ-6-13, 3231 - 3243	R.GWEEGVAQM*SVGQR.A	1550.67866	2	1.68E-04	0.96	4.64	-	1114.4
gi|24430192|ref|NP_005548.2|	keratin 16; keratin, type I cytoskeletal 16; cytokeratin 16 [Homo sapi			1.07E-07	4.33	50.30	16.30	51267.5
AHQ-6-10, 4132	R.DAETWFLSK.T	1097.20199	1	2.39E-04	0.67	2.60	-	490.0
AHQ-6-10, 4128	R.DAETWFLSK.T	1097.20199	2	2.72E-05	0.82	2.95	-	819.4
AHQ-6-1, 3688	R.GQTGGDVNVEM*DAAPGVDLSR.I	2105.22972	2	1.96E-04	0.85	4.29	-	565.9
AHQ-6-10, 3347	R.GQTGGDVNVEM*DAAPGVDLSR.I	2105.22972	2	8.58E-04	0.67	3.15	-	444.1
AHQ-6-1, 5171	K.IIAATIENAQPILQIDNAR.L	2065.35950	3	6.58E-04	0.98	5.41	-	2143.6
AHQ-6-1, 5167	K.IIAATIENAQPILQIDNAR.L	2065.35950	2	1.39E-04	0.88	4.31	-	522.8
AHQ-6-10, 4732	K.IIAATIENAQPILQIDNAR.L	2065.35950	2	2.71E-05	0.96	5.91	-	916.5
AHQ-6-10, 6018 - 6082	R.TDLEM*QIEGLKEELAYLR.K	2168.45360	3	3.96E-05	0.89	3.67	-	1071.7
AHQ-6-10, 2246	R.TKYEHELALR.Q	1260.42402	2	1.07E-07	0.80	2.97	-	649.7
gi|4505989|ref|NP_000299.1|	protective protein for beta-galactosidase; Protective protein for beta-			1.14E-07	0.97	10.22	2.70	54495.8
AHQ-6-12, 3517 - 3597	K.YGDSGEQIAGFVK.E	1371.47686	2	1.14E-07	0.97	4.30	-	2151.0
gi|4759082|ref|NP_004648.1|	serum deprivation response protein; serum deprivation response; phospha			1.17E-07	2.79	30.25	11.10	47172.9
AHQ-6-13-, 5932 - 5937	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.62E-04	0.97	5.09	-	1630.7
AHQ-6-13, 5985	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.55E-04	0.87	3.23	-	738.2
AHQ-6-11, 5693 - 5747	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.14E-04	0.60	3.00	-	389.5
AHQ-6-14-, 5927	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.05E-04	0.95	4.35	-	1317.6
AHQ-6-12, 3613	K.LVNMLDAVQENQHK.M	1639.85851	2	4.35E-04	0.89	3.42	-	890.7
AHQ-6-9, 5414 - 5472	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.87E-06	0.93	4.68	-	736.0
AHQ-6-8, 5722	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.02E-05	0.94	4.68	-	630.1
AHQ-6-6, 5774 - 5775	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.17E-07	0.95	4.52	-	1066.1
gi|5802966|ref|NP_006861.1|	destrin (actin depolymerizing factor); destrin [Homo sapiens]			1.19E-07	1.72	20.18	13.30	18505.6
AHQ-6-12, 3423	K.AVIFCLSADKK.C	1253.49298	2	3.97E-07	0.80	2.72	-	787.5
AHQ-6-12, 3719 - 3723	R.YALYDASFETK.E	1308.41754	2	1.19E-07	0.93	3.58	-	959.6
gi|10863927|ref|NP_066953.1|	peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]			1.21E-07	5.48	70.25	24.20	18012.4
AHQ-6-12, 3876 - 3935	K.FEDENFILK.H	1155.28144	2	2.88E-04	0.78	3.35	-	527.1
AHQ-6-13, 4115	K.FEDENFILK.H	1155.28144	2	2.47E-04	0.73	3.07	-	524.3
AHQ-6-12, 4417 - 4475	K.SIYGEKFEDENFILK.H	1833.03047	2	1.64E-05	0.82	3.40	-	793.4
AHQ-6-13, 4704	K.SIYGEKFEDENFILK.H	1833.03047	2	1.21E-07	0.79	3.45	-	445.0
AHQ-6-12, 4511	K.SIYGEKFEDENFILK.H	1833.03047	2	1.21E-07	0.96	5.05	-	1187.6
AHQ-6-13-, 4584	K.SIYGEKFEDENFILK.H	1833.03047	2	6.66E-06	0.95	4.72	-	1122.3
AHQ-6-14-, 4591	K.SIYGEKFEDENFILK.H	1833.03047	2	4.23E-07	0.95	5.06	-	979.5
AHQ-6-12, 3681	K.VKEGMNIVEAMER.F	1506.77390	2	2.09E-04	0.93	4.13	-	1086.7
AHQ-6-12, 3073	K.VKEGM*NIVEAMER.F	1522.77330	2	3.35E-04	0.80	2.91	-	738.4
AHQ-6-12, 2639	K.VKEGMNIVEAM*ER.F	1522.77330	2	7.78E-06	0.90	4.05	-	1125.6
AHQ-6-12, 3691	K.VKEGMNIVEAMER.F	1506.77390	3	2.74E-05	0.74	3.82	-	870.0
AHQ-6-13-, 4429	R.VSFELFADK.V	1056.19300	2	1.13E-04	0.87	3.21	-	862.8
AHQ-6-12, 4337	R.VSFELFADK.V	1056.19300	2	7.55E-05	0.78	2.98	-	841.3
AHQ-6-12, 4447	R.VSFELFADKVPK.T	1380.61317	2	3.66E-04	0.85	3.62	-	770.2
AHQ-6-12, 4456	R.VSFELFADKVPK.T	1380.61317	3	6.71E-07	0.57	3.38	-	326.7
gi|4507295|ref|NP_003560.1|	syntaxin 7 [Homo sapiens]			1.24E-07	0.70	10.16	5.40	29845.3
AHQ-6-13, 4893	R.LVAEFTTSLTNFQK.V	1599.80925	2	1.24E-07	0.70	3.13	-	524.8
gi|4507767|ref|NP_003326.1|	ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi			1.27E-07	2.43	30.21	4.20	111719.5
AHQ-6-4, 4656	R.VDGVAAALDSFQAR.R	1420.55265	2	1.27E-07	0.97	4.30	-	2084.3
AHQ-6-4, 4303 - 4317	K.VLEDGTPFWSGPK.Q	1433.58980	2	9.55E-05	0.61	2.88	-	476.3
AHQ-6-4, 4552	R.VLVSGLQGLGAEVAK.N	1441.69805	2	1.78E-06	0.85	2.77	-	1235.6
gi|14165439|ref|NP_002131.2|	heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch bindin			1.29E-07	0.89	10.19	4.10	51027.9
AHQ-6-7, 4760	R.GSYGDLGGPIITTQVTIPK.D	1918.18004	2	1.29E-07	0.89	3.84	-	818.8
gi|4507509|ref|NP_003245.1|	tissue inhibitor of metalloproteinase 1 precursor; Erythroid-potentiati			1.37E-07	0.96	10.19	5.80	23170.8
AHQ-6-10, 3599	K.GFQALGDAADIR.F	1234.34342	2	1.37E-07	0.96	3.74	-	2117.9
gi|5729875|ref|NP_006658.1|	progesterone receptor membrane component 1; progesterone binding protei			1.58E-07	1.81	20.18	17.90	21671.0
AHQ-6-11, 2905	R.GDQPAASGDSDDDEPPPLPR.L	2037.04410	2	1.46E-06	0.91	3.67	-	872.7
AHQ-6-11, 3984	R.KFYGPEGPYGVFAGR.D	1645.84140	2	1.58E-07	0.90	3.63	-	957.7
gi|5031573|ref|NP_005712.1|	ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye			1.67E-07	6.27	80.23	34.00	47370.9
AHQ-6-8, 2889 - 2892	R.DREVGIPPEQSLETAK.A	1769.93431	2	5.34E-04	0.96	4.56	-	918.4
AHQ-6-8, 3300	K.DYEEIGPSICR.H	1340.44122	2	6.66E-05	0.84	2.97	-	803.7
AHQ-6-13, 3657	K.DYEEIGPSICR.H	1340.44122	2	2.04E-05	0.79	2.75	-	503.8
AHQ-6-13-, 3506	K.DYEEIGPSICR.H	1340.44122	2	2.75E-05	0.93	3.63	-	1015.2
AHQ-6-7, 6382	R.FLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVR.R	4319.79733	3	7.54E-05	0.65	3.36	-	596.1
AHQ-6-8, 4150	R.HGIVEDWDLMER.F	1500.66127	2	2.24E-06	0.96	3.46	-	1887.3
AHQ-6-13, 3768	R.LPACVVDCGTGYTK.L	1543.74421	2	2.37E-04	0.41	2.59	-	587.5
AHQ-6-8, 3410	R.LPACVVDCGTGYTK.L	1543.74421	2	4.50E-04	0.47	2.81	-	560.0
AHQ-6-8, 3837	K.NIVLSGGSTMFR.D	1282.49463	2	1.67E-07	0.90	3.28	-	1376.6
AHQ-6-8, 5877 - 5956	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	1.71E-04	0.88	4.40	-	734.5
AHQ-6-8, 3501 - 3505	R.YSYVCPDLVK.E	1245.42618	2	3.19E-05	0.73	2.94	-	522.5
gi|5454152|ref|NP_006285.1|	ubiquinol-cytochrome c reductase binding protein [Homo sapiens]			1.78E-07	1.72	20.27	25.20	13530.4
AHQ-6-13, 3671	R.DDTIYEDEDVKEAIR.R	1811.88169	2	3.14E-06	0.75	3.07	-	630.1
AHQ-6-13-, 5025	K.YEEENFYLEPYLK.E	1737.88601	2	8.04E-06	0.97	4.63	-	1844.1
AHQ-6-13, 5127	K.YEEENFYLEPYLK.E	1737.88601	2	1.78E-07	0.97	5.46	-	1579.1
gi|7705849|ref|NP_057215.1|	ras-related GTP-binding protein RAB10; ras-related GTP-binding protein			1.83E-07	1.68	20.20	11.50	22540.8
AHQ-6-14-, 6087	K.AFLTLAEDILR.K	1262.47982	2	4.43E-06	0.96	3.80	-	1841.3
AHQ-6-11, 5907	K.AFLTLAEDILR.K	1262.47982	2	1.50E-05	0.88	3.31	-	1022.7
AHQ-6-13, 6183	K.AFLTLAEDILR.K	1262.47982	2	1.83E-07	0.92	2.91	-	1375.3
AHQ-6-10, 5864	K.AFLTLAEDILR.K	1262.47982	2	8.72E-06	0.95	3.01	-	2074.4
AHQ-6-11, 1937 - 2008	R.NIDEHANEDVER.M	1441.44245	2	3.37E-04	0.76	2.89	-	738.4
gi|4507651|ref|NP_003281.1|	tropomyosin 4 [Homo sapiens]			1.86E-07	3.60	40.24	17.70	28521.6
AHQ-6-9, 3792	R.AEVSELKCGDLEEELK.N	1851.02256	2	3.88E-05	0.84	3.11	-	856.5
AHQ-6-9, 2525 - 2600	K.IQALQQQADEAEDR.A	1615.68404	2	1.29E-05	0.97	4.72	-	1593.7
AHQ-6-10, 2595	K.IQALQQQADEAEDR.A	1615.68404	2	1.67E-04	0.79	2.78	-	817.9
AHQ-6-11, 2628	K.IQALQQQADEAEDR.A	1615.68404	2	4.74E-07	0.90	3.43	-	1124.5

AHQ-6-11, 2477	R.KIQALQQQADEAEDR.A	1743.85695	2	1.70E-05	0.89	3.71	-	1160.2
AHQ-6-10, 2432	R.KIQALQQQADEAEDR.A	1743.85695	2	9.45E-06	0.94	4.35	-	1281.9
AHQ-6-12, 2515	R.KIQALQQQADEAEDR.A	1743.85695	2	1.86E-07	0.94	4.22	-	1416.9
AHQ-6-9, 2112 - 2180	K.YSEKEDKYEEEIK.L	1690.78605	2	1.80E-04	0.92	3.72	-	1159.8
gi|4504515|ref|NP_002146.1|	heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B			1.94E-07	2.63	30.20	6.40	70853.4
AHQ-6-6, 4855 - 4859	R.ARFEELCSDLFR.S	1544.71384	2	1.62E-05	0.93	3.86	-	973.3
AHQ-6-6, 4718	R.IINEPTAAAIAYGLDR.R	1688.90603	2	3.36E-04	0.93	3.95	-	903.4
AHQ-6-11, 3388	R.TTPSYVAFTDTER.L	1488.58062	2	1.94E-07	0.77	2.51	-	748.9
AHQ-6-6, 3255	R.TTPSYVAFTDTER.L	1488.58062	2	1.91E-06	0.70	2.55	-	658.3
gi|4507149|ref|NP_000445.1|	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult			2.01E-07	0.81	10.17	9.10	15935.7
AHQ-6-12, 4257	K.GDGPVQGIINFEQK.E	1502.65366	2	2.01E-07	0.81	3.31	-	616.1
AHQ-6-11, 4188	K.GDGPVQGIINFEQK.E	1502.65366	2	2.80E-04	0.75	3.29	-	500.0
gi|4557385|ref|NP_000055.1|	complement component 3 precursor; acylation-stimulating protein cleavag			2.10E-07	3.49	40.26	4.40	187162.3
AHQ-6-6, 5655 - 5735	K.EYVLPSFEVIVEPTEK.F	1880.12704	2	7.62E-05	0.89	3.96	-	848.1
AHQ-6-6, 3564	R.IPIEDGSGEVVLSR.K	1471.63788	2	5.20E-07	0.92	3.44	-	1039.5
AHQ-6-4, 5647	K.VFSLAVNLIAIDSQVLCGAVK.W	2219.62984	2	6.27E-04	0.71	3.21	-	793.3
AHQ-6-6, 4399	R.VPVAVQGEDTVQSLTQGDGVAK.L	2199.40432	2	2.10E-07	0.96	5.29	-	997.2
gi|7706675|ref|NP_057661.1|	RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M			2.14E-07	1.55	20.22	12.50	23461.5
AHQ-6-11, 4531	R.GSDVIIMLVGNK.T	1246.50220	2	2.14E-07	0.97	4.49	-	2111.2
AHQ-6-11, 3132	R.VASALPGMENVQEK.S	1473.67727	2	1.07E-04	0.58	2.52	-	279.7
gi|19923457|ref|NP_057447.2|	glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M			2.24E-07	2.51	30.21	7.60	67308.6
AHQ-6-7, 4003 - 4020	R.ASFPIITVTAAHSGTYR.C	1793.01594	2	2.24E-07	0.69	2.95	-	629.0
AHQ-6-7, 5219	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	7.30E-07	0.91	4.25	-	1024.3
AHQ-6-7, 4539	R.YGFDQFALYK.E	1252.39881	2	2.63E-07	0.90	3.12	-	882.0
gi|30150022|ref|XP_300862.1|	similar to beta-tubulin 4Q [Homo sapiens]			2.25E-07	2.68	40.19	11.60	33545.2
AHQ-6-8, 3209 - 3265	R.FPGQLNADLR.K	1131.26634	2	1.38E-04	0.87	3.04	-	809.7
AHQ-6-13-, 3458	R.FPGQLNADLR.K	1131.26634	2	2.25E-07	0.67	2.60	-	709.1
AHQ-6-7, 3238 - 3304	R.FPGQLNADLR.K	1131.26634	2	3.11E-05	0.82	2.70	-	831.0
AHQ-6-11, 3916	R.KLAVNMVPFPR.L	1272.58771	2	3.27E-04	0.59	2.63	-	558.1
AHQ-6-10, 4219	K.LAVNMVPFPR.L	1144.41480	2	9.27E-05	0.61	2.59	-	412.5
AHQ-6-10, 4663	R.LHFFM*PGFAPLTSR.G	1637.92902	2	1.77E-04	0.82	3.01	-	658.5
AHQ-6-9, 4580	R.LHFFM*PGFAPLTSR.G	1637.92902	2	3.49E-04	0.84	3.00	-	722.8
gi|22547186|ref|NP_004160.3|	serine hydroxymethyltransferase 1 (soluble) isoform 1; cytoplasmic ser			2.48E-07	0.71	10.15	3.70	53082.3
AHQ-6-7, 4019	K.VNPDTGYINYDQLEENAR.L	2112.19894	2	2.48E-07	0.71	3.06	-	480.2
gi|14149680|ref|NP_056107.1|	KIAA0747 protein [Homo sapiens]			2.59E-07	3.44	40.21	5.80	122855.6
AHQ-6-4, 5835	R.ALTLGALTLPLAR.L	1310.61075	2	1.10E-06	0.92	3.53	-	1096.3
AHQ-6-4, 4916	R.FFLQDPQSQELDVQVK.D	1922.12725	2	3.36E-06	0.68	2.96	-	606.3
AHQ-6-12, 3949	R.LTHVDSPLEAPAGPLGQVK.L	1930.19405	2	2.59E-07	0.95	3.96	-	1280.0
AHQ-6-12, 4300	K.VQLDLAETDLSQGVAR.W	1715.88665	2	9.77E-05	0.89	4.12	-	635.3
gi|21361478|ref|NP_055944.2|	septin 6 isoform B; septin 2 [Homo sapiens]			2.67E-07	0.95	10.29	6.50	49716.3
AHQ-6-7, 3750	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L	3147.31508	3	2.67E-07	0.95	5.85	-	1108.8
gi|8922712|ref|NP_060713.1|	hypothetical protein FLJ10849 [Homo sapiens]			2.76E-07	0.51	10.19	4.20	49397.9
AHQ-6-7, 3432 - 3440	K.DTDPDSKPFSLQETYEAK.R	2072.17149	2	2.76E-07	0.51	2.95	-	246.8
gi|19923483|ref|NP_057406.2|	GTPase Rab14 [Homo sapiens]			2.90E-07	3.31	40.21	24.20	23896.8
AHQ-6-11, 3705 - 3708	R.GAAGALM*VYDITR.R	1354.55759	2	2.52E-05	0.95	4.13	-	1113.2
AHQ-6-11, 4791 - 4795	R.NLTNPNTVIILIGNK.A	1624.90662	2	2.90E-07	0.91	4.16	-	560.8
AHQ-6-10, 3238	K.SCLLHQFTEK.K	1264.43272	2	6.94E-04	0.79	2.51	-	1073.5
AHQ-6-14-, 4427 - 4499	K.TGENVEDAFLEAAK.K	1494.58517	2	3.21E-04	0.55	3.25	-	459.5
AHQ-6-10, 4262	K.TGENVEDAFLEAAK.K	1494.58517	2	3.50E-05	0.66	2.84	-	663.5
gi|4507951|ref|NP_003396.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept			2.92E-07	2.01	30.23	15.00	28218.5
AHQ-6-10, 2902 - 2959	K.AVTELNEPLSNEDR.N	1587.67060	2	2.92E-07	0.92	4.64	-	690.4
AHQ-6-13, 3208 - 3209	K.AVTELNEPLSNEDR.N	1587.67060	2	1.31E-04	0.93	3.85	-	934.3
AHQ-6-10, 2376	K.KNSVVEASEAAYK.E	1396.52786	2	4.76E-04	0.89	3.13	-	981.4
AHQ-6-10, 2207	R.YLAEVASGEK.K	1067.17419	1	1.79E-05	0.19	2.01	-	533.9
gi|10863873|ref|NP_000651.1|	transforming growth factor, beta 1 (Camurati-Engelmann disease); trans			2.95E-07	2.59	30.19	5.90	44422.0
AHQ-6-13-, 3362	R.ALDTNYCFSSTEK.N	1537.63010	2	2.95E-07	0.89	3.64	-	708.1
AHQ-6-13, 3519	R.ALDTNYCFSSTEK.N	1537.63010	2	1.02E-05	0.81	3.33	-	501.8
AHQ-6-13-, 2686 - 2748	K.VEQLSNM*IVR.S	1205.41014	2	9.31E-04	0.75	3.09	-	641.0
AHQ-6-13, 3713	K.VEQLSNMIVR.S	1189.41074	2	6.44E-06	0.95	3.84	-	1447.2
gi|16933567|ref|NP_005361.2|	mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]			2.98E-07	0.96	10.22	6.80	23668.1
AHQ-6-14-, 5632	K.ANINVENAFFTLAR.D	1580.76926	2	3.59E-07	0.77	3.07	-	590.1
AHQ-6-11, 5403 - 5471	K.ANINVENAFFTLAR.D	1580.76926	2	2.98E-07	0.96	4.41	-	1523.2
gi|4757886|ref|NP_004330.1|	pituitary tumor-transforming protein 1-interacting protein precursor; c			3.00E-07	0.68	10.17	10.00	20323.7
AHQ-6-11, 5235	K.ACLDYPVTSVLPPASLCK.L	1994.31817	2	3.00E-07	0.68	3.33	-	308.4
gi|30149221|ref|XP_291446.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			3.03E-07	0.95	10.22	3.90	45688.5
AHQ-6-7, 2406	R.STAGDTHLGGEDFDNR.M	1692.68222	2	1.06E-05	0.80	3.27	-	648.2
AHQ-6-6, 2498	R.STAGDTHLGGEDFDNR.M	1692.68222	2	3.03E-07	0.95	4.43	-	1366.1
gi|4504351|ref|NP_000510.1|	delta globin [Homo sapiens]			3.11E-07	1.79	20.24	21.80	16055.4
AHQ-6-13, 4873	R.FFESFGDLSSPDAVM*GNPK.V	2062.24491	2	1.65E-04	0.82	3.43	-	523.3
AHQ-6-13-, 3194	K.VNVDAVGGEALGR.L	1257.37853	2	3.11E-07	0.97	4.85	-	1906.4
gi|5802974|ref|NP_006784.1|	peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide			3.14E-07	2.64	30.24	22.30	27692.5
AHQ-6-11, 4353 - 4417	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	3.18E-05	0.90	4.82	-	517.0
AHQ-6-11, 5045	R.DYGVLLEGSGLALR.G	1463.66058	2	2.04E-06	0.96	4.08	-	1846.7
AHQ-6-10, 4982	R.DYGVLLEGSGLALR.G	1463.66058	2	3.14E-07	0.95	3.68	-	1511.0
AHQ-6-11, 5268	R.GLFIIDPNGVIK.H	1286.54452	2	3.70E-04	0.80	3.45	-	700.3
gi|4885063|ref|NP_005156.1|	aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase			3.31E-07	0.80	10.23	6.30	39455.6
AHQ-6-9, 4059 - 4119	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	9.39E-06	0.44	2.98	-	327.0
AHQ-6-8, 4264 - 4334	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	3.31E-07	0.80	4.63	-	592.4
gi|4505621|ref|NP_002558.1|	prostatic binding protein; phosphatidylethanolamine binding protein [Ho			3.55E-07	1.92	20.25	20.30	21056.6
AHQ-6-11, 4696 - 4701	R.APVAGTCYQAEWDDYVPK.L	2072.23961	2	3.55E-07	0.96	5.00	-	1375.3
AHQ-6-11, 4180	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	1.29E-06	0.95	4.22	-	1197.7
gi|5803225|ref|NP_006752.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon poly			3.79E-07	1.69	20.24	11.40	29173.7
AHQ-6-13-, 6144 - 6222	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	9.74E-05	0.94	4.72	-	895.3
AHQ-6-9, 6223	K.AAFDDAIAELDTLSEESYKDSTLIM*QLLR.D	3276.61426	3	3.79E-07	0.74	3.77	-	556.4
gi|4507645|ref|NP_000356.1|	triosephosphate isomerase 1 [Homo sapiens]			3.81E-07	3.50	40.27	31.30	26669.3
AHQ-6-10, 3680	K.DCGATWVVLGHSER.R	1588.72671	2	3.81E-07	0.84	3.02	-	796.6
AHQ-6-10, 6006 - 6063	K.ELASQPDVDGFLVGGASLKPEFVDIINAK.Q	3031.40532	3	8.34E-06	0.74	3.57	-	244.9
AHQ-6-10, 4218	R.KQSLGELIGTLNAAK.V	1543.79037	2	4.39E-04	0.96	3.60	-	2200.9
AHQ-6-10, 5066 - 5139	K.VPADTEVVCAPPTAYIDFAR.Q	2194.44943	2	2.74E-04	0.96	5.44	-	663.8
gi|5031839|ref|NP_005545.1|	keratin 6A; Keratin-6A; keratin, epidermal type II, K6A; cytokeratin 6A			4.13E-07	1.79	20.20	4.10	60044.6
AHQ-6-10, 4854 - 4860	K.ADTLTDEINFLR.A	1408.53864	2	4.98E-07	0.86	3.42	-	898.5
AHQ-6-1, 5274 - 5275	K.ADTLTDEINFLR.A	1408.53864	2	4.13E-07	0.92	4.07	-	1100.4
AHQ-6-10, 3112 - 3116	R.TAAENEFVTLK.K	1223.35732	2	1.92E-04	0.87	3.32	-	1007.6
gi|4507869|ref|NP_003361.1|	vasodilator-stimulated phosphoprotein [Homo sapiens]			4.14E-07	1.85	20.22	7.10	39829.4
AHQ-6-8, 5781	K.VKEEIIEAFVQELR.K	1703.96061	2	4.14E-07	0.95	4.36	-	1443.6
AHQ-6-13-, 2978	R.VQIYHNPTANSFR.V	1547.69936	2	4.43E-04	0.90	3.69	-	788.8
gi|6598323|ref|NP_001485.2|	GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom			4.24E-07	2.73	30.24	11.90	50662.9
AHQ-6-8, 4941	R.NPYYGGESASITPLEDLYK.R	2118.28499	2	4.24E-07	0.96	4.75	-	1258.0
AHQ-6-8, 6217	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	6.41E-04	0.86	3.78	-	451.6
AHQ-6-7, 6118	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	6.90E-05	0.95	4.61	-	937.8
AHQ-6-8, 3828	R.TDDYLDQPCYETINR.I	1904.98887	2	1.37E-06	0.83	3.94	-	341.7
gi|20357529|ref|NP_005264.2|	guanine nucleotide-binding protein, beta-2 subunit; G protein, beta-2			4.25E-07	0.83	10.18	5.90	37330.8
AHQ-6-9, 4527	R.KACGDSTLTQITAGLDPVGR.I	2062.29094	2	4.25E-07	0.83	3.61	-	669.7
gi|25188179|ref|NP_005653.3|	voltage-dependent anion channel 3 [Homo sapiens]			4.65E-07	2.42	30.20	16.30	30658.4
AHQ-6-11, 4747 - 4752	K.LTLDTIFVPNTGK.K	1419.64771	2	3.30E-05	0.63	2.66	-	521.7
AHQ-6-10, 4294	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	3.29E-05	0.59	2.88	-	468.5
AHQ-6-10, 4198	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	4.65E-07	0.85	3.69	-	575.4

AHQ-6-10, 3700	K.YKVCNYGLTFTQK.W	1623.85410	2	2.65E-05	0.94	3.92	-	1056.3
gi|29732955|ref|XP_291603.1|	similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA			4.80E-07	0.38	10.20	16.80	11173.0
AHQ-6-9, 3839 - 3906	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.40E-06	0.83	3.96	-	1065.9
AHQ-6-9, 3967 - 3972	K.NISNASCTTNCIAPLAK.M	1838.05353	2	3.23E-05	0.89	3.60	-	1482.6
AHQ-6-10, 3826	K.NISNASCTTNCIAPLAK.M	1838.05353	2	4.80E-07	0.38	2.75	-	550.0
AHQ-6-11, 4049	K.NISNASCTTNCIAPLAK.M	1838.05353	2	8.48E-04	0.73	3.30	-	963.4
AHQ-6-9, 3594 - 3662	K.NISNASCTTNCIAPLAK.M	1838.05353	2	6.66E-05	0.62	3.17	-	836.8
gi|4504071|ref|NP_000164.1|	platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA			4.84E-07	4.47	50.20	10.70	68955.0
AHQ-6-3, 3920	K.AMTSNVASVQCDNSDKFPVYK.Y	2363.60999	2	3.19E-06	0.76	2.63	-	711.0
AHQ-6-4, 3793	K.AMTSNVASVQCDNSDKFPVYK.Y	2363.60999	2	3.65E-06	0.87	3.81	-	595.2
AHQ-6-4, 4865 - 4873	R.GLGELQELYLK.G	1263.46458	1	8.70E-04	0.23	2.34	-	422.1
AHQ-6-3, 4828	R.GLGELQELYLK.G	1263.46458	2	2.06E-05	0.93	3.90	-	1235.1
AHQ-6-1, 4967	R.GLGELQELYLK.G	1263.46458	2	2.55E-05	0.93	3.90	-	1166.2
AHQ-6-13-, 4049 - 4050	R.GQDLLSTVSIR.Y	1189.34410	2	2.61E-06	0.96	3.77	-	1807.5
AHQ-6-3, 4068	R.GQDLLSTVSIR.Y	1189.34410	2	2.43E-04	0.89	3.15	-	969.8
AHQ-6-13, 4167 - 4187	R.GQDLLSTVSIR.Y	1189.34410	2	4.84E-07	0.94	3.28	-	1621.1
AHQ-6-1, 4244	R.GQDLLSTVSIR.Y	1189.34410	2	9.20E-06	0.95	3.62	-	1356.0
AHQ-6-12, 2240 - 2317	R.GVLQGHLESSR.N	1183.29965	2	5.68E-05	0.62	2.64	-	502.0
AHQ-6-3, 2229 - 2306	R.GVLQGHLESSR.N	1183.29965	2	8.23E-06	0.92	3.14	-	1101.7
AHQ-6-4, 2185	R.GVLQGHLESSR.N	1183.29965	2	4.80E-05	0.80	2.86	-	754.9
AHQ-6-3, 4880	R.WLQDNAENVYVWK.Q	1665.82948	2	6.25E-06	0.92	3.68	-	1192.2
gi|8922673|ref|NP_060692.1|	parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]			4.90E-07	0.96	10.23	3.50	42243.4
AHQ-6-9, 4234 - 4292	R.DAFDTLFDHAPDK.L	1492.57096	2	4.90E-07	0.96	4.64	-	1462.1
gi|4826657|ref|NP_004333.1|	caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]			5.18E-07	1.74	20.21	5.80	62662.9
AHQ-6-6, 2812 - 2890	R.LEQYTSAIEGTK.S	1340.46107	2	6.58E-04	0.84	3.00	-	1018.0
AHQ-6-7, 3566	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	3.49E-04	0.57	2.74	-	300.6
AHQ-6-6, 3663	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	5.18E-07	0.90	4.11	-	739.1
gi|29727317|ref|XP_298144.1|	hypothetical protein XP_298144 [Homo sapiens]			5.20E-07	0.78	10.15	8.00	22108.6
AHQ-6-4, 6069	K.GEYNLTLDTALTSNLK.T	1753.93165	2	5.20E-07	0.78	2.94	-	907.8
AHQ-6-3, 5997	K.GEYNLTLDTALTSNLK.T	1753.93165	2	2.07E-04	0.65	2.59	-	774.9
gi|4506045|ref|NP_002718.1|	proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p			5.31E-07	1.77	20.17	10.10	17623.6
AHQ-6-2, 4028	K.GPM*FELLPGESNK.I	1435.62747	2	9.05E-06	0.89	3.41	-	903.3
AHQ-6-1, 4163	K.GPM*FELLPGESNK.I	1435.62747	2	6.29E-05	0.79	2.94	-	667.3
AHQ-6-1, 4492	K.GPM*FELLPGESNKIPR.L	1802.08775	3	5.31E-07	0.88	3.43	-	1018.1
gi|4505667|ref|NP_001074.1|	phosphodiesterase 5A isoform 1; cGMP-binding cGMP-specific 3',5'-cyclic			5.35E-07	0.85	10.15	1.10	100012.4
AHQ-6-5, 3749	K.VIGVCQLVNK.M	1131.37098	2	5.35E-07	0.85	3.09	-	491.3
gi|4505813|ref|NP_003737.1|	cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain			5.75E-07	1.46	20.15	37.10	10365.8
AHQ-6-14, 4504	K.NADM*SEEM*QQDSVECATQALEK.Y	2548.67874	2	2.32E-05	0.78	3.07	-	576.8
AHQ-6-14-, 3603 - 3610	K.YNPTWHCIVGR.N	1404.57820	2	5.75E-07	0.67	2.54	-	633.6
gi|24497612|ref|NP_116262.2|	nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr			5.77E-07	0.94	10.18	1.80	72695.6
AHQ-6-6, 6110	K.LGCDWVATIFSR.D	1426.62208	2	5.77E-07	0.94	3.60	-	1226.4
gi|4758644|ref|NP_004511.1|	kinesin heavy chain member 2; Kinesin, heavy chain, 2 [Homo sapiens] [M			5.87E-07	0.91	10.22	2.40	76926.6
AHQ-6-6, 4151	R.FDYAFDDSAPNEM*VYR.F	1957.06565	2	5.87E-07	0.91	4.32	-	529.5
gi|10346135|ref|NP_055083.1|	microtubule-associated protein, RP/EB family, member 2; T-cell activat			5.96E-07	0.56	10.26	6.10	37031.1
AHQ-6-12, 4715	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	5.96E-07	0.56	3.08	-	544.3
AHQ-6-9, 4510 - 4511	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	3	1.29E-06	0.94	5.14	-	1038.6
gi|5901922|ref|NP_008996.1|	CDC37 homolog [Homo sapiens]			5.99E-07	0.93	10.24	5.60	44468.0
AHQ-6-8, 6104	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	5.99E-07	0.93	4.82	-	536.5
gi|4503291|ref|NP_001346.1|	D-dopachrome tautomerase [Homo sapiens]			6.10E-07	1.79	20.19	22.90	12711.7
AHQ-6-14-, 5383 - 5410	R.FFPLESWQIGK.I	1352.56151	2	6.10E-07	0.88	3.29	-	680.2
AHQ-6-14-, 3556	K.RLCAAAASILGKPADR.V	1671.94666	3	1.03E-05	0.91	3.89	-	1475.4
gi|4505591|ref|NP_002565.1|	peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc			6.35E-07	4.36	50.21	30.70	22110.2
AHQ-6-11, 3831	R.GLFIIDDK.G	921.07223	2	5.94E-05	0.85	2.92	-	987.4
AHQ-6-11, 3167	K.HGEVCPAGWKPGSDTIKPDVQK.S	2408.67532	3	4.11E-04	0.90	4.12	-	1180.5
AHQ-6-11, 3603 - 3607	R.LVQAFQFTDK.H	1197.36469	2	6.35E-07	0.92	3.48	-	995.0
AHQ-6-11, 3412 - 3467	R.QITVNDLPVGR.S	1212.38090	2	1.58E-04	0.87	3.82	-	547.7
AHQ-6-11, 3155 - 3212	R.TIAQDYGVLK.A	1108.26945	2	1.16E-04	0.82	2.97	-	607.4
gi|5803227|ref|NP_006817.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype			6.47E-07	1.77	20.20	12.70	27764.1
AHQ-6-10, 6004	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	6.47E-07	0.83	3.14	-	817.3
AHQ-6-10, 2667 - 2742	K.YLIANATNPESK.V	1321.46099	2	2.51E-04	0.94	3.95	-	1515.8
gi|4503743|ref|NP_002009.1|	flightless I homolog [Homo sapiens]			6.60E-07	1.74	20.16	1.70	144750.1
AHQ-6-3, 5337	K.ADLTALFLPR.Q	1117.32271	2	1.67E-05	0.90	2.97	-	1413.2
AHQ-6-3, 5041	R.VPECLYTLPSLR.R	1449.69710	2	6.60E-07	0.84	3.08	-	754.3
gi|4504073|ref|NP_000398.1|	glycoprotein Ib beta polypeptide precursor [Homo sapiens]			6.84E-07	2.61	30.20	15.50	21717.6
AHQ-6-1, 4780 - 4788	R.LLPYLAEDELR.A	1332.52691	2	2.88E-06	0.89	3.04	-	594.7
AHQ-6-3, 4658	R.LLPYLAEDELR.A	1332.52691	2	1.50E-06	0.83	2.76	-	603.6
AHQ-6-5, 4567	R.LLPYLAEDELR.A	1332.52691	2	2.70E-06	0.78	2.55	-	465.9
AHQ-6-6, 4522	R.LLPYLAEDELR.A	1332.52691	2	4.69E-06	0.86	2.94	-	700.6
AHQ-6-8, 4384	R.LLPYLAEDELR.A	1332.52691	2	4.89E-05	0.90	2.82	-	660.0
AHQ-6-10, 4327 - 4328	R.LLPYLAEDELR.A	1332.52691	2	1.21E-06	0.84	3.04	-	518.5
AHQ-6-10, 4338 - 4342	R.LLPYLAEDELR.A	1332.52691	1	3.86E-04	0.35	2.70	-	205.6
AHQ-6-13-, 4556 - 4566	R.LLPYLAEDELR.A	1332.52691	2	1.26E-05	0.84	2.73	-	568.4
AHQ-6-13, 4676 - 4693	R.LLPYLAEDELR.A	1332.52691	2	3.91E-05	0.86	3.02	-	676.1
AHQ-6-12, 4492 - 4493	R.LLPYLAEDELR.A	1332.52691	2	2.58E-04	0.52	2.72	-	319.5
AHQ-6-11, 4399 - 4421	R.LLPYLAEDELR.A	1332.52691	2	4.04E-06	0.84	3.08	-	563.7
AHQ-6-11, 4104	R.LSLTDPLVAER.A	1214.39356	2	1.80E-04	0.95	3.65	-	1597.4
AHQ-6-11, 4123	R.LSLTDPLVAER.A	1214.39356	2	6.84E-07	0.96	3.97	-	1621.0
AHQ-6-11, 2463 - 2480	R.TAHLGANPWR.C	1123.24913	2	5.49E-05	0.81	2.82	-	680.9
gi|4759140|ref|NP_004243.1|	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulato			6.90E-07	0.87	10.18	3.90	38868.2
AHQ-6-13-, 3776	R.LLVVDPETDEQLQK.L	1627.81777	2	7.80E-07	0.91	3.32	-	811.6
AHQ-6-13, 3865 - 3908	R.LLVVDPETDEQLQK.L	1627.81777	2	6.90E-07	0.87	3.53	-	663.9
gi|22042381|ref|XP_065237.3|	similar to FKSG30 [Homo sapiens]			7.43E-07	1.31	20.16	8.30	42016.0
AHQ-6-14-, 2447 - 2520	K.QEYDESGPSIVHR.K	1517.58206	2	2.01E-05	0.46	2.58	-	270.4
AHQ-6-13-, 2497 - 2506	K.QEYDESGPSIVHR.K	1517.58206	2	3.05E-05	0.75	3.07	-	433.9
AHQ-6-8, 2283 - 2342	K.QEYDESGPSIVHR.K	1517.58206	2	7.43E-07	0.63	2.81	-	357.3
AHQ-6-9, 3563 - 3635	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	1.81E-04	0.29	2.53	-	351.3
AHQ-6-8, 3592 - 3656	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	8.49E-06	0.68	3.15	-	367.4
gi|4757996|ref|NP_004060.1|	adaptor-related protein complex 2, sigma 1 subunit isoform AP17; clathr			7.65E-07	0.94	10.21	10.60	17017.6
AHQ-6-13-, 5090	K.VYTVVDEM*FLAGEIR.E	1759.01650	2	7.65E-07	0.94	4.19	-	1250.6
gi|5453549|ref|NP_006397.1|	thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho			8.26E-07	2.82	30.21	18.50	30539.7
AHQ-6-10, 3580 - 3586	K.DYGVYLEDSGHTLR.G	1625.72052	2	1.42E-06	0.96	3.89	-	1522.4
AHQ-6-10, 3958 - 3967	K.HGEVCPAGWKPGSETIIPDPAGK.L	2405.67144	3	1.37E-05	0.93	4.18	-	1298.6
AHQ-6-10, 4680 - 4699	R.IPLLSDLTHQISK.D	1465.71961	2	8.26E-07	0.94	3.60	-	1287.7
gi|30147623|ref|XP_293669.2|	similar to actinin, alpha 4 [Homo sapiens]			8.28E-07	0.93	10.23	3.50	57794.4
AHQ-6-4, 3980 - 4035	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	8.28E-07	0.93	4.63	-	663.0
gi|5031937|ref|NP_005822.1|	nuclear domain 10 protein [Homo sapiens]			8.60E-07	0.22	10.15	6.10	52253.6
AHQ-6-11, 4389 - 4433	R.EYYTFMWVTLPIDLNNKSAKQQEVQFK.A	3322.77755	3	8.60E-07	0.22	3.05	-	250.6
gi|4505735|ref|NP_002611.1|	platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H			8.62E-07	0.97	10.25	14.40	11552.6
AHQ-6-14-, 3670	R.AEAEEDGDLQCLCVK.T	1739.86036	2	3.56E-04	0.93	3.78	-	1229.2
AHQ-6-14-, 3751 - 3810	R.AEAEEDGDLQCLCVK.T	1739.86036	2	8.62E-07	0.97	4.98	-	1666.4
AHQ-6-14, 4462	R.AEAEEDGDLQCLCVK.T	1739.86036	2	1.76E-05	0.92	3.72	-	803.6
gi|4557032|ref|NP_002291.1|	lactate dehydrogenase B [Homo sapiens]			8.79E-07	4.29	50.22	25.70	36638.3
AHQ-6-9, 6101 - 6111	K.GM*YGIENEVFLSLPCILNAR.G	2314.66682	2	3.39E-06	0.66	2.80	-	317.3
AHQ-6-9, 6113 - 6175	K.GYTNWAIGLSVADLIESM*LK.N	2198.52454	2	1.62E-04	0.95	4.25	-	1278.8
AHQ-6-9, 6255 - 6281	K.ITVVGVGQVGMACAISILGK.S	1975.40611	2	8.79E-07	0.85	4.31	-	463.5
AHQ-6-9, 3560	K.MVVESAYEVIK.L	1268.50463	2	3.37E-05	0.88	3.07	-	940.5
AHQ-6-13-, 6216	K.SLADELALVDVLEDK.L	1630.81843	2	3.39E-04	0.96	4.16	-	1407.0

<table>
<tr><td>AHQ-6-13, 6255</td><td>K.SLADELALVDVLEDK.L</td><td>1630.81843</td><td>2</td><td>6.97E-04</td><td>0.95</td><td>4.17</td><td>-</td><td>1321.7</td></tr>
<tr><td>gi|5174393|ref|NP_006001.1|</td><td>arginine-rich, mutated in early stage tumors; arginine-rich protein [Ho</td><td></td><td></td><td>8.97E-07</td><td>0.97</td><td>10.26</td><td>7.30</td><td>26906.2</td></tr>
<tr><td>AHQ-6-12, 5313 - 5316</td><td>K.DRDVTFSPATIENELIK.F</td><td>1949.15100</td><td>2</td><td>8.97E-07</td><td>0.97</td><td>5.24</td><td>-</td><td>1885.1</td></tr>
<tr><td>gi|4502171|ref|NP_000476.1|</td><td>adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho</td><td></td><td></td><td>9.00E-07</td><td>0.93</td><td>10.17</td><td>5.60</td><td>19607.6</td></tr>
<tr><td>AHQ-6-11, 3527</td><td>R.IDYIAGLDSR.G</td><td>1123.24098</td><td>2</td><td>9.00E-07</td><td>0.93</td><td>3.32</td><td>-</td><td>1348.7</td></tr>
<tr><td>gi|5803181|ref|NP_006810.1|</td><td>stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo</td><td></td><td></td><td>9.33E-07</td><td>1.58</td><td>20.19</td><td>5.90</td><td>62638.9</td></tr>
<tr><td>AHQ-6-6, 5974</td><td>K.ALSVGNIDDALQCYSEAIK.L</td><td>2069.27871</td><td>2</td><td>9.33E-07</td><td>0.82</td><td>3.72</td><td>-</td><td>464.4</td></tr>
<tr><td>AHQ-6-6, 4398</td><td>R.LAYINPDLALEEK.N</td><td>1489.69480</td><td>2</td><td>4.96E-06</td><td>0.76</td><td>3.21</td><td>-</td><td>690.6</td></tr>
<tr><td>gi|4758208|ref|NP_004081.1|</td><td>dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;</td><td></td><td></td><td>9.38E-07</td><td>1.73</td><td>20.21</td><td>15.70</td><td>20478.2</td></tr>
<tr><td>AHQ-6-11, 5129</td><td>K.ANDTQEFNLSAYFER.A</td><td>1805.88207</td><td>2</td><td>1.55E-05</td><td>0.78</td><td>3.54</td><td>-</td><td>729.1</td></tr>
<tr><td>AHQ-6-11, 3935</td><td>R.IYVGNASVAQDIPK.L</td><td>1475.67136</td><td>2</td><td>3.31E-06</td><td>0.94</td><td>3.91</td><td>-</td><td>1156.5</td></tr>
<tr><td>AHQ-6-11, 3671</td><td>R.IYVGNASVAQDIPK.L</td><td>1475.67136</td><td>2</td><td>9.38E-07</td><td>0.96</td><td>4.15</td><td>-</td><td>1411.6</td></tr>
<tr><td>gi|22060072|ref|XP_088293.2|</td><td>similar to cytochrome c [Homo sapiens]</td><td></td><td></td><td>9.77E-07</td><td>0.79</td><td>10.16</td><td>10.50</td><td>11887.8</td></tr>
<tr><td>AHQ-6-13-, 3669</td><td>K.TGPNLHGLFGR.K</td><td>1169.31780</td><td>2</td><td>9.77E-07</td><td>0.79</td><td>3.07</td><td>-</td><td>592.3</td></tr>
<tr><td>gi|28178832|ref|NP_002159.2|</td><td>isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat</td><td></td><td></td><td>1.01E-06</td><td>2.80</td><td>30.25</td><td>8.20</td><td>50909.0</td></tr>
<tr><td>AHQ-6-8, 3893</td><td>K.DLAGCIHGLSNVK.L</td><td>1385.57150</td><td>2</td><td>1.18E-06</td><td>0.94</td><td>3.94</td><td>-</td><td>1456.1</td></tr>
<tr><td>AHQ-6-8, 4936</td><td>R.LIDDMVAQVLK.S</td><td>1245.51421</td><td>2</td><td>1.01E-06</td><td>0.96</td><td>4.64</td><td>-</td><td>1355.3</td></tr>
<tr><td>AHQ-6-8, 2047 - 2090</td><td>K.TIEAEAAHGTVTR.H</td><td>1356.46696</td><td>2</td><td>7.03E-05</td><td>0.90</td><td>3.47</td><td>-</td><td>870.2</td></tr>
<tr><td>gi|30158852|ref|XP_301583.1|</td><td>similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa</td><td></td><td></td><td>1.02E-06</td><td>0.61</td><td>10.14</td><td>6.50</td><td>19197.0</td></tr>
<tr><td>AHQ-6-10, 3058</td><td>K.IWHHTFYNKLR.V</td><td>1515.74533</td><td>2</td><td>1.03E-04</td><td>0.56</td><td>2.57</td><td>-</td><td>692.5</td></tr>
<tr><td>AHQ-6-12, 3193</td><td>K.IWHHTFYNKLR.V</td><td>1515.74533</td><td>2</td><td>1.90E-05</td><td>0.63</td><td>2.89</td><td>-</td><td>537.4</td></tr>
<tr><td>AHQ-6-9, 2915 - 2971</td><td>K.IWHHTFYNKLR.V</td><td>1515.74533</td><td>2</td><td>1.02E-06</td><td>0.61</td><td>2.84</td><td>-</td><td>654.8</td></tr>
<tr><td>gi|30154839|ref|XP_301540.1|</td><td>similar to keratin 8; cytokeratin 8; keratin, type II cytoskeletal 8 [</td><td></td><td></td><td>1.02E-06</td><td>0.89</td><td>10.19</td><td>3.40</td><td>39331.0</td></tr>
<tr><td>AHQ-6-4, 4616</td><td>K.SLNNKFASFIDK.V</td><td>1384.56191</td><td>2</td><td>4.16E-05</td><td>0.83</td><td>3.49</td><td>-</td><td>581.5</td></tr>
<tr><td>AHQ-6-6, 4486</td><td>K.SLNNKFASFIDK.V</td><td>1384.56191</td><td>2</td><td>2.91E-04</td><td>0.64</td><td>2.80</td><td>-</td><td>613.9</td></tr>
<tr><td>AHQ-6-7, 4607</td><td>K.SLNNKFASFIDK.V</td><td>1384.56191</td><td>2</td><td>5.34E-05</td><td>0.87</td><td>3.08</td><td>-</td><td>789.2</td></tr>
<tr><td>AHQ-6-10, 4523 - 4536</td><td>K.SLNNKFASFIDK.V</td><td>1384.56191</td><td>2</td><td>1.02E-06</td><td>0.89</td><td>3.27</td><td>-</td><td>967.3</td></tr>
<tr><td>AHQ-6-11, 4388 - 4469</td><td>K.SLNNKFASFIDK.V</td><td>1384.56191</td><td>2</td><td>2.39E-06</td><td>0.92</td><td>3.84</td><td>-</td><td>1117.3</td></tr>
<tr><td>AHQ-6-2, 4643</td><td>K.SLNNKFASFIDK.V</td><td>1384.56191</td><td>2</td><td>4.78E-04</td><td>0.83</td><td>3.33</td><td>-</td><td>774.8</td></tr>
<tr><td>gi|4557801|ref|NP_000261.1|</td><td>purine nucleoside phosphorylase [Homo sapiens]</td><td></td><td></td><td>1.05E-06</td><td>3.32</td><td>40.22</td><td>16.30</td><td>32147.7</td></tr>
<tr><td>AHQ-6-9, 3724</td><td>K.HRPQVAIICGSGLGGLTDK.L</td><td>1981.26589</td><td>3</td><td>6.40E-05</td><td>0.97</td><td>3.89</td><td>-</td><td>3455.2</td></tr>
<tr><td>AHQ-6-9, 4475</td><td>K.LGADAVGMSTVPEVIVAR.H</td><td>1786.08666</td><td>2</td><td>7.65E-04</td><td>0.78</td><td>3.16</td><td>-</td><td>651.0</td></tr>
<tr><td>AHQ-6-13-, 4126</td><td>K.LGADAVGM*STVPEVIVAR.H</td><td>1802.08606</td><td>2</td><td>2.77E-04</td><td>0.93</td><td>4.31</td><td>-</td><td>838.5</td></tr>
<tr><td>AHQ-6-13, 4849</td><td>K.LGADAVGMSTVPEVIVAR.H</td><td>1786.08666</td><td>2</td><td>7.29E-05</td><td>0.84</td><td>3.06</td><td>-</td><td>847.7</td></tr>
<tr><td>AHQ-6-9, 3810 - 3879</td><td>K.LGADAVGM*STVPEVIVAR.H</td><td>1802.08606</td><td>2</td><td>2.11E-04</td><td>0.82</td><td>3.28</td><td>-</td><td>678.5</td></tr>
<tr><td>AHQ-6-13-, 4901 - 4902</td><td>R.VFGFSLITNK.V</td><td>1126.32960</td><td>2</td><td>1.27E-04</td><td>0.91</td><td>3.17</td><td>-</td><td>801.0</td></tr>
<tr><td>AHQ-6-9, 4552 - 4556</td><td>R.VFGFSLITNK.V</td><td>1126.32960</td><td>2</td><td>1.05E-06</td><td>0.69</td><td>2.91</td><td>-</td><td>428.5</td></tr>
<tr><td>gi|20149637|ref|NP_057526.2|</td><td>type 1 tumor necrosis factor receptor shedding aminopeptidase regulato</td><td></td><td></td><td>1.09E-06</td><td>0.89</td><td>10.15</td><td>1.40</td><td>107761.4</td></tr>
<tr><td>AHQ-6-4, 5956</td><td>R.NPVGYPLAWQFLR.K</td><td>1561.81077</td><td>2</td><td>1.09E-06</td><td>0.89</td><td>2.94</td><td>-</td><td>786.8</td></tr>
<tr><td>gi|18104989|ref|NP_002822.2|</td><td>protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t</td><td></td><td></td><td>1.09E-06</td><td>2.52</td><td>30.18</td><td>6.40</td><td>67560.7</td></tr>
<tr><td>AHQ-6-6, 5614</td><td>K.AGFWEEFESLQK.Q</td><td>1471.59489</td><td>2</td><td>5.66E-06</td><td>0.90</td><td>3.65</td><td>-</td><td>1052.6</td></tr>
<tr><td>AHQ-6-6, 4759</td><td>R.DLSGLDAETLLK.G</td><td>1275.43053</td><td>2</td><td>1.09E-06</td><td>0.89</td><td>3.24</td><td>-</td><td>1140.9</td></tr>
<tr><td>AHQ-6-6, 4342</td><td>R.TLQVSPLDNGDLIR.E</td><td>1541.73134</td><td>2</td><td>1.96E-05</td><td>0.73</td><td>2.90</td><td>-</td><td>654.5</td></tr>
<tr><td>gi|5729779|ref|NP_006701.1|</td><td>COP9 homolog [Homo sapiens]</td><td></td><td></td><td>1.11E-06</td><td>0.86</td><td>10.16</td><td>6.70</td><td>23225.5</td></tr>
<tr><td>AHQ-6-11, 3513</td><td>K.GILEQGWQADSTTR.M</td><td>1562.66596</td><td>2</td><td>1.11E-06</td><td>0.86</td><td>3.20</td><td>-</td><td>979.8</td></tr>
<tr><td>gi|9966825|ref|NP_065089.1|</td><td>HEF like Protein [Homo sapiens]</td><td></td><td></td><td>1.15E-06</td><td>1.63</td><td>20.27</td><td>4.30</td><td>86696.2</td></tr>
<tr><td>AHQ-6-13-, 4165</td><td>K.AISAFHGSLSSSQPAEIITQSK.L</td><td>2260.48935</td><td>2</td><td>2.64E-05</td><td>0.97</td><td>5.30</td><td>-</td><td>1593.0</td></tr>
<tr><td>AHQ-6-13-, 3477</td><td>K.LVDTLCMETQER.D</td><td>1496.68930</td><td>2</td><td>1.15E-06</td><td>0.66</td><td>2.82</td><td>-</td><td>518.1</td></tr>
<tr><td>gi|13489087|ref|NP_109591.1|</td><td>serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member</td><td></td><td></td><td>1.18E-06</td><td>0.82</td><td>10.17</td><td>5.00</td><td>42741.5</td></tr>
<tr><td>AHQ-6-8, 3830 - 3848</td><td>K.TYGADLASVDFQHASEDAR.K</td><td>2054.11949</td><td>2</td><td>1.18E-06</td><td>0.82</td><td>3.42</td><td>-</td><td>568.6</td></tr>
<tr><td>gi|5123454|ref|NP_005336.2|</td><td>heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind</td><td></td><td></td><td>1.20E-06</td><td>4.43</td><td>50.21</td><td>12.00</td><td>70037.7</td></tr>
<tr><td>AHQ-6-6, 5084 - 5098</td><td>K.AAAIGIDLGTTYSCVGVFQHGK.V</td><td>2267.54677</td><td>2</td><td>2.04E-06</td><td>0.80</td><td>3.71</td><td>-</td><td>609.8</td></tr>
<tr><td>AHQ-6-6, 4730 - 4792</td><td>K.AFYPEEISSM*VLTK.M</td><td>1631.87149</td><td>2</td><td>1.20E-06</td><td>0.86</td><td>3.46</td><td>-</td><td>733.8</td></tr>
<tr><td>AHQ-6-6, 3276</td><td>K.AQIHDLVLVGGSTR.I</td><td>1466.66769</td><td>2</td><td>2.71E-06</td><td>0.92</td><td>3.75</td><td>-</td><td>1201.8</td></tr>
<tr><td>AHQ-6-6, 4610</td><td>K.DAGVIAGLNVLR.I</td><td>1198.39736</td><td>2</td><td>8.29E-06</td><td>0.95</td><td>3.69</td><td>-</td><td>1550.9</td></tr>
<tr><td>AHQ-6-6, 4015 - 4018</td><td>K.NQVALNPQNTVFDAK.R</td><td>1659.82478</td><td>2</td><td>1.80E-06</td><td>0.89</td><td>4.01</td><td>-</td><td>540.6</td></tr>
<tr><td>gi|28269681|ref|NP_783313.1|</td><td>NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]</td><td></td><td></td><td>1.26E-06</td><td>1.56</td><td>20.17</td><td>24.10</td><td>14852.0</td></tr>
<tr><td>AHQ-6-13-, 4977</td><td>K.AYSTTSIASVAGLTAAAYR.V</td><td>1875.07212</td><td>2</td><td>6.80E-04</td><td>0.75</td><td>3.39</td><td>-</td><td>522.0</td></tr>
<tr><td>AHQ-6-13-, 4789 - 4812</td><td>R.VTLNPPGTFLEGVAK.V</td><td>1543.78883</td><td>2</td><td>1.26E-06</td><td>0.81</td><td>2.95</td><td>-</td><td>564.3</td></tr>
<tr><td>gi|6715607|ref|NP_000175.1|</td><td>G-gamma globin [Homo sapiens]</td><td></td><td></td><td>1.28E-06</td><td>0.92</td><td>10.18</td><td>6.80</td><td>16126.3</td></tr>
<tr><td>AHQ-6-13-, 4744 - 4745</td><td>R.LLVVYPWTQR.F</td><td>1275.52342</td><td>2</td><td>5.34E-06</td><td>0.93</td><td>3.41</td><td>-</td><td>1056.8</td></tr>
<tr><td>AHQ-6-14-, 4760</td><td>R.LLVVYPWTQR.F</td><td>1275.52342</td><td>2</td><td>6.49E-06</td><td>0.91</td><td>3.24</td><td>-</td><td>1152.0</td></tr>
<tr><td>AHQ-6-13, 4871 - 4899</td><td>R.LLVVYPWTQR.F</td><td>1275.52342</td><td>2</td><td>1.28E-06</td><td>0.92</td><td>3.57</td><td>-</td><td>1014.9</td></tr>
<tr><td>gi|16933542|ref|NP_002017.1|</td><td>fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s</td><td></td><td></td><td>1.40E-06</td><td>4.80</td><td>60.25</td><td>3.90</td><td>259222.8</td></tr>
<tr><td>AHQ-6-2, 4319</td><td>R.ITYGETGGNSPVQEFTVPGSK.S</td><td>2169.33354</td><td>2</td><td>5.42E-04</td><td>0.86</td><td>3.63</td><td>-</td><td>585.0</td></tr>
<tr><td>AHQ-6-2, 4844</td><td>R.NLQPASEYTVSLVAIK.G</td><td>1733.98671</td><td>2</td><td>6.41E-05</td><td>0.64</td><td>3.37</td><td>-</td><td>337.7</td></tr>
<tr><td>AHQ-6-1, 4910</td><td>R.NLQPASEYTVSLVAIK.G</td><td>1733.98671</td><td>2</td><td>8.41E-04</td><td>0.78</td><td>3.10</td><td>-</td><td>446.1</td></tr>
<tr><td>AHQ-6-3, 4812 - 4814</td><td>R.NLQPASEYTVSLVAIK.G</td><td>1733.98671</td><td>2</td><td>2.02E-04</td><td>0.75</td><td>3.13</td><td>-</td><td>313.9</td></tr>
<tr><td>AHQ-6-2, 5740</td><td>R.NTFAEVTGLSPGVTYYFK.V</td><td>1995.21983</td><td>2</td><td>1.40E-06</td><td>0.95</td><td>4.95</td><td>-</td><td>827.3</td></tr>
<tr><td>AHQ-6-3, 4556 - 4558</td><td>R.SSPVVIDASTAIDAPSNLR.F</td><td>1914.10666</td><td>2</td><td>9.26E-04</td><td>0.90</td><td>4.04</td><td>-</td><td>963.5</td></tr>
<tr><td>AHQ-6-2, 3742</td><td>R.SYTITGLQPGTDYK.I</td><td>1544.68732</td><td>2</td><td>4.78E-04</td><td>0.85</td><td>3.03</td><td>-</td><td>784.9</td></tr>
<tr><td>AHQ-6-1, 4344</td><td>R.TKTETITGFQVDAVPANGQTPIQR.T</td><td>2573.84359</td><td>3</td><td>9.85E-04</td><td>0.60</td><td>3.19</td><td>-</td><td>531.4</td></tr>
<tr><td>gi|4506467|ref|NP_002897.1|</td><td>radixin [Homo sapiens]</td><td></td><td></td><td>1.46E-06</td><td>0.94</td><td>10.22</td><td>2.60</td><td>68563.4</td></tr>
<tr><td>AHQ-6-6, 5175 - 5182</td><td>K.NQEQLAAELAEFTAK.I</td><td>1663.81020</td><td>2</td><td>1.46E-06</td><td>0.94</td><td>4.38</td><td>-</td><td>1057.6</td></tr>
<tr><td>gi|30149327|ref|XP_293672.2|</td><td>similar to ebiP7687 [Homo sapiens]</td><td></td><td></td><td>1.47E-06</td><td>1.74</td><td>20.22</td><td>4.80</td><td>59404.3</td></tr>
<tr><td>AHQ-6-5, 3692</td><td>K.HLEINPNHPIVETLR.Q</td><td>1783.02428</td><td>3</td><td>2.16E-04</td><td>0.87</td><td>4.35</td><td>-</td><td>1312.8</td></tr>
<tr><td>AHQ-6-5, 2891</td><td>K.SIYYITGESK.E</td><td>1161.28598</td><td>2</td><td>1.47E-06</td><td>0.87</td><td>2.74</td><td>-</td><td>820.1</td></tr>
<tr><td>gi|22043610|ref|XP_171081.1|</td><td>similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1; rh</td><td></td><td></td><td>1.49E-06</td><td>1.76</td><td>20.22</td><td>16.70</td><td>21543.1</td></tr>
<tr><td>AHQ-6-11, 3893</td><td>K.KLTPITYPQGLAMAK.E</td><td>1632.99216</td><td>2</td><td>3.64E-04</td><td>0.82</td><td>3.22</td><td>-</td><td>515.0</td></tr>
<tr><td>AHQ-6-11, 4567</td><td>K.PVNLGLWDTAGQEDYDR.L</td><td>1950.05441</td><td>2</td><td>1.49E-06</td><td>0.94</td><td>3.55</td><td>-</td><td>1242.3</td></tr>
<tr><td>gi|4507949|ref|NP_003395.1|</td><td>tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,</td><td></td><td></td><td>1.59E-06</td><td>3.63</td><td>40.27</td><td>23.60</td><td>28082.2</td></tr>
<tr><td>AHQ-6-10, 6251</td><td>R.EKIEAELQDICNDVLELLDK.Y</td><td>2389.66216</td><td>3</td><td>1.59E-06</td><td>0.93</td><td>4.07</td><td>-</td><td>1586.1</td></tr>
<tr><td>AHQ-6-10, 6238</td><td>K.IEAELQDICNDVLELLDK.Y</td><td>2132.37471</td><td>2</td><td>8.46E-06</td><td>0.96</td><td>5.45</td><td>-</td><td>969.2</td></tr>
<tr><td>AHQ-6-10, 4020</td><td>K.QTTVSNSQQAYQEAFEISK.K</td><td>2160.28351</td><td>2</td><td>2.19E-06</td><td>0.82</td><td>3.26</td><td>-</td><td>554.2</td></tr>
<tr><td>AHQ-6-10, 3866</td><td>K.QTTVSNSQQAYQEAFEISK.K</td><td>2160.28351</td><td>2</td><td>5.55E-04</td><td>0.38</td><td>2.63</td><td>-</td><td>265.7</td></tr>
<tr><td>AHQ-6-14-, 6222</td><td>K.TAFDEAIAELDTLNEESYK.D</td><td>2160.27705</td><td>2</td><td>3.71E-06</td><td>0.93</td><td>4.14</td><td>-</td><td>1239.0</td></tr>
<tr><td>gi|10835242|ref|NP_006249.1|</td><td>protein kinase, cGMP-dependent, type I; Protein kinase, cGMP-dependent</td><td></td><td></td><td>1.63E-06</td><td>0.81</td><td>10.18</td><td>1.70</td><td>77803.3</td></tr>
<tr><td>AHQ-6-6, 3432</td><td>R.EDSPSEDPVFLR.T</td><td>1391.46494</td><td>2</td><td>1.63E-06</td><td>0.81</td><td>3.00</td><td>-</td><td>646.9</td></tr>
<tr><td>gi|4507793|ref|NP_003339.1|</td><td>ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast); ubiquitin-conj</td><td></td><td></td><td>1.67E-06</td><td>0.80</td><td>10.13</td><td>7.20</td><td>17137.7</td></tr>
<tr><td>AHQ-6-13, 2532</td><td>K.TNEAQAIETAR.A</td><td>1204.27249</td><td>2</td><td>1.67E-06</td><td>0.80</td><td>2.69</td><td>-</td><td>1196.4</td></tr>
<tr><td>gi|24307955|ref|NP_055191.1|</td><td>p53 inducible protein [Homo sapiens]</td><td></td><td></td><td>1.68E-06</td><td>1.77</td><td>20.16</td><td>2.00</td><td>145660.2</td></tr>
<tr><td>AHQ-6-3, 5978</td><td>K.DFVSEAYLLTLGK.F</td><td>1456.66481</td><td>2</td><td>2.38E-04</td><td>0.94</td><td>3.13</td><td>-</td><td>1299.6</td></tr>
<tr><td>AHQ-6-3, 4758</td><td>K.YAPLHLVPLIER.L</td><td>1421.71166</td><td>2</td><td>1.68E-06</td><td>0.83</td><td>2.65</td><td>-</td><td>991.8</td></tr>
<tr><td>gi|7657056|ref|NP_055415.1|</td><td>EH-domain containing 3; EH domain containing 3 [Homo sapiens]</td><td></td><td></td><td>1.71E-06</td><td>2.72</td><td>30.22</td><td>10.50</td><td>60886.7</td></tr>
<tr><td>AHQ-6-7, 4272</td><td>K.ELVNNLAEIYGR.I</td><td>1391.55445</td><td>2</td><td>6.75E-04</td><td>0.84</td><td>3.48</td><td>-</td><td>635.0</td></tr>
<tr><td>AHQ-6-7, 5190</td><td>K.GGAFEGTLHGPFGHGYGEGAGEGIDDAEWVVAR.D</td><td>3317.48513</td><td>3</td><td>3.94E-05</td><td>0.93</td><td>4.47</td><td>-</td><td>1278.5</td></tr>
<tr><td>AHQ-6-7, 4562</td><td>K.LFEAEEQDLFR.D</td><td>1397.51432</td><td>2</td><td>1.71E-06</td><td>0.95</td><td>3.10</td><td>-</td><td>1965.5</td></tr>
<tr><td>gi|20539300|ref|XP_088391.4|</td><td>similar to tropomyosin 4 [Homo sapiens]</td><td></td><td></td><td>1.71E-06</td><td>2.56</td><td>30.19</td><td>9.40</td><td>18592.1</td></tr>
<tr><td>AHQ-6-12, 3696</td><td>R.KLVILEGELER.A</td><td>1299.54160</td><td>2</td><td>2.17E-05</td><td>0.81</td><td>3.22</td><td>-</td><td>806.4</td></tr>
<tr><td>AHQ-6-11, 3633</td><td>R.KLVILEGELER.A</td><td>1299.54160</td><td>2</td><td>1.71E-06</td><td>0.92</td><td>3.28</td><td>-</td><td>1128.3</td></tr>
<tr><td>AHQ-6-9, 3730</td><td>R.KLVILEGELERAEER.A</td><td>1785.03525</td><td>2</td><td>1.34E-04</td><td>0.84</td><td>3.58</td><td>-</td><td>630.9</td></tr>
<tr><td>AHQ-6-9, 3682 - 3738</td><td>R.KLVILEGELERAEER.A</td><td>1785.03525</td><td>2</td><td>1.26E-04</td><td>0.79</td><td>3.76</td><td>-</td><td>550.6</td></tr>
<tr><td>AHQ-6-9, 3758</td><td>K.LVILEGELER.A</td><td>1171.36868</td><td>2</td><td>1.58E-05</td><td>0.86</td><td>2.82</td><td>-</td><td>1032.8</td></tr>
<tr><td>gi|4503117|ref|NP_000091.1|</td><td>cystatin B; stefin B; liver thiol proteinase inhibitor; CPI-B [Homo sap</td><td></td><td></td><td>1.78E-06</td><td>1.69</td><td>20.20</td><td>33.70</td><td>11139.5</td></tr>
<tr><td>AHQ-6-13-, 3678</td><td>K.SQVVAGTNYFIK.V</td><td>1327.51036</td><td>2</td><td>1.67E-05</td><td>0.94</td><td>3.96</td><td>-</td><td>1120.9</td></tr>
<tr><td>AHQ-6-13-, 3697</td><td>R.VFQSLPHENKPLTLSNYQTNK.A</td><td>2459.74218</td><td>3</td><td>1.83E-04</td><td>0.77</td><td>3.38</td><td>-</td><td>587.0</td></tr>
<tr><td>AHQ-6-13, 3819</td><td>R.VFQSLPHENKPLTLSNYQTNK.A</td><td>2459.74218</td><td>3</td><td>1.78E-06</td><td>0.76</td><td>3.49</td><td>-</td><td>475.1</td></tr>
</table>

gi|7705369|ref|NP_057535.1|	coatomer protein complex, subunit beta; beta coat protein [Homo sapiens			1.82E-06	0.82	10.18	1.90	107141.5
AHQ-6-4, 4604	K.YEAAGTLVTLSSAPTAIK.A	1794.03892	2	1.82E-06	0.82	3.57	-	620.7
gi|4557701|ref|NP_000413.1|	keratin 17 [Homo sapiens]			1.85E-06	1.89	20.22	5.60	48105.4
AHQ-6-10, 2134	R.EVATNSELVQSGK.S	1362.46828	2	3.93E-06	0.92	3.87	-	1057.3
AHQ-6-10, 3070 - 3091	K.TRLEQEIATYR.R	1380.53166	2	1.85E-06	0.97	4.31	-	1960.2
gi|30153966|ref|XP_293932.2|	similar to hypothetical protein BC013073 [Homo sapiens]			1.87E-06	0.46	10.20	9.00	21711.3
AHQ-6-3, 3826	R.MIFTLFTINVSKDIRHH	2073.44997	2	1.87E-06	0.46	2.77	-	369.8
AHQ-6-6, 3555	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.60E-04	0.49	2.76	-	449.3
AHQ-6-7, 3818	R.MIFTLFTINVSKDIRHH	2073.44997	2	7.75E-04	0.20	2.61	-	286.7
AHQ-6-2, 3946 - 4023	R.MIFTLFTINVSKDIRHH	2073.44997	2	1.45E-04	0.53	3.10	-	364.5
gi|10835002|ref|NP_001166.1|	Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]			2.02E-06	3.58	40.24	27.90	22987.8
AHQ-6-10, 2451	K.APEPHVEEDDDDELDSK.L	1940.90995	2	2.02E-06	0.96	4.85	-	1335.6
AHQ-6-10, 5298 - 5312	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	2.46E-04	0.86	4.27	-	485.5
AHQ-6-12, 5260 - 5269	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	3.45E-04	0.81	3.59	-	791.6
AHQ-6-13, 5407 - 5412	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	5.80E-04	0.86	3.91	-	941.3
AHQ-6-10, 3202 - 3270	K.TLLGDGPVVTDPK.A	1312.49400	2	1.01E-05	0.95	4.27	-	1309.4
gi|4506353|ref|NP_002854.1|	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease			2.03E-06	1.29	20.15	3.40	97147.8
AHQ-6-5, 4700	K.EYAQNIWNVEPSDLK.I	1806.95311	2	2.03E-06	0.46	2.85	-	351.0
AHQ-6-5, 5231	K.LVIDQIDNGFFSPK.Q	1593.80471	2	6.37E-05	0.83	3.06	-	706.9
gi|7705296|ref|NP_057271.1|	bridging integrator 2; bridging integrator-2; breast cancer associated			2.07E-06	3.33	50.21	15.10	61746.8
AHQ-6-7, 2766	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	9.50E-04	0.75	3.54	-	441.6
AHQ-6-10, 2791	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	2.23E-06	0.91	4.25	-	685.9
AHQ-6-14-, 6175	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.07E-06	0.64	2.89	-	486.3
AHQ-6-6, 6194 - 6208	R.IGCYVTIFQNISNLR.D	1800.07167	2	4.39E-04	0.72	3.07	-	598.0
AHQ-6-7, 3983	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	5.15E-04	0.30	2.52	-	416.6
AHQ-6-10, 4212 - 4220	R.TM*EIYVAQFSEIK.E	1575.80793	2	2.00E-05	0.94	3.61	-	1416.7
AHQ-6-14-, 4876 - 4884	R.VSETLQEIYSSEWDGHEELK.A	2380.50595	3	6.40E-05	0.54	3.06	-	481.2
gi|4758638|ref|NP_004896.1|	peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi			2.22E-06	3.16	40.21	26.80	25034.8
AHQ-6-10, 4127	K.DGDSVM*VLPTIPEEEAK.K	1847.03409	2	8.66E-04	0.53	2.88	-	475.4
AHQ-6-10, 5838	R.FHDFLGDSWGILFSHPR.D	2032.24831	3	6.85E-05	0.93	4.27	-	1154.2
AHQ-6-10, 5428 - 5436	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	2.22E-06	0.88	3.72	-	650.4
AHQ-6-10, 3722	R.VVFVFGPDK.K	1008.19471	2	4.18E-05	0.81	2.70	-	522.5
gi|24797067|ref|NP_002107.3|	major histocompatibility complex, class I, A precursor; HLA-A1 class I			2.32E-06	0.94	10.21	3.00	40840.5
AHQ-6-8, 2143	R.YLENGKETLQR.T	1351.49032	2	2.32E-06	0.94	2.93	-	1739.5
gi|4759342|ref|NP_004808.1|	tight junction protein 2 (zona occludens 2); Friedreich ataxia region g			2.45E-06	0.95	10.23	1.60	124661.6
AHQ-6-7, 3540	R.TFLRPSPEDEAIYGPNTK.M	2036.23035	2	2.45E-06	0.95	4.58	-	1353.8
gi|30149460|ref|XP_210540.2|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			2.65E-06	0.92	10.15	4.00	29287.8
AHQ-6-6, 2412	K.HIYYITGETK.D	1225.37490	2	1.15E-05	0.73	3.02	-	342.1
AHQ-6-5, 2335 - 2408	K.HIYYITGETK.D	1225.37490	2	2.65E-06	0.92	2.99	-	907.6
gi|29742410|ref|XP_291183.1|	similar to TREM-like transcript 1 [Homo sapiens]			2.70E-06	0.94	20.25	10.30	32678.3
AHQ-6-14-, 4260	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	2.70E-06	0.47	2.51	-	215.7
AHQ-6-13-, 4108	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	3.52E-05	0.64	2.83	-	262.2
AHQ-6-13-, 4230	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	5.01E-05	0.64	2.77	-	349.7
AHQ-6-13, 4235 - 4311	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	3.90E-04	0.83	3.34	-	395.8
AHQ-6-13-, 3885 - 3936	R.VSLNILPPEEEEETHK.I	1865.03087	2	1.67E-04	0.47	2.59	-	317.8
gi|10337595|ref|NP_066283.1|	protein phosphatase 1A isoform 1; protein phosphatase 2C alpha isoform			2.75E-06	0.81	10.17	4.70	42447.5
AHQ-6-7, 3515	K.GPTEQLVSPEPEVHDIER.S	2033.18486	2	2.75E-06	0.81	3.31	-	626.7
gi|4504085|ref|NP_000399.1|	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA			2.80E-06	4.14	50.18	6.90	80814.1
AHQ-6-6, 3610	R.CKDVLTGQEFDVR.A	1568.73370	2	2.80E-06	0.89	3.54	-	981.0
AHQ-6-6, 3047	R.SMAEDTINAAVK.T	1250.40457	2	6.63E-05	0.89	3.02	-	1336.4
AHQ-6-6, 5802	R.VIFFLPWQK.M	1178.44934	2	6.38E-05	0.78	2.98	-	532.5
AHQ-6-6, 5808	R.YGAATANYMEVVSLLK.K	1731.00632	2	9.37E-05	0.72	3.12	-	586.7
AHQ-6-6, 5311	R.YGAATANYM*EVVSLLK.K	1747.00572	2	1.60E-04	0.85	3.31	-	820.6
gi|4759044|ref|NP_004841.1|	Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]			2.84E-06	3.16	40.20	5.30	160883.4
AHQ-6-3, 6193 - 6250	K.AFVGNQLPFIGFTYYR.E	1894.16356	2	4.30E-04	0.65	3.01	-	423.8
AHQ-6-3, 6028	R.ETAAPVVPELSSDIDSSNFDDIEDDKGDVETFPIPK.A	3894.11183	3	1.25E-04	0.70	3.26	-	288.4
AHQ-6-3, 5694	K.NLICAFLTDR.E	1224.41173	2	2.84E-06	0.91	3.99	-	807.5
AHQ-6-3, 3017	R.SIAEEQYSDLEK.E	1412.48092	2	6.35E-05	0.91	3.40	-	1053.6
gi|5453607|ref|NP_006420.1|	chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co			2.99E-06	1.83	20.20	6.60	59366.3
AHQ-6-7, 4731	K.LPIGDVATQYFADR.D	1566.73935	2	2.99E-06	0.91	3.59	-	1039.5
AHQ-6-7, 6182	K.SQDAEVGDGTTSVTLLAAEFLK.Q	2253.44875	2	8.75E-06	0.92	4.09	-	781.1
gi|4759086|ref|NP_004883.1|	vesicle trafficking protein sec22b [Homo sapiens]			2.99E-06	0.77	10.17	6.50	24740.4
AHQ-6-12, 3863	R.NLGSINTELQDVQR.I	1587.71696	2	2.99E-06	0.77	3.50	-	766.5
gi|7657649|ref|NP_055362.1|	tropomodulin 3 (ubiquitous) [Homo sapiens]			2.99E-06	0.92	10.18	3.10	39594.5
AHQ-6-12, 3319 - 3321	K.FGYQFTQQGPR.T	1329.44490	2	2.99E-06	0.92	3.62	-	836.7
gi|4758970|ref|NP_004150.1|	proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be			3.06E-06	0.88	10.17	5.10	29769.4
AHQ-6-11, 3945 - 4015	K.VESTDVSDLLHQYR.E	1662.78230	2	3.06E-06	0.88	3.35	-	1207.9
gi|4506417|ref|NP_002877.1|	RAP2B, member of RAS oncogene family [Homo sapiens]			3.12E-06	2.56	30.20	26.20	20494.2
AHQ-6-11, 5733 - 5736	K.ASVDELFAEIVR.Q	1349.51434	2	3.12E-06	0.88	3.53	-	1087.3
AHQ-6-11, 6107	K.EIEVDSSPSVLEILDTAGTEQFASM*R.D	2842.08287	3	2.96E-05	0.90	3.98	-	830.9
AHQ-6-11, 4064	K.YDPTIEDFYR.K	1319.40042	2	4.41E-05	0.78	2.54	-	453.4
gi|17402865|ref|NP_003303.2|	thiosulfate sulfurtransferase; rhodanese [Homo sapiens]			3.36E-06	0.52	10.13	6.40	33428.7
AHQ-6-9, 3746	R.FLGTEPEPDAVGLDSGHIR.G	2011.18089	2	3.36E-06	0.52	2.58	-	420.6
gi|17149842|ref|NP_004461.2|	FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep			3.38E-06	2.45	30.20	9.20	15649.2
AHQ-6-13-, 4105 - 4116	K.GWDQGLLGM*CEGEK.R	1597.75215	2	1.22E-04	0.85	3.49	-	625.2
AHQ-6-13-, 3861	R.KLVIPSELGYGER.G	1461.68782	2	3.53E-06	0.91	3.91	-	740.7
AHQ-6-13-, 4141	K.LVIPSELGYGER.G	1333.51491	2	3.38E-06	0.69	2.80	-	393.3
gi|4557890|ref|NP_000415.1|	keratin 5; Keratin-5; 58 kda cytokeratin; keratin, type II cytoskeletal			3.46E-06	0.86	10.19	1.70	62461.1
AHQ-6-10, 3282 - 3294	K.WTLLQEQGTK.T	1204.35723	2	3.46E-06	0.86	3.12	-	984.2
gi|11496885|ref|NP_005442.2|	enigma protein; LIM domain protein [Homo sapiens]			3.48E-06	0.86	10.17	2.60	49844.4
AHQ-6-12, 4628	K.VVLEGPAPWGFR.L	1328.54318	2	4.60E-05	0.50	2.51	-	422.7
AHQ-6-13-, 4716	K.VVLEGPAPWGFR.L	1328.54318	2	9.52E-05	0.89	3.45	-	755.1
AHQ-6-11, 4572	K.VVLEGPAPWGFR.L	1328.54318	2	3.48E-06	0.86	2.85	-	964.4
gi|4557377|ref|NP_000052.1|	Bruton agammaglobulinemia tyrosine kinase [Homo sapiens]			3.65E-06	0.54	10.13	2.10	76280.8
AHQ-6-6, 3308 - 3370	R.YVLDDEYTSSVGSK.F	1563.64427	2	3.65E-06	0.54	2.53	-	293.8
gi|7019375|ref|NP_037373.1|	formin homology 2 domain containing 1; FH1/FH2 domain-containing protei			3.67E-06	1.72	20.20	2.60	126496.5
AHQ-6-13-, 5850	K.SGLGDDLVQALGLSK.G	1473.65377	2	2.84E-04	0.88	2.94	-	1130.2
AHQ-6-14-, 5827	K.SGLGDDLVQALGLSK.G	1473.65377	2	3.67E-06	0.95	3.95	-	1442.3
AHQ-6-6, 5742	K.VDFEQLTENLGQLER.R	1791.93998	2	1.06E-04	0.77	3.03	-	1036.0
gi|11056061|ref|NP_066932.1|	thymosin, beta 4 [Homo sapiens]			3.94E-06	1.41	20.18	43.20	5052.6
AHQ-6-14-, 2498	K.NPLPSKETIEQEK.Q	1513.67476	2	1.83E-05	0.64	2.52	-	378.3
AHQ-6-14-, 2608	K.TETQEKNPLPSKETIEQEK.Q	2230.41519	3	3.94E-06	0.77	3.62	-	425.1
gi|5031599|ref|NP_005722.1|	actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub			3.94E-06	2.66	30.24	15.00	34332.8
AHQ-6-9, 3718	R.DNTINLIHTFR.D	1344.50101	2	3.09E-04	0.78	2.94	-	747.2
AHQ-6-9, 6131 - 6133	K.DTDAAVGDNIGYITFVLFPR.H	2185.42094	2	3.94E-06	0.96	4.77	-	1405.6
AHQ-6-9, 2703 - 2705	K.YFQFQEEGKEGENR.A	1761.82929	2	2.30E-04	0.91	3.74	-	1039.2
gi|29731325|ref|XP_293023.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			4.20E-06	0.82	10.18	6.00	28867.8
AHQ-6-12, 3968	K.AGPNTNGSQFFICTAK.T	1714.88050	2	4.20E-06	0.82	3.56	-	517.0
gi|4502211|ref|NP_001654.1|	ADP-ribosylation factor 6 [Homo sapiens]			4.23E-06	0.88	10.15	6.30	20082.0
AHQ-6-12, 3952 - 3957	K.FNVWDVGGQDK.I	1265.35598	2	4.23E-06	0.88	3.00	-	1028.4
gi|30149555|ref|XP_301154.1|	similar to heat shock protein 86 [Homo sapiens]			4.23E-06	0.84	10.25	10.60	15781.6
AHQ-6-5, 5635	K.HSQFIGYPITLFVEK.E	1780.05877	3	4.23E-06	0.84	3.34	-	1063.5
AHQ-6-5, 5621 - 5628	K.HSQFIGYPITLFVEK.E	1780.05877	2	2.34E-05	0.97	5.02	-	1206.2
gi|5032041|ref|NP_005605.1|	Ras homolog enriched in brain 2 [Homo sapiens]			4.29E-06	0.88	10.17	8.70	20497.4
AHQ-6-12, 4744 - 4803	K.ALAESWNAAFLESSAK.E	1695.85389	2	4.29E-06	0.88	3.39	-	888.2
gi|5453722|ref|NP_006321.1|	lysophospholipase I; lysophospholipase 1; lysophospholipid-specific lys			4.54E-06	1.70	20.14	10.90	24669.5
AHQ-6-11, 6068	K.LAGVTALSCWLPLR.A	1558.86992	2	5.17E-05	0.83	2.85	-	909.5

AHQ-6-11, 3612	K.TLVNPANVTFK.T	1204.40037	2	4.54E-06	0.87	2.87	-	786.0
gi|14149734|ref|NP_065174.1|	coronin, actin binding protein, 1B [Homo sapiens]			4.61E-06	0.80	10.19	5.90	54234.4
AHQ-6-6, 6218 - 6294	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	4.61E-06	0.80	3.84	-	472.4
gi|4757818|ref|NP_004879.1|	ATPase, H+ transporting, lysosomal, V1 subunit G isoform 1; vacuolar H(			4.62E-06	0.81	10.14	9.30	13757.4
AHQ-6-13, 3024 - 3031	K.EEAQAEIEQYR.L	1366.41548	2	4.62E-06	0.81	2.80	-	1133.5
gi|24234688|ref|NP_004125.3|	heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre			4.77E-06	0.94	10.25	2.80	73680.1
AHQ-6-6, 5538 - 5551	K.STNGDTFLGGEDFDQALLR.H	2057.16328	2	4.77E-06	0.94	4.92	-	542.0
gi|4757812|ref|NP_004880.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso			4.82E-06	1.80	20.20	25.50	10917.8
AHQ-6-13-, 5668 - 5673	R.DFSPSGIFGAFQR.G	1429.56124	2	4.82E-06	0.93	3.94	-	993.0
AHQ-6-14-, 5651 - 5670	R.DFSPSGIFGAFQR.G	1429.56124	2	4.16E-04	0.83	3.10	-	803.3
AHQ-6-13, 5757 - 5759	R.DFSPSGIFGAFQR.G	1429.56124	2	1.21E-04	0.93	3.56	-	1147.3
AHQ-6-14-, 5316	K.LGELPSWILM*R.D	1331.60876	2	2.03E-05	0.87	3.37	-	562.8
gi|5453710|ref|NP_006139.1|	LIM and SH3 protein 1; Lasp-1 [Homo sapiens]			4.89E-06	0.94	10.19	5.00	29717.0
AHQ-6-13-, 3838 - 3913	K.GFSVVADTPELQR.I	1419.56466	2	1.19E-04	0.87	3.29	-	982.3
AHQ-6-14-, 3895	K.GFSVVADTPELQR.I	1419.56466	2	4.89E-06	0.94	3.73	-	1339.7
AHQ-6-12, 3840	K.GFSVVADTPELQR.I	1419.56466	2	6.77E-05	0.74	2.86	-	744.5
gi|4506405|ref|NP_002872.1|	v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP			5.09E-06	1.64	20.20	7.80	23408.4
AHQ-6-10, 3810	K.AEEWGVQYVETSAK.T	1597.70708	2	6.02E-04	0.72	2.63	-	646.1
AHQ-6-10, 3563	R.SKAEEWGVQYVETSAK.T	1812.95765	2	5.09E-06	0.92	3.93	-	1002.4
gi|16950601|ref|NP_005956.2|	myosin light chain kinase isoform 6; myosin light chain kinase [Homo s			5.27E-06	0.86	10.18	1.00	110074.8
AHQ-6-6, 3472	K.VSDFYDIEER.L	1273.33005	2	5.27E-06	0.86	2.70	-	1026.7
AHQ-6-5, 3484 - 3559	K.VSDFYDIEER.L	1273.33005	2	8.12E-06	0.94	3.64	-	1117.9
gi|5174727|ref|NP_005989.1|	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring			5.41E-06	2.45	30.18	6.60	60330.4
AHQ-6-6, 3775	R.AVAQALEVIPR.T	1167.38326	2	5.41E-06	0.93	3.59	-	1526.7
AHQ-6-6, 4232 - 4298	K.IPGGIIEDSCVLR.G	1430.65218	2	7.41E-05	0.81	2.88	-	1055.7
AHQ-6-6, 2886 - 2903	R.TLIQNCGASTIR.L	1335.51249	2	3.52E-04	0.71	2.92	-	557.3
gi|6005786|ref|NP_009214.1|	monoglyceride lipase; lysophospholipase-like [Homo sapiens]			5.51E-06	0.88	10.18	4.50	34292.3
AHQ-6-14-, 5767 - 5774	K.LTVPFLLLQGSADR.L	1530.79329	2	5.51E-06	0.88	3.63	-	773.3
AHQ-6-13-, 5785	K.LTVPFLLLQGSADR.L	1530.79329	2	4.28E-05	0.86	3.04	-	734.4
gi|4758266|ref|NP_004748.1|	small inducible cytokine subfamily E, member 1; endothelial monocyte-ac			5.58E-06	0.89	10.18	3.80	34326.4
AHQ-6-13, 4876	K.GAEADQIIEYLK.Q	1350.49910	2	5.58E-06	0.89	3.57	-	1137.9
gi|4502219|ref|NP_001656.1|	ras homolog gene family, member G (rho G); RhoG [Homo sapiens]			5.63E-06	0.70	10.16	8.90	21338.4
AHQ-6-11, 4653	R.TVNLNLWDTAGQEEYDR.L	2025.12129	2	5.63E-06	0.70	2.72	-	608.6
gi|4758988|ref|NP_004152.1|	RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho			5.82E-06	0.84	10.21	9.30	22677.6
AHQ-6-11, 5539 - 5556	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	6.19E-05	0.86	3.59	-	642.2
AHQ-6-14-, 5599	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.10E-05	0.93	3.86	-	961.5
AHQ-6-11, 5425 - 5479	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	5.82E-06	0.84	3.32	-	705.2
gi|6005826|ref|NP_009160.1|	protein kinase C and casein kinase substrate in neurons 2; pacsin 2 [Ho			5.86E-06	2.34	30.20	7.80	55904.6
AHQ-6-6, 3230	K.AIYHDLEQSIR.A	1345.48578	2	6.79E-06	0.87	2.77	-	966.9
AHQ-6-6, 3982	R.ALYDYEGQEHDELSFK.A	1945.03140	2	5.86E-06	0.90	4.05	-	679.8
AHQ-6-6, 3144	K.HLNLSNVAGYK.A	1216.37124	2	5.78E-04	0.57	2.73	-	525.8
gi|18570595|ref|XP_095590.1|	similar to myosin regulatory light chain [Homo sapiens]			5.90E-06	0.93	10.18	8.90	13951.5
AHQ-6-11, 3123 - 3196	K.LNGTDPEDVIR.H	1229.32195	2	1.04E-04	0.94	3.23	-	1328.3
AHQ-6-12, 3059 - 3128	K.LNGTDPEDVIR.H	1229.32195	2	1.50E-04	0.88	3.09	-	994.3
AHQ-6-11, 3031 - 3087	K.LNGTDPEDVIR.H	1229.32195	2	5.90E-06	0.93	3.52	-	1101.5
gi|27480842|ref|XP_208238.1|	similar to bA92K2.2 (similar to ubiquitin) [Homo sapiens]			6.04E-06	0.86	10.16	8.30	17966.9
AHQ-6-14-, 2135 - 2172	K.IQDKEGIPPDQQR.L	1524.66087	2	1.64E-04	0.74	2.91	-	507.2
AHQ-6-14-, 1996 - 2059	K.IQDKEGIPPDQQR.L	1524.66087	2	6.04E-06	0.86	3.28	-	644.6
gi|4758032|ref|NP_004757.1|	coatomer protein complex, subunit beta 2 (beta prime); coatomer binding			6.05E-06	0.88	10.20	2.10	102486.5
AHQ-6-5, 5868	K.AAESLADPTEYENLFPGLK.E	2066.25322	2	6.05E-06	0.88	3.94	-	596.2
gi|30147536|ref|XP_293762.2|	similar to bridging integrator 2; bridging integrator-2; breast cancer			6.15E-06	0.70	10.17	3.90	46870.6
AHQ-6-5, 2843	R.TSLEVSPNPEPPEKPVR.T	1877.08801	3	6.15E-06	0.70	3.41	-	471.2
gi|29729345|ref|XP_290995.1|	similar to speckle-type POZ protein [Homo sapiens]			6.27E-06	0.79	10.22	10.90	18703.4
AHQ-6-2, 5750	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	1.88E-04	0.95	4.41	-	1450.7
AHQ-6-3, 5693 - 5712	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	4.74E-05	0.32	2.97	-	392.4
AHQ-6-4, 5777 - 5780	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	6.27E-06	0.79	3.78	-	886.8
AHQ-6-5, 5700	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	4.34E-04	0.52	3.64	-	433.1
AHQ-6-1, 5808	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	6.52E-05	0.36	2.58	-	586.6
gi|10834976|ref|NP_000572.1|	glutathione peroxidase 1 [Homo sapiens]			6.28E-06	2.25	30.21	24.40	21909.0
AHQ-6-11, 5131	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	6.28E-06	0.77	2.96	-	647.4
AHQ-6-11, 4801 - 4877	R.GLVVLGFPCNQFGHQENAK.N	2117.37312	2	2.72E-04	0.67	3.78	-	411.6
AHQ-6-11, 3801	R.PLAGGEPVSLGSLR.G	1353.54935	2	6.60E-05	0.81	3.06	-	787.9
gi|21618359|ref|NP_004095.3|	fatty acid synthase [Homo sapiens]			6.36E-06	1.77	20.27	1.70	273262.0
AHQ-6-3, 5640	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	6.53E-04	0.94	5.36	-	883.6
AHQ-6-2, 5676	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	6.48E-05	0.73	3.88	-	677.1
AHQ-6-1, 5710 - 5718	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	6.36E-06	0.93	4.66	-	1162.8
AHQ-6-1, 6371	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	5.79E-04	0.84	3.00	-	851.0
gi|30156116|ref|XP_301571.1|	similar to Dual specificity protein phosphatase 3 (Dual specificity pr			6.62E-06	0.91	10.18	1.70	64164.4
AHQ-6-11, 3631	K.DSGITYLGIK.A	1067.21733	2	6.62E-06	0.91	3.52	-	894.1
gi|6912238|ref|NP_036226.1|	peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]			6.73E-06	1.83	20.23	15.40	22026.2
AHQ-6-12, 6224 - 6229	K.ETDLLLDDSLVSIFGNR.R	1908.09888	2	6.73E-06	0.96	4.56	-	1382.4
AHQ-6-12, 5029 - 5032	K.GVLFGVPGAFTPGCSK.T	1595.84389	2	1.05E-04	0.87	3.49	-	668.7
gi|17986273|ref|NP_524144.1|	fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2			7.28E-06	0.95	10.21	8.20	21145.0
AHQ-6-12, 3281 - 3343	R.VFDKEGNGTVMGAELR.H	1723.93228	2	7.28E-06	0.95	4.19	-	1265.7
gi|7706429|ref|NP_057293.1|	unknown [Homo sapiens]			7.42E-06	0.88	10.18	10.00	16145.6
AHQ-6-13-, 5528	R.ELYLGLLYPTEDYK.V	1717.93937	2	7.42E-06	0.88	3.66	-	756.2
gi|15306356|ref|XP_035638.2|	similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan			7.44E-06	1.68	20.21	5.20	18795.1
AHQ-6-13-, 3532	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.02E-04	0.75	2.95	-	471.2
AHQ-6-12, 3484 - 3485	R.ESDVPLKTEEFEVTK.T	1751.91253	2	3.28E-04	0.92	4.15	-	602.0
AHQ-6-13-, 4594	K.SYLYFTQFK.A	1197.36315	2	7.44E-06	0.93	3.50	-	1111.6
gi|18765729|ref|NP_003816.2|	synaptosomal-associated protein 23 isoform SNAP23A; synaptosomal-assoc			7.75E-06	0.93	10.18	6.60	23353.9
AHQ-6-14-, 4379	R.ILGLAIESQDAGIK.T	1428.65614	2	7.75E-06	0.93	3.51	-	1269.9
gi|20551618|ref|XP_167021.1|	similar to calponin 2; Calonin 2 [Homo sapiens]			7.84E-06	0.82	10.17	3.70	47327.9
AHQ-6-12, 5063 - 5068	R.SM*QNWHQLENLSNFIK.A	2006.23095	2	7.84E-06	0.82	3.38	-	559.9
gi|14917115|ref|NP_002268.2|	type I hair keratin 1; Ha-1; hard keratin, type I, 1; keratin, hair, a			8.90E-06	0.42	10.15	3.60	47236.9
AHQ-6-5, 4051	R.LNVEVDAAPTVDLNR.V	1626.79310	2	8.90E-06	0.42	2.97	-	250.8
gi|10835189|ref|NP_000628.1|	glutathione reductase [Homo sapiens]			9.25E-06	1.22	20.18	8.10	51700.3
AHQ-6-7, 4490	K.ADFDNTVAIHPTSSEELVTLR	2316.50977	2	9.25E-06	0.39	2.68	-	251.8
AHQ-6-7, 2608	R.GHAAFTSDPKPTIEVSGK.K	1843.03012	2	8.01E-05	0.83	3.55	-	439.8
gi|22035600|ref|NP_004570.2|	mitogen-activated protein kinase kinase kinase kinase 2; Rab8 interact			9.54E-06	0.29	10.13	2.20	91555.4
AHQ-6-14-, 5919 - 5976	K.LDPGDDISSLQQEITILR.E	2014.22299	2	9.54E-06	0.29	2.51	-	231.8
gi|4501993|ref|NP_003650.1|	alkylglycerone phosphate synthase precursor [Homo sapiens]			9.97E-06	0.95	10.23	2.60	72911.4
AHQ-6-6, 5622 - 5632	R.GISDPLTVFEQTEAAAR.E	1805.96665	2	9.97E-06	0.95	4.68	-	778.3
gi|13569962|ref|NP_112243.1|	RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap			1.05E-05	1.69	20.24	15.90	22171.0
AHQ-6-11, 2204	R.MGPGAASGGERPNLK.I	1442.62650	2	1.05E-05	0.76	2.61	-	1194.9
AHQ-6-11, 5740	K.NATNVEQAFM*TMAAEIK.K	1886.14019	3	1.44E-05	0.93	4.79	-	1707.5
gi|5454028|ref|NP_006261.1|	related RAS viral (r-ras) oncogene homolog; Oncogene RRAS [Homo sapiens			1.06E-05	0.92	10.16	5.50	23480.3
AHQ-6-10, 5343	R.LNVDEAFEQLVR.A	1433.59133	2	1.06E-05	0.92	3.20	-	1411.9
gi|4504111|ref|NP_002077.1|	growth factor receptor-bound protein 2 [Homo sapiens]			1.06E-05	1.53	20.18	18.90	25206.2
AHQ-6-10, 6142 - 6144	R.DIEQVPQQPTYVQALFDFDPQEDGELGFR.R	3383.62169	3	1.06E-05	0.79	3.58	-	365.9
AHQ-6-10, 3340	K.VLNEECDQNWYK.A	1599.70313	2	4.30E-05	0.74	2.91	-	637.9
gi|4504107|ref|NP_002076.1|	glutathione peroxidase 4; phospholipid hydroperoxidase; sperm nucleus g			1.07E-05	0.79	10.14	6.10	22137.7
AHQ-6-12, 3405	R.YGPM*EEPLVIEK.D	1421.64070	2	1.07E-05	0.79	2.73	-	680.7
gi|29743626|ref|XP_297123.1|	hypothetical protein XP_297123 [Homo sapiens]			1.07E-05	0.49	10.14	13.80	13908.9
AHQ-6-13-, 6328	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	1.07E-05	0.49	2.85	-	618.0
AHQ-6-12, 6267	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	5.40E-04	0.49	2.65	-	675.7
gi|4557797|ref|NP_000260.1|	non-metastatic cells 1 protein [Homo sapiens]			1.12E-05	3.45	40.21	29.60	17148.6

AHQ-6-12, 4073	K.DRPFFAGLVK.Y	1150.35439	2	2.54E-05	0.88	3.12	-	1147.1
AHQ-6-12, 3055 - 3057	R.GLVGEIIKR.F	985.20582	2	1.76E-05	0.90	3.30	-	1086.9
AHQ-6-12, 2248 - 2249	R.NIIHGSDSVESAEK.E	1486.56627	2	6.12E-04	0.89	4.20	-	998.9
AHQ-6-12, 3043 - 3103	R.TFIAIKPDGVQR.G	1345.57205	2	1.12E-05	0.78	3.24	-	627.6
gi|9966867|ref|NP_065123.1|	eIF-5A2 protein; eIF5AII [Homo sapiens]			1.13E-05	1.83	20.30	19.60	16793.1
AHQ-6-12, 3640	K.KYEDICPSTHNMDVPNIK.R	2163.41723	3	1.83E-04	0.97	5.97	-	1458.9
AHQ-6-12, 4663	K.VHLVGIDIFTGK.K	1299.54329	2	1.13E-05	0.86	2.99	-	791.1
gi|13129018|ref|NP_076956.1|	hypothetical protein MGC3077 [Homo sapiens]			1.13E-05	0.91	10.17	5.30	21007.6
AHQ-6-11, 3792	K.VSEEIEDIIK.K	1175.31097	2	1.13E-05	0.91	3.48	-	1236.3
gi|22538814|ref|NP_002976.2|	small inducible cytokine A5 precursor; T-cell specific protein p288; T			1.16E-05	1.26	20.18	20.90	9989.6
AHQ-6-14-, 3742 - 3758	K.CSNPAVVFVTR.K	1251.43718	2	1.16E-05	0.92	3.52	-	879.3
AHQ-6-14, 4586	K.CSNPAVVFVTR.K	1251.43718	2	8.24E-05	0.81	2.77	-	835.1
AHQ-6-14-, 2434	K.EYFYTSGK.C	995.06653	1	1.50E-05	0.34	2.32	-	242.6
gi|4503643|ref|NP_000121.1|	coagulation factor V precursor; labile factor; factor V Leiden [Homo sa			1.20E-05	3.21	40.19	2.50	251716.5
AHQ-6-4, 3197	R.AEVDDVIQVR.F	1144.26019	2	1.20E-05	0.93	3.31	-	1767.9
AHQ-6-5, 3117	K.EVIITGIQTQGAK.H	1358.56590	2	2.06E-05	0.90	3.44	-	997.0
AHQ-6-3, 3737 - 3801	K.LSEGASYLDHTFPAEK.M	1765.90099	2	4.10E-04	0.70	3.21	-	510.4
AHQ-6-1, 4050	R.M*PM*GLSTGIISDSQIK.A	1710.99516	2	4.15E-04	0.68	2.62	-	609.9
gi|20127528|ref|NP_037459.2|	parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]			1.26E-05	3.47	40.21	15.90	41714.0
AHQ-6-9, 3250 - 3275	K.ARPEDVVNLDLK.S	1369.54878	2	1.26E-05	0.81	3.64	-	538.0
AHQ-6-9, 4943	R.DAFDTLFDHAPDKLSVVK.K	2019.24293	2	6.22E-05	0.89	3.44	-	946.3
AHQ-6-9, 3404 - 3458	K.LNVAEVTQSEIGQK.Q	1516.67865	2	2.29E-05	0.82	2.82	-	966.4
AHQ-6-9, 6083 - 6095	K.VLLDWINDVLVEER.I	1713.95549	2	3.20E-05	0.94	4.12	-	1164.8
gi|23510338|ref|NP_003325.2|	ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity			1.31E-05	1.70	20.26	3.40	117848.1
AHQ-6-4, 5604	R.NEEDAAELVALAQAVNAR.A	1885.02541	2	5.14E-05	0.94	4.02	-	1548.9
AHQ-6-4, 6132	K.SLVASLAEPDFVVTDFAK.F	1910.15638	2	1.31E-05	0.77	3.39	-	524.7
gi|19923233|ref|NP_002970.2|	sterol carrier protein 2 [Homo sapiens]			1.31E-05	0.83	10.18	2.20	58993.3
AHQ-6-13-, 2778	K.LQNLQLQPGNAK.L	1324.51124	2	1.31E-05	0.83	3.37	-	734.6
gi|4506363|ref|NP_002861.1|	RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s			1.33E-05	1.83	20.17	10.80	22774.0
AHQ-6-11, 3543	K.LLLIGDSGVGK.T	1072.28025	2	5.97E-04	0.64	2.67	-	612.0
AHQ-6-11, 3644	K.LLLIGDSGVGK.T	1072.28025	2	1.33E-05	0.93	3.32	-	1200.2
AHQ-6-13-, 3784	K.LLLIGDSGVGK.T	1072.28025	2	9.35E-04	0.72	2.72	-	800.1
AHQ-6-14-, 3775	K.LLLIGDSGVGK.T	1072.28025	2	1.88E-05	0.89	3.08	-	955.0
AHQ-6-11, 3047	K.LQVWDTAGQER.F	1303.40576	2	1.53E-05	0.90	3.36	-	1120.8
gi|4758618|ref|NP_004684.1|	cytokeratin type II [Homo sapiens]			1.36E-05	1.69	20.22	3.60	59503.9
AHQ-6-10, 2479	R.AEAESWYQTK.Y	1213.27785	2	4.35E-04	0.72	2.55	-	780.4
AHQ-6-10, 2584 - 2586	K.YEELQVTAGR.H	1166.26586	2	1.36E-05	0.98	4.43	-	2385.9
gi|25306267|ref|NP_001700.2|	brain-derived neurotrophic factor isoform a preproprotein [Homo sapien			1.41E-05	0.88	10.17	6.10	27817.8
AHQ-6-13-, 3645	K.TAVDMSGGTVTVLEK.V	1508.71993	2	1.41E-05	0.88	3.32	-	992.3
gi|5031569|ref|NP_005727.1|	ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r			1.52E-05	1.71	20.26	9.00	42613.4
AHQ-6-8, 3761 - 3778	R.ACYLSINPQKDETLETEK.A	2141.34169	2	1.52E-05	0.92	4.59	-	609.6
AHQ-6-8, 6218 - 6220	R.TLFSNIVLSGGSTLFK.G	1684.95729	2	9.09E-04	0.79	3.31	-	557.5
gi|12545410|ref|NP_031394.1|	RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,			1.54E-05	1.82	20.25	5.90	95912.5
AHQ-6-5, 5989	R.FFAPAILSPNLFQLTPHHTDPQTSR.T	2837.18380	3	1.54E-05	0.86	3.56	-	1184.6
AHQ-6-5, 4921	K.SVYDGPEQEEYSTFVIDDPQETYK.T	2840.94215	2	5.56E-04	0.96	4.95	-	1133.4
gi|19743813|ref|NP_002202.2|	integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib			1.56E-05	2.40	30.24	6.00	88414.9
AHQ-6-3, 4926 - 4997	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	1.56E-05	0.93	4.14	-	1315.2
AHQ-6-3, 6424	K.LSENNIQTIFAVTEEFQPVYK.E	2471.74650	3	2.58E-05	0.96	4.78	-	1926.9
AHQ-6-3, 3244	K.WDTGENPIYK.S	1223.31587	2	5.75E-05	0.51	2.73	-	487.9
gi|21361827|ref|NP_062826.2|	putative methyltransferase M6A; putative methyltransferase [Homo sapie			1.59E-05	0.74	10.18	3.10	64473.6
AHQ-6-3, 3993	K.YVHYEIDACMDSEAPGSK.D	2074.23418	3	1.59E-05	0.74	3.53	-	805.9
gi|27764873|ref|NP_057070.2|	cytokine receptor-like factor 3; cytokine receptor-like molecule 9; cy			1.61E-05	1.62	20.15	6.10	49737.6
AHQ-6-7, 4422	R.APTYFCGQTLTFR.V	1563.75875	2	3.34E-05	0.81	2.85	-	676.8
AHQ-6-7, 3234	K.LIEHGVNTAEDLVR.E	1566.74089	2	1.61E-05	0.81	2.87	-	961.7
gi|4506063|ref|NP_002725.1|	protein kinase, cAMP-dependent, regulatory, type I, alpha; tissue-speci			1.63E-05	0.43	10.18	4.50	42981.4
AHQ-6-12, 4860 - 4871	R.LTVADALEPVQFEDGQK.I	1861.04222	2	1.63E-05	0.43	2.93	-	290.9
gi|4502643|ref|NP_001753.1|	chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing			1.67E-05	0.77	10.15	3.00	58023.9
AHQ-6-7, 4508	K.VLAQNSGFDLQETLVK.I	1762.98491	2	1.67E-05	0.77	3.10	-	680.1
gi|4557675|ref|NP_000201.1|	integrin alpha chain, alpha 6 [Homo sapiens]			1.67E-05	2.21	30.16	2.90	119509.5
AHQ-6-4, 3393	K.FGSCQQGVAATFTK.D	1503.66172	2	1.61E-04	0.84	3.07	-	853.9
AHQ-6-4, 2967	K.LETTSNQDNLAPITAK.A	1716.87141	2	4.01E-04	0.72	3.23	-	453.3
AHQ-6-3, 5117	K.LIATFPDTLTYSAYR.E	1732.95727	2	1.67E-05	0.65	2.99	-	402.6
gi|5031985|ref|NP_005787.1|	nuclear transport factor 2; placental protein 15 [Homo sapiens]			1.75E-05	0.70	10.19	11.00	14478.4
AHQ-6-14-, 4344	K.NINDAWVCTNDM*FR.L	1773.92828	2	1.75E-05	0.70	3.23	-	384.4
gi|4504743|ref|NP_002194.1|	integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o			1.76E-05	0.87	10.21	1.90	129294.4
AHQ-6-4, 4915	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	1.76E-05	0.87	3.67	-	732.9
AHQ-6-3, 4860	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	3.05E-05	0.90	4.23	-	565.3
gi|14211923|ref|NP_115982.1|	PKCI-1-related HIT protein [Homo sapiens]			1.78E-05	1.69	20.20	22.70	17161.6
AHQ-6-13-, 5872	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	1.78E-05	0.79	3.11	-	912.8
AHQ-6-13-, 5818 - 5824	K.SLPADILYEDQQCLVFR.D	2069.32354	2	3.14E-05	0.90	4.03	-	806.8
AHQ-6-13, 5815 - 5892	K.SLPADILYEDQQCLVFR.D	2069.32354	2	2.64E-04	0.32	2.58	-	176.8
gi|19913424|ref|NP_001681.2|	ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT			1.84E-05	2.64	30.27	8.10	68303.7
AHQ-6-6, 4130	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	4.42E-04	0.90	3.74	-	845.3
AHQ-6-6, 2347	K.LPANHPLLTGQR.V	1317.52194	2	5.02E-04	0.78	3.08	-	658.5
AHQ-6-6, 5152	R.VGSHITGGDIYGIVSENSLIK.H	2160.41292	2	1.84E-05	0.97	5.41	-	1250.5
gi|14745898|ref|XP_016144.2|	similar to tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat			1.94E-05	0.84	10.15	7.50	18201.0
AHQ-6-11, 6088	K.LLCCDILDVLDK.N	1479.74157	2	1.94E-05	0.84	2.92	-	473.7
gi|4557241|ref|NP_001095.1|	skeletal muscle specific actinin, alpha 3 [Homo sapiens]			1.96E-05	0.86	10.17	0.90	103293.7
AHQ-6-4, 3023	K.ALDFIASK.G	865.00867	2	6.26E-05	0.90	3.41	-	579.5
AHQ-6-5, 2984	K.ALDFIASK.G	865.00867	2	1.96E-05	0.86	2.82	-	572.8
AHQ-6-4, 2972 - 3035	K.ALDFIASK.G	865.00867	1	1.15E-04	0.57	2.21	-	802.9
gi|29731857|ref|XP_293042.1|	similar to ribosomal protein S12; 40S ribosomal protein S12 [Homo sapi			1.97E-05	0.87	10.17	8.90	19543.6
AHQ-6-13-, 4478	K.LVEALCAEHQINLIK.V	1753.05645	2	1.97E-05	0.87	3.50	-	795.7
gi|4503531|ref|NP_001958.1|	eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens] [			2.17E-05	0.93	10.20	3.90	46393.9
AHQ-6-8, 3454	R.GIYAYGFEKPSAIQQR.A	1829.04828	2	2.17E-05	0.93	4.01	-	974.8
gi|4507383|ref|NP_001052.1|	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil			2.18E-05	2.59	30.20	7.50	60675.3
AHQ-6-7, 2448	R.EAAQDCEVLGQR.I	1377.46310	2	5.26E-04	0.72	2.97	-	741.1
AHQ-6-7, 4075	R.FQACPETQVPLQLESK.S	1877.10807	2	2.18E-05	0.93	3.91	-	912.9
AHQ-6-7, 2984	R.YAESGDAFDIQR.C	1372.42172	2	4.03E-05	0.94	3.55	-	1385.9
gi|5803201|ref|NP_006818.1|	transmembrane trafficking protein [Homo sapiens]			2.26E-05	0.93	10.18	5.00	24975.8
AHQ-6-11, 4105	R.IPDQLVILDM*K.H	1301.57773	2	2.26E-05	0.93	3.50	-	1300.5
gi|9257232|ref|NP_000598.1|	orosomucoid 1 precursor; Orosomucoid-1 (alpha-1-acid glycoprotein-1); a			2.33E-05	0.82	10.16	7.00	23511.4
AHQ-6-8, 5785	K.EQLGEFYEALDCLR.I	1744.90337	2	3.12E-04	0.87	3.22	-	903.1
AHQ-6-1, 5895 - 5964	K.EQLGEFYEALDCLR.I	1744.90337	2	2.33E-05	0.82	3.19	-	635.9
gi|21735621|ref|NP_005909.2|	mitochondrial malate dehydrogenase precursor [Homo sapiens]			2.36E-05	0.95	10.26	6.50	35503.0
AHQ-6-13-, 5428	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	3	2.36E-05	0.95	5.10	-	1283.6
gi|4502565|ref|NP_001740.1|	calpain, small subunit 1; calpain, small polypeptide; calcium-dependent			2.38E-05	0.69	10.20	5.60	28315.5
AHQ-6-10, 2360	R.THYSNIEANESEEVR.Q	1778.81502	2	2.38E-05	0.69	2.59	-	687.4
gi|5453902|ref|NP_006214.1|	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting, 4 (parv			2.41E-05	0.53	10.16	22.90	13809.9
AHQ-6-13, 5727	R.GSM*VGPFQEAAFALPVSGM*DKPVFTDPPVK.T	3153.61740	3	2.41E-05	0.53	3.17	-	319.8
gi|4502011|ref|NP_000467.1|	adenylate kinase 1 [Homo sapiens]			2.52E-05	1.75	20.19	17.00	21634.7
AHQ-6-11, 5020	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	2	2.52E-05	0.80	3.52	-	635.2
AHQ-6-11, 3737	K.YGYTHLSTGDLLR.S	1496.64912	2	5.08E-05	0.96	3.71	-	1841.1
gi|29732170|ref|XP_291550.1|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			2.56E-05	1.82	20.20	13.60	13262.9
AHQ-6-5, 4080	K.HLEINPDHSIIETLR.Q	1787.99770	3	2.56E-05	0.95	4.04	-	1886.8
AHQ-6-5, 3656	K.KHLEINPDHSIIETLR.Q	1916.17061	2	7.08E-05	0.87	3.79	-	674.6
gi|19913373|ref|NP_079536.2|	G6B protein isoform G6b-A precursor; G6B protein; immunoglobulin recep			2.61E-05	0.90	10.14	3.80	25002.6

AHQ-6-11, 2573 - 2648	R.TVLHVLGDR.T	1010.17224	2	3.54E-04	0.89	2.74	-	1176.6
AHQ-6-10, 2512	R.TVLHVLGDR.T	1010.17224	2	2.61E-05	0.90	2.62	-	1262.0
gi|30153076|ref|XP_301485.1|	similar to ubiquitin-conjugating enzyme E2N; 1500026J17Rik [Homo sapie			2.67E-05	0.83	10.14	9.90	12235.8
AHQ-6-12, 2267 - 2303	K.TDEAQAIETAR.A	1205.25725	2	2.67E-05	0.83	2.82	-	908.2
gi|14043026|ref|NP_003752.2|	vesicle-associated membrane protein 8; endobrevin [Homo sapiens]			2.70E-05	0.95	10.21	14.00	11438.2
AHQ-6-13-, 2610	R.NKTEDLEATSEHFK.T	1649.74039	3	2.70E-05	0.95	4.14	-	1611.5
gi|30153852|ref|XP_171113.3|	similar to Moesin (Membrane-organizing extension spike protein) [Homo			2.73E-05	0.96	10.23	9.30	15601.7
AHQ-6-6, 2084 - 2087	R.RKPDTIEVQQMK.A	1473.72364	2	2.73E-05	0.96	4.59	-	1402.9
gi|29736622|ref|XP_293924.1|	similar to cytoplasmic beta-actin [Homo sapiens]			2.80E-05	0.87	10.20	8.00	42002.9
AHQ-6-8, 5793	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	2.80E-05	0.87	3.91	-	1263.3
gi|4505773|ref|NP_002625.1|	prohibitin [Homo sapiens]			2.88E-05	0.88	10.16	5.10	29803.9
AHQ-6-10, 4042	R.KLEAAEDIAYQLSR.S	1607.78978	2	2.88E-05	0.88	3.30	-	863.8
gi|18375655|ref|NP_055184.2|	protein tyrosine phosphatase, non-receptor type 18; brain-derived phos			3.07E-05	0.79	10.17	6.50	50482.1
AHQ-6-13, 4933	R.VPADQSPAGSGAYEDVAGGAQTGGLGFNLR.I	2864.03331	3	3.07E-05	0.79	3.45	-	876.8
gi|21361619|ref|NP_061882.2|	TOLLIP protein; Toll-interacting protein [Homo sapiens]			3.09E-05	0.90	10.20	5.10	30281.6
AHQ-6-11, 5328 - 5387	R.GPVYIGELPQDFLR.I	1604.83072	2	3.09E-05	0.90	3.99	-	771.5
gi|18426915|ref|NP_004386.2|	drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [			3.23E-05	1.85	20.25	5.40	71438.9
AHQ-6-13-, 4029	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	3.23E-05	0.94	4.99	-	834.1
AHQ-6-13-, 5326	K.YVLINWVGEDVPDAR.K	1746.94404	2	1.56E-04	0.91	4.10	-	763.8
gi|29788766|ref|NP_064424.2|	tubulin, beta polypeptide 4, member Q [Homo sapiens]			3.39E-05	1.30	20.26	10.90	48377.2
AHQ-6-13, 4564	R.AVLVDLEPGTMDSVR.S	1602.83495	2	4.88E-04	0.44	2.75	-	352.4
AHQ-6-7, 5636	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3315.65550	3	3.39E-05	0.85	3.80	-	789.4
gi|22748619|ref|NP_689476.1|	tropomyosin 3 [Homo sapiens]			3.43E-05	1.66	20.17	9.90	28222.6
AHQ-6-12, 3421	R.KLVIIEGDLER.T	1285.51492	2	3.27E-04	0.79	2.85	-	771.2
AHQ-6-10, 2155 - 2232	K.YSQKEDKYEEEIK.I	1689.80129	2	3.43E-05	0.87	3.37	-	1077.8
gi|4557415|ref|NP_000062.1|	cystathionine-beta-synthase; serine sulfhydrase; beta-thionase; methylc			3.52E-05	0.59	10.15	2.50	60586.2
AHQ-6-3, 3936	K.FLSDRWMLQKGFLK.E	1770.13375	2	3.52E-05	0.59	2.99	-	497.2
gi|4826762|ref|NP_005134.1|	haptoglobin [Homo sapiens]			3.55E-05	0.88	10.17	3.40	45205.0
AHQ-6-8, 4018	K.YVMLPVADQDQCIR.H	1709.96880	2	3.55E-05	0.88	3.41	-	595.9
gi|27500008|ref|XP_208872.1|	similar to tropomyosin 3 [Homo sapiens]			3.56E-05	0.93	10.24	6.50	28954.4
AHQ-6-9, 3674 - 3675	R.ALKDEEKMELQELQLK.E	1946.25520	2	3.56E-05	0.93	4.77	-	951.9
gi|4557251|ref|NP_001101.1|	a disintegrin and metalloprotease domain 10 [Homo sapiens]			3.57E-05	2.45	30.23	5.90	84141.7
AHQ-6-5, 4531	K.AIDTIYQTTDFSGIR.N	1701.85844	2	4.61E-04	0.96	4.59	-	1177.5
AHQ-6-5, 5327	K.NTCQLYIQTDHLFFK.Y	1930.17267	2	3.57E-05	0.73	3.40	-	355.7
AHQ-6-5, 3949 - 3967	R.TITLQPGSPCNDFR.G	1607.76993	2	4.24E-04	0.76	3.06	-	346.4
gi|13435359|ref|NP_001914.2|	damage-specific DNA binding protein 1; damage-specific DNA binding pro			3.66E-05	0.92	10.22	2.60	126987.0
AHQ-6-4, 3763	R.IEVQDTSGGTTALRPSASTQALSSSVSSSK.L	2954.15138	3	3.66E-05	0.92	4.40	-	1300.1
gi|7330335|ref|NP_039234.1|	chloride intracellular channel 4; chloride intracellular channel 4 like			3.92E-05	0.51	10.13	8.70	28771.9
AHQ-6-10, 4440	R.DEFTNTCPSDKEVEIAYSDVAK.R	2520.66487	2	3.92E-05	0.51	2.68	-	424.1
gi|18201911|ref|NP_000629.2|	vitronectin precursor; serum spreading factor; somatomedin B; compleme			3.93E-05	0.62	10.18	3.10	54335.4
AHQ-6-14-, 5363 - 5423	R.SIAQYWLGCPAPGHL	1671.90045	2	3.18E-04	0.81	3.52	-	573.0
AHQ-6-13-, 5352 - 5424	R.SIAQYWLGCPAPGHL	1671.90045	2	3.93E-05	0.62	2.80	-	416.6
gi|21361399|ref|NP_055040.2|	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp			3.95E-05	0.79	10.17	3.40	65308.3
AHQ-6-6, 5223	K.IGPILDNSTLQSEVKPILEK.L	2195.54185	3	3.95E-05	0.79	3.47	-	639.9
gi|9845511|ref|NP_008839.2|	ras-related C3 botulinum toxin substrate 1 isoform Rac1; rho family, sm			4.03E-05	0.82	10.15	5.20	21450.0
AHQ-6-11, 2947 - 3009	K.YLECSALTQR.G	1242.38392	2	4.03E-05	0.82	3.04	-	802.9
gi|4885417|ref|NP_005330.1|	huntingtin interacting protein 2; ubiquitin-conjugating enzyme E2-25 KD			4.10E-05	0.87	10.18	7.50	22406.5
AHQ-6-11, 2864 - 2876	R.GEIAGPPDTPYEGGR.Y	1516.59406	2	4.10E-05	0.87	3.51	-	541.6
gi|5174737|ref|NP_006077.1|	tubulin, beta, 4 [Homo sapiens]			4.15E-05	0.55	10.15	3.80	50517.5
AHQ-6-13-, 5686 - 5764	K.MSSTFIGNSTAIQELFK.R	1875.13553	2	4.15E-05	0.55	3.06	-	683.9
gi|18105037|ref|NP_004709.2|	cytochrome c oxidase subunit VIIa polypeptide 2 like; estrogen recepto			4.54E-05	0.82	10.21	28.90	12614.6
AHQ-6-14-, 5779	K.LAGAWASEAYSPQGLKPVVSTEAPPIIFATPTK.L	3399.87995	3	4.54E-05	0.82	4.18	-	530.1
gi|7706497|ref|NP_057392.1|	UMP-CMP kinase [Homo sapiens]			4.64E-05	0.87	10.17	5.70	25854.7
AHQ-6-11, 2729	R.KNPDSQYGELIEK.Y	1521.65375	2	4.64E-05	0.87	3.35	-	718.2
gi|29734623|ref|XP_299768.1|	hypothetical protein XP_299768 [Homo sapiens]			4.73E-05	0.43	10.12	7.50	14905.7
AHQ-6-9, 3372 - 3426	K.RMVPVKEIDR.L	1243.50477	1	4.73E-05	0.43	2.33	-	498.6
gi|29745994|ref|XP_290546.1|	similar to KIAA0830 protein [Homo sapiens]			4.79E-05	0.69	10.15	2.60	55016.4
AHQ-6-7, 3951 - 3958	K.ILEVVNQIQDEER.M	1585.74098	2	4.79E-05	0.69	3.10	-	683.6
gi|30147857|ref|XP_293007.2|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			4.90E-05	1.31	20.16	5.90	20789.8
AHQ-6-12, 3707	K.ITIADCGQLQ	1120.25869	2	9.84E-04	0.68	2.81	-	921.5
AHQ-6-13-, 3398	K.KITIADCGQLQ	1248.43160	2	5.52E-05	0.67	3.03	-	718.0
AHQ-6-12, 3257 - 3323	K.KITIADCGQLQ	1248.43160	2	4.90E-05	0.63	3.14	-	719.5
gi|13376282|ref|NP_079131.1|	hypothetical protein FLJ12785 [Homo sapiens]			4.90E-05	0.79	10.13	2.00	68298.1
AHQ-6-5, 3772 - 3783	K.YPGHLAAITLSR.M	1299.50338	2	4.90E-05	0.79	2.62	-	1091.3
gi|27478749|ref|XP_208411.1|	similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit			5.12E-05	0.94	10.26	7.40	25628.5
AHQ-6-9, 6156	K.LLIVSNPVDILTYVAWK.I	1945.33337	2	5.12E-05	0.94	5.28	-	779.1
gi|20270259|ref|NP_620061.1|	phosphoglycerate kinase 2; phosphoglycerate kinase 1, pseudogene 2 [Ho			5.19E-05	0.89	10.20	3.60	44895.0
AHQ-6-8, 3473	K.LGDVYVNDAFGTAHR.A	1635.76178	2	5.19E-05	0.89	4.01	-	854.9
gi|24307917|ref|NP_006819.1|	RNA helicase family [Homo sapiens]			5.34E-05	0.41	10.13	0.60	251471.2
AHQ-6-2, 4684 - 4744	K.M*ILPEGIQRENNK.L	1558.78537	2	5.34E-05	0.41	2.58	-	458.0
gi|4757952|ref|NP_001782.1|	cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p			5.84E-05	3.52	40.27	26.70	21258.5
AHQ-6-11, 2367	K.CVVVGDGAVGK.T	1062.22237	2	7.17E-04	0.86	2.72	-	1368.2
AHQ-6-11, 6129	K.NVFDEAILAALEPPEPK.K	1854.09282	3	5.84E-05	0.95	5.41	-	1077.4
AHQ-6-11, 5355 - 5368	K.TPFLLVGTQIDLR.D	1473.74174	2	8.61E-04	0.95	4.12	-	1543.2
AHQ-6-11, 2620 - 2677	K.YVECSALTQK.G	1200.34381	2	3.92E-04	0.76	3.05	-	476.2
gi|19913414|ref|NP_055018.2|	adaptor-related protein complex 2, alpha 1 subunit isoform 1; adaptin,			6.07E-05	0.13	10.09	1.10	107545.3
AHQ-6-12, 3703	R.YGGAPQALTLK.L	1119.29547	1	6.07E-05	0.13	1.89	-	391.0
gi|6912240|ref|NP_036227.1|	adaptor-related protein complex 3, mu 1 subunit; mu-adaptin 3A; AP-3 ad			6.26E-05	0.81	10.16	4.10	46938.9
AHQ-6-13, 5517	K.SVVSQSVCDYFFEAQEK.A	2025.18125	2	6.26E-05	0.81	3.16	-	743.3
gi|4505753|ref|NP_002620.1|	phosphoglycerate mutase 1 (brain); Phosphoglycerate mutase A, nonmuscle			6.29E-05	0.81	10.16	7.10	28803.7
AHQ-6-10, 3834	R.FSGWYDADLSPAGHEEAK.R	1981.06697	3	6.29E-05	0.81	3.19	-	1080.7
gi|7706563|ref|NP_057614.1|	RAB-8b protein [Homo sapiens]			6.46E-05	0.84	10.18	6.80	23584.0
AHQ-6-11, 5168 - 5237	K.SSANVEEAFFTLAR.D	1542.67465	2	6.46E-05	0.84	3.51	-	1127.2
gi|24307939|ref|NP_036205.1|	chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]			6.51E-05	0.91	10.17	3.00	59670.7
AHQ-6-7, 6011	K.LGFAGLVQEISFGTTK.D	1668.91472	2	6.51E-05	0.91	3.46	-	1164.1
gi|4506765|ref|NP_002952.1|	S100 calcium-binding protein A4; 18A2; 42A; S100 calcium-binding protei			6.57E-05	0.86	10.16	10.90	11728.5
AHQ-6-14-, 3523 - 3600	K.ALDVMVSTFHK.Y	1248.47665	2	6.57E-05	0.86	2.91	-	954.1
gi|21361334|ref|NP_001893.2|	cystathionase isoform 1; homoserine deaminase; homoserine dehydratase;			6.96E-05	0.82	10.18	3.50	44507.8
AHQ-6-14-, 5406	R.NCLEKAVAALDGAK.Y	1461.66628	2	6.96E-05	0.82	3.11	-	1269.3
gi|10835049|ref|NP_001655.1|	ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho			6.96E-05	1.74	20.21	18.70	21768.0
AHQ-6-10, 6170	K.DQFPEVYVPTVFENYVADIEVDGK.Q	2775.01481	3	6.96E-05	0.83	4.29	-	708.6
AHQ-6-10, 3631	R.IGAFGYMECSAK.T	1335.53122	2	9.93E-05	0.91	3.37	-	825.3
gi|5031987|ref|NP_005720.1|	peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]			7.18E-05	2.54	30.19	19.30	22040.1
AHQ-6-12, 3872	R.FPDENFTLK.H	1111.22866	2	7.18E-05	0.87	3.05	-	727.1
AHQ-6-12, 4837 - 4908	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	7.90E-05	0.77	3.52	-	742.1
AHQ-6-12, 3227 - 3305	K.KIVITDCGQLS	1235.43283	2	3.05E-04	0.90	3.52	-	926.6
gi|4504489|ref|NP_000403.1|	histidine-rich glycoprotein precursor; histidine-proline rich glycoprot			7.24E-05	0.95	10.22	2.70	59578.0
AHQ-6-5, 6153 - 6160	K.DSPVLIDFFEDTER.Y	1683.79674	2	7.24E-05	0.95	4.46	-	1254.0
gi|28827809|ref|NP_789797.1|	nucleoside diphosphate kinase B-like [Homo sapiens]			7.28E-05	0.92	10.19	6.60	15529.0
AHQ-6-12, 3360 - 3364	R.GDFCIQVGR.N	1053.17404	2	7.28E-05	0.92	3.76	-	1103.8
gi|29729616|ref|XP_292963.1|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			7.40E-05	0.85	10.29	16.40	18025.4
AHQ-6-14-, 4732 - 4812	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	9.82E-04	0.96	5.89	-	1418.8
AHQ-6-14-, 4822	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	7.40E-05	0.85	4.15	-	679.6
AHQ-6-13, 4845 - 4915	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.11E-04	0.95	5.49	-	1340.6
gi|29747201|ref|XP_290702.1|	similar to My016 protein [Homo sapiens]			7.51E-05	0.80	10.15	10.50	16932.3
AHQ-6-14, 4226	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	7.51E-05	0.80	2.97	-	714.0
gi|19882229|ref|NP_065871.1|	P-Rex1 [Homo sapiens]			7.65E-05	0.52	10.16	1.30	186232.7

AHQ-6-14-, 5018	R.FHADEEM*EGTSSKNKQLRNDFK.L	2628.81644	3	7.65E-05	0.52	3.15	-	308.8
gi|20553919|ref|XP_033811.2|	similar to hypothetical protein FLJ14775 [Homo sapiens]			7.66E-05	0.60	10.15	9.90	17460.4
AHQ-6-11, 5492 - 5553	R.NGSKEGNHHSTQPKR.N	1677.76352	2	7.66E-05	0.60	2.94	-	803.2
gi|5902134|ref|NP_009005.1|	coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin			7.95E-05	1.90	20.22	6.90	51026.0
AHQ-6-7, 6384 - 6443	K.FVALICEASGGGAFLVLPLGK.T	2121.52786	2	9.12E-04	0.96	4.42	-	1442.8
AHQ-6-7, 2298 - 2302	R.KLQATVQELQK.R	1286.50292	2	7.95E-05	0.95	3.94	-	1537.2
gi|14249382|ref|NP_116139.1|	hypothetical protein MGC15429 [Homo sapiens]			7.99E-05	0.72	10.16	6.70	22345.5
AHQ-6-11, 3921	R.FSSETWQNLGTLHR.L	1676.81390	3	7.99E-05	0.72	3.23	-	413.5
gi|27482573|ref|XP_208709.1|	similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro			8.56E-05	1.77	20.24	26.00	17875.4
AHQ-6-12, 4681	K.GQVCLPVISAENWKPATK.T	2000.30757	2	1.39E-04	0.94	4.74	-	678.3
AHQ-6-12, 6179 - 6180	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	8.56E-05	0.83	4.00	-	708.5
gi|4504505|ref|NP_000405.1|	hydroxysteroid (17-beta) dehydrogenase 4 [Homo sapiens]			8.64E-05	0.82	10.21	3.50	79685.9
AHQ-6-5, 5824	K.ICDFENASKPQSIQESTGSIIEVLSK.I	2883.17795	3	8.64E-05	0.82	4.23	-	693.0
gi|4506189|ref|NP_002783.1|	proteasome alpha 7 subunit isoform 1; proteasome subunit RC6-1; proteas			8.73E-05	0.84	10.17	6.00	27886.7
AHQ-6-10, 3880 - 3894	K.NYTDEAIETDDLTIK.L	1741.83137	2	8.73E-05	0.84	3.44	-	703.5
gi|4557395|ref|NP_000058.1|	carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase;			8.88E-05	0.72	10.18	7.30	29245.8
AHQ-6-10, 4244 - 4248	K.YDPSLKPLSVSYDQATSLR.I	2141.36647	2	8.88E-05	0.72	2.99	-	552.3
gi|10835121|ref|NP_000289.1|	pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H			8.97E-05	0.92	10.18	1.90	61829.8
AHQ-6-7, 3490 - 3506	R.GDLGIEIPAEK.V	1142.28420	2	8.97E-05	0.92	3.62	-	1056.3
AHQ-6-7, 3488	R.GDLGIEIPAEK.V	1142.28420	1	8.12E-04	0.63	2.32	-	760.1
gi|30157216|ref|XP_292133.2|	similar to genethonin 1 [Homo sapiens]			8.98E-05	0.75	20.17	4.50	39693.8
AHQ-6-14, 5029	K.PSDTIENVK.A	1003.08850	1	2.61E-04	0.32	2.17	-	286.0
AHQ-6-3, 4385 - 4461	K.TITLEVKPSDTIENVK.A	1788.03268	2	1.71E-04	0.38	2.79	-	292.7
AHQ-6-1, 4519	K.TITLEVKPSDTIENVK.A	1788.03268	2	8.98E-05	0.43	2.83	-	411.3
gi|6996010|ref|NP_002038.1|	glycyl-tRNA synthetase; GlyRS; glycine tRNA ligase [Homo sapiens]			9.10E-05	0.82	10.17	1.90	77530.3
AHQ-6-6, 6163	R.TFFSFPAVVAPFK.C	1458.72722	2	9.10E-05	0.82	3.30	-	603.8
AHQ-6-5, 6235	R.TFFSFPAVVAPFK.C	1458.72722	2	3.13E-04	0.82	3.29	-	470.5
gi|24497435|ref|NP_002796.4|	proteasome 26S ATPase subunit 5; thyroid receptor interactor 1; protea			9.27E-05	0.36	10.14	4.20	45625.7
AHQ-6-3, 4834 - 4893	K.ILPNKVDPLVSLMM*VEK.V	1943.40420	2	9.27E-05	0.36	2.74	-	364.3
gi|8923579|ref|NP_060377.1|	hypothetical protein FLJ20625 [Homo sapiens]			9.43E-05	0.69	10.16	19.30	17744.7
AHQ-6-14-, 5723	K.KLPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3411.89550	3	9.43E-05	0.69	3.30	-	513.4
gi|30148978|ref|XP_291520.2|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			9.61E-05	0.52	10.14	2.20	68413.1
AHQ-6-11, 4557 - 4561	R.DWSHYFKTIKDLR.A	1709.92863	2	9.61E-05	0.52	2.89	-	479.2
gi|4557235|ref|NP_000009.1|	acyl-Coenzyme A dehydrogenase, very long chain precursor [Homo sapiens]			9.75E-05	0.44	10.15	2.90	70389.7
AHQ-6-6, 5091 - 5155	R.AGLGSGLSLSGLVHPELSR.S	1851.09693	2	9.75E-05	0.44	2.95	-	512.2
gi|4502905|ref|NP_001822.1|	clusterin; complement-associated protein SP-40 [Homo sapiens]			1.01E-04	1.53	20.21	8.70	52494.3
AHQ-6-9, 2838 - 2844	R.EILSVDCSTNNPSQAK.L	1764.89299	2	1.01E-04	0.63	2.86	-	479.8
AHQ-6-9, 3294	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	2.81E-04	0.90	4.15	-	674.0
gi|4506193|ref|NP_002784.1|	proteasome beta 1 subunit; proteasome subunit HC5; proteasome component			1.01E-04	1.75	20.17	12.90	26489.2
AHQ-6-11, 3911	K.GAVYSFDPVGSYQR.D	1546.66500	2	5.82E-04	0.86	2.99	-	912.0
AHQ-6-11, 4121	K.TVIGCSGFHGDCLTLTK.I	1869.10923	2	1.01E-04	0.89	3.44	-	895.7
gi|4503481|ref|NP_001395.1|	eukaryotic translation elongation factor 1 gamma; elongation factor 1-g			1.06E-04	1.42	20.17	6.20	50118.5
AHQ-6-8, 2925	K.ALIAAQYSGAQVR.V	1348.53280	2	1.06E-04	0.88	3.43	-	746.2
AHQ-6-8, 2509 - 2573	R.KLDPGSEETQTLVR.E	1573.73020	2	1.65E-04	0.54	2.76	-	254.0
gi|23110942|ref|NP_002781.2|	proteasome alpha 5 subunit; proteasome component 5; macropain subunit			1.06E-04	0.84	10.13	5.00	26410.9
AHQ-6-10, 5218	R.LFQVEYAIEAIK.L	1424.66595	2	1.06E-04	0.84	2.53	-	1436.2
gi|18201905|ref|NP_000166.2|	glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras			1.08E-04	0.89	10.17	2.50	63146.7
AHQ-6-7, 3732	R.VWYVSNIDGTHIAK.T	1603.80282	2	1.08E-04	0.89	3.36	-	951.0
gi|4505395|ref|NP_002499.1|	nidogen (enactin); Nidogen; nidogen (entactin) [Homo sapiens]			1.08E-04	0.95	10.23	1.30	136488.3
AHQ-6-3, 5206	K.ALEGLQYPFAVTSYGK.N	1744.96805	2	1.08E-04	0.95	4.63	-	1035.6
gi|21361122|ref|NP_001440.2|	four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap			1.09E-04	2.33	30.23	14.30	31894.7
AHQ-6-10, 2458	K.AIVAGDQNVEYK.G	1307.43431	2	1.09E-04	0.83	3.14	-	715.4
AHQ-6-13-, 3788	R.FVFHQEQVYCPDCAK.K	1931.13758	3	1.74E-04	0.75	3.17	-	1078.7
AHQ-6-9, 3507	R.FVFHQEQVYCPDCAK.K	1931.13758	2	7.33E-04	0.71	2.78	-	630.0
AHQ-6-11, 3120	K.GEDFYCVTCHETK.F	1648.75260	2	3.26E-04	0.75	2.88	-	555.3
gi|5730118|ref|NP_006514.1|	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble; X-prolyl aminope			1.11E-04	0.74	10.17	2.60	69858.4
AHQ-6-6, 5846	R.GSLTFEPLTLVPIQTK.M	1745.05263	2	1.11E-04	0.74	3.43	-	493.8
gi|4757826|ref|NP_004039.1|	beta-2-microglobulin [Homo sapiens]			1.15E-04	0.81	10.19	18.50	13714.5
AHQ-6-14-, 6250 - 6251	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	3	1.15E-04	0.81	3.73	-	657.5
gi|4502297|ref|NP_001678.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit			1.16E-04	0.90	10.18	8.30	17489.8
AHQ-6-13-, 2606	K.AQAELVGTADEATR.A	1432.51860	2	1.16E-04	0.90	3.51	-	1025.7
gi|4506773|ref|NP_002956.1|	S100 calcium-binding protein A9; calgranulin B [Homo sapiens]			1.21E-04	0.89	10.21	13.20	13241.9
AHQ-6-13-, 5466	R.NIETIINTFHQYSVK.L	1808.02738	2	1.21E-04	0.89	4.26	-	572.8
gi|18079216|ref|NP_065815.1|	CASK-interacting protein 1 [Homo sapiens]			1.29E-04	0.73	10.17	1.30	149812.6
AHQ-6-2, 6486 - 6487	R.PGSPQALGGPHGPAPATAK.V	1711.90292	2	1.29E-04	0.73	3.49	-	709.7
AHQ-6-1, 6495 - 6572	R.PGSPQALGGPHGPAPATAK.V	1711.90292	2	6.49E-04	0.33	2.82	-	327.4
gi|6005717|ref|NP_009031.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit e; ATP			1.37E-04	0.90	10.18	20.30	7933.1
AHQ-6-14-, 5012	R.YSALFLGVAYGATR.Y	1489.69972	2	1.37E-04	0.90	3.58	-	1058.7
gi|16904381|ref|NP_006717.1|	LPS-responsive vesicle trafficking, beach and anchor containing; vesic			1.41E-04	0.78	10.18	0.60	319158.3
AHQ-6-4, 4323	R.SESYIGGNCYILSGSR.D	1764.89468	2	1.41E-04	0.78	3.59	-	377.9
gi|4503785|ref|NP_000135.1|	frataxin; Friedreich ataxia (frataxin) [Homo sapiens]			1.45E-04	0.90	10.20	5.70	23218.1
AHQ-6-13-, 3726 - 3797	K.LGGDLGTYVINK.Q	1250.42590	2	1.45E-04	0.90	3.21	-	1105.8
gi|4504751|ref|NP_002196.1|	integrin alpha 5 precursor; fibronectin receptor, alpha subunit; very l			1.50E-04	0.91	10.20	1.70	114507.7
AHQ-6-3, 3724	R.LLESSLSSSEGEEPVEYK.S	1984.10415	2	1.50E-04	0.91	4.09	-	799.4
gi|4502923|ref|NP_001830.1|	calponin 3; calponin, acidic [Homo sapiens]			1.50E-04	0.84	10.14	3.30	36413.4
AHQ-6-12, 2759 - 2760	K.GPSYGLSAEVK.N	1108.22631	2	1.50E-04	0.84	2.77	-	976.1
gi|19923534|ref|NP_060988.2|	MCM10 minichromosome maintenance deficient 10; homolog of yeast MCM10			1.52E-04	0.33	10.14	2.10	96134.1
AHQ-6-8, 6148 - 6221	R.EQLAYLESEEFQKILKAK.S	2168.47496	2	1.52E-04	0.33	2.90	-	118.5
gi|22035694|ref|NP_001487.2|	GDNF family receptor alpha 3 preproprotein; glial cell line-derived ne			1.70E-04	0.57	10.13	2.50	44510.7
AHQ-6-13, 3876	K.M*NLSKLNMLK.P	1208.52057	2	1.70E-04	0.57	2.57	-	690.5
gi|21361456|ref|NP_055425.2|	alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph			1.72E-04	0.83	10.16	0.90	109437.2
AHQ-6-4, 2944	R.GLLEFEHQR.A	1129.25045	2	1.72E-04	0.83	3.15	-	833.6
gi|30151752|ref|XP_294531.2|	similar to seven transmembrane helix receptor [Homo sapiens]			1.78E-04	0.25	10.15	5.50	46776.6
AHQ-6-2, 3070	R.HSRTSLSSM*QQPPELGKEVGQQR.E	2597.85025	3	1.78E-04	0.25	3.08	-	231.0
gi|19923499|ref|NP_061969.2|	GTP binding protein 2 [Homo sapiens]			1.83E-04	0.90	10.19	2.70	56683.9
AHQ-6-6, 3996	R.AGQAATLALGDFDR.A	1406.52598	2	1.83E-04	0.90	3.75	-	1024.8
gi|30158950|ref|XP_301585.1|	similar to natural killer cell transcript 4 [Homo sapiens]			1.86E-04	0.48	10.17	15.40	18547.1
AHQ-6-3, 4732 - 4760	R.EPTVNKDIHQRTCDLSKTIEAPAER.Q	2911.19785	3	2.73E-04	0.55	3.30	-	365.5
AHQ-6-2, 4759 - 4836	R.EPTVNKDIHQRTCDLSKTIEAPAER.Q	2911.19785	3	1.86E-04	0.48	3.04	-	409.8
gi|4505599|ref|NP_002568.1|	p21-activated kinase 2; novel serine kinase; hPAK65 [Homo sapiens] [MAS			1.88E-04	0.78	10.16	3.40	58075.3
AHQ-6-7, 4504	R.ALYLIATNGTPELQNPEK.L	1973.21570	2	1.88E-04	0.78	3.27	-	514.8
gi|5803115|ref|NP_006830.1|	inner membrane protein, mitochondrial (mitofilin); motor protein [Homo			1.92E-04	0.49	10.15	2.20	83667.3
AHQ-6-5, 6065	K.LFEMVLGPAAYNVPLPK.K	1860.25197	2	1.92E-04	0.49	3.07	-	337.5
gi|8922511|ref|NP_060605.1|	mitochondrial ribosomal protein S18A; mitochondrial ribosomal protein S			1.92E-04	0.31	10.14	8.20	22183.8
AHQ-6-4, 4053	R.EVVETQEGKTTIIEGR.I	1789.96553	2	1.92E-04	0.31	2.82	-	327.9
gi|6912494|ref|NP_036457.1|	microtubule-associated protein, RP/EB family, member 1; ADENOMATOUS POL			1.95E-04	0.63	10.14	6.30	29998.9
AHQ-6-12, 3897	K.FFDANYDGKDYDPVAAR.Q	1965.06754	2	1.95E-04	0.63	2.64	-	384.2
gi|9910156|ref|NP_064590.1|	zinc finger protein Cezanne [Homo sapiens]			1.95E-04	0.78	10.16	1.60	94400.5
AHQ-6-13-, 5152	K.EWNELIKLASSEPR.M	1672.86346	2	1.95E-04	0.78	3.22	-	792.5
gi|4502013|ref|NP_001616.1|	adenylate kinase 2 isoform a; adenylate kinase, mitochondrial; adenylat			2.01E-04	0.81	10.18	6.70	26477.6
AHQ-6-10, 3815	R.LQAYHTQTTPLIEYYR.K	1998.22695	2	2.01E-04	0.81	3.52	-	671.8
gi|7705704|ref|NP_057001.1|	glutathione S-transferase subunit 13 homolog [Homo sapiens]			2.10E-04	0.85	20.17	13.70	25496.7
AHQ-6-11, 4000	R.FLTAVNLEHPEM*LEK.A	1788.05785	2	2.26E-04	0.59	2.72	-	578.9
AHQ-6-11, 4672	R.NEDITEPQSILAAAEK.A	1729.86695	2	2.10E-04	0.26	2.55	-	302.4
gi|21281669|ref|NP_060899.1|	transcription factor-like nuclear regulator; putative transcription re			2.13E-04	0.54	10.13	0.80	252842.5
AHQ-6-3, 4438	K.NNSLEIDQTENVKPMLR.G	2002.23894	2	2.13E-04	0.54	2.69	-	680.5
gi|4758384|ref|NP_004108.1|	FK506 binding protein 5; FK506-binding protein 5; 51 kDa FK506-binding			2.17E-04	0.75	10.13	2.20	51211.8

AHQ-6-2, 3018	K.EKLEQAAIVK.E	1129.33180	2	2.17E-04	0.75	2.62	-	915.1
gi|4502693|ref|NP_001760.1|	CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen			2.18E-04	1.76	20.23	15.40	25415.9
AHQ-6-11, 6223	K.AIHYALNCCGLAGGVEQFISDICPK.K	2798.16446	3	2.18E-04	0.91	4.60	-	679.5
AHQ-6-12, 3435	K.KDVLETFTVK.S	1180.37558	2	8.13E-04	0.81	3.09	-	780.0
AHQ-6-11, 3387	K.KDVLETFTVK.S	1180.37558	2	6.85E-04	0.85	3.26	-	794.4
gi|4505585|ref|NP_002563.1|	platelet-activating factor acetylhydrolase, isoform Ib, beta subunit 30			2.31E-04	0.70	10.15	8.30	25569.1
AHQ-6-10, 5472	R.ELFSPLHALNFGIGGDTTR.H	2046.27160	2	2.31E-04	0.70	3.07	-	478.2
gi|4504483|ref|NP_000185.1|	hypoxanthine phosphoribosyltransferase 1 [Homo sapiens]			2.37E-04	0.76	10.15	7.30	24579.2
AHQ-6-10, 4496	R.SVGYKPDFVGFEIPDK.F	1799.01571	2	2.37E-04	0.76	3.09	-	442.8
gi|17450333|ref|XP_060887.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			2.38E-04	0.74	10.22	11.00	17503.9
AHQ-6-13-, 6021 - 6084	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	4.91E-04	0.52	2.78	-	517.1
AHQ-6-13, 6197 - 6276	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	2.38E-04	0.74	2.99	-	874.8
gi|6041669|ref|NP_004538.2|	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd			2.44E-04	0.88	10.19	14.00	15208.5
AHQ-6-13-, 4632	R.TLPETLDPAEYNISPETR.R	2047.20831	2	2.44E-04	0.88	3.75	-	560.2
AHQ-6-13, 4751	R.TLPETLDPAEYNISPETR.R	2047.20831	2	9.55E-04	0.62	2.52	-	366.6
gi|8923582|ref|NP_060378.1|	hypothetical protein FLJ20626 [Homo sapiens]			2.47E-04	0.04	10.13	2.70	48956.7
AHQ-6-8, 2724 - 2784	R.AFDWKSQLVIHR.K	1500.72897	1	2.47E-04	0.04	1.91	-	184.9
AHQ-6-8, 2673 - 2736	R.AFDWKSQLVIHR.K	1500.72897	2	5.67E-04	0.50	2.57	-	482.3
gi|27597085|ref|NP_000357.3|	tropomyosin 1 (alpha) [Homo sapiens]			2.49E-04	0.90	10.17	3.90	32865.7
AHQ-6-9, 3172	R.KLVIIESDLER.A	1315.54103	2	2.49E-04	0.90	3.25	-	1226.4
gi|10864047|ref|NP_067058.1|	epidermal growth factor receptor substrate EPS15R [Homo sapiens]			2.57E-04	0.91	10.19	1.90	94254.3
AHQ-6-6, 3575	R.LQQEETQLEQSIQAGR.V	1858.98795	2	2.57E-04	0.91	3.77	-	1008.8
gi|4502167|ref|NP_000475.1|	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disea			2.59E-04	0.78	10.15	2.10	86942.8
AHQ-6-4, 2489	K.YLETPGDENEHAHFQK.A	1915.99652	2	2.59E-04	0.78	2.69	-	762.3
gi|29729857|ref|XP_293567.1|	similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60)			2.64E-04	0.86	10.15	3.40	38427.8
AHQ-6-7, 3371	R.TVIIEQSWGSPK.V	1345.52569	2	2.64E-04	0.86	2.98	-	977.9
gi|14780596|ref|XP_033004.1|	hypothetical protein BC005107 [Homo sapiens]			2.66E-04	0.31	10.11	5.00	18127.9
AHQ-6-3, 2084	R.EQIIAKAK.A	901.08569	1	2.66E-04	0.31	2.19	-	369.5
AHQ-6-2, 2043	R.EQIIAKAK.A	901.08569	1	6.41E-04	0.38	2.20	-	336.5
gi|4757732|ref|NP_004199.1|	programmed cell death 8 isoform 1; apoptosis-inducing factor [Homo sapi			2.71E-04	0.70	10.15	2.10	66900.2
AHQ-6-6, 5184	R.ALGTEVIQLFPEK.G	1445.68516	2	2.71E-04	0.70	2.97	-	561.6
gi|30152949|ref|XP_301425.1|	similar to Heat shock protein HSP 90-beta (HSP 84) (HSP 90) [Homo sapi			2.75E-04	0.47	10.12	2.50	42437.9
AHQ-6-5, 2256	K.YINQEELNK.I	1151.25119	1	2.75E-04	0.47	2.42	-	637.6
gi|15718761|ref|NP_004976.2|	c-K-ras2 protein isoform b; Kirsten rat sarcoma-2 viral (v-Ki-ras2) on			2.81E-04	0.91	10.21	8.00	21424.4
AHQ-6-11, 3735	R.VKDSEDVPM*VLVGNK.C	1646.88770	2	2.81E-04	0.91	4.30	-	1015.8
gi|30158489|ref|XP_301421.1|	similar to Chloride intracellular channel protein 1 (Nuclear chloride			2.81E-04	0.57	10.16	6.60	28267.5
AHQ-6-10, 5458 - 5515	K.FLNGNELTLADCNLLPK.L	1934.20276	2	2.81E-04	0.57	3.06	-	722.2
gi|4506713|ref|NP_002945.1|	ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte			2.89E-04	0.83	10.22	10.30	17964.8
AHQ-6-14-, 4299 - 4318	K.TITLEVEPSDTIENVK.A	1788.97431	2	2.89E-04	0.83	4.45	-	565.1
gi|7669501|ref|NP_005552.2|	lysosomal-associated membrane protein 1 [Homo sapiens]			2.94E-04	0.93	10.24	3.80	44772.8
AHQ-6-4, 6473	R.FFLQGIQLNTILPDAR.D	1847.14988	2	2.94E-04	0.93	4.83	-	716.8
gi|4507191|ref|NP_003118.1|	spectrin, alpha, non-erythrocytic 1 (alpha-fodrin) [Homo sapiens]			2.95E-04	0.54	10.16	0.90	284279.3
AHQ-6-3, 4238	R.EKEPIVGSTDYGKDEDSAEALLK.K	2495.67840	3	2.95E-04	0.54	3.19	-	418.6
gi|4502989|ref|NP_001856.1|	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor; hepa			3.11E-04	0.89	10.18	15.70	9395.9
AHQ-6-14-, 5116 - 5182	K.LFQEDDEIPLYLK.G	1623.82758	2	3.11E-04	0.89	3.64	-	1013.9
AHQ-6-14, 5762 - 5837	K.LFQEDDEIPLYLK.G	1623.82758	2	6.61E-04	0.87	3.42	-	995.5
gi|20547107|ref|XP_114482.1|	similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN			3.19E-04	0.85	10.19	2.10	94330.3
AHQ-6-4, 6156	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	3.19E-04	0.85	3.79	-	653.5
gi|4502097|ref|NP_001142.1|	solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra			3.21E-04	0.74	10.16	4.00	33148.4
AHQ-6-10, 5258 - 5267	R.YFPTQALNFAFK.D	1447.66130	2	3.21E-04	0.74	2.54	-	535.3
gi|4758484|ref|NP_004823.1|	glutathione-S-transferase like; glutathione transferase omega [Homo sap			3.21E-04	1.33	20.14	10.00	27565.7
AHQ-6-10, 2866	R.HEVININLK.N	1080.26247	1	5.86E-04	0.51	2.30	-	517.4
AHQ-6-11, 2955 - 2968	R.HEVININLK.N	1080.26247	2	3.21E-04	0.82	2.89	-	908.4
AHQ-6-10, 2771 - 2787	R.SQNKEDYAGLKEEFR.K	1814.93364	2	6.65E-04	0.51	2.82	-	614.5
gi|4507143|ref|NP_003786.1|	sorting nexin 3 isoform a; sorting nexin 3A [Homo sapiens]			3.35E-04	0.72	10.13	6.20	18762.2
AHQ-6-12, 2901	R.KQGLEQFINK.V	1205.38836	2	3.35E-04	0.72	2.68	-	787.3
gi|4502285|ref|NP_001672.1|	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 2; ATP			3.41E-04	0.75	10.16	1.50	109690.3
AHQ-6-1, 4647	K.VGEATETALTCLVEK.M	1622.81958	2	3.41E-04	0.75	3.25	-	563.6
gi|21618338|ref|NP_003141.2|	signal transducer and activator of transcription 3 isoform 2; acute-ph			3.48E-04	0.81	10.18	2.30	87980.2
AHQ-6-6, 6432	R.SIVSELAGLLSAM*EYVQK.T	1955.26206	2	3.48E-04	0.81	3.62	-	529.6
gi|24111244|ref|NP_705691.1|	MAM domain containing glycosylphosphatidylinositol anchor 1; glycosyl-			3.48E-04	0.11	10.09	1.00	105789.7
AHQ-6-7, 3878 - 3935	R.PPVLWSRVDK.E	1197.41106	1	3.48E-04	0.11	1.81	-	442.9
gi|27478732|ref|XP_210750.1|	similar to ATP synthase, H+ transporting, mitochondrial F0 complex, su			3.53E-04	0.76	10.13	7.10	16272.9
AHQ-6-11, 3473	K.SCAEWVSLSK.A	1168.30181	2	3.53E-04	0.76	2.65	-	692.9
gi|6005902|ref|NP_009043.1|	thrombospondin 3 [Homo sapiens]			3.67E-04	0.86	10.14	0.70	104200.6
AHQ-6-7, 4296	R.FYVVMWK.Q	973.21547	1	3.87E-04	0.81	2.24	-	1075.5
AHQ-6-3, 4582	R.FYVVMWK.Q	973.21547	2	3.67E-04	0.86	2.77	-	717.4
gi|4506195|ref|NP_002785.1|	proteasome beta 2 subunit; proteasome subunit, beta type, 2; macropain			3.72E-04	0.91	10.18	5.50	22836.1
AHQ-6-11, 5703 - 5783	R.FILNLPTFSVR.I	1307.56542	2	3.72E-04	0.91	3.56	-	1005.4
gi|12707570|ref|NP_004083.2|	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor [Homo			4.03E-04	0.82	10.18	7.20	31371.2
AHQ-6-10, 4983	K.AQFAQPEILIGTIPGAGGTQR.L	2126.40140	2	4.03E-04	0.82	3.58	-	620.0
gi|21536449|ref|NP_002613.2|	prefoldin 1; prefoldin subunit 1 [Homo sapiens]			4.04E-04	0.96	10.22	9.00	14210.4
AHQ-6-13-, 3773	K.LADIQIEQLNR.T	1313.48523	2	4.04E-04	0.96	4.41	-	1612.6
gi|4504617|ref|NP_000589.1|	insulin-like growth factor binding protein 3 [Homo sapiens]			4.09E-04	0.71	10.13	3.40	31660.0
AHQ-6-6, 6590	R.EM*EDTLNHLK.F	1246.37275	2	4.09E-04	0.71	2.64	-	1045.0
gi|21361388|ref|NP_008868.2|	SMT3 suppressor of mif two 3 homolog 2; SMT3 (suppressor of mif two 3,			4.15E-04	0.69	10.14	12.60	10870.2
AHQ-6-12, 2720 - 2724	K.VAGQDGSVVQFK.I	1235.37133	2	4.15E-04	0.69	2.73	-	572.6
gi|29743324|ref|XP_293276.1|	similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote			4.17E-04	1.82	20.30	16.00	21244.7
AHQ-6-13-, 5280	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPMPK.L	3228.70228	3	4.17E-04	0.91	5.53	-	1264.3
AHQ-6-13-, 5057	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	4.86E-04	0.91	6.07	-	974.6
gi|4504205|ref|NP_001512.1|	general transcription factor IIIC, polypeptide 2, beta 110kDa; general			4.32E-04	0.26	10.13	2.10	100678.9
AHQ-6-14-, 5536 - 5539	K.KIRQPAACPGGEEVDGAPR.D	2010.22095	2	4.32E-04	0.26	2.59	-	163.3
gi|22267436|ref|NP_056284.1|	DKFZp564D177 protein [Homo sapiens]			4.33E-04	0.93	10.16	4.90	28466.4
AHQ-6-11, 2188	R.AVHAHVNLGYTK.L	1310.48626	3	4.33E-04	0.93	3.29	-	1422.3
gi|5902726|ref|NP_005800.1|	peroxiredoxin 2; thioredoxin-dependent peroxide reductase 1 (thiol-spec			4.39E-04	0.60	10.14	8.60	21856.8
AHQ-6-11, 6133	K.EGGLGPLNIPLLADVTR.R	1736.00583	2	4.39E-04	0.60	2.60	-	356.2
gi|4507795|ref|NP_003340.1|	ubiquitin-conjugating enzyme E2 variant 1 isoform b; DNA-binding protei			4.70E-04	0.83	10.15	4.10	25796.6
AHQ-6-12, 3471 - 3481	K.YPEAPPFVR.F	1076.22914	2	4.70E-04	0.83	3.01	-	587.3
gi|11496277|ref|NP_068805.1|	mitogen-activated protein kinase kinase 1 interacting protein 1; MEK p			4.82E-04	0.88	10.21	0.00	13622.6
AHQ-6-14-, 5108 - 5179	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	4.82E-04	0.88	4.30	-	621.1
gi|19923981|ref|NP_612460.1|	hypothetical protein BC013151 [Homo sapiens]			4.95E-04	0.56	10.13	4.30	40094.2
AHQ-6-14, 4802	R.SAEAQNFIDSLIELR.G	1706.87822	2	4.95E-04	0.56	2.60	-	780.1
gi|21389505|ref|NP_653321.1|	hypothetical protein FLJ31564 [Homo sapiens]			5.08E-04	0.66	10.16	0.00	73208.7
AHQ-6-14, 5221 - 5276	R.DSICCKLSNGADILFEPKLKFM	2590.03282	3	5.08E-04	0.66	3.15	-	589.3
gi|21361322|ref|NP_006078.2|	tubulin, beta, 5 [Homo sapiens]			5.17E-04	0.73	10.15	3.80	49585.5
AHQ-6-7, 2871	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	5.17E-04	0.73	3.02	-	737.6
gi|11968023|ref|NP_071918.1|	zinc finger protein 106 [Homo sapiens]			5.23E-04	0.81	10.16	0.70	208880.7
AHQ-6-12, 6199 - 6200	K.ERSQVDQLLNISLR.E	1671.88024	2	5.23E-04	0.81	3.28	-	1188.9
gi|4557317|ref|NP_001148.1|	annexin A11; annexin XI; autoantigen, 56-kD; calcyclin-associated annex			5.32E-04	0.91	10.19	3.20	54389.4
AHQ-6-7, 5168	K.GFGTDEQAIIDCLGSR.S	1740.87312	2	5.32E-04	0.91	3.74	-	1172.3
gi|8922122|ref|NP_061166.1|	elaC homolog 1 [Homo sapiens]			5.40E-04	0.11	10.09	2.80	40019.0
AHQ-6-7, 3222	K.KRPGKLNAQK.L	1140.36428	1	5.40E-04	0.11	1.87	-	254.5
gi|24308179|ref|NP_061174.1|	hypothetical protein DKFZp547A023 [Homo sapiens]			5.45E-04	0.18	10.15	3.30	70157.6
AHQ-6-3, 3250	K.ATNKAAEEGQKAGELSLKLEK.E	2216.47802	3	5.45E-04	0.18	3.04	-	342.1
gi|13376719|ref|NP_079413.1|	hypothetical protein FLJ21439 [Homo sapiens]			5.50E-04	0.82	10.16	2.40	48893.8
AHQ-6-12, 4401	K.GDFNYLEEFK.Q	1262.34887	2	5.50E-04	0.82	2.99	-	637.3
gi|4505409|ref|NP_002503.1|	non-metastatic cells 2, protein (NM23B) expressed in; Non-metastatic ce			5.67E-04	0.71	10.15	9.90	17297.9

<table>
<tr><td>AHQ-6-12, 5727</td><td>K.EISLWFKPEELVDYK.S</td><td>1897.15929</td><td>2</td><td>5.67E-04</td><td>0.71</td><td>2.92</td><td>-</td><td>515.8</td></tr>
<tr><td>gi|21361427|ref|NP_055182.2|</td><td>hypothetical protein, estradiol-induced [Homo sapiens]</td><td></td><td></td><td>5.70E-04</td><td>0.55</td><td>10.13</td><td>8.90</td><td>21551.0</td></tr>
<tr><td>AHQ-6-13-, 5417</td><td>K.EDEIPETVSLEMLDAAK.N</td><td>1891.08690</td><td>2</td><td>5.70E-04</td><td>0.55</td><td>2.63</td><td>-</td><td>324.6</td></tr>
<tr><td>gi|20149570|ref|NP_005816.2|</td><td>RAS guanyl releasing protein 2 isoform 1; calcium and diacylglycerol-r</td><td></td><td></td><td>6.00E-04</td><td>0.91</td><td>10.15</td><td>2.10</td><td>75547.0</td></tr>
<tr><td>AHQ-6-12, 3943</td><td>R.HSSLIDIDSVPTYK.W</td><td>1575.74455</td><td>2</td><td>6.00E-04</td><td>0.91</td><td>3.03</td><td>-</td><td>1248.3</td></tr>
<tr><td>gi|21265064|ref|NP_620688.1|</td><td>a disintegrin-like and metalloprotease (reprolysin type) with thrombos</td><td></td><td></td><td>6.30E-04</td><td>0.19</td><td>10.12</td><td>1.10</td><td>121099.3</td></tr>
<tr><td>AHQ-6-12, 4285</td><td>K.IGCDGIIGSAAK.E</td><td>1163.32670</td><td>1</td><td>6.30E-04</td><td>0.19</td><td>1.95</td><td>-</td><td>320.1</td></tr>
<tr><td>gi|20127517|ref|NP_009148.2|</td><td>programmed cell death 10; apoptosis-related protein 15 [Homo sapiens]</td><td></td><td></td><td>6.37E-04</td><td>0.81</td><td>10.19</td><td>11.30</td><td>24701.4</td></tr>
<tr><td>AHQ-6-10, 4783</td><td>R.M*AADDVEEYMIERPEPEFQDLNEK.A</td><td>2916.14381</td><td>3</td><td>6.37E-04</td><td>0.81</td><td>3.80</td><td>-</td><td>574.6</td></tr>
<tr><td>gi|21361358|ref|NP_006365.2|</td><td>serine/threonine kinase 25 (STE20 homolog, yeast); sterile 20 (oxidant</td><td></td><td></td><td>6.42E-04</td><td>0.88</td><td>10.18</td><td>3.80</td><td>48111.3</td></tr>
<tr><td>AHQ-6-7, 4327</td><td>K.LADFGVAGQLTDTQIK.R</td><td>1677.88001</td><td>2</td><td>6.42E-04</td><td>0.88</td><td>3.70</td><td>-</td><td>1026.7</td></tr>
<tr><td>gi|24308149|ref|NP_060035.1|</td><td>hypothetical protein DKFZp434F2322 [Homo sapiens]</td><td></td><td></td><td>6.52E-04</td><td>0.62</td><td>10.14</td><td>2.00</td><td>61404.2</td></tr>
<tr><td>AHQ-6-5, 5611</td><td>K.PSGVHLKLVLR.F</td><td>1219.50454</td><td>2</td><td>6.52E-04</td><td>0.62</td><td>2.87</td><td>-</td><td>617.9</td></tr>
<tr><td>gi|28461290|ref|NP_443728.2|</td><td>TRALPUSH; no opposite paired repeat protein [Homo sapiens]</td><td></td><td></td><td>6.62E-04</td><td>0.66</td><td>10.14</td><td>0.40</td><td>240073.5</td></tr>
<tr><td>AHQ-6-9, 3324</td><td>K.KKPQVNAK.D</td><td>913.09970</td><td>1</td><td>6.62E-04</td><td>0.66</td><td>2.64</td><td>-</td><td>536.3</td></tr>
<tr><td>gi|4557469|ref|NP_001273.1|</td><td>adaptor-related protein complex 2, beta 1 subunit; adaptin, beta 2 (bet</td><td></td><td></td><td>6.96E-04</td><td>0.82</td><td>10.16</td><td>1.50</td><td>104551.9</td></tr>
<tr><td>AHQ-6-6, 2802</td><td>R.LSHANSAVVLSAVK.V</td><td>1396.61737</td><td>2</td><td>6.96E-04</td><td>0.82</td><td>2.92</td><td>-</td><td>906.4</td></tr>
<tr><td>gi|29727204|ref|XP_290872.1|</td><td>similar to Pyruvate kinase, M2 isozyme [Homo sapiens]</td><td></td><td></td><td>7.33E-04</td><td>0.91</td><td>10.17</td><td>5.40</td><td>16297.7</td></tr>
<tr><td>AHQ-6-7, 2383 - 2458</td><td>R.APIIAVTR.N</td><td>841.03348</td><td>2</td><td>7.33E-04</td><td>0.91</td><td>2.61</td><td>-</td><td>1265.5</td></tr>
<tr><td>gi|5803135|ref|NP_006852.1|</td><td>RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind</td><td></td><td></td><td>7.50E-04</td><td>0.88</td><td>10.17</td><td>5.50</td><td>23025.1</td></tr>
<tr><td>AHQ-6-13, 3919 - 3927</td><td>K.LLIIGDSGVGK.S</td><td>1072.28025</td><td>2</td><td>7.50E-04</td><td>0.88</td><td>3.45</td><td>-</td><td>941.9</td></tr>
<tr><td>gi|5174553|ref|NP_005917.1|</td><td>microfibrillar-associated protein 1 [Homo sapiens]</td><td></td><td></td><td>7.66E-04</td><td>0.23</td><td>10.13</td><td>2.10</td><td>51854.9</td></tr>
<tr><td>AHQ-6-10, 2194</td><td>R.ANGKVITNK.A</td><td>945.09856</td><td>1</td><td>7.66E-04</td><td>0.23</td><td>2.70</td><td>-</td><td>345.8</td></tr>
<tr><td>gi|29741994|ref|XP_292459.1|</td><td>similar to alpha tubulin [Homo sapiens]</td><td></td><td></td><td>7.73E-04</td><td>0.42</td><td>10.13</td><td>5.00</td><td>39987.6</td></tr>
<tr><td>AHQ-6-12, 4261 - 4263</td><td>K.VGINYQPPNVVPGGDLAK.V</td><td>1839.08461</td><td>2</td><td>7.73E-04</td><td>0.42</td><td>2.68</td><td>-</td><td>384.1</td></tr>
<tr><td>gi|4557014|ref|NP_001743.1|</td><td>catalase [Homo sapiens]</td><td></td><td></td><td>7.83E-04</td><td>0.71</td><td>10.13</td><td>2.50</td><td>59755.8</td></tr>
<tr><td>AHQ-6-7, 2451</td><td>R.FNTANDDNVTQVR.A</td><td>1494.54849</td><td>2</td><td>7.83E-04</td><td>0.71</td><td>2.55</td><td>-</td><td>703.2</td></tr>
<tr><td>gi|5453597|ref|NP_006126.1|</td><td>F-actin capping protein alpha-1 subunit; Cap Z [Homo sapiens]</td><td></td><td></td><td>7.93E-04</td><td>0.38</td><td>10.15</td><td>7.00</td><td>32922.5</td></tr>
<tr><td>AHQ-6-9, 4991</td><td>K.TIDGQQTIIACIESHQFQPK.N</td><td>2316.57620</td><td>2</td><td>7.93E-04</td><td>0.38</td><td>2.58</td><td>-</td><td>229.0</td></tr>
<tr><td>gi|4557525|ref|NP_000099.1|</td><td>dihydrolipoamide dehydrogenase precursor; E3 component of pyruvate dehy</td><td></td><td></td><td>7.93E-04</td><td>0.91</td><td>10.18</td><td>2.60</td><td>54149.9</td></tr>
<tr><td>AHQ-6-7, 2520 - 2522</td><td>K.SEEQLKEEGIEYK.V</td><td>1582.69072</td><td>2</td><td>7.93E-04</td><td>0.91</td><td>3.68</td><td>-</td><td>968.4</td></tr>
<tr><td>gi|4758440|ref|NP_004868.1|</td><td>glia maturation factor, gamma [Homo sapiens]</td><td></td><td></td><td>8.02E-04</td><td>0.77</td><td>10.15</td><td>9.20</td><td>16801.2</td></tr>
<tr><td>AHQ-6-12, 4249</td><td>R.TTDDLTEAWLQEK.L</td><td>1550.64872</td><td>2</td><td>8.02E-04</td><td>0.77</td><td>3.06</td><td>-</td><td>953.4</td></tr>
<tr><td>gi|29734552|ref|XP_291269.1|</td><td>similar to KIAA1875 protein [Homo sapiens]</td><td></td><td></td><td>8.13E-04</td><td>0.45</td><td>10.14</td><td>1.70</td><td>93320.7</td></tr>
<tr><td>AHQ-6-13-, 4492</td><td>R.M*LAPKRSWGTPQLR.L</td><td>1657.96500</td><td>2</td><td>8.13E-04</td><td>0.45</td><td>2.89</td><td>-</td><td>496.2</td></tr>
<tr><td>gi|29743501|ref|XP_297109.1|</td><td>hypothetical protein XP_297109 [Homo sapiens]</td><td></td><td></td><td>8.34E-04</td><td>0.21</td><td>10.14</td><td>3.40</td><td>58170.9</td></tr>
<tr><td>AHQ-6-4, 5232</td><td>K.TESGQVGLPYALVEWKER.K</td><td>2063.29893</td><td>2</td><td>8.34E-04</td><td>0.21</td><td>2.73</td><td>-</td><td>299.7</td></tr>
<tr><td>gi|4506005|ref|NP_002700.1|</td><td>protein phosphatase 1, catalytic subunit, beta isoform [Homo sapiens] [</td><td></td><td></td><td>8.37E-04</td><td>0.88</td><td>10.14</td><td>4.30</td><td>37186.6</td></tr>
<tr><td>AHQ-6-9, 3711</td><td>R.AHQVVEDGYEFFAK.R</td><td>1640.77679</td><td>2</td><td>8.37E-04</td><td>0.88</td><td>2.85</td><td>-</td><td>953.2</td></tr>
<tr><td>gi|15618995|ref|NP_258259.1|</td><td>keratin 6 irs [Homo sapiens]</td><td></td><td></td><td>8.71E-04</td><td>0.85</td><td>10.20</td><td>2.30</td><td>57291.2</td></tr>
<tr><td>AHQ-6-6, 3146 - 3148</td><td>R.FLEQQNQVLETK.W</td><td>1477.64411</td><td>2</td><td>8.71E-04</td><td>0.85</td><td>3.91</td><td>-</td><td>491.0</td></tr>
<tr><td>gi|4506677|ref|NP_002942.1|</td><td>ribophorin II [Homo sapiens]</td><td></td><td></td><td>9.13E-04</td><td>0.52</td><td>10.14</td><td>2.70</td><td>69301.6</td></tr>
<tr><td>AHQ-6-1, 4888 - 4966</td><td>R.LQVTNVLSQPLTQATVK.L</td><td>1841.14195</td><td>2</td><td>9.13E-04</td><td>0.52</td><td>2.66</td><td>-</td><td>405.2</td></tr>
<tr><td>gi|5174613|ref|NP_005960.1|</td><td>nucleosome assembly protein 1-like 4; nucleosome assembly protein 2 [Ho</td><td></td><td></td><td>9.14E-04</td><td>0.90</td><td>10.16</td><td>2.70</td><td>42823.1</td></tr>
<tr><td>AHQ-6-7, 2862</td><td>K.FYEEVHDLER.K</td><td>1337.41897</td><td>2</td><td>9.14E-04</td><td>0.90</td><td>3.11</td><td>-</td><td>1231.5</td></tr>
<tr><td>gi|22749143|ref|NP_689761.1|</td><td>hypothetical protein FLJ25333 [Homo sapiens]</td><td></td><td></td><td>9.40E-04</td><td>0.12</td><td>10.13</td><td>5.80</td><td>47726.0</td></tr>
<tr><td>AHQ-6-7, 5520 - 5532</td><td>K.SENKM*EEKLLQLSSKVENFINTQK.Q</td><td>2855.21429</td><td>2</td><td>9.40E-04</td><td>0.12</td><td>2.55</td><td>-</td><td>90.1</td></tr>
<tr><td>gi|17482508|ref|XP_058957.1|</td><td>similar to QIL1 [Homo sapiens]</td><td></td><td></td><td>9.56E-04</td><td>0.83</td><td>10.19</td><td>18.60</td><td>13087.2</td></tr>
<tr><td>AHQ-6-14-, 5414 - 5420</td><td>K.GSVAGGAVYLVYDQELLGPSDK.S</td><td>2239.46691</td><td>2</td><td>9.56E-04</td><td>0.83</td><td>3.72</td><td>-</td><td>684.9</td></tr>
<tr><td>gi|4557773|ref|NP_000248.1|</td><td>myosin, heavy polypeptide 7, cardiac muscle, beta [Homo sapiens]</td><td></td><td></td><td>9.56E-04</td><td>0.61</td><td>10.17</td><td>0.50</td><td>223110.8</td></tr>
<tr><td>AHQ-6-5, 3124</td><td>R.CNGVLEGIR.I</td><td>1019.15759</td><td>2</td><td>9.56E-04</td><td>0.61</td><td>2.72</td><td>-</td><td>526.8</td></tr>
<tr><td>gi|19923748|ref|NP_001924.2|</td><td>dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarat</td><td></td><td></td><td>9.61E-04</td><td>0.92</td><td>10.20</td><td>3.10</td><td>48755.0</td></tr>
<tr><td>AHQ-6-7, 3252</td><td>K.TPAFAESVTEGDVR.W</td><td>1479.57373</td><td>2</td><td>9.61E-04</td><td>0.92</td><td>2.94</td><td>-</td><td>1803.8</td></tr>
<tr><td>gi|24307907|ref|NP_006207.1|</td><td>plasminogen activator inhibitor type 1, member 2; protease inhibitor 7</td><td></td><td></td><td>9.81E-04</td><td>0.80</td><td>10.15</td><td>3.50</td><td>44002.0</td></tr>
<tr><td>AHQ-6-8, 3145</td><td>K.FTAVAQTDLKEPLK.V</td><td>1561.80416</td><td>2</td><td>9.81E-04</td><td>0.80</td><td>2.95</td><td>-</td><td>656.1</td></tr>
</table>

Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				1.00E-30	102.50	1170.35	47.60	226529.8
AHQ-7-5, 2059	R.ALEEAMEQK.A	1049.18068	2	4.00E-04	0.77	2.71	-	751.2
AHQ-7-6, 2043	R.ALEEAMEQK.A	1049.18068	2	2.11E-04	0.86	2.81	-	966.9
AHQ-7-3, 2121 - 2128	R.ALEEAMEQK.A	1049.18068	2	6.27E-05	0.83	3.15	-	724.7
AHQ-7-2, 3844 - 3907	K.ALELDSNLYR.I	1194.31920	2	5.84E-07	0.95	3.99	-	1157.3
AHQ-7-3, 3779	K.ALELDSNLYR.I	1194.31920	2	1.17E-06	0.94	3.65	-	1334.6
AHQ-7-5, 3752	K.ALELDSNLYR.I	1194.31920	2	1.79E-06	0.93	3.43	-	1096.5
AHQ-7-14-, 3722	K.ALELDSNLYR.I	1194.31920	2	1.47E-07	0.91	3.06	-	1161.5
AHQ-7-1, 3891	K.ALELDSNLYR.I	1194.31920	2	2.89E-05	0.94	3.70	-	1201.1
AHQ-7-4, 3782	K.ALELDSNLYR.I	1194.31920	2	9.58E-08	0.96	4.05	-	1515.1
AHQ-7-6, 3689 - 3697	K.ALELDSNLYR.I	1194.31920	2	1.02E-04	0.92	3.52	-	1142.9
AHQ-7-2, 2985 - 2997	R.ALEQQVEEMK.T	1205.36380	2	1.36E-05	0.92	3.90	-	1146.9
AHQ-7-3, 2195	R.ALEQQVEEM*K.T	1221.36320	2	3.37E-04	0.79	3.12	-	845.5
AHQ-7-5, 2878 - 2880	R.ALEQQVEEMK.T	1205.36380	2	7.73E-05	0.83	3.22	-	1020.4
AHQ-7-2, 2227	R.ALEQQVEEM*K.T	1221.36320	2	1.17E-04	0.80	3.08	-	899.8
AHQ-7-1, 3125	R.ALEQQVEEMK.T	1205.36380	2	7.94E-05	0.89	3.36	-	1098.2
AHQ-7-7, 2812	R.ALEQQVEEMK.T	1205.36380	2	4.56E-04	0.91	3.31	-	1217.7
AHQ-7-6, 2869 - 2930	R.ALEQQVEEMK.T	1205.36380	2	3.97E-04	0.92	3.42	-	1056.1
AHQ-7-4, 2888	R.ALEQQVEEMK.T	1205.36380	2	1.89E-05	0.91	3.53	-	1194.7
AHQ-7-3, 2957 - 2975	R.ALEQQVEEMK.T	1205.36380	2	1.42E-07	0.90	3.67	-	1103.1
AHQ-7-2, 6312	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	3.66E-08	0.97	5.90	-	1531.9
AHQ-7-6, 6154	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.35E-08	0.89	4.04	-	1205.2
AHQ-7-3, 6155 - 6156	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.28E-04	0.96	5.54	-	1763.6
AHQ-7-5, 6244	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	7.23E-08	0.96	5.36	-	1718.3
AHQ-7-2, 6848	R.ALEQQVEEMKTQLEELEDELQATEDAK.L	3149.38454	3	5.74E-08	0.96	5.95	-	1395.6
AHQ-7-1, 6079	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	2.14E-05	0.96	5.61	-	1762.5
AHQ-7-1, 4973	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.74E-11	0.95	4.32	-	1227.5
AHQ-7-7, 4865 - 4942	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.81E-05	0.96	4.94	-	1201.5
AHQ-7-3, 5157	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.37E-04	0.93	4.52	-	976.1
AHQ-7-1, 5169 - 5188	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.65E-05	0.93	4.41	-	728.9
AHQ-7-3, 4708 - 4775	K.ANLQIDQINTDLNLER.S	1871.04187	2	9.85E-04	0.93	4.02	-	754.4
AHQ-7-2, 5196	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.76E-05	0.97	6.10	-	1207.7
AHQ-7-5, 4779	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.20E-05	0.94	4.42	-	843.1
AHQ-7-2, 5064 - 5131	K.ANLQIDQINTDLNLER.S	1871.04187	2	9.01E-07	0.98	6.20	-	1318.6
AHQ-7-2, 4867 - 4941	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.61E-09	0.97	5.56	-	1279.8
AHQ-7-11, 2387	K.ASITALEAK.I	904.04321	2	2.49E-05	0.94	3.23	-	1370.4
AHQ-7-4, 2417	K.ASITALEAK.I	904.04321	2	2.20E-07	0.93	3.09	-	1415.3
AHQ-7-6, 2367	K.ASITALEAK.I	904.04321	2	8.56E-05	0.87	2.84	-	847.1
AHQ-7-5, 2380	K.ASITALEAK.I	904.04321	2	3.41E-05	0.92	2.75	-	1301.3
AHQ-7-3, 2453	K.ASITALEAK.I	904.04321	2	5.24E-07	0.93	3.05	-	1130.5
AHQ-7-2, 2172	R.ASREEILAQAK.E	1216.36955	2	4.66E-04	0.94	3.39	-	1802.0
AHQ-7-3, 2167 - 2237	R.ASREEILAQAK.E	1216.36955	2	6.77E-05	0.78	2.86	-	991.5
AHQ-7-2, 3255	R.DELADEIANSSGK.G	1349.38323	2	9.57E-06	0.94	3.99	-	1280.5
AHQ-7-5, 3164	R.DELADEIANSSGK.G	1349.38323	2	2.06E-05	0.94	3.70	-	1428.1
AHQ-7-4, 3205	R.DELADEIANSSGK.G	1349.38323	2	1.32E-04	0.78	2.90	-	838.7
AHQ-7-2, 6375	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	2	4.21E-10	0.97	6.05	-	1360.3
AHQ-7-1, 6335 - 6340	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.86E-04	0.98	5.50	-	2526.7
AHQ-7-2, 6287	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	2	4.42E-05	0.85	3.97	-	784.3
AHQ-7-4, 6624 - 6628	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.96E-11	0.97	6.00	-	1548.4
AHQ-7-7, 6480 - 6513	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.01E-04	0.85	4.13	-	831.0
AHQ-7-1, 6041	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	8.00E-13	0.85	4.19	-	566.0
AHQ-7-2, 6271 - 6333	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	3.98E-09	0.86	4.15	-	739.7
AHQ-7-4, 2184 - 2186	K.DLEAHIDSANK.N	1213.27938	2	2.18E-06	0.98	4.05	-	2468.4
AHQ-7-5, 2160 - 2164	K.DLEAHIDSANK.N	1213.27938	2	2.96E-06	0.97	4.37	-	1904.5
AHQ-7-2, 2255	K.DLEAHIDSANK.N	1213.27938	2	5.26E-07	0.98	4.40	-	2533.6
AHQ-7-6, 2173	K.DLEAHIDSANK.N	1213.27938	2	4.87E-06	0.98	4.33	-	2402.8
AHQ-7-3, 2227 - 2229	K.DLEAHIDSANK.N	1213.27938	2	4.24E-08	0.98	4.31	-	2344.6
AHQ-7-3, 2228	K.DLEAHIDSANK.N	1213.27938	1	1.25E-05	0.59	1.83	-	792.4
AHQ-7-2, 2259	K.DLEAHIDSANK.N	1213.27938	1	6.43E-05	0.54	1.98	-	788.7
AHQ-7-3, 2353	K.DLEGLSQR.H	917.98683	1	3.21E-04	0.04	1.90	-	144.8
AHQ-7-6, 6761	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	2.80E-10	0.97	6.86	-	1603.3
AHQ-7-6, 3285	K.DVLLQVDDER.R	1202.29650	2	3.68E-06	0.91	3.19	-	1320.8
AHQ-7-4, 2920	K.DVLLQVDDERR.N	1358.48286	2	2.17E-05	0.79	2.98	-	990.7
AHQ-7-3, 2980	K.DVLLQVDDERR.N	1358.48286	2	3.07E-05	0.60	2.67	-	683.6
AHQ-7-5, 2907	K.DVLLQVDDERR.N	1358.48286	2	7.34E-04	0.80	3.18	-	766.4
AHQ-7-2, 2288	R.ELEDATETADAM*NR.E	1582.62946	2	3.15E-04	0.84	3.07	-	988.0
AHQ-7-2, 3091	R.ELEDATETADAMNR.E	1566.63006	2	2.45E-08	0.90	3.51	-	1022.3
AHQ-7-6, 2811	R.ELEDATETADAMNR.E	1566.63006	2	9.14E-06	0.90	3.69	-	983.2
AHQ-7-2, 2845 - 2911	R.ELEDATETADAMNR.E	1566.63006	2	5.78E-07	0.93	3.94	-	1075.9
AHQ-7-1, 3036	R.ELEDATETADAMNR.E	1566.63006	2	8.38E-07	0.93	3.51	-	1389.4
AHQ-7-5, 2830	R.ELEDATETADAMNR.E	1566.63006	2	1.26E-09	0.95	4.33	-	1215.1
AHQ-7-1, 5572 - 5573	R.ELESQISELQEDLESER.A	2035.10956	3	4.70E-05	0.98	5.90	-	2490.7
AHQ-7-5, 5683	R.ELESQISELQEDLESER.A	2035.10956	2	9.03E-08	0.96	4.80	-	1186.7
AHQ-7-2, 5961 - 5996	R.ELESQISELQEDLESER.A	2035.10956	2	7.06E-08	0.96	4.73	-	1247.9
AHQ-7-7, 5513 - 5594	R.ELESQISELQEDLESER.A	2035.10956	2	1.82E-07	0.91	4.30	-	848.3
AHQ-7-3, 5161	R.ELESQISELQEDLESER.A	2035.10956	2	9.37E-07	0.87	3.78	-	743.0
AHQ-7-4, 5753	R.ELESQISELQEDLESER.A	2035.10956	3	3.69E-05	0.98	6.11	-	2396.8
AHQ-7-3, 5571 - 5636	R.ELESQISELQEDLESER.A	2035.10956	2	3.43E-06	0.91	4.59	-	814.8
AHQ-7-2, 5671 - 5737	R.ELESQISELQEDLESER.A	2035.10956	2	2.64E-06	0.95	4.47	-	1098.7
AHQ-7-3, 5852	R.ELESQISELQEDLESER.A	2035.10956	2	1.78E-06	0.68	2.86	-	679.9
AHQ-7-3, 5275	R.ELESQISELQEDLESER.A	2035.10956	2	4.11E-07	0.92	4.07	-	828.4
AHQ-7-1, 5559 - 5560	R.ELESQISELQEDLESER.A	2035.10956	2	1.18E-07	0.94	4.34	-	913.2
AHQ-7-2, 5384	R.ELESQISELQEDLESER.A	2035.10956	2	1.03E-07	0.88	3.96	-	606.3
AHQ-7-4, 5752	R.ELESQISELQEDLESER.A	2035.10956	2	9.42E-06	0.95	4.95	-	1161.2
AHQ-7-4, 2244	R.EMEAELEDERK.Q	1379.47597	2	9.42E-05	0.90	3.27	-	1094.0
AHQ-7-2, 2245 - 2315	R.EMEAELEDERK.Q	1379.47597	2	4.22E-04	0.94	3.39	-	1557.4
AHQ-7-5, 2219	R.EMEAELEDERK.Q	1379.47597	2	1.10E-04	0.87	3.05	-	1033.4
AHQ-7-2, 2311	R.EMEAELEDERK.Q	1379.47597	2	8.47E-06	0.93	3.35	-	1431.1
AHQ-7-5, 4322 - 4386	K.EQADFAIEALAK.A	1306.44632	2	4.42E-04	0.81	2.63	-	843.9
AHQ-7-2, 4496	K.EQADFAIEALAK.A	1306.44632	1	4.64E-04	0.59	3.25	-	324.5
AHQ-7-7, 4238	K.EQADFAIEALAK.A	1306.44632	2	6.60E-04	0.53	2.65	-	366.8
AHQ-7-4, 2518	R.EQEVNILK.K	973.10554	1	5.83E-04	0.21	2.33	-	196.4
AHQ-7-2, 2507 - 2508	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.19E-05	0.91	4.52	-	679.2
AHQ-7-3, 2761	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.17E-04	0.77	3.53	-	615.7
AHQ-7-5, 2432	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	5.42E-04	0.90	4.02	-	770.4
AHQ-7-2, 2372	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	5.02E-06	0.86	3.55	-	870.3
AHQ-7-1, 2701	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.26E-06	0.94	4.59	-	1166.4
AHQ-7-2, 5124 - 5185	R.FLSNGHVTIPGQQDKDMFQETMEAM*R.I	3028.39040	3	7.38E-04	0.79	4.67	-	606.0
AHQ-7-4, 3712	K.FVSELWK.D	909.06314	1	1.44E-04	0.33	1.83	-	810.3
AHQ-7-4, 2486	K.HEAM*ITDLEER.L	1360.47586	2	3.79E-04	0.97	4.04	-	1612.7
AHQ-7-5, 2914	K.HEAMITDLEER.L	1344.47646	2	1.39E-06	0.95	3.82	-	1267.9
AHQ-7-2, 3015 - 3017	K.HEAMITDLEER.L	1344.47646	2	1.26E-08	0.97	3.78	-	1617.0
AHQ-7-3, 2993 - 3007	K.HEAMITDLEER.L	1344.47646	2	4.19E-07	0.96	3.97	-	1384.6
AHQ-7-10, 3380	R.HEMPPHIYAITDTAYR.S	1916.14944	3	6.80E-04	0.94	3.55	-	1942.1
AHQ-7-2, 3441	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	5.53E-06	0.88	3.34	-	723.9

AHQ-7-1, 3816	R.HEMPPHIYAITDTAYR.S	1916.14944	3	1.40E-04	0.93	3.88	-	1532.2
AHQ-7-4, 3373	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	1.64E-06	0.97	4.67	-	2206.4
AHQ-7-11, 3240	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	1.10E-04	0.86	3.50	-	1099.5
AHQ-7-4, 3374	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	1.07E-04	0.56	2.55	-	550.4
AHQ-7-3, 3420	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	1.44E-06	0.98	5.18	-	2280.6
AHQ-7-2, 3425	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	4.91E-05	0.92	4.24	-	1486.9
AHQ-7-2, 3704 - 3767	R.HEMPPHIYAITDTAYR.S	1916.14944	3	4.96E-08	0.98	5.10	-	3380.9
AHQ-7-2, 3732	R.HEMPPHIYAITDTAYR.S	1916.14944	2	6.43E-06	0.95	4.15	-	1126.1
AHQ-7-1, 4600	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.00E-30	0.98	6.27	-	2260.6
AHQ-7-3, 4516	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.76E-09	0.98	6.16	-	2730.5
AHQ-7-3, 4520	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.33E-07	0.96	4.74	-	1937.5
AHQ-7-1, 4604	K.HSQAVEELAEQLEQTK.R	1840.96940	3	3.55E-05	0.92	4.36	-	1439.7
AHQ-7-4, 4545	K.HSQAVEELAEQLEQTK.R	1840.96940	2	3.30E-06	0.98	6.41	-	2339.5
AHQ-7-2, 4604	K.HSQAVEELAEQLEQTK.R	1840.96940	2	4.25E-08	0.98	6.20	-	2638.9
AHQ-7-2, 4605	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.75E-07	0.96	4.77	-	2075.5
AHQ-7-4, 4121 - 4192	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	2.39E-08	0.98	6.18	-	2084.0
AHQ-7-4, 4190	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.33E-12	0.99	6.89	-	2609.2
AHQ-7-5, 4154	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	3.35E-09	0.96	5.35	-	1116.9
AHQ-7-6, 4089	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	7.02E-07	0.97	5.61	-	1662.7
AHQ-7-1, 4240 - 4299	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	4.64E-06	0.97	5.49	-	1491.6
AHQ-7-3, 4193	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.06E-07	0.98	6.47	-	2408.6
AHQ-7-2, 4263	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.82E-10	0.97	6.77	-	1397.7
AHQ-7-1, 4292	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	9.35E-10	0.98	6.28	-	2478.0
AHQ-7-2, 4267	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.51E-07	0.98	6.61	-	2111.4
AHQ-7-4, 4185	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	5.00E-05	0.97	5.51	-	1786.5
AHQ-7-3, 4192	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	7.31E-07	0.97	6.16	-	1614.3
AHQ-7-3, 3716 - 3743	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.71E-09	0.97	4.52	-	1898.6
AHQ-7-2, 3963 - 4035	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.97E-10	0.97	4.59	-	1895.9
AHQ-7-2, 3836 - 3899	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.44E-10	0.95	3.86	-	1718.6
AHQ-7-2, 3727 - 3799	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.53E-04	0.95	4.34	-	1176.0
AHQ-7-5, 3722	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.94E-08	0.97	4.77	-	1776.4
AHQ-7-3, 3947 - 3988	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.59E-05	0.97	4.38	-	2332.2
AHQ-7-4, 3740 - 3810	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.15E-07	0.97	4.81	-	2095.6
AHQ-7-1, 3845	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.22E-09	0.97	4.41	-	1999.4
AHQ-7-3, 3807 - 3868	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.03E-09	0.94	4.51	-	1306.6
AHQ-7-3, 3627	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.16E-05	0.68	2.78	-	684.6
AHQ-7-6, 3657	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.24E-07	0.95	3.79	-	1532.7
AHQ-7-7, 3546 - 3592	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.21E-07	0.91	3.40	-	1272.8
AHQ-7-2, 3613	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.54E-08	0.90	3.83	-	955.4
AHQ-7-13, 3806 - 3834	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.10E-06	0.93	4.02	-	1222.1
AHQ-7-8, 3555	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.07E-06	0.96	4.59	-	1675.2
AHQ-7-3, 5075 - 5076	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	1.24E-04	0.86	3.99	-	985.3
AHQ-7-2, 5467	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	4.71E-07	0.94	4.86	-	1052.5
AHQ-7-3, 5356 - 5363	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	9.32E-08	0.94	4.87	-	938.9
AHQ-7-2, 5463	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	2.28E-07	0.84	4.01	-	739.9
AHQ-7-4, 5472	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	2.38E-06	0.91	4.21	-	913.5
AHQ-7-1, 5312 - 5380	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	1.03E-04	0.66	3.71	-	542.7
AHQ-7-7, 3233 - 3270	K.IAQLEEQLDNETK.E	1531.64695	2	1.77E-05	0.91	4.03	-	790.4
AHQ-7-6, 3321	K.IAQLEEQLDNETK.E	1531.64695	2	7.06E-10	0.97	5.08	-	1727.1
AHQ-7-1, 3527	K.IAQLEEQLDNETK.E	1531.64695	2	1.63E-07	0.97	4.42	-	2258.3
AHQ-7-11, 3031	K.IAQLEEQLDNETK.E	1531.64695	2	6.54E-05	0.94	3.38	-	1534.1
AHQ-7-3, 3348 - 3400	K.IAQLEEQLDNETK.E	1531.64695	2	6.31E-08	0.96	3.84	-	2013.5
AHQ-7-2, 3587	K.IAQLEEQLDNETK.E	1531.64695	2	1.36E-06	0.87	3.32	-	817.0
AHQ-7-11, 3231	K.IAQLEEQLDNETK.E	1531.64695	2	4.45E-06	0.96	4.16	-	1581.9
AHQ-7-2, 3447 - 3515	K.IAQLEEQLDNETK.E	1531.64695	2	1.38E-07	0.97	4.28	-	1587.1
AHQ-7-8, 3262	K.IAQLEEQLDNETK.E	1531.64695	2	9.01E-09	0.96	4.75	-	1257.3
AHQ-7-3, 3171	K.IAQLEEQLDNETK.E	1531.64695	2	1.59E-08	0.97	4.75	-	1680.4
AHQ-7-4, 3158	K.IAQLEEQLDNETK.E	1531.64695	2	7.78E-06	0.93	3.82	-	1403.1
AHQ-7-4, 3380 - 3453	K.IAQLEEQLDNETK.E	1531.64695	2	2.37E-05	0.92	3.79	-	940.7
AHQ-7-2, 3224 - 3296	K.IAQLEEQLDNETK.E	1531.64695	2	1.83E-07	0.97	5.08	-	1788.2
AHQ-7-5, 3359	K.IAQLEEQLDNETK.E	1531.64695	2	1.12E-05	0.96	4.27	-	1668.9
AHQ-7-2, 3013	K.IAQLEEQLDNETK.E	1531.64695	2	1.35E-05	0.94	4.20	-	1045.6
AHQ-7-9, 3082	K.IAQLEEQLDNETK.E	1531.64695	2	5.10E-04	0.92	3.67	-	1094.6
AHQ-7-2, 3181	K.IAQLEEQLDNETKER.Q	1816.94784	2	8.14E-05	0.66	2.88	-	547.8
AHQ-7-2, 3605	K.IAQLEEQLDNETKER.Q	1816.94784	2	4.38E-09	0.91	4.25	-	799.7
AHQ-7-1, 6072 - 6145	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.64E-13	0.97	5.59	-	1357.4
AHQ-7-6, 6206	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.86E-05	0.95	5.08	-	967.3
AHQ-7-8, 6267	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	6.70E-06	0.96	4.71	-	1290.0
AHQ-7-6, 5517 - 5581	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	9.31E-04	0.77	3.90	-	627.3
AHQ-7-7, 6254 - 6258	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.85E-05	0.96	5.27	-	949.4
AHQ-7-14-, 5318	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.16E-05	0.94	4.17	-	997.6
AHQ-7-2, 6341 - 6399	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.83E-07	0.96	5.43	-	1106.5
AHQ-7-3, 6208 - 6280	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.68E-06	0.84	3.73	-	584.8
AHQ-7-5, 6298 - 6330	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.61E-04	0.91	4.24	-	819.7
AHQ-7-2, 5831 - 5861	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.50E-06	0.95	5.06	-	1004.3
AHQ-7-6, 5066 - 5125	R.IMGIPEEEQMGLLR.V	1616.92826	2	7.36E-07	0.90	4.16	-	514.8
AHQ-7-6, 4530	R.IM*GIPEEEQMGLLR.V	1632.92766	2	1.24E-04	0.83	2.94	-	652.0
AHQ-7-5, 5191 - 5263	R.IMGIPEEEQMGLLR.V	1616.92826	2	2.03E-08	0.82	3.39	-	321.4
AHQ-7-2, 5272 - 5281	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	4.74E-05	0.85	3.67	-	482.6
AHQ-7-2, 5256 - 5279	R.IMGIPEEEQMGLLR.V	1616.92826	2	7.33E-06	0.87	3.53	-	537.8
AHQ-7-2, 4652 - 4716	R.IM*GIPEEEQMGLLR.V	1632.92766	2	1.27E-08	0.96	4.64	-	964.4
AHQ-7-4, 5256	R.IMGIPEEEQMGLLR.V	1616.92826	2	8.13E-06	0.88	3.64	-	455.7
AHQ-7-4, 5772 - 5786	K.IRELESQISELQEDLESER.A	2304.45416	3	3.06E-05	0.93	4.47	-	1274.6
AHQ-7-4, 5757 - 5776	K.IRELESQISELQEDLESER.A	2304.45416	2	1.77E-06	0.98	6.31	-	1234.4
AHQ-7-1, 5607	K.IRELESQISELQEDLESER.A	2304.45416	2	8.38E-04	0.96	5.16	-	826.3
AHQ-7-3, 5648	K.IRELESQISELQEDLESER.A	2304.45416	2	3.38E-05	0.98	6.43	-	1295.0
AHQ-7-2, 5783 - 5797	K.IRELESQISELQEDLESER.A	2304.45416	3	2.15E-07	0.96	5.43	-	1877.9
AHQ-7-3, 5647 - 5659	K.IRELESQISELQEDLESER.A	2304.45416	3	9.26E-06	0.96	5.02	-	1701.7
AHQ-7-1, 5549 - 5608	K.IRELESQISELQEDLESER.A	2304.45416	2	4.81E-08	0.98	6.95	-	1625.1
AHQ-7-2, 5741 - 5803	K.IRELESQISELQEDLESER.A	2304.45416	2	3.07E-04	0.98	6.65	-	1832.2
AHQ-7-2, 5481	K.ITDVIIGFQACCR.G	1555.80136	2	2.25E-05	0.90	3.25	-	1075.2
AHQ-7-4, 4492 - 4565	K.KANLQIDQINTDLNLER.S	1999.21478	2	9.25E-07	0.96	5.19	-	1369.3
AHQ-7-2, 4765	K.KANLQIDQINTDLNLER.S	1999.21478	2	3.44E-07	0.94	4.60	-	1034.3
AHQ-7-2, 4457	K.KANLQIDQINTDLNLER.S	1999.21478	2	8.89E-09	0.97	5.73	-	1222.7
AHQ-7-2, 4601 - 4627	K.KANLQIDQINTDLNLER.S	1999.21478	3	2.05E-05	0.90	4.42	-	1041.6
AHQ-7-5, 4502	K.KANLQIDQINTDLNLER.S	1999.21478	2	9.22E-09	0.96	5.10	-	1219.3
AHQ-7-2, 4607	K.KANLQIDQINTDLNLER.S	1999.21478	2	4.07E-04	0.97	5.95	-	1253.8
AHQ-7-6, 4415	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.77E-11	0.97	5.23	-	1547.5
AHQ-7-3, 2691	R.KKVEAQLQELQVK.F	1541.81761	2	9.51E-08	0.97	4.97	-	1719.4
AHQ-7-1, 2933	R.KKVEAQLQELQVK.F	1541.81761	2	1.07E-05	0.94	4.45	-	1294.0
AHQ-7-4, 2646	R.KKVEAQLQELQVK.F	1541.81761	2	3.82E-09	0.97	4.90	-	1513.8
AHQ-7-2, 2704 - 2707	R.KKVEAQLQELQVK.F	1541.81761	2	1.43E-09	0.97	5.35	-	1375.4
AHQ-7-5, 2656	R.KKVEAQLQELQVK.F	1541.81761	2	3.34E-06	0.97	4.83	-	1548.7
AHQ-7-1, 3635 - 3696	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.54E-08	0.98	6.03	-	1707.7
AHQ-7-3, 3493 - 3575	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.56E-09	0.98	6.42	-	1989.6
AHQ-7-3, 3596	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.36E-12	0.98	5.56	-	1969.4
AHQ-7-2, 3548 - 3627	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.26E-04	0.96	5.27	-	1124.7

AHQ-7-4, 3492 - 3572	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.90E-09	0.98	6.10	-	2356.0
AHQ-7-5, 3467	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.74E-05	0.98	5.88	-	1890.4
AHQ-7-2, 3653	K.KLEEEQIILEDQNCK.L	1891.08992	3	4.70E-04	0.93	4.31	-	1423.9
AHQ-7-6, 3413	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.37E-04	0.95	4.84	-	891.0
AHQ-7-2, 3983	K.KLEEEQIILEDQNCKLAK.E	2203.49930	3	8.50E-04	0.96	4.95	-	1428.0
AHQ-7-3, 6593 - 6659	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	4.62E-08	0.97	5.94	-	1474.6
AHQ-7-4, 6796 - 6798	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	6.13E-08	0.91	5.03	-	714.2
AHQ-7-6, 6601	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	7.97E-08	0.86	4.12	-	1064.4
AHQ-7-3, 6516 - 6592	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	5.00E-06	0.93	5.67	-	930.3
AHQ-7-2, 6692 - 6767	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	6.92E-08	0.94	5.46	-	918.3
AHQ-7-2, 6057 - 6135	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	9.84E-05	0.92	4.34	-	1049.8
AHQ-7-7, 6688	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	4.49E-08	0.91	4.99	-	742.9
AHQ-7-1, 6480	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.15E-06	0.90	3.75	-	925.9
AHQ-7-1, 6475 - 6477	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	4.91E-06	0.95	6.03	-	891.2
AHQ-7-2, 6576	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	6.19E-06	0.96	5.14	-	1757.7
AHQ-7-5, 6710	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	8.42E-09	0.93	5.15	-	925.8
AHQ-7-3, 5911	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	1.53E-05	0.95	5.47	-	1538.1
AHQ-7-4, 6797 - 6874	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	1.62E-06	0.96	6.11	-	996.9
AHQ-7-6, 2813	K.KLVWVPSDK.S	1072.28194	2	4.82E-04	0.77	3.41	-	738.4
AHQ-7-4, 2868	K.KLVWVPSDK.S	1072.28194	2	1.07E-04	0.89	3.37	-	982.5
AHQ-7-2, 2947	K.KLVWVPSDK.S	1072.28194	1	8.64E-04	0.56	2.44	-	501.2
AHQ-7-3, 2936	K.KLVWVPSDK.S	1072.28194	2	3.39E-04	0.89	3.60	-	797.0
AHQ-7-2, 2944	K.KLVWVPSDK.S	1072.28194	2	3.21E-05	0.91	3.20	-	1141.6
AHQ-7-2, 3699	K.KMEDSVGCLETAEEVK.R	1827.02450	2	1.27E-04	0.89	4.03	-	819.6
AHQ-7-5, 3207	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	2.29E-04	0.91	3.47	-	1053.2
AHQ-7-3, 3620	K.KMEDSVGCLETAEEVK.R	1827.02450	2	5.27E-04	0.92	3.81	-	1375.9
AHQ-7-2, 3381	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	6.42E-08	0.95	5.25	-	1142.8
AHQ-7-3, 3017	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	1.07E-06	0.91	3.92	-	779.3
AHQ-7-3, 3336	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	6.28E-05	0.95	5.29	-	1230.6
AHQ-7-6, 3241	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.75E-09	0.97	5.16	-	1876.6
AHQ-7-4, 3325	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.23E-04	0.76	3.74	-	453.5
AHQ-7-2, 3289	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	2.42E-05	0.78	3.53	-	851.2
AHQ-7-2, 3043 - 3056	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	7.89E-04	0.93	4.66	-	1263.5
AHQ-7-2, 3040	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	1.63E-05	0.86	3.64	-	545.4
AHQ-7-4, 2953	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	2.88E-04	0.97	4.90	-	2108.0
AHQ-7-5, 2940	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	5.70E-04	0.94	4.18	-	1508.3
AHQ-7-3, 5227	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	1.98E-08	0.97	5.97	-	1183.4
AHQ-7-2, 5331	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	1.34E-08	0.97	5.36	-	1467.2
AHQ-7-3, 4788	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	7.96E-09	0.90	4.80	-	1207.0
AHQ-7-4, 5317	K.KMQQNIQELEEQLEEEESAR.Q	2462.63354	2	3.31E-05	0.87	3.72	-	908.6
AHQ-7-3, 4119 - 4135	K.KQELEEICHDLEAR.V	1771.93036	2	4.54E-06	0.98	5.88	-	2024.5
AHQ-7-5, 4107	K.KQELEEICHDLEAR.V	1771.93036	2	2.92E-06	0.96	4.72	-	1587.5
AHQ-7-3, 4121 - 4131	K.KQELEEICHDLEAR.V	1771.93036	3	2.98E-04	0.94	4.99	-	1091.9
AHQ-7-1, 4223	K.KQELEEICHDLEAR.V	1771.93036	3	5.35E-05	0.96	5.22	-	1639.5
AHQ-7-2, 4189	K.KQELEEICHDLEAR.V	1771.93036	2	5.79E-04	0.98	5.37	-	2136.7
AHQ-7-4, 4124	K.KQELEEICHDLEAR.V	1771.93036	2	4.15E-05	0.97	5.55	-	1572.5
AHQ-7-4, 4132	K.KQELEEICHDLEAR.V	1771.93036	3	5.33E-05	0.96	4.94	-	1570.4
AHQ-7-6, 2949	K.KVEAQLQELQVK.F	1413.64470	2	1.10E-06	0.96	4.67	-	1538.0
AHQ-7-1, 3231	K.KVEAQLQELQVK.F	1413.64470	2	1.36E-05	0.95	4.48	-	1325.2
AHQ-7-2, 3068	K.KVEAQLQELQVK.F	1413.64470	2	3.00E-06	0.96	4.86	-	1340.2
AHQ-7-3, 3043	K.KVEAQLQELQVK.F	1413.64470	2	1.82E-06	0.97	5.77	-	1417.9
AHQ-7-4, 2985	K.KVEAQLQELQVK.F	1413.64470	2	1.12E-05	0.97	4.92	-	1668.1
AHQ-7-5, 2876 - 2954	K.KVEAQLQELQVK.F	1413.64470	2	1.51E-06	0.96	4.50	-	1503.7
AHQ-7-1, 3889 - 3949	K.LEEEQIILEDQNCK.L	1762.91700	2	3.06E-07	0.97	5.73	-	1168.0
AHQ-7-2, 3883 - 3947	K.LEEEQIILEDQNCK.L	1762.91700	2	2.41E-10	0.97	5.38	-	1194.6
AHQ-7-2, 3897	K.LEEEQIILEDQNCK.L	1762.91700	3	4.13E-06	0.86	4.23	-	1128.8
AHQ-7-4, 3825 - 3848	K.LEEEQIILEDQNCK.L	1762.91700	2	1.43E-07	0.95	4.60	-	1172.2
AHQ-7-3, 6647	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	3.48E-07	0.93	5.98	-	816.5
AHQ-7-3, 2673	R.LEVNLQAM*K.A	1062.26570	2	1.30E-04	0.81	3.14	-	608.9
AHQ-7-4, 2638	R.LEVNLQAM*K.A	1062.26570	2	8.47E-04	0.85	2.76	-	802.0
AHQ-7-3, 3573	R.LEVNLQAMK.A	1046.26630	2	8.08E-05	0.85	3.42	-	650.4
AHQ-7-2, 2693	R.LEVNLQAM*K.A	1062.26570	2	4.31E-05	0.89	3.58	-	725.7
AHQ-7-3, 3536 - 3548	K.LKDVLLQVDDER.R	1443.62767	2	1.33E-05	0.94	3.71	-	1306.6
AHQ-7-3, 3207 - 3231	K.LKDVLLQVDDERR.N	1599.81402	2	3.79E-04	0.90	3.63	-	1344.8
AHQ-7-1, 3392	K.LKDVLLQVDDERR.N	1599.81402	3	1.64E-05	0.80	3.22	-	904.6
AHQ-7-2, 3227	K.LKDVLLQVDDERR.N	1599.81402	2	1.57E-05	0.91	3.93	-	1036.9
AHQ-7-2, 6888 - 6953	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	2.65E-07	0.93	3.82	-	1195.6
AHQ-7-2, 6944 - 7001	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	3	1.96E-04	0.92	4.13	-	1398.6
AHQ-7-2, 7012	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	5.79E-06	0.91	3.71	-	872.9
AHQ-7-3, 6737	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	7.59E-04	0.89	3.05	-	838.6
AHQ-7-2, 5991 - 6003	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.08E-09	0.97	4.96	-	2015.0
AHQ-7-1, 5445	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.61E-06	0.88	4.16	-	714.4
AHQ-7-2, 5987 - 6051	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	4.01E-06	0.91	4.06	-	845.9
AHQ-7-4, 5988	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.67E-05	0.93	4.74	-	890.3
AHQ-7-4, 5994	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.74E-10	0.98	5.49	-	2012.4
AHQ-7-5, 5948	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.32E-08	0.98	5.35	-	1827.7
AHQ-7-6, 5849	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	2.50E-07	0.85	4.03	-	711.1
AHQ-7-6, 5851	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	7.95E-10	0.96	4.65	-	1535.2
AHQ-7-3, 5864 - 5871	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	2.55E-04	0.90	4.40	-	659.1
AHQ-7-3, 5863 - 5867	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	9.51E-11	0.97	5.07	-	1971.4
AHQ-7-2, 5593	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.51E-10	0.94	4.82	-	1086.4
AHQ-7-2, 5592	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	9.36E-06	0.89	4.05	-	839.5
AHQ-7-7, 5856	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.80E-08	0.97	4.67	-	1602.2
AHQ-7-1, 5816	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.11E-06	0.97	5.05	-	1661.2
AHQ-7-1, 5731	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.08E-07	0.93	4.02	-	1045.6
AHQ-7-2, 5396 - 5415	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.30E-08	0.97	5.69	-	1108.0
AHQ-7-3, 5769	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.33E-06	0.93	4.42	-	1042.3
AHQ-7-3, 5676 - 5704	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.31E-07	0.95	4.83	-	1194.5
AHQ-7-2, 5675 - 5735	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.90E-06	0.98	5.77	-	1593.5
AHQ-7-2, 5721	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	2.88E-07	0.96	5.70	-	1337.0
AHQ-7-3, 5584 - 5643	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.53E-07	0.96	5.05	-	1131.6
AHQ-7-3, 5583	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	9.17E-09	0.97	5.17	-	1811.2
AHQ-7-6, 5550	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.08E-07	0.97	5.33	-	1218.1
AHQ-7-5, 5600 - 5658	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.77E-07	0.98	5.46	-	1897.0
AHQ-7-1, 5619 - 5677	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.02E-06	0.94	4.83	-	874.2
AHQ-7-7, 5536	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.17E-04	0.89	3.62	-	1088.2
AHQ-7-2, 5799 - 5869	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.29E-10	0.98	6.85	-	1688.6
AHQ-7-2, 6961	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.38E-05	0.93	4.67	-	676.9
AHQ-7-2, 6297	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.36E-04	0.88	4.02	-	565.6
AHQ-7-1, 5529	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	3.85E-07	0.95	4.58	-	1403.2
AHQ-7-1, 5499 - 5555	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.89E-10	0.97	5.15	-	1312.7
AHQ-7-3, 5280	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.20E-08	0.96	5.15	-	1138.5
AHQ-7-1, 5264	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.13E-07	0.94	4.84	-	764.6
AHQ-7-14-, 5354	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.24E-05	0.96	5.27	-	985.4
AHQ-7-4, 5700	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	7.00E-08	0.98	5.51	-	1744.2
AHQ-7-2, 5943 - 6012	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.22E-11	0.98	5.88	-	1743.8
AHQ-7-3, 4009 - 4071	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	3.59E-08	0.98	4.49	-	2644.5

AHQ-7-1, 3645	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	7.17E-05	0.93	3.94	-	1102.3
AHQ-7-3, 4969 - 4995	R.LTEMETLQSQLMAEK.L	1753.03211	2	4.04E-05	0.92	3.97	-	1045.5
AHQ-7-4, 4080	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	2.56E-08	0.98	4.42	-	2345.3
AHQ-7-2, 3631 - 3709	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	9.12E-06	0.96	4.42	-	1385.3
AHQ-7-2, 4095 - 4159	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	2.75E-05	0.96	4.56	-	1779.7
AHQ-7-3, 4485 - 4511	R.LTEMETLQSQLM*AEK.L	1769.03151	2	1.02E-04	0.93	3.94	-	1242.7
AHQ-7-1, 4091	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	1.03E-04	0.97	4.47	-	2260.0
AHQ-7-2, 4505 - 4580	R.LTEMETLQSQLM*AEK.L	1769.03151	2	5.19E-05	0.94	4.44	-	1131.5
AHQ-7-2, 6655	K.LTKDFSALESQLQDTQELLQEENR.Q	2837.04608	3	2.62E-05	0.91	4.50	-	1215.2
AHQ-7-3, 3897 - 3901	K.MEDSVGCLETAEEVK.R	1698.85159	2	2.78E-06	0.90	4.21	-	558.8
AHQ-7-4, 3917	K.MEDSVGCLETAEEVK.R	1698.85159	2	3.51E-06	0.93	3.84	-	990.8
AHQ-7-2, 3972	K.MEDSVGCLETAEEVK.R	1698.85159	2	7.75E-06	0.92	3.71	-	1018.4
AHQ-7-2, 3643 - 3645	K.MEDSVGCLETAEEVKR.K	1855.03794	3	9.52E-06	0.83	3.88	-	679.4
AHQ-7-2, 3640	K.MEDSVGCLETAEEVKR.K	1855.03794	2	5.27E-06	0.56	2.78	-	367.3
AHQ-7-3, 3565	K.MEDSVGCLETAEEVKR.K	1855.03794	2	4.66E-06	0.86	3.50	-	604.1
AHQ-7-3, 3292	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	1.08E-07	0.79	3.53	-	435.2
AHQ-7-2, 3344	K.M*EDSVGCLETAEEVKR.K	1871.03734	3	7.13E-05	0.78	3.55	-	609.3
AHQ-7-4, 3564	K.MEDSVGCLETAEEVKR.K	1855.03794	2	1.34E-09	0.80	3.24	-	484.6
AHQ-7-3, 5144 - 5151	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	4.30E-09	0.96	5.90	-	1704.7
AHQ-7-1, 5135	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	3.15E-09	0.97	5.06	-	2029.8
AHQ-7-2, 5251	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	5.05E-07	0.97	6.02	-	1556.7
AHQ-7-1, 5204	K.NFINNPLAQADWAAK.K	1673.85315	2	1.45E-09	0.96	4.76	-	1132.0
AHQ-7-1, 5591	K.NFINNPLAQADWAAK.K	1673.85315	2	3.21E-05	0.87	3.40	-	736.8
AHQ-7-10, 4745	K.NFINNPLAQADWAAK.K	1673.85315	2	1.50E-08	0.93	4.45	-	893.8
AHQ-7-2, 5288 - 5299	K.NFINNPLAQADWAAK.K	1673.85315	2	3.24E-07	0.96	4.83	-	1290.4
AHQ-7-4, 5290	K.NFINNPLAQADWAAK.K	1673.85315	2	3.43E-04	0.96	4.99	-	1376.1
AHQ-7-2, 5489	K.NFINNPLAQADWAAK.K	1673.85315	2	2.69E-09	0.95	4.37	-	1409.4
AHQ-7-13, 5507	K.NFINNPLAQADWAAK.K	1673.85315	2	2.28E-05	0.70	2.87	-	640.3
AHQ-7-13-, 5019	K.NFINNPLAQADWAAK.K	1673.85315	2	1.89E-10	0.97	5.15	-	1283.2
AHQ-7-6, 5150 - 5157	K.NFINNPLAQADWAAK.K	1673.85315	2	1.36E-08	0.95	4.90	-	1034.0
AHQ-7-5, 5190 - 5254	K.NFINNPLAQADWAAK.K	1673.85315	2	1.97E-04	0.95	4.96	-	1042.2
AHQ-7-3, 5203	K.NFINNPLAQADWAAK.K	1673.85315	2	8.76E-06	0.93	4.36	-	985.9
AHQ-7-2, 5776	K.NFINNPLAQADWAAK.K	1673.85315	2	2.63E-10	0.93	3.92	-	1040.0
AHQ-7-4, 2641	K.NKHEAMITDLEER.L	1586.75247	2	4.14E-08	0.91	3.52	-	1174.5
AHQ-7-3, 2703 - 2704	K.NKHEAMITDLEER.L	1586.75247	2	3.82E-09	0.92	3.58	-	1081.5
AHQ-7-2, 2715	K.NKHEAMITDLEER.L	1586.75247	2	4.41E-09	0.93	3.65	-	1302.8
AHQ-7-6, 5015 - 5042	K.NLPIYSEEIVEM*YK.G	1744.98660	2	8.71E-05	0.78	2.61	-	727.7
AHQ-7-2, 5716 - 5720	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.56E-06	0.94	4.35	-	801.2
AHQ-7-7, 4936	K.NLPIYSEEIVEM*YK.G	1744.98660	2	7.40E-04	0.89	3.27	-	790.6
AHQ-7-4, 5142	K.NLPIYSEEIVEM*YK.G	1744.98660	2	5.45E-05	0.92	3.90	-	784.3
AHQ-7-13, 4990	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.13E-05	0.84	3.46	-	555.0
AHQ-7-11, 5228 - 5230	K.NLPIYSEEIVEMYK.G	1728.98720	2	3.82E-06	0.78	3.06	-	685.1
AHQ-7-10, 5123 - 5131	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.08E-05	0.92	4.14	-	553.9
AHQ-7-3, 5587 - 5623	K.NLPIYSEEIVEMYK.G	1728.98720	2	7.61E-05	0.90	3.75	-	754.3
AHQ-7-2, 5167 - 5168	K.NLPIYSEEIVEM*YK.G	1744.98660	2	7.65E-09	0.96	5.13	-	1002.5
AHQ-7-5, 5094	K.NLPIYSEEIVEM*YK.G	1744.98660	2	3.28E-05	0.94	4.09	-	998.1
AHQ-7-6, 5555	K.NLPIYSEEIVEMYK.G	1728.98720	2	4.34E-04	0.86	3.32	-	564.4
AHQ-7-1, 5065 - 5105	K.NLPIYSEEIVEM*YK.G	1744.98660	2	3.33E-05	0.95	4.20	-	853.9
AHQ-7-2, 5069	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	2.54E-08	0.90	4.18	-	700.0
AHQ-7-3, 5321 - 5395	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.23E-04	0.81	3.81	-	628.0
AHQ-7-4, 5505	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	7.88E-05	0.94	4.36	-	981.0
AHQ-7-2, 5523	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	5.88E-05	0.60	2.60	-	487.5
AHQ-7-3, 5399	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	3	4.68E-06	0.69	3.04	-	440.1
AHQ-7-2, 5511	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	1.07E-04	0.89	4.43	-	640.1
AHQ-7-3, 3268 - 3271	R.QAQQERDELADEIANSSGK.G	2090.15168	3	3.90E-04	0.89	4.65	-	670.9
AHQ-7-2, 2915	R.QAQQERDELADEIANSSGK.G	2090.15168	2	1.05E-05	0.90	3.88	-	818.5
AHQ-7-2, 3249 - 3315	R.QAQQERDELADEIANSSGK.G	2090.15168	2	5.43E-04	0.92	4.21	-	636.8
AHQ-7-2, 2121	R.QLEEAEEEAQR.A	1332.35590	2	5.43E-04	0.82	3.23	-	711.6
AHQ-7-3, 2111	R.QLEEAEEEAQR.A	1332.35590	2	1.50E-06	0.65	3.08	-	431.6
AHQ-7-4, 2068	R.QLEEAEEEAQR.A	1332.35590	2	1.84E-05	0.72	3.04	-	508.5
AHQ-7-3, 3655	R.RGDLPFVVPR.R	1156.36217	2	3.84E-05	0.94	3.67	-	1497.1
AHQ-7-1, 3813	R.RGDLPFVVPR.R	1156.36217	2	6.45E-05	0.93	3.72	-	1324.9
AHQ-7-4, 3636	R.RGDLPFVVPR.R	1156.36217	2	1.17E-04	0.93	3.87	-	1020.3
AHQ-7-6, 3534	R.RGDLPFVVPR.R	1156.36217	2	2.37E-06	0.94	3.93	-	1247.1
AHQ-7-9, 3254	R.RGDLPFVVPR.R	1156.36217	2	1.06E-04	0.85	3.21	-	922.5
AHQ-7-7, 3468	R.RGDLPFVVPR.R	1156.36217	2	2.25E-05	0.78	3.05	-	625.0
AHQ-7-11, 3455	R.RGDLPFVVPR.R	1156.36217	2	2.47E-04	0.94	3.37	-	1443.8
AHQ-7-2, 3711 - 3757	R.RGDLPFVVPR.R	1156.36217	2	5.88E-06	0.93	3.82	-	1131.4
AHQ-7-5, 3598 - 3599	R.RGDLPFVVPR.R	1156.36217	2	7.46E-06	0.94	3.95	-	1113.4
AHQ-7-2, 3156	K.RHEM*PPHIYAITDTAYR.S	2088.33519	3	2.78E-06	0.95	4.62	-	1306.1
AHQ-7-2, 6591	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	6.39E-13	0.96	5.99	-	1419.5
AHQ-7-1, 6363 - 6372	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	5.32E-05	0.95	5.69	-	1133.8
AHQ-7-3, 6519	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	4.67E-06	0.95	5.44	-	1211.7
AHQ-7-3, 6428	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	2.17E-06	0.96	5.52	-	1574.1
AHQ-7-4, 6600	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	4.53E-08	0.97	5.76	-	1928.5
AHQ-7-3, 2087	K.RQLEEAEEEAQR.A	1488.54225	2	1.61E-09	0.97	4.81	-	2656.3
AHQ-7-2, 2105	K.RQLEEAEEEAQR.A	1488.54225	2	5.01E-08	0.98	5.77	-	3280.7
AHQ-7-5, 5975	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.62E-07	0.86	3.83	-	867.6
AHQ-7-2, 6112 - 6181	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	9.56E-09	0.96	5.25	-	1266.2
AHQ-7-2, 6929 - 6997	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.07E-04	0.80	3.69	-	744.9
AHQ-7-6, 6022	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	4.05E-09	0.93	4.95	-	1096.6
AHQ-7-1, 5968 - 5985	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.21E-05	0.89	4.30	-	966.0
AHQ-7-13-, 5789	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.04E-09	0.96	5.81	-	1095.5
AHQ-7-2, 6421 - 6489	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.70E-04	0.83	3.89	-	810.0
AHQ-7-1, 5512 - 5568	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	1.88E-05	0.91	4.78	-	1082.2
AHQ-7-3, 4669	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.48E-09	0.98	5.76	-	1544.6
AHQ-7-2, 5508	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	2.40E-04	0.85	4.05	-	875.6
AHQ-7-3, 4652	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	4.17E-07	0.93	3.99	-	1474.3
AHQ-7-7, 6481	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.42E-05	0.94	4.24	-	1365.2
AHQ-7-4, 6601 - 6629	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	1.75E-04	0.94	4.50	-	1335.7
AHQ-7-1, 4683	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.52E-09	0.96	5.02	-	1696.0
AHQ-7-2, 7020	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	4.92E-04	0.54	2.78	-	316.4
AHQ-7-2, 6600	K.SMEAEMIQLQEELAAAER.A	2050.30064	3	2.12E-04	0.91	4.43	-	965.0
AHQ-7-2, 5687 - 5759	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	4.51E-09	0.95	5.45	-	1690.8
AHQ-7-2, 4755 - 4835	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.14E-09	0.97	5.43	-	1472.7
AHQ-7-1, 5284 - 5348	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	1.19E-07	0.91	4.26	-	1305.3
AHQ-7-2, 4912	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	3.95E-07	0.95	4.65	-	1493.5
AHQ-7-2, 6543	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	2.90E-06	0.93	4.12	-	1276.9
AHQ-7-5, 6550	K.SMEAEMIQLQEELAAAER.A	2050.30064	2	6.79E-05	0.95	4.64	-	1373.5
AHQ-7-10, 3256	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	4.94E-04	0.69	2.75	-	697.4
AHQ-7-2, 3097	R.SMM*QDREDQSILCTGESGAGK.T	2318.50627	2	6.37E-04	0.91	4.77	-	487.1
AHQ-7-2, 3596	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	3.45E-08	0.96	5.06	-	1493.1
AHQ-7-3, 3519	R.SMMQDREDQSILCTGESGAGK.T	2302.50687	2	2.29E-05	0.98	6.18	-	1727.4
AHQ-7-7, 3581 - 3657	K.TDLLLEPYNK.Y	1206.36989	2	1.10E-04	0.61	2.64	-	736.0
AHQ-7-1, 3857 - 3865	K.TDLLLEPYNK.Y	1206.36989	2	1.75E-07	0.89	3.57	-	1099.1
AHQ-7-2, 3808 - 3809	K.TDLLLEPYNK.Y	1206.36989	2	2.81E-05	0.94	3.98	-	1154.1
AHQ-7-6, 3585 - 3645	K.TDLLLEPYNK.Y	1206.36989	2	4.19E-06	0.91	3.51	-	1050.6

AHQ-7-5, 3687	K.TDLLLEPYNK.Y	1206.36989	2	1.69E-05	0.85	3.73	-	838.0
AHQ-7-3, 3739	K.TDLLLEPYNK.Y	1206.36989	2	1.52E-05	0.93	3.78	-	1269.8
AHQ-7-4, 3742	K.TDLLLEPYNK.Y	1206.36989	2	9.48E-06	0.87	3.23	-	953.5
AHQ-7-2, 3987	K.TDLLLEPYNKYR.F	1525.73037	2	2.20E-06	0.78	2.98	-	641.1
AHQ-7-2, 4385	K.TELEDTLDSTAAQQELR.S	1921.00969	3	5.70E-07	0.96	4.83	-	2065.5
AHQ-7-4, 4246 - 4312	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.44E-04	0.94	3.92	-	1497.9
AHQ-7-2, 4367	K.TELEDTLDSTAAQQELR.S	1921.00969	2	2.37E-07	0.78	3.41	-	747.7
AHQ-7-1, 4307	K.TELEDTLDSTAAQQELR.S	1921.00969	2	8.71E-07	0.95	4.51	-	1388.4
AHQ-7-3, 4268	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.21E-08	0.93	4.37	-	1092.1
AHQ-7-5, 4256	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.25E-07	0.96	4.83	-	1620.8
AHQ-7-6, 3102	R.TEMEDLMSSK.D	1171.32449	2	3.21E-05	0.81	2.53	-	787.4
AHQ-7-4, 3126	R.TEMEDLMSSK.D	1171.32449	1	6.56E-05	0.38	1.97	-	489.7
AHQ-7-2, 3215	R.TEMEDLMSSK.D	1171.32449	2	6.74E-04	0.74	2.51	-	588.0
AHQ-7-3, 3393	R.TEMEDLMSSKDDVGK.S	1685.85626	2	2.93E-06	0.89	3.87	-	1018.9
AHQ-7-2, 2603	R.TEMEDLM*SSKDDVGK.S	1701.85566	2	8.33E-05	0.57	2.91	-	399.4
AHQ-7-6, 3297	R.TEMEDLMSSKDDVGK.S	1685.85626	2	2.88E-09	0.84	3.30	-	910.5
AHQ-7-4, 3376 - 3378	R.TEMEDLMSSKDDVGK.S	1685.85626	2	7.97E-06	0.81	3.17	-	823.9
AHQ-7-2, 3451	R.TEMEDLMSSKDDVGK.S	1685.85626	2	1.56E-05	0.90	3.31	-	1314.7
AHQ-7-5, 6338	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	9.67E-04	0.74	3.16	-	413.3
AHQ-7-2, 6381 - 6448	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	4.76E-10	0.96	5.66	-	1204.6
AHQ-7-6, 6250	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	2.94E-05	0.96	4.34	-	1975.0
AHQ-7-2, 6413	R.TFHIFYYLLSGAGEHLK.T	1997.28378	2	2.75E-06	0.97	4.93	-	1368.3
AHQ-7-4, 1897	K.THEAQIQEMR.Q	1243.37536	1	4.38E-06	0.55	2.48	-	430.9
AHQ-7-4, 1986	K.VAAYDKLEK.T	1037.19123	2	8.15E-07	0.79	3.01	-	490.4
AHQ-7-4, 3284 - 3352	K.VEAQLQELQVK.F	1285.47179	2	4.31E-05	0.93	3.78	-	1463.4
AHQ-7-3, 3367	K.VEAQLQELQVK.F	1285.47179	1	7.77E-04	0.73	2.93	-	825.9
AHQ-7-10, 4739 - 4772	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	7.92E-04	0.89	4.06	-	1096.2
AHQ-7-10, 5268	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	9.78E-04	0.75	3.30	-	563.1
AHQ-7-5, 5715 - 5784	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	6.56E-04	0.23	2.58	-	323.5
AHQ-7-13-, 4961 - 5001	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	2.11E-06	0.84	3.84	-	837.9
AHQ-7-6, 5721	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	1.48E-06	0.92	4.14	-	710.7
AHQ-7-10, 5208 - 5273	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.04E-07	0.77	3.66	-	482.7
AHQ-7-13, 5510 - 5571	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.08E-06	0.75	3.35	-	649.5
AHQ-7-3, 5751	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	5.10E-05	0.79	3.31	-	648.4
AHQ-7-2, 6041	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	8.82E-10	0.80	3.29	-	513.7
AHQ-7-4, 6065	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.75E-08	0.76	3.36	-	462.5
AHQ-7-1, 5199 - 5255	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	2.56E-04	0.88	4.07	-	673.8
AHQ-7-5, 5231	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	8.43E-04	0.90	3.99	-	883.7
AHQ-7-13, 5025 - 5098	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	4.55E-10	0.92	4.39	-	1143.1
AHQ-7-3, 5761	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.89E-09	0.89	4.21	-	458.6
AHQ-7-3, 5689 - 5767	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	7.81E-05	0.64	2.59	-	701.5
AHQ-7-2, 5264 - 5325	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	4.76E-08	0.87	3.92	-	761.2
AHQ-7-6, 5153 - 5155	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	4.58E-04	0.89	4.00	-	1074.7
AHQ-7-2, 5429 - 5497	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	2.70E-04	0.67	3.22	-	482.6
AHQ-7-5, 5815 - 5816	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	2.66E-09	0.89	4.18	-	877.8
AHQ-7-2, 2173	R.VEEEAAQKNMALK.K	1461.66649	2	2.32E-05	0.97	4.20	-	2515.3
AHQ-7-3, 2140	R.VEEEAAQKNMALK.K	1461.66649	2	1.94E-04	0.97	4.84	-	1836.8
AHQ-7-2, 2131	R.VEEEEERCQHLQAEK.K	1916.01642	2	5.27E-07	0.88	3.94	-	865.4
AHQ-7-6, 3885	K.VIQYLAYVASSHK.S	1479.70484	2	6.85E-06	0.96	3.79	-	1589.2
AHQ-7-5, 3970 - 3978	K.VIQYLAYVASSHK.S	1479.70484	2	1.34E-08	0.95	4.04	-	1204.9
AHQ-7-6, 3890	K.VIQYLAYVASSHK.S	1479.70484	3	2.58E-05	0.84	3.55	-	530.3
AHQ-7-5, 3976	K.VIQYLAYVASSHK.S	1479.70484	3	1.26E-04	0.83	3.82	-	730.9
AHQ-7-3, 4016	K.VIQYLAYVASSHK.S	1479.70484	2	4.24E-05	0.90	3.63	-	873.7
AHQ-7-2, 4180	K.VIQYLAYVASSHK.S	1479.70484	2	3.18E-05	0.92	3.18	-	1256.1
AHQ-7-2, 4079	K.VIQYLAYVASSHK.S	1479.70484	3	4.42E-04	0.83	3.46	-	636.6
AHQ-7-4, 3997	K.VIQYLAYVASSHK.S	1479.70484	2	1.22E-04	0.92	3.67	-	1160.6
AHQ-7-10, 3679	K.VIQYLAYVASSHK.S	1479.70484	2	3.10E-05	0.82	2.87	-	951.1
AHQ-7-2, 4075	K.VIQYLAYVASSHK.S	1479.70484	2	2.17E-05	0.90	3.36	-	989.0
AHQ-7-1, 4127 - 4132	K.VIQYLAYVASSHK.S	1479.70484	2	6.61E-05	0.94	3.86	-	1215.2
AHQ-7-8, 6226	R.VISGVLQLGNIVFK.K	1487.81155	2	1.48E-04	0.97	4.29	-	2259.8
AHQ-7-1, 6063 - 6131	R.VISGVLQLGNIVFK.K	1487.81155	2	3.62E-08	0.97	4.44	-	1703.1
AHQ-7-7, 6188	R.VISGVLQLGNIVFK.K	1487.81155	2	1.32E-08	0.97	4.46	-	1959.3
AHQ-7-5, 6274 - 6282	R.VISGVLQLGNIVFK.K	1487.81155	2	5.97E-06	0.94	3.79	-	1324.1
AHQ-7-9, 5634	R.VISGVLQLGNIVFK.K	1487.81155	2	8.37E-04	0.91	2.97	-	1371.4
AHQ-7-2, 6377	R.VISGVLQLGNIVFK.K	1487.81155	2	2.27E-06	0.94	3.47	-	1406.5
AHQ-7-2, 6251 - 6331	R.VISGVLQLGNIVFK.K	1487.81155	2	5.67E-05	0.96	4.55	-	1182.4
AHQ-7-4, 6352 - 6360	R.VISGVLQLGNIVFK.K	1487.81155	2	1.66E-05	0.78	2.70	-	839.4
AHQ-7-3, 5655 - 5701	R.VISGVLQLGNIVFKK.E	1615.98446	2	9.13E-05	0.90	4.20	-	969.0
AHQ-7-1, 5664 - 5680	R.VISGVLQLGNIVFKK.E	1615.98446	2	6.64E-05	0.90	3.66	-	1011.7
AHQ-7-2, 5819	R.VISGVLQLGNIVFKK.E	1615.98446	2	7.95E-10	0.91	3.88	-	982.0
AHQ-7-2, 2488	K.VKPLLQVSR.Q	1040.28462	1	8.83E-04	0.01	2.05	-	122.7
AHQ-7-5, 4874	K.VSHLLGINVTDFTR.G	1572.79026	3	3.41E-04	0.83	3.74	-	958.6
AHQ-7-9, 4421	K.VSHLLGINVTDFTR.G	1572.79026	2	1.14E-04	0.80	3.12	-	724.1
AHQ-7-5, 4863	K.VSHLLGINVTDFTR.G	1572.79026	2	4.74E-08	0.95	4.14	-	1371.7
AHQ-7-2, 4927 - 4987	K.VSHLLGINVTDFTR.G	1572.79026	2	9.35E-10	0.96	4.22	-	1524.4
AHQ-7-1, 4904 - 4964	K.VSHLLGINVTDFTR.G	1572.79026	2	3.35E-10	0.97	4.97	-	1484.0
AHQ-7-4, 4938	K.VSHLLGINVTDFTR.G	1572.79026	3	1.12E-04	0.92	4.22	-	1017.4
AHQ-7-7, 4712	K.VSHLLGINVTDFTR.G	1572.79026	2	2.73E-10	0.94	4.17	-	1214.9
AHQ-7-4, 4845 - 4918	K.VSHLLGINVTDFTR.G	1572.79026	2	6.46E-10	0.94	3.96	-	1143.5
AHQ-7-4, 3240	R.VVFQEFR.Q	925.06580	2	1.03E-04	0.77	2.59	-	498.1
AHQ-7-5, 3192 - 3194	R.VVFQEFR.Q	925.06580	2	6.30E-05	0.79	2.87	-	440.4
AHQ-7-6, 3177	R.VVFQEFR.Q	925.06580	2	1.23E-04	0.70	2.52	-	357.9
AHQ-7-2, 4265	R.YEILTPNSIPK.G	1275.47536	2	9.58E-05	0.88	3.24	-	966.3
AHQ-7-13, 4062	R.YEILTPNSIPK.G	1275.47536	2	6.32E-04	0.67	2.50	-	769.4
AHQ-7-3, 4191	R.YEILTPNSIPK.G	1275.47536	2	8.71E-05	0.84	3.10	-	673.3
AHQ-7-2, 4061	R.YEILTPNSIPK.G	1275.47536	1	3.43E-07	0.17	1.93	-	264.5
AHQ-7-2, 4048 - 4120	R.YEILTPNSIPK.G	1275.47536	2	1.48E-05	0.90	3.20	-	1100.1
AHQ-7-5, 3954	R.YEILTPNSIPK.G	1275.47536	2	1.91E-05	0.88	3.03	-	1160.1
AHQ-7-2, 6004	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	2	1.19E-10	0.97	5.12	-	1142.9
AHQ-7-2, 5999	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	3	1.88E-08	0.96	5.28	-	1577.9
gi|4501885|ref|NP_001092.1| beta actin; beta cytoskeletal actin [Homo sapiens]				2.22E-16	13.52	150.35	36.00	41736.5
AHQ-7-8, 6590 - 6650	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.83E-10	0.95	4.89	-	1001.0
AHQ-7-13-, 6104 - 6175	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	4.27E-07	0.67	3.50	-	596.1
AHQ-7-13-, 5735 - 5791	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	4.52E-04	0.88	4.32	-	444.3
AHQ-7-13, 5783 - 5841	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.36E-06	0.79	3.45	-	590.9
AHQ-7-8, 6138 - 6140	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.57E-04	0.68	3.61	-	372.2
AHQ-7-8, 6256 - 6314	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.15E-05	0.74	3.94	-	563.1
AHQ-7-8, 6342 - 6402	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	2.44E-05	0.85	4.56	-	691.9
AHQ-7-8, 6976	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	3.62E-04	0.90	4.77	-	575.7
AHQ-7-8, 6462 - 6546	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	4.60E-05	0.87	4.75	-	824.0
AHQ-7-8, 6686 - 6760	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	6.32E-09	0.95	5.64	-	808.2
AHQ-7-8, 5978 - 6044	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.42E-06	0.93	4.99	-	663.8
AHQ-7-8, 6826 - 6895	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	2.15E-06	0.95	5.62	-	756.0
AHQ-7-8, 6898 - 6963	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	3.52E-08	0.86	3.54	-	702.0
AHQ-7-8, 6840	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	6.78E-08	0.90	3.94	-	1059.8
AHQ-7-8, 6498	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	4.92E-07	0.81	3.61	-	535.1
AHQ-7-8, 6810 - 6835	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	3.44E-09	0.94	4.32	-	937.3

AHQ-7-8, 6918 - 6978	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	3.90E-09	0.91	5.31	-	807.2
AHQ-7-8, 6782 - 6855	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.15E-05	0.88	4.01	-	941.3
AHQ-7-8, 6690 - 6763	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.94E-06	0.92	5.11	-	1076.2
AHQ-7-8, 6923 - 6991	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	2.67E-05	0.82	3.75	-	1001.0
AHQ-7-8, 6678 - 6743	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	6.36E-06	0.92	4.46	-	813.7
AHQ-7-8, 6539 - 6607	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	5.55E-16	0.97	6.82	-	1125.1
AHQ-7-8, 6670 - 6712	R.FRCPEALFQPSFLGMESCGIHETTFNSIMK.C	3539.03813	3	1.77E-07	0.98	7.08	-	1846.7
AHQ-7-8, 2478 - 2542	R.GYSFTTTAER.E	1133.19273	2	3.42E-05	0.93	3.35	-	1075.9
AHQ-7-1, 2824	R.GYSFTTTAER.E	1133.19273	2	1.55E-04	0.92	2.95	-	1107.2
AHQ-7-8, 2387 - 2416	R.GYSFTTTAER.E	1133.19273	2	9.22E-06	0.93	3.12	-	1535.8
AHQ-7-6, 2546	R.GYSFTTTAER.E	1133.19273	2	3.71E-04	0.92	2.92	-	1081.0
AHQ-7-4, 2586	R.GYSFTTTAER.E	1133.19273	2	8.06E-04	0.88	3.05	-	877.2
AHQ-7-3, 2631	R.GYSFTTTAER.E	1133.19273	2	4.29E-04	0.86	2.68	-	1048.1
AHQ-7-10, 2479 - 2544	R.GYSFTTTAER.E	1133.19273	2	2.89E-05	0.92	3.54	-	1039.1
AHQ-7-13, 2775 - 2837	R.GYSFTTTAER.E	1133.19273	2	6.76E-04	0.85	2.92	-	913.6
AHQ-7-2, 2661	R.GYSFTTTAER.E	1133.19273	2	6.93E-06	0.94	3.03	-	1438.3
AHQ-7-7, 2509	R.GYSFTTTAER.E	1133.19273	2	1.01E-06	0.86	3.00	-	809.0
AHQ-7-8, 4818 - 4900	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	2.00E-04	0.81	3.51	-	621.0
AHQ-7-8, 4884	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	1.62E-06	0.85	3.54	-	1066.0
AHQ-7-10, 4336	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.56E-04	0.87	3.14	-	814.2
AHQ-7-14, 5101	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	7.74E-04	0.86	3.26	-	849.3
AHQ-7-13, 4273 - 4301	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	1.19E-05	0.92	4.93	-	1017.6
AHQ-7-13-, 4161 - 4193	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	8.41E-04	0.71	3.17	-	606.9
AHQ-7-8, 4167	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	5.64E-10	0.95	4.64	-	1556.8
AHQ-7-8, 4600 - 4648	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	8.84E-04	0.77	3.43	-	658.3
AHQ-7-8, 4610 - 4682	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	1.99E-06	0.93	5.16	-	1073.4
AHQ-7-8, 4640	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	8.21E-05	0.78	3.59	-	802.0
AHQ-7-8, 5910 - 5982	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	3.72E-04	0.95	4.93	-	1165.1
AHQ-7-8, 6919 - 6980	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	6.97E-04	0.97	5.67	-	2169.0
AHQ-7-8, 6166 - 6202	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	4.28E-05	0.91	3.73	-	1275.8
AHQ-7-8, 6850 - 6927	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	1.77E-05	0.86	3.69	-	783.2
AHQ-7-8, 6795 - 6874	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	1.48E-08	0.98	5.95	-	1952.0
AHQ-7-8, 6750 - 6783	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	4.11E-06	0.95	5.37	-	1379.9
AHQ-7-8, 5460	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	1.25E-04	0.88	3.08	-	1161.4
AHQ-7-8, 6667	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	6.58E-07	0.93	4.73	-	1276.9
AHQ-7-8, 6610 - 6675	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	6.60E-05	0.69	2.97	-	483.6
AHQ-7-8, 6982 - 6987	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	4.28E-08	0.97	5.99	-	2016.0
AHQ-7-13-, 5467	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.64E-13	0.98	6.29	-	2314.5
AHQ-7-7, 5661 - 5730	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.39E-05	0.95	5.09	-	1448.5
AHQ-7-8, 5462 - 5502	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.35E-08	0.96	5.39	-	1523.1
AHQ-7-6, 5686 - 5762	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.22E-16	0.96	6.08	-	1282.4
AHQ-7-1, 5465 - 5519	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.34E-07	0.94	5.16	-	1206.4
AHQ-7-14-, 5250 - 5267	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.85E-06	0.95	5.20	-	1277.1
AHQ-7-5, 5782 - 5851	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.65E-09	0.96	5.60	-	1596.0
AHQ-7-8, 5592 - 5615	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.95E-04	0.71	3.76	-	669.7
AHQ-7-14, 5958 - 6037	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.28E-05	0.71	3.82	-	733.7
AHQ-7-4, 5853 - 5930	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.49E-08	0.98	6.42	-	1665.8
AHQ-7-4, 5601 - 5609	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.47E-07	0.97	6.50	-	1494.6
AHQ-7-8, 5646 - 5710	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.51E-11	0.97	6.19	-	1677.8
AHQ-7-8, 5326 - 5403	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.96E-06	0.98	6.36	-	2453.3
AHQ-7-3, 5728 - 5787	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.20E-08	0.96	5.50	-	1411.8
AHQ-7-8, 5770 - 5830	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.44E-12	0.97	6.07	-	1726.6
AHQ-7-3, 5493 - 5552	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.56E-06	0.97	5.93	-	1555.2
AHQ-7-2, 5865	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.86E-10	0.97	5.71	-	1860.1
AHQ-7-13-, 5247	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.47E-07	0.95	5.49	-	1246.5
AHQ-7-1, 5696	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.27E-06	0.93	5.06	-	954.5
AHQ-7-9, 4881 - 4936	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.99E-10	0.97	6.05	-	1902.9
AHQ-7-9, 4924 - 4993	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.45E-07	0.96	5.94	-	1385.0
AHQ-7-9, 5144 - 5212	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.65E-06	0.92	4.69	-	1146.5
AHQ-7-2, 5624 - 5685	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.08E-05	0.91	4.79	-	956.7
AHQ-7-13, 5310	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.94E-06	0.94	5.05	-	1193.5
AHQ-7-8, 5200 - 5262	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.10E-09	0.97	6.15	-	1509.3
AHQ-7-10, 5215 - 5272	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.02E-12	0.97	6.57	-	1599.9
AHQ-7-10, 5327 - 5373	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.50E-06	0.95	5.61	-	1102.7
AHQ-7-10, 5448	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.50E-05	0.70	3.18	-	432.2
AHQ-7-6, 5447 - 5449	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.02E-06	0.93	4.62	-	1210.9
AHQ-7-11, 5120 - 5176	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.20E-08	0.95	6.22	-	759.1
AHQ-7-11, 5319 - 5374	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	7.06E-10	0.92	4.32	-	1360.0
AHQ-7-11, 5447	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.43E-07	0.78	3.19	-	861.4
AHQ-7-12, 5327 - 5395	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.66E-05	0.97	6.50	-	1255.1
AHQ-7-12, 5094	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.67E-08	0.96	5.56	-	1414.0
AHQ-7-14-, 5469	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.44E-06	0.96	5.78	-	1375.1
AHQ-7-2, 4063 - 4127	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.80E-05	0.81	3.54	-	572.7
AHQ-7-13, 4021	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.18E-04	0.93	4.47	-	766.7
AHQ-7-11, 3768	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.09E-06	0.92	4.56	-	770.6
AHQ-7-10, 3663 - 3719	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.91E-05	0.90	4.20	-	780.6
AHQ-7-9, 3534 - 3592	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.07E-05	0.94	5.08	-	828.2
AHQ-7-4, 4021 - 4097	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.98E-05	0.90	4.41	-	647.5
AHQ-7-5, 3963 - 4028	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.73E-05	0.90	4.08	-	787.1
AHQ-7-13-, 3893	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.41E-06	0.90	3.69	-	728.1
AHQ-7-7, 3820 - 3838	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.50E-04	0.89	4.41	-	630.9
AHQ-7-8, 3599 - 3666	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.51E-04	0.92	4.68	-	724.1
AHQ-7-8, 3730 - 3766	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.01E-07	0.93	4.48	-	846.9
AHQ-7-8, 3830 - 3894	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.70E-05	0.94	4.24	-	1068.0
AHQ-7-1, 4123	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.78E-06	0.89	4.28	-	652.7
AHQ-7-8, 3954 - 4027	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.96E-06	0.81	3.89	-	504.5
AHQ-7-12, 3782 - 3842	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.99E-04	0.94	4.94	-	946.8
gi|4501891|ref|NP_001093.1| actinin, alpha 1 [Homo sapiens]				5.55E-16	39.48	440.37	53.90	103056.9
AHQ-7-5, 6855	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	1.23E-04	0.70	3.62	-	568.0
AHQ-7-6, 6751	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	2.82E-04	0.86	4.14	-	648.2
AHQ-7-4, 5909	K.ACLISLGYDIGNDPQGEAEFAR.I	2398.59093	3	6.09E-04	0.92	4.42	-	1043.3
AHQ-7-6, 5306	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.13E-05	0.62	3.53	-	594.8
AHQ-7-5, 5379	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.07E-06	0.74	3.60	-	879.4
AHQ-7-4, 5416	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.45E-05	0.79	4.26	-	740.6
AHQ-7-4, 4826	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	2.00E-06	0.67	3.61	-	729.9
AHQ-7-5, 6332	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	2.69E-04	0.86	3.64	-	954.5
AHQ-7-4, 5636 - 5716	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	3.58E-07	0.94	4.77	-	779.5
AHQ-7-3, 6259	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	8.50E-07	0.80	3.76	-	575.5
AHQ-7-7, 6210 - 6273	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.24E-05	0.88	3.98	-	577.7
AHQ-7-5, 6334 - 6344	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.53E-08	0.94	4.70	-	765.8
AHQ-7-4, 6366 - 6381	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	3.33E-08	0.82	3.60	-	468.3
AHQ-7-4, 3457	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	2.99E-05	0.95	4.42	-	1189.7
AHQ-7-4, 3610	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	3.33E-06	0.87	3.32	-	1371.1
AHQ-7-4, 3605 - 3609	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	2	2.06E-06	0.89	3.43	-	769.5
AHQ-7-4, 2304 - 2306	K.ASIHEAWTDGK.E	1215.29697	2	9.30E-04	0.81	3.13	-	848.0
AHQ-7-4, 1716 - 1773	K.ATLPDADKER.L	1116.20684	2	5.43E-07	0.76	2.67	-	492.4
AHQ-7-1, 5475 - 5551	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.15E-04	0.51	2.69	-	433.7

AHQ-7-4, 5097 - 5157	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	6.88E-06	0.79	3.89	-	564.8
AHQ-7-5, 5044	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.08E-07	0.72	3.01	-	480.3
AHQ-7-5, 5572 - 5574	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	2.40E-07	0.96	5.44	-	1077.5
AHQ-7-4, 6088 - 6134	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.74E-05	0.93	4.45	-	1008.7
AHQ-7-9, 5013	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	5.39E-04	0.71	3.00	-	604.1
AHQ-7-6, 5498	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.84E-05	0.95	3.89	-	1451.4
AHQ-7-4, 5584 - 5642	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	7.56E-09	0.95	4.71	-	1142.5
AHQ-7-4, 5116	K.DGLGFCALIHR.H	1260.44730	2	1.31E-07	0.93	3.01	-	1534.5
AHQ-7-5, 2568 - 2583	R.DHSGTLGPEEFK.A	1317.38606	2	8.81E-07	0.89	3.12	-	921.4
AHQ-7-4, 2581	R.DHSGTLGPEEFK.A	1317.38606	2	1.19E-04	0.90	3.32	-	900.9
AHQ-7-6, 2539 - 2551	R.DHSGTLGPEEFK.A	1317.38606	2	7.54E-04	0.83	3.23	-	781.6
AHQ-7-4, 3801	K.DYETATLSEIK.A	1270.36761	2	9.53E-05	0.94	3.61	-	1201.6
AHQ-7-4, 3708	R.ELPPDQAEYCIAR.M	1563.71392	2	1.29E-05	0.75	2.73	-	300.0
AHQ-7-4, 4385 - 4453	R.ETADTDTADQVMASFK.I	1730.83208	2	9.83E-07	0.95	4.23	-	1097.3
AHQ-7-6, 4343	R.ETADTDTADQVMASFK.I	1730.83208	2	2.07E-12	0.97	4.57	-	1485.7
AHQ-7-4, 4452	R.ETADTDTADQVMASFK.I	1730.83208	2	6.25E-09	0.97	5.19	-	1435.1
AHQ-7-4, 3149 - 3229	R.ETADTDTADQVM*ASFK.I	1746.83148	2	1.50E-06	0.79	3.69	-	255.4
AHQ-7-5, 3215	R.ETADTDTADQVM*ASFK.I	1746.83148	2	3.24E-06	0.92	3.73	-	997.1
AHQ-7-4, 3885	R.ETADTDTADQVMASFK.I	1730.83208	2	5.56E-09	0.95	4.43	-	1167.0
AHQ-7-5, 4414 - 4430	R.ETADTDTADQVMASFK.I	1730.83208	2	1.17E-09	0.97	5.05	-	1496.9
AHQ-7-6, 3187	R.ETADTDTADQVM*ASFK.I	1746.83148	2	9.58E-06	0.89	3.79	-	977.2
AHQ-7-7, 4288 - 4337	R.ETADTDTADQVMASFK.I	1730.83208	2	6.18E-06	0.44	2.85	-	425.8
AHQ-7-11, 4139	R.ETADTDTADQVMASFK.I	1730.83208	2	3.53E-04	0.77	3.47	-	581.1
AHQ-7-6, 2989	K.GISQEQMNEFR.A	1339.45991	2	3.19E-05	0.89	3.22	-	1031.8
AHQ-7-6, 2290	K.GISQEQM*NEFR.A	1355.45931	2	1.31E-05	0.82	3.09	-	750.5
AHQ-7-11, 2948	K.GISQEQMNEFR.A	1339.45991	2	4.83E-05	0.85	2.86	-	909.9
AHQ-7-4, 3214	K.GISQEQMNEFR.A	1339.45991	2	2.52E-08	0.87	3.31	-	828.2
AHQ-7-4, 2718	K.GISQEQMNEFR.A	1339.45991	2	1.95E-07	0.80	3.27	-	911.4
AHQ-7-4, 2310 - 2337	K.GISQEQM*NEFR.A	1355.45931	2	1.36E-05	0.76	2.86	-	771.7
AHQ-7-4, 3024 - 3098	K.GISQEQMNEFR.A	1339.45991	2	1.55E-07	0.85	3.04	-	862.3
AHQ-7-5, 3008	K.GISQEQMNEFR.A	1339.45991	2	3.97E-07	0.86	3.36	-	781.0
AHQ-7-5, 2300	K.GISQEQM*NEFR.A	1355.45931	2	6.04E-05	0.84	2.98	-	875.9
AHQ-7-6, 2117 - 2194	R.HRPELIDYGK.L	1228.38202	2	7.41E-04	0.76	2.95	-	596.8
AHQ-7-4, 2162 - 2224	R.HRPELIDYGK.L	1228.38202	2	6.67E-06	0.84	3.11	-	600.5
AHQ-7-9, 2145	R.HRPELIDYGK.L	1228.38202	2	3.86E-04	0.85	2.80	-	819.6
AHQ-7-5, 2194	R.HRPELIDYGK.L	1228.38202	2	5.64E-04	0.91	3.75	-	704.2
AHQ-7-4, 4713	K.ICDQWDNLGALTQK.R	1663.83349	2	2.71E-05	0.56	2.54	-	725.2
AHQ-7-6, 4829	K.ICDQWDNLGALTQK.R	1663.83349	2	1.30E-06	0.97	4.87	-	1788.6
AHQ-7-6, 4683	K.ICDQWDNLGALTQK.R	1663.83349	2	4.38E-04	0.75	3.17	-	739.1
AHQ-7-4, 4548 - 4622	K.ICDQWDNLGALTQK.R	1663.83349	2	1.02E-04	0.87	3.60	-	954.8
AHQ-7-4, 4865 - 4928	K.ICDQWDNLGALTQK.R	1663.83349	2	5.43E-07	0.97	4.67	-	2151.6
AHQ-7-5, 4559 - 4592	K.ICDQWDNLGALTQK.R	1663.83349	2	1.79E-07	0.89	3.17	-	1231.8
AHQ-7-7, 4777	K.ICDQWDNLGALTQK.R	1663.83349	2	4.71E-06	0.97	4.46	-	2000.7
AHQ-7-5, 4856 - 4886	K.ICDQWDNLGALTQK.R	1663.83349	2	4.32E-08	0.96	4.13	-	1923.3
AHQ-7-4, 5734 - 5754	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	5.55E-16	0.95	5.28	-	1469.5
AHQ-7-7, 5712	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	3.38E-04	0.91	3.98	-	1207.0
AHQ-7-4, 5872 - 5952	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	8.35E-06	0.60	2.54	-	505.1
AHQ-7-4, 3588	K.ILAGDKNYITM*DELR.R	1769.01293	2	3.17E-04	0.93	3.98	-	788.7
AHQ-7-4, 4225 - 4302	K.ILAGDKNYITMDELR.R	1753.01353	2	1.33E-09	0.97	4.50	-	1651.6
AHQ-7-4, 5062	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	2	1.77E-04	0.95	4.63	-	1332.2
AHQ-7-5, 4432	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	3	9.41E-05	0.96	5.07	-	1871.3
AHQ-7-4, 4684	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	2.01E-05	0.90	4.31	-	735.1
AHQ-7-4, 4825	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	2	3.83E-10	0.96	5.05	-	1292.9
AHQ-7-4, 4104 - 4184	K.IVQTYHVNM*AGTNPYTTITPQEINGK.W	2908.23575	3	1.46E-05	0.87	4.56	-	515.9
AHQ-7-4, 4489	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	3.73E-06	0.96	4.84	-	1386.7
AHQ-7-5, 4914	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	8.12E-10	0.97	5.85	-	1388.3
AHQ-7-5, 4403	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.19E-05	0.80	3.21	-	735.4
AHQ-7-6, 4861	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	2.38E-05	0.90	4.34	-	574.4
AHQ-7-4, 4932 - 4993	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	2.76E-07	0.96	5.35	-	964.6
AHQ-7-5, 4420	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	3.28E-05	0.96	5.09	-	1242.2
AHQ-7-4, 3833 - 3897	R.LAILGIHNEVSK.I	1294.52505	2	5.61E-08	0.94	3.85	-	1119.1
AHQ-7-7, 3302	R.LAILGIHNEVSK.I	1294.52505	2	1.52E-05	0.91	3.58	-	1007.5
AHQ-7-4, 3902	R.LAILGIHNEVSK.I	1294.52505	2	1.72E-07	0.87	2.54	-	1211.8
AHQ-7-4, 3752	R.LAILGIHNEVSK.I	1294.52505	2	2.94E-08	0.95	3.73	-	1406.5
AHQ-7-3, 5915	K.LASDLLEWIR.R	1216.41115	2	5.82E-09	0.97	4.18	-	2090.1
AHQ-7-8, 5864	K.LASDLLEWIR.R	1216.41115	2	1.85E-07	0.95	3.93	-	1507.7
AHQ-7-5, 5962	K.LASDLLEWIR.R	1216.41115	2	1.49E-05	0.97	4.19	-	2112.7
AHQ-7-7, 5858	K.LASDLLEWIR.R	1216.41115	2	3.41E-07	0.97	4.07	-	2126.7
AHQ-7-4, 6020	K.LASDLLEWIR.R	1216.41115	1	5.71E-04	0.37	2.54	-	247.3
AHQ-7-1, 5851	K.LASDLLEWIR.R	1216.41115	2	5.52E-07	0.97	4.14	-	2238.9
AHQ-7-6, 5865	K.LASDLLEWIR.R	1216.41115	2	1.64E-08	0.96	3.96	-	1791.6
AHQ-7-4, 6012	K.LASDLLEWIR.R	1216.41115	2	1.42E-07	0.97	4.58	-	1952.9
AHQ-7-4, 6429	K.LLETIDQLYLEYAK.R	1712.96427	3	6.57E-07	0.98	5.12	-	2295.5
AHQ-7-2, 6433	K.LLETIDQLYLEYAK.R	1712.96427	2	2.99E-05	0.93	3.79	-	1039.5
AHQ-7-4, 5406	K.LLETIDQLYLEYAK.R	1712.96427	2	8.21E-05	0.83	2.99	-	695.8
AHQ-7-7, 6308	K.LLETIDQLYLEYAK.R	1712.96427	2	1.48E-07	0.96	4.53	-	1236.2
AHQ-7-5, 6356 - 6368	K.LLETIDQLYLEYAK.R	1712.96427	2	6.23E-04	0.97	4.80	-	1651.2
AHQ-7-6, 6259	K.LLETIDQLYLEYAK.R	1712.96427	2	3.77E-07	0.96	4.36	-	1291.4
AHQ-7-6, 6275	K.LLETIDQLYLEYAK.R	1712.96427	3	8.36E-04	0.94	3.42	-	1840.4
AHQ-7-4, 2241	R.LSNRPAFM*PSEGR.M	1478.65881	3	6.56E-04	0.72	3.09	-	959.3
AHQ-7-5, 3948 - 4010	K.MLDAEDIVGTARPDEK.A	1760.94769	2	5.83E-08	0.77	3.87	-	637.4
AHQ-7-8, 3956	K.MLDAEDIVGTARPDEK.A	1760.94769	2	3.99E-08	0.91	4.00	-	1043.4
AHQ-7-4, 3738	K.MLDAEDIVGTARPDEK.A	1760.94769	2	1.13E-04	0.42	2.61	-	423.9
AHQ-7-5, 3623	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	2.87E-05	0.89	3.75	-	656.4
AHQ-7-6, 3930 - 3939	K.MLDAEDIVGTARPDEK.A	1760.94769	2	1.80E-06	0.83	3.94	-	670.5
AHQ-7-6, 3547 - 3555	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	1.05E-04	0.85	3.55	-	652.8
AHQ-7-4, 4026	K.MLDAEDIVGTARPDEK.A	1760.94769	2	3.70E-04	0.91	4.25	-	801.1
AHQ-7-7, 3876	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.00E-04	0.84	3.29	-	894.4
AHQ-7-4, 4033	K.MLDAEDIVGTARPDEK.A	1760.94769	3	1.62E-08	0.88	4.39	-	596.1
AHQ-7-4, 3632	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	2.07E-04	0.82	3.71	-	481.5
AHQ-7-4, 5226	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	6.37E-08	0.95	4.27	-	1254.0
AHQ-7-4, 5688	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	1.32E-04	0.96	3.86	-	2085.2
AHQ-7-4, 5076 - 5141	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	2.47E-07	0.95	4.26	-	1025.2
AHQ-7-6, 5009	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	3.56E-08	0.95	4.76	-	1035.2
AHQ-7-4, 5496 - 5561	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	2.22E-08	0.96	4.46	-	1452.7
AHQ-7-6, 5239	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	5.16E-07	0.96	4.94	-	1021.0
AHQ-7-5, 5290	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	3.90E-05	0.87	3.69	-	519.9
AHQ-7-6, 5431	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.90E-04	0.62	2.77	-	512.2
AHQ-7-4, 5320 - 5393	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	7.52E-04	0.96	4.36	-	2000.0
AHQ-7-4, 4794	K.NVNIQNFHISWK.D	1500.68583	2	4.23E-06	0.95	3.71	-	1518.0
AHQ-7-5, 4738	K.NVNIQNFHISWK.D	1500.68583	2	7.40E-04	0.95	4.03	-	1182.4
AHQ-7-4, 3760	K.NYITMDELR.R	1155.30648	2	1.41E-05	0.84	2.99	-	650.8
AHQ-7-4, 5136	K.QFGAQANVIGPWIQTK.M	1759.00118	2	3.52E-04	0.90	3.90	-	855.6
AHQ-7-4, 3974	R.TINEVENQILTR.D	1430.58898	2	2.72E-04	0.89	3.77	-	847.6
AHQ-7-6, 3486	R.TINEVENQILTR.D	1430.58898	2	2.14E-05	0.81	2.99	-	676.5
AHQ-7-5, 3119 - 3126	R.TINEVENQILTR.D	1430.58898	2	1.27E-05	0.78	2.83	-	654.0
AHQ-7-4, 3573 - 3576	R.TINEVENQILTR.D	1430.58898	2	9.55E-06	0.74	3.14	-	478.5

AHQ-7-6, 3877 - 3889	R.TINEVENQILTR.D	1430.58898	2	2.87E-07	0.88	3.51	-	949.2
AHQ-7-4, 3993	R.TINEVENQILTR.D	1430.58898	1	8.43E-04	0.07	2.48	-	128.9
AHQ-7-4, 4141	R.TINEVENQILTR.D	1430.58898	1	5.36E-06	0.21	2.22	-	248.0
AHQ-7-4, 4133	R.TINEVENQILTR.D	1430.58898	2	4.34E-04	0.91	3.92	-	898.5
AHQ-7-4, 3152 - 3160	R.TINEVENQILTR.D	1430.58898	2	1.36E-04	0.83	3.38	-	743.3
AHQ-7-7, 6624	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	6.32E-06	0.90	3.86	-	852.8
AHQ-7-4, 6120	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.56E-10	0.87	4.07	-	676.3
AHQ-7-3, 6556	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	8.90E-09	0.96	5.53	-	1210.6
AHQ-7-4, 6738 - 6766	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	8.42E-06	0.97	5.60	-	1822.3
AHQ-7-5, 6662	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	7.56E-05	0.98	6.32	-	2600.6
AHQ-7-4, 6122 - 6125	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	3.54E-07	0.94	4.84	-	763.0
AHQ-7-2, 6731	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	7.72E-08	0.97	5.72	-	1573.1
AHQ-7-5, 6040	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	2.95E-04	0.85	3.71	-	918.7
AHQ-7-4, 6740 - 6744	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	2.99E-07	0.95	4.73	-	1141.8
AHQ-7-6, 6563	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	2.67E-09	0.93	4.91	-	969.3
AHQ-7-4, 6517	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	3.74E-09	0.97	5.61	-	1795.2
AHQ-7-6, 6558	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	9.40E-10	0.98	7.44	-	2139.8
AHQ-7-11, 5988 - 5999	R.VGWEQLLTTIAR.T	1387.60894	2	2.55E-07	0.93	3.65	-	1182.1
AHQ-7-4, 6520 - 6576	R.VGWEQLLTTIAR.T	1387.60894	2	6.71E-09	0.94	3.79	-	1398.0
AHQ-7-10, 5896 - 5899	R.VGWEQLLTTIAR.T	1387.60894	2	4.24E-05	0.94	3.91	-	1156.1
AHQ-7-7, 6408	R.VGWEQLLTTIAR.T	1387.60894	2	2.58E-08	0.96	4.48	-	1344.2
AHQ-7-3, 6392	R.VGWEQLLTTIAR.T	1387.60894	2	1.02E-07	0.95	3.84	-	1623.9
AHQ-7-5, 6470 - 6495	R.VGWEQLLTTIAR.T	1387.60894	2	2.80E-06	0.95	4.32	-	1261.0
AHQ-7-2, 6561	R.VGWEQLLTTIAR.T	1387.60894	2	9.78E-08	0.93	3.92	-	1207.2
AHQ-7-8, 6422	R.VGWEQLLTTIAR.T	1387.60894	2	5.06E-08	0.93	3.44	-	1137.4
AHQ-7-9, 5816 - 5821	R.VGWEQLLTTIAR.T	1387.60894	2	2.88E-05	0.83	3.14	-	1013.6
AHQ-7-7, 4141	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.76E-07	0.88	4.08	-	641.0
AHQ-7-6, 4163 - 4217	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.28E-08	0.95	5.07	-	923.8
AHQ-7-6, 3550 - 3558	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	4.51E-05	0.94	4.47	-	1092.1
AHQ-7-5, 4492	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	5.30E-09	0.94	4.59	-	705.5
AHQ-7-5, 4238	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.39E-09	0.93	4.19	-	925.9
AHQ-7-8, 4143	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	5.69E-09	0.95	4.56	-	1315.7
AHQ-7-5, 3626	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.79E-07	0.96	5.01	-	1206.1
AHQ-7-4, 4472 - 4544	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.44E-07	0.96	4.74	-	1168.1
AHQ-7-4, 4270 - 4336	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.17E-07	0.97	5.84	-	1496.3
AHQ-7-4, 4018 - 4096	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.25E-06	0.88	4.21	-	607.8
AHQ-7-4, 3789 - 3860	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	3.85E-07	0.95	4.75	-	973.2
AHQ-7-4, 3637 - 3700	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	4.55E-07	0.97	5.21	-	1516.3
AHQ-7-3, 4304	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.69E-05	0.93	3.86	-	1376.9
AHQ-7-2, 4403	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.36E-07	0.95	4.84	-	1036.5
AHQ-7-1, 4347	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	8.03E-07	0.95	4.36	-	1248.8
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				1.11E-15	6.35	70.29	24.10	61986.9
AHQ-7-4, 6276	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	8.38E-09	0.95	5.08	-	1444.3
AHQ-7-1, 5969 - 6040	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.71E-09	0.93	4.52	-	1272.9
AHQ-7-13-, 5903	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.87E-08	0.96	5.67	-	1638.0
AHQ-7-7, 6144	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.56E-05	0.94	4.76	-	1260.8
AHQ-7-6, 6118 - 6125	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.11E-15	0.97	5.68	-	1725.0
AHQ-7-14-, 5869	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.15E-05	0.95	5.33	-	1208.9
AHQ-7-3, 6121	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.65E-06	0.96	5.77	-	1117.2
AHQ-7-2, 6277	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.20E-06	0.93	4.73	-	1268.9
AHQ-7-2, 4673	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	4.68E-05	0.85	3.91	-	749.0
AHQ-7-6, 4474	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	4.07E-08	0.95	4.48	-	1655.7
AHQ-7-14-, 4422	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	2.85E-07	0.97	5.39	-	1856.7
AHQ-7-3, 4571	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	6.31E-06	0.93	5.16	-	964.7
AHQ-7-14-, 4846	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	1.45E-06	0.90	4.35	-	650.5
AHQ-7-5, 6739	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	8.26E-08	0.82	3.81	-	494.8
AHQ-7-1, 6459 - 6496	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	1.82E-13	0.80	3.83	-	427.1
AHQ-7-1, 6383 - 6399	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	2.93E-06	0.90	3.49	-	1395.7
AHQ-7-2, 3293	K.TLLDIDNTR.M	1061.17119	2	4.15E-04	0.87	3.04	-	878.9
AHQ-7-2, 3131	K.VQALEEANNDLENK.I	1587.67060	2	2.86E-04	0.96	4.20	-	1512.1
AHQ-7-1, 3239 - 3317	K.VQALEEANNDLENK.I	1587.67060	2	4.20E-05	0.96	4.27	-	1731.9
AHQ-7-11, 2958	K.VQALEEANNDLENK.I	1587.67060	2	2.09E-04	0.83	3.20	-	904.9
gi|27500274|ref|XP_113950.3| similar to Munc13-4 protein [Homo sapiens]				1.11E-15	5.67	60.28	10.10	123281.1
AHQ-7-4, 6322	R.ALLYEDALYTVLHR.L	1677.92484	2	4.90E-11	0.95	4.14	-	1490.9
AHQ-7-4, 5798	R.AVQMDELVPLGELTK.H	1643.92698	2	1.44E-06	0.90	3.73	-	771.7
AHQ-7-6, 3455	R.IQQQAETTSEELGAVTVK.A	1933.10674	2	6.33E-05	0.76	3.03	-	832.1
AHQ-7-4, 3548	R.IQQQAETTSEELGAVTVK.A	1933.10674	2	2.96E-08	0.97	5.16	-	1521.6
AHQ-7-4, 5497	K.LPAQLAWEALEQR.V	1525.73360	2	3.66E-10	0.96	4.44	-	1449.8
AHQ-7-4, 6898	R.LPLTYPAPNGDPILQLLEGR.K	2178.51621	2	1.11E-15	0.93	4.57	-	659.1
AHQ-7-4, 6801	R.VGAVLEQGQLQNTLHAQLQSALAGLGHEIR.T	3153.54178	3	2.41E-06	0.96	5.66	-	1259.1
gi|16753233|ref|NP_006280.2| talin 1 [Homo sapiens]				3.89E-15	112.28	1270.40	58.00	269665.3
AHQ-7-7, 3102	K.AAAFEEQENETVVVK.E	1664.79496	2	3.73E-08	0.95	4.72	-	1255.8
AHQ-7-2, 3695 - 3760	K.AAAFEEQENETVVVK.E	1664.79496	2	1.27E-04	0.96	5.05	-	1363.1
AHQ-7-5, 3198	K.AAAFEEQENETVVVK.E	1664.79496	2	1.61E-04	0.90	3.86	-	973.3
AHQ-7-14-, 3173	K.AAAFEEQENETVVVK.E	1664.79496	2	4.93E-05	0.90	3.91	-	1130.1
AHQ-7-4, 4074	K.AAAFEEQENETVVVK.E	1664.79496	2	4.76E-04	0.37	2.87	-	508.0
AHQ-7-1, 3291 - 3364	K.AAAFEEQENETVVVK.E	1664.79496	2	7.65E-06	0.84	3.58	-	914.5
AHQ-7-4, 3294 - 3368	K.AAAFEEQENETVVVK.E	1664.79496	2	7.83E-04	0.78	3.42	-	591.6
AHQ-7-6, 3158	K.AAAFEEQENETVVVK.E	1664.79496	2	1.81E-09	0.94	4.43	-	1210.5
AHQ-7-2, 3372	R.AAMEPIVISAK.T	1130.38320	1	3.65E-04	0.35	2.19	-	570.0
AHQ-7-3, 3339	R.AAMEPIVISAK.T	1130.38320	2	8.87E-04	0.56	2.63	-	393.7
AHQ-7-4, 2653	R.AAM*EPIVISAK.T	1146.38260	1	2.36E-04	0.16	2.07	-	195.6
AHQ-7-4, 2650	R.AAM*EPIVISAK.T	1146.38260	2	1.19E-05	0.88	2.91	-	876.0
AHQ-7-4, 3308	R.AAMEPIVISAK.T	1130.38320	2	8.29E-05	0.52	2.50	-	369.9
AHQ-7-2, 2708 - 2711	R.AAM*EPIVISAK.T	1146.38260	2	4.79E-06	0.82	2.54	-	839.8
AHQ-7-3, 2692 - 2695	R.AAM*EPIVISAK.T	1146.38260	2	3.24E-06	0.90	2.69	-	1165.4
AHQ-7-7, 4832 - 4901	K.ACEFAGFQCQIQFGPHNEQK.H	2399.60390	3	1.87E-05	0.71	3.65	-	521.3
AHQ-7-8, 4936 - 5016	K.ACEFAGFQCQIQFGPHNEQK.H	2399.60390	2	1.58E-04	0.89	4.09	-	689.5
AHQ-7-6, 1973	K.ADAEGESDLENSR.K	1393.35296	2	1.23E-07	0.87	2.96	-	966.5
AHQ-7-4, 1992	K.ADAEGESDLENSR.K	1393.35296	2	4.51E-07	0.92	3.53	-	1021.6
AHQ-7-3, 2039	K.ADAEGESDLENSR.K	1393.35296	2	7.12E-04	0.72	2.56	-	951.6
AHQ-7-2, 2052	K.ADAEGESDLENSR.K	1393.35296	2	2.33E-06	0.91	3.61	-	995.8
AHQ-7-3, 2675 - 2728	K.AGALQCSPSDAYTK.K	1470.58689	2	4.05E-05	0.86	3.18	-	833.2
AHQ-7-5, 2643	K.AGALQCSPSDAYTK.K	1470.58689	2	6.23E-04	0.79	3.17	-	592.8
AHQ-7-2, 2527 - 2577	K.AGALQCSPSDAYTK.K	1470.58689	2	4.21E-04	0.92	3.57	-	1214.7
AHQ-7-2, 4103 - 4168	K.AIAVTVQEMVTK.S	1290.55498	2	1.73E-06	0.94	4.40	-	1196.4
AHQ-7-3, 4024 - 4037	K.AIAVTVQEMVTK.S	1290.55498	2	4.38E-04	0.94	4.04	-	1111.7
AHQ-7-1, 4112	K.AIAVTVQEMVTK.S	1290.55498	2	4.13E-04	0.92	3.31	-	1082.6
AHQ-7-2, 3035 - 3104	K.AIAVTVQEM*VTK.S	1306.55438	2	9.05E-04	0.91	3.54	-	883.9
AHQ-7-1, 4115	K.AIAVTVQEMVTK.S	1290.55498	2	2.51E-04	0.95	4.02	-	1338.6
AHQ-7-4, 4016 - 4085	K.AIAVTVQEMVTK.S	1290.55498	2	4.65E-06	0.94	4.06	-	1085.8
AHQ-7-2, 4252	K.AIAVTVQEMVTK.S	1290.55498	2	2.60E-04	0.67	2.60	-	548.0
AHQ-7-1, 2920	K.ALDGAFTEENR.A	1223.27427	2	1.11E-05	0.95	3.37	-	1740.8
AHQ-7-4, 2685	K.ALDGAFTEENR.A	1223.27427	2	9.35E-07	0.95	3.96	-	1709.3
AHQ-7-4, 2509	K.ALDGAFTEENR.A	1223.27427	2	7.46E-06	0.94	3.67	-	1600.0
AHQ-7-2, 2579 - 2581	K.ALDGAFTEENR.A	1223.27427	2	4.47E-05	0.93	3.32	-	1322.2
AHQ-7-7, 3252	K.ALDYYM*LR.N	1061.23626	2	4.21E-04	0.90	2.65	-	1094.2

AHQ-7-13, 3529	K.ALDYYM*LR.N	1061.23626	2	4.08E-06	0.91	3.28	-	814.3
AHQ-7-7, 3832	K.ALDYYMLR.N	1045.23686	2	2.17E-07	0.94	3.64	-	925.2
AHQ-7-13-, 3935	K.ALDYYMLR.N	1045.23686	2	1.66E-06	0.93	3.33	-	922.7
AHQ-7-7, 4301	K.ALDYYMLRNGDTMEYR.K	2012.25579	2	4.78E-05	0.71	3.22	-	519.8
AHQ-7-3, 2096	R.ALEATTEHIR.Q	1141.25953	2	5.98E-04	0.75	3.01	-	822.9
AHQ-7-5, 2011	R.ALEATTEHIR.Q	1141.25953	2	6.08E-06	0.90	2.93	-	1375.3
AHQ-7-6, 2014	R.ALEATTEHIR.Q	1141.25953	2	2.69E-06	0.76	2.87	-	864.4
AHQ-7-2, 2104 - 2177	R.ALEATTEHIR.Q	1141.25953	2	1.47E-05	0.89	3.25	-	1066.5
AHQ-7-4, 2040	R.ALEATTEHIR.Q	1141.25953	2	1.54E-07	0.91	3.40	-	1200.7
AHQ-7-7, 1992 - 2049	R.ALEATTEHIR.Q	1141.25953	2	2.08E-04	0.57	2.71	-	607.2
AHQ-7-2, 3531	K.ALGDLISATK.A	989.14811	2	2.62E-06	0.90	3.58	-	756.6
AHQ-7-3, 3484	K.ALGDLISATK.A	989.14811	2	3.18E-07	0.88	3.30	-	796.2
AHQ-7-1, 3617	K.ALGDLISATK.A	989.14811	2	4.18E-06	0.92	3.51	-	896.4
AHQ-7-6, 3390	K.ALGDLISATK.A	989.14811	2	3.42E-05	0.89	3.43	-	661.7
AHQ-7-4, 3460	K.ALGDLISATK.A	989.14811	2	2.53E-07	0.95	4.04	-	961.9
AHQ-7-2, 3565 - 3633	K.ALGDLISATK.A	989.14811	1	9.38E-04	0.47	2.29	-	526.0
AHQ-7-5, 3431	K.ALGDLISATK.A	989.14811	2	1.65E-05	0.92	3.69	-	763.4
AHQ-7-4, 2684	K.ALSTDPAAPNLK.S	1198.35099	2	4.35E-06	0.83	3.06	-	681.5
AHQ-7-1, 2912	K.ALSTDPAAPNLK.S	1198.35099	2	1.21E-06	0.80	3.08	-	699.8
AHQ-7-2, 2733 - 2735	K.ALSTDPAAPNLK.S	1198.35099	2	9.26E-07	0.86	3.44	-	803.4
AHQ-7-3, 2712 - 2789	K.ALSTDPAAPNLK.S	1198.35099	2	5.83E-07	0.84	3.21	-	786.8
AHQ-7-6, 2642	K.ALSTDPAAPNLK.S	1198.35099	2	1.11E-05	0.76	2.81	-	626.3
AHQ-7-5, 2607 - 2671	K.ALSTDPAAPNLK.S	1198.35099	2	1.82E-06	0.61	2.76	-	403.9
AHQ-7-2, 3697	K.ALSTDPAAPNLKSQLAAAAR.A	1967.21592	2	3.01E-09	0.90	4.21	-	439.7
AHQ-7-1, 5715 - 5760	R.ANQAIQM*ACQSLGEPGCTQAQVLSAATIVAK.H	3236.64462	3	1.19E-06	0.86	4.46	-	635.3
AHQ-7-2, 6121	K.APGQLECETAIAALNSCLR.D	2077.32566	3	3.53E-07	0.90	4.72	-	852.1
AHQ-7-2, 6111	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.26E-09	0.98	5.62	-	1720.9
AHQ-7-3, 5964	K.APGQLECETAIAALNSCLR.D	2077.32566	2	6.32E-05	0.96	4.86	-	1262.7
AHQ-7-4, 5429 - 5494	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.48E-08	0.97	4.88	-	1576.2
AHQ-7-4, 6128	K.APGQLECETAIAALNSCLR.D	2077.32566	2	5.32E-09	0.97	5.41	-	1546.0
AHQ-7-3, 6169	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.13E-04	0.88	3.61	-	811.5
AHQ-7-3, 5313 - 5377	K.APGQLECETAIAALNSCLR.D	2077.32566	2	6.92E-09	0.98	5.53	-	1823.6
AHQ-7-2, 5423 - 5496	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.89E-09	0.97	5.44	-	1295.8
AHQ-7-3, 6460 - 6483	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	2	5.42E-09	0.81	2.96	-	986.9
AHQ-7-3, 6459	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	9.98E-05	0.96	4.98	-	1875.3
AHQ-7-4, 6641 - 6656	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	2.74E-06	0.95	4.84	-	1615.9
AHQ-7-4, 6642 - 6644	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	2	3.38E-07	0.88	3.42	-	1172.1
AHQ-7-5, 6595	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	3.42E-04	0.76	3.59	-	642.9
AHQ-7-5, 6570	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	3.82E-09	0.93	4.34	-	1739.2
AHQ-7-3, 5739	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	2.58E-05	0.93	4.37	-	1169.3
AHQ-7-1, 5697	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	1.99E-05	0.83	3.77	-	882.5
AHQ-7-2, 6631	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	6.74E-07	0.95	4.93	-	1491.8
AHQ-7-2, 6652	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	2.20E-05	0.87	3.80	-	1189.3
AHQ-7-6, 6469 - 6473	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	2.74E-07	0.95	4.89	-	1502.1
AHQ-7-2, 6628 - 6685	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	2	3.35E-06	0.71	2.70	-	809.1
AHQ-7-6, 2926	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.64E-06	0.67	2.56	-	461.3
AHQ-7-4, 2956 - 3021	K.ASAGPQPLLVQSCK.A	1457.67763	2	7.51E-08	0.88	3.73	-	499.9
AHQ-7-3, 3023	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.99E-05	0.76	2.74	-	546.2
AHQ-7-3, 3045	K.ASAGPQPLLVQSCK.A	1457.67763	1	2.69E-04	0.18	2.20	-	320.2
AHQ-7-5, 2932 - 2998	K.ASAGPQPLLVQSCK.A	1457.67763	2	4.51E-08	0.85	3.18	-	535.0
AHQ-7-2, 3088	K.ASAGPQPLLVQSCK.A	1457.67763	1	1.31E-04	0.32	2.48	-	460.4
AHQ-7-1, 3212	K.ASAGPQPLLVQSCK.A	1457.67763	2	3.43E-08	0.76	2.98	-	446.2
AHQ-7-2, 3032 - 3111	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.34E-09	0.72	3.04	-	414.3
AHQ-7-4, 3012	K.ASAGPQPLLVQSCK.A	1457.67763	1	5.26E-06	0.19	2.36	-	326.3
AHQ-7-2, 3781	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	8.58E-06	0.79	3.34	-	545.7
AHQ-7-6, 4131	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.45E-04	0.61	2.93	-	478.1
AHQ-7-4, 4242 - 4296	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	6.03E-07	0.93	4.55	-	596.4
AHQ-7-1, 3801	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	8.56E-05	0.74	3.55	-	303.9
AHQ-7-5, 3688	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.12E-05	0.90	4.10	-	808.8
AHQ-7-1, 4283	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.81E-09	0.89	3.98	-	516.7
AHQ-7-3, 3715 - 3717	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	4.75E-08	0.90	3.93	-	730.3
AHQ-7-6, 3629	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	4.83E-06	0.84	3.45	-	511.3
AHQ-7-2, 4363	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	9.56E-09	0.94	4.60	-	781.5
AHQ-7-7, 4097	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.36E-09	0.90	4.14	-	559.4
AHQ-7-5, 4208	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.47E-08	0.91	4.28	-	608.9
AHQ-7-2, 4481	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.05E-10	0.85	4.12	-	379.6
AHQ-7-7, 4098	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.72E-07	0.79	3.18	-	707.7
AHQ-7-2, 4257 - 4323	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.24E-05	0.81	3.84	-	368.7
AHQ-7-4, 3725	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	9.72E-07	0.81	3.49	-	485.2
AHQ-7-6, 4891	K.AVAEQIPLLVQGVR.G	1493.77619	3	3.70E-05	0.95	4.69	-	1661.9
AHQ-7-4, 5021	K.AVAEQIPLLVQGVR.G	1493.77619	3	2.14E-06	0.94	4.49	-	1739.2
AHQ-7-2, 5011 - 5071	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.19E-07	0.93	4.38	-	701.8
AHQ-7-2, 5039	K.AVAEQIPLLVQGVR.G	1493.77619	3	1.87E-06	0.93	4.26	-	1660.9
AHQ-7-6, 4874	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.57E-06	0.89	4.25	-	527.7
AHQ-7-5, 4952	K.AVAEQIPLLVQGVR.G	1493.77619	3	1.87E-09	0.98	5.43	-	2315.0
AHQ-7-3, 4927 - 4939	K.AVAEQIPLLVQGVR.G	1493.77619	2	3.40E-05	0.81	3.72	-	395.6
AHQ-7-1, 4959 - 4967	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.02E-05	0.94	3.94	-	893.6
AHQ-7-7, 4798 - 4805	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.29E-07	0.90	4.38	-	539.0
AHQ-7-5, 4939	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.91E-04	0.89	3.76	-	714.6
AHQ-7-4, 3924	K.AVASAAAALVLK.A	1085.32216	2	1.28E-06	0.97	4.20	-	1903.8
AHQ-7-5, 3878	K.AVASAAAALVLK.A	1085.32216	2	2.59E-06	0.96	3.64	-	1659.8
AHQ-7-1, 4023	K.AVASAAAALVLK.A	1085.32216	2	9.21E-06	0.95	4.15	-	1482.0
AHQ-7-2, 4093	K.AVASAAAALVLK.A	1085.32216	2	1.52E-04	0.96	3.96	-	1560.4
AHQ-7-6, 3791 - 3855	K.AVASAAAALVLK.A	1085.32216	2	5.31E-06	0.93	3.10	-	1355.3
AHQ-7-2, 4004 - 4011	K.AVASAAAALVLK.A	1085.32216	2	5.90E-06	0.96	4.25	-	1502.5
AHQ-7-2, 3940	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.43E-06	0.93	4.33	-	1415.6
AHQ-7-6, 3975	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.02E-04	0.92	4.03	-	1157.6
AHQ-7-1, 4043 - 4095	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.54E-07	0.92	4.35	-	1200.2
AHQ-7-2, 3847 - 3877	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.96E-07	0.97	4.90	-	2122.9
AHQ-7-6, 4071	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.71E-08	0.94	4.95	-	917.3
AHQ-7-5, 4026 - 4036	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.21E-07	0.94	4.95	-	1138.9
AHQ-7-2, 4119 - 4187	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	9.40E-07	0.95	4.96	-	1148.2
AHQ-7-2, 4121	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	9.34E-07	0.84	3.30	-	1093.5
AHQ-7-3, 4044 - 4067	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.97E-06	0.92	3.65	-	1294.2
AHQ-7-5, 4155	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.17E-08	0.91	3.84	-	1065.8
AHQ-7-4, 4069 - 4140	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.85E-08	0.97	5.11	-	1757.9
AHQ-7-3, 4152	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.01E-05	0.92	4.21	-	877.9
AHQ-7-2, 4231 - 4303	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.73E-08	0.96	4.24	-	1761.8
AHQ-7-2, 4369 - 4431	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.99E-07	0.96	5.10	-	1507.6
AHQ-7-4, 3770 - 3846	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	9.29E-04	0.68	3.61	-	652.8
AHQ-7-4, 7026	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.86E-05	0.64	2.75	-	924.4
AHQ-7-2, 4264	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.04E-07	0.97	5.10	-	2120.2
AHQ-7-4, 3849 - 3925	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.53E-05	0.56	3.14	-	329.6
AHQ-7-8, 3988	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	7.75E-05	0.68	2.90	-	593.5
AHQ-7-2, 4632	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	8.11E-07	0.96	4.90	-	1502.8
AHQ-7-5, 6754	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.95E-05	0.97	6.11	-	1435.1
AHQ-7-3, 6576 - 6639	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	3.36E-13	0.98	6.74	-	2141.5

AHQ-7-5, 6616 - 6691	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	4.12E-04	0.96	5.02	-	1884.1
AHQ-7-2, 6749 - 6811	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.47E-08	0.97	6.23	-	1953.6
AHQ-7-4, 6777 - 6845	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	2.24E-11	0.98	7.36	-	2381.1
AHQ-7-6, 6649 - 6698	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.58E-13	0.95	4.90	-	1476.4
AHQ-7-6, 5765	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	6.05E-06	0.71	3.43	-	380.4
AHQ-7-3, 5467 - 5487	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	2.57E-06	0.85	4.08	-	457.8
AHQ-7-2, 5597 - 5677	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	2.93E-04	0.67	3.77	-	257.1
AHQ-7-4, 5920	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	2.70E-04	0.47	3.01	-	256.3
AHQ-7-2, 5915	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	4.20E-08	0.88	3.96	-	559.1
AHQ-7-3, 5776	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	3.02E-06	0.89	4.28	-	498.2
AHQ-7-2, 4736	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	6.25E-07	0.85	4.03	-	485.9
AHQ-7-3, 4635 - 4649	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	3.77E-05	0.26	3.12	-	203.6
AHQ-7-5, 5862	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	4.48E-08	0.90	4.09	-	602.9
AHQ-7-5, 5930	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.05E-10	0.94	4.93	-	1106.2
AHQ-7-3, 5848 - 5849	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	8.09E-12	0.92	4.45	-	1046.3
AHQ-7-1, 5545 - 5548	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	2.64E-06	0.89	4.59	-	846.8
AHQ-7-6, 5831	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	6.27E-07	0.88	4.00	-	1011.1
AHQ-7-2, 5728 - 5804	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.42E-09	0.94	4.95	-	950.1
AHQ-7-7, 5842	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	5.40E-08	0.77	3.59	-	712.2
AHQ-7-4, 6016 - 6056	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.51E-10	0.94	5.17	-	986.0
AHQ-7-2, 5989 - 6052	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	2.80E-10	0.92	4.64	-	1050.2
AHQ-7-3, 5591	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	3.32E-04	0.66	3.24	-	757.0
AHQ-7-4, 2441	R.CVSCLPGQR.D	1079.23309	1	7.01E-05	0.10	1.88	-	79.6
AHQ-7-3, 2464	R.CVSCLPGQR.D	1079.23309	2	4.02E-06	0.81	2.81	-	793.2
AHQ-7-2, 2509	R.CVSCLPGQR.D	1079.23309	1	6.93E-04	0.30	2.01	-	245.8
AHQ-7-7, 3401 - 3436	R.DDILNGSHPVSFDK.A	1544.64741	2	1.83E-07	0.95	4.04	-	1250.4
AHQ-7-10, 3287	R.DDILNGSHPVSFDK.A	1544.64741	2	2.02E-05	0.90	3.07	-	974.4
AHQ-7-8, 3480 - 3559	R.DDILNGSHPVSFDK.A	1544.64741	2	1.38E-10	0.95	3.99	-	1476.8
AHQ-7-7, 4169	K.DHFGLEGDEESTM*LEDSVSPK.K	2339.43247	2	2.64E-04	0.76	3.02	-	458.2
AHQ-7-7, 4686 - 4692	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	5.21E-07	0.99	6.81	-	2490.7
AHQ-7-4, 5937	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.74E-10	0.93	4.17	-	935.6
AHQ-7-3, 5803	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.17E-11	0.97	5.40	-	1198.9
AHQ-7-2, 6153	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.22E-09	0.84	3.64	-	558.1
AHQ-7-3, 5799	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	7.57E-07	0.86	4.18	-	977.6
AHQ-7-2, 5269	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.00E-08	0.93	4.32	-	946.0
AHQ-7-2, 5937	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.22E-11	0.95	5.10	-	853.4
AHQ-7-1, 5744 - 5812	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.97E-08	0.94	4.31	-	893.3
AHQ-7-6, 5795	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.50E-07	0.95	5.18	-	757.6
AHQ-7-3, 5127 - 5173	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.13E-10	0.90	4.05	-	692.9
AHQ-7-3, 6012	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	9.59E-11	0.87	3.62	-	648.3
AHQ-7-7, 5793 - 5794	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.20E-08	0.92	4.28	-	680.4
AHQ-7-4, 6160	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.73E-09	0.93	4.15	-	1048.5
AHQ-7-7, 5798	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	6.16E-04	0.68	3.27	-	885.8
AHQ-7-4, 5260	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.50E-07	0.87	3.66	-	725.1
AHQ-7-1, 5145	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.60E-08	0.80	3.26	-	677.1
AHQ-7-5, 5883	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	6.44E-04	0.88	4.26	-	1033.3
AHQ-7-2, 6080 - 6147	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	2.58E-06	0.69	3.25	-	810.9
AHQ-7-3, 5128	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	5.36E-04	0.90	4.54	-	1102.6
AHQ-7-2, 5228	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.25E-06	0.91	4.23	-	1606.1
AHQ-7-2, 5227 - 5240	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.13E-08	0.96	5.21	-	888.7
AHQ-7-3, 5073 - 5140	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	4.28E-10	0.96	5.27	-	1063.2
AHQ-7-4, 5234	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	6.32E-08	0.96	5.09	-	1620.6
AHQ-7-2, 4644	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.54E-05	0.84	3.43	-	832.5
AHQ-7-1, 5055 - 5096	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.57E-06	0.55	3.33	-	564.0
AHQ-7-1, 5112	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	7.17E-07	0.89	4.40	-	1208.0
AHQ-7-4, 5182 - 5244	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.83E-05	0.87	4.02	-	621.1
AHQ-7-2, 3700 - 3715	R.DPPSWSVLAGHSR.T	1409.53156	2	5.74E-08	0.91	3.55	-	577.5
AHQ-7-3, 3631	R.DPPSWSVLAGHSR.T	1409.53156	2	5.95E-08	0.77	2.98	-	431.8
AHQ-7-3, 3639	R.DPPSWSVLAGHSR.T	1409.53156	3	1.13E-06	0.89	4.18	-	583.1
AHQ-7-5, 3586	R.DPPSWSVLAGHSR.T	1409.53156	2	5.68E-07	0.88	3.22	-	510.1
AHQ-7-2, 3708	R.DPPSWSVLAGHSR.T	1409.53156	3	3.61E-06	0.92	4.10	-	960.7
AHQ-7-4, 3592 - 3618	R.DPPSWSVLAGHSR.T	1409.53156	2	1.42E-07	0.86	3.25	-	469.7
AHQ-7-6, 3529	R.DPPSWSVLAGHSR.T	1409.53156	2	1.80E-08	0.78	3.12	-	481.3
AHQ-7-9, 4621	R.DPVQLNLLYVQAR.D	1529.76539	2	6.52E-10	0.94	4.03	-	1284.8
AHQ-7-13-, 4911	R.DPVQLNLLYVQAR.D	1529.76539	2	2.20E-06	0.81	3.03	-	770.6
AHQ-7-7, 4984	R.DPVQLNLLYVQAR.D	1529.76539	2	4.05E-07	0.95	4.31	-	1271.1
AHQ-7-8, 5023	R.DPVQLNLLYVQAR.D	1529.76539	2	1.58E-08	0.98	5.43	-	1936.0
AHQ-7-1, 5116	R.DPVQLNLLYVQAR.D	1529.76539	2	7.27E-06	0.86	2.98	-	1032.3
AHQ-7-3, 5129	R.DPVQLNLLYVQAR.D	1529.76539	2	1.81E-04	0.88	3.19	-	1042.3
AHQ-7-10, 4652 - 4656	R.DPVQLNLLYVQAR.D	1529.76539	2	1.15E-07	0.97	4.86	-	1687.3
AHQ-7-5, 2482	K.EAAYHPEVAPDVR.L	1454.56910	2	1.66E-04	0.58	2.58	-	528.2
AHQ-7-6, 2471	K.EAAYHPEVAPDVR.L	1454.56910	2	4.07E-06	0.72	2.90	-	570.8
AHQ-7-2, 2568	K.EAAYHPEVAPDVR.L	1454.56910	1	5.98E-04	0.50	2.17	-	443.9
AHQ-7-4, 2496	K.EAAYHPEVAPDVR.L	1454.56910	2	2.76E-06	0.72	2.89	-	505.5
AHQ-7-5, 2492	K.EAAYHPEVAPDVR.L	1454.56910	1	4.39E-04	0.27	1.92	-	300.6
AHQ-7-3, 2535	K.EAAYHPEVAPDVR.L	1454.56910	2	1.60E-07	0.83	2.65	-	935.3
AHQ-7-1, 2752	K.EAAYHPEVAPDVR.L	1454.56910	2	1.86E-04	0.83	2.63	-	987.4
AHQ-7-7, 2428	K.EAAYHPEVAPDVR.L	1454.56910	2	1.75E-04	0.70	2.77	-	623.0
AHQ-7-2, 5847 - 5907	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.45E-08	0.97	4.95	-	1760.7
AHQ-7-9, 5216	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.60E-06	0.43	2.80	-	616.2
AHQ-7-5, 5824 - 5891	K.EADESLNFEEQILEAAK.S	1937.05072	2	9.25E-07	0.94	4.38	-	1248.5
AHQ-7-3, 5757 - 5839	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.52E-07	0.97	5.49	-	1896.7
AHQ-7-4, 5681	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.47E-08	0.92	4.04	-	941.6
AHQ-7-2, 5901 - 5967	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.59E-09	0.96	5.03	-	1383.4
AHQ-7-10, 5284 - 5285	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.24E-06	0.96	4.85	-	1381.5
AHQ-7-4, 5848 - 5913	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.30E-08	0.97	5.63	-	1640.2
AHQ-7-7, 5740 - 5804	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.10E-05	0.95	4.93	-	1231.0
AHQ-7-6, 5725 - 5786	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.64E-09	0.95	4.37	-	1487.3
AHQ-7-3, 5907	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.09E-04	0.83	3.04	-	1045.0
AHQ-7-1, 5693 - 5756	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.73E-09	0.97	4.97	-	1849.0
AHQ-7-2, 6032 - 6035	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.77E-08	0.93	4.31	-	1155.4
AHQ-7-4, 5976	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.29E-06	0.96	4.84	-	1429.7
AHQ-7-11, 5388	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.20E-06	0.79	3.08	-	968.4
AHQ-7-2, 5637 - 5701	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.61E-07	0.89	4.29	-	675.4
AHQ-7-2, 6909 - 6968	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.22E-05	0.85	4.21	-	899.1
AHQ-7-3, 5559 - 5629	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.68E-05	0.46	2.75	-	343.4
AHQ-7-4, 6922	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	6.63E-08	0.94	5.43	-	1077.5
AHQ-7-3, 6707	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	1.03E-09	0.93	5.05	-	933.9
AHQ-7-6, 6721 - 6726	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	4.56E-06	0.96	6.05	-	1232.0
AHQ-7-2, 6883 - 6889	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	3.80E-10	0.97	6.10	-	1378.1
AHQ-7-6, 6677	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.47E-06	0.93	4.71	-	1136.4
AHQ-7-2, 6879 - 6949	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	3.81E-07	0.82	4.10	-	730.9
AHQ-7-6, 6770	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.38E-06	0.91	4.96	-	1055.4
AHQ-7-3, 6685 - 6749	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	3.49E-06	0.95	5.31	-	1167.5
AHQ-7-5, 6778	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.44E-06	0.92	4.85	-	928.6
AHQ-7-7, 6868	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	1.14E-11	0.98	6.95	-	1774.1
AHQ-7-2, 6813	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	5.52E-04	0.96	5.49	-	1736.0

AHQ-7-1, 6543	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.26E-07	0.94	5.38	-	890.6
AHQ-7-5, 6874	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	9.37E-09	0.97	5.83	-	1816.4
AHQ-7-4, 6757	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	3.74E-04	0.63	3.60	-	618.2
AHQ-7-2, 6727	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	2.16E-05	0.73	3.87	-	631.9
AHQ-7-7, 3020	R.EQGVEEHETLLLR.R	1553.69898	2	2.53E-06	0.78	3.06	-	410.7
AHQ-7-8, 3070	R.EQGVEEHETLLLR.R	1553.69898	2	8.13E-09	0.75	2.83	-	502.9
AHQ-7-8, 5500	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	7.44E-10	0.97	5.91	-	1898.7
AHQ-7-14-, 5323 - 5327	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	6.08E-09	0.98	7.30	-	2152.7
AHQ-7-13-, 5319	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	1.84E-08	0.98	7.24	-	1484.8
AHQ-7-7, 5460 - 5468	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	4.27E-11	0.97	6.75	-	1724.3
AHQ-7-10, 4744	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	9.10E-04	0.89	4.17	-	994.0
AHQ-7-14-, 5026 - 5082	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	9.48E-09	0.95	5.10	-	1339.3
AHQ-7-13-, 4953 - 5009	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.71E-05	0.98	6.05	-	2032.2
AHQ-7-7, 5001	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	3.67E-09	0.97	6.04	-	1943.3
AHQ-7-3, 2296	K.EVANSTANLVK.T	1146.27608	1	3.36E-05	0.15	2.22	-	150.1
AHQ-7-4, 2173 - 2201	K.EVANSTANLVK.T	1146.27608	2	8.53E-04	0.61	2.56	-	705.8
AHQ-7-8, 4650 - 4716	K.EVIQEWNLTNIK.R	1487.68214	2	4.62E-05	0.91	3.57	-	1168.8
AHQ-7-7, 4605	K.EVIQEWNLTNIK.R	1487.68214	1	5.71E-07	0.77	3.77	-	306.7
AHQ-7-8, 2935 - 2951	K.FFYSDQNVDSR.D	1378.42795	2	1.95E-05	0.93	3.55	-	1159.2
AHQ-7-7, 2956	K.FFYSDQNVDSR.D	1378.42795	2	6.50E-07	0.92	3.66	-	1054.9
AHQ-7-7, 5808	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	4.31E-10	0.98	6.67	-	2531.0
AHQ-7-4, 6194	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	1.12E-05	0.70	2.74	-	603.6
AHQ-7-2, 6171 - 6232	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	2.22E-04	0.91	4.49	-	791.0
AHQ-7-3, 6016 - 6075	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	2.30E-06	0.82	4.35	-	529.7
AHQ-7-4, 6182 - 6240	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	5.50E-06	0.84	4.07	-	624.7
AHQ-7-4, 6793	R.FGQDFSTFLEAGVEMAGQAPSQEDR.A	2718.89325	3	4.52E-07	0.84	3.83	-	778.7
AHQ-7-2, 6177 - 6179	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	1.49E-05	0.89	4.12	-	731.3
AHQ-7-14-, 2874	K.FLPSELRDEH	1243.35032	2	4.68E-05	0.32	2.55	-	283.9
AHQ-7-1, 3089	K.FLPSELRDEH	1243.35032	2	2.33E-05	0.68	2.64	-	371.1
AHQ-7-4, 2833	K.FLPSELRDEH	1243.35032	2	9.73E-06	0.54	2.57	-	332.0
AHQ-7-5, 2843	K.FLPSELRDEH	1243.35032	2	1.17E-04	0.39	2.71	-	211.3
AHQ-7-4, 5152	K.GLAGAVSELLR.S	1086.26701	2	2.27E-05	0.97	4.49	-	2043.5
AHQ-7-2, 4636	K.GLAGAVSELLR.S	1086.26701	2	1.32E-07	0.97	4.24	-	2042.8
AHQ-7-2, 5183	K.GLAGAVSELLR.S	1086.26701	2	1.73E-05	0.97	4.34	-	1965.2
AHQ-7-3, 5107	K.GLAGAVSELLR.S	1086.26701	2	2.55E-06	0.98	4.87	-	1999.5
AHQ-7-1, 5127 - 5129	K.GLAGAVSELLR.S	1086.26701	2	7.78E-07	0.98	4.73	-	2265.7
AHQ-7-5, 5118	K.GLAGAVSELLR.S	1086.26701	2	9.28E-07	0.97	4.98	-	1951.0
AHQ-7-6, 5045 - 5047	K.GLAGAVSELLR.S	1086.26701	2	5.09E-06	0.98	5.03	-	2058.0
AHQ-7-3, 6236 - 6303	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.37E-08	0.93	4.65	-	1169.8
AHQ-7-7, 6342 - 6344	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	6.56E-05	0.88	4.39	-	540.8
AHQ-7-2, 6239	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.67E-06	0.87	4.43	-	543.0
AHQ-7-2, 6243 - 6319	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.32E-10	0.97	6.15	-	1628.4
AHQ-7-6, 6302	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	3.72E-06	0.92	4.61	-	592.5
AHQ-7-2, 6396 - 6459	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	5.31E-06	0.95	5.25	-	1358.4
AHQ-7-2, 6479 - 6535	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	6.61E-05	0.87	4.37	-	749.9
AHQ-7-4, 6252	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.87E-06	0.95	5.08	-	1407.1
AHQ-7-3, 6359	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	5.32E-05	0.57	3.05	-	480.6
AHQ-7-3, 6307 - 6319	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	3.22E-05	0.92	4.81	-	806.6
AHQ-7-5, 6336 - 6398	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	7.20E-07	0.92	4.51	-	1043.6
AHQ-7-5, 6399	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	2.60E-04	0.91	4.41	-	704.4
AHQ-7-1, 6223 - 6279	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	4.45E-04	0.83	3.68	-	895.1
AHQ-7-5, 6890	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.30E-07	0.97	6.22	-	1371.2
AHQ-7-9, 6216	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.93E-08	0.92	5.24	-	970.4
AHQ-7-3, 6763	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	5.58E-09	0.94	5.13	-	1471.0
AHQ-7-7, 6888	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	5.89E-07	0.89	4.82	-	1092.7
AHQ-7-6, 6785	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.26E-10	0.96	6.37	-	1203.8
AHQ-7-1, 6631 - 6635	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	3.11E-07	0.89	4.29	-	1130.4
AHQ-7-2, 6927 - 6947	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.02E-12	0.95	5.20	-	1547.1
AHQ-7-2, 6713 - 6784	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	2.28E-04	0.74	2.52	-	721.7
AHQ-7-5, 6782	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.85E-09	0.99	7.96	-	3069.5
AHQ-7-5, 6783	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	6.28E-08	0.85	3.77	-	581.1
AHQ-7-1, 6539	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	2.11E-07	0.97	4.85	-	2631.1
AHQ-7-4, 6877 - 6878	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	4.96E-07	0.98	6.55	-	3243.1
AHQ-7-1, 6540	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	2.58E-07	0.91	4.08	-	721.5
AHQ-7-6, 6682 - 6683	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	3.28E-07	0.98	7.19	-	2015.7
AHQ-7-2, 6841	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.03E-05	0.98	7.01	-	2670.6
AHQ-7-2, 6895	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.60E-07	0.94	5.11	-	975.9
AHQ-7-9, 6160	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.44E-06	0.95	5.31	-	821.8
AHQ-7-3, 6719	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.71E-08	0.95	4.96	-	1319.6
AHQ-7-1, 6599	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.33E-04	0.88	4.47	-	693.1
AHQ-7-9, 6161	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.07E-07	0.94	4.86	-	947.9
AHQ-7-1, 6595 - 6596	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.63E-08	0.92	4.62	-	964.5
AHQ-7-2, 6896	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.16E-04	0.94	5.21	-	619.7
AHQ-7-2, 5753	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.51E-05	0.90	3.90	-	1169.4
AHQ-7-5, 6842	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.63E-04	0.96	5.14	-	1169.1
AHQ-7-2, 5756	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.33E-05	0.88	4.74	-	466.7
AHQ-7-6, 6738	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	7.31E-08	0.86	4.07	-	736.5
AHQ-7-4, 6934	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	6.88E-09	0.95	5.37	-	991.4
AHQ-7-6, 6739	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.24E-05	0.92	5.11	-	596.4
AHQ-7-5, 6838 - 6844	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.51E-07	0.93	4.79	-	953.7
AHQ-7-4, 6932 - 6933	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.13E-07	0.94	5.01	-	1083.4
AHQ-7-3, 6721	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.87E-04	0.94	5.24	-	767.6
AHQ-7-4, 5745	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	4.37E-05	0.86	3.98	-	772.6
AHQ-7-8, 6854	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.48E-07	0.93	4.93	-	820.3
AHQ-7-7, 6836 - 6838	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.10E-07	0.96	4.92	-	1447.1
AHQ-7-7, 6837 - 6885	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.10E-04	0.91	4.72	-	646.1
AHQ-7-4, 5746	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.90E-06	0.93	4.77	-	832.2
AHQ-7-7, 2845	K.IFQAHKNCGQMSEIEAK.V	1993.25380	2	1.13E-04	0.73	3.73	-	720.1
AHQ-7-9, 3077	R.IGITNHDEYSLVR.E	1517.66833	2	9.72E-08	0.86	2.87	-	1036.1
AHQ-7-13-, 3391	R.IGITNHDEYSLVR.E	1517.66833	3	1.47E-09	0.88	4.10	-	690.7
AHQ-7-10, 3193 - 3273	R.IGITNHDEYSLVR.E	1517.66833	2	3.46E-06	0.79	3.40	-	540.6
AHQ-7-13-, 3651	R.IGITNHDEYSLVR.E	1517.66833	2	7.89E-09	0.79	2.87	-	740.6
AHQ-7-13-, 3655	R.IGITNHDEYSLVR.E	1517.66833	3	3.19E-07	0.72	3.24	-	641.1
AHQ-7-13, 3537 - 3599	R.IGITNHDEYSLVR.E	1517.66833	2	2.74E-05	0.82	2.78	-	1071.3
AHQ-7-11, 3258	R.IGITNHDEYSLVR.E	1517.66833	2	4.31E-10	0.91	3.34	-	1060.6
AHQ-7-7, 3225	R.IGITNHDEYSLVR.E	1517.66833	2	1.39E-07	0.94	3.81	-	1190.1
AHQ-7-7, 3469 - 3529	R.IGITNHDEYSLVR.E	1517.66833	2	2.91E-06	0.83	3.10	-	1014.1
AHQ-7-7, 3576 - 3641	R.IGITNHDEYSLVR.E	1517.66833	2	4.02E-04	0.78	2.84	-	663.9
AHQ-7-13-, 3387	R.IGITNHDEYSLVR.E	1517.66833	2	1.68E-09	0.97	4.51	-	1697.4
AHQ-7-2, 4648	R.ILAQATSDLVNAIK.A	1457.69748	2	8.16E-05	0.98	4.99	-	2058.3
AHQ-7-5, 4996 - 5006	R.ILAQATSDLVNAIK.A	1457.69748	2	5.10E-09	0.98	5.37	-	1869.5
AHQ-7-4, 5040	R.ILAQATSDLVNAIK.A	1457.69748	2	1.32E-04	0.95	3.96	-	1402.9
AHQ-7-3, 4139 - 4144	R.ILAQATSDLVNAIK.A	1457.69748	2	3.16E-09	0.98	4.88	-	2903.0
AHQ-7-7, 4840	R.ILAQATSDLVNAIK.A	1457.69748	2	9.68E-05	0.94	3.92	-	1267.3
AHQ-7-3, 4975	R.ILAQATSDLVNAIK.A	1457.69748	2	3.83E-05	0.97	4.17	-	1859.8
AHQ-7-5, 4118	R.ILAQATSDLVNAIK.A	1457.69748	2	3.39E-06	0.96	4.09	-	1492.1
AHQ-7-1, 4989 - 4991	R.ILAQATSDLVNAIK.A	1457.69748	2	2.81E-07	0.98	5.68	-	2063.6

AHQ-7-2, 4212	R.ILAQATSDLVNAIK.A	1457.69748	2	1.51E-05	0.97	4.65	-	2001.6
AHQ-7-4, 4172	R.ILAQATSDLVNAIK.A	1457.69748	2	1.85E-08	0.96	4.04	-	1390.9
AHQ-7-2, 4448	R.ILAQATSDLVNAIK.A	1457.69748	2	7.09E-09	0.97	4.13	-	1903.0
AHQ-7-6, 4929	R.ILAQATSDLVNAIK.A	1457.69748	2	8.08E-08	0.98	4.67	-	1875.3
AHQ-7-6, 4057	R.ILAQATSDLVNAIK.A	1457.69748	2	9.62E-07	0.96	4.04	-	1652.0
AHQ-7-1, 4224	R.ILAQATSDLVNAIK.A	1457.69748	2	7.00E-09	0.97	4.30	-	1697.4
AHQ-7-8, 4055	R.ILAQATSDLVNAIK.A	1457.69748	2	3.28E-05	0.85	3.15	-	787.2
AHQ-7-13-, 5525 - 5603	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	3.04E-06	0.95	5.09	-	885.8
AHQ-7-8, 5790 - 5794	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	9.45E-04	0.97	5.08	-	1452.3
AHQ-7-13, 5635	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	8.52E-06	0.94	4.50	-	842.5
AHQ-7-13-, 5176 - 5249	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	3.65E-12	0.97	5.20	-	1681.0
AHQ-7-9, 4916 - 4922	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.98E-05	0.89	3.57	-	1315.8
AHQ-7-10, 4975 - 5011	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.32E-08	0.91	4.24	-	1237.6
AHQ-7-7, 5313 - 5337	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	2	1.36E-04	0.79	3.34	-	642.3
AHQ-7-13, 5278 - 5293	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.03E-11	0.95	4.60	-	1619.5
AHQ-7-8, 5264	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	9.22E-04	0.92	4.10	-	1214.6
AHQ-7-11, 5078 - 5136	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	3.06E-07	0.73	3.32	-	603.8
AHQ-7-7, 5296 - 5368	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	5.62E-12	0.96	4.70	-	1667.6
AHQ-7-8, 5272	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	2	1.61E-06	0.89	3.66	-	837.1
AHQ-7-1, 5437	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	8.97E-07	0.93	4.58	-	1168.6
AHQ-7-7, 1796 - 1860	K.KEEITGTLR.K	1047.18765	2	8.30E-04	0.53	2.57	-	466.1
AHQ-7-7, 2624	R.KFFYSDQNVDSR.D	1506.60087	2	4.66E-04	0.93	3.59	-	1153.7
AHQ-7-7, 2492	K.KGIWLEAGK.A	1002.19171	2	1.74E-04	0.88	3.12	-	847.7
AHQ-7-13-, 2792	K.LAQAAQSSVATITR.L	1417.59344	2	6.95E-06	0.91	3.23	-	1193.2
AHQ-7-4, 2753 - 2820	K.LAQAAQSSVATITR.L	1417.59344	2	1.42E-07	0.96	4.47	-	1506.8
AHQ-7-4, 2770	K.LAQAAQSSVATITR.L	1417.59344	1	9.97E-04	0.42	2.90	-	163.2
AHQ-7-7, 2517 - 2562	K.LAQAAQSSVATITR.L	1417.59344	2	7.79E-06	0.79	2.67	-	805.2
AHQ-7-6, 2569 - 2578	K.LAQAAQSSVATITR.L	1417.59344	2	6.40E-08	0.96	4.66	-	1297.9
AHQ-7-10, 2652	K.LAQAAQSSVATITR.L	1417.59344	2	7.50E-04	0.80	3.16	-	776.1
AHQ-7-6, 2719 - 2725	K.LAQAAQSSVATITR.L	1417.59344	2	1.40E-04	0.96	4.38	-	1415.6
AHQ-7-4, 2601 - 2612	K.LAQAAQSSVATITR.L	1417.59344	2	7.65E-10	0.97	4.96	-	1689.1
AHQ-7-11, 2699	K.LAQAAQSSVATITR.L	1417.59344	2	1.92E-08	0.95	4.04	-	1311.2
AHQ-7-2, 2816	K.LAQAAQSSVATITR.L	1417.59344	2	4.33E-05	0.95	3.77	-	1512.0
AHQ-7-5, 2595	K.LAQAAQSSVATITR.L	1417.59344	2	6.47E-08	0.97	4.06	-	1707.8
AHQ-7-1, 2984	K.LAQAAQSSVATITR.L	1417.59344	2	7.44E-05	0.91	2.94	-	1361.8
AHQ-7-3, 2625	K.LAQAAQSSVATITR.L	1417.59344	2	5.61E-06	0.97	3.56	-	2246.3
AHQ-7-2, 2651	K.LAQAAQSSVATITR.L	1417.59344	2	4.97E-08	0.93	3.70	-	1201.2
AHQ-7-3, 2797	K.LAQAAQSSVATITR.L	1417.59344	2	1.28E-09	0.96	4.23	-	1734.0
AHQ-7-5, 2746	K.LAQAAQSSVATITR.L	1417.59344	2	2.60E-10	0.97	4.44	-	1689.7
AHQ-7-14-, 2793	K.LAQAAQSSVATITR.L	1417.59344	2	3.24E-07	0.92	2.58	-	1774.4
AHQ-7-3, 3320 - 3323	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	9.70E-06	0.96	5.37	-	1962.4
AHQ-7-5, 3011	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.64E-09	0.95	5.16	-	1217.4
AHQ-7-2, 3375	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.67E-09	0.94	4.83	-	811.3
AHQ-7-1, 3440 - 3499	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	8.78E-06	0.95	5.35	-	1612.2
AHQ-7-5, 3271	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.16E-07	0.92	4.80	-	512.3
AHQ-7-4, 3288	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.73E-05	0.96	5.53	-	1674.8
AHQ-7-4, 3290 - 3300	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.70E-09	0.95	5.26	-	716.8
AHQ-7-2, 3329 - 3396	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.66E-08	0.97	5.95	-	1937.4
AHQ-7-3, 3281 - 3344	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	4.05E-07	0.96	5.48	-	752.1
AHQ-7-2, 5503	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.32E-05	0.96	5.30	-	970.7
AHQ-7-2, 5413 - 5479	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.29E-06	0.96	5.24	-	1187.5
AHQ-7-2, 5296 - 5313	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.46E-06	0.93	4.54	-	809.0
AHQ-7-2, 5201 - 5231	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.49E-07	0.93	4.42	-	881.3
AHQ-7-9, 4812	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.80E-05	0.49	2.51	-	393.6
AHQ-7-5, 5354 - 5355	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.94E-07	0.98	6.49	-	1194.1
AHQ-7-3, 5093 - 5155	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.13E-08	0.96	4.81	-	1280.5
AHQ-7-6, 5051 - 5109	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.66E-07	0.90	4.38	-	635.1
AHQ-7-5, 5362 - 5364	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	3.75E-09	0.98	5.81	-	3133.0
AHQ-7-11, 4804	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.97E-06	0.76	3.41	-	452.5
AHQ-7-3, 5471 - 5472	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.40E-11	0.94	4.50	-	1168.6
AHQ-7-5, 5158 - 5162	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.87E-07	0.92	4.20	-	862.4
AHQ-7-3, 5331 - 5335	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.45E-05	0.98	6.06	-	1408.2
AHQ-7-5, 5522	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.91E-10	0.93	4.43	-	925.5
AHQ-7-4, 5597 - 5613	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.45E-09	0.96	5.63	-	752.1
AHQ-7-1, 5124	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.33E-07	0.94	4.53	-	921.8
AHQ-7-6, 5223 - 5302	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.61E-12	0.97	5.91	-	1142.7
AHQ-7-7, 5370 - 5405	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.05E-04	0.54	2.52	-	511.6
AHQ-7-11, 4991	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.57E-04	0.88	3.82	-	645.8
AHQ-7-4, 5233 - 5298	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.70E-07	0.95	4.62	-	1238.1
AHQ-7-1, 5433 - 5439	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.47E-11	0.96	5.22	-	1094.8
AHQ-7-6, 5437 - 5439	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.31E-10	0.96	5.03	-	971.8
AHQ-7-2, 5591 - 5607	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	9.11E-12	0.97	5.56	-	1392.3
AHQ-7-4, 5448 - 5460	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	8.07E-07	0.98	6.40	-	2523.8
AHQ-7-4, 5445	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.37E-04	0.95	4.81	-	1034.9
AHQ-7-7, 5022	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.26E-06	0.95	4.90	-	1121.7
AHQ-7-10, 4880	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.83E-06	0.82	3.40	-	690.6
AHQ-7-7, 3704	K.LHTDDELNWLDHGR.T	1721.81153	3	1.19E-06	0.94	4.86	-	951.1
AHQ-7-9, 3417 - 3485	K.LHTDDELNWLDHGR.T	1721.81153	2	6.12E-05	0.96	4.12	-	1725.6
AHQ-7-10, 3601	K.LHTDDELNWLDHGR.T	1721.81153	2	7.52E-05	0.81	3.22	-	619.2
AHQ-7-8, 3603	K.LHTDDELNWLDHGR.T	1721.81153	3	8.72E-06	0.94	4.52	-	1353.7
AHQ-7-8, 3595	K.LHTDDELNWLDHGR.T	1721.81153	2	5.90E-07	0.97	4.76	-	1680.0
AHQ-7-2, 4456	K.LLAALLEDEGGSGR.P	1401.54764	2	3.01E-11	0.97	4.31	-	1834.3
AHQ-7-4, 4352 - 4373	K.LLAALLEDEGGSGR.P	1401.54764	2	2.07E-06	0.92	3.01	-	1459.2
AHQ-7-8, 5040	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.35E-07	0.93	5.23	-	960.0
AHQ-7-8, 5034	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.66E-11	0.98	6.73	-	1463.2
AHQ-7-3, 5215	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.19E-04	0.97	5.77	-	1223.2
AHQ-7-6, 5158	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.38E-08	0.95	4.90	-	1446.9
AHQ-7-6, 5162	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.80E-06	0.98	6.63	-	1747.4
AHQ-7-3, 5216 - 5217	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.20E-09	0.97	5.86	-	1718.1
AHQ-7-10, 4755	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.36E-08	0.93	4.61	-	812.1
AHQ-7-2, 5297 - 5300	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.67E-08	0.98	6.86	-	1864.2
AHQ-7-5, 5238 - 5243	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.38E-09	0.98	6.60	-	2031.0
AHQ-7-1, 5247	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.29E-10	0.96	6.02	-	969.0
AHQ-7-4, 5286 - 5348	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.36E-05	0.95	5.12	-	1349.0
AHQ-7-1, 5243	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	8.91E-10	0.96	5.21	-	1662.1
AHQ-7-11, 4879	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.51E-07	0.96	5.88	-	807.1
AHQ-7-12, 4880	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.49E-04	0.95	4.94	-	1067.1
AHQ-7-5, 5235 - 5236	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	5.18E-08	0.98	6.14	-	1849.1
AHQ-7-4, 5292	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.49E-11	0.98	6.27	-	1758.9
AHQ-7-2, 5295 - 5365	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	5.44E-08	0.96	5.35	-	1601.8
AHQ-7-7, 5032	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.18E-05	0.95	4.64	-	1451.9
AHQ-7-10, 4752	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.40E-07	0.74	3.27	-	583.7
AHQ-7-7, 5028	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.40E-08	0.98	6.50	-	1660.7
AHQ-7-9, 4689	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.80E-05	0.88	4.11	-	795.4
AHQ-7-5, 4202	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.74E-06	0.52	3.02	-	223.1
AHQ-7-2, 4133 - 4207	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.66E-06	0.82	3.55	-	429.9
AHQ-7-4, 4196 - 4264	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.74E-05	0.75	3.35	-	396.5

AHQ-7-2, 4268 - 4337	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	4.92E-04	0.85	3.98	-	304.4
AHQ-7-1, 4195 - 4213	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	7.58E-08	0.42	3.05	-	125.7
AHQ-7-5, 4072 - 4135	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	5.30E-08	0.59	3.33	-	289.8
AHQ-7-3, 4143 - 4207	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	6.71E-06	0.83	3.84	-	294.6
AHQ-7-11, 5072	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.22E-09	0.94	4.23	-	1271.4
AHQ-7-3, 4363	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.02E-11	0.95	4.78	-	982.9
AHQ-7-3, 5428 - 5504	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.50E-10	0.98	5.68	-	1967.7
AHQ-7-7, 5360	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.97E-12	0.98	5.42	-	2157.5
AHQ-7-4, 5846	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.30E-09	0.84	3.42	-	697.8
AHQ-7-10, 4977	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.14E-04	0.88	3.92	-	724.8
AHQ-7-4, 5544	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.01E-06	0.96	5.33	-	1692.2
AHQ-7-4, 5476 - 5540	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.25E-08	0.97	5.72	-	1359.0
AHQ-7-4, 5449	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.12E-06	0.86	3.70	-	668.6
AHQ-7-3, 5716 - 5792	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.90E-11	0.96	4.96	-	1327.6
AHQ-7-4, 5121 - 5122	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.73E-07	0.95	4.10	-	1552.7
AHQ-7-1, 5565	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.91E-06	0.84	2.82	-	765.5
AHQ-7-9, 4920	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.00E-08	0.86	3.70	-	683.6
AHQ-7-5, 4355	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.84E-05	0.95	4.66	-	915.0
AHQ-7-4, 4410	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.86E-10	0.96	4.98	-	1277.2
AHQ-7-1, 5401 - 5464	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.73E-10	0.97	5.20	-	1814.8
AHQ-7-2, 5765	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	5.81E-06	0.90	4.10	-	1053.3
AHQ-7-5, 5470 - 5542	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.08E-13	0.98	6.04	-	2313.4
AHQ-7-2, 5672 - 5748	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.69E-07	0.97	5.21	-	1363.0
AHQ-7-2, 5551	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.02E-07	0.98	6.40	-	2229.7
AHQ-7-2, 5545 - 5609	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.15E-08	0.97	4.95	-	1787.8
AHQ-7-2, 5449	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.36E-11	0.96	4.81	-	1063.1
AHQ-7-5, 5479	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	6.85E-04	0.97	4.71	-	2076.1
AHQ-7-2, 5348	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.59E-11	0.96	4.22	-	1468.1
AHQ-7-2, 4460	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.35E-13	0.97	5.35	-	1209.3
AHQ-7-5, 5690 - 5763	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.26E-06	0.96	5.24	-	1221.9
AHQ-7-6, 5397	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.18E-12	0.97	5.59	-	1488.7
AHQ-7-6, 5407	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.00E-06	0.98	6.50	-	1995.4
AHQ-7-1, 4400	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.27E-08	0.93	4.16	-	753.5
AHQ-7-2, 5156	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.90E-11	0.97	5.34	-	1473.5
AHQ-7-2, 5372	R.LNEAAAGLNQAATELVQASRGTPQDLAR.A	2867.12501	3	1.08E-05	0.92	4.59	-	1164.5
AHQ-7-4, 2046 - 2080	R.MATNAAAQNAIK.K	1204.38227	2	4.87E-07	0.69	3.16	-	708.4
AHQ-7-2, 2128	R.MATNAAAQNAIK.K	1204.38227	2	5.05E-05	0.76	3.31	-	551.9
AHQ-7-3, 2123	R.MATNAAAQNAIK.K	1204.38227	2	6.79E-04	0.76	3.17	-	875.1
AHQ-7-2, 4640	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.94E-05	0.98	5.77	-	2884.9
AHQ-7-2, 4312	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	4.49E-08	0.65	3.31	-	542.4
AHQ-7-2, 4232	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	7.19E-06	0.98	6.41	-	3192.2
AHQ-7-2, 4224	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	2	8.11E-07	0.79	3.20	-	608.5
AHQ-7-1, 4185	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.31E-06	0.95	4.93	-	1187.9
AHQ-7-2, 4404 - 4467	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	9.22E-06	0.97	5.25	-	2177.7
AHQ-7-2, 4213	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	9.79E-07	0.90	4.48	-	821.3
AHQ-7-2, 4723	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	6.34E-09	0.98	6.27	-	2457.5
AHQ-7-4, 4112	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.02E-09	0.81	3.71	-	849.2
AHQ-7-2, 4107	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.24E-06	0.87	3.50	-	989.3
AHQ-7-2, 3347	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	4.10E-07	0.93	4.07	-	1826.2
AHQ-7-5, 4426	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	6.77E-05	0.87	3.89	-	1057.4
AHQ-7-5, 4318	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	2.13E-04	0.81	3.43	-	1117.9
AHQ-7-4, 4488	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	3.28E-04	0.97	5.15	-	1941.1
AHQ-7-2, 5976 - 6047	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.94E-05	0.97	4.41	-	1705.5
AHQ-7-2, 6503	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	3	1.01E-07	0.97	5.42	-	2139.2
AHQ-7-14-, 5542 - 5610	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	6.84E-07	0.97	5.10	-	1500.8
AHQ-7-1, 5717	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	3.41E-04	0.95	4.88	-	1698.7
AHQ-7-4, 5970	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	9.86E-06	0.95	4.71	-	1207.9
AHQ-7-14-, 5619	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	5.05E-06	0.86	3.47	-	1085.9
AHQ-7-3, 6312 - 6328	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	2.45E-04	0.93	4.04	-	1359.4
AHQ-7-14-, 6070	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	2.51E-07	0.97	4.48	-	1813.6
AHQ-7-4, 6477 - 6486	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	4.44E-06	0.98	5.52	-	1911.6
AHQ-7-7, 2312	K.NCGQMSEIEAK.V	1268.40005	2	9.29E-07	0.89	3.36	-	1143.5
AHQ-7-8, 2303	K.NCGQMSEIEAK.V	1268.40005	2	1.25E-04	0.81	2.74	-	1036.3
AHQ-7-3, 4244	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.95E-06	0.80	3.27	-	438.4
AHQ-7-2, 4508	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.67E-04	0.82	3.61	-	427.9
AHQ-7-4, 4381 - 4400	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.95E-04	0.66	3.00	-	292.8
AHQ-7-3, 4339 - 4405	K.NGNLPEFGDAISTASK.A	1621.73018	2	8.72E-08	0.94	4.70	-	609.4
AHQ-7-6, 4198 - 4270	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.92E-08	0.83	3.21	-	521.0
AHQ-7-2, 4592	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.59E-08	0.91	3.86	-	698.6
AHQ-7-1, 4329 - 4384	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.71E-07	0.68	2.90	-	358.6
AHQ-7-1, 4311	K.NLGTALAELR.T	1058.21367	2	1.02E-04	0.84	3.21	-	897.5
AHQ-7-5, 4174	K.NLGTALAELR.T	1058.21367	2	1.66E-05	0.87	3.45	-	859.1
AHQ-7-3, 4217 - 4231	K.NLGTALAELR.T	1058.21367	2	3.56E-05	0.86	3.28	-	853.1
AHQ-7-6, 4085	K.NLGTALAELR.T	1058.21367	2	6.33E-06	0.79	3.10	-	568.8
AHQ-7-2, 4287 - 4296	K.NLGTALAELR.T	1058.21367	2	1.74E-04	0.84	3.03	-	847.5
AHQ-7-3, 2855	K.PAAVAAENEEIGSHIK.H	1636.78798	3	3.68E-10	0.97	5.64	-	1837.8
AHQ-7-3, 2856	K.PAAVAAENEEIGSHIK.H	1636.78798	2	7.03E-09	0.98	4.95	-	2357.5
AHQ-7-2, 2789	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.07E-08	0.98	5.34	-	1840.5
AHQ-7-2, 2791	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.46E-08	0.97	5.01	-	2286.0
AHQ-7-2, 2881 - 2887	K.PAAVAAENEEIGSHIK.H	1636.78798	3	5.60E-11	0.96	5.07	-	1658.5
AHQ-7-2, 2884	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.51E-05	0.98	5.26	-	1779.5
AHQ-7-6, 2754	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.06E-07	0.97	4.99	-	1768.5
AHQ-7-4, 2721 - 2792	K.PAAVAAENEEIGSHIK.H	1636.78798	2	5.66E-09	0.98	5.20	-	2299.7
AHQ-7-5, 2788	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.03E-10	0.98	5.23	-	1777.3
AHQ-7-5, 2786	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.89E-08	0.96	5.26	-	1406.0
AHQ-7-4, 2789	K.PAAVAAENEEIGSHIK.H	1636.78798	3	3.68E-08	0.97	5.02	-	1695.6
AHQ-7-2, 3251	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.98E-04	0.74	3.36	-	384.7
AHQ-7-2, 3436	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	7.17E-05	0.84	3.58	-	907.0
AHQ-7-3, 3380 - 3388	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	1.18E-05	0.86	3.33	-	1024.1
AHQ-7-6, 3263 - 3335	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	9.25E-05	0.92	4.16	-	770.5
AHQ-7-4, 3337 - 3364	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	1.13E-06	0.77	3.43	-	546.9
AHQ-7-3, 3384 - 3392	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	8.30E-07	0.92	4.82	-	687.7
AHQ-7-5, 3315	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.71E-05	0.95	5.11	-	1000.1
AHQ-7-4, 3338	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	3.54E-07	0.91	4.76	-	498.9
AHQ-7-2, 3433	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	4.29E-09	0.90	4.17	-	769.0
AHQ-7-1, 3201	R.QEDVIATANLSR.R	1317.43074	2	1.79E-04	0.85	3.36	-	566.8
AHQ-7-2, 4104	R.QELAVFCSPEPPAK.T	1574.77985	2	7.72E-05	0.93	3.59	-	1215.0
AHQ-7-1, 4065 - 4111	R.QELAVFCSPEPPAK.T	1574.77985	2	1.34E-05	0.91	3.56	-	918.6
AHQ-7-4, 4064 - 4068	R.QELAVFCSPEPPAK.T	1574.77985	2	3.93E-07	0.94	4.17	-	1151.0
AHQ-7-2, 6845 - 6851	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	1.11E-07	0.92	4.87	-	722.4
AHQ-7-1, 3935	K.QVAASTAQLLVACK.V	1461.70942	2	1.78E-06	0.76	3.02	-	433.3
AHQ-7-13, 3867 - 3874	K.QVAASTAQLLVACK.V	1461.70942	2	5.18E-06	0.80	3.22	-	394.2
AHQ-7-13-, 3727	K.QVAASTAQLLVACK.V	1461.70942	2	2.80E-07	0.94	4.53	-	777.1
AHQ-7-2, 3915	K.QVAASTAQLLVACK.V	1461.70942	2	8.72E-06	0.89	3.44	-	668.0
AHQ-7-2, 5885	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	3.65E-04	0.98	4.98	-	2298.5
AHQ-7-3, 5748	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	5.03E-07	0.97	4.81	-	1533.5
AHQ-7-2, 4955 - 5015	K.RVAGSVTELIQAAEAM*K.G	1791.06327	2	1.89E-04	0.87	3.75	-	515.8

AHQ-7-4, 5877	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	2.04E-04	0.90	4.04	-	807.3
AHQ-7-2, 3687 - 3688	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	1.28E-08	0.83	4.43	-	418.0
AHQ-7-5, 3588	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	1.61E-04	0.69	3.54	-	439.2
AHQ-7-7, 2941	K.SIAAATSALVK.A	1032.21612	2	5.72E-04	0.65	2.77	-	559.0
AHQ-7-3, 3139	K.SIAAATSALVK.A	1032.21612	2	1.87E-05	0.85	2.94	-	886.6
AHQ-7-2, 3164 - 3184	K.SIAAATSALVK.A	1032.21612	2	4.38E-04	0.90	3.70	-	838.6
AHQ-7-6, 3038 - 3041	K.SIAAATSALVK.A	1032.21612	2	9.72E-05	0.86	2.93	-	920.3
AHQ-7-13-, 3829	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	2.05E-04	0.94	4.84	-	1426.5
AHQ-7-7, 3784	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	1.27E-07	0.95	5.12	-	1126.2
AHQ-7-7, 4161 - 4225	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	8.66E-06	0.87	3.58	-	1230.8
AHQ-7-7, 4146 - 4196	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	5.18E-06	0.86	3.98	-	573.2
AHQ-7-4, 5252 - 5270	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.84E-08	0.83	3.48	-	584.8
AHQ-7-5, 5083 - 5148	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.03E-10	0.93	4.78	-	478.3
AHQ-7-7, 4997	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.91E-05	0.69	3.10	-	438.3
AHQ-7-2, 5009 - 5073	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.17E-07	0.78	3.91	-	430.4
AHQ-7-2, 4612 - 4615	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.10E-07	0.90	4.17	-	645.5
AHQ-7-4, 4582	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.68E-10	0.84	3.99	-	467.5
AHQ-7-1, 5080 - 5156	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.10E-04	0.83	3.88	-	368.8
AHQ-7-2, 4749	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.65E-05	0.34	2.69	-	231.4
AHQ-7-2, 4860	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.86E-05	0.53	2.54	-	495.5
AHQ-7-4, 5353 - 5418	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.75E-09	0.92	4.25	-	725.1
AHQ-7-2, 5504 - 5581	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.49E-04	0.64	3.06	-	467.0
AHQ-7-1, 4564	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	8.58E-09	0.88	3.93	-	572.7
AHQ-7-3, 4519	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.64E-06	0.69	3.11	-	378.2
AHQ-7-3, 4645	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.92E-07	0.78	3.64	-	292.7
AHQ-7-3, 5047 - 5119	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.34E-05	0.86	4.14	-	351.2
AHQ-7-6, 4458	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.39E-07	0.77	3.73	-	398.3
AHQ-7-3, 5163	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.36E-07	0.83	3.52	-	447.9
AHQ-7-2, 5284 - 5353	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.53E-06	0.91	4.77	-	478.9
AHQ-7-3, 5252 - 5284	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.84E-04	0.77	3.73	-	301.3
AHQ-7-5, 5312	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.27E-10	0.90	4.30	-	443.6
AHQ-7-5, 4522	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.93E-07	0.86	3.81	-	497.3
AHQ-7-2, 5139 - 5219	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.99E-06	0.90	4.27	-	528.6
AHQ-7-6, 5074	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.04E-04	0.79	3.46	-	452.2
AHQ-7-4, 5146 - 5208	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.08E-11	0.89	4.19	-	366.5
AHQ-7-5, 5207	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.01E-04	0.69	2.89	-	420.2
AHQ-7-2, 5408 - 5419	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.62E-08	0.91	3.95	-	640.6
AHQ-7-6, 5247	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.76E-04	0.80	3.62	-	356.4
AHQ-7-8, 6767 - 6772	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.09E-06	0.93	4.89	-	1138.4
AHQ-7-2, 7016 - 7025	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.83E-04	0.90	5.05	-	1046.4
AHQ-7-2, 6821	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	6.10E-08	0.96	5.56	-	1496.2
AHQ-7-3, 6644 - 6645	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	4.44E-15	0.98	6.13	-	2154.9
AHQ-7-7, 4221	K.TKEVIQEWNLTNIK.R	1716.95938	3	8.85E-07	0.92	4.65	-	1062.2
AHQ-7-8, 4204	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.79E-06	0.98	4.96	-	2070.5
AHQ-7-7, 4182 - 4224	K.TKEVIQEWNLTNIK.R	1716.95938	2	8.52E-06	0.96	4.33	-	1470.2
AHQ-7-7, 6181	K.TLAESALQLLYTAK.E	1522.76793	2	1.47E-04	0.91	3.42	-	957.4
AHQ-7-1, 6107 - 6109	K.TLAESALQLLYTAK.E	1522.76793	2	5.22E-08	0.96	5.12	-	1179.2
AHQ-7-2, 6309 - 6367	K.TLAESALQLLYTAK.E	1522.76793	2	3.56E-07	0.95	4.30	-	1279.5
AHQ-7-11, 5782	K.TLAESALQLLYTAK.E	1522.76793	2	6.58E-08	0.75	2.63	-	738.2
AHQ-7-3, 6167 - 6243	K.TLAESALQLLYTAK.E	1522.76793	2	6.70E-08	0.97	4.97	-	1307.9
AHQ-7-6, 6171	K.TLAESALQLLYTAK.E	1522.76793	2	7.56E-08	0.94	4.14	-	931.5
AHQ-7-4, 6494 - 6521	K.TLAESALQLLYTAK.E	1522.76793	2	4.25E-04	0.89	3.23	-	939.1
AHQ-7-2, 6320	K.TLAESALQLLYTAK.E	1522.76793	3	1.29E-06	0.97	4.89	-	2392.0
AHQ-7-5, 6254 - 6262	K.TLAESALQLLYTAK.E	1522.76793	2	1.89E-06	0.96	4.67	-	1241.5
AHQ-7-4, 2605	K.TLSHPQQM*ALLDQTK.T	1727.96404	3	2.24E-06	0.94	4.07	-	1361.2
AHQ-7-3, 3341	K.TLSHPQQMALLDQTK.T	1711.96464	3	4.34E-05	0.95	4.75	-	1577.4
AHQ-7-5, 2594	K.TLSHPQQM*ALLDQTK.T	1727.96404	3	3.84E-08	0.93	4.09	-	1285.7
AHQ-7-1, 3492	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.66E-04	0.95	4.67	-	817.6
AHQ-7-5, 3276	K.TLSHPQQMALLDQTK.T	1711.96464	3	4.65E-04	0.90	4.26	-	1139.2
AHQ-7-3, 3327	K.TLSHPQQMALLDQTK.T	1711.96464	2	6.97E-05	0.93	4.52	-	662.8
AHQ-7-4, 3297	K.TLSHPQQMALLDQTK.T	1711.96464	3	8.40E-04	0.94	4.91	-	1132.1
AHQ-7-5, 3270	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.57E-04	0.95	4.76	-	803.9
AHQ-7-6, 3238	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.97E-05	0.96	5.02	-	990.6
AHQ-7-1, 3649 - 3652	K.TM*LESAGGLIQTAR.A	1464.67035	2	4.88E-06	0.96	4.80	-	1564.2
AHQ-7-4, 4316	K.TMLESAGGLIQTAR.A	1448.67095	2	1.33E-05	0.96	4.26	-	1837.5
AHQ-7-11, 3342	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.22E-06	0.91	3.09	-	1414.3
AHQ-7-7, 4150	K.TMLESAGGLIQTAR.A	1448.67095	2	6.50E-08	0.91	3.65	-	1285.0
AHQ-7-6, 4203	K.TMLESAGGLIQTAR.A	1448.67095	2	2.38E-08	0.92	3.64	-	1751.7
AHQ-7-6, 3422 - 3438	K.TM*LESAGGLIQTAR.A	1464.67035	2	2.37E-04	0.70	3.30	-	791.0
AHQ-7-13, 4281	K.TMLESAGGLIQTAR.A	1448.67095	2	3.93E-07	0.87	3.21	-	1239.2
AHQ-7-2, 3577 - 3639	K.TM*LESAGGLIQTAR.A	1464.67035	2	4.02E-08	0.95	4.42	-	1486.1
AHQ-7-2, 4324 - 4388	K.TMLESAGGLIQTAR.A	1448.67095	2	6.25E-06	0.91	3.58	-	1392.9
AHQ-7-2, 4412 - 4413	K.TM*LESAGGLIQTAR.A	1464.67035	2	5.99E-06	0.74	2.86	-	970.9
AHQ-7-5, 4278	K.TMLESAGGLIQTAR.A	1448.67095	2	7.63E-10	0.91	3.81	-	1394.1
AHQ-7-1, 4303 - 4360	K.TMLESAGGLIQTAR.A	1448.67095	2	5.82E-10	0.96	4.32	-	2055.4
AHQ-7-3, 4272 - 4297	K.TMLESAGGLIQTAR.A	1448.67095	2	4.78E-06	0.94	3.77	-	1240.8
AHQ-7-13, 4333	K.TM*QFEPSTMVYDACR.I	1854.07511	2	5.35E-04	0.89	3.70	-	636.0
AHQ-7-13-, 4784	K.TVTDMLM*TICAR.I	1429.70947	2	7.10E-06	0.56	2.83	-	570.2
AHQ-7-13, 4895	K.TVTDMLM*TICAR.I	1429.70947	2	2.66E-05	0.85	2.77	-	1338.7
AHQ-7-13-, 3616 - 3684	K.TVTDM*LM*TICAR.I	1445.70887	2	1.36E-04	0.78	2.73	-	722.2
AHQ-7-7, 5305 - 5309	K.TVTDMLMTICAR.I	1413.71007	2	9.42E-04	0.86	2.66	-	1145.5
AHQ-7-13, 3759 - 3822	K.TVTDM*LM*TICAR.I	1445.70887	2	2.93E-04	0.85	3.01	-	723.0
AHQ-7-7, 5088	K.TYGVSFFLVK.E	1161.37395	2	4.40E-07	0.90	3.43	-	717.8
AHQ-7-8, 6118	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.27E-06	0.94	4.35	-	1126.4
AHQ-7-3, 5248	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	2.17E-06	0.95	4.28	-	1337.3
AHQ-7-4, 5332	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	3.50E-05	0.95	4.72	-	1304.8
AHQ-7-10, 5619	R.VAGSVTELIQAAEAMK.G	1618.87752	2	7.97E-04	0.79	2.63	-	902.9
AHQ-7-1, 6032 - 6036	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.68E-05	0.95	3.91	-	1499.8
AHQ-7-2, 6216 - 6276	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.55E-07	0.97	5.42	-	1542.2
AHQ-7-4, 6237 - 6262	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.33E-08	0.96	4.31	-	1500.8
AHQ-7-5, 5276	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	2.68E-07	0.96	4.47	-	1543.6
AHQ-7-9, 5493 - 5548	R.VAGSVTELIQAAEAMK.G	1618.87752	2	8.04E-04	0.77	3.00	-	717.4
AHQ-7-3, 6093	R.VAGSVTELIQAAEAMK.G	1618.87752	2	5.07E-05	0.95	4.29	-	1457.1
AHQ-7-6, 6083	R.VAGSVTELIQAAEAMK.G	1618.87752	2	3.83E-06	0.95	4.40	-	1068.7
AHQ-7-7, 6088	R.VAGSVTELIQAAEAMK.G	1618.87752	2	6.75E-07	0.93	3.78	-	1247.7
AHQ-7-1, 5235 - 5259	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	3.93E-06	0.91	3.86	-	1051.3
AHQ-7-5, 6171	R.VAGSVTELIQAAEAMK.G	1618.87752	2	5.35E-06	0.95	4.16	-	1357.3
AHQ-7-2, 5635 - 5695	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.34E-07	0.96	4.97	-	1061.7
AHQ-7-4, 5868 - 5926	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.22E-10	0.96	5.30	-	1005.9
AHQ-7-6, 5697	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.88E-09	0.96	5.27	-	1136.9
AHQ-7-2, 5703 - 5777	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	7.96E-06	0.96	5.62	-	1387.3
AHQ-7-1, 5669 - 5735	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.71E-09	0.96	5.28	-	852.1
AHQ-7-4, 5764 - 5806	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.98E-11	0.96	5.09	-	934.4
AHQ-7-2, 5768	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.51E-08	0.88	4.20	-	409.5
AHQ-7-2, 5851 - 5920	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.74E-10	0.93	4.88	-	723.7
AHQ-7-1, 5507 - 5575	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.81E-08	0.92	4.41	-	560.0
AHQ-7-4, 5626 - 5692	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.24E-05	0.93	4.72	-	693.8

AHQ-7-6, 5698	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	1.39E-05	0.94	4.62	-	1391.0
AHQ-7-10, 5175 - 5244	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.37E-08	0.94	4.77	-	805.8
AHQ-7-9, 5189 - 5256	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.08E-04	0.50	2.92	-	232.7
AHQ-7-6, 5598	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.35E-06	0.89	4.41	-	336.8
AHQ-7-3, 5508 - 5551	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.95E-07	0.92	4.92	-	629.0
AHQ-7-6, 5477 - 5529	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.53E-08	0.95	4.96	-	944.3
AHQ-7-5, 5559	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.43E-06	0.80	3.79	-	505.7
AHQ-7-7, 5486	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.68E-06	0.83	3.54	-	640.3
AHQ-7-7, 5604	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.50E-10	0.89	4.27	-	443.5
AHQ-7-7, 5701 - 5702	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.38E-09	0.96	5.40	-	956.1
AHQ-7-7, 5709	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	4.65E-07	0.54	3.07	-	527.3
AHQ-7-3, 5621 - 5637	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.89E-15	0.94	4.94	-	679.4
AHQ-7-5, 5684	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.34E-11	0.91	3.98	-	638.3
AHQ-7-3, 5720 - 5781	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.20E-04	0.59	3.31	-	573.0
AHQ-7-11, 5364	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.05E-10	0.90	3.99	-	608.0
AHQ-7-5, 5790 - 5791	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.04E-08	0.97	6.13	-	1246.3
AHQ-7-5, 5887	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.04E-09	0.92	4.51	-	793.1
AHQ-7-1, 5611 - 5667	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	1.61E-04	0.94	4.67	-	1349.0
AHQ-7-2, 3935	K.VGDDPAVWQLK.N	1228.37879	1	1.08E-06	0.34	2.46	-	303.3
AHQ-7-6, 3739	K.VGDDPAVWQLK.N	1228.37879	2	1.73E-08	0.80	2.77	-	678.5
AHQ-7-4, 3841 - 3861	K.VGDDPAVWQLK.N	1228.37879	1	4.68E-04	0.24	1.82	-	390.3
AHQ-7-6, 3729	K.VGDDPAVWQLK.N	1228.37879	2	3.17E-08	0.93	3.81	-	891.9
AHQ-7-5, 3807 - 3822	K.VGDDPAVWQLK.N	1228.37879	2	2.39E-08	0.92	3.78	-	822.2
AHQ-7-3, 3843	K.VGDDPAVWQLK.N	1228.37879	2	5.60E-08	0.92	3.79	-	812.5
AHQ-7-3, 3788 - 3851	K.VGDDPAVWQLK.N	1228.37879	2	6.43E-07	0.85	3.54	-	801.6
AHQ-7-7, 3673	K.VGDDPAVWQLK.N	1228.37879	2	1.12E-08	0.95	4.11	-	1030.1
AHQ-7-4, 3837 - 3840	K.VGDDPAVWQLK.N	1228.37879	2	1.33E-08	0.89	3.38	-	771.2
AHQ-7-1, 3901 - 3960	K.VGDDPAVWQLK.N	1228.37879	2	2.29E-08	0.91	3.79	-	727.5
AHQ-7-2, 3867 - 3927	K.VGDDPAVWQLK.N	1228.37879	2	2.52E-09	0.89	3.30	-	828.6
AHQ-7-2, 3376	K.VGDDPAVWQLKNSAK.V	1628.81068	2	1.55E-05	0.83	3.63	-	658.2
AHQ-7-3, 3216 - 3220	K.VLGEAMTGISQNAK.N	1419.62961	1	7.48E-04	0.56	2.72	-	506.6
AHQ-7-4, 3196	K.VLGEAMTGISQNAK.N	1419.62961	2	8.42E-05	0.92	3.88	-	1073.9
AHQ-7-4, 2408	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.00E-04	0.89	3.49	-	996.5
AHQ-7-2, 3404	K.VLGEAMTGISQNAK.N	1419.62961	2	2.55E-04	0.82	3.27	-	686.4
AHQ-7-2, 2480 - 2545	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.30E-07	0.96	4.45	-	1459.7
AHQ-7-2, 3263 - 3267	K.VLGEAMTGISQNAK.N	1419.62961	1	2.91E-06	0.84	2.93	-	746.6
AHQ-7-11, 3055	K.VLGEAMTGISQNAK.N	1419.62961	2	2.76E-05	0.89	3.58	-	1034.3
AHQ-7-1, 4796	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	3.77E-06	0.85	4.28	-	478.4
AHQ-7-2, 4812 - 4875	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	1.37E-11	0.92	5.25	-	592.6
AHQ-7-3, 5208 - 5271	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	1.41E-07	0.83	4.43	-	418.0
AHQ-7-3, 4723 - 4784	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	2.22E-06	0.85	4.67	-	447.9
AHQ-7-4, 4860	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	5.42E-06	0.87	4.59	-	477.3
AHQ-7-5, 5284	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	1.65E-04	0.92	4.96	-	904.2
AHQ-7-5, 1712 - 1770	K.VLVQNAAGSQEK.L	1244.37976	2	1.37E-06	0.93	3.65	-	1060.9
AHQ-7-4, 1729 - 1796	K.VLVQNAAGSQEK.L	1244.37976	2	4.17E-07	0.94	3.75	-	1150.8
AHQ-7-4, 1917 - 1977	K.VLVQNAAGSQEK.L	1244.37976	2	8.83E-05	0.74	2.85	-	544.5
AHQ-7-2, 1797 - 1863	K.VLVQNAAGSQEK.L	1244.37976	2	7.77E-09	0.93	3.62	-	1256.8
AHQ-7-4, 2045	K.VLVQNAAGSQEK.L	1244.37976	2	1.57E-04	0.52	2.60	-	520.7
AHQ-7-3, 1820 - 1877	K.VLVQNAAGSQEK.L	1244.37976	2	2.01E-06	0.93	3.62	-	1041.0
AHQ-7-6, 1959	K.VLVQNAAGSQEK.L	1244.37976	2	2.65E-06	0.83	3.08	-	751.6
AHQ-7-2, 2040 - 2055	K.VLVQNAAGSQEK.L	1244.37976	2	2.74E-06	0.92	3.51	-	925.3
AHQ-7-5, 1826	K.VLVQNAAGSQEK.L	1244.37976	2	8.61E-05	0.72	2.83	-	582.4
AHQ-7-6, 1749 - 1815	K.VLVQNAAGSQEK.L	1244.37976	2	7.40E-07	0.88	3.34	-	788.1
AHQ-7-4, 1821 - 1860	K.VLVQNAAGSQEK.L	1244.37976	2	6.43E-08	0.86	3.46	-	639.6
AHQ-7-7, 4158	K.VM*VTNVTSLLK.T	1221.49262	2	1.16E-04	0.77	2.98	-	629.4
AHQ-7-2, 4767	K.VMVTNVTSLLK.T	1205.49322	2	6.40E-06	0.92	3.79	-	887.9
AHQ-7-7, 4473	K.VMVTNVTSLLK.T	1205.49322	2	2.60E-04	0.78	3.43	-	620.0
AHQ-7-2, 4443	K.VM*VTNVTSLLK.T	1221.49262	2	3.54E-05	0.90	3.47	-	888.1
AHQ-7-6, 4562	K.VMVTNVTSLLK.T	1205.49322	2	8.18E-06	0.88	3.62	-	736.5
AHQ-7-5, 4646	K.VMVTNVTSLLK.T	1205.49322	2	5.68E-05	0.82	3.47	-	615.7
AHQ-7-4, 4368	K.VM*VTNVTSLLK.T	1221.49262	2	3.09E-05	0.68	2.88	-	538.6
AHQ-7-3, 4680	K.VMVTNVTSLLK.T	1205.49322	2	8.04E-05	0.91	3.80	-	865.1
AHQ-7-3, 4361 - 4364	K.VM*VTNVTSLLK.T	1221.49262	2	4.98E-05	0.82	3.38	-	656.5
AHQ-7-4, 4725	K.VMVTNVTSLLK.T	1205.49322	2	2.73E-04	0.91	3.69	-	877.0
AHQ-7-6, 2809	R.VQELGHGCAALVTK.A	1484.70307	2	3.26E-09	0.94	3.81	-	1275.7
AHQ-7-1, 3095	R.VQELGHGCAALVTK.A	1484.70307	2	1.29E-05	0.94	4.29	-	1165.9
AHQ-7-4, 2836 - 2861	R.VQELGHGCAALVTK.A	1484.70307	2	3.29E-04	0.98	5.07	-	2347.0
AHQ-7-2, 2940 - 2945	R.VQELGHGCAALVTK.A	1484.70307	3	2.80E-04	0.77	3.10	-	489.6
AHQ-7-2, 2932	R.VQELGHGCAALVTK.A	1484.70307	2	2.38E-06	0.95	4.20	-	1236.7
AHQ-7-7, 2738	R.VQELGHGCAALVTK.A	1484.70307	2	9.64E-10	0.98	4.88	-	2058.3
AHQ-7-5, 2842	R.VQELGHGCAALVTK.A	1484.70307	2	5.14E-05	0.97	4.69	-	1612.4
AHQ-7-5, 2775 - 2806	K.VSHVLAALQAGNR.G	1336.52525	2	2.22E-09	0.96	4.07	-	1471.2
AHQ-7-2, 2893	K.VSHVLAALQAGNR.G	1336.52525	1	5.86E-05	0.82	3.79	-	376.0
AHQ-7-2, 2876	K.VSHVLAALQAGNR.G	1336.52525	1	4.30E-05	0.76	3.07	-	423.9
AHQ-7-6, 2761	K.VSHVLAALQAGNR.G	1336.52525	2	5.34E-12	0.97	4.81	-	1780.1
AHQ-7-2, 2869	K.VSHVLAALQAGNR.G	1336.52525	2	1.12E-07	0.97	4.35	-	1916.3
AHQ-7-4, 2790	K.VSHVLAALQAGNR.G	1336.52525	1	2.66E-05	0.79	3.23	-	474.4
AHQ-7-1, 3081	K.VSHVLAALQAGNR.G	1336.52525	2	1.18E-09	0.97	4.48	-	1725.8
AHQ-7-3, 2864	K.VSHVLAALQAGNR.G	1336.52525	2	2.88E-10	0.97	4.64	-	1531.7
AHQ-7-6, 2778	K.VSHVLAALQAGNR.G	1336.52525	1	4.80E-06	0.57	2.67	-	231.2
AHQ-7-4, 2784 - 2793	K.VSHVLAALQAGNR.G	1336.52525	2	6.18E-10	0.98	5.00	-	2328.7
AHQ-7-3, 2871 - 2876	K.VSHVLAALQAGNR.G	1336.52525	1	3.61E-04	0.84	3.27	-	451.7
AHQ-7-7, 6428	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.30E-04	0.93	4.55	-	766.8
AHQ-7-5, 6507	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	9.28E-07	0.95	4.74	-	1432.5
AHQ-7-1, 6327	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	2.61E-06	0.94	4.29	-	1449.1
AHQ-7-9, 5836	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.05E-04	0.74	2.98	-	437.6
AHQ-7-1, 6319 - 6323	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	7.37E-05	0.93	4.32	-	843.4
AHQ-7-4, 6674 - 6726	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.84E-07	0.89	4.44	-	538.2
AHQ-7-11, 6011	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.35E-04	0.58	2.93	-	441.0
AHQ-7-6, 5670 - 5673	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	6.34E-06	0.96	4.85	-	1244.0
AHQ-7-4, 6568 - 6590	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	1.29E-06	0.92	4.35	-	1150.4
AHQ-7-1, 5672	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.74E-11	0.97	5.29	-	2103.2
AHQ-7-4, 6513 - 6572	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	8.17E-05	0.98	6.25	-	1156.6
AHQ-7-5, 5760	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.64E-05	0.86	3.69	-	723.4
AHQ-7-6, 6385 - 6387	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.38E-05	0.96	5.70	-	714.2
AHQ-7-4, 6504 - 6570	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	8.73E-07	0.97	5.44	-	1054.7
AHQ-7-3, 6395 - 6403	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	4.39E-05	0.94	4.62	-	1323.4
AHQ-7-3, 6320 - 6388	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.32E-06	0.91	4.22	-	679.3
AHQ-7-3, 5715	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	2.08E-08	0.96	4.65	-	1858.4
AHQ-7-4, 5844	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.23E-08	0.97	5.62	-	1136.1
AHQ-7-3, 5712	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.65E-08	0.94	4.41	-	1031.3
AHQ-7-1, 5592 - 5668	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	4.18E-07	0.93	4.55	-	997.4
AHQ-7-2, 5855	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	7.85E-07	0.90	3.50	-	1625.9
AHQ-7-4, 5845	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.86E-05	0.94	4.23	-	1093.4
AHQ-7-2, 6469 - 6547	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.51E-09	0.97	6.09	-	1256.6
AHQ-7-2, 6477	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.72E-06	0.94	4.85	-	749.1
AHQ-7-2, 6563 - 6571	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	2.51E-10	0.98	5.69	-	2206.9

AHQ-7-2, 6608 - 6667	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.64E-05	0.95	5.53	-	702.3
AHQ-7-3, 5709	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.16E-07	0.95	4.96	-	1039.8
AHQ-7-1, 4595	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.98E-07	0.95	4.60	-	889.9
AHQ-7-4, 4518	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.12E-06	0.82	4.21	-	253.0
AHQ-7-3, 4467	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.59E-09	0.92	4.03	-	696.1
AHQ-7-5, 4443	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.49E-07	0.93	4.58	-	590.0
AHQ-7-6, 4373	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.47E-07	0.83	3.77	-	394.9
AHQ-7-6, 4454 - 4481	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.07E-09	0.96	4.93	-	946.0
AHQ-7-4, 4620	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.01E-07	0.93	4.56	-	596.2
AHQ-7-5, 4546 - 4547	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.91E-08	0.97	5.44	-	968.3
AHQ-7-14, 5246	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.74E-06	0.91	4.14	-	643.0
AHQ-7-8, 4490 - 4496	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.97E-09	0.97	5.84	-	1068.8
AHQ-7-14-, 4407	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.61E-07	0.92	4.32	-	637.8
AHQ-7-8, 4506	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	2.83E-11	0.90	4.12	-	1061.9
AHQ-7-13, 4483	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.34E-08	0.95	5.09	-	783.2
AHQ-7-2, 4663 - 4743	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.07E-06	0.96	5.47	-	773.1
AHQ-7-2, 4555	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.84E-06	0.90	4.56	-	398.7
AHQ-7-11, 4284 - 4364	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.82E-05	0.63	3.74	-	315.4
gi|4504165|ref|NP_000168.1| gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]				3.89E-15	22.69	250.35	40.50	85696.9
AHQ-7-6, 3647	K.AGALNSNDAFVLK.T	1320.47622	2	2.90E-07	0.78	3.46	-	471.9
AHQ-7-6, 3751 - 3814	K.AGALNSNDAFVLK.T	1320.47622	2	1.32E-04	0.85	3.54	-	663.8
AHQ-7-5, 3644 - 3710	K.AGALNSNDAFVLK.T	1320.47622	2	1.55E-07	0.89	3.60	-	887.8
AHQ-7-5, 3906	K.AGALNSNDAFVLK.T	1320.47622	2	4.41E-10	0.88	3.63	-	713.4
AHQ-7-5, 3876	K.AGALNSNDAFVLK.T	1320.47622	1	1.45E-05	0.39	1.98	-	482.7
AHQ-7-5, 3227	K.AGKEPGLQIWR.V	1255.45060	2	3.57E-04	0.77	2.89	-	623.4
AHQ-7-5, 3230	K.AGKEPGLQIWR.V	1255.45060	3	4.04E-06	0.92	4.06	-	1284.0
AHQ-7-6, 5381 - 5441	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.53E-04	0.94	4.67	-	611.9
AHQ-7-8, 5578	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.46E-04	0.92	4.33	-	665.3
AHQ-7-11, 5270	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.98E-08	0.90	4.14	-	670.1
AHQ-7-5, 5670 - 5730	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.95E-07	0.97	6.01	-	736.2
AHQ-7-7, 5422 - 5429	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	8.12E-05	0.95	4.90	-	649.5
AHQ-7-10, 5171	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	8.28E-09	0.94	4.52	-	806.8
AHQ-7-7, 5589 - 5593	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.20E-09	0.97	6.20	-	1043.6
AHQ-7-9, 5109	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.05E-05	0.60	2.95	-	358.1
AHQ-7-7, 5514	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	2.54E-09	0.96	4.40	-	2029.1
AHQ-7-5, 5531 - 5594	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	5.85E-09	0.91	4.18	-	1038.4
AHQ-7-5, 5614	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.08E-10	0.95	4.84	-	1391.7
AHQ-7-6, 5525	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.31E-09	0.91	3.83	-	1492.8
AHQ-7-13, 2493	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.27E-07	0.89	3.41	-	1269.3
AHQ-7-13-, 2308 - 2311	K.DSQEEEKTEALTSAK.R	1666.72289	3	9.61E-05	0.94	4.26	-	1492.0
AHQ-7-11, 2226	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.49E-07	0.93	3.78	-	1586.0
AHQ-7-5, 2222 - 2299	K.DSQEEEKTEALTSAK.R	1666.72289	3	7.86E-07	0.98	5.33	-	2490.7
AHQ-7-7, 2196	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.71E-07	0.89	3.59	-	1057.9
AHQ-7-10, 2203	K.DSQEEEKTEALTSAK.R	1666.72289	2	8.68E-06	0.85	3.07	-	1080.4
AHQ-7-13-, 2300	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.53E-07	0.92	3.63	-	1180.0
AHQ-7-6, 2221	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.14E-07	0.91	3.50	-	1152.7
AHQ-7-5, 2218 - 2294	K.DSQEEEKTEALTSAK.R	1666.72289	2	6.09E-06	0.94	3.99	-	1498.7
AHQ-7-4, 2262	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.12E-05	0.91	3.58	-	1175.4
AHQ-7-2, 2341	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.57E-05	0.75	3.13	-	643.3
AHQ-7-6, 2229	K.DSQEEEKTEALTSAK.R	1666.72289	3	6.64E-08	0.95	4.28	-	1610.4
AHQ-7-5, 4094 - 4164	K.EPAHLMSLFGGK.P	1287.51287	2	3.56E-04	0.60	2.94	-	296.4
AHQ-7-5, 6611	R.EVQGFESATFLGYFK.S	1723.90570	2	1.26E-07	0.85	3.27	-	886.0
AHQ-7-5, 6519	R.EVQGFESATFLGYFK.S	1723.90570	2	9.84E-06	0.92	3.84	-	904.9
AHQ-7-13-, 5769 - 5835	R.EVQGFESATFLGYFK.S	1723.90570	2	1.81E-10	0.92	3.68	-	996.5
AHQ-7-5, 6199 - 6270	R.EVQGFESATFLGYFK.S	1723.90570	2	3.48E-10	0.95	4.24	-	1395.8
AHQ-7-11, 5652	R.EVQGFESATFLGYFK.S	1723.90570	2	1.93E-08	0.71	2.52	-	845.1
AHQ-7-1, 5976	R.EVQGFESATFLGYFK.S	1723.90570	2	3.53E-08	0.82	3.34	-	691.8
AHQ-7-5, 6880	R.EVQGFESATFLGYFK.S	1723.90570	2	1.02E-06	0.94	4.06	-	1114.8
AHQ-7-5, 6088 - 6154	R.EVQGFESATFLGYFK.S	1723.90570	2	5.94E-08	0.97	4.80	-	1873.5
AHQ-7-14-, 5798 - 5801	R.EVQGFESATFLGYFK.S	1723.90570	2	3.24E-05	0.97	4.98	-	1599.6
AHQ-7-5, 6850	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	3	1.91E-06	0.89	4.00	-	760.8
AHQ-7-5, 2318 - 2330	K.HVVPNEVVVQR.L	1276.46981	3	4.57E-04	0.70	3.66	-	672.1
AHQ-7-5, 2519 - 2527	K.HVVPNEVVVQR.L	1276.46981	2	1.81E-05	0.91	3.34	-	744.4
AHQ-7-11, 2339	K.HVVPNEVVVQR.L	1276.46981	2	9.25E-06	0.88	3.00	-	671.0
AHQ-7-5, 2314 - 2326	K.HVVPNEVVVQR.L	1276.46981	2	8.49E-08	0.93	3.61	-	707.9
AHQ-7-5, 6035 - 6108	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	3.71E-09	0.94	4.82	-	1216.3
AHQ-7-5, 6166 - 6226	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	2.03E-05	0.95	5.16	-	1409.7
AHQ-7-6, 6019 - 6086	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	1.16E-04	0.69	3.23	-	584.0
AHQ-7-5, 5566 - 5579	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	3.89E-15	0.98	7.04	-	2316.2
AHQ-7-5, 5303	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.51E-09	0.98	6.77	-	1760.2
AHQ-7-6, 5509	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	2.62E-11	0.98	6.06	-	2067.0
AHQ-7-5, 2507	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	3.30E-08	0.82	3.85	-	388.9
AHQ-7-5, 4747 - 4810	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	4.37E-04	0.87	3.75	-	421.9
AHQ-7-5, 3079	K.SEDCFILDHGK.D	1322.42590	1	8.99E-04	0.39	2.22	-	301.1
AHQ-7-5, 3080 - 3100	K.SEDCFILDHGK.D	1322.42590	3	4.73E-04	0.80	3.45	-	474.6
AHQ-7-5, 3068 - 3103	K.SEDCFILDHGK.D	1322.42590	2	3.03E-06	0.94	3.24	-	1318.1
AHQ-7-7, 2986	K.SEDCFILDHGK.D	1322.42590	2	2.68E-05	0.94	3.56	-	1281.8
AHQ-7-10, 2231	K.TGAQELLR.V	888.00387	2	8.82E-05	0.90	2.97	-	1222.1
AHQ-7-5, 2238	K.TGAQELLR.V	888.00387	2	1.86E-04	0.92	3.43	-	1201.0
AHQ-7-5, 2328	K.TGAQELLR.V	888.00387	2	2.82E-04	0.87	3.08	-	1001.6
AHQ-7-5, 4446 - 4510	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	2.47E-11	0.97	5.24	-	1328.1
AHQ-7-5, 4579	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	4.37E-06	0.93	4.39	-	883.1
AHQ-7-6, 4378	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	5.50E-05	0.95	3.68	-	1482.4
AHQ-7-11, 4183	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	4.04E-05	0.86	3.05	-	969.1
AHQ-7-5, 3827 - 3890	R.VHVSEEGTEPEAM*LQVLGPK.P	2167.42570	2	5.91E-04	0.97	5.74	-	1154.5
AHQ-7-5, 4935 - 5003	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	2.07E-08	0.97	5.79	-	1195.1
AHQ-7-5, 3816 - 3887	R.VHVSEEGTEPEAM*LQVLGPK.P	2167.42570	3	3.40E-04	0.92	4.31	-	950.8
AHQ-7-5, 5223	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	5.52E-07	0.96	5.56	-	1210.7
AHQ-7-5, 4343	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	1.12E-07	0.90	4.61	-	606.7
AHQ-7-5, 4016	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	3.85E-06	0.97	6.72	-	1199.9
AHQ-7-6, 3974	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	7.05E-07	0.97	6.27	-	1230.1
AHQ-7-5, 3883	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	7.85E-08	0.98	6.45	-	1884.4
AHQ-7-5, 3620 - 3686	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	2.59E-04	0.89	5.20	-	1199.1
AHQ-7-5, 4027	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	2	3.11E-10	0.90	4.26	-	749.8
AHQ-7-5, 3218	R.VPFDAATLHTSTAM*AAQHGM*DDDGTGQK.Q	2907.10021	3	2.89E-05	0.90	4.20	-	836.9
AHQ-7-5, 6376	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	2	2.15E-10	0.95	4.58	-	1112.1
AHQ-7-5, 6372 - 6451	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	3	1.74E-09	0.93	4.79	-	1219.4
AHQ-7-6, 6278 - 6285	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	3	4.23E-06	0.86	3.80	-	895.7
AHQ-7-5, 5350 - 5410	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	4.28E-10	0.88	3.59	-	787.3
AHQ-7-6, 5317	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	7.10E-10	0.94	4.08	-	1066.9
gi|13124879|ref|NP_002465.1| smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]				4.44E-15	8.78	110.34	6.10	227336.7
AHQ-7-3, 4712	R.DLGEELEALK.T	1117.23151	2	1.35E-04	0.94	3.79	-	1105.3
AHQ-7-2, 4823	R.DLGEELEALK.T	1117.23151	2	5.54E-06	0.90	3.60	-	872.0
AHQ-7-6, 2733	R.EDQSILCTGESGAGK.T	1553.63107	2	5.33E-07	0.86	3.82	-	486.0
AHQ-7-5, 2750	R.EDQSILCTGESGAGK.T	1553.63107	2	7.75E-04	0.47	2.83	-	387.3
AHQ-7-2, 3005	K.FDQLLAEEK.N	1093.21165	1	4.14E-04	0.51	2.17	-	938.4
AHQ-7-2, 3007	K.FDQLLAEEK.N	1093.21165	2	8.75E-06	0.92	3.04	-	1639.3

AHQ-7-3, 2979 - 2981	K.FDQLLAEEK.N	1093.21165	2	1.63E-05	0.93	3.64	-	1388.4
AHQ-7-1, 3152	K.FDQLLAEEK.N	1093.21165	2	1.79E-05	0.83	2.53	-	1192.2
AHQ-7-4, 2525	K.KEEELQAALAR.L	1258.40643	1	2.62E-06	0.17	1.88	-	457.0
AHQ-7-3, 2567 - 2597	K.KEEELQAALAR.L	1258.40643	2	4.03E-04	0.84	3.32	-	885.8
AHQ-7-4, 2517 - 2526	K.KEEELQAALAR.L	1258.40643	2	1.97E-04	0.88	3.37	-	1024.2
AHQ-7-2, 2609	K.KEEELQAALAR.L	1258.40643	3	9.22E-05	0.94	3.67	-	1954.9
AHQ-7-3, 2939	R.KFDQLLAEEK.N	1221.38456	1	9.23E-05	0.42	2.67	-	437.8
AHQ-7-4, 2857	R.KFDQLLAEEK.N	1221.38456	1	5.19E-05	0.44	2.16	-	780.3
AHQ-7-5, 2864	R.KFDQLLAEEK.N	1221.38456	1	8.31E-06	0.58	2.62	-	724.5
AHQ-7-3, 2924	R.KFDQLLAEEK.N	1221.38456	2	7.57E-04	0.90	3.29	-	1173.9
AHQ-7-5, 5902	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	7.90E-06	0.79	3.01	-	793.6
AHQ-7-2, 5931 - 5993	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	4.44E-15	0.98	6.43	-	3269.2
AHQ-7-7, 5765	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	6.72E-13	0.98	5.30	-	3460.3
AHQ-7-3, 5800	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	5.22E-14	0.97	5.73	-	2174.4
AHQ-7-5, 5884	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.24E-04	0.96	5.34	-	1482.2
AHQ-7-3, 5184 - 5193	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	8.81E-07	0.98	5.90	-	2168.9
AHQ-7-2, 6117 - 6193	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	1.75E-09	0.94	4.67	-	1421.1
AHQ-7-2, 5941	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	2	1.02E-07	0.94	3.50	-	1600.4
AHQ-7-2, 5283 - 5357	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	2.24E-09	0.98	6.14	-	2439.8
AHQ-7-2, 2453 - 2461	R.NCAAYLK.L	840.96726	1	1.00E-04	0.64	1.92	-	973.6
AHQ-7-4, 1876	R.NTDQASMPDNTAAQK.V	1592.67074	2	3.59E-04	0.69	3.00	-	534.3
AHQ-7-3, 1937	R.NTDQASMPDNTAAQK.V	1592.67074	2	1.61E-04	0.81	3.12	-	528.0
AHQ-7-1, 6048	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.44E-09	0.94	4.03	-	996.3
AHQ-7-2, 6255	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.80E-10	0.91	4.20	-	624.8
AHQ-7-3, 5945 - 6004	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.73E-04	0.97	4.77	-	1336.1
AHQ-7-3, 6113	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.20E-04	0.70	3.00	-	398.5
AHQ-7-13, 5835	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.77E-05	0.88	3.40	-	839.4
AHQ-7-7, 5977 - 5988	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.40E-04	0.83	3.34	-	631.5
AHQ-7-1, 5833 - 5888	K.QLLQANPILEAFGNAK.T	1727.98540	2	7.51E-13	0.97	4.61	-	1351.5
AHQ-7-9, 5440 - 5441	K.QLLQANPILEAFGNAK.T	1727.98540	2	8.54E-05	0.90	3.48	-	933.0
AHQ-7-2, 6163	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.90E-05	0.94	4.17	-	1039.0
AHQ-7-5, 6015 - 6082	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.05E-06	0.95	4.44	-	956.6
AHQ-7-2, 6017 - 6099	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.32E-10	0.95	4.06	-	1167.8
AHQ-7-4, 6096 - 6161	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.14E-06	0.96	5.09	-	941.6
AHQ-7-4, 6272	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.27E-10	0.87	3.47	-	644.8
AHQ-7-10, 5461 - 5516	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.12E-04	0.91	4.08	-	833.1
AHQ-7-6, 5923 - 5981	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.46E-06	0.95	4.49	-	973.9
AHQ-7-1, 5943	K.QLLQANPILEAFGNAK.T	1727.98540	2	8.46E-08	0.95	4.11	-	1158.7
AHQ-7-5, 5568 - 5640	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.46E-07	0.99	6.46	-	2954.9
AHQ-7-4, 5665	K.TQLEELEDELQATEDAK.L	1963.04334	3	6.93E-09	0.96	5.44	-	1122.7
AHQ-7-4, 5644 - 5648	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.94E-09	0.98	6.06	-	2595.4
AHQ-7-3, 5527	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.59E-05	0.97	5.72	-	1723.2
AHQ-7-6, 5497 - 5499	K.TQLEELEDELQATEDAK.L	1963.04334	2	3.29E-12	0.98	6.71	-	2370.8
AHQ-7-6, 5519	K.TQLEELEDELQATEDAK.L	1963.04334	3	3.47E-07	0.95	4.90	-	1424.3
AHQ-7-2, 5655	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.28E-04	0.96	5.28	-	1349.7
AHQ-7-7, 5500	K.TQLEELEDELQATEDAK.L	1963.04334	2	3.11E-05	0.97	5.21	-	1625.4
AHQ-7-2, 5651 - 5713	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.74E-09	0.97	4.69	-	2033.4
AHQ-7-2, 4064	K.TQLEELEDELQATEDAK.L	1963.04334	2	3.03E-09	0.97	5.30	-	1279.5
AHQ-7-8, 5528	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.08E-05	0.92	3.86	-	1187.0
AHQ-7-1, 5487	K.TQLEELEDELQATEDAK.L	1963.04334	3	6.00E-08	0.95	4.60	-	1559.6
AHQ-7-1, 5480 - 5484	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.19E-04	0.97	5.59	-	1553.5
AHQ-7-3, 5697	K.TQLEELEDELQATEDAK.L	1963.04334	2	9.19E-08	0.95	4.70	-	1143.4
gi|4505879|ref|NP_002655.1| pleckstrin; p47 [Homo sapiens]				5.00E-15	8.08	100.40	40.30	40082.5
AHQ-7-14-, 5418	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.14E-08	0.97	5.94	-	1588.8
AHQ-7-10, 5176 - 5188	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.79E-05	0.97	5.72	-	1843.3
AHQ-7-13-, 5413	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	7.52E-09	0.97	6.26	-	1669.6
AHQ-7-13, 5465 - 5467	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.84E-06	0.97	6.18	-	1607.5
AHQ-7-8, 5550 - 5570	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.45E-10	0.98	6.85	-	2075.5
AHQ-7-8, 5556 - 5559	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	9.70E-07	0.86	3.84	-	536.9
AHQ-7-12, 5254	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.34E-05	0.97	5.47	-	2026.1
AHQ-7-11, 5278	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	3.27E-07	0.96	5.39	-	1413.1
AHQ-7-9, 5105 - 5112	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.60E-06	0.96	6.20	-	1297.3
AHQ-7-8, 2520 - 2584	R.GCVVTSVESNSNGR.K	1467.54464	2	1.67E-06	0.89	3.41	-	1078.2
AHQ-7-8, 2446 - 2503	R.GCVVTSVESNSNGR.K	1467.54464	1	5.86E-04	0.11	1.96	-	153.6
AHQ-7-8, 3200	K.GSTLTSPCQDFGK.R	1399.50867	1	2.36E-04	0.24	2.45	-	261.5
AHQ-7-8, 2698	K.GSTLTSPCQDFGKR.M	1555.69502	2	2.21E-07	0.27	2.51	-	300.0
AHQ-7-8, 6664 - 6730	K.IFNHCFTGNCVIDWLVSNQSVR.N	2669.97641	2	1.65E-07	0.96	4.63	-	1581.4
AHQ-7-8, 6858 - 6926	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	5.00E-15	0.98	6.85	-	2759.7
AHQ-7-8, 7007	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.76E-05	0.97	5.84	-	1750.4
AHQ-7-9, 6169	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	2.52E-06	0.98	7.90	-	2490.4
AHQ-7-9, 5160	R.LPETIDLGALYLSM*K.D	1680.98719	2	3.63E-04	0.92	3.96	-	973.9
AHQ-7-13, 5489 - 5559	R.LPETIDLGALYLSM*K.D	1680.98719	2	4.02E-05	0.91	4.57	-	669.7
AHQ-7-12, 5300 - 5364	R.LPETIDLGALYLSM*K.D	1680.98719	2	1.09E-04	0.97	5.42	-	1152.1
AHQ-7-8, 6304 - 6366	R.LPETIDLGALYLSMK.D	1664.98779	2	9.72E-05	0.97	4.65	-	1747.2
AHQ-7-8, 5627	R.LPETIDLGALYLSM*K.D	1680.98719	2	2.32E-05	0.96	4.74	-	1404.9
AHQ-7-8, 6011 - 6084	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	6.49E-06	0.98	7.09	-	1323.2
AHQ-7-8, 6002	R.NRQEGLMIASSLLNEGYLQPAGDMSK.S	2824.18382	2	2.58E-04	0.96	4.92	-	1242.1
AHQ-7-8, 6914	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.32E-12	0.84	4.04	-	728.1
AHQ-7-9, 6212	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.45E-08	0.77	3.53	-	723.5
AHQ-7-8, 6911 - 6912	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	3.09E-06	0.83	4.31	-	380.1
AHQ-7-12, 6322	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	2.09E-06	0.71	3.26	-	758.5
AHQ-7-11, 6354 - 6355	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.96E-09	0.78	3.79	-	744.3
gi|4885609|ref|NP_005408.1| v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen				6.11E-15	4.28	50.39	17.90	59834.4
AHQ-7-7, 6766 - 6842	R.KEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL	3998.26826	3	6.16E-13	0.75	3.65	-	345.0
AHQ-7-7, 2925	R.KLDSGGFYITSR.T	1344.49778	2	4.53E-04	0.90	3.46	-	943.2
AHQ-7-7, 3734	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	6.43E-06	0.69	3.31	-	702.6
AHQ-7-7, 6825 - 6826	R.LPQLVDMAAQIASGMAYVER.M	2164.53485	2	6.11E-15	0.99	7.80	-	4471.5
AHQ-7-7, 6377	R.TQFNSLQQLVAYYSK.H	1790.99681	2	9.02E-06	0.90	3.48	-	1111.9
AHQ-7-7, 6193	R.TQFNSLQQLVAYYSK.H	1790.99681	2	1.03E-07	0.96	4.22	-	1544.2
AHQ-7-7, 5994 - 5996	R.TQFNSLQQLVAYYSK.H	1790.99681	2	2.14E-06	0.94	4.04	-	1111.3
gi|21361657|ref|NP_005304.3| glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom				7.77E-15	9.39	110.35	28.70	56782.0
AHQ-7-13-, 5468	R.ELSDFISYLQR.E	1371.52000	2	2.75E-04	0.94	3.49	-	1572.4
AHQ-7-13, 5551	R.ELSDFISYLQR.E	1371.52000	2	1.53E-04	0.93	3.20	-	1545.8
AHQ-7-14-, 5459	R.ELSDFISYLQR.E	1371.52000	2	4.45E-04	0.95	3.75	-	1491.3
AHQ-7-7, 6204 - 6274	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	3	1.05E-07	0.95	4.85	-	1232.9
AHQ-7-7, 6209	R.FAHTNVESLVNEYDDNGEGIILFR.P	2753.96046	2	8.12E-06	0.89	4.01	-	842.8
AHQ-7-7, 6716 - 6717	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	7.77E-15	0.98	7.07	-	3050.1
AHQ-7-7, 4610	R.FLQDYFDGNLK.R	1360.49568	1	2.20E-04	0.24	1.88	-	386.6
AHQ-7-7, 4608	R.FLQDYFDGNLK.R	1360.49568	2	3.59E-05	0.86	3.46	-	892.2
AHQ-7-7, 4526	R.GFPTIYFSPANK.K	1342.52349	2	4.20E-04	0.89	3.54	-	819.8
AHQ-7-7, 5686	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	3	5.33E-05	0.94	4.74	-	1137.8
AHQ-7-7, 2309	R.LAPEYEAAATR.L	1192.30331	2	3.96E-06	0.78	2.78	-	348.1
AHQ-7-7, 3362	K.MDATANDVPSPYEVR.G	1665.80646	2	1.45E-04	0.49	2.91	-	339.3
AHQ-7-7, 3509	K.MDATANDVPSPYEVR.G	1665.80646	2	1.34E-05	0.39	2.63	-	345.1
AHQ-7-7, 3060	K.M*DATANDVPSPYEVR.G	1681.80586	2	5.88E-05	0.82	3.46	-	521.6
AHQ-7-7, 6076	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	2	6.68E-08	0.95	4.16	-	1386.7
AHQ-7-7, 3089	K.YGVSGYPTLK.I	1085.23435	2	6.01E-06	0.89	3.23	-	649.9

gi|4505257|ref|NP_002435.1| moesin [Homo sapiens]				8.88E-15	13.54	150.32	28.80	67819.5
AHQ-7-6, 6493	R.AKFYPEDVSEELIQDITQR.L	2282.49179	3	8.25E-05	0.76	3.36	-	904.3
AHQ-7-6, 2247 - 2265	R.ALELEQER.K	988.07707	2	2.39E-04	0.92	2.87	-	1502.1
AHQ-7-6, 2586 - 2587	K.ALTSELANAR.D	1046.15975	2	2.89E-06	0.89	3.10	-	879.7
AHQ-7-6, 2005	K.AQM*VQEDLEK.T	1207.33653	2	6.95E-04	0.84	2.93	-	846.9
AHQ-7-6, 6673	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	3	6.32E-07	0.91	4.61	-	1204.6
AHQ-7-6, 6675 - 6747	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	2	4.44E-06	0.87	4.12	-	407.2
AHQ-7-6, 5925	R.EVWFFGLQYQDTK.G	1661.83760	2	1.95E-09	0.97	4.30	-	1532.3
AHQ-7-6, 5893 - 5966	R.EVWFFGLQYQDTK.G	1661.83760	2	5.66E-05	0.88	2.89	-	1018.8
AHQ-7-6, 6633	K.FYPEDVSEELIQDITQR.L	2083.24065	2	4.63E-08	0.96	4.93	-	1440.5
AHQ-7-6, 6637 - 6642	K.FYPEDVSEELIQDITQR.L	2083.24065	3	1.67E-08	0.95	5.32	-	1087.6
AHQ-7-6, 5793	K.IAQDLEMYGVNYFSIK.N	1892.16455	2	1.18E-05	0.97	4.22	-	2173.7
AHQ-7-6, 5450 - 5471	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	1.22E-08	0.96	4.43	-	1359.7
AHQ-7-6, 2031	R.IQVWHEEHR.G	1234.34835	2	1.71E-05	0.94	2.93	-	1637.5
AHQ-7-6, 2321	R.ISQLEMAR.Q	948.12272	2	1.42E-04	0.93	2.95	-	1448.4
AHQ-7-6, 4671 - 4729	K.KTQEQLALEMAELTAR.I	1833.10018	2	9.98E-05	0.97	5.03	-	1440.2
AHQ-7-6, 3671	K.KTQEQLALEM*AELTAR.I	1849.09958	2	9.30E-04	0.63	2.92	-	474.7
AHQ-7-6, 3521	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	1.18E-09	0.95	4.56	-	1792.3
AHQ-7-6, 3393 - 3457	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	1.78E-04	0.89	4.70	-	650.7
AHQ-7-6, 3069 - 3141	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	8.88E-15	0.97	6.34	-	1428.3
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				2.05E-14	25.88	300.35	59.70	75429.7
AHQ-7-6, 3313	K.AGDALWLR.F	902.03223	2	2.91E-04	0.87	3.53	-	1026.0
AHQ-7-6, 6343 - 6421	R.ARGEELDEDLFLQLTGGHEAF	2348.51032	2	8.66E-09	0.95	4.01	-	1257.1
AHQ-7-2, 6640	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.38E-04	0.92	3.57	-	789.2
AHQ-7-13-, 6261	R.ASFSQPLFQAVAAICR.L	1768.02967	2	7.28E-06	0.91	3.73	-	888.0
AHQ-7-10, 5971 - 5972	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.35E-05	0.86	3.48	-	735.2
AHQ-7-9, 5881 - 5896	R.ASFSQPLFQAVAAICR.L	1768.02967	2	9.19E-05	0.94	4.38	-	872.1
AHQ-7-6, 6389 - 6445	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.28E-08	0.94	4.42	-	941.0
AHQ-7-7, 6484	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.08E-07	0.92	4.00	-	717.8
AHQ-7-3, 6468 - 6488	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.95E-07	0.83	3.54	-	655.5
AHQ-7-6, 6449	R.ASFSQPLFQAVAAICR.L	1768.02967	3	1.90E-07	0.93	4.74	-	979.9
AHQ-7-4, 6657	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.07E-05	0.88	3.68	-	578.1
AHQ-7-6, 6501	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.90E-07	0.90	3.58	-	876.0
AHQ-7-6, 6605	R.ASFSQPLFQAVAAICR.L	1768.02967	2	9.25E-10	0.89	3.75	-	611.7
AHQ-7-5, 6575 - 6582	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.88E-06	0.92	3.99	-	769.6
AHQ-7-6, 3577 - 3637	K.EKEPEEELYDLSK.V	1609.71294	2	9.89E-07	0.86	3.56	-	495.9
AHQ-7-6, 6589	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	1.11E-04	0.95	5.09	-	652.0
AHQ-7-9, 3006	K.GCEVVPDVNVSGQK.F	1489.63335	1	7.43E-08	0.95	4.34	-	1212.8
AHQ-7-11, 3147 - 3228	K.GCEVVPDVNVSGQK.F	1489.63335	2	8.95E-04	0.81	2.85	-	853.6
AHQ-7-7, 3176	K.GCEVVPDVNVSGQK.F	1489.63335	1	6.93E-04	0.87	2.93	-	1091.8
AHQ-7-6, 3277	K.GCEVVPDVNVSGQK.F	1489.63335	2	3.68E-07	0.85	3.04	-	710.3
AHQ-7-6, 3217 - 3221	K.GCEVVPDVNVSGQK.F	1489.63335	1	3.32E-06	0.87	2.88	-	1016.2
AHQ-7-6, 6629 - 6630	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	3.04E-04	0.97	5.51	-	1396.5
AHQ-7-14-, 6335	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	6.40E-05	0.88	3.84	-	791.1
AHQ-7-6, 3949 - 4009	R.GMPAHFSDSAQTEACYHMLSR.P	2398.64117	3	6.89E-07	0.95	5.53	-	836.5
AHQ-7-6, 2857	R.HPEELSLLR.A	1094.24601	1	8.17E-06	0.16	1.83	-	234.9
AHQ-7-6, 3817	R.IDLAVGDVVK.T	1029.21223	1	3.75E-04	0.72	2.35	-	821.6
AHQ-7-12, 3736	R.IDLAVGDVVK.T	1029.21223	1	8.31E-04	0.43	2.58	-	335.4
AHQ-7-6, 4479	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.01E-10	0.98	6.01	-	2282.7
AHQ-7-6, 4425 - 4493	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	1.48E-04	0.82	4.79	-	429.8
AHQ-7-9, 4065	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.59E-06	0.98	5.78	-	2147.5
AHQ-7-6, 4353 - 4426	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.05E-14	0.97	5.82	-	1581.6
AHQ-7-13-, 2800	R.KDEILGIANNR.L	1243.39499	2	3.64E-06	0.92	3.57	-	1368.4
AHQ-7-9, 2541 - 2602	R.KDEILGIANNR.L	1243.39499	2	1.31E-04	0.92	3.41	-	1295.3
AHQ-7-12, 2707 - 2710	R.KDEILGIANNR.L	1243.39499	2	2.75E-06	0.95	3.56	-	1418.2
AHQ-7-6, 2649 - 2713	R.KDEILGIANNR.L	1243.39499	2	4.98E-05	0.96	4.48	-	1576.6
AHQ-7-13, 2938 - 2993	R.KDEILGIANNR.L	1243.39499	2	5.68E-04	0.93	3.60	-	1335.8
AHQ-7-12, 2852 - 2911	R.KDEILGIANNR.L	1243.39499	2	5.34E-04	0.70	2.93	-	646.6
AHQ-7-6, 4022	R.KQDWSDHAIWWEQK.R	1858.00504	3	7.94E-10	0.94	4.76	-	1234.7
AHQ-7-7, 5494	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	6.37E-04	0.82	3.59	-	601.2
AHQ-7-6, 6463	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	4.84E-06	0.74	3.23	-	508.9
AHQ-7-8, 6446	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.64E-04	0.57	2.79	-	431.6
AHQ-7-6, 6378 - 6401	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.65E-06	0.96	4.24	-	1509.2
AHQ-7-7, 6432	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.96E-05	0.59	2.77	-	519.8
AHQ-7-6, 6277	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.50E-05	0.92	4.67	-	687.7
AHQ-7-6, 6138	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	6.74E-06	0.81	3.67	-	528.1
AHQ-7-6, 5493	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.00E-05	0.87	3.69	-	736.4
AHQ-7-6, 6005 - 6075	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.21E-07	0.92	4.53	-	590.1
AHQ-7-6, 6161 - 6186	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	1.24E-06	0.77	3.98	-	408.6
AHQ-7-6, 5433	K.LLVPSPEGMSEIYLR.C	1705.01201	2	7.65E-07	0.78	2.82	-	538.4
AHQ-7-6, 5639 - 5701	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.08E-08	0.84	3.12	-	506.0
AHQ-7-7, 5698 - 5729	K.LLVPSPEGMSEIYLR.C	1705.01201	2	1.17E-05	0.46	2.54	-	330.0
AHQ-7-6, 4710 - 4773	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	4.10E-09	0.64	2.67	-	267.0
AHQ-7-3, 5765	K.LLVPSPEGMSEIYLR.C	1705.01201	2	2.58E-06	0.54	2.62	-	349.1
AHQ-7-2, 6729 - 6737	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	7.30E-06	0.82	3.42	-	1029.6
AHQ-7-8, 6631	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.27E-06	0.96	4.97	-	1896.8
AHQ-7-6, 6475 - 6553	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	5.80E-12	0.95	4.81	-	1556.9
AHQ-7-1, 6447	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.00E-09	0.92	4.60	-	1080.9
AHQ-7-9, 5909 - 5988	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.87E-08	0.94	4.90	-	1388.8
AHQ-7-4, 6756	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.89E-06	0.85	3.80	-	974.5
AHQ-7-6, 2377 - 2407	R.LTQLYEQAR.W	1122.25622	2	1.72E-04	0.83	2.89	-	887.7
AHQ-7-6, 5083 - 5105	R.QWLLQTHWTLDK.Y	1569.78807	2	4.44E-09	0.80	3.36	-	309.5
AHQ-7-11, 3887 - 3902	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.44E-08	0.87	3.58	-	598.8
AHQ-7-7, 3978	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	8.76E-09	0.89	4.09	-	465.3
AHQ-7-3, 4140	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.19E-04	0.77	2.94	-	423.9
AHQ-7-6, 4001 - 4050	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	7.47E-08	0.89	4.29	-	579.7
AHQ-7-9, 3724 - 3748	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	8.74E-04	0.92	4.56	-	528.3
AHQ-7-6, 4162	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	3.11E-05	0.76	3.08	-	487.8
AHQ-7-6, 5241	K.SQDEAPGDPIQQLNLKGCEVVPDVNVSGQK.F	3224.50249	3	8.75E-07	0.80	4.07	-	413.0
AHQ-7-13-, 4275	K.TASGDYIDSSWELR.V	1600.66783	2	3.00E-05	0.87	3.46	-	816.7
AHQ-7-13, 4405	K.TASGDYIDSSWELR.V	1600.66783	2	2.82E-04	0.87	3.48	-	979.8
AHQ-7-6, 4197	K.TASGDYIDSSWELR.V	1600.66783	2	1.24E-09	0.92	3.79	-	853.8
AHQ-7-9, 3969 - 3972	K.TASGDYIDSSWELR.V	1600.66783	2	5.39E-04	0.94	4.08	-	1026.4
AHQ-7-5, 4399	K.TASGDYIDSSWELR.V	1600.66783	2	6.05E-06	0.52	2.55	-	703.9
AHQ-7-3, 4416	K.TASGDYIDSSWELR.V	1600.66783	2	5.39E-10	0.90	3.52	-	729.8
AHQ-7-14-, 4295	K.TASGDYIDSSWELR.V	1600.66783	2	7.70E-10	0.91	3.37	-	1044.0
AHQ-7-6, 4295 - 4361	K.TASGDYIDSSWELR.V	1600.66783	2	1.55E-08	0.92	4.16	-	817.8
AHQ-7-6, 3869 - 3875	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	9.77E-07	0.94	4.88	-	736.4
AHQ-7-11, 3764 - 3771	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	1.82E-04	0.95	6.28	-	787.5
AHQ-7-6, 3854 - 3917	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	5.14E-07	0.97	6.91	-	1500.2
AHQ-7-7, 3816	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	1.46E-04	0.93	5.21	-	923.4
AHQ-7-7, 3822	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	6.86E-04	0.85	3.93	-	493.9
AHQ-7-6, 4006 - 4070	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	5.37E-12	0.97	6.61	-	1330.5
AHQ-7-6, 6757	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	2	9.88E-04	0.97	5.94	-	1702.0
AHQ-7-6, 6759	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	3.83E-07	0.93	4.98	-	1164.9
AHQ-7-9, 3652 - 3657	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.94E-06	0.65	2.70	-	768.6
AHQ-7-14-, 3906 - 3911	R.VFVGEEDPEAESVTLR.V	1777.91007	2	7.79E-12	0.94	4.82	-	1031.3

AHQ-7-2, 4152 - 4200	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.35E-06	0.90	3.94	-	941.6
AHQ-7-13, 4003 - 4061	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.68E-10	0.96	4.50	-	1527.2
AHQ-7-8, 3982 - 3983	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.74E-05	0.93	4.02	-	1003.4
AHQ-7-7, 3908	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.15E-05	0.94	4.25	-	1132.3
AHQ-7-6, 3938 - 4007	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.15E-08	0.93	4.19	-	1043.2
AHQ-7-10, 3745	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.38E-05	0.83	3.45	-	873.2
AHQ-7-13-, 3919	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.69E-07	0.94	4.44	-	1154.5
AHQ-7-3, 4029 - 4064	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.01E-06	0.78	3.23	-	881.9
AHQ-7-6, 3962	R.VFVGEEDPEAESVTLR.V	1777.91007	3	3.17E-04	0.97	4.38	-	2502.6
AHQ-7-12, 3844	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.42E-07	0.76	2.61	-	872.3
AHQ-7-5, 4048 - 4051	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.89E-11	0.95	4.91	-	1167.5
AHQ-7-11, 3822	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.46E-06	0.92	3.97	-	997.8
AHQ-7-11, 2870	R.VTGESHIGGVLLK.I	1310.52448	2	8.56E-10	0.93	3.87	-	1172.3
AHQ-7-14-, 2985	R.VTGESHIGGVLLK.I	1310.52448	2	2.06E-06	0.88	3.27	-	1297.4
AHQ-7-6, 2771 - 2850	R.VTGESHIGGVLLK.I	1310.52448	2	7.45E-11	0.95	4.59	-	1176.9
AHQ-7-9, 2729	R.VTGESHIGGVLLK.I	1310.52448	1	5.04E-05	0.10	2.13	-	257.6
AHQ-7-9, 2704 - 2718	R.VTGESHIGGVLLK.I	1310.52448	2	5.06E-06	0.94	3.95	-	1386.9
AHQ-7-8, 2692	R.VTGESHIGGVLLK.I	1310.52448	2	4.62E-07	0.92	3.84	-	1206.5
AHQ-7-7, 2776	R.VTGESHIGGVLLK.I	1310.52448	2	3.43E-07	0.86	3.32	-	1176.4
AHQ-7-6, 2885	R.VTGESHIGGVLLK.I	1310.52448	2	2.30E-07	0.95	4.07	-	1475.4
AHQ-7-4, 4949	K.VVLAGGVAPALFR.G	1270.54832	2	2.79E-06	0.97	4.64	-	1837.8
AHQ-7-6, 4762 - 4826	K.VVLAGGVAPALFR.G	1270.54832	2	2.51E-09	0.98	5.21	-	1961.4
AHQ-7-9, 4388 - 4392	K.VVLAGGVAPALFR.G	1270.54832	2	2.82E-06	0.97	4.86	-	1760.1
AHQ-7-10, 4435	K.VVLAGGVAPALFR.G	1270.54832	2	1.57E-07	0.95	4.22	-	1334.7
AHQ-7-7, 4713	K.VVLAGGVAPALFR.G	1270.54832	2	3.54E-07	0.95	4.46	-	1239.4
AHQ-7-7, 2558	K.YGILADAR.L	878.99544	2	4.83E-04	0.92	3.14	-	1046.3
AHQ-7-6, 5309	K.YYSFFDLDPK.T	1295.42046	2	1.73E-04	0.81	3.29	-	646.3
AHQ-7-7, 5254	K.YYSFFDLDPK.T	1295.42046	2	6.50E-05	0.82	3.35	-	691.9
gi|4557677|ref|NP_000203.1| integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu				2.33E-14	20.04	230.30	32.40	87185.6
AHQ-7-3, 3108	R.AKWDTANNPLYK.E	1421.58225	2	1.01E-06	0.88	3.44	-	638.2
AHQ-7-7, 2910	R.AKWDTANNPLYK.E	1421.58225	2	4.77E-06	0.86	3.04	-	708.7
AHQ-7-5, 3026 - 3098	R.AKWDTANNPLYK.E	1421.58225	2	4.52E-05	0.84	2.88	-	826.2
AHQ-7-4, 5352	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	5.36E-05	0.91	5.20	-	728.3
AHQ-7-7, 5174	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	5.40E-07	0.86	4.05	-	811.7
AHQ-7-5, 5310	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	7.73E-09	0.96	5.47	-	1404.5
AHQ-7-3, 5181 - 5249	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	2.03E-05	0.93	4.99	-	967.0
AHQ-7-3, 4216 - 4280	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.43E-11	0.83	4.16	-	522.9
AHQ-7-5, 4271 - 4275	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	3.71E-05	0.79	3.49	-	539.6
AHQ-7-6, 4213	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	1.48E-06	0.81	3.97	-	427.1
AHQ-7-1, 4323	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	9.15E-07	0.65	3.07	-	492.4
AHQ-7-2, 4400	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	9.71E-08	0.83	3.82	-	456.2
AHQ-7-7, 4172	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	6.86E-06	0.81	3.89	-	433.6
AHQ-7-3, 4349	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.61E-04	0.83	3.87	-	436.0
AHQ-7-4, 4253 - 4324	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.86E-04	0.78	3.71	-	477.7
AHQ-7-3, 6728 - 6761	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	3.59E-06	0.93	4.19	-	1065.1
AHQ-7-1, 5552	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	9.19E-04	0.87	3.70	-	726.4
AHQ-7-1, 4396	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.66E-05	0.95	4.19	-	1096.9
AHQ-7-2, 4492	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.26E-04	0.89	3.67	-	776.6
AHQ-7-6, 5617 - 5695	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.15E-06	0.93	4.62	-	591.5
AHQ-7-3, 5795	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	9.24E-08	0.90	3.80	-	756.6
AHQ-7-3, 4376 - 4377	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	2.96E-07	0.96	4.95	-	926.6
AHQ-7-4, 4436 - 4486	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.39E-04	0.93	4.31	-	777.4
AHQ-7-3, 5713	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.06E-10	0.95	5.09	-	603.9
AHQ-7-4, 5910	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	5.86E-10	0.90	4.10	-	536.2
AHQ-7-4, 5761 - 5821	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.04E-07	0.97	5.25	-	1351.3
AHQ-7-5, 4380 - 4388	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	2.79E-09	0.93	3.77	-	864.8
AHQ-7-5, 5726	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.86E-05	0.90	3.96	-	638.6
AHQ-7-3, 5601 - 5611	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	5.51E-05	0.87	3.81	-	795.7
AHQ-7-5, 4850	K.DDLWSIQNLGTK.L	1390.52332	1	2.00E-04	0.19	2.14	-	384.8
AHQ-7-3, 4832 - 4839	K.DDLWSIQNLGTK.L	1390.52332	2	9.35E-09	0.93	3.87	-	970.7
AHQ-7-5, 4838	K.DDLWSIQNLGTK.L	1390.52332	2	1.13E-04	0.83	2.84	-	871.1
AHQ-7-3, 4463	K.DNCAPESIEFPVSEAR.V	1822.93099	2	6.73E-10	0.95	3.97	-	1469.6
AHQ-7-7, 4220	K.DNCAPESIEFPVSEAR.V	1822.93099	2	4.49E-07	0.73	2.98	-	582.6
AHQ-7-5, 4328 - 4351	K.DNCAPESIEFPVSEAR.V	1822.93099	2	8.62E-05	0.89	3.37	-	1055.6
AHQ-7-3, 4283 - 4343	K.DNCAPESIEFPVSEAR.V	1822.93099	2	3.34E-04	0.72	2.92	-	576.6
AHQ-7-10, 3995	K.DNCAPESIEFPVSEAR.V	1822.93099	2	9.73E-04	0.63	2.84	-	520.8
AHQ-7-6, 4265 - 4273	K.DNCAPESIEFPVSEAR.V	1822.93099	2	6.30E-05	0.46	2.75	-	384.1
AHQ-7-4, 3382	K.EATSTFTNITYR.G	1404.50685	2	2.18E-07	0.77	2.95	-	614.5
AHQ-7-3, 3405	K.EATSTFTNITYR.G	1404.50685	2	7.58E-05	0.69	2.76	-	556.9
AHQ-7-5, 3358	K.EATSTFTNITYR.G	1404.50685	2	5.40E-06	0.77	2.99	-	542.7
AHQ-7-6, 3318	K.EATSTFTNITYR.G	1404.50685	2	2.17E-04	0.79	2.95	-	707.4
AHQ-7-1, 3543	K.EATSTFTNITYR.G	1404.50685	2	7.39E-07	0.82	2.96	-	782.1
AHQ-7-13, 3513	K.EATSTFTNITYR.G	1404.50685	2	8.62E-07	0.73	2.55	-	711.9
AHQ-7-4, 2373	R.FQYYEDSSGK.S	1224.25749	1	3.57E-05	0.69	3.17	-	468.5
AHQ-7-5, 3576 - 3578	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	9.47E-08	0.96	4.36	-	1661.6
AHQ-7-3, 3591	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	2.76E-06	0.91	3.88	-	900.7
AHQ-7-6, 3514 - 3519	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.28E-05	0.94	4.23	-	1453.2
AHQ-7-4, 3600	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.78E-04	0.91	4.08	-	917.5
AHQ-7-2, 3693	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	5.73E-05	0.93	4.16	-	1035.2
AHQ-7-1, 3700	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.09E-05	0.90	3.95	-	965.5
AHQ-7-1, 3709	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	5.09E-04	0.61	3.01	-	472.4
AHQ-7-3, 3595	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	1.04E-05	0.86	3.44	-	776.8
AHQ-7-3, 4228 - 4240	R.GKCECGSCVCIQPGSYGDTCEKCPTCPDACTFKK.E	4028.42584	3	1.28E-04	0.90	4.73	-	710.1
AHQ-7-5, 1931 - 1951	K.GSGDSSQVTQVSPQR.I	1533.58302	2	1.01E-04	0.85	3.07	-	1044.3
AHQ-7-4, 2773	K.HVLTLTDQVTR.F	1283.45912	1	6.94E-10	0.81	3.46	-	401.7
AHQ-7-5, 2756	K.HVLTLTDQVTR.F	1283.45912	2	2.37E-05	0.90	3.43	-	723.7
AHQ-7-8, 2644	K.HVLTLTDQVTR.F	1283.45912	2	2.26E-06	0.86	3.25	-	606.8
AHQ-7-2, 2848	K.HVLTLTDQVTR.F	1283.45912	2	5.14E-06	0.90	3.23	-	796.2
AHQ-7-9, 2525 - 2604	K.HVLTLTDQVTR.F	1283.45912	2	3.69E-05	0.89	3.44	-	818.5
AHQ-7-1, 3027	K.HVLTLTDQVTR.F	1283.45912	2	9.73E-08	0.94	3.71	-	981.7
AHQ-7-3, 2815 - 2881	K.HVLTLTDQVTR.F	1283.45912	2	4.58E-06	0.88	3.38	-	549.5
AHQ-7-4, 2764 - 2765	K.HVLTLTDQVTR.F	1283.45912	2	3.12E-07	0.92	3.96	-	557.8
AHQ-7-3, 4117	K.IGDTVSFSIEAK.V	1267.41009	2	1.13E-04	0.87	3.17	-	801.4
AHQ-7-3, 3605	K.IGDTVSFSIEAK.V	1267.41009	2	2.78E-05	0.75	2.93	-	511.5
AHQ-7-1, 4001	K.IGDTVSFSIEAK.V	1267.41009	2	9.11E-05	0.85	2.97	-	830.4
AHQ-7-1, 4059 - 4060	R.NDASHLLVFTTDAK.T	1532.67977	2	2.49E-05	0.97	5.26	-	1382.4
AHQ-7-4, 3912 - 3940	R.NDASHLLVFTTDAK.T	1532.67977	2	4.69E-10	0.97	4.80	-	1471.6
AHQ-7-1, 4408	R.NDASHLLVFTTDAK.T	1532.67977	2	3.68E-06	0.88	3.93	-	760.7
AHQ-7-7, 3744	R.NDASHLLVFTTDAK.T	1532.67977	2	4.66E-08	0.88	3.34	-	1063.0
AHQ-7-6, 3815 - 3827	R.NDASHLLVFTTDAK.T	1532.67977	2	3.64E-09	0.97	4.82	-	1519.4
AHQ-7-7, 4197	R.NDASHLLVFTTDAK.T	1532.67977	2	2.16E-07	0.92	3.64	-	1078.4
AHQ-7-4, 4380	R.NDASHLLVFTTDAK.T	1532.67977	2	1.08E-05	0.90	3.53	-	1047.8
AHQ-7-3, 3889 - 3951	R.NDASHLLVFTTDAK.T	1532.67977	2	6.26E-09	0.97	4.84	-	1721.5
AHQ-7-5, 4348	R.NDASHLLVFTTDAK.T	1532.67977	2	6.06E-09	0.93	3.86	-	1004.0
AHQ-7-3, 3953	R.NDASHLLVFTTDAK.T	1532.67977	3	1.23E-07	0.94	4.36	-	1318.1
AHQ-7-3, 4356 - 4396	R.NDASHLLVFTTDAK.T	1532.67977	2	2.39E-10	0.95	4.24	-	1229.3
AHQ-7-4, 4229 - 4300	R.NDASHLLVFTTDAK.T	1532.67977	2	5.35E-10	0.82	3.62	-	585.3

AHQ-7-5, 3915	R.NDASHLLVFTTDAK.T	1532.67977	3	1.51E-08	0.95	4.45	-	1447.4
AHQ-7-3, 4125 - 4199	R.NDASHLLVFTTDAK.T	1532.67977	2	4.91E-04	0.85	2.92	-	1061.5
AHQ-7-5, 3900 - 3979	R.NDASHLLVFTTDAK.T	1532.67977	2	2.61E-09	0.94	4.26	-	1139.4
AHQ-7-1, 3705	K.SFTIKPVGFK.D	1124.35685	2	7.50E-04	0.90	2.79	-	1343.6
AHQ-7-3, 3525	K.SFTIKPVGFK.D	1124.35685	2	8.99E-06	0.80	2.74	-	945.6
AHQ-7-5, 3454	K.SFTIKPVGFK.D	1124.35685	2	3.48E-06	0.85	2.69	-	1074.5
AHQ-7-5, 3535	R.TDTCMSSNGLLCSGR.G	1661.81786	2	7.96E-09	0.87	3.36	-	755.0
AHQ-7-3, 2825 - 2887	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.17E-08	0.92	3.79	-	1054.4
AHQ-7-5, 2784	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.57E-07	0.86	3.43	-	899.3
AHQ-7-3, 3555 - 3624	R.TDTCMSSNGLLCSGR.G	1661.81786	2	2.08E-08	0.90	3.72	-	886.5
AHQ-7-5, 2947	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.63E-06	0.93	3.50	-	1344.1
AHQ-7-4, 2978	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	9.60E-08	0.86	3.52	-	899.1
AHQ-7-3, 3453 - 3471	R.TDTCMSSNGLLCSGR.G	1661.81786	2	2.33E-14	0.95	4.28	-	1265.9
AHQ-7-4, 2801	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.01E-07	0.91	3.35	-	1195.5
AHQ-7-1, 3048	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.14E-08	0.93	3.75	-	1124.1
AHQ-7-4, 3482	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.75E-10	0.90	3.43	-	958.3
AHQ-7-7, 1906 - 1978	R.VLEDRPLSDK.G	1172.31354	2	8.49E-05	0.80	3.08	-	792.2
AHQ-7-3, 2048 - 2079	R.VLEDRPLSDK.G	1172.31354	2	4.12E-05	0.92	3.74	-	1050.5
AHQ-7-4, 2017	R.VLEDRPLSDK.G	1172.31354	2	6.49E-06	0.77	3.15	-	667.3
AHQ-7-5, 2803	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	3.92E-09	0.86	3.71	-	1033.6
AHQ-7-1, 3021	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	2.34E-06	0.96	5.50	-	1759.7
AHQ-7-3, 2851	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	1.11E-05	0.91	4.74	-	885.3
AHQ-7-3, 2859	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	2	3.40E-04	0.67	3.09	-	305.1
AHQ-7-4, 2804	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	3.73E-09	0.96	6.00	-	1487.0
AHQ-7-3, 3375 - 3391	K.WDTANNPLYK.E	1222.33111	2	2.90E-06	0.61	2.82	-	529.9
AHQ-7-4, 3582 - 3648	K.YCECDDFSCVR.Y	1514.59674	2	9.74E-07	0.96	3.79	-	1389.4
AHQ-7-5, 3607	K.YCECDDFSCVR.Y	1514.59674	2	6.82E-05	0.83	2.68	-	894.4
AHQ-7-1, 3667 - 3719	K.YCECDDFSCVR.Y	1514.59674	2	1.54E-05	0.93	3.39	-	1045.4
AHQ-7-2, 3712	K.YCECDDFSCVR.Y	1514.59674	2	4.54E-07	0.94	3.57	-	1213.9
AHQ-7-6, 2299	R.YCRDEIESVK.E	1300.42023	2	3.49E-04	0.56	2.56	-	655.0
AHQ-7-4, 2338	R.YCRDEIESVK.E	1300.42023	2	1.53E-04	0.93	3.54	-	1484.8
gi|4501881|ref|NP_001091.1| alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA				3.50E-14	11.83	160.26	36.60	42050.8
AHQ-7-8, 1712 - 1775	K.AGFAGDDAPR.A	977.01283	2	9.14E-04	0.91	3.51	-	992.7
AHQ-7-13, 2234 - 2289	K.AGFAGDDAPR.A	977.01283	2	1.09E-05	0.90	3.15	-	1155.2
AHQ-7-13-, 1893 - 1964	K.AGFAGDDAPR.A	977.01283	2	6.41E-04	0.87	2.68	-	1133.6
AHQ-7-12, 1995 - 2050	K.AGFAGDDAPR.A	977.01283	2	3.46E-05	0.91	2.90	-	1255.8
AHQ-7-8, 1834 - 1894	K.AGFAGDDAPR.A	977.01283	2	5.30E-07	0.91	3.32	-	1156.5
AHQ-7-8, 1954 - 2014	K.AGFAGDDAPR.A	977.01283	2	9.61E-04	0.78	2.57	-	1166.1
AHQ-7-12, 3566	R.AVFPSIVGR.P	946.12815	2	9.76E-04	0.75	2.55	-	763.2
AHQ-7-8, 3498 - 3562	R.AVFPSIVGR.P	946.12815	2	3.25E-04	0.67	2.60	-	557.8
AHQ-7-8, 3018 - 3090	R.AVFPSIVGRPR.H	1199.43018	2	3.19E-04	0.60	3.10	-	408.8
AHQ-7-7, 4304	R.DLTDYLMK.I	999.16326	1	9.28E-04	0.21	1.98	-	456.1
AHQ-7-9, 3992 - 4010	R.DLTDYLMK.I	999.16326	2	4.31E-04	0.63	2.61	-	385.8
AHQ-7-8, 3312	R.DLTDYLMK.I	999.16326	1	2.46E-04	0.52	2.31	-	455.4
AHQ-7-11, 4128 - 4134	R.DLTDYLMK.I	999.16326	2	9.05E-04	0.72	3.25	-	302.0
AHQ-7-10, 3451 - 3467	R.DLTDYLM*K.I	1015.16266	2	5.66E-04	0.65	2.62	-	390.1
AHQ-7-5, 4404	R.DLTDYLMK.I	999.16326	1	3.44E-04	0.54	2.15	-	657.0
AHQ-7-8, 4250 - 4319	R.DLTDYLMK.I	999.16326	2	9.04E-05	0.72	2.74	-	384.1
AHQ-7-8, 4246 - 4366	R.DLTDYLMK.I	999.16326	1	1.70E-05	0.51	2.61	-	506.7
AHQ-7-8, 3839 - 3904	R.DLTDYLMK.I	999.16326	1	4.26E-05	0.12	1.95	-	177.3
AHQ-7-8, 1528 - 1598	K.DSYVGDEAQSK.R	1199.20634	2	1.37E-04	0.72	3.16	-	584.8
AHQ-7-8, 1572 - 1631	K.DSYVGDEAQSK.R	1199.20634	1	5.12E-05	0.66	2.81	-	450.4
AHQ-7-8, 1562 - 1632	K.DSYVGDEAQSKR.G	1355.39270	2	6.29E-09	0.65	3.17	-	539.9
AHQ-7-8, 2314 - 2380	K.EITALAPSTM*K.I	1178.38146	2	5.15E-07	0.85	3.46	-	643.8
AHQ-7-13-, 3020 - 3021	K.EITALAPSTMK.I	1162.38206	1	5.86E-04	0.59	2.68	-	335.2
AHQ-7-10, 2793 - 2852	K.EITALAPSTMK.I	1162.38206	2	1.61E-04	0.77	2.74	-	617.5
AHQ-7-3, 3084	K.EITALAPSTMK.I	1162.38206	1	9.52E-04	0.56	2.35	-	363.0
AHQ-7-5, 3010	K.EITALAPSTMK.I	1162.38206	1	6.43E-06	0.48	2.46	-	323.7
AHQ-7-14-, 3023	K.EITALAPSTMK.I	1162.38206	1	7.75E-04	0.37	2.48	-	365.2
AHQ-7-14-, 3013 - 3014	K.EITALAPSTMK.I	1162.38206	2	1.90E-04	0.74	3.23	-	455.8
AHQ-7-6, 2993	K.EITALAPSTMK.I	1162.38206	2	9.58E-04	0.89	2.80	-	1064.6
AHQ-7-14, 3154 - 3225	K.EITALAPSTM*K.I	1178.38146	2	9.57E-04	0.59	2.54	-	564.4
AHQ-7-13, 3181	K.EITALAPSTMK.I	1162.38206	1	1.87E-04	0.33	2.16	-	244.1
AHQ-7-8, 6648 - 6711	K.EKLCYVALDFENEM*ATAASSSSLEK.S	2812.07683	2	2.33E-04	0.58	2.76	-	461.3
AHQ-7-8, 2659	R.HQGVMVGMGQKDSYVGDEAQSK.R	2352.59065	3	1.76E-08	0.89	3.77	-	1176.7
AHQ-7-8, 2647 - 2722	K.IWHHTFYNELR.V	1516.68695	2	3.84E-08	0.80	3.33	-	893.0
AHQ-7-12, 3111 - 3119	K.IWHHTFYNELR.V	1516.68695	3	2.04E-05	0.88	4.15	-	1176.5
AHQ-7-8, 2726 - 2794	K.IWHHTFYNELR.V	1516.68695	3	1.37E-05	0.96	4.43	-	1676.0
AHQ-7-8, 2790 - 2862	K.IWHHTFYNELR.V	1516.68695	2	1.54E-06	0.65	3.24	-	626.0
AHQ-7-8, 2834	K.IWHHTFYNELR.V	1516.68695	3	2.69E-05	0.92	4.34	-	1552.3
AHQ-7-8, 2930 - 2991	K.IWHHTFYNELR.V	1516.68695	2	9.06E-04	0.64	3.15	-	569.0
AHQ-7-8, 2978 - 3043	K.IWHHTFYNELR.V	1516.68695	3	6.23E-04	0.95	4.13	-	1745.6
AHQ-7-12, 3094 - 3150	K.IWHHTFYNELR.V	1516.68695	2	4.26E-06	0.85	3.27	-	1034.7
AHQ-7-12, 3250	K.IWHHTFYNELR.V	1516.68695	2	1.44E-05	0.86	3.26	-	842.7
AHQ-7-8, 3107 - 3184	K.IWHHTFYNELR.V	1516.68695	3	3.70E-05	0.92	3.88	-	1450.6
AHQ-7-8, 3226 - 3298	K.IWHHTFYNELR.V	1516.68695	2	1.64E-09	0.93	3.69	-	1102.7
AHQ-7-11, 3072	K.IWHHTFYNELR.V	1516.68695	2	5.78E-05	0.65	2.58	-	744.0
AHQ-7-10, 3004	K.IWHHTFYNELR.V	1516.68695	3	5.52E-04	0.93	4.35	-	1099.6
AHQ-7-10, 2991 - 3049	K.IWHHTFYNELR.V	1516.68695	2	5.85E-08	0.84	2.80	-	678.7
AHQ-7-4, 3169	K.IWHHTFYNELR.V	1516.68695	2	4.20E-08	0.84	3.22	-	994.3
AHQ-7-9, 2993 - 3052	K.IWHHTFYNELR.V	1516.68695	2	2.28E-07	0.87	3.55	-	727.9
AHQ-7-9, 2858	K.IWHHTFYNELR.V	1516.68695	3	4.27E-04	0.96	4.50	-	1600.1
AHQ-7-8, 3042 - 3102	K.IWHHTFYNELR.V	1516.68695	2	1.80E-08	0.93	4.27	-	1100.1
AHQ-7-8, 6836 - 6916	K.LCYVALDFENEM*ATAASSSSLEK.S	2554.78938	3	1.62E-04	0.90	4.39	-	1050.2
AHQ-7-8, 4328 - 4390	K.SYELPDGQVITIGNER.F	1791.93998	2	1.39E-05	0.87	3.15	-	726.4
AHQ-7-4, 4530	K.SYELPDGQVITIGNER.F	1791.93998	2	1.08E-06	0.82	2.90	-	790.7
AHQ-7-8, 4454 - 4518	K.SYELPDGQVITIGNER.F	1791.93998	2	1.01E-12	0.94	3.85	-	1249.5
AHQ-7-8, 4550 - 4579	K.SYELPDGQVITIGNER.F	1791.93998	2	1.37E-12	0.97	4.62	-	1443.0
AHQ-7-8, 4584	K.SYELPDGQVITIGNER.F	1791.93998	3	4.21E-08	0.91	4.29	-	1021.9
AHQ-7-8, 4660 - 4738	K.SYELPDGQVITIGNER.F	1791.93998	2	6.50E-11	0.96	4.77	-	1131.4
AHQ-7-8, 4671 - 4743	K.SYELPDGQVITIGNER.F	1791.93998	2	8.18E-10	0.96	5.03	-	983.9
AHQ-7-8, 4758 - 4827	K.SYELPDGQVITIGNER.F	1791.93998	3	1.75E-07	0.96	4.89	-	1624.6
AHQ-7-8, 4802 - 4874	K.SYELPDGQVITIGNER.F	1791.93998	2	1.52E-09	0.93	4.31	-	921.6
AHQ-7-8, 4927 - 5008	K.SYELPDGQVITIGNER.F	1791.93998	2	1.35E-10	0.95	4.79	-	939.7
AHQ-7-14, 5706 - 5761	K.SYELPDGQVITIGNER.F	1791.93998	2	2.51E-04	0.83	3.52	-	862.7
AHQ-7-8, 5050 - 5070	K.SYELPDGQVITIGNER.F	1791.93998	2	7.70E-09	0.95	4.36	-	1239.1
AHQ-7-4, 4616	K.SYELPDGQVITIGNER.F	1791.93998	2	9.18E-09	0.84	3.46	-	666.6
AHQ-7-13-, 4844 - 4904	K.SYELPDGQVITIGNER.F	1791.93998	2	2.72E-12	0.94	4.12	-	926.1
AHQ-7-5, 4543 - 4623	K.SYELPDGQVITIGNER.F	1791.93998	2	1.93E-11	0.94	4.04	-	943.1
AHQ-7-13-, 4295 - 4372	K.SYELPDGQVITIGNER.F	1791.93998	2	2.17E-06	0.82	3.15	-	700.2
AHQ-7-5, 5088 - 5156	K.SYELPDGQVITIGNER.F	1791.93998	2	9.91E-11	0.95	4.67	-	840.2
AHQ-7-9, 4174 - 4186	K.SYELPDGQVITIGNER.F	1791.93998	2	1.00E-05	0.92	3.95	-	962.0
AHQ-7-9, 4393 - 4473	K.SYELPDGQVITIGNER.F	1791.93998	2	4.53E-09	0.95	4.50	-	1045.9
AHQ-7-9, 4557 - 4612	K.SYELPDGQVITIGNER.F	1791.93998	2	5.85E-12	0.95	4.54	-	971.6
AHQ-7-3, 5071	K.SYELPDGQVITIGNER.F	1791.93998	2	3.52E-08	0.92	4.00	-	740.0
AHQ-7-13-, 4727 - 4729	K.SYELPDGQVITIGNER.F	1791.93998	2	5.15E-10	0.95	4.60	-	996.8
AHQ-7-6, 4469 - 4477	K.SYELPDGQVITIGNER.F	1791.93998	2	4.89E-10	0.92	3.82	-	837.4

AHQ-7-3, 4925	K.SYELPDGQVITIGNER.F	1791.93998	2	1.85E-06	0.75	3.00	-	576.7
AHQ-7-10, 4072 - 4135	K.SYELPDGQVITIGNER.F	1791.93998	2	1.76E-08	0.92	4.05	-	753.4
AHQ-7-10, 4220	K.SYELPDGQVITIGNER.F	1791.93998	2	3.50E-14	0.93	3.60	-	1033.7
AHQ-7-10, 4440 - 4495	K.SYELPDGQVITIGNER.F	1791.93998	2	8.19E-10	0.96	4.56	-	1119.7
AHQ-7-10, 4477	K.SYELPDGQVITIGNER.F	1791.93998	3	5.26E-08	0.95	4.58	-	1696.2
AHQ-7-10, 4559 - 4615	K.SYELPDGQVITIGNER.F	1791.93998	2	2.64E-11	0.96	4.63	-	1145.7
AHQ-7-10, 4669 - 4728	K.SYELPDGQVITIGNER.F	1791.93998	2	7.21E-05	0.76	3.03	-	743.3
AHQ-7-6, 4878	K.SYELPDGQVITIGNER.F	1791.93998	2	9.73E-07	0.94	3.44	-	1349.8
AHQ-7-3, 4560 - 4632	K.SYELPDGQVITIGNER.F	1791.93998	2	4.19E-12	0.93	4.04	-	820.8
AHQ-7-11, 4170 - 4246	K.SYELPDGQVITIGNER.F	1791.93998	2	2.95E-09	0.90	3.28	-	861.9
AHQ-7-11, 4262 - 4331	K.SYELPDGQVITIGNER.F	1791.93998	2	4.55E-07	0.94	4.28	-	1080.8
AHQ-7-11, 4558 - 4614	K.SYELPDGQVITIGNER.F	1791.93998	2	3.11E-04	0.93	4.24	-	840.2
AHQ-7-11, 4694 - 4750	K.SYELPDGQVITIGNER.F	1791.93998	2	6.48E-10	0.93	4.26	-	850.5
AHQ-7-2, 5179	K.SYELPDGQVITIGNER.F	1791.93998	2	8.61E-07	0.95	3.92	-	1144.4
AHQ-7-6, 4983 - 5018	K.SYELPDGQVITIGNER.F	1791.93998	2	1.28E-06	0.62	2.71	-	501.2
AHQ-7-6, 5086	K.SYELPDGQVITIGNER.F	1791.93998	2	2.72E-04	0.48	2.57	-	602.3
AHQ-7-7, 4800	K.SYELPDGQVITIGNER.F	1791.93998	2	5.62E-05	0.74	3.23	-	509.0
AHQ-7-2, 4668 - 4748	K.SYELPDGQVITIGNER.F	1791.93998	2	1.37E-07	0.90	3.85	-	658.7
AHQ-7-12, 4186	K.SYELPDGQVITIGNER.F	1791.93998	2	2.50E-04	0.75	2.85	-	603.6
AHQ-7-14, 5608	K.SYELPDGQVITIGNER.F	1791.93998	2	2.89E-04	0.91	3.93	-	838.0
AHQ-7-12, 4282 - 4283	K.SYELPDGQVITIGNER.F	1791.93998	2	8.26E-13	0.96	4.65	-	1179.3
AHQ-7-12, 4591	K.SYELPDGQVITIGNER.F	1791.93998	2	2.99E-05	0.94	3.86	-	1003.1
AHQ-7-12, 4710 - 4768	K.SYELPDGQVITIGNER.F	1791.93998	2	2.17E-08	0.95	4.67	-	796.5
AHQ-7-1, 5047 - 5120	K.SYELPDGQVITIGNER.F	1791.93998	2	1.44E-09	0.94	4.38	-	923.2
AHQ-7-7, 4993 - 5005	K.SYELPDGQVITIGNER.F	1791.93998	2	1.12E-08	0.93	3.83	-	985.6
AHQ-7-13, 4586	K.SYELPDGQVITIGNER.F	1791.93998	2	2.15E-04	0.82	3.41	-	603.6
AHQ-7-13, 4845 - 4846	K.SYELPDGQVITIGNER.F	1791.93998	2	1.37E-12	0.97	5.29	-	951.9
AHQ-7-13, 4966 - 5037	K.SYELPDGQVITIGNER.F	1791.93998	2	1.15E-11	0.94	4.29	-	965.5
AHQ-7-1, 4507 - 4587	K.SYELPDGQVITIGNER.F	1791.93998	2	1.73E-06	0.93	4.03	-	971.9
AHQ-7-14, 5566 - 5621	K.SYELPDGQVITIGNER.F	1791.93998	2	9.82E-06	0.55	2.74	-	525.3
AHQ-7-14-, 4903	K.SYELPDGQVITIGNER.F	1791.93998	2	7.73E-06	0.69	3.02	-	608.8
AHQ-7-8, 3640 - 3704	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	5.16E-04	0.76	3.47	-	437.9
AHQ-7-8, 4318 - 4382	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.14E-04	0.85	3.89	-	681.0
AHQ-7-8, 4227 - 4298	K.YPIEHGIITNWDDMEK.I	1962.17174	2	6.76E-05	0.90	4.34	-	700.4
AHQ-7-8, 4940	K.YPIEHGIITNWDDMEK.I	1962.17174	2	8.64E-07	0.87	3.90	-	623.2
AHQ-7-5, 4518	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.69E-04	0.87	3.95	-	717.1
AHQ-7-4, 4594	K.YPIEHGIITNWDDMEK.I	1962.17174	3	3.68E-04	0.83	3.36	-	1141.4
AHQ-7-4, 4577	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.07E-04	0.73	3.17	-	656.5
AHQ-7-12, 4256	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.21E-04	0.76	3.65	-	483.7
AHQ-7-8, 4426	K.YPIEHGIITNWDDMEK.I	1962.17174	3	5.37E-04	0.76	3.41	-	1131.9
gi|4504345|ref|NP_000508.1| alpha 2 globin [Homo sapiens]				3.55E-14	6.25	70.34	63.40	15257.4
AHQ-7-13-, 4203 - 4204	K.FLASVSTVLTSK.Y	1253.46970	2	9.28E-07	0.93	3.84	-	1115.3
AHQ-7-13, 4337	K.FLASVSTVLTSK.Y	1253.46970	2	7.77E-04	0.93	3.56	-	1253.8
AHQ-7-13, 3197	K.LRVDPVNFK.L	1088.28460	2	2.25E-04	0.85	3.17	-	696.0
AHQ-7-13-, 3959 - 3960	R.M*FLSFPTTK.T	1088.30161	2	7.00E-04	0.79	2.70	-	671.5
AHQ-7-13, 4125 - 4181	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	1.44E-08	0.91	4.10	-	744.3
AHQ-7-13, 4107 - 4166	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	1.01E-07	0.94	4.47	-	860.2
AHQ-7-13-, 3999	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	2.15E-07	0.96	4.19	-	1451.4
AHQ-7-13-, 3991 - 4029	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	1.30E-07	0.86	3.41	-	655.9
AHQ-7-14-, 3985	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	3.31E-13	0.94	3.73	-	1162.3
AHQ-7-13-, 5453	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	1.16E-10	0.83	4.22	-	1140.3
AHQ-7-13-, 5337	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	5.48E-08	0.97	6.55	-	1699.5
AHQ-7-13-, 4801	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	9.13E-08	0.97	6.72	-	1384.2
AHQ-7-13-, 5512	K.VADALTNAVAHVDDMPNALSALSDLHAHK.L	2998.32055	3	4.72E-10	0.93	5.31	-	850.4
AHQ-7-13, 2830 - 2885	K.VGAHAGEYGAEALER.M	1530.62397	2	3.55E-14	0.97	4.55	-	1944.6
AHQ-7-13-, 2632	K.VGAHAGEYGAEALER.M	1530.62397	2	2.57E-10	0.96	4.06	-	1735.6
AHQ-7-13, 2825 - 2881	K.VGAHAGEYGAEALER.M	1530.62397	3	2.23E-05	0.95	5.75	-	1405.6
AHQ-7-13-, 2633 - 2692	K.VGAHAGEYGAEALER.M	1530.62397	3	4.07E-06	0.98	6.22	-	2646.5
gi|4507877|ref|NP_003364.1| vinculin isoform VCL [Homo sapiens]				4.61E-14	48.89	580.31	52.30	116721.6
AHQ-7-14-, 6447 - 6453	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	6.92E-06	0.96	4.99	-	1065.2
AHQ-7-13-, 6483 - 6485	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.71E-05	0.90	3.94	-	696.0
AHQ-7-12, 6295	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.30E-07	0.80	3.60	-	394.9
AHQ-7-11, 6324	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.61E-14	0.97	5.40	-	1116.7
AHQ-7-1, 6608	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.09E-07	0.95	4.59	-	938.8
AHQ-7-5, 6796 - 6866	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.84E-06	0.97	5.46	-	1139.7
AHQ-7-10, 6215 - 6216	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.20E-09	0.98	5.99	-	1115.4
AHQ-7-6, 6754	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	6.98E-10	0.96	4.70	-	1054.1
AHQ-7-8, 6878 - 6922	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.45E-10	0.96	4.98	-	946.9
AHQ-7-3, 6689 - 6735	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.96E-04	0.74	2.91	-	615.7
AHQ-7-4, 6952 - 7012	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.66E-04	0.97	5.10	-	1223.7
AHQ-7-7, 6856	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.32E-05	0.95	4.16	-	1083.6
AHQ-7-6, 3329	R.ALASQLQDSLK.D	1174.32943	2	1.99E-04	0.92	3.88	-	1028.5
AHQ-7-6, 3330 - 3333	R.ALASQLQDSLK.D	1174.32943	1	1.89E-04	0.11	1.94	-	392.4
AHQ-7-3, 3447	R.ALASQLQDSLK.D	1174.32943	2	5.88E-04	0.73	2.89	-	571.9
AHQ-7-5, 3375 - 3452	R.ALASQLQDSLK.D	1174.32943	2	1.14E-04	0.91	3.33	-	1061.0
AHQ-7-7, 3485	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.05E-04	0.93	3.33	-	1183.9
AHQ-7-3, 3660 - 3663	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.34E-11	0.96	4.31	-	1179.5
AHQ-7-11, 3459	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.57E-04	0.94	3.60	-	1435.6
AHQ-7-5, 3595 - 3602	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.04E-08	0.97	4.86	-	1520.0
AHQ-7-6, 3526 - 3527	K.AQQVSQGLDVLTAK.V	1458.64233	2	9.92E-10	0.96	4.97	-	1216.2
AHQ-7-10, 3368	K.AQQVSQGLDVLTAK.V	1458.64233	2	5.82E-04	0.82	2.73	-	804.7
AHQ-7-1, 3731 - 3773	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.16E-07	0.93	3.36	-	1412.2
AHQ-7-7, 3496 - 3497	K.AQQVSQGLDVLTAK.V	1458.64233	1	2.09E-04	0.17	2.31	-	249.7
AHQ-7-4, 3652	K.AQQVSQGLDVLTAK.V	1458.64233	1	5.50E-08	0.69	3.37	-	377.7
AHQ-7-4, 3640	K.AQQVSQGLDVLTAK.V	1458.64233	1	3.14E-04	0.59	3.04	-	463.5
AHQ-7-4, 3578 - 3644	K.AQQVSQGLDVLTAK.V	1458.64233	2	4.53E-10	0.96	4.55	-	1413.5
AHQ-7-3, 2565	K.AVAGNISDPGLQK.S	1270.41721	2	3.45E-04	0.82	2.97	-	719.6
AHQ-7-5, 2502	K.AVAGNISDPGLQK.S	1270.41721	2	2.13E-06	0.89	3.56	-	734.6
AHQ-7-7, 2450	K.AVAGNISDPGLQK.S	1270.41721	2	4.57E-05	0.82	3.63	-	610.2
AHQ-7-4, 2516	K.AVAGNISDPGLQK.S	1270.41721	2	9.89E-05	0.88	3.85	-	634.9
AHQ-7-5, 5811 - 5812	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	1.83E-06	0.96	4.44	-	1632.5
AHQ-7-5, 5810	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	1.70E-05	0.91	4.26	-	1144.5
AHQ-7-3, 5752	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	8.48E-06	0.60	2.92	-	568.5
AHQ-7-6, 5718	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	3.72E-05	0.92	4.22	-	1352.9
AHQ-7-4, 5861 - 5876	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	2.59E-04	0.95	4.05	-	1464.6
AHQ-7-4, 5862 - 5865	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	3.04E-05	0.88	4.13	-	1092.7
AHQ-7-3, 2375	R.DPSASPGDAGEQAIR.Q	1471.51169	2	7.66E-04	0.77	3.07	-	522.3
AHQ-7-2, 2425	R.DPSASPGDAGEQAIR.Q	1471.51169	2	9.73E-05	0.76	2.75	-	638.1
AHQ-7-6, 2313	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.83E-07	0.87	3.59	-	522.0
AHQ-7-7, 2293	R.DPSASPGDAGEQAIR.Q	1471.51169	2	1.74E-04	0.74	3.09	-	418.2
AHQ-7-4, 2345 - 2349	R.DPSASPGDAGEQAIR.Q	1471.51169	1	4.91E-04	0.11	1.94	-	115.4
AHQ-7-4, 2284 - 2348	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.63E-06	0.91	3.74	-	892.4
AHQ-7-5, 2322	R.DPSASPGDAGEQAIR.Q	1471.51169	2	3.90E-04	0.84	3.14	-	701.5
AHQ-7-4, 2572 - 2636	R.DYLIDGSR.G	939.00451	1	7.62E-04	0.49	2.16	-	285.4
AHQ-7-5, 5842	K.ELLPVLISAMK.I	1214.54325	2	8.09E-05	0.81	3.15	-	561.3
AHQ-7-4, 5914 - 5924	K.ELLPVLISAMK.I	1214.54325	2	6.42E-07	0.84	3.17	-	669.7
AHQ-7-7, 2680	R.ELTPQVVSAAR.I	1171.32878	2	5.99E-04	0.91	3.10	-	1198.4

AHQ-7-4, 3052	K.ETVQTTEDQILKR.D	1561.71942	2	1.67E-08	0.88	3.63	-	809.6
AHQ-7-5, 3044	K.ETVQTTEDQILKR.D	1561.71942	2	3.30E-04	0.67	2.78	-	613.4
AHQ-7-7, 2922	K.ETVQTTEDQILKR.D	1561.71942	2	8.05E-05	0.56	2.78	-	518.8
AHQ-7-6, 3015	K.ETVQTTEDQILKR.D	1561.71942	2	1.36E-06	0.78	3.34	-	657.0
AHQ-7-4, 6804	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.19E-07	0.95	4.92	-	1022.9
AHQ-7-6, 6615 - 6686	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	8.99E-07	0.95	5.08	-	806.8
AHQ-7-1, 6489	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	5.61E-05	0.89	4.41	-	604.8
AHQ-7-5, 6719	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.48E-07	0.94	4.43	-	1008.2
AHQ-7-14-, 6321	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.74E-04	0.88	3.67	-	839.1
AHQ-7-7, 6694	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.07E-07	0.95	5.34	-	738.3
AHQ-7-5, 6584 - 6644	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	6.34E-05	0.60	3.07	-	379.5
AHQ-7-4, 6449	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	3	3.04E-08	0.87	3.67	-	889.5
AHQ-7-4, 1670	R.GQGSSPVAMQK.A	1090.23603	2	5.08E-04	0.73	2.94	-	744.8
AHQ-7-4, 3604 - 3676	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	3.28E-05	0.83	3.84	-	479.0
AHQ-7-4, 2260	K.IAELCDDPKER.D	1347.47690	2	4.75E-05	0.63	2.74	-	504.0
AHQ-7-4, 3177	R.IPTISTQLK.I	1001.20202	2	2.71E-05	0.76	2.58	-	547.3
AHQ-7-4, 3316	R.KIAELCDDPKERDDILR.S	2088.32839	2	7.17E-04	0.87	4.10	-	615.3
AHQ-7-4, 3321	R.KIAELCDDPKERDDILR.S	2088.32839	3	8.49E-05	0.75	3.34	-	567.4
AHQ-7-4, 4314 - 4325	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	3.63E-08	0.97	6.17	-	1317.5
AHQ-7-4, 4401	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	2.16E-05	0.63	3.02	-	708.4
AHQ-7-5, 4358	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	5.53E-06	0.77	3.40	-	301.5
AHQ-7-5, 4274	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.67E-07	0.84	3.27	-	501.2
AHQ-7-6, 4194	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	4.40E-07	0.91	4.38	-	922.5
AHQ-7-6, 4143 - 4206	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	5.51E-05	0.81	3.29	-	371.2
AHQ-7-4, 4428	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	3.63E-09	0.86	3.94	-	447.0
AHQ-7-5, 4270 - 4346	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	1.31E-05	0.96	5.70	-	1214.8
AHQ-7-4, 4290 - 4362	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	6.92E-09	0.91	4.43	-	527.9
AHQ-7-7, 4142	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.46E-04	0.63	3.18	-	250.4
AHQ-7-5, 2851 - 2928	R.LANVMM*GPYR.Q	1168.41500	2	2.50E-05	0.83	3.36	-	760.0
AHQ-7-6, 2922	R.LANVMM*GPYR.Q	1168.41500	2	2.55E-05	0.88	3.74	-	909.3
AHQ-7-5, 3424	R.LANVMMGPYR.Q	1152.41560	2	9.13E-05	0.87	3.31	-	775.4
AHQ-7-4, 4274 - 4340	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	6.16E-09	0.78	3.32	-	801.2
AHQ-7-4, 4444	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	2	1.74E-05	0.78	3.29	-	559.8
AHQ-7-1, 4365	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	8.29E-05	0.63	3.01	-	515.8
AHQ-7-5, 4508	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	4.22E-05	0.70	3.44	-	383.6
AHQ-7-4, 4538 - 4608	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	4.05E-04	0.84	3.82	-	705.3
AHQ-7-11, 3538	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	4.53E-06	0.76	3.06	-	520.0
AHQ-7-6, 3653	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.16E-05	0.85	3.27	-	618.1
AHQ-7-5, 3715	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	3.42E-07	0.95	4.99	-	828.6
AHQ-7-4, 4596	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	1.63E-05	0.94	4.68	-	1435.8
AHQ-7-4, 3768	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	5.31E-04	0.90	4.24	-	640.9
AHQ-7-4, 4402	R.MALLMAEMSR.L	1153.46531	2	4.40E-07	0.96	4.06	-	1805.9
AHQ-7-5, 2939	K.M*LGQM*TDQVADLR.A	1510.71935	2	9.98E-05	0.96	3.55	-	2047.7
AHQ-7-6, 4077	K.MLGQMTDQVADLR.A	1478.72055	2	2.94E-07	0.92	3.70	-	1212.0
AHQ-7-4, 4193	K.M*LGQM*TDQVADLR.A	1510.71935	2	8.83E-06	0.96	4.36	-	1595.5
AHQ-7-5, 3255 - 3299	K.MLGQM*TDQVADLR.A	1494.71995	2	4.66E-07	0.92	3.90	-	1402.9
AHQ-7-4, 4178 - 4180	K.MLGQMTDQVADLR.A	1478.72055	2	9.26E-08	0.96	4.44	-	1641.2
AHQ-7-5, 3772 - 3775	K.M*LGQMTDQVADLR.A	1494.71995	2	2.77E-05	0.98	4.77	-	2422.8
AHQ-7-5, 4142	K.MLGQMTDQVADLR.A	1478.72055	2	2.36E-10	0.97	4.91	-	1832.4
AHQ-7-6, 3698	K.M*LGQMTDQVADLR.A	1494.71995	2	3.05E-05	0.97	4.15	-	2449.4
AHQ-7-6, 4495	R.M*QEAM*TQEVSDVFSDTTTPIK.L	2391.61544	2	5.55E-05	0.89	3.60	-	651.1
AHQ-7-6, 3754	K.MSAEINEIIR.V	1176.36883	2	2.98E-05	0.90	3.43	-	1294.4
AHQ-7-4, 3929	K.MSAEINEIIR.V	1176.36883	2	1.59E-06	0.91	3.48	-	1277.8
AHQ-7-4, 3257	K.M*SAEINEIIR.V	1192.36823	2	6.88E-05	0.90	3.22	-	1000.5
AHQ-7-5, 3223	K.M*SAEINEIIR.V	1192.36823	2	1.23E-06	0.88	2.75	-	962.5
AHQ-7-6, 3518	K.MTGLVDEAIDTK.S	1293.46936	2	1.13E-04	0.96	4.07	-	1418.9
AHQ-7-4, 3612	K.MTGLVDEAIDTK.S	1293.46936	2	7.53E-08	0.96	4.20	-	1539.6
AHQ-7-4, 3162	K.M*TGLVDEAIDTK.S	1309.46876	2	9.28E-07	0.95	3.56	-	1381.7
AHQ-7-5, 3574	K.MTGLVDEAIDTK.S	1293.46936	2	1.65E-08	0.97	4.38	-	1765.1
AHQ-7-5, 3136 - 3151	K.M*TGLVDEAIDTK.S	1309.46876	2	1.91E-07	0.94	3.50	-	1332.9
AHQ-7-4, 2548 - 2616	R.NPGNQAAYEHFETM*K.N	1753.87377	2	7.51E-05	0.91	3.44	-	799.9
AHQ-7-5, 3048	R.NPGNQAAYEHFETMK.N	1737.87437	2	2.03E-05	0.83	3.15	-	704.1
AHQ-7-4, 3054	R.NPGNQAAYEHFETMK.N	1737.87437	2	7.46E-06	0.94	4.27	-	1003.2
AHQ-7-4, 3377	R.NPGNQAAYEHFETMK.N	1737.87437	2	3.63E-06	0.91	3.62	-	953.3
AHQ-7-4, 2992	K.NQWIDNVEK.M	1146.23464	1	5.92E-05	0.40	2.59	-	218.0
AHQ-7-4, 2942 - 3008	K.QVATALQNLQTK.T	1315.50112	2	4.34E-08	0.89	3.90	-	560.7
AHQ-7-4, 2976	K.SFLDSGYR.I	945.01074	1	4.84E-05	0.07	1.86	-	132.0
AHQ-7-4, 2968 - 3037	K.SFLDSGYR.I	945.01074	2	6.67E-05	0.86	2.63	-	836.0
AHQ-7-4, 3697	R.SLGEISALTSK.L	1106.25186	2	3.81E-04	0.92	3.45	-	896.4
AHQ-7-7, 3372	R.SLGEISALTSK.L	1106.25186	2	5.30E-05	0.94	3.89	-	965.2
AHQ-7-4, 3525 - 3526	R.SLGEISALTSK.L	1106.25186	2	2.05E-05	0.95	4.24	-	1029.5
AHQ-7-5, 3508	R.SLGEISALTSK.L	1106.25186	1	4.37E-09	0.41	2.63	-	127.4
AHQ-7-6, 3353	K.SLLDASEEAIKK.D	1304.47187	2	1.79E-05	0.82	2.85	-	971.0
AHQ-7-5, 3318 - 3382	K.SLLDASEEAIKK.D	1304.47187	2	8.36E-05	0.59	2.53	-	495.4
AHQ-7-8, 3272	K.SLLDASEEAIKK.D	1304.47187	2	2.24E-05	0.67	2.65	-	654.3
AHQ-7-4, 3400	K.SLLDASEEAIKK.D	1304.47187	2	3.82E-06	0.86	2.97	-	881.6
AHQ-7-4, 2445	K.STVEGIQASVK.T	1119.25064	2	5.03E-06	0.93	3.65	-	1004.8
AHQ-7-4, 2564	R.TDAGFTLR.W	880.96819	2	1.36E-05	0.90	2.70	-	1156.4
AHQ-7-4, 6921	R.TIESILEPVAQQISHLVIMHEEGEVDGK.A	3103.49334	3	1.05E-04	0.77	3.76	-	427.7
AHQ-7-3, 6607	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	8.31E-04	0.73	3.29	-	546.5
AHQ-7-4, 5666	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	3.68E-06	0.67	3.31	-	384.8
AHQ-7-4, 6606 - 6676	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	5.92E-09	0.79	4.48	-	515.2
AHQ-7-4, 6033 - 6112	R.TNISDEESEQATEMLVHNAQNLM*QSVK.E	3064.30957	3	1.25E-06	0.80	4.09	-	542.7
AHQ-7-7, 6630 - 6700	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	1.44E-04	0.77	3.62	-	488.8
AHQ-7-4, 6000	R.TNISDEESEQATEMLVHNAQNLMQSVK.E	3048.31017	3	2.61E-10	0.92	4.80	-	734.1
AHQ-7-5, 3310 - 3311	R.TNLLQVCER.I	1134.28859	2	7.20E-04	0.85	3.01	-	969.9
AHQ-7-6, 3218 - 3269	R.TNLLQVCER.I	1134.28859	2	5.48E-04	0.89	2.81	-	1076.3
AHQ-7-13-, 3295	R.TNLLQVCER.I	1134.28859	2	5.92E-04	0.87	3.02	-	910.3
AHQ-7-4, 4977	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	5.91E-06	0.96	4.62	-	2051.3
AHQ-7-5, 5880	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	3	1.71E-04	0.86	3.89	-	1087.1
AHQ-7-4, 5405 - 5477	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	2.60E-07	0.90	4.48	-	760.4
AHQ-7-7, 5170	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	5.51E-05	0.70	3.28	-	448.5
AHQ-7-6, 5415	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	3	9.01E-04	0.80	3.99	-	1093.0
AHQ-7-4, 5414	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	1.74E-05	0.89	4.56	-	1276.1
AHQ-7-4, 5944	K.VAMANIQPQMLVAGATSIAR.R	2043.44398	3	2.19E-08	0.96	4.72	-	2162.6
AHQ-7-6, 4949 - 4950	R.VDQLTAQLADLAAR.G	1485.66778	2	4.56E-08	0.98	4.85	-	2719.6
AHQ-7-5, 5019	R.VDQLTAQLADLAAR.G	1485.66778	2	1.01E-09	0.98	4.72	-	3005.4
AHQ-7-4, 5064	R.VDQLTAQLADLAAR.G	1485.66778	2	3.21E-05	0.97	3.89	-	2058.3
AHQ-7-4, 3260	R.VGKETVQTTEDQILK.R	1689.88910	2	6.85E-05	0.91	4.43	-	944.1
AHQ-7-6, 5285 - 5301	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.58E-11	0.95	4.01	-	1147.6
AHQ-7-3, 5347 - 5408	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.98E-06	0.94	4.24	-	981.2
AHQ-7-7, 5225	R.VLQLTSWDEDAWASK.D	1749.90156	2	9.99E-10	0.92	3.15	-	1142.6
AHQ-7-5, 5363	R.VLQLTSWDEDAWASK.D	1749.90156	2	5.37E-08	0.96	4.70	-	1221.6
AHQ-7-4, 5420 - 5440	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.07E-06	0.97	4.59	-	1470.7
AHQ-7-8, 5168 - 5196	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.43E-05	0.92	3.73	-	1156.4
AHQ-7-1, 5331 - 5389	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.52E-04	0.85	3.82	-	659.2
AHQ-7-2, 5460	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.49E-07	0.86	3.23	-	649.9

AHQ-7-4, 5322	R.VLQLTSWDEDAWASK.D	1749.90156	2	9.92E-06	0.88	2.97	-	944.3
AHQ-7-4, 3310	R.VMLVNSMNTVK.E	1236.53081	2	4.49E-04	0.94	3.88	-	1128.0
AHQ-7-5, 2892	R.WIDNPTVDDR.G	1231.29640	2	3.51E-06	0.86	2.75	-	961.8
gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]				7.16E-14	37.30	430.33	41.50	129351.8
AHQ-7-5, 4108	K.AGTLDLSLTVQGK.Q	1303.48711	2	8.10E-04	0.86	2.96	-	1160.2
AHQ-7-3, 4112	K.AGTLDLSLTVQGK.Q	1303.48711	2	1.50E-04	0.94	3.84	-	1514.4
AHQ-7-2, 2387 - 2388	R.AQGYSGLSVK.V	1010.12587	2	8.07E-04	0.63	2.76	-	333.6
AHQ-7-2, 2852	R.AQLYIDCEK.M	1141.27636	2	3.82E-04	0.87	3.32	-	823.6
AHQ-7-4, 2774	R.AQLYIDCEK.M	1141.27636	2	6.05E-05	0.88	3.10	-	738.7
AHQ-7-4, 6101	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	8.39E-04	0.64	3.27	-	502.6
AHQ-7-2, 4645	R.CDNCPYNHNPDQADTDNNGEGDACAADIDGDGILNER.D	4098.07237	3	2.25E-05	0.95	5.36	-	1142.6
AHQ-7-4, 3864 - 3916	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.80E-04	0.91	3.90	-	591.6
AHQ-7-5, 3859	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.40E-05	0.91	4.36	-	567.4
AHQ-7-4, 3777	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.30E-06	0.78	3.28	-	386.8
AHQ-7-5, 3746	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.70E-07	0.87	3.81	-	478.3
AHQ-7-3, 3731 - 3801	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.72E-10	0.82	3.19	-	399.7
AHQ-7-2, 3816	R.CENTDPGYNCLPCPPR.F	1954.10800	2	3.85E-05	0.89	3.71	-	543.9
AHQ-7-3, 3403	K.CNYLGHYSDPM*YR.C	1693.84162	2	3.87E-06	0.94	3.47	-	1005.3
AHQ-7-2, 3476 - 3480	K.CNYLGHYSDPM*YR.C	1693.84162	2	7.01E-06	0.92	3.79	-	751.9
AHQ-7-5, 3855 - 3862	K.CNYLGHYSDPMYR.C	1677.84222	2	1.31E-07	0.94	4.51	-	840.8
AHQ-7-2, 3493	K.CNYLGHYSDPM*YR.C	1693.84162	3	8.69E-05	0.81	3.09	-	1069.1
AHQ-7-3, 3871	K.CNYLGHYSDPMYR.C	1677.84222	2	3.10E-08	0.81	2.98	-	602.5
AHQ-7-4, 3877	K.CNYLGHYSDPMYR.C	1677.84222	2	1.99E-05	0.82	3.31	-	615.4
AHQ-7-5, 3282	K.DCVGDVTENQICNK.Q	1654.75869	2	2.71E-04	0.90	3.20	-	1118.0
AHQ-7-6, 3245	K.DCVGDVTENQICNK.Q	1654.75869	2	5.58E-06	0.94	3.96	-	990.2
AHQ-7-3, 3299	K.DCVGDVTENQICNK.Q	1654.75869	2	8.36E-07	0.86	3.12	-	945.7
AHQ-7-2, 3369	K.DCVGDVTENQICNK.Q	1654.75869	2	3.02E-06	0.94	4.28	-	1032.8
AHQ-7-4, 6124	K.DDFDHDSVPDIDDICPENVDISETDFR.R	3183.22991	3	7.55E-04	0.96	5.24	-	1846.3
AHQ-7-6, 2910 - 2965	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.34E-04	0.49	2.56	-	429.0
AHQ-7-10, 2675 - 2724	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.81E-05	0.86	3.63	-	567.1
AHQ-7-3, 2835 - 2911	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.89E-10	0.92	3.38	-	1097.8
AHQ-7-2, 3049	K.DHSGQVFSVVSNGK.A	1461.56164	2	9.09E-05	0.91	3.19	-	952.0
AHQ-7-2, 2856 - 2873	K.DHSGQVFSVVSNGK.A	1461.56164	2	5.22E-11	0.95	4.24	-	1262.8
AHQ-7-4, 2958	K.DHSGQVFSVVSNGK.A	1461.56164	2	6.80E-06	0.87	3.38	-	862.7
AHQ-7-2, 3241 - 3308	R.DNCQYVYNVDQR.D	1575.64166	2	2.05E-04	0.86	3.17	-	917.3
AHQ-7-7, 2996	R.DNCQYVYNVDQR.D	1575.64166	2	7.67E-08	0.89	3.36	-	909.1
AHQ-7-3, 3181 - 3243	R.DNCQYVYNVDQR.D	1575.64166	2	7.32E-07	0.83	2.99	-	889.8
AHQ-7-6, 3179	R.DNCQYVYNVDQR.D	1575.64166	2	2.85E-06	0.92	3.70	-	1282.3
AHQ-7-6, 3023	R.DNCQYVYNVDQR.D	1575.64166	2	2.71E-05	0.83	2.89	-	882.2
AHQ-7-5, 3062	R.DNCQYVYNVDQR.D	1575.64166	2	2.25E-05	0.93	3.79	-	1256.6
AHQ-7-7, 5688	K.DSDGDGRGDACKDDFDHDSVPDIDDICPENVDISETDFR.R	4418.43100	3	6.46E-07	0.88	4.65	-	569.4
AHQ-7-4, 4070 - 4136	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	7.66E-10	0.93	4.98	-	861.5
AHQ-7-2, 3807 - 3829	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.50E-13	0.91	4.51	-	962.8
AHQ-7-2, 3667 - 3741	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	5.24E-05	0.89	4.10	-	831.2
AHQ-7-3, 3683 - 3748	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.54E-06	0.86	4.07	-	728.4
AHQ-7-2, 4175	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.89E-08	0.92	4.76	-	560.1
AHQ-7-1, 3804	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.35E-04	0.70	4.07	-	256.1
AHQ-7-4, 3745 - 3812	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.68E-10	0.91	4.57	-	818.6
AHQ-7-7, 3869	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	2.20E-08	0.91	4.25	-	855.7
AHQ-7-5, 3951	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	8.30E-04	0.87	4.29	-	601.8
AHQ-7-6, 3913	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	3.76E-07	0.92	4.78	-	837.2
AHQ-7-5, 3727	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	6.63E-08	0.92	4.63	-	1026.7
AHQ-7-6, 3999	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	5.82E-04	0.77	3.61	-	574.8
AHQ-7-7, 3965 - 3988	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.24E-04	0.90	4.49	-	792.3
AHQ-7-3, 3649	K.FQDLVDAVR.A	1063.18877	2	7.00E-05	0.90	2.84	-	1104.8
AHQ-7-10, 3372 - 3373	K.FQDLVDAVR.A	1063.18877	2	7.71E-05	0.93	3.11	-	1364.2
AHQ-7-7, 3506	K.FQDLVDAVR.A	1063.18877	2	1.42E-05	0.91	3.12	-	1052.9
AHQ-7-2, 3725	K.FQDLVDAVR.A	1063.18877	2	8.03E-06	0.90	3.07	-	1052.5
AHQ-7-4, 3005 - 3006	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.10E-11	0.93	4.67	-	718.4
AHQ-7-7, 2793	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	8.97E-05	0.52	2.92	-	313.8
AHQ-7-6, 2886	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.50E-04	0.74	3.26	-	376.7
AHQ-7-2, 3036 - 3103	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.60E-11	0.93	4.80	-	590.6
AHQ-7-3, 3061	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.43E-09	0.79	3.52	-	401.0
AHQ-7-5, 2898	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	8.40E-06	0.87	3.83	-	671.0
AHQ-7-2, 2991	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.55E-04	0.70	3.04	-	532.1
AHQ-7-4, 2908	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.37E-07	0.89	4.14	-	478.1
AHQ-7-6, 2887 - 2894	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	8.61E-06	0.78	3.60	-	515.8
AHQ-7-13-, 5209	R.FVFGTTPEDILR.N	1395.58470	2	7.64E-05	0.84	2.99	-	713.8
AHQ-7-9, 4884	R.FVFGTTPEDILR.N	1395.58470	2	6.20E-04	0.85	2.77	-	900.7
AHQ-7-11, 5055	R.FVFGTTPEDILR.N	1395.58470	2	1.23E-04	0.83	3.09	-	697.8
AHQ-7-6, 5362	R.FVFGTTPEDILR.N	1395.58470	2	2.85E-04	0.72	2.74	-	654.9
AHQ-7-2, 5908	R.GDACKDDFDHDSVPDIDDICPENVDISETDFR.R	3715.80029	3	2.84E-04	0.70	3.14	-	434.4
AHQ-7-13-, 5344	K.GFLLLASLR.Q	990.22407	2	2.90E-05	0.96	3.66	-	1949.0
AHQ-7-1, 5527	K.GFLLLASLR.Q	990.22407	2	2.77E-04	0.96	3.32	-	2135.7
AHQ-7-2, 5643	K.GFLLLASLR.Q	990.22407	2	3.65E-06	0.97	4.21	-	2318.3
AHQ-7-6, 5475 - 5481	K.GFLLLASLR.Q	990.22407	2	7.28E-04	0.97	4.03	-	2080.2
AHQ-7-11, 5158	K.GFLLLASLR.Q	990.22407	2	4.90E-05	0.96	3.71	-	2108.7
AHQ-7-13, 5425	K.GFLLLASLR.Q	990.22407	2	3.62E-05	0.97	3.73	-	2285.3
AHQ-7-5, 5554	K.GFLLLASLR.Q	990.22407	2	2.71E-05	0.97	4.41	-	2225.4
AHQ-7-1, 4501 - 4559	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.32E-05	0.88	4.24	-	757.2
AHQ-7-5, 4498 - 4499	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.02E-07	0.92	4.29	-	933.2
AHQ-7-5, 4602 - 4603	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.88E-04	0.85	3.97	-	622.2
AHQ-7-3, 4293	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.69E-08	0.84	3.84	-	622.3
AHQ-7-7, 4365	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.43E-08	0.84	3.67	-	619.3
AHQ-7-3, 4445 - 4509	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.96E-06	0.84	3.55	-	697.3
AHQ-7-3, 4612	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.17E-05	0.82	3.67	-	866.1
AHQ-7-3, 4739	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.49E-06	0.87	3.46	-	1008.7
AHQ-7-7, 4272	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.36E-06	0.93	4.55	-	890.2
AHQ-7-1, 4663 - 4719	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.43E-04	0.84	3.85	-	630.6
AHQ-7-6, 4191	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.95E-07	0.65	2.89	-	568.9
AHQ-7-4, 4462 - 4505	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.30E-08	0.84	3.82	-	615.4
AHQ-7-9, 3989 - 4057	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.36E-07	0.85	4.06	-	588.3
AHQ-7-6, 4330	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.52E-04	0.88	4.02	-	664.6
AHQ-7-4, 4572 - 4589	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.03E-06	0.89	4.07	-	690.2
AHQ-7-4, 4661 - 4720	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.68E-06	0.82	3.58	-	680.2
AHQ-7-4, 4749	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.38E-06	0.56	2.86	-	313.0
AHQ-7-6, 4418	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.75E-08	0.90	4.29	-	718.9
AHQ-7-10, 4055 - 4127	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.41E-09	0.95	4.77	-	1105.9
AHQ-7-2, 4711	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.57E-06	0.78	3.50	-	514.5
AHQ-7-2, 4543 - 4611	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.04E-06	0.93	4.64	-	888.6
AHQ-7-6, 4519	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.14E-06	0.80	3.83	-	544.7
AHQ-7-5, 4411 - 4434	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.97E-05	0.90	4.28	-	819.3
AHQ-7-10, 4208 - 4212	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.22E-05	0.93	4.35	-	978.9
AHQ-7-11, 4143 - 4219	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.63E-04	0.90	4.15	-	782.1
AHQ-7-3, 2243	K.GPDPSSPAFR.I	1031.10364	2	6.53E-05	0.58	3.07	-	314.3
AHQ-7-4, 2194	K.GPDPSSPAFR.I	1031.10364	2	3.20E-05	0.74	3.06	-	460.4
AHQ-7-2, 2272	K.GPDPSSPAFR.I	1031.10364	2	3.97E-05	0.73	2.78	-	532.8

AHQ-7-5, 3094	R.GTLLALER.K	873.03234	2	9.29E-04	0.86	3.41	-	897.1
AHQ-7-1, 3381	R.GTLLALER.K	873.03234	2	5.01E-04	0.94	3.52	-	1218.2
AHQ-7-6, 3074	R.GTLLALER.K	873.03234	2	3.84E-04	0.83	2.91	-	820.4
AHQ-7-2, 2807	K.GTSQNDPNWVVR.H	1373.45608	2	1.52E-04	0.55	2.69	-	639.7
AHQ-7-13-, 5987 - 6064	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	7.13E-08	0.77	3.45	-	361.4
AHQ-7-1, 6140 - 6219	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.28E-04	0.78	3.95	-	519.0
AHQ-7-5, 6315 - 6384	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.82E-07	0.67	3.33	-	258.2
AHQ-7-8, 6239 - 6263	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.93E-04	0.39	2.57	-	167.9
AHQ-7-9, 5652 - 5653	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.11E-06	0.66	3.14	-	253.9
AHQ-7-3, 6215 - 6276	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.35E-04	0.79	3.41	-	459.5
AHQ-7-5, 6440	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.70E-06	0.85	4.06	-	545.7
AHQ-7-14-, 5953	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.32E-06	0.69	3.28	-	415.5
AHQ-7-13, 6013 - 6086	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.44E-07	0.65	3.04	-	357.9
AHQ-7-2, 6507 - 6523	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.52E-05	0.73	3.32	-	378.8
AHQ-7-2, 6376 - 6447	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.60E-06	0.88	4.35	-	490.7
AHQ-7-4, 6380 - 6457	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	6.07E-12	0.93	4.63	-	729.4
AHQ-7-4, 6393 - 6464	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.00E-04	0.56	2.79	-	259.9
AHQ-7-4, 6516	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.83E-08	0.63	3.22	-	351.3
AHQ-7-11, 5830 - 5898	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.04E-10	0.79	3.46	-	478.2
AHQ-7-10, 5732 - 5739	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	1.38E-05	0.68	3.33	-	267.0
AHQ-7-10, 5725	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.21E-08	0.62	3.08	-	328.5
AHQ-7-6, 6193 - 6253	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.24E-06	0.85	4.71	-	362.2
AHQ-7-12, 2664 - 2667	K.IMADSGPIYDK.T	1210.38204	2	2.71E-06	0.89	3.35	-	724.3
AHQ-7-11, 2608	K.IMADSGPIYDK.T	1210.38204	2	6.50E-07	0.92	3.70	-	839.6
AHQ-7-8, 2598 - 2606	K.IMADSGPIYDK.T	1210.38204	1	1.49E-04	0.37	2.66	-	552.6
AHQ-7-8, 2599	K.IMADSGPIYDK.T	1210.38204	2	1.53E-04	0.94	3.91	-	910.1
AHQ-7-6, 2629	K.IMADSGPIYDK.T	1210.38204	2	1.03E-06	0.87	3.09	-	682.4
AHQ-7-5, 2639 - 2664	K.IMADSGPIYDK.T	1210.38204	2	1.38E-04	0.79	2.58	-	563.6
AHQ-7-2, 2728 - 2732	K.IMADSGPIYDK.T	1210.38204	2	1.41E-04	0.86	3.14	-	744.0
AHQ-7-3, 2701	K.IMADSGPIYDK.T	1210.38204	1	1.92E-04	0.63	2.55	-	657.5
AHQ-7-11, 6140	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.93E-07	0.94	5.05	-	763.8
AHQ-7-5, 6660	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	8.34E-06	0.94	4.70	-	1481.0
AHQ-7-2, 6719	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	1.58E-04	0.89	3.83	-	1282.1
AHQ-7-9, 5968 - 6028	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.25E-08	0.96	5.29	-	1280.6
AHQ-7-4, 6745	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	3.92E-04	0.81	4.02	-	767.2
AHQ-7-2, 6711	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.67E-06	0.96	5.12	-	1091.6
AHQ-7-14-, 6274	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.70E-08	0.97	5.65	-	1127.4
AHQ-7-13, 6293	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.41E-11	0.97	5.40	-	1552.1
AHQ-7-7, 6664	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.43E-08	0.94	4.57	-	885.0
AHQ-7-5, 6647 - 6706	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.74E-12	0.97	5.78	-	1404.9
AHQ-7-1, 6439	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	4.83E-05	0.88	4.12	-	698.6
AHQ-7-7, 6526 - 6585	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.17E-10	0.96	4.96	-	1180.5
AHQ-7-13-, 6296 - 6300	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.38E-12	0.98	6.47	-	1315.8
AHQ-7-3, 6540 - 6563	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.27E-09	0.96	5.82	-	910.1
AHQ-7-6, 6546 - 6598	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	6.25E-09	0.97	5.54	-	1129.9
AHQ-7-4, 6730 - 6789	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.16E-14	0.98	6.54	-	1291.1
AHQ-7-4, 2409 - 2485	R.KDHSGQVFSVVSNGK.A	1589.73455	2	7.09E-10	0.91	3.63	-	1017.4
AHQ-7-2, 2553	R.KDHSGQVFSVVSNGK.A	1589.73455	3	3.07E-05	0.92	3.80	-	1211.9
AHQ-7-10, 2311	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.19E-06	0.65	2.92	-	623.8
AHQ-7-3, 2463 - 2525	R.KDHSGQVFSVVSNGK.A	1589.73455	2	6.68E-08	0.87	3.40	-	946.3
AHQ-7-5, 2359	R.KDHSGQVFSVVSNGK.A	1589.73455	2	9.10E-06	0.82	3.27	-	872.8
AHQ-7-2, 2499 - 2564	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.69E-08	0.96	4.53	-	1534.9
AHQ-7-9, 2284	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.11E-07	0.81	2.77	-	973.4
AHQ-7-2, 2539	K.KIMADSGPIYDK.T	1338.55496	2	1.13E-06	0.95	4.12	-	1057.7
AHQ-7-4, 2150	K.KIM*ADSGPIYDK.T	1354.55436	2	3.68E-04	0.84	3.11	-	832.8
AHQ-7-2, 2503	R.KVTEENKELANELR.R	1673.84976	2	1.37E-06	0.94	4.76	-	1242.7
AHQ-7-3, 2467	R.KVTEENKELANELR.R	1673.84976	2	2.23E-07	0.95	4.54	-	1589.1
AHQ-7-4, 2422 - 2424	R.KVTEENKELANELR.R	1673.84976	2	5.00E-08	0.95	4.53	-	1533.2
AHQ-7-3, 2199	R.KVTEENKELANELR.R	1673.84976	2	6.90E-10	0.89	3.99	-	1165.7
AHQ-7-4, 2421 - 2489	R.KVTEENKELANELR.R	1673.84976	3	8.88E-06	0.77	3.58	-	716.6
AHQ-7-2, 2241	R.KVTEENKELANELR.R	1673.84976	2	1.77E-10	0.91	3.99	-	1124.7
AHQ-7-8, 2299	R.KVTEENKELANELR.R	1673.84976	2	2.67E-08	0.91	3.98	-	1145.6
AHQ-7-5, 2134	R.KVTEENKELANELR.R	1673.84976	2	1.24E-09	0.86	3.60	-	1015.7
AHQ-7-6, 2366 - 2423	R.KVTEENKELANELR.R	1673.84976	3	1.10E-06	0.77	3.64	-	856.3
AHQ-7-5, 2391	R.KVTEENKELANELR.R	1673.84976	3	1.54E-06	0.85	3.92	-	853.9
AHQ-7-5, 2390	R.KVTEENKELANELR.R	1673.84976	2	8.52E-05	0.94	4.60	-	889.0
AHQ-7-4, 2670	R.LCNNPAPQFGGK.D	1304.45694	2	1.39E-04	0.91	4.04	-	725.3
AHQ-7-5, 2654	R.LCNNPAPQFGGK.D	1304.45694	2	9.60E-05	0.73	3.18	-	452.2
AHQ-7-2, 2723	R.LCNNPAPQFGGK.D	1304.45694	2	1.10E-05	0.92	3.88	-	764.2
AHQ-7-3, 2697 - 2699	R.LCNNPAPQFGGK.D	1304.45694	2	1.99E-04	0.87	3.97	-	473.0
AHQ-7-2, 4368	R.LCNNPAPQFGGKDCVGDVTENQICNK.Q	2940.19303	3	4.70E-05	0.88	4.13	-	749.5
AHQ-7-2, 2593	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.02E-12	0.92	4.27	-	693.0
AHQ-7-6, 2509	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	2.39E-07	0.86	3.78	-	494.4
AHQ-7-5, 2532	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	1.86E-08	0.81	3.61	-	481.0
AHQ-7-3, 2561	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	4.07E-08	0.86	3.80	-	467.7
AHQ-7-4, 2545	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	2.27E-08	0.87	4.22	-	692.9
AHQ-7-4, 2536 - 2540	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	3.80E-09	0.92	4.41	-	692.7
AHQ-7-3, 2569	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	3.25E-05	0.76	3.47	-	779.9
AHQ-7-6, 2510	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	2.87E-05	0.93	4.36	-	1182.4
AHQ-7-5, 2528	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	1.88E-06	0.87	3.54	-	1004.5
AHQ-7-6, 5422 - 5445	K.MENAELDVPIQSVFTR.D	1850.08607	2	8.67E-05	0.84	3.67	-	499.0
AHQ-7-6, 5245 - 5249	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	2.69E-08	0.94	4.75	-	813.4
AHQ-7-7, 5418	K.MENAELDVPIQSVFTR.D	1850.08607	2	6.78E-04	0.70	3.26	-	510.4
AHQ-7-2, 5397 - 5407	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	4.34E-07	0.85	3.60	-	587.5
AHQ-7-2, 5584 - 5647	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.36E-05	0.76	3.52	-	478.3
AHQ-7-4, 5617	K.MENAELDVPIQSVFTR.D	1850.08607	2	7.16E-08	0.90	4.18	-	506.2
AHQ-7-5, 5538	K.MENAELDVPIQSVFTR.D	1850.08607	2	4.78E-06	0.88	3.90	-	563.4
AHQ-7-5, 5324	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.44E-04	0.51	2.83	-	544.5
AHQ-7-3, 5499	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.58E-06	0.84	3.64	-	415.6
AHQ-7-4, 5400	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	9.39E-05	0.84	3.63	-	568.3
AHQ-7-8, 2984 - 3048	K.QVTQSYWDTNPTR.A	1596.68241	2	1.67E-07	0.81	3.08	-	606.9
AHQ-7-4, 3156	K.QVTQSYWDTNPTR.A	1596.68241	2	1.40E-06	0.71	2.69	-	590.5
AHQ-7-5, 3120	K.QVTQSYWDTNPTR.A	1596.68241	2	1.49E-07	0.80	3.12	-	511.0
AHQ-7-2, 3228 - 3292	K.QVTQSYWDTNPTR.A	1596.68241	2	5.38E-06	0.67	2.75	-	657.4
AHQ-7-1, 3321	K.QVTQSYWDTNPTR.A	1596.68241	2	2.34E-06	0.85	3.18	-	753.9
AHQ-7-7, 3002 - 3016	K.QVTQSYWDTNPTR.A	1596.68241	2	1.43E-05	0.79	2.93	-	532.6
AHQ-7-3, 3177 - 3255	K.QVTQSYWDTNPTR.A	1596.68241	2	6.53E-07	0.80	2.61	-	824.7
AHQ-7-6, 2847	R.RPPLCYHNGVQYR.N	1661.86889	2	2.03E-07	0.94	4.17	-	878.2
AHQ-7-5, 2856	R.RPPLCYHNGVQYR.N	1661.86889	2	8.59E-04	0.80	3.06	-	547.9
AHQ-7-2, 2804	R.RPPLCYHNGVQYR.N	1661.86889	2	1.91E-05	0.84	3.17	-	667.1
AHQ-7-2, 2964	R.RPPLCYHNGVQYR.N	1661.86889	2	1.61E-04	0.70	2.54	-	546.8
AHQ-7-2, 2960 - 2977	R.RPPLCYHNGVQYR.N	1661.86889	3	8.33E-07	0.95	3.72	-	1893.0
AHQ-7-4, 2734	R.RPPLCYHNGVQYR.N	1661.86889	2	2.55E-04	0.61	2.71	-	390.8
AHQ-7-3, 2313	R.SCDSLNNRCEGSSVQTR.T	1973.04966	2	1.14E-04	0.51	2.75	-	220.2
AHQ-7-5, 3854	K.SITLFVQEDR.A	1208.34588	2	1.95E-06	0.94	3.70	-	1192.6
AHQ-7-1, 3999	K.SITLFVQEDR.A	1208.34588	2	8.87E-07	0.93	3.59	-	1328.7
AHQ-7-4, 3882	K.SITLFVQEDR.A	1208.34588	2	7.92E-07	0.92	3.07	-	1345.3

AHQ-7-11, 3655	K.SITLFVQEDR.A	1208.34588	2	4.36E-06	0.90	3.25	-	1088.0
AHQ-7-13-, 3816	K.SITLFVQEDR.A	1208.34588	2	1.21E-06	0.90	2.72	-	1407.7
AHQ-7-7, 3714	K.SITLFVQEDR.A	1208.34588	2	1.22E-06	0.96	3.16	-	1850.4
AHQ-7-6, 3761 - 3763	K.SITLFVQEDR.A	1208.34588	2	1.47E-05	0.91	3.03	-	1255.9
AHQ-7-2, 3971 - 3996	K.SITLFVQEDR.A	1208.34588	2	1.14E-05	0.95	3.95	-	1356.3
AHQ-7-3, 3883	K.SITLFVQEDR.A	1208.34588	2	5.07E-05	0.89	3.05	-	1068.0
AHQ-7-9, 3489 - 3490	K.SITLFVQEDR.A	1208.34588	2	5.95E-05	0.88	2.99	-	1040.9
AHQ-7-14-, 3822	K.SITLFVQEDR.A	1208.34588	2	8.70E-06	0.90	3.01	-	1204.9
AHQ-7-13, 3966	K.SITLFVQEDR.A	1208.34588	2	2.50E-04	0.87	3.44	-	821.9
AHQ-7-1, 4515	R.TIVTTLQDSIR.K	1247.42355	2	2.24E-06	0.97	4.05	-	1913.2
AHQ-7-6, 3306	R.TIVTTLQDSIR.K	1247.42355	2	2.21E-07	0.93	3.28	-	1232.4
AHQ-7-2, 3648	R.TIVTTLQDSIR.K	1247.42355	2	3.42E-04	0.69	2.60	-	670.3
AHQ-7-4, 4441 - 4442	R.TIVTTLQDSIR.K	1247.42355	2	4.99E-08	0.96	4.26	-	1299.4
AHQ-7-5, 3360	R.TIVTTLQDSIR.K	1247.42355	2	9.27E-05	0.83	2.63	-	990.9
AHQ-7-11, 4147	R.TIVTTLQDSIR.K	1247.42355	2	1.20E-04	0.94	3.47	-	1502.1
AHQ-7-9, 3982	R.TIVTTLQDSIR.K	1247.42355	2	3.58E-06	0.95	3.69	-	1400.1
AHQ-7-6, 4313 - 4326	R.TIVTTLQDSIR.K	1247.42355	2	4.04E-08	0.96	4.44	-	1359.8
AHQ-7-4, 3385	R.TIVTTLQDSIR.K	1247.42355	2	5.14E-06	0.96	3.65	-	1737.3
AHQ-7-7, 4257	R.TIVTTLQDSIR.K	1247.42355	2	3.85E-07	0.96	3.83	-	1926.8
AHQ-7-3, 4440 - 4455	R.TIVTTLQDSIR.K	1247.42355	2	5.99E-08	0.97	3.99	-	1994.0
AHQ-7-2, 4532 - 4560	R.TIVTTLQDSIR.K	1247.42355	2	3.74E-07	0.96	4.05	-	1502.7
AHQ-7-5, 4406	R.TIVTTLQDSIR.K	1247.42355	2	1.26E-05	0.96	4.24	-	1413.0
AHQ-7-2, 6265 - 6340	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	3.32E-07	0.84	3.63	-	1015.7
AHQ-7-5, 6187	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	2.88E-06	0.83	3.63	-	683.9
AHQ-7-3, 6097	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	8.21E-06	0.83	3.56	-	877.7
AHQ-7-3, 2680 - 2759	K.VTEENKELANELR.R	1545.67685	2	1.20E-06	0.90	4.04	-	886.8
AHQ-7-5, 2632	K.VTEENKELANELR.R	1545.67685	2	1.77E-07	0.92	3.75	-	1177.8
AHQ-7-6, 2605	K.VTEENKELANELR.R	1545.67685	3	4.89E-07	0.83	4.10	-	955.8
AHQ-7-6, 2561 - 2598	K.VTEENKELANELR.R	1545.67685	2	1.87E-07	0.87	3.08	-	1145.2
AHQ-7-4, 2633	K.VTEENKELANELR.R	1545.67685	2	3.44E-05	0.81	3.71	-	687.6
AHQ-7-7, 2541	K.VTEENKELANELR.R	1545.67685	2	4.00E-05	0.79	3.23	-	882.9
AHQ-7-2, 3060	K.VTEENKELANELR.R	1545.67685	2	2.95E-04	0.79	3.13	-	773.6
gi|4503745|ref|NP_001447.1| filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act				9.16E-14	99.49	1150.35	53.80	280757.4
AHQ-7-2, 2389 - 2415	R.AEFTVETR.S	953.03118	2	2.10E-05	0.90	2.93	-	967.0
AHQ-7-5, 2304 - 2306	R.AEFTVETR.S	953.03118	2	1.28E-05	0.92	3.07	-	1266.2
AHQ-7-4, 2557	K.AEISFEDR.K	967.01472	2	8.50E-04	0.78	2.59	-	952.4
AHQ-7-1, 2796	K.AEISFEDR.K	967.01472	2	7.74E-04	0.81	2.75	-	833.8
AHQ-7-5, 2119	K.AEISFEDRK.D	1095.18763	2	3.46E-05	0.93	3.15	-	1402.6
AHQ-7-4, 2672	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	5.19E-09	0.88	3.05	-	958.4
AHQ-7-7, 2588	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.35E-04	0.83	2.73	-	908.4
AHQ-7-5, 2660 - 2663	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.52E-09	0.96	4.19	-	1778.3
AHQ-7-3, 2707 - 2708	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	7.28E-10	0.95	3.86	-	1385.2
AHQ-7-2, 2731 - 2775	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	5.50E-08	0.88	2.84	-	1204.5
AHQ-7-8, 2603	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	5.92E-05	0.81	2.65	-	1097.4
AHQ-7-2, 2841 - 2903	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.17E-08	0.80	3.21	-	855.4
AHQ-7-6, 2641	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	5.53E-05	0.95	3.45	-	1410.4
AHQ-7-4, 2821	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	6.79E-06	0.89	3.36	-	1176.4
AHQ-7-14-, 2847 - 2850	K.AGNNM*LLVGVHGPR.T	1451.67973	3	2.44E-05	0.94	4.40	-	1535.1
AHQ-7-14, 4232 - 4242	K.AGNNMLLVGVHGPR.T	1435.68033	2	2.36E-04	0.85	3.28	-	821.9
AHQ-7-14-, 3078	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.60E-07	0.81	2.96	-	747.8
AHQ-7-14-, 3281	K.AGNNMLLVGVHGPR.T	1435.68033	3	2.40E-05	0.81	3.30	-	900.7
AHQ-7-14, 3841 - 3896	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.69E-04	0.75	2.80	-	785.7
AHQ-7-14, 3730	K.AGNNM*LLVGVHGPR.T	1451.67973	3	4.32E-07	0.92	3.86	-	1396.3
AHQ-7-14-, 3285	K.AGNNM*LLVGVHGPR.T	1451.67973	2	5.81E-04	0.70	2.61	-	747.9
AHQ-7-14-, 3289	K.AGNNM*LLVGVHGPR.T	1451.67973	3	7.22E-04	0.82	3.09	-	1301.0
AHQ-7-14-, 3463	K.AGNNMLLVGVHGPR.T	1435.68033	3	1.26E-07	0.92	3.63	-	1465.5
AHQ-7-14-, 3458 - 3523	K.AGNNMLLVGVHGPR.T	1435.68033	2	6.38E-07	0.85	3.39	-	680.2
AHQ-7-11, 3350	K.AGNNMLLVGVHGPR.T	1435.68033	2	5.14E-06	0.60	3.05	-	603.5
AHQ-7-3, 1860	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	6.05E-05	0.86	3.37	-	838.6
AHQ-7-2, 1832 - 1896	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	2.46E-04	0.88	3.83	-	954.5
AHQ-7-3, 2417	K.AGVAPLQVK.V	883.07036	2	5.38E-04	0.88	3.00	-	750.7
AHQ-7-2, 2432	K.AGVAPLQVK.V	883.07036	2	9.30E-06	0.82	2.89	-	644.5
AHQ-7-5, 2340	K.AGVAPLQVK.V	883.07036	2	8.30E-04	0.85	2.58	-	746.2
AHQ-7-4, 2376	K.AGVAPLQVK.V	883.07036	2	2.24E-05	0.85	3.14	-	683.0
AHQ-7-6, 2323	K.AGVAPLQVK.V	883.07036	2	2.06E-04	0.73	2.74	-	563.1
AHQ-7-2, 6672 - 6745	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	4.49E-04	0.84	4.04	-	650.1
AHQ-7-1, 6653 - 6731	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	8.78E-05	0.91	4.32	-	1095.8
AHQ-7-2, 6975 - 7031	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	4.04E-05	0.94	5.12	-	1352.4
AHQ-7-4, 2706	K.AHVVPCFDASK.V	1232.39073	2	1.28E-04	0.74	2.53	-	607.8
AHQ-7-1, 2952	K.AHVVPCFDASK.V	1232.39073	2	2.55E-06	0.81	2.86	-	570.4
AHQ-7-4, 6060 - 6084	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.31E-07	0.91	4.56	-	764.7
AHQ-7-2, 5975 - 6044	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.26E-09	0.96	5.93	-	1115.9
AHQ-7-4, 6146 - 6216	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.16E-11	0.90	5.05	-	606.2
AHQ-7-2, 6113 - 6188	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.57E-09	0.93	5.11	-	789.7
AHQ-7-2, 6215 - 6289	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.60E-08	0.93	5.21	-	643.0
AHQ-7-1, 5849 - 5915	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.32E-12	0.93	5.00	-	746.6
AHQ-7-5, 6130	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.51E-09	0.93	4.94	-	884.6
AHQ-7-5, 5979 - 6054	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.36E-06	0.94	5.55	-	925.9
AHQ-7-3, 5916 - 5971	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.89E-05	0.60	3.19	-	535.4
AHQ-7-3, 6029	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	7.31E-06	0.75	3.59	-	420.3
AHQ-7-7, 5989 - 6052	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.11E-13	0.95	5.67	-	793.1
AHQ-7-6, 5973 - 6033	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.27E-09	0.90	4.52	-	777.7
AHQ-7-2, 1653	R.ALTQTGGPHVK.A	1109.26067	2	2.82E-04	0.81	2.90	-	754.4
AHQ-7-8, 3234	R.ANLPQSFQVDTSK.A	1435.56409	2	4.39E-09	0.86	3.34	-	594.3
AHQ-7-2, 3572 - 3644	R.ANLPQSFQVDTSK.A	1435.56409	2	6.81E-08	0.79	3.29	-	425.9
AHQ-7-2, 3416	R.ANLPQSFQVDTSK.A	1435.56409	1	4.92E-06	0.70	2.97	-	429.6
AHQ-7-3, 3300 - 3371	R.ANLPQSFQVDTSK.A	1435.56409	2	1.49E-06	0.90	3.59	-	626.0
AHQ-7-2, 3401 - 3477	R.ANLPQSFQVDTSK.A	1435.56409	2	1.99E-05	0.61	2.81	-	549.3
AHQ-7-6, 3377	R.APSVANVGSHCDLSLK.I	1656.84249	2	9.21E-07	0.95	4.69	-	1031.2
AHQ-7-5, 3430	R.APSVANVGSHCDLSLK.I	1656.84249	2	1.96E-06	0.94	4.72	-	781.5
AHQ-7-4, 3466 - 3485	R.APSVANVGSHCDLSLK.I	1656.84249	2	1.24E-04	0.91	4.26	-	601.7
AHQ-7-6, 1906	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	1.35E-04	0.92	3.72	-	864.5
AHQ-7-7, 1892	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	7.40E-04	0.90	3.98	-	561.2
AHQ-7-6, 3586	R.AWGPGLEGGVVGK.S	1227.39403	2	2.15E-06	0.89	3.53	-	775.4
AHQ-7-4, 3688 - 3709	R.AWGPGLEGGVVGK.S	1227.39403	2	1.55E-06	0.88	3.70	-	646.4
AHQ-7-7, 3534	R.AWGPGLEGGVVGK.S	1227.39403	2	1.00E-04	0.75	2.98	-	760.9
AHQ-7-5, 3638	R.AWGPGLEGGVVGK.S	1227.39403	2	5.36E-04	0.87	3.52	-	572.7
AHQ-7-3, 3691	R.AWGPGLEGGVVGK.S	1227.39403	2	2.29E-04	0.85	3.48	-	681.7
AHQ-7-1, 3811	R.AWGPGLEGGVVGK.S	1227.39403	2	1.41E-04	0.90	3.45	-	955.3
AHQ-7-2, 3759 - 3823	R.AWGPGLEGGVVGK.S	1227.39403	2	4.10E-05	0.84	3.24	-	708.2
AHQ-7-3, 3215 - 3288	R.AYGPGIEPTGNMVK.K	1434.64274	2	7.82E-04	0.64	2.79	-	455.0
AHQ-7-6, 2753	R.AYGPGIEPTGNM*VK.K	1450.64214	2	4.27E-06	0.69	2.86	-	436.2
AHQ-7-1, 3423 - 3484	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.44E-04	0.64	2.86	-	511.5
AHQ-7-4, 3198 - 3264	R.AYGPGIEPTGNMVK.K	1434.64274	2	3.00E-05	0.78	2.85	-	559.2
AHQ-7-5, 2768	R.AYGPGIEPTGNM*VK.K	1450.64214	2	8.65E-07	0.77	2.86	-	557.7
AHQ-7-3, 5705 - 5721	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	5.89E-04	0.56	3.34	-	546.5
AHQ-7-3, 5856 - 5932	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	6.86E-05	0.74	3.14	-	590.1

AHQ-7-5, 5944	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.27E-04	0.68	3.24	-	374.7
AHQ-7-6, 5866	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	8.33E-04	0.34	2.90	-	313.3
AHQ-7-1, 5795	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	4.15E-11	0.96	5.33	-	1418.4
AHQ-7-1, 5787 - 5860	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	4.97E-10	0.90	3.70	-	578.9
AHQ-7-2, 6011	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	2.15E-05	0.80	3.27	-	565.0
AHQ-7-2, 6027	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	4.18E-09	0.97	5.00	-	1867.9
AHQ-7-4, 6041	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	4.10E-07	0.83	3.22	-	507.8
AHQ-7-2, 3000 - 3067	K.CSGPGLSPGMVR.A	1219.41699	2	5.94E-06	0.68	2.50	-	636.0
AHQ-7-5, 2966 - 2970	K.CSGPGLSPGMVR.A	1219.41699	2	2.54E-05	0.73	2.87	-	606.9
AHQ-7-3, 5333	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	2.74E-10	0.90	3.60	-	770.1
AHQ-7-3, 4896	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	2.78E-05	0.93	4.44	-	798.4
AHQ-7-5, 4855 - 4918	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	7.57E-07	0.81	3.65	-	485.9
AHQ-7-2, 5404 - 5472	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	4.32E-11	0.92	4.43	-	797.3
AHQ-7-7, 5146	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	2	1.70E-04	0.73	2.97	-	651.2
AHQ-7-3, 5323	R.CSYQPTMEGVHTVHVTFAGVPIPR.S	2686.06233	3	4.28E-05	0.83	4.11	-	456.4
AHQ-7-2, 4593	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	3.92E-07	0.96	4.44	-	1446.4
AHQ-7-2, 4051	R.DAEM*PATEKDLAEDAPWK.K	2034.18987	2	4.16E-04	0.85	3.64	-	731.6
AHQ-7-1, 4552	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	1.48E-05	0.78	3.39	-	849.7
AHQ-7-5, 3930 - 3999	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	8.85E-08	0.96	5.16	-	1403.6
AHQ-7-8, 3888	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	3.83E-04	0.90	3.92	-	865.0
AHQ-7-4, 3964 - 4030	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.48E-08	0.95	4.82	-	1408.2
AHQ-7-13, 3985	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	5.60E-05	0.68	3.00	-	804.8
AHQ-7-11, 3735	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	9.23E-06	0.86	3.79	-	924.1
AHQ-7-13-, 3780 - 3839	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.99E-04	0.90	4.01	-	990.0
AHQ-7-8, 3978	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.54E-04	0.61	3.29	-	415.4
AHQ-7-1, 4783	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	3.54E-08	0.92	3.96	-	1087.1
AHQ-7-4, 4872	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	3.62E-07	0.91	3.88	-	1215.3
AHQ-7-3, 4720 - 4768	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	1.34E-07	0.78	3.09	-	1080.6
AHQ-7-2, 4441 - 4504	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.10E-09	0.92	4.36	-	1046.3
AHQ-7-7, 4198	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	9.73E-10	0.80	3.18	-	1055.6
AHQ-7-8, 4183	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.33E-08	0.94	4.36	-	1172.8
AHQ-7-7, 4188 - 4205	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.27E-04	0.84	3.88	-	786.9
AHQ-7-6, 4253	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.04E-09	0.96	4.52	-	1749.2
AHQ-7-4, 4384	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.79E-08	0.91	4.19	-	903.3
AHQ-7-11, 4080 - 4084	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.82E-08	0.95	4.68	-	1173.9
AHQ-7-3, 4367 - 4368	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	2.30E-09	0.95	4.33	-	1550.5
AHQ-7-3, 4421	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.69E-04	0.87	3.76	-	1006.0
AHQ-7-2, 4656 - 4665	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.94E-09	0.92	4.16	-	1075.5
AHQ-7-9, 3916 - 3924	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.24E-07	0.92	4.00	-	1101.8
AHQ-7-1, 4419 - 4431	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.27E-07	0.94	4.59	-	1164.8
AHQ-7-10, 3989	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.41E-08	0.90	3.88	-	956.0
AHQ-7-2, 4455 - 4525	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	5.23E-09	0.90	3.24	-	1217.7
AHQ-7-5, 4334	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.81E-08	0.94	4.90	-	1212.8
AHQ-7-3, 4567	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.40E-07	0.96	4.76	-	1242.8
AHQ-7-4, 4388	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	3.75E-06	0.88	3.54	-	1162.0
AHQ-7-2, 4569	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.29E-06	0.89	3.83	-	1000.8
AHQ-7-3, 4296 - 4357	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.10E-09	0.91	3.99	-	962.5
AHQ-7-6, 4379 - 4385	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	5.55E-09	0.96	4.79	-	1582.1
AHQ-7-3, 4464 - 4468	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.83E-12	0.95	4.77	-	1245.8
AHQ-7-5, 4210	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.02E-04	0.89	3.48	-	1093.3
AHQ-7-4, 4516	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.49E-07	0.93	3.96	-	1219.3
AHQ-7-2, 4568	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.22E-09	0.94	3.97	-	1465.2
AHQ-7-5, 4512	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.08E-07	0.91	4.27	-	743.6
AHQ-7-5, 4422 - 4442	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.55E-07	0.94	4.16	-	1119.2
AHQ-7-1, 4483 - 4509	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	6.13E-11	0.91	3.79	-	1002.5
AHQ-7-2, 2157	R.DAPQDFHPDR.V	1198.22650	2	2.44E-04	0.45	2.51	-	497.7
AHQ-7-5, 4830 - 4891	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	7.85E-04	0.63	3.38	-	369.3
AHQ-7-7, 4569 - 4636	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.42E-06	0.88	4.58	-	435.4
AHQ-7-1, 4691 - 4764	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.61E-06	0.76	3.71	-	407.9
AHQ-7-3, 4707	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	4.68E-06	0.83	4.09	-	477.8
AHQ-7-2, 4813	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.95E-04	0.91	4.51	-	736.9
AHQ-7-5, 4590	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	9.83E-06	0.93	4.85	-	794.3
AHQ-7-6, 4642 - 4665	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.94E-05	0.89	4.03	-	664.4
AHQ-7-4, 4968	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	3.01E-05	0.82	3.76	-	573.5
AHQ-7-3, 4869	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	3.26E-04	0.38	2.90	-	319.0
AHQ-7-4, 4781	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.09E-07	0.94	4.80	-	775.5
AHQ-7-5, 4707 - 4770	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	4.58E-05	0.84	3.99	-	518.0
AHQ-7-11, 2491	K.DKGEYTLVVK.W	1152.32223	2	2.39E-05	0.57	2.57	-	409.0
AHQ-7-14, 3368 - 3429	K.DKGEYTLVVK.W	1152.32223	2	3.38E-04	0.76	2.87	-	745.1
AHQ-7-6, 2505	K.DKGEYTLVVK.W	1152.32223	2	3.23E-04	0.69	2.51	-	621.1
AHQ-7-3, 2512 - 2588	K.DKGEYTLVVK.W	1152.32223	2	3.45E-05	0.45	2.58	-	468.0
AHQ-7-4, 2532	K.DKGEYTLVVK.W	1152.32223	1	3.13E-05	0.19	1.99	-	480.1
AHQ-7-3, 3235 - 3280	K.DNGNGTYSCSYVPR.K	1591.64109	2	7.28E-06	0.82	2.80	-	888.5
AHQ-7-1, 3332	K.DNGNGTYSCSYVPR.K	1591.64109	2	7.71E-06	0.76	2.53	-	873.3
AHQ-7-2, 3205 - 3243	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.32E-07	0.95	4.78	-	1026.3
AHQ-7-3, 3204	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.56E-05	0.92	4.23	-	729.4
AHQ-7-3, 3069 - 3133	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.57E-05	0.91	3.51	-	980.6
AHQ-7-4, 3225	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	8.06E-06	0.90	3.47	-	1020.6
AHQ-7-4, 3097	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	1.52E-04	0.54	3.02	-	400.5
AHQ-7-1, 3283	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	3.69E-06	0.87	3.27	-	873.8
AHQ-7-4, 3094	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.45E-07	0.90	3.76	-	791.1
AHQ-7-5, 3458 - 3530	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	4.88E-05	0.88	3.28	-	1140.3
AHQ-7-2, 3487 - 3560	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.04E-05	0.94	4.60	-	1019.9
AHQ-7-5, 3391	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	2.35E-07	0.68	3.51	-	288.6
AHQ-7-5, 3374 - 3443	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.56E-05	0.94	4.42	-	1153.6
AHQ-7-3, 3439 - 3464	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	5.54E-04	0.94	4.37	-	1261.2
AHQ-7-7, 3277	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.84E-05	0.94	3.82	-	1270.1
AHQ-7-8, 3208 - 3287	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	6.76E-04	0.87	2.82	-	1253.0
AHQ-7-6, 3345 - 3410	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.51E-04	0.85	3.19	-	1073.1
AHQ-7-4, 3432	R.EAGAGGLAIAVEGPSK.A	1427.58510	1	8.34E-09	0.77	3.43	-	341.2
AHQ-7-4, 3412 - 3481	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.87E-05	0.92	3.82	-	1134.3
AHQ-7-1, 3560 - 3620	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	7.31E-06	0.96	4.13	-	1507.4
AHQ-7-1, 2867	R.EATTEFSVDAR.A	1226.27493	2	2.32E-04	0.88	2.86	-	981.3
AHQ-7-5, 6067 - 6147	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.84E-05	0.91	5.20	-	725.7
AHQ-7-8, 6115	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.07E-05	0.87	4.76	-	546.6
AHQ-7-2, 6259	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	9.84E-10	0.96	5.92	-	953.7
AHQ-7-2, 6116 - 6199	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.18E-09	0.97	6.10	-	1233.1
AHQ-7-3, 6084 - 6139	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.02E-07	0.93	5.62	-	595.2
AHQ-7-4, 6141 - 6201	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.86E-07	0.93	5.20	-	735.9
AHQ-7-3, 5968 - 6031	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.75E-07	0.94	5.65	-	855.3
AHQ-7-6, 6049	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.65E-08	0.84	3.79	-	688.5
AHQ-7-1, 5895 - 5951	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	5.71E-09	0.91	5.24	-	667.3
AHQ-7-7, 6057	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.05E-05	0.85	4.47	-	578.2
AHQ-7-4, 6260	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	5.85E-08	0.90	4.67	-	698.6
AHQ-7-1, 6007 - 6009	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.83E-07	0.97	6.77	-	959.0
AHQ-7-3, 4957 - 5019	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.06E-08	0.93	4.50	-	1011.0
AHQ-7-3, 5004	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	4.75E-06	0.97	4.83	-	1912.1

AHQ-7-1, 4916 - 4979	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.02E-04	0.60	2.94	-	762.5
AHQ-7-8, 4907 - 4908	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.70E-06	0.94	4.62	-	872.9
AHQ-7-6, 4945 - 5022	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.28E-05	0.62	2.62	-	492.2
AHQ-7-3, 4705	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.01E-05	0.55	3.31	-	313.1
AHQ-7-5, 5022	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.64E-06	0.88	3.30	-	824.4
AHQ-7-2, 5032 - 5099	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	7.41E-10	0.92	4.56	-	949.4
AHQ-7-9, 4509 - 4512	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.67E-04	0.83	3.45	-	610.2
AHQ-7-4, 5006 - 5036	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.42E-07	0.82	2.97	-	883.3
AHQ-7-2, 4757 - 4799	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.06E-05	0.49	2.67	-	331.6
AHQ-7-5, 3482 - 3483	K.FADQHVPGSPFSVK.V	1516.68203	3	4.37E-05	0.91	3.91	-	1066.2
AHQ-7-5, 3475 - 3539	K.FADQHVPGSPFSVK.V	1516.68203	2	1.24E-05	0.62	2.96	-	458.1
AHQ-7-4, 3528	K.FADQHVPGSPFSVK.V	1516.68203	3	3.46E-05	0.88	3.40	-	1151.7
AHQ-7-6, 3421	K.FADQHVPGSPFSVK.V	1516.68203	2	1.17E-04	0.79	2.66	-	564.2
AHQ-7-4, 3516 - 3518	K.FADQHVPGSPFSVK.V	1516.68203	2	2.66E-04	0.53	2.95	-	452.2
AHQ-7-6, 3427	K.FADQHVPGSPFSVK.V	1516.68203	3	1.38E-06	0.84	3.40	-	846.7
AHQ-7-1, 3672	K.FADQHVPGSPFSVK.V	1516.68203	3	1.31E-07	0.95	4.06	-	1483.0
AHQ-7-1, 5405	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	9.40E-04	0.93	4.07	-	1033.3
AHQ-7-6, 5338 - 5401	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.76E-08	0.94	5.06	-	926.4
AHQ-7-7, 5284 - 5357	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.67E-04	0.92	4.73	-	957.6
AHQ-7-7, 5341	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	4.46E-07	0.94	4.84	-	817.7
AHQ-7-4, 5549 - 5562	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.21E-06	0.98	6.32	-	1329.2
AHQ-7-4, 5481 - 5541	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.71E-05	0.89	4.11	-	769.9
AHQ-7-2, 5608 - 5639	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.19E-05	0.88	4.66	-	594.4
AHQ-7-8, 5256	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	2.55E-08	0.95	4.63	-	1116.7
AHQ-7-3, 5417	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	8.62E-08	0.96	5.63	-	1044.0
AHQ-7-2, 5483 - 5543	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.20E-09	0.93	4.56	-	1181.1
AHQ-7-3, 5372 - 5431	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.04E-10	0.92	4.53	-	956.0
AHQ-7-2, 5521 - 5535	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	1.11E-06	0.96	5.30	-	1098.8
AHQ-7-3, 5264	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	7.14E-04	0.84	3.93	-	846.8
AHQ-7-1, 5375 - 5412	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.87E-13	0.95	5.32	-	1085.8
AHQ-7-6, 5037 - 5043	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	7.07E-07	0.95	5.01	-	772.4
AHQ-7-6, 5147 - 5151	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	5.49E-04	0.85	4.06	-	462.6
AHQ-7-3, 5092 - 5104	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	8.40E-04	0.75	3.24	-	541.0
AHQ-7-4, 5302	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	1.32E-04	0.76	3.16	-	511.8
AHQ-7-1, 5203 - 5260	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	3	3.76E-04	0.93	4.49	-	1368.7
AHQ-7-1, 5195	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	2.99E-05	0.66	2.84	-	406.8
AHQ-7-2, 5213	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	6.46E-07	0.90	3.38	-	999.8
AHQ-7-5, 3690 - 3700	K.FNGTHIPGSPFK.I	1302.46259	2	7.11E-04	0.85	3.26	-	611.1
AHQ-7-5, 3872 - 3935	K.FNGTHIPGSPFK.I	1302.46259	2	1.28E-04	0.36	2.52	-	329.5
AHQ-7-4, 3728	K.FNGTHIPGSPFK.I	1302.46259	2	2.39E-05	0.70	2.71	-	501.4
AHQ-7-7, 3805	K.FNGTHIPGSPFK.I	1302.46259	2	2.25E-04	0.71	2.64	-	497.3
AHQ-7-4, 3838 - 3856	K.FNGTHIPGSPFK.I	1302.46259	2	2.43E-06	0.63	2.95	-	488.1
AHQ-7-5, 3046 - 3047	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	8.97E-04	0.82	3.28	-	408.8
AHQ-7-5, 3034	R.FVPAEMGTHTVSVK.Y	1503.74821	2	6.54E-06	0.67	2.78	-	387.5
AHQ-7-4, 3074	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.35E-07	0.88	3.84	-	521.5
AHQ-7-3, 2471	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	2.30E-06	0.59	2.55	-	268.3
AHQ-7-1, 2676	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	2.09E-04	0.82	3.13	-	363.1
AHQ-7-6, 2389	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	9.44E-04	0.83	3.08	-	529.2
AHQ-7-7, 2344	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	2.25E-05	0.59	2.73	-	267.7
AHQ-7-1, 3292	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.06E-08	0.87	3.24	-	751.9
AHQ-7-2, 6495 - 6551	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	1.44E-05	0.95	5.34	-	1059.5
AHQ-7-1, 5683	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	1.85E-05	0.91	4.30	-	614.7
AHQ-7-4, 3389	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	8.73E-06	0.79	3.34	-	612.3
AHQ-7-2, 3452 - 3519	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.07E-06	0.87	3.69	-	674.3
AHQ-7-5, 3355	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.48E-05	0.83	3.12	-	801.0
AHQ-7-7, 3248 - 3268	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.80E-07	0.86	3.86	-	626.6
AHQ-7-8, 3264	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.02E-05	0.70	2.91	-	688.9
AHQ-7-6, 3317	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	8.52E-08	0.74	2.89	-	596.9
AHQ-7-3, 3411 - 3419	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	4.45E-05	0.90	4.10	-	720.4
AHQ-7-4, 4976 - 4992	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	3.82E-09	0.97	6.12	-	1562.8
AHQ-7-3, 5051	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.79E-06	0.94	4.26	-	1147.4
AHQ-7-3, 4673 - 4747	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.75E-07	0.90	4.48	-	732.9
AHQ-7-1, 4975 - 5036	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	8.53E-06	0.92	4.47	-	722.5
AHQ-7-2, 4760 - 4841	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.44E-07	0.97	6.53	-	1005.2
AHQ-7-2, 4903 - 4984	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	8.11E-07	0.97	6.07	-	1106.7
AHQ-7-3, 4787 - 4859	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	7.61E-10	0.92	4.45	-	745.8
AHQ-7-4, 4866 - 4922	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.67E-04	0.94	4.77	-	853.0
AHQ-7-2, 5044 - 5111	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	7.96E-08	0.96	5.05	-	1520.3
AHQ-7-5, 4847 - 4910	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	7.58E-12	0.97	5.71	-	1390.1
AHQ-7-2, 5173	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.36E-11	0.88	3.67	-	873.6
AHQ-7-1, 2524	K.GTVEPQLEAR.G	1100.20741	2	2.21E-05	0.79	2.76	-	580.2
AHQ-7-2, 2339 - 2403	K.GTVEPQLEAR.G	1100.20741	2	1.70E-05	0.88	3.17	-	755.0
AHQ-7-4, 2261 - 2292	K.GTVEPQLEAR.G	1100.20741	2	2.96E-04	0.83	3.07	-	538.2
AHQ-7-3, 2312 - 2336	K.GTVEPQLEAR.G	1100.20741	2	1.55E-06	0.67	2.91	-	520.0
AHQ-7-3, 5420 - 5433	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	2.38E-05	0.97	5.00	-	1195.3
AHQ-7-2, 5544	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	3	6.40E-04	0.87	4.54	-	796.5
AHQ-7-2, 5539	K.HTAMVSWGGVSIPNSPFR.V	1944.20601	2	7.06E-06	0.97	5.03	-	1349.8
AHQ-7-3, 5095 - 5099	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	6.05E-06	0.95	4.74	-	1148.5
AHQ-7-2, 5204	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	1.45E-04	0.71	3.48	-	677.7
AHQ-7-1, 5111 - 5113	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	6.10E-06	0.97	5.26	-	1250.3
AHQ-7-1, 5107	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	6.60E-04	0.86	4.45	-	589.3
AHQ-7-2, 5200 - 5209	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	4.41E-04	0.97	5.06	-	1606.6
AHQ-7-6, 4146 - 4219	R.IANLQTDLSDGLR.L	1416.56231	2	1.56E-06	0.94	3.95	-	1182.2
AHQ-7-1, 4291	R.IANLQTDLSDGLR.L	1416.56231	2	6.47E-07	0.94	4.00	-	940.9
AHQ-7-5, 3823 - 3839	R.IANLQTDLSDGLR.L	1416.56231	2	1.43E-06	0.95	4.41	-	1067.9
AHQ-7-8, 4111	R.IANLQTDLSDGLR.L	1416.56231	2	2.15E-05	0.72	2.99	-	691.3
AHQ-7-2, 3931 - 3941	R.IANLQTDLSDGLR.L	1416.56231	2	1.59E-06	0.95	4.17	-	1326.1
AHQ-7-2, 4319 - 4387	R.IANLQTDLSDGLR.L	1416.56231	2	1.28E-05	0.90	3.61	-	927.4
AHQ-7-7, 3720	R.IANLQTDLSDGLR.L	1416.56231	2	5.26E-05	0.89	3.62	-	879.0
AHQ-7-5, 4215 - 4235	R.IANLQTDLSDGLR.L	1416.56231	2	3.00E-07	0.89	3.31	-	994.6
AHQ-7-2, 4117 - 4195	R.IANLQTDLSDGLR.L	1416.56231	2	3.70E-07	0.96	4.51	-	1362.0
AHQ-7-11, 3958 - 3966	R.IANLQTDLSDGLR.L	1416.56231	2	2.22E-04	0.95	4.69	-	877.0
AHQ-7-2, 4033	R.IANLQTDLSDGLR.L	1416.56231	2	4.76E-08	0.94	4.13	-	1044.9
AHQ-7-12, 3986	R.IANLQTDLSDGLR.L	1416.56231	2	1.78E-04	0.87	3.03	-	833.6
AHQ-7-7, 4060	R.IANLQTDLSDGLR.L	1416.56231	2	6.36E-06	0.94	4.40	-	846.6
AHQ-7-10, 3892	R.IANLQTDLSDGLR.L	1416.56231	2	4.81E-05	0.89	3.15	-	1085.1
AHQ-7-4, 4256	R.IANLQTDLSDGLR.L	1416.56231	2	6.77E-06	0.96	4.41	-	1313.1
AHQ-7-3, 4239	R.IANLQTDLSDGLR.L	1416.56231	2	9.92E-07	0.93	3.62	-	1044.4
AHQ-7-4, 3876	R.IANLQTDLSDGLR.L	1416.56231	2	1.23E-05	0.93	4.00	-	1172.1
AHQ-7-3, 3844	R.IANLQTDLSDGLR.L	1416.56231	2	5.32E-07	0.95	4.29	-	1333.0
AHQ-7-4, 3962	R.IANLQTDLSDGLR.L	1416.56231	2	1.10E-05	0.75	2.67	-	705.7
AHQ-7-6, 3750	R.IANLQTDLSDGLR.L	1416.56231	2	8.03E-07	0.85	3.10	-	748.4
AHQ-7-9, 3809 - 3826	R.IANLQTDLSDGLR.L	1416.56231	2	3.40E-04	0.80	2.57	-	776.0
AHQ-7-13-, 4108	R.IANLQTDLSDGLR.L	1416.56231	2	4.00E-07	0.95	4.52	-	933.6
AHQ-7-1, 3931	R.IANLQTDLSDGLR.L	1416.56231	2	2.08E-04	0.77	2.97	-	721.9
AHQ-7-3, 4099	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	8.41E-04	0.91	3.85	-	901.8
AHQ-7-4, 4122 - 4153	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	8.88E-06	0.96	4.45	-	1865.4

AHQ-7-5, 5403	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	1.29E-04	0.93	4.55	-	1078.3
AHQ-7-4, 5492	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	1.85E-05	0.89	4.33	-	872.6
AHQ-7-6, 5342	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	6.01E-07	0.89	4.36	-	773.6
AHQ-7-3, 5369 - 5396	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.83E-04	0.89	4.08	-	894.4
AHQ-7-6, 4015	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	3.05E-08	0.97	4.89	-	1839.5
AHQ-7-2, 5491	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.00E-05	0.97	5.19	-	1258.6
AHQ-7-1, 5351	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	1.95E-05	0.90	4.60	-	822.4
AHQ-7-4, 5480	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.65E-07	0.97	5.08	-	1579.0
AHQ-7-6, 5319	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.02E-11	0.97	5.03	-	1540.3
AHQ-7-1, 5336	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.37E-08	0.97	4.86	-	1616.4
AHQ-7-5, 5390	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.84E-09	0.98	5.50	-	1831.3
AHQ-7-8, 3932 - 4006	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	9.49E-06	0.95	4.16	-	1346.6
AHQ-7-7, 5278 - 5292	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.94E-10	0.97	5.27	-	1660.2
AHQ-7-7, 3964	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.40E-08	0.97	5.08	-	1539.6
AHQ-7-7, 5301	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	6.69E-07	0.95	5.30	-	1050.8
AHQ-7-2, 4237	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.32E-04	0.96	5.00	-	1210.6
AHQ-7-5, 4070 - 4134	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	5.37E-07	0.98	5.03	-	1986.7
AHQ-7-1, 4129 - 4188	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.90E-09	0.97	5.01	-	1761.8
AHQ-7-8, 5248	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.58E-10	0.97	5.09	-	1607.9
AHQ-7-1, 4153 - 4233	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.15E-07	0.97	5.15	-	1491.0
AHQ-7-5, 2579	K.IVGPSGAAVPCK.V	1157.36530	2	1.51E-06	0.81	3.03	-	669.7
AHQ-7-2, 2627 - 2631	K.IVGPSGAAVPCK.V	1157.36530	2	7.99E-09	0.92	3.71	-	848.3
AHQ-7-4, 2546 - 2613	K.IVGPSGAAVPCK.V	1157.36530	2	8.59E-06	0.68	2.95	-	466.3
AHQ-7-1, 2795	K.IVGPSGAAVPCK.V	1157.36530	2	7.39E-05	0.78	2.64	-	689.3
AHQ-7-3, 2595	K.IVGPSGAAVPCK.V	1157.36530	2	6.93E-05	0.81	2.84	-	856.0
AHQ-7-2, 4244 - 4251	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	3.27E-06	0.95	5.17	-	610.1
AHQ-7-4, 4289	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.08E-06	0.89	4.06	-	974.3
AHQ-7-2, 4364	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	8.23E-09	0.66	3.20	-	624.5
AHQ-7-2, 4365	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	2.25E-04	0.90	4.11	-	454.8
AHQ-7-1, 4207 - 4263	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	4.10E-05	0.95	4.60	-	1518.4
AHQ-7-1, 4225 - 4227	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	8.12E-05	0.94	5.67	-	483.3
AHQ-7-4, 4197	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.55E-06	0.80	3.44	-	405.0
AHQ-7-4, 4188	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	7.13E-09	0.85	3.92	-	958.9
AHQ-7-3, 4284	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.06E-06	0.83	3.64	-	936.4
AHQ-7-3, 4273	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	6.57E-06	0.70	2.82	-	380.2
AHQ-7-5, 4139	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.09E-04	0.92	4.80	-	435.1
AHQ-7-3, 4156 - 4220	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.38E-11	0.96	5.91	-	1172.1
AHQ-7-6, 4075	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.11E-06	0.91	4.58	-	1103.5
AHQ-7-1, 4319	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.12E-06	0.86	3.98	-	724.5
AHQ-7-2, 4233 - 4299	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.04E-05	0.92	4.50	-	1091.9
AHQ-7-5, 4136	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	6.76E-06	0.96	5.20	-	1429.4
AHQ-7-6, 4317	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	6.35E-05	0.91	4.06	-	782.2
AHQ-7-1, 4376 - 4449	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	6.28E-05	0.91	4.65	-	1046.3
AHQ-7-5, 4310 - 4384	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	1.54E-06	0.96	5.66	-	1177.1
AHQ-7-1, 4452	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.55E-10	0.97	5.61	-	2285.8
AHQ-7-2, 4417 - 4485	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.74E-06	0.91	4.39	-	1271.6
AHQ-7-6, 4255	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	2.48E-07	0.90	4.18	-	514.4
AHQ-7-5, 4330	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	6.86E-10	0.97	5.37	-	1964.0
AHQ-7-1, 4461	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.13E-08	0.77	2.96	-	692.5
AHQ-7-3, 4383	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.11E-09	0.97	5.65	-	2244.9
AHQ-7-8, 4168	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	3.12E-07	0.92	4.08	-	779.1
AHQ-7-6, 4238	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	6.02E-12	0.96	5.18	-	1539.8
AHQ-7-3, 4384	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	5.30E-04	0.77	3.34	-	444.8
AHQ-7-5, 4326	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	7.64E-07	0.88	3.67	-	717.4
AHQ-7-7, 4177	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	2.84E-04	0.89	3.69	-	749.3
AHQ-7-4, 4377 - 4414	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	6.30E-06	0.91	4.31	-	706.2
AHQ-7-4, 4372	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	9.91E-08	0.97	5.53	-	1671.8
AHQ-7-4, 3584	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.68E-05	0.91	4.35	-	958.8
AHQ-7-3, 3468	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	5.36E-04	0.95	5.04	-	1201.4
AHQ-7-4, 3454	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.00E-06	0.87	4.05	-	951.4
AHQ-7-1, 3627 - 3689	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	5.81E-08	0.93	4.16	-	1288.7
AHQ-7-2, 3539	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	2.25E-09	0.96	4.98	-	1121.5
AHQ-7-2, 3647 - 3692	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.44E-08	0.96	4.95	-	1622.1
AHQ-7-3, 3477	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	4.87E-07	0.95	5.26	-	862.3
AHQ-7-3, 3592	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	4.89E-05	0.91	3.94	-	739.4
AHQ-7-3, 3952	K.LDVQFSGLTK.G	1108.26945	2	3.67E-04	0.93	3.90	-	1118.3
AHQ-7-1, 4040	K.LDVQFSGLTK.G	1108.26945	2	4.37E-05	0.90	3.34	-	903.1
AHQ-7-4, 3968	K.LDVQFSGLTK.G	1108.26945	2	4.02E-05	0.91	3.51	-	946.0
AHQ-7-2, 4031 - 4045	K.LDVQFSGLTK.G	1108.26945	2	4.98E-05	0.92	4.06	-	799.8
AHQ-7-2, 6639	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	1.74E-06	0.95	4.87	-	1376.7
AHQ-7-1, 6392	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	7.89E-06	0.93	4.75	-	1027.3
AHQ-7-4, 5090	K.LPQLPITNFSR.D	1286.50461	2	3.72E-05	0.89	3.20	-	726.5
AHQ-7-3, 5003	K.LPQLPITNFSR.D	1286.50461	2	7.51E-08	0.90	3.02	-	841.4
AHQ-7-10, 4381	K.LPQLPITNFSR.D	1286.50461	2	6.77E-05	0.79	2.52	-	620.2
AHQ-7-2, 4900 - 4901	K.LPQLPITNFSR.D	1286.50461	2	2.02E-06	0.92	3.24	-	1058.4
AHQ-7-2, 5100 - 5116	K.LPQLPITNFSR.D	1286.50461	2	1.06E-05	0.81	2.98	-	603.0
AHQ-7-4, 4873	K.LPQLPITNFSR.D	1286.50461	2	6.06E-04	0.83	2.79	-	630.1
AHQ-7-3, 5265 - 5276	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.29E-06	0.94	4.60	-	1035.3
AHQ-7-2, 5332 - 5395	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	9.99E-07	0.91	4.13	-	752.8
AHQ-7-2, 5341 - 5403	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.45E-13	0.98	6.47	-	2139.8
AHQ-7-7, 5224 - 5233	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.20E-07	0.95	4.89	-	953.5
AHQ-7-2, 5468 - 5531	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.56E-09	0.90	4.65	-	466.2
AHQ-7-4, 5413	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.87E-10	0.98	6.41	-	1150.5
AHQ-7-2, 5379	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	9.50E-08	0.92	4.37	-	689.4
AHQ-7-2, 5432 - 5500	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	5.15E-04	0.92	4.54	-	1530.9
AHQ-7-6, 5250	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.49E-05	0.89	3.86	-	581.1
AHQ-7-3, 5241 - 5301	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.10E-12	0.98	7.09	-	2106.5
AHQ-7-4, 3266	R.LRNGHVGISFVPK.E	1424.67564	3	3.62E-05	0.90	3.29	-	1504.2
AHQ-7-5, 2967	R.LRNGHVGISFVPK.E	1424.67564	3	2.89E-04	0.92	3.45	-	1548.3
AHQ-7-6, 3170	R.LRNGHVGISFVPK.E	1424.67564	2	1.97E-05	0.71	2.53	-	718.3
AHQ-7-4, 3124	R.LRNGHVGISFVPK.E	1424.67564	2	1.72E-04	0.86	2.80	-	784.7
AHQ-7-1, 3443	R.LRNGHVGISFVPK.E	1424.67564	3	3.95E-05	0.88	3.21	-	1600.0
AHQ-7-2, 4147 - 4164	R.LSPFMADIR.D	1050.25664	2	4.89E-04	0.74	2.57	-	516.4
AHQ-7-5, 4038	R.LSPFMADIR.D	1050.25664	2	1.31E-05	0.84	2.61	-	660.0
AHQ-7-3, 4075	R.LSPFMADIR.D	1050.25664	2	2.48E-04	0.73	2.57	-	586.4
AHQ-7-5, 3546	R.LTVSSLQESGLK.V	1262.43499	2	1.34E-04	0.66	2.56	-	850.3
AHQ-7-4, 3484 - 3500	R.LTVSSLQESGLK.V	1262.43499	2	4.77E-04	0.94	3.66	-	1137.8
AHQ-7-1, 3553 - 3623	R.LTVSSLQESGLK.V	1262.43499	2	2.75E-05	0.72	2.51	-	544.2
AHQ-7-5, 3440 - 3470	R.LTVSSLQESGLK.V	1262.43499	2	2.70E-07	0.90	3.18	-	938.4
AHQ-7-6, 3407 - 3475	R.LTVSSLQESGLK.V	1262.43499	2	2.58E-06	0.71	2.97	-	520.8
AHQ-7-4, 4476	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.19E-09	0.96	5.21	-	1461.9
AHQ-7-6, 4354	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.82E-10	0.95	4.65	-	1096.4
AHQ-7-1, 4537	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	9.16E-14	0.91	3.99	-	967.8
AHQ-7-1, 4287	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.05E-07	0.97	5.95	-	1016.3
AHQ-7-13-, 4305	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.30E-09	0.93	4.30	-	1025.5
AHQ-7-9, 3757	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	9.15E-08	0.47	2.58	-	451.9
AHQ-7-5, 4402	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	5.11E-10	0.97	5.26	-	1697.2

AHQ-7-5, 4408	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.84E-08	0.96	5.14	-	1038.4
AHQ-7-7, 3990	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.37E-07	0.96	4.78	-	1259.7
AHQ-7-6, 4087 - 4151	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	9.14E-04	0.92	4.25	-	977.9
AHQ-7-4, 4186	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.86E-05	0.96	5.12	-	1171.2
AHQ-7-4, 4478	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.64E-08	0.97	5.40	-	1702.5
AHQ-7-4, 4181	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.40E-07	0.96	5.37	-	1074.7
AHQ-7-5, 4146	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.42E-07	0.97	5.53	-	1162.9
AHQ-7-10, 3852	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.95E-06	0.96	4.29	-	2045.8
AHQ-7-1, 4284	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.60E-08	0.96	4.44	-	1854.5
AHQ-7-5, 4143 - 4214	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.77E-05	0.95	4.96	-	1257.6
AHQ-7-11, 3923	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	6.80E-07	0.94	4.49	-	1094.1
AHQ-7-3, 4476	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	5.81E-09	0.97	5.03	-	1588.1
AHQ-7-4, 4617	R.LYSVSYLLK.D	1086.30538	2	1.08E-05	0.76	2.82	-	492.1
AHQ-7-4, 2492 - 2493	K.MDCQECPEGYR.V	1447.55375	2	7.52E-05	0.89	3.73	-	717.6
AHQ-7-5, 2214	K.M*DCQECPEGYR.V	1463.55315	2	3.86E-08	0.95	3.97	-	1127.6
AHQ-7-4, 2234	K.M*DCQECPEGYR.V	1463.55315	2	5.23E-07	0.95	3.89	-	1507.7
AHQ-7-1, 4721	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	3.15E-05	0.90	3.90	-	1275.5
AHQ-7-4, 4742	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	6.23E-04	0.91	3.92	-	1733.8
AHQ-7-1, 4737	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	2.29E-06	0.88	3.62	-	751.9
AHQ-7-5, 4816	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	1.17E-05	0.95	4.49	-	1019.6
AHQ-7-4, 4886	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	2.25E-05	0.95	4.56	-	945.2
AHQ-7-5, 4660	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	5.76E-05	0.97	5.27	-	1531.5
AHQ-7-4, 4736	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	1.05E-06	0.93	3.74	-	1325.8
AHQ-7-6, 2085	K.RAEFTVETR.S	1109.21754	2	2.28E-05	0.90	3.13	-	1060.0
AHQ-7-3, 2152 - 2153	K.RAEFTVETR.S	1109.21754	2	2.64E-06	0.92	3.28	-	894.8
AHQ-7-5, 2056 - 2068	K.RAEFTVETR.S	1109.21754	2	2.58E-06	0.95	3.71	-	1009.7
AHQ-7-4, 2098	K.RAEFTVETR.S	1109.21754	2	6.36E-05	0.87	2.78	-	814.7
AHQ-7-7, 2040	K.RAEFTVETR.S	1109.21754	2	2.73E-06	0.91	3.33	-	946.8
AHQ-7-2, 2155	K.RAEFTVETR.S	1109.21754	2	1.07E-05	0.95	3.65	-	1159.9
AHQ-7-4, 3109 - 3110	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	8.11E-07	0.97	5.68	-	1999.8
AHQ-7-6, 3065 - 3067	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	6.27E-04	0.97	5.49	-	1784.7
AHQ-7-5, 3083	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	1.12E-04	0.97	5.38	-	1958.2
AHQ-7-4, 3120	R.RAPSVANVGSHCDLSLK.I	1813.02884	2	2.43E-05	0.96	4.51	-	1207.6
AHQ-7-1, 3329	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	6.47E-06	0.98	5.50	-	2293.3
AHQ-7-2, 3965	K.RIANLQTDLSDGLR.L	1572.74866	2	1.80E-06	0.86	3.54	-	620.3
AHQ-7-1, 3985	K.RIANLQTDLSDGLR.L	1572.74866	2	1.70E-04	0.73	2.89	-	603.3
AHQ-7-3, 3195	R.RLTVSSLQESGLK.V	1418.62134	2	1.24E-04	0.97	4.94	-	1802.1
AHQ-7-5, 3022 - 3096	R.RLTVSSLQESGLK.V	1418.62134	2	1.00E-05	0.97	4.23	-	2145.3
AHQ-7-4, 7030 - 7052	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	1.94E-06	0.87	3.88	-	966.6
AHQ-7-2, 6931 - 6988	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	1.83E-07	0.95	4.15	-	1762.2
AHQ-7-2, 6873 - 6937	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	3.91E-04	0.96	5.73	-	1383.1
AHQ-7-2, 7043	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	2.47E-04	0.86	3.35	-	1092.4
AHQ-7-2, 6932	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	3.28E-06	0.92	3.89	-	1241.8
AHQ-7-1, 4033 - 4113	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.41E-05	0.81	3.30	-	824.8
AHQ-7-3, 3937	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	9.74E-08	0.86	3.87	-	739.7
AHQ-7-8, 3808	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.36E-06	0.92	4.80	-	530.2
AHQ-7-5, 3903	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.46E-07	0.92	4.59	-	638.9
AHQ-7-1, 4035	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.44E-05	0.90	4.43	-	602.1
AHQ-7-2, 4304	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	8.45E-08	0.89	4.12	-	649.4
AHQ-7-7, 3772	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.46E-09	0.90	3.94	-	909.9
AHQ-7-2, 4136	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.31E-07	0.95	5.42	-	762.3
AHQ-7-7, 3769	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.18E-06	0.93	4.96	-	620.0
AHQ-7-2, 4007 - 4072	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	6.15E-08	0.96	5.42	-	1155.1
AHQ-7-2, 4005 - 4071	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	9.92E-06	0.93	4.78	-	669.5
AHQ-7-4, 3934 - 3944	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.78E-09	0.93	4.36	-	1150.5
AHQ-7-6, 3825	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.87E-07	0.92	4.54	-	666.6
AHQ-7-4, 3933	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.74E-09	0.94	4.72	-	802.4
AHQ-7-3, 3935 - 3995	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.14E-06	0.93	4.64	-	711.3
AHQ-7-13-, 3844	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.22E-10	0.79	3.75	-	911.8
AHQ-7-6, 3829	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.72E-05	0.93	4.30	-	1566.5
AHQ-7-5, 3904 - 3928	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	4.70E-08	0.86	3.59	-	988.1
AHQ-7-6, 3919	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.21E-04	0.42	2.73	-	221.7
AHQ-7-5, 3399	K.SPFEVYVDK.S	1084.20321	1	5.29E-04	0.67	2.18	-	905.7
AHQ-7-3, 3461	K.SPFEVYVDK.S	1084.20321	1	4.15E-04	0.80	2.85	-	891.2
AHQ-7-4, 3420	K.SPFEVYVDK.S	1084.20321	2	2.01E-05	0.92	3.40	-	975.9
AHQ-7-2, 3491	K.SPFEVYVDK.S	1084.20321	1	2.35E-04	0.58	2.10	-	916.8
AHQ-7-2, 3492 - 3511	K.SPFEVYVDK.S	1084.20321	2	1.23E-06	0.94	3.85	-	1130.7
AHQ-7-3, 3459	K.SPFEVYVDK.S	1084.20321	2	3.85E-06	0.91	3.46	-	987.0
AHQ-7-4, 3370 - 3440	K.SPFEVYVDK.S	1084.20321	1	9.09E-06	0.76	2.69	-	992.7
AHQ-7-6, 3354	K.SPFEVYVDK.S	1084.20321	2	6.00E-05	0.76	2.75	-	860.9
AHQ-7-5, 3398 - 3414	K.SPFEVYVDK.S	1084.20321	2	7.13E-06	0.93	3.24	-	1149.9
AHQ-7-2, 3497	K.SPFEVYVDK.S	1084.20321	1	5.11E-04	0.79	2.80	-	784.3
AHQ-7-3, 3455	K.SPFEVYVDK.S	1084.20321	1	3.40E-04	0.59	2.26	-	828.0
AHQ-7-2, 3188	K.SPFEVYVDKSQGDASK.V	1757.87886	2	1.32E-04	0.95	4.27	-	1133.4
AHQ-7-2, 4923 - 4983	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.02E-04	0.86	3.57	-	677.0
AHQ-7-3, 4833 - 4903	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.26E-06	0.93	3.79	-	969.3
AHQ-7-1, 4828 - 4888	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.31E-07	0.91	3.85	-	1059.3
AHQ-7-5, 4894 - 4898	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.96E-08	0.93	3.95	-	1028.0
AHQ-7-2, 4817	K.SPFSVAVSPSLDLSK.I	1534.73557	2	5.55E-07	0.85	3.67	-	622.2
AHQ-7-3, 4727	K.SPFSVAVSPSLDLSK.I	1534.73557	2	4.05E-04	0.83	3.65	-	565.1
AHQ-7-1, 4711 - 4755	K.SPFSVAVSPSLDLSK.I	1534.73557	2	6.95E-04	0.91	3.67	-	1012.1
AHQ-7-4, 4772	K.SPFSVAVSPSLDLSK.I	1534.73557	2	4.52E-04	0.53	2.82	-	472.4
AHQ-7-2, 3483 - 3551	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.38E-05	0.84	3.45	-	494.4
AHQ-7-1, 3525 - 3583	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.36E-05	0.93	4.54	-	616.2
AHQ-7-5, 3415	R.SPYTVTVGQACNPSACR.A	1871.04208	2	3.82E-04	0.94	4.69	-	675.7
AHQ-7-1, 3711	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.88E-08	0.78	3.20	-	467.0
AHQ-7-6, 3361	R.SPYTVTVGQACNPSACR.A	1871.04208	2	6.13E-05	0.81	3.12	-	481.2
AHQ-7-4, 2214	K.SSFTVDCSK.A	1032.10676	1	2.02E-05	0.30	2.06	-	423.4
AHQ-7-2, 5077 - 5080	R.TFSVWYVPEVTGTHK.V	1751.96228	3	9.67E-05	0.64	3.14	-	462.2
AHQ-7-1, 5029 - 5039	R.TFSVWYVPEVTGTHK.V	1751.96228	2	2.70E-04	0.80	2.87	-	623.2
AHQ-7-1, 3300	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	2.29E-05	0.91	4.06	-	678.4
AHQ-7-2, 3183 - 3240	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	4.93E-06	0.93	4.78	-	655.4
AHQ-7-2, 3245 - 3320	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	4.27E-04	0.73	3.45	-	486.0
AHQ-7-2, 3173 - 3196	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.40E-07	0.94	4.27	-	988.0
AHQ-7-3, 3156	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	7.79E-05	0.83	3.15	-	885.3
AHQ-7-4, 3108	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	4.15E-06	0.89	3.39	-	1240.5
AHQ-7-5, 3070	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	6.07E-04	0.78	3.35	-	581.0
AHQ-7-5, 3071	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.86E-09	0.92	3.63	-	1129.6
AHQ-7-6, 3055	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	1.68E-04	0.92	3.92	-	859.1
AHQ-7-2, 3105 - 3171	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	2.28E-06	0.89	4.13	-	709.7
AHQ-7-6, 3057	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	3.71E-08	0.75	3.12	-	597.6
AHQ-7-1, 3304	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	7.84E-06	0.93	3.99	-	1213.9
AHQ-7-1, 3184 - 3253	R.TGVELGKPTHFTVNAK.A	1699.93205	2	9.87E-04	0.92	4.27	-	701.1
AHQ-7-3, 3011 - 3083	R.TGVELGKPTHFTVNAK.A	1699.93205	2	3.09E-05	0.89	3.63	-	693.9
AHQ-7-4, 2925	R.TGVELGKPTHFTVNAK.A	1699.93205	2	7.30E-05	0.90	4.18	-	597.4
AHQ-7-1, 3252	R.TGVELGKPTHFTVNAK.A	1699.93205	3	1.68E-04	0.78	3.38	-	732.9
AHQ-7-4, 3034	R.TGVELGKPTHFTVNAK.A	1699.93205	2	9.54E-05	0.81	3.07	-	642.6

AHQ-7-6, 3181	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.93E-07	0.95	4.40	-	978.7
AHQ-7-5, 3074 - 3076	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.02E-05	0.95	4.54	-	1321.9
AHQ-7-6, 3062	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.24E-05	0.91	4.26	-	825.5
AHQ-7-4, 3105	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.11E-07	0.95	4.98	-	1183.1
AHQ-7-8, 3004	K.THEAEIVEGENHTYCIR.F	2060.19046	2	1.35E-12	0.98	5.93	-	2069.1
AHQ-7-5, 3222	K.THEAEIVEGENHTYCIR.F	2060.19046	3	3.97E-08	0.88	3.99	-	805.8
AHQ-7-2, 3252	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.49E-09	0.92	3.92	-	1397.6
AHQ-7-4, 3254	K.THEAEIVEGENHTYCIR.F	2060.19046	2	3.70E-12	0.98	5.71	-	1864.9
AHQ-7-4, 3246	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.48E-07	0.89	3.64	-	1280.3
AHQ-7-1, 3308	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.78E-08	0.97	5.27	-	1558.8
AHQ-7-1, 3307	K.THEAEIVEGENHTYCIR.F	2060.19046	3	3.63E-04	0.95	4.60	-	1316.1
AHQ-7-5, 3216	K.THEAEIVEGENHTYCIR.F	2060.19046	2	3.92E-10	0.98	4.85	-	2272.3
AHQ-7-2, 3831 - 3908	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	3	1.33E-05	0.93	4.79	-	843.6
AHQ-7-3, 3756	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	2	4.40E-04	0.88	2.99	-	984.9
AHQ-7-4, 3874	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	3	1.22E-04	0.79	3.55	-	680.1
AHQ-7-3, 3212	R.TPCEEILVK.H	1090.27249	2	1.07E-05	0.84	2.92	-	800.0
AHQ-7-14, 4013 - 4064	R.TPCEEILVK.H	1090.27249	2	1.51E-06	0.83	3.12	-	691.7
AHQ-7-4, 3166	R.TPCEEILVK.H	1090.27249	2	1.81E-05	0.75	2.79	-	786.8
AHQ-7-13-, 3147	R.TPCEEILVK.H	1090.27249	2	6.87E-05	0.83	3.52	-	594.9
AHQ-7-1, 3349	R.TPCEEILVK.H	1090.27249	2	4.12E-06	0.82	2.54	-	737.6
AHQ-7-5, 3150	R.TPCEEILVK.H	1090.27249	2	4.11E-06	0.79	2.99	-	540.5
AHQ-7-6, 3119	R.TPCEEILVK.H	1090.27249	2	2.77E-05	0.86	3.12	-	697.8
AHQ-7-7, 3040	R.TPCEEILVK.H	1090.27249	2	2.82E-05	0.71	2.62	-	540.1
AHQ-7-14-, 3137 - 3201	R.TPCEEILVK.H	1090.27249	2	2.21E-04	0.88	3.15	-	861.2
AHQ-7-14-, 3147	R.TPCEEILVK.H	1090.27249	1	1.36E-05	0.28	2.40	-	255.0
AHQ-7-2, 3257 - 3268	R.TPCEEILVK.H	1090.27249	2	5.62E-06	0.87	3.04	-	698.4
AHQ-7-11, 3056	R.TPCEEILVK.H	1090.27249	2	1.19E-04	0.79	3.00	-	706.0
AHQ-7-13, 3317	R.TPCEEILVK.H	1090.27249	2	7.70E-07	0.85	3.35	-	640.3
AHQ-7-1, 3444 - 3524	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.22E-09	0.96	4.58	-	1066.0
AHQ-7-1, 3477	R.VANPSGNLTETYVQDR.G	1764.87462	3	3.47E-04	0.88	3.66	-	978.2
AHQ-7-2, 3637	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.00E-05	0.75	2.61	-	894.6
AHQ-7-5, 3400 - 3468	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.51E-10	0.96	5.01	-	1177.0
AHQ-7-2, 3499 - 3571	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.65E-12	0.95	4.44	-	1110.4
AHQ-7-4, 3429 - 3508	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.12E-09	0.91	3.86	-	963.9
AHQ-7-1, 3601	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.43E-12	0.94	3.90	-	1027.8
AHQ-7-3, 3308 - 3373	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.05E-12	0.92	4.12	-	803.1
AHQ-7-5, 3279	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.24E-10	0.90	3.90	-	636.5
AHQ-7-2, 3367 - 3435	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.46E-10	0.94	4.38	-	884.3
AHQ-7-8, 3220 - 3223	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.11E-04	0.93	4.33	-	758.9
AHQ-7-2, 3229 - 3300	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.36E-08	0.92	3.92	-	881.1
AHQ-7-3, 3435 - 3503	R.VANPSGNLTETYVQDR.G	1764.87462	2	9.98E-13	0.96	4.57	-	1058.5
AHQ-7-6, 3242	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.32E-12	0.89	3.94	-	544.7
AHQ-7-6, 3343	R.VANPSGNLTETYVQDR.G	1764.87462	2	9.67E-10	0.92	3.96	-	808.3
AHQ-7-7, 3188	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.18E-08	0.89	3.59	-	800.3
AHQ-7-3, 2920	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.15E-04	0.84	3.72	-	464.0
AHQ-7-1, 2888	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	9.56E-06	0.84	3.23	-	633.4
AHQ-7-1, 3057	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.20E-08	0.83	3.27	-	764.5
AHQ-7-2, 2959	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.97E-04	0.82	3.48	-	502.2
AHQ-7-4, 2604 - 2661	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.95E-04	0.88	3.67	-	699.3
AHQ-7-5, 2822 - 2866	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.10E-07	0.93	4.71	-	775.5
AHQ-7-6, 2833	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.81E-08	0.76	3.26	-	416.7
AHQ-7-8, 2576	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.45E-06	0.82	3.32	-	531.7
AHQ-7-4, 2828	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.13E-07	0.89	4.02	-	548.3
AHQ-7-5, 2634	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	6.51E-07	0.89	3.77	-	706.0
AHQ-7-11, 2820	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.71E-04	0.64	2.76	-	429.6
AHQ-7-4, 3680 - 3694	K.VDINTEDLEDGTCR.V	1638.69283	2	8.71E-06	0.94	3.50	-	1246.9
AHQ-7-4, 3320	K.VDINTEDLEDGTCR.V	1638.69283	2	3.85E-06	0.91	3.92	-	1057.8
AHQ-7-5, 3280	K.VDINTEDLEDGTCR.V	1638.69283	2	1.15E-05	0.91	3.45	-	970.5
AHQ-7-13, 3635	K.VDINTEDLEDGTCR.V	1638.69283	2	2.29E-07	0.70	2.69	-	722.1
AHQ-7-7, 3473	K.VDINTEDLEDGTCR.V	1638.69283	2	1.99E-05	0.87	3.05	-	1086.9
AHQ-7-3, 3317	K.VDINTEDLEDGTCR.V	1638.69283	2	1.29E-04	0.83	2.98	-	840.3
AHQ-7-3, 3579 - 3580	K.VDINTEDLEDGTCR.V	1638.69283	2	3.66E-06	0.94	3.85	-	1302.7
AHQ-7-13-, 3476	K.VDINTEDLEDGTCR.V	1638.69283	2	2.46E-04	0.89	3.42	-	1184.3
AHQ-7-8, 3242	K.VDINTEDLEDGTCR.V	1638.69283	2	7.56E-06	0.84	3.19	-	869.8
AHQ-7-5, 3372	K.VDINTEDLEDGTCR.V	1638.69283	2	4.04E-06	0.90	3.79	-	859.0
AHQ-7-2, 3659	K.VDINTEDLEDGTCR.V	1638.69283	2	1.13E-06	0.93	3.23	-	1457.7
AHQ-7-1, 3419 - 3421	K.VDINTEDLEDGTCR.V	1638.69283	2	9.23E-06	0.94	4.13	-	1220.0
AHQ-7-6, 3246	K.VDINTEDLEDGTCR.V	1638.69283	2	1.20E-09	0.86	3.57	-	733.2
AHQ-7-1, 3671 - 3745	K.VDINTEDLEDGTCR.V	1638.69283	2	1.22E-08	0.93	3.66	-	1228.9
AHQ-7-8, 3372 - 3447	K.VDINTEDLEDGTCR.V	1638.69283	2	2.83E-06	0.89	3.58	-	1053.3
AHQ-7-3, 2664	K.VDVGKDQEFTVK.S	1365.51377	1	8.48E-08	0.44	2.91	-	315.4
AHQ-7-7, 2532	K.VDVGKDQEFTVK.S	1365.51377	2	5.98E-05	0.74	2.94	-	629.0
AHQ-7-4, 2617	K.VDVGKDQEFTVK.S	1365.51377	2	5.99E-07	0.87	3.42	-	556.0
AHQ-7-1, 2855	K.VDVGKDQEFTVK.S	1365.51377	2	1.91E-08	0.93	3.69	-	962.5
AHQ-7-3, 2644	K.VDVGKDQEFTVK.S	1365.51377	2	5.99E-09	0.85	3.18	-	745.1
AHQ-7-4, 2629	K.VDVGKDQEFTVK.S	1365.51377	1	6.98E-05	0.38	2.57	-	288.3
AHQ-7-2, 2667 - 2681	K.VDVGKDQEFTVK.S	1365.51377	2	4.45E-10	0.90	3.89	-	670.7
AHQ-7-3, 2796 - 2865	K.VEPGLGADNSVVR.F	1313.44209	2	1.34E-04	0.62	2.62	-	205.4
AHQ-7-3, 2961 - 2965	K.VEPGLGADNSVVR.F	1313.44209	2	1.04E-06	0.65	2.55	-	169.6
AHQ-7-1, 3117	K.VEPGLGADNSVVR.F	1313.44209	2	1.80E-04	0.78	2.58	-	431.0
AHQ-7-2, 2811 - 2880	K.VEPGLGADNSVVR.F	1313.44209	2	7.48E-09	0.85	3.22	-	408.4
AHQ-7-3, 2801 - 2803	K.VEPGLGADNSVVR.F	1313.44209	1	8.27E-05	0.22	2.34	-	177.1
AHQ-7-4, 2758	K.VEPGLGADNSVVR.F	1313.44209	2	7.14E-07	0.76	2.81	-	311.6
AHQ-7-1, 2983	K.VEPGLGADNSVVR.F	1313.44209	2	1.19E-07	0.92	3.60	-	553.2
AHQ-7-6, 5929 - 5990	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	6.66E-06	0.93	5.82	-	569.8
AHQ-7-5, 6018 - 6090	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.01E-07	0.93	5.98	-	678.6
AHQ-7-3, 6679	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.25E-04	0.69	3.13	-	561.3
AHQ-7-9, 6114	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	6.04E-04	0.58	2.77	-	525.1
AHQ-7-5, 6791	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	3.04E-04	0.81	3.42	-	557.0
AHQ-7-1, 6551	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.14E-07	0.95	5.35	-	935.1
AHQ-7-4, 4409 - 4481	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.90E-09	0.97	5.71	-	1299.6
AHQ-7-1, 4459	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	1.45E-06	0.72	3.07	-	974.0
AHQ-7-4, 4404 - 4413	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	6.01E-10	0.97	5.15	-	2367.9
AHQ-7-3, 4332 - 4393	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	2.08E-06	0.94	4.25	-	897.7
AHQ-7-2, 4493	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	3.45E-07	0.88	3.82	-	1255.0
AHQ-7-5, 4354	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.64E-07	0.97	5.43	-	1561.6
AHQ-7-5, 4352 - 4390	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	2.59E-05	0.97	6.63	-	1786.4
AHQ-7-1, 4463	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.75E-11	0.98	5.16	-	3071.8
AHQ-7-6, 4277 - 4282	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	1.36E-05	0.95	4.94	-	1602.9
AHQ-7-4, 4724 - 4732	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.07E-12	0.94	5.27	-	886.9
AHQ-7-4, 4730 - 4737	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	5.81E-09	0.92	4.45	-	987.2
AHQ-7-6, 4617 - 4618	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.43E-10	0.94	4.92	-	787.4
AHQ-7-7, 4542	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	9.62E-09	0.90	4.56	-	594.6
AHQ-7-3, 4728	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.38E-08	0.91	4.88	-	642.4
AHQ-7-8, 4587	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	8.99E-07	0.88	3.87	-	921.4
AHQ-7-2, 4805	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.77E-08	0.83	4.18	-	486.9
AHQ-7-5, 4575 - 4651	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.02E-11	0.95	5.87	-	704.5

AHQ-7-1, 4759	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	5.84E-11	0.92	4.68	-	778.2
AHQ-7-5, 4683	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	1.54E-09	0.92	4.36	-	911.6
AHQ-7-7, 3774	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.49E-07	0.84	3.40	-	469.1
AHQ-7-2, 3833 - 3903	K.VNQPASFAVSLNGAK.G	1503.68480	2	7.66E-09	0.91	4.20	-	644.0
AHQ-7-1, 3975 - 4055	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.76E-05	0.47	2.86	-	291.0
AHQ-7-3, 3751 - 3812	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.03E-04	0.92	4.31	-	647.6
AHQ-7-5, 3842 - 3902	K.VNQPASFAVSLNGAK.G	1503.68480	2	7.98E-08	0.92	3.80	-	747.5
AHQ-7-6, 3649 - 3713	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.01E-09	0.83	3.34	-	573.0
AHQ-7-3, 3933 - 3955	K.VNQPASFAVSLNGAK.G	1503.68480	2	6.61E-07	0.71	3.15	-	498.2
AHQ-7-5, 3714 - 3778	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.66E-08	0.94	4.50	-	755.8
AHQ-7-1, 3805 - 3863	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.28E-10	0.87	3.56	-	614.2
AHQ-7-8, 3547	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.59E-05	0.82	3.37	-	428.6
AHQ-7-7, 3584 - 3649	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.05E-05	0.70	3.12	-	387.6
AHQ-7-4, 3748 - 3821	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.21E-10	0.94	4.48	-	682.6
AHQ-7-4, 3836 - 3900	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.28E-08	0.81	3.47	-	518.7
AHQ-7-2, 1721 - 1784	K.VPVHDVTDASK.V	1168.28175	2	7.92E-08	0.94	3.02	-	1502.9
AHQ-7-3, 1753 - 1807	K.VPVHDVTDASK.V	1168.28175	2	1.65E-04	0.91	3.23	-	1027.2
AHQ-7-6, 1679	K.VPVHDVTDASK.V	1168.28175	2	3.39E-07	0.94	3.52	-	1113.4
AHQ-7-5, 1654	K.VPVHDVTDASK.V	1168.28175	2	2.26E-06	0.91	3.13	-	943.0
AHQ-7-4, 1693 - 1701	K.VPVHDVTDASK.V	1168.28175	2	4.03E-05	0.83	2.83	-	725.4
AHQ-7-2, 4185 - 4192	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.21E-06	0.96	5.05	-	1316.9
AHQ-7-2, 4281 - 4311	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.33E-10	0.96	4.68	-	1473.2
AHQ-7-3, 4195 - 4261	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.89E-04	0.91	4.10	-	922.5
AHQ-7-3, 4111	R.VQVQDNEGCPVEALVK.D	1786.98493	2	2.84E-06	0.96	4.85	-	1322.0
AHQ-7-6, 4033 - 4114	R.VQVQDNEGCPVEALVK.D	1786.98493	2	8.28E-04	0.91	3.70	-	1073.1
AHQ-7-2, 4375	R.VQVQDNEGCPVEALVK.D	1786.98493	2	5.83E-05	0.89	3.90	-	958.3
AHQ-7-1, 4183 - 4255	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.56E-08	0.96	5.05	-	1251.9
AHQ-7-4, 4241	R.VQVQDNEGCPVEALVK.D	1786.98493	2	7.00E-08	0.88	3.80	-	854.6
AHQ-7-4, 4137	R.VQVQDNEGCPVEALVK.D	1786.98493	2	7.42E-05	0.96	4.57	-	1284.6
AHQ-7-1, 5136 - 5196	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	3.56E-07	0.96	5.57	-	1645.7
AHQ-7-3, 5149 - 5207	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.66E-08	0.84	3.70	-	1341.6
AHQ-7-5, 5230	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	3.45E-07	0.66	3.14	-	775.2
AHQ-7-2, 5301 - 5380	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	6.22E-08	0.78	3.34	-	955.2
AHQ-7-4, 5098 - 5160	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	5.80E-06	0.89	3.65	-	1666.8
AHQ-7-3, 5027 - 5087	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	7.80E-09	0.93	4.65	-	1465.5
AHQ-7-2, 5025 - 5104	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	4.52E-08	0.95	5.00	-	1488.3
AHQ-7-2, 4893	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	2.84E-04	0.85	3.73	-	732.3
AHQ-7-7, 4570	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.55E-08	0.96	5.56	-	1135.5
AHQ-7-6, 4653	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.28E-06	0.97	6.07	-	1460.3
AHQ-7-2, 4887 - 4899	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.13E-08	0.93	4.63	-	1117.5
AHQ-7-1, 4856 - 4860	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	3.69E-05	0.94	4.88	-	766.9
AHQ-7-1, 4851	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	9.02E-08	0.96	5.39	-	1298.2
AHQ-7-8, 4615 - 4628	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.18E-11	0.96	5.67	-	1134.5
AHQ-7-3, 4800 - 4808	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.18E-08	0.96	5.36	-	1658.1
AHQ-7-4, 4784 - 4813	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	3.16E-08	0.95	5.10	-	1243.4
AHQ-7-6, 4655	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	4.12E-05	0.93	4.22	-	877.6
AHQ-7-5, 4698 - 4731	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.37E-09	0.97	6.03	-	1702.5
AHQ-7-5, 4703	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	1.90E-09	0.96	5.60	-	724.4
AHQ-7-4, 4782 - 4821	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	4.95E-05	0.93	4.51	-	683.6
AHQ-7-2, 2779 - 2847	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	5.76E-08	0.77	3.54	-	414.0
AHQ-7-3, 2743 - 2808	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	5.11E-05	0.85	4.16	-	450.0
AHQ-7-1, 2951 - 3013	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.46E-06	0.65	3.05	-	383.7
AHQ-7-5, 2782 - 2792	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.63E-06	0.91	4.57	-	573.4
AHQ-7-2, 2912	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.23E-11	0.84	3.97	-	529.2
AHQ-7-3, 2879 - 2880	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.13E-07	0.87	3.91	-	577.9
AHQ-7-6, 2701 - 2766	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.90E-04	0.88	4.06	-	510.5
AHQ-7-5, 2696 - 2727	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	3.32E-05	0.86	3.87	-	626.1
AHQ-7-7, 3110 - 3122	K.VTVLFAGQHIAK.S	1284.53185	2	5.19E-07	0.91	3.25	-	948.8
AHQ-7-1, 3491	K.VTVLFAGQHIAK.S	1284.53185	2	3.04E-06	0.93	4.14	-	991.8
AHQ-7-6, 3223	K.VTVLFAGQHIAK.S	1284.53185	2	2.02E-05	0.93	4.03	-	1001.5
AHQ-7-3, 3331	K.VTVLFAGQHIAK.S	1284.53185	2	4.09E-06	0.94	3.92	-	954.6
AHQ-7-4, 3296	K.VTVLFAGQHIAK.S	1284.53185	1	7.69E-05	0.36	1.90	-	630.5
AHQ-7-5, 3258 - 3322	K.VTVLFAGQHIAK.S	1284.53185	2	1.67E-05	0.89	4.12	-	774.1
AHQ-7-2, 3363	K.VTVLFAGQHIAK.S	1284.53185	2	2.39E-05	0.93	3.96	-	921.2
AHQ-7-1, 4832 - 4885	R.VTYCPTEPGNYIINIK.F	1884.14221	2	5.78E-10	0.83	3.69	-	341.7
AHQ-7-8, 4803 - 4880	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.87E-06	0.77	2.94	-	385.0
AHQ-7-8, 4886 - 4943	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.08E-07	0.93	4.45	-	570.5
AHQ-7-5, 4786 - 4846	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.97E-05	0.92	4.23	-	540.1
AHQ-7-1, 5100	R.VTYCPTEPGNYIINIK.F	1884.14221	2	8.56E-09	0.72	3.09	-	351.8
AHQ-7-6, 4925 - 4927	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.59E-04	0.80	3.51	-	359.6
AHQ-7-6, 4781	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.76E-05	0.75	3.26	-	391.4
AHQ-7-4, 4881 - 4892	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.06E-10	0.87	3.52	-	543.9
AHQ-7-3, 4837	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.51E-05	0.77	3.20	-	394.4
AHQ-7-5, 5080 - 5142	R.VTYCPTEPGNYIINIK.F	1884.14221	2	8.15E-09	0.86	3.80	-	523.2
AHQ-7-4, 5197	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.63E-09	0.75	3.22	-	312.9
AHQ-7-2, 5067	R.VTYCPTEPGNYIINIK.F	1884.14221	2	7.45E-04	0.81	3.55	-	405.0
AHQ-7-2, 4924	R.VTYCPTEPGNYIINIK.F	1884.14221	2	9.67E-04	0.50	2.79	-	289.5
AHQ-7-4, 5514 - 5528	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.83E-04	0.76	3.30	-	501.0
AHQ-7-13, 5290	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.56E-05	0.80	3.02	-	595.5
AHQ-7-2, 5547	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.22E-04	0.83	2.76	-	862.5
AHQ-7-13-, 5193	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.06E-05	0.75	3.17	-	387.3
AHQ-7-7, 5293	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.36E-04	0.83	3.40	-	474.1
AHQ-7-7, 5297	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.45E-05	0.54	2.76	-	386.7
AHQ-7-5, 5368 - 5438	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.23E-04	0.91	3.52	-	1026.7
AHQ-7-14-, 5209 - 5215	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.76E-05	0.79	2.99	-	622.6
AHQ-7-3, 1781	K.VYGPGVAK.T	790.92979	1	7.77E-04	0.50	2.13	-	654.7
AHQ-7-8, 3263	R.YAPSEAGLHEMDIR.Y	1589.75482	2	9.26E-05	0.82	3.33	-	691.6
AHQ-7-5, 2608 - 2676	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	4.08E-05	0.91	3.49	-	1030.8
AHQ-7-10, 3204 - 3207	R.YAPSEAGLHEMDIR.Y	1589.75482	2	5.40E-04	0.55	2.54	-	471.6
AHQ-7-10, 2595	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	6.81E-04	0.59	2.52	-	605.8
AHQ-7-4, 2692 - 2693	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	7.73E-04	0.84	3.14	-	799.5
AHQ-7-3, 3460	R.YAPSEAGLHEMDIR.Y	1589.75482	2	2.73E-04	0.90	3.45	-	916.0
AHQ-7-3, 4277	K.YGGDEIPFSPYR.V	1401.50466	1	9.78E-05	0.56	2.85	-	574.6
AHQ-7-12, 4008	K.YGGDEIPFSPYR.V	1401.50466	2	4.72E-04	0.60	2.72	-	409.5
AHQ-7-8, 4128 - 4135	K.YGGDEIPFSPYR.V	1401.50466	2	8.65E-06	0.71	2.98	-	475.2
AHQ-7-4, 4293	K.YGGDEIPFSPYR.V	1401.50466	1	2.93E-07	0.23	2.31	-	382.1
AHQ-7-13-, 3429	K.YGGPYHIGGSPFK.A	1380.53182	2	3.46E-06	0.96	3.87	-	1893.4
AHQ-7-8, 3256	K.YGGPYHIGGSPFK.A	1380.53182	2	1.62E-08	0.96	4.01	-	1662.7
AHQ-7-5, 3395	K.YGGPYHIGGSPFK.A	1380.53182	2	1.95E-09	0.92	4.13	-	1043.0
AHQ-7-7, 3204 - 3269	K.YGGPYHIGGSPFK.A	1380.53182	2	2.94E-07	0.96	3.93	-	1774.7
AHQ-7-6, 3357 - 3362	K.YGGPYHIGGSPFK.A	1380.53182	2	2.78E-08	0.96	3.88	-	1609.7
AHQ-7-1, 3611	K.YGGPYHIGGSPFK.A	1380.53182	2	2.77E-09	0.98	4.62	-	2225.3
AHQ-7-3, 3473	K.YGGPYHIGGSPFK.A	1380.53182	2	6.10E-08	0.97	4.48	-	1981.2
AHQ-7-4, 3406	K.YGGPYHIGGSPFK.A	1380.53182	2	1.92E-06	0.95	3.87	-	1453.8
AHQ-7-5, 3420	K.YGGPYHIGGSPFK.A	1380.53182	1	1.18E-05	0.88	3.71	-	450.9
AHQ-7-10, 3220	K.YGGPYHIGGSPFK.A	1380.53182	2	1.07E-04	0.90	3.37	-	1066.5
AHQ-7-4, 3426 - 3444	K.YGGPYHIGGSPFK.A	1380.53182	1	2.06E-04	0.79	2.69	-	624.0

AHQ-7-5, 3404	K.YGGPYHIGGSPFK.A	1380.53182	3	7.57E-06	0.86	3.74	-	555.8
AHQ-7-4, 2994 - 3076	K.YGGQPVPNFPSK.L	1291.43658	2	7.00E-05	0.86	3.64	-	352.4
AHQ-7-2, 3295	K.YGGQPVPNFPSK.L	1291.43658	2	5.69E-06	0.84	3.35	-	406.8
AHQ-7-5, 3043	K.YGGQPVPNFPSK.L	1291.43658	2	3.57E-04	0.83	3.22	-	386.1
AHQ-7-3, 3029 - 3107	K.YGGQPVPNFPSK.L	1291.43658	2	1.92E-04	0.88	3.55	-	412.9
AHQ-7-2, 3145	K.YGGQPVPNFPSK.L	1291.43658	1	3.95E-04	0.45	2.56	-	362.6
AHQ-7-3, 3249	K.YGGQPVPNFPSK.L	1291.43658	2	9.58E-06	0.88	3.65	-	496.0
AHQ-7-2, 3139 - 3140	K.YGGQPVPNFPSK.L	1291.43658	2	1.89E-05	0.93	3.65	-	677.8
AHQ-7-1, 3264	K.YGGQPVPNFPSK.L	1291.43658	2	1.03E-04	0.94	3.65	-	766.3
AHQ-7-7, 4149	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.38E-04	0.95	5.82	-	879.7
AHQ-7-3, 4395	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	6.16E-06	0.87	3.60	-	1051.1
AHQ-7-4, 4348	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	3.29E-06	0.80	3.41	-	847.3
AHQ-7-2, 2909 - 2987	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.63E-05	0.91	3.70	-	606.3
AHQ-7-1, 3132	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.69E-06	0.72	2.74	-	525.5
AHQ-7-4, 3104	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.14E-05	0.59	2.81	-	388.4
AHQ-7-3, 2889 - 2955	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.65E-06	0.89	3.59	-	530.0
AHQ-7-4, 3113	K.YNEQHVPGSPFTAR.V	1603.71978	3	4.30E-04	0.76	3.37	-	732.3
AHQ-7-5, 2867 - 2870	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.30E-06	0.89	3.35	-	642.1
AHQ-7-4, 2877 - 2892	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.72E-06	0.90	3.80	-	535.6
AHQ-7-8, 2686	K.YNEQHVPGSPFTAR.V	1603.71978	3	4.51E-04	0.84	3.59	-	900.8
AHQ-7-4, 2885	K.YNEQHVPGSPFTAR.V	1603.71978	3	3.86E-05	0.84	3.69	-	788.8
AHQ-7-4, 4504 - 4568	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.18E-07	0.92	4.15	-	718.1
AHQ-7-13, 4422	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.19E-06	0.70	3.34	-	410.2
AHQ-7-3, 4431 - 4495	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.72E-07	0.90	4.06	-	590.8
AHQ-7-3, 4592 - 4672	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.97E-06	0.87	3.97	-	500.7
AHQ-7-2, 4527 - 4591	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.18E-05	0.90	4.12	-	604.4
AHQ-7-2, 4697	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.24E-08	0.92	4.24	-	747.7
AHQ-7-3, 4329 - 4381	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.21E-05	0.90	3.99	-	762.0
AHQ-7-8, 4407	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.24E-04	0.95	4.48	-	888.2
AHQ-7-1, 4480 - 4535	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.14E-05	0.95	4.79	-	837.5
AHQ-7-7, 4340	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.23E-05	0.87	3.94	-	505.4
AHQ-7-4, 4673	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.44E-05	0.89	4.02	-	520.4
AHQ-7-5, 4436 - 4486	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.99E-05	0.92	4.22	-	702.7
AHQ-7-2, 6499 - 6555	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	1.66E-09	0.79	3.32	-	563.6
AHQ-7-2, 6203 - 6244	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.06E-11	0.90	3.83	-	812.1
AHQ-7-2, 6673	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	2.02E-04	0.76	2.56	-	742.7
AHQ-7-2, 6513 - 6515	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	2.05E-07	0.97	5.25	-	1523.3
AHQ-7-5, 6471	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	5.97E-08	0.86	3.28	-	614.4
AHQ-7-4, 6529 - 6553	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.72E-06	0.94	5.09	-	666.5
AHQ-7-3, 6080	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	8.73E-08	0.91	3.97	-	907.5
AHQ-7-3, 6343 - 6357	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	2.39E-07	0.54	3.03	-	450.1
gi|4827056|ref|NP_005103.1| WD repeat-containing protein 1 isoform 2 [Homo sapiens]				1.44E-13	11.50	130.36	45.10	58001.9
AHQ-7-6, 5071	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	2.14E-11	0.98	7.00	-	1708.6
AHQ-7-10, 4568	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	1.87E-05	0.95	4.79	-	1417.4
AHQ-7-6, 4973	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	1.28E-09	0.97	5.83	-	1633.5
AHQ-7-7, 4861	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	3.70E-09	0.97	6.11	-	1997.5
AHQ-7-8, 4904	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	9.27E-08	0.91	4.49	-	581.9
AHQ-7-6, 4987	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	1.94E-07	0.96	5.66	-	959.2
AHQ-7-9, 5017	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.95E-05	0.81	3.38	-	631.8
AHQ-7-6, 5486 - 5554	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.06E-09	0.89	4.28	-	745.0
AHQ-7-8, 5515	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	4.76E-12	0.89	4.50	-	541.8
AHQ-7-6, 3902 - 3971	R.FATASADGQIYIYDGK.T	1720.86021	2	1.54E-06	0.85	3.22	-	704.3
AHQ-7-6, 4135	R.FATASADGQIYIYDGK.T	1720.86021	2	2.92E-07	0.92	3.54	-	1197.9
AHQ-7-6, 5586	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	2	7.38E-08	0.91	4.27	-	831.5
AHQ-7-6, 5593	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	3	1.76E-04	0.81	3.96	-	735.5
AHQ-7-6, 4727 - 4731	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	8.52E-07	0.89	3.93	-	938.2
AHQ-7-6, 4573 - 4637	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	5.78E-07	0.97	5.35	-	1403.6
AHQ-7-6, 1897	R.IAVVGEGR.E	800.92621	2	1.33E-05	0.90	2.76	-	1180.0
AHQ-7-6, 2287 - 2369	K.IKDIAWTEDSKR.I	1462.63267	2	1.45E-05	0.64	2.82	-	565.6
AHQ-7-6, 5485 - 5545	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.44E-13	0.93	4.23	-	1125.7
AHQ-7-6, 5359 - 5425	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	8.87E-08	0.91	4.17	-	1056.4
AHQ-7-10, 3783 - 3787	R.LYSILGTTLKDEGK.L	1538.76736	2	2.44E-05	0.92	4.04	-	1022.4
AHQ-7-6, 3981 - 4046	R.LYSILGTTLKDEGK.L	1538.76736	2	3.45E-05	0.88	3.71	-	820.6
AHQ-7-7, 3920	R.LYSILGTTLKDEGK.L	1538.76736	2	5.17E-04	0.86	3.38	-	836.6
AHQ-7-12, 3891	R.LYSILGTTLKDEGK.L	1538.76736	2	4.13E-06	0.70	2.86	-	637.0
AHQ-7-6, 4301	R.M*TVDESGQLISCSMDDTVR.Y	2162.36305	2	1.84E-07	0.88	4.12	-	597.3
AHQ-7-6, 4287	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	1.72E-07	0.86	4.23	-	471.4
AHQ-7-6, 4285 - 4293	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	3	9.53E-05	0.71	3.26	-	437.0
AHQ-7-6, 4121 - 4183	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	5.75E-07	0.98	5.70	-	2314.5
AHQ-7-6, 4267	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	9.59E-10	0.98	7.14	-	2294.5
AHQ-7-12, 3778	K.YAPSGFYIASGDVSGK.L	1619.75589	2	5.63E-04	0.66	2.54	-	571.5
AHQ-7-11, 3760	K.YAPSGFYIASGDVSGK.L	1619.75589	2	4.15E-05	0.59	2.78	-	504.2
AHQ-7-6, 3893 - 3953	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.07E-11	0.94	4.22	-	886.2
gi|4557731|ref|NP_000618.1| latent transforming growth factor beta binding protein 1 precursor [Hom				1.73E-13	9.62	120.30	9.80	152790.9
AHQ-7-2, 3737	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	2.30E-08	0.98	5.99	-	2041.2
AHQ-7-1, 3761	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	6.37E-06	0.96	5.29	-	1311.1
AHQ-7-3, 3657 - 3661	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	9.45E-06	0.98	5.57	-	2091.1
AHQ-7-3, 3665	R.ASGLGDHCEDINECLEDK.S	2065.13910	3	9.69E-06	0.91	4.20	-	995.9
AHQ-7-2, 3977	R.ASGLGDHCEDINECLEDKSVCQR.G	2696.84428	3	2.93E-05	0.88	3.82	-	981.9
AHQ-7-2, 2381	R.CEYCDSGYR.M	1212.24846	1	2.04E-04	0.24	2.04	-	265.6
AHQ-7-5, 2588	R.CTCGQGYQLSAAK.D	1446.58862	2	1.22E-06	0.89	3.77	-	704.3
AHQ-7-2, 2655	R.CTCGQGYQLSAAK.D	1446.58862	2	7.99E-04	0.68	2.57	-	447.7
AHQ-7-2, 4163	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	1.40E-06	0.97	5.84	-	1401.4
AHQ-7-3, 4072	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	2.87E-06	0.95	5.14	-	929.9
AHQ-7-3, 2165	K.DQCEDIDECQHR.H	1607.61898	2	2.51E-06	0.63	2.55	-	796.2
AHQ-7-14-, 3170	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	1.73E-13	0.91	4.36	-	610.7
AHQ-7-1, 5637 - 5657	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	9.76E-06	0.93	5.28	-	873.3
AHQ-7-4, 3717	R.KCVDIDECTQVQHLCSQGR.C	2337.55401	3	3.37E-07	0.63	3.20	-	726.3
AHQ-7-2, 2973 - 2981	R.TSTDLDVDVDQPK.E	1433.50014	2	1.05E-06	0.86	3.49	-	894.8
AHQ-7-1, 3096	R.TSTDLDVDVDQPK.E	1433.50014	2	6.03E-07	0.84	2.71	-	1003.4
AHQ-7-4, 2681 - 2708	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.25E-04	0.66	3.02	-	683.9
AHQ-7-1, 2931	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	2.01E-05	0.93	4.19	-	1217.8
AHQ-7-2, 2771	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	8.91E-08	0.91	3.82	-	1205.8
AHQ-7-3, 2745	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	5.11E-07	0.93	4.02	-	1664.4
AHQ-7-2, 3651	R.YTCICYEGYR.F	1387.51964	2	1.90E-05	0.80	2.94	-	504.7
gi|7656991|ref|NP_055140.1| coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;				1.90E-13	8.68	100.35	31.00	53248.7
AHQ-7-7, 5769 - 5844	R.AIFLADGNVFTTGFSR.M	1716.91793	2	2.91E-05	0.96	4.80	-	1520.6
AHQ-7-6, 5890	R.AIFLADGNVFTTGFSR.M	1716.91793	2	1.34E-05	0.97	5.03	-	1540.3
AHQ-7-6, 5706 - 5783	R.AIFLADGNVFTTGFSR.M	1716.91793	2	1.52E-09	0.98	5.47	-	2055.7
AHQ-7-6, 5791 - 5821	R.AIFLADGNVFTTGFSR.M	1716.91793	2	2.98E-04	0.97	4.76	-	1796.7
AHQ-7-6, 3798 - 3802	K.CDLISIPK.K	947.13128	2	5.30E-04	0.87	3.24	-	779.3
AHQ-7-7, 2522	R.GLDVNKCEIAR.F	1276.44504	2	7.47E-04	0.80	2.64	-	1077.9
AHQ-7-6, 3145	R.HVFGQAVKNDQCYDDIR.V	2067.22783	3	1.23E-05	0.71	3.43	-	633.4
AHQ-7-6, 3385	R.KCEPIIMTVPR.K	1345.65706	2	2.01E-06	0.91	3.46	-	901.6
AHQ-7-7, 6728	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	1.21E-06	0.96	5.61	-	1224.0
AHQ-7-6, 6634 - 6635	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	1.90E-13	0.98	6.93	-	1420.0
AHQ-7-6, 4023 - 4031	K.NADPILISLK.H	1084.29103	2	2.60E-05	0.75	2.82	-	447.9

AHQ-7-6, 2410	K.SIKDTICNQDER.I	1480.58332	2	3.61E-07	0.84	2.86	-	1012.8
AHQ-7-7, 4266 - 4276	R.VTWDSSFCAVNPR.F	1540.68205	2	2.59E-07	0.90	3.58	-	1129.5
AHQ-7-7, 5880 - 5884	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	5.70E-07	0.94	4.88	-	731.3
AHQ-7-7, 5886	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	3.61E-05	0.90	3.85	-	861.0
AHQ-7-6, 5895	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	2.50E-06	0.85	3.46	-	768.9
AHQ-7-6, 5897 - 5970	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	3.70E-10	0.95	4.86	-	929.7
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				2.51E-13	24.41	290.31	30.30	138070.8
AHQ-7-4, 2404	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	2.16E-05	0.93	4.98	-	621.6
AHQ-7-4, 2401 - 2469	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	9.47E-04	0.93	4.33	-	1366.4
AHQ-7-3, 2509	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	3.93E-09	0.90	4.15	-	721.3
AHQ-7-3, 2428	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	2.78E-08	0.93	5.02	-	575.3
AHQ-7-3, 6072 - 6087	K.CTSDM*ETILTFIPQFHR.L	2114.38778	3	4.21E-08	0.91	4.70	-	1037.9
AHQ-7-4, 4010 - 4077	R.DQALQLQVLNSR.F	1385.55144	2	7.41E-06	0.95	3.98	-	1695.5
AHQ-7-6, 3950 - 4014	R.DQALQLQVLNSR.F	1385.55144	2	3.80E-06	0.95	3.99	-	1437.2
AHQ-7-3, 3909 - 3979	R.DQALQLQVLNSR.F	1385.55144	2	4.22E-08	0.95	4.14	-	1447.6
AHQ-7-3, 4189	R.DQALQLQVLNSR.F	1385.55144	2	2.79E-10	0.95	4.18	-	1368.3
AHQ-7-3, 3975 - 4040	R.DQALQLQVLNSR.F	1385.55144	2	4.05E-07	0.97	5.55	-	1636.3
AHQ-7-1, 4048	R.DQALQLQVLNSR.F	1385.55144	2	2.39E-08	0.68	2.53	-	1005.5
AHQ-7-4, 3256	K.ESLRGECEDMLSK.C	1555.71360	2	7.79E-04	0.92	3.81	-	906.7
AHQ-7-3, 2148	K.ETLSTIKDNSEIHHK.C	1752.90698	2	1.47E-07	0.87	3.40	-	947.4
AHQ-7-3, 2893	K.EVHEQLLSTEQVSDQK.N	1870.99550	2	1.14E-04	0.92	4.19	-	817.5
AHQ-7-2, 6281	K.FPPVTTFSGYLLYR.T	1661.92388	2	5.19E-05	0.82	3.10	-	568.8
AHQ-7-10, 5623 - 5629	K.FPPVTTFSGYLLYR.T	1661.92388	2	6.31E-07	0.94	4.12	-	867.3
AHQ-7-3, 5673 - 5692	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	5.58E-07	0.95	5.07	-	1090.2
AHQ-7-1, 5649	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	7.52E-05	0.87	3.61	-	942.4
AHQ-7-4, 5816	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.01E-07	0.93	4.33	-	1091.1
AHQ-7-2, 5820	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.02E-06	0.92	3.87	-	1224.2
AHQ-7-5, 5947	K.GLTEFVEPIIQIK.T	1487.76518	2	4.75E-06	0.90	3.96	-	682.6
AHQ-7-1, 5821	K.GLTEFVEPIIQIK.T	1487.76518	2	8.90E-05	0.74	2.91	-	705.9
AHQ-7-3, 5872	K.GLTEFVEPIIQIK.T	1487.76518	2	3.54E-06	0.91	3.89	-	890.2
AHQ-7-2, 6001	K.GLTEFVEPIIQIK.T	1487.76518	2	8.74E-06	0.86	3.26	-	869.4
AHQ-7-3, 2705	K.GPCGWTGGSCPQR.S	1422.52885	2	5.20E-04	0.84	2.74	-	836.9
AHQ-7-2, 2528	R.GVAEQQQQQGCGDPEVMQK.M	2119.27971	2	4.08E-07	0.95	4.41	-	1123.5
AHQ-7-5, 2447	R.GVAEQQQQQGCGDPEVMQK.M	2119.27971	2	2.91E-05	0.96	4.72	-	1319.2
AHQ-7-3, 3891	K.HSLPDIQLLQK.G	1292.50915	2	1.58E-07	0.90	3.40	-	832.5
AHQ-7-2, 4003	K.HSLPDIQLLQK.G	1292.50915	2	3.78E-08	0.85	3.04	-	744.2
AHQ-7-3, 6220 - 6289	K.IFQNDMQETVAQLFK.T	1813.06743	2	4.53E-05	0.95	4.25	-	1260.7
AHQ-7-1, 5048	K.IFQNDM*QETVAQLFK.T	1829.06683	2	8.34E-04	0.87	3.43	-	934.2
AHQ-7-5, 5067	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.41E-07	0.97	4.96	-	1780.2
AHQ-7-4, 6389 - 6460	K.IFQNDMQETVAQLFK.T	1813.06743	2	8.16E-04	0.70	3.13	-	772.4
AHQ-7-1, 6159	K.IFQNDMQETVAQLFK.T	1813.06743	2	3.96E-06	0.91	3.78	-	1127.3
AHQ-7-3, 5023 - 5025	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.72E-06	0.95	4.31	-	1334.1
AHQ-7-10, 5007	R.IPYLGVYVFK.Y	1199.46532	2	2.85E-06	0.85	3.12	-	785.3
AHQ-7-3, 5951	K.KIENLTSAVNSLNFIIK.E	1905.22764	2	9.35E-10	0.95	4.77	-	967.4
AHQ-7-10, 3543 - 3617	K.LAFESENINSEIHCDR.V	1936.04933	2	1.45E-04	0.82	3.85	-	401.7
AHQ-7-6, 2895	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	2.48E-06	0.93	4.59	-	800.3
AHQ-7-3, 2929 - 2995	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	4.51E-07	0.98	6.11	-	1615.6
AHQ-7-4, 2937	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	1.95E-05	0.96	4.90	-	1038.8
AHQ-7-2, 3916 - 3917	K.LVEENALAPDFSK.G	1433.58810	2	7.15E-05	0.88	3.59	-	635.5
AHQ-7-3, 3821	K.LVEENALAPDFSK.G	1433.58810	2	1.50E-05	0.75	2.78	-	654.6
AHQ-7-4, 6924	K.M*SEQLNDLTYDMEILQPLLEQGASLR.Q	3025.40122	3	1.34E-05	0.96	6.06	-	1662.7
AHQ-7-3, 6697	K.M*SEQLNDLTYDMEILQPLLEQGASLR.Q	3025.40122	3	3.73E-04	0.89	4.28	-	1437.4
AHQ-7-3, 6615 - 6624	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	2.51E-13	0.90	4.84	-	850.7
AHQ-7-3, 2395	K.M*TDQVNYQAMK.L	1345.52783	2	7.06E-07	0.91	3.44	-	1109.5
AHQ-7-3, 2011	R.NTYSSLEGK.V	999.05672	1	2.79E-05	0.11	1.81	-	207.5
AHQ-7-3, 2857 - 2875	R.QEMTLTCEKPIK.E	1479.74501	2	8.91E-04	0.38	2.63	-	469.8
AHQ-7-3, 6207	K.QSLMMLQM*FEDLHIQESK.I	2225.59529	2	7.07E-04	0.62	3.11	-	382.1
AHQ-7-3, 6360	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	2.34E-08	0.94	4.98	-	710.5
AHQ-7-3, 6544	K.TMTIINNAIDFIQDNYALK.E	2199.51256	3	8.60E-04	0.83	3.38	-	1104.6
AHQ-7-3, 6692	K.TMTIINNAIDFIQDNYALK.E	2199.51256	2	5.11E-09	0.80	3.90	-	468.3
AHQ-7-3, 6052	K.TM*TIINNAIDFIQDNYALK.E	2215.51196	2	2.30E-05	0.88	4.13	-	569.4
AHQ-7-3, 3073	K.TVSSLSEDLESTR.Q	1424.49324	2	1.01E-06	0.74	2.95	-	660.0
AHQ-7-6, 3406	K.TVSSLSEDLESTR.Q	1424.49324	2	1.36E-07	0.80	3.00	-	799.8
AHQ-7-5, 3462	K.TVSSLSEDLESTR.Q	1424.49324	2	1.86E-06	0.82	2.74	-	878.6
AHQ-7-4, 3476	K.TVSSLSEDLESTR.Q	1424.49324	2	3.58E-07	0.82	2.79	-	844.6
AHQ-7-4, 4109	R.YNFVLQVAK.T	1082.27683	2	3.08E-07	0.93	3.40	-	919.6
AHQ-7-1, 4189	R.YNFVLQVAK.T	1082.27683	2	3.36E-07	0.86	2.79	-	843.5
AHQ-7-3, 4089	R.YNFVLQVAK.T	1082.27683	2	2.42E-06	0.92	3.64	-	762.7
gi|27498332|ref|XP_212565.1| similar to tubulin, beta 5 [Homo sapiens]				2.70E-13	5.15	60.24	11.90	49670.5
AHQ-7-11, 5271	R.ALTVPELTQQVFDAK.N	1660.89259	2	1.46E-05	0.76	3.04	-	372.3
AHQ-7-7, 3809 - 3877	R.IMNTFSVVPSPK.V	1320.58277	2	8.92E-04	0.95	3.86	-	1446.2
AHQ-7-7, 3322	R.IM*NTFSVVPSPK.V	1336.58217	2	2.27E-05	0.88	3.26	-	898.2
AHQ-7-8, 3347	R.IM*NTFSVVPSPK.V	1336.58217	2	5.09E-06	0.76	2.84	-	758.0
AHQ-7-7, 6532	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.70E-13	0.97	4.76	-	1327.8
AHQ-7-7, 6597	K.MAVTFIGNSTAIQELFK.R	1871.19002	2	5.69E-04	0.90	3.68	-	1182.1
AHQ-7-7, 6262 - 6268	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	3.91E-07	0.96	4.76	-	1204.9
AHQ-7-10, 5765	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.38E-04	0.62	2.57	-	452.3
AHQ-7-14-, 5935 - 5989	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	6.68E-08	0.94	4.37	-	981.5
AHQ-7-13-, 6251	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	7.03E-09	0.95	4.60	-	987.3
AHQ-7-11, 5850	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	7.43E-06	0.91	4.11	-	796.9
AHQ-7-12, 6020 - 6076	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.03E-05	0.88	4.02	-	547.9
AHQ-7-13, 5971 - 6049	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.08E-06	0.76	3.39	-	374.7
AHQ-7-13, 6229	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.63E-09	0.93	4.07	-	888.0
AHQ-7-13-, 6023 - 6045	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.25E-06	0.96	4.81	-	1162.6
AHQ-7-14-, 6225	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.83E-08	0.88	4.06	-	448.3
AHQ-7-11, 4254	R.YLTVAAVFR.G	1040.23994	2	2.68E-05	0.83	2.60	-	750.1
AHQ-7-7, 4364	R.YLTVAAVFR.G	1040.23994	2	3.40E-07	0.82	2.68	-	790.9
gi|4885063|ref|NP_005156.1| aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase				2.78E-13	1.28	20.27	7.10	39455.6
AHQ-7-9, 4165	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	2.77E-11	0.92	4.38	-	555.7
AHQ-7-8, 4499 - 4562	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	2.78E-13	0.90	5.32	-	867.1
AHQ-7-8, 4155 - 4186	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	3.36E-06	0.86	4.59	-	900.8
AHQ-7-8, 4210	K.VDKGVVPLAGTDGETTTQGLDGLSER.C	2616.82041	2	2.01E-04	0.38	3.24	-	240.4
gi|5729770|ref|NP_000382.3| ceroid-lipofuscinosis, neuronal 2, late infantile (Jansky-Bielschowsky				2.82E-13	0.97	10.32	4.80	61247.6
AHQ-7-8, 6834	R.VPIPWVSGTSASTPVFGGILSLINEHR.I	2836.23725	3	2.82E-13	0.97	6.50	-	1394.7
gi|4759212|ref|NP_004598.1| beta-tubulin cofactor A [Homo sapiens]				2.85E-13	2.80	30.33	26.90	12854.8
AHQ-7-13-, 3388	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	3.43E-08	0.98	6.58	-	1817.2
AHQ-7-13, 3518 - 3519	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	2.85E-13	0.95	5.45	-	1177.4
AHQ-7-13, 3841 - 3849	R.LEAAYLDLQR.I	1192.34645	2	1.25E-05	0.97	4.19	-	1902.8
AHQ-7-13, 3595	R.RLEAAYLDLQR.I	1348.53280	2	1.29E-07	0.88	3.62	-	731.3
gi|4502549|ref|NP_001734.1| calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta				4.75E-13	2.40	30.24	19.50	16837.5
AHQ-7-12, 3444 - 3498	K.DTDSEEEIREAFR.V	1597.62234	2	3.23E-07	0.61	3.13	-	391.3
AHQ-7-11, 3978 - 4047	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	2.91E-04	0.82	3.19	-	622.2
AHQ-7-12, 3774	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	4.55E-04	0.59	3.01	-	522.5
AHQ-7-12, 3560	R.VFDKDGNGYISAAELR.H	1755.90933	2	6.30E-06	0.83	3.25	-	740.8
AHQ-7-12, 3694 - 3750	R.VFDKDGNGYISAAELR.H	1755.90933	2	4.75E-13	0.96	4.71	-	1286.6
AHQ-7-12, 3699 - 3754	R.VFDKDGNGYISAAELR.H	1755.90933	3	1.73E-06	0.93	4.11	-	1529.4
AHQ-7-11, 3712	R.VFDKDGNGYISAAELR.H	1755.90933	3	2.55E-06	0.94	4.24	-	1757.2

AHQ-7-11, 3651 - 3706	R.VFDKDGNGYISAAELR.H	1755.90933	2	6.97E-04	0.95	3.85	-	1618.9
gi|4826898|ref|NP_005013.1| profilin 1; profilin-1 [Homo sapiens]				4.90E-13	13.60	160.30	67.10	15054.2
AHQ-7-13, 2137 - 2194	K.CYEM*ASHLR.R	1184.32794	2	5.50E-06	0.85	2.97	-	934.5
AHQ-7-13-, 1931 - 1991	K.CYEM*ASHLR.R	1184.32794	2	3.82E-05	0.90	2.98	-	1325.2
AHQ-7-13-, 2015 - 2073	K.CYEM*ASHLR.R	1184.32794	2	1.23E-04	0.91	3.07	-	1203.0
AHQ-7-13-, 2397 - 2437	K.CYEMASHLR.R	1168.32854	2	9.83E-05	0.91	2.85	-	1568.0
AHQ-7-13-, 2496 - 2555	K.CYEMASHLR.R	1168.32854	2	5.37E-04	0.96	3.16	-	2102.9
AHQ-7-13, 2249 - 2310	K.CYEM*ASHLR.R	1184.32794	2	4.44E-05	0.87	2.97	-	993.3
AHQ-7-13, 4142	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.82E-09	0.97	4.97	-	1232.9
AHQ-7-13-, 4152	K.DRSSFYVNGLTLGGQK.C	1742.91379	3	7.07E-05	0.93	4.62	-	1149.2
AHQ-7-13-, 4003	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	4.90E-13	0.97	5.44	-	1372.2
AHQ-7-13, 4291	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.76E-08	0.97	5.85	-	1255.5
AHQ-7-13-, 4667 - 4669	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.94E-06	0.97	4.53	-	1900.2
AHQ-7-12, 5048 - 5104	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.49E-04	0.74	2.71	-	720.9
AHQ-7-12, 4352 - 4407	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.75E-10	0.96	4.31	-	1614.3
AHQ-7-13-, 4563 - 4600	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.45E-04	0.96	3.92	-	2073.8
AHQ-7-13-, 4445 - 4504	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.50E-07	0.97	4.02	-	2077.5
AHQ-7-13-, 4309 - 4371	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.30E-09	0.91	4.09	-	975.6
AHQ-7-14-, 4538	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.90E-05	0.96	3.93	-	1755.3
AHQ-7-13-, 4832 - 4900	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.87E-04	0.90	3.70	-	1057.0
AHQ-7-13-, 4899	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.78E-04	0.94	3.96	-	1307.9
AHQ-7-13-, 5013 - 5071	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.94E-08	0.96	3.70	-	1871.7
AHQ-7-13-, 5027 - 5036	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.06E-04	0.72	3.01	-	776.9
AHQ-7-13-, 5196 - 5197	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.59E-09	0.95	3.98	-	1563.1
AHQ-7-13-, 5207 - 5276	R.DSLLQDGEFSMDLR.T	1626.77023	2	8.49E-09	0.97	4.61	-	2386.2
AHQ-7-14-, 5233	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.66E-08	0.97	4.18	-	1859.7
AHQ-7-14, 5292 - 5361	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.37E-05	0.90	3.21	-	1135.9
AHQ-7-14, 5417	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.91E-06	0.94	3.60	-	1514.5
AHQ-7-13, 5491 - 5522	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.32E-08	0.94	3.75	-	1303.0
AHQ-7-13, 5405 - 5434	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.69E-04	0.92	3.00	-	1621.8
AHQ-7-13, 4485 - 4545	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.87E-07	0.94	3.91	-	1348.7
AHQ-7-14-, 4402	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.49E-04	0.91	3.44	-	977.7
AHQ-7-13, 5291 - 5349	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.77E-08	0.98	4.93	-	2247.1
AHQ-7-13, 4601 - 4643	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.79E-08	0.97	4.90	-	1691.3
AHQ-7-13, 4702 - 4763	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.02E-06	0.96	4.43	-	1705.7
AHQ-7-13, 4942 - 5013	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.13E-04	0.93	3.60	-	1511.6
AHQ-7-13, 5070 - 5121	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.32E-04	0.94	4.16	-	1561.9
AHQ-7-13, 5141 - 5221	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.38E-10	0.95	4.30	-	1291.8
AHQ-7-13-, 5336 - 5409	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.22E-04	0.86	3.11	-	1060.6
AHQ-7-13, 3690 - 3753	K.DSPSVWAAVPGK.T	1214.35211	2	7.75E-06	0.92	3.56	-	1054.2
AHQ-7-13-, 3492 - 3551	K.DSPSVWAAVPGK.T	1214.35211	2	5.43E-04	0.88	3.44	-	1002.1
AHQ-7-13, 4347	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.25E-07	0.53	2.80	-	391.4
AHQ-7-12, 4124 - 4150	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.80E-07	0.95	4.18	-	982.3
AHQ-7-12, 4134	R.SSFYVNGLTLGGQK.C	1471.63957	1	8.06E-07	0.85	2.66	-	798.9
AHQ-7-12, 4266 - 4331	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.34E-08	0.97	4.78	-	1258.4
AHQ-7-14, 5156	R.SSFYVNGLTLGGQK.C	1471.63957	2	6.57E-05	0.85	2.89	-	835.3
AHQ-7-13, 4262 - 4342	R.SSFYVNGLTLGGQK.C	1471.63957	2	4.62E-09	0.93	4.47	-	738.7
AHQ-7-13, 4401 - 4463	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.61E-06	0.93	4.26	-	758.5
AHQ-7-14-, 4463 - 4541	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.07E-07	0.96	4.07	-	1459.9
AHQ-7-13-, 4431 - 4487	R.SSFYVNGLTLGGQK.C	1471.63957	2	7.38E-11	0.97	4.66	-	1616.6
AHQ-7-13, 4489 - 4551	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.96E-08	0.61	2.79	-	388.5
AHQ-7-13-, 4355 - 4475	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.53E-11	0.50	2.31	-	394.0
AHQ-7-14-, 4281	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.21E-04	0.90	3.40	-	812.2
AHQ-7-13-, 4207 - 4268	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.10E-07	0.77	3.09	-	611.4
AHQ-7-13-, 4199 - 4263	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.33E-07	0.94	4.42	-	864.9
AHQ-7-13, 4498 - 4574	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.45E-05	0.97	4.30	-	1839.8
AHQ-7-12, 4280 - 4339	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.56E-04	0.79	3.39	-	478.0
AHQ-7-13-, 3084 - 3219	K.STGGAPTFNVTVTK.T	1380.52843	1	3.97E-06	0.48	2.71	-	267.9
AHQ-7-12, 3131	K.STGGAPTFNVTVTK.T	1380.52843	2	8.05E-04	0.79	2.97	-	467.0
AHQ-7-13-, 3029 - 3092	K.STGGAPTFNVTVTK.T	1380.52843	2	1.18E-07	0.93	4.01	-	655.8
AHQ-7-12, 3139	K.STGGAPTFNVTVTK.T	1380.52843	1	1.17E-06	0.24	2.34	-	290.8
AHQ-7-13, 3297 - 3354	K.STGGAPTFNVTVTK.T	1380.52843	2	3.89E-06	0.73	2.81	-	391.4
AHQ-7-13, 3413 - 3482	K.STGGAPTFNVTVTK.T	1380.52843	2	1.21E-06	0.84	3.59	-	362.1
AHQ-7-13, 3183 - 3238	K.STGGAPTFNVTVTK.T	1380.52843	2	4.45E-07	0.91	3.82	-	600.3
AHQ-7-13-, 2960	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	2.64E-07	0.86	3.60	-	526.9
AHQ-7-13, 3277	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	1.14E-04	0.90	3.42	-	777.5
AHQ-7-13, 3119	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	2.40E-04	0.86	3.52	-	607.5
AHQ-7-13, 3835	K.TDKTLVLLMGK.E	1219.51989	2	3.22E-07	0.93	3.56	-	1417.5
AHQ-7-13, 3161 - 3165	K.TDKTLVLLM*GK.E	1235.51929	2	1.48E-04	0.87	3.41	-	841.9
AHQ-7-13-, 3665 - 3668	K.TDKTLVLLMGK.E	1219.51989	2	2.27E-06	0.91	3.65	-	988.9
AHQ-7-12, 5418 - 5483	K.TFVNITPAEVGVLVGK.D	1644.93630	2	8.66E-04	0.91	3.64	-	1020.7
AHQ-7-11, 5439	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.66E-04	0.67	3.07	-	584.6
AHQ-7-13, 5689 - 5749	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.78E-07	0.92	4.39	-	861.8
AHQ-7-13, 5590 - 5649	K.TFVNITPAEVGVLVGK.D	1644.93630	3	9.13E-09	0.96	5.60	-	1175.2
AHQ-7-13, 5581 - 5645	K.TFVNITPAEVGVLVGK.D	1644.93630	2	4.51E-08	0.95	4.85	-	842.9
AHQ-7-13-, 5528 - 5596	K.TFVNITPAEVGVLVGK.D	1644.93630	3	2.24E-06	0.97	5.92	-	1404.3
AHQ-7-13-, 5576 - 5631	K.TFVNITPAEVGVLVGK.D	1644.93630	2	6.40E-08	0.95	5.34	-	993.7
AHQ-7-13-, 5475 - 5551	K.TFVNITPAEVGVLVGK.D	1644.93630	2	9.66E-09	0.94	4.72	-	865.1
AHQ-7-13-, 5308 - 5328	K.TFVNITPAEVGVLVGK.D	1644.93630	2	8.85E-04	0.79	3.48	-	603.5
AHQ-7-13-, 5687	K.TFVNITPAEVGVLVGK.D	1644.93630	2	6.25E-08	0.94	4.27	-	1011.3
AHQ-7-14-, 5589	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.30E-06	0.93	4.04	-	843.8
AHQ-7-13-, 5299	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	1.64E-04	0.86	3.71	-	1046.0
AHQ-7-13, 5305	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	6.30E-08	0.42	2.94	-	371.0
AHQ-7-13-, 5311	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	4.16E-06	0.87	3.68	-	854.3
AHQ-7-14-, 2895	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	4.04E-11	0.96	4.72	-	1220.0
AHQ-7-13-, 2820	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	4.89E-06	0.94	4.13	-	1029.3
AHQ-7-13, 3045	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	2.00E-04	0.83	3.28	-	618.2
AHQ-7-13-, 2903	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	2.00E-04	0.92	4.17	-	736.2
AHQ-7-13, 3245	K.TLVLLM*GK.E	891.15418	2	5.93E-04	0.55	2.52	-	417.5
AHQ-7-13, 3902 - 3961	K.TLVLLMGK.E	875.15478	2	5.36E-04	0.73	2.67	-	466.5
AHQ-7-13-, 3744 - 3815	K.TLVLLMGK.E	875.15478	2	2.04E-05	0.82	3.03	-	538.1
AHQ-7-13-, 3075 - 3135	K.TLVLLM*GK.E	891.15418	2	4.68E-04	0.79	2.64	-	676.6
gi|4507521|ref|NP_001055.1| transketolase [Homo sapiens]				5.82E-13	0.95	10.26	3.00	67877.3
AHQ-7-6, 4585 - 4593	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	5.82E-13	0.95	5.24	-	504.9
gi|6005942|ref|NP_009057.1| valosin-containing protein; yeast Cdc48p homolog; transitional endoplas				8.13E-13	14.53	160.32	30.60	89321.3
AHQ-7-5, 4628	K.DVDLEFLAK.M	1050.18677	2	7.92E-04	0.88	3.45	-	923.0
AHQ-7-5, 4182	R.EDEEESLNEVGYDDIGGCR.K	2188.18267	2	1.51E-05	0.83	3.08	-	668.3
AHQ-7-5, 3815 - 3840	R.ELQELVQYPVEHPDK.F	1825.01157	3	9.64E-04	0.76	3.03	-	916.0
AHQ-7-5, 3810	R.ELQELVQYPVEHPDK.F	1825.01157	2	3.15E-05	0.90	3.99	-	902.0
AHQ-7-5, 6044	R.ETVVEVPQVTWEDIGGLEDVKR.E	2499.75825	2	2.89E-05	0.87	3.88	-	371.7
AHQ-7-5, 3696	R.GILLYGPPGTGK.T	1173.38627	2	4.36E-04	0.88	3.44	-	920.0
AHQ-7-5, 6387 - 6395	K.GPELLTM*WFGESEANVR.E	1953.16482	2	3.52E-07	0.94	4.75	-	817.6
AHQ-7-5, 3847 - 3850	K.GVLFYGPPGCGK.T	1253.45154	2	6.17E-06	0.90	3.41	-	1007.6
AHQ-7-5, 6538	R.IVSQLLTLMDGLK.Q	1431.76657	2	1.32E-05	0.91	3.88	-	1056.0
AHQ-7-5, 3428	R.KYEMFAQTLQQSR.G	1630.85008	2	3.51E-09	0.95	4.18	-	1216.5
AHQ-7-5, 6683	K.LADDVDLEQVANETHGHVGADLAALCSEAALQAIR.K	3675.98140	3	8.13E-13	0.98	6.38	-	2288.5
AHQ-7-5, 5666 - 5668	R.LDQLIYIPLPDEK.S	1557.81228	2	1.95E-06	0.95	4.33	-	1123.0

AHQ-7-5, 4916 - 4995	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	1.80E-06	0.98	6.23	-	2349.0
AHQ-7-6, 6713	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	2.82E-07	0.96	4.36	-	1143.7
AHQ-7-4, 6912	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	1.34E-05	0.94	4.30	-	1083.7
AHQ-7-5, 6820	K.NAPAIIFIDELDAIAPK.R	1812.09907	3	3.70E-06	0.95	4.92	-	1531.4
AHQ-7-7, 6812	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	2.52E-04	0.90	3.97	-	739.9
AHQ-7-5, 6814	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	5.60E-05	0.90	4.02	-	604.8
AHQ-7-4, 5800	K.NVFIIGATNRPDIIDPAILRPGR.L	2519.93026	3	8.61E-06	0.78	3.94	-	649.5
AHQ-7-5, 5718	K.NVFIIGATNRPDIIDPAILRPGR.L	2519.93026	3	4.85E-05	0.77	3.83	-	525.6
AHQ-7-5, 6834	R.QAAPCVLFFDELDSIAK.A	1926.17909	2	8.25E-09	0.88	4.03	-	622.6
AHQ-7-5, 3570	R.WALSQSNPSALR.E	1330.47434	2	1.10E-06	0.95	4.07	-	1429.4
gi|27498267|ref|XP_209737.1| similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,				8.86E-13	2.50	30.34	32.60	11063.6
AHQ-7-10, 6125 - 6128	R.DICNDVLSLLEK.F	1420.61093	2	4.12E-05	0.85	3.05	-	1005.8
AHQ-7-13-, 6380 - 6392	R.DICNDVLSLLEK.F	1420.61093	2	4.29E-06	0.95	3.91	-	1470.5
AHQ-7-11, 5518	R.DICNDVLSLLEK.F	1420.61093	2	4.59E-05	0.95	3.19	-	1694.2
AHQ-7-10, 6137	R.DICNDVLSLLEK.F	1420.61093	1	4.41E-05	0.73	3.14	-	600.5
AHQ-7-14-, 6358 - 6370	R.DICNDVLSLLEK.F	1420.61093	2	3.54E-05	0.95	3.69	-	1485.1
AHQ-7-10, 5760	R.DICNDVLSLLEK.F	1420.61093	2	7.66E-05	0.95	3.13	-	2247.6
AHQ-7-10, 5416 - 5420	R.DICNDVLSLLEK.F	1420.61093	1	2.73E-08	0.57	2.62	-	585.8
AHQ-7-10, 5407 - 5408	R.DICNDVLSLLEK.F	1420.61093	2	4.89E-06	0.95	3.86	-	1406.2
AHQ-7-10, 4680 - 4757	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	4.48E-09	0.98	6.82	-	2249.6
AHQ-7-10, 4732 - 4787	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.33E-07	0.97	5.60	-	1541.9
AHQ-7-10, 4821 - 4876	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.51E-09	0.97	5.67	-	1571.3
AHQ-7-10, 4932	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.68E-07	0.96	4.95	-	1282.5
AHQ-7-10, 4617 - 4675	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.17E-07	0.98	5.87	-	1656.1
AHQ-7-10, 4436	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.60E-10	0.95	4.69	-	1062.9
AHQ-7-10, 4348	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	9.26E-11	0.97	5.30	-	1286.2
AHQ-7-14-, 4938 - 4939	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.73E-09	0.98	6.36	-	1504.0
AHQ-7-6, 5097	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.68E-07	0.88	3.42	-	874.0
AHQ-7-10, 6169 - 6211	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.75E-05	0.81	3.57	-	765.6
AHQ-7-10, 6272	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.57E-05	0.93	4.21	-	1070.4
AHQ-7-11, 4774 - 4851	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.86E-13	0.98	5.90	-	1907.1
AHQ-7-11, 4783 - 4839	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.55E-07	0.89	3.96	-	925.9
AHQ-7-9, 4636	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.66E-09	0.98	5.81	-	1514.6
AHQ-7-12, 4774	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.05E-07	0.97	4.91	-	1568.3
AHQ-7-13, 5033	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.89E-10	0.97	5.45	-	1547.3
AHQ-7-14, 5692	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	6.46E-08	0.96	5.44	-	1031.0
AHQ-7-13-, 4681	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.61E-07	0.66	3.12	-	466.1
AHQ-7-13-, 4872 - 4932	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.17E-09	0.98	6.14	-	1552.2
AHQ-7-1, 5099	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	9.19E-09	0.94	4.58	-	990.3
AHQ-7-10, 4243 - 4244	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	3	2.39E-04	0.96	4.90	-	2077.3
AHQ-7-10, 4211 - 4231	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	2.33E-05	0.96	5.08	-	1167.9
gi|4507953|ref|NP_003397.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep				9.17E-13	8.15	100.28	40.00	27744.9
AHQ-7-10, 3331 - 3412	K.FLIPNASQAESK.V	1305.46156	2	5.71E-04	0.67	3.04	-	356.0
AHQ-7-10, 3079 - 3140	K.FLIPNASQAESK.V	1305.46156	2	2.18E-05	0.76	2.98	-	420.0
AHQ-7-10, 3309 - 3391	K.FLIPNASQAESK.V	1305.46156	1	1.62E-04	0.27	2.34	-	387.1
AHQ-7-10, 4789	K.FLIPNASQAESKVFYLK.M	1956.27311	2	6.17E-04	0.73	2.96	-	646.7
AHQ-7-10, 5615	K.IETELRDICNDVLSLLEK.F	2162.44718	3	6.99E-05	0.86	4.37	-	597.4
AHQ-7-14-, 2386	K.SVTEQGAELSNEER.N	1549.57922	2	6.08E-08	0.90	3.57	-	1258.5
AHQ-7-11, 2242 - 2322	K.SVTEQGAELSNEER.N	1549.57922	2	1.76E-08	0.92	4.12	-	1003.2
AHQ-7-13, 2601	K.SVTEQGAELSNEER.N	1549.57922	2	1.26E-05	0.90	3.42	-	1103.4
AHQ-7-13-, 2395	K.SVTEQGAELSNEER.N	1549.57922	2	4.70E-09	0.81	3.18	-	917.2
AHQ-7-10, 2291 - 2299	K.SVTEQGAELSNEER.N	1549.57922	2	8.64E-10	0.96	5.12	-	1212.2
AHQ-7-11, 2324	K.SVTEQGAELSNEER.N	1549.57922	2	1.13E-06	0.77	3.09	-	827.8
AHQ-7-10, 4577	K.SVTEQGAELSNEERNLLSVAYK.N	2438.63331	2	2.02E-04	0.39	2.80	-	406.4
AHQ-7-10, 5559	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.14E-04	0.65	3.27	-	302.5
AHQ-7-13-, 6307 - 6375	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.96E-08	0.96	5.38	-	1114.6
AHQ-7-10, 6123 - 6124	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.87E-10	0.97	5.69	-	1377.7
AHQ-7-14-, 6291 - 6357	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	9.17E-13	0.95	4.61	-	1293.2
AHQ-7-13, 6373	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.10E-08	0.97	5.56	-	1289.9
AHQ-7-10, 6291	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	3.19E-09	0.92	4.60	-	870.2
AHQ-7-10, 2485 - 2496	R.YDDMAACMK.S	1106.27579	2	2.96E-04	0.87	2.92	-	886.8
AHQ-7-10, 2289	R.YLAEVAAGDDK.K	1152.23595	1	1.29E-05	0.83	2.85	-	1320.3
AHQ-7-10, 2019 - 2075	R.YLAEVAAGDDKK.G	1280.40887	2	7.91E-04	0.95	3.56	-	1478.4
AHQ-7-13-, 2027 - 2105	R.YLAEVAAGDDKK.G	1280.40887	2	1.56E-04	0.88	3.18	-	1229.8
gi|4507677|ref|NP_003290.1| tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu				1.03E-12	8.00	90.28	14.40	92468.2
AHQ-7-4, 2490	K.DISTNYYASQK.K	1290.36061	2	7.33E-05	0.83	3.20	-	643.0
AHQ-7-5, 2488	K.DISTNYYASQK.K	1290.36061	2	1.13E-05	0.84	3.44	-	553.5
AHQ-7-4, 3277	K.FAFQAEVNR.M	1082.19378	2	7.84E-06	0.93	3.65	-	1120.6
AHQ-7-4, 4061	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	1.62E-06	0.95	4.50	-	1752.1
AHQ-7-5, 4007	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	8.33E-05	0.95	4.42	-	1152.5
AHQ-7-5, 4012	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	1.03E-12	0.97	5.39	-	2327.7
AHQ-7-4, 4088 - 4092	K.GVVDSDDLPLNVSR.E	1486.60940	2	1.22E-07	0.96	4.79	-	1218.1
AHQ-7-6, 3965	K.GVVDSDDLPLNVSR.E	1486.60940	2	2.96E-06	0.91	4.17	-	937.2
AHQ-7-4, 6670	K.GYEVIYLTEPVDEYCIQALPEFDGKR.F	3107.43557	3	4.07E-07	0.91	4.64	-	673.5
AHQ-7-5, 6211 - 6283	K.KYSQFINFPIYVWSSK.T	2008.30657	2	2.83E-05	0.70	2.91	-	522.2
AHQ-7-4, 1890 - 1893	K.LGVIEDHSNR.T	1140.23163	2	4.59E-04	0.82	2.98	-	926.7
AHQ-7-5, 4147 - 4148	K.SILFVPTSAPR.G	1188.40094	2	4.68E-05	0.93	3.80	-	1210.3
AHQ-7-4, 6716 - 6754	K.YSQFINFPIYVWSSK.T	1880.13366	2	3.44E-05	0.97	5.51	-	1116.3
AHQ-7-6, 6535 - 6595	K.YSQFINFPIYVWSSK.T	1880.13366	2	5.51E-05	0.83	3.75	-	348.3
AHQ-7-5, 6639	K.YSQFINFPIYVWSSK.T	1880.13366	2	2.13E-06	0.93	4.14	-	871.7
gi|4504349|ref|NP_000509.1| beta globin [Homo sapiens]				1.38E-12	9.53	110.33	75.50	15998.3
AHQ-7-14-, 3183	K.EFTPPVQAAYQK.V	1379.54213	2	2.44E-05	0.54	2.58	-	432.0
AHQ-7-14-, 5377	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.94E-06	0.93	4.38	-	845.7
AHQ-7-13-, 5445	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	5.55E-08	0.94	4.45	-	824.4
AHQ-7-13-, 5288 - 5363	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	5.56E-05	0.96	4.56	-	992.6
AHQ-7-13-, 5184	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.22E-06	0.93	4.77	-	618.9
AHQ-7-13, 5531 - 5534	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.11E-06	0.95	4.47	-	970.7
AHQ-7-13-, 4875 - 4943	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	4.46E-08	0.95	4.65	-	882.3
AHQ-7-13, 5451 - 5463	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	3	5.15E-05	0.95	4.58	-	1732.0
AHQ-7-13, 5413 - 5470	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.18E-06	0.95	4.38	-	985.8
AHQ-7-13, 5042 - 5107	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	4.82E-06	0.91	4.23	-	714.7
AHQ-7-13, 4954 - 4971	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	4.19E-07	0.93	3.96	-	1438.6
AHQ-7-13-, 4849	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	2.64E-08	0.95	4.80	-	1486.9
AHQ-7-14, 5701 - 5704	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	4.28E-08	0.87	3.48	-	756.0
AHQ-7-13, 4929 - 4985	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	2.91E-06	0.93	4.62	-	701.9
AHQ-7-13, 3741 - 3797	K.GTFATLSELHCDK.L	1480.62492	2	1.59E-06	0.81	3.01	-	742.8
AHQ-7-13-, 3596 - 3671	K.GTFATLSELHCDK.L	1480.62492	2	8.85E-09	0.82	3.28	-	552.2
AHQ-7-13-, 4867	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	2	9.24E-09	0.92	4.68	-	532.9
AHQ-7-13-, 4921	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	1.60E-04	0.85	3.22	-	1213.5
AHQ-7-13, 4950 - 4958	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	6.34E-07	0.96	5.31	-	1388.3
AHQ-7-13-, 4781 - 4863	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	6.03E-10	0.97	6.18	-	1539.9
AHQ-7-13, 4599	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	3.39E-07	0.97	5.65	-	1718.9
AHQ-7-13, 4805 - 4807	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	1.38E-12	0.98	6.60	-	2207.6
AHQ-7-13-, 4697	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	3.52E-10	0.98	5.65	-	1672.0
AHQ-7-13-, 4695	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	4.10E-11	0.97	6.48	-	1643.8
AHQ-7-13-, 2881	K.LHVDPENFR.L	1127.23455	2	8.47E-04	0.77	2.69	-	1035.3
AHQ-7-13-, 6244	R.LLGNVLVCVLAHHFGK.E	1779.14197	2	5.62E-05	0.87	3.43	-	952.8

AHQ-7-14-, 5023	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	1.30E-07	0.81	3.34	-	601.0
AHQ-7-14, 5858	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	3.92E-04	0.94	3.91	-	1435.1
AHQ-7-14-, 5021	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.84E-10	0.96	5.39	-	1361.8
AHQ-7-13-, 5167 - 5168	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	8.98E-06	0.96	5.12	-	1429.5
AHQ-7-13-, 4984 - 4995	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	1.58E-07	0.73	3.01	-	500.5
AHQ-7-13, 5263	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	3.06E-09	0.96	5.42	-	1338.7
AHQ-7-13-, 4583	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	4.15E-04	0.96	4.41	-	1783.7
AHQ-7-13, 5082	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	7.92E-09	0.88	3.65	-	815.8
AHQ-7-13, 5081	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	7.42E-12	0.97	4.94	-	1946.8
AHQ-7-13, 4925	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	2.50E-08	0.91	3.96	-	675.4
AHQ-7-13-, 4813	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	7.62E-10	0.97	5.01	-	1468.2
AHQ-7-13-, 4820	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	1.08E-07	0.78	3.03	-	598.9
AHQ-7-13, 4921 - 4926	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.70E-08	0.96	5.12	-	1249.3
AHQ-7-13-, 4983 - 5045	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	7.93E-12	0.98	5.26	-	1980.2
AHQ-7-13-, 4897	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.97E-09	0.97	5.09	-	1843.9
AHQ-7-13, 3401 - 3479	K.VNVDEVGGEALGR.L	1315.41484	2	5.74E-05	0.97	5.09	-	1456.1
AHQ-7-13, 3415	K.VNVDEVGGEALGR.L	1315.41484	1	1.92E-06	0.36	2.75	-	258.6
AHQ-7-13-, 3264	K.VNVDEVGGEALGR.L	1315.41484	1	8.29E-07	0.75	3.55	-	312.5
AHQ-7-13-, 3259	K.VNVDEVGGEALGR.L	1315.41484	1	1.45E-06	0.38	2.46	-	285.0
AHQ-7-13-, 3255 - 3315	K.VNVDEVGGEALGR.L	1315.41484	2	9.04E-04	0.98	4.91	-	2161.1
AHQ-7-14-, 3251	K.VNVDEVGGEALGR.L	1315.41484	2	1.81E-04	0.97	4.44	-	1831.8
AHQ-7-13, 3405	K.VNVDEVGGEALGR.L	1315.41484	1	4.96E-05	0.24	2.01	-	329.5
AHQ-7-5, 3284	K.VNVDEVGGEALGR.L	1315.41484	2	2.92E-05	0.74	2.99	-	679.6
AHQ-7-13, 2399 - 2465	K.VVAGVANALAHK.Y	1150.35593	2	8.22E-04	0.91	3.09	-	1221.4
AHQ-7-13, 2749 - 2757	K.VVAGVANALAHK.Y	1150.35593	2	3.45E-04	0.92	3.16	-	1425.2
AHQ-7-13, 2973	K.VVAGVANALAHK.Y	1150.35593	2	5.23E-06	0.89	2.82	-	1222.9
AHQ-7-13-, 2772	K.VVAGVANALAHK.Y	1150.35593	2	1.94E-05	0.94	3.52	-	1370.4
AHQ-7-13-, 2540 - 2560	K.VVAGVANALAHK.Y	1150.35593	2	5.36E-09	0.97	4.08	-	1801.8
AHQ-7-13, 2699 - 2769	K.VVAGVANALAHK.Y	1150.35593	2	1.33E-06	0.96	3.63	-	1541.0
gi|4504351|ref|NP_000510.1| delta globin [Homo sapiens]				1.76E-12	3.76	40.24	29.90	16055.4
AHQ-7-13-, 5375	R.FFESFGDLSSPDAVM*GNPK.V	2062.24491	2	5.47E-05	0.83	3.51	-	616.2
AHQ-7-13-, 4777	R.FFESFGDLSSPDAVM*GNPK.V	2062.24491	2	1.00E-07	0.90	4.26	-	600.8
AHQ-7-13-, 5320	R.FFESFGDLSSPDAVMGNPK.V	2046.24551	2	1.76E-12	0.95	4.90	-	1125.3
AHQ-7-13, 4885 - 4887	R.FFESFGDLSSPDAVM*GNPK.V	2062.24491	2	1.69E-04	0.92	4.29	-	845.1
AHQ-7-13-, 5895	R.LLGNVLVCVLAR.N	1328.64936	2	4.46E-05	0.95	4.41	-	938.6
AHQ-7-13-, 3065 - 3141	K.VNVDAVGGEALGR.L	1257.37853	2	2.02E-04	0.96	4.36	-	1317.2
gi|10835143|ref|NP_000565.1| decay accelerating factor for complement (CD55, Cromer blood group sys				1.87E-12	0.93	10.20	5.00	41399.9
AHQ-7-5, 4804	R.EIYCPAPPQIDNGIIQGER.D	2172.40385	2	1.87E-12	0.93	4.01	-	683.7
gi|29741246|ref|XP_294070.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				1.87E-12	3.57	40.28	14.60	35032.0
AHQ-7-13-, 5155	K.AENGKLVINGNPITIFQER.D	2114.39062	2	1.80E-09	0.84	3.60	-	656.8
AHQ-7-13, 5247	K.AENGKLVINGNPITIFQER.D	2114.39062	3	2.89E-04	0.85	3.80	-	808.4
AHQ-7-9, 5133 - 5188	K.LVINGNPITIFQER.D	1614.87029	2	6.82E-10	0.93	3.51	-	981.6
AHQ-7-9, 5010 - 5069	K.LVINGNPITIFQER.D	1614.87029	2	4.20E-07	0.85	2.76	-	944.6
AHQ-7-13-, 5387 - 5463	K.LVINGNPITIFQER.D	1614.87029	2	4.16E-09	0.96	3.90	-	1394.1
AHQ-7-10, 5140 - 5199	K.LVINGNPITIFQER.D	1614.87029	2	6.51E-09	0.91	3.58	-	1088.6
AHQ-7-14-, 5501	K.LVINGNPITIFQER.D	1614.87029	2	1.91E-06	0.84	3.27	-	678.1
AHQ-7-14-, 5398 - 5446	K.LVINGNPITIFQER.D	1614.87029	2	1.80E-09	0.94	4.23	-	1106.9
AHQ-7-9, 5062 - 5124	K.LVINGNPITIFQER.D	1614.87029	2	1.87E-12	0.94	3.90	-	1184.4
AHQ-7-13, 5431 - 5509	K.LVINGNPITIFQER.D	1614.87029	2	7.76E-09	0.87	2.93	-	814.4
AHQ-7-13, 5565 - 5566	K.LVINGNPITIFQER.D	1614.87029	2	2.37E-06	0.90	2.98	-	1009.9
AHQ-7-12, 5175 - 5238	K.LVINGNPITIFQER.D	1614.87029	2	6.27E-06	0.86	2.80	-	867.1
AHQ-7-9, 4722 - 4785	K.LVINGNPITIFQERDPSK.I	2042.32440	2	4.92E-09	0.87	4.14	-	481.7
AHQ-7-9, 6080	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	2.23E-10	0.92	5.64	-	1230.6
AHQ-7-9, 6081	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	2	1.78E-06	0.90	3.95	-	1516.0
gi|5453595|ref|NP_006358.1| adenylyl cyclase-associated protein [Homo sapiens]				1.96E-12	10.00	120.28	36.00	51672.7
AHQ-7-13-, 2869	R.ALLVTASQCQQPAENK.L	1759.96271	2	3.37E-06	0.93	4.06	-	910.3
AHQ-7-11, 2814	R.ALLVTASQCQQPAENK.L	1759.96271	2	6.25E-05	0.92	3.54	-	1109.1
AHQ-7-7, 2754	R.ALLVTASQCQQPAENK.L	1759.96271	2	3.02E-04	0.92	4.14	-	731.0
AHQ-7-7, 2765	R.ALLVTASQCQQPAENK.L	1759.96271	3	1.82E-07	0.97	5.10	-	1961.8
AHQ-7-7, 2846	R.ALLVTASQCQQPAENK.L	1759.96271	2	1.80E-04	0.73	3.19	-	460.1
AHQ-7-7, 6313 - 6372	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	2.73E-04	0.73	3.63	-	900.0
AHQ-7-7, 3038	K.EFHTTGLAWSK.T	1277.40990	1	2.16E-04	0.73	3.36	-	263.5
AHQ-7-7, 3012	K.EMNDAAM*FYTNR.V	1479.62070	2	1.46E-04	0.47	2.61	-	335.5
AHQ-7-7, 2713	K.KEPAVLELEGK.K	1213.40557	2	2.38E-06	0.83	3.14	-	481.5
AHQ-7-7, 6929	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	2.10E-07	0.97	5.04	-	1682.9
AHQ-7-11, 4720	K.LSDLLAPISEQIK.E	1427.66814	2	2.29E-04	0.85	2.87	-	1015.7
AHQ-7-13-, 4880	K.LSDLLAPISEQIK.E	1427.66814	2	2.78E-07	0.86	3.32	-	777.1
AHQ-7-7, 4913	K.LSDLLAPISEQIK.E	1427.66814	1	1.78E-06	0.64	3.10	-	464.4
AHQ-7-13, 4982	K.LSDLLAPISEQIK.E	1427.66814	2	7.22E-05	0.82	2.93	-	839.0
AHQ-7-7, 4904	K.LSDLLAPISEQIK.E	1427.66814	2	2.92E-04	0.76	2.71	-	909.8
AHQ-7-7, 3418	K.NSLDCEIVSAK.S	1237.36245	1	2.60E-05	0.16	1.89	-	312.5
AHQ-7-7, 3428	K.NSLDCEIVSAK.S	1237.36245	2	9.30E-07	0.81	3.16	-	738.2
AHQ-7-7, 3265	K.NSLDCEIVSAK.S	1237.36245	1	6.28E-04	0.27	1.99	-	436.9
AHQ-7-7, 3033	K.NSLDCEIVSAK.S	1237.36245	2	2.14E-06	0.91	3.48	-	860.4
AHQ-7-14-, 3425	K.NSLDCEIVSAK.S	1237.36245	2	3.19E-09	0.94	3.64	-	1143.7
AHQ-7-7, 4664 - 4665	R.SALFAQINQGESITHALK.H	1929.16615	2	3.33E-06	0.89	4.33	-	598.6
AHQ-7-7, 4525 - 4598	R.SALFAQINQGESITHALK.H	1929.16615	2	9.17E-07	0.83	4.13	-	386.3
AHQ-7-7, 4386	R.SALFAQINQGESITHALK.H	1929.16615	2	3.00E-05	0.71	3.49	-	477.0
AHQ-7-9, 4378 - 4390	R.SALFAQINQGESITHALK.H	1929.16615	2	7.18E-04	0.80	3.49	-	637.2
AHQ-7-7, 4858	R.SALFAQINQGESITHALK.H	1929.16615	2	8.75E-05	0.85	4.04	-	523.1
AHQ-7-8, 4687	R.SALFAQINQGESITHALK.H	1929.16615	2	1.71E-08	0.93	4.94	-	643.9
AHQ-7-7, 2180	R.SGPKPFSAPKPQTSPSPK.R	1839.08461	2	5.49E-04	0.89	3.39	-	961.7
AHQ-7-7, 6357 - 6417	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	2.56E-05	0.75	3.24	-	278.4
AHQ-7-10, 4377 - 4379	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.01E-04	0.96	5.68	-	788.8
AHQ-7-8, 4683	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.96E-12	0.94	4.64	-	901.4
AHQ-7-11, 4475	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.93E-06	0.93	4.32	-	739.3
AHQ-7-7, 4672	R.VENQENVSNLVIEDTELK.Q	2074.23206	3	1.68E-04	0.92	4.68	-	1209.2
AHQ-7-7, 4652 - 4724	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.51E-04	0.93	4.01	-	996.7
AHQ-7-7, 4325	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.46E-08	0.91	4.09	-	739.4
AHQ-7-7, 4140	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.02E-08	0.93	4.34	-	861.8
AHQ-7-7, 4793 - 4873	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.20E-07	0.96	5.43	-	967.9
AHQ-7-14-, 4643	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	7.71E-05	0.94	4.38	-	884.1
gi|29568101|ref|NP_006467.3| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT				2.45E-12	0.95	10.24	14.60	11400.3
AHQ-7-14-, 3651 - 3662	K.TPALVNAAVTYSKPR.L	1588.83283	2	6.32E-07	0.94	4.19	-	1083.3
AHQ-7-14-, 3650	K.TPALVNAAVTYSKPR.L	1588.83283	3	2.45E-12	0.95	4.80	-	1454.7
gi|4506877|ref|NP_002996.1| selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;				2.53E-12	9.14	100.31	17.20	90844.7
AHQ-7-3, 5187 - 5189	K.AVQCQHLEAPSEGTMDCVHPLTAFAYGSSCK.F	3456.80579	3	2.43E-06	0.95	6.16	-	556.1
AHQ-7-2, 4824	K.AVQCQHLEAPSEGTM*DCVHPLTAFAYGSSCK.F	3472.80519	3	1.90E-05	0.78	3.80	-	593.1
AHQ-7-3, 4745	K.AVQCQHLEAPSEGTM*DCVHPLTAFAYGSSCK.F	3472.80519	3	8.69E-07	0.93	5.49	-	667.8
AHQ-7-3, 4471	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	2.13E-05	0.94	4.43	-	713.3
AHQ-7-2, 4576	K.CPELFAPEQGSLDCSDTR.G	2085.21515	2	4.02E-04	0.91	3.96	-	696.9
AHQ-7-3, 2357	K.FECQPGYR.V	1058.14914	2	8.27E-05	0.74	2.85	-	707.2
AHQ-7-3, 3021 - 3024	K.HALCYTASCQDMSCSK.Q	1923.11572	2	1.93E-08	0.98	4.81	-	1883.5
AHQ-7-2, 5800	K.LECLASGIWTNKPPQCLAAQCPPLK.I	2857.31818	3	4.19E-11	0.96	5.08	-	1362.0
AHQ-7-3, 5652	K.LECLASGIWTNKPPQCLAAQCPPLK.I	2857.31818	3	7.23E-07	0.86	4.08	-	903.6
AHQ-7-2, 5980	K.LECLASGIWTNKPPQCLAAQCPPLKIPER.G	3352.89300	3	2.78E-05	0.81	4.09	-	579.4
AHQ-7-3, 5833	K.LECLASGIWTNKPPQCLAAQCPPLKIPER.G	3352.89300	3	2.53E-12	0.89	4.36	-	875.9

AHQ-7-3, 3179	R.PSGQWTAVTPACR.A	1432.58672	2	5.36E-06	0.95	3.85	-	1364.5
AHQ-7-3, 4781 - 4783	K.STCQFICDEGYSLSGPER.L	2109.23671	2	4.50E-11	0.96	4.49	-	1102.0
AHQ-7-2, 4877	K.STCQFICDEGYSLSGPER.L	2109.23671	2	9.99E-05	0.95	4.34	-	1095.6
AHQ-7-4, 4850	K.STCQFICDEGYSLSGPER.L	2109.23671	2	4.37E-08	0.94	4.59	-	896.6
AHQ-7-6, 4750	K.STCQFICDEGYSLSGPER.L	2109.23671	2	4.45E-08	0.90	3.68	-	860.5
AHQ-7-3, 2991	R.YTDLVAIQNK.N	1165.32100	1	3.52E-05	0.13	2.07	-	419.8
AHQ-7-2, 3025	R.YTDLVAIQNK.N	1165.32100	2	2.32E-06	0.85	3.32	-	728.2
AHQ-7-3, 2999	R.YTDLVAIQNK.N	1165.32100	2	1.32E-05	0.96	3.40	-	1822.1
gi|18600882|ref|XP_089309.1| similar to Cyclophilin-LC [Homo sapiens]				2.53E-12	0.81	10.14	8.50	18166.6
AHQ-7-13, 4770 - 4781	R.IIPGFMCQGGDFTR.P	1600.84403	2	2.53E-12	0.81	2.88	-	299.8
gi|4504745|ref|NP_000410.1| integrin alpha 2b precursor [Homo sapiens]				3.13E-12	31.24	350.31	37.20	113374.2
AHQ-7-7, 5076	R.AEGGQCPSLLFDLR.D	1564.74505	2	8.80E-08	0.93	3.92	-	890.0
AHQ-7-13, 5163	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.73E-07	0.96	3.81	-	1524.4
AHQ-7-5, 5248	R.AEGGQCPSLLFDLR.D	1564.74505	2	6.93E-04	0.92	3.20	-	1122.7
AHQ-7-2, 5345	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.03E-05	0.94	4.01	-	957.0
AHQ-7-4, 5268 - 5333	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.74E-09	0.94	4.13	-	1107.1
AHQ-7-10, 4768 - 4769	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.21E-04	0.95	4.62	-	1040.6
AHQ-7-6, 5169	R.AEGGQCPSLLFDLR.D	1564.74505	2	8.43E-04	0.89	3.30	-	881.9
AHQ-7-3, 5237 - 5243	R.AEGGQCPSLLFDLR.D	1564.74505	2	9.04E-06	0.93	4.29	-	779.2
AHQ-7-4, 2873 - 2874	R.ALSNVEGFER.L	1122.21308	2	3.56E-05	0.89	3.66	-	875.9
AHQ-7-4, 4553	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.05E-05	0.44	2.65	-	512.5
AHQ-7-4, 5078 - 5150	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	6.75E-04	0.87	4.06	-	742.0
AHQ-7-5, 5043	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.70E-05	0.93	4.57	-	651.5
AHQ-7-4, 6078	K.ASVQLLVQDSLNPAVKSCVLPQTK.T	2598.01293	3	7.12E-04	0.94	4.12	-	1702.4
AHQ-7-4, 3261	R.DETRNVGSQTLQTFK.A	1724.85363	2	8.10E-08	0.72	3.17	-	532.8
AHQ-7-5, 3851 - 3874	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	8.95E-09	0.95	4.91	-	1015.2
AHQ-7-4, 3913	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	3	3.87E-04	0.77	3.53	-	1013.3
AHQ-7-4, 3880 - 3945	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	4.77E-07	0.85	3.74	-	587.0
AHQ-7-6, 3787	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.43E-06	0.86	3.28	-	675.7
AHQ-7-4, 4008 - 4048	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	3.45E-04	0.71	2.93	-	722.1
AHQ-7-3, 3875	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	4.41E-05	0.44	2.60	-	466.0
AHQ-7-6, 5567 - 5574	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	7.02E-04	0.90	4.47	-	929.9
AHQ-7-6, 5669	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.45E-04	0.69	3.50	-	599.1
AHQ-7-4, 5670 - 5732	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.11E-07	0.94	5.21	-	1014.4
AHQ-7-5, 5647 - 5714	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.03E-05	0.92	4.59	-	875.4
AHQ-7-4, 5936	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.03E-07	0.70	4.11	-	589.3
AHQ-7-4, 5796 - 5874	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.09E-09	0.94	5.26	-	1046.7
AHQ-7-5, 5778	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.54E-05	0.84	4.09	-	714.6
AHQ-7-5, 6092	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	4.73E-04	0.75	3.12	-	400.0
AHQ-7-4, 6046 - 6118	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.18E-08	0.93	5.03	-	599.5
AHQ-7-10, 4595 - 4657	R.GEAQVWTQLLR.A	1301.47614	2	3.22E-06	0.96	4.21	-	1501.5
AHQ-7-11, 4718	R.GEAQVWTQLLR.A	1301.47614	2	1.56E-05	0.88	3.90	-	772.0
AHQ-7-1, 5123	R.GEAQVWTQLLR.A	1301.47614	2	3.90E-07	0.91	3.78	-	1077.1
AHQ-7-4, 5278 - 5340	R.GNSFPASLVVAAEEGER.E	1733.86053	2	7.07E-05	0.55	2.63	-	703.6
AHQ-7-4, 5596 - 5662	R.GNSFPASLVVAAEEGER.E	1733.86053	2	2.92E-09	0.96	5.03	-	1061.2
AHQ-7-4, 5404 - 5469	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.65E-08	0.88	3.88	-	578.7
AHQ-7-4, 6537	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	1.30E-06	0.86	4.38	-	498.2
AHQ-7-4, 6341 - 6408	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	1.45E-06	0.93	5.12	-	953.2
AHQ-7-4, 6229 - 6282	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	9.58E-04	0.78	3.95	-	403.7
AHQ-7-7, 4972	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	4.11E-04	0.92	4.47	-	737.0
AHQ-7-4, 5086	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.65E-06	0.90	4.01	-	633.0
AHQ-7-4, 5224 - 5289	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.28E-04	0.97	5.28	-	1097.9
AHQ-7-5, 5202	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	1.35E-04	0.79	3.32	-	851.8
AHQ-7-3, 5209	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.43E-05	0.94	4.45	-	806.9
AHQ-7-6, 5130 - 5131	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	7.93E-09	0.97	5.52	-	1229.7
AHQ-7-5, 5206	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.20E-05	0.96	5.19	-	957.0
AHQ-7-6, 4943	R.GQVLVFLGQSEGLR.S	1503.72793	2	2.90E-06	0.97	4.27	-	1790.2
AHQ-7-7, 4860	R.GQVLVFLGQSEGLR.S	1503.72793	2	6.54E-05	0.87	3.15	-	1078.3
AHQ-7-5, 5016 - 5082	R.GQVLVFLGQSEGLR.S	1503.72793	2	4.78E-09	0.95	3.43	-	1767.0
AHQ-7-4, 5044 - 5108	R.GQVLVFLGQSEGLR.S	1503.72793	2	6.64E-08	0.97	4.38	-	1568.8
AHQ-7-4, 4464 - 4465	R.HDLLVGAPLYMESR.A	1601.85188	2	1.71E-09	0.97	4.50	-	1588.4
AHQ-7-4, 3928	R.HDLLVGAPLYM*ESR.A	1617.85128	2	2.27E-05	0.96	3.95	-	1462.4
AHQ-7-5, 4438	K.IVLLDVPVR.A	1024.28196	2	3.42E-05	0.92	3.78	-	877.2
AHQ-7-4, 4469	K.IVLLDVPVR.A	1024.28196	2	1.53E-05	0.89	3.23	-	800.1
AHQ-7-4, 4417	R.IYVENDFSWDK.R	1416.51610	1	2.46E-05	0.47	2.28	-	410.8
AHQ-7-4, 4406 - 4425	R.IYVENDFSWDK.R	1416.51610	2	1.24E-09	0.89	3.58	-	741.4
AHQ-7-6, 3882 - 3946	R.IYVENDFSWDKR.Y	1572.70245	2	4.19E-04	0.93	3.75	-	1229.5
AHQ-7-4, 3937 - 4001	R.IYVENDFSWDKR.Y	1572.70245	2	7.54E-09	0.95	4.43	-	1379.8
AHQ-7-4, 4224	R.IYVENDFSWDKR.Y	1572.70245	2	1.15E-08	0.91	3.37	-	1122.9
AHQ-7-4, 4421 - 4498	K.LSLNAELQLDR.Q	1272.43310	2	7.70E-05	0.90	3.29	-	1165.2
AHQ-7-11, 2152 - 2166	R.NRPPLEEDDEEGE	1529.50164	2	2.70E-06	0.93	3.78	-	1229.4
AHQ-7-7, 2802	R.NVGSQTLQTFK.A	1223.36055	2	3.16E-06	0.87	3.27	-	635.2
AHQ-7-4, 2766	R.NVGSQTLQTFK.A	1223.36055	2	2.24E-06	0.75	3.15	-	355.5
AHQ-7-4, 6318 - 6378	R.PSQVLDSPFPTGSAFGFSLR.G	2111.34205	2	1.39E-04	0.96	5.28	-	1122.9
AHQ-7-14-, 5637	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.31E-06	0.88	4.23	-	978.9
AHQ-7-5, 5923 - 5951	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	3.01E-09	0.94	4.58	-	694.4
AHQ-7-13, 5707	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	7.42E-04	0.83	3.30	-	1184.8
AHQ-7-6, 5843 - 5901	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	3.68E-05	0.96	4.96	-	1873.2
AHQ-7-6, 5857	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	3.13E-12	0.95	5.03	-	675.7
AHQ-7-4, 5977 - 6040	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.33E-09	0.97	6.27	-	1873.8
AHQ-7-7, 5833	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.02E-06	0.89	4.28	-	985.9
AHQ-7-1, 5828	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.53E-07	0.97	5.77	-	1808.2
AHQ-7-3, 5895	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	4.22E-07	0.96	6.08	-	1589.1
AHQ-7-4, 5768	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.29E-06	0.96	5.49	-	1860.7
AHQ-7-5, 5903 - 5963	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.52E-08	0.95	5.75	-	1068.5
AHQ-7-4, 3788	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	8.68E-10	0.94	4.73	-	836.7
AHQ-7-7, 3616	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.06E-05	0.87	4.16	-	400.3
AHQ-7-6, 3682	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	5.78E-06	0.94	4.73	-	710.7
AHQ-7-4, 3716 - 3784	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	1.71E-07	0.93	4.46	-	606.8
AHQ-7-4, 3437	K.TEEAEKTPVGSCFLAQPESGRR.A	2451.65537	3	3.52E-04	0.81	3.90	-	655.9
AHQ-7-5, 5546 - 5622	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	9.33E-07	0.90	4.27	-	722.6
AHQ-7-8, 5435	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.93E-05	0.79	3.09	-	837.5
AHQ-7-4, 5628 - 5686	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.35E-06	0.97	5.51	-	1233.5
AHQ-7-7, 5390 - 5452	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.14E-07	0.95	4.84	-	1008.4
AHQ-7-10, 5027 - 5093	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.14E-04	0.48	2.52	-	592.8
AHQ-7-2, 5580 - 5644	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.22E-06	0.26	3.04	-	332.3
AHQ-7-12, 5122	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.16E-07	0.93	4.28	-	932.4
AHQ-7-4, 5622 - 5689	R.TLGPSQEETGGVFLCPWR.A	2036.25364	3	3.17E-06	0.87	4.15	-	813.4
AHQ-7-1, 5429 - 5485	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.05E-08	0.94	4.30	-	1237.2
AHQ-7-13, 5379	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.53E-08	0.80	3.69	-	742.0
AHQ-7-13-, 5296	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.44E-06	0.94	4.59	-	910.4
AHQ-7-3, 5459 - 5519	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	8.73E-07	0.94	4.93	-	814.0
AHQ-7-6, 5429 - 5469	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.04E-06	0.95	4.96	-	932.7
AHQ-7-4, 3769 - 3786	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.09E-05	0.95	4.36	-	865.0
AHQ-7-5, 3751	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.43E-06	0.93	3.77	-	928.4
AHQ-7-7, 3629	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.89E-06	0.94	3.64	-	1016.5
AHQ-7-12, 3592	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.25E-05	0.74	3.15	-	491.1

AHQ-7-11, 3558	K.TPVGSCFLAQPESGR.R	1607.76993	2	9.54E-06	0.84	3.38	-	641.3
AHQ-7-3, 3721 - 3785	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.11E-08	0.74	3.28	-	546.0
AHQ-7-6, 3675 - 3693	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.15E-06	0.86	3.31	-	808.7
AHQ-7-4, 4564	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	1.86E-06	0.96	4.87	-	1538.9
AHQ-7-4, 4890 - 4970	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	1.75E-06	0.91	4.85	-	678.5
AHQ-7-5, 4516	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	8.31E-08	0.88	3.93	-	753.3
AHQ-7-6, 2623	R.VAIVVGAPR.T	882.08560	2	1.23E-05	0.93	2.94	-	1376.4
AHQ-7-4, 2652	R.VAIVVGAPR.T	882.08560	2	1.90E-06	0.95	3.48	-	1479.0
AHQ-7-11, 2615	R.VAIVVGAPR.T	882.08560	2	2.85E-05	0.93	3.39	-	1265.4
AHQ-7-5, 2644	R.VAIVVGAPR.T	882.08560	2	1.31E-04	0.94	3.35	-	1303.8
AHQ-7-4, 5946 - 6014	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	9.12E-04	0.95	4.88	-	1016.2
AHQ-7-4, 5668 - 5733	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.24E-07	0.98	5.90	-	1737.3
AHQ-7-4, 5820	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.98E-06	0.94	4.59	-	883.1
AHQ-7-4, 7005 - 7073	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.39E-06	0.98	6.19	-	1692.5
AHQ-7-4, 3372	R.VVLCELGNPM*K.K	1277.53632	2	1.95E-05	0.96	3.99	-	1606.2
AHQ-7-6, 4045	R.VVLCELGNPMK.K	1261.53692	2	1.25E-06	0.91	3.75	-	889.2
AHQ-7-4, 4165	R.VVLCELGNPMK.K	1261.53692	1	5.43E-05	0.53	2.78	-	620.0
AHQ-7-4, 4152	R.VVLCELGNPMK.K	1261.53692	2	2.19E-06	0.96	4.28	-	1377.8
AHQ-7-5, 4122	R.VVLCELGNPMK.K	1261.53692	2	8.37E-05	0.88	3.36	-	850.4
AHQ-7-4, 3681	R.VVLCELGNPMKK.N	1389.70984	2	4.94E-05	0.72	2.70	-	686.3
AHQ-7-6, 4165	R.VYLFLQPR.G	1036.25129	2	4.82E-06	0.94	3.28	-	1136.7
AHQ-7-4, 4309	R.VYLFLQPR.G	1036.25129	2	1.72E-05	0.95	3.61	-	1514.1
AHQ-7-5, 4268	R.VYLFLQPR.G	1036.25129	2	2.35E-06	0.95	3.17	-	1464.3
gi|4504183|ref|NP_000843.1| glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s				3.26E-12	6.95	80.25	61.00	23355.7
AHQ-7-14-, 5134	K.AFLASPEYVNLPINGNGKQ	2033.27283	2	2.10E-04	0.77	2.54	-	1068.7
AHQ-7-11, 5064 - 5128	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	1.45E-06	0.93	4.53	-	572.0
AHQ-7-11, 5070	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.76E-07	0.86	3.87	-	452.1
AHQ-7-11, 3178	K.ASCLYGQLPK.F	1138.31884	2	4.88E-07	0.90	3.49	-	880.3
AHQ-7-11, 4187	K.DQQEAALVDM*VNDGVEDLR.C	2134.26783	2	5.24E-06	0.94	4.79	-	808.1
AHQ-7-11, 5880 - 5882	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	3.21E-04	0.91	4.40	-	681.3
AHQ-7-11, 4896	K.DQQEAALVDM*VNDGVEDLR.C	2134.26783	2	1.04E-06	0.93	4.54	-	746.2
AHQ-7-11, 4894	K.DQQEAALVDMVNDGVEDLR.C	2118.26843	2	7.70E-06	0.73	3.37	-	510.8
AHQ-7-14-, 4798	K.FQDGDLTLYQSNTILR.H	1885.06701	2	4.19E-05	0.93	4.80	-	687.6
AHQ-7-11, 4743	K.FQDGDLTLYQSNTILR.H	1885.06701	2	8.95E-07	0.30	2.87	-	253.8
AHQ-7-14, 5570 - 5648	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.35E-04	0.89	4.02	-	722.3
AHQ-7-11, 4631	K.FQDGDLTLYQSNTILR.H	1885.06701	3	4.58E-07	0.92	4.85	-	866.6
AHQ-7-11, 4551 - 4606	K.FQDGDLTLYQSNTILR.H	1885.06701	2	3.26E-12	0.91	3.81	-	864.2
AHQ-7-11, 5642 - 5647	R.M*LLADQGQSWKEEVVTVETWQEGSLK.A	3009.33685	3	4.60E-05	0.92	4.92	-	1031.5
AHQ-7-11, 4280 - 4339	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	1.75E-06	0.93	4.46	-	882.8
AHQ-7-11, 4338 - 4352	K.YISLIYTNYEAGKDDYVK.A	2156.37637	3	2.46E-05	0.75	3.47	-	584.4
gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				3.67E-12	24.65	300.36	55.60	55901.8
AHQ-7-7, 2466 - 2536	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.59E-10	0.94	4.10	-	1116.2
AHQ-7-10, 2385	K.AHYGGFTVQNEANK.Y	1536.63020	2	6.91E-07	0.89	3.27	-	947.8
AHQ-7-6, 2402	K.AHYGGFTVQNEANK.Y	1536.63020	2	3.67E-12	0.94	4.54	-	1000.3
AHQ-7-6, 2518	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.01E-08	0.95	4.03	-	1243.7
AHQ-7-11, 2394	K.AHYGGFTVQNEANK.Y	1536.63020	2	4.25E-04	0.93	3.75	-	1110.3
AHQ-7-9, 2326	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.49E-05	0.90	3.13	-	908.5
AHQ-7-7, 2348	K.AHYGGFTVQNEANK.Y	1536.63020	2	3.01E-05	0.95	3.80	-	1248.0
AHQ-7-7, 6318	K.APDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	3961.41191	3	6.04E-06	0.83	3.97	-	471.6
AHQ-7-9, 3729 - 3782	K.DNENVVNEYSSELEK.H	1769.80167	2	1.97E-05	0.60	2.91	-	493.4
AHQ-7-10, 3841	K.DNENVVNEYSSELEK.H	1769.80167	2	8.04E-12	0.92	4.14	-	836.1
AHQ-7-4, 4208	K.DNENVVNEYSSELEK.H	1769.80167	2	4.54E-05	0.83	3.61	-	653.6
AHQ-7-8, 4000 - 4066	K.DNENVVNEYSSELEK.H	1769.80167	2	2.57E-05	0.79	3.39	-	607.7
AHQ-7-11, 3239	K.DNENVVNEYSSELEK.H	1769.80167	2	2.09E-04	0.57	2.98	-	385.8
AHQ-7-11, 3903	K.DNENVVNEYSSELEK.H	1769.80167	2	6.95E-09	0.86	3.86	-	754.3
AHQ-7-6, 4053 - 4117	K.DNENVVNEYSSELEK.H	1769.80167	2	1.69E-07	0.86	3.58	-	752.7
AHQ-7-7, 4204 - 4273	K.DNENVVNEYSSELEK.H	1769.80167	2	9.74E-08	0.96	5.51	-	753.7
AHQ-7-7, 4120 - 4201	K.DNENVVNEYSSELEK.H	1769.80167	2	6.99E-12	0.77	3.56	-	568.9
AHQ-7-6, 4178 - 4237	K.DNENVVNEYSSELEK.H	1769.80167	2	2.63E-09	0.92	4.49	-	808.0
AHQ-7-7, 3397	K.DNENVVNEYSSELEK.H	1769.80167	2	1.40E-05	0.56	2.82	-	578.8
AHQ-7-7, 3518 - 3580	K.DNENVVNEYSSELEK.H	1769.80167	2	4.57E-05	0.82	3.58	-	701.1
AHQ-7-13, 4110 - 4173	K.DNENVVNEYSSELEK.H	1769.80167	2	1.25E-04	0.87	4.09	-	684.9
AHQ-7-7, 3993 - 4056	K.DNENVVNEYSSELEK.H	1769.80167	2	1.94E-07	0.94	4.08	-	1043.0
AHQ-7-6, 3601	K.EDGGGWWYNR.C	1240.26508	2	2.02E-05	0.64	2.60	-	511.4
AHQ-7-11, 3486	K.EDGGGWWYNR.C	1240.26508	2	3.43E-04	0.59	2.56	-	388.2
AHQ-7-7, 3556 - 3620	K.EDGGGWWYNR.C	1240.26508	2	2.57E-04	0.70	2.67	-	519.3
AHQ-7-6, 3339 - 3414	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	3	4.22E-04	0.77	3.35	-	584.1
AHQ-7-6, 3397	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	1.53E-04	0.40	2.92	-	233.7
AHQ-7-8, 4052	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.58E-05	0.82	3.69	-	543.9
AHQ-7-7, 4014	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	7.30E-04	0.20	2.99	-	195.6
AHQ-7-7, 4001 - 4008	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	2.46E-06	0.94	4.70	-	1464.7
AHQ-7-6, 4090	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.31E-05	0.89	4.21	-	642.3
AHQ-7-6, 4081	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	4.68E-08	0.92	4.31	-	1068.0
AHQ-7-7, 3992	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	2.22E-04	0.82	3.89	-	615.0
AHQ-7-6, 4291	K.HGTDDGVVWMNWK.G	1545.70374	2	7.19E-09	0.96	4.42	-	1348.2
AHQ-7-7, 4176 - 4248	K.HGTDDGVVWMNWK.G	1545.70374	2	2.79E-05	0.95	4.15	-	1159.6
AHQ-7-6, 6113	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQER.P	3723.12454	3	2.99E-06	0.97	7.22	-	1302.7
AHQ-7-8, 6146	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQER.P	3723.12454	3	1.14E-07	0.90	3.91	-	1013.0
AHQ-7-7, 6030 - 6092	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	4089.58482	3	2.52E-04	0.71	3.90	-	254.1
AHQ-7-6, 6079 - 6081	R.KAPDAGGCLHADPDLGVLCPTGCQLQEALLQQERPIR.N	4089.58482	3	1.50E-05	0.89	4.96	-	392.4
AHQ-7-7, 3696	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	5.33E-06	0.72	3.23	-	581.4
AHQ-7-8, 3558	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	2.53E-04	0.79	3.57	-	544.5
AHQ-7-8, 3560	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	3.13E-04	0.88	3.65	-	907.0
AHQ-7-6, 3310	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	1.64E-10	0.89	4.50	-	873.6
AHQ-7-7, 3632 - 3640	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	2.51E-04	0.84	3.61	-	502.8
AHQ-7-6, 3722 - 3723	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	9.03E-04	0.79	3.43	-	938.4
AHQ-7-7, 3553 - 3633	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	4.05E-04	0.81	4.37	-	444.0
AHQ-7-8, 3230	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	8.84E-04	0.82	3.89	-	652.0
AHQ-7-7, 3216	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	1.06E-04	0.84	3.83	-	905.9
AHQ-7-6, 2909	K.KREEAPSLRPAPPPISGGGYR.A	2236.51908	3	1.55E-09	0.94	4.67	-	1205.1
AHQ-7-7, 3249 - 3326	K.LESDVSAQMEYCR.T	1589.73005	2	2.02E-07	0.91	3.44	-	1233.8
AHQ-7-7, 3414	K.LESDVSAQMEYCR.T	1589.73005	2	1.49E-04	0.77	2.57	-	732.2
AHQ-7-7, 2529	K.LESDVSAQM*EYCR.T	1605.72945	2	5.00E-05	0.90	3.47	-	817.0
AHQ-7-7, 3785	K.LESDVSAQMEYCR.T	1589.73005	2	1.49E-07	0.89	3.27	-	773.4
AHQ-7-8, 2567	K.LESDVSAQM*EYCR.T	1605.72945	2	7.55E-09	0.91	3.69	-	946.1
AHQ-7-6, 2575 - 2577	K.LESDVSAQM*EYCR.T	1605.72945	2	8.19E-08	0.94	4.20	-	945.4
AHQ-7-11, 5790 - 5855	R.M*GPTELLIEMEDWK.G	1708.97776	2	2.00E-04	0.69	2.72	-	809.8
AHQ-7-8, 6232	R.M*GPTELLIEMEDWK.G	1708.97776	2	2.00E-07	0.96	4.58	-	1431.0
AHQ-7-11, 4547	R.M*GPTELLIEM*EDWK.G	1724.97716	2	4.85E-04	0.81	3.23	-	578.4
AHQ-7-7, 6196	R.M*GPTELLIEMEDWK.G	1708.97776	2	4.26E-04	0.87	3.58	-	833.7
AHQ-7-6, 6177	R.M*GPTELLIEMEDWK.G	1708.97776	2	1.71E-04	0.82	2.95	-	922.5
AHQ-7-7, 5172	R.MGPTELLIEM*EDWK.G	1708.97776	2	8.53E-04	0.58	2.66	-	454.4
AHQ-7-7, 6364	R.MGPTELLIEMEDWK.G	1692.97836	2	3.79E-04	0.96	4.43	-	1579.9
AHQ-7-7, 6429 - 6498	R.NSVDELNNNVEAVSQTSSSSFQYMYLLK.D	3169.42237	3	5.03E-06	0.93	5.17	-	936.8
AHQ-7-7, 6556 - 6626	R.NSVDELNNNVEAVSQTSSSSFQYMYLLK.D	3169.42237	3	1.03E-04	0.90	4.61	-	914.9
AHQ-7-7, 5117 - 5185	K.NYCGLPGEYWLGNDK.I	1787.92994	2	1.95E-04	0.85	3.59	-	400.6
AHQ-7-6, 5774	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	2	2.47E-08	0.75	2.86	-	479.3

AHQ-7-7, 5772 - 5797	K.NYCGLPGEYWLGNDKISQLTR.M	2486.74455	2	5.28E-07	0.90	4.04	-	711.6
AHQ-7-6, 2213	K.QGFGNVATNTDGK.N	1309.36716	2	4.80E-05	0.71	2.93	-	530.1
AHQ-7-3, 3879	R.TPCTVSCNIPVVSGK.E	1621.85811	2	2.25E-04	0.80	3.20	-	591.4
AHQ-7-8, 3776	R.TPCTVSCNIPVVSGK.E	1621.85811	2	1.02E-05	0.87	4.18	-	422.3
AHQ-7-7, 3724	R.TPCTVSCNIPVVSGK.E	1621.85811	2	9.70E-04	0.89	3.55	-	641.2
AHQ-7-7, 4682 - 4689	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.10E-11	0.96	5.11	-	1475.5
AHQ-7-6, 4877	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	2.30E-08	0.70	3.14	-	359.8
AHQ-7-7, 4780 - 4784	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	1.98E-07	0.59	2.96	-	368.0
AHQ-7-8, 4828	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	8.42E-08	0.91	3.97	-	1206.9
AHQ-7-7, 4776 - 4804	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.03E-05	0.95	4.83	-	1196.2
AHQ-7-7, 4406	R.TPCTVSCNIPVVSGKECEEIIRK.G	2681.05731	3	2.87E-06	0.70	3.73	-	329.7
AHQ-7-8, 3963	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	1.17E-05	0.86	3.80	-	615.4
AHQ-7-6, 4039	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	8.60E-06	0.88	3.71	-	948.3
AHQ-7-8, 4438 - 4514	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.64E-09	0.97	4.82	-	1461.0
AHQ-7-7, 4513 - 4588	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.59E-09	0.97	4.86	-	1566.2
AHQ-7-7, 4342	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.39E-05	0.92	3.65	-	998.1
AHQ-7-7, 4033	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	1.92E-08	0.92	4.19	-	1104.3
AHQ-7-7, 3878 - 3952	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	9.99E-09	0.95	4.36	-	1164.1
AHQ-7-6, 4423 - 4486	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	3.71E-10	0.95	4.72	-	931.4
AHQ-7-6, 4558 - 4630	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	2.52E-06	0.84	3.40	-	733.7
AHQ-7-7, 4424 - 4454	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.52E-09	0.94	4.76	-	865.6
AHQ-7-6, 3933 - 3941	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	6.58E-08	0.95	4.52	-	1036.1
AHQ-7-7, 4370 - 4396	R.YYWGGQYTWDM*AK.H	1685.83949	2	2.53E-04	0.94	3.89	-	1123.7
AHQ-7-11, 4719	R.YYWGGQYTWDMAK.H	1669.84009	2	1.70E-08	0.84	2.96	-	950.7
AHQ-7-6, 5034	R.YYWGGQYTWDMAK.H	1669.84009	2	1.44E-10	0.95	4.05	-	1210.6
AHQ-7-6, 4457	R.YYWGGQYTWDM*AK.H	1685.83949	2	8.92E-06	0.93	3.58	-	980.2
AHQ-7-14-, 4918 - 4925	R.YYWGGQYTWDMAK.H	1669.84009	2	7.16E-06	0.97	3.87	-	2036.1
AHQ-7-7, 4928 - 4956	R.YYWGGQYTWDMAK.H	1669.84009	2	2.95E-04	0.94	3.62	-	1218.1
gi|4505877|ref|NP_000436.1| plectin 1, intermediate filament binding protein 500kDa; plectin 1, int				4.02E-12	9.78	110.24	3.40	518488.0
AHQ-7-2, 5147	R.APVPASELLASGVLSR.A	1567.81193	2	2.90E-09	0.94	3.87	-	1055.9
AHQ-7-3, 5040	R.APVPASELLASGVLSR.A	1567.81193	2	3.41E-07	0.93	3.62	-	1015.6
AHQ-7-1, 5049	R.APVPASELLASGVLSR.A	1567.81193	2	2.61E-05	0.86	3.29	-	686.8
AHQ-7-1, 3644	K.AQVEQELTTLR.L	1288.43253	2	2.28E-07	0.84	3.12	-	667.8
AHQ-7-2, 3332	K.AYSDPSTGEPATYGELQQR.C	2071.14682	2	4.02E-12	0.95	4.67	-	767.6
AHQ-7-3, 5401	R.DPYSGSTISLFQAMQK.G	1773.98806	2	2.55E-04	0.93	3.74	-	1293.4
AHQ-7-2, 5441 - 5484	R.DPYTGQSVSLFQALK.K	1654.84491	2	6.53E-05	0.92	3.99	-	978.3
AHQ-7-1, 5783 - 5791	K.EQELQQTLQQEQSVLDQLR.G	2314.49541	2	6.24E-06	0.95	4.73	-	1204.4
AHQ-7-7, 3945	R.LLDPEDVDVPQPDEK.S	1709.83251	2	4.43E-04	0.68	3.05	-	734.2
AHQ-7-1, 3841	K.NLLDEELQR.L	1130.23352	2	7.92E-04	0.79	3.12	-	714.1
AHQ-7-1, 4273	R.SIQEELQQLR.Q	1244.37976	2	4.13E-05	0.91	3.40	-	1510.7
AHQ-7-1, 4351	R.SQVEEELFSVR.V	1323.43374	2	2.22E-05	0.93	3.72	-	1153.3
AHQ-7-1, 5064	K.VQSGSESVIQEYVDLR.T	1809.95530	2	4.90E-06	0.94	4.23	-	1079.6
gi|4758086|ref|NP_004069.1| cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain				4.04E-12	6.61	70.25	50.30	20567.3
AHQ-7-11, 4043	K.GFGFGQGAGALVHSE	1434.53788	2	3.97E-07	0.96	4.41	-	1102.0
AHQ-7-13, 4321	K.GFGFGQGAGALVHSE	1434.53788	2	8.61E-04	0.86	3.07	-	925.4
AHQ-7-12, 4080	K.GFGFGQGAGALVHSE	1434.53788	2	6.57E-07	0.90	3.08	-	1083.5
AHQ-7-13-, 4183 - 4188	K.GFGFGQGAGALVHSE	1434.53788	2	8.00E-05	0.95	4.37	-	1194.3
AHQ-7-11, 3210 - 3266	K.GLESTTLADKDGEIYCK.G	1902.06957	2	5.97E-09	0.96	4.81	-	1257.4
AHQ-7-11, 2564	K.GYGYGQGAGTLSTDK.G	1475.54194	2	4.04E-12	0.95	3.95	-	1114.6
AHQ-7-13-, 3600	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	5.98E-09	0.79	3.15	-	604.9
AHQ-7-11, 3463	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	1.39E-08	0.83	3.68	-	788.6
AHQ-7-12, 3506 - 3507	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	6.30E-11	0.94	4.41	-	909.4
AHQ-7-11, 3462 - 3464	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	3.70E-11	0.94	5.07	-	623.2
AHQ-7-13, 3727	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	1.17E-04	0.75	3.36	-	488.8
AHQ-7-13, 3721	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	1.20E-10	0.79	3.80	-	498.0
AHQ-7-11, 3416	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	1.14E-09	0.96	5.04	-	968.8
AHQ-7-11, 4604	K.SCFLCMVCK.K	1208.47423	2	1.81E-04	0.91	3.61	-	682.9
AHQ-7-11, 4031	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	2.55E-05	0.83	3.89	-	516.3
AHQ-7-11, 3839	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	3.95E-09	0.94	4.52	-	929.3
gi|13562114|ref|NP_110400.1| beta tubulin 1, class VI [Homo sapiens]				4.07E-12	18.66	210.37	60.50	50326.6
AHQ-7-3, 6148	R.ALSVAELTQQMFDAR.N	1680.90740	2	8.75E-04	0.87	3.55	-	1146.2
AHQ-7-9, 5564 - 5572	R.ALSVAELTQQMFDAR.N	1680.90740	2	3.78E-05	0.91	3.39	-	1319.2
AHQ-7-8, 6152	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.74E-04	0.91	3.75	-	1347.0
AHQ-7-8, 4620	R.ALSVAELTQQM*FDAR.N	1696.90680	2	5.93E-06	0.95	4.10	-	1581.2
AHQ-7-10, 5643 - 5721	R.ALSVAELTQQMFDAR.N	1680.90740	2	9.42E-05	0.70	3.14	-	730.6
AHQ-7-7, 6121 - 6129	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.67E-06	0.96	5.14	-	1370.3
AHQ-7-7, 3766	K.AVLEEDEEVTEEAEMEPEDKGH	2516.58847	3	1.47E-05	0.28	3.05	-	231.9
AHQ-7-13-, 3532 - 3533	K.AVLEEDEEVTEEAEM*EPEDKGH	2532.58787	3	1.10E-06	0.85	3.77	-	723.6
AHQ-7-8, 4127	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	1.20E-04	0.72	3.39	-	449.3
AHQ-7-13, 4854	R.AVLVDLEPGTMDSIR.S	1616.86162	2	6.22E-06	0.94	3.86	-	1088.7
AHQ-7-12, 4614 - 4616	R.AVLVDLEPGTMDSIR.S	1616.86162	2	1.07E-05	0.69	3.00	-	478.1
AHQ-7-12, 3696 - 3758	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	3.55E-04	0.93	4.09	-	898.7
AHQ-7-7, 3880	R.EIVHIQIGQCGNQIGAK.F	1867.11965	3	4.78E-04	0.82	3.50	-	834.2
AHQ-7-14, 4665	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	3.81E-05	0.92	4.52	-	704.3
AHQ-7-14-, 3894	R.EIVHIQIGQCGNQIGAK.F	1867.11965	3	7.54E-05	0.80	3.19	-	1063.8
AHQ-7-7, 3889	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	7.04E-05	0.76	3.32	-	522.9
AHQ-7-13-, 5025	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.70E-07	0.98	5.82	-	2211.7
AHQ-7-14-, 4547	K.FWEM*IGEEHGIDLAGSDR.G	2079.23556	2	3.44E-05	0.93	3.83	-	769.5
AHQ-7-7, 5129	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	6.67E-06	0.96	4.77	-	1256.8
AHQ-7-13-, 4941 - 5017	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	3.07E-08	0.90	3.56	-	1168.8
AHQ-7-14-, 5029	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	2	2.62E-04	0.98	5.55	-	1775.6
AHQ-7-14-, 5033 - 5034	K.FWEMIGEEHGIDLAGSDR.G	2063.23616	3	3.74E-09	0.95	4.64	-	1369.9
AHQ-7-13, 6313 - 6315	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.08E-04	0.87	3.80	-	1420.0
AHQ-7-13, 6314	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	8.80E-09	0.98	6.45	-	2264.0
AHQ-7-7, 6608	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	4.51E-05	0.93	4.68	-	1899.7
AHQ-7-8, 6622	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.20E-06	0.98	6.36	-	2237.7
AHQ-7-12, 6136	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.38E-08	0.98	6.31	-	2635.3
AHQ-7-13-, 6316	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	4.24E-04	0.89	4.26	-	1627.4
AHQ-7-13-, 6319 - 6320	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.07E-12	0.99	7.33	-	2369.9
AHQ-7-11, 6168	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	8.49E-04	0.69	3.10	-	1045.8
AHQ-7-14-, 6297	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	3.46E-05	0.90	4.33	-	1554.2
AHQ-7-11, 6107 - 6163	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.16E-06	0.97	4.89	-	1803.5
AHQ-7-10, 6067	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.30E-05	0.95	4.74	-	1210.2
AHQ-7-9, 6004	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	5.12E-06	0.83	3.37	-	1176.9
AHQ-7-7, 6604 - 6669	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	7.42E-11	0.98	5.97	-	2211.2
AHQ-7-14-, 6298	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	6.10E-05	0.98	6.28	-	2514.9
AHQ-7-9, 5780 - 5794	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	6.78E-04	0.92	4.48	-	697.9
AHQ-7-13-, 6087 - 6121	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	7.04E-04	0.71	3.63	-	460.5
AHQ-7-14-, 6057 - 6086	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	7.76E-06	0.96	5.91	-	942.4
AHQ-7-7, 6345 - 6382	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.19E-05	0.94	4.88	-	745.3
AHQ-7-7, 6125 - 6137	R.HESESCDCLQGFQIVHSLGGGTGSGMGTLLMNK.I	3511.88634	3	8.53E-09	0.98	6.63	-	1979.6
AHQ-7-7, 3800 - 3868	R.IMNSFSVMPSPK.V	1338.62160	2	5.53E-08	0.94	3.56	-	1371.7
AHQ-7-7, 3132	R.ISVYYNEAYGR.K	1335.44622	2	6.41E-08	0.91	3.30	-	1065.2
AHQ-7-14-, 3230	R.ISVYYNEAYGR.K	1335.44622	1	1.37E-04	0.12	1.90	-	91.1
AHQ-7-14-, 3235	R.ISVYYNEAYGR.K	1335.44622	2	1.62E-07	0.92	3.29	-	1137.5
AHQ-7-11, 3134	R.ISVYYNEAYGR.K	1335.44622	2	4.42E-06	0.91	3.08	-	1118.9
AHQ-7-14, 4089 - 4145	R.ISVYYNEAYGR.K	1335.44622	2	5.27E-07	0.82	2.85	-	713.3

AHQ-7-13-, 3367	R.ISVYYNEAYGR.K	1335.44622	2	4.40E-06	0.89	2.71	-	954.5
AHQ-7-7, 4980	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	3.93E-09	0.86	3.73	-	765.5
AHQ-7-7, 5094 - 5161	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	2	3.86E-07	0.89	4.17	-	959.1
AHQ-7-13-, 4881 - 4939	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	5.41E-06	0.84	4.15	-	721.5
AHQ-7-14-, 4970 - 5045	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	4.02E-07	0.98	6.16	-	3076.0
AHQ-7-8, 5727	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	2.64E-06	0.79	3.62	-	328.3
AHQ-7-11, 5455	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	2.22E-06	0.92	4.19	-	603.0
AHQ-7-9, 5262	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	1.04E-05	0.93	4.71	-	529.1
AHQ-7-13, 5129 - 5130	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	5.96E-09	0.96	5.60	-	1323.2
AHQ-7-7, 5754	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	8.38E-07	0.97	6.08	-	2022.6
AHQ-7-8, 5731	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	1.80E-06	0.95	4.95	-	1325.3
AHQ-7-7, 5025	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	6.13E-05	0.96	5.25	-	745.0
AHQ-7-14-, 6227	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.09E-05	0.89	3.74	-	1195.9
AHQ-7-9, 6126	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.39E-10	0.94	4.88	-	813.0
AHQ-7-9, 5918 - 5980	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	7.55E-04	0.83	3.77	-	1045.4
AHQ-7-8, 6818	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	1.91E-07	0.88	3.96	-	702.3
AHQ-7-8, 6814 - 6819	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	2.29E-06	0.94	5.52	-	934.8
AHQ-7-7, 6796	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	2	3.38E-09	0.95	5.43	-	768.7
AHQ-7-7, 6557	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	7.02E-06	0.82	3.86	-	643.0
AHQ-7-9, 6128	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	5.56E-06	0.96	5.12	-	1477.4
AHQ-7-9, 4788 - 4848	R.NSSCFVEWIPNNVK.V	1695.87718	2	3.67E-05	0.81	3.26	-	730.0
AHQ-7-7, 5202 - 5276	R.NSSCFVEWIPNNVK.V	1695.87718	2	3.08E-04	0.42	2.83	-	357.9
AHQ-7-13, 5239	R.YLTVACIFR.G	1144.36822	2	2.76E-04	0.80	2.74	-	560.8
AHQ-7-7, 5132 - 5153	R.YLTVACIFR.G	1144.36822	2	2.14E-06	0.95	3.65	-	1021.9
gi|4758606|ref|NP_004508.1| integrin-linked kinase [Homo sapiens]				4.87E-12	11.34	130.29	27.40	51418.9
AHQ-7-7, 5465	R.EVPFADLSNMEIGMK.V	1681.95558	2	5.44E-04	0.82	3.08	-	438.2
AHQ-7-11, 4843	R.EVPFADLSNMEIGM*K.V	1697.95498	2	4.66E-04	0.46	2.53	-	249.9
AHQ-7-7, 5046 - 5052	R.EVPFADLSNMEIGM*K.V	1697.95498	2	2.78E-07	0.89	4.19	-	637.3
AHQ-7-7, 4433	K.FDM*IVPILEK.M	1221.49108	2	5.07E-07	0.85	3.34	-	744.1
AHQ-7-7, 5528	K.FDMIVPILEK.M	1205.49168	2	3.60E-04	0.92	3.38	-	1005.4
AHQ-7-7, 2066 - 2136	R.GDDTPLHLAASHGHR.D	1584.67809	2	1.14E-07	0.91	3.75	-	988.0
AHQ-7-7, 2138	R.GDDTPLHLAASHGHR.D	1584.67809	3	1.86E-09	0.90	3.62	-	1231.3
AHQ-7-7, 5026	R.GM*AFLHTLEPLIPR.H	1611.93301	2	2.50E-04	0.90	3.51	-	717.8
AHQ-7-7, 5820	R.GMAFLHTLEPLIPR.H	1595.93361	2	2.13E-07	0.96	3.94	-	1633.2
AHQ-7-8, 5774 - 5843	R.GMAFLHTLEPLIPR.H	1595.93361	2	6.16E-05	0.88	3.60	-	756.6
AHQ-7-7, 2316	K.LNENHSGELWK.G	1327.42732	2	4.24E-05	0.94	3.42	-	1570.7
AHQ-7-7, 5872 - 5873	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	9.00E-08	0.96	5.79	-	1218.3
AHQ-7-7, 5957	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	4.87E-12	0.94	5.04	-	1063.2
AHQ-7-7, 4624	R.MYAPAWVAPEALQK.K	1575.85602	2	1.80E-07	0.94	3.57	-	1180.8
AHQ-7-13, 4278 - 4343	R.M*YAPAWVAPEALQK.K	1591.85542	2	1.59E-05	0.78	2.77	-	640.2
AHQ-7-11, 4116	R.M*YAPAWVAPEALQK.K	1591.85542	2	4.65E-04	0.72	3.28	-	365.6
AHQ-7-7, 1921	K.SRDFNEECPR.L	1311.36321	2	8.26E-04	0.79	2.68	-	497.8
AHQ-7-7, 2886 - 2897	R.WQGNDIVVK.V	1059.20012	1	1.15E-05	0.71	2.30	-	753.3
gi|17986001|ref|NP_005505.2| major histocompatibility complex, class I, B; HLA class I histocompati				5.32E-12	0.95	10.24	3.90	40459.8
AHQ-7-8, 4718	R.APWIEQEGPEYWDR.N	1776.88556	2	5.32E-12	0.95	4.74	-	906.1
gi|7661678|ref|NP_056461.1| RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B				5.41E-12	4.25	50.31	26.60	20824.7
AHQ-7-14-, 5106	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	1.41E-10	0.96	5.36	-	1558.8
AHQ-7-11, 4959 - 5035	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	4.32E-06	0.94	4.72	-	1363.5
AHQ-7-11, 3988 - 4046	R.QWNNCAFLESSAK.S	1556.68148	2	1.13E-04	0.44	2.75	-	210.5
AHQ-7-11, 3680 - 3682	R.VKDTDDVPMILVGNK.C	1644.91497	3	1.01E-04	0.96	4.49	-	2093.6
AHQ-7-13-, 3860	R.VKDTDDVPMILVGNK.C	1644.91497	2	7.55E-07	0.96	4.43	-	1633.8
AHQ-7-13, 3999	R.VKDTDDVPMILVGNK.C	1644.91497	2	5.85E-06	0.85	3.36	-	1115.2
AHQ-7-6, 3819	R.VKDTDDVPMILVGNK.C	1644.91497	2	4.21E-04	0.85	3.23	-	1020.3
AHQ-7-13-, 3863	R.VKDTDDVPMILVGNK.C	1644.91497	3	1.89E-05	0.84	3.36	-	1346.1
AHQ-7-11, 3690	R.VKDTDDVPMILVGNK.C	1644.91497	2	5.76E-06	0.98	4.85	-	2102.8
AHQ-7-11, 4207 - 4266	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	5.41E-12	0.97	6.19	-	1359.9
AHQ-7-11, 4066 - 4131	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	2.44E-05	0.96	5.82	-	1373.9
AHQ-7-13-, 4160	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	2.59E-06	0.92	4.31	-	1087.7
AHQ-7-11, 4320 - 4383	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	1.06E-07	0.90	4.33	-	916.0
AHQ-7-11, 4240 - 4250	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	2	7.50E-05	0.87	3.34	-	686.4
gi|4557305|ref|NP_000025.1| aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho				5.45E-12	7.66	90.29	45.10	39419.7
AHQ-7-8, 5970 - 6004	K.CPLLKPWALTFSYGR.A	1811.13929	2	1.02E-07	0.90	4.04	-	595.4
AHQ-7-9, 3948 - 4026	K.FSHEEIAMATVTALR.R	1676.91875	2	6.29E-08	0.90	3.56	-	1047.7
AHQ-7-13-, 4337	K.FSHEEIAMATVTALR.R	1676.91875	2	1.20E-05	0.42	2.53	-	414.1
AHQ-7-8, 4230 - 4234	K.FSHEEIAMATVTALR.R	1676.91875	2	5.45E-12	0.96	4.70	-	1346.7
AHQ-7-8, 4236	K.FSHEEIAMATVTALR.R	1676.91875	3	1.49E-06	0.48	3.05	-	672.8
AHQ-7-14-, 2978	K.GILAADESTGSIAK.R	1333.47008	2	5.36E-06	0.94	3.96	-	1114.9
AHQ-7-13-, 2973	K.GILAADESTGSIAK.R	1333.47008	2	2.20E-11	0.95	4.12	-	1223.7
AHQ-7-8, 2822	K.GILAADESTGSIAK.R	1333.47008	2	3.62E-10	0.96	4.17	-	1608.3
AHQ-7-9, 2764 - 2774	K.GILAADESTGSIAK.R	1333.47008	2	6.51E-08	0.92	3.97	-	970.7
AHQ-7-12, 2948	K.GILAADESTGSIAK.R	1333.47008	2	1.12E-06	0.89	3.02	-	1097.6
AHQ-7-8, 2826	K.GILAADESTGSIAK.R	1333.47008	1	3.16E-06	0.59	2.79	-	412.6
AHQ-7-13, 3141	K.GILAADESTGSIAK.R	1333.47008	2	5.22E-09	0.97	4.14	-	1559.0
AHQ-7-8, 4386 - 4415	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	7.30E-07	0.62	4.46	-	323.9
AHQ-7-11, 4311	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	7.11E-06	0.70	3.74	-	567.5
AHQ-7-9, 3889 - 3908	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	7.53E-04	0.56	3.45	-	408.9
AHQ-7-8, 4954	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.88E-11	0.97	5.35	-	1039.2
AHQ-7-9, 4961	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	3.48E-06	0.87	3.97	-	561.6
AHQ-7-8, 5282 - 5283	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.54E-07	0.97	5.76	-	1021.6
AHQ-7-8, 2679	R.QLLLTADDR.V	1045.17176	2	4.17E-06	0.73	2.66	-	457.0
AHQ-7-8, 5802 - 5867	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	3.20E-04	0.94	4.45	-	817.4
AHQ-7-9, 5020	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	5.31E-04	0.71	3.38	-	678.2
AHQ-7-14-, 4399	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	1.21E-05	0.73	2.97	-	613.2
AHQ-7-8, 4396 - 4475	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	3.55E-09	0.88	3.73	-	596.8
gi|4505981|ref|NP_002695.1| pro-platelet basic protein (includes platelet basic protein, bet; Pro-p				5.46E-12	8.33	100.30	50.80	13894.1
AHQ-7-14, 5476 - 5536	K.EESLDSDLYAELR.C	1540.61070	2	9.43E-08	0.80	2.68	-	900.4
AHQ-7-14-, 4455	K.EESLDSDLYAELR.C	1540.61070	2	1.75E-04	0.89	3.40	-	838.4
AHQ-7-13, 4714 - 4722	K.EESLDSDLYAELR.C	1540.61070	2	9.34E-05	0.83	3.67	-	564.8
AHQ-7-14-, 4319 - 4381	K.EESLDSDLYAELR.C	1540.61070	2	1.50E-06	0.88	3.35	-	696.3
AHQ-7-14-, 4515 - 4591	K.EESLDSDLYAELR.C	1540.61070	2	1.92E-06	0.96	4.32	-	1426.0
AHQ-7-14-, 4810 - 4811	K.GKEESLDSDLYAELR.C	1725.83517	2	1.33E-08	0.95	4.01	-	1501.3
AHQ-7-12, 3976 - 4046	K.GKEESLDSDLYAELR.C	1725.83517	2	7.68E-09	0.96	4.37	-	1466.1
AHQ-7-14-, 4397	K.GKEESLDSDLYAELR.C	1725.83517	2	3.27E-11	0.97	4.83	-	2119.0
AHQ-7-13, 4293	K.GKEESLDSDLYAELR.C	1725.83517	3	1.54E-05	0.87	4.31	-	844.9
AHQ-7-14-, 4554	K.GKEESLDSDLYAELR.C	1725.83517	2	5.46E-12	0.99	6.07	-	3061.7
AHQ-7-14-, 4306	K.GKEESLDSDLYAELR.C	1725.83517	2	7.18E-06	0.97	4.09	-	2046.5
AHQ-7-14-, 4217 - 4291	K.GKEESLDSDLYAELR.C	1725.83517	3	1.55E-06	0.90	4.60	-	935.8
AHQ-7-14-, 4213 - 4286	K.GKEESLDSDLYAELR.C	1725.83517	2	9.84E-12	0.98	5.18	-	1984.5
AHQ-7-14-, 4169 - 4225	K.GKEESLDSDLYAELR.C	1725.83517	2	5.82E-09	0.98	6.05	-	2546.3
AHQ-7-14-, 4105 - 4161	K.GKEESLDSDLYAELR.C	1725.83517	3	2.38E-07	0.92	4.43	-	1179.7
AHQ-7-14-, 4042 - 4098	K.GKEESLDSDLYAELR.C	1725.83517	3	2.47E-04	0.74	3.11	-	936.5
AHQ-7-14-, 4021 - 4087	K.GKEESLDSDLYAELR.C	1725.83517	2	3.21E-10	0.98	5.89	-	2414.4
AHQ-7-14, 4733 - 4788	K.GKEESLDSDLYAELR.C	1725.83517	2	7.60E-10	0.97	5.22	-	1533.3
AHQ-7-14, 4844 - 4900	K.GKEESLDSDLYAELR.C	1725.83517	2	1.71E-10	0.98	5.52	-	2385.5
AHQ-7-14, 4958 - 5016	K.GKEESLDSDLYAELR.C	1725.83517	2	1.38E-09	0.98	5.61	-	3085.2
AHQ-7-14, 4993 - 5049	K.GKEESLDSDLYAELR.C	1725.83517	3	8.84E-06	0.86	4.30	-	743.7
AHQ-7-14-, 3903 - 3982	K.GKEESLDSDLYAELR.C	1725.83517	3	3.05E-07	0.92	4.65	-	926.5

AHQ-7-14, 5056 - 5112	K.GKEESLDSDLYAELR.C	1725.83517	2	4.07E-11	0.98	5.81	-	2594.8
AHQ-7-14, 5108 - 5164	K.GKEESLDSDLYAELR.C	1725.83517	3	4.88E-07	0.88	4.17	-	860.3
AHQ-7-14, 5168 - 5230	K.GKEESLDSDLYAELR.C	1725.83517	2	4.60E-11	0.98	5.43	-	2621.8
AHQ-7-14, 5260 - 5317	K.GKEESLDSDLYAELR.C	1725.83517	2	1.22E-08	0.98	4.99	-	2306.8
AHQ-7-14, 5373 - 5453	K.GKEESLDSDLYAELR.C	1725.83517	2	3.61E-09	0.97	5.06	-	1970.0
AHQ-7-1, 4363 - 4388	K.GKEESLDSDLYAELR.C	1725.83517	2	3.90E-05	0.94	3.90	-	1320.9
AHQ-7-14, 5478 - 5549	K.GKEESLDSDLYAELR.C	1725.83517	2	1.14E-07	0.97	4.88	-	2034.1
AHQ-7-14-, 3901 - 3961	K.GKEESLDSDLYAELR.C	1725.83517	2	7.86E-12	0.98	6.03	-	1942.8
AHQ-7-14, 5610 - 5668	K.GKEESLDSDLYAELR.C	1725.83517	2	8.26E-06	0.96	4.72	-	1369.1
AHQ-7-14-, 3766	K.GKEESLDSDLYAELR.C	1725.83517	2	1.28E-06	0.95	4.30	-	1281.1
AHQ-7-14-, 4927	K.GKEESLDSDLYAELR.C	1725.83517	2	3.15E-05	0.83	3.44	-	847.6
AHQ-7-13-, 4163	K.GKEESLDSDLYAELR.C	1725.83517	2	3.28E-10	0.98	5.10	-	2274.1
AHQ-7-13-, 4164 - 4168	K.GKEESLDSDLYAELR.C	1725.83517	3	6.31E-04	0.90	3.91	-	1145.6
AHQ-7-14-, 4707	K.GKEESLDSDLYAELRCM*CIK.T	2436.72245	3	7.65E-06	0.90	4.39	-	814.9
AHQ-7-13-, 3335 - 3408	K.GTHCNQVEVIATLK.D	1571.78073	2	1.16E-05	0.95	4.34	-	1071.4
AHQ-7-14, 4536 - 4596	K.GTHCNQVEVIATLK.D	1571.78073	2	1.74E-04	0.98	5.70	-	2263.2
AHQ-7-14, 5481	K.GTHCNQVEVIATLK.D	1571.78073	2	5.32E-04	0.82	3.27	-	874.6
AHQ-7-13, 3565 - 3622	K.GTHCNQVEVIATLK.D	1571.78073	2	9.14E-04	0.93	3.86	-	1118.0
AHQ-7-14-, 3926 - 3937	K.GTHCNQVEVIATLK.D	1571.78073	2	5.21E-04	0.95	4.60	-	1072.4
AHQ-7-14, 4298 - 4372	K.GTHCNQVEVIATLK.D	1571.78073	2	1.17E-06	0.97	4.93	-	1895.3
AHQ-7-14-, 3665 - 3721	K.GTHCNQVEVIATLK.D	1571.78073	2	4.45E-08	0.98	4.82	-	2026.7
AHQ-7-14-, 3570 - 3606	K.GTHCNQVEVIATLK.D	1571.78073	2	1.88E-05	0.97	4.42	-	1697.2
AHQ-7-14-, 3351 - 3413	K.GTHCNQVEVIATLK.D	1571.78073	2	1.63E-09	0.97	4.67	-	1558.2
AHQ-7-14, 4652 - 4714	K.GTHCNQVEVIATLK.D	1571.78073	2	5.24E-06	0.97	4.66	-	1792.6
AHQ-7-14-, 3446 - 3513	K.GTHCNQVEVIATLK.D	1571.78073	2	1.10E-07	0.97	4.55	-	1550.5
AHQ-7-14-, 3783 - 3842	K.GTHCNQVEVIATLK.D	1571.78073	2	5.86E-05	0.98	4.89	-	2157.9
AHQ-7-14-, 3202	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	3.76E-11	0.98	6.09	-	1886.8
AHQ-7-14, 4068 - 4129	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	4.01E-05	0.93	4.63	-	839.3
AHQ-7-14-, 3122 - 3181	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.95E-06	0.96	4.59	-	1581.8
AHQ-7-14-, 3110 - 3190	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	3.02E-08	0.98	5.41	-	1598.1
AHQ-7-14-, 3241 - 3266	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	8.37E-12	0.96	4.91	-	1658.8
AHQ-7-14-, 3347	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.13E-09	0.93	4.30	-	1226.1
AHQ-7-14-, 2799 - 2859	K.ICLDPDAPR.I	1058.19059	2	1.05E-04	0.74	2.51	-	839.8
AHQ-7-14, 3688 - 3758	K.ICLDPDAPR.I	1058.19059	2	2.75E-04	0.40	2.66	-	473.7
AHQ-7-13, 3122	K.ICLDPDAPR.I	1058.19059	2	1.18E-04	0.81	3.01	-	976.3
AHQ-7-14, 3801 - 3856	K.ICLDPDAPR.I	1058.19059	2	1.47E-04	0.89	3.95	-	855.0
AHQ-7-14-, 2918 - 2989	K.ICLDPDAPR.I	1058.19059	2	4.19E-04	0.83	2.99	-	917.3
AHQ-7-14, 3468 - 3536	R.KICLDPDAPR.I	1186.36350	2	3.39E-04	0.92	3.69	-	1028.1
AHQ-7-14-, 2605 - 2665	R.KICLDPDAPR.I	1186.36350	2	2.78E-05	0.90	3.25	-	1078.0
AHQ-7-14-, 2734 - 2798	R.KICLDPDAPR.I	1186.36350	2	7.46E-05	0.84	3.02	-	805.4
AHQ-7-14, 3356 - 3412	R.KICLDPDAPR.I	1186.36350	2	1.59E-05	0.81	2.95	-	832.7
AHQ-7-13, 2865	R.KICLDPDAPR.I	1186.36350	2	2.89E-04	0.41	2.58	-	371.4
AHQ-7-13-, 2676	R.KICLDPDAPR.I	1186.36350	2	7.67E-05	0.90	3.55	-	959.4
AHQ-7-14, 4240 - 4296	K.NIQSLEVIGK.G	1101.27845	2	1.28E-06	0.91	3.84	-	803.2
AHQ-7-14, 4352 - 4433	K.NIQSLEVIGK.G	1101.27845	2	2.01E-05	0.81	2.97	-	689.9
AHQ-7-14-, 4082	K.NIQSLEVIGK.G	1101.27845	2	9.73E-04	0.89	2.98	-	1249.4
AHQ-7-14-, 4071	K.NIQSLEVIGK.G	1101.27845	1	7.10E-04	0.34	2.17	-	498.1
AHQ-7-14-, 3703	K.NIQSLEVIGK.G	1101.27845	1	2.79E-04	0.81	2.70	-	928.8
AHQ-7-14, 4994	K.NIQSLEVIGK.G	1101.27845	1	1.24E-04	0.79	2.93	-	685.6
AHQ-7-14-, 3647 - 3706	K.NIQSLEVIGK.G	1101.27845	2	2.59E-06	0.89	2.82	-	1215.5
AHQ-7-14-, 3397 - 3457	K.NIQSLEVIGK.G	1101.27845	2	2.57E-05	0.91	3.62	-	900.3
AHQ-7-14-, 4515 - 4591	K.RNLAKGKEESLDSDLYAELR.C	2308.53401	3	3.64E-04	0.65	3.06	-	491.4
AHQ-7-14-, 3626	K.TTSGIHPKNIQSLEVIGK.G	1923.20305	3	1.66E-05	0.61	3.10	-	488.4
gi|5031973|ref|NP_005733.1| protein disulfide isomerase-related protein [Homo sapiens]				5.71E-12	5.51	60.30	20.70	48121.0
AHQ-7-7, 6828 - 6830	R.ALDLFSDNAPPPELLEIINEDIAK.R	2638.95072	3	1.79E-09	0.97	6.01	-	1683.8
AHQ-7-7, 6697	R.DGELPVEDDIDLSDVELDDLGKDEL	2759.86565	2	5.71E-12	0.96	5.08	-	1152.2
AHQ-7-7, 4729 - 4732	K.GSFSEQGINEFLR.E	1484.59520	2	2.56E-04	0.82	2.67	-	812.4
AHQ-7-7, 3957	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	8.87E-04	0.88	3.32	-	988.9
AHQ-7-7, 4704	K.LAAVDATVNQVLASR.Y	1528.73579	2	2.55E-05	0.94	4.04	-	1127.4
AHQ-7-13, 5886	R.TGEAIVDAALSALR.Q	1387.56411	2	1.67E-05	0.95	3.99	-	1778.2
AHQ-7-7, 6029 - 6044	R.TGEAIVDAALSALR.Q	1387.56411	2	8.76E-08	0.95	4.03	-	1688.5
gi|4507729|ref|NP_001060.1| tubulin, beta polypeptide [Homo sapiens]				7.13E-12	7.88	90.38	28.10	49906.7
AHQ-7-13-, 4653 - 4715	R.AILVDLEPGTMDSVR.S	1616.86162	2	2.99E-05	0.81	3.75	-	405.8
AHQ-7-14-, 5957	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.94E-08	0.98	6.26	-	2659.2
AHQ-7-13, 6018 - 6031	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	1.91E-04	0.91	4.79	-	1097.6
AHQ-7-12, 5808	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	9.87E-05	0.91	4.29	-	819.9
AHQ-7-7, 6192	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.13E-05	0.98	6.42	-	2743.5
AHQ-7-10, 5729 - 5744	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.79E-06	0.98	6.57	-	2435.5
AHQ-7-9, 5640	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	9.75E-06	0.97	5.32	-	1743.7
AHQ-7-13-, 5999	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	8.62E-08	0.99	6.63	-	2927.1
AHQ-7-8, 6230	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.84E-05	0.98	5.78	-	2199.6
AHQ-7-13, 6029	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.87E-07	0.99	6.28	-	3082.3
AHQ-7-13-, 4415	R.ISEQFTAMFR.R	1230.41818	2	5.44E-07	0.96	3.97	-	1859.0
AHQ-7-13, 4563	R.ISEQFTAMFR.R	1230.41818	2	5.07E-04	0.75	2.89	-	742.2
AHQ-7-13, 3781 - 3853	R.ISEQFTAM*FR.R	1246.41758	2	1.05E-05	0.85	2.84	-	844.6
AHQ-7-14-, 3622	R.ISEQFTAM*FR.R	1246.41758	2	2.13E-06	0.93	3.65	-	1234.5
AHQ-7-9, 6061	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	5.03E-06	0.78	3.07	-	569.0
AHQ-7-7, 6024	K.LTTPTYGDLNHLVSATM*SGVTTCLR.F	2727.06467	3	2.01E-05	0.79	3.20	-	1064.0
AHQ-7-9, 6060 - 6062	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	8.08E-04	0.68	3.12	-	885.3
AHQ-7-8, 6736	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	4.67E-07	0.88	4.26	-	1131.3
AHQ-7-7, 6724	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	1.62E-07	0.95	5.10	-	953.6
AHQ-7-8, 6063	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	4.59E-04	0.84	3.75	-	572.4
AHQ-7-13, 6054 - 6066	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	5.20E-04	0.27	2.89	-	347.4
AHQ-7-7, 6282 - 6349	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	2.40E-10	0.74	4.10	-	626.4
AHQ-7-14-, 5754 - 5821	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	6.25E-08	0.77	4.09	-	786.8
AHQ-7-14-, 5990	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	4.67E-05	0.82	3.99	-	820.0
AHQ-7-13, 5397	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.85E-04	0.63	2.65	-	600.1
AHQ-7-12, 5078 - 5139	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.65E-04	0.89	3.96	-	701.2
AHQ-7-13-, 5257 - 5317	K.NSSYFVEWIPNNVK.T	1697.87148	2	2.68E-04	0.92	4.20	-	848.2
AHQ-7-7, 5436 - 5512	K.NSSYFVEWIPNNVK.T	1697.87148	2	4.22E-08	0.73	3.25	-	564.4
AHQ-7-13-, 5907 - 5971	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	7.13E-12	0.98	7.56	-	1863.0
AHQ-7-9, 5608 - 5681	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	8.39E-07	0.84	4.43	-	810.6
AHQ-7-13-, 6027 - 6093	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.54E-09	0.97	6.21	-	1422.4
AHQ-7-8, 6190 - 6260	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	8.93E-07	0.90	4.17	-	792.0
AHQ-7-7, 6180 - 6245	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	2	5.93E-04	0.96	5.71	-	1017.6
AHQ-7-7, 6102 - 6170	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.62E-06	0.97	6.47	-	1719.3
AHQ-7-13, 5962 - 5997	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.03E-05	0.95	4.73	-	1698.0
gi|4557697|ref|NP_000412.1| keratin 10; Keratin-10 [Homo sapiens]				8.19E-12	4.56	50.23	10.90	57247.1
AHQ-7-1, 2987	R.ALEESNYELEGK.I	1382.45482	2	2.21E-06	0.93	3.83	-	1196.7
AHQ-7-14-, 2794	R.ALEESNYELEGK.I	1382.45482	2	8.71E-06	0.91	3.67	-	1024.3
AHQ-7-5, 2759	R.ALEESNYELEGK.I	1382.45482	2	1.22E-06	0.87	3.55	-	836.4
AHQ-7-13-, 2795	R.ALEESNYELEGK.I	1382.45482	2	4.83E-07	0.96	3.91	-	1676.2
AHQ-7-7, 2676	R.ALEESNYELEGK.I	1382.45482	2	1.03E-06	0.87	3.18	-	962.5
AHQ-7-6, 2755	R.ALEESNYELEGK.I	1382.45482	2	4.70E-04	0.83	2.96	-	930.6
AHQ-7-3, 2811	R.ALEESNYELEGK.I	1382.45482	2	5.23E-06	0.90	3.55	-	993.7
AHQ-7-1, 5299	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.24E-08	0.88	3.82	-	764.0
AHQ-7-1, 4551	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	5.67E-11	0.89	3.92	-	695.3

AHQ-7-7, 5265	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.56E-06	0.88	3.90	-	630.4
AHQ-7-2, 5447	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.85E-07	0.95	4.68	-	1017.8
AHQ-7-14-, 4363	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.48E-04	0.80	3.19	-	640.5
AHQ-7-5, 4120 - 4198	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	8.61E-06	0.61	2.72	-	611.7
AHQ-7-3, 4223 - 4249	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	2.51E-07	0.89	3.87	-	651.5
AHQ-7-2, 4313	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	4.39E-09	0.81	3.17	-	702.0
AHQ-7-12, 3962	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	2.77E-04	0.82	3.92	-	411.1
AHQ-7-13, 4209 - 4211	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	7.55E-05	0.85	3.50	-	650.4
AHQ-7-14-, 4031 - 4041	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	8.19E-12	0.91	4.65	-	659.8
AHQ-7-13-, 4075	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.15E-10	0.93	4.08	-	1054.4
AHQ-7-1, 4260	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.16E-06	0.83	3.62	-	643.7
AHQ-7-14-, 3258	K.IRLENEIQTYR.S	1435.61046	2	2.98E-07	0.92	3.88	-	1047.6
AHQ-7-1, 4999 - 5060	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	3.71E-04	0.88	4.09	-	959.0
AHQ-7-5, 5079	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	8.55E-04	0.70	2.97	-	518.0
gi|4504517|ref|NP_001531.1| heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M				8.22E-12	4.71	60.29	45.40	22782.3
AHQ-7-13-, 5316	R.KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK.L	3228.65914	3	2.47E-04	0.93	5.70	-	1364.5
AHQ-7-13, 5378	R.KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK.L	3228.65914	3	1.23E-04	0.90	5.31	-	1185.7
AHQ-7-14, 5776	R.KYTLPPGVDPTQVSSSLSPEGTLTVEAPM*PK.L	3244.65854	3	8.84E-04	0.72	4.17	-	747.6
AHQ-7-11, 5227	R.KYTLPPGVDPTQVSSSLSPEGTLTVEAPMPK.L	3228.65914	3	1.68E-06	0.90	5.83	-	943.3
AHQ-7-14-, 4657 - 4734	K.LATQSNEITIPVTFESR.A	1907.11412	2	4.11E-04	0.68	3.28	-	405.7
AHQ-7-13-, 4719	K.LATQSNEITIPVTFESR.A	1907.11412	2	4.02E-05	0.78	3.73	-	338.0
AHQ-7-13, 4741	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.49E-04	0.54	2.80	-	353.0
AHQ-7-11, 4511 - 4566	K.LATQSNEITIPVTFESR.A	1907.11412	2	4.17E-08	0.58	2.87	-	277.0
AHQ-7-10, 4287	R.LFDQAFGLPR.L	1164.33793	2	1.51E-05	0.96	4.43	-	1537.6
AHQ-7-14-, 4586	R.LFDQAFGLPR.L	1164.33793	2	4.11E-07	0.96	3.73	-	1446.3
AHQ-7-11, 4382	R.LFDQAFGLPR.L	1164.33793	2	1.21E-06	0.96	3.97	-	1504.8
AHQ-7-11, 3968	R.PLPPAAIESPAVAAPAYSR.A	1879.14874	2	2.41E-04	0.58	2.64	-	218.8
AHQ-7-11, 4419	R.VSLDVNHFAPDELTVK.T	1784.99058	3	3.22E-09	0.79	3.67	-	443.7
AHQ-7-13-, 4495 - 4555	R.VSLDVNHFAPDELTVK.T	1784.99058	2	8.22E-12	0.97	4.98	-	2157.2
AHQ-7-13-, 4544 - 4551	R.VSLDVNHFAPDELTVK.T	1784.99058	3	1.31E-06	0.89	4.38	-	494.3
AHQ-7-10, 4431 - 4456	R.VSLDVNHFAPDELTVK.T	1784.99058	2	3.55E-06	0.69	3.26	-	609.1
AHQ-7-10, 4295	R.VSLDVNHFAPDELTVK.T	1784.99058	2	6.56E-08	0.95	4.72	-	1184.6
AHQ-7-14, 5446	R.VSLDVNHFAPDELTVK.T	1784.99058	2	3.23E-05	0.63	2.93	-	526.0
AHQ-7-11, 4370 - 4435	R.VSLDVNHFAPDELTVK.T	1784.99058	2	7.75E-08	0.97	5.14	-	1445.4
AHQ-7-11, 4572 - 4632	R.VSLDVNHFAPDELTVK.T	1784.99058	2	4.31E-07	0.93	4.34	-	1003.1
gi|4501893|ref|NP_001094.1| actinin, alpha 2 [Homo sapiens]				9.30E-12	9.01	110.24	13.00	103853.1
AHQ-7-4, 4542	K.AGTQIENIEEDFR.N	1522.59861	2	3.41E-05	0.75	2.93	-	723.4
AHQ-7-12, 4970	K.AGTQIENIEEDFRNGLK.L	1935.08442	2	6.89E-05	0.16	2.62	-	339.3
AHQ-7-5, 4934	K.CQLEINFNTLQTK.L	1610.81373	2	9.43E-07	0.90	3.95	-	776.5
AHQ-7-4, 4416	K.CQLEINFNTLQTK.L	1610.81373	2	4.41E-06	0.70	2.70	-	655.7
AHQ-7-7, 4820 - 4828	K.CQLEINFNTLQTK.L	1610.81373	2	7.11E-04	0.70	3.37	-	531.3
AHQ-7-4, 5153	K.CQLEINFNTLQTK.L	1610.81373	2	1.63E-07	0.91	4.09	-	700.7
AHQ-7-5, 4844	K.EGLLLWCQR.K	1176.37031	2	8.13E-07	0.89	3.17	-	743.2
AHQ-7-6, 4157	R.FAIQDISVEETSAK.E	1538.68108	2	2.62E-07	0.90	3.47	-	953.2
AHQ-7-4, 4240 - 4304	R.FAIQDISVEETSAK.E	1538.68108	2	8.46E-05	0.90	3.60	-	1032.9
AHQ-7-4, 4257	R.FAIQDISVEETSAK.E	1538.68108	2	5.41E-11	0.93	4.27	-	927.8
AHQ-7-8, 4039 - 4116	R.FAIQDISVEETSAK.E	1538.68108	2	7.97E-05	0.30	2.66	-	319.9
AHQ-7-10, 3919	R.FAIQDISVEETSAK.E	1538.68108	2	4.31E-05	0.93	3.30	-	1325.9
AHQ-7-11, 3976 - 3982	R.FAIQDISVEETSAK.E	1538.68108	2	9.30E-12	0.95	4.49	-	1145.6
AHQ-7-4, 4130 - 4156	R.FAIQDISVEETSAK.E	1538.68108	2	1.40E-04	0.96	3.79	-	1775.1
AHQ-7-7, 4092	R.FAIQDISVEETSAK.E	1538.68108	2	2.65E-07	0.89	3.25	-	1043.4
AHQ-7-5, 4228	R.FAIQDISVEETSAK.E	1538.68108	2	2.00E-09	0.93	3.81	-	1346.4
AHQ-7-13, 4241 - 4246	R.FAIQDISVEETSAK.E	1538.68108	2	7.01E-04	0.78	2.61	-	1062.4
AHQ-7-1, 4296	R.FAIQDISVEETSAK.E	1538.68108	2	9.13E-05	0.82	3.04	-	810.3
AHQ-7-4, 5482	K.GYEEWLLNEIR.R	1422.56701	2	1.93E-07	0.93	3.30	-	1216.7
AHQ-7-4, 5960 - 5984	K.GYEEWLLNEIR.R	1422.56701	2	3.14E-07	0.97	4.66	-	1778.3
AHQ-7-2, 5988	K.GYEEWLLNEIR.R	1422.56701	2	4.99E-05	0.74	2.66	-	877.0
AHQ-7-7, 5832	K.GYEEWLLNEIR.R	1422.56701	2	1.30E-06	0.87	3.31	-	1071.0
AHQ-7-6, 5817	K.GYEEWLLNEIR.R	1422.56701	2	1.91E-07	0.96	4.41	-	1599.7
AHQ-7-4, 6100	K.GYEEWLLNEIR.R	1422.56701	2	8.04E-07	0.91	3.53	-	1184.6
AHQ-7-5, 5936	K.GYEEWLLNEIR.R	1422.56701	1	4.88E-04	0.55	2.52	-	361.0
AHQ-7-5, 5918 - 5922	K.GYEEWLLNEIR.R	1422.56701	2	1.70E-05	0.90	3.74	-	995.8
AHQ-7-4, 1994	K.HTNYTMEHIR.V	1302.44449	3	4.72E-04	0.79	3.34	-	946.8
AHQ-7-4, 2096 - 2168	R.KHEAFESDLAAHQDR.V	1754.84152	2	4.12E-08	0.93	4.10	-	929.2
AHQ-7-6, 2110	R.KHEAFESDLAAHQDR.V	1754.84152	2	4.22E-08	0.97	4.75	-	1384.1
AHQ-7-7, 2056	R.KHEAFESDLAAHQDR.V	1754.84152	2	1.39E-10	0.96	4.58	-	1380.0
AHQ-7-6, 2113	R.KHEAFESDLAAHQDR.V	1754.84152	3	1.07E-06	0.95	4.36	-	1333.8
AHQ-7-4, 3213	R.KTFTAWCNSHLR.K	1522.71309	3	7.25E-07	0.85	3.61	-	896.8
AHQ-7-4, 3224	R.KTFTAWCNSHLR.K	1522.71309	2	5.52E-07	0.87	3.44	-	836.9
AHQ-7-4, 4761	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.45E-05	0.87	2.88	-	1085.2
AHQ-7-4, 4974	K.LVSIGAEEIVDGNVK.M	1543.74400	2	2.88E-06	0.89	3.04	-	1102.0
AHQ-7-5, 4098	K.LVSIGAEEIVDGNVK.M	1543.74400	2	7.71E-04	0.88	3.73	-	807.6
AHQ-7-4, 4653	K.LVSIGAEEIVDGNVK.M	1543.74400	2	5.39E-05	0.83	3.44	-	547.1
AHQ-7-4, 4138 - 4216	K.LVSIGAEEIVDGNVK.M	1543.74400	2	5.95E-06	0.96	4.21	-	1391.0
AHQ-7-4, 4445 - 4461	K.LVSIGAEEIVDGNVK.M	1543.74400	2	8.58E-08	0.95	4.28	-	1140.0
AHQ-7-4, 3545 - 3624	K.TFTAWCNSHLR.K	1394.54018	2	5.06E-04	0.86	2.93	-	811.1
AHQ-7-5, 3608	K.TFTAWCNSHLR.K	1394.54018	2	2.63E-05	0.82	2.72	-	778.0
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				9.60E-12	15.77	180.34	60.20	49481.2
AHQ-7-7, 4004 - 4068	K.AIQLTYNPDESSKPNM*IDAATLK.S	2537.82826	3	1.99E-04	0.81	4.01	-	463.6
AHQ-7-7, 4322	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	5.22E-04	0.23	2.64	-	212.8
AHQ-7-7, 4442 - 4508	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	3	4.16E-08	0.86	3.76	-	734.7
AHQ-7-7, 6309 - 6384	K.ANQQFLVYCEIDGSGNGWTVFQK.R	2663.90221	2	6.60E-10	0.94	4.48	-	903.8
AHQ-7-14-, 5223 - 5282	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	6.17E-08	0.79	3.10	-	748.8
AHQ-7-13-, 5211 - 5271	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	4.40E-08	0.78	3.20	-	489.7
AHQ-7-7, 5352 - 5412	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.52E-07	0.79	3.14	-	677.9
AHQ-7-7, 5453 - 5516	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.05E-10	0.68	2.96	-	526.8
AHQ-7-14-, 5339 - 5403	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.04E-08	0.55	2.92	-	389.7
AHQ-7-7, 5580	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	8.65E-06	0.80	3.23	-	668.4
AHQ-7-13, 5330 - 5387	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	6.09E-08	0.71	3.32	-	424.1
AHQ-7-13-, 2804	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.97E-08	0.94	4.25	-	1000.5
AHQ-7-9, 2608	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.78E-04	0.73	3.14	-	576.0
AHQ-7-7, 2798	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.17E-07	0.91	4.32	-	541.4
AHQ-7-14-, 2814	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	1.58E-04	0.91	3.51	-	1319.7
AHQ-7-7, 2664 - 2728	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	8.61E-10	0.98	5.57	-	1648.9
AHQ-7-7, 3085 - 3108	R.DNCCILDER.F	1197.27847	2	2.79E-04	0.89	3.33	-	969.5
AHQ-7-11, 3060	R.DNCCILDER.F	1197.27847	2	3.89E-04	0.84	3.01	-	836.1
AHQ-7-7, 3254	R.DNCCILDER.F	1197.27847	2	1.35E-04	0.87	3.07	-	979.9
AHQ-7-7, 5073 - 5137	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	1.18E-04	0.95	5.08	-	1710.9
AHQ-7-7, 5100 - 5128	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.77E-08	0.95	4.96	-	755.6
AHQ-7-4, 5376	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	7.11E-04	0.87	3.60	-	1317.9
AHQ-7-7, 5194 - 5258	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.35E-06	0.96	5.04	-	1090.0
AHQ-7-1, 5288	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	5.78E-05	0.83	3.16	-	704.1
AHQ-7-4, 5372	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.28E-07	0.92	4.43	-	628.7
AHQ-7-4, 5454	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.66E-04	0.58	3.23	-	333.3
AHQ-7-8, 5090 - 5091	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	7.99E-06	0.93	4.42	-	723.5
AHQ-7-3, 5296	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	6.73E-04	0.45	2.70	-	336.1
AHQ-7-4, 6593	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	1.03E-04	0.72	3.49	-	684.5

AHQ-7-7, 6581 - 6648	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.20E-09	0.82	3.34	-	548.8
AHQ-7-7, 6452 - 6520	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.21E-09	0.95	4.95	-	934.6
AHQ-7-8, 6415 - 6475	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	1.70E-06	0.93	4.50	-	988.7
AHQ-7-6, 6419	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	7.03E-05	0.93	4.66	-	1325.2
AHQ-7-8, 6470	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	1.16E-05	0.81	3.57	-	893.0
AHQ-7-9, 5844 - 5846	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	2.65E-04	0.62	2.85	-	396.9
AHQ-7-6, 6398 - 6413	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	2.11E-05	0.84	3.24	-	652.3
AHQ-7-4, 4638 - 4716	K.IHLISTQSAIPYALR.V	1683.97576	2	9.25E-04	0.92	3.74	-	820.3
AHQ-7-9, 4160 - 4162	K.IHLISTQSAIPYALR.V	1683.97576	2	4.53E-09	0.96	4.80	-	1365.9
AHQ-7-7, 4464 - 4528	K.IHLISTQSAIPYALR.V	1683.97576	2	9.60E-12	0.96	5.39	-	1143.0
AHQ-7-3, 4683	K.IHLISTQSAIPYALR.V	1683.97576	2	1.82E-04	0.93	4.07	-	997.4
AHQ-7-6, 4569	K.IHLISTQSAIPYALR.V	1683.97576	2	6.76E-10	0.92	4.05	-	876.7
AHQ-7-8, 4435	K.IHLISTQSAIPYALR.V	1683.97576	2	2.85E-11	0.95	4.99	-	969.8
AHQ-7-7, 2060 - 2120	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.86E-10	0.96	4.41	-	1520.2
AHQ-7-8, 2098	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.82E-07	0.83	3.18	-	845.1
AHQ-7-13-, 2220 - 2285	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.07E-08	0.92	4.09	-	995.2
AHQ-7-4, 2146 - 2160	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.36E-06	0.89	4.05	-	917.9
AHQ-7-7, 6228	R.LTYAYFAGGDAGDAFDGFDFGDDPSDK.F	2835.88415	2	2.80E-05	0.82	3.48	-	481.3
AHQ-7-7, 6396 - 6462	R.LTYAYFAGGDAGDAFDGFDFGDDPSDK.F	2835.88415	2	7.18E-07	0.89	3.82	-	691.1
AHQ-7-7, 2225 - 2236	K.RLDGSVDFK.K	1037.15132	2	5.41E-04	0.84	3.29	-	427.7
AHQ-7-7, 3752 - 3824	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	2	2.11E-07	0.75	3.09	-	434.0
AHQ-7-7, 3825 - 3826	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	3.55E-05	0.91	4.65	-	845.7
AHQ-7-5, 3971	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	1.42E-04	0.87	3.93	-	931.3
AHQ-7-9, 3589 - 3610	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	1.26E-04	0.77	3.60	-	674.1
AHQ-7-7, 3986 - 4062	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	1.66E-08	0.97	6.88	-	1258.4
AHQ-7-4, 4212	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	1.03E-11	0.97	6.56	-	1761.5
AHQ-7-8, 4046 - 4059	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	9.01E-10	0.95	5.24	-	1371.1
AHQ-7-9, 3770	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	1.59E-04	0.86	4.10	-	955.7
AHQ-7-7, 3260	R.VELEDWNGR.T	1118.18129	2	1.93E-05	0.85	2.88	-	1018.8
AHQ-7-7, 3120 - 3194	R.VELEDWNGR.T	1118.18129	2	2.22E-04	0.83	3.01	-	900.6
AHQ-7-7, 1586	K.VGPEADKYR.L	1035.13542	2	2.36E-05	0.86	3.18	-	632.8
AHQ-7-7, 1514 - 1592	K.VGPEADKYR.L	1035.13542	1	3.09E-04	0.22	2.04	-	279.0
AHQ-7-11, 3014 - 3022	K.YEASILTHDSSIR.Y	1492.61564	2	6.68E-06	0.85	3.30	-	720.3
AHQ-7-9, 2828	K.YEASILTHDSSIR.Y	1492.61564	2	1.63E-06	0.83	3.15	-	635.7
AHQ-7-13-, 3120	K.YEASILTHDSSIR.Y	1492.61564	2	2.00E-04	0.80	3.13	-	653.5
AHQ-7-7, 2921 - 2988	K.YEASILTHDSSIR.Y	1492.61564	2	2.46E-05	0.90	3.63	-	746.3
AHQ-7-5, 3102	K.YEASILTHDSSIR.Y	1492.61564	2	5.77E-07	0.86	2.99	-	819.5
AHQ-7-1, 3320 - 3385	K.YEASILTHDSSIR.Y	1492.61564	2	5.54E-06	0.87	3.45	-	658.5
AHQ-7-4, 2832	R.YLQEIYNSNNQK.I	1514.62131	2	2.55E-08	0.93	4.41	-	1035.1
AHQ-7-10, 2659 - 2716	R.YLQEIYNSNNQK.I	1514.62131	2	4.34E-04	0.96	4.78	-	1188.0
AHQ-7-11, 2696 - 2768	R.YLQEIYNSNNQK.I	1514.62131	2	5.89E-08	0.92	4.51	-	827.4
AHQ-7-7, 2722 - 2766	R.YLQEIYNSNNQK.I	1514.62131	2	3.35E-04	0.96	4.57	-	1617.9
gi|10835187|ref|NP_000627.1| superoxide dismutase 2, mitochondrial [Homo sapiens]				1.04E-11	2.69	30.25	19.40	24733.0
AHQ-7-13, 5919	K.AIWNVINWENVTER.Y	1744.93137	2	7.42E-04	0.88	3.61	-	845.3
AHQ-7-13-, 5889	K.AIWNVINWENVTER.Y	1744.93137	2	9.65E-04	0.88	3.41	-	803.3
AHQ-7-14-, 5790 - 5854	K.AIWNVINWENVTER.Y	1744.93137	2	1.21E-07	0.95	4.31	-	1318.6
AHQ-7-11, 5632 - 5687	K.AIWNVINWENVTER.Y	1744.93137	2	1.04E-11	0.97	4.87	-	1416.8
AHQ-7-11, 5688	K.AIWNVINWENVTER.Y	1744.93137	3	7.11E-08	0.93	4.31	-	1139.2
AHQ-7-13-, 3847	K.GDVTAQIALQPALK.F	1425.65548	2	8.55E-07	0.87	3.63	-	776.8
AHQ-7-11, 3738 - 3811	K.GDVTAQIALQPALK.F	1425.65548	2	3.76E-09	0.75	3.21	-	626.8
AHQ-7-14-, 3857	K.GDVTAQIALQPALK.F	1425.65548	2	1.04E-05	0.87	3.87	-	739.0
AHQ-7-11, 3751	K.GDVTAQIALQPALK.F	1425.65548	1	8.07E-06	0.80	3.07	-	956.1
AHQ-7-11, 2362 - 2439	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	2.60E-10	0.97	5.09	-	1468.9
AHQ-7-14-, 2519	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	2.87E-06	0.49	2.55	-	390.7
gi|5729877|ref|NP_006588.1| heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD				1.16E-11	12.68	140.33	28.20	70897.6
AHQ-7-6, 4381	R.ARFEELNADLFR.G	1481.63768	2	5.82E-09	0.96	4.37	-	1035.2
AHQ-7-6, 4645 - 4646	R.FEELNADLFR.G	1254.37310	2	1.49E-05	0.90	3.80	-	973.0
AHQ-7-14-, 5077	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	1.16E-11	0.92	4.30	-	1045.4
AHQ-7-6, 5233 - 5237	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	4.69E-10	0.95	6.62	-	914.0
AHQ-7-6, 5238	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	2	2.55E-07	0.94	4.76	-	840.1
AHQ-7-6, 5553	K.ILDKCNEIINWLDK.N	1776.04688	2	2.16E-07	0.96	4.80	-	1462.6
AHQ-7-6, 3599	K.LDKSQIHDIVLVGGSTR.I	1839.08615	2	4.84E-07	0.94	3.96	-	1335.2
AHQ-7-6, 3442	K.NQVAMNPTNTVFDAK.R	1650.83816	2	2.23E-07	0.90	3.71	-	884.2
AHQ-7-6, 3979	K.NQVAMNPTNTVFDAK.R	1650.83816	2	2.90E-05	0.92	4.14	-	728.4
AHQ-7-6, 4571	K.NSLESYAFNMK.A	1304.45393	2	8.60E-05	0.73	3.18	-	520.7
AHQ-7-6, 4083 - 4105	K.NSLESYAFNMK.A	1304.45393	2	2.42E-05	0.91	3.89	-	865.6
AHQ-7-6, 5435	K.QTQTFTTYSDNQPGVLIQVYEGER.A	2775.96443	2	1.07E-05	0.61	2.80	-	276.2
AHQ-7-6, 2718	R.RFDDAVVQSDMK.H	1411.56603	2	6.83E-06	0.92	3.58	-	1267.6
AHQ-7-6, 2198	R.RFDDAVVQSDM*K.H	1427.56543	2	1.09E-04	0.92	3.68	-	812.2
AHQ-7-6, 5122 - 5187	K.SFYPEEVSSMVLTK.M	1617.84485	2	5.55E-07	0.94	3.78	-	823.9
AHQ-7-6, 6509 - 6513	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	5.25E-04	0.93	4.26	-	844.5
AHQ-7-6, 6518	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	8.68E-05	0.94	4.46	-	896.1
AHQ-7-7, 6565 - 6582	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	1.72E-08	0.95	4.91	-	998.3
AHQ-7-8, 2995	K.SQIHDIVLVGGSTR.I	1482.66712	2	8.22E-09	0.93	4.04	-	1166.4
AHQ-7-6, 3129 - 3203	K.SQIHDIVLVGGSTR.I	1482.66712	2	8.60E-07	0.97	4.20	-	2027.2
AHQ-7-6, 4537 - 4601	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	4.70E-06	0.91	4.37	-	498.7
gi|4506413|ref|NP_002875.1| RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				1.29E-11	7.49	90.25	54.90	20987.1
AHQ-7-11, 2471 - 2486	K.CDLEDERVVGK.E	1321.43945	2	1.02E-05	0.91	3.42	-	1040.0
AHQ-7-13-, 6355	K.INVNEIFYDLVR.Q	1495.70427	2	4.72E-10	0.96	5.06	-	1110.1
AHQ-7-5, 6735	K.INVNEIFYDLVR.Q	1495.70427	2	2.12E-06	0.92	4.07	-	832.7
AHQ-7-13, 6354	K.INVNEIFYDLVR.Q	1495.70427	2	1.44E-07	0.95	4.65	-	1067.8
AHQ-7-11, 6199	K.INVNEIFYDLVR.Q	1495.70427	1	4.24E-07	0.31	2.92	-	207.1
AHQ-7-11, 6194	K.INVNEIFYDLVR.Q	1495.70427	1	6.93E-07	0.47	3.07	-	242.1
AHQ-7-11, 6184 - 6248	K.INVNEIFYDLVR.Q	1495.70427	2	5.11E-09	0.96	4.71	-	1614.1
AHQ-7-11, 6080	K.INVNEIFYDLVR.Q	1495.70427	2	2.42E-04	0.91	3.32	-	1105.1
AHQ-7-14-, 6329	K.INVNEIFYDLVR.Q	1495.70427	2	2.78E-07	0.94	4.81	-	973.4
AHQ-7-11, 5635 - 5700	K.INVNEIFYDLVR.Q	1495.70427	2	9.86E-04	0.87	3.43	-	898.5
AHQ-7-11, 2730 - 2798	K.LVVLGSGGVGK.S	986.19059	2	3.04E-06	0.89	3.77	-	975.5
AHQ-7-13-, 2865	K.LVVLGSGGVGK.S	986.19059	2	1.37E-04	0.84	2.98	-	851.6
AHQ-7-11, 2750	K.LVVLGSGGVGK.S	986.19059	1	1.05E-04	0.80	3.06	-	714.4
AHQ-7-11, 6284 - 6343	K.NGQGFALVYSITAQSTFNDLQDLR.E	2659.89181	3	9.16E-04	0.67	3.40	-	561.4
AHQ-7-11, 6307	K.NGQGFALVYSITAQSTFNDLQDLR.E	2659.89181	2	4.45E-06	0.69	3.00	-	386.2
AHQ-7-11, 6346 - 6416	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.02E-04	0.96	4.43	-	1756.6
AHQ-7-13-, 5839 - 5899	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.17E-04	0.95	4.80	-	1477.2
AHQ-7-11, 6104 - 6171	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.23E-05	0.93	4.43	-	1164.4
AHQ-7-11, 5987 - 6047	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.66E-04	0.66	2.57	-	881.7
AHQ-7-11, 5762 - 5818	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.04E-06	0.96	4.72	-	1653.2
AHQ-7-11, 5651 - 5706	K.SALTVQFVQGIFVEK.Y	1666.94196	2	4.21E-05	0.93	3.96	-	1278.5
AHQ-7-11, 5702	K.SKINVNEIFYDLVR.Q	1710.95483	3	5.56E-08	0.93	3.94	-	1430.0
AHQ-7-14-, 5886	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.65E-10	0.95	4.46	-	1163.1
AHQ-7-11, 5002	K.SKINVNEIFYDLVR.Q	1710.95483	2	3.52E-08	0.74	3.39	-	401.0
AHQ-7-11, 5210 - 5215	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.98E-09	0.96	4.58	-	1096.9
AHQ-7-11, 5698	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.99E-08	0.97	4.72	-	1414.4
AHQ-7-11, 5936 - 5943	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.72E-06	0.87	4.08	-	819.3
AHQ-7-11, 6026	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.29E-11	0.90	3.69	-	964.7
AHQ-7-11, 3716	R.VKDTEDVPMILVGNK.C	1658.94164	2	3.05E-06	0.84	3.60	-	680.8
AHQ-7-14-, 2877	K.YDPTIEDSYR.K	1259.30338	2	1.13E-04	0.77	2.70	-	396.2

AHQ-7-11, 2772 - 2830	K.YDPTIEDSYR.K	1259.30338	2	2.38E-06	0.80	3.18	-	347.3
AHQ-7-12, 2836	K.YDPTIEDSYR.K	1259.30338	2	8.09E-06	0.64	2.53	-	410.9
AHQ-7-11, 2310	K.YDPTIEDSYRK.Q	1387.47629	2	1.24E-07	0.55	2.55	-	213.4
gi|7657431|ref|NP_055205.1| EBNA-2 co-activator (100kD) [Homo sapiens]				1.35E-11	0.84	10.27	2.40	99689.7
AHQ-7-5, 6242	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	1.10E-07	0.93	4.63	-	638.5
AHQ-7-6, 6150	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	1.35E-11	0.84	3.74	-	373.9
AHQ-7-4, 6314	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	2.03E-08	0.96	5.32	-	737.0
gi|4505733|ref|NP_002610.1| platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4				1.37E-11	7.47	80.27	39.60	10844.9
AHQ-7-14, 5010	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.82E-06	0.86	3.60	-	684.0
AHQ-7-14-, 4049	K.AGPHCPTAQLIATLK.N	1579.84600	3	3.05E-05	0.88	4.24	-	1022.4
AHQ-7-14-, 4045 - 4050	K.AGPHCPTAQLIATLK.N	1579.84600	2	1.25E-05	0.95	3.87	-	1175.7
AHQ-7-14, 5190 - 5221	K.AGPHCPTAQLIATLK.N	1579.84600	2	5.53E-07	0.94	3.89	-	1108.3
AHQ-7-13-, 4068 - 4148	K.AGPHCPTAQLIATLK.N	1579.84600	2	9.76E-09	0.85	3.44	-	568.2
AHQ-7-14, 4957	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.37E-11	0.98	5.20	-	2909.5
AHQ-7-14, 4796	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	5.97E-05	0.75	2.69	-	634.7
AHQ-7-14-, 3870	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	3.69E-06	0.92	3.95	-	911.5
AHQ-7-14-, 3975 - 3981	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	5.31E-09	0.95	4.51	-	1047.7
AHQ-7-14, 4964	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	2.54E-05	0.96	4.17	-	1338.7
AHQ-7-14-, 3641 - 3645	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	6.46E-07	0.95	4.44	-	1432.0
AHQ-7-14, 4570	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	8.67E-05	0.92	4.02	-	1179.4
AHQ-7-13, 2922 - 2985	R.HITSLEVIK.A	1040.23825	2	3.14E-04	0.79	2.91	-	404.4
AHQ-7-14-, 2614 - 2677	R.HITSLEVIK.A	1040.23825	2	1.43E-07	0.92	3.96	-	575.1
AHQ-7-14-, 2729 - 2789	R.HITSLEVIK.A	1040.23825	2	8.07E-07	0.92	3.39	-	750.9
AHQ-7-13-, 4779 - 4787	K.ICLDLQAPLYK.K	1335.59400	2	4.69E-05	0.95	3.92	-	1468.1
AHQ-7-14, 5666	K.ICLDLQAPLYK.K	1335.59400	2	2.61E-06	0.97	4.14	-	2476.0
AHQ-7-14-, 4773 - 4785	K.ICLDLQAPLYK.K	1335.59400	2	1.78E-05	0.97	4.72	-	1800.0
AHQ-7-13, 4891	K.ICLDLQAPLYK.K	1335.59400	2	2.00E-05	0.97	4.38	-	1853.4
AHQ-7-14-, 4781	K.ICLDLQAPLYK.K	1335.59400	1	4.15E-06	0.65	3.05	-	586.8
AHQ-7-14-, 4303	K.ICLDLQAPLYKK.I	1463.76691	2	3.33E-04	0.95	3.57	-	1877.8
AHQ-7-14, 5397 - 5400	R.KICLDLQAPLYK.K	1463.76691	2	8.13E-06	0.98	5.31	-	2190.6
AHQ-7-14-, 4398 - 4461	R.KICLDLQAPLYK.K	1463.76691	2	5.19E-06	0.97	5.09	-	1321.1
AHQ-7-14-, 4430 - 4465	R.KICLDLQAPLYK.K	1463.76691	3	1.79E-06	0.91	3.87	-	1768.6
AHQ-7-14, 5301	R.KICLDLQAPLYK.K	1463.76691	2	4.47E-04	0.64	3.33	-	651.1
AHQ-7-14-, 3994 - 4059	R.KICLDLQAPLYKK.I	1591.93982	3	5.19E-08	0.94	4.48	-	1261.5
AHQ-7-14-, 3995	R.KICLDLQAPLYKK.I	1591.93982	2	3.17E-04	0.92	3.83	-	1259.0
gi|5031857|ref|NP_005557.1| lactate dehydrogenase A [Homo sapiens]				1.45E-11	1.75	20.31	7.20	36688.5
AHQ-7-13, 6301	K.DLADELALVDVIEDK.L	1658.82864	2	1.81E-04	0.96	4.46	-	1670.4
AHQ-7-14-, 6281	K.DLADELALVDVIEDK.L	1658.82864	2	3.80E-08	0.96	4.29	-	1503.6
AHQ-7-13-, 6303 - 6304	K.DLADELALVDVIEDK.L	1658.82864	2	1.45E-11	0.98	6.13	-	1930.8
AHQ-7-9, 6000	K.DLADELALVDVIEDK.L	1658.82864	2	1.07E-04	0.91	3.32	-	1380.7
AHQ-7-13-, 2877	K.LVIITAGAR.Q	914.12760	2	4.01E-04	0.77	2.74	-	800.0
gi|14251209|ref|NP_001279.2| chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo				1.51E-11	4.92	60.28	28.20	26922.5
AHQ-7-9, 5185 - 5204	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	3	1.52E-04	0.82	3.17	-	1117.7
AHQ-7-9, 5398 - 5432	K.FLDGNELTLADCNLLPK.L	1935.18752	2	6.25E-05	0.81	3.66	-	562.0
AHQ-7-10, 5507 - 5585	K.FLDGNELTLADCNLLPK.L	1935.18752	2	1.10E-04	0.88	4.05	-	924.1
AHQ-7-13, 3593	K.GVTFNVTTVDTK.R	1282.42476	2	1.87E-07	0.93	4.07	-	1045.3
AHQ-7-9, 3150	K.GVTFNVTTVDTK.R	1282.42476	2	4.38E-07	0.56	2.51	-	522.2
AHQ-7-13, 3559 - 3585	K.GVTFNVTTVDTK.R	1282.42476	2	4.82E-06	0.89	3.46	-	787.4
AHQ-7-10, 3253	K.GVTFNVTTVDTK.R	1282.42476	2	3.50E-06	0.84	3.25	-	658.2
AHQ-7-13-, 3421 - 3439	K.GVTFNVTTVDTK.R	1282.42476	2	2.94E-07	0.93	3.59	-	1058.6
AHQ-7-13-, 5267	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.51E-11	0.97	5.57	-	960.4
AHQ-7-9, 4958 - 4960	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.29E-05	0.85	3.52	-	539.2
AHQ-7-13, 5202 - 5259	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.43E-05	0.97	5.52	-	1108.4
AHQ-7-13, 5345	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.23E-05	0.70	3.17	-	300.9
AHQ-7-14-, 5186	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.08E-05	0.92	4.66	-	641.4
AHQ-7-13-, 5171	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.15E-06	0.96	5.45	-	730.2
AHQ-7-9, 2674 - 2678	K.LHIVQVVCK.K	1097.35623	1	7.61E-04	0.55	2.16	-	640.4
AHQ-7-10, 2748 - 2755	K.LHIVQVVCK.K	1097.35623	2	2.50E-06	0.79	2.71	-	546.2
AHQ-7-10, 2267	K.NSNPALNDNLEK.G	1329.39838	2	4.07E-05	0.60	2.70	-	612.0
gi|4507487|ref|NP_003238.1| thrombospondin 2 [Homo sapiens]				1.57E-11	1.77	20.24	2.60	129954.5
AHQ-7-1, 5019	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.87E-05	0.92	3.37	-	1103.9
AHQ-7-11, 4754	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	2.51E-05	0.91	3.18	-	1295.8
AHQ-7-6, 4995 - 5053	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	6.66E-04	0.90	3.82	-	980.3
AHQ-7-2, 5119 - 5199	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.57E-11	0.96	4.80	-	1409.5
AHQ-7-5, 5170	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	7.34E-09	0.95	4.60	-	1224.7
AHQ-7-3, 5064	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	2.96E-06	0.93	3.69	-	1255.5
AHQ-7-4, 5166	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.07E-05	0.85	3.21	-	911.2
AHQ-7-4, 2990	R.NALWHTGNTPGQVR.T	1551.69124	2	9.31E-07	0.90	3.50	-	934.2
AHQ-7-5, 2742 - 2812	R.NALWHTGNTPGQVR.T	1551.69124	2	8.04E-05	0.74	2.78	-	651.9
AHQ-7-3, 3041	R.NALWHTGNTPGQVR.T	1551.69124	2	8.60E-05	0.83	3.21	-	787.5
AHQ-7-6, 2705	R.NALWHTGNTPGQVR.T	1551.69124	2	9.10E-04	0.83	3.45	-	784.7
AHQ-7-6, 2939	R.NALWHTGNTPGQVR.T	1551.69124	2	3.37E-05	0.69	3.01	-	535.7
AHQ-7-2, 3064	R.NALWHTGNTPGQVR.T	1551.69124	2	5.81E-04	0.93	3.45	-	1273.4
AHQ-7-7, 2576 - 2637	R.NALWHTGNTPGQVR.T	1551.69124	2	8.16E-06	0.78	3.08	-	753.9
AHQ-7-7, 2864	R.NALWHTGNTPGQVR.T	1551.69124	2	1.81E-07	0.81	3.17	-	746.6
AHQ-7-11, 2686 - 2694	R.NALWHTGNTPGQVR.T	1551.69124	2	4.97E-06	0.91	4.01	-	963.7
AHQ-7-2, 2823	R.NALWHTGNTPGQVR.T	1551.69124	3	1.73E-04	0.74	3.38	-	649.9
AHQ-7-14-, 2813	R.NALWHTGNTPGQVR.T	1551.69124	2	2.06E-04	0.91	3.14	-	1156.2
gi|20357552|ref|NP_005222.2| cortactin isoform a; oncogene EMS1 [Homo sapiens]				1.71E-11	5.25	60.29	19.60	61585.7
AHQ-7-14-, 4747 - 4758	K.ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK.E	3334.37643	3	5.77E-07	0.94	5.75	-	634.6
AHQ-7-11, 3931	R.GPVSGTEPEPVYSMEAADYR.E	2156.31513	2	8.53E-04	0.91	3.90	-	716.6
AHQ-7-13-, 3957	R.LPSSPVYEDAASFK.A	1511.65733	2	6.37E-05	0.73	2.62	-	630.4
AHQ-7-13, 3997	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	2.55E-08	0.93	4.39	-	1092.6
AHQ-7-12, 3764	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	3.97E-04	0.93	3.94	-	1075.7
AHQ-7-14-, 3859	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	1.71E-11	0.96	4.78	-	1324.0
AHQ-7-14, 4677	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	2.94E-07	0.88	3.61	-	877.7
AHQ-7-13-, 2943 - 2956	K.VDKSAVGFEYQGK.T	1428.57155	2	1.13E-05	0.85	3.55	-	607.0
AHQ-7-13, 3121	K.VDKSAVGFEYQGK.T	1428.57155	2	1.59E-04	0.81	2.94	-	774.8
AHQ-7-12, 5010	R.YGLFPANYVELR.Q	1442.64306	2	6.13E-08	0.85	3.26	-	632.8
gi|4504071|ref|NP_000164.1| platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA				1.80E-11	5.22	60.21	12.80	68955.0
AHQ-7-4, 3873	K.AMTSNVASVQCDNSDKFPVYK.Y	2363.60999	2	1.80E-11	0.88	3.80	-	853.0
AHQ-7-1, 4969	R.GLGELQELYLK.G	1263.46458	2	1.66E-04	0.94	3.91	-	1305.3
AHQ-7-4, 4921 - 4997	R.GLGELQELYLK.G	1263.46458	2	1.00E-04	0.89	3.55	-	995.1
AHQ-7-3, 4935	R.GLGELQELYLK.G	1263.46458	2	2.41E-06	0.93	3.99	-	1099.4
AHQ-7-12, 3919 - 3926	R.GQDLLSTVSIR.Y	1189.34410	2	6.72E-07	0.95	3.98	-	1261.8
AHQ-7-3, 4147 - 4155	R.GQDLLSTVSIR.Y	1189.34410	2	2.28E-05	0.94	3.53	-	1259.9
AHQ-7-1, 4235	R.GQDLLSTVSIR.Y	1189.34410	2	2.36E-05	0.95	3.81	-	1304.8
AHQ-7-13-, 4027 - 4057	R.GQDLLSTVSIR.Y	1189.34410	2	7.26E-07	0.94	3.75	-	1273.8
AHQ-7-12, 2222 - 2292	R.GVLQGHLESSR.N	1183.29965	2	8.24E-05	0.78	2.55	-	798.4
AHQ-7-3, 2141 - 2211	R.GVLQGHLESSR.N	1183.29965	2	6.66E-07	0.79	2.76	-	691.6
AHQ-7-4, 2158 - 2169	R.GVLQGHLESSR.N	1183.29965	2	1.07E-06	0.86	2.81	-	907.5
AHQ-7-3, 3687	R.LTQLNLDRCELTK.L	1605.83862	2	1.17E-04	0.81	3.58	-	755.6
AHQ-7-4, 3661 - 3692	R.LTQLNLDRCELTK.L	1605.83862	2	8.35E-04	0.50	2.67	-	664.2
AHQ-7-1, 4871 - 4889	R.WLQDNAENVYVWK.Q	1665.82948	2	8.05E-05	0.86	3.10	-	1072.9
AHQ-7-3, 4844 - 4885	R.WLQDNAENVYVWK.Q	1665.82948	2	2.91E-05	0.87	3.43	-	1248.1
gi|14249382|ref|NP_116139.1| hypothetical protein MGC15429 [Homo sapiens]				1.84E-11	0.65	10.16	6.70	22345.5
AHQ-7-11, 3890	R.FSSETWQNLGTLHR.L	1676.81390	2	1.84E-11	0.65	3.26	-	500.6

gi|7669492|ref|NP_002037.2| glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]				2.41E-11	6.83	80.32	28.40	36053.0
AHQ-7-9, 3377	R.GALQNIIPASTGAAK.A	1412.61680	1	1.34E-06	0.69	3.61	-	305.2
AHQ-7-10, 5779 - 5835	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	4.64E-04	0.96	6.13	-	1209.9
AHQ-7-11, 6240	K.VIHDNFGIVEGLMTTVHAITATQK.T	2596.98694	3	1.10E-10	0.98	6.48	-	1718.6
AHQ-7-11, 5871 - 5938	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	5.59E-04	0.97	6.21	-	1694.7
AHQ-7-10, 4205	R.VIISAPSADAPM*FVMGVNHEK.Y	2230.59327	2	2.50E-05	0.56	2.97	-	373.2
AHQ-7-9, 4568 - 4569	R.VIISAPSADAPMFVMGVNHEK.Y	2214.59387	2	7.76E-06	0.87	3.95	-	517.7
AHQ-7-10, 3851 - 3917	R.VPTANVSVVDLTCR.L	1532.74450	2	1.05E-08	0.96	4.44	-	1299.1
AHQ-7-5, 4183 - 4260	R.VPTANVSVVDLTCR.L	1532.74450	2	9.15E-07	0.89	3.32	-	802.4
AHQ-7-11, 3930 - 3932	R.VPTANVSVVDLTCR.L	1532.74450	2	7.93E-09	0.94	4.20	-	1039.4
AHQ-7-9, 3741 - 3840	R.VPTANVSVVDLTCR.L	1532.74450	2	6.82E-08	0.87	3.31	-	848.1
AHQ-7-9, 3896 - 3897	R.VPTANVSVVDLTCR.L	1532.74450	2	3.64E-05	0.84	3.25	-	588.8
AHQ-7-1, 4264 - 4324	R.VPTANVSVVDLTCR.L	1532.74450	2	5.91E-05	0.85	3.28	-	621.0
AHQ-7-12, 3964 - 4023	R.VPTANVSVVDLTCR.L	1532.74450	2	5.76E-07	0.89	3.64	-	737.5
AHQ-7-13, 4118 - 4177	R.VPTANVSVVDLTCR.L	1532.74450	2	4.48E-09	0.92	3.57	-	1002.2
AHQ-7-14, 4901 - 4905	R.VPTANVSVVDLTCR.L	1532.74450	2	1.83E-08	0.90	3.70	-	972.8
AHQ-7-13-, 4051	R.VPTANVSVVDLTCR.L	1532.74450	2	2.41E-11	0.95	4.42	-	1134.4
AHQ-7-14-, 4025	R.VPTANVSVVDLTCR.L	1532.74450	2	4.82E-11	0.95	4.32	-	1055.0
AHQ-7-13-, 5828 - 5892	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	1.03E-05	0.88	3.86	-	741.8
AHQ-7-13-, 5329	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	1.23E-06	0.95	4.73	-	952.4
gi|17986273|ref|NP_524144.1| fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2				2.50E-11	0.92	10.23	8.20	21145.0
AHQ-7-13, 3502	R.VFDKEGNGTVMGAELR.H	1723.93228	2	2.50E-11	0.92	3.60	-	1069.1
AHQ-7-13-, 3339 - 3419	R.VFDKEGNGTVMGAELR.H	1723.93228	2	1.49E-07	0.81	3.47	-	708.3
AHQ-7-12, 3227 - 3352	R.VFDKEGNGTVMGAELR.H	1723.93228	2	3.95E-09	0.96	4.55	-	1235.9
gi|10834976|ref|NP_000572.1| glutathione peroxidase 1 [Homo sapiens]				2.72E-11	6.61	80.21	42.80	21909.0
AHQ-7-11, 5144 - 5152	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	2.72E-11	0.92	4.20	-	754.8
AHQ-7-11, 2784 - 2842	R.DYTQMNELQR.R	1298.40778	2	7.95E-04	0.94	3.68	-	1224.0
AHQ-7-11, 3975	K.FLVGPDGVPLR.R	1170.38561	2	1.92E-08	0.93	3.57	-	906.4
AHQ-7-11, 3790	K.LITWSPVCR.N	1133.34543	2	4.37E-05	0.75	2.77	-	582.3
AHQ-7-11, 3267	R.NDVAWNFEK.F	1123.19953	1	4.41E-05	0.38	2.29	-	351.8
AHQ-7-11, 3778	R.PLAGGEPVSLGSLR.G	1353.54935	2	3.88E-08	0.92	3.61	-	839.6
AHQ-7-11, 5068	K.YVRPGGGFEPNFMLFEK.C	1989.28515	2	4.35E-04	0.94	4.29	-	1209.5
AHQ-7-11, 4800	K.YVRPGGGFEPNFM*LFEK.C	2005.28455	3	4.61E-05	0.83	3.38	-	851.6
gi|4503571|ref|NP_001419.1| enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n				2.86E-11	8.73	100.24	31.30	47168.7
AHQ-7-13-, 5119	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.86E-11	0.92	4.60	-	467.1
AHQ-7-11, 4966	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.77E-05	0.90	3.77	-	566.3
AHQ-7-14, 5901	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.35E-04	0.89	3.74	-	534.2
AHQ-7-13, 5209 - 5225	R.AAVPSGASTGIYEALELR.D	1806.00979	2	6.31E-05	0.94	4.50	-	591.1
AHQ-7-8, 5140	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.57E-04	0.85	3.11	-	556.1
AHQ-7-7, 6640	K.DYPVVSIEDPFDQDDWGAWQK.F	2511.63977	2	1.12E-06	0.86	3.28	-	798.6
AHQ-7-8, 4178 - 4179	R.GNPTVEVDLFTSK.G	1407.55065	2	2.38E-05	0.85	3.69	-	795.5
AHQ-7-8, 4182	R.GNPTVEVDLFTSK.G	1407.55065	1	9.26E-11	0.72	3.35	-	783.0
AHQ-7-8, 5746	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	4.15E-06	0.91	4.17	-	1363.0
AHQ-7-8, 2296 - 2298	R.IGAEVYHNLK.N	1144.30502	2	5.51E-05	0.93	4.00	-	1144.5
AHQ-7-8, 5956	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	1.79E-05	0.94	4.84	-	1133.8
AHQ-7-8, 6630	K.LAMQEFMILPVGAANFR.E	1909.30812	2	9.48E-05	0.92	4.68	-	501.7
AHQ-7-8, 5510	K.LAM*QEFM*ILPVGAANFR.E	1941.30692	2	5.71E-05	0.96	4.77	-	956.6
AHQ-7-14, 4572	K.VNQIGSVTESLQACK.L	1635.82159	2	1.33E-06	0.64	2.93	-	547.6
AHQ-7-13-, 3733	K.VNQIGSVTESLQACK.L	1635.82159	2	4.60E-06	0.95	4.46	-	1108.5
AHQ-7-8, 3967	K.VNQIGSVTESLQACK.L	1635.82159	2	1.58E-04	0.88	4.02	-	780.4
AHQ-7-8, 4728	R.YISPDQLADLYK.S	1426.59557	1	6.26E-06	0.84	3.49	-	758.5
AHQ-7-8, 4723 - 4724	R.YISPDQLADLYK.S	1426.59557	2	1.84E-09	0.94	4.47	-	708.7
AHQ-7-9, 4437 - 4441	R.YISPDQLADLYK.S	1426.59557	2	1.14E-06	0.90	3.99	-	604.4
AHQ-7-7, 4794	R.YISPDQLADLYK.S	1426.59557	2	1.58E-07	0.84	3.79	-	491.8
gi|13775198|ref|NP_112576.1| SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr				2.94E-11	3.25	40.27	31.20	10437.7
AHQ-7-14-, 4666	R.IQYQLVDISQDNALR.D	1776.97168	2	1.27E-04	0.90	3.49	-	1185.6
AHQ-7-14-, 4579	R.IQYQLVDISQDNALR.D	1776.97168	2	3.93E-11	0.98	5.26	-	2111.8
AHQ-7-13-, 4576	R.IQYQLVDISQDNALR.D	1776.97168	3	6.50E-07	0.94	4.99	-	1559.2
AHQ-7-13, 4669 - 4730	R.IQYQLVDISQDNALR.D	1776.97168	2	3.48E-08	0.96	4.13	-	1732.5
AHQ-7-13, 4695	R.IQYQLVDISQDNALR.D	1776.97168	3	3.10E-06	0.94	3.60	-	2117.4
AHQ-7-13, 4802	R.IQYQLVDISQDNALR.D	1776.97168	2	6.93E-09	0.97	5.14	-	1527.0
AHQ-7-13-, 4687 - 4691	R.IQYQLVDISQDNALR.D	1776.97168	2	2.94E-11	0.97	5.39	-	1587.3
AHQ-7-13-, 4556 - 4625	R.IQYQLVDISQDNALR.D	1776.97168	2	2.81E-09	0.95	4.51	-	1264.1
AHQ-7-13-, 4276 - 4335	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.11E-04	0.77	3.26	-	509.2
AHQ-7-13-, 4401 - 4465	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.08E-06	0.69	3.24	-	409.7
AHQ-7-14-, 4833 - 4890	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	2.90E-06	0.76	3.44	-	537.6
AHQ-7-13, 4231 - 4297	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	9.28E-06	0.75	3.47	-	593.8
AHQ-7-13-, 1799 - 1856	R.VYSTSVTGSR.E	1057.13940	2	9.89E-05	0.86	3.04	-	990.6
AHQ-7-13, 2162 - 2237	R.VYSTSVTGSR.E	1057.13940	2	4.26E-04	0.95	3.63	-	1361.4
AHQ-7-13-, 2023 - 2053	R.VYSTSVTGSR.E	1057.13940	2	5.20E-06	0.90	2.85	-	1034.8
AHQ-7-13-, 1915 - 1972	R.VYSTSVTGSR.E	1057.13940	2	1.17E-07	0.82	2.57	-	901.2
AHQ-7-13, 2066 - 2105	R.VYSTSVTGSR.E	1057.13940	2	1.77E-05	0.86	2.83	-	1049.1
gi|7705296|ref|NP_057271.1| bridging integrator 2; bridging integrator-2; breast cancer associated				3.00E-11	4.69	60.27	17.60	61746.8
AHQ-7-10, 5436 - 5495	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	4.58E-08	0.91	4.11	-	999.7
AHQ-7-10, 5573	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	2.38E-05	0.77	2.77	-	870.5
AHQ-7-10, 2752	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	7.06E-05	0.76	3.42	-	465.0
AHQ-7-10, 2611	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	1.03E-04	0.74	2.92	-	559.6
AHQ-7-5, 6571 - 6572	R.IGCYVTIFQNISNLR.D	1800.07167	2	3.00E-11	0.97	4.86	-	1582.6
AHQ-7-6, 6459	R.IGCYVTIFQNISNLR.D	1800.07167	2	5.46E-08	0.85	3.95	-	637.2
AHQ-7-7, 6485	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.76E-06	0.96	5.38	-	989.0
AHQ-7-10, 2892	K.LNHNLYEVMSK.L	1348.55307	2	7.86E-06	0.75	2.91	-	685.4
AHQ-7-5, 4299	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	1.73E-04	0.66	3.07	-	477.6
AHQ-7-7, 4144	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	5.01E-05	0.41	2.76	-	419.7
AHQ-7-14-, 4901	R.VSETLQEIYSSEWDGHEELK.A	2380.50595	3	3.69E-05	0.89	3.71	-	1365.4
gi|4757810|ref|NP_004037.1| ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,				3.09E-11	5.52	70.24	13.60	59750.3
AHQ-7-7, 3837	R.EAYPGDVFYLHSR.L	1554.68713	2	3.09E-11	0.78	2.99	-	519.8
AHQ-7-7, 3482	K.HALIIYDDLSK.Q	1288.47413	2	5.13E-04	0.88	2.54	-	1100.7
AHQ-7-7, 3688	R.ILGADTSVDLEETGR.V	1576.68772	2	2.36E-06	0.95	3.69	-	1626.6
AHQ-7-7, 2604	K.LELAQYR.E	893.02211	1	5.12E-04	0.18	1.84	-	216.2
AHQ-7-7, 5188 - 5189	R.TGAIVDVPVGEELLGR.V	1625.84824	2	4.76E-05	0.95	4.70	-	902.5
AHQ-7-7, 3741	K.TGTAEMSSILEER.I	1424.55988	2	4.17E-05	0.95	3.46	-	1662.0
AHQ-7-7, 2597	K.TGTAEM*SSILEER.I	1440.55928	2	1.55E-04	0.82	2.85	-	1271.5
gi|21389339|ref|NP_653174.1| likely ortholog of rat F-actin binding protein nexilin [Homo sapiens]				3.51E-11	0.96	10.29	6.30	60335.1
AHQ-7-13-, 5109 - 5177	K.RAEQIEDINNTGTESASEEGDDSLLITVVPVK.S	3431.66128	3	3.51E-11	0.96	5.70	-	1329.9
gi|17921989|ref|NP_005991.1| tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain				3.88E-11	14.70	170.28	48.70	49924.1
AHQ-7-13, 4679 - 4759	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	1.65E-04	0.89	3.97	-	1128.6
AHQ-7-13-, 4489 - 4548	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	4.72E-08	0.95	4.87	-	1301.3
AHQ-7-13-, 4999 - 5011	R.AFVHWYVGEGMEEGEFSEAR.E	2331.50495	3	1.55E-07	0.94	4.79	-	1326.8
AHQ-7-13, 5326 - 5331	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	6.86E-08	0.97	4.48	-	1698.8
AHQ-7-11, 5578 - 5596	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.55E-05	0.96	4.82	-	1480.1
AHQ-7-13, 5758 - 5817	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	4.18E-06	0.94	4.07	-	1460.2
AHQ-7-14-, 5718	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	5.15E-07	0.91	3.82	-	1264.0
AHQ-7-13-, 5736 - 5739	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.84E-08	0.96	5.03	-	1361.6
AHQ-7-14-, 5055	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	6.41E-05	0.94	3.93	-	1459.6
AHQ-7-13, 5133 - 5162	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.41E-06	0.96	4.71	-	1621.3
AHQ-7-13-, 5491	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	8.79E-05	0.84	3.49	-	942.7
AHQ-7-7, 5942 - 6004	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.58E-06	0.95	4.09	-	1315.0

AHQ-7-13-, 5008 - 5068	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	4.18E-05	0.94	4.41	-	1292.9
AHQ-7-7, 5125 - 5154	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.42E-05	0.93	4.36	-	916.7
AHQ-7-13-, 5217	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	8.96E-05	0.93	3.97	-	1131.6
AHQ-7-14-, 5714	R.AVFVDLEPTVIDEIR.N	1716.95615	2	4.71E-08	0.89	3.32	-	1355.3
AHQ-7-13-, 5692 - 5755	R.AVFVDLEPTVIDEIR.N	1716.95615	2	2.62E-07	0.93	3.89	-	1501.7
AHQ-7-11, 5590 - 5668	R.AVFVDLEPTVIDEIR.N	1716.95615	2	1.62E-07	0.79	3.00	-	972.1
AHQ-7-7, 5002	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	2	1.09E-05	0.97	5.65	-	1116.6
AHQ-7-7, 5373 - 5446	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	3	8.09E-05	0.87	4.10	-	705.7
AHQ-7-7, 3533	K.DVNAAIAAIK.T	986.14745	1	1.77E-05	0.84	2.60	-	1012.2
AHQ-7-12, 3279 - 3339	K.DVNAAIAAIK.T	986.14745	1	6.74E-05	0.47	2.50	-	411.4
AHQ-7-7, 3348	K.DVNAAIAAIK.T	986.14745	2	5.70E-04	0.91	2.82	-	1500.2
AHQ-7-12, 3026	K.DVNAAIAAIK.T	986.14745	1	3.95E-08	0.87	2.48	-	1304.7
AHQ-7-7, 6628 - 6629	R.FDGALNVDLTEFQTNLVPYPR.I	2410.66639	2	2.28E-04	0.92	4.42	-	768.6
AHQ-7-7, 3304 - 3344	K.FDLMYAK.R	888.06574	1	1.25E-04	0.31	2.10	-	342.0
AHQ-7-8, 4994 - 5068	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.09E-04	0.89	3.50	-	639.2
AHQ-7-7, 4924 - 4988	R.IHFPLATYAPVISAEK.A	1758.05310	2	5.46E-06	0.95	4.62	-	728.6
AHQ-7-9, 4624 - 4680	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.70E-06	0.89	3.79	-	454.0
AHQ-7-13-, 5000	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.57E-05	0.91	3.93	-	572.3
AHQ-7-13-, 6311	R.LISQIVSSITASLR.F	1488.75471	2	1.03E-10	0.94	4.32	-	1024.8
AHQ-7-7, 6600	R.LISQIVSSITASLR.F	1488.75471	2	5.48E-09	0.95	4.48	-	959.9
AHQ-7-8, 6628	R.LISQIVSSITASLR.F	1488.75471	2	2.98E-08	0.94	3.95	-	984.5
AHQ-7-14-, 6289 - 6290	R.LISQIVSSITASLR.F	1488.75471	2	9.03E-10	0.96	4.42	-	1465.0
AHQ-7-7, 5809	R.LISQIVSSITASLR.F	1488.75471	2	3.02E-04	0.85	3.13	-	823.4
AHQ-7-9, 5993	R.LISQIVSSITASLR.F	1488.75471	2	2.06E-07	0.91	3.52	-	1003.5
AHQ-7-10, 6055	R.LISQIVSSITASLR.F	1488.75471	2	5.44E-04	0.90	3.82	-	752.5
AHQ-7-11, 6172	R.LISQIVSSITASLR.F	1488.75471	2	6.91E-05	0.76	2.57	-	917.2
AHQ-7-13-, 3463 - 3483	R.NLDIERPTYTNLNR.L	1719.88022	2	5.18E-06	0.57	3.07	-	301.7
AHQ-7-7, 3385 - 3389	R.NLDIERPTYTNLNR.L	1719.88022	2	9.60E-05	0.50	3.12	-	379.2
AHQ-7-8, 3350	R.NLDIERPTYTNLNR.L	1719.88022	2	1.75E-06	0.81	3.46	-	632.3
AHQ-7-5, 3527	R.NLDIERPTYTNLNR.L	1719.88022	2	1.00E-04	0.22	2.52	-	295.3
AHQ-7-14-, 3502	R.NLDIERPTYTNLNR.L	1719.88022	2	5.12E-05	0.75	3.27	-	622.6
AHQ-7-14, 4322 - 4330	R.NLDIERPTYTNLNR.L	1719.88022	2	3.80E-04	0.53	2.91	-	364.1
AHQ-7-7, 5612 - 5625	R.SIQFVDWCPTGFK.V	1586.79232	2	4.69E-06	0.88	3.43	-	910.0
AHQ-7-14-, 5462	R.SIQFVDWCPTGFK.V	1586.79232	2	1.03E-04	0.87	3.21	-	739.2
AHQ-7-13-, 5472	R.SIQFVDWCPTGFK.V	1586.79232	2	4.02E-07	0.91	3.66	-	881.6
AHQ-7-12, 5283 - 5360	R.SIQFVDWCPTGFK.V	1586.79232	2	4.05E-05	0.76	2.67	-	701.8
AHQ-7-11, 5310 - 5322	R.SIQFVDWCPTGFK.V	1586.79232	2	6.31E-05	0.92	3.82	-	924.0
AHQ-7-14-, 5387 - 5393	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.88E-11	0.93	4.24	-	748.0
AHQ-7-10, 5157	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	5.82E-08	0.78	3.57	-	429.2
AHQ-7-14, 6230 - 6233	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.89E-08	0.86	3.84	-	625.4
AHQ-7-1, 5567	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.67E-06	0.63	3.06	-	337.7
AHQ-7-12, 5214 - 5218	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.29E-07	0.81	3.45	-	588.3
AHQ-7-7, 5520 - 5585	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.05E-08	0.93	4.48	-	843.0
AHQ-7-13-, 5396	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	7.31E-11	0.88	4.14	-	507.0
AHQ-7-11, 5254	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.31E-09	0.79	3.82	-	372.0
AHQ-7-9, 5030 - 5088	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	6.47E-07	0.87	3.60	-	737.3
AHQ-7-13, 5485	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.25E-09	0.88	3.94	-	672.9
AHQ-7-13-, 4269	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.07E-05	0.44	2.79	-	251.6
AHQ-7-13, 4393 - 4470	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	9.13E-07	0.73	3.66	-	269.6
AHQ-7-12, 4168 - 4250	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	7.78E-04	0.79	3.19	-	433.8
AHQ-7-14-, 4294 - 4354	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	5.14E-10	0.69	2.75	-	440.4
AHQ-7-7, 4376	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	9.35E-05	0.50	2.64	-	257.6
AHQ-7-1, 4548	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	3.14E-04	0.65	3.22	-	333.0
AHQ-7-7, 4361	K.YMACCLLYR.G	1252.50864	1	1.62E-04	0.60	3.20	-	278.7
AHQ-7-7, 3882	K.YM*ACCLLYR.G	1268.50804	2	6.91E-04	0.82	2.72	-	647.7
AHQ-7-7, 4353 - 4360	K.YMACCLLYR.G	1252.50864	2	4.36E-05	0.96	4.28	-	897.6
AHQ-7-11, 4224	K.YMACCLLYR.G	1252.50864	2	4.41E-05	0.92	2.82	-	1084.7
gi|27482573|ref|XP_208709.1| similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro				4.06E-11	1.67	20.24	26.00	17875.4
AHQ-7-12, 4624	K.GQVCLPVISAENWKPATK.T	2000.30757	2	8.97E-05	0.75	3.52	-	461.0
AHQ-7-12, 6135	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	4.06E-11	0.93	4.90	-	715.5
gi|17986260|ref|NP_524147.1| smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo				4.16E-11	0.97	10.32	23.30	12969.7
AHQ-7-14-, 5342	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	9.48E-07	0.95	5.29	-	1546.5
AHQ-7-12, 5183 - 5186	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	4.16E-11	0.97	6.32	-	1656.4
gi|4504391|ref|NP_000179.1| hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]				4.21E-11	3.53	40.20	5.60	102502.4
AHQ-7-4, 4496	K.ATDCVGHDVVTLLR.D	1557.75406	2	4.21E-11	0.94	3.83	-	1041.0
AHQ-7-4, 5484	K.KLPVGFTFSFPCQQSK.I	1873.16425	2	2.73E-06	0.93	3.88	-	1097.2
AHQ-7-4, 5901	K.LPVGFTFSFPCQQSK.I	1744.99134	2	1.53E-05	0.78	3.33	-	482.7
AHQ-7-4, 5981	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	4.16E-07	0.89	4.05	-	736.8
gi|4502027|ref|NP_000468.1| albumin precursor; PRO0883 protein [Homo sapiens]				4.39E-11	37.85	460.37	71.40	69366.4
AHQ-7-5, 2531 - 2562	K.AAFTECCQAADK.A	1374.47927	2	7.14E-04	0.88	3.33	-	872.5
AHQ-7-6, 2530	K.AAFTECCQAADK.A	1374.47927	1	9.72E-07	0.39	2.70	-	335.4
AHQ-7-6, 2517	K.AAFTECCQAADK.A	1374.47927	2	1.49E-06	0.87	3.17	-	981.2
AHQ-7-7, 2498	K.AAFTECCQAADK.A	1374.47927	1	1.93E-04	0.61	2.77	-	549.2
AHQ-7-6, 1850	K.ADDKETCFAEEGKK.L	1629.72754	2	4.46E-06	0.64	3.26	-	576.2
AHQ-7-6, 1786 - 1851	K.ADDKETCFAEEGKK.L	1629.72754	2	5.72E-05	0.80	2.59	-	1061.9
AHQ-7-5, 1819 - 1860	K.ADDKETCFAEEGKK.L	1629.72754	2	1.07E-05	0.93	4.06	-	1250.7
AHQ-7-6, 1855	K.ADDKETCFAEEGKK.L	1629.72754	3	4.81E-10	0.93	4.45	-	1481.0
AHQ-7-6, 1935 - 1994	K.AEFAEVSK.L	880.96496	2	4.59E-05	0.82	2.78	-	456.2
AHQ-7-5, 1974	K.AEFAEVSK.L	880.96496	1	4.15E-04	0.62	2.41	-	576.5
AHQ-7-5, 5400	K.AEFAEVSKLVTDLTK.V	1651.88247	2	7.59E-06	0.68	3.12	-	739.7
AHQ-7-6, 6703	K.ALVLIAFAQYLQQCPFEDHVK.L	2492.87697	3	2.21E-04	0.83	3.71	-	734.8
AHQ-7-5, 6806	K.ALVLIAFAQYLQQCPFEDHVK.L	2492.87697	3	3.97E-08	0.93	4.36	-	1106.6
AHQ-7-6, 4397 - 4461	K.AVM*DDFAAFVEK.C	1359.52946	2	4.05E-05	0.84	3.02	-	536.9
AHQ-7-11, 5074	K.AVMDDFAAFVEK.C	1343.53006	2	4.92E-07	0.95	4.38	-	1259.9
AHQ-7-3, 5443	K.AVMDDFAAFVEK.C	1343.53006	2	1.32E-06	0.86	2.99	-	1041.1
AHQ-7-12, 5063	K.AVMDDFAAFVEK.C	1343.53006	2	6.34E-05	0.81	2.74	-	1005.3
AHQ-7-10, 4972	K.AVMDDFAAFVEK.C	1343.53006	2	8.83E-09	0.95	4.22	-	1238.7
AHQ-7-1, 5409	K.AVMDDFAAFVEK.C	1343.53006	2	6.69E-07	0.90	3.65	-	941.9
AHQ-7-13, 5334	K.AVMDDFAAFVEK.C	1343.53006	2	4.70E-09	0.93	3.58	-	1044.9
AHQ-7-13-, 4357	K.AVM*DDFAAFVEK.C	1359.52946	2	1.46E-04	0.88	2.90	-	745.8
AHQ-7-13-, 5228 - 5231	K.AVMDDFAAFVEK.C	1343.53006	2	7.49E-09	0.93	3.70	-	1129.7
AHQ-7-14-, 4417	K.AVM*DDFAAFVEK.C	1359.52946	2	4.06E-06	0.89	3.34	-	813.9
AHQ-7-7, 5372	K.AVMDDFAAFVEK.C	1343.53006	2	6.32E-05	0.93	3.87	-	1024.2
AHQ-7-6, 5323 - 5389	K.AVMDDFAAFVEK.C	1343.53006	2	5.85E-09	0.95	4.42	-	1278.4
AHQ-7-5, 5480	K.AVMDDFAAFVEK.C	1343.53006	1	8.64E-07	0.82	3.56	-	756.1
AHQ-7-5, 5454	K.AVMDDFAAFVEK.C	1343.53006	2	5.81E-08	0.95	3.70	-	1418.4
AHQ-7-14-, 5234	K.AVMDDFAAFVEK.C	1343.53006	2	9.53E-08	0.97	4.25	-	1484.1
AHQ-7-6, 2165 - 2169	K.CCAAADPHECYAK.V	1556.67999	2	1.87E-07	0.93	4.04	-	891.1
AHQ-7-5, 2168	K.CCAAADPHECYAK.V	1556.67999	2	4.75E-04	0.76	3.21	-	587.8
AHQ-7-5, 2106	K.CCKADDKETCFAEEGKK.L	2080.26010	3	7.14E-07	0.97	5.91	-	2062.8
AHQ-7-6, 2417 - 2483	K.CCTESLVNR.R	1141.25805	1	3.83E-05	0.09	1.81	-	89.4
AHQ-7-7, 2400 - 2405	K.CCTESLVNR.R	1141.25805	2	5.50E-05	0.80	2.76	-	822.3
AHQ-7-5, 2412 - 2414	K.CCTESLVNR.R	1141.25805	1	4.40E-07	0.27	2.24	-	97.1
AHQ-7-5, 2410 - 2420	K.CCTESLVNR.R	1141.25805	2	2.68E-04	0.90	3.21	-	1113.7
AHQ-7-6, 2379 - 2445	K.CCTESLVNR.R	1141.25805	2	4.63E-04	0.94	2.93	-	1458.1
AHQ-7-5, 6598 - 6656	K.DVFLGM*FLYEYAR.R	1640.88331	2	1.24E-07	0.96	4.47	-	1133.3
AHQ-7-6, 6491	K.DVFLGM*FLYEYAR.R	1640.88331	2	4.58E-05	0.91	3.49	-	1002.8

AHQ-7-7, 6560 - 6638	K.DVFLGM*FLYEYAR.R	1640.88331	2	5.51E-04	0.82	3.36	-	530.0
AHQ-7-13-, 2723	R.ETYGEMADCCAK.Q	1437.55563	2	2.59E-05	0.60	2.86	-	393.8
AHQ-7-5, 2071 - 2079	R.ETYGEM*ADCCAK.Q	1453.55503	2	9.52E-05	0.83	2.89	-	669.6
AHQ-7-6, 2670	R.ETYGEMADCCAK.Q	1437.55563	1	1.33E-08	0.49	2.63	-	158.4
AHQ-7-5, 3016	R.ETYGEMADCCAKQEPER.N	2077.21652	2	9.66E-08	0.87	3.69	-	599.6
AHQ-7-6, 3926	R.ETYGEMADCCAKQEPERNECFLQHK.D	3135.38952	3	2.28E-10	0.68	3.61	-	395.3
AHQ-7-6, 2690	R.FKDLGEENFK.A	1227.34766	2	4.40E-07	0.83	3.51	-	703.3
AHQ-7-6, 2699	R.FKDLGEENFK.A	1227.34766	1	7.39E-05	0.31	1.99	-	437.5
AHQ-7-7, 2641	R.FKDLGEENFK.A	1227.34766	1	8.45E-05	0.22	1.83	-	396.6
AHQ-7-5, 2724 - 2730	R.FKDLGEENFK.A	1227.34766	1	2.43E-05	0.59	2.57	-	429.5
AHQ-7-13, 2986	R.FKDLGEENFK.A	1227.34766	2	7.60E-06	0.86	3.14	-	820.4
AHQ-7-13, 2991	R.FKDLGEENFK.A	1227.34766	3	3.71E-04	0.85	3.52	-	1084.8
AHQ-7-6, 2781	R.FKDLGEENFK.A	1227.34766	2	5.07E-06	0.76	3.00	-	550.3
AHQ-7-13-, 2815	R.FKDLGEENFK.A	1227.34766	2	1.52E-05	0.77	3.22	-	631.8
AHQ-7-10, 2933	K.FQNALLVR.Y	961.14282	2	7.45E-04	0.70	2.64	-	726.2
AHQ-7-5, 6446 - 6462	R.HPYFYAPELLFFAK.R	1744.02658	2	2.87E-04	0.65	2.51	-	386.9
AHQ-7-6, 6354	R.HPYFYAPELLFFAK.R	1744.02658	3	5.55E-06	0.91	4.06	-	1074.1
AHQ-7-5, 6450	R.HPYFYAPELLFFAK.R	1744.02658	3	1.03E-06	0.94	3.79	-	1539.4
AHQ-7-6, 6353	R.HPYFYAPELLFFAK.R	1744.02658	2	6.29E-04	0.83	3.10	-	390.0
AHQ-7-6, 2742 - 2743	K.KQTALVELVK.H	1129.37494	1	7.11E-05	0.25	2.20	-	306.0
AHQ-7-5, 2778	K.KQTALVELVK.H	1129.37494	1	9.11E-04	0.41	2.29	-	438.9
AHQ-7-9, 3252 - 3262	K.KVPQVSTPTLVEVSR.N	1640.90605	2	5.39E-06	0.70	2.50	-	561.6
AHQ-7-1, 3796	K.KVPQVSTPTLVEVSR.N	1640.90605	3	6.40E-07	0.95	4.59	-	1565.8
AHQ-7-6, 3295	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.18E-07	0.95	3.79	-	1175.0
AHQ-7-5, 3571 - 3646	K.KVPQVSTPTLVEVSR.N	1640.90605	3	3.23E-09	0.97	5.42	-	1612.8
AHQ-7-7, 3472	K.KVPQVSTPTLVEVSR.N	1640.90605	2	5.71E-04	0.72	3.15	-	704.5
AHQ-7-6, 3497 - 3561	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.16E-09	0.90	3.53	-	792.0
AHQ-7-5, 3326	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.51E-08	0.87	3.33	-	661.0
AHQ-7-5, 3550 - 3618	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.12E-08	0.92	3.71	-	925.9
AHQ-7-10, 3359	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.70E-04	0.74	2.97	-	356.5
AHQ-7-2, 3747	K.KVPQVSTPTLVEVSR.N	1640.90605	2	9.44E-06	0.93	3.75	-	1035.0
AHQ-7-1, 3791 - 3872	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.36E-08	0.83	3.35	-	552.1
AHQ-7-6, 3513 - 3515	K.KVPQVSTPTLVEVSR.N	1640.90605	3	5.75E-06	0.95	5.32	-	1326.1
AHQ-7-7, 3493	K.KVPQVSTPTLVEVSR.N	1640.90605	3	1.48E-08	0.94	4.72	-	1096.3
AHQ-7-6, 2703	K.KYLYEIAR.R	1056.23937	2	1.05E-04	0.80	2.72	-	615.1
AHQ-7-5, 1567 - 1639	K.LDELRDEGK.A	1075.15472	2	1.38E-05	0.70	2.78	-	606.8
AHQ-7-5, 2454 - 2466	K.LKECCEKPLLEK.S	1549.83503	3	1.48E-05	0.89	4.65	-	723.9
AHQ-7-13-, 4044	K.LVAASQAALGL	1014.20080	2	3.05E-06	0.94	3.53	-	1071.1
AHQ-7-5, 4162	K.LVAASQAALGL	1014.20080	2	2.62E-05	0.96	3.82	-	1383.3
AHQ-7-5, 3335 - 3370	K.LVNEVTEFAK.T	1150.30633	2	3.80E-05	0.88	2.89	-	767.6
AHQ-7-3, 3425	K.LVNEVTEFAK.T	1150.30633	2	5.30E-06	0.60	2.62	-	437.6
AHQ-7-5, 3338 - 3412	K.LVNEVTEFAK.T	1150.30633	1	9.28E-04	0.65	2.37	-	869.0
AHQ-7-14-, 3306	K.LVNEVTEFAK.T	1150.30633	1	3.03E-04	0.19	2.24	-	392.5
AHQ-7-6, 3287 - 3365	K.LVNEVTEFAK.T	1150.30633	2	3.76E-07	0.92	3.85	-	775.5
AHQ-7-6, 3185	K.LVNEVTEFAK.T	1150.30633	2	3.10E-05	0.75	2.97	-	437.8
AHQ-7-1, 3548	K.LVNEVTEFAK.T	1150.30633	2	1.66E-05	0.83	3.02	-	600.6
AHQ-7-5, 3226	K.LVNEVTEFAK.T	1150.30633	1	4.36E-05	0.37	2.07	-	331.6
AHQ-7-5, 3562	K.LVNEVTEFAK.T	1150.30633	2	7.77E-07	0.92	3.55	-	831.7
AHQ-7-14-, 3301	K.LVNEVTEFAK.T	1150.30633	2	5.16E-06	0.76	2.81	-	668.0
AHQ-7-10, 3160	K.LVNEVTEFAK.T	1150.30633	2	4.71E-05	0.82	2.94	-	555.2
AHQ-7-5, 3175 - 3238	K.LVNEVTEFAK.T	1150.30633	2	5.42E-05	0.58	2.70	-	326.2
AHQ-7-5, 3566	K.LVNEVTEFAK.T	1150.30633	1	1.53E-05	0.81	2.74	-	1034.4
AHQ-7-13, 3490 - 3558	K.LVNEVTEFAK.T	1150.30633	2	8.17E-06	0.76	2.98	-	486.8
AHQ-7-13-, 3355 - 3360	K.LVNEVTEFAK.T	1150.30633	1	4.56E-04	0.81	2.91	-	795.4
AHQ-7-7, 3228	K.LVNEVTEFAK.T	1150.30633	2	1.18E-04	0.92	3.41	-	964.5
AHQ-7-5, 4870 - 4920	R.LVRPEVDVM*CTAFHDNEETFLK.K	2668.98368	3	5.91E-04	0.95	5.53	-	1193.6
AHQ-7-5, 5724	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	3.63E-05	0.98	6.74	-	2561.8
AHQ-7-7, 5628	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	3.72E-06	0.98	6.65	-	2215.9
AHQ-7-6, 5629	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	1.17E-06	0.98	7.37	-	2211.7
AHQ-7-5, 5458	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	5.19E-09	0.97	6.62	-	1473.6
AHQ-7-6, 5365	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	1.51E-08	0.97	6.06	-	2060.4
AHQ-7-7, 5289	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	7.31E-07	0.97	6.58	-	1608.1
AHQ-7-5, 4423 - 4496	R.LVRPEVDVM*CTAFHDNEETFLKK.Y	2797.15659	3	3.66E-05	0.81	4.23	-	506.0
AHQ-7-5, 6798	R.M*PCAEDYLSVVLNQLCVLHEK.T	2537.91475	3	4.48E-10	0.97	5.59	-	1692.1
AHQ-7-6, 3043	R.NECFLQHKDDNPNLPR.L	1999.15349	3	4.07E-05	0.49	3.21	-	391.1
AHQ-7-6, 4985 - 4986	K.QNCELFEQLGEYK.F	1659.79847	2	3.69E-07	0.83	3.44	-	659.8
AHQ-7-5, 5062 - 5130	K.QNCELFEQLGEYK.F	1659.79847	2	1.25E-06	0.62	2.72	-	392.0
AHQ-7-6, 5079 - 5142	K.QNCELFEQLGEYK.F	1659.79847	2	2.76E-04	0.70	3.07	-	475.5
AHQ-7-5, 5228 - 5304	K.QNCELFEQLGEYK.F	1659.79847	2	2.69E-06	0.92	3.87	-	799.6
AHQ-7-5, 4180 - 4244	R.RHPDYSVVLLLR.L	1468.72842	3	8.58E-05	0.97	4.85	-	2489.0
AHQ-7-6, 5909 - 5967	R.RHPYFYAPELLFFAK.R	1900.21293	3	9.00E-10	0.97	5.49	-	2062.3
AHQ-7-5, 6002 - 6066	R.RHPYFYAPELLFFAK.R	1900.21293	3	6.70E-10	0.97	5.95	-	2092.0
AHQ-7-5, 6007	R.RHPYFYAPELLFFAK.R	1900.21293	2	3.61E-06	0.97	5.01	-	1772.3
AHQ-7-6, 5910 - 5975	R.RHPYFYAPELLFFAK.R	1900.21293	2	4.39E-11	0.98	5.16	-	2632.4
AHQ-7-5, 6766	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	8.78E-07	0.97	6.02	-	1648.4
AHQ-7-6, 6661	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	3.44E-05	0.90	4.48	-	1066.3
AHQ-7-1, 4781	R.RPCFSALEVDETYVPK.E	1913.14041	3	5.23E-05	0.89	4.45	-	786.1
AHQ-7-6, 4531	R.RPCFSALEVDETYVPK.E	1913.14041	2	8.22E-04	0.89	4.21	-	645.8
AHQ-7-6, 4542	R.RPCFSALEVDETYVPK.E	1913.14041	3	8.65E-07	0.95	5.26	-	1294.2
AHQ-7-6, 4621 - 4685	R.RPCFSALEVDETYVPK.E	1913.14041	2	4.94E-05	0.90	3.96	-	634.2
AHQ-7-6, 4629	R.RPCFSALEVDETYVPK.E	1913.14041	3	9.21E-08	0.85	4.25	-	710.6
AHQ-7-11, 4440 - 4451	R.RPCFSALEVDETYVPK.E	1913.14041	2	8.51E-05	0.87	4.03	-	516.0
AHQ-7-13, 4674	R.RPCFSALEVDETYVPK.E	1913.14041	2	7.99E-04	0.91	4.13	-	640.5
AHQ-7-5, 4594 - 4611	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.81E-05	0.95	4.61	-	876.7
AHQ-7-5, 4620 - 4694	R.RPCFSALEVDETYVPK.E	1913.14041	3	2.67E-05	0.85	4.66	-	715.8
AHQ-7-5, 4688 - 4754	R.RPCFSALEVDETYVPK.E	1913.14041	2	8.33E-04	0.93	4.10	-	673.4
AHQ-7-3, 4760	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.00E-04	0.92	4.42	-	541.1
AHQ-7-5, 4759 - 4763	R.RPCFSALEVDETYVPK.E	1913.14041	3	3.57E-06	0.93	4.66	-	924.0
AHQ-7-1, 4776	R.RPCFSALEVDETYVPK.E	1913.14041	2	3.09E-05	0.87	3.62	-	562.7
AHQ-7-5, 6650	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	2	7.77E-05	0.90	4.00	-	712.5
AHQ-7-7, 6592 - 6594	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	7.67E-05	0.97	7.14	-	936.2
AHQ-7-6, 6059 - 6141	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	9.10E-08	0.96	6.65	-	866.1
AHQ-7-5, 6200	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	2	1.41E-04	0.94	4.33	-	1203.6
AHQ-7-3, 6116 - 6124	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	1.74E-07	0.96	6.75	-	831.8
AHQ-7-6, 6437	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	4.25E-04	0.65	3.27	-	595.7
AHQ-7-6, 6498 - 6557	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	2.68E-06	0.93	5.31	-	770.5
AHQ-7-5, 6191 - 6198	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	2	3.41E-04	0.95	5.12	-	983.0
AHQ-7-5, 5126	K.SLHTLFGDKLCTVATLR.E	1934.24913	3	1.03E-06	0.94	4.29	-	1355.3
AHQ-7-5, 5138	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	1.28E-06	0.97	4.58	-	1589.6
AHQ-7-6, 5061 - 5127	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	7.40E-05	0.89	3.58	-	799.1
AHQ-7-5, 1871 - 1934	K.TCVADESAENCDK.S	1501.53308	2	5.69E-09	0.98	4.35	-	2703.6
AHQ-7-6, 1853 - 1910	K.TCVADESAENCDK.S	1501.53308	2	1.82E-08	0.97	4.30	-	2217.2
AHQ-7-5, 5848	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.65E-06	0.91	4.12	-	1003.5
AHQ-7-6, 5526 - 5601	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.42E-05	0.80	3.88	-	637.2
AHQ-7-1, 5600 - 5655	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.03E-09	0.90	4.13	-	535.0
AHQ-7-4, 5836	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.60E-07	0.97	5.21	-	1480.3
AHQ-7-5, 5602	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.16E-05	0.95	4.85	-	1197.8

AHQ-7-5, 5580 - 5648	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	8.17E-05	0.60	2.97	-	300.0
AHQ-7-4, 5832	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	4.89E-07	0.89	4.24	-	432.3
AHQ-7-5, 5731 - 5738	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.56E-09	0.93	4.68	-	511.5
AHQ-7-3, 5703	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.68E-09	0.95	4.94	-	1063.8
AHQ-7-7, 5646	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	7.28E-07	0.90	4.08	-	439.5
AHQ-7-7, 5652	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.61E-04	0.92	4.25	-	1128.7
AHQ-7-5, 5732	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	7.01E-06	0.96	5.06	-	1447.5
AHQ-7-2, 5843	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.71E-07	0.90	4.15	-	537.1
AHQ-7-5, 5448	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.33E-06	0.83	4.13	-	361.6
AHQ-7-9, 5145	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.61E-04	0.72	3.47	-	305.6
AHQ-7-3, 5700	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.75E-04	0.90	4.14	-	512.6
AHQ-7-13-, 5469	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.08E-05	0.64	3.04	-	326.0
AHQ-7-6, 5571 - 5634	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.88E-07	0.91	4.42	-	431.2
AHQ-7-1, 5651	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.77E-04	0.86	3.95	-	440.3
AHQ-7-10, 5216	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	6.07E-04	0.87	3.91	-	399.7
AHQ-7-1, 5647	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.67E-06	0.93	5.17	-	875.6
AHQ-7-5, 3132	K.VHTECCHGDLLECADDR.A	2091.20307	2	3.29E-06	0.96	4.51	-	1426.2
AHQ-7-6, 3098	K.VHTECCHGDLLECADDR.A	2091.20307	2	2.47E-07	0.97	4.74	-	1513.5
AHQ-7-6, 3694	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	8.61E-05	0.90	3.88	-	873.9
AHQ-7-5, 3512 - 3532	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	9.12E-04	0.55	3.33	-	559.6
AHQ-7-7, 3669 - 3672	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	3.47E-06	0.93	4.35	-	1225.7
AHQ-7-7, 3668	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	3.12E-04	0.93	4.82	-	685.8
AHQ-7-5, 3770 - 3774	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	6.51E-05	0.96	5.13	-	1231.8
AHQ-7-7, 3821	K.VPQVSTPTLVEVSR.N	1512.73313	2	2.90E-04	0.85	2.65	-	989.3
AHQ-7-11, 3747	K.VPQVSTPTLVEVSR.N	1512.73313	2	7.56E-06	0.87	3.03	-	783.1
AHQ-7-6, 3857 - 3858	K.VPQVSTPTLVEVSR.N	1512.73313	2	2.12E-08	0.94	3.60	-	1164.3
AHQ-7-3, 2419	K.YICENQDSISSK.L	1445.53420	2	3.33E-04	0.88	3.26	-	779.8
AHQ-7-5, 2278 - 2354	K.YICENQDSISSK.L	1445.53420	2	2.64E-05	0.90	3.73	-	718.5
AHQ-7-2, 2469	K.YICENQDSISSK.L	1445.53420	2	7.42E-05	0.82	3.33	-	505.3
AHQ-7-5, 2467 - 2484	K.YICENQDSISSK.L	1445.53420	2	3.28E-06	0.86	3.61	-	549.3
AHQ-7-6, 2462	K.YICENQDSISSK.L	1445.53420	2	1.04E-06	0.86	3.29	-	631.6
AHQ-7-5, 2372	K.YICENQDSISSK.L	1445.53420	1	6.18E-05	0.72	3.17	-	346.5
AHQ-7-5, 2476	K.YICENQDSISSK.L	1445.53420	1	1.85E-06	0.59	2.20	-	538.2
AHQ-7-6, 2345	K.YICENQDSISSK.L	1445.53420	2	1.99E-06	0.85	3.63	-	630.7
AHQ-7-6, 2958	K.YLYEIAR.R	928.06646	1	9.15E-04	0.24	2.07	-	279.6
gi|21624607|ref|NP_066972.1| coactosin-like 1 [Homo sapiens]				5.08E-11	3.53	40.29	45.10	15944.9
AHQ-7-13-, 5056 - 5069	R.DDGSAVIWVTFK.Y	1338.49001	2	1.44E-07	0.97	4.85	-	1157.6
AHQ-7-13, 6381 - 6387	K.FALITWIGENVSGLQR.A	1805.06986	2	3.29E-05	0.98	5.82	-	2555.3
AHQ-7-13-, 6379	K.FALITWIGENVSGLQR.A	1805.06986	3	8.66E-08	0.97	5.20	-	1889.0
AHQ-7-13-, 6376 - 6437	K.FALITWIGENVSGLQR.A	1805.06986	2	2.54E-05	0.98	5.61	-	2089.5
AHQ-7-13-, 2947 - 2951	R.KELEEDFIK.S	1151.29110	2	6.52E-04	0.85	3.37	-	727.0
AHQ-7-12, 2891	R.KELEEDFIK.S	1151.29110	2	5.70E-05	0.77	2.91	-	698.3
AHQ-7-12, 4915 - 4971	K.YDGSTIVPGEQGAEYQHFIQQCTDDVR.L	3116.27790	3	5.08E-11	0.83	4.11	-	437.9
gi|9507215|ref|NP_061816.1| tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]				5.26E-11	3.57	40.25	10.90	50093.2
AHQ-7-7, 5186	R.AVMIDLEPTVVDEVR.A	1686.95185	2	2.97E-05	0.84	2.89	-	1160.1
AHQ-7-14-, 4767	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	6.30E-10	0.97	5.07	-	1354.7
AHQ-7-13, 4858	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	6.22E-07	0.86	3.98	-	568.7
AHQ-7-14-, 4703 - 4769	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	4.19E-04	0.91	3.70	-	1040.8
AHQ-7-14-, 5117	R.AVMIDLEPTVVDEVR.A	1686.95185	2	4.46E-06	0.92	3.71	-	1226.7
AHQ-7-7, 5529	R.IHFPLVTYAPIISAEK.A	1800.13312	2	3.47E-06	0.81	3.56	-	494.9
AHQ-7-14-, 5091	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	5.26E-11	0.88	4.02	-	483.4
AHQ-7-13, 5371	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	1.73E-08	0.46	2.72	-	381.5
AHQ-7-13, 5135 - 5215	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	1.38E-07	0.79	3.86	-	491.7
gi|16507237|ref|NP_005338.1| heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he				5.40E-11	9.10	100.30	24.50	72332.5
AHQ-7-6, 5002	R.AKFEELNMDLFR.S	1513.74309	3	1.27E-07	0.87	3.69	-	1038.4
AHQ-7-6, 4923 - 5001	R.AKFEELNMDLFR.S	1513.74309	2	2.53E-07	0.94	3.81	-	1183.8
AHQ-7-6, 5482	K.DNHLLGTFDLTGIPPAPR.G	1935.17239	2	2.00E-06	0.92	3.82	-	933.0
AHQ-7-6, 5879	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	2.52E-04	0.49	2.61	-	565.8
AHQ-7-6, 5750 - 5782	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	1.63E-05	0.93	4.06	-	1190.8
AHQ-7-6, 4681	K.IEWLESHQDADIEDFK.A	1976.08864	3	1.68E-08	0.89	4.29	-	535.0
AHQ-7-6, 4674	K.IEWLESHQDADIEDFK.A	1976.08864	2	5.40E-11	0.98	5.96	-	1946.3
AHQ-7-6, 4421	R.IINEPTAAAIAYGLDKR.E	1817.07894	2	6.28E-11	0.87	4.34	-	956.7
AHQ-7-6, 3785	K.KSDIDEIVLVGGSTR.I	1589.77277	3	5.22E-06	0.74	3.39	-	813.1
AHQ-7-6, 3786	K.KSDIDEIVLVGGSTR.I	1589.77277	2	3.30E-08	0.94	3.93	-	1564.0
AHQ-7-6, 3666	K.NQLTSNPENTVFDAK.R	1678.78173	2	6.00E-04	0.80	3.95	-	359.5
AHQ-7-6, 3742	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	5.36E-06	0.88	3.83	-	830.7
AHQ-7-7, 3701	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	3.36E-07	0.96	4.88	-	1170.7
AHQ-7-6, 3070	K.TKPYIQVDIGGGQTK.T	1605.81703	2	5.52E-06	0.88	3.32	-	935.1
AHQ-7-6, 3879 - 3942	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	5.39E-09	0.94	4.50	-	670.5
gi|20149594|ref|NP_031381.2| heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea				5.60E-11	5.27	60.28	10.60	83263.6
AHQ-7-5, 3162	R.ELISNASDALDK.I	1276.37539	2	1.87E-06	0.86	2.99	-	844.2
AHQ-7-4, 3204	R.ELISNASDALDK.I	1276.37539	2	7.87E-05	0.71	3.01	-	587.5
AHQ-7-5, 5632	K.HSQFIGYPITLYLEK.E	1810.08487	2	1.00E-06	0.95	4.10	-	1051.9
AHQ-7-5, 4058 - 4132	R.NPDDITQEEYGEFYK.S	1848.90048	2	5.60E-11	0.98	5.56	-	1625.7
AHQ-7-5, 4063	K.SLTNDWEDHLAVK.H	1528.64798	2	1.56E-09	0.85	3.65	-	688.6
AHQ-7-5, 4294 - 4296	R.TLTLVDTGIGMTK.A	1350.60718	2	1.03E-07	0.95	4.07	-	1055.9
AHQ-7-6, 2262	K.YIDQEELNK.T	1152.23595	2	4.21E-04	0.68	2.59	-	448.5
gi|24797067|ref|NP_002107.3| major histocompatibility complex, class I, A precursor; HLA-A1 class I				5.72E-11	4.35	50.27	22.70	40840.5
AHQ-7-8, 4926	R.APWIEQEGPEYWDQETR.N	2135.23420	2	5.72E-11	0.97	5.46	-	988.5
AHQ-7-8, 3288	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	2	9.59E-08	0.68	3.71	-	446.0
AHQ-7-8, 3390	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	3	5.43E-06	0.70	3.32	-	458.0
AHQ-7-8, 4935 - 5000	R.FIAVGYVDDTQFVR.F	1630.82504	2	5.12E-08	0.98	4.74	-	2186.5
AHQ-7-1, 5008	R.FIAVGYVDDTQFVR.F	1630.82504	2	4.98E-08	0.97	4.07	-	1967.7
AHQ-7-8, 2194	R.YLENGKETLQR.T	1351.49032	2	5.59E-07	0.78	2.85	-	790.0
AHQ-7-8, 3238	R.YTCHVQHEGLPKPLTLR.W	2051.35781	2	1.90E-04	0.96	4.94	-	1762.0
gi|29732955|ref|XP_291603.1| similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA				5.85E-11	0.85	10.21	16.80	11173.0
AHQ-7-9, 3824 - 3901	K.NISNASCTTNCIAPLAK.M	1838.05353	2	7.18E-10	0.91	3.79	-	956.3
AHQ-7-10, 3655 - 3725	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.53E-04	0.56	3.03	-	700.4
AHQ-7-11, 3742 - 3802	K.NISNASCTTNCIAPLAK.M	1838.05353	2	2.63E-05	0.81	3.59	-	1193.8
AHQ-7-11, 4048 - 4060	K.NISNASCTTNCIAPLAK.M	1838.05353	2	7.96E-05	0.27	2.56	-	546.0
AHQ-7-9, 3588 - 3668	K.NISNASCTTNCIAPLAK.M	1838.05353	2	5.85E-11	0.85	4.18	-	1089.2
gi|7661818|ref|NP_054900.1| HSPC159 protein [Homo sapiens]				6.44E-11	3.14	40.21	37.80	19011.6
AHQ-7-14-, 6315	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	8.07E-06	0.65	2.74	-	327.1
AHQ-7-13-, 6331	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	5.47E-05	0.85	3.60	-	434.0
AHQ-7-11, 6178	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.92E-04	0.82	3.66	-	286.0
AHQ-7-13, 6321	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.49E-07	0.83	3.59	-	334.7
AHQ-7-11, 4627 - 4683	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	3	1.04E-08	0.90	4.20	-	1120.4
AHQ-7-11, 3904	R.LIVPFCGHIK.G	1185.46348	2	9.12E-05	0.51	2.56	-	280.8
AHQ-7-11, 4620	R.VFVDGHQLFDFYHR.I	1780.96540	3	6.44E-11	0.91	4.06	-	831.6
AHQ-7-11, 4563 - 4618	R.VFVDGHQLFDFYHR.I	1780.96540	2	4.75E-06	0.96	4.19	-	1534.8
gi|30159830|ref|XP_302246.1| similar to HSPC280 [Homo sapiens]				6.69E-11	1.92	20.25	3.90	45644.4
AHQ-7-14-, 6397	K.CANLFEALVGTLK.A	1437.68632	2	4.99E-06	0.97	5.02	-	1403.4
AHQ-7-14-, 6354 - 6414	R.DDKCANLFEALVGTLK.A	1796.03496	3	6.89E-05	0.91	4.06	-	1613.4
AHQ-7-14-, 6353	R.DDKCANLFEALVGTLK.A	1796.03496	2	6.69E-11	0.95	3.80	-	1567.5
gi|4503689|ref|NP_000499.1| fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M				6.87E-11	17.63	230.29	36.00	94972.5
AHQ-7-10, 5180 - 5183	K.DSDWPFCSDEDWNYK.C	1965.98609	2	8.64E-07	0.90	3.96	-	609.9
AHQ-7-9, 5113	K.DSDWPFCSDEDWNYK.C	1965.98609	2	4.80E-05	0.90	3.72	-	454.4

AHQ-7-7, 5621 - 5622	K.DSDWPFCSDEDWNYK.C	1965.98609	2	1.54E-04	0.90	3.61	-	571.4
AHQ-7-6, 5597 - 5599	K.DSDWPFCSDEDWNYK.C	1965.98609	2	2.07E-07	0.94	4.33	-	644.9
AHQ-7-6, 5647 - 5683	K.DSHSLTTNIMEILR.G	1630.84839	2	3.96E-05	0.95	3.79	-	1472.9
AHQ-7-8, 5644	K.DSHSLTTNIMEILR.G	1630.84839	2	9.14E-04	0.95	4.20	-	1173.9
AHQ-7-10, 4515 - 4520	K.DSHSLTTNIM*EILR.G	1646.84779	2	2.08E-05	0.91	3.44	-	1158.3
AHQ-7-9, 5168 - 5176	K.DSHSLTTNIMEILR.G	1630.84839	2	2.95E-04	0.97	4.74	-	1646.3
AHQ-7-6, 4919	K.DSHSLTTNIM*EILR.G	1646.84779	2	8.43E-05	0.82	2.90	-	938.1
AHQ-7-7, 5641 - 5644	K.DSHSLTTNIMEILR.G	1630.84839	2	5.73E-04	0.96	4.17	-	1548.8
AHQ-7-7, 2285	K.ESSSHHPGIAEFPSR.G	1638.72252	2	6.38E-04	0.74	2.58	-	695.3
AHQ-7-6, 2329 - 2343	K.ESSSHHPGIAEFPSR.G	1638.72252	2	2.94E-05	0.84	3.07	-	563.3
AHQ-7-11, 2354 - 2355	K.ESSSHHPGIAEFPSR.G	1638.72252	3	6.70E-04	0.67	3.08	-	758.0
AHQ-7-8, 2586 - 2587	R.EVDLKDYEDQQK.Q	1510.58460	2	2.90E-07	0.90	3.76	-	801.0
AHQ-7-13-, 2696	R.EVDLKDYEDQQK.Q	1510.58460	2	2.34E-08	0.60	2.79	-	422.4
AHQ-7-6, 2617	R.EVDLKDYEDQQK.Q	1510.58460	2	3.18E-06	0.72	2.82	-	598.0
AHQ-7-7, 2565	R.EVDLKDYEDQQK.Q	1510.58460	2	1.93E-04	0.67	3.00	-	503.4
AHQ-7-10, 2563 - 2640	R.EVDLKDYEDQQK.Q	1510.58460	2	6.93E-07	0.88	3.12	-	1011.1
AHQ-7-7, 6264	K.EVVTSEDGSDCPEAMDLGTLSGIGTLDGFR.H	3131.34937	3	3.44E-08	0.78	3.71	-	725.0
AHQ-7-6, 1827 - 1887	R.GGSTSYGTGSETESPR.N	1573.55765	2	8.18E-06	0.63	2.64	-	541.8
AHQ-7-7, 1829	R.GGSTSYGTGSETESPR.N	1573.55765	2	8.40E-05	0.56	2.91	-	394.1
AHQ-7-6, 4034	K.GLIDEVNQDFTNR.I	1521.61384	2	2.92E-05	0.93	4.27	-	730.5
AHQ-7-9, 4598	K.GLIDEVNQDFTNR.I	1521.61384	2	1.05E-06	0.87	3.18	-	832.0
AHQ-7-10, 4275 - 4284	K.GLIDEVNQDFTNR.I	1521.61384	2	3.73E-06	0.96	4.34	-	1344.6
AHQ-7-6, 4579 - 4605	K.GLIDEVNQDFTNR.I	1521.61384	2	1.41E-05	0.90	3.59	-	806.8
AHQ-7-12, 4390 - 4391	K.GLIDEVNQDFTNR.I	1521.61384	2	7.90E-05	0.93	4.20	-	944.4
AHQ-7-8, 4619 - 4630	K.GLIDEVNQDFTNR.I	1521.61384	2	2.98E-09	0.95	4.23	-	1207.5
AHQ-7-13, 4565 - 4645	K.GLIDEVNQDFTNR.I	1521.61384	2	4.88E-06	0.95	4.05	-	1114.2
AHQ-7-8, 4034 - 4035	K.GLIDEVNQDFTNR.I	1521.61384	2	7.92E-07	0.88	3.95	-	627.8
AHQ-7-9, 4229 - 4288	K.GLIDEVNQDFTNR.I	1521.61384	2	5.74E-05	0.96	4.36	-	1335.2
AHQ-7-7, 3984	K.GLIDEVNQDFTNR.I	1521.61384	2	8.07E-07	0.91	4.21	-	693.2
AHQ-7-7, 4576	K.GLIDEVNQDFTNR.I	1521.61384	2	8.19E-10	0.89	3.69	-	773.1
AHQ-7-2, 4792 - 4816	K.GLIDEVNQDFTNR.I	1521.61384	2	2.50E-07	0.94	4.32	-	998.1
AHQ-7-5, 4675	K.GLIDEVNQDFTNR.I	1521.61384	2	3.01E-08	0.96	4.59	-	1228.6
AHQ-7-3, 4677	K.GLIDEVNQDFTNR.I	1521.61384	2	2.79E-05	0.65	2.97	-	643.6
AHQ-7-6, 4757	K.GLIDEVNQDFTNR.I	1521.61384	2	5.37E-06	0.24	2.51	-	383.4
AHQ-7-6, 2206 - 2277	R.GSESGIFTNTK.E	1141.21317	2	4.13E-05	0.80	2.96	-	796.0
AHQ-7-11, 2278	R.GSESGIFTNTK.E	1141.21317	1	1.64E-04	0.30	2.26	-	284.6
AHQ-7-11, 2244 - 2286	R.GSESGIFTNTK.E	1141.21317	2	1.24E-05	0.76	2.72	-	735.4
AHQ-7-13, 3398	R.HPDEAAFFDTASTGK.T	1594.66329	2	7.59E-04	0.42	2.54	-	318.1
AHQ-7-7, 3022 - 3088	R.HPDEAAFFDTASTGK.T	1594.66329	2	1.01E-05	0.84	3.68	-	423.8
AHQ-7-12, 3118	R.HPDEAAFFDTASTGK.T	1594.66329	2	3.62E-04	0.69	2.81	-	415.6
AHQ-7-6, 2614 - 2619	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	5.51E-09	0.97	5.54	-	1983.7
AHQ-7-6, 2618	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	6.71E-06	0.97	5.66	-	1373.5
AHQ-7-10, 2588	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	2.30E-06	0.96	4.40	-	1761.1
AHQ-7-7, 2557	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	1.68E-06	0.96	4.62	-	1793.2
AHQ-7-13-, 2764 - 2803	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	4.74E-07	0.95	4.46	-	1597.8
AHQ-7-13-, 2781	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	3.92E-06	0.97	4.91	-	1374.8
AHQ-7-9, 2498 - 2570	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	7.70E-04	0.94	4.51	-	824.2
AHQ-7-13, 3014 - 3094	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	3.07E-05	0.97	5.11	-	2142.0
AHQ-7-11, 2618	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	3.66E-09	0.97	5.29	-	1240.4
AHQ-7-6, 2942	K.LKNSLFEYQK.N	1270.45881	2	1.36E-05	0.54	2.63	-	501.1
AHQ-7-9, 2769 - 2770	K.LKNSLFEYQK.N	1270.45881	1	1.19E-04	0.19	2.11	-	316.5
AHQ-7-6, 2785	R.MELERPGGNEITR.G	1502.67870	2	6.59E-05	0.80	3.13	-	875.7
AHQ-7-7, 3912	K.MKPVPDLVPGNFK.S	1442.75114	2	3.06E-05	0.48	2.81	-	286.8
AHQ-7-8, 3756	K.MKPVPDLVPGNFK.S	1442.75114	2	5.06E-04	0.55	2.55	-	391.8
AHQ-7-7, 5317	K.NNKDSHSLTTNIMEILR.G	1987.22751	2	1.76E-05	0.81	3.46	-	684.6
AHQ-7-6, 3278	R.NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPR.P	4123.15285	3	6.97E-06	0.92	5.26	-	604.3
AHQ-7-8, 3231	R.NPGSSGTGGTATWKPGSSGPGSTGSWNSGSSGTGSTGNQNPGSPR.P	4123.15285	3	1.95E-08	0.93	5.02	-	1044.4
AHQ-7-7, 2157 - 2216	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	3.26E-10	0.97	5.73	-	1113.8
AHQ-7-6, 2185 - 2259	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	7.51E-08	0.97	5.03	-	1373.2
AHQ-7-8, 2215	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	6.87E-11	0.95	4.80	-	827.7
AHQ-7-8, 2690	K.NSLFEYQK.N	1029.12765	1	6.30E-05	0.13	2.00	-	197.0
AHQ-7-13, 2534	R.PGSTGTWNPGSSER.G	1433.46515	2	8.40E-05	0.62	2.62	-	522.5
AHQ-7-8, 2202	R.PGSTGTWNPGSSER.G	1433.46515	2	7.11E-08	0.91	3.85	-	708.9
AHQ-7-13-, 4532 - 4581	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	2.67E-07	0.86	3.82	-	699.5
AHQ-7-11, 4444	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	1.12E-10	0.88	4.21	-	510.6
AHQ-7-6, 6705	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.05E-04	0.88	3.90	-	438.2
AHQ-7-13-, 6292	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.97E-04	0.71	3.03	-	245.4
AHQ-7-6, 6547	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	2.37E-04	0.60	3.08	-	210.5
AHQ-7-9, 6132	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.47E-06	0.82	3.51	-	367.9
AHQ-7-13-, 6427	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.41E-06	0.90	3.95	-	539.2
AHQ-7-13, 6209 - 6281	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	7.51E-04	0.59	2.94	-	214.7
AHQ-7-7, 6804	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	2.88E-07	0.84	3.57	-	457.3
AHQ-7-9, 2317	K.VQHIQLLQK.N	1107.33106	1	4.51E-04	0.73	2.98	-	559.4
AHQ-7-7, 2342	K.VQHIQLLQK.N	1107.33106	2	3.82E-04	0.79	2.76	-	669.3
AHQ-7-7, 2336	K.VQHIQLLQK.N	1107.33106	1	1.72E-04	0.56	2.33	-	715.5
AHQ-7-8, 2312	K.VQHIQLLQK.N	1107.33106	1	9.00E-04	0.58	2.83	-	371.4
AHQ-7-10, 2359 - 2373	K.VQHIQLLQK.N	1107.33106	2	4.15E-04	0.86	2.77	-	852.9
gi|4503631|ref|NP_000120.1| coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,				7.83E-11	23.23	280.30	39.90	83232.8
AHQ-7-5, 5358 - 5423	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	8.01E-08	0.44	3.15	-	164.4
AHQ-7-5, 5222 - 5295	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	4.16E-07	0.62	3.25	-	116.2
AHQ-7-7, 2569	R.CLGIPAR.I	787.95073	1	5.05E-05	0.52	2.10	-	370.0
AHQ-7-8, 2572	K.DGTHVVENVDATHIGK.L	1692.81163	2	8.40E-07	0.95	4.25	-	1102.0
AHQ-7-6, 2599	K.DGTHVVENVDATHIGK.L	1692.81163	3	2.14E-05	0.84	3.84	-	781.5
AHQ-7-5, 2616	K.DGTHVVENVDATHIGK.L	1692.81163	2	2.15E-09	0.95	4.30	-	1116.4
AHQ-7-5, 2614	K.DGTHVVENVDATHIGK.L	1692.81163	3	1.36E-05	0.85	3.75	-	960.2
AHQ-7-5, 2760 - 2800	K.DGTHVVENVDATHIGK.L	1692.81163	2	2.40E-04	0.81	3.52	-	642.8
AHQ-7-5, 6994	K.EAVLIQAGEYMGQLLEQASLHFFVTAR.I	3023.45475	3	1.18E-07	0.84	4.11	-	674.1
AHQ-7-5, 5688 - 5722	K.ETFDVTLEPLSFK.K	1526.71190	2	1.28E-04	0.83	3.26	-	724.2
AHQ-7-5, 5042	K.ETFDVTLEPLSFKK.E	1654.88482	2	1.37E-05	0.74	3.21	-	427.5
AHQ-7-5, 5070	R.GTQVVGSDM*TVTVQFTNPLK.E	2139.41549	2	1.21E-08	0.91	3.91	-	851.3
AHQ-7-6, 5542 - 5615	K.GTYIPVPIVSELQSGK.W	1688.94594	2	3.22E-04	0.61	3.03	-	231.2
AHQ-7-5, 5606 - 5615	K.GTYIPVPIVSELQSGK.W	1688.94594	2	1.73E-04	0.66	2.88	-	302.9
AHQ-7-5, 5707	K.GTYIPVPIVSELQSGK.W	1688.94594	2	4.53E-05	0.60	2.85	-	264.9
AHQ-7-11, 5220 - 5226	K.GTYIPVPIVSELQSGK.W	1688.94594	2	8.04E-04	0.78	3.39	-	320.1
AHQ-7-5, 6714 - 6715	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	8.53E-10	0.85	3.96	-	688.2
AHQ-7-7, 6680 - 6681	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.88E-07	0.97	5.55	-	1384.3
AHQ-7-9, 6037	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.55E-04	0.95	3.95	-	1347.1
AHQ-7-6, 6610	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.65E-10	0.95	4.91	-	1065.8
AHQ-7-5, 6711	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	6.25E-10	0.97	4.75	-	1600.9
AHQ-7-13, 6329	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.59E-05	0.91	3.75	-	861.4
AHQ-7-12, 6090 - 6151	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	6.30E-04	0.92	4.62	-	806.0
AHQ-7-13-, 6267 - 6339	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.90E-05	0.97	5.92	-	1213.8
AHQ-7-5, 3814	R.HVYGELDVQIQR.R	1457.61612	2	1.03E-06	0.91	3.25	-	767.9
AHQ-7-5, 3472 - 3536	R.HVYGELDVQIQR.R	1457.61612	2	3.28E-10	0.94	4.19	-	825.4
AHQ-7-5, 2266	K.KDGTHVVENVDATHIGK.L	1820.98455	3	2.47E-07	0.97	5.28	-	2417.1
AHQ-7-5, 2458	K.KDGTHVVENVDATHIGK.L	1820.98455	2	5.99E-09	0.84	3.66	-	673.0
AHQ-7-6, 2255 - 2331	K.KDGTHVVENVDATHIGK.L	1820.98455	3	1.34E-05	0.80	3.06	-	1045.8

AHQ-7-5, 2463	K.KDGTHVVENVDATHIGK.L	1820.98455	3	1.39E-05	0.98	5.61	-	2825.9
AHQ-7-5, 2271	K.KDGTHVVENVDATHIGK.L	1820.98455	2	3.66E-05	0.90	3.34	-	1139.6
AHQ-7-10, 4700	K.KETFDVTLEPLSFK.K	1654.88482	2	7.80E-05	0.91	3.71	-	1325.3
AHQ-7-11, 4819	K.KETFDVTLEPLSFK.K	1654.88482	2	5.48E-08	0.93	3.70	-	1288.2
AHQ-7-6, 5115	K.KETFDVTLEPLSFK.K	1654.88482	2	8.85E-05	0.95	3.91	-	1605.7
AHQ-7-5, 5124 - 5186	K.KETFDVTLEPLSFK.K	1654.88482	2	6.55E-08	0.96	4.57	-	1591.6
AHQ-7-5, 2802 - 2804	R.KLIASMSSDSLR.H	1308.53039	2	1.01E-09	0.96	4.04	-	1509.9
AHQ-7-5, 2114	R.KLIASM*SSDSLR.H	1324.52979	2	1.21E-05	0.86	3.07	-	900.0
AHQ-7-5, 4702 - 4743	R.LALETALMYGAK.K	1281.54655	2	1.54E-04	0.96	3.91	-	1737.4
AHQ-7-6, 4639 - 4669	R.LALETALMYGAK.K	1281.54655	2	9.72E-08	0.96	3.67	-	1743.6
AHQ-7-5, 4718	R.LALETALM*YGAK.K	1297.54595	2	2.46E-07	0.93	3.66	-	1210.1
AHQ-7-5, 2262	K.LIASM*SSDSLR.H	1196.35688	2	2.12E-04	0.87	3.26	-	638.7
AHQ-7-5, 6042 - 6051	R.MYVAVWTPYGVLR.T	1555.86794	2	9.00E-04	0.94	4.41	-	906.4
AHQ-7-5, 5571 - 5650	R.M*YVAVWTPYGVLR.T	1571.86734	2	2.93E-04	0.67	2.92	-	551.9
AHQ-7-5, 6635 - 6712	R.NPETDTYILFNPWCEDDAVYLDNEK.E	3064.23814	3	1.66E-04	0.64	3.06	-	723.8
AHQ-7-5, 6464	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	7.83E-11	0.93	4.75	-	995.1
AHQ-7-7, 6397	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	9.05E-07	0.92	4.75	-	938.1
AHQ-7-11, 3544	R.NVWVHLDGPGVTR.P	1450.62682	2	7.10E-06	0.86	3.21	-	959.3
AHQ-7-8, 3542	R.NVWVHLDGPGVTR.P	1450.62682	2	3.30E-05	0.74	2.77	-	597.1
AHQ-7-5, 3724	R.NVWVHLDGPGVTR.P	1450.62682	2	3.24E-08	0.93	3.63	-	1257.8
AHQ-7-5, 4263 - 4266	K.QIGGDGMMDITDTYK.F	1645.83696	2	1.28E-08	0.91	4.01	-	680.5
AHQ-7-5, 3671 - 3738	K.QIGGDGMM*DITDTYK.F	1661.83636	2	8.26E-04	0.36	2.68	-	388.9
AHQ-7-5, 4576 - 4642	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	4.93E-07	0.97	4.94	-	1891.7
AHQ-7-6, 4565 - 4567	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	3.46E-10	0.97	4.36	-	1939.1
AHQ-7-6, 5213	R.SNVDMDFEVENAVLGK.D	1767.93869	2	1.20E-05	0.91	3.61	-	1290.5
AHQ-7-5, 5280 - 5306	R.SNVDMDFEVENAVLGK.D	1767.93869	2	3.94E-09	0.97	5.48	-	2019.1
AHQ-7-5, 4114	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	2.43E-07	0.73	2.69	-	727.7
AHQ-7-5, 5375	R.SNVDMDFEVENAVLGK.D	1767.93869	2	6.26E-06	0.84	3.60	-	817.2
AHQ-7-6, 5643 - 5705	K.STVLTIPEIIIK.V	1327.63485	2	2.00E-04	0.80	2.73	-	1101.9
AHQ-7-7, 5638 - 5642	K.STVLTIPEIIIK.V	1327.63485	2	2.66E-04	0.88	3.45	-	1019.5
AHQ-7-13-, 5503	K.STVLTIPEIIIK.V	1327.63485	2	9.60E-04	0.89	2.86	-	1386.9
AHQ-7-11, 5350 - 5419	K.STVLTIPEIIIK.V	1327.63485	2	1.20E-04	0.92	4.01	-	992.2
AHQ-7-5, 6868	R.YGQCWVFAGVFNTFLR.C	1967.23783	2	2.41E-08	0.95	4.56	-	1030.4
gi|4506467|ref|NP_002897.1| radixin [Homo sapiens]				8.54E-11	0.96	10.23	2.60	68563.4
AHQ-7-6, 5351	K.NQEQLAAELAEFTAK.I	1663.81020	2	8.54E-11	0.96	4.60	-	1379.8
gi|4507725|ref|NP_000362.1| transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum				8.59E-11	6.27	70.29	69.40	15886.9
AHQ-7-13, 3933 - 3937	K.AADDTWEPFASGK.T	1395.45529	2	1.41E-04	0.91	3.69	-	943.4
AHQ-7-13-, 4451	K.ALGISPFHEHAEVVFTANDSGPR.R	2452.66660	3	1.68E-06	0.89	3.27	-	1567.3
AHQ-7-13, 4138 - 4145	R.GSPAINVAVHVFR.K	1367.58095	2	3.23E-07	0.94	4.23	-	1081.3
AHQ-7-13-, 4015 - 4028	R.GSPAINVAVHVFR.K	1367.58095	2	1.56E-09	0.96	4.53	-	1157.1
AHQ-7-13, 3459	R.KAADDTWEPFASGK.T	1523.62820	2	1.45E-05	0.94	3.40	-	1500.8
AHQ-7-13, 5709	R.RYTIAALLSPYSYSTTAVVTNPKE	2646.97608	3	3.26E-04	0.70	3.07	-	785.6
AHQ-7-13-, 5335	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	2.11E-08	0.96	5.34	-	1305.8
AHQ-7-13-, 5341	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	8.59E-11	0.98	5.87	-	1668.3
AHQ-7-13, 5401	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	6.98E-06	0.88	3.47	-	968.0
AHQ-7-13-, 6136	K.TSESGELHGLTTEEEFVEGIYKVEIDTK.S	3142.37019	3	2.08E-04	0.91	5.13	-	623.4
gi|21361547|ref|NP_002930.2| ribonuclease/angiogenin inhibitor; Placental ribonuclease inhibitor [H				8.65E-11	0.91	10.19	3.30	49973.3
AHQ-7-7, 6414	R.WAELLPLLQQCQVVR.L	1855.19360	2	8.65E-11	0.91	3.81	-	726.4
gi|13994151|ref|NP_066272.1| PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H				9.28E-11	12.07	140.27	51.40	36071.5
AHQ-7-14-, 6182 - 6245	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	6.53E-06	0.95	5.45	-	938.6
AHQ-7-13-, 6252	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.01E-05	0.94	5.37	-	653.5
AHQ-7-13-, 6272 - 6347	K.AALANLCIGDVITAIDGENTSNMTHLEAQNR.I	3315.63867	3	1.28E-06	0.90	4.55	-	599.0
AHQ-7-13, 6278	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.74E-06	0.89	4.42	-	597.5
AHQ-7-13-, 5732	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	3.07E-07	0.86	4.23	-	530.8
AHQ-7-14-, 4421 - 4446	K.CGTGIVGVFVK.L	1138.36198	2	2.15E-04	0.91	2.89	-	1299.5
AHQ-7-13-, 4389	K.CGTGIVGVFVK.L	1138.36198	2	1.83E-05	0.93	3.58	-	1298.3
AHQ-7-13, 4526 - 4539	K.CGTGIVGVFVK.L	1138.36198	2	5.60E-04	0.91	3.41	-	988.5
AHQ-7-11, 3483 - 3560	K.DFEQPLAISR.V	1176.30388	2	2.45E-06	0.91	3.39	-	1056.4
AHQ-7-12, 3524	K.DFEQPLAISR.V	1176.30388	2	1.56E-06	0.92	3.45	-	1116.0
AHQ-7-14-, 3597 - 3614	K.DFEQPLAISR.V	1176.30388	2	4.89E-05	0.91	3.67	-	905.0
AHQ-7-13, 3523	K.GCTDNLTLTVAR.S	1322.47058	2	2.69E-07	0.71	3.20	-	565.6
AHQ-7-13-, 3363	K.GCTDNLTLTVAR.S	1322.47058	2	5.75E-05	0.87	3.73	-	735.2
AHQ-7-13, 4111 - 4183	K.GHFFVEDQIYCEK.H	1673.82684	2	1.75E-05	0.94	3.89	-	1020.8
AHQ-7-14-, 3959 - 3965	K.GHFFVEDQIYCEK.H	1673.82684	2	2.49E-05	0.97	4.98	-	1217.6
AHQ-7-11, 3856	K.GHFFVEDQIYCEK.H	1673.82684	2	3.39E-05	0.94	3.80	-	1200.2
AHQ-7-13-, 3971	K.GHFFVEDQIYCEK.H	1673.82684	2	3.01E-05	0.97	4.43	-	1707.9
AHQ-7-13-, 2787	R.HRHPECYVCTDCGTNLK.Q	2151.34648	3	3.80E-04	0.96	5.10	-	1332.7
AHQ-7-13-, 3256	R.IKGCTDNLTLTVAR.S	1563.80174	2	4.26E-09	0.94	3.87	-	1068.1
AHQ-7-14-, 3233 - 3234	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.01E-10	0.96	4.77	-	1108.6
AHQ-7-13-, 3381 - 3459	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.48E-04	0.40	2.55	-	497.5
AHQ-7-12, 3166	R.IKGCTDNLTLTVAR.S	1563.80174	2	9.28E-11	0.92	3.88	-	971.5
AHQ-7-11, 3148	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.88E-10	0.94	3.93	-	1046.1
AHQ-7-13, 3387 - 3397	R.IKGCTDNLTLTVAR.S	1563.80174	2	6.13E-09	0.94	3.84	-	1147.5
AHQ-7-13, 3539 - 3554	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.29E-05	0.78	3.29	-	740.6
AHQ-7-14, 4126	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.59E-06	0.85	3.14	-	666.3
AHQ-7-14-, 4667	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	3	1.49E-06	0.82	3.40	-	971.0
AHQ-7-13, 3875	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.72E-06	0.92	4.01	-	960.2
AHQ-7-13-, 3703	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	7.71E-05	0.86	3.85	-	545.1
AHQ-7-13-, 3691 - 3696	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	2.19E-09	0.76	3.72	-	528.3
AHQ-7-12, 3576	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	8.43E-04	0.42	2.71	-	232.2
AHQ-7-13, 3810 - 3829	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	3	9.37E-04	0.73	3.44	-	654.6
AHQ-7-13-, 6255	K.QSTSFLVLQEILESEEK.G	1981.18977	2	2.48E-06	0.94	4.06	-	1328.7
AHQ-7-13, 6266	K.QSTSFLVLQEILESEEK.G	1981.18977	2	6.23E-08	0.97	4.30	-	1731.3
AHQ-7-13-, 5884 - 5887	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	1.43E-05	0.79	3.76	-	547.7
AHQ-7-13-, 3080	R.SAMPFTASPASSTTAR.V	1583.74859	2	2.65E-04	0.44	2.60	-	449.0
AHQ-7-11, 2992	R.SAMPFTASPASSTTAR.V	1583.74859	2	3.34E-06	0.68	2.74	-	632.5
gi|25188179|ref|NP_005653.3| voltage-dependent anion channel 3 [Homo sapiens]				9.67E-11	2.61	30.22	16.30	30658.4
AHQ-7-10, 4608	K.LTLDTIFVPNTGK.K	1419.64771	2	7.31E-05	0.85	3.38	-	649.5
AHQ-7-10, 4264	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	9.67E-11	0.80	3.46	-	592.0
AHQ-7-10, 4153	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	4.90E-08	0.85	3.74	-	686.3
AHQ-7-14, 5369	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	9.37E-05	0.71	2.93	-	463.2
AHQ-7-10, 3656 - 3669	K.YKVCNYGLTFTQK.W	1623.85410	2	6.29E-05	0.96	4.43	-	1405.7
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				9.82E-11	2.69	30.30	13.10	32164.8
AHQ-7-1, 4897 - 4899	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.48E-06	0.92	4.56	-	721.1
AHQ-7-1, 5325 - 5328	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.78E-04	0.95	5.13	-	997.8
AHQ-7-2, 5019 - 5091	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.15E-06	0.95	4.83	-	1159.7
AHQ-7-3, 4916	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.16E-04	0.93	4.52	-	861.1
AHQ-7-3, 5196	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.55E-05	0.91	3.78	-	988.2
AHQ-7-4, 4864	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.15E-06	0.92	4.35	-	690.7
AHQ-7-4, 5012	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.12E-04	0.89	3.99	-	723.8
AHQ-7-5, 4795	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.58E-08	0.94	4.57	-	854.4
AHQ-7-5, 4892 - 4954	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.46E-05	0.95	4.89	-	1088.1
AHQ-7-5, 5242	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.91E-05	0.81	3.54	-	354.5
AHQ-7-5, 5414	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.98E-04	0.88	3.88	-	779.5
AHQ-7-6, 4883	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.29E-05	0.97	5.29	-	1559.1
AHQ-7-6, 5057	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.67E-04	0.86	3.60	-	719.2
AHQ-7-6, 5166	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.81E-05	0.84	3.73	-	332.4

AHQ-7-6, 5337	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.26E-04	0.81	3.70	-	537.4
AHQ-7-7, 5141	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.68E-06	0.95	4.54	-	1081.1
AHQ-7-7, 5326 - 5328	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.64E-05	0.95	5.05	-	900.1
AHQ-7-14-, 5054 - 5109	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.70E-07	0.94	4.68	-	842.9
AHQ-7-8, 4652 - 4714	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.07E-09	0.97	5.19	-	1363.8
AHQ-7-8, 4778 - 4838	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.33E-07	0.94	4.76	-	857.5
AHQ-7-8, 4856 - 4863	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	3	1.71E-04	0.81	3.78	-	741.7
AHQ-7-8, 4870 - 4930	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.76E-07	0.95	5.17	-	893.4
AHQ-7-8, 4902	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.06E-04	0.92	4.71	-	818.7
AHQ-7-8, 5075 - 5127	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.25E-07	0.96	5.40	-	1110.5
AHQ-7-8, 5174 - 5242	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.65E-08	0.96	5.32	-	1062.3
AHQ-7-8, 5538 - 5606	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.68E-06	0.96	5.38	-	951.2
AHQ-7-8, 6174 - 6246	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.28E-04	0.95	4.72	-	1148.2
AHQ-7-8, 6182	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.77E-04	0.89	3.76	-	865.3
AHQ-7-8, 6803 - 6868	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.10E-05	0.84	3.93	-	507.6
AHQ-7-8, 6938	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.11E-04	0.90	4.44	-	663.5
AHQ-7-9, 4452	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.59E-05	0.93	4.31	-	1048.9
AHQ-7-10, 4359 - 4428	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.27E-06	0.96	5.21	-	1002.0
AHQ-7-10, 4483 - 4545	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.74E-05	0.94	4.99	-	856.3
AHQ-7-10, 4643	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.75E-06	0.91	3.95	-	832.2
AHQ-7-10, 4872 - 4935	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.84E-06	0.95	5.09	-	894.4
AHQ-7-11, 4474	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.82E-11	0.95	5.04	-	871.6
AHQ-7-11, 4586	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.78E-05	0.90	4.16	-	728.5
AHQ-7-11, 4863 - 4864	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.76E-05	0.93	4.93	-	749.0
AHQ-7-12, 4478 - 4487	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.46E-09	0.95	5.27	-	1057.0
AHQ-7-13, 4689 - 4761	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.05E-05	0.95	5.09	-	959.0
AHQ-7-13, 4817 - 4841	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.00E-05	0.97	5.49	-	1190.5
AHQ-7-13, 4989 - 5005	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.23E-06	0.97	5.31	-	1289.2
AHQ-7-13, 5079 - 5137	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.43E-04	0.89	3.93	-	903.9
AHQ-7-13, 5203 - 5261	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.44E-06	0.95	4.83	-	967.1
AHQ-7-14, 5353 - 5409	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.59E-05	0.94	4.61	-	887.6
AHQ-7-14, 5468 - 5524	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.17E-05	0.94	4.92	-	728.5
AHQ-7-14, 5580 - 5642	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.79E-05	0.92	4.63	-	655.9
AHQ-7-14, 5702 - 5768	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.04E-05	0.95	4.40	-	1240.0
AHQ-7-14, 5748	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.12E-04	0.92	4.25	-	687.3
AHQ-7-13-, 4772	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.94E-05	0.89	3.65	-	934.4
AHQ-7-13-, 4861	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.44E-07	0.97	5.02	-	1421.1
AHQ-7-13-, 5095 - 5164	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.58E-06	0.96	5.91	-	928.4
AHQ-7-14-, 4543 - 4602	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.89E-08	0.97	5.78	-	1077.6
AHQ-7-14-, 4661 - 4722	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.33E-05	0.96	5.26	-	1129.9
AHQ-7-14-, 4790 - 4851	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.09E-05	0.94	4.69	-	823.9
AHQ-7-14-, 4879 - 4941	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.79E-08	0.95	4.74	-	937.0
AHQ-7-14-, 4947 - 5005	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.76E-04	0.95	4.99	-	1072.7
AHQ-7-14-, 5293 - 5294	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.66E-06	0.96	5.86	-	924.0
AHQ-7-8, 4063 - 4075	K.YPIEHSIITNWDDMEK.I	1992.19784	2	3.15E-04	0.78	3.31	-	891.6
gi|4502051|ref|NP_000688.1| arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]				9.93E-11	6.97	80.22	17.60	75721.8
AHQ-7-6, 4802	R.AAAQLTYCSLCPPDDLADR.G	2140.33708	2	2.83E-05	0.84	3.40	-	555.2
AHQ-7-6, 3470	K.GDPELQAWCR.E	1233.33558	2	1.04E-06	0.74	2.56	-	505.5
AHQ-7-6, 5458	R.GLLGLPGALYAHDALR.L	1637.90708	2	9.93E-11	0.94	4.41	-	803.3
AHQ-7-6, 5033	R.ITVQGPGACAEVAFPCYR.W	1999.25659	2	5.46E-04	0.79	3.35	-	784.5
AHQ-7-6, 4509	R.LPGDNALDMFQK.H	1349.53784	2	2.74E-05	0.88	3.45	-	858.6
AHQ-7-6, 4047	R.TQLISDGGIFDK.A	1294.43554	2	1.22E-06	0.92	3.71	-	1007.8
AHQ-7-6, 4673	R.VATGAWLFSGSYNR.V	1529.68080	2	1.93E-04	0.91	3.35	-	1099.4
AHQ-7-6, 4966	R.WVQGEDILSLPEGTAR.L	1771.95190	2	1.34E-05	0.94	4.31	-	1000.7
gi|29742410|ref|XP_291183.1| similar to TREM-like transcript 1 [Homo sapiens]				9.93E-11	1.57	20.21	10.30	32678.3
AHQ-7-11, 4123	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	9.93E-11	0.84	3.60	-	504.4
AHQ-7-13-, 4103 - 4107	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.96E-07	0.90	4.06	-	520.6
AHQ-7-13-, 4185 - 4259	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	3.10E-07	0.89	3.55	-	613.6
AHQ-7-13-, 3868 - 3933	R.VSLNILPPEEEEETHK.I	1865.03087	3	1.42E-04	0.73	3.22	-	770.2
AHQ-7-11, 3723	R.VSLNILPPEEEEETHK.I	1865.03087	3	2.94E-04	0.56	3.14	-	595.6
gi|5031635|ref|NP_005498.1| cofilin 1 (non-muscle) [Homo sapiens]				1.07E-10	7.32	80.33	57.80	18502.4
AHQ-7-12, 3443 - 3500	K.AVLFCLSEDKK.N	1311.52930	2	2.84E-06	0.74	2.69	-	686.1
AHQ-7-11, 5286	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.07E-10	0.94	4.48	-	1124.9
AHQ-7-13, 5469 - 5471	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.40E-06	0.98	6.15	-	1663.0
AHQ-7-13-, 5404	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.98E-07	0.96	5.17	-	1285.8
AHQ-7-12, 5296	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.68E-07	0.50	2.88	-	375.3
AHQ-7-12, 5192 - 5239	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.50E-09	0.98	6.17	-	1720.2
AHQ-7-14-, 5411	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	6.28E-09	0.96	5.21	-	1073.8
AHQ-7-14, 6149	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	5.31E-04	0.94	4.69	-	915.6
AHQ-7-12, 2608 - 2683	K.HELQANCYEEVKDR.C	1792.90812	2	7.39E-05	0.83	3.24	-	530.2
AHQ-7-12, 2446 - 2511	K.HELQANCYEEVKDR.C	1792.90812	2	2.65E-09	0.97	5.42	-	1405.0
AHQ-7-12, 3063 - 3132	K.KAVLFCLSEDKK.N	1439.70221	2	1.08E-04	0.91	3.71	-	888.3
AHQ-7-12, 3087	K.KAVLFCLSEDKK.N	1439.70221	3	1.17E-08	0.90	3.88	-	1061.7
AHQ-7-11, 5984	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	9.59E-04	0.65	2.77	-	553.6
AHQ-7-12, 5959 - 6034	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	2.34E-06	0.93	4.36	-	872.7
AHQ-7-13-, 6113 - 6148	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	6.26E-05	0.94	4.59	-	967.0
AHQ-7-13-, 6149	K.KEDLVFIFWAPESAPLK.S	1991.31745	3	8.62E-04	0.92	5.17	-	620.7
AHQ-7-12, 4222 - 4303	K.LGGSAVISLEGKPL	1341.57848	2	5.53E-08	0.96	5.03	-	1310.1
AHQ-7-14-, 4365	K.LGGSAVISLEGKPL	1341.57848	2	1.39E-06	0.95	4.43	-	1209.3
AHQ-7-12, 3928 - 3930	K.LGGSAVISLEGKPL	1341.57848	2	1.38E-06	0.95	4.23	-	1439.3
AHQ-7-12, 4227 - 4296	K.LGGSAVISLEGKPL	1341.57848	1	4.29E-04	0.33	2.46	-	403.2
AHQ-7-12, 4359	K.LGGSAVISLEGKPL	1341.57848	2	5.63E-04	0.90	3.53	-	1100.5
AHQ-7-13-, 4329	K.LGGSAVISLEGKPL	1341.57848	2	8.11E-05	0.90	3.66	-	971.3
AHQ-7-11, 6147	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	4.59E-05	0.92	5.00	-	859.0
AHQ-7-12, 6119	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	4.79E-10	0.96	6.55	-	1365.3
AHQ-7-12, 3115 - 3178	R.YALYDATYETK.E	1338.44364	2	1.48E-06	0.95	3.95	-	1075.7
AHQ-7-11, 3194 - 3264	R.YALYDATYETK.E	1338.44364	2	2.95E-09	0.91	3.37	-	932.9
AHQ-7-12, 3182	R.YALYDATYETK.E	1338.44364	1	1.97E-06	0.53	2.79	-	301.4
gi|13518026|ref|NP_004978.2| LIM and senescent cell antigen-like domains 1 [Homo sapiens]				1.07E-10	2.60	30.23	12.00	37251.2
AHQ-7-9, 4129 - 4140	K.CHAIIDEQPLIFK.N	1585.84900	2	2.44E-04	0.95	4.61	-	1390.5
AHQ-7-8, 4404 - 4418	K.CHAIIDEQPLIFK.N	1585.84900	2	1.07E-10	0.96	4.65	-	1233.0
AHQ-7-11, 4319 - 4327	K.CHAIIDEQPLIFK.N	1585.84900	2	3.10E-07	0.95	4.60	-	1170.5
AHQ-7-8, 3318	R.ELKGELYCLPCHDK.M	1765.00101	2	9.81E-06	0.70	2.86	-	504.0
AHQ-7-8, 3327	R.VIEGDVVSALNK.A	1244.41966	2	6.43E-06	0.90	3.37	-	892.1
AHQ-7-10, 3351	R.VIEGDVVSALNK.A	1244.41966	2	8.80E-04	0.71	2.80	-	456.6
AHQ-7-11, 3423 - 3434	R.VIEGDVVSALNK.A	1244.41966	2	5.09E-05	0.95	4.28	-	952.3
AHQ-7-9, 3265	R.VIEGDVVSALNK.A	1244.41966	1	1.63E-04	0.63	2.58	-	675.6
AHQ-7-8, 3414	R.VIEGDVVSALNK.A	1244.41966	2	1.82E-07	0.94	4.17	-	1145.6
gi|5729887|ref|NP_006624.1| IQ motif containing GTPase activating protein 2 [Homo sapiens]				1.14E-10	5.40	60.27	6.00	180611.0
AHQ-7-3, 3749	K.AWVNQLETQTGEASK.L	1662.78230	2	7.05E-04	0.70	3.00	-	658.3
AHQ-7-3, 5536	K.GVLLDIDDLQTNQFK.N	1719.91690	2	1.15E-07	0.95	4.63	-	1246.2
AHQ-7-3, 4753	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	1.14E-10	0.97	4.74	-	1896.1
AHQ-7-3, 4475	K.SLIINTNPVEVYK.A	1490.72593	2	4.50E-04	0.85	2.93	-	1238.8
AHQ-7-3, 4116 - 4187	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	1.19E-08	0.95	4.88	-	1137.2
AHQ-7-3, 5680	R.VVAVGYINEAIDEGNPLR.T	1930.15092	2	7.48E-10	0.98	5.37	-	2180.2
gi|5453607|ref|NP_006420.1| chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co				1.25E-10	1.88	20.24	6.60	59366.3
AHQ-7-7, 4941	K.LPIGDVATQYFADR.D	1566.73935	2	1.25E-10	0.93	3.57	-	1136.4

AHQ-7-7, 6676	K.SQDAEVGDGTTSVTLLAAEFLK.Q	2253.44875	2	6.48E-06	0.95	4.89	-	1076.5
gi|10835002|ref|NP_001166.1| Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]				1.53E-10	4.19	50.25	40.80	22987.8
AHQ-7-10, 2419	K.APEPHVEEDDDDELDSK.L	1940.90995	2	3.25E-09	0.97	4.67	-	1737.7
AHQ-7-10, 2356 - 2437	K.APEPHVEEDDDDELDSK.L	1940.90995	3	1.53E-10	0.96	5.09	-	1650.6
AHQ-7-10, 5100 - 5155	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	4.77E-10	0.88	4.25	-	737.4
AHQ-7-10, 5292 - 5299	K.ATFMVGSYGPRPEEYEFLTPVEEAPK.G	2946.27924	3	2.58E-05	0.85	4.09	-	782.8
AHQ-7-13-, 5372	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	4.80E-04	0.82	3.54	-	781.0
AHQ-7-11, 5236 - 5238	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	7.50E-06	0.87	4.02	-	903.9
AHQ-7-10, 3021 - 3075	K.ELQEMDKDDESLIK.Y	1693.85489	2	8.42E-04	0.84	3.77	-	820.8
AHQ-7-10, 5751 - 5808	R.LTLVCESAPGPITM*DLTGDLEALKK.E	2691.11214	3	2.09E-07	0.66	3.13	-	593.5
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				1.55E-10	13.26	150.24	12.00	191612.6
AHQ-7-3, 4456	R.ALEHFTDLYDIK.R	1465.63179	2	2.25E-05	0.90	3.30	-	934.3
AHQ-7-3, 4752	R.GQFSTDELVAEVEK.R	1552.66462	2	9.49E-08	0.94	4.54	-	1128.9
AHQ-7-3, 4703	R.GQFSTDELVAEVEKR.N	1708.85097	2	1.12E-07	0.89	3.89	-	942.8
AHQ-7-3, 2156	R.IHEGCEEPATHNALAK.I	1778.92458	2	9.06E-04	0.87	3.36	-	803.5
AHQ-7-3, 5212	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	1.55E-10	0.91	4.10	-	1366.7
AHQ-7-3, 4479	R.LASTLVHLGEYQAAVDGAR.K	1972.19103	2	9.25E-05	0.92	3.92	-	1021.1
AHQ-7-3, 5857	K.LLLPWLEAR.I	1111.36131	2	1.37E-04	0.60	2.86	-	395.5
AHQ-7-3, 6421 - 6500	R.LPVVIGGLLDVDCSEDVIK.N	2043.36744	2	6.70E-04	0.91	3.94	-	844.6
AHQ-7-4, 6209	R.NLQNLLILTAIK.A	1354.66353	2	3.42E-05	0.97	4.64	-	1703.5
AHQ-7-3, 6059 - 6079	R.NLQNLLILTAIK.A	1354.66353	2	2.05E-05	0.97	4.47	-	2204.3
AHQ-7-5, 4862 - 4923	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	8.79E-07	0.78	3.22	-	776.7
AHQ-7-3, 3295	K.VANVELYYR.A	1127.27446	2	3.22E-07	0.92	3.54	-	931.4
AHQ-7-3, 6581	K.VGYTPDWIFLLR.N	1480.73443	2	2.14E-07	0.77	3.21	-	382.9
AHQ-7-3, 3192	K.VIQCFAETGQVQK.I	1509.70940	2	1.08E-07	0.96	3.78	-	2082.8
AHQ-7-3, 3815	R.VVGAMQLYSVDR.K	1338.55819	2	8.37E-08	0.94	3.64	-	1223.7
AHQ-7-3, 5188	K.WLLLTGISAQQNR.V	1500.72728	2	1.64E-06	0.98	4.84	-	2438.9
AHQ-7-5, 5208	K.WLLLTGISAQQNR.V	1500.72728	2	1.19E-04	0.93	3.08	-	1747.7
gi|4759300|ref|NP_004772.1| vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated				1.71E-10	2.90	30.30	33.00	11309.0
AHQ-7-14-, 3582	R.ADALQAGASQFETSAAK.L	1666.77095	2	5.87E-09	0.94	4.18	-	1183.5
AHQ-7-13-, 3569	R.ADALQAGASQFETSAAK.L	1666.77095	2	6.26E-10	0.95	4.94	-	1039.9
AHQ-7-13-, 3515 - 3575	R.ADALQAGASQFETSAAK.L	1666.77095	2	6.30E-08	0.91	4.00	-	973.2
AHQ-7-13, 3689	R.ADALQAGASQFETSAAK.L	1666.77095	2	4.89E-05	0.90	3.66	-	889.8
AHQ-7-13-, 3680 - 3681	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	2.36E-08	0.98	6.06	-	1824.0
AHQ-7-13-, 4745	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	1.71E-10	0.97	4.78	-	1778.3
AHQ-7-13, 4850	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	8.12E-08	0.97	4.91	-	1532.1
AHQ-7-13, 3811	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	1.04E-05	0.97	4.99	-	1562.1
gi|5729875|ref|NP_006658.1| progesterone receptor membrane component 1; progesterone binding protei				1.78E-10	1.77	20.20	17.40	21671.0
AHQ-7-11, 4356 - 4362	K.FYGPEGPYGVFAGR.D	1517.66849	2	1.78E-10	0.94	3.99	-	1095.7
AHQ-7-11, 2864	R.GDQPAASGDSDDDEPPPLPR.L	2037.04410	2	2.50E-04	0.83	3.72	-	518.0
gi|4502011|ref|NP_000467.1| adenylate kinase 1 [Homo sapiens]				1.87E-10	2.32	30.24	24.20	21634.7
AHQ-7-11, 6311	K.GQLVPLETVLDMLR.D	1584.90590	2	1.87E-10	0.95	4.80	-	543.4
AHQ-7-11, 5014	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	2	2.21E-05	0.56	2.75	-	561.1
AHQ-7-11, 3676 - 3732	K.YGYTHLSTGDLLR.S	1496.64912	2	2.77E-05	0.81	3.24	-	635.5
gi|5453549|ref|NP_006397.1| thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho				2.07E-10	2.79	30.20	18.50	30539.7
AHQ-7-10, 3548	K.DYGVYLEDSGHTLR.G	1625.72052	2	2.07E-10	0.96	4.05	-	1465.1
AHQ-7-10, 3935	K.HGEVCPAGWKPGSETIIPDPAGK.L	2405.67144	3	4.01E-05	0.87	3.52	-	1402.3
AHQ-7-10, 4648	R.IPLLSDLTHQISK.D	1465.71961	2	7.02E-09	0.96	4.08	-	1164.1
gi|30160191|ref|XP_294035.2| similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme				2.25E-10	0.70	10.22	2.80	50222.2
AHQ-7-7, 5009	K.IYVDDGLISLQVK.Q	1463.70048	1	2.25E-10	0.70	3.19	-	584.7
AHQ-7-7, 4990	K.IYVDDGLISLQVK.Q	1463.70048	2	9.67E-07	0.97	4.43	-	2098.9
gi|17986258|ref|NP_066299.2| smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo				2.32E-10	6.15	70.23	37.10	16930.0
AHQ-7-13-, 4144	K.DQGTYEDYVEGLR.V	1545.58904	2	8.23E-04	0.91	3.56	-	1073.5
AHQ-7-14-, 4195	K.DQGTYEDYVEGLR.V	1545.58904	2	1.44E-06	0.93	3.68	-	1245.2
AHQ-7-12, 4038 - 4114	K.DQGTYEDYVEGLR.V	1545.58904	2	5.69E-05	0.91	3.76	-	1021.5
AHQ-7-13, 2653 - 2679	R.HVLVTLGEK.M	996.18547	2	3.73E-06	0.86	2.86	-	691.7
AHQ-7-12, 2367	R.HVLVTLGEK.M	996.18547	1	5.81E-05	0.66	3.18	-	431.6
AHQ-7-12, 2362 - 2418	R.HVLVTLGEK.M	996.18547	2	6.48E-06	0.89	3.41	-	644.9
AHQ-7-13-, 2404	R.HVLVTLGEK.M	996.18547	2	5.21E-06	0.86	3.46	-	568.7
AHQ-7-12, 3698 - 3775	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.23E-08	0.95	4.09	-	1379.4
AHQ-7-12, 3594 - 3615	K.NKDQGTYEDYVEGLR.V	1787.86505	3	7.85E-06	0.93	4.49	-	1210.8
AHQ-7-12, 3587 - 3644	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.12E-04	0.72	3.24	-	476.5
AHQ-7-14-, 3742	K.NKDQGTYEDYVEGLR.V	1787.86505	2	5.82E-08	0.89	3.68	-	1041.4
AHQ-7-13-, 3757	K.NKDQGTYEDYVEGLR.V	1787.86505	3	4.35E-04	0.91	4.20	-	1037.8
AHQ-7-13-, 3731 - 3735	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.89E-10	0.90	4.04	-	877.3
AHQ-7-12, 2890 - 2959	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.07E-05	0.72	3.84	-	495.0
AHQ-7-13, 3869	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.52E-06	0.86	3.49	-	883.4
AHQ-7-12, 3872 - 3947	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.32E-10	0.93	4.29	-	1030.2
AHQ-7-14, 4584	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.64E-04	0.85	3.33	-	865.0
AHQ-7-12, 2679 - 2735	R.VFDKEGNGTVM*GAEIR.H	1739.93168	2	2.46E-05	0.83	3.01	-	899.7
AHQ-7-12, 3235 - 3243	R.VFDKEGNGTVMGAEIR.H	1723.93228	3	4.50E-04	0.75	3.26	-	1026.2
AHQ-7-12, 5819 - 5874	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	1.31E-04	0.62	3.03	-	514.6
AHQ-7-12, 6162	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	4.63E-05	0.93	4.58	-	710.5
AHQ-7-13-, 6012 - 6015	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	5.53E-05	0.83	3.69	-	719.0
AHQ-7-13-, 6356	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	9.51E-06	0.93	4.56	-	722.4
AHQ-7-13-, 6359	K.VLDFEHFLPMLQTVAK.N	1889.25017	3	1.94E-04	0.89	4.08	-	1121.1
AHQ-7-13-, 6011	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	3.69E-07	0.93	4.16	-	672.8
AHQ-7-12, 5866 - 5928	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	3.68E-05	0.84	3.70	-	474.2
AHQ-7-13, 6037	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	1.70E-04	0.73	3.32	-	489.4
AHQ-7-14-, 5971	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	2.78E-05	0.94	4.36	-	928.5
gi|10863977|ref|NP_067000.1| LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-				2.57E-10	0.97	10.30	20.00	10834.5
AHQ-7-14-, 5213	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	2.57E-10	0.97	6.07	-	1462.0
AHQ-7-14, 5934 - 5937	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	8.83E-06	0.98	6.07	-	1429.6
gi|4505753|ref|NP_002620.1| phosphoglycerate mutase 1 (brain); Phosphoglycerate mutase A, nonmuscle				2.69E-10	0.85	10.19	8.30	28803.7
AHQ-7-10, 4569	R.YADLTEDQLPSCESLKDTIAR.A	2427.62735	3	2.69E-10	0.85	3.49	-	765.7
gi|5902128|ref|NP_008880.1| syntaxin binding protein 2; Hunc18b [Homo sapiens]				3.06E-10	8.05	90.32	26.30	66438.1
AHQ-7-6, 6695 - 6710	R.AADPVSPLLHELTFQAM*AYDLLDIEQDTYR.Y	3453.81998	3	2.07E-06	0.88	4.43	-	756.5
AHQ-7-6, 6106	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	3	6.61E-05	0.90	4.01	-	1153.6
AHQ-7-6, 6115 - 6122	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	2	7.90E-07	0.98	6.36	-	1395.0
AHQ-7-6, 6321	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	3.64E-04	0.69	2.59	-	569.0
AHQ-7-6, 3323	R.KGPEDTAQLAHAVLAK.L	1649.87303	2	1.00E-08	0.95	4.26	-	1386.7
AHQ-7-6, 4129	K.LCSVEQDLAMGSDAEGEK.I	1941.08446	2	5.69E-05	0.91	3.99	-	887.5
AHQ-7-7, 6173	K.LIVPVLLDAAVPAYDK.I	1698.03911	2	1.05E-05	0.92	3.49	-	1165.6
AHQ-7-6, 6173	K.LIVPVLLDAAVPAYDK.I	1698.03911	3	2.23E-05	0.93	4.98	-	1051.6
AHQ-7-6, 6631	K.M*SDILAEGITIVEDINKR.R	2034.32082	3	3.06E-10	0.83	3.89	-	704.4
AHQ-7-6, 3253	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	1.99E-09	0.91	4.25	-	615.4
AHQ-7-6, 5873	R.REPIPSLEAIYLLSPTEK.S	2057.37574	3	5.13E-06	0.85	3.73	-	985.0
AHQ-7-6, 5882 - 5899	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	2.47E-07	0.98	6.18	-	1853.0
gi|19923457|ref|NP_057447.2| glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M				3.27E-10	3.49	40.23	10.80	67308.6
AHQ-7-7, 5524	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	3.27E-10	0.91	3.98	-	1134.5
AHQ-7-7, 5534	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	2	8.64E-05	0.93	4.68	-	631.3
AHQ-7-7, 3684	K.PSLSAQPGPAVSSGGDVTLQCQTR.Y	2415.62303	2	3.82E-05	0.73	2.72	-	783.7
AHQ-7-7, 4752	R.YGFDQFALYK.E	1252.39881	2	1.45E-07	0.93	3.47	-	900.5
AHQ-7-7, 4949	R.YQDQAVLFIPAMK.R	1524.80902	2	1.44E-04	0.93	3.89	-	1138.9
gi|18860900|ref|NP_002834.2| protein tyrosine phosphatase, receptor type, J precursor; protein tyro				3.36E-10	7.16	80.28	10.00	145926.2
AHQ-7-1, 3523	R.AGSPTAPVHDESLVGPVDPSSGQQSR.D	2576.71806	3	7.06E-09	0.93	4.59	-	1256.9
AHQ-7-1, 4280 - 4357	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	2	3.01E-06	0.98	5.54	-	1919.1

AHQ-7-1, 4859	R.DTEVLLVGLEPGTR.Y	1499.69122	2	6.36E-04	0.91	3.57	-	1361.8
AHQ-7-1, 3064	K.FSGFEASHGPIK.A	1277.40990	2	1.45E-05	0.90	3.38	-	960.0
AHQ-7-1, 3092 - 3160	K.GDPLGTEGGLDASNTER.S	1689.71978	2	4.90E-09	0.84	3.32	-	736.7
AHQ-7-1, 5012 - 5088	K.GLIDGAESYVSFSR.Y	1501.62253	2	3.81E-06	0.92	3.49	-	1244.2
AHQ-7-1, 3785	K.TPSSTGPSPVFDIK.A	1433.58810	2	5.92E-05	0.73	3.07	-	596.6
AHQ-7-1, 3895 - 3907	R.VLLESIGSHEELTQDSR.L	1914.06352	2	1.66E-05	0.91	4.09	-	833.5
AHQ-7-1, 3904	R.VLLESIGSHEELTQDSR.L	1914.06352	3	3.36E-10	0.95	4.66	-	1124.4
gi|4504973|ref|NP_002292.1| lactate dehydrogenase C [Homo sapiens]				3.53E-10	0.90	10.17	3.60	36311.0
AHQ-7-9, 2365	R.VIGSGCNLDSAR.F	1250.36445	2	3.53E-10	0.90	3.49	-	765.6
gi|27413156|ref|NP_000338.2| spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)				3.77E-10	0.89	10.19	0.70	246320.0
AHQ-7-2, 2668	R.LLSGEDVGQDEGATR.A	1547.60647	2	3.77E-10	0.89	3.82	-	562.3
gi|20535366|ref|XP_053177.4| similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap				3.88E-10	2.55	30.22	9.60	49858.2
AHQ-7-7, 3064	K.DVNAAIATIK.T	1016.17355	2	8.35E-06	0.86	3.19	-	873.5
AHQ-7-7, 3220	K.DVNAAIATIK.T	1016.17355	1	1.33E-04	0.19	1.85	-	274.1
AHQ-7-11, 3063	K.DVNAAIATIK.T	1016.17355	2	1.35E-04	0.90	3.66	-	934.4
AHQ-7-8, 3252	K.DVNAAIATIK.T	1016.17355	1	3.99E-04	0.34	1.88	-	290.9
AHQ-7-8, 3059	K.DVNAAIATIK.T	1016.17355	1	5.56E-04	0.26	2.30	-	194.2
AHQ-7-12, 2899	K.DVNAAIATIK.T	1016.17355	1	1.76E-04	0.37	2.18	-	422.0
AHQ-7-14-, 4895 - 4967	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.28E-07	0.84	3.71	-	510.4
AHQ-7-7, 5044 - 5124	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.08E-06	0.87	3.81	-	559.8
AHQ-7-7, 4929	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.45E-06	0.82	3.75	-	531.2
AHQ-7-7, 4678 - 4709	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	6.29E-08	0.94	4.43	-	694.3
AHQ-7-11, 4483	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.95E-06	0.75	3.26	-	405.0
AHQ-7-11, 4822	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	6.04E-08	0.81	3.57	-	484.1
AHQ-7-14-, 4631	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.88E-10	0.92	4.22	-	635.3
AHQ-7-7, 5130 - 5193	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.92E-09	0.94	4.22	-	1118.3
AHQ-7-14, 5944	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	3.48E-04	0.82	3.79	-	446.3
AHQ-7-13, 5101 - 5117	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.06E-07	0.93	4.18	-	812.9
AHQ-7-14, 5736 - 5796	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.54E-04	0.73	3.40	-	409.4
AHQ-7-14, 5505	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.84E-07	0.69	3.46	-	215.9
AHQ-7-14-, 5025	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.18E-07	0.95	4.40	-	1092.8
AHQ-7-11, 5280 - 5346	R.TIQFVDWCPTGFK.V	1600.81899	2	3.46E-04	0.63	2.98	-	492.9
AHQ-7-7, 5608 - 5672	R.TIQFVDWCPTGFK.V	1600.81899	2	9.41E-05	0.86	2.87	-	923.5
AHQ-7-12, 5255 - 5322	R.TIQFVDWCPTGFK.V	1600.81899	2	3.48E-04	0.48	2.57	-	471.6
AHQ-7-13, 5503 - 5577	R.TIQFVDWCPTGFK.V	1600.81899	2	1.41E-04	0.88	3.69	-	730.3
AHQ-7-14-, 5497 - 5553	R.TIQFVDWCPTGFK.V	1600.81899	2	3.57E-05	0.76	2.91	-	569.1
gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]				3.93E-10	9.77	120.27	55.80	22391.3
AHQ-7-12, 5390	R.DDGLFSGDPNWFPK.K	1595.69288	2	7.09E-06	0.81	2.82	-	827.0
AHQ-7-11, 5414 - 5474	R.DDGLFSGDPNWFPK.K	1595.69288	2	4.05E-07	0.90	3.54	-	1045.1
AHQ-7-11, 5516 - 5587	R.DDGLFSGDPNWFPK.K	1595.69288	2	8.14E-05	0.95	4.81	-	1109.3
AHQ-7-13-, 5904	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.85E-04	0.58	2.74	-	429.8
AHQ-7-13-, 6471	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	3.14E-05	0.80	3.30	-	478.9
AHQ-7-11, 5738	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	7.70E-06	0.74	3.12	-	533.7
AHQ-7-12, 5730	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	5.82E-04	0.84	4.01	-	477.7
AHQ-7-11, 6259 - 6315	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.09E-05	0.93	4.67	-	695.0
AHQ-7-11, 6320 - 6323	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	3	3.28E-07	0.90	4.95	-	751.1
AHQ-7-11, 6208 - 6270	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	4.10E-07	0.95	5.42	-	945.0
AHQ-7-12, 6230 - 6234	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	5.42E-04	0.85	3.83	-	738.1
AHQ-7-11, 5347 - 5352	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.42E-04	0.63	2.96	-	492.9
AHQ-7-12, 6240	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	1.11E-09	0.61	2.90	-	490.1
AHQ-7-13-, 6424	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	7.44E-07	0.86	4.03	-	938.4
AHQ-7-14-, 6405	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.11E-07	0.68	3.09	-	570.8
AHQ-7-12, 2646	K.IQASTMAFK.Q	997.19374	1	1.54E-04	0.48	2.40	-	483.5
AHQ-7-12, 2306 - 2307	R.NFSDNQLQEGK.N	1280.32582	2	8.42E-05	0.67	2.73	-	763.5
AHQ-7-11, 2372	R.NFSDNQLQEGK.N	1280.32582	2	1.11E-04	0.83	3.23	-	752.6
AHQ-7-12, 2322	R.NFSDNQLQEGK.N	1280.32582	1	9.72E-04	0.16	2.03	-	186.0
AHQ-7-11, 3084	K.NVIGLQMGTNR.G	1203.39751	2	4.71E-06	0.90	3.19	-	1223.8
AHQ-7-11, 2463	K.NVIGLQM*GTNR.G	1219.39691	2	2.40E-04	0.84	3.22	-	882.5
AHQ-7-11, 2303 - 2375	K.NVIGLQM*GTNR.G	1219.39691	2	2.51E-05	0.83	2.86	-	802.5
AHQ-7-11, 3183 - 3256	K.NVIGLQMGTNR.G	1203.39751	2	1.48E-05	0.88	3.25	-	1353.9
AHQ-7-11, 4484	K.QM*EQISQFLQAAER.Y	1695.87890	3	1.58E-05	0.93	4.25	-	1502.3
AHQ-7-12, 5080	K.QMEQISQFLQAAER.Y	1679.87950	2	2.49E-05	0.73	2.98	-	749.2
AHQ-7-11, 5082 - 5090	K.QMEQISQFLQAAER.Y	1679.87950	2	2.30E-04	0.96	4.51	-	1338.8
AHQ-7-11, 4244 - 4302	R.TLMNLGGLAVAR.D	1216.47932	2	1.68E-05	0.93	4.20	-	1171.3
AHQ-7-11, 4512	R.TLMNLGGLAVAR.D	1216.47932	2	3.81E-07	0.94	3.89	-	1312.7
AHQ-7-11, 3526	R.TLM*NLGGLAVAR.D	1232.47872	2	8.64E-06	0.92	3.53	-	1115.6
AHQ-7-12, 4326 - 4327	R.TLMNLGGLAVAR.D	1216.47932	2	2.23E-05	0.92	4.10	-	954.1
AHQ-7-13, 4561	R.TLMNLGGLAVAR.D	1216.47932	2	1.18E-05	0.88	3.54	-	1034.4
AHQ-7-11, 4283	R.TLM*NLGGLAVAR.D	1232.47872	2	4.91E-04	0.83	3.44	-	887.2
AHQ-7-13-, 4440	R.TLMNLGGLAVAR.D	1216.47932	2	2.60E-06	0.95	4.72	-	1239.6
AHQ-7-11, 3835	R.TLM*NLGGLAVAR.D	1232.47872	2	5.04E-05	0.86	2.63	-	1113.5
AHQ-7-11, 6134 - 6207	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	7.09E-09	0.97	5.33	-	1266.5
AHQ-7-14-, 6341	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	4.03E-08	0.96	5.05	-	1152.5
AHQ-7-12, 6166	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	5.92E-07	0.93	4.70	-	864.0
AHQ-7-13, 6353	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.93E-10	0.96	5.33	-	1169.0
gi|30147105|ref|XP_210550.2| similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48				4.15E-10	0.95	10.22	2.20	61339.9
AHQ-7-5, 4644	K.ADLINNLGTIAK.S	1243.43490	2	4.15E-10	0.95	4.08	-	1113.7
AHQ-7-5, 4251	K.ADLINNLGTIAK.S	1243.43490	2	2.19E-06	0.95	4.50	-	981.1
gi|9966825|ref|NP_065089.1| HEF like Protein [Homo sapiens]				4.26E-10	1.79	20.25	4.30	86696.2
AHQ-7-13-, 4147	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	5.43E-04	0.96	4.98	-	1378.6
AHQ-7-13-, 4149	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	3	4.43E-05	0.87	4.11	-	686.1
AHQ-7-13-, 3448	K.LVDTLCMETQER.D	1496.68930	2	4.26E-10	0.92	3.74	-	781.7
gi|5031677|ref|NP_005681.1| dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [				4.63E-10	10.88	120.24	24.20	78060.6
AHQ-7-6, 4734	K.ALQGASQIIAEIR.E	1370.57991	2	8.83E-04	0.91	3.64	-	1335.4
AHQ-7-13, 4767	K.ALQGASQIIAEIR.E	1370.57991	2	1.89E-05	0.90	3.96	-	1104.1
AHQ-7-13-, 4660	K.ALQGASQIIAEIR.E	1370.57991	2	5.27E-08	0.93	3.97	-	1489.1
AHQ-7-6, 2903	R.CVELVHEEMQR.I	1431.62054	2	1.91E-07	0.88	3.57	-	777.2
AHQ-7-14-, 5013	K.DTLQSELVGQLYK.S	1494.67144	2	4.76E-07	0.67	2.90	-	624.5
AHQ-7-13-, 4988 - 4996	K.DTLQSELVGQLYK.S	1494.67144	2	6.52E-08	0.89	3.10	-	1130.2
AHQ-7-13, 5106	K.DTLQSELVGQLYK.S	1494.67144	2	5.60E-04	0.91	3.51	-	1172.5
AHQ-7-13-, 4332 - 4399	K.GHAVNLLDVPVPVAR.K	1557.82197	2	3.22E-06	0.95	4.14	-	1207.8
AHQ-7-6, 6577 - 6581	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	2.27E-06	0.92	4.03	-	1012.8
AHQ-7-6, 6145	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	3.74E-04	0.91	3.61	-	933.7
AHQ-7-5, 6686	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	1.16E-07	0.95	4.84	-	1181.8
AHQ-7-6, 3305	R.IIQHCSNYSTQELLR.F	1864.07262	2	5.54E-04	0.93	3.90	-	1019.1
AHQ-7-6, 5958	K.LYTDFDEIRQEIENETER.I	2301.40883	3	4.63E-10	0.90	4.01	-	990.0
AHQ-7-13, 5970	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	6.21E-07	0.86	3.03	-	881.7
AHQ-7-14-, 5919	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	1.96E-08	0.83	3.42	-	722.8
AHQ-7-6, 4726	K.SVTDSIRDEYAFLQK.K	1772.93666	2	6.37E-04	0.90	3.57	-	1219.7
AHQ-7-6, 6697 - 6699	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	2.15E-07	0.94	4.50	-	917.4
AHQ-7-7, 6793	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	5.10E-08	0.92	4.23	-	723.0
AHQ-7-6, 2990	K.YIETSELCGGAR.I	1357.47179	2	1.01E-04	0.91	3.40	-	1123.7
gi|21361755|ref|NP_004090.3| stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie				4.86E-10	7.61	90.27	40.60	31708.5
AHQ-7-1, 4248 - 4259	K.EASM*VITESPAALQLR.Y	1732.98059	2	7.75E-07	0.86	3.85	-	675.4
AHQ-7-13, 4171	K.EASM*VITESPAALQLR.Y	1732.98059	2	1.30E-04	0.63	2.78	-	552.4
AHQ-7-10, 4272 - 4273	K.EASMVITESPAALQLR.Y	1716.98119	2	3.00E-04	0.94	4.35	-	1165.1
AHQ-7-10, 3847 - 3860	K.EASM*VITESPAALQLR.Y	1732.98059	2	1.86E-05	0.93	4.52	-	960.6

AHQ-7-14-, 4030	K.EASM*VITESPAALQLR.Y	1732.98059	2	2.51E-05	0.94	4.34	-	930.5
AHQ-7-9, 6124 - 6125	K.GPGLFFILPCTDSFIK.V	1814.13672	2	7.56E-05	0.96	4.60	-	1139.4
AHQ-7-13-, 6423 - 6425	K.GPGLFFILPCTDSFIK.V	1814.13672	2	4.97E-05	0.94	4.76	-	744.9
AHQ-7-3, 6687	K.GPGLFFILPCTDSFIK.V	1814.13672	2	7.58E-04	0.93	4.36	-	891.7
AHQ-7-1, 6559 - 6560	K.GPGLFFILPCTDSFIK.V	1814.13672	2	5.51E-04	0.96	4.77	-	1142.8
AHQ-7-10, 2349	R.LLAQTTLR.N	916.10035	2	6.58E-05	0.63	2.59	-	565.6
AHQ-7-9, 6224 - 6226	K.NSTIVFPLPIDMLQGIIGAK.H	2128.56375	2	2.82E-04	0.85	3.94	-	449.6
AHQ-7-1, 5343 - 5424	R.TISFDIPPQEILTK.D	1602.85305	2	7.61E-04	0.53	2.66	-	228.4
AHQ-7-10, 2232 - 2240	K.VIAAEGEMNASR.A	1248.39191	2	1.05E-08	0.97	4.31	-	1550.8
AHQ-7-1, 4149 - 4211	R.VQNATLAVANITNADSATR.L	1931.09731	2	7.77E-10	0.96	5.31	-	1032.5
AHQ-7-1, 4496	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.05E-07	0.92	4.29	-	719.4
AHQ-7-1, 3899 - 3961	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.75E-08	0.94	4.77	-	756.8
AHQ-7-10, 3744 - 3816	R.VQNATLAVANITNADSATR.L	1931.09731	2	6.04E-08	0.95	4.87	-	1092.8
AHQ-7-1, 4019 - 4084	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.86E-10	0.96	4.86	-	1264.9
AHQ-7-10, 4087	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.42E-09	0.94	3.94	-	981.7
AHQ-7-1, 4007	R.VQNATLAVANITNADSATR.L	1931.09731	3	4.96E-05	0.89	4.39	-	870.9
AHQ-7-1, 3880	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.88E-08	0.95	4.65	-	935.6
AHQ-7-2, 4012	R.YLQTLTTIAAEK.N	1352.55813	2	3.92E-04	0.87	3.12	-	981.5
AHQ-7-1, 3937 - 4011	R.YLQTLTTIAAEK.N	1352.55813	2	1.55E-05	0.93	3.66	-	1399.7
gi|21956645|ref|NP_665807.1| myotrophin; granule cell differentiation protein [Homo sapiens]				5.25E-10	2.89	30.28	41.50	12894.7
AHQ-7-13, 4074 - 4129	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.00E-08	0.97	5.41	-	1691.1
AHQ-7-13, 4202 - 4206	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	5.25E-10	0.97	5.56	-	1286.1
AHQ-7-14, 4732 - 4790	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.12E-04	0.96	5.27	-	1148.0
AHQ-7-14, 4846 - 4928	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	8.14E-04	0.97	5.57	-	1354.6
AHQ-7-13-, 4071	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.79E-09	0.98	5.52	-	1585.1
AHQ-7-14-, 3927 - 4001	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.72E-06	0.84	3.15	-	763.3
AHQ-7-13-, 3987	K.HHITPLLSAVYEGHVSCVK.L	2149.45825	3	1.97E-09	0.98	5.55	-	2396.2
AHQ-7-13-, 3647	K.NGDLDEVKDYVAK.G	1466.57496	2	3.59E-07	0.80	2.99	-	774.2
AHQ-7-14-, 3565	K.NGDLDEVKDYVAK.G	1466.57496	2	9.10E-08	0.88	3.73	-	726.3
AHQ-7-13, 3695	K.NGDLDEVKDYVAK.G	1466.57496	2	1.09E-09	0.94	4.05	-	1159.5
gi|4505763|ref|NP_000282.1| phosphoglycerate kinase 1 [Homo sapiens]				5.64E-10	5.75	70.27	25.40	44614.4
AHQ-7-8, 5714	K.ACANPAAGSVILLENLR.F	1771.03187	2	6.75E-06	0.89	3.75	-	1074.6
AHQ-7-8, 5327	K.ALESPERPFLAILGGAK.V	1770.06542	2	3.74E-06	0.97	5.43	-	1688.4
AHQ-7-10, 5072	K.ALESPERPFLAILGGAK.V	1770.06542	2	3.35E-04	0.82	3.91	-	941.4
AHQ-7-8, 4642	K.DVLFLKDCVGPEVEK.A	1750.00620	2	5.64E-10	0.92	3.92	-	1057.9
AHQ-7-8, 4159	K.IQLINNMLDK.V	1202.44942	2	5.14E-06	0.57	3.15	-	342.6
AHQ-7-8, 5234	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	4.75E-06	0.94	4.79	-	850.9
AHQ-7-8, 5111	K.VLNNMEIGTSLFDEEGAK.I	1968.17459	2	1.82E-04	0.89	4.32	-	539.1
AHQ-7-8, 5306	K.VLPGVDALSNI	1098.27456	1	1.32E-04	0.57	2.15	-	335.0
gi|5454152|ref|NP_006285.1| ubiquinol-cytochrome c reductase binding protein [Homo sapiens]				5.69E-10	1.57	20.20	25.20	13530.4
AHQ-7-13-, 3520	R.DDTIYEDEDVKEAIR.R	1811.88169	2	8.92E-07	0.86	3.42	-	735.8
AHQ-7-13, 3655	R.DDTIYEDEDVKEAIR.R	1811.88169	2	5.69E-10	0.63	2.82	-	560.4
AHQ-7-13-, 4997 - 5055	K.YEEENFYLEPYLK.E	1737.88601	2	2.05E-05	0.94	4.07	-	1241.9
AHQ-7-13, 5131 - 5207	K.YEEENFYLEPYLK.E	1737.88601	2	3.42E-06	0.94	3.45	-	1356.9
gi|29737978|ref|XP_290747.1| similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy				5.83E-10	4.51	50.25	2.60	191380.7
AHQ-7-2, 3115	K.ADEWLMK.N	893.04238	2	2.31E-04	0.86	2.77	-	676.8
AHQ-7-3, 4007 - 4008	K.ADFCIIHYAGK.V	1296.47641	2	1.46E-06	0.96	3.83	-	1533.2
AHQ-7-1, 4104	K.ADFCIIHYAGK.V	1296.47641	2	4.41E-06	0.94	3.88	-	1186.0
AHQ-7-2, 4100	K.ADFCIIHYAGK.V	1296.47641	1	1.64E-04	0.78	2.93	-	669.0
AHQ-7-5, 3975	K.ADFCIIHYAGK.V	1296.47641	2	1.38E-05	0.95	4.10	-	1187.4
AHQ-7-6, 3891	K.ADFCIIHYAGK.V	1296.47641	2	8.01E-07	0.94	3.97	-	1100.3
AHQ-7-2, 4076 - 4115	K.ADFCIIHYAGK.V	1296.47641	2	2.46E-06	0.93	3.56	-	1268.1
AHQ-7-4, 3998 - 4006	K.ADFCIIHYAGK.V	1296.47641	2	2.05E-06	0.93	3.63	-	1069.8
AHQ-7-3, 3033 - 3095	R.AGVLAHLEEER.D	1224.34854	2	1.98E-07	0.96	4.38	-	1710.6
AHQ-7-7, 2902	R.AGVLAHLEEER.D	1224.34854	2	3.30E-07	0.89	3.63	-	1028.9
AHQ-7-2, 3112	R.AGVLAHLEEER.D	1224.34854	2	5.35E-07	0.94	4.08	-	1288.2
AHQ-7-13-, 3096	R.AGVLAHLEEER.D	1224.34854	2	1.27E-05	0.92	3.42	-	1236.8
AHQ-7-4, 3025	R.AGVLAHLEEER.D	1224.34854	2	2.60E-08	0.95	4.31	-	1511.9
AHQ-7-1, 3279	R.AGVLAHLEEER.D	1224.34854	2	7.80E-07	0.96	4.31	-	1637.8
AHQ-7-6, 3006	R.AGVLAHLEEER.D	1224.34854	2	2.33E-06	0.97	4.59	-	1705.9
AHQ-7-5, 3007	R.AGVLAHLEEER.D	1224.34854	2	1.45E-06	0.95	4.18	-	1470.7
AHQ-7-3, 3784	K.DKADFCIIHYAGK.V	1539.73719	2	5.83E-10	0.96	4.14	-	1487.4
AHQ-7-2, 3855	K.DKADFCIIHYAGK.V	1539.73719	3	5.22E-06	0.93	4.15	-	1463.3
AHQ-7-6, 3673	K.DKADFCIIHYAGK.V	1539.73719	2	2.06E-07	0.97	4.42	-	1777.2
AHQ-7-2, 3851 - 3853	K.DKADFCIIHYAGK.V	1539.73719	2	8.95E-10	0.98	4.92	-	2060.0
AHQ-7-2, 4784	K.LDPHLVLDQLR.C	1319.53460	3	1.47E-05	0.85	3.38	-	775.3
AHQ-7-5, 4671	K.LDPHLVLDQLR.C	1319.53460	3	9.75E-07	0.67	3.05	-	622.3
AHQ-7-5, 4662 - 4663	K.LDPHLVLDQLR.C	1319.53460	2	7.18E-07	0.80	2.87	-	561.6
AHQ-7-4, 4744 - 4753	K.LDPHLVLDQLR.C	1319.53460	2	9.98E-07	0.79	2.78	-	657.0
AHQ-7-3, 4681	K.LDPHLVLDQLR.C	1319.53460	2	9.84E-06	0.74	2.65	-	582.7
gi|28178832|ref|NP_002159.2| isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat				6.20E-10	3.38	40.22	12.20	50909.0
AHQ-7-8, 4074 - 4079	K.DLAGCIHGLSNVK.L	1385.57150	2	6.20E-10	0.96	4.50	-	1592.3
AHQ-7-14-, 5431 - 5442	K.LNEHFLNTTDFLDTIK.S	1922.12725	2	7.97E-05	0.92	4.20	-	988.6
AHQ-7-8, 5656	K.LNEHFLNTTDFLDTIK.S	1922.12725	2	1.06E-05	0.79	3.32	-	813.3
AHQ-7-8, 2078	K.TIEAEAAHGTVTR.H	1356.46696	2	3.14E-04	0.76	2.84	-	714.2
AHQ-7-8, 3106	K.VCVETVESGAMTK.D	1412.61230	2	7.04E-04	0.87	3.20	-	966.2
gi|5031597|ref|NP_005710.1| actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub				6.35E-10	2.53	30.21	15.20	20546.5
AHQ-7-11, 6012 - 6034	K.DTDIVDEAIYYFK.A	1592.72721	2	4.10E-06	0.93	4.14	-	1090.1
AHQ-7-14-, 6173	K.DTDIVDEAIYYFK.A	1592.72721	2	6.35E-10	0.92	3.25	-	1407.2
AHQ-7-11, 5571	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	2.64E-07	0.67	2.72	-	608.3
AHQ-7-11, 4858	K.LIGNMALLPIR.S	1211.54582	2	2.30E-05	0.94	3.43	-	1680.6
gi|4504523|ref|NP_002148.1| heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (				6.56E-10	1.82	20.20	25.50	10931.6
AHQ-7-14-, 2834 - 2893	K.VLQATVVAVGSGSK.G	1316.52902	2	3.27E-08	0.95	3.92	-	1360.8
AHQ-7-14-, 4882	K.VVLDDKDYFLFR.D	1530.74861	2	4.08E-09	0.92	2.98	-	1264.1
AHQ-7-14, 5780 - 5857	K.VVLDDKDYFLFR.D	1530.74861	2	6.56E-10	0.87	3.11	-	862.6
gi|5453832|ref|NP_006380.1| oxygen regulated protein precursor; oxygen regulated protein (150kD) [H				7.28E-10	1.89	20.22	2.80	111334.8
AHQ-7-3, 3303	K.LYQPEYQEVSTEEQR.E	1899.99217	2	7.28E-10	0.94	4.39	-	744.3
AHQ-7-3, 6267	R.VEFEELCADLFER.V	1658.81048	2	1.10E-09	0.95	4.22	-	1307.3
gi|10346135|ref|NP_055083.1| microtubule-associated protein, RP/EB family, member 2; T-cell activat				7.46E-10	1.89	20.27	9.80	37031.1
AHQ-7-9, 6032 - 6038	R.FQDNLDFIQWFK.K	1601.78539	2	3.96E-07	0.97	5.30	-	1362.9
AHQ-7-9, 4504	K.SDKDLETQVIQLNEQVHSLK.L	2325.56134	2	7.46E-10	0.92	4.63	-	815.2
gi|21314617|ref|NP_000433.2| platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e				7.86E-10	4.33	50.24	6.90	82449.6
AHQ-7-1, 5864	R.DQNFVILEFPVEEQDR.V	1979.13566	2	4.99E-04	0.94	4.43	-	1084.9
AHQ-7-4, 6105 - 6106	R.DQNFVILEFPVEEQDR.V	1979.13566	2	7.86E-10	0.91	4.41	-	909.0
AHQ-7-3, 5949	R.DQNFVILEFPVEEQDR.V	1979.13566	2	6.67E-06	0.95	4.88	-	1026.7
AHQ-7-6, 5927	R.DQNFVILEFPVEEQDR.V	1979.13566	2	4.53E-04	0.79	3.81	-	525.1
AHQ-7-5, 3455	K.EDTIVSQTQDFTK.I	1512.60049	2	5.41E-05	0.84	3.35	-	623.3
AHQ-7-4, 4218	R.ISYDAQFEVIK.G	1313.48046	2	6.83E-05	0.93	3.68	-	1010.4
AHQ-7-4, 4168 - 4169	K.STESYFIPEVR.I	1328.45199	2	5.38E-05	0.79	2.85	-	609.8
AHQ-7-3, 5412	K.VIAPVDEVQISILSSK.V	1698.98227	2	3.21E-04	0.85	3.41	-	552.8
AHQ-7-4, 5522 - 5593	K.VIAPVDEVQISILSSK.V	1698.98227	2	4.29E-04	0.81	3.11	-	423.1
gi|5453740|ref|NP_006462.1| myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat				7.87E-10	5.75	70.29	32.70	19794.0
AHQ-7-11, 5622 - 5680	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	5.32E-08	0.98	5.75	-	2342.8
AHQ-7-14-, 5206 - 5253	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.95E-06	0.97	5.22	-	1693.1
AHQ-7-13-, 5888	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	2.22E-07	0.98	5.14	-	2042.5
AHQ-7-13-, 5248	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	6.10E-06	0.97	4.59	-	1571.8
AHQ-7-14, 5968	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.18E-08	0.96	4.55	-	1479.6

AHQ-7-11, 4919	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	3.47E-08	0.91	3.99	-	804.2
AHQ-7-11, 5020 - 5086	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	7.87E-10	0.98	5.62	-	1517.2
AHQ-7-11, 5142 - 5224	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	7.09E-08	0.97	5.35	-	1716.2
AHQ-7-11, 5279 - 5294	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	3.00E-06	0.96	5.26	-	1066.6
AHQ-7-12, 5686	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.45E-05	0.89	3.58	-	930.0
AHQ-7-12, 5070	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.78E-06	0.93	4.15	-	1231.2
AHQ-7-11, 5511 - 5567	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	8.97E-06	0.94	3.99	-	1038.6
AHQ-7-11, 5990	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.27E-05	0.85	3.51	-	743.2
AHQ-7-11, 5858	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.27E-05	0.91	3.79	-	866.8
AHQ-7-14-, 5846 - 5853	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	8.67E-07	0.98	5.67	-	1820.9
AHQ-7-11, 5759	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	5.40E-05	0.90	3.82	-	792.6
AHQ-7-11, 5560	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	2.18E-08	0.91	3.76	-	1477.6
AHQ-7-11, 5554 - 5563	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	7.92E-07	0.90	4.20	-	928.3
AHQ-7-11, 4236 - 4312	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	4.87E-06	0.94	4.06	-	1106.4
AHQ-7-11, 5470	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	7.60E-09	0.96	4.45	-	1450.5
AHQ-7-12, 5474 - 5487	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	2.97E-04	0.94	4.44	-	1198.0
AHQ-7-12, 5478 - 5479	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	1.78E-07	0.95	4.37	-	1648.0
AHQ-7-11, 5468	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	9.59E-08	0.88	3.95	-	1012.3
AHQ-7-11, 4314	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	3	4.96E-05	0.90	3.80	-	1344.9
AHQ-7-11, 2679	R.ELLTTMGDR.F	1036.18513	1	1.52E-04	0.13	1.84	-	145.7
AHQ-7-11, 4002 - 4006	K.GNFNYIEFTR.I	1261.36733	2	3.92E-04	0.80	3.53	-	657.2
AHQ-7-12, 4050 - 4059	K.GNFNYIEFTR.I	1261.36733	2	9.12E-05	0.84	3.59	-	733.3
AHQ-7-13-, 4176 - 4180	K.GNFNYIEFTR.I	1261.36733	2	4.56E-05	0.87	3.37	-	857.4
AHQ-7-11, 3514	K.KGNFNYIEFTR.I	1389.54025	2	3.85E-06	0.89	3.14	-	845.6
gi|29730023|ref|XP_291482.1| similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno				8.04E-10	4.49	60.21	11.50	63563.0
AHQ-7-10, 4365	R.IINKPTAAAIAYGLDK.R	1659.95097	2	2.58E-06	0.34	3.09	-	376.9
AHQ-7-6, 3493 - 3557	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	2.63E-05	0.91	4.09	-	1010.9
AHQ-7-7, 3470	K.NQLTSNPKNTVFDAK.R	1677.84011	2	2.96E-05	0.87	3.88	-	1034.5
AHQ-7-6, 3489	K.NQLTSNPKNTVFDAK.R	1677.84011	2	2.29E-04	0.78	4.15	-	639.0
AHQ-7-7, 4654	K.PTAAAIAYGLDK.R	1191.35846	1	5.30E-04	0.70	2.62	-	699.1
AHQ-7-6, 5565	K.TFAPKEISAMVLTK.M	1536.86124	2	8.04E-10	0.80	3.20	-	948.9
AHQ-7-6, 4833	K.TFAPKEISAM*VLTK.M	1552.86064	2	8.09E-09	0.87	3.62	-	1052.7
AHQ-7-6, 4675 - 4741	K.TFAPKEISAM*VLTK.M	1552.86064	2	4.69E-05	0.83	3.51	-	989.1
gi|4758984|ref|NP_004654.1| RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho				8.06E-10	4.13	50.30	23.10	24393.3
AHQ-7-13-, 2880	K.AQIWDTAGQER.Y	1275.35241	2	2.47E-05	0.89	3.02	-	1116.3
AHQ-7-11, 2778 - 2791	K.AQIWDTAGQER.Y	1275.35241	2	3.82E-07	0.96	3.81	-	1933.8
AHQ-7-11, 4062 - 4070	R.DHADSNIVIM*LVGNK.S	1642.85914	2	5.69E-07	0.98	6.01	-	2727.9
AHQ-7-11, 4554 - 4624	R.DHADSNIVIMLVGNK.S	1626.85974	2	8.06E-10	0.97	4.47	-	1751.0
AHQ-7-11, 4806	R.GAVGALLVYDIAK.H	1290.53317	2	1.53E-06	0.96	4.14	-	1695.0
AHQ-7-11, 2856	K.VVLIGDSGVGK.S	1044.22690	1	4.66E-05	0.25	2.56	-	487.7
AHQ-7-11, 2846	K.VVLIGDSGVGK.S	1044.22690	1	1.83E-04	0.43	2.15	-	801.9
gi|5802974|ref|NP_006784.1| peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide				8.19E-10	3.69	40.28	26.60	27692.5
AHQ-7-11, 4359	K.AFQYVETHGEVCPANWTPDSPTIKPSPAASK.E	3388.70790	3	8.19E-10	0.95	5.50	-	1182.8
AHQ-7-11, 5060	R.DYGVLLEGSGLALR.G	1463.66058	2	1.51E-08	0.96	3.89	-	1937.8
AHQ-7-10, 4973	R.DYGVLLEGSGLALR.G	1463.66058	2	2.17E-04	0.92	2.87	-	1651.6
AHQ-7-11, 5150	R.GLFIIDPNGVIK.H	1286.54452	2	2.90E-05	0.88	2.93	-	1214.7
AHQ-7-11, 5300	R.GLFIIDPNGVIK.H	1286.54452	2	1.37E-05	0.87	3.60	-	870.2
AHQ-7-11, 2971 - 3032	K.HLSVNDLPVGR.S	1207.36435	2	3.80E-07	0.90	3.57	-	649.6
gi|20127528|ref|NP_037459.2| parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]				8.41E-10	3.01	40.25	15.90	41714.0
AHQ-7-9, 3196	K.ARPEDVVNLDLK.S	1369.54878	2	1.91E-06	0.81	3.54	-	662.7
AHQ-7-9, 3208	K.ARPEDVVNLDLK.S	1369.54878	1	1.73E-05	0.31	2.71	-	199.4
AHQ-7-13-, 3513	K.ARPEDVVNLDLK.S	1369.54878	2	6.89E-05	0.81	3.49	-	581.8
AHQ-7-13, 3653	K.ARPEDVVNLDLK.S	1369.54878	2	1.43E-06	0.71	3.13	-	626.2
AHQ-7-14-, 3529	K.ARPEDVVNLDLK.S	1369.54878	2	3.38E-05	0.92	4.20	-	908.3
AHQ-7-9, 4941	R.DAFDTLFDHAPDKLSVVK.K	2019.24293	2	3.53E-07	0.63	3.35	-	491.9
AHQ-7-9, 3385 - 3448	K.LNVAEVTQSEIGQK.Q	1516.67865	2	8.41E-10	0.97	5.02	-	1687.0
AHQ-7-9, 3694	K.QLEEDLYDGQVLQK.L	1678.82164	2	3.27E-05	0.92	3.50	-	1171.2
AHQ-7-9, 3486	K.QLEEDLYDGQVLQK.L	1678.82164	2	6.85E-06	0.70	2.68	-	694.7
gi|4505839|ref|NP_002645.1| pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro				9.20E-10	15.03	170.27	45.80	57913.6
AHQ-7-7, 5586 - 5657	R.AEGSDVANAVLDGADCIM*LSGETAK.G	2512.71089	2	3.79E-04	0.89	3.84	-	708.8
AHQ-7-7, 6161	R.AGKPVICATQMLESMIK.K	1879.29869	3	2.17E-05	0.91	4.15	-	1363.1
AHQ-7-7, 5786 - 5852	R.EAEAAIYHLQLFEELR.R	1933.15326	2	9.20E-10	0.94	4.28	-	993.6
AHQ-7-7, 6797	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	1.01E-06	0.97	5.37	-	1294.8
AHQ-7-7, 4769	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	4.79E-09	0.96	4.79	-	1258.0
AHQ-7-7, 5014 - 5024	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.41E-07	0.96	4.82	-	1622.7
AHQ-7-10, 4457	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	3.00E-05	0.87	3.77	-	791.0
AHQ-7-7, 4434 - 4501	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	9.73E-05	0.52	3.27	-	199.7
AHQ-7-7, 2828 - 2860	K.GDYPLEAVR.M	1020.12076	2	3.72E-06	0.52	2.54	-	396.5
AHQ-7-14-, 6185	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	8.54E-04	0.94	4.64	-	1322.0
AHQ-7-7, 6469	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	9.76E-08	0.95	4.98	-	1687.1
AHQ-7-8, 4580	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	6.64E-04	0.69	3.10	-	508.1
AHQ-7-7, 4500 - 4516	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	2.30E-06	0.94	4.58	-	715.3
AHQ-7-7, 3173	K.ITLDNAYMEK.C	1198.37126	2	2.37E-04	0.77	3.03	-	598.4
AHQ-7-7, 4061	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	2.67E-06	0.90	3.94	-	1276.4
AHQ-7-11, 5331	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	3.30E-04	0.94	4.33	-	1123.4
AHQ-7-7, 5660 - 5728	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.18E-08	0.97	5.45	-	1357.4
AHQ-7-7, 5676	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	3	1.74E-06	0.94	4.21	-	1560.1
AHQ-7-12, 5310	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	4.90E-05	0.67	3.09	-	436.7
AHQ-7-13, 5539	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.72E-04	0.83	3.39	-	593.4
AHQ-7-9, 5166	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	7.45E-06	0.50	2.51	-	376.3
AHQ-7-7, 5325	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	6.09E-05	0.92	4.30	-	723.3
AHQ-7-1, 5643	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.51E-05	0.67	2.69	-	561.3
AHQ-7-13-, 3431	R.LDIDSPPITAR.N	1198.35099	2	3.72E-04	0.87	3.00	-	981.2
AHQ-7-11, 3339	R.LDIDSPPITAR.N	1198.35099	2	8.58E-04	0.93	3.94	-	1034.0
AHQ-7-7, 2384	R.LNFSHGTHEYHAETIK.N	1885.02879	2	3.22E-04	0.84	3.82	-	602.3
AHQ-7-7, 2397	R.LNFSHGTHEYHAETIK.N	1885.02879	3	2.19E-07	0.95	4.88	-	1490.5
AHQ-7-7, 3852	R.NTGIICTIGPASR.S	1361.54994	2	8.31E-05	0.83	3.26	-	1049.7
AHQ-7-10, 3279 - 3281	R.NTGIICTIGPASR.S	1361.54994	2	1.67E-05	0.93	3.75	-	1148.1
AHQ-7-13-, 3456 - 3469	R.NTGIICTIGPASR.S	1361.54994	2	8.62E-06	0.94	3.75	-	1265.1
AHQ-7-7, 4693 - 4718	R.RFDEILEASDGIMVAR.G	1823.06385	2	1.61E-05	0.96	5.01	-	905.0
AHQ-7-7, 4982	R.RFDEILEASDGIMVAR.G	1823.06385	2	5.71E-09	0.97	5.44	-	1444.9
AHQ-7-7, 4036	R.TATESFASDPILYR.P	1571.71277	2	1.66E-08	0.81	3.33	-	634.3
AHQ-7-7, 5613 - 5617	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	5.26E-04	0.78	3.33	-	750.1
AHQ-7-13, 5453 - 5526	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	9.99E-04	0.49	3.43	-	553.8
gi|16933567|ref|NP_005361.2| mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]				9.96E-10	0.97	10.27	6.80	23668.1
AHQ-7-11, 5435 - 5498	K.ANINVENAFFTLAR.D	1580.76926	2	9.96E-10	0.97	5.41	-	1533.7
AHQ-7-11, 5575 - 5650	K.ANINVENAFFTLAR.D	1580.76926	2	1.74E-07	0.91	3.61	-	734.9
AHQ-7-11, 4890	K.ANINVENAFFTLAR.D	1580.76926	2	2.78E-04	0.54	2.71	-	511.6
gi|4759082|ref|NP_004648.1| serum deprivation response protein; serum deprivation response; phospha				1.09E-09	3.79	40.27	14.40	47172.9
AHQ-7-11, 5839	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	6.18E-06	0.91	3.72	-	1115.0
AHQ-7-13-, 5985 - 5993	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	3.39E-04	0.96	4.53	-	1377.6
AHQ-7-13, 6101	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	6.40E-04	0.75	3.34	-	747.5
AHQ-7-9, 5613 - 5668	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.13E-06	0.89	4.22	-	657.4
AHQ-7-9, 5698 - 5757	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.17E-05	0.92	4.25	-	964.1
AHQ-7-13, 6011	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	4.97E-05	0.79	3.17	-	643.0
AHQ-7-12, 5772 - 5814	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.94E-05	0.90	3.42	-	1112.7
AHQ-7-14-, 5958	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.08E-07	0.97	5.08	-	1629.8

AHQ-7-11, 3511 - 3522	K.LVNMLDAVQENQHK.M	1639.85851	2	1.39E-05	0.94	4.44	-	1122.8
AHQ-7-14-, 5765 - 5766	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	5.73E-05	0.96	5.34	-	877.3
AHQ-7-11, 5602 - 5638	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.74E-06	0.97	5.23	-	1100.1
AHQ-7-11, 5755	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.36E-05	0.84	3.36	-	536.5
AHQ-7-7, 6008	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.60E-06	0.94	4.42	-	921.0
AHQ-7-10, 5527	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	5.03E-07	0.96	5.15	-	1013.1
AHQ-7-9, 5417 - 5448	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.73E-08	0.95	5.08	-	752.8
AHQ-7-13-, 5793	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.23E-05	0.83	3.30	-	778.1
AHQ-7-6, 6006 - 6013	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.09E-09	0.95	4.92	-	850.8
AHQ-7-12, 2882	R.YEGSYALTSEEAER.S	1605.64124	2	2.99E-04	0.78	2.77	-	684.8
AHQ-7-13, 3095 - 3151	R.YEGSYALTSEEAER.S	1605.64124	2	1.31E-06	0.92	3.60	-	892.8
gi|4507907|ref|NP_000543.1| von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille				1.12E-09	20.99	250.29	13.00	309296.7
AHQ-7-1, 3911 - 3989	R.CLPSACEVVTGSPR.G	1535.72531	2	4.68E-05	0.89	3.92	-	820.3
AHQ-7-1, 4327	R.CM*VQVGVISGFK.L	1342.61000	2	8.93E-04	0.72	2.69	-	767.2
AHQ-7-3, 4911 - 4985	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	1.13E-05	0.26	2.73	-	407.4
AHQ-7-1, 4684 - 4697	R.EQAPNLVYM*VTGNPASDEIK.R	2193.42002	2	1.74E-05	0.94	4.14	-	1080.9
AHQ-7-2, 5631	R.EQAPNLVYMVTGNPASDEIK.R	2177.42062	2	6.31E-04	0.74	3.56	-	388.0
AHQ-7-2, 4149	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	3.09E-07	0.80	3.29	-	702.4
AHQ-7-1, 4128	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	2.40E-06	0.84	3.78	-	637.2
AHQ-7-1, 3357	R.HIVTFDGQNFK.L	1306.45124	2	6.50E-08	0.87	3.34	-	597.1
AHQ-7-1, 6547	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	1.47E-06	0.91	4.57	-	432.7
AHQ-7-1, 2877	R.ILAGPAGDSNVVK.L	1241.41901	2	1.85E-07	0.87	3.06	-	968.5
AHQ-7-2, 3832	R.ILTSDVFQDCNK.L	1441.58869	2	4.69E-07	0.93	3.87	-	945.9
AHQ-7-1, 3839	R.ILTSDVFQDCNK.L	1441.58869	2	5.78E-07	0.90	3.51	-	790.6
AHQ-7-1, 3713	K.IPGTCCDTCEEPECNDITAR.L	2403.54132	2	1.18E-05	0.54	2.63	-	525.9
AHQ-7-1, 6428	R.LLDLVFLLDGSSR.L	1448.68905	2	1.66E-05	0.88	3.26	-	934.1
AHQ-7-1, 4253	R.LSEAEFEVLK.A	1165.31777	2	1.74E-05	0.89	3.45	-	957.9
AHQ-7-4, 3286	K.LSGEAYGFVAR.I	1170.29934	2	1.77E-05	0.95	3.84	-	1476.7
AHQ-7-3, 4967	R.NSQWICSNEECPGECLVTGQSHFK.S	2872.07402	3	3.36E-06	0.86	4.18	-	601.6
AHQ-7-1, 5391 - 5457	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	5.91E-06	0.97	5.83	-	2035.0
AHQ-7-1, 4037 - 4109	R.SGFTYVLHEGECCGR.C	1774.91285	2	3.53E-09	0.96	4.32	-	1426.6
AHQ-7-2, 4935	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	1.12E-09	0.91	4.41	-	567.2
AHQ-7-3, 4851	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	7.04E-08	0.91	4.63	-	495.6
AHQ-7-1, 4843	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	3.40E-04	0.79	3.63	-	386.8
AHQ-7-4, 3217	R.TCQSLHINEMCQER.C	1808.99579	2	1.55E-04	0.89	3.49	-	718.4
AHQ-7-1, 5329 - 5379	K.TYGLCGICDENGANDFM*LR.D	2225.42231	2	1.51E-06	0.96	4.71	-	1296.4
AHQ-7-1, 4545	K.VIVIPVGIGPHANLK.Q	1527.87891	2	2.86E-05	0.49	2.60	-	413.6
AHQ-7-1, 4607	R.VTVFPIGIGDR.Y	1174.37426	2	1.49E-07	0.94	3.39	-	1551.2
AHQ-7-2, 4657	R.VTVFPIGIGDR.Y	1174.37426	2	1.97E-06	0.94	3.46	-	1351.8
AHQ-7-1, 3123	K.YAGSQVASTSEVLK.Y	1440.58064	2	2.69E-07	0.94	4.22	-	953.8
AHQ-7-2, 2999	K.YAGSQVASTSEVLK.Y	1440.58064	2	4.60E-04	0.92	4.03	-	865.3
AHQ-7-3, 2964 - 2972	K.YAGSQVASTSEVLK.Y	1440.58064	2	4.44E-08	0.96	4.93	-	1167.8
AHQ-7-1, 3597	R.YLSDHSFLVSQGDR.E	1624.73576	2	3.79E-06	0.94	3.99	-	1122.2
AHQ-7-1, 5747	K.YTLFQIFSK.I	1147.34728	2	2.91E-05	0.92	3.22	-	906.8
gi|4507869|ref|NP_003361.1| vasodilator-stimulated phosphoprotein [Homo sapiens]				1.17E-09	0.95	10.21	3.70	39829.4
AHQ-7-8, 6082	K.VKEEIIEAFVQELR.K	1703.96061	2	1.17E-09	0.95	4.22	-	1377.8
gi|13129150|ref|NP_005339.1| heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H				1.19E-09	1.86	20.27	3.40	84659.1
AHQ-7-8, 4002	R.NPDDITNEEYGEFYK.S	1834.87381	2	7.99E-07	0.96	4.42	-	1473.1
AHQ-7-6, 3994	R.NPDDITNEEYGEFYK.S	1834.87381	2	2.33E-09	0.96	4.52	-	1157.3
AHQ-7-7, 3946	R.NPDDITNEEYGEFYK.S	1834.87381	2	2.29E-06	0.92	4.02	-	1116.2
AHQ-7-5, 4047 - 4050	R.NPDDITNEEYGEFYK.S	1834.87381	2	1.19E-09	0.97	5.47	-	1247.9
AHQ-7-5, 4095 - 4170	R.RAPFDLFENR.K	1265.40235	2	5.62E-06	0.89	3.36	-	851.5
gi|13489087|ref|NP_109591.1| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member				1.27E-09	1.55	20.22	8.70	42741.5
AHQ-7-9, 3721	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	7.17E-05	0.60	2.83	-	471.9
AHQ-7-13-, 3988	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	2.05E-05	0.88	3.72	-	803.0
AHQ-7-8, 4024	K.TYGADLASVDFQHASEDAR.K	2054.11949	3	1.27E-09	0.90	4.38	-	692.3
AHQ-7-14-, 5871	K.TYNFLPEFLVSTQK.T	1687.91650	2	7.59E-04	0.60	2.62	-	407.3
AHQ-7-13, 5882 - 5938	K.TYNFLPEFLVSTQK.T	1687.91650	2	3.48E-05	0.66	2.96	-	330.6
gi|17444699|ref|XP_017966.4| similar to Reticulon protein 3 (Neuroendocrine-specific protein-like 2				1.32E-09	0.82	10.16	4.70	25522.7
AHQ-7-1, 3093	K.TQIDHYVGIAR.H	1273.42279	2	1.32E-09	0.82	3.27	-	864.1
gi|18104967|ref|NP_000953.2| prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland				1.38E-09	4.09	50.24	17.20	68686.0
AHQ-7-6, 3993	K.AEHPTWGDEQLFQTTR.L	1917.02765	3	2.84E-04	0.91	4.19	-	1257.7
AHQ-7-6, 5117	R.FGMKPYTSFQELVGEK.E	1862.13845	2	2.57E-07	0.80	3.62	-	393.5
AHQ-7-6, 6585	K.GLLGNPICSPEYWKPSTFGGEVGFNIVK.T	3069.47853	3	1.47E-05	0.77	3.86	-	392.7
AHQ-7-6, 3227 - 3303	R.VPDASQDDGPAVERPSTEL	1984.06747	2	1.38E-09	0.95	4.86	-	929.0
AHQ-7-6, 5310	K.YQVLDGEMYPPSVEEAPVLM*HYPR.G	2838.20739	3	9.57E-08	0.65	3.18	-	464.7
gi|21361478|ref|NP_055944.2| septin 6 isoform B; septin 2 [Homo sapiens]				1.42E-09	1.92	20.26	11.10	49716.3
AHQ-7-7, 3881	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L	3147.31508	3	1.42E-09	0.95	5.24	-	1347.5
AHQ-7-7, 4954 - 4960	R.TVPLAGHVGFDSLPDQLVNK.S	2108.38284	2	7.17E-08	0.97	5.27	-	1272.4
gi|29742827|ref|XP_294099.1| similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]				1.42E-09	2.17	30.23	14.20	17094.0
AHQ-7-11, 2843 - 2851	K.EAFNMIDQNR.D	1238.35558	2	8.01E-05	0.63	2.80	-	442.2
AHQ-7-11, 2962	K.EAFNMIDQNR.D	1238.35558	2	2.89E-04	0.81	3.29	-	644.4
AHQ-7-11, 2964	K.EAFNM*IDQNR.D	1254.35498	2	4.72E-05	0.55	2.64	-	543.4
AHQ-7-14-, 3079 - 3133	K.EAFNMIDQNR.D	1238.35558	2	2.41E-05	0.66	2.73	-	709.6
AHQ-7-11, 3150	K.EAFNMIDQNR.D	1238.35558	2	9.47E-05	0.85	3.29	-	779.2
AHQ-7-11, 3624 - 3674	R.FTDEEVDELYR.E	1416.47127	2	1.15E-08	0.97	4.13	-	2182.7
AHQ-7-11, 3675	R.FTDEEVDELYR.E	1416.47127	1	8.01E-06	0.32	1.92	-	403.7
AHQ-7-11, 3136 - 3195	R.FTDEEVDELYR.E	1416.47127	2	3.44E-05	0.84	2.94	-	780.5
AHQ-7-12, 3714	R.FTDEEVDELYR.E	1416.47127	2	3.20E-08	0.97	3.99	-	1814.8
AHQ-7-12, 3724	R.FTDEEVDELYR.E	1416.47127	1	5.23E-09	0.64	2.75	-	519.2
AHQ-7-13, 3969 - 4041	R.FTDEEVDELYR.E	1416.47127	2	1.54E-05	0.96	3.98	-	1955.3
AHQ-7-14, 4676	R.FTDEEVDELYR.E	1416.47127	2	5.11E-08	0.95	3.48	-	1768.7
AHQ-7-13-, 3828 - 3897	R.FTDEEVDELYR.E	1416.47127	2	1.91E-06	0.96	3.94	-	1522.8
AHQ-7-11, 3695	R.FTDEEVDELYR.E	1416.47127	1	1.52E-09	0.58	2.59	-	428.4
AHQ-7-14-, 3831	R.FTDEEVDELYR.E	1416.47127	2	1.42E-09	0.96	4.52	-	1499.3
gi|29739414|ref|XP_294015.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				1.67E-09	2.45	30.23	17.70	26916.7
AHQ-7-9, 3713 - 3778	K.IISNASCTTNCLAPLAK.V	1837.10868	2	8.22E-06	0.86	4.17	-	1195.3
AHQ-7-10, 3960	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.06E-09	0.59	3.10	-	751.3
AHQ-7-10, 3743 - 3800	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.50E-08	0.83	3.53	-	1233.7
AHQ-7-11, 3824 - 3900	K.IISNASCTTNCLAPLAK.V	1837.10868	2	7.35E-08	0.91	4.53	-	1366.6
AHQ-7-9, 4670	K.LISWYDNEFGYSNR.V	1764.87478	2	9.34E-05	0.67	3.03	-	513.2
AHQ-7-9, 4498 - 4553	K.LISWYDNEFGYSNR.V	1764.87478	2	5.46E-07	0.96	4.30	-	1208.5
AHQ-7-9, 4369 - 4425	K.LISWYDNEFGYSNR.V	1764.87478	2	9.51E-04	0.56	2.82	-	385.6
AHQ-7-14-, 4858 - 4930	K.LISWYDNEFGYSNR.V	1764.87478	2	8.90E-08	0.94	4.58	-	923.0
AHQ-7-10, 4576 - 4583	K.LISWYDNEFGYSNR.V	1764.87478	2	8.33E-08	0.94	4.00	-	1215.9
AHQ-7-11, 4651 - 4706	K.LISWYDNEFGYSNR.V	1764.87478	2	6.06E-09	0.91	3.70	-	741.2
AHQ-7-13, 4965 - 4974	K.LISWYDNEFGYSNR.V	1764.87478	2	1.67E-09	0.96	4.56	-	1339.1
AHQ-7-14, 5741 - 5742	K.LISWYDNEFGYSNR.V	1764.87478	2	1.92E-05	0.94	4.39	-	1020.7
AHQ-7-13-, 4847	K.LISWYDNEFGYSNR.V	1764.87478	2	3.55E-08	0.93	3.77	-	1071.6
AHQ-7-9, 2957	R.VVDLMAHMASKE	1331.58746	2	1.20E-05	0.90	3.21	-	1076.7
gi|4557871|ref|NP_001054.1| transferrin [Homo sapiens]				1.70E-09	8.52	100.26	19.50	77049.5
AHQ-7-5, 4638	K.CSTSSLLEACTFR.R	1534.69418	2	4.60E-04	0.89	3.10	-	956.7
AHQ-7-5, 5050	K.EDPQTFYYAVAVVK.K	1630.82181	2	8.14E-04	0.37	2.63	-	488.1
AHQ-7-5, 3666	K.EGYYGYTGAFR.C	1284.35776	2	4.42E-05	0.78	2.55	-	835.6
AHQ-7-5, 4138	R.FDEFFSEGCAPGSK.K	1579.66868	2	6.88E-06	0.96	3.92	-	1618.5
AHQ-7-6, 4073 - 4079	R.FDEFFSEGCAPGSK.K	1579.66868	2	1.64E-05	0.96	4.22	-	1382.1
AHQ-7-5, 2983	K.HSTIFENLANK.A	1274.40755	2	3.22E-05	0.95	3.93	-	1223.5

AHQ-7-6, 3378	K.IECVSAETTEDCIAK.I	1728.87748	2	1.39E-04	0.77	3.48	-	539.9
AHQ-7-5, 3422	K.IECVSAETTEDCIAK.I	1728.87748	2	1.57E-05	0.91	3.20	-	1022.3
AHQ-7-5, 3220 - 3231	R.LKCDEWSVNSVGK.I	1523.69293	2	1.70E-09	0.87	3.64	-	739.2
AHQ-7-5, 4652	K.M*YLGYEYVTAIR.N	1495.72451	2	1.31E-06	0.94	3.13	-	1406.9
AHQ-7-5, 6763	R.SAGWNIPIGLLYCDLPEPR.K	2173.47658	2	2.32E-06	0.96	5.13	-	940.9
AHQ-7-5, 5983 - 5990	R.TAGWNIPMGLLYNK.I	1578.85991	2	5.90E-06	0.87	3.93	-	504.0
gi|4507651|ref|NP_003281.1| tropomyosin 4 [Homo sapiens]				1.80E-09	4.46	50.27	22.60	28521.6
AHQ-7-9, 3792	R.AEVSELKCGDLEEELK.N	1851.02256	2	7.00E-06	0.85	3.74	-	710.5
AHQ-7-9, 1940 - 1956	R.EKAEGDVAALNR.R	1273.37796	2	4.07E-05	0.74	2.87	-	717.6
AHQ-7-9, 2504 - 2561	K.IQALQQQADEAEDR.A	1615.68404	2	5.30E-05	0.84	3.29	-	877.5
AHQ-7-13, 2867	K.IQALQQQADEAEDR.A	1615.68404	2	6.41E-04	0.81	3.02	-	591.9
AHQ-7-10, 2572 - 2573	K.IQALQQQADEAEDR.A	1615.68404	2	1.80E-09	0.96	4.11	-	1673.0
AHQ-7-11, 2594 - 2655	K.IQALQQQADEAEDR.A	1615.68404	2	6.59E-08	0.95	4.28	-	1323.0
AHQ-7-11, 2426	R.KIQALQQQADEAEDR.A	1743.85695	2	9.19E-06	0.97	5.42	-	2019.3
AHQ-7-9, 2332 - 2388	R.KIQALQQQADEAEDR.A	1743.85695	2	6.28E-05	0.95	4.94	-	1145.5
AHQ-7-9, 2088 - 2150	K.YSEKEDKYEEEIK.L	1690.78605	3	1.23E-04	0.95	4.80	-	1346.7
gi|4758460|ref|NP_004479.1| glycoprotein V (platelet) [Homo sapiens]				1.83E-09	7.08	80.24	24.80	60958.9
AHQ-7-5, 5495	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	1.95E-06	0.86	4.12	-	728.9
AHQ-7-6, 5414	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	8.73E-09	0.84	4.20	-	790.9
AHQ-7-6, 4625	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	1.19E-06	0.93	3.88	-	1286.5
AHQ-7-5, 4680 - 4686	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	1.15E-08	0.96	4.80	-	1403.5
AHQ-7-5, 3944	R.GVLQSQSFSGM*TVLQR.L	1754.98948	2	4.72E-07	0.96	4.56	-	1755.0
AHQ-7-5, 5547	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	3	1.49E-06	0.93	4.77	-	1058.7
AHQ-7-5, 5550	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	2	1.83E-09	0.96	4.78	-	1086.9
AHQ-7-6, 5474	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	3	9.13E-09	0.90	4.26	-	1076.6
AHQ-7-6, 4589	R.LPNLSSLTLSR.N	1201.39802	2	5.72E-05	0.74	2.97	-	871.9
AHQ-7-5, 4687	R.LPNLSSLTLSR.N	1201.39802	2	7.07E-05	0.88	3.25	-	1061.4
AHQ-7-5, 6826	R.LSALPQGAFQGLGELQVLALHSNGLTALPDGLLR.G	3471.99408	3	2.15E-05	0.80	4.11	-	445.8
AHQ-7-5, 6803	R.LVSLDSGLLNSLGALTELQFHR.N	2384.71675	3	8.17E-07	0.72	3.23	-	525.6
AHQ-7-6, 6701	R.LVSLDSGLLNSLGALTELQFHR.N	2384.71675	3	5.21E-08	0.77	3.31	-	576.9
AHQ-7-5, 6707	R.LVSLDSGLLNSLGALTELQFHR.N	2384.71675	3	2.12E-09	0.90	4.25	-	983.1
AHQ-7-5, 3459	R.YLGVTLSPR.L	1006.18036	2	8.29E-04	0.91	3.28	-	1196.8
gi|4506353|ref|NP_002854.1| phosphorylase, glycogen; liver (Hers disease, glycogen storage disease				1.90E-09	1.80	20.26	3.70	97147.8
AHQ-7-5, 4848	K.EYAQNIWNVEPSDLK.I	1806.95311	2	7.66E-07	0.84	3.72	-	531.6
AHQ-7-5, 6251	R.WLLLCNPGLAELIAEK.I	1842.19160	2	1.90E-09	0.95	5.16	-	1412.3
gi|4758208|ref|NP_004081.1| dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;				2.05E-09	3.67	40.24	32.40	20478.2
AHQ-7-11, 5154	K.ANDTQEFNLSAYFER.A	1805.88207	2	2.05E-09	0.95	4.38	-	1264.6
AHQ-7-11, 5628	R.EIGPNDGFLAQLCQLNDR.L	2062.24949	2	1.69E-06	0.89	4.01	-	703.2
AHQ-7-11, 3935	R.IYVGNASVAQDIPK.L	1475.67136	2	2.35E-08	0.94	3.18	-	1525.4
AHQ-7-11, 3639 - 3650	R.IYVGNASVAQDIPK.L	1475.67136	2	3.01E-04	0.95	4.73	-	1085.6
AHQ-7-11, 3376	K.LGITHVLNAAEGR.S	1351.53669	2	1.80E-07	0.89	3.17	-	1015.2
AHQ-7-11, 3051	K.LGITHVLNAAEGR.S	1351.53669	2	1.69E-05	0.91	3.57	-	992.9
gi|4507109|ref|NP_000336.1| alpha-synuclein isoform NACP140; non A4 component of amyloid precursor				2.15E-09	3.53	40.30	36.40	14460.1
AHQ-7-12, 2298 - 2332	K.EGVVHGVATVAEK.T	1296.45466	2	1.52E-04	0.73	2.76	-	668.6
AHQ-7-13-, 4517	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	3.34E-08	0.95	5.39	-	832.6
AHQ-7-12, 4399 - 4410	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	2.39E-05	0.96	5.50	-	1005.1
AHQ-7-13, 4617	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.36E-05	0.96	5.07	-	1143.9
AHQ-7-14-, 4533	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	1.20E-07	0.97	5.91	-	1387.7
AHQ-7-13, 4305 - 4319	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	3	8.81E-05	0.81	3.93	-	1337.7
AHQ-7-12, 4096	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	2.15E-09	0.96	5.17	-	1171.1
AHQ-7-13, 4313	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.86E-04	0.89	4.22	-	641.3
AHQ-7-13, 4198 - 4254	K.TVEGAGSIAAATGFVK.K	1479.66001	2	1.50E-06	0.89	3.37	-	1019.6
gi|5031571|ref|NP_005713.1| actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog				2.28E-09	1.83	20.23	6.30	44760.5
AHQ-7-8, 3482	R.GYAFNHSADFETVR.M	1614.69943	2	5.57E-06	0.95	3.90	-	1058.9
AHQ-7-8, 3299	R.GYAFNHSADFETVR.M	1614.69943	2	2.28E-09	0.91	4.43	-	741.8
AHQ-7-8, 4134	K.HLWDYTFGPEK.L	1393.52736	2	7.69E-07	0.92	3.26	-	794.1
gi|21361122|ref|NP_001440.2| four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap				2.38E-09	2.20	30.20	14.30	31894.7
AHQ-7-12, 2523	K.AIVAGDQNVEYK.G	1307.43431	2	9.34E-04	0.77	2.61	-	632.9
AHQ-7-11, 2470	K.AIVAGDQNVEYK.G	1307.43431	2	9.45E-05	0.93	3.85	-	879.4
AHQ-7-9, 2382	K.AIVAGDQNVEYK.G	1307.43431	2	1.96E-05	0.76	2.73	-	650.8
AHQ-7-10, 3588	R.FVFHQEQVYCPDCAK.K	1931.13758	2	1.13E-06	0.85	3.59	-	749.5
AHQ-7-9, 3488	R.FVFHQEQVYCPDCAK.K	1931.13758	2	7.53E-04	0.91	3.62	-	972.4
AHQ-7-13-, 3775 - 3776	R.FVFHQEQVYCPDCAK.K	1931.13758	3	1.91E-04	0.89	3.94	-	1171.8
AHQ-7-11, 3075	K.GEDFYCVTCHETK.F	1648.75260	2	2.38E-09	0.59	2.66	-	387.8
AHQ-7-9, 2936	K.GEDFYCVTCHETK.F	1648.75260	2	1.35E-04	0.80	2.80	-	787.1
gi|4502295|ref|NP_001677.1| ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti				2.45E-09	8.22	100.28	28.90	57955.2
AHQ-7-7, 5472	R.AIAELGIYPAVDPLDSTSR.I	1989.21513	2	7.89E-04	0.68	2.72	-	422.5
AHQ-7-7, 6060	R.FLSQPFQVAEVFTGHMGK.L	2024.33104	3	3.64E-07	0.85	3.86	-	530.4
AHQ-7-7, 4408	R.FTQAGSEVSALLGR.I	1436.59522	2	3.44E-08	0.93	4.02	-	1079.9
AHQ-7-7, 4409	R.FTQAGSEVSALLGR.I	1436.59522	1	3.39E-04	0.08	2.22	-	102.6
AHQ-7-7, 6708	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	2.45E-09	0.95	5.55	-	999.5
AHQ-7-7, 2893	K.IPVGPETLGR.I	1039.21035	2	9.11E-05	0.85	2.70	-	745.3
AHQ-7-7, 4132	R.LVLEVAQHLGESTVR.T	1651.88893	2	1.30E-06	0.96	4.62	-	1188.5
AHQ-7-7, 6705	K.TVLIMELINNVAK.A	1458.79202	2	7.43E-06	0.98	4.92	-	2847.8
AHQ-7-7, 5637	R.VALTGLTVAEYFR.D	1440.66861	2	1.51E-04	0.95	3.98	-	1953.8
AHQ-7-7, 3453	K.VALVYGQMNQPPGAR.A	1601.85511	2	5.66E-09	0.85	3.42	-	648.7
AHQ-7-7, 2097	K.VLDSGAPIK.I	900.05456	1	9.87E-04	0.22	1.97	-	396.4
gi|19557677|ref|NP_002108.3| major histocompatibility complex, class I, C precursor; HLA class I hi				2.72E-09	0.96	10.21	3.30	40994.6
AHQ-7-8, 5087	R.AYLEGTCVEWLR.R	1498.68507	2	2.72E-09	0.96	4.18	-	1233.5
gi|6598323|ref|NP_001485.2| GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom				2.84E-09	2.88	30.30	12.80	50662.9
AHQ-7-7, 5252	R.NPYYGGESASITPLEDLYK.R	2118.28499	2	2.84E-09	0.94	4.46	-	1047.8
AHQ-7-7, 6568 - 6636	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	3.30E-05	0.91	4.32	-	673.6
AHQ-7-8, 6584 - 6586	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	3.09E-05	0.96	4.95	-	944.7
AHQ-7-6, 6483 - 6549	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.05E-06	0.97	5.75	-	907.7
AHQ-7-8, 6870	K.VPSTEAEALASSLMGLFEK.R	1981.25641	2	1.81E-08	0.97	5.94	-	1106.3
gi|4503743|ref|NP_002009.1| flightless I homolog [Homo sapiens]				2.89E-09	2.01	30.21	3.40	144750.1
AHQ-7-3, 6051	R.TGLCYLPEELAALQK.L	1707.96931	2	8.55E-04	0.64	3.20	-	364.3
AHQ-7-4, 6445	K.VGLGLGYLELPQINYK.L	1778.08432	2	1.62E-05	0.47	2.87	-	423.1
AHQ-7-3, 5172	R.VPECLYTLPSLR.R	1449.69710	2	2.89E-09	0.90	3.14	-	1050.6
gi|9257257|ref|NP_059830.1| WD repeat-containing protein 1 isoform 1 [Homo sapiens]				2.92E-09	1.62	20.20	7.90	66193.1
AHQ-7-6, 4155 - 4222	R.LHHVSSLAWLDEHTLVTTSHDASVK.E	2785.06406	3	2.61E-07	0.76	3.32	-	812.0
AHQ-7-13-, 4949	K.VVTVFSVADGYSENNVFYGHHAK.I	2541.75861	3	2.92E-09	0.86	4.01	-	724.2
gi|11496885|ref|NP_005442.2| enigma protein; LIM domain protein [Homo sapiens]				2.96E-09	0.83	10.19	2.60	49844.4
AHQ-7-13, 4839	K.VVLEGPAPWGFR.L	1328.54318	2	7.30E-07	0.94	3.63	-	1151.9
AHQ-7-13-, 4725 - 4763	K.VVLEGPAPWGFR.L	1328.54318	2	4.43E-05	0.93	3.73	-	1013.6
AHQ-7-11, 4567	K.VVLEGPAPWGFR.L	1328.54318	2	2.96E-09	0.83	3.16	-	751.8
gi|4557419|ref|NP_000063.1| CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36				3.07E-09	2.71	30.20	10.20	53052.1
AHQ-7-1, 4692	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	7.66E-05	0.84	3.30	-	675.6
AHQ-7-5, 4647	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	9.43E-05	0.82	3.34	-	564.9
AHQ-7-3, 4668	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.55E-07	0.85	3.73	-	488.6
AHQ-7-2, 4773	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.40E-04	0.70	3.19	-	498.0
AHQ-7-1, 5463	K.SQVLQFFSSDICR.S	1588.76661	2	6.80E-06	0.89	3.26	-	996.6
AHQ-7-5, 5524	K.SQVLQFFSSDICR.S	1588.76661	2	2.69E-08	0.92	3.57	-	1213.9
AHQ-7-6, 5462	K.SQVLQFFSSDICR.S	1588.76661	2	7.46E-08	0.93	3.76	-	1277.0
AHQ-7-5, 6730	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	3.07E-09	0.94	4.06	-	1000.6
AHQ-7-1, 6487 - 6495	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.16E-08	0.92	4.06	-	1006.5
gi|4504085|ref|NP_000399.1| glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA				3.24E-09	2.70	30.23	6.50	80814.1

AHQ-7-6, 5566	R.LVQDYGLESEVAQHLAATYGDK.A	2408.60567	3	5.62E-04	0.85	3.31	-	1072.5
AHQ-7-6, 5559	R.LVQDYGLESEVAQHLAATYGDK.A	2408.60567	2	2.54E-06	0.90	3.36	-	988.0
AHQ-7-6, 6026 - 6027	R.VIFFLPWQK.M	1178.44934	2	1.29E-05	0.84	2.74	-	666.8
AHQ-7-6, 6037 - 6051	R.YGAATANYMEVVSLLK.K	1731.00632	2	3.24E-09	0.95	4.55	-	1102.6
gi|5803201|ref|NP_006818.1| transmembrane trafficking protein [Homo sapiens]				3.37E-09	1.91	20.20	10.50	24975.8
AHQ-7-11, 4092 - 4095	R.IPDQLVILDM*K.H	1301.57773	2	6.88E-04	0.94	3.93	-	1361.8
AHQ-7-11, 2459	K.ITDSAGHILYSK.E	1305.46156	2	3.37E-09	0.97	4.06	-	1751.7
gi|4758970|ref|NP_004150.1| proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be				3.60E-09	1.86	20.19	9.20	29769.4
AHQ-7-11, 3274	R.ASAGSYISALR.V	1096.21876	2	1.02E-04	0.91	3.45	-	1104.5
AHQ-7-11, 4004	K.VESTDVSDLLHQYR.E	1662.78230	2	3.60E-09	0.96	3.86	-	1629.0
gi|23110925|ref|NP_002789.1| proteasome beta 6 subunit; proteasome subunit Y; proteasome subunit be				3.61E-09	0.95	10.19	4.60	25357.6
AHQ-7-11, 2474	R.LAAIAESGVER.Q	1116.24998	2	3.61E-09	0.95	3.82	-	1401.2
gi|6005846|ref|NP_009215.1| PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro				3.67E-09	4.41	50.25	24.90	39547.7
AHQ-7-13-, 6192	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	1.21E-08	0.96	4.75	-	996.2
AHQ-7-9, 5861	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	2.55E-06	0.72	3.00	-	488.3
AHQ-7-13, 6142 - 6219	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	8.35E-04	0.89	3.92	-	631.7
AHQ-7-14-, 6151	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	4.95E-08	0.78	3.33	-	477.9
AHQ-7-11, 3990	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	2.32E-05	0.81	4.02	-	469.8
AHQ-7-9, 3836	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	4.85E-04	0.85	3.82	-	628.3
AHQ-7-11, 4235	K.HQTLQGLAFPLQPEAQR.A	1935.17562	3	7.15E-05	0.87	3.61	-	1081.5
AHQ-7-11, 4227	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	3.67E-09	0.97	4.95	-	1234.1
AHQ-7-9, 4053	K.HQTLQGLAFPLQPEAQR.A	1935.17562	2	2.35E-04	0.91	3.97	-	748.4
AHQ-7-11, 4968	R.LLDSVEQDFHLEIAK.K	1757.96513	2	1.43E-06	0.72	3.10	-	532.3
AHQ-7-12, 4439 - 4442	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	1.64E-06	0.95	3.84	-	1650.9
gi|24119203|ref|NP_705935.1| tropomyosin 3 [Homo sapiens]				3.69E-09	4.71	50.22	14.50	29032.5
AHQ-7-9, 3342 - 3396	R.IQLVEEELDR.A	1244.37653	2	1.72E-06	0.94	3.94	-	1120.4
AHQ-7-10, 3452	R.IQLVEEELDR.A	1244.37653	2	3.71E-05	0.77	3.07	-	668.3
AHQ-7-11, 3506 - 3542	R.IQLVEEELDR.A	1244.37653	2	8.01E-05	0.79	2.70	-	844.5
AHQ-7-9, 3256 - 3464	R.IQLVEEELDR.A	1244.37653	1	2.42E-04	0.64	2.90	-	581.2
AHQ-7-10, 2735	K.IQVLQQQADDAEER.A	1643.73738	2	2.13E-08	0.92	3.59	-	1484.7
AHQ-7-9, 2664 - 2672	K.IQVLQQQADDAEER.A	1643.73738	2	3.69E-09	0.97	4.31	-	2223.6
AHQ-7-9, 2456	R.KIQVLQQQADDAEER.A	1771.91030	2	1.97E-04	0.95	4.42	-	1429.6
AHQ-7-10, 3219 - 3228	R.RIQLVEEELDR.A	1400.56288	2	7.61E-06	0.97	4.24	-	1742.7
AHQ-7-9, 2945 - 2950	K.TIDDLEDKLK.C	1190.32563	2	1.55E-06	0.88	3.53	-	714.3
gi|4504521|ref|NP_002147.1| heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P				3.81E-09	1.58	20.19	8.00	61024.2
AHQ-7-7, 5306	K.ISSIQSIVPALEIANAHR.K	1920.20240	2	3.81E-09	0.79	3.83	-	323.2
AHQ-7-7, 6904	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D	2870.28530	3	1.45E-08	0.79	3.45	-	858.3
gi|10716563|ref|NP_001737.1| calnexin [Homo sapiens]				3.99E-09	5.28	60.27	14.00	67567.8
AHQ-7-1, 4956	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.90E-05	0.91	3.60	-	1135.0
AHQ-7-2, 5055	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.35E-05	0.85	3.10	-	892.2
AHQ-7-5, 4950	K.APVPTGEVYFADSFDR.G	1771.90722	2	3.99E-09	0.95	4.28	-	1116.2
AHQ-7-12, 4622	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.68E-06	0.84	3.35	-	638.4
AHQ-7-5, 4247	R.CESAPGCGVWQRPVIDNPNYK.G	2450.69236	2	5.66E-07	0.67	3.02	-	313.6
AHQ-7-5, 3980	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	2	6.73E-04	0.90	4.05	-	643.2
AHQ-7-5, 3986	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	3	3.22E-08	0.96	4.72	-	1622.3
AHQ-7-5, 6580	K.IPNPDFFEDLEPFR.M	1736.90447	2	1.39E-06	0.86	3.26	-	776.3
AHQ-7-5, 6144	R.KIPNPDFFEDLEPFR.M	1865.07739	3	9.35E-06	0.97	5.33	-	2031.5
AHQ-7-5, 6142	R.KIPNPDFFEDLEPFR.M	1865.07739	2	3.34E-07	0.94	4.34	-	824.2
AHQ-7-5, 3619	K.TPELNLDQFHDK.T	1457.56976	2	5.83E-04	0.90	3.56	-	1036.1
gi|22042381|ref|XP_065237.3| similar to FKSG30 [Homo sapiens]				5.02E-09	1.56	20.19	8.30	42016.0
AHQ-7-14-, 2947	K.QEYDESGPSIVHR.K	1517.58206	2	7.98E-04	0.69	3.09	-	581.4
AHQ-7-13-, 2476	K.QEYDESGPSIVHR.K	1517.58206	2	1.49E-08	0.60	2.95	-	368.9
AHQ-7-14-, 2454 - 2471	K.QEYDESGPSIVHR.K	1517.58206	2	5.02E-09	0.82	3.40	-	484.2
AHQ-7-3, 3016	K.QEYDESGPSIVHR.K	1517.58206	2	4.17E-06	0.55	2.53	-	507.3
AHQ-7-8, 3726 - 3791	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	2.04E-04	0.74	3.30	-	496.8
gi|30150448|ref|XP_293066.2| similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose				5.21E-09	1.75	20.23	5.10	58788.2
AHQ-7-6, 3954	K.DAGQISGLNVLR.V	1243.39499	2	2.35E-04	0.81	2.89	-	913.6
AHQ-7-6, 4599 - 4602	R.VINEPTAAALAYGLDK.S	1646.86592	2	5.21E-09	0.94	4.65	-	839.7
gi|4557321|ref|NP_000030.1| apolipoprotein A-I precursor [Homo sapiens]				5.26E-09	5.09	60.29	25.50	30777.6
AHQ-7-13, 5782	R.EQLGPVTQEFWDNLEK.E	1934.09489	2	2.73E-05	0.68	2.74	-	460.7
AHQ-7-11, 5538	R.EQLGPVTQEFWDNLEK.E	1934.09489	2	2.44E-06	0.83	3.49	-	488.2
AHQ-7-13, 5149	K.LLDNWDSVTSTFSK.L	1613.74965	2	1.37E-04	0.56	2.64	-	425.5
AHQ-7-10, 4783	K.LLDNWDSVTSTFSK.L	1613.74965	2	1.67E-07	0.68	2.84	-	462.5
AHQ-7-14-, 5061	K.LLDNWDSVTSTFSK.L	1613.74965	2	2.75E-07	0.91	3.90	-	969.5
AHQ-7-11, 5366	K.LREQLGPVTQEFWDNLEK.E	2203.43949	2	1.25E-05	0.97	5.72	-	1564.5
AHQ-7-11, 5343	R.QGLLPVLESFK.V	1231.46572	2	2.10E-05	0.75	2.57	-	569.9
AHQ-7-11, 4342 - 4348	R.VKDLATVYVDVLK.D	1463.74362	2	2.75E-07	0.91	3.46	-	1049.4
AHQ-7-10, 5659 - 5673	K.VSFLSALEEYTK.K	1387.55934	2	5.26E-09	0.94	4.33	-	781.7
gi|12408656|ref|NP_005177.2| calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ				5.27E-09	10.26	120.27	23.10	81889.4
AHQ-7-6, 5114	K.APSDLYQIILK.A	1261.49183	2	2.86E-07	0.90	3.16	-	1233.4
AHQ-7-6, 6073 - 6147	R.DM*ETIGFAVYEVPPELVGQPAVHLK.R	2757.15391	3	6.13E-06	0.87	3.75	-	812.8
AHQ-7-6, 5863	R.FRLPPGEYVVVPSTFEPNKEGDFVLR.F	2994.39160	3	7.05E-07	0.92	4.81	-	1215.1
AHQ-7-6, 2954	K.IRLDETDDPDDYGDR.E	1795.79921	2	3.64E-07	0.85	3.37	-	766.6
AHQ-7-6, 4879	R.LEICNLTPDALK.S	1388.61207	2	8.24E-04	0.92	3.30	-	1331.6
AHQ-7-6, 5630 - 5631	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	5.27E-09	0.90	4.58	-	612.5
AHQ-7-6, 6242	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	2	5.05E-06	0.96	5.34	-	1285.8
AHQ-7-6, 3977	K.LYELIITR.Y	1021.23493	2	6.00E-04	0.95	3.61	-	1692.9
AHQ-7-6, 5163	R.NYPATFWVNPQFK.I	1612.81141	2	3.35E-07	0.95	3.93	-	1221.8
AHQ-7-6, 4533	K.RPTELLSNPQFIVDGATR.T	2015.25904	3	6.00E-07	0.97	5.07	-	1959.0
AHQ-7-6, 3201	R.SEQFINLR.E	1007.12521	2	8.46E-04	0.84	2.78	-	817.3
AHQ-7-6, 3207	R.SEQFINLR.E	1007.12521	1	4.59E-05	0.17	1.89	-	251.1
AHQ-7-6, 3319 - 3325	K.YLGQDYEQLR.V	1285.38720	2	9.97E-08	0.90	3.73	-	618.0
gi|27477800|ref|XP_208313.1| similar to tropomyosin 4 [Homo sapiens]				5.36E-09	0.91	10.24	10.10	18426.7
AHQ-7-9, 4652 - 4653	K.CGDLEEELKNVTNNLK.S	1878.05124	2	3.80E-07	0.94	4.75	-	970.7
AHQ-7-9, 5072	K.CGDLEEELKNVTNNLK.S	1878.05124	2	3.27E-04	0.84	3.67	-	822.3
AHQ-7-9, 5081	K.CGDLEEELKNVTNNLK.S	1878.05124	3	1.60E-08	0.80	3.64	-	784.1
AHQ-7-9, 5184 - 5186	K.CGDLEEELKNVTNNLK.S	1878.05124	2	3.66E-08	0.92	4.74	-	792.2
AHQ-7-9, 4205 - 4208	K.CGDLEEELKNVTNNLK.S	1878.05124	3	5.36E-09	0.91	4.43	-	1076.1
gi|18201905|ref|NP_000166.2| glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras				5.60E-09	3.67	40.22	10.90	63146.7
AHQ-7-7, 6832	K.ILLANFLAQTEALMR.G	1705.05838	2	5.60E-09	0.96	3.53	-	1738.9
AHQ-7-7, 2994	K.TFTTQETITNAETAK.E	1656.77283	2	1.00E-07	0.86	3.47	-	727.9
AHQ-7-7, 5952 - 5953	K.TLAQLNPESSLFIIASK.T	1833.11828	2	2.97E-07	0.90	4.37	-	417.6
AHQ-7-7, 3841	R.VWYVSNIDGTHIAK.T	1603.80282	2	1.44E-08	0.96	4.26	-	1281.6
gi|5901944|ref|NP_008977.1| elastin microfibril interface located protein; TNF? elastin microfibril				5.74E-09	5.37	60.28	12.30	106694.7
AHQ-7-3, 2988 - 3027	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	3.26E-05	0.77	2.94	-	672.4
AHQ-7-3, 3169	R.GTELGGAAGQGGHPPGYTSLASR.L	2142.27464	2	1.66E-05	0.87	4.21	-	301.3
AHQ-7-3, 3671	R.LDTVAGGLQGLR.E	1200.37012	2	3.36E-04	0.96	3.51	-	1995.9
AHQ-7-3, 5285	R.LGQLEGLLQAHGDEGCGACGGVQEELGR.L	2914.13552	3	5.59E-05	0.95	5.39	-	1094.5
AHQ-7-3, 2883 - 2960	R.LVGSGLHTVEAAGEAR.Q	1567.72888	2	5.74E-09	0.86	3.13	-	923.0
AHQ-7-3, 3768	R.PARPNLSGSSAGSPLSGLGGEGPGESEK.V	2596.74928	3	5.35E-07	0.96	5.66	-	1212.4
gi|7706497|ref|NP_057392.1| UMP-CMP kinase [Homo sapiens]				5.96E-09	1.91	20.21	11.40	25854.7
AHQ-7-11, 2670 - 2678	R.KNPDSQYGELIEK.Y	1521.65375	2	5.96E-09	0.94	4.28	-	869.8
AHQ-7-11, 3740	K.YGYTHLSAGELLR.D	1480.64969	2	8.86E-06	0.97	3.80	-	2249.5
gi|4505303|ref|NP_002466.1| myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m				6.16E-09	2.24	30.21	11.50	22763.8
AHQ-7-12, 2756	R.ALGQNPTNAEVLK.V	1355.52211	1	1.50E-06	0.38	2.78	-	368.5
AHQ-7-12, 2931	R.ALGQNPTNAEVLK.V	1355.52211	1	1.51E-05	0.20	2.57	-	336.6
AHQ-7-12, 2746 - 2806	R.ALGQNPTNAEVLK.V	1355.52211	2	7.01E-06	0.85	4.15	-	366.0

AHQ-7-12, 3226	K.ILYSQCGDVMR.A	1343.55489	1	4.54E-04	0.25	2.59	-	213.9
AHQ-7-13-, 2724	K.ILYSQCGDVM*R.A	1359.55429	2	6.16E-09	0.91	3.21	-	1076.4
AHQ-7-14-, 2715	K.ILYSQCGDVM*R.A	1359.55429	2	4.32E-05	0.75	2.98	-	610.5
AHQ-7-12, 3176 - 3234	K.ILYSQCGDVMR.A	1343.55489	2	4.44E-04	0.95	3.82	-	1239.7
gi|24307939|ref|NP_036205.1| chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]				6.38E-09	0.98	10.28	3.00	59670.7
AHQ-7-7, 6454	K.LGFAGLVQEISFGTTK.D	1668.91472	2	6.38E-09	0.98	5.56	-	1764.6
gi|15306356|ref|XP_035638.2| similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan				6.79E-09	2.64	30.21	20.80	18795.1
AHQ-7-13-, 3445 - 3505	R.ESDVPLKTEEFEVTK.T	1751.91253	2	6.79E-09	0.89	4.17	-	473.8
AHQ-7-13, 3633 - 3637	R.ESDVPLKTEEFEVTK.T	1751.91253	2	2.77E-06	0.88	3.90	-	502.6
AHQ-7-13-, 3464 - 3507	R.GAEIEYAMAYSK.A	1333.49204	2	6.17E-04	0.92	3.85	-	1024.8
AHQ-7-13, 3681	R.GAEIEYAMAYSK.A	1333.49204	2	5.78E-05	0.91	3.95	-	1002.3
AHQ-7-13, 4699	K.SYLYFTQFK.A	1197.36315	2	7.73E-06	0.83	2.76	-	763.5
gi|4502303|ref|NP_001688.1| mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m				7.52E-09	2.76	30.25	22.10	23277.2
AHQ-7-11, 5183 - 5242	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	7.52E-09	0.94	4.95	-	876.7
AHQ-7-14-, 5379	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	2.65E-05	0.91	4.38	-	759.0
AHQ-7-11, 3592	K.LVRPPVQVYGIEGR.Y	1583.85942	3	1.14E-04	0.96	4.43	-	1960.9
AHQ-7-11, 3271	K.VAASVLNPYVK.R	1161.37549	2	9.55E-08	0.86	3.42	-	693.2
gi|4758304|ref|NP_004902.1| protein disulfide isomerase related protein (calcium-binding protein, i				7.63E-09	6.88	80.21	16.10	72931.9
AHQ-7-6, 4575	K.DLGLSESGEDVNAAILDESGKK.F	2248.38737	2	7.63E-09	0.90	3.62	-	1264.2
AHQ-7-6, 3797	K.FAM*EPEEFDSDTLR.E	1703.80830	2	1.20E-04	0.72	2.95	-	400.0
AHQ-7-6, 4583	K.FAMEPEEFDSDTLR.E	1687.80890	2	1.55E-04	0.72	3.22	-	375.8
AHQ-7-6, 3685	R.FDVSGYPTIK.I	1127.27123	2	8.67E-07	0.91	2.97	-	1221.7
AHQ-7-6, 3907	K.GESDPAYQQYQDAANNLR.E	2041.08081	2	1.75E-07	0.85	3.44	-	1016.7
AHQ-7-6, 2929	K.IDATSASVLASR.F	1191.31686	2	9.56E-08	0.94	3.84	-	1330.0
AHQ-7-6, 5134	K.VEGFPTIYFAPSGDK.K	1628.80592	2	3.54E-05	0.94	4.13	-	993.6
AHQ-7-6, 3005	K.VSQGQLVVMQPEK.F	1443.69431	2	2.61E-05	0.90	3.35	-	1241.1
gi|5123454|ref|NP_005336.2| heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind				8.56E-09	3.74	40.25	12.50	70037.7
AHQ-7-6, 4725 - 4730	K.DAGVIAGLNVLR.I	1198.39736	2	6.88E-07	0.96	3.91	-	1745.5
AHQ-7-6, 5969 - 6042	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G	3058.37100	3	6.03E-04	0.93	4.46	-	1455.2
AHQ-7-6, 3665	K.HWPFQVINDGDKPK.V	1681.87528	3	5.97E-07	0.96	4.93	-	1623.3
AHQ-7-6, 6489	K.SINPDEAVAYGAAVQAAILM*GDK.S	2321.59293	2	8.56E-09	0.90	3.69	-	828.4
gi|4758950|ref|NP_000933.1| peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]				8.59E-09	4.56	50.19	30.10	23742.4
AHQ-7-12, 3022	R.DKPLKDVIIADCGK.I	1573.83653	2	7.54E-07	0.91	3.76	-	940.3
AHQ-7-11, 2995 - 3002	R.DKPLKDVIIADCGK.I	1573.83653	2	1.72E-08	0.94	3.60	-	1485.9
AHQ-7-11, 4064 - 4130	K.DTNGSQFFITTVK.T	1458.59766	2	8.59E-09	0.93	3.80	-	1264.1
AHQ-7-12, 4086 - 4155	K.DTNGSQFFITTVK.T	1458.59766	2	8.99E-06	0.73	3.00	-	612.6
AHQ-7-12, 3186	K.IEVEKPFAIAK.E	1245.49240	2	1.87E-06	0.94	3.74	-	1308.2
AHQ-7-11, 4192	K.TVDNFVALATGEK.G	1365.51377	2	1.15E-04	0.83	3.18	-	632.1
AHQ-7-11, 4023	R.VIKDFMIQGGDFTR.G	1627.88933	2	2.13E-07	0.92	3.40	-	1131.2
gi|30148492|ref|XP_293610.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				9.00E-09	1.58	20.22	2.60	72113.4
AHQ-7-6, 4689 - 4713	R.IINEPTAAAIAYGLDK.K	1660.89259	2	4.84E-06	0.83	4.32	-	735.1
AHQ-7-6, 4290	R.IINEPTAAAIAYGLDKK.V	1789.06550	3	9.00E-09	0.75	3.37	-	406.4
AHQ-7-6, 4286	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	7.67E-07	0.86	4.09	-	700.6
gi|29731460|ref|XP_293027.1| similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl				1.04E-08	0.98	10.23	6.10	23572.2
AHQ-7-10, 4265	K.DFLAGGVAAAISK.M	1220.39980	2	1.04E-08	0.98	4.61	-	2830.1
gi|4501993|ref|NP_003650.1| alkylglycerone phosphate synthase precursor [Homo sapiens]				1.10E-08	0.87	10.19	2.60	72911.4
AHQ-7-6, 5842	R.GISDPLTVFEQTEAAAR.E	1805.96665	2	1.10E-08	0.87	3.84	-	546.1
gi|30159310|ref|XP_301899.1| similar to beta-actin [Homo sapiens]				1.12E-08	0.82	20.17	9.20	32376.4
AHQ-7-8, 1531 - 2083	K.DSYVGNEAQSK.R	1198.22158	1	7.09E-08	0.54	2.85	-	295.2
AHQ-7-8, 1647 - 1724	K.DSYVGNEAQSK.R	1198.22158	2	4.78E-05	0.85	3.46	-	718.5
AHQ-7-8, 1886 - 1956	K.DSYVGNEAQSK.R	1198.22158	2	2.26E-05	0.76	3.10	-	807.3
AHQ-7-8, 2024	K.DSYVGNEAQSK.R	1198.22158	2	3.24E-04	0.58	3.07	-	376.5
AHQ-7-8, 2195	K.DSYVGNEAQSK.R	1198.22158	1	1.12E-08	0.30	2.15	-	268.3
AHQ-7-12, 1823 - 1846	K.DSYVGNEAQSK.R	1198.22158	1	4.50E-05	0.33	2.14	-	488.5
AHQ-7-12, 1808 - 1878	K.DSYVGNEAQSK.R	1198.22158	2	1.25E-04	0.83	2.94	-	891.2
AHQ-7-8, 4570	K.SYKLLDGQVITIGNER.F	1807.04092	2	4.64E-04	0.68	2.80	-	662.4
AHQ-7-8, 4448 - 4516	K.SYKLLDGQVITIGNER.F	1807.04092	2	2.37E-06	0.51	2.58	-	421.5
AHQ-7-8, 4982 - 5062	K.SYKLLDGQVITIGNER.F	1807.04092	2	7.22E-07	0.52	2.81	-	463.8
gi|4505621|ref|NP_002558.1| prostatic binding protein; phosphatidylethanolamine binding protein [Ho				1.13E-08	1.88	20.26	20.30	21056.6
AHQ-7-11, 4695	R.APVAGTCYQAEWDDYVPK.L	2072.23961	2	1.85E-05	0.92	3.84	-	1152.8
AHQ-7-11, 4306	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	1.13E-08	0.96	5.13	-	1025.6
AHQ-7-11, 4167 - 4178	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	1.90E-07	0.97	4.95	-	1549.1
gi|5031987|ref|NP_005720.1| peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]				1.14E-08	1.68	20.22	18.40	22040.1
AHQ-7-12, 3739	R.FPDENFTLK.H	1111.22866	1	8.92E-04	0.10	1.80	-	346.6
AHQ-7-12, 3855	R.FPDENFTLK.H	1111.22866	2	9.59E-04	0.71	2.62	-	625.1
AHQ-7-12, 3703 - 3762	R.FPDENFTLK.H	1111.22866	2	2.39E-05	0.79	2.56	-	639.4
AHQ-7-12, 4778 - 4846	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	1.14E-08	0.89	4.38	-	929.1
gi|4503643|ref|NP_000121.1| coagulation factor V precursor; labile factor; factor V Leiden [Homo sa				1.23E-08	5.24	60.18	3.10	251716.5
AHQ-7-3, 5717	R.AADIEQQAVFAVFDENK.S	1896.04666	2	4.99E-04	0.88	3.52	-	1153.8
AHQ-7-5, 3183	R.AEVDDVIQVR.F	1144.26019	2	1.28E-05	0.96	3.33	-	2387.4
AHQ-7-1, 3896	R.AWAYYSAVNPEK.D	1399.53190	2	5.41E-05	0.90	2.57	-	1495.3
AHQ-7-2, 3568	R.ETDIEDSDDIPEDTTYK.K	1986.97539	2	9.26E-07	0.79	3.59	-	361.0
AHQ-7-4, 3065	R.ETDIEDSDDIPEDTTYKK.V	2115.14831	2	1.23E-08	0.81	3.46	-	396.9
AHQ-7-5, 3095 - 3168	K.EVIITGIQTQGAK.H	1358.56590	2	2.12E-06	0.88	3.12	-	1181.1
AHQ-7-3, 3233	K.EVIITGIQTQGAK.H	1358.56590	2	4.67E-05	0.93	3.68	-	1355.7
AHQ-7-2, 3277	K.EVIITGIQTQGAK.H	1358.56590	2	1.72E-06	0.89	3.27	-	954.5
gi|4557703|ref|NP_000414.1| keratin 2a [Homo sapiens]				1.25E-08	6.40	70.26	19.70	65864.9
AHQ-7-5, 6626	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	8.28E-05	0.92	5.20	-	629.9
AHQ-7-4, 6729	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	7.06E-05	0.70	3.23	-	716.1
AHQ-7-3, 6524	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	1.25E-04	0.94	5.16	-	1125.2
AHQ-7-2, 6699	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	2.39E-04	0.89	4.91	-	479.2
AHQ-7-1, 6419	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	6.61E-05	0.87	4.04	-	878.9
AHQ-7-6, 6525	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	5.37E-05	0.91	4.97	-	740.7
AHQ-7-2, 3137	R.FLEQQNQVLQTK.W	1476.65935	2	1.41E-08	0.98	5.13	-	2704.1
AHQ-7-13, 3201	R.FLEQQNQVLQTK.W	1476.65935	2	2.24E-06	0.90	3.18	-	1627.7
AHQ-7-12, 2998	R.FLEQQNQVLQTK.W	1476.65935	2	1.93E-05	0.97	4.55	-	2001.2
AHQ-7-1, 3411	R.FLEQQNQVLQTK.W	1476.65935	2	8.87E-04	0.93	3.30	-	1765.9
AHQ-7-3, 3101	R.FLEQQNQVLQTK.W	1476.65935	2	7.60E-05	0.97	4.25	-	2225.6
AHQ-7-11, 2966	R.FLEQQNQVLQTK.W	1476.65935	2	6.67E-04	0.97	4.52	-	1905.3
AHQ-7-10, 2899 - 2903	R.FLEQQNQVLQTK.W	1476.65935	2	3.47E-07	0.96	4.48	-	1951.2
AHQ-7-7, 2960	R.FLEQQNQVLQTK.W	1476.65935	2	9.85E-05	0.94	3.12	-	1944.2
AHQ-7-13-, 3043	R.FLEQQNQVLQTK.W	1476.65935	2	3.85E-07	0.96	3.80	-	2235.8
AHQ-7-4, 3077 - 3078	R.FLEQQNQVLQTK.W	1476.65935	2	3.59E-08	0.98	4.72	-	2784.6
AHQ-7-1, 3244	R.FLEQQNQVLQTK.W	1476.65935	2	1.24E-05	0.96	3.80	-	1918.4
AHQ-7-14, 3892	R.FLEQQNQVLQTK.W	1476.65935	2	1.91E-05	0.96	3.99	-	1821.8
AHQ-7-14-, 3055	R.FLEQQNQVLQTK.W	1476.65935	2	4.69E-07	0.98	5.11	-	2410.8
AHQ-7-6, 3017	R.FLEQQNQVLQTK.W	1476.65935	2	6.88E-08	0.97	5.02	-	2073.3
AHQ-7-5, 3032 - 3040	R.FLEQQNQVLQTK.W	1476.65935	2	1.25E-08	0.97	5.27	-	2149.6
AHQ-7-6, 2845	K.IEISELNR.V	974.09353	2	9.17E-05	0.78	2.65	-	817.2
AHQ-7-5, 2888	K.IEISELNR.V	974.09353	2	2.27E-04	0.83	2.66	-	835.5
AHQ-7-1, 3119	K.IEISELNR.V	974.09353	2	5.83E-04	0.79	3.14	-	606.0
AHQ-7-6, 5961	R.NLDLDSIIAEVK.A	1330.50933	2	9.12E-07	0.94	3.76	-	1244.5
AHQ-7-1, 5896	R.NLDLDSIIAEVK.A	1330.50933	2	5.18E-06	0.96	4.45	-	1128.5
AHQ-7-13-, 5759	R.NLDLDSIIAEVK.A	1330.50933	2	3.12E-05	0.96	4.55	-	1259.5
AHQ-7-3, 5983 - 5984	R.NLDLDSIIAEVK.A	1330.50933	2	1.01E-06	0.97	5.17	-	1227.6
AHQ-7-12, 5578	R.NLDLDSIIAEVK.A	1330.50933	2	2.47E-05	0.90	3.18	-	1010.4
AHQ-7-5, 6062	R.NLDLDSIIAEVK.A	1330.50933	2	2.64E-07	0.96	4.81	-	1239.5

AHQ-7-2, 6131	R.NLDLDSIIAEVK.A	1330.50933	2	1.11E-05	0.95	4.64	-	1148.0
AHQ-7-1, 3361	K.NVQDAIADAEQR.G	1330.38637	2	4.71E-08	0.91	3.90	-	932.6
AHQ-7-3, 3248	K.NVQDAIADAEQR.G	1330.38637	2	2.69E-07	0.79	3.27	-	648.7
AHQ-7-6, 5815	K.VDLLNQEIEFLK.V	1461.68459	2	4.36E-05	0.79	3.21	-	700.1
AHQ-7-5, 5914	K.VDLLNQEIEFLK.V	1461.68459	2	1.11E-06	0.94	4.63	-	933.6
AHQ-7-2, 5983 - 6025	K.VDLLNQEIEFLK.V	1461.68459	2	8.93E-05	0.91	4.07	-	911.8
AHQ-7-3, 5847	K.VDLLNQEIEFLK.V	1461.68459	2	7.39E-06	0.95	4.47	-	1065.3
AHQ-7-14-, 5427	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	1.37E-07	0.92	3.91	-	1490.1
gi|4503747|ref|NP_001448.1| filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a				1.28E-08	4.56	60.25	2.00	278191.4
AHQ-7-3, 3068	K.DLAEDAPWKK.I	1173.29999	2	7.80E-04	0.72	2.88	-	794.6
AHQ-7-5, 2996 - 3000	K.DLAEDAPWKK.I	1173.29999	2	3.26E-04	0.70	2.62	-	938.8
AHQ-7-2, 6332	R.LIALLEVLSQK.R	1227.51852	2	1.52E-06	0.97	4.12	-	1719.9
AHQ-7-10, 5696 - 5700	R.LIALLEVLSQK.R	1227.51852	2	8.55E-06	0.95	3.85	-	1151.8
AHQ-7-9, 5637	R.LIALLEVLSQK.R	1227.51852	2	5.04E-04	0.86	2.74	-	974.1
AHQ-7-7, 6184	R.LIALLEVLSQK.R	1227.51852	2	6.90E-07	0.96	4.36	-	1084.7
AHQ-7-11, 5784 - 5786	R.LIALLEVLSQK.R	1227.51852	2	1.28E-08	0.97	4.59	-	1544.7
AHQ-7-1, 6123	R.LIALLEVLSQK.R	1227.51852	2	6.15E-05	0.97	4.30	-	1607.9
AHQ-7-3, 6188	R.LIALLEVLSQK.R	1227.51852	2	2.42E-08	0.97	4.52	-	1465.2
AHQ-7-6, 6182	R.LIALLEVLSQK.R	1227.51852	2	8.19E-08	0.96	4.15	-	1283.1
AHQ-7-13, 6026	R.LIALLEVLSQK.R	1227.51852	2	6.16E-08	0.97	3.83	-	1755.9
AHQ-7-4, 6344	R.LIALLEVLSQK.R	1227.51852	2	1.22E-06	0.97	4.95	-	1309.4
AHQ-7-5, 6271	R.LIALLEVLSQK.R	1227.51852	2	2.53E-07	0.97	4.48	-	1395.2
AHQ-7-4, 3721	R.LLGWIQNK.I	972.16560	2	3.91E-04	0.87	2.99	-	701.3
AHQ-7-5, 3628 - 3694	R.LLGWIQNK.I	972.16560	2	5.30E-04	0.82	2.71	-	718.7
AHQ-7-3, 1989	K.LVSIDSK.A	761.88676	1	1.91E-05	0.15	2.01	-	293.8
AHQ-7-2, 6743	R.QMQLENVSVALEFLDR.E	1893.15408	2	1.84E-06	0.93	4.23	-	866.9
AHQ-7-2, 6315 - 6327	R.QM*QLENVSVALEFLDR.E	1909.15348	2	4.56E-04	0.95	4.62	-	1160.8
AHQ-7-1, 6091	R.QM*QLENVSVALEFLDR.E	1909.15348	2	4.11E-05	0.94	3.63	-	1374.6
AHQ-7-2, 6831 - 6832	R.QMQLENVSVALEFLDR.E	1893.15408	2	2.91E-05	0.90	3.49	-	913.7
gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre				1.35E-08	5.87	70.30	30.70	48141.1
AHQ-7-7, 5777	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	2	4.78E-06	0.90	3.70	-	898.5
AHQ-7-7, 5764	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	1.35E-08	0.97	6.01	-	1706.1
AHQ-7-13-, 3891	K.EQFLDGDGWTSR.W	1411.45795	2	2.86E-05	0.72	2.88	-	647.5
AHQ-7-7, 3844	K.EQFLDGDGWTSR.W	1411.45795	2	1.11E-04	0.77	3.10	-	637.3
AHQ-7-14-, 3889	K.EQFLDGDGWTSR.W	1411.45795	2	2.07E-04	0.81	2.60	-	829.0
AHQ-7-14, 6036	R.FYALSASFEPFSNK.G	1608.77470	2	1.58E-07	0.92	2.94	-	1280.1
AHQ-7-14-, 5197 - 5258	R.FYALSASFEPFSNK.G	1608.77470	2	9.01E-08	0.94	3.60	-	1290.6
AHQ-7-7, 3564 - 3574	K.IDDPTDSKPEDWDKPEHIPDPDAK.K	2761.89139	3	1.11E-05	0.86	4.66	-	606.6
AHQ-7-7, 5165 - 5242	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	2.62E-05	0.71	3.33	-	626.5
AHQ-7-7, 5346	K.KPEDWDEEMDGEWEPPVIQNPEYK.G	2962.14926	3	9.47E-06	0.90	4.43	-	840.0
AHQ-7-7, 5369	K.KPEDWDEEMDGEWEPPVIQNPEYK.G	2962.14926	2	1.27E-04	0.79	3.20	-	472.7
AHQ-7-7, 2396	K.KVHVIFNYK.G	1148.38164	1	1.87E-06	0.77	2.60	-	637.0
gi|4504743|ref|NP_002194.1| integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o				1.51E-08	6.81	80.24	11.10	129294.4
AHQ-7-3, 3689	K.AGDISCNADINPLK.I	1489.63335	2	1.04E-05	0.90	4.00	-	898.9
AHQ-7-3, 3044	K.AVIDQCNHDNILR.F	1569.72493	2	8.10E-07	0.81	3.11	-	965.7
AHQ-7-3, 3549	K.FVQGLDIGPTK.T	1175.35903	2	5.31E-07	0.95	3.17	-	1956.6
AHQ-7-3, 6263 - 6279	K.GNWLLVGSPWSGFPENR.M	1917.11562	2	1.72E-04	0.59	3.14	-	469.2
AHQ-7-3, 5197 - 5259	K.IPLLYDAEIHLTR.S	1554.81485	2	1.91E-07	0.89	3.68	-	740.2
AHQ-7-3, 6361	R.STNINFYEISSDGNVPSIVHSFEDVGPK.F	3054.26956	3	5.61E-04	0.82	3.74	-	750.8
AHQ-7-3, 6447 - 6521	R.STNINFYEISSDGNVPSIVHSFEDVGPK.F	3054.26956	3	9.66E-04	0.89	4.83	-	759.6
AHQ-7-3, 3443	K.TQVGLIQYANNPR.V	1474.64668	2	2.49E-05	0.94	3.55	-	1614.3
AHQ-7-4, 5092	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	6.84E-05	0.85	3.76	-	464.6
AHQ-7-3, 4928 - 4992	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	1.51E-08	0.91	3.99	-	812.8
gi|16933542|ref|NP_002017.1| fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s				1.56E-08	5.10	60.23	3.50	259222.8
AHQ-7-1, 4921	R.NLQPASEYTVSLVAIK.G	1733.98671	2	4.56E-06	0.90	3.41	-	690.7
AHQ-7-1, 6189	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	7.17E-06	0.87	3.79	-	499.9
AHQ-7-1, 5749 - 5803	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	5.50E-07	0.91	4.18	-	825.2
AHQ-7-1, 4679 - 4680	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	2.01E-05	0.93	4.60	-	996.2
AHQ-7-3, 4655	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	5.18E-04	0.86	3.76	-	826.5
AHQ-7-1, 3871 - 3913	R.SYTITGLQPGTDYK.I	1544.68732	2	1.58E-04	0.71	2.97	-	511.0
AHQ-7-1, 4093	R.VDVIPVNLPGEHGQR.L	1630.82981	3	1.41E-04	0.74	3.23	-	510.7
AHQ-7-1, 3549 - 3629	R.VPGTSTSATLTGLTR.G	1462.63098	2	1.56E-08	0.89	3.54	-	868.9
gi|12545410|ref|NP_031394.1| RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,				1.57E-08	1.88	30.19	8.20	95912.5
AHQ-7-5, 5052	R.APSDSAPGCSPCTGGLPANIQLDIDGDRETER.I	3360.54658	3	2.64E-04	0.55	3.50	-	302.2
AHQ-7-5, 6182	K.SKGDQPLYSIPIENILAVEK.L	2215.53162	3	3.86E-04	0.76	3.85	-	673.1
AHQ-7-5, 6184	K.SKGDQPLYSIPIENILAVEK.L	2215.53162	2	4.69E-04	0.78	3.69	-	449.1
AHQ-7-5, 6104	K.SLCPFYGEDFYCEIPR.S	2056.26024	2	2.12E-08	0.89	3.42	-	681.3
AHQ-7-4, 6193	K.SLCPFYGEDFYCEIPR.S	2056.26024	2	1.57E-08	0.57	2.79	-	376.8
gi|6857820|ref|NP_005019.2| phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl				1.64E-08	2.64	30.29	11.30	46224.3
AHQ-7-7, 4492 - 4493	R.FGIDDQDFQNSLTR.S	1656.73462	2	1.64E-08	0.89	4.13	-	803.1
AHQ-7-7, 4284	R.FGIDDQDFQNSLTR.S	1656.73462	2	1.23E-05	0.84	3.47	-	880.8
AHQ-7-7, 2758	K.HGAGAEISTVNPEQYSK.R	1788.89618	2	6.30E-07	0.98	5.79	-	2124.9
AHQ-7-7, 4226	K.TITSEDVAEMHNILK.K	1701.92338	2	2.30E-07	0.76	3.64	-	470.7
gi|30147623|ref|XP_293669.2| similar to actinin, alpha 4 [Homo sapiens]				1.66E-08	0.90	10.22	3.50	57794.4
AHQ-7-5, 4082 - 4083	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	4.56E-06	0.90	4.30	-	765.2
AHQ-7-4, 4106 - 4120	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	1.66E-08	0.90	3.88	-	534.5
gi|18426915|ref|NP_004386.2| drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [				1.67E-08	4.43	50.25	12.80	71438.9
AHQ-7-13-, 5452	R.EESAADWALYTYEDGSDDLK.L	2279.31212	2	2.44E-05	0.78	3.67	-	581.3
AHQ-7-8, 3971 - 4030	K.LAASGEGGLQELSGHFENQK.V	2073.20908	2	5.08E-05	0.93	4.15	-	1177.3
AHQ-7-13-, 4001	K.LAASGEGGLQELSGHFENQK.V	2073.20908	3	3.06E-07	0.75	3.65	-	516.8
AHQ-7-13, 5842	R.LELLAAYEEVIR.E	1419.64771	2	7.30E-05	0.96	3.50	-	1914.5
AHQ-7-8, 2222	R.LREDENAEPVGTTYQK.T	1850.96428	2	5.65E-05	0.97	5.10	-	1647.0
AHQ-7-13-, 5359 - 5360	K.YVLINWVGEDVPDAR.K	1746.94404	2	1.67E-08	0.97	5.06	-	1725.1
AHQ-7-13, 5429	K.YVLINWVGEDVPDAR.K	1746.94404	2	5.16E-06	0.93	4.00	-	1225.2
gi|10863927|ref|NP_066953.1| peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]				1.82E-08	6.25	70.24	24.20	18012.4
AHQ-7-13-, 3968	K.FEDENFILK.H	1155.28144	2	4.23E-04	0.63	2.80	-	507.4
AHQ-7-13, 4105	K.FEDENFILK.H	1155.28144	2	1.04E-04	0.78	3.07	-	568.9
AHQ-7-13-, 4596	K.SIYGEKFEDENFILK.H	1833.03047	2	4.40E-06	0.94	4.51	-	1089.5
AHQ-7-13, 4691	K.SIYGEKFEDENFILK.H	1833.03047	2	1.08E-04	0.84	4.10	-	539.8
AHQ-7-14-, 4613	K.SIYGEKFEDENFILK.H	1833.03047	2	1.82E-08	0.95	4.77	-	987.9
AHQ-7-12, 4431 - 4490	K.SIYGEKFEDENFILK.H	1833.03047	2	2.37E-05	0.92	3.82	-	1205.8
AHQ-7-14-, 3125	K.VKEGM*NIVEAMER.F	1522.77330	2	8.21E-04	0.88	3.00	-	1057.9
AHQ-7-12, 3627	K.VKEGMNIVEAMER.F	1506.77390	2	6.74E-08	0.89	4.09	-	882.7
AHQ-7-12, 2576 - 2600	K.VKEGMNIVEAM*ER.F	1522.77330	2	5.31E-04	0.96	4.65	-	1621.8
AHQ-7-12, 4254	R.VSFELFADK.V	1056.19300	2	3.73E-06	0.90	3.51	-	1127.3
AHQ-7-12, 4260	R.VSFELFADK.V	1056.19300	1	1.92E-04	0.63	2.61	-	599.5
AHQ-7-12, 4402	R.VSFELFADKVPK.T	1380.61317	2	1.45E-05	0.89	3.74	-	879.6
gi|4502201|ref|NP_001649.1| ADP-ribosylation factor 1 [Homo sapiens]				1.90E-08	5.59	70.26	46.40	20696.6
AHQ-7-12, 4374	R.DAVLLVFANK.Q	1090.29726	1	5.53E-05	0.59	2.33	-	675.4
AHQ-7-12, 4600	R.HYFQNTQGLIFVVDSNDR.E	2154.32702	2	4.21E-05	0.68	3.30	-	580.5
AHQ-7-12, 4643 - 4698	R.HYFQNTQGLIFVVDSNDRER.V	2439.62792	3	3.50E-07	0.88	3.66	-	847.1
AHQ-7-12, 3172	R.ILM*VGLDAAGK.T	1104.34572	2	1.96E-05	0.95	3.47	-	1621.0
AHQ-7-13-, 6041 - 6055	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	7.58E-05	0.64	3.31	-	188.8
AHQ-7-14-, 5995	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	2.14E-04	0.34	2.55	-	164.5
AHQ-7-12, 6194 - 6195	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	3	1.50E-07	0.97	5.27	-	1998.8
AHQ-7-13-, 4937	K.NISFTVWDVGGQDK.I	1566.69621	2	1.76E-04	0.90	3.51	-	793.0
AHQ-7-12, 4766 - 4819	K.NISFTVWDVGGQDK.I	1566.69621	2	3.43E-05	0.81	3.06	-	629.8

AHQ-7-14-, 4953	K.NISFTVWDVGGQDK.I	1566.69621	2	1.90E-08	0.88	3.24	-	779.9
AHQ-7-11, 4696 - 4766	K.NISFTVWDVGGQDK.I	1566.69621	2	3.18E-06	0.68	2.67	-	538.2
AHQ-7-13, 5049 - 5071	K.NISFTVWDVGGQDK.I	1566.69621	2	2.43E-04	0.88	3.86	-	626.8
gi|4502985|ref|NP_001854.1| cytochrome c oxidase subunit VIb; human cytochrome oxidase subunit VIb				2.19E-08	0.97	10.25	20.90	10192.3
AHQ-7-14-, 5895	R.VYQSLCPTSWVTDWDEQR.A	2272.43560	2	2.19E-08	0.97	5.05	-	1621.6
gi|4557597|ref|NP_001449.1| gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);				2.19E-08	2.00	30.29	1.80	288897.4
AHQ-7-4, 4666	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	2.19E-08	0.96	5.71	-	754.9
AHQ-7-7, 4393	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.13E-07	0.95	5.28	-	631.4
AHQ-7-2, 4735 - 4739	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	1.36E-07	0.72	3.47	-	386.4
AHQ-7-6, 4498 - 4505	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	3.74E-08	0.88	4.60	-	442.0
AHQ-7-5, 4583	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	5.40E-05	0.94	4.85	-	589.9
AHQ-7-4, 4660	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	5.54E-08	0.82	4.01	-	476.3
AHQ-7-7, 4394	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	1.47E-05	0.74	3.47	-	544.0
AHQ-7-5, 4582	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.18E-06	0.94	5.22	-	788.6
AHQ-7-3, 1921 - 1999	K.IECDDKGDGSCDVR.Y	1628.67809	2	6.86E-04	0.58	2.88	-	464.9
AHQ-7-2, 2015	K.IECDDKGDGSCDVR.Y	1628.67809	2	6.45E-04	0.92	3.42	-	1083.2
AHQ-7-4, 1958	K.IECDDKGDGSCDVR.Y	1628.67809	2	9.98E-06	0.73	2.92	-	633.8
AHQ-7-2, 4360	K.YGGDEIPYSPFR.I	1401.50466	1	9.03E-05	0.31	2.77	-	315.5
gi|4503445|ref|NP_001944.1| endothelial cell growth factor 1 (platelet-derived); thymidine phosphor				2.24E-08	3.55	40.25	16.40	49955.2
AHQ-7-7, 6497	R.ALPLALVLHELGAGR.S	1530.83966	2	2.24E-08	0.97	4.61	-	1703.3
AHQ-7-7, 4233	R.AREQEELLAPADGTVELVR.A	2097.31523	2	8.82E-07	0.92	4.75	-	735.3
AHQ-7-7, 6889	R.DLVTTLGGALLWLSGHAGTQAQGAAR.V	2565.86952	3	5.12E-07	0.96	5.00	-	1679.7
AHQ-7-7, 6774	R.DVTATVDSLPLITASILSK.K	1945.24371	2	3.58E-06	0.70	3.60	-	270.7
gi|4502097|ref|NP_001142.1| solute carrier family 25 (mitochondrial carrier; adenine nucleotide tra				2.27E-08	0.88	10.17	4.00	33148.4
AHQ-7-10, 5256 - 5257	R.YFPTQALNFAFK.D	1447.66130	2	2.27E-08	0.88	3.43	-	609.4
gi|5902134|ref|NP_009005.1| coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin				2.28E-08	1.86	20.22	5.90	51026.0
AHQ-7-7, 2273	R.KLQATVQELQK.R	1286.50292	2	5.25E-04	0.92	4.11	-	1192.4
AHQ-7-13, 4238 - 4245	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	3.73E-04	0.79	3.64	-	623.1
AHQ-7-13-, 4109 - 4111	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	7.23E-06	0.68	3.32	-	492.4
AHQ-7-7, 4048 - 4108	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	2.28E-08	0.94	4.49	-	872.8
gi|20539300|ref|XP_088391.4| similar to tropomyosin 4 [Homo sapiens]				2.38E-08	1.42	20.19	6.90	18592.1
AHQ-7-9, 3354	R.KLVILEGELER.A	1299.54160	1	2.38E-08	0.47	2.59	-	282.8
AHQ-7-11, 3516 - 3587	R.KLVILEGELER.A	1299.54160	2	1.46E-06	0.94	3.77	-	1446.4
AHQ-7-10, 3509	R.KLVILEGELER.A	1299.54160	2	4.05E-05	0.88	3.27	-	942.1
AHQ-7-9, 3340	R.KLVILEGELER.A	1299.54160	2	4.04E-06	0.93	3.62	-	1112.6
AHQ-7-9, 3736 - 3737	K.LVILEGELER.A	1171.36868	2	8.26E-06	0.95	3.82	-	1532.2
gi|20127408|ref|NP_000173.2| hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub				2.53E-08	3.36	40.21	8.70	82999.1
AHQ-7-6, 6166	R.DSIFSNLTGQLDYQGFEK.A	2063.20943	2	2.53E-08	0.92	4.17	-	820.1
AHQ-7-6, 2673	K.DTSASAVAVGLK.Q	1119.25064	2	3.09E-04	0.85	2.94	-	1082.8
AHQ-7-6, 4610	R.FGGGNPELLTQMVSK.G	1578.81508	2	1.61E-04	0.84	3.26	-	592.0
AHQ-7-6, 5885	K.TVLGTPEVLLGALPGAGGTQR.L	2008.30795	2	1.30E-04	0.76	3.59	-	282.2
gi|7705849|ref|NP_057215.1| ras-related GTP-binding protein RAB10; ras-related GTP-binding protein				2.61E-08	2.36	30.19	23.00	22540.8
AHQ-7-14-, 6105	K.AFLTLAEDILR.K	1262.47982	2	2.26E-05	0.93	3.34	-	1446.7
AHQ-7-11, 5935	K.AFLTLAEDILR.K	1262.47982	2	5.65E-06	0.96	3.81	-	1731.7
AHQ-7-13, 6203	K.AFLTLAEDILR.K	1262.47982	2	2.61E-08	0.96	3.70	-	1898.6
AHQ-7-13-, 6145	K.AFLTLAEDILR.K	1262.47982	2	5.75E-04	0.94	3.68	-	1498.0
AHQ-7-11, 1906 - 1971	R.NIDEHANEDVER.M	1441.44245	2	2.39E-05	0.67	2.73	-	578.2
AHQ-7-11, 3518 - 3594	K.TPVKEPNSENVDISSGGGVTGWK.S	2359.53465	3	5.51E-05	0.74	3.32	-	835.2
gi|4503725|ref|NP_000792.1| FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei				2.90E-08	1.75	20.25	13.00	11950.6
AHQ-7-13, 3939 - 4001	R.GWEEGVAQMSVGQR.A	1534.67926	2	3.56E-04	0.84	3.54	-	1129.8
AHQ-7-13-, 3051	R.GWEEGVAQM*SVGQR.A	1550.67866	2	5.35E-07	0.95	4.90	-	921.4
AHQ-7-13-, 3851 - 3861	R.GWEEGVAQMSVGQR.A	1534.67926	2	2.90E-08	0.95	3.99	-	1474.9
AHQ-7-14-, 3067	R.GWEEGVAQM*SVGQR.A	1550.67866	2	3.15E-05	0.94	3.93	-	1172.6
AHQ-7-13, 3199	R.GWEEGVAQM*SVGQR.A	1550.67866	2	4.44E-07	0.81	3.06	-	752.2
gi|7705827|ref|NP_057187.1| GTP-binding protein Sara [Homo sapiens]				2.93E-08	0.95	10.19	5.60	22409.7
AHQ-7-11, 4287 - 4291	K.LVFLGLDNAGK.T	1147.34882	2	2.93E-08	0.95	3.80	-	1327.2
gi|17318569|ref|NP_006112.2| keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]				3.02E-08	10.96	120.25	22.70	66066.3
AHQ-7-1, 4005 - 4067	K.LNDLEDALQQAK.E	1358.47963	2	1.12E-04	0.92	3.61	-	1490.4
AHQ-7-14-, 3882	K.LNDLEDALQQAK.E	1358.47963	2	2.61E-04	0.97	4.60	-	2120.5
AHQ-7-13, 4025	K.LNDLEDALQQAK.E	1358.47963	2	5.29E-05	0.94	3.72	-	1596.0
AHQ-7-1, 4499	K.NKLNDLEDALQQAK.E	1600.75564	2	3.33E-04	0.95	3.95	-	1633.0
AHQ-7-3, 2943	K.NMQDM*VEDYR.N	1317.43134	2	9.57E-04	0.86	2.89	-	1009.9
AHQ-7-1, 3859	K.QISNLQQSISDAEQR.G	1717.81950	2	4.42E-08	0.89	3.68	-	774.7
AHQ-7-13-, 3679	K.QISNLQQSISDAEQR.G	1717.81950	2	2.66E-04	0.84	3.03	-	725.4
AHQ-7-3, 3767	K.QISNLQQSISDAEQR.G	1717.81950	2	3.02E-08	0.84	3.64	-	554.4
AHQ-7-1, 3717	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	4.06E-04	0.86	2.63	-	1272.3
AHQ-7-6, 5957	R.SLDLDSIIAEVK.A	1303.48388	2	3.39E-08	0.96	4.50	-	1353.0
AHQ-7-2, 6127	R.SLDLDSIIAEVK.A	1303.48388	2	1.08E-06	0.93	3.88	-	1208.0
AHQ-7-5, 6058	R.SLDLDSIIAEVK.A	1303.48388	2	7.45E-07	0.95	4.18	-	1372.4
AHQ-7-13, 5818	R.SLDLDSIIAEVK.A	1303.48388	2	5.09E-06	0.93	3.80	-	1162.1
AHQ-7-4, 6136	R.SLDLDSIIAEVK.A	1303.48388	2	1.14E-07	0.94	3.89	-	1376.9
AHQ-7-13-, 5763	R.SLDLDSIIAEVK.A	1303.48388	2	5.11E-05	0.55	2.57	-	585.8
AHQ-7-11, 5586 - 5598	R.SLDLDSIIAEVK.A	1303.48388	2	1.65E-07	0.96	4.41	-	1440.2
AHQ-7-3, 5980 - 5981	R.SLDLDSIIAEVK.A	1303.48388	2	7.94E-07	0.96	4.13	-	1412.6
AHQ-7-13, 4659 - 4671	K.SLNNQFASFIDK.V	1384.51877	2	9.21E-04	0.87	3.27	-	891.0
AHQ-7-1, 4760 - 4761	K.SLNNQFASFIDK.V	1384.51877	2	3.18E-04	0.85	3.86	-	669.8
AHQ-7-3, 4299	R.SLVNLGGSKSISISVAR.G	1688.95071	2	1.68E-06	0.92	4.26	-	820.4
AHQ-7-13-, 6068 - 6147	R.THNLEPYFESFINNLR.R	1995.18315	3	1.85E-05	0.95	4.90	-	1488.6
AHQ-7-2, 6533	R.THNLEPYFESFINNLR.R	1995.18315	2	8.96E-04	0.66	3.40	-	329.2
AHQ-7-1, 6297	R.THNLEPYFESFINNLR.R	1995.18315	3	3.07E-07	0.92	4.27	-	1267.8
AHQ-7-6, 6349	R.THNLEPYFESFINNLR.R	1995.18315	3	3.72E-05	0.92	4.35	-	1137.0
AHQ-7-1, 3379	R.TNAENEFVTIK.K	1266.38219	2	1.43E-04	0.94	3.34	-	1276.9
AHQ-7-6, 3139	R.TNAENEFVTIK.K	1266.38219	2	1.78E-04	0.75	2.56	-	703.6
AHQ-7-5, 4527	K.WELLQQVDTSTR.T	1476.61621	2	3.76E-07	0.95	3.71	-	1802.0
AHQ-7-1, 4596 - 4660	K.WELLQQVDTSTR.T	1476.61621	2	3.80E-08	0.95	3.73	-	1689.9
AHQ-7-14-, 4409 - 4470	K.WELLQQVDTSTR.T	1476.61621	2	4.93E-08	0.83	3.18	-	908.5
AHQ-7-2, 4643	K.WELLQQVDTSTR.T	1476.61621	2	4.58E-08	0.94	3.42	-	1766.6
AHQ-7-6, 4438 - 4502	K.WELLQQVDTSTR.T	1476.61621	2	4.23E-06	0.94	3.65	-	1746.0
AHQ-7-3, 4544	K.WELLQQVDTSTR.T	1476.61621	2	8.08E-07	0.89	3.37	-	1248.8
AHQ-7-3, 3079	K.YEELQITAGR.H	1180.29253	2	7.18E-06	0.96	3.81	-	1829.1
AHQ-7-2, 3133	K.YEELQITAGR.H	1180.29253	2	6.40E-04	0.94	3.63	-	1658.4
AHQ-7-1, 3233	K.YEELQITAGR.H	1180.29253	2	8.42E-05	0.94	3.58	-	1704.3
AHQ-7-7, 2914	K.YEELQITAGR.H	1180.29253	2	6.16E-04	0.89	3.47	-	1180.0
gi|4758638|ref|NP_004896.1| peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi				3.07E-08	4.96	60.25	36.60	25034.8
AHQ-7-10, 3643	R.DFTPVCTTELGR.A	1397.53591	2	3.07E-07	0.81	2.83	-	578.2
AHQ-7-10, 3968	K.DGDSVM*VLPTIPEEEAK.K	1847.03409	2	6.01E-05	0.44	2.81	-	333.2
AHQ-7-10, 5631	R.ELAILLGMLDPAEKDEK.G	1886.19976	2	1.82E-05	0.96	4.72	-	1097.2
AHQ-7-10, 5429 - 5489	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	1.32E-06	0.92	4.37	-	680.9
AHQ-7-10, 5435 - 5437	K.LIALSIDSVEDHLAWSK.D	1898.14883	3	2.52E-05	0.78	3.87	-	489.1
AHQ-7-14-, 5673	K.LIALSIDSVEDHLAWSK.D	1898.14883	2	3.07E-08	0.94	3.69	-	1406.3
AHQ-7-10, 4233 - 4239	K.LPFPIIDDR.N	1086.26548	2	5.82E-05	0.93	3.58	-	939.2
AHQ-7-10, 3088 - 3089	R.VVFVFGPDKK.L	1136.36763	2	5.18E-04	0.87	3.05	-	980.3
gi|4504515|ref|NP_002146.1| heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B				3.09E-08	4.60	50.21	8.40	70853.4
AHQ-7-6, 4994	R.ARFEELCSDLFR.S	1544.71384	2	4.46E-05	0.95	4.18	-	1221.7
AHQ-7-6, 5003	R.FEELCSDLFR.S	1317.44926	2	2.38E-06	0.95	4.12	-	1257.3
AHQ-7-6, 4855	R.IINEPTAAAIAYGLDR.R	1688.90603	2	7.83E-08	0.93	4.15	-	992.4
AHQ-7-6, 4351	K.LLQDFFNGKELNK.S	1566.78249	2	4.96E-04	0.87	3.64	-	798.5

AHQ-7-13-, 3475 - 3480	R.TTPSYVAFTDTER.L	1488.58062	2	6.21E-07	0.80	2.70	-	773.1
AHQ-7-6, 3441	R.TTPSYVAFTDTER.L	1488.58062	2	3.09E-08	0.90	2.87	-	1084.1
gi|16950601|ref|NP_005956.2| myosin light chain kinase isoform 6; myosin light chain kinase [Homo s				3.28E-08	3.51	40.17	5.00	110074.8
AHQ-7-5, 5595	K.IEGYPDPEVVWFK.D	1579.77650	2	8.09E-06	0.88	3.20	-	621.2
AHQ-7-5, 3650	K.LVQCVDAFEEK.A	1339.49637	2	2.65E-04	0.90	3.05	-	1127.7
AHQ-7-5, 5110	R.STSFNVQDLLPDHEYK.F	1894.03076	2	4.10E-05	0.80	3.50	-	416.5
AHQ-7-6, 3517	K.VSDFYDIEER.L	1273.33005	2	7.83E-07	0.93	3.01	-	1440.8
AHQ-7-5, 3564	K.VSDFYDIEER.L	1273.33005	2	3.28E-08	0.93	3.42	-	1123.5
gi|4507171|ref|NP_003109.1| secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec				3.42E-08	3.57	40.19	19.80	34632.0
AHQ-7-8, 3174	R.LEAGDHPVELLAR.D	1420.59579	2	1.67E-07	0.92	3.83	-	844.5
AHQ-7-8, 5058	K.NVLVTLYERDEDNNLLTEK.Q	2279.48944	2	3.89E-04	0.89	3.75	-	1005.5
AHQ-7-8, 3408	K.TFDSSCHFFATK.C	1449.56938	2	3.42E-08	0.90	3.66	-	933.7
AHQ-7-9, 5661 - 5662	K.YIPPCLDSELTEFPLR.M	1952.21655	2	8.76E-07	0.85	3.78	-	248.8
gi|6005749|ref|NP_009193.1| RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA				3.44E-08	2.33	30.18	24.30	19846.9
AHQ-7-11, 3367	R.DVVICPDASLEDAKK.E	1661.85581	2	3.44E-08	0.81	2.94	-	680.3
AHQ-7-11, 4082	K.GAEEM*ETVIPVDVMR.R	1692.93673	2	2.75E-05	0.67	3.22	-	428.7
AHQ-7-11, 3158	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	1.18E-07	0.84	3.28	-	629.2
gi|4507231|ref|NP_003134.1| single-stranded DNA binding protein; single-stranded DNA-binding protei				3.48E-08	3.51	40.25	32.40	17259.5
AHQ-7-13-, 5724	K.NPVTIFSLATNEM*WR.S	1796.04007	2	3.48E-08	0.87	3.42	-	607.7
AHQ-7-13-, 6325	K.NPVTIFSLATNEMWR.S	1780.04067	2	4.78E-04	0.86	2.94	-	979.3
AHQ-7-13-, 5777	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	1.36E-05	0.90	3.88	-	740.1
AHQ-7-13-, 3232 - 3233	R.SGDSEVYQLGDVSQK.T	1612.67692	2	5.73E-07	0.96	4.98	-	1264.3
AHQ-7-13, 3385	R.SGDSEVYQLGDVSQK.T	1612.67692	2	3.04E-07	0.88	3.33	-	853.1
gi|18375655|ref|NP_055184.2| protein tyrosine phosphatase, non-receptor type 18; brain-derived phos				3.53E-08	0.97	10.31	6.50	50482.1
AHQ-7-13, 4939	R.VPADQSPAGSGAYEDVAGGAQTGGLGFNLR.I	2864.03331	3	3.53E-08	0.97	6.15	-	1462.9
gi|11321601|ref|NP_002618.1| phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom				3.57E-08	6.26	70.28	16.10	85595.6
AHQ-7-5, 3736	K.AIGVLTSGGDAQGMNAAVR.A	1789.00750	2	2.76E-07	0.97	5.68	-	1517.4
AHQ-7-5, 4974	K.ASYDVSDSGQLEHVQPWSV	2105.20640	2	2.84E-06	0.69	3.38	-	326.7
AHQ-7-5, 5867 - 5876	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	3.57E-08	0.92	4.15	-	911.0
AHQ-7-5, 6192	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	1.46E-06	0.97	5.24	-	1324.0
AHQ-7-5, 3912 - 3952	K.IKELVVTQLGYDTR.V	1635.88627	2	2.98E-04	0.83	3.36	-	795.1
AHQ-7-5, 6352 - 6354	R.NESCSENYTTDFIYQLYSEEGK.G	2679.76407	2	4.55E-07	0.94	4.82	-	860.1
AHQ-7-5, 3683	K.YLEEIATQMR.T	1254.43805	2	3.11E-06	0.94	3.92	-	1480.3
gi|7657056|ref|NP_055415.1| EH-domain containing 3; EH domain containing 3 [Homo sapiens]				3.74E-08	5.61	60.33	24.10	60886.7
AHQ-7-7, 4965	R.FHEFHSPALEDADFDNKPM*VLLVGQYSTGK.T	3410.75689	3	3.74E-08	0.94	4.88	-	1002.9
AHQ-7-7, 6822	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	3.57E-05	0.82	3.51	-	643.3
AHQ-7-7, 5498	K.GGAFEGTLHGPFGHGYGEGAGEGIDDAEWVVAR.D	3317.48513	3	1.08E-04	0.98	6.69	-	2415.5
AHQ-7-7, 4782	K.LFEAEEQDLFR.D	1397.51432	2	2.48E-07	0.97	3.96	-	2196.7
AHQ-7-7, 5958	R.VYIGSFWSHPLLIPDNR.K	2015.30234	2	8.49E-04	0.93	4.43	-	808.2
AHQ-7-7, 4668 - 4681	R.YLLEQDFPGMR.I	1369.57075	2	4.46E-05	0.96	3.65	-	2005.8
gi|18570595|ref|XP_095590.1| similar to myosin regulatory light chain [Homo sapiens]				3.80E-08	0.94	10.20	8.90	13951.5
AHQ-7-11, 3070	K.LNGTDPEDVIR.H	1229.32195	2	3.80E-08	0.94	4.06	-	1105.9
AHQ-7-12, 3090	K.LNGTDPEDVIR.H	1229.32195	2	5.30E-04	0.83	2.80	-	992.9
AHQ-7-11, 2923 - 2994	K.LNGTDPEDVIR.H	1229.32195	2	8.37E-05	0.91	3.11	-	1339.9
gi|4506417|ref|NP_002877.1| RAP2B, member of RAS oncogene family [Homo sapiens]				3.86E-08	2.35	30.21	20.80	20494.2
AHQ-7-11, 4886 - 4948	K.ALAEEWSCPFMETSAK.N	1859.06988	2	2.05E-04	0.56	3.00	-	164.5
AHQ-7-11, 5764	K.ASVDELFAEIVR.Q	1349.51434	2	1.69E-07	0.93	4.14	-	1177.8
AHQ-7-11, 4059 - 4072	K.YDPTIEDFYR.K	1319.40042	2	3.86E-08	0.86	2.80	-	640.8
gi|4502695|ref|NP_001779.1| cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c				3.90E-08	2.57	30.22	13.60	48786.6
AHQ-7-8, 3970	K.IYEFPETDDEEENKLVK.K	2099.23685	2	1.90E-04	0.76	3.94	-	312.9
AHQ-7-13-, 5244	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	1.74E-04	0.95	4.37	-	1087.5
AHQ-7-8, 6443 - 6448	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	1.76E-07	0.83	3.82	-	554.4
AHQ-7-8, 6400 - 6452	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	2	3.90E-08	0.87	4.13	-	457.7
gi|14249348|ref|NP_116120.1| hypothetical protein MGC14353 [Homo sapiens]				4.26E-08	0.93	10.19	11.40	13940.7
AHQ-7-13-, 4012	K.SWCPDCVQAEPVVR.E	1705.89366	2	4.26E-08	0.93	3.75	-	1037.5
AHQ-7-13, 4146	K.SWCPDCVQAEPVVR.E	1705.89366	2	4.67E-04	0.83	2.85	-	748.1
gi|4757812|ref|NP_004880.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso				4.38E-08	1.79	20.19	25.50	10917.8
AHQ-7-13, 5779	R.DFSPSGIFGAFQR.G	1429.56124	2	3.23E-05	0.81	2.92	-	747.8
AHQ-7-13-, 5715	R.DFSPSGIFGAFQR.G	1429.56124	2	4.38E-08	0.95	3.72	-	1290.5
AHQ-7-13-, 5353	K.LGELPSWILM*R.D	1331.60876	2	2.20E-04	0.86	3.22	-	489.4
AHQ-7-14-, 5338	K.LGELPSWILM*R.D	1331.60876	2	2.01E-06	0.84	3.37	-	495.7
AHQ-7-13, 5426	K.LGELPSWILM*R.D	1331.60876	2	1.60E-05	0.93	3.73	-	653.3
gi|20532885|ref|XP_086931.2| similar to epsilon isoform of 14-3-3 protein [Homo sapiens]				4.41E-08	2.44	30.24	13.70	29380.0
AHQ-7-9, 2481	K.EAAKNSIVAYK.A	1194.36234	2	5.53E-05	0.59	2.89	-	500.8
AHQ-7-10, 6035 - 6036	K.LICCDILDVLDK.H	1479.74157	2	4.41E-08	0.96	4.89	-	961.2
AHQ-7-11, 6142	K.LICCDILDVLDK.H	1479.74157	2	1.29E-04	0.90	3.45	-	699.0
AHQ-7-13-, 6297	K.LICCDILDVLDK.H	1479.74157	2	1.82E-05	0.92	3.51	-	820.2
AHQ-7-9, 2620	R.YLAEFATGNDRK.E	1385.50677	2	5.89E-07	0.89	3.03	-	987.6
gi|6715607|ref|NP_000175.1| G-gamma globin [Homo sapiens]				4.48E-08	0.92	10.19	6.80	16126.3
AHQ-7-13-, 4743 - 4744	R.LLVVYPWTQR.F	1275.52342	2	4.48E-08	0.92	3.75	-	931.7
AHQ-7-13, 4853 - 4874	R.LLVVYPWTQR.F	1275.52342	2	8.93E-05	0.90	3.52	-	910.7
gi|4507951|ref|NP_003396.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept				4.60E-08	4.93	60.22	26.80	28218.5
AHQ-7-10, 2863 - 2925	K.AVTELNEPLSNEDR.N	1587.67060	2	9.60E-07	0.92	4.43	-	593.2
AHQ-7-10, 5404 - 5484	K.ELETVCNDVLSLLDK.F	1749.96137	2	2.33E-04	0.57	2.65	-	368.8
AHQ-7-10, 6095 - 6168	K.ELETVCNDVLSLLDK.F	1749.96137	2	1.48E-07	0.76	3.57	-	418.1
AHQ-7-10, 3903	K.FLIKNCNDFQYESK.V	1808.00430	2	4.60E-08	0.88	3.59	-	587.6
AHQ-7-10, 2343	K.KNSVVEASEAAYK.E	1396.52786	2	2.92E-04	0.83	3.09	-	759.5
AHQ-7-10, 2528 - 2591	K.NSVVEASEAAYK.E	1268.35495	2	9.56E-05	0.91	3.92	-	801.1
AHQ-7-10, 2179	R.YLAEVASGEK.K	1067.17419	1	2.62E-04	0.39	2.03	-	643.6
AHQ-7-10, 2139 - 2195	R.YLAEVASGEK.K	1067.17419	2	2.61E-05	0.83	3.04	-	895.5
AHQ-7-10, 2189	R.YLAEVASGEK.K	1067.17419	1	1.79E-05	0.63	2.81	-	376.8
gi|11128019|ref|NP_061820.1| cytochrome c [Homo sapiens]				4.80E-08	0.84	10.15	13.30	11748.7
AHQ-7-13-, 2228	K.TGQAPGYSYTAANK.N	1429.51641	2	4.80E-08	0.84	2.91	-	763.6
gi|4826762|ref|NP_005134.1| haptoglobin [Homo sapiens]				5.02E-08	2.66	30.21	9.90	45205.0
AHQ-7-8, 4231	R.VMPICLPSKDYAEVGR.V	1837.15372	2	5.02E-08	0.88	3.51	-	555.9
AHQ-7-8, 3512	K.VTSIQDWVQK.T	1204.35723	2	1.46E-04	0.92	3.24	-	1136.8
AHQ-7-8, 4200	K.YVMLPVADQDQCIR.H	1709.96880	2	2.48E-04	0.87	3.18	-	741.8
gi|30149460|ref|XP_210540.2| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				5.34E-08	0.91	10.17	4.00	29287.8
AHQ-7-5, 2392	K.HIYYITGETK.D	1225.37490	2	5.34E-08	0.91	3.35	-	676.5
gi|10835189|ref|NP_000628.1| glutathione reductase [Homo sapiens]				5.56E-08	1.55	20.21	7.50	51700.3
AHQ-7-7, 4685	K.ADFDNTVAIHPTSSEELVTLR	2316.50977	2	5.56E-08	0.84	4.15	-	387.9
AHQ-7-7, 3548	K.TYSTSFTPMYHAVTK.R	1734.95353	2	2.39E-04	0.71	3.01	-	537.0
gi|5802966|ref|NP_006861.1| destrin (actin depolymerizing factor); destrin [Homo sapiens]				6.16E-08	1.75	20.19	14.50	18505.6
AHQ-7-12, 2071 - 2136	K.HECQANGPEDLNR.A	1541.58530	2	4.96E-04	0.83	2.82	-	728.3
AHQ-7-12, 3632 - 3687	R.YALYDASFETK.E	1308.41754	2	6.16E-08	0.92	3.89	-	888.0
gi|4507745|ref|NP_003320.1| thioredoxin [Homo sapiens]				6.35E-08	0.92	10.18	12.40	11693.3
AHQ-7-14, 4718	K.TAFQEALDAAGDK.L	1337.41728	2	1.81E-07	0.93	3.27	-	1706.6
AHQ-7-13-, 3832	K.TAFQEALDAAGDK.L	1337.41728	2	1.88E-06	0.87	2.99	-	1171.9
AHQ-7-14-, 3837	K.TAFQEALDAAGDK.L	1337.41728	2	3.60E-06	0.89	3.29	-	1221.8
AHQ-7-13, 3978 - 3979	K.TAFQEALDAAGDK.L	1337.41728	2	6.35E-08	0.92	3.19	-	1452.8
gi|4506675|ref|NP_002941.1| ribophorin I [Homo sapiens]				6.62E-08	2.46	30.20	6.80	68569.0
AHQ-7-1, 4639	K.ALTSEIALLQSR.L	1302.50235	2	6.62E-08	0.95	3.92	-	1703.2
AHQ-7-6, 5570	R.FVDHVFDEQVIDSLTVK.I	1992.21748	2	6.03E-05	0.67	3.22	-	511.2
AHQ-7-1, 4075	K.NIEIDSPYEISR.A	1436.54885	2	2.52E-05	0.85	3.48	-	745.1
gi|4557361|ref|NP_001187.1| BH3 interacting domain death agonist; BH3-interacting domain death agon				6.74E-08	0.92	10.15	6.70	21994.6
AHQ-7-11, 2759 - 2823	R.IEADSESQEDIIR.N	1505.56635	2	6.74E-08	0.92	3.10	-	1544.5
gi|4505759|ref|NP_002622.1| phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo				6.87E-08	1.87	20.27	7.00	53151.7

<table>
<tr><td>AHQ-7-14-, 4510</td><td>R.DYFGAHTYELLAK.P</td><td>1528.68958</td><td>2</td><td>6.21E-07</td><td>0.90</td><td>3.16</td><td>-</td><td>1072.4</td></tr>
<tr><td>AHQ-7-8, 6559</td><td>K.IKDAFDRNPELQNLLLDDFFK.S</td><td>2552.86598</td><td>3</td><td>6.87E-08</td><td>0.97</td><td>5.48</td><td>-</td><td>1665.3</td></tr>
<tr><td colspan="2">gi|21361198|ref|NP_000286.2| serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei</td><td></td><td></td><td>7.12E-08</td><td>4.46</td><td>50.23</td><td>19.90</td><td>46722.2</td></tr>
<tr><td>AHQ-7-7, 3429 - 3449</td><td>K.DTEEEDFHVDQVTTVK.V</td><td>1892.95480</td><td>2</td><td>1.13E-05</td><td>0.93</td><td>3.57</td><td>-</td><td>1268.6</td></tr>
<tr><td>AHQ-7-7, 3674 - 3690</td><td>K.LQHLENELTHDIITK.F</td><td>1805.02503</td><td>2</td><td>3.82E-05</td><td>0.96</td><td>4.51</td><td>-</td><td>1572.7</td></tr>
<tr><td>AHQ-7-7, 3884</td><td>K.SVLGQLGITK.V</td><td>1016.21669</td><td>2</td><td>1.86E-06</td><td>0.90</td><td>2.99</td><td>-</td><td>901.0</td></tr>
<tr><td>AHQ-7-7, 5846</td><td>R.TLNQPDSQLQLTTGNGLFLSEGLK.L</td><td>2575.85625</td><td>2</td><td>4.61E-06</td><td>0.78</td><td>3.62</td><td>-</td><td>379.3</td></tr>
<tr><td>AHQ-7-8, 4520</td><td>K.VFSNGADLSGVTEEAPLK.L</td><td>1835.00476</td><td>2</td><td>7.12E-08</td><td>0.89</td><td>3.74</td><td>-</td><td>904.0</td></tr>
<tr><td>AHQ-7-7, 4457 - 4537</td><td>K.VFSNGADLSGVTEEAPLK.L</td><td>1835.00476</td><td>2</td><td>5.26E-06</td><td>0.92</td><td>4.52</td><td>-</td><td>940.2</td></tr>
<tr><td colspan="2">gi|4507645|ref|NP_000356.1| triosephosphate isomerase 1 [Homo sapiens]</td><td></td><td></td><td>7.14E-08</td><td>3.35</td><td>40.28</td><td>26.50</td><td>26669.3</td></tr>
<tr><td>AHQ-7-10, 3623 - 3700</td><td>K.DCGATWVVLGHSER.R</td><td>1588.72671</td><td>2</td><td>1.58E-04</td><td>0.62</td><td>2.93</td><td>-</td><td>712.8</td></tr>
<tr><td>AHQ-7-10, 4853 - 4861</td><td>K.QSLGELIGTLNAAK.V</td><td>1415.61746</td><td>2</td><td>2.52E-07</td><td>0.86</td><td>3.60</td><td>-</td><td>614.3</td></tr>
<tr><td>AHQ-7-10, 5056</td><td>K.VAHALAEGLGVIACIGEK.L</td><td>1810.10800</td><td>2</td><td>7.14E-08</td><td>0.98</td><td>5.53</td><td>-</td><td>2196.2</td></tr>
<tr><td>AHQ-7-10, 5048 - 5104</td><td>K.VPADTEVVCAPPTAYIDFAR.Q</td><td>2194.44943</td><td>2</td><td>4.75E-05</td><td>0.89</td><td>3.87</td><td>-</td><td>685.1</td></tr>
<tr><td colspan="2">gi|4758756|ref|NP_004528.1| nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr</td><td></td><td></td><td>7.44E-08</td><td>1.67</td><td>20.27</td><td>7.40</td><td>45373.8</td></tr>
<tr><td>AHQ-7-7, 6748</td><td>K.GIPEFWLTVFK.N</td><td>1337.58999</td><td>2</td><td>1.65E-07</td><td>0.70</td><td>2.51</td><td>-</td><td>261.2</td></tr>
<tr><td>AHQ-7-7, 5432</td><td>K.NVDLLSDMVQEHDEPILK.H</td><td>2096.34751</td><td>2</td><td>7.44E-08</td><td>0.97</td><td>5.43</td><td>-</td><td>1370.8</td></tr>
<tr><td colspan="2">gi|5453722|ref|NP_006321.1| lysophospholipase I; lysophospholipase 1; lysophospholipid-specific lys</td><td></td><td></td><td>8.12E-08</td><td>1.72</td><td>20.17</td><td>11.30</td><td>24669.5</td></tr>
<tr><td>AHQ-7-11, 3020</td><td>K.ALIDQEVKNGIPSNR.I</td><td>1654.84968</td><td>2</td><td>8.12E-08</td><td>0.82</td><td>2.72</td><td>-</td><td>875.7</td></tr>
<tr><td>AHQ-7-11, 3575 - 3579</td><td>K.TLVNPANVTFK.T</td><td>1204.40037</td><td>2</td><td>8.38E-04</td><td>0.89</td><td>3.28</td><td>-</td><td>923.3</td></tr>
<tr><td colspan="2">gi|4557395|ref|NP_000058.1| carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase;</td><td></td><td></td><td>8.90E-08</td><td>4.62</td><td>50.23</td><td>35.00</td><td>29245.8</td></tr>
<tr><td>AHQ-7-10, 6119 - 6120</td><td>K.AVQQPDGLAVLGIFLK.V</td><td>1669.98899</td><td>2</td><td>8.90E-08</td><td>0.94</td><td>4.63</td><td>-</td><td>706.1</td></tr>
<tr><td>AHQ-7-10, 3945</td><td>R.ILNNGHAFNVEFDDSQDK.A</td><td>2064.15751</td><td>2</td><td>8.45E-04</td><td>0.47</td><td>2.53</td><td>-</td><td>568.1</td></tr>
<tr><td>AHQ-7-10, 3796</td><td>R.ILNNGHAFNVEFDDSQDK.A</td><td>2064.15751</td><td>2</td><td>4.19E-07</td><td>0.93</td><td>4.19</td><td>-</td><td>1296.3</td></tr>
<tr><td>AHQ-7-10, 4549</td><td>R.KLNFNGEGEPEELM*VDNWRPAQPLK.N</td><td>2929.25665</td><td>3</td><td>3.57E-04</td><td>0.87</td><td>3.77</td><td>-</td><td>871.0</td></tr>
<tr><td>AHQ-7-10, 3444</td><td>K.YAAELHLVHWNTK.Y</td><td>1582.78684</td><td>2</td><td>1.85E-07</td><td>0.92</td><td>3.18</td><td>-</td><td>1619.5</td></tr>
<tr><td>AHQ-7-10, 4176 - 4219</td><td>K.YDPSLKPLSVSYDQATSLR.I</td><td>2141.36647</td><td>2</td><td>9.19E-06</td><td>0.87</td><td>3.50</td><td>-</td><td>604.0</td></tr>
<tr><td>AHQ-7-10, 4149 - 4217</td><td>K.YDPSLKPLSVSYDQATSLR.I</td><td>2141.36647</td><td>3</td><td>2.35E-07</td><td>0.95</td><td>4.08</td><td>-</td><td>1711.0</td></tr>
<tr><td colspan="2">gi|7705704|ref|NP_057001.1| glutathione S-transferase subunit 13 homolog [Homo sapiens]</td><td></td><td></td><td>8.94E-08</td><td>0.88</td><td>10.23</td><td>7.10</td><td>25496.7</td></tr>
<tr><td>AHQ-7-11, 4358</td><td>R.NEDITEPQSILAAAEK.A</td><td>1729.86695</td><td>2</td><td>8.94E-08</td><td>0.88</td><td>3.60</td><td>-</td><td>584.5</td></tr>
<tr><td colspan="2">gi|13376181|ref|NP_079079.1| hypothetical protein FLJ21665 [Homo sapiens]</td><td></td><td></td><td>9.60E-08</td><td>0.81</td><td>10.18</td><td>3.80</td><td>49908.5</td></tr>
<tr><td>AHQ-7-7, 5300</td><td>R.SFGGGTGSGFTSLLMER.L</td><td>1704.88582</td><td>2</td><td>9.60E-08</td><td>0.81</td><td>3.57</td><td>-</td><td>679.5</td></tr>
<tr><td colspan="2">gi|4505989|ref|NP_000299.1| protective protein for beta-galactosidase; Protective protein for beta-</td><td></td><td></td><td>9.79E-08</td><td>0.96</td><td>10.20</td><td>2.70</td><td>54495.8</td></tr>
<tr><td>AHQ-7-12, 3466</td><td>K.YGDSGEQIAGFVK.E</td><td>1371.47686</td><td>2</td><td>9.79E-08</td><td>0.96</td><td>4.10</td><td>-</td><td>1582.9</td></tr>
<tr><td colspan="2">gi|4557251|ref|NP_001101.1| a disintegrin and metalloprotease domain 10 [Homo sapiens]</td><td></td><td></td><td>9.81E-08</td><td>0.95</td><td>10.26</td><td>2.00</td><td>84141.7</td></tr>
<tr><td>AHQ-7-5, 4674</td><td>K.AIDTIYQTTDFSGIR.N</td><td>1701.85844</td><td>2</td><td>9.81E-08</td><td>0.95</td><td>5.16</td><td>-</td><td>826.6</td></tr>
<tr><td colspan="2">gi|7657647|ref|NP_055363.1| tropomodulin 2 (neuronal) [Homo sapiens]</td><td></td><td></td><td>9.83E-08</td><td>0.84</td><td>10.14</td><td>3.10</td><td>39594.8</td></tr>
<tr><td>AHQ-7-11, 3238</td><td>K.FGYQFTKQGPR.T</td><td>1329.48804</td><td>2</td><td>9.83E-08</td><td>0.84</td><td>2.78</td><td>-</td><td>813.0</td></tr>
<tr><td colspan="2">gi|4502565|ref|NP_001740.1| calpain, small subunit 1; calpain, small polypeptide; calcium-dependent</td><td></td><td></td><td>1.01E-07</td><td>0.97</td><td>10.25</td><td>5.60</td><td>28315.5</td></tr>
<tr><td>AHQ-7-11, 2351 - 2352</td><td>R.THYSNIEANESEEVR.Q</td><td>1778.81502</td><td>2</td><td>7.78E-06</td><td>0.95</td><td>4.24</td><td>-</td><td>1329.4</td></tr>
<tr><td>AHQ-7-10, 2328 - 2333</td><td>R.THYSNIEANESEEVR.Q</td><td>1778.81502</td><td>2</td><td>1.01E-07</td><td>0.97</td><td>4.92</td><td>-</td><td>1797.4</td></tr>
<tr><td colspan="2">gi|4885417|ref|NP_005330.1| huntingtin interacting protein 2; ubiquitin-conjugating enzyme E2-25 KD</td><td></td><td></td><td>1.03E-07</td><td>0.86</td><td>10.15</td><td>6.00</td><td>22406.5</td></tr>
<tr><td>AHQ-7-11, 4458</td><td>K.VDLVDENFTELR.G</td><td>1450.57553</td><td>2</td><td>1.03E-07</td><td>0.86</td><td>3.02</td><td>-</td><td>981.6</td></tr>
<tr><td colspan="2">gi|4507767|ref|NP_003326.1| ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi</td><td></td><td></td><td>1.04E-07</td><td>0.96</td><td>10.20</td><td>1.40</td><td>111719.5</td></tr>
<tr><td>AHQ-7-4, 4785</td><td>R.VDGVAAALDSFQAR.R</td><td>1420.55265</td><td>2</td><td>1.04E-07</td><td>0.96</td><td>4.05</td><td>-</td><td>1958.3</td></tr>
<tr><td colspan="2">gi|5729997|ref|NP_004154.2| RAB27B, member RAS oncogene family [Homo sapiens]</td><td></td><td></td><td>1.05E-07</td><td>3.52</td><td>40.21</td><td>19.30</td><td>24607.7</td></tr>
<tr><td>AHQ-7-11, 6164 - 6166</td><td>K.AVETLLDLIMK.R</td><td>1246.54211</td><td>2</td><td>4.45E-04</td><td>0.89</td><td>3.93</td><td>-</td><td>661.2</td></tr>
<tr><td>AHQ-7-11, 5406</td><td>K.AVETLLDLIM*K.R</td><td>1262.54151</td><td>2</td><td>1.08E-05</td><td>0.87</td><td>3.65</td><td>-</td><td>710.7</td></tr>
<tr><td>AHQ-7-11, 3583</td><td>K.VHLQLWDTAGQER.F</td><td>1553.70390</td><td>2</td><td>1.77E-05</td><td>0.90</td><td>3.11</td><td>-</td><td>1025.5</td></tr>
<tr><td>AHQ-7-13-, 3777</td><td>K.VHLQLWDTAGQER.F</td><td>1553.70390</td><td>2</td><td>4.29E-05</td><td>0.94</td><td>3.81</td><td>-</td><td>1195.2</td></tr>
<tr><td>AHQ-7-10, 3505</td><td>K.VHLQLWDTAGQER.F</td><td>1553.70390</td><td>2</td><td>2.40E-05</td><td>0.96</td><td>4.15</td><td>-</td><td>1553.2</td></tr>
<tr><td>AHQ-7-11, 4296</td><td>K.YGIPYFETSAATGQNVEK.A</td><td>1976.13177</td><td>2</td><td>1.54E-06</td><td>0.91</td><td>4.13</td><td>-</td><td>694.1</td></tr>
<tr><td>AHQ-7-11, 4228 - 4310</td><td>K.YGIPYFETSAATGQNVEK.A</td><td>1976.13177</td><td>2</td><td>1.05E-07</td><td>0.86</td><td>4.05</td><td>-</td><td>524.7</td></tr>
<tr><td>AHQ-7-10, 4133 - 4187</td><td>K.YGIPYFETSAATGQNVEK.A</td><td>1976.13177</td><td>2</td><td>1.52E-06</td><td>0.90</td><td>3.62</td><td>-</td><td>789.3</td></tr>
<tr><td colspan="2">gi|13899317|ref|NP_113657.1| SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M</td><td></td><td></td><td>1.07E-07</td><td>3.85</td><td>50.30</td><td>72.00</td><td>12326.0</td></tr>
<tr><td>AHQ-7-13, 5406 - 5417</td><td>K.ESNTVFSFLGLKPR.L</td><td>1595.82383</td><td>2</td><td>2.28E-04</td><td>0.74</td><td>3.33</td><td>-</td><td>390.2</td></tr>
<tr><td>AHQ-7-13-, 5340</td><td>K.ESNTVFSFLGLKPR.L</td><td>1595.82383</td><td>2</td><td>1.88E-07</td><td>0.70</td><td>3.60</td><td>-</td><td>394.3</td></tr>
<tr><td>AHQ-7-13-, 4797</td><td>R.FLEANKIEFEEVDITM*SEEQR.Q</td><td>2574.80223</td><td>3</td><td>5.75E-06</td><td>0.97</td><td>5.93</td><td>-</td><td>1660.2</td></tr>
<tr><td>AHQ-7-14-, 4830</td><td>R.FLEANKIEFEEVDITM*SEEQR.Q</td><td>2574.80223</td><td>2</td><td>7.31E-04</td><td>0.65</td><td>2.88</td><td>-</td><td>514.8</td></tr>
<tr><td>AHQ-7-14-, 4822 - 4887</td><td>R.FLEANKIEFEEVDITM*SEEQR.Q</td><td>2574.80223</td><td>3</td><td>8.26E-07</td><td>0.97</td><td>5.60</td><td>-</td><td>2227.4</td></tr>
<tr><td>AHQ-7-13, 4907</td><td>R.FLEANKIEFEEVDITM*SEEQR.Q</td><td>2574.80223</td><td>3</td><td>3.02E-04</td><td>0.90</td><td>4.57</td><td>-</td><td>945.4</td></tr>
<tr><td>AHQ-7-14-, 3743</td><td>K.KPTQGNPLPPQIFNGDR.Y</td><td>1880.09682</td><td>2</td><td>4.29E-05</td><td>0.56</td><td>2.79</td><td>-</td><td>388.9</td></tr>
<tr><td>AHQ-7-14-, 5513 - 5590</td><td>K.KPTQGNPLPPQIFNGDRYCGDYDSFFESK.E</td><td>3380.64432</td><td>3</td><td>2.88E-05</td><td>0.65</td><td>3.41</td><td>-</td><td>556.8</td></tr>
<tr><td>AHQ-7-13-, 4316</td><td>R.VFIASSSGFVAIK.K</td><td>1326.56551</td><td>2</td><td>1.75E-06</td><td>0.97</td><td>3.73</td><td>-</td><td>2109.8</td></tr>
<tr><td>AHQ-7-14-, 4339</td><td>R.VFIASSSGFVAIK.K</td><td>1326.56551</td><td>2</td><td>1.07E-07</td><td>0.98</td><td>4.53</td><td>-</td><td>2438.2</td></tr>
<tr><td colspan="2">gi|5031569|ref|NP_005727.1| ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r</td><td></td><td></td><td>1.15E-07</td><td>1.89</td><td>20.31</td><td>10.60</td><td>42613.4</td></tr>
<tr><td>AHQ-7-8, 3935</td><td>R.ACYLSINPQKDETLETEK.A</td><td>2141.34169</td><td>2</td><td>8.51E-04</td><td>0.92</td><td>4.60</td><td>-</td><td>641.1</td></tr>
<tr><td>AHQ-7-8, 5204</td><td>K.DQLQTFSEEHPVLLTEAPLNPR.K</td><td>2535.79382</td><td>2</td><td>1.15E-07</td><td>0.97</td><td>6.28</td><td>-</td><td>929.0</td></tr>
<tr><td colspan="2">gi|4505145|ref|NP_002387.1| malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochon</td><td></td><td></td><td>1.16E-07</td><td>5.40</td><td>60.23</td><td>16.80</td><td>65443.3</td></tr>
<tr><td>AHQ-7-7, 3517</td><td>K.ALTSQLTDEELAQGR.L</td><td>1632.75450</td><td>2</td><td>4.84E-05</td><td>0.91</td><td>3.59</td><td>-</td><td>1343.9</td></tr>
<tr><td>AHQ-7-6, 4854</td><td>R.CLFASGSPFGPVK.L</td><td>1368.58254</td><td>2</td><td>1.16E-07</td><td>0.95</td><td>3.83</td><td>-</td><td>1507.5</td></tr>
<tr><td>AHQ-7-6, 3355</td><td>R.HISDSVFLEAAK.A</td><td>1317.47234</td><td>2</td><td>5.70E-04</td><td>0.81</td><td>3.03</td><td>-</td><td>545.4</td></tr>
<tr><td>AHQ-7-6, 3027</td><td>K.IETQDIQALR.F</td><td>1187.32821</td><td>2</td><td>1.34E-05</td><td>0.88</td><td>2.99</td><td>-</td><td>1073.8</td></tr>
<tr><td>AHQ-7-6, 6414</td><td>R.ILGLGDLGVYGMGIPVGK.L</td><td>1760.13394</td><td>2</td><td>5.06E-05</td><td>0.94</td><td>4.54</td><td>-</td><td>1109.7</td></tr>
<tr><td>AHQ-7-7, 6668</td><td>R.ILQDDIESLM*PIVYTPTVGLACSQYGHIFR.R</td><td>3455.94544</td><td>3</td><td>2.85E-04</td><td>0.91</td><td>4.36</td><td>-</td><td>970.2</td></tr>
<tr><td colspan="2">gi|21361370|ref|NP_002853.2| phosphorylase, glycogen; brain [Homo sapiens]</td><td></td><td></td><td>1.19E-07</td><td>1.72</td><td>20.16</td><td>3.20</td><td>96695.3</td></tr>
<tr><td>AHQ-7-7, 3600</td><td>R.HLDHVAALFPGDVDR.L</td><td>1662.83036</td><td>2</td><td>2.92E-05</td><td>0.82</td><td>2.95</td><td>-</td><td>880.0</td></tr>
<tr><td>AHQ-7-5, 5819</td><td>K.LLPLVSDEVFIR.D</td><td>1401.67552</td><td>2</td><td>1.19E-07</td><td>0.90</td><td>3.10</td><td>-</td><td>754.9</td></tr>
<tr><td colspan="2">gi|4506063|ref|NP_002725.1| protein kinase, cAMP-dependent, regulatory, type I, alpha; tissue-speci</td><td></td><td></td><td>1.22E-07</td><td>2.65</td><td>30.23</td><td>10.80</td><td>42981.4</td></tr>
<tr><td>AHQ-7-8, 5007 - 5080</td><td>R.LTVADALEPVQFEDGQK.I</td><td>1861.04222</td><td>2</td><td>7.00E-05</td><td>0.84</td><td>3.85</td><td>-</td><td>488.2</td></tr>
<tr><td>AHQ-7-8, 3232</td><td>K.NVLFSHLDDNER.S</td><td>1459.54574</td><td>2</td><td>1.22E-07</td><td>0.84</td><td>3.46</td><td>-</td><td>725.9</td></tr>
<tr><td>AHQ-7-7, 2414</td><td>R.RSENEEFVEVGR.L</td><td>1451.52361</td><td>2</td><td>3.27E-06</td><td>0.97</td><td>4.53</td><td>-</td><td>2204.6</td></tr>
<tr><td colspan="2">gi|4504557|ref|NP_000864.1| intercellular adhesion molecule 2 precursor [Homo sapiens]</td><td></td><td></td><td>1.25E-07</td><td>0.88</td><td>10.21</td><td>5.80</td><td>30653.1</td></tr>
<tr><td>AHQ-7-7, 6872</td><td>R.VPTVEPLDSLTLFLFR.G</td><td>1848.17455</td><td>2</td><td>1.25E-07</td><td>0.88</td><td>4.10</td><td>-</td><td>484.3</td></tr>
<tr><td colspan="2">gi|4557801|ref|NP_000261.1| purine nucleoside phosphorylase [Homo sapiens]</td><td></td><td></td><td>1.36E-07</td><td>2.84</td><td>30.29</td><td>18.70</td><td>32147.7</td></tr>
<tr><td>AHQ-7-13-, 3997</td><td>K.HRPQVAIICGSGLGGLTDK.L</td><td>1981.26589</td><td>3</td><td>4.82E-07</td><td>0.98</td><td>5.66</td><td>-</td><td>4087.7</td></tr>
<tr><td>AHQ-7-9, 3690 - 3697</td><td>K.HRPQVAIICGSGLGGLTDK.L</td><td>1981.26589</td><td>3</td><td>1.36E-07</td><td>0.98</td><td>5.83</td><td>-</td><td>3363.0</td></tr>
<tr><td>AHQ-7-9, 6172</td><td>K.LEQFVSILMASIPLPDK.A</td><td>1902.28716</td><td>2</td><td>8.33E-05</td><td>0.92</td><td>4.25</td><td>-</td><td>699.9</td></tr>
<tr><td>AHQ-7-9, 3873 - 3876</td><td>K.LGADAVGM*STVPEVIVAR.H</td><td>1802.08606</td><td>2</td><td>1.41E-06</td><td>0.94</td><td>4.07</td><td>-</td><td>1085.8</td></tr>
<tr><td colspan="2">gi|4507789|ref|NP_003338.1| ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]</td><td></td><td></td><td>1.38E-07</td><td>0.92</td><td>10.19</td><td>9.70</td><td>17861.5</td></tr>
<tr><td>AHQ-7-12, 4956</td><td>R.IEINFPAEYPFKPPK.I</td><td>1791.08155</td><td>3</td><td>1.38E-07</td><td>0.92</td><td>3.88</td><td>-</td><td>1226.8</td></tr>
<tr><td colspan="2">gi|4504077|ref|NP_000165.1| glycoprotein IX (platelet) [Homo sapiens]</td><td></td><td></td><td>1.41E-07</td><td>3.57</td><td>40.20</td><td>27.10</td><td>19046.0</td></tr>
<tr><td>AHQ-7-11, 4018</td><td>R.ALETM*GLWVDCR.G</td><td>1468.68075</td><td>2</td><td>2.69E-04</td><td>0.88</td><td>3.67</td><td>-</td><td>785.6</td></tr>
<tr><td>AHQ-7-11, 2698</td><td>R.CASPSLAAHGPLGR.L</td><td>1395.56962</td><td>2</td><td>4.73E-07</td><td>0.88</td><td>2.98</td><td>-</td><td>1012.9</td></tr>
<tr><td>AHQ-7-11, 3398</td><td>R.GHGLTALPALPAR.T</td><td>1274.49706</td><td>3</td><td>3.17E-05</td><td>0.92</td><td>3.91</td><td>-</td><td>1235.8</td></tr>
<tr><td>AHQ-7-11, 3392</td><td>R.GHGLTALPALPAR.T</td><td>1274.49706</td><td>2</td><td>6.51E-05</td><td>0.91</td><td>3.68</td><td>-</td><td>672.6</td></tr>
<tr><td>AHQ-7-12, 3459 - 3462</td><td>R.GHGLTALPALPAR.T</td><td>1274.49706</td><td>2</td><td>3.84E-04</td><td>0.94</td><td>3.93</td><td>-</td><td>857.1</td></tr>
<tr><td>AHQ-7-14-, 3297 - 3299</td><td>R.TPEALLQVR.C</td><td>1027.19957</td><td>2</td><td>1.41E-07</td><td>0.89</td><td>3.03</td><td>-</td><td>1059.0</td></tr>
<tr><td>AHQ-7-11, 3182</td><td>R.TPEALLQVR.C</td><td>1027.19957</td><td>2</td><td>2.43E-05</td><td>0.90</td><td>3.21</td><td>-</td><td>1074.9</td></tr>
<tr><td colspan="2">gi|29568111|ref|NP_006088.2| myosin, light polypeptide 9, regulatory; myosin regulatory light chain</td><td></td><td></td><td>1.68E-07</td><td>2.49</td><td>30.19</td><td>12.20</td><td>19827.1</td></tr>
<tr><td>AHQ-7-11, 3355</td><td>R.FTDEEVDEM*YR.E</td><td>1450.50949</td><td>2</td><td>8.31E-04</td><td>0.78</td><td>2.54</td><td>-</td><td>941.3</td></tr>
<tr><td>AHQ-7-11, 3347</td><td>R.FTDEEVDEMYR.E</td><td>1434.51009</td><td>2</td><td>1.68E-07</td><td>0.89</td><td>3.04</td><td>-</td><td>919.1</td></tr>
<tr><td>AHQ-7-11, 4035</td><td>K.GNFNYVEFTR.I</td><td>1247.34066</td><td>2</td><td>2.57E-05</td><td>0.82</td><td>3.04</td><td>-</td><td>762.5</td></tr>
<tr><td>AHQ-7-14-, 3897</td><td>K.GNFNYVEFTR.I</td><td>1247.34066</td><td>2</td><td>1.27E-04</td><td>0.62</td><td>2.52</td><td>-</td><td>680.6</td></tr>
<tr><td>AHQ-7-11, 3722 - 3726</td><td>K.GNFNYVEFTR.I</td><td>1247.34066</td><td>2</td><td>6.34E-04</td><td>0.94</td><td>3.87</td><td>-</td><td>1055.0</td></tr>
<tr><td colspan="2">gi|27597085|ref|NP_000357.3| tropomyosin 1 (alpha) [Homo sapiens]</td><td></td><td></td><td>1.77E-07</td><td>1.82</td><td>20.20</td><td>3.90</td><td>32865.7</td></tr>
<tr><td>AHQ-7-9, 3116 - 3126</td><td>R.KLVIIESDLER.A</td><td>1315.54103</td><td>2</td><td>8.05E-07</td><td>0.94</td><td>4.01</td><td>-</td><td>1352.8</td></tr>
</table>

AHQ-7-10, 3592	K.LVIIESDLER.A	1187.36811	2	1.77E-07	0.88	2.92	-	937.0
gi|30153852|ref|XP_171113.3| similar to Moesin (Membrane-organizing extension spike protein) [Homo				1.79E-07	0.97	10.23	9.30	15601.7
AHQ-7-6, 2049	R.RKPDTIEVQQMK.A	1473.72364	2	1.79E-07	0.97	4.52	-	1804.5
gi|4885183|ref|NP_005210.1| diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS				1.85E-07	5.25	60.25	6.80	138977.7
AHQ-7-3, 3316	R.DVQNFPAATDEKDKFVEK.M	2082.25588	2	1.33E-04	0.85	3.69	-	646.0
AHQ-7-3, 3629	R.EMVSQYLYTSK.A	1349.53461	2	1.15E-05	0.81	2.91	-	704.3
AHQ-7-3, 4591	R.LGLHQVLQDLR.E	1292.51238	2	1.31E-04	0.84	3.35	-	768.4
AHQ-7-3, 5079	K.LVAEDLSQDCFWTK.V	1713.88927	2	1.85E-07	0.91	3.76	-	828.9
AHQ-7-3, 5777 - 5779	K.TAQNLSIFLGSFR.M	1454.65537	2	4.65E-06	0.88	3.75	-	779.5
AHQ-7-3, 4797 - 4867	R.VQLNVFDEQGEEDSYDLK.G	2129.22304	2	1.95E-05	0.97	4.91	-	1487.7
gi|5803225|ref|NP_006752.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon poly				1.86E-07	0.97	10.24	7.50	29173.7
AHQ-7-10, 6040	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	2.05E-07	0.94	4.14	-	1169.6
AHQ-7-13, 6231 - 6289	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	2.88E-06	0.84	3.88	-	596.8
AHQ-7-14-, 6277	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	1.86E-07	0.97	4.77	-	1500.2
AHQ-7-9, 5925 - 5985	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	1.75E-04	0.94	4.15	-	1070.7
gi|9945439|ref|NP_002679.2| peanut-like 1; septin HCDCREL-1 [Homo sapiens]				1.88E-07	0.89	10.17	3.30	42776.7
AHQ-7-8, 2892 - 2970	K.DVTCDVHYENYR.A	1572.63777	2	1.88E-07	0.89	3.39	-	862.2
gi|18765729|ref|NP_003816.2| synaptosomal-associated protein 23 isoform SNAP23A; synaptosomal-assoc				1.95E-07	0.96	10.21	6.60	23353.9
AHQ-7-14, 5365	R.ILGLAIESQDAGIK.T	1428.65614	2	4.96E-04	0.94	3.53	-	1381.1
AHQ-7-14-, 4405 - 4482	R.ILGLAIESQDAGIK.T	1428.65614	2	3.22E-04	0.97	4.13	-	1972.6
AHQ-7-11, 4248	R.ILGLAIESQDAGIK.T	1428.65614	2	1.95E-07	0.96	3.62	-	1718.3
gi|4506925|ref|NP_003013.1| SH3 domain binding glutamic acid-rich protein like; SH3-binding domain				2.04E-07	3.62	40.30	58.80	12774.2
AHQ-7-13, 5974 - 6014	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	3.81E-04	0.82	3.15	-	629.2
AHQ-7-13-, 5717 - 5775	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	4.29E-07	0.94	4.76	-	970.9
AHQ-7-13-, 5865 - 5945	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	1.20E-04	0.57	2.88	-	419.7
AHQ-7-13, 5109	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.37E-05	0.81	3.86	-	594.5
AHQ-7-13, 4882 - 4938	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	3.34E-07	0.96	5.85	-	1286.9
AHQ-7-13-, 4795 - 4864	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.63E-05	0.96	5.80	-	1095.6
AHQ-7-13, 4993 - 5054	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.04E-07	0.96	5.94	-	1034.2
AHQ-7-13, 4158 - 4213	R.GDYDAFFEAR.E	1191.23073	2	3.33E-04	0.82	2.98	-	826.8
AHQ-7-13, 2666 - 2722	R.VYIASSSGSTAIK.K	1284.44065	2	1.96E-05	0.89	3.43	-	1391.0
AHQ-7-13-, 2459 - 2485	R.VYIASSSGSTAIK.K	1284.44065	2	2.11E-05	0.95	3.75	-	1823.7
gi|18104989|ref|NP_002822.2| protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t				2.13E-07	4.88	60.23	15.50	67560.7
AHQ-7-6, 5829 - 5830	K.AGFWEEFESLQK.Q	1471.59489	2	8.16E-07	0.96	4.66	-	1396.4
AHQ-7-6, 4911	R.DLSGLDAETLLK.G	1275.43053	2	2.27E-07	0.93	3.55	-	1203.0
AHQ-7-6, 6458 - 6490	R.ESLSQPGDFVLSVLSDQPK.A	2047.25144	2	7.33E-04	0.69	3.48	-	320.5
AHQ-7-6, 4058	R.IQNSGDFYDLYGGEK.F	1706.79040	2	8.34E-07	0.86	3.62	-	652.6
AHQ-7-6, 4450	R.TLQVSPLDNGDLIR.E	1541.73134	2	2.70E-05	0.67	2.83	-	611.6
AHQ-7-6, 6694	R.YTVGGLETFDSLTDLVEHFK.K	2272.49536	3	2.13E-07	0.78	3.45	-	523.5
gi|24307955|ref|NP_055191.1| p53 inducible protein [Homo sapiens]				2.21E-07	1.61	20.14	2.00	145660.2
AHQ-7-3, 3251	R.AVGPSSTQLYM*VR.T	1425.63581	2	5.32E-06	0.68	2.72	-	639.4
AHQ-7-3, 4857	K.YAPLHLVPLIER.L	1421.71166	2	2.21E-07	0.93	2.77	-	1493.2
gi|4557032|ref|NP_002291.1| lactate dehydrogenase B [Homo sapiens]				2.23E-07	5.83	70.28	21.90	36638.3
AHQ-7-9, 4432	K.GEMMDLQHGSLFLQTPK.I	1933.24171	2	1.79E-06	0.91	3.75	-	994.5
AHQ-7-9, 6190	K.GYTNWAIGLSVADLIESM*LK.N	2198.52454	2	1.48E-04	0.70	2.69	-	781.9
AHQ-7-13-, 2601	K.IVVVTAGVR.Q	914.12760	2	3.26E-05	0.85	3.09	-	772.1
AHQ-7-13-, 3407	K.LIAPVAEEEATVPNNK.I	1695.89534	2	4.49E-04	0.85	3.32	-	694.4
AHQ-7-9, 2148 - 2149	K.LKDDEVAQLK.K	1159.31477	2	5.58E-05	0.74	3.13	-	524.9
AHQ-7-11, 6130	K.SLADELALVDVLEDK.L	1630.81843	2	1.95E-04	0.91	3.57	-	1076.5
AHQ-7-13-, 6283	K.SLADELALVDVLEDK.L	1630.81843	2	2.23E-07	0.92	3.67	-	1061.7
AHQ-7-14-, 6265	K.SLADELALVDVLEDK.L	1630.81843	2	1.13E-05	0.96	4.53	-	1534.1
AHQ-7-13, 6285 - 6286	K.SLADELALVDVLEDK.L	1630.81843	2	4.09E-07	0.98	5.55	-	1968.0
AHQ-7-14-, 6350	K.SLADELALVDVLEDKLK.G	1872.14959	2	8.22E-06	0.86	3.37	-	879.4
gi|5803011|ref|NP_001966.1| enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron				2.25E-07	0.87	10.19	3.70	47268.3
AHQ-7-8, 6375	R.YITGDQLGALYQDFVR.D	1860.05915	2	2.25E-07	0.87	3.73	-	872.5
gi|17986283|ref|NP_006000.2| tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu				2.28E-07	0.93	10.22	3.30	50135.3
AHQ-7-7, 5497	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.33E-05	0.74	3.02	-	528.5
AHQ-7-7, 5588	R.AVFVDLEPTVIDEVR.T	1702.92947	2	2.28E-07	0.93	4.37	-	849.4
AHQ-7-13, 5494 - 5502	R.AVFVDLEPTVIDEVR.T	1702.92947	2	7.75E-07	0.89	4.28	-	651.4
AHQ-7-1, 5623	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.98E-04	0.83	3.58	-	621.2
gi|29788766|ref|NP_064424.2| tubulin, beta polypeptide 4, member Q [Homo sapiens]				2.33E-07	2.64	30.32	11.10	48377.2
AHQ-7-14-, 4489	R.AVLVDLEPGTMDSVR.S	1602.83495	2	2.33E-07	0.85	3.65	-	542.9
AHQ-7-7, 3840 - 3842	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	3.48E-04	0.82	3.57	-	467.9
AHQ-7-7, 5744	R.KEAESCDCLQGFQLTHSLGGGTGSGMGTLLLSK.I	3443.82841	3	5.58E-05	0.97	6.35	-	1669.5
gi|4505735|ref|NP_002611.1| platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H				2.35E-07	1.93	20.24	25.00	11552.6
AHQ-7-14-, 3809	R.AEAEEDGDLQCLCVK.T	1739.86036	2	2.35E-07	0.97	4.82	-	1779.9
AHQ-7-14-, 3702	R.AEAEEDGDLQCLCVK.T	1739.86036	2	3.83E-05	0.91	3.78	-	793.3
AHQ-7-14-, 5950	K.ICLDLQALLYK.K	1351.63656	2	8.64E-07	0.96	4.13	-	1318.1
gi|4507949|ref|NP_003395.1| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,				2.38E-07	3.51	40.23	27.60	28082.2
AHQ-7-10, 6247	K.IEAELQDICNDVLELLDK.Y	2132.37471	2	1.65E-06	0.86	4.52	-	528.0
AHQ-7-10, 3836	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	3.20E-05	0.75	3.38	-	533.1
AHQ-7-10, 6148 - 6199	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	3.38E-05	0.71	3.36	-	410.4
AHQ-7-10, 6017 - 6019	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	5.67E-06	0.96	4.68	-	1190.6
AHQ-7-13-, 6279	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	1.48E-04	0.79	3.28	-	781.3
AHQ-7-14-, 6258	K.TAFDEAIAELDTLNEESYK.D	2160.27705	2	1.13E-05	0.95	4.07	-	1474.2
AHQ-7-10, 2819 - 2877	K.YLIPNATQPESK.V	1361.52512	2	2.38E-07	0.94	4.31	-	845.6
gi|4506005|ref|NP_002700.1| protein phosphatase 1, catalytic subunit, beta isoform [Homo sapiens] [				2.45E-07	2.78	30.25	15.00	37186.6
AHQ-7-9, 3688	R.AHQVVEDGYEFFAK.R	1640.77679	2	2.17E-05	0.92	3.74	-	1016.2
AHQ-7-9, 6110	R.EIFLSQPILLELEAPLK.I	1954.33857	2	2.45E-07	0.94	4.92	-	632.9
AHQ-7-14-, 6385	R.EIFLSQPILLELEAPLK.I	1954.33857	2	3.09E-04	0.80	3.07	-	571.9
AHQ-7-9, 6009 - 6065	K.TFTDCFNCLPIAAIVDEK.I	2117.38502	2	2.07E-06	0.92	4.13	-	718.1
gi|27480842|ref|XP_208238.1| similar to bA92K2.2 (similar to ubiquitin) [Homo sapiens]				2.51E-07	0.91	10.17	8.30	17966.9
AHQ-7-14-, 2153 - 2211	K.IQDKEGIPPDQQR.L	1524.66087	2	4.41E-04	0.86	3.43	-	737.1
AHQ-7-14-, 1991 - 2062	K.IQDKEGIPPDQQR.L	1524.66087	2	2.51E-07	0.91	3.48	-	910.8
gi|29731857|ref|XP_293042.1| similar to ribosomal protein S12; 40S ribosomal protein S12 [Homo sapi				2.77E-07	0.96	10.28	8.90	19543.6
AHQ-7-13-, 4473	K.LVEALCAEHQINLIK.V	1753.05645	2	2.77E-07	0.96	5.56	-	1368.0
gi|4557471|ref|NP_001274.1| adaptor-related protein complex 1, sigma 1 subunit isoform 1; clathrin-				2.98E-07	0.92	10.19	10.10	18732.9
AHQ-7-12, 3503	K.AIEQADLLQEEDESPR.S	1843.92692	2	2.98E-07	0.92	3.78	-	1402.5
gi|19923483|ref|NP_057406.2| GTPase Rab14 [Homo sapiens]				2.99E-07	2.23	30.19	20.90	23896.8
AHQ-7-10, 4593 - 4668	R.NLTNPNTVIILIGNK.A	1624.90662	2	1.50E-04	0.60	2.95	-	527.4
AHQ-7-14-, 5454	K.QFAEENGLLFLEASAK.T	1767.96002	2	2.99E-07	0.88	3.89	-	623.2
AHQ-7-10, 4227	K.TGENVEDAFLEAAK.K	1494.58517	2	7.86E-05	0.75	3.21	-	466.8
gi|4826657|ref|NP_004333.1| caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]				3.04E-07	1.78	20.22	5.80	62662.9
AHQ-7-13-, 2793 - 2871	R.LEQYTSAIEGTK.S	1340.46107	2	2.87E-04	0.86	2.98	-	1198.0
AHQ-7-10, 3541 - 3545	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	3.04E-07	0.92	4.40	-	886.3
AHQ-7-6, 3735	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	7.49E-07	0.93	4.05	-	912.2
gi|5031573|ref|NP_005712.1| ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye				3.32E-07	7.05	80.27	27.00	47370.9
AHQ-7-7, 4888	R.AEPEDHYFLLTEPPLNTPENR.E	2483.67423	2	1.25E-04	0.73	2.69	-	563.9
AHQ-7-7, 6854	R.DITYFIQQLLR.D	1410.64250	2	6.17E-04	0.95	4.09	-	1262.4
AHQ-7-7, 2998 - 3074	R.DREVGIPPEQSLETAK.A	1769.93431	2	1.13E-06	0.97	5.43	-	919.7
AHQ-7-7, 3477	K.DYEEIGPSICR.H	1340.44122	2	3.32E-07	0.87	2.94	-	886.8
AHQ-7-13-, 3488	K.DYEEIGPSICR.H	1340.44122	2	1.01E-04	0.84	2.74	-	1050.1
AHQ-7-7, 3949	R.FMEQVIFK.Y	1042.27611	2	2.24E-04	0.81	2.74	-	643.7
AHQ-7-7, 4358 - 4362	R.HGIVEDWDLMER.F	1500.66127	2	2.25E-05	0.95	4.10	-	1292.7
AHQ-7-7, 6168	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	6.77E-05	0.88	3.85	-	697.4
AHQ-7-7, 6037 - 6065	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	4.06E-04	0.46	3.22	-	326.4
AHQ-7-13-, 5819	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	7.45E-04	0.31	2.81	-	324.2

AHQ-7-7, 3588	R.LPACVVDCGTGYTK.L	1543.74421	2	1.93E-04	0.90	3.57	-	908.2
gi|18543899|ref|XP_086916.1|	similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic			3.33E-07	0.95	10.20	8.00	21265.8
AHQ-7-11, 3338	K.NRPTSISWDGLDSGK.L	1633.74419	2	3.33E-07	0.95	3.99	-	1095.3
gi|30147857|ref|XP_293007.2|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			3.33E-07	0.84	10.18	5.90	20789.8
AHQ-7-14, 4222	K.KITIADCGQLQ	1248.43160	2	3.34E-04	0.50	2.59	-	694.0
AHQ-7-14-, 3353	K.KITIADCGQLQ	1248.43160	2	3.33E-07	0.84	3.59	-	1050.4
AHQ-7-12, 3274 - 3350	K.KITIADCGQLQ	1248.43160	2	5.30E-05	0.73	3.37	-	789.9
gi|4505329|ref|NP_003818.1|	N-ethylmaleimide-sensitive factor attachment protein, alpha; alpha-SNAP			3.37E-07	0.94	10.23	6.10	33246.6
AHQ-7-9, 3105	K.LLEAHEEQNVDSYTESVK.E	2092.20594	2	3.37E-07	0.94	4.52	-	1254.8
gi|8922673|ref|NP_060692.1|	parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]			3.45E-07	0.95	10.22	3.50	42243.4
AHQ-7-9, 4216 - 4270	R.DAFDTLFDHAPDK.L	1492.57096	2	3.45E-07	0.95	4.34	-	1124.3
gi|4503609|ref|NP_001976.1|	electron-transfer-flavoprotein, beta polypeptide; electron-transferring			3.92E-07	0.70	10.14	6.70	27843.4
AHQ-7-10, 3555	K.EVIAVSCGPAQCQETIR.T	1921.14254	2	3.92E-07	0.70	2.88	-	528.7
gi|18702323|ref|NP_570967.1|	dynein, cytoplasmic, light polypeptide 2B; dynein light chain 2B; bith			4.17E-07	0.76	10.13	12.50	10854.6
AHQ-7-14-, 4841	R.DIDPQNDLTFLR.I	1447.57487	2	4.17E-07	0.76	2.60	-	555.2
gi|27500008|ref|XP_208872.1|	similar to tropomyosin 3 [Homo sapiens]			4.19E-07	1.93	20.29	12.10	28954.4
AHQ-7-9, 3664	R.ALKDEEKMELQELQLK.E	1946.25520	2	4.19E-07	0.95	4.74	-	1381.7
AHQ-7-9, 2346 - 2356	R.ARKQAEAEVASLNR.R	1543.71055	2	2.74E-06	0.98	5.77	-	2785.3
gi|4503971|ref|NP_001484.1|	GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r			4.26E-07	3.34	40.27	17.40	50582.4
AHQ-7-7, 4292	R.FQLLEGPPESMGR.G	1461.66818	2	6.69E-07	0.91	3.82	-	939.6
AHQ-7-7, 5166	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	4.26E-07	0.91	3.78	-	826.9
AHQ-7-7, 5173	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	3.89E-06	0.95	5.31	-	721.2
AHQ-7-7, 4170	R.TDDYLDQPCLETVNR.I	1840.94632	2	3.71E-04	0.85	4.38	-	387.9
AHQ-7-6, 6574	K.YIAIASTTVETTDPEKEVEPALELLEPIDQK.F	3444.82460	3	4.27E-05	0.68	3.09	-	718.7
gi|30148644|ref|XP_293716.2|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			4.36E-07	0.92	10.18	1.20	105150.3
AHQ-7-5, 3675	R.TLTIVDTGIGM*TK.A	1366.60658	2	4.36E-07	0.92	3.29	-	1048.9
gi|21361456|ref|NP_055425.2|	alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph			4.47E-07	3.41	40.22	6.60	109437.2
AHQ-7-4, 4100 - 4101	R.DENSVELTMAEGPYK.I	1683.81855	2	1.16E-05	0.81	3.12	-	658.1
AHQ-7-4, 4897	R.FGAVWTGDNTAEWDHLK.I	1948.08335	2	4.47E-07	0.93	4.44	-	931.3
AHQ-7-4, 4592	R.LSFQHDPETSVLVLR.K	1741.96893	2	9.82E-06	0.71	3.13	-	416.1
AHQ-7-4, 3808	K.MMDYLQGSGETPQTDVR.W	1929.12196	2	3.38E-05	0.96	4.37	-	1562.0
gi|21614520|ref|NP_000393.2|	glucose-6-phosphate dehydrogenase [Homo sapiens]			4.57E-07	3.36	40.26	11.10	59257.4
AHQ-7-7, 3062	K.GYLDDPTVPR.G	1133.23587	2	4.73E-05	0.89	2.74	-	952.6
AHQ-7-7, 6549 - 6596	R.LFYLALPPTVYEAVTK.N	1826.16735	2	3.89E-05	0.66	2.51	-	345.2
AHQ-7-7, 5945	R.LILDVFCGSQMHFVR.S	1824.15987	2	5.25E-04	0.83	3.32	-	871.3
AHQ-7-7, 4333	R.LQFHDVAGDIFHQQCK.R	1945.14742	2	4.57E-07	0.98	5.14	-	1806.8
gi|4557797|ref|NP_000260.1|	non-metastatic cells 1 protein [Homo sapiens]			4.60E-07	2.40	30.21	23.70	17148.6
AHQ-7-12, 4015	K.DRPFFAGLVK.Y	1150.35439	2	3.04E-04	0.88	3.44	-	919.2
AHQ-7-12, 2228 - 2235	R.NIIHGSDSVESAEK.E	1486.56627	2	4.60E-07	0.71	4.28	-	470.8
AHQ-7-12, 3003 - 3058	R.TFIAIKPDGVQR.G	1345.57205	2	7.98E-04	0.81	3.21	-	736.0
gi|4502989|ref|NP_001856.1|	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor; hepa			4.74E-07	0.95	10.23	15.70	9395.9
AHQ-7-14-, 5137 - 5191	K.LFQEDDEIPLYLK.G	1623.82758	2	6.63E-04	0.92	4.01	-	1078.0
AHQ-7-14, 5924 - 5936	K.LFQEDDEIPLYLK.G	1623.82758	2	4.74E-07	0.95	4.66	-	1378.1
gi|5453898|ref|NP_006212.1|	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1; dod;			4.91E-07	0.92	10.17	11.70	18243.2
AHQ-7-12, 4724	R.TGEM*SGPVFTDSGIHIILR.T	2047.32128	3	4.91E-07	0.92	3.47	-	1778.8
gi|30150022|ref|XP_300862.1|	similar to beta-tubulin 4Q [Homo sapiens]			4.97E-07	5.31	60.20	22.20	33545.2
AHQ-7-7, 5969 - 6036	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	5.80E-05	0.90	4.06	-	1113.6
AHQ-7-7, 3441	R.FPGQLNADLR.K	1131.26634	2	3.40E-04	0.93	3.61	-	1051.5
AHQ-7-13, 3561 - 3609	R.FPGQLNADLR.K	1131.26634	2	6.22E-06	0.82	2.85	-	681.2
AHQ-7-9, 3132 - 3189	R.FPGQLNADLR.K	1131.26634	2	5.23E-06	0.77	2.95	-	739.1
AHQ-7-8, 3315 - 3375	R.FPGQLNADLR.K	1131.26634	2	2.98E-05	0.90	3.42	-	833.2
AHQ-7-7, 3292 - 3360	R.FPGQLNADLR.K	1131.26634	2	2.63E-05	0.84	3.01	-	726.7
AHQ-7-7, 3924	R.KLAVNMVPFPR.L	1272.58771	2	4.97E-07	0.94	3.83	-	1239.3
AHQ-7-7, 4380 - 4381	K.LAVNMVPFPR.L	1144.41480	2	3.61E-06	0.92	3.31	-	827.9
AHQ-7-11, 4275	K.LAVNMVPFPR.L	1144.41480	2	3.56E-05	0.87	3.23	-	700.4
AHQ-7-7, 3812	K.LAVNM*VPFPR.L	1160.41420	2	2.19E-05	0.94	3.61	-	1251.8
AHQ-7-13-, 4417	K.LAVNMVPFPR.L	1144.41480	2	5.46E-07	0.81	2.70	-	672.1
AHQ-7-7, 5668 - 5690	R.LHFFMPGFAPLTSR.G	1621.92962	2	6.93E-04	0.95	3.95	-	1010.6
gi|4506077|ref|NP_002734.1|	protein kinase C substrate 80K-H; glucosidase II, beta subunit; AGE-bin			5.36E-07	0.91	10.16	2.50	59296.0
AHQ-7-5, 3287	K.AQQEQELAADAFK.E	1449.54763	2	5.36E-07	0.91	3.17	-	1389.3
gi|4504489|ref|NP_000403.1|	histidine-rich glycoprotein precursor; histidine-proline rich glycoprot			5.42E-07	0.84	10.15	2.70	59578.0
AHQ-7-5, 6359 - 6426	K.DSPVLIDFFEDTER.Y	1683.79674	2	5.42E-07	0.84	3.02	-	937.3
gi|27436929|ref|NP_005518.2|	heat shock 70kDa protein 1-like; heat shock 70kD protein-like 1 [Homo			5.47E-07	0.94	10.18	2.20	70404.7
AHQ-7-6, 3286	K.AKIHDIVLVGGSTR.I	1466.71083	2	5.47E-07	0.94	3.66	-	1518.9
gi|11993943|ref|NP_055419.1|	Tax interaction protein 1 [Homo sapiens]			5.70E-07	0.77	10.14	13.70	13734.6
AHQ-7-13, 4191	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	5.70E-07	0.77	2.78	-	771.0
gi|13027638|ref|NP_006750.2|	UDP-glucose pyrophosphorylase 2; UTP-glucose-1-phosphate uridyltransfe			5.71E-07	1.11	20.17	7.50	56964.9
AHQ-7-7, 6293	R.NENTFLDLTVQQIEHLNK.T	2157.36913	2	2.33E-04	0.29	2.66	-	209.5
AHQ-7-7, 6678	K.TLDGGLNVIQLETAVGAAIK.S	1984.28316	2	5.71E-07	0.82	3.42	-	736.4
gi|4503327|ref|NP_000389.1|	cytochrome b5 reductase membrane-bound isoform; diaphorase (NADH) [Homo			5.91E-07	2.04	30.21	15.30	34234.6
AHQ-7-9, 4333 - 4402	K.DILLRPELEELR.N	1496.73370	2	2.98E-05	0.33	2.64	-	464.6
AHQ-7-9, 5489	R.FALPSPQHILGLPVGQHIYLSAR.I	2515.94007	3	5.91E-07	0.74	3.11	-	623.6
AHQ-7-9, 2853	R.GPSGLLVYQGK.G	1119.29547	2	8.38E-04	0.97	4.30	-	1797.2
gi|20536967|ref|XP_115812.1|	similar to Latent transforming growth factor beta binding protein 1L p			5.98E-07	0.89	10.18	12.00	13416.2
AHQ-7-1, 3535 - 3541	K.GISGEQSTEGSFPLR.Y	1565.66662	2	5.98E-07	0.89	3.53	-	961.7
gi|24234688|ref|NP_004125.3|	heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre			6.04E-07	1.66	20.19	4.40	73680.1
AHQ-7-6, 5759 - 5838	K.STNGDTFLGGEDFDQALLR.H	2057.16328	2	6.04E-07	0.75	3.88	-	321.7
AHQ-7-6, 3738	K.VQQTVQDLFGR.A	1291.43811	2	5.40E-04	0.91	3.54	-	1218.8
gi|5453603|ref|NP_006422.1|	chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c			6.11E-07	3.17	40.20	8.40	57487.9
AHQ-7-7, 3105	R.EALLSSAVDHGSDEVK.F	1657.76083	2	6.11E-07	0.67	2.69	-	847.7
AHQ-7-7, 5540	R.LALVTGGEIASTFDHPELVK.L	2098.38473	2	6.05E-04	0.91	4.03	-	974.1
AHQ-7-7, 6009	K.LGGSLADSYLDEGFLLDK.K	1914.10189	2	5.15E-04	0.77	3.14	-	604.1
AHQ-7-7, 3642	K.LIEEVMIGEDK.L	1276.48193	2	3.37E-05	0.82	3.02	-	730.0
gi|4826659|ref|NP_004921.1|	F-actin capping protein beta subunit; Cap Z [Homo sapiens]			6.13E-07	1.37	20.19	10.70	30628.5
AHQ-7-9, 3774	K.GCWDSIHVVEVQEK.S	1687.85505	2	6.13E-07	0.88	3.57	-	968.2
AHQ-7-10, 3864	K.GCWDSIHVVEVQEK.S	1687.85505	2	4.29E-04	0.86	3.47	-	921.1
AHQ-7-9, 3325	K.SKQEALKNDLVEALK.R	1686.93158	2	3.61E-04	0.50	2.57	-	770.2
gi|5453599|ref|NP_006127.1|	capping protein (actin filament) muscle Z-line, alpha 2; F-actin cappin			6.53E-07	0.61	10.18	5.20	32948.9
AHQ-7-13, 5205	K.FTITPSTTQVVGILK.I	1605.90007	2	6.53E-07	0.61	3.08	-	252.4
AHQ-7-9, 4790 - 4806	K.FTITPSTTQVVGILK.I	1605.90007	2	2.52E-04	0.70	2.82	-	399.4
gi|4557385|ref|NP_000055.1|	complement component 3 precursor; acylation-stimulating protein cleavag			6.59E-07	2.80	30.28	3.40	187162.3
AHQ-7-6, 5190	R.AYYENSPQQVFSTEFEVK.E	2167.31611	2	8.01E-05	0.89	4.11	-	706.0
AHQ-7-6, 5867	K.EYVLPSFEVIVEPTEK.F	1880.12704	2	5.36E-06	0.95	4.63	-	801.7
AHQ-7-6, 4525	R.VPVAVQGEDTVQSLTQGDGVAK.L	2199.40432	2	6.59E-07	0.96	5.51	-	954.9
gi|29736622|ref|XP_293924.1|	similar to cytoplasmic beta-actin [Homo sapiens]			6.84E-07	3.04	40.22	27.10	42002.9
AHQ-7-10, 4911	K.DLYANTVLSGGSTM*YPGIADR.M	2218.42957	2	7.27E-04	0.84	4.36	-	580.7
AHQ-7-14-, 4987 - 5063	K.DLYANTVLSGGSTM*YPGIADR.M	2218.42957	2	6.81E-05	0.84	4.23	-	686.4
AHQ-7-8, 6599 - 6608	R.FRCPEAIFQPSFLGIESSGIHETTFNSIMK.C	3446.89713	3	4.10E-04	0.66	3.00	-	444.0
AHQ-7-8, 6116	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	6.84E-07	0.89	4.35	-	949.2
AHQ-7-8, 4090	R.VAPDEHPILLTEAPLNPKINR.E	2338.69122	3	6.42E-04	0.66	3.28	-	746.6
gi|4758988|ref|NP_004152.1|	RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho			6.86E-07	2.63	30.20	25.40	22677.6
AHQ-7-11, 5704 - 5758	K.EFADSLGIPFLETSAK.N	1725.91990	2	6.86E-07	0.87	4.00	-	582.4
AHQ-7-11, 5526	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.82E-04	0.72	3.25	-	393.0
AHQ-7-14-, 5633	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.92E-05	0.92	3.76	-	1074.1
AHQ-7-11, 5306	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.78E-04	0.90	3.89	-	865.3
AHQ-7-11, 5422 - 5488	K.LLLIGDSGVGKSCLLLR.F	1816.19882	2	8.28E-05	0.83	3.80	-	596.8
gi|18491024|ref|NP_005691.2|	dipeptidylpeptidase III isoform 1; dipeptidylpeptidase III [Homo sapie			7.46E-07	0.93	10.20	2.70	82588.6

AHQ-7-6, 6427	R.LEGSDVQLLEYEASAAGLIR.S	2135.36023	2	7.46E-07	0.93	4.07	-	1067.4
gi|4503531|ref|NP_001958.1|	eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens] [			7.51E-07	0.93	10.20	3.90	46393.9
AHQ-7-8, 3554	R.GIYAYGFEKPSAIQQR.A	1829.04828	2	7.51E-07	0.93	4.05	-	810.5
gi|21464101|ref|NP_036611.2|	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein			7.73E-07	2.31	30.22	17.40	28302.4
AHQ-7-10, 2941	K.NVTELNEPLSNEER.N	1644.72215	2	7.73E-07	0.93	4.00	-	826.1
AHQ-7-11, 3024	K.NVTELNEPLSNEER.N	1644.72215	2	6.88E-04	0.51	2.81	-	391.3
AHQ-7-14-, 3109	K.NVTELNEPLSNEER.N	1644.72215	2	1.88E-05	0.91	4.37	-	800.8
AHQ-7-10, 5907 - 5928	K.TAFDDAIAELDTLNEDSYK.D	2132.22370	2	2.13E-06	0.48	2.93	-	476.0
AHQ-7-10, 2279	R.YLAEVATGEK.R	1081.20087	2	9.01E-07	0.90	3.49	-	870.0
gi|23110942|ref|NP_002781.2|	proteasome alpha 5 subunit; proteasome component 5; macropain subunit			8.60E-07	0.97	10.23	5.80	26410.9
AHQ-7-10, 5633	R.PFGVALLFGGVDEK.G	1449.67550	2	8.60E-07	0.97	4.63	-	1752.8
gi|29727204|ref|XP_290872.1|	similar to Pyruvate kinase, M2 isozyme [Homo sapiens]			8.83E-07	1.86	20.23	22.10	16297.7
AHQ-7-7, 3801 - 3874	K.CCSGAIIVLTK.S	1224.47324	2	1.39E-04	0.95	4.02	-	1070.8
AHQ-7-7, 5268	K.KGDVVIVLTGWRPGSGFTNTMR.V	2392.76561	3	8.83E-07	0.91	4.61	-	987.3
gi|4757826|ref|NP_004039.1|	beta-2-microglobulin [Homo sapiens]			8.97E-07	1.82	20.22	21.80	13714.5
AHQ-7-14-, 6285	K.SNFLNCYVSGFHPSDIEVDLLK.N	2556.83155	3	8.97E-07	0.90	4.25	-	771.6
AHQ-7-14-, 6066	K.SNFLNCYVSGFHPSDIEVDLLKNGER.I	3013.28710	3	2.91E-06	0.91	4.49	-	1025.2
gi|5803227|ref|NP_006817.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype			9.19E-07	2.45	30.22	18.40	27764.1
AHQ-7-10, 2243	K.AVTEQGAELSNEER.N	1533.57979	2	1.33E-05	0.78	2.86	-	784.0
AHQ-7-10, 6007	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	1.17E-05	0.91	4.35	-	754.7
AHQ-7-14-, 6255	K.TAFDEAIAELDTLNEDSYK.D	2146.25037	2	9.19E-07	0.87	3.65	-	673.6
AHQ-7-10, 2777	K.YLIANATNPESK.V	1321.46099	2	2.03E-04	0.92	3.27	-	1361.3
AHQ-7-10, 2695	K.YLIANATNPESK.V	1321.46099	2	1.57E-04	0.80	2.95	-	995.4
gi|30158852|ref|XP_301583.1|	similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa			9.34E-07	0.77	10.16	6.50	19197.0
AHQ-7-6, 3131	K.IWHHTFYNKLR.V	1515.74533	2	1.51E-06	0.55	2.63	-	668.6
AHQ-7-9, 2848 - 2913	K.IWHHTFYNKLR.V	1515.74533	2	9.34E-07	0.77	3.23	-	719.4
AHQ-7-3, 3256	K.IWHHTFYNKLR.V	1515.74533	2	2.95E-05	0.56	3.00	-	600.3
gi|5803135|ref|NP_006852.1|	RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind			9.42E-07	0.69	10.18	5.50	23025.1
AHQ-7-11, 3626	K.LLIIGDSGVGK.S	1072.28025	1	9.42E-07	0.69	2.62	-	559.9
AHQ-7-11, 3614	K.LLIIGDSGVGK.S	1072.28025	2	9.73E-07	0.94	3.61	-	1172.7
gi|9966867|ref|NP_065123.1|	eIF-5A2 protein; eIF5AII [Homo sapiens]			9.89E-07	1.84	20.25	19.60	16793.1
AHQ-7-12, 3590	K.KYEDICPSTHNMDVPNIK.R	2163.41723	3	9.41E-04	0.97	5.07	-	2133.5
AHQ-7-12, 3586	K.KYEDICPSTHNMDVPNIK.R	2163.41723	2	2.40E-04	0.89	3.54	-	945.7
AHQ-7-12, 4611 - 4618	K.VHLVGIDIFTGK.K	1299.54329	2	9.89E-07	0.95	4.15	-	1178.6
gi|22059949|ref|XP_114617.2|	similar to tubulin, beta 5 [Homo sapiens]			9.90E-07	1.74	20.29	18.80	22810.8
AHQ-7-7, 5220	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	1.94E-05	0.95	5.74	-	1210.3
AHQ-7-7, 5318	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	4.71E-04	0.90	4.63	-	884.8
AHQ-7-7, 2706 - 2709	R.ISVYYNEATGGK.Y	1302.41453	2	1.03E-05	0.80	3.10	-	788.3
AHQ-7-13, 2950 - 3005	R.ISVYYNEATGGK.Y	1302.41453	2	9.90E-07	0.79	2.90	-	676.3
AHQ-7-13-, 2761 - 2836	R.ISVYYNEATGGK.Y	1302.41453	2	2.87E-05	0.90	3.52	-	982.3
AHQ-7-7, 2705	R.ISVYYNEATGGK.Y	1302.41453	1	6.69E-04	0.21	2.21	-	319.7
gi|29826319|ref|NP_001110.2|	adducin 1 (alpha) isoform a; erythrocyte adducin alpha subunit [Homo s			1.05E-06	0.92	10.22	2.40	80954.7
AHQ-7-7, 4502	R.TLASAGGPDNLVLLNPEK.Y	1810.04158	2	1.05E-06	0.92	4.44	-	918.0
gi|4758032|ref|NP_004757.1|	coatomer protein complex, subunit beta 2 (beta prime); coatomer binding			1.07E-06	0.90	10.21	2.10	102486.5
AHQ-7-5, 6136	K.AAESLADPTEYENLFPGLK.E	2066.25322	2	1.07E-06	0.90	4.28	-	629.1
gi|7019375|ref|NP_037373.1|	formin homology 2 domain containing 1; FH1/FH2 domain-containing protei			1.07E-06	1.88	20.20	2.60	126496.5
AHQ-7-14-, 5858	K.SGLGDDLVQALGLSK.G	1473.65377	2	1.07E-06	0.97	3.53	-	2227.0
AHQ-7-6, 5979	K.VDFEQLTENLGQLER.R	1791.93998	2	1.18E-05	0.91	3.92	-	1111.8
gi|5803181|ref|NP_006810.1|	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo			1.07E-06	1.80	20.21	5.90	62638.9
AHQ-7-6, 6195 - 6229	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	4.94E-06	0.93	4.16	-	784.6
AHQ-7-6, 4503	R.LAYINPDLALEEK.N	1489.69480	2	1.07E-06	0.87	3.46	-	766.2
gi|4507195|ref|NP_003119.1|	spectrin, beta, non-erythrocytic 1; Spectrin, beta, nonerythrocytic-1 (			1.08E-06	1.64	20.21	1.50	274628.5
AHQ-7-1, 5681	R.LVSQDNFGFDLPAVEAATK.K	2023.23158	2	1.31E-04	0.70	3.12	-	386.2
AHQ-7-1, 4108	R.SQNIVTDSSSLSAEAIR.Q	1778.89960	2	1.08E-06	0.94	4.12	-	1280.3
gi|30148978|ref|XP_291520.2|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			1.09E-06	0.72	10.16	2.20	68413.1
AHQ-7-11, 4714	R.DWSHYFKTIKDLR.A	1709.92863	2	1.09E-06	0.72	3.21	-	696.2
AHQ-7-11, 4568 - 4570	R.DWSHYFKTIKDLR.A	1709.92863	2	1.01E-04	0.66	3.15	-	588.1
gi|4505093|ref|NP_000889.1|	monoamine oxidase B [Homo sapiens]			1.20E-06	2.74	30.20	8.80	58762.6
AHQ-7-7, 4193	K.LLHDSGLNVVVLEAR.D	1635.88950	2	1.20E-06	0.96	4.04	-	1481.2
AHQ-7-7, 4478	K.VLGSLEALEPVHYEEK.N	1814.02869	2	8.18E-06	0.84	3.54	-	720.9
AHQ-7-7, 3282	K.YVDLGGSYVGPTQNR.I	1626.75165	2	7.23E-06	0.93	4.09	-	965.7
gi|4502171|ref|NP_000476.1|	adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho			1.20E-06	1.89	20.24	16.70	19607.6
AHQ-7-11, 6330 - 6331	R.GFLFGPSLAQELGLGCVLIR.K	2149.54130	2	4.91E-06	0.96	4.80	-	1416.7
AHQ-7-11, 3504	R.IDYIAGLDSR.G	1123.24098	2	1.20E-06	0.93	3.35	-	1377.6
gi|10835121|ref|NP_000289.1|	pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H			1.20E-06	0.67	10.13	1.90	61829.8
AHQ-7-7, 3604	R.GDLGIEIPAEK.V	1142.28420	1	1.20E-06	0.67	2.65	-	586.2
gi|22060072|ref|XP_088293.2|	similar to cytochrome c [Homo sapiens]			1.20E-06	1.76	20.16	18.10	11887.8
AHQ-7-13, 4339	R.ADLIAYLK.K	907.08869	2	8.18E-06	0.87	2.73	-	972.1
AHQ-7-13-, 3612 - 3632	K.TGPNLHGLFGR.K	1169.31780	2	1.20E-06	0.88	3.14	-	729.4
gi|24431935|ref|NP_065393.1|	reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sap			1.21E-06	0.86	10.16	1.10	129930.3
AHQ-7-1, 3405	R.GPLPAAPPVAPER.Q	1272.47793	2	1.21E-06	0.86	3.17	-	732.2
gi|20543399|ref|XP_116396.1|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			1.22E-06	0.79	10.13	5.00	19852.7
AHQ-7-13, 4547	R.VSFKLFADK.F	1055.25138	2	1.22E-06	0.79	2.55	-	989.7
AHQ-7-12, 4251 - 4306	R.VSFKLFADK.F	1055.25138	1	2.12E-04	0.78	2.52	-	1202.2
gi|18201911|ref|NP_000629.2|	vitronectin precursor; serum spreading factor; somatomedin B; compleme			1.23E-06	0.93	10.22	3.10	54335.4
AHQ-7-14-, 5399 - 5453	R.SIAQYWLGCPAPGHL	1671.90045	2	1.23E-06	0.93	4.45	-	739.6
AHQ-7-13-, 5401 - 5460	R.SIAQYWLGCPAPGHL	1671.90045	2	2.97E-04	0.67	2.79	-	587.9
gi|30154839|ref|XP_301540.1|	similar to keratin 8; cytokeratin 8; keratin, type II cytoskeletal 8 [			1.28E-06	0.78	10.17	3.40	39331.0
AHQ-7-7, 4529	K.SLNNKFASFIDK.V	1384.56191	2	2.29E-06	0.89	3.48	-	1075.9
AHQ-7-14-, 4534 - 4581	K.SLNNKFASFIDK.V	1384.56191	2	1.28E-06	0.78	2.94	-	687.8
AHQ-7-2, 4800	K.SLNNKFASFIDK.V	1384.56191	2	4.10E-04	0.73	2.92	-	691.9
gi|4759044|ref|NP_004841.1|	Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]			1.29E-06	1.76	20.23	2.10	160883.4
AHQ-7-3, 5827	K.ELQDQLEAEQYFSTLYK.T	2106.27421	2	1.29E-06	0.95	4.51	-	1136.2
AHQ-7-3, 3449	R.ENLLLSDSPSCR.E	1392.51767	2	2.65E-04	0.81	3.22	-	735.4
gi|11056061|ref|NP_066932.1|	thymosin, beta 4 [Homo sapiens]			1.29E-06	0.74	10.15	29.50	5052.6
AHQ-7-14-, 2509	K.NPLPSKETIEQEK.Q	1513.67476	2	1.29E-06	0.74	3.05	-	462.4
gi|4757952|ref|NP_001782.1|	cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p			1.30E-06	1.72	20.26	14.10	21258.5
AHQ-7-11, 6174 - 6187	K.NVFDEAILAALEPPEPK.K	1854.09282	3	1.30E-06	0.95	5.17	-	1047.7
AHQ-7-11, 2578 - 2636	K.YVECSALTQK.G	1200.34381	2	1.76E-04	0.77	3.24	-	492.6
gi|4504073|ref|NP_000398.1|	glycoprotein Ib beta polypeptide precursor [Homo sapiens]			1.32E-06	2.45	30.19	15.50	21717.6
AHQ-7-1, 4788	R.LLPYLAEDELR.A	1332.52691	2	7.41E-06	0.88	3.36	-	670.4
AHQ-7-3, 4749	R.LLPYLAEDELR.A	1332.52691	2	4.48E-06	0.79	2.70	-	438.3
AHQ-7-4, 4788	R.LLPYLAEDELR.A	1332.52691	2	1.82E-05	0.85	3.15	-	575.0
AHQ-7-5, 4708	R.LLPYLAEDELR.A	1332.52691	2	2.10E-04	0.83	2.53	-	600.2
AHQ-7-7, 4572	R.LLPYLAEDELR.A	1332.52691	2	1.99E-06	0.84	2.59	-	518.9
AHQ-7-8, 4616	R.LLPYLAEDELR.A	1332.52691	2	6.93E-06	0.67	2.72	-	412.5
AHQ-7-13-, 4560 - 4565	R.LLPYLAEDELR.A	1332.52691	2	4.24E-06	0.90	3.23	-	695.6
AHQ-7-13-, 4577	R.LLPYLAEDELR.A	1332.52691	1	6.05E-04	0.18	2.17	-	219.8
AHQ-7-10, 4288 - 4309	R.LLPYLAEDELR.A	1332.52691	2	1.32E-06	0.65	2.82	-	519.9
AHQ-7-13, 4670 - 4678	R.LLPYLAEDELR.A	1332.52691	2	4.02E-06	0.87	3.35	-	429.7
AHQ-7-11, 4386 - 4448	R.LLPYLAEDELR.A	1332.52691	2	2.13E-05	0.84	3.11	-	510.8
AHQ-7-11, 4408	R.LLPYLAEDELR.A	1332.52691	1	2.83E-04	0.60	3.06	-	312.1
AHQ-7-10, 4016	R.LSLTDPLVAER.A	1214.39356	2	8.42E-06	0.83	3.14	-	694.2
AHQ-7-11, 4088 - 4090	R.LSLTDPLVAER.A	1214.39356	2	1.59E-06	0.95	3.79	-	1381.4
AHQ-7-10, 2352	R.TAHLGANPWR.C	1123.24913	2	1.27E-04	0.85	3.13	-	710.3
gi|22043610|ref|XP_171081.1|	similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1; rh			1.33E-06	3.17	40.23	24.00	21543.1
AHQ-7-11, 2850 - 2902	R.HHCPNTPIILVGTK.L	1588.85612	2	3.65E-04	0.74	2.92	-	551.8

AHQ-7-11, 3458	K.KLTPITYPQGLAM*AK.E	1648.99156	2	1.36E-04	0.79	2.86	-	581.8
AHQ-7-11, 3762	K.LTPITYPQGLAM*AK.E	1520.81864	2	6.42E-04	0.67	2.76	-	259.1
AHQ-7-11, 4571	K.PVNLGLWDTAGQEDYDR.L	1950.05441	2	1.33E-06	0.97	4.58	-	1780.2
gi|4506045|ref|NP_002718.1| proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p				1.33E-06	1.65	20.17	8.20	17623.6
AHQ-7-2, 4768	K.GPMFELLPGESNK.I	1419.62807	2	6.46E-05	0.92	3.35	-	1148.4
AHQ-7-3, 4664	K.GPMFELLPGESNK.I	1419.62807	2	1.33E-06	0.87	3.29	-	752.0
AHQ-7-1, 4165 - 4171	K.GPM*FELLPGESNK.I	1435.62747	2	5.44E-05	0.77	3.14	-	476.1
gi|14149680|ref|NP_056107.1| KIAA0747 protein [Homo sapiens]				1.34E-06	0.93	10.20	1.70	122855.6
AHQ-7-12, 3906	R.LTHVDSPLEAPAGPLGQVK.L	1930.19405	2	1.34E-06	0.93	4.09	-	1003.6
gi|29732725|ref|XP_291587.1| similar to Endoplasmin precursor (94 kDa glucose-regulated protein) (G				1.35E-06	0.10	10.10	2.70	37967.5
AHQ-7-4, 3293	R.GLFDEYGSK.K	1016.08574	1	1.35E-06	0.10	1.89	-	307.1
gi|4503481|ref|NP_001395.1| eukaryotic translation elongation factor 1 gamma; elongation factor 1-g				1.48E-06	0.95	10.18	3.00	50118.5
AHQ-7-8, 2999	K.ALIAAQYSGAQVR.V	1348.53280	2	1.48E-06	0.95	3.61	-	1726.5
gi|5031599|ref|NP_005722.1| actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub				1.55E-06	3.37	40.22	24.70	34332.8
AHQ-7-9, 6138	K.DTDAAVGDNIGYITFVLFPR.H	2185.42094	2	1.63E-05	0.91	3.42	-	1337.5
AHQ-7-9, 2624	K.ELQAHGADELLK.R	1324.46487	2	7.66E-05	0.67	2.80	-	764.8
AHQ-7-9, 6109	R.VYGSFLVNPESGYNVSLLYDLENLPASK.D	3090.42808	3	3.65E-05	0.87	4.39	-	425.5
AHQ-7-9, 2652	K.YFQFQEEGKEGENR.A	1761.82929	2	1.55E-06	0.92	3.96	-	964.5
gi|29729345|ref|XP_290995.1| similar to speckle-type POZ protein [Homo sapiens]				1.61E-06	1.43	20.20	10.90	18703.4
AHQ-7-2, 5992	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	7.55E-05	0.80	3.61	-	1024.0
AHQ-7-3, 5868	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	5.38E-06	0.73	3.68	-	819.9
AHQ-7-4, 5997 - 6066	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	5.43E-06	0.81	3.91	-	923.8
AHQ-7-5, 5950	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	2.42E-04	0.73	3.69	-	730.7
AHQ-7-6, 5854	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	1.76E-04	0.76	3.35	-	682.2
AHQ-7-1, 5824	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	1.61E-06	0.70	3.19	-	465.5
gi|22748619|ref|NP_689476.1| tropomyosin 3 [Homo sapiens]				1.66E-06	1.85	20.22	9.90	28222.6
AHQ-7-9, 3108 - 3173	R.KLVIIEGDLER.T	1285.51492	2	1.66E-06	0.94	3.71	-	1449.3
AHQ-7-10, 3244 - 3248	R.KLVIIEGDLER.T	1285.51492	2	1.21E-05	0.82	2.97	-	968.0
AHQ-7-9, 2076 - 2144	K.YSQKEDKYEEEIK.I	1689.80129	2	3.45E-04	0.91	4.44	-	1137.7
gi|29729950|ref|XP_293759.1| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				1.67E-06	0.75	10.15	5.00	39776.4
AHQ-7-5, 5103	K.CLELFTELAEDKENYKK.F	2132.37640	3	1.67E-06	0.75	3.09	-	673.7
gi|4557525|ref|NP_000099.1| dihydrolipoamide dehydrogenase precursor; E3 component of pyruvate dehy				1.67E-06	0.78	10.15	2.60	54149.9
AHQ-7-7, 2524	K.SEEQLKEEGIEYK.V	1582.69072	2	1.67E-06	0.78	3.10	-	801.7
gi|23510338|ref|NP_003325.2| ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity				1.75E-06	3.19	40.21	5.90	117848.1
AHQ-7-4, 4669	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	1.30E-05	0.88	3.83	-	434.5
AHQ-7-4, 3620	K.DNPGVVTCLDEAR.H	1447.55333	2	1.75E-06	0.59	2.68	-	500.9
AHQ-7-4, 6398 - 6401	K.SLVASLAEPDFVVTDFAK.F	1910.15638	2	4.79E-05	0.88	4.16	-	447.1
AHQ-7-4, 4078	R.YDGQVAVFGSDLQEK.L	1656.77453	2	6.37E-06	0.83	3.16	-	778.0
gi|17999541|ref|NP_060676.2| vacuolar protein sorting 35; maternal-embryonic 3 [Homo sapiens]				1.75E-06	0.88	10.14	1.30	91706.5
AHQ-7-5, 3604	K.LLDEAIQAVK.V	1100.29046	2	1.75E-06	0.88	2.84	-	1263.3
gi|10835242|ref|NP_006249.1| protein kinase, cGMP-dependent, type I; Protein kinase, cGMP-dependent				1.83E-06	0.83	10.17	1.70	77803.3
AHQ-7-6, 2786	K.HLIGGLDDVSNK.A	1268.40132	2	1.83E-06	0.83	2.65	-	769.5
gi|7705819|ref|NP_057181.1| HSPC039 protein [Homo sapiens]				1.83E-06	0.92	10.21	24.40	8968.7
AHQ-7-14-, 4946	K.NIGWGTDQGIGGFGEEPGIK.S	2033.18655	2	1.83E-06	0.92	4.15	-	888.2
gi|21735621|ref|NP_005909.2| mitochondrial malate dehydrogenase precursor [Homo sapiens]				1.85E-06	2.81	30.24	17.20	35503.0
AHQ-7-9, 5149	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	3	1.85E-06	0.95	4.85	-	1655.6
AHQ-7-9, 4981 - 5012	K.SQETECTYFSTPLLLGK.K	1976.19328	2	3.59E-06	0.94	4.45	-	986.2
AHQ-7-13, 6221	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	5.14E-04	0.93	4.10	-	1046.0
AHQ-7-13-, 6195	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	3.89E-05	0.92	3.87	-	1235.1
AHQ-7-9, 5805 - 5860	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	1.40E-04	0.65	3.05	-	526.3
gi|11559923|ref|NP_071496.1| eukaryotic translation initiation factor 4H isoform 1 [Homo sapiens] [				2.01E-06	0.48	10.14	8.50	27384.8
AHQ-7-10, 4464	R.TVATPLNQVANPNSAIFGGAR.P	2099.33604	2	2.01E-06	0.48	2.74	-	334.7
gi|5031595|ref|NP_005709.1| actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub				2.02E-06	1.86	20.21	11.30	19666.9
AHQ-7-11, 4234	R.AENFFILR.R	1010.17070	2	1.02E-04	0.95	3.89	-	1627.9
AHQ-7-12, 4264	R.AENFFILR.R	1010.17070	2	4.97E-05	0.95	3.47	-	1648.6
AHQ-7-11, 3142 - 3192	K.VLIEGSINSVR.V	1187.37134	2	2.02E-06	0.91	3.46	-	959.8
gi|4506363|ref|NP_002861.1| RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s				2.07E-06	0.89	10.18	5.40	22774.0
AHQ-7-13-, 3771	K.LLLIGDSGVGK.T	1072.28025	2	1.35E-04	0.91	3.55	-	991.6
AHQ-7-14-, 3781	K.LLLIGDSGVGK.T	1072.28025	2	1.21E-05	0.77	3.06	-	739.7
AHQ-7-13, 3919	K.LLLIGDSGVGK.T	1072.28025	2	2.07E-06	0.89	3.16	-	929.1
gi|4505591|ref|NP_002565.1| peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc				2.30E-06	3.52	40.30	24.10	22110.2
AHQ-7-11, 2424	K.ADEGISFR.G	894.95173	2	2.30E-06	0.77	2.68	-	568.6
AHQ-7-11, 3807	R.GLFIIDDK.G	921.07223	2	2.03E-04	0.87	3.38	-	888.5
AHQ-7-11, 3123	K.HGEVCPAGWKPGSDTIKPDVQK.S	2408.67532	3	3.72E-06	0.97	5.91	-	1786.1
AHQ-7-11, 3571	R.LVQAFQFTDK.H	1197.36469	2	1.67E-04	0.91	3.17	-	978.8
gi|5453597|ref|NP_006126.1| F-actin capping protein alpha-1 subunit; Cap Z [Homo sapiens]				2.37E-06	3.35	50.23	28.00	32922.5
AHQ-7-13-, 2860	K.DVQDSLTVSNEAQTAK.E	1706.79025	2	2.37E-06	0.95	4.69	-	1069.9
AHQ-7-9, 2709	K.DVQDSLTVSNEAQTAK.E	1706.79025	2	5.34E-04	0.63	2.80	-	435.0
AHQ-7-9, 4052	R.EGAAHAFAQYNMDQFTPVK.I	2126.33709	2	2.01E-04	0.67	3.36	-	439.8
AHQ-7-13-, 5151	K.FTITPPTAQVVGVLK.I	1571.88532	2	1.16E-04	0.68	2.64	-	309.2
AHQ-7-9, 3793	R.LLLNNDNLLR.E	1198.39736	2	2.12E-04	0.57	2.60	-	528.0
AHQ-7-9, 4984 - 4988	K.TIDGQQTIIACIESHQFQPK.N	2316.57620	2	1.71E-05	0.49	2.81	-	359.7
gi|6996010|ref|NP_002038.1| glycyl-tRNA synthetase; GlyRS; glycine tRNA ligase [Homo sapiens]				2.39E-06	1.49	20.16	4.80	77530.3
AHQ-7-6, 6410	R.TFFSFPAVVAPFK.C	1458.72722	2	5.08E-04	0.84	3.23	-	591.9
AHQ-7-6, 6477	K.TLYVEEVVPNVIEPSFGLGR.I	2219.52197	2	2.39E-06	0.65	3.27	-	414.3
gi|28827809|ref|NP_789797.1| nucleoside diphosphate kinase B-like [Homo sapiens]				2.42E-06	1.61	20.19	19.00	15529.0
AHQ-7-12, 3311	R.GDFCIQVGR.N	1053.17404	2	2.42E-06	0.91	3.66	-	1015.9
AHQ-7-12, 3314	R.GDFCIQVGR.N	1053.17404	1	5.00E-04	0.10	1.93	-	185.7
AHQ-7-12, 2894 - 2958	R.VMLGETNPADSKPGTIR.G	1787.03151	3	4.64E-06	0.71	3.72	-	371.5
gi|19913424|ref|NP_001681.2| ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT				2.53E-06	0.86	10.15	2.80	68303.7
AHQ-7-6, 4227	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	2.53E-06	0.86	3.02	-	777.2
gi|4502297|ref|NP_001678.1| ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit				2.56E-06	0.91	10.19	8.30	17489.8
AHQ-7-13-, 2587	K.AQAELVGTADEATR.A	1432.51860	2	2.56E-06	0.91	3.81	-	673.6
AHQ-7-13, 2777	K.AQAELVGTADEATR.A	1432.51860	2	2.33E-05	0.75	3.04	-	531.3
gi|6912638|ref|NP_036557.1| ras suppressor protein 1 [Homo sapiens]				2.60E-06	2.60	30.21	21.30	31540.1
AHQ-7-10, 5571 - 5627	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	2.60E-06	0.93	4.16	-	558.9
AHQ-7-10, 5580 - 5637	R.ALYLSDNDFEILPPDIGK.L	2021.25559	3	1.01E-04	0.59	3.27	-	561.9
AHQ-7-10, 5340 - 5395	R.LTVLPPELGNLDLTGQK.Q	1809.09672	3	9.66E-04	0.95	4.26	-	1845.2
AHQ-7-10, 5335 - 5399	R.LTVLPPELGNLDLTGQK.Q	1809.09672	2	6.90E-06	0.92	4.14	-	631.1
AHQ-7-10, 6140	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	2	3.50E-05	0.75	2.95	-	522.3
gi|30154095|ref|XP_293967.2| similar to gamma actin-like protein [Homo sapiens]				2.65E-06	1.04	20.18	12.20	19259.0
AHQ-7-8, 4784 - 4866	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.15E-04	0.59	3.44	-	284.4
AHQ-7-8, 5039	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.65E-06	0.82	3.60	-	652.3
AHQ-7-8, 5290 - 5310	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	1.37E-05	0.22	2.53	-	297.4
AHQ-7-13, 4697 - 4777	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	5.09E-05	0.78	3.66	-	552.9
AHQ-7-14, 5393	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.66E-04	0.58	2.94	-	496.5
AHQ-7-14, 5477 - 5532	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	7.98E-05	0.22	2.53	-	415.4
AHQ-7-13-, 4575 - 4644	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.51E-04	0.55	3.34	-	425.7
AHQ-7-13-, 4703	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	6.74E-06	0.32	2.66	-	403.0
AHQ-7-14-, 4683 - 4717	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.11E-04	0.73	3.32	-	468.9
AHQ-7-14-, 4893	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	9.14E-05	0.71	3.31	-	649.1
gi|30156116|ref|XP_301571.1| similar to Dual specificity protein phosphatase 3 (Dual specificity pr				2.85E-06	0.88	10.15	1.70	64164.4
AHQ-7-11, 3608 - 3611	K.DSGITYLGIK.A	1067.21733	2	2.85E-06	0.88	3.07	-	1078.6
gi|13786129|ref|NP_112586.1| RAB33B, member RAS oncogene family; likely ortholog of mouse RAB33b [H				3.20E-06	0.90	10.19	4.80	25717.4
AHQ-7-11, 3472 - 3482	K.IQLWDTAGQER.F	1317.43243	2	2.86E-04	0.88	3.16	-	935.9
AHQ-7-14-, 3498	K.IQLWDTAGQER.F	1317.43243	2	3.20E-06	0.90	3.34	-	945.4
AHQ-7-11, 3311 - 3366	K.IQLWDTAGQER.F	1317.43243	2	6.40E-05	0.90	3.87	-	780.7

gi|21361322|ref|NP_006078.2| tubulin, beta, 5 [Homo sapiens]				3.24E-06	2.55	30.27	13.70	49585.5
AHQ-7-7, 3017	R.EIVHLQAGQCGNQIGAK.F	1825.03962	2	1.57E-04	0.84	3.23	-	684.7
AHQ-7-7, 5212	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	3.24E-06	0.95	5.40	-	1029.8
AHQ-7-7, 6301	K.M*AATFIGNSTAIQELFK.R	1859.13607	2	1.10E-04	0.76	2.82	-	1194.3
gi|5729873|ref|NP_006656.1| heparanase; heparanase-1 [Homo sapiens]				3.28E-06	0.94	10.25	3.30	61176.4
AHQ-7-7, 6841	R.EDFLNPDVLDIFISSVQK.V	2080.32304	2	3.28E-06	0.94	5.00	-	658.8
gi|17149842|ref|NP_004461.2| FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep				3.33E-06	2.67	30.25	19.00	15649.2
AHQ-7-13-, 4100	K.GWDQGLLGM*CEGEK.R	1597.75215	2	9.88E-05	0.89	3.18	-	1001.1
AHQ-7-13-, 3840	R.KLVIPSELGYGER.G	1461.68782	2	1.80E-04	0.92	3.84	-	760.7
AHQ-7-13-, 4132	K.LVIPSELGYGER.G	1333.51491	2	3.33E-06	0.86	3.01	-	579.0
AHQ-7-13, 4265	K.LVIPSELGYGER.G	1333.51491	2	1.05E-05	0.81	2.98	-	455.9
gi|5031593|ref|NP_005708.1| actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub				3.40E-06	4.40	50.22	53.60	16320.3
AHQ-7-14-, 3117 - 3186	K.ALAAGGVGSIVR.V	1071.25558	2	1.29E-05	0.97	4.13	-	2160.8
AHQ-7-12, 3054	K.ALAAGGVGSIVR.V	1071.25558	2	3.40E-06	0.97	4.14	-	1834.7
AHQ-7-12, 3946 - 4003	K.AVQSLDKNGVDLLMK.Y	1631.91943	2	1.53E-05	0.86	4.03	-	645.1
AHQ-7-12, 3474 - 3530	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	6.13E-05	0.79	3.61	-	379.6
AHQ-7-12, 4392	K.GFESPSDNSSAMLLQWHEK.A	2164.34049	2	1.59E-05	0.92	4.41	-	766.9
AHQ-7-12, 4162	R.KVDVDEYDENKFVDEEDGGDGQAGPDEGEVDSCLR.Q	3890.92031	3	8.90E-04	0.86	3.85	-	908.7
gi|7706675|ref|NP_057661.1| RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M				3.43E-06	1.79	20.21	12.50	23461.5
AHQ-7-11, 4522	R.GSDVIIMLVGNK.T	1246.50220	2	5.90E-05	0.96	4.22	-	1764.3
AHQ-7-11, 3098 - 3099	R.VASALPGMENVQEK.S	1473.67727	2	3.43E-06	0.83	3.69	-	323.1
gi|5803121|ref|NP_006801.1| for protein disulfide isomerase-related [Homo sapiens]				3.47E-06	0.79	10.17	6.60	59594.0
AHQ-7-7, 6362	K.NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK.E	3870.10181	3	3.47E-06	0.79	3.44	-	539.2
gi|4505813|ref|NP_003737.1| cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain				3.47E-06	1.90	30.16	37.10	10365.8
AHQ-7-14-, 4309	K.NADM*SEEMQQDSVECATQALEK.Y	2532.67934	2	2.93E-04	0.68	3.14	-	720.8
AHQ-7-14-, 3806	K.NADM*SEEM*QQDSVECATQALEK.Y	2548.67874	2	1.17E-04	0.72	2.76	-	637.6
AHQ-7-14, 4606 - 4609	K.NADM*SEEM*QQDSVECATQALEK.Y	2548.67874	2	3.47E-06	0.43	3.08	-	250.9
AHQ-7-14-, 3625 - 3627	K.YNPTWHCIVGR.N	1404.57820	2	2.52E-04	0.79	3.02	-	430.8
gi|4758018|ref|NP_004359.1| calponin 2; Calonin 2 [Homo sapiens]				3.54E-06	1.81	20.22	9.10	33696.9
AHQ-7-11, 2867	K.GLQSGVDIGVK.Y	1073.22510	2	2.05E-04	0.87	3.09	-	1089.0
AHQ-7-12, 5803 - 5858	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	3.48E-05	0.94	4.00	-	1278.7
AHQ-7-13, 5998 - 6069	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	3.54E-06	0.94	4.34	-	1102.1
AHQ-7-13-, 6031 - 6065	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	2.13E-04	0.94	3.92	-	1147.1
AHQ-7-11, 5862 - 5942	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	7.46E-05	0.87	3.62	-	955.8
gi|12025678|ref|NP_004915.2| actinin, alpha 4 [Homo sapiens]				3.58E-06	7.02	80.28	12.00	104853.3
AHQ-7-4, 4642	K.AGTQIENIDEDFRDGLK.L	1922.04251	2	3.49E-05	0.93	4.34	-	940.8
AHQ-7-4, 4728	R.ETTDTDTADQVIASFK.V	1742.81936	2	8.35E-06	0.96	4.51	-	1488.8
AHQ-7-6, 3018	K.GISQEQMQEFR.A	1353.48658	2	2.82E-05	0.68	2.92	-	964.3
AHQ-7-4, 4438	R.KDDPVTNLNNAFEVAEK.Y	1905.05509	2	1.03E-04	0.97	5.69	-	1239.1
AHQ-7-4, 3981	R.M*APYQGPDAVPGALDYK.S	1810.02037	2	7.07E-04	0.92	3.69	-	1052.5
AHQ-7-4, 3865	K.M*LDAEDIVNTARPDEK.A	1833.99864	2	6.85E-04	0.76	3.32	-	476.8
AHQ-7-4, 4232	K.MLDAEDIVNTARPDEK.A	1817.99924	2	1.53E-04	0.87	3.76	-	813.9
AHQ-7-6, 4122	K.MLDAEDIVNTARPDEK.A	1817.99924	2	6.17E-04	0.77	3.14	-	685.6
AHQ-7-4, 3986 - 3989	K.VLAGDKNFITAEELR.R	1676.89525	2	3.58E-06	0.91	3.66	-	1348.1
gi|4557319|ref|NP_000029.1| adenomatosis polyposis coli [Homo sapiens]				3.68E-06	0.43	10.16	0.80	311658.1
AHQ-7-11, 5828	R.NPKDQEALWDM*GAVSMLKNLIHSK.H	2743.15551	3	3.68E-06	0.43	3.08	-	398.1
gi|29743324|ref|XP_293276.1| similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote				3.70E-06	0.89	10.29	16.00	21244.7
AHQ-7-13, 5166 - 5229	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	3.70E-06	0.89	5.89	-	731.5
AHQ-7-11, 4983 - 5050	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	3.52E-04	0.92	5.77	-	1288.5
gi|20070125|ref|NP_000909.2| prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke				3.79E-06	3.17	50.23	13.60	57115.9
AHQ-7-7, 5056	K.HNQLPLVIEFTEQTAPK.I	1966.22639	2	1.23E-05	0.94	4.51	-	922.9
AHQ-7-7, 2669 - 2690	K.LGETYKDHENIVIAK.M	1730.94291	2	2.32E-05	0.77	3.69	-	387.4
AHQ-7-13, 5586 - 5714	K.QPVKVLVGK.N	968.21840	1	7.54E-04	0.03	1.81	-	223.1
AHQ-7-7, 3732 - 3749	K.VDATEESDLAQQYGVR.G	1781.85882	2	3.79E-06	0.94	4.14	-	1440.8
AHQ-7-7, 2208 - 2210	K.YKPESEELTAER.I	1452.54828	2	4.76E-05	0.48	2.60	-	231.3
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				3.98E-06	3.37	40.20	22.30	22006.2
AHQ-7-10, 4347	K.HFCPNVPIILVGNK.K	1609.91693	2	1.70E-04	0.95	3.85	-	1481.7
AHQ-7-10, 3967	K.HFCPNVPIILVGNKK.D	1738.08985	2	3.98E-06	0.89	3.36	-	924.1
AHQ-7-10, 2665	K.LVIVGDGACGK.T	1090.27572	1	6.55E-06	0.59	2.29	-	802.1
AHQ-7-10, 4607	K.QVELALWDTAGQEDYDR.L	2010.10662	2	6.74E-06	0.94	4.05	-	1271.8
gi|4557485|ref|NP_000087.1| ceruloplasmin (ferroxidase); Ceruloplasmin [Homo sapiens]				4.04E-06	0.68	10.14	1.20	122204.3
AHQ-7-3, 4663	K.GAYPLSIEPIGVR.F	1372.59427	2	4.04E-06	0.68	2.75	-	557.1
gi|20149545|ref|NP_002717.2| prolyl endopeptidase [Homo sapiens]				4.19E-06	0.70	10.16	2.50	80733.0
AHQ-7-6, 6467 - 6506	R.LWYCDLQQESSGIAGILK.W	2083.35021	2	4.19E-06	0.70	3.27	-	743.6
gi|24307969|ref|NP_055423.1| cytoplasmic FMR1 interacting protein 1; selective hybridizing clone (m				4.30E-06	1.58	20.21	1.80	145181.2
AHQ-7-3, 6261	K.NVIQSVLQAIR.K	1241.46538	2	4.30E-06	0.96	4.22	-	1580.2
AHQ-7-3, 4628	R.TVLPFSQEFQR.D	1352.51991	2	6.08E-05	0.62	2.66	-	377.6
gi|5803133|ref|NP_006825.1| RAB32, member RAS oncogene family [Homo sapiens]				4.37E-06	0.46	10.13	7.60	24997.1
AHQ-7-10, 4535 - 4609	K.VHLPNGSPIPAVLLANK.C	1741.07044	2	4.37E-06	0.46	2.51	-	413.1
gi|14389309|ref|NP_116093.1| tubulin alpha 6 [Homo sapiens]				4.43E-06	0.69	10.14	3.80	49895.0
AHQ-7-13, 4782	R.AVCM*LSNTTAVAEAWAR.L	1869.11264	2	4.43E-06	0.69	2.83	-	961.5
gi|7706244|ref|NP_057005.1| divalent cation tolerant protein CUTA [Homo sapiens]				4.45E-06	0.90	10.17	9.00	16832.5
AHQ-7-13, 5525	K.TQSSLVPALTDFVR.S	1534.73880	2	4.45E-06	0.90	3.43	-	572.0
gi|4557014|ref|NP_001743.1| catalase [Homo sapiens]				4.98E-06	0.94	10.19	2.30	59755.8
AHQ-7-7, 4136	R.AFYVNVLNEEQR.K	1482.62245	2	4.98E-06	0.94	3.79	-	1183.7
gi|27481323|ref|XP_208234.1| similar to unactive progesterone receptor, 23 kD; likely ortholog of m				5.12E-06	0.81	10.14	8.10	18694.3
AHQ-7-11, 4294	K.LTFSCLGGSDNFK.H	1447.59493	2	5.12E-06	0.81	2.89	-	743.0
gi|27478749|ref|XP_208411.1| similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit				5.15E-06	0.93	10.24	7.40	25628.5
AHQ-7-9, 6166	K.LLIVSNPVDILTYVAWK.I	1945.33337	2	5.15E-06	0.93	4.88	-	784.5
gi|4503987|ref|NP_003869.1| gamma-glutamyl hydrolase precursor; conjugase; folylpolygammaglutamyl h				5.15E-06	0.83	10.20	4.10	35964.1
AHQ-7-14-, 5135 - 5178	R.LDLTEKDYEILFK.S	1627.85937	2	5.15E-06	0.83	4.00	-	685.3
gi|20127517|ref|NP_009148.2| programmed cell death 10; apoptosis-related protein 15 [Homo sapiens]				5.21E-06	1.39	20.19	17.50	24701.4
AHQ-7-10, 4025	R.LIHQTNLILQTFK.T	1569.87265	2	2.86E-05	0.52	2.68	-	431.2
AHQ-7-10, 4780	R.M*AADDVEEYMIERPEPEFQDLNEK.A	2916.14381	3	5.21E-06	0.86	3.81	-	1039.7
gi|30157216|ref|XP_292133.2| similar to genethonin 1 [Homo sapiens]				5.51E-06	0.37	10.16	0.00	39693.8
AHQ-7-1, 4532	K.TITLEVKPSDTIENVK.A	1788.03268	2	5.51E-06	0.37	2.97	-	298.9
gi|23065552|ref|NP_000840.2| glutathione S-transferase M3; glutathione S-transferase, Mu-3; brain G				5.59E-06	0.80	10.16	6.20	26559.4
AHQ-7-10, 3991	K.LKPQYLEELPGQLK.Q	1656.94708	2	5.59E-06	0.80	3.26	-	682.1
gi|4505773|ref|NP_002625.1| prohibitin [Homo sapiens]				5.59E-06	0.97	10.23	5.10	29803.9
AHQ-7-10, 3997	R.KLEAAEDIAYQLSR.S	1607.78978	2	5.59E-06	0.97	4.63	-	2187.6
gi|21361670|ref|NP_054782.2| src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo				5.75E-06	0.77	10.17	3.70	48294.0
AHQ-7-11, 3328 - 3391	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	5.75E-06	0.77	3.15	-	676.4
gi|18640750|ref|NP_570138.1| regulator of G-protein signalling 18; regulator of G-protein signaling				5.80E-06	0.71	10.14	8.90	27582.0
AHQ-7-10, 3985	K.EVITNSITQPTLHSFDAAQSR.V	2316.51300	2	5.80E-06	0.71	2.86	-	434.2
gi|4506677|ref|NP_002942.1| ribophorin II [Homo sapiens]				6.28E-06	1.45	20.18	5.50	69301.6
AHQ-7-1, 4909 - 4987	R.LQVTNVLSQPLTQATVK.L	1841.14195	2	6.28E-06	0.70	3.53	-	457.6
AHQ-7-1, 6184 - 6245	K.TSFTPVGDVFELNFM*NVK.F	2062.33118	2	2.83E-05	0.75	2.90	-	548.2
gi|5453760|ref|NP_006147.1| neural precursor cell expressed, developmentally down-regulated 8 [Homo				6.74E-06	0.67	10.17	17.30	9071.5
AHQ-7-14-, 3661 - 3717	K.EIEIDIEPTDKVER.I	1686.84208	2	6.74E-06	0.67	3.43	-	286.5
gi|29729616|ref|XP_292963.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [				6.78E-06	0.95	10.27	16.40	18025.4
AHQ-7-12, 4658 - 4714	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	6.49E-05	0.95	5.40	-	1066.1
AHQ-7-13, 4747 - 4825	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	9.66E-04	0.89	4.37	-	772.5
AHQ-7-13-, 4724	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	3.00E-05	0.68	3.53	-	685.2
AHQ-7-14-, 4750	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.16E-04	0.94	4.78	-	1515.4
AHQ-7-12, 4547 - 4602	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	6.78E-06	0.95	5.40	-	1405.6
gi|4885387|ref|NP_005318.1| L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain; L-3-hydroxyacyl-				7.30E-06	0.95	10.28	9.60	34286.3
AHQ-7-9, 6225	K.TLSTIATSTDAASVVHSTDLVVEAIVENLK.V	3086.43759	3	7.30E-06	0.95	5.52	-	1184.4

gi|27480104|ref|XP_208215.1| similar to triosephosphate isomerase 1 [Homo sapiens]				7.55E-06	5.31	70.21	32.10	26942.6
AHQ-7-10, 2264	K.IAVAAQNCYK.V	1139.30684	2	6.28E-05	0.86	3.08	-	797.9
AHQ-7-10, 2265	K.IAVAAQNCYK.V	1139.30684	1	2.11E-05	0.28	2.15	-	319.9
AHQ-7-10, 2673 - 2679	R.IIYGGSVTGATCK.E	1328.51672	2	2.19E-05	0.79	3.14	-	528.9
AHQ-7-10, 2661 - 2715	R.RHVFGESDELIGQK.V	1615.77200	2	7.44E-04	0.96	4.16	-	1906.1
AHQ-7-10, 2111	K.SNVSDAVAQSTR.I	1235.28659	2	7.55E-06	0.90	3.57	-	1326.8
AHQ-7-10, 3761	K.VTNGAFTGEISPGM*IK.D	1638.86726	2	1.99E-04	0.84	3.21	-	827.6
AHQ-7-11, 4103	K.VTNGAFTGEISPGMIK.D	1622.86786	2	1.02E-04	0.59	2.89	-	626.9
AHQ-7-10, 3547 - 3615	K.VTNGAFTGEISPGM*IK.D	1638.86726	2	7.51E-04	0.54	2.75	-	660.5
AHQ-7-14-, 5283	K.VVLAYEPVWAIGTGK.T	1603.88587	2	4.64E-05	0.95	3.97	-	1436.0
gi|13637631|ref|XP_016625.1| similar to voltage-dependent anion channel isoform 2 [Homo sapiens] [M				7.98E-06	0.44	10.13	6.80	31479.2
AHQ-7-9, 3868	K.VNNSSLIGVGYTQTLRPGVK.L	2104.39573	2	7.98E-06	0.44	2.62	-	304.2
gi|29732344|ref|XP_297644.1| hypothetical protein XP_297644 [Homo sapiens]				8.22E-06	0.73	10.14	5.60	22228.5
AHQ-7-4, 1736	K.MLGLGSSSPLR.S	1118.33251	2	8.22E-06	0.73	2.78	-	744.6
gi|21614499|ref|NP_003370.2| villin 2; Villin-2; cytovillin [Homo sapiens]				8.32E-06	1.89	20.21	3.20	69412.3
AHQ-7-6, 4345 - 4362	K.APDFVFYAPR.L	1183.33971	2	8.32E-06	0.96	4.12	-	1241.6
AHQ-7-6, 5145 - 5161	K.IGFPWSEIR.N	1105.27049	2	2.22E-05	0.93	2.89	-	1076.3
gi|4506505|ref|NP_002916.1| regulator of G-protein signaling 10 [Homo sapiens]				8.35E-06	1.57	20.18	16.80	19607.9
AHQ-7-11, 3642	K.ILEEPHPLMFQK.L	1482.77213	2	9.46E-04	0.87	3.06	-	951.9
AHQ-7-11, 2550	R.TEEEEEDLPDAQTAAK.R	1776.79097	2	8.35E-06	0.71	3.31	-	474.8
gi|29727317|ref|XP_298144.1| hypothetical protein XP_298144 [Homo sapiens]				8.41E-06	0.52	10.14	8.00	22108.6
AHQ-7-3, 6105 - 6175	K.GEYNLTLDTALTSNLK.T	1753.93165	2	8.41E-06	0.52	2.62	-	717.6
AHQ-7-2, 6325	K.GEYNLTLDTALTSNLK.T	1753.93165	2	1.59E-04	0.58	2.89	-	515.2
gi|4501865|ref|NP_001087.1| ATP citrate lyase [Homo sapiens]				8.68E-06	0.93	10.18	1.00	121419.0
AHQ-7-4, 3000	K.FICTTSAIQNR.F	1312.47738	2	8.68E-06	0.93	3.64	-	1305.2
gi|4505185|ref|NP_002406.1| macrophage migration inhibitory factor (glycosylation-inhibiting factor				8.75E-06	0.95	10.21	7.80	12476.2
AHQ-7-14-, 4486 - 4487	K.LLCGLLAER.L	1046.26608	2	8.75E-06	0.95	4.14	-	1258.1
gi|4557773|ref|NP_000248.1| myosin, heavy polypeptide 7, cardiac muscle, beta [Homo sapiens]				9.14E-06	0.83	10.17	0.50	223110.8
AHQ-7-4, 3249	R.CNGVLEGIR.I	1019.15759	2	6.20E-05	0.74	2.72	-	663.2
AHQ-7-1, 3371 - 3373	R.CNGVLEGIR.I	1019.15759	2	9.14E-06	0.83	3.24	-	603.1
gi|4507793|ref|NP_003339.1| ubiquitin-conjugating enzyme E2N (UBC13 homolog, yeast); ubiquitin-conj				9.14E-06	0.84	10.17	7.20	17137.7
AHQ-7-13, 2521	K.TNEAQAIETAR.A	1204.27249	2	1.66E-04	0.94	3.42	-	1722.1
AHQ-7-12, 2275 - 2282	K.TNEAQAIETAR.A	1204.27249	2	9.14E-06	0.84	3.15	-	1090.1
gi|4557675|ref|NP_000201.1| integrin alpha chain, alpha 6 [Homo sapiens]				9.58E-06	3.15	40.20	6.00	119509.5
AHQ-7-4, 3450	K.FGSCQQGVAATFTK.D	1503.66172	2	7.60E-04	0.76	2.70	-	825.1
AHQ-7-5, 5536	K.NIGDINQDGYPDIAVGAPYDDLGK.V	2521.67764	2	5.72E-05	0.81	3.20	-	647.4
AHQ-7-4, 3733	K.TACGAPSGICLQVK.S	1464.69022	2	9.58E-06	0.75	2.96	-	564.6
AHQ-7-4, 3244	R.TGGLYSCDITAR.G	1315.43490	2	1.87E-04	0.83	3.01	-	802.0
gi|7706312|ref|NP_057105.1| non-canonical ubquitin conjugating enzyme 1 [Homo sapiens]				9.65E-06	0.68	10.14	4.60	35979.3
AHQ-7-10, 3300	K.GEGAIGSLDYTPEER.R	1594.66159	2	9.65E-06	0.68	2.84	-	649.8
gi|20547107|ref|XP_114482.1| similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN				1.04E-05	0.93	10.20	2.10	94330.3
AHQ-7-4, 6425 - 6428	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	1.04E-05	0.93	4.05	-	1033.4
gi|4507367|ref|NP_003182.1| threonyl-tRNA synthetase; threonine--tRNA ligase [Homo sapiens]				1.05E-05	0.95	10.19	1.80	82123.1
AHQ-7-5, 5178	K.FLGDIEVWDQAEK.Q	1550.69355	2	1.05E-05	0.95	3.84	-	1365.8
gi|4502107|ref|NP_001145.1| annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoag				1.05E-05	1.67	20.18	9.10	35936.5
AHQ-7-9, 5758	R.DLLDDLKSELTGK.F	1447.61309	2	1.63E-05	0.80	2.63	-	773.8
AHQ-7-9, 6001	K.GLGTDEESILTLLTSR.S	1705.88853	2	1.05E-05	0.88	3.68	-	749.0
gi|10047092|ref|NP_037391.1| neuronal protein [Homo sapiens]				1.10E-05	0.85	10.14	5.00	31454.0
AHQ-7-11, 5607	R.TTDIFQTVDLWEGK.D	1653.81378	2	1.10E-05	0.85	2.87	-	1102.1
gi|5174727|ref|NP_005989.1| chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring				1.11E-05	2.23	30.21	6.80	60330.4
AHQ-7-6, 3833	R.AVAQALEVIPR.T	1167.38326	2	1.11E-05	0.94	4.30	-	1367.1
AHQ-7-6, 2905 - 2907	R.TLIQNCGASTIR.L	1335.51249	2	2.72E-05	0.48	2.52	-	457.1
AHQ-7-6, 5399	R.WSSLACNIALDAVK.M	1549.77353	2	8.77E-05	0.81	2.98	-	837.2
gi|11321561|ref|NP_000604.1| hemopexin [Homo sapiens]				1.15E-05	1.71	20.22	8.90	51676.1
AHQ-7-6, 5739 - 5818	K.SLGPNSCSANGPGLYLIHGPNLYCYSDVEK.L	3286.59404	3	3.68E-05	0.88	4.40	-	601.7
AHQ-7-6, 4557	R.YYCFQGNQFLR.F	1497.65886	2	1.15E-05	0.83	2.83	-	761.0
gi|30149221|ref|XP_291446.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				1.19E-05	0.73	10.18	3.90	45688.5
AHQ-7-7, 2420	R.STAGDTHLGGEDFDNR.M	1692.68222	2	1.19E-05	0.73	2.89	-	763.5
gi|4826643|ref|NP_005130.1| annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III,				1.30E-05	0.50	10.14	5.00	36375.0
AHQ-7-9, 3981	R.DYPDFSPSVDAEAIQK.A	1782.88518	2	1.30E-05	0.50	2.68	-	363.6
gi|15723376|ref|NP_277050.1| MacGAP protein [Homo sapiens]				1.33E-05	0.70	10.16	3.20	70163.1
AHQ-7-5, 6592	K.TKDSGLFCVPLTALLEQDQR.K	2293.58254	3	1.33E-05	0.70	3.20	-	867.3
gi|6041669|ref|NP_004538.2| NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd				1.37E-05	0.83	10.18	14.00	15208.5
AHQ-7-13-, 4657	R.TLPETLDPAEYNISPETR.R	2047.20831	2	9.16E-05	0.81	3.24	-	447.5
AHQ-7-13, 4762	R.TLPETLDPAEYNISPETR.R	2047.20831	2	1.37E-05	0.83	3.62	-	482.2
gi|4502167|ref|NP_000475.1| amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disea				1.37E-05	1.61	20.20	4.40	86942.8
AHQ-7-4, 6612	R.CLVGEFVSDALLVPDKCK.F	2053.38561	3	1.37E-05	0.69	3.29	-	480.6
AHQ-7-4, 2481	K.YLETPGDENEHAHFQK.A	1915.99652	2	9.85E-05	0.93	3.96	-	859.6
gi|20270259|ref|NP_620061.1| phosphoglycerate kinase 2; phosphoglycerate kinase 1, pseudogene 2 [Ho				1.38E-05	0.76	10.20	3.60	44895.0
AHQ-7-8, 3568	K.LGDVYVNDAFGTAHR.A	1635.76178	2	4.18E-05	0.91	3.95	-	962.7
AHQ-7-8, 3439	K.LGDVYVNDAFGTAHR.A	1635.76178	2	1.38E-05	0.76	2.84	-	675.7
gi|4507383|ref|NP_001052.1| thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil				1.45E-05	0.96	10.21	3.00	60675.3
AHQ-7-7, 4262 - 4282	R.FQACPETQVPLQLESK.S	1877.10807	2	1.45E-05	0.96	4.28	-	1504.0
gi|29740995|ref|XP_291768.1| similar to Proteasome activator complex subunit 2 (Proteasome activato				1.47E-05	0.81	10.16	9.60	19192.6
AHQ-7-10, 6088	R.AFYAELYHIISSNLEK.T	1899.13528	2	1.47E-05	0.81	3.18	-	634.0
gi|16753212|ref|NP_003921.2| src family associated phosphoprotein 2; src kinase-associated phosphop				1.52E-05	0.82	10.19	2.80	41216.5
AHQ-7-13, 3510	K.RGDVIYILSK.E	1164.37938	2	1.52E-05	0.82	3.04	-	963.7
gi|9845297|ref|NP_063940.1| second mitochondria-derived activator of caspase isoform Smac-alpha, pr				1.52E-05	0.94	10.18	4.20	27130.6
AHQ-7-11, 3218	K.LAEAQIEELR.Q	1172.31354	2	1.52E-05	0.94	3.65	-	1450.7
gi|5031601|ref|NP_005711.1| actin related protein 2/3 complex subunit 1B; ARP2/3 protein complex su				1.54E-05	2.02	30.20	13.20	40949.5
AHQ-7-9, 2333	K.ASSEGGTAAGAGLDSLHK.N	1629.71071	2	1.54E-05	0.44	2.69	-	511.5
AHQ-7-9, 2465	K.EVEERPAPTPWGSK.M	1583.72678	2	6.21E-04	0.65	2.84	-	472.8
AHQ-7-9, 3245	R.TQIAICPNNHEVHIYEK.S	2068.29887	2	8.66E-04	0.92	4.04	-	786.7
gi|22749247|ref|NP_689822.1| hypothetical protein FLJ32001 [Homo sapiens]				1.62E-05	0.65	10.15	2.50	79570.3
AHQ-7-12, 5783	K.RIEIAEVVPTEGLVSILK.K	1967.33888	2	1.62E-05	0.65	2.91	-	328.3
gi|4506381|ref|NP_002863.1| ras-related C3 botulinum toxin substrate 2; Ras-related C3 botulinum to				1.71E-05	0.54	10.13	7.80	21428.7
AHQ-7-11, 4026	K.KLAPITYPQGLALAK.E	1584.92723	2	1.71E-05	0.54	2.63	-	429.1
gi|22267436|ref|NP_056284.1| DKFZp564D177 protein [Homo sapiens]				1.79E-05	1.87	20.18	10.50	28466.4
AHQ-7-11, 2134	R.AVHAHVNLGYTK.L	1310.48626	3	1.79E-05	0.93	3.53	-	1567.4
AHQ-7-11, 3670	K.LVGVFHTEYGALNR.V	1576.78061	2	2.03E-05	0.94	3.33	-	1332.5
gi|4504045|ref|NP_002063.1| guanine nucleotide binding protein (G protein), q polypeptide [Homo sap				1.86E-05	1.69	20.28	9.50	42142.8
AHQ-7-8, 4098 - 4110	R.VADPAYLPTQQDVLR.V	1686.89014	2	4.21E-05	0.76	3.24	-	647.2
AHQ-7-8, 6794 - 6799	R.VPTTGIIEYPFDLQSVIFR.M	2196.53000	2	1.86E-05	0.93	4.50	-	802.1
gi|14780596|ref|XP_033004.1| hypothetical protein BC005107 [Homo sapiens]				2.00E-05	0.37	10.13	5.00	18127.9
AHQ-7-3, 2049	R.EQIIAKAK.A	901.08569	1	3.15E-04	0.40	2.64	-	331.0
AHQ-7-4, 2004 - 2016	R.EQIIAKAK.A	901.08569	1	2.00E-05	0.37	2.57	-	266.5
AHQ-7-2, 2051 - 2191	R.EQIIAKAK.A	901.08569	1	5.05E-04	0.31	2.43	-	301.8
gi|6912238|ref|NP_036226.1| peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]				2.01E-05	0.95	10.22	7.90	22026.2
AHQ-7-12, 4496 - 4506	K.KGVLFGVPGAFTPGCSK.T	1724.01680	2	2.01E-05	0.95	4.39	-	965.0
gi|4508047|ref|NP_003452.1| zyxin [Homo sapiens]				2.04E-05	1.73	20.22	7.70	61277.0
AHQ-7-9, 3600	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	2	2.69E-04	0.84	3.54	-	601.8
AHQ-7-12, 3779	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	2	6.48E-04	0.75	3.10	-	325.2
AHQ-7-13-, 3849	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	2.04E-05	0.89	4.32	-	635.2
AHQ-7-9, 2728	K.VNPFRPGDSEPPPAPGAQR.A	1990.16814	2	5.64E-04	0.84	3.44	-	567.7
gi|4502693|ref|NP_001760.1| CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen				2.05E-05	1.79	20.19	10.10	25415.9
AHQ-7-11, 3330 - 3331	K.KDVLETFTVK.S	1180.37558	2	2.39E-05	0.79	3.12	-	738.0
AHQ-7-1, 3701 - 3707	K.KDVLETFTVK.S	1180.37558	2	2.05E-05	0.90	3.43	-	1027.5

AHQ-7-11, 3694	K.SCPDAIKEVFDNK.F	1524.67770	2	4.79E-04	0.89	3.23	-	955.4
gi|5032161|ref|NP_005639.1| elongin C; transcription elongation factor B (SIII), polypeptide 1 (15k				2.08E-05	0.82	10.15	12.50	12473.1
AHQ-7-13-, 2776 - 2840	K.TYGGCEGPDAM*YVK.L	1565.70692	2	2.08E-05	0.82	2.96	-	728.5
gi|7705501|ref|NP_057546.1| hypothetical protein HSPC194 [Homo sapiens]				2.08E-05	1.53	20.20	41.10	11564.5
AHQ-7-14-, 6469	K.AGSVPSLAAGLLFGSLAGLGAYQLSQDPR.N	2818.17710	3	2.08E-05	0.57	3.19	-	449.5
AHQ-7-14-, 5665	K.FM*PAGLIAGASLLM*VAK.V	1723.13705	2	9.80E-04	0.96	4.06	-	1589.0
gi|14779875|ref|XP_032693.1| similar to KIAA0420 [Homo sapiens]				2.11E-05	0.30	10.13	1.90	78941.3
AHQ-7-3, 5628	R.FLRAHDFHLDKAR.E	1626.84608	2	2.11E-05	0.30	2.61	-	308.9
gi|20270343|ref|NP_620150.1| hypothetical protein BC015408 [Homo sapiens]				2.15E-05	1.76	20.21	17.20	21415.8
AHQ-7-11, 2838	K.MNLSAIQDR.E	1048.19914	2	2.15E-05	0.93	2.97	-	1725.6
AHQ-7-11, 5542 - 5606	K.NELHNLLDKPQLQGIPVLVLGNK.R	2553.98492	3	9.28E-04	0.83	4.12	-	354.8
gi|4507149|ref|NP_000445.1| superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult				2.19E-05	0.59	10.14	9.10	15935.7
AHQ-7-12, 4194	K.GDGPVQGIINFEQK.E	1502.65366	2	2.19E-05	0.59	2.57	-	600.2
gi|8923812|ref|NP_060943.1| uncharacterized hypothalamus protein HT012 [Homo sapiens]				2.26E-05	0.90	10.16	8.60	14960.4
AHQ-7-13-, 4047	K.TLAFTSVDLTNK.A	1310.47811	2	3.22E-04	0.83	3.22	-	671.4
AHQ-7-13, 4185 - 4193	K.TLAFTSVDLTNK.A	1310.47811	2	2.26E-05	0.90	3.23	-	964.3
gi|5031985|ref|NP_005787.1| nuclear transport factor 2; placental protein 15 [Homo sapiens]				2.27E-05	2.59	30.24	32.30	14478.4
AHQ-7-14-, 5279	K.IQHSITAQDHQPTPDSCIISM*VVGQLK.A	3022.40358	3	2.27E-05	0.95	4.90	-	1466.8
AHQ-7-14-, 5183	K.NINDAWVCTNDMFR.L	1757.92888	2	2.39E-05	0.87	3.90	-	599.9
AHQ-7-14-, 4386	K.NINDAWVCTNDM*FR.L	1773.92828	2	7.66E-04	0.77	3.36	-	452.0
gi|23111030|ref|NP_037478.2| sorting nexin 12 [Homo sapiens]				2.37E-05	0.94	10.21	8.60	18884.4
AHQ-7-12, 4716 - 4719	R.GDEGIFEESFIEER.R	1657.71615	2	2.37E-05	0.94	4.20	-	975.5
gi|6005826|ref|NP_009160.1| protein kinase C and casein kinase substrate in neurons 2; pacsin 2 [Ho				2.47E-05	1.49	20.13	4.50	55904.6
AHQ-7-6, 3958	K.AYAQQLTEWAR.R	1337.46534	2	2.47E-05	0.79	2.55	-	1064.9
AHQ-7-6, 3167	K.HLNLSNVAGYK.A	1216.37124	2	8.00E-05	0.70	2.56	-	647.2
gi|4758618|ref|NP_004684.1| cytokeratin type II [Homo sapiens]				2.58E-05	0.97	10.22	2.20	59503.9
AHQ-7-3, 3104	R.FLEQQNKVLETK.W	1477.68725	2	2.58E-05	0.97	4.43	-	1937.7
gi|4557241|ref|NP_001095.1| skeletal muscle specific actinin, alpha 3 [Homo sapiens]				2.95E-05	0.90	10.16	0.90	103293.7
AHQ-7-5, 3003	K.ALDFIASK.G	865.00867	2	4.39E-05	0.89	3.15	-	733.6
AHQ-7-4, 3022	K.ALDFIASK.G	865.00867	2	2.95E-05	0.90	3.22	-	627.7
gi|7656999|ref|NP_004380.1| catenin (cadherin-associated protein), alpha 2; Catenin, alpha-2 (cadhe				2.98E-05	0.57	10.15	2.00	105281.3
AHQ-7-14-, 4917	K.KAHVLAASVEQATQNFLEK.G	2085.34928	2	8.44E-04	0.16	2.64	-	296.2
AHQ-7-5, 5152	K.KAHVLAASVEQATQNFLEK.G	2085.34928	2	2.98E-05	0.57	3.02	-	638.9
gi|4502905|ref|NP_001822.1| clusterin; complement-associated protein SP-40 [Homo sapiens]				3.01E-05	2.38	30.27	11.40	52494.3
AHQ-7-9, 5264	R.ASSIIDELFQDR.F	1394.51197	2	1.79E-04	0.54	2.62	-	688.4
AHQ-7-9, 2810 - 2814	R.EILSVDCSTNNPSQAK.L	1764.89299	2	5.18E-05	0.92	4.20	-	839.3
AHQ-7-11, 3451	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	3.24E-05	0.95	5.36	-	656.1
AHQ-7-9, 3261	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	3.01E-05	0.92	4.31	-	833.2
gi|4758484|ref|NP_004823.1| glutathione-S-transferase like; glutathione transferase omega [Homo sap				3.07E-05	1.27	20.16	8.70	27565.7
AHQ-7-10, 3904 - 3948	K.EFTKLEEVLTNK.K	1451.64657	2	2.02E-04	0.74	3.25	-	544.4
AHQ-7-10, 2808	R.HEVININLK.N	1080.26247	1	3.07E-05	0.53	2.50	-	476.6
AHQ-7-10, 2803	R.HEVININLK.N	1080.26247	2	5.86E-04	0.91	3.18	-	992.8
gi|6005902|ref|NP_009043.1| thrombospondin 3 [Homo sapiens]				3.08E-05	1.30	20.13	0.70	104200.6
AHQ-7-3, 4659	R.FYVVMWK.Q	973.21547	1	1.62E-04	0.71	2.18	-	828.1
AHQ-7-6, 4534 - 4538	R.FYVVMWK.Q	973.21547	1	2.21E-04	0.76	2.22	-	912.8
AHQ-7-6, 4541	R.FYVVMWK.Q	973.21547	2	7.72E-04	0.86	2.52	-	750.7
AHQ-7-7, 4446	R.FYVVMWK.Q	973.21547	1	2.11E-04	0.60	2.12	-	730.0
AHQ-7-9, 4145	R.FYVVMWK.Q	973.21547	1	3.08E-05	0.71	2.02	-	846.6
AHQ-7-3, 4136	R.FYVVM*WK.Q	989.21487	1	8.87E-04	0.59	2.23	-	162.5
gi|4506193|ref|NP_002784.1| proteasome beta 1 subunit; proteasome subunit HC5; proteasome component				3.13E-05	2.23	30.24	17.00	26489.2
AHQ-7-11, 3858 - 3916	K.GAVYSFDPVGSYQR.D	1546.66500	2	3.13E-05	0.69	2.70	-	616.7
AHQ-7-11, 2614	R.LSEGFSIHTR.D	1147.26577	2	4.03E-05	0.61	2.89	-	506.2
AHQ-7-11, 4106 - 4107	K.TVIGCSGFHGDCLTLTK.I	1869.10923	2	6.70E-04	0.94	4.87	-	957.2
gi|4557894|ref|NP_000230.1| lysozyme precursor [Homo sapiens]				3.16E-05	0.83	10.17	8.10	16537.0
AHQ-7-13, 4275	R.STDYGIFQINSR.Y	1401.50620	2	3.16E-05	0.83	3.34	-	655.4
gi|4504107|ref|NP_002076.1| glutathione peroxidase 4; phospholipid hydroperoxidase; sperm nucleus g				3.17E-05	0.82	10.15	6.10	22137.7
AHQ-7-11, 3878	R.YGPMEEPLVIEK.D	1405.64130	2	3.17E-05	0.82	2.99	-	646.6
gi|30149555|ref|XP_301154.1| similar to heat shock protein 86 [Homo sapiens]				3.18E-05	0.96	10.24	10.60	15781.6
AHQ-7-5, 5838	K.HSQFIGYPITLFVEK.E	1780.05877	2	3.18E-05	0.96	4.82	-	1030.6
gi|13569962|ref|NP_112243.1| RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap				3.33E-05	2.87	40.29	26.40	22171.0
AHQ-7-11, 4351	R.GAHGIIVVYDVTDQESYANVK.Q	2279.49113	2	3.33E-05	0.98	5.84	-	2127.5
AHQ-7-11, 2150 - 2228	R.MGPGAASGGERPNLK.I	1442.62650	2	1.78E-04	0.81	3.30	-	772.1
AHQ-7-11, 1834 - 1902	R.M*GPGAASGGERPNLK.I	1458.62590	2	7.78E-04	0.69	2.96	-	632.4
AHQ-7-11, 6022 - 6091	K.NATNVEQAFMTM*AAEIK.K	1886.14019	2	8.07E-04	0.39	2.74	-	415.9
gi|18087855|ref|NP_542408.1| dynein light chain 2 [Homo sapiens]				3.45E-05	0.65	10.10	7.90	10349.8
AHQ-7-14-, 3154	K.DIAAYIK.K	793.93045	1	3.45E-05	0.65	1.94	-	747.5
gi|5032041|ref|NP_005605.1| Ras homolog enriched in brain 2 [Homo sapiens]				3.48E-05	0.86	10.16	8.70	20497.4
AHQ-7-12, 4694	K.ALAESWNAAFLESSAK.E	1695.85389	2	3.48E-05	0.86	3.11	-	861.4
gi|7661728|ref|NP_054736.1| HSPC003 protein [Homo sapiens]				3.58E-05	0.59	10.15	14.40	13507.4
AHQ-7-14-, 6207 - 6209	K.AQALVQYLEEPLTQVAAS	1932.16358	2	3.58E-05	0.59	2.97	-	368.9
gi|4758038|ref|NP_004246.1| cytochrome c oxidase subunit Va precursor; cytochrome c oxidase polypep				3.62E-05	1.88	20.24	10.00	16774.1
AHQ-7-13-, 4140	K.GINTLVTYDM*VPEPK.I	1693.94282	2	9.79E-05	0.88	3.27	-	1324.3
AHQ-7-13-, 4717 - 4721	K.GINTLVTYDMVPEPK.I	1677.94342	2	4.88E-05	0.92	4.02	-	1251.2
AHQ-7-13, 4267 - 4270	K.GINTLVTYDM*VPEPK.I	1693.94282	2	3.62E-05	0.96	4.74	-	1481.2
gi|10835049|ref|NP_001655.1| ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho				3.62E-05	0.93	10.19	6.20	21768.0
AHQ-7-10, 3587 - 3591	R.IGAFGYMECSAK.T	1335.53122	2	3.62E-05	0.93	3.77	-	872.7
gi|4557469|ref|NP_001273.1| adaptor-related protein complex 2, beta 1 subunit; adaptin, beta 2 (bet				3.67E-05	0.91	10.19	1.30	104551.9
AHQ-7-6, 5891	R.CVSTLLDLIQTK.V	1392.64385	2	3.67E-05	0.91	3.73	-	931.7
gi|24497612|ref|NP_116262.2| nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr				3.80E-05	0.85	10.21	3.90	72695.6
AHQ-7-6, 5347 - 5355	R.RPYEDQGLGETTPLTIICQPM*QPLR.V	2932.32204	3	3.80E-05	0.85	4.21	-	712.7
gi|4757786|ref|NP_004306.1| N-acylsphingosine amidohydrolase (acid ceramidase) 1; N-acylsphingosine				3.96E-05	0.70	10.18	6.30	44649.3
AHQ-7-14-, 5863	K.VM*QVVDEKLPGLLGNFPGPFEEEM*K.G	2837.26081	3	3.96E-05	0.70	3.45	-	604.8
gi|19923437|ref|NP_057366.2| adenylate kinase 3 alpha like [Homo sapiens]				4.17E-05	1.51	20.16	12.80	25565.2
AHQ-7-10, 5880 - 5943	K.NLTQYSWLLDGFPR.T	1710.91339	2	4.17E-05	0.81	2.71	-	813.1
AHQ-7-10, 4337 - 4415	K.TVGIDDLTGEPLIQR.E	1627.82100	2	4.22E-04	0.70	2.91	-	676.9
gi|5803009|ref|NP_006786.1| EH-domain containing 1; homolog of Drosophila past; EH domain containin				4.29E-05	0.78	10.22	2.80	60844.7
AHQ-7-7, 5493	K.LLDTVDDMLANDIAR.L	1675.88593	2	4.29E-05	0.78	2.89	-	627.5
gi|4758384|ref|NP_004108.1| FK506 binding protein 5; FK506-binding protein 5; 51 kDa FK506-binding				4.33E-05	0.66	10.13	2.20	51211.8
AHQ-7-2, 3063	K.EKLEQAAIVK.E	1129.33180	2	4.33E-05	0.66	2.63	-	960.5
gi|8922950|ref|NP_060835.1| hypothetical protein FLJ11222 [Homo sapiens]				4.47E-05	0.84	10.14	2.60	60570.9
AHQ-7-10, 2244	K.ERAAQIAEKDAIK.Y	1443.63090	2	4.47E-05	0.84	2.84	-	718.5
gi|14589893|ref|NP_001785.2| cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-				4.54E-05	0.28	10.15	2.00	100279.9
AHQ-7-9, 4256	K.VENPIDLYIYVIDM*NDNR.P	2213.45293	2	2.13E-04	0.32	2.98	-	321.0
AHQ-7-7, 4562	K.VENPIDLYIYVIDM*NDNR.P	2213.45293	2	4.54E-05	0.28	2.65	-	406.9
gi|19743813|ref|NP_002202.2| integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib				4.56E-05	3.54	40.26	7.40	88414.9
AHQ-7-3, 3239	K.FCECDNFNCDR.S	1540.59429	2	5.84E-04	0.94	3.68	-	1304.0
AHQ-7-3, 3693	K.GEVFNELVGK.Q	1092.22688	2	7.60E-04	0.72	2.77	-	749.0
AHQ-7-4, 5218	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	3.35E-04	0.93	4.29	-	806.0
AHQ-7-3, 6628 - 6672	K.LSENNIQTIFAVTEEFQPVYK.E	2471.74650	3	4.56E-05	0.96	5.18	-	1583.3
gi|5729779|ref|NP_006701.1| COP9 homolog [Homo sapiens]				4.63E-05	0.69	10.15	6.70	23225.5
AHQ-7-11, 3487	K.GILEQGWQADSTTR.M	1562.66596	2	4.63E-05	0.69	2.91	-	606.8
gi|24308149|ref|NP_060035.1| hypothetical protein DKFZp434F2322 [Homo sapiens]				4.65E-05	0.72	10.15	2.00	61404.2
AHQ-7-4, 5908	K.PSGVHLKLVLR.F	1219.50454	2	4.65E-05	0.72	3.08	-	714.8
gi|9506667|ref|NP_061907.1| ras homolog gene family, member F [Homo sapiens]				4.72E-05	0.65	10.16	8.10	23593.2
AHQ-7-11, 4068	K.EVTLNLYDTAGQEDYDR.L	2003.06925	2	4.72E-05	0.65	3.10	-	406.6
gi|4507509|ref|NP_003245.1| tissue inhibitor of metalloproteinase 1 precursor; Erythroid-potentiati				4.73E-05	0.92	10.17	5.80	23170.8
AHQ-7-10, 3561 - 3568	K.GFQALGDAADIR.F	1234.34342	2	4.73E-05	0.92	3.44	-	1127.0

gi|10863873|ref|NP_000651.1| transforming growth factor, beta 1 (Camurati-Engelmann disease); trans				4.73E-05	2.73	30.20	5.90	44422.0
AHQ-7-13-, 3344	R.ALDTNYCFSSTEK.N	1537.63010	2	1.58E-04	0.88	3.82	-	616.9
AHQ-7-13-, 2725	K.VEQLSNM*IVR.S	1205.41014	2	4.73E-05	0.90	3.78	-	942.2
AHQ-7-13, 3685	K.VEQLSNMIVR.S	1189.41074	2	2.30E-04	0.95	4.03	-	1415.5
gi|28269681|ref|NP_783313.1| NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]				4.98E-05	0.94	10.22	16.30	14852.0
AHQ-7-13-, 6223	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	4.98E-05	0.94	4.36	-	1591.1
gi|7661922|ref|NP_055814.1| RAB21, member RAS oncogene family [Homo sapiens]				5.36E-05	0.82	10.16	7.60	24347.4
AHQ-7-10, 4048	R.HVSIQEAESYAESVGAK.H	1805.92351	2	5.36E-05	0.82	3.17	-	613.1
gi|4759086|ref|NP_004883.1| vesicle trafficking protein sec22b [Homo sapiens]				5.36E-05	0.88	10.18	6.50	24740.4
AHQ-7-12, 3827	R.NLGSINTELQDVQR.I	1587.71696	2	5.36E-05	0.88	3.57	-	1126.3
gi|4557225|ref|NP_000005.1| alpha 2 macroglobulin precursor [Homo sapiens]				5.43E-05	1.70	20.21	2.00	163276.5
AHQ-7-3, 5517	R.VSVQLEASPAFLAVPVEK.E	1885.19319	2	2.16E-04	0.85	3.73	-	639.4
AHQ-7-2, 5645	R.VSVQLEASPAFLAVPVEK.E	1885.19319	2	4.53E-04	0.81	3.27	-	656.2
AHQ-7-4, 3009	R.VTAAPQSVCALR.A	1274.47229	2	5.43E-05	0.85	2.96	-	700.7
gi|5453704|ref|NP_006398.1| cytoskeleton related vitamin A responsive protein; glutamate transporte				5.46E-05	0.84	10.15	5.90	21614.6
AHQ-7-1, 4948	R.AWDDFFPGSDR.F	1313.35597	2	5.46E-05	0.84	2.93	-	697.8
gi|4506765|ref|NP_002952.1| S100 calcium-binding protein A4; 18A2; 42A; S100 calcium-binding protei				5.60E-05	1.60	20.15	10.90	11728.5
AHQ-7-14-, 3519	K.ALDVMVSTFHK.Y	1248.47665	2	5.60E-05	0.68	2.69	-	577.7
AHQ-7-14-, 3077	K.ALDVM*VSTFHK.Y	1264.47605	2	6.09E-04	0.92	2.91	-	1314.3
gi|29727565|ref|XP_291384.1| similar to Cytochrome c, somatic [Homo sapiens]				5.73E-05	0.94	10.20	16.20	11621.4
AHQ-7-13-, 6076	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	5.73E-05	0.94	4.06	-	1146.7
AHQ-7-13, 6118	K.GIIWGEDTLM*EYLENPK.K	2025.26771	2	2.27E-04	0.60	2.68	-	561.3
gi|4501867|ref|NP_001089.1| aconitase 2 [Homo sapiens]				5.91E-05	1.60	20.19	4.60	85424.8
AHQ-7-5, 6574	K.DINQEVYNFLATAGAK.Y	1754.92134	2	5.91E-05	0.91	3.78	-	898.8
AHQ-7-5, 6176	R.DLGGIVLANACGPCIGQWDR.K	2175.43103	2	7.73E-04	0.70	3.22	-	594.1
gi|4503069|ref|NP_001306.1| mitogen-activated protein kinase 14 isoform 1; cytokine suppressive ant				6.23E-05	0.92	10.18	4.20	41493.2
AHQ-7-9, 5378	K.HENVIGLLDVFTPAR.S	1681.91672	2	6.23E-05	0.92	3.64	-	1118.5
gi|21359837|ref|NP_003312.2| Tu translation elongation factor, mitochondrial [Homo sapiens]				6.44E-05	0.69	10.17	3.10	49541.2
AHQ-7-8, 5026	K.LLDAVDTYIPVPAR.D	1543.78883	2	6.44E-05	0.69	2.78	-	606.1
gi|20070272|ref|NP_057110.2| androgen-regulated short-chain dehydrogenase/reductase 1; prostate sho				6.56E-05	0.67	10.15	6.30	35414.1
AHQ-7-9, 3369	K.GSGVTTYSVHPGTVQSELVR.H	2075.26811	2	6.56E-05	0.67	2.91	-	454.9
gi|22749499|ref|NP_689979.1| hypothetical protein MGC40107 [Homo sapiens]				6.73E-05	0.91	10.21	24.80	11741.6
AHQ-7-14-, 5434	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	6.73E-05	0.91	4.12	-	1157.8
gi|5803013|ref|NP_006808.1| endoplasmic reticulum protein 29 precursor; endoplasmic reticulum lumen				6.76E-05	0.88	10.16	5.70	28993.2
AHQ-7-10, 3724 - 3749	K.ILDQGEDFPASEMTR.I	1709.85924	2	6.76E-05	0.88	3.19	-	913.7
gi|29732170|ref|XP_291550.1| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				6.79E-05	0.96	10.25	12.70	13262.9
AHQ-7-5, 4179	K.HLEINPDHSIIETLR.Q	1787.99770	3	6.79E-05	0.96	5.06	-	1488.3
gi|17017988|ref|NP_001853.2| cytochrome c oxidase subunit Vb precursor; cytochrome c oxidase polype				6.84E-05	0.46	10.14	9.30	13695.6
AHQ-7-13-, 3571	K.KGLDPYNVLAPK.G	1315.54272	2	6.84E-05	0.46	2.71	-	457.4
gi|4757766|ref|NP_004299.1| Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa				6.85E-05	0.95	10.26	4.60	50435.4
AHQ-7-7, 6018	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	3	1.75E-04	0.59	3.28	-	369.2
AHQ-7-7, 6016	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	6.85E-05	0.95	5.20	-	757.6
gi|19913441|ref|NP_002140.2| hippocalcin-like 1; visinin-like protein 3; calcium-binding protein BD				6.87E-05	1.46	20.15	11.90	22313.1
AHQ-7-11, 3272	K.LRPEVLQDLR.E	1239.44948	2	8.94E-04	0.55	2.78	-	443.9
AHQ-7-11, 3630 - 3643	R.TFDTNGDGTIDFR.E	1459.49937	2	6.87E-05	0.92	2.97	-	1154.0
gi|7662338|ref|NP_054735.1| suppressor of actin 1 [Homo sapiens]				6.88E-05	0.81	10.17	2.70	66966.5
AHQ-7-1, 5061	R.LSNTSPEFQEMSLLER.A	1882.08493	2	6.88E-05	0.81	3.35	-	518.7
gi|5453990|ref|NP_006254.1| proteasome (prosome, macropain) activator subunit 1 (PA28 alpha); Prote				7.14E-05	0.66	10.14	4.80	28722.9
AHQ-7-10, 6023	R.NAYAVLYDIILK.N	1396.65574	2	7.14E-05	0.66	2.60	-	544.6
gi|4507295|ref|NP_003560.1| syntaxin 7 [Homo sapiens]				7.15E-05	0.47	10.13	5.70	29845.3
AHQ-7-13-, 3373	R.TLNQLGTPQDSPELR.Q	1669.81798	2	9.92E-05	0.64	2.60	-	591.0
AHQ-7-10, 3208	R.TLNQLGTPQDSPELR.Q	1669.81798	2	7.15E-05	0.47	2.68	-	389.5
gi|22538814|ref|NP_002976.2| small inducible cytokine A5 precursor; T-cell specific protein p288; T				7.18E-05	0.87	10.15	12.10	9989.6
AHQ-7-14-, 3757 - 3769	K.CSNPAVVFVTR.K	1251.43718	2	3.31E-04	0.83	2.89	-	652.3
AHQ-7-14, 4696	K.CSNPAVVFVTR.K	1251.43718	2	7.18E-05	0.87	2.98	-	810.4
gi|19923262|ref|NP_004153.2| RAB5A, member RAS oncogene family; RAS-associated protein RAB5A [Homo				7.30E-05	1.36	20.14	9.80	23658.5
AHQ-7-10, 3705 - 3751	K.FEIWDTAGQER.Y	1352.43364	2	7.30E-05	0.86	2.82	-	1144.7
AHQ-7-10, 2883	R.YHSLAPMYYR.G	1301.49810	2	7.02E-04	0.50	2.52	-	606.5
gi|29731062|ref|XP_293011.1| hypothetical protein XP_293011 [Homo sapiens]				7.41E-05	0.53	10.15	14.50	20147.8
AHQ-7-9, 6009 - 6065	K.QYYKHQEFDNHINSYDHAHKQRTSK.I	3176.36627	3	7.41E-05	0.53	3.04	-	387.9
gi|11321585|ref|NP_002065.1| guanine nucleotide-binding protein, beta-1 subunit; G protein, beta-1				7.90E-05	0.36	10.15	5.90	37376.8
AHQ-7-9, 3746	R.KACADATLSQITNNIDPVGR.I	2146.36794	2	7.90E-05	0.36	2.65	-	336.4
gi|14211923|ref|NP_115982.1| PKCI-1-related HIT protein [Homo sapiens]				8.18E-05	1.75	20.26	22.70	17161.6
AHQ-7-13-, 5927	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	2	8.18E-05	0.95	5.13	-	1459.9
AHQ-7-13, 5931 - 5961	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	3.32E-04	0.75	3.37	-	903.5
AHQ-7-13-, 5875	K.SLPADILYEDQQCLVFR.D	2069.32354	2	3.15E-04	0.80	3.26	-	540.1
gi|27477132|ref|NP_061934.2| phosphatidylinositol-3 phosphate 3-phosphatase adaptor subunit; 3-phos				8.22E-05	0.31	10.14	2.40	86147.2
AHQ-7-5, 5712	R.LPAYFVVPTPLPEENVQR.F	2070.37621	2	8.22E-05	0.31	2.52	-	323.0
gi|4506713|ref|NP_002945.1| ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte				8.53E-05	0.77	10.19	10.30	17964.8
AHQ-7-14, 5224 - 5281	K.TITLEVEPSDTIENVK.A	1788.97431	2	8.53E-05	0.77	3.72	-	776.9
gi|5174393|ref|NP_006001.1| arginine-rich, mutated in early stage tumors; arginine-rich protein [Ho				8.65E-05	0.93	10.24	7.30	26906.2
AHQ-7-12, 5208 - 5266	K.DRDVTFSPATIENELIK.F	1949.15100	2	8.65E-05	0.93	4.77	-	909.7
gi|11496277|ref|NP_068805.1| mitogen-activated protein kinase kinase 1 interacting protein 1; MEK p				8.76E-05	0.92	10.24	22.60	13622.6
AHQ-7-14-, 5119	K.VANDNAPEHALRPGFLSTFALATDQGSK.L	2929.19327	3	8.76E-05	0.92	4.73	-	1018.5
gi|13376689|ref|NP_079390.1| hypothetical protein FLJ13615 [Homo sapiens]				9.01E-05	0.25	10.13	2.30	67925.5
AHQ-7-9, 3888	R.LDLKKKNSSNGSR.K	1447.62278	1	9.01E-05	0.25	2.03	-	513.1
gi|9910542|ref|NP_064535.1| SAR1a gene homolog 1; SAR1 protein [Homo sapiens]				9.02E-05	0.92	10.21	11.60	22366.6
AHQ-7-11, 6162	K.VELNALM*TDETISNVPILILGNK.I	2514.92088	2	5.23E-04	0.62	2.78	-	456.6
AHQ-7-11, 6095 - 6158	K.VELNALM*TDETISNVPILILGNK.I	2514.92088	3	9.02E-05	0.92	4.22	-	927.8
gi|4502211|ref|NP_001654.1| ADP-ribosylation factor 6 [Homo sapiens]				9.08E-05	0.89	10.16	6.30	20082.0
AHQ-7-12, 3910 - 3911	K.FNVWDVGGQDK.I	1265.35598	2	9.08E-05	0.89	3.20	-	1165.1
gi|30153966|ref|XP_293932.2| similar to hypothetical protein BC013073 [Homo sapiens]				9.30E-05	0.26	10.20	9.00	21711.3
AHQ-7-1, 3976	R.MIFTLFTINVSKDIRHH	2073.44997	2	1.48E-04	0.54	2.89	-	425.0
AHQ-7-1, 4147	R.MIFTLFTINVSKDIRHH	2073.44997	3	9.38E-04	0.77	3.70	-	968.5
AHQ-7-2, 3789	R.MIFTLFTINVSKDIRHH	2073.44997	3	8.11E-04	0.60	3.25	-	666.7
AHQ-7-2, 3985	R.MIFTLFTINVSKDIRHH	2073.44997	2	7.95E-04	0.74	3.22	-	714.8
AHQ-7-2, 4236 - 4307	R.MIFTLFTINVSKDIRHH	2073.44997	2	8.22E-04	0.38	2.88	-	422.6
AHQ-7-3, 3703	R.MIFTLFTINVSKDIRHH	2073.44997	2	7.54E-04	0.53	3.25	-	357.5
AHQ-7-3, 3907	R.MIFTLFTINVSKDIRHH	2073.44997	2	9.30E-05	0.26	2.63	-	331.6
AHQ-7-3, 4088	R.MIFTLFTINVSKDIRHH	2073.44997	3	9.35E-04	0.71	3.38	-	954.4
AHQ-7-7, 3968	R.MIFTLFTINVSKDIRHH	2073.44997	2	5.10E-04	0.37	2.90	-	389.2
gi|4502923|ref|NP_001830.1| calponin 3; calponin, acidic [Homo sapiens]				9.50E-05	0.89	10.15	3.30	36413.4
AHQ-7-12, 2716	K.GPSYGLSAEVK.N	1108.22631	2	9.50E-05	0.89	3.06	-	986.8
gi|5729999|ref|NP_006561.1| Ras-related GTP-binding protein RAGA [Homo sapiens]				1.02E-04	0.61	10.11	1.90	36565.9
AHQ-7-13, 3906 - 3965	K.VLLMGK.S	660.89221	1	1.02E-04	0.61	2.21	-	709.2
gi|4503477|ref|NP_001950.1| eukaryotic translation elongation factor 1 beta 2; eukaryotic translati				1.05E-04	0.76	10.16	6.70	24763.6
AHQ-7-9, 4932 - 4997	K.SPAGLQVLNDYLADK.S	1604.78589	2	1.05E-04	0.76	3.15	-	563.1
gi|28461290|ref|NP_443728.2| TRALPUSH; no opposite paired repeat protein [Homo sapiens]				1.07E-04	0.53	10.15	0.40	240073.5
AHQ-7-8, 3538	K.KKPQVNAK.D	913.09970	1	1.07E-04	0.53	2.24	-	478.2
AHQ-7-6, 3573	K.KKPQVNAK.D	913.09970	1	6.52E-04	0.58	2.57	-	450.9
gi|21361565|ref|NP_001679.2| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, is				1.09E-04	0.90	10.20	5.90	28908.4
AHQ-7-11, 6335 - 6336	R.YGLIPEEFFQFLYPK.T	1892.18434	2	1.09E-04	0.90	3.98	-	405.0
gi|4506181|ref|NP_002778.1| proteasome alpha 2 subunit; proteasome subunit HC3; proteasome componen				1.16E-04	0.85	10.16	6.00	25898.4
AHQ-7-11, 3555	K.HIGLVYSGMGPDYR.V	1565.77809	2	1.16E-04	0.85	3.13	-	747.8
gi|29743626|ref|XP_297123.1| hypothetical protein XP_297123 [Homo sapiens]				1.20E-04	0.72	10.16	13.80	13908.9
AHQ-7-13, 6425	R.M*EQKNVRSNNVWELAK.I	1963.20761	2	1.20E-04	0.72	3.12	-	746.9
gi|27484943|ref|XP_084514.3| similar to heat shock 90kDa protein 1, alpha; heat shock 90kD protein				1.21E-04	0.80	10.17	3.50	39364.6

AHQ-7-5, 2690	R.ELISNSSDALDK.I	1292.37482	2	1.21E-04	0.80	3.33	-	608.3
gi|4503117|ref|NP_000091.1| cystatin B; stefin B; liver thiol proteinase inhibitor; CPI-B [Homo sap				1.23E-04	0.89	10.21	21.40	11139.5
AHQ-7-13-, 3621 - 3672	R.VFQSLPHENKPLTLSNYQTNK.A	2459.74218	3	1.23E-04	0.89	4.28	-	820.9
AHQ-7-13, 3802	R.VFQSLPHENKPLTLSNYQTNK.A	2459.74218	3	9.65E-04	0.84	4.13	-	618.9
gi|4503573|ref|NP_001967.1| enolase 3; enolase-3, beta, muscle; muscle specific enolase; beta enola				1.29E-04	0.88	10.17	3.50	46958.5
AHQ-7-8, 3843	K.VNQIGSVTESIQACK.L	1635.82159	2	1.29E-04	0.88	3.47	-	925.2
gi|4557323|ref|NP_000031.1| apolipoprotein C-III precursor [Homo sapiens]				1.37E-04	0.86	10.16	16.20	10852.2
AHQ-7-14-, 3189	K.DALSSVQESQVAQQAR.G	1717.81950	2	1.37E-04	0.86	3.23	-	1195.7
gi|8923904|ref|NP_061158.1| bridging integrator 3 [Homo sapiens]				1.38E-04	0.63	10.17	5.50	29664.7
AHQ-7-7, 5180	R.M*DAFNQEKVNQIQK.T	1709.90558	2	1.38E-04	0.63	3.32	-	401.3
gi|4505409|ref|NP_002503.1| non-metastatic cells 2, protein (NM23B) expressed in; Non-metastatic ce				1.41E-04	0.80	10.15	9.90	17297.9
AHQ-7-14-, 5830 - 5834	K.EISLWFKPEELVDYK.S	1897.15929	2	1.41E-04	0.80	2.99	-	646.1
gi|19923142|ref|NP_002256.2| karyopherin beta 1; nuclear factor p97; importin 90; importin beta-1 s				1.46E-04	0.69	10.17	1.70	97169.7
AHQ-7-4, 5738	R.ESCLEAYTGIVQGLK.G	1669.87794	2	1.46E-04	0.69	2.91	-	635.4
gi|21361399|ref|NP_055040.2| protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alp				1.56E-04	0.83	10.18	3.20	65308.3
AHQ-7-6, 5613 - 5681	K.SEIIPMFSNLASDEQDSVR.L	2139.32924	2	1.56E-04	0.83	3.69	-	619.8
gi|4506189|ref|NP_002783.1| proteasome alpha 7 subunit isoform 1; proteasome subunit RC6-1; proteas				1.57E-04	0.77	10.16	6.00	27886.7
AHQ-7-10, 3855	K.NYTDEAIETDDLTIK.L	1741.83137	2	1.57E-04	0.77	2.84	-	733.2
gi|21361397|ref|NP_037409.2| Rac GTPase activating protein 1; GTPase activating protein [Homo sapie				1.57E-04	0.33	10.13	1.70	71026.2
AHQ-7-8, 3215	R.IKFGKLSLKCR.D	1351.68616	2	1.57E-04	0.33	2.57	-	531.8
gi|4502013|ref|NP_001616.1| adenylate kinase 2 isoform a; adenylate kinase, mitochondrial; adenylat				1.57E-04	0.94	10.22	6.70	26477.6
AHQ-7-10, 3776	R.LQAYHTQTTPLIEYYR.K	1998.22695	2	1.57E-04	0.94	4.31	-	1230.0
gi|6005786|ref|NP_009214.1| monoglyceride lipase; lysophospholipase-like [Homo sapiens]				1.58E-04	0.81	10.23	4.50	34292.3
AHQ-7-13, 5866 - 5874	K.LTVPFLLLQGSADR.L	1530.79329	2	1.58E-04	0.81	3.27	-	611.0
gi|21618359|ref|NP_004095.3| fatty acid synthase [Homo sapiens]				1.70E-04	2.84	30.28	2.30	273262.0
AHQ-7-3, 5801	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	3.57E-04	0.95	5.55	-	988.8
AHQ-7-2, 6669	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	6.00E-04	0.95	4.14	-	1479.9
AHQ-7-1, 5128	K.VVVQVLAEEPEAVLK.G	1623.91540	2	1.70E-04	0.94	4.42	-	1276.1
gi|4504751|ref|NP_002196.1| integrin alpha 5 precursor; fibronectin receptor, alpha subunit; very l				1.73E-04	0.90	10.20	1.70	114507.7
AHQ-7-3, 3793	R.LLESSLSSSEGEEPVEYK.S	1984.10415	2	1.73E-04	0.90	4.01	-	580.9
gi|9257232|ref|NP_000598.1| orosomucoid 1 precursor; Orosomucoid-1 (alpha-1-acid glycoprotein-1); a				1.79E-04	0.87	10.15	7.00	23511.4
AHQ-7-1, 5992	K.EQLGEFYEALDCLR.I	1744.90337	2	1.79E-04	0.87	2.98	-	1033.0
gi|14210536|ref|NP_115914.1| similar to chicken tubulin beta 5 [Homo sapiens]				1.83E-04	0.67	10.18	3.80	49856.8
AHQ-7-12, 5596 - 5655	K.M*ASTFIGNSTAIQELFK.R	1875.13550	2	1.83E-04	0.67	3.55	-	682.5
gi|20540570|ref|XP_116321.1| similar to 60 kDa heat shock protein, mitochondrial precursor (Hsp60)				1.99E-04	0.88	10.20	6.10	24274.4
AHQ-7-4, 6334	K.TLNDELEIMEGMK.F	1523.75487	3	1.99E-04	0.88	3.96	-	1296.3
gi|4502419|ref|NP_000704.1| biliverdin reductase B (flavin reductase (NADPH)); flavin reductase (NA				2.02E-04	0.90	10.18	11.70	22119.2
AHQ-7-11, 4472	R.LPSEGPRPAHVVVGDVLQAADVDK.T	2470.76651	3	2.02E-04	0.90	3.70	-	1372.0
gi|20149637|ref|NP_057526.2| type 1 tumor necrosis factor receptor shedding aminopeptidase regulato				2.04E-04	0.49	10.13	1.40	107761.4
AHQ-7-4, 6222	R.NPVGYPLAWQFLR.K	1561.81077	2	2.04E-04	0.49	2.56	-	347.4
gi|4505237|ref|NP_002427.1| palmitoylated membrane protein 1; membrane protein, palmitoylated 1 (55				2.07E-04	0.78	10.17	6.90	52296.2
AHQ-7-13-, 3915	R.SRPEAVSHPLNTVTEDMYTNGSPAPGSPAQVK.G	3339.63863	3	2.07E-04	0.78	3.49	-	568.3
gi|8922712|ref|NP_060713.1| hypothetical protein FLJ10849 [Homo sapiens]				2.12E-04	1.87	20.21	6.80	49397.9
AHQ-7-7, 2554	K.AAAQLLQSQAQQSGAQQTK.K	1958.12276	2	2.12E-04	0.93	4.25	-	1092.0
AHQ-7-7, 2889	K.RNEFLGELQK.K	1234.38656	2	7.01E-04	0.94	3.31	-	1698.5
gi|28872861|ref|NP_055987.1| HBxAg transactivated protein 2 [Homo sapiens]				2.22E-04	0.51	10.13	0.40	295826.6
AHQ-7-10, 2324 - 2369	R.EPNLEPMVEK.Q	1186.36048	2	2.22E-04	0.51	2.56	-	434.8
gi|21361427|ref|NP_055182.2| hypothetical protein, estradiol-induced [Homo sapiens]				2.24E-04	0.88	10.20	8.90	21551.0
AHQ-7-13-, 5456	K.EDEIPETVSLEMLDAAK.N	1891.08690	2	2.24E-04	0.88	3.90	-	390.4
gi|23065544|ref|NP_000552.2| glutathione S-transferase M1 isoform 1; HB subunit 4; glutathione S-al				2.25E-04	0.76	10.15	7.80	25711.6
AHQ-7-10, 5855	K.LGLDFPNLPYLIDGAHK.I	1884.16698	3	2.25E-04	0.76	3.05	-	823.9
gi|22748717|ref|NP_689541.1| hypothetical protein FLJ38602 [Homo sapiens]				2.27E-04	0.37	10.14	2.60	50208.1
AHQ-7-14, 4198	K.RRCGWLDLMILR.Y	1590.94188	2	2.27E-04	0.37	2.77	-	382.7
gi|4885583|ref|NP_005397.1| Rho-associated, coiled-coil containing protein kinase 1; p160ROCK; p160				2.29E-04	0.26	10.13	1.30	158173.3
AHQ-7-3, 4631	R.CDTAVGTPDYISPEVLK.S	1867.06682	2	2.29E-04	0.26	2.64	-	297.9
gi|19745148|ref|NP_056078.1| rabconnectin-3 [Homo sapiens]				2.38E-04	0.56	10.17	1.00	339754.9
AHQ-7-14-, 5299	R.GLHMKLDHDLSLDRESEAGTGSSEHEDGER.E	3309.44151	3	2.38E-04	0.56	3.30	-	413.0
gi|22538465|ref|NP_002786.2| proteasome beta 3 subunit; proteasome theta chain; proteasome chain 13				2.41E-04	0.77	10.14	7.80	22948.8
AHQ-7-11, 4932	R.FGPYYTEPVIAGLDPK.T	1768.00162	2	2.41E-04	0.77	2.80	-	718.8
gi|7706563|ref|NP_057614.1| RAB-8b protein [Homo sapiens]				2.44E-04	0.93	10.20	6.80	23584.0
AHQ-7-11, 5263 - 5264	K.SSANVEEAFFTLAR.D	1542.67465	2	2.44E-04	0.93	4.03	-	1277.2
gi|4506405|ref|NP_002872.1| v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP				2.46E-04	1.80	20.22	15.50	23408.4
AHQ-7-10, 3511	R.SKAEEWGVQYVETSAK.T	1812.95765	2	2.47E-04	0.97	4.48	-	1871.7
AHQ-7-10, 3456	R.VKAEEDKIPLLVVGNK.S	1753.07630	2	2.46E-04	0.83	3.85	-	620.5
gi|4506265|ref|NP_000954.1| prostaglandin-endoperoxide synthase 2 precursor; prostaglandin G/H synt				2.53E-04	0.57	10.13	1.50	68995.7
AHQ-7-6, 4095	R.LILIGETIK.I	1000.25717	2	2.53E-04	0.57	2.63	-	537.0
gi|20357529|ref|NP_005264.2| guanine nucleotide-binding protein, beta-2 subunit; G protein, beta-2				2.60E-04	0.81	10.18	5.90	37330.8
AHQ-7-9, 4521	R.KACGDSTLTQITAGLDPVGR.I	2062.29094	2	2.60E-04	0.81	3.53	-	547.5
gi|6005727|ref|NP_006576.1| chaperonin containing TCP1, subunit 8 (theta); T-complex protein 1, the				2.66E-04	0.88	10.18	2.90	59662.4
AHQ-7-7, 5109	K.IAVYSCPFDGMITETK.G	1834.10347	2	2.66E-04	0.88	3.54	-	583.7
gi|13376539|ref|NP_079295.1| hypothetical protein FLJ13940 [Homo sapiens]				2.69E-04	0.79	10.16	5.00	27546.1
AHQ-7-13-, 4036 - 4048	R.QIFHPEQLITGK.E	1411.63050	2	2.69E-04	0.79	3.23	-	338.0
gi|29729329|ref|XP_291459.1| similar to Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18) [				2.70E-04	0.71	10.19	5.20	17172.9
AHQ-7-12, 2442	K.NIILEEGK.E	916.05399	1	2.70E-04	0.71	3.25	-	480.3
gi|4507669|ref|NP_003286.1| tumor protein, translationally-controlled 1; fortilin; histamine-releas				2.73E-04	0.81	10.15	8.10	19595.2
AHQ-7-11, 4044	R.DLISHDEM*FSDIYK.I	1729.88889	2	2.73E-04	0.81	3.06	-	875.3
gi|25121940|ref|NP_004482.2| glucocorticoid receptor DNA binding factor 1 isoform b [Homo sapiens]				2.76E-04	0.35	10.11	0.70	172174.1
AHQ-7-7, 3297	R.EDTSLPSLSK.D	1077.16739	1	2.76E-04	0.35	1.87	-	593.2
gi|20149570|ref|NP_005816.2| RAS guanyl releasing protein 2 isoform 1; calcium and diacylglycerol-r				2.80E-04	0.92	10.16	2.10	75547.0
AHQ-7-12, 3894	R.HSSLIDIDSVPTYK.W	1575.74455	2	2.80E-04	0.92	3.19	-	1398.7
gi|22065448|ref|XP_084610.2| similar to tubulin alpha-1 chain - Chinese hamster [Homo sapiens] [MAS				2.80E-04	0.79	10.14	2.40	41009.4
AHQ-7-11, 4658	K.EIIDLVLDR.I	1086.26378	2	2.80E-04	0.79	2.89	-	820.0
gi|4758986|ref|NP_004209.1| RAB11B, member RAS oncogene family; RAB11B, member of RAS oncogene fami				2.82E-04	0.80	10.16	9.60	24573.4
AHQ-7-11, 5798	K.NNLSFIETSALDSTNVEEAFK.N	2330.49008	2	2.82E-04	0.80	3.28	-	658.6
gi|21071030|ref|NP_570602.2| alpha 1B-glycoprotein [Homo sapiens]				2.83E-04	0.93	10.28	7.50	54253.2
AHQ-7-6, 6537 - 6539	R.LHDNQNGWSGDSAPVELILSDETLPAPEFSPEPESGR.A	3993.21165	3	2.83E-04	0.93	5.52	-	612.8
gi|30158950|ref|XP_301585.1| similar to natural killer cell transcript 4 [Homo sapiens]				2.84E-04	0.32	10.18	15.40	18547.1
AHQ-7-1, 4853 - 4923	R.EPTVNKDIHQRTCDLSKTIEAPAER.Q	2911.19785	3	2.84E-04	0.32	3.22	-	267.1
gi|5031611|ref|NP_005859.1| BET1 homolog; Golgi vesicular membrane trafficking protein p18; Bet1p h				2.89E-04	1.83	20.22	15.30	13289.4
AHQ-7-14-, 5275 - 5290	K.LLAEMDSQFDSTTGFLGK.T	1961.18205	2	8.75E-04	0.88	3.74	-	849.9
AHQ-7-14, 5462	K.LLAEM*DSQFDSTTGFLGK.T	1977.18145	2	2.89E-04	0.95	4.32	-	1000.4
gi|19923264|ref|NP_004571.2| RAB27A, member RAS oncogene family [Homo sapiens]				2.93E-04	0.85	10.16	4.50	24867.9
AHQ-7-14-, 4577	K.FITTVGIDFR.E	1169.35448	2	7.97E-04	0.91	3.10	-	869.6
AHQ-7-10, 4316	K.FITTVGIDFR.E	1169.35448	2	2.93E-04	0.85	2.97	-	827.5
gi|29731325|ref|XP_293023.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				3.07E-04	0.74	10.16	6.00	28867.8
AHQ-7-12, 3899	K.AGPNTNGSQFFICTAK.T	1714.88050	2	3.07E-04	0.74	3.26	-	348.7
gi|4503141|ref|NP_001805.1| cathepsin C isoform a preproprotein; dipeptidyl-peptidase I; dipeptidyl				3.07E-04	0.93	10.22	4.10	51841.5
AHQ-7-14-, 5237	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	3.07E-04	0.93	4.45	-	858.7
AHQ-7-14, 5978 - 5985	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	5.15E-04	0.89	4.04	-	696.4
gi|4504041|ref|NP_002061.1| guanine nucleotide binding protein (G protein), alpha inhibiting activi				3.12E-04	0.60	10.17	5.10	40450.7
AHQ-7-9, 4412	K.ITHSPLTICFPEYTGANK.Y	2051.30821	2	3.12E-04	0.60	3.10	-	418.1
gi|11386143|ref|NP_000925.1| alpha-2-plasmin inhibitor; alpha-2-antiplasmin [Homo sapiens]				3.22E-04	0.58	10.16	5.30	54595.5
AHQ-7-7, 6385	K.GFPIKEDFLEQSEQLFGAKPVSLTGK.Q	2867.24489	3	3.22E-04	0.58	3.13	-	661.5
gi|21245108|ref|NP_631960.1| TGFB-induced factor 2-like, Y-linked [Homo sapiens]				3.23E-04	0.69	10.14	4.90	20813.6
AHQ-7-13, 5729	R.CQERSNQIR.S	1192.28823	2	3.23E-04	0.69	2.81	-	822.4
gi|30158489|ref|XP_301421.1| similar to Chloride intracellular channel protein 1 (Nuclear chloride				3.27E-04	0.88	10.19	6.60	28267.5
AHQ-7-9, 5446 - 5524	K.FLNGNELTLADCNLLPK.L	1934.20276	2	3.27E-04	0.88	3.70	-	915.6

gi|9910280|ref|NP_064505.1|	UDP-glucose ceramide glucosyltransferase-like 1; UDP-glucose:glycoprote			3.28E-04	0.79	10.19	1.10	177187.7
AHQ-7-3, 5380	R.YVLEPEISFTSDNSFAK.G	1948.11833	2	3.28E-04	0.79	3.83	-	316.4
gi|4503823|ref|NP_002028.1|	protein-tyrosine kinase fyn isoform a; proto-oncogene tyrosine-protein			3.32E-04	0.76	10.15	2.00	60761.5
AHQ-7-7, 3665	K.WTAPEAALYGR.F	1235.37302	2	3.32E-04	0.76	3.01	-	563.7
gi|4503443|ref|NP_001388.1|	endothelin converting enzyme 1 [Homo sapiens]			3.33E-04	1.24	20.17	4.20	87163.2
AHQ-7-3, 5063	K.DNFQDTLQVVTAHYR.T	1807.94433	2	3.33E-04	0.45	2.70	-	534.6
AHQ-7-3, 6501	K.NEIVFPAGILQAPFYTR.S	1937.22988	2	4.25E-04	0.80	3.34	-	772.8
gi|4504795|ref|NP_002215.1|	inositol 1,4,5-triphosphate receptor, type 3 [Homo sapiens]			3.35E-04	0.40	10.15	1.10	304113.7
AHQ-7-14, 5928 - 5989	K.PLVQAELSVLVDVLHWPELLFLEGSEAYQR.C	3452.94285	3	3.35E-04	0.40	3.06	-	316.7
gi|7657649|ref|NP_055362.1|	tropomodulin 3 (ubiquitous) [Homo sapiens]			3.43E-04	1.86	30.16	14.20	39594.5
AHQ-7-11, 2548	K.DREDYVPYTGEK.K	1472.53805	2	9.68E-04	0.49	2.60	-	553.0
AHQ-7-11, 5315	K.ILPVFDEPPNPTNVEESLK.R	2139.39048	2	7.69E-04	0.55	3.05	-	298.7
AHQ-7-12, 4894	K.YKDLDEDELLGNLSETELK.Q	2225.39217	2	3.43E-04	0.82	3.17	-	709.2
gi|30148456|ref|XP_293602.2|	similar to glutathione-S-transferase like; glutathione transferase ome			3.50E-04	0.94	10.17	3.90	29139.6
AHQ-7-11, 4431	K.VPSLVGSFLR.T	1075.28583	2	7.19E-04	0.87	2.98	-	1008.0
AHQ-7-10, 4296 - 4303	K.VPSLVGSFLR.T	1075.28583	2	3.50E-04	0.94	3.43	-	1277.3
gi|16418461|ref|NP_443195.1|	mitochondrial topoisomerase I [Homo sapiens]			3.51E-04	0.24	10.13	2.20	69871.5
AHQ-7-14, 4890	R.WEKEKHEDGVKWR.Q	1727.90404	2	3.51E-04	0.24	2.55	-	273.7
gi|4505881|ref|NP_000292.1|	plasminogen [Homo sapiens]			3.51E-04	0.73	10.16	2.00	90568.6
AHQ-7-4, 4824 - 4830	K.VIPACLPSPNYVVADR.T	1773.04622	2	3.51E-04	0.73	3.23	-	332.8
gi|4826864|ref|NP_005001.1|	neuronal cell adhesion molecule; Bravo [Homo sapiens]			3.54E-04	0.18	10.12	0.70	130627.1
AHQ-7-2, 4356	R.EDYICYAR.F	1091.17590	1	3.54E-04	0.18	1.96	-	367.7
gi|29732431|ref|XP_039259.5|	similar to modifier of cell adhesion [Homo sapiens]			3.61E-04	0.38	10.15	1.10	153585.7
AHQ-7-8, 4402 - 4416	K.EFLLKIFCVFRNLM*K.M	1976.43736	2	3.61E-04	0.38	3.01	-	370.5
gi|4506773|ref|NP_002956.1|	S100 calcium-binding protein A9; calgranulin B [Homo sapiens]			3.65E-04	0.91	10.22	13.20	13241.9
AHQ-7-13-, 5496 - 5499	R.NIETIINTFHQYSVK.L	1808.02738	2	3.65E-04	0.91	4.47	-	703.9
AHQ-7-13, 5570	R.NIETIINTFHQYSVK.L	1808.02738	2	5.42E-04	0.68	2.95	-	623.2
gi|16975484|ref|NP_056057.1|	centaurin delta 2 isoform b; ARF-GAP, RHO-GAP, ankyrin repeat, and ple			3.67E-04	0.70	10.15	1.20	136262.7
AHQ-7-3, 4940	R.AVFPEGPCEEPLQLR.K	1743.96175	2	3.67E-04	0.70	2.91	-	485.5
gi|8922835|ref|NP_060776.1|	hypothetical protein FLJ11036 [Homo sapiens]			3.76E-04	0.94	10.20	6.90	22353.4
AHQ-7-13, 5863	R.IHSVLQGFIPLFQK.F	1627.95380	2	3.76E-04	0.94	3.97	-	1066.4
gi|11072091|ref|NP_057736.2|	Crn, crooked neck-like 1; CGI-201 protein; crooked neck protein (crn);			3.84E-04	0.33	10.10	1.10	99200.7
AHQ-7-3, 3151	R.FVLVHPDVK.N	1054.26662	1	3.84E-04	0.33	1.97	-	714.7
gi|22041780|ref|XP_059066.2|	similar to 14-3-3 protein sigma (Stratifin) (Epithelial cell marker pr			3.92E-04	0.93	10.22	4.00	27773.9
AHQ-7-13-, 5639 - 5640	K.DSTLIMQLLR.D	1190.43864	2	3.92E-04	0.93	4.40	-	1257.2
gi|7656894|ref|NP_055093.1|	heat shock protein (hsp110 family) [Homo sapiens]			3.98E-04	0.95	10.22	1.70	94504.9
AHQ-7-4, 5453 - 5466	R.GCALQCAILSPAFK.V	1538.81393	2	3.98E-04	0.95	4.39	-	1273.3
gi|4507649|ref|NP_003280.1|	tropomyosin 2 (beta) [Homo sapiens]			3.99E-04	0.75	10.14	4.60	32989.6
AHQ-7-9, 4074	K.TIDDLEETLASAK.E	1406.51783	2	3.99E-04	0.75	2.53	-	793.8
gi|4503507|ref|NP_001406.1|	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa; euk			4.06E-04	0.88	10.19	3.00	51109.2
AHQ-7-7, 2813	K.VGQEIEVRPGIVSK.D	1511.74837	2	4.06E-04	0.88	3.72	-	843.4
gi|7662318|ref|NP_055644.1|	Prp5-like DEAD-box protein [Homo sapiens]			4.09E-04	0.26	10.11	0.80	117460.5
AHQ-7-11, 3862	R.DSIINDFK.N	952.04319	1	4.09E-04	0.26	2.26	-	352.0
gi|4757768|ref|NP_004300.1|	Rho GDP dissociation inhibitor (GDI) alpha [Homo sapiens]			4.23E-04	1.72	20.20	8.30	23206.9
AHQ-7-10, 3632	K.SIQEIQELDKDDESLR.K	1919.03693	2	4.23E-04	0.87	4.02	-	849.6
AHQ-7-10, 3292	K.SIQEIQELDKDDESLRK.Y	2047.20984	2	4.96E-04	0.85	3.74	-	759.6
gi|4759302|ref|NP_004729.1|	VAMP (vesicle-associated membrane protein)-associated protein B and C;			4.24E-04	0.87	10.17	5.30	27228.2
AHQ-7-14-, 2491	K.SLSSSLDDTEVKK.V	1409.52171	2	4.24E-04	0.87	3.33	-	980.0
gi|29745118|ref|XP_292125.1|	similar to submaxillary apomucin [Homo sapiens]			4.32E-04	0.11	10.09	0.80	117947.5
AHQ-7-6, 3290	K.TATISPGASR.T	961.05485	1	4.32E-04	0.11	1.83	-	271.1
gi|20127450|ref|NP_002729.2|	protein kinase C, beta 1; Protein kinase C, beta 1 polypeptide [Homo s			4.52E-04	0.79	10.14	2.40	77011.7
AHQ-7-5, 4272	K.DVVIQDDDVECTMVEK.R	1897.07159	2	4.52E-04	0.79	2.84	-	863.2
gi|4885153|ref|NP_005198.1|	v-crk sarcoma virus CT10 oncogene homolog (avian)-like; v-crk avian sar			4.56E-04	0.85	10.16	5.00	33776.7
AHQ-7-11, 3954	K.IHYLDTTTLIEPAPR.Y	1740.98094	2	4.56E-04	0.85	3.18	-	888.2
gi|6005768|ref|NP_009216.1|	GABA(A) receptor-associated protein-like 2; ganglioside expression fact			4.58E-04	0.75	10.17	9.40	13666.8
AHQ-7-13-, 2859	K.VSGSQIVDIDK.R	1161.28752	2	4.58E-04	0.75	3.08	-	653.4
gi|18585927|ref|XP_097006.1|	similar to MUSP1 [Homo sapiens]			4.60E-04	0.02	10.10	7.20	12657.6
AHQ-7-11, 3826	R.YNQRQKNK.N	1079.19466	1	4.60E-04	0.02	2.09	-	71.7
gi|21536449|ref|NP_002613.2|	prefoldin 1; prefoldin subunit 1 [Homo sapiens]			4.61E-04	0.93	10.18	9.00	14210.4
AHQ-7-13-, 3688 - 3755	K.LADIQIEQLNR.T	1313.48523	2	4.61E-04	0.93	3.59	-	1588.0
gi|4759096|ref|NP_004252.1|	15 kDa selenoprotein [Homo sapiens]			4.71E-04	0.71	10.13	8.00	17640.3
AHQ-7-13, 5443	K.WNTDSVEEFLSEK.L	1584.66517	2	4.71E-04	0.71	2.61	-	683.2
gi|5032009|ref|NP_005600.1|	glycogen phosphorylase; phosphorylase, glycogen, muscle; myophosphoryla			4.72E-04	0.82	10.14	1.00	97091.4
AHQ-7-5, 3958	R.VIFLENYR.V	1054.22348	2	4.72E-04	0.82	2.86	-	614.8
gi|4507797|ref|NP_003341.1|	ubiquitin-conjugating enzyme E2 variant 2; 1 alpha,25-dihydroxyvitamin			4.81E-04	0.88	10.16	6.90	16362.7
AHQ-7-12, 3019	R.LLEELEEGQK.G	1188.30974	2	4.81E-04	0.88	3.27	-	1076.5
gi|5453591|ref|NP_006435.1|	SMC2 structural maintenance of chromosomes 2-like 1; structural mainten			5.00E-04	0.31	10.13	0.80	135779.4
AHQ-7-13-, 3977	K.YEVLENKMK.N	1154.36162	1	5.00E-04	0.31	2.42	-	489.8
gi|22748683|ref|NP_689522.1|	hypothetical protein FLJ35564 [Homo sapiens]			5.15E-04	0.04	10.13	1.80	70407.8
AHQ-7-7, 2310	K.HGHYPNTIAEK.H	1267.37511	1	5.15E-04	0.04	1.97	-	125.7
gi|4502993|ref|NP_001858.1|	cytochrome c oxidase subunit VIIc precursor; cytochrome-c oxidase chain			5.21E-04	0.91	10.18	27.00	7245.5
AHQ-7-14-, 6361	K.M*CLYFGSAFATPFLVVR.H	1997.36876	2	5.21E-04	0.91	3.58	-	1110.5
gi|28373103|ref|NP_005164.2|	sarco/endoplasmic reticulum Ca2+ -ATPase isoform a; ATPase, Ca(2+)-tra			5.26E-04	0.89	10.16	1.30	109255.5
AHQ-7-14-, 3942	R.LGIFGDTEDVAGK.A	1322.44575	2	5.26E-04	0.89	3.29	-	877.6
gi|13435359|ref|NP_001914.2|	damage-specific DNA binding protein 1; damage-specific DNA binding pro			5.31E-04	0.78	10.20	2.60	126987.0
AHQ-7-4, 3854	R.IEVQDTSGGTTALRPSASTQALSSSVSSSK.L	2954.15138	3	5.31E-04	0.78	3.91	-	579.3
gi|10880989|ref|NP_067075.1|	RAB18, member RAS oncogene family; RAB18 small GTPase [Homo sapiens] [			5.52E-04	0.71	10.17	6.80	22976.9
AHQ-7-11, 5828	K.LDNWLNELETYCTR.N	1828.98037	2	5.52E-04	0.71	3.38	-	496.8
gi|22749489|ref|NP_689973.1|	hypothetical protein FLJ30934 [Homo sapiens]			5.87E-04	0.55	10.15	5.40	31378.3
AHQ-7-5, 5167	R.ADRVMRAHKCTQGPR.G	1785.04860	2	5.87E-04	0.55	2.82	-	390.3
gi|11545777|ref|NP_071349.1|	likely ortholog of mouse ubiquitin-conjugating enzyme E2-230K [Homo sa			5.92E-04	0.68	10.14	2.00	81876.4
AHQ-7-7, 6464	K.SGYPDIGFPLFPLSK.G	1638.88708	2	5.92E-04	0.68	2.85	-	503.4
gi|8922297|ref|NP_060502.1|	LUC7-like; sarcoplasmic reticulum protein LUC7B1 [Homo sapiens]			5.97E-04	0.21	10.12	2.20	38405.1
AHQ-7-9, 3049 - 3081	R.EKLDQLR.K	902.03054	1	5.97E-04	0.21	2.33	-	244.2
gi|28376635|ref|NP_783865.1|	Rab37-like [Homo sapiens]			6.22E-04	0.94	10.18	5.60	24169.2
AHQ-7-10, 3916 - 3924	R.AWLTEIHEYAQR.D	1517.67002	2	6.22E-04	0.94	3.67	-	1342.8
gi|7705777|ref|NP_057095.1|	CGI-63 protein [Homo sapiens]			6.57E-04	0.31	10.11	3.50	40057.0
AHQ-7-7, 4125	K.QPVVASVSLLIFK.D	1401.71866	1	6.57E-04	0.31	2.10	-	503.8
gi|17450333|ref|XP_060887.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			6.69E-04	0.67	10.14	11.00	17503.9
AHQ-7-12, 5888 - 5943	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	6.69E-04	0.67	2.72	-	706.2
gi|4757996|ref|NP_004060.1|	adaptor-related protein complex 2, sigma 1 subunit isoform AP17; clathr			6.81E-04	0.93	10.17	8.50	17017.6
AHQ-7-13-, 3489	K.LIEEVHAVVTVR.D	1365.60327	2	6.81E-04	0.93	3.34	-	1425.2
gi|4503291|ref|NP_001346.1|	D-dopachrome tautomerase [Homo sapiens]			6.82E-04	0.70	10.13	9.30	12711.7
AHQ-7-14-, 5406	R.FFPLESWQIGK.I	1352.56151	2	6.82E-04	0.70	2.55	-	341.4
gi|4505395|ref|NP_002499.1|	nidogen (enactin); Nidogen; nidogen (entactin) [Homo sapiens]			6.87E-04	0.86	10.17	1.30	136488.3
AHQ-7-2, 5464	K.ALEGLQYPFAVTSYGK.N	1744.96805	2	6.87E-04	0.86	3.33	-	869.8
gi|14745898|ref|XP_016144.2|	similar to tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activat			7.02E-04	0.92	10.17	7.50	18201.0
AHQ-7-9, 5978	K.LLCCDILDVLDK.N	1479.74157	2	7.02E-04	0.92	3.41	-	949.4
gi|5453555|ref|NP_006316.1|	ras-related nuclear protein [Homo sapiens]			7.07E-04	0.58	10.16	6.50	24422.9
AHQ-7-10, 5331	K.SNYNFEKPFLWLAR.K	1786.02509	2	7.07E-04	0.58	3.13	-	359.7
gi|11496891|ref|NP_000662.2|	class III alcohol dehydrogenase 5 chi subunit; Alcohol dehydrogenase (			7.24E-04	0.74	10.15	4.30	39738.1
AHQ-7-8, 4443	K.VDEFVTHNLSFDEINK.A	1908.05744	2	7.24E-04	0.74	3.00	-	564.2
gi|16904381|ref|NP_006717.1|	LPS-responsive vesicle trafficking, beach and anchor containing; vesic			7.66E-04	0.90	10.23	1.00	319158.3
AHQ-7-4, 4878	K.FPSNSPVTHVAANTQPGLATPAVITVTANR.L	3033.38776	3	7.66E-04	0.90	4.62	-	895.7
gi|5453629|ref|NP_006391.1|	dynactin 2; dynactin complex 50 kD subunit; dynamitin; 50 kD dynein-ass			7.71E-04	0.65	10.14	3.40	44819.3
AHQ-7-11, 4124	R.LLHEVQELTTEVEK.I	1668.86989	2	7.71E-04	0.65	2.79	-	400.6
gi|20546215|ref|XP_115639.1|	similar to leukocyte immunoglobulin-like receptor, subfamily B (with T			7.76E-04	0.37	10.15	4.70	42748.2

AHQ-7-7, 4590 - 4614	R.CSREVNSREDNVLYRVVK.P	2225.47152	2	7.76E-04	0.37	2.55	-	621.2
gi|4505301|ref|NP_002463.1| myosin, heavy polypeptide 8, skeletal muscle, perinatal [Homo sapiens]				7.86E-04	0.38	10.19	1.40	222660.8
AHQ-7-4, 3637 - 3700	K.AGLLGLLEEM*RDEKLAQIITRTQAVCR.G	3103.60765	3	7.86E-04	0.38	3.02	-	245.0
gi|4502153|ref|NP_000375.1| apolipoprotein B precursor; apoB-100; apoB-48 [Homo sapiens]				7.91E-04	0.63	10.13	0.40	515560.6
AHQ-7-1, 6312	K.ATFQTPDFIVPLTDLR.I	1835.09273	2	7.91E-04	0.63	2.67	-	425.9
gi|5453916|ref|NP_006311.1| progesterone membrane binding protein [Homo sapiens]				8.55E-04	0.89	10.19	8.50	23818.3
AHQ-7-10, 3025	R.GLGAGAGAGEESPATSLPR.M	1698.81618	2	8.55E-04	0.89	3.88	-	859.8
gi|21070997|ref|NP_003147.2| stromal interaction molecule 1 precursor [Homo sapiens]				8.57E-04	0.83	10.17	2.00	77422.9
AHQ-7-7, 5981	K.ALDTVLFGPPLLTR.H	1513.80587	2	8.57E-04	0.83	3.37	-	619.2
gi|9845255|ref|NP_000574.1| group-specific component (vitamin D binding protein); hDBP [Homo sapien				8.65E-04	0.45	10.15	4.60	53049.5
AHQ-7-6, 6807	K.VPTADLEDVLPLAEDITNILSK.C	2367.67804	3	8.65E-04	0.45	3.05	-	369.2
gi|30157526|ref|XP_297980.2| hypothetical protein XP_297980 [Homo sapiens]				8.67E-04	0.31	10.16	6.90	48376.1
AHQ-7-5, 5135 - 5204	K.QTARNHHGQEDSFRHPSSVGVFTAAHMLSR.A	3362.64690	3	8.67E-04	0.31	3.10	-	324.2
gi|30158009|ref|XP_210183.2| similar to 60S ribosomal protein L7a (Surfeit locus protein 3) (PLA-X				8.68E-04	0.65	10.18	8.20	33293.0
AHQ-7-4, 4248	K.GDIPNKRPPVLQAGVKTVTNLVENK.K	2689.10724	3	8.68E-04	0.65	3.55	-	555.0
gi|11321640|ref|NP_066301.1| basic beta 1 syntrophin; 59-DAP; syntrophin, beta 1; syntrophin, beta				8.72E-04	0.72	10.16	3.30	58060.8
AHQ-7-6, 4581	R.TAFTDLPEQVPESISNQK.R	2005.17142	2	8.72E-04	0.72	3.23	-	419.3
gi|4502219|ref|NP_001656.1| ras homolog gene family, member G (rho G); RhoG [Homo sapiens]				8.96E-04	1.30	20.16	13.10	21338.4
AHQ-7-11, 2472	K.EVFAEAVR.A	921.03232	2	9.29E-04	0.52	2.57	-	434.9
AHQ-7-11, 4648	R.TVNLNLWDTAGQEEYDR.L	2025.12129	2	8.96E-04	0.79	3.22	-	729.2
gi|22027538|ref|NP_037506.2| programmed cell death 6 interacting protein; ALG-2 interacting protein				8.98E-04	0.96	10.23	1.80	96022.6
AHQ-7-5, 5219 - 5224	R.SVIEQGGIQTVDQLIK.E	1728.96847	2	8.98E-04	0.96	4.68	-	1686.7
gi|30155531|ref|XP_305444.1| hypothetical protein XP_305444 [Homo sapiens]				9.00E-04	0.33	10.13	14.00	13692.9
AHQ-7-4, 6326	K.TELVENGCGKLADQWKK.K	1978.21563	2	9.00E-04	0.33	2.61	-	301.0
gi|5453710|ref|NP_006139.1| LIM and SH3 protein 1; Lasp-1 [Homo sapiens]				9.14E-04	0.69	10.14	5.00	29717.0
AHQ-7-13, 4030	K.GFSVVADTPELQR.I	1419.56466	2	9.14E-04	0.69	2.82	-	755.5
gi|4757714|ref|NP_004291.1| acid phosphatase 1 isoform c; acid phosphatase of erythrocyte; red cell				9.15E-04	0.84	10.18	7.00	18042.4
AHQ-7-11, 3672 - 3730	K.IELLGSYDPQK.Q	1263.42144	2	9.15E-04	0.84	3.53	-	904.6
gi|17864092|ref|NP_061720.1| axonemal dynein heavy chain 7 [Homo sapiens]				9.86E-04	0.37	10.17	0.30	461142.7
AHQ-7-7, 3154	R.LYDKYDFLITRK.A	1575.83252	2	9.86E-04	0.37	2.65	-	402.3

Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|12667788|ref|NP_002464.1|	myosin, heavy polypeptide 9, non-muscle [Homo sapiens]			1.00E-30	89.97	1020.36	44.20	226529.8
AHQ-8-2, 2156	R.ALEEAMEQK.A	1049.18068	2	1.37E-04	0.76	3.08	-	666.0
AHQ-8-5, 3676	K.ALELDSNLYR.I	1194.31920	2	5.84E-07	0.95	4.06	-	1324.0
AHQ-8-3, 3702	K.ALELDSNLYR.I	1194.31920	2	2.68E-06	0.95	3.89	-	1292.0
AHQ-8-2, 3653	K.ALELDSNLYR.I	1194.31920	2	9.12E-07	0.95	3.64	-	1681.2
AHQ-8-2, 3764 - 3768	K.ALELDSNLYR.I	1194.31920	2	1.95E-06	0.96	3.89	-	1410.4
AHQ-8-2, 3781	K.ALELDSNLYR.I	1194.31920	1	1.82E-04	0.26	2.15	-	284.9
AHQ-8-1, 3864	K.ALELDSNLYR.I	1194.31920	2	3.73E-06	0.94	3.73	-	1319.5
AHQ-8-2, 3911	K.ALELDSNLYR.I	1194.31920	2	4.74E-05	0.73	2.57	-	587.2
AHQ-8-14-, 3702 - 3711	K.ALELDSNLYR.I	1194.31920	2	2.26E-06	0.82	3.12	-	747.7
AHQ-8-4, 3705 - 3706	K.ALELDSNLYR.I	1194.31920	2	3.76E-06	0.95	3.84	-	1310.8
AHQ-8-6, 2823 - 2899	R.ALEQQVEEMK.T	1205.36380	2	2.86E-05	0.85	3.15	-	984.7
AHQ-8-5, 2909	R.ALEQQVEEMK.T	1205.36380	2	5.12E-05	0.89	3.38	-	979.5
AHQ-8-3, 2940 - 2941	R.ALEQQVEEMK.T	1205.36380	2	2.42E-06	0.91	3.70	-	1002.4
AHQ-8-2, 2228	R.ALEQQVEEM*K.T	1221.36320	2	8.62E-04	0.83	2.97	-	845.0
AHQ-8-7, 2856	R.ALEQQVEEMK.T	1205.36380	2	1.48E-04	0.77	2.99	-	803.2
AHQ-8-4, 2905	R.ALEQQVEEMK.T	1205.36380	2	3.49E-05	0.86	3.18	-	1068.7
AHQ-8-2, 5996 - 6007	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	2.28E-12	0.98	6.65	-	2149.4
AHQ-8-5, 5941 - 5972	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.24E-07	0.98	6.12	-	2462.4
AHQ-8-1, 5992	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	8.03E-05	0.86	4.05	-	788.0
AHQ-8-6, 5838	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.06E-11	0.92	4.51	-	1168.6
AHQ-8-4, 5993 - 6029	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	3.36E-07	0.97	6.01	-	1909.8
AHQ-8-8, 4774	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.24E-04	0.71	2.86	-	550.4
AHQ-8-5, 4910	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.19E-06	0.89	4.02	-	742.2
AHQ-8-2, 5069	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.70E-07	0.96	4.73	-	1289.3
AHQ-8-6, 4738	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.64E-05	0.96	4.68	-	1182.7
AHQ-8-1, 4920	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.72E-09	0.96	4.75	-	1381.5
AHQ-8-2, 4880	K.ANLQIDQINTDLNLER.S	1871.04187	3	4.80E-04	0.98	5.35	-	2854.7
AHQ-8-2, 4959	K.ANLQIDQINTDLNLER.S	1871.04187	2	8.01E-10	0.95	4.70	-	991.6
AHQ-8-2, 4687 - 4761	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.60E-11	0.97	5.47	-	1180.6
AHQ-8-2, 4871	K.ANLQIDQINTDLNLER.S	1871.04187	2	7.66E-08	0.97	5.41	-	1605.4
AHQ-8-3, 4741 - 4797	K.ANLQIDQINTDLNLER.S	1871.04187	2	8.31E-08	0.97	5.68	-	1494.3
AHQ-8-3, 4800	K.ANLQIDQINTDLNLER.S	1871.04187	3	5.46E-04	0.97	4.80	-	2499.0
AHQ-8-4, 2439	K.ASITALEAK.I	904.04321	2	1.99E-04	0.92	3.22	-	940.3
AHQ-8-3, 2481	K.ASITALEAK.I	904.04321	2	6.27E-06	0.93	3.22	-	1219.6
AHQ-8-2, 2501	K.ASITALEAK.I	904.04321	2	5.32E-06	0.94	3.46	-	1198.4
AHQ-8-5, 2430	K.ASITALEAK.I	904.04321	2	2.43E-05	0.90	3.35	-	840.0
AHQ-8-5, 2145	R.ASREEILAQAK.E	1216.36955	2	8.46E-04	0.90	3.19	-	1415.1
AHQ-8-4, 2151	R.ASREEILAQAK.E	1216.36955	2	2.43E-04	0.92	3.56	-	1385.5
AHQ-8-2, 2204	R.ASREEILAQAK.E	1216.36955	2	3.25E-06	0.95	3.44	-	1775.3
AHQ-8-4, 2738	R.DELADEIANSSGK.G	1349.38323	2	1.25E-04	0.87	2.54	-	999.8
AHQ-8-2, 3175	R.DELADEIANSSGK.G	1349.38323	2	6.16E-08	0.92	3.65	-	1258.1
AHQ-8-5, 3125	R.DELADEIANSSGK.G	1349.38323	2	9.27E-07	0.93	3.14	-	1436.6
AHQ-8-2, 2800 - 2812	R.DELADEIANSSGK.G	1349.38323	2	1.42E-06	0.96	3.63	-	1660.1
AHQ-8-2, 6265 - 6308	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	8.40E-10	0.95	5.12	-	1459.5
AHQ-8-2, 6048	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	2	1.07E-05	0.91	3.37	-	1124.5
AHQ-8-3, 5948 - 5950	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	5.73E-05	0.86	3.82	-	1069.6
AHQ-8-3, 6164 - 6186	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.04E-11	0.97	5.59	-	2302.9
AHQ-8-3, 6165 - 6166	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	2	1.30E-04	0.77	3.24	-	538.3
AHQ-8-5, 6228	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	5.72E-05	0.95	4.06	-	2043.7
AHQ-8-2, 6371	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	1.37E-06	0.67	3.38	-	785.4
AHQ-8-1, 5960	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	8.02E-08	0.82	3.59	-	730.8
AHQ-8-6, 2212 - 2259	K.DLEAHIDSANK.N	1213.27938	2	2.03E-04	0.95	3.29	-	1784.5
AHQ-8-2, 2260	K.DLEAHIDSANK.N	1213.27938	2	7.10E-06	0.98	3.91	-	2618.3
AHQ-8-4, 2155 - 2213	K.DLEAHIDSANK.N	1213.27938	2	4.44E-06	0.98	4.14	-	2678.0
AHQ-8-5, 2209 - 2234	K.DLEAHIDSANK.N	1213.27938	2	8.80E-05	0.98	4.29	-	2631.4
AHQ-8-3, 2200 - 2257	K.DLEAHIDSANK.N	1213.27938	2	1.35E-07	0.97	3.86	-	1874.1
AHQ-8-3, 6460	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	3.91E-08	0.97	4.91	-	2294.7
AHQ-8-2, 6567	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	3.25E-11	0.96	5.14	-	1930.8
AHQ-8-4, 3307 - 3342	K.DVLLQVDDER.R	1202.29650	2	1.26E-07	0.81	2.51	-	1138.2
AHQ-8-2, 3363	K.DVLLQVDDER.R	1202.29650	2	7.57E-07	0.90	3.30	-	960.2
AHQ-8-2, 3007	K.DVLLQVDDERR.N	1358.48286	2	8.14E-04	0.44	2.87	-	554.4
AHQ-8-3, 2264	R.ELEDATETADAM*NR.E	1582.62946	2	1.34E-08	0.94	4.51	-	883.9
AHQ-8-4, 2821	R.ELEDATETADAMNR.E	1566.63006	2	5.14E-09	0.91	3.90	-	967.5
AHQ-8-2, 2865 - 2887	R.ELEDATETADAMNR.E	1566.63006	2	1.52E-07	0.91	3.43	-	1153.7
AHQ-8-4, 2226	R.ELEDATETADAM*NR.E	1582.62946	2	1.51E-05	0.90	3.87	-	723.8
AHQ-8-11, 2792 - 2809	R.ELEDATETADAMNR.E	1566.63006	2	2.72E-08	0.89	3.30	-	962.1
AHQ-8-6, 2806	R.ELEDATETADAMNR.E	1566.63006	2	1.87E-07	0.90	2.73	-	1476.3
AHQ-8-3, 2770 - 2846	R.ELEDATETADAMNR.E	1566.63006	2	7.33E-05	0.40	2.54	-	339.0
AHQ-8-2, 5416 - 5485	R.ELESQISELQEDLESER.A	2035.10956	3	2.27E-05	0.97	5.04	-	2260.7
AHQ-8-4, 5457	R.ELESQISELQEDLESER.A	2035.10956	2	1.64E-09	0.96	4.32	-	1389.3
AHQ-8-2, 5464	R.ELESQISELQEDLESER.A	2035.10956	2	3.23E-04	0.72	3.33	-	599.2
AHQ-8-6, 5327	R.ELESQISELQEDLESER.A	2035.10956	2	1.27E-07	0.88	3.62	-	823.3
AHQ-8-3, 5389 - 5392	R.ELESQISELQEDLESER.A	2035.10956	3	3.87E-08	0.98	5.79	-	2632.4
AHQ-8-2, 5155	R.ELESQISELQEDLESER.A	2035.10956	2	3.68E-05	0.85	3.62	-	587.2
AHQ-8-2, 5707 - 5780	R.ELESQISELQEDLESER.A	2035.10956	2	7.70E-04	0.80	3.35	-	649.7
AHQ-8-3, 4294	R.ELESQISELQEDLESER.A	2035.10956	2	3.66E-06	0.79	3.38	-	547.1
AHQ-8-3, 5077	R.ELESQISELQEDLESER.A	2035.10956	2	1.72E-06	0.59	2.61	-	459.5
AHQ-8-5, 5432	R.ELESQISELQEDLESER.A	2035.10956	2	2.76E-06	0.93	4.19	-	980.0
AHQ-8-3, 5384 - 5418	R.ELESQISELQEDLESER.A	2035.10956	2	4.90E-06	0.92	4.79	-	659.3
AHQ-8-7, 5266	R.ELESQISELQEDLESER.A	2035.10956	2	1.05E-05	0.80	3.24	-	571.9
AHQ-8-1, 5485	R.ELESQISELQEDLESER.A	2035.10956	2	2.21E-07	0.92	4.42	-	935.1
AHQ-8-4, 2554	R.EMEAELEDER.K	1251.30306	2	4.50E-04	0.43	2.52	-	536.0
AHQ-8-2, 2323	R.EMEAELEDERK.Q	1379.47597	2	2.85E-08	0.87	3.06	-	1106.0
AHQ-8-4, 2270	R.EMEAELEDERK.Q	1379.47597	2	2.67E-06	0.92	3.37	-	1085.5
AHQ-8-5, 2269 - 2282	R.EMEAELEDERK.Q	1379.47597	2	1.72E-06	0.91	3.29	-	1157.8
AHQ-8-2, 4339 - 4383	K.EQADFAIEALAK.A	1306.44632	2	1.16E-04	0.81	2.56	-	668.0
AHQ-8-4, 4287	K.EQADFAIEALAK.A	1306.44632	2	4.00E-04	0.75	2.67	-	614.4
AHQ-8-2, 2531	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.68E-06	0.90	4.29	-	704.5
AHQ-8-5, 2465	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	3.34E-04	0.89	3.80	-	716.9
AHQ-8-2, 3436	R.FLSNGHVTIPGQQDK.D	1641.80946	2	2.76E-05	0.88	3.60	-	901.2
AHQ-8-5, 2962	K.HEAMITDLEER.L	1344.47646	2	5.78E-05	0.96	3.76	-	1957.2
AHQ-8-4, 2955 - 3022	K.HEAMITDLEER.L	1344.47646	2	3.30E-06	0.89	3.14	-	899.6
AHQ-8-3, 2993	K.HEAMITDLEER.L	1344.47646	2	2.48E-06	0.95	3.95	-	1185.8
AHQ-8-2, 3377 - 3435	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	1.50E-04	0.98	4.90	-	2534.7
AHQ-8-5, 3520 - 3594	R.HEMPPHIYAITDTAYR.S	1916.14944	3	6.58E-04	0.87	3.88	-	884.8
AHQ-8-2, 3677 - 3695	R.HEMPPHIYAITDTAYR.S	1916.14944	3	1.73E-10	0.97	4.95	-	2313.8
AHQ-8-2, 3433	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	1.82E-04	0.92	3.59	-	853.7
AHQ-8-4, 4415	K.HSQAVEELAEQLEQTK.R	1840.96940	2	6.03E-08	0.98	5.28	-	1892.4
AHQ-8-4, 4418	K.HSQAVEELAEQLEQTK.R	1840.96940	3	5.51E-06	0.95	4.18	-	1913.6
AHQ-8-5, 4388	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.25E-05	0.94	4.52	-	1501.0
AHQ-8-3, 4408 - 4409	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.91E-05	0.97	5.04	-	1987.5
AHQ-8-3, 4404 - 4465	K.HSQAVEELAEQLEQTK.R	1840.96940	2	2.09E-07	0.98	5.54	-	2477.7
AHQ-8-2, 4464 - 4476	K.HSQAVEELAEQLEQTK.R	1840.96940	3	9.46E-06	0.97	5.15	-	2074.7
AHQ-8-2, 4463 - 4527	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.61E-11	0.98	6.36	-	2292.3

AHQ-8-2, 4167	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.00E-30	0.99	6.84	-	2900.8
AHQ-8-6, 4036	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	5.15E-06	0.97	5.46	-	1663.0
AHQ-8-4, 4105	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	5.23E-08	0.98	5.77	-	2884.1
AHQ-8-1, 4273	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.02E-06	0.97	5.79	-	1415.0
AHQ-8-2, 4179 - 4249	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.14E-10	0.97	5.81	-	1596.6
AHQ-8-3, 4100	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.25E-08	0.97	5.96	-	1650.2
AHQ-8-3, 4101	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.48E-09	0.98	6.13	-	2590.9
AHQ-8-5, 4082 - 4158	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.93E-06	0.96	5.83	-	1203.1
AHQ-8-1, 3815 - 3817	R.IAEFTTNLTEEEEK.S	1654.75371	2	6.87E-07	0.95	3.83	-	2018.7
AHQ-8-3, 3602 - 3660	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.95E-08	0.95	4.10	-	1749.3
AHQ-8-13-, 3683	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.54E-06	0.74	2.59	-	807.8
AHQ-8-2, 3859 - 3921	R.IAEFTTNLTEEEEK.S	1654.75371	2	6.87E-08	0.97	4.89	-	1723.1
AHQ-8-2, 3732 - 3800	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.24E-04	0.67	2.54	-	728.6
AHQ-8-3, 3780 - 3850	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.16E-09	0.98	5.16	-	1955.1
AHQ-8-5, 3644	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.13E-07	0.90	3.28	-	1337.9
AHQ-8-7, 3548	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.56E-07	0.93	3.56	-	1474.4
AHQ-8-4, 3634 - 3683	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.39E-08	0.96	4.14	-	1647.4
AHQ-8-2, 3637 - 3700	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.07E-06	0.96	4.32	-	1538.6
AHQ-8-4, 3859	R.IAEFTTNLTEEEEK.S	1654.75371	2	6.20E-08	0.86	3.38	-	809.9
AHQ-8-2, 3759	R.IAEFTTNLTEEEEK.S	1654.75371	2	8.33E-10	0.98	5.12	-	2368.8
AHQ-8-3, 3354 - 3412	R.IAEFTTNLTEEEEKSK.S	1870.00428	2	1.08E-04	0.93	4.44	-	1012.0
AHQ-8-3, 4852 - 4908	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	4.57E-06	0.72	3.70	-	750.6
AHQ-8-4, 5205	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	4.43E-07	0.82	3.74	-	606.8
AHQ-8-2, 5223	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	1.41E-07	0.81	3.89	-	695.0
AHQ-8-4, 3111	K.IAQLEEQLDNETK.E	1531.64695	2	1.64E-07	0.97	4.64	-	1982.4
AHQ-8-7, 3254	K.IAQLEEQLDNETK.E	1531.64695	2	1.75E-05	0.93	3.52	-	1307.9
AHQ-8-2, 3163	K.IAQLEEQLDNETK.E	1531.64695	2	7.82E-10	0.97	4.87	-	1830.1
AHQ-8-6, 3298	K.IAQLEEQLDNETK.E	1531.64695	2	4.01E-04	0.93	4.00	-	1229.3
AHQ-8-4, 3337	K.IAQLEEQLDNETK.E	1531.64695	2	1.37E-08	0.97	4.53	-	1925.2
AHQ-8-3, 3693	K.IAQLEEQLDNETK.E	1531.64695	2	1.43E-04	0.87	3.12	-	964.8
AHQ-8-11, 3052 - 3060	K.IAQLEEQLDNETK.E	1531.64695	2	7.92E-05	0.82	3.30	-	838.3
AHQ-8-11, 3201 - 3271	K.IAQLEEQLDNETK.E	1531.64695	2	1.04E-05	0.92	3.70	-	1180.3
AHQ-8-2, 3395	K.IAQLEEQLDNETK.E	1531.64695	2	8.51E-06	0.96	4.16	-	1507.3
AHQ-8-2, 2992	K.IAQLEEQLDNETK.E	1531.64695	2	1.18E-04	0.93	3.70	-	1180.4
AHQ-8-2, 3505	K.IAQLEEQLDNETK.E	1531.64695	2	1.09E-06	0.89	3.36	-	841.1
AHQ-8-3, 3116	K.IAQLEEQLDNETK.E	1531.64695	2	8.59E-09	0.97	4.25	-	1893.3
AHQ-8-8, 3286 - 3287	K.IAQLEEQLDNETK.E	1531.64695	2	3.00E-05	0.96	4.82	-	1432.7
AHQ-8-5, 3093	K.IAQLEEQLDNETK.E	1531.64695	2	2.51E-06	0.97	4.57	-	1782.0
AHQ-8-1, 3528	K.IAQLEEQLDNETK.E	1531.64695	2	3.67E-09	0.96	4.27	-	1672.5
AHQ-8-2, 3248	K.IAQLEEQLDNETK.E	1531.64695	2	7.59E-04	0.85	3.13	-	995.5
AHQ-8-5, 3332	K.IAQLEEQLDNETK.E	1531.64695	2	2.08E-08	0.97	4.57	-	1818.9
AHQ-8-3, 3352	K.IAQLEEQLDNETK.E	1531.64695	2	1.12E-07	0.96	4.43	-	1497.3
AHQ-8-10, 3226	K.IAQLEEQLDNETK.E	1531.64695	2	5.49E-08	0.93	3.12	-	1548.3
AHQ-8-3, 3085	K.IAQLEEQLDNETKER.Q	1816.94784	2	1.44E-07	0.87	3.59	-	743.3
AHQ-8-2, 3527	K.IAQLEEQLDNETKER.Q	1816.94784	3	9.97E-04	0.71	3.03	-	639.8
AHQ-8-3, 3473	K.IAQLEEQLDNETKER.Q	1816.94784	2	4.28E-08	0.93	4.26	-	1049.1
AHQ-8-2, 3539	K.IAQLEEQLDNETKER.Q	1816.94784	2	7.83E-14	0.94	3.86	-	1252.5
AHQ-8-3, 5956 - 5957	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.27E-07	0.96	5.20	-	1158.1
AHQ-8-5, 5969 - 5985	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.49E-06	0.92	3.96	-	1044.3
AHQ-8-4, 6045	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.78E-06	0.97	5.81	-	1231.6
AHQ-8-2, 5028	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	9.24E-04	0.92	4.15	-	944.5
AHQ-8-2, 5553 - 5565	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.69E-04	0.72	3.53	-	285.6
AHQ-8-2, 6055 - 6059	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	6.46E-07	0.98	6.26	-	1541.1
AHQ-8-1, 6048	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	7.71E-04	0.90	3.72	-	907.3
AHQ-8-1, 4569	R.IMGIPEEEQM*GLLR.V	1632.92766	2	2.17E-04	0.69	3.04	-	323.7
AHQ-8-2, 5521 - 5532	K.IRELESQISELQEDLESER.A	2304.45416	2	1.16E-04	0.97	6.12	-	1057.1
AHQ-8-3, 5432	K.IRELESQISELQEDLESER.A	2304.45416	2	2.52E-04	0.98	6.28	-	1926.6
AHQ-8-3, 5428 - 5430	K.IRELESQISELQEDLESER.A	2304.45416	3	4.74E-10	0.98	6.46	-	2309.0
AHQ-8-2, 5443 - 5519	K.IRELESQISELQEDLESER.A	2304.45416	3	2.17E-07	0.96	5.31	-	1619.7
AHQ-8-1, 5545	K.IRELESQISELQEDLESER.A	2304.45416	2	1.37E-05	0.98	5.85	-	1467.8
AHQ-8-4, 5505	K.IRELESQISELQEDLESER.A	2304.45416	2	1.29E-04	0.98	6.96	-	1398.7
AHQ-8-2, 4952 - 5016	K.ITDVIIGFQACCR.G	1555.80136	2	1.63E-04	0.87	3.46	-	751.2
AHQ-8-5, 4372	K.KANLQIDQINTDLNLER.S	1999.21478	2	5.02E-07	0.96	5.41	-	1225.8
AHQ-8-2, 4303	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.60E-06	0.94	4.94	-	999.9
AHQ-8-3, 4398 - 4405	K.KANLQIDQINTDLNLER.S	1999.21478	3	1.81E-06	0.81	4.24	-	714.8
AHQ-8-6, 4318	K.KANLQIDQINTDLNLER.S	1999.21478	2	2.95E-08	0.95	5.13	-	821.7
AHQ-8-2, 4459	K.KANLQIDQINTDLNLER.S	1999.21478	3	1.86E-04	0.85	4.09	-	771.7
AHQ-8-2, 2756	R.KKVEAQLQELQVK.F	1541.81761	2	3.38E-08	0.98	5.41	-	1846.1
AHQ-8-5, 2697	R.KKVEAQLQELQVK.F	1541.81761	2	3.38E-09	0.96	4.42	-	1486.5
AHQ-8-4, 2685	R.KKVEAQLQELQVK.F	1541.81761	2	6.32E-08	0.98	5.01	-	2046.4
AHQ-8-2, 3567	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.54E-12	0.98	5.21	-	1942.0
AHQ-8-2, 3447 - 3495	K.KLEEEQIILEDQNCK.L	1891.08992	2	8.72E-04	0.95	4.58	-	1244.0
AHQ-8-2, 3499 - 3579	K.KLEEEQIILEDQNCK.L	1891.08992	3	2.13E-05	0.94	4.86	-	1476.5
AHQ-8-4, 3519	K.KLEEEQIILEDQNCK.L	1891.08992	3	9.11E-04	0.91	4.16	-	1253.7
AHQ-8-3, 3444 - 3505	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.42E-09	0.98	6.54	-	1964.5
AHQ-8-4, 3437 - 3511	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.01E-10	0.98	6.37	-	2292.2
AHQ-8-1, 3620	K.KLEEEQIILEDQNCK.L	1891.08992	2	4.66E-04	0.97	5.04	-	1861.6
AHQ-8-5, 3489	K.KLEEEQIILEDQNCK.L	1891.08992	3	6.72E-04	0.82	3.38	-	952.2
AHQ-8-3, 3820	K.KLEEEQIILEDQNCKLAK.E	2203.49930	2	6.42E-08	0.91	4.52	-	574.3
AHQ-8-3, 3816	K.KLEEEQIILEDQNCKLAK.E	2203.49930	3	8.69E-05	0.96	5.66	-	1227.7
AHQ-8-3, 6320 - 6400	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	7.88E-07	0.97	5.92	-	1368.4
AHQ-8-4, 6409	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	9.87E-07	0.92	5.67	-	579.8
AHQ-8-3, 6316	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	5.93E-08	0.92	5.20	-	920.0
AHQ-8-7, 6200 - 6201	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	3.81E-08	0.94	4.85	-	1416.1
AHQ-8-5, 6356	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	6.84E-05	0.79	3.65	-	807.4
AHQ-8-2, 6416 - 6419	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	5.05E-08	0.98	6.67	-	1371.9
AHQ-8-6, 6250	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	8.20E-06	0.88	4.47	-	801.8
AHQ-8-2, 6349 - 6415	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	6.85E-06	0.90	5.13	-	707.1
AHQ-8-1, 6399	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	3.72E-07	0.93	5.38	-	852.3
AHQ-8-5, 2898	K.KLVWVPSDK.S	1072.28194	2	4.30E-05	0.88	3.15	-	948.3
AHQ-8-2, 2971	K.KLVWVPSDK.S	1072.28194	2	4.03E-04	0.86	3.23	-	830.6
AHQ-8-2, 3265	K.KM*EDSVGCLETAEEVK.R	1843.02390	2	4.70E-04	0.89	3.53	-	850.6
AHQ-8-2, 3625	K.KMEDSVGCLETAEEVK.R	1827.02450	2	4.36E-04	0.88	4.09	-	790.8
AHQ-8-2, 3016	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	3.03E-08	0.97	5.72	-	1862.8
AHQ-8-3, 2980	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	1.99E-05	0.95	4.87	-	1510.3
AHQ-8-4, 2958	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	2.10E-07	0.96	5.80	-	1451.1
AHQ-8-3, 2982	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	5.40E-05	0.67	2.72	-	533.3
AHQ-8-3, 3312	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	4.48E-06	0.94	5.19	-	1044.2
AHQ-8-2, 3360	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.61E-08	0.96	4.99	-	1837.7
AHQ-8-5, 3280	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	4.94E-10	0.94	4.98	-	1212.7
AHQ-8-2, 3025	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	5.99E-06	0.92	3.89	-	839.2
AHQ-8-5, 2944	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	6.87E-05	0.90	4.46	-	971.1
AHQ-8-4, 4670	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	1.89E-05	0.87	4.04	-	1065.3
AHQ-8-2, 4716 - 4724	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	6.61E-06	0.89	4.10	-	498.0
AHQ-8-2, 4099	K.KQELEEICHDLEAR.V	1771.93036	2	5.28E-05	0.96	4.83	-	1683.8
AHQ-8-6, 3983	K.KQELEEICHDLEAR.V	1771.93036	3	4.68E-04	0.97	5.69	-	2283.6
AHQ-8-3, 4040	K.KQELEEICHDLEAR.V	1771.93036	2	7.66E-04	0.97	5.47	-	1863.3

AHQ-8-2, 4100	K.KQELEEICHDLEAR.V	1771.93036	3	2.12E-04	0.95	4.57	-	1714.8
AHQ-8-1, 4177 - 4203	K.KQELEEICHDLEAR.V	1771.93036	2	2.38E-06	0.97	5.31	-	1883.0
AHQ-8-5, 2992	K.KVEAQLQELQVK.F	1413.64470	2	4.09E-04	0.95	4.25	-	1331.6
AHQ-8-2, 3075	K.KVEAQLQELQVK.F	1413.64470	2	1.77E-04	0.96	4.64	-	1623.0
AHQ-8-6, 3735	K.KVIQYLAYVASSHK.S	1607.87775	3	3.41E-09	0.96	4.90	-	1620.6
AHQ-8-2, 3889	K.KVIQYLAYVASSHK.S	1607.87775	2	3.95E-06	0.88	3.65	-	857.2
AHQ-8-4, 3713 - 3773	K.LEEEQIILEDQNCK.L	1762.91700	2	1.53E-06	0.97	5.28	-	1247.7
AHQ-8-2, 3772 - 3831	K.LEEEQIILEDQNCK.L	1762.91700	2	1.57E-09	0.97	5.44	-	1523.5
AHQ-8-3, 3700 - 3772	K.LEEEQIILEDQNCK.L	1762.91700	2	2.11E-04	0.94	4.16	-	1066.1
AHQ-8-5, 3690	K.LEEEQIILEDQNCK.L	1762.91700	2	3.70E-04	0.94	4.03	-	1000.8
AHQ-8-3, 6369	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	2	2.64E-08	0.74	3.25	-	614.5
AHQ-8-3, 6368	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	6.77E-04	0.90	4.72	-	941.8
AHQ-8-2, 3571	R.LEVNLQAMK.A	1046.26630	2	1.61E-04	0.84	3.22	-	571.4
AHQ-8-2, 2711 - 2713	R.LEVNLQAM*K.A	1062.26570	2	4.91E-05	0.81	3.33	-	556.2
AHQ-8-6, 3460 - 3536	R.LEVNLQAMK.A	1046.26630	2	5.17E-05	0.57	2.87	-	359.8
AHQ-8-4, 3494 - 3501	K.LKDVLLQVDDER.R	1443.62767	2	2.70E-06	0.96	4.05	-	1779.0
AHQ-8-3, 3425 - 3501	K.LKDVLLQVDDER.R	1443.62767	2	2.72E-09	0.95	3.64	-	1783.3
AHQ-8-2, 3565 - 3572	K.LKDVLLQVDDER.R	1443.62767	2	1.80E-08	0.95	4.37	-	1434.4
AHQ-8-2, 3233	K.LKDVLLQVDDERR.N	1599.81402	3	2.80E-04	0.90	3.70	-	1364.4
AHQ-8-3, 3169 - 3200	K.LKDVLLQVDDERR.N	1599.81402	2	1.32E-05	0.86	3.16	-	1111.4
AHQ-8-2, 3232	K.LKDVLLQVDDERR.N	1599.81402	2	6.55E-04	0.95	3.74	-	1625.6
AHQ-8-4, 3167	K.LKDVLLQVDDERR.N	1599.81402	2	1.68E-05	0.83	3.28	-	1130.4
AHQ-8-2, 6592 - 6656	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	1.03E-07	0.84	3.34	-	579.3
AHQ-8-1, 5707 - 5748	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.97E-07	0.96	5.03	-	1341.2
AHQ-8-2, 5731	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.28E-10	0.97	5.32	-	1672.4
AHQ-8-5, 5676	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	5.43E-06	0.76	3.42	-	653.1
AHQ-8-3, 5553 - 5633	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.59E-08	0.94	4.26	-	1358.8
AHQ-8-3, 5632	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.73E-05	0.91	4.17	-	863.4
AHQ-8-3, 5637	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	4.21E-09	0.97	5.67	-	1534.2
AHQ-8-6, 5583	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.89E-07	0.94	4.49	-	1270.6
AHQ-8-2, 5347	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.75E-05	0.94	5.03	-	996.4
AHQ-8-2, 5355	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	7.31E-08	0.98	5.54	-	2018.0
AHQ-8-3, 5272	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.34E-04	0.91	3.84	-	1159.1
AHQ-8-5, 5680 - 5682	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	6.25E-12	0.98	5.50	-	1786.2
AHQ-8-4, 5714	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.73E-10	0.97	5.16	-	1546.1
AHQ-8-4, 5713	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	5.72E-07	0.89	4.19	-	759.9
AHQ-8-2, 5727	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.50E-06	0.94	4.96	-	1068.8
AHQ-8-2, 5424 - 5483	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.93E-11	0.98	6.25	-	1842.8
AHQ-8-13-, 5274	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.68E-06	0.94	4.64	-	812.6
AHQ-8-2, 6687	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.97E-06	0.83	3.16	-	763.3
AHQ-8-7, 5212	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.04E-08	0.90	3.81	-	838.2
AHQ-8-1, 5196	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.15E-06	0.91	4.05	-	794.5
AHQ-8-1, 5384 - 5441	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.15E-08	0.96	5.46	-	1090.8
AHQ-8-4, 5434	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	2.17E-05	0.84	3.95	-	812.5
AHQ-8-3, 5437 - 5454	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.85E-07	0.95	5.29	-	767.7
AHQ-8-2, 5168	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.67E-13	0.96	5.40	-	1155.0
AHQ-8-4, 5153	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.83E-07	0.92	4.58	-	778.9
AHQ-8-1, 5463	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	2.26E-08	0.96	4.70	-	1753.8
AHQ-8-6, 5284	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.91E-07	0.96	5.24	-	1013.8
AHQ-8-3, 5074	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.34E-06	0.96	5.10	-	1257.8
AHQ-8-5, 5094	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.09E-07	0.94	4.22	-	1135.3
AHQ-8-2, 5543	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.53E-07	0.98	6.43	-	1623.0
AHQ-8-2, 5645 - 5709	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	8.55E-14	0.98	6.44	-	1777.3
AHQ-8-5, 5362	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.00E-04	0.87	3.98	-	608.7
AHQ-8-3, 5325 - 5380	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.47E-08	0.98	6.09	-	1422.3
AHQ-8-3, 5354	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	2.44E-07	0.95	4.80	-	1381.0
AHQ-8-4, 5421 - 5498	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.44E-06	0.96	5.00	-	1075.5
AHQ-8-2, 4165	K.LRLEVNLQAMK.A	1315.61090	2	4.18E-05	0.92	3.48	-	1196.5
AHQ-8-2, 3525 - 3588	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	2.59E-06	0.95	4.10	-	1305.0
AHQ-8-2, 3979	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	3.12E-04	0.98	5.20	-	2738.9
AHQ-8-4, 3926 - 3963	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	1.28E-04	0.96	4.40	-	1781.9
AHQ-8-4, 4865 - 4867	R.LTEMETLQSQLMAEK.L	1753.03211	2	4.26E-05	0.94	4.15	-	1323.3
AHQ-8-3, 3905	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	6.75E-07	0.95	3.96	-	1632.1
AHQ-8-2, 3803 - 3876	K.MEDSVGCLETAEEVK.R	1698.85159	2	3.88E-05	0.66	2.52	-	669.6
AHQ-8-2, 3573	K.MEDSVGCLETAEEVKR.K	1855.03794	2	2.04E-05	0.63	2.92	-	372.6
AHQ-8-2, 3292 - 3296	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	1.63E-07	0.93	4.36	-	756.4
AHQ-8-2, 3289	K.M*EDSVGCLETAEEVKR.K	1871.03734	3	7.08E-04	0.73	3.06	-	696.2
AHQ-8-3, 3258	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	1.16E-06	0.88	3.87	-	581.4
AHQ-8-5, 3469	K.MEDSVGCLETAEEVKR.K	1855.03794	2	2.51E-04	0.47	2.58	-	426.4
AHQ-8-2, 5027	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	2	5.19E-07	0.81	2.68	-	961.8
AHQ-8-1, 5063	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	3.61E-07	0.88	3.92	-	814.5
AHQ-8-3, 4898 - 4956	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	6.17E-05	0.96	5.79	-	1254.8
AHQ-8-3, 5040 - 5041	K.MQQNIQELEEQLEEEESAR.Q	2334.46063	2	3.07E-05	0.42	3.47	-	316.4
AHQ-8-6, 5346 - 5408	K.NFINNPLAQADWAAK.K	1673.85315	2	1.08E-09	0.87	3.50	-	743.1
AHQ-8-2, 5099 - 5107	K.NFINNPLAQADWAAK.K	1673.85315	2	5.27E-10	0.95	4.68	-	1074.1
AHQ-8-5, 5445	K.NFINNPLAQADWAAK.K	1673.85315	2	1.39E-06	0.88	3.54	-	804.1
AHQ-8-3, 5416	K.NFINNPLAQADWAAK.K	1673.85315	2	3.26E-11	0.92	4.04	-	897.9
AHQ-8-4, 5077 - 5078	K.NFINNPLAQADWAAK.K	1673.85315	2	8.86E-06	0.97	4.98	-	1326.3
AHQ-8-5, 5040	K.NFINNPLAQADWAAK.K	1673.85315	2	2.21E-07	0.93	4.02	-	1078.5
AHQ-8-2, 5440 - 5505	K.NFINNPLAQADWAAK.K	1673.85315	2	4.79E-07	0.91	3.74	-	1002.7
AHQ-8-3, 5025	K.NFINNPLAQADWAAK.K	1673.85315	2	1.33E-09	0.97	5.43	-	1152.4
AHQ-8-6, 4960 - 4966	K.NFINNPLAQADWAAK.K	1673.85315	2	5.33E-10	0.97	5.54	-	1152.7
AHQ-8-2, 5252	K.NFINNPLAQADWAAK.K	1673.85315	2	3.68E-07	0.93	4.36	-	943.1
AHQ-8-1, 5144	K.NFINNPLAQADWAAK.K	1673.85315	2	2.52E-06	0.96	4.90	-	1274.4
AHQ-8-2, 5503	K.NFINNPLAQADWAAK.K	1673.85315	2	1.40E-10	0.93	4.72	-	900.6
AHQ-8-7, 4854	K.NFINNPLAQADWAAK.K	1673.85315	2	1.65E-05	0.88	3.82	-	718.1
AHQ-8-2, 2795	K.NKHEAMITDLEER.L	1586.75247	2	1.18E-09	0.91	3.45	-	1142.7
AHQ-8-3, 2745	K.NKHEAMITDLEER.L	1586.75247	2	1.97E-04	0.63	2.65	-	513.1
AHQ-8-3, 5381 - 5390	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.35E-10	0.93	3.87	-	862.6
AHQ-8-1, 5005 - 5017	K.NLPIYSEEIVEM*YK.G	1744.98660	2	4.80E-04	0.94	4.25	-	937.7
AHQ-8-4, 4931 - 4937	K.NLPIYSEEIVEM*YK.G	1744.98660	2	4.04E-10	0.95	4.62	-	854.4
AHQ-8-2, 5461 - 5467	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.16E-11	0.96	4.66	-	1086.1
AHQ-8-3, 4882	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.63E-07	0.95	4.03	-	1032.5
AHQ-8-6, 4819 - 4838	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.60E-05	0.94	4.48	-	968.3
AHQ-8-5, 4904 - 4968	K.NLPIYSEEIVEM*YK.G	1744.98660	2	3.76E-05	0.95	4.30	-	1056.5
AHQ-8-2, 4963	K.NLPIYSEEIVEM*YK.G	1744.98660	2	4.62E-04	0.87	3.32	-	859.2
AHQ-8-2, 5283	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	5.18E-07	0.94	4.37	-	927.2
AHQ-8-2, 4895	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	9.02E-08	0.86	3.22	-	1064.1
AHQ-8-2, 5284 - 5285	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	3	2.16E-06	0.83	3.50	-	510.1
AHQ-8-2, 4892 - 4896	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	8.35E-07	0.92	4.89	-	883.9
AHQ-8-2, 2917	R.QAQQERDELADEIANSSGK.G	2090.15168	2	5.01E-06	0.88	3.80	-	714.2
AHQ-8-2, 3275	R.QAQQERDELADEIANSSGK.G	2090.15168	2	1.95E-04	0.94	4.42	-	762.6
AHQ-8-3, 3238	R.QAQQERDELADEIANSSGK.G	2090.15168	2	6.57E-05	0.85	3.98	-	422.7
AHQ-8-2, 3268 - 3269	R.QAQQERDELADEIANSSGK.G	2090.15168	3	5.14E-05	0.92	4.43	-	1310.8
AHQ-8-3, 3236	R.QAQQERDELADEIANSSGK.G	2090.15168	3	7.74E-04	0.81	3.82	-	665.2
AHQ-8-3, 2877	R.QAQQERDELADEIANSSGK.G	2090.15168	2	2.64E-06	0.79	3.69	-	465.1
AHQ-8-2, 2988	K.QIATLHAQVADMK.K	1426.66697	2	9.48E-05	0.72	3.13	-	376.6

AHQ-8-2, 2143 - 2144	R.QLEEAEEEAQR.A	1332.35590	2	1.07E-05	0.70	3.03	-	550.3
AHQ-8-3, 2133	R.QLEEAEEEAQR.A	1332.35590	2	1.29E-04	0.64	3.04	-	384.7
AHQ-8-2, 2297	K.REQEVNILK.K	1129.29189	2	5.01E-04	0.87	2.65	-	1178.8
AHQ-8-5, 3580	R.RGDLPFVVPR.R	1156.36217	2	1.59E-04	0.93	3.97	-	1179.8
AHQ-8-6, 3546 - 3547	R.RGDLPFVVPR.R	1156.36217	2	5.38E-06	0.95	3.81	-	1209.3
AHQ-8-11, 3519	R.RGDLPFVVPR.R	1156.36217	2	2.78E-05	0.90	3.38	-	912.7
AHQ-8-3, 3612	R.RGDLPFVVPR.R	1156.36217	2	1.71E-04	0.93	3.56	-	1202.3
AHQ-8-1, 3801	R.RGDLPFVVPR.R	1156.36217	2	5.65E-06	0.95	3.90	-	1088.7
AHQ-8-12, 3538	R.RGDLPFVVPR.R	1156.36217	2	2.66E-05	0.91	3.29	-	1196.2
AHQ-8-8, 3474	R.RGDLPFVVPR.R	1156.36217	2	2.43E-04	0.72	2.68	-	702.6
AHQ-8-13-, 3640	R.RGDLPFVVPR.R	1156.36217	2	4.47E-04	0.76	2.68	-	769.3
AHQ-8-2, 3671	R.RGDLPFVVPR.R	1156.36217	2	5.62E-06	0.92	3.46	-	1160.4
AHQ-8-2, 6263	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	8.53E-13	0.98	7.11	-	1523.0
AHQ-8-3, 6184	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	3.65E-08	0.96	6.15	-	1102.0
AHQ-8-2, 6609 - 6673	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.72E-05	0.89	4.25	-	945.3
AHQ-8-2, 6341	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.46E-07	0.70	3.23	-	738.0
AHQ-8-2, 5888 - 5956	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.48E-09	0.97	6.02	-	1548.9
AHQ-8-5, 5745 - 5817	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.64E-06	0.79	3.97	-	779.3
AHQ-8-3, 5800	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.25E-05	0.75	3.22	-	888.1
AHQ-8-13-, 5546 - 5626	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.86E-08	0.90	4.54	-	891.3
AHQ-8-3, 5386	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	4.60E-06	0.96	5.60	-	1706.2
AHQ-8-1, 5477	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	4.27E-06	0.92	4.34	-	1456.5
AHQ-8-1, 4629	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	4.05E-07	0.96	4.34	-	1850.9
AHQ-8-3, 4510	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.60E-08	0.94	4.20	-	1152.9
AHQ-8-2, 4580	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	7.73E-11	0.98	5.55	-	2159.9
AHQ-8-2, 4663 - 4741	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	6.33E-05	0.92	4.04	-	992.3
AHQ-8-4, 4463 - 4535	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.41E-08	0.97	5.13	-	1509.1
AHQ-8-5, 4422 - 4496	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.56E-10	0.96	4.66	-	1376.3
AHQ-8-2, 5188 - 5247	K.SMEAEM*IQLQEELAAAER.A	2066.30004	2	3.62E-07	0.95	5.35	-	1465.8
AHQ-8-6, 3583 - 3598	K.TDLLLEPYNK.Y	1206.36989	2	2.83E-06	0.86	3.29	-	609.0
AHQ-8-2, 3675 - 3745	K.TDLLLEPYNK.Y	1206.36989	2	1.38E-04	0.91	4.12	-	999.4
AHQ-8-3, 3669 - 3676	K.TDLLLEPYNK.Y	1206.36989	2	2.51E-06	0.94	4.31	-	1258.7
AHQ-8-5, 3637	K.TDLLLEPYNK.Y	1206.36989	2	2.27E-05	0.89	3.90	-	885.9
AHQ-8-4, 3669	K.TDLLLEPYNK.Y	1206.36989	2	2.15E-06	0.93	4.15	-	1111.2
AHQ-8-1, 3844	K.TDLLLEPYNK.Y	1206.36989	2	2.55E-05	0.93	3.91	-	1121.1
AHQ-8-7, 3550	K.TDLLLEPYNK.Y	1206.36989	2	6.13E-06	0.89	3.43	-	895.2
AHQ-8-2, 3880	K.TDLLLEPYNKYR.F	1525.73037	2	2.98E-06	0.59	2.77	-	631.4
AHQ-8-4, 4153	K.TELEDTLDSTAAQQELR.S	1921.00969	2	3.22E-07	0.96	4.56	-	1407.8
AHQ-8-3, 4134	K.TELEDTLDSTAAQQELR.S	1921.00969	2	3.15E-05	0.96	5.19	-	1229.6
AHQ-8-2, 4205	K.TELEDTLDSTAAQQELR.S	1921.00969	2	9.10E-11	0.97	5.37	-	1719.9
AHQ-8-2, 6091 - 6157	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	1.39E-07	0.93	4.62	-	1148.7
AHQ-8-5, 6104 - 6120	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	5.09E-04	0.93	4.74	-	1148.1
AHQ-8-5, 2040	K.VAAYDKLEK.T	1037.19123	2	5.78E-06	0.60	2.53	-	533.0
AHQ-8-2, 2117	K.VAAYDKLEK.T	1037.19123	2	3.56E-05	0.76	2.63	-	552.1
AHQ-8-7, 4852 - 4861	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.03E-06	0.91	4.11	-	1052.8
AHQ-8-2, 5049 - 5103	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.70E-09	0.95	5.31	-	1065.8
AHQ-8-2, 5547 - 5617	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	5.05E-06	0.68	3.41	-	656.4
AHQ-8-2, 5625	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	2.25E-09	0.91	4.12	-	668.8
AHQ-8-3, 5024 - 5105	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	4.85E-04	0.80	3.78	-	766.4
AHQ-8-2, 5104 - 5173	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	3.64E-10	0.94	4.45	-	924.8
AHQ-8-5, 4986 - 5044	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	8.91E-04	0.87	4.21	-	789.8
AHQ-8-2, 2145 - 2221	R.VEEEEERCQHLQAEK.K	1916.01642	2	1.13E-04	0.70	3.29	-	548.0
AHQ-8-5, 3909	K.VIQYLAYVASSHK.S	1479.70484	2	8.93E-05	0.86	3.12	-	927.6
AHQ-8-2, 3999	K.VIQYLAYVASSHK.S	1479.70484	2	3.23E-04	0.94	3.68	-	1230.5
AHQ-8-3, 3944	K.VIQYLAYVASSHK.S	1479.70484	2	2.64E-05	0.92	3.35	-	1188.2
AHQ-8-4, 3930	K.VIQYLAYVASSHK.S	1479.70484	2	3.11E-04	0.90	3.44	-	1046.4
AHQ-8-6, 3854	K.VIQYLAYVASSHK.S	1479.70484	2	7.38E-06	0.94	3.84	-	1293.9
AHQ-8-1, 4047 - 4111	K.VIQYLAYVASSHK.S	1479.70484	2	5.90E-05	0.90	3.62	-	983.1
AHQ-8-2, 4004	K.VIQYLAYVASSHK.S	1479.70484	3	4.09E-05	0.63	3.09	-	504.8
AHQ-8-5, 3914	K.VIQYLAYVASSHK.S	1479.70484	3	1.31E-04	0.63	3.24	-	455.6
AHQ-8-7, 3792	K.VIQYLAYVASSHK.S	1479.70484	2	2.33E-04	0.88	3.79	-	787.1
AHQ-8-2, 5955 - 6035	R.VISGVLQLGNIVFK.K	1487.81155	2	3.84E-07	0.95	4.80	-	1138.3
AHQ-8-6, 5875 - 5882	R.VISGVLQLGNIVFK.K	1487.81155	2	2.85E-08	0.98	5.24	-	2027.1
AHQ-8-5, 5976 - 5978	R.VISGVLQLGNIVFK.K	1487.81155	2	6.37E-07	0.96	4.00	-	1537.1
AHQ-8-8, 6029	R.VISGVLQLGNIVFK.K	1487.81155	2	2.89E-05	0.96	4.42	-	1418.4
AHQ-8-7, 5805	R.VISGVLQLGNIVFK.K	1487.81155	2	8.91E-06	0.94	3.58	-	1554.2
AHQ-8-1, 6043 - 6045	R.VISGVLQLGNIVFK.K	1487.81155	2	2.96E-07	0.98	4.85	-	2350.2
AHQ-8-4, 5557	R.VISGVLQLGNIVFKK.E	1615.98446	2	1.81E-04	0.95	4.54	-	1179.6
AHQ-8-3, 5420 - 5490	R.VISGVLQLGNIVFKK.E	1615.98446	2	2.46E-05	0.89	3.29	-	1080.1
AHQ-8-2, 5573 - 5575	R.VISGVLQLGNIVFKK.E	1615.98446	2	1.55E-09	0.93	4.23	-	986.2
AHQ-8-5, 5510	R.VISGVLQLGNIVFKK.E	1615.98446	2	7.73E-04	0.94	4.01	-	1102.2
AHQ-8-7, 4574	K.VSHLLGINVTDFTR.G	1572.79026	2	1.22E-11	0.96	4.55	-	1433.4
AHQ-8-3, 4750	K.VSHLLGINVTDFTR.G	1572.79026	3	3.14E-06	0.90	3.92	-	933.9
AHQ-8-5, 4738	K.VSHLLGINVTDFTR.G	1572.79026	2	4.95E-04	0.88	3.32	-	1187.1
AHQ-8-4, 4774 - 4846	K.VSHLLGINVTDFTR.G	1572.79026	2	7.49E-04	0.89	3.59	-	935.8
AHQ-8-6, 4670	K.VSHLLGINVTDFTR.G	1572.79026	3	3.19E-05	0.91	3.83	-	1396.2
AHQ-8-4, 3223	R.VVFQEFR.Q	925.06580	2	4.18E-05	0.76	2.58	-	700.1
AHQ-8-1, 3432	R.VVFQEFR.Q	925.06580	2	1.36E-04	0.76	2.54	-	624.0
AHQ-8-3, 3884 - 3953	R.YEILTPNSIPK.G	1275.47536	2	3.28E-05	0.97	4.23	-	1840.2
AHQ-8-2, 3948 - 4027	R.YEILTPNSIPK.G	1275.47536	2	1.27E-04	0.92	3.63	-	1179.0
AHQ-8-4, 3887	R.YEILTPNSIPK.G	1275.47536	2	1.06E-07	0.94	3.77	-	1274.1
AHQ-8-2, 4140 - 4141	R.YEILTPNSIPK.G	1275.47536	2	7.52E-05	0.78	3.10	-	787.4
AHQ-8-2, 5712	K.YLYVDKNFINNPLAQADWAAK.K	2455.75199	3	1.76E-07	0.92	4.30	-	1184.0
gi|4504165|ref|NP_000168.1|	gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]			1.00E-30	21.42	250.34	41.20	85696.9
AHQ-8-6, 3616	K.AGALNSNDAFVLK.T	1320.47622	2	7.19E-07	0.86	3.75	-	610.7
AHQ-8-5, 3808 - 3857	K.AGALNSNDAFVLK.T	1320.47622	2	3.05E-06	0.75	3.06	-	515.9
AHQ-8-5, 3593 - 3664	K.AGALNSNDAFVLK.T	1320.47622	2	5.12E-05	0.92	3.95	-	818.4
AHQ-8-5, 3268	K.AGKEPGLQIWR.V	1255.45060	3	2.75E-04	0.86	3.70	-	1066.1
AHQ-8-5, 3261	K.AGKEPGLQIWR.V	1255.45060	2	5.86E-06	0.57	2.66	-	469.3
AHQ-8-6, 5336 - 5339	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.60E-04	0.96	5.14	-	824.6
AHQ-8-5, 5268	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.47E-06	0.94	4.91	-	660.5
AHQ-8-5, 5625	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.86E-04	0.65	2.92	-	412.0
AHQ-8-8, 5441	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.87E-07	0.96	5.67	-	909.3
AHQ-8-10, 5170	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.95E-05	0.81	3.13	-	640.1
AHQ-8-5, 5429 - 5496	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	6.37E-07	0.95	5.15	-	662.4
AHQ-8-7, 5281 - 5285	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.41E-08	0.96	5.31	-	893.7
AHQ-8-11, 5243	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.54E-06	0.83	3.49	-	574.1
AHQ-8-5, 5458	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.13E-05	0.88	3.91	-	989.8
AHQ-8-6, 5279	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	2.74E-09	0.92	4.22	-	1162.7
AHQ-8-5, 5324 - 5380	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.65E-07	0.94	4.29	-	1447.2
AHQ-8-11, 2277	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.98E-07	0.88	3.74	-	996.3
AHQ-8-6, 2271	K.DSQEEEKTEALTSAK.R	1666.72289	3	2.96E-05	0.96	4.42	-	1881.2
AHQ-8-6, 2266	K.DSQEEEKTEALTSAK.R	1666.72289	2	9.08E-06	0.91	3.74	-	1240.9
AHQ-8-7, 2257	K.DSQEEEKTEALTSAK.R	1666.72289	2	5.13E-07	0.94	4.07	-	1291.6
AHQ-8-5, 2265 - 2333	K.DSQEEEKTEALTSAK.R	1666.72289	3	1.20E-04	0.97	4.78	-	2130.7
AHQ-8-5, 2264 - 2329	K.DSQEEEKTEALTSAK.R	1666.72289	2	9.29E-07	0.93	3.79	-	1270.1
AHQ-8-13-, 2342	K.DSQEEEKTEALTSAK.R	1666.72289	2	7.43E-05	0.77	2.90	-	835.2

AHQ-8-8, 2243	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.91E-07	0.93	3.46	-	1450.6
AHQ-8-7, 5676 - 5749	R.EVQGFESATFLGYFK.S	1723.90570	2	3.39E-08	0.94	4.17	-	1038.5
AHQ-8-5, 5880 - 5936	R.EVQGFESATFLGYFK.S	1723.90570	2	9.99E-06	0.96	4.15	-	1408.3
AHQ-8-5, 5789 - 5844	R.EVQGFESATFLGYFK.S	1723.90570	2	3.61E-11	0.97	5.06	-	1538.3
AHQ-8-13-, 5706	R.EVQGFESATFLGYFK.S	1723.90570	2	2.61E-08	0.95	4.31	-	1163.4
AHQ-8-6, 5740 - 5742	R.EVQGFESATFLGYFK.S	1723.90570	2	1.25E-06	0.94	4.21	-	1205.8
AHQ-8-8, 5829 - 5909	R.EVQGFESATFLGYFK.S	1723.90570	2	2.17E-05	0.76	2.93	-	883.3
AHQ-8-14-, 5721	R.EVQGFESATFLGYFK.S	1723.90570	2	1.13E-04	0.88	3.04	-	1046.6
AHQ-8-5, 6484 - 6490	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	2	4.01E-07	0.95	5.02	-	629.3
AHQ-8-5, 2386	K.HVVPNEVVVQR.L	1276.46981	1	2.68E-05	0.21	1.89	-	295.4
AHQ-8-5, 2360 - 2380	K.HVVPNEVVVQR.L	1276.46981	2	6.32E-06	0.93	3.71	-	653.0
AHQ-8-5, 2558	K.HVVPNEVVVQR.L	1276.46981	2	2.51E-04	0.87	3.00	-	582.6
AHQ-8-5, 5780 - 5836	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	1.57E-07	0.96	4.90	-	1687.6
AHQ-8-5, 5360 - 5361	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.00E-30	0.98	6.80	-	1868.0
AHQ-8-6, 5282	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	5.83E-10	0.95	5.26	-	1354.2
AHQ-8-5, 2165	K.PALPAGTEDTAK.E	1171.28241	2	1.23E-06	0.83	2.94	-	411.7
AHQ-8-5, 2081 - 2149	K.PALPAGTEDTAK.E	1171.28241	2	1.92E-04	0.60	2.61	-	274.3
AHQ-8-5, 2529	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	1.70E-06	0.94	4.44	-	641.9
AHQ-8-5, 4642 - 4688	K.QTQVSVLPEGGETPLFK.Q	1831.05925	2	3.13E-04	0.51	3.00	-	235.7
AHQ-8-6, 3108	K.SEDCFILDHGK.D	1322.42590	3	7.59E-06	0.82	3.18	-	756.0
AHQ-8-6, 3099	K.SEDCFILDHGK.D	1322.42590	2	1.03E-06	0.91	3.39	-	965.7
AHQ-8-5, 3100	K.SEDCFILDHGK.D	1322.42590	2	3.12E-04	0.97	4.26	-	1865.7
AHQ-8-5, 2830	K.SEDCFILDHGKDGK.I	1622.73823	2	1.05E-04	0.61	2.78	-	715.9
AHQ-8-5, 2141 - 2206	K.TASDFITK.M	882.98086	2	1.78E-04	0.68	2.81	-	394.9
AHQ-8-5, 2293 - 2353	K.TGAQELLR.V	888.00387	2	4.40E-05	0.91	3.07	-	1278.6
AHQ-8-7, 2282	K.TGAQELLR.V	888.00387	2	5.30E-05	0.84	2.80	-	858.4
AHQ-8-5, 4321 - 4380	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.13E-05	0.97	5.11	-	1513.9
AHQ-8-6, 4271	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	6.78E-10	0.96	4.89	-	1139.4
AHQ-8-8, 4262	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.82E-05	0.90	3.75	-	942.1
AHQ-8-11, 4213	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	4.72E-04	0.71	2.87	-	642.7
AHQ-8-5, 3733 - 3794	R.VHVSEEGTEPEAM*LQVLGPK.P	2167.42570	3	3.72E-04	0.78	3.37	-	673.3
AHQ-8-5, 4782 - 4838	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	3	6.33E-04	0.83	3.55	-	686.0
AHQ-8-5, 4781 - 4804	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	1.71E-04	0.97	5.81	-	1066.6
AHQ-8-5, 5050	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	1.70E-08	0.96	5.88	-	1079.7
AHQ-8-5, 3564 - 3620	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	2.99E-06	0.91	5.34	-	1137.7
AHQ-8-5, 3940	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	2.51E-11	0.97	6.78	-	1457.2
AHQ-8-6, 3516 - 3526	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	1.03E-04	0.87	4.71	-	884.6
AHQ-8-5, 6053	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	2	1.03E-06	0.70	3.22	-	445.4
AHQ-8-5, 5138	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	1.07E-07	0.77	3.43	-	491.5
AHQ-8-6, 5066	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	3.30E-04	0.70	2.77	-	488.6
gi|4505879|ref|NP_002655.1|	pleckstrin; p47 [Homo sapiens]			5.55E-16	6.50	80.39	23.70	40082.5
AHQ-8-8, 5418 - 5429	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.93E-13	0.98	6.94	-	1956.6
AHQ-8-12, 5179 - 5251	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	5.14E-05	0.80	4.42	-	455.0
AHQ-8-8, 2434 - 2447	R.GCVVTSVESNSNGR.K	1467.54464	1	1.02E-05	0.14	2.01	-	115.9
AHQ-8-8, 2179 - 2226	R.GCVVTSVESNSNGRK.S	1595.71755	2	1.47E-07	0.74	3.02	-	579.2
AHQ-8-11, 6251	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	4.18E-06	0.99	7.77	-	3320.2
AHQ-8-12, 6274	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.32E-08	0.98	6.58	-	2475.3
AHQ-8-10, 6202	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.16E-10	0.98	7.35	-	1869.4
AHQ-8-8, 6546 - 6551	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	5.55E-16	0.98	6.81	-	2406.1
AHQ-8-13-, 5334 - 5392	R.LPETIDLGALYLSM*K.D	1680.98719	2	2.69E-04	0.93	4.11	-	1098.8
AHQ-8-8, 5485 - 5486	R.LPETIDLGALYLSM*K.D	1680.98719	2	4.24E-07	0.95	5.09	-	857.8
AHQ-8-8, 6093 - 6154	R.LPETIDLGALYLSMK.D	1664.98779	2	6.05E-07	0.97	4.56	-	1815.1
AHQ-8-12, 4991	R.LPETIDLGALYLSM*KDTEK.G	2154.46684	2	1.38E-04	0.86	3.61	-	567.5
AHQ-8-12, 6314	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	5.34E-08	0.66	3.10	-	558.6
AHQ-8-8, 6589	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	3.69E-04	0.56	3.47	-	313.2
AHQ-8-8, 6585 - 6654	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	5.61E-14	0.89	3.94	-	814.0
gi|4557305|ref|NP_000025.1|	aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho			1.67E-15	8.78	100.25	47.80	39419.7
AHQ-8-8, 4202 - 4214	K.ALSDHHIYLEGTLLKPNMVTPGHACTQK.F	3134.57879	3	6.20E-04	0.89	4.50	-	790.9
AHQ-8-8, 2825	K.GILAADESTGSIAK.R	1333.47008	2	2.04E-10	0.97	4.58	-	1658.5
AHQ-8-8, 2831	K.GILAADESTGSIAK.R	1333.47008	1	2.15E-04	0.55	3.00	-	339.4
AHQ-8-14-, 2990	K.GILAADESTGSIAK.R	1333.47008	2	2.83E-09	0.95	3.75	-	1437.9
AHQ-8-12, 4326	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	1.41E-09	0.68	4.01	-	438.5
AHQ-8-8, 4379 - 4445	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	1.67E-15	0.88	4.96	-	680.4
AHQ-8-8, 4093	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	2.67E-05	0.67	3.93	-	631.3
AHQ-8-8, 4875 - 4942	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.91E-06	0.92	4.28	-	773.6
AHQ-8-8, 5285	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	7.72E-05	0.93	4.21	-	863.1
AHQ-8-8, 4047 - 4082	K.IGEHTPSALAIM*ENANVLAR.Y	2124.40728	2	1.58E-05	0.95	4.93	-	821.5
AHQ-8-8, 2785	R.QLLLTADDR.V	1045.17176	2	3.33E-04	0.74	2.56	-	608.1
AHQ-8-8, 6577	R.TVPPAVTGITFLSGGQSEEEASINLNAINK.C	3059.37393	3	2.91E-04	0.88	4.48	-	1168.3
AHQ-8-8, 5677	R.YASICQQNGIVPIVEPEILPDGDHDLK.R	3023.36334	3	2.40E-04	0.84	4.80	-	458.4
AHQ-8-8, 5361	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	1.39E-06	0.93	4.66	-	1022.0
AHQ-8-8, 4391 - 4454	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	3.64E-06	0.79	3.37	-	446.3
gi|4502549|ref|NP_001734.1|	calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta			3.33E-15	1.78	20.23	22.10	16837.5
AHQ-8-12, 4014 - 4082	K.EAFSLFDKDGDGTITTK.E	1845.98441	3	9.57E-05	0.78	3.04	-	839.4
AHQ-8-12, 4010 - 4038	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	2.38E-04	0.92	3.88	-	1104.0
AHQ-8-12, 4094	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	8.62E-08	0.83	3.12	-	638.2
AHQ-8-12, 3842	R.VFDKDGNGYISAAELR.H	1755.90933	2	3.09E-05	0.85	3.34	-	972.3
AHQ-8-12, 3706 - 3766	R.VFDKDGNGYISAAELR.H	1755.90933	2	3.33E-15	0.95	4.66	-	1075.5
AHQ-8-11, 3705	R.VFDKDGNGYISAAELR.H	1755.90933	3	2.69E-05	0.92	3.75	-	1576.5
gi|16753233|ref|NP_006280.2|	talin 1 [Homo sapiens]			5.00E-15	104.42	1180.38	56.20	269665.3
AHQ-8-13-, 3174 - 3175	K.AAAFEEQENETVVVK.E	1664.79496	2	6.37E-07	0.92	4.38	-	1172.9
AHQ-8-4, 3231 - 3295	K.AAAFEEQENETVVVK.E	1664.79496	2	4.18E-04	0.93	4.34	-	1301.2
AHQ-8-14-, 3155	K.AAAFEEQENETVVVK.E	1664.79496	2	1.66E-06	0.92	4.71	-	958.7
AHQ-8-1, 3349	K.AAAFEEQENETVVVK.E	1664.79496	2	1.05E-05	0.95	4.92	-	1236.1
AHQ-8-2, 3225 - 3300	K.AAAFEEQENETVVVK.E	1664.79496	2	2.42E-05	0.92	4.24	-	1031.5
AHQ-8-5, 3168	K.AAAFEEQENETVVVK.E	1664.79496	2	3.46E-07	0.94	4.43	-	1226.0
AHQ-8-3, 2700	R.AAM*EPIVISAK.T	1146.38260	2	3.09E-07	0.90	2.67	-	1112.9
AHQ-8-2, 2744	R.AAM*EPIVISAK.T	1146.38260	1	1.46E-04	0.22	2.17	-	205.4
AHQ-8-2, 2731	R.AAM*EPIVISAK.T	1146.38260	2	5.83E-06	0.72	2.63	-	633.4
AHQ-8-5, 3266	R.AAMEPIVISAK.T	1130.38320	2	4.88E-04	0.60	2.51	-	410.0
AHQ-8-4, 2667	R.AAM*EPIVISAK.T	1146.38260	1	1.51E-05	0.10	2.06	-	151.2
AHQ-8-7, 4630 - 4696	K.ACEFAGFQCQIQFGPHNEQK.H	2399.60390	3	1.21E-04	0.73	3.46	-	460.9
AHQ-8-3, 2074	K.ADAEGESDLENSR.K	1393.35296	2	3.71E-05	0.85	2.71	-	1153.4
AHQ-8-4, 2026	K.ADAEGESDLENSR.K	1393.35296	2	1.05E-07	0.93	3.74	-	1183.3
AHQ-8-5, 2030	K.ADAEGESDLENSR.K	1393.35296	2	2.15E-06	0.88	3.67	-	794.0
AHQ-8-2, 2072	K.ADAEGESDLENSR.K	1393.35296	2	1.26E-07	0.94	3.91	-	1185.7
AHQ-8-6, 2039	K.ADAEGESDLENSR.K	1393.35296	2	2.58E-05	0.87	3.21	-	874.0
AHQ-8-4, 2641	K.AGALQCSPSDAYTK.K	1470.58689	2	5.88E-06	0.90	3.42	-	819.7
AHQ-8-6, 2635	K.AGALQCSPSDAYTK.K	1470.58689	2	3.99E-04	0.62	2.79	-	545.2
AHQ-8-7, 5737	K.AGFLDLKDFLPK.E	1364.61374	2	9.65E-04	0.87	3.30	-	1183.5
AHQ-8-5, 3905	K.AIAVTVQEMVTK.S	1290.55498	2	8.48E-08	0.94	3.58	-	1251.5
AHQ-8-4, 3925 - 4002	K.AIAVTVQEMVTK.S	1290.55498	2	1.92E-07	0.90	3.36	-	971.4
AHQ-8-2, 3019 - 3032	K.AIAVTVQEM*VTK.S	1306.55438	2	4.96E-05	0.92	3.98	-	806.8
AHQ-8-4, 2942 - 2949	K.AIAVTVQEM*VTK.S	1306.55438	2	1.77E-07	0.95	3.74	-	1260.2
AHQ-8-5, 2937 - 2954	K.AIAVTVQEM*VTK.S	1306.55438	2	2.75E-04	0.88	3.21	-	845.2
AHQ-8-3, 2968	K.AIAVTVQEM*VTK.S	1306.55438	2	3.71E-06	0.92	3.66	-	837.0
AHQ-8-3, 3933 - 3934	K.AIAVTVQEMVTK.S	1290.55498	2	4.05E-07	0.97	4.97	-	1465.6

AHQ-8-4, 2689	K.ALDGAFTEENR.A	1223.27427	2	1.19E-04	0.95	4.03	-	1526.3
AHQ-8-2, 2759	K.ALDGAFTEENR.A	1223.27427	2	5.48E-06	0.95	3.89	-	1452.8
AHQ-8-4, 2506	K.ALDGAFTEENR.A	1223.27427	2	3.80E-06	0.88	3.25	-	1192.4
AHQ-8-3, 2552	K.ALDGAFTEENR.A	1223.27427	2	3.90E-06	0.92	3.49	-	1247.1
AHQ-8-3, 2684 - 2728	K.ALDGAFTEENR.A	1223.27427	2	1.48E-05	0.95	3.72	-	1551.6
AHQ-8-6, 2694	K.ALDGAFTEENR.A	1223.27427	2	3.26E-06	0.95	3.71	-	1676.2
AHQ-8-7, 3806	K.ALDYYMLR.N	1045.23686	2	1.78E-06	0.90	3.25	-	645.2
AHQ-8-5, 2073 - 2084	R.ALEATTEHIR.Q	1141.25953	2	1.37E-05	0.86	2.85	-	1204.7
AHQ-8-6, 2083 - 2084	R.ALEATTEHIR.Q	1141.25953	2	5.70E-05	0.79	2.63	-	969.9
AHQ-8-4, 2082 - 2086	R.ALEATTEHIR.Q	1141.25953	2	4.43E-06	0.88	3.42	-	1096.8
AHQ-8-2, 2140 - 2167	R.ALEATTEHIR.Q	1141.25953	2	2.71E-07	0.90	3.34	-	1280.3
AHQ-8-3, 2138	R.ALEATTEHIR.Q	1141.25953	2	8.83E-06	0.88	2.98	-	1323.0
AHQ-8-3, 3433 - 3446	K.ALGDLISATK.A	989.14811	2	2.33E-06	0.95	4.13	-	904.8
AHQ-8-5, 3409	K.ALGDLISATK.A	989.14811	2	3.92E-06	0.91	3.48	-	846.1
AHQ-8-2, 3477	K.ALGDLISATK.A	989.14811	2	3.92E-04	0.87	3.34	-	616.3
AHQ-8-4, 3419	K.ALGDLISATK.A	989.14811	2	1.56E-06	0.92	3.46	-	900.0
AHQ-8-2, 2573	K.ALSTDPAAPNLK.S	1198.35099	2	8.54E-05	0.58	2.88	-	415.9
AHQ-8-2, 2761 - 2764	K.ALSTDPAAPNLK.S	1198.35099	1	8.07E-04	0.19	1.98	-	312.2
AHQ-8-3, 2710 - 2720	K.ALSTDPAAPNLK.S	1198.35099	2	1.59E-06	0.82	3.08	-	674.1
AHQ-8-5, 2686	K.ALSTDPAAPNLK.S	1198.35099	2	1.38E-05	0.53	2.60	-	598.8
AHQ-8-4, 2686	K.ALSTDPAAPNLK.S	1198.35099	2	1.10E-08	0.64	2.77	-	607.8
AHQ-8-6, 2678	K.ALSTDPAAPNLK.S	1198.35099	2	4.46E-06	0.71	2.89	-	722.1
AHQ-8-2, 2741 - 2755	K.ALSTDPAAPNLK.S	1198.35099	2	1.35E-07	0.85	3.59	-	635.8
AHQ-8-2, 5808	K.APGQLECETAIAALNSCLR.D	2077.32566	2	3.61E-07	0.96	4.66	-	1214.7
AHQ-8-4, 5797	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.11E-06	0.97	4.82	-	1458.4
AHQ-8-2, 5195 - 5255	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.48E-10	0.95	4.67	-	1193.3
AHQ-8-2, 5812	K.APGQLECETAIAALNSCLR.D	2077.32566	3	1.15E-04	0.78	3.58	-	717.1
AHQ-8-3, 5425 - 5496	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	1.31E-05	0.91	4.55	-	1046.2
AHQ-8-3, 6193	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	2	1.02E-07	0.62	2.51	-	536.3
AHQ-8-2, 5599	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	2.25E-04	0.88	3.53	-	1197.5
AHQ-8-2, 6292	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	7.74E-06	0.95	5.10	-	1023.8
AHQ-8-2, 5591	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	2	2.75E-06	0.90	3.52	-	1053.3
AHQ-8-3, 5501 - 5506	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	2	7.88E-04	0.64	3.24	-	662.8
AHQ-8-2, 3048	K.ASAGPQPLLVQSCK.A	1457.67763	2	4.01E-05	0.59	2.64	-	398.7
AHQ-8-5, 2960	K.ASAGPQPLLVQSCK.A	1457.67763	2	5.99E-07	0.63	2.90	-	394.0
AHQ-8-4, 2967	K.ASAGPQPLLVQSCK.A	1457.67763	2	3.51E-06	0.56	2.89	-	332.1
AHQ-8-3, 2994	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.23E-04	0.59	2.74	-	348.8
AHQ-8-7, 2920	K.ASAGPQPLLVQSCK.A	1457.67763	2	4.06E-11	0.83	3.90	-	415.3
AHQ-8-1, 3219	K.ASAGPQPLLVQSCK.A	1457.67763	2	4.94E-06	0.90	3.81	-	562.2
AHQ-8-6, 2939 - 2994	K.ASAGPQPLLVQSCK.A	1457.67763	2	6.69E-08	0.88	3.83	-	503.9
AHQ-8-3, 4104	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.66E-04	0.87	3.41	-	826.2
AHQ-8-4, 4122 - 4123	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.73E-06	0.87	4.34	-	409.6
AHQ-8-1, 3777	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	1.05E-05	0.78	3.74	-	384.9
AHQ-8-4, 4129	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	3	1.90E-05	0.56	3.02	-	364.3
AHQ-8-5, 3608	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	3.64E-06	0.89	3.90	-	582.8
AHQ-8-2, 4145 - 4149	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	8.01E-06	0.82	3.96	-	418.3
AHQ-8-6, 4039	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	5.27E-07	0.92	4.30	-	686.3
AHQ-8-4, 3630	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	9.46E-08	0.87	3.97	-	449.9
AHQ-8-3, 4120	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	3	1.21E-07	0.91	3.95	-	1394.0
AHQ-8-5, 4096	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.68E-07	0.94	4.39	-	742.7
AHQ-8-2, 3608 - 3687	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	8.30E-04	0.91	4.73	-	395.0
AHQ-8-2, 4864	K.AVAEQIPLLVQGVR.G	1493.77619	3	2.98E-09	0.97	5.09	-	2285.5
AHQ-8-2, 4845 - 4847	K.AVAEQIPLLVQGVR.G	1493.77619	2	7.87E-05	0.90	3.90	-	645.1
AHQ-8-1, 4912 - 4924	K.AVAEQIPLLVQGVR.G	1493.77619	2	6.77E-05	0.90	3.84	-	697.9
AHQ-8-3, 4790	K.AVAEQIPLLVQGVR.G	1493.77619	3	3.80E-04	0.97	4.82	-	2523.5
AHQ-8-6, 4720	K.AVAEQIPLLVQGVR.G	1493.77619	3	1.08E-05	0.95	4.40	-	2060.7
AHQ-8-4, 4830	K.AVAEQIPLLVQGVR.G	1493.77619	3	6.48E-07	0.97	5.15	-	1955.2
AHQ-8-5, 4808	K.AVAEQIPLLVQGVR.G	1493.77619	3	2.70E-05	0.96	5.08	-	1774.9
AHQ-8-4, 4811 - 4825	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.60E-08	0.93	4.35	-	767.1
AHQ-8-4, 3833 - 3903	K.AVASAAAALVLK.A	1085.32216	2	3.52E-06	0.96	4.12	-	1551.4
AHQ-8-6, 3751	K.AVASAAAALVLK.A	1085.32216	2	3.36E-05	0.91	3.57	-	1049.6
AHQ-8-1, 3999	K.AVASAAAALVLK.A	1085.32216	2	1.36E-05	0.96	3.83	-	1482.8
AHQ-8-5, 3770 - 3828	K.AVASAAAALVLK.A	1085.32216	2	4.92E-04	0.94	3.94	-	1315.8
AHQ-8-2, 3909 - 3969	K.AVASAAAALVLK.A	1085.32216	2	1.02E-06	0.95	4.09	-	1333.0
AHQ-8-2, 4127	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.21E-05	0.69	2.72	-	887.9
AHQ-8-3, 3958	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.18E-07	0.96	4.75	-	1282.7
AHQ-8-2, 4008 - 4068	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.22E-07	0.95	4.79	-	1293.3
AHQ-8-5, 3933	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.14E-06	0.92	3.95	-	1190.9
AHQ-8-1, 4061	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.66E-05	0.91	4.07	-	1102.9
AHQ-8-2, 3896	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.87E-06	0.93	4.18	-	1045.7
AHQ-8-4, 3947 - 4027	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.94E-08	0.94	4.61	-	1068.2
AHQ-8-2, 4280	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.77E-06	0.82	3.26	-	818.0
AHQ-8-2, 3795 - 3797	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.07E-07	0.96	4.92	-	1309.8
AHQ-8-6, 3892	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.71E-07	0.94	4.13	-	1281.6
AHQ-8-2, 4529	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.09E-06	0.83	3.47	-	701.0
AHQ-8-2, 6463	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	6.14E-08	0.95	4.71	-	1598.4
AHQ-8-3, 6344 - 6354	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.64E-07	0.98	6.10	-	2257.8
AHQ-8-4, 6394 - 6453	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	5.00E-15	0.97	6.48	-	1757.0
AHQ-8-1, 6364 - 6423	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.52E-10	0.97	5.21	-	2575.4
AHQ-8-6, 6290	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	1.63E-10	0.97	5.36	-	1825.0
AHQ-8-4, 5317 - 5326	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	1.03E-05	0.87	4.14	-	540.3
AHQ-8-2, 5631	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	8.16E-07	0.81	3.36	-	611.9
AHQ-8-2, 5700	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	1.16E-08	0.76	3.55	-	654.9
AHQ-8-6, 5312	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	3.34E-04	0.88	4.12	-	906.4
AHQ-8-2, 5456 - 5517	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	2.45E-09	0.96	5.64	-	1299.4
AHQ-8-3, 5368 - 5434	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.16E-09	0.75	3.69	-	812.9
AHQ-8-3, 2468	R.CVSCLPGQR.D	1079.23309	2	7.00E-05	0.72	2.78	-	514.2
AHQ-8-7, 3492 - 3554	R.DDILNGSHPVSFDK.A	1544.64741	2	8.36E-10	0.96	4.31	-	1316.9
AHQ-8-8, 3334 - 3385	R.DDILNGSHPVSFDK.A	1544.64741	2	3.99E-06	0.86	3.28	-	827.5
AHQ-8-3, 3670	R.DDILNGSHPVSFDK.A	1544.64741	2	6.33E-06	0.77	3.28	-	513.3
AHQ-8-7, 3368 - 3441	R.DDILNGSHPVSFDK.A	1544.64741	2	1.69E-09	0.92	3.67	-	1057.7
AHQ-8-8, 4573	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	3.79E-06	0.97	5.34	-	1768.0
AHQ-8-7, 4496	K.DHFGLEGDEESTMLEDSVSPK.K	2323.43307	2	8.01E-06	0.96	5.07	-	1130.1
AHQ-8-4, 5638	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.30E-07	0.91	4.24	-	776.4
AHQ-8-2, 5592 - 5653	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	1.89E-04	0.44	3.00	-	623.5
AHQ-8-2, 5656	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.05E-10	0.75	3.05	-	594.3
AHQ-8-3, 5561	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	4.98E-09	0.92	4.30	-	776.8
AHQ-8-3, 4964 - 4970	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.29E-11	0.94	4.23	-	1109.9
AHQ-8-2, 4997 - 5055	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	7.81E-06	0.84	3.22	-	858.9
AHQ-8-11, 4776 - 4783	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.39E-04	0.88	3.41	-	820.2
AHQ-8-1, 5048	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	4.42E-05	0.92	4.27	-	1398.1
AHQ-8-4, 4979 - 4997	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	8.97E-05	0.94	4.37	-	1005.1
AHQ-8-3, 4926 - 4933	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	3.08E-07	0.96	5.04	-	2024.1
AHQ-8-2, 5009 - 5015	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.12E-07	0.96	5.34	-	1829.8
AHQ-8-4, 4990	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	3.22E-06	0.93	4.52	-	1406.5
AHQ-8-3, 4916	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	4.52E-06	0.69	2.69	-	840.4
AHQ-8-5, 4961	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	1.73E-05	0.96	4.44	-	2191.0

AHQ-8-2, 4953 - 5000	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.51E-05	0.94	4.15	-	1209.6
AHQ-8-5, 4948	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.90E-04	0.54	2.51	-	587.6
AHQ-8-6, 4879	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	2.93E-08	0.92	4.50	-	1218.7
AHQ-8-1, 5033 - 5041	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.49E-05	0.88	3.49	-	780.5
AHQ-8-4, 3570	R.DPPSWSVLAGHSR.T	1409.53156	2	9.02E-07	0.89	2.71	-	883.4
AHQ-8-3, 3588	R.DPPSWSVLAGHSR.T	1409.53156	3	1.34E-08	0.93	5.07	-	667.2
AHQ-8-2, 3639	R.DPPSWSVLAGHSR.T	1409.53156	2	2.42E-07	0.95	4.30	-	932.1
AHQ-8-4, 3575	R.DPPSWSVLAGHSR.T	1409.53156	3	1.94E-07	0.92	4.13	-	880.1
AHQ-8-2, 3649	R.DPPSWSVLAGHSR.T	1409.53156	3	5.11E-07	0.92	4.68	-	687.2
AHQ-8-3, 3580	R.DPPSWSVLAGHSR.T	1409.53156	2	5.07E-05	0.83	3.02	-	480.8
AHQ-8-10, 4680	R.DPVQLNLLYVQAR.D	1529.76539	2	8.08E-04	0.88	2.71	-	1230.7
AHQ-8-7, 4721 - 4752	R.DPVQLNLLYVQAR.D	1529.76539	2	3.42E-04	0.97	5.06	-	1550.5
AHQ-8-8, 4899 - 4902	R.DPVQLNLLYVQAR.D	1529.76539	2	5.29E-08	0.98	5.72	-	1669.4
AHQ-8-3, 4934	R.DPVQLNLLYVQAR.D	1529.76539	2	9.34E-07	0.94	3.60	-	1643.5
AHQ-8-4, 2509	K.EAAYHPEVAPDVR.L	1454.56910	2	3.30E-08	0.78	2.85	-	779.4
AHQ-8-3, 2560	K.EAAYHPEVAPDVR.L	1454.56910	2	8.28E-06	0.83	2.91	-	925.2
AHQ-8-6, 2510	K.EAAYHPEVAPDVR.L	1454.56910	2	1.16E-04	0.82	2.65	-	843.1
AHQ-8-2, 5671	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.27E-07	0.93	4.24	-	1212.9
AHQ-8-3, 5474 - 5536	K.EADESLNFEEQILEAAK.S	1937.05072	2	8.14E-08	0.97	5.37	-	1499.1
AHQ-8-5, 5554 - 5624	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.09E-07	0.96	4.90	-	1745.1
AHQ-8-2, 5793	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.60E-05	0.71	3.14	-	851.8
AHQ-8-3, 5592	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.08E-07	0.93	4.32	-	1053.4
AHQ-8-1, 5621 - 5684	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.69E-07	0.96	4.91	-	1553.7
AHQ-8-8, 5549 - 5625	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.07E-05	0.96	4.43	-	1492.3
AHQ-8-3, 5274 - 5332	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.36E-06	0.93	4.74	-	637.1
AHQ-8-4, 5799	K.EADESLNFEEQILEAAK.S	1937.05072	2	8.14E-07	0.58	3.25	-	450.6
AHQ-8-2, 5559 - 5615	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.26E-07	0.96	4.46	-	1616.8
AHQ-8-4, 5654	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.19E-10	0.96	4.83	-	1333.6
AHQ-8-6, 5450 - 5519	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.93E-07	0.95	4.76	-	1205.5
AHQ-8-4, 5539 - 5597	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.48E-08	0.97	4.99	-	1845.9
AHQ-8-4, 5399 - 5473	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.40E-07	0.75	3.24	-	615.1
AHQ-8-7, 5394 - 5461	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.86E-07	0.94	4.56	-	1273.7
AHQ-8-6, 5267 - 5322	K.EADESLNFEEQILEAAK.S	1937.05072	2	9.02E-06	0.64	3.44	-	419.2
AHQ-8-2, 5375 - 5415	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.54E-05	0.87	3.56	-	726.0
AHQ-8-5, 6464	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	2.86E-04	0.67	3.49	-	733.6
AHQ-8-7, 6348	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	5.73E-08	0.96	5.49	-	1661.9
AHQ-8-6, 6315	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	8.74E-06	0.95	5.45	-	1283.8
AHQ-8-2, 6459	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	9.04E-11	0.91	4.96	-	884.1
AHQ-8-7, 6264	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	4.07E-05	0.93	4.28	-	1425.4
AHQ-8-4, 5811 - 5869	R.ELLENPVQPINDM*SYFGCLDSVM*ENSK.V	3164.48754	3	9.12E-07	0.86	4.18	-	543.4
AHQ-8-2, 6376	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	4.84E-04	0.72	3.62	-	413.8
AHQ-8-8, 3035 - 3093	R.EQGVEEHETLLLR.R	1553.69898	2	4.88E-04	0.83	2.98	-	579.5
AHQ-8-8, 5357	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	9.54E-13	0.98	6.85	-	1971.3
AHQ-8-14-, 5202 - 5262	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	3.02E-06	0.93	4.77	-	1265.3
AHQ-8-13-, 4978	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	8.92E-04	0.89	3.79	-	1143.7
AHQ-8-8, 5022	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	2.98E-07	0.96	5.29	-	1409.1
AHQ-8-8, 4569	K.EVIQEWNLTNIK.R	1487.68214	1	8.52E-06	0.46	3.14	-	203.3
AHQ-8-8, 4557	K.EVIQEWNLTNIK.R	1487.68214	2	3.67E-06	0.91	3.96	-	841.3
AHQ-8-7, 4457	K.EVIQEWNLTNIK.R	1487.68214	2	2.29E-05	0.87	3.61	-	770.1
AHQ-8-8, 2958	K.FFYSDQNVDSR.D	1378.42795	2	7.84E-08	0.93	3.41	-	1094.0
AHQ-8-7, 2966	K.FFYSDQNVDSR.D	1378.42795	2	2.97E-07	0.94	3.59	-	1215.0
AHQ-8-7, 5408 - 5465	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	8.92E-04	0.89	4.15	-	879.5
AHQ-8-3, 5602	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	7.26E-06	0.96	5.75	-	1085.2
AHQ-8-1, 5704	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	1.45E-04	0.91	4.40	-	1280.3
AHQ-8-8, 5681	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	4.30E-11	0.97	5.20	-	2109.0
AHQ-8-2, 5868	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	3.06E-05	0.60	2.70	-	699.6
AHQ-8-2, 5919	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	1.47E-06	0.86	3.67	-	844.1
AHQ-8-2, 5783 - 5863	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	9.54E-05	0.67	3.58	-	538.8
AHQ-8-1, 5776 - 5857	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	6.49E-05	0.80	4.08	-	459.7
AHQ-8-3, 5801	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	1.85E-04	0.78	2.95	-	708.1
AHQ-8-3, 2898	K.FLPSELRDEH	1243.35032	2	1.01E-05	0.73	2.65	-	425.7
AHQ-8-2, 2931 - 2935	K.FLPSELRDEH	1243.35032	2	8.91E-07	0.49	2.51	-	342.0
AHQ-8-1, 5075	K.GLAGAVSELLR.S	1086.26701	2	2.35E-06	0.98	4.79	-	2400.6
AHQ-8-4, 4970 - 4978	K.GLAGAVSELLR.S	1086.26701	2	1.05E-06	0.98	5.11	-	2134.8
AHQ-8-5, 4952	K.GLAGAVSELLR.S	1086.26701	2	1.53E-04	0.97	4.09	-	2034.1
AHQ-8-3, 4941	K.GLAGAVSELLR.S	1086.26701	2	2.06E-06	0.97	4.33	-	2073.1
AHQ-8-7, 4777	K.GLAGAVSELLR.S	1086.26701	2	2.34E-06	0.97	4.84	-	1943.9
AHQ-8-2, 5019	K.GLAGAVSELLR.S	1086.26701	2	1.23E-07	0.98	4.65	-	2041.4
AHQ-8-4, 6169 - 6235	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.54E-04	0.78	3.47	-	700.9
AHQ-8-4, 6134	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.55E-04	0.87	4.50	-	538.7
AHQ-8-5, 6082	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.75E-04	0.84	3.77	-	687.7
AHQ-8-3, 6052 - 6053	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	6.83E-08	0.95	5.57	-	680.9
AHQ-8-2, 6337 - 6405	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.49E-04	0.89	4.51	-	768.4
AHQ-8-2, 6083 - 6153	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.70E-06	0.91	4.93	-	871.7
AHQ-8-3, 5970 - 6044	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	1.33E-08	0.96	5.86	-	1294.8
AHQ-8-5, 6524 - 6526	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.37E-09	0.97	6.09	-	1871.1
AHQ-8-3, 6480 - 6484	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.51E-12	0.96	5.76	-	1420.6
AHQ-8-2, 6587	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	2.59E-13	0.97	5.84	-	1918.1
AHQ-8-4, 6581	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	6.32E-10	0.88	4.55	-	1056.4
AHQ-8-4, 6482	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.10E-07	0.98	6.61	-	2778.4
AHQ-8-6, 6318 - 6319	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	3.94E-11	0.97	6.17	-	1781.7
AHQ-8-2, 6489	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.56E-08	0.98	6.81	-	2824.4
AHQ-8-5, 6425	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	7.34E-08	0.94	5.51	-	1248.1
AHQ-8-2, 6487 - 6488	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	2.86E-11	0.98	7.53	-	1242.0
AHQ-8-5, 6476	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.55E-06	0.95	5.17	-	1180.3
AHQ-8-1, 6511	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.86E-07	0.92	4.23	-	1163.1
AHQ-8-3, 6436	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.30E-08	0.92	4.20	-	1052.2
AHQ-8-5, 6477	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.89E-04	0.94	5.16	-	807.9
AHQ-8-6, 6370	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.70E-09	0.95	4.99	-	1360.6
AHQ-8-2, 5512	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.13E-04	0.83	3.86	-	534.5
AHQ-8-7, 6320	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.76E-08	0.94	5.06	-	1049.0
AHQ-8-2, 5504	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	7.60E-07	0.95	4.52	-	1255.7
AHQ-8-2, 6540	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.66E-06	0.94	5.52	-	569.5
AHQ-8-7, 6322	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	6.32E-05	0.85	4.21	-	484.1
AHQ-8-4, 6515 - 6533	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.52E-07	0.87	4.09	-	936.5
AHQ-8-4, 6534	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.03E-06	0.94	5.17	-	793.4
AHQ-8-3, 6437 - 6438	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	6.91E-07	0.96	5.39	-	1169.5
AHQ-8-2, 6539	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.55E-07	0.86	4.20	-	654.4
AHQ-8-7, 3272	R.IGITNHDEYSLVR.E	1517.66833	2	3.29E-04	0.94	3.55	-	1459.5
AHQ-8-11, 3313	R.IGITNHDEYSLVR.E	1517.66833	2	5.44E-04	0.85	2.73	-	1096.6
AHQ-8-7, 3485 - 3544	R.IGITNHDEYSLVR.E	1517.66833	2	1.29E-05	0.93	3.11	-	1641.7
AHQ-8-13-, 3424	R.IGITNHDEYSLVR.E	1517.66833	2	7.05E-10	0.94	3.86	-	1183.7
AHQ-8-8, 3546 - 3610	R.IGITNHDEYSLVR.E	1517.66833	2	3.14E-06	0.88	3.21	-	939.7
AHQ-8-1, 4939	R.ILAQATSDLVNAIK.A	1457.69748	2	6.03E-08	0.98	4.95	-	2206.1
AHQ-8-6, 4740 - 4742	R.ILAQATSDLVNAIK.A	1457.69748	2	9.67E-08	0.98	5.74	-	1793.1
AHQ-8-7, 4645	R.ILAQATSDLVNAIK.A	1457.69748	2	6.02E-06	0.96	4.20	-	1361.2
AHQ-8-4, 4842 - 4866	R.ILAQATSDLVNAIK.A	1457.69748	2	1.07E-06	0.96	3.97	-	1678.0

AHQ-8-2, 4107 - 4128	R.ILAQATSDLVNAIK.A	1457.69748	2	9.91E-07	0.98	4.67	-	2317.9
AHQ-8-4, 4051	R.ILAQATSDLVNAIK.A	1457.69748	2	4.51E-08	0.97	4.24	-	1945.2
AHQ-8-5, 4021	R.ILAQATSDLVNAIK.A	1457.69748	2	1.00E-07	0.96	3.74	-	1862.8
AHQ-8-5, 4817 - 4841	R.ILAQATSDLVNAIK.A	1457.69748	2	4.52E-08	0.95	3.87	-	1361.8
AHQ-8-3, 4809 - 4810	R.ILAQATSDLVNAIK.A	1457.69748	2	1.34E-10	0.98	5.93	-	1495.2
AHQ-8-6, 3960	R.ILAQATSDLVNAIK.A	1457.69748	2	2.32E-08	0.97	4.61	-	2073.7
AHQ-8-1, 4189	R.ILAQATSDLVNAIK.A	1457.69748	2	2.39E-06	0.97	4.44	-	1626.2
AHQ-8-2, 4883	R.ILAQATSDLVNAIK.A	1457.69748	2	1.06E-08	0.97	4.66	-	1741.1
AHQ-8-3, 4041	R.ILAQATSDLVNAIK.A	1457.69748	2	2.29E-07	0.98	4.94	-	2606.9
AHQ-8-3, 5246 - 5262	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.36E-11	0.91	4.50	-	1022.5
AHQ-8-1, 5355	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	4.06E-07	0.85	4.04	-	709.2
AHQ-8-8, 5225 - 5302	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.49E-10	0.92	4.37	-	1255.6
AHQ-8-13, 5284	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.07E-05	0.90	3.66	-	1401.1
AHQ-8-7, 2596	K.KGIWLEAGK.A	1002.19171	2	2.77E-04	0.72	2.74	-	779.3
AHQ-8-3, 2640	K.LAQAAQSSVATITR.L	1417.59344	2	4.87E-08	0.95	3.54	-	1510.3
AHQ-8-4, 2606	K.LAQAAQSSVATITR.L	1417.59344	2	2.18E-09	0.97	4.70	-	1737.2
AHQ-8-6, 2746	K.LAQAAQSSVATITR.L	1417.59344	2	2.50E-07	0.96	4.43	-	1380.0
AHQ-8-7, 2709	K.LAQAAQSSVATITR.L	1417.59344	2	1.20E-07	0.95	4.09	-	1459.7
AHQ-8-5, 2760	K.LAQAAQSSVATITR.L	1417.59344	2	4.90E-10	0.96	4.30	-	1497.3
AHQ-8-3, 2796 - 2818	K.LAQAAQSSVATITR.L	1417.59344	2	1.36E-08	0.97	4.26	-	1779.5
AHQ-8-2, 2669 - 2704	K.LAQAAQSSVATITR.L	1417.59344	2	1.04E-04	0.93	3.44	-	1253.4
AHQ-8-14-, 2801	K.LAQAAQSSVATITR.L	1417.59344	2	7.87E-04	0.87	3.13	-	1152.2
AHQ-8-1, 2991	K.LAQAAQSSVATITR.L	1417.59344	2	9.10E-06	0.94	3.23	-	1583.2
AHQ-8-11, 2755	K.LAQAAQSSVATITR.L	1417.59344	2	1.65E-04	0.92	3.37	-	1119.3
AHQ-8-4, 2758	K.LAQAAQSSVATITR.L	1417.59344	2	2.40E-10	0.96	3.79	-	1776.2
AHQ-8-2, 3339	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	7.32E-10	0.97	5.61	-	2462.4
AHQ-8-4, 3262	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	3.37E-07	0.93	4.72	-	1117.9
AHQ-8-3, 3296	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	7.42E-10	0.95	5.27	-	712.1
AHQ-8-4, 3277	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	8.71E-10	0.96	5.36	-	878.1
AHQ-8-3, 3214 - 3288	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	2.12E-07	0.95	4.94	-	1700.6
AHQ-8-6, 5058 - 5062	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	5.21E-04	0.95	4.74	-	1701.5
AHQ-8-4, 5334	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.58E-05	0.83	3.14	-	1368.4
AHQ-8-4, 5322	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.85E-08	0.87	4.07	-	609.8
AHQ-8-4, 5201 - 5203	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.08E-07	0.97	5.54	-	2072.5
AHQ-8-4, 5193 - 5197	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.51E-05	0.96	4.92	-	1236.1
AHQ-8-5, 5145	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.84E-06	0.97	5.90	-	1159.1
AHQ-8-5, 5148 - 5156	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	9.04E-06	0.97	5.41	-	2340.7
AHQ-8-2, 4996 - 5031	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.99E-10	0.96	5.07	-	1138.5
AHQ-8-6, 5182 - 5231	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.33E-04	0.90	4.34	-	671.4
AHQ-8-2, 5184 - 5243	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.76E-05	0.97	5.15	-	1467.4
AHQ-8-2, 5321 - 5336	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.28E-05	0.84	4.04	-	498.6
AHQ-8-6, 4875 - 4903	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.43E-09	0.97	5.11	-	1611.1
AHQ-8-1, 5247 - 5315	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.58E-07	0.95	4.51	-	1068.8
AHQ-8-5, 4933 - 4998	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.92E-05	0.59	2.88	-	432.2
AHQ-8-5, 5278	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.08E-08	0.90	4.68	-	469.1
AHQ-8-4, 5005	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.06E-07	0.94	4.61	-	875.1
AHQ-8-7, 4785	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.22E-07	0.93	4.49	-	797.0
AHQ-8-3, 5136 - 5198	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.85E-04	0.97	5.07	-	1498.5
AHQ-8-1, 5079	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.06E-05	0.94	4.60	-	931.1
AHQ-8-3, 4940 - 4958	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.65E-06	0.95	4.99	-	843.4
AHQ-8-3, 5256 - 5296	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.51E-04	0.91	4.04	-	787.6
AHQ-8-8, 3657	K.LHTDDELNWLDHGR.T	1721.81153	2	3.26E-06	0.97	5.01	-	1819.3
AHQ-8-8, 3662	K.LHTDDELNWLDHGR.T	1721.81153	3	2.14E-07	0.91	4.63	-	823.6
AHQ-8-7, 3697	K.LHTDDELNWLDHGR.T	1721.81153	2	3.45E-06	0.96	4.67	-	1742.1
AHQ-8-2, 4292 - 4355	K.LLAALLEDEGGSGR.P	1401.54764	2	1.52E-05	0.72	2.72	-	287.4
AHQ-8-1, 5183	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.24E-06	0.95	4.69	-	1382.3
AHQ-8-7, 4864	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	8.04E-11	0.96	4.80	-	1794.3
AHQ-8-7, 4865	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.36E-08	0.97	6.17	-	1211.1
AHQ-8-4, 5093	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.32E-09	0.95	4.93	-	1224.1
AHQ-8-2, 5120	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.42E-07	0.97	5.34	-	1734.5
AHQ-8-2, 5123 - 5124	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.29E-12	0.97	6.44	-	1170.8
AHQ-8-6, 4974	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	8.73E-08	0.97	6.20	-	1145.2
AHQ-8-6, 4971	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.21E-07	0.94	5.28	-	1186.5
AHQ-8-5, 5060	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	6.53E-10	0.97	6.48	-	1268.9
AHQ-8-2, 6568 - 6569	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.62E-04	0.82	3.78	-	744.2
AHQ-8-5, 5058	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.65E-09	0.97	5.73	-	1723.8
AHQ-8-3, 5046	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.43E-06	0.98	6.72	-	1729.5
AHQ-8-4, 5094	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.44E-11	0.98	6.36	-	1751.1
AHQ-8-3, 5044	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.66E-08	0.95	4.91	-	1481.0
AHQ-8-1, 5135 - 5191	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.35E-08	0.96	5.67	-	960.7
AHQ-8-8, 5018	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.97E-09	0.96	5.77	-	974.0
AHQ-8-3, 4076 - 4136	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	6.88E-06	0.87	3.95	-	337.9
AHQ-8-3, 3962 - 4020	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.26E-09	0.88	3.71	-	429.8
AHQ-8-2, 4092 - 4151	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.79E-08	0.80	3.38	-	351.3
AHQ-8-4, 4098 - 4171	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.15E-04	0.91	4.20	-	412.5
AHQ-8-4, 3973 - 4037	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	4.31E-04	0.88	3.55	-	432.8
AHQ-8-5, 4209	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.65E-06	0.94	4.81	-	920.7
AHQ-8-1, 5337	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.10E-12	0.98	6.02	-	2362.5
AHQ-8-2, 5576	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.17E-13	0.97	5.33	-	1760.2
AHQ-8-2, 4281	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.20E-08	0.92	4.01	-	857.6
AHQ-8-2, 5476 - 5479	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.71E-07	0.95	4.36	-	1072.7
AHQ-8-3, 5232	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.02E-07	0.98	5.96	-	2066.1
AHQ-8-6, 5328	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.98E-07	0.83	3.44	-	813.5
AHQ-8-4, 4243	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.14E-09	0.96	4.91	-	1021.7
AHQ-8-6, 4148	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.00E-08	0.95	4.59	-	937.7
AHQ-8-3, 5489	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.65E-10	0.97	5.11	-	1626.6
AHQ-8-4, 5559 - 5618	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.38E-08	0.96	4.98	-	1439.7
AHQ-8-1, 4356	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.61E-07	0.93	4.56	-	668.5
AHQ-8-6, 5172	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	4.11E-04	0.97	6.09	-	1947.8
AHQ-8-6, 5171	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.49E-08	0.93	4.51	-	955.8
AHQ-8-7, 5090	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.06E-08	0.97	5.33	-	1484.5
AHQ-8-4, 5462	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.66E-05	0.96	4.78	-	1201.1
AHQ-8-5, 5210 - 5269	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.27E-09	0.97	5.52	-	1437.1
AHQ-8-2, 4944	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.27E-08	0.94	4.25	-	1137.2
AHQ-8-5, 5308	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.56E-06	0.92	4.07	-	813.5
AHQ-8-4, 5289	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.65E-06	0.98	5.64	-	1915.9
AHQ-8-2, 5305 - 5373	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.19E-12	0.98	5.94	-	1409.8
AHQ-8-6, 5167	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.02E-09	0.98	5.92	-	1720.3
AHQ-8-3, 5224 - 5245	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.27E-06	0.96	4.87	-	1683.7
AHQ-8-3, 4220	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.93E-09	0.96	4.84	-	1221.2
AHQ-8-2, 5152	R.LNEAAAGLNQAATELVQASRGTPQDLAR.A	2867.12501	3	1.53E-05	0.56	3.11	-	607.1
AHQ-8-2, 2149	R.MATNAAAQNAIK.K	1204.38227	2	1.67E-07	0.81	3.36	-	715.4
AHQ-8-4, 4009	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.09E-09	0.84	3.57	-	715.8
AHQ-8-2, 3976	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.92E-07	0.71	3.49	-	657.8
AHQ-8-5, 3998	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	4.74E-08	0.83	3.59	-	826.4
AHQ-8-2, 4065 - 4079	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.93E-09	0.95	5.95	-	966.9
AHQ-8-4, 3915	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.52E-12	0.92	4.36	-	969.7

AHQ-8-3, 4009	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	3.36E-11	0.89	4.53	-	869.2
AHQ-8-2, 3055	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	6.98E-05	0.76	3.49	-	600.5
AHQ-8-5, 4176	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	9.46E-04	0.96	5.83	-	1451.7
AHQ-8-3, 3917	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.43E-09	0.78	3.57	-	655.7
AHQ-8-2, 4256	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	4.90E-04	0.97	5.80	-	2004.3
AHQ-8-4, 6157	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	3	3.08E-05	0.94	4.58	-	1376.8
AHQ-8-2, 5639 - 5717	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	3.13E-09	0.97	6.14	-	1722.0
AHQ-8-13-, 5446 - 5522	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	2.36E-05	0.90	3.72	-	966.9
AHQ-8-2, 6177	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	3	3.50E-10	0.96	5.42	-	1489.2
AHQ-8-2, 5629 - 5703	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.11E-06	0.97	5.46	-	1584.6
AHQ-8-2, 5769	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	3	4.89E-04	0.89	3.49	-	2123.5
AHQ-8-2, 6121 - 6176	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	5.60E-09	0.98	5.52	-	1840.1
AHQ-8-14-, 5473 - 5538	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.08E-07	0.97	5.46	-	1496.2
AHQ-8-4, 6146	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	4.09E-04	0.91	4.11	-	1056.0
AHQ-8-4, 5678	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	1.02E-08	0.97	5.88	-	2069.7
AHQ-8-4, 5685	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	6.98E-07	0.93	4.56	-	858.1
AHQ-8-7, 2297 - 2373	K.NCGQMSEIEAK.V	1268.40005	2	5.92E-04	0.88	2.88	-	1300.9
AHQ-8-7, 4216	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.71E-06	0.73	3.09	-	416.0
AHQ-8-5, 4349 - 4374	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.85E-06	0.90	4.20	-	559.1
AHQ-8-3, 4178 - 4198	K.NGNLPEFGDAISTASK.A	1621.73018	2	7.74E-04	0.81	3.25	-	412.6
AHQ-8-2, 4287	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.76E-07	0.92	3.90	-	701.6
AHQ-8-1, 4475	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.88E-08	0.86	3.60	-	479.6
AHQ-8-1, 4337 - 4349	K.NGNLPEFGDAISTASK.A	1621.73018	2	8.48E-04	0.71	3.42	-	304.6
AHQ-8-3, 4036 - 4096	K.NGNLPEFGDAISTASK.A	1621.73018	2	8.41E-06	0.84	3.63	-	400.6
AHQ-8-1, 4285	K.NLGTALAELR.T	1058.21367	2	5.70E-04	0.83	3.36	-	711.6
AHQ-8-2, 4192	K.NLGTALAELR.T	1058.21367	2	1.22E-04	0.91	3.40	-	940.4
AHQ-8-3, 4124	K.NLGTALAELR.T	1058.21367	2	9.98E-06	0.92	3.61	-	1106.0
AHQ-8-3, 2848	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.13E-08	0.95	5.05	-	1189.9
AHQ-8-4, 2811 - 2873	K.PAAVAAENEEIGSHIK.H	1636.78798	2	2.01E-09	0.97	4.87	-	1508.5
AHQ-8-3, 2849	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.12E-09	0.97	5.02	-	1734.0
AHQ-8-6, 2794	K.PAAVAAENEEIGSHIK.H	1636.78798	3	6.96E-07	0.96	4.50	-	1885.4
AHQ-8-2, 2888	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.47E-07	0.96	5.10	-	1586.2
AHQ-8-2, 2885	K.PAAVAAENEEIGSHIK.H	1636.78798	2	4.09E-11	0.98	5.51	-	1849.6
AHQ-8-5, 2816	K.PAAVAAENEEIGSHIK.H	1636.78798	2	9.76E-09	0.97	5.14	-	1458.7
AHQ-8-4, 2807 - 2839	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.60E-05	0.96	4.82	-	1713.1
AHQ-8-5, 2808	K.PAAVAAENEEIGSHIK.H	1636.78798	3	6.52E-08	0.97	5.96	-	1954.9
AHQ-8-4, 2715	K.PAAVAAENEEIGSHIK.H	1636.78798	2	2.96E-13	0.97	4.85	-	1543.8
AHQ-8-5, 3300	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	7.21E-04	0.89	3.83	-	831.2
AHQ-8-6, 3236 - 3274	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	1.17E-06	0.73	3.10	-	599.4
AHQ-8-4, 3305	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	2.68E-05	0.71	3.11	-	562.0
AHQ-8-2, 3387 - 3389	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	4.61E-08	0.94	4.78	-	852.6
AHQ-8-2, 3383 - 3459	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	2.76E-04	0.77	3.57	-	775.7
AHQ-8-6, 3278	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.03E-04	0.89	4.24	-	656.6
AHQ-8-3, 3336	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	3.97E-07	0.90	4.21	-	627.4
AHQ-8-1, 3511	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	4.32E-07	0.70	3.11	-	826.7
AHQ-8-3, 3332 - 3410	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	6.71E-12	0.73	3.09	-	645.1
AHQ-8-1, 3520	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	8.97E-08	0.74	3.24	-	668.4
AHQ-8-4, 3313	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	4.53E-04	0.85	3.94	-	520.0
AHQ-8-5, 3306	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.46E-06	0.93	4.32	-	900.3
AHQ-8-2, 3987	R.QELAVFCSPEPPAK.T	1574.77985	2	1.57E-07	0.94	3.53	-	1312.0
AHQ-8-6, 3852	R.QELAVFCSPEPPAK.T	1574.77985	2	1.79E-07	0.88	3.12	-	889.3
AHQ-8-5, 3900 - 3908	R.QELAVFCSPEPPAK.T	1574.77985	2	1.91E-05	0.87	3.51	-	873.8
AHQ-8-3, 3920 - 3930	R.QELAVFCSPEPPAK.T	1574.77985	2	3.56E-04	0.82	3.01	-	793.2
AHQ-8-2, 6493 - 6545	R.QNLLQAAGNVGQASGELLQQIGESDTDPHFQDALM*QLAK.A	4154.52584	3	8.68E-04	0.77	3.88	-	416.9
AHQ-8-2, 3819	K.QVAASTAQLLVACK.V	1461.70942	2	1.80E-07	0.86	3.50	-	526.3
AHQ-8-13-, 3748	K.QVAASTAQLLVACK.V	1461.70942	2	5.15E-06	0.81	2.72	-	696.5
AHQ-8-4, 3745	K.QVAASTAQLLVACK.V	1461.70942	2	1.22E-09	0.92	4.00	-	684.3
AHQ-8-4, 5607	K.RVAGSVTELIQAAEAMK.G	1775.06387	2	2.69E-04	0.95	4.68	-	1202.8
AHQ-8-6, 3216	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	5.86E-05	0.79	3.59	-	661.0
AHQ-8-4, 3538	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	5.79E-07	0.78	4.22	-	489.2
AHQ-8-4, 3737	R.SGASGPENFQVGSMPPAQQQITSGQM*HR.G	2945.19807	3	3.05E-04	0.66	3.36	-	369.2
AHQ-8-6, 3476	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	2.69E-04	0.79	3.72	-	458.1
AHQ-8-3, 3461 - 3540	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	2.85E-05	0.71	3.70	-	355.0
AHQ-8-4, 3257	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	5.80E-06	0.84	4.30	-	728.6
AHQ-8-2, 3316	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	2.28E-04	0.89	4.54	-	741.1
AHQ-8-2, 3813 - 3821	R.SGASGPENFQVGSMPPAQQQITSGQM*HR.G	2945.19807	3	1.05E-05	0.82	4.06	-	448.9
AHQ-8-3, 3269	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	3.75E-07	0.92	4.74	-	991.2
AHQ-8-2, 3600	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	2.58E-04	0.83	4.05	-	744.6
AHQ-8-6, 3074	K.SIAAATSALVK.A	1032.21612	2	9.09E-04	0.81	2.55	-	756.5
AHQ-8-2, 3160	K.SIAAATSALVK.A	1032.21612	2	6.24E-04	0.90	3.23	-	1032.5
AHQ-8-8, 4171	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	2	2.51E-04	0.89	3.22	-	1028.5
AHQ-8-7, 3708	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	6.39E-06	0.96	5.06	-	1838.8
AHQ-8-8, 4169	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	2.13E-06	0.95	4.72	-	1468.9
AHQ-8-7, 4110	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	1.96E-10	0.98	5.68	-	2276.0
AHQ-8-8, 3791	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	2	3.80E-04	0.65	2.93	-	360.2
AHQ-8-5, 5078	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.33E-09	0.84	3.61	-	465.3
AHQ-8-5, 4370	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.08E-07	0.88	3.86	-	568.9
AHQ-8-2, 4440 - 4448	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.25E-08	0.88	4.18	-	468.1
AHQ-8-4, 5115	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.24E-06	0.85	3.64	-	478.7
AHQ-8-7, 4780	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.86E-06	0.40	2.78	-	189.5
AHQ-8-3, 5058	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.78E-07	0.81	3.63	-	354.5
AHQ-8-3, 4377 - 4392	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.56E-08	0.89	3.99	-	616.6
AHQ-8-4, 4407	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.50E-10	0.91	4.26	-	657.8
AHQ-8-1, 5185	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.82E-04	0.88	4.25	-	406.6
AHQ-8-3, 4901 - 4968	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.72E-07	0.92	4.43	-	578.5
AHQ-8-6, 4862	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.50E-07	0.71	3.38	-	305.0
AHQ-8-2, 5140 - 5159	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.87E-07	0.92	4.46	-	614.6
AHQ-8-2, 4916 - 4984	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.98E-06	0.87	4.05	-	441.9
AHQ-8-6, 4292 - 4312	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.16E-05	0.89	4.08	-	586.7
AHQ-8-1, 4516	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.10E-05	0.76	3.35	-	434.9
AHQ-8-4, 5239 - 5242	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.77E-05	0.42	2.69	-	289.2
AHQ-8-4, 4950 - 5009	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.40E-07	0.86	4.03	-	439.9
AHQ-8-2, 5043	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.11E-06	0.85	4.09	-	446.7
AHQ-8-5, 4929 - 4984	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.78E-05	0.88	4.03	-	503.6
AHQ-8-14-, 6277	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.82E-05	0.90	3.57	-	1328.4
AHQ-8-1, 6439	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.87E-12	0.97	5.84	-	2060.0
AHQ-8-2, 6467 - 6500	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	2.78E-09	0.97	6.01	-	1541.2
AHQ-8-8, 6465 - 6535	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	4.63E-07	0.97	5.89	-	1961.9
AHQ-8-3, 6364	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	3.15E-11	0.97	6.35	-	1687.3
AHQ-8-8, 4185	K.TKEVIQEWNLTNIK.R	1716.95938	3	6.53E-07	0.95	4.66	-	1442.9
AHQ-8-7, 4073 - 4136	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.69E-08	0.97	4.13	-	2201.0
AHQ-8-8, 4181	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.71E-07	0.96	4.57	-	1601.8
AHQ-8-14-, 5861 - 5867	K.TLAESALQLLYTAK.E	1522.76793	2	2.16E-05	0.83	3.08	-	642.5
AHQ-8-2, 6016	K.TLAESALQLLYTAK.E	1522.76793	2	6.31E-06	0.94	3.83	-	1147.0
AHQ-8-4, 6003 - 6083	K.TLAESALQLLYTAK.E	1522.76793	2	1.54E-10	0.95	4.55	-	1028.3
AHQ-8-5, 5956	K.TLAESALQLLYTAK.E	1522.76793	2	5.93E-06	0.78	3.01	-	658.2
AHQ-8-4, 6015	K.TLAESALQLLYTAK.E	1522.76793	3	1.39E-05	0.96	4.65	-	1898.9

AHQ-8-7, 5800 - 5870	K.TLAESALQLLYTAK.E	1522.76793	2	9.31E-07	0.92	3.54	-	973.0
AHQ-8-8, 6014	K.TLAESALQLLYTAK.E	1522.76793	2	4.56E-04	0.91	3.32	-	1011.6
AHQ-8-3, 5929	K.TLAESALQLLYTAK.E	1522.76793	3	1.64E-04	0.96	4.84	-	1849.4
AHQ-8-1, 6023	K.TLAESALQLLYTAK.E	1522.76793	2	8.62E-07	0.92	3.72	-	879.2
AHQ-8-3, 5917	K.TLAESALQLLYTAK.E	1522.76793	2	1.61E-07	0.96	4.35	-	1166.4
AHQ-8-5, 3274	K.TLSHPQQMALLDQTK.T	1711.96464	3	4.27E-07	0.96	4.95	-	1539.7
AHQ-8-5, 3276	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.56E-05	0.93	4.04	-	859.3
AHQ-8-2, 3357	K.TLSHPQQMALLDQTK.T	1711.96464	3	4.83E-05	0.93	4.44	-	1103.6
AHQ-8-3, 3314	K.TLSHPQQMALLDQTK.T	1711.96464	3	2.92E-05	0.94	4.53	-	1300.4
AHQ-8-4, 3287	K.TLSHPQQMALLDQTK.T	1711.96464	3	6.79E-05	0.93	4.50	-	1223.4
AHQ-8-2, 3347 - 3359	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.04E-04	0.96	4.93	-	1018.8
AHQ-8-6, 4106	K.TMLESAGGLIQTAR.A	1448.67095	2	4.95E-07	0.92	4.06	-	1269.8
AHQ-8-2, 4197 - 4255	K.TMLESAGGLIQTAR.A	1448.67095	2	8.55E-10	0.96	4.40	-	1658.6
AHQ-8-1, 3639	K.TM*LESAGGLIQTAR.A	1464.67035	2	5.25E-07	0.92	3.22	-	1318.1
AHQ-8-4, 4187	K.TMLESAGGLIQTAR.A	1448.67095	2	1.28E-07	0.96	3.78	-	2104.6
AHQ-8-1, 4248 - 4323	K.TMLESAGGLIQTAR.A	1448.67095	2	1.19E-06	0.94	4.27	-	1604.8
AHQ-8-3, 3430 - 3497	K.TM*LESAGGLIQTAR.A	1464.67035	2	3.05E-04	0.96	4.60	-	1439.9
AHQ-8-3, 4140 - 4172	K.TMLESAGGLIQTAR.A	1448.67095	2	1.41E-07	0.91	3.75	-	1511.5
AHQ-8-7, 4042 - 4044	K.TMLESAGGLIQTAR.A	1448.67095	2	2.64E-05	0.96	4.31	-	1741.6
AHQ-8-8, 4114	K.TMLESAGGLIQTAR.A	1448.67095	2	9.37E-05	0.91	3.72	-	1156.8
AHQ-8-2, 3504 - 3563	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.85E-08	0.95	3.72	-	1838.7
AHQ-8-2, 4197 - 4255	K.TMLESAGGLIQTARALAVNPR.D	2170.52235	3	5.63E-05	0.58	3.13	-	529.8
AHQ-8-8, 4166	K.TM*QFEPSTMVYDACR.I	1854.07511	2	1.40E-04	0.91	3.93	-	687.4
AHQ-8-13, 3660	K.TM*QFEPSTM*VYDACR.I	1870.07451	2	3.34E-04	0.78	3.01	-	503.9
AHQ-8-7, 4080	K.TM*QFEPSTMVYDACR.I	1854.07511	2	5.47E-04	0.87	3.77	-	659.9
AHQ-8-8, 4138	K.TVTDM*LMTICAR.I	1429.70947	2	2.74E-05	0.64	2.90	-	860.5
AHQ-8-7, 4920	K.TYGVSFFLVK.E	1161.37395	2	3.14E-07	0.90	3.41	-	760.4
AHQ-8-8, 5058	K.TYGVSFFLVK.E	1161.37395	2	1.40E-06	0.89	3.50	-	664.9
AHQ-8-1, 5252	K.TYGVSFFLVK.E	1161.37395	2	6.10E-06	0.88	3.23	-	657.0
AHQ-8-3, 5846	R.VAGSVTELIQAAEAMK.G	1618.87752	2	3.93E-05	0.95	4.06	-	1330.1
AHQ-8-2, 5947	R.VAGSVTELIQAAEAMK.G	1618.87752	2	5.80E-10	0.94	4.11	-	1082.0
AHQ-8-7, 4909	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.85E-06	0.87	3.35	-	839.3
AHQ-8-4, 5917 - 5955	R.VAGSVTELIQAAEAMK.G	1618.87752	2	6.86E-07	0.91	3.85	-	811.7
AHQ-8-5, 5080 - 5088	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	4.71E-05	0.97	5.19	-	1389.9
AHQ-8-4, 5102	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	4.48E-06	0.87	3.82	-	913.8
AHQ-8-1, 5917 - 5955	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.69E-05	0.89	3.55	-	921.1
AHQ-8-6, 5780 - 5795	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.38E-04	0.87	3.04	-	946.5
AHQ-8-7, 5722	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.61E-05	0.85	2.84	-	1086.7
AHQ-8-2, 5163	R.VAGSVTELIQAAEAM*K.G	1634.87692	3	1.30E-08	0.92	4.42	-	1337.7
AHQ-8-2, 5131	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	1.16E-05	0.81	2.84	-	953.8
AHQ-8-3, 5049 - 5056	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	4.17E-06	0.96	4.00	-	1901.0
AHQ-8-2, 3765	K.VEHGSVALPAIMR.S	1380.64144	2	4.12E-10	0.85	3.15	-	948.9
AHQ-8-7, 5368 - 5369	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	1.49E-04	0.96	5.01	-	1839.0
AHQ-8-7, 5365	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.87E-11	0.95	4.60	-	1426.6
AHQ-8-6, 5423 - 5494	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.90E-11	0.97	5.64	-	1081.3
AHQ-8-4, 5566 - 5629	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.36E-09	0.97	5.83	-	919.7
AHQ-8-6, 5270 - 5340	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.09E-07	0.85	3.71	-	407.8
AHQ-8-2, 5495 - 5569	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.83E-08	0.83	4.05	-	446.5
AHQ-8-1, 5591 - 5652	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.22E-05	0.94	4.83	-	871.1
AHQ-8-3, 5492 - 5548	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	3.01E-10	0.91	4.24	-	814.3
AHQ-8-4, 5485	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.44E-12	0.91	4.54	-	478.5
AHQ-8-3, 5406	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.53E-10	0.87	3.88	-	520.7
AHQ-8-5, 5358	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.83E-05	0.61	2.99	-	320.6
AHQ-8-3, 5346 - 5405	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	1.19E-08	0.93	4.84	-	1354.3
AHQ-8-2, 5372 - 5432	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.29E-08	0.91	4.52	-	627.1
AHQ-8-5, 5446 - 5466	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.20E-04	0.90	4.47	-	415.1
AHQ-8-5, 5528	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	3.46E-05	0.77	3.07	-	802.7
AHQ-8-5, 5529	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.29E-11	0.92	4.57	-	578.5
AHQ-8-4, 5359	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.80E-07	0.86	3.92	-	521.7
AHQ-8-4, 3758	K.VGDDPAVWQLK.N	1228.37879	2	8.79E-08	0.93	3.73	-	858.4
AHQ-8-2, 3832	K.VGDDPAVWQLK.N	1228.37879	2	6.62E-08	0.95	4.42	-	901.6
AHQ-8-7, 3636 - 3664	K.VGDDPAVWQLK.N	1228.37879	2	8.52E-09	0.84	3.33	-	637.8
AHQ-8-2, 3780 - 3847	K.VGDDPAVWQLK.N	1228.37879	2	2.37E-08	0.88	3.53	-	708.1
AHQ-8-6, 3686 - 3744	K.VGDDPAVWQLK.N	1228.37879	2	3.80E-07	0.78	2.69	-	675.0
AHQ-8-5, 3734	K.VGDDPAVWQLK.N	1228.37879	2	4.61E-09	0.90	3.23	-	893.1
AHQ-8-3, 3760	K.VGDDPAVWQLK.N	1228.37879	2	5.68E-08	0.93	3.79	-	883.1
AHQ-8-1, 3929	K.VGDDPAVWQLK.N	1228.37879	2	7.27E-09	0.95	4.16	-	960.8
AHQ-8-5, 3117	K.VLGEAMTGISQNAK.N	1419.62961	2	5.47E-07	0.97	4.01	-	2047.6
AHQ-8-4, 2409	K.VLGEAM*TGISQNAK.N	1435.62901	2	9.06E-05	0.83	3.44	-	731.6
AHQ-8-3, 2549	K.VLGEAM*TGISQNAK.N	1435.62901	2	2.55E-06	0.94	3.83	-	1278.5
AHQ-8-3, 2454	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.10E-04	0.96	4.02	-	1655.8
AHQ-8-4, 2426 - 2498	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.89E-04	0.89	3.49	-	1215.2
AHQ-8-2, 2569	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.18E-04	0.87	3.09	-	951.1
AHQ-8-2, 3188 - 3211	K.VLGEAMTGISQNAK.N	1419.62961	2	1.20E-04	0.97	4.38	-	2280.6
AHQ-8-3, 4554 - 4621	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	5.68E-08	0.91	5.23	-	526.3
AHQ-8-2, 5145 - 5217	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	1.04E-04	0.74	4.15	-	425.2
AHQ-8-3, 4990 - 5053	K.VLGEAMTGISQNAKNGNLPEFGDAISTASK.A	3022.33719	3	1.82E-06	0.88	5.27	-	596.0
AHQ-8-2, 4633 - 4691	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	1.24E-12	0.92	4.98	-	849.9
AHQ-8-4, 4610 - 4669	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	1.78E-06	0.86	4.32	-	686.0
AHQ-8-4, 1893 - 1958	K.VLVQNAAGSQEK.L	1244.37976	2	2.35E-05	0.88	3.66	-	690.8
AHQ-8-4, 1782 - 1838	K.VLVQNAAGSQEK.L	1244.37976	2	4.88E-06	0.93	3.60	-	1027.5
AHQ-8-2, 2069	K.VLVQNAAGSQEK.L	1244.37976	2	9.99E-06	0.89	3.51	-	844.9
AHQ-8-6, 1920 - 1944	K.VLVQNAAGSQEK.L	1244.37976	2	3.27E-05	0.55	2.64	-	399.1
AHQ-8-2, 1857 - 1912	K.VLVQNAAGSQEK.L	1244.37976	2	8.13E-08	0.94	3.98	-	1087.2
AHQ-8-5, 1794 - 1849	K.VLVQNAAGSQEK.L	1244.37976	2	1.50E-08	0.90	3.43	-	908.0
AHQ-8-2, 1971 - 2000	K.VLVQNAAGSQEK.L	1244.37976	2	7.16E-05	0.76	3.12	-	605.9
AHQ-8-3, 1905	K.VLVQNAAGSQEK.L	1244.37976	2	4.89E-06	0.94	3.86	-	996.1
AHQ-8-6, 4446	K.VMVTNVTSLLK.T	1205.49322	2	3.27E-04	0.90	3.48	-	910.0
AHQ-8-4, 4563	K.VMVTNVTSLLK.T	1205.49322	2	6.92E-06	0.89	3.80	-	748.3
AHQ-8-4, 4249	K.VM*VTNVTSLLK.T	1221.49262	2	9.99E-06	0.86	3.49	-	804.1
AHQ-8-2, 4300	K.VM*VTNVTSLLK.T	1221.49262	2	2.72E-06	0.70	2.92	-	640.4
AHQ-8-6, 4146 - 4151	K.VM*VTNVTSLLK.T	1221.49262	2	9.05E-04	0.73	3.16	-	603.1
AHQ-8-3, 4552 - 4564	K.VMVTNVTSLLK.T	1205.49322	2	3.23E-05	0.93	4.28	-	870.3
AHQ-8-2, 4625	K.VMVTNVTSLLK.T	1205.49322	2	9.30E-05	0.89	3.59	-	836.1
AHQ-8-5, 4213	K.VM*VTNVTSLLK.T	1221.49262	2	4.98E-04	0.39	2.51	-	487.8
AHQ-8-3, 4233 - 4241	K.VM*VTNVTSLLK.T	1221.49262	2	2.42E-05	0.89	3.53	-	854.1
AHQ-8-4, 2861	R.VQELGHGCAALVTK.A	1484.70307	2	3.51E-04	0.97	4.71	-	1776.6
AHQ-8-7, 2816	R.VQELGHGCAALVTK.A	1484.70307	2	6.92E-05	0.96	4.45	-	1296.0
AHQ-8-5, 2872	R.VQELGHGCAALVTK.A	1484.70307	2	9.38E-05	0.95	4.12	-	1270.1
AHQ-8-2, 2943	R.VQELGHGCAALVTK.A	1484.70307	2	3.53E-06	0.97	4.74	-	1980.7
AHQ-8-1, 3097	R.VQELGHGCAALVTK.A	1484.70307	2	3.18E-05	0.95	4.28	-	1148.8
AHQ-8-6, 2854	R.VQELGHGCAALVTK.A	1484.70307	2	5.21E-07	0.95	4.40	-	1286.7
AHQ-8-4, 2837 - 2855	K.VSHVLAALQAGNR.G	1336.52525	2	3.36E-10	0.97	4.37	-	1985.1
AHQ-8-6, 2834	K.VSHVLAALQAGNR.G	1336.52525	2	1.25E-09	0.97	4.77	-	1689.6
AHQ-8-3, 2885	K.VSHVLAALQAGNR.G	1336.52525	2	4.71E-10	0.96	4.21	-	1812.1
AHQ-8-2, 2915	K.VSHVLAALQAGNR.G	1336.52525	2	2.61E-08	0.96	4.28	-	1429.8
AHQ-8-6, 6072	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.23E-05	0.92	4.44	-	749.4

AHQ-8-4, 6209	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.49E-06	0.77	3.39	-	537.9
AHQ-8-4, 5562	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	2.15E-08	0.94	4.36	-	1279.2
AHQ-8-1, 5532 - 5596	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.50E-04	0.91	3.40	-	1606.0
AHQ-8-2, 5579	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	5.32E-07	0.96	4.94	-	1015.6
AHQ-8-2, 5584	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	4.25E-06	0.94	4.43	-	1401.4
AHQ-8-7, 6014	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	7.51E-09	0.94	4.76	-	872.4
AHQ-8-2, 6165 - 6227	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.66E-05	0.94	4.66	-	920.6
AHQ-8-2, 6237 - 6244	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	1.29E-08	0.94	5.00	-	1474.6
AHQ-8-7, 5352	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.15E-05	0.87	3.53	-	701.3
AHQ-8-4, 5561 - 5563	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.08E-06	0.95	5.09	-	1074.9
AHQ-8-6, 5422	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.06E-08	0.87	3.95	-	807.3
AHQ-8-3, 5484 - 5493	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	3.66E-12	0.94	4.71	-	1284.4
AHQ-8-3, 6133	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.40E-06	0.93	4.44	-	794.6
AHQ-8-5, 5450 - 5516	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.35E-07	0.96	5.27	-	1082.9
AHQ-8-7, 4260	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.42E-07	0.86	3.74	-	685.4
AHQ-8-4, 4454 - 4455	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	3.87E-11	0.94	4.87	-	1281.4
AHQ-8-4, 4518	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.51E-05	0.36	3.10	-	157.9
AHQ-8-3, 4412	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.22E-08	0.75	3.49	-	422.7
AHQ-8-2, 4568	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.93E-06	0.47	2.82	-	214.6
AHQ-8-2, 4479 - 4480	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.73E-06	0.96	5.27	-	847.1
AHQ-8-6, 4330	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.29E-08	0.95	4.75	-	827.3
AHQ-8-2, 4379 - 4388	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.51E-08	0.95	5.41	-	506.5
AHQ-8-14-, 4362	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	4.40E-04	0.79	3.24	-	494.9
AHQ-8-5, 4310	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.16E-06	0.82	4.01	-	260.3
AHQ-8-5, 4398	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.31E-09	0.93	4.53	-	599.8
AHQ-8-8, 4378	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.96E-06	0.97	5.36	-	1197.9
AHQ-8-3, 4325	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.25E-05	0.77	3.70	-	231.7
gi|4503745|ref|NP_001447.1|	filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act			5.55E-15	91.13	1060.32	52.20	280757.4
AHQ-8-4, 2189	K.AEISFEDRK.D	1095.18763	2	4.51E-04	0.71	2.88	-	590.2
AHQ-8-3, 2712	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.06E-07	0.95	3.37	-	1491.1
AHQ-8-2, 2747	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	9.03E-08	0.94	3.52	-	1280.1
AHQ-8-1, 2909	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.54E-09	0.94	3.76	-	1343.6
AHQ-8-7, 2648	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.25E-05	0.92	3.34	-	1238.1
AHQ-8-6, 2595 - 2674	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.49E-04	0.90	3.09	-	1268.1
AHQ-8-5, 2684 - 2693	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.27E-07	0.92	3.61	-	1260.6
AHQ-8-4, 2678 - 2681	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.67E-08	0.95	3.98	-	1536.5
AHQ-8-14-, 2862 - 2883	K.AGNNM*LLVGVHGPR.T	1451.67973	3	8.45E-07	0.81	3.29	-	1275.5
AHQ-8-14-, 2982	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.43E-04	0.67	2.69	-	652.3
AHQ-8-14-, 3321	K.AGNNMLLVGVHGPR.T	1435.68033	3	2.67E-06	0.78	3.22	-	961.5
AHQ-8-14, 3846 - 3915	K.AGNNM*LLVGVHGPR.T	1451.67973	3	1.31E-05	0.83	3.23	-	1093.3
AHQ-8-14-, 3502	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.34E-06	0.83	3.02	-	717.1
AHQ-8-14-, 2813 - 2870	K.AGNNM*LLVGVHGPR.T	1451.67973	2	2.00E-06	0.93	3.79	-	1034.7
AHQ-8-14, 3827 - 3886	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.27E-06	0.73	2.84	-	665.1
AHQ-8-4, 2974	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.66E-05	0.72	2.87	-	663.7
AHQ-8-14-, 3485 - 3505	K.AGNNMLLVGVHGPR.T	1435.68033	2	4.84E-06	0.89	3.36	-	997.7
AHQ-8-14-, 3317	K.AGNNMLLVGVHGPR.T	1435.68033	2	1.01E-04	0.65	2.92	-	539.4
AHQ-8-3, 2441	K.AGVAPLQVK.V	883.07036	2	1.45E-06	0.77	2.76	-	597.5
AHQ-8-2, 2455	K.AGVAPLQVK.V	883.07036	2	7.75E-05	0.90	3.41	-	676.6
AHQ-8-4, 2391	K.AGVAPLQVK.V	883.07036	2	3.52E-04	0.79	2.77	-	664.2
AHQ-8-2, 6589 - 6651	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	4.39E-04	0.87	3.94	-	1076.8
AHQ-8-2, 2787	K.AHVVPCFDASK.V	1232.39073	2	6.09E-04	0.79	2.69	-	693.3
AHQ-8-3, 2753	K.AHVVPCFDASK.V	1232.39073	2	3.92E-04	0.68	2.53	-	462.1
AHQ-8-2, 5768 - 5840	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.55E-15	0.94	5.70	-	658.8
AHQ-8-4, 5831 - 5886	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.28E-07	0.88	4.82	-	446.6
AHQ-8-3, 5649 - 5710	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	8.98E-04	0.59	3.42	-	412.8
AHQ-8-2, 5895	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.61E-08	0.93	5.14	-	765.3
AHQ-8-7, 5618 - 5677	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.50E-07	0.90	4.50	-	598.5
AHQ-8-8, 5894	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	8.01E-04	0.77	3.40	-	608.7
AHQ-8-6, 5672 - 5736	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.02E-04	0.90	4.98	-	509.3
AHQ-8-5, 5834 - 5897	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.83E-07	0.80	4.08	-	396.4
AHQ-8-3, 5792	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.86E-05	0.78	3.98	-	356.7
AHQ-8-5, 5718 - 5777	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.16E-06	0.91	4.58	-	763.9
AHQ-8-1, 5839 - 5895	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.21E-06	0.89	4.85	-	629.0
AHQ-8-4, 3310	R.ANLPQSFQVDTSK.A	1435.56409	2	3.03E-09	0.88	3.44	-	616.9
AHQ-8-2, 3427 - 3500	R.ANLPQSFQVDTSK.A	1435.56409	2	1.72E-04	0.84	3.30	-	663.3
AHQ-8-1, 3601	R.APSVANVGSHCDLSLK.I	1656.84249	2	1.74E-07	0.92	4.08	-	772.2
AHQ-8-5, 1958	K.ATCAPQHGAPGPGPADASK.V	1791.92336	3	1.43E-06	0.75	3.10	-	880.3
AHQ-8-4, 1947	K.ATCAPQHGAPGPGPADASK.V	1791.92336	3	1.01E-04	0.86	3.38	-	991.0
AHQ-8-2, 3684 - 3713	R.AWGPGLEGGVVGK.S	1227.39403	2	2.68E-06	0.94	3.89	-	958.7
AHQ-8-4, 3621	R.AWGPGLEGGVVGK.S	1227.39403	2	6.24E-05	0.88	3.43	-	755.0
AHQ-8-6, 3555	R.AWGPGLEGGVVGK.S	1227.39403	2	2.26E-04	0.80	2.80	-	697.2
AHQ-8-3, 3622	R.AWGPGLEGGVVGK.S	1227.39403	2	5.87E-07	0.84	3.00	-	731.6
AHQ-8-5, 3588	R.AWGPGLEGGVVGK.S	1227.39403	2	3.17E-07	0.87	3.26	-	808.7
AHQ-8-7, 3512	R.AWGPGLEGGVVGK.S	1227.39403	2	9.65E-05	0.88	3.03	-	867.2
AHQ-8-1, 3787	R.AWGPGLEGGVVGK.S	1227.39403	2	3.67E-05	0.92	3.73	-	1084.8
AHQ-8-3, 3172 - 3245	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.12E-04	0.55	2.99	-	344.4
AHQ-8-5, 2672	R.AYGPGIEPTGNM*VK.K	1450.64214	2	6.13E-05	0.70	3.20	-	397.6
AHQ-8-5, 3354	R.AYGPGIEPTGNMVK.K	1434.64274	2	4.72E-05	0.81	2.87	-	723.5
AHQ-8-2, 2833 - 2847	R.AYGPGIEPTGNM*VK.K	1450.64214	2	5.93E-04	0.38	2.52	-	327.4
AHQ-8-3, 3254 - 3324	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.65E-04	0.81	3.32	-	529.1
AHQ-8-2, 2725	R.AYGPGIEPTGNM*VK.K	1450.64214	2	3.91E-05	0.64	2.72	-	381.2
AHQ-8-1, 5656 - 5731	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	3.35E-04	0.82	3.67	-	459.6
AHQ-8-1, 5724	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	2.15E-10	0.96	5.18	-	1898.2
AHQ-8-2, 5719	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	3.44E-09	0.95	4.83	-	1432.9
AHQ-8-3, 5609 - 5676	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	4.60E-05	0.92	4.59	-	556.7
AHQ-8-4, 5705	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	6.41E-05	0.39	2.67	-	378.5
AHQ-8-3, 5617	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.37E-09	0.92	4.59	-	994.0
AHQ-8-2, 5715 - 5775	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	6.77E-09	0.95	4.26	-	983.9
AHQ-8-2, 4804 - 4815	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	2.56E-08	0.86	4.62	-	438.4
AHQ-8-2, 4441 - 4457	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	4.47E-07	0.65	2.96	-	599.2
AHQ-8-2, 3919	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	9.64E-09	0.90	3.37	-	1124.7
AHQ-8-5, 3825 - 3884	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.31E-06	0.95	4.83	-	1423.5
AHQ-8-8, 3790	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	5.21E-04	0.92	4.04	-	1013.9
AHQ-8-4, 4038	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	4.21E-06	0.62	2.99	-	727.3
AHQ-8-4, 3854 - 3917	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	8.47E-04	0.92	4.14	-	1136.6
AHQ-8-1, 3979	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	4.59E-04	0.90	4.12	-	944.6
AHQ-8-3, 4602	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	2.28E-08	0.94	3.82	-	1498.8
AHQ-8-2, 4671 - 4703	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	1.35E-04	0.82	2.97	-	1091.3
AHQ-8-1, 4725	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	2.87E-06	0.85	3.31	-	1148.3
AHQ-8-8, 4158 - 4165	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.86E-05	0.94	4.37	-	1229.7
AHQ-8-4, 4261 - 4262	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.62E-06	0.89	3.88	-	1102.3
AHQ-8-5, 4216	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	3.75E-05	0.88	3.91	-	1009.2
AHQ-8-1, 4384	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.95E-08	0.91	4.25	-	860.1
AHQ-8-3, 4232	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.51E-05	0.94	4.38	-	1241.7
AHQ-8-6, 4150	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.49E-07	0.95	4.24	-	1604.5
AHQ-8-11, 4096 - 4103	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.94E-04	0.89	3.33	-	1070.1
AHQ-8-2, 4301	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	2.55E-06	0.79	3.04	-	828.8

AHQ-8-7, 4081	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	9.25E-06	0.90	4.16	-	802.0
AHQ-8-3, 4237	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	5.04E-07	0.88	3.25	-	1170.1
AHQ-8-3, 4424	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.39E-05	0.93	3.84	-	1203.8
AHQ-8-2, 4299 - 4363	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.29E-09	0.95	4.46	-	1433.5
AHQ-8-3, 4313	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	3.04E-04	0.69	3.13	-	803.0
AHQ-8-4, 4107	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	9.14E-05	0.82	3.12	-	991.1
AHQ-8-6, 4232	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.42E-10	0.92	3.69	-	1268.1
AHQ-8-2, 4380 - 4400	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	5.71E-06	0.94	3.96	-	1371.8
AHQ-8-5, 4081	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.99E-07	0.90	3.61	-	1063.8
AHQ-8-5, 4294	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	3.79E-11	0.96	4.27	-	1703.2
AHQ-8-1, 4431 - 4433	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	6.23E-11	0.94	4.31	-	1294.7
AHQ-8-4, 4274 - 4337	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.45E-09	0.96	4.43	-	1408.4
AHQ-8-3, 2065	R.DAPQDFHPDR.V	1198.22650	2	4.96E-06	0.73	2.71	-	715.9
AHQ-8-4, 2035	R.DAPQDFHPDR.V	1198.22650	2	1.81E-05	0.85	2.80	-	842.9
AHQ-8-2, 2065	R.DAPQDFHPDR.V	1198.22650	2	8.58E-06	0.61	2.64	-	465.1
AHQ-8-5, 4690	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	5.12E-04	0.55	3.26	-	302.3
AHQ-8-5, 4540	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	8.88E-07	0.90	4.31	-	793.1
AHQ-8-7, 4400 - 4410	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.55E-04	0.66	3.39	-	356.6
AHQ-8-4, 4575 - 4579	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.57E-05	0.81	4.05	-	412.5
AHQ-8-6, 4472	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.02E-07	0.84	3.76	-	585.3
AHQ-8-8, 4494 - 4522	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	6.49E-04	0.82	4.04	-	517.1
AHQ-8-6, 2552	K.DKGEYTLVVK.W	1152.32223	2	5.45E-05	0.74	2.66	-	568.7
AHQ-8-14-, 2585	K.DKGEYTLVVK.W	1152.32223	1	5.35E-04	0.41	2.38	-	515.8
AHQ-8-5, 3172	K.DNGNGTYSCSYVPR.K	1591.64109	2	5.71E-06	0.71	2.69	-	654.4
AHQ-8-1, 3293	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	9.85E-06	0.95	4.20	-	1282.6
AHQ-8-5, 3077	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.89E-05	0.90	3.90	-	819.1
AHQ-8-3, 3108	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.18E-06	0.94	4.07	-	1125.2
AHQ-8-6, 3059	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	8.94E-05	0.59	2.54	-	519.0
AHQ-8-2, 3149	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	5.83E-05	0.86	3.37	-	826.0
AHQ-8-3, 3104	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	1.56E-05	0.76	3.37	-	451.5
AHQ-8-2, 3151	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	6.39E-05	0.66	3.09	-	422.4
AHQ-8-2, 3441 - 3445	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.72E-04	0.95	4.12	-	1352.6
AHQ-8-5, 3352 - 3418	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	2.31E-05	0.92	3.48	-	1253.4
AHQ-8-4, 3371 - 3415	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	6.35E-07	0.72	2.52	-	1001.6
AHQ-8-6, 3326 - 3388	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.32E-08	0.85	3.15	-	940.3
AHQ-8-8, 3309	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	4.21E-06	0.90	3.60	-	1211.3
AHQ-8-3, 3384 - 3450	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.32E-06	0.89	3.36	-	1168.6
AHQ-8-7, 3274	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.39E-09	0.94	3.88	-	1220.2
AHQ-8-5, 2660	R.EATTEFSVDAR.A	1226.27493	2	1.58E-04	0.85	3.00	-	735.6
AHQ-8-1, 2871	R.EATTEFSVDAR.A	1226.27493	2	2.04E-04	0.79	2.77	-	834.9
AHQ-8-2, 2712 - 2785	R.EATTEFSVDAR.A	1226.27493	2	5.44E-05	0.84	2.73	-	805.5
AHQ-8-4, 2645 - 2657	R.EATTEFSVDAR.A	1226.27493	2	2.91E-04	0.92	3.05	-	1028.7
AHQ-8-2, 5827 - 5883	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.79E-08	0.95	5.49	-	942.1
AHQ-8-5, 5813 - 5868	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.01E-09	0.95	6.42	-	609.2
AHQ-8-1, 5823 - 5888	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	6.69E-07	0.90	4.82	-	587.2
AHQ-8-3, 5828 - 5885	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.04E-09	0.95	5.59	-	830.1
AHQ-8-4, 5825 - 5870	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	8.36E-05	0.85	4.26	-	572.0
AHQ-8-3, 5714 - 5772	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.21E-05	0.93	4.94	-	754.1
AHQ-8-4, 5925	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.31E-09	0.92	4.82	-	831.8
AHQ-8-7, 5705	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.25E-05	0.83	3.69	-	639.6
AHQ-8-1, 5943	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	5.09E-09	0.91	5.11	-	625.3
AHQ-8-11, 4653	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.70E-05	0.77	2.93	-	721.4
AHQ-8-5, 4832	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.65E-04	0.70	3.14	-	571.1
AHQ-8-7, 4656 - 4660	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.09E-05	0.93	4.40	-	963.0
AHQ-8-6, 4684 - 4750	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.64E-07	0.95	4.15	-	1279.4
AHQ-8-3, 4818	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	1.02E-07	0.97	6.11	-	1558.8
AHQ-8-2, 4813 - 4879	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.55E-07	0.86	3.69	-	738.2
AHQ-8-8, 4770 - 4783	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.48E-07	0.91	3.97	-	800.4
AHQ-8-10, 4574 - 4578	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.10E-04	0.46	2.68	-	374.8
AHQ-8-1, 4944	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	2.04E-05	0.86	3.84	-	782.8
AHQ-8-1, 4881 - 4935	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.66E-10	0.94	4.24	-	1289.1
AHQ-8-3, 4744 - 4808	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.11E-09	0.90	4.44	-	865.5
AHQ-8-2, 4629	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	8.79E-07	0.92	4.36	-	840.5
AHQ-8-2, 4908	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	1.19E-06	0.96	4.97	-	1746.0
AHQ-8-4, 3858	R.ENGVYLIDVK.F	1150.30633	2	8.04E-04	0.75	2.59	-	589.6
AHQ-8-5, 3830	R.ENGVYLIDVK.F	1150.30633	2	5.41E-06	0.87	3.11	-	669.5
AHQ-8-1, 3659	K.FADQHVPGSPFSVK.V	1516.68203	2	8.84E-08	0.81	2.95	-	645.6
AHQ-8-3, 3484 - 3545	K.FADQHVPGSPFSVK.V	1516.68203	2	1.30E-04	0.78	3.46	-	432.2
AHQ-8-6, 3416	K.FADQHVPGSPFSVK.V	1516.68203	3	7.83E-10	0.93	4.41	-	1144.9
AHQ-8-4, 3467	K.FADQHVPGSPFSVK.V	1516.68203	3	4.46E-05	0.92	3.84	-	1188.3
AHQ-8-4, 3463 - 3531	K.FADQHVPGSPFSVK.V	1516.68203	2	1.97E-06	0.74	2.98	-	610.3
AHQ-8-5, 3448	K.FADQHVPGSPFSVK.V	1516.68203	3	2.63E-07	0.94	4.14	-	1297.7
AHQ-8-1, 5276 - 5331	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.55E-10	0.93	5.03	-	828.8
AHQ-8-5, 5188 - 5249	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.27E-09	0.96	5.52	-	1270.5
AHQ-8-3, 5164 - 5228	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.05E-06	0.94	4.55	-	1214.4
AHQ-8-13-, 5114	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.71E-04	0.89	4.36	-	710.3
AHQ-8-2, 5249 - 5315	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.58E-05	0.85	4.33	-	634.2
AHQ-8-1, 5189	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.74E-04	0.81	3.48	-	946.9
AHQ-8-12, 5042	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.65E-06	0.75	3.35	-	597.8
AHQ-8-2, 5371	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	7.03E-07	0.84	3.86	-	826.4
AHQ-8-4, 5186 - 5254	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.19E-09	0.90	4.01	-	901.8
AHQ-8-5, 4900 - 4964	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	3	2.48E-04	0.91	4.15	-	953.0
AHQ-8-1, 5044 - 5045	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	8.49E-05	0.84	3.45	-	618.8
AHQ-8-6, 4926 - 5006	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	3	4.33E-05	0.86	3.81	-	857.1
AHQ-8-4, 4957 - 4967	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	5.94E-04	0.67	2.81	-	484.3
AHQ-8-7, 4720	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	3	5.94E-04	0.87	3.35	-	1259.6
AHQ-8-4, 3649 - 3659	K.FNGTHIPGSPFK.I	1302.46259	2	8.53E-07	0.79	2.99	-	588.3
AHQ-8-5, 3722	K.FNGTHIPGSPFK.I	1302.46259	3	1.13E-05	0.69	3.26	-	633.1
AHQ-8-4, 3089	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.14E-07	0.87	3.02	-	756.4
AHQ-8-6, 2428 - 2430	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	3.40E-05	0.75	3.16	-	334.7
AHQ-8-5, 3065 - 3066	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.44E-05	0.92	3.85	-	751.9
AHQ-8-4, 2438 - 2449	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	1.32E-06	0.83	3.16	-	370.1
AHQ-8-1, 6191	R.GAGSYTIMVLFADQATPTSPIR.V	2297.61623	2	4.04E-05	0.48	2.92	-	315.6
AHQ-8-1, 5609	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	3.80E-05	0.89	4.25	-	593.9
AHQ-8-2, 5612 - 5684	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	1.33E-07	0.94	4.81	-	786.4
AHQ-8-6, 3308	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.24E-04	0.87	3.60	-	781.9
AHQ-8-4, 3306 - 3365	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.11E-05	0.89	3.90	-	724.5
AHQ-8-5, 3341	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	7.24E-07	0.90	3.95	-	761.8
AHQ-8-8, 3291	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	4.41E-08	0.90	3.85	-	796.4
AHQ-8-1, 3543	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	3.63E-07	0.79	3.32	-	697.8
AHQ-8-7, 3258	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.12E-04	0.63	2.67	-	492.9
AHQ-8-2, 3568	K.GKLDVQFSGLTK.G	1293.49392	3	4.15E-05	0.88	4.00	-	987.7
AHQ-8-1, 3687	K.GKLDVQFSGLTK.G	1293.49392	2	3.03E-06	0.89	3.78	-	770.8
AHQ-8-3, 3502	K.GKLDVQFSGLTK.G	1293.49392	2	1.42E-06	0.94	4.07	-	1156.4
AHQ-8-3, 4520 - 4600	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.41E-07	0.89	3.82	-	759.3
AHQ-8-2, 4935	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.53E-07	0.76	2.71	-	731.4
AHQ-8-3, 4641 - 4696	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	3	4.61E-04	0.77	3.43	-	615.3

AHQ-8-1, 4800	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.02E-10	0.94	4.04	-	1103.3
AHQ-8-3, 4632 - 4688	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	3.46E-04	0.54	2.56	-	522.9
AHQ-8-2, 4719 - 4775	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	9.60E-10	0.97	5.72	-	1188.8
AHQ-8-6, 4556 - 4619	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.55E-04	0.88	3.68	-	808.2
AHQ-8-2, 4807 - 4872	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	5.12E-05	0.65	2.90	-	749.5
AHQ-8-5, 4700	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	4.52E-07	0.80	2.92	-	744.0
AHQ-8-3, 4862	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	8.91E-09	0.91	3.26	-	1156.5
AHQ-8-2, 2345 - 2412	K.GTVEPQLEAR.G	1100.20741	2	1.84E-06	0.78	3.03	-	538.9
AHQ-8-3, 2337	K.GTVEPQLEAR.G	1100.20741	2	2.00E-04	0.71	2.85	-	563.3
AHQ-8-1, 2535	K.GTVEPQLEAR.G	1100.20741	2	5.59E-04	0.73	2.89	-	512.5
AHQ-8-4, 4966	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	2.57E-05	0.97	4.93	-	1592.4
AHQ-8-2, 5007	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	6.16E-07	0.94	4.22	-	1038.1
AHQ-8-2, 5003 - 5008	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	7.15E-04	0.87	4.00	-	753.4
AHQ-8-3, 4918 - 4928	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	5.63E-05	0.95	5.12	-	881.8
AHQ-8-3, 4924	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	3.05E-05	0.85	3.69	-	983.6
AHQ-8-1, 5053	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	7.23E-04	0.94	4.05	-	1254.2
AHQ-8-7, 3972 - 3980	R.IANLQTDLSDGLR.L	1416.56231	2	2.90E-08	0.90	4.06	-	635.2
AHQ-8-2, 3929 - 3997	R.IANLQTDLSDGLR.L	1416.56231	2	4.05E-07	0.96	4.59	-	1229.5
AHQ-8-2, 3823 - 3824	R.IANLQTDLSDGLR.L	1416.56231	2	3.24E-07	0.93	4.08	-	1054.8
AHQ-8-2, 4076	R.IANLQTDLSDGLR.L	1416.56231	2	1.40E-06	0.95	4.39	-	1078.3
AHQ-8-1, 4260	R.IANLQTDLSDGLR.L	1416.56231	2	1.61E-06	0.93	3.91	-	957.0
AHQ-8-4, 3761	R.IANLQTDLSDGLR.L	1416.56231	2	1.07E-05	0.94	3.77	-	1090.0
AHQ-8-13-, 4063 - 4120	R.IANLQTDLSDGLR.L	1416.56231	2	1.63E-04	0.57	2.52	-	423.6
AHQ-8-5, 4102 - 4108	R.IANLQTDLSDGLR.L	1416.56231	2	1.75E-05	0.89	3.75	-	770.5
AHQ-8-4, 4127 - 4151	R.IANLQTDLSDGLR.L	1416.56231	2	4.32E-06	0.90	3.52	-	889.4
AHQ-8-12, 4006	R.IANLQTDLSDGLR.L	1416.56231	2	1.26E-07	0.92	3.59	-	1215.5
AHQ-8-13, 4263	R.IANLQTDLSDGLR.L	1416.56231	2	1.58E-05	0.81	3.16	-	574.9
AHQ-8-3, 4113 - 4117	R.IANLQTDLSDGLR.L	1416.56231	2	4.40E-06	0.96	4.63	-	1309.6
AHQ-8-6, 4046 - 4124	R.IANLQTDLSDGLR.L	1416.56231	2	5.50E-06	0.94	4.21	-	1070.6
AHQ-8-2, 4173 - 4252	R.IANLQTDLSDGLR.L	1416.56231	2	6.85E-06	0.93	3.90	-	1002.6
AHQ-8-3, 3756	R.IANLQTDLSDGLR.L	1416.56231	2	4.50E-07	0.92	3.76	-	1057.3
AHQ-8-5, 3728 - 3732	R.IANLQTDLSDGLR.L	1416.56231	2	4.64E-06	0.96	4.53	-	1145.7
AHQ-8-11, 3989 - 3997	R.IANLQTDLSDGLR.L	1416.56231	2	3.40E-05	0.93	4.16	-	931.4
AHQ-8-1, 3901	R.IANLQTDLSDGLR.L	1416.56231	2	4.54E-07	0.95	4.59	-	1048.7
AHQ-8-4, 5225	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.50E-08	0.97	4.83	-	1518.7
AHQ-8-2, 4049	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.94E-07	0.97	5.36	-	1578.4
AHQ-8-1, 5272	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.05E-12	0.97	5.32	-	1556.7
AHQ-8-4, 3990	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.14E-04	0.97	5.17	-	1837.4
AHQ-8-1, 5279 - 5357	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	7.33E-05	0.95	5.03	-	1378.7
AHQ-8-6, 5104	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	5.31E-07	0.83	3.56	-	934.0
AHQ-8-5, 5174 - 5193	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.29E-11	0.98	5.90	-	2161.1
AHQ-8-6, 5090	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	7.90E-07	0.96	5.40	-	1120.4
AHQ-8-3, 5168 - 5169	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.51E-09	0.97	5.45	-	1400.2
AHQ-8-5, 3956 - 4016	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.99E-08	0.97	5.36	-	1717.4
AHQ-8-2, 5263	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.93E-11	0.98	6.38	-	1910.1
AHQ-8-3, 3980 - 4050	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	6.81E-06	0.96	4.39	-	1764.0
AHQ-8-4, 5237	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	5.81E-06	0.75	3.72	-	690.6
AHQ-8-6, 3904 - 3948	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.86E-06	0.98	5.98	-	1844.1
AHQ-8-5, 4732	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.08E-04	0.91	4.62	-	538.8
AHQ-8-7, 4969 - 5016	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.97E-09	0.97	5.10	-	1823.1
AHQ-8-8, 5159	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.12E-07	0.97	4.99	-	1353.8
AHQ-8-7, 3846	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.43E-07	0.98	5.00	-	2455.2
AHQ-8-4, 2581	K.IVGPSGAAVPCK.V	1157.36530	2	4.64E-08	0.86	3.18	-	782.3
AHQ-8-2, 2639 - 2640	K.IVGPSGAAVPCK.V	1157.36530	2	4.25E-09	0.85	3.13	-	783.2
AHQ-8-3, 2614	K.IVGPSGAAVPCK.V	1157.36530	2	4.61E-10	0.92	3.46	-	1002.8
AHQ-8-5, 2590	K.IVGPSGAAVPCK.V	1157.36530	2	1.81E-06	0.84	2.96	-	776.0
AHQ-8-1, 4184	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.78E-08	0.93	4.87	-	1234.6
AHQ-8-1, 4197	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.64E-06	0.81	3.57	-	470.1
AHQ-8-3, 4022 - 4080	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.63E-10	0.86	4.01	-	905.0
AHQ-8-3, 4042 - 4044	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	9.77E-04	0.89	4.60	-	398.9
AHQ-8-4, 4065	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.71E-04	0.72	3.34	-	285.2
AHQ-8-4, 4057	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.42E-06	0.96	5.55	-	1286.5
AHQ-8-5, 4029	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.69E-05	0.96	5.04	-	1599.7
AHQ-8-1, 4275	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.33E-07	0.86	4.30	-	659.5
AHQ-8-2, 4113	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	4.04E-04	0.81	3.27	-	447.4
AHQ-8-2, 4108	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.19E-04	0.91	4.44	-	1020.8
AHQ-8-3, 4133	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	7.12E-09	0.74	3.47	-	1110.3
AHQ-8-1, 4335	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	9.09E-04	0.70	3.32	-	764.1
AHQ-8-4, 4294	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	4.46E-04	0.60	3.28	-	486.8
AHQ-8-5, 4244	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	5.26E-06	0.88	4.23	-	863.5
AHQ-8-5, 4189 - 4258	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	2	4.07E-04	0.78	3.61	-	705.9
AHQ-8-5, 4212	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.44E-10	0.97	5.21	-	2316.3
AHQ-8-2, 4257 - 4336	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	7.03E-05	0.89	4.47	-	970.6
AHQ-8-5, 4220	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.73E-08	0.91	3.85	-	894.8
AHQ-8-8, 4161	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.07E-06	0.85	3.55	-	607.2
AHQ-8-8, 4153	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.07E-07	0.95	5.06	-	1397.9
AHQ-8-7, 4101	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	7.84E-05	0.95	4.92	-	1804.4
AHQ-8-1, 4403 - 4481	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	3.00E-12	0.97	5.90	-	1775.2
AHQ-8-4, 4271	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	1.54E-07	0.87	3.41	-	769.7
AHQ-8-3, 4270 - 4342	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	2.66E-07	0.96	4.95	-	2298.5
AHQ-8-4, 4257 - 4263	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	8.87E-13	0.98	6.23	-	2576.7
AHQ-8-5, 4084 - 4148	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	9.26E-06	0.94	4.72	-	1674.3
AHQ-8-2, 3492	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.52E-09	0.96	5.17	-	1263.2
AHQ-8-2, 3496	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	7.94E-05	0.83	3.61	-	484.5
AHQ-8-2, 3581	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	4.47E-05	0.69	2.80	-	551.4
AHQ-8-4, 3411	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.74E-06	0.93	4.55	-	1051.4
AHQ-8-1, 3619	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	3.32E-04	0.91	4.08	-	1071.7
AHQ-8-3, 3537 - 3594	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	3.29E-04	0.93	5.44	-	840.4
AHQ-8-3, 3445	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	8.64E-07	0.91	4.45	-	860.3
AHQ-8-3, 3456	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	2	1.70E-05	0.88	3.42	-	738.4
AHQ-8-4, 3862	K.LDVQFSGLTK.G	1108.26945	2	5.79E-05	0.92	3.42	-	1112.3
AHQ-8-2, 3931 - 3935	K.LDVQFSGLTK.G	1108.26945	2	2.85E-05	0.93	3.45	-	972.4
AHQ-8-3, 3856	K.LDVQFSGLTK.G	1108.26945	2	3.11E-05	0.93	3.98	-	888.5
AHQ-8-1, 4009	K.LDVQFSGLTK.G	1108.26945	2	2.43E-04	0.90	3.41	-	826.5
AHQ-8-5, 6248	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	1.06E-04	0.82	3.53	-	697.0
AHQ-8-3, 6204	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	4.66E-04	0.79	3.48	-	857.6
AHQ-8-2, 6300	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	2.92E-04	0.93	4.53	-	1324.5
AHQ-8-3, 4598 - 4673	K.LPQLPITNFSR.D	1286.50461	2	2.80E-04	0.73	2.80	-	491.5
AHQ-8-5, 4842	K.LPQLPITNFSR.D	1286.50461	2	1.12E-05	0.90	3.31	-	943.0
AHQ-8-1, 4805	K.LPQLPITNFSR.D	1286.50461	2	3.53E-04	0.85	3.01	-	605.4
AHQ-8-2, 4737	K.LPQLPITNFSR.D	1286.50461	2	1.55E-04	0.86	3.05	-	595.3
AHQ-8-1, 4947	K.LPQLPITNFSR.D	1286.50461	2	1.27E-04	0.88	2.99	-	837.3
AHQ-8-2, 4901 - 4911	K.LPQLPITNFSR.D	1286.50461	2	2.62E-06	0.89	3.33	-	712.6
AHQ-8-6, 4587	K.LPQLPITNFSR.D	1286.50461	2	6.72E-05	0.69	2.83	-	458.9
AHQ-8-2, 5271	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	9.76E-07	0.81	3.31	-	653.3
AHQ-8-2, 5191	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	1.24E-04	0.97	5.79	-	1595.6
AHQ-8-2, 5167	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.77E-08	0.96	5.10	-	1003.7

AHQ-8-3, 5085	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.33E-09	0.97	5.67	-	1047.7
AHQ-8-1, 5195	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	7.90E-06	0.89	4.05	-	496.9
AHQ-8-3, 3988	R.LSPFMADIR.D	1050.25664	2	6.14E-05	0.65	2.53	-	330.2
AHQ-8-4, 3357 - 3427	R.LTVSSLQESGLK.V	1262.43499	2	5.21E-05	0.83	2.99	-	776.3
AHQ-8-1, 3615	R.LTVSSLQESGLK.V	1262.43499	2	1.69E-05	0.84	2.89	-	734.3
AHQ-8-4, 4091	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.60E-08	0.97	5.76	-	1200.3
AHQ-8-8, 4049	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.26E-04	0.89	3.77	-	674.1
AHQ-8-4, 4345	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	2.98E-06	0.92	3.65	-	1118.1
AHQ-8-4, 4346	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	4.03E-09	0.94	4.77	-	773.3
AHQ-8-5, 4074	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	8.58E-05	0.95	4.85	-	991.1
AHQ-8-4, 4089	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	7.10E-11	0.97	5.71	-	1330.0
AHQ-8-5, 4316	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.72E-08	0.94	4.37	-	1011.6
AHQ-8-1, 4264 - 4343	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	9.22E-07	0.95	5.01	-	1184.6
AHQ-8-3, 2522	K.MDCQECPEGYR.V	1447.55375	2	3.14E-04	0.72	2.94	-	617.6
AHQ-8-5, 2254	K.M*DCQECPEGYR.V	1463.55315	2	1.05E-06	0.89	3.38	-	922.2
AHQ-8-4, 2238	K.M*DCQECPEGYR.V	1463.55315	2	1.09E-05	0.80	2.72	-	817.2
AHQ-8-5, 4521	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	5.06E-04	0.84	3.15	-	756.0
AHQ-8-3, 4542	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	1.54E-06	0.92	4.19	-	1683.6
AHQ-8-5, 4656	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	6.39E-12	0.93	4.58	-	1654.3
AHQ-8-8, 4491	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	5.32E-04	0.96	4.17	-	1494.0
AHQ-8-1, 4663	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	1.57E-04	0.85	3.76	-	921.3
AHQ-8-5, 2132	K.RAEFTVETR.S	1109.21754	2	2.61E-06	0.90	2.82	-	976.7
AHQ-8-4, 2147 - 2215	K.RAEFTVETR.S	1109.21754	2	8.93E-06	0.88	3.25	-	803.0
AHQ-8-3, 2186	K.RAEFTVETR.S	1109.21754	2	3.96E-06	0.88	2.98	-	759.1
AHQ-8-1, 3345	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	1.15E-05	0.94	4.69	-	1066.4
AHQ-8-3, 3158	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	3.38E-05	0.96	5.24	-	1568.1
AHQ-8-5, 3109	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	1.41E-04	0.98	5.67	-	2371.7
AHQ-8-5, 3114	R.RAPSVANVGSHCDLSLK.I	1813.02884	2	2.79E-04	0.93	4.60	-	753.6
AHQ-8-2, 3855 - 3873	K.RIANLQTDLSDGLR.L	1572.74866	2	5.59E-07	0.91	3.47	-	1064.8
AHQ-8-1, 3368	R.RLTVSSLQESGLK.V	1418.62134	2	2.40E-06	0.98	4.93	-	2449.6
AHQ-8-5, 3145	R.RLTVSSLQESGLK.V	1418.62134	2	1.42E-04	0.96	3.79	-	1731.5
AHQ-8-2, 6561 - 6619	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	4.66E-06	0.95	4.87	-	1283.1
AHQ-8-2, 6444 - 6503	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	1.90E-05	0.92	4.44	-	1022.6
AHQ-8-5, 3832	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.07E-07	0.91	3.93	-	1147.7
AHQ-8-4, 3857	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.19E-07	0.95	4.80	-	904.0
AHQ-8-4, 3853	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.78E-06	0.84	3.42	-	957.8
AHQ-8-1, 4003	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	7.99E-14	0.95	5.10	-	1215.9
AHQ-8-5, 3833 - 3834	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.12E-05	0.93	4.65	-	741.5
AHQ-8-1, 4005	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.52E-05	0.90	4.13	-	628.0
AHQ-8-6, 3782	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.09E-07	0.81	4.03	-	540.4
AHQ-8-2, 3920	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.48E-06	0.94	4.54	-	1306.4
AHQ-8-7, 3724	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.12E-06	0.90	3.67	-	1337.4
AHQ-8-2, 3923 - 3924	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.13E-08	0.94	4.67	-	827.4
AHQ-8-6, 3776	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	8.54E-05	0.74	3.60	-	585.4
AHQ-8-3, 3836 - 3894	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.40E-10	0.89	3.77	-	951.4
AHQ-8-2, 4017	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	2.22E-06	0.80	3.33	-	514.7
AHQ-8-3, 3852 - 3914	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.52E-06	0.93	4.53	-	693.5
AHQ-8-7, 3722	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.65E-06	0.80	3.75	-	544.3
AHQ-8-1, 3591	K.SPFEVYVDK.S	1084.20321	2	2.46E-06	0.89	2.89	-	950.1
AHQ-8-4, 3401	K.SPFEVYVDK.S	1084.20321	1	1.84E-04	0.55	2.13	-	847.5
AHQ-8-5, 3392	K.SPFEVYVDK.S	1084.20321	1	9.04E-05	0.81	2.68	-	1100.0
AHQ-8-5, 3384	K.SPFEVYVDK.S	1084.20321	2	5.14E-07	0.93	3.06	-	1202.5
AHQ-8-3, 3420	K.SPFEVYVDK.S	1084.20321	1	1.05E-05	0.83	3.01	-	810.2
AHQ-8-2, 3455	K.SPFEVYVDK.S	1084.20321	2	6.40E-06	0.85	3.03	-	857.7
AHQ-8-4, 3397	K.SPFEVYVDK.S	1084.20321	2	2.85E-05	0.89	3.04	-	1020.7
AHQ-8-3, 3414	K.SPFEVYVDK.S	1084.20321	2	2.49E-06	0.94	3.39	-	1160.5
AHQ-8-1, 4832 - 4895	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.15E-04	0.87	3.52	-	992.0
AHQ-8-2, 4648	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.07E-05	0.72	3.20	-	509.1
AHQ-8-3, 4570	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.45E-05	0.91	3.31	-	1037.6
AHQ-8-5, 4728 - 4798	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.27E-06	0.80	3.17	-	688.2
AHQ-8-6, 4650 - 4706	K.SPFSVAVSPSLDLSK.I	1534.73557	2	6.75E-05	0.74	3.03	-	688.5
AHQ-8-7, 4568	K.SPFSVAVSPSLDLSK.I	1534.73557	2	9.34E-06	0.64	2.88	-	628.9
AHQ-8-7, 3292	R.SPYTVTVGQACNPSACR.A	1871.04208	2	8.59E-05	0.84	3.62	-	467.7
AHQ-8-4, 3321 - 3381	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.03E-04	0.86	4.06	-	445.6
AHQ-8-6, 3334	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.13E-06	0.95	5.13	-	505.8
AHQ-8-2, 3404 - 3464	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.50E-05	0.83	3.81	-	421.5
AHQ-8-1, 3527 - 3547	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.33E-05	0.86	3.45	-	515.4
AHQ-8-6, 3279 - 3338	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.27E-04	0.87	3.98	-	419.4
AHQ-8-5, 3360	R.SPYTVTVGQACNPSACR.A	1871.04208	2	9.51E-04	0.84	3.47	-	487.5
AHQ-8-3, 4850	R.TFSVWYVPEVTGTHK.V	1751.96228	3	1.04E-05	0.64	3.29	-	400.6
AHQ-8-6, 4776	R.TFSVWYVPEVTGTHK.V	1751.96228	3	5.51E-07	0.81	3.51	-	622.2
AHQ-8-1, 4989 - 4995	R.TFSVWYVPEVTGTHK.V	1751.96228	3	7.49E-05	0.67	3.07	-	541.4
AHQ-8-1, 4980 - 4984	R.TFSVWYVPEVTGTHK.V	1751.96228	2	3.46E-07	0.82	3.06	-	535.0
AHQ-8-4, 4889	R.TFSVWYVPEVTGTHK.V	1751.96228	3	8.26E-07	0.76	3.63	-	459.9
AHQ-8-5, 4853	R.TFSVWYVPEVTGTHK.V	1751.96228	3	7.12E-05	0.72	3.19	-	478.9
AHQ-8-3, 3124	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	3.59E-05	0.83	3.24	-	687.4
AHQ-8-1, 3311	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.10E-04	0.83	3.45	-	719.9
AHQ-8-6, 3075	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	9.42E-04	0.88	4.23	-	388.1
AHQ-8-5, 3054 - 3090	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.79E-05	0.79	3.34	-	706.9
AHQ-8-4, 3110	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	3.06E-07	0.86	3.33	-	843.4
AHQ-8-2, 3171	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	2.24E-07	0.80	3.12	-	744.8
AHQ-8-3, 3061	R.TGVELGKPTHFTVNAK.A	1699.93205	2	1.87E-04	0.68	2.79	-	616.1
AHQ-8-2, 3033 - 3104	R.TGVELGKPTHFTVNAK.A	1699.93205	2	1.64E-05	0.86	3.76	-	510.2
AHQ-8-3, 2910 - 2985	R.TGVELGKPTHFTVNAK.A	1699.93205	2	9.43E-04	0.91	4.06	-	713.9
AHQ-8-4, 3215	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.48E-06	0.91	4.26	-	859.4
AHQ-8-4, 3098	K.THEAEIVEGENHTYCIR.F	2060.19046	3	5.62E-13	0.90	4.08	-	946.4
AHQ-8-6, 3078	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.55E-10	0.94	4.71	-	1181.3
AHQ-8-5, 3085 - 3096	K.THEAEIVEGENHTYCIR.F	2060.19046	2	1.27E-04	0.98	5.44	-	1859.1
AHQ-8-5, 3089 - 3101	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.36E-07	0.94	4.58	-	1130.9
AHQ-8-6, 3082 - 3086	K.THEAEIVEGENHTYCIR.F	2060.19046	2	7.44E-05	0.97	4.78	-	1522.3
AHQ-8-3, 3140	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.56E-05	0.86	3.31	-	1071.7
AHQ-8-7, 3040	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.40E-04	0.90	3.56	-	1207.2
AHQ-8-8, 3050	K.THEAEIVEGENHTYCIR.F	2060.19046	3	3.58E-06	0.86	3.46	-	1128.3
AHQ-8-2, 3179	K.THEAEIVEGENHTYCIR.F	2060.19046	3	3.98E-05	0.66	3.04	-	632.5
AHQ-8-5, 3218	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.89E-14	0.98	5.05	-	1902.5
AHQ-8-5, 3206 - 3282	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.54E-04	0.83	3.45	-	828.3
AHQ-8-3, 3173	R.TPCEEILVK.H	1090.27249	2	3.40E-04	0.91	3.23	-	881.3
AHQ-8-1, 3351	R.TPCEEILVK.H	1090.27249	2	9.55E-06	0.85	2.99	-	772.8
AHQ-8-6, 3128	R.TPCEEILVK.H	1090.27249	2	4.87E-06	0.70	2.72	-	603.7
AHQ-8-4, 3141	R.TPCEEILVK.H	1090.27249	2	4.94E-06	0.64	2.86	-	513.0
AHQ-8-14-, 3167	R.TPCEEILVK.H	1090.27249	1	1.72E-05	0.53	2.75	-	353.0
AHQ-8-5, 3141	R.TPCEEILVK.H	1090.27249	2	1.80E-05	0.75	2.94	-	556.3
AHQ-8-3, 6560 - 6564	K.TTYFEIFTAGAGTGEVEVVIQDPM*GQK.G	2906.21339	3	3.92E-04	0.86	3.44	-	1357.6
AHQ-8-5, 3333 - 3406	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.00E-13	0.94	4.53	-	939.0
AHQ-8-7, 3194	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.23E-05	0.91	3.72	-	946.9
AHQ-8-5, 3252	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.01E-07	0.82	3.40	-	555.9
AHQ-8-4, 3187 - 3261	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.48E-05	0.78	3.02	-	470.1

AHQ-8-5, 3192 - 3264	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.82E-11	0.93	3.95	-	983.5
AHQ-8-1, 3467 - 3523	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.24E-13	0.92	3.95	-	878.2
AHQ-8-3, 3137 - 3205	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.30E-05	0.82	3.56	-	577.7
AHQ-8-8, 3225 - 3306	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.60E-06	0.93	4.88	-	471.4
AHQ-8-2, 3397 - 3437	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.26E-09	0.95	4.57	-	1136.9
AHQ-8-3, 3272 - 3334	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.06E-07	0.78	3.30	-	374.6
AHQ-8-2, 3305	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.90E-05	0.46	2.75	-	241.5
AHQ-8-2, 3183 - 3243	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.07E-11	0.94	4.15	-	1132.3
AHQ-8-6, 3230 - 3303	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.10E-10	0.92	3.93	-	971.3
AHQ-8-3, 3424	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.13E-10	0.93	4.20	-	797.1
AHQ-8-1, 3079	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.07E-06	0.85	3.55	-	591.3
AHQ-8-4, 2845	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.11E-06	0.88	3.69	-	665.5
AHQ-8-6, 2856	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.25E-04	0.57	2.80	-	310.0
AHQ-8-2, 2939 - 2987	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.02E-05	0.93	3.95	-	895.3
AHQ-8-3, 2893	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.49E-08	0.86	3.86	-	424.1
AHQ-8-4, 2651	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.73E-06	0.71	3.05	-	485.1
AHQ-8-5, 2665	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.65E-05	0.92	4.05	-	800.6
AHQ-8-14-, 2895	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.10E-05	0.77	3.18	-	346.7
AHQ-8-5, 2840 - 2868	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	1.55E-06	0.85	3.55	-	614.6
AHQ-8-3, 3257 - 3338	K.VDINTEDLEDGTCR.V	1638.69283	2	2.06E-07	0.92	3.69	-	1056.0
AHQ-8-13-, 3498	K.VDINTEDLEDGTCR.V	1638.69283	2	1.13E-06	0.81	2.94	-	880.8
AHQ-8-6, 3204 - 3282	K.VDINTEDLEDGTCR.V	1638.69283	2	1.23E-07	0.85	3.15	-	854.3
AHQ-8-4, 3490 - 3509	K.VDINTEDLEDGTCR.V	1638.69283	2	1.18E-06	0.93	4.06	-	903.8
AHQ-8-8, 3215	K.VDINTEDLEDGTCR.V	1638.69283	2	2.06E-07	0.56	2.60	-	645.1
AHQ-8-5, 3470 - 3540	K.VDINTEDLEDGTCR.V	1638.69283	2	2.99E-05	0.95	4.21	-	1210.4
AHQ-8-2, 3561	K.VDINTEDLEDGTCR.V	1638.69283	2	1.08E-05	0.91	3.86	-	1112.8
AHQ-8-1, 3647 - 3649	K.VDINTEDLEDGTCR.V	1638.69283	2	5.60E-07	0.93	4.18	-	1013.2
AHQ-8-4, 3327	K.VDINTEDLEDGTCR.V	1638.69283	2	7.59E-05	0.92	3.54	-	1195.2
AHQ-8-5, 3309 - 3381	K.VDINTEDLEDGTCR.V	1638.69283	2	2.24E-07	0.91	3.21	-	1211.5
AHQ-8-3, 3492 - 3550	K.VDINTEDLEDGTCR.V	1638.69283	2	5.08E-06	0.80	3.26	-	745.8
AHQ-8-4, 3242	K.VDINTEDLEDGTCR.V	1638.69283	2	1.93E-07	0.88	3.75	-	769.3
AHQ-8-5, 3228	K.VDINTEDLEDGTCR.V	1638.69283	2	7.00E-06	0.86	3.27	-	908.2
AHQ-8-8, 3425	K.VDINTEDLEDGTCR.V	1638.69283	2	2.37E-06	0.96	4.78	-	1212.0
AHQ-8-6, 2624	K.VDVGKDQEFTVK.S	1365.51377	2	8.40E-10	0.89	3.40	-	771.9
AHQ-8-2, 2693	K.VDVGKDQEFTVK.S	1365.51377	2	7.43E-08	0.86	3.36	-	637.9
AHQ-8-4, 2626	K.VDVGKDQEFTVK.S	1365.51377	2	1.11E-07	0.82	3.08	-	599.7
AHQ-8-1, 2861	K.VDVGKDQEFTVK.S	1365.51377	2	7.46E-10	0.90	3.59	-	738.0
AHQ-8-3, 2660	K.VDVGKDQEFTVK.S	1365.51377	2	1.22E-08	0.70	3.10	-	460.5
AHQ-8-3, 2801	K.VEPGLGADNSVVR.F	1313.44209	1	1.59E-06	0.05	1.91	-	136.7
AHQ-8-1, 2983	K.VEPGLGADNSVVR.F	1313.44209	2	1.10E-04	0.69	2.73	-	335.0
AHQ-8-2, 5739 - 5795	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	2.54E-05	0.93	5.51	-	799.4
AHQ-8-1, 5791 - 5847	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	3.88E-06	0.96	6.08	-	931.0
AHQ-8-6, 5667	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	8.75E-04	0.75	3.63	-	428.3
AHQ-8-2, 6443 - 6499	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	2.24E-04	0.81	4.28	-	358.1
AHQ-8-5, 6429	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.39E-04	0.44	2.70	-	227.9
AHQ-8-4, 6491 - 6493	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	5.02E-06	0.85	4.00	-	382.7
AHQ-8-1, 6472 - 6473	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.37E-06	0.86	3.69	-	686.0
AHQ-8-3, 6396	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	2.00E-05	0.93	4.23	-	772.7
AHQ-8-8, 6501 - 6567	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	3.05E-04	0.81	3.32	-	514.1
AHQ-8-2, 6501	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	8.38E-04	0.55	2.83	-	358.5
AHQ-8-2, 1600 - 1639	R.VHGPGIQSGTTNKPNK.F	1635.80645	2	4.67E-07	0.87	3.60	-	771.8
AHQ-8-1, 4411	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	2.36E-04	0.90	3.58	-	919.3
AHQ-8-4, 4266	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.43E-06	0.97	5.59	-	1354.9
AHQ-8-5, 4233 - 4248	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	5.95E-05	0.95	4.73	-	1666.2
AHQ-8-6, 4184	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	2.73E-04	0.90	4.25	-	1321.9
AHQ-8-5, 4237	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	7.35E-09	0.97	5.42	-	1391.3
AHQ-8-8, 4177	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	5.21E-06	0.97	4.97	-	1772.2
AHQ-8-1, 4408	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	3.40E-05	0.93	3.37	-	1987.0
AHQ-8-7, 4108	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	3.09E-06	0.94	4.80	-	928.6
AHQ-8-4, 4621	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	8.58E-10	0.93	4.85	-	783.4
AHQ-8-3, 4582	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.28E-08	0.93	4.92	-	701.3
AHQ-8-5, 4550 - 4562	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.77E-15	0.89	4.40	-	498.1
AHQ-8-6, 4507	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	8.59E-05	0.86	4.05	-	553.0
AHQ-8-1, 4713	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	5.55E-15	0.94	5.12	-	847.2
AHQ-8-5, 4572	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	2	5.66E-07	0.80	3.81	-	555.8
AHQ-8-2, 4660	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	9.78E-12	0.86	4.29	-	617.6
AHQ-8-1, 3949	K.VNQPASFAVSLNGAK.G	1503.68480	2	9.60E-12	0.91	3.97	-	657.6
AHQ-8-7, 3546 - 3606	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.25E-04	0.79	3.20	-	446.7
AHQ-8-3, 3666 - 3724	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.98E-09	0.84	3.73	-	442.2
AHQ-8-5, 3636 - 3696	K.VNQPASFAVSLNGAK.G	1503.68480	2	8.39E-04	0.89	3.69	-	625.2
AHQ-8-5, 3760 - 3824	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.91E-10	0.87	3.60	-	608.8
AHQ-8-3, 3788 - 3849	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.77E-06	0.58	2.94	-	346.4
AHQ-8-1, 3821	K.VNQPASFAVSLNGAK.G	1503.68480	2	7.10E-08	0.94	4.41	-	775.5
AHQ-8-4, 3793 - 3850	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.70E-09	0.83	3.54	-	450.2
AHQ-8-4, 3662 - 3725	K.VNQPASFAVSLNGAK.G	1503.68480	2	9.17E-08	0.84	3.67	-	438.7
AHQ-8-2, 3744 - 3805	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.90E-07	0.87	3.67	-	575.0
AHQ-8-8, 3553 - 3617	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.83E-09	0.91	3.83	-	697.7
AHQ-8-6, 3594 - 3650	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.42E-08	0.83	3.40	-	506.0
AHQ-8-2, 3925	K.VNQPASFAVSLNGAK.G	1503.68480	2	7.40E-05	0.77	2.97	-	428.1
AHQ-8-3, 1790	K.VPVHDVTDASK.V	1168.28175	2	6.37E-06	0.95	3.38	-	1484.8
AHQ-8-2, 1729 - 1796	K.VPVHDVTDASK.V	1168.28175	2	4.36E-05	0.92	3.19	-	1151.0
AHQ-8-1, 4119 - 4179	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.76E-07	0.96	4.19	-	1816.6
AHQ-8-5, 3989 - 4056	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.27E-07	0.96	5.02	-	1310.4
AHQ-8-4, 4023 - 4099	R.VQVQDNEGCPVEALVK.D	1786.98493	2	6.82E-08	0.96	4.59	-	1529.3
AHQ-8-2, 4069 - 4144	R.VQVQDNEGCPVEALVK.D	1786.98493	2	5.01E-10	0.97	5.48	-	1300.1
AHQ-8-1, 4120 - 4175	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.34E-06	0.98	5.14	-	1881.0
AHQ-8-3, 4028 - 4072	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.37E-04	0.96	5.73	-	1039.4
AHQ-8-1, 4952 - 5007	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	6.71E-07	0.95	5.12	-	1448.5
AHQ-8-3, 4840 - 4896	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	2.99E-04	0.95	5.03	-	1624.5
AHQ-8-2, 5048 - 5113	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	7.67E-06	0.91	4.30	-	1170.8
AHQ-8-2, 4749	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.02E-07	0.96	5.41	-	1378.9
AHQ-8-4, 4682	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	1.34E-06	0.94	4.98	-	713.3
AHQ-8-1, 4803 - 4863	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	3.53E-07	0.95	5.13	-	1371.5
AHQ-8-3, 4666 - 4669	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	8.96E-08	0.95	5.27	-	1075.0
AHQ-8-8, 4559 - 4563	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.12E-09	0.94	4.43	-	1462.2
AHQ-8-5, 4625 - 4684	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	7.82E-10	0.97	5.87	-	1638.9
AHQ-8-6, 4564 - 4576	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	3.52E-06	0.92	4.27	-	1049.9
AHQ-8-7, 4476	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.59E-09	0.93	4.61	-	1123.2
AHQ-8-6, 2718 - 2738	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.75E-05	0.79	3.19	-	601.4
AHQ-8-2, 2772 - 2835	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.14E-05	0.82	3.54	-	533.9
AHQ-8-1, 2955	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.96E-06	0.89	3.87	-	665.7
AHQ-8-2, 2903	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	6.81E-06	0.92	4.23	-	713.0
AHQ-8-6, 2832	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.17E-06	0.44	2.55	-	367.4
AHQ-8-5, 2745 - 2800	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.23E-09	0.89	4.44	-	443.4
AHQ-8-3, 2748 - 2812	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	8.16E-07	0.90	4.38	-	551.4
AHQ-8-3, 2873	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	8.88E-06	0.81	3.24	-	479.3
AHQ-8-4, 2734 - 2797	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.94E-04	0.74	2.94	-	604.3

AHQ-8-7, 3180	K.VTVLFAGQHIAK.S	1284.53185	2	3.00E-07	0.89	3.59	-	751.9
AHQ-8-4, 3291	K.VTVLFAGQHIAK.S	1284.53185	2	5.57E-07	0.95	4.24	-	1052.5
AHQ-8-3, 3317	K.VTVLFAGQHIAK.S	1284.53185	3	5.34E-06	0.75	3.31	-	672.1
AHQ-8-3, 3308	K.VTVLFAGQHIAK.S	1284.53185	2	2.59E-04	0.94	3.86	-	1162.3
AHQ-8-2, 3351 - 3356	K.VTVLFAGQHIAK.S	1284.53185	2	6.97E-07	0.93	3.71	-	1041.2
AHQ-8-2, 3353	K.VTVLFAGQHIAK.S	1284.53185	3	1.40E-04	0.81	3.63	-	561.3
AHQ-8-8, 3127	K.VTVLFAGQHIAK.S	1284.53185	2	2.07E-06	0.91	3.84	-	850.4
AHQ-8-1, 4919	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.34E-04	0.77	2.96	-	434.2
AHQ-8-5, 4754 - 4813	R.VTYCPTEPGNYIINIK.F	1884.14221	2	6.87E-07	0.92	4.45	-	494.5
AHQ-8-6, 4595	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.86E-04	0.77	3.20	-	423.9
AHQ-8-5, 4673	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.99E-04	0.90	3.65	-	602.8
AHQ-8-8, 4765 - 4837	R.VTYCPTEPGNYIINIK.F	1884.14221	2	4.21E-07	0.88	3.97	-	444.5
AHQ-8-3, 4658	R.VTYCPTEPGNYIINIK.F	1884.14221	2	4.75E-06	0.78	3.01	-	463.7
AHQ-8-1, 4775	R.VTYCPTEPGNYIINIK.F	1884.14221	2	5.95E-07	0.85	3.14	-	599.8
AHQ-8-5, 4886 - 4940	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.41E-10	0.79	3.70	-	340.1
AHQ-8-4, 4703	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.01E-10	0.93	4.36	-	707.6
AHQ-8-7, 4641	R.VTYCPTEPGNYIINIK.F	1884.14221	2	4.70E-05	0.84	3.25	-	417.4
AHQ-8-4, 4801 - 4861	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.90E-04	0.92	4.26	-	561.9
AHQ-8-4, 5275 - 5278	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.17E-06	0.87	3.64	-	698.9
AHQ-8-1, 5328	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.40E-04	0.69	2.78	-	522.3
AHQ-8-13-, 4735	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	7.43E-05	0.66	2.71	-	415.6
AHQ-8-14, 5574 - 5587	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	2.13E-04	0.75	3.12	-	491.6
AHQ-8-14-, 5143 - 5218	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.09E-05	0.82	3.00	-	567.1
AHQ-8-5, 4801	R.VTYTPM*APGSYLISIK.Y	1758.07165	3	9.18E-04	0.93	3.87	-	1251.0
AHQ-8-3, 2740	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	1.89E-05	0.84	2.80	-	905.9
AHQ-8-2, 3399 - 3472	R.YAPSEAGLHEMDIR.Y	1589.75482	2	7.07E-05	0.60	2.59	-	579.2
AHQ-8-4, 3386 - 3462	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.64E-05	0.77	3.15	-	707.0
AHQ-8-1, 3584	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.44E-05	0.54	2.66	-	599.5
AHQ-8-4, 2646 - 2709	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	5.00E-04	0.64	2.66	-	567.7
AHQ-8-5, 2700	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	2.25E-04	0.79	2.58	-	792.9
AHQ-8-2, 2777	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	7.36E-04	0.66	2.73	-	677.2
AHQ-8-4, 4143 - 4213	K.YGGDEIPFSPYR.V	1401.50466	2	7.59E-07	0.70	3.14	-	451.4
AHQ-8-7, 3304	K.YGGPYHIGGSPFK.A	1380.53182	2	2.04E-06	0.90	3.58	-	1138.8
AHQ-8-1, 3621	K.YGGPYHIGGSPFK.A	1380.53182	2	5.37E-04	0.95	4.39	-	1114.8
AHQ-8-8, 3329	K.YGGPYHIGGSPFK.A	1380.53182	2	7.62E-09	0.97	4.64	-	1669.4
AHQ-8-5, 3393	K.YGGPYHIGGSPFK.A	1380.53182	2	1.16E-06	0.90	3.61	-	946.5
AHQ-8-6, 3376	K.YGGPYHIGGSPFK.A	1380.53182	2	2.98E-07	0.96	4.27	-	1244.2
AHQ-8-4, 3398	K.YGGPYHIGGSPFK.A	1380.53182	2	6.08E-08	0.97	4.76	-	1745.1
AHQ-8-2, 3497	K.YGGPYHIGGSPFK.A	1380.53182	2	5.22E-04	0.97	4.30	-	1904.0
AHQ-8-4, 3410	K.YGGPYHIGGSPFK.A	1380.53182	3	1.91E-05	0.93	4.59	-	669.3
AHQ-8-11, 3331 - 3343	K.YGGPYHIGGSPFK.A	1380.53182	2	2.69E-06	0.97	4.37	-	1760.1
AHQ-8-5, 3405	K.YGGPYHIGGSPFK.A	1380.53182	3	3.54E-07	0.91	4.00	-	753.1
AHQ-8-3, 3434	K.YGGPYHIGGSPFK.A	1380.53182	2	7.93E-08	0.98	4.58	-	2129.4
AHQ-8-1, 3267	K.YGGQPVPNFPSK.L	1291.43658	2	2.05E-05	0.93	3.38	-	763.7
AHQ-8-2, 3065 - 3127	K.YGGQPVPNFPSK.L	1291.43658	2	5.03E-04	0.86	3.18	-	429.7
AHQ-8-3, 3080	K.YGGQPVPNFPSK.L	1291.43658	2	1.65E-05	0.90	3.39	-	539.1
AHQ-8-1, 4468 - 4547	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	8.70E-07	0.90	3.97	-	954.7
AHQ-8-5, 4240 - 4282	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.56E-05	0.90	4.48	-	836.0
AHQ-8-6, 4175	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	9.74E-06	0.89	4.77	-	625.4
AHQ-8-3, 4296	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	1.38E-05	0.67	3.37	-	569.0
AHQ-8-7, 4094	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	8.10E-05	0.79	3.45	-	619.9
AHQ-8-4, 2906	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.20E-05	0.84	3.03	-	526.6
AHQ-8-10, 2762 - 2834	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.14E-07	0.82	3.38	-	444.3
AHQ-8-4, 3095	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.60E-07	0.86	3.02	-	499.6
AHQ-8-4, 2915	K.YNEQHVPGSPFTAR.V	1603.71978	3	4.16E-04	0.97	5.38	-	1629.4
AHQ-8-3, 2948	K.YNEQHVPGSPFTAR.V	1603.71978	2	9.58E-06	0.83	3.10	-	539.5
AHQ-8-8, 2790	K.YNEQHVPGSPFTAR.V	1603.71978	2	7.01E-05	0.88	3.40	-	536.2
AHQ-8-4, 3101	K.YNEQHVPGSPFTAR.V	1603.71978	3	5.46E-05	0.84	3.32	-	916.4
AHQ-8-5, 4336	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	8.17E-07	0.90	4.08	-	699.3
AHQ-8-3, 4192	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.65E-06	0.90	3.74	-	733.2
AHQ-8-3, 4452 - 4496	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.71E-04	0.92	4.57	-	588.5
AHQ-8-3, 4297 - 4345	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.46E-06	0.92	4.34	-	687.2
AHQ-8-7, 4202	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.35E-06	0.86	3.74	-	602.3
AHQ-8-2, 4260	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.73E-07	0.90	4.12	-	526.7
AHQ-8-6, 4267	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.18E-05	0.84	3.49	-	565.2
AHQ-8-2, 4356 - 4415	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.26E-05	0.95	5.02	-	823.5
AHQ-8-1, 4564	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.54E-06	0.82	3.57	-	568.3
AHQ-8-2, 4515 - 4573	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	7.70E-07	0.89	3.81	-	606.8
AHQ-8-1, 4449 - 4503	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.43E-06	0.88	4.15	-	510.0
AHQ-8-4, 4385	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.31E-06	0.87	4.10	-	490.3
AHQ-8-2, 6164 - 6239	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	3.08E-06	0.74	3.55	-	455.9
AHQ-8-2, 5852 - 5920	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	4.51E-05	0.90	3.93	-	911.9
AHQ-8-3, 6076 - 6132	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	4.23E-07	0.75	3.69	-	455.1
gi|4503571|ref|NP_001419.1|	enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n			5.55E-15	9.17	110.27	31.80	47168.7
AHQ-8-7, 4924 - 4982	R.AAVPSGASTGIYEALELR.D	1806.00979	2	5.25E-04	0.59	2.84	-	245.8
AHQ-8-13-, 5015 - 5070	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.03E-12	0.97	5.40	-	1124.7
AHQ-8-13, 5199	R.AAVPSGASTGIYEALELR.D	1806.00979	2	5.06E-08	0.85	3.60	-	363.4
AHQ-8-11, 4957	R.AAVPSGASTGIYEALELR.D	1806.00979	2	4.45E-05	0.58	2.55	-	284.1
AHQ-8-8, 5107	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.02E-04	0.77	3.16	-	305.6
AHQ-8-8, 4993	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.11E-05	0.85	3.93	-	320.1
AHQ-8-14-, 5022 - 5102	R.AAVPSGASTGIYEALELR.D	1806.00979	2	5.55E-15	0.96	5.29	-	694.5
AHQ-8-10, 4170	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	7.08E-07	0.71	3.00	-	524.6
AHQ-8-8, 5090	K.FTASAGIQVVGDDLTVTNPK.R	2034.25590	2	7.84E-05	0.90	4.09	-	725.9
AHQ-8-8, 4154	R.GNPTVEVDLFTSK.G	1407.55065	1	4.22E-07	0.53	3.25	-	476.9
AHQ-8-8, 4145	R.GNPTVEVDLFTSK.G	1407.55065	1	6.31E-04	0.15	1.90	-	413.1
AHQ-8-8, 2366	R.IGAEVYHNLK.N	1144.30502	2	4.38E-05	0.95	3.92	-	1535.6
AHQ-8-8, 5941 - 5963	K.LAMQEFM*ILPVGAANFR.E	1925.30752	2	3.98E-04	0.93	5.26	-	766.8
AHQ-8-8, 5769 - 5770	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	2.10E-04	0.93	5.25	-	828.4
AHQ-8-8, 5365	K.LAM*QEFM*ILPVGAANFR.E	1941.30692	2	6.09E-05	0.94	4.49	-	832.3
AHQ-8-8, 3469	K.LAQANGWGVMVSHR.S	1526.74832	2	1.08E-09	0.85	3.00	-	1075.8
AHQ-8-14, 4621	K.VNQIGSVTESLQACK.L	1635.82159	2	5.87E-04	0.60	2.52	-	469.3
AHQ-8-8, 4649	R.YISPDQLADLYK.S	1426.59557	1	2.04E-05	0.81	3.52	-	715.5
AHQ-8-8, 4642	R.YISPDQLADLYK.S	1426.59557	1	2.75E-04	0.22	2.10	-	525.9
AHQ-8-8, 4641	R.YISPDQLADLYK.S	1426.59557	2	1.07E-05	0.87	3.25	-	687.8
gi|4505257|ref|NP_002435.1|	moesin [Homo sapiens]			7.22E-15	10.90	120.34	25.30	67819.5
AHQ-8-6, 2302 - 2303	R.ALELEQER.K	988.07707	2	2.10E-04	0.90	2.99	-	1489.5
AHQ-8-6, 2630	K.ALTSELANAR.D	1046.15975	2	6.90E-05	0.94	3.55	-	1371.5
AHQ-8-6, 6311	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	3	8.07E-09	0.87	4.30	-	792.9
AHQ-8-6, 5636	R.EVWFFGLQYQDTK.G	1661.83760	2	1.24E-06	0.91	3.36	-	1050.3
AHQ-8-6, 6276	K.FYPEDVSEELIQDITQR.L	2083.24065	2	1.79E-08	0.92	4.35	-	889.4
AHQ-8-6, 6279	K.FYPEDVSEELIQDITQR.L	2083.24065	3	8.73E-07	0.95	4.75	-	1340.2
AHQ-8-6, 5124 - 5195	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	1.26E-06	0.95	4.35	-	1269.0
AHQ-8-6, 5504	K.IAQDLEMYGVNYFSIK.N	1892.16455	2	2.72E-06	0.71	3.12	-	779.6
AHQ-8-6, 2110	R.IQVWHEEHR.G	1234.34835	2	2.30E-05	0.81	2.85	-	904.8
AHQ-8-6, 4560	K.KTQEQLALEMAELTAR.I	1833.10018	2	6.34E-07	0.98	4.99	-	2084.3
AHQ-8-6, 4566 - 4567	K.KTQEQLALEMAELTAR.I	1833.10018	3	3.78E-05	0.96	4.83	-	1965.7
AHQ-8-6, 3350 - 3406	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	3.82E-12	0.96	5.59	-	1433.8

AHQ-8-6, 3178 - 3234	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	3.16E-10	0.97	6.24	-	2127.3
AHQ-8-6, 3054 - 3115	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	7.22E-15	0.97	6.74	-	1605.6
AHQ-8-6, 3463 - 3464	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	1.17E-09	0.96	5.44	-	1807.2
AHQ-8-6, 5050	K.TQEQLALEMAELTAR.I	1704.92727	2	3.80E-08	0.97	3.69	-	2463.2
gi|4557697|ref|NP_000412.1|	keratin 10; Keratin-10 [Homo sapiens]			7.77E-15	14.16	160.30	26.20	57247.1
AHQ-8-1, 2979	R.ALEESNYELEGK.I	1382.45482	2	4.01E-06	0.95	4.11	-	1393.9
AHQ-8-10, 2703	R.ALEESNYELEGK.I	1382.45482	2	1.55E-06	0.83	3.04	-	877.3
AHQ-8-4, 2754	R.ALEESNYELEGK.I	1382.45482	2	1.26E-07	0.92	3.52	-	1247.5
AHQ-8-11, 2749 - 2751	R.ALEESNYELEGK.I	1382.45482	2	1.52E-07	0.92	3.77	-	1064.4
AHQ-8-12, 2703 - 2768	R.ALEESNYELEGK.I	1382.45482	2	8.53E-04	0.69	2.80	-	369.5
AHQ-8-3, 2797	R.ALEESNYELEGK.I	1382.45482	2	5.49E-07	0.93	3.87	-	1109.9
AHQ-8-13, 2971	R.ALEESNYELEGK.I	1382.45482	2	1.73E-04	0.76	3.12	-	660.6
AHQ-8-14-, 2799 - 2806	R.ALEESNYELEGK.I	1382.45482	2	6.55E-10	0.94	3.81	-	1300.4
AHQ-8-2, 2828	R.ALEESNYELEGK.I	1382.45482	2	9.85E-08	0.94	3.96	-	1237.2
AHQ-8-8, 2726	R.ALEESNYELEGK.I	1382.45482	2	1.41E-06	0.82	3.19	-	768.5
AHQ-8-14, 3611	R.ALEESNYELEGK.I	1382.45482	2	1.40E-04	0.48	2.53	-	497.8
AHQ-8-13-, 2831	R.ALEESNYELEGK.I	1382.45482	2	5.72E-07	0.94	4.16	-	1142.6
AHQ-8-4, 3465	K.DAEAWFNEK.S	1110.15762	2	2.05E-05	0.73	2.78	-	881.0
AHQ-8-14-, 3490	K.DAEAWFNEK.S	1110.15762	2	1.06E-04	0.73	2.84	-	732.8
AHQ-8-2, 3531	K.DAEAWFNEK.S	1110.15762	2	1.99E-04	0.84	2.94	-	1038.4
AHQ-8-2, 4427 - 4503	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.89E-14	0.96	5.13	-	926.8
AHQ-8-8, 5141	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.87E-04	0.83	3.67	-	665.1
AHQ-8-13-, 5058	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.61E-04	0.89	4.10	-	755.1
AHQ-8-13-, 5168	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.88E-07	0.92	4.25	-	816.7
AHQ-8-13, 4475	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.50E-09	0.86	3.36	-	867.4
AHQ-8-2, 5203	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.24E-06	0.95	4.59	-	1101.6
AHQ-8-4, 4398 - 4475	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.02E-07	0.90	3.99	-	768.7
AHQ-8-13-, 4319	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	8.16E-11	0.92	3.69	-	871.6
AHQ-8-3, 4372	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	4.64E-08	0.92	4.09	-	866.9
AHQ-8-1, 4501	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.44E-08	0.91	4.44	-	673.6
AHQ-8-1, 5229	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	4.73E-08	0.96	5.02	-	1050.1
AHQ-8-3, 5124 - 5176	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.90E-05	0.75	3.56	-	544.0
AHQ-8-3, 5238	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	8.77E-04	0.78	3.52	-	608.4
AHQ-8-14-, 5078	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.38E-07	0.96	5.07	-	1104.4
AHQ-8-10, 4156	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.38E-06	0.54	2.70	-	327.6
AHQ-8-13, 5187 - 5188	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.14E-07	0.95	4.59	-	995.7
AHQ-8-13-, 4010 - 4071	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	5.89E-05	0.90	3.77	-	888.8
AHQ-8-6, 3956 - 4026	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	9.43E-04	0.47	2.70	-	436.0
AHQ-8-1, 4229	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	7.77E-11	0.95	4.28	-	1244.5
AHQ-8-7, 3956	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.19E-06	0.94	4.58	-	898.9
AHQ-8-2, 4156 - 4229	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	5.22E-13	0.93	3.97	-	956.6
AHQ-8-14-, 4034	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	6.77E-07	0.79	3.49	-	721.8
AHQ-8-12, 3975 - 3982	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	5.17E-08	0.95	4.51	-	1134.8
AHQ-8-8, 4051 - 4079	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.11E-04	0.86	3.57	-	692.5
AHQ-8-2, 3345	K.IRLENEIQTYR.S	1435.61046	3	9.69E-06	0.74	3.66	-	648.3
AHQ-8-13-, 3331	K.IRLENEIQTYR.S	1435.61046	2	5.16E-08	0.97	4.20	-	1770.2
AHQ-8-10, 3087 - 3146	K.IRLENEIQTYR.S	1435.61046	2	2.97E-08	0.98	4.70	-	2360.5
AHQ-8-4, 2511	R.LENEIQTYR.S	1166.26586	2	3.96E-06	0.92	4.19	-	1189.7
AHQ-8-14-, 2794	R.LKYENEVALR.Q	1235.41446	2	4.68E-07	0.72	3.20	-	459.1
AHQ-8-13-, 2788 - 2830	R.LKYENEVALR.Q	1235.41446	2	1.60E-04	0.64	2.88	-	388.0
AHQ-8-2, 6129	K.NQILNLTTDNANILLQIDNAR.L	2368.63258	3	5.05E-05	0.97	4.95	-	2246.3
AHQ-8-1, 5483 - 5561	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	3.25E-04	0.96	5.72	-	1057.9
AHQ-8-14-, 6073	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	7.80E-05	0.72	3.50	-	590.9
AHQ-8-2, 5480	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	2	1.58E-06	0.85	4.45	-	285.2
AHQ-8-2, 5475	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	1.17E-04	0.94	5.31	-	733.5
AHQ-8-2, 6243	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	2.12E-05	0.93	4.84	-	948.8
AHQ-8-8, 6222	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	5.13E-04	0.72	3.45	-	776.6
AHQ-8-13-, 5287	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	6.22E-07	0.92	4.96	-	783.3
AHQ-8-13-, 5656	R.NVSTGDVNVEMNAAPGVDLTQLLNNM*R.N	2890.20063	3	1.23E-04	0.79	3.58	-	648.5
AHQ-8-7, 5257	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	1.12E-04	0.93	5.28	-	833.3
AHQ-8-14-, 6078 - 6083	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	2	9.54E-04	0.85	3.81	-	388.2
AHQ-8-2, 3429	K.QSLEASLAETEGR.Y	1391.46648	2	6.11E-05	0.79	3.45	-	430.2
AHQ-8-13-, 4826	K.SKELTTEIDNNIEQISSYK.S	2213.38462	3	4.19E-07	0.72	3.04	-	623.8
AHQ-8-2, 4907 - 4965	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	5.36E-09	0.97	5.52	-	1544.7
AHQ-8-2, 5132	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	1.43E-10	0.95	4.90	-	854.6
AHQ-8-3, 4813 - 4884	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	1.18E-04	0.83	3.74	-	619.1
AHQ-8-7, 3929	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	4.70E-04	0.60	2.84	-	367.9
AHQ-8-3, 5050	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	1.94E-05	0.70	3.13	-	213.7
AHQ-8-2, 4137	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	7.77E-15	0.97	5.90	-	1415.9
AHQ-8-1, 5091 - 5172	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	1.18E-06	0.40	2.62	-	251.3
AHQ-8-14-, 4997	K.SKELTTEIDNNIEQISSYK.S	2213.38462	3	1.83E-06	0.69	3.04	-	710.4
AHQ-8-14-, 4758 - 4831	K.SKELTTEIDNNIEQISSYK.S	2213.38462	3	8.74E-04	0.73	3.38	-	624.1
AHQ-8-2, 2189	R.SLLEGEGSSGGGGR.G	1263.29680	2	2.22E-06	0.88	3.01	-	1146.4
AHQ-8-4, 2133	R.SLLEGEGSSGGGGR.G	1263.29680	2	3.16E-05	0.88	3.36	-	800.0
AHQ-8-13-, 6280	K.TIDDLKNQILNLTTDNANILLQIDNAR.L	3054.40205	3	1.48E-09	0.92	4.97	-	1199.4
AHQ-8-2, 2309	K.VTMQNLNDR.L	1091.22402	2	1.25E-05	0.83	2.87	-	851.2
gi|21361657|ref|NP_005304.3|	glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom			1.22E-14	4.56	60.30	16.80	56782.0
AHQ-8-7, 6225	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	1.22E-14	0.98	6.07	-	3236.2
AHQ-8-7, 4440	R.FLQDYFDGNLK.R	1360.49568	2	1.19E-04	0.90	3.72	-	889.2
AHQ-8-7, 4405	R.GFPTIYFSPANK.K	1342.52349	2	2.68E-04	0.87	3.20	-	803.8
AHQ-8-7, 5370	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	3	7.11E-05	0.65	3.35	-	489.6
AHQ-8-7, 2416	K.LSKDPNIVIAK.M	1198.43727	2	1.59E-06	0.60	2.56	-	519.4
AHQ-8-7, 2397 - 2400	K.SEPIPESNDGPVK.V	1369.45928	2	6.12E-04	0.56	2.65	-	310.2
gi|4758460|ref|NP_004479.1|	glycoprotein V (platelet) [Homo sapiens]			1.83E-14	7.77	90.26	24.80	60958.9
AHQ-8-5, 5272 - 5276	R.CAGPGAHAGLPLWALPGGDAECPGPR.G	2587.87539	3	2.04E-06	0.90	4.47	-	814.7
AHQ-8-5, 3838	R.GVLQSQSFSGM*TVLQR.L	1754.98948	2	2.53E-06	0.96	4.61	-	1421.9
AHQ-8-5, 4544	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	1.87E-08	0.98	5.11	-	2236.5
AHQ-8-5, 5312	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	3	1.74E-05	0.91	3.96	-	1284.2
AHQ-8-5, 4510 - 4525	R.LPNLSSLTLSR.N	1201.39802	2	3.56E-06	0.88	3.38	-	1090.2
AHQ-8-6, 6354	R.LSALPQGAFQGLGELQVLALHSNGLTALPDGLLR.G	3471.99408	3	4.41E-08	0.75	3.42	-	453.4
AHQ-8-5, 6460	R.LSALPQGAFQGLGELQVLALHSNGLTALPDGLLR.G	3471.99408	3	1.83E-14	0.85	4.28	-	463.6
AHQ-8-5, 6445	R.LVSLDSGLLNSLGALTELQFHR.N	2384.71675	3	4.84E-12	0.77	3.50	-	517.8
AHQ-8-5, 5806	K.M*VLLEQLFLDHNALR.G	1829.15633	2	5.42E-05	0.61	2.68	-	501.2
AHQ-8-5, 3429 - 3432	R.YLGVTLSPR.L	1006.18036	2	2.21E-05	0.92	3.34	-	1274.1
AHQ-8-6, 3399	R.YLGVTLSPR.L	1006.18036	2	5.93E-04	0.93	3.19	-	1405.7
gi|18104967|ref|NP_000953.2|	prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland			2.00E-14	3.64	40.28	11.90	68686.0
AHQ-8-6, 3928 - 4002	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	1.22E-05	0.93	4.04	-	793.4
AHQ-8-6, 3847 - 3859	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	3	1.02E-07	0.81	3.14	-	896.1
AHQ-8-6, 6398	K.IVIEEYVQQLSGYFLQLK.F	2171.52045	3	2.00E-14	0.97	5.65	-	1722.2
AHQ-8-6, 6402	K.IVIEEYVQQLSGYFLQLK.F	2171.52045	2	1.19E-05	0.97	4.84	-	1658.4
AHQ-8-6, 3319	R.VPDASQDDGPAVERPSTEL	1984.06747	2	6.62E-07	0.93	4.22	-	854.4
AHQ-8-6, 3208 - 3259	R.VPDASQDDGPAVERPSTEL	1984.06747	2	3.38E-06	0.93	4.54	-	858.5
gi|7656991|ref|NP_055140.1|	coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;			2.66E-14	6.92	80.30	25.50	53248.7
AHQ-8-6, 5554	R.AIFLADGNVFTTGFSR.M	1716.91793	2	7.95E-06	0.90	3.75	-	967.6
AHQ-8-6, 5442 - 5498	R.AIFLADGNVFTTGFSR.M	1716.91793	2	1.88E-07	0.97	4.84	-	1681.2
AHQ-8-6, 3402 - 3407	R.KCEPIIMTVPR.K	1345.65706	2	1.31E-05	0.89	3.13	-	839.9
AHQ-8-6, 6278	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	2.66E-14	0.97	6.02	-	1390.0

AHQ-8-6, 2342 - 2356	K.NDQCYDDIR.V	1200.21762	2	9.51E-04	0.82	2.91	-	1025.7
AHQ-8-6, 2431	K.SIKDTICNQDER.I	1480.58332	2	6.66E-05	0.88	2.84	-	1136.4
AHQ-8-6, 3119	R.VGIVAWHPTAR.N	1207.40918	3	1.71E-04	0.79	3.41	-	719.0
AHQ-8-7, 4125	R.VTWDSSFCAVNPR.F	1540.68205	2	1.32E-04	0.89	3.73	-	882.9
AHQ-8-6, 4127 - 4191	R.VTWDSSFCAVNPR.F	1540.68205	2	9.20E-09	0.85	3.42	-	1083.4
AHQ-8-7, 5546	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	1.78E-07	0.76	3.29	-	592.9
AHQ-8-6, 5604	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	2.01E-07	0.92	4.75	-	859.7
gi|4507485|ref|NP_003237.1|	thrombospondin 1 [Homo sapiens]			6.49E-14	29.98	350.32	31.20	129351.8
AHQ-8-5, 3961	K.AGTLDLSLTVQGK.Q	1303.48711	2	2.83E-05	0.95	3.91	-	1462.4
AHQ-8-3, 4006	K.AGTLDLSLTVQGK.Q	1303.48711	2	2.32E-06	0.94	3.49	-	1605.3
AHQ-8-5, 2781	R.AQLYIDCEK.M	1141.27636	2	1.33E-04	0.81	2.85	-	817.0
AHQ-8-4, 5647 - 5703	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	4.16E-04	0.88	4.29	-	817.4
AHQ-8-2, 5655 - 5721	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	1.97E-07	0.93	5.45	-	900.7
AHQ-8-6, 5486 - 5542	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	1.94E-05	0.88	4.69	-	409.8
AHQ-8-4, 3597 - 3647	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.67E-06	0.84	3.52	-	407.9
AHQ-8-5, 3626	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.27E-09	0.75	2.88	-	453.7
AHQ-8-2, 3820	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.48E-06	0.85	3.39	-	409.7
AHQ-8-5, 3746	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.39E-05	0.74	3.04	-	541.8
AHQ-8-3, 3749	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.55E-04	0.81	3.09	-	522.0
AHQ-8-2, 3707	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.18E-10	0.85	3.39	-	505.4
AHQ-8-3, 3624 - 3689	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.57E-05	0.67	2.90	-	418.6
AHQ-8-3, 3792	K.CNYLGHYSDPMYR.C	1677.84222	2	6.78E-06	0.90	3.82	-	643.8
AHQ-8-2, 3396	K.CNYLGHYSDPM*YR.C	1693.84162	2	8.35E-05	0.87	2.90	-	748.0
AHQ-8-3, 3345	K.CNYLGHYSDPM*YR.C	1693.84162	2	7.39E-04	0.93	3.48	-	1244.4
AHQ-8-2, 3276 - 3280	K.DCVGDVTENQICNK.Q	1654.75869	2	7.33E-08	0.96	4.77	-	1367.6
AHQ-8-2, 2857 - 2861	K.DHSGQVFSVVSNGK.A	1461.56164	2	3.93E-06	0.94	3.89	-	1213.7
AHQ-8-5, 2953	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.72E-10	0.84	2.95	-	815.3
AHQ-8-3, 3161	R.DNCQYVYNVDQR.D	1575.64166	2	2.23E-06	0.88	3.62	-	932.1
AHQ-8-5, 3021	R.DNCQYVYNVDQR.D	1575.64166	2	1.45E-04	0.83	2.62	-	1128.9
AHQ-8-2, 3079	R.DNCQYVYNVDQR.D	1575.64166	2	1.22E-04	0.80	2.59	-	980.9
AHQ-8-7, 2964	R.DNCQYVYNVDQR.D	1575.64166	2	2.54E-05	0.89	3.54	-	915.7
AHQ-8-7, 3092	R.DNCQYVYNVDQR.D	1575.64166	2	2.16E-06	0.84	3.42	-	880.6
AHQ-8-6, 3120	R.DNCQYVYNVDQR.D	1575.64166	2	3.63E-05	0.54	2.73	-	537.1
AHQ-8-6, 3008	R.DNCQYVYNVDQR.D	1575.64166	2	1.79E-04	0.94	3.60	-	1563.1
AHQ-8-3, 3038 - 3040	R.DNCQYVYNVDQR.D	1575.64166	2	5.56E-07	0.92	3.92	-	989.5
AHQ-8-5, 3153	R.DNCQYVYNVDQR.D	1575.64166	2	1.18E-06	0.92	3.59	-	1217.7
AHQ-8-5, 3609	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	6.49E-14	0.86	3.74	-	799.6
AHQ-8-4, 3629	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.40E-09	0.90	4.52	-	810.7
AHQ-8-2, 4021	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	6.94E-06	0.91	4.67	-	541.9
AHQ-8-2, 3752	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.25E-07	0.90	4.64	-	678.4
AHQ-8-3, 3582 - 3661	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	8.10E-11	0.88	4.31	-	621.0
AHQ-8-6, 3486 - 3556	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	8.43E-09	0.83	3.40	-	909.0
AHQ-8-7, 3540	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.34E-04	0.74	3.09	-	985.4
AHQ-8-4, 3977	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	1.89E-10	0.88	4.49	-	585.0
AHQ-8-2, 3617 - 3679	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	3.00E-11	0.81	3.99	-	497.2
AHQ-8-3, 3956	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	4.07E-08	0.83	3.80	-	511.9
AHQ-8-4, 3587	K.FQDLVDAVR.A	1063.18877	2	5.14E-07	0.90	3.11	-	940.2
AHQ-8-2, 3655	K.FQDLVDAVR.A	1063.18877	2	1.22E-06	0.90	3.52	-	942.8
AHQ-8-6, 3531	K.FQDLVDAVR.A	1063.18877	2	8.60E-04	0.82	2.68	-	958.2
AHQ-8-3, 4164 - 4165	R.FQMIPLDPK.G	1089.33277	2	2.01E-04	0.81	2.74	-	586.1
AHQ-8-3, 2892 - 2952	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.82E-04	0.86	3.98	-	411.3
AHQ-8-3, 3049	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.22E-06	0.67	3.07	-	331.3
AHQ-8-6, 2915 - 2920	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	9.10E-08	0.49	3.26	-	383.5
AHQ-8-2, 2996	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.15E-06	0.80	3.67	-	354.1
AHQ-8-7, 2860	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.60E-05	0.73	3.43	-	419.0
AHQ-8-4, 2917	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.58E-06	0.94	4.96	-	613.8
AHQ-8-8, 2793	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	9.99E-04	0.91	3.86	-	785.3
AHQ-8-4, 2919 - 2922	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	2.91E-04	0.69	3.46	-	405.6
AHQ-8-3, 2953 - 2954	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	5.73E-06	0.81	3.76	-	627.2
AHQ-8-6, 2911	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	5.00E-04	0.85	3.96	-	376.5
AHQ-8-11, 5155	K.GFLLLASLR.Q	990.22407	2	6.18E-05	0.96	3.50	-	2046.9
AHQ-8-5, 5344 - 5348	K.GFLLLASLR.Q	990.22407	2	2.38E-04	0.97	4.11	-	2246.0
AHQ-8-4, 5393	K.GFLLLASLR.Q	990.22407	2	5.72E-04	0.97	3.88	-	2067.0
AHQ-8-1, 5468	K.GFLLLASLR.Q	990.22407	2	4.24E-05	0.96	3.61	-	1932.8
AHQ-8-2, 5420	K.GFLLLASLR.Q	990.22407	2	8.94E-05	0.97	3.80	-	1982.1
AHQ-8-3, 5341	K.GFLLLASLR.Q	990.22407	2	1.10E-04	0.97	4.20	-	2086.4
AHQ-8-6, 4223 - 4299	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.67E-04	0.77	3.51	-	545.8
AHQ-8-3, 4472 - 4476	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.10E-04	0.86	4.05	-	661.4
AHQ-8-2, 4636 - 4657	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.49E-06	0.86	3.63	-	852.3
AHQ-8-2, 4447	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.14E-08	0.94	4.41	-	1039.7
AHQ-8-6, 4090	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.14E-05	0.49	2.93	-	413.2
AHQ-8-2, 4327 - 4387	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.77E-06	0.88	4.20	-	701.8
AHQ-8-6, 4490	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.41E-06	0.43	2.68	-	513.9
AHQ-8-3, 4312 - 4368	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.17E-05	0.90	4.43	-	765.9
AHQ-8-4, 4494	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.35E-04	0.65	3.11	-	542.3
AHQ-8-4, 4322 - 4399	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.31E-05	0.91	4.65	-	764.9
AHQ-8-7, 4152 - 4221	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.65E-05	0.90	3.99	-	871.1
AHQ-8-10, 4056 - 4111	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.84E-06	0.86	3.15	-	868.7
AHQ-8-4, 4179	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.46E-06	0.84	3.58	-	718.7
AHQ-8-11, 4176 - 4231	K.GGVNDNFQGVLQNVR.F	1617.74799	2	9.16E-05	0.67	3.47	-	514.0
AHQ-8-6, 4386	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.99E-06	0.69	3.34	-	525.7
AHQ-8-5, 4288 - 4356	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.25E-06	0.91	4.08	-	825.6
AHQ-8-1, 4460 - 4520	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.25E-04	0.87	3.68	-	879.9
AHQ-8-2, 2283	K.GPDPSSPAFR.I	1031.10364	2	5.43E-04	0.78	2.98	-	545.9
AHQ-8-3, 2277	K.GPDPSSPAFR.I	1031.10364	2	3.22E-06	0.91	3.42	-	864.9
AHQ-8-4, 3153 - 3157	R.GTLLALER.K	873.03234	2	8.58E-04	0.89	3.38	-	908.5
AHQ-8-6, 3122	R.GTLLALER.K	873.03234	2	9.41E-04	0.76	3.05	-	849.5
AHQ-8-11, 5787 - 5851	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.83E-07	0.57	3.17	-	304.0
AHQ-8-2, 5984 - 6056	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.68E-07	0.80	3.66	-	376.0
AHQ-8-3, 5960 - 6018	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	6.94E-08	0.85	4.04	-	530.6
AHQ-8-5, 5988 - 6056	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.01E-07	0.70	3.54	-	304.9
AHQ-8-13-, 5858	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	6.44E-06	0.57	3.17	-	342.8
AHQ-8-4, 6042 - 6103	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.94E-05	0.65	3.37	-	319.5
AHQ-8-4, 6062	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.11E-04	0.50	2.69	-	284.1
AHQ-8-4, 6166	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	7.87E-09	0.75	3.62	-	383.7
AHQ-8-3, 5968 - 6025	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	2.75E-05	0.55	2.69	-	172.9
AHQ-8-7, 5836 - 5894	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.90E-10	0.66	3.84	-	462.4
AHQ-8-6, 5883 - 5960	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.36E-07	0.78	3.76	-	391.5
AHQ-8-3, 2708	K.IMADSGPIYDK.T	1210.38204	2	8.49E-05	0.84	3.43	-	521.6
AHQ-8-6, 2666	K.IMADSGPIYDK.T	1210.38204	2	8.12E-05	0.86	3.16	-	669.3
AHQ-8-2, 2740	K.IMADSGPIYDK.T	1210.38204	2	1.95E-06	0.83	3.16	-	574.3
AHQ-8-6, 2380 - 2446	K.IM*ADSGPIYDK.T	1226.38144	2	2.94E-04	0.75	2.68	-	692.3
AHQ-8-11, 2668	K.IMADSGPIYDK.T	1210.38204	2	2.11E-06	0.89	3.13	-	790.5
AHQ-8-2, 2459	K.IM*ADSGPIYDK.T	1226.38144	2	4.62E-05	0.84	3.12	-	719.5
AHQ-8-3, 6274 - 6305	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.60E-08	0.97	6.48	-	1144.6
AHQ-8-4, 6339 - 6399	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.43E-09	0.98	5.93	-	1546.6
AHQ-8-5, 6305 - 6312	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.58E-09	0.98	6.11	-	1801.5

AHQ-8-2, 6379	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	5.09E-04	0.76	3.86	-	766.7
AHQ-8-11, 6084	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	2.16E-04	0.76	2.76	-	738.0
AHQ-8-13-, 6184	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.20E-05	0.92	4.04	-	822.4
AHQ-8-2, 6368 - 6375	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.37E-08	0.96	5.62	-	920.9
AHQ-8-6, 6207	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	4.76E-04	0.84	3.55	-	945.9
AHQ-8-6, 6202 - 6252	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.44E-11	0.95	4.78	-	1132.3
AHQ-8-14-, 6198	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	5.21E-09	0.95	4.57	-	1050.2
AHQ-8-4, 2487	R.KDHSGQVFSVVSNGK.A	1589.73455	3	1.19E-06	0.91	3.77	-	1237.9
AHQ-8-2, 2576	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.83E-10	0.92	3.34	-	1270.9
AHQ-8-3, 2492	R.KDHSGQVFSVVSNGK.A	1589.73455	2	4.08E-06	0.56	2.70	-	573.9
AHQ-8-2, 2513	R.KDHSGQVFSVVSNGK.A	1589.73455	3	2.53E-05	0.95	4.16	-	1933.2
AHQ-8-6, 2423 - 2500	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.11E-08	0.86	3.54	-	777.2
AHQ-8-2, 2559	K.KIMADSGPIYDK.T	1338.55496	2	4.27E-05	0.87	3.51	-	802.7
AHQ-8-8, 2373	R.KVTEENKELANELR.R	1673.84976	2	4.15E-05	0.90	4.02	-	1011.4
AHQ-8-2, 2464 - 2528	R.KVTEENKELANELR.R	1673.84976	2	3.34E-09	0.95	4.32	-	1524.9
AHQ-8-5, 2453	R.KVTEENKELANELR.R	1673.84976	3	5.76E-07	0.74	3.73	-	780.6
AHQ-8-3, 2497	R.KVTEENKELANELR.R	1673.84976	2	5.45E-08	0.95	4.89	-	1272.4
AHQ-8-6, 2442 - 2507	R.KVTEENKELANELR.R	1673.84976	2	2.28E-04	0.92	4.28	-	1135.4
AHQ-8-4, 2446	R.KVTEENKELANELR.R	1673.84976	3	2.49E-08	0.62	3.11	-	495.6
AHQ-8-5, 2452	R.KVTEENKELANELR.R	1673.84976	2	8.09E-09	0.96	4.97	-	1570.7
AHQ-8-7, 2422	R.KVTEENKELANELR.R	1673.84976	2	4.99E-06	0.95	4.55	-	1436.4
AHQ-8-2, 2536	R.KVTEENKELANELR.R	1673.84976	3	9.46E-06	0.87	4.07	-	883.0
AHQ-8-5, 2541	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	6.36E-06	0.87	3.80	-	915.3
AHQ-8-4, 2527	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	2.37E-04	0.82	3.71	-	397.4
AHQ-8-4, 2535	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	2.40E-05	0.83	3.29	-	955.4
AHQ-8-4, 2194	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	3	5.65E-07	0.79	3.49	-	608.4
AHQ-8-6, 5068	K.MENAELDVPIQSVFTR.D	1850.08607	2	3.57E-04	0.73	3.32	-	603.7
AHQ-8-5, 5109	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	8.36E-06	0.90	3.93	-	668.2
AHQ-8-4, 5162	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	7.64E-07	0.86	3.59	-	527.1
AHQ-8-6, 5016	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	5.47E-04	0.82	3.34	-	597.0
AHQ-8-3, 5092	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.18E-04	0.37	2.65	-	289.3
AHQ-8-6, 3087	K.QVTQSYWDTNPTR.A	1596.68241	2	1.93E-06	0.85	3.00	-	743.1
AHQ-8-11, 3071	K.QVTQSYWDTNPTR.A	1596.68241	2	6.78E-08	0.57	2.68	-	436.1
AHQ-8-4, 3113	K.QVTQSYWDTNPTR.A	1596.68241	2	2.80E-06	0.84	3.56	-	567.9
AHQ-8-3, 2850 - 2928	R.RPPLCYHNGVQYR.N	1661.86889	2	1.00E-04	0.79	3.28	-	502.3
AHQ-8-3, 2784	R.RPPLCYHNGVQYR.N	1661.86889	3	8.94E-06	0.87	3.13	-	1145.1
AHQ-8-5, 2752	R.RPPLCYHNGVQYR.N	1661.86889	3	3.53E-10	0.97	4.61	-	1784.6
AHQ-8-5, 2905	R.RPPLCYHNGVQYR.N	1661.86889	2	1.87E-04	0.53	2.57	-	446.4
AHQ-8-11, 3697	K.SITLFVQEDR.A	1208.34588	2	4.74E-06	0.76	2.60	-	784.5
AHQ-8-4, 3801	K.SITLFVQEDR.A	1208.34588	2	6.48E-06	0.95	3.55	-	1539.7
AHQ-8-5, 3778	K.SITLFVQEDR.A	1208.34588	2	4.61E-07	0.93	3.60	-	1249.5
AHQ-8-6, 3726	K.SITLFVQEDR.A	1208.34588	2	3.91E-06	0.92	2.98	-	1314.0
AHQ-8-3, 3804	K.SITLFVQEDR.A	1208.34588	2	1.56E-05	0.89	3.09	-	1205.9
AHQ-8-7, 4153	R.TIVTTLQDSIR.K	1247.42355	2	3.28E-04	0.95	3.78	-	1447.5
AHQ-8-5, 3326	R.TIVTTLQDSIR.K	1247.42355	2	8.09E-04	0.94	3.17	-	1545.4
AHQ-8-3, 4318	R.TIVTTLQDSIR.K	1247.42355	2	2.04E-04	0.97	4.18	-	2031.8
AHQ-8-4, 4329 - 4333	R.TIVTTLQDSIR.K	1247.42355	2	1.79E-04	0.97	4.16	-	1847.2
AHQ-8-1, 4483	R.TIVTTLQDSIR.K	1247.42355	2	1.96E-08	0.96	3.79	-	1513.4
AHQ-8-5, 4300	R.TIVTTLQDSIR.K	1247.42355	2	1.37E-08	0.96	3.67	-	1730.2
AHQ-8-2, 3409	R.TIVTTLQDSIR.K	1247.42355	2	4.18E-05	0.95	3.54	-	1564.6
AHQ-8-2, 4389 - 4396	R.TIVTTLQDSIR.K	1247.42355	2	1.16E-06	0.97	4.20	-	1738.5
AHQ-8-6, 4234 - 4275	R.TIVTTLQDSIR.K	1247.42355	2	2.49E-07	0.97	4.08	-	1872.2
AHQ-8-6, 3295	R.TIVTTLQDSIR.K	1247.42355	2	3.79E-05	0.95	3.63	-	1526.3
AHQ-8-2, 5953	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	2.37E-05	0.75	3.79	-	536.3
AHQ-8-4, 2654	K.VTEENKELANELR.R	1545.67685	2	1.47E-09	0.88	3.89	-	830.2
AHQ-8-6, 2590 - 2667	K.VTEENKELANELR.R	1545.67685	2	5.18E-06	0.79	3.44	-	681.4
AHQ-8-5, 2674	K.VTEENKELANELR.R	1545.67685	2	5.25E-06	0.84	3.47	-	815.0
AHQ-8-2, 2736	K.VTEENKELANELR.R	1545.67685	2	1.21E-05	0.88	3.79	-	805.2
gi|4507729|ref|NP_001060.1|	tubulin, beta polypeptide [Homo sapiens]			1.13E-13	7.70	90.36	30.80	49906.7
AHQ-8-13, 4833	R.AILVDLEPGTMDSVR.S	1616.86162	2	6.09E-04	0.45	2.57	-	368.4
AHQ-8-13-, 4666 - 4723	R.AILVDLEPGTMDSVR.S	1616.86162	2	1.75E-04	0.78	3.43	-	434.0
AHQ-8-7, 2892	K.EVDEQMLNVQNK.N	1447.59668	2	3.98E-05	0.67	3.19	-	723.5
AHQ-8-7, 4385	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	8.14E-07	0.95	4.50	-	1260.7
AHQ-8-13-, 5872 - 5874	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.13E-13	0.99	7.20	-	3323.2
AHQ-8-8, 6042	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	4.12E-04	0.79	3.91	-	1105.3
AHQ-8-8, 6038	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.00E-10	0.98	5.63	-	2634.8
AHQ-8-8, 5987 - 6054	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	8.60E-05	0.96	4.85	-	1978.7
AHQ-8-7, 5824	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	3.46E-10	0.98	6.55	-	2367.6
AHQ-8-7, 5820 - 5822	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	2.31E-04	0.88	4.23	-	1154.6
AHQ-8-14-, 5882	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.33E-05	0.96	4.32	-	1573.6
AHQ-8-7, 4293	R.ISEQFTAMFR.R	1230.41818	2	9.50E-09	0.92	3.55	-	1003.4
AHQ-8-13-, 4426 - 4427	R.ISEQFTAMFR.R	1230.41818	2	1.95E-08	0.95	4.13	-	1338.0
AHQ-8-13, 3827 - 3889	R.ISEQFTAM*FR.R	1246.41758	2	1.05E-06	0.86	3.10	-	792.6
AHQ-8-7, 3516 - 3578	R.ISEQFTAM*FR.R	1246.41758	2	6.12E-04	0.73	2.69	-	673.3
AHQ-8-7, 6224	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	1.68E-07	0.89	4.39	-	779.7
AHQ-8-7, 5614	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	1.98E-06	0.83	4.15	-	914.9
AHQ-8-7, 5858	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	8.73E-05	0.37	2.71	-	469.5
AHQ-8-14-, 5678	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	6.33E-06	0.82	3.81	-	952.2
AHQ-8-7, 5572 - 5634	K.NSSYFVEWIPNNVK.T	1697.87148	2	3.15E-04	0.86	3.21	-	996.6
AHQ-8-13-, 5198 - 5263	K.NSSYFVEWIPNNVK.T	1697.87148	2	2.46E-06	0.79	3.67	-	501.1
AHQ-8-13-, 5323 - 5364	K.NSSYFVEWIPNNVK.T	1697.87148	2	1.96E-06	0.78	3.30	-	698.0
AHQ-8-7, 5106 - 5164	K.NSSYFVEWIPNNVK.T	1697.87148	2	8.70E-06	0.94	4.58	-	1008.8
AHQ-8-7, 5229 - 5309	K.NSSYFVEWIPNNVK.T	1697.87148	2	8.12E-05	0.37	2.70	-	354.5
AHQ-8-8, 6013	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	9.94E-08	0.95	5.59	-	1149.6
AHQ-8-7, 5742 - 5789	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.12E-06	0.95	5.08	-	1183.9
AHQ-8-13-, 5824 - 5884	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	9.95E-12	0.98	6.97	-	1987.0
gi|4501881|ref|NP_001091.1|	alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA			1.15E-13	12.63	150.25	43.50	42050.8
AHQ-8-8, 1989 - 2045	K.AGFAGDDAPR.A	977.01283	2	1.60E-05	0.89	3.19	-	1043.9
AHQ-8-5, 3656	R.AVFPSIVGR.P	946.12815	2	3.99E-04	0.81	2.51	-	721.7
AHQ-8-8, 4871	K.DLYANNVMSGGTTMYPGIADR.M	2247.49444	2	5.96E-04	0.35	2.61	-	274.0
AHQ-8-8, 1561 - 1619	K.DSYVGDEAQSK.R	1199.20634	2	1.23E-04	0.74	3.08	-	717.4
AHQ-8-8, 1677 - 1733	K.DSYVGDEAQSK.R	1199.20634	2	3.93E-06	0.86	3.60	-	871.2
AHQ-8-14-, 2977 - 3037	K.EITALAPSTMK.I	1162.38206	2	6.16E-04	0.70	2.60	-	520.1
AHQ-8-8, 2814 - 2881	K.EITALAPSTMK.I	1162.38206	1	5.22E-05	0.46	2.56	-	281.3
AHQ-8-8, 2377 - 2437	K.EITALAPSTM*K.I	1178.38146	2	6.46E-04	0.88	3.29	-	794.0
AHQ-8-14-, 2505 - 2506	K.EITALAPSTM*K.I	1178.38146	2	5.60E-04	0.85	2.91	-	763.0
AHQ-8-13-, 3090 - 3091	K.EITALAPSTMK.I	1162.38206	1	4.72E-05	0.73	3.41	-	270.7
AHQ-8-8, 2817 - 2886	K.EITALAPSTMK.I	1162.38206	2	1.67E-04	0.84	2.71	-	827.8
AHQ-8-11, 2927 - 2992	K.EITALAPSTMK.I	1162.38206	2	8.27E-04	0.73	2.79	-	488.2
AHQ-8-14-, 3041	K.EITALAPSTMK.I	1162.38206	1	7.72E-04	0.20	1.97	-	263.3
AHQ-8-8, 1882 - 1943	R.HQGVMVGMGQK.D	1172.40691	2	6.33E-06	0.91	3.49	-	716.7
AHQ-8-8, 2003 - 2043	R.HQGVMVGMGQK.D	1172.40691	2	4.05E-04	0.88	3.58	-	619.9
AHQ-8-8, 3370 - 3431	K.IWHHTFYNELR.V	1516.68695	3	1.31E-04	0.94	4.03	-	1617.5
AHQ-8-8, 3009 - 3066	K.IWHHTFYNELR.V	1516.68695	3	5.00E-06	0.93	4.30	-	1860.8
AHQ-8-8, 3422 - 3486	K.IWHHTFYNELR.V	1516.68695	2	3.02E-06	0.87	3.11	-	845.5
AHQ-8-5, 3200	K.IWHHTFYNELR.V	1516.68695	3	1.72E-04	0.85	4.20	-	1045.1
AHQ-8-8, 3293 - 3369	K.IWHHTFYNELR.V	1516.68695	2	2.87E-04	0.88	3.47	-	925.0

AHQ-8-8, 3173 - 3233	K.IWHHTFYNELR.V	1516.68695	2	4.55E-07	0.94	3.84	-	1086.2
AHQ-8-8, 2898 - 2957	K.IWHHTFYNELR.V	1516.68695	3	4.38E-06	0.96	4.68	-	1529.0
AHQ-8-8, 2953 - 2981	K.IWHHTFYNELR.V	1516.68695	2	4.55E-09	0.84	3.69	-	839.3
AHQ-8-8, 3131 - 3194	K.IWHHTFYNELR.V	1516.68695	3	2.62E-04	0.91	4.13	-	1443.5
AHQ-8-8, 6637	K.LCYVALDFENEM*ATAASSSSLEK.S	2554.78938	2	1.88E-06	0.95	4.84	-	1366.7
AHQ-8-8, 5115	R.LDLAGRDLTDYLMK.I	1624.88375	2	2.43E-04	0.94	4.35	-	1197.6
AHQ-8-4, 4785	K.SYELPDGQVITIGNER.F	1791.93998	2	2.05E-05	0.92	3.87	-	864.1
AHQ-8-5, 4761 - 4765	K.SYELPDGQVITIGNER.F	1791.93998	2	3.06E-06	0.92	3.79	-	916.0
AHQ-8-3, 4876	K.SYELPDGQVITIGNER.F	1791.93998	2	3.09E-05	0.78	3.15	-	502.4
AHQ-8-2, 4835	K.SYELPDGQVITIGNER.F	1791.93998	2	1.68E-09	0.92	3.55	-	851.5
AHQ-8-2, 4780 - 4843	K.SYELPDGQVITIGNER.F	1791.93998	2	8.53E-05	0.90	3.88	-	775.8
AHQ-8-5, 4894 - 4949	K.SYELPDGQVITIGNER.F	1791.93998	2	7.00E-06	0.94	3.73	-	1351.2
AHQ-8-8, 4227 - 4306	K.SYELPDGQVITIGNER.F	1791.93998	2	2.62E-11	0.93	4.31	-	981.7
AHQ-8-13-, 4818 - 4876	K.SYELPDGQVITIGNER.F	1791.93998	2	8.69E-10	0.95	4.11	-	1250.6
AHQ-8-8, 4363 - 4371	K.SYELPDGQVITIGNER.F	1791.93998	3	6.74E-06	0.96	5.01	-	1448.2
AHQ-8-8, 4365 - 4425	K.SYELPDGQVITIGNER.F	1791.93998	2	1.46E-12	0.97	5.02	-	1332.1
AHQ-8-8, 4482	K.SYELPDGQVITIGNER.F	1791.93998	2	6.10E-09	0.95	4.42	-	1021.5
AHQ-8-13-, 4695 - 4718	K.SYELPDGQVITIGNER.F	1791.93998	2	6.81E-11	0.95	4.53	-	884.7
AHQ-8-8, 4594 - 4665	K.SYELPDGQVITIGNER.F	1791.93998	2	2.35E-11	0.96	4.81	-	1211.7
AHQ-8-8, 4662	K.SYELPDGQVITIGNER.F	1791.93998	3	4.29E-05	0.94	4.23	-	1306.9
AHQ-8-8, 4721 - 4790	K.SYELPDGQVITIGNER.F	1791.93998	2	5.71E-11	0.95	4.42	-	1105.4
AHQ-8-8, 4725	K.SYELPDGQVITIGNER.F	1791.93998	2	3.25E-08	0.96	4.41	-	1130.5
AHQ-8-1, 5001	K.SYELPDGQVITIGNER.F	1791.93998	2	6.85E-07	0.80	2.79	-	856.4
AHQ-8-8, 4845 - 4905	K.SYELPDGQVITIGNER.F	1791.93998	2	1.15E-13	0.96	4.48	-	1202.0
AHQ-8-14, 5541 - 5613	K.SYELPDGQVITIGNER.F	1791.93998	2	9.07E-05	0.88	3.80	-	630.9
AHQ-8-1, 4868	K.SYELPDGQVITIGNER.F	1791.93998	2	7.30E-06	0.90	3.48	-	773.8
AHQ-8-8, 4930 - 4970	K.SYELPDGQVITIGNER.F	1791.93998	2	7.22E-10	0.94	4.19	-	1022.7
AHQ-8-8, 4966 - 4989	K.SYELPDGQVITIGNER.F	1791.93998	2	7.98E-12	0.93	4.13	-	821.9
AHQ-8-4, 4442	K.SYELPDGQVITIGNER.F	1791.93998	2	1.49E-10	0.92	3.49	-	1069.0
AHQ-8-8, 4219	K.SYELPDGQVITIGNER.F	1791.93998	2	2.34E-09	0.88	3.46	-	1065.7
AHQ-8-10, 4194	K.SYELPDGQVITIGNER.F	1791.93998	3	7.17E-05	0.81	3.22	-	935.4
AHQ-8-10, 4248	K.SYELPDGQVITIGNER.F	1791.93998	2	1.03E-04	0.87	3.01	-	697.8
AHQ-8-10, 4456 - 4530	K.SYELPDGQVITIGNER.F	1791.93998	2	6.04E-11	0.97	5.00	-	1219.3
AHQ-8-10, 4514 - 4528	K.SYELPDGQVITIGNER.F	1791.93998	3	1.44E-08	0.96	4.89	-	1554.5
AHQ-8-10, 4611 - 4666	K.SYELPDGQVITIGNER.F	1791.93998	2	5.16E-11	0.93	3.95	-	1001.8
AHQ-8-7, 4601	K.SYELPDGQVITIGNER.F	1791.93998	2	6.52E-05	0.47	2.54	-	511.5
AHQ-8-11, 4571	K.SYELPDGQVITIGNER.F	1791.93998	2	1.28E-09	0.90	3.94	-	566.9
AHQ-8-11, 4683 - 4740	K.SYELPDGQVITIGNER.F	1791.93998	2	3.65E-10	0.94	4.23	-	1042.3
AHQ-8-13, 4983	K.SYELPDGQVITIGNER.F	1791.93998	2	6.76E-06	0.94	4.18	-	951.5
AHQ-8-12, 4280	K.SYELPDGQVITIGNER.F	1791.93998	2	3.77E-06	0.93	3.92	-	1003.5
AHQ-8-12, 4598 - 4602	K.SYELPDGQVITIGNER.F	1791.93998	2	1.36E-07	0.95	4.16	-	1066.8
AHQ-8-12, 4716 - 4780	K.SYELPDGQVITIGNER.F	1791.93998	2	5.17E-04	0.82	3.27	-	525.1
AHQ-8-13, 4511 - 4576	K.SYELPDGQVITIGNER.F	1791.93998	2	4.19E-09	0.92	3.46	-	935.8
AHQ-8-13, 4851 - 4853	K.SYELPDGQVITIGNER.F	1791.93998	2	1.20E-07	0.90	3.96	-	631.7
AHQ-8-1, 4497 - 4545	K.SYELPDGQVITIGNER.F	1791.93998	2	5.70E-06	0.62	2.52	-	450.1
AHQ-8-8, 4833 - 4914	K.SYELPDGQVITIGNERFR.C	2095.30102	2	4.14E-05	0.90	3.83	-	878.8
AHQ-8-8, 3857	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	5.39E-06	0.94	4.44	-	763.2
AHQ-8-8, 4337 - 4409	K.YPIEHGIITNWDDMEK.I	1962.17174	2	4.98E-04	0.86	3.64	-	805.4
AHQ-8-8, 3897 - 3953	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	1.76E-04	0.84	3.98	-	441.3
AHQ-8-8, 4555	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.68E-05	0.87	3.85	-	564.1
AHQ-8-8, 4865 - 4931	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.04E-05	0.85	3.76	-	595.0
AHQ-8-12, 4274	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.50E-04	0.89	3.83	-	830.7
gi|13562114|ref|NP_110400.1|	beta tubulin 1, class VI [Homo sapiens]			4.45E-13	11.01	130.32	44.30	50326.6
AHQ-8-8, 5962	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.85E-07	0.96	4.66	-	1477.2
AHQ-8-7, 5669 - 5748	R.ALSVAELTQQMFDAR.N	1680.90740	2	1.83E-04	0.93	3.64	-	1593.2
AHQ-8-14-, 4643 - 4702	R.AVLVDLEPGTMDSIR.S	1616.86162	2	2.34E-07	0.92	4.64	-	540.2
AHQ-8-7, 3630 - 3688	R.EIVHIQIGQCGNQIGAK.F	1867.11965	3	5.07E-04	0.68	3.00	-	622.3
AHQ-8-11, 3223	K.EVDQQLLSVQTR.N	1416.56231	2	8.51E-04	0.80	3.05	-	714.0
AHQ-8-8, 3211 - 3238	K.EVDQQLLSVQTR.N	1416.56231	2	7.77E-04	0.57	2.62	-	537.1
AHQ-8-13, 6249	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	7.21E-04	0.79	3.29	-	1315.6
AHQ-8-13, 6248	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	7.84E-06	0.98	5.86	-	2326.9
AHQ-8-13-, 6206	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.36E-07	0.98	5.75	-	2193.0
AHQ-8-13-, 6202 - 6204	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.14E-04	0.86	4.60	-	922.3
AHQ-8-7, 6180	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	1.98E-06	0.94	4.29	-	2230.7
AHQ-8-11, 6113	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	5.26E-04	0.66	3.18	-	963.1
AHQ-8-8, 6395	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.95E-05	0.98	5.84	-	2227.9
AHQ-8-8, 6151	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.50E-05	0.91	3.68	-	1080.0
AHQ-8-7, 5928 - 5968	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	3	5.64E-04	0.67	3.12	-	945.2
AHQ-8-14-, 5989 - 6034	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.11E-04	0.87	3.91	-	743.8
AHQ-8-14, 4090 - 4157	R.ISVYYNEAYGR.K	1335.44622	2	2.16E-06	0.63	2.75	-	477.9
AHQ-8-13-, 3276 - 3286	R.ISVYYNEAYGR.K	1335.44622	2	1.17E-07	0.94	3.70	-	1081.3
AHQ-8-8, 3169	R.ISVYYNEAYGR.K	1335.44622	2	3.04E-04	0.87	3.30	-	672.8
AHQ-8-7, 3148 - 3184	R.ISVYYNEAYGR.K	1335.44622	2	1.11E-05	0.90	3.05	-	855.8
AHQ-8-7, 4881	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	4.80E-07	0.78	3.31	-	669.8
AHQ-8-13-, 4932 - 4998	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	3.96E-07	0.78	3.26	-	732.6
AHQ-8-7, 4784	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	8.37E-06	0.78	3.81	-	661.7
AHQ-8-8, 5619	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	9.87E-06	0.96	5.13	-	1484.3
AHQ-8-7, 5452 - 5482	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	5.79E-09	0.98	6.08	-	2271.8
AHQ-8-7, 5466	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	6.33E-05	0.95	4.70	-	801.8
AHQ-8-7, 4866 - 4890	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	4.45E-13	0.98	6.36	-	2720.2
AHQ-8-7, 6062 - 6117	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.80E-08	0.79	3.40	-	559.5
AHQ-8-8, 6317	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	4.54E-07	0.85	3.70	-	1006.3
AHQ-8-7, 4956 - 5028	R.NSSCFVEWIPNNVK.V	1695.87718	2	1.59E-04	0.74	3.69	-	361.5
AHQ-8-7, 4940	R.YLTVACIFR.G	1144.36822	2	2.90E-04	0.79	2.73	-	654.6
gi|4501885|ref|NP_001092.1|	beta actin; beta cytoskeletal actin [Homo sapiens]			4.57E-13	13.36	150.33	36.00	41736.5
AHQ-8-8, 6301 - 6358	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.37E-06	0.72	4.34	-	471.6
AHQ-8-13-, 5983 - 6052	R.CPEALFQPSFLGM*ESCGIHETTFNSIMK.C	3251.67648	3	1.96E-05	0.84	4.64	-	647.6
AHQ-8-8, 5841 - 5913	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.74E-04	0.91	4.45	-	681.7
AHQ-8-8, 6165 - 6246	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	9.27E-05	0.75	4.32	-	383.4
AHQ-8-8, 6413	R.CPEALFQPSFLGMESCGIHETTFNSIMK.C	3235.67708	3	5.43E-07	0.88	4.17	-	539.0
AHQ-8-13, 5752 - 5809	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	3.14E-07	0.88	4.38	-	544.5
AHQ-8-8, 6409 - 6469	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.64E-05	0.90	4.11	-	686.7
AHQ-8-8, 6481 - 6542	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	5.83E-07	0.94	5.12	-	1423.7
AHQ-8-8, 6506 - 6573	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	3.52E-06	0.90	4.14	-	1041.0
AHQ-8-8, 6363 - 6421	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	3.38E-06	0.93	5.19	-	1154.6
AHQ-8-8, 5238 - 5305	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	2.42E-06	0.91	4.18	-	1203.0
AHQ-8-8, 6602 - 6663	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.40E-08	0.93	5.04	-	946.6
AHQ-8-8, 6633	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.79E-05	0.91	4.10	-	1308.4
AHQ-8-8, 6261 - 6329	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	2.61E-05	0.74	3.48	-	718.1
AHQ-8-8, 5763 - 5877	R.FRCPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3571.03693	3	9.15E-04	0.79	3.44	-	659.8
AHQ-8-8, 2462 - 2523	R.GYSFTTTAER.E	1133.19273	2	4.19E-04	0.84	2.95	-	1020.0
AHQ-8-4, 2593	R.GYSFTTTAER.E	1133.19273	2	2.03E-04	0.87	2.74	-	955.7
AHQ-8-9, 6555	R.GYSFTTTAER.E	1133.19273	2	2.90E-04	0.91	2.74	-	1290.8
AHQ-8-10, 2486 - 2543	R.GYSFTTTAER.E	1133.19273	2	6.59E-06	0.92	3.33	-	1116.9
AHQ-8-3, 2641	R.GYSFTTTAER.E	1133.19273	2	8.74E-04	0.90	3.08	-	995.1
AHQ-8-13-, 2676 - 2738	R.GYSFTTTAER.E	1133.19273	2	1.77E-05	0.90	3.33	-	909.1
AHQ-8-8, 2585 - 2654	R.GYSFTTTAER.E	1133.19273	2	1.47E-04	0.91	3.30	-	1070.2

AHQ-8-11, 2579	R.GYSFTTTAER.E	1133.19273	2	6.29E-05	0.88	2.78	-	1118.7
AHQ-8-8, 4753 - 4755	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	1.65E-07	0.95	5.27	-	1515.3
AHQ-8-8, 4691 - 4758	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	8.88E-10	0.96	4.72	-	1437.1
AHQ-8-8, 4325 - 4386	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	2	8.50E-05	0.95	4.31	-	1210.9
AHQ-8-8, 4471 - 4534	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	2.12E-05	0.95	5.22	-	1368.2
AHQ-8-8, 4602	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	3.17E-08	0.94	4.43	-	1001.4
AHQ-8-8, 4473 - 4533	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	7.12E-05	0.95	4.22	-	1202.2
AHQ-8-13-, 4147 - 4202	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	1.11E-06	0.95	4.69	-	1430.5
AHQ-8-8, 6393 - 6457	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	4.50E-07	0.87	3.99	-	1022.6
AHQ-8-8, 5698 - 5777	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	3.64E-06	0.95	4.72	-	941.3
AHQ-8-8, 6557 - 6614	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	6.23E-07	0.96	6.61	-	1515.6
AHQ-8-8, 6513 - 6541	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	9.96E-09	0.97	5.11	-	1690.3
AHQ-8-8, 5378 - 5446	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	8.86E-04	0.80	3.10	-	1079.9
AHQ-8-8, 5786 - 5850	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	1.91E-05	0.89	3.73	-	1065.4
AHQ-8-8, 6617 - 6673	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	4.57E-13	0.98	6.28	-	2082.2
AHQ-8-8, 6077 - 6133	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	6.20E-05	0.88	3.68	-	1034.2
AHQ-8-8, 6081 - 6145	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	1.43E-04	0.86	3.32	-	1706.3
AHQ-8-8, 6626 - 6658	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	3.45E-09	0.98	5.51	-	2389.1
AHQ-8-8, 6315 - 6369	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	7.16E-06	0.88	3.49	-	991.5
AHQ-8-8, 6202 - 6257	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	2.27E-04	0.95	4.56	-	1810.1
AHQ-8-8, 6670	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	1.78E-04	0.84	3.37	-	1276.4
AHQ-8-8, 6525 - 6558	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	1.65E-04	0.95	4.28	-	1980.2
AHQ-8-8, 6194 - 6258	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	9.53E-08	0.92	4.27	-	1062.0
AHQ-8-8, 5771	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.34E-06	0.96	5.45	-	1345.7
AHQ-8-8, 5670 - 5726	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.68E-08	0.96	5.86	-	1075.5
AHQ-8-8, 5547 - 5613	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.42E-05	0.95	5.60	-	966.9
AHQ-8-8, 5470 - 5529	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.34E-04	0.77	4.06	-	634.5
AHQ-8-8, 5450 - 5513	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.77E-08	0.97	5.92	-	1639.6
AHQ-8-8, 5410 - 5439	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.01E-04	0.91	4.71	-	776.6
AHQ-8-8, 5291 - 5349	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.83E-07	0.97	5.73	-	2281.1
AHQ-8-8, 5122 - 5194	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.08E-04	0.80	4.20	-	349.5
AHQ-8-12, 5330 - 5387	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.10E-04	0.89	4.36	-	1142.3
AHQ-8-7, 5357 - 5413	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.90E-06	0.95	4.97	-	1376.9
AHQ-8-5, 5256 - 5318	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.74E-05	0.64	3.12	-	643.2
AHQ-8-4, 5590	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.29E-07	0.91	4.56	-	1073.0
AHQ-8-4, 5349 - 5410	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.87E-07	0.96	5.80	-	1304.2
AHQ-8-13-, 5183 - 5248	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.80E-06	0.94	5.35	-	977.2
AHQ-8-3, 5280	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.45E-07	0.94	4.73	-	1246.3
AHQ-8-12, 5103 - 5158	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.49E-07	0.94	5.31	-	1125.5
AHQ-8-13-, 5398	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.67E-06	0.91	4.31	-	1140.5
AHQ-8-11, 5096 - 5152	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.79E-05	0.94	5.29	-	1036.4
AHQ-8-10, 5010 - 5066	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.37E-04	0.96	5.61	-	1554.3
AHQ-8-14-, 5183	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.31E-04	0.96	4.94	-	1651.4
AHQ-8-11, 3811	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.74E-04	0.87	3.67	-	671.2
AHQ-8-10, 3734	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.47E-04	0.83	3.42	-	475.4
AHQ-8-12, 3756 - 3822	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	3.66E-06	0.82	4.22	-	746.4
AHQ-8-12, 3810 - 3880	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.55E-05	0.91	4.31	-	817.3
AHQ-8-9, 6671 - 6672	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.45E-05	0.95	4.83	-	1071.7
AHQ-8-8, 3797 - 3877	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.18E-04	0.89	5.05	-	517.7
AHQ-8-8, 3658 - 3754	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.20E-06	0.88	3.80	-	671.2
AHQ-8-7, 3786	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.81E-05	0.85	4.13	-	556.2
AHQ-8-13-, 3915	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.08E-07	0.87	4.13	-	582.9
AHQ-8-6, 3839 - 3850	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.86E-04	0.90	4.36	-	718.6
AHQ-8-4, 3882 - 3941	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.82E-06	0.92	4.81	-	672.6
AHQ-8-3, 3937 - 3954	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.52E-04	0.92	4.50	-	846.7
AHQ-8-2, 4013 - 4028	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.75E-04	0.86	4.24	-	439.2
AHQ-8-14-, 3885	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.91E-08	0.91	4.19	-	1032.3
AHQ-8-1, 4100	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.53E-04	0.84	3.95	-	663.7
gi|4501891|ref|NP_001093.1|	actinin, alpha 1 [Homo sapiens]			4.86E-13	34.32	390.37	48.10	103056.9
AHQ-8-5, 6492 - 6493	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	6.30E-08	0.97	6.11	-	1580.1
AHQ-8-5, 5176	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	6.55E-07	0.82	4.41	-	745.7
AHQ-8-4, 5214	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	4.10E-06	0.85	4.41	-	887.8
AHQ-8-4, 6070	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	1.56E-08	0.95	4.59	-	1119.7
AHQ-8-5, 6026	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	1.28E-06	0.65	3.14	-	606.9
AHQ-8-4, 6067	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	6.61E-05	0.76	3.46	-	830.0
AHQ-8-4, 5407 - 5467	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	3	2.78E-06	0.83	3.44	-	788.1
AHQ-8-6, 5940 - 6010	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	6.74E-05	0.66	3.34	-	384.6
AHQ-8-6, 5943 - 5944	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	3.52E-06	0.70	3.31	-	630.7
AHQ-8-4, 3438	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	7.51E-04	0.96	4.20	-	2642.2
AHQ-8-4, 2329	K.ASIHEAWTDGK.E	1215.29697	2	1.66E-04	0.80	2.89	-	787.8
AHQ-8-4, 2339 - 2346	K.ASIHEAWTDGK.E	1215.29697	1	1.64E-06	0.70	2.67	-	763.5
AHQ-8-3, 5313	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.04E-04	0.74	2.91	-	528.9
AHQ-8-4, 5758	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	5.03E-04	0.60	2.92	-	389.7
AHQ-8-5, 5322	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.78E-07	0.95	4.51	-	1153.0
AHQ-8-4, 5323 - 5382	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	5.59E-08	0.95	4.71	-	1055.3
AHQ-8-6, 5234	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	5.22E-06	0.89	3.49	-	967.9
AHQ-8-7, 5169	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.10E-04	0.62	3.22	-	422.4
AHQ-8-5, 2612	R.DHSGTLGPEEFK.A	1317.38606	2	2.26E-09	0.78	3.01	-	633.4
AHQ-8-4, 2590 - 2602	R.DHSGTLGPEEFK.A	1317.38606	2	5.48E-06	0.89	3.43	-	885.8
AHQ-8-7, 3597	K.DYETATLSEIK.A	1270.36761	2	5.15E-05	0.88	2.82	-	1304.1
AHQ-8-4, 3702	K.DYETATLSEIK.A	1270.36761	2	6.00E-07	0.92	3.60	-	1102.8
AHQ-8-4, 3481 - 3541	R.ELPPDQAEYCIAR.M	1563.71392	2	3.11E-09	0.87	2.98	-	428.8
AHQ-8-4, 3355 - 3418	R.ELPPDQAEYCIAR.M	1563.71392	2	1.56E-05	0.59	2.91	-	137.3
AHQ-8-6, 3160	R.ETADTDTADQVM*ASFK.I	1746.83148	2	2.59E-06	0.93	4.42	-	782.0
AHQ-8-13, 3376	R.ETADTDTADQVM*ASFK.I	1746.83148	2	6.59E-04	0.81	3.19	-	745.2
AHQ-8-13-, 4282	R.ETADTDTADQVMASFK.I	1730.83208	2	3.57E-04	0.74	3.09	-	557.9
AHQ-8-4, 4265 - 4313	R.ETADTDTADQVMASFK.I	1730.83208	2	6.23E-05	0.95	4.13	-	1323.8
AHQ-8-4, 3181	R.ETADTDTADQVM*ASFK.I	1746.83148	2	7.13E-06	0.92	4.31	-	811.6
AHQ-8-5, 3181	R.ETADTDTADQVM*ASFK.I	1746.83148	2	2.94E-07	0.95	4.66	-	1045.6
AHQ-8-6, 2330	K.GISQEQM*NEFR.A	1355.45931	2	6.87E-05	0.76	3.31	-	526.4
AHQ-8-4, 2713	K.GISQEQMNEFR.A	1339.45991	2	1.73E-08	0.92	3.53	-	1058.0
AHQ-8-6, 3012	K.GISQEQMNEFR.A	1339.45991	2	4.65E-07	0.89	3.14	-	951.4
AHQ-8-4, 2319	K.GISQEQM*NEFR.A	1355.45931	2	5.48E-06	0.83	2.89	-	791.9
AHQ-8-5, 3016 - 3017	K.GISQEQMNEFR.A	1339.45991	2	6.02E-05	0.84	3.12	-	850.2
AHQ-8-7, 2902 - 2962	K.GISQEQMNEFR.A	1339.45991	2	3.27E-08	0.91	3.29	-	1208.0
AHQ-8-5, 2332	K.GISQEQM*NEFR.A	1355.45931	2	7.65E-06	0.78	3.02	-	561.2
AHQ-8-4, 2403	K.GISQEQM*NEFR.A	1355.45931	2	6.78E-04	0.86	2.86	-	1002.4
AHQ-8-11, 2340	K.GISQEQM*NEFR.A	1355.45931	2	9.79E-07	0.77	2.52	-	810.8
AHQ-8-4, 3171	K.GISQEQMNEFR.A	1339.45991	2	3.30E-06	0.82	3.04	-	837.1
AHQ-8-4, 3017	K.GISQEQMNEFR.A	1339.45991	2	2.65E-07	0.91	3.70	-	1033.0
AHQ-8-4, 2257	R.HRPELIDYGK.L	1228.38202	3	5.45E-05	0.94	3.80	-	1341.5
AHQ-8-5, 2290	R.HRPELIDYGK.L	1228.38202	2	7.77E-04	0.82	2.61	-	702.4
AHQ-8-7, 2245	R.HRPELIDYGK.L	1228.38202	2	3.01E-05	0.92	3.17	-	866.3
AHQ-8-4, 2253	R.HRPELIDYGK.L	1228.38202	2	4.94E-04	0.93	3.68	-	747.7
AHQ-8-4, 4435 - 4515	K.ICDQWDNLGALTQK.R	1663.83349	2	1.15E-04	0.95	4.43	-	1336.7
AHQ-8-4, 4609	K.ICDQWDNLGALTQK.R	1663.83349	2	2.14E-05	0.88	3.41	-	1123.0
AHQ-8-6, 4632	K.ICDQWDNLGALTQK.R	1663.83349	2	4.30E-09	0.95	3.86	-	1540.3

AHQ-8-4, 4713 - 4753	K.ICDQWDNLGALTQK.R	1663.83349	2	6.36E-07	0.98	4.75	-	2471.1
AHQ-8-5, 4701 - 4717	K.ICDQWDNLGALTQK.R	1663.83349	2	1.31E-05	0.90	3.42	-	1172.2
AHQ-8-7, 4565	K.ICDQWDNLGALTQK.R	1663.83349	2	1.79E-05	0.95	4.08	-	1590.5
AHQ-8-4, 5545 - 5605	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	3.06E-08	0.96	4.84	-	1395.2
AHQ-8-4, 5458	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	8.73E-10	0.96	5.70	-	1609.6
AHQ-8-7, 5373 - 5389	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	6.47E-05	0.91	4.28	-	1076.6
AHQ-8-5, 5556 - 5560	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	8.93E-06	0.95	5.44	-	1394.7
AHQ-8-6, 5458	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	4.11E-06	0.75	2.66	-	809.1
AHQ-8-4, 4101	K.ILAGDKNYITMDELR.R	1753.01353	2	1.04E-08	0.96	4.20	-	1253.3
AHQ-8-4, 4227	K.ILAGDKNYITMDELR.R	1753.01353	2	2.30E-06	0.91	4.34	-	636.4
AHQ-8-4, 3527	K.ILAGDKNYITM*DELR.R	1769.01293	2	5.22E-04	0.95	4.82	-	787.3
AHQ-8-4, 3554	K.ILAGDKNYITM*DELR.R	1769.01293	3	1.37E-06	0.75	3.48	-	575.6
AHQ-8-4, 4495	K.IVQTYHVNMAGTNPYTTITPQEINGK.W	2892.23635	3	1.08E-05	0.90	4.38	-	850.0
AHQ-8-6, 4714	R.KAGTQIENIEEDFRDGLK.L	2064.24210	3	1.34E-05	0.91	4.46	-	1018.9
AHQ-8-4, 4770	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.34E-05	0.97	5.20	-	1486.4
AHQ-8-5, 4764	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	4.32E-04	0.94	4.68	-	901.0
AHQ-8-6, 4686	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	8.48E-06	0.94	4.68	-	1051.1
AHQ-8-4, 4357	R.KQFGAQANVIGPWIQTK.M	1887.17410	3	2.33E-04	0.95	4.60	-	1670.4
AHQ-8-5, 4324 - 4340	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	3.82E-04	0.94	4.29	-	1059.8
AHQ-8-4, 3790 - 3847	R.LAILGIHNEVSK.I	1294.52505	2	7.26E-06	0.94	3.25	-	1469.7
AHQ-8-5, 3461	R.LAILGIHNEVSK.I	1294.52505	2	2.31E-08	0.95	3.47	-	1290.7
AHQ-8-4, 3690	R.LAILGIHNEVSK.I	1294.52505	2	3.28E-10	0.93	3.45	-	1076.0
AHQ-8-4, 5741	K.LASDLLEWIR.R	1216.41115	1	8.76E-06	0.45	2.66	-	302.9
AHQ-8-6, 5595	K.LASDLLEWIR.R	1216.41115	2	9.64E-08	0.96	3.91	-	1629.9
AHQ-8-7, 5536	K.LASDLLEWIR.R	1216.41115	2	7.46E-07	0.95	3.77	-	1545.6
AHQ-8-4, 5729 - 5730	K.LASDLLEWIR.R	1216.41115	2	7.56E-07	0.97	4.11	-	1914.6
AHQ-8-5, 5696	K.LASDLLEWIR.R	1216.41115	2	4.54E-07	0.96	3.97	-	1695.3
AHQ-8-4, 6085 - 6158	K.LLETIDQLYLEYAK.R	1712.96427	2	8.97E-06	0.96	4.77	-	1103.2
AHQ-8-7, 5821 - 5888	K.LLETIDQLYLEYAK.R	1712.96427	2	3.55E-08	0.89	3.36	-	984.0
AHQ-8-4, 6094	K.LLETIDQLYLEYAK.R	1712.96427	3	8.30E-07	0.97	5.45	-	1434.7
AHQ-8-4, 5159	K.LLETIDQLYLEYAK.R	1712.96427	2	4.55E-06	0.89	3.76	-	564.3
AHQ-8-6, 5884 - 5939	K.LLETIDQLYLEYAK.R	1712.96427	2	2.49E-05	0.95	4.10	-	1099.1
AHQ-8-5, 6041	K.LLETIDQLYLEYAK.R	1712.96427	2	5.15E-10	0.97	4.79	-	1354.3
AHQ-8-3, 6016	K.LLETIDQLYLEYAK.R	1712.96427	2	5.64E-06	0.92	3.58	-	1096.7
AHQ-8-4, 2753	R.LSNRPAFMPSEGR.M	1462.65941	2	1.69E-04	0.80	3.64	-	520.5
AHQ-8-4, 2697 - 2770	R.LSNRPAFMPSEGR.M	1462.65941	2	5.20E-05	0.79	3.17	-	711.6
AHQ-8-4, 2206 - 2278	R.LSNRPAFM*PSEGR.M	1478.65881	3	4.94E-04	0.69	3.35	-	669.3
AHQ-8-5, 3545	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	6.86E-05	0.80	3.40	-	477.4
AHQ-8-4, 3923	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.14E-05	0.66	3.12	-	692.5
AHQ-8-4, 3929	K.MLDAEDIVGTARPDEK.A	1760.94769	3	2.98E-06	0.70	3.66	-	499.2
AHQ-8-6, 3514 - 3590	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	4.03E-05	0.69	3.36	-	400.3
AHQ-8-4, 3566	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	7.72E-05	0.91	3.93	-	814.6
AHQ-8-5, 3922	K.MLDAEDIVGTARPDEK.A	1760.94769	2	8.66E-08	0.91	4.15	-	976.5
AHQ-8-4, 5147	R.M*VSDINNAWGCLEQVEK.G	2011.22273	3	1.01E-04	0.93	4.82	-	1140.0
AHQ-8-4, 5305	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.40E-05	0.86	3.29	-	821.3
AHQ-8-5, 5098	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.16E-06	0.94	4.51	-	917.6
AHQ-8-6, 4796	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	2.18E-05	0.61	3.15	-	573.4
AHQ-8-4, 5135 - 5138	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	2.58E-10	0.97	5.21	-	1371.6
AHQ-8-6, 5018	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.41E-04	0.95	4.44	-	1071.1
AHQ-8-4, 4666 - 4675	K.NVNIQNFHISWK.D	1500.68583	2	2.51E-07	0.96	4.50	-	1253.7
AHQ-8-6, 4575	K.NVNIQNFHISWK.D	1500.68583	2	4.89E-06	0.97	4.55	-	1361.2
AHQ-8-6, 4828	K.QFGAQANVIGPWIQTK.M	1759.00118	2	1.41E-04	0.74	3.07	-	697.8
AHQ-8-4, 4925	K.QFGAQANVIGPWIQTK.M	1759.00118	2	6.47E-05	0.88	3.78	-	793.1
AHQ-8-5, 3081	R.QKDYETATLSEIK.A	1526.67030	2	7.73E-05	0.24	2.70	-	171.2
AHQ-8-6, 3088	R.TINEVENQILTR.D	1430.58898	2	5.07E-04	0.88	3.61	-	745.3
AHQ-8-4, 3486	R.TINEVENQILTR.D	1430.58898	2	7.08E-04	0.70	2.68	-	511.1
AHQ-8-5, 4001	R.TINEVENQILTR.D	1430.58898	2	1.68E-06	0.91	3.88	-	1018.4
AHQ-8-6, 3826 - 3827	R.TINEVENQILTR.D	1430.58898	2	5.19E-07	0.90	3.85	-	905.1
AHQ-8-4, 3902	R.TINEVENQILTR.D	1430.58898	1	5.31E-06	0.31	2.57	-	219.6
AHQ-8-7, 3889	R.TINEVENQILTR.D	1430.58898	2	7.93E-05	0.66	2.99	-	493.3
AHQ-8-4, 4018 - 4019	R.TINEVENQILTR.D	1430.58898	2	3.17E-05	0.91	3.91	-	1012.7
AHQ-8-5, 3105	R.TINEVENQILTR.D	1430.58898	2	5.32E-04	0.84	3.23	-	764.2
AHQ-8-4, 3885	R.TINEVENQILTR.D	1430.58898	2	3.76E-07	0.92	4.17	-	968.1
AHQ-8-5, 3874	R.TINEVENQILTR.D	1430.58898	2	1.99E-06	0.90	3.55	-	956.1
AHQ-8-3, 6281	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.78E-06	0.89	4.09	-	828.4
AHQ-8-5, 6313	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	4.70E-06	0.95	5.82	-	1013.2
AHQ-8-5, 6314 - 6316	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	5.89E-05	0.95	5.14	-	1017.6
AHQ-8-4, 6366 - 6367	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	5.23E-09	0.97	6.14	-	1570.6
AHQ-8-6, 6211	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	4.82E-11	0.98	7.46	-	2765.3
AHQ-8-7, 5996	R.VGWEQLLTTIAR.T	1387.60894	2	8.06E-09	0.94	3.29	-	1805.4
AHQ-8-8, 6206	R.VGWEQLLTTIAR.T	1387.60894	2	2.75E-07	0.96	4.25	-	1504.9
AHQ-8-6, 6063	R.VGWEQLLTTIAR.T	1387.60894	2	5.67E-07	0.93	3.63	-	1191.1
AHQ-8-4, 6195 - 6266	R.VGWEQLLTTIAR.T	1387.60894	2	7.20E-06	0.95	4.18	-	1384.6
AHQ-8-11, 5947	R.VGWEQLLTTIAR.T	1387.60894	2	3.67E-04	0.70	2.79	-	723.8
AHQ-8-5, 6160 - 6168	R.VGWEQLLTTIAR.T	1387.60894	2	2.67E-06	0.97	4.35	-	1763.4
AHQ-8-4, 3443 - 3505	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	8.14E-06	0.91	3.88	-	781.1
AHQ-8-4, 3565 - 3641	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.26E-09	0.97	5.31	-	1355.7
AHQ-8-4, 4541	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.09E-05	0.91	4.08	-	668.4
AHQ-8-7, 4028	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.09E-08	0.95	4.11	-	1408.4
AHQ-8-4, 3558	K.VLAVNQENEQLM*EDYEK.L	2069.23575	3	4.86E-13	0.97	6.21	-	1726.2
AHQ-8-5, 4330	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.53E-10	0.95	4.41	-	1106.6
AHQ-8-5, 4152	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.53E-06	0.96	5.40	-	1146.1
AHQ-8-5, 3589	K.VLAVNQENEQLM*EDYEK.L	2069.23575	3	1.24E-09	0.94	4.17	-	1469.4
AHQ-8-5, 3542 - 3553	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.13E-07	0.96	5.30	-	1238.5
AHQ-8-4, 4303 - 4365	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	3.00E-07	0.96	5.05	-	1254.4
AHQ-8-8, 4083 - 4111	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.66E-08	0.95	4.43	-	1153.9
AHQ-8-6, 3498	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	7.29E-06	0.97	5.18	-	1542.5
AHQ-8-4, 3723	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	6.33E-07	0.81	3.47	-	816.3
AHQ-8-4, 4126 - 4185	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	6.93E-07	0.97	5.56	-	1387.6
AHQ-8-6, 4043 - 4099	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.36E-06	0.96	5.46	-	1128.9
AHQ-8-2, 4240	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.13E-05	0.88	3.80	-	811.2
gi|4502051|ref|NP_000688.1|	arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]			5.70E-13	8.45	100.24	21.60	75721.8
AHQ-8-6, 4607	R.AAAQLTYCSLCPPDDLADR.G	2140.33708	2	5.42E-04	0.77	3.51	-	271.6
AHQ-8-6, 2470 - 2472	K.AVSTGGGGHVQLLR.R	1352.52468	2	1.66E-10	0.88	3.16	-	1075.0
AHQ-8-6, 3703 - 3706	K.EGLPLTIAADR.K	1156.31411	2	3.60E-05	0.81	2.97	-	651.2
AHQ-8-6, 3126 - 3206	R.EITEVGLCQAQDR.G	1520.64745	2	4.26E-04	0.86	3.07	-	796.5
AHQ-8-6, 3439	K.GDPELQAWCR.E	1233.33558	2	1.46E-07	0.54	2.62	-	339.7
AHQ-8-6, 5232 - 5240	R.GLLGLPGALYAHDALR.L	1637.90708	2	5.70E-13	0.95	4.72	-	751.6
AHQ-8-6, 4820	R.ITVQGPGACAEVAFPCYR.W	1999.25659	2	4.07E-05	0.91	3.49	-	1247.9
AHQ-8-6, 3671 - 3675	R.LPGDNALDM*FQK.H	1365.53724	2	3.58E-05	0.94	4.31	-	1026.5
AHQ-8-6, 4551	R.VATGAWLFSGSYNR.V	1529.68080	2	1.04E-04	0.90	3.92	-	790.7
AHQ-8-6, 4771	R.WVQGEDILSLPEGTAR.L	1771.95190	2	7.19E-06	0.91	4.12	-	749.4
gi|4827056|ref|NP_005103.1|	WD repeat-containing protein 1 isoform 2 [Homo sapiens]			9.13E-13	12.24	140.31	50.20	58001.9
AHQ-8-6, 4788 - 4806	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	9.13E-13	0.97	6.21	-	1282.6
AHQ-8-8, 5347	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.54E-06	0.90	3.72	-	1105.6
AHQ-8-6, 4014	R.FATASADGQIYIYDGK.T	1720.86021	2	5.91E-04	0.81	3.08	-	666.0
AHQ-8-6, 3800 - 3864	R.FATASADGQIYIYDGK.T	1720.86021	2	1.79E-06	0.69	2.94	-	767.8

AHQ-8-6, 5351	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	3	1.20E-09	0.87	4.13	-	679.5
AHQ-8-6, 4420 - 4480	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	3	4.29E-06	0.94	5.00	-	1117.7
AHQ-8-6, 4434 - 4498	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	3.12E-08	0.97	5.75	-	1575.3
AHQ-8-6, 1951	R.IAVVGEGR.E	800.92621	2	9.06E-05	0.78	2.85	-	644.4
AHQ-8-6, 2454	K.IKDIAWTEDSKR.I	1462.63267	2	2.66E-06	0.91	3.68	-	922.8
AHQ-8-6, 5318 - 5386	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.83E-11	0.70	3.67	-	454.0
AHQ-8-6, 5186 - 5262	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	3.30E-10	0.94	4.98	-	963.4
AHQ-8-6, 5092 - 5147	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.55E-05	0.76	3.16	-	693.4
AHQ-8-7, 5209	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	3.77E-04	0.44	2.67	-	512.1
AHQ-8-7, 5114 - 5129	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	1.04E-06	0.89	3.77	-	957.4
AHQ-8-6, 3930 - 3934	R.LYSILGTTLKDEGK.L	1538.76736	2	4.14E-08	0.79	3.19	-	681.7
AHQ-8-7, 3881 - 3946	R.LYSILGTTLKDEGK.L	1538.76736	2	1.36E-04	0.75	3.10	-	583.3
AHQ-8-6, 4160	R.M*TVDESGQLISCSMDDTVR.Y	2162.36305	2	2.83E-04	0.95	4.43	-	934.4
AHQ-8-6, 4212 - 4288	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	3	8.95E-05	0.86	3.88	-	595.6
AHQ-8-6, 4218	R.NIDNPALADIYTEHAHQVVVAK.Y	2419.67805	2	2.11E-05	0.91	4.20	-	601.3
AHQ-8-6, 2142	K.SIQCLTVHKNGGK.S	1443.65418	2	1.07E-05	0.87	3.64	-	967.2
AHQ-8-6, 4071 - 4079	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	2.06E-11	0.98	6.12	-	3013.7
AHQ-8-6, 4163	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	7.32E-07	0.94	4.56	-	1187.3
AHQ-8-5, 3896	K.YAPSGFYIASGDVSGK.L	1619.75589	2	2.64E-04	0.51	2.60	-	390.5
AHQ-8-6, 3758 - 3830	K.YAPSGFYIASGDVSGK.L	1619.75589	2	5.98E-08	0.95	4.13	-	919.6
AHQ-8-11, 3785 - 3791	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.26E-05	0.92	3.27	-	1111.7
gi|16507237|ref|NP_005338.1|	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he			9.18E-13	9.52	110.26	23.90	72332.5
AHQ-8-5, 4926	R.AKFEELNMDLFR.S	1513.74309	2	8.55E-04	0.79	2.58	-	793.0
AHQ-8-5, 4174	R.AKFEELNM*DLFR.S	1529.74249	2	8.59E-05	0.74	3.17	-	550.7
AHQ-8-5, 5592	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	5.42E-06	0.94	4.26	-	889.6
AHQ-8-5, 4637	K.IEWLESHQDADIEDFK.A	1976.08864	3	3.21E-10	0.90	4.35	-	704.5
AHQ-8-5, 4617	K.IEWLESHQDADIEDFK.A	1976.08864	2	1.26E-07	0.97	5.20	-	1715.6
AHQ-8-5, 4397 - 4400	R.IINEPTAAAIAYGLDKR.E	1817.07894	2	9.18E-13	0.89	4.27	-	1122.9
AHQ-8-5, 3840 - 3849	R.ITPSYVAFTPEGER.L	1567.72412	2	7.27E-04	0.62	2.64	-	532.1
AHQ-8-6, 3802	R.ITPSYVAFTPEGER.L	1567.72412	2	6.99E-04	0.68	2.72	-	629.8
AHQ-8-14-, 3843	R.ITPSYVAFTPEGER.L	1567.72412	2	1.70E-05	0.81	3.63	-	372.9
AHQ-8-5, 3790	K.KSDIDEIVLVGGSTR.I	1589.77277	2	7.30E-10	0.98	4.92	-	3121.2
AHQ-8-5, 3809	K.NQLTSNPENTVFDAK.R	1678.78173	2	6.29E-04	0.60	3.62	-	428.9
AHQ-8-5, 3229	K.NQLTSNPENTVFDAK.R	1678.78173	2	8.79E-09	0.89	3.73	-	786.2
AHQ-8-6, 3678 - 3679	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	9.19E-10	0.96	5.14	-	1135.1
AHQ-8-5, 3724 - 3725	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	1.31E-08	0.95	4.75	-	960.5
AHQ-8-7, 3626	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	8.32E-07	0.94	4.55	-	920.0
AHQ-8-6, 3104	K.TKPYIQVDIGGGQTK.T	1605.81703	2	4.81E-07	0.68	2.84	-	674.1
AHQ-8-5, 3930	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	2	4.82E-04	0.93	4.63	-	635.5
gi|11761631|ref|NP_005132.1|	fibrinogen, beta chain preproprotein [Homo sapiens]			1.06E-12	17.23	210.27	39.50	55901.8
AHQ-8-7, 2540	K.AHYGGFTVQNEANK.Y	1536.63020	2	6.14E-09	0.88	3.67	-	778.0
AHQ-8-11, 2465	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.27E-07	0.92	3.37	-	1154.5
AHQ-8-6, 2462	K.AHYGGFTVQNEANK.Y	1536.63020	2	3.71E-06	0.91	3.77	-	843.7
AHQ-8-7, 2432 - 2433	K.AHYGGFTVQNEANK.Y	1536.63020	2	6.60E-07	0.96	4.56	-	1455.7
AHQ-8-7, 3538 - 3558	K.AHYGGFTVQNEANKYQISVNK.Y	2369.57759	3	7.17E-04	0.89	3.81	-	674.9
AHQ-8-8, 4014	K.DNENVVNEYSSELEK.H	1769.80167	2	6.08E-04	0.80	3.40	-	631.7
AHQ-8-8, 4013	K.DNENVVNEYSSELEK.H	1769.80167	2	2.66E-04	0.85	3.99	-	512.7
AHQ-8-7, 4036 - 4112	K.DNENVVNEYSSELEK.H	1769.80167	2	3.47E-08	0.95	4.88	-	917.5
AHQ-8-11, 3911 - 3968	K.DNENVVNEYSSELEK.H	1769.80167	2	3.41E-07	0.91	4.43	-	890.9
AHQ-8-6, 3906 - 3971	K.DNENVVNEYSSELEK.H	1769.80167	2	1.18E-08	0.94	4.61	-	929.7
AHQ-8-7, 3334	K.DNENVVNEYSSELEK.H	1769.80167	2	1.61E-04	0.78	3.30	-	639.6
AHQ-8-7, 3245 - 3310	K.DNENVVNEYSSELEK.H	1769.80167	2	4.59E-04	0.88	3.82	-	670.7
AHQ-8-6, 4094 - 4174	K.DNENVVNEYSSELEK.H	1769.80167	2	1.35E-05	0.87	4.03	-	563.2
AHQ-8-9, 6547	K.DNENVVNEYSSELEK.H	1769.80167	2	2.89E-06	0.80	3.35	-	587.5
AHQ-8-8, 3295	K.DNENVVNEYSSELEK.H	1769.80167	2	5.09E-04	0.67	3.24	-	421.1
AHQ-8-6, 3283	K.DNENVVNEYSSELEK.H	1769.80167	2	2.28E-06	0.80	3.50	-	634.2
AHQ-8-8, 4133	K.DNENVVNEYSSELEK.H	1769.80167	2	6.56E-04	0.50	2.64	-	698.3
AHQ-8-6, 3574 - 3575	K.EDGGGWWYNR.C	1240.26508	2	6.04E-05	0.73	3.03	-	461.2
AHQ-8-6, 3386	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	7.26E-05	0.21	3.00	-	156.4
AHQ-8-7, 3893	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	6.00E-09	0.91	3.92	-	1189.4
AHQ-8-7, 3924	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	8.74E-07	0.84	3.90	-	463.7
AHQ-8-6, 4006	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	3.72E-06	0.89	4.13	-	543.1
AHQ-8-8, 4018	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	2.91E-07	0.90	4.50	-	457.9
AHQ-8-8, 4025	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	1.71E-05	0.90	4.17	-	1007.0
AHQ-8-6, 4000	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	1.58E-05	0.85	3.50	-	989.4
AHQ-8-7, 3536	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	9.72E-06	0.57	3.32	-	237.3
AHQ-8-7, 4041 - 4117	K.HGTDDGVVWMNWK.G	1545.70374	2	1.28E-04	0.91	3.48	-	717.3
AHQ-8-7, 3545 - 3614	K.HGTDDGVVWM*NWK.G	1561.70314	2	4.65E-06	0.94	4.17	-	800.4
AHQ-8-6, 3694	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	3.60E-07	0.88	4.11	-	593.0
AHQ-8-8, 3619	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	3.87E-04	0.83	4.34	-	467.2
AHQ-8-6, 3322	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	4.27E-04	0.86	4.04	-	842.9
AHQ-8-7, 3260	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	2.15E-04	0.88	4.41	-	782.3
AHQ-8-7, 3589 - 3645	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	6.21E-07	0.84	3.84	-	738.5
AHQ-8-8, 3623 - 3627	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	7.16E-06	0.94	5.35	-	794.1
AHQ-8-7, 3434 - 3509	K.LESDVSAQMEYCR.T	1589.73005	2	5.83E-06	0.71	2.72	-	712.8
AHQ-8-7, 3212 - 3268	K.LESDVSAQMEYCR.T	1589.73005	2	3.68E-07	0.88	3.57	-	900.9
AHQ-8-6, 5874	R.M*GPTELLIEMEDWK.G	1708.97776	2	1.78E-05	0.94	4.22	-	1161.1
AHQ-8-11, 4543	R.M*GPTELLIEM*EDWK.G	1724.97716	2	1.32E-05	0.55	2.59	-	425.3
AHQ-8-8, 6027	R.M*GPTELLIEMEDWK.G	1708.97776	2	3.09E-05	0.83	2.94	-	906.4
AHQ-8-6, 4583 - 4646	R.M*GPTELLIEM*EDWK.G	1724.97716	2	1.03E-05	0.79	3.15	-	629.6
AHQ-8-7, 5796	R.M*GPTELLIEMEDWK.G	1708.97776	2	8.78E-06	0.97	4.82	-	1984.1
AHQ-8-7, 4901 - 4912	K.NYCGLPGEYWLGNDK.I	1787.92994	2	1.48E-05	0.70	3.05	-	314.0
AHQ-8-7, 3633	R.TPCTVSCNIPVVSGK.E	1621.85811	2	2.14E-05	0.53	3.22	-	234.2
AHQ-8-7, 3588 - 3644	R.TPCTVSCNIPVVSGK.E	1621.85811	2	3.62E-04	0.79	3.32	-	518.7
AHQ-8-8, 3666	R.TPCTVSCNIPVVSGK.E	1621.85811	2	2.78E-05	0.92	3.84	-	747.0
AHQ-8-7, 4612 - 4648	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	7.90E-07	0.87	4.15	-	774.4
AHQ-8-7, 4493 - 4556	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	6.03E-07	0.92	3.98	-	1231.2
AHQ-8-6, 4615 - 4678	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	9.09E-05	0.91	4.40	-	864.8
AHQ-8-1, 4876	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.39E-05	0.74	3.36	-	675.4
AHQ-8-3, 4756	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.80E-05	0.88	4.18	-	734.9
AHQ-8-7, 3772 - 3828	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	2.86E-07	0.94	4.86	-	740.1
AHQ-8-6, 3831 - 3887	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	8.39E-08	0.95	4.53	-	1141.7
AHQ-8-7, 4222	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	1.82E-05	0.39	2.59	-	470.4
AHQ-8-6, 4283 - 4284	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	4.65E-06	0.91	4.17	-	783.6
AHQ-8-7, 4209 - 4210	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	9.57E-11	0.97	4.79	-	1465.1
AHQ-8-7, 3892	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	1.91E-05	0.89	3.80	-	1028.6
AHQ-8-7, 4300	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.06E-12	0.94	4.19	-	1353.5
AHQ-8-7, 4217 - 4261	R.YYWGGQYTWDM*AK.H	1685.83949	2	6.49E-05	0.89	3.45	-	741.3
AHQ-8-7, 4732	R.YYWGGQYTWDMAK.H	1669.84009	2	6.06E-04	0.89	3.05	-	968.1
AHQ-8-6, 4843 - 4907	R.YYWGGQYTWDMAK.H	1669.84009	2	1.14E-04	0.94	3.63	-	1192.7
AHQ-8-6, 4343	R.YYWGGQYTWDM*AK.H	1685.83949	2	4.21E-04	0.92	3.27	-	952.3
gi|4501893|ref|NP_001094.1|	actinin, alpha 2 [Homo sapiens]			1.69E-12	9.10	100.25	12.50	103853.1
AHQ-8-5, 4377 - 4390	K.AGTQIENIEEDFR.N	1522.59861	2	2.93E-04	0.90	3.65	-	1050.4
AHQ-8-4, 4913	K.CQLEINFNTLQTK.L	1610.81373	2	1.26E-05	0.87	3.20	-	826.6
AHQ-8-4, 4614	K.CQLEINFNTLQTK.L	1610.81373	2	7.57E-09	0.95	3.93	-	1463.1
AHQ-8-5, 4757 - 4760	K.CQLEINFNTLQTK.L	1610.81373	2	2.58E-10	0.95	4.75	-	1158.6
AHQ-8-4, 4254	K.CQLEINFNTLQTK.L	1610.81373	2	5.15E-06	0.93	4.13	-	1206.5

AHQ-8-6, 4659 - 4674	K.CQLEINFNTLQTK.L	1610.81373	2	3.23E-06	0.93	4.12	-	901.2
AHQ-8-4, 4707	R.DLLLDPAWEK.Q	1200.36535	2	4.20E-04	0.72	2.97	-	757.9
AHQ-8-4, 4741	K.EGLLLWCQR.K	1176.37031	2	1.01E-05	0.81	2.70	-	800.8
AHQ-8-6, 4023 - 4078	R.FAIQDISVEETSAK.E	1538.68108	2	1.63E-06	0.77	3.16	-	801.5
AHQ-8-10, 3942	R.FAIQDISVEETSAK.E	1538.68108	2	5.50E-05	0.91	3.11	-	1154.9
AHQ-8-11, 3995	R.FAIQDISVEETSAK.E	1538.68108	2	2.27E-05	0.84	3.20	-	698.6
AHQ-8-8, 4073	R.FAIQDISVEETSAK.E	1538.68108	2	1.02E-05	0.92	3.32	-	1154.8
AHQ-8-7, 3981	R.FAIQDISVEETSAK.E	1538.68108	2	9.51E-07	0.94	4.42	-	982.3
AHQ-8-4, 4102 - 4161	R.FAIQDISVEETSAK.E	1538.68108	2	6.24E-09	0.95	3.73	-	1210.8
AHQ-8-13-, 4112	R.FAIQDISVEETSAK.E	1538.68108	2	1.51E-06	0.83	3.25	-	837.0
AHQ-8-3, 4137	R.FAIQDISVEETSAK.E	1538.68108	2	8.96E-06	0.89	3.30	-	1032.6
AHQ-8-5, 4109	R.FAIQDISVEETSAK.E	1538.68108	2	1.13E-05	0.93	3.62	-	1272.4
AHQ-8-14-, 4067	R.FAIQDISVEETSAK.E	1538.68108	2	1.88E-04	0.78	2.89	-	584.3
AHQ-8-6, 5128 - 5130	K.GYEEWLLNEIR.R	1422.56701	2	1.11E-07	0.85	3.02	-	905.8
AHQ-8-4, 5775 - 5782	K.GYEEWLLNEIR.R	1422.56701	2	6.33E-04	0.73	3.09	-	857.3
AHQ-8-6, 5544	K.GYEEWLLNEIR.R	1422.56701	2	1.08E-07	0.94	3.73	-	1396.9
AHQ-8-5, 5200	K.GYEEWLLNEIR.R	1422.56701	2	1.37E-04	0.84	2.82	-	1072.2
AHQ-8-4, 5669	K.GYEEWLLNEIR.R	1422.56701	2	9.64E-05	0.94	3.38	-	1939.2
AHQ-8-4, 5245	K.GYEEWLLNEIR.R	1422.56701	2	2.60E-04	0.90	3.20	-	1166.5
AHQ-8-5, 5644	K.GYEEWLLNEIR.R	1422.56701	2	8.99E-05	0.92	3.48	-	1254.7
AHQ-8-4, 2375	K.HEAFESDLAAHQDR.V	1626.66861	2	2.10E-07	0.97	4.83	-	1582.7
AHQ-8-4, 2369 - 2442	K.HEAFESDLAAHQDR.V	1626.66861	3	1.26E-05	0.93	4.21	-	1144.1
AHQ-8-4, 2165	R.KHEAFESDLAAHQDR.V	1754.84152	3	4.25E-08	0.90	4.30	-	833.0
AHQ-8-5, 2192	R.KHEAFESDLAAHQDR.V	1754.84152	2	1.20E-07	0.90	3.16	-	1107.8
AHQ-8-6, 2183	R.KHEAFESDLAAHQDR.V	1754.84152	2	1.40E-07	0.91	3.83	-	865.6
AHQ-8-4, 2163	R.KHEAFESDLAAHQDR.V	1754.84152	2	1.69E-12	0.97	5.04	-	1316.1
AHQ-8-4, 3974 - 4033	K.LVSIGAEEIVDGNVK.M	1543.74400	2	2.69E-05	0.95	4.45	-	1329.5
AHQ-8-4, 6634	K.LVSIGAEEIVDGNVK.M	1543.74400	2	2.37E-04	0.84	2.73	-	902.3
AHQ-8-4, 4519	K.LVSIGAEEIVDGNVK.M	1543.74400	2	8.24E-07	0.83	2.96	-	996.7
AHQ-8-5, 3994	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.49E-05	0.88	3.66	-	814.6
AHQ-8-4, 4373 - 4451	K.LVSIGAEEIVDGNVK.M	1543.74400	2	3.97E-04	0.73	3.48	-	582.4
AHQ-8-4, 4239 - 4310	K.LVSIGAEEIVDGNVK.M	1543.74400	2	3.25E-08	0.96	4.48	-	1300.8
AHQ-8-4, 6403	K.M*TLGM*IWTIILR.F	1480.86426	2	1.95E-07	0.93	3.63	-	1190.8
gi|4504745|ref|NP_000410.1|	integrin alpha 2b precursor [Homo sapiens]			2.04E-12	27.76	320.34	35.60	113374.2
AHQ-8-7, 4870 - 4884	R.AEGGQCPSLLFDLR.D	1564.74505	2	8.85E-08	0.92	3.83	-	983.3
AHQ-8-5, 5064	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.04E-04	0.86	3.17	-	779.7
AHQ-8-3, 5048 - 5060	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.45E-07	0.94	4.05	-	961.6
AHQ-8-12, 4906	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.22E-04	0.86	3.66	-	610.6
AHQ-8-4, 5001 - 5070	R.AEGGQCPSLLFDLR.D	1564.74505	2	4.68E-07	0.94	4.43	-	899.6
AHQ-8-6, 4970 - 4979	R.AEGGQCPSLLFDLR.D	1564.74505	2	8.25E-06	0.90	3.40	-	871.3
AHQ-8-4, 5109	R.AEGGQCPSLLFDLR.D	1564.74505	2	6.08E-05	0.93	3.46	-	1125.7
AHQ-8-6, 2887 - 2946	R.ALSNVEGFER.L	1122.21308	2	2.18E-06	0.81	3.12	-	596.0
AHQ-8-7, 2845 - 2849	R.ALSNVEGFER.L	1122.21308	2	3.92E-06	0.82	2.99	-	748.8
AHQ-8-5, 2908	R.ALSNVEGFER.L	1122.21308	2	3.94E-06	0.84	3.34	-	758.2
AHQ-8-5, 4856 - 4858	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.53E-04	0.88	4.08	-	761.0
AHQ-8-4, 4638 - 4702	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	7.83E-05	0.82	3.46	-	763.2
AHQ-8-7, 4681	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.44E-05	0.78	3.48	-	601.8
AHQ-8-5, 4646 - 4693	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	6.53E-04	0.46	2.82	-	424.8
AHQ-8-6, 4774	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	5.91E-04	0.74	3.41	-	458.9
AHQ-8-4, 4894	K.ASVQLLVQDSLNPAVK.S	1682.94293	3	1.23E-05	0.82	3.66	-	805.8
AHQ-8-4, 3217	R.DETRNVGSQTLQTFK.A	1724.85363	3	1.52E-04	0.72	3.15	-	692.7
AHQ-8-4, 3082	R.DETRNVGSQTLQTFK.A	1724.85363	2	4.34E-04	0.93	4.05	-	1069.0
AHQ-8-4, 3846 - 3898	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.65E-11	0.91	4.34	-	634.0
AHQ-8-4, 3749 - 3757	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.98E-08	0.96	4.40	-	1216.7
AHQ-8-5, 3730 - 3761	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	5.81E-11	0.82	3.43	-	648.6
AHQ-8-4, 3957	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	5.56E-04	0.85	3.44	-	719.7
AHQ-8-4, 3135	R.EQNSLDSWGPK.V	1261.32250	2	9.82E-04	0.63	2.64	-	600.5
AHQ-8-6, 5404	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.29E-05	0.80	3.77	-	700.5
AHQ-8-4, 5586 - 5645	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	9.32E-05	0.91	4.64	-	1006.2
AHQ-8-4, 5327 - 5409	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	5.45E-07	0.89	4.40	-	846.9
AHQ-8-5, 5412	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.00E-03	0.67	3.85	-	436.7
AHQ-8-6, 5315 - 5335	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.94E-08	0.77	3.75	-	719.6
AHQ-8-4, 5465 - 5527	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	3.59E-11	0.95	6.39	-	722.4
AHQ-8-3, 5410 - 5470	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	2.09E-05	0.86	4.24	-	812.2
AHQ-8-10, 4652	R.GEAQVWTQLLR.A	1301.47614	2	5.36E-05	0.71	2.83	-	629.3
AHQ-8-11, 4731 - 4755	R.GEAQVWTQLLR.A	1301.47614	2	2.17E-05	0.93	4.21	-	940.6
AHQ-8-1, 5072 - 5077	R.GEAQVWTQLLR.A	1301.47614	2	7.63E-08	0.88	4.05	-	688.4
AHQ-8-4, 5295 - 5357	R.GNSFPASLVVAAEEGER.E	1733.86053	2	1.25E-08	0.92	4.36	-	951.0
AHQ-8-5, 5293 - 5350	R.GNSFPASLVVAAEEGER.E	1733.86053	2	7.29E-04	0.54	2.96	-	446.9
AHQ-8-6, 5151	R.GNSFPASLVVAAEEGER.E	1733.86053	2	4.18E-04	0.57	2.67	-	732.5
AHQ-8-4, 5170 - 5234	R.GNSFPASLVVAAEEGER.E	1733.86053	2	8.42E-08	0.91	4.18	-	710.4
AHQ-8-4, 6163	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	3.08E-04	0.75	3.36	-	639.7
AHQ-8-4, 5015 - 5075	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	2.99E-06	0.89	4.34	-	789.9
AHQ-8-3, 5028 - 5030	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	2.63E-04	0.81	3.42	-	1149.3
AHQ-8-5, 5037	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.39E-05	0.96	5.43	-	950.4
AHQ-8-7, 4820	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.67E-04	0.93	4.56	-	733.1
AHQ-8-4, 5045	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.11E-04	0.98	5.74	-	1462.0
AHQ-8-7, 4816	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	4.35E-04	0.77	3.27	-	784.1
AHQ-8-6, 4943	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	6.65E-06	0.79	3.24	-	1014.0
AHQ-8-5, 4840 - 4844	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.47E-08	0.97	5.21	-	1227.1
AHQ-8-6, 4766	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.27E-05	0.94	4.03	-	1335.7
AHQ-8-4, 4841 - 4921	R.GQVLVFLGQSEGLR.S	1503.72793	2	8.04E-10	0.97	5.06	-	1622.1
AHQ-8-4, 4981 - 5062	R.GQVLVFLGQSEGLR.S	1503.72793	2	3.88E-05	0.90	3.05	-	1203.5
AHQ-8-4, 4286 - 4351	R.HDLLVGAPLYMESR.A	1601.85188	2	1.54E-07	0.95	3.61	-	1419.4
AHQ-8-4, 3785	K.HSPICHTTMAFLR.D	1572.83705	3	1.50E-04	0.77	3.21	-	811.3
AHQ-8-4, 3219	K.HSPICHTTM*AFLR.D	1588.83645	2	1.06E-05	0.72	3.21	-	405.6
AHQ-8-4, 4361	K.IVLLDVPVR.A	1024.28196	2	1.78E-05	0.93	3.52	-	1173.6
AHQ-8-4, 3899	R.IYVENDFSWDKR.Y	1572.70245	3	1.17E-06	0.64	3.14	-	400.2
AHQ-8-4, 3913 - 3978	R.IYVENDFSWDKR.Y	1572.70245	2	1.68E-07	0.93	3.85	-	1197.7
AHQ-8-6, 4188	K.LSLNAELQLDR.Q	1272.43310	2	1.34E-06	0.86	2.93	-	787.2
AHQ-8-4, 4235 - 4302	K.LSLNAELQLDR.Q	1272.43310	2	2.22E-06	0.94	3.98	-	1256.6
AHQ-8-10, 2164 - 2178	R.NRPPLEEDDEEGE	1529.50164	2	2.55E-06	0.79	2.97	-	787.9
AHQ-8-4, 2783	R.NVGSQTLQTFK.A	1223.36055	2	9.16E-09	0.83	3.04	-	508.4
AHQ-8-4, 2111 - 2131	K.SCVLPQTK.T	934.09260	2	3.69E-04	0.80	2.96	-	795.6
AHQ-8-4, 5501 - 5578	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	9.44E-11	0.97	5.57	-	1849.3
AHQ-8-7, 5453 - 5508	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	3.00E-12	0.98	6.87	-	2077.3
AHQ-8-5, 5669	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.89E-08	0.97	6.06	-	1491.3
AHQ-8-4, 5697 - 5755	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.09E-08	0.95	5.68	-	1049.3
AHQ-8-3, 5640 - 5648	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	9.97E-05	0.97	5.38	-	1849.0
AHQ-8-5, 3677	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	4.31E-07	0.67	3.25	-	402.6
AHQ-8-4, 3693	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	7.15E-07	0.93	4.31	-	663.6
AHQ-8-7, 3574	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	2.35E-05	0.82	3.50	-	454.2
AHQ-8-7, 5157	R.TLGPSQEETGGVFLCPWR.A	2036.25364	3	1.45E-04	0.81	4.30	-	538.0
AHQ-8-3, 5250 - 5324	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.04E-05	0.26	2.89	-	328.2
AHQ-8-12, 5123	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.10E-04	0.82	3.17	-	633.2
AHQ-8-7, 5142 - 5202	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.61E-07	0.92	4.20	-	797.0
AHQ-8-13-, 5234 - 5240	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.15E-07	0.88	4.00	-	785.5

AHQ-8-5, 5313 - 5376	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.40E-06	0.95	4.40	-	1316.4
AHQ-8-4, 5353 - 5419	R.TLGPSQEETGGVFLCPWR.A	2036.25364	3	4.48E-04	0.70	3.41	-	620.4
AHQ-8-4, 5369 - 5401	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	8.86E-08	0.95	4.85	-	1096.7
AHQ-8-10, 3526	K.TPVGSCFLAQPESGR.R	1607.76993	2	6.85E-06	0.85	3.16	-	822.2
AHQ-8-7, 3518 - 3576	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.06E-06	0.89	3.48	-	912.6
AHQ-8-5, 3669	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.89E-07	0.95	3.87	-	1275.6
AHQ-8-11, 3589	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.94E-04	0.81	3.21	-	623.1
AHQ-8-4, 3677 - 3681	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.07E-07	0.95	4.61	-	897.1
AHQ-8-4, 4406	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	8.77E-07	0.94	4.54	-	1436.8
AHQ-8-4, 4839	K.TPVSCFNIQMCVGATGHNIPQK.L	2462.81122	3	2.04E-05	0.94	4.95	-	1129.4
AHQ-8-11, 2680	R.VAIVVGAPR.T	882.08560	2	9.94E-06	0.93	3.26	-	1215.9
AHQ-8-4, 2661	R.VAIVVGAPR.T	882.08560	2	7.40E-07	0.94	3.35	-	1400.5
AHQ-8-4, 5398 - 5474	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.04E-12	0.95	4.99	-	1177.6
AHQ-8-4, 5537	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.27E-04	0.92	4.15	-	938.2
AHQ-8-4, 5643 - 5701	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	3.28E-05	0.94	4.65	-	975.1
AHQ-8-4, 6670 - 6678	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.67E-04	0.97	5.35	-	1340.8
AHQ-8-4, 3333 - 3350	R.VVLCELGNPM*K.K	1277.53632	2	3.32E-05	0.95	3.95	-	1543.1
AHQ-8-4, 4039	R.VVLCELGNPMK.K	1261.53692	2	1.35E-06	0.96	4.50	-	1633.8
AHQ-8-6, 3299	R.VVLCELGNPM*K.K	1277.53632	2	1.08E-05	0.77	2.55	-	901.1
AHQ-8-5, 4022	R.VVLCELGNPMK.K	1261.53692	2	2.34E-05	0.87	3.24	-	897.5
AHQ-8-7, 4038	R.VYLFLQPR.G	1036.25129	2	7.71E-05	0.89	2.92	-	852.6
AHQ-8-5, 4156	R.VYLFLQPR.G	1036.25129	2	3.54E-06	0.94	3.51	-	1275.3
AHQ-8-4, 4167	R.VYLFLQPR.G	1036.25129	2	3.82E-06	0.92	3.27	-	1058.5
AHQ-8-6, 4107	R.VYLFLQPR.G	1036.25129	2	1.00E-06	0.95	3.69	-	1191.4
gi|4502027|ref|NP_000468.1|	albumin precursor; PRO0883 protein [Homo sapiens]			2.23E-12	35.16	400.34	69.10	69366.4
AHQ-8-7, 2504 - 2538	K.AAFTECCQAADK.A	1374.47927	2	6.98E-04	0.44	2.59	-	415.7
AHQ-8-5, 2654	K.AAFTECCQAADK.A	1374.47927	2	3.42E-04	0.83	2.76	-	848.2
AHQ-8-6, 2546 - 2547	K.AAFTECCQAADK.A	1374.47927	2	7.42E-05	0.90	3.44	-	1004.6
AHQ-8-5, 2556	K.AAFTECCQAADK.A	1374.47927	1	2.90E-04	0.63	2.84	-	510.0
AHQ-8-5, 1998 - 2068	K.AEFAEVSK.L	880.96496	2	2.27E-04	0.42	2.95	-	282.8
AHQ-8-5, 5196	K.AEFAEVSKLVTDLTK.V	1651.88247	2	2.43E-07	0.87	3.44	-	931.2
AHQ-8-5, 6444	K.ALVLIAFAQYLQQCPFEDHVK.L	2492.87697	3	2.18E-09	0.96	5.37	-	1351.9
AHQ-8-14-, 5167	K.AVMDDFAAFVEK.C	1343.53006	2	1.82E-06	0.95	3.73	-	1492.0
AHQ-8-7, 5086	K.AVMDDFAAFVEK.C	1343.53006	2	4.47E-08	0.94	3.80	-	1294.6
AHQ-8-5, 4346 - 4408	K.AVM*DDFAAFVEK.C	1359.52946	2	7.60E-05	0.92	3.70	-	958.5
AHQ-8-13-, 4390	K.AVM*DDFAAFVEK.C	1359.52946	2	6.31E-04	0.77	2.59	-	459.2
AHQ-8-13-, 5164	K.AVMDDFAAFVEK.C	1343.53006	2	2.41E-09	0.92	3.31	-	1064.1
AHQ-8-5, 5228	K.AVMDDFAAFVEK.C	1343.53006	2	1.05E-08	0.95	3.93	-	1309.5
AHQ-8-6, 5111 - 5154	K.AVMDDFAAFVEK.C	1343.53006	2	5.25E-08	0.94	3.80	-	1322.7
AHQ-8-7, 2197	K.CCAAADPHECYAK.V	1556.67999	2	5.23E-04	0.64	2.91	-	497.8
AHQ-8-5, 2208	K.CCAAADPHECYAK.V	1556.67999	2	3.35E-06	0.79	3.55	-	567.3
AHQ-8-5, 2402 - 2425	K.CCTESLVNR.R	1141.25805	2	7.86E-04	0.90	2.92	-	1148.5
AHQ-8-5, 6252 - 6256	K.DVFLGM*FLYEYAR.R	1640.88331	2	1.15E-05	0.94	3.79	-	922.1
AHQ-8-6, 6106 - 6162	K.DVFLGM*FLYEYAR.R	1640.88331	2	5.04E-04	0.89	3.67	-	832.7
AHQ-8-1, 6307	K.DVFLGM*FLYEYAR.R	1640.88331	2	1.66E-05	0.78	2.51	-	827.3
AHQ-8-5, 2761 - 2826	R.FKDLGEENFK.A	1227.34766	2	8.31E-06	0.90	3.84	-	786.5
AHQ-8-5, 2929	R.FKDLGEENFK.A	1227.34766	2	1.41E-04	0.86	3.18	-	815.9
AHQ-8-6, 2760	R.FKDLGEENFK.A	1227.34766	2	1.52E-05	0.85	3.32	-	663.0
AHQ-8-10, 3014	K.FQNALLVR.Y	961.14282	2	9.88E-05	0.82	2.54	-	947.0
AHQ-8-6, 6054 - 6060	R.HPYFYAPELLFFAK.R	1744.02658	3	2.21E-07	0.95	4.64	-	1393.1
AHQ-8-5, 6144 - 6204	R.HPYFYAPELLFFAK.R	1744.02658	3	6.63E-07	0.94	4.71	-	1198.8
AHQ-8-1, 6239	R.HPYFYAPELLFFAK.R	1744.02658	3	4.95E-05	0.83	3.37	-	731.7
AHQ-8-7, 5993	R.HPYFYAPELLFFAK.R	1744.02658	3	4.88E-06	0.91	4.33	-	1033.2
AHQ-8-5, 3686	K.KLVAASQAALGL	1142.37371	2	2.57E-04	0.89	3.18	-	911.7
AHQ-8-5, 2836	K.KQTALVELVK.H	1129.37494	2	1.14E-05	0.75	2.85	-	714.0
AHQ-8-3, 3605 - 3685	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.09E-06	0.73	2.84	-	573.4
AHQ-8-6, 3506 - 3586	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.97E-08	0.85	3.64	-	541.0
AHQ-8-7, 3476	K.KVPQVSTPTLVEVSR.N	1640.90605	3	3.62E-08	0.96	4.61	-	1775.9
AHQ-8-5, 3536	K.KVPQVSTPTLVEVSR.N	1640.90605	3	9.27E-05	0.96	4.78	-	1557.8
AHQ-8-5, 3556 - 3600	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.51E-04	0.86	3.65	-	470.6
AHQ-8-7, 3402 - 3472	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.99E-04	0.59	2.96	-	460.5
AHQ-8-5, 3321	K.KVPQVSTPTLVEVSR.N	1640.90605	2	7.84E-08	0.94	3.59	-	1343.6
AHQ-8-10, 3428 - 3434	K.KVPQVSTPTLVEVSR.N	1640.90605	3	1.97E-05	0.71	3.23	-	839.1
AHQ-8-6, 3510 - 3587	K.KVPQVSTPTLVEVSR.N	1640.90605	3	6.42E-06	0.85	3.79	-	938.3
AHQ-8-4, 3605 - 3614	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.31E-08	0.92	4.06	-	769.6
AHQ-8-5, 3952 - 3980	K.KVPQVSTPTLVEVSRNLGK.V	2053.39186	3	5.06E-08	0.92	4.65	-	1010.1
AHQ-8-5, 2790 - 2794	K.KYLYEIAR.R	1056.23937	2	6.81E-04	0.74	2.84	-	557.2
AHQ-8-5, 1638 - 1710	K.LDELRDEGK.A	1075.15472	2	3.42E-04	0.66	2.93	-	640.0
AHQ-8-5, 2480	K.LKECCEKPLLEK.S	1549.83503	3	2.19E-04	0.89	4.56	-	1073.0
AHQ-8-14-, 4021	K.LVAASQAALGL	1014.20080	2	5.24E-05	0.93	3.32	-	1124.9
AHQ-8-5, 4044 - 4065	K.LVAASQAALGL	1014.20080	2	1.31E-04	0.93	3.18	-	1182.1
AHQ-8-2, 3425	K.LVNEVTEFAK.T	1150.30633	2	2.85E-05	0.82	3.49	-	549.0
AHQ-8-13, 3533 - 3539	K.LVNEVTEFAK.T	1150.30633	2	1.61E-05	0.91	3.30	-	916.8
AHQ-8-5, 3194	K.LVNEVTEFAK.T	1150.30633	1	1.53E-05	0.47	2.29	-	409.5
AHQ-8-5, 3518	K.LVNEVTEFAK.T	1150.30633	1	8.17E-04	0.44	2.32	-	517.2
AHQ-8-5, 3512	K.LVNEVTEFAK.T	1150.30633	2	8.12E-06	0.92	3.50	-	807.1
AHQ-8-6, 3302	K.LVNEVTEFAK.T	1150.30633	2	1.21E-05	0.66	2.71	-	465.6
AHQ-8-5, 3324 - 3353	K.LVNEVTEFAK.T	1150.30633	2	1.41E-06	0.87	3.57	-	650.0
AHQ-8-5, 5493	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	1.86E-05	0.98	6.81	-	1821.3
AHQ-8-5, 4713 - 4718	R.LVRPEVDVM*CTAFHDNEETFLK.K	2668.98368	3	1.58E-08	0.98	6.45	-	1652.3
AHQ-8-5, 5198 - 5238	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	3.15E-09	0.98	6.75	-	1808.8
AHQ-8-5, 3158	R.NECFLQHKDDNPNLPR.L	1999.15349	3	4.79E-04	0.76	3.58	-	740.6
AHQ-8-5, 3026	K.QEPERNECFLQHKDDNPNLPR.L	2638.81438	3	1.22E-04	0.75	3.79	-	496.2
AHQ-8-6, 4794	K.QNCELFEQLGEYK.F	1659.79847	2	1.32E-07	0.87	3.25	-	610.5
AHQ-8-5, 4876 - 4936	K.QNCELFEQLGEYK.F	1659.79847	2	1.50E-04	0.76	3.16	-	499.0
AHQ-8-7, 4006	R.RHPDYSVVLLLR.L	1468.72842	2	2.23E-04	0.90	3.16	-	937.2
AHQ-8-5, 4128 - 4188	R.RHPDYSVVLLLR.L	1468.72842	3	3.42E-05	0.95	4.83	-	1757.9
AHQ-8-5, 4192	R.RHPDYSVVLLLR.L	1468.72842	2	6.87E-06	0.96	3.33	-	1621.2
AHQ-8-6, 5678 - 5735	R.RHPYFYAPELLFFAK.R	1900.21293	3	3.09E-07	0.97	5.55	-	2027.7
AHQ-8-7, 5613	R.RHPYFYAPELLFFAK.R	1900.21293	3	2.25E-08	0.97	5.58	-	2175.0
AHQ-8-5, 5756 - 5812	R.RHPYFYAPELLFFAK.R	1900.21293	3	5.72E-10	0.97	5.49	-	1709.2
AHQ-8-5, 5818 - 5884	R.RHPYFYAPELLFFAK.R	1900.21293	2	4.37E-04	0.94	4.00	-	1494.4
AHQ-8-5, 5881	R.RHPYFYAPELLFFAK.R	1900.21293	3	9.02E-06	0.94	4.48	-	1419.2
AHQ-8-5, 5690 - 5758	R.RHPYFYAPELLFFAK.R	1900.21293	2	1.82E-11	0.98	5.64	-	2328.0
AHQ-8-5, 6408	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	9.02E-06	0.95	5.78	-	1255.0
AHQ-8-6, 6302	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	3.05E-05	0.96	5.83	-	1408.0
AHQ-8-5, 4461	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.78E-05	0.95	5.20	-	701.6
AHQ-8-6, 4502	R.RPCFSALEVDETYVPK.E	1913.14041	3	1.46E-06	0.85	4.30	-	746.1
AHQ-8-5, 4545 - 4604	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.95E-05	0.93	4.34	-	632.5
AHQ-8-6, 4406	R.RPCFSALEVDETYVPK.E	1913.14041	3	6.34E-04	0.74	3.34	-	676.9
AHQ-8-6, 4486 - 4487	R.RPCFSALEVDETYVPK.E	1913.14041	2	8.04E-06	0.93	4.29	-	715.3
AHQ-8-5, 4553 - 4630	R.RPCFSALEVDETYVPK.E	1913.14041	3	3.37E-05	0.91	4.84	-	648.7
AHQ-8-6, 4403	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.65E-05	0.73	3.30	-	368.2
AHQ-8-7, 5734	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	4.76E-06	0.90	4.44	-	772.5
AHQ-8-5, 5908	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	7.43E-05	0.96	5.94	-	991.7
AHQ-8-5, 5896	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	2	3.58E-06	0.82	3.58	-	605.6
AHQ-8-4, 5958 - 6017	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	4.08E-04	0.81	3.86	-	412.4

AHQ-8-3, 5817 - 5874	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	6.04E-05	0.84	4.33	-	601.6
AHQ-8-6, 4898	K.SLHTLFGDKLCTVATLR.E	1934.24913	3	4.91E-05	0.81	3.50	-	686.7
AHQ-8-6, 4890	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	3.91E-05	0.87	3.85	-	669.7
AHQ-8-5, 4962	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	1.56E-06	0.96	4.70	-	1133.8
AHQ-8-5, 4957	K.SLHTLFGDKLCTVATLR.E	1934.24913	3	1.41E-06	0.94	4.36	-	1225.3
AHQ-8-5, 1922 - 1981	K.TCVADESAENCDK.S	1501.53308	2	1.93E-09	0.95	3.76	-	1445.1
AHQ-8-6, 1983 - 2050	K.TCVADESAENCDK.S	1501.53308	2	2.66E-04	0.97	4.02	-	2360.3
AHQ-8-5, 4384	K.TCVADESAENCDKSLHTLFGDK.L	2500.65848	3	2.23E-12	0.90	3.85	-	921.3
AHQ-8-5, 3776 - 3777	K.TYETTLEKCCAAADPHECYAK.V	2522.72734	3	2.21E-09	0.93	5.07	-	918.1
AHQ-8-6, 5406	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	6.67E-05	0.96	4.78	-	1451.0
AHQ-8-5, 5570	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	4.45E-05	0.88	3.92	-	496.0
AHQ-8-5, 5485	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.60E-05	0.89	4.03	-	459.0
AHQ-8-7, 5324 - 5336	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.05E-05	0.96	4.74	-	1421.7
AHQ-8-5, 5673	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.92E-04	0.44	2.77	-	224.4
AHQ-8-1, 5583	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.05E-06	0.96	4.80	-	1811.6
AHQ-8-5, 5373	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.20E-09	0.94	4.50	-	662.3
AHQ-8-1, 5521 - 5580	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	5.86E-04	0.78	3.72	-	313.3
AHQ-8-5, 5370	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	7.89E-06	0.93	4.42	-	1150.3
AHQ-8-5, 5225	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	4.33E-05	0.80	3.52	-	430.2
AHQ-8-5, 3130 - 3210	K.VHTECCHGDLLECADDR.A	2091.20307	2	1.90E-06	0.96	5.09	-	1420.0
AHQ-8-5, 3126 - 3205	K.VHTECCHGDLLECADDR.A	2091.20307	3	2.44E-04	0.93	4.43	-	917.3
AHQ-8-6, 3660 - 3674	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	6.63E-05	0.94	5.78	-	628.0
AHQ-8-5, 3692	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	9.74E-05	0.93	5.11	-	684.3
AHQ-8-5, 3810	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	1.10E-07	0.86	4.36	-	697.3
AHQ-8-5, 3704	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	1.49E-04	0.86	3.57	-	703.2
AHQ-8-7, 2368 - 2381	K.YICENQDSISSK.L	1445.53420	2	6.36E-06	0.80	3.28	-	527.6
AHQ-8-6, 2374 - 2390	K.YICENQDSISSK.L	1445.53420	2	2.72E-08	0.93	4.12	-	973.5
AHQ-8-6, 2502	K.YICENQDSISSK.L	1445.53420	2	4.28E-06	0.86	3.45	-	586.8
AHQ-8-8, 2361	K.YICENQDSISSK.L	1445.53420	2	1.47E-04	0.90	3.44	-	787.7
AHQ-8-4, 2390	K.YICENQDSISSK.L	1445.53420	2	2.94E-04	0.74	3.40	-	474.9
AHQ-8-5, 2476	K.YICENQDSISSK.L	1445.53420	2	2.60E-06	0.89	3.26	-	697.8
AHQ-8-5, 2390	K.YICENQDSISSK.L	1445.53420	1	3.05E-04	0.70	3.21	-	301.0
AHQ-8-5, 2302 - 2381	K.YICENQDSISSK.L	1445.53420	2	5.92E-08	0.90	3.71	-	801.3
gi|4826898|ref|NP_005013.1|	profilin 1; profilin-1 [Homo sapiens]			2.64E-12	13.94	160.29	58.60	15054.2
AHQ-8-12, 2540 - 2562	K.CYEMASHLR.R	1168.32854	2	7.49E-05	0.90	2.83	-	1419.7
AHQ-8-13-, 2080	K.CYEM*ASHLR.R	1184.32794	2	1.46E-04	0.78	2.64	-	865.5
AHQ-8-13-, 1967 - 2023	K.CYEM*ASHLR.R	1184.32794	2	1.24E-04	0.92	3.13	-	1448.6
AHQ-8-13-, 1854 - 1910	K.CYEM*ASHLR.R	1184.32794	2	3.27E-05	0.92	3.17	-	1416.1
AHQ-8-13, 2179 - 2237	K.CYEM*ASHLR.R	1184.32794	2	4.33E-04	0.91	3.11	-	1289.8
AHQ-8-13, 4317 - 4373	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.27E-06	0.92	4.42	-	675.0
AHQ-8-13-, 4160 - 4220	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	4.76E-12	0.98	5.53	-	1660.3
AHQ-8-13, 4176 - 4179	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	4.54E-12	0.98	5.84	-	1319.4
AHQ-8-13-, 4022 - 4026	K.DRSSFYVNGLTLGGQK.C	1742.91379	3	5.44E-05	0.88	3.79	-	1057.9
AHQ-8-13-, 4028	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	2.64E-12	0.97	5.50	-	1253.7
AHQ-8-12, 5054 - 5120	R.DSLLQDGEFSMDLR.T	1626.77023	2	6.02E-04	0.93	3.48	-	1446.4
AHQ-8-12, 4275 - 4351	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.94E-05	0.87	3.46	-	974.6
AHQ-8-13-, 5174 - 5230	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.77E-11	0.97	4.43	-	2145.0
AHQ-8-13-, 4318 - 4374	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.50E-07	0.93	4.04	-	1156.2
AHQ-8-13-, 5080 - 5124	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.51E-04	0.93	3.67	-	1423.4
AHQ-8-14-, 4361 - 4363	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.83E-05	0.93	4.20	-	1053.7
AHQ-8-14-, 4483	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.16E-04	0.88	3.12	-	1381.4
AHQ-8-14-, 5149	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.79E-11	0.97	4.89	-	1961.9
AHQ-8-13, 4343 - 4399	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.08E-04	0.87	3.15	-	1082.7
AHQ-8-13-, 4434 - 4490	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.39E-07	0.95	4.30	-	1616.6
AHQ-8-14, 5911	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.10E-06	0.96	3.97	-	1677.4
AHQ-8-13, 4483 - 4539	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.67E-08	0.95	4.31	-	1109.0
AHQ-8-14, 5390	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.90E-04	0.89	3.14	-	1269.5
AHQ-8-14, 5287	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.35E-04	0.94	3.74	-	1464.2
AHQ-8-13, 4599 - 4671	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.11E-08	0.96	4.04	-	1746.4
AHQ-8-13, 4727 - 4785	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.55E-04	0.94	3.72	-	1792.5
AHQ-8-13, 4801 - 4861	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.88E-04	0.95	4.32	-	1513.3
AHQ-8-13, 5195 - 5251	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.34E-05	0.96	3.92	-	1812.2
AHQ-8-13-, 4976 - 5030	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.27E-05	0.94	3.84	-	1464.2
AHQ-8-13, 5296 - 5356	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.38E-04	0.95	3.66	-	1802.7
AHQ-8-13, 5307 - 5363	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.17E-08	0.98	5.19	-	2377.6
AHQ-8-13, 5419	R.DSLLQDGEFSMDLR.T	1626.77023	2	9.26E-06	0.95	3.85	-	1697.5
AHQ-8-13-, 4952 - 5022	R.DSLLQDGEFSMDLR.T	1626.77023	2	5.72E-09	0.94	3.43	-	1684.1
AHQ-8-13-, 4548 - 4624	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.34E-07	0.96	3.74	-	2021.6
AHQ-8-13, 3700 - 3755	K.DSPSVWAAVPGK.T	1214.35211	2	4.69E-04	0.86	3.41	-	990.8
AHQ-8-13-, 3578 - 3643	K.DSPSVWAAVPGK.T	1214.35211	2	3.04E-04	0.89	3.03	-	1115.4
AHQ-8-13, 4387	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.23E-06	0.62	2.42	-	546.9
AHQ-8-13, 4376 - 4432	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.88E-08	0.91	3.98	-	673.0
AHQ-8-13-, 4360 - 4418	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.81E-08	0.51	2.49	-	448.2
AHQ-8-12, 4272 - 4339	R.SSFYVNGLTLGGQK.C	1471.63957	2	6.41E-09	0.96	4.60	-	1293.8
AHQ-8-13-, 4342 - 4422	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.74E-07	0.93	3.93	-	971.2
AHQ-8-13, 4499	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.53E-04	0.81	2.85	-	658.0
AHQ-8-13-, 4234 - 4235	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.31E-06	0.35	2.59	-	335.5
AHQ-8-13-, 4226 - 4286	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.31E-05	0.95	4.85	-	910.3
AHQ-8-14-, 4241 - 4251	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.35E-07	0.93	3.94	-	848.8
AHQ-8-14-, 4437 - 4501	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.17E-06	0.95	3.44	-	1492.9
AHQ-8-12, 4138 - 4142	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.23E-05	0.94	4.20	-	990.0
AHQ-8-13, 4523 - 4588	R.SSFYVNGLTLGGQK.C	1471.63957	1	9.20E-06	0.68	2.67	-	527.2
AHQ-8-12, 3162 - 3239	K.STGGAPTFNVTVTK.T	1380.52843	2	2.25E-05	0.75	2.81	-	464.5
AHQ-8-13-, 3278 - 3334	K.STGGAPTFNVTVTK.T	1380.52843	2	7.09E-06	0.77	3.21	-	371.6
AHQ-8-13-, 3230	K.STGGAPTFNVTVTK.T	1380.52843	1	1.02E-04	0.54	2.72	-	425.8
AHQ-8-13, 3435 - 3503	K.STGGAPTFNVTVTK.T	1380.52843	2	2.13E-07	0.85	3.59	-	397.4
AHQ-8-13, 3217 - 3287	K.STGGAPTFNVTVTK.T	1380.52843	2	4.96E-05	0.84	3.35	-	549.9
AHQ-8-13-, 3079 - 3134	K.STGGAPTFNVTVTK.T	1380.52843	2	2.54E-07	0.89	3.65	-	553.3
AHQ-8-13, 3387	K.STGGAPTFNVTVTK.T	1380.52843	1	1.09E-04	0.11	2.19	-	212.4
AHQ-8-12, 3171	K.STGGAPTFNVTVTK.T	1380.52843	1	1.84E-04	0.39	2.44	-	332.1
AHQ-8-13-, 3022	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	1.75E-04	0.65	2.81	-	411.9
AHQ-8-13-, 3184	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	2.05E-05	0.72	2.94	-	529.3
AHQ-8-13-, 3059	K.TDKTLVLLM*GK.E	1235.51929	2	1.69E-04	0.90	3.12	-	986.4
AHQ-8-13, 3195 - 3215	K.TDKTLVLLM*GK.E	1235.51929	2	1.14E-04	0.91	3.24	-	1074.2
AHQ-8-12, 3631 - 3635	K.TDKTLVLLMGK.E	1219.51989	2	6.16E-04	0.69	2.69	-	687.2
AHQ-8-13-, 5454 - 5510	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.97E-06	0.95	4.67	-	884.2
AHQ-8-13-, 5554 - 5610	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.24E-08	0.93	4.35	-	909.7
AHQ-8-13, 5631 - 5707	K.TFVNITPAEVGVLVGK.D	1644.93630	2	8.70E-05	0.94	4.55	-	968.8
AHQ-8-13, 5587 - 5623	K.TFVNITPAEVGVLVGK.D	1644.93630	3	7.13E-06	0.96	5.37	-	1409.1
AHQ-8-13-, 5438 - 5498	K.TFVNITPAEVGVLVGK.D	1644.93630	2	8.00E-06	0.92	4.74	-	652.4
AHQ-8-13-, 5450 - 5463	K.TFVNITPAEVGVLVGK.D	1644.93630	3	3.86E-06	0.94	3.31	-	1912.6
AHQ-8-13, 5288 - 5359	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	5.34E-04	0.78	3.64	-	920.9
AHQ-8-13-, 5184	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	1.74E-06	0.85	3.90	-	487.0
AHQ-8-13-, 5166 - 5238	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	7.24E-06	0.70	3.32	-	708.9
AHQ-8-13, 3083	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	1.79E-06	0.79	3.01	-	728.1
AHQ-8-13-, 3146 - 3207	K.TLVLLM*GK.E	891.15418	2	2.84E-04	0.77	2.85	-	603.6
AHQ-8-13, 3991	K.TLVLLMGK.E	875.15478	2	1.73E-05	0.87	2.91	-	759.5

AHQ-8-13-, 3819	K.TLVLLMGK.E	875.15478	1	4.62E-04	0.24	2.71	-	189.5
gi|13775198|ref|NP_112576.1|	SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr			2.69E-12	3.06	40.29	31.20	10437.7
AHQ-8-13-, 4530 - 4604	R.IQYQLVDISQDNALR.D	1776.97168	2	2.69E-12	0.98	5.66	-	1867.8
AHQ-8-13, 4699 - 4759	R.IQYQLVDISQDNALR.D	1776.97168	2	8.15E-11	0.97	5.60	-	1502.7
AHQ-8-13-, 4542	R.IQYQLVDISQDNALR.D	1776.97168	3	1.28E-04	0.96	5.43	-	1935.9
AHQ-8-14-, 4538 - 4539	R.IQYQLVDISQDNALR.D	1776.97168	2	5.51E-12	0.98	5.81	-	1871.2
AHQ-8-14-, 4331 - 4393	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	4.50E-06	0.58	3.14	-	481.5
AHQ-8-13-, 4886 - 4934	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	5.46E-05	0.84	3.94	-	604.4
AHQ-8-13, 4980	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.50E-08	0.69	3.22	-	601.5
AHQ-8-13-, 4702 - 4774	R.IQYQLVDISQDNALRDEMR.A	2308.55751	3	1.16E-05	0.57	3.28	-	486.3
AHQ-8-13, 4411 - 4477	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.99E-05	0.78	3.86	-	430.4
AHQ-8-13-, 1775 - 1834	R.VYSTSVTGSR.E	1057.13940	2	6.85E-04	0.89	3.20	-	878.6
AHQ-8-13-, 2070	R.VYSTSVTGSR.E	1057.13940	2	8.06E-06	0.82	2.60	-	972.3
AHQ-8-13-, 1890 - 1954	R.VYSTSVTGSR.E	1057.13940	2	3.67E-04	0.86	2.95	-	876.1
gi|4507877|ref|NP_003364.1|	vinculin isoform VCL [Homo sapiens]			2.93E-12	37.32	440.32	47.70	116721.6
AHQ-8-14-, 6371 - 6374	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.08E-06	0.94	4.25	-	818.5
AHQ-8-12, 6282	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.31E-04	0.85	3.28	-	651.0
AHQ-8-11, 6259 - 6317	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.96E-08	0.96	4.41	-	1178.2
AHQ-8-10, 6210 - 6214	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	7.41E-09	0.97	4.78	-	1353.4
AHQ-8-7, 6277 - 6336	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.53E-07	0.93	4.36	-	763.0
AHQ-8-3, 6397 - 6457	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	7.12E-07	0.86	3.96	-	637.4
AHQ-8-3, 6456	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	3	2.13E-04	0.88	3.74	-	1277.5
AHQ-8-4, 6485 - 6566	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.66E-06	0.90	4.13	-	697.7
AHQ-8-6, 6387 - 6388	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.41E-11	0.96	5.11	-	859.8
AHQ-8-4, 6549	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	3	7.69E-04	0.91	4.23	-	1086.6
AHQ-8-5, 6496	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.93E-12	0.97	5.76	-	1152.9
AHQ-8-3, 3401	R.ALASQLQDSLK.D	1174.32943	2	2.17E-04	0.64	2.89	-	634.8
AHQ-8-6, 3331 - 3332	R.ALASQLQDSLK.D	1174.32943	2	5.25E-06	0.91	3.74	-	890.3
AHQ-8-7, 3209 - 3284	R.ALASQLQDSLK.D	1174.32943	2	2.24E-04	0.87	2.79	-	1013.5
AHQ-8-5, 3364	R.ALASQLQDSLK.D	1174.32943	2	2.33E-05	0.90	3.12	-	1053.7
AHQ-8-5, 3513 - 3581	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.40E-08	0.90	3.30	-	1346.2
AHQ-8-4, 3573	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.83E-10	0.96	4.50	-	1384.0
AHQ-8-8, 3450	K.AQQVSQGLDVLTAK.V	1458.64233	2	5.75E-08	0.96	3.85	-	1474.1
AHQ-8-3, 3589	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.09E-07	0.97	4.11	-	1743.4
AHQ-8-5, 2528	K.AVAGNISDPGLQK.S	1270.41721	2	9.04E-05	0.78	2.92	-	590.7
AHQ-8-6, 2516 - 2522	K.AVAGNISDPGLQK.S	1270.41721	2	7.42E-06	0.68	2.91	-	565.8
AHQ-8-7, 2497	K.AVAGNISDPGLQK.S	1270.41721	2	2.26E-05	0.81	2.98	-	651.1
AHQ-8-4, 2517	K.AVAGNISDPGLQK.S	1270.41721	2	8.68E-05	0.84	3.33	-	731.5
AHQ-8-5, 5549	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	6.64E-07	0.89	4.57	-	1204.2
AHQ-8-4, 5581	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	1.07E-04	0.94	4.47	-	1666.8
AHQ-8-6, 5456	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	6.58E-04	0.83	3.28	-	883.7
AHQ-8-5, 5552	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	9.08E-08	0.91	3.76	-	989.1
AHQ-8-6, 5446	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	5.14E-06	0.93	4.61	-	1336.6
AHQ-8-5, 2342 - 2348	R.DPSASPGDAGEQAIR.Q	1471.51169	2	4.00E-09	0.95	4.11	-	1008.1
AHQ-8-7, 2329 - 2330	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.75E-07	0.92	4.10	-	830.4
AHQ-8-4, 2335	R.DPSASPGDAGEQAIR.Q	1471.51169	2	9.21E-05	0.78	3.33	-	455.0
AHQ-8-6, 2338	R.DPSASPGDAGEQAIR.Q	1471.51169	2	6.77E-05	0.80	3.17	-	569.6
AHQ-8-8, 2339	R.DPSASPGDAGEQAIR.Q	1471.51169	2	9.09E-04	0.80	3.44	-	577.5
AHQ-8-4, 4630 - 4637	K.ELLPVLISAM*K.I	1230.54265	2	2.70E-04	0.84	3.66	-	671.8
AHQ-8-5, 2778	R.ELTPQVVSAAR.I	1171.32878	2	5.72E-04	0.92	3.01	-	1349.0
AHQ-8-6, 3050	K.ETVQTTEDQILKR.D	1561.71942	2	6.81E-05	0.85	3.10	-	931.2
AHQ-8-4, 3054 - 3058	K.ETVQTTEDQILKR.D	1561.71942	2	2.60E-05	0.84	3.35	-	670.8
AHQ-8-5, 3061	K.ETVQTTEDQILKR.D	1561.71942	2	1.83E-06	0.70	2.83	-	579.2
AHQ-8-14-, 3101	K.ETVQTTEDQILKR.D	1561.71942	2	1.47E-04	0.57	2.94	-	416.6
AHQ-8-4, 6557 - 6615	K.GILEYLTVAEVVETM*EDLVTYTK.N	2633.99263	3	6.34E-10	0.96	5.27	-	1608.3
AHQ-8-5, 6506 - 6580	K.GILEYLTVAEVVETM*EDLVTYTK.N	2633.99263	3	7.78E-09	0.96	5.00	-	1980.0
AHQ-8-5, 6364	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.70E-06	0.93	4.07	-	1103.1
AHQ-8-6, 6200 - 6262	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.12E-06	0.93	4.53	-	861.8
AHQ-8-4, 6417	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.08E-05	0.97	5.97	-	1119.3
AHQ-8-4, 6135 - 6203	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	1.54E-10	0.93	4.55	-	906.6
AHQ-8-4, 3542	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	3	1.04E-10	0.90	4.79	-	771.6
AHQ-8-4, 3547	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	2.62E-04	0.86	3.99	-	609.3
AHQ-8-4, 2277	K.IAELCDDPKER.D	1347.47690	2	1.50E-05	0.56	2.66	-	426.8
AHQ-8-4, 4279	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	1.81E-06	0.97	6.37	-	1797.7
AHQ-8-7, 4037 - 4097	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	7.05E-07	0.87	4.44	-	830.9
AHQ-8-5, 4161 - 4225	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	5.06E-08	0.93	5.05	-	874.6
AHQ-8-6, 4031 - 4102	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	5.72E-04	0.80	4.10	-	519.5
AHQ-8-4, 4282	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	4.75E-06	0.83	3.67	-	505.6
AHQ-8-4, 3429	R.LANVMMGPYR.Q	1152.41560	2	1.80E-04	0.87	3.28	-	732.7
AHQ-8-4, 2306	R.LANVM*M*GPYR.Q	1184.41440	2	3.78E-04	0.93	3.97	-	899.3
AHQ-8-4, 2954	R.LANVMM*GPYR.Q	1168.41500	2	2.65E-05	0.69	3.30	-	535.6
AHQ-8-4, 4141 - 4201	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	1.17E-04	0.82	3.65	-	731.4
AHQ-8-3, 4176 - 4194	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	1.30E-05	0.75	3.26	-	725.6
AHQ-8-4, 4210	R.LTDELAPPKPPLPEGEVPPPRPPPPEEK.D	3025.44391	3	3.60E-05	0.69	3.38	-	761.4
AHQ-8-8, 4311	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	7.62E-05	0.66	3.04	-	478.5
AHQ-8-4, 4425	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	5.68E-06	0.90	3.93	-	1200.6
AHQ-8-5, 3638 - 3640	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.05E-06	0.94	4.69	-	812.4
AHQ-8-11, 3555	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.40E-04	0.89	3.32	-	831.1
AHQ-8-4, 3661	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	9.26E-07	0.93	4.17	-	722.1
AHQ-8-4, 2315	R.M*ALLM*AEM*SR.L	1201.46351	2	6.18E-05	0.91	3.06	-	1207.0
AHQ-8-4, 2929	K.M*LGQM*TDQVADLR.A	1510.71935	2	3.40E-04	0.96	3.82	-	1844.9
AHQ-8-6, 3642	K.M*LGQMTDQVADLR.A	1494.71995	2	1.23E-04	0.97	3.92	-	2063.5
AHQ-8-5, 2930	K.M*LGQM*TDQVADLR.A	1510.71935	2	2.28E-05	0.88	3.24	-	1092.6
AHQ-8-4, 4058	K.MLGQMTDQVADLR.A	1478.72055	2	4.69E-06	0.97	4.40	-	1719.1
AHQ-8-5, 3680 - 3689	K.M*LGQMTDQVADLR.A	1494.71995	2	1.21E-04	0.95	3.66	-	1654.2
AHQ-8-5, 4412 - 4413	R.M*QEAM*TQEVSDVFSDTTTPIK.L	2391.61544	2	1.78E-06	0.68	3.05	-	424.6
AHQ-8-4, 3237 - 3250	K.M*SAEINEIIR.V	1192.36823	2	4.71E-08	0.96	3.89	-	1678.0
AHQ-8-5, 3224	K.M*SAEINEIIR.V	1192.36823	2	2.25E-08	0.94	3.49	-	1297.4
AHQ-8-4, 2869	K.M*SAEINEIIR.V	1192.36823	2	2.28E-08	0.82	2.62	-	836.1
AHQ-8-6, 3722	K.MSAEINEIIR.V	1176.36883	2	4.01E-05	0.86	2.76	-	1291.2
AHQ-8-5, 3533 - 3598	K.MTGLVDEAIDTK.S	1293.46936	2	8.64E-04	0.95	3.46	-	1495.3
AHQ-8-4, 3557	K.MTGLVDEAIDTK.S	1293.46936	2	2.56E-08	0.97	4.09	-	2001.9
AHQ-8-6, 3111	K.M*TGLVDEAIDTK.S	1309.46876	2	1.12E-05	0.83	3.05	-	1010.7
AHQ-8-5, 3133	K.M*TGLVDEAIDTK.S	1309.46876	2	2.41E-04	0.93	3.90	-	1077.4
AHQ-8-4, 3133	K.M*TGLVDEAIDTK.S	1309.46876	2	4.89E-05	0.94	3.94	-	1211.9
AHQ-8-4, 3079	R.NPGNQAAYEHFETMK.N	1737.87437	2	3.53E-05	0.92	3.56	-	1050.6
AHQ-8-4, 3471 - 3546	R.SLGEISALTSK.L	1106.25186	2	3.69E-05	0.90	3.60	-	705.5
AHQ-8-7, 3373	R.SLGEISALTSK.L	1106.25186	2	2.09E-05	0.93	3.38	-	1008.7
AHQ-8-3, 3421	K.SLLDASEEAIKK.D	1304.47187	2	7.70E-04	0.76	2.55	-	838.0
AHQ-8-5, 3322 - 3388	K.SLLDASEEAIKK.D	1304.47187	2	1.16E-07	0.82	2.96	-	689.1
AHQ-8-4, 2453	K.STVEGIQASVK.T	1119.25064	2	3.55E-05	0.89	3.22	-	802.4
AHQ-8-11, 6209	R.TIESILEPVAQQISHLVIM*HEEGEVDGK.A	3119.49274	3	1.97E-04	0.64	3.24	-	326.3
AHQ-8-4, 6309 - 6355	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	4.13E-04	0.47	3.06	-	396.2
AHQ-8-4, 5394 - 5463	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	5.23E-04	0.59	3.40	-	349.3
AHQ-8-4, 5178	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	1.06E-05	0.85	3.71	-	1560.9
AHQ-8-4, 5177	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	1.56E-05	0.95	4.79	-	1056.7
AHQ-8-4, 4773	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	7.11E-05	0.95	4.48	-	1678.3

AHQ-8-5, 5117	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	7.13E-05	0.85	3.46	-	871.8
AHQ-8-6, 5036	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	8.44E-07	0.77	3.68	-	675.7
AHQ-8-4, 4915	R.VDQLTAQLADLAAR.G	1485.66778	2	8.08E-06	0.90	2.92	-	1524.6
AHQ-8-6, 4752 - 4754	R.VDQLTAQLADLAAR.G	1485.66778	2	6.00E-09	0.98	5.11	-	3337.6
AHQ-8-4, 4786 - 4855	R.VDQLTAQLADLAAR.G	1485.66778	2	5.92E-06	0.98	4.70	-	2679.0
AHQ-8-5, 4833 - 4834	R.VDQLTAQLADLAAR.G	1485.66778	2	4.79E-08	0.98	5.68	-	3197.8
AHQ-8-5, 5074 - 5153	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.62E-07	0.95	4.37	-	1041.9
AHQ-8-6, 5071 - 5082	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.78E-05	0.94	4.67	-	807.7
AHQ-8-3, 5149	R.VLQLTSWDEDAWASK.D	1749.90156	2	7.26E-06	0.95	4.47	-	1045.6
AHQ-8-4, 5191 - 5270	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.71E-06	0.95	4.01	-	1529.9
AHQ-8-4, 5083	R.VLQLTSWDEDAWASK.D	1749.90156	2	7.56E-09	0.94	3.74	-	1268.9
AHQ-8-4, 2894 - 2963	R.WIDNPTVDDR.G	1231.29640	2	9.67E-05	0.94	3.34	-	1252.5
AHQ-8-5, 2900	R.WIDNPTVDDR.G	1231.29640	2	1.87E-06	0.92	3.54	-	1066.1
AHQ-8-6, 2886 - 2951	R.WIDNPTVDDR.G	1231.29640	2	2.13E-04	0.95	3.84	-	1328.5
gi|5031635|ref|NP_005498.1|	cofilin 1 (non-muscle) [Homo sapiens]			3.26E-12	7.34	80.34	60.80	18502.4
AHQ-8-12, 5246	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	8.29E-06	0.97	5.42	-	1296.5
AHQ-8-13-, 5326	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.26E-12	0.97	5.29	-	1280.6
AHQ-8-14, 6022	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.29E-09	0.64	2.85	-	501.2
AHQ-8-13, 5448 - 5452	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.86E-04	0.97	5.24	-	1568.3
AHQ-8-14-, 5342	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	9.48E-06	0.96	4.69	-	1327.0
AHQ-8-12, 2636	K.HELQANCYEEVKDR.C	1792.90812	2	3.08E-06	0.70	2.96	-	476.4
AHQ-8-12, 2498 - 2550	K.HELQANCYEEVKDR.C	1792.90812	3	5.31E-06	0.98	5.88	-	2810.8
AHQ-8-12, 3115	K.KAVLFCLSEDKK.N	1439.70221	3	1.22E-04	0.94	4.64	-	1324.7
AHQ-8-12, 5936 - 5942	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	3.33E-04	0.66	3.15	-	492.9
AHQ-8-13-, 6022	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	4.36E-05	0.88	3.68	-	667.2
AHQ-8-12, 4234 - 4294	K.LGGSAVISLEGKPL	1341.57848	2	1.22E-07	0.96	4.83	-	1204.9
AHQ-8-12, 3947 - 3951	K.LGGSAVISLEGKPL	1341.57848	2	1.03E-05	0.97	4.24	-	1681.3
AHQ-8-14-, 4329	K.LGGSAVISLEGKPL	1341.57848	2	4.93E-07	0.92	4.14	-	851.4
AHQ-8-12, 4243	K.LGGSAVISLEGKPL	1341.57848	1	3.49E-06	0.42	2.58	-	398.2
AHQ-8-12, 3046 - 3114	K.LTGIKHELQANCYEEVKDR.C	2305.55341	3	2.74E-06	0.95	4.79	-	1400.4
AHQ-8-11, 6091	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	4.03E-05	0.92	3.96	-	1366.5
AHQ-8-13-, 6170	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	8.12E-10	0.98	6.75	-	2049.9
AHQ-8-13, 3432 - 3492	R.YALYDATYETK.E	1338.44364	2	4.22E-07	0.94	3.65	-	1306.3
AHQ-8-12, 3214	R.YALYDATYETK.E	1338.44364	1	6.58E-07	0.77	3.13	-	432.2
AHQ-8-12, 3206 - 3238	R.YALYDATYETK.E	1338.44364	2	3.45E-07	0.96	3.84	-	1273.1
AHQ-8-13-, 3282 - 3339	R.YALYDATYETK.E	1338.44364	2	1.52E-06	0.95	4.03	-	1201.7
gi|4557677|ref|NP_000203.1|	integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu			6.07E-12	17.80	210.28	30.30	87185.6
AHQ-8-3, 5042	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	1.31E-04	0.94	5.50	-	801.7
AHQ-8-3, 5138 - 5160	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	1.79E-04	0.80	3.69	-	640.3
AHQ-8-3, 4085 - 4144	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	6.02E-05	0.46	3.28	-	409.2
AHQ-8-4, 4158	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	7.20E-10	0.73	3.55	-	390.3
AHQ-8-1, 4280	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	1.77E-05	0.63	3.02	-	381.3
AHQ-8-5, 4136	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	1.39E-04	0.56	3.33	-	444.5
AHQ-8-1, 4353	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	5.76E-04	0.94	4.12	-	1022.7
AHQ-8-3, 5397 - 5469	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	8.31E-07	0.96	5.24	-	865.3
AHQ-8-3, 4218	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.22E-05	0.86	3.52	-	685.7
AHQ-8-5, 4169 - 4236	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	4.49E-05	0.50	2.90	-	235.6
AHQ-8-5, 5476	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	1.47E-04	0.88	3.19	-	910.1
AHQ-8-3, 5385	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	5.67E-06	0.91	3.45	-	951.9
AHQ-8-6, 4166	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	9.13E-10	0.79	3.30	-	529.2
AHQ-8-4, 4709 - 4721	K.DDLWSIQNLGTK.L	1390.52332	2	4.42E-04	0.91	3.93	-	903.9
AHQ-8-5, 4201	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.44E-05	0.88	3.71	-	885.7
AHQ-8-4, 4229	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.41E-04	0.60	2.72	-	529.1
AHQ-8-1, 4267 - 4339	K.DNCAPESIEFPVSEAR.V	1822.93099	2	4.37E-06	0.87	3.04	-	973.6
AHQ-8-6, 4135	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.71E-05	0.83	2.78	-	1086.9
AHQ-8-3, 4304	K.DNCAPESIEFPVSEAR.V	1822.93099	2	5.95E-07	0.79	2.90	-	878.3
AHQ-8-5, 3344	K.EATSTFTNITYR.G	1404.50685	2	1.48E-04	0.83	3.23	-	606.8
AHQ-8-4, 3266 - 3346	K.EATSTFTNITYR.G	1404.50685	2	1.23E-07	0.64	2.67	-	608.0
AHQ-8-3, 3361	K.EATSTFTNITYR.G	1404.50685	2	2.88E-08	0.68	2.73	-	532.2
AHQ-8-1, 3540	K.EATSTFTNITYR.G	1404.50685	2	1.60E-07	0.57	2.66	-	389.7
AHQ-8-4, 2385 - 2386	R.FQYYEDSSGK.S	1224.25749	1	8.68E-04	0.82	2.99	-	644.9
AHQ-8-3, 3513 - 3586	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	8.25E-05	0.92	3.99	-	996.9
AHQ-8-6, 3466	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	6.81E-06	0.93	4.20	-	1172.4
AHQ-8-3, 3516 - 3577	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	5.92E-06	0.79	3.39	-	793.1
AHQ-8-5, 3494	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	8.39E-05	0.92	4.11	-	976.4
AHQ-8-4, 3513	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.80E-07	0.92	3.79	-	1157.9
AHQ-8-6, 2008	K.GSGDSSQVTQVSPQR.I	1533.58302	2	1.35E-04	0.71	2.77	-	929.7
AHQ-8-4, 1955 - 2013	K.GSGDSSQVTQVSPQR.I	1533.58302	2	9.82E-04	0.78	2.95	-	845.7
AHQ-8-4, 2786	K.HVLTLTDQVTR.F	1283.45912	2	2.36E-09	0.93	3.85	-	816.4
AHQ-8-4, 2793	K.HVLTLTDQVTR.F	1283.45912	1	2.13E-04	0.40	2.22	-	326.8
AHQ-8-6, 2776	K.HVLTLTDQVTR.F	1283.45912	2	1.89E-06	0.92	3.53	-	741.9
AHQ-8-8, 2739	K.HVLTLTDQVTR.F	1283.45912	2	8.53E-06	0.87	3.10	-	723.2
AHQ-8-3, 2828 - 2830	K.HVLTLTDQVTR.F	1283.45912	2	1.76E-08	0.92	3.33	-	732.2
AHQ-8-7, 2733	K.HVLTLTDQVTR.F	1283.45912	2	3.11E-06	0.87	3.09	-	600.8
AHQ-8-5, 2793 - 2802	K.HVLTLTDQVTR.F	1283.45912	2	2.01E-09	0.90	3.48	-	661.5
AHQ-8-3, 3993 - 4012	K.IGDTVSFSIEAK.V	1267.41009	2	2.47E-06	0.89	3.26	-	803.8
AHQ-8-4, 3522	K.IGDTVSFSIEAK.V	1267.41009	2	1.36E-06	0.76	2.63	-	726.5
AHQ-8-3, 4206	K.IGDTVSFSIEAK.V	1267.41009	2	2.99E-04	0.84	3.09	-	701.0
AHQ-8-3, 3572	K.IGDTVSFSIEAK.V	1267.41009	2	7.52E-06	0.94	3.75	-	1282.0
AHQ-8-4, 4070	K.IGDTVSFSIEAK.V	1267.41009	2	2.21E-06	0.89	3.50	-	840.8
AHQ-8-3, 4094	K.IGDTVSFSIEAK.V	1267.41009	2	3.76E-06	0.89	3.26	-	797.4
AHQ-8-4, 4245 - 4247	R.NDASHLLVFTTDAK.T	1532.67977	2	4.56E-09	0.94	4.28	-	1144.8
AHQ-8-5, 4226 - 4297	R.NDASHLLVFTTDAK.T	1532.67977	2	7.15E-10	0.92	3.87	-	1011.7
AHQ-8-4, 3866	R.NDASHLLVFTTDAK.T	1532.67977	3	2.77E-06	0.96	4.61	-	1540.1
AHQ-8-4, 3861	R.NDASHLLVFTTDAK.T	1532.67977	2	5.16E-10	0.96	4.78	-	1154.0
AHQ-8-6, 3786	R.NDASHLLVFTTDAK.T	1532.67977	2	1.85E-09	0.96	4.66	-	1167.3
AHQ-8-6, 3791	R.NDASHLLVFTTDAK.T	1532.67977	3	6.78E-10	0.93	4.36	-	1042.8
AHQ-8-7, 3718 - 3725	R.NDASHLLVFTTDAK.T	1532.67977	2	4.47E-05	0.96	4.76	-	1086.4
AHQ-8-5, 3836	R.NDASHLLVFTTDAK.T	1532.67977	2	9.81E-06	0.87	3.24	-	848.1
AHQ-8-3, 3878	R.NDASHLLVFTTDAK.T	1532.67977	3	1.14E-07	0.95	4.81	-	1464.6
AHQ-8-5, 3472 - 3476	K.SFTIKPVGFK.D	1124.35685	2	8.89E-05	0.91	2.96	-	1296.1
AHQ-8-3, 2078	R.SKVELEVR.D	960.10999	2	2.24E-04	0.69	2.53	-	594.8
AHQ-8-4, 2765	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.43E-08	0.89	3.18	-	1094.3
AHQ-8-3, 3468 - 3533	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.46E-07	0.71	3.03	-	568.9
AHQ-8-3, 3385	R.TDTCMSSNGLLCSGR.G	1661.81786	2	6.23E-09	0.93	3.74	-	1111.9
AHQ-8-3, 2789 - 2870	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.70E-11	0.93	4.10	-	1098.7
AHQ-8-4, 3379	R.TDTCMSSNGLLCSGR.G	1661.81786	2	2.00E-10	0.91	3.69	-	825.3
AHQ-8-4, 2851	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.33E-07	0.84	3.25	-	940.2
AHQ-8-4, 2042 - 2115	R.VLEDRPLSDK.G	1172.31354	2	7.02E-05	0.80	2.93	-	777.3
AHQ-8-3, 2088	R.VLEDRPLSDK.G	1172.31354	2	2.37E-05	0.95	3.73	-	1512.0
AHQ-8-4, 2803	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	9.25E-07	0.93	4.38	-	1370.3
AHQ-8-3, 2829	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	6.07E-12	0.95	4.38	-	1665.9
AHQ-8-4, 3317 - 3394	K.WDTANNPLYK.E	1222.33111	2	1.27E-04	0.66	2.54	-	652.2
AHQ-8-7, 3452	K.YCECDDFSCVR.Y	1514.59674	2	8.72E-06	0.85	2.62	-	954.6
AHQ-8-3, 3525	K.YCECDDFSCVR.Y	1514.59674	2	7.74E-07	0.90	3.04	-	959.7
gi|4758086|ref|NP_004069.1|	cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain			6.65E-12	4.57	50.24	36.80	20567.3
AHQ-8-11, 4067 - 4128	K.GFGFGQGAGALVHSE	1434.53788	2	1.35E-06	0.92	4.06	-	822.4

AHQ-8-11, 3239 - 3295	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.10E-06	0.90	3.97	-	815.1
AHQ-8-11, 3236 - 3297	K.GLESTTLADKDGEIYCK.G	1902.06957	3	6.65E-12	0.92	4.60	-	847.4
AHQ-8-11, 2611	K.GYGYGQGAGTLSTDK.G	1475.54194	2	5.90E-06	0.94	3.44	-	1361.3
AHQ-8-11, 3503	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	7.96E-06	0.90	4.44	-	644.5
AHQ-8-13-, 3627	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	3.31E-07	0.82	4.17	-	354.4
AHQ-8-12, 3527	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	4.51E-04	0.42	2.69	-	305.3
AHQ-8-14-, 3539	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	8.31E-06	0.78	3.28	-	530.8
AHQ-8-11, 3455	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	9.32E-08	0.97	4.84	-	1420.8
gi|7661678|ref|NP_056461.1|	RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B			7.08E-12	4.15	50.25	35.90	20824.7
AHQ-8-14-, 5049	R.KQVEVDAQQCM*LEILDTAGTEQFTAM*R.D	3147.50488	3	1.50E-05	0.91	4.43	-	1086.9
AHQ-8-11, 3891 - 3947	R.QWNNCAFLESSAK.S	1556.68148	2	4.34E-07	0.56	2.52	-	316.8
AHQ-8-11, 4059 - 4116	R.QWNNCAFLESSAK.S	1556.68148	2	3.02E-04	0.43	2.69	-	208.0
AHQ-8-11, 3743	R.VKDTDDVPMILVGNK.C	1644.91497	2	2.32E-06	0.91	3.62	-	1185.5
AHQ-8-11, 3747	R.VKDTDDVPMILVGNK.C	1644.91497	3	1.05E-05	0.95	4.34	-	1877.9
AHQ-8-11, 4089 - 4107	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	2.09E-04	0.88	4.07	-	1211.6
AHQ-8-12, 3996 - 3999	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	3.49E-06	0.95	5.00	-	1359.1
AHQ-8-13-, 4095	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	1.49E-04	0.81	3.65	-	841.6
AHQ-8-11, 3975 - 4033	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	7.08E-12	0.88	4.60	-	1148.4
AHQ-8-11, 4139	R.VKDTDDVPM*ILVGNKCDLEDERVVGK.E	2963.33122	3	9.32E-05	0.89	4.28	-	1049.8
gi|10863977|ref|NP_067000.1|	LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-			7.96E-12	0.96	10.25	20.00	10834.5
AHQ-8-14-, 5153	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	7.96E-12	0.96	4.96	-	1263.4
AHQ-8-14, 5865	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	2.37E-10	0.96	4.33	-	1575.8
gi|4505733|ref|NP_002610.1|	platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4			8.63E-12	7.48	80.27	39.60	10844.9
AHQ-8-14, 5189 - 5246	K.AGPHCPTAQLIATLK.N	1579.84600	2	2.33E-04	0.93	4.59	-	664.9
AHQ-8-14-, 4065 - 4086	K.AGPHCPTAQLIATLK.N	1579.84600	3	5.67E-04	0.90	4.52	-	985.3
AHQ-8-14, 5025	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	8.63E-12	0.97	4.27	-	2608.4
AHQ-8-14-, 3862	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	2.67E-09	0.97	5.26	-	1231.9
AHQ-8-14-, 3977 - 4014	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	8.97E-10	0.97	5.36	-	2233.7
AHQ-8-14-, 3854 - 3861	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	4.80E-09	0.97	5.13	-	2298.5
AHQ-8-14-, 3987 - 3994	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	4.64E-09	0.97	5.31	-	1167.1
AHQ-8-14-, 3634	K.AGPHCPTAQLIATLKNGRK.I	2035.35992	3	3.79E-06	0.93	4.54	-	1235.2
AHQ-8-14-, 2661 - 2729	R.HITSLEVIK.A	1040.23825	2	8.17E-07	0.90	3.74	-	512.7
AHQ-8-14, 3742 - 3797	R.HITSLEVIK.A	1040.23825	2	3.63E-05	0.80	3.08	-	414.5
AHQ-8-14, 3617 - 3685	R.HITSLEVIK.A	1040.23825	2	4.31E-06	0.90	3.52	-	629.6
AHQ-8-13, 4905	K.ICLDLQAPLYK.K	1335.59400	2	4.88E-05	0.95	3.59	-	1755.6
AHQ-8-13-, 4742	K.ICLDLQAPLYK.K	1335.59400	2	2.50E-05	0.95	4.17	-	1461.4
AHQ-8-14, 5585	K.ICLDLQAPLYK.K	1335.59400	2	1.64E-07	0.97	4.79	-	2065.7
AHQ-8-14-, 4717	K.ICLDLQAPLYK.K	1335.59400	2	4.18E-06	0.98	4.70	-	2272.9
AHQ-8-14-, 4273	K.ICLDLQAPLYKK.I	1463.76691	2	3.41E-04	0.89	3.07	-	1519.5
AHQ-8-14-, 4401	R.KICLDLQAPLYK.K	1463.76691	2	5.03E-06	0.97	4.61	-	1597.4
AHQ-8-14-, 4405 - 4410	R.KICLDLQAPLYK.K	1463.76691	3	4.88E-04	0.89	3.70	-	1393.1
AHQ-8-14, 5301 - 5381	R.KICLDLQAPLYK.K	1463.76691	2	1.34E-06	0.94	4.36	-	1126.4
AHQ-8-14-, 3989	R.KICLDLQAPLYKK.I	1591.93982	3	2.38E-07	0.94	4.89	-	1252.1
gi|4507953|ref|NP_003397.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep			9.44E-12	5.13	60.28	27.30	27744.9
AHQ-8-10, 3152 - 3206	K.FLIPNASQAESK.V	1305.46156	2	4.55E-06	0.76	3.00	-	438.4
AHQ-8-10, 3222	K.FLIPNASQAESK.V	1305.46156	2	2.75E-04	0.73	2.72	-	426.2
AHQ-8-9, 5830 - 5968	K.SVTEQGAELSNEER.N	1549.57922	2	2.59E-04	0.68	2.69	-	562.2
AHQ-8-10, 2326 - 2384	K.SVTEQGAELSNEER.N	1549.57922	2	9.44E-12	0.95	4.32	-	1383.7
AHQ-8-11, 2297 - 2375	K.SVTEQGAELSNEER.N	1549.57922	2	3.84E-08	0.96	4.32	-	1675.5
AHQ-8-13-, 2422	K.SVTEQGAELSNEER.N	1549.57922	2	2.72E-05	0.79	3.13	-	899.0
AHQ-8-14-, 2407	K.SVTEQGAELSNEER.N	1549.57922	2	2.92E-08	0.84	3.21	-	840.1
AHQ-8-10, 6121 - 6130	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	2.92E-06	0.88	3.85	-	738.4
AHQ-8-13, 6295	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	3.34E-06	0.96	5.06	-	1262.3
AHQ-8-9, 6682	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	5.16E-07	0.96	4.90	-	1272.4
AHQ-8-13-, 6186 - 6254	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	6.39E-11	0.97	5.64	-	990.9
AHQ-8-10, 6218	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	2.00E-05	0.83	3.48	-	915.6
AHQ-8-10, 2342	R.YLAEVAAGDDK.K	1152.23595	1	7.17E-07	0.69	2.26	-	1162.3
AHQ-8-10, 2063 - 2118	R.YLAEVAAGDDKK.G	1280.40887	2	2.23E-07	0.93	3.65	-	1313.9
AHQ-8-10, 2082	R.YLAEVAAGDDKK.G	1280.40887	3	8.03E-07	0.93	3.65	-	1405.5
gi|4505981|ref|NP_002695.1|	pro-platelet basic protein (includes platelet basic protein, bet; Pro-p			9.97E-12	7.11	80.32	46.90	13894.1
AHQ-8-13-, 4572	K.EESLDSDLYAELR.C	1540.61070	2	4.55E-07	0.88	3.58	-	769.0
AHQ-8-14, 5314	K.EESLDSDLYAELR.C	1540.61070	2	9.43E-05	0.86	3.21	-	714.1
AHQ-8-14, 5441 - 5502	K.EESLDSDLYAELR.C	1540.61070	2	5.33E-06	0.92	3.93	-	886.8
AHQ-8-14-, 4294 - 4346	K.EESLDSDLYAELR.C	1540.61070	2	2.21E-07	0.84	3.38	-	527.0
AHQ-8-14-, 4549 - 4607	K.EESLDSDLYAELR.C	1540.61070	2	1.91E-06	0.90	3.91	-	751.1
AHQ-8-14-, 4514	K.GKEESLDSDLYAELR.C	1725.83517	2	3.48E-11	0.98	5.27	-	2288.6
AHQ-8-14-, 4343	K.GKEESLDSDLYAELR.C	1725.83517	2	3.05E-07	0.97	4.79	-	2344.9
AHQ-8-13, 4327	K.GKEESLDSDLYAELR.C	1725.83517	3	2.56E-04	0.88	4.10	-	1071.1
AHQ-8-14-, 4234 - 4235	K.GKEESLDSDLYAELR.C	1725.83517	2	2.20E-10	0.98	5.94	-	2882.3
AHQ-8-14, 4698	K.GKEESLDSDLYAELR.C	1725.83517	2	2.18E-04	0.93	3.44	-	1373.1
AHQ-8-13, 4324	K.GKEESLDSDLYAELR.C	1725.83517	2	1.67E-07	0.98	4.62	-	2506.1
AHQ-8-14, 4969	K.GKEESLDSDLYAELR.C	1725.83517	2	1.28E-05	0.94	4.18	-	1501.6
AHQ-8-14, 5102 - 5158	K.GKEESLDSDLYAELR.C	1725.83517	2	2.05E-10	0.98	6.36	-	2699.5
AHQ-8-14, 5117	K.GKEESLDSDLYAELR.C	1725.83517	3	1.06E-05	0.87	4.06	-	884.7
AHQ-8-14, 5203	K.GKEESLDSDLYAELR.C	1725.83517	3	1.23E-04	0.76	3.70	-	742.6
AHQ-8-14, 5217 - 5274	K.GKEESLDSDLYAELR.C	1725.83517	2	1.67E-11	0.98	6.03	-	2871.2
AHQ-8-14-, 4861 - 4881	K.GKEESLDSDLYAELR.C	1725.83517	2	5.40E-04	0.79	3.22	-	926.2
AHQ-8-14, 5346	K.GKEESLDSDLYAELR.C	1725.83517	2	3.31E-06	0.97	4.76	-	1970.4
AHQ-8-14, 5434	K.GKEESLDSDLYAELR.C	1725.83517	2	2.23E-08	0.97	5.01	-	1922.2
AHQ-8-14, 4829 - 4909	K.GKEESLDSDLYAELR.C	1725.83517	2	6.23E-10	0.98	5.07	-	2308.6
AHQ-8-14, 5515 - 5590	K.GKEESLDSDLYAELR.C	1725.83517	2	1.89E-05	0.98	5.63	-	3195.9
AHQ-8-14, 5647 - 5707	K.GKEESLDSDLYAELR.C	1725.83517	2	5.26E-06	0.96	4.31	-	1637.2
AHQ-8-14, 5801 - 5870	K.GKEESLDSDLYAELR.C	1725.83517	2	4.26E-04	0.72	3.29	-	614.4
AHQ-8-14-, 4185	K.GKEESLDSDLYAELR.C	1725.83517	3	2.06E-04	0.87	4.50	-	732.8
AHQ-8-13-, 4190	K.GKEESLDSDLYAELR.C	1725.83517	2	5.44E-11	0.98	5.78	-	2617.8
AHQ-8-12, 4059	K.GKEESLDSDLYAELR.C	1725.83517	2	8.03E-08	0.97	4.78	-	1572.1
AHQ-8-14-, 4109 - 4173	K.GKEESLDSDLYAELR.C	1725.83517	2	1.16E-11	0.98	5.95	-	2312.7
AHQ-8-14-, 5119	K.GKEESLDSDLYAELR.C	1725.83517	2	2.03E-04	0.84	3.03	-	839.4
AHQ-8-14-, 4013	K.GKEESLDSDLYAELR.C	1725.83517	3	6.94E-07	0.89	3.65	-	1078.0
AHQ-8-14-, 3993 - 4051	K.GKEESLDSDLYAELR.C	1725.83517	2	1.18E-10	0.98	5.43	-	2528.1
AHQ-8-14-, 3894 - 3957	K.GKEESLDSDLYAELR.C	1725.83517	3	5.60E-08	0.82	3.36	-	934.3
AHQ-8-14-, 3893 - 3949	K.GKEESLDSDLYAELR.C	1725.83517	2	9.89E-10	0.98	5.57	-	2523.2
AHQ-8-14-, 3754	K.GKEESLDSDLYAELR.C	1725.83517	2	9.97E-12	0.95	4.40	-	1390.6
AHQ-8-14-, 3653	K.GTHCNQVEVIATLK.D	1571.78073	2	1.15E-06	0.95	4.08	-	1302.9
AHQ-8-14-, 3417 - 3481	K.GTHCNQVEVIATLK.D	1571.78073	2	2.33E-06	0.94	3.72	-	1401.9
AHQ-8-14-, 3454 - 3511	K.GTHCNQVEVIATLK.D	1571.78073	3	4.18E-04	0.84	3.36	-	1202.8
AHQ-8-14-, 3541 - 3597	K.GTHCNQVEVIATLK.D	1571.78073	2	2.25E-11	0.97	5.19	-	1625.8
AHQ-8-14, 4342 - 4397	K.GTHCNQVEVIATLK.D	1571.78073	2	1.53E-06	0.97	4.75	-	1718.3
AHQ-8-14, 4453 - 4509	K.GTHCNQVEVIATLK.D	1571.78073	2	9.98E-06	0.98	5.38	-	1817.2
AHQ-8-13-, 3580	K.GTHCNQVEVIATLK.D	1571.78073	2	3.04E-04	0.79	3.04	-	663.9
AHQ-8-14-, 3290 - 3373	K.GTHCNQVEVIATLK.D	1571.78073	2	1.02E-10	0.97	5.06	-	1546.6
AHQ-8-14-, 3774 - 3830	K.GTHCNQVEVIATLK.D	1571.78073	2	6.17E-05	0.96	5.09	-	1406.0
AHQ-8-14, 4565 - 4629	K.GTHCNQVEVIATLK.D	1571.78073	2	9.95E-11	0.98	4.72	-	2206.6
AHQ-8-14-, 3231	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	9.85E-05	0.98	5.75	-	2215.9
AHQ-8-14-, 3150	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	2.09E-11	0.97	5.55	-	1212.5
AHQ-8-14-, 2897 - 2957	K.ICLDPDAPR.I	1058.19059	2	1.49E-04	0.91	3.73	-	1031.2
AHQ-8-14, 3749 - 3806	K.ICLDPDAPR.I	1058.19059	2	1.88E-04	0.87	3.53	-	803.3

AHQ-8-14-, 2683 - 2741	R.KICLDPDAPR.I	1186.36350	2	8.83E-04	0.85	3.37	-	726.5
AHQ-8-14, 3593 - 3649	R.KICLDPDAPR.I	1186.36350	2	7.67E-04	0.71	2.69	-	678.5
AHQ-8-13, 2869 - 2928	R.KICLDPDAPR.I	1186.36350	2	1.44E-04	0.53	2.61	-	591.4
AHQ-8-14-, 2709	R.KICLDPDAPR.I	1186.36350	2	2.19E-05	0.87	3.64	-	772.2
AHQ-8-14-, 2587 - 2645	R.KICLDPDAPR.I	1186.36350	2	1.93E-04	0.84	3.06	-	901.2
AHQ-8-14-, 3547 - 3603	K.NIQSLEVIGK.G	1101.27845	2	4.42E-05	0.78	3.08	-	659.1
AHQ-8-14-, 3338 - 3397	K.NIQSLEVIGK.G	1101.27845	2	6.40E-05	0.91	3.53	-	935.1
AHQ-8-14-, 3617	K.TTSGIHPKNIQSLEVIGK.G	1923.20305	3	4.12E-05	0.82	3.39	-	897.5
gi|5803011|ref|NP_001966.1|	enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron			1.12E-11	0.97	10.26	3.70	47268.3
AHQ-8-8, 6161	R.YITGDQLGALYQDFVR.D	1860.05915	2	1.12E-11	0.97	5.10	-	1191.3
gi|17986260|ref|NP_524147.1|	smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo			1.42E-11	0.95	10.27	23.30	12969.7
AHQ-8-14-, 5269	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	1.42E-11	0.95	5.49	-	1304.6
AHQ-8-13-, 5264	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	2.57E-05	0.93	5.05	-	885.8
gi|13124879|ref|NP_002465.1|	smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]			1.46E-11	5.71	70.32	4.00	227336.7
AHQ-8-3, 2965	K.FDQLLAEEK.N	1093.21165	2	5.83E-06	0.90	2.92	-	1325.1
AHQ-8-2, 3003	K.FDQLLAEEK.N	1093.21165	1	2.39E-04	0.47	2.09	-	760.5
AHQ-8-2, 3000	K.FDQLLAEEK.N	1093.21165	2	1.33E-05	0.92	3.36	-	1438.6
AHQ-8-5, 2925 - 2926	K.FDQLLAEEK.N	1093.21165	2	1.47E-05	0.92	3.18	-	1354.7
AHQ-8-2, 2619 - 2621	K.KEEELQAALAR.L	1258.40643	2	1.91E-05	0.90	3.39	-	1150.2
AHQ-8-6, 2543	K.KEEELQAALAR.L	1258.40643	2	7.62E-04	0.81	3.28	-	890.0
AHQ-8-5, 2554	K.KEEELQAALAR.L	1258.40643	2	4.27E-05	0.89	3.29	-	1094.9
AHQ-8-5, 2888 - 2956	R.KFDQLLAEEK.N	1221.38456	2	1.07E-05	0.67	2.67	-	737.4
AHQ-8-1, 3123	R.KFDQLLAEEK.N	1221.38456	2	1.91E-04	0.90	3.46	-	1091.6
AHQ-8-2, 5080 - 5156	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	1.02E-10	0.98	6.47	-	2011.5
AHQ-8-3, 5069	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	2.16E-06	0.97	5.70	-	1693.1
AHQ-8-2, 5268	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	4.84E-08	0.97	5.72	-	2535.5
AHQ-8-6, 4948 - 5008	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	9.16E-05	0.95	5.00	-	1333.9
AHQ-8-4, 5134	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	3.46E-05	0.86	4.31	-	948.2
AHQ-8-2, 4557 - 4563	R.NWQWWR.L	976.07459	1	7.60E-04	0.36	2.15	-	146.9
AHQ-8-2, 5959 - 5963	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.00E-08	0.96	4.24	-	1290.2
AHQ-8-2, 5744 - 5799	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.55E-10	0.96	4.42	-	1117.9
AHQ-8-6, 5634 - 5683	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.46E-11	0.95	4.59	-	821.1
AHQ-8-14-, 5694	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.01E-04	0.71	2.80	-	440.9
AHQ-8-1, 5968	K.QLLQANPILEAFGNAK.T	1727.98540	2	8.13E-06	0.87	3.35	-	682.5
AHQ-8-3, 5692 - 5754	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.90E-05	0.96	4.83	-	966.9
AHQ-8-3, 5858	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.04E-05	0.91	3.82	-	749.3
AHQ-8-6, 5798	K.QLLQANPILEAFGNAK.T	1727.98540	2	5.57E-07	0.82	3.28	-	525.9
AHQ-8-5, 5732 - 5786	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.59E-07	0.94	4.77	-	690.1
AHQ-8-4, 5791 - 5845	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.03E-04	0.95	4.19	-	1034.6
AHQ-8-1, 5799	K.QLLQANPILEAFGNAK.T	1727.98540	2	6.88E-08	0.91	3.53	-	903.7
AHQ-8-7, 5576 - 5632	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.04E-06	0.93	4.07	-	815.7
AHQ-8-2, 5855	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.15E-08	0.94	4.02	-	983.4
AHQ-8-5, 5340	K.TQLEELEDELQATEDAK.L	1963.04334	2	6.12E-09	0.98	6.25	-	1941.6
AHQ-8-4, 5387	K.TQLEELEDELQATEDAK.L	1963.04334	3	1.26E-06	0.95	5.18	-	1155.7
AHQ-8-3, 5316 - 5317	K.TQLEELEDELQATEDAK.L	1963.04334	3	3.36E-11	0.96	5.51	-	1097.8
AHQ-8-2, 5395	K.TQLEELEDELQATEDAK.L	1963.04334	3	2.23E-09	0.94	5.34	-	953.5
AHQ-8-6, 5254 - 5332	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.19E-04	0.97	5.21	-	1745.6
AHQ-8-2, 5143	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.73E-06	0.97	5.15	-	1473.2
AHQ-8-2, 3943	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.60E-09	0.98	5.99	-	1470.9
AHQ-8-1, 5408 - 5467	K.TQLEELEDELQATEDAK.L	1963.04334	2	7.09E-11	0.98	5.91	-	1712.7
AHQ-8-3, 5257 - 5312	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.85E-07	0.96	5.02	-	1161.9
gi|4503689|ref|NP_000499.1|	fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M			1.55E-11	9.11	120.26	17.00	94972.5
AHQ-8-6, 4744	K.DSHSLTTNIM*EILR.G	1646.84779	2	2.45E-05	0.95	3.63	-	1479.6
AHQ-8-10, 4559 - 4564	K.DSHSLTTNIM*EILR.G	1646.84779	2	1.73E-04	0.93	3.78	-	1152.0
AHQ-8-7, 2625 - 2705	R.EVDLKDYEDQQK.Q	1510.58460	2	1.41E-07	0.91	3.43	-	937.8
AHQ-8-8, 2645	R.EVDLKDYEDQQK.Q	1510.58460	2	1.49E-05	0.77	2.95	-	573.8
AHQ-8-6, 2650 - 2656	R.EVDLKDYEDQQK.Q	1510.58460	2	3.38E-05	0.85	3.29	-	700.6
AHQ-8-10, 2610 - 2675	R.EVDLKDYEDQQK.Q	1510.58460	2	7.29E-07	0.84	3.06	-	765.1
AHQ-8-8, 1849 - 1854	R.GGSTSYGTGSETESPR.N	1573.55765	2	1.12E-06	0.78	3.33	-	466.3
AHQ-8-6, 1880 - 1940	R.GGSTSYGTGSETESPR.N	1573.55765	2	1.12E-07	0.81	3.23	-	600.4
AHQ-8-7, 1842 - 1900	R.GGSTSYGTGSETESPR.N	1573.55765	2	1.68E-06	0.63	2.93	-	430.6
AHQ-8-9, 5187 - 5243	R.GGSTSYGTGSETESPR.N	1573.55765	2	2.87E-05	0.77	2.81	-	820.3
AHQ-8-11, 4371	K.GLIDEVNQDFTNR.I	1521.61384	2	1.21E-07	0.89	3.23	-	851.0
AHQ-8-10, 4303	K.GLIDEVNQDFTNR.I	1521.61384	2	1.09E-04	0.66	3.15	-	522.3
AHQ-8-12, 4390 - 4398	K.GLIDEVNQDFTNR.I	1521.61384	2	6.90E-05	0.88	3.31	-	779.6
AHQ-8-7, 4328 - 4384	K.GLIDEVNQDFTNR.I	1521.61384	2	2.42E-05	0.85	3.17	-	810.5
AHQ-8-7, 3850 - 3870	K.GLIDEVNQDFTNR.I	1521.61384	2	6.60E-04	0.84	3.63	-	570.9
AHQ-8-8, 4418 - 4498	K.GLIDEVNQDFTNR.I	1521.61384	2	1.54E-07	0.92	3.55	-	1026.9
AHQ-8-5, 4518	K.GLIDEVNQDFTNR.I	1521.61384	2	9.11E-09	0.91	3.67	-	938.4
AHQ-8-8, 3961	K.GLIDEVNQDFTNR.I	1521.61384	2	1.87E-05	0.88	3.73	-	675.6
AHQ-8-4, 4557 - 4565	K.GLIDEVNQDFTNR.I	1521.61384	2	1.61E-07	0.96	3.86	-	1568.7
AHQ-8-14-, 2381 - 2383	R.GSESGIFTNTK.E	1141.21317	2	3.97E-05	0.71	2.53	-	819.6
AHQ-8-6, 2326	R.GSESGIFTNTK.E	1141.21317	2	9.58E-04	0.68	2.53	-	791.2
AHQ-8-13, 2481 - 2543	R.GSESGIFTNTK.E	1141.21317	2	1.54E-05	0.81	2.69	-	963.8
AHQ-8-7, 2310	R.GSESGIFTNTK.E	1141.21317	2	1.61E-04	0.72	2.51	-	773.4
AHQ-8-13-, 2380 - 2408	R.GSESGIFTNTK.E	1141.21317	2	1.30E-05	0.74	2.68	-	658.4
AHQ-8-13-, 3272	R.HPDEAAFFDTASTGK.T	1594.66329	2	1.11E-04	0.42	2.99	-	189.6
AHQ-8-6, 3138 - 3195	R.HPDEAAFFDTASTGK.T	1594.66329	2	1.44E-04	0.55	2.59	-	377.2
AHQ-8-6, 2704 - 2782	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	1.65E-05	0.94	4.55	-	1323.4
AHQ-8-6, 2711	R.HRHPDEAAFFDTASTGK.T	1887.98954	2	1.33E-06	0.97	5.12	-	1266.1
AHQ-8-7, 2669	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	2.84E-05	0.97	5.29	-	2022.5
AHQ-8-7, 2216	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	3.66E-07	0.80	3.77	-	466.5
AHQ-8-6, 2226	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	6.72E-11	0.94	4.42	-	914.6
AHQ-8-8, 2218	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	1.55E-11	0.95	4.74	-	1216.8
AHQ-8-7, 2300	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	2.00E-04	0.76	3.03	-	737.1
AHQ-8-8, 2257	R.PGSTGTWNPGSSER.G	1433.46515	2	2.29E-08	0.84	3.48	-	527.5
AHQ-8-7, 2186 - 2264	R.PGSTGTWNPGSSER.G	1433.46515	2	1.95E-05	0.58	2.82	-	494.9
AHQ-8-6, 6332 - 6343	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	4.82E-04	0.72	3.29	-	315.2
AHQ-8-13-, 6174	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	2.49E-04	0.55	2.73	-	155.7
AHQ-8-6, 2491	K.VQHIQLLQK.N	1107.33106	1	2.27E-04	0.35	1.95	-	579.7
AHQ-8-7, 2461	K.VQHIQLLQK.N	1107.33106	1	8.36E-04	0.60	2.35	-	655.8
AHQ-8-7, 2456 - 2457	K.VQHIQLLQK.N	1107.33106	2	8.36E-04	0.77	2.82	-	599.5
gi|8393159|ref|NP_059118.1|	calmodulin-like skin protein [Homo sapiens]			1.73E-11	0.95	10.25	15.80	15920.4
AHQ-8-14-, 4902	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	1.73E-11	0.95	5.03	-	936.9
gi|21361755|ref|NP_004090.3|	stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie			1.77E-11	4.44	50.27	26.00	31708.5
AHQ-8-13, 4197	K.EASM*VITESPAALQLR.Y	1732.98059	2	4.10E-05	0.69	2.94	-	574.7
AHQ-8-10, 6162	K.GPGLFFILPCTDSFIK.V	1814.13672	2	3.48E-05	0.95	4.37	-	943.8
AHQ-8-13-, 6298	K.GPGLFFILPCTDSFIK.V	1814.13672	2	2.34E-04	0.90	4.16	-	567.5
AHQ-8-10, 2279	K.VIAAEGEMNASR.A	1248.39191	2	9.90E-07	0.92	3.52	-	832.7
AHQ-8-10, 3644 - 3648	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.30E-04	0.87	3.57	-	925.2
AHQ-8-1, 4448 - 4511	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.71E-07	0.89	4.18	-	613.8
AHQ-8-1, 4068	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.87E-06	0.84	3.34	-	671.8
AHQ-8-1, 3977	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.63E-08	0.96	4.78	-	971.0
AHQ-8-1, 3852 - 3925	R.VQNATLAVANITNADSATR.L	1931.09731	2	1.77E-11	0.96	5.33	-	1233.5
AHQ-8-13, 3983	R.YLQTLTTIAAEK.N	1352.55813	2	9.35E-04	0.92	3.55	-	1250.7
gi|4557419|ref|NP_000063.1|	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36			2.07E-11	4.32	50.22	12.90	53052.1
AHQ-8-5, 4488	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	6.43E-06	0.91	4.21	-	715.2

AHQ-8-4, 4545	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	4.32E-04	0.87	3.26	-	758.1
AHQ-8-1, 4633 - 4703	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	2.63E-07	0.76	3.25	-	517.6
AHQ-8-5, 3452	R.LQVNLLVKPSEK.I	1368.64707	2	4.54E-06	0.79	3.39	-	690.4
AHQ-8-5, 3154	K.RLQVNLLVKPSEK.I	1524.83342	3	1.67E-05	0.93	3.88	-	1466.5
AHQ-8-5, 5297	K.SQVLQFFSSDICR.S	1588.76661	2	3.12E-10	0.96	4.09	-	1566.2
AHQ-8-6, 5215	K.SQVLQFFSSDICR.S	1588.76661	2	2.22E-06	0.91	3.73	-	1090.1
AHQ-8-1, 5393	K.SQVLQFFSSDICR.S	1588.76661	2	3.10E-10	0.90	3.07	-	1235.9
AHQ-8-5, 6309 - 6372	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	2.07E-11	0.96	4.43	-	1193.3
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				2.11E-11	1.94	20.29	7.40	32164.8
AHQ-8-1, 4849	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.29E-05	0.90	4.11	-	673.9
AHQ-8-4, 4653	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.97E-07	0.77	3.17	-	522.0
AHQ-8-4, 4781	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.56E-04	0.94	4.62	-	908.5
AHQ-8-5, 4744 - 4748	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.54E-04	0.93	4.90	-	846.9
AHQ-8-5, 5178	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.11E-05	0.46	2.91	-	332.2
AHQ-8-7, 4592 - 4594	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.09E-05	0.95	4.88	-	975.0
AHQ-8-8, 4525 - 4585	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.30E-09	0.96	5.11	-	1106.5
AHQ-8-8, 4646 - 4709	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.47E-04	0.93	4.30	-	954.1
AHQ-8-8, 4697 - 4757	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	3	9.45E-04	0.87	3.55	-	1264.6
AHQ-8-8, 4778	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.75E-07	0.96	5.69	-	909.2
AHQ-8-8, 4869 - 4929	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.41E-07	0.96	5.45	-	884.1
AHQ-8-8, 4963 - 5021	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.68E-08	0.97	5.70	-	1416.2
AHQ-8-8, 5053 - 5114	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.20E-04	0.96	5.41	-	905.7
AHQ-8-8, 5173 - 5211	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.54E-04	0.95	5.14	-	857.0
AHQ-8-8, 5273 - 5335	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.22E-04	0.91	4.18	-	894.1
AHQ-8-8, 5398	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.37E-05	0.95	4.98	-	965.9
AHQ-8-8, 5483 - 5551	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.92E-04	0.65	3.44	-	389.4
AHQ-8-8, 6018 - 6075	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.87E-05	0.76	3.54	-	471.9
AHQ-8-9, 6603 - 6607	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.26E-05	0.95	4.78	-	959.4
AHQ-8-10, 4443 - 4498	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.83E-05	0.95	5.08	-	1049.2
AHQ-8-10, 4651	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.73E-05	0.77	3.12	-	520.0
AHQ-8-11, 4565	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.28E-05	0.91	4.46	-	709.3
AHQ-8-12, 4594	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.71E-05	0.91	4.11	-	929.3
AHQ-8-13, 4669 - 4697	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.11E-11	0.96	5.55	-	1122.0
AHQ-8-13, 4767 - 4823	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.34E-04	0.95	4.88	-	1059.1
AHQ-8-13, 4987	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.06E-07	0.96	4.50	-	1342.7
AHQ-8-13, 5212 - 5277	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.75E-04	0.87	4.34	-	555.2
AHQ-8-14, 5358 - 5430	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.40E-06	0.95	5.29	-	856.1
AHQ-8-14, 5485 - 5546	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.49E-06	0.96	4.53	-	1292.4
AHQ-8-14, 5601	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.26E-08	0.91	4.08	-	785.9
AHQ-8-14, 5794 - 5850	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.68E-05	0.92	4.68	-	842.9
AHQ-8-13-, 4603 - 4658	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.56E-05	0.97	5.24	-	1275.4
AHQ-8-13-, 4919 - 4975	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.99E-06	0.97	5.73	-	1184.0
AHQ-8-13-, 5039 - 5094	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	5.33E-04	0.95	5.34	-	886.6
AHQ-8-14-, 4605 - 4663	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.53E-07	0.95	4.93	-	981.0
AHQ-8-14-, 4747 - 4819	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.10E-08	0.96	5.76	-	964.4
AHQ-8-14-, 4882 - 4943	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.03E-04	0.96	5.75	-	993.7
AHQ-8-14-, 4977 - 5035	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.58E-04	0.93	4.63	-	978.1
AHQ-8-14-, 5089	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.15E-05	0.95	5.18	-	721.0
AHQ-8-14-, 5229	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.04E-05	0.82	3.49	-	695.0
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				2.15E-11	8.62	100.31	33.10	61986.9
AHQ-8-3, 5860	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.12E-05	0.93	4.77	-	1151.4
AHQ-8-14-, 5798	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.26E-08	0.96	5.53	-	1191.1
AHQ-8-13-, 5744 - 5786	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.82E-10	0.96	5.11	-	1828.0
AHQ-8-11, 5679	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.32E-04	0.82	3.68	-	1043.0
AHQ-8-2, 5961	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.48E-05	0.96	6.02	-	1171.1
AHQ-8-6, 5800	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.17E-05	0.89	4.43	-	818.2
AHQ-8-1, 5952	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.59E-04	0.95	4.92	-	1379.9
AHQ-8-5, 5904	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	5.33E-06	0.91	4.72	-	967.3
AHQ-8-4, 5941	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.84E-05	0.97	6.17	-	1806.0
AHQ-8-13-, 5443	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.80E-04	0.89	4.14	-	969.1
AHQ-8-4, 4439	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	6.74E-08	0.93	4.88	-	1279.8
AHQ-8-1, 4479 - 4548	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	8.98E-05	0.95	5.14	-	1311.9
AHQ-8-14, 5293	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	5.43E-05	0.84	3.57	-	803.5
AHQ-8-7, 4278 - 4281	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	6.14E-05	0.94	5.10	-	1113.5
AHQ-8-10, 4198	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	5.43E-09	0.95	4.65	-	1846.8
AHQ-8-13, 4993 - 5003	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	3	3.95E-04	0.65	3.38	-	618.1
AHQ-8-14-, 4787	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	1.65E-06	0.65	2.82	-	428.4
AHQ-8-13-, 4779	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	8.27E-07	0.69	3.23	-	411.4
AHQ-8-13-, 2567	R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	3225.08711	3	7.50E-06	0.96	5.90	-	1325.3
AHQ-8-1, 5123	R.HGVQELEIELQSQLSK.K	1839.03978	3	7.16E-06	0.85	4.11	-	970.0
AHQ-8-1, 5128	R.HGVQELEIELQSQLSK.K	1839.03978	2	2.38E-07	0.96	4.60	-	1534.5
AHQ-8-13-, 4931 - 4988	R.HGVQELEIELQSQLSK.K	1839.03978	2	4.32E-08	0.97	5.39	-	1606.0
AHQ-8-1, 5024	R.LASYLDKVQALEEANNDLENK.I	2378.57787	3	1.22E-04	0.78	3.35	-	951.6
AHQ-8-2, 6441	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	6.66E-05	0.86	3.98	-	610.1
AHQ-8-13-, 6230 - 6232	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	2.15E-11	0.89	4.60	-	661.1
AHQ-8-14-, 6254	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	8.45E-05	0.75	3.59	-	363.2
AHQ-8-4, 6435 - 6437	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	5.58E-08	0.91	4.54	-	538.4
AHQ-8-13, 6180	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	8.79E-04	0.65	3.08	-	902.7
AHQ-8-1, 6269 - 6323	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	6.80E-06	0.60	3.02	-	810.5
AHQ-8-2, 6304 - 6359	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	5.48E-05	0.74	3.26	-	750.0
AHQ-8-13, 3397	K.TLLDIDNTR.M	1061.17119	2	6.49E-04	0.74	2.71	-	575.4
AHQ-8-2, 3257	K.TLLDIDNTR.M	1061.17119	2	4.74E-04	0.82	2.74	-	762.1
AHQ-8-1, 3392	K.TLLDIDNTR.M	1061.17119	2	2.07E-04	0.71	2.75	-	558.0
AHQ-8-10, 3055 - 3128	K.TLLDIDNTR.M	1061.17119	2	1.29E-04	0.89	3.00	-	931.1
AHQ-8-4, 3185 - 3198	K.TLLDIDNTR.M	1061.17119	2	5.53E-05	0.85	3.11	-	788.9
AHQ-8-13-, 3180 - 3248	K.TLLDIDNTR.M	1061.17119	2	4.25E-04	0.68	2.63	-	613.9
AHQ-8-4, 3027	K.VQALEEANNDLENK.I	1587.67060	2	5.10E-08	0.97	4.79	-	1966.2
AHQ-8-3, 3054	K.VQALEEANNDLENK.I	1587.67060	2	5.58E-07	0.97	4.36	-	2055.5
AHQ-8-7, 2960	K.VQALEEANNDLENK.I	1587.67060	2	2.34E-08	0.95	3.88	-	1588.7
AHQ-8-8, 2990	K.VQALEEANNDLENK.I	1587.67060	2	2.15E-05	0.96	3.96	-	1780.9
AHQ-8-10, 2590 - 2666	K.VQALEEANNDLENK.I	1587.67060	2	1.56E-07	0.94	4.41	-	1229.5
AHQ-8-12, 3006	K.VQALEEANNDLENK.I	1587.67060	2	2.16E-05	0.88	3.69	-	880.8
AHQ-8-1, 3237	K.VQALEEANNDLENK.I	1587.67060	2	8.62E-07	0.97	4.62	-	1900.4
AHQ-8-13-, 3082 - 3095	K.VQALEEANNDLENK.I	1587.67060	2	1.06E-08	0.97	4.66	-	1959.3
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				2.37E-11	24.20	280.32	56.30	75429.7
AHQ-8-6, 3342	K.AGDALWLR.F	902.03223	2	1.08E-04	0.89	3.67	-	1065.8
AHQ-8-7, 6072	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.61E-05	0.77	3.08	-	425.8
AHQ-8-6, 6232	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.94E-04	0.56	2.81	-	403.0
AHQ-8-3, 6213	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.74E-05	0.65	2.70	-	424.6
AHQ-8-6, 6100 - 6154	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.37E-11	0.95	4.79	-	915.0
AHQ-8-5, 6242 - 6244	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.56E-07	0.96	4.87	-	925.6
AHQ-8-2, 6312	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.74E-04	0.47	2.81	-	284.2
AHQ-8-6, 6007 - 6074	R.ASFSQPLFQAVAAICR.L	1768.02967	2	3.73E-06	0.90	3.64	-	862.4
AHQ-8-6, 3143	K.DEILGIANNR.L	1115.22208	2	1.04E-05	0.94	3.21	-	1470.2
AHQ-8-6, 3551 - 3626	K.EKEPEEELYDLSK.V	1609.71294	2	8.55E-09	0.82	3.13	-	547.5
AHQ-8-6, 6234 - 6235	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	1.16E-05	0.94	4.84	-	609.0
AHQ-8-6, 3202	K.GCEVVPDVNVSGQK.F	1489.63335	1	8.88E-05	0.65	2.17	-	805.7

AHQ-8-6, 6270 - 6274	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	1.37E-07	0.95	4.54	-	1334.9
AHQ-8-6, 3146 - 3174	R.GM*PAHFSDSAQTEACYHM*LSR.P	2430.63997	3	2.04E-07	0.96	4.63	-	1939.9
AHQ-8-6, 3750	R.IDLAVGDVVK.T	1029.21223	1	4.11E-04	0.41	2.19	-	460.3
AHQ-8-6, 3760	R.IDLAVGDVVK.T	1029.21223	1	1.94E-04	0.37	2.49	-	320.6
AHQ-8-12, 3746	R.IDLAVGDVVK.T	1029.21223	1	4.24E-04	0.33	2.10	-	498.6
AHQ-8-6, 4324	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.65E-11	0.98	6.38	-	1846.7
AHQ-8-12, 4296	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.90E-07	0.97	5.70	-	1668.5
AHQ-8-6, 4598	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	2.15E-04	0.67	3.17	-	907.0
AHQ-8-6, 1819 - 1875	K.IVEQINR.K	872.00444	2	5.26E-04	0.75	2.77	-	573.9
AHQ-8-6, 2766 - 2846	R.KDEILGIANNR.L	1243.39499	2	1.58E-04	0.89	2.89	-	1328.1
AHQ-8-6, 2707 - 2767	R.KDEILGIANNR.L	1243.39499	3	5.45E-05	0.90	3.52	-	1311.5
AHQ-8-6, 2680 - 2751	R.KDEILGIANNR.L	1243.39499	2	5.76E-07	0.95	4.11	-	1521.5
AHQ-8-12, 2728 - 2742	R.KDEILGIANNR.L	1243.39499	2	5.56E-04	0.94	3.27	-	1596.1
AHQ-8-6, 2906	R.KDEILGIANNR.L	1243.39499	2	7.36E-06	0.88	2.85	-	1373.4
AHQ-8-6, 3936 - 3994	R.KQDWSDHAIWWEQK.R	1858.00504	2	4.01E-04	0.87	3.96	-	816.1
AHQ-8-6, 3988 - 3995	R.KQDWSDHAIWWEQK.R	1858.00504	3	5.49E-08	0.95	4.74	-	1407.4
AHQ-8-6, 5956	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	6.60E-05	0.66	3.05	-	500.4
AHQ-8-7, 5172	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.76E-04	0.74	3.45	-	371.2
AHQ-8-7, 6009 - 6012	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	9.54E-06	0.91	4.11	-	804.1
AHQ-8-6, 5238	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.20E-07	0.89	3.60	-	801.8
AHQ-8-6, 6058 - 6115	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	2.33E-07	0.89	4.02	-	701.3
AHQ-8-5, 6180	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	4.10E-04	0.76	3.33	-	615.8
AHQ-8-6, 5455	K.LLVPSPEGMSEIYLR.C	1705.01201	3	3.05E-04	0.97	4.68	-	2063.0
AHQ-8-7, 4529 - 4593	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	2.56E-05	0.48	2.86	-	189.2
AHQ-8-6, 5426 - 5482	K.LLVPSPEGMSEIYLR.C	1705.01201	2	4.19E-04	0.87	3.31	-	621.3
AHQ-8-8, 6377	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	5.90E-07	0.92	4.35	-	1175.8
AHQ-8-6, 6210	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	4.48E-11	0.96	5.43	-	1303.6
AHQ-8-4, 6374	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	3.18E-04	0.82	3.59	-	1003.8
AHQ-8-3, 6282	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	9.94E-05	0.86	3.74	-	1136.8
AHQ-8-7, 6161 - 6168	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.84E-07	0.91	4.40	-	1010.1
AHQ-8-6, 2407 - 2467	R.LTQLYEQAR.W	1122.25622	2	2.38E-06	0.89	2.97	-	1127.9
AHQ-8-7, 2420 - 2428	R.LTQLYEQAR.W	1122.25622	2	2.69E-04	0.85	3.05	-	949.2
AHQ-8-6, 3796	R.PQPPPDPLLLQR.L	1371.60951	3	1.48E-06	0.84	3.59	-	1000.3
AHQ-8-5, 4017 - 4018	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	9.62E-08	0.88	3.70	-	543.2
AHQ-8-6, 3951	K.SQDEAPGDPIQQLNLK.G	1753.89174	3	2.61E-05	0.88	3.55	-	1099.8
AHQ-8-6, 3895 - 3970	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.44E-10	0.86	3.51	-	452.9
AHQ-8-6, 5019	K.SQDEAPGDPIQQLNLKGCEVVPDVNVSGQK.F	3224.50249	3	1.38E-06	0.67	3.30	-	468.7
AHQ-8-6, 4186 - 4251	K.TASGDYIDSSWELR.V	1600.66783	2	1.52E-08	0.95	4.20	-	1084.6
AHQ-8-13-, 4280	K.TASGDYIDSSWELR.V	1600.66783	2	3.97E-04	0.94	3.87	-	1140.1
AHQ-8-7, 4130	K.TASGDYIDSSWELR.V	1600.66783	2	9.04E-07	0.90	3.66	-	838.1
AHQ-8-14-, 4262	K.TASGDYIDSSWELR.V	1600.66783	2	2.55E-07	0.92	3.80	-	944.8
AHQ-8-6, 3823	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	5.57E-05	0.89	4.15	-	576.2
AHQ-8-6, 6390	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	8.71E-09	0.95	5.31	-	1499.2
AHQ-8-7, 3813 - 3817	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.53E-07	0.94	4.22	-	1038.8
AHQ-8-6, 3872	R.VFVGEEDPEAESVTLR.V	1777.91007	3	8.24E-05	0.97	5.10	-	2322.3
AHQ-8-6, 3851 - 3890	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.27E-08	0.96	4.65	-	1458.2
AHQ-8-13-, 3930	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.71E-07	0.85	3.34	-	1139.3
AHQ-8-3, 3949	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.05E-04	0.86	3.16	-	945.2
AHQ-8-14-, 3891 - 3918	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.25E-06	0.88	3.54	-	903.8
AHQ-8-14, 4797	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.01E-04	0.87	3.18	-	1357.0
AHQ-8-12, 3850	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.74E-06	0.78	3.01	-	630.8
AHQ-8-4, 3969	R.VFVGEEDPEAESVTLR.V	1777.91007	2	9.38E-08	0.91	3.85	-	951.1
AHQ-8-8, 3925	R.VFVGEEDPEAESVTLR.V	1777.91007	2	8.44E-08	0.92	3.95	-	981.0
AHQ-8-5, 3938	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.10E-09	0.95	4.64	-	1191.1
AHQ-8-11, 3831	R.VFVGEEDPEAESVTLR.V	1777.91007	2	7.11E-06	0.67	2.62	-	632.7
AHQ-8-2, 4024 - 4101	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.64E-04	0.82	3.37	-	1018.4
AHQ-8-5, 2948	R.VTGESHIGGVLLK.I	1310.52448	2	1.20E-04	0.91	3.74	-	1131.5
AHQ-8-7, 2873	R.VTGESHIGGVLLK.I	1310.52448	2	6.03E-06	0.96	4.45	-	1523.3
AHQ-8-6, 2910 - 2966	R.VTGESHIGGVLLK.I	1310.52448	2	1.60E-08	0.96	4.28	-	1596.0
AHQ-8-11, 4511 - 4580	K.VVLAGGVAPALFR.G	1270.54832	2	8.89E-04	0.96	3.46	-	1972.9
AHQ-8-7, 4566	K.VVLAGGVAPALFR.G	1270.54832	2	1.56E-07	0.97	4.97	-	1887.1
AHQ-8-5, 4736	K.VVLAGGVAPALFR.G	1270.54832	2	9.70E-07	0.97	4.88	-	1706.2
AHQ-8-6, 4630	K.VVLAGGVAPALFR.G	1270.54832	2	2.04E-06	0.97	4.75	-	1590.5
AHQ-8-3, 4753	K.VVLAGGVAPALFR.G	1270.54832	2	2.19E-08	0.93	3.87	-	1131.6
AHQ-8-6, 2566 - 2662	K.YGILADAR.L	878.99544	2	3.83E-05	0.91	3.30	-	957.2
gi|4504349|ref|NP_000509.1|	beta globin [Homo sapiens]			2.71E-11	8.06	90.29	64.60	15998.3
AHQ-8-14-, 3189 - 3247	K.EFTPPVQAAYQK.V	1379.54213	2	5.03E-04	0.61	2.86	-	515.0
AHQ-8-13, 4896 - 4971	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	3.44E-04	0.85	3.52	-	831.9
AHQ-8-13-, 4802 - 4851	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.65E-06	0.93	4.75	-	487.5
AHQ-8-13, 4995 - 5060	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	2.00E-07	0.88	3.99	-	518.3
AHQ-8-13-, 4722 - 4795	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	9.87E-06	0.93	4.20	-	788.2
AHQ-8-13-, 5288 - 5292	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	2.48E-10	0.97	5.31	-	1012.9
AHQ-8-13-, 4812	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	1.06E-06	0.93	3.95	-	1459.1
AHQ-8-14-, 5314	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	2.57E-09	0.94	4.73	-	718.0
AHQ-8-13-, 3630 - 3631	K.GTFATLSELHCDK.L	1480.62492	2	1.22E-09	0.78	3.34	-	524.0
AHQ-8-13-, 4831	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	2.46E-10	0.95	4.67	-	1493.4
AHQ-8-13-, 4678 - 4686	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	2.40E-09	0.95	5.43	-	1150.6
AHQ-8-13, 4873	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	9.37E-07	0.92	4.56	-	879.7
AHQ-8-13-, 4684	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	6.99E-10	0.96	4.80	-	1304.9
AHQ-8-13-, 4794 - 4863	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	2.22E-07	0.88	3.93	-	645.2
AHQ-8-13, 4947	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.18E-04	0.74	3.20	-	613.6
AHQ-8-14-, 4961	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	3.81E-07	0.82	3.24	-	641.8
AHQ-8-13-, 4782	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	4.84E-10	0.95	4.90	-	1022.1
AHQ-8-13, 5077 - 5111	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	9.04E-09	0.97	5.17	-	1632.1
AHQ-8-13-, 4864	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.66E-10	0.97	4.61	-	1915.6
AHQ-8-13-, 4954 - 5014	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.71E-11	0.98	5.85	-	1991.9
AHQ-8-13-, 4955	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	2.15E-08	0.79	3.42	-	492.6
AHQ-8-13-, 5115	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	6.86E-08	0.59	3.08	-	402.9
AHQ-8-14-, 4953	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.09E-08	0.96	4.30	-	1614.9
AHQ-8-14-, 3261	K.VNVDEVGGEALGR.L	1315.41484	2	1.81E-06	0.97	5.24	-	1769.6
AHQ-8-13, 3377 - 3440	K.VNVDEVGGEALGR.L	1315.41484	2	3.15E-06	0.98	4.97	-	2075.6
AHQ-8-13-, 3228 - 3291	K.VNVDEVGGEALGR.L	1315.41484	2	5.19E-06	0.96	4.66	-	1366.1
AHQ-8-13-, 2543 - 2606	K.VVAGVANALAHK.Y	1150.35593	2	2.22E-06	0.95	3.88	-	1568.3
AHQ-8-13-, 2779 - 2838	K.VVAGVANALAHK.Y	1150.35593	2	4.83E-04	0.81	2.69	-	903.4
gi|17921989|ref|NP_005991.1|	tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain			2.97E-11	11.07	130.27	40.20	49924.1
AHQ-8-13-, 4488 - 4560	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	2.24E-05	0.97	5.31	-	1884.1
AHQ-8-7, 4434	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	4.01E-05	0.94	4.12	-	1346.5
AHQ-8-12, 5024 - 5078	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.12E-07	0.84	3.37	-	827.7
AHQ-8-7, 5584 - 5653	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	6.18E-06	0.95	4.48	-	1467.7
AHQ-8-13-, 4990	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.07E-04	0.94	3.96	-	1330.1
AHQ-8-13-, 5630	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	9.85E-09	0.96	4.98	-	1553.8
AHQ-8-7, 4880	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	8.08E-05	0.82	3.20	-	885.7
AHQ-8-13-, 5636	R.AVCMLSNTTAIAEAWAR.L	1867.13992	3	2.11E-04	0.82	3.96	-	951.2
AHQ-8-13, 5132	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	2.04E-04	0.91	3.50	-	1245.0
AHQ-8-13-, 5638	R.AVFVDLEPTVIDEIR.N	1716.95615	2	3.75E-07	0.91	3.56	-	1459.3
AHQ-8-7, 5521 - 5593	R.AVFVDLEPTVIDEIR.N	1716.95615	2	6.06E-05	0.56	2.94	-	700.6
AHQ-8-7, 4629	K.AYHEQLSVAEITNACFEPANQM*VK.C	2769.06010	3	2.75E-05	0.87	3.59	-	1022.8

AHQ-8-7, 4828 - 4889	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.84E-04	0.94	4.04	-	808.7
AHQ-8-7, 4726 - 4808	R.IHFPLATYAPVISAEK.A	1758.05310	2	8.46E-04	0.95	4.52	-	754.2
AHQ-8-13-, 6194 - 6195	R.LISQIVSSITASLR.F	1488.75471	2	2.40E-07	0.95	4.74	-	1004.7
AHQ-8-8, 6389	R.LISQIVSSITASLR.F	1488.75471	2	2.76E-07	0.85	3.20	-	713.9
AHQ-8-7, 6172	R.LISQIVSSITASLR.F	1488.75471	2	5.11E-04	0.91	3.94	-	907.2
AHQ-8-14-, 6217	R.LISQIVSSITASLR.F	1488.75471	2	4.87E-08	0.94	4.18	-	1007.0
AHQ-8-13-, 3506 - 3519	R.NLDIERPTYTNLNR.L	1719.88022	2	7.91E-07	0.56	3.15	-	261.0
AHQ-8-14-, 3495	R.NLDIERPTYTNLNR.L	1719.88022	2	5.46E-05	0.65	2.81	-	474.9
AHQ-8-12, 5286 - 5287	R.SIQFVDWCPTGFK.V	1586.79232	2	1.76E-04	0.63	2.95	-	490.5
AHQ-8-7, 5313 - 5332	R.SIQFVDWCPTGFK.V	1586.79232	2	2.35E-04	0.94	3.94	-	1130.6
AHQ-8-13-, 5390	R.SIQFVDWCPTGFK.V	1586.79232	2	5.48E-05	0.78	2.98	-	649.3
AHQ-8-11, 5279 - 5292	R.SIQFVDWCPTGFK.V	1586.79232	2	4.05E-04	0.90	3.20	-	1025.7
AHQ-8-14-, 5298 - 5326	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	4.66E-08	0.91	4.45	-	575.4
AHQ-8-13, 5457	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.97E-11	0.80	3.50	-	535.1
AHQ-8-7, 5186 - 5244	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	4.92E-09	0.86	3.68	-	554.6
AHQ-8-12, 5218	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.56E-07	0.58	3.09	-	305.7
AHQ-8-7, 5206	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	8.95E-09	0.90	4.07	-	656.8
AHQ-8-13-, 5320	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	6.52E-09	0.88	3.95	-	525.2
AHQ-8-11, 5173 - 5204	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.87E-04	0.81	3.61	-	481.3
AHQ-8-7, 5300	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	4.81E-06	0.82	3.61	-	516.1
AHQ-8-13, 4379 - 4435	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.02E-04	0.80	3.22	-	447.9
AHQ-8-14-, 4275 - 4354	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	8.66E-05	0.75	3.10	-	453.4
AHQ-8-13, 4428 - 4497	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.02E-06	0.73	3.25	-	318.1
AHQ-8-12, 4179 - 4242	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.45E-08	0.84	3.70	-	437.8
AHQ-8-12, 3807	K.YM*ACCLLYR.G	1268.50804	2	1.19E-04	0.73	2.61	-	432.8
AHQ-8-7, 3797	K.YM*ACCLLYR.G	1268.50804	2	6.50E-04	0.72	2.65	-	477.9
AHQ-8-7, 4224 - 4236	K.YMACCLLYR.G	1252.50864	2	1.21E-05	0.95	3.47	-	1000.9
gi|4503715|ref|NP_000500.1|	fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]			3.25E-11	12.31	150.27	46.70	49481.2
AHQ-8-8, 4530	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	4.50E-04	0.60	3.09	-	338.1
AHQ-8-7, 4349	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	1.88E-04	0.80	3.83	-	410.7
AHQ-8-7, 3969	K.AIQLTYNPDESSKPNM*IDAATLK.S	2537.82826	2	2.93E-04	0.61	2.96	-	309.9
AHQ-8-8, 4011	K.AIQLTYNPDESSKPNM*IDAATLK.S	2537.82826	3	8.20E-06	0.80	3.54	-	717.0
AHQ-8-7, 4436	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	8.59E-07	0.83	3.86	-	554.0
AHQ-8-13-, 5154 - 5211	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	9.06E-07	0.84	3.71	-	507.0
AHQ-8-13-, 5282 - 5346	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	5.79E-07	0.72	2.62	-	739.3
AHQ-8-7, 5068 - 5125	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.37E-07	0.69	2.74	-	709.3
AHQ-8-7, 5170 - 5224	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	2.46E-07	0.79	3.33	-	476.7
AHQ-8-14-, 5282 - 5337	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	6.59E-04	0.71	3.19	-	444.7
AHQ-8-7, 2801 - 2822	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	1.63E-06	0.98	5.19	-	2495.1
AHQ-8-7, 2689 - 2744	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	2.39E-04	0.97	5.47	-	1870.6
AHQ-8-8, 2722	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.10E-04	0.91	4.12	-	849.3
AHQ-8-7, 2728 - 2804	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	1.22E-07	0.97	5.15	-	1113.0
AHQ-8-7, 3054	R.DNCCILDER.F	1197.27847	2	8.20E-05	0.84	3.09	-	737.7
AHQ-8-7, 4988 - 5008	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.22E-08	0.93	4.52	-	805.4
AHQ-8-8, 5059	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.11E-06	0.85	3.84	-	400.0
AHQ-8-7, 4896 - 4952	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.01E-04	0.94	4.66	-	744.1
AHQ-8-7, 4897 - 4968	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	3	1.43E-05	0.93	4.54	-	1588.9
AHQ-8-8, 4426 - 4474	K.IHLISTQSAIPYALR.V	1683.97576	2	3.25E-11	0.95	4.47	-	1017.2
AHQ-8-10, 4295	K.IHLISTQSAIPYALR.V	1683.97576	2	1.07E-04	0.89	3.60	-	894.8
AHQ-8-7, 4312 - 4348	K.IHLISTQSAIPYALR.V	1683.97576	2	3.17E-08	0.95	4.27	-	1281.7
AHQ-8-8, 2169	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	5.19E-07	0.94	4.05	-	1415.2
AHQ-8-7, 2148 - 2204	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.87E-08	0.94	4.10	-	1196.0
AHQ-8-13-, 2263 - 2324	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	3.42E-05	0.83	3.60	-	674.7
AHQ-8-14-, 2230	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	8.17E-05	0.90	3.56	-	964.9
AHQ-8-7, 3726 - 3784	K.QSGLYFIKPLK.A	1294.56665	2	9.25E-04	0.70	2.87	-	411.8
AHQ-8-7, 3016	R.TSTADYAMFK.V	1135.27203	1	2.54E-05	0.10	2.18	-	130.2
AHQ-8-7, 3752	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	8.05E-06	0.91	4.25	-	1006.7
AHQ-8-7, 3845 - 3849	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	1.12E-05	0.54	3.20	-	496.3
AHQ-8-7, 3905 - 3982	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	1.73E-10	0.94	5.30	-	1057.2
AHQ-8-8, 4006	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	1.22E-05	0.83	3.82	-	689.2
AHQ-8-7, 3198 - 3257	R.VELEDWNGR.T	1118.18129	2	3.80E-05	0.88	2.87	-	1094.1
AHQ-8-12, 3079	K.YEASILTHDSSIR.Y	1492.61564	2	2.28E-05	0.65	2.59	-	494.4
AHQ-8-7, 3004 - 3065	K.YEASILTHDSSIR.Y	1492.61564	2	6.24E-08	0.94	4.32	-	900.1
AHQ-8-11, 3069	K.YEASILTHDSSIR.Y	1492.61564	2	9.07E-07	0.76	2.58	-	711.8
AHQ-8-8, 2702 - 2761	R.YLQEIYNSNNQK.I	1514.62131	2	1.63E-06	0.90	3.76	-	952.0
AHQ-8-7, 2724 - 2780	R.YLQEIYNSNNQK.I	1514.62131	2	1.66E-04	0.97	5.26	-	1564.5
AHQ-8-11, 2748 - 2804	R.YLQEIYNSNNQK.I	1514.62131	2	1.10E-04	0.96	4.78	-	1352.6
gi|29730023|ref|XP_291482.1|	similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno			3.51E-11	4.84	60.26	13.80	63563.0
AHQ-8-5, 4344 - 4352	K.ELEEIVQPIISK.L	1398.62680	2	3.30E-05	0.96	4.04	-	1488.9
AHQ-8-5, 4624	R.IINKPTAAAIAYGLDK.R	1659.95097	2	3.51E-11	0.92	5.12	-	955.7
AHQ-8-6, 4327	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	4.02E-06	0.52	3.17	-	563.2
AHQ-8-6, 3454	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	5.35E-06	0.86	3.99	-	478.2
AHQ-8-5, 3486	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	6.41E-04	0.85	3.54	-	750.6
AHQ-8-7, 3418	K.NQLTSNPKNTVFDAK.R	1677.84011	2	7.27E-04	0.27	2.67	-	336.2
AHQ-8-5, 3500 - 3516	K.NQLTSNPKNTVFDAK.R	1677.84011	2	3.77E-04	0.73	3.84	-	632.7
AHQ-8-6, 3470	K.NQLTSNPKNTVFDAK.R	1677.84011	2	6.41E-05	0.65	3.97	-	412.5
AHQ-8-6, 4582 - 4658	K.TFAPKEISAM*VLTK.M	1552.86064	2	2.04E-04	0.55	2.74	-	691.6
AHQ-8-5, 4729	K.TFAPKEISAM*VLTK.M	1552.86064	2	5.68E-08	0.93	3.74	-	1490.3
AHQ-8-5, 4593 - 4654	K.TFAPKEISAM*VLTK.M	1552.86064	2	1.16E-04	0.82	2.89	-	1087.0
gi|5802974|ref|NP_006784.1|	peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide			3.95E-11	1.85	20.29	9.80	27692.5
AHQ-8-11, 5044 - 5121	R.DYGVLLEGSGLALR.G	1463.66058	2	3.95E-11	0.98	5.79	-	1922.5
AHQ-8-11, 3012 - 3083	K.HLSVNDLPVGR.S	1207.36435	2	1.60E-05	0.87	3.46	-	682.0
gi|4757712|ref|NP_004026.1|	acyl-Coenzyme A oxidase isoform a; acyl-coenzyme A oxidase 1 [Homo sapi			4.14E-11	0.91	10.21	3.60	74745.4
AHQ-8-6, 5850	R.INEGIGQGDLSELPELHALTAGLK.A	2476.76782	3	4.14E-11	0.91	4.11	-	930.1
gi|4505735|ref|NP_002611.1|	platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H			4.60E-11	1.89	20.30	25.00	11552.6
AHQ-8-14-, 3679	R.AEAEEDGDLQCLCVK.T	1739.86036	2	3.07E-05	0.84	3.43	-	544.4
AHQ-8-14-, 3789 - 3790	R.AEAEEDGDLQCLCVK.T	1739.86036	2	4.60E-11	0.98	6.00	-	1565.8
AHQ-8-14, 4706	R.AEAEEDGDLQCLCVK.T	1739.86036	2	1.88E-06	0.95	4.17	-	1355.3
AHQ-8-14-, 4721	K.ICLDLQALLYK.K	1351.63656	2	3.64E-04	0.91	3.52	-	1286.6
gi|29741246|ref|XP_294070.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			5.58E-11	0.90	10.18	4.30	35032.0
AHQ-8-13-, 5316 - 5374	K.LVINGNPITIFQER.D	1614.87029	2	5.58E-11	0.90	3.24	-	1109.6
AHQ-8-13-, 5430	K.LVINGNPITIFQER.D	1614.87029	2	2.42E-05	0.91	3.60	-	933.9
AHQ-8-14-, 5327	K.LVINGNPITIFQER.D	1614.87029	2	2.56E-09	0.92	3.30	-	1002.4
AHQ-8-13, 5375 - 5445	K.LVINGNPITIFQER.D	1614.87029	2	2.98E-06	0.84	2.55	-	967.4
gi|5902134|ref|NP_009005.1|	coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin			7.15E-11	1.79	20.28	10.60	51026.0
AHQ-8-7, 6176	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	7.15E-11	0.94	5.50	-	621.7
AHQ-8-7, 6244	R.YFEITSEAPFLHYLSM*FSSK.E	2414.71688	3	9.05E-06	0.85	4.11	-	700.8
gi|21956645|ref|NP_665807.1|	myotrophin; granule cell differentiation protein [Homo sapiens]			7.37E-11	1.93	20.28	25.40	12894.7
AHQ-8-14-, 3997 - 4053	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	4.50E-05	0.96	4.56	-	1336.1
AHQ-8-13, 4107 - 4187	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.37E-11	0.97	5.63	-	1092.4
AHQ-8-14, 4730 - 4789	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	4.91E-05	0.81	3.27	-	749.0
AHQ-8-14, 4785 - 4845	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.59E-07	0.97	5.31	-	1161.3
AHQ-8-14, 4849 - 4911	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.92E-04	0.87	3.58	-	805.5
AHQ-8-14, 4901 - 4966	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.49E-09	0.96	5.00	-	1286.9
AHQ-8-14-, 3950	K.GPDGLTAFEATDNQAIK.A	1748.87196	3	8.16E-04	0.90	3.62	-	1204.0
AHQ-8-14-, 3858 - 3934	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.09E-07	0.97	4.81	-	1432.9
AHQ-8-13-, 3938 - 3994	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.06E-08	0.96	4.42	-	1205.8

AHQ-8-13-, 4075 - 4091	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.35E-10	0.96	4.97	-	1234.2
AHQ-8-13-, 3663 - 3728	K.NGDLDEVKDYVAK.G	1466.57496	2	1.96E-08	0.84	3.32	-	848.0
AHQ-8-13-, 3574	K.NGDLDEVKDYVAK.G	1466.57496	2	4.74E-07	0.94	3.89	-	1188.3
AHQ-8-14-, 3557	K.NGDLDEVKDYVAK.G	1466.57496	2	1.62E-08	0.96	4.22	-	1413.3
AHQ-8-13, 3741 - 3817	K.NGDLDEVKDYVAK.G	1466.57496	2	1.21E-05	0.81	3.09	-	768.1
gi|24797067|ref|NP_002107.3|	major histocompatibility complex, class I, A precursor; HLA-A1 class I			8.42E-11	4.20	50.29	16.70	40840.5
AHQ-8-8, 4813	R.APWIEQEGPEYWDQETR.N	2135.23420	2	1.36E-06	0.93	4.20	-	916.5
AHQ-8-8, 3375	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	3	1.81E-05	0.77	3.30	-	643.6
AHQ-8-8, 3282	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	2	2.08E-06	0.72	3.43	-	349.7
AHQ-8-8, 4785 - 4843	R.FIAVGYVDDTQFVR.F	1630.82504	2	8.42E-11	0.98	5.70	-	2246.4
AHQ-8-11, 3337	K.WAAVVVPSGEEQR.Y	1428.57478	2	2.86E-05	0.62	2.52	-	728.3
AHQ-8-8, 3311	R.YTCHVQHEGLPKPLTLR.W	2051.35781	3	1.30E-06	0.94	4.89	-	1699.6
gi|4759300|ref|NP_004772.1|	vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated			8.62E-11	2.87	30.26	33.00	11309.0
AHQ-8-13-, 3579	R.ADALQAGASQFETSAAK.L	1666.77095	2	4.48E-04	0.94	4.54	-	829.7
AHQ-8-14-, 3493 - 3561	R.ADALQAGASQFETSAAK.L	1666.77095	2	7.86E-07	0.93	4.06	-	1066.8
AHQ-8-13-, 4563	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	2.20E-05	0.97	4.75	-	1456.3
AHQ-8-13-, 4720	R.LQQTQNQVDEVVDIMR.V	1917.13404	2	1.86E-05	0.97	5.13	-	1606.5
AHQ-8-13-, 3692	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	8.62E-11	0.96	4.53	-	1756.3
AHQ-8-13, 3837	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	5.71E-04	0.93	3.64	-	1290.7
gi|4504345|ref|NP_000508.1|	alpha 2 globin [Homo sapiens]			8.77E-11	4.71	50.31	50.70	15257.4
AHQ-8-13-, 4218	K.FLASVSTVLTSK.Y	1253.46970	2	4.00E-04	0.90	3.61	-	1137.2
AHQ-8-13, 4375	K.FLASVSTVLTSK.Y	1253.46970	2	1.40E-06	0.92	3.81	-	1229.7
AHQ-8-14, 5299	K.FLASVSTVLTSK.Y	1253.46970	2	6.00E-04	0.88	3.24	-	1002.9
AHQ-8-13, 4181 - 4193	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	8.06E-06	0.85	3.29	-	698.2
AHQ-8-13, 4175 - 4231	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	2.26E-08	0.89	3.77	-	726.6
AHQ-8-13-, 3979 - 4034	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	1.15E-08	0.91	4.52	-	650.1
AHQ-8-13-, 4007 - 4066	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	3.30E-09	0.93	4.47	-	764.5
AHQ-8-13-, 5912	K.VADALTNAVAHVDDMPNALSALSDLHAHK.L	2998.32055	3	1.69E-04	0.93	4.26	-	1545.6
AHQ-8-13-, 5279	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	1.28E-04	0.97	6.19	-	1484.6
AHQ-8-13, 2969	K.VGAHAGEYGAEALER.M	1530.62397	2	2.83E-06	0.86	2.77	-	959.6
AHQ-8-13, 2856 - 2911	K.VGAHAGEYGAEALER.M	1530.62397	2	7.25E-05	0.97	4.45	-	1743.6
AHQ-8-13-, 2683 - 2747	K.VGAHAGEYGAEALER.M	1530.62397	3	8.65E-05	0.96	4.88	-	2048.0
AHQ-8-13-, 2684 - 2748	K.VGAHAGEYGAEALER.M	1530.62397	2	8.77E-11	0.96	4.22	-	1512.4
AHQ-8-13, 2852 - 2927	K.VGAHAGEYGAEALER.M	1530.62397	3	8.36E-04	0.96	5.69	-	1688.9
AHQ-8-14-, 2637	K.VGAHAGEYGAEALER.M	1530.62397	2	2.68E-09	0.96	4.23	-	1485.5
AHQ-8-14-, 2638	K.VGAHAGEYGAEALER.M	1530.62397	3	9.74E-04	0.95	5.18	-	1607.3
gi|30148492|ref|XP_293610.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			9.71E-11	2.71	30.24	4.30	72113.4
AHQ-8-6, 2327 - 2350	R.FDDAVVQSDM*K.H	1271.37908	2	7.26E-05	0.93	3.68	-	906.3
AHQ-8-6, 4479 - 4558	R.IINEPTAAAIAYGLDK.K	1660.89259	2	9.71E-11	0.89	4.82	-	909.9
AHQ-8-7, 4477	R.IINEPTAAAIAYGLDK.K	1660.89259	2	8.15E-10	0.82	4.06	-	755.5
AHQ-8-6, 4222	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	2.15E-09	0.89	3.97	-	618.0
gi|4758012|ref|NP_004850.1|	clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]			9.94E-11	9.98	120.31	12.80	191612.6
AHQ-8-3, 6353 - 6418	K.AFM*TADLPNELIELLEK.I	1964.26896	2	6.54E-04	0.31	2.80	-	239.3
AHQ-8-3, 6448	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	1.20E-09	0.96	5.56	-	1564.1
AHQ-8-4, 4622	R.GQFSTDELVAEVEK.R	1552.66462	2	7.35E-08	0.94	4.34	-	1106.4
AHQ-8-3, 2116 - 2184	R.IHEGCEEPATHNALAK.I	1778.92458	2	4.53E-04	0.69	2.82	-	471.0
AHQ-8-3, 4952 - 5029	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	4.45E-10	0.93	4.21	-	1127.1
AHQ-8-3, 5036	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	5.70E-07	0.92	4.04	-	1250.2
AHQ-8-3, 6321	R.KFDVNTSAVQVLIEHIGNLDR.A	2369.66218	3	4.44E-06	0.98	6.26	-	2375.9
AHQ-8-3, 6148	R.LPVVIGGLLDVDCSEDVIK.N	2043.36744	2	6.00E-04	0.94	4.11	-	1104.3
AHQ-8-3, 5812	R.NLQNLLILTAIK.A	1354.66353	2	4.51E-04	0.97	4.95	-	1728.2
AHQ-8-3, 6256 - 6258	R.RPLIDQVVQTALSETQDPEEVSVTVK.A	2883.20103	3	4.01E-04	0.90	4.11	-	983.7
AHQ-8-3, 6310	K.VGYTPDWIFLLR.N	1480.73443	2	9.94E-11	0.81	3.38	-	515.5
AHQ-8-3, 3138	K.VIQCFAETGQVQK.I	1509.70940	2	6.41E-04	0.84	2.63	-	1514.7
AHQ-8-3, 5001 - 5078	K.WLLLTGISAQQNR.V	1500.72728	2	2.34E-05	0.72	3.13	-	586.8
gi|9257257|ref|NP_059830.1|	WD repeat-containing protein 1 isoform 1 [Homo sapiens]			1.02E-10	0.74	10.16	3.80	66193.1
AHQ-8-6, 4864 - 4891	K.VVTVFSVADGYSENNVFYGHHAK.I	2541.75861	3	1.02E-10	0.74	3.29	-	623.2
gi|4557703|ref|NP_000414.1|	keratin 2a [Homo sapiens]			1.10E-10	20.35	230.28	42.60	65864.9
AHQ-8-2, 2199 - 2265	K.AQYEEIAQR.S	1108.18640	2	7.59E-04	0.84	3.30	-	971.2
AHQ-8-2, 2919	K.DVDNAYMIK.V	1069.21359	2	1.43E-04	0.88	3.57	-	565.5
AHQ-8-2, 3524 - 3532	R.DYQELMNVK.L	1140.29181	2	3.82E-04	0.89	3.39	-	1015.4
AHQ-8-1, 6335	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	9.15E-05	0.95	5.69	-	942.2
AHQ-8-4, 6338	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	3.92E-06	0.94	5.61	-	913.1
AHQ-8-7, 6129	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	4.21E-04	0.68	3.21	-	649.7
AHQ-8-11, 3008 - 3075	R.FLEQQNQVLQTK.W	1476.65935	2	1.40E-07	0.96	4.37	-	1814.7
AHQ-8-10, 3082 - 3084	R.FLEQQNQVLQTK.W	1476.65935	2	1.33E-05	0.93	4.18	-	1370.0
AHQ-8-12, 3022	R.FLEQQNQVLQTK.W	1476.65935	2	1.70E-06	0.97	4.09	-	2000.8
AHQ-8-13, 3221 - 3243	R.FLEQQNQVLQTK.W	1476.65935	2	3.51E-05	0.96	4.42	-	1637.1
AHQ-8-13-, 3088	R.FLEQQNQVLQTK.W	1476.65935	2	1.15E-07	0.97	4.95	-	2172.4
AHQ-8-6, 3019	R.FLEQQNQVLQTK.W	1476.65935	2	1.81E-07	0.97	4.52	-	2282.7
AHQ-8-5, 3036 - 3073	R.FLEQQNQVLQTK.W	1476.65935	2	1.48E-08	0.96	4.04	-	2281.8
AHQ-8-1, 3248 - 3249	R.FLEQQNQVLQTK.W	1476.65935	2	6.03E-06	0.97	4.51	-	2031.1
AHQ-8-2, 3279	R.FLEQQNQVLQTK.W	1476.65935	2	1.89E-06	0.96	4.83	-	2082.8
AHQ-8-10, 2934	R.FLEQQNQVLQTK.W	1476.65935	2	1.10E-05	0.90	3.84	-	987.3
AHQ-8-4, 3041	R.FLEQQNQVLQTK.W	1476.65935	2	1.84E-04	0.97	5.19	-	2271.5
AHQ-8-3, 3230	R.FLEQQNQVLQTK.W	1476.65935	2	5.93E-04	0.88	3.88	-	1123.7
AHQ-8-3, 3064 - 3065	R.FLEQQNQVLQTK.W	1476.65935	2	5.94E-07	0.97	4.68	-	2142.1
AHQ-8-2, 2353	R.GFSSGSAVVSGGSR.R	1255.31950	2	6.91E-04	0.95	3.95	-	1399.6
AHQ-8-4, 2289 - 2362	R.GFSSGSAVVSGGSR.R	1255.31950	2	8.52E-06	0.86	2.96	-	949.3
AHQ-8-13-, 2344 - 2363	R.GFSSGSAVVSGGSR.R	1255.31950	2	7.92E-06	0.95	3.70	-	1563.9
AHQ-8-4, 2187	R.HGGGGGGFGGGGFGSR.S	1321.34296	2	1.27E-04	0.90	3.25	-	1152.1
AHQ-8-2, 2252	R.HGGGGGGFGGGGFGSR.S	1321.34296	2	5.62E-05	0.85	3.26	-	725.8
AHQ-8-6, 2882	K.IEISELNR.V	974.09353	2	2.75E-04	0.72	2.84	-	547.5
AHQ-8-11, 2876	K.IEISELNR.V	974.09353	2	4.16E-04	0.76	2.95	-	572.9
AHQ-8-10, 2818	K.IEISELNR.V	974.09353	2	7.43E-04	0.73	2.89	-	587.2
AHQ-8-7, 2840	K.IEISELNR.V	974.09353	2	2.19E-04	0.84	2.85	-	853.9
AHQ-8-7, 2841	K.IEISELNR.V	974.09353	1	5.78E-04	0.16	1.85	-	207.0
AHQ-8-4, 4069 - 4134	K.LNDLEEALQQAK.E	1372.50630	2	3.56E-06	0.97	4.74	-	1846.8
AHQ-8-13-, 4122 - 4199	K.LNDLEEALQQAK.E	1372.50630	2	2.52E-06	0.97	4.47	-	2056.8
AHQ-8-3, 4126	K.LNDLEEALQQAK.E	1372.50630	2	2.79E-05	0.95	4.45	-	1397.2
AHQ-8-13, 4211 - 4279	K.LNDLEEALQQAK.E	1372.50630	2	4.13E-05	0.95	4.54	-	1366.6
AHQ-8-2, 4115 - 4183	K.LNDLEEALQQAK.E	1372.50630	2	3.53E-06	0.97	4.62	-	1709.5
AHQ-8-10, 3939	K.LNDLEEALQQAK.E	1372.50630	2	3.44E-04	0.80	3.08	-	1034.2
AHQ-8-7, 3989	K.LNDLEEALQQAK.E	1372.50630	2	2.03E-05	0.95	4.27	-	1429.3
AHQ-8-1, 4617	R.NKLNDLEEALQQAK.E	1614.78232	2	2.39E-04	0.95	3.86	-	1613.1
AHQ-8-2, 5884	R.NKLNDLEEALQQAKEDLAR.L	2199.40755	3	3.50E-04	0.95	5.38	-	1051.3
AHQ-8-4, 5807	R.NLDLDSIIAEVK.A	1330.50933	2	6.73E-07	0.96	4.42	-	1463.4
AHQ-8-7, 5597	R.NLDLDSIIAEVK.A	1330.50933	2	1.23E-05	0.96	4.75	-	1275.6
AHQ-8-12, 5562	R.NLDLDSIIAEVK.A	1330.50933	2	4.97E-04	0.90	3.60	-	954.5
AHQ-8-14-, 5653	R.NLDLDSIIAEVK.A	1330.50933	2	3.49E-06	0.95	4.41	-	1191.7
AHQ-8-13, 5780	R.NLDLDSIIAEVK.A	1330.50933	2	1.09E-06	0.96	4.48	-	1252.1
AHQ-8-1, 5819	R.NLDLDSIIAEVK.A	1330.50933	2	2.53E-06	0.96	5.03	-	1083.4
AHQ-8-6, 5659 - 5662	R.NLDLDSIIAEVK.A	1330.50933	2	1.76E-06	0.97	5.09	-	1288.0
AHQ-8-2, 5815	R.NLDLDSIIAEVK.A	1330.50933	2	2.50E-06	0.96	4.38	-	1333.2
AHQ-8-13-, 5642	R.NLDLDSIIAEVK.A	1330.50933	2	6.43E-07	0.96	4.80	-	1260.2
AHQ-8-3, 5720 - 5725	R.NLDLDSIIAEVK.A	1330.50933	2	8.98E-07	0.97	5.09	-	1208.4
AHQ-8-2, 3224	K.NVQDAIADAEQR.G	1330.38637	2	6.91E-08	0.95	4.38	-	1161.7

AHQ-8-4, 3166	K.NVQDAIADAEQR.G	1330.38637	2	3.11E-06	0.97	4.35	-	1865.6
AHQ-8-3, 3202	K.NVQDAIADAEQR.G	1330.38637	2	7.80E-10	0.90	3.28	-	1101.6
AHQ-8-13-, 3199	K.NVQDAIADAEQR.G	1330.38637	2	1.17E-06	0.95	4.01	-	1577.7
AHQ-8-14-, 3186	K.NVQDAIADAEQR.G	1330.38637	2	2.68E-10	0.94	4.14	-	1285.3
AHQ-8-13, 3365 - 3369	K.NVQDAIADAEQR.G	1330.38637	2	9.92E-09	0.94	3.81	-	1156.9
AHQ-8-2, 4977	K.SISISVAGGGGGFGAAGGFGGR.G	1839.98956	2	1.45E-04	0.68	2.75	-	744.5
AHQ-8-2, 3272	R.TAAENDFVTLK.K	1209.33064	2	2.37E-04	0.69	2.51	-	695.1
AHQ-8-2, 2757	R.TAAENDFVTLKK.D	1337.50356	2	1.69E-05	0.75	2.98	-	719.9
AHQ-8-2, 5047	R.TSQNSELNNMQDLVEDYK.K	2129.24808	2	3.35E-09	0.97	4.64	-	1481.9
AHQ-8-2, 4504 - 4577	R.TSQNSELNNMQDLVEDYK.K	2129.24808	2	2.62E-06	0.84	3.53	-	590.4
AHQ-8-4, 4558	R.TSQNSELNNMQDLVEDYKK.K	2257.42100	3	3.60E-07	0.80	3.27	-	782.4
AHQ-8-2, 4608	R.TSQNSELNNMQDLVEDYKK.K	2257.42100	2	1.10E-10	0.89	3.58	-	960.9
AHQ-8-4, 5677	K.VDLLNQEIEFLK.V	1461.68459	2	3.96E-07	0.93	4.15	-	960.1
AHQ-8-5, 5645	K.VDLLNQEIEFLK.V	1461.68459	2	6.58E-08	0.94	4.49	-	983.5
AHQ-8-13, 5637 - 5661	K.VDLLNQEIEFLK.V	1461.68459	2	2.88E-07	0.92	4.06	-	993.2
AHQ-8-3, 5604 - 5605	K.VDLLNQEIEFLK.V	1461.68459	2	3.76E-06	0.95	4.87	-	964.7
AHQ-8-14-, 5533 - 5553	K.VDLLNQEIEFLK.V	1461.68459	2	3.60E-06	0.84	3.59	-	689.5
AHQ-8-7, 5416 - 5472	K.VDLLNQEIEFLK.V	1461.68459	2	3.73E-07	0.87	3.73	-	722.7
AHQ-8-2, 5695	K.VDLLNQEIEFLK.V	1461.68459	2	1.51E-05	0.95	4.91	-	934.5
AHQ-8-13-, 5512 - 5588	K.VDLLNQEIEFLK.V	1461.68459	2	1.82E-04	0.89	3.87	-	1003.7
AHQ-8-13-, 5332 - 5340	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	2.25E-10	0.94	5.04	-	1036.4
AHQ-8-14-, 5343	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	2.31E-05	0.95	4.69	-	1427.9
AHQ-8-2, 5520 - 5577	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	1.68E-07	0.94	5.01	-	1033.1
AHQ-8-13-, 5654	K.VLYDAEISQIHQSVTDTNVILSMDNSR.N	3050.34740	3	3.72E-07	0.73	3.26	-	624.9
AHQ-8-2, 3204	K.YEELQVTVGR.H	1194.31920	2	9.57E-07	0.95	3.55	-	1745.8
AHQ-8-13-, 3191	K.YEELQVTVGR.H	1194.31920	2	1.64E-07	0.96	4.19	-	1801.3
AHQ-8-13, 3353 - 3359	K.YEELQVTVGR.H	1194.31920	2	4.19E-04	0.82	2.76	-	1089.0
AHQ-8-1, 3336	K.YEELQVTVGR.H	1194.31920	2	1.49E-07	0.95	3.43	-	1793.6
AHQ-8-2, 3035	R.YLDGLTAER.T	1038.13608	2	2.24E-04	0.88	3.44	-	613.6
gi|4759212|ref|NP_004598.1|	beta-tubulin cofactor A [Homo sapiens]			1.22E-10	1.91	20.29	26.90	12854.8
AHQ-8-13-, 3407	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	1.22E-10	0.97	5.84	-	1880.7
AHQ-8-13-, 3411	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	4.86E-09	0.95	4.88	-	956.0
AHQ-8-13, 3508 - 3576	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	1.14E-05	0.92	4.16	-	1084.8
AHQ-8-13-, 3495	R.RLEAAYLDLQR.I	1348.53280	2	1.84E-06	0.94	3.76	-	896.7
gi|20357552|ref|NP_005222.2|	cortactin isoform a; oncogene EMS1 [Homo sapiens]			1.23E-10	2.66	30.21	7.80	61585.7
AHQ-8-12, 3770	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	4.00E-08	0.77	3.06	-	570.3
AHQ-8-14-, 3839	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	1.23E-10	0.96	4.11	-	1353.2
AHQ-8-13-, 2994 - 2995	K.VDKSAVGFEYQGK.T	1428.57155	2	1.56E-07	0.87	3.81	-	757.3
AHQ-8-14-, 2963	R.VDQSAVGFEYQGK.T	1428.52841	2	6.11E-07	0.84	3.43	-	678.0
AHQ-8-11, 2916	R.VDQSAVGFEYQGK.T	1428.52841	2	3.55E-04	0.76	2.84	-	635.3
gi|27500274|ref|XP_113950.3|	similar to Munc13-4 protein [Homo sapiens]			1.27E-10	4.39	50.31	8.30	123281.1
AHQ-8-4, 4693 - 4699	R.AVQM*DELVPLGELTK.H	1659.92638	2	4.61E-05	0.72	2.98	-	444.8
AHQ-8-4, 5181 - 5261	K.LPAQLAWEALEQR.V	1525.73360	2	1.64E-10	0.94	3.75	-	1437.7
AHQ-8-4, 6498	R.LPLTYPAPNGDPILQLLEGR.K	2178.51621	2	1.27E-10	0.88	3.71	-	728.0
AHQ-8-4, 4061 - 4067	R.SVFPLSVSDSPAR.L	1362.51311	2	4.36E-06	0.88	2.78	-	1152.1
AHQ-8-4, 6415	R.VGAVLEQGQLQNTLHAQLQSALAGLGHEIR.T	3153.54178	3	3.34E-05	0.97	6.20	-	1721.9
gi|27498332|ref|XP_212565.1|	similar to tubulin, beta 5 [Homo sapiens]			1.31E-10	2.75	30.25	8.60	49670.5
AHQ-8-13, 3624	R.IM*NTFSVVPSPK.V	1336.58217	2	1.10E-04	0.80	2.78	-	765.7
AHQ-8-7, 3324 - 3341	R.IM*NTFSVVPSPK.V	1336.58217	2	8.64E-06	0.90	3.27	-	1103.1
AHQ-8-7, 6033 - 6110	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.23E-07	0.95	4.80	-	1007.4
AHQ-8-11, 5800 - 5807	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	3.63E-06	0.85	3.82	-	516.3
AHQ-8-12, 5820	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	8.92E-04	0.91	3.69	-	875.0
AHQ-8-12, 6006 - 6064	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	5.18E-07	0.88	4.04	-	513.5
AHQ-8-7, 5848 - 5853	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.49E-05	0.97	5.04	-	1234.0
AHQ-8-14-, 5909	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.90E-07	0.89	3.72	-	746.7
AHQ-8-13, 6019	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	2.73E-08	0.95	4.49	-	1193.3
AHQ-8-13-, 5860 - 5890	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.04E-05	0.80	3.42	-	523.0
AHQ-8-14-, 6102 - 6161	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.31E-10	0.97	5.08	-	1276.1
AHQ-8-7, 4266 - 4274	R.YLTVAAVFR.G	1040.23994	2	1.88E-05	0.87	2.87	-	859.3
gi|4502295|ref|NP_001677.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti			1.39E-10	10.13	120.30	33.00	57955.2
AHQ-8-7, 5168	R.AIAELGIYPAVDPLDSTSR.I	1989.21513	2	6.21E-04	0.81	3.18	-	601.9
AHQ-8-7, 6304 - 6373	R.DQEGQDVLLFIDNIFR.F	1923.11524	2	1.44E-08	0.95	4.80	-	1024.9
AHQ-8-7, 4286 - 4288	R.FTQAGSEVSALLGR.I	1436.59522	2	1.39E-10	0.96	4.70	-	1424.5
AHQ-8-7, 6212 - 6216	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	6.94E-06	0.96	6.07	-	1462.4
AHQ-8-7, 3224	R.IM*DPNIVGSEHYDVAR.G	1833.01557	3	5.19E-05	0.63	3.36	-	650.0
AHQ-8-7, 3549	R.IMDPNIVGSEHYDVAR.G	1817.01617	2	3.95E-05	0.93	3.83	-	986.8
AHQ-8-7, 4016 - 4017	R.IPSAVGYQPTLATDMGTM*QER.I	2283.56820	2	2.37E-04	0.89	4.93	-	689.0
AHQ-8-7, 4052	R.LVLEVAQHLGESTVR.T	1651.88893	2	6.72E-08	0.97	4.92	-	1761.7
AHQ-8-7, 5348	R.VALTGLTVAEYFR.D	1440.66861	2	3.94E-07	0.88	3.31	-	1009.6
AHQ-8-7, 2912	K.VALVYGQM*NQPPGAR.A	1617.85451	2	3.84E-04	0.57	2.51	-	381.2
AHQ-8-7, 3437	K.VALVYGQMNQPPGAR.A	1601.85511	2	2.99E-05	0.68	2.81	-	463.7
AHQ-8-7, 4458 - 4518	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	3	3.13E-06	0.90	3.35	-	1319.9
AHQ-8-7, 4452	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	5.17E-05	0.55	2.86	-	283.8
gi|10716563|ref|NP_001737.1|	calnexin [Homo sapiens]			1.70E-10	3.54	40.25	8.40	67567.8
AHQ-8-7, 4614	K.APVPTGEVYFADSFDR.G	1771.90722	2	3.62E-04	0.84	3.18	-	795.1
AHQ-8-5, 4777	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.70E-10	0.95	4.33	-	1044.8
AHQ-8-6, 4638 - 4711	K.APVPTGEVYFADSFDR.G	1771.90722	2	3.25E-04	0.74	3.11	-	639.7
AHQ-8-5, 3888	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	2	6.46E-04	0.90	4.02	-	640.8
AHQ-8-5, 3876	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	3	8.84E-07	0.91	3.89	-	1325.7
AHQ-8-5, 6224	K.IPNPDFFEDLEPFR.M	1736.90447	2	1.51E-04	0.75	2.93	-	652.7
AHQ-8-5, 5852 - 5854	R.KIPNPDFFEDLEPFR.M	1865.07739	3	8.31E-06	0.94	5.09	-	1496.9
AHQ-8-5, 5846	R.KIPNPDFFEDLEPFR.M	1865.07739	2	1.43E-05	0.88	3.29	-	939.7
gi|4507357|ref|NP_003555.1|	transgelin 2; SM22-alpha homolog [Homo sapiens]			1.88E-10	12.77	150.28	64.80	22391.3
AHQ-8-11, 5249 - 5304	R.DDGLFSGDPNWFPK.K	1595.69288	2	5.76E-04	0.94	3.74	-	1361.5
AHQ-8-11, 5460	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.25E-05	0.90	3.20	-	1112.7
AHQ-8-13, 5584	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.94E-06	0.87	3.41	-	886.0
AHQ-8-11, 5543 - 5553	R.DDGLFSGDPNWFPK.K	1595.69288	2	5.77E-04	0.66	2.69	-	651.8
AHQ-8-12, 5427 - 5482	R.DDGLFSGDPNWFPK.K	1595.69288	2	5.34E-05	0.84	3.10	-	733.4
AHQ-8-11, 4657 - 4719	R.DDGLFSGDPNWFPKK.S	1723.86579	2	2.01E-09	0.69	3.16	-	515.7
AHQ-8-12, 4746	R.DDGLFSGDPNWFPKK.S	1723.86579	2	2.03E-04	0.70	3.11	-	451.6
AHQ-8-11, 6193 - 6252	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	5.66E-05	0.37	2.72	-	282.7
AHQ-8-13-, 5782	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.04E-07	0.79	3.28	-	533.4
AHQ-8-11, 5696	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	1.42E-07	0.82	3.53	-	602.9
AHQ-8-12, 6207 - 6275	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.97E-04	0.74	3.79	-	375.1
AHQ-8-11, 6211 - 6213	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	5.69E-05	0.74	3.68	-	452.1
AHQ-8-11, 6203	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.79E-07	0.86	4.02	-	762.7
AHQ-8-11, 2195 - 2225	R.GASQAGMTGYGM*PR.Q	1400.56672	2	1.41E-06	0.89	3.52	-	1055.0
AHQ-8-11, 2280	R.GPAYGLSREVQQK.I	1433.59456	2	2.11E-04	0.76	3.36	-	712.6
AHQ-8-11, 2383 - 2440	R.NFSDNQLQEGK.N	1280.32582	2	1.90E-04	0.82	3.49	-	619.6
AHQ-8-11, 3727	R.NFSDNQLQEGKNVIGLQM*GTNR.G	2480.70013	3	1.71E-04	0.71	3.29	-	679.9
AHQ-8-11, 2379 - 2443	K.NVIGLQM*GTNR.G	1219.39691	2	2.31E-05	0.94	4.18	-	888.6
AHQ-8-11, 3131 - 3187	K.NVIGLQMGTNR.G	1203.39751	2	6.16E-04	0.80	3.10	-	878.9
AHQ-8-11, 2512	K.NVIGLQM*GTNR.G	1219.39691	2	3.07E-04	0.77	2.80	-	568.2
AHQ-8-13-, 5206	K.QMEQISQFLQAAER.Y	1679.87950	2	4.67E-05	0.95	4.31	-	1198.8
AHQ-8-13-, 5598 - 5655	K.QMEQISQFLQAAER.Y	1679.87950	2	9.50E-04	0.85	2.98	-	1223.3
AHQ-8-11, 4479	K.QM*EQISQFLQAAER.Y	1695.87890	3	2.50E-05	0.94	4.14	-	1907.1
AHQ-8-12, 5091 - 5092	K.QMEQISQFLQAAER.Y	1679.87950	2	2.80E-06	0.88	3.50	-	866.4

AHQ-8-11, 5084	K.QMEQISQFLQAAER.Y	1679.87950	3	5.84E-06	0.98	5.27	-	2986.7
AHQ-8-11, 4472	K.QM*EQISQFLQAAER.Y	1695.87890	2	1.13E-04	0.73	3.17	-	431.6
AHQ-8-11, 5025 - 5079	K.QMEQISQFLQAAER.Y	1679.87950	2	2.31E-07	0.95	4.53	-	1037.6
AHQ-8-13, 3832 - 3847	R.TLM*NLGGLAVAR.D	1232.47872	2	5.34E-06	0.87	3.21	-	923.1
AHQ-8-13, 4605	R.TLMNLGGLAVAR.D	1216.47932	2	3.16E-06	0.85	3.35	-	830.5
AHQ-8-12, 4340 - 4347	R.TLMNLGGLAVAR.D	1216.47932	2	1.20E-07	0.93	4.02	-	1308.2
AHQ-8-11, 4319 - 4320	R.TLMNLGGLAVAR.D	1216.47932	2	3.63E-06	0.94	4.15	-	1189.8
AHQ-8-11, 3787 - 3843	R.TLM*NLGGLAVAR.D	1232.47872	2	2.27E-04	0.91	3.61	-	1312.0
AHQ-8-11, 3563 - 3601	R.TLM*NLGGLAVAR.D	1232.47872	2	2.29E-04	0.94	4.00	-	1034.8
AHQ-8-12, 6046 - 6087	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	2.43E-04	0.83	3.84	-	690.9
AHQ-8-13, 6199 - 6279	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	3.73E-07	0.97	5.61	-	952.6
AHQ-8-13-, 6187 - 6244	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.88E-10	0.96	4.84	-	1237.7
AHQ-8-14-, 6261	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.64E-09	0.96	5.11	-	1123.6
gi|28178832|ref|NP_002159.2|	isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat			1.90E-10	4.25	50.26	15.00	50909.0
AHQ-8-8, 5119	R.LIDDMVAQVLK.S	1245.51421	2	1.23E-04	0.93	4.32	-	1046.5
AHQ-8-8, 5451	K.LNEHFLNTTDFLDTIK.S	1922.12725	2	1.90E-10	0.97	5.04	-	1259.4
AHQ-8-8, 2138	K.TIEAEAAHGTVTR.H	1356.46696	2	3.69E-06	0.81	3.01	-	707.7
AHQ-8-8, 2801	K.VAKPVVEMDGDEMTR.I	1677.92533	2	9.65E-05	0.62	3.15	-	325.1
AHQ-8-8, 2637 - 2639	K.VCVETVESGAM*TK.D	1428.61170	2	2.57E-04	0.93	4.12	-	981.0
gi|4557731|ref|NP_000618.1|	latent transforming growth factor beta binding protein 1 precursor [Hom			2.06E-10	7.84	90.30	8.70	152790.9
AHQ-8-3, 3510 - 3584	R.ASGLGDHCEDINECLEDK.S	2065.13910	3	4.09E-04	0.85	4.19	-	509.8
AHQ-8-3, 3581	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	7.52E-05	0.98	6.04	-	2027.5
AHQ-8-2, 3643 - 3720	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	1.75E-04	0.95	4.99	-	1178.0
AHQ-8-2, 2637 - 2717	R.CTCGQGYQLSAAK.D	1446.58862	2	1.75E-06	0.92	3.87	-	701.6
AHQ-8-3, 2606	R.CTCGQGYQLSAAK.D	1446.58862	2	6.45E-06	0.90	3.77	-	650.3
AHQ-8-3, 3966	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	7.67E-07	0.81	3.45	-	585.2
AHQ-8-14-, 3173	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	2.58E-05	0.76	2.81	-	567.4
AHQ-8-1, 3371 - 3436	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	5.01E-04	0.73	3.08	-	443.9
AHQ-8-1, 3984	K.EEPVEALTFSR.E	1278.39297	2	8.10E-04	0.85	3.12	-	748.1
AHQ-8-1, 5572	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	6.55E-06	0.88	4.45	-	509.8
AHQ-8-3, 5472	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	4.28E-05	0.75	3.52	-	497.5
AHQ-8-5, 2878 - 2880	R.TSTDLDVDVDQPK.E	1433.50014	2	5.64E-09	0.91	3.43	-	1263.1
AHQ-8-4, 2882	R.TSTDLDVDVDQPK.E	1433.50014	2	2.27E-06	0.89	3.31	-	1094.9
AHQ-8-2, 2953	R.TSTDLDVDVDQPK.E	1433.50014	2	1.09E-08	0.88	3.28	-	935.5
AHQ-8-3, 2741	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	7.68E-07	0.87	3.48	-	1144.9
AHQ-8-5, 2712	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	2.76E-05	0.58	2.71	-	862.0
AHQ-8-2, 2779	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	2.06E-10	0.89	3.98	-	1028.9
AHQ-8-4, 2701	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	2.85E-06	0.92	3.64	-	1366.9
AHQ-8-1, 3651 - 3663	R.YTCICYEGYR.F	1387.51964	2	6.07E-06	0.85	2.77	-	675.1
gi|4507907|ref|NP_000543.1|	von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille			2.81E-10	17.75	200.35	10.00	309296.7
AHQ-8-2, 3857	R.CLPSACEVVTGSPR.G	1535.72531	2	9.82E-05	0.75	3.00	-	830.5
AHQ-8-1, 3923	R.CLPSACEVVTGSPR.G	1535.72531	2	2.74E-07	0.93	4.64	-	668.1
AHQ-8-3, 4014	R.CLPTACTIQLR.G	1335.57568	2	5.41E-04	0.61	2.65	-	432.2
AHQ-8-1, 4149	R.CLPTACTIQLR.G	1335.57568	2	1.08E-04	0.74	3.03	-	436.8
AHQ-8-2, 4887	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	2.22E-04	0.78	3.47	-	461.2
AHQ-8-1, 4940	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	2.43E-04	0.74	2.58	-	792.9
AHQ-8-1, 5389	R.EQAPNLVYMVTGNPASDEIK.R	2177.42062	2	1.90E-05	0.49	2.65	-	316.8
AHQ-8-1, 4088	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	7.87E-07	0.88	3.62	-	928.3
AHQ-8-1, 4037	R.IALLLM*ASQEPQR.M	1486.76229	2	1.89E-05	0.86	3.06	-	829.7
AHQ-8-1, 6465 - 6528	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	4.66E-04	0.96	4.91	-	1006.5
AHQ-8-1, 2889	R.ILAGPAGDSNVVK.L	1241.41901	2	1.02E-07	0.92	3.84	-	1013.2
AHQ-8-2, 2721	R.ILAGPAGDSNVVK.L	1241.41901	2	5.91E-09	0.91	3.47	-	941.5
AHQ-8-1, 6337 - 6416	R.LLDLVFLLDGSSR.L	1448.68905	2	9.55E-06	0.96	4.78	-	1723.5
AHQ-8-3, 4081	R.LSEAEFEVLK.A	1165.31777	2	3.72E-06	0.88	3.36	-	944.5
AHQ-8-1, 4223	R.LSEAEFEVLK.A	1165.31777	2	1.10E-06	0.93	3.80	-	1257.4
AHQ-8-4, 3253	K.LSGEAYGFVAR.I	1170.29934	2	9.39E-06	0.95	3.91	-	1265.3
AHQ-8-3, 3265	K.LSGEAYGFVAR.I	1170.29934	2	3.13E-07	0.95	3.44	-	1549.5
AHQ-8-2, 4104	K.LTGSCSYVLFQNK.E	1518.71629	2	3.18E-05	0.83	3.45	-	810.5
AHQ-8-1, 4168 - 4231	K.LTGSCSYVLFQNK.E	1518.71629	2	6.44E-08	0.93	3.81	-	1078.7
AHQ-8-1, 5553	R.NSM*VLDVAFVLEGSDK.I	1740.95635	2	4.31E-05	0.92	2.97	-	1748.3
AHQ-8-1, 5153 - 5228	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	1.80E-04	0.96	5.30	-	1420.5
AHQ-8-2, 5207 - 5209	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	2.81E-10	0.98	6.98	-	2564.5
AHQ-8-1, 5311 - 5324	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	1.68E-04	0.98	6.11	-	2117.0
AHQ-8-2, 4759	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	2.83E-06	0.87	3.91	-	515.3
AHQ-8-1, 5253 - 5317	K.TYGLCGICDENGANDFM*LR.D	2225.42231	2	2.79E-05	0.89	4.14	-	619.7
AHQ-8-1, 4561	R.VTVFPIGIGDR.Y	1174.37426	2	1.69E-07	0.94	3.61	-	1237.0
AHQ-8-2, 4500	R.VTVFPIGIGDR.Y	1174.37426	2	2.41E-05	0.94	3.54	-	1248.5
AHQ-8-1, 3131	K.YAGSQVASTSEVLK.Y	1440.58064	2	8.89E-07	0.93	3.93	-	1012.4
AHQ-8-2, 2997	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.33E-04	0.90	3.21	-	896.5
AHQ-8-1, 3585 - 3635	R.YLSDHSFLVSQGDR.E	1624.73576	2	1.66E-09	0.95	3.95	-	1488.5
AHQ-8-1, 5677 - 5680	K.YTLFQIFSK.I	1147.34728	2	4.84E-06	0.95	3.38	-	1320.2
gi|5031987|ref|NP_005720.1|	peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]			3.03E-10	0.90	10.19	14.00	22040.1
AHQ-8-12, 4779 - 4818	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	3.03E-10	0.90	3.84	-	1230.9
gi|4504523|ref|NP_002148.1|	heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (			3.13E-10	0.88	10.16	11.80	10931.6
AHQ-8-14-, 4830	K.VVLDDKDYFLFR.D	1530.74861	2	3.13E-10	0.88	3.13	-	740.8
AHQ-8-14, 5689	K.VVLDDKDYFLFR.D	1530.74861	2	1.01E-06	0.79	2.75	-	603.4
gi|10835002|ref|NP_001166.1|	Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]			3.16E-10	2.79	30.26	27.90	22987.8
AHQ-8-10, 2466	K.APEPHVEEDDDDELDSK.L	1940.90995	2	3.16E-10	0.96	5.11	-	1295.1
AHQ-8-11, 5211 - 5219	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	6.05E-09	0.93	4.57	-	1130.2
AHQ-8-13, 5401 - 5403	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.96E-05	0.68	3.23	-	487.4
AHQ-8-10, 3271 - 3334	K.TLLGDGPVVTDPK.A	1312.49400	2	6.61E-05	0.90	3.66	-	976.5
gi|6005942|ref|NP_009057.1|	valosin-containing protein; yeast Cdc48p homolog; transitional endoplas			3.66E-10	9.31	110.29	23.70	89321.3
AHQ-8-5, 4013 - 4072	K.AIANECQANFISIK.G	1580.78762	2	1.20E-05	0.90	3.70	-	696.2
AHQ-8-4, 4095	K.AIANECQANFISIK.G	1580.78762	2	1.23E-04	0.81	3.26	-	781.1
AHQ-8-5, 3738	R.ELQELVQYPVEHPDK.F	1825.01157	2	1.34E-05	0.76	2.98	-	604.7
AHQ-8-5, 3706 - 3765	K.GVLFYGPPGCGK.T	1253.45154	2	4.85E-06	0.55	2.53	-	547.6
AHQ-8-5, 6229	R.IVSQLLTLMDGLK.Q	1431.76657	2	8.73E-08	0.94	4.10	-	1045.0
AHQ-8-5, 6333	K.LADDVDLEQVANETHGHVGADLAALCSEAALQAIR.K	3675.98140	3	2.33E-05	0.95	4.93	-	1509.5
AHQ-8-5, 5420	R.LDQLIYIPLPDEK.S	1557.81228	2	4.40E-06	0.79	2.97	-	800.5
AHQ-8-5, 4793	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	2.88E-08	0.98	5.76	-	1757.2
AHQ-8-7, 6297	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	2.72E-05	0.79	2.85	-	863.8
AHQ-8-4, 6509 - 6513	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	1.12E-05	0.74	2.93	-	650.2
AHQ-8-5, 6456	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	3.66E-10	0.98	5.66	-	1646.7
AHQ-8-5, 5481	K.NVFIIGATNRPDIIDPAILRPGR.L	2519.93026	3	1.35E-04	0.64	3.47	-	428.4
AHQ-8-5, 6468	R.QAAPCVLFFDELDSIAK.A	1926.17909	2	2.62E-06	0.89	3.96	-	700.3
AHQ-8-5, 3537 - 3538	R.WALSQSNPSALR.E	1330.47434	2	1.62E-06	0.93	3.75	-	1128.8
gi|13129150|ref|NP_005339.1|	heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H			4.25E-10	1.74	20.23	3.40	84659.1
AHQ-8-8, 3939	R.NPDDITNEEYGEFYK.S	1834.87381	2	2.32E-05	0.92	4.43	-	913.4
AHQ-8-6, 3894	R.NPDDITNEEYGEFYK.S	1834.87381	2	4.25E-10	0.96	4.55	-	1526.0
AHQ-8-5, 3869 - 3936	R.NPDDITNEEYGEFYK.S	1834.87381	2	3.91E-09	0.96	4.64	-	1066.2
AHQ-8-5, 4070 - 4116	R.RAPFDLFENR.K	1265.40235	2	9.57E-04	0.78	2.90	-	634.9
gi|24119203|ref|NP_705935.1|	tropomyosin 3 [Homo sapiens]			4.37E-10	1.87	20.27	9.70	29032.5
AHQ-8-9, 6626	R.IQLVEEELDR.A	1244.37653	2	1.86E-07	0.89	3.33	-	956.5
AHQ-8-9, 6627	R.IQLVEEELDR.A	1244.37653	1	3.03E-04	0.10	1.80	-	363.9
AHQ-8-11, 3567 - 3572	R.IQLVEEELDR.A	1244.37653	2	2.33E-06	0.86	3.07	-	883.8
AHQ-8-9, 6503	K.IQVLQQQADDAEER.A	1643.73738	2	4.37E-10	0.98	5.35	-	2657.6
gi|4505839|ref|NP_002645.1|	pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro			4.45E-10	13.69	150.26	35.80	57913.6

AHQ-8-7, 5477	R.EAEAAIYHLQLFEELR.R	1933.15326	2	2.02E-07	0.93	4.44		-	904.8
AHQ-8-7, 6288	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	9.95E-09	0.97	5.11		-	1511.5
AHQ-8-7, 4276 - 4340	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	8.49E-06	0.94	4.39		-	1122.0
AHQ-8-7, 4758 - 4812	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	3.74E-08	0.96	5.12		-	1315.9
AHQ-8-7, 4478	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.43E-04	0.91	4.01		-	925.1
AHQ-8-7, 6005 - 6060	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	4.45E-10	0.95	4.80		-	1474.7
AHQ-8-7, 4360	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	1.45E-06	0.91	3.58		-	1096.5
AHQ-8-7, 3985	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	8.66E-05	0.83	3.53		-	1090.8
AHQ-8-7, 5004	K.KGVNLPGAAVDLPAVSEKDIQDLK.F	2478.82685	3	2.40E-05	0.93	4.74		-	1294.3
AHQ-8-7, 5328	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	3	9.14E-05	0.96	5.07		-	1639.7
AHQ-8-7, 5049 - 5121	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	5.07E-07	0.92	4.35		-	698.5
AHQ-8-7, 5322 - 5386	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	2.15E-09	0.95	4.36		-	1053.0
AHQ-8-7, 3326 - 3342	R.LDIDSPPITAR.N	1198.35099	2	7.69E-06	0.94	4.06		-	1241.5
AHQ-8-7, 2488	R.LNFSHGTHEYHAETIK.N	1885.02879	2	2.91E-06	0.95	4.20		-	1382.7
AHQ-8-7, 3340	R.NTGIICTIGPASR.S	1361.54994	2	1.08E-04	0.95	4.24		-	1309.1
AHQ-8-7, 3712	R.NTGIICTIGPASR.S	1361.54994	2	3.53E-04	0.88	2.92		-	1149.4
AHQ-8-6, 3408	R.NTGIICTIGPASR.S	1361.54994	2	3.07E-05	0.81	3.63		-	774.3
AHQ-8-13-, 3484 - 3490	R.NTGIICTIGPASR.S	1361.54994	2	1.03E-05	0.91	3.90		-	980.7
AHQ-8-7, 2314	R.PVAVALDTK.G	914.08123	2	2.85E-05	0.88	2.83		-	756.2
AHQ-8-7, 3961	R.TATESFASDPILYR.P	1571.71277	2	1.64E-05	0.92	3.97		-	780.6
AHQ-8-7, 5341 - 5344	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	2	2.47E-05	0.86	4.15		-	307.9
AHQ-8-7, 5306 - 5364	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	8.42E-04	0.76	3.19		-	913.1
AHQ-8-7, 2946	R.VNFAMNVGK.A	980.16641	2	8.00E-04	0.80	2.69		-	569.7
gi|4758304|ref|NP_004902.1|	protein disulfide isomerase related protein (calcium-binding protein, i			5.35E-10	4.11	50.19	5.70		72931.9
AHQ-8-6, 4436	K.FAMEPEEFDSDTLR.E	1687.80890	2	3.14E-08	0.74	3.15		-	520.7
AHQ-8-6, 3666 - 3727	K.FAM*EPEEFDSDTLR.E	1703.80830	2	1.61E-05	0.73	3.10		-	506.1
AHQ-8-6, 3559 - 3630	R.FDVSGYPTLK.I	1127.27123	2	9.68E-06	0.83	2.63		-	1122.0
AHQ-8-6, 2919 - 2927	K.IDATSASVLASR.F	1191.31686	2	5.35E-10	0.94	3.84		-	1510.5
AHQ-8-6, 3400 - 3403	K.RFDVSGYPTLK.I	1283.45758	2	5.55E-06	0.87	3.27		-	938.5
gi|4503445|ref|NP_001944.1|	endothelial cell growth factor 1 (platelet-derived); thymidine phosphor			7.69E-10	2.81	30.21	9.80		49955.2
AHQ-8-7, 6097 - 6105	R.ALPLALVLHELGAGR.S	1530.83966	2	7.69E-10	0.95	4.18		-	1318.7
AHQ-8-7, 6098	R.ALPLALVLHELGAGR.S	1530.83966	3	6.94E-07	0.86	3.46		-	581.4
AHQ-8-7, 4138	R.AREQEELLAPADGTVELVR.A	2097.31523	2	9.66E-06	0.91	4.17		-	748.3
AHQ-8-7, 2722	R.VAAALDDGSALGR.F	1216.32641	2	7.32E-06	0.95	4.15		-	1287.8
gi|20535366|ref|XP_053177.4|	similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap			7.90E-10	2.35	30.24	6.70		49858.2
AHQ-8-13-, 3188	K.DVNAAIATIK.T	1016.17355	2	5.33E-04	0.66	2.65		-	658.6
AHQ-8-7, 4805 - 4860	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.42E-09	0.93	4.05		-	979.2
AHQ-8-7, 5026	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.20E-06	0.76	3.25		-	501.0
AHQ-8-14-, 4905 - 4955	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.14E-09	0.92	4.51		-	749.2
AHQ-8-13, 5093	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.63E-05	0.82	3.49		-	701.3
AHQ-8-14, 5670 - 5737	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.90E-10	0.94	4.81		-	983.5
AHQ-8-7, 4704	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.21E-04	0.84	3.45		-	914.8
AHQ-8-7, 4484	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	6.26E-07	0.86	3.90		-	382.3
AHQ-8-13-, 4947	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.94E-07	0.94	4.36		-	1060.0
AHQ-8-14-, 4574	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.29E-07	0.90	4.06		-	554.3
AHQ-8-14-, 5385 - 5429	R.TIQFVDWCPTGFK.V	1600.81899	2	8.25E-04	0.74	3.02		-	579.0
AHQ-8-7, 5278 - 5353	R.TIQFVDWCPTGFK.V	1600.81899	2	6.55E-04	0.75	2.93		-	572.4
gi|4503631|ref|NP_000120.1|	coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,			8.06E-10	18.63	210.29	32.50		83232.8
AHQ-8-5, 2641 - 2646	K.DGTHVVENVDATHIGK.L	1692.81163	2	1.06E-08	0.93	4.15		-	973.9
AHQ-8-7, 2605	K.DGTHVVENVDATHIGK.L	1692.81163	2	4.59E-04	0.95	4.53		-	1201.3
AHQ-8-5, 2644	K.DGTHVVENVDATHIGK.L	1692.81163	3	2.21E-06	0.91	4.35		-	996.6
AHQ-8-8, 2629 - 2706	K.DGTHVVENVDATHIGK.L	1692.81163	2	1.95E-04	0.59	2.95		-	390.5
AHQ-8-5, 6604 - 6605	K.EAVLIQAGEYM*GQLLEQASLHFFVTAR.I	3039.45415	3	3.39E-05	0.91	4.35		-	904.7
AHQ-8-11, 5263	K.ETFDVTLEPLSFK.K	1526.71190	2	4.60E-05	0.73	2.97		-	604.3
AHQ-8-5, 4814	R.GTQVVGSDM*TVTVQFTNPLK.E	2139.41549	2	5.73E-06	0.93	4.13		-	1022.6
AHQ-8-7, 5204 - 5216	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.91E-04	0.41	2.65		-	215.5
AHQ-8-5, 5374	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.69E-04	0.52	2.64		-	337.8
AHQ-8-8, 5366	K.GTYIPVPIVSELQSGK.W	1688.94594	2	3.77E-04	0.55	2.78		-	284.1
AHQ-8-5, 6360	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	2.06E-09	0.77	3.09		-	646.2
AHQ-8-13-, 6147 - 6219	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.56E-06	0.94	4.69		-	1163.1
AHQ-8-11, 6128	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	9.81E-04	0.78	3.16		-	839.6
AHQ-8-7, 6205	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	3.13E-09	0.89	4.09		-	721.6
AHQ-8-7, 6204 - 6266	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	6.15E-07	0.94	4.63		-	941.1
AHQ-8-5, 6285 - 6361	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	8.06E-10	0.97	5.35		-	1445.2
AHQ-8-5, 3366 - 3449	R.HVYGELDVQIQR.R	1457.61612	2	4.20E-04	0.89	3.32		-	779.2
AHQ-8-5, 2324	K.KDGTHVVENVDATHIGK.L	1820.98455	3	3.83E-08	0.98	5.86		-	3019.1
AHQ-8-5, 2321	K.KDGTHVVENVDATHIGK.L	1820.98455	2	1.93E-06	0.93	3.99		-	1170.7
AHQ-8-5, 2500	K.KDGTHVVENVDATHIGK.L	1820.98455	3	6.27E-05	0.95	4.83		-	1723.9
AHQ-8-5, 2417	K.KDGTHVVENVDATHIGK.L	1820.98455	3	1.85E-04	0.78	3.19		-	831.7
AHQ-8-5, 5004 - 5077	K.KETFDVTLEPLSFK.K	1654.88482	2	2.23E-04	0.95	4.18		-	1544.2
AHQ-8-5, 2834	R.KLIASMSSDSLR.H	1308.53039	2	2.80E-06	0.92	3.90		-	997.0
AHQ-8-5, 2177	R.KLIASM*SSDSLR.H	1324.52979	2	1.56E-04	0.90	3.21		-	1218.0
AHQ-8-5, 4565	R.LALETALMYGAK.K	1281.54655	2	3.62E-07	0.96	3.88		-	1866.8
AHQ-8-5, 2304	K.LIASM*SSDSLR.H	1196.35688	2	1.80E-05	0.91	3.19		-	903.3
AHQ-8-6, 5216 - 5283	R.M*YVAVWTPYGVLR.T	1571.86734	2	3.07E-04	0.85	3.20		-	676.7
AHQ-8-7, 5184	R.M*YVAVWTPYGVLR.T	1571.86734	2	2.71E-04	0.93	4.02		-	790.7
AHQ-8-5, 5345 - 5364	R.M*YVAVWTPYGVLR.T	1571.86734	2	2.58E-04	0.84	2.94		-	977.9
AHQ-8-5, 6140 - 6145	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	3.59E-06	0.93	4.88		-	926.6
AHQ-8-5, 3673	R.NVWVHLDGPGVTR.P	1450.62682	2	1.37E-05	0.91	3.32		-	1328.8
AHQ-8-5, 3433	R.NVWVHLDGPGVTRPM*K.K	1823.11188	3	4.45E-07	0.83	3.74		-	628.5
AHQ-8-5, 4464	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	6.43E-07	0.97	4.71		-	2026.3
AHQ-8-5, 4428 - 4490	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	2.22E-04	0.87	2.99		-	1162.0
AHQ-8-6, 4996	R.SNVDMDFEVENAVLGK.D	1767.93869	2	9.21E-04	0.70	2.74		-	919.9
AHQ-8-10, 4215 - 4271	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	2.11E-04	0.59	2.65		-	619.1
AHQ-8-5, 5068 - 5124	R.SNVDMDFEVENAVLGK.D	1767.93869	2	3.72E-08	0.96	4.67		-	1787.4
AHQ-8-5, 4618	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	2.92E-04	0.62	3.17		-	689.7
AHQ-8-13-, 5426	K.STVLTIPEIIIK.V	1327.63485	2	1.40E-04	0.87	2.78		-	1144.9
AHQ-8-7, 5349	K.STVLTIPEIIIK.V	1327.63485	2	7.42E-04	0.91	2.78		-	1538.5
AHQ-8-14-, 5431 - 5434	K.STVLTIPEIIIK.V	1327.63485	2	4.72E-04	0.86	2.98		-	1084.6
AHQ-8-5, 2426	R.VEYVIGR.Y	835.97056	2	7.58E-04	0.81	2.53		-	673.0
gi|29568111|ref|NP_006088.2|	myosin, light polypeptide 9, regulatory; myosin regulatory light chain			8.09E-10	2.43	30.17	12.20		19827.1
AHQ-8-12, 2795	R.FTDEEVDEM*YR.E	1450.50949	2	7.97E-06	0.81	3.11		-	784.9
AHQ-8-11, 3387 - 3428	R.FTDEEVDEMYR.E	1434.51009	2	8.09E-10	0.88	3.20		-	1087.5
AHQ-8-14-, 3878 - 3882	K.GNFNYVEFTR.I	1247.34066	2	5.09E-06	0.74	2.53		-	587.6
AHQ-8-11, 3921 - 3923	K.GNFNYVEFTR.I	1247.34066	2	2.85E-05	0.87	3.29		-	772.4
gi|13994151|ref|NP_066272.1|	PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H			8.37E-10	6.19	70.24	27.40		36071.5
AHQ-8-14-, 6149 - 6205	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	6.76E-06	0.91	4.90		-	602.5
AHQ-8-13, 6204	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	8.33E-04	0.83	4.25		-	412.8
AHQ-8-13-, 6132 - 6191	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	7.89E-04	0.88	4.59		-	649.0
AHQ-8-14-, 3587	K.DFEQPLAISR.V	1176.30388	2	1.73E-05	0.92	3.75		-	1030.8
AHQ-8-11, 3508 - 3509	K.DFEQPLAISR.V	1176.30388	2	2.34E-06	0.85	3.37		-	776.5
AHQ-8-13-, 3592 - 3616	K.DFEQPLAISR.V	1176.30388	2	1.25E-04	0.93	3.25		-	1287.2
AHQ-8-13, 3761	K.DFEQPLAISR.V	1176.30388	2	3.27E-05	0.87	3.33		-	820.2
AHQ-8-12, 3531 - 3539	K.DFEQPLAISR.V	1176.30388	2	2.41E-04	0.85	2.83		-	936.1
AHQ-8-14-, 3343	K.GCTDNLTLTVAR.S	1322.47058	2	2.12E-04	0.72	2.80		-	828.2
AHQ-8-13, 3555 - 3557	K.GCTDNLTLTVAR.S	1322.47058	2	2.71E-06	0.64	3.15		-	586.8
AHQ-8-13, 4148 - 4167	K.GHFFVEDQIYCEK.H	1673.82684	2	3.78E-04	0.87	3.52		-	725.3

AHQ-8-12, 3891 - 3892	K.GHFFVEDQIYCEK.H	1673.82684	2	8.25E-06	0.97	4.60	-	1345.4
AHQ-8-13-, 3980 - 3995	K.GHFFVEDQIYCEK.H	1673.82684	2	8.80E-04	0.92	3.74	-	913.3
AHQ-8-14-, 3958	K.GHFFVEDQIYCEK.H	1673.82684	2	1.65E-04	0.91	3.51	-	1073.6
AHQ-8-13-, 3427 - 3483	R.IKGCTDNLTLTVAR.S	1563.80174	2	4.34E-06	0.57	2.73	-	477.5
AHQ-8-13-, 3299	R.IKGCTDNLTLTVAR.S	1563.80174	2	8.37E-10	0.95	4.16	-	1130.5
AHQ-8-12, 3194	R.IKGCTDNLTLTVAR.S	1563.80174	2	3.57E-04	0.72	3.37	-	503.8
AHQ-8-14-, 3257	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.33E-08	0.94	4.05	-	999.2
AHQ-8-14, 4154	R.IKGCTDNLTLTVAR.S	1563.80174	2	6.94E-05	0.75	2.64	-	713.4
AHQ-8-13, 3443	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.87E-09	0.92	3.53	-	1003.7
AHQ-8-11, 3203	R.IKGCTDNLTLTVAR.S	1563.80174	2	3.78E-06	0.81	3.00	-	717.3
AHQ-8-13-, 3780	R.LVGGKDFEQPLAISR.V	1630.86972	2	2.03E-06	0.93	4.39	-	1046.0
AHQ-8-14-, 3725 - 3749	R.LVGGKDFEQPLAISR.V	1630.86972	2	3.34E-04	0.38	2.76	-	565.6
AHQ-8-13-, 6142	K.QSTSFLVLQEILESEEK.G	1981.18977	2	4.26E-06	0.95	4.24	-	1363.9
gi|7669492|ref|NP_002037.2|	glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]			9.26E-10	3.25	40.23	14.90	36053.0
AHQ-8-9, 6612	R.GALQNIIPASTGAAK.A	1412.61680	2	1.74E-05	0.72	3.18	-	485.2
AHQ-8-9, 6602	R.VPTANVSVVDLTCR.L	1532.74450	2	4.79E-09	0.95	4.43	-	1091.3
AHQ-8-11, 3917 - 3971	R.VPTANVSVVDLTCR.L	1532.74450	2	2.20E-08	0.94	4.04	-	979.3
AHQ-8-12, 3978 - 4035	R.VPTANVSVVDLTCR.L	1532.74450	2	6.72E-05	0.96	4.11	-	1313.6
AHQ-8-13, 4201 - 4261	R.VPTANVSVVDLTCR.L	1532.74450	2	8.77E-07	0.82	2.93	-	709.3
AHQ-8-13-, 4050	R.VPTANVSVVDLTCR.L	1532.74450	2	3.31E-09	0.95	4.44	-	1067.9
AHQ-8-14-, 4017	R.VPTANVSVVDLTCR.L	1532.74450	2	9.26E-10	0.93	4.29	-	774.4
AHQ-8-13-, 5651 - 5708	K.WGDAGAEYVVESTGVFTTMEK.A	2278.48027	2	5.54E-04	0.66	3.25	-	441.9
AHQ-8-13-, 5251	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	6.10E-05	0.94	4.59	-	743.4
gi|4557377|ref|NP_000052.1|	Bruton agammaglobulinemia tyrosine kinase [Homo sapiens]			1.06E-09	0.88	10.19	2.30	76280.8
AHQ-8-6, 3396	R.FTNSETAEHIAQGLR.L	1674.79631	2	1.06E-09	0.88	3.87	-	828.0
gi|5453595|ref|NP_006358.1|	adenylyl cyclase-associated protein [Homo sapiens]			1.10E-09	6.89	80.35	26.90	51672.7
AHQ-8-5, 2860	R.ALLVTASQCQQPAENK.L	1759.96271	2	3.18E-04	0.79	3.33	-	474.5
AHQ-8-7, 2802 - 2808	R.ALLVTASQCQQPAENK.L	1759.96271	3	4.68E-06	0.92	4.34	-	1141.9
AHQ-8-11, 2851	R.ALLVTASQCQQPAENK.L	1759.96271	2	2.25E-05	0.78	2.93	-	556.4
AHQ-8-8, 2777 - 2779	R.ALLVTASQCQQPAENK.L	1759.96271	2	1.18E-04	0.96	4.33	-	1420.6
AHQ-8-13-, 2911	R.ALLVTASQCQQPAENK.L	1759.96271	2	3.06E-06	0.87	3.49	-	670.6
AHQ-8-7, 2812 - 2889	K.KEPAVLELEGK.K	1213.40557	2	1.46E-07	0.82	2.63	-	595.1
AHQ-8-7, 6177	K.LFNHLSAVSESIQALGWVAM*APK.P	2486.87415	3	8.35E-06	0.69	3.07	-	739.1
AHQ-8-7, 6412	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	1.10E-09	0.98	6.96	-	1879.3
AHQ-8-8, 4799	K.LSDLLAPISEQIK.E	1427.66814	2	3.06E-05	0.81	3.07	-	673.1
AHQ-8-13, 5001	K.LSDLLAPISEQIK.E	1427.66814	2	9.39E-04	0.57	2.85	-	443.8
AHQ-8-7, 3038 - 3089	K.NSLDCEIVSAK.S	1237.36245	2	2.36E-05	0.91	3.68	-	832.4
AHQ-8-7, 3332	K.NSLDCEIVSAK.S	1237.36245	2	3.74E-09	0.91	3.41	-	1117.3
AHQ-8-7, 4336 - 4397	R.SALFAQINQGESITHALK.H	1929.16615	2	1.46E-05	0.87	4.39	-	447.3
AHQ-8-7, 4689	R.SALFAQINQGESITHALK.H	1929.16615	2	9.81E-05	0.28	2.74	-	353.1
AHQ-8-7, 4465 - 4524	R.SALFAQINQGESITHALK.H	1929.16615	2	1.20E-04	0.89	4.32	-	640.7
AHQ-8-7, 4473 - 4554	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.79E-07	0.93	4.81	-	699.9
AHQ-8-7, 4325	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	7.43E-05	0.79	3.12	-	703.9
AHQ-8-8, 4582	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	9.97E-07	0.93	4.37	-	821.6
gi|4505667|ref|NP_001074.1|	phosphodiesterase 5A isoform 1; cGMP-binding cGMP-specific 3',5'-cyclic			1.24E-09	2.29	30.21	5.00	100012.4
AHQ-8-5, 3726	R.FNAEVDQITGYK.T	1385.50354	2	6.54E-07	0.75	3.17	-	706.5
AHQ-8-4, 4162	R.FPWTTENTGNVNQQCIR.S	2067.22783	2	8.10E-06	0.59	3.16	-	658.9
AHQ-8-5, 5292	R.IAELVATEFFDQGDR.E	1711.85332	2	5.61E-08	0.96	4.21	-	1240.8
AHQ-8-4, 5343	R.IAELVATEFFDQGDR.E	1711.85332	2	1.24E-09	0.95	4.04	-	1287.1
gi|17318569|ref|NP_006112.2|	keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]			1.33E-09	17.80	200.29	37.60	66066.3
AHQ-8-4, 2947	R.DYQELMNTK.L	1142.26457	2	1.41E-04	0.91	3.13	-	1062.0
AHQ-8-2, 3012	R.DYQELMNTK.L	1142.26457	2	7.00E-05	0.87	2.89	-	977.4
AHQ-8-13-, 2274 - 2275	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	2.60E-07	0.78	3.53	-	570.0
AHQ-8-4, 2221 - 2222	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	3.92E-07	0.90	4.65	-	569.4
AHQ-8-13-, 2618	R.GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR.G	3314.18235	3	1.92E-08	0.93	4.49	-	1592.4
AHQ-8-10, 3098	K.KQISNLQQSISDAEQR.G	1845.99241	2	2.99E-04	0.87	3.70	-	755.1
AHQ-8-10, 4715	K.LALDLEIATYR.T	1278.47925	2	1.23E-04	0.91	2.65	-	1605.8
AHQ-8-13-, 4884	K.LALDLEIATYR.T	1278.47925	2	1.14E-07	0.91	3.75	-	1452.9
AHQ-8-13-, 3883 - 3942	K.LNDLEDALQQAK.E	1358.47963	2	1.23E-07	0.98	5.36	-	2117.5
AHQ-8-2, 3955	K.LNDLEDALQQAK.E	1358.47963	2	3.56E-06	0.97	4.36	-	2012.5
AHQ-8-13, 4039 - 4111	K.LNDLEDALQQAK.E	1358.47963	2	1.55E-07	0.97	4.93	-	1834.5
AHQ-8-4, 3889	K.LNDLEDALQQAK.E	1358.47963	2	6.05E-06	0.97	4.76	-	1752.9
AHQ-8-12, 3776	K.LNDLEDALQQAK.E	1358.47963	2	5.49E-05	0.94	3.81	-	1452.9
AHQ-8-3, 3885 - 3888	K.LNDLEDALQQAK.E	1358.47963	2	3.84E-09	0.96	4.57	-	1868.2
AHQ-8-10, 3704	K.LNDLEDALQQAK.E	1358.47963	2	2.20E-04	0.96	4.24	-	1732.0
AHQ-8-1, 4031	K.LNDLEDALQQAK.E	1358.47963	2	8.34E-08	0.97	4.65	-	1878.3
AHQ-8-5, 3873	K.LNDLEDALQQAK.E	1358.47963	2	7.16E-07	0.96	3.94	-	2111.6
AHQ-8-1, 4445	K.NKLNDLEDALQQAK.E	1600.75564	2	2.26E-04	0.96	4.51	-	1663.3
AHQ-8-2, 4373	K.NKLNDLEDALQQAK.E	1600.75564	2	4.40E-07	0.97	4.19	-	2092.3
AHQ-8-10, 4058 - 4100	K.NKLNDLEDALQQAK.E	1600.75564	2	7.83E-05	0.92	3.56	-	1224.9
AHQ-8-1, 3089	K.NMQDM*VEDYR.N	1317.43134	2	9.78E-05	0.83	3.08	-	818.5
AHQ-8-10, 2758 - 2814	K.NMQDM*VEDYR.N	1317.43134	2	3.04E-04	0.96	4.07	-	1527.8
AHQ-8-1, 3828	K.QISNLQQSISDAEQR.G	1717.81950	2	5.66E-08	0.94	4.10	-	977.6
AHQ-8-6, 3618	K.QISNLQQSISDAEQR.G	1717.81950	2	1.37E-04	0.79	2.92	-	695.0
AHQ-8-2, 3751	K.QISNLQQSISDAEQR.G	1717.81950	2	2.03E-05	0.84	3.56	-	579.4
AHQ-8-3, 3678	K.QISNLQQSISDAEQR.G	1717.81950	2	2.74E-07	0.86	3.34	-	711.8
AHQ-8-12, 3574	K.QISNLQQSISDAEQR.G	1717.81950	2	1.15E-05	0.77	2.91	-	599.0
AHQ-8-13, 3831	K.QISNLQQSISDAEQR.G	1717.81950	2	2.63E-06	0.82	3.32	-	629.8
AHQ-8-4, 3666	K.QISNLQQSISDAEQR.G	1717.81950	2	3.92E-06	0.95	4.59	-	1131.7
AHQ-8-14-, 3661	K.QISNLQQSISDAEQR.G	1717.81950	2	2.56E-06	0.94	4.10	-	956.3
AHQ-8-13-, 3694	K.QISNLQQSISDAEQR.G	1717.81950	2	1.18E-05	0.89	3.32	-	895.6
AHQ-8-14-, 3522 - 3586	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	1.56E-05	0.89	2.94	-	1315.7
AHQ-8-6, 3468	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	2.37E-05	0.89	3.39	-	990.8
AHQ-8-13-, 3460 - 3531	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	4.50E-04	0.90	3.14	-	1327.8
AHQ-8-10, 3294 - 3363	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	5.82E-06	0.94	3.49	-	1974.6
AHQ-8-2, 2061	K.SKAEAESLYQSK.Y	1341.44907	2	2.01E-08	0.92	3.77	-	1034.6
AHQ-8-4, 2002	K.SKAEAESLYQSK.Y	1341.44907	2	2.03E-08	0.87	3.51	-	692.8
AHQ-8-7, 1988	K.SKAEAESLYQSK.Y	1341.44907	2	5.36E-04	0.42	2.69	-	551.7
AHQ-8-1, 5837	R.SLDLDSIIAEVK.A	1303.48388	2	9.40E-07	0.95	4.20	-	1340.6
AHQ-8-8, 5807	R.SLDLDSIIAEVK.A	1303.48388	2	3.10E-05	0.91	3.58	-	1145.9
AHQ-8-7, 5609	R.SLDLDSIIAEVK.A	1303.48388	2	2.78E-06	0.94	4.03	-	1291.2
AHQ-8-13, 5779 - 5781	R.SLDLDSIIAEVK.A	1303.48388	2	6.05E-07	0.95	4.37	-	1238.2
AHQ-8-6, 5587 - 5655	R.SLDLDSIIAEVK.A	1303.48388	2	6.81E-05	0.90	3.43	-	1102.6
AHQ-8-12, 5559	R.SLDLDSIIAEVK.A	1303.48388	2	3.92E-04	0.88	2.69	-	1278.8
AHQ-8-1, 5743 - 5820	R.SLDLDSIIAEVK.A	1303.48388	2	1.46E-06	0.95	3.80	-	1201.7
AHQ-8-5, 5689 - 5762	R.SLDLDSIIAEVK.A	1303.48388	2	2.79E-05	0.93	3.92	-	1261.0
AHQ-8-10, 5478	R.SLDLDSIIAEVK.A	1303.48388	2	4.42E-05	0.90	3.58	-	1162.9
AHQ-8-2, 5819	R.SLDLDSIIAEVK.A	1303.48388	2	2.80E-06	0.96	4.30	-	1616.2
AHQ-8-3, 5645 - 5718	R.SLDLDSIIAEVK.A	1303.48388	2	1.80E-06	0.94	4.03	-	1199.0
AHQ-8-4, 5809 - 5810	R.SLDLDSIIAEVK.A	1303.48388	2	3.46E-07	0.96	4.71	-	1287.5
AHQ-8-7, 5525 - 5600	R.SLDLDSIIAEVK.A	1303.48388	2	2.24E-07	0.96	4.08	-	1511.0
AHQ-8-4, 4594	K.SLNNQFASFIDK.V	1384.51877	2	1.20E-04	0.77	3.14	-	640.5
AHQ-8-14, 5465	K.SLNNQFASFIDK.V	1384.51877	2	1.07E-06	0.80	3.06	-	741.6
AHQ-8-3, 4572	K.SLNNQFASFIDK.V	1384.51877	2	3.09E-06	0.92	4.01	-	930.5
AHQ-8-13, 4679 - 4739	K.SLNNQFASFIDK.V	1384.51877	2	4.54E-08	0.90	3.42	-	1034.2
AHQ-8-14-, 4506 - 4535	K.SLNNQFASFIDK.V	1384.51877	2	3.23E-05	0.87	3.03	-	920.5
AHQ-8-7, 4409 - 4481	K.SLNNQFASFIDK.V	1384.51877	2	6.96E-04	0.67	2.94	-	461.3

AHQ-8-2, 2556	R.SLVNLGGSK.S	875.00510	2	7.05E-04	0.72	2.81	-	440.4
AHQ-8-1, 4331	R.SLVNLGGSKSISISVAR.G	1688.95071	2	7.95E-07	0.73	3.17	-	505.9
AHQ-8-6, 6031	R.THNLEPYFESFINNLR.R	1995.18315	3	1.36E-05	0.94	4.37	-	1650.4
AHQ-8-2, 6183 - 6208	R.THNLEPYFESFINNLR.R	1995.18315	2	1.33E-09	0.94	4.57	-	580.4
AHQ-8-13-, 6003 - 6014	R.THNLEPYFESFINNLR.R	1995.18315	3	5.92E-07	0.97	5.72	-	1740.0
AHQ-8-4, 6174 - 6254	R.THNLEPYFESFINNLR.R	1995.18315	2	5.05E-04	0.77	3.51	-	334.4
AHQ-8-1, 6200	R.THNLEPYFESFINNLR.R	1995.18315	2	2.68E-05	0.84	3.32	-	534.5
AHQ-8-3, 6096	R.THNLEPYFESFINNLR.R	1995.18315	3	2.89E-05	0.93	4.91	-	1266.3
AHQ-8-13, 6135	R.THNLEPYFESFINNLR.R	1995.18315	3	1.56E-07	0.95	5.01	-	1765.7
AHQ-8-13-, 6012	R.THNLEPYFESFINNLR.R	1995.18315	2	7.78E-04	0.91	4.16	-	473.2
AHQ-8-13-, 6111	R.THNLEPYFESFINNLR.R	1995.18315	3	4.27E-05	0.83	3.72	-	948.3
AHQ-8-10, 5126 - 5143	R.THNLEPYFESFINNLR.R	1995.18315	2	6.42E-04	0.80	3.32	-	454.2
AHQ-8-1, 6195 - 6232	R.THNLEPYFESFINNLR.R	1995.18315	3	3.86E-05	0.98	5.29	-	2405.4
AHQ-8-6, 3142	R.TNAENEFVTIK.K	1266.38219	2	1.27E-05	0.80	2.89	-	576.2
AHQ-8-10, 3047 - 3123	R.TNAENEFVTIK.K	1266.38219	2	2.83E-04	0.89	3.42	-	857.9
AHQ-8-4, 3161	R.TNAENEFVTIK.K	1266.38219	2	1.02E-05	0.74	2.89	-	605.2
AHQ-8-13-, 3232	R.TNAENEFVTIK.K	1266.38219	2	1.35E-05	0.93	3.83	-	891.3
AHQ-8-7, 3080 - 3085	R.TNAENEFVTIK.K	1266.38219	2	8.95E-07	0.91	3.30	-	1014.1
AHQ-8-3, 3197	R.TNAENEFVTIK.K	1266.38219	2	5.87E-05	0.88	3.01	-	974.1
AHQ-8-1, 3379	R.TNAENEFVTIK.K	1266.38219	2	7.29E-07	0.87	3.28	-	768.8
AHQ-8-13, 3375 - 3381	R.TNAENEFVTIK.K	1266.38219	2	4.14E-04	0.88	3.56	-	701.3
AHQ-8-5, 3162	R.TNAENEFVTIK.K	1266.38219	2	8.57E-06	0.91	3.16	-	1031.4
AHQ-8-2, 3236	R.TNAENEFVTIK.K	1266.38219	2	3.90E-05	0.91	3.38	-	984.9
AHQ-8-10, 2622 - 2624	R.TNAENEFVTIKK.D	1394.55511	2	4.70E-05	0.75	2.90	-	564.5
AHQ-8-13-, 2774 - 2776	R.TNAENEFVTIKK.D	1394.55511	2	5.62E-09	0.88	3.61	-	981.3
AHQ-8-6, 4334 - 4352	K.WELLQQVDTSTR.T	1476.61621	2	3.39E-06	0.89	3.29	-	1161.2
AHQ-8-4, 4433 - 4461	K.WELLQQVDTSTR.T	1476.61621	2	1.31E-05	0.92	3.59	-	1356.8
AHQ-8-3, 4406 - 4473	K.WELLQQVDTSTR.T	1476.61621	2	1.83E-06	0.87	3.35	-	1102.1
AHQ-8-11, 4256 - 4291	K.WELLQQVDTSTR.T	1476.61621	2	2.46E-04	0.84	2.76	-	1035.3
AHQ-8-12, 4270 - 4330	K.WELLQQVDTSTR.T	1476.61621	2	1.56E-04	0.83	3.18	-	891.1
AHQ-8-7, 4250	K.WELLQQVDTSTR.T	1476.61621	2	1.10E-04	0.94	3.62	-	1571.5
AHQ-8-5, 4405	K.WELLQQVDTSTR.T	1476.61621	2	3.32E-05	0.65	2.62	-	667.3
AHQ-8-1, 4541 - 4600	K.WELLQQVDTSTR.T	1476.61621	2	3.13E-08	0.92	3.76	-	1225.3
AHQ-8-2, 4472 - 4495	K.WELLQQVDTSTR.T	1476.61621	2	7.45E-07	0.96	4.45	-	1470.6
AHQ-8-14, 3934	K.YEELQITAGR.H	1180.29253	2	5.17E-04	0.84	3.13	-	1137.1
AHQ-8-13, 3156 - 3223	K.YEELQITAGR.H	1180.29253	2	9.95E-04	0.92	3.17	-	1610.0
AHQ-8-12, 2947 - 3002	K.YEELQITAGR.H	1180.29253	2	3.50E-04	0.92	3.39	-	1307.2
AHQ-8-6, 2999	K.YEELQITAGR.H	1180.29253	2	2.47E-04	0.93	3.43	-	1569.2
AHQ-8-2, 3085	K.YEELQITAGR.H	1180.29253	2	6.14E-06	0.97	4.22	-	2134.3
AHQ-8-3, 3036	K.YEELQITAGR.H	1180.29253	2	4.64E-05	0.96	3.91	-	1988.1
AHQ-8-1, 3223	K.YEELQITAGR.H	1180.29253	2	3.02E-04	0.96	4.04	-	1753.9
AHQ-8-4, 3021	K.YEELQITAGR.H	1180.29253	2	3.13E-05	0.96	4.01	-	1679.6
gi|11056061|ref|NP_066932.1|	thymosin, beta 4 [Homo sapiens]			1.38E-09	1.68	20.22	43.20	5052.6
AHQ-8-14-, 2533	K.NPLPSKETIEQEK.Q	1513.67476	2	1.38E-09	0.80	3.57	-	440.5
AHQ-8-14-, 2625	K.TETQEKNPLPSKETIEQEK.Q	2230.41519	2	1.59E-05	0.88	4.49	-	518.6
gi|4502167|ref|NP_000475.1|	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disea			1.39E-09	0.78	10.17	2.30	86942.8
AHQ-8-4, 5661	R.LALENYITALQAVPPRPR.H	2023.36745	3	1.39E-09	0.78	3.30	-	811.3
gi|4504515|ref|NP_002146.1|	heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B			1.45E-09	3.57	40.23	8.60	70853.4
AHQ-8-6, 2506	K.ATAGDTHLGGEDFDNR.L	1676.68279	2	1.45E-09	0.89	3.31	-	1019.9
AHQ-8-6, 4799	R.FEELCSDLFR.S	1317.44926	2	2.55E-05	0.80	2.97	-	813.7
AHQ-8-6, 4683	R.IINEPTAAAIAYGLDR.R	1688.90603	3	1.59E-04	0.93	4.10	-	1539.5
AHQ-8-6, 4672	R.IINEPTAAAIAYGLDR.R	1688.90603	2	3.07E-04	0.89	3.50	-	806.9
AHQ-8-6, 4263	K.LLQDFFNGKELNK.S	1566.78249	2	6.72E-04	0.96	4.58	-	1413.0
gi|4505763|ref|NP_000282.1|	phosphoglycerate kinase 1 [Homo sapiens]			1.45E-09	5.29	60.29	23.00	44614.4
AHQ-8-8, 5570 - 5590	K.ACANPAAGSVILLENLR.F	1771.03187	2	5.34E-07	0.93	4.23	-	1056.4
AHQ-8-8, 5326	K.ALESPERPFLAILGGAK.V	1770.06542	2	1.45E-09	0.98	5.83	-	1807.8
AHQ-8-8, 4543	K.DVLFLKDCVGPEVEK.A	1750.00620	2	7.30E-09	0.94	4.44	-	967.0
AHQ-8-8, 5223	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	3.33E-07	0.86	3.59	-	722.3
AHQ-8-8, 5123	K.VLNNMEIGTSLFDEEGAK.I	1968.17459	2	1.08E-05	0.67	3.18	-	304.3
AHQ-8-8, 4162	K.YSLEPVAVELK.S	1248.44991	2	1.10E-06	0.91	3.27	-	1045.6
gi|4759082|ref|NP_004648.1|	serum deprivation response protein; serum deprivation response; phospha			1.54E-09	1.87	20.26	7.80	47172.9
AHQ-8-6, 5880 - 5892	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.37E-04	0.71	2.68	-	809.9
AHQ-8-13, 6016	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.54E-09	0.96	4.63	-	1347.8
AHQ-8-7, 5810 - 5876	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.74E-04	0.69	3.52	-	555.5
AHQ-8-13-, 5871	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.68E-05	0.96	4.48	-	1395.4
AHQ-8-11, 5713	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	6.34E-04	0.55	2.54	-	448.0
AHQ-8-12, 5608	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.29E-05	0.84	3.50	-	599.4
AHQ-8-8, 5851 - 5857	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.09E-04	0.96	5.13	-	1050.1
AHQ-8-7, 5637	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.08E-05	0.91	4.20	-	718.8
AHQ-8-13-, 5691	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.90E-04	0.83	3.81	-	511.2
AHQ-8-6, 5651 - 5706	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	3.87E-05	0.96	5.14	-	1034.3
AHQ-8-14-, 5693	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	6.65E-04	0.90	3.82	-	673.6
gi|4557361|ref|NP_001187.1|	BH3 interacting domain death agonist; BH3-interacting domain death agon			1.69E-09	1.76	20.18	14.40	21994.6
AHQ-8-11, 6260	R.DLATALEQLLQAYPR.D	1702.93270	2	1.67E-04	0.82	3.28	-	715.8
AHQ-8-11, 2791	R.IEADSESQEDIIR.N	1505.56635	2	1.69E-09	0.94	3.12	-	1870.2
gi|4507725|ref|NP_000362.1|	transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum			1.81E-09	4.51	50.24	49.00	15886.9
AHQ-8-13, 3893 - 3959	K.AADDTWEPFASGK.T	1395.45529	2	9.27E-04	0.69	2.58	-	741.5
AHQ-8-13-, 4308	K.ALGISPFHEHAEVVFTANDSGPR.R	2452.66660	3	1.28E-06	0.96	4.03	-	2598.8
AHQ-8-13, 4199	R.GSPAINVAVHVFR.K	1367.58095	2	1.12E-07	0.93	3.90	-	1075.3
AHQ-8-13-, 4038	R.GSPAINVAVHVFR.K	1367.58095	2	1.81E-09	0.95	4.05	-	1207.0
AHQ-8-13-, 3382	R.KAADDTWEPFASGK.T	1523.62820	2	6.17E-05	0.95	4.08	-	1457.2
AHQ-8-13, 3519	R.KAADDTWEPFASGK.T	1523.62820	2	9.24E-04	0.85	2.94	-	887.7
AHQ-8-13-, 5267	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	6.20E-08	0.96	4.75	-	1360.6
AHQ-8-13, 5379	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	2.29E-04	0.95	4.25	-	1693.6
gi|30159310|ref|XP_301899.1|	similar to beta-actin [Homo sapiens]			1.83E-09	1.40	20.18	9.20	32376.4
AHQ-8-8, 1789 - 1845	K.DSYVGNEAQSK.R	1198.22158	2	8.36E-06	0.73	3.23	-	653.8
AHQ-8-8, 1922	K.DSYVGNEAQSK.R	1198.22158	2	6.96E-05	0.65	2.55	-	795.3
AHQ-8-8, 2046 - 2119	K.DSYVGNEAQSK.R	1198.22158	2	1.22E-06	0.71	2.97	-	686.0
AHQ-8-9, 5313 - 5369	K.DSYVGNEAQSK.R	1198.22158	1	2.27E-04	0.54	2.03	-	460.0
AHQ-8-9, 5297 - 5353	K.DSYVGNEAQSK.R	1198.22158	2	3.52E-06	0.83	3.27	-	865.8
AHQ-8-8, 1565 - 2047	K.DSYVGNEAQSK.R	1198.22158	1	1.83E-09	0.61	2.67	-	415.9
AHQ-8-8, 4862 - 4938	K.SYKLLDGQVITIGNER.F	1807.04092	2	1.95E-06	0.79	3.62	-	499.1
AHQ-8-8, 4439	K.SYKLLDGQVITIGNER.F	1807.04092	2	2.73E-05	0.70	3.14	-	556.7
gi|19557677|ref|NP_002108.3|	major histocompatibility complex, class I, C precursor; HLA class I hi			2.02E-09	0.97	10.24	3.80	40994.6
AHQ-8-8, 3603	R.SWTAADTAAQITQR.K	1520.62908	2	2.02E-09	0.97	4.69	-	2114.6
gi|12025678|ref|NP_004915.2|	actinin, alpha 4 [Homo sapiens]			2.18E-09	8.94	100.27	13.30	104853.3
AHQ-8-4, 3526	R.DYETATLSDIK.A	1256.34094	2	1.43E-04	0.94	3.27	-	1444.7
AHQ-8-4, 4542	R.ETTDTDTADQVIASFK.V	1742.81936	2	1.48E-07	0.93	3.88	-	1179.6
AHQ-8-4, 2679	K.HRDYETATLSDIK.A	1549.66719	2	5.38E-05	0.90	3.24	-	992.9
AHQ-8-4, 3873	R.M*APYQGPDAVPGALDYK.S	1810.02037	2	2.18E-09	0.95	4.02	-	1324.5
AHQ-8-4, 3759	K.M*LDAEDIVNTARPDEK.A	1833.99864	2	6.91E-04	0.84	3.94	-	544.8
AHQ-8-4, 4537	R.QFASQANVVGPWIQTK.M	1775.00061	2	2.92E-08	0.75	3.23	-	538.4
AHQ-8-4, 6410	R.SIVDYKPNLDLLEQQHQLIQEALIFDNK.H	3326.74423	3	2.60E-09	0.94	5.46	-	903.0
AHQ-8-6, 5954	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	2.25E-04	0.89	4.47	-	821.0
AHQ-8-4, 3927	K.VLAGDKNFITAEELR.R	1676.89525	2	6.79E-06	0.86	3.57	-	813.1
AHQ-8-4, 3729 - 3741	K.VLAVNQENEHLMEDYEK.L	2062.24648	2	3.39E-05	0.95	4.68	-	1150.6
gi|4506877|ref|NP_002996.1|	selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;			2.20E-09	3.74	40.24	8.00	90844.7

AHQ-8-3, 5429	K.LECLASGIWTNKPPQCLAAQCPPLK.I	2857.31818	3	2.05E-05	0.94	4.64	-	1222.4
AHQ-8-3, 3141	R.PSGQWTAVTPACR.A	1432.58672	2	1.35E-05	0.91	3.58	-	977.1
AHQ-8-3, 4608	K.STCQFICDEGYSLSGPER.L	2109.23671	2	2.20E-09	0.95	4.78	-	982.1
AHQ-8-4, 4659	K.STCQFICDEGYSLSGPER.L	2109.23671	2	5.59E-07	0.94	4.00	-	1151.9
AHQ-8-3, 2972	R.YTDLVAIQNK.N	1165.32100	2	1.19E-06	0.94	3.70	-	1267.3
gi|29568101|ref|NP_006467.3|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT			2.24E-09	0.95	10.21	14.60	11400.3
AHQ-8-14-, 3642	K.TPALVNAAVTYSKPR.L	1588.83283	2	9.80E-08	0.91	3.62	-	1085.4
AHQ-8-14-, 3633	K.TPALVNAAVTYSKPR.L	1588.83283	3	2.24E-09	0.95	4.21	-	1588.5
gi|20149594|ref|NP_031381.2|	heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea			2.25E-09	4.15	50.24	9.50	83263.6
AHQ-8-5, 2522	K.EDQTEYLEER.R	1312.32145	2	3.25E-05	0.68	2.74	-	462.5
AHQ-8-4, 3142	R.ELISNASDALDK.I	1276.37539	2	1.00E-06	0.86	3.05	-	774.0
AHQ-8-14, 4869	R.NPDDITQEEYGEFYK.S	1848.90048	2	4.32E-06	0.86	3.85	-	579.9
AHQ-8-5, 4004	R.NPDDITQEEYGEFYK.S	1848.90048	2	3.16E-06	0.93	4.32	-	911.9
AHQ-8-6, 3963	R.NPDDITQEEYGEFYK.S	1848.90048	2	2.25E-09	0.96	4.76	-	1141.5
AHQ-8-14-, 3975	R.NPDDITQEEYGEFYK.S	1848.90048	2	4.88E-05	0.87	3.33	-	998.3
AHQ-8-5, 3969	K.SLTNDWEDHLAVK.H	1528.64798	2	1.79E-04	0.86	3.71	-	629.1
AHQ-8-5, 3958	R.YHTSQSGDEMTSLSEYVSR.M	2178.27920	2	1.48E-04	0.78	3.17	-	633.6
gi|27498267|ref|XP_209737.1|	similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,			2.34E-09	2.77	30.32	32.60	11063.6
AHQ-8-10, 6122 - 6133	R.DICNDVLSLLEK.F	1420.61093	2	9.92E-04	0.88	3.23	-	1282.5
AHQ-8-14-, 6294	R.DICNDVLSLLEK.F	1420.61093	2	1.28E-06	0.87	3.02	-	1504.1
AHQ-8-10, 4459	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.07E-04	0.88	3.40	-	890.7
AHQ-8-10, 4626 - 4682	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.34E-09	0.98	5.53	-	1792.0
AHQ-8-10, 4683 - 4690	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	1.04E-08	0.98	6.47	-	2601.6
AHQ-8-10, 4370	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.58E-05	0.77	3.58	-	423.7
AHQ-8-14-, 4878 - 4879	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	7.25E-08	0.97	5.22	-	1373.9
AHQ-8-11, 4743	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	7.36E-06	0.93	4.20	-	1040.5
AHQ-8-11, 4749 - 4817	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	2.48E-04	0.95	4.26	-	1937.5
AHQ-8-12, 4774	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.72E-04	0.94	4.06	-	1124.4
AHQ-8-13, 5023 - 5025	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.11E-09	0.97	5.67	-	1385.1
AHQ-8-14, 5621	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.14E-06	0.93	4.40	-	805.9
AHQ-8-13-, 4862	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.83E-08	0.97	5.79	-	1143.8
AHQ-8-10, 4270	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	2	2.07E-04	0.81	3.38	-	765.3
AHQ-8-10, 4272 - 4274	K.KGIVDQSQQAYQEAFEISK.K	2170.36467	3	1.13E-05	0.92	3.90	-	1462.8
gi|17986258|ref|NP_066299.2|	smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo			2.37E-09	5.63	70.23	42.40	16930.0
AHQ-8-12, 4044 - 4119	K.DQGTYEDYVEGLR.V	1545.58904	2	7.00E-07	0.93	3.83	-	1062.4
AHQ-8-13, 4311 - 4312	K.DQGTYEDYVEGLR.V	1545.58904	2	1.71E-06	0.94	4.01	-	1147.0
AHQ-8-12, 3867	K.EAFQLFDR.T	1026.12699	1	5.88E-06	0.24	2.21	-	103.1
AHQ-8-12, 2510 - 2572	R.HVLVTLGEK.M	996.18547	2	1.45E-05	0.86	2.96	-	680.3
AHQ-8-12, 2459	R.HVLVTLGEK.M	996.18547	1	4.13E-04	0.85	2.96	-	747.3
AHQ-8-12, 2406 - 2467	R.HVLVTLGEK.M	996.18547	2	8.50E-07	0.85	3.15	-	558.6
AHQ-8-12, 3718 - 3774	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.14E-04	0.95	4.42	-	1354.6
AHQ-8-12, 3608	K.NKDQGTYEDYVEGLR.V	1787.86505	3	6.23E-04	0.92	4.57	-	1058.2
AHQ-8-12, 3606 - 3664	K.NKDQGTYEDYVEGLR.V	1787.86505	2	7.52E-08	0.94	4.38	-	1081.2
AHQ-8-14-, 3722	K.NKDQGTYEDYVEGLR.V	1787.86505	3	5.70E-05	0.94	4.66	-	1331.6
AHQ-8-14-, 3966	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.03E-04	0.73	3.31	-	513.8
AHQ-8-14-, 3719	K.NKDQGTYEDYVEGLR.V	1787.86505	2	4.95E-07	0.93	4.09	-	1086.9
AHQ-8-13-, 3763	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.50E-09	0.96	4.43	-	1596.8
AHQ-8-13, 3900	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.88E-04	0.71	3.28	-	461.4
AHQ-8-12, 3831 - 3886	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.25E-05	0.85	3.39	-	816.0
AHQ-8-14, 4649	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.89E-05	0.88	3.37	-	886.0
AHQ-8-13-, 3762	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.91E-06	0.87	3.61	-	984.1
AHQ-8-12, 3255 - 3310	R.VFDKEGNGTVMGAEIR.H	1723.93228	2	2.37E-09	0.94	4.55	-	1035.7
AHQ-8-12, 5802 - 5864	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	4.65E-05	0.85	3.44	-	1017.9
AHQ-8-12, 5760 - 5818	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	1.29E-04	0.93	4.48	-	645.8
AHQ-8-12, 6150	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	2.23E-04	0.87	4.02	-	551.3
AHQ-8-14-, 5901 - 5923	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	4.95E-06	0.84	3.56	-	844.4
gi|30160191|ref|XP_294035.2|	similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme			2.42E-09	0.97	10.23	2.80	50222.2
AHQ-8-7, 4761 - 4776	K.IYVDDGLISLQVK.Q	1463.70048	2	2.42E-09	0.97	4.58	-	2069.0
AHQ-8-7, 4596 - 4662	K.IYVDDGLISLQVK.Q	1463.70048	2	5.19E-06	0.89	3.59	-	1017.0
gi|5729887|ref|NP_006624.1|	IQ motif containing GTPase activating protein 2 [Homo sapiens]			2.43E-09	3.53	40.28	4.10	180611.0
AHQ-8-4, 4641	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	7.76E-08	0.94	3.77	-	1365.2
AHQ-8-3, 4596	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	2.43E-09	0.95	4.30	-	1293.1
AHQ-8-3, 4045	K.TLVGSENPPLTVIR.K	1496.73370	2	3.27E-04	0.72	2.86	-	512.9
AHQ-8-3, 4065	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	8.70E-05	0.97	5.63	-	1367.0
AHQ-8-3, 5442	R.VVAVGYINEAIDEGNPLR.T	1930.15092	2	8.26E-04	0.89	3.84	-	1038.6
gi|6598323|ref|NP_001485.2|	GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom			2.79E-09	2.70	30.28	11.90	50662.9
AHQ-8-8, 5137	R.NPYYGGESASITPLEDLYK.R	2118.28499	2	2.79E-09	0.97	5.54	-	1636.0
AHQ-8-8, 6355	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	3	5.00E-07	0.85	3.40	-	943.5
AHQ-8-8, 6349	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.30E-07	0.94	4.61	-	789.0
AHQ-8-7, 6140 - 6190	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	2.21E-05	0.90	4.11	-	475.9
AHQ-8-8, 3957	R.TDDYLDQPCYETINR.I	1904.98887	2	4.89E-06	0.79	3.56	-	356.2
gi|14251209|ref|NP_001279.2|	chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo			3.80E-09	2.72	30.24	21.60	26922.5
AHQ-8-9, 6610	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	2	1.95E-06	0.87	3.84	-	639.1
AHQ-8-14-, 3439	K.GVTFNVTTVDTK.R	1282.42476	2	6.94E-06	0.94	3.98	-	1105.4
AHQ-8-10, 3299	K.GVTFNVTTVDTK.R	1282.42476	2	3.76E-04	0.86	3.04	-	888.7
AHQ-8-13, 3627	K.GVTFNVTTVDTK.R	1282.42476	2	1.22E-06	0.92	3.88	-	908.2
AHQ-8-13-, 3439 - 3474	K.GVTFNVTTVDTK.R	1282.42476	2	8.25E-06	0.92	3.75	-	1132.4
AHQ-8-13-, 5196	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.80E-09	0.93	4.27	-	741.1
AHQ-8-9, 6652	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	5.99E-07	0.89	3.84	-	484.8
AHQ-8-14-, 5117	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	9.16E-04	0.96	4.84	-	963.5
AHQ-8-13-, 5106 - 5110	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.64E-04	0.96	4.78	-	956.9
gi|5453740|ref|NP_006462.1|	myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat			3.95E-09	5.21	60.27	32.20	19794.0
AHQ-8-14-, 5777	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	3.44E-06	0.96	4.18	-	1576.8
AHQ-8-14-, 5177	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.61E-06	0.96	4.62	-	1589.8
AHQ-8-13-, 5768	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	7.71E-05	0.96	4.19	-	1502.7
AHQ-8-12, 5594 - 5663	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.22E-04	0.78	3.73	-	457.1
AHQ-8-13-, 5187 - 5252	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.28E-06	0.81	3.51	-	574.7
AHQ-8-11, 4916 - 4991	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.36E-05	0.79	3.37	-	625.5
AHQ-8-11, 5056 - 5117	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.99E-08	0.98	5.30	-	1650.1
AHQ-8-11, 5172 - 5199	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	3.15E-06	0.93	3.93	-	1033.8
AHQ-8-12, 5039 - 5094	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	3.95E-09	0.97	4.93	-	1479.4
AHQ-8-11, 5583 - 5641	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	2.00E-04	0.94	4.03	-	1235.0
AHQ-8-13, 5303	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	4.22E-07	0.90	3.44	-	871.3
AHQ-8-11, 5448	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	4.70E-09	0.90	3.47	-	1361.0
AHQ-8-11, 4333	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	1.56E-04	0.88	3.76	-	625.2
AHQ-8-12, 4359 - 4363	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	3	8.79E-06	0.93	3.90	-	1642.5
AHQ-8-11, 2655 - 2735	R.ELLTTMGDR.F	1036.18513	2	3.58E-05	0.71	2.64	-	507.6
AHQ-8-11, 4200	K.GNFNYIEFTR.I	1261.36733	2	6.00E-04	0.76	2.91	-	791.8
AHQ-8-14-, 4126	K.GNFNYIEFTR.I	1261.36733	2	1.67E-05	0.76	2.76	-	648.7
AHQ-8-11, 3965 - 4039	K.GNFNYIEFTR.I	1261.36733	2	8.17E-05	0.64	3.13	-	549.2
AHQ-8-12, 4058 - 4060	K.GNFNYIEFTR.I	1261.36733	2	4.20E-04	0.85	3.50	-	791.4
AHQ-8-11, 4343	K.GNFNYIEFTR.I	1261.36733	2	4.03E-04	0.73	3.41	-	692.1
gi|5031677|ref|NP_005681.1|	dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [			4.03E-09	4.26	50.20	10.00	78060.6
AHQ-8-13-, 4640	K.ALQGASQIIAEIR.E	1370.57991	2	1.21E-08	0.94	3.83	-	1660.4
AHQ-8-5, 4658	K.ALQGASQIIAEIR.E	1370.57991	2	1.17E-04	0.83	3.01	-	939.0
AHQ-8-5, 5008	K.DTLQSELVGQLYK.S	1494.67144	2	9.65E-04	0.87	3.41	-	871.2
AHQ-8-6, 5831	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	1.01E-04	0.74	3.28	-	633.0

AHQ-8-5, 5933 - 5949	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	5.19E-06	0.83	3.68	-	684.6
AHQ-8-13, 5935	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	2.86E-04	0.63	2.81	-	637.7
AHQ-8-13-, 5807	K.SSLLDDLLTESEDM*AQR.R	1940.07638	2	4.03E-09	0.72	2.78	-	847.7
AHQ-8-5, 6440	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	3.65E-05	0.89	3.92	-	669.9
gi|12408656|ref|NP_005177.2|	calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ			4.27E-09	7.38	90.25	16.10	81889.4
AHQ-8-6, 4914	K.APSDLYQIILK.A	1261.49183	2	2.90E-05	0.94	3.97	-	1145.0
AHQ-8-5, 5829 - 5886	R.DM*ETIGFAVYEVPPELVGQPAVHLK.R	2757.15391	3	9.64E-07	0.93	5.03	-	899.4
AHQ-8-6, 4358	R.KAPSDLYQIILK.A	1389.66474	2	4.34E-05	0.86	3.18	-	934.2
AHQ-8-6, 4688	R.LEICNLTPDALK.S	1388.61207	2	9.33E-05	0.78	2.77	-	850.4
AHQ-8-5, 4772 - 4774	R.LEICNLTPDALK.S	1388.61207	2	8.92E-04	0.94	4.66	-	865.3
AHQ-8-6, 4559	R.LPPGEYVVVPSTFEPNK.E	1874.12573	2	3.90E-05	0.74	2.96	-	467.0
AHQ-8-6, 5382 - 5383	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	4.27E-09	0.84	3.92	-	664.6
AHQ-8-5, 4476	K.RPTELLSNPQFIVDGATR.T	2015.25904	2	2.70E-05	0.93	4.44	-	543.4
AHQ-8-5, 3246	R.SEQFINLR.E	1007.12521	2	4.47E-04	0.73	2.66	-	684.3
AHQ-8-6, 3222	R.SEQFINLR.E	1007.12521	2	6.00E-04	0.82	2.66	-	854.2
AHQ-8-6, 6255	K.TLDTDLDGVVTFDLFK.W	1799.99879	2	3.23E-04	0.63	2.90	-	530.2
gi|5901944|ref|NP_008977.1|	elastin microfibril interface located protein; TNF? elastin microfibril			4.81E-09	2.32	30.18	4.60	106694.7
AHQ-8-3, 2964 - 2984	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	4.83E-05	0.84	3.57	-	688.4
AHQ-8-3, 2950	R.LVGSGLHTVEAAGEAR.Q	1567.72888	2	4.81E-09	0.89	3.31	-	951.7
AHQ-8-3, 3800 - 3857	K.VQQLEEQVQSLTK.E	1530.70532	2	1.56E-05	0.59	3.15	-	709.6
gi|16933542|ref|NP_002017.1|	fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s			4.96E-09	1.79	20.23	1.60	259222.8
AHQ-8-2, 5724	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	4.96E-09	0.92	4.54	-	700.1
AHQ-8-2, 4575	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	1.93E-05	0.87	3.75	-	773.4
AHQ-8-3, 4506	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	4.91E-04	0.81	3.75	-	581.9
AHQ-8-1, 4625	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	7.44E-04	0.67	2.74	-	731.8
gi|4504073|ref|NP_000398.1|	glycoprotein Ib beta polypeptide precursor [Homo sapiens]			5.51E-09	2.47	30.19	15.50	21717.6
AHQ-8-1, 4732 - 4745	R.LLPYLAEDELR.A	1332.52691	2	3.16E-04	0.71	2.68	-	505.2
AHQ-8-4, 4633	R.LLPYLAEDELR.A	1332.52691	2	2.99E-06	0.77	2.72	-	478.2
AHQ-8-5, 4592	R.LLPYLAEDELR.A	1332.52691	2	3.48E-06	0.79	2.60	-	614.4
AHQ-8-6, 4499	R.LLPYLAEDELR.A	1332.52691	2	7.60E-07	0.64	2.76	-	386.1
AHQ-8-8, 4513	R.LLPYLAEDELR.A	1332.52691	2	1.14E-04	0.50	2.53	-	358.1
AHQ-8-13-, 4551	R.LLPYLAEDELR.A	1332.52691	2	2.20E-05	0.87	3.07	-	716.2
AHQ-8-13, 4719 - 4720	R.LLPYLAEDELR.A	1332.52691	2	9.69E-07	0.93	3.27	-	823.2
AHQ-8-11, 4411	R.LLPYLAEDELR.A	1332.52691	2	4.47E-06	0.83	3.05	-	479.0
AHQ-8-11, 4112	R.LSLTDPLVAER.A	1214.39356	2	5.51E-09	0.95	3.74	-	1487.4
AHQ-8-11, 2475	R.TAHLGANPWR.C	1123.24913	2	4.20E-05	0.88	3.19	-	697.3
gi|29739414|ref|XP_294015.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			5.52E-09	1.85	20.22	12.80	26916.7
AHQ-8-10, 3770 - 3827	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.53E-06	0.56	2.71	-	654.8
AHQ-8-9, 6590 - 6660	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.05E-08	0.90	4.40	-	1246.3
AHQ-8-13, 4981	K.LISWYDNEFGYSNR.V	1764.87478	2	3.02E-07	0.94	4.31	-	871.8
AHQ-8-13-, 4819	K.LISWYDNEFGYSNR.V	1764.87478	2	1.56E-06	0.90	3.69	-	899.2
AHQ-8-14-, 4803	K.LISWYDNEFGYSNR.V	1764.87478	2	5.52E-09	0.94	4.12	-	987.1
AHQ-8-11, 4655 - 4725	K.LISWYDNEFGYSNR.V	1764.87478	2	8.01E-08	0.95	4.19	-	1176.9
gi|4503747|ref|NP_001448.1|	filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a			6.05E-09	2.66	30.25	1.00	278191.4
AHQ-8-3, 5940	R.LIALLEVLSQK.R	1227.51852	2	8.21E-06	0.96	4.20	-	1332.5
AHQ-8-1, 6047	R.LIALLEVLSQK.R	1227.51852	2	1.04E-05	0.96	4.12	-	1362.3
AHQ-8-10, 5702	R.LIALLEVLSQK.R	1227.51852	2	3.37E-04	0.72	2.69	-	459.8
AHQ-8-2, 5823	R.LIALLEVLSQK.R	1227.51852	2	1.48E-05	0.97	4.27	-	1743.8
AHQ-8-2, 6039	R.LIALLEVLSQK.R	1227.51852	2	2.52E-06	0.97	4.44	-	1688.7
AHQ-8-7, 5806	R.LIALLEVLSQK.R	1227.51852	2	4.81E-07	0.94	3.64	-	1160.1
AHQ-8-11, 5759	R.LIALLEVLSQK.R	1227.51852	2	4.37E-06	0.90	3.56	-	786.5
AHQ-8-4, 6026	R.LIALLEVLSQK.R	1227.51852	2	6.05E-09	0.96	4.20	-	1157.1
AHQ-8-5, 5970 - 5977	R.LIALLEVLSQK.R	1227.51852	2	1.12E-07	0.97	4.94	-	1683.7
AHQ-8-2, 6475	R.QMQLENVSVALEFLDR.E	1893.15408	2	4.46E-07	0.92	3.90	-	900.5
AHQ-8-1, 6447	R.QMQLENVSVALEFLDR.E	1893.15408	2	9.77E-06	0.92	3.89	-	986.3
AHQ-8-1, 6005	R.QM*QLENVSVALEFLDR.E	1909.15348	2	1.64E-05	0.86	3.60	-	560.9
AHQ-8-5, 5952	R.QM*QLENVSVALEFLDR.E	1909.15348	2	7.35E-06	0.78	2.86	-	811.4
gi|4507869|ref|NP_003361.1|	vasodilator-stimulated phosphoprotein [Homo sapiens]			6.18E-09	1.70	20.24	7.10	39829.4
AHQ-8-8, 5925	K.VKEEIIEAFVQELR.K	1703.96061	2	6.18E-09	0.96	4.88	-	1336.7
AHQ-8-14-, 2941 - 2949	R.VQIYHNPTANSFR.V	1547.69936	2	2.91E-05	0.74	3.07	-	595.8
gi|5902128|ref|NP_008880.1|	syntaxin binding protein 2; Hunc18b [Homo sapiens]			6.31E-09	7.24	80.28	25.10	66438.1
AHQ-8-6, 6339	R.AADPVSPLLHELTFQAM*AYDLLDIEQDTYR.Y	3453.81998	3	1.39E-04	0.92	4.66	-	1186.2
AHQ-8-6, 5812	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	2	2.21E-05	0.96	5.56	-	909.1
AHQ-8-6, 2862	K.DVMEDAVEDR.L	1179.24007	2	4.35E-04	0.86	2.76	-	1102.1
AHQ-8-6, 3670	K.GPEDTAQLAHAVLAK.L	1521.70012	2	1.79E-08	0.88	3.73	-	879.3
AHQ-8-6, 3591	K.LCSVEQDLAM*GSDAEGEK.I	1957.08386	2	6.31E-09	0.93	3.83	-	1120.4
AHQ-8-6, 6275	K.M*SDILAEGITIVEDINKR.R	2034.32082	3	1.05E-06	0.79	3.65	-	697.8
AHQ-8-6, 3242	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	1.10E-04	0.92	4.25	-	994.9
AHQ-8-6, 5607	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	5.52E-07	0.97	5.56	-	1404.1
gi|13899317|ref|NP_113657.1|	SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M			8.03E-09	4.15	50.29	56.10	12326.0
AHQ-8-13, 5404	K.ESNTVFSFLGLKPR.L	1595.82383	2	1.77E-05	0.54	2.69	-	288.0
AHQ-8-13-, 5283	K.ESNTVFSFLGLKPR.L	1595.82383	2	4.55E-08	0.68	3.10	-	413.9
AHQ-8-14, 6095	K.ESNTVFSFLGLKPR.L	1595.82383	2	9.75E-07	0.67	2.74	-	476.9
AHQ-8-14-, 5265 - 5271	K.ESNTVFSFLGLKPR.L	1595.82383	2	8.03E-09	0.82	3.80	-	457.0
AHQ-8-13-, 4760	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	1.01E-07	0.86	4.03	-	929.4
AHQ-8-14-, 4761 - 4762	R.FLEANKIEFEEVDITM*SEEQR.Q	2574.80223	3	5.09E-05	0.97	5.82	-	1786.2
AHQ-8-14-, 4133	K.IEFEEVDITM*SEEQR.Q	1872.00051	2	1.49E-04	0.53	2.59	-	652.8
AHQ-8-14, 5045	K.IEFEEVDITM*SEEQR.Q	1872.00051	2	5.24E-04	0.65	2.53	-	610.2
AHQ-8-14-, 4305	R.VFIASSSGFVAIK.K	1326.56551	2	1.53E-06	0.98	4.75	-	2492.2
AHQ-8-13-, 4320	R.VFIASSSGFVAIK.K	1326.56551	2	8.75E-04	0.97	4.09	-	2131.4
AHQ-8-14-, 4306 - 4381	R.YCGDYDSFFESK.E	1519.57010	2	8.36E-05	0.96	3.53	-	1453.7
gi|29742410|ref|XP_291183.1|	similar to TREM-like transcript 1 [Homo sapiens]			8.78E-09	1.62	20.17	10.30	32678.3
AHQ-8-11, 4144	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	8.78E-09	0.89	3.46	-	781.7
AHQ-8-13-, 4228	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.15E-05	0.86	3.06	-	558.4
AHQ-8-11, 3763	R.VSLNILPPEEEEETHK.I	1865.03087	3	3.43E-05	0.73	3.07	-	705.2
gi|4757810|ref|NP_004037.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,			9.60E-09	5.67	70.22	15.90	59750.3
AHQ-8-7, 3730 - 3800	R.EAYPGDVFYLHSR.L	1554.68713	2	7.09E-05	0.41	2.62	-	389.9
AHQ-8-7, 5097	K.GM*SLNLEPDNVGVVVFGNDK.L	2121.35703	2	9.60E-09	0.91	4.48	-	596.4
AHQ-8-7, 3496	K.HALIIYDDLSK.Q	1288.47413	2	3.14E-06	0.96	3.63	-	1391.3
AHQ-8-7, 3593 - 3662	R.ILGADTSVDLEETGR.V	1576.68772	2	2.08E-07	0.89	3.31	-	1074.5
AHQ-8-14-, 3678	R.ILGADTSVDLEETGR.V	1576.68772	2	1.03E-05	0.73	2.82	-	1039.9
AHQ-8-7, 4941 - 4945	R.TGAIVDVPVGEELLGR.V	1625.84824	2	6.87E-05	0.88	3.60	-	696.8
AHQ-8-7, 3685	K.TGTAEMSSILEER.I	1424.55988	2	6.92E-04	0.82	3.12	-	869.9
AHQ-8-7, 2656	K.TGTAEM*SSILEER.I	1440.55928	2	1.48E-04	0.80	2.73	-	1082.0
gi|29729616|ref|XP_292963.1|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			1.01E-08	0.94	10.30	16.40	18025.4
AHQ-8-13, 4855 - 4936	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	8.01E-04	0.96	6.05	-	1217.0
AHQ-8-13-, 4694	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	5.56E-05	0.91	4.58	-	1219.6
AHQ-8-14-, 4694 - 4773	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	1.01E-08	0.94	5.18	-	1249.2
AHQ-8-12, 4622	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	2	7.48E-04	0.74	3.32	-	419.9
gi|5729877|ref|NP_006588.1|	heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD			1.03E-08	9.39	110.24	19.50	70897.6
AHQ-8-6, 4303 - 4310	R.ARFEELNADLFR.G	1481.63768	2	7.87E-08	0.97	4.81	-	1295.2
AHQ-8-7, 4225	R.ARFEELNADLFR.G	1481.63768	2	1.72E-06	0.96	4.62	-	1164.9
AHQ-8-6, 4311	R.ARFEELNADLFR.G	1481.63768	3	1.38E-04	0.91	3.98	-	1219.1
AHQ-8-6, 4512 - 4514	R.FEELNADLFR.G	1254.37310	2	2.92E-07	0.91	3.93	-	1007.5
AHQ-8-6, 5310	K.ILDKCNEIINWLDK.N	1776.04688	2	3.07E-05	0.77	3.24	-	744.7
AHQ-8-6, 5324	K.ILDKCNEIINWLDK.N	1776.04688	3	5.37E-05	0.92	4.75	-	924.1
AHQ-8-6, 2626	K.M*KEIAEAYLGK.T	1269.49260	2	2.99E-07	0.82	3.10	-	890.9

AHQ-8-7, 3501	K.NQVAMNPTNTVFDAK.R	1650.83816	2	4.96E-04	0.77	3.24	-	463.3
AHQ-8-6, 3716	K.NQVAMNPTNTVFDAK.R	1650.83816	2	9.26E-06	0.90	3.50	-	699.7
AHQ-8-6, 2814	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	5.80E-06	0.91	3.86	-	674.8
AHQ-8-6, 3534	K.NQVAMNPTNTVFDAK.R	1650.83816	2	8.60E-04	0.93	4.14	-	816.2
AHQ-8-6, 3268 - 3347	K.NSLESYAFNM*K.A	1320.45333	2	5.25E-05	0.90	3.17	-	1096.5
AHQ-8-6, 2254	R.RFDDAVVQSDM*K.H	1427.56543	2	5.60E-06	0.93	3.65	-	835.1
AHQ-8-6, 4240 - 4286	K.SFYPEEVSSM*VLTK.M	1633.84425	2	3.44E-04	0.63	2.62	-	441.8
AHQ-8-6, 4348	K.SFYPEEVSSM*VLTK.M	1633.84425	2	3.90E-04	0.84	3.52	-	528.9
AHQ-8-7, 6132	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	1.30E-05	0.70	3.12	-	461.8
AHQ-8-6, 6171 - 6174	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	3	4.67E-05	0.80	3.71	-	955.2
AHQ-8-6, 3154 - 3155	K.SQIHDIVLVGGSTR.I	1482.66712	2	1.03E-08	0.97	4.36	-	1800.3
AHQ-8-6, 3168	K.SQIHDIVLVGGSTR.I	1482.66712	1	1.25E-05	0.47	2.54	-	634.0
AHQ-8-7, 3097 - 3130	K.SQIHDIVLVGGSTR.I	1482.66712	2	1.35E-06	0.95	3.97	-	1462.2
gi|5031571|ref|NP_005713.1|	actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog			1.11E-08	4.55	50.20	12.70	44760.5
AHQ-8-8, 3629	K.DLMVGDEASELR.S	1335.46633	2	2.69E-06	0.91	3.33	-	1051.9
AHQ-8-8, 3301	K.DLM*VGDEASELR.S	1351.46573	2	1.48E-06	0.90	3.17	-	1059.1
AHQ-8-8, 3511	R.GYAFNHSADFETVR.M	1614.69943	2	9.63E-07	0.94	3.95	-	949.8
AHQ-8-8, 3341 - 3401	R.GYAFNHSADFETVR.M	1614.69943	2	2.45E-05	0.84	3.45	-	832.8
AHQ-8-8, 4113	K.HLWDYTFGPEK.L	1393.52736	2	3.15E-07	0.86	3.31	-	541.3
AHQ-8-8, 3663	K.LCYVGYNIEQEQK.L	1645.81494	2	1.11E-08	0.94	3.91	-	1115.5
gi|4507171|ref|NP_003109.1|	secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec			1.11E-08	2.64	30.22	11.60	34632.0
AHQ-8-8, 3181	R.LEAGDHPVELLAR.D	1420.59579	2	1.11E-08	0.97	4.33	-	1632.1
AHQ-8-8, 3303 - 3361	K.LHLDYIGPCK.Y	1217.41920	2	1.87E-05	0.78	3.20	-	548.7
AHQ-8-8, 3465	K.TFDSSCHFFATK.C	1449.56938	2	5.24E-05	0.89	3.93	-	814.2
gi|5454152|ref|NP_006285.1|	ubiquinol-cytochrome c reductase binding protein [Homo sapiens]			1.14E-08	1.82	20.21	25.20	13530.4
AHQ-8-13-, 3534	R.DDTIYEDEDVKEAIR.R	1811.88169	2	1.14E-08	0.86	3.42	-	920.5
AHQ-8-13-, 4994	K.YEEENFYLEPYLK.E	1737.88601	2	1.17E-04	0.96	4.15	-	1609.2
gi|4885183|ref|NP_005210.1|	diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS			1.15E-08	5.11	60.21	7.80	138977.7
AHQ-8-3, 4486 - 4492	R.LGLHQVLQDLR.E	1292.51238	2	2.45E-05	0.73	3.04	-	608.9
AHQ-8-3, 5926	K.LQFSEQVENIKPEIVSVTAACEELR.K	2892.23121	3	3.93E-05	0.84	3.84	-	822.9
AHQ-8-3, 4885 - 4892	K.LVAEDLSQDCFWTK.V	1713.88927	2	1.15E-08	0.92	4.19	-	759.7
AHQ-8-3, 5378	K.QDLEAEVSQLTGEVAK.L	1717.85617	2	7.82E-05	0.89	3.82	-	763.0
AHQ-8-3, 5545 - 5554	K.TAQNLSIFLGSFR.M	1454.65537	2	1.57E-05	0.81	3.34	-	569.9
AHQ-8-3, 4692	R.VQLNVFDEQGEEDSYDLK.G	2129.22304	2	7.05E-06	0.92	4.20	-	827.4
gi|4506413|ref|NP_002875.1|	RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s			1.20E-08	5.45	60.26	25.00	20987.1
AHQ-8-11, 2519 - 2523	K.CDLEDERVVGK.E	1321.43945	2	4.36E-05	0.86	3.13	-	933.3
AHQ-8-14-, 5557 - 5558	K.INVNEIFYDLVR.Q	1495.70427	2	6.15E-05	0.91	3.65	-	934.6
AHQ-8-13-, 6235	K.INVNEIFYDLVR.Q	1495.70427	2	8.47E-08	0.96	4.99	-	1349.9
AHQ-8-13, 6280	K.INVNEIFYDLVR.Q	1495.70427	2	1.92E-05	0.91	3.98	-	790.0
AHQ-8-11, 6121 - 6188	K.INVNEIFYDLVR.Q	1495.70427	2	1.20E-08	0.96	4.97	-	1412.6
AHQ-8-14-, 6253	K.INVNEIFYDLVR.Q	1495.70427	2	4.88E-08	0.93	4.08	-	1045.5
AHQ-8-11, 2800 - 2860	K.LVVLGSGGVGK.S	986.19059	2	2.99E-06	0.92	3.69	-	1057.7
AHQ-8-11, 5839 - 5895	K.SALTVQFVQGIFVEK.Y	1666.94196	2	5.04E-04	0.96	4.35	-	1640.3
AHQ-8-11, 5727 - 5783	K.SALTVQFVQGIFVEK.Y	1666.94196	2	3.02E-04	0.96	3.98	-	1788.1
AHQ-8-11, 4999 - 5016	K.SKINVNEIFYDLVR.Q	1710.95483	2	5.90E-08	0.88	4.15	-	653.4
AHQ-8-11, 5901 - 5980	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.37E-08	0.95	4.43	-	1108.1
AHQ-8-11, 5687	K.SKINVNEIFYDLVR.Q	1710.95483	2	3.95E-04	0.86	3.67	-	686.9
AHQ-8-11, 5691 - 5705	K.SKINVNEIFYDLVR.Q	1710.95483	3	3.04E-08	0.94	4.67	-	1392.7
AHQ-8-11, 2737 - 2812	K.YDPTIEDSYR.K	1259.30338	2	5.90E-06	0.79	2.58	-	423.8
AHQ-8-11, 2823 - 2885	K.YDPTIEDSYR.K	1259.30338	2	4.20E-08	0.81	2.62	-	445.8
gi|14211923|ref|NP_115982.1|	PKCI-1-related HIT protein [Homo sapiens]			1.25E-08	1.68	20.23	22.70	17161.6
AHQ-8-13-, 5795	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	1.25E-08	0.84	3.91	-	656.4
AHQ-8-13-, 5751	K.SLPADILYEDQQCLVFR.D	2069.32354	2	1.91E-04	0.84	3.13	-	729.6
gi|4557597|ref|NP_001449.1|	gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);			1.28E-08	1.51	20.25	1.40	288897.4
AHQ-8-2, 4600 - 4604	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	4.45E-06	0.91	4.81	-	483.9
AHQ-8-7, 4324	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.59E-05	0.90	4.71	-	678.0
AHQ-8-5, 4468 - 4472	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	6.62E-05	0.80	3.66	-	615.5
AHQ-8-5, 4484	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	1.65E-05	0.91	4.71	-	397.5
AHQ-8-6, 4411	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	3.94E-05	0.91	5.01	-	572.8
AHQ-8-1, 4672 - 4721	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	1.28E-08	0.89	4.24	-	588.3
AHQ-8-3, 2032	K.IECDDKGDGSCDVR.Y	1628.67809	2	5.00E-05	0.63	2.85	-	599.6
gi|4503291|ref|NP_001346.1|	D-dopachrome tautomerase [Homo sapiens]			1.33E-08	0.91	10.17	9.30	12711.7
AHQ-8-14-, 5351 - 5353	R.FFPLESWQIGK.I	1352.56151	2	1.33E-08	0.91	3.34	-	1000.4
gi|7662651|ref|NP_054778.1|	RGC32 protein [Homo sapiens]			1.41E-08	0.94	10.22	18.80	12924.1
AHQ-8-14-, 3567	R.SSASVSDSSGFSDSESADSLYR.N	2242.21028	2	1.41E-08	0.94	4.45	-	808.7
gi|6681259|ref|NP_031377.1|	multimerin [Homo sapiens]			1.41E-08	16.97	190.32	21.70	138070.8
AHQ-8-2, 2489	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	6.28E-06	0.88	3.91	-	1025.3
AHQ-8-3, 2460	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	7.54E-07	0.90	4.29	-	558.8
AHQ-8-4, 2413	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	6.31E-04	0.88	4.18	-	839.9
AHQ-8-3, 5820	K.CTSDM*ETILTFIPQFHR.L	2114.38778	3	1.35E-07	0.85	3.69	-	828.0
AHQ-8-3, 3864 - 3921	R.DQALQLQVLNSR.F	1385.55144	2	2.56E-07	0.97	5.14	-	1923.9
AHQ-8-3, 4066	R.DQALQLQVLNSR.F	1385.55144	2	8.48E-04	0.76	2.96	-	874.0
AHQ-8-2, 3993	R.DQALQLQVLNSR.F	1385.55144	2	1.08E-06	0.96	4.69	-	1435.6
AHQ-8-5, 2852	K.EVHEQLLSTEQVSDQK.N	1870.99550	2	2.20E-05	0.92	3.83	-	1080.0
AHQ-8-2, 5968 - 5980	K.FPPVTTFSGYLLYR.T	1661.92388	2	3.63E-05	0.70	3.31	-	452.3
AHQ-8-14-, 5801	K.FPPVTTFSGYLLYR.T	1661.92388	2	6.47E-04	0.95	4.00	-	954.7
AHQ-8-3, 5452	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.79E-08	0.92	4.09	-	1331.7
AHQ-8-4, 5534	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	6.71E-08	0.91	4.46	-	807.0
AHQ-8-2, 5555	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	3.29E-07	0.94	4.00	-	1312.3
AHQ-8-6, 5566 - 5570	K.GLTEFVEPIIQIK.T	1487.76518	2	1.01E-04	0.68	2.67	-	694.4
AHQ-8-2, 5743	K.GLTEFVEPIIQIK.T	1487.76518	2	2.99E-04	0.83	3.39	-	705.1
AHQ-8-3, 5630 - 5646	K.GLTEFVEPIIQIK.T	1487.76518	2	1.32E-07	0.94	4.01	-	1229.9
AHQ-8-3, 2693	K.GPCGWTGGSCPQR.S	1422.52885	2	3.72E-05	0.88	2.90	-	1003.8
AHQ-8-3, 4086	K.GSVVTNERDQALQLQVLNSR.F	2228.45212	3	1.64E-05	0.90	4.07	-	1199.8
AHQ-8-3, 2485	R.GVAEQQQQQGCGDPEVMQK.M	2119.27971	2	2.57E-04	0.90	4.35	-	655.2
AHQ-8-2, 3845 - 3917	K.HSLPDIQLLQK.G	1292.50915	2	2.34E-08	0.92	3.71	-	839.9
AHQ-8-3, 3828 - 3830	K.HSLPDIQLLQK.G	1292.50915	2	9.98E-08	0.88	3.76	-	642.9
AHQ-8-3, 4937 - 4992	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.05E-05	0.77	3.13	-	705.3
AHQ-8-3, 4773 - 4854	K.IFQNDM*QETVAQLFK.T	1829.06683	2	2.92E-08	0.97	5.01	-	1619.1
AHQ-8-2, 5388	R.IPYLGVYVFK.Y	1199.46532	2	5.55E-04	0.80	3.00	-	707.9
AHQ-8-3, 5196	K.KIENLTSAVNSLNFIIK.E	1905.22764	2	1.45E-08	0.89	4.03	-	582.3
AHQ-8-3, 2949	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	5.47E-06	0.98	6.49	-	1822.4
AHQ-8-4, 2931	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	1.08E-04	0.95	5.31	-	772.4
AHQ-8-3, 3740	K.LVEENALAPDFSK.G	1433.58810	2	2.24E-05	0.83	3.09	-	875.2
AHQ-8-2, 3785 - 3809	K.LVEENALAPDFSK.G	1433.58810	2	8.52E-05	0.67	2.63	-	553.5
AHQ-8-4, 6439	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	1.02E-04	0.58	3.20	-	461.5
AHQ-8-3, 6336 - 6349	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	1.41E-08	0.95	5.05	-	1526.8
AHQ-8-2, 6449	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	7.04E-05	0.62	3.15	-	676.7
AHQ-8-3, 3428	K.TVSSLSEDLESTR.Q	1424.49324	2	9.35E-07	0.82	3.05	-	936.9
AHQ-8-3, 3992	R.YNFVLQVAK.T	1082.27683	2	6.26E-05	0.92	3.11	-	1002.2
gi|30150448|ref|XP_293066.2|	similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose			1.61E-08	0.92	10.20	2.90	58788.2
AHQ-8-6, 4456	R.VINEPTAAALAYGLDK.S	1646.86592	2	1.61E-08	0.92	4.02	-	790.6
gi|21314617|ref|NP_000433.2|	platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e			1.62E-08	5.28	70.20	13.00	82449.6
AHQ-8-5, 5480 - 5482	R.CESISGTLPISYQLLK.T	1811.08954	2	3.40E-04	0.45	2.77	-	223.1
AHQ-8-4, 5913	R.DQNFVILEFPVEEQDR.V	1979.13566	2	2.98E-04	0.67	3.44	-	466.8
AHQ-8-4, 5769 - 5774	R.DQNFVILEFPVEEQDR.V	1979.13566	2	1.26E-04	0.89	3.78	-	792.0
AHQ-8-5, 5721	R.DQNFVILEFPVEEQDR.V	1979.13566	2	5.48E-04	0.79	3.56	-	668.3

AHQ-8-4, 3402	K.EDTIVSQTQDFTK.I	1512.60049	2	1.30E-04	0.83	3.21	-	644.0
AHQ-8-4, 3529	K.EQEGEYYCTAFNR.A	1668.72232	2	3.42E-07	0.69	2.74	-	468.1
AHQ-8-4, 4081	R.ISYDAQFEVIK.G	1313.48046	2	2.32E-08	0.83	3.41	-	590.6
AHQ-8-4, 4063	K.STESYFIPEVR.I	1328.45199	2	6.92E-05	0.82	2.96	-	740.9
AHQ-8-3, 4061	K.STESYFIPEVR.I	1328.45199	2	6.69E-08	0.73	2.81	-	533.4
AHQ-8-3, 5209 - 5234	K.VIAPVDEVQISILSSK.V	1698.98227	2	1.23E-04	0.64	2.80	-	333.3
AHQ-8-1, 5316	K.VIAPVDEVQISILSSK.V	1698.98227	2	1.01E-05	0.91	3.64	-	729.0
AHQ-8-4, 5269	K.VIAPVDEVQISILSSK.V	1698.98227	2	1.62E-08	0.86	3.14	-	752.8
gi|29737978|ref|XP_290747.1|	similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy			1.71E-08	3.29	40.24	1.50	191380.7
AHQ-8-1, 4076	K.ADFCIIHYAGK.V	1296.47641	2	1.09E-07	0.96	3.73	-	1591.4
AHQ-8-6, 3846	K.ADFCIIHYAGK.V	1296.47641	2	1.47E-06	0.95	3.83	-	1382.8
AHQ-8-4, 3914 - 3918	K.ADFCIIHYAGK.V	1296.47641	2	2.98E-06	0.95	3.73	-	1350.7
AHQ-8-5, 3892 - 3893	K.ADFCIIHYAGK.V	1296.47641	2	2.14E-07	0.95	3.82	-	1135.2
AHQ-8-2, 3983 - 3984	K.ADFCIIHYAGK.V	1296.47641	2	1.71E-08	0.97	4.12	-	2076.6
AHQ-8-3, 3906 - 3928	K.ADFCIIHYAGK.V	1296.47641	2	1.26E-06	0.96	3.82	-	1725.3
AHQ-8-3, 3084	R.AGVLAHLEEER.D	1224.34854	2	2.70E-06	0.94	3.76	-	1478.0
AHQ-8-2, 3124	R.AGVLAHLEEER.D	1224.34854	2	7.09E-07	0.95	4.05	-	1478.3
AHQ-8-5, 3049	R.AGVLAHLEEER.D	1224.34854	2	6.01E-07	0.91	3.61	-	1056.2
AHQ-8-6, 3056	R.AGVLAHLEEER.D	1224.34854	2	5.26E-06	0.96	4.20	-	1680.2
AHQ-8-4, 3051 - 3070	R.AGVLAHLEEER.D	1224.34854	2	4.59E-06	0.97	4.78	-	1758.7
AHQ-8-7, 2990	R.AGVLAHLEEER.D	1224.34854	2	5.57E-07	0.90	3.73	-	1023.2
AHQ-8-3, 3713	K.DKADFCIIHYAGK.V	1539.73719	2	3.52E-05	0.93	3.83	-	1240.3
AHQ-8-6, 3632	K.DKADFCIIHYAGK.V	1539.73719	2	8.54E-06	0.85	2.91	-	908.1
AHQ-8-2, 3776 - 3853	K.DKADFCIIHYAGK.V	1539.73719	2	2.78E-04	0.93	3.78	-	1373.7
AHQ-8-4, 3619 - 3691	K.DKADFCIIHYAGK.V	1539.73719	2	3.55E-05	0.80	3.23	-	880.6
AHQ-8-4, 4582	K.LDPHLVLDQLR.C	1319.53460	2	2.65E-06	0.57	2.53	-	384.1
AHQ-8-1, 4692	K.LDPHLVLDQLR.C	1319.53460	2	8.10E-06	0.72	2.83	-	508.1
AHQ-8-2, 4615	K.LDPHLVLDQLR.C	1319.53460	2	5.40E-04	0.86	2.97	-	664.1
AHQ-8-2, 4628	K.LDPHLVLDQLR.C	1319.53460	3	8.75E-06	0.93	4.07	-	945.5
gi|7657056|ref|NP_055415.1|	EH-domain containing 3; EH domain containing 3 [Homo sapiens]			1.74E-08	3.52	40.23	10.70	60886.7
AHQ-8-7, 4329	K.ELVNNLAEIYGR.I	1391.55445	2	1.04E-05	0.79	3.14	-	733.1
AHQ-8-7, 5166 - 5225	K.GGAFEGTLHGPFGHGYGEGAGEGIDDAEWVVAR.D	3317.48513	3	1.60E-05	0.91	4.53	-	1122.3
AHQ-8-7, 4133	R.KLFEAEEQDLFR.D	1525.68723	2	2.58E-04	0.86	3.56	-	735.7
AHQ-8-7, 4576	K.LFEAEEQDLFR.D	1397.51432	2	1.74E-08	0.96	3.61	-	1720.5
gi|4885063|ref|NP_005156.1|	aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase			1.88E-08	0.94	10.21	6.30	39455.6
AHQ-8-9, 6595	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.88E-08	0.94	4.27	-	789.6
gi|28395033|ref|NP_786886.1|	ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco			1.90E-08	1.87	20.19	16.10	22006.2
AHQ-8-10, 4408	K.HFCPNVPIILVGNK.K	1609.91693	2	8.21E-05	0.93	3.34	-	1330.3
AHQ-8-10, 4640	K.QVELALWDTAGQEDYDR.L	2010.10662	2	1.90E-08	0.94	3.80	-	1257.3
gi|4504517|ref|NP_001531.1|	heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M			1.90E-08	2.48	30.29	21.00	22782.3
AHQ-8-11, 4505 - 4579	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.10E-04	0.75	3.77	-	298.0
AHQ-8-13, 4784 - 4849	K.LATQSNEITIPVTFESR.A	1907.11412	2	1.63E-04	0.71	3.43	-	343.4
AHQ-8-11, 4404	R.LFDQAFGLPR.L	1164.33793	2	1.99E-05	0.96	4.14	-	1568.8
AHQ-8-10, 4328 - 4331	R.LFDQAFGLPR.L	1164.33793	2	1.25E-04	0.95	4.36	-	1399.3
AHQ-8-14-, 4542	R.LFDQAFGLPR.L	1164.33793	2	1.03E-06	0.92	3.28	-	1268.7
AHQ-8-14, 5411	R.VSLDVNHFAPDELTVK.T	1784.99058	2	4.86E-04	0.55	2.74	-	503.7
AHQ-8-13-, 4526	R.VSLDVNHFAPDELTVK.T	1784.99058	3	1.90E-08	0.81	3.81	-	438.9
AHQ-8-13-, 4536	R.VSLDVNHFAPDELTVK.T	1784.99058	2	5.31E-05	0.87	3.86	-	702.6
AHQ-8-10, 4330	R.VSLDVNHFAPDELTVK.T	1784.99058	2	9.33E-06	0.90	3.60	-	1169.9
AHQ-8-11, 4413 - 4417	R.VSLDVNHFAPDELTVK.T	1784.99058	3	1.54E-05	0.82	4.01	-	420.1
gi|17149842|ref|NP_004461.2|	FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep			1.91E-08	1.63	20.20	9.20	15649.2
AHQ-8-13, 4007	R.KLVIPSELGYGER.G	1461.68782	3	5.72E-05	0.95	3.93	-	1868.1
AHQ-8-13-, 4138	K.LVIPSELGYGER.G	1333.51491	2	1.91E-08	0.68	2.63	-	329.5
AHQ-8-13, 4291	K.LVIPSELGYGER.G	1333.51491	2	6.66E-05	0.82	2.97	-	471.9
gi|29742827|ref|XP_294099.1|	similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]			2.06E-08	1.77	20.23	14.20	17094.0
AHQ-8-11, 3000 - 3080	K.EAFNMIDQNR.D	1238.35558	2	8.12E-04	0.84	3.18	-	795.8
AHQ-8-11, 3703 - 3723	R.FTDEEVDELYR.E	1416.47127	2	2.06E-08	0.93	3.52	-	1038.4
AHQ-8-12, 3643 - 3723	R.FTDEEVDELYR.E	1416.47127	2	7.81E-08	0.97	4.55	-	1790.7
AHQ-8-13, 3995 - 4061	R.FTDEEVDELYR.E	1416.47127	2	2.09E-07	0.95	3.17	-	1632.6
AHQ-8-14, 4729	R.FTDEEVDELYR.E	1416.47127	2	1.34E-05	0.96	3.46	-	1732.8
AHQ-8-13-, 3842 - 3912	R.FTDEEVDELYR.E	1416.47127	2	4.50E-08	0.96	3.50	-	1804.7
AHQ-8-14-, 3806	R.FTDEEVDELYR.E	1416.47127	2	1.00E-05	0.85	2.85	-	1156.1
AHQ-8-11, 3091 - 3169	R.FTDEEVDELYR.E	1416.47127	2	8.27E-04	0.82	2.94	-	714.9
gi|4826657|ref|NP_004333.1|	caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]			2.36E-08	4.57	50.26	13.60	62662.9
AHQ-8-5, 4756	K.EFDPTITDASLSLPSR.R	1749.89986	2	3.40E-07	0.81	3.52	-	722.2
AHQ-8-6, 4604 - 4676	K.EFDPTITDASLSLPSR.R	1749.89986	2	2.69E-07	0.90	3.85	-	747.6
AHQ-8-6, 2631	K.GNVFSSPTAAGTPNK.E	1448.56286	2	5.64E-05	0.92	3.40	-	1255.7
AHQ-8-5, 2642	K.GNVFSSPTAAGTPNK.E	1448.56286	2	2.68E-04	0.92	3.80	-	941.8
AHQ-8-5, 2856 - 2857	R.LEQYTSAIEGTK.S	1340.46107	2	1.94E-04	0.89	3.42	-	1053.3
AHQ-8-6, 3676	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	3.04E-05	0.94	4.07	-	1220.2
AHQ-8-5, 3729	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	2.36E-08	0.96	5.20	-	1090.4
AHQ-8-6, 2744 - 2750	R.YEIEETETVTK.S	1342.43060	2	8.82E-05	0.90	3.39	-	897.7
AHQ-8-5, 2762	R.YEIEETETVTK.S	1342.43060	2	1.12E-04	0.67	2.76	-	609.5
gi|5032161|ref|NP_005639.1|	elongin C; transcription elongation factor B (SIII), polypeptide 1 (15k			2.52E-08	1.83	20.24	30.40	12473.1
AHQ-8-13, 4521	K.AM*LSGPGQFAENETNEVNFR.E	2228.38455	2	2.52E-08	0.96	4.79	-	1389.4
AHQ-8-13-, 2820	K.TYGGCEGPDAM*YVK.L	1565.70692	2	3.37E-04	0.87	2.84	-	906.6
gi|30147623|ref|XP_293669.2|	similar to actinin, alpha 4 [Homo sapiens]			2.62E-08	0.61	10.19	3.50	57794.4
AHQ-8-5, 3986	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	2.18E-05	0.87	3.90	-	848.5
AHQ-8-4, 3998	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	2.62E-08	0.61	2.85	-	531.2
gi|18570595|ref|XP_095590.1|	similar to myosin regulatory light chain [Homo sapiens]			2.63E-08	0.96	10.23	8.90	13951.5
AHQ-8-12, 3054 - 3110	K.LNGTDPEDVIR.H	1229.32195	2	2.63E-08	0.96	4.52	-	1459.2
AHQ-8-13, 3339	K.LNGTDPEDVIR.H	1229.32195	2	4.28E-04	0.76	2.67	-	714.5
AHQ-8-14, 3990 - 4027	K.LNGTDPEDVIR.H	1229.32195	2	3.79E-04	0.79	2.72	-	932.4
AHQ-8-13-, 3190	K.LNGTDPEDVIR.H	1229.32195	2	5.17E-05	0.93	3.60	-	1144.7
AHQ-8-11, 3035 - 3115	K.LNGTDPEDVIR.H	1229.32195	2	2.71E-04	0.92	3.41	-	1067.2
gi|21361370|ref|NP_002853.2|	phosphorylase, glycogen; brain [Homo sapiens]			2.69E-08	2.70	30.20	4.70	96695.3
AHQ-8-5, 3768	R.GLAGLGDVAEVR.K	1157.30210	2	3.84E-05	0.95	4.01	-	1380.3
AHQ-8-5, 5564 - 5565	K.LLPLVSDEVFIR.D	1401.67552	2	2.69E-08	0.90	3.40	-	806.2
AHQ-8-5, 6061 - 6078	R.WLLLCNPGLADTIVEK.I	1844.16436	2	1.25E-05	0.84	3.85	-	699.4
gi|7705849|ref|NP_057215.1|	ras-related GTP-binding protein RAB10; ras-related GTP-binding protein			2.70E-08	0.94	10.19	5.50	22540.8
AHQ-8-14-, 6031	K.AFLTLAEDILR.K	1262.47982	2	2.86E-06	0.93	3.28	-	1707.7
AHQ-8-11, 5903 - 5904	K.AFLTLAEDILR.K	1262.47982	2	2.70E-08	0.94	3.71	-	1318.0
gi|17986283|ref|NP_006000.2|	tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu			3.09E-08	0.80	10.24	3.30	50135.3
AHQ-8-11, 5265	R.AVFVDLEPTVIDEVR.T	1702.92947	2	4.22E-04	0.89	3.64	-	887.1
AHQ-8-12, 5275 - 5278	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.39E-05	0.76	3.55	-	449.9
AHQ-8-13, 5481	R.AVFVDLEPTVIDEVR.T	1702.92947	2	4.34E-05	0.87	3.97	-	573.2
AHQ-8-13-, 5350	R.AVFVDLEPTVIDEVR.T	1702.92947	2	9.77E-08	0.96	4.87	-	1194.5
AHQ-8-14-, 5350 - 5366	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.09E-06	0.93	4.74	-	795.0
AHQ-8-7, 5284	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.09E-08	0.80	3.74	-	546.9
gi|4504071|ref|NP_000164.1|	platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA			3.18E-08	4.39	50.21	10.70	68955.0
AHQ-8-4, 3477	K.AM*TSNVASVQCDNSDKFPVYK.Y	2379.60939	3	2.43E-04	0.72	3.10	-	498.9
AHQ-8-3, 4777	R.GLGELQELYLK.G	1263.46458	2	1.09E-04	0.92	3.75	-	1172.7
AHQ-8-4, 4810	R.GLGELQELYLK.G	1263.46458	2	9.78E-05	0.91	3.54	-	1152.8
AHQ-8-3, 4048	R.GQDLLSTVSIR.Y	1189.34410	2	2.21E-07	0.92	3.12	-	1230.9
AHQ-8-13, 4200	R.GQDLLSTVSIR.Y	1189.34410	2	1.75E-05	0.96	3.65	-	1699.8
AHQ-8-1, 4205	R.GQDLLSTVSIR.Y	1189.34410	2	1.22E-07	0.95	3.60	-	1337.8
AHQ-8-13-, 4051 - 4064	R.GQDLLSTVSIR.Y	1189.34410	2	2.04E-06	0.94	3.54	-	1600.1

AHQ-8-2, 4132	R.GQDLLSTVSIR.Y	1189.34410	2	2.24E-04	0.81	2.77	-	810.1
AHQ-8-12, 3934 - 3935	R.GQDLLSTVSIR.Y	1189.34410	2	5.39E-07	0.94	3.62	-	1234.8
AHQ-8-14-, 4009 - 4071	R.GQDLLSTVSIR.Y	1189.34410	2	5.35E-04	0.92	3.00	-	1265.3
AHQ-8-3, 2260	R.GVLQGHLESSR.N	1183.29965	2	3.73E-04	0.88	3.48	-	785.5
AHQ-8-3, 4870	R.WLQDNAENVYVWK.Q	1665.82948	2	9.00E-07	0.96	4.24	-	1583.7
AHQ-8-4, 4902 - 4922	R.WLQDNAENVYVWK.Q	1665.82948	2	3.18E-08	0.93	3.43	-	1415.4
gi|4506077|ref|NP_002734.1|	protein kinase C substrate 80K-H; glucosidase II, beta subunit; AGE-bin			3.40E-08	0.95	10.20	2.50	59296.0
AHQ-8-5, 3272	K.AQQEQELAADAFK.E	1449.54763	2	3.40E-08	0.95	3.99	-	1438.6
gi|4507677|ref|NP_003290.1|	tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu			3.59E-08	5.07	60.28	11.20	92468.2
AHQ-8-4, 3238 - 3239	K.FAFQAEVNR.M	1082.19378	2	1.98E-05	0.81	3.27	-	777.7
AHQ-8-5, 3233	K.FAFQAEVNR.M	1082.19378	2	5.47E-04	0.79	2.62	-	934.7
AHQ-8-4, 3951	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	4.93E-07	0.97	4.92	-	2451.3
AHQ-8-4, 3955	R.FQSSHHPTDITSLDQYVER.M	2261.39276	2	5.74E-08	0.96	5.05	-	994.7
AHQ-8-5, 3924	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	2.65E-06	0.95	4.63	-	1571.4
AHQ-8-4, 3953	K.GVVDSDDLPLNVSR.E	1486.60940	2	1.16E-04	0.93	3.98	-	1277.7
AHQ-8-5, 3920	K.GVVDSDDLPLNVSR.E	1486.60940	2	6.33E-06	0.89	3.64	-	975.3
AHQ-8-5, 6521	R.IKEDEDDKTVLDLAVVLFETATLR.S	2735.07994	3	1.29E-05	0.89	4.40	-	750.0
AHQ-8-4, 2830	R.SGYLLPDTK.A	994.12321	1	1.09E-04	0.55	2.16	-	776.6
AHQ-8-4, 6350 - 6351	K.YSQFINFPIYVWSSK.T	1880.13366	2	1.00E-05	0.95	4.68	-	975.0
AHQ-8-5, 6300 - 6302	K.YSQFINFPIYVWSSK.T	1880.13366	2	3.59E-08	0.97	5.54	-	1229.6
gi|9506667|ref|NP_061907.1|	ras homolog gene family, member F [Homo sapiens]			3.84E-08	0.83	10.17	8.10	23593.2
AHQ-8-11, 4081	K.EVTLNLYDTAGQEDYDR.L	2003.06925	2	3.84E-08	0.83	3.30	-	722.7
gi|10834976|ref|NP_000572.1|	glutathione peroxidase 1 [Homo sapiens]			4.48E-08	2.38	30.22	22.90	21909.0
AHQ-8-11, 5364	R.LAAAAAQSVYAFSARPLAGGEPVSLGSLR.G	2832.20700	3	1.02E-04	0.90	4.04	-	1185.9
AHQ-8-11, 3815 - 3816	R.PLAGGEPVSLGSLR.G	1353.54935	2	4.48E-08	0.96	4.33	-	1175.0
AHQ-8-11, 4808	K.YVRPGGGFEPNFM*LFEK.C	2005.28455	2	2.31E-04	0.53	2.89	-	211.2
gi|29747201|ref|XP_290702.1|	similar to My016 protein [Homo sapiens]			4.77E-08	0.87	10.17	10.50	16932.3
AHQ-8-14-, 3498	R.DLEAEHVEVEDTTLNR.C	1870.95236	2	4.77E-08	0.87	3.44	-	890.5
gi|30147105|ref|XP_210550.2|	similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48			4.96E-08	0.94	10.22	2.20	61339.9
AHQ-8-5, 4138 - 4144	K.ADLINNLGTIAK.S	1243.43490	2	4.96E-08	0.94	4.45	-	819.2
AHQ-8-5, 4489	K.ADLINNLGTIAK.S	1243.43490	2	9.22E-05	0.92	4.02	-	938.7
AHQ-8-5, 3902	K.ADLINNLGTIAK.S	1243.43490	2	1.38E-04	0.82	3.31	-	505.9
gi|20070125|ref|NP_000909.2|	prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke			5.13E-08	1.68	20.22	8.30	57115.9
AHQ-8-7, 6296 - 6353	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	3	2.62E-06	0.89	4.37	-	909.0
AHQ-8-7, 2284 - 2285	K.YKPESEELTAER.I	1452.54828	2	5.13E-08	0.79	3.11	-	441.8
gi|21361565|ref|NP_001679.2|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit b, is			5.13E-08	0.92	10.25	7.80	28908.4
AHQ-8-11, 6243	K.TGVTGPYVLGTGLILYALSK.E	2024.38889	2	5.13E-08	0.92	5.03	-	591.6
gi|23110925|ref|NP_002789.1|	proteasome beta 6 subunit; proteasome subunit Y; proteasome subunit be			5.70E-08	0.97	10.21	4.60	25357.6
AHQ-8-11, 2527	R.LAAIAESGVER.Q	1116.24998	2	5.70E-08	0.97	4.21	-	2023.3
gi|5031973|ref|NP_005733.1|	protein disulfide isomerase-related protein [Homo sapiens]			5.89E-08	1.76	20.21	6.40	48121.0
AHQ-8-7, 4557 - 4636	K.GSFSEQGINEFLR.E	1484.59520	2	2.64E-06	0.82	2.81	-	782.5
AHQ-8-7, 4521	K.LAAVDATVNQVLASR.Y	1528.73579	2	5.89E-08	0.94	4.21	-	1122.2
gi|7706563|ref|NP_057614.1|	RAB-8b protein [Homo sapiens]			5.90E-08	0.93	10.19	6.80	23584.0
AHQ-8-11, 5177 - 5235	K.SSANVEEAFFTLAR.D	1542.67465	2	5.90E-08	0.93	3.79	-	1193.5
gi|10863927|ref|NP_066953.1|	peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]			6.04E-08	5.23	60.26	30.90	18012.4
AHQ-8-12, 3846 - 3902	K.FEDENFILK.H	1155.28144	2	3.95E-04	0.88	3.55	-	645.8
AHQ-8-14-, 3342	K.KITIADCGQLE	1249.41637	2	6.04E-08	0.84	3.75	-	986.4
AHQ-8-12, 3272 - 3326	K.KITIADCGQLE	1249.41637	2	4.99E-05	0.85	3.54	-	1224.3
AHQ-8-12, 4443 - 4478	K.SIYGEKFEDENFILK.H	1833.03047	2	4.54E-05	0.94	4.56	-	925.3
AHQ-8-13-, 4580	K.SIYGEKFEDENFILK.H	1833.03047	2	1.02E-06	0.96	5.20	-	1214.0
AHQ-8-12, 3650	K.VKEGMNIVEAMER.F	1506.77390	2	2.83E-04	0.86	3.59	-	758.3
AHQ-8-13-, 4428	R.VSFELFADK.V	1056.19300	2	5.33E-06	0.82	3.02	-	838.2
AHQ-8-12, 4284	R.VSFELFADK.V	1056.19300	2	1.65E-04	0.87	3.23	-	1114.1
AHQ-8-12, 4395 - 4414	R.VSFELFADKVPK.T	1380.61317	2	1.32E-07	0.86	3.77	-	814.0
gi|18860900|ref|NP_002834.2|	protein tyrosine phosphatase, receptor type, J precursor; protein tyro			6.92E-08	4.00	50.26	5.50	145926.2
AHQ-8-1, 4328	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	2	9.02E-08	0.97	5.19	-	1837.5
AHQ-8-1, 4808	R.DTEVLLVGLEPGTR.Y	1499.69122	2	1.81E-04	0.56	2.56	-	695.8
AHQ-8-1, 4955	K.GLIDGAESYVSFSR.Y	1501.62253	2	6.92E-08	0.85	3.05	-	1123.3
AHQ-8-1, 3772	K.TPSSTGPSPVFDIK.A	1433.58810	2	7.79E-04	0.81	3.37	-	702.2
AHQ-8-1, 4243	K.VITEPIPVSDLR.V	1339.56259	2	3.05E-05	0.80	2.88	-	495.9
gi|4757952|ref|NP_001782.1|	cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p			7.42E-08	1.77	20.24	14.70	21258.5
AHQ-8-11, 2377	K.CVVVGDGAVGK.T	1062.22237	2	2.19E-05	0.82	3.10	-	980.1
AHQ-8-11, 6116	K.NVFDEAILAALEPPEPK.K	1854.09282	3	7.42E-08	0.95	4.79	-	1033.3
AHQ-8-11, 6111	K.NVFDEAILAALEPPEPK.K	1854.09282	2	8.47E-06	0.57	2.69	-	431.5
gi|4507651|ref|NP_003281.1|	tropomyosin 4 [Homo sapiens]			7.62E-08	2.84	30.22	10.10	28521.6
AHQ-8-9, 6214 - 6272	K.AEGDVAALNR.R	1016.09051	2	3.59E-06	0.93	3.49	-	1347.9
AHQ-8-11, 2636	K.IQALQQQADEAEDR.A	1615.68404	2	4.67E-06	0.91	3.39	-	1063.6
AHQ-8-10, 2614	K.IQALQQQADEAEDR.A	1615.68404	2	2.62E-05	0.81	3.18	-	794.9
AHQ-8-9, 6296 - 6353	K.IQALQQQADEAEDR.A	1615.68404	2	7.62E-08	0.96	4.46	-	1680.4
AHQ-8-11, 2489	R.KIQALQQQADEAEDR.A	1743.85695	2	4.54E-07	0.95	3.82	-	1644.9
AHQ-8-10, 2450	R.KIQALQQQADEAEDR.A	1743.85695	2	9.38E-05	0.82	3.21	-	784.6
gi|4757812|ref|NP_004880.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso			7.89E-08	1.87	20.21	25.50	10917.8
AHQ-8-14-, 5614 - 5621	R.DFSPSGIFGAFQR.G	1429.56124	2	9.70E-08	0.95	4.18	-	1066.1
AHQ-8-13, 5751	R.DFSPSGIFGAFQR.G	1429.56124	2	2.56E-06	0.89	3.39	-	1045.1
AHQ-8-14-, 5278	K.LGELPSWILM*R.D	1331.60876	2	7.89E-08	0.92	3.77	-	604.3
gi|10835187|ref|NP_000627.1|	superoxide dismutase 2, mitochondrial [Homo sapiens]			8.66E-08	3.37	40.20	22.50	24733.0
AHQ-8-11, 5665	K.AIWNVINWENVTER.Y	1744.93137	3	9.06E-05	0.82	3.06	-	1138.5
AHQ-8-11, 3713 - 3767	K.GDVTAQIALQPALK.F	1425.65548	2	8.66E-08	0.76	3.06	-	692.8
AHQ-8-11, 2448 - 2508	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	3.30E-06	0.95	4.03	-	1098.1
AHQ-8-11, 3643	K.HHAAYVNNLNVTEEKYQEALAK.G	2543.77604	3	1.32E-06	0.84	3.92	-	588.0
gi|5031593|ref|NP_005708.1|	actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub			8.66E-08	1.82	20.19	17.90	16320.3
AHQ-8-12, 3082	K.ALAAGGVGSIVR.V	1071.25558	2	9.03E-04	0.95	3.27	-	1607.7
AHQ-8-12, 3494 - 3550	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	8.66E-08	0.87	3.81	-	515.5
gi|10863873|ref|NP_000651.1|	transforming growth factor, beta 1 (Camurati-Engelmann disease); trans			8.82E-08	1.71	20.18	5.90	44422.0
AHQ-8-13-, 3372	R.ALDTNYCFSSTEK.N	1537.63010	2	5.10E-05	0.73	3.04	-	558.6
AHQ-8-13, 3528 - 3532	R.ALDTNYCFSSTEK.N	1537.63010	2	8.82E-08	0.83	3.59	-	650.5
AHQ-8-13-, 2766	K.VEQLSNM*IVR.S	1205.41014	2	1.82E-04	0.89	3.36	-	867.0
gi|29732955|ref|XP_291603.1|	similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA			1.01E-07	0.78	10.22	16.80	11173.0
AHQ-8-11, 3760 - 3839	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.01E-07	0.78	4.36	-	826.6
gi|11321601|ref|NP_002618.1|	phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom			1.08E-07	5.28	60.28	13.30	85595.6
AHQ-8-5, 3661	K.AIGVLTSGGDAQGMNAAVR.A	1789.00750	2	8.07E-04	0.96	4.43	-	1536.3
AHQ-8-5, 3492 - 3560	R.DLQSNVEHLTEK.M	1413.51529	2	5.17E-04	0.70	2.82	-	642.4
AHQ-8-6, 5490	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	3.89E-05	0.76	3.30	-	485.2
AHQ-8-5, 5590	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	2.00E-05	0.93	4.10	-	1032.1
AHQ-8-5, 4564	K.FTTDDSICVLGISK.R	1557.74760	2	3.57E-04	0.79	3.36	-	521.9
AHQ-8-5, 5914 - 5922	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	1.42E-05	0.96	5.64	-	906.7
AHQ-8-5, 5305	R.IIEVVDAIMTTAQSHQR.T	1913.18853	2	1.08E-07	0.94	4.48	-	1293.6
gi|4505591|ref|NP_002565.1|	peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc			1.13E-07	2.71	30.21	20.10	22110.2
AHQ-8-11, 3840	R.GLFIIDDK.G	921.07223	2	4.81E-05	0.87	2.95	-	936.8
AHQ-8-11, 3179	K.HGEVCPAGWKPGSDTIKPDVQK.S	2408.67532	3	1.13E-07	0.90	4.24	-	969.2
AHQ-8-11, 3604 - 3619	R.LVQAFQFTDK.H	1197.36469	2	3.32E-06	0.94	3.50	-	1002.0
gi|7019375|ref|NP_037373.1|	formin homology 2 domain containing 1; FH1/FH2 domain-containing protei			1.14E-07	0.93	10.14	1.30	126496.5
AHQ-8-14-, 5789	K.SGLGDDLVQALGLSK.G	1473.65377	2	1.14E-07	0.93	2.84	-	1773.4
gi|18765729|ref|NP_003816.2|	synaptosomal-associated protein 23 isoform SNAP23A; synaptosomal-assoc			1.28E-07	0.94	10.22	6.60	23353.9
AHQ-8-14-, 4370	R.ILGLAIESQDAGIK.T	1428.65614	2	1.28E-07	0.94	4.43	-	1176.7
gi|16751921|ref|NP_444513.1|	dermcidin precursor; AIDD protein [Homo sapiens]			1.28E-07	0.93	10.20	12.70	11283.8
AHQ-8-14-, 3723	K.LGKDAVEDLESVGK.G	1460.61186	2	1.28E-07	0.93	4.07	-	1342.2

gi|5123454|ref|NP_005336.2|	heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind			1.30E-07	4.33	50.20	13.40	70037.7
AHQ-8-6, 5023 - 5027	K.AAAIGIDLGTTYSCVGVFQHGK.V	2267.54677	3	9.89E-04	0.64	3.26	-	573.0
AHQ-8-6, 3324 - 3398	K.AQIHDLVLVGGSTR.I	1466.66769	2	2.37E-05	0.94	3.80	-	1884.8
AHQ-8-6, 4574	K.DAGVIAGLNVLR.I	1198.39736	2	1.06E-06	0.96	3.90	-	1647.2
AHQ-8-6, 3990 - 4003	K.NQVALNPQNTVFDAK.R	1659.82478	2	1.30E-07	0.87	3.70	-	625.0
AHQ-8-6, 6152	K.SINPDEAVAYGAAVQAAILM*GDK.S	2321.59293	2	2.86E-05	0.92	4.06	-	773.2
gi|4885609|ref|NP_005408.1|	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen			1.30E-07	2.83	30.21	9.30	59834.4
AHQ-8-7, 6118	R.AGPLAGGVTTFVALYDYESR.T	2088.30526	2	3.46E-06	0.95	4.25	-	1232.7
AHQ-8-7, 4148	K.GAYCLSVSDFDNAK.G	1548.65612	2	6.70E-04	0.94	4.21	-	1002.3
AHQ-8-7, 3842	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	1.30E-07	0.93	4.02	-	857.9
AHQ-8-7, 3668	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	2.01E-05	0.78	3.27	-	812.7
gi|21614544|ref|NP_002955.2|	S100 calcium-binding protein A8; cystic fibrosis antigen; calgranulin			1.31E-07	0.84	10.15	11.80	10834.4
AHQ-8-14-, 3551	K.LLETECPQYIR.K	1423.61651	2	1.31E-07	0.84	2.97	-	831.2
gi|4504085|ref|NP_000399.1|	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA			1.48E-07	2.44	30.23	6.10	80814.1
AHQ-8-6, 6246	R.ANLLEIAPHLSAPLPIM*LPVYK.W	2417.93800	3	1.48E-07	0.93	4.70	-	1116.6
AHQ-8-6, 3624	R.CKDVLTGQEFDVR.A	1568.73370	3	1.83E-04	0.73	3.12	-	869.4
AHQ-8-6, 5738	R.VIFFLPWQK.M	1178.44934	2	9.42E-07	0.78	2.77	-	675.7
gi|30147536|ref|XP_293762.2|	similar to bridging integrator 2; bridging integrator-2; breast cancer			1.49E-07	0.78	10.18	3.90	46870.6
AHQ-8-5, 2890	R.TSLEVSPNPEPPEKPVR.T	1877.08801	2	1.49E-07	0.78	3.56	-	402.6
AHQ-8-5, 2886	R.TSLEVSPNPEPPEKPVR.T	1877.08801	3	6.34E-06	0.78	3.22	-	610.0
gi|4504521|ref|NP_002147.1|	heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P			1.56E-07	0.93	10.21	4.90	61024.2
AHQ-8-7, 6380	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D	2870.28530	3	1.56E-07	0.93	4.22	-	1189.8
gi|5729997|ref|NP_004154.2|	RAB27B, member RAS oncogene family [Homo sapiens]			1.59E-07	1.79	20.21	14.20	24607.7
AHQ-8-11, 3644	K.VHLQLWDTAGQER.F	1553.70390	2	1.59E-07	0.94	4.14	-	1080.4
AHQ-8-11, 4307	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	4.43E-07	0.85	3.26	-	746.2
gi|4557471|ref|NP_001274.1|	adaptor-related protein complex 1, sigma 1 subunit isoform 1; clathrin-			1.59E-07	0.89	10.18	10.10	18732.9
AHQ-8-12, 3511	K.AIEQADLLQEEDESPR.S	1843.92692	2	1.59E-07	0.89	3.70	-	1098.6
gi|18426915|ref|NP_004386.2|	drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [			1.64E-07	1.74	20.22	5.20	71438.9
AHQ-8-8, 2262	R.LREDENAEPVGTTYQK.T	1850.96428	2	2.45E-05	0.96	4.50	-	1173.8
AHQ-8-8, 2747	R.SPSDSSTASTPVAEQIER.A	1862.93023	2	1.64E-07	0.78	3.32	-	460.7
gi|30154839|ref|XP_301540.1|	similar to keratin 8; cytokeratin 8; keratin, type II cytoskeletal 8 [			1.78E-07	0.84	10.20	3.40	39331.0
AHQ-8-2, 4607 - 4659	K.SLNNKFASFIDK.V	1384.56191	2	4.70E-07	0.91	3.61	-	928.2
AHQ-8-4, 4509 - 4574	K.SLNNKFASFIDK.V	1384.56191	2	1.21E-06	0.82	3.22	-	702.8
AHQ-8-5, 4541	K.SLNNKFASFIDK.V	1384.56191	2	9.93E-05	0.86	3.47	-	711.6
AHQ-8-10, 4308 - 4314	K.SLNNKFASFIDK.V	1384.56191	2	1.78E-07	0.84	3.25	-	732.2
AHQ-8-10, 4535	K.SLNNKFASFIDK.V	1384.56191	2	9.70E-04	0.74	2.65	-	713.3
AHQ-8-1, 4699	K.SLNNKFASFIDK.V	1384.56191	2	3.20E-07	0.94	3.92	-	1121.3
gi|13518026|ref|NP_004978.2|	LIM and senescent cell antigen-like domains 1 [Homo sapiens]			1.88E-07	1.90	20.21	7.70	37251.2
AHQ-8-8, 4374	K.CHAIIDEQPLIFK.N	1585.84900	2	3.17E-04	0.94	4.16	-	1235.3
AHQ-8-10, 3399	R.VIEGDVVSALNK.A	1244.41966	2	5.14E-07	0.85	2.76	-	879.5
AHQ-8-8, 3438 - 3441	R.VIEGDVVSALNK.A	1244.41966	2	1.88E-07	0.96	4.25	-	1399.8
gi|9507215|ref|NP_061816.1|	tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]			2.00E-07	2.93	40.22	6.90	50093.2
AHQ-8-13, 4808 - 4877	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	3.52E-06	0.91	4.45	-	764.6
AHQ-8-13-, 4716	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	6.01E-07	0.87	3.64	-	700.7
AHQ-8-14-, 4710 - 4713	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	7.33E-06	0.93	4.40	-	1014.7
AHQ-8-14-, 4987 - 5041	R.AVMIDLEPTVVDEVR.A	1686.95185	2	2.37E-04	0.85	3.74	-	712.8
AHQ-8-7, 5276	R.IHFPLVTYAPIISAEK.A	1800.13312	2	2.00E-07	0.81	2.96	-	523.6
AHQ-8-14-, 5021	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	1.16E-05	0.41	3.00	-	233.9
gi|17450333|ref|XP_060887.1|	similar to peptidyl-Pro cis trans isomerase [Homo sapiens]			2.03E-07	0.89	10.18	11.00	17503.9
AHQ-8-14-, 6145 - 6170	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	2.03E-07	0.89	3.34	-	1071.9
AHQ-8-14-, 5966	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	2.97E-06	0.84	3.09	-	824.5
gi|4504415|ref|NP_002118.1|	major histocompatibility complex, class I, G precursor; HLA-G histocomp			2.03E-07	0.39	10.15	7.10	38223.9
AHQ-8-8, 3381	R.DGEDQTQDVELVETRPAGDGTFQK.W	2636.72390	2	2.03E-07	0.39	3.02	-	444.5
gi|7661818|ref|NP_054900.1|	HSPC159 protein [Homo sapiens]			2.29E-07	1.68	20.19	19.20	19011.6
AHQ-8-13, 6251 - 6311	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	9.43E-05	0.68	3.45	-	251.5
AHQ-8-13-, 6211 - 6214	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	2.36E-06	0.85	3.71	-	365.7
AHQ-8-11, 4624	R.VFVDGHQLFDFYHR.I	1780.96540	3	2.29E-07	0.83	3.68	-	589.7
gi|4557871|ref|NP_001054.1|	transferrin [Homo sapiens]			2.46E-07	3.23	40.21	8.00	77049.5
AHQ-8-5, 4872	K.EDPQTFYYAVAVVK.K	1630.82181	2	1.91E-04	0.82	2.63	-	927.9
AHQ-8-6, 3978	R.FDEFFSEGCAPGSK.K	1579.66868	2	2.04E-04	0.95	4.21	-	1085.1
AHQ-8-5, 3281 - 3361	K.IECVSAETTEDCIAK.I	1728.87748	2	2.46E-07	0.65	2.90	-	579.0
AHQ-8-5, 3214	R.LKCDEWSVNSVGK.I	1523.69293	2	5.63E-07	0.81	3.12	-	696.4
gi|27482573|ref|XP_208709.1|	similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro			2.65E-07	1.73	20.26	26.00	17875.4
AHQ-8-12, 4643	K.GQVCLPVISAENWKPATK.T	2000.30757	2	4.82E-04	0.77	3.60	-	431.5
AHQ-8-12, 6122 - 6123	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	2.65E-07	0.95	5.19	-	1265.1
gi|4504183|ref|NP_000843.1|	glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s			2.77E-07	3.56	40.23	34.80	23355.7
AHQ-8-11, 5059 - 5135	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.07E-06	0.89	4.23	-	375.1
AHQ-8-11, 5055 - 5112	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	3	8.73E-06	0.86	3.67	-	965.1
AHQ-8-11, 4877	K.DQQEAALVDM*VNDGVEDLR.C	2134.26783	2	3.66E-04	0.90	3.77	-	776.7
AHQ-8-11, 4652 - 4729	K.FQDGDLTLYQSNTILR.H	1885.06701	2	4.56E-05	0.92	4.48	-	739.4
AHQ-8-11, 4540 - 4595	K.FQDGDLTLYQSNTILR.H	1885.06701	2	3.85E-05	0.83	3.52	-	562.5
AHQ-8-14-, 4679 - 4743	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.26E-04	0.77	3.67	-	486.7
AHQ-8-11, 4364	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	2.77E-07	0.94	4.66	-	776.2
AHQ-8-11, 4363	K.YISLIYTNYEAGKDDYVK.A	2156.37637	3	2.31E-05	0.77	3.04	-	582.8
gi|19923457|ref|NP_057447.2|	glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M			3.11E-07	1.44	20.22	3.20	67308.6
AHQ-8-7, 4049	R.ASFPIITVTAAHSGTYR.C	1793.01594	2	3.11E-07	0.50	2.92	-	468.5
AHQ-8-7, 5245	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	2	4.82E-05	0.75	3.27	-	487.1
AHQ-8-7, 5240	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	5.49E-06	0.94	4.37	-	1445.6
gi|7706675|ref|NP_057661.1|	RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M			3.25E-07	1.86	20.19	11.10	23461.5
AHQ-8-11, 4539	R.GSDVIIMLVGNK.T	1246.50220	2	5.55E-05	0.96	3.73	-	1984.2
AHQ-8-11, 3521 - 3524	R.LQLWDTAGQER.F	1317.43243	2	3.25E-07	0.91	3.42	-	944.2
AHQ-8-14-, 3507	R.LQLWDTAGQER.F	1317.43243	2	3.28E-04	0.87	3.30	-	707.9
AHQ-8-11, 3317 - 3399	R.LQLWDTAGQER.F	1317.43243	2	1.91E-05	0.80	3.11	-	692.6
gi|21618359|ref|NP_004095.3|	fatty acid synthase [Homo sapiens]			3.27E-07	0.90	10.22	1.00	273262.0
AHQ-8-1, 5668	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	3.27E-07	0.90	4.30	-	810.7
gi|4503643|ref|NP_000121.1|	coagulation factor V precursor; labile factor; factor V Leiden [Homo sa			3.38E-07	6.00	70.25	4.20	251716.5
AHQ-8-5, 3161	R.AEVDDVIQVR.F	1144.26019	2	7.90E-05	0.94	3.81	-	1486.1
AHQ-8-2, 3247	R.AEVDDVIQVR.F	1144.26019	2	9.97E-05	0.95	3.63	-	1840.1
AHQ-8-5, 4702	K.ASEFLGYWEPR.L	1355.47913	2	6.97E-04	0.89	3.43	-	912.0
AHQ-8-3, 6365	K.EKPQSTISGLLGPTLYAEVGDIIK.V	2530.89853	3	6.03E-06	0.92	4.96	-	995.5
AHQ-8-5, 3122 - 3157	K.EVIITGIQTQGAK.H	1358.56590	2	3.38E-07	0.90	3.59	-	830.2
AHQ-8-4, 3175	K.EVIITGIQTQGAK.H	1358.56590	2	2.25E-06	0.92	3.37	-	1160.8
AHQ-8-4, 4843 - 4917	R.GEYEEHLGILGPIIR.A	1696.92816	2	5.84E-05	0.77	3.16	-	628.7
AHQ-8-3, 3832	K.SWYLEDNINK.F	1282.38331	2	3.26E-04	0.81	3.17	-	722.9
AHQ-8-3, 4789	K.SWYLEDNINKFCENPDEVKR.D	2558.76440	3	5.53E-04	0.76	3.60	-	485.5
gi|4758756|ref|NP_004528.1|	nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr			3.39E-07	2.68	30.23	10.00	45373.8
AHQ-8-7, 6252	K.GIPEFWLTVFK.N	1337.58999	2	3.39E-07	0.82	2.85	-	334.4
AHQ-8-7, 5161	R.LDGLVETPTGYIESLPR.V	1861.08535	2	3.44E-05	0.95	4.56	-	1113.9
AHQ-8-8, 5266 - 5341	R.LDGLVETPTGYIESLPR.V	1861.08535	2	3.21E-04	0.78	3.04	-	654.6
AHQ-8-7, 4586	K.YAVLYQPLFDK.R	1357.57807	2	4.03E-04	0.91	3.57	-	798.0
gi|30150022|ref|XP_300862.1|	similar to beta-tubulin 4Q [Homo sapiens]			3.52E-07	4.55	50.21	11.30	33545.2
AHQ-8-7, 3429	R.FPGQLNADLR.K	1131.26634	2	3.72E-07	0.86	2.97	-	922.2
AHQ-8-8, 3322 - 3383	R.FPGQLNADLR.K	1131.26634	2	8.28E-04	0.83	2.95	-	690.5
AHQ-8-7, 3305 - 3369	R.FPGQLNADLR.K	1131.26634	2	1.53E-05	0.90	3.56	-	860.5
AHQ-8-11, 3749 - 3789	K.LAVNM*VPFPR.L	1160.41420	2	1.55E-04	0.91	3.30	-	1049.3
AHQ-8-13-, 3854	K.LAVNM*VPFPR.L	1160.41420	2	2.43E-04	0.87	2.77	-	1203.8
AHQ-8-7, 4226 - 4285	K.LAVNMVPFPR.L	1144.41480	2	1.39E-04	0.94	3.88	-	876.5

AHQ-8-7, 3710	K.LAVNM*VPFPR.L	1160.41420	2	7.71E-06	0.93	3.50	-	1046.6
AHQ-8-11, 4747	R.LHFFM*PGFAPLTSR.G	1637.92902	2	1.24E-04	0.92	3.47	-	923.1
AHQ-8-7, 5409	R.LHFFMPGFAPLTSR.G	1621.92962	2	3.52E-07	0.89	3.58	-	730.8
AHQ-8-7, 4736	R.LHFFM*PGFAPLTSR.G	1637.92902	2	1.26E-04	0.95	4.21	-	1066.7
gi|30148644|ref|XP_293716.2|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			3.72E-07	0.94	10.17	1.20	105150.3
AHQ-8-5, 3612	R.TLTIVDTGIGM*TK.A	1366.60658	2	3.72E-07	0.94	3.42	-	1229.7
gi|21361621|ref|NP_002624.2|	phosphoglucomutase 1 [Homo sapiens]			3.78E-07	1.52	20.18	6.20	61448.7
AHQ-8-7, 3552	K.FNISNGGPAPEAITDK.I	1631.76820	2	3.78E-07	0.95	3.70	-	1618.6
AHQ-8-7, 5746 - 5816	R.LVIGQNGILSTPAVSCIIR.K	2013.39093	2	2.53E-04	0.57	2.98	-	509.6
gi|4505877|ref|NP_000436.1|	plectin 1, intermediate filament binding protein 500kDa; plectin 1, int			3.94E-07	4.17	50.20	1.70	518488.0
AHQ-8-3, 3821	K.AGVVGPELHEQLLSAEK.A	1777.99958	2	3.94E-07	0.92	3.98	-	1031.6
AHQ-8-2, 3521	K.AQVEQELTTLR.L	1288.43253	2	1.77E-04	0.85	2.94	-	726.8
AHQ-8-3, 3218	K.AYSDPSTGEPATYGELQQR.C	2071.14682	2	4.81E-05	0.91	4.04	-	549.8
AHQ-8-2, 4097	R.LQEAGILSAEELQR.L	1557.73077	2	4.73E-04	0.88	3.44	-	1068.2
AHQ-8-1, 4459	K.VLALPEPSPAAPTLR.S	1532.80918	2	8.62E-06	0.60	2.65	-	355.1
gi|5453607|ref|NP_006420.1|	chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co			3.99E-07	0.95	10.28	4.10	59366.3
AHQ-8-7, 6196	K.SQDAEVGDGTTSVTLLAAEFLK.Q	2253.44875	2	3.99E-07	0.95	5.51	-	753.9
gi|21614499|ref|NP_003370.2|	villin 2; Villin-2; cytovillin [Homo sapiens]			4.02E-07	2.66	30.19	3.40	69412.3
AHQ-8-6, 4254	K.APDFVFYAPR.L	1183.33971	2	1.40E-06	0.95	3.71	-	1175.3
AHQ-8-6, 4967	K.IGFPWSEIR.N	1105.27049	2	8.07E-06	0.84	2.53	-	924.6
AHQ-8-6, 3818 - 3819	K.KAPDFVFYAPR.L	1311.51262	2	4.02E-07	0.88	3.27	-	763.6
gi|29729345|ref|XP_290995.1|	similar to speckle-type POZ protein [Homo sapiens]			4.52E-07	0.84	10.21	10.90	18703.4
AHQ-8-4, 5717	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	2.03E-04	0.83	4.01	-	1027.0
AHQ-8-5, 5681	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	4.52E-07	0.84	4.16	-	986.9
AHQ-8-3, 5636	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	1.59E-06	0.89	3.92	-	956.2
gi|7657431|ref|NP_055205.1|	EBNA-2 co-activator (100kD) [Homo sapiens]			4.58E-07	2.68	30.20	7.20	99689.7
AHQ-8-4, 5873	K.DTNGENIAESLVAEGLATR.R	1961.07704	2	4.58E-07	0.92	3.87	-	1346.5
AHQ-8-4, 5986	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	2.05E-06	0.82	3.90	-	338.4
AHQ-8-4, 4723	K.VNVTVDYIRPASPATETVPAFSER.T	2620.89872	3	3.74E-06	0.94	3.92	-	1668.9
gi|4507521|ref|NP_001055.1|	transketolase [Homo sapiens]			4.70E-07	1.83	20.20	5.00	67877.3
AHQ-8-6, 4431	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	4.70E-07	0.88	3.96	-	455.0
AHQ-8-6, 5499 - 5507	K.LDNLVAILDINR.L	1369.59192	2	8.29E-07	0.94	4.03	-	1222.5
gi|5730118|ref|NP_006514.1|	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble; X-prolyl aminope			4.79E-07	0.78	10.18	2.70	69858.4
AHQ-8-6, 5302	R.TLSLDEVYLIDSGAQYK.D	1916.11778	2	4.79E-07	0.78	3.63	-	445.9
gi|5031573|ref|NP_005712.1|	ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye			4.84E-07	6.99	80.26	31.80	47370.9
AHQ-8-8, 4847	R.AEPEDHYFLLTEPPLNTPENR.E	2483.67423	2	7.66E-04	0.84	3.39	-	554.2
AHQ-8-7, 4718	R.AEPEDHYFLLTEPPLNTPENR.E	2483.67423	3	4.01E-04	0.67	3.07	-	504.3
AHQ-8-8, 6561	R.DITYFIQQLLR.D	1410.64250	2	4.84E-07	0.97	4.58	-	1428.7
AHQ-8-8, 3029 - 3106	R.DREVGIPPEQSLETAK.A	1769.93431	2	2.16E-05	0.96	5.21	-	1177.0
AHQ-8-13, 3681	K.DYEEIGPSICR.H	1340.44122	2	2.07E-06	0.86	2.75	-	956.7
AHQ-8-13-, 3512	K.DYEEIGPSICR.H	1340.44122	2	3.26E-05	0.75	2.67	-	596.7
AHQ-8-8, 5541	K.GVDDLDFFIGDEAIEKPTYATK.W	2445.66268	2	4.41E-06	0.90	3.97	-	855.1
AHQ-8-8, 5543	K.GVDDLDFFIGDEAIEKPTYATK.W	2445.66268	3	6.13E-04	0.65	3.26	-	473.4
AHQ-8-8, 4303	R.HGIVEDWDLMER.F	1500.66127	2	1.15E-04	0.94	3.36	-	1520.5
AHQ-8-8, 6089 - 6147	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	1.72E-04	0.85	4.26	-	938.6
AHQ-8-8, 3661	R.YSYVCPDLVK.E	1245.42618	2	9.91E-05	0.85	3.44	-	511.6
gi|4758018|ref|NP_004359.1|	calponin 2; Calonin 2 [Homo sapiens]			5.11E-07	1.75	20.19	9.10	33696.9
AHQ-8-12, 2943 - 2944	K.GLQSGVDIGVK.Y	1073.22510	2	1.10E-06	0.92	3.19	-	1335.3
AHQ-8-12, 5838	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.07E-04	0.95	3.76	-	1723.7
AHQ-8-14-, 5929	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	5.11E-07	0.84	2.79	-	1023.9
AHQ-8-11, 5811	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	4.12E-06	0.89	2.72	-	1155.3
gi|21361670|ref|NP_054782.2|	src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo			5.34E-07	0.76	10.17	3.70	48294.0
AHQ-8-10, 3290 - 3339	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	5.21E-04	0.81	3.21	-	815.4
AHQ-8-8, 3358	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	5.34E-07	0.76	3.16	-	590.3
gi|18600882|ref|XP_089309.1|	similar to Cyclophilin-LC [Homo sapiens]			5.53E-07	0.81	10.14	8.50	18166.6
AHQ-8-13-, 4626	R.IIPGFMCQGGDFTR.P	1600.84403	2	5.53E-07	0.81	2.71	-	361.6
gi|6005846|ref|NP_009215.1|	PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro			5.55E-07	2.62	30.18	14.90	39547.7
AHQ-8-14-, 6093	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	5.27E-06	0.83	3.29	-	569.5
AHQ-8-12, 2743	K.HLSSCAAPAPLTSAER.E	1669.84126	2	5.55E-07	0.83	3.15	-	586.8
AHQ-8-12, 4450	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	2.18E-06	0.96	3.12	-	2365.8
gi|4505621|ref|NP_002558.1|	prostatic binding protein; phosphatidylethanolamine binding protein [Ho			5.64E-07	1.92	20.23	20.30	21056.6
AHQ-8-11, 4684	R.APVAGTCYQAEWDDYVPK.L	2072.23961	2	5.64E-07	0.97	4.70	-	1925.6
AHQ-8-11, 4187	K.GNDISSGTVLSDYVGSGPPK.G	1951.08062	2	2.41E-06	0.94	4.41	-	1013.0
gi|7705296|ref|NP_057271.1|	bridging integrator 2; bridging integrator-2; breast cancer associated			5.78E-07	3.09	40.19	12.10	61746.8
AHQ-8-5, 5709	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	2.77E-06	0.79	3.19	-	791.8
AHQ-8-7, 5553 - 5554	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	2.73E-05	0.54	2.73	-	585.8
AHQ-8-7, 2834	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	5.60E-04	0.88	3.86	-	776.0
AHQ-8-10, 2815	R.FEQSASNFYQQQAEGHK.L	2000.07352	2	5.78E-07	0.87	3.68	-	683.9
AHQ-8-6, 6122	R.IGCYVTIFQNISNLR.D	1800.07167	2	1.71E-05	0.88	3.28	-	1046.8
AHQ-8-7, 6068	R.IGCYVTIFQNISNLR.D	1800.07167	2	1.09E-05	0.82	3.71	-	579.2
AHQ-8-5, 6225	R.IGCYVTIFQNISNLR.D	1800.07167	2	7.98E-05	0.88	3.69	-	877.3
AHQ-8-5, 4181	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	1.77E-05	0.61	2.62	-	487.8
gi|5729875|ref|NP_006658.1|	progesterone receptor membrane component 1; progesterone binding protei			6.06E-07	0.87	10.17	7.70	21671.0
AHQ-8-11, 4000	R.KFYGPEGPYGVFAGR.D	1645.84140	2	6.06E-07	0.87	3.48	-	807.1
gi|21361478|ref|NP_055944.2|	septin 6 isoform B; septin 2 [Homo sapiens]			6.48E-07	1.92	20.32	11.10	49716.3
AHQ-8-7, 3796	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L	3147.31508	3	6.48E-07	0.98	6.50	-	1882.4
AHQ-8-7, 4765	R.TVPLAGHVGFDSLPDQLVNK.S	2108.38284	2	9.49E-07	0.95	4.58	-	991.0
gi|19743813|ref|NP_002202.2|	integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib			6.94E-07	1.88	20.28	4.80	88414.9
AHQ-8-3, 4944	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	6.94E-07	0.92	4.41	-	745.5
AHQ-8-3, 4938	K.LKPEDITQIQPQQLVLR.L	2020.36187	3	9.06E-07	0.95	4.73	-	1353.0
AHQ-8-3, 6269 - 6348	K.LSENNIQTIFAVTEEFQPVYK.E	2471.74650	3	8.10E-07	0.96	5.62	-	1318.2
gi|4506925|ref|NP_003013.1|	SH3 domain binding glutamic acid-rich protein like; SH3-binding domain			7.14E-07	3.54	40.27	58.80	12774.2
AHQ-8-13, 5749 - 5803	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	1.49E-05	0.93	4.25	-	1009.1
AHQ-8-13-, 5614 - 5676	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.22E-04	0.92	3.52	-	1121.9
AHQ-8-13, 4916 - 4972	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	3.46E-04	0.96	5.35	-	1123.4
AHQ-8-13-, 4943	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	7.14E-07	0.80	3.87	-	766.4
AHQ-8-13-, 4758 - 4827	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	4.96E-05	0.90	4.82	-	617.3
AHQ-8-13, 4224 - 4247	R.GDYDAFFEAR.E	1191.23073	2	1.43E-05	0.94	4.21	-	985.9
AHQ-8-13-, 2507 - 2514	R.VYIASSSGSTAIK.K	1284.44065	2	4.74E-04	0.95	4.27	-	1705.9
AHQ-8-13, 2581 - 2647	R.VYIASSSGSTAIK.K	1284.44065	2	2.23E-04	0.87	3.31	-	1333.7
gi|4758158|ref|NP_004395.1|	neural precursor cell expressed, developmentally down-regulated 5 [Homo			7.77E-07	0.85	10.17	4.70	41487.2
AHQ-8-8, 4985	K.ASIPFSVVGSNQLIEAK.G	1761.01216	2	7.77E-07	0.85	3.47	-	660.0
gi|4503481|ref|NP_001395.1|	eukaryotic translation elongation factor 1 gamma; elongation factor 1-g			7.94E-07	1.88	20.23	6.20	50118.5
AHQ-8-8, 3053	K.ALIAAQYSGAQVR.V	1348.53280	2	7.94E-07	0.95	3.99	-	1369.7
AHQ-8-8, 2687 - 2690	R.KLDPGSEETQTLVR.E	1573.73020	2	1.99E-05	0.93	4.52	-	556.7
gi|9845511|ref|NP_008839.2|	ras-related C3 botulinum toxin substrate 1 isoform Rac1; rho family, sm			8.04E-07	0.82	10.17	5.20	21450.0
AHQ-8-11, 3101 - 3159	K.YLECSALTQR.G	1242.38392	2	8.04E-07	0.82	2.87	-	835.1
gi|5453559|ref|NP_006347.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; ATP			8.26E-07	0.89	10.19	10.60	18491.1
AHQ-8-11, 5179 - 5187	R.LAALPENPPAIDWAYYK.A	1933.19486	2	8.26E-07	0.89	3.73	-	568.6
gi|4503725|ref|NP_000792.1|	FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei			9.27E-07	1.90	20.22	13.00	11950.6
AHQ-8-13-, 3104	R.GWEEGVAQM*SVGQR.A	1550.67866	2	6.94E-06	0.95	4.28	-	1194.2
AHQ-8-13-, 3874	R.GWEEGVAQMSVGQR.A	1534.67926	2	9.27E-07	0.95	4.48	-	1094.0
AHQ-8-14-, 3071	R.GWEEGVAQM*SVGQR.A	1550.67866	2	9.44E-05	0.94	3.78	-	1332.6
AHQ-8-14-, 3837	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.12E-04	0.91	3.77	-	1019.4
AHQ-8-13, 3244	R.GWEEGVAQM*SVGQR.A	1550.67866	2	1.62E-05	0.94	3.70	-	1243.0
gi|5174727|ref|NP_005989.1|	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring			9.29E-07	3.77	40.22	8.50	60330.4
AHQ-8-6, 3790	R.AVAQALEVIPR.T	1167.38326	2	7.97E-05	0.96	4.37	-	1625.2

AHQ-8-6, 4295 - 4340	K.IPGGIIEDSCVLR.G	1430.65218	2	1.25E-06	0.92	3.97	-	927.4
AHQ-8-6, 4304	R.IVLLDSSLEYK.K	1280.49191	2	1.79E-06	0.94	3.45	-	1257.1
AHQ-8-6, 4675	K.TAVETAVLLLR.I	1186.42649	2	9.29E-07	0.94	3.57	-	1869.7
gi|22748619|ref|NP_689476.1|	tropomyosin 3 [Homo sapiens]			9.32E-07	0.76	10.18	5.30	28222.6
AHQ-8-9, 6686	K.YSQKEDKYEEEIK.I	1689.80129	2	9.32E-07	0.76	3.60	-	773.7
gi|6005826|ref|NP_009160.1|	protein kinase C and casein kinase substrate in neurons 2; pacsin 2 [Ho			9.46E-07	0.89	10.17	2.30	55904.6
AHQ-8-6, 3903	K.AYAQQLTEWAR.R	1337.46534	2	9.46E-07	0.89	3.32	-	1060.4
gi|18201905|ref|NP_000166.2|	glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras			1.04E-06	1.65	20.20	2.70	63146.7
AHQ-8-7, 6316	K.ILLANFLAQTEALMR.G	1705.05838	2	1.53E-04	0.94	4.01	-	1243.8
AHQ-8-7, 5954 - 6008	K.ILLANFLAQTEALM*R.G	1721.05778	2	1.04E-06	0.71	3.25	-	414.5
gi|30150299|ref|XP_293010.2|	similar to keratin 8, type II cytoskeletal - human [Homo sapiens] [MAS			1.05E-06	0.94	10.21	2.70	44500.6
AHQ-8-1, 5064	K.LALDIEIATYR.Q	1278.47925	2	1.05E-06	0.94	4.27	-	1841.7
gi|20547107|ref|XP_114482.1|	similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN			1.12E-06	0.89	10.19	2.10	94330.3
AHQ-8-4, 6086	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	1.12E-06	0.89	3.88	-	715.9
gi|21361198|ref|NP_000286.2|	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei			1.14E-06	1.77	20.19	6.70	46722.2
AHQ-8-7, 3818	K.SVLGQLGITK.V	1016.21669	2	2.69E-04	0.86	3.28	-	775.2
AHQ-8-7, 4197	K.VFSNGADLSGVTEEAPLK.L	1835.00476	2	1.14E-06	0.91	3.83	-	1047.9
gi|21361322|ref|NP_006078.2|	tubulin, beta, 5 [Homo sapiens]			1.14E-06	0.93	10.25	6.10	49585.5
AHQ-8-7, 4981	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	1.14E-06	0.93	5.08	-	945.2
gi|4502201|ref|NP_001649.1|	ADP-ribosylation factor 1 [Homo sapiens]			1.19E-06	1.92	20.25	16.00	20696.6
AHQ-8-13, 3437	R.ILM*VGLDAAGK.T	1104.34572	2	5.76E-04	0.87	2.66	-	1187.3
AHQ-8-12, 3207	R.ILM*VGLDAAGK.T	1104.34572	2	2.08E-04	0.95	3.26	-	1856.0
AHQ-8-13-, 6258	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	3	5.67E-04	0.94	3.75	-	1934.7
AHQ-8-12, 6182	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	3	1.19E-06	0.97	4.97	-	2107.7
gi|4507767|ref|NP_003326.1|	ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi			1.20E-06	2.80	30.25	4.90	111719.5
AHQ-8-4, 3493	R.APASAAASEDAPYPVCTVR.Y	1935.10448	2	1.20E-06	0.94	5.04	-	770.7
AHQ-8-4, 4886	R.TEEEPLEEPLDEALVR.T	1870.00428	2	3.42E-05	0.89	3.42	-	932.8
AHQ-8-4, 4513	R.VLVSGLQGLGAEVAK.N	1441.69805	2	2.41E-04	0.97	4.55	-	1612.4
gi|4758950|ref|NP_000933.1|	peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]			1.22E-06	2.44	30.21	18.50	23742.4
AHQ-8-12, 3062	R.DKPLKDVIIADCGK.I	1573.83653	2	1.22E-06	0.90	3.33	-	1191.9
AHQ-8-11, 3055	R.DKPLKDVIIADCGK.I	1573.83653	3	9.89E-04	0.76	3.51	-	666.0
AHQ-8-12, 4096 - 4160	K.DTNGSQFFITTVK.T	1458.59766	2	6.81E-05	0.95	4.19	-	1409.5
AHQ-8-11, 4153 - 4229	K.TVDNFVALATGEK.G	1365.51377	2	3.17E-05	0.59	2.76	-	444.7
gi|15431310|ref|NP_000517.2|	keratin 14; cytokeratin 14 [Homo sapiens]			1.24E-06	2.64	30.19	7.00	51621.2
AHQ-8-10, 2831	R.ALEEANADLEVK.I	1302.41284	2	1.24E-06	0.91	3.16	-	1352.9
AHQ-8-10, 2571	R.APSTYGGGLSVSSSR.F	1426.51406	2	2.67E-04	0.88	3.20	-	812.6
AHQ-8-13, 3864 - 3943	R.GQVGGDVNVEM*DAAPGVDLSR.I	2103.25697	2	6.32E-04	0.63	2.84	-	344.7
AHQ-8-13-, 3718	R.GQVGGDVNVEM*DAAPGVDLSR.I	2103.25697	2	2.49E-04	0.84	3.65	-	528.2
AHQ-8-2, 3812	R.GQVGGDVNVEM*DAAPGVDLSR.I	2103.25697	2	7.75E-05	0.85	3.90	-	443.2
gi|20452464|ref|NP_620411.1|	similar to endothelial cell-selective adhesion molecule; likely orthol			1.26E-06	0.69	10.14	3.60	41208.1
AHQ-8-8, 2685	K.DSGPYSCSVNVQDK.Q	1557.62141	2	1.26E-06	0.69	2.85	-	781.0
gi|17986001|ref|NP_005505.2|	major histocompatibility complex, class I, B; HLA class I histocompati			1.28E-06	0.67	10.15	5.50	40459.8
AHQ-8-8, 2671 - 2746	R.DGEDQTQDTELVETRPAGDR.T	2233.24975	3	1.28E-06	0.67	3.06	-	690.0
gi|24234688|ref|NP_004125.3|	heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre			1.30E-06	0.77	10.19	2.80	73680.1
AHQ-8-6, 5470 - 5484	K.STNGDTFLGGEDFDQALLR.H	2057.16328	2	1.30E-06	0.77	3.89	-	311.0
gi|4557321|ref|NP_000030.1|	apolipoprotein A-I precursor [Homo sapiens]			1.30E-06	1.75	20.18	9.70	30777.6
AHQ-8-14-, 5003	K.LLDNWDSVTSTFSK.L	1613.74965	2	2.27E-04	0.85	3.50	-	652.3
AHQ-8-11, 5708	K.VSFLSALEEYTK.K	1387.55934	2	1.30E-06	0.89	3.47	-	805.9
gi|21359837|ref|NP_003312.2|	Tu translation elongation factor, mitochondrial [Homo sapiens]			1.33E-06	0.77	10.17	3.50	49541.2
AHQ-8-8, 3275	R.GITINAAHVEYSTAAR.H	1674.83945	2	1.33E-06	0.77	3.43	-	725.7
gi|16950601|ref|NP_005956.2|	myosin light chain kinase isoform 6; myosin light chain kinase [Homo s			1.42E-06	3.08	40.21	5.20	110074.8
AHQ-8-5, 4094	K.AAM*PPQIIQFPEDQK.V	1729.97839	2	8.89E-05	0.67	2.65	-	528.5
AHQ-8-5, 3885	R.IIDEDFELTER.E	1380.48206	2	2.17E-05	0.87	3.21	-	695.2
AHQ-8-5, 4938	R.STSFNVQDLLPDHEYK.F	1894.03076	2	2.67E-04	0.69	3.13	-	305.8
AHQ-8-6, 3492	K.VSDFYDIEER.L	1273.33005	2	1.42E-06	0.86	3.14	-	788.6
AHQ-8-5, 3521	K.VSDFYDIEER.L	1273.33005	2	2.93E-06	0.94	3.45	-	1139.5
gi|4502693|ref|NP_001760.1|	CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen			1.43E-06	1.75	20.18	9.60	25415.9
AHQ-8-11, 2699	K.EVQEFYKDTYNK.L	1564.67709	2	8.09E-04	0.88	2.83	-	1219.7
AHQ-8-11, 3401	K.KDVLETFTVK.S	1180.37558	2	1.39E-05	0.90	3.64	-	875.9
AHQ-8-1, 3708	K.KDVLETFTVK.S	1180.37558	2	1.43E-06	0.86	3.26	-	922.5
gi|5453605|ref|NP_006421.1|	chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-			1.44E-06	1.91	20.21	4.80	57838.8
AHQ-8-7, 5901	R.DALSDLALHFLNK.M	1457.65603	2	1.44E-06	0.97	4.27	-	2312.0
AHQ-8-7, 3486	K.VIDPATATSVDLR.D	1358.52277	2	1.43E-04	0.94	3.42	-	1295.6
gi|4506045|ref|NP_002718.1|	proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p			1.44E-06	0.81	10.15	8.20	17623.6
AHQ-8-1, 4128	K.GPM*FELLPGESNK.I	1435.62747	2	1.44E-06	0.81	3.02	-	893.2
gi|5803225|ref|NP_006752.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, epsilon poly			1.45E-06	0.96	10.25	7.50	29173.7
AHQ-8-13-, 6178	K.AAFDDAIAELDTLSEESYK.D	2089.19882	2	1.45E-06	0.96	4.90	-	1185.5
gi|4557385|ref|NP_000055.1|	complement component 3 precursor; acylation-stimulating protein cleavag			1.49E-06	2.81	30.26	3.10	187162.3
AHQ-8-6, 5516 - 5584	K.EYVLPSFEVIVEPTEK.F	1880.12704	2	2.00E-05	0.94	4.45	-	952.8
AHQ-8-6, 3570	R.IPIEDGSGEVVLSR.K	1471.63788	2	9.95E-06	0.91	3.53	-	791.2
AHQ-8-6, 4376	R.VPVAVQGEDTVQSLTQGDGVAK.L	2199.40432	2	1.49E-06	0.97	5.19	-	1313.0
gi|9845297|ref|NP_063940.1|	second mitochondria-derived activator of caspase isoform Smac-alpha, pr			1.51E-06	0.94	10.15	4.20	27130.6
AHQ-8-11, 3251	K.LAEAQIEELR.Q	1172.31354	2	1.51E-06	0.94	2.72	-	2030.9
gi|19913424|ref|NP_001681.2|	ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT			1.51E-06	0.92	10.21	2.80	68303.7
AHQ-8-6, 4118 - 4128	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	1.51E-06	0.92	4.24	-	942.6
gi|7705827|ref|NP_057187.1|	GTP-binding protein Sara [Homo sapiens]			1.56E-06	0.95	10.19	5.60	22409.7
AHQ-8-11, 4183	K.LVFLGLDNAGK.T	1147.34882	2	1.56E-06	0.95	3.87	-	1332.7
AHQ-8-11, 4108 - 4184	K.LVFLGLDNAGK.T	1147.34882	2	6.13E-05	0.84	2.66	-	911.4
gi|18104989|ref|NP_002822.2|	protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t			1.56E-06	3.66	50.20	11.60	67560.7
AHQ-8-6, 5550	K.AGFWEEFESLQK.Q	1471.59489	2	1.56E-06	0.93	3.19	-	1609.2
AHQ-8-6, 4634 - 4698	R.DLSGLDAETLLK.G	1275.43053	2	5.08E-04	0.90	3.20	-	1291.0
AHQ-8-6, 6118	R.ESLSQPGDFVLSVLSDQPK.A	2047.25144	3	4.65E-06	0.84	3.94	-	1154.1
AHQ-8-6, 4264 - 4322	R.TLQVSPLDNGDLIR.E	1541.73134	2	3.85E-04	0.61	3.01	-	310.5
AHQ-8-7, 4253	R.TLQVSPLDNGDLIR.E	1541.73134	2	5.76E-04	0.35	2.63	-	403.2
AHQ-8-6, 2695	K.YPLNCSDPTSER.W	1440.51765	2	3.41E-04	0.38	2.63	-	357.1
gi|16933567|ref|NP_005361.2|	mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]			1.58E-06	0.93	10.18	6.80	23668.1
AHQ-8-11, 5399 - 5475	K.ANINVENAFFTLAR.D	1580.76926	2	1.58E-06	0.93	3.67	-	1335.2
gi|4557675|ref|NP_000201.1|	integrin alpha chain, alpha 6 [Homo sapiens]			1.59E-06	4.74	60.20	8.20	119509.5
AHQ-8-4, 3391	K.FGSCQQGVAATFTK.D	1503.66172	2	1.59E-06	0.81	2.59	-	1301.4
AHQ-8-3, 3901	K.GIVSKDEITFVSGAPR.A	1676.89525	2	1.63E-06	0.76	3.29	-	696.8
AHQ-8-4, 4195	K.LRPIPITASVEIQEPSSR.R	1994.28128	2	1.23E-04	0.85	3.74	-	653.9
AHQ-8-4, 5437	K.SEDEVGSLIEYEFR.V	1673.75872	2	1.75E-05	0.95	4.00	-	1351.2
AHQ-8-5, 3616	K.TACGAPSGICLQVK.S	1464.69022	2	7.55E-04	0.44	2.69	-	306.7
AHQ-8-4, 3201	R.TGGLYSCDITAR.G	1315.43490	2	9.29E-06	0.93	3.71	-	991.3
gi|4502285|ref|NP_001672.1|	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 isoform 2; ATP			1.64E-06	0.92	10.20	1.50	109690.3
AHQ-8-1, 4612	K.VGEATETALTCLVEK.M	1622.81958	2	1.64E-06	0.92	4.00	-	892.6
gi|6005786|ref|NP_009214.1|	monoglyceride lipase; lysophospholipase-like [Homo sapiens]			1.66E-06	0.92	10.20	4.50	34292.3
AHQ-8-14-, 5726 - 5727	K.LTVPFLLLQGSADR.L	1530.79329	2	1.66E-06	0.92	3.94	-	917.3
gi|20149637|ref|NP_057526.2|	type 1 tumor necrosis factor receptor shedding aminopeptidase regulato			1.66E-06	0.79	10.13	1.40	107761.4
AHQ-8-4, 5899	R.NPVGYPLAWQFLR.K	1561.81077	2	1.66E-06	0.79	2.58	-	759.8
gi|5803181|ref|NP_006810.1|	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo			1.68E-06	1.69	20.20	5.90	62638.9
AHQ-8-6, 5899	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	1.68E-06	0.80	3.19	-	720.7
AHQ-8-6, 4375 - 4378	R.LAYINPDLALEEK.N	1489.69480	2	1.26E-04	0.89	3.99	-	655.5
gi|7705704|ref|NP_057001.1|	glutathione S-transferase subunit 13 homolog [Homo sapiens]			1.70E-06	0.82	10.16	6.60	25496.7
AHQ-8-11, 4012	R.FLTAVNLEHPEM*LEK.A	1788.05785	2	1.70E-06	0.82	3.01	-	800.8
gi|20127408|ref|NP_000173.2|	hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub			1.71E-06	1.76	20.18	4.60	82999.1
AHQ-8-6, 5847	R.DSIFSNLTGQLDYQGFEK.A	2063.20943	2	1.71E-06	0.84	3.60	-	545.5

AHQ-8-6, 3106	K.TGIEQGSDAGYLCESQK.F	1844.93497	2	1.84E-04	0.92	3.63	-	1100.5
gi|6715607|ref|NP_000175.1|	G-gamma globin [Homo sapiens]			1.72E-06	0.93	10.18	6.80	16126.3
AHQ-8-14-, 4729 - 4741	R.LLVVYPWTQR.F	1275.52342	2	4.59E-06	0.89	3.01	-	1077.1
AHQ-8-13-, 4730 - 4731	R.LLVVYPWTQR.F	1275.52342	2	1.72E-06	0.93	3.53	-	1143.7
gi|4507745|ref|NP_003320.1|	thioredoxin [Homo sapiens]			1.72E-06	1.90	30.18	22.90	11693.3
AHQ-8-13-, 3872 - 3878	K.EKLEATINELV	1259.43110	2	5.70E-04	0.85	3.12	-	948.9
AHQ-8-14-, 4443	K.LEATINELV	1002.14365	1	6.03E-04	0.11	1.82	-	188.0
AHQ-8-14-, 3817	K.TAFQEALDAAGDK.L	1337.41728	2	1.72E-06	0.94	3.50	-	1606.1
AHQ-8-13-, 3788 - 3846	K.TAFQEALDAAGDK.L	1337.41728	2	4.53E-05	0.90	3.30	-	1346.9
AHQ-8-14, 4777	K.TAFQEALDAAGDK.L	1337.41728	2	4.13E-04	0.66	2.78	-	662.7
gi|20539300|ref|XP_088391.4|	similar to tropomyosin 4 [Homo sapiens]			1.83E-06	0.93	10.17	6.90	18592.1
AHQ-8-11, 3648	R.KLVILEGELER.A	1299.54160	2	1.83E-06	0.93	3.44	-	1559.0
gi|13569962|ref|NP_112243.1|	RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap			1.87E-06	0.87	10.23	8.50	22171.0
AHQ-8-11, 5676 - 5736	K.NATNVEQAFM*TMAAEIK.K	1886.14019	2	1.87E-06	0.87	4.64	-	838.2
gi|4502171|ref|NP_000476.1|	adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho			1.92E-06	0.97	10.21	5.60	19607.6
AHQ-8-11, 3535 - 3537	R.IDYIAGLDSR.G	1123.24098	2	1.92E-06	0.97	4.11	-	1915.8
gi|4503531|ref|NP_001958.1|	eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens] [			2.03E-06	0.92	10.21	3.90	46393.9
AHQ-8-8, 3609	R.GIYAYGFEKPSAIQQR.A	1829.04828	2	2.03E-06	0.92	4.24	-	793.7
gi|4504557|ref|NP_000864.1|	intercellular adhesion molecule 2 precursor [Homo sapiens]			2.12E-06	0.90	10.19	5.80	30653.1
AHQ-8-7, 6354 - 6426	R.VPTVEPLDSLTLFLFR.G	1848.17455	2	2.12E-06	0.90	3.83	-	507.4
gi|4507231|ref|NP_003134.1|	single-stranded DNA binding protein; single-stranded DNA-binding protei			2.16E-06	1.82	20.22	22.30	17259.5
AHQ-8-13-, 5668	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	5.63E-05	0.88	3.92	-	811.2
AHQ-8-13-, 3271	R.SGDSEVYQLGDVSQK.T	1612.67692	2	2.16E-06	0.94	4.34	-	1034.8
gi|14149680|ref|NP_056107.1|	KIAA0747 protein [Homo sapiens]			2.17E-06	0.68	10.19	1.40	122855.6
AHQ-8-6, 5159	K.AVYSTNCPVWEEAFR.F	1830.99795	2	2.17E-06	0.68	2.84	-	538.9
gi|5802966|ref|NP_006861.1|	destrin (actin depolymerizing factor); destrin [Homo sapiens]			2.19E-06	0.94	10.18	6.70	18505.6
AHQ-8-12, 3640 - 3695	R.YALYDASFETK.E	1308.41754	2	2.19E-06	0.94	3.63	-	1168.5
gi|21464101|ref|NP_036611.2|	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein			2.26E-06	0.93	10.22	5.70	28302.4
AHQ-8-14-, 3122 - 3187	K.NVTELNEPLSNEER.N	1644.72215	2	3.76E-05	0.81	3.31	-	675.7
AHQ-8-10, 2994 - 2999	K.NVTELNEPLSNEER.N	1644.72215	2	2.26E-06	0.93	4.44	-	774.9
gi|5453832|ref|NP_006380.1|	oxygen regulated protein precursor; oxygen regulated protein (150kD) [H			2.34E-06	0.95	10.20	1.30	111334.8
AHQ-8-3, 6005	R.VEFEELCADLFER.V	1658.81048	2	2.34E-06	0.95	4.01	-	1133.9
gi|4506417|ref|NP_002877.1|	RAP2B, member of RAS oncogene family [Homo sapiens]			2.47E-06	2.45	30.22	26.20	20494.2
AHQ-8-11, 5729	K.ASVDELFAEIVR.Q	1349.51434	2	6.84E-05	0.78	2.91	-	942.8
AHQ-8-11, 6101 - 6103	K.EIEVDSSPSVLEILDTAGTEQFASM*R.D	2842.08287	3	6.17E-06	0.93	4.43	-	1114.1
AHQ-8-11, 4071	K.YDPTIEDFYR.K	1319.40042	2	2.47E-06	0.73	2.77	-	283.8
gi|6005749|ref|NP_009193.1|	RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA			2.48E-06	0.86	10.17	8.50	19846.9
AHQ-8-11, 3204	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	2.48E-06	0.86	3.45	-	643.0
gi|30148978|ref|XP_291520.2|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			2.61E-06	0.49	10.14	2.20	68413.1
AHQ-8-11, 4567 - 4568	R.DWSHYFKTIKDLR.A	1709.92863	2	2.61E-06	0.49	2.87	-	513.2
gi|4757900|ref|NP_004334.1|	calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre			2.71E-06	4.12	50.28	24.50	48141.1
AHQ-8-7, 3408	R.AKIDDPTDSKPEDWDKPEHIPDPDAK.K	2961.14253	3	4.26E-04	0.61	3.17	-	670.4
AHQ-8-7, 5458	R.CKDDEFTHLYTLIVRPDNTYEVK.I	2859.15977	3	8.22E-06	0.96	5.58	-	1430.5
AHQ-8-14-, 5194	R.FYALSASFEPFSNK.G	1608.77470	2	2.71E-06	0.95	3.66	-	1324.5
AHQ-8-13-, 5159 - 5194	R.FYALSASFEPFSNK.G	1608.77470	2	6.63E-05	0.94	3.43	-	1488.5
AHQ-8-7, 2537	K.IKDPDASKPEDWDER.A	1801.89173	2	6.62E-05	0.91	3.57	-	937.0
AHQ-8-7, 4553	K.KPEDWDEEM*DGEWEPPVIQNPEYK.G	2978.14866	3	4.27E-04	0.69	3.14	-	522.4
gi|4502011|ref|NP_000467.1|	adenylate kinase 1 [Homo sapiens]			2.94E-06	2.56	30.19	23.20	21634.7
AHQ-8-11, 5008	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	3	7.12E-05	0.77	3.12	-	777.1
AHQ-8-11, 5007	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	2	7.32E-04	0.82	2.95	-	845.3
AHQ-8-11, 3443 - 3507	K.IIFVVGGPGSGK.G	1131.34939	2	3.29E-05	0.96	3.87	-	2330.2
AHQ-8-11, 3752	K.YGYTHLSTGDLLR.S	1496.64912	3	2.94E-06	0.82	3.05	-	803.9
gi|4757826|ref|NP_004039.1|	beta-2-microglobulin [Homo sapiens]			2.97E-06	0.86	10.15	8.40	13714.5
AHQ-8-14-, 2070 - 2090	R.VNHVTLSQPK.I	1123.28735	2	2.97E-06	0.86	2.89	-	884.8
AHQ-8-14-, 1933 - 2005	R.VNHVTLSQPK.I	1123.28735	2	2.82E-05	0.87	2.99	-	771.8
gi|29743324|ref|XP_293276.1|	similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote			3.00E-06	0.85	10.34	16.00	21244.7
AHQ-8-14-, 5033 - 5098	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	3.00E-06	0.85	5.25	-	840.7
AHQ-8-13-, 5023 - 5051	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	7.97E-04	0.94	6.79	-	1106.6
gi|4506365|ref|NP_002856.1|	RAB2, member RAS oncogene family [Homo sapiens]			3.04E-06	0.94	10.20	6.10	23545.4
AHQ-8-11, 4235 - 4301	K.LQIWDTAGQESFR.S	1551.68478	2	3.04E-06	0.94	4.06	-	1425.8
gi|4502303|ref|NP_001688.1|	mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m			3.35E-06	2.29	30.24	22.10	23277.2
AHQ-8-11, 5207	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	2.65E-04	0.52	2.82	-	320.8
AHQ-8-11, 3641	K.LVRPPVQVYGIEGR.Y	1583.85942	3	1.19E-05	0.95	4.74	-	1781.8
AHQ-8-11, 3316	K.VAASVLNPYVK.R	1161.37549	2	3.35E-06	0.82	3.08	-	562.6
gi|5453603|ref|NP_006422.1|	chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c			3.52E-06	0.86	10.17	3.00	57487.9
AHQ-8-7, 3142	R.EALLSSAVDHGSDEVK.F	1657.76083	2	3.52E-06	0.86	3.18	-	1190.9
gi|5803227|ref|NP_006817.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype			3.65E-06	1.67	20.16	10.60	27764.1
AHQ-8-10, 2266 - 2335	K.AVTEQGAELSNEER.N	1533.57979	2	3.65E-06	0.81	3.14	-	862.3
AHQ-8-10, 2676 - 2750	K.YLIANATNPESK.V	1321.46099	2	6.83E-04	0.86	3.15	-	1117.7
gi|29731460|ref|XP_293027.1|	similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl			3.86E-06	0.97	10.16	6.10	23572.2
AHQ-8-10, 4287	K.DFLAGGVAAAISK.M	1220.39980	2	3.86E-06	0.97	3.26	-	2730.2
gi|4507109|ref|NP_000336.1|	alpha-synuclein isoform NACP140; non A4 component of amyloid precursor			3.92E-06	2.50	30.28	15.70	14460.1
AHQ-8-13-, 4496 - 4504	K.EQVTNVGGAVVTGVTAVAQK.T	1929.16446	2	3.92E-06	0.82	3.59	-	576.8
AHQ-8-12, 4116 - 4127	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	1.52E-05	0.97	5.68	-	1034.5
AHQ-8-2, 4219	K.TVEGAGSIAAATGFVK.K	1479.66001	2	5.64E-04	0.71	2.58	-	917.4
gi|11993943|ref|NP_055419.1|	Tax interaction protein 1 [Homo sapiens]			4.17E-06	0.93	10.18	13.70	13734.6
AHQ-8-13, 4212	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	4.17E-06	0.93	3.69	-	1221.8
gi|4507487|ref|NP_003238.1|	thrombospondin 2 [Homo sapiens]			4.29E-06	1.65	20.19	2.60	129954.5
AHQ-8-3, 4872 - 4946	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	5.31E-06	0.89	3.43	-	953.2
AHQ-8-5, 4914	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	8.82E-05	0.93	3.73	-	1229.1
AHQ-8-6, 4839	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	4.42E-05	0.92	3.60	-	1082.2
AHQ-8-2, 4948 - 5021	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	4.29E-06	0.92	3.54	-	1016.6
AHQ-8-11, 2767 - 2847	R.NALWHTGNTPGQVR.T	1551.69124	2	1.13E-04	0.73	2.62	-	808.0
AHQ-8-7, 2922	R.NALWHTGNTPGQVR.T	1551.69124	2	1.83E-04	0.69	2.62	-	699.9
gi|4504505|ref|NP_000405.1|	hydroxysteroid (17-beta) dehydrogenase 4 [Homo sapiens]			4.82E-06	0.79	10.19	2.20	79685.9
AHQ-8-5, 2917	R.ATSTATSGFAGAIGQK.L	1468.59408	2	4.82E-06	0.79	3.40	-	680.1
gi|4506353|ref|NP_002854.1|	phosphorylase, glycogen; liver (Hers disease, glycogen storage disease			4.95E-06	0.92	10.17	1.70	97147.8
AHQ-8-5, 5208 - 5216	K.LVIDQIDNGFFSPK.Q	1593.80471	2	4.95E-06	0.92	3.43	-	1190.6
gi|4505759|ref|NP_002622.1|	phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo			5.17E-06	0.96	10.25	4.10	53151.7
AHQ-8-8, 5875	K.LVPLLDTGDIIIDGGNSEYR.D	2161.39768	2	5.17E-06	0.96	4.93	-	1419.4
gi|13378141|ref|NP_054752.1|	DKFZP586A0522 protein [Homo sapiens]			5.17E-06	0.61	10.14	6.10	28318.9
AHQ-8-1, 4965	R.ELFSNLQEFAGPSGK.L	1624.77567	2	5.17E-06	0.61	2.85	-	423.9
gi|29736622|ref|XP_293924.1|	similar to cytoplasmic beta-actin [Homo sapiens]			5.22E-06	1.47	20.20	8.00	42002.9
AHQ-8-8, 5839 - 5921	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	6.38E-04	0.84	3.66	-	880.1
AHQ-8-8, 6055	R.TTGIVM*DSGDGVTHIVPIYEGYALPHAILR.L	3213.65260	3	5.22E-06	0.83	4.09	-	686.1
AHQ-8-8, 5559 - 5633	R.TTGIVMDSGDGVTHIVPIYEGYALPHAILR.L	3197.65320	3	5.21E-04	0.64	3.28	-	624.7
gi|21070997|ref|NP_003147.2|	stromal interaction molecule 1 precursor [Homo sapiens]			5.41E-06	0.82	10.16	1.50	77422.9
AHQ-8-7, 2852	K.YAEEELEQVR.E	1266.33905	2	5.41E-06	0.82	3.17	-	1155.6
gi|4758984|ref|NP_004654.1|	RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho			5.84E-06	2.53	30.20	16.20	24393.3
AHQ-8-11, 4143	R.DDEYDYLFK.V	1208.25483	2	1.78E-04	0.82	3.04	-	885.7
AHQ-8-11, 4088	R.DHADSNIVIM*LVGNK.S	1642.85914	2	5.84E-06	0.93	3.95	-	980.2
AHQ-8-11, 2841 - 2895	K.VVLIGDSGVGK.S	1044.22690	2	2.41E-04	0.77	3.14	-	900.3
gi|21735621|ref|NP_005909.2|	mitochondrial malate dehydrogenase precursor [Homo sapiens]			6.88E-06	0.83	10.14	5.60	35503.0
AHQ-8-14-, 6107	K.VAVLGASGGIGQPLSLLLK.N	1794.17156	2	6.88E-06	0.83	2.83	-	960.3
gi|4503823|ref|NP_002028.1|	protein-tyrosine kinase fyn isoform a; proto-oncogene tyrosine-protein			7.42E-06	0.74	10.14	2.00	60761.5
AHQ-8-7, 3625	K.WTAPEAALYGR.F	1235.37302	2	7.42E-06	0.74	2.71	-	621.3
gi|4506773|ref|NP_002956.1|	S100 calcium-binding protein A9; calgranulin B [Homo sapiens]			7.66E-06	1.67	20.17	24.60	13241.9

AHQ-8-13-, 2764	K.LGHPDTLNQGEFK.E	1456.58499	3	4.30E-04	0.81	3.21	-	1268.0
AHQ-8-13-, 5411	R.NIETIINTFHQYSVK.L	1808.02738	2	4.00E-04	0.80	3.19	-	773.9
AHQ-8-13, 5549	R.NIETIINTFHQYSVK.L	1808.02738	2	7.66E-06	0.86	3.45	-	634.7
gi|18543899|ref|XP_086916.1|	similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic			7.91E-06	0.94	10.21	8.00	21265.8
AHQ-8-11, 3395	K.NRPTSISWDGLDSGK.L	1633.74419	2	7.91E-06	0.94	4.18	-	1037.6
gi|4503545|ref|NP_001961.1|	eukaryotic translation initiation factor 5A; eIF5AI; eIF5A [Homo sapien			8.09E-06	0.78	10.18	11.00	16832.2
AHQ-8-12, 3819 - 3879	R.EDLRLPEGDLGKEIEQK.Y	1970.17021	3	8.09E-06	0.78	3.55	-	780.0
gi|13489087|ref|NP_109591.1|	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member			8.21E-06	1.75	20.19	8.70	42741.5
AHQ-8-8, 3973	K.TYGADLASVDFQHASEDAR.K	2054.11949	3	8.21E-06	0.88	3.78	-	713.2
AHQ-8-8, 5919	K.TYNFLPEFLVSTQK.T	1687.91650	2	1.35E-05	0.87	3.59	-	516.0
gi|4501867|ref|NP_001089.1|	aconitase 2 [Homo sapiens]			8.45E-06	0.90	10.18	2.10	85424.8
AHQ-8-5, 6234	K.DINQEVYNFLATAGAK.Y	1754.92134	2	8.45E-06	0.90	3.59	-	765.2
gi|30149460|ref|XP_210540.2|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			8.65E-06	0.79	10.13	4.00	29287.8
AHQ-8-5, 2374 - 2454	K.HIYYITGETK.D	1225.37490	2	8.65E-06	0.79	2.58	-	703.8
gi|4501993|ref|NP_003650.1|	alkylglycerone phosphate synthase precursor [Homo sapiens]			8.95E-06	0.54	10.16	2.60	72911.4
AHQ-8-6, 5555	R.GISDPLTVFEQTEAAAR.E	1805.96665	2	8.95E-06	0.54	2.76	-	353.1
gi|29788766|ref|NP_064424.2|	tubulin, beta polypeptide 4, member Q [Homo sapiens]			1.09E-05	1.24	20.16	3.50	48377.2
AHQ-8-13-, 3882	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	1.09E-05	0.63	2.84	-	489.8
AHQ-8-7, 4320	R.AVLVDLEPGTMDSVR.S	1602.83495	2	1.12E-04	0.61	2.94	-	360.4
gi|5729808|ref|NP_006557.1|	adhesion glycoprotein; platelet and T cell activation antigen 1; DNAX a			1.13E-05	0.95	10.20	6.00	38583.7
AHQ-8-6, 4824	K.IGTQQDSIAIFSPTHGMVIR.K	2172.49357	3	1.13E-05	0.95	4.03	-	1954.3
gi|4504351|ref|NP_000510.1|	delta globin [Homo sapiens]			1.16E-05	1.44	20.24	21.80	16055.4
AHQ-8-13-, 4734	R.FFESFGDLSSPDAVM*GNPK.V	2062.24491	2	1.16E-05	0.48	2.83	-	436.5
AHQ-8-13, 4885 - 4895	R.FFESFGDLSSPDAVM*GNPK.V	2062.24491	2	1.64E-04	0.87	3.77	-	637.0
AHQ-8-13-, 3204	K.VNVDAVGGEALGR.L	1257.37853	2	8.59E-04	0.96	4.88	-	1120.8
gi|4502695|ref|NP_001779.1|	cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c			1.20E-05	1.58	20.19	8.10	48786.6
AHQ-8-8, 3921	K.IYEFPETDDEEENKLVK.K	2099.23685	2	1.20E-05	0.72	3.21	-	293.5
AHQ-8-14-, 5174	K.NLEGYVGFANLPNQVYR.K	1955.16216	2	4.50E-04	0.86	3.83	-	693.8
gi|4505303|ref|NP_002466.1|	myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m			1.20E-05	1.21	20.20	11.50	22763.8
AHQ-8-12, 2791	R.ALGQNPTNAEVLK.V	1355.52211	1	1.20E-05	0.41	3.08	-	344.8
AHQ-8-12, 2904 - 2958	R.ALGQNPTNAEVLK.V	1355.52211	2	8.23E-05	0.84	3.31	-	732.6
AHQ-8-13-, 2850	R.ALGQNPTNAEVLK.V	1355.52211	2	9.41E-05	0.85	3.96	-	719.2
AHQ-8-14-, 2726	K.ILYSQCGDVM*R.A	1359.55429	2	1.71E-04	0.91	3.00	-	1325.7
AHQ-8-12, 2694 - 2730	K.ILYSQCGDVM*R.A	1359.55429	2	1.18E-04	0.80	2.94	-	667.0
gi|28269681|ref|NP_783313.1|	NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]			1.21E-05	1.56	20.19	29.80	14852.0
AHQ-8-13-, 4942 - 5019	K.AYSTTSIASVAGLTAAAYR.V	1875.07212	2	2.34E-05	0.75	2.85	-	685.1
AHQ-8-13-, 6100 - 6180	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	1.21E-05	0.81	3.80	-	819.9
gi|4758970|ref|NP_004150.1|	proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be			1.25E-05	1.82	20.19	9.20	29769.4
AHQ-8-11, 3325	R.ASAGSYISALR.V	1096.21876	2	1.09E-04	0.92	2.97	-	1273.7
AHQ-8-11, 2545	K.KGPGLYYVDEHGTR.L	1592.73690	3	1.25E-05	0.91	3.83	-	1203.8
gi|15306356|ref|XP_035638.2|	similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan			1.30E-05	0.45	10.14	8.70	18795.1
AHQ-8-12, 3451 - 3455	R.ESDVPLKTEEFEVTK.T	1751.91253	2	1.30E-05	0.45	2.75	-	321.2
gi|4507649|ref|NP_003280.1|	tropomyosin 2 (beta) [Homo sapiens]			1.30E-05	0.81	10.13	4.60	32989.6
AHQ-8-9, 6361	K.ATDAEADVASLNR.R	1333.38703	2	1.30E-05	0.81	2.50	-	1183.0
gi|4758606|ref|NP_004508.1|	integrin-linked kinase [Homo sapiens]			1.32E-05	7.54	100.21	23.90	51418.9
AHQ-8-7, 5250	K.FDMIVPILEK.M	1205.49168	2	3.01E-04	0.79	2.73	-	665.0
AHQ-8-7, 4292	K.FDM*IVPILEK.M	1221.49108	2	2.68E-05	0.68	2.67	-	563.7
AHQ-8-7, 3182	K.FSFQCPGR.M	1000.11283	1	2.71E-04	0.13	2.08	-	107.0
AHQ-8-7, 2229	R.GDDTPLHLAASHGHR.D	1584.67809	3	1.68E-05	0.86	3.24	-	1162.4
AHQ-8-7, 5528	R.GMAFLHTLEPLIPR.H	1595.93361	2	7.08E-05	0.93	3.85	-	1035.5
AHQ-8-7, 4888	R.GM*AFLHTLEPLIPR.H	1611.93301	2	2.16E-04	0.82	3.24	-	657.5
AHQ-8-7, 2418	K.LNENHSGELWK.G	1327.42732	2	3.06E-05	0.82	3.03	-	1018.2
AHQ-8-7, 5538	R.LWLDNTENDLNQGDDHGFSPLHWACR.E	3113.28217	3	2.53E-04	0.90	4.21	-	834.6
AHQ-8-7, 4482	R.MYAPAWVAPEALQK.K	1575.85602	2	9.51E-05	0.87	3.03	-	872.4
AHQ-8-7, 3888	R.SAVVEM*LIMR.G	1165.45256	2	1.32E-05	0.74	2.98	-	700.1
gi|11968045|ref|NP_071934.1|	hypothetical protein FLJ22056 [Homo sapiens]			1.38E-05	0.93	10.22	8.00	36010.3
AHQ-8-11, 6199 - 6201	K.DPTSLLGVLQAEADSTSEGLEDAVHSR.G	2798.95471	3	1.38E-05	0.93	4.48	-	1055.4
gi|20270259|ref|NP_620061.1|	phosphoglycerate kinase 2; phosphoglycerate kinase 1, pseudogene 2 [Ho			1.38E-05	0.53	10.17	3.60	44895.0
AHQ-8-8, 3618	K.LGDVYVNDAFGTAHR.A	1635.76178	2	1.38E-05	0.53	3.31	-	528.5
gi|4507949|ref|NP_003395.1|	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,			1.44E-05	2.34	30.17	18.30	28082.2
AHQ-8-10, 1955 - 1958	K.AVTEQGHELSNEER.N	1599.64147	2	1.86E-04	0.87	3.47	-	821.6
AHQ-8-10, 3884	K.QTTVSNSQQAYQEAFEISK.K	2160.28351	2	1.44E-05	0.65	2.83	-	551.0
AHQ-8-10, 2878	K.YLIPNATQPESK.V	1361.52512	2	1.60E-04	0.83	2.85	-	931.1
gi|28466991|ref|NP_775771.2|	tau-tubulin kinase [Homo sapiens]			1.44E-05	0.81	10.21	0.70	182465.3
AHQ-8-14-, 4895	K.LALDIKIATYR.K	1277.53762	2	1.44E-05	0.81	3.23	-	1231.7
AHQ-8-13, 5084 - 5092	K.LALDIKIATYR.K	1277.53762	2	2.97E-04	0.94	4.18	-	1695.9
gi|4506195|ref|NP_002785.1|	proteasome beta 2 subunit; proteasome subunit, beta type, 2; macropain			1.47E-05	0.70	10.18	8.50	22836.1
AHQ-8-11, 3636	K.MRNGYELSPTAAANFTR.R	1900.10841	3	1.47E-05	0.70	3.06	-	1254.1
gi|29727317|ref|XP_298144.1|	hypothetical protein XP_298144 [Homo sapiens]			1.52E-05	0.42	10.13	8.00	22108.6
AHQ-8-5, 5957	K.GEYNLTLDTALTSNLK.T	1753.93165	2	1.52E-05	0.42	2.62	-	688.9
gi|28373103|ref|NP_005164.2|	sarco/endoplasmic reticulum Ca2+ -ATPase isoform a; ATPase, Ca(2+)-tra			1.53E-05	0.81	10.14	1.50	109255.5
AHQ-8-1, 3747	R.VDQSILTGESVSVTK.H	1563.73208	2	1.53E-05	0.81	2.80	-	677.7
gi|30157216|ref|XP_292133.2|	similar to genethonin 1 [Homo sapiens]			1.58E-05	0.83	10.18	4.50	39693.8
AHQ-8-4, 4381	K.TITLEVKPSDTIENVK.A	1788.03268	2	3.74E-04	0.44	2.61	-	485.0
AHQ-8-13, 4444	K.TITLEVKPSDTIENVK.A	1788.03268	2	1.58E-05	0.83	3.64	-	768.8
AHQ-8-1, 4484	K.TITLEVKPSDTIENVK.A	1788.03268	2	8.64E-04	0.42	3.14	-	271.0
gi|4506363|ref|NP_002861.1|	RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s			1.63E-05	0.88	10.15	5.40	22774.0
AHQ-8-14-, 3767	K.LLLIGDSGVGK.T	1072.28025	2	1.63E-05	0.88	3.09	-	977.6
AHQ-8-13-, 3786	K.LLLIGDSGVGK.T	1072.28025	2	5.02E-04	0.65	2.89	-	669.3
gi|4557032|ref|NP_002291.1|	lactate dehydrogenase B [Homo sapiens]			1.64E-05	0.83	10.23	4.50	36638.3
AHQ-8-13-, 6166	K.SLADELALVDVLEDK.L	1630.81843	2	2.33E-04	0.96	4.69	-	1326.2
AHQ-8-13, 6215	K.SLADELALVDVLEDK.L	1630.81843	2	1.64E-05	0.83	3.30	-	897.7
gi|22749499|ref|NP_689979.1|	hypothetical protein MGC40107 [Homo sapiens]			1.66E-05	0.91	10.19	24.80	11741.6
AHQ-8-14-, 5371	R.LGALSGAAALGFASYGAHGAQFPDAYGK.E	2669.93152	3	1.66E-05	0.91	3.72	-	1410.3
gi|4758988|ref|NP_004152.1|	RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho			1.81E-05	1.61	20.21	17.10	22677.6
AHQ-8-14-, 5815 - 5837	K.EFADSLGIPFLETSAK.N	1725.91990	2	7.67E-05	0.67	3.42	-	379.7
AHQ-8-14-, 5561	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	1.81E-05	0.94	4.19	-	1126.3
AHQ-8-13-, 5556	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	3.70E-04	0.80	3.49	-	453.6
AHQ-8-11, 5264	R.FADDTYTESYISTIGVDFK.I	2173.31742	2	2.17E-04	0.89	3.65	-	824.6
gi|6679056|ref|NP_031387.1|	nidogen 2 (osteonidogen); nidogen 2 [Homo sapiens]			1.83E-05	0.49	10.14	1.20	151153.0
AHQ-8-2, 5064 - 5072	R.ITQTAEGLDPENYLSIK.T	1893.08421	2	1.83E-05	0.49	2.75	-	494.1
gi|4507951|ref|NP_003396.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept			1.84E-05	0.88	10.18	5.70	28218.5
AHQ-8-10, 2920 - 2975	K.AVTELNEPLSNEDR.N	1587.67060	2	1.84E-05	0.88	3.64	-	623.5
gi|15723376|ref|NP_277050.1|	MacGAP protein [Homo sapiens]			1.85E-05	1.67	20.15	4.00	70163.1
AHQ-8-5, 3312 - 3320	R.FLSQESGVAQTLK.K	1408.58178	2	1.85E-05	0.89	3.06	-	1312.9
AHQ-8-5, 4641	K.FYEGTFNWESVK.Q	1507.62723	2	4.46E-05	0.78	2.90	-	636.1
gi|5032009|ref|NP_005600.1|	glycogen phosphorylase; phosphorylase, glycogen, muscle; myophosphoryla			1.89E-05	0.81	10.13	1.00	97091.4
AHQ-8-5, 3894	R.VIFLENYR.V	1054.22348	2	1.89E-05	0.81	2.69	-	613.5
gi|27499681|ref|XP_045792.6|	similar to RIKEN cDNA G431004K08 [Homo sapiens]			1.91E-05	0.45	10.15	1.10	292883.2
AHQ-8-8, 6433 - 6438	R.EEFAIM*QTPAGELYDKSIIQSAQQDSIKK.A	3286.65552	3	1.91E-05	0.45	3.07	-	315.3
gi|5031597|ref|NP_005710.1|	actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub			1.91E-05	0.90	10.17	7.30	20546.5
AHQ-8-14-, 6099	K.DTDIVDEAIYYFK.A	1592.72721	2	2.49E-04	0.81	2.60	-	1006.2
AHQ-8-12, 5987	K.DTDIVDEAIYYFK.A	1592.72721	2	1.91E-05	0.90	3.24	-	856.3
gi|30154095|ref|XP_293967.2|	similar to gamma actin-like protein [Homo sapiens]			1.97E-05	0.87	20.16	12.80	19259.0
AHQ-8-8, 4561	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	6.69E-05	0.40	2.72	-	393.8
AHQ-8-8, 4693 - 4759	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.27E-04	0.67	3.21	-	450.9
AHQ-8-10, 4503	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	8.35E-04	0.62	3.00	-	534.3

AHQ-8-13, 4831	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.34E-04	0.16	2.57	-	286.0
AHQ-8-14-, 4626	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.97E-05	0.30	2.76	-	246.2
AHQ-8-8, 4501	R.KDLYTSTVLSGGTTMYPGIADR.M	2347.63041	2	9.24E-05	0.57	2.98	-	623.0
gi|25188179|ref|NP_005653.3|	voltage-dependent anion channel 3 [Homo sapiens]			2.04E-05	0.44	10.18	7.10	30658.4
AHQ-8-10, 4210	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	2.04E-05	0.44	2.64	-	350.9
AHQ-8-10, 4199 - 4211	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	3	3.29E-04	0.68	3.53	-	545.8
gi|4504391|ref|NP_000179.1|	hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]			2.05E-05	3.29	40.17	6.30	102502.4
AHQ-8-4, 4353	K.ATDCVGHDVVTLLR.D	1557.75406	2	2.05E-05	0.89	2.71	-	1136.4
AHQ-8-4, 2841	K.FLSQIESDR.L	1095.18763	2	1.55E-04	0.79	3.37	-	469.5
AHQ-8-4, 5339	K.GDFIALDLGGSSFR.I	1455.59700	2	3.00E-05	0.91	2.92	-	1524.8
AHQ-8-4, 5657	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	2.27E-05	0.70	3.03	-	500.4
gi|4758208|ref|NP_004081.1|	dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;			2.16E-05	0.96	10.22	7.60	20478.2
AHQ-8-11, 3940 - 3944	R.IYVGNASVAQDIPK.L	1475.67136	2	2.16E-05	0.96	4.32	-	1423.7
AHQ-8-11, 3687 - 3688	R.IYVGNASVAQDIPK.L	1475.67136	2	9.57E-04	0.95	4.12	-	1227.5
gi|29737976|ref|XP_290742.1|	similar to Phosphoribosylformylglycinamidine synthase (FGAM synthase)			2.17E-05	0.54	10.16	2.10	144733.3
AHQ-8-3, 6300	R.LGGTALAQCFSQLGEHPPDLDLPENLVR.A	3050.39201	3	2.17E-05	0.54	3.21	-	453.1
gi|17986273|ref|NP_524144.1|	fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2			2.17E-05	0.90	10.18	8.20	21145.0
AHQ-8-13-, 3378 - 3440	R.VFDKEGNGTVMGAELR.H	1723.93228	2	2.17E-05	0.90	3.54	-	1093.9
AHQ-8-12, 3260 - 3319	R.VFDKEGNGTVMGAELR.H	1723.93228	3	2.80E-05	0.80	3.43	-	1404.9
gi|4757996|ref|NP_004060.1|	adaptor-related protein complex 2, sigma 1 subunit isoform AP17; clathr			2.21E-05	0.92	10.19	10.60	17017.6
AHQ-8-13-, 5050	K.VYTVVDEM*FLAGEIR.E	1759.01650	2	2.21E-05	0.92	3.82	-	1348.8
gi|24497612|ref|NP_116262.2|	nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr			2.31E-05	1.68	20.20	5.70	72695.6
AHQ-8-6, 6040	K.LGCDWVATIFSR.D	1426.62208	2	2.31E-05	0.83	2.66	-	680.9
AHQ-8-6, 5087 - 5126	R.RPYEDQGLGETTPLTIICQPM*QPLR.V	2932.32204	3	2.45E-05	0.84	4.00	-	703.4
gi|4504743|ref|NP_002194.1|	integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o			2.34E-05	2.21	30.18	5.40	129294.4
AHQ-8-3, 3608	K.AGDISCNADINPLK.I	1489.63335	2	1.10E-04	0.87	3.53	-	835.7
AHQ-8-3, 6189 - 6265	R.STNINFYEISSDGNVPSIVHSFEDVGPK.F	3054.26956	3	2.34E-05	0.50	3.02	-	650.0
AHQ-8-3, 4801	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	2.10E-04	0.84	3.50	-	638.3
gi|29731857|ref|XP_293042.1|	similar to ribosomal protein S12; 40S ribosomal protein S12 [Homo sapi			2.53E-05	0.93	10.22	8.90	19543.6
AHQ-8-13-, 4462	K.LVEALCAEHQINLIK.V	1753.05645	2	2.53E-05	0.93	4.34	-	1129.8
gi|4557241|ref|NP_001095.1|	skeletal muscle specific actinin, alpha 3 [Homo sapiens]			2.56E-05	0.91	10.17	0.90	103293.7
AHQ-8-4, 3042	K.ALDFIASK.G	865.00867	1	1.33E-04	0.59	2.29	-	781.4
AHQ-8-4, 3034 - 3038	K.ALDFIASK.G	865.00867	2	2.56E-05	0.91	3.43	-	655.0
gi|4501841|ref|NP_001596.1|	alanyl-tRNA synthetase [Homo sapiens]			2.58E-05	0.61	10.13	1.30	106800.7
AHQ-8-4, 3146 - 3210	K.AVYTQDCPLAAAK.A	1409.58983	2	2.58E-05	0.61	2.63	-	679.0
gi|4505813|ref|NP_003737.1|	cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain			2.64E-05	0.82	10.15	12.40	10365.8
AHQ-8-14-, 2510	R.NFGSYVTHETK.H	1283.37131	2	2.64E-05	0.82	3.08	-	761.1
gi|4503377|ref|NP_001377.1|	dihydropyrimidinase-like 2; collapsin response mediator protein hCRMP-2			2.75E-05	1.04	20.16	7.30	62293.3
AHQ-8-6, 3979	R.GLYDGPVCEVSVTPK.T	1622.82128	2	3.69E-04	0.33	2.65	-	310.6
AHQ-8-7, 4849	R.ILDLGITGPEGHVLSRPEEVEAEAVNR.A	2902.20927	3	2.75E-05	0.71	3.26	-	417.6
gi|30149221|ref|XP_291446.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			3.12E-05	0.97	10.21	3.90	45688.5
AHQ-8-7, 2476	R.STAGDTHLGGEDFDNR.M	1692.68222	2	4.46E-04	0.80	3.28	-	627.6
AHQ-8-6, 2487	R.STAGDTHLGGEDFDNR.M	1692.68222	2	3.12E-05	0.97	4.15	-	2086.6
gi|6912638|ref|NP_036557.1|	ras suppressor protein 1 [Homo sapiens]			3.13E-05	0.90	10.18	6.10	31540.1
AHQ-8-10, 5360	R.LTVLPPELGNLDLTGQK.Q	1809.09672	3	3.13E-05	0.90	3.60	-	1127.1
gi|4557014|ref|NP_001743.1|	catalase [Homo sapiens]			3.18E-05	0.93	10.17	2.30	59755.8
AHQ-8-7, 4045	R.AFYVNVLNEEQR.K	1482.62245	2	3.18E-05	0.93	3.50	-	1190.9
gi|4759044|ref|NP_004841.1|	Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]			3.21E-05	1.85	20.21	2.10	160883.4
AHQ-8-3, 3098 - 3102	K.DATIASLEETNR.T	1320.38826	2	3.21E-05	0.92	3.25	-	1239.3
AHQ-8-3, 5580	K.ELQDQLEAEQYFSTLYK.T	2106.27421	2	1.19E-04	0.94	4.11	-	904.5
gi|5031985|ref|NP_005787.1|	nuclear transport factor 2; placental protein 15 [Homo sapiens]			3.24E-05	0.79	10.21	21.30	14478.4
AHQ-8-14-, 5213 - 5217	K.IQHSITAQDHQPTPDSCIISM*VVGQLK.A	3022.40358	3	3.24E-05	0.79	4.17	-	556.2
gi|4504077|ref|NP_000165.1|	glycoprotein IX (platelet) [Homo sapiens]			3.26E-05	3.25	40.19	30.50	19046.0
AHQ-8-12, 4054	R.ALETM*GLWVDCR.G	1468.68075	2	1.89E-04	0.86	3.00	-	839.0
AHQ-8-11, 3981 - 4037	R.ALETM*GLWVDCR.G	1468.68075	2	1.09E-04	0.91	3.37	-	1180.6
AHQ-8-14-, 2814 - 2831	R.CASPSLAAHGPLGR.L	1395.56962	2	4.28E-05	0.91	3.47	-	1112.2
AHQ-8-12, 3478	R.GHGLTALPALPAR.T	1274.49706	2	4.59E-05	0.94	3.69	-	1058.4
AHQ-8-11, 3459 - 3471	R.GHGLTALPALPAR.T	1274.49706	3	3.26E-05	0.88	3.65	-	876.9
AHQ-8-11, 3457	R.GHGLTALPALPAR.T	1274.49706	2	7.99E-05	0.93	3.71	-	815.4
AHQ-8-12, 5106	R.LWLEDRTPEALLQVR.C	1840.11574	2	3.10E-04	0.55	2.80	-	581.6
gi|4757768|ref|NP_004300.1|	Rho GDP dissociation inhibitor (GDI) alpha [Homo sapiens]			3.35E-05	1.39	20.18	8.30	23206.9
AHQ-8-10, 3682	K.SIQEIQELDKDDESLR.K	1919.03693	2	3.35E-05	0.54	2.69	-	579.9
AHQ-8-10, 3362 - 3364	K.SIQEIQELDKDDESLRK.Y	2047.20984	3	3.54E-05	0.85	3.67	-	1108.2
AHQ-8-10, 3356 - 3367	K.SIQEIQELDKDDESLRK.Y	2047.20984	2	3.77E-04	0.79	3.04	-	753.1
gi|4504973|ref|NP_002292.1|	lactate dehydrogenase C [Homo sapiens]			3.40E-05	0.73	10.14	3.60	36311.0
AHQ-8-10, 2463	R.VIGSGCNLDSAR.F	1250.36445	2	3.40E-05	0.73	2.70	-	534.5
gi|23503239|ref|NP_699160.1|	hypothetical protein MGC10204 [Homo sapiens]			3.72E-05	0.86	10.18	2.00	85113.0
AHQ-8-5, 4068	R.AWDQEAEGAGPELGLR.V	1699.80263	2	3.72E-05	0.86	3.45	-	1056.9
gi|4507149|ref|NP_000445.1|	superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult			3.76E-05	1.11	20.22	15.60	15935.7
AHQ-8-12, 4228	K.GDGPVQGIINFEQK.E	1502.65366	2	3.76E-05	0.65	2.95	-	381.6
AHQ-8-12, 3936	R.LACGVIGIAQ	1003.19807	1	7.90E-04	0.46	2.61	-	575.6
gi|17999541|ref|NP_060676.2|	vacuolar protein sorting 35; maternal-embryonic 3 [Homo sapiens]			3.80E-05	1.68	20.18	3.60	91706.5
AHQ-8-5, 5574	K.IPVDTYNNILTVLK.L	1603.88418	2	3.80E-05	0.91	3.56	-	931.1
AHQ-8-5, 4012	R.SEDPDQQYLILNTAR.K	1763.88663	2	5.66E-04	0.77	2.95	-	941.9
gi|21624607|ref|NP_066972.1|	coactosin-like 1 [Homo sapiens]			3.82E-05	1.83	20.22	19.70	15944.9
AHQ-8-13-, 5002	R.DDGSAVIWVTFK.Y	1338.49001	2	6.18E-05	0.88	3.63	-	749.3
AHQ-8-13-, 6255	K.FALITWIGENVSGLQR.A	1805.06986	2	3.82E-05	0.96	4.39	-	1548.3
gi|6857820|ref|NP_005019.2|	phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl			4.07E-05	1.82	20.23	7.60	46224.3
AHQ-8-7, 4061 - 4122	R.FGIDDQDFQNSLTR.S	1656.73462	2	1.20E-04	0.23	2.78	-	212.2
AHQ-8-7, 4321	R.FGIDDQDFQNSLTR.S	1656.73462	2	4.07E-05	0.86	3.69	-	840.6
AHQ-8-7, 2806 - 2828	K.HGAGAEISTVNPEQYSK.R	1788.89618	2	1.07E-04	0.96	4.69	-	1144.3
gi|4504045|ref|NP_002063.1|	guanine nucleotide binding protein (G protein), q polypeptide [Homo sap			4.08E-05	0.80	10.16	4.20	42142.8
AHQ-8-8, 4061	R.VADPAYLPTQQDVLR.V	1686.89014	2	4.08E-05	0.80	3.20	-	493.0
gi|22060072|ref|XP_088293.2|	similar to cytochrome c [Homo sapiens]			4.20E-05	0.93	10.15	10.50	11887.8
AHQ-8-13-, 3690	K.TGPNLHGLFGR.K	1169.31780	2	4.20E-05	0.93	3.04	-	1235.3
gi|6041669|ref|NP_004538.2|	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd			4.21E-05	0.87	10.18	14.00	15208.5
AHQ-8-13-, 4618	R.TLPETLDPAEYNISPETR.R	2047.20831	2	4.21E-05	0.87	3.60	-	506.6
AHQ-8-13, 4780	R.TLPETLDPAEYNISPETR.R	2047.20831	2	1.89E-04	0.46	2.65	-	323.0
gi|4506713|ref|NP_002945.1|	ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte			4.21E-05	0.68	10.18	0.00	17964.8
AHQ-8-14-, 4229 - 4286	K.TITLEVEPSDTIENVK.A	1788.97431	2	4.21E-05	0.68	3.56	-	511.6
gi|4507789|ref|NP_003338.1|	ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]			4.56E-05	0.67	10.15	0.00	17861.5
AHQ-8-12, 4958 - 4959	R.IEINFPAEYPFKPPK.I	1791.08155	2	4.56E-05	0.67	3.06	-	576.9
gi|30149555|ref|XP_301154.1|	similar to heat shock protein 86 [Homo sapiens]			4.66E-05	0.92	10.21	10.60	15781.6
AHQ-8-5, 5605	K.HSQFIGYPITLFVEK.E	1780.05877	3	4.66E-05	0.92	4.25	-	1127.4
gi|14765644|ref|XP_037574.1|	similar to PTPL1-associated RhoGAP 1 [Homo sapiens]			4.73E-05	0.80	10.19	2.90	124613.7
AHQ-8-6, 6394	R.SPLTAASPGELPTEGAGPDVVEDISHLLADVAR.F	3286.59214	3	4.73E-05	0.80	3.88	-	297.2
gi|10835121|ref|NP_000289.1|	pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H			4.80E-05	0.88	10.16	1.90	61829.8
AHQ-8-7, 3553	R.GDLGIEIPAEK.V	1142.28420	2	4.80E-05	0.88	3.16	-	874.8
gi|4757766|ref|NP_004299.1|	Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa			4.81E-05	0.87	10.22	4.60	50435.4
AHQ-8-7, 5644	R.VPATLQVLQTLPEENYQVLR.F	2312.65053	2	4.81E-05	0.87	4.36	-	533.3
gi|7657649|ref|NP_055362.1|	tropomodulin 3 (ubiquitous) [Homo sapiens]			4.92E-05	0.65	10.13	3.10	39594.5
AHQ-8-11, 3288	K.FGYQFTQQGPR.T	1329.44490	2	4.92E-05	0.65	2.63	-	546.1
gi|5803121|ref|NP_006801.1|	for protein disulfide isomerase-related [Homo sapiens]			4.94E-05	0.65	10.14	2.30	59594.0
AHQ-8-7, 2826	K.DVVHLDSEKDFR.R	1460.57364	2	4.94E-05	0.65	2.64	-	818.3
gi|19923483|ref|NP_057406.2|	GTPase Rab14 [Homo sapiens]			4.95E-05	2.14	30.21	19.50	23896.8
AHQ-8-11, 3712	R.GAAGALM*VYDITR.R	1354.55759	2	4.95E-05	0.94	3.79	-	1238.0
AHQ-8-11, 4775 - 4777	R.NLTNPNTVIILIGNK.A	1624.90662	2	6.38E-05	0.32	2.62	-	240.7

AHQ-8-14-, 4474 - 4551	K.TGENVEDAFLEAAK.K	1494.58517	2	4.10E-04	0.59	2.53	-	608.5
AHQ-8-11, 4344 - 4405	K.TGENVEDAFLEAAK.K	1494.58517	2	9.42E-05	0.88	4.12	-	565.7
gi|4502923|ref|NP_001830.1|	calponin 3; calponin, acidic [Homo sapiens]			5.32E-05	0.82	10.13	3.30	36413.4
AHQ-8-12, 2751	K.GPSYGLSAEVK.N	1108.22631	2	5.32E-05	0.82	2.59	-	763.0
gi|8923812|ref|NP_060943.1|	uncharacterized hypothalamus protein HT012 [Homo sapiens]			5.61E-05	0.94	10.19	8.60	14960.4
AHQ-8-13, 4219 - 4220	K.TLAFTSVDLTNK.A	1310.47811	2	5.61E-05	0.94	3.84	-	1024.9
gi|4502297|ref|NP_001678.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit			5.87E-05	0.75	10.14	8.30	17489.8
AHQ-8-13-, 2616	K.AQAELVGTADEATR.A	1432.51860	2	5.87E-05	0.75	2.78	-	605.8
gi|4507157|ref|NP_003096.1|	sortilin-related receptor containing LDLR class A repeats preproprotein			5.91E-05	0.40	10.16	0.80	248439.0
AHQ-8-13-, 6124	K.NNTCVKEENTCLRNQYR.C	2202.37174	2	5.91E-05	0.40	3.11	-	443.2
gi|4504489|ref|NP_000403.1|	histidine-rich glycoprotein precursor; histidine-proline rich glycoprot			5.95E-05	0.65	10.13	2.70	59578.0
AHQ-8-5, 6101	K.DSPVLIDFFEDTER.Y	1683.79674	2	5.95E-05	0.65	2.57	-	550.8
gi|16753212|ref|NP_003921.2|	src family associated phosphoprotein 2; src kinase-associated phosphop			5.97E-05	0.80	10.16	2.80	41216.5
AHQ-8-7, 4057	K.DAEEWVQQLK.F	1246.35097	2	5.97E-05	0.80	3.16	-	814.5
gi|5174393|ref|NP_006001.1|	arginine-rich, mutated in early stage tumors; arginine-rich protein [Ho			6.20E-05	0.84	10.19	7.30	26906.2
AHQ-8-12, 5260 - 5266	K.DRDVTFSPATIENELIK.F	1949.15100	2	6.20E-05	0.84	3.81	-	697.5
gi|21361456|ref|NP_055425.2|	alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph			6.22E-05	1.52	20.16	3.30	109437.2
AHQ-8-4, 2969	R.GLLEFEHQR.A	1129.25045	2	6.90E-05	0.75	2.79	-	899.3
AHQ-8-4, 5689	R.QYASLTGTQALPPLFSLGYHQSR.W	2536.82664	3	6.22E-05	0.77	3.07	-	769.6
gi|4507383|ref|NP_001052.1|	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil			6.22E-05	1.85	20.18	4.70	60675.3
AHQ-8-7, 5493	R.DFLQM*VLDAR.H	1224.41192	2	6.22E-05	0.94	3.66	-	1566.5
AHQ-8-7, 3938	R.HSASPMGVQDFDIVR.D	1659.84828	2	4.66E-04	0.91	3.07	-	1200.8
gi|4557890|ref|NP_000415.1|	keratin 5; Keratin-5; 58 kda cytokeratin; keratin, type II cytoskeletal			6.28E-05	0.89	10.16	1.70	62461.1
AHQ-8-2, 3517	K.LAELEEALQK.A	1144.30010	2	6.28E-05	0.89	3.21	-	1204.9
gi|4507947|ref|NP_003671.1|	tyrosyl-tRNA synthetase; tyrosyl-tRNA synthetase; tyrosyl tRNA ligase [			6.34E-05	0.84	10.17	2.30	59143.1
AHQ-8-7, 4818	R.TVVSGLVQFVPK.E	1274.53374	2	6.34E-05	0.84	3.44	-	678.0
gi|4506405|ref|NP_002872.1|	v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP			6.52E-05	0.82	10.14	7.80	23408.4
AHQ-8-10, 3574	R.SKAEEWGVQYVETSAK.T	1812.95765	2	6.52E-05	0.82	2.75	-	999.3
gi|4557801|ref|NP_000261.1|	purine nucleoside phosphorylase [Homo sapiens]			6.57E-05	0.86	10.18	6.20	32147.7
AHQ-8-13, 4273	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	6.57E-05	0.86	3.54	-	625.5
gi|4506189|ref|NP_002783.1|	proteasome alpha 7 subunit isoform 1; proteasome subunit RC6-1; proteas			6.58E-05	1.53	20.15	10.50	27886.7
AHQ-8-10, 3040	K.ALLEVVQSGGK.N	1101.27845	2	6.58E-05	0.69	2.57	-	636.9
AHQ-8-10, 3887	K.NYTDEAIETDDLTIK.L	1741.83137	2	5.37E-04	0.84	3.02	-	771.9
gi|4505395|ref|NP_002499.1|	nidogen (enactin); Nidogen; nidogen (entactin) [Homo sapiens]			6.64E-05	0.72	10.15	1.80	136488.3
AHQ-8-2, 4576	R.SDIDAVYVTTNGIIATSEPPAK.E	2263.48678	2	6.64E-05	0.72	3.01	-	592.5
gi|22748811|ref|NP_689590.1|	hypothetical protein MGC34837 [Homo sapiens]			6.88E-05	0.52	10.16	4.90	62034.3
AHQ-8-3, 4925	R.GSPEMVNYEKLLWFLNSAASDYPQQNK.A	3131.46380	3	6.88E-05	0.52	3.19	-	567.2
gi|8923579|ref|NP_060377.1|	hypothetical protein FLJ20625 [Homo sapiens]			7.09E-05	0.78	10.16	18.60	17744.7
AHQ-8-14-, 5913	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	7.09E-05	0.78	3.12	-	699.7
gi|16904381|ref|NP_006717.1|	LPS-responsive vesicle trafficking, beach and anchor containing; vesic			7.77E-05	0.51	10.17	0.50	319158.3
AHQ-8-4, 5982	R.IEPFTTYFLNLQGGK.F	1728.96862	2	7.77E-05	0.51	3.01	-	273.0
gi|6912324|ref|NP_036266.1|	leiomodin 1 (smooth muscle); thyroid and eye muscle autoantigen D1 (64k			7.83E-05	0.30	10.14	3.00	63737.1
AHQ-8-14-, 4979	K.GEKKDLLEVPKAGAVAK.G	1754.06430	2	7.83E-05	0.30	2.74	-	423.2
gi|5803013|ref|NP_006808.1|	endoplasmic reticulum protein 29 precursor; endoplasmic reticulum lumen			8.47E-05	0.77	10.15	5.70	28993.2
AHQ-8-10, 3095	K.ILDQGEDFPASEM*TR.I	1725.85864	2	8.47E-05	0.77	2.92	-	473.7
gi|27480842|ref|XP_208238.1|	similar to bA92K2.2 (similar to ubiquitin) [Homo sapiens]			8.71E-05	0.77	10.15	8.30	17966.9
AHQ-8-14-, 2018 - 2086	K.IQDKEGIPPDQQR.L	1524.66087	2	8.71E-05	0.77	2.82	-	528.1
gi|5453710|ref|NP_006139.1|	LIM and SH3 protein 1; Lasp-1 [Homo sapiens]			9.48E-05	0.47	10.16	5.00	29717.0
AHQ-8-13-, 3911	K.GFSVVADTPELQR.I	1419.56466	2	9.48E-05	0.47	2.94	-	409.1
AHQ-8-13, 4064	K.GFSVVADTPELQR.I	1419.56466	2	4.32E-04	0.77	3.20	-	685.9
gi|30152949|ref|XP_301425.1|	similar to Heat shock protein HSP 90-beta (HSP 84) (HSP 90) [Homo sapi			9.62E-05	0.62	10.13	2.50	42437.9
AHQ-8-5, 2297 - 2378	K.YINQEELNK.I	1151.25119	2	9.62E-05	0.62	2.62	-	467.0
gi|6005745|ref|NP_009165.1|	dynactin 3 isoform 1; dynactin light chain [Homo sapiens]			9.78E-05	0.86	10.14	5.90	21119.3
AHQ-8-11, 2932	K.VQVALGNISSK.R	1116.29312	2	9.78E-05	0.86	2.85	-	910.8
gi|17475428|ref|XP_062849.1|	similar to Proteasome subunit alpha type 6 (Proteasome iota chain) (Ma			9.96E-05	0.91	10.18	4.80	30918.3
AHQ-8-10, 2910 - 2915	K.AINQGGLTSVAVR.K	1286.46301	2	9.96E-05	0.91	3.68	-	1155.6
gi|18201911|ref|NP_000629.2|	vitronectin precursor; serum spreading factor; somatomedin B; compleme			1.01E-04	1.40	20.16	6.30	54335.4
AHQ-8-6, 5791 - 5852	R.DVWGIEGPIDAAFTR.I	1647.81246	2	1.29E-04	0.61	2.53	-	474.5
AHQ-8-14-, 5321 - 5382	R.SIAQYWLGCPAPGHL	1671.90045	2	1.01E-04	0.79	3.19	-	550.6
gi|30155257|ref|XP_299313.2|	hypothetical protein XP_299313 [Homo sapiens]			1.03E-04	0.18	10.14	9.00	20734.9
AHQ-8-8, 6506 - 6573	R.GGKCRQFTAASESDELK.L	1886.03346	2	1.03E-04	0.18	2.52	-	364.8
gi|13435359|ref|NP_001914.2|	damage-specific DNA binding protein 1; damage-specific DNA binding pro			1.09E-04	0.92	10.21	2.60	126987.0
AHQ-8-4, 3746	R.IEVQDTSGGTTALRPSASTQALSSSVSSSK.L	2954.15138	3	1.09E-04	0.92	4.28	-	1411.4
gi|4501865|ref|NP_001087.1|	ATP citrate lyase [Homo sapiens]			1.16E-04	0.45	10.14	1.40	121419.0
AHQ-8-4, 3202	R.TTDGVYEGVAIGGDR.Y	1510.58783	2	1.16E-04	0.45	2.77	-	406.5
gi|4502687|ref|NP_003865.1|	CD84 antigen (leukocyte antigen); leukocyte antigen CD84 [Homo sapiens]			1.16E-04	0.65	10.15	4.30	36870.6
AHQ-8-7, 2485	K.ADINTQADPYTTTK.R	1539.62594	2	1.16E-04	0.65	2.90	-	458.7
gi|9966867|ref|NP_065123.1|	eIF-5A2 protein; eIF5AII [Homo sapiens]			1.16E-04	0.90	10.16	7.80	16793.1
AHQ-8-12, 4631 - 4638	K.VHLVGIDIFTGK.K	1299.54329	2	1.16E-04	0.90	3.26	-	1091.2
gi|24307939|ref|NP_036205.1|	chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]			1.20E-04	0.86	10.18	3.00	59670.7
AHQ-8-7, 6032	K.LGFAGLVQEISFGTTK.D	1668.91472	2	1.20E-04	0.86	3.60	-	803.6
gi|30152584|ref|XP_305800.1|	hypothetical protein XP_305800 [Homo sapiens]			1.23E-04	0.56	10.17	8.70	24751.1
AHQ-8-2, 5391	K.MGKSSLSTPLSMLVM*AWNLR.A	2239.71147	2	1.23E-04	0.56	3.33	-	594.6
AHQ-8-1, 5404	K.MGKSSLSTPLSMLVM*AWNLR.A	2239.71147	2	4.06E-04	0.63	3.47	-	699.2
gi|4557797|ref|NP_000260.1|	non-metastatic cells 1 protein [Homo sapiens]			1.29E-04	0.82	10.15	7.90	17148.6
AHQ-8-12, 3063	R.TFIAIKPDGVQR.G	1345.57205	2	1.29E-04	0.82	2.97	-	744.8
gi|29740132|ref|XP_299177.1|	hypothetical protein XP_299177 [Homo sapiens]			1.32E-04	0.46	10.16	2.70	114488.9
AHQ-8-3, 4944	R.RCHEEKLPLSAGTASHKGQASAQPITPR.Q	3030.36879	3	1.32E-04	0.46	3.17	-	243.9
gi|5453629|ref|NP_006391.1|	dynactin 2; dynactin complex 50 kD subunit; dynamitin; 50 kD dynein-ass			1.33E-04	0.91	10.20	4.70	44819.3
AHQ-8-8, 5017	K.LLGPDAAINLTDPDGALAK.R	1866.10514	2	1.33E-04	0.91	3.97	-	807.9
gi|4759342|ref|NP_004808.1|	tight junction protein 2 (zona occludens 2); Friedreich ataxia region g			1.34E-04	0.88	10.14	1.10	124661.6
AHQ-8-4, 6053	R.EDAVLYLLEIPK.G	1403.64505	2	1.34E-04	0.88	2.65	-	1470.1
gi|4557251|ref|NP_001101.1|	a disintegrin and metalloprotease domain 10 [Homo sapiens]			1.35E-04	0.94	10.20	2.00	84141.7
AHQ-8-5, 4530	K.AIDTIYQTTDFSGIR.N	1701.85844	2	1.35E-04	0.94	4.04	-	976.2
gi|24307907|ref|NP_006207.1|	plasminogen activator inhibitor type 1, member 2; protease inhibitor 7			1.46E-04	0.39	10.13	3.50	44002.0
AHQ-8-8, 3285	K.FTAVAQTDLKEPLK.V	1561.80416	2	1.46E-04	0.39	2.57	-	436.5
gi|7706497|ref|NP_057392.1|	UMP-CMP kinase [Homo sapiens]			1.50E-04	0.93	10.18	5.70	25854.7
AHQ-8-11, 3729 - 3795	K.YGYTHLSAGELLR.D	1480.64969	2	1.50E-04	0.93	3.51	-	1154.2
gi|20070158|ref|NP_003567.2|	serine/threonine kinase 24 (STE20 homolog, yeast); STE20-like kinase 3			1.58E-04	0.89	10.17	3.40	49307.6
AHQ-8-7, 3716	K.SQACGGNLGSIEELR.G	1592.71366	2	1.58E-04	0.89	3.33	-	1112.8
gi|27499572|ref|XP_058577.2|	similar to chromosome 11 open reading frame 25 [Homo sapiens]			1.61E-04	0.48	10.16	2.30	107611.6
AHQ-8-14-, 5898 - 5974	K.ETFFNNATRSRIVHHILQRIK.Y	2581.96338	3	1.61E-04	0.48	3.20	-	310.6
gi|4503971|ref|NP_001484.1|	GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r			1.61E-04	0.59	10.19	3.40	50582.4
AHQ-8-7, 4032 - 4069	R.TDDYLDQPCLETVNR.I	1840.94632	2	1.61E-04	0.59	3.05	-	299.6
gi|30158852|ref|XP_301583.1|	similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa			1.62E-04	0.57	10.14	0.00	19197.0
AHQ-8-4, 3211	K.IWHHTFYNKLR.V	1515.74533	2	1.62E-04	0.57	2.73	-	644.2
gi|5031595|ref|NP_005709.1|	actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub			1.68E-04	0.79	10.16	6.50	19666.9
AHQ-8-12, 3191 - 3240	K.VLIEGSINSVR.V	1187.37134	2	1.68E-04	0.79	3.15	-	714.4
gi|4503359|ref|NP_003965.1|	docking protein 2, 56kD [Homo sapiens]			1.69E-04	0.62	10.15	3.60	45547.8
AHQ-8-7, 3957	R.GQEGEYAVPFDAVAR.S	1609.72109	2	1.69E-04	0.62	3.02	-	403.7
gi|8922712|ref|NP_060713.1|	hypothetical protein FLJ10849 [Homo sapiens]			1.72E-04	2.67	30.19	11.00	49397.9
AHQ-8-7, 2598	K.AAAQLLQSQAQQSGAQQTK.K	1958.12276	2	4.55E-04	0.86	3.25	-	990.1
AHQ-8-7, 3502	K.DTDPDSKPFSLQETYEAK.R	2072.17149	3	7.05E-04	0.89	3.80	-	879.5
AHQ-8-7, 2424	R.SYELQESNVR.L	1225.29016	2	1.72E-04	0.92	2.88	-	1365.7
gi|30153852|ref|XP_171113.3|	similar to Moesin (Membrane-organizing extension spike protein) [Homo			1.72E-04	0.89	10.18	9.30	15601.7
AHQ-8-6, 2111	R.RKPDTIEVQQMK.A	1473.72364	2	1.72E-04	0.89	3.53	-	948.0
gi|18104998|ref|NP_001119.2|	adaptor-related protein complex 1, gamma 1 subunit; gamma adaptin; cla			1.73E-04	0.81	10.20	3.30	91679.3

AHQ-8-13-, 6262	K.TFQLQLLSPSSSIVPAFNTGTITQVIK.V	2892.33903	3	1.73E-04	0.81	4.03	-	901.7
gi|4506675|ref|NP_002941.1|	ribophorin I [Homo sapiens]			1.76E-04	0.79	10.17	3.60	68569.0
AHQ-8-6, 5119	R.APDELHYTYLDTFGRPVIVAYK.K	2569.89500	3	1.76E-04	0.79	3.37	-	711.7
gi|4503743|ref|NP_002009.1|	flightless I homolog [Homo sapiens]			1.77E-04	0.86	10.19	1.30	144750.1
AHQ-8-4, 6121 - 6185	K.VGLGLGYLELPQINYK.L	1778.08432	2	1.77E-04	0.86	3.72	-	682.5
gi|22059949|ref|XP_114617.2|	similar to tubulin, beta 5 [Homo sapiens]			1.78E-04	1.85	20.25	13.00	22810.8
AHQ-8-7, 4977	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	2.49E-04	0.94	4.95	-	1355.1
AHQ-8-7, 2696 - 2764	R.ISVYYNEATGGK.Y	1302.41453	2	1.78E-04	0.91	3.74	-	779.7
gi|30158844|ref|XP_292513.2|	similar to KIAA1879 protein [Homo sapiens]			1.81E-04	0.94	10.19	0.70	203894.8
AHQ-8-7, 3990	K.TSIAIDTIINQK.H	1317.51378	2	1.81E-04	0.94	3.86	-	1423.3
gi|28461290|ref|NP_443728.2|	TRALPUSH; no opposite paired repeat protein [Homo sapiens]			1.82E-04	0.26	10.14	0.40	240073.5
AHQ-8-7, 3465	K.KKPQVNAK.D	913.09970	1	1.82E-04	0.26	2.37	-	328.9
AHQ-8-6, 3515	K.KKPQVNAK.D	913.09970	1	2.74E-04	0.67	2.72	-	562.9
gi|14249348|ref|NP_116120.1|	hypothetical protein MGC14353 [Homo sapiens]			1.87E-04	0.91	10.18	11.40	13940.7
AHQ-8-13, 4163 - 4168	K.SWCPDCVQAEPVVR.E	1705.89366	2	1.87E-04	0.91	3.59	-	850.8
gi|4758618|ref|NP_004684.1|	cytokeratin type II [Homo sapiens]			2.01E-04	0.98	10.26	2.20	59503.9
AHQ-8-2, 3107	R.FLEQQNKVLETK.W	1477.68725	2	2.01E-04	0.98	5.10	-	2251.7
gi|4508047|ref|NP_003452.1|	zyxin [Homo sapiens]			2.03E-04	0.78	10.19	4.40	61277.0
AHQ-8-8, 3839	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	6.09E-04	0.70	3.51	-	505.8
AHQ-8-5, 3889	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	2.03E-04	0.78	3.85	-	604.9
gi|21361553|ref|NP_003168.2|	spleen tyrosine kinase [Homo sapiens]			2.15E-04	1.33	20.17	5.70	72065.7
AHQ-8-6, 5370	K.QTWNLQGQALEQAIISQKPQLEK.L	2652.98708	3	4.84E-04	0.76	3.31	-	854.0
AHQ-8-6, 4440 - 4484	K.TGPFEDLKENLIR.E	1532.72291	2	2.15E-04	0.57	2.93	-	573.1
gi|13775186|ref|NP_112567.1|	ring finger protein 17 isoform long [Homo sapiens]			2.20E-04	0.81	10.16	1.70	73736.0
AHQ-8-10, 4964 - 5038	K.TADQLTTGLER.S	1205.30039	2	2.20E-04	0.81	3.27	-	1052.9
gi|30150883|ref|XP_305873.1|	hypothetical protein XP_305873 [Homo sapiens]			2.21E-04	0.43	10.16	5.40	41521.9
AHQ-8-13-, 3368	K.AGFACSVTHFIKSQMRWTRK.N	2413.80980	3	2.21E-04	0.43	3.26	-	229.6
gi|21536449|ref|NP_002613.2|	prefoldin 1; prefoldin subunit 1 [Homo sapiens]			2.24E-04	0.94	10.20	9.00	14210.4
AHQ-8-13-, 3770 - 3782	K.LADIQIEQLNR.T	1313.48523	2	2.24E-04	0.94	4.02	-	1583.3
AHQ-8-13, 3915	K.LADIQIEQLNR.T	1313.48523	2	8.14E-04	0.92	3.10	-	1436.8
gi|20127528|ref|NP_037459.2|	parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]			2.27E-04	0.88	10.19	3.30	41714.0
AHQ-8-14-, 3533	K.ARPEDVVNLDLK.S	1369.54878	2	2.27E-04	0.88	3.83	-	695.4
gi|25306267|ref|NP_001700.2|	brain-derived neurotrophic factor isoform a preproprotein [Homo sapien			2.36E-04	1.70	20.24	14.20	27817.8
AHQ-8-13-, 5519	R.RGELSVCDSISEWVTAADKK.T	2253.47527	3	2.36E-04	0.96	4.86	-	1574.4
AHQ-8-13-, 3642 - 3644	K.TAVDMSGGTVTVLEK.V	1508.71993	2	5.35E-04	0.74	3.17	-	750.3
gi|17448269|ref|XP_069750.1|	similar to GDP dissociation inhibitor isoform 2; GDI-2 [Homo sapiens]			2.48E-04	0.90	10.17	4.20	32024.9
AHQ-8-8, 4106	K.DLGTESQIFISR.A	1366.50176	2	2.48E-04	0.90	3.41	-	1353.1
gi|4557773|ref|NP_000248.1|	myosin, heavy polypeptide 7, cardiac muscle, beta [Homo sapiens]			2.49E-04	1.46	20.17	1.20	223110.8
AHQ-8-4, 3177	R.CNGVLEGIR.I	1019.15759	2	7.12E-04	0.91	3.24	-	874.0
AHQ-8-2, 4061	R.IEELEEELESERTAR.A	1833.93203	2	2.49E-04	0.54	3.26	-	642.0
gi|5453549|ref|NP_006397.1|	thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho			2.52E-04	0.79	10.20	5.20	30539.7
AHQ-8-10, 3588 - 3595	K.DYGVYLEDSGHTLR.G	1625.72052	2	2.52E-04	0.79	2.76	-	766.3
gi|12545410|ref|NP_031394.1|	RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,			2.65E-04	1.53	20.17	5.00	95912.5
AHQ-8-5, 4860	R.APSDSAPGCSPCTGGLPANIQLDIDGDRETER.I	3360.54658	3	2.82E-04	0.60	3.26	-	270.8
AHQ-8-5, 4650	K.FGDEFLGELR.I	1183.29488	2	2.65E-04	0.93	3.44	-	1155.7
gi|4758638|ref|NP_004896.1|	peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi			2.67E-04	0.83	20.14	10.30	25034.8
AHQ-8-10, 2547 - 2587	K.DINAYNCEEPTEK.L	1584.64363	2	4.66E-04	0.70	2.72	-	609.4
AHQ-8-10, 3182	R.VVFVFGPDKK.L	1136.36763	1	2.67E-04	0.13	2.04	-	383.3
gi|7669501|ref|NP_005552.2|	lysosomal-associated membrane protein 1 [Homo sapiens]			2.85E-04	0.87	10.21	3.80	44772.8
AHQ-8-4, 6393	R.FFLQGIQLNTILPDAR.D	1847.14988	2	2.85E-04	0.87	4.13	-	532.7
gi|24308149|ref|NP_060035.1|	hypothetical protein DKFZp434F2322 [Homo sapiens]			2.85E-04	0.73	10.14	2.00	61404.2
AHQ-8-4, 5619 - 5653	K.PSGVHLKLVLR.F	1219.50454	2	2.85E-04	0.73	2.83	-	703.9
gi|29733950|ref|XP_293814.1|	similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK			2.90E-04	0.54	10.13	2.00	49024.0
AHQ-8-13, 2187 - 2252	R.AQYDELAQK.N	1066.14629	2	2.90E-04	0.54	2.63	-	457.2
gi|14589893|ref|NP_001785.2|	cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-			2.93E-04	0.28	10.15	2.00	100279.9
AHQ-8-8, 4493	K.VENPIDLYIYVIDM*NDNR.P	2213.45293	2	2.93E-04	0.28	2.92	-	373.3
gi|22267436|ref|NP_056284.1|	DKFZp564D177 protein [Homo sapiens]			3.08E-04	0.86	10.16	5.70	28466.4
AHQ-8-11, 3737 - 3740	K.LVGVFHTEYGALNR.V	1576.78061	2	3.08E-04	0.86	3.28	-	700.1
gi|22095371|ref|NP_079434.2|	RUN and FYVE domain-containing 1 [Homo sapiens]			3.09E-04	0.64	10.14	2.00	69077.6
AHQ-8-6, 3159	R.ICSLQEEQQQLR.E	1533.68936	2	3.09E-04	0.64	2.87	-	734.9
gi|4502261|ref|NP_000479.1|	serine (or cysteine) proteinase inhibitor, clade C (antithrombin), memb			3.18E-04	0.73	10.14	3.40	52602.1
AHQ-8-7, 5782	K.EQLQDMGLVDLFSPEK.S	1850.08284	2	3.18E-04	0.73	2.71	-	612.0
gi|4502989|ref|NP_001856.1|	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor; hepa			3.31E-04	0.80	10.15	15.70	9395.9
AHQ-8-14, 5846	K.LFQEDDEIPLYLK.G	1623.82758	2	3.31E-04	0.80	3.09	-	895.7
gi|28827809|ref|NP_789797.1|	nucleoside diphosphate kinase B-like [Homo sapiens]			3.40E-04	0.62	10.15	7.30	15529.0
AHQ-8-12, 3844	K.DRPFFPGLVK.Y	1176.39185	2	3.40E-04	0.62	2.52	-	676.1
gi|18087855|ref|NP_542408.1|	dynein light chain 2 [Homo sapiens]			3.61E-04	1.38	20.13	13.50	10349.8
AHQ-8-14-, 3165	K.DIAAYIK.K	793.93045	1	3.61E-04	0.61	2.17	-	627.3
AHQ-8-14, 5657	K.YNIEKDIAAYIK.K	1441.65337	2	6.75E-04	0.78	2.52	-	892.3
gi|13128974|ref|NP_076933.1|	hypothetical protein MGC3265 [Homo sapiens]			3.63E-04	0.60	10.17	4.50	46867.3
AHQ-8-7, 3221	K.ANVIHATVTSVTLHSTEGK.A	1966.18479	3	3.63E-04	0.60	3.36	-	558.1
gi|9845255|ref|NP_000574.1|	group-specific component (vitamin D binding protein); hDBP [Homo sapien			3.67E-04	0.90	10.19	4.60	53049.5
AHQ-8-6, 6435	K.VPTADLEDVLPLAEDITNILSK.C	2367.67804	3	3.67E-04	0.90	3.83	-	1086.1
gi|4757714|ref|NP_004291.1|	acid phosphatase 1 isoform c; acid phosphatase of erythrocyte; red cell			3.69E-04	0.89	10.16	7.00	18042.4
AHQ-8-11, 3704	K.IELLGSYDPQK.Q	1263.42144	2	3.69E-04	0.89	3.28	-	960.8
gi|30148456|ref|XP_293602.2|	similar to glutathione-S-transferase like; glutathione transferase ome			3.80E-04	0.87	10.13	3.90	29139.6
AHQ-8-10, 4359	K.VPSLVGSFLR.T	1075.28583	2	3.80E-04	0.87	2.69	-	985.5
gi|23510338|ref|NP_003325.2|	ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity			3.93E-04	1.47	20.19	2.90	117848.1
AHQ-8-4, 5967 - 5971	R.AAVATFLQSVQVPEFTPK.S	1934.22430	3	9.51E-04	0.76	3.80	-	615.4
AHQ-8-4, 3537	K.DNPGVVTCLDEAR.H	1447.55333	2	3.93E-04	0.71	2.82	-	523.4
gi|19913373|ref|NP_079536.2|	G6B protein isoform G6b-A precursor; G6B protein; immunoglobulin recep			4.02E-04	0.92	10.13	3.80	25002.6
AHQ-8-11, 2599 - 2647	R.TVLHVLGDR.T	1010.17224	2	4.02E-04	0.92	2.53	-	1596.8
gi|18375611|ref|NP_542937.1|	dachshund homolog isoform a [Homo sapiens]			4.07E-04	0.07	10.14	2.10	73029.7
AHQ-8-7, 4156	K.EGDLAGHDMGHESKR.M	1639.73233	2	4.07E-04	0.07	2.82	-	193.0
gi|4557323|ref|NP_000031.1|	apolipoprotein C-III precursor [Homo sapiens]			4.21E-04	0.71	10.15	16.20	10852.2
AHQ-8-14-, 3183	K.DALSSVQESQVAQQAR.G	1717.81950	2	4.21E-04	0.71	2.92	-	901.6
gi|9910280|ref|NP_064505.1|	UDP-glucose ceramide glucosyltransferase-like 1; UDP-glucose:glycoprote			4.41E-04	0.62	10.16	1.10	177187.7
AHQ-8-3, 5177 - 5178	R.YVLEPEISFTSDNSFAK.G	1948.11833	2	4.41E-04	0.62	3.20	-	339.0
gi|22042381|ref|XP_065237.3|	similar to FKSG30 [Homo sapiens]			4.45E-04	0.70	10.19	4.80	42016.0
AHQ-8-8, 3759 - 3809	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	4.45E-04	0.70	3.33	-	492.9
AHQ-8-8, 3667 - 3747	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	5.62E-04	0.86	3.74	-	580.5
gi|27480104|ref|XP_208215.1|	similar to triosephosphate isomerase 1 [Homo sapiens]			4.48E-04	0.79	10.15	4.80	26942.6
AHQ-8-10, 2107 - 2163	K.SNVSDAVAQSTR.I	1235.28659	2	4.48E-04	0.79	2.73	-	979.9
gi|14150056|ref|NP_115676.1|	hypothetical protein MGC10854 [Homo sapiens]			4.50E-04	0.75	10.15	2.00	61071.3
AHQ-8-8, 2371	K.LKEVEATKLK.K	1159.40104	2	4.50E-04	0.75	2.94	-	738.6
gi|30153966|ref|XP_293932.2|	similar to hypothetical protein BC013073 [Homo sapiens]			4.70E-04	0.74	10.17	9.00	21711.3
AHQ-8-2, 3672	R.MIFTLFTINVSKDIRHH	2073.44997	2	4.73E-04	0.45	3.02	-	329.5
AHQ-8-2, 4031 - 4091	R.MIFTLFTINVSKDIRHH	2073.44997	2	9.00E-04	0.35	3.26	-	344.8
AHQ-8-2, 4035	R.MIFTLFTINVSKDIRHH	2073.44997	3	6.36E-04	0.64	3.27	-	714.9
AHQ-8-3, 3972 - 3976	R.MIFTLFTINVSKDIRHH	2073.44997	3	6.92E-04	0.77	3.48	-	948.7
AHQ-8-7, 3864	R.MIFTLFTINVSKDIRHH	2073.44997	2	7.41E-04	0.29	2.64	-	328.6
AHQ-8-1, 4085 - 4115	R.MIFTLFTINVSKDIRHH	2073.44997	2	4.70E-04	0.74	3.42	-	578.9
gi|4505881|ref|NP_000292.1|	plasminogen [Homo sapiens]			4.87E-04	0.78	10.18	1.40	90568.6
AHQ-8-4, 2483	R.HSIFTPETNPR.A	1299.41711	2	4.87E-04	0.78	2.99	-	568.3
gi|27480017|ref|XP_038288.7|	similar to The KIAA0191 gene is expressed ubiquitously.~The KIAA0191 p			5.04E-04	0.35	10.17	1.00	184703.1
AHQ-8-1, 4801	R.M*DDFQLKGIVEEKFVK.W	1943.25298	2	5.04E-04	0.35	2.72	-	477.4
gi|30156349|ref|XP_301652.1|	similar to Eukaryotic initiation factor 4A-II (eIF-4A-II) (eIF4A-II) [			5.49E-04	0.19	10.13	9.30	21450.7

<table>
<tr><td>AHQ-8-8, 3510 - 3571</td><td>K.M*HAADLTVSALRGDM*DEK.E</td><td>1993.20912</td><td>2</td><td>5.49E-04</td><td>0.19</td><td>2.69</td><td>-</td><td>190.9</td></tr>
<tr><td>gi|4757818|ref|NP_004879.1|</td><td>ATPase, H+ transporting, lysosomal, V1 subunit G isoform 1; vacuolar H(</td><td></td><td></td><td>5.56E-04</td><td>0.54</td><td>10.14</td><td>0.00</td><td>13757.4</td></tr>
<tr><td>AHQ-8-13-, 2884</td><td>K.EEAQAEIEQYR.L</td><td>1366.41548</td><td>2</td><td>5.56E-04</td><td>0.54</td><td>2.72</td><td>-</td><td>640.5</td></tr>
<tr><td>gi|20127450|ref|NP_002729.2|</td><td>protein kinase C, beta 1; Protein kinase C, beta 1 polypeptide [Homo s</td><td></td><td></td><td>5.66E-04</td><td>0.93</td><td>10.18</td><td>1.80</td><td>77011.7</td></tr>
<tr><td>AHQ-8-5, 6022</td><td>K.LTDFNFLM*VLGK.G</td><td>1414.69453</td><td>2</td><td>5.66E-04</td><td>0.93</td><td>3.69</td><td>-</td><td>1156.4</td></tr>
<tr><td>gi|29740531|ref|XP_296644.1|</td><td>hypothetical protein XP_296644 [Homo sapiens]</td><td></td><td></td><td>5.73E-04</td><td>0.29</td><td>10.13</td><td>6.60</td><td>24615.3</td></tr>
<tr><td>AHQ-8-2, 5729 - 5801</td><td>K.KVAPTLTVSGSSLAK.K</td><td>1459.71337</td><td>2</td><td>5.73E-04</td><td>0.29</td><td>2.60</td><td>-</td><td>472.2</td></tr>
<tr><td>gi|4506407|ref|NP_002873.1|</td><td>RAN binding protein 1 [Homo sapiens]</td><td></td><td></td><td>6.28E-04</td><td>0.82</td><td>10.13</td><td>5.50</td><td>23310.0</td></tr>
<tr><td>AHQ-8-10, 4195</td><td>K.TLEEDEEELFK.M</td><td>1382.45159</td><td>2</td><td>6.28E-04</td><td>0.82</td><td>2.64</td><td>-</td><td>760.4</td></tr>
<tr><td>gi|5901922|ref|NP_008996.1|</td><td>CDC37 homolog [Homo sapiens]</td><td></td><td></td><td>6.35E-04</td><td>0.87</td><td>10.21</td><td>5.60</td><td>44468.0</td></tr>
<tr><td>AHQ-8-8, 6235</td><td>R.LGPGGLDPVEVYESLPEELQK.C</td><td>2270.52091</td><td>2</td><td>6.35E-04</td><td>0.87</td><td>4.11</td><td>-</td><td>381.1</td></tr>
<tr><td>gi|22054400|ref|XP_096852.2|</td><td>hypothetical protein XP_096852 [Homo sapiens]</td><td></td><td></td><td>6.66E-04</td><td>0.48</td><td>10.13</td><td>3.30</td><td>39743.5</td></tr>
<tr><td>AHQ-8-2, 3861</td><td>K.ESLLLGGPPAPR.P</td><td>1207.40425</td><td>2</td><td>6.66E-04</td><td>0.48</td><td>2.62</td><td>-</td><td>643.0</td></tr>
<tr><td>gi|4506265|ref|NP_000954.1|</td><td>prostaglandin-endoperoxide synthase 2 precursor; prostaglandin G/H synt</td><td></td><td></td><td>6.87E-04</td><td>0.74</td><td>10.16</td><td>1.50</td><td>68995.7</td></tr>
<tr><td>AHQ-8-6, 4038</td><td>R.LILIGETIK.I</td><td>1000.25717</td><td>2</td><td>6.87E-04</td><td>0.74</td><td>3.13</td><td>-</td><td>584.9</td></tr>
<tr><td>gi|4501889|ref|NP_001606.1|</td><td>actin, gamma 2 propeptide; actin, alpha-3 [Homo sapiens]</td><td></td><td></td><td>7.04E-04</td><td>0.50</td><td>10.14</td><td>5.60</td><td>41876.7</td></tr>
<tr><td>AHQ-8-8, 4694 - 4751</td><td>K.DLYANNVLSGGTTM*YPGIADR.M</td><td>2245.45502</td><td>2</td><td>7.04E-04</td><td>0.50</td><td>2.78</td><td>-</td><td>432.3</td></tr>
<tr><td>gi|21361374|ref|NP_009168.2|</td><td>SP140 nuclear body protein; nuclear body protein Sp140 [Homo sapiens]</td><td></td><td></td><td>7.24E-04</td><td>0.11</td><td>10.13</td><td>2.30</td><td>99869.6</td></tr>
<tr><td>AHQ-8-2, 5580</td><td>-.M*AQQGQQGQM*ASGDSNLNFR.M</td><td>2201.34420</td><td>2</td><td>7.24E-04</td><td>0.11</td><td>2.57</td><td>-</td><td>176.7</td></tr>
<tr><td>gi|7706495|ref|NP_057390.1|</td><td>DnaJ (Hsp40) homolog, subfamily B, member 11; ER-associated DNAJ; ER-as</td><td></td><td></td><td>7.34E-04</td><td>0.96</td><td>10.17</td><td>4.50</td><td>40513.6</td></tr>
<tr><td>AHQ-8-8, 4977</td><td>K.FQDLGAAYEVLSDSEK.R</td><td>1772.89029</td><td>2</td><td>7.34E-04</td><td>0.96</td><td>3.33</td><td>-</td><td>1936.1</td></tr>
<tr><td>gi|30159830|ref|XP_302246.1|</td><td>similar to HSPC280 [Homo sapiens]</td><td></td><td></td><td>7.60E-04</td><td>0.95</td><td>10.24</td><td>3.90</td><td>45644.4</td></tr>
<tr><td>AHQ-8-14-, 6242 - 6278</td><td>R.DDKCANLFEALVGTLK.A</td><td>1796.03496</td><td>3</td><td>7.60E-04</td><td>0.95</td><td>4.78</td><td>-</td><td>1743.8</td></tr>
<tr><td>gi|20546215|ref|XP_115639.1|</td><td>similar to leukocyte immunoglobulin-like receptor, subfamily B (with T</td><td></td><td></td><td>7.73E-04</td><td>0.48</td><td>10.15</td><td>4.70</td><td>42748.2</td></tr>
<tr><td>AHQ-8-13, 4704</td><td>R.CSREVNSREDNVLYRVVK.P</td><td>2225.47152</td><td>2</td><td>7.73E-04</td><td>0.48</td><td>2.89</td><td>-</td><td>629.0</td></tr>
<tr><td>gi|14149817|ref|NP_115523.1|</td><td>hypothetical protein DKFZp434D0127 [Homo sapiens]</td><td></td><td></td><td>7.79E-04</td><td>0.65</td><td>10.10</td><td>1.00</td><td>81154.7</td></tr>
<tr><td>AHQ-8-12, 3722</td><td>R.RRILMGK.I</td><td>874.13334</td><td>1</td><td>7.79E-04</td><td>0.65</td><td>2.02</td><td>-</td><td>904.0</td></tr>
<tr><td>gi|17445600|ref|XP_059465.1|</td><td>similar to ribosomal protein S15 [Homo sapiens]</td><td></td><td></td><td>7.82E-04</td><td>0.66</td><td>10.19</td><td>17.80</td><td>15238.9</td></tr>
<tr><td>AHQ-8-3, 3000</td><td>K.THLRDM*IILPEMVGSM*VGVYNGK.T</td><td>2594.07144</td><td>3</td><td>7.82E-04</td><td>0.66</td><td>3.84</td><td>-</td><td>444.9</td></tr>
<tr><td>gi|4758484|ref|NP_004823.1|</td><td>glutathione-S-transferase like; glutathione transferase omega [Homo sap</td><td></td><td></td><td>7.92E-04</td><td>0.59</td><td>10.14</td><td>6.20</td><td>27565.7</td></tr>
<tr><td>AHQ-8-10, 2768 - 2811</td><td>R.SQNKEDYAGLKEEFR.K</td><td>1814.93364</td><td>2</td><td>7.92E-04</td><td>0.59</td><td>2.53</td><td>-</td><td>458.5</td></tr>
<tr><td>gi|7662096|ref|NP_055517.1|</td><td>KIAA0408 gene product [Homo sapiens]</td><td></td><td></td><td>8.38E-04</td><td>0.46</td><td>10.16</td><td>4.50</td><td>64957.3</td></tr>
<tr><td>AHQ-8-6, 4686</td><td>K.TNAHMPVPMENVPDNPTKKSTTGLVR.Q</td><td>2836.24097</td><td>3</td><td>8.38E-04</td><td>0.46</td><td>3.26</td><td>-</td><td>257.9</td></tr>
<tr><td>gi|4758078|ref|NP_004374.1|</td><td>c-src tyrosine kinase [Homo sapiens]</td><td></td><td></td><td>8.51E-04</td><td>0.67</td><td>10.13</td><td>2.90</td><td>50704.1</td></tr>
<tr><td>AHQ-8-7, 5518 - 5529</td><td>R.LLYPPETGLFLVR.E</td><td>1518.82411</td><td>2</td><td>8.51E-04</td><td>0.67</td><td>2.58</td><td>-</td><td>494.7</td></tr>
<tr><td>gi|11321640|ref|NP_066301.1|</td><td>basic beta 1 syntrophin; 59-DAP; syntrophin, beta 1; syntrophin, beta</td><td></td><td></td><td>8.68E-04</td><td>0.76</td><td>10.17</td><td>3.30</td><td>58060.8</td></tr>
<tr><td>AHQ-8-6, 4423</td><td>R.TAFTDLPEQVPESISNQK.R</td><td>2005.17142</td><td>2</td><td>8.68E-04</td><td>0.76</td><td>3.30</td><td>-</td><td>549.4</td></tr>
<tr><td>gi|27481160|ref|XP_208217.1|</td><td>similar to elongation factor 1 alpha [Homo sapiens]</td><td></td><td></td><td>8.78E-04</td><td>0.85</td><td>10.13</td><td>2.60</td><td>50171.6</td></tr>
<tr><td>AHQ-8-7, 3804</td><td>R.EHALLAYTLGVK.Q</td><td>1315.54272</td><td>2</td><td>8.78E-04</td><td>0.85</td><td>2.60</td><td>-</td><td>813.4</td></tr>
<tr><td>gi|4757762|ref|NP_004281.1|</td><td>ring finger protein 14; androgen receptor associated protein 54 [Homo s</td><td></td><td></td><td>9.47E-04</td><td>0.39</td><td>10.13</td><td>3.40</td><td>53837.2</td></tr>
<tr><td>AHQ-8-7, 3150</td><td>R.YGKRVIQKALEEMESK.E</td><td>1910.22778</td><td>2</td><td>9.47E-04</td><td>0.39</td><td>2.62</td><td>-</td><td>421.3</td></tr>
<tr><td>gi|30148842|ref|XP_292982.2|</td><td>similar to FKSG30 [Homo sapiens]</td><td></td><td></td><td>9.51E-04</td><td>0.75</td><td>10.20</td><td>3.90</td><td>66046.0</td></tr>
<tr><td>AHQ-8-8, 6527 - 6533</td><td>K.LCYVALDFEQEMATVASSSSLEK.S</td><td>2580.87000</td><td>3</td><td>9.51E-04</td><td>0.75</td><td>3.95</td><td>-</td><td>952.8</td></tr>
<tr><td>gi|11072091|ref|NP_057736.2|</td><td>Crn, crooked neck-like 1; CGI-201 protein; crooked neck protein (crn);</td><td></td><td></td><td>9.53E-04</td><td>0.38</td><td>10.11</td><td>1.10</td><td>99200.7</td></tr>
<tr><td>AHQ-8-2, 3141</td><td>R.FVLVHPDVK.N</td><td>1054.26662</td><td>1</td><td>9.53E-04</td><td>0.38</td><td>1.80</td><td>-</td><td>556.8</td></tr>
<tr><td>gi|7661732|ref|NP_054738.1|</td><td>HSPC009 protein [Homo sapiens]</td><td></td><td></td><td>9.69E-04</td><td>0.70</td><td>10.14</td><td>9.40</td><td>11731.2</td></tr>
<tr><td>AHQ-8-13-, 3732</td><td>R.FLDELEDEAK.A</td><td>1209.28427</td><td>2</td><td>9.69E-04</td><td>0.70</td><td>2.72</td><td>-</td><td>716.0</td></tr>
</table>

Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|4557705|ref|NP_000217.1|	keratin 9 [Homo sapiens]			1.00E-30	11.23	130.33	36.20	61986.9
AHQ-9-14-, 5786	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.49E-04	0.80	3.53	-	693.8
AHQ-9-13-, 5746 - 5786	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.72E-14	0.96	5.28	-	1547.7
AHQ-9-13, 5884 - 5898	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.11E-16	0.96	5.41	-	1523.1
AHQ-9-4, 5765 - 5820	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	9.75E-07	0.98	6.09	-	2188.0
AHQ-9-3, 5757	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.28E-07	0.94	4.92	-	1247.4
AHQ-9-2, 5925	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.33E-15	0.97	6.22	-	1424.4
AHQ-9-11, 5677	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.84E-06	0.85	3.60	-	689.2
AHQ-9-10, 5668 - 5675	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.50E-04	0.83	4.02	-	490.1
AHQ-9-7, 5694 - 5748	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.44E-15	0.97	5.87	-	1634.5
AHQ-9-2, 5590	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.27E-04	0.75	3.58	-	514.1
AHQ-9-1, 5599	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	5.52E-07	0.88	4.03	-	970.1
AHQ-9-6, 5753	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.12E-09	0.95	5.67	-	1163.2
AHQ-9-1, 5883 - 5938	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.47E-12	0.97	6.19	-	1724.5
AHQ-9-5, 5503	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.00E-30	0.96	5.28	-	1671.0
AHQ-9-5, 5916 - 5972	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.88E-05	0.91	4.47	-	1136.1
AHQ-9-5, 5835	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	5.12E-06	0.97	5.78	-	1745.0
AHQ-9-6, 4330	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	2.11E-07	0.74	3.22	-	569.7
AHQ-9-1, 4534	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	2.46E-07	0.96	5.61	-	1280.2
AHQ-9-1, 4539	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	3.00E-04	0.82	3.36	-	686.2
AHQ-9-7, 4296	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	1.20E-08	0.94	4.83	-	1379.0
AHQ-9-3, 4365 - 4373	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	1.84E-05	0.94	5.05	-	1501.5
AHQ-9-5, 4379	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	2.67E-04	0.83	3.41	-	667.6
AHQ-9-5, 4373	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	1.27E-07	0.95	6.02	-	1191.3
AHQ-9-4, 4314 - 4381	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	5.90E-05	0.94	4.70	-	1491.4
AHQ-9-5, 4824	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	1.34E-07	0.77	3.18	-	628.8
AHQ-9-2, 4914	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	2.23E-07	0.85	3.79	-	527.8
AHQ-9-1, 4938	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	1.11E-07	0.93	4.56	-	817.2
AHQ-9-5, 2629	R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	3225.08711	3	1.54E-06	0.91	4.27	-	1039.3
AHQ-9-1, 2714 - 2764	R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	3225.08711	3	2.12E-06	0.96	5.71	-	1287.4
AHQ-9-7, 4865	R.HGVQELEIELQSQLSK.K	1839.03978	2	2.69E-04	0.94	4.03	-	1400.7
AHQ-9-5, 4952	R.HGVQELEIELQSQLSK.K	1839.03978	3	7.76E-05	0.84	3.60	-	1357.1
AHQ-9-4, 4945	R.HGVQELEIELQSQLSK.K	1839.03978	3	4.20E-05	0.94	5.44	-	1299.1
AHQ-9-1, 5098	R.HGVQELEIELQSQLSK.K	1839.03978	2	8.21E-11	0.95	4.67	-	1203.2
AHQ-9-7, 4868	R.HGVQELEIELQSQLSK.K	1839.03978	3	1.26E-04	0.80	3.53	-	1042.0
AHQ-9-1, 5102	R.HGVQELEIELQSQLSK.K	1839.03978	3	1.10E-06	0.96	5.24	-	2022.9
AHQ-9-2, 5047	R.HGVQELEIELQSQLSK.K	1839.03978	2	5.86E-08	0.96	4.58	-	1274.7
AHQ-9-1, 5524	R.KDIENQYETQITQIEHEVSSSGQEVQSSAK.E	3394.55959	3	8.15E-11	0.97	6.52	-	1592.6
AHQ-9-5, 5421	R.KDIENQYETQITQIEHEVSSSGQEVQSSAK.E	3394.55959	3	2.64E-06	0.95	5.26	-	1689.7
AHQ-9-4, 5372 - 5429	R.KDIENQYETQITQIEHEVSSSGQEVQSSAK.E	3394.55959	3	7.22E-07	0.81	3.68	-	812.8
AHQ-9-1, 5002	R.LASYLDKVQALEEANNDLENK.I	2378.57787	3	9.39E-05	0.80	3.51	-	977.7
AHQ-9-7, 6217	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	1.01E-06	0.92	4.88	-	617.5
AHQ-9-13-, 6216	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	5.96E-06	0.83	3.81	-	550.7
AHQ-9-2, 6401	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	3.88E-11	0.88	4.07	-	475.2
AHQ-9-5, 6312 - 6371	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	6.21E-06	0.87	4.34	-	504.6
AHQ-9-4, 6254 - 6293	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	9.62E-09	0.79	3.40	-	451.4
AHQ-9-3, 6237	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	2.01E-08	0.92	4.92	-	738.0
AHQ-9-6, 6234	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	1.66E-08	0.87	4.08	-	637.9
AHQ-9-1, 6435 - 6456	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	2.66E-04	0.55	3.16	-	434.2
AHQ-9-1, 6344 - 6350	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	7.01E-08	0.94	4.87	-	946.4
AHQ-9-1, 3044	R.QVLDNLTM*EK.S	1207.37967	2	1.07E-04	0.49	2.59	-	290.3
AHQ-9-2, 6266 - 6273	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	2.73E-04	0.89	4.00	-	1216.0
AHQ-9-1, 6243 - 6298	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	5.33E-05	0.88	3.98	-	873.6
AHQ-9-13-, 6137	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	1.40E-06	0.83	3.37	-	915.3
AHQ-9-5, 6176 - 6235	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	2.06E-06	0.93	4.11	-	1519.3
AHQ-9-5, 5731 - 5740	K.SDLEM*QYETLQEELM*ALKK.N	2332.63427	3	7.83E-06	0.64	3.06	-	609.4
AHQ-9-1, 5836 - 5894	K.SDLEM*QYETLQEELM*ALKK.N	2332.63427	3	3.02E-06	0.82	3.69	-	815.7
AHQ-9-5, 3163 - 3241	K.TLLDIDNTR.M	1061.17119	2	4.15E-04	0.71	2.61	-	605.3
AHQ-9-11, 3150 - 3154	K.TLLDIDNTR.M	1061.17119	2	2.10E-05	0.58	2.54	-	569.6
AHQ-9-4, 3176 - 3177	K.TLLDIDNTR.M	1061.17119	2	1.05E-05	0.79	2.95	-	568.0
AHQ-9-7, 3004 - 3008	K.VQALEEANNDLENK.I	1587.67060	2	1.79E-08	0.98	5.21	-	1821.6
AHQ-9-7, 2637	K.VQALEEANNDLENK.I	1587.67060	2	1.53E-09	0.95	4.46	-	1452.7
AHQ-9-6, 3019 - 3022	K.VQALEEANNDLENK.I	1587.67060	2	4.87E-08	0.97	4.87	-	1563.0
AHQ-9-8, 2983	K.VQALEEANNDLENK.I	1587.67060	2	3.80E-05	0.96	4.68	-	1656.2
AHQ-9-2, 3117	K.VQALEEANNDLENK.I	1587.67060	2	3.05E-09	0.97	5.15	-	1784.9
AHQ-9-5, 3244 - 3252	K.VQALEEANNDLENK.I	1587.67060	2	4.14E-06	0.96	4.94	-	1561.8
AHQ-9-5, 3023	K.VQALEEANNDLENK.I	1587.67060	2	1.57E-08	0.97	4.99	-	1716.9
AHQ-9-1, 3215	K.VQALEEANNDLENK.I	1587.67060	2	4.55E-06	0.98	5.14	-	2154.9
AHQ-9-13-, 3076	K.VQALEEANNDLENK.I	1587.67060	2	3.08E-07	0.88	3.68	-	988.3
AHQ-9-3, 3044	K.VQALEEANNDLENK.I	1587.67060	2	9.07E-06	0.96	4.08	-	1871.6
AHQ-9-4, 2637 - 2698	K.VQALEEANNDLENK.I	1587.67060	2	3.60E-05	0.95	4.14	-	1357.5
AHQ-9-4, 3014	K.VQALEEANNDLENK.I	1587.67060	2	1.64E-05	0.97	4.43	-	1878.4
AHQ-9-5, 2641 - 2645	K.VQALEEANNDLENK.I	1587.67060	2	1.06E-05	0.96	4.90	-	1668.6
gi|4507729|ref|NP_001060.1|	tubulin, beta polypeptide [Homo sapiens]			1.11E-16	5.65	70.38	21.30	49906.7
AHQ-9-7, 4592 - 4666	R.AILVDLEPGTMDSVR.S	1616.86162	2	2.33E-04	0.34	2.77	-	335.1
AHQ-9-7, 2936	K.EVDEQMLNVQNK.N	1447.59668	2	1.81E-04	0.94	3.49	-	1451.8
AHQ-9-8, 5923	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	5.43E-05	0.92	4.04	-	1177.0
AHQ-9-11, 5791	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	8.22E-04	0.91	3.03	-	1486.2
AHQ-9-8, 5919 - 5924	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	2.55E-04	0.71	3.45	-	828.4
AHQ-9-7, 5834 - 5870	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	7.96E-07	0.98	5.54	-	2052.0
AHQ-9-7, 5833 - 5844	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	3.50E-05	0.90	4.41	-	1055.1
AHQ-9-13-, 5888	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.94E-10	0.98	5.80	-	2146.4
AHQ-9-7, 3554 - 3626	R.ISEQFTAM*FR.R	1246.41758	2	1.19E-04	0.72	2.66	-	624.1
AHQ-9-7, 4325	R.ISEQFTAMFR.R	1230.41818	2	6.59E-07	0.71	2.95	-	782.1
AHQ-9-13-, 4425	R.ISEQFTAMFR.R	1230.41818	2	1.93E-07	0.88	3.08	-	985.4
AHQ-9-7, 5136 - 5193	K.NSSYFVEWIPNNVK.T	1697.87148	2	4.81E-05	0.81	3.50	-	660.8
AHQ-9-13-, 5884 - 5948	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.42E-07	0.95	5.60	-	1366.6
AHQ-9-8, 5876 - 5939	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	7.30E-08	0.98	6.62	-	2177.2
AHQ-9-7, 5776 - 5856	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	1.11E-16	0.98	7.58	-	2801.3
gi|4505879|ref|NP_002655.1|	pleckstrin; p47 [Homo sapiens]			3.89E-15	5.39	60.38	26.60	40082.5
AHQ-9-12, 5286 - 5289	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.09E-04	0.86	4.14	-	914.9
AHQ-9-8, 5364 - 5366	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	8.49E-09	0.98	6.88	-	2484.2
AHQ-9-8, 5374	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	2	7.10E-05	0.80	3.22	-	492.8
AHQ-9-11, 5253	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.31E-06	0.91	3.77	-	1179.6
AHQ-9-13-, 5325 - 5326	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	4.40E-07	0.97	7.00	-	1848.3
AHQ-9-8, 2272	R.GCVVTSVESNSNGRK.S	1595.71755	2	1.46E-07	0.63	3.12	-	463.6
AHQ-9-10, 6287	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	7.77E-15	0.98	7.67	-	2960.3
AHQ-9-8, 6344 - 6406	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	3.89E-15	0.98	7.64	-	2289.4
AHQ-9-9, 6139 - 6153	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.03E-07	0.97	6.65	-	1595.4
AHQ-9-8, 5414 - 5479	R.LPETIDLGALYLSM*K.D	1680.98719	2	3.06E-05	0.96	4.83	-	1129.3
AHQ-9-8, 4468	K.QQDHFFQAAFLEER.D	1766.89390	3	2.37E-04	0.89	4.53	-	759.1
AHQ-9-10, 6323 - 6324	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.04E-10	0.94	5.16	-	1126.2
AHQ-9-9, 6187	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	8.00E-09	0.86	3.81	-	771.9
AHQ-9-8, 6446	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	4.15E-06	0.82	3.93	-	454.7
AHQ-9-12, 6344 - 6345	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	7.59E-09	0.91	5.04	-	566.1

AHQ-9-8, 6443	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	2.65E-08	0.91	4.45	-	964.6
gi|4507485|ref|NP_003237.1|	thrombospondin 1 [Homo sapiens]			5.00E-15	27.53	340.33	32.60	129351.8
AHQ-9-5, 3953 - 3967	K.AGTLDLSLTVQGK.Q	1303.48711	2	5.31E-05	0.90	3.50	-	1137.9
AHQ-9-6, 2715 - 2779	R.AQLYIDCEK.M	1141.27636	2	2.71E-05	0.82	2.92	-	610.3
AHQ-9-3, 5469 - 5525	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	1.72E-05	0.96	6.58	-	975.1
AHQ-9-5, 5520 - 5575	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	1.87E-04	0.96	5.76	-	974.2
AHQ-9-4, 5522 - 5581	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	6.38E-05	0.89	4.43	-	714.3
AHQ-9-6, 5441 - 5489	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	2.19E-05	0.95	5.92	-	846.9
AHQ-9-2, 5623 - 5677	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	1.04E-06	0.94	5.65	-	646.9
AHQ-9-4, 3598 - 3617	R.CENTDPGYNCLPCPPR.F	1954.10800	2	9.07E-11	0.90	4.13	-	530.6
AHQ-9-2, 3821	R.CENTDPGYNCLPCPPR.F	1954.10800	2	6.24E-05	0.91	4.30	-	565.9
AHQ-9-3, 3589 - 3602	R.CENTDPGYNCLPCPPR.F	1954.10800	2	4.44E-08	0.91	3.90	-	612.6
AHQ-9-2, 3686	R.CENTDPGYNCLPCPPR.F	1954.10800	2	8.88E-08	0.85	3.58	-	447.1
AHQ-9-2, 3859	K.CNYLGHYSDPMYR.C	1677.84222	2	1.11E-05	0.83	3.26	-	533.4
AHQ-9-3, 3761	K.CNYLGHYSDPMYR.C	1677.84222	2	8.71E-05	0.85	2.93	-	796.1
AHQ-9-4, 3749	K.CNYLGHYSDPMYR.C	1677.84222	2	4.61E-04	0.69	2.55	-	540.3
AHQ-9-4, 3186	K.DCVGDVTENQICNK.Q	1654.75869	2	1.00E-05	0.83	3.46	-	612.8
AHQ-9-3, 3197	K.DCVGDVTENQICNK.Q	1654.75869	2	2.55E-04	0.82	3.31	-	613.2
AHQ-9-2, 3278	K.DCVGDVTENQICNK.Q	1654.75869	2	2.04E-05	0.85	2.96	-	841.5
AHQ-9-5, 3201	K.DCVGDVTENQICNK.Q	1654.75869	2	4.58E-04	0.93	4.02	-	1136.7
AHQ-9-5, 2796	K.DHSGQVFSVVSNGK.A	1461.56164	2	3.49E-06	0.93	3.85	-	1052.4
AHQ-9-6, 2850	K.DHSGQVFSVVSNGK.A	1461.56164	2	7.79E-05	0.80	2.67	-	1040.4
AHQ-9-7, 3005	R.DNCQYVYNVDQR.D	1575.64166	2	5.18E-04	0.87	3.44	-	864.7
AHQ-9-2, 3094	R.DNCQYVYNVDQR.D	1575.64166	2	1.97E-04	0.87	3.67	-	838.1
AHQ-9-6, 3113	R.DNCQYVYNVDQR.D	1575.64166	2	2.81E-06	0.81	3.08	-	834.5
AHQ-9-4, 3001	R.DNCQYVYNVDQR.D	1575.64166	2	6.74E-05	0.66	2.57	-	769.6
AHQ-9-2, 3209	R.DNCQYVYNVDQR.D	1575.64166	2	1.30E-05	0.91	3.39	-	1247.5
AHQ-9-6, 3001	R.DNCQYVYNVDQR.D	1575.64166	2	2.96E-06	0.87	3.24	-	953.1
AHQ-9-5, 3012	R.DNCQYVYNVDQR.D	1575.64166	2	6.11E-04	0.90	3.68	-	997.0
AHQ-9-3, 3024 - 3097	R.DNCQYVYNVDQR.D	1575.64166	2	2.11E-04	0.74	3.17	-	576.4
AHQ-9-2, 3643 - 3709	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	8.85E-09	0.94	5.72	-	811.7
AHQ-9-5, 3609 - 3685	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.84E-09	0.93	5.09	-	840.4
AHQ-9-6, 3555	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	5.65E-12	0.83	4.12	-	738.6
AHQ-9-4, 3577 - 3634	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.37E-10	0.89	4.14	-	809.1
AHQ-9-7, 3877	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	7.69E-05	0.86	4.20	-	601.4
AHQ-9-3, 3546 - 3613	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	5.00E-15	0.95	5.81	-	722.6
AHQ-9-2, 3974	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	7.43E-04	0.88	4.32	-	729.6
AHQ-9-5, 3929	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	3.01E-08	0.61	3.31	-	491.8
AHQ-9-2, 3657	K.FQDLVDAVR.A	1063.18877	2	4.84E-05	0.90	3.07	-	1063.9
AHQ-9-6, 3523	K.FQDLVDAVR.A	1063.18877	2	2.45E-05	0.87	2.97	-	1017.5
AHQ-9-3, 3558	K.FQDLVDAVR.A	1063.18877	2	1.18E-04	0.80	2.78	-	844.9
AHQ-9-2, 4219 - 4229	R.FQMIPLDPK.G	1089.33277	2	5.82E-04	0.80	3.06	-	708.1
AHQ-9-6, 2929	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.50E-04	0.67	2.94	-	403.3
AHQ-9-3, 2901 - 2960	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	6.21E-09	0.73	3.36	-	437.0
AHQ-9-3, 2953	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	1.29E-05	0.80	3.90	-	454.6
AHQ-9-2, 3018	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	8.19E-05	0.86	4.22	-	422.8
AHQ-9-3, 2954	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.81E-07	0.91	4.35	-	450.6
AHQ-9-4, 2928	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	5.61E-07	0.83	3.61	-	618.9
AHQ-9-8, 5146	R.FVFGTTPEDILR.N	1395.58470	2	7.46E-04	0.78	3.36	-	482.4
AHQ-9-10, 5146	K.GFLLLASLR.Q	990.22407	2	5.57E-05	0.95	2.98	-	1928.8
AHQ-9-2, 5397 - 5398	K.GFLLLASLR.Q	990.22407	2	1.06E-04	0.97	4.18	-	2157.6
AHQ-9-4, 5297	K.GFLLLASLR.Q	990.22407	2	2.87E-04	0.97	3.86	-	1983.3
AHQ-9-6, 5223	K.GFLLLASLR.Q	990.22407	2	1.79E-04	0.94	3.07	-	1498.0
AHQ-9-11, 5171	K.GFLLLASLR.Q	990.22407	2	6.71E-06	0.95	3.46	-	1583.2
AHQ-9-5, 5301	K.GFLLLASLR.Q	990.22407	2	4.12E-05	0.96	3.53	-	2020.7
AHQ-9-3, 5252	K.GFLLLASLR.Q	990.22407	2	2.33E-04	0.97	4.07	-	2289.9
AHQ-9-3, 4409	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.02E-06	0.93	4.28	-	1040.4
AHQ-9-5, 4420	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.28E-04	0.85	4.15	-	668.4
AHQ-9-2, 4213 - 4273	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.97E-05	0.79	3.09	-	614.6
AHQ-9-2, 4365 - 4425	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.48E-06	0.96	4.95	-	1239.2
AHQ-9-6, 4014 - 4063	K.GGVNDNFQGVLQNVR.F	1617.74799	2	8.07E-05	0.62	2.91	-	601.6
AHQ-9-2, 4526	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.59E-04	0.91	4.17	-	823.1
AHQ-9-10, 4153 - 4206	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.93E-05	0.84	3.44	-	800.2
AHQ-9-3, 4250 - 4309	K.GGVNDNFQGVLQNVR.F	1617.74799	2	6.69E-05	0.94	4.51	-	1046.6
AHQ-9-7, 4197 - 4253	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.93E-06	0.88	3.87	-	776.5
AHQ-9-6, 4205	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.25E-05	0.56	2.89	-	608.4
AHQ-9-6, 4218	K.GGVNDNFQGVLQNVR.F	1617.74799	3	1.52E-04	0.78	3.62	-	771.4
AHQ-9-6, 4362 - 4437	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.76E-05	0.90	4.14	-	781.5
AHQ-9-9, 4109	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.71E-04	0.74	3.07	-	747.1
AHQ-9-4, 4256 - 4326	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.46E-05	0.88	4.08	-	616.4
AHQ-9-4, 4109	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.76E-06	0.50	3.09	-	347.4
AHQ-9-2, 2307	K.GPDPSSPAFR.I	1031.10364	2	2.54E-04	0.83	3.01	-	543.6
AHQ-9-3, 2253	K.GPDPSSPAFR.I	1031.10364	2	1.32E-04	0.68	2.97	-	409.3
AHQ-9-5, 3143	R.GTLLALER.K	873.03234	2	5.81E-04	0.88	3.33	-	927.5
AHQ-9-3, 3173	R.GTLLALER.K	873.03234	2	4.82E-04	0.91	3.46	-	1000.4
AHQ-9-3, 5853 - 5910	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.53E-05	0.73	3.40	-	515.8
AHQ-9-5, 6048	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.51E-05	0.66	3.03	-	391.9
AHQ-9-4, 5921 - 5990	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.75E-05	0.90	4.52	-	609.5
AHQ-9-13, 5978 - 5982	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.63E-05	0.76	3.42	-	487.3
AHQ-9-5, 5941 - 5943	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	3.29E-07	0.70	3.09	-	248.1
AHQ-9-5, 5923 - 5992	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.45E-05	0.76	3.18	-	480.1
AHQ-9-6, 5833 - 5894	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	8.51E-07	0.59	3.04	-	364.0
AHQ-9-14-, 5897 - 5901	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	7.69E-05	0.62	3.34	-	377.2
AHQ-9-2, 6081 - 6155	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.33E-08	0.78	3.94	-	435.0
AHQ-9-11, 2409 - 2410	K.IM*ADSGPIYDK.T	1226.38144	2	8.95E-04	0.56	2.75	-	401.6
AHQ-9-6, 2674	K.IMADSGPIYDK.T	1210.38204	2	1.37E-06	0.89	3.32	-	829.4
AHQ-9-2, 2767	K.IMADSGPIYDK.T	1210.38204	2	2.79E-05	0.84	3.29	-	553.9
AHQ-9-7, 2668	K.IMADSGPIYDK.T	1210.38204	2	4.53E-05	0.81	2.98	-	526.2
AHQ-9-4, 6230	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.41E-06	0.93	4.66	-	624.2
AHQ-9-13, 6255	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.19E-06	0.93	4.25	-	650.4
AHQ-9-3, 6162 - 6165	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.82E-11	0.98	6.46	-	1445.8
AHQ-9-2, 6334 - 6345	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.96E-13	0.98	6.59	-	1412.7
AHQ-9-2, 6338	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	2.71E-07	0.62	3.22	-	739.7
AHQ-9-5, 6244	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.45E-09	0.97	5.55	-	1154.7
AHQ-9-7, 6140	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.76E-07	0.95	4.36	-	1070.2
AHQ-9-1, 6332	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.61E-04	0.83	3.37	-	589.0
AHQ-9-6, 6157 - 6207	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.24E-08	0.93	4.67	-	644.0
AHQ-9-6, 2443 - 2501	R.KDHSGQVFSVVSNGK.A	1589.73455	2	1.96E-08	0.78	2.98	-	871.6
AHQ-9-4, 2454	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.82E-05	0.67	3.16	-	396.4
AHQ-9-2, 2650	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.80E-10	0.88	3.46	-	911.6
AHQ-9-3, 2489	R.KDHSGQVFSVVSNGK.A	1589.73455	2	5.04E-08	0.82	3.17	-	852.2
AHQ-9-4, 2469	R.KVTEENKELANELR.R	1673.84976	2	1.71E-08	0.88	3.88	-	967.5
AHQ-9-7, 2456	R.KVTEENKELANELR.R	1673.84976	2	2.95E-06	0.94	4.85	-	1200.5
AHQ-9-6, 2442 - 2463	R.KVTEENKELANELR.R	1673.84976	2	3.37E-08	0.91	4.12	-	1189.2
AHQ-9-5, 2452 - 2463	R.KVTEENKELANELR.R	1673.84976	2	5.66E-09	0.93	4.70	-	894.2
AHQ-9-1, 2687 - 2691	R.KVTEENKELANELR.R	1673.84976	2	6.83E-05	0.87	3.82	-	964.5
AHQ-9-3, 2501	R.KVTEENKELANELR.R	1673.84976	3	3.55E-07	0.79	3.35	-	850.3

AHQ-9-3, 2500 - 2580	R.KVTEENKELANELR.R	1673.84976	2	1.37E-08	0.96	4.75	-	1624.0
AHQ-9-2, 2473 - 2554	R.KVTEENKELANELR.R	1673.84976	2	5.01E-08	0.94	4.43	-	1494.5
AHQ-9-5, 2577	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	9.48E-04	0.36	2.59	-	227.5
AHQ-9-4, 4997 - 5054	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	6.22E-06	0.76	3.23	-	475.2
AHQ-9-5, 5105	K.MENAELDVPIQSVFTR.D	1850.08607	2	2.84E-04	0.41	2.94	-	408.0
AHQ-9-3, 5012	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	4.69E-05	0.87	3.06	-	817.6
AHQ-9-5, 5060	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	5.70E-10	0.91	4.81	-	434.3
AHQ-9-6, 4982	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	2.79E-05	0.56	3.20	-	355.9
AHQ-9-3, 3122 - 3194	K.QVTQSYWDTNPTR.A	1596.68241	2	3.71E-04	0.67	3.13	-	589.2
AHQ-9-6, 3094 - 3095	K.QVTQSYWDTNPTR.A	1596.68241	2	8.29E-07	0.89	3.62	-	747.1
AHQ-9-4, 3101	K.QVTQSYWDTNPTR.A	1596.68241	2	1.65E-07	0.87	3.28	-	686.7
AHQ-9-5, 3105	K.QVTQSYWDTNPTR.A	1596.68241	2	2.13E-07	0.69	2.90	-	470.5
AHQ-9-11, 3079 - 3139	K.QVTQSYWDTNPTR.A	1596.68241	2	8.56E-06	0.75	3.12	-	466.3
AHQ-9-2, 2998	R.RPPLCYHNGVQYR.N	1661.86889	2	1.49E-06	0.90	3.63	-	856.3
AHQ-9-6, 2899 - 2903	R.RPPLCYHNGVQYR.N	1661.86889	2	3.09E-04	0.87	3.69	-	475.6
AHQ-9-4, 2806	R.RPPLCYHNGVQYR.N	1661.86889	3	5.73E-04	0.90	3.22	-	1236.6
AHQ-9-3, 2242 - 2317	R.SCDSLNNRCEGSSVQTR.T	1973.04966	2	2.56E-07	0.38	2.59	-	251.1
AHQ-9-4, 3769	K.SITLFVQEDR.A	1208.34588	2	8.51E-07	0.91	3.21	-	1229.9
AHQ-9-13, 4000	K.SITLFVQEDR.A	1208.34588	2	3.60E-04	0.66	2.74	-	663.0
AHQ-9-3, 3769 - 3773	K.SITLFVQEDR.A	1208.34588	2	4.02E-06	0.94	3.63	-	1383.5
AHQ-9-11, 3647 - 3723	K.SITLFVQEDR.A	1208.34588	2	7.20E-04	0.84	3.09	-	859.7
AHQ-9-2, 3873	K.SITLFVQEDR.A	1208.34588	2	8.75E-07	0.94	3.51	-	1369.6
AHQ-9-5, 3735 - 3795	K.SITLFVQEDR.A	1208.34588	2	7.56E-04	0.89	3.11	-	1120.3
AHQ-9-5, 3775	K.SITLFVQEDR.A	1208.34588	2	7.65E-06	0.91	3.44	-	1195.6
AHQ-9-4, 3330	R.TIVTTLQDSIR.K	1247.42355	2	6.08E-05	0.94	3.02	-	1895.8
AHQ-9-7, 4200 - 4212	R.TIVTTLQDSIR.K	1247.42355	2	1.35E-05	0.97	4.18	-	2156.7
AHQ-9-5, 4276	R.TIVTTLQDSIR.K	1247.42355	2	1.12E-05	0.95	4.04	-	1348.2
AHQ-9-8, 4254	R.TIVTTLQDSIR.K	1247.42355	2	6.57E-04	0.97	3.58	-	1971.5
AHQ-9-6, 3303	R.TIVTTLQDSIR.K	1247.42355	2	4.72E-06	0.93	3.18	-	1487.1
AHQ-9-9, 4064	R.TIVTTLQDSIR.K	1247.42355	2	1.64E-06	0.97	3.89	-	2189.8
AHQ-9-3, 4260 - 4274	R.TIVTTLQDSIR.K	1247.42355	2	1.03E-07	0.97	4.33	-	1826.2
AHQ-9-6, 4217	R.TIVTTLQDSIR.K	1247.42355	2	8.62E-07	0.96	4.07	-	1683.3
AHQ-9-4, 4268 - 4269	R.TIVTTLQDSIR.K	1247.42355	2	3.33E-07	0.97	4.18	-	1806.2
AHQ-9-2, 4374 - 4385	R.TIVTTLQDSIR.K	1247.42355	2	4.52E-07	0.97	4.33	-	1621.5
AHQ-9-1, 4468	R.TIVTTLQDSIR.K	1247.42355	2	4.36E-08	0.96	3.68	-	1512.2
AHQ-9-6, 5715	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	7.57E-06	0.81	3.34	-	947.0
AHQ-9-2, 5917	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	1.67E-05	0.91	4.10	-	1299.5
AHQ-9-6, 2673	K.VTEENKELANELR.R	1545.67685	2	1.93E-09	0.83	3.65	-	681.0
AHQ-9-2, 2755 - 2761	K.VTEENKELANELR.R	1545.67685	2	2.44E-07	0.89	3.86	-	797.9
AHQ-9-5, 2677	K.VTEENKELANELR.R	1545.67685	2	7.75E-07	0.93	3.84	-	1317.5
AHQ-9-3, 2708	K.VTEENKELANELR.R	1545.67685	2	2.32E-05	0.71	3.11	-	570.6
AHQ-9-4, 2669	K.VTEENKELANELR.R	1545.67685	2	3.72E-06	0.74	3.27	-	639.3
gi|16753233|ref|NP_006280.2| talin 1 [Homo sapiens]				6.66E-15	91.68	1020.35	50.50	269665.3
AHQ-9-2, 3245 - 3309	K.AAAFEEQENETVVVK.E	1664.79496	2	1.27E-08	0.96	5.23	-	1127.7
AHQ-9-1, 3344	K.AAAFEEQENETVVVK.E	1664.79496	2	3.40E-06	0.96	4.29	-	1573.7
AHQ-9-14-, 3198	K.AAAFEEQENETVVVK.E	1664.79496	2	6.86E-05	0.84	3.53	-	897.7
AHQ-9-4, 3160 - 3238	K.AAAFEEQENETVVVK.E	1664.79496	2	5.29E-05	0.97	5.20	-	1669.7
AHQ-9-3, 3312	K.AAAFEEQENETVVVK.E	1664.79496	2	1.88E-04	0.84	3.09	-	1067.2
AHQ-9-2, 3990	K.AAAFEEQENETVVVK.E	1664.79496	2	4.28E-04	0.67	2.67	-	633.8
AHQ-9-13-, 3170 - 3173	K.AAAFEEQENETVVVK.E	1664.79496	2	3.97E-06	0.92	4.22	-	1024.2
AHQ-9-5, 3160 - 3227	K.AAAFEEQENETVVVK.E	1664.79496	2	3.45E-07	0.96	4.86	-	1376.6
AHQ-9-2, 2750	R.AAM*EPIVISAK.T	1146.38260	2	1.03E-04	0.82	2.93	-	652.8
AHQ-9-3, 2696 - 2710	R.AAM*EPIVISAK.T	1146.38260	2	1.64E-05	0.93	3.22	-	1163.5
AHQ-9-4, 2674	R.AAM*EPIVISAK.T	1146.38260	2	7.14E-05	0.88	2.97	-	1004.2
AHQ-9-2, 2102	K.ADAEGESDLENSR.K	1393.35296	2	1.79E-09	0.92	3.37	-	1221.6
AHQ-9-4, 2033	K.ADAEGESDLENSR.K	1393.35296	2	1.35E-05	0.91	3.29	-	1043.1
AHQ-9-3, 2068	K.ADAEGESDLENSR.K	1393.35296	2	3.61E-07	0.84	3.19	-	706.1
AHQ-9-6, 2650	K.AGALQCSPSDAYTK.K	1470.58689	2	2.70E-05	0.88	3.37	-	846.5
AHQ-9-3, 2678 - 2698	K.AGALQCSPSDAYTK.K	1470.58689	2	1.32E-04	0.86	3.70	-	683.5
AHQ-9-2, 2725	K.AGALQCSPSDAYTK.K	1470.58689	2	2.02E-05	0.91	3.68	-	961.7
AHQ-9-7, 5732	K.AGFLDLKDFLPK.E	1364.61374	2	7.12E-05	0.91	3.26	-	1392.0
AHQ-9-8, 5810	K.AGFLDLKDFLPK.E	1364.61374	2	3.15E-04	0.94	3.89	-	1555.9
AHQ-9-2, 3031	K.AIAVTVQEM*VTK.S	1306.55438	2	6.05E-07	0.93	3.33	-	1199.8
AHQ-9-4, 2941	K.AIAVTVQEM*VTK.S	1306.55438	2	3.27E-04	0.96	4.42	-	1368.0
AHQ-9-4, 3892	K.AIAVTVQEMVTK.S	1290.55498	2	1.66E-07	0.95	4.16	-	1082.4
AHQ-9-5, 3892	K.AIAVTVQEMVTK.S	1290.55498	2	2.51E-05	0.88	3.35	-	913.8
AHQ-9-5, 2943	K.AIAVTVQEM*VTK.S	1306.55438	2	2.52E-06	0.96	3.94	-	1258.1
AHQ-9-3, 2926 - 2988	K.AIAVTVQEM*VTK.S	1306.55438	2	2.41E-04	0.93	3.30	-	1118.5
AHQ-9-3, 3892 - 3893	K.AIAVTVQEMVTK.S	1290.55498	2	6.26E-06	0.95	4.29	-	1285.4
AHQ-9-4, 2693	K.ALDGAFTEENR.A	1223.27427	2	4.96E-04	0.93	3.47	-	1460.7
AHQ-9-2, 2777	K.ALDGAFTEENR.A	1223.27427	2	4.83E-06	0.94	3.43	-	1774.0
AHQ-9-3, 2725	K.ALDGAFTEENR.A	1223.27427	2	9.32E-06	0.96	3.90	-	1617.3
AHQ-9-4, 2520 - 2525	K.ALDGAFTEENR.A	1223.27427	2	2.83E-05	0.95	3.54	-	1703.8
AHQ-9-3, 2544	K.ALDGAFTEENR.A	1223.27427	2	3.42E-06	0.88	3.33	-	1093.0
AHQ-9-2, 2602	K.ALDGAFTEENR.A	1223.27427	2	5.29E-08	0.92	2.77	-	1515.1
AHQ-9-7, 3322	K.ALDYYM*LR.N	1061.23626	2	9.96E-04	0.89	2.85	-	962.9
AHQ-9-3, 2133	R.ALEATTEHIR.Q	1141.25953	2	1.63E-04	0.89	3.03	-	1215.5
AHQ-9-5, 2084	R.ALEATTEHIR.Q	1141.25953	2	6.04E-04	0.88	2.84	-	1258.0
AHQ-9-4, 2093 - 2158	R.ALEATTEHIR.Q	1141.25953	2	6.44E-07	0.84	2.83	-	1076.5
AHQ-9-2, 2169	R.ALEATTEHIR.Q	1141.25953	2	8.68E-06	0.77	2.88	-	881.6
AHQ-9-4, 3404	K.ALGDLISATK.A	989.14811	2	2.77E-04	0.89	3.17	-	801.0
AHQ-9-3, 3406	K.ALGDLISATK.A	989.14811	2	1.30E-05	0.94	4.10	-	914.1
AHQ-9-6, 3374	K.ALGDLISATK.A	989.14811	2	8.81E-04	0.89	3.40	-	704.8
AHQ-9-5, 3401	K.ALGDLISATK.A	989.14811	2	1.57E-06	0.94	4.02	-	980.8
AHQ-9-7, 3365	K.ALGDLISATK.A	989.14811	2	2.74E-04	0.90	3.20	-	838.2
AHQ-9-2, 3486	K.ALGDLISATK.A	989.14811	2	1.44E-04	0.87	3.58	-	688.2
AHQ-9-5, 2697	K.ALSTDPAAPNLK.S	1198.35099	2	3.31E-05	0.63	2.84	-	553.7
AHQ-9-2, 2766	K.ALSTDPAAPNLK.S	1198.35099	2	2.99E-05	0.84	2.98	-	690.4
AHQ-9-6, 2689	K.ALSTDPAAPNLK.S	1198.35099	2	5.27E-06	0.73	2.55	-	834.8
AHQ-9-3, 2716	K.ALSTDPAAPNLK.S	1198.35099	2	1.71E-05	0.71	2.79	-	703.6
AHQ-9-2, 3625	K.ALSTDPAAPNLKSQLAAAAR.A	1967.21592	2	3.94E-05	0.67	2.88	-	487.6
AHQ-9-4, 5670	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.65E-07	0.92	3.95	-	768.6
AHQ-9-2, 5167 - 5230	K.APGQLECETAIAALNSCLR.D	2077.32566	2	5.68E-06	0.76	3.10	-	482.2
AHQ-9-2, 5782	K.APGQLECETAIAALNSCLR.D	2077.32566	3	3.05E-04	0.84	3.69	-	719.4
AHQ-9-2, 5774	K.APGQLECETAIAALNSCLR.D	2077.32566	2	7.64E-07	0.95	4.76	-	933.8
AHQ-9-3, 5602 - 5625	K.APGQLECETAIAALNSCLR.D	2077.32566	2	5.77E-04	0.86	3.58	-	741.1
AHQ-9-2, 5555 - 5561	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	2	3.62E-04	0.85	3.71	-	788.0
AHQ-9-2, 5559	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	8.12E-05	0.82	3.86	-	765.8
AHQ-9-4, 5452	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	2.47E-05	0.87	3.87	-	1127.7
AHQ-9-7, 2960	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.58E-06	0.58	3.16	-	315.0
AHQ-9-6, 2959 - 2970	K.ASAGPQPLLVQSCK.A	1457.67763	2	3.23E-07	0.77	3.00	-	433.8
AHQ-9-3, 3013	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.54E-08	0.79	3.23	-	397.9
AHQ-9-4, 2962 - 2978	K.ASAGPQPLLVQSCK.A	1457.67763	2	6.49E-08	0.72	3.01	-	477.8
AHQ-9-2, 3046 - 3110	K.ASAGPQPLLVQSCK.A	1457.67763	2	1.94E-04	0.78	3.10	-	469.8
AHQ-9-4, 4061 - 4120	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	7.19E-04	0.95	5.18	-	749.6
AHQ-9-3, 4048	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	5.44E-04	0.87	3.91	-	639.6
AHQ-9-5, 3591	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	7.59E-05	0.89	3.73	-	645.7

AHQ-9-6, 4022	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.15E-08	0.83	3.57	-	511.3
AHQ-9-2, 3677	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	4.68E-06	0.71	3.02	-	475.2
AHQ-9-5, 4063	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	4.90E-09	0.88	4.06	-	578.9
AHQ-9-6, 3553 - 3563	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.05E-06	0.92	4.28	-	834.5
AHQ-9-3, 3584 - 3585	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	3.74E-04	0.82	3.56	-	492.1
AHQ-9-2, 4153	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.09E-07	0.86	3.51	-	673.2
AHQ-9-1, 3768	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	6.41E-05	0.93	4.02	-	840.5
AHQ-9-4, 3593	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	4.40E-05	0.89	4.00	-	534.0
AHQ-9-4, 4750	K.AVAEQIPLLVQGVR.G	1493.77619	3	1.20E-07	0.96	5.30	-	1770.8
AHQ-9-2, 4845	K.AVAEQIPLLVQGVR.G	1493.77619	3	2.40E-05	0.96	4.45	-	2041.7
AHQ-9-2, 4826 - 4829	K.AVAEQIPLLVQGVR.G	1493.77619	2	1.83E-05	0.93	4.28	-	835.0
AHQ-9-1, 4900 - 4908	K.AVAEQIPLLVQGVR.G	1493.77619	2	9.73E-06	0.94	4.29	-	841.1
AHQ-9-6, 4687	K.AVAEQIPLLVQGVR.G	1493.77619	3	1.85E-04	0.97	4.76	-	2707.0
AHQ-9-5, 3801 - 3811	K.AVASAAAALVLK.A	1085.32216	2	1.42E-04	0.91	3.47	-	1070.8
AHQ-9-3, 3733 - 3804	K.AVASAAAALVLK.A	1085.32216	2	5.97E-04	0.94	3.39	-	1482.4
AHQ-9-2, 3863 - 3921	K.AVASAAAALVLK.A	1085.32216	2	7.04E-07	0.95	4.08	-	1424.6
AHQ-9-6, 3895	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.16E-04	0.96	4.54	-	1356.5
AHQ-9-2, 3997 - 4059	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.51E-07	0.68	3.02	-	747.2
AHQ-9-2, 4215	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.22E-05	0.58	2.83	-	571.6
AHQ-9-5, 3904 - 3964	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.31E-05	0.57	3.12	-	668.6
AHQ-9-4, 3901	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	8.36E-07	0.88	3.50	-	1013.3
AHQ-9-4, 3696 - 3753	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.42E-04	0.63	2.89	-	748.2
AHQ-9-1, 3983 - 4048	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	6.64E-06	0.87	3.49	-	911.3
AHQ-9-2, 4122	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.62E-04	0.81	3.33	-	976.2
AHQ-9-3, 3894 - 3942	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.38E-07	0.95	4.79	-	1387.8
AHQ-9-2, 3794	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.56E-07	0.94	4.29	-	1209.2
AHQ-9-5, 6331	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	6.49E-07	0.97	5.47	-	2110.8
AHQ-9-2, 6417 - 6439	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	4.51E-10	0.98	6.64	-	1878.4
AHQ-9-6, 6250	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	9.66E-09	0.98	6.03	-	2378.5
AHQ-9-4, 5206	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	7.47E-04	0.61	2.92	-	462.2
AHQ-9-2, 5298 - 5302	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	8.06E-05	0.59	3.34	-	316.0
AHQ-9-1, 5450	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.39E-07	0.88	4.54	-	580.3
AHQ-9-2, 5421	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.14E-06	0.86	4.22	-	687.1
AHQ-9-2, 5665	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	6.94E-08	0.88	3.85	-	904.0
AHQ-9-3, 5269 - 5334	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	2.91E-07	0.87	4.19	-	923.1
AHQ-9-4, 2440	R.CVSCLPGQR.D	1079.23309	2	2.22E-05	0.87	3.09	-	913.1
AHQ-9-8, 3488 - 3534	R.DDILNGSHPVSFDK.A	1544.64741	2	1.82E-07	0.96	4.43	-	1483.2
AHQ-9-7, 3408 - 3481	R.DDILNGSHPVSFDK.A	1544.64741	2	5.69E-06	0.91	3.78	-	766.1
AHQ-9-2, 5621	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	9.85E-04	0.76	3.07	-	1054.9
AHQ-9-2, 5823	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	1.42E-04	0.78	3.30	-	766.3
AHQ-9-3, 4882	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.24E-05	0.91	3.96	-	902.2
AHQ-9-2, 5750 - 5819	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.19E-08	0.88	3.56	-	794.3
AHQ-9-4, 4925	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.07E-06	0.77	3.11	-	646.1
AHQ-9-2, 5023 - 5043	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.70E-07	0.93	4.47	-	988.8
AHQ-9-4, 5521	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	7.52E-10	0.92	4.54	-	727.0
AHQ-9-3, 5473	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	6.18E-10	0.90	3.89	-	666.0
AHQ-9-2, 5626 - 5627	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	5.27E-08	0.96	5.14	-	1162.2
AHQ-9-1, 5036	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	6.85E-08	0.93	4.60	-	1251.8
AHQ-9-1, 5026	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.71E-04	0.88	3.63	-	671.4
AHQ-9-6, 4838	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	3.48E-06	0.90	3.92	-	1227.3
AHQ-9-2, 4931 - 4989	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	8.66E-08	0.96	5.24	-	956.1
AHQ-9-3, 4844 - 4850	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	3.85E-06	0.94	5.02	-	1431.0
AHQ-9-4, 4874 - 4908	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	1.28E-09	0.90	3.88	-	957.9
AHQ-9-5, 4907	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	5.43E-06	0.90	3.67	-	1544.7
AHQ-9-3, 3552 - 3554	R.DPPSWSVLAGHSR.T	1409.53156	2	4.99E-08	0.88	3.11	-	598.5
AHQ-9-4, 3549	R.DPPSWSVLAGHSR.T	1409.53156	2	2.36E-09	0.89	3.55	-	455.5
AHQ-9-3, 3572	R.DPPSWSVLAGHSR.T	1409.53156	3	3.47E-06	0.92	4.54	-	784.0
AHQ-9-2, 3641	R.DPPSWSVLAGHSR.T	1409.53156	2	1.51E-07	0.70	2.86	-	281.7
AHQ-9-2, 3651	R.DPPSWSVLAGHSR.T	1409.53156	3	4.75E-06	0.88	3.86	-	884.4
AHQ-9-8, 4850 - 4851	R.DPVQLNLLYVQAR.D	1529.76539	2	5.19E-09	0.97	5.12	-	1506.9
AHQ-9-7, 4734 - 4788	R.DPVQLNLLYVQAR.D	1529.76539	2	3.13E-04	0.95	4.05	-	1320.2
AHQ-9-7, 4813	R.DPVQLNLLYVQAR.D	1529.76539	2	2.63E-04	0.87	2.84	-	1182.1
AHQ-9-6, 2525	K.EAAYHPEVAPDVR.L	1454.56910	2	2.30E-04	0.82	2.73	-	869.3
AHQ-9-6, 5414 - 5477	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.29E-06	0.95	4.76	-	1385.6
AHQ-9-8, 5442 - 5499	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.38E-04	0.77	3.16	-	687.6
AHQ-9-4, 5544	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.57E-06	0.88	3.88	-	953.6
AHQ-9-2, 5574 - 5653	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.14E-07	0.97	5.45	-	2043.6
AHQ-9-3, 5436 - 5489	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.14E-06	0.94	4.70	-	1200.5
AHQ-9-9, 5263	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.99E-06	0.83	3.02	-	964.4
AHQ-9-3, 5202 - 5237	K.EADESLNFEEQILEAAK.S	1937.05072	2	5.91E-05	0.56	2.79	-	388.2
AHQ-9-7, 5404 - 5473	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.61E-07	0.94	4.43	-	1219.4
AHQ-9-4, 5430 - 5488	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.24E-07	0.97	5.18	-	1786.8
AHQ-9-1, 5598 - 5660	K.EADESLNFEEQILEAAK.S	1937.05072	2	7.82E-08	0.94	4.74	-	1123.3
AHQ-9-3, 5380 - 5432	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.30E-07	0.97	4.79	-	2060.2
AHQ-9-5, 5491 - 5571	K.EADESLNFEEQILEAAK.S	1937.05072	2	6.47E-07	0.96	5.07	-	1525.9
AHQ-9-5, 6399	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	4.71E-07	0.91	4.30	-	1078.8
AHQ-9-2, 6485	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	3.37E-08	0.95	5.59	-	1101.6
AHQ-9-2, 6347 - 6419	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	3.51E-06	0.93	5.35	-	926.7
AHQ-9-2, 6450	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	5.23E-08	0.93	5.57	-	913.5
AHQ-9-4, 6265 - 6334	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	9.69E-07	0.96	5.69	-	1409.8
AHQ-9-6, 6273	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.16E-07	0.95	5.53	-	1235.7
AHQ-9-4, 5637 - 5692	R.ELLENPVQPINDM*SYFGCLDSVM*ENSK.V	3164.48754	3	8.16E-07	0.79	3.47	-	636.3
AHQ-9-3, 6169	R.ELLENPVQPINDM*SYFGCLDSVMENSK.V	3148.48814	3	1.10E-04	0.61	3.20	-	413.4
AHQ-9-3, 5608 - 5676	R.ELLENPVQPINDM*SYFGCLDSVM*ENSK.V	3164.48754	3	1.64E-05	0.87	4.05	-	644.4
AHQ-9-13-, 5244	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	2.39E-08	0.96	5.69	-	1377.2
AHQ-9-8, 5275 - 5338	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	6.71E-08	0.96	4.71	-	1627.0
AHQ-9-2, 2310	K.EVANSTANLVK.T	1146.27608	2	2.98E-05	0.77	2.87	-	713.1
AHQ-9-8, 2970	K.FFYSDQNVDSR.D	1378.42795	2	7.47E-06	0.93	3.88	-	980.2
AHQ-9-8, 5554	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	8.58E-10	0.98	6.18	-	2457.7
AHQ-9-7, 5469 - 5541	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	2.41E-05	0.98	6.91	-	1683.3
AHQ-9-2, 5835 - 5839	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	2	1.47E-07	0.81	3.27	-	835.6
AHQ-9-2, 5826 - 5882	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	3.67E-07	0.84	4.09	-	747.3
AHQ-9-6, 5666	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	1.41E-07	0.68	3.16	-	660.8
AHQ-9-2, 2953 - 2954	K.FLPSELRDEH	1243.35032	2	1.73E-06	0.61	2.56	-	429.3
AHQ-9-4, 2860	K.FLPSELRDEH	1243.35032	2	4.42E-06	0.60	2.61	-	306.4
AHQ-9-3, 2894 - 2910	K.FLPSELRDEH	1243.35032	2	2.28E-05	0.50	2.64	-	310.6
AHQ-9-4, 4890	K.GLAGAVSELLR.S	1086.26701	2	4.09E-07	0.97	4.09	-	2066.8
AHQ-9-5, 4915	K.GLAGAVSELLR.S	1086.26701	2	5.75E-07	0.95	3.50	-	1618.4
AHQ-9-3, 4878 - 4892	K.GLAGAVSELLR.S	1086.26701	2	3.75E-07	0.98	5.02	-	2132.0
AHQ-9-2, 5001	K.GLAGAVSELLR.S	1086.26701	2	1.05E-06	0.97	4.57	-	2110.6
AHQ-9-7, 4829	K.GLAGAVSELLR.S	1086.26701	2	3.45E-06	0.95	3.59	-	1719.7
AHQ-9-6, 4843 - 4849	K.GLAGAVSELLR.S	1086.26701	2	5.93E-05	0.95	3.61	-	1486.1
AHQ-9-9, 4680	K.GLAGAVSELLR.S	1086.26701	2	5.79E-04	0.98	3.77	-	2768.9
AHQ-9-1, 5072	K.GLAGAVSELLR.S	1086.26701	2	1.45E-06	0.97	4.70	-	2031.7
AHQ-9-4, 5936 - 6008	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	7.10E-04	0.89	4.12	-	1136.6
AHQ-9-4, 5806 - 5862	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.92E-04	0.80	3.96	-	803.7
AHQ-9-3, 5876 - 5933	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	6.48E-04	0.85	4.18	-	1043.1

AHQ-9-7, 5874 - 5928	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	5.01E-04	0.66	3.66	-	546.9
AHQ-9-6, 5917 - 5981	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.85E-06	0.93	5.33	-	823.8
AHQ-9-5, 6459	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.31E-05	0.93	4.96	-	1342.9
AHQ-9-3, 6376 - 6446	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.44E-14	0.98	6.27	-	2324.8
AHQ-9-6, 6375	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.09E-05	0.92	4.50	-	1488.8
AHQ-9-2, 6541 - 6543	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.69E-10	0.96	5.46	-	1723.0
AHQ-9-2, 6446	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	1.77E-04	0.82	3.99	-	785.6
AHQ-9-3, 6280	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	5.11E-07	0.98	5.60	-	2374.5
AHQ-9-5, 6360	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	1.07E-07	0.97	6.31	-	1073.3
AHQ-9-1, 6431	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	7.06E-04	0.62	2.78	-	465.3
AHQ-9-4, 6340	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	3.00E-08	0.97	6.50	-	1764.3
AHQ-9-7, 6262	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	3.09E-05	0.95	5.98	-	1360.0
AHQ-9-6, 6330	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.03E-04	0.79	4.16	-	497.8
AHQ-9-2, 5473	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	5.20E-06	0.89	4.06	-	775.0
AHQ-9-3, 6332	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.32E-08	0.92	4.48	-	1093.1
AHQ-9-2, 6498	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.50E-09	0.96	5.23	-	1065.6
AHQ-9-2, 6497	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.13E-09	0.94	5.24	-	822.6
AHQ-9-3, 6334	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	9.20E-07	0.91	4.61	-	559.4
AHQ-9-1, 6482	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.24E-07	0.92	4.25	-	1166.6
AHQ-9-8, 6402 - 6404	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.29E-06	0.94	4.56	-	1129.4
AHQ-9-4, 6390	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.03E-08	0.95	5.61	-	841.5
AHQ-9-4, 6388	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	8.51E-05	0.95	5.10	-	1232.6
AHQ-9-5, 6411	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.40E-07	0.91	4.17	-	1084.5
AHQ-9-5, 6412	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	9.51E-09	0.95	5.42	-	756.1
AHQ-9-7, 6312	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	3.05E-07	0.93	4.38	-	1166.2
AHQ-9-6, 6329	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	1.65E-07	0.87	3.31	-	1220.8
AHQ-9-7, 3324	R.IGITNHDEYSLVR.E	1517.66833	3	1.41E-07	0.95	4.45	-	1337.0
AHQ-9-7, 3317	R.IGITNHDEYSLVR.E	1517.66833	2	2.09E-09	0.92	3.87	-	973.2
AHQ-9-13-, 3425	R.IGITNHDEYSLVR.E	1517.66833	2	6.44E-06	0.91	3.79	-	855.0
AHQ-9-8, 3502 - 3559	R.IGITNHDEYSLVR.E	1517.66833	2	3.58E-08	0.95	3.80	-	1589.0
AHQ-9-7, 4692	R.ILAQATSDLVNAIK.A	1457.69748	2	1.53E-05	0.95	3.36	-	1693.0
AHQ-9-1, 4922 - 4924	R.ILAQATSDLVNAIK.A	1457.69748	2	1.43E-07	0.98	5.36	-	2878.5
AHQ-9-7, 3933	R.ILAQATSDLVNAIK.A	1457.69748	2	1.52E-06	0.91	3.37	-	1320.2
AHQ-9-3, 4738	R.ILAQATSDLVNAIK.A	1457.69748	2	7.90E-08	0.97	4.89	-	1746.7
AHQ-9-4, 3953 - 4008	R.ILAQATSDLVNAIK.A	1457.69748	2	6.60E-09	0.97	4.55	-	1718.9
AHQ-9-3, 3989	R.ILAQATSDLVNAIK.A	1457.69748	2	1.09E-09	0.98	4.50	-	2880.0
AHQ-9-5, 4776	R.ILAQATSDLVNAIK.A	1457.69748	2	3.67E-09	0.98	5.22	-	1892.4
AHQ-9-5, 3992	R.ILAQATSDLVNAIK.A	1457.69748	2	1.94E-05	0.96	3.77	-	1767.1
AHQ-9-2, 4097	R.ILAQATSDLVNAIK.A	1457.69748	2	5.11E-07	0.96	3.96	-	1618.7
AHQ-9-8, 3992	R.ILAQATSDLVNAIK.A	1457.69748	2	1.78E-06	0.89	2.98	-	1093.7
AHQ-9-4, 4760	R.ILAQATSDLVNAIK.A	1457.69748	2	2.06E-08	0.98	4.53	-	2376.0
AHQ-9-2, 4865	R.ILAQATSDLVNAIK.A	1457.69748	2	1.25E-07	0.97	4.64	-	1683.5
AHQ-9-6, 3945	R.ILAQATSDLVNAIK.A	1457.69748	2	9.59E-08	0.96	3.62	-	1754.0
AHQ-9-6, 4709 - 4717	R.ILAQATSDLVNAIK.A	1457.69748	2	1.78E-08	0.98	5.02	-	2147.9
AHQ-9-8, 5514	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	1.79E-04	0.80	3.21	-	641.8
AHQ-9-14-, 5161 - 5175	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.05E-05	0.92	4.56	-	971.6
AHQ-9-13-, 5160 - 5186	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.15E-07	0.95	4.54	-	1751.3
AHQ-9-13, 5260 - 5284	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	8.64E-04	0.73	3.08	-	1028.3
AHQ-9-8, 2755	R.KFFYSDQNVDSR.D	1506.60087	2	8.40E-05	0.96	4.03	-	1401.6
AHQ-9-11, 2774 - 2778	K.LAQAAQSSVATITR.L	1417.59344	2	3.75E-04	0.84	3.31	-	767.0
AHQ-9-4, 2761 - 2773	K.LAQAAQSSVATITR.L	1417.59344	2	7.54E-08	0.94	3.61	-	1402.3
AHQ-9-6, 2610	K.LAQAAQSSVATITR.L	1417.59344	2	1.35E-06	0.95	3.57	-	1576.8
AHQ-9-1, 2978	K.LAQAAQSSVATITR.L	1417.59344	2	6.12E-05	0.95	3.24	-	1772.9
AHQ-9-13-, 2829	K.LAQAAQSSVATITR.L	1417.59344	2	4.68E-04	0.90	3.28	-	1103.4
AHQ-9-3, 2632	K.LAQAAQSSVATITR.L	1417.59344	2	3.36E-07	0.94	4.04	-	1165.8
AHQ-9-8, 2759 - 2762	K.LAQAAQSSVATITR.L	1417.59344	2	2.48E-07	0.94	4.13	-	1161.9
AHQ-9-6, 2757 - 2758	K.LAQAAQSSVATITR.L	1417.59344	2	1.63E-08	0.97	5.03	-	1784.2
AHQ-9-2, 2689 - 2727	K.LAQAAQSSVATITR.L	1417.59344	2	8.81E-07	0.87	3.31	-	842.7
AHQ-9-2, 2807 - 2845	K.LAQAAQSSVATITR.L	1417.59344	2	6.13E-11	0.96	4.37	-	1467.8
AHQ-9-3, 2794	K.LAQAAQSSVATITR.L	1417.59344	2	2.08E-09	0.96	4.23	-	1713.1
AHQ-9-5, 2767 - 2789	K.LAQAAQSSVATITR.L	1417.59344	2	7.96E-05	0.97	4.56	-	1722.2
AHQ-9-5, 2615	K.LAQAAQSSVATITR.L	1417.59344	2	6.94E-06	0.91	3.00	-	1410.6
AHQ-9-4, 2614	K.LAQAAQSSVATITR.L	1417.59344	2	1.01E-06	0.86	2.79	-	1293.1
AHQ-9-4, 3033 - 3106	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.87E-06	0.89	3.94	-	1269.1
AHQ-9-1, 3476	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	9.64E-09	0.98	5.84	-	2629.7
AHQ-9-4, 3268	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	1.06E-07	0.91	4.25	-	617.7
AHQ-9-3, 3288	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	3.12E-09	0.93	4.39	-	702.6
AHQ-9-2, 3595	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	3.01E-07	0.96	4.57	-	2150.5
AHQ-9-3, 3272	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.68E-06	0.96	5.09	-	1650.9
AHQ-9-3, 3054	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.76E-06	0.87	4.00	-	929.1
AHQ-9-2, 5193	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	6.17E-10	0.98	6.66	-	3189.8
AHQ-9-2, 5185 - 5250	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.67E-06	0.96	5.49	-	976.0
AHQ-9-1, 5235	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.19E-08	0.97	4.98	-	1569.9
AHQ-9-1, 5239	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.07E-05	0.96	4.78	-	1943.2
AHQ-9-4, 5216 - 5221	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.04E-10	0.95	5.12	-	742.8
AHQ-9-2, 5309	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.12E-10	0.93	4.65	-	696.3
AHQ-9-3, 5168 - 5172	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.02E-07	0.95	5.03	-	922.1
AHQ-9-5, 5219	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.37E-09	0.93	4.32	-	859.2
AHQ-9-4, 5093 - 5094	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.18E-08	0.95	4.98	-	1003.1
AHQ-9-2, 5005	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	7.89E-09	0.89	3.47	-	1389.6
AHQ-9-5, 5099	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.22E-06	0.97	5.74	-	1066.2
AHQ-9-3, 5049 - 5066	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	4.03E-05	0.89	3.38	-	1462.6
AHQ-9-4, 4901 - 4926	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.20E-06	0.96	4.70	-	1433.5
AHQ-9-3, 5048	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.29E-04	0.93	4.39	-	893.4
AHQ-9-2, 4970 - 5033	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.16E-11	0.94	4.54	-	790.9
AHQ-9-6, 4837	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.18E-07	0.93	4.59	-	766.4
AHQ-9-6, 5021	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.48E-05	0.95	4.33	-	1293.5
AHQ-9-6, 5023 - 5086	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	6.55E-04	0.91	4.25	-	1544.1
AHQ-9-6, 5151	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	8.74E-07	0.92	4.44	-	712.0
AHQ-9-5, 4913	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.74E-08	0.90	4.11	-	682.5
AHQ-9-4, 5100	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	2.43E-07	0.97	5.58	-	2092.9
AHQ-9-3, 4865	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.70E-07	0.92	4.53	-	848.1
AHQ-9-7, 4821	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.05E-08	0.92	4.21	-	940.2
AHQ-9-5, 5103	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	2.18E-09	0.97	5.82	-	2226.2
AHQ-9-8, 3676	K.LHTDDELNWLDHGR.T	1721.81153	2	1.79E-05	0.97	4.49	-	1813.4
AHQ-9-8, 3686	K.LHTDDELNWLDHGR.T	1721.81153	3	3.24E-05	0.89	4.07	-	1007.1
AHQ-9-7, 3740	K.LHTDDELNWLDHGR.T	1721.81153	2	2.76E-05	0.93	3.47	-	1398.2
AHQ-9-2, 4287	K.LLAALLEDEGGSGR.P	1401.54764	2	1.18E-06	0.95	3.77	-	1118.5
AHQ-9-3, 4972 - 4990	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.05E-09	0.95	5.06	-	1354.2
AHQ-9-5, 5023	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.80E-05	0.97	6.70	-	1292.2
AHQ-9-1, 5154 - 5176	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	8.03E-10	0.96	4.61	-	1591.6
AHQ-9-1, 5183	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.76E-08	0.93	4.97	-	906.9
AHQ-9-7, 4925	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.21E-06	0.98	6.91	-	1208.8
AHQ-9-2, 5101	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.40E-10	0.95	5.06	-	1402.5
AHQ-9-8, 4987	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.11E-08	0.94	4.73	-	1117.4
AHQ-9-4, 5008 - 5009	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.15E-07	0.98	6.67	-	1599.2
AHQ-9-5, 5020	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	6.09E-06	0.97	5.57	-	1616.4

AHQ-9-4, 5001 - 5002	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	6.65E-09	0.98	6.14	-	2674.6
AHQ-9-8, 4984	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.30E-10	0.98	6.26	-	1452.9
AHQ-9-2, 5102	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.29E-11	0.98	6.36	-	1480.3
AHQ-9-7, 4922 - 4929	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	8.20E-08	0.96	5.77	-	1601.1
AHQ-9-3, 4976	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	4.62E-09	0.97	6.31	-	1461.0
AHQ-9-6, 4941	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	3.05E-07	0.94	5.04	-	988.2
AHQ-9-6, 4945	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.40E-09	0.98	6.11	-	1581.8
AHQ-9-1, 5324	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.21E-12	0.98	5.52	-	1797.4
AHQ-9-4, 4169	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.12E-09	0.92	4.33	-	693.9
AHQ-9-5, 5201	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.48E-09	0.98	5.64	-	1831.3
AHQ-9-2, 5690	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.71E-06	0.95	3.97	-	1388.5
AHQ-9-6, 5138	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.72E-04	0.98	5.53	-	2827.4
AHQ-9-6, 5074 - 5130	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.13E-08	0.93	4.53	-	947.8
AHQ-9-2, 5442	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.05E-08	0.96	5.08	-	1151.6
AHQ-9-2, 5286	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.73E-07	0.98	5.65	-	2345.1
AHQ-9-2, 5282 - 5341	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.88E-08	0.98	5.80	-	1922.5
AHQ-9-11, 5063	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.16E-05	0.70	2.59	-	754.1
AHQ-9-3, 5388 - 5445	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.50E-06	0.94	4.63	-	1316.7
AHQ-9-4, 5440 - 5501	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.48E-11	0.94	4.53	-	1213.3
AHQ-9-6, 4130	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.77E-04	0.83	3.44	-	726.4
AHQ-9-2, 5122	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.67E-06	0.95	4.47	-	1061.8
AHQ-9-4, 5344	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.25E-04	0.94	4.26	-	1243.0
AHQ-9-5, 4180	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.15E-07	0.97	5.29	-	1168.1
AHQ-9-3, 5134 - 5144	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.08E-10	0.97	5.47	-	1534.7
AHQ-9-1, 5334	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	3.52E-04	0.96	4.93	-	1675.0
AHQ-9-2, 5537	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.52E-08	0.97	4.74	-	1773.9
AHQ-9-2, 4270	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	9.51E-11	0.95	4.86	-	1002.6
AHQ-9-7, 5121	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.15E-05	0.97	4.79	-	1618.8
AHQ-9-3, 5138	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	2.85E-05	0.97	5.65	-	1960.4
AHQ-9-3, 4157	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.66E-15	0.97	5.45	-	1304.9
AHQ-9-4, 5149 - 5196	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.25E-06	0.96	4.15	-	1592.8
AHQ-9-5, 5207	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	3.91E-08	0.97	5.54	-	1930.4
AHQ-9-5, 3884	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	4.28E-06	0.67	3.34	-	656.1
AHQ-9-4, 3960	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	7.77E-05	0.92	4.81	-	934.6
AHQ-9-4, 4044 - 4054	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.88E-09	0.93	4.85	-	1319.2
AHQ-9-2, 4150	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.05E-08	0.86	3.91	-	768.5
AHQ-9-5, 3975	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.93E-10	0.96	5.54	-	1247.5
AHQ-9-3, 3953 - 3956	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.78E-09	0.96	5.73	-	1754.5
AHQ-9-2, 4338 - 4395	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	1.12E-05	0.95	5.50	-	1222.2
AHQ-9-2, 3969	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	3.79E-09	0.90	4.15	-	1033.0
AHQ-9-2, 4062 - 4066	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.51E-09	0.96	5.98	-	1224.4
AHQ-9-3, 4044 - 4094	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.70E-06	0.77	3.56	-	622.4
AHQ-9-4, 5566	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	8.22E-09	0.95	4.98	-	1569.8
AHQ-9-4, 5568	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	2.60E-10	0.97	4.94	-	1822.4
AHQ-9-2, 5669	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	2.92E-08	0.97	5.60	-	1856.7
AHQ-9-2, 6142	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	3	9.63E-06	0.96	4.97	-	1644.9
AHQ-9-2, 5597 - 5670	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	5.81E-08	0.98	5.35	-	1688.5
AHQ-9-2, 5737	K.MVGGIAQIIAAQEEM*LR.K	1847.19347	3	6.81E-04	0.95	3.24	-	2892.8
AHQ-9-5, 5589	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	5.59E-05	0.93	3.77	-	1122.7
AHQ-9-6, 5434 - 5507	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.34E-06	0.97	4.77	-	1963.5
AHQ-9-13, 5667	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	8.74E-06	0.48	2.55	-	496.6
AHQ-9-6, 5435	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	4.21E-06	0.95	3.91	-	2204.7
AHQ-9-3, 5520 - 5530	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.95E-06	0.96	4.75	-	1386.6
AHQ-9-2, 5317	K.M*VGGIAQIIAAQEEM*LRK.E	1991.36578	3	4.46E-04	0.91	3.88	-	986.5
AHQ-9-2, 4143	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.89E-04	0.85	3.53	-	482.1
AHQ-9-5, 4157 - 4163	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.43E-04	0.36	2.62	-	264.9
AHQ-9-1, 4463	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.38E-10	0.90	3.40	-	714.2
AHQ-9-5, 4313	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.46E-05	0.87	3.84	-	498.3
AHQ-9-4, 4153	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.24E-10	0.90	4.00	-	596.1
AHQ-9-4, 4070 - 4072	K.NLGTALAELR.T	1058.21367	2	6.24E-05	0.87	3.36	-	818.2
AHQ-9-6, 4037 - 4050	K.NLGTALAELR.T	1058.21367	2	2.33E-04	0.94	3.82	-	1186.6
AHQ-9-3, 4080	K.NLGTALAELR.T	1058.21367	2	2.75E-04	0.82	3.13	-	683.4
AHQ-9-2, 4185	K.NLGTALAELR.T	1058.21367	2	5.47E-04	0.93	3.56	-	1049.4
AHQ-9-5, 4091	K.NLGTALAELR.T	1058.21367	2	1.33E-04	0.75	2.76	-	742.1
AHQ-9-5, 2815	K.PAAVAAENEEIGSHIK.H	1636.78798	3	3.73E-07	0.97	5.65	-	1667.1
AHQ-9-3, 2849	K.PAAVAAENEEIGSHIK.H	1636.78798	3	3.32E-09	0.97	5.21	-	2182.6
AHQ-9-3, 2814 - 2846	K.PAAVAAENEEIGSHIK.H	1636.78798	2	7.89E-08	0.98	5.47	-	2515.3
AHQ-9-2, 2901	K.PAAVAAENEEIGSHIK.H	1636.78798	3	6.96E-08	0.96	4.60	-	1609.0
AHQ-9-4, 2813	K.PAAVAAENEEIGSHIK.H	1636.78798	2	3.41E-06	0.96	4.10	-	1624.8
AHQ-9-2, 2902	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.90E-08	0.97	5.24	-	1648.4
AHQ-9-4, 2721	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.21E-07	0.96	4.77	-	1691.8
AHQ-9-6, 2811 - 2818	K.PAAVAAENEEIGSHIK.H	1636.78798	3	7.58E-05	0.93	4.54	-	1199.1
AHQ-9-6, 3281	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	3.65E-08	0.87	3.90	-	590.6
AHQ-9-2, 3393	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	4.79E-05	0.74	3.08	-	621.2
AHQ-9-5, 3307	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	2.00E-06	0.80	3.77	-	536.9
AHQ-9-5, 3300 - 3303	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	2.73E-05	0.64	3.09	-	459.7
AHQ-9-4, 3289	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	8.36E-07	0.80	3.60	-	511.6
AHQ-9-3, 3313	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	6.32E-05	0.91	4.56	-	572.3
AHQ-9-4, 3300	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.26E-06	0.91	4.32	-	652.7
AHQ-9-1, 3892 - 3946	K.QVAASTAQLLVACK.V	1461.70942	2	1.20E-05	0.86	3.41	-	591.8
AHQ-9-2, 3809	K.QVAASTAQLLVACK.V	1461.70942	2	3.23E-08	0.89	3.58	-	724.8
AHQ-9-2, 3326 - 3327	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	6.39E-05	0.95	5.39	-	1104.7
AHQ-9-4, 3240	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	2.94E-06	0.92	4.90	-	812.5
AHQ-9-5, 3240	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	8.39E-05	0.82	3.96	-	583.1
AHQ-9-2, 3599	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	9.05E-05	0.85	4.17	-	638.4
AHQ-9-3, 3244	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	1.94E-05	0.85	3.85	-	855.0
AHQ-9-3, 3118	K.SIAAATSALVK.A	1032.21612	2	3.65E-05	0.91	3.37	-	1067.4
AHQ-9-7, 3749 - 3758	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	2.14E-08	0.95	5.50	-	1267.6
AHQ-9-8, 4191	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	3.38E-05	0.90	3.70	-	1351.5
AHQ-9-1, 5027	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.13E-06	0.72	3.39	-	310.0
AHQ-9-5, 4869 - 4895	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.65E-07	0.90	4.11	-	604.4
AHQ-9-5, 4339	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.08E-12	0.78	3.55	-	376.3
AHQ-9-6, 4833	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.24E-05	0.72	3.33	-	374.9
AHQ-9-2, 4426	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.39E-07	0.86	3.91	-	500.4
AHQ-9-2, 5113 - 5117	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.84E-06	0.87	4.37	-	391.9
AHQ-9-3, 4978	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.56E-07	0.75	3.11	-	352.3
AHQ-9-2, 5026	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.14E-05	0.84	3.84	-	393.8
AHQ-9-2, 4899 - 4969	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	8.14E-08	0.83	3.66	-	375.6
AHQ-9-4, 4868	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	5.48E-06	0.92	4.49	-	503.8
AHQ-9-4, 5020	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.62E-06	0.82	3.54	-	472.1
AHQ-9-4, 4341	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.56E-05	0.83	3.54	-	598.0
AHQ-9-4, 4860 - 4916	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	9.35E-08	0.86	3.63	-	479.2
AHQ-9-3, 4826 - 4888	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.94E-05	0.81	3.83	-	362.1
AHQ-9-2, 6265 - 6330	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	6.46E-04	0.91	4.28	-	1318.6
AHQ-9-2, 6425	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.34E-11	0.97	6.34	-	1471.3
AHQ-9-8, 6326	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	3.81E-11	0.96	5.79	-	1328.6
AHQ-9-7, 6241 - 6242	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.04E-09	0.97	5.86	-	2032.3

AHQ-9-1, 6410 - 6440	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	1.40E-10	0.96	5.22	-	1841.0
AHQ-9-8, 4234	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.60E-07	0.96	4.69	-	1642.0
AHQ-9-5, 5904 - 5907	K.TLAESALQLLYTAK.E	1522.76793	2	1.57E-10	0.96	4.73	-	1218.6
AHQ-9-4, 5884 - 5900	K.TLAESALQLLYTAK.E	1522.76793	2	1.23E-04	0.97	4.71	-	1274.2
AHQ-9-7, 5813	K.TLAESALQLLYTAK.E	1522.76793	2	5.68E-04	0.90	3.81	-	706.5
AHQ-9-8, 5894	K.TLAESALQLLYTAK.E	1522.76793	2	6.91E-07	0.89	3.34	-	728.2
AHQ-9-3, 5824 - 5834	K.TLAESALQLLYTAK.E	1522.76793	2	7.78E-06	0.94	4.09	-	1010.3
AHQ-9-4, 6045 - 6094	K.TLAESALQLLYTAK.E	1522.76793	2	4.34E-04	0.57	2.69	-	538.1
AHQ-9-2, 6003	K.TLAESALQLLYTAK.E	1522.76793	3	1.91E-06	0.96	5.01	-	1996.4
AHQ-9-3, 5836	K.TLAESALQLLYTAK.E	1522.76793	3	1.17E-06	0.97	5.30	-	2174.1
AHQ-9-2, 5986 - 6066	K.TLAESALQLLYTAK.E	1522.76793	2	7.89E-08	0.94	4.50	-	856.6
AHQ-9-6, 5817	K.TLAESALQLLYTAK.E	1522.76793	2	8.85E-05	0.81	2.82	-	626.3
AHQ-9-1, 6003 - 6030	K.TLAESALQLLYTAK.E	1522.76793	2	1.79E-07	0.93	3.87	-	1011.2
AHQ-9-4, 2632 - 2633	K.TLSHPQQM*ALLDQTK.T	1727.96404	3	3.41E-06	0.91	4.25	-	978.2
AHQ-9-4, 3209 - 3280	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.77E-06	0.90	3.97	-	530.2
AHQ-9-3, 3294	K.TLSHPQQMALLDQTK.T	1711.96464	3	7.64E-06	0.94	4.55	-	1440.6
AHQ-9-5, 3296	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.29E-05	0.91	4.47	-	492.6
AHQ-9-2, 3365	K.TLSHPQQMALLDQTK.T	1711.96464	2	2.17E-04	0.94	4.54	-	816.0
AHQ-9-2, 3518	K.TM*LESAGGLIQTAR.A	1464.67035	2	8.60E-10	0.97	5.02	-	1651.6
AHQ-9-2, 3499 - 3557	K.TM*LESAGGLIQTAR.A	1464.67035	2	8.87E-08	0.95	4.18	-	1429.2
AHQ-9-7, 4077	K.TMLESAGGLIQTAR.A	1448.67095	2	5.31E-04	0.80	3.14	-	1081.6
AHQ-9-3, 4092 - 4106	K.TMLESAGGLIQTAR.A	1448.67095	2	1.10E-04	0.80	2.81	-	1187.3
AHQ-9-2, 4238	K.TMLESAGGLIQTAR.A	1448.67095	3	2.08E-05	0.90	3.90	-	1413.9
AHQ-9-6, 4086	K.TMLESAGGLIQTAR.A	1448.67095	2	5.45E-07	0.93	3.73	-	1570.1
AHQ-9-2, 4183 - 4241	K.TMLESAGGLIQTAR.A	1448.67095	2	2.40E-08	0.95	4.34	-	1647.4
AHQ-9-3, 3402 - 3461	K.TM*LESAGGLIQTAR.A	1464.67035	2	6.62E-04	0.93	4.38	-	1198.9
AHQ-9-4, 4125	K.TMLESAGGLIQTAR.A	1448.67095	2	1.19E-07	0.91	3.52	-	1383.7
AHQ-9-7, 4070 - 4125	K.TM*QFEPSTMVYDACR.I	1854.07511	2	5.21E-04	0.92	4.27	-	702.1
AHQ-9-8, 5031	K.TYGVSFFLVK.E	1161.37395	2	3.83E-06	0.86	3.28	-	585.9
AHQ-9-7, 4980	K.TYGVSFFLVK.E	1161.37395	2	2.46E-06	0.86	3.01	-	773.4
AHQ-9-1, 5948	R.VAGSVTELIQAAEAMK.G	1618.87752	2	6.88E-09	0.67	2.98	-	647.5
AHQ-9-1, 5167	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.22E-05	0.94	3.64	-	1338.4
AHQ-9-7, 5736	R.VAGSVTELIQAAEAMK.G	1618.87752	2	8.27E-08	0.91	3.39	-	1200.5
AHQ-9-4, 5800	R.VAGSVTELIQAAEAMK.G	1618.87752	2	6.62E-05	0.93	3.58	-	1311.2
AHQ-9-3, 4973	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	2.79E-05	0.82	2.62	-	1121.8
AHQ-9-4, 5000	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	3.07E-05	0.91	3.65	-	1048.6
AHQ-9-6, 5741	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.98E-08	0.96	4.53	-	1263.9
AHQ-9-2, 5045 - 5105	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.69E-04	0.94	3.99	-	1353.1
AHQ-9-2, 5913	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.47E-05	0.84	3.26	-	901.4
AHQ-9-5, 5828	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.14E-08	0.96	4.24	-	1805.5
AHQ-9-2, 3769	K.VEHGSVALPAIMR.S	1380.64144	2	1.64E-07	0.89	3.05	-	1057.2
AHQ-9-2, 5474 - 5549	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	3.81E-07	0.92	4.84	-	1116.6
AHQ-9-3, 5398 - 5452	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.01E-05	0.96	5.19	-	923.6
AHQ-9-3, 5309 - 5345	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	7.71E-06	0.77	3.51	-	1153.7
AHQ-9-3, 5240 - 5320	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.11E-06	0.93	4.75	-	570.5
AHQ-9-1, 5571 - 5627	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	5.36E-04	0.78	3.39	-	1054.7
AHQ-9-2, 5463 - 5543	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.45E-13	0.95	5.62	-	523.0
AHQ-9-1, 5576	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.28E-08	0.94	4.65	-	937.6
AHQ-9-2, 5346 - 5407	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.34E-11	0.94	4.74	-	824.9
AHQ-9-5, 5401 - 5472	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.76E-11	0.94	4.74	-	718.6
AHQ-9-2, 5345 - 5401	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	2.94E-04	0.95	5.06	-	1159.5
AHQ-9-7, 5373	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.07E-06	0.76	3.53	-	491.5
AHQ-9-4, 5368 - 5445	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	3.49E-08	0.93	4.72	-	1257.3
AHQ-9-4, 5293 - 5365	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.87E-09	0.93	4.89	-	583.2
AHQ-9-6, 5385	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.27E-08	0.95	4.70	-	895.1
AHQ-9-5, 3725	K.VGDDPAVWQLK.N	1228.37879	2	3.27E-07	0.85	3.09	-	723.2
AHQ-9-4, 3722	K.VGDDPAVWQLK.N	1228.37879	2	6.11E-09	0.94	3.99	-	939.0
AHQ-9-3, 3726	K.VGDDPAVWQLK.N	1228.37879	2	3.60E-07	0.94	4.11	-	924.5
AHQ-9-6, 3689	K.VGDDPAVWQLK.N	1228.37879	2	6.76E-08	0.92	3.67	-	835.5
AHQ-9-2, 3779 - 3837	K.VGDDPAVWQLK.N	1228.37879	2	6.42E-09	0.92	3.68	-	866.2
AHQ-9-4, 2518	K.VLGEAM*TGISQNAK.N	1435.62901	2	2.01E-06	0.93	3.27	-	1335.6
AHQ-9-2, 3206	K.VLGEAMTGISQNAK.N	1419.62961	2	3.79E-06	0.93	3.94	-	1226.8
AHQ-9-3, 2545	K.VLGEAM*TGISQNAK.N	1435.62901	2	2.04E-04	0.87	2.98	-	950.1
AHQ-9-2, 2501	K.VLGEAM*TGISQNAK.N	1435.62901	2	6.39E-04	0.95	4.07	-	1346.9
AHQ-9-4, 2421 - 2433	K.VLGEAM*TGISQNAK.N	1435.62901	2	5.70E-04	0.97	4.50	-	1946.9
AHQ-9-4, 3061 - 3128	K.VLGEAMTGISQNAK.N	1419.62961	2	4.79E-05	0.95	3.82	-	1764.0
AHQ-9-2, 4681	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	4.11E-11	0.88	4.55	-	652.7
AHQ-9-3, 4482 - 4548	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	6.36E-10	0.95	5.63	-	834.5
AHQ-9-4, 4576	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	8.28E-07	0.89	4.50	-	605.9
AHQ-9-4, 1913 - 1978	K.VLVQNAAGSQEK.L	1244.37976	2	2.96E-04	0.82	3.07	-	609.0
AHQ-9-6, 1839 - 1899	K.VLVQNAAGSQEK.L	1244.37976	2	2.54E-06	0.80	3.10	-	743.3
AHQ-9-2, 1927	K.VLVQNAAGSQEK.L	1244.37976	2	9.05E-07	0.92	3.53	-	949.3
AHQ-9-3, 1881	K.VLVQNAAGSQEK.L	1244.37976	2	2.16E-06	0.84	3.18	-	833.5
AHQ-9-4, 1801 - 1857	K.VLVQNAAGSQEK.L	1244.37976	2	1.81E-05	0.93	3.74	-	1081.0
AHQ-9-5, 1841 - 1900	K.VLVQNAAGSQEK.L	1244.37976	2	6.12E-04	0.83	3.18	-	664.6
AHQ-9-4, 4512	K.VMVTNVTSLLK.T	1205.49322	2	2.19E-07	0.92	4.21	-	785.8
AHQ-9-2, 4610 - 4611	K.VMVTNVTSLLK.T	1205.49322	2	1.94E-06	0.91	4.22	-	792.1
AHQ-9-6, 4425	K.VMVTNVTSLLK.T	1205.49322	2	2.66E-04	0.81	3.05	-	631.9
AHQ-9-1, 4384	K.VM*VTNVTSLLK.T	1221.49262	2	3.06E-04	0.68	2.69	-	528.5
AHQ-9-3, 4170	K.VM*VTNVTSLLK.T	1221.49262	2	9.07E-04	0.78	3.07	-	760.8
AHQ-9-5, 4497	K.VMVTNVTSLLK.T	1205.49322	2	5.18E-04	0.81	3.18	-	591.6
AHQ-9-2, 4289 - 4290	K.VM*VTNVTSLLK.T	1221.49262	2	7.56E-04	0.91	3.76	-	884.6
AHQ-9-3, 4500	K.VMVTNVTSLLK.T	1205.49322	2	5.58E-05	0.90	3.97	-	812.3
AHQ-9-4, 4194	K.VM*VTNVTSLLK.T	1221.49262	2	7.10E-05	0.86	3.39	-	798.5
AHQ-9-7, 4112	K.VM*VTNVTSLLK.T	1221.49262	2	5.04E-04	0.74	2.98	-	596.2
AHQ-9-4, 2876	R.VQELGHGCAALVTK.A	1484.70307	2	9.02E-09	0.97	4.68	-	1749.3
AHQ-9-3, 2900	R.VQELGHGCAALVTK.A	1484.70307	2	1.23E-04	0.98	4.91	-	1964.6
AHQ-9-5, 2877 - 2884	R.VQELGHGCAALVTK.A	1484.70307	2	1.58E-08	0.97	4.79	-	1331.9
AHQ-9-6, 2861	R.VQELGHGCAALVTK.A	1484.70307	2	1.15E-06	0.96	4.71	-	1386.6
AHQ-9-3, 2842 - 2905	R.VQELGHGCAALVTK.A	1484.70307	2	2.21E-04	0.94	3.97	-	1110.2
AHQ-9-2, 2958	R.VQELGHGCAALVTK.A	1484.70307	2	1.43E-08	0.96	4.51	-	1220.8
AHQ-9-7, 2852	R.VQELGHGCAALVTK.A	1484.70307	2	4.70E-04	0.62	2.80	-	353.1
AHQ-9-5, 2864	K.VSHVLAALQAGNR.G	1336.52525	2	8.01E-11	0.97	4.10	-	1716.6
AHQ-9-2, 2939	K.VSHVLAALQAGNR.G	1336.52525	2	7.24E-07	0.97	4.80	-	1644.8
AHQ-9-3, 2888	K.VSHVLAALQAGNR.G	1336.52525	2	2.35E-10	0.97	4.77	-	1928.9
AHQ-9-6, 2839 - 2846	K.VSHVLAALQAGNR.G	1336.52525	2	7.76E-11	0.97	4.69	-	1887.8
AHQ-9-4, 2850	K.VSHVLAALQAGNR.G	1336.52525	2	7.39E-09	0.97	4.62	-	1668.2
AHQ-9-6, 6030	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.50E-06	0.90	3.66	-	820.0
AHQ-9-2, 6319	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	6.61E-05	0.79	3.71	-	421.1
AHQ-9-2, 6205	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	3.07E-06	0.84	3.54	-	958.6
AHQ-9-7, 5372	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.74E-06	0.89	3.61	-	1068.0
AHQ-9-1, 6222	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.30E-06	0.79	3.19	-	551.4
AHQ-9-3, 6026	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	7.43E-05	0.88	3.74	-	698.2
AHQ-9-7, 6010	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	5.75E-06	0.95	4.90	-	948.9
AHQ-9-4, 6100	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	4.28E-04	0.87	4.01	-	511.1
AHQ-9-1, 5575 - 5582	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.67E-06	0.97	5.64	-	1539.6
AHQ-9-3, 6030	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	5.61E-07	0.84	3.64	-	904.6

AHQ-9-1, 5567	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.27E-06	0.90	4.12	-	803.9
AHQ-9-4, 5444 - 5465	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	8.88E-09	0.96	5.20	-	1326.4
AHQ-9-6, 5386	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	4.59E-05	0.94	4.72	-	776.9
AHQ-9-5, 5453	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.56E-07	0.95	4.56	-	1106.1
AHQ-9-3, 5392 - 5400	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.21E-06	0.91	3.85	-	1294.7
AHQ-9-2, 6197	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.01E-04	0.90	4.05	-	676.9
AHQ-9-3, 5390	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	5.36E-04	0.92	3.98	-	1037.5
AHQ-9-5, 6119	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	1.98E-06	0.94	4.64	-	914.1
AHQ-9-9, 4159	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	6.15E-04	0.69	3.07	-	346.5
AHQ-9-2, 4366	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.99E-05	0.90	4.32	-	376.5
AHQ-9-5, 4363	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.48E-06	0.94	4.79	-	680.3
AHQ-9-12, 4332	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.56E-05	0.86	3.64	-	558.0
AHQ-9-4, 4288	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.39E-05	0.85	3.70	-	458.1
AHQ-9-4, 4380	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.90E-07	0.88	4.11	-	518.6
AHQ-9-4, 4385 - 4388	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	8.48E-07	0.92	4.71	-	1212.3
AHQ-9-1, 4535 - 4536	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.32E-07	0.93	4.78	-	613.3
AHQ-9-6, 4306	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.66E-07	0.96	5.28	-	888.3
AHQ-9-8, 4331 - 4346	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	3.89E-08	0.95	5.10	-	805.2
AHQ-9-3, 4350	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.25E-06	0.95	4.90	-	952.1
AHQ-9-2, 4466	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.23E-07	0.93	4.79	-	609.8
AHQ-9-7, 4288	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.38E-08	0.93	4.73	-	668.7
gi|4503745|ref|NP_001447.1|	filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act			1.11E-14	90.24	1040.35	54.70	280757.4
AHQ-9-8, 4979	R.AEAGVPAEFSIWTR.E	1534.69735	2	8.79E-05	0.77	3.06	-	465.1
AHQ-9-1, 2898	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.29E-05	0.94	3.24	-	1566.6
AHQ-9-2, 2765	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	7.65E-10	0.93	3.27	-	1322.2
AHQ-9-3, 2714	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	5.80E-06	0.88	3.06	-	1080.3
AHQ-9-6, 2690 - 2763	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.16E-06	0.75	2.87	-	829.2
AHQ-9-4, 2692	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	9.53E-09	0.95	3.59	-	1643.4
AHQ-9-5, 2692 - 2695	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.20E-05	0.95	3.80	-	1616.1
AHQ-9-7, 2680	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	2.35E-07	0.93	3.23	-	1368.5
AHQ-9-4, 2980	K.AGNNM*LLVGVHGPR.T	1451.67973	2	7.92E-05	0.74	2.53	-	603.3
AHQ-9-14-, 2846 - 2901	K.AGNNM*LLVGVHGPR.T	1451.67973	2	1.63E-05	0.84	3.21	-	655.7
AHQ-9-14-, 2898 - 2914	K.AGNNM*LLVGVHGPR.T	1451.67973	3	3.53E-05	0.89	3.61	-	1349.6
AHQ-9-2, 1911	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	9.30E-06	0.48	2.59	-	416.4
AHQ-9-4, 1790 - 1858	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	1.17E-04	0.82	3.08	-	788.7
AHQ-9-3, 2438	K.AGVAPLQVK.V	883.07036	2	2.06E-05	0.73	2.71	-	562.8
AHQ-9-4, 2413	K.AGVAPLQVK.V	883.07036	2	3.40E-05	0.68	2.78	-	397.8
AHQ-9-2, 6511 - 6579	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	5.40E-04	0.91	4.70	-	968.4
AHQ-9-2, 6293 - 6295	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	4.38E-04	0.81	3.78	-	630.3
AHQ-9-4, 2745	K.AHVVPCFDASK.V	1232.39073	2	7.69E-05	0.68	2.53	-	572.6
AHQ-9-2, 2805	K.AHVVPCFDASK.V	1232.39073	2	4.48E-06	0.81	2.82	-	680.2
AHQ-9-1, 5784 - 5823	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.58E-06	0.79	3.56	-	584.3
AHQ-9-6, 5551 - 5630	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.10E-04	0.88	4.73	-	449.4
AHQ-9-4, 5764	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.32E-07	0.93	4.53	-	912.7
AHQ-9-7, 5626	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	2.30E-07	0.82	3.58	-	560.1
AHQ-9-5, 5712 - 5776	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.14E-09	0.88	4.43	-	677.2
AHQ-9-6, 5637	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	4.16E-04	0.76	3.44	-	380.7
AHQ-9-4, 3250 - 3308	R.ANLPQSFQVDTSK.A	1435.56409	2	5.12E-09	0.76	3.17	-	412.9
AHQ-9-6, 3259 - 3273	R.ANLPQSFQVDTSK.A	1435.56409	2	3.75E-11	0.88	3.25	-	752.8
AHQ-9-1, 3416 - 3475	R.ANLPQSFQVDTSK.A	1435.56409	2	1.30E-04	0.44	2.57	-	488.1
AHQ-9-4, 3332 - 3397	R.APSVANVGSHCDLSLK.I	1656.84249	2	3.47E-05	0.88	3.84	-	706.1
AHQ-9-4, 1969	K.ATCAPQHGAPGPGPADASK.V	1791.92336	3	1.05E-08	0.89	3.53	-	1338.0
AHQ-9-4, 1908 - 1964	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	2.36E-05	0.82	3.73	-	468.0
AHQ-9-6, 3558 - 3559	R.AWGPGLEGGVVGK.S	1227.39403	2	1.60E-06	0.93	3.90	-	952.7
AHQ-9-3, 3592	R.AWGPGLEGGVVGK.S	1227.39403	2	1.82E-05	0.92	3.50	-	996.3
AHQ-9-4, 3597	R.AWGPGLEGGVVGK.S	1227.39403	2	1.21E-05	0.79	3.31	-	557.6
AHQ-9-7, 3556	R.AWGPGLEGGVVGK.S	1227.39403	2	5.98E-06	0.79	3.12	-	645.0
AHQ-9-1, 3778	R.AWGPGLEGGVVGK.S	1227.39403	2	1.18E-05	0.94	3.79	-	1061.5
AHQ-9-2, 3685 - 3687	R.AWGPGLEGGVVGK.S	1227.39403	2	7.04E-06	0.93	3.80	-	956.0
AHQ-9-5, 3587	R.AWGPGLEGGVVGK.S	1227.39403	2	6.87E-04	0.93	3.60	-	1152.3
AHQ-9-2, 2843	R.AYGPGIEPTGNM*VK.K	1450.64214	2	5.33E-07	0.77	3.30	-	390.5
AHQ-9-2, 3422	R.AYGPGIEPTGNMVK.K	1434.64274	2	4.90E-05	0.49	2.62	-	411.9
AHQ-9-5, 2760	R.AYGPGIEPTGNM*VK.K	1450.64214	2	1.21E-04	0.55	2.53	-	391.2
AHQ-9-5, 3212	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.18E-07	0.90	3.48	-	838.1
AHQ-9-2, 5681	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.93E-08	0.90	3.90	-	1128.2
AHQ-9-3, 5521 - 5590	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	8.44E-05	0.92	4.32	-	620.3
AHQ-9-1, 5707	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.89E-04	0.81	3.42	-	716.6
AHQ-9-1, 5691	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.80E-06	0.84	3.45	-	538.1
AHQ-9-2, 5673	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	4.35E-08	0.91	3.78	-	863.5
AHQ-9-3, 4664	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	6.84E-11	0.94	5.13	-	609.6
AHQ-9-1, 4843	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	4.11E-04	0.84	3.61	-	529.0
AHQ-9-5, 4700	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	7.41E-07	0.85	4.10	-	513.8
AHQ-9-2, 4789	R.CSYQPTM*EGVHTVHVTFAGVPIPR.S	2702.06173	3	2.24E-08	0.84	4.03	-	386.7
AHQ-9-1, 3894 - 3966	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	8.69E-06	0.87	3.74	-	894.4
AHQ-9-2, 3907	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	2.11E-04	0.89	3.17	-	1232.9
AHQ-9-4, 3804 - 3876	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	3.51E-04	0.90	4.13	-	773.7
AHQ-9-5, 3808 - 3867	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.17E-04	0.75	3.32	-	832.1
AHQ-9-3, 3768 - 3797	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	8.35E-04	0.88	2.94	-	1065.6
AHQ-9-2, 4654 - 4662	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	1.18E-07	0.96	4.36	-	1479.6
AHQ-9-3, 4537	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	9.08E-08	0.94	3.99	-	1416.6
AHQ-9-7, 4117	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.65E-06	0.82	3.76	-	648.6
AHQ-9-6, 4137	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.84E-11	0.94	4.54	-	1293.1
AHQ-9-3, 4174 - 4180	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.75E-08	0.95	4.63	-	1300.4
AHQ-9-3, 4182	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	1.98E-06	0.91	3.46	-	1282.2
AHQ-9-12, 4172	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.49E-04	0.72	2.84	-	856.4
AHQ-9-2, 4235 - 4294	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.78E-08	0.94	4.59	-	1135.3
AHQ-9-1, 4371	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.83E-07	0.95	4.47	-	1347.2
AHQ-9-1, 4383	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	5.78E-09	0.86	3.57	-	917.9
AHQ-9-5, 4156 - 4189	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.07E-08	0.94	4.11	-	1186.8
AHQ-9-8, 4162	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	8.82E-07	0.76	3.37	-	648.8
AHQ-9-4, 4192	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.50E-07	0.92	4.25	-	1120.6
AHQ-9-1, 4422	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.44E-09	0.95	3.88	-	1700.0
AHQ-9-2, 4363	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	8.89E-08	0.95	4.03	-	1488.0
AHQ-9-5, 4047	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	2.82E-05	0.81	3.07	-	1069.6
AHQ-9-4, 4042 - 4097	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.31E-04	0.91	4.21	-	935.2
AHQ-9-5, 4259	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	6.61E-08	0.94	4.02	-	1385.1
AHQ-9-3, 4248	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	8.67E-05	0.83	3.28	-	1076.9
AHQ-9-4, 4260 - 4324	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.14E-08	0.94	4.34	-	1124.6
AHQ-9-8, 4252	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.52E-06	0.91	4.18	-	849.9
AHQ-9-6, 4214	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	6.39E-08	0.89	3.89	-	897.2
AHQ-9-2, 2094	R.DAPQDFHPDR.V	1198.22650	2	7.75E-06	0.83	2.83	-	750.6
AHQ-9-4, 4488	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	3.35E-07	0.84	4.36	-	448.0
AHQ-9-2, 4595	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	7.60E-05	0.68	3.41	-	468.1
AHQ-9-5, 4651	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	9.67E-04	0.90	4.32	-	789.8
AHQ-9-4, 4640	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	4.50E-04	0.58	3.61	-	248.0
AHQ-9-5, 4495	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	6.43E-06	0.91	4.47	-	762.7
AHQ-9-3, 4464 - 4521	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.47E-05	0.64	3.49	-	405.2

AHQ-9-6, 2562	K.DKGEYTLVVK.W	1152.32223	2	1.01E-06	0.81	2.70	-	678.4
AHQ-9-5, 3155	K.DNGNGTYSCSYVPR.K	1591.64109	2	2.00E-04	0.87	3.27	-	896.1
AHQ-9-5, 3083	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	5.51E-07	0.84	3.28	-	664.1
AHQ-9-2, 3166 - 3226	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.94E-04	0.88	3.43	-	909.0
AHQ-9-3, 3057 - 3116	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.44E-06	0.96	4.89	-	1304.3
AHQ-9-6, 3323 - 3325	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	7.34E-06	0.94	4.06	-	1119.3
AHQ-9-5, 3351 - 3419	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	7.71E-05	0.86	3.19	-	987.0
AHQ-9-7, 3316 - 3389	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	8.26E-05	0.90	3.38	-	1199.2
AHQ-9-4, 3352 - 3396	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	5.44E-06	0.83	3.10	-	956.2
AHQ-9-8, 3311	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	4.51E-05	0.87	3.44	-	864.4
AHQ-9-1, 3544	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.40E-05	0.96	4.21	-	1532.9
AHQ-9-2, 3441	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.43E-05	0.88	3.48	-	919.0
AHQ-9-1, 2860	R.EATTEFSVDAR.A	1226.27493	2	1.23E-05	0.89	3.28	-	955.5
AHQ-9-3, 2684	R.EATTEFSVDAR.A	1226.27493	2	1.45E-04	0.75	2.72	-	577.8
AHQ-9-2, 2730 - 2801	R.EATTEFSVDAR.A	1226.27493	2	8.62E-04	0.68	2.79	-	687.7
AHQ-9-3, 5644 - 5700	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.73E-07	0.89	4.60	-	613.0
AHQ-9-2, 5779 - 5837	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.25E-08	0.92	4.89	-	732.4
AHQ-9-4, 5721 - 5749	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.70E-05	0.88	4.37	-	653.4
AHQ-9-3, 5756 - 5814	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.30E-08	0.95	5.67	-	1010.5
AHQ-9-7, 5700 - 5766	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	8.08E-07	0.84	4.16	-	641.3
AHQ-9-2, 5873 - 5929	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.38E-06	0.91	4.84	-	668.7
AHQ-9-6, 5709	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.83E-06	0.87	4.44	-	568.4
AHQ-9-5, 5743 - 5801	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.59E-08	0.96	6.38	-	994.0
AHQ-9-4, 5804 - 5860	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.42E-07	0.89	4.17	-	785.0
AHQ-9-12, 4713 - 4724	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.53E-04	0.51	2.81	-	638.0
AHQ-9-3, 4749	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	1.02E-06	0.97	5.41	-	1924.2
AHQ-9-3, 4682 - 4737	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.08E-10	0.92	4.20	-	1047.5
AHQ-9-5, 4704 - 4781	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.59E-05	0.34	2.74	-	382.0
AHQ-9-11, 4663	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.25E-06	0.71	2.86	-	620.5
AHQ-9-2, 4795 - 4861	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.07E-05	0.82	4.10	-	699.5
AHQ-9-8, 4734 - 4762	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.74E-07	0.91	3.68	-	811.8
AHQ-9-1, 4838 - 4912	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	5.03E-06	0.87	3.99	-	693.8
AHQ-9-7, 4634 - 4694	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.20E-06	0.46	3.02	-	255.3
AHQ-9-4, 4690 - 4766	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.16E-04	0.67	3.40	-	579.5
AHQ-9-6, 4715	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	4.54E-06	0.83	3.48	-	766.1
AHQ-9-1, 3646 - 3710	K.FADQHVPGSPFSVK.V	1516.68203	2	2.81E-06	0.83	3.21	-	586.7
AHQ-9-6, 3410	K.FADQHVPGSPFSVK.V	1516.68203	3	4.10E-06	0.94	3.76	-	1607.0
AHQ-9-4, 3453	K.FADQHVPGSPFSVK.V	1516.68203	3	1.19E-06	0.93	4.28	-	1047.2
AHQ-9-2, 3549	K.FADQHVPGSPFSVK.V	1516.68203	2	3.03E-09	0.87	3.24	-	591.1
AHQ-9-4, 3448	K.FADQHVPGSPFSVK.V	1516.68203	2	5.81E-06	0.83	3.61	-	522.6
AHQ-9-3, 3462	K.FADQHVPGSPFSVK.V	1516.68203	3	3.63E-11	0.89	3.98	-	861.9
AHQ-9-5, 3448	K.FADQHVPGSPFSVK.V	1516.68203	3	3.92E-08	0.89	3.49	-	1204.8
AHQ-9-1, 5240 - 5318	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	8.20E-10	0.92	5.06	-	735.5
AHQ-9-12, 5082 - 5089	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.51E-04	0.84	4.09	-	430.1
AHQ-9-3, 5081 - 5146	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.47E-06	0.93	4.78	-	860.3
AHQ-9-1, 5326 - 5387	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.55E-06	0.89	4.20	-	890.5
AHQ-9-2, 5223 - 5297	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.83E-08	0.91	5.13	-	735.8
AHQ-9-2, 5353 - 5419	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.02E-04	0.78	3.75	-	503.4
AHQ-9-5, 5141 - 5184	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.69E-06	0.96	5.51	-	1338.1
AHQ-9-2, 5271	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	2	6.10E-07	0.95	4.29	-	1171.9
AHQ-9-2, 5086 - 5145	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.24E-05	0.89	4.55	-	838.6
AHQ-9-6, 5059 - 5113	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.67E-07	0.92	5.24	-	733.6
AHQ-9-13-, 5106	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	6.67E-05	0.87	4.44	-	677.6
AHQ-9-1, 5032	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	8.97E-04	0.81	3.22	-	532.1
AHQ-9-7, 4793	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	7.55E-05	0.84	3.14	-	648.1
AHQ-9-4, 3538	K.FNGTHIPGSPFK.I	1302.46259	2	4.08E-06	0.75	3.21	-	516.0
AHQ-9-4, 3084	R.FVPAEMGTHTVSVK.Y	1503.74821	2	7.39E-07	0.81	2.81	-	583.2
AHQ-9-5, 3085	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	1.28E-04	0.47	2.73	-	347.0
AHQ-9-4, 2456 - 2478	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	1.42E-05	0.77	3.47	-	273.8
AHQ-9-5, 3080	R.FVPAEMGTHTVSVK.Y	1503.74821	2	5.10E-07	0.86	2.64	-	801.0
AHQ-9-2, 5551 - 5602	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	2.79E-05	0.94	4.79	-	783.8
AHQ-9-4, 5505	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	2.45E-04	0.67	3.23	-	434.4
AHQ-9-1, 5606 - 5672	R.GAGSYTIM*VLFADQATPTSPIR.V	2313.61563	2	7.44E-05	0.82	3.73	-	482.4
AHQ-9-8, 3303 - 3315	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.13E-04	0.82	3.73	-	598.4
AHQ-9-2, 3399 - 3457	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.55E-06	0.84	3.86	-	599.0
AHQ-9-6, 3314	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.70E-06	0.91	4.35	-	693.7
AHQ-9-5, 3339	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	9.57E-04	0.80	3.12	-	690.2
AHQ-9-1, 3530 - 3532	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	4.40E-06	0.93	4.03	-	891.4
AHQ-9-1, 3675 - 3679	K.GKLDVQFSGLTK.G	1293.49392	2	1.48E-04	0.90	3.66	-	911.8
AHQ-9-6, 4590 - 4619	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.85E-05	0.45	2.95	-	199.2
AHQ-9-2, 4569 - 4629	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.80E-07	0.90	3.94	-	934.0
AHQ-9-2, 4847 - 4906	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.00E-06	0.93	4.48	-	907.3
AHQ-9-3, 4581 - 4637	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	3	4.20E-05	0.89	4.22	-	690.9
AHQ-9-2, 4702	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	5.60E-05	0.84	4.02	-	512.1
AHQ-9-3, 2326	K.GTVEPQLEAR.G	1100.20741	2	8.35E-04	0.62	2.78	-	387.9
AHQ-9-5, 2263 - 2297	K.GTVEPQLEAR.G	1100.20741	2	1.87E-05	0.72	2.86	-	488.3
AHQ-9-2, 2371 - 2399	K.GTVEPQLEAR.G	1100.20741	2	6.58E-04	0.69	2.83	-	490.8
AHQ-9-3, 4856	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.09E-04	0.87	3.54	-	835.3
AHQ-9-2, 4981	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.03E-08	0.96	4.60	-	1506.2
AHQ-9-2, 4983	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	5.49E-04	0.75	3.60	-	759.8
AHQ-9-3, 4857	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	1.54E-06	0.90	3.33	-	1818.9
AHQ-9-4, 3725	R.IANLQTDLSDGLR.L	1416.56231	2	1.60E-07	0.94	3.79	-	1208.4
AHQ-9-5, 4079	R.IANLQTDLSDGLR.L	1416.56231	2	6.97E-05	0.92	3.99	-	797.6
AHQ-9-5, 3721	R.IANLQTDLSDGLR.L	1416.56231	2	3.98E-06	0.87	3.32	-	862.4
AHQ-9-1, 3886	R.IANLQTDLSDGLR.L	1416.56231	2	5.59E-05	0.90	3.15	-	889.0
AHQ-9-13-, 4049 - 4104	R.IANLQTDLSDGLR.L	1416.56231	2	3.01E-08	0.85	3.16	-	766.5
AHQ-9-4, 4068	R.IANLQTDLSDGLR.L	1416.56231	2	1.08E-06	0.93	3.65	-	985.7
AHQ-9-1, 4246	R.IANLQTDLSDGLR.L	1416.56231	2	6.80E-05	0.94	4.04	-	932.8
AHQ-9-6, 4003 - 4031	R.IANLQTDLSDGLR.L	1416.56231	2	1.36E-04	0.93	3.46	-	1337.1
AHQ-9-13, 4251 - 4263	R.IANLQTDLSDGLR.L	1416.56231	2	1.10E-05	0.94	4.42	-	995.0
AHQ-9-11, 4001	R.IANLQTDLSDGLR.L	1416.56231	2	1.39E-06	0.94	3.59	-	1277.9
AHQ-9-3, 4064 - 4126	R.IANLQTDLSDGLR.L	1416.56231	2	9.21E-06	0.95	4.05	-	1306.8
AHQ-9-3, 3709	R.IANLQTDLSDGLR.L	1416.56231	2	7.35E-08	0.95	3.54	-	1432.5
AHQ-9-7, 4012	R.IANLQTDLSDGLR.L	1416.56231	2	2.14E-07	0.94	3.70	-	1222.4
AHQ-9-2, 3815	R.IANLQTDLSDGLR.L	1416.56231	2	1.98E-08	0.92	3.96	-	809.6
AHQ-9-2, 4069	R.IANLQTDLSDGLR.L	1416.56231	2	6.13E-04	0.92	3.61	-	1175.4
AHQ-9-6, 3677	R.IANLQTDLSDGLR.L	1416.56231	2	3.57E-06	0.79	3.29	-	715.7
AHQ-9-2, 4151 - 4189	R.IANLQTDLSDGLR.L	1416.56231	2	2.04E-05	0.93	4.33	-	854.3
AHQ-9-1, 5258	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.43E-12	0.98	5.59	-	1652.4
AHQ-9-6, 5057	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	4.54E-10	0.97	5.60	-	1393.6
AHQ-9-2, 4039	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.13E-04	0.96	4.58	-	1203.5
AHQ-9-3, 5080	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.22E-09	0.96	4.77	-	1205.3
AHQ-9-5, 3931 - 3988	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	5.63E-07	0.97	5.30	-	1695.3
AHQ-9-7, 5052	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	7.91E-09	0.97	5.78	-	1375.1
AHQ-9-4, 3940 - 3978	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	3	4.29E-04	0.83	3.88	-	724.4
AHQ-9-4, 5117	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.11E-07	0.97	5.03	-	1408.5
AHQ-9-3, 3901 - 3957	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	2.81E-05	0.95	4.30	-	1182.4

AHQ-9-5, 5139	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.90E-05	0.82	3.30	-	692.4
AHQ-9-5, 5131	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	8.50E-07	0.65	3.61	-	511.4
AHQ-9-7, 3880	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.86E-04	0.96	4.97	-	1296.3
AHQ-9-5, 5123	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.19E-07	0.97	5.01	-	1661.0
AHQ-9-4, 3936	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.42E-06	0.97	5.54	-	1448.6
AHQ-9-6, 3890	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.10E-05	0.96	5.28	-	1262.4
AHQ-9-2, 5225	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.69E-10	0.95	5.14	-	925.3
AHQ-9-4, 2598 - 2618	K.IVGPSGAAVPCK.V	1157.36530	2	2.75E-07	0.83	2.93	-	678.8
AHQ-9-2, 2657	K.IVGPSGAAVPCK.V	1157.36530	2	4.10E-05	0.79	3.06	-	730.3
AHQ-9-3, 2616	K.IVGPSGAAVPCK.V	1157.36530	2	9.04E-07	0.88	3.12	-	838.6
AHQ-9-5, 2599	K.IVGPSGAAVPCK.V	1157.36530	2	8.47E-06	0.73	3.07	-	645.1
AHQ-9-2, 4093 - 4109	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	5.54E-11	0.94	4.48	-	1597.6
AHQ-9-2, 4190	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	8.69E-10	0.87	3.70	-	993.0
AHQ-9-5, 3999	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.39E-05	0.92	4.50	-	1029.5
AHQ-9-3, 3969 - 4024	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.59E-06	0.90	4.13	-	1031.0
AHQ-9-4, 4098	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.00E-10	0.94	4.34	-	1394.0
AHQ-9-3, 3996	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	7.22E-06	0.77	3.44	-	342.3
AHQ-9-1, 4166	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.85E-11	0.95	5.18	-	1445.8
AHQ-9-3, 4081	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.21E-06	0.89	4.03	-	969.4
AHQ-9-4, 4214	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	8.87E-05	0.84	4.24	-	627.3
AHQ-9-8, 4176	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	9.37E-11	0.96	5.42	-	1555.6
AHQ-9-1, 4404	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	3.33E-10	0.98	6.19	-	2149.5
AHQ-9-4, 4146 - 4204	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	5.62E-11	0.96	5.59	-	1404.5
AHQ-9-2, 4275 - 4339	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.15E-05	0.96	5.57	-	1493.4
AHQ-9-5, 4205	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	2.47E-05	0.81	3.44	-	566.2
AHQ-9-6, 4095 - 4149	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	3.15E-08	0.95	4.60	-	1588.6
AHQ-9-5, 4064 - 4140	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.13E-10	0.97	6.27	-	1987.2
AHQ-9-5, 4195	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	3.65E-11	0.96	5.57	-	1607.0
AHQ-9-3, 4208	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	3.15E-05	0.96	5.07	-	1818.2
AHQ-9-4, 4216	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	5.94E-06	0.82	3.47	-	525.2
AHQ-9-3, 3513	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	9.02E-04	0.95	4.40	-	1560.6
AHQ-9-2, 3502	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	3.87E-06	0.94	4.56	-	1130.1
AHQ-9-2, 3590 - 3645	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.10E-06	0.93	4.30	-	1228.9
AHQ-9-3, 3416	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	5.65E-06	0.96	5.14	-	1565.0
AHQ-9-2, 3923	K.LDVQFSGLTK.G	1108.26945	2	1.70E-06	0.92	3.59	-	924.4
AHQ-9-3, 3814	K.LDVQFSGLTK.G	1108.26945	2	1.47E-05	0.91	3.26	-	1036.7
AHQ-9-6, 3775	K.LDVQFSGLTK.G	1108.26945	2	4.84E-06	0.78	2.74	-	727.1
AHQ-9-1, 6302	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	1.60E-05	0.75	3.25	-	695.4
AHQ-9-2, 6267	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	1.40E-06	0.87	4.08	-	821.8
AHQ-9-4, 4638	K.LPQLPITNFSR.D	1286.50461	2	1.18E-05	0.87	3.02	-	866.8
AHQ-9-2, 4879	K.LPQLPITNFSR.D	1286.50461	2	1.94E-04	0.85	2.66	-	927.1
AHQ-9-3, 4757	K.LPQLPITNFSR.D	1286.50461	2	1.35E-06	0.85	3.21	-	618.3
AHQ-9-5, 4795	K.LPQLPITNFSR.D	1286.50461	2	4.60E-05	0.76	3.07	-	557.6
AHQ-9-1, 4792	K.LPQLPITNFSR.D	1286.50461	2	2.29E-04	0.91	3.25	-	860.4
AHQ-9-2, 4726	K.LPQLPITNFSR.D	1286.50461	2	2.02E-05	0.91	3.21	-	858.0
AHQ-9-6, 4567 - 4574	K.LPQLPITNFSR.D	1286.50461	2	1.69E-05	0.89	3.52	-	612.2
AHQ-9-5, 5063	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.48E-04	0.93	3.97	-	893.2
AHQ-9-2, 5111 - 5169	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	1.57E-08	0.95	4.71	-	1272.3
AHQ-9-3, 5013	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	2.91E-06	0.94	4.82	-	787.3
AHQ-9-4, 5056	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.90E-08	0.94	4.83	-	820.1
AHQ-9-4, 5052	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.26E-04	0.78	2.93	-	656.2
AHQ-9-6, 4910 - 4981	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	7.34E-04	0.83	3.78	-	476.4
AHQ-9-3, 5024 - 5092	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.57E-06	0.96	5.31	-	1471.9
AHQ-9-1, 5190	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.19E-07	0.94	3.97	-	1175.8
AHQ-9-6, 4990	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.11E-07	0.88	3.70	-	672.1
AHQ-9-1, 5151 - 5206	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	2.07E-07	0.97	5.94	-	1797.0
AHQ-9-3, 3946	R.LSPFMADIR.D	1050.25664	2	1.20E-05	0.74	3.02	-	356.2
AHQ-9-8, 3355 - 3358	R.LTVSSLQESGLK.V	1262.43499	2	4.91E-06	0.84	2.91	-	803.3
AHQ-9-4, 3336 - 3416	R.LTVSSLQESGLK.V	1262.43499	2	9.45E-05	0.88	3.02	-	963.5
AHQ-9-4, 4056	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.98E-06	0.95	4.98	-	1002.9
AHQ-9-4, 4052 - 4110	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.39E-05	0.95	4.95	-	1311.5
AHQ-9-3, 4065 - 4122	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	9.15E-04	0.87	3.59	-	1084.9
AHQ-9-4, 4296	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.89E-10	0.90	3.97	-	834.4
AHQ-9-5, 4288	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	3.04E-09	0.89	4.08	-	725.6
AHQ-9-5, 4068	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.10E-08	0.94	4.58	-	979.7
AHQ-9-4, 4284	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.76E-07	0.87	3.83	-	613.8
AHQ-9-2, 4553	R.LYSVSYLLK.D	1086.30538	2	3.42E-05	0.81	2.67	-	611.9
AHQ-9-4, 2178 - 2245	K.M*DCQECPEGYR.V	1463.55315	2	8.97E-06	0.89	2.93	-	977.8
AHQ-9-4, 2494	K.MDCQECPEGYR.V	1447.55375	2	1.96E-06	0.80	2.77	-	661.0
AHQ-9-4, 4612	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	9.25E-05	0.77	3.17	-	1056.7
AHQ-9-1, 4659 - 4730	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	3	3.45E-06	0.96	4.38	-	2610.9
AHQ-9-5, 3107 - 3179	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	1.29E-08	0.97	5.59	-	1505.8
AHQ-9-4, 3121 - 3180	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	4.52E-04	0.95	4.72	-	1347.9
AHQ-9-3, 3150	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	3.47E-05	0.94	3.94	-	1701.9
AHQ-9-2, 3870	K.RIANLQTDLSDGLR.L	1572.74866	2	1.82E-06	0.95	4.41	-	957.7
AHQ-9-5, 3148	R.RLTVSSLQESGLK.V	1418.62134	3	4.16E-04	0.92	4.22	-	1087.1
AHQ-9-6, 3106 - 3134	R.RLTVSSLQESGLK.V	1418.62134	2	3.66E-04	0.94	4.13	-	1323.8
AHQ-9-4, 3156	R.RLTVSSLQESGLK.V	1418.62134	2	2.54E-04	0.97	4.36	-	2387.4
AHQ-9-2, 6469 - 6519	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	8.38E-04	0.90	4.53	-	1048.9
AHQ-9-2, 6577 - 6589	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	2.27E-08	0.87	3.91	-	1004.8
AHQ-9-2, 6637	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	2.07E-05	0.94	3.95	-	1269.3
AHQ-9-2, 6402 - 6461	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	6.05E-06	0.96	4.06	-	1731.1
AHQ-9-3, 6305 - 6361	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	8.20E-04	0.87	3.90	-	936.6
AHQ-9-7, 3768	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.41E-06	0.90	4.38	-	575.3
AHQ-9-1, 3990	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.90E-09	0.92	4.25	-	1286.6
AHQ-9-1, 3994	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.24E-09	0.88	4.14	-	519.1
AHQ-9-6, 3774	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.93E-05	0.77	3.43	-	717.0
AHQ-9-7, 3766	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.81E-07	0.96	4.64	-	1720.6
AHQ-9-4, 3821	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	1.36E-07	0.96	4.48	-	1960.2
AHQ-9-4, 3822	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	7.67E-06	0.85	4.01	-	392.1
AHQ-9-5, 3819	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	7.46E-09	0.92	4.56	-	798.5
AHQ-9-3, 3816	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	7.89E-07	0.95	4.67	-	1554.0
AHQ-9-2, 3913	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	2.05E-09	0.95	4.17	-	1726.7
AHQ-9-5, 3824	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.81E-08	0.93	4.73	-	682.9
AHQ-9-2, 3917	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.23E-06	0.91	4.16	-	747.7
AHQ-9-3, 3813 - 3818	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	6.00E-05	0.92	4.62	-	617.4
AHQ-9-6, 3777	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	7.66E-08	0.86	3.91	-	535.8
AHQ-9-5, 3387	K.SPFEVYVDK.S	1084.20321	2	7.52E-06	0.93	3.05	-	1168.3
AHQ-9-2, 3469	K.SPFEVYVDK.S	1084.20321	2	3.27E-05	0.94	3.50	-	1170.0
AHQ-9-3, 3388	K.SPFEVYVDK.S	1084.20321	2	6.01E-06	0.91	3.14	-	1046.9
AHQ-9-4, 3382	K.SPFEVYVDK.S	1084.20321	2	2.28E-06	0.93	3.04	-	1440.7
AHQ-9-2, 3470	K.SPFEVYVDK.S	1084.20321	1	6.40E-04	0.79	2.48	-	1195.1
AHQ-9-1, 3578	K.SPFEVYVDK.S	1084.20321	2	1.09E-06	0.91	3.11	-	991.5
AHQ-9-4, 3386 - 3389	K.SPFEVYVDK.S	1084.20321	1	4.43E-06	0.58	2.39	-	743.7
AHQ-9-2, 3511 - 3513	K.SPFEVYVDKSQGDASK.V	1757.87886	2	3.97E-07	0.56	3.35	-	440.1
AHQ-9-9, 4455	K.SPFSVAVSPSLDLSK.I	1534.73557	2	4.63E-05	0.68	2.69	-	707.1
AHQ-9-2, 4765 - 4822	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.53E-06	0.85	3.50	-	785.9

AHQ-9-1, 4818 - 4888	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.57E-04	0.89	3.29	-	1094.7
AHQ-9-2, 4631 - 4710	K.SPFSVAVSPSLDLSK.I	1534.73557	2	7.79E-05	0.86	3.56	-	681.8
AHQ-9-3, 4648 - 4704	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.10E-04	0.89	3.61	-	924.1
AHQ-9-3, 4524 - 4593	K.SPFSVAVSPSLDLSK.I	1534.73557	2	6.62E-04	0.66	3.02	-	732.7
AHQ-9-4, 4602 - 4676	K.SPFSVAVSPSLDLSK.I	1534.73557	2	4.82E-07	0.92	4.32	-	889.9
AHQ-9-6, 4621 - 4678	K.SPFSVAVSPSLDLSK.I	1534.73557	2	6.19E-04	0.51	2.69	-	501.4
AHQ-9-6, 4535 - 4614	K.SPFSVAVSPSLDLSK.I	1534.73557	2	6.41E-04	0.68	3.11	-	609.4
AHQ-9-5, 4683 - 4743	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.94E-04	0.91	4.39	-	799.8
AHQ-9-5, 3359	R.SPYTVTVGQACNPSACR.A	1871.04208	2	5.24E-06	0.89	4.15	-	422.9
AHQ-9-4, 3301 - 3364	R.SPYTVTVGQACNPSACR.A	1871.04208	2	3.38E-05	0.91	3.79	-	633.2
AHQ-9-2, 3402 - 3462	R.SPYTVTVGQACNPSACR.A	1871.04208	2	1.25E-04	0.91	4.24	-	625.8
AHQ-9-4, 3353	R.SPYTVTVGQACNPSACR.A	1871.04208	2	3.60E-07	0.90	4.02	-	554.8
AHQ-9-6, 3330	R.SPYTVTVGQACNPSACR.A	1871.04208	2	3.52E-04	0.92	4.25	-	554.2
AHQ-9-5, 4811	R.TFSVWYVPEVTGTHK.V	1751.96228	3	3.28E-07	0.70	3.19	-	465.1
AHQ-9-3, 4784	R.TFSVWYVPEVTGTHK.V	1751.96228	3	1.38E-06	0.66	3.25	-	512.0
AHQ-9-1, 3300	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	2.23E-05	0.85	3.40	-	907.2
AHQ-9-5, 3088	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	6.37E-05	0.90	4.06	-	890.6
AHQ-9-3, 3112	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	1.84E-04	0.91	4.09	-	760.1
AHQ-9-4, 3110	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.98E-07	0.90	3.72	-	1036.7
AHQ-9-2, 3178 - 3233	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	5.53E-04	0.92	3.96	-	846.8
AHQ-9-2, 3182 - 3185	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	4.30E-08	0.83	3.62	-	692.7
AHQ-9-3, 3117	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	3.20E-04	0.86	3.43	-	748.2
AHQ-9-1, 3294	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	4.88E-04	0.94	4.21	-	900.7
AHQ-9-2, 3054 - 3125	R.TGVELGKPTHFTVNAK.A	1699.93205	2	5.97E-04	0.93	4.42	-	666.3
AHQ-9-2, 3053 - 3123	R.TGVELGKPTHFTVNAK.A	1699.93205	3	2.43E-07	0.80	3.77	-	836.3
AHQ-9-4, 3085	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.99E-08	0.96	5.36	-	1396.7
AHQ-9-5, 3092	K.THEAEIVEGENHTYCIR.F	2060.19046	3	4.68E-11	0.90	3.77	-	1054.3
AHQ-9-4, 3096 - 3097	K.THEAEIVEGENHTYCIR.F	2060.19046	2	3.31E-05	0.98	5.65	-	1891.8
AHQ-9-6, 3085 - 3086	K.THEAEIVEGENHTYCIR.F	2060.19046	3	4.75E-07	0.94	4.58	-	1299.7
AHQ-9-1, 3296	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.50E-07	0.82	3.56	-	801.1
AHQ-9-4, 3132	R.TPCEEILVK.H	1090.27249	2	4.73E-06	0.80	2.67	-	709.2
AHQ-9-14-, 3227	R.TPCEEILVK.H	1090.27249	1	1.61E-05	0.63	2.69	-	460.0
AHQ-9-4, 3150	R.TPCEEILVK.H	1090.27249	1	7.92E-04	0.66	2.81	-	613.0
AHQ-9-7, 3104	R.TPCEEILVK.H	1090.27249	2	3.48E-06	0.83	2.99	-	684.3
AHQ-9-3, 3156	R.TPCEEILVK.H	1090.27249	2	4.49E-04	0.87	3.09	-	870.2
AHQ-9-1, 3334	R.TPCEEILVK.H	1090.27249	2	2.15E-05	0.78	3.07	-	584.1
AHQ-9-5, 3137	R.TPCEEILVK.H	1090.27249	2	8.47E-07	0.80	2.72	-	641.6
AHQ-9-3, 6346 - 6404	K.TTYFEIFTAGAGTGEVEVVIQDPM*GQK.G	2906.21339	3	8.14E-06	0.92	4.42	-	1394.4
AHQ-9-3, 6460	K.TTYFEIFTAGAGTGEVEVVIQDPM*GQK.G	2906.21339	3	4.52E-07	0.68	3.14	-	815.8
AHQ-9-3, 3174 - 3245	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.84E-04	0.82	3.09	-	508.8
AHQ-9-2, 3325 - 3401	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.63E-13	0.94	4.48	-	859.4
AHQ-9-4, 3241 - 3321	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.57E-10	0.95	4.85	-	985.8
AHQ-9-3, 3316 - 3380	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.70E-11	0.87	3.52	-	671.0
AHQ-9-1, 3439 - 3506	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.21E-10	0.96	4.58	-	1217.4
AHQ-9-6, 3233 - 3301	R.VANPSGNLTETYVQDR.G	1764.87462	2	5.11E-13	0.96	4.81	-	1012.3
AHQ-9-2, 3467	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.82E-05	0.65	2.84	-	468.8
AHQ-9-5, 3253 - 3259	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.66E-14	0.94	4.17	-	878.0
AHQ-9-7, 3234	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.13E-11	0.90	3.66	-	749.1
AHQ-9-6, 2870	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.03E-07	0.42	2.71	-	331.5
AHQ-9-2, 2955	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.82E-04	0.80	3.30	-	441.1
AHQ-9-4, 2833	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.00E-07	0.89	3.60	-	547.6
AHQ-9-5, 2841	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.36E-04	0.74	3.08	-	503.5
AHQ-9-1, 3066	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.65E-08	0.88	3.63	-	618.1
AHQ-9-8, 2807 - 2842	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	7.11E-06	0.87	3.52	-	801.1
AHQ-9-4, 2670	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.03E-05	0.80	3.53	-	450.4
AHQ-9-3, 2889	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.17E-04	0.89	3.64	-	639.2
AHQ-9-1, 3071	K.VAQPTITDNKDGTVTVR.Y	1816.00621	3	3.24E-04	0.70	3.10	-	468.3
AHQ-9-5, 3463 - 3524	K.VDINTEDLEDGTCR.V	1638.69283	2	8.75E-08	0.97	4.78	-	1638.4
AHQ-9-2, 3554 - 3566	K.VDINTEDLEDGTCR.V	1638.69283	2	4.58E-05	0.83	3.85	-	688.0
AHQ-9-1, 3630	K.VDINTEDLEDGTCR.V	1638.69283	2	4.19E-05	0.92	3.71	-	1075.8
AHQ-9-4, 3454 - 3472	K.VDINTEDLEDGTCR.V	1638.69283	2	1.49E-06	0.96	4.51	-	1206.3
AHQ-9-6, 3429	K.VDINTEDLEDGTCR.V	1638.69283	2	5.03E-07	0.93	4.05	-	1061.0
AHQ-9-6, 3199	K.VDINTEDLEDGTCR.V	1638.69283	2	2.15E-06	0.54	2.57	-	451.6
AHQ-9-3, 3450	K.VDINTEDLEDGTCR.V	1638.69283	2	1.44E-04	0.78	2.77	-	986.6
AHQ-9-5, 3219 - 3297	K.VDINTEDLEDGTCR.V	1638.69283	2	3.17E-07	0.90	3.68	-	999.1
AHQ-9-3, 3224	K.VDINTEDLEDGTCR.V	1638.69283	2	5.62E-06	0.92	3.89	-	953.4
AHQ-9-4, 3212 - 3288	K.VDINTEDLEDGTCR.V	1638.69283	2	1.55E-07	0.85	3.14	-	869.0
AHQ-9-4, 2642	K.VDVGKDQEFTVK.S	1365.51377	2	5.11E-08	0.85	3.65	-	595.7
AHQ-9-3, 2668	K.VDVGKDQEFTVK.S	1365.51377	2	2.04E-06	0.94	3.90	-	912.7
AHQ-9-2, 2714 - 2717	K.VDVGKDQEFTVK.S	1365.51377	2	5.69E-07	0.93	4.04	-	910.6
AHQ-9-5, 2644	K.VDVGKDQEFTVK.S	1365.51377	2	5.01E-08	0.72	2.96	-	598.2
AHQ-9-6, 2637	K.VDVGKDQEFTVK.S	1365.51377	2	1.12E-07	0.89	3.34	-	811.2
AHQ-9-1, 2851	K.VDVGKDQEFTVK.S	1365.51377	2	5.94E-07	0.87	3.35	-	671.0
AHQ-9-2, 2830 - 2870	K.VEPGLGADNSVVR.F	1313.44209	2	7.67E-07	0.79	2.92	-	298.1
AHQ-9-2, 5745 - 5801	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	3.91E-11	0.97	7.05	-	799.9
AHQ-9-4, 5660 - 5716	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	1.17E-07	0.90	4.60	-	703.7
AHQ-9-1, 5758 - 5814	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	3.65E-07	0.66	3.42	-	308.0
AHQ-9-7, 6268 - 6270	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	1.45E-04	0.74	3.76	-	529.0
AHQ-9-2, 6458	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	1.47E-06	0.90	4.09	-	604.3
AHQ-9-1, 6438 - 6439	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	7.86E-05	0.93	4.52	-	729.5
AHQ-9-4, 6304 - 6364	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	5.77E-04	0.73	3.79	-	436.0
AHQ-9-2, 1618	R.VHGPGIQSGTTNKPNK.F	1635.80645	3	2.15E-07	0.91	3.54	-	1182.2
AHQ-9-7, 4145	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.71E-06	0.95	4.17	-	1495.4
AHQ-9-7, 4144	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	4.02E-04	0.82	3.50	-	1180.5
AHQ-9-4, 4193	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	9.71E-04	0.81	3.28	-	1231.9
AHQ-9-5, 4228	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.53E-08	0.98	5.75	-	2263.0
AHQ-9-5, 4211	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	1.52E-07	0.95	4.95	-	1720.6
AHQ-9-6, 4163	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	7.69E-05	0.94	4.31	-	1663.9
AHQ-9-4, 4208	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.05E-04	0.97	5.26	-	1451.2
AHQ-9-8, 4195	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	7.57E-04	0.91	4.14	-	840.8
AHQ-9-1, 4703	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	7.34E-09	0.92	4.90	-	626.6
AHQ-9-2, 4647	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.88E-11	0.92	4.47	-	655.7
AHQ-9-6, 4485	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	9.65E-10	0.94	4.90	-	997.4
AHQ-9-4, 4540	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.11E-14	0.95	5.37	-	974.7
AHQ-9-5, 4535 - 4547	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	2.18E-12	0.96	6.03	-	851.6
AHQ-9-2, 3914	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.02E-06	0.66	2.81	-	682.3
AHQ-9-5, 3748 - 3803	K.VNQPASFAVSLNGAK.G	1503.68480	2	6.39E-07	0.84	3.70	-	517.1
AHQ-9-4, 3757 - 3812	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.52E-08	0.81	3.76	-	441.5
AHQ-9-7, 3580 - 3636	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.64E-05	0.71	3.15	-	387.6
AHQ-9-5, 3625 - 3683	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.03E-07	0.83	3.53	-	441.1
AHQ-9-3, 3624 - 3680	K.VNQPASFAVSLNGAK.G	1503.68480	2	4.83E-05	0.90	3.69	-	759.4
AHQ-9-2, 3725 - 3786	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.81E-07	0.91	3.79	-	823.5
AHQ-9-4, 3629 - 3688	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.44E-07	0.94	4.18	-	727.9
AHQ-9-6, 3585 - 3642	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.78E-10	0.93	3.98	-	817.7
AHQ-9-1, 3808	K.VNQPASFAVSLNGAK.G	1503.68480	2	9.29E-08	0.90	3.69	-	690.6
AHQ-9-5, 1755	K.VPVHDVTDASK.V	1168.28175	2	9.66E-04	0.85	2.76	-	1068.0
AHQ-9-2, 1846	K.VPVHDVTDASK.V	1168.28175	2	1.12E-07	0.90	3.31	-	915.7

AHQ-9-4, 3973 - 4038	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.59E-07	0.96	5.10	-	1289.9
AHQ-9-1, 4107 - 4168	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.04E-04	0.88	3.47	-	883.5
AHQ-9-2, 4061 - 4127	R.VQVQDNEGCPVEALVK.D	1786.98493	2	1.35E-05	0.96	5.13	-	1095.0
AHQ-9-3, 3906 - 3960	R.VQVQDNEGCPVEALVK.D	1786.98493	2	5.38E-05	0.97	4.17	-	1926.5
AHQ-9-5, 3960	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.80E-06	0.95	4.41	-	1270.9
AHQ-9-3, 3948 - 4020	R.VQVQDNEGCPVEALVK.D	1786.98493	2	9.87E-05	0.94	4.67	-	945.6
AHQ-9-6, 3929	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.88E-05	0.78	3.12	-	712.9
AHQ-9-7, 3917 - 3921	R.VQVQDNEGCPVEALVK.D	1786.98493	2	8.30E-07	0.87	3.55	-	878.5
AHQ-9-2, 5015 - 5085	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.06E-07	0.83	3.54	-	1230.8
AHQ-9-1, 4943 - 4948	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	4.93E-08	0.96	5.25	-	1598.5
AHQ-9-4, 4562 - 4616	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	7.82E-08	0.96	5.93	-	1020.1
AHQ-9-8, 4540	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	1.37E-06	0.92	4.38	-	650.5
AHQ-9-3, 4612	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	5.73E-06	0.95	5.12	-	1322.1
AHQ-9-5, 4601 - 4659	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.69E-10	0.92	4.86	-	860.8
AHQ-9-4, 4648	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.29E-07	0.93	4.75	-	1161.5
AHQ-9-9, 4368 - 4371	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	7.92E-05	0.91	3.98	-	1086.7
AHQ-9-6, 4558	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	9.80E-05	0.93	4.53	-	1143.3
AHQ-9-1, 4794 - 4854	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.35E-09	0.97	6.51	-	1614.1
AHQ-9-2, 4734	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	4.04E-06	0.95	5.01	-	1134.8
AHQ-9-5, 4617	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	2.76E-05	0.88	3.60	-	836.2
AHQ-9-8, 2730	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.10E-04	0.60	2.87	-	387.0
AHQ-9-3, 2761	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.89E-07	0.73	3.69	-	444.0
AHQ-9-6, 2729	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.19E-06	0.87	3.62	-	579.8
AHQ-9-2, 2929	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.53E-07	0.84	3.35	-	565.8
AHQ-9-2, 2794 - 2873	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	5.80E-06	0.90	4.36	-	504.1
AHQ-9-3, 2866	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.10E-07	0.54	2.76	-	442.6
AHQ-9-5, 3279	K.VTVLFAGQHIAK.S	1284.53185	2	3.05E-07	0.95	3.99	-	1107.3
AHQ-9-4, 3286	K.VTVLFAGQHIAK.S	1284.53185	2	1.93E-05	0.94	4.42	-	878.5
AHQ-9-2, 3366 - 3369	K.VTVLFAGQHIAK.S	1284.53185	2	2.97E-05	0.93	3.82	-	1171.3
AHQ-9-3, 3296 - 3297	K.VTVLFAGQHIAK.S	1284.53185	2	8.74E-06	0.85	3.55	-	886.6
AHQ-9-2, 3374	K.VTVLFAGQHIAK.S	1284.53185	3	2.92E-05	0.76	3.55	-	613.8
AHQ-9-1, 3494	K.VTVLFAGQHIAK.S	1284.53185	2	3.83E-06	0.62	3.20	-	503.0
AHQ-9-7, 3230	K.VTVLFAGQHIAK.S	1284.53185	2	3.65E-05	0.82	3.15	-	677.1
AHQ-9-5, 4764 - 4783	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.62E-08	0.86	3.69	-	446.8
AHQ-9-4, 4610	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.65E-11	0.90	4.08	-	498.5
AHQ-9-3, 4596	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.20E-04	0.85	3.26	-	458.4
AHQ-9-4, 4749	R.VTYCPTEPGNYIINIK.F	1884.14221	2	9.07E-04	0.84	3.82	-	350.6
AHQ-9-7, 4682 - 4684	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.91E-04	0.72	3.01	-	416.0
AHQ-9-6, 4701	R.VTYCPTEPGNYIINIK.F	1884.14221	2	9.90E-06	0.68	3.36	-	275.5
AHQ-9-1, 4916	R.VTYCPTEPGNYIINIK.F	1884.14221	3	1.05E-04	0.81	3.60	-	795.8
AHQ-9-5, 4624 - 4625	R.VTYCPTEPGNYIINIK.F	1884.14221	2	9.51E-09	0.90	4.34	-	467.5
AHQ-9-6, 4563	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.67E-09	0.86	3.17	-	608.8
AHQ-9-4, 4764 - 4765	R.VTYCPTEPGNYIINIK.F	1884.14221	3	5.24E-07	0.95	5.14	-	1040.0
AHQ-9-2, 4853	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.27E-05	0.63	2.77	-	309.6
AHQ-9-1, 4903 - 4983	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.01E-05	0.77	2.99	-	479.5
AHQ-9-4, 4748	R.VTYTPM*APGSYLISIK.Y	1758.07165	3	3.30E-04	0.90	3.80	-	1102.9
AHQ-9-6, 5107	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.62E-04	0.83	3.12	-	611.0
AHQ-9-14-, 4726	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	3.51E-05	0.55	2.56	-	297.9
AHQ-9-5, 4759	R.VTYTPM*APGSYLISIK.Y	1758.07165	3	3.47E-05	0.86	3.47	-	1150.1
AHQ-9-2, 5287	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.42E-04	0.85	2.94	-	808.5
AHQ-9-5, 2708	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	9.05E-04	0.85	2.97	-	1024.9
AHQ-9-5, 3375	R.YAPSEAGLHEMDIR.Y	1589.75482	2	7.84E-04	0.70	3.00	-	586.4
AHQ-9-2, 3479	R.YAPSEAGLHEMDIR.Y	1589.75482	2	9.80E-07	0.82	2.50	-	918.2
AHQ-9-8, 3330	R.YAPSEAGLHEMDIR.Y	1589.75482	2	8.12E-04	0.81	2.86	-	845.0
AHQ-9-7, 4026 - 4033	K.YGGDEIPFSPYR.V	1401.50466	2	1.57E-04	0.51	3.04	-	400.6
AHQ-9-3, 4073	K.YGGDEIPFSPYR.V	1401.50466	2	8.41E-05	0.76	2.94	-	671.3
AHQ-9-13-, 3473	K.YGGPYHIGGSPFK.A	1380.53182	2	1.25E-05	0.91	3.44	-	1276.3
AHQ-9-8, 3346 - 3351	K.YGGPYHIGGSPFK.A	1380.53182	2	7.40E-10	0.95	3.94	-	1403.1
AHQ-9-4, 3384	K.YGGPYHIGGSPFK.A	1380.53182	2	1.22E-07	0.96	4.02	-	1466.4
AHQ-9-3, 3412	K.YGGPYHIGGSPFK.A	1380.53182	2	1.37E-07	0.94	3.97	-	1315.5
AHQ-9-5, 3400 - 3403	K.YGGPYHIGGSPFK.A	1380.53182	2	8.48E-11	0.96	4.42	-	1491.4
AHQ-9-7, 3353	K.YGGPYHIGGSPFK.A	1380.53182	2	8.50E-04	0.95	3.64	-	1921.8
AHQ-9-4, 3394	K.YGGPYHIGGSPFK.A	1380.53182	3	9.40E-05	0.84	4.02	-	539.8
AHQ-9-5, 3404	K.YGGPYHIGGSPFK.A	1380.53182	3	3.72E-06	0.84	3.91	-	432.6
AHQ-9-6, 3375	K.YGGPYHIGGSPFK.A	1380.53182	2	4.49E-09	0.97	4.24	-	1629.0
AHQ-9-3, 3072	K.YGGQPVPNFPSK.L	1291.43658	2	4.19E-04	0.91	3.60	-	606.5
AHQ-9-1, 3252	K.YGGQPVPNFPSK.L	1291.43658	2	2.24E-04	0.91	3.26	-	672.0
AHQ-9-5, 3052 - 3053	K.YGGQPVPNFPSK.L	1291.43658	2	2.86E-06	0.90	3.54	-	604.6
AHQ-9-2, 3135	K.YGGQPVPNFPSK.L	1291.43658	2	3.17E-04	0.93	3.65	-	711.0
AHQ-9-1, 4480	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	7.01E-04	0.82	3.41	-	879.9
AHQ-9-8, 2854	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.27E-04	0.79	3.29	-	392.4
AHQ-9-5, 3072	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.27E-04	0.66	2.94	-	335.8
AHQ-9-5, 2912	K.YNEQHVPGSPFTAR.V	1603.71978	3	1.66E-05	0.88	4.05	-	926.8
AHQ-9-4, 2912	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.43E-05	0.92	3.88	-	548.8
AHQ-9-4, 2917 - 2922	K.YNEQHVPGSPFTAR.V	1603.71978	3	1.81E-06	0.94	4.62	-	1246.4
AHQ-9-4, 3069	K.YNEQHVPGSPFTAR.V	1603.71978	2	5.30E-05	0.74	2.85	-	433.2
AHQ-9-3, 2922 - 2942	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.32E-05	0.86	3.30	-	461.5
AHQ-9-8, 2859	K.YNEQHVPGSPFTAR.V	1603.71978	3	4.62E-04	0.83	3.55	-	896.1
AHQ-9-1, 3054 - 3132	K.YNEQHVPGSPFTAR.V	1603.71978	2	6.16E-06	0.89	3.48	-	612.1
AHQ-9-5, 2911	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.37E-07	0.81	2.81	-	493.0
AHQ-9-12, 2878 - 2938	K.YNEQHVPGSPFTAR.V	1603.71978	2	3.08E-04	0.53	2.72	-	308.0
AHQ-9-9, 4105	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.61E-05	0.68	2.70	-	593.6
AHQ-9-4, 4321	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.18E-04	0.89	4.02	-	528.9
AHQ-9-2, 4347 - 4405	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.21E-09	0.93	4.53	-	764.2
AHQ-9-3, 4378	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	8.98E-08	0.70	3.05	-	387.8
AHQ-9-3, 4237 - 4292	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.32E-06	0.94	4.45	-	793.0
AHQ-9-3, 4130	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.68E-04	0.75	3.25	-	486.2
AHQ-9-6, 4249	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.75E-04	0.94	4.49	-	848.0
AHQ-9-2, 4250	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.93E-05	0.88	3.92	-	556.0
AHQ-9-1, 4474	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.87E-06	0.92	4.35	-	730.0
AHQ-9-5, 4307	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	3.58E-07	0.90	4.10	-	618.4
AHQ-9-7, 4232	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.75E-07	0.91	4.17	-	621.8
AHQ-9-2, 4497 - 4574	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.76E-06	0.90	4.31	-	511.2
AHQ-9-2, 4415	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.12E-07	0.93	4.66	-	641.7
AHQ-9-3, 5977 - 6020	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	2.82E-07	0.62	3.20	-	307.9
AHQ-9-2, 6137 - 6193	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	7.34E-07	0.80	3.72	-	353.6
AHQ-9-2, 5885 - 5890	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	3.15E-09	0.90	3.75	-	743.2
gi|4501881|ref|NP_001091.1| alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA				1.44E-14	7.61	110.28	22.00	42050.8
AHQ-9-8, 2031 - 2091	K.AGFAGDDAPR.A	977.01283	2	5.93E-05	0.85	3.04	-	982.6
AHQ-9-12, 3620 - 3629	R.AVFPSIVGR.P	946.12815	2	2.77E-04	0.68	2.68	-	450.4
AHQ-9-8, 4204	R.DLTDYLMK.I	999.16326	1	2.91E-04	0.66	2.96	-	647.3
AHQ-9-8, 4200	R.DLTDYLMK.I	999.16326	2	1.72E-04	0.69	2.67	-	395.9
AHQ-9-8, 3568	R.DLTDYLM*K.I	1015.16266	2	4.43E-04	0.67	2.67	-	410.2
AHQ-9-8, 3567	R.DLTDYLM*K.I	1015.16266	1	7.63E-05	0.37	2.57	-	118.6
AHQ-9-12, 4189	R.DLTDYLMK.I	999.16326	1	7.35E-04	0.46	2.04	-	787.8
AHQ-9-9, 3415	R.DLTDYLM*K.I	1015.16266	1	8.45E-04	0.06	1.96	-	107.3
AHQ-9-8, 1810 - 1890	K.DSYVGDEAQSK.R	1199.20634	2	8.96E-06	0.76	3.15	-	721.2

AHQ-9-8, 1567 - 1644	K.DSYVGDEAQSK.R	1199.20634	2	4.80E-05	0.45	2.54	-	330.9
AHQ-9-8, 1907 - 1968	K.DSYVGDEAQSK.R	1199.20634	2	3.88E-05	0.78	3.29	-	495.3
AHQ-9-13-, 3086	K.EITALAPSTMK.I	1162.38206	1	7.95E-04	0.11	2.09	-	215.1
AHQ-9-9, 2367 - 2368	K.EITALAPSTM*K.I	1178.38146	2	1.18E-04	0.78	2.95	-	604.5
AHQ-9-9, 2999 - 3039	K.IWHHTFYNELR.V	1516.68695	2	9.54E-04	0.60	2.80	-	735.3
AHQ-9-9, 3000	K.IWHHTFYNELR.V	1516.68695	3	6.57E-05	0.91	4.50	-	1306.1
AHQ-9-12, 3301 - 3356	K.IWHHTFYNELR.V	1516.68695	2	3.67E-04	0.84	3.51	-	1021.1
AHQ-9-12, 3186 - 3240	K.IWHHTFYNELR.V	1516.68695	2	1.54E-06	0.85	3.14	-	884.7
AHQ-9-8, 2930 - 3002	K.IWHHTFYNELR.V	1516.68695	2	7.33E-06	0.73	2.98	-	814.5
AHQ-9-8, 3063 - 3130	K.IWHHTFYNELR.V	1516.68695	2	9.05E-06	0.80	3.40	-	872.7
AHQ-9-8, 3123	K.IWHHTFYNELR.V	1516.68695	3	2.69E-06	0.93	4.54	-	1468.7
AHQ-9-8, 3202 - 3258	K.IWHHTFYNELR.V	1516.68695	2	2.62E-07	0.94	3.81	-	1100.9
AHQ-9-5, 4372 - 4437	K.SYELPDGQVITIGNER.F	1791.93998	2	5.56E-09	0.88	3.18	-	905.8
AHQ-9-4, 4841	K.SYELPDGQVITIGNER.F	1791.93998	2	5.01E-06	0.74	3.13	-	553.1
AHQ-9-4, 4696 - 4776	K.SYELPDGQVITIGNER.F	1791.93998	2	5.67E-05	0.81	3.04	-	707.1
AHQ-9-4, 4312 - 4378	K.SYELPDGQVITIGNER.F	1791.93998	2	7.82E-04	0.72	2.84	-	749.5
AHQ-9-8, 4208 - 4280	K.SYELPDGQVITIGNER.F	1791.93998	2	1.07E-09	0.96	4.83	-	1098.5
AHQ-9-8, 4266 - 4334	K.SYELPDGQVITIGNER.F	1791.93998	2	6.42E-08	0.88	3.32	-	791.1
AHQ-9-13-, 4681 - 4692	K.SYELPDGQVITIGNER.F	1791.93998	2	1.80E-10	0.96	4.65	-	1122.7
AHQ-9-3, 4672	K.SYELPDGQVITIGNER.F	1791.93998	2	1.22E-04	0.72	2.50	-	779.9
AHQ-9-8, 4390 - 4400	K.SYELPDGQVITIGNER.F	1791.93998	2	1.44E-14	0.96	4.26	-	1353.8
AHQ-9-13-, 4266 - 4344	K.SYELPDGQVITIGNER.F	1791.93998	2	2.18E-09	0.92	4.08	-	822.5
AHQ-9-5, 4713 - 4773	K.SYELPDGQVITIGNER.F	1791.93998	2	2.15E-06	0.94	4.46	-	845.0
AHQ-9-8, 4559 - 4622	K.SYELPDGQVITIGNER.F	1791.93998	2	5.88E-07	0.87	3.36	-	824.9
AHQ-9-8, 4640	K.SYELPDGQVITIGNER.F	1791.93998	3	2.83E-06	0.94	4.52	-	1456.7
AHQ-9-8, 4682 - 4740	K.SYELPDGQVITIGNER.F	1791.93998	2	7.73E-11	0.94	4.19	-	989.2
AHQ-9-7, 4776 - 4857	K.SYELPDGQVITIGNER.F	1791.93998	2	1.26E-04	0.72	3.02	-	359.7
AHQ-9-8, 4854 - 4926	K.SYELPDGQVITIGNER.F	1791.93998	2	1.33E-11	0.97	4.65	-	1424.8
AHQ-9-8, 5003	K.SYELPDGQVITIGNER.F	1791.93998	2	7.50E-06	0.86	3.20	-	712.4
AHQ-9-7, 4638 - 4662	K.SYELPDGQVITIGNER.F	1791.93998	2	8.39E-06	0.88	3.85	-	754.5
AHQ-9-6, 4790	K.SYELPDGQVITIGNER.F	1791.93998	2	6.02E-07	0.59	2.82	-	304.9
AHQ-9-6, 4659	K.SYELPDGQVITIGNER.F	1791.93998	2	3.12E-09	0.93	3.91	-	1061.9
AHQ-9-2, 4943	K.SYELPDGQVITIGNER.F	1791.93998	2	2.16E-08	0.91	3.70	-	992.6
AHQ-9-9, 4207 - 4265	K.SYELPDGQVITIGNER.F	1791.93998	2	1.01E-06	0.87	3.80	-	710.3
AHQ-9-9, 4447 - 4503	K.SYELPDGQVITIGNER.F	1791.93998	2	2.66E-11	0.98	5.63	-	1470.9
AHQ-9-9, 4480	K.SYELPDGQVITIGNER.F	1791.93998	3	1.85E-07	0.92	4.03	-	1294.3
AHQ-9-9, 4588 - 4660	K.SYELPDGQVITIGNER.F	1791.93998	2	4.66E-08	0.96	4.70	-	1239.9
AHQ-9-10, 4160 - 4238	K.SYELPDGQVITIGNER.F	1791.93998	2	1.54E-04	0.85	3.21	-	683.6
AHQ-9-10, 4507 - 4561	K.SYELPDGQVITIGNER.F	1791.93998	3	8.78E-10	0.90	3.79	-	1065.9
AHQ-9-10, 4517 - 4573	K.SYELPDGQVITIGNER.F	1791.93998	2	8.01E-08	0.90	3.49	-	933.2
AHQ-9-10, 4658 - 4713	K.SYELPDGQVITIGNER.F	1791.93998	2	2.26E-06	0.81	2.82	-	661.6
AHQ-9-11, 4270 - 4327	K.SYELPDGQVITIGNER.F	1791.93998	2	8.32E-07	0.89	3.58	-	846.3
AHQ-9-11, 4597	K.SYELPDGQVITIGNER.F	1791.93998	3	1.13E-06	0.90	3.96	-	1012.5
AHQ-9-11, 4690 - 4746	K.SYELPDGQVITIGNER.F	1791.93998	2	9.84E-07	0.91	3.36	-	960.4
AHQ-9-8, 4488 - 4490	K.SYELPDGQVITIGNER.F	1791.93998	2	7.30E-05	0.55	2.81	-	393.6
AHQ-9-5, 4848	K.SYELPDGQVITIGNER.F	1791.93998	2	1.17E-07	0.86	3.24	-	845.3
AHQ-9-8, 4318 - 4319	K.SYELPDGQVITIGNER.F	1791.93998	3	1.26E-08	0.93	4.68	-	1124.1
AHQ-9-1, 4863	K.SYELPDGQVITIGNER.F	1791.93998	2	5.82E-07	0.91	3.51	-	832.2
AHQ-9-12, 4240 - 4297	K.SYELPDGQVITIGNER.F	1791.93998	2	2.67E-08	0.89	3.80	-	692.5
AHQ-9-12, 4596 - 4672	K.SYELPDGQVITIGNER.F	1791.93998	2	7.93E-11	0.96	5.01	-	1181.5
AHQ-9-12, 4729 - 4804	K.SYELPDGQVITIGNER.F	1791.93998	2	1.47E-10	0.97	4.80	-	1537.6
AHQ-9-13, 4847 - 4851	K.SYELPDGQVITIGNER.F	1791.93998	2	4.31E-07	0.93	4.13	-	916.8
AHQ-9-13, 4972 - 4988	K.SYELPDGQVITIGNER.F	1791.93998	2	1.30E-05	0.90	3.64	-	838.2
AHQ-9-13-, 4802	K.SYELPDGQVITIGNER.F	1791.93998	2	2.49E-11	0.83	3.15	-	589.4
AHQ-9-8, 4800 - 4858	K.SYELPDGQVITIGNERFR.C	2095.30102	2	6.24E-04	0.74	3.25	-	429.3
AHQ-9-8, 4304	K.YPIEHGIITNWDDMEK.I	1962.17174	3	6.90E-04	0.83	3.48	-	1331.1
AHQ-9-8, 4414	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.75E-07	0.73	3.43	-	449.7
gi|4504165|ref|NP_000168.1|	gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]			2.28E-14	22.01	250.34	35.70	85696.9
AHQ-9-6, 3606 - 3663	K.AGALNSNDAFVLK.T	1320.47622	2	6.90E-04	0.77	3.36	-	535.6
AHQ-9-5, 3592 - 3651	K.AGALNSNDAFVLK.T	1320.47622	2	2.84E-05	0.89	3.84	-	679.2
AHQ-9-5, 3277	K.AGKEPGLQIWR.V	1255.45060	3	8.48E-05	0.84	4.01	-	805.3
AHQ-9-5, 3273	K.AGKEPGLQIWR.V	1255.45060	2	2.49E-07	0.72	2.91	-	390.5
AHQ-9-8, 5372	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	3.14E-06	0.93	4.80	-	565.4
AHQ-9-5, 5212	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.10E-07	0.94	4.86	-	819.0
AHQ-9-5, 5367	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.39E-05	0.94	4.91	-	709.5
AHQ-9-7, 5296	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	2.05E-05	0.95	4.93	-	847.0
AHQ-9-6, 5309	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	4.70E-06	0.95	5.20	-	752.4
AHQ-9-6, 5195 - 5249	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	9.64E-12	0.94	4.50	-	1357.3
AHQ-9-5, 5251 - 5307	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	1.13E-10	0.93	4.50	-	1472.0
AHQ-9-5, 5309	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	2	2.71E-07	0.71	3.12	-	483.6
AHQ-9-8, 2274	K.DSQEEEKTEALTSAK.R	1666.72289	2	7.98E-07	0.93	3.70	-	1268.7
AHQ-9-13-, 2333	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.66E-05	0.85	3.42	-	1106.7
AHQ-9-6, 2281 - 2294	K.DSQEEEKTEALTSAK.R	1666.72289	2	8.18E-09	0.95	3.93	-	1675.6
AHQ-9-5, 2264 - 2336	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.79E-07	0.95	4.13	-	1561.5
AHQ-9-7, 2292	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.57E-04	0.93	3.92	-	1466.5
AHQ-9-10, 2272	K.DSQEEEKTEALTSAK.R	1666.72289	2	6.26E-05	0.86	3.40	-	851.3
AHQ-9-5, 2275 - 2283	K.DSQEEEKTEALTSAK.R	1666.72289	3	3.93E-06	0.97	5.39	-	1999.8
AHQ-9-5, 5725 - 5783	R.EVQGFESATFLGYFK.S	1723.90570	2	4.21E-06	0.94	3.47	-	1398.2
AHQ-9-5, 5837 - 5920	R.EVQGFESATFLGYFK.S	1723.90570	2	1.47E-06	0.95	4.81	-	991.2
AHQ-9-7, 5684 - 5746	R.EVQGFESATFLGYFK.S	1723.90570	2	1.99E-05	0.63	2.67	-	648.9
AHQ-9-5, 6085	R.EVQGFESATFLGYFK.S	1723.90570	2	1.66E-05	0.89	3.21	-	907.9
AHQ-9-13-, 5716	R.EVQGFESATFLGYFK.S	1723.90570	2	1.49E-04	0.86	2.85	-	1072.9
AHQ-9-5, 6419	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	3	7.81E-05	0.76	3.20	-	677.5
AHQ-9-5, 6420	K.FDLVPVPTNLYGDFFTGDAYVILK.T	2706.08359	2	2.49E-10	0.87	3.92	-	451.3
AHQ-9-5, 2399	K.HVVPNEVVVQR.L	1276.46981	3	8.86E-04	0.72	3.38	-	733.5
AHQ-9-5, 2367 - 2391	K.HVVPNEVVVQR.L	1276.46981	2	1.83E-07	0.90	3.43	-	592.8
AHQ-9-5, 2397	K.HVVPNEVVVQR.L	1276.46981	1	2.09E-04	0.15	1.90	-	265.5
AHQ-9-5, 5751 - 5813	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	3.80E-07	0.93	4.46	-	1173.4
AHQ-9-5, 5303	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	2.28E-14	0.98	6.70	-	1952.2
AHQ-9-6, 5245	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	1.67E-08	0.95	5.34	-	1096.9
AHQ-9-5, 5068	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	9.52E-07	0.94	4.84	-	1136.0
AHQ-9-5, 2532	K.PALPAGTEDTAKEDAANR.K	1827.93072	3	3.59E-10	0.66	3.02	-	376.1
AHQ-9-5, 3065 - 3127	K.SEDCFILDHGK.D	1322.42590	2	9.09E-05	0.86	3.10	-	818.6
AHQ-9-6, 3110	K.SEDCFILDHGK.D	1322.42590	2	1.48E-05	0.89	3.52	-	879.2
AHQ-9-7, 3086	K.SEDCFILDHGK.D	1322.42590	2	1.79E-06	0.86	3.24	-	793.2
AHQ-9-5, 2836	K.SEDCFILDHGKDGK.I	1622.73823	2	6.93E-06	0.85	3.17	-	650.9
AHQ-9-10, 2313	K.TGAQELLR.V	888.00387	2	1.42E-05	0.87	2.92	-	871.4
AHQ-9-5, 2293 - 2373	K.TGAQELLR.V	888.00387	2	9.56E-05	0.87	2.91	-	971.4
AHQ-9-5, 4587	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	4.01E-05	0.79	3.28	-	573.2
AHQ-9-6, 4253 - 4309	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.16E-04	0.95	4.67	-	1069.6
AHQ-9-9, 4091 - 4103	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.05E-04	0.83	3.26	-	811.3
AHQ-9-5, 4295 - 4351	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	2.06E-05	0.95	4.17	-	1294.8
AHQ-9-5, 4199	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	2.46E-04	0.91	3.64	-	1009.7
AHQ-9-8, 4270 - 4335	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	5.90E-04	0.94	4.41	-	1069.8
AHQ-9-5, 3745	R.VHVSEEGTEPEAM*LQVLGPK.P	2167.42570	2	4.57E-04	0.95	4.57	-	912.7
AHQ-9-5, 4765	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	1.10E-05	0.97	5.21	-	1215.2
AHQ-9-5, 5007 - 5065	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	2.19E-05	0.93	5.17	-	699.1

AHQ-9-5, 4175	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	1.58E-06	0.95	5.70	-	737.5
AHQ-9-6, 3538	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	3.61E-05	0.72	3.83	-	710.6
AHQ-9-5, 3203 - 3261	R.VPFDAATLHTSTAM*AAQHGM*DDDGTGQK.Q	2907.10021	3	7.33E-05	0.93	5.19	-	1008.3
AHQ-9-5, 3925	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	1.67E-04	0.92	4.76	-	872.6
AHQ-9-5, 5965 - 6027	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	3	6.83E-05	0.82	3.30	-	905.2
AHQ-9-5, 5091	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	4.95E-09	0.79	3.01	-	603.8
AHQ-9-6, 5041 - 5046	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	2	1.23E-11	0.92	4.06	-	867.4
AHQ-9-5, 5100 - 5157	K.VSNGAGTM*SVSLVADENPFAQGALK.S	2480.73680	3	2.05E-08	0.86	3.92	-	1163.7
AHQ-9-5, 5531 - 5587	K.VSNGAGTMSVSLVADENPFAQGALK.S	2464.73740	2	2.56E-04	0.65	2.81	-	419.1
gi|6005942|ref|NP_009057.1|	valosin-containing protein; yeast Cdc48p homolog; transitional endoplas			1.35E-13	6.30	70.32	15.40	89321.3
AHQ-9-5, 3731	R.ELQELVQYPVEHPDK.F	1825.01157	2	2.20E-04	0.81	3.26	-	664.8
AHQ-9-5, 3756	K.GVLFYGPPGCGK.T	1253.45154	2	8.25E-06	0.84	2.79	-	930.6
AHQ-9-5, 6268	K.LADDVDLEQVANETHGHVGADLAALCSEAALQAIR.K	3675.98140	3	1.35E-13	0.89	3.89	-	975.9
AHQ-9-5, 5359	R.LDQLIYIPLPDEK.S	1557.81228	2	2.20E-08	0.91	3.71	-	1006.0
AHQ-9-4, 5373	R.LDQLIYIPLPDEK.S	1557.81228	2	2.86E-07	0.89	3.25	-	891.5
AHQ-9-5, 4677 - 4747	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	1.51E-09	0.98	6.49	-	1759.1
AHQ-9-4, 6368 - 6370	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	4.33E-04	0.90	3.89	-	745.3
AHQ-9-5, 6387 - 6447	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	4.64E-06	0.95	4.29	-	1188.4
AHQ-9-6, 6309	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	5.42E-04	0.89	2.94	-	1178.7
AHQ-9-5, 3535	R.WALSQSNPSALR.E	1330.47434	2	9.04E-04	0.92	3.57	-	1062.1
gi|4557419|ref|NP_000063.1|	CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36			1.45E-13	2.72	30.24	10.20	53052.1
AHQ-9-5, 4456	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	3.72E-04	0.92	4.24	-	750.1
AHQ-9-6, 4423	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	4.95E-07	0.85	3.38	-	540.9
AHQ-9-5, 5243 - 5255	K.SQVLQFFSSDICR.S	1588.76661	2	4.40E-09	0.91	3.70	-	1030.6
AHQ-9-6, 5182	K.SQVLQFFSSDICR.S	1588.76661	2	2.23E-06	0.91	3.40	-	1400.3
AHQ-9-3, 5198	K.SQVLQFFSSDICR.S	1588.76661	2	2.96E-04	0.77	2.92	-	621.3
AHQ-9-7, 5168	K.SQVLQFFSSDICR.S	1588.76661	2	1.07E-04	0.96	4.21	-	1681.6
AHQ-9-5, 6307 - 6308	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.45E-13	0.96	4.70	-	1256.0
AHQ-9-1, 6383 - 6448	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	7.02E-07	0.93	4.01	-	934.9
gi|24119203|ref|NP_705935.1|	tropomyosin 3 [Homo sapiens]			1.77E-13	5.41	70.31	21.80	29032.5
AHQ-9-9, 2397 - 2413	R.AREQAEAEVASLNR.R	1544.65218	2	1.04E-04	0.98	6.01	-	2985.5
AHQ-9-9, 3435	R.IQLVEEELDR.A	1244.37653	1	8.15E-05	0.22	2.58	-	387.0
AHQ-9-9, 3600 - 3601	R.IQLVEEELDRAQER.L	1728.88542	2	2.08E-04	0.52	3.68	-	463.7
AHQ-9-9, 2731 - 2747	K.IQVLQQQADDAEER.A	1643.73738	2	6.45E-10	0.98	5.03	-	2168.2
AHQ-9-10, 2807	K.IQVLQQQADDAEER.A	1643.73738	2	4.82E-07	0.89	2.69	-	1298.1
AHQ-9-9, 2523	R.KIQVLQQQADDAEER.A	1771.91030	3	3.74E-09	0.94	4.71	-	1367.3
AHQ-9-9, 2515	R.KIQVLQQQADDAEER.A	1771.91030	2	1.77E-13	0.98	6.17	-	1640.6
AHQ-9-9, 3199	R.RIQLVEEELDR.A	1400.56288	2	9.49E-06	0.97	4.29	-	1778.7
AHQ-9-9, 3027 - 3032	K.TIDDLEDKLK.C	1190.32563	2	1.19E-04	0.75	2.94	-	586.1
gi|4504349|ref|NP_000509.1|	beta globin [Homo sapiens]			2.77E-13	9.56	110.31	73.50	15998.3
AHQ-9-14-, 5301	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	7.79E-07	0.88	3.86	-	596.6
AHQ-9-13-, 4760 - 4822	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	8.51E-07	0.89	3.91	-	631.8
AHQ-9-13, 4982 - 5038	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	6.56E-06	0.94	4.74	-	715.7
AHQ-9-13-, 5376	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	3.42E-06	0.94	4.51	-	790.8
AHQ-9-13-, 5280	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.60E-06	0.94	4.36	-	826.8
AHQ-9-13, 4959	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	1.04E-04	0.70	3.22	-	850.7
AHQ-9-13, 5442 - 5511	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	6.34E-08	0.92	3.99	-	684.0
AHQ-9-13, 3792	K.GTFATLSELHCDK.L	1480.62492	2	3.69E-05	0.56	2.75	-	446.4
AHQ-9-13-, 4821	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	4.68E-09	0.88	4.29	-	1035.3
AHQ-9-13, 4859	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	2.21E-09	0.94	5.09	-	1005.4
AHQ-9-13-, 4673	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	1.10E-07	0.98	5.64	-	1940.8
AHQ-9-13-, 4668	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	6.11E-09	0.97	6.21	-	1539.2
AHQ-9-13-, 2936	K.LHVDPENFR.L	1127.23455	2	6.63E-05	0.90	2.70	-	1330.9
AHQ-9-13-, 6152	R.LLGNVLVCVLAHHFGK.E	1779.14197	3	4.71E-05	0.81	3.32	-	538.7
AHQ-9-13-, 3544	K.SAVTALWGK.V	933.08624	2	3.84E-04	0.82	2.98	-	669.7
AHQ-9-14-, 4965	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.77E-13	0.96	4.76	-	1544.6
AHQ-9-13, 4936	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	3.06E-05	0.82	3.31	-	547.0
AHQ-9-13, 5095	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.18E-11	0.97	5.47	-	1366.4
AHQ-9-13-, 4764	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	6.03E-08	0.94	3.75	-	1414.4
AHQ-9-13-, 4774	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	2.87E-10	0.88	3.80	-	692.7
AHQ-9-13, 5094 - 5096	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	5.44E-10	0.81	3.31	-	496.4
AHQ-9-13, 4939	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	6.34E-05	0.86	3.17	-	1007.1
AHQ-9-13-, 4945 - 5000	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.69E-08	0.95	4.84	-	1098.9
AHQ-9-13-, 5104	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	3.40E-06	0.56	3.06	-	386.8
AHQ-9-13-, 4944	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	9.31E-10	0.73	3.11	-	425.8
AHQ-9-14, 4104 - 4143	K.VNVDEVGGEALGR.L	1315.41484	2	6.78E-05	0.95	4.12	-	1382.7
AHQ-9-13, 3527 - 3528	K.VNVDEVGGEALGR.L	1315.41484	2	3.44E-05	0.93	3.87	-	1250.6
AHQ-9-14-, 3279 - 3313	K.VNVDEVGGEALGR.L	1315.41484	2	5.81E-04	0.94	3.49	-	1570.8
AHQ-9-13-, 2822	K.VVAGVANALAHK.Y	1150.35593	2	2.02E-05	0.91	3.08	-	1288.0
AHQ-9-13-, 2608	K.VVAGVANALAHK.Y	1150.35593	2	1.63E-09	0.96	3.87	-	1745.1
gi|4503689|ref|NP_000499.1|	fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M			3.19E-13	12.16	150.25	23.90	94972.5
AHQ-9-7, 5293	K.DSDWPFCSDEDWNYK.C	1965.98609	2	4.01E-05	0.94	4.29	-	724.1
AHQ-9-6, 5294 - 5299	K.DSDWPFCSDEDWNYK.C	1965.98609	2	1.09E-07	0.96	4.62	-	963.3
AHQ-9-6, 4721 - 4797	K.DSHSLTTNIM*EILR.G	1646.84779	2	1.56E-05	0.95	3.66	-	1592.1
AHQ-9-7, 5382	K.DSHSLTTNIMEILR.G	1630.84839	2	5.20E-07	0.95	3.92	-	1208.1
AHQ-9-9, 4535	K.DSHSLTTNIM*EILR.G	1646.84779	2	7.85E-04	0.73	2.60	-	857.1
AHQ-9-7, 4690 - 4697	K.DSHSLTTNIM*EILR.G	1646.84779	2	6.20E-04	0.94	4.07	-	1259.4
AHQ-9-6, 2419 - 2433	K.ESSSHHPGIAEFPSR.G	1638.72252	3	3.17E-04	0.64	3.16	-	783.7
AHQ-9-6, 2665 - 2667	R.EVDLKDYEDQQK.Q	1510.58460	2	7.51E-10	0.83	3.30	-	602.9
AHQ-9-8, 2682	R.EVDLKDYEDQQK.Q	1510.58460	2	2.45E-07	0.77	2.81	-	694.0
AHQ-9-9, 2556 - 2557	R.EVDLKDYEDQQK.Q	1510.58460	2	4.55E-10	0.93	3.91	-	981.6
AHQ-9-7, 2658	R.EVDLKDYEDQQK.Q	1510.58460	2	8.34E-06	0.62	2.73	-	548.5
AHQ-9-14-, 5759	K.EVVTSEDGSDCPEAM*DLGTLSGIGTLDGFR.H	3147.34877	3	8.74E-04	0.87	3.63	-	938.0
AHQ-9-8, 1904	R.GGSTSYGTGSETESPR.N	1573.55765	2	4.76E-06	0.40	2.60	-	412.7
AHQ-9-6, 1915	R.GGSTSYGTGSETESPR.N	1573.55765	2	8.37E-04	0.61	2.75	-	382.9
AHQ-9-7, 4405 - 4409	K.GLIDEVNQDFTNR.I	1521.61384	2	1.03E-08	0.96	4.65	-	1006.4
AHQ-9-14-, 4509 - 4563	K.GLIDEVNQDFTNR.I	1521.61384	2	8.41E-08	0.77	3.31	-	534.6
AHQ-9-9, 4189 - 4268	K.GLIDEVNQDFTNR.I	1521.61384	2	2.19E-07	0.88	3.38	-	898.4
AHQ-9-9, 3740 - 3748	K.GLIDEVNQDFTNR.I	1521.61384	2	2.92E-04	0.69	3.16	-	575.7
AHQ-9-7, 3881	K.GLIDEVNQDFTNR.I	1521.61384	2	1.36E-05	0.76	2.81	-	641.3
AHQ-9-5, 4479	K.GLIDEVNQDFTNR.I	1521.61384	2	8.05E-07	0.81	3.05	-	743.3
AHQ-9-3, 4466	K.GLIDEVNQDFTNR.I	1521.61384	2	6.01E-04	0.84	2.96	-	870.2
AHQ-9-12, 4429	K.GLIDEVNQDFTNR.I	1521.61384	2	5.09E-05	0.80	2.80	-	784.2
AHQ-9-8, 3942	K.GLIDEVNQDFTNR.I	1521.61384	2	4.39E-06	0.85	3.44	-	581.8
AHQ-9-6, 2343 - 2405	R.GSESGIFTNTK.E	1141.21317	2	5.08E-05	0.83	3.13	-	737.6
AHQ-9-13-, 3274 - 3282	R.HPDEAAFFDTASTGK.T	1594.66329	2	1.35E-04	0.37	2.70	-	305.8
AHQ-9-6, 2733	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	4.41E-08	0.96	4.62	-	1701.3
AHQ-9-13-, 2889	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	2.62E-04	0.87	3.35	-	1313.8
AHQ-9-7, 2261	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	8.33E-11	0.93	4.45	-	894.3
AHQ-9-8, 2275	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	1.31E-10	0.94	4.19	-	943.7
AHQ-9-6, 2243	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	3.19E-13	0.97	4.90	-	1361.2
AHQ-9-8, 2290 - 2291	R.PGSTGTWNPGSSER.G	1433.46515	2	1.14E-06	0.75	3.34	-	448.2
AHQ-9-6, 6301	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	3.55E-06	0.84	3.48	-	494.2
AHQ-9-7, 2492	K.VQHIQLLQK.N	1107.33106	2	4.15E-04	0.59	2.54	-	481.4
AHQ-9-8, 2460	K.VQHIQLLQK.N	1107.33106	2	2.71E-04	0.78	2.76	-	709.1
gi|5803181|ref|NP_006810.1|	stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo			7.90E-13	0.93	10.20	3.50	62638.9
AHQ-9-6, 5858 - 5859	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	7.90E-13	0.93	4.10	-	1165.7

gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				8.22E-13	17.01	200.27	38.50	55901.8
AHQ-9-6, 2485	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.22E-05	0.91	3.78	-	950.6
AHQ-9-11, 2486	K.AHYGGFTVQNEANK.Y	1536.63020	2	2.59E-04	0.87	2.92	-	876.1
AHQ-9-7, 2622	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.72E-08	0.90	3.62	-	892.5
AHQ-9-7, 2429 - 2468	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.19E-05	0.92	3.58	-	1063.1
AHQ-9-6, 3145	R.DNDGWLTSDPR.K	1276.29403	2	4.20E-05	0.72	2.75	-	801.0
AHQ-9-7, 4066 - 4140	K.DNENVVNEYSSELEK.H	1769.80167	2	1.60E-07	0.94	5.14	-	861.9
AHQ-9-7, 3876 - 3936	K.DNENVVNEYSSELEK.H	1769.80167	2	8.34E-05	0.80	3.78	-	519.8
AHQ-9-8, 3998 - 4055	K.DNENVVNEYSSELEK.H	1769.80167	2	1.90E-06	0.84	3.71	-	559.1
AHQ-9-6, 3282	K.DNENVVNEYSSELEK.H	1769.80167	2	8.07E-06	0.87	3.63	-	676.4
AHQ-9-12, 3972 - 3981	K.DNENVVNEYSSELEK.H	1769.80167	2	1.36E-04	0.78	3.79	-	456.8
AHQ-9-7, 3280 - 3348	K.DNENVVNEYSSELEK.H	1769.80167	2	2.50E-07	0.78	3.14	-	541.9
AHQ-9-6, 3915 - 3973	K.DNENVVNEYSSELEK.H	1769.80167	2	3.59E-07	0.93	4.44	-	893.7
AHQ-9-8, 4127	K.DNENVVNEYSSELEK.H	1769.80167	2	1.11E-06	0.59	3.04	-	495.0
AHQ-9-6, 4019 - 4077	K.DNENVVNEYSSELEK.H	1769.80167	2	6.95E-09	0.90	4.61	-	557.8
AHQ-9-6, 4153	K.DNENVVNEYSSELEK.H	1769.80167	2	2.03E-09	0.93	4.26	-	827.4
AHQ-9-7, 3540	K.DNENVVNEYSSELEK.H	1769.80167	2	1.03E-04	0.89	3.51	-	872.7
AHQ-9-6, 3383	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	1.97E-06	0.73	3.31	-	383.7
AHQ-9-7, 3368	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	1.72E-05	0.19	2.85	-	196.1
AHQ-9-7, 3968	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	7.11E-07	0.89	4.02	-	1131.5
AHQ-9-7, 3961 - 3976	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.57E-05	0.82	3.98	-	488.8
AHQ-9-6, 3586	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	3	3.39E-06	0.84	3.75	-	846.5
AHQ-9-7, 3574	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	3.60E-04	0.67	2.95	-	429.6
AHQ-9-6, 3990 - 3993	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	2.61E-04	0.87	4.23	-	515.7
AHQ-9-7, 3573 - 3576	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	3	9.76E-06	0.70	3.33	-	847.2
AHQ-9-7, 4130 - 4198	K.HGTDDGVVWMNWK.G	1545.70374	2	8.79E-07	0.95	4.57	-	1348.8
AHQ-9-7, 3681 - 3690	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	2.09E-04	0.71	3.37	-	570.6
AHQ-9-6, 3321	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	3.63E-06	0.82	4.04	-	516.8
AHQ-9-6, 3685 - 3733	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	1.24E-04	0.76	3.29	-	732.3
AHQ-9-7, 3393 - 3453	K.LESDVSAQMEYCR.T	1589.73005	2	3.42E-05	0.49	2.53	-	625.1
AHQ-9-7, 2588	K.LESDVSAQM*EYCR.T	1605.72945	2	1.91E-04	0.39	2.54	-	334.1
AHQ-9-6, 2599 - 2626	K.LESDVSAQM*EYCR.T	1605.72945	2	7.52E-04	0.96	4.58	-	1219.9
AHQ-9-8, 2618	K.LESDVSAQM*EYCR.T	1605.72945	2	4.55E-08	0.90	3.74	-	742.1
AHQ-9-7, 3245 - 3308	K.LESDVSAQMEYCR.T	1589.73005	2	2.55E-04	0.72	3.01	-	700.6
AHQ-9-7, 5808	R.M*GPTELLIEMEDWK.G	1708.97776	2	9.30E-04	0.89	3.61	-	885.9
AHQ-9-6, 5823 - 5831	R.M*GPTELLIEMEDWK.G	1708.97776	2	4.41E-07	0.97	4.74	-	1646.9
AHQ-9-6, 4955 - 4970	K.NYCGLPGEYWLGNDK.I	1787.92994	2	7.04E-05	0.59	2.74	-	278.3
AHQ-9-6, 4830 - 4886	K.NYCGLPGEYWLGNDK.I	1787.92994	2	3.01E-07	0.87	3.85	-	332.0
AHQ-9-7, 4854 - 4920	K.NYCGLPGEYWLGNDK.I	1787.92994	2	7.77E-04	0.71	3.36	-	250.9
AHQ-9-6, 3114 - 3174	K.REEAPSLRPAPPPISGGGYR.A	2108.34617	3	1.14E-04	0.97	5.48	-	2026.3
AHQ-9-7, 3674	R.TPCTVSCNIPVVSGK.E	1621.85811	2	8.77E-07	0.63	3.23	-	305.3
AHQ-9-7, 4628 - 4668	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.73E-07	0.93	4.05	-	1132.0
AHQ-9-7, 4546	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	3.55E-04	0.91	3.79	-	1310.0
AHQ-9-6, 4649	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	8.22E-13	0.96	4.66	-	1791.0
AHQ-9-6, 4566 - 4582	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.01E-04	0.83	3.74	-	723.2
AHQ-9-6, 3810 - 3885	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	6.04E-06	0.94	4.58	-	987.6
AHQ-9-7, 4236 - 4294	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	2.79E-08	0.88	3.85	-	850.0
AHQ-9-7, 3806 - 3885	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	3.88E-06	0.94	4.79	-	911.9
AHQ-9-6, 3911	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	3.22E-09	0.89	3.51	-	1098.7
AHQ-9-7, 4297 - 4377	R.YYWGGQYTWDM*AK.H	1685.83949	2	8.25E-04	0.97	4.26	-	1702.9
AHQ-9-7, 4785	R.YYWGGQYTWDMAK.H	1669.84009	2	3.27E-06	0.91	2.86	-	1063.1
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				8.60E-13	22.41	250.29	56.70	75429.7
AHQ-9-6, 3349	K.AGDALWLR.F	902.03223	2	9.79E-05	0.89	3.37	-	1327.7
AHQ-9-2, 6289	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.75E-05	0.71	2.58	-	557.9
AHQ-9-7, 6077	R.ASFSQPLFQAVAAICR.L	1768.02967	3	2.38E-04	0.91	3.71	-	1318.6
AHQ-9-6, 6019 - 6081	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.08E-08	0.96	4.87	-	960.1
AHQ-9-6, 6082 - 6098	R.ASFSQPLFQAVAAICR.L	1768.02967	3	2.41E-08	0.74	3.60	-	776.5
AHQ-9-7, 6060 - 6084	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.23E-04	0.92	4.09	-	707.2
AHQ-9-6, 6214	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.01E-08	0.86	3.28	-	668.3
AHQ-9-5, 6183	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.14E-04	0.79	2.92	-	884.9
AHQ-9-6, 6193	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	2	2.80E-04	0.94	5.05	-	647.8
AHQ-9-6, 6194	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	3	2.16E-07	0.97	5.10	-	1682.8
AHQ-9-6, 3205 - 3249	K.GCEVVPDVNVSGQK.F	1489.63335	2	4.86E-08	0.88	2.91	-	921.1
AHQ-9-6, 6233	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	2.48E-07	0.94	4.62	-	914.0
AHQ-9-6, 3149	R.GM*PAHFSDSAQTEACYHM*LSR.P	2430.63997	3	2.03E-04	0.80	3.26	-	1024.9
AHQ-9-12, 4344	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	2.90E-05	0.96	4.87	-	1269.4
AHQ-9-6, 4573	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	3	1.13E-04	0.90	3.93	-	1286.1
AHQ-9-6, 4307	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	8.60E-13	0.98	5.84	-	1857.3
AHQ-9-9, 4149 - 4188	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	8.68E-04	0.94	4.50	-	1118.4
AHQ-9-6, 2717 - 2773	R.KDEILGIANNR.L	1243.39499	2	1.92E-05	0.96	4.42	-	1599.3
AHQ-9-6, 2849 - 2917	R.KDEILGIANNR.L	1243.39499	2	4.96E-04	0.77	3.05	-	928.3
AHQ-9-11, 2734	R.KDEILGIANNR.L	1243.39499	2	3.59E-04	0.85	2.84	-	1309.1
AHQ-9-6, 3978	R.KQDWSDHAIWWEQK.R	1858.00504	3	1.07E-06	0.92	3.99	-	1224.4
AHQ-9-6, 5655 - 5713	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	8.91E-04	0.71	3.31	-	439.4
AHQ-9-7, 6000	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.03E-06	0.88	3.90	-	582.0
AHQ-9-6, 5909	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.02E-04	0.69	2.96	-	563.6
AHQ-9-5, 6115 - 6116	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	3.58E-04	0.90	3.95	-	605.5
AHQ-9-6, 5201 - 5250	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	4.76E-05	0.90	3.94	-	767.3
AHQ-9-8, 6094 - 6096	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	7.15E-05	0.75	3.78	-	384.0
AHQ-9-6, 5802 - 5821	K.LEGSAPTDVLDSLTTIPELKDHLR.I	2621.92493	3	1.19E-10	0.93	4.67	-	699.9
AHQ-9-6, 2663 - 2677	R.LFFGPQHR.P	1002.15349	2	4.20E-04	0.52	2.54	-	452.0
AHQ-9-6, 2114 - 2174	R.LPRPSSLSDK.T	1100.25055	2	3.36E-04	0.85	3.05	-	843.7
AHQ-9-7, 6148 - 6149	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.11E-06	0.95	4.87	-	1591.9
AHQ-9-4, 6241 - 6244	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.80E-08	0.94	5.03	-	1222.8
AHQ-9-3, 6176 - 6177	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.34E-04	0.80	3.67	-	789.7
AHQ-9-5, 2467	R.LTQLYEQAR.W	1122.25622	2	7.30E-07	0.84	2.95	-	850.2
AHQ-9-6, 2410 - 2469	R.LTQLYEQAR.W	1122.25622	2	1.40E-05	0.91	3.49	-	1057.5
AHQ-9-7, 2453	R.LTQLYEQAR.W	1122.25622	2	2.01E-04	0.93	3.37	-	1516.4
AHQ-9-6, 4347	K.RQWLLQTHWTLDK.Y	1725.97442	3	1.61E-05	0.91	3.78	-	1298.0
AHQ-9-6, 4001 - 4074	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	1.58E-05	0.73	3.26	-	299.0
AHQ-9-7, 3920	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	2.93E-05	0.74	3.10	-	516.2
AHQ-9-11, 3922	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	2.30E-05	0.72	3.03	-	338.6
AHQ-9-6, 3886 - 3925	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	3.17E-10	0.94	4.58	-	704.7
AHQ-9-9, 3773	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	8.38E-04	0.64	2.76	-	371.1
AHQ-9-6, 3935	K.SQDEAPGDPIQQLNLK.G	1753.89174	3	3.42E-08	0.71	3.27	-	623.9
AHQ-9-6, 4175 - 4237	K.TASGDYIDSSWELR.V	1600.66783	2	1.12E-07	0.94	4.07	-	892.1
AHQ-9-6, 4065	K.TASGDYIDSSWELR.V	1600.66783	2	3.89E-07	0.80	3.11	-	532.9
AHQ-9-7, 4173	K.TASGDYIDSSWELR.V	1600.66783	2	4.37E-10	0.92	3.84	-	955.1
AHQ-9-6, 3966	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	3.46E-06	0.95	5.72	-	1003.8
AHQ-9-6, 3821	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	6.64E-05	0.63	3.12	-	360.9
AHQ-9-6, 6349 - 6350	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	2	5.32E-05	0.97	5.48	-	1232.1
AHQ-9-7, 3852 - 3853	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.71E-09	0.97	5.10	-	1596.1
AHQ-9-14-, 3931 - 3947	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.14E-08	0.75	3.16	-	744.3
AHQ-9-6, 3865	R.VFVGEEDPEAESVTLR.V	1777.91007	3	3.42E-04	0.97	4.59	-	2594.3
AHQ-9-6, 3839 - 3843	R.VFVGEEDPEAESVTLR.V	1777.91007	2	8.58E-06	0.95	4.41	-	1458.8
AHQ-9-11, 3846	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.15E-06	0.84	3.23	-	662.2
AHQ-9-12, 3886	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.25E-05	0.69	2.72	-	781.1

AHQ-9-4, 3917 - 3924	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.97E-12	0.94	4.36	-	1269.0
AHQ-9-3, 3905	R.VFVGEEDPEAESVTLR.V	1777.91007	2	7.55E-05	0.81	3.29	-	976.5
AHQ-9-13, 4066	R.VFVGEEDPEAESVTLR.V	1777.91007	2	4.74E-06	0.92	3.60	-	944.4
AHQ-9-8, 3908	R.VFVGEEDPEAESVTLR.V	1777.91007	2	3.20E-10	0.93	4.44	-	1229.4
AHQ-9-1, 4076 - 4090	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.25E-06	0.84	3.68	-	556.1
AHQ-9-6, 2922 - 2965	R.VTGESHIGGVLLK.I	1310.52448	2	3.65E-09	0.96	4.53	-	1502.7
AHQ-9-7, 2917	R.VTGESHIGGVLLK.I	1310.52448	2	3.84E-04	0.94	3.77	-	1566.0
AHQ-9-5, 2952	R.VTGESHIGGVLLK.I	1310.52448	2	1.40E-04	0.81	2.73	-	1284.6
AHQ-9-10, 4538	K.VVLAGGVAPALFR.G	1270.54832	2	1.21E-04	0.76	2.65	-	872.9
AHQ-9-9, 4441 - 4453	K.VVLAGGVAPALFR.G	1270.54832	2	1.93E-04	0.97	4.25	-	2254.1
AHQ-9-6, 4609	K.VVLAGGVAPALFR.G	1270.54832	2	2.32E-08	0.96	4.35	-	1493.8
AHQ-9-5, 4693	K.VVLAGGVAPALFR.G	1270.54832	2	2.39E-06	0.97	4.62	-	1675.7
AHQ-9-11, 4582 - 4655	K.VVLAGGVAPALFR.G	1270.54832	2	3.64E-05	0.91	3.67	-	1091.9
AHQ-9-7, 4605	K.VVLAGGVAPALFR.G	1270.54832	2	1.16E-08	0.97	4.95	-	2006.4
AHQ-9-2, 4813	K.VVLAGGVAPALFR.G	1270.54832	2	4.87E-04	0.96	3.99	-	1854.6
AHQ-9-4, 4709	K.VVLAGGVAPALFR.G	1270.54832	2	2.64E-05	0.94	4.09	-	1336.6
AHQ-9-6, 2566 - 2706	K.YGILADAR.L	878.99544	2	9.53E-05	0.90	2.87	-	867.7
AHQ-9-9, 4911	K.YYSFFDLDPK.T	1295.42046	2	1.13E-05	0.93	3.51	-	763.2
gi|4505257|ref|NP_002435.1| moesin [Homo sapiens]				1.14E-12	8.99	100.29	22.40	67819.5
AHQ-9-6, 2319 - 2321	R.ALELEQER.K	988.07707	2	5.80E-05	0.83	3.11	-	1024.4
AHQ-9-6, 2645 - 2646	K.ALTSELANAR.D	1046.15975	2	4.29E-05	0.88	3.24	-	687.3
AHQ-9-6, 2415	K.AQMVQEDLEK.T	1191.33713	2	7.26E-05	0.67	2.92	-	449.7
AHQ-9-6, 5593	R.EVWFFGLQYQDTK.G	1661.83760	2	7.55E-09	0.93	3.77	-	1013.5
AHQ-9-6, 6238 - 6242	K.FYPEDVSEELIQDITQR.L	2083.24065	3	3.18E-07	0.96	5.21	-	1425.0
AHQ-9-6, 6241 - 6295	K.FYPEDVSEELIQDITQR.L	2083.24065	2	7.56E-07	0.88	3.65	-	724.9
AHQ-9-6, 5165	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	3.81E-06	0.94	4.69	-	781.4
AHQ-9-6, 2137 - 2215	R.IQVWHEEHR.G	1234.34835	2	2.35E-05	0.91	2.93	-	1442.2
AHQ-9-6, 3054	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	1.14E-12	0.96	5.84	-	1663.9
AHQ-9-6, 3185	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	1.35E-07	0.96	5.11	-	1799.2
AHQ-9-6, 3342 - 3401	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	6.44E-12	0.96	5.84	-	1573.8
AHQ-9-6, 5017	K.TQEQLALEMAELTAR.I	1704.92727	2	2.69E-08	0.94	3.45	-	1518.9
AHQ-9-6, 5030	K.TQEQLALEMAELTAR.I	1704.92727	3	5.89E-04	0.95	4.29	-	1729.2
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				1.21E-12	80.02	890.36	43.10	226529.8
AHQ-9-3, 2154	R.ALEEAMEQK.A	1049.18068	2	3.53E-04	0.80	3.10	-	803.3
AHQ-9-2, 2194	R.ALEEAMEQK.A	1049.18068	2	7.21E-04	0.91	3.78	-	837.7
AHQ-9-4, 3666 - 3672	K.ALELDSNLYR.I	1194.31920	2	1.70E-06	0.95	4.21	-	1057.1
AHQ-9-2, 3654	K.ALELDSNLYR.I	1194.31920	2	2.61E-06	0.93	3.49	-	1297.6
AHQ-9-1, 3858	K.ALELDSNLYR.I	1194.31920	2	1.27E-06	0.95	4.03	-	1350.1
AHQ-9-5, 3671 - 3732	K.ALELDSNLYR.I	1194.31920	2	4.01E-05	0.84	2.74	-	892.4
AHQ-9-3, 3665	K.ALELDSNLYR.I	1194.31920	2	1.20E-06	0.93	3.77	-	1194.0
AHQ-9-2, 3766 - 3771	K.ALELDSNLYR.I	1194.31920	2	5.01E-07	0.94	3.75	-	1281.3
AHQ-9-3, 2218	R.ALEQQVEEM*K.T	1221.36320	2	5.49E-04	0.91	3.78	-	1068.5
AHQ-9-5, 2187	R.ALEQQVEEM*K.T	1221.36320	2	5.45E-04	0.82	2.86	-	818.2
AHQ-9-3, 2936 - 2941	R.ALEQQVEEMK.T	1205.36380	2	2.46E-05	0.89	3.50	-	1164.2
AHQ-9-6, 2851 - 2911	R.ALEQQVEEMK.T	1205.36380	2	9.21E-05	0.87	3.37	-	922.7
AHQ-9-2, 3001 - 3015	R.ALEQQVEEMK.T	1205.36380	2	2.23E-05	0.89	3.73	-	1052.0
AHQ-9-2, 5965	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	3.23E-11	0.98	6.60	-	2047.4
AHQ-9-1, 5924 - 5986	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	9.78E-09	0.92	4.63	-	983.1
AHQ-9-3, 5800	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	9.55E-06	0.95	5.14	-	1734.4
AHQ-9-5, 5877	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	5.87E-07	0.95	5.28	-	1366.9
AHQ-9-1, 4987	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.49E-05	0.52	2.62	-	540.1
AHQ-9-2, 4849	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.45E-09	0.96	4.87	-	1325.0
AHQ-9-5, 4772	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.19E-04	0.71	2.71	-	711.5
AHQ-9-8, 4750 - 4827	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.57E-04	0.87	3.53	-	1015.7
AHQ-9-1, 4906	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.93E-05	0.96	4.93	-	1293.8
AHQ-9-6, 4705	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.85E-06	0.95	4.64	-	1145.7
AHQ-9-4, 4705 - 4773	K.ANLQIDQINTDLNLER.S	1871.04187	2	7.92E-07	0.97	5.23	-	1346.8
AHQ-9-9, 4543	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.84E-05	0.94	4.36	-	985.8
AHQ-9-3, 4541	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.81E-06	0.86	3.66	-	551.5
AHQ-9-2, 4935 - 5010	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.24E-08	0.95	4.69	-	1064.2
AHQ-9-2, 4665 - 4738	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.56E-11	0.96	5.59	-	922.2
AHQ-9-3, 4722	K.ANLQIDQINTDLNLER.S	1871.04187	2	7.21E-09	0.95	4.55	-	1035.4
AHQ-9-3, 2470	K.ASITALEAK.I	904.04321	2	1.22E-04	0.89	3.17	-	975.4
AHQ-9-2, 2530	K.ASITALEAK.I	904.04321	2	7.41E-05	0.93	3.27	-	1235.8
AHQ-9-5, 2441	K.ASITALEAK.I	904.04321	2	5.94E-06	0.79	2.61	-	694.5
AHQ-9-3, 2190	R.ASREEILAQAK.E	1216.36955	2	1.31E-06	0.95	3.71	-	1770.9
AHQ-9-4, 2164	R.ASREEILAQAK.E	1216.36955	2	5.52E-05	0.76	2.86	-	877.6
AHQ-9-6, 6059 - 6061	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.96E-06	0.92	4.27	-	1334.9
AHQ-9-4, 6128 - 6129	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.40E-06	0.98	6.28	-	2297.2
AHQ-9-2, 6225 - 6229	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.49E-06	0.91	4.54	-	1374.3
AHQ-9-1, 6230	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.61E-04	0.69	3.09	-	781.6
AHQ-9-2, 5933	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	5.54E-08	0.91	4.06	-	1057.1
AHQ-9-2, 2314	K.DLEAHIDSANK.N	1213.27938	2	1.28E-05	0.97	3.95	-	1934.8
AHQ-9-4, 2233	K.DLEAHIDSANK.N	1213.27938	2	5.69E-05	0.96	3.32	-	1901.8
AHQ-9-1, 6503	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	5.21E-10	0.89	3.54	-	1223.9
AHQ-9-3, 6356	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	9.93E-06	0.87	3.98	-	1110.1
AHQ-9-3, 3286	K.DVLLQVDDER.R	1202.29650	2	1.61E-05	0.86	2.82	-	984.3
AHQ-9-2, 3371 - 3377	K.DVLLQVDDER.R	1202.29650	2	3.59E-07	0.92	3.63	-	959.1
AHQ-9-2, 2121	R.EEILAQAK.E	902.02731	1	1.56E-04	0.37	2.39	-	304.1
AHQ-9-4, 2816	R.ELEDATETADAMNR.E	1566.63006	2	4.26E-06	0.92	3.81	-	1078.5
AHQ-9-6, 2815 - 2821	R.ELEDATETADAMNR.E	1566.63006	2	4.72E-08	0.94	4.31	-	1064.6
AHQ-9-2, 2311	R.ELEDATETADAM*NR.E	1582.62946	2	2.20E-05	0.84	3.05	-	868.3
AHQ-9-3, 2840	R.ELEDATETADAMNR.E	1566.63006	2	9.40E-08	0.93	3.69	-	1414.5
AHQ-9-2, 2891 - 2898	R.ELEDATETADAMNR.E	1566.63006	2	4.05E-09	0.90	3.96	-	1141.6
AHQ-9-5, 2820	R.ELEDATETADAMNR.E	1566.63006	2	2.73E-07	0.90	3.58	-	1066.2
AHQ-9-5, 5365	R.ELESQISELQEDLESER.A	2035.10956	2	2.71E-06	0.93	4.17	-	970.1
AHQ-9-2, 5394 - 5453	R.ELESQISELQEDLESER.A	2035.10956	2	1.82E-05	0.93	4.52	-	1126.2
AHQ-9-4, 5352	R.ELESQISELQEDLESER.A	2035.10956	2	1.55E-12	0.97	5.99	-	1015.4
AHQ-9-3, 5293	R.ELESQISELQEDLESER.A	2035.10956	3	5.45E-05	0.98	6.05	-	2316.9
AHQ-9-3, 5256 - 5304	R.ELESQISELQEDLESER.A	2035.10956	2	1.33E-05	0.96	5.48	-	1055.5
AHQ-9-2, 5129	R.ELESQISELQEDLESER.A	2035.10956	2	6.01E-07	0.86	3.67	-	600.7
AHQ-9-1, 5467 - 5468	R.ELESQISELQEDLESER.A	2035.10956	2	1.64E-07	0.94	4.64	-	1032.0
AHQ-9-6, 5293 - 5301	R.ELESQISELQEDLESER.A	2035.10956	2	4.95E-09	0.97	5.23	-	1220.7
AHQ-9-3, 2310	R.EMEAELEDERK.Q	1379.47597	2	7.02E-07	0.82	3.13	-	773.7
AHQ-9-2, 2358 - 2370	R.EMEAELEDERK.Q	1379.47597	2	6.41E-07	0.95	3.59	-	1815.8
AHQ-9-5, 2272	R.EMEAELEDERK.Q	1379.47597	2	3.75E-05	0.85	3.06	-	998.0
AHQ-9-5, 2476	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	8.99E-04	0.80	3.67	-	599.1
AHQ-9-2, 2558 - 2559	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.32E-07	0.87	4.23	-	598.3
AHQ-9-2, 3439	R.FLSNGHVTIPGQQDK.D	1641.80946	2	4.46E-05	0.79	2.93	-	613.9
AHQ-9-3, 2997	K.HEAMITDLEER.L	1344.47646	2	4.04E-06	0.96	3.92	-	1528.1
AHQ-9-2, 3062	K.HEAMITDLEER.L	1344.47646	2	4.72E-06	0.95	4.03	-	1012.8
AHQ-9-2, 3437	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	3.32E-07	0.98	4.91	-	2415.6
AHQ-9-2, 3690	R.HEMPPHIYAITDTAYR.S	1916.14944	3	3.66E-10	0.95	3.86	-	2057.6
AHQ-9-3, 3370	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	8.67E-04	0.51	2.53	-	356.2
AHQ-9-2, 3443	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	2.66E-05	0.89	3.26	-	767.0
AHQ-9-2, 4465	K.HSQAVEELAEQLEQTK.R	1840.96940	3	3.68E-07	0.96	4.65	-	1984.5
AHQ-9-3, 4353	K.HSQAVEELAEQLEQTK.R	1840.96940	3	1.29E-07	0.97	4.88	-	2606.0

AHQ-9-3, 4356	K.HSQAVEELAEQLEQTK.R	1840.96940	2	3.54E-09	0.98	5.86	-	2185.6
AHQ-9-4, 4368	K.HSQAVEELAEQLEQTK.R	1840.96940	3	5.77E-07	0.95	4.98	-	1836.7
AHQ-9-2, 4469	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.38E-08	0.98	5.60	-	2203.3
AHQ-9-2, 4158	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.08E-05	0.98	6.24	-	2288.9
AHQ-9-3, 4056	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.96E-07	0.96	5.22	-	1405.0
AHQ-9-3, 4061	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.52E-07	0.98	6.12	-	1608.7
AHQ-9-5, 4071	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.01E-08	0.98	5.99	-	1839.0
AHQ-9-2, 4161	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.19E-05	0.99	6.60	-	2424.0
AHQ-9-4, 4057	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	1.64E-06	0.98	5.94	-	2094.9
AHQ-9-6, 4039	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.33E-05	0.93	4.48	-	1041.7
AHQ-9-2, 3834	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.15E-04	0.96	4.13	-	1598.4
AHQ-9-1, 3806	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.12E-07	0.96	4.42	-	1870.8
AHQ-9-6, 3591 - 3597	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.37E-10	0.98	5.25	-	2282.2
AHQ-9-2, 3621 - 3678	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.43E-08	0.91	3.27	-	1101.4
AHQ-9-5, 3632	R.IAEFTTNLTEEEEK.S	1654.75371	2	5.39E-07	0.97	4.36	-	1903.4
AHQ-9-7, 3588	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.02E-06	0.94	3.71	-	1563.3
AHQ-9-2, 3737	R.IAEFTTNLTEEEEK.S	1654.75371	2	6.86E-06	0.96	4.20	-	1747.6
AHQ-9-3, 3744 - 3812	R.IAEFTTNLTEEEEK.S	1654.75371	2	7.36E-04	0.96	4.45	-	1329.2
AHQ-9-4, 3624 - 3625	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.55E-06	0.97	4.88	-	1853.1
AHQ-9-3, 3580 - 3636	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.51E-08	0.96	4.87	-	1553.2
AHQ-9-2, 3477	R.IAEFTTNLTEEEEKSK.S	1870.00428	3	8.13E-06	0.65	3.07	-	391.1
AHQ-9-5, 4863	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	1.05E-05	0.78	3.69	-	615.6
AHQ-9-3, 5050	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	2.14E-09	0.86	4.27	-	774.4
AHQ-9-1, 5224 - 5236	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	5.22E-05	0.61	3.24	-	501.3
AHQ-9-4, 5097	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	6.60E-11	0.86	4.09	-	706.8
AHQ-9-2, 5201	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	2	6.10E-04	0.85	3.99	-	600.6
AHQ-9-3, 3105	K.IAQLEEQLDNETK.E	1531.64695	2	1.29E-07	0.94	3.62	-	1520.3
AHQ-9-3, 3277 - 3336	K.IAQLEEQLDNETK.E	1531.64695	2	3.01E-06	0.97	4.71	-	1673.0
AHQ-9-2, 3409	K.IAQLEEQLDNETK.E	1531.64695	2	3.40E-08	0.97	4.32	-	1752.2
AHQ-9-5, 3327 - 3335	K.IAQLEEQLDNETK.E	1531.64695	2	9.88E-09	0.96	4.83	-	1567.5
AHQ-9-2, 3011 - 3077	K.IAQLEEQLDNETK.E	1531.64695	2	6.62E-04	0.90	3.19	-	1140.4
AHQ-9-4, 3030 - 3093	K.IAQLEEQLDNETK.E	1531.64695	2	2.34E-07	0.93	3.97	-	1169.3
AHQ-9-8, 3298	K.IAQLEEQLDNETK.E	1531.64695	2	4.39E-05	0.95	3.67	-	1604.2
AHQ-9-6, 3078	K.IAQLEEQLDNETK.E	1531.64695	2	1.19E-05	0.94	3.68	-	1471.4
AHQ-9-4, 3318	K.IAQLEEQLDNETK.E	1531.64695	2	2.23E-05	0.97	4.62	-	2006.1
AHQ-9-10, 3258 - 3320	K.IAQLEEQLDNETK.E	1531.64695	2	4.39E-04	0.89	2.90	-	1147.9
AHQ-9-2, 3169	K.IAQLEEQLDNETK.E	1531.64695	2	1.55E-09	0.97	4.21	-	2311.7
AHQ-9-11, 3285 - 3286	K.IAQLEEQLDNETK.E	1531.64695	2	5.44E-10	0.97	4.83	-	1571.6
AHQ-9-6, 3302	K.IAQLEEQLDNETK.E	1531.64695	2	1.63E-09	0.95	4.43	-	1334.9
AHQ-9-7, 3301	K.IAQLEEQLDNETK.E	1531.64695	2	4.07E-06	0.77	2.80	-	817.1
AHQ-9-1, 3512 - 3579	K.IAQLEEQLDNETK.E	1531.64695	2	1.89E-05	0.96	4.44	-	1470.3
AHQ-9-2, 3535	K.IAQLEEQLDNETKER.Q	1816.94784	2	7.96E-08	0.93	4.39	-	996.4
AHQ-9-2, 4993	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	4.23E-04	0.91	3.81	-	771.7
AHQ-9-2, 6009 - 6083	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.41E-06	0.97	5.85	-	1324.5
AHQ-9-1, 5360 - 5427	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	1.17E-04	0.96	5.48	-	804.9
AHQ-9-3, 5856	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	8.41E-06	0.96	4.48	-	1349.5
AHQ-9-6, 3797	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	3.25E-05	0.92	3.90	-	790.9
AHQ-9-2, 5038	R.IMGIPEEEQMGLLR.V	1616.92826	2	1.23E-04	0.75	3.08	-	392.9
AHQ-9-2, 4481 - 4537	R.IM*GIPEEEQMGLLR.V	1632.92766	2	8.21E-04	0.94	3.99	-	1016.3
AHQ-9-5, 3843	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	1.52E-04	0.90	3.75	-	771.0
AHQ-9-2, 3930	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	6.83E-07	0.91	3.76	-	774.0
AHQ-9-2, 5410 - 5487	K.IRELESQISELQEDLESER.A	2304.45416	3	1.78E-08	0.97	5.99	-	1556.9
AHQ-9-2, 5490 - 5509	K.IRELESQISELQEDLESER.A	2304.45416	2	2.18E-10	0.98	7.17	-	1668.2
AHQ-9-3, 5272 - 5337	K.IRELESQISELQEDLESER.A	2304.45416	3	1.56E-06	0.96	5.13	-	1597.3
AHQ-9-3, 5340	K.IRELESQISELQEDLESER.A	2304.45416	2	1.58E-07	0.97	5.44	-	1133.1
AHQ-9-1, 5510 - 5523	K.IRELESQISELQEDLESER.A	2304.45416	3	3.83E-06	0.95	5.01	-	1446.3
AHQ-9-2, 4919 - 4998	K.ITDVIIGFQACCR.G	1555.80136	2	3.56E-09	0.95	4.46	-	1251.8
AHQ-9-2, 4277	K.KANLQIDQINTDLNLER.S	1999.21478	3	4.96E-05	0.43	3.02	-	432.4
AHQ-9-2, 4387 - 4457	K.KANLQIDQINTDLNLER.S	1999.21478	2	7.11E-07	0.97	5.35	-	1437.1
AHQ-9-2, 4453 - 4519	K.KANLQIDQINTDLNLER.S	1999.21478	3	1.02E-05	0.85	4.15	-	828.1
AHQ-9-3, 4340	K.KANLQIDQINTDLNLER.S	1999.21478	3	1.41E-05	0.82	3.65	-	1147.1
AHQ-9-3, 2745	R.KKVEAQLQELQVK.F	1541.81761	3	1.26E-04	0.76	3.20	-	1039.2
AHQ-9-3, 2744 - 2806	R.KKVEAQLQELQVK.F	1541.81761	2	9.72E-06	0.96	4.14	-	1592.3
AHQ-9-4, 2709	R.KKVEAQLQELQVK.F	1541.81761	2	2.83E-08	0.95	4.33	-	1322.1
AHQ-9-2, 2778	R.KKVEAQLQELQVK.F	1541.81761	2	3.23E-07	0.97	4.80	-	1540.3
AHQ-9-5, 3483	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.23E-05	0.93	3.99	-	1161.3
AHQ-9-2, 3577 - 3619	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.46E-11	0.97	5.38	-	1383.4
AHQ-9-3, 3418 - 3477	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.34E-11	0.98	6.06	-	2149.1
AHQ-9-2, 3451 - 3517	K.KLEEEQIILEDQNCK.L	1891.08992	2	1.25E-05	0.98	5.17	-	2006.6
AHQ-9-3, 3784	K.KLEEEQIILEDQNCKLAK.E	2203.49930	3	2.02E-04	0.97	5.30	-	1819.4
AHQ-9-5, 6291 - 6292	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	7.47E-05	0.91	4.71	-	896.4
AHQ-9-3, 5564	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	8.08E-04	0.91	3.86	-	1391.7
AHQ-9-2, 6315 - 6377	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	3.66E-08	0.94	5.72	-	959.9
AHQ-9-1, 6368 - 6382	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	3.26E-07	0.91	4.86	-	759.6
AHQ-9-6, 6209	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.52E-06	0.87	4.59	-	532.1
AHQ-9-3, 6136 - 6212	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.49E-07	0.95	5.57	-	991.2
AHQ-9-4, 6272	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.35E-08	0.92	5.05	-	779.8
AHQ-9-2, 6379	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	3.49E-08	0.98	6.27	-	1637.4
AHQ-9-2, 2993 - 2999	K.KLVWVPSDK.S	1072.28194	2	2.42E-04	0.93	3.52	-	1239.0
AHQ-9-2, 3037	K.KM*EDSVGCLETAEEVKR.K	1999.21025	2	8.03E-11	0.93	4.17	-	872.4
AHQ-9-3, 2973	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	9.37E-06	0.96	4.95	-	1845.1
AHQ-9-5, 2953	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	2.02E-05	0.86	3.83	-	833.6
AHQ-9-4, 3276	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	6.51E-07	0.87	4.01	-	806.2
AHQ-9-2, 3373	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	5.44E-09	0.96	5.50	-	1181.4
AHQ-9-5, 3281	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.07E-11	0.80	3.75	-	746.3
AHQ-9-2, 4698	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	5.39E-04	0.93	4.79	-	1104.6
AHQ-9-5, 4011	K.KQELEEICHDLEAR.V	1771.93036	2	2.17E-04	0.98	5.42	-	2092.6
AHQ-9-4, 3997 - 4010	K.KQELEEICHDLEAR.V	1771.93036	2	5.81E-05	0.96	4.56	-	1513.8
AHQ-9-6, 3969	K.KQELEEICHDLEAR.V	1771.93036	3	3.32E-04	0.95	4.77	-	1581.4
AHQ-9-3, 3993	K.KQELEEICHDLEAR.V	1771.93036	3	1.87E-04	0.95	5.32	-	1269.9
AHQ-9-3, 3037	K.KVEAQLQELQVK.F	1413.64470	2	5.27E-04	0.96	4.14	-	1762.1
AHQ-9-2, 3101	K.KVEAQLQELQVK.F	1413.64470	2	4.12E-07	0.96	4.49	-	1537.0
AHQ-9-4, 3008	K.KVEAQLQELQVK.F	1413.64470	2	1.26E-04	0.95	4.28	-	1442.8
AHQ-9-5, 3004	K.KVEAQLQELQVK.F	1413.64470	2	4.35E-07	0.96	4.52	-	1646.6
AHQ-9-2, 3765 - 3822	K.LEEEQIILEDQNCK.L	1762.91700	2	1.40E-08	0.98	5.76	-	1577.2
AHQ-9-3, 3638 - 3720	K.LEEEQIILEDQNCK.L	1762.91700	2	5.30E-10	0.97	5.85	-	1049.7
AHQ-9-2, 6429	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	1.51E-06	0.90	4.60	-	780.3
AHQ-9-2, 2734	R.LEVNLQAM*K.A	1062.26570	2	1.84E-04	0.82	3.20	-	548.0
AHQ-9-4, 3494	R.LEVNLQAMK.A	1046.26630	2	3.82E-04	0.82	2.86	-	683.4
AHQ-9-2, 3579 - 3583	R.LEVNLQAMK.A	1046.26630	2	4.14E-05	0.90	3.80	-	684.0
AHQ-9-2, 3563	K.LKDVLLQVDDER.R	1443.62767	2	1.28E-10	0.95	4.21	-	1345.5
AHQ-9-3, 3185	K.LKDVLLQVDDERR.N	1599.81402	3	1.29E-05	0.87	3.98	-	741.6
AHQ-9-2, 3187 - 3254	K.LKDVLLQVDDERR.N	1599.81402	2	2.58E-04	0.59	2.82	-	627.1
AHQ-9-2, 6558 - 6635	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	3	4.07E-05	0.85	3.49	-	1259.7
AHQ-9-1, 5726	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.68E-11	0.97	5.26	-	2026.5
AHQ-9-4, 5596 - 5676	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	9.95E-04	0.91	4.17	-	839.0
AHQ-9-4, 5601	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	3.57E-09	0.97	4.81	-	1807.6

AHQ-9-6, 5539 - 5546	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.18E-08	0.96	4.64	-	1579.5
AHQ-9-2, 5327 - 5383	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.06E-07	0.94	4.51	-	1093.4
AHQ-9-5, 5619 - 5624	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	2.04E-07	0.88	3.91	-	857.8
AHQ-9-2, 5699 - 5718	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.60E-11	0.97	5.36	-	1630.9
AHQ-9-7, 5537	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.19E-09	0.83	3.53	-	732.7
AHQ-9-5, 5623	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	9.94E-07	0.96	5.18	-	1311.3
AHQ-9-3, 5546 - 5569	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	4.89E-07	0.94	5.15	-	992.3
AHQ-9-3, 5548	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	5.63E-11	0.98	5.03	-	2539.2
AHQ-9-2, 5697 - 5698	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	2.18E-08	0.91	4.56	-	829.9
AHQ-9-4, 5292 - 5348	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.62E-05	0.97	5.48	-	1308.4
AHQ-9-7, 5237	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.90E-04	0.91	4.16	-	671.2
AHQ-9-2, 5415	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	2.79E-06	0.97	6.19	-	1691.2
AHQ-9-2, 6574	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.45E-05	0.82	3.09	-	763.1
AHQ-9-3, 5302 - 5332	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.29E-05	0.96	4.73	-	1284.0
AHQ-9-4, 5405	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.27E-05	0.94	4.54	-	894.2
AHQ-9-2, 5386 - 5445	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.41E-11	0.98	6.00	-	1775.5
AHQ-9-2, 5501	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.21E-12	0.98	6.96	-	1439.4
AHQ-9-3, 5260	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	2.80E-05	0.96	5.21	-	1714.6
AHQ-9-2, 5133	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.50E-07	0.94	4.21	-	1217.9
AHQ-9-1, 5448	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	1.63E-05	0.93	4.23	-	1387.6
AHQ-9-5, 5300 - 5356	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.96E-06	0.96	5.21	-	1271.0
AHQ-9-3, 5194 - 5249	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.19E-12	0.98	6.71	-	1651.0
AHQ-9-1, 5180	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.83E-07	0.91	3.47	-	1178.7
AHQ-9-3, 4941 - 4996	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	6.20E-07	0.97	5.35	-	1304.0
AHQ-9-5, 5049	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.95E-05	0.87	3.56	-	817.9
AHQ-9-2, 5617 - 5689	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.02E-05	0.95	4.89	-	1012.3
AHQ-9-6, 5230 - 5286	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	8.49E-06	0.90	4.35	-	832.7
AHQ-9-1, 5420 - 5446	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	4.84E-08	0.98	5.43	-	1960.4
AHQ-9-14-, 5283	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.67E-08	0.92	4.16	-	1110.5
AHQ-9-2, 3967	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	8.73E-04	0.96	3.68	-	2218.8
AHQ-9-2, 4811 - 4885	R.LTEMETLQSQLMAEK.L	1753.03211	2	6.91E-07	0.97	4.14	-	2219.6
AHQ-9-3, 3425 - 3490	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	5.46E-04	0.86	3.44	-	880.8
AHQ-9-1, 3615	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	3.40E-04	0.84	3.12	-	884.0
AHQ-9-2, 3526 - 3585	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	3.15E-04	0.94	4.29	-	1100.8
AHQ-9-2, 4407 - 4479	R.LTEMETLQSQLM*AEK.L	1769.03151	2	5.65E-05	0.96	5.00	-	1342.9
AHQ-9-4, 3872	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	2.70E-04	0.96	3.94	-	1874.4
AHQ-9-3, 4253 - 4308	R.LTEMETLQSQLM*AEK.L	1769.03151	2	3.00E-05	0.83	3.18	-	903.7
AHQ-9-3, 3226	K.M*EDSVGCLETAEEVKR.K	1871.03734	3	2.64E-04	0.74	3.32	-	638.7
AHQ-9-6, 5310	K.NFINNPLAQADWAAK.K	1673.85315	2	3.18E-06	0.89	3.25	-	1192.6
AHQ-9-7, 4914 - 4968	K.NFINNPLAQADWAAK.K	1673.85315	2	8.89E-04	0.89	3.77	-	717.4
AHQ-9-1, 5136	K.NFINNPLAQADWAAK.K	1673.85315	2	2.32E-05	0.93	4.22	-	921.6
AHQ-9-5, 4997	K.NFINNPLAQADWAAK.K	1673.85315	2	8.64E-06	0.96	5.00	-	1195.3
AHQ-9-2, 5469	K.NFINNPLAQADWAAK.K	1673.85315	2	5.06E-12	0.94	4.14	-	1048.3
AHQ-9-4, 4986	K.NFINNPLAQADWAAK.K	1673.85315	2	3.94E-07	0.95	4.55	-	1173.2
AHQ-9-3, 4945	K.NFINNPLAQADWAAK.K	1673.85315	2	4.41E-07	0.95	4.80	-	1053.2
AHQ-9-6, 4922	K.NFINNPLAQADWAAK.K	1673.85315	2	6.34E-09	0.93	4.11	-	961.6
AHQ-9-2, 5078 - 5097	K.NFINNPLAQADWAAK.K	1673.85315	2	9.13E-09	0.96	4.86	-	1152.8
AHQ-9-3, 2777	K.NKHEAMITDLEER.L	1586.75247	2	2.18E-05	0.71	2.80	-	689.4
AHQ-9-2, 2813	K.NKHEAMITDLEER.L	1586.75247	2	5.35E-09	0.88	3.29	-	1035.8
AHQ-9-2, 4939	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.48E-06	0.95	4.34	-	886.8
AHQ-9-2, 5433 - 5446	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.48E-06	0.97	4.92	-	1168.3
AHQ-9-5, 5336 - 5349	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.05E-05	0.96	4.99	-	943.4
AHQ-9-7, 4772 - 4773	K.NLPIYSEEIVEM*YK.G	1744.98660	2	9.54E-06	0.96	4.39	-	1228.7
AHQ-9-6, 4787	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.07E-04	0.86	3.46	-	551.7
AHQ-9-1, 4952 - 5000	K.NLPIYSEEIVEM*YK.G	1744.98660	2	5.30E-04	0.93	3.84	-	966.6
AHQ-9-4, 4845	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.79E-04	0.89	3.64	-	742.5
AHQ-9-3, 4801 - 4821	K.NLPIYSEEIVEM*YK.G	1744.98660	2	5.03E-07	0.89	3.39	-	731.2
AHQ-9-2, 5438	K.NLPIYSEEIVEM*YK.G	1744.98660	2	7.89E-04	0.78	3.20	-	401.2
AHQ-9-2, 4883	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	1.28E-04	0.89	3.29	-	1008.2
AHQ-9-2, 5257	K.NMDPLNDNIATLLHQSSDK.F	2127.32169	2	3.11E-06	0.85	3.30	-	639.5
AHQ-9-2, 3351	R.QAQQERDELADEIANSSGK.G	2090.15168	2	8.62E-05	0.86	3.52	-	687.1
AHQ-9-2, 3005 - 3075	K.QIATLHAQVADMK.K	1426.66697	2	8.69E-04	0.66	2.80	-	473.1
AHQ-9-13-, 3624	R.RGDLPFVVPR.R	1156.36217	2	4.61E-05	0.70	3.00	-	581.4
AHQ-9-2, 3673 - 3689	R.RGDLPFVVPR.R	1156.36217	2	8.94E-06	0.95	3.81	-	1387.9
AHQ-9-3, 3593	R.RGDLPFVVPR.R	1156.36217	2	1.75E-05	0.94	3.78	-	1373.3
AHQ-9-4, 3594 - 3654	R.RGDLPFVVPR.R	1156.36217	2	6.46E-07	0.90	3.24	-	1111.5
AHQ-9-6, 3550	R.RGDLPFVVPR.R	1156.36217	2	6.62E-06	0.94	3.75	-	1302.4
AHQ-9-11, 3543 - 3561	R.RGDLPFVVPR.R	1156.36217	2	4.20E-05	0.95	3.71	-	1490.3
AHQ-9-5, 3588	R.RGDLPFVVPR.R	1156.36217	2	1.32E-05	0.96	4.02	-	1577.1
AHQ-9-7, 3545	R.RGDLPFVVPR.R	1156.36217	2	1.45E-05	0.81	2.97	-	701.8
AHQ-9-4, 6145	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	5.29E-04	0.96	6.01	-	1623.3
AHQ-9-2, 6234 - 6303	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	1.66E-07	0.97	5.99	-	1737.3
AHQ-9-3, 6065	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	4.39E-06	0.83	4.19	-	953.0
AHQ-9-5, 5777	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.09E-07	0.77	3.48	-	650.0
AHQ-9-2, 5730 - 5797	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	4.93E-09	0.92	5.41	-	769.6
AHQ-9-13-, 5673	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	3.19E-06	0.79	3.61	-	605.6
AHQ-9-2, 5853 - 5918	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.96E-11	0.96	5.73	-	1328.1
AHQ-9-2, 6483 - 6553	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	8.38E-07	0.87	4.13	-	851.6
AHQ-9-2, 5389 - 5435	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	9.78E-05	0.90	4.36	-	1222.0
AHQ-9-3, 4452	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.28E-05	0.93	4.51	-	1063.1
AHQ-9-2, 4567 - 4645	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	7.58E-08	0.97	5.45	-	1623.6
AHQ-9-4, 4468	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	3.15E-08	0.95	4.35	-	1445.0
AHQ-9-4, 3640	K.TDLLLEPYNK.Y	1206.36989	2	2.20E-06	0.91	4.00	-	1138.8
AHQ-9-5, 3637	K.TDLLLEPYNK.Y	1206.36989	2	8.45E-05	0.92	4.02	-	1060.5
AHQ-9-1, 3827	K.TDLLLEPYNK.Y	1206.36989	2	3.59E-05	0.91	3.77	-	963.0
AHQ-9-2, 3733	K.TDLLLEPYNK.Y	1206.36989	2	1.36E-05	0.91	3.96	-	982.4
AHQ-9-6, 3598	K.TDLLLEPYNK.Y	1206.36989	2	2.16E-06	0.93	3.81	-	1248.1
AHQ-9-7, 3594 - 3601	K.TDLLLEPYNK.Y	1206.36989	2	1.54E-04	0.87	3.54	-	900.3
AHQ-9-3, 3640	K.TDLLLEPYNK.Y	1206.36989	2	1.52E-05	0.89	3.59	-	1019.3
AHQ-9-5, 4101 - 4159	K.TELEDTLDSTAAQQELR.S	1921.00969	2	2.79E-07	0.97	5.07	-	1837.5
AHQ-9-2, 4187	K.TELEDTLDSTAAQQELR.S	1921.00969	2	8.89E-07	0.98	5.13	-	2413.7
AHQ-9-4, 4066 - 4085	K.TELEDTLDSTAAQQELR.S	1921.00969	2	1.44E-04	0.52	2.90	-	628.5
AHQ-9-3, 4076	K.TELEDTLDSTAAQQELR.S	1921.00969	2	8.06E-10	0.96	4.80	-	1441.6
AHQ-9-2, 3407	R.TEMEDLMSSKDDVGK.S	1685.85626	2	4.24E-09	0.84	3.33	-	927.0
AHQ-9-5, 6148	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	3.84E-05	0.73	3.16	-	664.2
AHQ-9-2, 6350	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	6.03E-06	0.75	3.25	-	762.7
AHQ-9-3, 2102	K.VAAYDKLEK.T	1037.19123	2	9.73E-05	0.64	2.68	-	541.2
AHQ-9-2, 5083	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	3.91E-08	0.93	4.55	-	915.1
AHQ-9-2, 5583	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	4.45E-04	0.76	3.42	-	503.4
AHQ-9-5, 4936 - 5000	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	4.86E-05	0.90	4.17	-	731.6
AHQ-9-2, 5514 - 5585	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	3	4.66E-05	0.85	3.98	-	770.7
AHQ-9-2, 2173 - 2326	R.VEEEEERCQHLQAEK.K	1916.01642	2	1.76E-07	0.91	3.96	-	1042.2
AHQ-9-2, 4001	K.VIQYLAYVASSHK.S	1479.70484	2	4.04E-04	0.95	3.68	-	1523.3
AHQ-9-5, 3901 - 3911	K.VIQYLAYVASSHK.S	1479.70484	2	1.12E-05	0.94	3.92	-	1211.8
AHQ-9-3, 3904	K.VIQYLAYVASSHK.S	1479.70484	2	1.03E-07	0.93	3.81	-	1136.0
AHQ-9-2, 4006	K.VIQYLAYVASSHK.S	1479.70484	3	2.06E-05	0.76	3.44	-	452.8
AHQ-9-6, 3854 - 3917	K.VIQYLAYVASSHK.S	1479.70484	2	4.31E-05	0.58	2.62	-	561.1

AHQ-9-5, 5919	R.VISGVLQLGNIVFK.K	1487.81155	2	7.97E-09	0.96	3.93	-	1752.4
AHQ-9-2, 5967 - 6021	R.VISGVLQLGNIVFK.K	1487.81155	2	5.86E-07	0.98	5.30	-	1931.4
AHQ-9-3, 5848 - 5858	R.VISGVLQLGNIVFK.K	1487.81155	2	1.04E-08	0.97	4.50	-	1830.6
AHQ-9-6, 5829 - 5842	R.VISGVLQLGNIVFK.K	1487.81155	2	4.55E-07	0.95	4.55	-	1357.2
AHQ-9-7, 5816	R.VISGVLQLGNIVFK.K	1487.81155	2	1.46E-06	0.96	3.95	-	1898.6
AHQ-9-1, 6028 - 6034	R.VISGVLQLGNIVFK.K	1487.81155	2	1.25E-06	0.97	4.62	-	1481.3
AHQ-9-8, 5902 - 5907	R.VISGVLQLGNIVFK.K	1487.81155	2	4.21E-07	0.97	4.99	-	1905.9
AHQ-9-3, 5397 - 5477	R.VISGVLQLGNIVFKK.E	1615.98446	2	1.40E-04	0.89	3.48	-	960.6
AHQ-9-4, 5449	R.VISGVLQLGNIVFKK.E	1615.98446	2	2.58E-05	0.94	3.60	-	1552.3
AHQ-9-1, 5579	R.VISGVLQLGNIVFKK.E	1615.98446	2	6.47E-04	0.63	3.09	-	582.9
AHQ-9-2, 5541	R.VISGVLQLGNIVFKK.E	1615.98446	2	5.80E-04	0.92	3.74	-	968.9
AHQ-9-7, 4617	K.VSHLLGINVTDFTR.G	1572.79026	2	7.59E-06	0.96	4.57	-	1395.6
AHQ-9-5, 4707 - 4715	K.VSHLLGINVTDFTR.G	1572.79026	3	3.17E-05	0.80	3.60	-	910.1
AHQ-9-4, 4681 - 4701	K.VSHLLGINVTDFTR.G	1572.79026	2	1.07E-06	0.90	3.81	-	1096.1
AHQ-9-4, 4704	K.VSHLLGINVTDFTR.G	1572.79026	3	6.27E-05	0.88	3.73	-	1007.6
AHQ-9-1, 4874	K.VSHLLGINVTDFTR.G	1572.79026	2	5.43E-09	0.96	4.62	-	1275.3
AHQ-9-3, 4021	R.YEILTPNSIPK.G	1275.47536	2	9.51E-04	0.83	2.73	-	1073.5
AHQ-9-2, 3941 - 4015	R.YEILTPNSIPK.G	1275.47536	2	1.04E-05	0.91	3.69	-	995.6
gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]				1.67E-12	11.32	130.29	64.80	22391.3
AHQ-9-11, 5381 - 5437	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.12E-04	0.93	4.09	-	1029.0
AHQ-9-14-, 5450	R.DDGLFSGDPNWFPK.K	1595.69288	2	4.42E-06	0.96	4.23	-	1426.2
AHQ-9-11, 5697	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.19E-05	0.74	3.39	-	498.2
AHQ-9-11, 6151 - 6213	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	5.75E-04	0.90	4.60	-	646.7
AHQ-9-11, 6205 - 6206	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	2.44E-09	0.88	4.18	-	818.5
AHQ-9-13-, 6292	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	1.59E-08	0.85	3.78	-	798.6
AHQ-9-11, 2214	R.GASQAGMTGYGM*PR.Q	1400.56672	2	2.68E-04	0.63	2.59	-	629.9
AHQ-9-11, 2297	R.GPAYGLSREVQQK.I	1433.59456	2	2.35E-04	0.81	2.93	-	1226.1
AHQ-9-11, 2406 - 2461	R.NFSDNQLQEGK.N	1280.32582	2	6.82E-04	0.88	3.52	-	841.9
AHQ-9-11, 2395 - 2447	K.NVIGLQM*GTNR.G	1219.39691	2	3.83E-04	0.87	3.09	-	908.2
AHQ-9-11, 3153	K.NVIGLQMGTNR.G	1203.39751	2	7.12E-07	0.95	3.68	-	1726.0
AHQ-9-11, 3250 - 3310	K.NVIGLQMGTNR.G	1203.39751	2	7.20E-04	0.67	2.91	-	780.1
AHQ-9-11, 5017 - 5094	K.QMEQISQFLQAAER.Y	1679.87950	2	6.60E-07	0.95	4.42	-	1146.5
AHQ-9-11, 4491	K.QM*EQISQFLQAAER.Y	1695.87890	3	7.10E-06	0.93	3.93	-	1646.3
AHQ-9-11, 5091	K.QMEQISQFLQAAER.Y	1679.87950	3	2.04E-05	0.97	4.76	-	2035.2
AHQ-9-11, 4329 - 4350	R.TLMNLGGLAVAR.D	1216.47932	2	3.37E-05	0.87	3.76	-	823.1
AHQ-9-11, 4215 - 4275	R.TLMNLGGLAVAR.D	1216.47932	2	1.49E-04	0.68	2.80	-	834.7
AHQ-9-11, 3790 - 3866	R.TLM*NLGGLAVAR.D	1232.47872	2	2.80E-05	0.89	3.30	-	1077.4
AHQ-9-11, 3581 - 3586	R.TLM*NLGGLAVAR.D	1232.47872	2	8.49E-06	0.90	3.74	-	786.6
AHQ-9-13-, 6224	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	4.46E-10	0.97	5.34	-	1280.2
AHQ-9-12, 6180 - 6181	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.66E-10	0.97	5.71	-	1086.9
AHQ-9-11, 6074 - 6145	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.67E-12	0.95	5.01	-	824.5
AHQ-9-13, 6310	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.02E-10	0.95	4.79	-	1039.2
gi|4501891|ref|NP_001093.1| actinin, alpha 1 [Homo sapiens]				1.75E-12	32.30	360.39	46.30	103056.9
AHQ-9-5, 6424	R.AAPFNNWM*EGAM*EDLQDTFIVHTIEEIQGLTTAHEQFK.A	4396.81902	3	1.32E-06	0.94	5.50	-	1020.7
AHQ-9-4, 5106	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	3.75E-06	0.83	4.78	-	683.3
AHQ-9-4, 5953 - 5956	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	2.23E-05	0.64	3.10	-	427.4
AHQ-9-4, 5954	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	8.81E-07	0.90	3.99	-	725.5
AHQ-9-5, 5976 - 5983	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	3	3.35E-04	0.75	3.51	-	619.6
AHQ-9-4, 5304	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	4.81E-07	0.89	4.38	-	518.2
AHQ-9-4, 5301 - 5357	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	3	1.04E-04	0.72	3.08	-	786.4
AHQ-9-4, 3413 - 3434	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	3.09E-06	0.97	5.59	-	2440.0
AHQ-9-4, 5172 - 5212	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.92E-08	0.89	4.37	-	705.7
AHQ-9-6, 5197	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.87E-07	0.83	3.24	-	785.3
AHQ-9-7, 5202	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	3.19E-04	0.65	2.66	-	573.2
AHQ-9-4, 5268	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	9.38E-10	0.96	4.86	-	1296.2
AHQ-9-5, 5263	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	2.16E-06	0.92	3.95	-	1073.6
AHQ-9-4, 4664 - 4722	K.DGLGFCALIHR.H	1260.44730	2	5.84E-07	0.95	3.17	-	1921.8
AHQ-9-5, 4680	K.DGLGFCALIHR.H	1260.44730	2	5.84E-07	0.90	2.72	-	1304.5
AHQ-9-5, 3673 - 3680	K.DYETATLSEIK.A	1270.36761	2	1.08E-07	0.90	3.40	-	1013.5
AHQ-9-4, 3496 - 3552	R.ELPPDQAEYCIAR.M	1563.71392	2	5.94E-06	0.77	2.91	-	268.1
AHQ-9-6, 4199	R.ETADTDTADQVMASFK.I	1730.83208	2	1.17E-07	0.92	3.78	-	1016.8
AHQ-9-6, 3153	R.ETADTDTADQVM*ASFK.I	1746.83148	2	1.39E-07	0.94	3.95	-	1100.2
AHQ-9-4, 2842	R.ETADTDTADQVM*ASFK.I	1746.83148	2	3.99E-07	0.68	2.66	-	713.0
AHQ-9-4, 4166 - 4246	R.ETADTDTADQVMASFK.I	1730.83208	2	6.18E-06	0.95	4.51	-	1011.1
AHQ-9-5, 2340	K.GISQEQM*NEFR.A	1355.45931	2	2.04E-04	0.83	2.94	-	892.4
AHQ-9-4, 2337	K.GISQEQM*NEFR.A	1355.45931	2	7.32E-05	0.88	3.21	-	914.3
AHQ-9-6, 2349	K.GISQEQM*NEFR.A	1355.45931	2	9.77E-06	0.82	3.07	-	746.8
AHQ-9-5, 2961 - 3028	K.GISQEQMNEFR.A	1339.45991	2	1.18E-05	0.74	2.58	-	920.1
AHQ-9-4, 2716	K.GISQEQMNEFR.A	1339.45991	2	7.26E-09	0.87	3.28	-	852.8
AHQ-9-4, 2968 - 3028	K.GISQEQMNEFR.A	1339.45991	2	7.17E-08	0.82	2.98	-	843.3
AHQ-9-5, 2285	R.HRPELIDYGK.L	1228.38202	2	4.56E-05	0.79	2.83	-	534.7
AHQ-9-4, 2290	R.HRPELIDYGK.L	1228.38202	2	8.53E-04	0.90	3.83	-	535.4
AHQ-9-5, 4668	K.ICDQWDNLGALTQK.R	1663.83349	2	3.50E-07	0.96	4.13	-	1886.0
AHQ-9-4, 4884 - 4950	K.ICDQWDNLGALTQK.R	1663.83349	2	2.71E-05	0.96	3.77	-	2081.4
AHQ-9-4, 4361	K.ICDQWDNLGALTQK.R	1663.83349	2	6.78E-08	0.79	3.11	-	742.2
AHQ-9-4, 4661	K.ICDQWDNLGALTQK.R	1663.83349	3	3.26E-07	0.81	4.51	-	477.9
AHQ-9-6, 4545 - 4605	K.ICDQWDNLGALTQK.R	1663.83349	2	2.97E-05	0.90	3.90	-	1056.1
AHQ-9-7, 4596	K.ICDQWDNLGALTQK.R	1663.83349	2	8.85E-04	0.77	3.03	-	933.3
AHQ-9-4, 5464 - 5526	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	2.24E-07	0.95	4.96	-	1696.2
AHQ-9-4, 5468 - 5469	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	4.42E-07	0.96	4.81	-	1240.5
AHQ-9-9, 5259 - 5267	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	2.94E-04	0.88	3.70	-	1162.3
AHQ-9-4, 5340 - 5400	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	2.66E-05	0.95	5.06	-	1344.8
AHQ-9-4, 3993 - 4050	K.ILAGDKNYITMDELR.R	1753.01353	2	2.50E-07	0.92	4.36	-	805.5
AHQ-9-4, 3433 - 3504	K.ILAGDKNYITM*DELR.R	1769.01293	2	3.99E-05	0.92	3.91	-	768.1
AHQ-9-4, 4297	R.ISIEM*HGTLEDQLSHLR.Q	1996.23437	2	6.60E-06	0.87	3.86	-	525.7
AHQ-9-4, 4833	R.ISIEMHGTLEDQLSHLR.Q	1980.23497	3	1.75E-12	0.87	3.92	-	1110.1
AHQ-9-4, 4689	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	8.86E-07	0.95	4.61	-	1130.5
AHQ-9-5, 4264	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.92E-04	0.82	3.27	-	659.0
AHQ-9-5, 4708	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	4.80E-07	0.97	5.60	-	1020.8
AHQ-9-6, 4654	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	7.77E-05	0.90	4.00	-	657.2
AHQ-9-4, 4264	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.45E-07	0.94	4.47	-	1111.7
AHQ-9-4, 4294	R.KQFGAQANVIGPWIQTK.M	1887.17410	2	3.63E-06	0.94	4.51	-	1023.5
AHQ-9-4, 4293	R.KQFGAQANVIGPWIQTK.M	1887.17410	3	3.26E-04	0.90	3.64	-	1480.5
AHQ-9-4, 3450 - 3528	R.LAILGIHNEVSK.I	1294.52505	2	1.08E-06	0.77	3.01	-	761.5
AHQ-9-4, 3661	R.LAILGIHNEVSK.I	1294.52505	2	3.28E-05	0.94	3.21	-	1372.7
AHQ-9-4, 3756	R.LAILGIHNEVSK.I	1294.52505	2	2.61E-08	0.95	4.07	-	1285.4
AHQ-9-5, 3425 - 3460	R.LAILGIHNEVSK.I	1294.52505	2	8.71E-08	0.93	3.37	-	1358.9
AHQ-9-5, 3763	R.LAILGIHNEVSK.I	1294.52505	2	4.23E-06	0.88	2.88	-	1084.6
AHQ-9-7, 5554	K.LASDLLEWIR.R	1216.41115	2	4.56E-05	0.96	4.00	-	1669.8
AHQ-9-4, 5612 - 5626	K.LASDLLEWIR.R	1216.41115	2	5.95E-07	0.98	4.33	-	2491.2
AHQ-9-5, 5636 - 5639	K.LASDLLEWIR.R	1216.41115	2	1.87E-07	0.97	3.85	-	1970.3
AHQ-9-3, 5912 - 5981	K.LLETIDQLYLEYAK.R	1712.96427	2	1.49E-05	0.77	3.32	-	555.0
AHQ-9-6, 5893 - 5913	K.LLETIDQLYLEYAK.R	1712.96427	2	2.37E-06	0.96	4.05	-	1682.1
AHQ-9-4, 5964 - 5989	K.LLETIDQLYLEYAK.R	1712.96427	2	1.90E-07	0.96	4.38	-	1458.5
AHQ-9-4, 5972 - 5973	K.LLETIDQLYLEYAK.R	1712.96427	3	2.56E-06	0.96	5.23	-	1412.8
AHQ-9-5, 5980	K.LLETIDQLYLEYAK.R	1712.96427	2	1.38E-08	0.95	4.53	-	1178.9
AHQ-9-4, 2285	R.LSNRPAFM*PSEGR.M	1478.65881	3	2.85E-05	0.66	3.21	-	868.3

AHQ-9-4, 2769	R.LSNRPAFMPSEGR.M	1462.65941	3	3.43E-05	0.82	3.39	-	938.0
AHQ-9-4, 3884	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.83E-05	0.90	3.67	-	1127.8
AHQ-9-5, 3545 - 3559	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	1.30E-05	0.86	3.43	-	702.4
AHQ-9-6, 3515 - 3526	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	3.04E-04	0.90	3.78	-	784.5
AHQ-9-4, 3540 - 3586	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	1.18E-09	0.79	3.32	-	559.3
AHQ-9-6, 4847	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	7.58E-05	0.82	3.51	-	537.2
AHQ-9-4, 4952	R.MVSDINNAWGCLEQVEK.G	1995.22333	2	5.85E-06	0.96	4.11	-	1970.7
AHQ-9-5, 5051 - 5061	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	8.11E-04	0.97	5.16	-	1467.2
AHQ-9-6, 4763	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	3.34E-04	0.92	3.85	-	1057.4
AHQ-9-4, 5193	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.44E-06	0.96	4.73	-	1403.7
AHQ-9-6, 4979	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	5.24E-05	0.83	3.68	-	454.4
AHQ-9-4, 4888	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.20E-05	0.97	5.08	-	1477.6
AHQ-9-4, 5024	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	7.41E-05	0.77	3.32	-	589.5
AHQ-9-4, 3840	R.TINEVENQILTR.D	1430.58898	2	3.74E-07	0.87	3.24	-	1026.8
AHQ-9-5, 3468 - 3527	R.TINEVENQILTR.D	1430.58898	2	1.26E-04	0.65	2.57	-	519.9
AHQ-9-4, 3964	R.TINEVENQILTR.D	1430.58898	2	7.47E-04	0.94	4.11	-	1207.6
AHQ-9-7, 3812	R.TINEVENQILTR.D	1430.58898	2	8.11E-04	0.86	3.27	-	857.6
AHQ-9-5, 3856 - 3861	R.TINEVENQILTR.D	1430.58898	2	1.50E-05	0.79	3.27	-	646.5
AHQ-9-5, 3980	R.TINEVENQILTR.D	1430.58898	2	5.70E-04	0.83	3.46	-	757.7
AHQ-9-6, 3926	R.TINEVENQILTR.D	1430.58898	2	9.62E-04	0.82	3.14	-	748.7
AHQ-9-4, 3104	R.TINEVENQILTR.D	1430.58898	2	4.38E-04	0.91	3.54	-	976.9
AHQ-9-5, 6251 - 6252	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	6.03E-12	0.98	7.87	-	2009.8
AHQ-9-6, 6171	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	1.97E-08	0.86	3.55	-	632.4
AHQ-9-4, 6236 - 6238	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	7.74E-07	0.97	6.14	-	1187.4
AHQ-9-8, 6086	R.VGWEQLLTTIAR.T	1387.60894	2	1.45E-07	0.93	3.55	-	1439.1
AHQ-9-5, 6103	R.VGWEQLLTTIAR.T	1387.60894	2	1.17E-08	0.91	3.46	-	1133.6
AHQ-9-7, 5998	R.VGWEQLLTTIAR.T	1387.60894	2	2.61E-08	0.94	3.89	-	1358.8
AHQ-9-4, 6088 - 6150	R.VGWEQLLTTIAR.T	1387.60894	2	5.45E-06	0.95	4.02	-	1452.2
AHQ-9-6, 6014	R.VGWEQLLTTIAR.T	1387.60894	2	8.44E-06	0.94	3.99	-	1242.4
AHQ-9-5, 3452 - 3532	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	8.67E-06	0.93	4.69	-	965.5
AHQ-9-4, 3412	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	7.00E-06	0.93	4.45	-	730.0
AHQ-9-4, 4281	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.94E-06	0.72	3.47	-	412.3
AHQ-9-6, 4075 - 4082	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.37E-05	0.93	4.34	-	976.2
AHQ-9-5, 4053 - 4124	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	5.28E-06	0.96	5.09	-	1183.6
AHQ-9-6, 3494	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.31E-04	0.91	4.31	-	809.7
AHQ-9-4, 4060 - 4108	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.92E-08	0.96	4.89	-	1322.0
AHQ-9-4, 3521 - 3580	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	9.40E-06	0.93	4.39	-	1006.2
AHQ-9-4, 3529	K.VLAVNQENEQLM*EDYEK.L	2069.23575	3	2.00E-12	0.94	5.23	-	1145.7
AHQ-9-4, 3692	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	3.25E-10	0.96	5.02	-	1111.6
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				1.84E-12	1.91	20.34	7.40	32164.8
AHQ-9-1, 4824	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.15E-04	0.71	2.98	-	519.5
AHQ-9-2, 4783	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.25E-04	0.93	4.61	-	812.2
AHQ-9-3, 4652 - 4662	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.17E-05	0.86	3.79	-	711.6
AHQ-9-4, 4685	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.21E-05	0.94	4.56	-	1038.7
AHQ-9-4, 5132	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.19E-04	0.73	3.07	-	494.7
AHQ-9-5, 4695	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.35E-07	0.95	4.95	-	948.1
AHQ-9-6, 4633	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.47E-05	0.88	3.80	-	972.5
AHQ-9-8, 4567 - 4626	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.39E-06	0.94	4.79	-	924.3
AHQ-9-8, 4686 - 4742	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.67E-07	0.95	4.99	-	946.6
AHQ-9-8, 4838 - 4903	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.05E-07	0.96	5.33	-	798.1
AHQ-9-8, 4942 - 4999	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.66E-08	0.97	5.72	-	1277.2
AHQ-9-8, 5268 - 5340	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.07E-04	0.91	4.49	-	740.3
AHQ-9-8, 6459 - 6519	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.05E-04	0.43	2.78	-	437.6
AHQ-9-9, 4351 - 4416	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.07E-04	0.81	3.79	-	605.0
AHQ-9-9, 4472	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.13E-04	0.86	3.62	-	736.6
AHQ-9-9, 4737	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.61E-05	0.82	3.63	-	548.6
AHQ-9-10, 4363 - 4413	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.41E-05	0.53	2.92	-	385.4
AHQ-9-10, 4483 - 4550	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.74E-05	0.95	5.16	-	875.3
AHQ-9-10, 4529 - 4606	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.20E-05	0.95	4.97	-	875.8
AHQ-9-11, 4573	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.01E-05	0.82	3.66	-	633.5
AHQ-9-12, 4442 - 4524	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.48E-07	0.92	5.00	-	615.3
AHQ-9-12, 4568 - 4624	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.34E-06	0.97	5.29	-	1326.5
AHQ-9-12, 4685	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.64E-06	0.88	3.93	-	582.7
AHQ-9-12, 4708 - 4781	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.61E-04	0.93	4.35	-	1046.7
AHQ-9-12, 4844 - 4905	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.43E-04	0.68	3.81	-	290.9
AHQ-9-12, 4857 - 4913	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.02E-07	0.83	4.06	-	438.8
AHQ-9-12, 5070	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.64E-04	0.84	4.10	-	491.8
AHQ-9-13, 4682 - 4755	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.91E-07	0.94	4.56	-	1056.3
AHQ-9-13, 4810 - 4875	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.26E-04	0.95	5.09	-	929.4
AHQ-9-13, 4984	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.56E-07	0.94	4.62	-	1034.7
AHQ-9-14, 5311 - 5383	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.94E-07	0.97	5.53	-	1179.8
AHQ-9-14, 5431 - 5496	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.77E-06	0.97	5.59	-	1378.4
AHQ-9-14, 5551	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.85E-07	0.94	4.67	-	923.3
AHQ-9-13-, 4497 - 4521	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.62E-04	0.80	3.99	-	446.9
AHQ-9-13-, 4589 - 4652	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.88E-04	0.96	5.51	-	1067.7
AHQ-9-13-, 4805	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.56E-07	0.98	5.96	-	1551.9
AHQ-9-13-, 4908 - 4965	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.14E-07	0.96	5.37	-	1138.9
AHQ-9-13-, 5052	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.41E-05	0.96	4.91	-	1174.4
AHQ-9-13-, 5208	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.62E-06	0.94	4.51	-	762.9
AHQ-9-14-, 4494 - 4555	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.84E-12	0.95	4.52	-	979.2
AHQ-9-14-, 4767 - 4822	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.93E-08	0.97	5.63	-	1088.1
AHQ-9-14-, 4877	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.92E-04	0.89	3.98	-	768.8
AHQ-9-14-, 4927 - 4994	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.99E-08	0.97	5.71	-	1456.7
AHQ-9-14-, 5038 - 5093	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.03E-08	0.97	6.74	-	965.9
gi|4501885|ref|NP_001092.1| beta actin; beta cytoskeletal actin [Homo sapiens]				2.03E-12	10.96	120.34	39.70	41736.5
AHQ-9-13-, 5624 - 5669	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.55E-04	0.90	4.60	-	703.1
AHQ-9-12, 5596 - 5660	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	4.72E-04	0.75	3.72	-	491.8
AHQ-9-8, 5652 - 5707	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	1.02E-04	0.63	3.23	-	324.1
AHQ-9-8, 5160 - 5228	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	5.68E-07	0.86	3.81	-	784.9
AHQ-9-8, 6272 - 6278	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	1.11E-05	0.85	3.59	-	709.4
AHQ-9-8, 6458 - 6527	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	7.09E-07	0.90	4.48	-	785.3
AHQ-9-8, 5247 - 5315	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.68E-07	0.89	4.32	-	1093.5
AHQ-9-8, 5466	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	5.66E-04	0.77	3.16	-	842.0
AHQ-9-8, 6275 - 6335	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.79E-04	0.90	3.74	-	1298.1
AHQ-9-9, 2485	R.GYSFTTTAER.E	1133.19273	2	5.28E-04	0.95	3.43	-	1361.3
AHQ-9-6, 2603	R.GYSFTTTAER.E	1133.19273	2	7.18E-06	0.92	2.77	-	1214.8
AHQ-9-10, 2521 - 2569	R.GYSFTTTAER.E	1133.19273	2	1.29E-04	0.81	2.71	-	786.6
AHQ-9-4, 2609	R.GYSFTTTAER.E	1133.19273	2	2.89E-05	0.89	3.03	-	1107.2
AHQ-9-8, 2650 - 2706	R.GYSFTTTAER.E	1133.19273	2	6.50E-04	0.91	2.76	-	1151.5
AHQ-9-7, 2604	R.GYSFTTTAER.E	1133.19273	2	2.01E-04	0.88	2.60	-	901.0
AHQ-9-5, 2608 - 2609	R.GYSFTTTAER.E	1133.19273	2	1.47E-04	0.92	3.07	-	1109.9
AHQ-9-8, 2512 - 2592	R.GYSFTTTAER.E	1133.19273	2	2.46E-04	0.89	2.92	-	972.1
AHQ-9-12, 2601 - 2656	R.GYSFTTTAER.E	1133.19273	2	4.72E-04	0.87	3.31	-	817.5
AHQ-9-8, 2510 - 2575	R.GYSFTTTAER.E	1133.19273	2	1.92E-04	0.91	2.77	-	1052.5
AHQ-9-8, 4500	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	4.62E-08	0.95	4.14	-	1182.2
AHQ-9-8, 4132 - 4175	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	6.40E-04	0.93	4.51	-	1175.8
AHQ-9-14-, 4225 - 4227	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	1.25E-04	0.95	5.70	-	1101.0

AHQ-9-8, 6286 - 6346	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	1.25E-10	0.97	6.27	-	1839.8
AHQ-9-8, 6358 - 6398	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	5.30E-06	0.95	4.22	-	1418.8
AHQ-9-8, 5982 - 6038	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	2.61E-04	0.85	3.39	-	1553.0
AHQ-9-8, 6452 - 6514	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	1.17E-07	0.98	5.62	-	2447.6
AHQ-9-8, 6454	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	4.98E-06	0.83	2.77	-	1486.0
AHQ-9-8, 6466 - 6523	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	6.24E-09	0.98	6.74	-	2076.2
AHQ-9-8, 6486 - 6487	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	1.62E-06	0.95	5.42	-	1853.4
AHQ-9-12, 5254 - 5312	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	5.31E-04	0.76	2.64	-	950.7
AHQ-9-8, 5312 - 5382	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	6.51E-06	0.88	3.62	-	992.6
AHQ-9-8, 6450 - 6506	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	3.51E-04	0.81	3.18	-	817.7
AHQ-9-8, 6354 - 6414	K.LCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNER.F	4325.73403	3	1.02E-11	0.95	5.46	-	1131.5
AHQ-9-8, 5359 - 5418	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.17E-04	0.90	4.70	-	777.5
AHQ-9-8, 5410 - 5470	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.79E-12	0.97	6.22	-	1715.4
AHQ-9-8, 5112 - 5170	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.22E-09	0.96	6.03	-	1268.2
AHQ-9-8, 5526	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.03E-06	0.96	5.37	-	1385.8
AHQ-9-8, 5076	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.96E-06	0.86	3.83	-	996.5
AHQ-9-13-, 5382 - 5446	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.05E-09	0.94	5.57	-	1014.8
AHQ-9-13-, 5173	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.15E-06	0.87	4.18	-	927.9
AHQ-9-12, 5345 - 5409	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.03E-12	0.98	6.31	-	1991.5
AHQ-9-12, 5316 - 5377	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.08E-04	0.73	3.18	-	772.3
AHQ-9-8, 5230 - 5291	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.43E-08	0.97	6.03	-	2008.1
AHQ-9-7, 5374 - 5429	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.07E-04	0.69	3.38	-	530.7
AHQ-9-7, 5149	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	4.05E-05	0.95	5.12	-	1332.9
AHQ-9-12, 5200 - 5256	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.03E-09	0.96	5.83	-	1477.7
AHQ-9-6, 5395	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	1.03E-04	0.60	3.68	-	386.0
AHQ-9-6, 5170	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.45E-05	0.93	4.58	-	1338.0
AHQ-9-12, 5090 - 5144	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.50E-10	0.97	5.53	-	2174.8
AHQ-9-3, 5193 - 5196	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.64E-05	0.93	4.99	-	1077.3
AHQ-9-4, 5245	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.13E-06	0.95	5.20	-	1290.7
AHQ-9-11, 5333	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	4.04E-05	0.74	3.11	-	712.9
AHQ-9-9, 5092	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	2.61E-07	0.92	4.86	-	1198.7
AHQ-9-9, 5220 - 5291	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	8.31E-09	0.97	6.36	-	1310.1
AHQ-9-1, 5388	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.78E-04	0.86	3.87	-	934.3
AHQ-9-11, 5107 - 5161	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	5.89E-04	0.89	4.65	-	897.7
AHQ-9-10, 5062 - 5118	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.09E-05	0.92	4.40	-	1007.0
AHQ-9-11, 3802 - 3865	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	6.89E-04	0.36	3.07	-	470.4
AHQ-9-11, 3830 - 3837	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.04E-08	0.92	4.56	-	827.7
AHQ-9-10, 3778	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.74E-06	0.78	3.09	-	537.6
AHQ-9-9, 3621 - 3675	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.18E-07	0.89	4.11	-	702.1
AHQ-9-5, 3895	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.52E-10	0.91	4.60	-	731.5
AHQ-9-12, 3784 - 3840	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.49E-04	0.91	4.27	-	830.3
AHQ-9-12, 3789 - 3845	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	3.17E-04	0.83	4.34	-	727.8
AHQ-9-12, 3896 - 3952	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.59E-06	0.86	3.84	-	702.3
AHQ-9-6, 3841	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.24E-04	0.91	4.46	-	785.1
AHQ-9-7, 3822	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.05E-05	0.90	4.00	-	848.5
AHQ-9-3, 3822 - 3897	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.96E-05	0.84	3.57	-	679.8
AHQ-9-8, 3679 - 3738	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.47E-04	0.91	4.45	-	805.1
AHQ-9-8, 3690 - 3751	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	9.18E-04	0.63	3.51	-	659.4
AHQ-9-2, 4007	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.38E-04	0.77	3.92	-	431.0
AHQ-9-13, 4056	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.59E-04	0.88	3.64	-	815.5
AHQ-9-13-, 3910	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.13E-04	0.88	3.71	-	734.3
AHQ-9-8, 3768 - 3830	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.03E-07	0.95	4.93	-	1005.7
AHQ-9-8, 3972 - 4052	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.59E-04	0.87	3.91	-	528.1
AHQ-9-4, 3908	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.20E-04	0.86	3.79	-	704.3
AHQ-9-1, 4087	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	4.61E-04	0.78	3.97	-	914.3
gi|29741246|ref|XP_294070.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				2.34E-12	3.52	40.30	13.40	35032.0
AHQ-9-13-, 5088	K.AENGKLVINGNPITIFQER.D	2114.39062	3	4.42E-04	0.76	3.18	-	917.1
AHQ-9-9, 4893 - 4956	K.AENGKLVINGNPITIFQER.D	2114.39062	2	3.53E-04	0.77	3.47	-	537.8
AHQ-9-13-, 5316 - 5372	K.LVINGNPITIFQER.D	1614.87029	2	2.34E-12	0.93	3.77	-	893.5
AHQ-9-9, 5229	K.LVINGNPITIFQER.D	1614.87029	2	3.25E-07	0.89	3.44	-	811.0
AHQ-9-13, 5466 - 5546	K.LVINGNPITIFQER.D	1614.87029	2	1.43E-08	0.89	3.50	-	1076.9
AHQ-9-9, 5100 - 5175	K.LVINGNPITIFQER.D	1614.87029	2	9.51E-12	0.91	3.79	-	953.0
AHQ-9-9, 6079 - 6080	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	2.88E-10	0.93	6.06	-	1203.7
AHQ-9-9, 5757 - 5827	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	4.38E-06	0.89	5.09	-	1120.5
gi|4826898|ref|NP_005013.1| profilin 1; profilin-1 [Homo sapiens]				2.68E-12	12.70	150.32	65.70	15054.2
AHQ-9-13-, 1910 - 1974	K.CYEM*ASHLR.R	1184.32794	2	3.74E-04	0.94	3.29	-	1249.4
AHQ-9-13-, 2004 - 2061	K.CYEM*ASHLR.R	1184.32794	2	2.83E-05	0.86	3.05	-	918.6
AHQ-9-13-, 4017 - 4025	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	2.68E-12	0.98	6.31	-	1313.0
AHQ-9-13, 4166	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	6.24E-05	0.93	4.38	-	864.6
AHQ-9-13, 4366	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	3.91E-04	0.61	2.84	-	450.6
AHQ-9-13-, 4150	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.78E-06	0.87	3.94	-	738.3
AHQ-9-14-, 4514	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.03E-09	0.95	3.64	-	1763.3
AHQ-9-13-, 4564 - 4633	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.41E-04	0.92	3.36	-	1500.5
AHQ-9-13-, 4846 - 4917	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.81E-05	0.89	3.08	-	1396.3
AHQ-9-12, 5108	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.20E-04	0.96	3.11	-	2377.9
AHQ-9-13-, 4937 - 4997	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.82E-10	0.98	4.78	-	2400.9
AHQ-9-14-, 4373	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.10E-04	0.93	3.97	-	1011.0
AHQ-9-13-, 4332 - 4397	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.14E-07	0.96	4.66	-	1571.5
AHQ-9-13-, 4964	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.54E-07	0.94	4.54	-	856.1
AHQ-9-13-, 5037 - 5092	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.16E-06	0.97	4.52	-	2107.5
AHQ-9-13, 4479 - 4534	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.50E-05	0.95	4.16	-	1151.4
AHQ-9-13-, 4452 - 4509	R.DSLLQDGEFSM*DLR.T	1642.76963	2	5.82E-09	0.96	4.58	-	1699.7
AHQ-9-14-, 4982	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.91E-05	0.96	3.96	-	1743.8
AHQ-9-13, 4590 - 4650	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.24E-09	0.97	4.70	-	1906.8
AHQ-9-13, 4594 - 4667	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.02E-04	0.92	3.32	-	1430.7
AHQ-9-13, 4706 - 4790	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.03E-09	0.97	4.91	-	1792.5
AHQ-9-13, 5004 - 5058	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.10E-04	0.76	2.98	-	902.3
AHQ-9-13, 5120 - 5198	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.20E-10	0.95	4.30	-	1324.6
AHQ-9-13, 5211 - 5282	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.87E-08	0.98	4.79	-	2246.5
AHQ-9-13, 5338 - 5394	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.54E-09	0.98	4.73	-	2369.5
AHQ-9-13, 5422 - 5495	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.86E-07	0.98	4.25	-	2867.1
AHQ-9-13-, 5077	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.72E-06	0.90	3.65	-	1014.3
AHQ-9-13-, 5148 - 5218	R.DSLLQDGEFSMDLR.T	1626.77023	2	3.42E-08	0.97	4.76	-	2286.7
AHQ-9-13-, 4698	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.28E-04	0.94	3.76	-	1323.2
AHQ-9-13, 3916 - 3994	K.DSPSVWAAVPGK.T	1214.35211	2	4.55E-05	0.72	2.81	-	797.2
AHQ-9-13-, 6085 - 6097	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	3.09E-05	0.75	3.13	-	1097.2
AHQ-9-13, 4455 - 4514	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.56E-08	0.87	3.90	-	619.9
AHQ-9-12, 4321 - 4380	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.14E-08	0.94	3.46	-	1087.5
AHQ-9-13, 4386	R.SSFYVNGLTLGGQK.C	1471.63957	1	5.13E-09	0.63	2.41	-	578.7
AHQ-9-12, 4384	R.SSFYVNGLTLGGQK.C	1471.63957	1	9.83E-04	0.25	2.00	-	394.6
AHQ-9-13-, 4348 - 4416	R.SSFYVNGLTLGGQK.C	1471.63957	1	1.89E-07	0.44	2.76	-	318.0
AHQ-9-13, 4310 - 4383	R.SSFYVNGLTLGGQK.C	1471.63957	2	9.56E-08	0.94	4.14	-	819.8
AHQ-9-13, 4527 - 4598	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.91E-08	0.54	2.46	-	456.8
AHQ-9-13, 4570 - 4626	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.95E-08	0.97	4.42	-	1672.6
AHQ-9-14-, 4447	R.SSFYVNGLTLGGQK.C	1471.63957	2	3.71E-07	0.91	2.87	-	1345.6
AHQ-9-13-, 4194 - 4269	R.SSFYVNGLTLGGQK.C	1471.63957	2	5.73E-07	0.95	4.23	-	986.2
AHQ-9-13-, 4220	R.SSFYVNGLTLGGQK.C	1471.63957	1	4.85E-08	0.25	2.01	-	280.4

AHQ-9-13-, 4229	R.SSFYVNGLTLGGQK.C	1471.63957	1	8.56E-05	0.46	2.51	-	368.7
AHQ-9-13-, 4324 - 4392	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.59E-05	0.93	3.73	-	918.3
AHQ-9-13-, 3225	K.STGGAPTFNVTVTK.T	1380.52843	1	9.58E-04	0.18	2.26	-	316.0
AHQ-9-13-, 3188 - 3248	K.STGGAPTFNVTVTK.T	1380.52843	2	6.69E-07	0.86	3.35	-	483.9
AHQ-9-13-, 3084 - 3140	K.STGGAPTFNVTVTK.T	1380.52843	2	2.09E-09	0.86	3.88	-	459.5
AHQ-9-13, 3350 - 3407	K.STGGAPTFNVTVTK.T	1380.52843	2	5.30E-06	0.88	3.61	-	525.8
AHQ-9-13, 3230 - 3290	K.STGGAPTFNVTVTK.T	1380.52843	2	3.28E-09	0.89	3.57	-	585.1
AHQ-9-12, 3206	K.STGGAPTFNVTVTK.T	1380.52843	1	3.20E-05	0.26	2.13	-	429.0
AHQ-9-13-, 3181	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	7.36E-04	0.74	3.03	-	518.4
AHQ-9-13-, 3058	K.TDKTLVLLM*GK.E	1235.51929	2	3.32E-04	0.89	2.97	-	1027.1
AHQ-9-13, 3139 - 3219	K.TDKTLVLLM*GK.E	1235.51929	2	7.11E-04	0.81	2.81	-	708.0
AHQ-9-13-, 3689 - 3745	K.TDKTLVLLMGK.E	1219.51989	2	1.65E-06	0.93	3.62	-	1145.3
AHQ-9-13, 5606 - 5682	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.48E-08	0.92	4.07	-	961.8
AHQ-9-13, 5608 - 5616	K.TFVNITPAEVGVLVGK.D	1644.93630	3	8.03E-07	0.97	5.90	-	1798.1
AHQ-9-13-, 5389 - 5445	K.TFVNITPAEVGVLVGK.D	1644.93630	2	8.47E-05	0.95	5.08	-	902.1
AHQ-9-13-, 5458 - 5465	K.TFVNITPAEVGVLVGK.D	1644.93630	3	3.87E-06	0.96	5.21	-	1613.3
AHQ-9-13-, 5500 - 5568	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.26E-04	0.93	3.96	-	965.8
AHQ-9-13, 5516 - 5570	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.94E-04	0.86	3.60	-	622.5
AHQ-9-13-, 5162 - 5220	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	1.60E-06	0.90	4.66	-	547.5
AHQ-9-12, 5186	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	9.99E-05	0.42	2.69	-	419.4
AHQ-9-13-, 3820 - 3878	K.TLVLLMGK.E	875.15478	2	6.99E-05	0.79	2.55	-	559.4
AHQ-9-13, 3320 - 3334	K.TLVLLM*GK.E	891.15418	2	3.21E-04	0.82	2.58	-	810.7
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				3.23E-12	12.00	140.29	49.20	49481.2
AHQ-9-7, 4369 - 4385	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	1.91E-05	0.67	3.56	-	280.9
AHQ-9-13, 5315	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.68E-05	0.60	2.69	-	533.2
AHQ-9-13-, 5290 - 5332	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.37E-07	0.80	3.32	-	444.8
AHQ-9-7, 2770 - 2838	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	3.23E-12	0.97	5.71	-	1170.4
AHQ-9-7, 2840 - 2845	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	1.87E-06	0.94	4.56	-	1162.0
AHQ-9-8, 2772	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	1.15E-05	0.94	4.46	-	800.3
AHQ-9-7, 2726 - 2785	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	5.58E-05	0.79	3.54	-	823.9
AHQ-9-7, 3089 - 3106	R.DNCCILDER.F	1197.27847	2	1.29E-05	0.88	3.01	-	1047.2
AHQ-9-9, 4820	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	1.25E-07	0.86	3.88	-	572.7
AHQ-9-7, 4956 - 5022	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	2.12E-05	0.88	4.00	-	619.2
AHQ-9-8, 5036	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.92E-05	0.84	3.70	-	483.5
AHQ-9-7, 6004 - 6024	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	3	2.11E-04	0.93	5.09	-	999.7
AHQ-9-8, 4424	K.IHLISTQSAIPYALR.V	1683.97576	2	1.52E-07	0.94	4.23	-	1098.5
AHQ-9-8, 2202	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	1.68E-09	0.66	2.66	-	651.0
AHQ-9-7, 2184 - 2240	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	7.19E-12	0.95	4.13	-	1397.5
AHQ-9-7, 3824	K.QSGLYFIKPLK.A	1294.56665	2	9.10E-04	0.60	2.74	-	287.0
AHQ-9-7, 3801 - 3808	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	2	1.42E-06	0.89	4.29	-	387.7
AHQ-9-9, 3819	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	7.01E-04	0.80	3.57	-	776.1
AHQ-9-7, 3148 - 3176	R.VELEDWNGR.T	1118.18129	2	1.80E-05	0.90	3.31	-	1190.0
AHQ-9-8, 3148	R.VELEDWNGR.T	1118.18129	2	4.66E-06	0.88	2.89	-	1061.5
AHQ-9-5, 3113	K.YEASILTHDSSIR.Y	1492.61564	2	3.51E-04	0.66	2.56	-	564.2
AHQ-9-7, 3017 - 3088	K.YEASILTHDSSIR.Y	1492.61564	2	1.34E-06	0.86	3.86	-	536.3
AHQ-9-7, 3061	K.YEASILTHDSSIR.Y	1492.61564	3	6.28E-06	0.69	3.05	-	610.9
AHQ-9-7, 2908	K.YEASILTHDSSIR.Y	1492.61564	2	7.90E-04	0.67	2.75	-	385.7
AHQ-9-8, 2996	K.YEASILTHDSSIR.Y	1492.61564	2	3.68E-06	0.71	2.71	-	474.2
AHQ-9-11, 3089	K.YEASILTHDSSIR.Y	1492.61564	2	2.74E-06	0.81	3.09	-	532.1
AHQ-9-12, 3042 - 3112	K.YEASILTHDSSIR.Y	1492.61564	2	1.48E-05	0.88	3.19	-	839.9
AHQ-9-7, 2764 - 2820	R.YLQEIYNSNNQK.I	1514.62131	2	6.24E-08	0.96	5.05	-	1265.4
AHQ-9-7, 2876 - 2945	R.YLQEIYNSNNQK.I	1514.62131	2	5.03E-05	0.93	4.30	-	1061.4
gi|4557697|ref|NP_000412.1| keratin 10; Keratin-10 [Homo sapiens]				3.38E-12	13.26	160.29	31.60	57247.1
AHQ-9-1, 2967	R.ALEESNYELEGK.I	1382.45482	2	4.91E-07	0.94	3.78	-	1350.4
AHQ-9-7, 2748	R.ALEESNYELEGK.I	1382.45482	2	2.00E-07	0.91	3.34	-	1403.7
AHQ-9-8, 2766	R.ALEESNYELEGK.I	1382.45482	2	7.00E-07	0.96	4.44	-	1318.0
AHQ-9-3, 2792	R.ALEESNYELEGK.I	1382.45482	2	2.51E-07	0.92	3.68	-	1099.1
AHQ-9-6, 2761	R.ALEESNYELEGK.I	1382.45482	2	1.97E-06	0.88	3.89	-	882.5
AHQ-9-4, 2757	R.ALEESNYELEGK.I	1382.45482	2	2.54E-06	0.95	4.12	-	1225.6
AHQ-9-9, 2655 - 2668	R.ALEESNYELEGK.I	1382.45482	2	1.20E-04	0.79	2.97	-	866.8
AHQ-9-14-, 2833	R.ALEESNYELEGK.I	1382.45482	2	2.44E-05	0.89	2.92	-	1350.2
AHQ-9-5, 2768	R.ALEESNYELEGK.I	1382.45482	2	7.23E-07	0.95	4.13	-	1340.1
AHQ-9-11, 2758 - 2762	R.ALEESNYELEGK.I	1382.45482	2	2.30E-07	0.95	3.81	-	1386.6
AHQ-9-2, 2847	R.ALEESNYELEGK.I	1382.45482	2	2.36E-08	0.92	3.79	-	938.9
AHQ-9-13-, 2828	R.ALEESNYELEGK.I	1382.45482	2	5.17E-06	0.90	3.72	-	875.3
AHQ-9-12, 2754 - 2808	R.ALEESNYELEGK.I	1382.45482	2	4.55E-05	0.72	2.92	-	590.8
AHQ-9-4, 2765 - 2768	R.ALEESNYELEGK.I	1382.45482	1	6.13E-05	0.29	2.39	-	445.8
AHQ-9-14, 3599	R.ALEESNYELEGK.I	1382.45482	2	2.25E-05	0.70	2.74	-	923.3
AHQ-9-14-, 3549	K.DAEAWFNEK.S	1110.15762	2	3.32E-04	0.76	2.75	-	700.2
AHQ-9-6, 3434	K.DAEAWFNEK.S	1110.15762	2	1.56E-04	0.73	2.57	-	959.4
AHQ-9-2, 3542	K.DAEAWFNEK.S	1110.15762	2	4.15E-04	0.82	3.17	-	943.2
AHQ-9-4, 3441	K.DAEAWFNEK.S	1110.15762	2	7.88E-04	0.81	3.32	-	872.1
AHQ-9-7, 4973 - 5028	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.24E-05	0.78	3.47	-	835.2
AHQ-9-3, 4313 - 4389	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.17E-04	0.83	3.52	-	489.2
AHQ-9-3, 5040	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	5.12E-09	0.87	3.82	-	712.4
AHQ-9-7, 4249	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	5.84E-07	0.87	3.95	-	694.8
AHQ-9-1, 4482	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.46E-10	0.95	4.68	-	967.8
AHQ-9-14, 5711	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.08E-05	0.70	3.17	-	444.5
AHQ-9-8, 5075	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.25E-05	0.83	3.40	-	777.6
AHQ-9-12, 4932 - 5000	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.98E-04	0.70	2.94	-	489.3
AHQ-9-2, 5177 - 5253	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	4.48E-06	0.91	4.19	-	791.1
AHQ-9-6, 5146	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.24E-05	0.84	3.26	-	736.2
AHQ-9-4, 5078	K.ELTTEIDNNIEQISSYK.S	1998.13406	3	1.43E-07	0.75	3.35	-	714.3
AHQ-9-4, 5188	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.43E-05	0.63	3.62	-	548.4
AHQ-9-6, 5027	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	9.33E-06	0.92	3.84	-	950.5
AHQ-9-6, 4271	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.45E-04	0.80	3.64	-	537.6
AHQ-9-13-, 4309	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.87E-10	0.93	4.44	-	796.5
AHQ-9-9, 4868	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	7.95E-05	0.41	2.63	-	398.9
AHQ-9-9, 4115	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	4.87E-07	0.36	2.81	-	312.9
AHQ-9-13-, 5164	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.10E-10	0.88	3.49	-	873.6
AHQ-9-14-, 4333	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.34E-07	0.95	4.28	-	1088.9
AHQ-9-5, 4324 - 4337	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.47E-08	0.92	4.52	-	593.4
AHQ-9-5, 5092	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.40E-06	0.84	3.43	-	575.4
AHQ-9-1, 5212	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.62E-05	0.91	4.02	-	1082.3
AHQ-9-7, 5129 - 5154	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	7.27E-04	0.12	2.51	-	254.5
AHQ-9-9, 3851	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	9.09E-05	0.94	4.35	-	1027.2
AHQ-9-6, 4005	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	9.13E-05	0.86	3.63	-	745.8
AHQ-9-11, 3974	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	6.59E-05	0.86	3.59	-	649.2
AHQ-9-2, 4145 - 4223	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	7.94E-08	0.89	3.87	-	704.3
AHQ-9-12, 4014	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	4.01E-06	0.73	3.07	-	702.6
AHQ-9-13-, 4009 - 4065	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	3.70E-08	0.93	4.89	-	654.2
AHQ-9-8, 4044	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	5.15E-10	0.75	3.56	-	523.7
AHQ-9-13, 4156 - 4218	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	4.68E-06	0.86	3.58	-	716.9
AHQ-9-1, 4164 - 4210	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	3.38E-12	0.94	4.52	-	980.5
AHQ-9-7, 3988	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	7.81E-07	0.78	3.38	-	578.1
AHQ-9-14, 4951 - 5008	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	3.24E-06	0.81	3.47	-	896.4
AHQ-9-14-, 4074	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	2.91E-05	0.91	4.33	-	787.2

AHQ-9-3, 3965 - 4040	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.58E-11	0.93	4.07	-	906.1
AHQ-9-13-, 3316	K.IRLENEIQTYR.S	1435.61046	2	4.00E-06	0.88	3.16	-	1035.5
AHQ-9-3, 3282 - 3353	K.IRLENEIQTYR.S	1435.61046	2	1.87E-05	0.95	3.79	-	1710.7
AHQ-9-5, 3196 - 3272	K.IRLENEIQTYR.S	1435.61046	2	1.44E-05	0.96	3.85	-	1699.7
AHQ-9-5, 2521	R.LENEIQTYR.S	1166.26586	2	6.18E-05	0.87	3.62	-	961.3
AHQ-9-7, 2444 - 2516	R.LENEIQTYR.S	1166.26586	2	9.37E-04	0.68	3.01	-	539.3
AHQ-9-2, 2605	R.LENEIQTYR.S	1166.26586	2	3.07E-05	0.87	3.69	-	894.6
AHQ-9-13-, 2826	R.LKYENEVALR.Q	1235.41446	2	8.40E-06	0.60	2.64	-	402.4
AHQ-9-2, 2837	R.LKYENEVALR.Q	1235.41446	2	2.94E-04	0.75	2.79	-	474.2
AHQ-9-4, 2754	R.LKYENEVALR.Q	1235.41446	2	1.69E-06	0.69	2.74	-	501.9
AHQ-9-5, 2759	R.LKYENEVALR.Q	1235.41446	2	3.10E-05	0.57	2.70	-	368.4
AHQ-9-2, 6101	K.NQILNLTTDNANILLQIDNAR.L	2368.63258	3	1.64E-04	0.84	3.65	-	1091.3
AHQ-9-2, 5957	R.NVQALEIELQSQLALK.Q	1798.07394	2	3.31E-04	0.51	2.96	-	611.7
AHQ-9-13-, 5729 - 5805	R.NVQALEIELQSQLALK.Q	1798.07394	2	6.51E-04	0.90	3.76	-	1103.2
AHQ-9-13, 6168 - 6178	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	5.61E-04	0.74	3.52	-	698.7
AHQ-9-5, 5296 - 5351	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	1.42E-04	0.86	3.96	-	686.7
AHQ-9-6, 6029	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	4.58E-04	0.72	3.19	-	1054.0
AHQ-9-2, 6203 - 6206	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	1.84E-05	0.95	5.39	-	1325.6
AHQ-9-14-, 5295	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	7.34E-04	0.88	4.17	-	745.3
AHQ-9-13-, 5278	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	1.62E-05	0.93	5.28	-	1063.4
AHQ-9-4, 6104	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	1.69E-06	0.85	3.62	-	829.9
AHQ-9-1, 5470 - 5542	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	5.83E-04	0.94	5.74	-	839.0
AHQ-9-4, 3344	K.QSLEASLAETEGR.Y	1391.46648	2	1.60E-06	0.79	2.77	-	604.4
AHQ-9-1, 5159	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	1.11E-04	0.63	2.90	-	249.2
AHQ-9-1, 4991	K.SKELTTEIDNNIEQISSYK.S	2213.38462	3	3.73E-04	0.76	3.04	-	850.8
AHQ-9-1, 4918 - 4988	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	8.02E-08	0.93	4.66	-	754.0
AHQ-9-4, 4025	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	1.97E-10	0.95	4.81	-	1056.6
AHQ-9-7, 4686 - 4768	K.SKELTTEIDNNIEQISSYK.S	2213.38462	3	1.12E-04	0.84	4.52	-	776.8
AHQ-9-4, 2141	R.SLLEGEGSSGGGGR.G	1263.29680	2	3.66E-06	0.84	3.08	-	950.8
AHQ-9-5, 2136	R.SLLEGEGSSGGGGR.G	1263.29680	2	9.24E-05	0.80	2.91	-	774.9
AHQ-9-6, 6281	K.TIDDLKNQILNLTTDNANILLQIDNAR.L	3054.40205	3	2.78E-04	0.76	3.97	-	599.0
AHQ-9-5, 2252	K.VTMQNLNDR.L	1091.22402	2	7.69E-06	0.82	2.74	-	922.2
gi|17318569|ref|NP_006112.2| keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]				3.56E-12	19.37	220.31	39.60	66066.3
AHQ-9-4, 2118	K.AEAESLYQSK.Y	1126.19850	2	1.28E-07	0.83	2.72	-	841.2
AHQ-9-5, 2100	K.AEAESLYQSK.Y	1126.19850	2	1.79E-06	0.90	3.20	-	929.1
AHQ-9-4, 2085 - 2096	K.AQYEDIAQK.S	1066.14629	2	1.39E-04	0.57	3.05	-	358.3
AHQ-9-6, 2090	K.AQYEDIAQK.S	1066.14629	2	1.16E-04	0.57	2.69	-	436.7
AHQ-9-4, 2236	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	1.20E-09	0.93	5.02	-	684.0
AHQ-9-7, 2265	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	2.52E-06	0.58	3.00	-	426.0
AHQ-9-5, 2241	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	6.21E-06	0.55	2.59	-	350.5
AHQ-9-3, 2260	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	1.78E-04	0.59	3.06	-	261.7
AHQ-9-1, 2434	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	1.91E-09	0.90	4.75	-	497.7
AHQ-9-8, 2252	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	2.75E-04	0.54	2.57	-	396.2
AHQ-9-4, 2561	R.GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR.G	3314.18235	3	2.93E-07	0.91	5.10	-	1033.2
AHQ-9-1, 5043	K.LALDLEIATYR.T	1278.47925	2	1.73E-06	0.92	4.33	-	1420.4
AHQ-9-4, 3841	K.LNDLEDALQQAK.E	1358.47963	2	2.98E-05	0.96	5.07	-	1618.9
AHQ-9-7, 3734 - 3794	K.LNDLEDALQQAK.E	1358.47963	2	9.53E-08	0.97	4.69	-	1995.2
AHQ-9-6, 3809	K.LNDLEDALQQAK.E	1358.47963	2	6.24E-05	0.95	4.46	-	1669.3
AHQ-9-13, 4034	K.LNDLEDALQQAK.E	1358.47963	2	6.26E-04	0.89	3.78	-	1069.1
AHQ-9-13-, 3873 - 3880	K.LNDLEDALQQAK.E	1358.47963	2	9.69E-04	0.96	4.35	-	1676.7
AHQ-9-14-, 3910	K.LNDLEDALQQAK.E	1358.47963	2	1.41E-06	0.97	5.04	-	1867.3
AHQ-9-3, 3844	K.LNDLEDALQQAK.E	1358.47963	2	7.74E-07	0.95	4.62	-	1412.9
AHQ-9-2, 3945	K.LNDLEDALQQAK.E	1358.47963	2	6.27E-07	0.96	4.28	-	1870.1
AHQ-9-5, 3793 - 3852	K.LNDLEDALQQAK.E	1358.47963	2	2.76E-05	0.98	5.14	-	2175.6
AHQ-9-2, 4367	K.NKLNDLEDALQQAK.E	1600.75564	2	3.01E-09	0.97	4.89	-	1823.6
AHQ-9-8, 4163 - 4236	K.NKLNDLEDALQQAK.E	1600.75564	2	1.18E-05	0.91	3.51	-	1187.3
AHQ-9-4, 4262	K.NKLNDLEDALQQAK.E	1600.75564	2	5.00E-05	0.54	2.81	-	486.9
AHQ-9-5, 4263	K.NKLNDLEDALQQAK.E	1600.75564	2	6.80E-08	0.97	5.13	-	1722.9
AHQ-9-3, 4254	K.NKLNDLEDALQQAK.E	1600.75564	2	1.62E-06	0.84	3.22	-	1047.2
AHQ-9-1, 4434 - 4436	K.NKLNDLEDALQQAK.E	1600.75564	2	3.56E-12	0.97	4.71	-	1728.7
AHQ-9-13-, 4277	K.NKLNDLEDALQQAK.E	1600.75564	2	6.90E-04	0.91	3.71	-	1042.8
AHQ-9-2, 5771	K.NKLNDLEDALQQAKEDLAR.L	2185.38087	3	5.83E-06	0.95	4.93	-	1206.8
AHQ-9-6, 5597	K.NKLNDLEDALQQAKEDLAR.L	2185.38087	3	1.76E-08	0.93	4.52	-	1212.9
AHQ-9-4, 5666	K.NKLNDLEDALQQAKEDLAR.L	2185.38087	3	2.21E-09	0.93	4.72	-	1094.3
AHQ-9-3, 2897	K.NMQDM*VEDYR.N	1317.43134	2	9.58E-08	0.65	2.57	-	753.2
AHQ-9-11, 2805 - 2870	K.NMQDM*VEDYR.N	1317.43134	2	2.56E-04	0.50	2.75	-	534.9
AHQ-9-4, 2760 - 2822	K.NMQDM*VEDYR.N	1317.43134	2	3.14E-05	0.71	2.78	-	712.0
AHQ-9-5, 2745 - 2823	K.NMQDM*VEDYR.N	1317.43134	2	1.43E-04	0.86	3.03	-	913.1
AHQ-9-2, 2911 - 2974	K.NMQDM*VEDYR.N	1317.43134	2	2.09E-07	0.88	3.41	-	845.6
AHQ-9-3, 3642	K.QISNLQQSISDAEQR.G	1717.81950	2	1.95E-05	0.80	3.25	-	680.7
AHQ-9-1, 3811	K.QISNLQQSISDAEQR.G	1717.81950	2	3.88E-06	0.92	3.41	-	1251.9
AHQ-9-14-, 3709	K.QISNLQQSISDAEQR.G	1717.81950	2	4.11E-06	0.75	3.02	-	519.5
AHQ-9-5, 3641	K.QISNLQQSISDAEQR.G	1717.81950	2	2.52E-08	0.88	3.44	-	919.7
AHQ-9-4, 3633 - 3702	K.QISNLQQSISDAEQR.G	1717.81950	2	1.41E-07	0.91	4.29	-	654.9
AHQ-9-8, 3592	K.QISNLQQSISDAEQR.G	1717.81950	2	3.65E-06	0.87	3.60	-	682.1
AHQ-9-7, 3602	K.QISNLQQSISDAEQR.G	1717.81950	2	1.56E-06	0.91	3.95	-	966.8
AHQ-9-13-, 3684	K.QISNLQQSISDAEQR.G	1717.81950	2	5.14E-05	0.87	3.50	-	665.9
AHQ-9-2, 3586	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	1.87E-06	0.95	3.82	-	1523.9
AHQ-9-4, 3493	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	1.37E-05	0.89	3.36	-	1076.2
AHQ-9-6, 3461	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	1.03E-06	0.94	3.90	-	1246.6
AHQ-9-6, 2005	K.SKAEAESLYQSK.Y	1341.44907	2	5.81E-04	0.68	3.10	-	450.1
AHQ-9-5, 2008	K.SKAEAESLYQSK.Y	1341.44907	2	7.75E-07	0.94	3.86	-	1071.6
AHQ-9-4, 2026	K.SKAEAESLYQSK.Y	1341.44907	2	5.85E-04	0.82	3.08	-	587.8
AHQ-9-7, 2024 - 2040	K.SKAEAESLYQSK.Y	1341.44907	2	2.49E-06	0.74	2.96	-	681.2
AHQ-9-4, 3976	K.SKAEAESLYQSKYEELQITAGR.H	2502.71900	3	1.02E-04	0.90	3.76	-	1148.8
AHQ-9-5, 5720	R.SLDLDSIIAEVK.A	1303.48388	2	5.32E-06	0.95	4.16	-	1178.4
AHQ-9-11, 5550	R.SLDLDSIIAEVK.A	1303.48388	2	4.14E-06	0.94	3.52	-	1474.0
AHQ-9-6, 5625	R.SLDLDSIIAEVK.A	1303.48388	2	5.03E-07	0.96	4.49	-	1633.7
AHQ-9-1, 5815	R.SLDLDSIIAEVK.A	1303.48388	2	4.63E-07	0.96	4.26	-	1671.5
AHQ-9-1, 5722 - 5791	R.SLDLDSIIAEVK.A	1303.48388	2	6.34E-04	0.83	2.89	-	748.8
AHQ-9-3, 5557 - 5629	R.SLDLDSIIAEVK.A	1303.48388	2	3.38E-07	0.95	4.44	-	1236.4
AHQ-9-8, 5690	R.SLDLDSIIAEVK.A	1303.48388	2	7.57E-07	0.93	3.87	-	1201.3
AHQ-9-7, 5533 - 5605	R.SLDLDSIIAEVK.A	1303.48388	2	8.12E-08	0.95	4.15	-	1303.9
AHQ-9-12, 5604	R.SLDLDSIIAEVK.A	1303.48388	2	9.70E-04	0.86	3.16	-	1028.1
AHQ-9-13, 5779	R.SLDLDSIIAEVK.A	1303.48388	2	3.64E-07	0.95	4.18	-	1321.2
AHQ-9-2, 5710 - 5787	R.SLDLDSIIAEVK.A	1303.48388	2	2.95E-06	0.95	4.33	-	1207.9
AHQ-9-5, 5635 - 5691	R.SLDLDSIIAEVK.A	1303.48388	2	3.38E-06	0.95	4.20	-	1246.2
AHQ-9-7, 5604	R.SLDLDSIIAEVK.A	1303.48388	2	7.66E-06	0.96	4.90	-	1279.7
AHQ-9-9, 5456 - 5457	R.SLDLDSIIAEVK.A	1303.48388	2	3.87E-06	0.95	3.93	-	1254.4
AHQ-9-5, 4493 - 4561	K.SLNNQFASFIDK.V	1384.51877	2	6.97E-07	0.91	3.73	-	954.8
AHQ-9-5, 4320	K.SLNNQFASFIDK.V	1384.51877	2	6.75E-04	0.57	2.53	-	537.6
AHQ-9-2, 4834	K.SLNNQFASFIDK.V	1384.51877	2	3.62E-07	0.86	3.00	-	810.9
AHQ-9-11, 4413 - 4414	K.SLNNQFASFIDK.V	1384.51877	2	5.19E-05	0.94	3.86	-	1364.7
AHQ-9-10, 4379	K.SLNNQFASFIDK.V	1384.51877	2	4.02E-05	0.48	2.74	-	417.5
AHQ-9-2, 4593 - 4655	K.SLNNQFASFIDK.V	1384.51877	2	3.93E-07	0.87	3.65	-	724.8
AHQ-9-8, 4467 - 4474	K.SLNNQFASFIDK.V	1384.51877	2	5.58E-07	0.80	3.47	-	576.3
AHQ-9-14-, 4523 - 4551	K.SLNNQFASFIDK.V	1384.51877	2	1.72E-06	0.77	3.03	-	707.4

AHQ-9-1, 4879	K.SLNNQFASFIDK.V	1384.51877	2	3.30E-07	0.90	3.54	-	855.8
AHQ-9-1, 4494	K.SLNNQFASFIDK.V	1384.51877	2	1.76E-07	0.76	2.71	-	581.3
AHQ-9-1, 5264 - 5267	K.SLNNQFASFIDKVR.F	1639.83670	2	1.45E-06	0.94	3.46	-	1487.8
AHQ-9-1, 4314	R.SLVNLGGSKSISISVAR.G	1688.95071	2	4.56E-06	0.91	3.43	-	919.4
AHQ-9-3, 4132	R.SLVNLGGSKSISISVAR.G	1688.95071	2	1.06E-09	0.77	3.16	-	500.6
AHQ-9-13-, 4138	R.SLVNLGGSKSISISVAR.G	1688.95071	2	3.83E-11	0.88	3.71	-	572.0
AHQ-9-2, 4247 - 4258	R.SLVNLGGSKSISISVAR.G	1688.95071	2	8.84E-11	0.78	3.34	-	564.5
AHQ-9-5, 6071	R.THNLEPYFESFINNLR.R	1995.18315	2	1.71E-06	0.93	4.56	-	513.7
AHQ-9-5, 6059 - 6067	R.THNLEPYFESFINNLR.R	1995.18315	3	6.37E-08	0.96	5.28	-	1545.9
AHQ-9-6, 5977 - 5989	R.THNLEPYFESFINNLR.R	1995.18315	3	4.56E-04	0.96	5.72	-	1688.4
AHQ-9-2, 6141 - 6175	R.THNLEPYFESFINNLR.R	1995.18315	3	7.91E-05	0.89	4.14	-	1286.1
AHQ-9-13-, 6040 - 6045	R.THNLEPYFESFINNLR.R	1995.18315	3	2.23E-05	0.95	4.76	-	1539.3
AHQ-9-4, 6056	R.THNLEPYFESFINNLR.R	1995.18315	3	6.78E-04	0.93	4.50	-	1332.2
AHQ-9-1, 6188 - 6250	R.THNLEPYFESFINNLR.R	1995.18315	3	5.36E-07	0.96	6.12	-	1362.5
AHQ-9-1, 5492	R.THNLEPYFESFINNLR.R	1995.18315	2	1.54E-04	0.85	3.19	-	528.4
AHQ-9-1, 6192 - 6260	R.THNLEPYFESFINNLR.R	1995.18315	2	1.51E-06	0.88	3.86	-	489.5
AHQ-9-2, 6159	R.THNLEPYFESFINNLR.R	1995.18315	2	4.02E-09	0.92	4.12	-	627.6
AHQ-9-5, 5353	R.THNLEPYFESFINNLR.R	1995.18315	2	4.44E-06	0.90	4.06	-	526.3
AHQ-9-7, 5960 - 5964	R.THNLEPYFESFINNLR.R	1995.18315	3	3.54E-07	0.96	5.82	-	1429.3
AHQ-9-3, 3184	R.TNAENEFVTIK.K	1266.38219	2	2.17E-05	0.90	3.70	-	719.4
AHQ-9-7, 3117	R.TNAENEFVTIK.K	1266.38219	2	7.63E-05	0.86	2.97	-	894.9
AHQ-9-1, 3358	R.TNAENEFVTIK.K	1266.38219	2	1.00E-04	0.91	3.08	-	1001.3
AHQ-9-14-, 3265	R.TNAENEFVTIK.K	1266.38219	2	9.60E-06	0.78	2.81	-	732.2
AHQ-9-6, 3351	R.TNAENEFVTIK.K	1266.38219	2	5.76E-06	0.94	3.25	-	1466.4
AHQ-9-4, 3158	R.TNAENEFVTIK.K	1266.38219	2	1.26E-05	0.88	3.60	-	804.5
AHQ-9-2, 3253	R.TNAENEFVTIK.K	1266.38219	2	1.24E-05	0.91	3.47	-	874.8
AHQ-9-6, 3143 - 3151	R.TNAENEFVTIK.K	1266.38219	2	8.62E-07	0.90	3.47	-	908.4
AHQ-9-5, 3153 - 3167	R.TNAENEFVTIK.K	1266.38219	2	2.55E-05	0.88	3.31	-	765.8
AHQ-9-8, 2696	R.TNAENEFVTIKK.D	1394.55511	2	7.66E-04	0.51	2.74	-	473.0
AHQ-9-6, 2685	R.TNAENEFVTIKK.D	1394.55511	2	1.63E-04	0.80	2.87	-	785.2
AHQ-9-11, 2691 - 2699	R.TNAENEFVTIKK.D	1394.55511	2	7.34E-04	0.57	2.75	-	485.4
AHQ-9-5, 2691	R.TNAENEFVTIKK.D	1394.55511	2	4.23E-06	0.80	2.92	-	849.2
AHQ-9-13-, 2765 - 2766	R.TNAENEFVTIKK.D	1394.55511	2	1.21E-04	0.86	3.38	-	834.2
AHQ-9-5, 4356 - 4417	K.WELLQQVDTSTR.T	1476.61621	2	4.06E-07	0.95	4.27	-	1405.2
AHQ-9-12, 4325 - 4382	K.WELLQQVDTSTR.T	1476.61621	2	1.02E-06	0.79	2.95	-	862.8
AHQ-9-6, 4302 - 4371	K.WELLQQVDTSTR.T	1476.61621	2	7.36E-07	0.94	3.74	-	1557.7
AHQ-9-7, 4225 - 4290	K.WELLQQVDTSTR.T	1476.61621	2	1.58E-08	0.92	3.87	-	1177.8
AHQ-9-2, 4461 - 4530	K.WELLQQVDTSTR.T	1476.61621	2	6.22E-08	0.92	3.75	-	1270.4
AHQ-9-9, 4135	K.WELLQQVDTSTR.T	1476.61621	2	4.50E-05	0.83	2.85	-	1055.9
AHQ-9-3, 4348 - 4408	K.WELLQQVDTSTR.T	1476.61621	2	1.21E-07	0.92	3.30	-	1515.0
AHQ-9-5, 2999 - 3003	K.YEELQITAGR.H	1180.29253	2	2.13E-05	0.96	4.35	-	1701.9
AHQ-9-13-, 3072 - 3074	K.YEELQITAGR.H	1180.29253	2	2.36E-04	0.94	3.66	-	1642.1
AHQ-9-13, 3242 - 3243	K.YEELQITAGR.H	1180.29253	2	3.35E-04	0.93	3.59	-	1433.7
AHQ-9-7, 2985 - 3001	K.YEELQITAGR.H	1180.29253	2	8.54E-05	0.95	3.44	-	1796.2
AHQ-9-11, 2998	K.YEELQITAGR.H	1180.29253	2	3.84E-04	0.95	3.78	-	1769.3
AHQ-9-4, 3005	K.YEELQITAGR.H	1180.29253	2	4.13E-04	0.93	3.64	-	1365.5
AHQ-9-2, 3105	K.YEELQITAGR.H	1180.29253	2	3.15E-05	0.95	3.75	-	1639.5
AHQ-9-6, 2987 - 2997	K.YEELQITAGR.H	1180.29253	2	6.76E-04	0.94	3.60	-	1435.9
AHQ-9-3, 3041	K.YEELQITAGR.H	1180.29253	2	5.01E-04	0.96	3.97	-	1839.3
AHQ-9-1, 3206	K.YEELQITAGR.H	1180.29253	2	2.66E-05	0.96	4.21	-	1899.9
AHQ-9-10, 2957	K.YEELQITAGR.H	1180.29253	2	9.99E-06	0.96	3.51	-	2058.3
gi|4507877|ref|NP_003364.1| vinculin isoform VCL [Homo sapiens]				3.72E-12	36.99	430.29	46.50	116721.6
AHQ-9-14-, 6374	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.30E-06	0.92	3.28	-	1043.0
AHQ-9-5, 6431	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.14E-06	0.97	5.06	-	1321.0
AHQ-9-8, 6424	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.04E-05	0.88	3.48	-	624.1
AHQ-9-7, 6272 - 6334	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.55E-07	0.96	4.79	-	1044.1
AHQ-9-11, 6198 - 6262	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.10E-06	0.93	4.10	-	786.2
AHQ-9-4, 6346 - 6408	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	2.45E-05	0.97	5.29	-	1240.9
AHQ-9-6, 6346	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.63E-08	0.96	4.92	-	1038.9
AHQ-9-10, 6295	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.27E-05	0.95	5.00	-	729.3
AHQ-9-4, 3293 - 3356	R.ALASQLQDSLK.D	1174.32943	2	4.68E-04	0.86	3.15	-	779.6
AHQ-9-8, 3336	R.ALASQLQDSLK.D	1174.32943	2	1.00E-04	0.93	3.51	-	1101.7
AHQ-9-5, 3363	R.ALASQLQDSLK.D	1174.32943	2	5.62E-05	0.93	3.61	-	1178.4
AHQ-9-3, 3376	R.ALASQLQDSLK.D	1174.32943	2	5.47E-05	0.81	2.72	-	778.8
AHQ-9-7, 3268 - 3332	R.ALASQLQDSLK.D	1174.32943	2	5.04E-04	0.71	2.85	-	553.1
AHQ-9-7, 3512	K.AQQVSQGLDVLTAK.V	1458.64233	2	2.04E-09	0.95	4.02	-	1343.3
AHQ-9-3, 3553	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.67E-04	0.94	3.00	-	1499.7
AHQ-9-5, 3505 - 3563	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.91E-07	0.97	4.61	-	1708.1
AHQ-9-4, 3489 - 3548	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.75E-08	0.97	4.78	-	1587.2
AHQ-9-8, 3454 - 3524	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.37E-04	0.95	4.03	-	1479.1
AHQ-9-8, 2507	K.AVAGNISDPGLQK.S	1270.41721	2	1.61E-06	0.80	3.09	-	608.9
AHQ-9-5, 2533	K.AVAGNISDPGLQK.S	1270.41721	2	3.26E-04	0.89	3.79	-	707.5
AHQ-9-6, 2522 - 2533	K.AVAGNISDPGLQK.S	1270.41721	2	4.86E-04	0.77	3.04	-	592.0
AHQ-9-7, 2528	K.AVAGNISDPGLQK.S	1270.41721	2	1.23E-04	0.55	3.10	-	368.8
AHQ-9-3, 2566 - 2568	K.AVAGNISDPGLQK.S	1270.41721	2	3.83E-05	0.87	3.80	-	647.5
AHQ-9-4, 2536	K.AVAGNISDPGLQK.S	1270.41721	2	1.15E-04	0.81	3.36	-	651.6
AHQ-9-5, 5480	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	1.91E-04	0.89	4.34	-	1197.8
AHQ-9-4, 5462 - 5473	K.CDRVDQLTAQLADLAAR.G	1918.12182	2	7.05E-04	0.96	4.55	-	1369.3
AHQ-9-6, 5410	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	7.54E-06	0.92	4.47	-	1246.3
AHQ-9-4, 5460	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	6.60E-06	0.95	4.66	-	1675.9
AHQ-9-5, 2347	R.DPSASPGDAGEQAIR.Q	1471.51169	2	5.56E-07	0.83	2.95	-	638.4
AHQ-9-7, 2305 - 2360	R.DPSASPGDAGEQAIR.Q	1471.51169	2	9.21E-07	0.78	3.43	-	459.7
AHQ-9-3, 2378	R.DPSASPGDAGEQAIR.Q	1471.51169	2	4.96E-04	0.76	3.01	-	495.0
AHQ-9-4, 2348	R.DPSASPGDAGEQAIR.Q	1471.51169	2	2.97E-06	0.87	3.47	-	646.5
AHQ-9-4, 5280 - 5336	R.EAFQPQEPDFPPPPPDLEQLR.L	2448.67149	3	1.80E-04	0.89	4.04	-	891.2
AHQ-9-4, 5528	K.ELLPVLISAMK.I	1214.54325	2	4.04E-04	0.55	2.64	-	385.9
AHQ-9-6, 3057	K.ETVQTTEDQILKR.D	1561.71942	2	1.31E-05	0.84	3.23	-	867.8
AHQ-9-7, 3036	K.ETVQTTEDQILKR.D	1561.71942	2	1.56E-05	0.87	3.25	-	833.3
AHQ-9-4, 3050 - 3056	K.ETVQTTEDQILKR.D	1561.71942	2	2.83E-05	0.84	3.27	-	821.9
AHQ-9-5, 3063	K.ETVQTTEDQILKR.D	1561.71942	2	5.32E-07	0.80	3.25	-	658.6
AHQ-9-6, 6154 - 6221	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.55E-09	0.86	4.01	-	665.3
AHQ-9-4, 6280	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.19E-07	0.97	5.59	-	1391.4
AHQ-9-3, 6228 - 6230	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	2.90E-04	0.83	3.82	-	433.1
AHQ-9-5, 6232 - 6301	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.09E-09	0.97	5.61	-	1252.2
AHQ-9-4, 6034	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	2	4.12E-06	0.83	3.63	-	824.9
AHQ-9-4, 6024	R.GILSGTSDLLLTFDEAEVRK.I	2165.42947	3	7.10E-05	0.82	3.61	-	822.0
AHQ-9-4, 3520	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	3	3.24E-06	0.92	4.20	-	1248.2
AHQ-9-5, 3521	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	3	1.18E-04	0.88	3.78	-	1174.0
AHQ-9-4, 2301 - 2370	K.IAELCDDPKER.D	1347.47690	2	9.71E-04	0.79	2.69	-	809.0
AHQ-9-5, 3439	K.IAELCDDPKERDDILR.S	1960.15548	3	1.52E-04	0.87	3.59	-	1207.5
AHQ-9-5, 4136 - 4200	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	2.45E-07	0.89	4.68	-	872.9
AHQ-9-7, 4072 - 4136	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	7.38E-05	0.74	3.96	-	531.1
AHQ-9-4, 4129 - 4201	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	2	1.11E-05	0.91	4.29	-	458.9
AHQ-9-6, 4085 - 4143	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	1.51E-05	0.90	4.42	-	1013.3
AHQ-9-4, 2952	R.LANVMM*GPYR.Q	1168.41500	2	1.53E-04	0.72	3.07	-	559.8
AHQ-9-4, 3420	R.LANVMMGPYR.Q	1152.41560	2	5.08E-05	0.90	3.08	-	1004.9
AHQ-9-4, 4082 - 4140	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	1.05E-07	0.87	4.28	-	796.3

AHQ-9-6, 4070 - 4150	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	2.01E-05	0.75	3.30	-	502.2
AHQ-9-4, 4360	R.LTDELAPPKPPLPEGEVPPPRPPPPEEKDEEFPEQK.A	4028.46845	3	1.07E-04	0.80	3.14	-	776.5
AHQ-9-11, 3569	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	5.60E-08	0.87	3.19	-	677.8
AHQ-9-4, 4362 - 4364	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	2	3.48E-04	0.88	3.64	-	692.9
AHQ-9-4, 4370	K.LVQAAQMLQSDPYSVPAR.D	1975.25833	3	1.55E-04	0.88	4.07	-	940.6
AHQ-9-4, 3620	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	1.97E-05	0.87	3.21	-	580.4
AHQ-9-5, 3624	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	8.43E-05	0.44	2.76	-	346.6
AHQ-9-4, 3630	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	3	3.72E-10	0.98	5.74	-	3062.7
AHQ-9-4, 2329 - 2333	R.M*ALLM*AEM*SR.L	1201.46351	2	6.25E-06	0.92	3.02	-	1407.2
AHQ-9-5, 2928	K.M*LGQM*TDQVADLR.A	1510.71935	2	6.28E-05	0.96	3.86	-	2007.1
AHQ-9-6, 3641	K.M*LGQMTDQVADLR.A	1494.71995	2	1.03E-06	0.86	3.34	-	942.4
AHQ-9-5, 3681	K.M*LGQMTDQVADLR.A	1494.71995	2	4.23E-05	0.94	3.45	-	1656.1
AHQ-9-4, 2930 - 2932	K.M*LGQM*TDQVADLR.A	1510.71935	2	3.35E-05	0.97	4.56	-	1737.3
AHQ-9-4, 5262 - 5330	R.MQEAMTQEVSDVFSDTTTPIK.L	2359.61664	2	9.27E-05	0.51	2.80	-	373.1
AHQ-9-4, 3220	K.M*SAEINEIIR.V	1192.36823	2	8.44E-07	0.92	3.40	-	1132.3
AHQ-9-6, 3213	K.M*SAEINEIIR.V	1192.36823	2	1.18E-05	0.95	3.43	-	1592.5
AHQ-9-5, 3176 - 3231	K.M*SAEINEIIR.V	1192.36823	2	5.42E-06	0.89	3.08	-	1001.2
AHQ-9-4, 3682 - 3750	K.MSAEINEIIR.V	1176.36883	2	8.46E-06	0.96	3.96	-	2202.8
AHQ-9-6, 3115	K.M*TGLVDEAIDTK.S	1309.46876	2	3.42E-06	0.77	2.82	-	820.8
AHQ-9-4, 3062 - 3125	K.M*TGLVDEAIDTK.S	1309.46876	2	2.79E-06	0.94	3.80	-	1149.0
AHQ-9-5, 3059 - 3128	K.M*TGLVDEAIDTK.S	1309.46876	2	2.51E-05	0.93	3.74	-	1125.4
AHQ-9-4, 3077	R.NPGNQAAYEHFETMK.N	1737.87437	2	2.97E-07	0.95	4.30	-	1242.7
AHQ-9-7, 2942	K.QVATALQNLQTK.T	1315.50112	2	8.29E-04	0.61	2.96	-	287.1
AHQ-9-7, 3421	R.SLGEISALTSK.L	1106.25186	2	1.45E-07	0.90	3.30	-	851.0
AHQ-9-4, 3456	R.SLGEISALTSK.L	1106.25186	2	1.22E-05	0.94	3.72	-	931.9
AHQ-9-3, 3469 - 3470	R.SLGEISALTSK.L	1106.25186	2	4.29E-05	0.94	3.71	-	958.8
AHQ-9-6, 3433	R.SLGEISALTSK.L	1106.25186	2	2.33E-06	0.90	3.58	-	786.1
AHQ-9-6, 3298 - 3379	K.SLLDASEEAIKK.D	1304.47187	2	4.05E-04	0.80	2.81	-	866.9
AHQ-9-8, 3275 - 3344	K.SLLDASEEAIKK.D	1304.47187	2	6.32E-06	0.82	3.02	-	880.5
AHQ-9-4, 2470	K.STVEGIQASVK.T	1119.25064	2	3.98E-08	0.93	3.52	-	1193.9
AHQ-9-4, 4461	R.TNISDEESEQATEM*LVHNAQNLM*QSVK.E	3080.30897	3	2.34E-07	0.70	3.39	-	386.0
AHQ-9-4, 6140 - 6176	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	8.88E-07	0.76	4.08	-	592.1
AHQ-9-7, 3258	R.TNLLQVCER.I	1134.28859	2	1.61E-04	0.82	2.50	-	1021.0
AHQ-9-4, 5201 - 5210	K.VAMANIQPQM*LVAGATSIAR.R	2059.44338	3	1.10E-08	0.95	5.56	-	1866.0
AHQ-9-4, 5081	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	8.57E-04	0.47	2.68	-	464.1
AHQ-9-4, 4680	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	5.66E-08	0.95	4.83	-	1873.7
AHQ-9-5, 4685	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	7.54E-05	0.91	4.33	-	706.6
AHQ-9-6, 5005	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	1.56E-07	0.92	4.53	-	731.1
AHQ-9-4, 5074	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	5.30E-05	0.79	3.57	-	624.2
AHQ-9-5, 5052 - 5079	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	6.82E-04	0.75	3.63	-	338.2
AHQ-9-4, 4770	R.VDQLTAQLADLAAR.G	1485.66778	2	5.60E-08	0.98	5.01	-	2656.2
AHQ-9-5, 4787 - 4793	R.VDQLTAQLADLAAR.G	1485.66778	2	2.04E-09	0.98	5.04	-	3148.7
AHQ-9-6, 4722	R.VDQLTAQLADLAAR.G	1485.66778	2	1.06E-08	0.97	4.64	-	2285.1
AHQ-9-4, 3201	R.VGKETVQTTEDQILKR.D	1846.07546	3	1.45E-04	0.81	3.79	-	600.1
AHQ-9-7, 5033	R.VLQLTSWDEDAWASK.D	1749.90156	2	9.39E-06	0.92	3.78	-	887.5
AHQ-9-6, 5038 - 5043	R.VLQLTSWDEDAWASK.D	1749.90156	2	3.72E-12	0.96	4.52	-	1267.1
AHQ-9-4, 5084 - 5165	R.VLQLTSWDEDAWASK.D	1749.90156	2	9.78E-11	0.98	5.62	-	1707.8
AHQ-9-2, 5211	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.36E-05	0.90	3.59	-	752.2
AHQ-9-5, 2903 - 2917	R.WIDNPTVDDR.G	1231.29640	2	4.12E-04	0.93	3.83	-	1156.8
AHQ-9-6, 2889	R.WIDNPTVDDR.G	1231.29640	2	9.78E-05	0.74	3.01	-	556.8
AHQ-9-4, 2889	R.WIDNPTVDDR.G	1231.29640	2	8.28E-05	0.88	3.21	-	859.7
gi|7656991|ref|NP_055140.1| coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;				9.38E-12	5.40	60.30	21.30	53248.7
AHQ-9-6, 5525	R.AIFLADGNVFTTGFSR.M	1716.91793	2	6.65E-07	0.86	2.95	-	939.4
AHQ-9-7, 5397 - 5460	R.AIFLADGNVFTTGFSR.M	1716.91793	2	7.51E-09	0.93	4.34	-	846.7
AHQ-9-6, 5406 - 5461	R.AIFLADGNVFTTGFSR.M	1716.91793	2	9.38E-12	0.96	4.91	-	1472.2
AHQ-9-6, 6237	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	2.25E-04	0.96	5.90	-	1253.3
AHQ-9-6, 2402 - 2447	K.SIKDTICNQDER.I	1480.58332	2	1.47E-07	0.82	2.83	-	1158.5
AHQ-9-6, 3131	R.VGIVAWHPTAR.N	1207.40918	3	2.77E-04	0.84	3.31	-	979.4
AHQ-9-7, 4170	R.VTWDSSFCAVNPR.F	1540.68205	2	1.28E-04	0.74	2.54	-	823.2
AHQ-9-6, 4179	R.VTWDSSFCAVNPR.F	1540.68205	2	4.25E-09	0.93	4.00	-	1134.3
AHQ-9-6, 5557 - 5565	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	4.49E-06	0.92	4.02	-	986.3
AHQ-9-7, 5553	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	2.19E-09	0.88	3.84	-	764.3
gi|29732955|ref|XP_291603.1| similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA				9.88E-12	0.94	10.23	16.80	11173.0
AHQ-9-9, 3837 - 3900	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.13E-06	0.93	4.62	-	925.6
AHQ-9-9, 3704 - 3783	K.NISNASCTTNCIAPLAK.M	1838.05353	2	9.88E-12	0.94	3.76	-	1361.1
gi|16507237|ref|NP_005338.1| heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he				1.31E-11	9.45	110.23	23.50	72332.5
AHQ-9-5, 3140	K.DAGTIAGLNVM*R.I	1234.40834	2	5.22E-04	0.73	2.94	-	540.8
AHQ-9-5, 5511 - 5512	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	1.21E-05	0.85	3.42	-	804.8
AHQ-9-6, 5437	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	3.01E-06	0.96	4.69	-	1206.6
AHQ-9-6, 4522	K.IEWLESHQDADIEDFK.A	1976.08864	2	2.86E-06	0.95	4.51	-	1226.7
AHQ-9-6, 4314	R.IINEPTAAAIAYGLDKR.E	1817.07894	3	1.31E-11	0.68	3.12	-	524.2
AHQ-9-5, 4381	R.IINEPTAAAIAYGLDKR.E	1817.07894	2	3.69E-07	0.62	3.55	-	645.5
AHQ-9-5, 4375	R.IINEPTAAAIAYGLDKR.E	1817.07894	3	1.17E-06	0.66	3.27	-	371.7
AHQ-9-5, 3832	R.ITPSYVAFTPEGER.L	1567.72412	2	4.20E-04	0.46	2.62	-	469.7
AHQ-9-6, 3790	R.ITPSYVAFTPEGER.L	1567.72412	2	2.95E-04	0.76	2.91	-	503.6
AHQ-9-5, 3771 - 3784	K.KSDIDEIVLVGGSTR.I	1589.77277	2	7.10E-06	0.97	4.59	-	2055.7
AHQ-9-6, 3685 - 3733	K.KSDIDEIVLVGGSTR.I	1589.77277	2	2.10E-05	0.93	4.01	-	1110.5
AHQ-9-5, 3785	K.KSDIDEIVLVGGSTR.I	1589.77277	2	2.23E-04	0.83	2.64	-	1205.6
AHQ-9-5, 3500 - 3508	K.NQLTSNPENTVFDAK.R	1678.78173	2	2.62E-07	0.80	4.29	-	539.3
AHQ-9-6, 3670	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	2.86E-06	0.92	3.99	-	986.6
AHQ-9-5, 3716	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	4.78E-09	0.93	4.63	-	816.6
AHQ-9-6, 3109	K.TKPYIQVDIGGGQTK.T	1605.81703	2	6.34E-04	0.85	3.24	-	723.4
AHQ-9-6, 3119	K.TKPYIQVDIGGGQTK.T	1605.81703	3	9.72E-04	0.87	3.45	-	1196.5
AHQ-9-5, 3125 - 3129	R.TWNDPSVQQDIK.F	1431.53230	2	3.75E-05	0.96	4.05	-	1558.9
AHQ-9-5, 3921	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	3	9.88E-04	0.86	3.51	-	909.0
gi|5031571|ref|NP_005713.1| actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog				1.43E-11	3.44	40.20	18.50	44760.5
AHQ-9-8, 3300	K.DLM*VGDEASELR.S	1351.46573	2	6.80E-07	0.94	3.66	-	1273.6
AHQ-9-9, 6183 - 6233	R.FEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTR.S	3940.40927	3	1.69E-04	0.65	3.08	-	360.6
AHQ-9-8, 3352	R.GYAFNHSADFETVR.M	1614.69943	2	1.43E-11	0.94	3.97	-	1023.6
AHQ-9-8, 4119	K.HLWDYTFGPEK.L	1393.52736	2	7.47E-07	0.91	3.80	-	598.2
gi|4507869|ref|NP_003361.1| vasodilator-stimulated phosphoprotein [Homo sapiens]				1.55E-11	0.96	10.25	3.70	39829.4
AHQ-9-8, 5824	K.VKEEIIEAFVQELR.K	1703.96061	3	3.82E-05	0.95	4.95	-	1614.7
AHQ-9-8, 5811	K.VKEEIIEAFVQELR.K	1703.96061	2	1.55E-11	0.96	4.56	-	1513.3
gi|4504745|ref|NP_000410.1| integrin alpha 2b precursor [Homo sapiens]				1.76E-11	27.34	310.32	35.00	113374.2
AHQ-9-6, 4943 - 4962	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.17E-04	0.95	4.87	-	846.4
AHQ-9-4, 4982 - 5025	R.AEGGQCPSLLFDLR.D	1564.74505	2	4.42E-04	0.80	3.26	-	452.0
AHQ-9-3, 4970 - 4981	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.36E-05	0.85	3.77	-	607.3
AHQ-9-13-, 5008 - 5012	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.59E-04	0.92	3.98	-	793.8
AHQ-9-5, 4945 - 5027	R.AEGGQCPSLLFDLR.D	1564.74505	2	4.33E-06	0.91	3.38	-	989.2
AHQ-9-7, 4924 - 4936	R.AEGGQCPSLLFDLR.D	1564.74505	2	1.01E-08	0.95	4.18	-	1168.5
AHQ-9-4, 4581	R.AEGGQCPSLLFDLRDETR.N	2066.23814	3	2.55E-07	0.77	3.52	-	494.1
AHQ-9-3, 2938	R.ALSNVEGFER.L	1122.21308	2	1.97E-05	0.87	2.93	-	1055.3
AHQ-9-4, 2906	R.ALSNVEGFER.L	1122.21308	1	3.56E-04	0.68	2.76	-	180.1
AHQ-9-4, 2892	R.ALSNVEGFER.L	1122.21308	2	1.48E-05	0.87	2.81	-	1087.9
AHQ-9-4, 4814	K.ASVQLLVQDSLNPAVK.S	1682.94293	3	1.98E-04	0.92	4.55	-	989.3
AHQ-9-5, 4812 - 4887	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.96E-05	0.78	3.60	-	508.3
AHQ-9-3, 4781 - 4836	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	6.82E-04	0.80	2.60	-	1095.6

AHQ-9-4, 5644	K.ASVQLLVQDSLNPAVKSCVLPQTK.T	2598.01293	3	1.99E-04	0.87	3.70	-	1177.9
AHQ-9-4, 3072	R.DETRNVGSQTLQTFK.A	1724.85363	2	7.34E-05	0.71	3.03	-	707.4
AHQ-9-3, 3696	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.81E-05	0.76	2.91	-	679.0
AHQ-9-5, 3713 - 3749	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	5.84E-05	0.80	3.59	-	557.6
AHQ-9-4, 3704 - 3752	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	3.91E-07	0.93	4.39	-	951.7
AHQ-9-4, 3810 - 3886	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	5.52E-07	0.77	3.57	-	563.7
AHQ-9-4, 4310 - 4344	R.FGSAIAPLGDLDR.D	1332.48700	2	6.22E-06	0.93	3.70	-	984.6
AHQ-9-6, 5271 - 5317	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	3.40E-04	0.87	4.11	-	907.9
AHQ-9-5, 5347 - 5352	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.99E-05	0.91	4.63	-	799.5
AHQ-9-4, 5493 - 5497	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	6.50E-05	0.84	3.77	-	882.8
AHQ-9-4, 5376 - 5432	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	3.12E-06	0.94	5.27	-	977.8
AHQ-9-4, 5585	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	6.31E-05	0.88	3.99	-	543.3
AHQ-9-4, 5693	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.97E-06	0.95	4.49	-	959.2
AHQ-9-4, 5794 - 5856	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	3.56E-08	0.76	3.50	-	772.8
AHQ-9-4, 5572 - 5630	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	6.90E-04	0.73	3.41	-	632.3
AHQ-9-11, 4745	R.GEAQVWTQLLR.A	1301.47614	2	3.11E-07	0.89	3.31	-	940.6
AHQ-9-10, 4710 - 4771	R.GEAQVWTQLLR.A	1301.47614	2	8.77E-05	0.68	3.10	-	625.1
AHQ-9-4, 5113 - 5182	R.GNSFPASLVVAAEEGER.E	1733.86053	2	9.35E-09	0.90	4.24	-	638.1
AHQ-9-4, 5240 - 5305	R.GNSFPASLVVAAEEGER.E	1733.86053	2	3.29E-06	0.91	3.98	-	864.8
AHQ-9-4, 5857 - 5928	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	5.63E-05	0.76	3.84	-	372.7
AHQ-9-4, 5726 - 5801	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	1.21E-05	0.76	3.95	-	395.5
AHQ-9-4, 5984 - 6042	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	9.14E-06	0.75	3.56	-	424.9
AHQ-9-3, 4953 - 4956	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	2.78E-07	0.89	4.03	-	896.6
AHQ-9-6, 4917	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	3.32E-04	0.81	3.42	-	954.2
AHQ-9-5, 4991	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	1.65E-05	0.88	3.37	-	1514.5
AHQ-9-5, 5001	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	6.59E-07	0.96	5.17	-	897.5
AHQ-9-4, 4964	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	3.46E-10	0.97	5.46	-	1343.4
AHQ-9-4, 4960 - 5021	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	1.89E-05	0.86	3.76	-	1022.5
AHQ-9-6, 4925	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	8.44E-06	0.92	4.32	-	723.6
AHQ-9-3, 4966	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	7.07E-04	0.94	4.63	-	903.2
AHQ-9-4, 4741 - 4808	R.GQVLVFLGQSEGLR.S	1503.72793	2	2.84E-06	0.97	5.15	-	1657.7
AHQ-9-4, 4844 - 4900	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.09E-04	0.90	3.65	-	1002.5
AHQ-9-6, 4730 - 4737	R.GQVLVFLGQSEGLR.S	1503.72793	2	2.72E-08	0.96	3.92	-	1785.4
AHQ-9-5, 4803	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.14E-08	0.97	4.95	-	1365.9
AHQ-9-4, 3814	R.HDLLVGAPLYM*ESR.A	1617.85128	3	6.36E-04	0.83	3.72	-	971.5
AHQ-9-4, 4304	R.HDLLVGAPLYMESR.A	1601.85188	3	3.92E-05	0.91	3.74	-	1408.4
AHQ-9-6, 4255	K.IVLLDVPVR.A	1024.28196	2	2.29E-04	0.85	3.30	-	635.7
AHQ-9-4, 4309	K.IVLLDVPVR.A	1024.28196	2	1.46E-05	0.91	3.71	-	833.5
AHQ-9-5, 3872 - 3881	R.IYVENDFSWDKR.Y	1572.70245	2	4.66E-04	0.90	3.91	-	906.7
AHQ-9-3, 3869	R.IYVENDFSWDKR.Y	1572.70245	2	4.11E-06	0.96	4.28	-	1376.4
AHQ-9-4, 3852 - 3909	R.IYVENDFSWDKR.Y	1572.70245	2	9.24E-06	0.88	3.86	-	877.1
AHQ-9-4, 4041	R.IYVENDFSWDKR.Y	1572.70245	2	5.01E-06	0.92	3.47	-	1218.3
AHQ-9-4, 4173	K.LSLNAELQLDR.Q	1272.43310	2	1.32E-07	0.90	3.83	-	941.6
AHQ-9-6, 5529 - 5586	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	6.85E-11	0.97	6.37	-	1263.0
AHQ-9-7, 5512	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.04E-04	0.94	5.15	-	1039.0
AHQ-9-4, 5584 - 5652	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.76E-11	0.95	5.81	-	1031.6
AHQ-9-3, 5553 - 5568	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.31E-07	0.96	6.19	-	1172.0
AHQ-9-4, 5389	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	6.06E-09	0.93	4.63	-	1204.0
AHQ-9-4, 5490	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	5.34E-05	0.96	5.44	-	1945.7
AHQ-9-4, 5597 - 5598	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	2	6.23E-08	0.94	5.09	-	635.1
AHQ-9-4, 3657	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	3.67E-04	0.94	4.64	-	682.0
AHQ-9-4, 3390	K.TEEAEKTPVGSCFLAQPESGRR.A	2451.65537	3	1.78E-05	0.50	3.26	-	290.1
AHQ-9-7, 5172	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	6.48E-06	0.80	3.58	-	602.4
AHQ-9-7, 5180	R.TLGPSQEETGGVFLCPWR.A	2036.25364	3	1.24E-05	0.71	3.19	-	649.5
AHQ-9-5, 5264	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	7.51E-09	0.93	4.29	-	767.2
AHQ-9-11, 5123 - 5179	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.34E-06	0.86	3.60	-	829.3
AHQ-9-13-, 5222	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.95E-04	0.93	4.47	-	823.2
AHQ-9-4, 5205 - 5264	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.14E-06	0.97	5.76	-	1354.4
AHQ-9-4, 5129 - 5208	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	7.84E-04	0.78	3.04	-	587.5
AHQ-9-11, 3566 - 3597	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.09E-04	0.62	2.70	-	500.7
AHQ-9-5, 3659	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.29E-07	0.85	3.64	-	754.7
AHQ-9-4, 3645 - 3668	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.04E-07	0.95	4.59	-	1102.6
AHQ-9-4, 4349 - 4376	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	5.89E-09	0.96	5.17	-	1624.5
AHQ-9-4, 5385	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	2.06E-06	0.90	4.30	-	817.4
AHQ-9-4, 5485	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.60E-04	0.94	3.97	-	1176.2
AHQ-9-5, 4004	R.VVLCELGNPMK.K	1261.53692	2	9.73E-04	0.76	2.85	-	576.7
AHQ-9-4, 3316	R.VVLCELGNPM*K.K	1277.53632	2	1.25E-05	0.93	4.22	-	1202.6
AHQ-9-6, 3295	R.VVLCELGNPM*K.K	1277.53632	2	6.72E-05	0.80	2.95	-	844.6
AHQ-9-4, 3985	R.VVLCELGNPMK.K	1261.53692	2	1.62E-04	0.94	3.80	-	1297.0
AHQ-9-4, 3602	R.VVLCELGNPMKK.N	1389.70984	2	2.16E-05	0.90	3.12	-	1066.2
AHQ-9-4, 4141	R.VYLFLQPR.G	1036.25129	2	1.28E-04	0.94	3.44	-	1125.3
AHQ-9-3, 4142	R.VYLFLQPR.G	1036.25129	2	1.24E-05	0.94	3.44	-	1368.8
AHQ-9-5, 4147 - 4155	R.VYLFLQPR.G	1036.25129	2	1.12E-05	0.95	3.70	-	1219.7
AHQ-9-4, 4130	R.VYLFLQPR.G	1036.25129	2	5.40E-06	0.95	4.00	-	1150.8
gi|13124879|ref|NP_002465.1| smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]				1.92E-11	7.09	80.40	4.20	227336.7
AHQ-9-2, 4607	R.DLGEELEALK.T	1117.23151	2	9.32E-04	0.91	3.00	-	1048.9
AHQ-9-3, 2952	K.FDQLLAEEK.N	1093.21165	2	9.60E-06	0.90	2.67	-	1501.9
AHQ-9-5, 2929	K.FDQLLAEEK.N	1093.21165	2	4.83E-05	0.90	2.88	-	1408.7
AHQ-9-2, 3014	K.FDQLLAEEK.N	1093.21165	2	1.98E-05	0.91	3.10	-	1469.3
AHQ-9-2, 2566 - 2641	K.KEEELQAALAR.L	1258.40643	2	6.49E-04	0.73	2.82	-	845.1
AHQ-9-6, 2813 - 2882	R.KFDQLLAEEK.N	1221.38456	2	1.18E-04	0.85	3.11	-	965.6
AHQ-9-3, 2920 - 2994	R.KFDQLLAEEK.N	1221.38456	2	4.06E-05	0.65	2.52	-	761.5
AHQ-9-4, 2890 - 2970	R.KFDQLLAEEK.N	1221.38456	2	1.04E-04	0.86	3.44	-	923.8
AHQ-9-2, 2977 - 3051	R.KFDQLLAEEK.N	1221.38456	2	2.25E-04	0.56	2.92	-	687.4
AHQ-9-2, 5618 - 5650	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	4.44E-08	0.97	5.59	-	2259.2
AHQ-9-6, 4957 - 5025	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	5.32E-05	0.78	3.63	-	1083.3
AHQ-9-2, 5073 - 5130	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	8.16E-09	0.98	8.01	-	2619.8
AHQ-9-2, 5825	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.63E-07	0.96	4.26	-	1231.6
AHQ-9-2, 5926	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.21E-07	0.78	3.31	-	497.1
AHQ-9-2, 5714 - 5769	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.99E-08	0.96	4.63	-	1181.4
AHQ-9-6, 5511 - 5587	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.90E-07	0.84	3.28	-	684.4
AHQ-9-6, 5646 - 5662	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.38E-04	0.86	3.75	-	667.8
AHQ-9-7, 5632	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.52E-05	0.65	2.87	-	493.4
AHQ-9-3, 5768	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.57E-06	0.88	3.63	-	609.9
AHQ-9-1, 5952 - 5956	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.93E-04	0.85	3.32	-	810.5
AHQ-9-3, 5661	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.55E-04	0.85	3.32	-	659.8
AHQ-9-4, 5834	K.QLLQANPILEAFGNAK.T	1727.98540	2	9.97E-07	0.92	3.62	-	928.8
AHQ-9-4, 5725	K.QLLQANPILEAFGNAK.T	1727.98540	2	5.91E-07	0.92	3.68	-	854.9
AHQ-9-4, 5272	K.TQLEELEDELQATEDAK.L	1963.04334	3	4.39E-09	0.96	6.11	-	1032.3
AHQ-9-4, 5237 - 5265	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.67E-09	0.98	6.44	-	1936.0
AHQ-9-5, 5283	K.TQLEELEDELQATEDAK.L	1963.04334	2	5.28E-04	0.98	5.20	-	2322.9
AHQ-9-5, 5292	K.TQLEELEDELQATEDAK.L	1963.04334	3	2.34E-05	0.91	3.98	-	1257.5
AHQ-9-3, 5220 - 5221	K.TQLEELEDELQATEDAK.L	1963.04334	3	8.17E-06	0.96	6.17	-	1126.6
AHQ-9-2, 5365 - 5370	K.TQLEELEDELQATEDAK.L	1963.04334	3	6.78E-09	0.92	4.86	-	862.8
AHQ-9-6, 5215 - 5221	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.92E-11	0.98	6.53	-	2076.1
AHQ-9-2, 5361	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.43E-11	0.96	4.88	-	1404.2
AHQ-9-2, 3931	K.TQLEELEDELQATEDAK.L	1963.04334	2	5.63E-06	0.97	5.00	-	1412.1

AHQ-9-7, 5209	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.88E-05	0.97	5.12	-	1644.2
AHQ-9-1, 5396 - 5456	K.TQLEELEDELQATEDAK.L	1963.04334	2	6.55E-07	0.97	4.97	-	1552.4
gi|13775198|ref|NP_112576.1| SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr				2.62E-11	2.45	30.25	31.20	10437.7
AHQ-9-13-, 4528	R.IQYQLVDISQDNALR.D	1776.97168	2	2.62E-11	0.95	4.42	-	1475.4
AHQ-9-13, 4694 - 4750	R.IQYQLVDISQDNALR.D	1776.97168	2	5.38E-07	0.96	5.00	-	1492.2
AHQ-9-13-, 4389 - 4454	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	1.06E-05	0.67	3.64	-	376.5
AHQ-9-13-, 4258 - 4316	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	3.89E-04	0.45	3.20	-	250.7
AHQ-9-14-, 4345	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	6.64E-04	0.52	3.04	-	340.9
AHQ-9-13-, 1853 - 1917	R.VYSTSVTGSR.E	1057.13940	2	4.32E-04	0.83	2.82	-	832.1
gi|4507953|ref|NP_003397.1| tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep				2.62E-11	2.66	30.22	18.40	27744.9
AHQ-9-14-, 2426	K.SVTEQGAELSNEER.N	1549.57922	2	6.23E-08	0.88	3.15	-	1265.0
AHQ-9-10, 2367 - 2423	K.SVTEQGAELSNEER.N	1549.57922	2	3.00E-07	0.94	3.99	-	1273.8
AHQ-9-11, 2382	K.SVTEQGAELSNEER.N	1549.57922	2	2.62E-11	0.89	3.46	-	1067.9
AHQ-9-13-, 2428 - 2497	K.SVTEQGAELSNEER.N	1549.57922	2	1.64E-09	0.92	3.88	-	1108.3
AHQ-9-9, 2291	K.SVTEQGAELSNEER.N	1549.57922	2	3.08E-07	0.78	2.82	-	891.4
AHQ-9-13, 6330	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	1.10E-04	0.95	4.46	-	1186.0
AHQ-9-10, 2092 - 2147	R.YLAEVAAGDDKK.G	1280.40887	2	4.18E-04	0.82	3.28	-	833.9
gi|4504345|ref|NP_000508.1| alpha 2 globin [Homo sapiens]				2.62E-11	3.69	40.35	50.70	15257.4
AHQ-9-13, 4374 - 4380	K.FLASVSTVLTSK.Y	1253.46970	2	3.05E-04	0.88	3.25	-	950.7
AHQ-9-13-, 3997 - 4066	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	6.70E-08	0.87	3.98	-	669.0
AHQ-9-13, 4136 - 4190	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	6.08E-06	0.89	3.82	-	728.8
AHQ-9-13, 4162	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	3.82E-04	0.66	2.87	-	461.7
AHQ-9-13-, 4002	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	7.01E-05	0.80	3.44	-	576.6
AHQ-9-13-, 5264 - 5266	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	7.78E-06	0.98	7.09	-	1776.3
AHQ-9-13-, 4745	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	5.76E-05	0.93	5.37	-	797.1
AHQ-9-13, 3018 - 3083	K.VGAHAGEYGAEALER.M	1530.62397	2	6.71E-05	0.59	2.67	-	584.4
AHQ-9-13, 2895 - 2959	K.VGAHAGEYGAEALER.M	1530.62397	3	9.45E-05	0.96	5.01	-	2065.6
AHQ-9-13-, 2685 - 2746	K.VGAHAGEYGAEALER.M	1530.62397	2	2.62E-11	0.97	4.40	-	1664.9
AHQ-9-13-, 2684 - 2758	K.VGAHAGEYGAEALER.M	1530.62397	3	2.70E-04	0.97	5.59	-	2303.3
AHQ-9-13, 2890 - 2962	K.VGAHAGEYGAEALER.M	1530.62397	2	3.86E-06	0.95	4.23	-	1107.5
AHQ-9-14-, 2690 - 2691	K.VGAHAGEYGAEALER.M	1530.62397	2	5.57E-10	0.97	4.31	-	1953.8
gi|14149734|ref|NP_065174.1| coronin, actin binding protein, 1B [Homo sapiens]				2.89E-11	0.93	10.22	5.90	54234.4
AHQ-9-6, 6177	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	2.89E-11	0.93	4.36	-	1144.6
gi|10835063|ref|NP_002511.1| nucleophosmin (nucleolar phosphoprotein B23, numatrin); Nucleophosmin				4.04E-11	1.62	20.22	17.00	32574.8
AHQ-9-9, 3289	K.LAADEDDDDDDEEDDDEDDDDDDFDDEEAEEKAPVK.K	4120.75940	3	4.04E-11	0.92	4.44	-	961.5
AHQ-9-9, 5325 - 5391	R.M*TDQEAIQDLWQWR.K	1837.00591	2	3.60E-04	0.70	3.13	-	859.3
gi|4505981|ref|NP_002695.1| pro-platelet basic protein (includes platelet basic protein, bet; Pro-p				4.12E-11	6.12	70.30	44.50	13894.1
AHQ-9-13-, 4550 - 4577	K.EESLDSDLYAELR.C	1540.61070	2	8.38E-06	0.52	2.76	-	408.0
AHQ-9-14, 5391 - 5399	K.EESLDSDLYAELR.C	1540.61070	2	2.99E-08	0.93	4.25	-	871.7
AHQ-9-14-, 4297 - 4355	K.EESLDSDLYAELR.C	1540.61070	2	1.03E-10	0.89	3.50	-	696.9
AHQ-9-14-, 4415	K.EESLDSDLYAELR.C	1540.61070	2	6.04E-07	0.85	3.26	-	636.5
AHQ-9-14-, 4557 - 4627	K.EESLDSDLYAELR.C	1540.61070	2	1.97E-06	0.93	3.88	-	1077.9
AHQ-9-14-, 4519	K.GKEESLDSDLYAELR.C	1725.83517	2	2.88E-10	0.98	5.64	-	2146.7
AHQ-9-13, 4327	K.GKEESLDSDLYAELR.C	1725.83517	3	5.08E-04	0.87	3.78	-	980.8
AHQ-9-13, 4326	K.GKEESLDSDLYAELR.C	1725.83517	2	6.67E-08	0.98	4.82	-	2102.9
AHQ-9-14-, 4278 - 4350	K.GKEESLDSDLYAELR.C	1725.83517	2	5.68E-06	0.95	4.35	-	1364.9
AHQ-9-14-, 4161 - 4221	K.GKEESLDSDLYAELR.C	1725.83517	2	7.40E-10	0.98	5.29	-	2421.0
AHQ-9-11, 4078	K.GKEESLDSDLYAELR.C	1725.83517	2	3.99E-04	0.89	3.27	-	910.1
AHQ-9-14-, 4045 - 4102	K.GKEESLDSDLYAELR.C	1725.83517	2	8.36E-08	0.98	5.64	-	2411.5
AHQ-9-14-, 3937 - 3998	K.GKEESLDSDLYAELR.C	1725.83517	2	6.40E-11	0.98	5.92	-	2634.0
AHQ-9-14, 4824 - 4887	K.GKEESLDSDLYAELR.C	1725.83517	2	3.77E-06	0.98	5.41	-	1985.7
AHQ-9-14, 4947 - 4955	K.GKEESLDSDLYAELR.C	1725.83517	2	2.91E-07	0.96	4.66	-	1740.5
AHQ-9-14, 5063 - 5127	K.GKEESLDSDLYAELR.C	1725.83517	2	4.12E-11	0.98	5.61	-	2194.6
AHQ-9-14, 5069	K.GKEESLDSDLYAELR.C	1725.83517	3	6.76E-05	0.92	4.45	-	1216.1
AHQ-9-14, 5183 - 5248	K.GKEESLDSDLYAELR.C	1725.83517	2	8.22E-07	0.98	4.82	-	2286.5
AHQ-9-14, 5388 - 5461	K.GKEESLDSDLYAELR.C	1725.83517	2	3.92E-04	0.96	4.46	-	1471.2
AHQ-9-14-, 4149 - 4181	K.GKEESLDSDLYAELR.C	1725.83517	3	3.89E-06	0.90	4.22	-	988.6
AHQ-9-6, 4107	K.GKEESLDSDLYAELR.C	1725.83517	2	2.19E-05	0.88	3.66	-	1103.1
AHQ-9-14-, 4869 - 4870	K.GKEESLDSDLYAELR.C	1725.83517	2	1.90E-04	0.48	2.67	-	393.2
AHQ-9-13-, 3572	K.GTHCNQVEVIATLK.D	1571.78073	2	2.10E-05	0.81	3.02	-	714.7
AHQ-9-14, 4409 - 4479	K.GTHCNQVEVIATLK.D	1571.78073	2	6.55E-10	0.97	4.64	-	1704.9
AHQ-9-14, 4507 - 4569	K.GTHCNQVEVIATLK.D	1571.78073	2	1.58E-06	0.95	4.31	-	1438.7
AHQ-9-14, 4648 - 4660	K.GTHCNQVEVIATLK.D	1571.78073	2	5.14E-05	0.90	3.34	-	1026.1
AHQ-9-14-, 3389 - 3459	K.GTHCNQVEVIATLK.D	1571.78073	2	8.55E-09	0.98	4.83	-	2132.7
AHQ-9-14-, 3517	K.GTHCNQVEVIATLK.D	1571.78073	2	8.99E-07	0.98	5.11	-	1864.0
AHQ-9-14-, 3601 - 3626	K.GTHCNQVEVIATLK.D	1571.78073	2	8.60E-07	0.94	4.37	-	1220.1
AHQ-9-13-, 3433 - 3444	K.GTHCNQVEVIATLK.D	1571.78073	2	3.43E-06	0.96	4.33	-	1499.7
AHQ-9-14, 3763 - 3820	K.ICLDPDAPR.I	1058.19059	2	1.07E-04	0.85	3.01	-	1006.1
AHQ-9-14-, 2671 - 2729	R.KICLDPDAPR.I	1186.36350	2	5.91E-05	0.91	3.28	-	972.7
AHQ-9-14-, 2787 - 2858	R.KICLDPDAPR.I	1186.36350	2	3.10E-05	0.92	3.28	-	1190.0
AHQ-9-14, 3535 - 3592	R.KICLDPDAPR.I	1186.36350	2	4.98E-05	0.83	3.07	-	826.4
AHQ-9-13-, 2721	R.KICLDPDAPR.I	1186.36350	2	1.86E-05	0.72	2.75	-	614.2
AHQ-9-14, 3349 - 3407	R.KICLDPDAPR.I	1186.36350	2	7.57E-04	0.65	2.81	-	585.3
AHQ-9-14, 4207 - 4287	K.NIQSLEVIGK.G	1101.27845	2	1.68E-05	0.86	3.55	-	649.3
AHQ-9-14-, 4118	K.NIQSLEVIGK.G	1101.27845	1	8.16E-04	0.76	2.65	-	685.3
AHQ-9-14-, 3722	K.NIQSLEVIGK.G	1101.27845	1	1.20E-04	0.43	2.53	-	477.3
AHQ-9-14, 4343 - 4423	K.NIQSLEVIGK.G	1101.27845	2	1.29E-06	0.89	3.62	-	732.6
AHQ-9-14, 4297	K.NIQSLEVIGK.G	1101.27845	1	9.12E-04	0.49	2.49	-	269.6
AHQ-9-14-, 3669	K.TTSGIHPKNIQSLEVIGK.G	1923.20305	3	1.01E-05	0.83	3.68	-	887.0
gi|4502549|ref|NP_001734.1| calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta				4.35E-11	1.73	20.22	22.10	16837.5
AHQ-9-11, 4017 - 4091	K.EAFSLFDKDGDGTITTK.E	1845.98441	3	2.24E-04	0.80	3.49	-	754.4
AHQ-9-11, 4021 - 4077	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	2.39E-04	0.93	4.38	-	1025.3
AHQ-9-11, 3717	R.VFDKDGNGYISAAELR.H	1755.90933	3	4.46E-06	0.93	3.58	-	2021.2
AHQ-9-12, 3744 - 3782	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.31E-09	0.93	4.11	-	923.2
AHQ-9-11, 3713 - 3722	R.VFDKDGNGYISAAELR.H	1755.90933	2	4.35E-11	0.93	4.11	-	922.2
gi|30148492|ref|XP_293610.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				5.27E-11	1.83	20.24	4.30	72113.4
AHQ-9-6, 2887 - 2962	R.FDDAVVQSDMK.H	1255.37968	2	1.45E-07	0.88	3.03	-	853.2
AHQ-9-6, 4211	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	5.27E-11	0.95	4.77	-	779.0
gi|21361657|ref|NP_005304.3| glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom				5.76E-11	6.16	70.32	21.00	56782.0
AHQ-9-7, 5318	R.ELSDFISYLQR.E	1371.52000	2	4.62E-05	0.95	3.53	-	1349.1
AHQ-9-7, 6216	K.FISDKDASIVGFFDDSFSEAHSEFLK.A	2940.16492	3	5.76E-11	0.98	6.39	-	2746.8
AHQ-9-7, 4462 - 4517	R.FLQDYFDGNLK.R	1360.49568	2	8.38E-04	0.85	3.79	-	585.5
AHQ-9-7, 4429	R.GFPTIYFSPANK.K	1342.52349	2	6.54E-05	0.74	2.81	-	643.0
AHQ-9-7, 5389 - 5390	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	3	9.82E-08	0.87	4.30	-	657.6
AHQ-9-7, 2450	K.LSKDPNIVIAK.M	1198.43727	2	1.87E-06	0.89	3.19	-	1074.0
AHQ-9-7, 3164 - 3166	K.YGVSGYPTLK.I	1085.23435	2	3.50E-04	0.87	2.90	-	716.0
gi|13489087|ref|NP_109591.1| serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member				7.35E-11	0.89	10.21	5.00	42741.5
AHQ-9-8, 3918 - 3974	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	1.29E-08	0.90	4.07	-	795.1
AHQ-9-8, 3911 - 3966	K.TYGADLASVDFQHASEDAR.K	2054.11949	3	7.35E-11	0.89	4.16	-	696.8
gi|4827056|ref|NP_005103.1| WD repeat-containing protein 1 isoform 2 [Homo sapiens]				8.57E-11	9.10	110.38	36.50	58001.9
AHQ-9-6, 4767	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	2	3.07E-06	0.63	2.61	-	620.2
AHQ-9-6, 4739 - 4814	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	1.34E-04	0.91	4.00	-	1137.1
AHQ-9-6, 5202	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	3.12E-10	0.93	4.32	-	994.1
AHQ-9-6, 3794 - 3875	R.FATASADGQIYIYDGK.T	1720.86021	2	9.85E-09	0.91	3.44	-	1058.5
AHQ-9-6, 4010 - 4015	R.FATASADGQIYIYDGK.T	1720.86021	2	4.19E-05	0.62	3.05	-	652.2
AHQ-9-6, 5313	K.FGAVFLWDSGSSVGEITGHNK.V	2209.40259	3	5.49E-06	0.89	4.36	-	990.3
AHQ-9-6, 4414 - 4473	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	3	1.91E-07	0.96	5.25	-	1694.9

AHQ-9-6, 4422 - 4483	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	2.29E-07	0.98	5.98	-	2094.5
AHQ-9-6, 2471	K.IKDIAWTEDSKR.I	1462.63267	2	2.47E-05	0.81	3.23	-	731.3
AHQ-9-7, 5137 - 5174	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	8.90E-06	0.67	3.13	-	625.5
AHQ-9-6, 5097 - 5159	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	9.46E-09	0.93	4.46	-	907.9
AHQ-9-6, 5217 - 5273	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	8.57E-11	0.96	4.99	-	1352.0
AHQ-9-6, 4057 - 4133	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	2.76E-09	0.98	7.55	-	1957.9
AHQ-9-6, 3533	K.VFASLPQVER.G	1146.32091	2	2.83E-04	0.57	2.50	-	403.4
AHQ-9-6, 3803	K.YAPSGFYIASGDVSGK.L	1619.75589	2	8.83E-04	0.61	2.98	-	387.1
AHQ-9-6, 2909 - 2958	K.YEYQPFAGK.I	1103.20822	2	5.92E-05	0.84	2.86	-	663.9
gi|27498267|ref|XP_209737.1|	similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,			8.73E-11	1.91	20.29	31.60	11063.6
AHQ-9-11, 6179	R.DICNDVLSLLEK.F	1420.61093	2	2.11E-05	0.93	3.47	-	1609.7
AHQ-9-10, 5437	R.DICNDVLSLLEK.F	1420.61093	2	1.31E-04	0.81	2.59	-	814.7
AHQ-9-13-, 6257	R.DICNDVLSLLEK.F	1420.61093	2	2.35E-05	0.95	3.32	-	1824.7
AHQ-9-10, 4733 - 4745	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	3.58E-05	0.98	5.75	-	2197.8
AHQ-9-11, 4750	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	6.78E-07	0.93	4.35	-	973.4
AHQ-9-10, 4501 - 4509	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.82E-05	0.95	4.73	-	1052.9
AHQ-9-9, 4679	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	9.60E-04	0.83	3.25	-	980.2
AHQ-9-13, 5023	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	4.93E-05	0.94	4.31	-	1046.1
AHQ-9-13-, 4845	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.43E-07	0.94	4.06	-	1217.8
AHQ-9-9, 4671	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.78E-04	0.68	3.09	-	525.0
AHQ-9-14-, 4871 - 4873	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	8.73E-11	0.98	5.67	-	1552.2
gi|29730023|ref|XP_291482.1|	similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno			9.15E-11	6.07	80.21	15.70	63563.0
AHQ-9-6, 4257 - 4262	K.ELEEIVQPIISK.L	1398.62680	2	1.33E-04	0.66	2.87	-	617.4
AHQ-9-6, 4525	R.IINKPTAAAIAYGLDK.R	1659.95097	2	7.16E-05	0.92	4.14	-	1254.6
AHQ-9-5, 4595	R.IINKPTAAAIAYGLDK.R	1659.95097	2	9.73E-09	0.91	4.19	-	1281.4
AHQ-9-7, 4508	R.IINKPTAAAIAYGLDK.R	1659.95097	2	6.22E-08	0.91	4.04	-	1206.4
AHQ-9-6, 4318	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	3.24E-08	0.78	3.66	-	862.0
AHQ-9-6, 3447 - 3501	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	2.97E-04	0.90	4.04	-	730.6
AHQ-9-5, 3488	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	3.71E-05	0.89	4.20	-	557.1
AHQ-9-6, 3939 - 3958	R.NELESYAYSLK.N	1317.42597	2	2.37E-05	0.74	3.09	-	618.3
AHQ-9-6, 3394 - 3462	K.NQLTSNPKNTVFDAK.R	1677.84011	2	2.04E-06	0.80	3.87	-	807.8
AHQ-9-5, 4621	K.TFAPKEISAM*VLTK.M	1552.86064	2	5.04E-04	0.54	2.75	-	654.3
AHQ-9-5, 5361	K.TFAPKEISAMVLTK.M	1536.86124	2	9.15E-11	0.75	3.26	-	948.4
gi|4507907|ref|NP_000543.1|	von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille			9.34E-11	9.97	120.32	5.60	309296.7
AHQ-9-2, 3781 - 3842	R.CLPSACEVVTGSPR.G	1535.72531	2	4.40E-05	0.81	3.57	-	576.0
AHQ-9-2, 4071	R.CLPTACTIQLR.G	1335.57568	2	7.20E-05	0.62	2.71	-	431.5
AHQ-9-3, 4733	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	2.26E-06	0.42	2.51	-	482.8
AHQ-9-3, 4561	K.GLWEQCQLLK.S	1276.48664	2	3.05E-05	0.77	3.18	-	828.7
AHQ-9-2, 2745	R.ILAGPAGDSNVVK.L	1241.41901	2	7.60E-05	0.92	3.63	-	1171.3
AHQ-9-1, 3731 - 3794	R.ILTSDVFQDCNK.L	1441.58869	2	7.45E-06	0.87	3.18	-	921.8
AHQ-9-3, 3249	K.LSGEAYGFVAR.I	1170.29934	2	5.41E-07	0.97	4.32	-	1840.0
AHQ-9-1, 5218 - 5227	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	9.34E-11	0.98	6.43	-	2462.6
AHQ-9-2, 5178	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	1.69E-04	0.97	6.50	-	1726.0
AHQ-9-2, 4490	R.VTVFPIGIGDR.Y	1174.37426	2	2.12E-07	0.93	3.44	-	1095.3
AHQ-9-1, 3572	R.WTCPCVCTGSSTR.H	1575.72645	2	8.62E-04	0.81	3.15	-	683.8
AHQ-9-2, 3006	K.YAGSQVASTSEVLK.Y	1440.58064	2	6.64E-10	0.94	4.15	-	1117.4
AHQ-9-3, 2945	K.YAGSQVASTSEVLK.Y	1440.58064	2	4.50E-07	0.90	3.76	-	745.1
AHQ-9-1, 5658	K.YTLFQIFSK.I	1147.34728	2	5.21E-06	0.91	2.73	-	1042.8
AHQ-9-2, 5639	K.YTLFQIFSK.I	1147.34728	2	6.71E-06	0.84	2.78	-	570.3
gi|21956645|ref|NP_665807.1|	myotrophin; granule cell differentiation protein [Homo sapiens]			9.62E-11	1.84	20.27	25.40	12894.7
AHQ-9-13-, 3940 - 3996	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	9.62E-11	0.95	4.36	-	932.7
AHQ-9-13, 4114 - 4170	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.64E-05	0.97	5.17	-	1434.7
AHQ-9-13, 4226 - 4227	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	2.74E-07	0.93	4.32	-	990.4
AHQ-9-14, 4825 - 4859	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.34E-10	0.94	4.79	-	886.2
AHQ-9-14, 4963 - 4965	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	4.02E-04	0.71	3.03	-	581.7
AHQ-9-14-, 3903 - 3977	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	4.71E-06	0.97	5.42	-	1444.7
AHQ-9-14-, 4005 - 4082	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	5.05E-06	0.96	4.37	-	1474.3
AHQ-9-13-, 4068	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	7.29E-09	0.95	4.42	-	1089.2
AHQ-9-14-, 3674	K.NGDLDEVKDYVAK.G	1466.57496	2	2.76E-08	0.90	3.59	-	1105.3
AHQ-9-13-, 3649	K.NGDLDEVKDYVAK.G	1466.57496	2	3.49E-09	0.84	3.35	-	769.0
AHQ-9-13, 3726	K.NGDLDEVKDYVAK.G	1466.57496	2	3.27E-06	0.84	2.81	-	957.0
AHQ-9-14-, 3593	K.NGDLDEVKDYVAK.G	1466.57496	2	5.22E-10	0.89	3.37	-	1010.7
gi|5454152|ref|NP_006285.1|	ubiquinol-cytochrome c reductase binding protein [Homo sapiens]			1.05E-10	1.80	20.23	25.20	13530.4
AHQ-9-13-, 3529 - 3534	R.DDTIYEDEDVKEAIR.R	1811.88169	2	1.05E-10	0.84	3.21	-	713.4
AHQ-9-13-, 4980 - 4986	K.YEEENFYLEPYLK.E	1737.88601	2	3.28E-04	0.96	4.50	-	1463.3
gi|4557305|ref|NP_000025.1|	aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho			1.17E-10	3.53	40.27	18.10	39419.7
AHQ-9-8, 4300	K.FSHEEIAMATVTALR.R	1676.91875	2	1.17E-10	0.96	4.26	-	1599.4
AHQ-9-9, 4111	K.FSHEEIAMATVTALR.R	1676.91875	2	4.42E-05	0.82	3.28	-	788.0
AHQ-9-13-, 3024	K.GILAADESTGSIAK.R	1333.47008	2	2.16E-07	0.93	3.68	-	1070.3
AHQ-9-9, 2827	K.GILAADESTGSIAK.R	1333.47008	2	6.86E-09	0.97	4.19	-	1723.6
AHQ-9-8, 2895 - 2896	K.GILAADESTGSIAK.R	1333.47008	2	6.11E-10	0.97	5.46	-	1444.0
AHQ-9-11, 2969 - 2970	K.GILAADESTGSIAK.R	1333.47008	2	2.38E-06	0.93	3.77	-	1316.4
AHQ-9-8, 2834	R.QLLLTADDR.V	1045.17176	2	2.20E-05	0.72	2.71	-	505.8
AHQ-9-8, 5292 - 5352	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	1.53E-05	0.88	4.50	-	900.9
gi|4505735|ref|NP_002611.1|	platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H			1.17E-10	0.98	10.28	14.40	11552.6
AHQ-9-14-, 3777 - 3834	R.AEAEEDGDLQCLCVK.T	1739.86036	2	1.17E-10	0.98	5.53	-	1750.9
gi|4504183|ref|NP_000843.1|	glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s			1.20E-10	1.79	20.24	16.20	23355.7
AHQ-9-11, 4555 - 4623	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.79E-06	0.85	3.94	-	534.7
AHQ-9-11, 4383 - 4386	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	1.20E-10	0.94	4.74	-	660.0
AHQ-9-11, 4378 - 4385	K.YISLIYTNYEAGKDDYVK.A	2156.37637	3	8.08E-04	0.74	3.22	-	710.9
gi|4505733|ref|NP_002610.1|	platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4			1.25E-10	6.36	70.28	39.60	10844.9
AHQ-9-14, 5087 - 5109	K.AGPHCPTAQLIATLK.N	1579.84600	2	7.27E-06	0.83	3.42	-	559.2
AHQ-9-14-, 4122	K.AGPHCPTAQLIATLK.N	1579.84600	2	9.55E-07	0.85	3.33	-	602.2
AHQ-9-14, 4995	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	4.39E-08	0.96	4.92	-	1486.2
AHQ-9-14, 5009	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	6.92E-04	0.90	3.19	-	1008.7
AHQ-9-14-, 3909	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	8.13E-10	0.95	4.59	-	1152.8
AHQ-9-14-, 4111	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.25E-10	0.98	5.70	-	2365.3
AHQ-9-14-, 3901	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	2.01E-07	0.98	5.22	-	2558.9
AHQ-9-14-, 4035	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	4.00E-07	0.96	4.85	-	1237.0
AHQ-9-14, 3707 - 3768	R.HITSLEVIK.A	1040.23825	2	1.50E-04	0.77	2.76	-	536.7
AHQ-9-14-, 2706 - 2785	R.HITSLEVIK.A	1040.23825	2	1.97E-05	0.90	3.73	-	530.3
AHQ-9-14, 3623 - 3648	R.HITSLEVIK.A	1040.23825	2	1.52E-05	0.80	3.05	-	455.2
AHQ-9-13, 4896	K.ICLDLQAPLYK.K	1335.59400	2	3.96E-05	0.96	4.18	-	1654.7
AHQ-9-13-, 4724	K.ICLDLQAPLYK.K	1335.59400	2	1.48E-05	0.96	3.94	-	1851.2
AHQ-9-14, 5539	K.ICLDLQAPLYK.K	1335.59400	2	3.04E-04	0.92	3.24	-	1614.6
AHQ-9-14-, 4599	K.ICLDLQAPLYK.K	1335.59400	2	5.79E-04	0.76	2.67	-	775.4
AHQ-9-14-, 4718 - 4721	K.ICLDLQAPLYK.K	1335.59400	2	4.57E-05	0.97	4.62	-	2000.4
AHQ-9-14-, 4285 - 4289	K.ICLDLQAPLYKK.I	1463.76691	3	3.22E-06	0.86	3.38	-	1157.3
AHQ-9-13-, 4414	R.KICLDLQAPLYK.K	1463.76691	2	2.80E-04	0.89	3.12	-	1234.7
AHQ-9-14-, 4377 - 4433	R.KICLDLQAPLYK.K	1463.76691	2	4.93E-05	0.96	4.41	-	1360.9
AHQ-9-14, 5319 - 5320	R.KICLDLQAPLYK.K	1463.76691	2	1.62E-05	0.97	4.41	-	1632.8
AHQ-9-14-, 4034	R.KICLDLQAPLYKK.I	1591.93982	3	7.28E-09	0.94	5.00	-	1457.8
AHQ-9-14-, 4039	R.KICLDLQAPLYKK.I	1591.93982	2	5.25E-04	0.97	5.01	-	1581.3
gi|17921989|ref|NP_005991.1|	tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain			1.40E-10	11.48	140.24	42.40	49924.1
AHQ-9-7, 4450 - 4512	R.AFVHWYVGEGM*EEGEFSEAR.E	2347.50435	3	8.16E-06	0.76	3.40	-	786.2
AHQ-9-7, 5118	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.63E-06	0.93	3.59	-	1267.6
AHQ-9-7, 5592	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	1.93E-09	0.93	3.73	-	1344.4

AHQ-9-13-, 4922 - 4976	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	3.01E-07	0.94	3.98	-	1220.2
AHQ-9-7, 4928	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	9.48E-04	0.92	3.80	-	1205.9
AHQ-9-13, 5766 - 5768	R.AVFVDLEPTVIDEIR.N	1716.95615	2	2.60E-06	0.58	2.69	-	686.2
AHQ-9-7, 4434	K.AYHEQLSVAEITNACFEPANQM*VK.C	2769.06010	3	5.73E-06	0.64	3.22	-	473.3
AHQ-9-7, 3358	K.DVNAAIAAIK.T	986.14745	2	8.98E-05	0.91	3.80	-	928.2
AHQ-9-7, 4840 - 4896	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.60E-04	0.93	3.82	-	737.9
AHQ-9-8, 4916	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.92E-04	0.74	2.84	-	473.8
AHQ-9-8, 6255 - 6264	R.LISQIVSSITASLR.F	1488.75471	2	1.43E-05	0.93	3.80	-	1086.4
AHQ-9-7, 6158 - 6160	R.LISQIVSSITASLR.F	1488.75471	2	3.68E-08	0.96	4.83	-	1089.3
AHQ-9-13-, 6190	R.LISQIVSSITASLR.F	1488.75471	2	1.98E-05	0.92	3.09	-	1280.7
AHQ-9-8, 3394	R.NLDIERPTYTNLNR.L	1719.88022	2	7.41E-06	0.60	3.14	-	415.3
AHQ-9-14-, 3545	R.NLDIERPTYTNLNR.L	1719.88022	2	3.46E-05	0.63	2.98	-	479.3
AHQ-9-9, 3275	R.NLDIERPTYTNLNR.L	1719.88022	2	3.20E-04	0.37	2.71	-	297.3
AHQ-9-6, 5370	R.SIQFVDWCPTGFK.V	1586.79232	2	1.18E-04	0.82	2.78	-	961.8
AHQ-9-7, 5332 - 5333	R.SIQFVDWCPTGFK.V	1586.79232	2	1.83E-06	0.93	3.71	-	1056.0
AHQ-9-13, 5527	R.SIQFVDWCPTGFK.V	1586.79232	2	6.71E-04	0.74	2.70	-	693.6
AHQ-9-14-, 5313	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.52E-08	0.81	3.75	-	420.0
AHQ-9-11, 5209 - 5210	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.80E-05	0.80	3.34	-	471.8
AHQ-9-7, 5218 - 5273	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.40E-10	0.95	4.59	-	982.5
AHQ-9-13, 5458	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	2.72E-06	0.81	3.37	-	590.9
AHQ-9-9, 5116	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	4.10E-05	0.58	2.88	-	335.2
AHQ-9-13-, 5308 - 5309	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	4.13E-09	0.92	4.23	-	628.3
AHQ-9-7, 4309	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	4.58E-04	0.43	2.55	-	261.2
AHQ-9-14, 5136	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	2.66E-04	0.55	2.80	-	335.0
AHQ-9-12, 4252 - 4326	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	6.99E-04	0.70	3.11	-	367.5
AHQ-9-11, 4194 - 4249	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	8.65E-04	0.34	2.65	-	255.2
AHQ-9-7, 3832 - 3864	K.YM*ACCLLYR.G	1268.50804	2	5.44E-04	0.86	2.64	-	667.6
AHQ-9-7, 4258	K.YMACCLLYR.G	1252.50864	2	5.80E-06	0.93	3.28	-	913.3
gi|4502027|ref|NP_000468.1|	albumin precursor; PRO0883 protein [Homo sapiens]			1.47E-10	32.49	370.30	70.60	69366.4
AHQ-9-6, 2557	K.AAFTECCQAADK.A	1374.47927	2	5.36E-05	0.94	3.63	-	1391.6
AHQ-9-5, 1876 - 1931	K.ADDKETCFAEEGKK.L	1629.72754	2	1.25E-04	0.83	3.20	-	894.0
AHQ-9-5, 5153	K.AEFAEVSKLVTDLTK.V	1651.88247	3	1.49E-04	0.81	3.42	-	520.1
AHQ-9-5, 6379	K.ALVLIAFAQYLQQCPFEDHVK.L	2492.87697	3	1.99E-09	0.95	4.73	-	1130.9
AHQ-9-14-, 5167	K.AVMDDFAAFVEK.C	1343.53006	2	6.12E-06	0.94	3.76	-	1228.8
AHQ-9-6, 5082 - 5119	K.AVMDDFAAFVEK.C	1343.53006	2	4.82E-07	0.95	3.97	-	1307.8
AHQ-9-5, 5181 - 5191	K.AVMDDFAAFVEK.C	1343.53006	2	9.13E-10	0.97	5.01	-	1362.1
AHQ-9-5, 2207	K.CCAAADPHECYAK.V	1556.67999	2	3.16E-04	0.75	2.96	-	706.8
AHQ-9-5, 2421 - 2425	K.CCTESLVNR.R	1141.25805	2	7.63E-06	0.94	3.10	-	1414.0
AHQ-9-1, 6290 - 6314	K.DVFLGM*FLYEYAR.R	1640.88331	2	7.01E-05	0.95	3.55	-	1326.3
AHQ-9-6, 6105 - 6117	K.DVFLGM*FLYEYAR.R	1640.88331	2	5.65E-05	0.96	4.28	-	1108.4
AHQ-9-5, 6191 - 6199	K.DVFLGM*FLYEYAR.R	1640.88331	2	1.78E-09	0.96	4.34	-	1309.8
AHQ-9-5, 2684 - 2687	R.ETYGEMADCCAK.Q	1437.55563	2	8.73E-05	0.64	2.54	-	404.2
AHQ-9-5, 2772 - 2832	R.FKDLGEENFK.A	1227.34766	2	1.08E-05	0.90	3.86	-	793.4
AHQ-9-6, 2775	R.FKDLGEENFK.A	1227.34766	2	5.78E-06	0.80	3.12	-	615.5
AHQ-9-6, 3097 - 3177	K.FQNALLVR.Y	961.14282	2	8.81E-06	0.73	2.82	-	639.5
AHQ-9-6, 6007	R.HPYFYAPELLFFAK.R	1744.02658	3	2.72E-06	0.89	3.91	-	941.2
AHQ-9-5, 6091 - 6112	R.HPYFYAPELLFFAK.R	1744.02658	3	8.68E-04	0.72	3.74	-	514.5
AHQ-9-5, 2855	K.KQTALVELVK.H	1129.37494	2	4.11E-05	0.87	2.94	-	903.6
AHQ-9-3, 3578	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.79E-06	0.67	2.55	-	518.7
AHQ-9-4, 3581	K.KVPQVSTPTLVEVSR.N	1640.90605	2	4.72E-04	0.83	3.34	-	599.9
AHQ-9-5, 3471 - 3551	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.66E-07	0.91	3.50	-	961.2
AHQ-9-6, 3507 - 3587	K.KVPQVSTPTLVEVSR.N	1640.90605	2	5.01E-09	0.91	3.77	-	764.6
AHQ-9-5, 3547	K.KVPQVSTPTLVEVSR.N	1640.90605	3	4.71E-08	0.95	4.87	-	1368.1
AHQ-9-5, 3583 - 3655	K.KVPQVSTPTLVEVSR.N	1640.90605	2	1.31E-06	0.92	3.74	-	1041.0
AHQ-9-7, 3510	K.KVPQVSTPTLVEVSR.N	1640.90605	2	7.23E-07	0.82	2.77	-	761.8
AHQ-9-6, 3511	K.KVPQVSTPTLVEVSR.N	1640.90605	3	1.31E-08	0.95	4.79	-	1339.0
AHQ-9-5, 2491 - 2492	K.LKECCEKPLLEK.S	1549.83503	3	9.98E-04	0.90	4.97	-	671.6
AHQ-9-5, 4020	K.LVAASQAALGL	1014.20080	2	2.86E-06	0.93	3.45	-	1102.0
AHQ-9-5, 3193	K.LVNEVTEFAK.T	1150.30633	1	1.67E-05	0.63	2.34	-	499.8
AHQ-9-6, 3305	K.LVNEVTEFAK.T	1150.30633	2	1.51E-04	0.87	3.15	-	665.2
AHQ-9-5, 3324	K.LVNEVTEFAK.T	1150.30633	2	8.01E-06	0.93	3.64	-	863.0
AHQ-9-5, 3183	K.LVNEVTEFAK.T	1150.30633	2	1.15E-04	0.48	2.77	-	277.1
AHQ-9-5, 3504	K.LVNEVTEFAK.T	1150.30633	2	1.04E-06	0.90	3.87	-	622.5
AHQ-9-6, 4610	R.LVRPEVDVM*CTAFHDNEETFLK.K	2668.98368	3	1.32E-04	0.95	4.48	-	1634.2
AHQ-9-5, 4667	R.LVRPEVDVM*CTAFHDNEETFLK.K	2668.98368	3	1.47E-10	0.97	5.98	-	1335.6
AHQ-9-5, 4355 - 4416	R.LVRPEVDVM*CTAFHDNEETFLKK.Y	2797.15659	3	5.95E-05	0.69	3.65	-	338.6
AHQ-9-5, 6375	R.M*PCAEDYLSVVLNQLCVLHEK.T	2537.91475	3	7.14E-06	0.93	4.68	-	945.7
AHQ-9-5, 3073	R.NECFLQHKDDNPNLPR.L	1999.15349	3	7.92E-05	0.78	3.44	-	743.5
AHQ-9-5, 4829 - 4891	K.QNCELFEQLGEYK.F	1659.79847	2	1.33E-04	0.80	3.16	-	526.0
AHQ-9-6, 4081	R.RHPDYSVVLLLR.L	1468.72842	3	8.49E-05	0.94	4.46	-	1647.2
AHQ-9-6, 4030 - 4089	R.RHPDYSVVLLLR.L	1468.72842	2	4.66E-07	0.91	3.58	-	829.1
AHQ-9-5, 4052 - 4133	R.RHPDYSVVLLLR.L	1468.72842	2	7.39E-09	0.95	3.58	-	1256.8
AHQ-9-5, 4123 - 4181	R.RHPDYSVVLLLR.L	1468.72842	3	2.05E-04	0.97	5.00	-	1928.8
AHQ-9-5, 5711 - 5767	R.RHPYFYAPELLFFAK.R	1900.21293	3	6.63E-08	0.98	5.74	-	2142.8
AHQ-9-5, 5825	R.RHPYFYAPELLFFAK.R	1900.21293	3	5.30E-05	0.97	4.85	-	2091.8
AHQ-9-6, 5647	R.RHPYFYAPELLFFAK.R	1900.21293	2	2.74E-05	0.92	3.74	-	941.9
AHQ-9-6, 5641 - 5653	R.RHPYFYAPELLFFAK.R	1900.21293	3	2.03E-10	0.97	5.75	-	1899.5
AHQ-9-5, 5652 - 5715	R.RHPYFYAPELLFFAK.R	1900.21293	2	1.42E-04	0.98	4.96	-	1971.1
AHQ-9-6, 6261	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	1.46E-05	0.94	5.52	-	868.5
AHQ-9-5, 6343	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	2.20E-04	0.94	5.16	-	1072.1
AHQ-9-5, 4524 - 4537	R.RPCFSALEVDETYVPK.E	1913.14041	2	2.81E-07	0.94	4.80	-	727.0
AHQ-9-6, 4486 - 4495	R.RPCFSALEVDETYVPK.E	1913.14041	3	3.95E-06	0.93	4.80	-	1029.0
AHQ-9-6, 4478	R.RPCFSALEVDETYVPK.E	1913.14041	2	6.59E-06	0.87	3.77	-	582.3
AHQ-9-5, 4533 - 4592	R.RPCFSALEVDETYVPK.E	1913.14041	3	7.86E-07	0.87	4.61	-	738.0
AHQ-9-5, 6240	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	2.97E-05	0.84	3.99	-	579.5
AHQ-9-6, 5773 - 5830	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	1.63E-05	0.92	4.98	-	855.7
AHQ-9-5, 2801 - 2807	K.SLHTLFGDK.L	1018.14800	2	9.12E-05	0.87	2.67	-	857.6
AHQ-9-5, 4931	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	4.82E-07	0.91	3.94	-	801.0
AHQ-9-5, 4920 - 4921	K.SLHTLFGDKLCTVATLR.E	1934.24913	3	1.40E-06	0.83	3.67	-	767.4
AHQ-9-5, 1921 - 1960	K.TCVADESAENCDK.S	1501.53308	2	6.40E-07	0.96	4.15	-	1585.5
AHQ-9-6, 1991	K.TCVADESAENCDK.S	1501.53308	2	6.75E-06	0.81	2.89	-	828.0
AHQ-9-5, 2049	K.TCVADESAENCDK.S	1501.53308	2	2.00E-06	0.90	2.99	-	1058.6
AHQ-9-5, 4345	K.TCVADESAENCDKSLHTLFGDK.L	2500.65848	3	2.40E-05	0.82	3.68	-	648.4
AHQ-9-5, 3751	K.TYETTLEKCCAAADPHECYAK.V	2522.72734	3	2.41E-07	0.89	4.45	-	689.8
AHQ-9-7, 5337	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.38E-05	0.87	4.20	-	384.5
AHQ-9-5, 5423 - 5496	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.42E-05	0.95	4.61	-	1393.5
AHQ-9-5, 5420 - 5495	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.06E-07	0.92	4.87	-	434.0
AHQ-9-5, 5316	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.43E-08	0.93	4.23	-	737.0
AHQ-9-6, 5315 - 5369	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.14E-06	0.91	4.41	-	787.9
AHQ-9-6, 5347	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	9.24E-07	0.85	3.77	-	438.7
AHQ-9-4, 5436	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	9.22E-06	0.95	4.35	-	1333.6
AHQ-9-1, 5555	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	6.64E-05	0.91	4.34	-	916.9
AHQ-9-5, 3696	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	2.05E-04	0.77	3.21	-	607.8
AHQ-9-6, 3653	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	2.93E-06	0.94	5.44	-	756.1
AHQ-9-6, 3789	K.VPQVSTPTLVEVSR.N	1512.73313	2	1.59E-07	0.88	2.88	-	1028.0
AHQ-9-5, 3757 - 3828	K.VPQVSTPTLVEVSR.N	1512.73313	2	4.03E-04	0.56	2.52	-	361.2
AHQ-9-5, 2384	K.YICENQDSISSK.L	1445.53420	2	4.60E-07	0.87	3.42	-	723.6

AHQ-9-7, 2396	K.YICENQDSISSK.L	1445.53420	2	7.13E-05	0.82	3.36	-	533.7
AHQ-9-5, 2480	K.YICENQDSISSK.L	1445.53420	2	1.08E-06	0.93	3.92	-	733.4
AHQ-9-6, 2314 - 2387	K.YICENQDSISSK.L	1445.53420	2	1.92E-04	0.92	3.69	-	687.5
gi|4501893|ref|NP_001094.1| actinin, alpha 2 [Homo sapiens]				1.92E-10	10.12	120.27	13.30	103853.1
AHQ-9-4, 4594	K.AGTQIENIEEDFRNGLK.L	1935.08442	2	9.05E-04	0.55	3.49	-	512.7
AHQ-9-6, 4642	K.CQLEINFNTLQTK.L	1610.81373	2	1.50E-04	0.94	4.09	-	1280.7
AHQ-9-4, 4678 - 4745	K.CQLEINFNTLQTK.L	1610.81373	2	1.10E-09	0.96	4.70	-	1139.8
AHQ-9-4, 4821	K.CQLEINFNTLQTK.L	1610.81373	2	8.56E-05	0.92	3.58	-	1047.9
AHQ-9-5, 4701 - 4723	K.CQLEINFNTLQTK.L	1610.81373	2	3.31E-09	0.94	4.73	-	880.6
AHQ-9-4, 4541	K.CQLEINFNTLQTK.L	1610.81373	2	5.15E-06	0.90	3.69	-	791.8
AHQ-9-6, 4629	K.EGLLLWCQR.K	1176.37031	2	1.90E-04	0.92	3.18	-	904.1
AHQ-9-5, 4687 - 4689	K.EGLLLWCQR.K	1176.37031	2	7.03E-04	0.95	3.41	-	1408.2
AHQ-9-6, 4033 - 4113	R.FAIQDISVEETSAK.E	1538.68108	2	3.57E-09	0.90	3.98	-	757.9
AHQ-9-4, 4069 - 4096	R.FAIQDISVEETSAK.E	1538.68108	2	1.49E-07	0.95	4.02	-	1280.4
AHQ-9-5, 4081	R.FAIQDISVEETSAK.E	1538.68108	2	1.92E-10	0.95	3.58	-	1406.2
AHQ-9-9, 3887	R.FAIQDISVEETSAK.E	1538.68108	2	8.35E-05	0.90	3.38	-	983.1
AHQ-9-3, 4082	R.FAIQDISVEETSAK.E	1538.68108	2	5.66E-05	0.75	2.84	-	782.5
AHQ-9-4, 5137	K.GYEEWLLNEIR.R	1422.56701	2	2.64E-06	0.93	3.72	-	1235.4
AHQ-9-6, 5093	K.GYEEWLLNEIR.R	1422.56701	2	1.13E-04	0.88	2.90	-	956.4
AHQ-9-5, 5584 - 5595	K.GYEEWLLNEIR.R	1422.56701	2	4.54E-07	0.92	4.16	-	1003.2
AHQ-9-4, 5552 - 5553	K.GYEEWLLNEIR.R	1422.56701	2	1.54E-07	0.97	4.59	-	1688.8
AHQ-9-7, 5505	K.GYEEWLLNEIR.R	1422.56701	2	1.96E-04	0.76	2.80	-	879.8
AHQ-9-4, 2410	K.HEAFESDLAAHQDR.V	1626.66861	2	5.32E-07	0.97	4.55	-	2013.2
AHQ-9-4, 3842 - 3912	R.KAGTQIENIEEDFR.N	1650.77152	2	5.60E-04	0.36	2.79	-	377.9
AHQ-9-4, 2202	R.KHEAFESDLAAHQDR.V	1754.84152	3	3.33E-09	0.97	5.43	-	1792.8
AHQ-9-5, 2201	R.KHEAFESDLAAHQDR.V	1754.84152	2	2.39E-10	0.95	4.06	-	1332.2
AHQ-9-4, 2129 - 2208	R.KHEAFESDLAAHQDR.V	1754.84152	2	5.82E-09	0.96	4.12	-	1488.3
AHQ-9-4, 3116	R.KTFTAWCNSHLR.K	1522.71309	3	1.19E-06	0.95	4.44	-	1346.1
AHQ-9-4, 5700	K.LM*LLLEVISGER.L	1389.68652	2	1.09E-05	0.96	4.26	-	1831.3
AHQ-9-5, 3963	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.11E-04	0.82	3.28	-	639.4
AHQ-9-4, 3965 - 4024	K.LVSIGAEEIVDGNVK.M	1543.74400	2	5.40E-06	0.97	5.11	-	1658.7
AHQ-9-4, 4202 - 4278	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.42E-05	0.94	3.98	-	1220.4
AHQ-9-4, 4317 - 4397	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.41E-05	0.93	3.62	-	1138.3
AHQ-9-4, 3568 - 3626	K.TFTAWCNSHLR.K	1394.54018	2	2.89E-04	0.62	2.65	-	318.8
gi|13562114|ref|NP_110400.1| beta tubulin 1, class VI [Homo sapiens]				2.36E-10	11.82	140.32	39.70	50326.6
AHQ-9-8, 4399 - 4466	R.ALSVAELTQQM*FDAR.N	1696.90680	2	6.71E-04	0.95	4.11	-	1485.1
AHQ-9-7, 5768	R.ALSVAELTQQMFDAR.N	1680.90740	3	1.00E-08	0.98	5.53	-	2506.7
AHQ-9-10, 4377	R.ALSVAELTQQM*FDAR.N	1696.90680	2	3.11E-04	0.88	3.30	-	836.7
AHQ-9-9, 5541 - 5619	R.ALSVAELTQQMFDAR.N	1680.90740	2	5.39E-05	0.93	3.80	-	1229.4
AHQ-9-9, 5625	R.ALSVAELTQQMFDAR.N	1680.90740	3	7.42E-05	0.97	4.38	-	2613.3
AHQ-9-8, 5839 - 5880	R.ALSVAELTQQMFDAR.N	1680.90740	2	7.27E-05	0.92	3.74	-	1291.3
AHQ-9-13-, 3540	K.AVLEEDEEVTEEAEM*EPEDKGH	2532.58787	3	1.88E-07	0.51	3.01	-	417.4
AHQ-9-7, 3468 - 3469	K.AVLEEDEEVTEEAEM*EPEDKGH	2532.58787	3	5.47E-07	0.68	3.82	-	383.0
AHQ-9-14, 5031	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	2.76E-05	0.85	3.18	-	836.5
AHQ-9-14-, 4062 - 4121	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	2.28E-04	0.92	4.05	-	871.6
AHQ-9-8, 4076 - 4079	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	6.17E-04	0.76	3.12	-	494.3
AHQ-9-14-, 4701	R.AVLVDLEPGTMDSIR.S	1616.86162	2	4.45E-07	0.90	3.44	-	856.4
AHQ-9-7, 3826 - 3840	R.EIVHIQIGQCGNQIGAK.F	1867.11965	2	6.94E-04	0.49	3.04	-	313.3
AHQ-9-8, 6266	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.69E-06	0.98	6.42	-	2405.7
AHQ-9-11, 6117	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	6.97E-07	0.86	3.29	-	1412.4
AHQ-9-7, 6170 - 6177	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	6.50E-05	0.92	4.23	-	1732.6
AHQ-9-13-, 6193	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	3.51E-04	0.88	4.05	-	1480.5
AHQ-9-12, 6149	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.13E-06	0.98	6.27	-	2621.9
AHQ-9-13-, 6194	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	4.49E-08	0.98	6.26	-	2142.3
AHQ-9-7, 5930 - 5949	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	3.04E-05	0.92	4.85	-	757.5
AHQ-9-7, 3181 - 3188	R.ISVYYNEAYGR.K	1335.44622	2	8.12E-09	0.94	3.45	-	1217.8
AHQ-9-8, 3163	R.ISVYYNEAYGR.K	1335.44622	2	1.79E-05	0.90	3.36	-	889.0
AHQ-9-11, 3129 - 3186	R.ISVYYNEAYGR.K	1335.44622	2	7.01E-04	0.85	2.69	-	1102.8
AHQ-9-14, 4116 - 4179	R.ISVYYNEAYGR.K	1335.44622	2	3.04E-04	0.92	3.37	-	1118.8
AHQ-9-7, 4782 - 4842	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	2.27E-08	0.82	4.23	-	767.3
AHQ-9-13, 5119	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	2.36E-06	0.73	3.05	-	580.6
AHQ-9-7, 5476 - 5485	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	1.15E-05	0.97	5.71	-	1934.6
AHQ-9-9, 4795 - 4797	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	1.80E-06	0.94	4.81	-	1227.2
AHQ-9-8, 6186	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.36E-10	0.81	3.73	-	767.0
AHQ-9-7, 4992	R.YLTVACIFR.G	1144.36822	2	3.24E-05	0.83	2.91	-	661.8
AHQ-9-9, 4843 - 4848	R.YLTVACIFR.G	1144.36822	2	4.03E-04	0.91	3.05	-	1069.4
gi|4502295|ref|NP_001677.1| ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti				3.28E-10	8.04	90.27	26.30	57955.2
AHQ-9-7, 5188	R.AIAELGIYPAVDPLDSTSR.I	1989.21513	2	3.31E-05	0.80	3.29	-	438.4
AHQ-9-7, 6300 - 6364	R.DQEGQDVLLFIDNIFR.F	1923.11524	2	1.55E-05	0.88	4.21	-	527.1
AHQ-9-7, 4320	R.FTQAGSEVSALLGR.I	1436.59522	2	2.22E-06	0.91	3.46	-	1137.8
AHQ-9-7, 6204	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	3.45E-07	0.94	5.32	-	938.9
AHQ-9-7, 3589	R.IMDPNIVGSEHYDVAR.G	1817.01617	2	7.48E-07	0.84	3.42	-	555.5
AHQ-9-7, 3266	R.IM*DPNIVGSEHYDVAR.G	1833.01557	2	9.20E-05	0.91	3.67	-	840.0
AHQ-9-7, 4032 - 4089	R.LVLEVAQHLGESTVR.T	1651.88893	2	2.78E-09	0.96	4.28	-	1357.5
AHQ-9-7, 5369	R.VALTGLTVAEYFR.D	1440.66861	2	3.28E-10	0.93	3.51	-	1470.1
AHQ-9-7, 4478 - 4545	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	3	2.57E-05	0.87	3.59	-	1195.6
AHQ-9-7, 4473 - 4474	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	8.69E-05	0.80	3.62	-	305.2
gi|5031635|ref|NP_005498.1| cofilin 1 (non-muscle) [Homo sapiens]				3.68E-10	4.49	50.33	31.90	18502.4
AHQ-9-13-, 5312	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	7.03E-07	0.96	5.18	-	1251.8
AHQ-9-11, 5249	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.05E-06	0.93	3.76	-	1047.1
AHQ-9-13, 5444	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	4.20E-08	0.97	5.32	-	1696.1
AHQ-9-12, 5288	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	6.09E-09	0.97	5.64	-	1431.1
AHQ-9-14-, 5333	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	4.20E-05	0.93	4.23	-	945.7
AHQ-9-12, 5994 - 6068	K.KEDLVFIFWAPESAPLK.S	1991.31745	2	1.35E-05	0.94	4.70	-	928.9
AHQ-9-14-, 4337 - 4354	K.LGGSAVISLEGKPL	1341.57848	2	3.56E-05	0.84	3.69	-	665.0
AHQ-9-11, 4250	K.LGGSAVISLEGKPL	1341.57848	2	1.20E-05	0.92	3.77	-	895.3
AHQ-9-12, 4284 - 4356	K.LGGSAVISLEGKPL	1341.57848	2	1.75E-06	0.93	4.30	-	1113.4
AHQ-9-13-, 6156	K.NIILEEGKEILVGDVGQTVDDPYATFVK.M	3064.43208	3	1.33E-09	0.97	6.57	-	1427.8
AHQ-9-13-, 3320	R.YALYDATYETK.E	1338.44364	2	6.10E-07	0.94	3.62	-	1070.8
AHQ-9-12, 3193 - 3268	R.YALYDATYETK.E	1338.44364	2	3.44E-04	0.95	3.71	-	1205.2
AHQ-9-11, 3229 - 3249	R.YALYDATYETK.E	1338.44364	2	3.43E-06	0.94	4.20	-	989.8
AHQ-9-12, 3250	R.YALYDATYETK.E	1338.44364	1	3.68E-10	0.67	3.12	-	339.7
gi|4504447|ref|NP_002128.1| heterogeneous nuclear ribonucleoprotein A2/B1 isoform A2; heterogeneous				3.76E-10	2.28	30.22	16.40	36005.7
AHQ-9-9, 4253 - 4256	R.GFGFVTFDDHDPVDK.I	1696.79721	2	4.77E-07	0.87	3.55	-	797.4
AHQ-9-9, 5356 - 5361	K.LFIGGLSFETTEESLR.N	1800.00202	2	3.76E-10	0.95	4.40	-	1244.6
AHQ-9-9, 2879	R.NMGGPYGGGNYGPGGSGGSGGYGGR.S	2191.24298	2	1.80E-07	0.46	2.70	-	407.5
gi|12056465|ref|NP_001427.2| fibrillarin; 34-kD nucleolar scleroderma antigen; RNA, U3 small nucleo				4.21E-10	0.81	10.13	4.00	33784.0
AHQ-9-9, 2792	R.VSISEGDDKIEYR.A	1511.61573	2	4.21E-10	0.81	2.64	-	981.1
gi|4506877|ref|NP_002996.1| selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;				4.60E-10	1.78	20.21	3.70	90844.7
AHQ-9-3, 3130	R.PSGQWTAVTPACR.A	1432.58672	2	2.20E-05	0.84	3.00	-	853.4
AHQ-9-3, 4544	K.STCQFICDEGYSLSGPER.L	2109.23671	2	3.06E-08	0.90	3.73	-	891.8
AHQ-9-4, 4573	K.STCQFICDEGYSLSGPER.L	2109.23671	2	2.39E-05	0.93	4.22	-	915.5
AHQ-9-2, 4674 - 4754	K.STCQFICDEGYSLSGPER.L	2109.23671	2	4.60E-10	0.94	4.28	-	977.9
gi|4503631|ref|NP_000120.1| coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,				6.76E-10	19.23	230.25	34.30	83232.8
AHQ-9-5, 5003 - 5072	R.AVPPNNSNAAEDDLPTVELQGVVPR.G	2603.82656	2	2.92E-06	0.76	3.72	-	191.0
AHQ-9-5, 2353 - 2379	R.CGPASVQAIK.H	1032.19627	2	4.48E-04	0.74	2.76	-	669.2
AHQ-9-5, 2648 - 2652	K.DGTHVVENVDATHIGK.L	1692.81163	2	1.30E-08	0.97	4.76	-	1675.7

AHQ-9-7, 2634	K.DGTHVVENVDATHIGK.L	1692.81163	2	7.15E-05	0.82	3.26	-	800.0
AHQ-9-5, 6401 - 6463	K.EAVLIQAGEYM*GQLLEQASLHFFVTAR.I	3039.45415	3	8.14E-06	0.92	4.90	-	797.9
AHQ-9-11, 5231 - 5265	K.ETFDVTLEPLSFK.K	1526.71190	2	1.39E-04	0.79	2.74	-	787.8
AHQ-9-5, 5383 - 5415	K.ETFDVTLEPLSFK.K	1526.71190	2	1.04E-04	0.87	3.61	-	757.7
AHQ-9-7, 5312	K.ETFDVTLEPLSFK.K	1526.71190	2	5.35E-05	0.74	2.76	-	775.4
AHQ-9-5, 4757	R.GTQVVGSDM*TVTVQFTNPLK.E	2139.41549	2	1.75E-09	0.94	4.54	-	796.5
AHQ-9-5, 5315	K.GTYIPVPIVSELQSGK.W	1688.94594	2	4.73E-04	0.59	2.71	-	269.8
AHQ-9-5, 5344	K.GTYIPVPIVSELQSGK.W	1688.94594	3	1.43E-04	0.90	3.57	-	1133.9
AHQ-9-11, 6130	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	1.22E-04	0.91	3.47	-	1046.5
AHQ-9-7, 6196 - 6260	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	6.76E-10	0.93	4.51	-	833.4
AHQ-9-5, 6296 - 6297	R.GVNLQEFLNVTSVHLFK.E	1946.23831	3	1.27E-07	0.82	3.87	-	834.2
AHQ-9-5, 6295	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	2.58E-07	0.96	5.05	-	1227.6
AHQ-9-5, 3361 - 3421	R.HVYGELDVQIQR.R	1457.61612	2	1.83E-09	0.92	3.67	-	786.9
AHQ-9-5, 2320 - 2335	K.KDGTHVVENVDATHIGK.L	1820.98455	2	1.00E-06	0.86	3.11	-	1064.3
AHQ-9-5, 2513	K.KDGTHVVENVDATHIGK.L	1820.98455	3	8.46E-06	0.96	4.75	-	2164.7
AHQ-9-5, 4963 - 5044	K.KETFDVTLEPLSFK.K	1654.88482	2	2.88E-06	0.94	3.90	-	1182.6
AHQ-9-5, 2849	R.KLIASMSSDSLR.H	1308.53039	2	2.96E-05	0.81	2.97	-	892.7
AHQ-9-5, 2011	K.KPLNTEGVMK.S	1117.34452	2	2.89E-05	0.52	2.65	-	388.1
AHQ-9-6, 4102	R.LALETALM*YGAK.K	1297.54595	2	1.65E-07	0.91	3.29	-	844.8
AHQ-9-5, 4541 - 4544	R.LALETALMYGAK.K	1281.54655	2	1.43E-06	0.95	3.33	-	1905.9
AHQ-9-5, 4143 - 4177	R.LALETALM*YGAK.K	1297.54595	2	9.97E-07	0.96	4.08	-	1225.8
AHQ-9-5, 2311	K.LIASM*SSDSLR.H	1196.35688	2	2.65E-04	0.94	3.31	-	1151.8
AHQ-9-7, 5338	R.MYVAVWTPYGVLR.T	1555.86794	2	3.19E-04	0.44	2.58	-	551.7
AHQ-9-7, 5213	R.M*YVAVWTPYGVLR.T	1571.86734	2	2.20E-07	0.93	3.70	-	934.6
AHQ-9-5, 6076	R.NPETDTYILFNPWCEDDAVYLDNEKER.E	3349.53903	3	9.42E-06	0.84	3.70	-	936.0
AHQ-9-5, 4589	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	3.02E-06	0.94	4.50	-	1088.3
AHQ-9-5, 4399 - 4455	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	1.36E-07	0.95	3.97	-	1661.2
AHQ-9-6, 4961	R.SNVDMDFEVENAVLGK.D	1767.93869	2	4.81E-06	0.92	3.67	-	1312.5
AHQ-9-6, 4394	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	6.09E-08	0.94	3.54	-	1775.8
AHQ-9-5, 4439	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	3.84E-08	0.96	4.67	-	1633.4
AHQ-9-5, 5021	R.SNVDMDFEVENAVLGK.D	1767.93869	2	5.72E-08	0.94	4.30	-	1193.9
AHQ-9-5, 3973	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	2.05E-08	0.74	3.26	-	839.1
AHQ-9-13, 5550	K.STVLTIPEIIIK.V	1327.63485	2	7.82E-05	0.77	2.70	-	791.0
AHQ-9-6, 5366 - 5405	K.STVLTIPEIIIK.V	1327.63485	2	1.81E-04	0.89	3.22	-	1063.0
AHQ-9-8, 5447	K.STVLTIPEIIIK.V	1327.63485	2	1.76E-04	0.73	2.90	-	818.5
AHQ-9-5, 2431	R.VEYVIGR.Y	835.97056	2	7.58E-04	0.84	2.70	-	724.0
gi|21361198|ref|NP_000286.2|	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei			8.44E-10	1.53	20.15	5.70	46722.2
AHQ-9-7, 6180	K.ITPNLAEFAFSLYR.Q	1642.87896	2	8.44E-10	0.78	2.56	-	617.6
AHQ-9-7, 3858	K.SVLGQLGITK.V	1016.21669	2	1.40E-05	0.74	2.98	-	539.0
gi|20535366|ref|XP_053177.4|	similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap			9.56E-10	2.46	30.22	9.60	49858.2
AHQ-9-11, 3113	K.DVNAAIATIK.T	1016.17355	2	2.81E-06	0.94	3.66	-	1325.1
AHQ-9-7, 3093	K.DVNAAIATIK.T	1016.17355	2	3.66E-04	0.88	3.61	-	959.5
AHQ-9-8, 4956	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.89E-07	0.80	3.23	-	629.3
AHQ-9-9, 4723 - 4800	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.02E-05	0.78	3.25	-	666.5
AHQ-9-7, 4982 - 5062	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	8.46E-09	0.91	4.22	-	741.8
AHQ-9-7, 4845 - 4900	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.77E-09	0.93	4.35	-	796.3
AHQ-9-11, 4810	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.28E-07	0.50	2.83	-	299.0
AHQ-9-13-, 4868 - 4936	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.15E-05	0.62	3.25	-	392.9
AHQ-9-13, 5099	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.11E-05	0.90	4.14	-	574.5
AHQ-9-14, 5631 - 5679	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.04E-05	0.73	3.28	-	444.1
AHQ-9-14-, 4939	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	9.56E-10	0.93	4.42	-	764.2
AHQ-9-13-, 5416	R.TIQFVDWCPTGFK.V	1600.81899	2	3.23E-06	0.92	3.75	-	894.3
AHQ-9-11, 5237 - 5318	R.TIQFVDWCPTGFK.V	1600.81899	2	2.84E-06	0.60	2.71	-	635.7
AHQ-9-14-, 5375 - 5422	R.TIQFVDWCPTGFK.V	1600.81899	2	2.47E-05	0.84	2.93	-	776.3
gi|13994151|ref|NP_066272.1|	PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H			9.75E-10	8.45	100.24	40.70	36071.5
AHQ-9-13-, 6128 - 6133	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	5.66E-06	0.91	4.78	-	634.4
AHQ-9-13-, 5622	K.AALANLCIGDVITAIDGENTSNM*THLEAQNR.I	3331.63807	3	1.43E-09	0.88	4.30	-	585.1
AHQ-9-11, 3521 - 3522	K.DFEQPLAISR.V	1176.30388	2	4.48E-04	0.81	3.33	-	606.9
AHQ-9-13, 3764	K.DFEQPLAISR.V	1176.30388	2	1.82E-05	0.91	3.57	-	971.8
AHQ-9-14-, 3625	K.DFEQPLAISR.V	1176.30388	2	3.37E-06	0.95	4.09	-	1322.1
AHQ-9-13-, 3382 - 3458	K.GCTDNLTLTVAR.S	1322.47058	2	2.43E-04	0.62	3.06	-	545.5
AHQ-9-9, 3073	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.01E-06	0.86	2.99	-	902.5
AHQ-9-13-, 3288	R.IKGCTDNLTLTVAR.S	1563.80174	2	9.75E-10	0.91	3.57	-	982.1
AHQ-9-13, 3444	R.IKGCTDNLTLTVAR.S	1563.80174	2	7.68E-07	0.88	3.27	-	841.6
AHQ-9-11, 3213	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.98E-06	0.82	3.09	-	678.7
AHQ-9-14-, 3322	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.75E-09	0.88	3.46	-	831.8
AHQ-9-13-, 3700 - 3764	R.LVGGKDFEQPLAISR.V	1630.86972	2	1.21E-05	0.95	4.23	-	1245.7
AHQ-9-13-, 3721	K.M*NLASEPQEVLHIGSAHNR.S	2120.33559	2	8.40E-05	0.83	3.38	-	365.5
AHQ-9-13-, 6141	K.QSTSFLVLQEILESEEK.G	1981.18977	2	5.01E-09	0.96	4.15	-	1518.1
AHQ-9-13-, 5782	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	6.36E-04	0.68	3.30	-	496.9
AHQ-9-13-, 3124	R.SAMPFTASPASSTTAR.V	1583.74859	2	1.83E-04	0.78	3.11	-	627.6
AHQ-9-11, 5061 - 5139	R.VITNQYNNPAGLYSSENISNFNNALESK.T	3103.30221	3	7.42E-05	0.90	4.65	-	555.4
gi|5174539|ref|NP_005908.1|	cytosolic malate dehydrogenase; soluble malate dehydrogenase [Homo sapi			9.85E-10	0.81	10.20	5.10	36425.9
AHQ-9-9, 3425	K.VIVVGNPANTNCLTASK.S	1760.00585	2	9.85E-10	0.81	3.06	-	719.6
AHQ-9-9, 3340	K.VIVVGNPANTNCLTASK.S	1760.00585	2	2.61E-08	0.91	3.93	-	761.7
gi|7669492|ref|NP_002037.2|	glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]			1.17E-09	4.01	60.22	28.70	36053.0
AHQ-9-9, 3456	R.GALQNIIPASTGAAK.A	1412.61680	1	4.09E-06	0.70	3.32	-	357.7
AHQ-9-11, 3582 - 3638	R.GALQNIIPASTGAAK.A	1412.61680	2	6.51E-04	0.84	3.97	-	504.7
AHQ-9-9, 3907 - 3963	K.RVIISAPSADAPM*FVMGVNHEK.Y	2386.77962	3	1.89E-04	0.68	3.73	-	573.1
AHQ-9-11, 5854 - 5910	K.VIHDNFGIVEGLM*TTVHAITATQK.T	2612.98634	3	7.83E-05	0.88	4.45	-	1412.0
AHQ-9-9, 4229 - 4296	R.VIISAPSADAPM*FVMGVNHEK.Y	2230.59327	2	4.06E-04	0.20	3.00	-	186.1
AHQ-9-9, 3960 - 3972	R.VPTANVSVVDLTCR.L	1532.74450	2	6.32E-05	0.75	2.91	-	625.1
AHQ-9-9, 3807 - 3897	R.VPTANVSVVDLTCR.L	1532.74450	2	2.03E-07	0.95	3.97	-	1271.8
AHQ-9-11, 3961	R.VPTANVSVVDLTCR.L	1532.74450	2	3.21E-07	0.82	3.25	-	580.5
AHQ-9-6, 3997	R.VPTANVSVVDLTCR.L	1532.74450	2	1.91E-06	0.94	4.01	-	1108.6
AHQ-9-13, 4186 - 4246	R.VPTANVSVVDLTCR.L	1532.74450	2	3.73E-07	0.93	3.64	-	997.3
AHQ-9-14, 4940	R.VPTANVSVVDLTCR.L	1532.74450	2	2.40E-07	0.78	2.82	-	816.9
AHQ-9-13-, 4040	R.VPTANVSVVDLTCR.L	1532.74450	2	2.20E-08	0.93	3.50	-	1136.5
AHQ-9-14-, 4057	R.VPTANVSVVDLTCR.L	1532.74450	2	1.17E-09	0.90	3.52	-	845.1
AHQ-9-13-, 5237	K.WGDAGAEYVVESTGVFTTM*EK.A	2294.47967	2	2.60E-04	0.66	3.23	-	450.9
gi|4502201|ref|NP_001649.1|	ADP-ribosylation factor 1 [Homo sapiens]			1.23E-09	3.47	40.22	23.80	20696.6
AHQ-9-12, 4448	R.DAVLLVFANK.Q	1090.29726	1	2.37E-05	0.79	2.64	-	941.2
AHQ-9-11, 3221	R.ILM*VGLDAAGK.T	1104.34572	2	1.04E-04	0.92	2.81	-	1517.0
AHQ-9-12, 6204 - 6208	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	3	1.23E-09	0.95	4.35	-	1904.8
AHQ-9-12, 6209 - 6210	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	2	2.78E-06	0.68	3.04	-	441.6
AHQ-9-12, 4821 - 4832	K.NISFTVWDVGGQDK.I	1566.69621	2	2.01E-04	0.80	3.05	-	637.8
gi|4758086|ref|NP_004069.1|	cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain			1.33E-09	3.53	40.25	36.80	20567.3
AHQ-9-11, 4081 - 4099	K.GFGFGQGAGALVHSE	1434.53788	2	9.67E-05	0.93	3.63	-	1077.0
AHQ-9-11, 3289	K.GLESTTLADKDGEIYCK.G	1902.06957	2	6.19E-04	0.92	4.36	-	876.3
AHQ-9-11, 3247 - 3313	K.GLESTTLADKDGEIYCK.G	1902.06957	3	4.14E-04	0.74	3.68	-	528.6
AHQ-9-11, 3525	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	1.33E-09	0.94	4.95	-	787.0
AHQ-9-13-, 3562 - 3617	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	5.49E-08	0.76	3.52	-	530.7
AHQ-9-11, 3475	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	6.39E-07	0.91	3.71	-	758.5
gi|4557703|ref|NP_000414.1|	keratin 2a [Homo sapiens]			1.40E-09	11.69	140.31	28.40	65864.9
AHQ-9-6, 2225	K.AQYEEIAQR.S	1108.18640	2	2.65E-05	0.74	2.61	-	868.5
AHQ-9-4, 6216 - 6218	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	4.75E-08	0.96	6.12	-	1178.3
AHQ-9-1, 6310	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	4.73E-05	0.64	4.06	-	420.8

AHQ-9-13-, 6134	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	6.07E-04	0.70	3.33	-	763.9
AHQ-9-14-, 3101	R.FLEQQNQVLQTK.W	1476.65935	2	1.70E-07	0.96	4.58	-	1875.2
AHQ-9-2, 3121	R.FLEQQNQVLQTK.W	1476.65935	2	1.26E-06	0.95	4.23	-	1504.8
AHQ-9-13-, 3078 - 3089	R.FLEQQNQVLQTK.W	1476.65935	2	8.69E-08	0.97	4.75	-	2477.4
AHQ-9-5, 3027 - 3100	R.FLEQQNQVLQTK.W	1476.65935	2	3.00E-08	0.97	5.20	-	2205.4
AHQ-9-5, 3120 - 3189	R.FLEQQNQVLQTK.W	1476.65935	2	6.05E-05	0.93	3.96	-	1377.6
AHQ-9-6, 3014	R.FLEQQNQVLQTK.W	1476.65935	2	6.63E-05	0.96	4.59	-	1761.8
AHQ-9-13, 3234 - 3240	R.FLEQQNQVLQTK.W	1476.65935	2	4.01E-08	0.97	5.00	-	1865.5
AHQ-9-11, 3017	R.FLEQQNQVLQTK.W	1476.65935	2	9.35E-04	0.95	4.34	-	1401.4
AHQ-9-3, 3056	R.FLEQQNQVLQTK.W	1476.65935	2	5.53E-04	0.97	4.73	-	1936.4
AHQ-9-10, 2973 - 2974	R.FLEQQNQVLQTK.W	1476.65935	2	2.71E-05	0.92	3.72	-	1175.8
AHQ-9-9, 2887 - 2895	R.FLEQQNQVLQTK.W	1476.65935	2	1.40E-07	0.97	4.86	-	2005.1
AHQ-9-7, 3000 - 3074	R.FLEQQNQVLQTK.W	1476.65935	2	3.60E-06	0.97	4.53	-	2391.5
AHQ-9-1, 3224 - 3298	R.FLEQQNQVLQTK.W	1476.65935	2	2.75E-06	0.96	5.35	-	1405.0
AHQ-9-4, 3036	R.FLEQQNQVLQTK.W	1476.65935	2	1.77E-04	0.97	5.16	-	2279.5
AHQ-9-8, 3146	R.FLEQQNQVLQTK.W	1476.65935	2	2.35E-05	0.83	3.04	-	1075.1
AHQ-9-8, 2962 - 2972	R.FLEQQNQVLQTK.W	1476.65935	2	8.71E-04	0.91	3.76	-	1155.2
AHQ-9-4, 3197	R.FLEQQNQVLQTK.W	1476.65935	2	6.35E-06	0.92	4.04	-	1397.3
AHQ-9-4, 2306 - 2369	R.GFSSGSAVVSGGSR.R	1255.31950	2	1.83E-06	0.92	3.83	-	1105.9
AHQ-9-2, 2391	R.GFSSGSAVVSGGSR.R	1255.31950	2	2.05E-04	0.91	3.37	-	1159.8
AHQ-9-7, 2232 - 2306	R.GFSSGSAVVSGGSR.R	1255.31950	2	3.59E-06	0.74	2.58	-	880.8
AHQ-9-13-, 2274 - 2344	R.GFSSGSAVVSGGSR.R	1255.31950	2	1.10E-06	0.78	2.99	-	892.1
AHQ-9-6, 2298	R.GFSSGSAVVSGGSR.R	1255.31950	2	3.01E-06	0.92	3.64	-	996.9
AHQ-9-14-, 2958	K.IEISELNR.V	974.09353	2	7.77E-04	0.89	3.21	-	783.7
AHQ-9-9, 2772 - 2775	K.IEISELNR.V	974.09353	2	3.86E-04	0.62	2.60	-	570.2
AHQ-9-5, 2899	K.IEISELNR.V	974.09353	2	3.87E-04	0.72	3.00	-	506.4
AHQ-9-6, 4042	K.LNDLEEALQQAK.E	1372.50630	2	1.11E-05	0.97	4.26	-	1948.9
AHQ-9-2, 4113 - 4177	K.LNDLEEALQQAK.E	1372.50630	2	9.21E-04	0.90	3.65	-	1131.6
AHQ-9-4, 4076 - 4078	K.LNDLEEALQQAK.E	1372.50630	2	3.06E-05	0.97	5.13	-	1646.5
AHQ-9-5, 5692	R.NLDLDSIIAEVK.A	1330.50933	2	2.16E-06	0.95	4.53	-	1208.6
AHQ-9-1, 5790	R.NLDLDSIIAEVK.A	1330.50933	2	1.66E-06	0.96	4.35	-	1361.1
AHQ-9-13-, 5638 - 5648	R.NLDLDSIIAEVK.A	1330.50933	2	5.86E-06	0.96	4.98	-	1200.9
AHQ-9-13, 5778	R.NLDLDSIIAEVK.A	1330.50933	2	6.62E-05	0.94	4.39	-	1089.0
AHQ-9-11, 5553 - 5554	R.NLDLDSIIAEVK.A	1330.50933	2	4.48E-09	0.96	4.50	-	1530.7
AHQ-9-2, 5785	R.NLDLDSIIAEVK.A	1330.50933	2	1.24E-07	0.95	4.43	-	1064.9
AHQ-9-3, 5632	R.NLDLDSIIAEVK.A	1330.50933	2	1.65E-06	0.96	4.90	-	1075.3
AHQ-9-6, 5610	R.NLDLDSIIAEVK.A	1330.50933	2	9.11E-07	0.94	4.25	-	1128.9
AHQ-9-4, 5677 - 5702	R.NLDLDSIIAEVK.A	1330.50933	2	3.76E-06	0.96	4.84	-	1265.4
AHQ-9-7, 5601	R.NLDLDSIIAEVK.A	1330.50933	2	4.69E-06	0.95	4.51	-	1089.8
AHQ-9-14-, 5649	R.NLDLDSIIAEVK.A	1330.50933	2	5.35E-07	0.93	3.71	-	1023.9
AHQ-9-14-, 3241	K.NVQDAIADAEQR.G	1330.38637	2	1.12E-07	0.93	3.97	-	1001.4
AHQ-9-5, 3159	K.NVQDAIADAEQR.G	1330.38637	2	3.53E-06	0.97	4.07	-	1985.0
AHQ-9-13-, 3193	K.NVQDAIADAEQR.G	1330.38637	2	3.57E-05	0.91	3.67	-	1142.5
AHQ-9-8, 3128	K.NVQDAIADAEQR.G	1330.38637	2	8.71E-09	0.90	3.70	-	895.0
AHQ-9-4, 3140	K.NVQDAIADAEQR.G	1330.38637	2	6.69E-07	0.92	3.71	-	1137.8
AHQ-9-2, 3237	K.NVQDAIADAEQR.G	1330.38637	2	6.54E-06	0.93	3.96	-	1134.1
AHQ-9-7, 3134	K.NVQDAIADAEQR.G	1330.38637	2	3.80E-05	0.77	2.78	-	863.5
AHQ-9-3, 3165	K.NVQDAIADAEQR.G	1330.38637	2	9.09E-05	0.90	3.29	-	1206.8
AHQ-9-6, 3141	K.NVQDAIADAEQR.G	1330.38637	2	8.11E-09	0.86	3.37	-	876.0
AHQ-9-14-, 3266	R.TAAENDFVTLK.K	1209.33064	2	6.54E-04	0.89	2.81	-	1131.1
AHQ-9-2, 3266	R.TAAENDFVTLK.K	1209.33064	2	4.09E-04	0.73	2.63	-	703.0
AHQ-9-13-, 4910	R.TSQNSELNNMQDLVEDYK.K	2129.24808	2	1.79E-04	0.53	2.68	-	429.5
AHQ-9-13, 5646	K.VDLLNQEIEFLK.V	1461.68459	2	1.99E-07	0.93	4.28	-	853.7
AHQ-9-14-, 5501 - 5527	K.VDLLNQEIEFLK.V	1461.68459	2	3.34E-07	0.91	3.76	-	961.8
AHQ-9-3, 5516	K.VDLLNQEIEFLK.V	1461.68459	2	7.12E-07	0.93	4.09	-	1018.9
AHQ-9-6, 5493 - 5513	K.VDLLNQEIEFLK.V	1461.68459	2	5.77E-06	0.92	3.42	-	1053.0
AHQ-9-1, 5678 - 5752	K.VDLLNQEIEFLK.V	1461.68459	2	9.22E-06	0.94	4.66	-	888.5
AHQ-9-5, 5507 - 5585	K.VDLLNQEIEFLK.V	1461.68459	2	3.40E-08	0.95	4.96	-	1007.0
AHQ-9-7, 5402 - 5480	K.VDLLNQEIEFLK.V	1461.68459	2	1.50E-06	0.89	3.30	-	935.9
AHQ-9-2, 5661 - 5693	K.VDLLNQEIEFLK.V	1461.68459	2	6.04E-06	0.85	3.99	-	630.8
AHQ-9-11, 5355 - 5433	K.VDLLNQEIEFLK.V	1461.68459	2	4.66E-05	0.64	2.73	-	529.4
AHQ-9-13-, 5505 - 5520	K.VDLLNQEIEFLK.V	1461.68459	2	1.40E-09	0.95	4.05	-	1209.1
AHQ-9-4, 5554 - 5574	K.VDLLNQEIEFLK.V	1461.68459	2	2.40E-06	0.94	4.15	-	1164.0
AHQ-9-14-, 5327 - 5337	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	8.03E-05	0.90	4.12	-	1215.0
AHQ-9-13, 5454 - 5524	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	2.53E-05	0.77	3.50	-	698.7
AHQ-9-13-, 5321	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	1.32E-04	0.81	3.62	-	637.8
AHQ-9-5, 3147	K.YEELQVTVGR.H	1194.31920	2	4.55E-07	0.94	3.62	-	1461.2
AHQ-9-14-, 3202	K.YEELQVTVGR.H	1194.31920	2	2.15E-05	0.92	3.46	-	1345.8
AHQ-9-1, 3322	K.YEELQVTVGR.H	1194.31920	2	1.45E-06	0.97	3.93	-	2079.9
AHQ-9-13-, 3182	K.YEELQVTVGR.H	1194.31920	2	3.07E-08	0.97	4.09	-	2266.4
AHQ-9-4, 3141 - 3144	K.YEELQVTVGR.H	1194.31920	2	5.54E-07	0.95	4.01	-	1386.0
AHQ-9-5, 2967	R.YLDGLTAER.T	1038.13608	2	6.36E-05	0.87	3.24	-	680.1
gi|5031839|ref|NP_005545.1|	keratin 6A; Keratin-6A; keratin, epidermal type II, K6A; cytokeratin 6A			1.57E-09	1.77	20.21	5.10	60044.6
AHQ-9-3, 5030	K.ADTLTDEINFLR.A	1408.53864	2	1.73E-04	0.87	3.07	-	1101.7
AHQ-9-7, 4997	K.ADTLTDEINFLR.A	1408.53864	2	5.34E-06	0.84	3.05	-	701.3
AHQ-9-1, 3262	R.AIGGGLSSVGGGSSTIK.Y	1448.60431	2	1.57E-09	0.93	4.06	-	938.8
gi|29739414|ref|XP_294015.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			1.78E-09	2.35	30.23	17.70	26916.7
AHQ-9-9, 3669 - 3723	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.48E-09	0.84	3.97	-	854.1
AHQ-9-11, 3771 - 3849	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.73E-06	0.79	3.10	-	1087.9
AHQ-9-9, 4597	K.LISWYDNEFGYSNR.V	1764.87478	3	4.86E-04	0.85	3.38	-	739.8
AHQ-9-14-, 4805	K.LISWYDNEFGYSNR.V	1764.87478	2	4.54E-07	0.91	3.52	-	823.0
AHQ-9-9, 4523 - 4583	K.LISWYDNEFGYSNR.V	1764.87478	2	9.52E-09	0.95	4.47	-	1022.3
AHQ-9-9, 4641 - 4699	K.LISWYDNEFGYSNR.V	1764.87478	2	1.78E-09	0.96	4.58	-	1307.9
AHQ-9-11, 4613 - 4681	K.LISWYDNEFGYSNR.V	1764.87478	2	1.63E-04	0.74	2.96	-	682.0
AHQ-9-11, 4734 - 4785	K.LISWYDNEFGYSNR.V	1764.87478	2	8.47E-04	0.61	2.67	-	430.7
AHQ-9-9, 2297 - 2369	R.VVDLMAHM*ASKE	1347.58686	2	7.14E-05	0.55	3.14	-	577.9
gi|4758950|ref|NP_000933.1|	peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]			1.79E-09	4.22	50.19	29.20	23742.4
AHQ-9-11, 3070	R.DKPLKDVIIADCGK.I	1573.83653	2	3.88E-07	0.91	3.48	-	1000.8
AHQ-9-11, 4087 - 4153	K.DTNGSQFFITTVK.T	1458.59766	2	1.79E-09	0.92	3.62	-	1209.5
AHQ-9-14-, 4369	K.TVDNFVALATGEK.G	1365.51377	2	6.94E-06	0.91	3.80	-	850.4
AHQ-9-11, 3634 - 3711	R.VIKDFM*IQGGDFTR.G	1643.88873	2	2.59E-04	0.59	2.57	-	452.4
AHQ-9-11, 3073 - 3082	K.VLEGMEVVR.K	1032.23962	2	2.99E-05	0.89	3.16	-	912.6
gi|16751921|ref|NP_444513.1|	dermcidin precursor; AIDD protein [Homo sapiens]			1.88E-09	0.92	10.19	12.70	11283.8
AHQ-9-14-, 3770	K.LGKDAVEDLESVGK.G	1460.61186	2	1.88E-09	0.92	3.78	-	1326.1
AHQ-9-3, 3702	K.LGKDAVEDLESVGK.G	1460.61186	2	4.62E-06	0.84	3.17	-	1076.1
gi|4757810|ref|NP_004037.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,			2.21E-09	4.53	50.24	10.50	59750.3
AHQ-9-7, 3845	R.EAYPGDVFYLHSR.L	1554.68713	2	2.21E-09	0.90	3.69	-	662.1
AHQ-9-7, 5448 - 5478	K.FENAFLSHVVSQHQALLGTIR.A	2368.67911	3	4.95E-07	0.94	4.73	-	1304.2
AHQ-9-7, 3544	K.HALIIYDDLSK.Q	1288.47413	2	1.17E-07	0.95	3.69	-	1278.7
AHQ-9-7, 3728	K.TGTAEMSSILEER.I	1424.55988	2	5.04E-05	0.86	3.09	-	1208.7
AHQ-9-7, 2688	K.TGTAEM*SSILEER.I	1440.55928	2	2.11E-06	0.88	2.85	-	1414.7
gi|4503571|ref|NP_001419.1|	enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n			2.29E-09	4.30	50.24	20.50	47168.7
AHQ-9-13-, 5053	R.AAVPSGASTGIYEALELR.D	1806.00979	2	1.45E-04	0.94	4.82	-	642.6
AHQ-9-13, 5194 - 5216	R.AAVPSGASTGIYEALELR.D	1806.00979	2	5.67E-04	0.87	3.70	-	522.2
AHQ-9-12, 5005 - 5012	R.AAVPSGASTGIYEALELR.D	1806.00979	2	7.73E-06	0.92	4.34	-	611.4
AHQ-9-8, 5062	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.08E-05	0.81	3.26	-	367.2
AHQ-9-9, 4867	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.83E-05	0.79	3.01	-	517.4

AHQ-9-14-, 5059	R.AAVPSGASTGIYEALELR.D	1806.00979	2	5.01E-07	0.71	2.87	-	317.7
AHQ-9-9, 4116 - 4123	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	1.75E-04	0.91	4.42	-	662.4
AHQ-9-7, 4257	K.DATNVGDEGGFAPNILENK.E	1962.06350	2	6.05E-04	0.72	3.10	-	601.5
AHQ-9-8, 5612	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	4.76E-06	0.87	4.58	-	670.2
AHQ-9-8, 2411 - 2480	R.IGAEVYHNLK.N	1144.30502	2	2.09E-04	0.93	3.65	-	1457.8
AHQ-9-8, 4630 - 4634	R.YISPDQLADLYK.S	1426.59557	2	6.26E-07	0.94	4.22	-	963.3
AHQ-9-8, 4643	R.YISPDQLADLYK.S	1426.59557	1	2.07E-04	0.40	2.39	-	626.9
AHQ-9-9, 4464 - 4469	R.YISPDQLADLYK.S	1426.59557	2	2.29E-09	0.88	3.21	-	708.4
AHQ-9-11, 4577	R.YISPDQLADLYK.S	1426.59557	2	8.15E-06	0.83	2.99	-	630.0
gi|4505763|ref|NP_000282.1|	phosphoglycerate kinase 1 [Homo sapiens]			2.33E-09	3.79	40.25	15.10	44614.4
AHQ-9-8, 5504 - 5506	K.ACANPAAGSVILLENLR.F	1771.03187	2	2.33E-09	0.97	4.95	-	1586.6
AHQ-9-12, 5421	K.ACANPAAGSVILLENLR.F	1771.03187	2	6.17E-06	0.73	3.30	-	709.6
AHQ-9-8, 5270	K.ALESPERPFLAILGGAK.V	1770.06542	2	8.65E-06	0.96	4.81	-	1637.6
AHQ-9-8, 5155	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	2.46E-06	0.94	4.43	-	757.5
AHQ-9-8, 4172	K.YSLEPVAVELK.S	1248.44991	2	2.30E-05	0.91	3.27	-	1091.9
gi|29728393|ref|XP_293689.1|	similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabili			2.53E-09	0.86	10.22	4.50	37463.6
AHQ-9-9, 4147 - 4148	R.GFAFVTFDNHDSVDK.I	1699.80110	2	2.53E-09	0.86	4.35	-	869.9
gi|4506413|ref|NP_002875.1|	RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s			2.53E-09	3.54	40.24	21.70	20987.1
AHQ-9-11, 2529	K.CDLEDERVVGK.E	1321.43945	2	5.66E-04	0.74	2.69	-	785.6
AHQ-9-11, 5445 - 5446	K.INVNEIFYDLVR.Q	1495.70427	2	2.04E-04	0.77	3.12	-	755.0
AHQ-9-11, 6137	K.INVNEIFYDLVR.Q	1495.70427	2	5.09E-07	0.95	4.75	-	1077.7
AHQ-9-14-, 5553	K.INVNEIFYDLVR.Q	1495.70427	2	6.39E-05	0.91	3.76	-	1005.3
AHQ-9-11, 5685 - 5761	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.42E-06	0.91	4.20	-	891.3
AHQ-9-13-, 5721 - 5777	K.SALTVQFVQGIFVEK.Y	1666.94196	2	7.25E-04	0.80	2.84	-	897.4
AHQ-9-11, 5837 - 5914	K.SKINVNEIFYDLVR.Q	1710.95483	2	5.66E-06	0.85	3.53	-	931.8
AHQ-9-11, 5702 - 5703	K.SKINVNEIFYDLVR.Q	1710.95483	3	8.46E-06	0.96	4.65	-	1787.7
AHQ-9-11, 5701	K.SKINVNEIFYDLVR.Q	1710.95483	2	2.53E-09	0.94	4.20	-	1045.4
gi|4885063|ref|NP_005156.1|	aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase			2.67E-09	1.62	20.25	7.10	39455.6
AHQ-9-12, 4352 - 4432	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	2.10E-05	0.42	3.06	-	322.1
AHQ-9-8, 4320 - 4378	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	1.87E-06	0.85	4.91	-	612.2
AHQ-9-8, 4090	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	2.67E-09	0.86	5.03	-	683.9
AHQ-9-8, 4148	K.VDKGVVPLAGTDGETTTQGLDGLSER.C	2616.82041	3	8.34E-06	0.76	4.04	-	906.2
gi|4507171|ref|NP_003109.1|	secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec			2.88E-09	1.76	20.21	4.60	34632.0
AHQ-9-8, 3187	R.LEAGDHPVELLAR.D	1420.59579	2	2.88E-09	0.94	4.18	-	861.5
AHQ-9-8, 2979	K.RLEAGDHPVELLAR.D	1576.78214	3	4.03E-06	0.82	3.28	-	874.0
AHQ-9-8, 2976	K.RLEAGDHPVELLAR.D	1576.78214	2	5.76E-06	0.55	2.69	-	360.7
gi|4505813|ref|NP_003737.1|	cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain			2.99E-09	1.57	20.14	24.70	10365.8
AHQ-9-14-, 2546	R.NFGSYVTHETK.H	1283.37131	2	2.62E-04	0.87	2.88	-	944.4
AHQ-9-14-, 3665	K.YNPTWHCIVGR.N	1404.57820	2	2.99E-09	0.70	2.80	-	368.4
gi|4503747|ref|NP_001448.1|	filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a			3.01E-09	3.47	40.24	1.40	278191.4
AHQ-9-2, 3126	K.DLAEDAPWKK.I	1173.29999	2	2.60E-05	0.62	2.55	-	781.5
AHQ-9-1, 6031 - 6032	R.LIALLEVLSQK.R	1227.51852	2	3.01E-09	0.97	4.26	-	1461.0
AHQ-9-11, 5765	R.LIALLEVLSQK.R	1227.51852	2	1.73E-04	0.93	3.55	-	897.0
AHQ-9-2, 6007	R.LIALLEVLSQK.R	1227.51852	2	1.59E-07	0.97	4.70	-	1623.5
AHQ-9-8, 5903	R.LIALLEVLSQK.R	1227.51852	2	2.59E-06	0.92	3.47	-	987.3
AHQ-9-3, 5849 - 5850	R.LIALLEVLSQK.R	1227.51852	2	4.61E-09	0.97	4.75	-	1557.3
AHQ-9-4, 5910	R.LIALLEVLSQK.R	1227.51852	2	1.38E-07	0.98	4.89	-	1637.9
AHQ-9-5, 5915	R.LIALLEVLSQK.R	1227.51852	2	5.53E-08	0.96	4.39	-	1331.6
AHQ-9-6, 5834	R.LIALLEVLSQK.R	1227.51852	2	2.86E-08	0.96	4.42	-	1259.7
AHQ-9-7, 5820 - 5829	R.LIALLEVLSQK.R	1227.51852	2	5.10E-07	0.96	3.96	-	1472.2
AHQ-9-13, 6002	R.LIALLEVLSQK.R	1227.51852	2	1.50E-04	0.96	4.09	-	1236.0
AHQ-9-2, 5977	R.QM*QLENVSVALEFLDR.E	1909.15348	2	2.84E-07	0.94	4.41	-	933.8
AHQ-9-2, 6433 - 6435	R.QMQLENVSVALEFLDR.E	1893.15408	2	1.51E-05	0.95	4.44	-	1172.4
gi|30147536|ref|XP_293762.2|	similar to bridging integrator 2; bridging integrator-2; breast cancer			3.05E-09	0.84	10.19	3.90	46870.6
AHQ-9-5, 2897	R.TSLEVSPNPEPPEKPVR.T	1877.08801	2	3.05E-09	0.84	3.82	-	420.4
AHQ-9-5, 2893	R.TSLEVSPNPEPPEKPVR.T	1877.08801	3	1.27E-06	0.82	3.47	-	687.5
gi|29568101|ref|NP_006467.3|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT			3.14E-09	0.95	10.20	14.60	11400.3
AHQ-9-14-, 3681	K.TPALVNAAVTYSKPR.L	1588.83283	3	3.14E-09	0.95	3.99	-	1372.8
gi|5031677|ref|NP_005681.1|	dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [			3.27E-09	3.40	40.23	8.90	78060.6
AHQ-9-5, 4635	K.ALQGASQIIAEIR.E	1370.57991	2	1.00E-05	0.92	3.48	-	1613.2
AHQ-9-14-, 4642 - 4645	K.ALQGASQIIAEIR.E	1370.57991	2	3.27E-09	0.91	3.90	-	1231.9
AHQ-9-13-, 4626	K.ALQGASQIIAEIR.E	1370.57991	2	1.00E-08	0.94	3.80	-	1628.4
AHQ-9-13-, 4934	K.DTLQSELVGQLYK.S	1494.67144	2	1.01E-04	0.89	3.03	-	1023.8
AHQ-9-5, 4613	K.SVTDSIRDEYAFLQK.K	1772.93666	2	3.45E-04	0.67	2.67	-	836.2
AHQ-9-6, 6290 - 6369	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	7.03E-06	0.92	4.30	-	849.4
AHQ-9-5, 6376	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	4.16E-04	0.90	4.11	-	615.3
gi|13129150|ref|NP_005339.1|	heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H			4.42E-09	1.42	20.23	3.40	84659.1
AHQ-9-5, 3907	R.NPDDITNEEYGEFYK.S	1834.87381	2	4.42E-09	0.95	4.53	-	1061.7
AHQ-9-7, 3868	R.NPDDITNEEYGEFYK.S	1834.87381	2	7.47E-09	0.84	3.78	-	624.7
AHQ-9-6, 3873	R.NPDDITNEEYGEFYK.S	1834.87381	2	1.82E-04	0.76	3.07	-	602.5
AHQ-9-5, 3825	R.NPDDITNEEYGEFYK.S	1834.87381	2	5.50E-07	0.95	4.47	-	896.2
AHQ-9-5, 4001 - 4069	R.RAPFDLFENR.K	1265.40235	2	5.17E-07	0.47	2.90	-	417.6
gi|4758460|ref|NP_004479.1|	glycoprotein V (platelet) [Homo sapiens]			4.49E-09	6.36	70.23	17.00	60958.9
AHQ-9-5, 3823	R.GVLQSQSFSGM*TVLQR.L	1754.98948	2	1.68E-06	0.96	4.40	-	1790.9
AHQ-9-5, 4521	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	9.74E-07	0.95	4.40	-	1268.4
AHQ-9-5, 5253 - 5259	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	3	8.74E-07	0.91	4.27	-	1121.4
AHQ-9-5, 3912	R.LTEVLLGHNSWR.C	1425.61726	2	4.49E-09	0.92	3.01	-	1254.1
AHQ-9-5, 3739	R.LTEVLLGHNSWR.C	1425.61726	2	8.46E-04	0.88	2.95	-	1022.5
AHQ-9-6, 6293	R.LVSLDSGLLNSLGALTELQFHR.N	2384.71675	3	8.77E-08	0.84	3.67	-	908.8
AHQ-9-5, 5901	K.MVLLEQLFLDHNALR.G	1813.15693	3	3.99E-04	0.95	4.59	-	1722.9
AHQ-9-5, 3427	R.YLGVTLSPR.L	1006.18036	2	2.34E-04	0.82	3.18	-	1015.6
AHQ-9-6, 3398	R.YLGVTLSPR.L	1006.18036	2	3.29E-04	0.92	2.99	-	1318.6
gi|21361478|ref|NP_055944.2|	septin 6 isoform B; septin 2 [Homo sapiens]			4.51E-09	1.85	20.32	11.10	49716.3
AHQ-9-7, 3836	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L	3147.31508	3	4.51E-09	0.98	6.42	-	2375.7
AHQ-9-7, 3149	K.TAAELLQSQGSQAGGSQTLK.R	1976.13485	2	8.11E-05	0.87	3.88	-	647.8
gi|4885609|ref|NP_005408.1|	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen			4.93E-09	2.66	30.19	9.50	59834.4
AHQ-9-7, 6105	R.AGPLAGGVTTFVALYDYESR.T	2088.30526	2	1.38E-08	0.89	3.81	-	786.7
AHQ-9-7, 3872	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	1.42E-08	0.89	3.72	-	720.9
AHQ-9-7, 3708	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	7.55E-07	0.79	3.43	-	596.7
AHQ-9-7, 5806	R.TQFNSLQQLVAYYSK.H	1790.99681	2	2.55E-08	0.79	3.16	-	729.0
AHQ-9-7, 5629 - 5641	R.TQFNSLQQLVAYYSK.H	1790.99681	2	4.93E-09	0.88	3.81	-	701.1
gi|4507487|ref|NP_003238.1|	thrombospondin 2 [Homo sapiens]			5.05E-09	1.85	20.22	2.60	129954.5
AHQ-9-2, 4921 - 4985	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	5.05E-09	0.94	4.37	-	1176.6
AHQ-9-4, 4810 - 4832	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	2.25E-05	0.91	3.89	-	935.8
AHQ-9-5, 4831 - 4847	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	2.79E-05	0.75	3.16	-	687.2
AHQ-9-6, 4778	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	8.85E-06	0.84	2.96	-	786.1
AHQ-9-5, 2747 - 2808	R.NALWHTGNTPGQVR.T	1551.69124	2	8.97E-04	0.85	3.63	-	924.6
AHQ-9-2, 2827 - 2885	R.NALWHTGNTPGQVR.T	1551.69124	2	2.62E-04	0.90	3.54	-	1039.0
gi|4557677|ref|NP_000203.1|	integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu			5.14E-09	17.67	210.26	28.60	87185.6
AHQ-9-5, 3069	R.AKWDTANNPLYK.E	1421.58225	2	1.11E-04	0.71	2.62	-	680.4
AHQ-9-3, 3084 - 3134	R.AKWDTANNPLYK.E	1421.58225	2	1.57E-06	0.76	2.99	-	800.9
AHQ-9-3, 2964	R.CDLKENLLK.D	1134.32850	2	9.30E-04	0.75	2.58	-	927.6
AHQ-9-3, 5052	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	7.40E-06	0.59	3.16	-	655.3
AHQ-9-3, 4958	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	2.35E-05	0.83	3.66	-	691.0
AHQ-9-4, 4092 - 4100	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.40E-06	0.83	4.13	-	519.2
AHQ-9-3, 4077	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.75E-06	0.79	3.71	-	438.4
AHQ-9-6, 4146	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.98E-05	0.94	4.11	-	1080.0

AHQ-9-7, 4132	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	3.11E-06	0.76	3.03	-	558.0
AHQ-9-3, 4152 - 4176	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.35E-06	0.92	3.83	-	845.8
AHQ-9-3, 5280 - 5336	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.61E-04	0.95	5.15	-	786.6
AHQ-9-3, 4238	K.DNCAPESIEFPVSEAR.V	1822.93099	2	6.63E-05	0.84	2.65	-	1076.5
AHQ-9-7, 4104 - 4106	K.DNCAPESIEFPVSEAR.V	1822.93099	2	2.13E-06	0.81	2.98	-	752.9
AHQ-9-4, 4164	K.DNCAPESIEFPVSEAR.V	1822.93099	2	7.38E-04	0.86	3.31	-	1003.5
AHQ-9-3, 4140 - 4141	K.DNCAPESIEFPVSEAR.V	1822.93099	2	4.34E-08	0.91	3.28	-	1366.1
AHQ-9-8, 4160	K.DNCAPESIEFPVSEAR.V	1822.93099	2	2.03E-04	0.84	3.06	-	858.0
AHQ-9-6, 4114	K.DNCAPESIEFPVSEAR.V	1822.93099	2	7.79E-06	0.80	3.08	-	1005.5
AHQ-9-4, 3262 - 3329	K.EATSTFTNITYR.G	1404.50685	2	1.66E-05	0.84	3.22	-	772.3
AHQ-9-3, 3333 - 3349	K.EATSTFTNITYR.G	1404.50685	2	1.06E-07	0.74	3.10	-	483.0
AHQ-9-3, 2409	R.FQYYEDSSGK.S	1224.25749	2	7.30E-05	0.72	2.58	-	473.5
AHQ-9-5, 3489 - 3492	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	3.60E-06	0.97	4.95	-	1796.8
AHQ-9-3, 3476	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	3.46E-05	0.94	4.11	-	1332.9
AHQ-9-4, 3484	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	3.60E-08	0.96	4.40	-	1690.0
AHQ-9-4, 3486	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	9.69E-07	0.84	3.79	-	640.5
AHQ-9-6, 3466 - 3467	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	7.21E-04	0.86	3.69	-	915.6
AHQ-9-8, 2790	K.HVLTLTDQVTR.F	1283.45912	2	1.07E-04	0.89	3.44	-	561.8
AHQ-9-7, 2776	K.HVLTLTDQVTR.F	1283.45912	2	5.85E-04	0.40	2.76	-	348.3
AHQ-9-3, 3928 - 3986	K.IGDTVSFSIEAK.V	1267.41009	2	9.73E-06	0.94	3.56	-	1091.0
AHQ-9-3, 4050	K.IGDTVSFSIEAK.V	1267.41009	2	6.93E-04	0.93	3.65	-	982.2
AHQ-9-4, 3990	K.IGDTVSFSIEAK.V	1267.41009	2	1.92E-07	0.86	3.32	-	794.5
AHQ-9-3, 4137	K.IGDTVSFSIEAK.V	1267.41009	2	5.81E-05	0.79	3.00	-	649.7
AHQ-9-3, 3529	K.IGDTVSFSIEAK.V	1267.41009	2	2.85E-05	0.86	2.99	-	846.1
AHQ-9-3, 3540	K.ITGKYCECDDFSCVR.Y	1914.08378	2	5.25E-07	0.69	3.36	-	346.7
AHQ-9-3, 3760 - 3824	R.NDASHLLVFTTDAK.T	1532.67977	2	6.72E-05	0.95	3.69	-	1513.4
AHQ-9-6, 3779	R.NDASHLLVFTTDAK.T	1532.67977	2	4.02E-05	0.93	3.89	-	1058.8
AHQ-9-4, 3764 - 3826	R.NDASHLLVFTTDAK.T	1532.67977	2	5.25E-05	0.94	4.18	-	1179.5
AHQ-9-3, 3821	R.NDASHLLVFTTDAK.T	1532.67977	2	4.33E-06	0.93	4.12	-	843.8
AHQ-9-1, 4026	R.NDASHLLVFTTDAK.T	1532.67977	2	2.38E-04	0.74	2.62	-	851.9
AHQ-9-7, 3770	R.NDASHLLVFTTDAK.T	1532.67977	2	7.24E-07	0.95	4.02	-	1407.7
AHQ-9-4, 4185	R.NDASHLLVFTTDAK.T	1532.67977	2	1.01E-07	0.86	3.53	-	868.7
AHQ-9-3, 3838	R.NDASHLLVFTTDAK.T	1532.67977	3	2.89E-08	0.95	4.80	-	1341.1
AHQ-9-5, 3831	R.NDASHLLVFTTDAK.T	1532.67977	2	3.71E-04	0.66	2.63	-	680.5
AHQ-9-6, 4138	R.NDASHLLVFTTDAK.T	1532.67977	2	3.10E-05	0.81	3.19	-	873.1
AHQ-9-6, 3451 - 3457	K.SFTIKPVGFK.D	1124.35685	2	2.42E-05	0.87	2.77	-	1197.8
AHQ-9-3, 3480 - 3481	K.SFTIKPVGFK.D	1124.35685	2	7.61E-06	0.80	2.81	-	949.7
AHQ-9-3, 2913 - 2976	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.42E-08	0.89	3.98	-	919.2
AHQ-9-4, 2841	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	4.45E-08	0.81	2.95	-	874.8
AHQ-9-3, 2780 - 2848	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	3.63E-07	0.92	3.62	-	1289.0
AHQ-9-4, 2748	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	6.11E-06	0.47	2.65	-	624.2
AHQ-9-3, 3344	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.49E-07	0.88	2.79	-	1095.6
AHQ-9-4, 2074	R.VLEDRPLSDK.G	1172.31354	2	1.69E-05	0.84	3.28	-	912.1
AHQ-9-3, 2088 - 2118	R.VLEDRPLSDK.G	1172.31354	2	9.73E-06	0.93	3.50	-	1166.0
AHQ-9-3, 2825 - 2882	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	5.14E-09	0.93	4.85	-	1229.3
AHQ-9-4, 2805	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	2.94E-07	0.95	4.93	-	1200.5
AHQ-9-5, 3308 - 3312	K.WDTANNPLYK.E	1222.33111	2	1.85E-05	0.77	2.58	-	733.5
AHQ-9-5, 3507	K.YCECDDFSCVR.Y	1514.59674	2	4.70E-07	0.95	3.54	-	1284.1
AHQ-9-3, 3504	K.YCECDDFSCVR.Y	1514.59674	2	3.00E-07	0.94	3.82	-	986.7
gi|5031931|ref|NP_005585.1|	nascent-polypeptide-associated complex alpha polypeptide [Homo sapiens]			5.35E-09	1.89	20.22	13.50	23383.7
AHQ-9-9, 3175	K.IEDLSQQAQLAAAEK.F	1615.76708	2	5.35E-09	0.94	4.37	-	1944.9
AHQ-9-9, 3727 - 3733	K.SPASDTYIVFGEAK.I	1485.61987	2	2.75E-08	0.95	4.24	-	1295.6
gi|4503445|ref|NP_001944.1|	endothelial cell growth factor 1 (platelet-derived); thymidine phosphor			6.06E-09	1.83	20.21	5.40	49955.2
AHQ-9-7, 6085 - 6097	R.ALPLALVLHELGAGR.S	1530.83966	2	6.06E-09	0.95	4.10	-	1456.5
AHQ-9-7, 3504	R.ALQEALVLSDR.A	1215.38155	2	7.13E-07	0.88	3.20	-	1131.5
gi|19923457|ref|NP_057447.2|	glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M			6.13E-09	2.63	30.24	6.90	67308.6
AHQ-9-7, 5264	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	6.13E-09	0.94	4.83	-	1293.7
AHQ-9-7, 4606	R.YGFDQFALYK.E	1252.39881	2	2.64E-07	0.92	3.33	-	974.8
AHQ-9-7, 4822	R.YQDQAVLFIPAMK.R	1524.80902	2	9.51E-04	0.77	2.65	-	982.4
gi|8393159|ref|NP_059118.1|	calmodulin-like skin protein [Homo sapiens]			6.16E-09	0.80	10.19	15.80	15920.4
AHQ-9-14-, 4899	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	6.16E-09	0.80	3.71	-	572.1
gi|4507651|ref|NP_003281.1|	tropomyosin 4 [Homo sapiens]			6.75E-09	3.74	40.30	15.30	28521.6
AHQ-9-9, 3823 - 3827	R.AEVSELKCGDLEEELK.N	1851.02256	2	6.75E-09	0.90	4.09	-	858.0
AHQ-9-9, 5337 - 5393	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	1.69E-08	0.97	5.99	-	1819.9
AHQ-9-9, 2547	K.IQALQQQADEAEDR.A	1615.68404	2	2.84E-06	0.97	4.52	-	1839.3
AHQ-9-11, 2653 - 2655	K.IQALQQQADEAEDR.A	1615.68404	2	1.09E-08	0.97	4.21	-	1807.7
AHQ-9-13-, 2729	K.IQALQQQADEAEDR.A	1615.68404	2	2.24E-06	0.91	3.11	-	1350.5
AHQ-9-11, 2497	R.KIQALQQQADEAEDR.A	1743.85695	2	7.38E-07	0.90	3.62	-	1043.8
AHQ-9-11, 2494 - 2543	R.KIQALQQQADEAEDR.A	1743.85695	3	2.91E-04	0.79	3.32	-	985.9
AHQ-9-10, 2483	R.KIQALQQQADEAEDR.A	1743.85695	2	5.49E-04	0.81	2.51	-	963.7
AHQ-9-9, 2379	R.KIQALQQQADEAEDR.A	1743.85695	3	3.55E-06	0.95	4.54	-	1432.1
gi|21624607|ref|NP_066972.1|	coactosin-like 1 [Homo sapiens]			7.32E-09	0.95	10.20	8.50	15944.9
AHQ-9-13-, 4992	R.DDGSAVIWVTFK.Y	1338.49001	2	7.32E-09	0.95	4.06	-	1063.4
gi|27477800|ref|XP_208313.1|	similar to tropomyosin 4 [Homo sapiens]			7.79E-09	0.86	10.19	10.10	18426.7
AHQ-9-9, 4704	K.CGDLEEELKNVTNNLK.S	1878.05124	3	8.75E-06	0.87	3.00	-	1235.9
AHQ-9-9, 4247	K.CGDLEEELKNVTNNLK.S	1878.05124	2	7.79E-09	0.86	3.81	-	841.1
gi|4557597|ref|NP_001449.1|	gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);			7.97E-09	1.53	20.24	1.40	288897.4
AHQ-9-2, 4597	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.10E-05	0.89	4.58	-	628.4
AHQ-9-7, 4356 - 4421	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	3.20E-05	0.84	4.11	-	568.5
AHQ-9-4, 4490	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	2.07E-05	0.89	4.43	-	369.2
AHQ-9-6, 4393 - 4395	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	7.97E-09	0.83	4.03	-	462.1
AHQ-9-1, 4667	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	8.99E-08	0.85	3.99	-	724.0
AHQ-9-5, 2004	K.IECDDKGDGSCDVR.Y	1628.67809	2	1.07E-04	0.70	2.63	-	773.0
AHQ-9-3, 2048	K.IECDDKGDGSCDVR.Y	1628.67809	2	4.69E-04	0.85	3.34	-	772.1
gi|21361322|ref|NP_006078.2|	tubulin, beta, 5 [Homo sapiens]			8.92E-09	0.93	10.29	6.10	49585.5
AHQ-9-7, 5021 - 5026	K.FWEVISDEHGIDPTGTYHGDSDLQLER.I	3118.27220	3	8.92E-09	0.93	5.88	-	637.5
gi|4502303|ref|NP_001688.1|	mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m			8.97E-09	2.29	30.18	22.10	23277.2
AHQ-9-11, 5214	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	6.12E-04	0.78	3.41	-	523.2
AHQ-9-11, 3659	K.LVRPPVQVYGIEGR.Y	1583.85942	2	9.02E-04	0.61	2.86	-	286.7
AHQ-9-11, 3334	K.VAASVLNPYVK.R	1161.37549	2	8.97E-09	0.90	3.29	-	802.3
gi|5031973|ref|NP_005733.1|	protein disulfide isomerase-related protein [Homo sapiens]			9.27E-09	2.58	30.17	9.50	48121.0
AHQ-9-7, 4578 - 4652	K.GSFSEQGINEFLR.E	1484.59520	2	2.30E-06	0.82	3.04	-	795.8
AHQ-9-7, 4554	K.LAAVDATVNQVLASR.Y	1528.73579	2	6.07E-06	0.86	3.48	-	869.8
AHQ-9-7, 5673 - 5674	R.TGEAIVDAALSALR.Q	1387.56411	2	9.27E-09	0.90	3.12	-	1524.3
gi|5453740|ref|NP_006462.1|	myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat			1.15E-08	5.43	60.29	27.50	19794.0
AHQ-9-14-, 5171	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	4.32E-06	0.97	5.15	-	1393.3
AHQ-9-14, 5831 - 5833	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.42E-05	0.94	4.49	-	1020.2
AHQ-9-12, 5129	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.12E-04	0.81	3.33	-	496.9
AHQ-9-11, 4994 - 5034	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	3.39E-08	0.92	4.31	-	778.8
AHQ-9-11, 5069 - 5101	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.15E-08	0.97	5.87	-	1284.8
AHQ-9-11, 5154 - 5211	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.25E-04	0.90	4.15	-	667.0
AHQ-9-11, 5581 - 5650	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	7.89E-05	0.97	5.08	-	1496.7
AHQ-9-13, 5306	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	7.90E-08	0.94	4.60	-	923.1
AHQ-9-11, 4345	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	6.08E-06	0.92	3.83	-	1054.7
AHQ-9-11, 5442 - 5463	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	4.08E-06	0.88	3.67	-	1242.2
AHQ-9-14-, 4179	K.GNFNYIEFTR.I	1261.36733	2	4.85E-05	0.80	3.43	-	697.7
AHQ-9-11, 4061	K.GNFNYIEFTR.I	1261.36733	2	1.57E-04	0.88	3.95	-	701.5

AHQ-9-11, 3594	K.KGNFNYIEFTR.I	1389.54025	2	4.24E-08	0.88	2.67	-	1073.0
gi|4557361|ref|NP_001187.1|	BH3 interacting domain death agonist; BH3-interacting domain death agon			1.15E-08	0.96	10.18	6.70	21994.6
AHQ-9-11, 2811	R.IEADSESQEDIIR.N	1505.56635	2	1.15E-08	0.96	3.63	-	2091.2
gi|5729877|ref|NP_006588.1|	heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD			1.19E-08	9.71	110.26	23.80	70897.6
AHQ-9-7, 4268	R.ARFEELNADLFR.G	1481.63768	2	3.30E-08	0.97	5.23	-	1408.1
AHQ-9-6, 4293	R.ARFEELNADLFR.G	1481.63768	3	1.14E-04	0.92	3.93	-	1239.0
AHQ-9-6, 4242 - 4297	R.ARFEELNADLFR.G	1481.63768	2	3.84E-08	0.95	4.32	-	1028.1
AHQ-9-6, 4498 - 4505	R.FEELNADLFR.G	1254.37310	2	1.03E-06	0.93	3.79	-	1166.8
AHQ-9-7, 4477	R.FEELNADLFR.G	1254.37310	2	7.18E-06	0.85	3.36	-	976.3
AHQ-9-6, 4993	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	8.34E-06	0.88	4.28	-	652.0
AHQ-9-6, 3474	K.HWPFM*VVNDAGRPK.V	1670.91910	3	9.14E-05	0.84	3.23	-	1159.0
AHQ-9-6, 5287	K.ILDKCNEIINWLDK.N	1776.04688	2	2.25E-04	0.94	3.78	-	1212.8
AHQ-9-6, 3265	R.M*VNHFIAEFK.R	1252.46696	2	1.87E-05	0.94	3.52	-	1301.7
AHQ-9-6, 3406	K.NQVAMNPTNTVFDAK.R	1650.83816	2	5.86E-04	0.65	2.73	-	391.2
AHQ-9-6, 2265	R.RFDDAVVQSDM*K.H	1427.56543	2	5.59E-05	0.82	2.57	-	737.9
AHQ-9-6, 6125 - 6129	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	1.19E-08	0.93	4.52	-	802.7
AHQ-9-6, 6126	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	3	4.80E-04	0.79	3.07	-	1072.9
AHQ-9-6, 3157	K.SQIHDIVLVGGSTR.I	1482.66712	2	2.79E-08	0.96	3.82	-	1807.7
AHQ-9-6, 4490 - 4569	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	4.32E-04	0.50	2.90	-	197.7
AHQ-9-6, 4365 - 4421	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	1.28E-05	0.85	4.00	-	399.1
gi|4504505|ref|NP_000405.1|	hydroxysteroid (17-beta) dehydrogenase 4 [Homo sapiens]			1.22E-08	0.98	10.22	1.80	79685.9
AHQ-9-5, 3256	R.VVLVTGAGAGLGR.A	1170.38715	2	1.22E-08	0.98	4.49	-	2185.8
gi|4557032|ref|NP_002291.1|	lactate dehydrogenase B [Homo sapiens]			1.24E-08	6.68	80.23	31.70	36638.3
AHQ-9-9, 4232 - 4235	K.FIIPQIVK.Y	958.22198	2	5.09E-04	0.77	2.92	-	657.9
AHQ-9-9, 4471	K.GEMMDLQHGSLFLQTPK.I	1933.24171	2	4.26E-06	0.93	4.27	-	986.0
AHQ-9-9, 6090 - 6167	K.GYTNWAIGLSVADLIESM*LK.N	2198.52454	2	3.16E-06	0.92	4.62	-	690.7
AHQ-9-9, 2475	K.IVVVTAGVR.Q	914.12760	2	2.01E-04	0.81	2.93	-	761.5
AHQ-9-9, 3364 - 3367	K.LIAPVAEEEATVPNNK.I	1695.89534	2	1.10E-04	0.65	2.74	-	479.8
AHQ-9-9, 3613	K.MVVESAYEVIK.L	1268.50463	2	1.24E-08	0.95	3.86	-	1220.5
AHQ-9-9, 3383 - 3445	K.SADTLWDIQK.D	1177.28864	2	1.27E-04	0.69	3.06	-	812.9
AHQ-9-13-, 6161	K.SLADELALVDVLEDK.L	1630.81843	2	2.91E-06	0.96	3.97	-	1649.2
gi|29737978|ref|XP_290747.1|	similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy			1.25E-08	3.74	40.21	1.50	191380.7
AHQ-9-3, 3878 - 3881	K.ADFCIIHYAGK.V	1296.47641	2	5.51E-08	0.96	4.14	-	1383.4
AHQ-9-6, 3842	K.ADFCIIHYAGK.V	1296.47641	2	9.56E-07	0.93	3.08	-	1306.9
AHQ-9-4, 3877	K.ADFCIIHYAGK.V	1296.47641	2	1.36E-05	0.92	3.31	-	1108.0
AHQ-9-2, 3977	K.ADFCIIHYAGK.V	1296.47641	2	5.75E-07	0.96	3.86	-	1457.6
AHQ-9-5, 3879	K.ADFCIIHYAGK.V	1296.47641	2	3.83E-05	0.91	3.36	-	981.2
AHQ-9-3, 3088	R.AGVLAHLEEER.D	1224.34854	2	1.88E-06	0.95	4.22	-	1555.1
AHQ-9-2, 3142	R.AGVLAHLEEER.D	1224.34854	2	5.10E-06	0.94	3.95	-	1455.1
AHQ-9-4, 3058	R.AGVLAHLEEER.D	1224.34854	2	2.75E-06	0.95	4.14	-	1401.1
AHQ-9-5, 3068	R.AGVLAHLEEER.D	1224.34854	2	1.45E-06	0.96	4.14	-	1725.9
AHQ-9-6, 3059 - 3065	R.AGVLAHLEEER.D	1224.34854	2	2.58E-07	0.95	4.18	-	1439.6
AHQ-9-7, 3042	R.AGVLAHLEEER.D	1224.34854	2	6.50E-07	0.85	3.42	-	877.0
AHQ-9-2, 3777	K.DKADFCIIHYAGK.V	1539.73719	3	1.25E-08	0.94	4.06	-	1752.7
AHQ-9-2, 3775	K.DKADFCIIHYAGK.V	1539.73719	2	2.56E-07	0.95	3.70	-	1530.7
AHQ-9-2, 4603	K.LDPHLVLDQLR.C	1319.53460	2	8.82E-05	0.76	2.87	-	594.8
AHQ-9-2, 4613	K.LDPHLVLDQLR.C	1319.53460	3	8.52E-07	0.90	3.58	-	920.1
gi|4758304|ref|NP_004902.1|	protein disulfide isomerase related protein (calcium-binding protein, i			1.29E-08	2.29	30.18	5.70	72931.9
AHQ-9-6, 3710	K.FAM*EPEEFDSDTLR.E	1703.80830	2	1.85E-04	0.46	2.58	-	298.1
AHQ-9-6, 2915 - 2921	K.IDATSASVLASR.F	1191.31686	2	1.29E-08	0.93	3.53	-	1353.3
AHQ-9-6, 3403	K.RFDVSGYPTLK.I	1283.45758	2	2.80E-08	0.91	3.37	-	921.3
gi|24430192|ref|NP_005548.2|	keratin 16; keratin, type I cytoskeletal 16; cytokeratin 16 [Homo sapi			1.32E-08	3.56	40.31	12.30	51267.5
AHQ-9-7, 3897	R.GQTGGDVNVEMDAAPGVDLSR.I	2089.23032	2	3.84E-04	0.76	3.76	-	594.6
AHQ-9-1, 3636 - 3639	R.GQTGGDVNVEM*DAAPGVDLSR.I	2105.22972	2	4.02E-05	0.89	4.31	-	877.9
AHQ-9-1, 5108 - 5111	K.IIAATIENAQPILQIDNAR.L	2065.35950	3	2.73E-07	0.98	6.28	-	2932.4
AHQ-9-1, 5068 - 5110	K.IIAATIENAQPILQIDNAR.L	2065.35950	2	9.17E-04	0.89	3.75	-	840.9
AHQ-9-1, 6379	R.TDLEM*QIEGLKEELAYLR.K	2168.45360	3	1.32E-08	0.93	4.67	-	1088.3
gi|4758984|ref|NP_004654.1|	RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho			1.36E-08	2.59	30.28	15.70	24393.3
AHQ-9-10, 2818	K.AQIWDTAGQER.Y	1275.35241	2	2.96E-04	0.95	3.59	-	1415.1
AHQ-9-14-, 4959	R.GAVGALLVYDIAK.H	1290.53317	2	1.36E-08	0.95	3.41	-	1728.3
AHQ-9-11, 4825 - 4837	R.GAVGALLVYDIAK.H	1290.53317	2	1.73E-07	0.98	5.61	-	1857.0
AHQ-9-10, 4798 - 4814	R.GAVGALLVYDIAK.H	1290.53317	2	2.15E-05	0.86	3.57	-	887.4
AHQ-9-11, 3142 - 3145	K.STIGVEFATR.S	1081.20410	2	3.66E-05	0.69	2.58	-	576.8
gi|4507677|ref|NP_003290.1|	tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu			1.42E-08	6.33	70.26	12.20	92468.2
AHQ-9-4, 2496	K.DISTNYYASQK.K	1290.36061	2	3.25E-05	0.90	3.50	-	781.8
AHQ-9-4, 3224	K.FAFQAEVNR.M	1082.19378	2	6.61E-06	0.90	3.16	-	986.8
AHQ-9-4, 3904	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	1.01E-06	0.96	5.26	-	1657.7
AHQ-9-4, 3896	K.GVVDSDDLPLNVSR.E	1486.60940	2	3.22E-04	0.93	4.04	-	1135.8
AHQ-9-6, 3853	K.GVVDSDDLPLNVSR.E	1486.60940	2	8.24E-04	0.90	3.86	-	913.1
AHQ-9-4, 4733	R.LISLTDENALSGNEELTVK.I	2047.24975	2	3.90E-06	0.82	3.72	-	598.4
AHQ-9-5, 4036	K.SILFVPTSAPR.G	1188.40094	2	4.14E-04	0.86	3.13	-	960.8
AHQ-9-5, 6165 - 6239	K.YSQFINFPIYVWSSK.T	1880.13366	2	1.42E-08	0.97	4.81	-	1485.8
AHQ-9-4, 6228 - 6229	K.YSQFINFPIYVWSSK.T	1880.13366	2	8.64E-07	0.93	4.41	-	792.7
gi|10716563|ref|NP_001737.1|	calnexin [Homo sapiens]			1.51E-08	3.55	40.22	10.10	67567.8
AHQ-9-7, 4661	K.APVPTGEVYFADSFDR.G	1771.90722	2	4.14E-06	0.85	3.18	-	849.7
AHQ-9-5, 4731	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.99E-07	0.93	3.57	-	1372.6
AHQ-9-6, 4615 - 4689	K.APVPTGEVYFADSFDR.G	1771.90722	2	1.30E-05	0.91	3.83	-	988.9
AHQ-9-5, 4353	R.GTLSGWILSK.A	1062.24392	2	2.29E-05	0.83	2.85	-	883.7
AHQ-9-5, 3865	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	2	2.62E-05	0.93	4.40	-	754.9
AHQ-9-5, 5816	R.KIPNPDFFEDLEPFR.M	1865.07739	2	1.51E-08	0.85	3.30	-	584.6
AHQ-9-5, 5804	R.KIPNPDFFEDLEPFR.M	1865.07739	3	4.35E-06	0.93	4.29	-	1706.0
gi|7661818|ref|NP_054900.1|	HSPC159 protein [Homo sapiens]			1.56E-08	1.69	20.23	19.20	19011.6
AHQ-9-11, 6119	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	2.30E-06	0.75	3.55	-	253.0
AHQ-9-13, 6278	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	2.23E-04	0.24	2.53	-	229.6
AHQ-9-13-, 6201	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	6.17E-04	0.80	3.30	-	362.8
AHQ-9-11, 4634 - 4641	R.VFVDGHQLFDFYHR.I	1780.96540	3	1.56E-08	0.94	4.67	-	972.7
gi|5902134|ref|NP_009005.1|	coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin			1.61E-08	3.31	40.28	15.00	51026.0
AHQ-9-7, 2694	R.DGGLICTSCR.D	1141.25805	2	3.31E-04	0.84	2.61	-	894.2
AHQ-9-7, 6164	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	1.61E-08	0.94	5.65	-	554.6
AHQ-9-7, 2466 - 2544	K.LQATVQELQK.R	1158.33000	2	1.29E-04	0.80	3.25	-	615.4
AHQ-9-7, 6240	R.YFEITSEAPFLHYLSM*FSSK.E	2414.71688	2	9.11E-08	0.72	2.81	-	424.5
gi|10863977|ref|NP_067000.1|	LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-			1.74E-08	0.97	10.25	20.00	10834.5
AHQ-9-14-, 5149	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	1.74E-08	0.97	5.01	-	1503.2
AHQ-9-14, 5803	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	1.18E-07	0.87	3.37	-	881.1
gi|24797067|ref|NP_002107.3|	major histocompatibility complex, class I, A precursor; HLA-A1 class I			1.83E-08	2.68	30.21	13.40	40840.5
AHQ-9-8, 3374	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	3	8.88E-07	0.88	4.22	-	788.8
AHQ-9-12, 4714 - 4717	R.FIAVGYVDDTQFVR.F	1630.82504	2	4.34E-04	0.79	2.85	-	931.4
AHQ-9-8, 4759	R.FIAVGYVDDTQFVR.F	1630.82504	2	1.83E-08	0.97	4.26	-	1887.6
AHQ-9-5, 4789	R.FIAVGYVDDTQFVR.F	1630.82504	2	1.85E-05	0.91	3.55	-	928.7
AHQ-9-8, 2270	R.YLENGKETLQR.T	1351.49032	2	7.74E-04	0.83	2.85	-	916.7
gi|4757756|ref|NP_004030.1|	annexin A2; annexin II; annexin II (lipocortin II); calpactin I, heavy			2.00E-08	9.14	110.25	36.30	38603.8
AHQ-9-9, 4224 - 4231	R.AEDGSVIDYELIDQDAR.D	1909.98536	2	1.45E-06	0.89	3.85	-	775.3
AHQ-9-9, 4219	K.ALLYLCGGDD	1098.20835	1	1.20E-06	0.86	3.23	-	737.5
AHQ-9-9, 2963 - 3043	K.LSLEGDHSTPPSAYGSVK.A	1845.98764	2	7.10E-04	0.68	3.35	-	389.3
AHQ-9-9, 3911	R.RAEDGSVIDYELIDQDAR.D	2066.17172	2	1.03E-05	0.92	3.81	-	913.4
AHQ-9-9, 6071 - 6072	K.SALSGHLETVILGLLK.T	1651.97197	2	1.57E-07	0.98	4.90	-	2261.3
AHQ-9-9, 3653 - 3655	K.SLYYYIQQDTK.G	1422.56378	2	3.79E-05	0.94	3.98	-	1412.3

AHQ-9-9, 4993	K.SYSPYDMLESIR.K	1461.62182	2	2.00E-08	0.90	3.24	-	857.8
AHQ-9-9, 4279	K.TDLEKDIISDTSGDFR.K	1812.91282	2	1.98E-06	0.92	4.10	-	958.9
AHQ-9-9, 3952 - 3987	K.TDLEKDIISDTSGDFRK.L	1941.08573	2	5.33E-04	0.68	3.03	-	728.0
AHQ-9-9, 2235 - 2309	R.TNQELQEINR.V	1245.32461	2	5.01E-05	0.85	3.44	-	988.5
AHQ-9-9, 2329	K.TPAQYDASELK.A	1223.31418	2	3.44E-04	0.53	2.68	-	519.5
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				2.03E-08	14.04	160.30	21.30	138070.8
AHQ-9-3, 2457 - 2525	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	3	1.44E-06	0.95	5.23	-	1296.4
AHQ-9-3, 5726 - 5728	K.CTSDM*ETILTFIPQFHR.L	2114.38778	3	1.73E-05	0.81	3.60	-	735.1
AHQ-9-2, 3998	R.DQALQLQVLNSR.F	1385.55144	2	4.13E-08	0.97	4.14	-	1787.6
AHQ-9-4, 3890	R.DQALQLQVLNSR.F	1385.55144	2	6.05E-05	0.90	3.04	-	1338.7
AHQ-9-3, 3817 - 3882	R.DQALQLQVLNSR.F	1385.55144	2	9.53E-08	0.97	4.83	-	1989.3
AHQ-9-2, 5521	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.18E-07	0.90	4.18	-	820.9
AHQ-9-3, 5373	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	1.46E-04	0.52	3.26	-	254.1
AHQ-9-3, 5366 - 5386	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	2.03E-08	0.94	4.43	-	1268.3
AHQ-9-6, 5357	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.14E-04	0.85	3.85	-	705.5
AHQ-9-1, 5727	K.GLTEFVEPIIQIK.T	1487.76518	2	2.93E-06	0.87	3.38	-	963.0
AHQ-9-3, 5545	K.GLTEFVEPIIQIK.T	1487.76518	2	4.71E-04	0.86	3.19	-	952.4
AHQ-9-2, 5706 - 5711	K.GLTEFVEPIIQIK.T	1487.76518	2	2.32E-04	0.86	3.78	-	724.7
AHQ-9-3, 2697	K.GPCGWTGGSCPQR.S	1422.52885	2	1.32E-05	0.89	3.19	-	893.8
AHQ-9-3, 4036	K.GSVVTNERDQALQLQVLNSR.F	2228.45212	3	8.89E-07	0.94	4.19	-	1605.6
AHQ-9-4, 2461	R.GVAEQQQQQGCGDPEVMQK.M	2119.27971	2	1.44E-04	0.77	3.33	-	429.6
AHQ-9-3, 4776	K.IFQNDM*QETVAQLFK.T	1829.06683	2	8.24E-05	0.90	3.51	-	1111.0
AHQ-9-4, 4820	K.IFQNDM*QETVAQLFK.T	1829.06683	2	1.78E-04	0.91	4.11	-	1002.0
AHQ-9-3, 5113	K.KIENLTSAVNSLNFIIK.E	1905.22764	2	9.15E-08	0.91	3.52	-	1041.9
AHQ-9-3, 2944	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	3	7.86E-07	0.97	5.43	-	2124.0
AHQ-9-3, 2946	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	2.27E-05	0.98	5.93	-	1640.6
AHQ-9-2, 5390 - 5449	K.LQNLTLPTNASIKFNPGAESVVLSNSTLK.F	3058.47544	3	7.58E-04	0.60	3.40	-	329.8
AHQ-9-2, 3801	K.LVEENALAPDFSK.G	1433.58810	2	7.84E-05	0.90	3.17	-	1067.2
AHQ-9-4, 6298 - 6300	K.M*SEQLNDLTYDM*EILQPLLEQGASLR.Q	3041.40062	3	5.36E-07	0.90	4.72	-	812.5
AHQ-9-5, 3349 - 3420	K.TVSSLSEDLESTR.Q	1424.49324	2	7.82E-04	0.50	2.77	-	567.2
AHQ-9-2, 3501	K.TVSSLSEDLESTR.Q	1424.49324	2	2.77E-05	0.88	3.34	-	1036.2
AHQ-9-2, 4073	R.YNFVLQVAK.T	1082.27683	2	9.73E-06	0.91	2.84	-	1038.6
AHQ-9-3, 3952	R.YNFVLQVAK.T	1082.27683	2	1.65E-06	0.86	3.11	-	633.5
gi|4507521|ref|NP_001055.1| transketolase [Homo sapiens]				2.05E-08	1.88	20.24	5.00	67877.3
AHQ-9-6, 4417	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	2.05E-08	0.95	4.72	-	860.2
AHQ-9-6, 5467	K.LDNLVAILDINR.L	1369.59192	2	5.26E-05	0.93	3.70	-	1083.1
gi|21361370|ref|NP_002853.2| phosphorylase, glycogen; brain [Homo sapiens]				2.17E-08	2.29	30.19	4.60	96695.3
AHQ-9-5, 3767	R.GLAGLGDVAEVR.K	1157.30210	2	1.43E-07	0.93	3.81	-	1057.8
AHQ-9-5, 5381	K.IVNGWQVEEADDWLR.Y	1830.97790	2	4.28E-04	0.62	2.78	-	580.3
AHQ-9-5, 5497	K.LLPLVSDEVFIR.D	1401.67552	2	2.17E-08	0.74	2.54	-	463.3
gi|27478749|ref|XP_208411.1| similar to L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit				2.27E-08	0.92	10.22	6.10	25628.5
AHQ-9-9, 4339 - 4340	K.GEMMDLQHGSLFLR.T	1634.90537	2	2.27E-08	0.92	4.37	-	821.0
gi|4505641|ref|NP_002583.1| proliferating cell nuclear antigen [Homo sapiens]				2.78E-08	0.80	10.16	7.30	28768.6
AHQ-9-9, 4697 - 4765	R.AEDNADTLALVFEAPNQEK.V	2076.20651	2	2.78E-08	0.80	3.17	-	755.3
gi|4503971|ref|NP_001484.1| GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r				3.15E-08	3.55	50.21	16.10	50582.4
AHQ-9-7, 5206	K.FLVFVANFDENDPK.T	1655.83136	2	1.67E-04	0.66	2.54	-	776.6
AHQ-9-7, 3702 - 3721	R.FQLLEGPPESM*GR.G	1477.66758	2	7.58E-04	0.70	3.13	-	590.6
AHQ-9-7, 2446	R.KQNDVFGEAEQ	1265.31115	2	9.56E-05	0.87	3.03	-	1094.6
AHQ-9-7, 4989	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	3.15E-08	0.86	3.63	-	685.8
AHQ-9-7, 4064	R.TDDYLDQPCLETVNR.I	1840.94632	2	5.50E-04	0.45	2.69	-	323.1
gi|4503327|ref|NP_000389.1| cytochrome b5 reductase membrane-bound isoform; diaphorase (NADH) [Homo				3.24E-08	0.94	20.14	12.30	34234.6
AHQ-9-9, 5095	R.APEAWDYGQGFVNEEMIR.D	2113.29517	2	2.91E-06	0.70	2.86	-	763.5
AHQ-9-9, 4667	K.SVGMIAGGTGITPM*LQVIR.A	1918.31483	2	3.24E-08	0.24	2.59	-	303.1
gi|7657056|ref|NP_055415.1| EH-domain containing 3; EH domain containing 3 [Homo sapiens]				3.46E-08	1.77	20.20	4.10	60886.7
AHQ-9-7, 2388	K.ADQIETQQLM*R.V	1349.49621	2	3.44E-04	0.81	3.17	-	847.8
AHQ-9-7, 4608	K.LFEAEEQDLFR.D	1397.51432	2	3.46E-08	0.96	3.98	-	1909.9
gi|21314617|ref|NP_000433.2| platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e				3.62E-08	4.56	60.21	11.00	82449.6
AHQ-9-5, 5656	R.DQNFVILEFPVEEQDR.V	1979.13566	2	2.52E-05	0.62	3.11	-	494.0
AHQ-9-3, 5589	R.DQNFVILEFPVEEQDR.V	1979.13566	2	4.65E-06	0.38	2.74	-	497.1
AHQ-9-5, 3389 - 3449	K.EDTIVSQTQDFTK.I	1512.60049	2	3.38E-04	0.53	2.79	-	521.1
AHQ-9-4, 4030 - 4033	R.ISYDAQFEVIK.G	1313.48046	2	3.62E-08	0.93	3.48	-	1120.1
AHQ-9-5, 4043 - 4044	R.ISYDAQFEVIK.G	1313.48046	2	3.37E-06	0.91	3.24	-	1225.2
AHQ-9-4, 3174 - 3245	K.SDSGTYICTAGIDK.V	1489.58698	2	1.02E-05	0.96	4.25	-	1636.1
AHQ-9-4, 4016	K.STESYFIPEVR.I	1328.45199	2	4.21E-05	0.84	2.93	-	760.5
AHQ-9-4, 5169 - 5180	K.VIAPVDEVQISILSSK.V	1698.98227	2	9.34E-06	0.92	4.13	-	598.9
gi|13518026|ref|NP_004978.2| LIM and senescent cell antigen-like domains 1 [Homo sapiens]				3.75E-08	1.64	20.20	7.70	37251.2
AHQ-9-11, 4358	K.CHAIIDEQPLIFK.N	1585.84900	2	1.01E-04	0.73	3.06	-	715.5
AHQ-9-11, 3473	R.VIEGDVVSALNK.A	1244.41966	2	3.75E-08	0.91	3.38	-	1000.0
AHQ-9-13-, 3552 - 3616	R.VIEGDVVSALNK.A	1244.41966	2	1.76E-07	0.92	3.21	-	1255.3
AHQ-9-8, 3443	R.VIEGDVVSALNK.A	1244.41966	2	4.05E-06	0.90	3.67	-	792.8
gi|10835187|ref|NP_000627.1| superoxide dismutase 2, mitochondrial [Homo sapiens]				3.89E-08	1.56	20.20	13.10	24733.0
AHQ-9-11, 3739 - 3793	K.GDVTAQIALQPALK.F	1425.65548	2	3.16E-06	0.91	3.99	-	929.1
AHQ-9-11, 3789 - 3855	K.GDVTAQIALQPALK.F	1425.65548	2	1.08E-04	0.81	3.30	-	931.9
AHQ-9-11, 2530	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	3.89E-08	0.64	2.76	-	482.7
gi|5902128|ref|NP_008880.1| syntaxin binding protein 2; Hunc18b [Homo sapiens]				4.00E-08	9.59	110.24	29.80	66438.1
AHQ-9-6, 6298	R.AADPVSPLLHELTFQAM*AYDLLDIEQDTYR.Y	3453.81998	3	9.76E-04	0.91	4.38	-	962.1
AHQ-9-6, 5757 - 5777	K.AAHIFFTDTCPEPLFSELGR.S	2310.57011	3	3.81E-06	0.91	4.69	-	842.8
AHQ-9-6, 5955	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	5.49E-04	0.88	3.50	-	699.5
AHQ-9-6, 3367	R.KGPEDTAQLAHAVLAK.L	1649.87303	3	3.49E-05	0.81	3.48	-	947.7
AHQ-9-6, 3549 - 3618	K.LCSVEQDLAM*GSDAEGEK.I	1957.08386	2	4.00E-08	0.90	3.60	-	1052.0
AHQ-9-6, 6235	K.M*SDILAEGITIVEDINKR.R	2034.32082	3	8.49E-07	0.82	3.55	-	786.9
AHQ-9-6, 6247	K.MSDILAEGITIVEDINKR.R	2018.32142	3	5.56E-04	0.78	3.52	-	1192.7
AHQ-9-6, 3245 - 3246	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	9.26E-07	0.94	4.87	-	656.9
AHQ-9-6, 5127	R.NLWPFVSDPAPTASSQAAVSAR.F	2273.48981	2	8.21E-06	0.77	3.47	-	388.2
AHQ-9-6, 5570	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	5.88E-07	0.94	4.81	-	982.8
AHQ-9-6, 5562 - 5563	R.REPIPSLEAIYLLSPTEK.S	2057.37574	3	1.14E-05	0.61	3.11	-	674.8
AHQ-9-6, 4647	K.WEVLIGSSHILTPTR.F	1709.97007	2	5.73E-06	0.95	4.10	-	1286.9
gi|6598323|ref|NP_001485.2| GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom				4.07E-08	2.68	30.27	11.90	50662.9
AHQ-9-8, 5079	R.NPYYGGESASITPLEDLYK.R	2118.28499	2	4.07E-08	0.91	3.70	-	1112.6
AHQ-9-8, 6220	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	2.38E-05	0.95	4.70	-	876.0
AHQ-9-7, 6125 - 6128	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	3.80E-05	0.97	5.33	-	1044.4
AHQ-9-8, 3947 - 3948	R.TDDYLDQPCYETINR.I	1904.98887	2	1.05E-04	0.82	3.89	-	363.8
gi|4826657|ref|NP_004333.1| caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]				4.55E-08	3.15	40.23	12.30	62662.9
AHQ-9-6, 4643	K.EFDPTITDASLSLPSR.R	1749.89986	2	1.42E-05	0.93	4.36	-	941.4
AHQ-9-6, 2878	K.SAKPTKPAASDLPVPAEGVR.N	1992.26539	3	1.61E-04	0.78	3.30	-	952.8
AHQ-9-6, 3669	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	4.55E-08	0.96	4.68	-	1373.3
AHQ-9-6, 2749	R.YEIEETETVTK.S	1342.43060	2	6.37E-05	0.48	2.97	-	492.0
gi|4502905|ref|NP_001822.1| clusterin; complement-associated protein SP-40 [Homo sapiens]				4.88E-08	1.55	20.19	8.70	52494.3
AHQ-9-9, 2872	R.EILSVDCSTNNPSQAK.L	1764.89299	2	4.88E-08	0.73	3.18	-	697.8
AHQ-9-9, 3347	R.VTTVASHTSDSDVPSGVTEVVVK.L	2315.52008	2	1.27E-04	0.82	3.86	-	449.7
gi|7661678|ref|NP_056461.1| RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B				4.90E-08	3.14	40.26	19.00	20824.7
AHQ-9-11, 3909 - 3967	R.QWNNCAFLESSAK.S	1556.68148	2	4.82E-06	0.48	2.89	-	237.6
AHQ-9-11, 4075 - 4129	R.QWNNCAFLESSAK.S	1556.68148	2	1.16E-04	0.33	2.72	-	209.5
AHQ-9-11, 3765	R.VKDTDDVPMILVGNK.C	1644.91497	2	4.25E-06	0.96	4.43	-	1615.3
AHQ-9-13-, 3426 - 3484	R.VKDTDDVPM*ILVGNK.C	1660.91437	2	7.15E-04	0.77	2.56	-	880.6
AHQ-9-11, 3706 - 3766	R.VKDTDDVPMILVGNK.C	1644.91497	3	2.23E-07	0.93	3.86	-	1645.7
AHQ-9-13, 4232	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	3.62E-04	0.90	3.76	-	1124.2

AHQ-9-11, 4013 - 4074	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	4.90E-08	0.96	5.24	-	2073.5
AHQ-9-13-, 4092 - 4153	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	2.78E-05	0.88	4.10	-	1131.3
AHQ-9-11, 4130 - 4191	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	3.08E-05	0.90	4.35	-	977.8
gi|4504517|ref|NP_001531.1|	heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M			5.08E-08	1.38	20.24	13.20	22782.3
AHQ-9-13-, 4598 - 4664	K.LATQSNEITIPVTFESR.A	1907.11412	2	7.58E-04	0.42	2.64	-	287.4
AHQ-9-11, 4425	R.LFDQAFGLPR.L	1164.33793	2	4.19E-06	0.86	3.01	-	1124.4
AHQ-9-10, 4390	R.LFDQAFGLPR.L	1164.33793	2	5.08E-08	0.96	3.62	-	1737.4
gi|15723376|ref|NP_277050.1|	MacGAP protein [Homo sapiens]			5.42E-08	0.90	10.17	2.10	70163.1
AHQ-9-5, 3315	R.FLSQESGVAQTLK.K	1408.58178	2	5.42E-08	0.90	3.46	-	1084.2
gi|16950601|ref|NP_005956.2|	myosin light chain kinase isoform 6; myosin light chain kinase [Homo s			5.48E-08	1.85	20.17	2.10	110074.8
AHQ-9-5, 3571	K.LVQCVDAFEEK.A	1339.49637	2	2.42E-04	0.93	3.29	-	1255.8
AHQ-9-6, 3490	K.VSDFYDIEER.L	1273.33005	2	1.31E-06	0.79	2.52	-	907.4
AHQ-9-5, 3516	K.VSDFYDIEER.L	1273.33005	2	5.48E-08	0.92	3.38	-	1040.2
gi|4557731|ref|NP_000618.1|	latent transforming growth factor beta binding protein 1 precursor [Hom			5.58E-08	4.40	50.21	6.50	152790.9
AHQ-9-3, 3550	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	5.48E-04	0.95	4.20	-	1441.3
AHQ-9-2, 3647 - 3718	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	4.00E-05	0.91	4.04	-	1164.4
AHQ-9-2, 3257	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	2.96E-04	0.86	3.15	-	755.1
AHQ-9-1, 5554	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	2.03E-04	0.84	3.90	-	481.6
AHQ-9-1, 2906	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	6.78E-06	0.83	3.06	-	913.9
AHQ-9-3, 2737	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.29E-05	0.89	3.67	-	1064.1
AHQ-9-4, 2722	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	2.19E-07	0.83	3.22	-	911.2
AHQ-9-2, 2793	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.52E-04	0.92	3.72	-	1364.9
AHQ-9-6, 2705	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	5.58E-08	0.89	3.11	-	1241.9
AHQ-9-2, 3558	R.YTCICYEGYR.F	1387.51964	2	3.89E-04	0.90	2.94	-	818.9
gi|20149594|ref|NP_031381.2|	heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea			5.61E-08	6.07	70.25	10.60	83263.6
AHQ-9-5, 2524 - 2528	K.EDQTEYLEER.R	1312.32145	2	2.26E-04	0.80	3.01	-	659.4
AHQ-9-4, 3134	R.ELISNASDALDK.I	1276.37539	2	9.50E-04	0.83	3.50	-	506.5
AHQ-9-11, 4149	R.GVVDSEDLPLNISR.E	1514.66275	2	3.70E-04	0.72	2.61	-	696.7
AHQ-9-5, 3979	R.NPDDITQEEYGEFYK.S	1848.90048	2	5.68E-08	0.98	4.97	-	1836.3
AHQ-9-5, 3952	K.SLTNDWEDHLAVK.H	1528.64798	2	2.96E-06	0.88	3.54	-	871.2
AHQ-9-5, 4148	R.TLTLVDTGIGMTK.A	1350.60718	2	5.61E-08	0.93	3.23	-	1244.6
AHQ-9-5, 3709	R.TLTLVDTGIGM*TK.A	1366.60658	2	2.65E-06	0.93	3.51	-	1191.3
gi|5453595|ref|NP_006358.1|	adenylyl cyclase-associated protein [Homo sapiens]			5.79E-08	6.49	80.32	25.10	51672.7
AHQ-9-7, 2832	R.ALLVTASQCQQPAENK.L	1759.96271	2	9.00E-05	0.91	3.72	-	940.9
AHQ-9-7, 5822 - 5877	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	9.58E-05	0.88	4.31	-	863.4
AHQ-9-7, 6404	K.LGLVFDDVVGIVEIINSK.D	1931.26186	2	1.00E-06	0.98	6.42	-	1685.8
AHQ-9-7, 4756 - 4830	K.LSDLLAPISEQIK.E	1427.66814	2	4.64E-04	0.87	3.52	-	767.7
AHQ-9-7, 3361	K.NSLDCEIVSAK.S	1237.36245	2	5.25E-05	0.89	3.33	-	1020.0
AHQ-9-7, 3081	K.NSLDCEIVSAK.S	1237.36245	2	4.58E-07	0.88	3.47	-	785.8
AHQ-9-14-, 3186	K.NSLDCEIVSAK.S	1237.36245	2	5.51E-04	0.83	2.71	-	982.7
AHQ-9-7, 4321	R.SALFAQINQGESITHALK.H	1929.16615	2	6.51E-04	0.79	3.67	-	421.6
AHQ-9-7, 4574	R.SALFAQINQGESITHALK.H	1929.16615	2	7.14E-06	0.68	3.68	-	279.3
AHQ-9-7, 5716	K.SSEM*NVLIPTEGGDFNEFPVPEQFK.T	2829.08749	2	4.07E-05	0.35	2.73	-	135.2
AHQ-9-7, 4052	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.59E-07	0.73	3.20	-	539.2
AHQ-9-8, 4548	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.39E-04	0.90	3.86	-	726.3
AHQ-9-12, 4528	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.58E-04	0.77	3.69	-	428.6
AHQ-9-7, 4620 - 4678	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	5.79E-08	0.94	4.71	-	938.2
AHQ-9-7, 4494 - 4548	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.24E-07	0.96	5.13	-	1186.4
gi|4507231|ref|NP_003134.1|	single-stranded DNA binding protein; single-stranded DNA-binding protei			6.86E-08	1.85	20.20	22.30	17259.5
AHQ-9-13-, 5676	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	1.22E-06	0.92	4.00	-	807.1
AHQ-9-13-, 3238 - 3262	R.SGDSEVYQLGDVSQK.T	1612.67692	2	6.86E-08	0.93	3.99	-	1105.4
AHQ-9-13, 3426 - 3436	R.SGDSEVYQLGDVSQK.T	1612.67692	2	2.47E-07	0.85	3.88	-	584.8
gi|4504515|ref|NP_002146.1|	heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B			6.90E-08	3.62	40.20	8.60	70853.4
AHQ-9-6, 2529	K.ATAGDTHLGGEDFDNR.L	1676.68279	2	3.88E-04	0.85	3.59	-	677.9
AHQ-9-6, 4769 - 4773	R.FEELCSDLFR.S	1317.44926	2	6.90E-08	0.92	3.42	-	1155.1
AHQ-9-6, 4657	R.IINEPTAAAIAYGLDR.R	1688.90603	3	4.90E-06	0.93	4.04	-	1690.8
AHQ-9-6, 4646	R.IINEPTAAAIAYGLDR.R	1688.90603	2	9.17E-06	0.92	3.61	-	1257.2
AHQ-9-6, 4246	K.LLQDFFNGKELNK.S	1566.78249	2	1.36E-05	0.93	4.05	-	1395.2
gi|10835143|ref|NP_000565.1|	decay accelerating factor for complement (CD55, Cromer blood group sys			7.63E-08	0.71	10.15	5.00	41399.9
AHQ-9-5, 4583	R.EIYCPAPPQIDNGIIQGER.D	2172.40385	2	7.63E-08	0.71	2.93	-	654.8
gi|6857820|ref|NP_005019.2|	phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl			7.68E-08	0.79	10.16	3.40	46224.3
AHQ-9-7, 4348	R.FGIDDQDFQNSLTR.S	1656.73462	2	1.08E-05	0.79	3.26	-	766.5
AHQ-9-7, 4149	R.FGIDDQDFQNSLTR.S	1656.73462	2	7.68E-08	0.79	3.27	-	834.2
gi|4758756|ref|NP_004528.1|	nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr			7.73E-08	0.73	10.19	2.80	45373.8
AHQ-9-7, 6248	K.GIPEFWLTVFK.N	1337.58999	2	7.73E-08	0.73	2.75	-	254.3
gi|30150354|ref|XP_301830.1|	similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabili			8.00E-08	1.91	20.27	6.50	29305.3
AHQ-9-9, 4840 - 4851	R.KLFIGGLSFETTDESLR.S	1914.14826	2	9.21E-05	0.93	4.05	-	1189.3
AHQ-9-9, 5243 - 5324	K.LFIGGLSFETTDESLR.S	1785.97534	2	8.00E-08	0.97	5.48	-	1682.7
gi|14211923|ref|NP_115982.1|	PKCI-1-related HIT protein [Homo sapiens]			8.27E-08	1.67	20.18	22.70	17161.6
AHQ-9-13-, 5797	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	8.27E-08	0.78	3.02	-	925.6
AHQ-9-13-, 5752	K.SLPADILYEDQQCLVFR.D	2069.32354	2	3.97E-05	0.89	3.62	-	891.9
gi|30147105|ref|XP_210550.2|	similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48			8.41E-08	0.94	10.21	2.20	61339.9
AHQ-9-5, 4108	K.ADLINNLGTIAK.S	1243.43490	2	1.61E-07	0.94	4.20	-	1035.9
AHQ-9-5, 4457	K.ADLINNLGTIAK.S	1243.43490	2	8.41E-08	0.94	3.89	-	933.6
AHQ-9-5, 3887	K.ADLINNLGTIAK.S	1243.43490	2	2.38E-06	0.77	3.47	-	461.9
gi|30157216|ref|XP_292133.2|	similar to genethonin 1 [Homo sapiens]			8.80E-08	0.81	10.17	4.50	39693.8
AHQ-9-13, 4442	K.TITLEVKPSDTIENVK.A	1788.03268	2	3.62E-05	0.76	2.80	-	669.1
AHQ-9-14, 5139 - 5151	K.TITLEVKPSDTIENVK.A	1788.03268	2	8.80E-08	0.81	3.47	-	472.3
AHQ-9-3, 4285 - 4357	K.TITLEVKPSDTIENVK.A	1788.03268	2	4.92E-04	0.23	2.54	-	202.2
gi|30154095|ref|XP_293967.2|	similar to gamma actin-like protein [Homo sapiens]			8.88E-08	0.37	10.18	12.20	19259.0
AHQ-9-7, 4625	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	3.85E-04	0.32	2.71	-	349.6
AHQ-9-8, 4663	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.26E-05	0.40	2.96	-	329.6
AHQ-9-9, 4476	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.44E-04	0.34	2.83	-	327.1
AHQ-9-11, 4583	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.46E-04	0.31	2.59	-	312.8
AHQ-9-12, 4581 - 4645	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	4.67E-05	0.43	2.88	-	317.1
AHQ-9-13, 4687	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	8.88E-08	0.37	2.80	-	384.3
AHQ-9-13, 4814	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.72E-04	0.30	2.84	-	303.6
AHQ-9-14-, 4534	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.50E-05	0.75	3.61	-	593.7
AHQ-9-14-, 4619 - 4674	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.61E-06	0.67	3.50	-	384.3
gi|4506723|ref|NP_000997.1|	ribosomal protein S3a; 40S ribosomal protein S3a; v-fos transformation			9.15E-08	1.58	20.18	10.20	29944.7
AHQ-9-9, 4335 - 4336	K.ACQSIYPLHDVFVR.K	1706.94633	2	1.05E-05	0.82	3.51	-	539.2
AHQ-9-9, 3928	K.NCLTNFHGMDLTR.D	1580.77122	2	9.15E-08	0.75	2.81	-	850.6
gi|30154839|ref|XP_301540.1|	similar to keratin 8; cytokeratin 8; keratin, type II cytoskeletal 8 [			9.41E-08	0.92	10.18	3.40	39331.0
AHQ-9-4, 4316	K.SLNNKFASFIDK.V	1384.56191	2	3.24E-04	0.74	2.74	-	694.3
AHQ-9-4, 4526	K.SLNNKFASFIDK.V	1384.56191	2	5.36E-06	0.87	3.56	-	751.7
AHQ-9-7, 4361 - 4422	K.SLNNKFASFIDK.V	1384.56191	2	9.41E-08	0.92	3.55	-	1083.4
AHQ-9-9, 4284 - 4285	K.SLNNKFASFIDK.V	1384.56191	1	3.52E-04	0.32	2.54	-	338.2
AHQ-9-13, 4688	K.SLNNKFASFIDK.V	1384.56191	2	6.97E-04	0.67	2.63	-	620.5
AHQ-9-1, 4654 - 4720	K.SLNNKFASFIDK.V	1384.56191	2	1.91E-07	0.79	3.17	-	536.3
gi|4557675|ref|NP_000201.1|	integrin alpha chain, alpha 6 [Homo sapiens]			9.45E-08	3.12	40.21	5.60	119509.5
AHQ-9-10, 4367 - 4373	R.AFIDVTAAAENIR.L	1391.55445	2	5.04E-06	0.84	2.81	-	1056.0
AHQ-9-6, 3341	K.FGSCQQGVAATFTK.D	1503.66172	2	9.45E-08	0.74	2.63	-	602.4
AHQ-9-3, 4969	K.LIATFPDTLTYSAYR.E	1732.95727	2	4.48E-04	0.61	2.71	-	364.0
AHQ-9-3, 4129	K.LRPIPITASVEIQEPSSR.R	1994.28128	2	8.35E-04	0.93	4.12	-	844.6
gi|4507745|ref|NP_003320.1|	thioredoxin [Homo sapiens]			9.49E-08	0.93	10.18	12.40	11693.3
AHQ-9-13-, 3810 - 3865	K.TAFQEALDAAGDK.L	1337.41728	2	1.49E-05	0.88	3.02	-	1216.7
AHQ-9-14-, 3869 - 3870	K.TAFQEALDAAGDK.L	1337.41728	2	9.49E-08	0.93	3.51	-	1389.5

AHQ-9-13, 4002 - 4014	K.TAFQEALDAAGDK.L	1337.41728	2	3.28E-07	0.90	2.94	-	1350.4
gi|5803227|ref|NP_006817.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, theta polype			1.06E-07	0.89	10.18	5.70	27764.1
AHQ-9-10, 2295	K.AVTEQGAELSNEER.N	1533.57979	2	1.06E-07	0.89	3.00	-	1275.6
gi|4502693|ref|NP_001760.1|	CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen			1.12E-07	1.65	20.17	10.10	25415.9
AHQ-9-14-, 3581	K.KDVLETFTVK.S	1180.37558	2	6.59E-04	0.67	2.81	-	614.4
AHQ-9-11, 3425	K.KDVLETFTVK.S	1180.37558	2	2.25E-05	0.86	3.42	-	811.6
AHQ-9-11, 3753	K.SCPDAIKEVFDNK.F	1524.67770	2	1.12E-07	0.79	2.64	-	876.4
gi|30159310|ref|XP_301899.1|	similar to beta-actin [Homo sapiens]			1.13E-07	1.99	30.17	9.60	32376.4
AHQ-9-8, 1698 - 1754	K.DSYVGNEAQSK.R	1198.22158	2	1.77E-05	0.59	2.76	-	595.4
AHQ-9-8, 1672 - 1954	K.DSYVGNEAQSK.R	1198.22158	1	1.13E-07	0.73	2.78	-	468.9
AHQ-9-8, 1836 - 1854	K.DSYVGNEAQSKR.G	1354.40793	2	7.25E-06	0.75	2.75	-	749.6
AHQ-9-12, 4328 - 4385	K.SYKLLDGQVITIGNER.F	1807.04092	2	1.71E-05	0.51	2.90	-	489.0
AHQ-9-8, 4380 - 4395	K.SYKLLDGQVITIGNER.F	1807.04092	2	1.62E-04	0.77	3.41	-	769.9
gi|19557677|ref|NP_002108.3|	major histocompatibility complex, class I, C precursor; HLA class I hi			1.20E-07	1.55	20.18	7.90	40994.6
AHQ-9-8, 4955	R.AYLEGTCVEWLR.R	1498.68507	2	1.20E-07	0.69	2.64	-	806.6
AHQ-9-8, 3316	R.YTCHVQHEGLPEPLTLR.W	2052.29944	3	5.67E-06	0.86	3.61	-	891.9
gi|11321601|ref|NP_002618.1|	phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom			1.25E-07	1.67	20.19	4.20	85595.6
AHQ-9-5, 5527	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	3.24E-05	0.91	3.77	-	781.4
AHQ-9-5, 3869	K.ELVVTQLGYDTR.V	1394.55511	2	1.25E-07	0.76	2.65	-	511.3
gi|21614499|ref|NP_003370.2|	villin 2; Villin-2; cytovillin [Homo sapiens]			1.26E-07	1.49	20.22	1.90	69412.3
AHQ-9-6, 4241	K.APDFVFYAPR.L	1183.33971	2	1.26E-07	0.96	4.46	-	1082.8
AHQ-9-6, 3814	K.KAPDFVFYAPR.L	1311.51262	2	1.26E-04	0.53	2.51	-	543.7
gi|4505839|ref|NP_002645.1|	pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro			1.33E-07	9.54	110.31	29.80	57913.6
AHQ-9-7, 4601 - 4602	K.DPVQEAWAEDVDLR.V	1643.73585	2	3.37E-04	0.56	2.87	-	620.9
AHQ-9-7, 5492	R.EAEAAIYHLQLFEELR.R	1933.15326	2	3.24E-06	0.91	3.83	-	931.7
AHQ-9-7, 6280 - 6292	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	2.63E-06	0.94	4.59	-	978.3
AHQ-9-7, 6282	K.FGVEQDVDM*VFASFIR.K	1877.10995	3	4.69E-07	0.97	5.07	-	1736.5
AHQ-9-7, 4820 - 4833	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	7.74E-06	0.77	3.17	-	739.3
AHQ-9-7, 4304 - 4365	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	4.57E-06	0.93	3.88	-	1316.2
AHQ-9-7, 4493 - 4573	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	4.31E-05	0.91	3.83	-	1086.6
AHQ-9-7, 4020	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	3	2.25E-05	0.94	4.60	-	1464.3
AHQ-9-7, 4017 - 4024	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	5.62E-05	0.97	6.12	-	1206.7
AHQ-9-7, 5336 - 5392	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	1.33E-07	0.95	4.75	-	904.8
AHQ-9-7, 5342 - 5348	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	3	5.80E-04	0.93	4.85	-	1085.5
AHQ-9-7, 5084 - 5144	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	5.03E-05	0.93	4.34	-	764.0
AHQ-9-7, 3360 - 3376	R.LDIDSPPITAR.N	1198.35099	2	4.84E-07	0.95	3.91	-	1391.7
AHQ-9-7, 3380	R.NTGIICTIGPASR.S	1361.54994	2	1.93E-06	0.93	3.95	-	1128.3
AHQ-9-6, 3405	R.NTGIICTIGPASR.S	1361.54994	2	6.78E-06	0.84	3.08	-	1046.1
AHQ-9-7, 4345	R.RFDEILEASDGIM*VAR.G	1839.06325	3	3.12E-07	0.97	5.16	-	2020.7
AHQ-9-7, 3996	R.TATESFASDPILYR.P	1571.71277	2	2.27E-04	0.57	2.66	-	456.0
AHQ-9-7, 5328 - 5384	R.TATESFASDPILYRPVAVALDTK.G	2466.77140	3	5.15E-04	0.85	3.93	-	844.5
gi|4557871|ref|NP_001054.1|	transferrin [Homo sapiens]			1.46E-07	3.26	40.21	7.90	77049.5
AHQ-9-5, 4475	K.DLLFRDDTVCLAK.L	1567.78885	2	3.95E-04	0.84	3.27	-	864.4
AHQ-9-5, 4003	R.FDEFFSEGCAPGSK.K	1579.66868	2	8.36E-06	0.92	3.61	-	1128.1
AHQ-9-5, 3357 - 3416	K.IECVSAETTEDCIAK.I	1728.87748	2	7.82E-04	0.73	2.62	-	539.9
AHQ-9-5, 3204	R.LKCDEWSVNSVGK.I	1523.69293	2	1.46E-07	0.77	3.29	-	576.0
gi|22059949|ref|XP_114617.2|	similar to tubulin, beta 5 [Homo sapiens]			1.48E-07	1.84	20.28	18.80	22810.8
AHQ-9-7, 5016	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	1.48E-07	0.95	5.52	-	1546.5
AHQ-9-7, 2788 - 2864	R.ISVYYNEATGGK.Y	1302.41453	2	5.32E-06	0.89	3.46	-	797.2
gi|5729887|ref|NP_006624.1|	IQ motif containing GTPase activating protein 2 [Homo sapiens]			1.50E-07	2.72	30.24	3.20	180611.0
AHQ-9-4, 4554	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	1.50E-07	0.96	4.11	-	2025.9
AHQ-9-3, 4533	K.LPYDVTTEQALTYPEVK.N	1968.19269	2	4.06E-05	0.97	4.81	-	1748.0
AHQ-9-4, 4029	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	4.18E-04	0.83	3.22	-	791.5
AHQ-9-3, 5350	R.VVAVGYINEAIDEGNPLR.T	1930.15092	2	5.80E-05	0.92	4.08	-	1179.5
gi|4507725|ref|NP_000362.1|	transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum			1.52E-07	4.27	50.31	64.60	15886.9
AHQ-9-13-, 3792 - 3793	K.AADDTWEPFASGK.T	1395.45529	2	1.57E-07	0.94	4.42	-	839.5
AHQ-9-13-, 4449	K.ALGISPFHEHAEVVFTANDSGPR.R	2452.66660	3	2.56E-04	0.79	3.42	-	1064.8
AHQ-9-13-, 4036 - 4109	R.GSPAINVAVHVFR.K	1367.58095	2	1.52E-07	0.87	3.52	-	825.9
AHQ-9-13, 4198 - 4278	R.GSPAINVAVHVFR.K	1367.58095	2	7.59E-04	0.62	2.58	-	559.5
AHQ-9-13-, 5558	R.RYTIAALLSPYSYSTTAVVTNPKE	2646.97608	3	9.88E-04	0.69	3.48	-	515.0
AHQ-9-13-, 5260	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	2.96E-07	0.98	6.22	-	2122.4
gi|21070997|ref|NP_003147.2|	stromal interaction molecule 1 precursor [Homo sapiens]			1.52E-07	0.94	10.17	1.50	77422.9
AHQ-9-6, 2894 - 2901	K.YAEEELEQVR.E	1266.33905	2	1.52E-07	0.94	3.50	-	1556.6
gi|4502491|ref|NP_001203.1|	complement component 1, q subcomponent binding protein precursor; hyalu			1.62E-07	1.83	20.20	12.10	31362.0
AHQ-9-9, 4975	K.AFVDFLSDEIKEER.K	1698.85455	3	1.08E-06	0.82	3.27	-	638.2
AHQ-9-9, 4961 - 4967	K.AFVDFLSDEIKEER.K	1698.85455	2	1.62E-07	0.91	3.33	-	1266.3
AHQ-9-9, 5271	K.VEEQEPELTSTPNFVVEVIK.N	2288.53624	2	2.44E-05	0.92	3.91	-	838.0
gi|30160191|ref|XP_294035.2|	similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme			1.67E-07	0.96	10.23	2.80	50222.2
AHQ-9-7, 4812	K.IYVDDGLISLQVK.Q	1463.70048	2	1.67E-07	0.96	4.54	-	1487.7
gi|27498332|ref|XP_212565.1|	similar to tubulin, beta 5 [Homo sapiens]			1.67E-07	3.18	40.22	6.50	49670.5
AHQ-9-7, 3730 - 3793	R.IMNTFSVVPSPK.V	1320.58277	2	1.83E-05	0.96	3.85	-	2022.6
AHQ-9-8, 3367	R.IM*NTFSVVPSPK.V	1336.58217	2	1.11E-05	0.89	3.26	-	1044.8
AHQ-9-7, 3282 - 3362	R.IM*NTFSVVPSPK.V	1336.58217	2	6.73E-06	0.42	2.82	-	513.9
AHQ-9-7, 6078	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	8.49E-05	0.92	4.09	-	828.9
AHQ-9-7, 5850	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	9.26E-07	0.92	4.23	-	832.7
AHQ-9-12, 6010 - 6086	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	6.46E-07	0.84	3.51	-	621.8
AHQ-9-8, 5940	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	7.52E-06	0.86	3.30	-	669.9
AHQ-9-13-, 6138	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.67E-07	0.94	3.98	-	988.3
AHQ-9-7, 4312	R.YLTVAAVFR.G	1040.23994	2	1.24E-04	0.86	2.72	-	852.2
gi|11968045|ref|NP_071934.1|	hypothetical protein FLJ22056 [Homo sapiens]			1.78E-07	0.87	10.19	9.50	36010.3
AHQ-9-11, 3665	R.GARPPAAGPGGDEDEDEEDTAPESALDTSLDK.S	3214.22226	3	1.78E-07	0.87	3.84	-	799.6
gi|23503239|ref|NP_699160.1|	hypothetical protein MGC10204 [Homo sapiens]			1.97E-07	0.71	10.17	2.00	85113.0
AHQ-9-5, 4039	R.AWDQEAEGAGPELGLR.V	1699.80263	2	1.97E-07	0.71	3.32	-	813.7
gi|25453472|ref|NP_001951.2|	eukaryotic translation elongation factor 1 delta isoform 2; guanine nu			2.01E-07	4.16	50.20	26.70	31121.6
AHQ-9-9, 2881	R.FYEQMNGPVAGASR.Q	1527.68672	2	5.38E-04	0.60	2.60	-	402.4
AHQ-9-9, 4604	R.GVVQELQQAISK.L	1300.48645	2	2.01E-07	0.94	3.78	-	1237.8
AHQ-9-9, 3067	R.IASLEVENQSLR.G	1359.51076	2	1.26E-05	0.87	3.03	-	972.4
AHQ-9-9, 4675 - 4705	R.SIQLDGLVWGASK.L	1374.56703	2	4.35E-05	0.92	3.63	-	1081.8
AHQ-9-9, 2653 - 2659	K.SLAGSSGPGASSGTSGDHGELVVR.I	2186.28259	2	8.77E-05	0.82	3.92	-	594.7
gi|4557801|ref|NP_000261.1|	purine nucleoside phosphorylase [Homo sapiens]			2.01E-07	3.18	40.23	16.30	32147.7
AHQ-9-9, 3769	K.HRPQVAIICGSGLGGLTDK.L	1981.26589	3	8.41E-04	0.96	4.50	-	2247.4
AHQ-9-9, 4509	K.LGADAVGMSTVPEVIVAR.H	1786.08666	2	3.58E-05	0.40	2.50	-	414.4
AHQ-9-13-, 4090 - 4118	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	6.33E-05	0.53	2.67	-	436.7
AHQ-9-13, 4276	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	2.33E-05	0.89	3.90	-	606.7
AHQ-9-9, 3919	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	9.83E-06	0.95	4.21	-	1126.6
AHQ-9-9, 4607	R.VFGFSLITNK.V	1126.32960	2	2.01E-07	0.88	3.07	-	667.1
gi|7705296|ref|NP_057271.1|	bridging integrator 2; bridging integrator-2; breast cancer associated			2.11E-07	2.80	40.18	12.10	61746.8
AHQ-9-7, 5566	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	7.47E-05	0.78	3.18	-	558.0
AHQ-9-5, 5648	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	2.11E-07	0.84	3.64	-	659.0
AHQ-9-7, 2882	R.FEQSASNFYQQQAEGHK.L	2000.07352	3	1.39E-05	0.70	3.13	-	584.8
AHQ-9-6, 6077	R.IGCYVTIFQNISNLR.D	1800.07167	2	2.21E-04	0.70	3.19	-	524.1
AHQ-9-5, 6163	R.IGCYVTIFQNISNLR.D	1800.07167	2	3.61E-06	0.82	3.50	-	595.9
AHQ-9-7, 4060	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	7.22E-06	0.44	2.80	-	409.0
gi|15431310|ref|NP_000517.2|	keratin 14; cytokeratin 14 [Homo sapiens]			2.24E-07	4.25	50.23	13.30	51621.2
AHQ-9-5, 2908	R.ALEEANADLEVK.I	1302.41284	2	5.91E-05	0.77	2.62	-	873.1
AHQ-9-1, 3090	R.ALEEANADLEVK.I	1302.41284	2	1.46E-06	0.95	4.09	-	1520.6
AHQ-9-3, 2652	R.APSTYGGGLSVSSSR.F	1426.51406	2	2.41E-06	0.92	3.16	-	1110.1

AHQ-9-7, 2742 - 2758	K.ASLENSLEETK.G	1221.29659	2	2.19E-05	0.60	2.88	-	487.2
AHQ-9-1, 3859	R.GQVGGDVNVEM*DAAPGVDLSR.I	2103.25697	2	1.74E-05	0.89	4.56	-	346.7
AHQ-9-2, 5329	K.ILTATVDNANVLLQIDNAR.L	2055.32148	2	1.47E-04	0.78	3.12	-	892.8
AHQ-9-1, 5356	K.ILTATVDNANVLLQIDNAR.L	2055.32148	2	2.24E-07	0.89	3.73	-	1012.1
AHQ-9-1, 5354	K.ILTATVDNANVLLQIDNAR.L	2055.32148	3	9.05E-05	0.95	4.53	-	1973.9
gi|30149555|ref|XP_301154.1| similar to heat shock protein 86 [Homo sapiens]				2.37E-07	0.90	10.22	10.60	15781.6
AHQ-9-5, 5548 - 5555	K.HSQFIGYPITLFVEK.E	1780.05877	3	2.37E-07	0.90	4.20	-	866.2
gi|5453599|ref|NP_006127.1| capping protein (actin filament) muscle Z-line, alpha 2; F-actin cappin				2.40E-07	0.64	10.13	5.20	32948.9
AHQ-9-9, 4863 - 4864	K.FTITPSTTQVVGILK.I	1605.90007	2	2.40E-07	0.64	2.62	-	393.0
gi|5453603|ref|NP_006422.1| chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c				2.48E-07	1.62	20.17	6.40	57487.9
AHQ-9-7, 3180	R.EALLSSAVDHGSDEVK.F	1657.76083	2	2.48E-07	0.84	3.32	-	885.9
AHQ-9-7, 5630 - 5644	K.LGGSLADSYLDEGFLLDK.K	1914.10189	2	7.15E-04	0.78	3.07	-	678.2
gi|4504557|ref|NP_000864.1| intercellular adhesion molecule 2 precursor [Homo sapiens]				2.62E-07	0.92	10.21	5.80	30653.1
AHQ-9-7, 6348 - 6413	R.VPTVEPLDSLTLFLFR.G	1848.17455	2	2.62E-07	0.92	4.20	-	593.9
gi|20539300|ref|XP_088391.4| similar to tropomyosin 4 [Homo sapiens]				2.94E-07	1.89	20.20	6.90	18592.1
AHQ-9-9, 3477	R.KLVILEGELER.A	1299.54160	3	1.26E-04	0.85	3.19	-	1118.2
AHQ-9-9, 3467 - 3523	R.KLVILEGELER.A	1299.54160	2	5.82E-06	0.95	3.95	-	1444.4
AHQ-9-9, 3793	K.LVILEGELER.A	1171.36868	2	2.94E-07	0.94	3.58	-	1518.2
gi|9845255|ref|NP_000574.1| group-specific component (vitamin D binding protein); hDBP [Homo sapien				3.01E-07	0.88	10.17	4.60	53049.5
AHQ-9-6, 6394	K.VPTADLEDVLPLAEDITNILSK.C	2367.67804	3	3.01E-07	0.88	3.48	-	982.5
gi|4557385|ref|NP_000055.1| complement component 3 precursor; acylation-stimulating protein cleavag				3.06E-07	1.87	20.25	2.30	187162.3
AHQ-9-6, 5534	K.EYVLPSFEVIVEPTEK.F	1880.12704	2	7.59E-05	0.90	3.58	-	790.5
AHQ-9-6, 4353	R.VPVAVQGEDTVQSLTQGDGVAK.L	2199.40432	2	3.06E-07	0.97	4.94	-	1488.8
gi|4503531|ref|NP_001958.1| eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens] [				3.09E-07	1.58	20.18	7.40	46393.9
AHQ-9-8, 3610	R.GIYAYGFEKPSAIQQR.A	1829.04828	2	3.09E-07	0.88	3.69	-	689.2
AHQ-9-8, 2858	K.GYDVIAQAQSGTGK.T	1395.49996	2	3.35E-05	0.70	2.57	-	888.2
gi|30147623|ref|XP_293669.2| similar to actinin, alpha 4 [Homo sapiens]				3.34E-07	0.93	10.23	3.50	57794.4
AHQ-9-4, 3949 - 3962	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	3.34E-07	0.93	4.55	-	988.7
gi|4885183|ref|NP_005210.1| diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS				3.51E-07	0.77	10.16	1.00	138977.7
AHQ-9-3, 5461	K.TAQNLSIFLGSFR.M	1454.65537	2	3.51E-07	0.77	3.16	-	636.4
gi|10834976|ref|NP_000572.1| glutathione peroxidase 1 [Homo sapiens]				3.54E-07	1.57	20.20	14.90	21909.0
AHQ-9-11, 5153 - 5155	K.CEVNGAGAHPLFAFLR.E	1760.99723	2	3.54E-07	0.87	3.54	-	780.6
AHQ-9-11, 3826	R.PLAGGEPVSLGSLR.G	1353.54935	2	7.36E-04	0.70	3.07	-	712.1
gi|29742827|ref|XP_294099.1| similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]				3.58E-07	1.65	20.20	14.20	17094.0
AHQ-9-11, 3013	K.EAFNMIDQNR.D	1238.35558	2	1.54E-04	0.73	2.80	-	618.8
AHQ-9-11, 3542	R.FTDEEVDELYR.E	1416.47127	2	3.89E-06	0.93	3.07	-	1357.9
AHQ-9-11, 3721	R.FTDEEVDELYR.E	1416.47127	2	1.61E-06	0.96	3.85	-	1602.1
AHQ-9-11, 3735	R.FTDEEVDELYR.E	1416.47127	1	5.37E-05	0.50	2.39	-	427.3
AHQ-9-12, 3765 - 3776	R.FTDEEVDELYR.E	1416.47127	2	1.02E-05	0.96	3.85	-	1623.9
AHQ-9-13, 3986	R.FTDEEVDELYR.E	1416.47127	2	3.02E-06	0.85	2.68	-	1078.0
AHQ-9-14, 4715 - 4721	R.FTDEEVDELYR.E	1416.47127	2	1.21E-05	0.95	3.99	-	1472.9
AHQ-9-13-, 3834 - 3904	R.FTDEEVDELYR.E	1416.47127	2	5.56E-07	0.93	3.16	-	1660.8
AHQ-9-14-, 3854	R.FTDEEVDELYR.E	1416.47127	2	3.58E-07	0.92	3.59	-	995.4
gi|4504073|ref|NP_000398.1| glycoprotein Ib beta polypeptide precursor [Homo sapiens]				3.60E-07	2.41	30.22	15.50	21717.6
AHQ-9-6, 4487 - 4499	R.LLPYLAEDELR.A	1332.52691	2	3.60E-07	0.86	3.23	-	542.5
AHQ-9-13-, 4542	R.LLPYLAEDELR.A	1332.52691	2	4.67E-06	0.84	3.24	-	571.0
AHQ-9-13, 4710 - 4714	R.LLPYLAEDELR.A	1332.52691	2	8.03E-06	0.76	2.57	-	535.8
AHQ-9-11, 4433 - 4434	R.LLPYLAEDELR.A	1332.52691	2	6.48E-06	0.83	2.94	-	561.2
AHQ-9-2, 4667	R.LLPYLAEDELR.A	1332.52691	2	8.10E-06	0.81	2.98	-	495.2
AHQ-9-11, 4133 - 4134	R.LSLTDPLVAER.A	1214.39356	2	4.47E-05	0.96	4.33	-	1353.0
AHQ-9-11, 2499 - 2502	R.TAHLGANPWR.C	1123.24913	2	4.11E-05	0.59	2.74	-	431.1
gi|6005854|ref|NP_009204.1| repressor of estrogen receptor activity; B-cell associated protein [Hom				3.81E-07	1.35	20.24	9.70	33296.1
AHQ-9-9, 3979 - 3980	K.LLLGAGAVAYGVR.E	1260.51029	2	3.81E-07	0.98	4.71	-	2949.1
AHQ-9-9, 3296	R.VLSRPNAQELPSMYQR.L	1890.15666	2	6.51E-04	0.37	2.76	-	324.0
gi|4505877|ref|NP_000436.1| plectin 1, intermediate filament binding protein 500kDa; plectin 1, int				4.45E-07	4.97	60.18	2.30	518488.0
AHQ-9-2, 4917 - 4942	R.APVPASELLASGVLSR.A	1567.81193	2	1.11E-06	0.89	3.58	-	727.8
AHQ-9-2, 3271	K.AYSDPSTGEPATYGELQQR.C	2071.14682	2	5.11E-07	0.87	3.40	-	589.9
AHQ-9-1, 5686	K.EQELQQTLQQEQSVLDQLR.G	2314.49541	3	7.52E-04	0.80	3.16	-	914.8
AHQ-9-3, 5076	R.IISLETYNLLR.E	1335.57394	2	8.62E-04	0.85	3.29	-	762.0
AHQ-9-1, 6159	K.SEEM*QTVQQEQLLQETQALQQSFLSEK.D	3198.46199	3	4.45E-07	0.89	3.51	-	1265.6
AHQ-9-2, 4643	R.SLVPAAELLESR.V	1285.47179	2	3.37E-05	0.66	2.80	-	436.5
gi|12025678|ref|NP_004915.2| actinin, alpha 4 [Homo sapiens]				4.64E-07	3.26	40.20	7.40	104853.3
AHQ-9-4, 4469	R.ETTDTDTADQVIASFK.V	1742.81936	2	4.64E-07	0.91	3.59	-	1127.1
AHQ-9-4, 2992 - 3053	K.GISQEQMQEFR.A	1353.48658	2	6.70E-06	0.62	3.05	-	716.9
AHQ-9-4, 4604	K.ICDQWDALGSLTHSR.R	1760.90926	2	1.66E-05	0.87	3.94	-	712.9
AHQ-9-6, 5902 - 5963	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	2.05E-04	0.87	3.92	-	695.0
gi|21464101|ref|NP_036611.2| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein				4.90E-07	0.80	10.20	5.70	28302.4
AHQ-9-11, 3078	K.NVTELNEPLSNEER.N	1644.72215	2	4.90E-07	0.80	2.75	-	752.4
AHQ-9-14-, 3174	K.NVTELNEPLSNEER.N	1644.72215	2	3.15E-06	0.93	4.07	-	928.0
AHQ-9-10, 3025 - 3026	K.NVTELNEPLSNEER.N	1644.72215	2	6.04E-05	0.78	3.62	-	465.1
gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre				5.30E-07	3.57	40.23	15.30	48141.1
AHQ-9-7, 5085 - 5141	R.FYALSASFEPFSNK.G	1608.77470	2	4.98E-04	0.93	3.69	-	1253.3
AHQ-9-7, 2277	K.HEQNIDCGGGYVK.L	1478.56912	2	5.24E-04	0.91	3.76	-	794.7
AHQ-9-7, 4886 - 4957	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	1.14E-05	0.79	3.53	-	1083.2
AHQ-9-7, 2560	K.IKDPDASKPEDWDER.A	1801.89783	2	5.30E-07	0.94	4.09	-	1074.9
gi|4502107|ref|NP_001145.1| annexin V; endonexin II; anchorin CII; lipocortin V; placental anticoag				5.49E-07	1.72	20.20	6.90	35936.5
AHQ-9-9, 5785	R.DLLDDLKSELTGK.F	1447.61309	2	5.49E-07	0.85	3.01	-	934.3
AHQ-9-9, 4427	R.SEIDLFNIR.K	1107.24155	2	6.38E-05	0.88	3.03	-	1080.7
gi|20070125|ref|NP_000909.2| prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke				5.64E-07	2.67	30.26	11.40	57115.9
AHQ-9-7, 6289 - 6354	R.TGPAATTLPDGAAAESLVESSEVAVIGFFK.D	2937.24716	3	5.64E-07	0.93	5.28	-	1148.2
AHQ-9-7, 3672	K.VDATEESDLAQQYGVR.G	1781.85882	2	1.53E-05	0.89	3.65	-	1068.3
AHQ-9-7, 3980	K.YQLDKDGVVLFK.K	1425.65394	2	1.49E-06	0.85	3.16	-	1183.4
gi|30149221|ref|XP_291446.2| similar to Heat shock cognate 71 kDa protein [Homo sapiens]				5.68E-07	0.88	10.20	3.90	45688.5
AHQ-9-6, 2507	R.STAGDTHLGGEDFDNR.M	1692.68222	2	5.68E-07	0.88	3.91	-	678.0
gi|9507215|ref|NP_061816.1| tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]				5.72E-07	1.85	30.22	9.60	50093.2
AHQ-9-14-, 4713 - 4722	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	1.50E-05	0.95	4.46	-	1177.4
AHQ-9-12, 3501	K.DVNVAIAAIK.T	1014.20080	1	8.54E-04	0.30	2.01	-	577.3
AHQ-9-14-, 5027	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	5.72E-07	0.61	2.71	-	405.0
AHQ-9-13-, 5022	K.INDDDSFTTFFSETGNGK.H	1996.03358	2	3.18E-04	0.51	2.62	-	344.5
gi|4505667|ref|NP_001074.1| phosphodiesterase 5A isoform 1; cGMP-binding cGMP-specific 3',5'-cyclic				5.86E-07	0.94	10.22	1.70	100012.4
AHQ-9-5, 5247	R.IAELVATEFFDQGDR.E	1711.85332	2	5.86E-07	0.94	4.36	-	1012.2
AHQ-9-4, 5238	R.IAELVATEFFDQGDR.E	1711.85332	2	8.83E-07	0.93	4.12	-	880.9
gi|18570595|ref|XP_095590.1| similar to myosin regulatory light chain [Homo sapiens]				6.26E-07	0.94	10.20	8.90	13951.5
AHQ-9-13, 3346	K.LNGTDPEDVIR.H	1229.32195	2	2.03E-06	0.89	3.41	-	786.5
AHQ-9-13-, 3172	K.LNGTDPEDVIR.H	1229.32195	2	6.26E-07	0.94	3.66	-	1311.6
AHQ-9-11, 3045 - 3106	K.LNGTDPEDVIR.H	1229.32195	2	9.27E-07	0.94	3.97	-	1012.7
gi|4885423|ref|NP_005454.1| heterogeneous nuclear ribonucleoprotein D-like; A+U-rich element RNA bi				6.39E-07	0.87	10.16	2.40	46437.2
AHQ-9-9, 3191	R.FGEVVDCTIK.T	1169.32971	2	6.39E-07	0.87	2.86	-	820.6
gi|4506077|ref|NP_002734.1| protein kinase C substrate 80K-H; glucosidase II, beta subunit; AGE-bin				7.12E-07	1.49	20.13	4.40	59296.0
AHQ-9-5, 3271	K.AQQEQELAADAFK.E	1449.54763	2	7.12E-07	0.87	2.59	-	1329.5
AHQ-9-5, 3432	K.LWEEQLAAAK.A	1159.31646	2	3.49E-05	0.63	2.59	-	499.1
gi|30150022|ref|XP_300862.1| similar to beta-tubulin 4Q [Homo sapiens]				7.60E-07	3.50	40.21	11.30	33545.2
AHQ-9-7, 3341 - 3396	R.FPGQLNADLR.K	1131.26634	2	5.53E-05	0.88	3.16	-	909.6
AHQ-9-13-, 3853	K.LAVNM*VPFPR.L	1160.41420	2	3.72E-04	0.86	2.50	-	1113.5
AHQ-9-8, 4367	K.LAVNMVPFPR.L	1144.41480	2	3.32E-04	0.44	2.57	-	348.9
AHQ-9-9, 4164 - 4177	K.LAVNMVPFPR.L	1144.41480	2	7.11E-06	0.82	2.80	-	653.2
AHQ-9-7, 4316	K.LAVNMVPFPR.L	1144.41480	2	2.31E-05	0.90	3.29	-	774.6

AHQ-9-9, 5299 - 5308	R.LHFFMPGFAPLTSR.G	1621.92962	2	7.60E-07	0.93	4.23	-	736.0
AHQ-9-7, 5433 - 5494	R.LHFFMPGFAPLTSR.G	1621.92962	2	2.41E-04	0.93	3.87	-	815.0
gi|6005846|ref|NP_009215.1|	PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro			8.08E-07	2.53	30.17	10.30	39547.7
AHQ-9-12, 6040	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	8.08E-07	0.85	3.19	-	579.8
AHQ-9-11, 4023 - 4034	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	3	5.07E-04	0.75	3.22	-	876.6
AHQ-9-12, 4484 - 4485	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	1.57E-04	0.92	3.36	-	1619.1
gi|4504077|ref|NP_000165.1|	glycoprotein IX (platelet) [Homo sapiens]			8.38E-07	3.56	40.18	30.50	19046.0
AHQ-9-11, 3997 - 4053	R.ALETM*GLWVDCR.G	1468.68075	2	5.33E-04	0.91	3.07	-	1155.0
AHQ-9-11, 2777	R.CASPSLAAHGPLGR.L	1395.56962	2	8.38E-07	0.84	2.80	-	948.5
AHQ-9-11, 3477	R.GHGLTALPALPAR.T	1274.49706	2	5.37E-04	0.89	3.28	-	798.9
AHQ-9-11, 5118	R.LWLEDRTPEALLQVR.C	1840.11574	3	1.95E-05	0.92	3.55	-	1149.8
gi|17986260|ref|NP_524147.1|	smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo			8.61E-07	0.80	10.21	23.30	12969.7
AHQ-9-13-, 5254	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	8.61E-07	0.80	4.02	-	729.0
AHQ-9-14-, 5261	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	9.20E-05	0.88	4.17	-	818.8
AHQ-9-13, 5392 - 5398	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	8.21E-06	0.81	3.95	-	635.4
gi|4758606|ref|NP_004508.1|	integrin-linked kinase [Homo sapiens]			8.62E-07	5.82	70.20	13.90	51418.9
AHQ-9-7, 4108 - 4110	R.EVPFADLSNM*EIGM*K.V	1713.95438	2	1.43E-05	0.59	2.99	-	350.8
AHQ-9-7, 5285	K.FDMIVPILEK.M	1205.49168	2	1.88E-05	0.88	3.50	-	728.2
AHQ-9-7, 4317	K.FDM*IVPILEK.M	1221.49108	2	8.62E-07	0.82	2.84	-	911.3
AHQ-9-7, 4974	R.GM*AFLHTLEPLIPR.H	1611.93301	3	2.64E-06	0.78	3.19	-	907.4
AHQ-9-7, 5557	R.GMAFLHTLEPLIPR.H	1595.93361	2	1.05E-04	0.94	4.01	-	1160.5
AHQ-9-7, 4142	R.M*YAPAWVAPEALQK.K	1591.85542	2	5.30E-04	0.91	3.32	-	822.9
AHQ-9-7, 4090	R.SAVVEMLIM*R.G	1165.45256	2	7.40E-06	0.90	3.34	-	1069.9
gi|4759082|ref|NP_004648.1|	serum deprivation response protein; serum deprivation response; phospha			8.93E-07	2.24	30.22	11.10	47172.9
AHQ-9-6, 5798 - 5835	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.77E-04	0.92	4.31	-	868.6
AHQ-9-7, 5789 - 5825	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	3.00E-06	0.93	3.88	-	1187.2
AHQ-9-9, 5635 - 5692	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	9.47E-04	0.93	4.32	-	911.7
AHQ-9-12, 5800 - 5841	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.73E-04	0.92	3.54	-	1194.4
AHQ-9-11, 5713 - 5779	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	1.27E-06	0.96	3.76	-	2047.7
AHQ-9-13-, 5877	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.50E-05	0.88	3.45	-	945.3
AHQ-9-11, 3585 - 3654	K.LVNMLDAVQENQHK.M	1639.85851	2	1.66E-06	0.75	3.00	-	636.3
AHQ-9-11, 3587	K.LVNMLDAVQENQHK.M	1639.85851	3	8.93E-07	0.71	3.23	-	458.5
AHQ-9-11, 5597	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.43E-05	0.56	2.93	-	367.0
AHQ-9-12, 5652 - 5656	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.02E-05	0.88	3.87	-	648.8
AHQ-9-14-, 5707	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	6.21E-05	0.62	2.62	-	526.7
gi|16933567|ref|NP_005361.2|	mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]			9.05E-07	0.96	10.21	6.80	23668.1
AHQ-9-11, 5403 - 5479	K.ANINVENAFFTLAR.D	1580.76926	2	9.05E-07	0.96	4.11	-	1606.2
gi|27481160|ref|XP_208217.1|	similar to elongation factor 1 alpha [Homo sapiens]			9.36E-07	0.84	10.14	2.60	50171.6
AHQ-9-9, 3291	K.YYVTIIDAPGHR.D	1405.58282	2	9.36E-07	0.84	2.78	-	995.2
gi|4757714|ref|NP_004291.1|	acid phosphatase 1 isoform c; acid phosphatase of erythrocyte; red cell			9.42E-07	0.92	10.15	5.70	18042.4
AHQ-9-11, 3343	R.SPIAEAVFR.K	990.13779	2	9.42E-07	0.92	2.97	-	1145.4
gi|14251209|ref|NP_001279.2|	chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo			9.55E-07	2.72	30.27	21.60	26922.5
AHQ-9-9, 5208 - 5216	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	3	9.55E-07	0.94	4.63	-	1406.2
AHQ-9-13, 3627	K.GVTFNVTTVDTK.R	1282.42476	2	7.33E-06	0.91	3.34	-	1213.6
AHQ-9-13-, 3402 - 3462	K.GVTFNVTTVDTK.R	1282.42476	2	1.67E-05	0.94	4.07	-	1110.4
AHQ-9-11, 5026 - 5105	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	8.76E-05	0.67	3.08	-	371.8
AHQ-9-13-, 5184	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.70E-06	0.86	3.56	-	602.8
AHQ-9-14-, 5105 - 5122	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.54E-05	0.94	4.40	-	954.4
AHQ-9-9, 4907 - 4908	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.11E-04	0.95	5.42	-	695.6
gi|5031573|ref|NP_005712.1|	ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye			1.00E-06	2.41	30.20	11.70	47370.9
AHQ-9-8, 6418	R.DITYFIQQLLR.D	1410.64250	2	1.00E-06	0.94	3.76	-	1333.5
AHQ-9-8, 3031	R.DREVGIPPEQSLETAK.A	1769.93431	2	8.94E-04	0.91	3.94	-	734.2
AHQ-9-8, 5484 - 5556	K.GVDDLDFFIGDEAIEKPTYATK.W	2445.66268	2	4.85E-05	0.55	2.90	-	577.4
gi|5031597|ref|NP_005710.1|	actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub			1.01E-06	1.67	20.17	9.00	20546.5
AHQ-9-11, 5958 - 5981	K.DTDIVDEAIYYFK.A	1592.72721	2	3.47E-04	0.93	3.29	-	1183.6
AHQ-9-14-, 6103	K.DTDIVDEAIYYFK.A	1592.72721	2	1.01E-06	0.91	3.31	-	1209.0
AHQ-9-11, 5541	R.ETKDTDIVDEAIYYFK.A	1951.11899	2	2.33E-05	0.76	2.74	-	716.7
gi|10835002|ref|NP_001166.1|	Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]			1.02E-06	2.45	30.19	27.90	22987.8
AHQ-9-10, 2496	K.APEPHVEEDDDDELDSK.L	1940.90995	2	1.02E-06	0.77	3.04	-	610.6
AHQ-9-10, 5194	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	2.12E-04	0.85	3.88	-	795.7
AHQ-9-11, 5217	K.ATFM*VGSYGPRPEEYEFLTPVEEAPK.G	2962.27864	3	1.27E-04	0.86	3.58	-	917.3
AHQ-9-10, 3314 - 3370	K.TLLGDGPVVTDPK.A	1312.49400	2	6.80E-04	0.82	2.97	-	1000.8
gi|4557435|ref|NP_001242.1|	CD68 antigen; Macrophage antigen CD68 (microsialin); macrosialin; scave			1.10E-06	0.89	10.21	6.20	37408.0
AHQ-9-5, 4476	R.LQAAQLPHTGVFGQSFSCPSDR.S	2405.63153	3	1.10E-06	0.89	4.19	-	822.1
gi|21361122|ref|NP_001440.2|	four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap			1.12E-06	1.87	20.25	9.60	31894.7
AHQ-9-9, 2419 - 2428	K.AIVAGDQNVEYK.G	1307.43431	2	1.12E-06	0.92	3.45	-	1013.5
AHQ-9-9, 3548 - 3551	R.FVFHQEQVYCPDCAK.K	1931.13758	2	1.11E-05	0.95	4.95	-	940.7
gi|14724206|ref|XP_042500.1|	similar to ribosomal protein S2; 40S ribosomal protein S2 [Homo sapien			1.13E-06	1.77	20.19	12.00	25535.7
AHQ-9-9, 4185 - 4257	K.AFVAIGDYNGHVGLGVK.C	1717.94906	2	1.13E-06	0.94	3.82	-	1417.9
AHQ-9-9, 4572 - 4623	K.TYSYLTPDLWK.E	1387.56103	2	1.54E-05	0.83	3.01	-	675.7
gi|24497612|ref|NP_116262.2|	nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr			1.20E-06	1.79	20.21	5.70	72695.6
AHQ-9-6, 5993	K.LGCDWVATIFSR.D	1426.62208	2	8.53E-05	0.93	3.03	-	1299.9
AHQ-9-6, 5077	R.RPYEDQGLGETTPLTIICQPM*QPLR.V	2932.32204	3	1.20E-06	0.86	4.24	-	783.6
gi|4758018|ref|NP_004359.1|	calponin 2; Calonin 2 [Homo sapiens]			1.20E-06	0.81	10.18	5.50	33696.9
AHQ-9-13-, 5916 - 5990	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.20E-06	0.81	3.00	-	817.1
AHQ-9-12, 5878	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.32E-06	0.93	3.52	-	1131.9
gi|4759300|ref|NP_004772.1|	vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated			1.22E-06	0.94	10.22	17.00	11309.0
AHQ-9-13-, 3573 - 3578	R.ADALQAGASQFETSAAK.L	1666.77095	2	1.22E-06	0.94	4.47	-	1002.5
gi|4506925|ref|NP_003013.1|	SH3 domain binding glutamic acid-rich protein like; SH3-binding domain			1.23E-06	2.61	30.27	47.40	12774.2
AHQ-9-13-, 5833 - 5897	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	3.73E-06	0.76	3.37	-	471.7
AHQ-9-13-, 5608 - 5665	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.65E-04	0.44	2.62	-	377.1
AHQ-9-13-, 4744 - 4809	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.23E-06	0.94	5.17	-	937.4
AHQ-9-13-, 4861 - 4921	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.58E-05	0.93	5.43	-	732.2
AHQ-9-13, 5003 - 5059	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.57E-05	0.88	4.37	-	629.4
AHQ-9-13, 4892 - 4954	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	1.16E-04	0.90	4.82	-	746.6
AHQ-9-13-, 4006 - 4064	R.GDYDAFFEAR.E	1191.23073	2	9.86E-05	0.91	3.70	-	963.2
gi|7657431|ref|NP_055205.1|	EBNA-2 co-activator (100kD) [Homo sapiens]			1.24E-06	1.78	20.21	4.50	99689.7
AHQ-9-4, 5742	K.DTNGENIAESLVAEGLATR.R	1961.07704	2	1.24E-06	0.94	4.10	-	1381.2
AHQ-9-4, 5861	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	2.17E-06	0.84	3.41	-	531.8
gi|4758970|ref|NP_004150.1|	proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be			1.27E-06	1.70	20.17	9.20	29769.4
AHQ-9-11, 3342	R.ASAGSYISALR.V	1096.21876	2	5.67E-05	0.79	2.54	-	1002.4
AHQ-9-11, 4045 - 4047	K.VESTDVSDLLHQYR.E	1662.78230	2	1.27E-06	0.91	3.48	-	1243.7
gi|7705849|ref|NP_057215.1|	ras-related GTP-binding protein RAB10; ras-related GTP-binding protein			1.29E-06	0.95	10.21	5.50	22540.8
AHQ-9-11, 5913 - 5921	K.AFLTLAEDILR.K	1262.47982	2	1.29E-06	0.95	4.20	-	1445.4
gi|12408656|ref|NP_005177.2|	calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ			1.34E-06	9.53	110.25	18.30	81889.4
AHQ-9-6, 4883	K.APSDLYQIILK.A	1261.49183	2	9.89E-05	0.90	3.23	-	1287.0
AHQ-9-6, 3589	R.DFFLANASR.A	1041.14166	2	5.39E-05	0.91	2.77	-	1370.9
AHQ-9-5, 5811	R.DM*ETIGFAVYEVPPELVGQPAVHLK.R	2757.15391	3	2.51E-04	0.75	3.49	-	528.0
AHQ-9-6, 5550	R.FRLPPGEYVVVPSTFEPNKEGDFVLR.F	2994.39160	3	2.65E-04	0.92	4.46	-	1331.8
AHQ-9-6, 4341	R.KAPSDLYQIILK.A	1389.66474	2	1.33E-05	0.90	3.47	-	956.2
AHQ-9-6, 6063	K.LGLVEFNILWNR.I	1474.73142	2	1.34E-06	0.84	3.17	-	813.3
AHQ-9-6, 4542	R.LPPGEYVVVPSTFEPNK.E	1874.12573	2	2.40E-05	0.76	3.38	-	467.7
AHQ-9-6, 3897	K.LYELIITR.Y	1021.23493	2	3.16E-04	0.97	3.90	-	2125.9
AHQ-9-6, 4937	R.NYPATFWVNPQFK.I	1612.81141	2	6.32E-04	0.75	2.88	-	622.0
AHQ-9-5, 4449	K.RPTELLSNPQFIVDGATR.T	2015.25904	3	2.10E-05	0.96	5.07	-	1616.1
AHQ-9-6, 3229	R.SEQFINLR.E	1007.12521	2	2.94E-06	0.87	2.87	-	978.7
gi|30149327|ref|XP_293672.2|	similar to ebiP7687 [Homo sapiens]			1.39E-06	0.91	10.15	1.90	59404.3

AHQ-9-5, 2941	K.SIYYITGESK.E	1161.28598	2	1.39E-06	0.91	2.93	-	1291.6
gi|4759212|ref|NP_004598.1|	beta-tubulin cofactor A [Homo sapiens]			1.40E-06	3.82	40.31	26.90	12854.8
AHQ-9-13-, 3561	R.ILENEKDLEEAEEYK.E	1852.97372	2	5.73E-05	0.93	4.15	-	1020.8
AHQ-9-13-, 3404	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	2.02E-06	0.98	6.20	-	2081.3
AHQ-9-13-, 3657 - 3714	R.LEAAYLDLQR.I	1192.34645	2	5.35E-04	0.96	4.01	-	1466.7
AHQ-9-13, 3826 - 3884	R.LEAAYLDLQR.I	1192.34645	2	9.65E-04	0.96	4.09	-	1668.5
AHQ-9-13-, 3489	R.RLEAAYLDLQR.I	1348.53280	2	1.40E-06	0.95	4.42	-	905.9
gi|4557014|ref|NP_001743.1|	catalase [Homo sapiens]			1.47E-06	5.99	70.29	19.70	59755.8
AHQ-9-7, 2745	K.ADVLTTGAGNPVGDK.L	1415.53118	2	4.25E-04	0.77	2.75	-	1109.8
AHQ-9-7, 4076 - 4084	R.AFYVNVLNEEQR.K	1482.62245	2	7.76E-06	0.95	4.37	-	1203.1
AHQ-9-7, 2534 - 2536	R.FNTANDDNVTQVR.A	1494.54849	2	4.33E-04	0.81	3.25	-	708.5
AHQ-9-7, 4376 - 4448	K.GAGAFGYFEVTHDITK.Y	1713.87091	2	5.27E-04	0.85	3.45	-	852.2
AHQ-9-7, 5792	R.GPLLVQDVVFTDEMAHFDR.E	2190.46422	3	1.47E-06	0.84	3.87	-	646.9
AHQ-9-7, 5178	R.GPLLVQDVVFTDEM*AHFDR.E	2206.46362	3	8.31E-05	0.80	3.44	-	648.6
AHQ-9-7, 6228	R.NPVNYFAEVEQIAFDPSNM*PPGIEASPDK.M	3194.47350	3	5.10E-05	0.95	5.77	-	1140.0
gi|4504521|ref|NP_002147.1|	heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P			1.50E-06	1.63	20.22	7.70	61024.2
AHQ-9-7, 4146	R.CIPALDSLTPANEDQK.I	1773.94302	2	6.40E-04	0.70	3.37	-	390.2
AHQ-9-7, 6376	R.TALLDAAGVASLLTTAEVVVTEIPKEEK.D	2870.28530	3	1.50E-06	0.93	4.48	-	1389.4
gi|29727317|ref|XP_298144.1|	hypothetical protein XP_298144 [Homo sapiens]			1.51E-06	0.68	10.15	8.00	22108.6
AHQ-9-4, 5886	K.GEYNLTLDTALTSNLK.T	1753.93165	2	1.51E-06	0.68	3.03	-	717.7
gi|29742410|ref|XP_291183.1|	similar to TREM-like transcript 1 [Homo sapiens]			1.52E-06	0.67	10.16	5.10	32678.3
AHQ-9-14-, 4259 - 4267	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	1.52E-06	0.67	3.27	-	347.0
AHQ-9-13-, 4110	R.FLPEGCQPLVSSAVDR.R	1776.99174	2	3.01E-05	0.52	2.60	-	261.3
gi|17986258|ref|NP_066299.2|	smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo			1.72E-06	3.77	50.21	25.80	16930.0
AHQ-9-12, 4082 - 4088	K.DQGTYEDYVEGLR.V	1545.58904	2	1.72E-06	0.86	3.31	-	879.0
AHQ-9-13, 4304	K.DQGTYEDYVEGLR.V	1545.58904	2	1.23E-04	0.66	2.85	-	614.6
AHQ-9-12, 3916	K.EAFQLFDR.T	1026.12699	1	3.60E-05	0.29	1.89	-	170.8
AHQ-9-13-, 3985	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.04E-05	0.61	3.09	-	602.8
AHQ-9-13, 3894	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.32E-05	0.77	3.21	-	570.3
AHQ-9-12, 3657	K.NKDQGTYEDYVEGLR.V	1787.86505	2	4.15E-05	0.82	3.17	-	922.4
AHQ-9-13-, 3752	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.42E-05	0.89	3.83	-	903.3
AHQ-9-14-, 3778	K.NKDQGTYEDYVEGLR.V	1787.86505	2	6.10E-04	0.77	2.98	-	730.2
AHQ-9-13-, 5910	K.VLDFEHFLPM*LQTVAK.N	1905.24957	2	7.22E-06	0.94	4.26	-	975.9
AHQ-9-13-, 5900	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	4.80E-04	0.88	4.08	-	762.2
AHQ-9-12, 6182	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	6.02E-04	0.90	4.19	-	662.6
gi|5123454|ref|NP_005336.2|	heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind			1.76E-06	1.53	20.20	4.20	70037.7
AHQ-9-6, 4554	K.DAGVIAGLNVLR.I	1198.39736	2	1.76E-06	0.95	3.95	-	1523.1
AHQ-9-7, 3670	K.NQVALNPQNTVFDAK.R	1659.82478	2	7.95E-04	0.58	2.77	-	449.2
gi|11993943|ref|NP_055419.1|	Tax interaction protein 1 [Homo sapiens]			1.85E-06	0.93	10.17	13.70	13734.6
AHQ-9-13, 4199 - 4212	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	1.85E-06	0.93	3.43	-	1399.2
gi|4504071|ref|NP_000164.1|	platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA			1.97E-06	5.24	60.21	12.30	68955.0
AHQ-9-3, 3444	K.AM*TSNVASVQCDNSDKFPVYK.Y	2379.60939	3	1.97E-06	0.90	4.22	-	630.6
AHQ-9-9, 4519	R.GLGELQELYLK.G	1263.46458	2	7.76E-05	0.82	3.24	-	770.0
AHQ-9-3, 4712 - 4725	R.GLGELQELYLK.G	1263.46458	2	1.32E-04	0.95	3.78	-	1620.2
AHQ-9-13, 4187 - 4202	R.GQDLLSTVSIR.Y	1189.34410	2	4.04E-05	0.93	3.97	-	1118.0
AHQ-9-3, 4000	R.GQDLLSTVSIR.Y	1189.34410	2	3.68E-04	0.94	3.49	-	1436.2
AHQ-9-13-, 4044 - 4062	R.GQDLLSTVSIR.Y	1189.34410	2	4.78E-06	0.95	3.46	-	1580.5
AHQ-9-4, 2225	R.GVLQGHLESSR.N	1183.29965	2	6.69E-06	0.88	2.92	-	1012.2
AHQ-9-3, 4060 - 4062	R.LTSLPLGALR.G	1041.26938	2	9.28E-04	0.84	3.18	-	729.9
AHQ-9-3, 4576 - 4626	R.WLQDNAENVYVWK.Q	1665.82948	2	1.78E-04	0.90	3.66	-	975.1
AHQ-9-3, 4770 - 4797	R.WLQDNAENVYVWK.Q	1665.82948	2	5.96E-05	0.85	3.60	-	797.9
AHQ-9-4, 4636 - 4644	R.WLQDNAENVYVWK.Q	1665.82948	2	2.34E-04	0.87	3.61	-	913.8
gi|24234688|ref|NP_004125.3|	heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre			2.04E-06	0.48	10.14	2.80	73680.1
AHQ-9-6, 5433	K.STNGDTFLGGEDFDQALLR.H	2057.16328	2	2.04E-06	0.48	2.76	-	294.1
gi|4557701|ref|NP_000413.1|	keratin 17 [Homo sapiens]			2.16E-06	1.86	20.19	4.60	48105.4
AHQ-9-7, 3178 - 3244	K.TRLEQEIATYR.R	1380.53166	2	5.71E-04	0.95	3.74	-	1481.3
AHQ-9-1, 3738	R.VLDELTLAR.A	1030.20023	2	2.16E-06	0.91	3.45	-	995.3
gi|20127408|ref|NP_000173.2|	hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub			2.19E-06	0.90	10.21	2.20	82999.1
AHQ-9-6, 3111	K.TGIEQGSDAGYLCESQK.F	1844.93497	2	2.19E-06	0.90	4.10	-	687.6
gi|27500274|ref|XP_113950.3|	similar to Munc13-4 protein [Homo sapiens]			2.22E-06	1.85	20.20	2.80	123281.1
AHQ-9-4, 3445	R.IQQQAETTSEELGAVTVK.A	1933.10674	2	2.92E-04	0.94	3.93	-	1241.8
AHQ-9-4, 5130 - 5157	K.LPAQLAWEALEQR.V	1525.73360	2	2.22E-06	0.91	3.15	-	1230.6
gi|17986273|ref|NP_524144.1|	fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2			2.64E-06	1.85	20.21	8.20	21145.0
AHQ-9-12, 3340 - 3409	R.VFDKEGNGTVMGAELR.H	1723.93228	2	2.64E-06	0.94	4.13	-	1242.5
AHQ-9-12, 2714 - 2768	R.VFDKEGNGTVM*GAELR.H	1739.93168	2	1.43E-05	0.91	3.59	-	972.9
gi|28178832|ref|NP_002159.2|	isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat			2.70E-06	1.84	20.17	4.90	50909.0
AHQ-9-8, 2170 - 2206	K.TIEAEAAHGTVTR.H	1356.46696	2	2.70E-06	0.91	3.26	-	939.7
AHQ-9-8, 4138	K.YFDLGLPNR.D	1095.23246	2	2.34E-05	0.94	3.33	-	1400.2
gi|5803036|ref|NP_006796.1|	heterogeneous nuclear ribonucleoprotein A0; hnRNA binding protein [Homo			2.70E-06	0.92	10.18	5.20	30840.3
AHQ-9-9, 4555 - 4563	K.LFIGGLNVQTSESGLR.G	1691.90992	2	2.70E-06	0.92	3.60	-	1217.3
gi|19743813|ref|NP_002202.2|	integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib			2.71E-06	2.36	30.21	6.00	88414.9
AHQ-9-3, 4872	K.LKPEDITQIQPQQLVLR.L	2020.36187	3	5.14E-05	0.84	3.99	-	758.1
AHQ-9-3, 4874	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	2.71E-06	0.88	4.18	-	616.3
AHQ-9-3, 6244 - 6245	K.LSENNIQTIFAVTEEFQPVYK.E	2471.74650	2	3.07E-06	0.81	3.49	-	407.1
AHQ-9-3, 3210	K.WDTGENPIYK.S	1223.31587	2	2.44E-04	0.67	2.99	-	532.7
gi|23510338|ref|NP_003325.2|	ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity			2.72E-06	1.81	20.23	2.80	117848.1
AHQ-9-4, 5061 - 5062	R.LAGTQPLEVLEAVQR.S	1624.86348	2	2.72E-06	0.91	4.64	-	505.0
AHQ-9-4, 5934	K.YFLVGAGAIGCELLK.N	1612.91436	2	2.82E-04	0.90	3.25	-	1108.5
gi|4504045|ref|NP_002063.1|	guanine nucleotide binding protein (G protein), q polypeptide [Homo sap			2.86E-06	0.77	10.17	4.20	42142.8
AHQ-9-8, 4046 - 4050	R.VADPAYLPTQQDVLR.V	1686.89014	2	2.86E-06	0.77	3.40	-	657.7
gi|14249348|ref|NP_116120.1|	hypothetical protein MGC14353 [Homo sapiens]			3.06E-06	0.69	10.16	11.40	13940.7
AHQ-9-13-, 4122	R.YEEVSVSGFEEFHR.A	1715.80053	2	3.06E-06	0.69	3.12	-	373.2
gi|5031857|ref|NP_005557.1|	lactate dehydrogenase A [Homo sapiens]			3.07E-06	4.08	50.20	13.60	36688.5
AHQ-9-9, 6002	K.DLADELALVDVIEDK.L	1658.82864	2	3.07E-06	0.96	3.99	-	1777.2
AHQ-9-13-, 6176	K.DLADELALVDVIEDK.L	1658.82864	2	3.19E-04	0.96	4.07	-	1764.7
AHQ-9-9, 2717	K.LVIITAGAR.Q	914.12760	2	6.40E-05	0.91	2.91	-	1103.1
AHQ-9-9, 3521	K.QVVESAYEVIK.L	1265.43734	2	4.59E-05	0.85	3.07	-	821.2
AHQ-9-9, 3248 - 3260	K.SADTLWGIQK.E	1119.25233	2	8.06E-06	0.84	3.44	-	628.2
AHQ-9-9, 2493	K.TLHPDLGTDKDKEQWK.E	1912.09245	2	7.66E-04	0.51	2.88	-	251.2
gi|5031987|ref|NP_005720.1|	peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]			3.32E-06	0.76	10.17	14.00	22040.1
AHQ-9-13, 5042	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	3.32E-06	0.76	3.39	-	709.0
AHQ-9-11, 4777 - 4849	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	7.72E-05	0.82	3.36	-	889.9
gi|20127528|ref|NP_037459.2|	parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]			3.70E-06	2.77	30.21	11.00	41714.0
AHQ-9-9, 3299 - 3301	K.ARPEDVVNLDLK.S	1369.54878	2	3.70E-06	0.93	4.16	-	937.6
AHQ-9-9, 3497	K.LNVAEVTQSEIGQK.Q	1516.67865	2	3.50E-05	0.92	3.67	-	1239.1
AHQ-9-9, 3731	K.QLEEDLYDGQVLQK.L	1678.82164	2	3.45E-04	0.91	3.69	-	1061.1
gi|13899317|ref|NP_113657.1|	SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M			4.13E-06	2.32	30.22	23.40	12326.0
AHQ-9-14-, 5267	K.ESNTVFSFLGLKPR.L	1595.82383	2	5.53E-04	0.53	2.85	-	391.7
AHQ-9-14-, 4310	R.VFIASSSGFVAIK.K	1326.56551	2	4.13E-06	0.97	4.38	-	2305.5
AHQ-9-13-, 4298	R.VFIASSSGFVAIK.K	1326.56551	2	5.68E-06	0.97	4.11	-	1902.2
AHQ-9-14-, 4326	R.YCGDYDSFFESK.E	1519.57010	2	7.65E-05	0.81	2.59	-	869.7
gi|17438583|ref|XP_059067.1|	similar to nucleophosmin (nucleolar phosphoprotein B23, numatrin); Nuc			4.24E-06	0.38	10.13	5.10	28274.3
AHQ-9-9, 2331	K.VDNDENEHQLSLR.T	1569.61536	2	4.24E-06	0.38	2.66	-	308.1
gi|29568111|ref|NP_006088.2|	myosin, light polypeptide 9, regulatory; myosin regulatory light chain			4.36E-06	2.61	30.19	12.20	19827.1
AHQ-9-11, 3402 - 3421	R.FTDEEVDEMYR.E	1434.51009	2	7.66E-05	0.91	3.28	-	907.3
AHQ-9-11, 2765 - 2766	R.FTDEEVDEM*YR.E	1450.50949	2	4.75E-06	0.93	3.28	-	1216.1
AHQ-9-13-, 3905	K.GNFNYVEFTR.I	1247.34066	2	8.46E-05	0.69	2.70	-	617.9

AHQ-9-14-, 3925	K.GNFNYVEFTR.I	1247.34066	2	4.36E-06	0.77	2.61	-	780.5
AHQ-9-11, 3930 - 3939	K.GNFNYVEFTR.I	1247.34066	2	2.37E-04	0.94	3.73	-	1026.1
gi|4506417|ref|NP_002877.1|	RAP2B, member of RAS oncogene family [Homo sapiens]			4.39E-06	3.27	40.22	31.10	20494.2
AHQ-9-11, 5735	K.ASVDELFAEIVR.Q	1349.51434	2	4.39E-06	0.69	2.74	-	818.5
AHQ-9-11, 6101	K.EIEVDSSPSVLEILDTAGTEQFASM*R.D	2842.08287	3	9.30E-06	0.90	4.38	-	1028.9
AHQ-9-11, 3283 - 3287	R.VPMILVGNK.V	971.24256	2	8.15E-04	0.81	2.72	-	781.5
AHQ-9-11, 4085 - 4086	K.YDPTIEDFYR.K	1319.40042	2	2.98E-04	0.87	3.12	-	451.5
gi|27597085|ref|NP_000357.3|	tropomyosin 1 (alpha) [Homo sapiens]			4.59E-06	0.85	10.18	3.90	32865.7
AHQ-9-9, 3235	R.KLVIIESDLER.A	1315.54103	2	4.59E-06	0.85	2.96	-	1166.3
gi|18491024|ref|NP_005691.2|	dipeptidylpeptidase III isoform 1; dipeptidylpeptidase III [Homo sapie			4.80E-06	0.92	10.19	2.30	82588.6
AHQ-9-6, 4374	K.LAQDFLDSQNLSAYNTR.L	1957.09009	2	4.80E-06	0.92	3.83	-	1209.6
gi|4557241|ref|NP_001095.1|	skeletal muscle specific actinin, alpha 3 [Homo sapiens]			4.96E-06	0.75	10.13	0.90	103293.7
AHQ-9-4, 3038	K.ALDFIASK.G	865.00867	2	4.96E-06	0.75	2.59	-	463.5
AHQ-9-5, 3047	K.ALDFIASK.G	865.00867	1	4.83E-04	0.50	1.82	-	817.2
AHQ-9-4, 2969 - 3041	K.ALDFIASK.G	865.00867	1	8.85E-04	0.52	2.45	-	789.6
gi|14591909|ref|NP_000960.2|	ribosomal protein L5; 60S ribosomal protein L5 [Homo sapiens]			5.00E-06	1.83	20.17	7.40	34362.4
AHQ-9-9, 4100	R.DIICQIAYAR.I	1224.41173	2	5.00E-06	0.95	3.34	-	1710.3
AHQ-9-9, 3087 - 3149	K.HIMGQNVADYMR.Y	1435.65746	2	2.52E-04	0.87	3.06	-	1283.2
gi|4502101|ref|NP_000691.1|	annexin I; annexin I (lipocortin I); lipocortin I [Homo sapiens]			5.05E-06	2.43	30.16	11.60	38714.0
AHQ-9-9, 5875 - 5876	K.GLGTDEDTLIEILASR.T	1703.87264	2	8.30E-06	0.74	3.23	-	786.2
AHQ-9-9, 5584 - 5588	K.GVDEATIIDILTK.R	1388.58878	2	9.82E-04	0.86	3.20	-	974.8
AHQ-9-9, 2975	K.TPAQFDADELR.A	1263.33840	2	5.05E-06	0.83	3.02	-	939.5
gi|18104967|ref|NP_000953.2|	prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland			5.14E-06	3.45	40.21	13.50	68686.0
AHQ-9-6, 3927	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	5.14E-06	0.94	4.25	-	988.4
AHQ-9-6, 3845 - 3850	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	3	1.43E-05	0.79	3.53	-	818.1
AHQ-9-6, 6195	K.GLLGNPICSPEYWKPSTFGGEVGFNIVK.T	3069.47853	3	1.47E-04	0.84	4.02	-	528.6
AHQ-9-6, 3207 - 3266	R.VPDASQDDGPAVERPSTEL	1984.06747	2	6.35E-05	0.88	3.51	-	820.1
gi|5174447|ref|NP_006089.1|	guanine nucleotide binding protein (G protein), beta polypeptide 2-like			5.14E-06	1.82	20.20	6.60	35076.5
AHQ-9-9, 3824	K.DVLSVAFSSDNR.Q	1310.39506	2	5.14E-06	0.92	3.73	-	906.2
AHQ-9-9, 3304 - 3309	R.VWQVTIGTR	1060.23125	2	7.00E-04	0.90	3.26	-	1069.5
gi|21361755|ref|NP_004090.3|	stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie			5.27E-06	2.73	30.24	11.10	31708.5
AHQ-9-13, 4179	K.EASM*VITESPAALQLR.Y	1732.98059	2	1.52E-04	0.84	3.31	-	815.8
AHQ-9-10, 6243	K.GPGLFFILPCTDSFIK.V	1814.13672	2	5.27E-06	0.95	4.39	-	1031.5
AHQ-9-1, 6450 - 6451	K.GPGLFFILPCTDSFIK.V	1814.13672	2	7.25E-05	0.94	4.40	-	702.5
AHQ-9-1, 3958	R.VQNATLAVANITNADSATR.L	1931.09731	2	2.94E-05	0.94	4.90	-	990.9
gi|24307939|ref|NP_036205.1|	chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]			5.63E-06	0.91	10.18	3.00	59670.7
AHQ-9-7, 6025	K.LGFAGLVQEISFGTTK.D	1668.91472	2	5.63E-06	0.91	3.58	-	1114.9
AHQ-9-6, 6049	K.LGFAGLVQEISFGTTK.D	1668.91472	2	4.70E-05	0.91	3.48	-	1017.8
gi|4503551|ref|NP_001410.1|	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen			5.76E-06	0.91	10.19	4.30	36061.6
AHQ-9-9, 3968	K.NVALLSQLYHSPAR.R	1569.78961	2	5.76E-06	0.91	3.72	-	974.6
gi|5901944|ref|NP_008977.1|	elastin microfibril interface located protein; TNF? elastin microfibril			5.77E-06	4.34	50.25	9.00	106694.7
AHQ-9-4, 3506	R.APAPASAPPGPSEELLR.Q	1660.85268	2	5.77E-06	0.73	3.30	-	348.6
AHQ-9-4, 2956	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	1.11E-04	0.82	3.26	-	589.5
AHQ-9-3, 3566	R.LDTVAGGLQGLR.E	1200.37012	2	5.54E-05	0.96	4.05	-	1918.8
AHQ-9-3, 2950	R.LVGSGLHTVEAAGEAR.Q	1567.72888	2	1.16E-04	0.90	3.53	-	1073.0
AHQ-9-3, 3649	R.PARPNLSGSSAGSPLSGLGGEGPGESEK.V	2596.74928	3	1.45E-05	0.93	4.98	-	1007.1
gi|10863927|ref|NP_066953.1|	peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]			5.78E-06	4.03	50.28	23.00	18012.4
AHQ-9-12, 3878 - 3944	K.FEDENFILK.H	1155.28144	2	8.90E-05	0.70	2.69	-	564.0
AHQ-9-14-, 3413 - 3417	K.KITIADCGQLE	1249.41637	2	2.13E-04	0.89	4.18	-	1018.8
AHQ-9-12, 4488 - 4490	K.SIYGEKFEDENFILK.H	1833.03047	2	5.78E-06	0.96	5.59	-	1116.3
AHQ-9-12, 4349	R.VSFELFADK.V	1056.19300	1	3.36E-04	0.61	2.77	-	674.1
AHQ-9-12, 4458	R.VSFELFADKVPK.T	1380.61317	2	3.63E-05	0.87	3.56	-	880.9
gi|6005749|ref|NP_009193.1|	RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA			6.01E-06	0.59	10.13	8.50	19846.9
AHQ-9-11, 3225	K.VTVAGLAGKDPVQCSR.D	1659.88952	2	6.01E-06	0.59	2.54	-	407.4
gi|18201905|ref|NP_000166.2|	glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras			6.01E-06	0.86	10.19	3.00	63146.7
AHQ-9-7, 5609	K.TLAQLNPESSLFIIASK.T	1833.11828	2	6.01E-06	0.86	3.74	-	502.4
gi|19882251|ref|NP_001889.2|	cystatin SN precursor; cystatin 1; cystatin SA-I; cysteine proteinase			6.16E-06	0.51	10.16	12.80	16387.6
AHQ-9-13, 5082	R.IIPGGIYNADLNDEWVQR.A	2074.28181	2	6.16E-06	0.51	3.11	-	183.8
gi|18543899|ref|XP_086916.1|	similar to Phosphatidylethanolamine-binding protein (PEBP) (Prostatic			6.19E-06	0.81	10.14	7.50	21265.8
AHQ-9-11, 4225	K.LYTLVLTDPDAPSR.K	1561.76102	2	6.19E-06	0.81	2.86	-	851.7
gi|4505185|ref|NP_002406.1|	macrophage migration inhibitory factor (glycosylation-inhibiting factor			6.29E-06	0.92	10.16	7.80	12476.2
AHQ-9-13-, 4453	K.LLCGLLAER.L	1046.26608	2	6.29E-06	0.92	3.12	-	1143.7
AHQ-9-13, 4628	K.LLCGLLAER.L	1046.26608	2	9.59E-04	0.82	2.62	-	709.2
gi|5453607|ref|NP_006420.1|	chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co			6.41E-06	1.87	20.26	6.60	59366.3
AHQ-9-7, 4710 - 4786	K.LPIGDVATQYFADR.D	1566.73935	2	6.41E-06	0.91	3.89	-	667.5
AHQ-9-7, 6188 - 6189	K.SQDAEVGDGTTSVTLLAAEFLK.Q	2253.44875	2	3.47E-05	0.96	5.12	-	1116.8
gi|20547663|ref|XP_166266.1|	similar to Esterase D [Homo sapiens]			6.48E-06	0.46	10.15	6.40	31462.6
AHQ-9-9, 5641	K.SVSAFAPICNPVLCPWGK.K	2006.33387	2	6.48E-06	0.46	2.95	-	222.6
gi|4759274|ref|NP_004777.1|	thioredoxin-like, 32kDa; thioredoxin-related 32 kDa protein; thioredoxi			6.67E-06	0.95	10.19	5.20	32251.1
AHQ-9-9, 2991	R.IDQYQGADAVGLEEK.I	1636.74162	2	6.67E-06	0.95	3.79	-	1933.7
gi|6912638|ref|NP_036557.1|	ras suppressor protein 1 [Homo sapiens]			6.67E-06	2.19	30.17	24.50	31540.1
AHQ-9-10, 5600 - 5671	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	2.10E-04	0.69	3.23	-	323.8
AHQ-9-10, 6255 - 6256	R.GISNM*LDVNGLFTLSHITQLVLSHNK.L	2869.28903	3	6.67E-06	0.74	3.49	-	748.8
AHQ-9-10, 6173 - 6247	K.NLEVLNFFNNQIEELPTQISSLQK.L	2820.14663	3	4.98E-04	0.76	3.27	-	738.4
gi|18104989|ref|NP_002822.2|	protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t			7.07E-06	2.42	30.19	6.10	67560.7
AHQ-9-6, 4617 - 4677	R.DLSGLDAETLLK.G	1275.43053	2	1.93E-04	0.83	2.91	-	1201.0
AHQ-9-6, 3234	K.GLDCDIDIQK.T	1178.29500	2	7.07E-06	0.93	3.78	-	1028.6
AHQ-9-6, 4294	R.TLQVSPLDNGDLIR.E	1541.73134	2	1.96E-05	0.67	2.72	-	591.2
gi|29727204|ref|XP_290872.1|	similar to Pyruvate kinase, M2 isozyme [Homo sapiens]			7.08E-06	0.95	10.16	5.40	16297.7
AHQ-9-7, 2484 - 2493	R.APIIAVTR.N	841.03348	2	7.08E-06	0.95	3.29	-	1326.7
gi|5174727|ref|NP_005989.1|	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring			7.56E-06	1.64	20.19	6.30	60330.4
AHQ-9-6, 4285	R.IVSRPEELREDDVGTGAGLLEIK.K	2497.78703	3	2.78E-04	0.71	3.71	-	646.9
AHQ-9-6, 4663	K.TAVETAVLLLR.I	1186.42649	2	7.56E-06	0.93	3.67	-	1637.2
gi|4505989|ref|NP_000299.1|	protective protein for beta-galactosidase; Protective protein for beta-			7.70E-06	0.88	10.16	2.70	54495.8
AHQ-9-11, 3493	K.YGDSGEQIAGFVK.E	1371.47686	2	7.70E-06	0.88	3.18	-	968.6
gi|4507383|ref|NP_001052.1|	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil			8.42E-06	1.84	20.23	4.90	60675.3
AHQ-9-7, 4154	R.FQACPETQVPLQLESK.S	1877.10807	2	8.42E-06	0.96	4.69	-	1281.2
AHQ-9-7, 4396	K.SVADSVLFLR.D	1107.28469	2	1.85E-04	0.88	3.28	-	778.0
gi|4757812|ref|NP_004880.1|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso			8.64E-06	1.64	20.16	11.70	10917.8
AHQ-9-14-, 5605	R.DFSPSGIFGAFQR.G	1429.56124	2	8.64E-06	0.78	2.57	-	744.7
AHQ-9-14-, 5270	K.LGELPSWILM*R.D	1331.60876	2	7.41E-05	0.86	3.12	-	507.6
gi|4507767|ref|NP_003326.1|	ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi			8.93E-06	1.90	20.18	2.90	111719.5
AHQ-9-4, 4550	R.VDGVAAALDSFQAR.R	1420.55265	2	7.84E-05	0.96	3.61	-	2066.3
AHQ-9-4, 4450	R.VLVSGLQGLGAEVAK.N	1441.69805	2	8.93E-06	0.94	3.53	-	1520.8
gi|4504489|ref|NP_000403.1|	histidine-rich glycoprotein precursor; histidine-proline rich glycoprot			9.05E-06	0.73	10.13	2.70	59578.0
AHQ-9-5, 6049	K.DSPVLIDFFEDTER.Y	1683.79674	2	9.05E-06	0.73	2.66	-	728.2
gi|8922804|ref|NP_060760.1|	hypothetical protein FLJ10983 [Homo sapiens]			9.52E-06	0.86	10.14	1.60	68268.9
AHQ-9-6, 3465	R.LDQETAQWLR.W	1260.38088	2	9.52E-06	0.86	2.90	-	1110.8
gi|4504391|ref|NP_000179.1|	hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]			9.63E-06	1.98	30.18	5.90	102502.4
AHQ-9-4, 5570	R.AILQQLGLNSTCDDSILVK.T	2090.38419	2	3.48E-04	0.35	2.65	-	366.7
AHQ-9-4, 5230	K.GDFIALDLGGSSFR.I	1455.59700	2	2.83E-04	0.83	2.57	-	1239.2
AHQ-9-4, 5537	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	9.63E-06	0.81	3.58	-	738.9
gi|4504085|ref|NP_000399.1|	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA			9.75E-06	1.44	20.16	3.40	80814.1
AHQ-9-6, 5697 - 5705	R.VIFFLPWQK.M	1178.44934	2	7.89E-04	0.86	3.04	-	745.0
AHQ-9-6, 5218	R.YGAATANYM*EVVSLLK.K	1747.00572	2	9.75E-06	0.59	3.11	-	286.9
gi|13637631|ref|XP_016625.1|	similar to voltage-dependent anion channel isoform 2 [Homo sapiens] [M			9.97E-06	0.92	10.16	3.40	31479.2
AHQ-9-9, 3916	K.LTLSALVDGK.S	1017.20145	2	9.97E-06	0.92	3.30	-	1021.6

gi|11056061|ref|NP_066932.1| thymosin, beta 4 [Homo sapiens]				1.03E-05	3.11	40.24	54.50	5052.6
AHQ-9-14-, 2549	K.NPLPSKETIEQEK.Q	1513.67476	2	1.03E-05	0.58	2.65	-	326.7
AHQ-9-14-, 2710	K.NPLPSKETIEQEKQAGES	1986.12651	2	3.03E-04	0.87	4.28	-	477.6
AHQ-9-14-, 1983	K.TETQEKNPLPSK.E	1372.50630	2	7.65E-04	0.75	2.85	-	867.1
AHQ-9-14-, 1835 - 1895	K.TETQEKNPLPSK.E	1372.50630	2	3.18E-04	0.85	3.39	-	873.3
AHQ-9-14-, 2647	K.TETQEKNPLPSKETIEQEK.Q	2230.41519	2	7.49E-04	0.81	3.78	-	469.8
gi|5031595|ref|NP_005709.1| actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub				1.08E-05	1.84	20.21	13.10	19666.9
AHQ-9-11, 4059 - 4139	K.ELLLQPVTISR.N	1269.51549	2	5.38E-05	0.88	3.57	-	721.0
AHQ-9-11, 3193 - 3254	K.VLIEGSINSVR.V	1187.37134	2	1.08E-05	0.96	4.12	-	1691.6
gi|9257232|ref|NP_000598.1| orosomucoid 1 precursor; Orosomucoid-1 (alpha-1-acid glycoprotein-1); a				1.14E-05	0.73	10.13	7.00	23511.4
AHQ-9-1, 5880	K.EQLGEFYEALDCLR.I	1744.90337	2	1.14E-05	0.73	2.60	-	681.1
gi|5729873|ref|NP_006656.1| heparanase; heparanase-1 [Homo sapiens]				1.17E-05	0.78	10.17	3.30	61176.4
AHQ-9-7, 6316	R.EDFLNPDVLDIFISSVQK.V	2080.32304	2	1.17E-05	0.78	3.37	-	406.4
gi|30147736|ref|XP_301750.1| similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabili				1.17E-05	1.92	20.20	3.80	29717.3
AHQ-9-9, 4223	K.IEVIEIMTDR.G	1219.43361	2	3.89E-05	0.96	3.74	-	1636.8
AHQ-9-9, 3261 - 3271	K.IEVIEIM*TDR.G	1235.43301	2	1.17E-05	0.96	4.00	-	1598.0
gi|27413156|ref|NP_000338.2| spectrin, beta, erythrocytic (includes spherocytosis, clinical type I)				1.20E-05	0.83	10.15	0.70	246320.0
AHQ-9-2, 6294	R.YFYTGAEILGLIDEK.H	1732.95404	2	1.20E-05	0.83	2.52	-	1070.5
gi|5453559|ref|NP_006347.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d; ATP				1.20E-05	0.87	10.18	10.60	18491.1
AHQ-9-11, 5187 - 5197	R.LAALPENPPAIDWAYYK.A	1933.19486	2	1.20E-05	0.87	3.60	-	501.3
gi|14165439|ref|NP_002131.2| heterogeneous nuclear ribonucleoprotein K isoform a; dC-stretch bindin				1.26E-05	0.66	10.15	4.10	51027.9
AHQ-9-6, 4831	R.GSYGDLGGPIITTQVTIPK.D	1918.18004	2	1.26E-05	0.66	2.95	-	635.5
gi|5901922|ref|NP_008996.1| CDC37 homolog [Homo sapiens]				1.29E-05	0.81	10.18	5.60	44468.0
AHQ-9-8, 6108	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	1.29E-05	0.81	3.68	-	394.5
gi|4503725|ref|NP_000792.1| FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei				1.41E-05	0.65	10.23	13.00	11950.6
AHQ-9-14-, 3142	R.GWEEGVAQM*SVGQR.A	1550.67866	2	1.41E-05	0.65	2.51	-	674.4
AHQ-9-13-, 3088 - 3092	R.GWEEGVAQM*SVGQR.A	1550.67866	2	3.47E-05	0.95	4.58	-	1153.5
gi|4507879|ref|NP_003365.1| voltage-dependent anion channel 1 [Homo sapiens]				1.53E-05	0.70	10.13	3.90	30772.3
AHQ-9-9, 4124	R.WTEYGLTFTEK.W	1375.50711	2	1.53E-05	0.70	2.65	-	530.3
gi|18860900|ref|NP_002834.2| protein tyrosine phosphatase, receptor type, J precursor; protein tyro				1.62E-05	0.90	10.16	0.90	145926.2
AHQ-9-1, 4227	K.VITEPIPVSDLR.V	1339.56259	2	1.62E-05	0.90	3.16	-	828.2
gi|13786129|ref|NP_112586.1| RAB33B, member RAS oncogene family; likely ortholog of mouse RAB33b [H				1.63E-05	0.93	10.20	4.80	25717.4
AHQ-9-11, 3417 - 3479	K.IQLWDTAGQER.F	1317.43243	2	1.63E-05	0.93	3.99	-	947.8
gi|4826643|ref|NP_005130.1| annexin A3; Annexin III (lipocortin III); annexin III (lipocortin III,				1.65E-05	1.75	20.19	8.40	36375.0
AHQ-9-9, 4007 - 4012	R.DYPDFSPSVDAEAIQK.A	1782.88518	2	1.65E-05	0.90	3.89	-	549.5
AHQ-9-9, 3369	K.GIGTDEFTLNR.I	1223.31741	2	3.89E-05	0.85	2.64	-	1033.3
gi|4758618|ref|NP_004684.1| cytokeratin type II [Homo sapiens]				1.72E-05	0.94	10.17	1.80	59503.9
AHQ-9-7, 2650	K.YEELQVTAGR.H	1166.26586	2	1.72E-05	0.94	3.34	-	1723.6
gi|4506773|ref|NP_002956.1| S100 calcium-binding protein A9; calgranulin B [Homo sapiens]				1.78E-05	0.84	10.20	13.20	13241.9
AHQ-9-13-, 5413	R.NIETIINTFHQYSVK.L	1808.02738	2	1.78E-05	0.84	4.01	-	524.6
gi|4502171|ref|NP_000476.1| adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho				1.90E-05	0.94	10.17	5.60	19607.6
AHQ-9-11, 3551	R.IDYIAGLDSR.G	1123.24098	2	1.90E-05	0.94	3.44	-	1557.6
gi|17482508|ref|XP_058957.1| similar to QIL1 [Homo sapiens]				1.94E-05	0.81	10.16	18.60	13087.2
AHQ-9-14-, 5373	K.GSVAGGAVYLVYDQELLGPSDK.S	2239.46691	2	1.94E-05	0.81	3.18	-	693.2
gi|30149460|ref|XP_210540.2| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA				1.96E-05	0.86	10.16	4.00	29287.8
AHQ-9-5, 2396 - 2473	K.HIYYITGETK.D	1225.37490	2	1.96E-05	0.86	3.11	-	640.4
gi|4502051|ref|NP_000688.1| arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]				2.01E-05	4.10	50.17	11.60	75721.8
AHQ-9-6, 4581	R.AAAQLTYCSLCPPDDLADR.G	2140.33708	2	3.20E-04	0.85	3.29	-	606.1
AHQ-9-6, 2486	K.AVSTGGGGHVQLLR.R	1352.52468	2	2.01E-05	0.87	3.35	-	1026.4
AHQ-9-6, 4791	R.ITVQGPGACAEVAFPCYR.W	1999.25659	2	6.09E-04	0.80	3.03	-	1077.3
AHQ-9-6, 3667	R.LPGDNALDM*FQK.H	1365.53724	2	4.79E-04	0.92	3.14	-	1221.6
AHQ-9-6, 4530	R.VATGAWLFSGSYNR.V	1529.68080	2	1.06E-04	0.66	2.62	-	610.9
gi|4507949|ref|NP_003395.1| tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein,				2.05E-05	0.83	10.15	5.70	28082.2
AHQ-9-10, 1993 - 2048	K.AVTEQGHELSNEER.N	1599.64147	2	2.05E-05	0.83	3.05	-	787.5
gi|4505093|ref|NP_000889.1| monoamine oxidase B [Homo sapiens]				2.08E-05	0.87	10.17	2.90	58762.6
AHQ-9-7, 3305	K.YVDLGGSYVGPTQNR.I	1626.75165	2	2.08E-05	0.87	3.45	-	775.9
gi|30147184|ref|XP_060320.2| similar to ATP-dependent DNA helicase II, 70 kDa subunit (Lupus Ku aut				2.16E-05	0.95	10.21	1.60	72387.2
AHQ-9-9, 4072	K.IIQLLDDYPK.C	1218.42381	2	2.16E-05	0.95	4.30	-	1306.6
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				2.16E-05	4.33	50.25	5.90	191612.6
AHQ-9-4, 6400	R.FQSVPAQPGQTSPLLQYFGILLDQGQLNK.Y	3189.60926	3	4.26E-04	0.76	3.38	-	696.5
AHQ-9-4, 4548 - 4557	R.GQFSTDELVAEVEK.R	1552.66462	2	2.16E-05	0.74	2.93	-	1103.5
AHQ-9-3, 4946 - 4954	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	3.38E-04	0.93	3.74	-	2013.2
AHQ-9-2, 5089 - 5093	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	4.12E-04	0.83	3.84	-	966.0
AHQ-9-3, 6226	R.KFDVNTSAVQVLIEHIGNLDR.A	2369.66218	3	1.20E-04	0.94	4.98	-	1059.3
AHQ-9-4, 5785	R.NLQNLLILTAIK.A	1354.66353	2	8.32E-04	0.94	3.78	-	1584.3
AHQ-9-3, 5720	R.NLQNLLILTAIK.A	1354.66353	2	3.00E-05	0.96	4.07	-	1664.9
gi|4506661|ref|NP_000963.1| ribosomal protein L7a; 60S ribosomal protein L7a; surfeit 3; surfeit lo				2.26E-05	0.91	10.20	4.90	29995.4
AHQ-9-9, 3333 - 3335	R.AGVNTVTTLVENK.K	1346.51199	2	2.26E-05	0.91	3.91	-	794.7
gi|30150299|ref|XP_293010.2| similar to keratin 8, type II cytoskeletal - human [Homo sapiens] [MAS				2.37E-05	0.94	10.21	2.70	44500.6
AHQ-9-2, 5031	K.LALDIEIATYR.Q	1278.47925	2	2.37E-05	0.94	4.17	-	1811.6
gi|5803011|ref|NP_001966.1| enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron				2.38E-05	0.86	10.19	3.70	47268.3
AHQ-9-8, 6035	R.YITGDQLGALYQDFVR.D	1860.05915	2	2.38E-05	0.86	3.72	-	643.8
gi|4885079|ref|NP_005165.1| ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypept				2.43E-05	1.68	20.15	7.40	32880.7
AHQ-9-9, 2444	K.HLLIGVSSDR.G	1097.24989	2	2.82E-04	0.80	3.06	-	823.1
AHQ-9-9, 4653	R.IYGLGSLALYEK.A	1327.55027	2	2.43E-05	0.89	2.81	-	993.1
gi|4505753|ref|NP_002620.1| phosphoglycerate mutase 1 (brain); Phosphoglycerate mutase A, nonmuscle				2.50E-05	0.81	10.16	8.30	28803.7
AHQ-9-10, 4638	R.YADLTEDQLPSCESLKDTIAR.A	2427.62735	3	2.50E-05	0.81	3.17	-	677.5
gi|9910280|ref|NP_064505.1| UDP-glucose ceramide glucosyltransferase-like 1; UDP-glucose:glycoprote				2.55E-05	0.79	10.15	1.10	177187.7
AHQ-9-3, 5594	K.EGETYFDVVAVVDPVTR.E	1897.07456	2	2.55E-05	0.79	3.00	-	699.0
gi|4557251|ref|NP_001101.1| a disintegrin and metalloprotease domain 10 [Homo sapiens]				2.57E-05	0.83	10.16	2.00	84141.7
AHQ-9-5, 4507	K.AIDTIYQTTDFSGIR.N	1701.85844	2	2.57E-05	0.83	3.25	-	773.8
gi|4505671|ref|NP_002592.1| phosphodiesterase 6D, cGMP-specific, rod, delta [Homo sapiens]				2.58E-05	0.17	10.09	6.00	17419.9
AHQ-9-9, 3943	K.DERAREILR.G	1158.29332	1	2.58E-05	0.17	1.88	-	392.3
gi|9845511|ref|NP_008839.2| ras-related C3 botulinum toxin substrate 1 isoform Rac1; rho family, sm				2.69E-05	0.89	10.14	5.20	21450.0
AHQ-9-14-, 3309	K.YLECSALTQR.G	1242.38392	2	8.51E-05	0.78	2.74	-	862.0
AHQ-9-11, 3115 - 3177	K.YLECSALTQR.G	1242.38392	2	2.69E-05	0.89	2.89	-	1132.4
gi|8922712|ref|NP_060713.1| hypothetical protein FLJ10849 [Homo sapiens]				2.79E-05	1.79	20.18	6.50	49397.9
AHQ-9-7, 3538	K.DTDPDSKPFSLQETYEAK.R	2072.17149	3	2.79E-05	0.88	3.27	-	1340.5
AHQ-9-7, 3032	K.RNEFLGELQK.K	1234.38656	2	3.57E-04	0.91	3.67	-	1169.4
gi|6715607|ref|NP_000175.1| G-gamma globin [Homo sapiens]				2.98E-05	0.89	10.18	6.80	16126.3
AHQ-9-13, 4898	R.LLVVYPWTQR.F	1275.52342	2	5.85E-05	0.91	3.06	-	1085.3
AHQ-9-13-, 4712 - 4728	R.LLVVYPWTQR.F	1275.52342	2	2.98E-05	0.89	3.10	-	945.9
AHQ-9-14-, 4737 - 4749	R.LLVVYPWTQR.F	1275.52342	2	1.81E-04	0.94	3.61	-	1290.9
AHQ-9-13, 4886 - 4887	R.LLVVYPWTQR.F	1275.52342	2	1.66E-04	0.89	3.59	-	857.5
gi|27482573|ref|XP_208709.1| similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro				3.00E-05	0.89	10.17	14.30	17875.4
AHQ-9-12, 6148	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	3.00E-05	0.89	3.46	-	1011.0
gi|5032009|ref|NP_005600.1| glycogen phosphorylase; phosphorylase, glycogen, muscle; myophosphoryla				3.04E-05	0.81	10.14	1.00	97091.4
AHQ-9-5, 3877	R.VIFLENYR.V	1054.22348	2	3.04E-05	0.81	2.80	-	643.9
gi|17986283|ref|NP_006000.2| tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu				3.08E-05	0.94	10.24	3.30	50135.3
AHQ-9-7, 5310	R.AVFVDLEPTVIDEVR.T	1702.92947	3	8.55E-05	0.96	4.18	-	1989.2
AHQ-9-8, 5386 - 5392	R.AVFVDLEPTVIDEVR.T	1702.92947	2	4.80E-04	0.85	3.79	-	585.0
AHQ-9-11, 5266	R.AVFVDLEPTVIDEVR.T	1702.92947	2	5.41E-05	0.74	2.91	-	643.2
AHQ-9-14, 6039	R.AVFVDLEPTVIDEVR.T	1702.92947	2	8.66E-05	0.79	3.11	-	657.6
AHQ-9-13-, 5336 - 5337	R.AVFVDLEPTVIDEVR.T	1702.92947	2	9.24E-04	0.91	4.58	-	756.1
AHQ-9-7, 5300 - 5324	R.AVFVDLEPTVIDEVR.T	1702.92947	2	3.08E-05	0.94	4.85	-	931.9
gi|4507109|ref|NP_000336.1| alpha-synuclein isoform NACP140; non A4 component of amyloid precursor				3.21E-05	0.90	10.18	0.00	14460.1
AHQ-9-13-, 4105	K.TVEGAGSIAAATGFVK.K	1479.66001	2	3.21E-05	0.90	3.68	-	1038.5

<table>
<tr><td>gi|6912238|ref|NP_036226.1|</td><td>peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]</td><td></td><td></td><td>3.21E-05</td><td>0.96</td><td>10.21</td><td>7.90</td><td>22026.2</td></tr>
<tr><td>AHQ-9-12, 6196 - 6197</td><td>K.ETDLLLDDSLVSIFGNR.R</td><td>1908.09888</td><td>2</td><td>3.21E-05</td><td>0.96</td><td>4.17</td><td>-</td><td>1516.8</td></tr>
<tr><td>gi|4502695|ref|NP_001779.1|</td><td>cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c</td><td></td><td></td><td>3.26E-05</td><td>0.66</td><td>10.15</td><td>4.10</td><td>48786.6</td></tr>
<tr><td>AHQ-9-8, 3907</td><td>K.IYEFPETDDEEENKLVK.K</td><td>2099.23685</td><td>2</td><td>3.26E-05</td><td>0.66</td><td>2.97</td><td>-</td><td>283.3</td></tr>
<tr><td>gi|30156347|ref|XP_293277.2|</td><td>similar to keratin 8; cytokeratin 8; keratin, type II cytoskeletal 8 [</td><td></td><td></td><td>3.32E-05</td><td>0.81</td><td>10.17</td><td>2.00</td><td>68049.8</td></tr>
<tr><td>AHQ-9-9, 5051</td><td>R.LEGLTDQINFLR.Q</td><td>1419.60780</td><td>2</td><td>3.32E-05</td><td>0.81</td><td>3.41</td><td>-</td><td>792.2</td></tr>
<tr><td>gi|5031569|ref|NP_005727.1|</td><td>ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r</td><td></td><td></td><td>3.35E-05</td><td>1.16</td><td>20.14</td><td>9.00</td><td>42613.4</td></tr>
<tr><td>AHQ-9-8, 3880</td><td>R.ACYLSINPQKDETLETEK.A</td><td>2141.34169</td><td>2</td><td>3.35E-05</td><td>0.44</td><td>2.85</td><td>-</td><td>255.2</td></tr>
<tr><td>AHQ-9-8, 6224</td><td>R.TLFSNIVLSGGSTLFK.G</td><td>1684.95729</td><td>2</td><td>1.49E-04</td><td>0.72</td><td>2.89</td><td>-</td><td>656.1</td></tr>
<tr><td>gi|6005727|ref|NP_006576.1|</td><td>chaperonin containing TCP1, subunit 8 (theta); T-complex protein 1, the</td><td></td><td></td><td>3.37E-05</td><td>0.29</td><td>10.13</td><td>2.60</td><td>59662.4</td></tr>
<tr><td>AHQ-9-7, 3413</td><td>R.LVPGGGATEIELAK.Q</td><td>1355.56202</td><td>2</td><td>3.37E-05</td><td>0.29</td><td>2.61</td><td>-</td><td>144.6</td></tr>
<tr><td>gi|4503607|ref|NP_000117.1|</td><td>electron transfer flavoprotein, alpha polypeptide; electron-transferrin</td><td></td><td></td><td>3.46E-05</td><td>0.87</td><td>10.17</td><td>3.90</td><td>35079.3</td></tr>
<tr><td>AHQ-9-9, 5191 - 5199</td><td>K.LEVAPISDIIAIK.S</td><td>1382.67051</td><td>2</td><td>3.46E-05</td><td>0.87</td><td>3.31</td><td>-</td><td>710.0</td></tr>
<tr><td>gi|20547107|ref|XP_114482.1|</td><td>similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN</td><td></td><td></td><td>3.48E-05</td><td>1.74</td><td>20.20</td><td>3.70</td><td>94330.3</td></tr>
<tr><td>AHQ-9-4, 5974</td><td>K.SNLAYDIVQLPTGLTGIK.V</td><td>1904.19651</td><td>2</td><td>3.48E-05</td><td>0.82</td><td>3.92</td><td>-</td><td>425.8</td></tr>
<tr><td>AHQ-9-4, 3933</td><td>K.VLATAFDTTLGGR.K</td><td>1322.49212</td><td>2</td><td>2.63E-04</td><td>0.92</td><td>3.42</td><td>-</td><td>1078.6</td></tr>
<tr><td>gi|29729616|ref|XP_292963.1|</td><td>similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [</td><td></td><td></td><td>3.63E-05</td><td>0.90</td><td>10.24</td><td>16.40</td><td>18025.4</td></tr>
<tr><td>AHQ-9-13-, 4688</td><td>K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S</td><td>2810.11545</td><td>3</td><td>3.63E-05</td><td>0.90</td><td>4.28</td><td>-</td><td>1000.5</td></tr>
<tr><td>AHQ-9-12, 4653</td><td>K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S</td><td>2810.11545</td><td>2</td><td>2.46E-04</td><td>0.73</td><td>3.54</td><td>-</td><td>384.1</td></tr>
<tr><td>gi|9257257|ref|NP_059830.1|</td><td>WD repeat-containing protein 1 isoform 1 [Homo sapiens]</td><td></td><td></td><td>3.66E-05</td><td>0.82</td><td>10.18</td><td>4.10</td><td>66193.1</td></tr>
<tr><td>AHQ-9-6, 4210</td><td>R.LHHVSSLAWLDEHTLVTTSHDASVK.E</td><td>2785.06406</td><td>3</td><td>3.66E-05</td><td>0.82</td><td>3.52</td><td>-</td><td>528.9</td></tr>
<tr><td>gi|8922673|ref|NP_060692.1|</td><td>parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]</td><td></td><td></td><td>4.18E-05</td><td>0.75</td><td>10.16</td><td>3.50</td><td>42243.4</td></tr>
<tr><td>AHQ-9-9, 4275 - 4337</td><td>R.DAFDTLFDHAPDK.L</td><td>1492.57096</td><td>2</td><td>4.18E-05</td><td>0.75</td><td>3.20</td><td>-</td><td>602.0</td></tr>
<tr><td>gi|15306356|ref|XP_035638.2|</td><td>similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan</td><td></td><td></td><td>4.26E-05</td><td>0.61</td><td>10.14</td><td>8.70</td><td>18795.1</td></tr>
<tr><td>AHQ-9-13-, 3536</td><td>R.ESDVPLKTEEFEVTK.T</td><td>1751.91253</td><td>2</td><td>4.26E-05</td><td>0.61</td><td>2.63</td><td>-</td><td>289.4</td></tr>
<tr><td>gi|6715600|ref|NP_002069.2|</td><td>golgi autoantigen, golgin subfamily a, 4; golgin 245; golgin-240; p230</td><td></td><td></td><td>4.34E-05</td><td>0.61</td><td>10.14</td><td>0.80</td><td>261137.0</td></tr>
<tr><td>AHQ-9-1, 5100</td><td>K.M*EKKESNLETELKSQTAR.I</td><td>2139.37389</td><td>2</td><td>4.34E-05</td><td>0.61</td><td>2.72</td><td>-</td><td>623.7</td></tr>
<tr><td>gi|21361553|ref|NP_003168.2|</td><td>spleen tyrosine kinase [Homo sapiens]</td><td></td><td></td><td>4.36E-05</td><td>0.62</td><td>10.15</td><td>3.60</td><td>72065.7</td></tr>
<tr><td>AHQ-9-6, 5326</td><td>K.QTWNLQGQALEQAIISQKPQLEK.L</td><td>2652.98708</td><td>3</td><td>4.36E-05</td><td>0.62</td><td>3.03</td><td>-</td><td>531.7</td></tr>
<tr><td>gi|5031593|ref|NP_005708.1|</td><td>actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub</td><td></td><td></td><td>4.40E-05</td><td>0.79</td><td>10.18</td><td>9.90</td><td>16320.3</td></tr>
<tr><td>AHQ-9-12, 3524 - 3589</td><td>K.AVQSLDKNGVDLLM*K.Y</td><td>1647.91883</td><td>2</td><td>4.40E-05</td><td>0.79</td><td>3.60</td><td>-</td><td>526.7</td></tr>
<tr><td>gi|4506363|ref|NP_002861.1|</td><td>RAB13, member RAS oncogene family; RAS-associated protein RAB13 [Homo s</td><td></td><td></td><td>4.50E-05</td><td>0.87</td><td>10.16</td><td>5.40</td><td>22774.0</td></tr>
<tr><td>AHQ-9-13, 3944</td><td>K.LLLIGDSGVGK.T</td><td>1072.28025</td><td>2</td><td>9.75E-05</td><td>0.83</td><td>2.54</td><td>-</td><td>1035.5</td></tr>
<tr><td>AHQ-9-11, 3673 - 3701</td><td>K.LLLIGDSGVGK.T</td><td>1072.28025</td><td>2</td><td>4.50E-05</td><td>0.87</td><td>3.17</td><td>-</td><td>948.3</td></tr>
<tr><td>gi|4503573|ref|NP_001967.1|</td><td>enolase 3; enolase-3, beta, muscle; muscle specific enolase; beta enola</td><td></td><td></td><td>4.66E-05</td><td>0.91</td><td>10.20</td><td>3.50</td><td>46958.5</td></tr>
<tr><td>AHQ-9-14-, 3758 - 3762</td><td>K.VNQIGSVTESIQACK.L</td><td>1635.82159</td><td>2</td><td>4.66E-05</td><td>0.91</td><td>3.91</td><td>-</td><td>940.8</td></tr>
<tr><td>gi|14589893|ref|NP_001785.2|</td><td>cadherin 4, type 1 preproprotein; cadherin 4, R-cadherin (retinal); R-</td><td></td><td></td><td>5.07E-05</td><td>0.28</td><td>10.16</td><td>2.00</td><td>100279.9</td></tr>
<tr><td>AHQ-9-4, 4506</td><td>K.VENPIDLYIYVIDM*NDNR.P</td><td>2213.45293</td><td>2</td><td>5.07E-05</td><td>0.28</td><td>2.82</td><td>-</td><td>351.2</td></tr>
<tr><td>AHQ-9-14-, 4501</td><td>K.VENPIDLYIYVIDM*NDNR.P</td><td>2213.45293</td><td>2</td><td>3.69E-04</td><td>0.54</td><td>3.28</td><td>-</td><td>442.2</td></tr>
<tr><td>AHQ-9-1, 4555</td><td>K.VENPIDLYIYVIDM*NDNR.P</td><td>2213.45293</td><td>2</td><td>4.71E-04</td><td>0.23</td><td>2.82</td><td>-</td><td>293.2</td></tr>
<tr><td>gi|22042381|ref|XP_065237.3|</td><td>similar to FKSG30 [Homo sapiens]</td><td></td><td></td><td>5.38E-05</td><td>0.94</td><td>20.18</td><td>4.80</td><td>42016.0</td></tr>
<tr><td>AHQ-9-8, 2864 - 2926</td><td>K.QEYDESGPSIVHR.K</td><td>1517.58206</td><td>2</td><td>5.38E-05</td><td>0.58</td><td>2.96</td><td>-</td><td>592.5</td></tr>
<tr><td>AHQ-9-8, 3831</td><td>R.VAPEEHPILLTEAPLNPK.A</td><td>1969.27019</td><td>2</td><td>4.51E-04</td><td>0.59</td><td>2.94</td><td>-</td><td>357.5</td></tr>
<tr><td>AHQ-9-9, 3645 - 3647</td><td>R.VAPEEHPILLTEAPLNPK.A</td><td>1969.27019</td><td>2</td><td>6.22E-04</td><td>0.50</td><td>2.98</td><td>-</td><td>355.7</td></tr>
<tr><td>AHQ-9-12, 3822 - 3877</td><td>R.VAPEEHPILLTEAPLNPK.A</td><td>1969.27019</td><td>2</td><td>1.17E-04</td><td>0.37</td><td>2.69</td><td>-</td><td>294.9</td></tr>
<tr><td>AHQ-9-8, 3707 - 3775</td><td>R.VAPEEHPILLTEAPLNPK.A</td><td>1969.27019</td><td>2</td><td>5.60E-04</td><td>0.73</td><td>3.60</td><td>-</td><td>380.8</td></tr>
<tr><td>gi|4502297|ref|NP_001678.1|</td><td>ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit</td><td></td><td></td><td>5.42E-05</td><td>0.68</td><td>10.13</td><td>8.30</td><td>17489.8</td></tr>
<tr><td>AHQ-9-13-, 2620</td><td>K.AQAELVGTADEATR.A</td><td>1432.51860</td><td>2</td><td>5.42E-05</td><td>0.68</td><td>2.66</td><td>-</td><td>600.3</td></tr>
<tr><td>gi|10346135|ref|NP_055083.1|</td><td>microtubule-associated protein, RP/EB family, member 2; T-cell activat</td><td></td><td></td><td>5.50E-05</td><td>0.86</td><td>10.21</td><td>6.10</td><td>37031.1</td></tr>
<tr><td>AHQ-9-9, 4573</td><td>K.SDKDLETQVIQLNEQVHSLK.L</td><td>2325.56134</td><td>3</td><td>5.50E-05</td><td>0.86</td><td>4.11</td><td>-</td><td>750.4</td></tr>
<tr><td>gi|4505145|ref|NP_002387.1|</td><td>malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochon</td><td></td><td></td><td>5.63E-05</td><td>0.84</td><td>10.21</td><td>1.70</td><td>65443.3</td></tr>
<tr><td>AHQ-9-6, 3037</td><td>K.IETQDIQALR.F</td><td>1187.32821</td><td>2</td><td>5.63E-05</td><td>0.84</td><td>3.00</td><td>-</td><td>919.0</td></tr>
<tr><td>gi|21362062|ref|NP_115744.2|</td><td>leucine zipper and CTNNBIP1 domain containing [Homo sapiens]</td><td></td><td></td><td>6.04E-05</td><td>0.74</td><td>10.13</td><td>11.60</td><td>21494.4</td></tr>
<tr><td>AHQ-9-11, 6157 - 6183</td><td>K.LTADDEAFLSANAGAILSQFEK.V</td><td>2312.51789</td><td>2</td><td>6.04E-05</td><td>0.74</td><td>2.64</td><td>-</td><td>742.7</td></tr>
<tr><td>gi|4757996|ref|NP_004060.1|</td><td>adaptor-related protein complex 2, sigma 1 subunit isoform AP17; clathr</td><td></td><td></td><td>6.07E-05</td><td>0.92</td><td>10.17</td><td>8.50</td><td>17017.6</td></tr>
<tr><td>AHQ-9-13-, 3509</td><td>K.LIEEVHAVVTVR.D</td><td>1365.60327</td><td>2</td><td>6.07E-05</td><td>0.92</td><td>3.31</td><td>-</td><td>1277.8</td></tr>
<tr><td>gi|7705827|ref|NP_057187.1|</td><td>GTP-binding protein Sara [Homo sapiens]</td><td></td><td></td><td>6.10E-05</td><td>0.89</td><td>10.16</td><td>5.60</td><td>22409.7</td></tr>
<tr><td>AHQ-9-11, 4190 - 4198</td><td>K.LVFLGLDNAGK.T</td><td>1147.34882</td><td>2</td><td>6.10E-05</td><td>0.89</td><td>3.22</td><td>-</td><td>966.4</td></tr>
<tr><td>gi|17450333|ref|XP_060887.1|</td><td>similar to peptidyl-Pro cis trans isomerase [Homo sapiens]</td><td></td><td></td><td>6.53E-05</td><td>0.92</td><td>10.22</td><td>11.00</td><td>17503.9</td></tr>
<tr><td>AHQ-9-13-, 6146</td><td>-.M*VNPTVFDIAVDGKPLGR.V</td><td>1946.26009</td><td>2</td><td>6.53E-05</td><td>0.92</td><td>3.95</td><td>-</td><td>1117.7</td></tr>
<tr><td>AHQ-9-12, 6070 - 6125</td><td>-.M*VNPTVFDIAVDGKPLGR.V</td><td>1946.26009</td><td>2</td><td>1.28E-04</td><td>0.93</td><td>4.48</td><td>-</td><td>967.1</td></tr>
<tr><td>gi|5453605|ref|NP_006421.1|</td><td>chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-</td><td></td><td></td><td>6.65E-05</td><td>1.46</td><td>20.20</td><td>5.90</td><td>57838.8</td></tr>
<tr><td>AHQ-9-7, 5906</td><td>R.DALSDLALHFLNK.M</td><td>1457.65603</td><td>2</td><td>6.65E-05</td><td>0.95</td><td>4.05</td><td>-</td><td>1599.6</td></tr>
<tr><td>AHQ-9-7, 5705</td><td>K.LGGTIDDCELVEGLVLTQK.V</td><td>2062.32762</td><td>2</td><td>3.21E-04</td><td>0.51</td><td>2.70</td><td>-</td><td>564.9</td></tr>
<tr><td>gi|4759044|ref|NP_004841.1|</td><td>Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]</td><td></td><td></td><td>6.94E-05</td><td>1.74</td><td>20.17</td><td>1.90</td><td>160883.4</td></tr>
<tr><td>AHQ-9-3, 5490</td><td>K.ELQDQLEAEQYFSTLYK.T</td><td>2106.27421</td><td>2</td><td>2.47E-04</td><td>0.84</td><td>3.45</td><td>-</td><td>626.9</td></tr>
<tr><td>AHQ-9-3, 5532</td><td>K.NLICAFLTDR.E</td><td>1224.41173</td><td>2</td><td>6.94E-05</td><td>0.90</td><td>3.14</td><td>-</td><td>1060.5</td></tr>
<tr><td>gi|18765729|ref|NP_003816.2|</td><td>synaptosomal-associated protein 23 isoform SNAP23A; synaptosomal-assoc</td><td></td><td></td><td>6.94E-05</td><td>1.43</td><td>20.20</td><td>18.50</td><td>23353.9</td></tr>
<tr><td>AHQ-9-14-, 4387</td><td>R.ILGLAIESQDAGIK.T</td><td>1428.65614</td><td>2</td><td>6.94E-05</td><td>0.84</td><td>3.10</td><td>-</td><td>822.0</td></tr>
<tr><td>AHQ-9-13-, 5302</td><td>R.ITNDAREDEM*EENLTQVGSILGNLK.D</td><td>2807.04176</td><td>3</td><td>7.79E-04</td><td>0.59</td><td>3.18</td><td>-</td><td>652.0</td></tr>
<tr><td>gi|21361621|ref|NP_002624.2|</td><td>phosphoglucomutase 1 [Homo sapiens]</td><td></td><td></td><td>7.32E-05</td><td>0.99</td><td>20.13</td><td>6.20</td><td>61448.7</td></tr>
<tr><td>AHQ-9-7, 3653</td><td>K.ADNFEYSDPVDGSISR.N</td><td>1772.80725</td><td>2</td><td>7.32E-05</td><td>0.63</td><td>2.53</td><td>-</td><td>571.3</td></tr>
<tr><td>AHQ-9-6, 5754</td><td>R.LVIGQNGILSTPAVSCIIR.K</td><td>2013.39093</td><td>2</td><td>3.34E-04</td><td>0.36</td><td>2.55</td><td>-</td><td>340.7</td></tr>
<tr><td>gi|22027538|ref|NP_037506.2|</td><td>programmed cell death 6 interacting protein; ALG-2 interacting protein</td><td></td><td></td><td>7.38E-05</td><td>0.82</td><td>10.19</td><td>3.90</td><td>96022.6</td></tr>
<tr><td>AHQ-9-4, 6369</td><td>R.EATTLANGVLASLNLPAAIEDVSGDTVPQSILTK.S</td><td>3410.81462</td><td>3</td><td>7.38E-05</td><td>0.82</td><td>3.74</td><td>-</td><td>623.5</td></tr>
<tr><td>gi|5803201|ref|NP_006818.1|</td><td>transmembrane trafficking protein [Homo sapiens]</td><td></td><td></td><td>7.41E-05</td><td>0.92</td><td>10.17</td><td>5.00</td><td>24975.8</td></tr>
<tr><td>AHQ-9-11, 4131</td><td>R.IPDQLVILDM*K.H</td><td>1301.57773</td><td>2</td><td>7.41E-05</td><td>0.92</td><td>3.02</td><td>-</td><td>1333.9</td></tr>
<tr><td>gi|30148842|ref|XP_292982.2|</td><td>similar to FKSG30 [Homo sapiens]</td><td></td><td></td><td>7.59E-05</td><td>0.78</td><td>10.19</td><td>3.90</td><td>66046.0</td></tr>
<tr><td>AHQ-9-8, 6386</td><td>K.LCYVALDFEQEMATVASSSSLEK.S</td><td>2580.87000</td><td>3</td><td>7.59E-05</td><td>0.78</td><td>3.82</td><td>-</td><td>805.8</td></tr>
<tr><td>AHQ-9-8, 6303 - 6370</td><td>K.LCYVALDFEQEMATVASSSSLEK.S</td><td>2580.87000</td><td>2</td><td>3.47E-04</td><td>0.72</td><td>2.99</td><td>-</td><td>869.7</td></tr>
<tr><td>gi|6680033|ref|NP_031379.1|</td><td>guanine nucleotide binding protein (G protein) alpha 12 [Homo sapiens]</td><td></td><td></td><td>7.94E-05</td><td>0.85</td><td>10.14</td><td>2.90</td><td>44250.9</td></tr>
<tr><td>AHQ-9-9, 3205</td><td>K.ILLLGAGESGK.S</td><td>1058.25357</td><td>2</td><td>7.94E-05</td><td>0.85</td><td>2.79</td><td>-</td><td>869.6</td></tr>
<tr><td>gi|4503141|ref|NP_001805.1|</td><td>cathepsin C isoform a preproprotein; dipeptidyl-peptidase I; dipeptidyl</td><td></td><td></td><td>8.65E-05</td><td>0.85</td><td>10.14</td><td>4.10</td><td>51841.5</td></tr>
<tr><td>AHQ-9-14-, 5173</td><td>R.GTDECAIESIAVAATPIPK.L</td><td>1945.18072</td><td>2</td><td>8.65E-05</td><td>0.85</td><td>2.74</td><td>-</td><td>985.3</td></tr>
<tr><td>gi|21735621|ref|NP_005909.2|</td><td>mitochondrial malate dehydrogenase precursor [Homo sapiens]</td><td></td><td></td><td>8.76E-05</td><td>1.70</td><td>20.23</td><td>8.90</td><td>35503.0</td></tr>
<tr><td>AHQ-9-9, 4879</td><td>K.IFGVTTLDIVR.A</td><td>1234.46961</td><td>2</td><td>6.49E-04</td><td>0.93</td><td>3.40</td><td>-</td><td>1329.3</td></tr>
<tr><td>AHQ-9-13, 6195</td><td>K.VAVLGASGGIGQPLSLLLK.N</td><td>1794.17156</td><td>2</td><td>8.76E-05</td><td>0.77</td><td>2.63</td><td>-</td><td>842.5</td></tr>
<tr><td>gi|21614520|ref|NP_000393.2|</td><td>glucose-6-phosphate dehydrogenase [Homo sapiens]</td><td></td><td></td><td>8.97E-05</td><td>0.86</td><td>10.16</td><td>2.90</td><td>59257.4</td></tr>
<tr><td>AHQ-9-7, 5253</td><td>R.DGLLPENTFIVGYAR.S</td><td>1665.87093</td><td>2</td><td>8.97E-05</td><td>0.86</td><td>3.28</td><td>-</td><td>613.4</td></tr>
<tr><td>gi|13775186|ref|NP_112567.1|</td><td>ring finger protein 17 isoform long [Homo sapiens]</td><td></td><td></td><td>9.00E-05</td><td>0.63</td><td>10.16</td><td>1.70</td><td>73736.0</td></tr>
<tr><td>AHQ-9-10, 5020 - 5078</td><td>K.TADQLTTGLER.S</td><td>1205.30039</td><td>2</td><td>9.00E-05</td><td>0.63</td><td>3.11</td><td>-</td><td>772.5</td></tr>
<tr><td>gi|4505303|ref|NP_002466.1|</td><td>myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m</td><td></td><td></td><td>9.01E-05</td><td>0.82</td><td>10.18</td><td>6.30</td><td>22763.8</td></tr>
<tr><td>AHQ-9-14-, 2849 - 2855</td><td>R.ALGQNPTNAEVLK.V</td><td>1355.52211</td><td>2</td><td>9.01E-05</td><td>0.82</td><td>3.22</td><td>-</td><td>629.0</td></tr>
<tr><td>gi|16933542|ref|NP_002017.1|</td><td>fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s</td><td></td><td></td><td>9.33E-05</td><td>2.04</td><td>30.21</td><td>2.20</td><td>259222.8</td></tr>
<tr><td>AHQ-9-1, 4855</td><td>R.NLQPASEYTVSLVAIK.G</td><td>1733.98671</td><td>2</td><td>9.33E-05</td><td>0.60</td><td>2.55</td><td>-</td><td>339.3</td></tr>
<tr><td>AHQ-9-1, 5704 - 5711</td><td>R.NTFAEVTGLSPGVTYYFK.V</td><td>1995.21983</td><td>2</td><td>3.41E-04</td><td>0.93</td><td>4.27</td><td>-</td><td>973.4</td></tr>
<tr><td>AHQ-9-1, 6375</td><td>R.VTWAPPPSIDLTNFLVR.Y</td><td>1927.23500</td><td>2</td><td>1.28E-04</td><td>0.51</td><td>2.61</td><td>-</td><td>312.5</td></tr>
<tr><td>gi|4506713|ref|NP_002945.1|</td><td>ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte</td><td></td><td></td><td>9.60E-05</td><td>0.62</td><td>10.20</td><td>10.30</td><td>17964.8</td></tr>
<tr><td>AHQ-9-14-, 4237 - 4298</td><td>K.TITLEVEPSDTIENVK.A</td><td>1788.97431</td><td>2</td><td>9.60E-05</td><td>0.62</td><td>3.33</td><td>-</td><td>571.1</td></tr>
<tr><td>gi|10863873|ref|NP_000651.1|</td><td>transforming growth factor, beta 1 (Camurati-Engelmann disease); trans</td><td></td><td></td><td>1.00E-04</td><td>1.56</td><td>20.16</td><td>7.40</td><td>44422.0</td></tr>
<tr><td>AHQ-9-8, 3027</td><td>R.VAGESAEPEPEPEADYYAK.E</td><td>2053.12504</td><td>2</td><td>1.02E-04</td><td>0.70</td><td>3.12</td><td>-</td><td>352.7</td></tr>
<tr><td>AHQ-9-13-, 3574</td><td>K.VEQLSNMIVR.S</td><td>1189.41074</td><td>2</td><td>1.00E-04</td><td>0.87</td><td>3.01</td><td>-</td><td>1100.4</td></tr>
<tr><td>gi|4757952|ref|NP_001782.1|</td><td>cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p</td><td></td><td></td><td>1.00E-04</td><td>1.60</td><td>20.18</td><td>14.10</td><td>21258.5</td></tr>
<tr><td>AHQ-9-11, 6109 - 6129</td><td>K.NVFDEAILAALEPPEPK.K</td><td>1854.09282</td><td>2</td><td>3.22E-04</td><td>0.68</td><td>3.15</td><td>-</td><td>418.4</td></tr>
<tr><td>AHQ-9-11, 2641 - 2698</td><td>K.YVECSALTQK.G</td><td>1200.34381</td><td>2</td><td>1.00E-04</td><td>0.92</td><td>3.55</td><td>-</td><td>738.0</td></tr>
<tr><td>gi|7706563|ref|NP_057614.1|</td><td>RAB-8b protein [Homo sapiens]</td><td></td><td></td><td>1.02E-04</td><td>0.84</td><td>10.15</td><td>6.80</td><td>23584.0</td></tr>
<tr><td>AHQ-9-11, 5241</td><td>K.SSANVEEAFFTLAR.D</td><td>1542.67465</td><td>2</td><td>1.02E-04</td><td>0.84</td><td>2.91</td><td>-</td><td>977.9</td></tr>
</table>

gi|5730118|ref|NP_006514.1|	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble; X-prolyl aminope			1.02E-04	0.80	10.16	2.20	69858.4
AHQ-9-6, 5614	R.VGVDPLIIPTDYWK.K	1616.88141	2	1.02E-04	0.80	3.17	-	543.5
gi|27499559|ref|XP_062669.7|	similar to lactate dehydrogenase A -like [Homo sapiens]			1.09E-04	0.71	10.14	5.60	33375.6
AHQ-9-9, 6149	K.LIIVSNPVDILTYVAWK.L	1945.33337	2	1.09E-04	0.71	2.82	-	487.3
gi|29729345|ref|XP_290995.1|	similar to speckle-type POZ protein [Homo sapiens]			1.17E-04	1.41	20.19	10.90	18703.4
AHQ-9-2, 5702	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	1.17E-04	0.60	3.31	-	701.8
AHQ-9-3, 5552	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	9.64E-04	0.82	3.71	-	1040.6
AHQ-9-1, 5736	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	7.31E-04	0.84	3.11	-	1091.1
gi|21618359|ref|NP_004095.3|	fatty acid synthase [Homo sapiens]			1.19E-04	1.70	20.20	1.30	273262.0
AHQ-9-2, 6311	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	1.72E-04	0.89	3.78	-	734.2
AHQ-9-1, 5056 - 5127	K.VVVQVLAEEPEAVLK.G	1623.91540	2	1.19E-04	0.81	3.25	-	841.5
gi|29732170|ref|XP_291550.1|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			1.26E-04	0.91	10.26	12.70	13262.9
AHQ-9-5, 4092	K.HLEINPDHSIIETLR.Q	1787.99770	3	1.90E-04	0.98	5.11	-	2407.1
AHQ-9-5, 4083	K.HLEINPDHSIIETLR.Q	1787.99770	2	1.26E-04	0.91	3.70	-	883.1
gi|4506117|ref|NP_000304.1|	protein S (alpha); Protein S, alpha [Homo sapiens]			1.26E-04	0.85	10.16	1.60	75072.2
AHQ-9-4, 3830	R.SFQTGLFTAAR.Q	1199.34068	2	1.26E-04	0.85	3.17	-	554.3
gi|30148644|ref|XP_293716.2|	similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA			1.26E-04	0.90	10.17	1.20	105150.3
AHQ-9-5, 3608	R.TLTIVDTGIGM*TK.A	1366.60658	2	1.26E-04	0.90	3.33	-	1006.0
gi|30153966|ref|XP_293932.2|	similar to hypothetical protein BC013073 [Homo sapiens]			1.29E-04	0.75	10.18	9.00	21711.3
AHQ-9-4, 3921 - 3977	R.MIFTLFTINVSKDIRHH	2073.44997	2	6.62E-04	0.51	3.37	-	387.4
AHQ-9-5, 3935 - 3991	R.MIFTLFTINVSKDIRHH	2073.44997	2	1.90E-04	0.34	3.16	-	281.0
AHQ-9-6, 3903	R.MIFTLFTINVSKDIRHH	2073.44997	3	1.29E-04	0.75	3.33	-	786.1
AHQ-9-2, 3951 - 4021	R.MIFTLFTINVSKDIRHH	2073.44997	2	3.98E-04	0.68	3.36	-	553.4
gi|29739002|ref|XP_294006.1|	similar to 60S ribosomal protein L6 (TAX-responsive enhancer element b			1.30E-04	0.79	10.14	11.10	13435.5
AHQ-9-9, 3903	R.SVFALTNGIYPHK.L	1447.66284	2	1.30E-04	0.79	2.88	-	736.0
gi|4503821|ref|NP_001456.1|	FYN binding protein (FYB-120/130); FYN-binding protein (FYB-120/130) [H			1.40E-04	0.95	10.20	1.50	85450.5
AHQ-9-6, 3659	K.TTAVEIDYDSLK.L	1355.47251	2	1.40E-04	0.95	3.98	-	1310.3
gi|22053085|ref|XP_087939.3|	similar to tubulin, beta 5 [Homo sapiens]			1.54E-04	0.68	10.16	16.00	12104.0
AHQ-9-7, 5657	K.MAVTFIGNSSAIQELFK.R	1857.16334	2	1.54E-04	0.68	3.17	-	764.9
gi|4505759|ref|NP_002622.1|	phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo			1.54E-04	0.77	10.19	4.30	53151.7
AHQ-9-8, 6175 - 6231	K.IKDAFDRNPELQNLLLDDFFK.S	2552.86598	3	1.54E-04	0.77	3.74	-	799.7
gi|4508047|ref|NP_003452.1|	zyxin [Homo sapiens]			1.56E-04	0.86	10.19	4.40	61277.0
AHQ-9-8, 3852	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	1.56E-04	0.86	3.83	-	826.1
gi|6041669|ref|NP_004538.2|	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd			1.60E-04	0.44	10.13	14.00	15208.5
AHQ-9-13-, 4610	R.TLPETLDPAEYNISPETR.R	2047.20831	2	1.60E-04	0.44	2.52	-	346.4
gi|20546215|ref|XP_115639.1|	similar to leukocyte immunoglobulin-like receptor, subfamily B (with T			1.61E-04	0.63	10.16	4.70	42748.2
AHQ-9-2, 4627 - 4685	R.CSREVNSREDNVLYRVVK.P	2225.47152	2	1.61E-04	0.63	3.13	-	736.6
gi|23463289|ref|NP_695023.1|	family with sequence similarity 10, member A5 [Homo sapiens]			1.66E-04	0.92	10.17	3.50	41377.4
AHQ-9-8, 3143	R.AIEINPDSAQPYK.W	1446.58688	2	1.66E-04	0.92	3.31	-	986.7
gi|4503291|ref|NP_001346.1|	D-dopachrome tautomerase [Homo sapiens]			1.67E-04	0.83	10.14	9.30	12711.7
AHQ-9-14-, 5341	R.FFPLESWQIGK.I	1352.56151	2	1.67E-04	0.83	2.71	-	526.9
gi|6005826|ref|NP_009160.1|	protein kinase C and casein kinase substrate in neurons 2; pacsin 2 [Ho			1.69E-04	0.80	10.14	2.30	55904.6
AHQ-9-6, 3891	K.AYAQQLTEWAR.R	1337.46534	2	1.69E-04	0.80	2.82	-	1002.0
gi|18558709|ref|XP_087572.1|	similar to bA291L22.2 (similar to CDC10 (cell division cycle 10, S. ce			1.72E-04	0.93	10.15	10.90	9988.5
AHQ-9-8, 3155 - 3159	K.FEDYLNAESR.V	1244.29194	2	1.72E-04	0.93	3.06	-	1574.4
gi|27477134|ref|NP_079199.2|	nucleoporin 210; nuclear pore membrane glycoprotein 210; gp210 [Homo s			1.72E-04	0.51	10.14	1.00	205108.8
AHQ-9-2, 3862	R.CDAIVDLIHDIQIVSTTR.E	2071.34097	2	1.72E-04	0.51	2.74	-	655.9
gi|22043610|ref|XP_171081.1|	similar to ras-related C3 botulinum toxin substrate 1 isoform Rac1; rh			1.84E-04	0.71	10.17	7.80	21543.1
AHQ-9-11, 3537 - 3538	K.KLTPITYPQGLAM*AK.E	1648.99156	2	1.84E-04	0.71	3.40	-	342.5
gi|4504351|ref|NP_000510.1|	delta globin [Homo sapiens]			1.92E-04	1.71	20.19	21.80	16055.4
AHQ-9-13, 4880	R.FFESFGDLSSPDAVM*GNPK.V	2062.24491	2	8.98E-04	0.66	3.06	-	447.4
AHQ-9-13-, 4716	R.FFESFGDLSSPDAVM*GNPK.V	2062.24491	2	2.47E-04	0.77	3.44	-	417.9
AHQ-9-13-, 3194	K.VNVDAVGGEALGR.L	1257.37853	2	1.92E-04	0.94	3.83	-	1082.9
AHQ-9-13, 3368	K.VNVDAVGGEALGR.L	1257.37853	2	3.07E-04	0.94	3.81	-	1362.2
gi|20543399|ref|XP_116396.1|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			1.92E-04	0.58	10.15	5.00	19852.7
AHQ-9-12, 4336	R.VSFKLFADK.F	1055.25138	1	1.92E-04	0.58	2.43	-	838.0
gi|4504743|ref|NP_002194.1|	integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o			2.12E-04	0.79	10.17	1.90	129294.4
AHQ-9-3, 4724	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	2.12E-04	0.79	3.41	-	516.7
gi|4758208|ref|NP_004081.1|	dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;			2.22E-04	0.77	10.16	7.60	20478.2
AHQ-9-11, 3694 - 3755	R.IYVGNASVAQDIPK.L	1475.67136	2	2.22E-04	0.77	3.11	-	758.6
gi|4757766|ref|NP_004299.1|	Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa			2.23E-04	0.49	10.13	4.10	50435.4
AHQ-9-7, 5577	K.FLLDHQGELFPSPDPSGL	1970.17037	2	2.23E-04	0.49	2.65	-	477.1
gi|22045984|ref|XP_036408.3|	similar to KIAA1228 protein [Homo sapiens]			2.23E-04	0.72	10.13	1.70	80295.6
AHQ-9-11, 3945	K.VLVALASEELAK.G	1243.47481	2	2.23E-04	0.72	2.67	-	645.0
gi|24307975|ref|NP_054733.1|	U5 snRNP-specific protein, 200-KD [Homo sapiens]			2.35E-04	0.61	10.18	0.90	207190.6
AHQ-9-11, 5001 - 5058	K.M*IDKRMWQSMCPLRQFR.K	2301.76788	3	2.35E-04	0.61	3.56	-	577.3
gi|8922599|ref|NP_060653.1|	hypothetical protein FLJ10701 [Homo sapiens]			2.36E-04	0.14	10.11	3.60	31649.2
AHQ-9-4, 3846	R.NNKKTAILVK.E	1129.37817	1	2.36E-04	0.14	2.21	-	383.6
gi|4758076|ref|NP_004068.1|	citrate synthase precursor; Citrate synthase, mitochondrial [Homo sapie			2.38E-04	0.86	10.17	3.40	51706.2
AHQ-9-8, 4483	K.GLVYETSVLDPDEGIR.F	1763.92654	2	2.38E-04	0.86	3.39	-	673.8
gi|4506005|ref|NP_002700.1|	protein phosphatase 1, catalytic subunit, beta isoform [Homo sapiens] [			2.53E-04	0.88	10.16	4.30	37186.6
AHQ-9-9, 3752	R.AHQVVEDGYEFFAK.R	1640.77679	2	2.53E-04	0.88	3.24	-	836.4
gi|4758038|ref|NP_004246.1|	cytochrome c oxidase subunit Va precursor; cytochrome c oxidase polypep			2.56E-04	0.68	10.14	10.00	16774.1
AHQ-9-13-, 4140	K.GINTLVTYDM*VPEPK.I	1693.94282	2	2.56E-04	0.68	2.55	-	885.9
gi|6912322|ref|NP_036208.1|	crumbs homolog 1 [Homo sapiens]			2.66E-04	0.28	10.13	1.50	151412.1
AHQ-9-10, 4415	K.IDWNHITLENISSGSSLNVK.A	2228.44735	2	2.66E-04	0.28	2.69	-	501.5
gi|29788766|ref|NP_064424.2|	tubulin, beta polypeptide 4, member Q [Homo sapiens]			2.67E-04	0.60	10.15	3.50	48377.2
AHQ-9-14-, 3886 - 3890	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	2.67E-04	0.60	2.68	-	434.0
gi|5031599|ref|NP_005722.1|	actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub			2.68E-04	0.88	10.19	3.70	34332.8
AHQ-9-9, 3775	R.DNTINLIHTFR.D	1344.50101	2	2.68E-04	0.88	3.13	-	895.7
gi|4502011|ref|NP_000467.1|	adenylate kinase 1 [Homo sapiens]			2.76E-04	0.95	10.19	6.20	21634.7
AHQ-9-11, 3518 - 3530	K.IIFVVGGPGSGK.G	1131.34939	2	2.76E-04	0.95	3.83	-	1960.8
gi|14042953|ref|NP_114420.1|	FKSG17 [Homo sapiens]			2.84E-04	0.85	10.16	6.10	23305.9
AHQ-9-9, 4415	K.NILFVITKPDVYK.S	1550.86611	2	2.84E-04	0.85	3.28	-	740.6
gi|5803135|ref|NP_006852.1|	RAB35, member RAS oncogene family; ras-related protein rab-1c (GTP-bind			2.86E-04	0.90	10.16	5.50	23025.1
AHQ-9-13-, 3781 - 3786	K.LLIIGDSGVGK.S	1072.28025	2	2.86E-04	0.90	3.14	-	1177.0
gi|5174613|ref|NP_005960.1|	nucleosome assembly protein 1-like 4; nucleosome assembly protein 2 [Ho			2.87E-04	0.89	10.15	2.70	42823.1
AHQ-9-7, 2980	K.FYEEVHDLER.K	1337.41897	2	2.87E-04	0.89	3.06	-	1039.6
gi|20373153|ref|NP_115997.4|	myosin XVIIIB; myosin 18B [Homo sapiens]			2.88E-04	0.91	10.20	0.70	285231.7
AHQ-9-7, 6176	R.ITAAQLQTMLLEKSRVAR.Q	2030.42494	2	2.88E-04	0.91	4.09	-	1281.0
gi|24497438|ref|NP_002178.2|	interleukin 12B precursor; natural killer cell stimulatory factor-2; i			2.98E-04	0.17	10.13	5.80	37168.7
AHQ-9-13-, 5884 - 5948	R.GSSDPQGVTCGAATLSAER.V	1865.95741	2	2.98E-04	0.17	2.67	-	244.5
gi|4501889|ref|NP_001606.1|	actin, gamma 2 propeptide; actin, alpha-3 [Homo sapiens]			3.03E-04	0.64	10.17	5.60	41876.7
AHQ-9-14, 5428	K.DLYANNVLSGGTTM*YPGIADR.M	2245.45502	2	3.03E-04	0.64	3.39	-	461.3
gi|16753212|ref|NP_003921.2|	src family associated phosphoprotein 2; src kinase-associated phosphop			3.05E-04	0.86	10.17	2.80	41216.5
AHQ-9-7, 4093	K.DAEEWVQQLK.F	1246.35097	2	3.05E-04	0.86	3.39	-	1033.7
gi|30158852|ref|XP_301583.1|	similar to actin CA15 - sea squirt (Styela clava) (fragments) [Homo sa			3.12E-04	0.82	10.18	6.50	19197.0
AHQ-9-12, 3225	K.IWHHTFYNKLR.V	1515.74533	3	3.12E-04	0.82	3.55	-	1295.3
gi|4503377|ref|NP_001377.1|	dihydropyrimidinase-like 2; collapsin response mediator protein hCRMP-2			3.19E-04	0.81	10.15	2.60	62293.3
AHQ-9-6, 3967	R.GLYDGPVCEVSVTPK.T	1622.82128	2	3.19E-04	0.81	2.92	-	691.1
gi|4503635|ref|NP_000497.1|	coagulation factor II precursor; prothrombin [Homo sapiens]			3.22E-04	0.29	10.13	2.70	70036.5
AHQ-9-5, 4445	R.TFGSGEADCGLRPLFEK.K	1886.07506	2	3.22E-04	0.29	2.55	-	243.6
gi|4505669|ref|NP_000274.1|	phosphodiesterase 6B, cGMP-specific, rod, beta [Homo sapiens]			3.41E-04	0.41	10.16	2.70	98406.2
AHQ-9-7, 5853 - 5922	R.HHLEFGKFLLSEETLNIYQNLNR.R	2817.15089	3	3.41E-04	0.41	3.13	-	375.3
gi|4503785|ref|NP_000135.1|	frataxin; Friedreich ataxia (frataxin) [Homo sapiens]			3.45E-04	0.90	10.18	5.70	23218.1
AHQ-9-13-, 3729 - 3730	K.LGGDLGTYVINK.Q	1250.42590	2	3.45E-04	0.90	3.56	-	1020.7
gi|4557890|ref|NP_000415.1|	keratin 5; Keratin-5; 58 kda cytokeratin; keratin, type II cytoskeletal			3.45E-04	0.93	10.18	1.70	62461.1

AHQ-9-5, 3441 - 3444	K.WTLLQEQGTK.T	1204.35723	2	3.56E-04	0.89	2.90	-	988.9
AHQ-9-1, 3626	K.WTLLQEQGTK.T	1204.35723	2	3.45E-04	0.93	3.67	-	1115.1
gi|29731325|ref|XP_293023.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				3.77E-04	0.75	10.16	6.00	28867.8
AHQ-9-12, 3976	K.AGPNTNGSQFFICTAK.T	1714.88050	2	3.77E-04	0.75	3.23	-	512.7
gi|10835121|ref|NP_000289.1| pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H				3.96E-04	0.88	10.16	1.90	61829.8
AHQ-9-7, 3592	R.GDLGIEIPAEK.V	1142.28420	2	3.96E-04	0.88	3.22	-	870.7
gi|27498919|ref|XP_031992.8| similar to RRP5 protein homolog [Homo sapiens]				3.96E-04	0.48	10.15	0.70	208698.2
AHQ-9-6, 4641	R.IPLLLTSLSFKVLK.H	1572.99949	2	3.96E-04	0.48	2.94	-	507.2
gi|7705855|ref|NP_057226.1| steroid dehydrogenase homolog; likely ortholog of mouse Kik1 steroid de				3.98E-04	0.47	10.13	4.80	34323.9
AHQ-9-9, 5629 - 5639	K.GVFVQSVLPYFVATK.L	1655.96078	2	3.98E-04	0.47	2.54	-	313.2
gi|23110925|ref|NP_002789.1| proteasome beta 6 subunit; proteasome subunit Y; proteasome subunit be				4.03E-04	0.86	10.15	4.60	25357.6
AHQ-9-11, 2538	R.LAAIAESGVER.Q	1116.24998	2	4.03E-04	0.86	3.10	-	994.8
gi|7661948|ref|NP_055545.1| KIAA0152 gene product [Homo sapiens]				4.04E-04	0.88	10.17	4.50	32233.6
AHQ-9-9, 3315 - 3317	R.SNPEDQILYQTER.Y	1593.67683	2	4.04E-04	0.88	3.49	-	703.2
gi|29729918|ref|XP_294951.1| hypothetical protein XP_294951 [Homo sapiens]				4.19E-04	0.71	10.17	20.90	9159.6
AHQ-9-6, 4315	R.RPLQAQIVPKSVSPVGLCR.P	2107.50918	2	4.19E-04	0.71	3.41	-	930.8
gi|4505197|ref|NP_003473.1| myeloid/lymphoid or mixed-lineage leukemia 2; ALL1-related gene [Homo s				4.36E-04	0.45	10.16	0.50	564185.0
AHQ-9-1, 3958	R.PPPAADASEPRLASVLPEVKPKVEEGGR.H	2898.26376	3	4.36E-04	0.45	3.27	-	267.2
gi|19923142|ref|NP_002256.2| karyopherin beta 1; nuclear factor p97; importin 90; importin beta-1 s				4.36E-04	1.67	20.18	3.40	97169.7
AHQ-9-4, 6181	R.AAVENLPTFLVELSR.V	1659.90783	2	4.36E-04	0.86	3.52	-	559.5
AHQ-9-4, 5341	R.ESCLEAYTGIVQGLK.G	1669.87794	2	6.16E-04	0.81	2.61	-	937.8
gi|5803187|ref|NP_006746.1| transaldolase 1; dihydroxyacetone transferase; glycerone transferase [H				4.41E-04	0.86	10.14	3.90	37539.9
AHQ-9-9, 4448	K.ALAGCDFLTISPK.L	1394.61830	2	4.41E-04	0.86	2.84	-	865.2
gi|9966827|ref|NP_065090.1| PEST-containing nuclear protein [Homo sapiens]				4.46E-04	0.61	10.13	11.80	18924.8
AHQ-9-8, 4803	K.SQRAGAAGGPEEEAEKPVKTK.T	2141.32810	2	4.46E-04	0.61	2.68	-	687.6
gi|4501867|ref|NP_001089.1| aconitase 2 [Homo sapiens]				4.54E-04	0.84	10.18	2.10	85424.8
AHQ-9-5, 3433	K.IVYGHLDDPASQEIER.G	1842.98698	3	4.54E-04	0.84	3.51	-	896.3
gi|7656999|ref|NP_004380.1| catenin (cadherin-associated protein), alpha 2; Catenin, alpha-2 (cadhe				4.62E-04	0.35	10.16	2.00	105281.3
AHQ-9-14-, 4862	K.KAHVLAASVEQATQNFLEK.G	2085.34928	2	4.62E-04	0.35	2.69	-	425.8
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				4.79E-04	0.61	10.13	8.80	22006.2
AHQ-9-10, 4673 - 4683	K.QVELALWDTAGQEDYDR.L	2010.10662	2	4.79E-04	0.61	2.55	-	684.6
gi|29733417|ref|XP_294548.1| similar to hypothetical protein FLJ90396 [Homo sapiens]				4.90E-04	0.16	10.10	2.10	48468.3
AHQ-9-3, 5420	R.DIPFTNLAK.T	1019.17590	1	4.90E-04	0.16	1.97	-	400.1
gi|5453832|ref|NP_006380.1| oxygen regulated protein precursor; oxygen regulated protein (150kD) [H				4.96E-04	0.94	10.21	1.30	111334.8
AHQ-9-3, 5900 - 5901	R.VEFEELCADLFER.V	1658.81048	2	4.96E-04	0.94	4.25	-	1170.7
gi|30152584|ref|XP_305800.1| hypothetical protein XP_305800 [Homo sapiens]				5.04E-04	0.45	10.20	8.70	24751.1
AHQ-9-14-, 5225	K.MGKSSLSTPLSMLVM*AWNLR.A	2239.71147	2	5.04E-04	0.45	3.29	-	493.9
AHQ-9-2, 5358 - 5375	K.MGKSSLSTPLSMLVM*AWNLR.A	2239.71147	2	8.13E-04	0.61	2.98	-	728.7
gi|28557709|ref|NP_787082.1| hypothetical protein LOC221823 [Homo sapiens]				5.36E-04	0.51	10.13	5.30	34839.1
AHQ-9-9, 4751	R.VYAILTHGIFSGPAISR.I	1803.09710	2	5.36E-04	0.51	2.54	-	387.0
gi|30155465|ref|XP_292801.2| similar to RIKEN cDNA 2310076L09 [Homo sapiens]				5.83E-04	0.24	10.18	6.70	52773.6
AHQ-9-8, 4663	R.SLTQELQGTVEALESSVRGLPAGAQEKVAEVR.R	3354.71438	3	5.83E-04	0.24	3.54	-	266.8
gi|4506381|ref|NP_002863.1| ras-related C3 botulinum toxin substrate 2; Ras-related C3 botulinum to				5.91E-04	0.76	10.16	7.80	21428.7
AHQ-9-11, 4090	K.KLAPITYPQGLALAK.E	1584.92723	2	5.91E-04	0.76	3.11	-	463.2
gi|30148728|ref|XP_291501.2| similar to Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabili				5.99E-04	0.75	10.17	6.70	26333.9
AHQ-9-9, 4151	R.GFAFVTFDDHDSVDK.I	1700.78586	3	5.99E-04	0.75	3.34	-	468.7
gi|4504215|ref|NP_000848.1| guanylate cyclase 1, soluble, beta 3 [Homo sapiens]				6.02E-04	0.81	10.14	1.80	70514.1
AHQ-9-6, 4147	K.LTQELEILTDR.L	1331.49732	2	6.02E-04	0.81	2.90	-	926.8
gi|4503643|ref|NP_000121.1| coagulation factor V precursor; labile factor; factor V Leiden [Homo sa				6.10E-04	0.94	10.25	1.10	251716.5
AHQ-9-3, 6262	K.EKPQSTISGLLGPTLYAEVGDIIK.V	2530.89853	3	6.10E-04	0.94	4.92	-	1275.8
gi|4759140|ref|NP_004243.1| solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulato				6.13E-04	0.91	10.19	3.90	38868.2
AHQ-9-7, 3700	R.LLVVDPETDEQLQK.L	1627.81777	2	6.13E-04	0.91	3.88	-	723.6
gi|4506675|ref|NP_002941.1| ribophorin I [Homo sapiens]				6.18E-04	0.63	10.15	4.10	68569.0
AHQ-9-6, 6054 - 6118	K.THYIVGYNLPSYEYLYNLGDQYALK.M	2999.32033	3	6.18E-04	0.63	3.01	-	745.5
gi|6005902|ref|NP_009043.1| thrombospondin 3 [Homo sapiens]				6.25E-04	0.85	10.13	0.70	104200.6
AHQ-9-6, 4429	R.FYVVMWK.Q	973.21547	2	6.25E-04	0.85	2.53	-	693.6
gi|24307969|ref|NP_055423.1| cytoplasmic FMR1 interacting protein 1; selective hybridizing clone (m				6.29E-04	0.81	10.15	1.00	145181.2
AHQ-9-3, 5169	R.YLTLDGFDAM*FR.E	1465.65527	2	6.29E-04	0.81	2.93	-	682.4
gi|30149452|ref|XP_305804.1| hypothetical protein XP_305804 [Homo sapiens]				6.50E-04	0.61	10.16	2.10	82533.5
AHQ-9-4, 4880 - 4885	R.WRDDPELSGGNGQPAGK.A	1784.86762	3	6.50E-04	0.61	3.16	-	669.0
gi|9910542|ref|NP_064535.1| SAR1a gene homolog 1; SAR1 protein [Homo sapiens]				6.76E-04	0.86	10.20	11.60	22366.6
AHQ-9-11, 6099	K.VELNALM*TDETISNVPILILGNK.I	2514.92088	3	6.76E-04	0.86	3.91	-	800.7
gi|24432022|ref|NP_115956.2| testis-specific protein NYD-TSP1 [Homo sapiens]				6.85E-04	0.71	10.15	4.90	49458.7
AHQ-9-13, 5106	K.FNNLLKEIKDILKNM*AGFEEK.I	2511.92191	3	6.85E-04	0.71	3.01	-	1046.9
gi|21361670|ref|NP_054782.2| src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo				7.43E-04	0.70	10.14	3.70	48294.0
AHQ-9-10, 3327 - 3383	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	7.43E-04	0.70	2.71	-	599.3
gi|20070272|ref|NP_057110.2| androgen-regulated short-chain dehydrogenase/reductase 1; prostate sho				7.50E-04	0.71	10.13	4.40	35414.1
AHQ-9-9, 2595	K.EIQTTTGNQQVLVR.K	1587.76010	2	7.50E-04	0.71	2.57	-	731.8
gi|4557321|ref|NP_000030.1| apolipoprotein A-I precursor [Homo sapiens]				7.57E-04	0.91	10.21	0.00	30777.6
AHQ-9-14-, 4995 - 4999	K.LLDNWDSVTSTFSK.L	1613.74965	2	7.57E-04	0.91	4.19	-	619.1
gi|28372565|ref|NP_777604.1| hypothetical protein LOC283629 [Homo sapiens]				7.94E-04	0.51	10.14	4.30	28953.5
AHQ-9-11, 3813 - 3877	R.DLKLENLLLDK.W	1314.55303	2	7.94E-04	0.51	2.83	-	586.1
gi|4758440|ref|NP_004868.1| glia maturation factor, gamma [Homo sapiens]				8.06E-04	0.23	10.10	4.90	16801.2
AHQ-9-12, 3024	R.FVVYSYK.Y	906.05925	1	8.06E-04	0.23	1.98	-	427.4
gi|30148978|ref|XP_291520.2| similar to Keratin, type I cytoskeletal 18 (Cytokeratin 18) (K18) (CK				8.49E-04	0.49	10.14	2.20	68413.1
AHQ-9-11, 4579 - 4594	R.DWSHYFKTIKDLR.A	1709.92863	2	8.49E-04	0.49	2.79	-	535.5
gi|11545789|ref|NP_071357.1| hypothetical protein FLJ22794; KIAA1895 protein [Homo sapiens]				8.59E-04	0.22	10.13	12.00	18011.3
AHQ-9-3, 5056	R.SIIEFGSTM*ESILLDIKQR.H	2197.53808	2	8.59E-04	0.22	2.65	-	244.2
gi|15618995|ref|NP_258259.1| keratin 6 irs [Homo sapiens]				8.68E-04	0.97	10.23	2.30	57291.2
AHQ-9-1, 3383	R.FLEQQNQVLETK.W	1477.64411	2	8.68E-04	0.97	4.54	-	2112.8
gi|4504973|ref|NP_002292.1| lactate dehydrogenase C [Homo sapiens]				8.71E-04	0.82	10.16	3.60	36311.0
AHQ-9-11, 2506	R.VIGSGCNLDSAR.F	1250.36445	2	8.71E-04	0.82	3.28	-	651.7
gi|30150422|ref|XP_294438.2| similar to ribosomal protein L5; 60S ribosomal protein L5 [Homo sapien				9.81E-04	0.90	10.19	2.80	48674.6
AHQ-9-9, 2599 - 2601	R.YLMEQDEDAYKK.H	1533.68480	2	9.81E-04	0.90	3.71	-	1423.1
gi|7706244|ref|NP_057005.1| divalent cation tolerant protein CUTA [Homo sapiens]				9.91E-04	0.53	10.14	9.00	16832.5
AHQ-9-13-, 5349 - 5364	K.TQSSLVPALTDFVR.S	1534.73880	2	9.91E-04	0.53	2.73	-	239.8
gi|29738713|ref|XP_291660.1| similar to RIKEN cDNA 5730509K17 gene [Homo sapiens]				9.95E-04	0.16	10.10	0.90	91446.4
AHQ-9-8, 3043	R.IKPITLR.P	841.07662	1	9.95E-04	0.16	1.85	-	203.3

Reference				P (pro)	Sf	Score	Coverage	MW
File, Scan(s)	Peptide	MH+	z	P (pep)	Sf	XC		Sp
gi|4501885|ref|NP_001092.1| beta actin; beta cytoskeletal actin [Homo sapiens]				3.33E-15	11.54	130.33	36.00	41736.5
AHQ-10-13-, 5625 - 5680	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	2.03E-05	0.89	4.47	-	538.9
AHQ-10-8, 6018 - 6082	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	5.51E-04	0.66	4.04	-	344.3
AHQ-10-8, 5705 - 5769	R.CPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3267.67588	3	4.33E-06	0.85	4.00	-	572.0
AHQ-10-8, 6121 - 6193	R.CPEALFQPSFLGMESCGIHETTFNSIM*K.C	3251.67648	3	6.99E-04	0.87	4.57	-	586.2
AHQ-10-8, 6443	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	1.26E-04	0.73	3.29	-	821.0
AHQ-10-8, 6426 - 6507	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.87E-05	0.93	4.97	-	974.3
AHQ-10-8, 5602 - 5679	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	8.38E-05	0.83	3.71	-	1131.3
AHQ-10-8, 5369	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.50E-10	0.91	4.22	-	1187.2
AHQ-10-8, 6322 - 6323	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	2	2.52E-08	0.91	4.14	-	876.0
AHQ-10-8, 6313 - 6375	K.EKLCYVALDFEQEMATAASSSSLEK.S	2810.10410	3	2.96E-07	0.89	3.99	-	1230.5
AHQ-10-8, 6297 - 6363	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.20E-04	0.76	3.21	-	1068.4
AHQ-10-8, 5245 - 5314	K.EKLCYVALDFEQEM*ATAASSSSLEK.S	2826.10350	3	1.76E-04	0.77	3.80	-	545.6
AHQ-10-8, 5721 - 5781	R.FRCPEALFQPSFLGM*ESCGIHETTFNSIM*K.C	3571.03693	3	1.93E-05	0.72	3.19	-	633.9
AHQ-10-6, 2592	R.GYSFTTTAER.E	1133.19273	2	5.53E-05	0.89	2.70	-	990.1
AHQ-10-8, 2617 - 2673	R.GYSFTTTAER.E	1133.19273	2	3.96E-06	0.92	3.22	-	1365.6
AHQ-10-10, 2520 - 2590	R.GYSFTTTAER.E	1133.19273	2	1.87E-05	0.91	3.25	-	1064.4
AHQ-10-11, 2600 - 2602	R.GYSFTTTAER.E	1133.19273	2	1.07E-05	0.93	3.46	-	1120.1
AHQ-10-4, 2621	R.GYSFTTTAER.E	1133.19273	2	3.77E-04	0.95	3.34	-	1477.1
AHQ-10-8, 2498 - 2555	R.GYSFTTTAER.E	1133.19273	2	4.88E-04	0.86	2.66	-	1097.5
AHQ-10-3, 2645	R.GYSFTTTAER.E	1133.19273	2	8.48E-05	0.89	2.71	-	1000.3
AHQ-10-8, 4489	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	2	2.68E-05	0.91	4.36	-	788.5
AHQ-10-8, 4118 - 4153	R.KDLYANTVLSGGTTM*YPGIADR.M	2360.62916	3	4.79E-07	0.96	4.97	-	1871.9
AHQ-10-8, 4453 - 4530	R.KDLYANTVLSGGTTMYPGIADR.M	2344.62976	3	4.33E-05	0.97	6.19	-	1797.3
AHQ-10-8, 6525	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	1.14E-04	0.82	2.79	-	1120.4
AHQ-10-8, 6505 - 6562	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	8.18E-10	0.98	5.52	-	2120.1
AHQ-10-8, 6485 - 6542	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	2.69E-07	0.98	6.51	-	2683.1
AHQ-10-8, 6413 - 6469	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	1.50E-04	0.85	3.59	-	1141.5
AHQ-10-8, 6405 - 6465	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	7.87E-04	0.84	4.00	-	988.3
AHQ-10-8, 6385 - 6447	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	2	8.91E-05	0.96	4.46	-	1682.0
AHQ-10-8, 6374 - 6429	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	8.24E-06	0.94	4.47	-	1745.2
AHQ-10-8, 6270 - 6341	K.LCYVALDFEQEMATAASSSSLEK.S	2552.81665	3	3.83E-09	0.97	5.94	-	1953.1
AHQ-10-8, 6249 - 6309	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	3	1.06E-04	0.96	6.00	-	1538.6
AHQ-10-8, 6190 - 6247	K.LCYVALDFEQEM*ATAASSSSLEK.S	2568.81605	2	3.80E-08	0.92	4.21	-	828.7
AHQ-10-8, 5779 - 5821	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.08E-05	0.93	4.76	-	1259.4
AHQ-10-11, 5295 - 5343	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.48E-06	0.95	4.99	-	1645.2
AHQ-10-11, 5099 - 5155	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.66E-06	0.91	5.17	-	670.1
AHQ-10-10, 5287 - 5344	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	9.13E-04	0.95	4.77	-	1668.9
AHQ-10-10, 5126 - 5199	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.55E-06	0.96	6.70	-	1158.9
AHQ-10-8, 5617 - 5678	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.67E-07	0.96	5.48	-	1616.6
AHQ-10-7, 5117 - 5196	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.00E-04	0.90	4.56	-	831.3
AHQ-10-6, 5193	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.13E-05	0.92	5.06	-	749.9
AHQ-10-10, 5042 - 5098	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.26E-05	0.87	3.98	-	706.6
AHQ-10-4, 5325	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	8.20E-04	0.94	5.34	-	1035.3
AHQ-10-8, 5533 - 5613	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	3.33E-15	0.98	6.56	-	2233.5
AHQ-10-8, 5418 - 5482	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.22E-05	0.91	4.74	-	848.1
AHQ-10-8, 5417 - 5477	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	2.51E-10	0.96	5.80	-	1424.2
AHQ-10-9, 5243 - 5299	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L	3185.59928	3	5.47E-11	0.95	4.88	-	1361.1
AHQ-10-9, 5051	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	7.15E-05	0.83	3.38	-	1012.1
AHQ-10-9, 4955 - 5011	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.66E-07	0.97	6.38	-	1407.7
AHQ-10-8, 5305 - 5361	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	3.21E-09	0.98	6.67	-	2420.3
AHQ-10-8, 5169 - 5249	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	1.60E-06	0.96	6.31	-	1120.0
AHQ-10-3, 5258	R.TTGIVM*DSGDGVTHTVPIYEGYALPHAILR.L	3201.59868	3	6.39E-04	0.91	4.59	-	988.8
AHQ-10-9, 3639 - 3696	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.33E-04	0.91	4.63	-	623.9
AHQ-10-8, 4051	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.29E-04	0.76	3.17	-	669.2
AHQ-10-5, 3923 - 3952	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	5.46E-04	0.77	3.93	-	729.4
AHQ-10-5, 3925	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.35E-04	0.91	4.47	-	823.8
AHQ-10-8, 3925 - 3990	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	5.78E-05	0.76	3.66	-	532.8
AHQ-10-6, 3849	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.87E-04	0.92	4.07	-	921.6
AHQ-10-8, 3826	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	3.08E-05	0.90	4.38	-	651.7
AHQ-10-8, 3825 - 3901	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	9.09E-04	0.84	4.43	-	793.6
AHQ-10-4, 3892 - 3951	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	9.35E-06	0.74	3.81	-	557.9
AHQ-10-11, 3827	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.61E-04	0.91	4.28	-	627.4
AHQ-10-8, 3693 - 3753	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.40E-07	0.89	4.50	-	596.2
AHQ-10-8, 3809 - 3869	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	7.81E-06	0.93	4.84	-	856.9
AHQ-10-12, 3834 - 3905	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	8.98E-04	0.93	4.74	-	622.7
AHQ-10-12, 3928	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	6.54E-05	0.92	4.06	-	1028.3
AHQ-10-13, 4259 - 4283	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	2.01E-04	0.94	5.22	-	859.0
AHQ-10-13-, 3901	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	1.96E-05	0.90	4.41	-	811.5
AHQ-10-9, 3635 - 3717	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	3	2.84E-04	0.80	4.82	-	517.2
AHQ-10-14-, 3902	R.VAPEEHPVLLTEAPLNPK.A	1955.24351	2	4.45E-09	0.84	3.73	-	504.4
gi|16753233|ref|NP_006280.2| talin 1 [Homo sapiens]				4.44E-15	99.28	1130.38	53.90	269665.3
AHQ-10-5, 3264	K.AAAFEEQENETVVVK.E	1664.79496	2	6.14E-05	0.95	4.32	-	1284.1
AHQ-10-2, 3247 - 3312	K.AAAFEEQENETVVVK.E	1664.79496	2	3.12E-08	0.96	5.43	-	1331.6
AHQ-10-5, 3176 - 3185	K.AAAFEEQENETVVVK.E	1664.79496	2	1.19E-05	0.89	4.53	-	850.5
AHQ-10-1, 3359	K.AAAFEEQENETVVVK.E	1664.79496	2	1.02E-08	0.97	5.19	-	1463.0
AHQ-10-14-, 3142	K.AAAFEEQENETVVVK.E	1664.79496	2	9.08E-06	0.96	4.38	-	1519.9
AHQ-10-1, 3459	K.AAAFEEQENETVVVK.E	1664.79496	2	3.91E-05	0.41	2.60	-	362.5
AHQ-10-2, 3400	K.AAAFEEQENETVVVK.E	1664.79496	2	8.18E-07	0.97	4.99	-	1843.5
AHQ-10-6, 3275	K.AAAFEEQENETVVVK.E	1664.79496	2	7.23E-05	0.29	2.60	-	362.5
AHQ-10-4, 2677	R.AAM*EPIVISAK.T	1146.38260	1	2.85E-04	0.21	1.99	-	199.6
AHQ-10-4, 2667	R.AAM*EPIVISAK.T	1146.38260	2	1.53E-05	0.91	3.10	-	963.9
AHQ-10-7, 4684 - 4740	K.ACEFAGFQCQIQFGPHNEQK.H	2399.60390	3	5.10E-06	0.85	4.10	-	587.1
AHQ-10-4, 2035	K.ADAEGESDLENSR.K	1393.35296	2	9.68E-06	0.89	3.35	-	996.3
AHQ-10-2, 2091	K.ADAEGESDLENSR.K	1393.35296	2	1.72E-07	0.90	3.25	-	1051.6
AHQ-10-3, 2682 - 2730	K.AGALQCSPSDAYTK.K	1470.58689	2	1.85E-05	0.81	2.96	-	703.0
AHQ-10-4, 2556	K.AGALQCSPSDAYTK.K	1470.58689	2	7.07E-04	0.65	2.69	-	692.3
AHQ-10-4, 2655	K.AGALQCSPSDAYTK.K	1470.58689	2	2.69E-05	0.82	2.96	-	777.5
AHQ-10-3, 2467	K.AGALQCSPSDAYTKK.E	1598.75981	2	1.21E-04	0.50	2.52	-	449.7
AHQ-10-8, 5838	K.AGFLDLKDFLPK.E	1364.61374	2	5.28E-04	0.90	3.74	-	1124.9
AHQ-10-3, 3923	K.AIAVTVQEMVTK.S	1290.55498	2	1.01E-04	0.93	3.94	-	1118.5
AHQ-10-4, 3932	K.AIAVTVQEMVTK.S	1290.55498	2	5.28E-05	0.95	4.39	-	1243.2
AHQ-10-5, 3924	K.AIAVTVQEMVTK.S	1290.55498	2	2.36E-05	0.95	4.06	-	1241.8
AHQ-10-5, 2957	K.AIAVTVQEM*VTK.S	1306.55438	2	4.00E-05	0.95	4.05	-	1079.1
AHQ-10-7, 3845	K.AIAVTVQEMVTK.S	1290.55498	2	1.43E-04	0.85	3.18	-	801.8
AHQ-10-2, 3024	K.AIAVTVQEM*VTK.S	1306.55438	2	9.28E-07	0.96	4.14	-	1274.2
AHQ-10-3, 2979	K.AIAVTVQEM*VTK.S	1306.55438	2	5.30E-06	0.92	3.63	-	822.7
AHQ-10-4, 2539	K.ALDGAFTEENR.A	1223.27427	2	1.88E-06	0.95	3.80	-	1616.1
AHQ-10-3, 2554 - 2562	K.ALDGAFTEENR.A	1223.27427	2	7.42E-07	0.92	3.37	-	1110.7
AHQ-10-3, 2742	K.ALDGAFTEENR.A	1223.27427	2	1.88E-07	0.95	3.36	-	1659.2
AHQ-10-7, 3829	K.ALDYYMLR.N	1045.23686	2	3.30E-04	0.91	3.34	-	705.0
AHQ-10-4, 2103	R.ALEATTEHIR.Q	1141.25953	2	8.28E-05	0.80	2.88	-	1128.7
AHQ-10-7, 2096	R.ALEATTEHIR.Q	1141.25953	2	6.05E-05	0.85	3.26	-	976.7
AHQ-10-3, 2127	R.ALEATTEHIR.Q	1141.25953	2	6.64E-05	0.85	2.88	-	1131.0
AHQ-10-4, 2119	R.ALEATTEHIR.Q	1141.25953	1	2.68E-05	0.26	1.94	-	303.2

AHQ-10-5, 2072	R.ALEATTEHIR.Q	1141.25953	2	8.26E-06	0.82	2.70	-	1179.5
AHQ-10-6, 2081 - 2091	R.ALEATTEHIR.Q	1141.25953	2	5.31E-05	0.81	2.88	-	941.1
AHQ-10-2, 2158	R.ALEATTEHIR.Q	1141.25953	2	1.88E-05	0.89	3.12	-	1124.0
AHQ-10-2, 3490	K.ALGDLISATK.A	989.14811	2	7.91E-07	0.92	3.82	-	885.9
AHQ-10-3, 3433	K.ALGDLISATK.A	989.14811	2	4.63E-05	0.80	2.78	-	722.5
AHQ-10-6, 3375	K.ALGDLISATK.A	989.14811	2	2.50E-05	0.89	3.02	-	657.3
AHQ-10-5, 3427 - 3429	K.ALGDLISATK.A	989.14811	2	1.10E-05	0.92	4.32	-	789.7
AHQ-10-4, 3433 - 3435	K.ALGDLISATK.A	989.14811	2	3.38E-05	0.93	3.97	-	797.3
AHQ-10-6, 2604 - 2687	K.ALSTDPAAPNLK.S	1198.35099	2	2.94E-04	0.59	2.55	-	534.0
AHQ-10-3, 2666 - 2722	K.ALSTDPAAPNLK.S	1198.35099	2	8.17E-05	0.60	2.84	-	538.2
AHQ-10-4, 2687	K.ALSTDPAAPNLK.S	1198.35099	2	7.89E-06	0.46	2.58	-	530.0
AHQ-10-2, 3630	K.ALSTDPAAPNLKSQLAAAAR.A	1967.21592	2	2.60E-08	0.85	3.69	-	465.2
AHQ-10-1, 5621 - 5629	R.ANQAIQM*ACQSLGEPGCTQAQVLSAATIVAK.H	3236.64462	3	9.53E-04	0.80	3.88	-	580.0
AHQ-10-2, 5778	K.APGQLECETAIAALNSCLR.D	2077.32566	3	6.15E-04	0.46	3.00	-	630.8
AHQ-10-4, 5788	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.46E-05	0.84	3.33	-	873.8
AHQ-10-3, 5082 - 5139	K.APGQLECETAIAALNSCLR.D	2077.32566	2	2.88E-08	0.92	4.12	-	869.3
AHQ-10-2, 5774	K.APGQLECETAIAALNSCLR.D	2077.32566	2	1.50E-09	0.94	4.41	-	993.2
AHQ-10-3, 5683	K.APGQLECETAIAALNSCLR.D	2077.32566	2	7.40E-06	0.91	4.32	-	689.3
AHQ-10-4, 5540	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	2	1.14E-04	0.55	2.69	-	505.1
AHQ-10-4, 5547 - 5569	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	1.35E-09	0.95	5.17	-	1262.7
AHQ-10-2, 6251	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	7.01E-04	0.59	3.02	-	634.2
AHQ-10-4, 6248 - 6249	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	3.55E-04	0.95	5.35	-	1294.5
AHQ-10-3, 5462	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	5.65E-08	0.93	4.65	-	1176.8
AHQ-10-3, 6153 - 6158	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	6.13E-04	0.83	3.90	-	843.4
AHQ-10-2, 5562 - 5571	K.AQEACGPLEM*DSALSVVQNLEK.D	2407.66105	3	1.46E-04	0.95	5.08	-	1501.4
AHQ-10-5, 6247	K.AQEACGPLEMDSALSVVQNLEK.D	2391.66165	3	4.77E-08	0.81	3.35	-	1071.9
AHQ-10-1, 3226	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.19E-07	0.89	3.61	-	638.7
AHQ-10-4, 2980	K.ASAGPQPLLVQSCK.A	1457.67763	2	3.36E-04	0.58	2.71	-	383.3
AHQ-10-3, 3007 - 3037	K.ASAGPQPLLVQSCK.A	1457.67763	2	5.15E-08	0.85	3.68	-	459.6
AHQ-10-2, 3044 - 3106	K.ASAGPQPLLVQSCK.A	1457.67763	2	2.55E-12	0.85	3.63	-	398.8
AHQ-10-4, 4108	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	7.86E-06	0.40	2.78	-	305.6
AHQ-10-5, 3621 - 3623	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	2.15E-09	0.95	4.82	-	951.8
AHQ-10-2, 4158	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.08E-07	0.93	4.45	-	740.2
AHQ-10-1, 4238	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	1.19E-05	0.80	3.45	-	479.9
AHQ-10-6, 4027	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	2.49E-08	0.77	2.99	-	517.7
AHQ-10-5, 4107	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	3.43E-08	0.92	4.68	-	579.2
AHQ-10-3, 4087 - 4098	K.ASVPTIQDQASAMQLSQCAK.N	2136.39332	2	9.13E-09	0.94	4.93	-	798.9
AHQ-10-1, 3777 - 3779	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	4.33E-04	0.87	3.85	-	641.6
AHQ-10-6, 3559 - 3563	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	5.42E-09	0.92	4.15	-	699.9
AHQ-10-3, 3609	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	3.58E-04	0.71	3.32	-	408.1
AHQ-10-4, 3631	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	6.90E-06	0.89	3.74	-	654.3
AHQ-10-2, 3679 - 3690	K.ASVPTIQDQASAM*QLSQCAK.N	2152.39272	2	9.71E-05	0.94	4.49	-	962.3
AHQ-10-6, 4697	K.AVAEQIPLLVQGVR.G	1493.77619	3	2.62E-05	0.96	4.53	-	1835.1
AHQ-10-3, 4766	K.AVAEQIPLLVQGVR.G	1493.77619	3	3.89E-06	0.97	5.18	-	1991.0
AHQ-10-7, 4677	K.AVAEQIPLLVQGVR.G	1493.77619	2	9.56E-06	0.78	3.17	-	483.8
AHQ-10-3, 4751	K.AVAEQIPLLVQGVR.G	1493.77619	2	5.56E-05	0.70	3.01	-	412.6
AHQ-10-2, 4838	K.AVAEQIPLLVQGVR.G	1493.77619	3	3.91E-06	0.96	4.69	-	1977.0
AHQ-10-4, 4812	K.AVAEQIPLLVQGVR.G	1493.77619	3	4.33E-06	0.96	4.50	-	1951.8
AHQ-10-4, 4787	K.AVAEQIPLLVQGVR.G	1493.77619	2	9.78E-05	0.93	3.92	-	839.5
AHQ-10-2, 4826 - 4888	K.AVAEQIPLLVQGVR.G	1493.77619	2	3.36E-06	0.91	4.01	-	786.0
AHQ-10-5, 4767 - 4773	K.AVAEQIPLLVQGVR.G	1493.77619	2	2.46E-06	0.93	4.20	-	692.1
AHQ-10-4, 3803 - 3859	K.AVASAAAALVLK.A	1085.32216	2	3.42E-06	0.96	3.99	-	1670.4
AHQ-10-1, 3991	K.AVASAAAALVLK.A	1085.32216	2	1.63E-05	0.93	3.60	-	1326.6
AHQ-10-5, 3823	K.AVASAAAALVLK.A	1085.32216	2	6.42E-05	0.84	3.11	-	837.1
AHQ-10-8, 3710	K.AVASAAAALVLK.A	1085.32216	2	1.44E-06	0.96	3.59	-	1942.8
AHQ-10-7, 3736	K.AVASAAAALVLK.A	1085.32216	2	2.81E-07	0.96	4.17	-	1711.9
AHQ-10-2, 3735 - 3794	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.40E-08	0.95	3.98	-	1772.3
AHQ-10-2, 3995 - 4054	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	1.50E-09	0.93	3.86	-	1301.8
AHQ-10-6, 3875	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.54E-04	0.93	4.13	-	1227.7
AHQ-10-1, 4059	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	5.26E-10	0.93	3.96	-	1135.4
AHQ-10-2, 4112 - 4136	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	7.23E-10	0.97	5.18	-	1507.0
AHQ-10-5, 3957 - 4032	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	7.19E-07	0.95	4.70	-	1283.7
AHQ-10-2, 4646	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	3.59E-04	0.89	3.50	-	1069.6
AHQ-10-2, 4371 - 4439	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	4.44E-05	0.82	3.47	-	779.5
AHQ-10-4, 4056	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	8.03E-06	0.91	4.14	-	981.0
AHQ-10-4, 3672 - 3743	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	2.62E-05	0.88	3.89	-	1117.2
AHQ-10-3, 3939 - 4015	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	7.97E-05	0.91	3.98	-	1178.3
AHQ-10-4, 3959	K.AVEGCVSASQAATEDGQLLR.G	2064.22056	2	7.05E-07	0.96	4.95	-	1562.2
AHQ-10-7, 6324	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	8.31E-13	0.98	6.53	-	1914.0
AHQ-10-2, 6414 - 6455	K.AVSSAIAQLLGEVAQGNENYAGIAAR.D	2574.83158	3	4.94E-14	0.98	7.23	-	2371.5
AHQ-10-3, 5495	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.28E-04	0.70	2.96	-	460.3
AHQ-10-2, 5590	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	1.85E-04	0.50	2.73	-	318.6
AHQ-10-4, 5221 - 5292	R.AVTDSINQLITM*CTQQAPGQK.E	2322.60252	2	2.07E-05	0.52	3.07	-	239.5
AHQ-10-2, 4535	R.AVTDSINQLITMCTQQAPGQK.E	2306.60312	2	7.43E-07	0.74	3.24	-	389.3
AHQ-10-2, 5423	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.74E-09	0.91	4.67	-	857.9
AHQ-10-3, 5565 - 5642	R.AVTDSINQLITMCTQQAPGQKECDNALR.E	3166.51128	3	4.39E-04	0.60	3.03	-	545.6
AHQ-10-4, 5411	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	6.04E-10	0.90	4.30	-	937.5
AHQ-10-1, 5458	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.00E-03	0.80	3.53	-	644.8
AHQ-10-3, 5329 - 5387	R.AVTDSINQLITM*CTQQAPGQKECDNALR.E	3182.51068	3	1.91E-04	0.89	4.93	-	654.4
AHQ-10-8, 3495 - 3561	R.DDILNGSHPVSFDK.A	1544.64741	2	8.65E-10	0.95	3.79	-	1611.0
AHQ-10-9, 3268 - 3333	R.DDILNGSHPVSFDK.A	1544.64741	2	5.31E-04	0.74	2.68	-	784.2
AHQ-10-8, 3402	R.DDILNGSHPVSFDK.A	1544.64741	2	6.28E-05	0.87	3.26	-	874.8
AHQ-10-7, 3398 - 3421	R.DDILNGSHPVSFDK.A	1544.64741	2	3.31E-09	0.94	4.01	-	1043.5
AHQ-10-8, 3601	R.DDILNGSHPVSFDK.A	1544.64741	2	1.77E-05	0.91	4.07	-	1029.6
AHQ-10-7, 3597	R.DDILNGSHPVSFDK.A	1544.64741	2	7.74E-11	0.95	4.26	-	1366.6
AHQ-10-3, 3479	R.DDILNGSHPVSFDK.A	1544.64741	2	2.48E-04	0.47	2.59	-	352.2
AHQ-10-3, 4943	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	3.90E-06	0.88	3.39	-	894.5
AHQ-10-3, 5529 - 5594	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	2.61E-07	0.89	3.73	-	815.8
AHQ-10-2, 5622 - 5688	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.29E-08	0.91	4.32	-	762.0
AHQ-10-2, 5019 - 5036	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.40E-10	0.93	4.10	-	1151.9
AHQ-10-2, 5744 - 5814	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	3	4.70E-05	0.84	4.19	-	770.4
AHQ-10-7, 5505	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	1.14E-08	0.86	3.48	-	757.7
AHQ-10-4, 5627	R.DKAPGQLECETAIAALNSCLR.D	2320.58644	2	9.34E-07	0.94	4.56	-	1000.8
AHQ-10-2, 4927 - 4986	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	5.07E-07	0.94	4.45	-	1119.1
AHQ-10-1, 5033 - 5034	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	3.72E-04	0.92	3.94	-	950.9
AHQ-10-3, 4889	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	3.22E-05	0.97	5.01	-	2213.3
AHQ-10-3, 4849 - 4905	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	4.61E-11	0.93	4.56	-	744.1
AHQ-10-4, 4913 - 4967	R.DLDQASLAAVSQQLAPR.E	1783.96422	2	2.85E-08	0.95	5.16	-	924.2
AHQ-10-2, 4975	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	1.26E-05	0.95	4.44	-	1938.0
AHQ-10-1, 5050	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	5.62E-04	0.93	3.79	-	1687.4
AHQ-10-4, 4956	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	4.64E-05	0.93	4.31	-	1536.4
AHQ-10-6, 4860	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	3.91E-07	0.93	4.39	-	1630.5
AHQ-10-5, 4953	R.DLDQASLAAVSQQLAPR.E	1783.96422	3	4.67E-06	0.95	4.61	-	1843.1
AHQ-10-4, 3588	R.DPPSWSVLAGHSR.T	1409.53156	2	1.25E-07	0.73	2.84	-	352.1
AHQ-10-3, 3579 - 3581	R.DPPSWSVLAGHSR.T	1409.53156	2	1.41E-06	0.90	3.55	-	622.0
AHQ-10-2, 3646	R.DPPSWSVLAGHSR.T	1409.53156	2	2.70E-07	0.68	2.70	-	406.5
AHQ-10-3, 3582	R.DPPSWSVLAGHSR.T	1409.53156	3	1.94E-05	0.91	3.89	-	779.7

AHQ-10-4, 3603	R.DPPSWSVLAGHSR.T	1409.53156	3	1.46E-06	0.87	4.09	-	581.3
AHQ-10-2, 3658	R.DPPSWSVLAGHSR.T	1409.53156	3	9.87E-07	0.92	4.56	-	809.6
AHQ-10-1, 3755	R.DPPSWSVLAGHSR.T	1409.53156	2	3.67E-07	0.71	2.91	-	462.9
AHQ-10-10, 4708	R.DPVQLNLLYVQAR.D	1529.76539	2	2.10E-04	0.94	3.72	-	1176.7
AHQ-10-7, 4813 - 4829	R.DPVQLNLLYVQAR.D	1529.76539	2	6.09E-06	0.95	3.95	-	1579.8
AHQ-10-9, 4623	R.DPVQLNLLYVQAR.D	1529.76539	2	9.18E-05	0.94	3.65	-	1366.3
AHQ-10-3, 4898	R.DPVQLNLLYVQAR.D	1529.76539	2	6.17E-08	0.96	4.19	-	1452.9
AHQ-10-8, 4873 - 4887	R.DPVQLNLLYVQAR.D	1529.76539	2	9.88E-09	0.97	5.32	-	1459.7
AHQ-10-2, 2611	K.EAAYHPEVAPDVR.L	1454.56910	2	1.21E-06	0.91	3.42	-	1040.1
AHQ-10-2, 5583 - 5638	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.36E-08	0.96	4.48	-	1649.7
AHQ-10-7, 5229 - 5262	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.24E-05	0.61	3.03	-	709.1
AHQ-10-4, 5365 - 5424	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.91E-04	0.28	2.51	-	417.5
AHQ-10-4, 5525 - 5583	K.EADESLNFEEQILEAAK.S	1937.05072	2	4.40E-07	0.96	4.92	-	1701.9
AHQ-10-7, 5541	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.82E-04	0.46	2.89	-	538.8
AHQ-10-1, 5610 - 5673	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.82E-07	0.97	5.17	-	1817.9
AHQ-10-13-, 5386 - 5444	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.78E-07	0.88	3.53	-	1035.7
AHQ-10-3, 5437 - 5505	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.69E-07	0.96	5.31	-	1377.9
AHQ-10-3, 5485	K.EADESLNFEEQILEAAK.S	1937.05072	3	4.11E-04	0.70	3.01	-	937.7
AHQ-10-4, 5623 - 5681	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.40E-05	0.95	4.85	-	1285.8
AHQ-10-3, 5549	K.EADESLNFEEQILEAAK.S	1937.05072	2	3.06E-07	0.95	4.53	-	1608.7
AHQ-10-6, 5436 - 5513	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.59E-09	0.97	4.95	-	1830.3
AHQ-10-5, 5555 - 5627	K.EADESLNFEEQILEAAK.S	1937.05072	2	1.07E-07	0.96	4.64	-	1587.9
AHQ-10-7, 5452 - 5454	K.EADESLNFEEQILEAAK.S	1937.05072	2	2.67E-04	0.97	4.89	-	1915.6
AHQ-10-2, 6480	R.ECANGYLELLDHVLLTLQKPSPELK.Q	2883.30906	3	1.62E-08	0.96	5.39	-	1372.6
AHQ-10-2, 6391 - 6416	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	6.30E-05	0.91	4.81	-	808.9
AHQ-10-6, 6291	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.45E-06	0.94	5.62	-	867.9
AHQ-10-4, 6443	R.EGISQEALHTQMLTAVQEISHLIEPLANAAR.A	3372.79804	3	7.61E-04	0.53	3.46	-	522.2
AHQ-10-3, 6227 - 6306	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.65E-08	0.90	4.46	-	1018.5
AHQ-10-4, 6383	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	3.35E-07	0.93	4.87	-	1038.5
AHQ-10-5, 6416	R.EGISQEALHTQM*LTAVQEISHLIEPLANAAR.A	3388.79744	3	1.95E-10	0.97	6.06	-	1742.9
AHQ-10-3, 5697 - 5761	R.ELLENPVQPINDM*SYFGCLDSVM*ENSK.V	3164.48754	3	3.88E-06	0.92	5.18	-	553.0
AHQ-10-4, 5753 - 5809	R.ELLENPVQPINDM*SYFGCLDSVM*ENSK.V	3164.48754	3	1.96E-08	0.85	3.57	-	770.2
AHQ-10-3, 6101	R.ELLENPVQPINDMSYFGCLDSVM*ENSK.V	3148.48814	3	2.31E-04	0.62	3.18	-	309.8
AHQ-10-7, 3116	R.EQGVEEHETLLLR.R	1553.69898	2	2.42E-04	0.87	3.52	-	557.4
AHQ-10-7, 5253	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	2.60E-10	0.98	7.59	-	2143.3
AHQ-10-14-, 5269 - 5274	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	2.83E-06	0.98	6.18	-	2091.5
AHQ-10-13-, 5201 - 5256	R.ERIPEAPAGPPSDFGLFLSDDDPK.K	2571.77979	3	6.58E-08	0.97	6.55	-	1626.0
AHQ-10-7, 4896	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	1.61E-04	0.81	3.56	-	977.6
AHQ-10-8, 4979	R.ERIPEAPAGPPSDFGLFLSDDDPKK.G	2699.95270	3	5.05E-14	0.98	6.62	-	2383.9
AHQ-10-2, 2318	K.EVANSTANLVK.T	1146.27608	2	5.85E-04	0.82	2.83	-	862.4
AHQ-10-3, 2278	K.EVANSTANLVK.T	1146.27608	2	8.05E-05	0.69	2.78	-	547.5
AHQ-10-7, 4460 - 4517	K.EVIQEWNLTNIK.R	1487.68214	2	2.95E-04	0.60	2.87	-	514.9
AHQ-10-7, 2993	K.FFYSDQNVDSR.D	1378.42795	2	2.15E-06	0.93	3.48	-	1087.9
AHQ-10-8, 2971	K.FFYSDQNVDSR.D	1378.42795	2	3.44E-06	0.91	3.37	-	918.0
AHQ-10-8, 5593 - 5594	K.FFYSDQNVDSRDPVQLNLLYVQAR.D	2889.17074	3	4.19E-06	0.97	5.77	-	1963.4
AHQ-10-1, 5846 - 5901	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	3.25E-05	0.84	3.74	-	846.1
AHQ-10-4, 5821 - 5875	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	6.48E-06	0.91	4.35	-	887.9
AHQ-10-3, 5725 - 5781	R.FGQDFSTFLEAGVEM*AGQAPSQEDR.A	2734.89265	3	8.70E-07	0.88	4.43	-	873.4
AHQ-10-4, 2875 - 2901	K.FLPSELRDEH	1243.35032	2	9.07E-07	0.65	2.66	-	407.3
AHQ-10-6, 4859	K.GLAGAVSELLR.S	1086.26701	2	4.34E-04	0.88	2.63	-	1346.3
AHQ-10-3, 4922	K.GLAGAVSELLR.S	1086.26701	2	1.59E-06	0.98	4.64	-	2445.2
AHQ-10-1, 5079	K.GLAGAVSELLR.S	1086.26701	2	1.00E-06	0.96	4.11	-	1734.3
AHQ-10-4, 4976	K.GLAGAVSELLR.S	1086.26701	2	2.01E-06	0.97	4.62	-	2131.6
AHQ-10-5, 4933	K.GLAGAVSELLR.S	1086.26701	2	7.97E-08	0.97	4.02	-	1857.4
AHQ-10-2, 4998	K.GLAGAVSELLR.S	1086.26701	2	2.44E-06	0.97	4.25	-	2149.4
AHQ-10-5, 6029 - 6100	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.31E-04	0.81	4.05	-	603.9
AHQ-10-3, 6025	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	2	1.61E-04	0.89	3.18	-	1064.9
AHQ-10-3, 5939 - 6011	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	3.03E-04	0.83	4.23	-	674.9
AHQ-10-3, 5738 - 5806	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.94E-05	0.81	3.72	-	918.8
AHQ-10-4, 6088 - 6155	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	7.19E-04	0.94	4.98	-	1287.7
AHQ-10-2, 5952 - 6022	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	2.66E-05	0.74	3.88	-	586.3
AHQ-10-6, 5880 - 5951	R.GSQAQPDSPSAQLALIAASQSFLQPGGK.M	2756.02103	3	9.95E-05	0.75	3.82	-	715.9
AHQ-10-2, 6538	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	7.89E-10	0.96	5.75	-	1426.6
AHQ-10-5, 6516	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.11E-04	0.87	4.22	-	870.5
AHQ-10-3, 6422 - 6425	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	5.22E-06	0.97	6.07	-	1499.4
AHQ-10-4, 6503	K.GTEWVDPEDPTVIAENELLGAAAAIEAAAK.K	3053.32301	3	1.57E-07	0.96	5.59	-	1665.1
AHQ-10-7, 6353	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	7.97E-05	0.97	6.35	-	1894.3
AHQ-10-5, 6419	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	5.96E-05	0.96	5.44	-	1674.9
AHQ-10-4, 6407 - 6413	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	2.75E-11	0.98	6.70	-	2847.4
AHQ-10-6, 6296	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	4.23E-09	0.98	6.39	-	3472.6
AHQ-10-8, 6389	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	2	6.88E-05	0.93	4.34	-	914.5
AHQ-10-1, 6434 - 6513	R.GVAALTSDPAVQAIVLDTASDVLDK.A	2470.75835	3	7.09E-07	0.98	6.76	-	3165.3
AHQ-10-4, 6467	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	1.83E-07	0.92	4.57	-	737.3
AHQ-10-2, 6490	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	6.26E-06	0.95	5.22	-	979.2
AHQ-10-5, 6471	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.91E-07	0.92	4.32	-	966.0
AHQ-10-4, 6463 - 6541	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	6.82E-08	0.96	5.70	-	1250.8
AHQ-10-5, 6473	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	8.87E-05	0.95	5.47	-	771.4
AHQ-10-8, 6445	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	5.04E-07	0.93	4.44	-	952.8
AHQ-10-2, 5470	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	3.47E-08	0.91	4.11	-	823.4
AHQ-10-3, 6391	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	2.53E-05	0.94	4.51	-	1267.8
AHQ-10-6, 6353	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	2	4.62E-05	0.83	4.02	-	618.3
AHQ-10-6, 6351	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	2.19E-08	0.89	3.92	-	956.3
AHQ-10-3, 6385	R.GVGAAATAVTQALNELLQHVK.A	2092.38495	3	3.89E-08	0.91	4.42	-	985.2
AHQ-10-7, 3525 - 3572	R.IGITNHDEYSLVR.E	1517.66833	2	1.03E-04	0.86	3.22	-	955.5
AHQ-10-7, 3253 - 3312	R.IGITNHDEYSLVR.E	1517.66833	2	1.63E-09	0.91	3.44	-	1209.1
AHQ-10-13-, 3406	R.IGITNHDEYSLVR.E	1517.66833	3	2.03E-07	0.84	3.44	-	722.7
AHQ-10-8, 3641 - 3647	R.IGITNHDEYSLVR.E	1517.66833	2	8.54E-07	0.85	2.96	-	872.6
AHQ-10-13-, 3402	R.IGITNHDEYSLVR.E	1517.66833	2	8.84E-10	0.94	4.03	-	1144.7
AHQ-10-8, 3513 - 3573	R.IGITNHDEYSLVR.E	1517.66833	2	3.43E-09	0.94	3.87	-	1483.1
AHQ-10-7, 3308 - 3310	R.IGITNHDEYSLVR.E	1517.66833	3	2.33E-06	0.94	4.75	-	900.4
AHQ-10-13-, 3402	R.IGITNHDEYSLVRELMEEK.K	2277.54018	3	2.35E-04	0.45	3.10	-	412.3
AHQ-10-2, 4284	R.ILAQATSDLVNAIK.A	1457.69748	2	2.46E-07	0.94	3.44	-	1397.3
AHQ-10-1, 4933	R.ILAQATSDLVNAIK.A	1457.69748	2	4.70E-05	0.96	4.22	-	1553.1
AHQ-10-3, 4785	R.ILAQATSDLVNAIK.A	1457.69748	2	5.79E-07	0.97	4.67	-	1998.0
AHQ-10-4, 4043 - 4044	R.ILAQATSDLVNAIK.A	1457.69748	2	5.73E-07	0.97	4.03	-	2021.3
AHQ-10-2, 4450 - 4472	R.ILAQATSDLVNAIK.A	1457.69748	2	3.30E-05	0.88	3.39	-	970.5
AHQ-10-7, 4720 - 4782	R.ILAQATSDLVNAIK.A	1457.69748	2	2.16E-05	0.95	4.24	-	1458.5
AHQ-10-2, 4560	R.ILAQATSDLVNAIK.A	1457.69748	2	4.82E-07	0.94	3.63	-	1389.2
AHQ-10-2, 4027 - 4094	R.ILAQATSDLVNAIK.A	1457.69748	2	5.24E-06	0.97	4.59	-	2028.7
AHQ-10-6, 3953 - 3963	R.ILAQATSDLVNAIK.A	1457.69748	2	9.62E-10	0.98	4.38	-	2673.7
AHQ-10-7, 3930	R.ILAQATSDLVNAIK.A	1457.69748	2	5.70E-08	0.95	3.71	-	1465.2
AHQ-10-5, 4795 - 4807	R.ILAQATSDLVNAIK.A	1457.69748	2	8.31E-10	0.98	4.96	-	2492.9
AHQ-10-6, 4724 - 4791	R.ILAQATSDLVNAIK.A	1457.69748	2	3.06E-09	0.98	5.09	-	2098.4
AHQ-10-4, 4836 - 4847	R.ILAQATSDLVNAIK.A	1457.69748	2	1.78E-08	0.98	5.28	-	1770.0
AHQ-10-5, 4036 - 4043	R.ILAQATSDLVNAIK.A	1457.69748	2	1.63E-07	0.98	4.37	-	2396.3
AHQ-10-2, 4863	R.ILAQATSDLVNAIK.A	1457.69748	2	1.01E-09	0.97	3.93	-	2021.4
AHQ-10-3, 4022	R.ILAQATSDLVNAIK.A	1457.69748	2	1.82E-06	0.96	3.69	-	1805.8

AHQ-10-13-, 5485	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	3.94E-05	0.93	3.84	-	1092.9
AHQ-10-8, 5502 - 5557	R.IPEAPAGPPSDFGLFLSDDDPK.K	2286.47890	2	3.00E-06	0.93	4.29	-	981.5
AHQ-10-3, 5214	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	2.59E-06	0.82	3.76	-	649.9
AHQ-10-8, 5194 - 5259	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.21E-08	0.92	4.26	-	1101.4
AHQ-10-13-, 5148 - 5161	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	5.79E-10	0.91	4.11	-	981.7
AHQ-10-13, 5440 - 5501	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	4.77E-07	0.91	4.80	-	933.9
AHQ-10-1, 5354	R.IPEAPAGPPSDFGLFLSDDDPKK.G	2414.65181	3	1.75E-06	0.90	3.74	-	1198.9
AHQ-10-8, 2731	R.KFFYSDQNVDSR.D	1506.60087	2	1.41E-04	0.87	2.82	-	994.6
AHQ-10-7, 2661 - 2734	R.KFFYSDQNVDSR.D	1506.60087	2	4.38E-05	0.88	3.62	-	740.0
AHQ-10-7, 2736 - 2738	K.LAQAAQSSVATITR.L	1417.59344	2	6.58E-09	0.95	3.72	-	1815.8
AHQ-10-2, 2850	K.LAQAAQSSVATITR.L	1417.59344	2	1.69E-06	0.94	3.65	-	1360.6
AHQ-10-8, 2743 - 2754	K.LAQAAQSSVATITR.L	1417.59344	2	8.56E-05	0.68	2.88	-	740.1
AHQ-10-6, 2743	K.LAQAAQSSVATITR.L	1417.59344	2	2.97E-06	0.94	3.77	-	1286.9
AHQ-10-6, 2588 - 2595	K.LAQAAQSSVATITR.L	1417.59344	2	9.74E-06	0.97	4.81	-	1865.1
AHQ-10-1, 2995	K.LAQAAQSSVATITR.L	1417.59344	2	1.04E-05	0.95	3.50	-	1548.9
AHQ-10-3, 2763 - 2821	K.LAQAAQSSVATITR.L	1417.59344	2	2.59E-09	0.97	4.86	-	1479.9
AHQ-10-3, 2647	K.LAQAAQSSVATITR.L	1417.59344	2	7.33E-07	0.94	3.82	-	1403.4
AHQ-10-4, 2767	K.LAQAAQSSVATITR.L	1417.59344	2	7.79E-09	0.96	4.20	-	1612.4
AHQ-10-2, 2686 - 2726	K.LAQAAQSSVATITR.L	1417.59344	2	2.18E-04	0.89	3.42	-	898.8
AHQ-10-5, 2775 - 2797	K.LAQAAQSSVATITR.L	1417.59344	2	1.93E-09	0.96	4.21	-	1357.8
AHQ-10-4, 2620	K.LAQAAQSSVATITR.L	1417.59344	2	1.37E-05	0.95	3.69	-	1773.9
AHQ-10-6, 3203 - 3265	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	4.77E-06	0.88	4.01	-	910.2
AHQ-10-2, 3594	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.35E-07	0.96	4.67	-	2177.5
AHQ-10-2, 3362 - 3364	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	5.89E-07	0.96	5.40	-	1769.1
AHQ-10-3, 3070	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	4.33E-04	0.66	3.23	-	753.7
AHQ-10-3, 3306	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	2	2.61E-06	0.88	4.06	-	502.5
AHQ-10-1, 3486	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.17E-08	0.97	5.75	-	2386.3
AHQ-10-4, 3296	R.LASEAKPAAVAAENEEIGSHIK.H	2236.46779	3	1.70E-04	0.95	5.04	-	1705.1
AHQ-10-5, 5151	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	8.66E-07	0.98	5.66	-	2526.5
AHQ-10-2, 4967 - 5022	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.38E-07	0.94	4.96	-	686.9
AHQ-10-4, 5296	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	2.66E-05	0.90	3.44	-	1664.3
AHQ-10-4, 5285	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.09E-11	0.89	4.42	-	603.1
AHQ-10-5, 5144	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.76E-07	0.95	4.70	-	1121.7
AHQ-10-4, 5167	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	6.27E-09	0.98	5.61	-	2760.3
AHQ-10-1, 5065	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.32E-05	0.86	3.54	-	613.8
AHQ-10-4, 5163	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.75E-04	0.95	5.18	-	826.0
AHQ-10-13-, 5044	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.14E-05	0.83	3.10	-	777.6
AHQ-10-4, 4968 - 4975	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	3.59E-10	0.97	5.09	-	1698.4
AHQ-10-1, 5241 - 5243	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	3.71E-05	0.94	4.64	-	1430.2
AHQ-10-6, 4835 - 4855	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.00E-06	0.87	4.12	-	586.1
AHQ-10-3, 5222 - 5266	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.16E-04	0.75	3.57	-	393.6
AHQ-10-6, 4857	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	2.25E-05	0.85	3.40	-	1263.4
AHQ-10-6, 5036 - 5043	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	5.40E-06	0.96	5.24	-	1053.3
AHQ-10-6, 5169	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	6.99E-09	0.94	4.66	-	783.3
AHQ-10-1, 5358 - 5381	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.16E-07	0.86	4.09	-	504.9
AHQ-10-3, 5103 - 5106	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	8.02E-06	0.89	3.77	-	1272.2
AHQ-10-14-, 5069	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.10E-05	0.90	3.97	-	753.4
AHQ-10-3, 5097 - 5101	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.38E-05	0.96	5.35	-	1170.2
AHQ-10-2, 5158 - 5215	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.04E-08	0.97	5.42	-	1423.1
AHQ-10-2, 5184 - 5208	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.57E-06	0.97	5.23	-	2431.7
AHQ-10-2, 5310 - 5314	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	3	1.06E-04	0.89	3.95	-	1083.8
AHQ-10-5, 5276	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	2.96E-09	0.88	4.13	-	635.4
AHQ-10-5, 4951	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	4.84E-11	0.91	4.14	-	869.7
AHQ-10-7, 5037 - 5046	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	7.63E-05	0.97	5.27	-	1567.4
AHQ-10-2, 5306 - 5307	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.15E-10	0.95	5.05	-	864.8
AHQ-10-3, 4885 - 4951	K.LGAASLGAEDPETQVVLINAVK.D	2196.48671	2	1.71E-04	0.80	3.67	-	490.6
AHQ-10-8, 3701 - 3703	K.LHTDDELNWLDHGR.T	1721.81153	2	1.63E-06	0.97	5.00	-	1962.8
AHQ-10-8, 3702	K.LHTDDELNWLDHGR.T	1721.81153	3	5.94E-06	0.95	5.01	-	1365.9
AHQ-10-7, 3741	K.LHTDDELNWLDHGR.T	1721.81153	2	5.26E-07	0.97	4.76	-	1837.9
AHQ-10-7, 3744	K.LHTDDELNWLDHGR.T	1721.81153	3	2.59E-06	0.91	4.20	-	1055.4
AHQ-10-7, 4949	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.79E-05	0.96	5.46	-	1065.0
AHQ-10-7, 4941 - 4942	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.11E-07	0.97	5.54	-	1802.5
AHQ-10-5, 5052	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	3.46E-06	0.98	7.19	-	1469.3
AHQ-10-3, 5025	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	6.70E-07	0.94	5.08	-	999.4
AHQ-10-3, 5029	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	5.02E-09	0.97	6.19	-	1205.4
AHQ-10-6, 4959	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	4.40E-08	0.93	4.66	-	1166.0
AHQ-10-6, 4960	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	6.20E-08	0.98	6.68	-	1441.2
AHQ-10-2, 5098	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.20E-11	0.98	6.57	-	1546.4
AHQ-10-8, 4990	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	8.84E-07	0.97	6.13	-	1173.5
AHQ-10-4, 5087	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	9.75E-09	0.97	5.75	-	1360.6
AHQ-10-2, 5095	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.00E-08	0.97	5.76	-	1769.5
AHQ-10-5, 5049 - 5051	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	8.12E-08	0.96	5.39	-	1396.8
AHQ-10-9, 4755	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.03E-06	0.79	3.47	-	678.0
AHQ-10-4, 5092 - 5095	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	2.15E-08	0.98	7.17	-	1336.3
AHQ-10-8, 4993	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	2.18E-09	0.97	5.60	-	1723.0
AHQ-10-1, 5191	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	2	1.13E-06	0.97	5.50	-	1240.4
AHQ-10-9, 4751	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.13E-06	0.93	4.54	-	1033.9
AHQ-10-1, 5185	K.LLAALLEDEGGSGRPLLQAAK.G	2123.43896	3	1.33E-08	0.94	4.46	-	1452.6
AHQ-10-2, 4186 - 4243	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.08E-12	0.73	3.08	-	321.5
AHQ-10-2, 4074 - 4130	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	6.44E-08	0.92	4.56	-	429.9
AHQ-10-2, 3944 - 4015	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	8.52E-04	0.73	3.04	-	319.3
AHQ-10-3, 4039 - 4095	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	5.40E-05	0.82	3.57	-	364.9
AHQ-10-4, 4053 - 4111	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.92E-08	0.91	4.32	-	413.4
AHQ-10-3, 3953 - 4017	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	1.77E-09	0.94	5.11	-	398.3
AHQ-10-4, 3963 - 4028	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	5.42E-13	0.90	4.13	-	521.9
AHQ-10-5, 3968 - 4027	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.11E-12	0.94	4.07	-	721.6
AHQ-10-3, 4154	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	6.13E-06	0.65	3.04	-	326.0
AHQ-10-3, 3902 - 3958	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	2.25E-06	0.25	2.64	-	159.4
AHQ-10-4, 4176 - 4184	R.LLSDSLPPSTGTFQEAQSR.L	2035.20076	2	3.27E-06	0.71	3.44	-	284.5
AHQ-10-3, 5166 - 5221	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.46E-08	0.97	5.15	-	1545.2
AHQ-10-3, 5343	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	8.87E-05	0.64	2.57	-	629.8
AHQ-10-6, 5152	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.91E-10	0.97	5.23	-	1648.1
AHQ-10-6, 5155	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.97E-06	0.95	5.52	-	1100.3
AHQ-10-1, 5326	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.75E-07	0.93	3.65	-	1115.0
AHQ-10-4, 4240	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.21E-05	0.97	5.55	-	1765.3
AHQ-10-2, 4924	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.66E-05	0.93	4.48	-	656.6
AHQ-10-2, 4274 - 4354	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	7.30E-05	0.59	3.37	-	284.3
AHQ-10-4, 4232	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.44E-15	0.96	5.36	-	1055.6
AHQ-10-4, 5679	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.17E-04	0.62	2.81	-	562.4
AHQ-10-4, 5271 - 5289	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.92E-08	0.97	6.10	-	1690.0
AHQ-10-4, 5272 - 5333	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	5.21E-07	0.97	4.91	-	1733.2
AHQ-10-5, 4227	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.67E-10	0.96	4.91	-	1103.6
AHQ-10-9, 4936	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.56E-06	0.96	4.56	-	1511.8
AHQ-10-3, 5459	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.19E-09	0.98	5.73	-	2457.1
AHQ-10-1, 5574	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	2.61E-05	0.78	3.13	-	613.1
AHQ-10-7, 5165	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.82E-04	0.98	5.94	-	2295.5
AHQ-10-7, 5158 - 5160	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	3.97E-11	0.97	5.52	-	1513.7

AHQ-10-4, 5431	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.20E-11	0.97	4.53	-	1503.9
AHQ-10-2, 5438	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.30E-06	0.96	4.66	-	1314.5
AHQ-10-3, 5023	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.22E-04	0.87	3.30	-	851.2
AHQ-10-2, 4280	R.LNEAAAGLNQAATELVQASR.G	2028.21299	3	1.73E-09	0.95	4.90	-	1494.8
AHQ-10-2, 5543 - 5544	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.10E-12	0.98	5.76	-	2016.0
AHQ-10-5, 5243 - 5309	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	1.11E-14	0.97	5.72	-	1517.7
AHQ-10-2, 5275 - 5346	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	6.05E-11	0.98	6.29	-	1601.6
AHQ-10-4, 5541 - 5544	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.44E-15	0.98	5.83	-	1936.4
AHQ-10-2, 5687	R.LNEAAAGLNQAATELVQASR.G	2028.21299	2	4.30E-06	0.86	3.54	-	671.5
AHQ-10-2, 5124	R.LNEAAAGLNQAATELVQASRGTPQDLAR.A	2867.12501	3	7.63E-05	0.71	3.39	-	548.0
AHQ-10-4, 2129 - 2193	R.MATNAAAQNAIK.K	1204.38227	2	6.71E-05	0.74	3.50	-	550.3
AHQ-10-5, 4011 - 4072	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	1.36E-09	0.84	4.08	-	588.6
AHQ-10-5, 3907	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	3.35E-09	0.87	3.82	-	697.3
AHQ-10-3, 3997 - 4055	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.09E-12	0.93	5.19	-	850.3
AHQ-10-6, 3932	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	4.96E-05	0.65	3.20	-	700.5
AHQ-10-3, 3897	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.86E-04	0.80	3.56	-	697.8
AHQ-10-2, 4063 - 4140	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	6.06E-11	0.94	4.81	-	1123.8
AHQ-10-2, 4044 - 4076	R.MVAAATNNLCEAANAAVQGHASQEK.L	2558.79098	3	3.10E-04	0.98	5.64	-	2496.2
AHQ-10-2, 3966	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	6.05E-08	0.91	4.12	-	987.8
AHQ-10-4, 4023	R.M*VAAATNNLCEAANAAVQGHASQEK.L	2574.79038	3	2.72E-10	0.91	4.53	-	757.2
AHQ-10-4, 5673	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	6.61E-06	0.90	3.89	-	802.7
AHQ-10-1, 5703	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.18E-08	0.91	3.34	-	1126.1
AHQ-10-5, 5655	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	4.73E-06	0.97	5.41	-	1679.0
AHQ-10-4, 6065 - 6144	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	1.71E-04	0.96	4.33	-	1704.1
AHQ-10-3, 5507	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	4.08E-06	0.95	4.51	-	1478.7
AHQ-10-3, 5583	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	3.05E-05	0.74	3.23	-	576.7
AHQ-10-4, 5591 - 5665	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	4.38E-08	0.97	5.74	-	2099.0
AHQ-10-14-, 5456	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	2.82E-05	0.82	3.76	-	986.3
AHQ-10-14-, 5462 - 5537	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	5.63E-07	0.96	4.96	-	1221.1
AHQ-10-3, 6021 - 6054	K.M*VGGIAQIIAAQEEMLR.K	1847.19347	2	4.87E-05	0.91	3.73	-	1134.7
AHQ-10-2, 5595 - 5668	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	2	1.97E-08	0.98	6.12	-	1597.9
AHQ-10-2, 5599 - 5667	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	1.12E-07	0.97	5.87	-	2016.2
AHQ-10-1, 5706	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	9.76E-04	0.94	4.48	-	1546.8
AHQ-10-14-, 5538	K.M*VGGIAQIIAAQEEM*LR.K	1863.19287	3	8.87E-10	0.92	4.15	-	1343.9
AHQ-10-2, 5316	K.M*VGGIAQIIAAQEEM*LRK.E	1991.36578	3	2.24E-04	0.79	3.34	-	836.1
AHQ-10-4, 5304	K.M*VGGIAQIIAAQEEM*LRK.E	1991.36578	3	7.06E-04	0.86	3.65	-	786.0
AHQ-10-8, 2391	K.NCGQMSEIEAK.V	1268.40005	2	1.05E-04	0.92	3.10	-	1494.9
AHQ-10-2, 4251	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.17E-06	0.67	2.72	-	477.6
AHQ-10-1, 4455	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.23E-05	0.77	3.22	-	427.1
AHQ-10-3, 4177 - 4178	K.NGNLPEFGDAISTASK.A	1621.73018	2	8.59E-06	0.82	4.01	-	334.4
AHQ-10-4, 4113 - 4173	K.NGNLPEFGDAISTASK.A	1621.73018	2	1.51E-05	0.70	2.89	-	513.8
AHQ-10-4, 4231	K.NGNLPEFGDAISTASK.A	1621.73018	2	2.04E-05	0.72	3.28	-	364.2
AHQ-10-2, 4148	K.NGNLPEFGDAISTASK.A	1621.73018	2	3.36E-04	0.69	2.86	-	436.5
AHQ-10-1, 4327	K.NGNLPEFGDAISTASK.A	1621.73018	2	5.01E-05	0.83	3.39	-	428.1
AHQ-10-2, 4187 - 4195	K.NLGTALAELR.T	1058.21367	2	6.49E-05	0.92	3.88	-	928.1
AHQ-10-4, 4141	K.NLGTALAELR.T	1058.21367	2	9.66E-06	0.88	3.45	-	930.5
AHQ-10-3, 4118	K.NLGTALAELR.T	1058.21367	2	7.24E-06	0.94	3.25	-	1295.1
AHQ-10-1, 4278	K.NLGTALAELR.T	1058.21367	2	1.04E-04	0.88	3.23	-	1006.8
AHQ-10-2, 4712	K.NLGTALAELR.T	1058.21367	2	4.87E-05	0.83	2.91	-	957.3
AHQ-10-6, 2799	K.PAAVAAENEEIGSHIK.H	1636.78798	3	9.21E-08	0.96	4.75	-	1729.5
AHQ-10-7, 2780	K.PAAVAAENEEIGSHIK.H	1636.78798	3	2.93E-06	0.92	4.15	-	1464.3
AHQ-10-5, 2829	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.93E-08	0.96	4.98	-	1701.5
AHQ-10-3, 2857	K.PAAVAAENEEIGSHIK.H	1636.78798	3	5.53E-08	0.97	5.70	-	1869.1
AHQ-10-3, 2859	K.PAAVAAENEEIGSHIK.H	1636.78798	2	1.48E-08	0.98	5.34	-	2128.2
AHQ-10-2, 2816 - 2878	K.PAAVAAENEEIGSHIK.H	1636.78798	2	7.75E-07	0.96	4.82	-	1454.8
AHQ-10-5, 2828	K.PAAVAAENEEIGSHIK.H	1636.78798	2	3.27E-10	0.97	4.67	-	1889.0
AHQ-10-4, 2827	K.PAAVAAENEEIGSHIK.H	1636.78798	2	3.27E-11	0.97	4.93	-	1871.9
AHQ-10-4, 2823 - 2831	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.79E-10	0.97	5.90	-	1686.1
AHQ-10-2, 2904	K.PAAVAAENEEIGSHIK.H	1636.78798	3	1.40E-07	0.97	6.17	-	1729.9
AHQ-10-6, 3281	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.15E-04	0.83	3.91	-	434.3
AHQ-10-4, 3344	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	3.61E-08	0.92	4.44	-	766.5
AHQ-10-2, 3402	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	3	1.71E-05	0.76	3.26	-	829.9
AHQ-10-5, 3319 - 3320	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	6.05E-05	0.91	4.43	-	686.0
AHQ-10-2, 3403	K.QAAASATQTIAAAQHAASTPK.A	1996.17099	2	1.61E-08	0.91	4.48	-	629.7
AHQ-10-4, 3873 - 3937	R.QELAVFCSPEPPAK.T	1574.77985	2	2.24E-04	0.81	3.20	-	884.0
AHQ-10-1, 4017 - 4066	R.QELAVFCSPEPPAK.T	1574.77985	2	3.08E-04	0.65	2.78	-	582.1
AHQ-10-6, 3851	R.QELAVFCSPEPPAK.T	1574.77985	2	2.38E-07	0.93	3.71	-	1191.1
AHQ-10-2, 3974	R.QELAVFCSPEPPAK.T	1574.77985	2	4.75E-07	0.91	3.09	-	1118.1
AHQ-10-13-, 3736	K.QVAASTAQLLVACK.V	1461.70942	2	1.39E-05	0.84	3.25	-	632.7
AHQ-10-5, 3735	K.QVAASTAQLLVACK.V	1461.70942	2	8.60E-06	0.84	3.26	-	644.0
AHQ-10-4, 3273	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	2.67E-07	0.92	4.95	-	915.2
AHQ-10-6, 3224	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	6.96E-04	0.77	3.47	-	580.6
AHQ-10-2, 3604	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	8.81E-05	0.82	4.34	-	451.7
AHQ-10-1, 3447	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	2.95E-04	0.89	4.42	-	788.6
AHQ-10-2, 3334	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	7.90E-06	0.95	5.48	-	917.4
AHQ-10-3, 3267	R.SGASGPENFQVGSM*PPAQQQITSGQM*HR.G	2961.19747	3	2.85E-05	0.87	4.31	-	756.1
AHQ-10-3, 3533	R.SGASGPENFQVGSM*PPAQQQITSGQMHR.G	2945.19807	3	7.52E-04	0.65	3.13	-	565.1
AHQ-10-3, 3131	K.SIAAATSALVK.A	1032.21612	2	4.08E-05	0.94	3.29	-	1390.5
AHQ-10-7, 4069 - 4145	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	5.33E-07	0.92	4.36	-	1513.2
AHQ-10-8, 4167	K.SKDHFGLEGDEESTMLEDSVSPK.K	2538.68364	3	7.61E-10	0.96	4.92	-	1841.3
AHQ-10-7, 3752	K.SKDHFGLEGDEESTM*LEDSVSPK.K	2554.68304	3	9.77E-05	0.93	4.14	-	1267.2
AHQ-10-4, 4403	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.04E-10	0.93	4.26	-	741.7
AHQ-10-3, 4955 - 5034	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.04E-04	0.77	3.86	-	296.9
AHQ-10-3, 4837 - 4897	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.49E-05	0.86	3.93	-	399.1
AHQ-10-1, 4990 - 5043	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.06E-05	0.77	3.20	-	378.2
AHQ-10-7, 4852	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.23E-08	0.72	3.04	-	374.8
AHQ-10-6, 4995	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.11E-06	0.52	3.02	-	275.0
AHQ-10-3, 4361 - 4366	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.58E-09	0.92	4.36	-	769.1
AHQ-10-6, 4844 - 4845	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.94E-05	0.81	3.47	-	416.2
AHQ-10-2, 4912 - 4970	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.34E-08	0.89	4.35	-	357.2
AHQ-10-5, 4928 - 4939	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.29E-07	0.87	4.03	-	485.4
AHQ-10-2, 5142	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.39E-06	0.86	3.88	-	408.8
AHQ-10-1, 4505	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	7.18E-05	0.68	3.21	-	341.0
AHQ-10-4, 4944 - 5021	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.02E-05	0.84	3.87	-	405.3
AHQ-10-5, 5077	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	1.78E-04	0.69	3.14	-	373.5
AHQ-10-5, 4383	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	8.33E-09	0.92	4.72	-	460.4
AHQ-10-2, 4787 - 4842	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	6.22E-04	0.58	2.90	-	379.0
AHQ-10-2, 5014 - 5087	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.83E-07	0.89	4.15	-	476.3
AHQ-10-2, 4431 - 4462	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	2.39E-07	0.90	4.44	-	420.5
AHQ-10-4, 5108 - 5149	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	4.67E-06	0.93	4.72	-	681.6
AHQ-10-6, 4281 - 4292	K.SNTSPEELGPLANQLTSDYGR.L	2250.36505	2	3.80E-06	0.74	3.39	-	416.8
AHQ-10-8, 6365	R.TEDSGLQTQVIAAATQCALSTSQLVACTK.V	3056.37009	3	9.91E-04	0.89	4.32	-	1088.4
AHQ-10-8, 4169	K.TKEVIQEWNLTNIK.R	1716.95938	2	1.64E-07	0.96	4.64	-	1743.4
AHQ-10-7, 4194	K.TKEVIQEWNLTNIK.R	1716.95938	2	3.09E-04	0.96	4.86	-	1597.5
AHQ-10-11, 4204	K.TKEVIQEWNLTNIK.R	1716.95938	2	6.03E-06	0.85	2.97	-	896.8
AHQ-10-4, 5987 - 5992	K.TLAESALQLLYTAK.E	1522.76793	2	8.27E-09	0.90	3.59	-	873.5
AHQ-10-6, 5852	K.TLAESALQLLYTAK.E	1522.76793	2	4.76E-07	0.87	3.04	-	1008.1

AHQ-10-3, 5895	K.TLAESALQLLYTAK.E	1522.76793	2	4.15E-06	0.93	3.82	-	938.7
AHQ-10-2, 5978 - 5995	K.TLAESALQLLYTAK.E	1522.76793	2	2.30E-09	0.95	4.30	-	1011.2
AHQ-10-7, 5892	K.TLAESALQLLYTAK.E	1522.76793	2	2.92E-04	0.87	3.46	-	597.9
AHQ-10-3, 5909 - 5910	K.TLAESALQLLYTAK.E	1522.76793	3	4.55E-06	0.97	5.29	-	2245.8
AHQ-10-8, 5937	K.TLAESALQLLYTAK.E	1522.76793	2	1.40E-07	0.82	3.29	-	697.7
AHQ-10-4, 5999	K.TLAESALQLLYTAK.E	1522.76793	3	2.59E-05	0.97	5.46	-	1965.6
AHQ-10-7, 3230	K.TLSHPQQMALLDQTK.T	1711.96464	2	3.13E-04	0.42	2.93	-	263.8
AHQ-10-3, 3318	K.TLSHPQQMALLDQTK.T	1711.96464	3	2.68E-05	0.91	4.40	-	1154.5
AHQ-10-4, 3307	K.TLSHPQQMALLDQTK.T	1711.96464	2	4.52E-05	0.92	3.96	-	704.3
AHQ-10-6, 3257	K.TLSHPQQMALLDQTK.T	1711.96464	2	4.80E-05	0.93	4.23	-	832.4
AHQ-10-2, 3371 - 3378	K.TLSHPQQMALLDQTK.T	1711.96464	2	6.77E-09	0.95	4.87	-	848.6
AHQ-10-5, 3297	K.TLSHPQQMALLDQTK.T	1711.96464	2	1.99E-04	0.85	3.68	-	436.4
AHQ-10-4, 3309 - 3325	K.TLSHPQQMALLDQTK.T	1711.96464	3	2.47E-08	0.95	4.46	-	1774.6
AHQ-10-2, 3383	K.TLSHPQQMALLDQTK.T	1711.96464	3	6.63E-06	0.95	5.15	-	1124.5
AHQ-10-4, 4145 - 4207	K.TMLESAGGLIQTAR.A	1448.67095	2	1.08E-09	0.94	4.03	-	1500.8
AHQ-10-7, 4080 - 4082	K.TMLESAGGLIQTAR.A	1448.67095	2	5.98E-09	0.94	4.00	-	1421.6
AHQ-10-3, 3967	K.TMLESAGGLIQTAR.A	1448.67095	2	8.19E-06	0.74	2.75	-	877.5
AHQ-10-5, 3397 - 3468	K.TM*LESAGGLIQTAR.A	1464.67035	2	6.86E-05	0.94	4.31	-	1288.7
AHQ-10-2, 3510 - 3566	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.44E-07	0.96	4.82	-	1540.2
AHQ-10-3, 4167	K.TM*LESAGGLIQTAR.A	1464.67035	2	3.27E-06	0.86	3.03	-	1228.9
AHQ-10-1, 3641	K.TM*LESAGGLIQTAR.A	1464.67035	2	9.24E-05	0.72	2.64	-	812.9
AHQ-10-2, 4183 - 4242	K.TMLESAGGLIQTAR.A	1448.67095	2	9.83E-11	0.96	4.41	-	1648.0
AHQ-10-2, 3526	K.TM*LESAGGLIQTAR.A	1464.67035	2	3.68E-06	0.96	4.19	-	1470.5
AHQ-10-6, 4096	K.TMLESAGGLIQTAR.A	1448.67095	2	1.01E-07	0.91	3.56	-	1390.9
AHQ-10-5, 4139 - 4179	K.TMLESAGGLIQTAR.A	1448.67095	2	1.09E-05	0.82	3.20	-	962.3
AHQ-10-2, 4239	K.TMLESAGGLIQTAR.A	1448.67095	3	1.63E-06	0.94	3.67	-	1989.7
AHQ-10-4, 3511	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.46E-07	0.97	4.59	-	2030.1
AHQ-10-3, 4126 - 4153	K.TMLESAGGLIQTAR.A	1448.67095	2	7.54E-09	0.94	3.94	-	1764.4
AHQ-10-3, 3455	K.TM*LESAGGLIQTAR.A	1464.67035	2	1.21E-06	0.96	4.31	-	1347.3
AHQ-10-8, 5045	K.TYGVSFFLVK.E	1161.37395	2	1.69E-05	0.82	3.14	-	538.3
AHQ-10-7, 4993 - 4998	K.TYGVSFFLVK.E	1161.37395	2	2.11E-05	0.83	3.07	-	665.6
AHQ-10-9, 4808	K.TYGVSFFLVK.E	1161.37395	2	5.38E-06	0.91	2.80	-	1036.1
AHQ-10-11, 4947	K.TYGVSFFLVK.E	1161.37395	2	1.67E-04	0.85	2.66	-	762.3
AHQ-10-1, 5166	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	2.03E-05	0.63	2.51	-	674.6
AHQ-10-5, 5884	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.50E-05	0.93	3.44	-	1412.5
AHQ-10-2, 5100	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	5.49E-06	0.92	3.06	-	1362.0
AHQ-10-4, 5099	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	6.94E-06	0.93	3.50	-	1349.2
AHQ-10-6, 5771	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.21E-06	0.79	2.92	-	755.5
AHQ-10-6, 4969 - 4971	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	8.46E-06	0.91	3.78	-	1002.2
AHQ-10-2, 5131	R.VAGSVTELIQAAEAM*K.G	1634.87692	3	2.00E-07	0.92	4.33	-	1159.8
AHQ-10-4, 5880 - 5935	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.43E-06	0.98	5.24	-	1826.6
AHQ-10-9, 5556	R.VAGSVTELIQAAEAMK.G	1618.87752	2	5.60E-04	0.86	2.87	-	1200.2
AHQ-10-1, 5939 - 5951	R.VAGSVTELIQAAEAMK.G	1618.87752	2	2.43E-06	0.92	4.00	-	1064.5
AHQ-10-7, 5800	R.VAGSVTELIQAAEAMK.G	1618.87752	2	1.38E-04	0.95	3.90	-	1453.0
AHQ-10-5, 5067 - 5135	R.VAGSVTELIQAAEAM*K.G	1634.87692	2	1.58E-06	0.86	3.53	-	840.9
AHQ-10-2, 5888	R.VAGSVTELIQAAEAMK.G	1618.87752	2	3.50E-09	0.94	4.11	-	1314.2
AHQ-10-2, 3772	K.VEHGSVALPAIMR.S	1380.64144	2	6.87E-05	0.87	3.26	-	890.2
AHQ-10-3, 5455 - 5509	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.96E-06	0.92	4.50	-	690.8
AHQ-10-5, 5532 - 5609	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.14E-10	0.96	5.51	-	1060.4
AHQ-10-4, 5605 - 5609	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.10E-06	0.95	4.88	-	1105.7
AHQ-10-5, 5361 - 5440	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	8.38E-09	0.93	4.49	-	642.6
AHQ-10-3, 5298 - 5378	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	1.16E-06	0.94	4.90	-	1263.6
AHQ-10-2, 5454 - 5494	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	5.94E-08	0.92	4.94	-	486.5
AHQ-10-6, 5341 - 5407	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	4.48E-10	0.94	5.08	-	625.5
AHQ-10-2, 5331 - 5388	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.69E-07	0.94	4.69	-	849.4
AHQ-10-3, 5259	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	7.71E-07	0.54	2.76	-	411.3
AHQ-10-3, 5369	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.15E-08	0.84	3.68	-	337.4
AHQ-10-1, 5586 - 5649	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	2.73E-05	0.80	3.93	-	431.3
AHQ-10-2, 5547 - 5606	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.99E-08	0.96	5.82	-	892.2
AHQ-10-4, 5531 - 5612	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	7.34E-07	0.87	3.89	-	1176.3
AHQ-10-5, 5535 - 5604	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	3	5.63E-07	0.94	5.18	-	1088.7
AHQ-10-4, 5329 - 5369	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.87E-08	0.95	5.27	-	770.7
AHQ-10-7, 5424	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	1.02E-06	0.94	4.70	-	833.7
AHQ-10-4, 5437	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	6.08E-10	0.90	4.34	-	471.5
AHQ-10-4, 5528	K.VGAIPANALDDGQWSQGLISAAR.M	2311.53959	2	9.09E-09	0.97	5.45	-	1375.8
AHQ-10-6, 3691	K.VGDDPAVWQLK.N	1228.37879	2	3.79E-06	0.91	3.79	-	851.5
AHQ-10-2, 3755 - 3826	K.VGDDPAVWQLK.N	1228.37879	2	6.54E-07	0.93	3.46	-	1046.9
AHQ-10-2, 3774 - 3835	K.VGDDPAVWQLK.N	1228.37879	2	6.03E-10	0.91	3.61	-	805.7
AHQ-10-1, 3929	K.VGDDPAVWQLK.N	1228.37879	2	1.96E-08	0.93	3.55	-	910.3
AHQ-10-3, 3749	K.VGDDPAVWQLK.N	1228.37879	2	8.04E-08	0.91	3.93	-	885.5
AHQ-10-5, 3747	K.VGDDPAVWQLK.N	1228.37879	2	6.36E-07	0.84	3.26	-	621.4
AHQ-10-7, 3678	K.VGDDPAVWQLK.N	1228.37879	2	1.57E-06	0.89	3.75	-	770.3
AHQ-10-5, 3281	K.VGDDPAVWQLKNSAK.V	1628.81068	2	3.49E-05	0.61	2.80	-	535.4
AHQ-10-4, 2528	K.VLGEAM*TGISQNAK.N	1435.62901	2	4.14E-04	0.82	3.06	-	807.4
AHQ-10-2, 2503 - 2574	K.VLGEAM*TGISQNAK.N	1435.62901	2	6.83E-05	0.88	3.62	-	799.0
AHQ-10-4, 3237 - 3305	K.VLGEAMTGISQNAK.N	1419.62961	2	6.26E-06	0.96	3.45	-	1974.7
AHQ-10-4, 2432 - 2435	K.VLGEAM*TGISQNAK.N	1435.62901	2	1.01E-04	0.95	4.12	-	1147.2
AHQ-10-4, 3093 - 3156	K.VLGEAMTGISQNAK.N	1419.62961	2	2.41E-05	0.92	3.77	-	1165.2
AHQ-10-2, 3158 - 3226	K.VLGEAMTGISQNAK.N	1419.62961	2	1.78E-07	0.96	4.25	-	1514.2
AHQ-10-2, 4619 - 4678	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	3.50E-07	0.91	5.08	-	624.4
AHQ-10-4, 4591 - 4647	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	1.97E-09	0.95	5.52	-	1063.8
AHQ-10-1, 4747	K.VLGEAM*TGISQNAKNGNLPEFGDAISTASK.A	3038.33659	3	5.72E-04	0.50	3.16	-	241.7
AHQ-10-4, 2009 - 2073	K.VLVQNAAGSQEK.L	1244.37976	2	2.82E-06	0.81	2.98	-	690.1
AHQ-10-5, 1752 - 1761	K.VLVQNAAGSQEK.L	1244.37976	2	1.10E-07	0.88	3.61	-	720.5
AHQ-10-3, 1891 - 1946	K.VLVQNAAGSQEK.L	1244.37976	2	4.75E-08	0.93	3.72	-	929.3
AHQ-10-4, 1893 - 1949	K.VLVQNAAGSQEK.L	1244.37976	2	2.26E-07	0.92	3.74	-	732.1
AHQ-10-2, 1884 - 1938	K.VLVQNAAGSQEK.L	1244.37976	2	1.03E-05	0.93	3.73	-	1095.3
AHQ-10-2, 1996 - 2067	K.VLVQNAAGSQEK.L	1244.37976	2	1.59E-07	0.83	3.24	-	684.6
AHQ-10-4, 1780 - 1853	K.VLVQNAAGSQEK.L	1244.37976	2	1.41E-05	0.90	3.47	-	805.1
AHQ-10-5, 1932	K.VLVQNAAGSQEK.L	1244.37976	2	7.38E-04	0.75	2.77	-	645.4
AHQ-10-2, 4611	K.VMVTNVTSLLK.T	1205.49322	2	5.65E-08	0.87	3.46	-	797.4
AHQ-10-5, 4235	K.VM*VTNVTSLLK.T	1221.49262	2	2.41E-04	0.73	2.97	-	600.9
AHQ-10-3, 4215	K.VM*VTNVTSLLK.T	1221.49262	2	2.46E-05	0.89	3.70	-	853.3
AHQ-10-3, 4542 - 4543	K.VMVTNVTSLLK.T	1205.49322	2	7.69E-06	0.91	3.99	-	875.9
AHQ-10-6, 4435	K.VMVTNVTSLLK.T	1205.49322	2	3.94E-05	0.79	3.06	-	704.1
AHQ-10-2, 4290 - 4291	K.VM*VTNVTSLLK.T	1221.49262	2	9.05E-04	0.85	3.27	-	793.0
AHQ-10-7, 4117	K.VM*VTNVTSLLK.T	1221.49262	2	3.08E-05	0.73	3.19	-	617.1
AHQ-10-4, 4560	K.VMVTNVTSLLK.T	1205.49322	2	1.56E-05	0.89	3.71	-	895.7
AHQ-10-1, 4391	K.VM*VTNVTSLLK.T	1221.49262	2	3.99E-05	0.50	2.62	-	506.7
AHQ-10-7, 4413	K.VMVTNVTSLLK.T	1205.49322	2	1.79E-05	0.88	3.86	-	672.1
AHQ-10-4, 4235 - 4247	K.VM*VTNVTSLLK.T	1221.49262	2	1.84E-06	0.91	3.67	-	954.1
AHQ-10-6, 4141	K.VM*VTNVTSLLK.T	1221.49262	2	1.78E-04	0.73	2.81	-	670.7
AHQ-10-4, 2879	R.VQELGHGCAALVTK.A	1484.70307	2	9.92E-04	0.95	4.25	-	1403.3
AHQ-10-1, 3109 - 3147	R.VQELGHGCAALVTK.A	1484.70307	2	1.93E-04	0.97	4.88	-	1422.4
AHQ-10-7, 2848	R.VQELGHGCAALVTK.A	1484.70307	2	3.33E-05	0.95	3.77	-	1578.3
AHQ-10-5, 2895	R.VQELGHGCAALVTK.A	1484.70307	2	1.91E-04	0.96	4.54	-	1273.0
AHQ-10-6, 2855	R.VQELGHGCAALVTK.A	1484.70307	2	2.21E-06	0.97	4.38	-	1767.7

AHQ-10-2, 2960	R.VQELGHGCAALVTK.A	1484.70307	2	4.27E-07	0.98	4.75	-	2238.7
AHQ-10-3, 2913	R.VQELGHGCAALVTK.A	1484.70307	2	2.18E-05	0.97	4.67	-	1591.5
AHQ-10-2, 2879 - 2939	K.VSHVLAALQAGNR.G	1336.52525	2	5.84E-11	0.97	4.07	-	2261.1
AHQ-10-7, 2813 - 2816	K.VSHVLAALQAGNR.G	1336.52525	2	2.19E-06	0.95	3.70	-	1349.4
AHQ-10-4, 2867	K.VSHVLAALQAGNR.G	1336.52525	2	6.36E-10	0.97	4.53	-	1870.0
AHQ-10-5, 2879	K.VSHVLAALQAGNR.G	1336.52525	2	3.20E-10	0.97	4.47	-	1623.4
AHQ-10-3, 2890 - 2893	K.VSHVLAALQAGNR.G	1336.52525	2	5.32E-09	0.97	4.51	-	1770.3
AHQ-10-5, 6187	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.12E-04	0.86	3.83	-	595.0
AHQ-10-7, 6108	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.05E-06	0.92	4.51	-	651.7
AHQ-10-3, 5449	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.10E-07	0.91	4.42	-	782.5
AHQ-10-4, 5651	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.19E-04	0.55	2.66	-	337.8
AHQ-10-4, 5529	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	7.58E-09	0.95	4.65	-	1597.1
AHQ-10-5, 6193	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	5.53E-04	0.76	3.37	-	946.8
AHQ-10-2, 6198	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	5.63E-06	0.88	3.32	-	1368.3
AHQ-10-4, 5527	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	8.73E-04	0.95	4.52	-	1117.0
AHQ-10-5, 5520	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	5.17E-07	0.96	3.69	-	2252.1
AHQ-10-1, 6218	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	2.20E-04	0.88	3.14	-	968.0
AHQ-10-1, 5585	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	1.21E-05	0.88	3.20	-	1589.7
AHQ-10-5, 5519 - 5521	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	1.04E-07	0.96	5.25	-	1052.0
AHQ-10-1, 5582	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	9.24E-07	0.91	3.98	-	922.4
AHQ-10-2, 5539	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	2.56E-08	0.95	4.63	-	1009.8
AHQ-10-6, 6071	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	3	2.52E-04	0.87	3.59	-	1147.4
AHQ-10-6, 6060	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	3.64E-05	0.88	4.00	-	546.7
AHQ-10-2, 6146 - 6202	K.VSQMAQYFEPLTLAAVGAASK.T	2183.51313	2	9.67E-05	0.94	4.52	-	792.4
AHQ-10-2, 5548	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	4.12E-10	0.97	5.46	-	1812.1
AHQ-10-3, 5450 - 5457	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	3	6.60E-12	0.97	5.34	-	1724.7
AHQ-10-6, 5404	K.VSQM*AQYFEPLTLAAVGAASK.T	2199.51253	2	3.12E-07	0.94	4.71	-	872.7
AHQ-10-1, 4533 - 4541	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.22E-07	0.95	5.18	-	1010.6
AHQ-10-9, 4143 - 4217	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.15E-06	0.58	3.25	-	259.7
AHQ-10-8, 4357	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.03E-07	0.92	4.13	-	600.5
AHQ-10-5, 4319	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.04E-08	0.94	5.11	-	429.1
AHQ-10-5, 4411	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.17E-10	0.95	5.33	-	671.5
AHQ-10-3, 4402	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	3	1.76E-06	0.85	3.10	-	984.8
AHQ-10-3, 4311	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	8.21E-05	0.81	3.41	-	390.4
AHQ-10-2, 4463	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.57E-06	0.81	3.73	-	503.9
AHQ-10-6, 4316 - 4317	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	2.29E-07	0.98	5.89	-	1510.9
AHQ-10-2, 4372	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.69E-07	0.92	4.47	-	495.7
AHQ-10-4, 4427 - 4431	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	5.79E-06	0.96	5.62	-	776.2
AHQ-10-4, 4329	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	7.10E-08	0.95	5.23	-	536.7
AHQ-10-12, 4342	K.VVAPTISSPVCQEQLVEAGR.L	2142.41919	2	1.43E-06	0.54	2.88	-	321.3
gi|4507729|ref|NP_001060.1|	tubulin, beta polypeptide [Homo sapiens]			4.44E-15	7.73	90.36	32.40	49906.7
AHQ-10-13-, 4657 - 4662	R.AILVDLEPGTMDSVR.S	1616.86162	2	4.25E-07	0.84	3.38	-	552.6
AHQ-10-13-, 5886	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	4.02E-07	0.98	5.81	-	2018.2
AHQ-10-9, 5605 - 5680	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.75E-04	0.81	2.78	-	1069.4
AHQ-10-14-, 5912 - 5918	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	8.07E-07	0.98	5.51	-	2338.9
AHQ-10-8, 5974	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	1.19E-07	0.99	7.10	-	3276.8
AHQ-10-7, 5920	K.GHYTEGAELVDSVLDVVR.K	1960.13388	3	6.23E-04	0.89	4.28	-	1214.3
AHQ-10-7, 5917	K.GHYTEGAELVDSVLDVVR.K	1960.13388	2	2.63E-13	0.98	6.27	-	2212.1
AHQ-10-7, 4336	R.ISEQFTAMFR.R	1230.41818	2	2.54E-07	0.94	3.81	-	1399.1
AHQ-10-11, 4315	R.ISEQFTAMFR.R	1230.41818	2	6.11E-06	0.91	3.11	-	1168.6
AHQ-10-7, 3540	R.ISEQFTAM*FR.R	1246.41758	2	1.16E-06	0.87	3.11	-	866.9
AHQ-10-13-, 4416	R.ISEQFTAMFR.R	1230.41818	2	2.92E-05	0.97	3.62	-	2127.4
AHQ-10-7, 5706	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	1.89E-08	0.78	3.12	-	1061.5
AHQ-10-7, 6310	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	2	3.49E-11	0.94	4.76	-	949.5
AHQ-10-7, 6308	K.LTTPTYGDLNHLVSATMSGVTTCLR.F	2711.06527	3	7.68E-05	0.77	3.71	-	652.4
AHQ-10-7, 2817	-.M*REIVHIQAGQCGNQIGAK.F	2128.42245	3	1.79E-04	0.77	3.16	-	846.8
AHQ-10-13-, 5673 - 5716	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	6.34E-07	0.54	2.95	-	670.1
AHQ-10-14-, 5681	K.M*SATFIGNSTAIQELFK.R	1875.13550	2	2.37E-04	0.69	3.87	-	621.5
AHQ-10-7, 5162 - 5244	K.NSSYFVEWIPNNVK.T	1697.87148	2	6.24E-06	0.88	3.82	-	721.9
AHQ-10-13-, 5889 - 5953	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.25E-08	0.95	5.58	-	1059.0
AHQ-10-13-, 5776 - 5832	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	6.20E-05	0.90	4.13	-	1189.3
AHQ-10-7, 5876 - 5936	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	4.44E-15	0.98	7.07	-	1908.6
AHQ-10-11, 5772 - 5828	R.SGPFGQIFRPDNFVFGQSGAGNNWAK.G	2800.03898	3	3.69E-04	0.78	3.49	-	751.9
gi|4503745|ref|NP_001447.1|	filamin 1 (actin-binding protein-280); filamin 1; filamin A, alpha (act			8.33E-15	90.47	1040.35	52.60	280757.4
AHQ-10-2, 2431	R.AEFTVETR.S	953.03118	2	5.47E-05	0.92	3.32	-	1217.3
AHQ-10-5, 2175	K.AEISFEDRK.D	1095.18763	2	1.48E-04	0.86	2.92	-	1056.8
AHQ-10-4, 2695	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.53E-06	0.93	3.36	-	1570.6
AHQ-10-1, 2870 - 2933	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.14E-09	0.94	3.40	-	1538.9
AHQ-10-5, 2700	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.86E-07	0.77	2.83	-	866.2
AHQ-10-1, 2915	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.39E-08	0.95	3.78	-	1491.4
AHQ-10-2, 2767	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	1.21E-05	0.92	3.46	-	1114.6
AHQ-10-9, 2588	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	8.08E-05	0.84	2.57	-	1144.8
AHQ-10-7, 2669 - 2672	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	9.68E-06	0.92	3.24	-	1284.7
AHQ-10-3, 2719	K.AFGPGLQGGSAGSPAR.F	1430.55077	2	4.27E-06	0.90	3.05	-	1273.0
AHQ-10-14-, 3312	K.AGNNMLLVGVHGPR.T	1435.68033	3	4.33E-07	0.92	3.89	-	1414.8
AHQ-10-14-, 3505	K.AGNNMLLVGVHGPR.T	1435.68033	2	4.82E-06	0.66	2.71	-	649.9
AHQ-10-14-, 2968 - 2989	K.AGNNM*LLVGVHGPR.T	1451.67973	2	2.53E-08	0.59	2.96	-	431.0
AHQ-10-14-, 2858 - 2860	K.AGNNM*LLVGVHGPR.T	1451.67973	2	3.43E-07	0.88	3.44	-	829.2
AHQ-10-14-, 3506	K.AGNNMLLVGVHGPR.T	1435.68033	3	4.75E-04	0.78	3.08	-	955.9
AHQ-10-4, 3361	K.AGNNMLLVGVHGPR.T	1435.68033	3	6.83E-06	0.93	3.66	-	1770.0
AHQ-10-2, 1890	R.AGQSAAGAAPGGGVDTR.D	1443.50471	2	1.92E-04	0.76	2.76	-	752.5
AHQ-10-6, 2387	K.AGVAPLQVK.V	883.07036	2	4.24E-05	0.82	3.05	-	599.2
AHQ-10-4, 2404	K.AGVAPLQVK.V	883.07036	2	4.40E-05	0.78	2.82	-	557.9
AHQ-10-2, 6540 - 6612	K.AHEPTYFTVDCAEAGQGDVSIGIK.C	2567.76960	3	6.05E-05	0.79	3.52	-	928.5
AHQ-10-3, 2778	K.AHVVPCFDASK.V	1232.39073	1	2.99E-04	0.20	2.28	-	294.7
AHQ-10-1, 2967	K.AHVVPCFDASK.V	1232.39073	2	1.50E-04	0.80	2.84	-	616.2
AHQ-10-3, 2765	K.AHVVPCFDASK.V	1232.39073	2	4.18E-05	0.70	2.54	-	581.9
AHQ-10-2, 5727 - 5795	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.42E-06	0.90	4.79	-	496.0
AHQ-10-5, 5791 - 5849	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	9.29E-08	0.94	5.62	-	682.2
AHQ-10-3, 5702 - 5769	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	3.63E-10	0.91	5.53	-	531.0
AHQ-10-6, 5664 - 5720	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.36E-07	0.91	5.05	-	475.4
AHQ-10-4, 5855	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	1.11E-10	0.86	4.05	-	568.2
AHQ-10-2, 5852	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	5.18E-09	0.90	4.43	-	552.0
AHQ-10-7, 5682 - 5745	R.ALGALVDSCAPGLCPDWDSWDASKPVTNAR.E	3233.53437	3	6.32E-11	0.93	5.38	-	718.9
AHQ-10-8, 3278 - 3354	R.ANLPQSFQVDTSK.A	1435.56409	2	7.89E-06	0.71	2.83	-	495.2
AHQ-10-5, 3425	R.APSVANVGSHCDLSLK.I	1656.84249	2	1.34E-04	0.81	3.41	-	575.5
AHQ-10-4, 1948 - 1980	K.ATCAPQHGAPGPGPADASK.V	1791.92336	2	3.66E-04	0.92	4.15	-	651.4
AHQ-10-2, 3686	R.AWGPGLEGGVVGK.S	1227.39403	2	1.55E-05	0.86	3.20	-	668.7
AHQ-10-1, 3785	R.AWGPGLEGGVVGK.S	1227.39403	2	3.70E-06	0.95	3.83	-	1239.6
AHQ-10-4, 3636 - 3637	R.AWGPGLEGGVVGK.S	1227.39403	2	1.63E-07	0.90	3.61	-	1019.3
AHQ-10-5, 3607	R.AWGPGLEGGVVGK.S	1227.39403	2	1.69E-07	0.87	3.37	-	828.2
AHQ-10-7, 3548	R.AWGPGLEGGVVGK.S	1227.39403	2	2.68E-04	0.85	3.35	-	788.6
AHQ-10-3, 3618	R.AWGPGLEGGVVGK.S	1227.39403	2	1.73E-08	0.91	3.76	-	862.6
AHQ-10-6, 3509 - 3565	R.AWGPGLEGGVVGK.S	1227.39403	2	6.53E-04	0.92	3.62	-	887.9
AHQ-10-3, 2702	R.AYGPGIEPTGNM*VK.K	1450.64214	2	2.16E-04	0.26	2.53	-	206.7
AHQ-10-3, 3362	R.AYGPGIEPTGNMVK.K	1434.64274	2	2.81E-05	0.70	2.85	-	599.5
AHQ-10-2, 3430	R.AYGPGIEPTGNMVK.K	1434.64274	2	8.32E-05	0.67	2.70	-	467.6

AHQ-10-3, 2810	R.AYGPGIEPTGNM*VK.K	1450.64214	2	4.05E-04	0.56	2.62	-	325.0
AHQ-10-2, 2851	R.AYGPGIEPTGNM*VK.K	1450.64214	2	7.79E-08	0.87	3.73	-	498.9
AHQ-10-2, 5679	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	8.27E-10	0.96	4.85	-	1623.0
AHQ-10-4, 5660 - 5675	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	7.72E-04	0.78	3.40	-	578.7
AHQ-10-1, 5697	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	5.08E-06	0.80	3.53	-	531.6
AHQ-10-1, 5705	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	1.23E-06	0.89	3.47	-	1308.1
AHQ-10-3, 5589	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	3	3.56E-08	0.93	4.45	-	1196.0
AHQ-10-3, 5573	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	1.45E-05	0.44	2.51	-	495.5
AHQ-10-7, 5545	K.CAPGVVGPAEADIDFDIIR.N	2017.24863	2	6.54E-04	0.53	2.94	-	318.9
AHQ-10-3, 2998 - 2999	K.CSGPGLSPGMVR.A	1219.41699	2	2.25E-07	0.72	2.94	-	507.4
AHQ-10-2, 4436	R.DAEMPATEKDLAEDAPWK.K	2018.19047	2	9.83E-07	0.86	3.55	-	792.3
AHQ-10-8, 3778	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	6.41E-07	0.87	3.73	-	860.4
AHQ-10-4, 3852 - 3917	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.74E-04	0.78	3.31	-	778.2
AHQ-10-1, 3975	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.35E-05	0.73	3.12	-	851.7
AHQ-10-5, 3835 - 3899	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	1.80E-05	0.93	4.30	-	1344.6
AHQ-10-11, 3758 - 3828	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	3.16E-06	0.64	2.87	-	663.9
AHQ-10-6, 3716 - 3772	K.DAGEGGLSLAIEGPSK.A	1501.62084	2	5.04E-04	0.66	2.92	-	630.5
AHQ-10-1, 4718	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	4.29E-06	0.93	4.18	-	1187.3
AHQ-10-2, 4652	K.DAGEGLLAVQITDPEGK.P	1713.86752	2	3.59E-05	0.84	3.19	-	936.5
AHQ-10-6, 4148 - 4153	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	4.01E-05	0.95	4.49	-	1429.5
AHQ-10-8, 4154	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.03E-07	0.95	4.55	-	1168.4
AHQ-10-5, 4232 - 4247	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.46E-06	0.94	4.47	-	1047.6
AHQ-10-2, 4240 - 4310	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.00E-06	0.94	4.44	-	1160.6
AHQ-10-9, 3975	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	2.25E-04	0.87	3.69	-	881.4
AHQ-10-7, 4125	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.03E-06	0.95	4.12	-	1504.1
AHQ-10-2, 4498	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	5.48E-05	0.85	3.59	-	791.9
AHQ-10-1, 4377	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	6.26E-06	0.95	4.54	-	1342.1
AHQ-10-2, 4403	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.55E-05	0.84	3.61	-	945.8
AHQ-10-11, 4122	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	1.09E-05	0.91	3.97	-	907.1
AHQ-10-3, 4221	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	2	9.36E-08	0.96	4.67	-	1405.1
AHQ-10-2, 4294	K.DAGEGLLAVQITDPEGKPK.K	1939.15612	3	1.71E-07	0.90	3.41	-	1134.7
AHQ-10-6, 4228 - 4231	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.38E-09	0.95	4.22	-	1366.6
AHQ-10-1, 4421	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	9.70E-06	0.84	3.26	-	986.0
AHQ-10-5, 4301 - 4363	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.31E-04	0.86	3.13	-	1113.8
AHQ-10-4, 4480	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	2.14E-05	0.91	3.88	-	1010.9
AHQ-10-4, 4321 - 4348	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	5.61E-05	0.82	3.33	-	725.7
AHQ-10-3, 4294	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	7.30E-06	0.86	2.65	-	1060.5
AHQ-10-8, 4255	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	1.28E-07	0.90	3.71	-	1015.8
AHQ-10-2, 4367 - 4375	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	5.90E-09	0.92	3.99	-	1198.3
AHQ-10-5, 4461	R.DAGYGGLSLSIEGPSK.V	1551.67986	2	4.94E-05	0.91	4.06	-	737.2
AHQ-10-1, 5483	R.DAGYGGLSLSIEGPSKVDINTEDLEDGTCR.V	3171.35009	3	1.60E-04	0.88	4.23	-	667.5
AHQ-10-4, 2041	R.DAPQDFHPDR.V	1198.22650	2	6.28E-06	0.74	2.81	-	580.5
AHQ-10-6, 2033	R.DAPQDFHPDR.V	1198.22650	2	3.43E-04	0.74	2.62	-	892.7
AHQ-10-2, 2082	R.DAPQDFHPDR.V	1198.22650	2	2.01E-06	0.88	3.05	-	861.1
AHQ-10-5, 4535 - 4597	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.36E-05	0.86	4.11	-	563.5
AHQ-10-3, 4509 - 4510	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.39E-06	0.80	3.84	-	466.4
AHQ-10-4, 4555	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.12E-05	0.89	4.67	-	518.7
AHQ-10-2, 4594	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	2.16E-04	0.68	3.19	-	507.4
AHQ-10-8, 4482 - 4501	K.DGSCGVAYVVQEPGDYEVSVK.F	2260.41990	2	1.66E-05	0.82	3.83	-	463.7
AHQ-10-5, 2565	K.DKGEYTLVVK.W	1152.32223	2	1.90E-06	0.70	2.87	-	530.0
AHQ-10-14-, 2581	K.DKGEYTLVVK.W	1152.32223	2	2.42E-05	0.70	3.00	-	562.7
AHQ-10-1, 2797	K.DKGEYTLVVK.W	1152.32223	2	4.68E-07	0.73	2.56	-	566.7
AHQ-10-3, 2606	K.DKGEYTLVVK.W	1152.32223	2	9.85E-04	0.65	2.58	-	543.5
AHQ-10-14-, 2588	K.DKGEYTLVVK.W	1152.32223	1	7.57E-07	0.28	2.26	-	507.4
AHQ-10-5, 3169	K.DNGNGTYSCSYVPR.K	1591.64109	2	4.86E-08	0.74	2.80	-	750.6
AHQ-10-4, 3187	K.DNGNGTYSCSYVPR.K	1591.64109	2	1.81E-05	0.84	3.00	-	889.6
AHQ-10-1, 3331 - 3334	K.DNGNGTYSCSYVPR.K	1591.64109	2	3.39E-06	0.47	2.50	-	544.3
AHQ-10-1, 3261 - 3295	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	2.42E-04	0.92	3.32	-	1178.9
AHQ-10-5, 3093	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.60E-06	0.81	2.99	-	794.0
AHQ-10-1, 3294	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	1.67E-04	0.71	3.31	-	453.5
AHQ-10-4, 3100	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	1.07E-04	0.71	2.81	-	616.2
AHQ-10-6, 3061	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	1.70E-04	0.56	3.08	-	575.5
AHQ-10-4, 3107	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	7.80E-05	0.72	3.26	-	404.5
AHQ-10-2, 3171	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	6.47E-08	0.95	4.61	-	1186.4
AHQ-10-3, 3113 - 3174	R.DVDIIDHHDNTYTVK.Y	1785.89230	2	8.05E-06	0.92	3.96	-	862.2
AHQ-10-3, 3114	R.DVDIIDHHDNTYTVK.Y	1785.89230	3	1.08E-05	0.59	3.03	-	445.0
AHQ-10-9, 3180	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	2.93E-07	0.92	3.07	-	1442.2
AHQ-10-1, 3557	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.00E-06	0.94	4.11	-	1263.0
AHQ-10-7, 3300	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.51E-06	0.92	3.47	-	1248.5
AHQ-10-5, 3373 - 3436	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	3.84E-04	0.96	4.37	-	1596.0
AHQ-10-6, 3325	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	4.25E-05	0.91	3.54	-	1082.3
AHQ-10-2, 3450	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.10E-06	0.89	3.00	-	1047.2
AHQ-10-8, 3326 - 3331	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	8.84E-05	0.88	3.14	-	1073.1
AHQ-10-4, 3379	R.EAGAGGLAIAVEGPSK.A	1427.58510	2	1.40E-04	0.89	3.31	-	1314.1
AHQ-10-6, 2649 - 2659	R.EATTEFSVDAR.A	1226.27493	2	7.97E-06	0.69	2.68	-	517.5
AHQ-10-1, 2877	R.EATTEFSVDAR.A	1226.27493	2	3.41E-06	0.87	3.00	-	872.2
AHQ-10-4, 5793 - 5851	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.60E-04	0.83	4.15	-	553.0
AHQ-10-3, 5829 - 5906	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.08E-04	0.93	5.05	-	787.7
AHQ-10-1, 5806 - 5873	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	4.32E-05	0.94	5.41	-	887.2
AHQ-10-1, 5929	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.43E-05	0.85	3.78	-	716.5
AHQ-10-5, 5833 - 5887	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.08E-10	0.95	5.74	-	962.6
AHQ-10-3, 5703 - 5757	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	1.46E-07	0.94	4.84	-	1257.1
AHQ-10-3, 5795 - 5849	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	8.33E-15	0.97	6.91	-	981.5
AHQ-10-7, 5744	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	2.50E-07	0.84	4.09	-	562.3
AHQ-10-4, 5896 - 5955	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.47E-04	0.89	4.61	-	620.5
AHQ-10-2, 5786 - 5842	R.EEGPYEVEVTYDGVPVPGSPFPLEAVAPTKPSK.V	3487.85286	3	3.71E-07	0.94	5.55	-	844.2
AHQ-10-2, 4802 - 4859	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.60E-04	0.90	3.81	-	842.5
AHQ-10-6, 4728	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.92E-05	0.51	2.58	-	591.0
AHQ-10-9, 4523	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	2.06E-06	0.79	3.03	-	782.0
AHQ-10-8, 4761 - 4786	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	9.40E-07	0.86	3.36	-	776.5
AHQ-10-5, 4816	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	7.48E-11	0.87	3.54	-	806.6
AHQ-10-7, 4713	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	3.11E-05	0.62	3.18	-	510.4
AHQ-10-4, 4771 - 4840	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.19E-06	0.76	3.45	-	537.5
AHQ-10-4, 4855 - 4856	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.69E-08	0.92	3.89	-	965.8
AHQ-10-6, 4744	R.EGPYSISVLYGDEEVPR.S	1911.05809	3	1.58E-06	0.78	3.65	-	1049.3
AHQ-10-1, 4853 - 4930	R.EGPYSISVLYGDEEVPR.S	1911.05809	2	1.51E-04	0.71	3.34	-	688.1
AHQ-10-4, 3493	K.FADQHVPGSPFSVK.V	1516.68203	3	8.10E-07	0.92	3.71	-	1322.2
AHQ-10-2, 3484 - 3563	K.FADQHVPGSPFSVK.V	1516.68203	2	5.42E-06	0.78	3.12	-	428.9
AHQ-10-7, 3406	K.FADQHVPGSPFSVK.V	1516.68203	2	1.59E-04	0.60	2.70	-	355.7
AHQ-10-6, 3417	K.FADQHVPGSPFSVK.V	1516.68203	3	3.79E-05	0.92	3.70	-	1328.2
AHQ-10-1, 3665	K.FADQHVPGSPFSVK.V	1516.68203	3	8.12E-07	0.94	3.87	-	1490.2
AHQ-10-3, 3491	K.FADQHVPGSPFSVK.V	1516.68203	3	1.08E-06	0.96	4.91	-	1373.0
AHQ-10-5, 3469	K.FADQHVPGSPFSVK.V	1516.68203	3	8.45E-06	0.89	3.57	-	948.3
AHQ-10-1, 3658 - 3682	K.FADQHVPGSPFSVK.V	1516.68203	2	2.63E-05	0.71	2.88	-	411.5
AHQ-10-13-, 5110	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.72E-05	0.92	4.47	-	960.8
AHQ-10-1, 5274 - 5346	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	5.57E-09	0.91	4.77	-	684.0
AHQ-10-8, 5181	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.25E-06	0.91	4.39	-	928.9

AHQ-10-2, 5222 - 5278	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	4.28E-05	0.90	4.53	-	683.6
AHQ-10-6, 5079 - 5135	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	2.25E-04	0.91	4.17	-	1018.2
AHQ-10-5, 5149 - 5207	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	3.32E-05	0.90	4.26	-	786.2
AHQ-10-2, 5335	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	8.43E-09	0.84	3.68	-	661.0
AHQ-10-4, 5201 - 5259	R.FGGEHVPNSPFQVTALAGDQPSVQPPLR.S	2947.25342	3	1.61E-08	0.91	4.45	-	900.5
AHQ-10-4, 4940	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	1.14E-05	0.75	3.32	-	488.2
AHQ-10-3, 4899	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	5.55E-04	0.63	2.65	-	451.8
AHQ-10-6, 4837	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	9.26E-08	0.68	2.99	-	383.4
AHQ-10-2, 4988	K.FNEEHIPDSPFVVPVASPSGDAR.R	2468.66280	2	6.17E-06	0.57	2.98	-	297.0
AHQ-10-4, 3765 - 3823	K.FNGTHIPGSPFK.I	1302.46259	2	5.05E-06	0.68	2.97	-	463.7
AHQ-10-5, 2451	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	4.58E-07	0.60	2.86	-	172.1
AHQ-10-7, 3018	R.FVPAEMGTHTVSVK.Y	1503.74821	2	8.94E-09	0.82	3.28	-	417.4
AHQ-10-4, 2459	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	7.88E-04	0.60	2.79	-	312.1
AHQ-10-5, 3088	R.FVPAEMGTHTVSVK.Y	1503.74821	2	3.63E-13	0.80	2.93	-	523.2
AHQ-10-4, 3099	R.FVPAEMGTHTVSVK.Y	1503.74821	2	1.22E-10	0.81	2.83	-	506.1
AHQ-10-2, 2540	R.FVPAEM*GTHTVSVK.Y	1519.74761	2	7.97E-04	0.46	2.51	-	246.0
AHQ-10-11, 3320	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	7.45E-04	0.79	2.85	-	822.7
AHQ-10-8, 3313	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.06E-05	0.86	3.12	-	829.8
AHQ-10-1, 3493 - 3545	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	1.25E-05	0.89	3.54	-	866.9
AHQ-10-7, 3284 - 3286	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.59E-04	0.90	3.94	-	679.7
AHQ-10-4, 3368	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	5.23E-06	0.85	3.34	-	689.3
AHQ-10-5, 3361	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	2.29E-07	0.90	3.64	-	899.3
AHQ-10-6, 3313	R.GAGTGGLGLAVEGPSEAK.M	1571.71430	2	4.39E-06	0.87	3.79	-	599.9
AHQ-10-3, 3458 - 3519	K.GKLDVQFSGLTK.G	1293.49392	2	7.49E-05	0.90	3.70	-	1014.7
AHQ-10-3, 4653 - 4702	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	6.38E-06	0.94	4.63	-	917.0
AHQ-10-5, 4657 - 4715	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	9.36E-05	0.90	3.94	-	861.1
AHQ-10-2, 4914	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	1.23E-05	0.75	2.74	-	901.4
AHQ-10-2, 4779 - 4851	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.18E-08	0.97	6.30	-	1268.0
AHQ-10-3, 4502 - 4582	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	4.57E-04	0.66	2.78	-	632.6
AHQ-10-2, 4564 - 4628	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	6.51E-09	0.94	4.73	-	850.9
AHQ-10-2, 4674 - 4734	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	7.66E-04	0.64	2.88	-	611.0
AHQ-10-1, 4722 - 4789	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	2.65E-04	0.83	3.35	-	658.5
AHQ-10-4, 4625 - 4703	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	5.91E-07	0.95	5.33	-	913.8
AHQ-10-7, 4601 - 4629	K.GLVEPVDVVDNADGTQTVNYVPSR.E	2545.74387	2	4.31E-04	0.52	2.59	-	314.6
AHQ-10-4, 2311 - 2325	K.GTVEPQLEAR.G	1100.20741	2	1.48E-04	0.75	2.56	-	595.8
AHQ-10-2, 2378	K.GTVEPQLEAR.G	1100.20741	2	6.89E-05	0.84	3.44	-	459.9
AHQ-10-2, 2332 - 2390	K.GTVEPQLEAR.G	1100.20741	2	1.76E-04	0.82	2.63	-	602.3
AHQ-10-3, 2341	K.GTVEPQLEAR.G	1100.20741	2	3.57E-04	0.72	2.93	-	423.2
AHQ-10-1, 2535	K.GTVEPQLEAR.G	1100.20741	2	1.64E-05	0.87	3.42	-	604.8
AHQ-10-3, 4902	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	1.37E-06	0.96	4.60	-	1442.1
AHQ-10-2, 4978	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	2	3.84E-05	0.91	3.92	-	1048.2
AHQ-10-3, 4903	K.HTAM*VSWGGVSIPNSPFR.V	1960.20541	3	1.94E-04	0.88	3.88	-	1138.7
AHQ-10-7, 4002 - 4008	R.IANLQTDLSDGLR.L	1416.56231	2	2.58E-04	0.76	2.92	-	701.9
AHQ-10-6, 4041	R.IANLQTDLSDGLR.L	1416.56231	2	9.23E-04	0.96	4.08	-	1480.2
AHQ-10-2, 4058	R.IANLQTDLSDGLR.L	1416.56231	2	3.71E-06	0.83	3.16	-	679.2
AHQ-10-2, 3767 - 3822	R.IANLQTDLSDGLR.L	1416.56231	2	7.15E-06	0.93	3.98	-	1062.3
AHQ-10-2, 3919	R.IANLQTDLSDGLR.L	1416.56231	2	5.20E-07	0.95	3.94	-	1251.1
AHQ-10-1, 4139	R.IANLQTDLSDGLR.L	1416.56231	2	4.00E-04	0.86	3.14	-	773.4
AHQ-10-4, 3764	R.IANLQTDLSDGLR.L	1416.56231	2	1.56E-05	0.93	3.70	-	1084.0
AHQ-10-5, 3745	R.IANLQTDLSDGLR.L	1416.56231	2	3.28E-06	0.91	3.78	-	785.5
AHQ-10-2, 4170	R.IANLQTDLSDGLR.L	1416.56231	2	1.50E-04	0.94	3.94	-	1220.8
AHQ-10-10, 3962 - 3966	R.IANLQTDLSDGLR.L	1416.56231	2	8.07E-04	0.85	2.92	-	780.9
AHQ-10-1, 4254	R.IANLQTDLSDGLR.L	1416.56231	2	3.14E-08	0.95	4.32	-	1188.9
AHQ-10-12, 4076	R.IANLQTDLSDGLR.L	1416.56231	2	6.18E-06	0.92	3.71	-	1084.9
AHQ-10-3, 4101	R.IANLQTDLSDGLR.L	1416.56231	2	2.23E-05	0.91	3.50	-	946.3
AHQ-10-3, 3734	R.IANLQTDLSDGLR.L	1416.56231	2	4.60E-06	0.96	4.49	-	1335.1
AHQ-10-5, 4116	R.IANLQTDLSDGLR.L	1416.56231	2	3.95E-05	0.91	3.47	-	930.0
AHQ-10-4, 4135 - 4139	R.IANLQTDLSDGLR.L	1416.56231	2	2.06E-06	0.94	4.69	-	1125.0
AHQ-10-1, 3901 - 3902	R.IANLQTDLSDGLR.L	1416.56231	2	3.07E-06	0.96	4.76	-	1360.7
AHQ-10-6, 3685	R.IANLQTDLSDGLR.L	1416.56231	2	4.66E-07	0.67	2.65	-	629.8
AHQ-10-11, 4006	R.IANLQTDLSDGLR.L	1416.56231	2	8.70E-07	0.84	3.81	-	583.2
AHQ-10-3, 3918 - 3991	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	4.94E-06	0.97	4.52	-	1945.6
AHQ-10-2, 5218	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.30E-10	0.96	4.76	-	1238.5
AHQ-10-5, 4604	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.48E-09	0.94	4.40	-	1013.0
AHQ-10-4, 5197 - 5203	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	9.78E-10	0.98	6.24	-	1771.7
AHQ-10-4, 5207 - 5209	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	4.94E-05	0.92	5.18	-	712.7
AHQ-10-1, 5261	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	3.64E-07	0.95	4.39	-	1230.8
AHQ-10-6, 5075	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	5.83E-14	0.97	5.56	-	1582.1
AHQ-10-4, 3979	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.41E-06	0.97	5.00	-	1511.2
AHQ-10-3, 5145	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	7.68E-07	0.75	3.67	-	799.7
AHQ-10-1, 5266	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	3	1.06E-04	0.84	3.37	-	1104.7
AHQ-10-7, 5077	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	8.63E-10	0.95	4.54	-	1121.5
AHQ-10-6, 3899	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.12E-08	0.97	5.18	-	1804.7
AHQ-10-5, 5168	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	2.04E-09	0.96	4.74	-	1131.5
AHQ-10-1, 4105	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	5.83E-05	0.95	4.47	-	1109.6
AHQ-10-3, 5135	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	6.19E-07	0.95	4.61	-	1158.1
AHQ-10-5, 3969 - 4028	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	1.48E-08	0.98	5.24	-	2030.7
AHQ-10-8, 5127	K.IPEISIQDMTAQVTSPSGK.T	2003.26361	2	1.44E-09	0.98	5.69	-	1817.7
AHQ-10-2, 4038	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	6.77E-04	0.96	4.47	-	1477.1
AHQ-10-7, 3882 - 3914	K.IPEISIQDM*TAQVTSPSGK.T	2019.26301	2	3.90E-06	0.96	4.78	-	1281.5
AHQ-10-5, 2607	K.IVGPSGAAVPCK.V	1157.36530	2	3.30E-06	0.85	2.96	-	784.9
AHQ-10-4, 2592	K.IVGPSGAAVPCK.V	1157.36530	2	1.09E-05	0.91	3.37	-	857.1
AHQ-10-3, 2607 - 2613	K.IVGPSGAAVPCK.V	1157.36530	2	2.14E-04	0.83	3.08	-	704.3
AHQ-10-2, 2663	K.IVGPSGAAVPCK.V	1157.36530	2	1.95E-05	0.79	2.65	-	711.7
AHQ-10-3, 4025	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	2.37E-06	0.75	3.65	-	312.0
AHQ-10-5, 4041	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	6.12E-04	0.82	4.32	-	737.2
AHQ-10-3, 4018 - 4019	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	3.37E-05	0.90	4.32	-	1066.9
AHQ-10-6, 3967 - 3993	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.36E-04	0.93	4.56	-	1211.7
AHQ-10-1, 4185	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	9.79E-05	0.65	3.30	-	277.0
AHQ-10-3, 4115	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	1.58E-09	0.93	4.48	-	1243.4
AHQ-10-1, 4175 - 4255	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.42E-08	0.94	4.59	-	1422.1
AHQ-10-4, 4073	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	2	1.65E-05	0.51	2.56	-	289.8
AHQ-10-4, 4039 - 4115	K.IVGPSGAAVPCKVEPGLGADNSVVR.F	2451.78478	3	2.25E-09	0.89	4.33	-	1040.8
AHQ-10-1, 4329 - 4402	R.KDGSCGVAYVVQEPGDYEVSVK.F	2388.59282	3	8.99E-06	0.91	5.09	-	725.9
AHQ-10-8, 4163	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	4.07E-06	0.91	4.41	-	453.2
AHQ-10-3, 4257 - 4261	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	4.71E-12	0.97	5.94	-	2023.7
AHQ-10-5, 4159 - 4236	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.02E-08	0.96	5.25	-	1697.7
AHQ-10-8, 4086 - 4155	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	7.01E-10	0.97	6.18	-	1659.1
AHQ-10-4, 4248	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	5.21E-10	0.97	5.56	-	1740.7
AHQ-10-1, 4399	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	3	1.18E-11	0.96	5.68	-	1758.7
AHQ-10-5, 4243 - 4244	K.KNGQHVASSPIPVVISQSEIGDASR.V	2577.83547	2	6.27E-07	0.95	4.86	-	952.9
AHQ-10-4, 3457	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.48E-06	0.78	3.63	-	649.1
AHQ-10-1, 3623 - 3695	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	1.15E-04	0.89	4.23	-	754.2
AHQ-10-2, 3506 - 3568	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	9.30E-06	0.87	3.90	-	831.1
AHQ-10-4, 3559	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	8.29E-04	0.67	3.00	-	675.9
AHQ-10-3, 3443 - 3503	K.KTHIQDNHDGTYTVAYVPDVTGR.Y	2588.77367	3	4.44E-06	0.87	4.24	-	924.0
AHQ-10-3, 3846	K.LDVQFSGLTK.G	1108.26945	1	4.04E-04	0.36	2.36	-	290.9

AHQ-10-3, 3839	K.LDVQFSGLTK.G	1108.26945	2	7.98E-07	0.95	4.01	-	968.6
AHQ-10-2, 3920	K.LDVQFSGLTK.G	1108.26945	2	1.20E-04	0.91	3.25	-	981.2
AHQ-10-1, 4009	K.LDVQFSGLTK.G	1108.26945	2	1.05E-04	0.91	3.35	-	926.4
AHQ-10-4, 3867	K.LDVQFSGLTK.G	1108.26945	2	1.69E-04	0.93	3.82	-	909.3
AHQ-10-2, 6266	R.LLGWIQNKLPQLPITNFSR.D	2239.64761	3	7.76E-05	0.93	4.53	-	1086.2
AHQ-10-1, 4794	K.LPQLPITNFSR.D	1286.50461	2	5.44E-05	0.79	2.66	-	557.2
AHQ-10-5, 4817	K.LPQLPITNFSR.D	1286.50461	2	5.87E-06	0.81	3.29	-	577.1
AHQ-10-3, 4805	K.LPQLPITNFSR.D	1286.50461	2	1.44E-06	0.76	2.99	-	443.5
AHQ-10-4, 4692 - 4704	K.LPQLPITNFSR.D	1286.50461	2	1.27E-05	0.93	3.11	-	1125.5
AHQ-10-3, 4647	K.LPQLPITNFSR.D	1286.50461	2	2.43E-06	0.82	3.05	-	495.5
AHQ-10-2, 4718	K.LPQLPITNFSR.D	1286.50461	2	1.35E-05	0.90	2.94	-	1011.5
AHQ-10-2, 5108 - 5166	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.91E-05	0.81	3.31	-	590.5
AHQ-10-6, 5011	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	4.49E-06	0.90	3.86	-	653.9
AHQ-10-7, 5001	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	8.39E-07	0.84	3.70	-	535.9
AHQ-10-4, 5123 - 5131	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	5.53E-06	0.97	5.27	-	2228.6
AHQ-10-1, 5135 - 5194	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	3	3.73E-08	0.97	6.33	-	1377.2
AHQ-10-1, 5190	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	3.93E-06	0.89	3.76	-	636.2
AHQ-10-5, 5107	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.57E-05	0.88	3.86	-	603.6
AHQ-10-4, 5127	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.54E-10	0.94	4.64	-	886.4
AHQ-10-3, 5061	K.LQVEPAVDTSGVQCYGPGIEGQGVFR.E	2766.03597	2	1.10E-04	0.87	4.06	-	620.4
AHQ-10-5, 3141	R.LRNGHVGISFVPK.E	1424.67564	3	3.96E-05	0.88	3.29	-	1454.3
AHQ-10-5, 3240	R.LRNGHVGISFVPK.E	1424.67564	3	7.10E-06	0.88	3.18	-	1679.1
AHQ-10-3, 3275	R.LRNGHVGISFVPK.E	1424.67564	3	6.14E-05	0.83	3.54	-	1045.9
AHQ-10-3, 3434 - 3437	R.LSPFM*ADIR.D	1066.25604	2	4.19E-04	0.66	2.56	-	530.1
AHQ-10-1, 3613	R.LTVSSLQESGLK.V	1262.43499	2	3.93E-04	0.86	3.35	-	691.5
AHQ-10-8, 3373	R.LTVSSLQESGLK.V	1262.43499	2	1.53E-08	0.84	2.78	-	889.4
AHQ-10-5, 3431	R.LTVSSLQESGLK.V	1262.43499	2	4.37E-08	0.76	2.87	-	603.0
AHQ-10-5, 4320	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.64E-04	0.78	3.41	-	509.8
AHQ-10-1, 4275	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.09E-04	0.83	3.14	-	1018.5
AHQ-10-8, 4230	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	1.18E-08	0.93	3.74	-	1205.9
AHQ-10-4, 4133	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.46E-04	0.96	4.73	-	1525.9
AHQ-10-13-, 4085 - 4146	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	1.46E-09	0.96	5.27	-	1692.1
AHQ-10-5, 4096 - 4164	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	3	6.73E-04	0.90	3.70	-	1035.9
AHQ-10-4, 4137	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	3.25E-06	0.94	4.30	-	970.1
AHQ-10-5, 4104	R.LVSNHSLHETSSVFVDSLTK.A	2201.42190	2	2.88E-05	0.94	5.11	-	808.7
AHQ-10-4, 2273	K.M*DCQECPEGYR.V	1463.55315	2	3.09E-07	0.91	3.38	-	896.0
AHQ-10-8, 4470	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	4.29E-08	0.95	4.38	-	1052.4
AHQ-10-5, 4531	K.NGQHVASSPIPVVISQSEIGDASR.V	2449.66256	2	5.99E-08	0.95	4.65	-	1036.1
AHQ-10-2, 2215	K.RAEFTVETR.S	1109.21754	2	1.72E-06	0.92	3.24	-	1130.4
AHQ-10-5, 2067 - 2129	K.RAEFTVETR.S	1109.21754	2	5.19E-07	0.83	2.65	-	771.7
AHQ-10-4, 3148	R.RAPSVANVGSHCDLSLK.I	1813.02884	2	3.83E-04	0.96	4.42	-	1425.7
AHQ-10-1, 3347	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	7.94E-09	0.95	4.99	-	1444.6
AHQ-10-5, 3123	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	5.19E-05	0.94	4.79	-	1435.5
AHQ-10-4, 3143 - 3205	R.RAPSVANVGSHCDLSLK.I	1813.02884	3	4.13E-04	0.96	4.99	-	1792.5
AHQ-10-1, 3374	R.RLTVSSLQESGLK.V	1418.62134	2	7.02E-05	0.98	5.05	-	2731.5
AHQ-10-2, 6507 - 6564	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	4.93E-04	0.92	4.96	-	1022.9
AHQ-10-4, 6511 - 6545	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	1.37E-04	0.84	3.58	-	875.6
AHQ-10-2, 6523 - 6588	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	2.44E-04	0.90	3.70	-	1059.7
AHQ-10-5, 6323 - 6384	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	2	7.12E-06	0.89	3.57	-	881.9
AHQ-10-3, 6513	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	7.87E-04	0.77	3.40	-	762.7
AHQ-10-2, 6406 - 6470	K.SADFVVEAIGDDVGTLGFSVEGPSQAK.I	2696.90399	3	1.65E-04	0.90	4.15	-	1223.6
AHQ-10-2, 3914	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.57E-07	0.91	4.12	-	750.9
AHQ-10-1, 4005	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.23E-10	0.96	5.03	-	1635.8
AHQ-10-5, 3848	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	3.98E-07	0.88	4.34	-	513.7
AHQ-10-3, 3841	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	4.03E-07	0.80	3.47	-	661.4
AHQ-10-3, 3842	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	4.45E-06	0.87	3.64	-	580.6
AHQ-10-2, 3912 - 3979	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	4.82E-07	0.90	3.68	-	1193.4
AHQ-10-1, 4006	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	7.47E-06	0.90	4.22	-	654.7
AHQ-10-6, 3784	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	1.68E-06	0.91	4.40	-	637.2
AHQ-10-6, 3776	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	3.56E-07	0.90	3.76	-	1220.4
AHQ-10-5, 3847 - 3855	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	3	5.72E-09	0.93	4.67	-	1090.3
AHQ-10-4, 3871	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.24E-05	0.88	4.31	-	549.5
AHQ-10-7, 3764	R.SAGQGEVLVYVEDPAGHQEEAK.V	2314.45074	2	5.91E-07	0.92	4.25	-	638.3
AHQ-10-1, 3590	K.SPFEVYVDK.S	1084.20321	2	1.48E-05	0.90	3.05	-	1017.4
AHQ-10-3, 3415	K.SPFEVYVDK.S	1084.20321	2	8.69E-06	0.93	3.54	-	1135.3
AHQ-10-5, 3409	K.SPFEVYVDK.S	1084.20321	1	2.09E-04	0.86	2.69	-	1224.9
AHQ-10-5, 3403 - 3404	K.SPFEVYVDK.S	1084.20321	2	4.34E-06	0.95	3.16	-	1302.1
AHQ-10-2, 3474	K.SPFEVYVDK.S	1084.20321	2	3.24E-06	0.92	3.14	-	1084.8
AHQ-10-4, 3424	K.SPFEVYVDK.S	1084.20321	2	7.62E-07	0.92	3.18	-	1195.8
AHQ-10-2, 3486	K.SPFEVYVDK.S	1084.20321	1	3.47E-05	0.87	3.08	-	1034.0
AHQ-10-4, 3427	K.SPFEVYVDK.S	1084.20321	1	5.60E-04	0.66	2.37	-	869.5
AHQ-10-1, 3598	K.SPFEVYVDK.S	1084.20321	1	3.80E-04	0.74	2.67	-	919.7
AHQ-10-2, 4719 - 4774	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.35E-05	0.87	3.22	-	998.3
AHQ-10-5, 4637 - 4716	K.SPFSVAVSPSLDLSK.I	1534.73557	2	1.19E-05	0.89	3.58	-	919.2
AHQ-10-2, 4626	K.SPFSVAVSPSLDLSK.I	1534.73557	2	2.91E-05	0.62	3.11	-	412.0
AHQ-10-4, 4680 - 4739	K.SPFSVAVSPSLDLSK.I	1534.73557	2	7.75E-06	0.88	3.61	-	958.1
AHQ-10-3, 4554 - 4634	K.SPFSVAVSPSLDLSK.I	1534.73557	2	8.88E-07	0.88	3.30	-	915.2
AHQ-10-3, 4686 - 4754	K.SPFSVAVSPSLDLSK.I	1534.73557	2	3.46E-06	0.89	3.95	-	823.6
AHQ-10-1, 3546	R.SPYTVTVGQACNPSACR.A	1871.04208	2	6.84E-04	0.92	4.36	-	558.0
AHQ-10-6, 3277 - 3335	R.SPYTVTVGQACNPSACR.A	1871.04208	2	4.49E-06	0.85	3.55	-	401.7
AHQ-10-5, 3375 - 3384	R.SPYTVTVGQACNPSACR.A	1871.04208	2	2.00E-06	0.93	4.29	-	585.4
AHQ-10-7, 3317	R.SPYTVTVGQACNPSACR.A	1871.04208	2	7.92E-05	0.82	3.31	-	435.5
AHQ-10-3, 3346 - 3401	R.SPYTVTVGQACNPSACR.A	1871.04208	2	5.07E-07	0.82	3.48	-	445.4
AHQ-10-1, 4981	R.TFSVWYVPEVTGTHK.V	1751.96228	3	1.37E-05	0.64	3.06	-	386.1
AHQ-10-2, 4902 - 4907	R.TFSVWYVPEVTGTHK.V	1751.96228	3	3.64E-06	0.75	3.37	-	557.2
AHQ-10-6, 3072	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	6.07E-04	0.85	3.59	-	502.5
AHQ-10-5, 3099	K.TGVAVNKPAEFTVDAK.H	1647.85391	2	4.48E-04	0.91	3.87	-	798.0
AHQ-10-3, 3130	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	5.76E-07	0.86	3.67	-	770.7
AHQ-10-4, 3119	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	1.70E-06	0.91	3.97	-	926.4
AHQ-10-1, 3317	K.TGVAVNKPAEFTVDAK.H	1647.85391	3	6.33E-07	0.92	3.79	-	1106.0
AHQ-10-2, 3050 - 3130	R.TGVELGKPTHFTVNAK.A	1699.93205	3	6.77E-06	0.84	4.50	-	574.4
AHQ-10-1, 3206 - 3265	R.TGVELGKPTHFTVNAK.A	1699.93205	2	6.99E-05	0.90	4.11	-	591.8
AHQ-10-2, 3047 - 3126	R.TGVELGKPTHFTVNAK.A	1699.93205	2	3.34E-05	0.93	4.34	-	774.6
AHQ-10-3, 3139	K.THEAEIVEGENHTYCIR.F	2060.19046	3	4.93E-06	0.90	3.85	-	1057.7
AHQ-10-6, 3080	K.THEAEIVEGENHTYCIR.F	2060.19046	3	4.65E-09	0.94	4.23	-	1331.7
AHQ-10-6, 3077 - 3085	K.THEAEIVEGENHTYCIR.F	2060.19046	2	6.39E-04	0.97	4.69	-	2229.2
AHQ-10-1, 3314	K.THEAEIVEGENHTYCIR.F	2060.19046	3	3.41E-07	0.93	4.46	-	1051.5
AHQ-10-1, 3430	K.THEAEIVEGENHTYCIR.F	2060.19046	3	6.95E-09	0.84	3.59	-	633.3
AHQ-10-4, 3259	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.59E-07	0.95	4.37	-	1405.2
AHQ-10-5, 3101	K.THEAEIVEGENHTYCIR.F	2060.19046	2	2.87E-05	0.98	5.23	-	1885.7
AHQ-10-5, 3220	K.THEAEIVEGENHTYCIR.F	2060.19046	3	2.62E-09	0.90	3.94	-	1123.9
AHQ-10-4, 3085 - 3151	K.THEAEIVEGENHTYCIR.F	2060.19046	3	9.06E-13	0.96	5.22	-	1277.3
AHQ-10-2, 3198	K.THEAEIVEGENHTYCIR.F	2060.19046	3	1.14E-07	0.92	4.33	-	1108.6
AHQ-10-2, 3754	K.THIQDNHDGTYTVAYVPDVTGR.Y	2460.60076	2	1.46E-07	0.80	3.16	-	448.9
AHQ-10-4, 3159	R.TPCEEILVK.H	1090.27249	2	2.21E-04	0.81	3.03	-	717.2
AHQ-10-3, 3175 - 3247	R.TPCEEILVK.H	1090.27249	2	3.54E-06	0.86	2.94	-	742.2
AHQ-10-14-, 3154	R.TPCEEILVK.H	1090.27249	1	3.62E-06	0.57	2.61	-	414.7

AHQ-10-14-, 3140 - 3169	R.TPCEEILVK.H	1090.27249	2	3.03E-04	0.85	2.60	-	950.7
AHQ-10-5, 3149	R.TPCEEILVK.H	1090.27249	2	1.52E-05	0.89	3.42	-	747.8
AHQ-10-11, 3110	R.TPCEEILVK.H	1090.27249	2	5.23E-05	0.80	2.92	-	661.6
AHQ-10-1, 3354	R.TPCEEILVK.H	1090.27249	2	1.78E-05	0.90	3.40	-	824.4
AHQ-10-2, 3186	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.44E-07	0.90	3.53	-	824.9
AHQ-10-4, 3127	R.VANPSGNLTETYVQDR.G	1764.87462	2	8.69E-06	0.73	2.72	-	731.3
AHQ-10-7, 3216	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.39E-05	0.86	3.55	-	522.9
AHQ-10-5, 3261 - 3329	R.VANPSGNLTETYVQDR.G	1764.87462	2	3.33E-13	0.92	4.39	-	600.0
AHQ-10-3, 3382	R.VANPSGNLTETYVQDR.G	1764.87462	2	6.46E-04	0.68	2.92	-	416.9
AHQ-10-2, 3315 - 3374	R.VANPSGNLTETYVQDR.G	1764.87462	2	7.98E-12	0.93	4.31	-	902.6
AHQ-10-3, 3265 - 3341	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.44E-10	0.95	4.65	-	948.4
AHQ-10-1, 3453 - 3509	R.VANPSGNLTETYVQDR.G	1764.87462	2	1.53E-11	0.97	5.05	-	1414.7
AHQ-10-6, 3220 - 3301	R.VANPSGNLTETYVQDR.G	1764.87462	2	2.35E-11	0.95	4.56	-	1016.3
AHQ-10-4, 3284 - 3359	R.VANPSGNLTETYVQDR.G	1764.87462	2	4.17E-07	0.85	3.60	-	639.4
AHQ-10-2, 3434 - 3494	R.VANPSGNLTETYVQDR.G	1764.87462	2	9.76E-11	0.95	4.64	-	954.0
AHQ-10-5, 2675	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	8.69E-07	0.92	4.18	-	703.1
AHQ-10-8, 2809	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	8.35E-04	0.84	3.48	-	554.3
AHQ-10-5, 2864	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	5.14E-06	0.80	3.31	-	611.8
AHQ-10-4, 2852	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.62E-07	0.91	3.97	-	725.5
AHQ-10-3, 2706	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	2.14E-05	0.77	3.04	-	568.4
AHQ-10-2, 2958	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	4.38E-05	0.89	3.39	-	763.7
AHQ-10-4, 2660	K.VAQPTITDNKDGTVTVR.Y	1816.00621	2	3.39E-07	0.92	3.85	-	961.0
AHQ-10-4, 3255	K.VDINTEDLEDGTCR.V	1638.69283	2	6.55E-06	0.78	2.91	-	1045.1
AHQ-10-13-, 3490	K.VDINTEDLEDGTCR.V	1638.69283	2	2.88E-06	0.75	2.57	-	827.5
AHQ-10-7, 3433	K.VDINTEDLEDGTCR.V	1638.69283	2	3.62E-05	0.84	3.09	-	966.6
AHQ-10-5, 3236 - 3316	K.VDINTEDLEDGTCR.V	1638.69283	2	3.51E-07	0.94	3.85	-	1250.6
AHQ-10-6, 3431	K.VDINTEDLEDGTCR.V	1638.69283	2	2.58E-06	0.85	3.31	-	879.2
AHQ-10-4, 3515 - 3572	K.VDINTEDLEDGTCR.V	1638.69283	2	2.71E-06	0.94	4.22	-	1334.8
AHQ-10-8, 3217 - 3282	K.VDINTEDLEDGTCR.V	1638.69283	2	9.41E-06	0.77	2.95	-	769.1
AHQ-10-5, 3437 - 3495	K.VDINTEDLEDGTCR.V	1638.69283	2	4.91E-05	0.95	4.31	-	1169.3
AHQ-10-4, 3436 - 3507	K.VDINTEDLEDGTCR.V	1638.69283	2	3.79E-05	0.80	3.07	-	577.0
AHQ-10-1, 3643	K.VDINTEDLEDGTCR.V	1638.69283	2	3.91E-06	0.93	4.42	-	926.2
AHQ-10-2, 3560	K.VDINTEDLEDGTCR.V	1638.69283	2	1.54E-06	0.92	3.78	-	1121.6
AHQ-10-6, 3199 - 3272	K.VDINTEDLEDGTCR.V	1638.69283	2	5.63E-08	0.93	3.75	-	1287.3
AHQ-10-4, 3349	K.VDINTEDLEDGTCR.V	1638.69283	2	1.85E-04	0.64	2.57	-	676.1
AHQ-10-1, 3410	K.VDINTEDLEDGTCR.V	1638.69283	2	9.89E-07	0.94	3.70	-	1329.3
AHQ-10-3, 2671	K.VDVGKDQEFTVK.S	1365.51377	2	2.92E-08	0.90	3.51	-	718.1
AHQ-10-2, 2719	K.VDVGKDQEFTVK.S	1365.51377	2	2.59E-08	0.95	4.08	-	1049.7
AHQ-10-6, 2627	K.VDVGKDQEFTVK.S	1365.51377	2	3.33E-06	0.80	2.98	-	652.9
AHQ-10-7, 2625	K.VDVGKDQEFTVK.S	1365.51377	2	4.80E-08	0.59	2.60	-	463.4
AHQ-10-1, 2867	K.VDVGKDQEFTVK.S	1365.51377	2	6.40E-09	0.87	3.29	-	656.0
AHQ-10-4, 2647	K.VDVGKDQEFTVK.S	1365.51377	2	2.21E-08	0.89	3.50	-	783.2
AHQ-10-5, 2773	K.VEPGLGADNSVVR.F	1313.44209	2	1.88E-05	0.60	2.55	-	268.8
AHQ-10-1, 2987	K.VEPGLGADNSVVR.F	1313.44209	2	4.75E-06	0.80	3.18	-	241.7
AHQ-10-1, 5829 - 5831	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	5.39E-04	0.91	5.00	-	706.2
AHQ-10-3, 5654 - 5709	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	3.19E-04	0.91	5.05	-	735.4
AHQ-10-2, 5794 - 5872	K.VEYTPYEEGLHSVDVTYDGSPVPSSPFQVPVTEGCDPSR.V	4300.57494	3	1.79E-08	0.96	6.36	-	891.0
AHQ-10-5, 6428	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	2	8.85E-08	0.94	5.13	-	743.3
AHQ-10-5, 6369 - 6427	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	6.70E-04	0.86	4.51	-	471.6
AHQ-10-2, 6450	K.VGSAADIPINISETDLSLLTATVVPPSGR.E	2895.25495	3	9.65E-08	0.83	4.28	-	386.9
AHQ-10-5, 4248	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	5.45E-10	0.97	5.55	-	1521.1
AHQ-10-4, 4288	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.65E-04	0.95	4.89	-	1044.0
AHQ-10-4, 4251 - 4292	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	5.12E-05	0.94	4.54	-	1618.0
AHQ-10-5, 4241	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	7.21E-09	0.96	4.60	-	2197.2
AHQ-10-7, 4153	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	8.87E-08	0.96	5.39	-	1096.8
AHQ-10-3, 4262	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	2	1.47E-05	0.87	3.76	-	864.1
AHQ-10-1, 4397	K.VHSPSGALEECYVTEIDQDK.Y	2279.42322	3	3.58E-05	0.91	3.88	-	1477.2
AHQ-10-2, 4647	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.22E-09	0.84	3.98	-	486.1
AHQ-10-5, 4544	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	3.53E-09	0.83	4.47	-	471.9
AHQ-10-4, 4549 - 4616	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	1.45E-08	0.85	4.10	-	535.0
AHQ-10-3, 4566	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	9.68E-11	0.81	3.76	-	520.9
AHQ-10-8, 4495	K.VHSPSGALEECYVTEIDQDKYAVR.F	2768.99349	3	9.05E-05	0.87	3.98	-	619.4
AHQ-10-4, 3664 - 3723	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.85E-06	0.90	3.99	-	539.1
AHQ-10-5, 3776 - 3843	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.64E-08	0.86	3.55	-	607.6
AHQ-10-3, 3653 - 3710	K.VNQPASFAVSLNGAK.G	1503.68480	2	3.76E-08	0.86	3.66	-	549.3
AHQ-10-8, 3599	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.09E-06	0.76	2.98	-	573.4
AHQ-10-7, 3582 - 3640	K.VNQPASFAVSLNGAK.G	1503.68480	2	8.07E-05	0.77	3.28	-	428.2
AHQ-10-2, 3736	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.83E-07	0.83	3.11	-	475.1
AHQ-10-5, 3651 - 3711	K.VNQPASFAVSLNGAK.G	1503.68480	2	2.99E-08	0.91	4.08	-	607.9
AHQ-10-4, 3797 - 3855	K.VNQPASFAVSLNGAK.G	1503.68480	2	1.05E-08	0.89	3.82	-	562.0
AHQ-10-1, 3818 - 3873	K.VNQPASFAVSLNGAK.G	1503.68480	2	9.81E-09	0.93	4.08	-	791.5
AHQ-10-6, 3592 - 3651	K.VNQPASFAVSLNGAK.G	1503.68480	2	5.29E-08	0.90	3.94	-	693.9
AHQ-10-3, 1807	K.VPVHDVTDASK.V	1168.28175	2	4.33E-07	0.84	2.87	-	876.9
AHQ-10-2, 1816	K.VPVHDVTDASK.V	1168.28175	2	2.71E-06	0.91	3.33	-	923.4
AHQ-10-3, 3931 - 3989	R.VQVQDNEGCPVEALVK.D	1786.98493	2	3.40E-05	0.91	4.12	-	770.0
AHQ-10-1, 4143 - 4218	R.VQVQDNEGCPVEALVK.D	1786.98493	2	5.94E-06	0.93	4.28	-	1002.8
AHQ-10-5, 4004	R.VQVQDNEGCPVEALVK.D	1786.98493	2	8.48E-06	0.93	4.08	-	972.5
AHQ-10-2, 4056 - 4126	R.VQVQDNEGCPVEALVK.D	1786.98493	2	2.05E-06	0.96	4.76	-	1292.8
AHQ-10-4, 3952 - 4027	R.VQVQDNEGCPVEALVK.D	1786.98493	2	4.47E-05	0.97	4.89	-	1473.3
AHQ-10-2, 4894 - 4950	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.99E-07	0.94	4.85	-	1445.6
AHQ-10-3, 4813 - 4869	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	1.58E-08	0.95	5.34	-	1478.8
AHQ-10-1, 4953 - 5009	R.VQVQDNEGCPVEALVKDNGNGTYSCSYVPR.K	3359.60342	3	5.54E-08	0.95	5.39	-	1346.2
AHQ-10-3, 4657	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.74E-09	0.96	5.47	-	1359.9
AHQ-10-8, 4558	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.31E-09	0.97	5.95	-	1570.4
AHQ-10-8, 4562	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	2.79E-04	0.84	3.96	-	406.1
AHQ-10-6, 4556	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	8.77E-07	0.92	4.73	-	989.2
AHQ-10-5, 4615 - 4675	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.36E-07	0.96	5.41	-	1204.0
AHQ-10-5, 4623 - 4660	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	2	2.97E-04	0.91	4.48	-	590.9
AHQ-10-2, 4730	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	1.20E-05	0.91	4.37	-	885.7
AHQ-10-1, 4805 - 4862	R.VSGQGLHEGHTFEPAEFIIDTR.D	2441.64058	3	2.88E-06	0.96	5.31	-	1447.5
AHQ-10-1, 2961	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	7.22E-05	0.81	3.72	-	457.9
AHQ-10-2, 2803 - 2868	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	1.16E-05	0.91	4.93	-	446.2
AHQ-10-4, 2740 - 2809	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.07E-04	0.90	4.35	-	485.8
AHQ-10-5, 2861 - 2935	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	2.09E-04	0.63	3.64	-	302.0
AHQ-10-5, 2725 - 2795	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	3.46E-05	0.91	4.59	-	572.5
AHQ-10-2, 2926	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.36E-09	0.80	3.80	-	444.7
AHQ-10-3, 2881	K.VTAQGPGLEPSGNIANK.T	1653.81855	2	4.74E-05	0.82	3.44	-	512.2
AHQ-10-2, 3375 - 3382	K.VTVLFAGQHIAK.S	1284.53185	2	5.21E-06	0.92	3.44	-	1045.8
AHQ-10-2, 3384	K.VTVLFAGQHIAK.S	1284.53185	3	2.63E-05	0.84	3.46	-	912.5
AHQ-10-4, 3313 - 3385	K.VTVLFAGQHIAK.S	1284.53185	2	2.71E-06	0.92	3.47	-	992.1
AHQ-10-5, 3295 - 3365	K.VTVLFAGQHIAK.S	1284.53185	2	1.76E-05	0.92	3.83	-	831.6
AHQ-10-7, 3217	K.VTVLFAGQHIAK.S	1284.53185	2	9.39E-06	0.85	3.54	-	604.6
AHQ-10-4, 4951	R.VTYCPTEPGNYIINIK.F	1884.14221	2	7.85E-04	0.56	2.72	-	248.6
AHQ-10-4, 4823	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.31E-04	0.89	3.83	-	532.7
AHQ-10-3, 4774 - 4775	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.28E-05	0.93	4.51	-	592.2
AHQ-10-2, 4722	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.38E-06	0.73	3.10	-	356.7
AHQ-10-1, 4917	R.VTYCPTEPGNYIINIK.F	1884.14221	2	8.05E-04	0.83	3.33	-	384.3

AHQ-10-5, 4756 - 4815	R.VTYCPTEPGNYIINIK.F	1884.14221	2	3.30E-08	0.88	3.95	-	415.3
AHQ-10-1, 4770	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.42E-11	0.81	3.10	-	406.5
AHQ-10-4, 4848	R.VTYCPTEPGNYIINIK.F	1884.14221	3	4.40E-07	0.94	4.58	-	1138.1
AHQ-10-2, 4854 - 4858	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.47E-04	0.68	2.93	-	338.8
AHQ-10-6, 4572	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.10E-06	0.79	3.23	-	355.4
AHQ-10-3, 4639 - 4718	R.VTYCPTEPGNYIINIK.F	1884.14221	2	2.40E-08	0.82	3.67	-	431.1
AHQ-10-5, 4896 - 4931	R.VTYCPTEPGNYIINIK.F	1884.14221	2	1.16E-09	0.89	3.91	-	451.3
AHQ-10-4, 4677	R.VTYCPTEPGNYIINIK.F	1884.14221	2	5.80E-12	0.85	3.76	-	446.5
AHQ-10-6, 4695 - 4696	R.VTYTPM*APGSYLISIK.Y	1758.07165	2	9.38E-04	0.74	3.19	-	361.0
AHQ-10-11, 5042 - 5043	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	8.78E-04	0.76	3.26	-	518.7
AHQ-10-6, 5127	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	6.51E-05	0.83	3.02	-	698.5
AHQ-10-7, 5121	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.84E-04	0.55	2.56	-	462.4
AHQ-10-3, 5185	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	2.29E-05	0.81	3.26	-	740.2
AHQ-10-13-, 5138	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	4.19E-04	0.79	2.69	-	650.2
AHQ-10-4, 5240 - 5247	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	1.15E-05	0.89	3.29	-	951.1
AHQ-10-2, 5282	R.VTYTPMAPGSYLISIK.Y	1742.07225	2	3.80E-04	0.77	3.00	-	594.5
AHQ-10-5, 3392	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.99E-04	0.45	2.66	-	564.0
AHQ-10-8, 3334 - 3341	R.YAPSEAGLHEMDIR.Y	1589.75482	2	1.74E-04	0.91	3.64	-	928.4
AHQ-10-3, 2745 - 2750	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	4.38E-05	0.86	3.18	-	952.5
AHQ-10-5, 2719 - 2789	R.YAPSEAGLHEM*DIR.Y	1605.75422	2	9.35E-05	0.70	2.78	-	661.4
AHQ-10-1, 4261 - 4263	K.YGGDEIPFSPYR.V	1401.50466	2	1.26E-06	0.71	3.03	-	478.2
AHQ-10-8, 4078 - 4081	K.YGGDEIPFSPYR.V	1401.50466	2	3.98E-05	0.77	3.34	-	483.8
AHQ-10-10, 3323 - 3331	K.YGGPYHIGGSPFK.A	1380.53182	2	2.52E-05	0.54	2.82	-	533.2
AHQ-10-6, 3379	K.YGGPYHIGGSPFK.A	1380.53182	2	7.30E-08	0.97	4.53	-	1898.5
AHQ-10-8, 3347	K.YGGPYHIGGSPFK.A	1380.53182	2	1.18E-07	0.97	4.29	-	1889.4
AHQ-10-4, 3447	K.YGGPYHIGGSPFK.A	1380.53182	3	1.06E-06	0.87	4.11	-	523.9
AHQ-10-5, 3412	K.YGGPYHIGGSPFK.A	1380.53182	2	6.20E-07	0.95	3.77	-	1595.4
AHQ-10-1, 3617	K.YGGPYHIGGSPFK.A	1380.53182	2	1.17E-08	0.98	4.47	-	2340.9
AHQ-10-11, 3360	K.YGGPYHIGGSPFK.A	1380.53182	3	1.46E-06	0.89	3.98	-	597.0
AHQ-10-5, 3417	K.YGGPYHIGGSPFK.A	1380.53182	3	4.38E-05	0.71	3.27	-	455.8
AHQ-10-13-, 3456	K.YGGPYHIGGSPFK.A	1380.53182	2	6.54E-07	0.86	3.30	-	905.9
AHQ-10-4, 3440	K.YGGPYHIGGSPFK.A	1380.53182	2	6.75E-06	0.96	3.93	-	1654.6
AHQ-10-3, 3439	K.YGGPYHIGGSPFK.A	1380.53182	2	1.05E-07	0.93	3.47	-	1180.8
AHQ-10-2, 3147 - 3150	K.YGGQPVPNFPSK.L	1291.43658	1	1.85E-04	0.33	2.25	-	366.0
AHQ-10-4, 3079	K.YGGQPVPNFPSK.L	1291.43658	2	6.35E-06	0.89	3.38	-	547.3
AHQ-10-1, 3267	K.YGGQPVPNFPSK.L	1291.43658	2	5.93E-04	0.91	3.45	-	598.2
AHQ-10-3, 3089	K.YGGQPVPNFPSK.L	1291.43658	2	3.28E-07	0.92	3.80	-	635.6
AHQ-10-5, 3067	K.YGGQPVPNFPSK.L	1291.43658	2	1.98E-05	0.65	2.75	-	250.4
AHQ-10-2, 3138	K.YGGQPVPNFPSK.L	1291.43658	2	4.72E-07	0.94	4.06	-	762.0
AHQ-10-5, 4256 - 4257	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	9.51E-08	0.88	4.18	-	774.5
AHQ-10-3, 4310	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	7.10E-04	0.88	3.50	-	1117.7
AHQ-10-4, 4296	K.YKGQHVPGSPFQFTVGPLGEGGAHK.V	2596.88377	3	5.37E-05	0.77	3.64	-	805.6
AHQ-10-2, 3015	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.75E-06	0.82	3.46	-	421.8
AHQ-10-4, 2932	K.YNEQHVPGSPFTAR.V	1603.71978	2	9.68E-06	0.90	3.08	-	739.8
AHQ-10-1, 3143	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.60E-07	0.86	3.11	-	659.6
AHQ-10-1, 3153 - 3154	K.YNEQHVPGSPFTAR.V	1603.71978	3	2.11E-05	0.88	4.23	-	785.1
AHQ-10-6, 2899	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.58E-04	0.86	3.04	-	661.8
AHQ-10-5, 2923	K.YNEQHVPGSPFTAR.V	1603.71978	2	2.97E-05	0.88	3.20	-	851.5
AHQ-10-3, 2955	K.YNEQHVPGSPFTAR.V	1603.71978	2	1.16E-05	0.87	3.28	-	639.3
AHQ-10-8, 2834	K.YNEQHVPGSPFTAR.V	1603.71978	2	8.43E-04	0.68	2.74	-	385.6
AHQ-10-8, 2837	K.YNEQHVPGSPFTAR.V	1603.71978	3	5.74E-07	0.91	4.19	-	998.9
AHQ-10-4, 2935	K.YNEQHVPGSPFTAR.V	1603.71978	3	1.03E-07	0.95	4.98	-	1265.9
AHQ-10-5, 3092	K.YNEQHVPGSPFTAR.V	1603.71978	3	5.62E-04	0.88	3.71	-	1206.1
AHQ-10-3, 4281 - 4338	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.12E-06	0.95	4.49	-	1022.0
AHQ-10-3, 4419	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	9.75E-08	0.85	3.71	-	665.9
AHQ-10-5, 4353 - 4355	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.23E-06	0.91	4.47	-	475.2
AHQ-10-2, 4496	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.57E-07	0.91	4.28	-	530.4
AHQ-10-1, 4422 - 4477	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.34E-05	0.94	4.75	-	753.4
AHQ-10-4, 4471	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	2.16E-04	0.86	3.83	-	532.3
AHQ-10-6, 4261	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	4.97E-06	0.90	4.00	-	574.6
AHQ-10-4, 4309 - 4363	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.67E-06	0.94	4.54	-	802.0
AHQ-10-2, 4212 - 4254	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.32E-06	0.91	4.11	-	551.8
AHQ-10-2, 4347 - 4410	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.31E-08	0.96	4.94	-	958.6
AHQ-10-1, 4598	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	1.76E-05	0.71	3.05	-	330.3
AHQ-10-1, 4478	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	3	5.65E-05	0.86	3.67	-	1051.4
AHQ-10-7, 4246 - 4252	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	5.25E-06	0.94	4.82	-	756.9
AHQ-10-1, 4313	K.YTPVQQGPVGVNVTYGGDPIPK.S	2287.55640	2	6.27E-04	0.65	2.91	-	297.0
AHQ-10-2, 6163	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	6.45E-08	0.69	3.10	-	452.0
AHQ-10-2, 6139 - 6196	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	3	2.07E-07	0.62	3.10	-	537.4
AHQ-10-2, 5816 - 5870	R.YWPQEAGEYAVHVLCNSEDIR.L	2538.73318	2	1.85E-07	0.70	2.75	-	607.8
gi|12667788|ref|NP_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens]				8.33E-15	82.67	940.35	41.70	226529.8
AHQ-10-5, 2091	R.ALEEAMEQK.A	1049.18068	2	5.72E-04	0.78	2.71	-	780.7
AHQ-10-2, 2188	R.ALEEAMEQK.A	1049.18068	2	5.72E-04	0.80	3.15	-	660.6
AHQ-10-5, 3691	K.ALELDSNLYR.I	1194.31920	2	1.89E-06	0.92	3.36	-	1192.0
AHQ-10-2, 3766 - 3770	K.ALELDSNLYR.I	1194.31920	2	1.82E-06	0.94	3.77	-	1273.2
AHQ-10-4, 3715	K.ALELDSNLYR.I	1194.31920	2	2.02E-06	0.90	3.53	-	952.9
AHQ-10-3, 3689	K.ALELDSNLYR.I	1194.31920	2	1.57E-06	0.96	4.04	-	1406.6
AHQ-10-2, 3650	K.ALELDSNLYR.I	1194.31920	2	8.41E-08	0.96	4.02	-	1777.5
AHQ-10-1, 3861 - 3865	K.ALELDSNLYR.I	1194.31920	2	1.34E-07	0.95	3.99	-	1273.6
AHQ-10-4, 2200	R.ALEQQVEEM*K.T	1221.36320	2	6.08E-05	0.79	3.14	-	751.9
AHQ-10-5, 2928	R.ALEQQVEEMK.T	1205.36380	2	3.94E-05	0.87	3.27	-	1012.4
AHQ-10-3, 2873 - 2945	R.ALEQQVEEMK.T	1205.36380	2	4.15E-04	0.75	2.94	-	720.0
AHQ-10-4, 2933	R.ALEQQVEEMK.T	1205.36380	2	1.82E-04	0.89	3.35	-	1105.2
AHQ-10-2, 2995	R.ALEQQVEEMK.T	1205.36380	2	2.71E-05	0.91	3.24	-	1320.9
AHQ-10-2, 2258 - 2259	R.ALEQQVEEM*K.T	1221.36320	2	3.90E-06	0.84	3.81	-	692.8
AHQ-10-6, 2896	R.ALEQQVEEMK.T	1205.36380	2	4.88E-06	0.89	3.68	-	947.9
AHQ-10-3, 5870 - 5950	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	1.34E-05	0.98	6.96	-	2082.2
AHQ-10-4, 5895 - 5963	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	4.95E-06	0.95	5.15	-	1355.4
AHQ-10-2, 5954 - 5998	R.ALEQQVEEM*KTQLEELEDELQATEDAK.L	3165.38394	3	4.31E-11	0.97	6.46	-	1656.2
AHQ-10-2, 5043	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.33E-06	0.96	4.36	-	1365.3
AHQ-10-7, 4708	K.ANLQIDQINTDLNLER.S	1871.04187	2	5.07E-06	0.95	4.32	-	1230.3
AHQ-10-2, 4582 - 4659	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.39E-12	0.97	5.78	-	1210.4
AHQ-10-3, 4782	K.ANLQIDQINTDLNLER.S	1871.04187	3	5.50E-05	0.97	5.74	-	2120.4
AHQ-10-1, 4921	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.66E-08	0.93	4.38	-	814.2
AHQ-10-2, 4702	K.ANLQIDQINTDLNLER.S	1871.04187	2	7.70E-04	0.94	4.24	-	953.8
AHQ-10-6, 4656 - 4723	K.ANLQIDQINTDLNLER.S	1871.04187	2	2.31E-04	0.94	4.08	-	1100.6
AHQ-10-2, 4850	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.26E-04	0.96	4.43	-	1516.2
AHQ-10-3, 4499 - 4578	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.93E-08	0.96	5.04	-	1034.6
AHQ-10-8, 4763	K.ANLQIDQINTDLNLER.S	1871.04187	2	6.83E-05	0.97	5.25	-	1416.8
AHQ-10-2, 4954	K.ANLQIDQINTDLNLER.S	1871.04187	2	4.81E-06	0.97	5.45	-	1538.2
AHQ-10-3, 4875	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.75E-04	0.94	4.23	-	1099.7
AHQ-10-4, 4829 - 4831	K.ANLQIDQINTDLNLER.S	1871.04187	2	9.17E-05	0.97	5.19	-	1257.5
AHQ-10-4, 4636	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.46E-08	0.94	4.61	-	805.5
AHQ-10-3, 4983	K.ANLQIDQINTDLNLER.S	1871.04187	2	3.75E-04	0.73	3.09	-	578.1
AHQ-10-1, 4731	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.23E-09	0.89	3.51	-	868.7
AHQ-10-3, 4729 - 4773	K.ANLQIDQINTDLNLER.S	1871.04187	2	1.83E-08	0.97	5.60	-	1401.8
AHQ-10-3, 2486 - 2494	K.ASITALEAK.I	904.04321	2	2.81E-05	0.92	3.25	-	1110.5

AHQ-10-2, 2527	K.ASITALEAK.I	904.04321	2	1.19E-05	0.89	3.14	-	884.6
AHQ-10-5, 2432	K.ASITALEAK.I	904.04321	2	5.86E-06	0.92	3.30	-	1016.2
AHQ-10-4, 2453	K.ASITALEAK.I	904.04321	2	2.16E-05	0.91	3.13	-	977.7
AHQ-10-2, 2232	R.ASREEILAQAK.E	1216.36955	2	2.11E-04	0.90	3.41	-	1238.6
AHQ-10-3, 2202	R.ASREEILAQAK.E	1216.36955	2	3.91E-06	0.92	3.88	-	1239.2
AHQ-10-4, 2760	R.DELADEIANSSGK.G	1349.38323	2	4.07E-04	0.89	3.38	-	1085.1
AHQ-10-2, 2815	R.DELADEIANSSGK.G	1349.38323	2	5.11E-04	0.93	3.58	-	1248.1
AHQ-10-2, 3196	R.DELADEIANSSGK.G	1349.38323	2	1.92E-06	0.96	4.11	-	1484.7
AHQ-10-6, 6087 - 6096	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	3.13E-05	0.92	4.38	-	1140.4
AHQ-10-4, 5915	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	9.07E-05	0.84	3.37	-	1207.2
AHQ-10-1, 6241 - 6242	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	5.52E-05	0.97	5.67	-	2231.5
AHQ-10-4, 6216	K.DFSALESQLQDTQELLQEENR.Q	2494.61059	3	2.13E-06	0.96	4.90	-	1509.1
AHQ-10-3, 5791 - 5845	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	6.28E-07	0.86	4.08	-	614.5
AHQ-10-2, 5820 - 5876	K.DFSALESQLQDTQELLQEENRQK.L	2750.91328	3	1.77E-04	0.76	3.54	-	437.8
AHQ-10-3, 2258	K.DLEAHIDSANK.N	1213.27938	2	1.06E-06	0.94	3.49	-	1505.9
AHQ-10-2, 2298	K.DLEAHIDSANK.N	1213.27938	2	7.31E-08	0.97	4.22	-	2068.6
AHQ-10-4, 6483	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	9.08E-07	0.90	4.08	-	1110.0
AHQ-10-3, 6331 - 6406	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	8.47E-05	0.89	4.24	-	1170.7
AHQ-10-2, 6518	R.DLGEELEALKTELEDTLDSTAAQQELR.S	3019.21860	3	9.09E-09	0.93	4.33	-	1463.9
AHQ-10-3, 3314	K.DVLLQVDDER.R	1202.29650	2	2.17E-07	0.91	3.24	-	1079.1
AHQ-10-2, 2944 - 3022	K.DVLLQVDDERR.N	1358.48286	2	4.52E-04	0.55	2.74	-	556.2
AHQ-10-1, 3038	R.ELEDATETADAMNR.E	1566.63006	2	3.99E-07	0.83	3.01	-	890.1
AHQ-10-5, 2839	R.ELEDATETADAMNR.E	1566.63006	2	2.28E-07	0.89	3.37	-	971.9
AHQ-10-3, 2275 - 2343	R.ELEDATETADAM*NR.E	1582.62946	2	8.68E-04	0.85	3.16	-	898.9
AHQ-10-3, 2773 - 2847	R.ELEDATETADAMNR.E	1566.63006	2	1.73E-08	0.87	2.97	-	969.6
AHQ-10-2, 2251 - 2306	R.ELEDATETADAM*NR.E	1582.62946	2	1.63E-06	0.90	3.77	-	749.3
AHQ-10-4, 2833	R.ELEDATETADAMNR.E	1566.63006	2	5.45E-06	0.90	3.22	-	1144.7
AHQ-10-3, 5297 - 5355	R.ELESQISELQEDLESER.A	2035.10956	3	1.34E-04	0.97	5.99	-	2143.4
AHQ-10-3, 5350	R.ELESQISELQEDLESER.A	2035.10956	2	5.84E-07	0.96	5.00	-	1230.1
AHQ-10-8, 5395	R.ELESQISELQEDLESER.A	2035.10956	2	4.96E-05	0.88	4.05	-	627.4
AHQ-10-1, 5414 - 5486	R.ELESQISELQEDLESER.A	2035.10956	2	1.75E-04	0.95	5.26	-	1155.3
AHQ-10-2, 5123	R.ELESQISELQEDLESER.A	2035.10956	2	8.79E-05	0.89	4.32	-	485.5
AHQ-10-2, 5664 - 5746	R.ELESQISELQEDLESER.A	2035.10956	2	2.90E-07	0.72	2.88	-	648.5
AHQ-10-6, 5312	R.ELESQISELQEDLESER.A	2035.10956	2	2.40E-06	0.94	4.96	-	805.3
AHQ-10-4, 5444	R.ELESQISELQEDLESER.A	2035.10956	3	2.52E-04	0.98	5.90	-	2308.5
AHQ-10-4, 5439	R.ELESQISELQEDLESER.A	2035.10956	2	4.70E-10	0.95	4.22	-	1214.5
AHQ-10-2, 5370 - 5442	R.ELESQISELQEDLESER.A	2035.10956	2	2.84E-07	0.95	4.86	-	1001.3
AHQ-10-5, 5427	R.ELESQISELQEDLESER.A	2035.10956	2	2.07E-06	0.94	4.60	-	933.4
AHQ-10-3, 2317	R.EMEAELEDERK.Q	1379.47597	2	4.18E-04	0.91	3.43	-	1165.3
AHQ-10-5, 2263	R.EMEAELEDERK.Q	1379.47597	2	6.62E-05	0.93	3.24	-	1411.3
AHQ-10-7, 4157	K.EQADFAIEALAK.A	1306.44632	2	7.57E-04	0.82	2.99	-	590.0
AHQ-10-3, 2506	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.72E-05	0.82	3.89	-	543.7
AHQ-10-2, 2556	R.EQLEEEEEAKHNLEK.Q	1855.93770	2	1.21E-04	0.83	3.53	-	613.3
AHQ-10-3, 3009	K.HEAMITDLEER.L	1344.47646	2	8.19E-05	0.95	3.94	-	1228.4
AHQ-10-2, 3048	K.HEAMITDLEER.L	1344.47646	2	9.61E-06	0.96	3.80	-	1201.6
AHQ-10-2, 3451	R.HEM*PPHIYAITDTAYR.S	1932.14884	2	2.43E-05	0.79	2.99	-	586.9
AHQ-10-7, 3296	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	4.71E-04	0.93	3.81	-	1538.0
AHQ-10-5, 3364	R.HEM*PPHIYAITDTAYR.S	1932.14884	3	5.76E-04	0.97	4.12	-	2349.3
AHQ-10-2, 3675	R.HEMPPHIYAITDTAYR.S	1916.14944	3	5.33E-10	0.96	4.21	-	2125.0
AHQ-10-3, 4403	K.HSQAVEELAEQLEQTK.R	1840.96940	2	7.68E-09	0.98	5.68	-	1752.0
AHQ-10-2, 4467	K.HSQAVEELAEQLEQTK.R	1840.96940	3	2.34E-07	0.95	4.64	-	1596.9
AHQ-10-4, 4443	K.HSQAVEELAEQLEQTK.R	1840.96940	3	2.22E-06	0.97	5.01	-	2007.0
AHQ-10-2, 4466	K.HSQAVEELAEQLEQTK.R	1840.96940	2	6.31E-09	0.98	6.16	-	2105.4
AHQ-10-3, 4405	K.HSQAVEELAEQLEQTK.R	1840.96940	3	2.40E-08	0.96	5.55	-	1627.8
AHQ-10-4, 4445	K.HSQAVEELAEQLEQTK.R	1840.96940	2	1.09E-13	0.98	5.94	-	2023.6
AHQ-10-2, 4163	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	2.68E-09	0.98	6.44	-	2119.9
AHQ-10-3, 4102	K.HSQAVEELAEQLEQTKR.V	1997.15575	2	7.39E-08	0.99	6.39	-	3320.6
AHQ-10-1, 4262	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.12E-10	0.95	4.79	-	1217.2
AHQ-10-4, 4129 - 4183	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	2.64E-09	0.96	5.33	-	1505.6
AHQ-10-3, 4097	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	1.17E-05	0.97	6.18	-	1650.5
AHQ-10-2, 4162 - 4190	K.HSQAVEELAEQLEQTKR.V	1997.15575	3	7.57E-07	0.97	6.28	-	1353.0
AHQ-10-2, 3786 - 3844	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.50E-06	0.94	4.27	-	1088.1
AHQ-10-1, 3813 - 3871	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.08E-06	0.96	4.34	-	1602.5
AHQ-10-3, 3559 - 3613	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.65E-05	0.94	3.45	-	1346.5
AHQ-10-13-, 3661	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.08E-04	0.87	2.96	-	1184.3
AHQ-10-2, 3911	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.87E-06	0.97	4.14	-	2005.8
AHQ-10-5, 3659	R.IAEFTTNLTEEEEK.S	1654.75371	2	4.29E-07	0.95	4.28	-	1490.2
AHQ-10-2, 3683 - 3743	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.52E-09	0.97	4.86	-	1843.0
AHQ-10-3, 3834	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.80E-08	0.96	3.94	-	1685.5
AHQ-10-2, 3539	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.68E-06	0.77	2.76	-	957.2
AHQ-10-3, 3751	R.IAEFTTNLTEEEEK.S	1654.75371	2	9.15E-07	0.96	4.14	-	1844.6
AHQ-10-7, 3588	R.IAEFTTNLTEEEEK.S	1654.75371	2	1.41E-04	0.94	3.97	-	1331.9
AHQ-10-3, 3669	R.IAEFTTNLTEEEEK.S	1654.75371	2	6.65E-07	0.96	4.37	-	1679.1
AHQ-10-6, 3596 - 3664	R.IAEFTTNLTEEEEK.S	1654.75371	2	2.35E-07	0.91	3.75	-	1405.4
AHQ-10-4, 3669	R.IAEFTTNLTEEEEK.S	1654.75371	2	3.51E-05	0.93	3.74	-	1501.6
AHQ-10-2, 3424 - 3491	R.IAEFTTNLTEEEEKSK.S	1870.00428	3	1.29E-04	0.60	3.13	-	461.1
AHQ-10-3, 4810 - 4865	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	3.54E-06	0.88	4.43	-	804.8
AHQ-10-2, 4939	R.IAQLEEELEEEQGNTELINDR.L	2473.58969	3	5.87E-06	0.92	5.31	-	868.3
AHQ-10-2, 5182 - 5207	R.IAQLEEELEEEQGNTELINDRLK.K	2714.92085	3	8.09E-05	0.89	4.00	-	912.4
AHQ-10-6, 3069	K.IAQLEEQLDNETK.E	1531.64695	2	1.36E-05	0.89	3.43	-	945.3
AHQ-10-2, 3759	K.IAQLEEQLDNETK.E	1531.64695	2	1.95E-05	0.96	4.39	-	1465.6
AHQ-10-4, 3367 - 3392	K.IAQLEEQLDNETK.E	1531.64695	2	1.22E-08	0.95	4.43	-	1330.9
AHQ-10-6, 3299	K.IAQLEEQLDNETK.E	1531.64695	2	3.94E-07	0.94	3.61	-	1409.2
AHQ-10-5, 3105	K.IAQLEEQLDNETK.E	1531.64695	2	2.44E-08	0.96	4.06	-	1825.0
AHQ-10-5, 3340	K.IAQLEEQLDNETK.E	1531.64695	2	1.19E-06	0.97	4.69	-	1711.1
AHQ-10-9, 3153 - 3155	K.IAQLEEQLDNETK.E	1531.64695	2	1.38E-05	0.97	4.69	-	1665.5
AHQ-10-2, 3414	K.IAQLEEQLDNETK.E	1531.64695	2	1.31E-08	0.96	4.28	-	1433.9
AHQ-10-1, 3526	K.IAQLEEQLDNETK.E	1531.64695	2	9.44E-09	0.97	4.61	-	1836.4
AHQ-10-3, 3349	K.IAQLEEQLDNETK.E	1531.64695	2	4.10E-04	0.96	4.68	-	1503.2
AHQ-10-2, 3502	K.IAQLEEQLDNETK.E	1531.64695	2	2.24E-04	0.95	4.06	-	1224.5
AHQ-10-2, 3174	K.IAQLEEQLDNETK.E	1531.64695	2	1.55E-09	0.96	4.29	-	1594.5
AHQ-10-7, 3282	K.IAQLEEQLDNETK.E	1531.64695	2	1.12E-05	0.93	3.85	-	1206.4
AHQ-10-3, 3118	K.IAQLEEQLDNETK.E	1531.64695	2	2.86E-11	0.92	3.62	-	1138.7
AHQ-10-10, 3254	K.IAQLEEQLDNETK.E	1531.64695	2	1.13E-05	0.95	3.78	-	1405.3
AHQ-10-2, 3543	K.IAQLEEQLDNETKER.Q	1816.94784	2	5.86E-08	0.87	3.38	-	838.4
AHQ-10-3, 5922	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.03E-06	0.80	3.14	-	528.9
AHQ-10-2, 5955 - 6011	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.38E-06	0.97	5.42	-	1371.7
AHQ-10-2, 5480 - 5518	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.60E-07	0.83	3.57	-	778.9
AHQ-10-4, 6001 - 6003	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	1.27E-06	0.95	5.00	-	861.7
AHQ-10-3, 5265 - 5293	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	3.13E-05	0.93	4.69	-	769.9
AHQ-10-6, 5799 - 5868	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.31E-05	0.92	4.31	-	987.3
AHQ-10-2, 5003	R.IIGLDQVAGM*SETALPGAFK.T	2035.35041	2	3.91E-05	0.89	3.93	-	732.6
AHQ-10-5, 6007	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	3	2.16E-04	0.85	3.55	-	1042.9
AHQ-10-5, 6001 - 6003	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	4.47E-07	0.97	6.33	-	1305.8
AHQ-10-1, 5967 - 6041	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	3.00E-04	0.80	3.60	-	392.9
AHQ-10-7, 5906	R.IIGLDQVAGMSETALPGAFK.T	2019.35101	2	5.23E-04	0.94	4.39	-	1105.6
AHQ-10-5, 3872	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	2.02E-07	0.61	2.61	-	405.3

AHQ-10-2, 3928 - 3951	R.IM*GIPEEEQM*GLLR.V	1648.92706	2	2.23E-04	0.92	3.41	-	952.2
AHQ-10-2, 5484	K.IRELESQISELQEDLESER.A	2304.45416	2	1.39E-05	0.97	6.15	-	821.5
AHQ-10-5, 5476	K.IRELESQISELQEDLESER.A	2304.45416	2	4.10E-04	0.95	5.09	-	812.0
AHQ-10-3, 5401	K.IRELESQISELQEDLESER.A	2304.45416	2	3.05E-05	0.98	6.53	-	1330.7
AHQ-10-6, 5305 - 5359	K.IRELESQISELQEDLESER.A	2304.45416	3	3.46E-07	0.95	4.93	-	1424.4
AHQ-10-2, 5179	K.ITDVIIGFQACCR.G	1555.80136	2	1.19E-05	0.77	2.63	-	824.4
AHQ-10-2, 5315 - 5324	K.ITDVIIGFQACCR.G	1555.80136	2	1.85E-06	0.65	3.01	-	535.9
AHQ-10-3, 4331 - 4390	K.KANLQIDQINTDLNLER.S	1999.21478	2	1.02E-06	0.93	4.91	-	942.1
AHQ-10-1, 4531	K.KANLQIDQINTDLNLER.S	1999.21478	3	8.88E-07	0.89	4.47	-	885.6
AHQ-10-6, 4307	K.KANLQIDQINTDLNLER.S	1999.21478	2	9.41E-04	0.95	5.06	-	1024.9
AHQ-10-9, 4115	K.KANLQIDQINTDLNLER.S	1999.21478	2	4.46E-04	0.92	3.92	-	1027.5
AHQ-10-2, 4454 - 4455	K.KANLQIDQINTDLNLER.S	1999.21478	3	9.70E-08	0.83	4.25	-	688.8
AHQ-10-2, 2730 - 2790	R.KKVEAQLQELQVK.F	1541.81761	2	2.48E-08	0.97	5.24	-	1655.2
AHQ-10-2, 2794	R.KKVEAQLQELQVK.F	1541.81761	3	1.83E-04	0.86	3.66	-	986.1
AHQ-10-6, 2696	R.KKVEAQLQELQVK.F	1541.81761	2	1.65E-05	0.93	3.95	-	1266.5
AHQ-10-3, 2741	R.KKVEAQLQELQVK.F	1541.81761	2	3.88E-07	0.96	4.95	-	1266.9
AHQ-10-4, 2707	R.KKVEAQLQELQVK.F	1541.81761	2	5.82E-07	0.97	5.18	-	1672.7
AHQ-10-5, 2732	R.KKVEAQLQELQVK.F	1541.81761	2	3.48E-08	0.97	4.89	-	1788.0
AHQ-10-3, 3514	K.KLEEEQIILEDQNCK.L	1891.08992	3	2.60E-08	0.89	4.35	-	1033.0
AHQ-10-2, 3572	K.KLEEEQIILEDQNCK.L	1891.08992	2	3.22E-11	0.98	5.93	-	2047.6
AHQ-10-1, 3626	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.41E-05	0.95	4.54	-	1114.3
AHQ-10-2, 3448 - 3515	K.KLEEEQIILEDQNCK.L	1891.08992	2	2.06E-05	0.98	6.10	-	1864.2
AHQ-10-3, 3390 - 3445	K.KLEEEQIILEDQNCK.L	1891.08992	2	9.61E-05	0.98	5.82	-	1941.6
AHQ-10-4, 3463 - 3532	K.KLEEEQIILEDQNCK.L	1891.08992	2	5.03E-09	0.98	6.16	-	1493.6
AHQ-10-3, 3505	K.KLEEEQIILEDQNCK.L	1891.08992	2	9.62E-12	0.97	5.27	-	1194.2
AHQ-10-2, 3511 - 3586	K.KLEEEQIILEDQNCK.L	1891.08992	3	5.73E-04	0.85	4.11	-	935.9
AHQ-10-2, 3879	K.KLEEEQIILEDQNCKLAK.E	2203.49930	3	2.35E-07	0.94	5.00	-	948.7
AHQ-10-1, 6374	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.70E-07	0.91	4.73	-	990.3
AHQ-10-5, 6355	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	2.69E-07	0.91	4.88	-	768.2
AHQ-10-6, 6231	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	1.68E-06	0.88	4.40	-	727.5
AHQ-10-3, 6269	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	2.83E-04	0.90	3.94	-	944.4
AHQ-10-2, 6375	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	2	3.22E-10	0.96	5.35	-	1272.7
AHQ-10-3, 6265	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	6.33E-06	0.95	5.85	-	1145.2
AHQ-10-2, 6307 - 6374	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	5.02E-09	0.94	6.00	-	842.8
AHQ-10-2, 5718	R.KLEGDSTDLSDQIAELQAQIAELK.M	2616.86032	3	1.51E-06	0.93	4.44	-	1476.1
AHQ-10-6, 2889 - 2895	K.KLVWVPSDK.S	1072.28194	2	5.51E-05	0.71	2.89	-	630.8
AHQ-10-2, 2994	K.KLVWVPSDK.S	1072.28194	2	3.85E-06	0.89	3.16	-	1000.7
AHQ-10-2, 3616	K.KMEDSVGCLETAEEVK.R	1827.02450	2	1.35E-04	0.81	2.96	-	1150.1
AHQ-10-2, 3380	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.86E-06	0.96	5.67	-	1088.2
AHQ-10-2, 3032	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	1.23E-09	0.95	4.83	-	1462.5
AHQ-10-4, 3328	K.KMEDSVGCLETAEEVKR.K	1983.21085	3	1.46E-04	0.96	5.60	-	1222.3
AHQ-10-3, 2983	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	1.10E-06	0.98	5.88	-	2005.6
AHQ-10-4, 2984	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	3.38E-04	0.92	4.79	-	814.1
AHQ-10-5, 2960	K.KM*EDSVGCLETAEEVKR.K	1999.21025	3	1.88E-05	0.76	3.35	-	805.2
AHQ-10-2, 4639 - 4694	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	1.61E-05	0.91	4.60	-	919.1
AHQ-10-1, 4763 - 4769	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	3	5.03E-04	0.60	3.27	-	737.0
AHQ-10-2, 4703	K.KM*QQNIQELEEQLEEEESAR.Q	2478.63294	2	1.83E-04	0.77	3.31	-	315.5
AHQ-10-6, 3979	K.KQELEEICHDLEAR.V	1771.93036	3	7.53E-06	0.95	5.15	-	1535.5
AHQ-10-1, 4198	K.KQELEEICHDLEAR.V	1771.93036	3	3.13E-06	0.94	4.84	-	1439.6
AHQ-10-2, 4096	K.KQELEEICHDLEAR.V	1771.93036	2	3.07E-05	0.97	5.01	-	1755.7
AHQ-10-2, 3095 - 3098	K.KVEAQLQELQVK.F	1413.64470	2	2.59E-05	0.96	5.15	-	1448.1
AHQ-10-3, 3047 - 3057	K.KVEAQLQELQVK.F	1413.64470	2	1.91E-04	0.96	4.78	-	1512.0
AHQ-10-6, 2979 - 2985	K.KVEAQLQELQVK.F	1413.64470	2	8.92E-05	0.90	3.04	-	1306.0
AHQ-10-4, 3721 - 3791	K.LEEEQIILEDQNCK.L	1762.91700	2	1.85E-07	0.93	3.98	-	1021.2
AHQ-10-1, 3853 - 3930	K.LEEEQIILEDQNCK.L	1762.91700	2	2.74E-06	0.88	3.48	-	958.5
AHQ-10-2, 3763 - 3834	K.LEEEQIILEDQNCK.L	1762.91700	2	3.10E-09	0.97	5.58	-	1152.1
AHQ-10-2, 3818	K.LEEEQIILEDQNCK.L	1762.91700	2	7.99E-09	0.97	4.99	-	1673.7
AHQ-10-3, 6309	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	2.22E-08	0.92	4.79	-	1078.3
AHQ-10-2, 6423	K.LEGDSTDLSDQIAELQAQIAELK.M	2488.68740	3	1.14E-04	0.93	4.37	-	1290.1
AHQ-10-2, 3583	R.LEVNLQAMK.A	1046.26630	2	9.73E-06	0.78	3.19	-	584.9
AHQ-10-4, 3528	R.LEVNLQAMK.A	1046.26630	2	6.19E-04	0.79	3.24	-	483.7
AHQ-10-2, 2735	R.LEVNLQAM*K.A	1062.26570	2	4.23E-04	0.84	3.34	-	542.2
AHQ-10-3, 2703	R.LEVNLQAM*K.A	1062.26570	2	2.30E-05	0.76	2.81	-	550.3
AHQ-10-3, 3507	K.LKDVLLQVDDER.R	1443.62767	2	1.86E-09	0.97	5.01	-	1739.6
AHQ-10-2, 3570	K.LKDVLLQVDDER.R	1443.62767	2	8.81E-08	0.94	3.35	-	1647.3
AHQ-10-2, 3578	K.LKDVLLQVDDER.R	1443.62767	2	4.11E-08	0.97	4.65	-	1738.9
AHQ-10-4, 3199	K.LKDVLLQVDDERR.N	1599.81402	2	1.07E-04	0.55	2.68	-	613.0
AHQ-10-2, 3254 - 3318	K.LKDVLLQVDDERR.N	1599.81402	2	1.28E-04	0.93	4.02	-	1119.4
AHQ-10-2, 3255 - 3276	K.LKDVLLQVDDERR.N	1599.81402	3	1.52E-04	0.89	3.60	-	929.8
AHQ-10-3, 3201	K.LKDVLLQVDDERR.N	1599.81402	2	1.50E-04	0.95	3.77	-	1985.3
AHQ-10-2, 6570 - 6627	K.LQLQEQLQAETELCAEAEELR.A	2503.72536	2	6.92E-07	0.71	2.70	-	539.6
AHQ-10-6, 5561	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	1.79E-05	0.86	3.83	-	769.6
AHQ-10-5, 5695	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.74E-10	0.97	5.16	-	1486.7
AHQ-10-7, 5582	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.92E-06	0.85	3.86	-	818.5
AHQ-10-3, 5239	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	7.35E-04	0.74	3.34	-	551.1
AHQ-10-1, 5738	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.64E-05	0.80	3.24	-	772.7
AHQ-10-2, 5694 - 5720	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	7.91E-07	0.91	4.48	-	956.5
AHQ-10-2, 5696 - 5748	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	8.33E-15	0.97	5.37	-	1383.3
AHQ-10-2, 5318	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	3.06E-05	0.95	5.23	-	1083.5
AHQ-10-6, 5564	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.19E-11	0.96	4.56	-	1327.3
AHQ-10-4, 5707 - 5779	R.LQQELDDLLVDLDHQR.Q	1951.12699	3	5.53E-06	0.87	3.89	-	757.9
AHQ-10-4, 5709	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.37E-11	0.98	5.91	-	1898.1
AHQ-10-3, 5606 - 5613	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	1.76E-09	0.97	5.16	-	1741.1
AHQ-10-2, 5255 - 5319	R.LQQELDDLLVDLDHQR.Q	1951.12699	2	2.69E-11	0.91	4.12	-	994.9
AHQ-10-2, 5127	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.56E-07	0.95	4.41	-	1354.4
AHQ-10-3, 5382 - 5439	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	3.85E-08	0.95	5.13	-	913.3
AHQ-10-7, 5276	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.03E-06	0.97	5.23	-	1410.2
AHQ-10-1, 5450	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	3.36E-06	0.96	4.62	-	1525.7
AHQ-10-4, 5641	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	5.27E-06	0.94	4.14	-	1151.6
AHQ-10-3, 5322	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	7.59E-10	0.97	5.88	-	1893.5
AHQ-10-1, 5533	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.95E-04	0.83	3.70	-	607.5
AHQ-10-2, 5380 - 5452	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	7.01E-13	0.98	6.41	-	1612.2
AHQ-10-4, 5125	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.88E-07	0.97	5.21	-	1325.4
AHQ-10-2, 5414	K.LQVELDNVTGLLSQSDSK.S	1947.13342	3	1.37E-04	0.96	5.25	-	1465.7
AHQ-10-2, 5510 - 5511	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.07E-11	0.97	5.77	-	1466.1
AHQ-10-2, 6626	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	9.04E-07	0.91	3.34	-	1096.5
AHQ-10-3, 5294 - 5365	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.27E-06	0.96	4.63	-	1468.3
AHQ-10-3, 5043 - 5115	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	2.06E-07	0.97	5.24	-	1600.2
AHQ-10-2, 5612 - 5690	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.47E-04	0.83	3.61	-	543.8
AHQ-10-5, 5352 - 5377	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	8.33E-09	0.97	5.57	-	1396.0
AHQ-10-6, 5267	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.05E-05	0.90	3.96	-	762.1
AHQ-10-14-, 5288	K.LQVELDNVTGLLSQSDSK.S	1947.13342	2	1.87E-06	0.95	5.01	-	1115.8
AHQ-10-2, 4412	R.LTEMETLQSQLM*AEK.L	1769.03151	2	5.24E-07	0.95	4.89	-	1094.0
AHQ-10-2, 4366 - 4422	R.LTEMETLQSQLM*AEK.L	1769.03151	2	7.79E-08	0.97	5.10	-	1564.7
AHQ-10-2, 4862 - 4896	R.LTEMETLQSQLMAEK.L	1753.03211	2	2.11E-04	0.79	2.91	-	824.4
AHQ-10-3, 3890	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	3.66E-05	0.95	3.81	-	2011.0
AHQ-10-3, 3459 - 3522	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	1.21E-04	0.94	4.09	-	1323.9

AHQ-10-2, 3962	R.LTEM*ETLQSQLMAEK.L	1769.03151	2	6.67E-05	0.96	4.21	-	2052.1
AHQ-10-2, 3591	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	2.58E-05	0.95	4.34	-	1202.0
AHQ-10-2, 3468 - 3534	R.LTEM*ETLQSQLM*AEK.L	1785.03091	2	3.95E-06	0.94	3.99	-	1105.9
AHQ-10-2, 3548 - 3607	K.M*EDSVGCLETAEEVK.R	1714.85099	2	4.41E-06	0.96	4.46	-	1430.3
AHQ-10-2, 3574	K.MEDSVGCLETAEEVKR.K	1855.03794	3	2.15E-07	0.66	3.46	-	361.1
AHQ-10-5, 3232	K.M*EDSVGCLETAEEVKR.K	1871.03734	3	5.60E-06	0.86	3.61	-	792.3
AHQ-10-5, 3201 - 3247	K.MEDSVGCLETAEEVKR.K	1855.03794	3	1.14E-04	0.74	3.28	-	821.7
AHQ-10-3, 3246	K.M*EDSVGCLETAEEVKR.K	1871.03734	3	6.07E-04	0.87	3.71	-	914.2
AHQ-10-3, 3242	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	3.62E-07	0.85	3.39	-	702.8
AHQ-10-2, 3310	K.M*EDSVGCLETAEEVKR.K	1871.03734	2	4.26E-08	0.82	3.28	-	534.6
AHQ-10-2, 4930 - 5002	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	4.08E-06	0.88	4.04	-	1037.7
AHQ-10-4, 4995	K.M*QQNIQELEEQLEEEESAR.Q	2350.46003	3	3.45E-07	0.93	4.10	-	1534.7
AHQ-10-1, 5146 - 5149	K.NFINNPLAQADWAAK.K	1673.85315	2	8.93E-06	0.93	4.32	-	971.2
AHQ-10-2, 5074 - 5139	K.NFINNPLAQADWAAK.K	1673.85315	2	1.69E-07	0.95	4.90	-	974.0
AHQ-10-7, 4921	K.NFINNPLAQADWAAK.K	1673.85315	2	2.29E-04	0.95	4.55	-	1062.4
AHQ-10-3, 5001 - 5002	K.NFINNPLAQADWAAK.K	1673.85315	2	1.24E-04	0.96	5.26	-	1053.0
AHQ-10-13-, 5329	K.NFINNPLAQADWAAK.K	1673.85315	2	8.62E-06	0.88	3.74	-	734.8
AHQ-10-2, 5466	K.NFINNPLAQADWAAK.K	1673.85315	2	3.87E-12	0.94	4.32	-	871.6
AHQ-10-14-, 4965	K.NFINNPLAQADWAAK.K	1673.85315	2	9.79E-07	0.91	4.31	-	815.3
AHQ-10-5, 5449	K.NFINNPLAQADWAAK.K	1673.85315	2	6.81E-08	0.92	3.70	-	981.4
AHQ-10-6, 4935	K.NFINNPLAQADWAAK.K	1673.85315	2	9.89E-09	0.91	3.82	-	974.5
AHQ-10-5, 5028	K.NFINNPLAQADWAAK.K	1673.85315	2	1.04E-10	0.96	5.14	-	1243.6
AHQ-10-13, 5225 - 5279	K.NFINNPLAQADWAAK.K	1673.85315	2	3.34E-04	0.92	4.04	-	978.4
AHQ-10-3, 2783	K.NKHEAMITDLEER.L	1586.75247	3	7.00E-05	0.90	3.86	-	1107.6
AHQ-10-3, 2775	K.NKHEAMITDLEER.L	1586.75247	2	2.32E-08	0.92	3.08	-	1208.3
AHQ-10-1, 5003	K.NLPIYSEEIVEM*YK.G	1744.98660	2	2.25E-06	0.95	3.95	-	1160.0
AHQ-10-9, 4595	K.NLPIYSEEIVEM*YK.G	1744.98660	2	3.86E-04	0.61	2.63	-	421.7
AHQ-10-4, 4919	K.NLPIYSEEIVEM*YK.G	1744.98660	2	4.39E-04	0.88	3.42	-	598.1
AHQ-10-5, 5392 - 5407	K.NLPIYSEEIVEMYK.G	1728.98720	2	1.42E-04	0.88	3.42	-	573.1
AHQ-10-7, 5308	K.NLPIYSEEIVEMYK.G	1728.98720	2	4.67E-04	0.91	3.52	-	717.2
AHQ-10-5, 4888	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.65E-07	0.95	4.87	-	821.7
AHQ-10-3, 5345	K.NLPIYSEEIVEMYK.G	1728.98720	2	4.56E-04	0.56	2.62	-	342.3
AHQ-10-2, 4940 - 4942	K.NLPIYSEEIVEM*YK.G	1744.98660	2	1.90E-04	0.97	4.89	-	1295.2
AHQ-10-3, 4857 - 4858	K.NLPIYSEEIVEM*YK.G	1744.98660	2	4.53E-08	0.95	4.23	-	1346.0
AHQ-10-2, 5427 - 5430	K.NLPIYSEEIVEMYK.G	1728.98720	2	9.92E-09	0.89	3.79	-	653.7
AHQ-10-4, 5427 - 5428	K.NLPIYSEEIVEMYK.G	1728.98720	2	2.13E-05	0.93	3.99	-	844.5
AHQ-10-2, 5247	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	2.20E-05	0.64	3.07	-	639.0
AHQ-10-2, 4880	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	2	1.91E-06	0.92	3.61	-	1124.6
AHQ-10-2, 4876 - 4883	K.NM*DPLNDNIATLLHQSSDK.F	2143.32109	3	5.07E-07	0.83	3.46	-	934.4
AHQ-10-2, 3287	R.QAQQERDELADEIANSSGK.G	2090.15168	3	4.37E-05	0.89	4.21	-	738.6
AHQ-10-2, 3355	R.QAQQERDELADEIANSSGK.G	2090.15168	2	8.12E-05	0.59	3.16	-	360.8
AHQ-10-3, 2883	R.QAQQERDELADEIANSSGK.G	2090.15168	2	2.03E-04	0.76	3.57	-	341.5
AHQ-10-2, 2931	R.QAQQERDELADEIANSSGK.G	2090.15168	3	4.95E-04	0.89	4.19	-	1031.5
AHQ-10-2, 2930	R.QAQQERDELADEIANSSGK.G	2090.15168	2	1.65E-04	0.76	3.37	-	472.5
AHQ-10-2, 2454	K.QIATLHAQVADM*K.K	1442.66637	2	5.62E-04	0.79	3.25	-	481.4
AHQ-10-2, 2152	R.QLEEAEEEAQR.A	1332.35590	2	6.93E-06	0.75	3.10	-	591.5
AHQ-10-2, 3020 - 3064	K.QTLENERGELANEVK.V	1730.85818	2	8.14E-04	0.71	3.41	-	421.9
AHQ-10-6, 3560	R.RGDLPFVVPR.R	1156.36217	2	3.40E-05	0.90	3.26	-	996.8
AHQ-10-8, 3501	R.RGDLPFVVPR.R	1156.36217	2	2.11E-05	0.91	3.23	-	1222.9
AHQ-10-11, 3534	R.RGDLPFVVPR.R	1156.36217	2	1.24E-04	0.90	3.58	-	1073.8
AHQ-10-4, 3619	R.RGDLPFVVPR.R	1156.36217	2	1.97E-04	0.92	3.68	-	1135.8
AHQ-10-12, 3618	R.RGDLPFVVPR.R	1156.36217	2	1.00E-04	0.89	3.40	-	839.1
AHQ-10-3, 3617 - 3633	R.RGDLPFVVPR.R	1156.36217	2	1.96E-06	0.95	3.92	-	1160.9
AHQ-10-13-, 3621 - 3700	R.RGDLPFVVPR.R	1156.36217	2	4.09E-05	0.89	3.23	-	912.2
AHQ-10-13, 4019	R.RGDLPFVVPR.R	1156.36217	2	2.89E-05	0.70	2.62	-	610.2
AHQ-10-1, 3807	R.RGDLPFVVPR.R	1156.36217	2	7.05E-07	0.95	3.87	-	1306.1
AHQ-10-5, 3603 - 3613	R.RGDLPFVVPR.R	1156.36217	2	1.04E-04	0.93	3.41	-	1264.3
AHQ-10-3, 6161	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	3.34E-06	0.96	5.75	-	1538.3
AHQ-10-2, 6230 - 6302	R.RKLEGDSTDLSDQIAELQAQIAELK.M	2773.04667	3	4.59E-08	0.94	5.55	-	945.7
AHQ-10-13-, 5696	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	1.81E-08	0.88	3.76	-	1035.4
AHQ-10-2, 5704 - 5764	K.SGFEPASLKEEVGEEAIVELVENGKK.V	2790.07246	3	2.80E-09	0.95	5.28	-	1180.8
AHQ-10-4, 4552	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.08E-10	0.98	6.28	-	1776.0
AHQ-10-2, 5392 - 5450	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	7.11E-07	0.96	5.69	-	1695.2
AHQ-10-1, 5467	K.SM*EAEMIQLQEELAAAER.A	2066.30004	2	1.13E-04	0.83	3.88	-	1123.8
AHQ-10-5, 4503	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	8.65E-08	0.96	5.22	-	1672.1
AHQ-10-2, 4563 - 4642	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	3.52E-09	0.98	5.73	-	1845.3
AHQ-10-6, 4425	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	1.24E-05	0.91	4.17	-	951.8
AHQ-10-1, 4623	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	2.67E-08	0.95	5.06	-	1271.5
AHQ-10-3, 4491	K.SM*EAEM*IQLQEELAAAER.A	2082.29944	2	4.93E-07	0.92	4.47	-	1028.2
AHQ-10-4, 3679 - 3680	K.TDLLLEPYNK.Y	1206.36989	2	3.76E-05	0.93	4.09	-	1197.7
AHQ-10-7, 3586	K.TDLLLEPYNK.Y	1206.36989	2	1.54E-04	0.76	3.29	-	779.9
AHQ-10-1, 3830	K.TDLLLEPYNK.Y	1206.36989	2	2.08E-05	0.85	3.38	-	922.5
AHQ-10-5, 3655	K.TDLLLEPYNK.Y	1206.36989	2	4.13E-05	0.95	4.21	-	1282.4
AHQ-10-2, 3734	K.TDLLLEPYNK.Y	1206.36989	2	2.55E-05	0.94	4.15	-	1336.1
AHQ-10-3, 3663 - 3670	K.TDLLLEPYNK.Y	1206.36989	2	4.13E-05	0.91	4.23	-	934.2
AHQ-10-2, 3884	K.TDLLLEPYNKYR.F	1525.73037	2	4.31E-06	0.83	3.39	-	579.9
AHQ-10-4, 4157	K.TELEDTLDSTAAQQELR.S	1921.00969	2	4.84E-08	0.97	4.49	-	1955.3
AHQ-10-6, 4063	K.TELEDTLDSTAAQQELR.S	1921.00969	2	5.54E-05	0.83	3.08	-	1305.9
AHQ-10-5, 4144 - 4216	K.TELEDTLDSTAAQQELR.S	1921.00969	2	5.76E-06	0.75	3.41	-	734.9
AHQ-10-2, 4194	K.TELEDTLDSTAAQQELR.S	1921.00969	2	4.40E-08	0.97	5.03	-	1842.7
AHQ-10-3, 4117	K.TELEDTLDSTAAQQELR.S	1921.00969	2	4.23E-09	0.95	4.63	-	1373.4
AHQ-10-1, 4259	K.TELEDTLDSTAAQQELR.S	1921.00969	2	4.44E-05	0.95	3.78	-	1950.1
AHQ-10-2, 6119 - 6174	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	7.45E-06	0.96	5.09	-	1404.2
AHQ-10-2, 6258 - 6328	R.TFHIFYYLLSGAGEHLK.T	1997.28378	3	2.72E-05	0.96	4.57	-	1911.3
AHQ-10-6, 4944 - 5004	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	2.86E-07	0.86	4.36	-	628.7
AHQ-10-2, 5584	K.VEDMAELTCLNEASVLHNLK.E	2288.58457	2	9.29E-09	0.88	4.23	-	527.7
AHQ-10-13, 5188 - 5255	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	1.31E-04	0.89	3.87	-	1039.6
AHQ-10-5, 5027 - 5091	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	3.52E-06	0.89	4.59	-	585.2
AHQ-10-2, 5075	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	2	3.12E-07	0.82	3.85	-	477.2
AHQ-10-2, 5027 - 5104	K.VEDM*AELTCLNEASVLHNLK.E	2304.58397	3	3.18E-07	0.91	4.41	-	964.0
AHQ-10-2, 2162	R.VEEEEERCQHLQAEK.K	1916.01642	2	4.06E-05	0.94	4.08	-	1264.5
AHQ-10-3, 2135	R.VEEEEERCQHLQAEK.K	1916.01642	3	7.43E-05	0.84	3.93	-	640.6
AHQ-10-5, 3935	K.VIQYLAYVASSHK.S	1479.70484	2	4.15E-06	0.91	3.40	-	1017.9
AHQ-10-1, 4098	K.VIQYLAYVASSHK.S	1479.70484	2	1.71E-04	0.90	3.41	-	1121.6
AHQ-10-5, 3932	K.VIQYLAYVASSHK.S	1479.70484	3	2.36E-06	0.81	3.32	-	718.4
AHQ-10-10, 3795	K.VIQYLAYVASSHK.S	1479.70484	2	2.55E-06	0.82	2.69	-	702.7
AHQ-10-2, 3998	K.VIQYLAYVASSHK.S	1479.70484	2	4.42E-06	0.95	3.93	-	1322.7
AHQ-10-2, 4003	K.VIQYLAYVASSHK.S	1479.70484	3	1.40E-05	0.85	3.95	-	619.8
AHQ-10-4, 3957	K.VIQYLAYVASSHK.S	1479.70484	3	3.52E-05	0.66	3.18	-	526.7
AHQ-10-8, 5949 - 5950	R.VISGVLQLGNIVFK.K	1487.81155	2	1.11E-07	0.97	5.28	-	1490.7
AHQ-10-3, 5917 - 5921	R.VISGVLQLGNIVFK.K	1487.81155	2	4.68E-05	0.92	3.41	-	1228.3
AHQ-10-4, 6005 - 6007	R.VISGVLQLGNIVFK.K	1487.81155	2	3.16E-04	0.73	2.82	-	837.4
AHQ-10-2, 6020	R.VISGVLQLGNIVFK.K	1487.81155	3	1.92E-06	0.97	4.77	-	2597.2
AHQ-10-1, 6033	R.VISGVLQLGNIVFK.K	1487.81155	2	6.26E-07	0.95	3.82	-	1462.3
AHQ-10-7, 5900 - 5901	R.VISGVLQLGNIVFK.K	1487.81155	2	2.33E-08	0.98	5.87	-	1706.5
AHQ-10-2, 6030	R.VISGVLQLGNIVFK.K	1487.81155	2	5.76E-08	0.96	4.38	-	1454.3
AHQ-10-6, 5865	R.VISGVLQLGNIVFK.K	1487.81155	2	1.40E-06	0.91	3.30	-	1146.8

AHQ-10-2, 5920 - 6000	R.VISGVLQLGNIVFK.K	1487.81155	2	6.98E-05	0.96	4.42	-	1547.2
AHQ-10-2, 5538 - 5542	R.VISGVLQLGNIVFKK.E	1615.98446	2	8.52E-08	0.94	4.35	-	1061.2
AHQ-10-3, 5383 - 5458	R.VISGVLQLGNIVFKK.E	1615.98446	2	1.20E-04	0.84	3.37	-	717.5
AHQ-10-5, 5513	R.VISGVLQLGNIVFKK.E	1615.98446	2	1.21E-04	0.92	4.15	-	905.4
AHQ-10-2, 2552	K.VKPLLQVSR.Q	1040.28462	1	3.70E-04	0.31	2.44	-	291.3
AHQ-10-1, 4841 - 4885	K.VSHLLGINVTDFTR.G	1572.79026	2	1.24E-08	0.89	3.31	-	1043.5
AHQ-10-4, 4741 - 4777	K.VSHLLGINVTDFTR.G	1572.79026	2	4.22E-06	0.93	3.39	-	1433.1
AHQ-10-5, 4725 - 4753	K.VSHLLGINVTDFTR.G	1572.79026	2	9.01E-11	0.96	4.45	-	1604.0
AHQ-10-7, 4638	K.VSHLLGINVTDFTR.G	1572.79026	2	2.24E-08	0.88	3.56	-	1028.1
AHQ-10-3, 4685 - 4734	K.VSHLLGINVTDFTR.G	1572.79026	2	3.25E-07	0.93	3.73	-	1241.7
AHQ-10-3, 4735	K.VSHLLGINVTDFTR.G	1572.79026	3	9.72E-06	0.95	4.44	-	1648.5
AHQ-10-6, 4657	K.VSHLLGINVTDFTR.G	1572.79026	3	1.84E-07	0.91	4.17	-	1056.6
AHQ-10-5, 3227 - 3228	R.VVFQEFR.Q	925.06580	2	9.46E-05	0.75	2.74	-	474.5
AHQ-10-5, 3880 - 3953	R.YEILTPNSIPK.G	1275.47536	2	8.07E-06	0.93	3.73	-	1183.7
AHQ-10-5, 4076	R.YEILTPNSIPK.G	1275.47536	2	5.38E-05	0.95	3.22	-	1694.1
AHQ-10-3, 3866 - 3937	R.YEILTPNSIPK.G	1275.47536	2	1.90E-04	0.87	3.54	-	804.9
AHQ-10-3, 4062	R.YEILTPNSIPK.G	1275.47536	2	6.36E-05	0.75	2.94	-	784.7
AHQ-10-2, 3938 - 4011	R.YEILTPNSIPK.G	1275.47536	2	1.88E-06	0.83	3.07	-	970.3
AHQ-10-4, 4087	R.YEILTPNSIPK.G	1275.47536	2	9.00E-05	0.72	2.71	-	728.4
AHQ-10-4, 3887 - 3961	R.YEILTPNSIPK.G	1275.47536	2	5.02E-07	0.92	3.51	-	1047.0
gi|4557705|ref|NP_000217.1| keratin 9 [Homo sapiens]				1.11E-14	10.44	120.35	36.80	61986.9
AHQ-10-14-, 5893	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.41E-05	0.87	4.07	-	898.2
AHQ-10-14-, 5452	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.36E-09	0.91	4.25	-	1142.8
AHQ-10-4, 5919 - 5928	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	7.96E-10	0.98	7.07	-	2043.3
AHQ-10-3, 5758 - 5825	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	2.16E-05	0.97	5.91	-	1521.9
AHQ-10-5, 5571	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.11E-07	0.84	3.76	-	811.5
AHQ-10-5, 6004	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.60E-06	0.87	4.28	-	723.4
AHQ-10-6, 5779 - 5781	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	3.62E-06	0.97	5.47	-	1655.3
AHQ-10-1, 5619	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.85E-07	0.85	3.83	-	703.6
AHQ-10-1, 5941	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.56E-06	0.98	5.96	-	2195.9
AHQ-10-7, 5816	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.74E-10	0.97	5.43	-	1660.6
AHQ-10-11, 5690	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	8.42E-04	0.89	3.84	-	1088.9
AHQ-10-13-, 5458	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	9.49E-04	0.73	3.29	-	638.2
AHQ-10-2, 5915 - 5918	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	1.11E-14	0.97	5.87	-	1615.8
AHQ-10-13, 6003 - 6007	K.DIENQYETQITQIEHEVSSSGQEVQSSAK.E	3266.38667	3	4.43E-04	0.94	5.10	-	1175.3
AHQ-10-2, 4423 - 4484	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	2.83E-05	0.95	4.88	-	1744.9
AHQ-10-1, 4554	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	1.85E-04	0.76	3.02	-	590.7
AHQ-10-3, 4406	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	5.38E-07	0.96	5.29	-	1658.6
AHQ-10-14-, 4358	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	2	1.13E-06	0.92	4.57	-	791.0
AHQ-10-7, 4310	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	5.91E-04	0.79	3.70	-	899.7
AHQ-10-5, 4404 - 4405	K.EIETYHNLLEGGQEDFESSGAGK.I	2511.59648	3	7.38E-06	0.94	5.25	-	1486.7
AHQ-10-14-, 4770	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	7.98E-11	0.93	4.50	-	947.9
AHQ-10-5, 4869 - 4871	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	2.89E-07	0.90	4.57	-	734.7
AHQ-10-1, 4954	R.GGGGSFGYSYGGGSGGGFSASSLGGGFGGGSR.G	2706.73770	2	1.29E-04	0.71	2.80	-	569.9
AHQ-10-13-, 2560	R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	3225.08711	3	1.75E-04	0.83	4.42	-	841.6
AHQ-10-14-, 2538	R.GGSGGSHGGGSGFGGESGGSYGGGEEASGSGGGYGGGSGK.S	3225.08711	3	5.92E-07	0.88	4.13	-	876.0
AHQ-10-5, 4992	R.HGVQELEIELQSQLSK.K	1839.03978	3	1.35E-04	0.81	3.63	-	1121.7
AHQ-10-1, 5122 - 5174	R.HGVQELEIELQSQLSK.K	1839.03978	2	1.05E-04	0.91	4.03	-	1032.6
AHQ-10-3, 4982	R.HGVQELEIELQSQLSK.K	1839.03978	3	3.10E-06	0.88	4.59	-	1016.6
AHQ-10-1, 5117	R.HGVQELEIELQSQLSK.K	1839.03978	3	9.37E-06	0.92	4.61	-	1158.8
AHQ-10-7, 4892	R.HGVQELEIELQSQLSK.K	1839.03978	3	2.56E-04	0.88	4.56	-	958.1
AHQ-10-14-, 4824	R.LASYLDKVQALEEANNDLENK.I	2378.57787	3	6.19E-08	0.96	5.16	-	1771.6
AHQ-10-3, 4874	R.LASYLDKVQALEEANNDLENK.I	2378.57787	3	1.99E-05	0.93	4.61	-	1490.6
AHQ-10-7, 6305	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	2	3.05E-08	0.82	3.64	-	419.3
AHQ-10-1, 6355 - 6393	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	4.68E-10	0.83	3.96	-	498.7
AHQ-10-7, 6304	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	1.10E-08	0.90	4.51	-	505.2
AHQ-10-2, 6395	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	2.41E-09	0.85	4.13	-	375.2
AHQ-10-6, 6252 - 6303	K.NYSPYYNTIDDLKDQIVDLTVGNNK.T	2904.13412	3	9.36E-09	0.87	4.32	-	530.9
AHQ-10-2, 6263 - 6318	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	9.52E-07	0.82	3.88	-	818.2
AHQ-10-4, 6264 - 6291	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	9.16E-05	0.65	3.14	-	687.3
AHQ-10-7, 6193	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	3.20E-07	0.95	4.49	-	1322.3
AHQ-10-13-, 6137	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	6.14E-06	0.68	2.79	-	843.0
AHQ-10-5, 6204 - 6261	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	2.07E-04	0.61	3.01	-	584.4
AHQ-10-3, 6165 - 6234	K.SDLEM*QYETLQEELM*ALK.K	2204.46135	2	4.03E-06	0.95	4.53	-	1425.6
AHQ-10-5, 5995	K.SDLEM*QYETLQEELMALKK.N	2316.63487	3	1.78E-04	0.75	3.19	-	667.1
AHQ-10-1, 3389	K.TLLDIDNTR.M	1061.17119	2	7.69E-05	0.73	3.00	-	534.5
AHQ-10-3, 3205	K.TLLDIDNTR.M	1061.17119	2	1.29E-04	0.67	2.58	-	596.8
AHQ-10-2, 3267	K.TLLDIDNTR.M	1061.17119	2	2.42E-06	0.74	2.95	-	610.9
AHQ-10-5, 3187	K.TLLDIDNTR.M	1061.17119	2	4.40E-05	0.83	3.09	-	728.2
AHQ-10-6, 3151 - 3176	K.TLLDIDNTR.M	1061.17119	2	3.23E-04	0.65	2.75	-	582.6
AHQ-10-14-, 3197	K.TLLDIDNTR.M	1061.17119	2	1.22E-05	0.80	2.76	-	661.2
AHQ-10-14-, 4682	K.TLNDMRQEYEQLIAK.N	1853.08996	2	6.95E-04	0.62	3.09	-	549.1
AHQ-10-8, 3001	K.VQALEEANNDLENK.I	1587.67060	2	1.04E-04	0.95	3.47	-	1758.6
AHQ-10-3, 3061	K.VQALEEANNDLENK.I	1587.67060	2	2.43E-06	0.98	5.37	-	1776.7
AHQ-10-2, 3332	K.VQALEEANNDLENK.I	1587.67060	2	6.43E-05	0.72	3.05	-	695.4
AHQ-10-7, 2985	K.VQALEEANNDLENK.I	1587.67060	2	2.82E-05	0.97	5.05	-	1829.8
AHQ-10-13-, 3065	K.VQALEEANNDLENK.I	1587.67060	2	4.15E-05	0.96	4.24	-	1532.7
AHQ-10-2, 3120	K.VQALEEANNDLENK.I	1587.67060	2	8.33E-09	0.97	5.44	-	1724.0
AHQ-10-7, 2617 - 2677	K.VQALEEANNDLENK.I	1587.67060	2	3.08E-08	0.93	4.15	-	1248.1
AHQ-10-2, 3114	K.VQALEEANNDLENK.I	1587.67060	3	5.83E-04	0.86	3.04	-	1378.4
AHQ-10-3, 3067	K.VQALEEANNDLENK.I	1587.67060	3	8.03E-07	0.90	4.07	-	1145.4
AHQ-10-6, 3009	K.VQALEEANNDLENK.I	1587.67060	2	3.76E-08	0.95	4.35	-	1293.6
AHQ-10-3, 2673	K.VQALEEANNDLENK.I	1587.67060	2	1.41E-09	0.93	4.26	-	1311.0
AHQ-10-6, 2629	K.VQALEEANNDLENK.I	1587.67060	2	7.42E-11	0.90	3.84	-	911.6
AHQ-10-5, 3033 - 3036	K.VQALEEANNDLENK.I	1587.67060	2	4.77E-11	0.98	5.75	-	2205.0
AHQ-10-1, 3367 - 3442	K.VQALEEANNDLENK.I	1587.67060	2	4.24E-04	0.81	2.99	-	896.8
AHQ-10-1, 3242	K.VQALEEANNDLENK.I	1587.67060	2	4.32E-08	0.97	4.61	-	1801.3
gi|4505257|ref|NP_002435.1| moesin [Homo sapiens]				1.11E-14	8.61	100.30	23.70	67819.5
AHQ-10-6, 4017	R.EDAVLEYLK.I	1080.21287	1	2.80E-04	0.17	1.94	-	331.3
AHQ-10-6, 6289	K.EGILNDDIYCPPETAVLLASYAVQSK.Y	2869.19288	3	2.03E-07	0.93	5.21	-	844.0
AHQ-10-6, 5568 - 5623	R.EVWFFGLQYQDTK.G	1661.83760	2	1.34E-05	0.97	4.43	-	1544.0
AHQ-10-6, 6255	K.FYPEDVSEELIQDITQR.L	2083.24065	3	6.89E-07	0.95	4.65	-	1642.9
AHQ-10-6, 6259	K.FYPEDVSEELIQDITQR.L	2083.24065	2	2.03E-11	0.96	5.18	-	1192.9
AHQ-10-6, 5116 - 5183	K.IAQDLEM*YGVNYFSIK.N	1908.16395	2	9.79E-06	0.95	4.54	-	1149.3
AHQ-10-6, 2115 - 2184	R.IQVWHEEHR.G	1234.34835	2	9.12E-04	0.90	2.88	-	1286.3
AHQ-10-6, 4551 - 4561	K.KTQEQLALEMAELTAR.I	1833.10018	2	1.28E-04	0.82	3.56	-	589.6
AHQ-10-6, 4547 - 4553	K.KTQEQLALEMAELTAR.I	1833.10018	3	8.58E-04	0.90	4.11	-	1530.1
AHQ-10-6, 3468 - 3481	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	1.14E-06	0.95	5.34	-	1033.6
AHQ-10-6, 3352 - 3411	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A	3314.36856	3	1.11E-14	0.97	5.55	-	1922.9
AHQ-10-6, 3183	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	4.89E-09	0.93	5.11	-	1106.9
AHQ-10-6, 3051 - 3111	K.TAM*STPHVAEPAENEQDEQDENGAEASADLR.A	3330.36796	3	3.94E-14	0.97	6.09	-	1936.6
AHQ-10-6, 5045	K.TQEQLALEMAELTAR.I	1704.92727	3	1.34E-06	0.96	5.10	-	2053.9
AHQ-10-6, 5035	K.TQEQLALEMAELTAR.I	1704.92727	2	1.03E-04	0.96	4.20	-	1697.7
gi|8393159|ref|NP_059118.1| calmodulin-like skin protein [Homo sapiens]				2.89E-14	0.97	10.30	15.80	15920.4
AHQ-10-3, 4946	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	4.91E-07	0.49	2.94	-	422.0
AHQ-10-14, 5463 - 5524	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	2.15E-08	0.97	5.45	-	1539.1
AHQ-10-14-, 4848 - 4904	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	2.89E-14	0.97	6.00	-	1316.0

AHQ-10-14-, 4964	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	3.40E-06	0.95	5.23	-	830.2
AHQ-10-1, 5077	K.AFSAVDTDGNGTINAQELGAALK.A	2264.43486	2	2.27E-05	0.86	3.69	-	647.0
gi|4507485|ref|NP_003237.1| thrombospondin 1 [Homo sapiens]				6.88E-14	28.96	340.32	33.40	129351.8
AHQ-10-2, 4060	K.AGTLDLSLTVQGK.Q	1303.48711	2	1.21E-04	0.94	4.22	-	1395.3
AHQ-10-6, 3905 - 3965	K.AGTLDLSLTVQGK.Q	1303.48711	2	4.14E-05	0.95	4.16	-	1512.6
AHQ-10-2, 3952 - 3999	K.AGTLDLSLTVQGK.Q	1303.48711	2	2.97E-04	0.80	3.14	-	691.7
AHQ-10-6, 2689 - 2767	R.AQLYIDCEK.M	1141.27636	2	1.16E-04	0.87	2.95	-	770.6
AHQ-10-5, 2793	R.AQLYIDCEK.M	1141.27636	2	2.69E-04	0.78	2.66	-	702.3
AHQ-10-6, 2765	R.AQLYIDCEK.M	1141.27636	2	3.40E-04	0.80	3.00	-	611.1
AHQ-10-3, 2817	R.AQLYIDCEK.M	1141.27636	2	5.07E-04	0.72	2.54	-	546.1
AHQ-10-2, 5626 - 5682	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	4.22E-07	0.96	6.01	-	929.0
AHQ-10-4, 5604 - 5680	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	7.30E-05	0.91	5.04	-	666.8
AHQ-10-6, 5467 - 5528	R.AQLYIDCEKM*ENAELDVPIQSVFTR.D	2988.33923	3	1.07E-07	0.96	6.49	-	1042.7
AHQ-10-2, 3807 - 3810	R.CENTDPGYNCLPCPPR.F	1954.10800	2	1.33E-08	0.92	3.93	-	700.1
AHQ-10-3, 3675 - 3737	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.36E-05	0.81	3.33	-	574.9
AHQ-10-4, 3644	R.CENTDPGYNCLPCPPR.F	1954.10800	2	3.50E-09	0.94	4.25	-	694.5
AHQ-10-2, 3698 - 3704	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.31E-11	0.92	4.65	-	615.6
AHQ-10-3, 3610 - 3682	R.CENTDPGYNCLPCPPR.F	1954.10800	2	2.91E-06	0.91	3.88	-	560.9
AHQ-10-5, 3749	R.CENTDPGYNCLPCPPR.F	1954.10800	2	9.28E-05	0.70	2.93	-	412.2
AHQ-10-3, 3787	K.CNYLGHYSDPMYR.C	1677.84222	2	3.61E-04	0.79	3.37	-	509.2
AHQ-10-4, 3820	K.CNYLGHYSDPMYR.C	1677.84222	2	4.17E-05	0.83	2.79	-	711.1
AHQ-10-2, 3863	K.CNYLGHYSDPMYR.C	1677.84222	2	5.89E-06	0.80	2.80	-	587.4
AHQ-10-3, 3217	K.DCVGDVTENQICNK.Q	1654.75869	2	5.03E-07	0.74	2.56	-	646.0
AHQ-10-2, 3283 - 3284	K.DCVGDVTENQICNK.Q	1654.75869	2	5.96E-07	0.97	4.86	-	1314.1
AHQ-10-4, 3241	K.DCVGDVTENQICNK.Q	1654.75869	2	4.06E-06	0.91	3.78	-	793.6
AHQ-10-5, 3213	K.DCVGDVTENQICNK.Q	1654.75869	2	5.98E-04	0.75	3.00	-	707.4
AHQ-10-2, 3060 - 3082	K.DHSGQVFSVVSNGK.A	1461.56164	2	9.54E-05	0.72	3.08	-	488.2
AHQ-10-3, 2834	K.DHSGQVFSVVSNGK.A	1461.56164	2	2.12E-05	0.90	3.71	-	956.2
AHQ-10-4, 2865	K.DHSGQVFSVVSNGK.A	1461.56164	2	3.82E-07	0.85	3.17	-	757.2
AHQ-10-3, 3154 - 3155	R.DNCQYVYNVDQR.D	1575.64166	2	5.45E-07	0.90	3.96	-	957.8
AHQ-10-4, 3133 - 3176	R.DNCQYVYNVDQR.D	1575.64166	2	3.34E-05	0.88	3.05	-	1292.9
AHQ-10-3, 3035	R.DNCQYVYNVDQR.D	1575.64166	2	8.79E-04	0.85	3.10	-	869.5
AHQ-10-6, 2995	R.DNCQYVYNVDQR.D	1575.64166	2	1.04E-04	0.84	3.31	-	780.8
AHQ-10-2, 3214	R.DNCQYVYNVDQR.D	1575.64166	2	3.35E-05	0.93	3.87	-	1078.5
AHQ-10-7, 2988	R.DNCQYVYNVDQR.D	1575.64166	2	1.40E-05	0.87	2.95	-	1262.3
AHQ-10-7, 3112	R.DNCQYVYNVDQR.D	1575.64166	2	4.54E-04	0.74	2.92	-	772.7
AHQ-10-2, 3091	R.DNCQYVYNVDQR.D	1575.64166	2	3.25E-06	0.91	3.91	-	956.2
AHQ-10-5, 3028	R.DNCQYVYNVDQR.D	1575.64166	2	5.30E-05	0.77	3.34	-	811.9
AHQ-10-5, 3153	R.DNCQYVYNVDQR.D	1575.64166	2	6.70E-05	0.78	3.25	-	772.2
AHQ-10-4, 3047	R.DNCQYVYNVDQR.D	1575.64166	2	8.52E-07	0.93	3.50	-	1199.1
AHQ-10-6, 3112	R.DNCQYVYNVDQR.D	1575.64166	2	9.08E-04	0.86	3.15	-	886.4
AHQ-10-5, 3624	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	2.55E-08	0.84	3.59	-	980.1
AHQ-10-3, 3487 - 3567	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	6.70E-08	0.90	4.66	-	644.5
AHQ-10-3, 3570 - 3630	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	6.88E-14	0.93	5.08	-	741.5
AHQ-10-3, 3929 - 3946	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	5.65E-07	0.91	4.72	-	655.7
AHQ-10-2, 3795	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	7.63E-08	0.76	3.68	-	436.8
AHQ-10-6, 3540 - 3599	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	5.87E-11	0.90	4.52	-	752.0
AHQ-10-2, 3714	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	1.30E-10	0.93	4.72	-	990.8
AHQ-10-4, 3628 - 3668	R.DTDM*DGVGDQCDNCPLEHNPDQLDSDSDR.I	3340.31822	3	6.75E-10	0.93	5.09	-	702.3
AHQ-10-7, 3876	R.DTDMDGVGDQCDNCPLEHNPDQLDSDSDR.I	3324.31882	3	4.38E-09	0.88	4.41	-	466.5
AHQ-10-2, 3651	K.FQDLVDAVR.A	1063.18877	2	2.75E-06	0.91	3.25	-	1115.8
AHQ-10-2, 4218 - 4223	R.FQMIPLDPK.G	1089.33277	2	4.98E-04	0.90	3.53	-	913.6
AHQ-10-6, 2912	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.81E-06	0.84	3.64	-	575.3
AHQ-10-3, 3063	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.22E-05	0.82	3.49	-	493.5
AHQ-10-5, 2908 - 2943	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	3.48E-06	0.76	3.46	-	694.9
AHQ-10-5, 2959	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	2.37E-06	0.94	4.88	-	610.3
AHQ-10-3, 2957 - 2959	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	2.08E-06	0.74	3.37	-	565.3
AHQ-10-2, 3006	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	1.33E-06	0.83	3.62	-	598.4
AHQ-10-7, 2888	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	3.61E-05	0.89	4.28	-	436.9
AHQ-10-4, 2877 - 2939	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	8.54E-07	0.68	3.36	-	375.6
AHQ-10-7, 2896	R.FTGSQPFGQGVEHATANK.Q	1877.00666	3	1.98E-07	0.79	3.47	-	530.7
AHQ-10-3, 2878 - 2953	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	4.17E-06	0.87	3.91	-	528.4
AHQ-10-8, 2841	R.FTGSQPFGQGVEHATANK.Q	1877.00666	2	5.69E-07	0.81	3.72	-	378.7
AHQ-10-5, 5221 - 5223	R.FVFGTTPEDILR.N	1395.58470	2	8.05E-04	0.83	3.12	-	664.3
AHQ-10-3, 5181	R.FVFGTTPEDILR.N	1395.58470	2	5.16E-04	0.77	2.83	-	594.4
AHQ-10-1, 5323	R.FVFGTTPEDILR.N	1395.58470	2	5.41E-04	0.73	2.52	-	544.1
AHQ-10-6, 5120 - 5124	R.FVFGTTPEDILR.N	1395.58470	2	4.88E-05	0.82	3.03	-	668.3
AHQ-10-6, 5243	K.GFLLLASLR.Q	990.22407	2	9.73E-05	0.97	3.64	-	2055.1
AHQ-10-3, 5313 - 5314	K.GFLLLASLR.Q	990.22407	2	4.13E-06	0.97	4.39	-	2090.5
AHQ-10-11, 5160	K.GFLLLASLR.Q	990.22407	2	5.03E-04	0.96	3.18	-	2134.1
AHQ-10-4, 5379	K.GFLLLASLR.Q	990.22407	2	1.56E-04	0.97	3.83	-	2000.5
AHQ-10-1, 5457	K.GFLLLASLR.Q	990.22407	2	4.30E-05	0.95	3.05	-	1985.9
AHQ-10-9, 5024 - 5032	K.GFLLLASLR.Q	990.22407	2	1.15E-04	0.97	3.46	-	2207.6
AHQ-10-2, 5390	K.GFLLLASLR.Q	990.22407	2	7.64E-05	0.97	3.92	-	2076.2
AHQ-10-7, 5245	K.GFLLLASLR.Q	990.22407	2	3.82E-04	0.94	3.36	-	1655.8
AHQ-10-10, 5119	K.GFLLLASLR.Q	990.22407	2	3.96E-06	0.94	3.44	-	1617.0
AHQ-10-5, 5348	K.GFLLLASLR.Q	990.22407	2	2.19E-04	0.97	3.91	-	2167.4
AHQ-10-5, 4568	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.14E-05	0.69	3.17	-	646.3
AHQ-10-2, 4224	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.81E-05	0.86	3.61	-	769.0
AHQ-10-2, 4370 - 4430	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.01E-10	0.94	4.37	-	1222.9
AHQ-10-6, 4223 - 4283	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.92E-06	0.91	4.42	-	795.5
AHQ-10-10, 4138 - 4194	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.20E-05	0.90	3.89	-	908.8
AHQ-10-5, 4297 - 4367	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.13E-05	0.91	4.30	-	933.7
AHQ-10-3, 4453 - 4457	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.72E-05	0.82	3.78	-	762.6
AHQ-10-8, 4247	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.99E-04	0.86	3.88	-	702.3
AHQ-10-7, 4200 - 4260	K.GGVNDNFQGVLQNVR.F	1617.74799	2	3.31E-04	0.93	4.24	-	1065.4
AHQ-10-3, 4297 - 4357	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.18E-08	0.92	4.25	-	964.7
AHQ-10-1, 4449 - 4507	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.88E-04	0.70	3.72	-	360.4
AHQ-10-9, 4047 - 4104	K.GGVNDNFQGVLQNVR.F	1617.74799	2	7.71E-06	0.93	4.37	-	1091.3
AHQ-10-5, 4459 - 4471	K.GGVNDNFQGVLQNVR.F	1617.74799	2	5.18E-05	0.87	4.08	-	752.8
AHQ-10-4, 4164 - 4241	K.GGVNDNFQGVLQNVR.F	1617.74799	2	2.53E-04	0.55	3.15	-	466.3
AHQ-10-4, 4320 - 4399	K.GGVNDNFQGVLQNVR.F	1617.74799	2	4.31E-06	0.93	4.58	-	957.6
AHQ-10-4, 4612	K.GGVNDNFQGVLQNVR.F	1617.74799	2	1.07E-05	0.88	3.69	-	813.1
AHQ-10-5, 2208	K.GPDPSSPAFR.I	1031.10364	2	2.36E-04	0.65	2.63	-	549.9
AHQ-10-6, 2217 - 2227	K.GPDPSSPAFR.I	1031.10364	2	7.37E-05	0.82	2.90	-	677.7
AHQ-10-3, 2267	K.GPDPSSPAFR.I	1031.10364	2	3.73E-04	0.73	2.77	-	550.3
AHQ-10-2, 2302	K.GPDPSSPAFR.I	1031.10364	2	4.69E-05	0.69	2.61	-	533.7
AHQ-10-3, 3183	R.GTLLALER.K	873.03234	2	8.01E-04	0.87	3.04	-	914.0
AHQ-10-6, 3119	R.GTLLALER.K	873.03234	2	1.69E-04	0.88	3.46	-	878.4
AHQ-10-9, 2984	R.GTLLALER.K	873.03234	2	8.47E-04	0.81	2.74	-	758.4
AHQ-10-10, 3091	R.GTLLALER.K	873.03234	2	4.51E-04	0.86	2.81	-	1035.7
AHQ-10-4, 3164 - 3168	R.GTLLALER.K	873.03234	2	3.62E-04	0.87	3.28	-	910.2
AHQ-10-4, 2871	K.GTSQNDPNWVVR.H	1373.45608	2	9.53E-04	0.28	2.59	-	467.5
AHQ-10-5, 5999 - 6061	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.61E-07	0.88	4.46	-	496.5
AHQ-10-14-, 5900 - 5964	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.75E-05	0.67	3.22	-	319.1
AHQ-10-3, 5926 - 5985	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	3.13E-05	0.87	4.32	-	504.4
AHQ-10-6, 5861 - 5915	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	4.49E-05	0.54	3.17	-	281.9

AHQ-10-7, 5921	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	2	5.12E-06	0.78	3.28	-	343.7
AHQ-10-13, 6107 - 6123	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	5.57E-05	0.84	4.34	-	318.4
AHQ-10-4, 5995 - 6032	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.17E-09	0.85	4.36	-	539.8
AHQ-10-1, 6049 - 6113	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	7.10E-06	0.57	3.10	-	294.9
AHQ-10-2, 6014 - 6078	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	2.07E-08	0.93	5.08	-	727.1
AHQ-10-6, 5971 - 5996	R.IEDANLIPPVPDDKFQDLVDAVR.A	2580.87450	3	1.45E-05	0.67	3.31	-	563.0
AHQ-10-7, 2660	K.IMADSGPIYDK.T	1210.38204	2	1.18E-06	0.87	3.09	-	740.2
AHQ-10-6, 2660	K.IMADSGPIYDK.T	1210.38204	2	1.37E-05	0.92	3.42	-	811.3
AHQ-10-11, 2670	K.IMADSGPIYDK.T	1210.38204	2	1.67E-05	0.81	3.19	-	573.7
AHQ-10-2, 2766	K.IMADSGPIYDK.T	1210.38204	2	3.92E-06	0.93	3.69	-	926.2
AHQ-10-2, 6330 - 6331	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.46E-11	0.97	5.66	-	1157.6
AHQ-10-11, 6099	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.18E-04	0.89	4.28	-	606.1
AHQ-10-7, 6233	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	2.43E-10	0.94	4.73	-	899.3
AHQ-10-13, 6359	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	3.05E-06	0.93	4.54	-	774.7
AHQ-10-3, 6229	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	7.66E-14	0.96	5.70	-	974.6
AHQ-10-13-, 6172 - 6178	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.73E-08	0.95	5.01	-	1103.1
AHQ-10-3, 6235 - 6239	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	3.95E-04	0.80	3.63	-	875.0
AHQ-10-5, 6273 - 6315	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.43E-09	0.97	6.01	-	1388.3
AHQ-10-5, 6320	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	4.92E-05	0.81	3.72	-	860.8
AHQ-10-4, 6308	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.91E-04	0.76	2.98	-	623.7
AHQ-10-14-, 6209 - 6212	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	1.45E-11	0.93	4.70	-	846.6
AHQ-10-6, 6183	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	2	8.64E-09	0.96	5.28	-	1079.8
AHQ-10-2, 6335	R.IPESGGDNSVFDIFELTGAAR.K	2196.35899	3	1.99E-06	0.82	4.05	-	601.1
AHQ-10-9, 2352	R.KDHSGQVFSVVSNGK.A	1589.73455	2	4.49E-05	0.68	2.72	-	699.9
AHQ-10-4, 2468	R.KDHSGQVFSVVSNGK.A	1589.73455	3	2.63E-05	0.88	3.88	-	1056.9
AHQ-10-2, 2595	R.KDHSGQVFSVVSNGK.A	1589.73455	2	7.27E-09	0.74	3.00	-	707.9
AHQ-10-2, 2554	R.KVTEENKELANELR.R	1673.84976	2	7.44E-07	0.93	4.65	-	1100.8
AHQ-10-6, 2447 - 2509	R.KVTEENKELANELR.R	1673.84976	2	5.47E-06	0.92	4.31	-	1218.9
AHQ-10-3, 2505	R.KVTEENKELANELR.R	1673.84976	2	6.91E-10	0.94	4.75	-	1176.5
AHQ-10-3, 2509	R.KVTEENKELANELR.R	1673.84976	3	1.27E-07	0.66	3.28	-	491.5
AHQ-10-8, 2422	R.KVTEENKELANELR.R	1673.84976	2	4.78E-06	0.85	3.69	-	1012.6
AHQ-10-4, 2472	R.KVTEENKELANELR.R	1673.84976	2	5.95E-08	0.92	4.07	-	1395.2
AHQ-10-2, 2550	R.KVTEENKELANELR.R	1673.84976	3	2.04E-05	0.67	3.48	-	567.2
AHQ-10-7, 2448	R.KVTEENKELANELR.R	1673.84976	2	1.20E-10	0.93	4.60	-	1071.3
AHQ-10-5, 2467	R.KVTEENKELANELR.R	1673.84976	2	6.49E-11	0.93	4.23	-	1312.3
AHQ-10-2, 2619	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	2	2.67E-04	0.76	3.63	-	451.0
AHQ-10-4, 2547	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	2.15E-07	0.87	3.70	-	955.8
AHQ-10-2, 2284	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	2	3.84E-06	0.91	4.02	-	689.2
AHQ-10-5, 2548	R.LCNSPSPQMNGKPCEGEAR.E	2135.34557	3	1.38E-04	0.87	3.83	-	867.5
AHQ-10-5, 2201	R.LCNSPSPQM*NGKPCEGEAR.E	2151.34497	3	8.10E-04	0.49	3.17	-	409.8
AHQ-10-11, 4932	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	1.26E-05	0.70	3.12	-	394.2
AHQ-10-6, 4997	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	4.72E-04	0.65	3.02	-	398.4
AHQ-10-4, 5083 - 5157	K.M*ENAELDVPIQSVFTR.D	1866.08547	2	9.83E-08	0.95	4.66	-	825.5
AHQ-10-5, 3121	K.QVTQSYWDTNPTR.A	1596.68241	2	1.72E-05	0.81	3.16	-	612.1
AHQ-10-2, 3195	K.QVTQSYWDTNPTR.A	1596.68241	2	3.17E-07	0.87	3.62	-	649.9
AHQ-10-4, 3135	K.QVTQSYWDTNPTR.A	1596.68241	2	2.75E-07	0.90	3.38	-	830.9
AHQ-10-3, 3141 - 3158	K.QVTQSYWDTNPTR.A	1596.68241	2	3.06E-06	0.90	3.65	-	937.1
AHQ-10-11, 3071 - 3086	K.QVTQSYWDTNPTR.A	1596.68241	2	1.09E-05	0.58	2.77	-	438.2
AHQ-10-7, 3070	K.QVTQSYWDTNPTR.A	1596.68241	2	3.30E-06	0.77	3.34	-	569.8
AHQ-10-6, 3088	K.QVTQSYWDTNPTR.A	1596.68241	2	6.09E-07	0.78	3.07	-	611.3
AHQ-10-5, 2892	R.RPPLCYHNGVQYR.N	1661.86889	3	6.06E-05	0.92	3.92	-	1146.5
AHQ-10-5, 2889	R.RPPLCYHNGVQYR.N	1661.86889	2	7.87E-07	0.75	2.77	-	559.2
AHQ-10-2, 2964	R.RPPLCYHNGVQYR.N	1661.86889	2	4.80E-05	0.63	2.82	-	508.5
AHQ-10-2, 2370	R.SCDSLNNRCEGSSVQTR.T	1973.04966	2	1.84E-08	0.52	2.70	-	318.0
AHQ-10-3, 3794 - 3814	K.SITLFVQEDR.A	1208.34588	2	1.71E-06	0.96	4.10	-	1702.3
AHQ-10-5, 3791	K.SITLFVQEDR.A	1208.34588	2	2.45E-05	0.92	3.50	-	1267.3
AHQ-10-6, 3728	K.SITLFVQEDR.A	1208.34588	2	4.12E-07	0.93	3.08	-	1459.8
AHQ-10-11, 3715	K.SITLFVQEDR.A	1208.34588	2	1.38E-05	0.89	3.17	-	1044.8
AHQ-10-1, 3983	K.SITLFVQEDR.A	1208.34588	2	5.98E-05	0.88	3.15	-	844.3
AHQ-10-13-, 3816	K.SITLFVQEDR.A	1208.34588	2	3.23E-07	0.91	2.94	-	1346.1
AHQ-10-2, 3872	K.SITLFVQEDR.A	1208.34588	2	4.71E-05	0.95	3.92	-	1515.2
AHQ-10-4, 3811	K.SITLFVQEDR.A	1208.34588	2	2.71E-05	0.89	3.07	-	1028.7
AHQ-10-9, 3560	K.SITLFVQEDR.A	1208.34588	2	1.18E-05	0.88	3.06	-	1073.8
AHQ-10-2, 4376 - 4392	R.TIVTTLQDSIR.K	1247.42355	2	8.34E-08	0.97	4.58	-	1663.7
AHQ-10-9, 4055 - 4071	R.TIVTTLQDSIR.K	1247.42355	2	1.03E-06	0.97	3.84	-	2075.4
AHQ-10-5, 3341	R.TIVTTLQDSIR.K	1247.42355	2	2.81E-05	0.95	3.30	-	1588.1
AHQ-10-7, 4204 - 4205	R.TIVTTLQDSIR.K	1247.42355	2	4.89E-07	0.96	4.05	-	1573.7
AHQ-10-3, 4309	R.TIVTTLQDSIR.K	1247.42355	2	2.83E-07	0.97	3.76	-	2212.3
AHQ-10-1, 4463	R.TIVTTLQDSIR.K	1247.42355	2	1.41E-06	0.95	3.77	-	1269.8
AHQ-10-5, 4307 - 4328	R.TIVTTLQDSIR.K	1247.42355	2	2.45E-07	0.97	4.01	-	2189.9
AHQ-10-6, 4229 - 4236	R.TIVTTLQDSIR.K	1247.42355	2	5.72E-06	0.96	3.84	-	1606.3
AHQ-10-4, 3369	R.TIVTTLQDSIR.K	1247.42355	2	8.53E-06	0.96	3.68	-	1993.0
AHQ-10-6, 3295	R.TIVTTLQDSIR.K	1247.42355	2	6.45E-04	0.97	3.99	-	2480.4
AHQ-10-2, 5890	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	5.59E-08	0.95	4.42	-	1619.3
AHQ-10-6, 5747 - 5767	K.TKDLQAICGISCDELSSM*VLELR.G	2658.02070	3	4.14E-05	0.91	4.43	-	1078.6
AHQ-10-4, 2684	K.VTEENKELANELR.R	1545.67685	2	2.91E-09	0.93	4.12	-	1163.4
AHQ-10-3, 2709	K.VTEENKELANELR.R	1545.67685	2	5.94E-07	0.75	3.53	-	583.1
AHQ-10-5, 2685 - 2689	K.VTEENKELANELR.R	1545.67685	2	1.36E-08	0.91	3.77	-	899.3
AHQ-10-5, 2688	K.VTEENKELANELR.R	1545.67685	3	3.19E-07	0.84	3.72	-	950.3
AHQ-10-6, 2655 - 2656	K.VTEENKELANELR.R	1545.67685	2	1.65E-07	0.89	4.03	-	868.3
AHQ-10-2, 2754 - 2764	K.VTEENKELANELR.R	1545.67685	2	1.98E-07	0.85	3.44	-	875.2
gi|4501891|ref|NP_001093.1| actinin, alpha 1 [Homo sapiens]				7.61E-14	29.03	340.34	41.40	103056.9
AHQ-10-5, 5179	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	1.44E-05	0.75	4.10	-	620.3
AHQ-10-4, 5212 - 5215	K.AGTQIENIEEDFRDGLK.L	1936.06918	2	3.56E-06	0.88	4.71	-	887.1
AHQ-10-5, 5413 - 5420	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	6.49E-04	0.82	3.87	-	579.1
AHQ-10-8, 6023	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	3.25E-05	0.21	2.56	-	158.2
AHQ-10-5, 6056	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	7.06E-04	0.88	3.99	-	702.7
AHQ-10-4, 5408	K.AIM*TYVSSFYHAFSGAQK.A	2025.27263	2	4.54E-07	0.87	3.82	-	627.9
AHQ-10-4, 6085	K.AIMTYVSSFYHAFSGAQK.A	2009.27323	2	9.22E-06	0.78	3.32	-	506.6
AHQ-10-4, 3467	R.ASFNHFDRDHSGTLGPEEFK.A	2292.40855	3	1.58E-07	0.93	3.86	-	1747.7
AHQ-10-6, 2343	K.ASIHEAWTDGK.E	1215.29697	2	8.61E-04	0.38	2.53	-	506.4
AHQ-10-5, 5327 - 5328	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	4.04E-09	0.95	5.23	-	1051.1
AHQ-10-4, 4827	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	1.17E-06	0.94	4.16	-	974.1
AHQ-10-6, 5215 - 5233	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	7.80E-04	0.49	2.92	-	354.0
AHQ-10-4, 5327	K.DDPLTNLNTAFDVAEK.Y	1763.88340	2	6.04E-08	0.94	4.87	-	877.2
AHQ-10-5, 4712	K.DGLGFCALIHR.H	1260.44730	2	2.24E-07	0.93	2.73	-	1736.5
AHQ-10-4, 4748	K.DGLGFCALIHR.H	1260.44730	2	6.98E-07	0.93	3.55	-	1302.4
AHQ-10-4, 2617 - 2631	R.DHSGTLGPEEFK.A	1317.38606	2	2.19E-05	0.94	3.98	-	1034.9
AHQ-10-6, 2603	R.DHSGTLGPEEFK.A	1317.38606	2	1.72E-06	0.72	2.73	-	620.5
AHQ-10-5, 3695	K.DYETATLSEIK.A	1270.36761	2	2.05E-05	0.90	3.00	-	1191.8
AHQ-10-4, 3207	R.ETADTDTADQVM*ASFK.I	1746.83148	2	8.91E-08	0.93	4.67	-	837.3
AHQ-10-6, 4219	R.ETADTDTADQVMASFK.I	1730.83208	2	1.14E-07	0.93	4.01	-	1005.9
AHQ-10-13-, 4265 - 4268	R.ETADTDTADQVMASFK.I	1730.83208	2	7.42E-05	0.73	3.02	-	592.7
AHQ-10-5, 3195	R.ETADTDTADQVM*ASFK.I	1746.83148	2	8.54E-06	0.92	3.99	-	836.6
AHQ-10-4, 2736	K.GISQEQMNEFR.A	1339.45991	2	2.30E-06	0.88	3.36	-	999.4
AHQ-10-4, 3053 - 3132	K.GISQEQMNEFR.A	1339.45991	2	3.64E-06	0.88	3.34	-	917.5
AHQ-10-4, 3203	K.GISQEQMNEFR.A	1339.45991	2	5.82E-05	0.82	2.99	-	952.2

AHQ-10-4, 2351	K.GISQEQM*NEFR.A	1355.45931	2	1.68E-05	0.79	3.17	-	620.2
AHQ-10-6, 2333	K.GISQEQM*NEFR.A	1355.45931	2	1.08E-07	0.61	2.78	-	404.4
AHQ-10-5, 2336	K.GISQEQM*NEFR.A	1355.45931	2	3.29E-05	0.89	3.26	-	937.2
AHQ-10-4, 2300	R.HRPELIDYGK.L	1228.38202	2	6.00E-04	0.90	3.38	-	651.2
AHQ-10-5, 4699 - 4752	K.ICDQWDNLGALTQK.R	1663.83349	2	3.54E-08	0.96	3.64	-	2123.8
AHQ-10-6, 4617 - 4619	K.ICDQWDNLGALTQK.R	1663.83349	2	3.69E-10	0.97	5.27	-	1915.0
AHQ-10-6, 5440	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	1.69E-04	0.79	2.85	-	741.1
AHQ-10-5, 5552 - 5612	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	2	1.62E-04	0.68	2.64	-	564.7
AHQ-10-6, 5364 - 5441	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	4.78E-05	0.93	5.04	-	1043.5
AHQ-10-4, 5435 - 5497	K.IDQLEGDHQLIQEALIFDNK.H	2340.57447	3	8.87E-12	0.97	5.99	-	1706.1
AHQ-10-4, 4103	K.ILAGDKNYITMDELR.R	1753.01353	2	2.13E-04	0.94	4.78	-	852.6
AHQ-10-4, 3485 - 3545	K.ILAGDKNYITM*DELR.R	1769.01293	3	9.64E-06	0.76	3.45	-	463.8
AHQ-10-4, 3543	K.ILAGDKNYITM*DELR.R	1769.01293	2	4.53E-04	0.93	4.02	-	722.0
AHQ-10-4, 4107	K.ILAGDKNYITMDELR.R	1753.01353	3	6.11E-06	0.86	4.63	-	730.0
AHQ-10-5, 4739 - 4757	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	7.61E-08	0.97	5.23	-	1283.9
AHQ-10-4, 4767	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	2.21E-06	0.97	5.44	-	1184.8
AHQ-10-5, 4304	R.KDDPLTNLNTAFDVAEK.Y	1892.05631	2	1.19E-05	0.68	2.88	-	377.6
AHQ-10-4, 3707	R.LAILGIHNEVSK.I	1294.52505	2	1.06E-08	0.96	3.92	-	1387.7
AHQ-10-6, 3423 - 3459	R.LAILGIHNEVSK.I	1294.52505	2	1.45E-06	0.84	3.00	-	752.5
AHQ-10-7, 3390	R.LAILGIHNEVSK.I	1294.52505	2	3.03E-04	0.75	2.61	-	636.1
AHQ-10-4, 3477	R.LAILGIHNEVSK.I	1294.52505	2	6.70E-07	0.95	3.64	-	1407.7
AHQ-10-5, 5703	K.LASDLLEWIR.R	1216.41115	2	4.43E-07	0.97	4.50	-	2233.9
AHQ-10-6, 5576	K.LASDLLEWIR.R	1216.41115	2	1.45E-07	0.94	3.54	-	1546.7
AHQ-10-7, 5592	K.LASDLLEWIR.R	1216.41115	2	2.55E-04	0.96	3.68	-	1799.6
AHQ-10-6, 5925 - 5931	K.LLETIDQLYLEYAK.R	1712.96427	2	4.91E-09	0.97	5.02	-	1536.6
AHQ-10-4, 6063 - 6071	K.LLETIDQLYLEYAK.R	1712.96427	2	1.23E-08	0.96	4.69	-	1259.0
AHQ-10-4, 6072 - 6073	K.LLETIDQLYLEYAK.R	1712.96427	3	2.18E-06	0.98	5.82	-	2134.5
AHQ-10-5, 6053 - 6080	K.LLETIDQLYLEYAK.R	1712.96427	2	2.85E-07	0.97	4.42	-	1620.4
AHQ-10-7, 5972 - 5974	K.LLETIDQLYLEYAK.R	1712.96427	2	3.60E-09	0.97	5.75	-	1349.2
AHQ-10-3, 5983 - 5994	K.LLETIDQLYLEYAK.R	1712.96427	2	2.76E-04	0.92	3.88	-	1034.0
AHQ-10-2, 6067 - 6086	K.LLETIDQLYLEYAK.R	1712.96427	2	7.31E-04	0.95	3.99	-	1390.4
AHQ-10-8, 2742	R.LSNRPAFMPSEGR.M	1462.65941	2	3.36E-04	0.69	3.11	-	572.8
AHQ-10-4, 3583	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	3.14E-05	0.88	3.35	-	701.0
AHQ-10-6, 3523	K.M*LDAEDIVGTARPDEK.A	1776.94709	2	2.49E-04	0.57	2.81	-	418.4
AHQ-10-4, 3947 - 3948	K.MLDAEDIVGTARPDEK.A	1760.94769	2	2.95E-04	0.86	3.84	-	782.7
AHQ-10-4, 5275 - 5331	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	8.07E-07	0.89	3.80	-	870.4
AHQ-10-5, 4864	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.39E-04	0.79	3.60	-	426.5
AHQ-10-4, 4984	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.77E-06	0.97	4.51	-	1624.8
AHQ-10-5, 4955	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.30E-05	0.89	4.01	-	660.6
AHQ-10-6, 4999	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	2.91E-07	0.88	3.60	-	702.2
AHQ-10-4, 4883 - 4952	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	4.26E-05	0.85	3.93	-	560.1
AHQ-10-4, 5129	R.M*VSDINNAWGCLEQVEK.G	2011.22273	2	1.38E-04	0.94	4.09	-	1163.2
AHQ-10-5, 4632	K.NVNIQNFHISWK.D	1500.68583	2	4.02E-07	0.97	4.08	-	1923.4
AHQ-10-4, 4691	K.NVNIQNFHISWK.D	1500.68583	2	1.73E-08	0.96	4.20	-	1340.5
AHQ-10-5, 4887	K.QFGAQANVIGPWIQTK.M	1759.00118	2	5.35E-04	0.90	3.90	-	827.1
AHQ-10-4, 4908	K.QFGAQANVIGPWIQTK.M	1759.00118	2	1.26E-04	0.64	2.83	-	526.0
AHQ-10-4, 3233	R.QKDYETATLSEIK.A	1526.67030	2	9.10E-04	0.55	2.54	-	480.5
AHQ-10-6, 3825	R.TINEVENQILTR.D	1430.58898	2	5.60E-07	0.95	4.47	-	1522.5
AHQ-10-5, 3883	R.TINEVENQILTR.D	1430.58898	2	1.20E-07	0.79	2.83	-	820.5
AHQ-10-4, 3901 - 3903	R.TINEVENQILTR.D	1430.58898	2	4.31E-07	0.96	4.26	-	1524.6
AHQ-10-6, 3083	R.TINEVENQILTR.D	1430.58898	2	1.97E-07	0.83	2.75	-	986.5
AHQ-10-4, 3499	R.TINEVENQILTR.D	1430.58898	2	1.24E-05	0.66	2.94	-	502.2
AHQ-10-7, 3812 - 3813	R.TINEVENQILTR.D	1430.58898	2	1.77E-04	0.86	3.73	-	817.1
AHQ-10-4, 4031 - 4048	R.TINEVENQILTR.D	1430.58898	2	1.48E-06	0.94	4.34	-	951.6
AHQ-10-5, 6319	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	3.18E-08	0.98	6.83	-	2296.8
AHQ-10-4, 6319	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	3.73E-07	0.96	5.47	-	1001.3
AHQ-10-6, 6192 - 6193	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	9.25E-12	0.97	6.76	-	1552.2
AHQ-10-4, 5755	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.25E-05	0.77	3.32	-	658.0
AHQ-10-6, 6208	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	1.50E-04	0.69	2.68	-	534.1
AHQ-10-7, 6240	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	3	1.18E-04	0.96	5.61	-	1309.0
AHQ-10-4, 6315	R.VEQIAAIAQELNELDYYDSPSVNAR.C	2810.02233	2	1.56E-04	0.72	2.50	-	868.4
AHQ-10-5, 6179	R.VGWEQLLTTIAR.T	1387.60894	2	9.47E-09	0.92	3.47	-	1149.5
AHQ-10-11, 5971	R.VGWEQLLTTIAR.T	1387.60894	2	2.13E-04	0.83	2.94	-	815.8
AHQ-10-7, 6109 - 6114	R.VGWEQLLTTIAR.T	1387.60894	2	7.56E-07	0.95	4.16	-	1350.7
AHQ-10-4, 6195 - 6269	R.VGWEQLLTTIAR.T	1387.60894	2	2.06E-07	0.95	4.05	-	1482.7
AHQ-10-8, 6141 - 6146	R.VGWEQLLTTIAR.T	1387.60894	2	1.42E-06	0.95	4.01	-	1205.3
AHQ-10-4, 3725 - 3751	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.02E-07	0.97	5.72	-	1375.9
AHQ-10-6, 4260	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.24E-07	0.88	3.79	-	620.8
AHQ-10-4, 4191	K.VLAVNQENEQLMEDYEK.L	2053.23635	3	1.55E-04	0.90	3.86	-	1021.6
AHQ-10-7, 3497 - 3502	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	4.30E-04	0.79	3.25	-	691.7
AHQ-10-6, 4087	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	9.66E-08	0.95	5.05	-	994.1
AHQ-10-7, 4074	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	2.86E-06	0.93	4.57	-	1126.6
AHQ-10-4, 4127 - 4187	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	8.56E-08	0.96	5.33	-	1097.8
AHQ-10-6, 3495	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	2.38E-05	0.95	4.34	-	1308.1
AHQ-10-4, 3575 - 3647	K.VLAVNQENEQLM*EDYEK.L	2069.23575	3	1.22E-05	0.95	4.88	-	1584.1
AHQ-10-4, 3571 - 3648	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	4.72E-09	0.95	4.88	-	1157.0
AHQ-10-4, 3460	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	4.72E-05	0.87	3.47	-	742.9
AHQ-10-8, 4106	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	4.53E-06	0.91	4.18	-	858.4
AHQ-10-5, 3551 - 3628	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.74E-08	0.93	4.47	-	909.1
AHQ-10-4, 4315 - 4375	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	7.61E-14	0.96	4.90	-	1248.6
AHQ-10-5, 4119	K.VLAVNQENEQLMEDYEK.L	2053.23635	2	1.09E-10	0.94	4.65	-	891.2
AHQ-10-4, 3916 - 3989	K.VLAVNQENEQLM*EDYEK.L	2069.23575	2	1.51E-10	0.93	4.67	-	771.3
gi|4557697|ref|NP_000412.1| keratin 10; Keratin-10 [Homo sapiens]				1.17E-13	13.27	150.30	28.70	57247.1
AHQ-10-1, 2989	R.ALEESNYELEGK.I	1382.45482	2	9.86E-10	0.95	4.08	-	1285.5
AHQ-10-11, 2752 - 2754	R.ALEESNYELEGK.I	1382.45482	2	1.56E-06	0.92	3.47	-	1120.7
AHQ-10-10, 2736	R.ALEESNYELEGK.I	1382.45482	2	2.80E-06	0.68	2.72	-	568.7
AHQ-10-9, 2657	R.ALEESNYELEGK.I	1382.45482	2	2.93E-07	0.89	3.19	-	928.7
AHQ-10-12, 2850	R.ALEESNYELEGK.I	1382.45482	2	2.55E-05	0.78	2.98	-	804.4
AHQ-10-8, 2746	R.ALEESNYELEGK.I	1382.45482	2	5.70E-06	0.86	3.27	-	848.6
AHQ-10-13, 3195	R.ALEESNYELEGK.I	1382.45482	2	2.75E-06	0.87	3.40	-	800.1
AHQ-10-2, 2854	R.ALEESNYELEGK.I	1382.45482	2	4.16E-09	0.94	4.04	-	1444.7
AHQ-10-7, 2744	R.ALEESNYELEGK.I	1382.45482	2	4.14E-07	0.90	3.80	-	987.7
AHQ-10-6, 2747	R.ALEESNYELEGK.I	1382.45482	2	1.85E-05	0.88	3.12	-	1015.7
AHQ-10-5, 2779	R.ALEESNYELEGK.I	1382.45482	2	5.78E-08	0.94	4.11	-	1139.2
AHQ-10-4, 2780	R.ALEESNYELEGK.I	1382.45482	2	2.13E-06	0.94	3.97	-	1216.5
AHQ-10-13-, 2817 - 2878	R.ALEESNYELEGK.I	1382.45482	2	3.24E-04	0.86	3.51	-	810.7
AHQ-10-14-, 2793	R.ALEESNYELEGK.I	1382.45482	2	2.33E-06	0.91	3.67	-	931.5
AHQ-10-13-, 3504	K.DAEAWFNEK.S	1110.15762	2	1.98E-05	0.91	3.42	-	825.3
AHQ-10-1, 3654	K.DAEAWFNEK.S	1110.15762	2	2.48E-04	0.82	3.03	-	889.8
AHQ-10-3, 3486	K.DAEAWFNEK.S	1110.15762	1	1.90E-04	0.17	1.96	-	466.3
AHQ-10-3, 3475	K.DAEAWFNEK.S	1110.15762	2	1.11E-04	0.90	3.31	-	853.6
AHQ-10-6, 3440 - 3444	K.DAEAWFNEK.S	1110.15762	2	6.89E-04	0.69	2.82	-	809.8
AHQ-10-1, 5221 - 5298	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.21E-05	0.82	3.75	-	453.7
AHQ-10-1, 4490 - 4491	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	4.62E-12	0.95	4.70	-	983.4
AHQ-10-13-, 4313	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.88E-06	0.80	3.44	-	445.1
AHQ-10-14-, 5165 - 5221	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	7.07E-11	0.88	3.77	-	583.7
AHQ-10-12, 5012 - 5018	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.53E-06	0.80	3.70	-	624.5

AHQ-10-3, 5087	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.76E-07	0.75	3.33	-	619.6
AHQ-10-14-, 5061	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.39E-10	0.95	5.18	-	888.2
AHQ-10-2, 5176	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	8.35E-09	0.91	3.90	-	849.5
AHQ-10-7, 5048	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	4.03E-06	0.95	4.93	-	971.8
AHQ-10-4, 5181	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.70E-09	0.94	4.78	-	822.4
AHQ-10-2, 4424	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	7.79E-09	0.91	4.28	-	548.4
AHQ-10-5, 4368	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	4.40E-08	0.91	3.85	-	960.5
AHQ-10-7, 4262	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.85E-08	0.87	3.79	-	677.4
AHQ-10-5, 5136	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	6.61E-07	0.87	3.56	-	780.0
AHQ-10-5, 5268	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	1.39E-05	0.89	3.72	-	616.5
AHQ-10-14-, 5004 - 5064	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	6.59E-05	0.82	4.27	-	814.6
AHQ-10-13, 5340	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.98E-04	0.82	3.34	-	742.8
AHQ-10-13-, 5058	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	3.19E-07	0.94	4.79	-	858.5
AHQ-10-6, 5048	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	2.08E-07	0.94	4.46	-	869.1
AHQ-10-11, 4891 - 4952	K.ELTTEIDNNIEQISSYK.S	1998.13406	2	4.19E-06	0.92	4.38	-	793.4
AHQ-10-2, 4147 - 4150	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	2.04E-09	0.92	4.20	-	893.5
AHQ-10-1, 4217	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.52E-06	0.76	3.05	-	657.4
AHQ-10-13-, 4001 - 4064	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	5.70E-07	0.95	5.05	-	855.7
AHQ-10-8, 3966 - 4041	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	4.18E-08	0.88	3.62	-	818.2
AHQ-10-7, 3984 - 4050	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	8.54E-06	0.90	3.69	-	865.1
AHQ-10-12, 4044	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	1.02E-05	0.80	3.06	-	603.5
AHQ-10-14-, 4016	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	9.00E-07	0.92	3.93	-	1017.8
AHQ-10-13, 4416 - 4427	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	8.57E-06	0.89	3.75	-	783.0
AHQ-10-3, 4070 - 4134	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	8.47E-08	0.82	3.40	-	558.5
AHQ-10-6, 3943 - 4020	K.GSLGGGFSSGGFSGGSFSR.G	1708.76962	2	6.21E-07	0.74	3.12	-	613.0
AHQ-10-7, 3213 - 3221	K.IRLENEIQTYR.S	1435.61046	2	3.68E-08	0.97	4.40	-	1926.4
AHQ-10-13-, 3308	K.IRLENEIQTYR.S	1435.61046	2	2.70E-07	0.97	3.99	-	2371.9
AHQ-10-6, 2504	R.LENEIQTYR.S	1166.26586	2	3.78E-05	0.89	3.63	-	1089.5
AHQ-10-3, 2551 - 2553	R.LENEIQTYR.S	1166.26586	2	3.09E-05	0.86	3.96	-	916.9
AHQ-10-3, 2790	R.LKYENEVALR.Q	1235.41446	2	1.92E-05	0.52	2.52	-	360.4
AHQ-10-7, 2720 - 2721	R.LKYENEVALR.Q	1235.41446	2	6.39E-07	0.81	2.88	-	646.1
AHQ-10-11, 2747	R.LKYENEVALR.Q	1235.41446	2	5.60E-05	0.60	2.52	-	464.1
AHQ-10-13-, 2818	R.LKYENEVALR.Q	1235.41446	2	2.08E-05	0.74	2.84	-	472.6
AHQ-10-13-, 2745 - 2820	R.LKYENEVALR.Q	1235.41446	2	8.82E-08	0.68	2.97	-	390.9
AHQ-10-8, 2725	R.LKYENEVALR.Q	1235.41446	2	3.75E-07	0.78	3.25	-	480.1
AHQ-10-1, 6110	K.NQILNLTTDNANILLQIDNAR.L	2368.63258	3	1.64E-05	0.95	4.13	-	1900.6
AHQ-10-7, 5984	K.NQILNLTTDNANILLQIDNAR.L	2368.63258	3	2.44E-04	0.93	4.19	-	1550.8
AHQ-10-12, 5252	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	2.60E-04	0.84	3.51	-	953.5
AHQ-10-7, 6097	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	2.55E-06	0.92	5.07	-	807.9
AHQ-10-2, 5444	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	7.60E-05	0.82	3.34	-	881.9
AHQ-10-8, 6149	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	5.74E-06	0.84	3.34	-	1036.7
AHQ-10-6, 5295	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	2.92E-04	0.90	4.20	-	945.7
AHQ-10-13-, 5292	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	2	9.52E-05	0.60	3.15	-	255.8
AHQ-10-2, 6210	R.NVSTGDVNVEM*NAAPGVDLTQLLNNMR.N	2890.20063	3	3.26E-04	0.91	4.50	-	1135.5
AHQ-10-3, 5267 - 5349	R.NVSTGDVNVEM*NAAPGVDLTQLLNNM*R.N	2906.20003	3	3.71E-07	0.96	6.07	-	1320.1
AHQ-10-14-, 5689	R.NVSTGDVNVEMNAAPGVDLTQLLNNM*R.N	2890.20063	2	9.44E-04	0.81	3.51	-	430.9
AHQ-10-3, 3377 - 3381	K.QSLEASLAETEGR.Y	1391.46648	2	2.37E-06	0.69	3.28	-	320.1
AHQ-10-8, 3330	K.QSLEASLAETEGR.Y	1391.46648	2	1.51E-06	0.61	2.75	-	350.3
AHQ-10-3, 4798 - 4853	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	7.59E-09	0.94	4.70	-	1011.8
AHQ-10-2, 4138	K.SKELTTEIDNNIEQISSYK.S	2213.38462	3	5.97E-06	0.88	4.16	-	965.8
AHQ-10-5, 4801 - 4875	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	6.53E-06	0.89	3.94	-	1077.4
AHQ-10-3, 4057	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	1.17E-13	0.96	4.87	-	1196.4
AHQ-10-2, 4871 - 4931	K.SKELTTEIDNNIEQISSYK.S	2213.38462	2	1.01E-04	0.82	3.65	-	776.2
AHQ-10-2, 2214	R.SLLEGEGSSGGGGR.G	1263.29680	2	5.71E-06	0.87	3.13	-	952.8
AHQ-10-3, 2166	R.SLLEGEGSSGGGGR.G	1263.29680	2	4.61E-04	0.74	2.77	-	588.6
AHQ-10-7, 6360	K.TIDDLKNQILNLTTDNANILLQIDNAR.L	3054.40205	3	2.25E-05	0.94	5.39	-	1154.9
AHQ-10-3, 6338	K.TIDDLKNQILNLTTDNANILLQIDNAR.L	3054.40205	3	1.29E-04	0.78	3.43	-	713.4
gi|5031987|ref|NP_005720.1| peptidylprolyl isomerase F (cyclophilin F) [Homo sapiens]				1.22E-13	1.47	20.21	18.40	22040.1
AHQ-10-12, 3797 - 3861	R.FPDENFTLK.H	1111.22866	2	6.69E-04	0.59	2.67	-	419.9
AHQ-10-12, 4814 - 4868	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	1.22E-13	0.89	4.22	-	740.6
AHQ-10-11, 4796 - 4856	K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V	2834.99028	3	4.68E-08	0.89	4.06	-	803.3
gi|4504165|ref|NP_000168.1| gelsolin (amyloidosis, Finnish type); Gelsolin [Homo sapiens]				1.67E-13	19.16	210.32	31.70	85696.9
AHQ-10-5, 3819	K.AGALNSNDAFVLK.T	1320.47622	2	2.15E-07	0.85	3.84	-	491.4
AHQ-10-5, 3289 - 3303	K.AGKEPGLQIWR.V	1255.45060	3	3.09E-04	0.91	3.98	-	1271.1
AHQ-10-5, 3287	K.AGKEPGLQIWR.V	1255.45060	2	1.90E-06	0.79	2.99	-	569.7
AHQ-10-6, 5324 - 5327	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.65E-08	0.95	5.13	-	621.1
AHQ-10-5, 5431 - 5487	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	5.99E-06	0.97	5.87	-	902.6
AHQ-10-7, 5340	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	1.18E-06	0.86	3.84	-	574.4
AHQ-10-5, 5220 - 5292	R.AQPVQVAEGSEPDGFWEALGGK.A	2273.44345	2	7.89E-08	0.96	5.75	-	742.5
AHQ-10-5, 5457	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	9.85E-08	0.89	3.66	-	1435.0
AHQ-10-5, 5299 - 5367	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	3.75E-09	0.94	4.65	-	1372.7
AHQ-10-6, 5225 - 5279	R.DPDQTDGLGLSYLSSHIANVER.V	2388.53285	3	8.08E-06	0.93	3.98	-	1611.7
AHQ-10-7, 2285	K.DSQEEEKTEALTSAK.R	1666.72289	3	5.02E-05	0.87	3.18	-	1427.0
AHQ-10-7, 2281	K.DSQEEEKTEALTSAK.R	1666.72289	2	8.48E-07	0.84	3.55	-	841.1
AHQ-10-5, 2268 - 2337	K.DSQEEEKTEALTSAK.R	1666.72289	3	1.66E-06	0.97	4.58	-	2278.7
AHQ-10-8, 2281	K.DSQEEEKTEALTSAK.R	1666.72289	2	5.43E-07	0.71	2.91	-	903.2
AHQ-10-10, 2267	K.DSQEEEKTEALTSAK.R	1666.72289	2	2.79E-07	0.85	3.27	-	931.7
AHQ-10-6, 2276	K.DSQEEEKTEALTSAK.R	1666.72289	3	1.20E-04	0.93	3.78	-	1837.5
AHQ-10-6, 2271 - 2327	K.DSQEEEKTEALTSAK.R	1666.72289	2	1.02E-05	0.95	3.91	-	1593.4
AHQ-10-5, 2267 - 2335	K.DSQEEEKTEALTSAK.R	1666.72289	2	3.94E-08	0.93	3.91	-	1236.7
AHQ-10-8, 5825 - 5833	R.EVQGFESATFLGYFK.S	1723.90570	2	9.70E-05	0.59	2.86	-	567.7
AHQ-10-11, 5587 - 5658	R.EVQGFESATFLGYFK.S	1723.90570	2	5.03E-06	0.38	2.72	-	350.4
AHQ-10-5, 5947 - 6005	R.EVQGFESATFLGYFK.S	1723.90570	2	2.01E-07	0.97	4.46	-	1635.2
AHQ-10-7, 5742 - 5753	R.EVQGFESATFLGYFK.S	1723.90570	2	8.77E-04	0.91	3.77	-	928.0
AHQ-10-5, 6211	R.EVQGFESATFLGYFK.S	1723.90570	2	1.87E-04	0.77	2.94	-	595.2
AHQ-10-5, 6076 - 6136	R.EVQGFESATFLGYFK.S	1723.90570	2	1.33E-06	0.84	3.56	-	583.5
AHQ-10-5, 5817 - 5891	R.EVQGFESATFLGYFK.S	1723.90570	2	1.08E-08	0.95	4.25	-	1324.2
AHQ-10-13-, 5712	R.EVQGFESATFLGYFK.S	1723.90570	2	5.50E-04	0.84	2.88	-	915.3
AHQ-10-8, 2385	K.HVVPNEVVVQR.L	1276.46981	2	2.24E-04	0.93	3.20	-	918.5
AHQ-10-5, 2376 - 2435	K.HVVPNEVVVQR.L	1276.46981	2	1.84E-08	0.93	3.55	-	748.8
AHQ-10-5, 5863 - 5933	R.IEGSNKVPVDPATYGQFYGGDSYIILYNYR.H	3401.72499	3	1.40E-04	0.96	5.82	-	1424.3
AHQ-10-6, 5273	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	8.32E-08	0.97	6.22	-	1648.2
AHQ-10-5, 5363 - 5411	K.NWRDPDQTDGLGLSYLSSHIANVER.V	2845.03323	3	3.98E-07	0.98	6.34	-	2011.3
AHQ-10-5, 2553	K.PALPAGTEDTAKEDAANR.K	1827.93072	2	1.67E-13	0.94	4.79	-	556.8
AHQ-10-7, 3066	K.SEDCFILDHGK.D	1322.42590	2	2.58E-05	0.89	3.20	-	874.5
AHQ-10-6, 3101 - 3107	K.SEDCFILDHGK.D	1322.42590	2	6.79E-07	0.94	3.54	-	1138.1
AHQ-10-5, 3137	K.SEDCFILDHGK.D	1322.42590	3	7.23E-05	0.87	3.45	-	722.4
AHQ-10-5, 3125 - 3139	K.SEDCFILDHGK.D	1322.42590	2	6.90E-07	0.92	3.67	-	1029.8
AHQ-10-5, 3012	K.SEDCFILDHGK.D	1322.42590	2	6.51E-04	0.83	3.36	-	841.6
AHQ-10-5, 2865	K.SEDCFILDHGKDGK.I	1622.73823	2	1.06E-05	0.87	3.47	-	962.0
AHQ-10-8, 2302	K.TGAQELLR.V	888.00387	2	1.56E-05	0.66	2.91	-	607.2
AHQ-10-5, 2287	K.TGAQELLR.V	888.00387	2	1.23E-05	0.89	2.91	-	1211.1
AHQ-10-10, 2314	K.TGAQELLR.V	888.00387	2	7.77E-05	0.89	2.84	-	1078.3
AHQ-10-8, 4266	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	2.41E-05	0.94	3.88	-	1273.7
AHQ-10-5, 4351 - 4425	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	3.48E-10	0.97	5.50	-	1276.5
AHQ-10-6, 4263	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	4.22E-04	0.88	3.61	-	736.1
AHQ-10-5, 4339	K.TPSAAYLWVGTGASEAEK.T	1838.99510	2	1.25E-05	0.96	4.38	-	1571.3

AHQ-10-5, 3757 - 3785	R.VHVSEEGTEPEAM*LQVLGPK.P	2167.42570	2	1.21E-05	0.97	5.35	-	1176.1
AHQ-10-5, 4769	R.VHVSEEGTEPEAMLQVLGPK.P	2151.42630	2	3.60E-06	0.97	5.50	-	1205.8
AHQ-10-5, 5060	R.VHVSEEGTEPEAMLQVLGPKPALPAGTEDTAK.E	3303.68611	3	4.27E-10	0.93	5.20	-	862.4
AHQ-10-5, 4228	R.VHVSEEGTEPEAM*LQVLGPKPALPAGTEDTAK.E	3319.68551	3	7.08E-05	0.92	4.85	-	688.1
AHQ-10-5, 3579 - 3640	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	2.97E-04	0.92	5.31	-	1341.4
AHQ-10-6, 3525	R.VPFDAATLHTSTAMAAQHGM*DDDGTGQK.Q	2891.10081	3	9.90E-04	0.98	6.37	-	2272.2
AHQ-10-7, 3873	R.VPFDAATLHTSTAMAAQHGMDDDGTGQK.Q	2875.10141	3	4.20E-06	0.95	4.98	-	1287.1
AHQ-10-5, 6067 - 6079	K.VPVDPATYGQFYGGDSYIILYNYR.H	2773.04698	3	8.65E-08	0.61	3.11	-	702.7
gi|4507651|ref|NP_003281.1| tropomyosin 4 [Homo sapiens]				1.99E-13	3.78	40.26	15.30	28521.6
AHQ-10-9, 3831	R.AEVSELKCGDLEEELK.N	1851.02256	3	5.90E-06	0.91	4.52	-	898.5
AHQ-10-9, 3753 - 3827	R.AEVSELKCGDLEEELK.N	1851.02256	2	3.81E-05	0.86	3.81	-	646.5
AHQ-10-9, 5316 - 5371	R.AEVSELKCGDLEEELKNVTNNLK.S	2634.89893	3	1.65E-07	0.96	5.20	-	1554.0
AHQ-10-9, 2545	K.IQALQQQADEAEDR.A	1615.68404	2	6.38E-07	0.97	4.48	-	1913.1
AHQ-10-13-, 2717	K.IQALQQQADEAEDR.A	1615.68404	2	3.95E-07	0.95	3.67	-	1652.2
AHQ-10-10, 2636	K.IQALQQQADEAEDR.A	1615.68404	2	1.93E-07	0.94	3.57	-	1286.7
AHQ-10-11, 2652	K.IQALQQQADEAEDR.A	1615.68404	2	3.06E-06	0.94	3.79	-	1218.3
AHQ-10-9, 2391	R.KIQALQQQADEAEDR.A	1743.85695	3	1.99E-13	0.96	5.03	-	1730.0
AHQ-10-11, 2498	R.KIQALQQQADEAEDR.A	1743.85695	2	2.61E-06	0.93	4.26	-	1214.2
gi|4557677|ref|NP_000203.1| integrin beta chain, beta 3 precursor; platelet glycoprotein IIIa precu				4.81E-13	20.73	240.24	31.50	87185.6
AHQ-10-3, 3099 - 3151	R.AKWDTANNPLYK.E	1421.58225	2	9.51E-05	0.82	3.31	-	779.6
AHQ-10-4, 3101 - 3181	R.AKWDTANNPLYK.E	1421.58225	2	6.10E-06	0.91	3.71	-	860.9
AHQ-10-3, 5006 - 5066	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	9.20E-07	0.90	4.46	-	966.0
AHQ-10-4, 5120	R.CDLKENLLKDNCAPESIEFPVSEAR.V	2938.23689	3	7.91E-07	0.90	4.30	-	912.1
AHQ-10-4, 4168	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	2.71E-08	0.84	4.01	-	514.5
AHQ-10-5, 4145	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	3.14E-06	0.68	3.42	-	330.7
AHQ-10-3, 4129 - 4190	R.CGPGWLGSQCECSEEDYRPSQQDECSPR.E	3380.49342	3	4.05E-11	0.84	4.22	-	579.0
AHQ-10-4, 4268	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	4.69E-06	0.92	4.00	-	869.1
AHQ-10-6, 4151	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.77E-04	0.80	3.00	-	607.2
AHQ-10-7, 5333	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	2.80E-04	0.88	3.43	-	844.2
AHQ-10-4, 5432	R.DAPEGGFDAIMQATVCDEK.I	2056.21716	2	3.09E-08	0.71	2.94	-	481.1
AHQ-10-4, 4177 - 4244	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	1.43E-04	0.56	3.40	-	223.4
AHQ-10-5, 4223	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	3.34E-05	0.88	3.51	-	858.0
AHQ-10-1, 4343	R.DAPEGGFDAIM*QATVCDEK.I	2072.21656	2	2.30E-05	0.94	4.18	-	950.2
AHQ-10-6, 4584	K.DDLWSIQNLGTK.L	1390.52332	2	5.48E-06	0.90	3.58	-	941.2
AHQ-10-4, 4695	K.DDLWSIQNLGTK.L	1390.52332	2	4.13E-04	0.76	2.57	-	804.4
AHQ-10-4, 4332	K.DNCAPESIEFPVSEAR.V	1822.93099	2	8.31E-05	0.53	2.51	-	531.6
AHQ-10-9, 3963 - 3964	K.DNCAPESIEFPVSEAR.V	1822.93099	2	6.19E-05	0.73	3.06	-	688.6
AHQ-10-7, 4116	K.DNCAPESIEFPVSEAR.V	1822.93099	2	5.74E-06	0.82	3.03	-	919.6
AHQ-10-8, 4149	K.DNCAPESIEFPVSEAR.V	1822.93099	2	2.36E-04	0.72	2.76	-	792.7
AHQ-10-6, 4127 - 4140	K.DNCAPESIEFPVSEAR.V	1822.93099	2	2.26E-06	0.83	3.24	-	772.0
AHQ-10-5, 4209 - 4219	K.DNCAPESIEFPVSEAR.V	1822.93099	2	1.69E-04	0.94	3.63	-	1298.1
AHQ-10-3, 4182 - 4189	K.DNCAPESIEFPVSEAR.V	1822.93099	2	5.55E-06	0.92	3.71	-	1146.1
AHQ-10-4, 3371	K.EATSTFTNITYR.G	1404.50685	2	1.39E-04	0.67	2.86	-	498.3
AHQ-10-6, 3315	K.EATSTFTNITYR.G	1404.50685	2	2.92E-05	0.86	3.06	-	890.9
AHQ-10-3, 2423	R.FQYYEDSSGK.S	1224.25749	2	8.74E-08	0.81	3.19	-	463.8
AHQ-10-5, 3508	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.37E-04	0.91	4.09	-	848.2
AHQ-10-3, 3506	R.GECLCGQCVCHSSDFGK.I	2006.16137	3	2.52E-06	0.91	4.08	-	1017.8
AHQ-10-6, 3467	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	9.35E-05	0.74	3.10	-	634.4
AHQ-10-3, 3502 - 3513	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	1.52E-05	0.96	4.27	-	1634.7
AHQ-10-4, 3537 - 3540	R.GECLCGQCVCHSSDFGK.I	2006.16137	2	3.82E-05	0.95	4.04	-	1610.8
AHQ-10-5, 1971	K.GSGDSSQVTQVSPQR.I	1533.58302	2	2.04E-05	0.76	3.01	-	756.2
AHQ-10-3, 2839	K.HVLTLTDQVTR.F	1283.45912	2	5.03E-06	0.89	3.41	-	665.9
AHQ-10-8, 2771	K.HVLTLTDQVTR.F	1283.45912	2	6.69E-04	0.68	2.65	-	632.5
AHQ-10-4, 2803 - 2816	K.HVLTLTDQVTR.F	1283.45912	2	6.34E-08	0.91	3.49	-	760.8
AHQ-10-6, 2741 - 2776	K.HVLTLTDQVTR.F	1283.45912	2	1.89E-04	0.84	2.66	-	609.5
AHQ-10-5, 2815	K.HVLTLTDQVTR.F	1283.45912	2	5.03E-07	0.80	2.81	-	566.5
AHQ-10-3, 3998 - 4063	K.IGDTVSFSIEAK.V	1267.41009	2	2.43E-04	0.92	3.63	-	1076.1
AHQ-10-3, 3563	K.ITGKYCECDDFSCVR.Y	1914.08378	2	5.67E-04	0.62	2.77	-	479.9
AHQ-10-3, 3867	R.NDASHLLVFTTDAK.T	1532.67977	3	1.30E-05	0.96	4.79	-	1698.2
AHQ-10-4, 3799 - 3875	R.NDASHLLVFTTDAK.T	1532.67977	2	4.60E-05	0.95	4.32	-	1172.4
AHQ-10-4, 4236	R.NDASHLLVFTTDAK.T	1532.67977	2	4.14E-10	0.93	4.10	-	925.8
AHQ-10-3, 4023 - 4082	R.NDASHLLVFTTDAK.T	1532.67977	2	8.08E-05	0.88	3.31	-	946.9
AHQ-10-3, 3869	R.NDASHLLVFTTDAK.T	1532.67977	2	3.21E-07	0.96	4.01	-	1658.2
AHQ-10-3, 3785 - 3853	R.NDASHLLVFTTDAK.T	1532.67977	2	1.24E-10	0.94	4.47	-	963.3
AHQ-10-4, 3885	R.NDASHLLVFTTDAK.T	1532.67977	3	1.43E-10	0.96	4.82	-	1805.4
AHQ-10-6, 3792	R.NDASHLLVFTTDAK.T	1532.67977	2	5.39E-09	0.96	4.72	-	1240.7
AHQ-10-7, 3766	R.NDASHLLVFTTDAK.T	1532.67977	2	1.40E-06	0.95	3.95	-	1314.3
AHQ-10-3, 4202 - 4263	R.NDASHLLVFTTDAK.T	1532.67977	2	3.69E-10	0.95	4.18	-	1243.6
AHQ-10-6, 3443	K.SFTIKPVGFK.D	1124.35685	2	1.15E-04	0.85	2.61	-	1232.8
AHQ-10-4, 3496	K.SFTIKPVGFK.D	1124.35685	2	7.84E-06	0.84	2.82	-	1116.7
AHQ-10-4, 4249 - 4252	K.SILYVVEEPECPK.G	1564.78173	2	6.03E-05	0.84	3.46	-	631.2
AHQ-10-3, 2791 - 2865	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.72E-10	0.94	4.08	-	1408.7
AHQ-10-3, 3461 - 3525	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.03E-08	0.87	3.21	-	966.2
AHQ-10-3, 2946	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	2.29E-05	0.91	3.60	-	1127.1
AHQ-10-4, 2776 - 2855	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.45E-09	0.93	3.78	-	1151.8
AHQ-10-5, 2777	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.18E-08	0.93	3.51	-	1184.4
AHQ-10-4, 2937	R.TDTCM*SSNGLLCSGR.G	1677.81726	2	1.05E-08	0.94	3.87	-	1468.6
AHQ-10-4, 3480 - 3552	R.TDTCMSSNGLLCSGR.G	1661.81786	2	1.03E-08	0.81	2.88	-	950.7
AHQ-10-4, 3340 - 3401	R.TDTCMSSNGLLCSGR.G	1661.81786	2	2.37E-06	0.58	3.00	-	752.0
AHQ-10-3, 2103	R.VLEDRPLSDK.G	1172.31354	2	2.05E-06	0.90	3.47	-	958.3
AHQ-10-4, 2061 - 2079	R.VLEDRPLSDK.G	1172.31354	2	1.01E-04	0.90	3.28	-	969.1
AHQ-10-4, 2813	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	3.84E-08	0.93	4.89	-	1136.4
AHQ-10-9, 2679	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	2.77E-04	0.86	3.51	-	1131.4
AHQ-10-5, 2825	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	3.78E-09	0.92	4.27	-	1253.1
AHQ-10-3, 2837	R.VLEDRPLSDKGSGDSSQVTQVSPQR.I	2686.87396	3	4.81E-13	0.93	4.68	-	1208.2
AHQ-10-3, 3329	K.WDTANNPLYK.E	1222.33111	2	3.86E-04	0.76	2.74	-	760.1
AHQ-10-3, 3471 - 3530	K.YCECDDFSCVR.Y	1514.59674	2	6.79E-07	0.97	4.61	-	1300.1
AHQ-10-7, 3476	K.YCECDDFSCVR.Y	1514.59674	2	4.72E-05	0.93	3.42	-	1078.5
AHQ-10-4, 3487 - 3556	K.YCECDDFSCVR.Y	1514.59674	2	1.24E-04	0.92	3.74	-	828.4
AHQ-10-2, 3596	K.YCECDDFSCVR.Y	1514.59674	2	2.11E-06	0.91	3.14	-	1077.6
AHQ-10-4, 2376	R.YCRDEIESVK.E	1300.42023	2	8.84E-06	0.94	3.73	-	1615.9
AHQ-10-3, 2399	R.YCRDEIESVK.E	1300.42023	2	2.33E-05	0.83	3.14	-	804.4
gi|4505879|ref|NP_002655.1| pleckstrin; p47 [Homo sapiens]				6.51E-13	5.73	60.39	22.60	40082.5
AHQ-10-8, 5391	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.83E-12	0.98	6.37	-	2260.7
AHQ-10-12, 5284	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	1.68E-05	0.92	4.13	-	1680.9
AHQ-10-11, 5262	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	9.57E-05	0.94	5.07	-	1027.7
AHQ-10-13-, 5332	R.EDPAYLHYYDPAGAEDPLGAIHLR.G	2684.89982	3	2.99E-07	0.97	5.45	-	1788.2
AHQ-10-8, 2461	R.GCVVTSVESNSNGR.K	1467.54464	2	1.54E-04	0.94	3.66	-	1553.4
AHQ-10-8, 6446 - 6453	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	8.04E-08	0.98	7.76	-	2739.4
AHQ-10-10, 6235	R.KSEEENLFEIITADEVHYFLQAATPK.E	3024.32650	3	1.18E-06	0.94	4.72	-	1222.6
AHQ-10-8, 6061	R.LPETIDLGALYLSMK.D	1664.98779	2	2.40E-04	0.96	3.90	-	1895.0
AHQ-10-8, 5443 - 5514	R.LPETIDLGALYLSM*K.D	1680.98719	2	2.02E-05	0.95	4.72	-	1030.3
AHQ-10-10, 6272	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.40E-05	0.84	3.61	-	853.5
AHQ-10-11, 6304	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	1.47E-06	0.73	3.47	-	558.6
AHQ-10-8, 6489	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	2	1.09E-04	0.74	3.62	-	450.1
AHQ-10-8, 6486	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	6.51E-13	0.92	4.32	-	1242.5
AHQ-10-9, 6061 - 6190	K.SEEENLFEIITADEVHYFLQAATPK.E	2896.15359	3	6.08E-06	0.68	3.36	-	472.6

gi|4502303|ref|NP_001688.1| mitochondrial ATP synthase, O subunit; ATP synthase, H+ transporting, m				7.64E-13	3.69	40.26	30.00	23277.2
AHQ-10-11, 6148	R.FSPLTTNLINLLAENGR.L	1874.13050	2	1.09E-08	0.92	4.06	-	1168.4
AHQ-10-11, 5167 - 5222	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	7.01E-07	0.88	4.12	-	593.7
AHQ-10-11, 5219	R.GEVPCTVTSASPLEEATLSELK.T	2320.55669	2	7.64E-13	0.94	5.16	-	947.0
AHQ-10-11, 3654	K.LVRPPVQVYGIEGR.Y	1583.85942	3	7.25E-05	0.93	4.05	-	1369.0
AHQ-10-11, 3326 - 3330	K.VAASVLNPYVK.R	1161.37549	2	1.19E-07	0.90	3.72	-	707.6
gi|30151108|ref|XP_301187.1| similar to actin beta, cytoskeletal - Kenyan clawed frog [Homo sapiens				9.05E-13	2.39	30.30	13.10	32164.8
AHQ-10-2, 4788	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.01E-05	0.91	4.44	-	643.0
AHQ-10-3, 4705 - 4706	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.70E-04	0.95	4.95	-	828.0
AHQ-10-4, 4752	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.53E-05	0.93	4.27	-	932.5
AHQ-10-5, 4735	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.30E-06	0.95	5.18	-	829.8
AHQ-10-6, 4651	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.48E-05	0.93	4.56	-	731.8
AHQ-10-14-, 5078 - 5096	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.23E-04	0.71	3.61	-	385.6
AHQ-10-8, 4502 - 4561	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.50E-10	0.94	4.69	-	896.3
AHQ-10-8, 4621 - 4694	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	8.17E-05	0.94	4.86	-	1011.5
AHQ-10-8, 4745 - 4809	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.59E-05	0.96	5.34	-	1180.5
AHQ-10-8, 4754	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.75E-04	0.94	4.58	-	955.0
AHQ-10-8, 4869 - 4930	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.70E-06	0.97	6.00	-	1196.3
AHQ-10-8, 4911 - 4985	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.47E-09	0.97	5.75	-	1472.9
AHQ-10-8, 5009 - 5070	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	8.38E-04	0.94	4.89	-	790.6
AHQ-10-8, 5125 - 5186	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	1.52E-06	0.96	5.54	-	851.0
AHQ-10-8, 5253 - 5309	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.73E-06	0.96	5.16	-	979.4
AHQ-10-8, 5365	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	9.76E-05	0.94	4.59	-	890.6
AHQ-10-9, 4431 - 4435	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	6.01E-05	0.96	5.46	-	1115.4
AHQ-10-9, 4605	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.30E-04	0.85	3.36	-	692.7
AHQ-10-9, 4704	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.49E-08	0.86	3.70	-	619.3
AHQ-10-10, 4358 - 4414	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.50E-04	0.78	3.49	-	592.5
AHQ-10-10, 4480 - 4518	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.26E-04	0.70	3.33	-	521.2
AHQ-10-10, 4680 - 4755	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.44E-05	0.75	3.65	-	494.5
AHQ-10-11, 4578	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.01E-04	0.94	4.15	-	1104.5
AHQ-10-13, 4931 - 4987	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	1.39E-06	0.97	5.65	-	1066.9
AHQ-10-13, 5149	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	7.11E-07	0.95	4.49	-	1164.0
AHQ-10-13, 5244	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	2.63E-05	0.72	3.04	-	583.4
AHQ-10-14, 5203 - 5284	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.87E-08	0.94	4.94	-	905.7
AHQ-10-14, 5327 - 5340	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	4.37E-04	0.96	5.32	-	992.4
AHQ-10-14, 5443	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.16E-05	0.88	3.76	-	678.6
AHQ-10-13-, 4501 - 4536	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	5.94E-08	0.93	4.50	-	873.4
AHQ-10-13-, 4594 - 4652	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.17E-05	0.95	4.90	-	905.8
AHQ-10-13-, 4808	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	3.61E-07	0.96	5.34	-	1031.7
AHQ-10-13-, 4912 - 4980	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	4.17E-07	0.96	4.89	-	1145.0
AHQ-10-13-, 5217	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	3.53E-05	0.90	3.85	-	843.4
AHQ-10-14-, 4489 - 4548	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.05E-13	0.95	5.22	-	1072.0
AHQ-10-14-, 4602 - 4660	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	2.17E-04	0.92	4.56	-	673.7
AHQ-10-14-, 4774 - 4836	K.DLYANTVLSGGTTM*YPGIADR.M	2232.45624	2	9.59E-07	0.97	5.67	-	1150.3
AHQ-10-14-, 4864 - 4928	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.49E-08	0.96	5.44	-	1086.1
AHQ-10-14-, 5046 - 5104	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	7.57E-05	0.96	5.54	-	857.7
AHQ-10-14-, 5232 - 5236	K.DLYANTVLSGGTTMYPGIADR.M	2216.45684	2	6.71E-06	0.95	5.02	-	866.0
AHQ-10-8, 4275 - 4337	K.YPIEHSIITNWDDM*EK.I	2008.19724	2	2.08E-06	0.47	2.68	-	513.6
gi|4501881|ref|NP_001091.1| alpha 1 actin precursor; alpha skeletal muscle actin [Homo sapiens] [MA				1.02E-12	10.37	130.27	27.60	42050.8
AHQ-10-8, 1906 - 1965	K.AGFAGDDAPR.A	977.01283	2	6.66E-06	0.91	3.65	-	1026.9
AHQ-10-8, 3174 - 3233	R.AVFPSIVGRPR.H	1199.43018	2	6.30E-04	0.72	3.18	-	480.6
AHQ-10-10, 4098	R.DLTDYLMK.I	999.16326	2	5.75E-04	0.32	2.52	-	248.2
AHQ-10-8, 4174 - 4234	R.DLTDYLMK.I	999.16326	2	2.85E-04	0.75	2.92	-	369.2
AHQ-10-9, 3421	R.DLTDYLM*K.I	1015.16266	1	9.26E-04	0.28	2.73	-	120.9
AHQ-10-9, 4008	R.DLTDYLMK.I	999.16326	1	3.83E-04	0.45	2.31	-	655.4
AHQ-10-8, 4175 - 4305	R.DLTDYLMK.I	999.16326	1	3.34E-04	0.70	3.04	-	626.2
AHQ-10-8, 1938 - 2003	K.DSYVGDEAQSK.R	1199.20634	2	1.09E-04	0.87	2.83	-	729.2
AHQ-10-8, 1817 - 1873	K.DSYVGDEAQSK.R	1199.20634	2	2.64E-05	0.69	2.84	-	676.1
AHQ-10-8, 1757 - 1815	K.DSYVGDEAQSK.R	1199.20634	1	7.19E-04	0.48	3.14	-	373.2
AHQ-10-8, 1586 - 1641	K.DSYVGDEAQSK.R	1199.20634	2	2.77E-05	0.82	3.16	-	643.6
AHQ-10-8, 1697 - 1762	K.DSYVGDEAQSK.R	1199.20634	2	3.92E-06	0.84	3.33	-	642.8
AHQ-10-10, 2900 - 2958	K.EITALAPSTMK.I	1162.38206	2	8.81E-04	0.80	2.98	-	562.7
AHQ-10-11, 2474 - 2475	K.EITALAPSTM*K.I	1178.38146	2	5.14E-05	0.64	2.77	-	485.7
AHQ-10-11, 2932 - 3000	K.EITALAPSTMK.I	1162.38206	2	3.10E-05	0.80	2.86	-	682.1
AHQ-10-10, 2955	K.EITALAPSTMK.I	1162.38206	1	8.48E-05	0.51	2.23	-	369.6
AHQ-10-8, 2002 - 2063	R.HQGVMVGMGQK.D	1172.40691	2	4.67E-04	0.91	3.34	-	776.1
AHQ-10-8, 1870 - 1941	R.HQGVMVGMGQK.D	1172.40691	2	9.21E-05	0.88	3.32	-	620.8
AHQ-10-8, 2997 - 3054	K.IWHHTFYNELR.V	1516.68695	2	1.75E-06	0.84	3.77	-	888.1
AHQ-10-8, 3113 - 3169	K.IWHHTFYNELR.V	1516.68695	2	1.56E-04	0.81	3.49	-	788.8
AHQ-10-8, 3117 - 3173	K.IWHHTFYNELR.V	1516.68695	3	8.41E-05	0.91	4.53	-	1332.4
AHQ-10-9, 3003	K.IWHHTFYNELR.V	1516.68695	3	1.10E-05	0.91	3.99	-	1597.8
AHQ-10-8, 3333 - 3389	K.IWHHTFYNELR.V	1516.68695	2	9.27E-04	0.78	2.80	-	1112.2
AHQ-10-10, 3139 - 3168	K.IWHHTFYNELR.V	1516.68695	3	2.36E-05	0.67	3.20	-	965.9
AHQ-10-13, 5156 - 5211	K.SYELPDGQVITIGNER.F	1791.93998	2	8.47E-06	0.74	3.26	-	499.7
AHQ-10-13, 5031 - 5044	K.SYELPDGQVITIGNER.F	1791.93998	2	5.52E-08	0.85	3.68	-	586.0
AHQ-10-12, 4770 - 4829	K.SYELPDGQVITIGNER.F	1791.93998	2	2.52E-05	0.73	2.78	-	545.9
AHQ-10-12, 4661 - 4662	K.SYELPDGQVITIGNER.F	1791.93998	2	1.39E-05	0.94	4.45	-	1017.5
AHQ-10-6, 4671 - 4719	K.SYELPDGQVITIGNER.F	1791.93998	2	4.51E-04	0.75	2.94	-	643.9
AHQ-10-5, 4895 - 4921	K.SYELPDGQVITIGNER.F	1791.93998	2	5.53E-08	0.95	4.07	-	1242.0
AHQ-10-8, 4215 - 4294	K.SYELPDGQVITIGNER.F	1791.93998	2	5.72E-12	0.96	4.90	-	875.0
AHQ-10-8, 4323 - 4381	K.SYELPDGQVITIGNER.F	1791.93998	2	1.39E-09	0.94	4.10	-	965.3
AHQ-10-12, 4336	K.SYELPDGQVITIGNER.F	1791.93998	2	1.69E-05	0.92	3.61	-	950.5
AHQ-10-8, 4370	K.SYELPDGQVITIGNER.F	1791.93998	3	2.73E-10	0.94	4.60	-	1229.7
AHQ-10-11, 4706	K.SYELPDGQVITIGNER.F	1791.93998	2	7.40E-12	0.96	4.03	-	1309.5
AHQ-10-11, 4586 - 4652	K.SYELPDGQVITIGNER.F	1791.93998	2	9.56E-05	0.91	3.46	-	874.8
AHQ-10-13-, 4688	K.SYELPDGQVITIGNER.F	1791.93998	2	4.40E-06	0.91	3.72	-	780.9
AHQ-10-13-, 4816	K.SYELPDGQVITIGNER.F	1791.93998	2	2.63E-09	0.88	3.72	-	614.7
AHQ-10-8, 4602 - 4661	K.SYELPDGQVITIGNER.F	1791.93998	2	7.10E-11	0.94	4.17	-	1064.1
AHQ-10-8, 4646 - 4662	K.SYELPDGQVITIGNER.F	1791.93998	3	1.32E-08	0.94	4.44	-	1172.0
AHQ-10-8, 4725 - 4787	K.SYELPDGQVITIGNER.F	1791.93998	2	1.02E-12	0.97	5.34	-	1209.1
AHQ-10-8, 4845 - 4905	K.SYELPDGQVITIGNER.F	1791.93998	2	1.34E-12	0.97	5.00	-	1343.5
AHQ-10-11, 4200 - 4282	K.SYELPDGQVITIGNER.F	1791.93998	2	3.30E-09	0.95	4.52	-	1045.6
AHQ-10-8, 4858	K.SYELPDGQVITIGNER.F	1791.93998	3	1.62E-09	0.86	3.59	-	1090.7
AHQ-10-8, 4945 - 5006	K.SYELPDGQVITIGNER.F	1791.93998	2	1.39E-05	0.95	4.35	-	948.4
AHQ-10-7, 4666 - 4670	K.SYELPDGQVITIGNER.F	1791.93998	2	1.41E-06	0.92	4.10	-	826.5
AHQ-10-5, 4681 - 4747	K.SYELPDGQVITIGNER.F	1791.93998	2	2.93E-08	0.88	3.58	-	845.4
AHQ-10-5, 4413	K.SYELPDGQVITIGNER.F	1791.93998	2	6.17E-09	0.91	3.23	-	1065.5
AHQ-10-9, 4051 - 4109	K.SYELPDGQVITIGNER.F	1791.93998	2	7.72E-06	0.89	3.70	-	789.3
AHQ-10-4, 4437	K.SYELPDGQVITIGNER.F	1791.93998	2	5.09E-09	0.78	3.04	-	625.3
AHQ-10-9, 4417 - 4461	K.SYELPDGQVITIGNER.F	1791.93998	2	1.70E-11	0.97	5.43	-	1388.7
AHQ-10-9, 4455	K.SYELPDGQVITIGNER.F	1791.93998	3	3.15E-08	0.94	4.16	-	1487.6
AHQ-10-9, 4567 - 4639	K.SYELPDGQVITIGNER.F	1791.93998	2	1.02E-10	0.96	5.25	-	1012.3
AHQ-10-3, 4739	K.SYELPDGQVITIGNER.F	1791.93998	3	2.59E-04	0.88	4.10	-	1033.3
AHQ-10-3, 4721	K.SYELPDGQVITIGNER.F	1791.93998	2	7.26E-04	0.79	3.19	-	637.4
AHQ-10-8, 4437 - 4441	K.SYELPDGQVITIGNER.F	1791.93998	2	3.64E-11	0.95	4.16	-	1131.8
AHQ-10-2, 4824	K.SYELPDGQVITIGNER.F	1791.93998	2	3.43E-06	0.96	4.70	-	1101.6
AHQ-10-1, 4870 - 4873	K.SYELPDGQVITIGNER.F	1791.93998	2	1.33E-07	0.93	4.13	-	986.9

AHQ-10-10, 4514 - 4570	K.SYELPDGQVITIGNER.F	1791.93998	2	1.46E-12	0.96	4.89	-	1148.2
AHQ-10-10, 4540 - 4548	K.SYELPDGQVITIGNER.F	1791.93998	3	1.48E-07	0.93	4.19	-	1348.9
AHQ-10-10, 4647 - 4690	K.SYELPDGQVITIGNER.F	1791.93998	2	7.26E-09	0.95	4.24	-	997.1
AHQ-10-8, 3729 - 3789	R.VAPEEHPTLLTEAPLNPK.A	1957.21627	2	1.47E-05	0.90	4.72	-	531.8
AHQ-10-9, 4079 - 4147	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.11E-04	0.81	3.81	-	748.6
AHQ-10-8, 4849	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.08E-04	0.78	3.66	-	471.0
AHQ-10-11, 4279	K.YPIEHGIITNWDDMEK.I	1962.17174	3	1.21E-04	0.76	3.78	-	812.1
AHQ-10-8, 4429 - 4434	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	6.65E-04	0.51	2.99	-	455.1
AHQ-10-8, 4405 - 4406	K.YPIEHGIITNWDDMEK.I	1962.17174	3	1.62E-04	0.86	4.46	-	771.0
AHQ-10-8, 4362 - 4421	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.07E-06	0.93	4.61	-	762.5
AHQ-10-8, 4142 - 4201	K.YPIEHGIITNWDDMEK.I	1962.17174	2	5.19E-04	0.89	4.05	-	909.0
AHQ-10-8, 4079	K.YPIEHGIITNWDDM*EK.I	1978.17114	3	7.04E-04	0.73	3.30	-	1118.4
AHQ-10-8, 4057	K.YPIEHGIITNWDDMEK.I	1962.17174	2	1.56E-05	0.91	4.20	-	921.7
AHQ-10-8, 4029 - 4110	K.YPIEHGIITNWDDM*EK.I	1978.17114	2	5.47E-04	0.91	4.07	-	805.4
AHQ-10-10, 4164 - 4235	K.YPIEHGIITNWDDMEK.I	1962.17174	2	3.47E-05	0.67	3.20	-	599.2
AHQ-10-8, 4553	K.YPIEHGIITNWDDMEK.I	1962.17174	2	2.35E-04	0.86	3.93	-	572.0
gi|13775198|ref|NP_112576.1|	SH3 domain binding glutamic acid-rich protein like 3; SH3BGRL3-like pr			2.38E-12	2.55	30.26	31.20	10437.7
AHQ-10-14-, 4529	R.IQYQLVDISQDNALR.D	1776.97168	2	4.29E-12	0.97	4.75	-	1739.5
AHQ-10-13, 4863 - 4933	R.IQYQLVDISQDNALR.D	1776.97168	2	5.38E-11	0.96	4.59	-	1509.3
AHQ-10-14, 5263	R.IQYQLVDISQDNALR.D	1776.97168	2	7.06E-06	0.91	3.70	-	1137.5
AHQ-10-13-, 4524 - 4596	R.IQYQLVDISQDNALR.D	1776.97168	2	2.38E-12	0.97	5.11	-	1568.4
AHQ-10-13-, 4157 - 4160	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	2.37E-05	0.85	3.51	-	845.0
AHQ-10-13-, 4270	R.IQYQLVDISQDNALRDEM*R.A	2324.55691	3	7.70E-06	0.65	3.06	-	431.2
AHQ-10-13-, 1993 - 2061	R.VYSTSVTGSR.E	1057.13940	2	9.23E-05	0.80	2.94	-	829.0
AHQ-10-13-, 1861 - 1920	R.VYSTSVTGSR.E	1057.13940	2	1.40E-05	0.93	3.52	-	1210.5
AHQ-10-13-, 1746 - 1805	R.VYSTSVTGSR.E	1057.13940	2	7.39E-05	0.90	2.90	-	1070.5
AHQ-10-13, 2280 - 2335	R.VYSTSVTGSR.E	1057.13940	2	2.80E-04	0.87	3.05	-	931.7
gi|30148492|ref|XP_293610.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			2.38E-12	2.78	30.28	4.30	72113.4
AHQ-10-6, 2955	R.FDDAVVQSDMK.H	1255.37968	2	2.15E-07	0.90	3.14	-	1036.1
AHQ-10-6, 4532 - 4533	R.IINEPTAAAIAYGLDK.K	1660.89259	2	1.09E-09	0.94	5.55	-	1045.0
AHQ-10-6, 4221	R.IINEPTAAAIAYGLDKK.V	1789.06550	2	2.38E-12	0.94	4.11	-	942.3
gi|18860900|ref|NP_002834.2|	protein tyrosine phosphatase, receptor type, J precursor; protein tyro			3.49E-12	6.56	80.26	9.00	145926.2
AHQ-10-1, 5481	K.AVSISPTNVILTWK.S	1529.80530	2	4.55E-05	0.60	2.57	-	422.5
AHQ-10-1, 4315	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	3	2.90E-07	0.94	3.97	-	1549.8
AHQ-10-1, 4246 - 4321	K.AYAVILTTGEAGHPSADVLK.Y	2014.26782	2	3.17E-07	0.97	5.12	-	1799.6
AHQ-10-1, 3166	K.GDPLGTEGGLDASNTER.S	1689.71978	2	3.49E-12	0.77	2.74	-	786.3
AHQ-10-1, 4958	K.GLIDGAESYVSFSR.Y	1501.62253	2	1.14E-04	0.94	3.46	-	1618.5
AHQ-10-1, 5114	K.SPDGASEYVYHLVIESK.H	1895.05866	2	7.84E-04	0.77	3.21	-	688.2
AHQ-10-1, 5111	K.SPDGASEYVYHLVIESK.H	1895.05866	3	4.03E-07	0.95	4.39	-	1571.5
AHQ-10-1, 4423	R.VENFEAYFK.K	1147.26100	2	1.54E-05	0.78	3.34	-	529.3
AHQ-10-1, 4233	K.VITEPIPVSDLR.V	1339.56259	2	7.86E-06	0.73	2.87	-	450.6
AHQ-10-1, 3870 - 3938	R.VLLESIGSHEELTQDSR.L	1914.06352	2	3.11E-05	0.84	3.53	-	687.1
AHQ-10-1, 3883	R.VLLESIGSHEELTQDSR.L	1914.06352	3	4.22E-04	0.85	3.69	-	910.0
gi|4502295|ref|NP_001677.1|	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypepti			3.58E-12	7.82	90.35	26.50	57955.2
AHQ-10-7, 5232 - 5293	R.AIAELGIYPAVDPLDSTSR.I	1989.21513	2	6.50E-04	0.86	3.94	-	441.4
AHQ-10-7, 5345	R.FLSQPFQVAEVFTGHM*GK.L	2040.33044	3	1.31E-05	0.71	3.02	-	677.2
AHQ-10-7, 4329	R.FTQAGSEVSALLGR.I	1436.59522	2	8.65E-09	0.93	4.12	-	909.5
AHQ-10-7, 6294 - 6296	K.GFQQILAGEYDHLPEQAFYM*VGPIEEAVAK.A	3368.75991	3	3.58E-12	0.97	6.97	-	1408.0
AHQ-10-7, 3590	R.IMDPNIVGSEHYDVAR.G	1817.01617	2	2.28E-04	0.80	3.02	-	658.7
AHQ-10-7, 4092	R.LVLEVAQHLGESTVR.T	1651.88893	2	1.85E-07	0.95	3.69	-	1384.0
AHQ-10-7, 4100	R.LVLEVAQHLGESTVR.T	1651.88893	3	9.22E-09	0.89	3.61	-	725.4
AHQ-10-7, 5413	R.VALTGLTVAEYFR.D	1440.66861	2	2.88E-05	0.90	3.57	-	1004.0
AHQ-10-7, 3445	K.VALVYGQMNQPPGAR.A	1601.85511	2	5.27E-06	0.89	3.66	-	765.9
AHQ-10-7, 4509	K.VLDSGAPIKIPVGPETLGR.I	1920.24231	2	8.37E-09	0.88	3.58	-	506.5
gi|4504349|ref|NP_000509.1|	beta globin [Homo sapiens]			3.92E-12	7.54	90.31	64.60	15998.3
AHQ-10-14-, 3180 - 3198	K.EFTPPVQAAYQK.V	1379.54213	2	1.77E-04	0.89	3.58	-	874.1
AHQ-10-13-, 3202	K.EFTPPVQAAYQK.V	1379.54213	1	1.91E-04	0.16	2.22	-	168.0
AHQ-10-13-, 5113	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	4.73E-05	0.90	3.73	-	761.2
AHQ-10-13-, 4900	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	6.15E-04	0.90	4.51	-	576.4
AHQ-10-13, 5139	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	2.21E-05	0.96	4.41	-	1932.3
AHQ-10-13, 5231 - 5276	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.72E-04	0.93	4.34	-	782.3
AHQ-10-13-, 4798	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	3	7.66E-06	0.88	4.03	-	1033.8
AHQ-10-13, 5023 - 5089	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	7.67E-04	0.90	4.05	-	684.1
AHQ-10-13-, 4788 - 4844	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.05E-06	0.90	4.49	-	594.0
AHQ-10-14, 5467 - 5471	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	4.32E-05	0.88	3.59	-	632.7
AHQ-10-13-, 5388	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	4.94E-08	0.91	3.88	-	851.6
AHQ-10-14-, 4814 - 4882	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.93E-06	0.91	4.65	-	578.2
AHQ-10-14-, 4797	R.FFESFGDLSTPDAVM*GNPK.V	2076.27158	2	1.45E-05	0.50	2.90	-	410.9
AHQ-10-13, 5583 - 5589	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	7.05E-07	0.86	3.54	-	662.9
AHQ-10-14-, 5313	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	1.23E-05	0.87	3.21	-	774.3
AHQ-10-13-, 5288	R.FFESFGDLSTPDAVMGNPK.V	2060.27218	2	2.59E-08	0.94	4.71	-	862.4
AHQ-10-13-, 3617	K.GTFATLSELHCDK.L	1480.62492	2	1.82E-06	0.84	3.30	-	735.0
AHQ-10-13-, 4822 - 4824	K.GTFATLSELHCDKLHVDPENFR.L	2588.83687	3	1.06E-09	0.94	4.61	-	1258.7
AHQ-10-13-, 4469 - 4470	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	3.79E-09	0.97	6.13	-	2026.0
AHQ-10-13-, 4668	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	1.78E-09	0.97	5.67	-	1699.8
AHQ-10-13-, 4670	K.KVLGAFSDGLAHLDNLK.G	1799.06362	2	1.21E-05	0.97	5.17	-	1261.7
AHQ-10-13, 5033	K.KVLGAFSDGLAHLDNLK.G	1799.06362	3	2.53E-07	0.94	4.62	-	1122.9
AHQ-10-13, 5252	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	3.13E-09	0.95	4.44	-	1478.8
AHQ-10-13-, 4550	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	1.19E-11	0.93	4.47	-	1202.9
AHQ-10-13, 5111	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	6.85E-06	0.90	3.51	-	1010.2
AHQ-10-13-, 4945 - 5002	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	3.92E-12	0.98	5.76	-	2003.9
AHQ-10-13-, 5104	K.VLGAFSDGLAHLDNLK.G	1670.89071	3	1.87E-04	0.80	3.34	-	526.0
AHQ-10-14-, 4954	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	3.12E-10	0.96	4.65	-	1364.8
AHQ-10-13-, 4776	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	2.09E-10	0.97	5.06	-	1679.7
AHQ-10-14, 5623	K.VLGAFSDGLAHLDNLK.G	1670.89071	2	7.36E-07	0.74	2.57	-	760.3
AHQ-10-13-, 3264 - 3326	K.VNVDEVGGEALGR.L	1315.41484	2	9.71E-05	0.98	4.48	-	2511.1
AHQ-10-14-, 3249	K.VNVDEVGGEALGR.L	1315.41484	2	5.28E-06	0.97	4.46	-	2212.2
AHQ-10-6, 3236	K.VNVDEVGGEALGR.L	1315.41484	2	9.74E-05	0.94	4.00	-	1149.0
AHQ-10-14, 3991 - 3993	K.VNVDEVGGEALGR.L	1315.41484	2	8.22E-04	0.91	3.77	-	974.6
AHQ-10-13-, 3274	K.VNVDEVGGEALGR.L	1315.41484	1	3.38E-07	0.14	1.83	-	290.0
AHQ-10-13-, 2186 - 2244	K.VVAGVANALAHK.Y	1150.35593	2	5.59E-05	0.85	2.74	-	1074.3
AHQ-10-13-, 2506 - 2584	K.VVAGVANALAHK.Y	1150.35593	2	4.24E-05	0.94	3.29	-	1448.2
gi|17318569|ref|NP_006112.2|	keratin 1; Keratin-1; cytokeratin 1; hair alpha protein [Homo sapiens]			4.19E-12	18.75	220.26	39.00	66066.3
AHQ-10-7, 2125	K.AEAESLYQSK.Y	1126.19850	2	9.94E-04	0.75	2.91	-	577.4
AHQ-10-6, 2111 - 2112	K.AEAESLYQSK.Y	1126.19850	2	6.99E-05	0.83	2.81	-	838.4
AHQ-10-14-, 2118	K.AQYEDIAQK.S	1066.14629	2	6.90E-05	0.66	2.55	-	496.3
AHQ-10-7, 2092 - 2162	K.AQYEDIAQK.S	1066.14629	2	8.96E-05	0.69	2.56	-	453.0
AHQ-10-6, 2080	K.AQYEDIAQK.S	1066.14629	2	8.75E-05	0.48	2.64	-	358.8
AHQ-10-7, 2246	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	5.56E-04	0.75	3.39	-	545.1
AHQ-10-5, 2236	R.GGGGGGYGSGGSSYGSGGGSYGSGGGGGGGR.G	2385.27982	2	4.51E-07	0.31	2.67	-	272.5
AHQ-10-14-, 2577	R.GSYGSGGSSYGSGGGSYGSGGGGGGHGSYGSGSSSGGYR.G	3314.18235	3	9.81E-07	0.91	4.82	-	1293.2
AHQ-10-1, 5055	K.LALDLEIATYR.T	1278.47925	2	5.33E-09	0.97	4.26	-	2088.4
AHQ-10-1, 4023	K.LNDLEDALQQAK.E	1358.47963	2	3.91E-08	0.97	4.93	-	1724.0
AHQ-10-6, 3764 - 3823	K.LNDLEDALQQAK.E	1358.47963	2	1.01E-05	0.97	4.73	-	1911.1
AHQ-10-5, 3827 - 3887	K.LNDLEDALQQAK.E	1358.47963	2	1.73E-07	0.98	5.07	-	2325.4
AHQ-10-3, 3865	K.LNDLEDALQQAK.E	1358.47963	2	3.93E-06	0.96	4.70	-	1616.7
AHQ-10-4, 3905	K.LNDLEDALQQAK.E	1358.47963	2	1.64E-08	0.95	4.17	-	1496.0

AHQ-10-14-, 3852	K.LNDLEDALQQAK.E	1358.47963	2	1.85E-05	0.97	5.24	-	1953.5
AHQ-10-14, 4672	K.LNDLEDALQQAK.E	1358.47963	2	2.51E-04	0.90	2.83	-	1918.2
AHQ-10-11, 3776	K.LNDLEDALQQAK.E	1358.47963	2	2.76E-05	0.98	4.74	-	2665.9
AHQ-10-13-, 3880	K.LNDLEDALQQAK.E	1358.47963	2	1.72E-06	0.96	4.55	-	1819.5
AHQ-10-2, 3946 - 3947	K.LNDLEDALQQAK.E	1358.47963	2	1.83E-05	0.95	4.07	-	1666.5
AHQ-10-2, 4378	K.NKLNDLEDALQQAK.E	1600.75564	2	1.75E-06	0.96	4.43	-	1720.8
AHQ-10-13, 4613	K.NKLNDLEDALQQAK.E	1600.75564	2	1.15E-04	0.89	3.61	-	761.5
AHQ-10-13-, 4272 - 4281	K.NKLNDLEDALQQAK.E	1600.75564	2	4.80E-07	0.95	3.90	-	1548.8
AHQ-10-3, 4293	K.NKLNDLEDALQQAK.E	1600.75564	2	4.13E-04	0.95	4.54	-	1208.8
AHQ-10-5, 4296	K.NKLNDLEDALQQAK.E	1600.75564	2	4.31E-10	0.97	4.54	-	2027.1
AHQ-10-1, 4425 - 4441	K.NKLNDLEDALQQAK.E	1600.75564	2	1.57E-05	0.91	3.45	-	1249.4
AHQ-10-3, 4298	K.NKLNDLEDALQQAK.E	1600.75564	3	1.16E-06	0.97	4.94	-	2316.5
AHQ-10-5, 2843 - 2903	K.NMQDM*VEDYR.N	1317.43134	2	8.85E-06	0.92	3.55	-	940.6
AHQ-10-3, 2914 - 2937	K.NMQDM*VEDYR.N	1317.43134	2	5.82E-04	0.84	3.01	-	799.3
AHQ-10-11, 2795 - 2855	K.NMQDM*VEDYR.N	1317.43134	2	7.18E-04	0.91	3.36	-	1116.9
AHQ-10-3, 3641 - 3673	K.QISNLQQSISDAEQR.G	1717.81950	2	8.84E-07	0.93	4.29	-	781.9
AHQ-10-6, 3605	K.QISNLQQSISDAEQR.G	1717.81950	2	1.45E-05	0.85	3.35	-	626.3
AHQ-10-5, 3667	K.QISNLQQSISDAEQR.G	1717.81950	2	8.64E-07	0.88	3.70	-	643.3
AHQ-10-8, 3611	K.QISNLQQSISDAEQR.G	1717.81950	2	5.20E-07	0.84	3.58	-	724.1
AHQ-10-1, 3826	K.QISNLQQSISDAEQR.G	1717.81950	2	6.31E-05	0.88	3.66	-	762.3
AHQ-10-7, 3601	K.QISNLQQSISDAEQR.G	1717.81950	2	1.07E-07	0.82	3.30	-	688.0
AHQ-10-14-, 3653	K.QISNLQQSISDAEQR.G	1717.81950	2	6.83E-06	0.95	4.27	-	1194.7
AHQ-10-11, 3578 - 3583	K.QISNLQQSISDAEQR.G	1717.81950	2	5.24E-07	0.88	4.07	-	594.5
AHQ-10-2, 3744	K.QISNLQQSISDAEQR.G	1717.81950	2	2.24E-05	0.79	3.24	-	579.3
AHQ-10-14-, 3441 - 3521	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	7.57E-05	0.87	3.38	-	1073.4
AHQ-10-1, 3689	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	4.95E-05	0.80	2.84	-	1027.9
AHQ-10-5, 3515	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	2.03E-07	0.91	3.55	-	1227.1
AHQ-10-11, 3438	R.SGGGFSSGSAGIINYQR.R	1658.75374	2	8.70E-05	0.81	2.60	-	1139.4
AHQ-10-13-, 2045	K.SKAEAESLYQSK.Y	1341.44907	2	1.36E-05	0.92	3.20	-	1151.6
AHQ-10-5, 1952 - 1959	K.SKAEAESLYQSK.Y	1341.44907	2	4.53E-07	0.91	3.41	-	961.4
AHQ-10-2, 2088	K.SKAEAESLYQSK.Y	1341.44907	2	1.05E-08	0.92	3.75	-	829.9
AHQ-10-3, 2058 - 2063	K.SKAEAESLYQSK.Y	1341.44907	2	1.85E-08	0.93	3.61	-	1048.8
AHQ-10-6, 2005	K.SKAEAESLYQSK.Y	1341.44907	2	6.12E-08	0.91	3.60	-	926.7
AHQ-10-7, 1962 - 2028	K.SKAEAESLYQSK.Y	1341.44907	2	1.24E-08	0.86	3.63	-	612.2
AHQ-10-5, 4016	K.SKAEAESLYQSKYEELQITAGR.H	2502.71900	3	4.19E-12	0.94	5.08	-	1030.2
AHQ-10-3, 4005	K.SKAEAESLYQSKYEELQITAGR.H	2502.71900	3	3.89E-08	0.92	4.26	-	1186.6
AHQ-10-9, 5360 - 5431	R.SLDLDSIIAEVK.A	1303.48388	2	4.86E-06	0.93	3.69	-	1140.5
AHQ-10-10, 5514	R.SLDLDSIIAEVK.A	1303.48388	2	5.54E-05	0.90	2.92	-	1245.4
AHQ-10-8, 5717	R.SLDLDSIIAEVK.A	1303.48388	2	2.13E-07	0.94	3.75	-	1332.9
AHQ-10-7, 5656	R.SLDLDSIIAEVK.A	1303.48388	2	9.12E-07	0.94	4.04	-	1400.3
AHQ-10-2, 5782 - 5858	R.SLDLDSIIAEVK.A	1303.48388	2	9.40E-08	0.96	4.70	-	1233.7
AHQ-10-13, 5923 - 5924	R.SLDLDSIIAEVK.A	1303.48388	2	8.45E-07	0.97	5.14	-	1799.9
AHQ-10-6, 5639 - 5651	R.SLDLDSIIAEVK.A	1303.48388	2	2.42E-06	0.96	4.84	-	1194.6
AHQ-10-11, 5558 - 5580	R.SLDLDSIIAEVK.A	1303.48388	2	1.33E-06	0.94	3.83	-	1320.2
AHQ-10-7, 4444	K.SLNNQFASFIDK.V	1384.51877	2	1.35E-05	0.88	3.20	-	933.7
AHQ-10-4, 4592 - 4609	K.SLNNQFASFIDK.V	1384.51877	2	5.22E-05	0.91	3.86	-	860.8
AHQ-10-13-, 4525 - 4532	K.SLNNQFASFIDK.V	1384.51877	2	2.24E-07	0.88	3.57	-	675.1
AHQ-10-1, 4902	K.SLNNQFASFIDK.V	1384.51877	2	5.96E-06	0.86	3.42	-	729.4
AHQ-10-1, 4657 - 4702	K.SLNNQFASFIDK.V	1384.51877	2	1.82E-06	0.92	4.05	-	834.3
AHQ-10-1, 4498	K.SLNNQFASFIDK.V	1384.51877	2	4.38E-04	0.73	2.93	-	646.7
AHQ-10-11, 4400	K.SLNNQFASFIDK.V	1384.51877	2	2.39E-05	0.79	3.06	-	647.3
AHQ-10-14-, 4510	K.SLNNQFASFIDK.V	1384.51877	2	1.77E-04	0.64	2.66	-	606.8
AHQ-10-8, 4487	K.SLNNQFASFIDK.V	1384.51877	2	1.62E-06	0.88	3.69	-	692.9
AHQ-10-3, 5126	K.SLNNQFASFIDKVR.F	1639.83670	3	9.55E-05	0.85	3.22	-	911.0
AHQ-10-3, 5122	K.SLNNQFASFIDKVR.F	1639.83670	2	1.27E-07	0.73	3.09	-	507.8
AHQ-10-3, 2514 - 2519	R.SLVNLGGSK.S	875.00510	1	7.80E-04	0.17	2.26	-	228.7
AHQ-10-5, 2473	R.SLVNLGGSK.S	875.00510	2	6.38E-04	0.66	2.65	-	484.4
AHQ-10-1, 4322	R.SLVNLGGSKSISISVAR.G	1688.95071	2	6.18E-04	0.81	3.32	-	608.2
AHQ-10-3, 4175 - 4191	R.SLVNLGGSKSISISVAR.G	1688.95071	2	2.11E-11	0.86	3.44	-	718.6
AHQ-10-1, 5490	R.THNLEPYFESFINNLR.R	1995.18315	3	4.26E-04	0.61	3.13	-	551.3
AHQ-10-1, 5487	R.THNLEPYFESFINNLR.R	1995.18315	2	5.65E-05	0.67	2.80	-	408.6
AHQ-10-13-, 6024 - 6049	R.THNLEPYFESFINNLR.R	1995.18315	3	9.11E-04	0.88	4.03	-	1009.6
AHQ-10-6, 6016 - 6017	R.THNLEPYFESFINNLR.R	1995.18315	3	1.84E-04	0.95	5.18	-	1425.7
AHQ-10-2, 6155 - 6215	R.THNLEPYFESFINNLR.R	1995.18315	2	2.96E-04	0.81	3.50	-	449.1
AHQ-10-1, 6209 - 6265	R.THNLEPYFESFINNLR.R	1995.18315	3	8.92E-06	0.90	4.39	-	1204.6
AHQ-10-3, 6085	R.THNLEPYFESFINNLR.R	1995.18315	3	4.29E-06	0.94	4.71	-	1416.0
AHQ-10-8, 6109	R.THNLEPYFESFINNLR.R	1995.18315	3	7.23E-06	0.94	4.63	-	1437.5
AHQ-10-5, 6143	R.THNLEPYFESFINNLR.R	1995.18315	3	1.48E-04	0.93	4.52	-	1559.0
AHQ-10-4, 3195	R.TNAENEFVTIK.K	1266.38219	2	2.53E-05	0.93	3.70	-	995.4
AHQ-10-2, 3260	R.TNAENEFVTIK.K	1266.38219	2	4.48E-06	0.92	3.39	-	1027.1
AHQ-10-1, 3381 - 3390	R.TNAENEFVTIK.K	1266.38219	2	1.53E-05	0.95	3.73	-	1237.4
AHQ-10-10, 3103	R.TNAENEFVTIK.K	1266.38219	2	1.99E-05	0.85	3.45	-	605.0
AHQ-10-13-, 3213	R.TNAENEFVTIK.K	1266.38219	2	3.19E-05	0.92	3.06	-	1309.3
AHQ-10-7, 3258 - 3325	R.TNAENEFVTIK.K	1266.38219	2	6.00E-04	0.87	2.88	-	1046.3
AHQ-10-8, 3066	R.TNAENEFVTIK.K	1266.38219	2	5.23E-07	0.85	3.04	-	816.4
AHQ-10-6, 3136	R.TNAENEFVTIK.K	1266.38219	2	1.76E-05	0.93	3.49	-	1097.5
AHQ-10-5, 3167 - 3173	R.TNAENEFVTIK.K	1266.38219	2	7.44E-05	0.93	3.62	-	1029.9
AHQ-10-3, 3193 - 3213	R.TNAENEFVTIK.K	1266.38219	2	1.26E-04	0.94	3.65	-	1136.2
AHQ-10-7, 3106	R.TNAENEFVTIK.K	1266.38219	2	1.50E-04	0.84	3.03	-	734.4
AHQ-10-13-, 2752	R.TNAENEFVTIKK.D	1394.55511	2	1.02E-04	0.92	3.57	-	1100.4
AHQ-10-5, 2699	R.TNAENEFVTIKK.D	1394.55511	2	1.10E-07	0.90	3.38	-	1075.2
AHQ-10-3, 2726	R.TNAENEFVTIKK.D	1394.55511	2	4.08E-06	0.78	2.70	-	986.8
AHQ-10-6, 4321 - 4379	K.WELLQQVDTSTR.T	1476.61621	2	7.12E-08	0.93	3.33	-	1662.4
AHQ-10-1, 4530	K.WELLQQVDTSTR.T	1476.61621	2	2.56E-08	0.96	3.84	-	2094.7
AHQ-10-7, 4214 - 4296	K.WELLQQVDTSTR.T	1476.61621	2	1.89E-08	0.93	4.33	-	1041.2
AHQ-10-3, 4393 - 4454	K.WELLQQVDTSTR.T	1476.61621	2	5.29E-07	0.96	4.17	-	1802.4
AHQ-10-14, 5127 - 5196	K.WELLQQVDTSTR.T	1476.61621	2	6.88E-05	0.79	2.81	-	934.0
AHQ-10-2, 4468 - 4530	K.WELLQQVDTSTR.T	1476.61621	2	1.20E-05	0.93	4.03	-	1386.2
AHQ-10-11, 4266 - 4326	K.WELLQQVDTSTR.T	1476.61621	2	5.30E-05	0.83	3.24	-	939.1
AHQ-10-10, 4232	K.WELLQQVDTSTR.T	1476.61621	2	1.49E-05	0.74	2.75	-	844.0
AHQ-10-8, 4307 - 4377	K.WELLQQVDTSTR.T	1476.61621	2	6.42E-06	0.74	3.23	-	791.6
AHQ-10-5, 4396 - 4475	K.WELLQQVDTSTR.T	1476.61621	2	6.31E-07	0.89	3.66	-	1162.4
AHQ-10-7, 2972	K.YEELQITAGR.H	1180.29253	2	2.66E-05	0.96	3.78	-	2149.1
AHQ-10-6, 2992	K.YEELQITAGR.H	1180.29253	2	2.17E-04	0.95	3.78	-	1979.8
AHQ-10-13, 3479	K.YEELQITAGR.H	1180.29253	2	3.20E-05	0.96	4.23	-	2036.7
AHQ-10-3, 3041	K.YEELQITAGR.H	1180.29253	2	5.02E-07	0.94	4.23	-	1448.2
AHQ-10-11, 2986	K.YEELQITAGR.H	1180.29253	2	4.91E-04	0.93	3.54	-	1539.1
AHQ-10-4, 3039	K.YEELQITAGR.H	1180.29253	2	1.47E-04	0.95	3.56	-	1775.0
AHQ-10-1, 3233	K.YEELQITAGR.H	1180.29253	2	1.71E-05	0.96	4.21	-	1775.3
AHQ-10-2, 3100	K.YEELQITAGR.H	1180.29253	2	8.20E-04	0.95	3.90	-	1572.8
gi|4505981|ref|NP_002695.1| pro-platelet basic protein (includes platelet basic protein, bet; Pro-p				4.38E-12	7.85	90.31	53.90	13894.1
AHQ-10-13-, 4564 - 4581	K.EESLDSDLYAELR.C	1540.61070	2	6.05E-07	0.75	2.79	-	755.6
AHQ-10-14, 5280 - 5349	K.EESLDSDLYAELR.C	1540.61070	2	1.18E-06	0.87	3.59	-	700.0
AHQ-10-14-, 4254 - 4325	K.EESLDSDLYAELR.C	1540.61070	2	4.13E-07	0.75	3.03	-	473.9
AHQ-10-14-, 4520 - 4576	K.EESLDSDLYAELR.C	1540.61070	2	4.04E-08	0.95	4.19	-	1315.4
AHQ-10-13, 4519 - 4521	K.GKEESLDSDLYAELR.C	1725.83517	3	7.22E-04	0.81	3.95	-	694.8
AHQ-10-14-, 4485	K.GKEESLDSDLYAELR.C	1725.83517	2	8.48E-09	0.97	5.27	-	1816.0

AHQ-10-13, 4515 - 4517	K.GKEESLDSDLYAELR.C	1725.83517	2	1.09E-09	0.98	6.26	-	2606.0
AHQ-10-14-, 4246	K.GKEESLDSDLYAELR.C	1725.83517	2	1.15E-06	0.97	5.06	-	1880.2
AHQ-10-14-, 4120 - 4190	K.GKEESLDSDLYAELR.C	1725.83517	2	9.26E-11	0.98	6.08	-	2476.8
AHQ-10-14-, 3996 - 4064	K.GKEESLDSDLYAELR.C	1725.83517	2	6.88E-12	0.98	5.67	-	2604.1
AHQ-10-14-, 3885 - 3941	K.GKEESLDSDLYAELR.C	1725.83517	3	1.06E-04	0.92	4.42	-	1068.8
AHQ-10-9, 3928 - 3952	K.GKEESLDSDLYAELR.C	1725.83517	2	1.63E-06	0.98	5.29	-	2168.8
AHQ-10-14, 4635 - 4692	K.GKEESLDSDLYAELR.C	1725.83517	2	2.50E-05	0.97	4.92	-	1419.1
AHQ-10-14-, 3884 - 3946	K.GKEESLDSDLYAELR.C	1725.83517	2	4.38E-12	0.98	5.49	-	2074.2
AHQ-10-14, 4751 - 4807	K.GKEESLDSDLYAELR.C	1725.83517	2	3.21E-05	0.95	4.81	-	1276.8
AHQ-10-14-, 3757 - 3830	K.GKEESLDSDLYAELR.C	1725.83517	2	6.02E-08	0.97	5.25	-	1681.0
AHQ-10-14, 4948 - 5023	K.GKEESLDSDLYAELR.C	1725.83517	2	4.13E-08	0.98	5.21	-	2254.4
AHQ-10-14, 4956 - 4960	K.GKEESLDSDLYAELR.C	1725.83517	3	3.37E-04	0.91	4.21	-	1086.5
AHQ-10-14, 5080 - 5143	K.GKEESLDSDLYAELR.C	1725.83517	2	2.32E-08	0.97	4.82	-	1979.5
AHQ-10-14, 5181	K.GKEESLDSDLYAELR.C	1725.83517	2	2.88E-05	0.80	3.10	-	770.5
AHQ-10-14, 5269 - 5275	K.GKEESLDSDLYAELR.C	1725.83517	2	2.48E-08	0.98	5.10	-	2433.5
AHQ-10-14, 4633 - 4695	K.GKEESLDSDLYAELR.C	1725.83517	2	4.54E-11	0.98	5.50	-	1753.6
AHQ-10-14, 5824 - 5885	K.GKEESLDSDLYAELR.C	1725.83517	2	5.05E-04	0.82	3.30	-	892.5
AHQ-10-13-, 4188	K.GKEESLDSDLYAELR.C	1725.83517	3	6.49E-07	0.83	3.64	-	850.1
AHQ-10-13-, 4036	K.GKEESLDSDLYAELR.C	1725.83517	2	3.81E-06	0.96	4.14	-	1511.9
AHQ-10-13-, 4166	K.GKEESLDSDLYAELR.C	1725.83517	2	3.17E-09	0.97	4.96	-	2079.1
AHQ-10-14-, 4737	K.GKEESLDSDLYAELR.C	1725.83517	2	3.89E-05	0.79	2.91	-	845.1
AHQ-10-13-, 3448	K.GTHCNQVEVIATLK.D	1571.78073	2	3.92E-08	0.96	3.73	-	1659.0
AHQ-10-14, 4223 - 4279	K.GTHCNQVEVIATLK.D	1571.78073	2	2.13E-08	0.97	4.33	-	1575.4
AHQ-10-14, 4339 - 4396	K.GTHCNQVEVIATLK.D	1571.78073	2	5.57E-06	0.97	4.94	-	1741.1
AHQ-10-14, 4451 - 4508	K.GTHCNQVEVIATLK.D	1571.78073	2	2.54E-05	0.97	4.97	-	1609.3
AHQ-10-14-, 3617	K.GTHCNQVEVIATLK.D	1571.78073	2	2.78E-09	0.97	4.87	-	1573.9
AHQ-10-14-, 3449 - 3504	K.GTHCNQVEVIATLK.D	1571.78073	2	2.06E-10	0.98	5.01	-	2031.3
AHQ-10-14, 4680 - 4744	K.GTHCNQVEVIATLK.D	1571.78073	2	1.73E-04	0.92	2.96	-	1518.6
AHQ-10-14-, 3306 - 3385	K.GTHCNQVEVIATLK.D	1571.78073	2	1.98E-10	0.97	4.51	-	1845.9
AHQ-10-14-, 3137	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	1.30E-05	0.97	5.36	-	1358.3
AHQ-10-14-, 3228	K.GTHCNQVEVIATLKDGR.K	1900.10650	2	9.06E-07	0.97	4.83	-	1549.6
AHQ-10-14-, 3181 - 3242	K.GTHCNQVEVIATLKDGR.K	1900.10650	3	1.24E-04	0.96	4.59	-	1552.3
AHQ-10-14-, 2913 - 2990	K.ICLDPDAPR.I	1058.19059	2	1.98E-05	0.82	2.99	-	923.1
AHQ-10-9, 2792	K.ICLDPDAPR.I	1058.19059	2	1.41E-04	0.79	2.54	-	864.6
AHQ-10-14-, 2672 - 2740	R.KICLDPDAPR.I	1186.36350	2	5.05E-05	0.94	3.68	-	1234.1
AHQ-10-14-, 2801 - 2857	R.KICLDPDAPR.I	1186.36350	2	1.01E-06	0.87	2.94	-	940.9
AHQ-10-14, 3188 - 3235	R.KICLDPDAPR.I	1186.36350	2	5.64E-05	0.80	3.24	-	696.0
AHQ-10-14, 3403 - 3435	R.KICLDPDAPR.I	1186.36350	2	8.45E-05	0.92	3.39	-	1059.0
AHQ-10-14, 1400 - 1467	K.KLAGDESAD	905.92969	1	6.09E-05	0.51	2.15	-	478.4
AHQ-10-14-, 3693	K.NIQSLEVIGK.G	1101.27845	1	2.59E-04	0.42	2.58	-	428.5
AHQ-10-14, 4187 - 4251	K.NIQSLEVIGK.G	1101.27845	2	6.41E-07	0.89	3.79	-	735.7
AHQ-10-14-, 4062	K.NIQSLEVIGK.G	1101.27845	1	5.75E-05	0.57	2.14	-	694.2
AHQ-10-14, 4893	K.NIQSLEVIGK.G	1101.27845	1	1.68E-04	0.24	2.09	-	430.7
AHQ-10-14-, 3684 - 3698	K.NIQSLEVIGK.G	1101.27845	2	6.81E-06	0.89	2.62	-	1288.0
AHQ-10-14-, 3642	K.TTSGIHPKNIQSLEVIGK.G	1923.20305	2	2.21E-07	0.80	3.75	-	459.8
AHQ-10-14-, 3641	K.TTSGIHPKNIQSLEVIGK.G	1923.20305	3	4.10E-09	0.89	4.49	-	841.2
gi|6681259|ref|NP_031377.1| multimerin [Homo sapiens]				5.63E-12	16.77	200.30	21.20	138070.8
AHQ-10-3, 2466	R.AQEQQSLIHTNQAESHTAVGR.G	2306.43830	2	1.38E-06	0.95	4.75	-	883.7
AHQ-10-3, 5786	K.CTSDM*ETILTFIPQFHR.L	2114.38778	3	8.28E-05	0.73	3.33	-	644.8
AHQ-10-3, 3843 - 3905	R.DQALQLQVLNSR.F	1385.55144	2	1.71E-08	0.97	4.88	-	1632.8
AHQ-10-3, 4027 - 4050	R.DQALQLQVLNSR.F	1385.55144	2	6.34E-07	0.94	3.67	-	1470.3
AHQ-10-4, 3945	R.DQALQLQVLNSR.F	1385.55144	2	5.52E-06	0.85	3.60	-	931.7
AHQ-10-4, 5509	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	2.60E-05	0.91	4.04	-	1036.0
AHQ-10-2, 5522	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.97E-07	0.89	4.14	-	846.9
AHQ-10-3, 5426 - 5491	K.FVLVQENRPTLTDIVELR.N	2143.47187	3	1.20E-10	0.93	4.32	-	1119.2
AHQ-10-3, 5433	K.FVLVQENRPTLTDIVELR.N	2143.47187	2	2.07E-06	0.86	4.29	-	508.0
AHQ-10-5, 5680	K.GLTEFVEPIIQIK.T	1487.76518	2	1.42E-05	0.87	3.43	-	895.5
AHQ-10-3, 5601	K.GLTEFVEPIIQIK.T	1487.76518	2	1.47E-07	0.95	4.24	-	1169.0
AHQ-10-4, 5687 - 5688	K.GLTEFVEPIIQIK.T	1487.76518	2	2.05E-04	0.90	3.46	-	1053.5
AHQ-10-2, 5703	K.GLTEFVEPIIQIK.T	1487.76518	2	2.01E-05	0.80	2.88	-	797.3
AHQ-10-3, 2694	K.GPCGWTGGSCPQR.S	1422.52885	2	9.27E-04	0.88	3.20	-	936.5
AHQ-10-3, 3821 - 3883	K.HSLPDIQLLQK.G	1292.50915	2	4.68E-05	0.87	3.32	-	697.6
AHQ-10-4, 3843 - 3861	K.HSLPDIQLLQK.G	1292.50915	2	3.56E-05	0.81	2.90	-	691.9
AHQ-10-3, 5486	K.IENLTSAVNSLNFIIK.E	1777.05472	2	2.09E-04	0.83	3.77	-	599.3
AHQ-10-3, 6063 - 6073	K.IENLTSAVNSLNFIIK.E	1777.05472	2	3.55E-06	0.95	4.48	-	1151.9
AHQ-10-4, 6047	K.IFQNDMQETVAQLFK.T	1813.06743	2	3.42E-07	0.91	3.75	-	996.2
AHQ-10-10, 5075	R.IPYLGVYVFK.Y	1199.46532	2	4.70E-06	0.90	3.45	-	886.4
AHQ-10-3, 5673	K.KIENLTSAVNSLNFIIK.E	1905.22764	2	8.85E-05	0.94	4.44	-	943.3
AHQ-10-3, 5162	K.KIENLTSAVNSLNFIIK.E	1905.22764	2	5.98E-07	0.81	3.15	-	881.3
AHQ-10-10, 3718	K.LAFESENINSEIHCDR.V	1936.04933	2	4.72E-04	0.72	2.56	-	705.9
AHQ-10-5, 2948	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	3	5.81E-06	0.97	5.21	-	2248.6
AHQ-10-3, 2954	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	2	2.01E-07	0.98	6.02	-	1657.7
AHQ-10-3, 2901 - 2961	K.LKEVHEQLLSTEQVSDQK.N	2112.32666	3	5.63E-12	0.97	5.31	-	2397.2
AHQ-10-2, 3802	K.LVEENALAPDFSK.G	1433.58810	2	1.13E-04	0.93	3.82	-	853.6
AHQ-10-3, 2427	K.M*TDQVNYQAMK.L	1345.52783	2	1.07E-07	0.92	3.76	-	1187.1
AHQ-10-3, 2263	K.QTHLEGALEQEHSR.S	1635.72018	2	1.69E-05	0.70	2.72	-	422.8
AHQ-10-3, 6313	K.TM*TIINNAIDFIQDNYALK.E	2215.51196	3	1.36E-06	0.71	3.02	-	692.5
AHQ-10-3, 5694 - 5770	K.TM*TIINNAIDFIQDNYALK.E	2215.51196	2	2.65E-04	0.83	3.84	-	437.0
AHQ-10-4, 3461	K.TVSSLSEDLESTR.Q	1424.49324	2	1.15E-04	0.85	2.97	-	997.8
AHQ-10-6, 3387	K.TVSSLSEDLESTR.Q	1424.49324	2	9.55E-04	0.85	2.94	-	916.9
AHQ-10-5, 3432	K.TVSSLSEDLESTR.Q	1424.49324	2	7.06E-06	0.67	2.80	-	689.5
AHQ-10-2, 3508	K.TVSSLSEDLESTR.Q	1424.49324	2	3.06E-05	0.77	3.13	-	571.6
AHQ-10-3, 4907	K.VTQTLIPYYISVK.K	1525.81342	2	1.16E-04	0.45	2.76	-	268.8
AHQ-10-2, 4064	R.YNFVLQVAK.T	1082.27683	2	4.58E-06	0.81	2.66	-	669.8
AHQ-10-3, 3977	R.YNFVLQVAK.T	1082.27683	2	1.87E-06	0.91	3.26	-	871.9
gi|4826898|ref|NP_005013.1| profilin 1; profilin-1 [Homo sapiens]				5.73E-12	14.31	160.26	67.10	15054.2
AHQ-10-13-, 1882 - 1941	K.CYEM*ASHLR.R	1184.32794	2	1.03E-05	0.88	2.78	-	1254.7
AHQ-10-13-, 2524 - 2590	K.CYEMASHLR.R	1168.32854	2	4.87E-05	0.94	2.73	-	1922.6
AHQ-10-13-, 1790 - 1857	K.CYEM*ASHLR.R	1184.32794	2	6.50E-04	0.86	3.11	-	1129.8
AHQ-10-13, 2459 - 2508	K.CYEM*ASHLR.R	1184.32794	2	1.37E-05	0.81	2.64	-	1081.5
AHQ-10-13-, 4153	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	5.73E-12	0.96	4.97	-	1050.1
AHQ-10-13-, 4012	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	3.15E-09	0.94	4.84	-	748.9
AHQ-10-13, 4375	K.DRSSFYVNGLTLGGQK.C	1742.91379	2	1.11E-06	0.96	4.38	-	1219.1
AHQ-10-13-, 4861 - 4864	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.09E-04	0.94	3.82	-	1296.1
AHQ-10-13-, 4305 - 4360	R.DSLLQDGEFSM*DLR.T	1642.76963	2	3.16E-08	0.94	4.03	-	1103.0
AHQ-10-13-, 5074 - 5146	R.DSLLQDGEFSMDLR.T	1626.77023	2	4.19E-09	0.98	5.14	-	2032.5
AHQ-10-13-, 4960 - 5016	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.67E-05	0.97	4.15	-	2257.1
AHQ-10-14-, 4470 - 4484	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.00E-07	0.97	4.23	-	1956.2
AHQ-10-13-, 4608 - 4682	R.DSLLQDGEFSM*DLR.T	1642.76963	2	2.77E-07	0.94	3.61	-	1715.1
AHQ-10-12, 5057 - 5113	R.DSLLQDGEFSMDLR.T	1626.77023	2	7.36E-08	0.93	3.30	-	1400.8
AHQ-10-12, 4413 - 4469	R.DSLLQDGEFSM*DLR.T	1642.76963	2	8.23E-07	0.93	3.78	-	1246.4
AHQ-10-13, 4680 - 4736	R.DSLLQDGEFSM*DLR.T	1642.76963	2	9.36E-05	0.87	2.96	-	1083.8
AHQ-10-13-, 4428 - 4484	R.DSLLQDGEFSM*DLR.T	1642.76963	2	6.69E-09	0.96	3.93	-	1775.5
AHQ-10-13, 4700	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.96E-09	0.95	4.50	-	1141.1
AHQ-10-14, 5232	R.DSLLQDGEFSM*DLR.T	1642.76963	2	1.73E-04	0.81	2.87	-	1005.1
AHQ-10-13, 4788 - 4847	R.DSLLQDGEFSM*DLR.T	1642.76963	2	4.55E-09	0.97	4.68	-	2038.0
AHQ-10-13, 4903 - 4972	R.DSLLQDGEFSM*DLR.T	1642.76963	2	7.08E-04	0.89	3.61	-	1095.9

AHQ-10-13, 5377 - 5452	R.DSLLQDGEFSMDLR.T	1626.77023	2	2.76E-09	0.97	4.61	-	2175.3
AHQ-10-13, 5507 - 5563	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.27E-05	0.97	4.05	-	2556.1
AHQ-10-14-, 4976 - 4978	R.DSLLQDGEFSMDLR.T	1626.77023	2	1.41E-04	0.89	3.04	-	1093.3
AHQ-10-13, 3979 - 4056	K.DSPSVWAAVPGK.T	1214.35211	2	4.89E-05	0.85	2.93	-	1035.1
AHQ-10-13-, 3565 - 3624	K.DSPSVWAAVPGK.T	1214.35211	2	2.85E-04	0.93	3.58	-	1133.3
AHQ-10-13-, 6076	K.DSPSVWAAVPGKTFVNITPAEVGVLVGK.D	2840.26581	3	2.23E-05	0.92	3.73	-	1723.1
AHQ-10-13, 4712 - 4777	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.50E-07	0.64	2.75	-	460.3
AHQ-10-13, 4692 - 4747	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.05E-09	0.96	4.33	-	1511.3
AHQ-10-13, 4588	R.SSFYVNGLTLGGQK.C	1471.63957	1	3.33E-09	0.27	2.29	-	433.7
AHQ-10-13, 4575 - 4641	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.44E-08	0.94	4.11	-	916.1
AHQ-10-13-, 4218 - 4280	R.SSFYVNGLTLGGQK.C	1471.63957	2	2.76E-07	0.95	4.48	-	1056.8
AHQ-10-13-, 4352 - 4420	R.SSFYVNGLTLGGQK.C	1471.63957	1	2.23E-09	0.63	2.70	-	491.1
AHQ-10-13-, 4224	R.SSFYVNGLTLGGQK.C	1471.63957	1	6.83E-08	0.54	2.42	-	510.4
AHQ-10-14-, 4229	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.18E-08	0.86	3.05	-	782.7
AHQ-10-13-, 4330 - 4388	R.SSFYVNGLTLGGQK.C	1471.63957	2	1.24E-04	0.90	3.38	-	834.5
AHQ-10-13, 3453 - 3511	K.STGGAPTFNVTVTK.T	1380.52843	2	1.38E-08	0.87	3.45	-	532.7
AHQ-10-13-, 3168 - 3238	K.STGGAPTFNVTVTK.T	1380.52843	2	1.62E-08	0.86	3.55	-	500.2
AHQ-10-13, 3581 - 3649	K.STGGAPTFNVTVTK.T	1380.52843	2	2.72E-05	0.74	2.93	-	397.4
AHQ-10-13-, 3062 - 3120	K.STGGAPTFNVTVTK.T	1380.52843	2	5.88E-07	0.92	4.17	-	529.9
AHQ-10-13, 3695 - 3733	K.STGGAPTFNVTVTK.T	1380.52843	2	5.71E-05	0.78	3.14	-	404.0
AHQ-10-13-, 3169	K.STGGAPTFNVTVTKTDK.T	1724.89354	2	4.66E-05	0.82	3.54	-	508.2
AHQ-10-13, 3460 - 3499	K.TDKTLVLLM*GK.E	1235.51929	2	1.96E-04	0.88	2.87	-	974.0
AHQ-10-13-, 3680 - 3744	K.TDKTLVLLMGK.E	1219.51989	2	1.48E-05	0.91	3.62	-	950.3
AHQ-10-13-, 3040	K.TDKTLVLLM*GK.E	1235.51929	2	8.19E-05	0.86	3.39	-	848.4
AHQ-10-13, 4079 - 4147	K.TDKTLVLLMGK.E	1219.51989	2	1.33E-06	0.94	3.38	-	1481.4
AHQ-10-12, 5374 - 5452	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.36E-04	0.93	4.25	-	717.2
AHQ-10-13, 5663 - 5727	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.33E-05	0.85	3.74	-	604.2
AHQ-10-13, 5783 - 5859	K.TFVNITPAEVGVLVGK.D	1644.93630	2	2.10E-05	0.93	4.43	-	1006.3
AHQ-10-13-, 5508 - 5569	K.TFVNITPAEVGVLVGK.D	1644.93630	2	3.71E-08	0.91	3.94	-	877.9
AHQ-10-12, 5454 - 5456	K.TFVNITPAEVGVLVGK.D	1644.93630	3	1.89E-04	0.75	3.15	-	911.2
AHQ-10-13-, 5396 - 5453	K.TFVNITPAEVGVLVGK.D	1644.93630	2	1.69E-04	0.93	4.61	-	787.8
AHQ-10-13, 5408 - 5455	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	2.90E-04	0.58	3.09	-	472.6
AHQ-10-13, 5512 - 5513	K.TFVNITPAEVGVLVGKDR.S	1916.21052	3	9.91E-08	0.80	3.59	-	687.7
AHQ-10-13-, 5176 - 5234	K.TFVNITPAEVGVLVGKDR.S	1916.21052	2	1.24E-08	0.93	4.74	-	638.9
AHQ-10-13-, 2934 - 2957	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	5.69E-05	0.86	3.53	-	670.1
AHQ-10-13, 3320	R.TKSTGGAPTFNVTVTK.T	1609.80568	2	6.91E-04	0.71	2.92	-	489.8
AHQ-10-13-, 3808 - 3837	K.TLVLLMGK.E	875.15478	2	3.80E-05	0.65	2.64	-	489.5
gi|4507357|ref|NP_003555.1| transgelin 2; SM22-alpha homolog [Homo sapiens]				7.64E-12	11.59	130.27	53.30	22391.3
AHQ-10-11, 5271 - 5331	R.DDGLFSGDPNWFPK.K	1595.69288	2	8.36E-06	0.94	3.71	-	1290.2
AHQ-10-11, 5498 - 5568	R.DDGLFSGDPNWFPK.K	1595.69288	2	6.25E-06	0.87	3.93	-	718.2
AHQ-10-14-, 5449 - 5460	R.DDGLFSGDPNWFPK.K	1595.69288	2	7.70E-05	0.94	4.15	-	1071.5
AHQ-10-13-, 5440	R.DDGLFSGDPNWFPK.K	1595.69288	2	1.82E-08	0.96	4.45	-	1426.5
AHQ-10-12, 5362 - 5416	R.DDGLFSGDPNWFPK.K	1595.69288	2	2.39E-04	0.82	3.29	-	827.1
AHQ-10-11, 5386 - 5444	R.DDGLFSGDPNWFPK.K	1595.69288	2	6.85E-05	0.95	3.79	-	1419.6
AHQ-10-11, 4738	R.DDGLFSGDPNWFPKK.S	1723.86579	2	1.83E-05	0.91	4.39	-	677.9
AHQ-10-11, 5720	K.DGTVLCELINALYPEGQAPVK.K	2289.59066	2	2.11E-04	0.90	4.02	-	616.0
AHQ-10-11, 5327 - 5340	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	2	3.02E-06	0.77	3.30	-	468.0
AHQ-10-11, 5491	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	6.72E-08	0.59	3.22	-	414.3
AHQ-10-11, 6219 - 6226	K.DGTVLCELINALYPEGQAPVKK.I	2417.76357	3	5.16E-08	0.91	4.46	-	845.5
AHQ-10-11, 2208 - 2210	R.GASQAGMTGYGM*PR.Q	1400.56672	2	1.29E-05	0.89	3.13	-	1026.6
AHQ-10-11, 1770 - 1771	R.GASQAGM*TGYGM*PR.Q	1416.56612	2	8.31E-04	0.53	2.58	-	589.2
AHQ-10-11, 2310 - 2314	R.GASQAGM*TGYGMPR.Q	1400.56672	2	1.27E-04	0.86	3.39	-	679.9
AHQ-10-11, 2442	K.NVIGLQM*GTNR.G	1219.39691	2	2.23E-06	0.95	3.77	-	1170.1
AHQ-10-11, 2523 - 2532	K.NVIGLQM*GTNR.G	1219.39691	2	4.97E-05	0.90	2.94	-	962.2
AHQ-10-11, 4490	K.QM*EQISQFLQAAER.Y	1695.87890	3	1.97E-06	0.96	4.51	-	2162.0
AHQ-10-11, 5619 - 5699	K.QMEQISQFLQAAER.Y	1679.87950	2	3.69E-05	0.50	2.62	-	489.0
AHQ-10-11, 5090	K.QMEQISQFLQAAER.Y	1679.87950	3	4.04E-07	0.97	5.15	-	2455.4
AHQ-10-11, 5023 - 5078	K.QMEQISQFLQAAER.Y	1679.87950	2	1.55E-08	0.92	3.99	-	994.2
AHQ-10-12, 4409	R.TLMNLGGLAVAR.D	1216.47932	2	3.32E-04	0.73	2.91	-	718.0
AHQ-10-11, 3579 - 3582	R.TLM*NLGGLAVAR.D	1232.47872	2	2.49E-05	0.93	3.83	-	1044.9
AHQ-10-13-, 4440	R.TLMNLGGLAVAR.D	1216.47932	2	1.58E-05	0.69	2.69	-	885.1
AHQ-10-11, 3800 - 3854	R.TLM*NLGGLAVAR.D	1232.47872	2	9.46E-05	0.91	3.60	-	909.8
AHQ-10-11, 4338	R.TLMNLGGLAVAR.D	1216.47932	2	1.22E-06	0.91	3.88	-	1007.5
AHQ-10-11, 6090 - 6162	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	9.52E-11	0.96	5.34	-	1058.2
AHQ-10-14-, 6268	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	1.23E-06	0.81	3.22	-	702.0
AHQ-10-13-, 6225	R.YGINTTDIFQTVDLWEGK.N	2101.30080	2	7.64E-12	0.96	5.15	-	1232.0
gi|5454152|ref|NP_006285.1| ubiquinol-cytochrome c reductase binding protein [Homo sapiens]				8.60E-12	0.82	10.20	13.50	13530.4
AHQ-10-13-, 3522	R.DDTIYEDEDVKEAIR.R	1811.88169	2	8.60E-12	0.82	3.97	-	415.0
gi|4557305|ref|NP_000025.1| aldolase A; fructose-bisphosphate aldolase; Aldolase A, fructose-bispho				9.94E-12	8.44	100.24	41.50	39419.7
AHQ-10-9, 2240	R.ALANSLACQGK.Y	1134.28859	2	2.06E-04	0.60	2.65	-	647.2
AHQ-10-8, 4353 - 4409	R.ALANSLACQGKYTPSGQAGAAASESLFVSNHAY	3344.61352	3	4.34E-08	0.73	3.58	-	496.9
AHQ-10-8, 4390 - 4466	R.ALANSLACQGKYTPSGQAGAAASESLFVSNHAY	3344.61352	3	1.08E-05	0.59	3.22	-	421.7
AHQ-10-8, 4263	K.FSHEEIAMATVTALR.R	1676.91875	2	8.75E-09	0.94	4.03	-	1314.3
AHQ-10-14-, 2988	K.GILAADESTGSIAK.R	1333.47008	2	1.16E-05	0.95	4.06	-	1202.2
AHQ-10-13-, 2942 - 3018	K.GILAADESTGSIAK.R	1333.47008	2	8.18E-07	0.86	3.32	-	784.9
AHQ-10-8, 2874	K.GILAADESTGSIAK.R	1333.47008	1	2.05E-04	0.60	2.74	-	328.8
AHQ-10-8, 2867	K.GILAADESTGSIAK.R	1333.47008	2	9.94E-12	0.97	4.55	-	1495.5
AHQ-10-8, 4089	K.GVVPLAGTNGETTTQGLDGLSER.C	2273.44329	2	8.52E-10	0.88	4.74	-	899.7
AHQ-10-9, 5000	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	1.68E-05	0.87	3.61	-	658.6
AHQ-10-8, 5251	K.IGEHTPSALAIMENANVLAR.Y	2108.40788	2	2.04E-04	0.90	3.94	-	634.9
AHQ-10-8, 5538	R.VNPCIGGVILFHETLYQK.A	2090.43072	2	1.74E-08	0.95	4.68	-	1006.4
AHQ-10-8, 5595 - 5657	R.YASICQQNGIVPIVEPEILPDGDHDLK.R	3023.36334	3	4.66E-05	0.82	4.43	-	475.5
AHQ-10-9, 5047 - 5116	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	2.80E-04	0.75	3.74	-	645.8
AHQ-10-8, 5326 - 5383	R.YASICQQNGIVPIVEPEILPDGDHDLKR.C	3179.54969	3	9.61E-08	0.90	4.81	-	651.2
AHQ-10-8, 4353 - 4409	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	5.84E-09	0.77	3.62	-	519.3
AHQ-10-8, 4130	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	3.31E-04	0.40	2.69	-	330.6
AHQ-10-8, 4390 - 4466	K.YTPSGQAGAAASESLFVSNHAY	2229.34753	2	5.00E-06	0.78	3.59	-	430.5
gi|4504745|ref|NP_000410.1| integrin alpha 2b precursor [Homo sapiens]				1.02E-11	26.51	290.33	34.30	113374.2
AHQ-10-4, 5072 - 5101	R.AEGGQCPSLLFDLR.D	1564.74505	2	4.82E-05	0.90	3.30	-	914.3
AHQ-10-3, 5017 - 5031	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.18E-06	0.95	3.95	-	1225.7
AHQ-10-13-, 5012 - 5014	R.AEGGQCPSLLFDLR.D	1564.74505	2	3.30E-05	0.95	4.38	-	1149.4
AHQ-10-11, 4870	R.AEGGQCPSLLFDLR.D	1564.74505	2	5.11E-04	0.70	2.90	-	528.4
AHQ-10-7, 4937	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.42E-04	0.74	2.62	-	651.2
AHQ-10-5, 5056	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.14E-06	0.92	3.38	-	1048.0
AHQ-10-6, 4956 - 4957	R.AEGGQCPSLLFDLR.D	1564.74505	2	2.83E-06	0.90	4.02	-	738.4
AHQ-10-4, 4652	R.AEGGQCPSLLFDLRDETR.N	2066.23814	3	6.62E-07	0.81	3.58	-	763.8
AHQ-10-6, 2817 - 2892	R.ALSNVEGFER.L	1122.21308	2	6.99E-05	0.89	3.30	-	944.9
AHQ-10-4, 2911	R.ALSNVEGFER.L	1122.21308	2	8.78E-07	0.86	3.28	-	816.8
AHQ-10-4, 3239	R.ALSNVEGFER.L	1122.21308	2	4.02E-05	0.93	3.27	-	1118.2
AHQ-10-5, 2921 - 2927	R.ALSNVEGFER.L	1122.21308	2	3.93E-05	0.83	3.26	-	629.4
AHQ-10-5, 4837 - 4916	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	1.07E-05	0.62	3.08	-	536.3
AHQ-10-6, 4753 - 4755	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	2.41E-04	0.95	4.83	-	1320.4
AHQ-10-4, 4688 - 4724	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	6.90E-04	0.84	3.64	-	720.9
AHQ-10-4, 4867 - 4933	K.ASVQLLVQDSLNPAVK.S	1682.94293	2	6.43E-07	0.92	4.70	-	781.1
AHQ-10-4, 4889	K.ASVQLLVQDSLNPAVK.S	1682.94293	3	2.05E-06	0.95	5.01	-	1461.4
AHQ-10-4, 3104	R.DETRNVGSQTLQTFK.A	1724.85363	2	3.42E-04	0.96	3.81	-	1852.9
AHQ-10-4, 3839	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	8.77E-09	0.86	3.59	-	745.9

AHQ-10-6, 3676	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	2.35E-06	0.84	3.02	-	841.5
AHQ-10-4, 3940	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	4.83E-09	0.92	4.06	-	950.8
AHQ-10-5, 3764	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	3.16E-04	0.72	2.89	-	551.1
AHQ-10-4, 3747 - 3772	R.DGYNDIAVAAPYGGPSGR.G	1780.87574	2	1.39E-09	0.92	4.35	-	779.1
AHQ-10-4, 5317 - 5387	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	6.27E-09	0.93	5.24	-	764.8
AHQ-10-4, 5443 - 5503	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.02E-11	0.95	5.79	-	871.3
AHQ-10-7, 5400	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	9.46E-04	0.43	3.12	-	451.2
AHQ-10-5, 5508	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	1.90E-05	0.49	3.03	-	554.1
AHQ-10-5, 5419 - 5423	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.23E-06	0.88	4.35	-	952.6
AHQ-10-5, 5593	R.FGSAIAPLGDLDRDGYNDIAVAAPYGGPSGR.G	3094.34015	3	4.51E-04	0.57	3.04	-	745.1
AHQ-10-4, 5883 - 5944	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	5.07E-08	0.79	3.57	-	642.5
AHQ-10-4, 5737 - 5792	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	3	1.86E-06	0.88	4.00	-	1090.0
AHQ-10-4, 5664	R.GAVDIDDNGYPDLIVGAYGANQVAVYR.A	2827.05458	2	1.65E-06	0.82	3.42	-	432.9
AHQ-10-1, 5069	R.GEAQVWTQLLR.A	1301.47614	2	2.10E-04	0.92	3.68	-	958.2
AHQ-10-11, 4750	R.GEAQVWTQLLR.A	1301.47614	2	9.23E-07	0.86	3.51	-	848.5
AHQ-10-10, 4688 - 4696	R.GEAQVWTQLLR.A	1301.47614	2	3.37E-06	0.95	4.25	-	1173.3
AHQ-10-4, 5291 - 5315	R.GNSFPASLVVAAEEGER.E	1733.86053	2	6.13E-07	0.91	3.70	-	803.2
AHQ-10-4, 5168 - 5231	R.GNSFPASLVVAAEEGER.E	1733.86053	2	5.71E-10	0.91	4.21	-	743.8
AHQ-10-4, 6179	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	2.27E-08	0.75	3.39	-	366.8
AHQ-10-4, 5848 - 5904	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	4.40E-04	0.65	3.59	-	370.9
AHQ-10-4, 6067 - 6124	R.GNSFPASLVVAAEEGEREQNSLDSWGPK.V	2976.16043	3	1.96E-10	0.92	4.79	-	593.7
AHQ-10-6, 4928	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	8.78E-04	0.87	3.67	-	1295.7
AHQ-10-4, 5044 - 5045	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	1.06E-06	0.97	5.74	-	1197.4
AHQ-10-6, 4939	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	2.50E-09	0.95	4.76	-	935.1
AHQ-10-7, 4900 - 4901	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	7.30E-05	0.97	5.34	-	1046.7
AHQ-10-5, 5009 - 5025	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	3	2.63E-05	0.94	4.56	-	1201.3
AHQ-10-5, 5013	R.GPHALGAPSLLLTGTQLYGR.F	2023.32431	2	4.53E-07	0.97	5.55	-	1086.5
AHQ-10-4, 4853 - 4924	R.GQVLVFLGQSEGLR.S	1503.72793	2	4.23E-09	0.97	4.85	-	1493.8
AHQ-10-5, 4825	R.GQVLVFLGQSEGLR.S	1503.72793	2	1.11E-08	0.96	4.69	-	1417.7
AHQ-10-7, 4737	R.GQVLVFLGQSEGLR.S	1503.72793	2	7.36E-05	0.95	3.69	-	1499.6
AHQ-10-4, 3849	R.HDLLVGAPLYM*ESR.A	1617.85128	2	5.29E-04	0.95	4.10	-	1107.3
AHQ-10-6, 4264 - 4265	K.IVLLDVPVR.A	1024.28196	2	3.08E-04	0.90	3.78	-	781.2
AHQ-10-5, 4356	K.IVLLDVPVR.A	1024.28196	2	1.70E-05	0.85	3.18	-	744.6
AHQ-10-11, 4240	K.IVLLDVPVR.A	1024.28196	2	9.07E-04	0.90	3.53	-	794.2
AHQ-10-4, 4345	K.IVLLDVPVR.A	1024.28196	2	6.51E-04	0.85	2.96	-	741.2
AHQ-10-7, 3809	R.IYVENDFSWDKR.Y	1572.70245	2	2.11E-06	0.79	2.70	-	817.1
AHQ-10-4, 3915	R.IYVENDFSWDKR.Y	1572.70245	3	6.99E-08	0.64	3.08	-	488.1
AHQ-10-4, 4017	R.IYVENDFSWDKR.Y	1572.70245	2	5.45E-10	0.96	4.25	-	1584.8
AHQ-10-4, 4409	K.LSLNAELQLDR.Q	1272.43310	2	4.70E-04	0.95	3.57	-	1675.9
AHQ-10-4, 4091	K.LSLNAELQLDR.Q	1272.43310	2	1.53E-05	0.86	3.28	-	969.9
AHQ-10-4, 4300 - 4313	K.LSLNAELQLDR.Q	1272.43310	2	4.03E-05	0.73	2.88	-	759.7
AHQ-10-6, 2916	R.NVGSQTLQTFK.A	1223.36055	2	2.70E-04	0.86	3.03	-	580.4
AHQ-10-11, 2911 - 2918	R.NVGSQTLQTFK.A	1223.36055	2	8.17E-06	0.92	3.61	-	649.3
AHQ-10-7, 2892 - 2901	R.NVGSQTLQTFK.A	1223.36055	2	4.96E-04	0.88	3.53	-	594.2
AHQ-10-5, 5683	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	8.60E-08	0.94	5.61	-	1095.3
AHQ-10-4, 5472 - 5548	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	2.10E-04	0.97	5.66	-	1987.5
AHQ-10-4, 5683 - 5704	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	1.08E-06	0.92	4.98	-	910.4
AHQ-10-3, 5617	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	6.15E-05	0.91	4.85	-	1031.6
AHQ-10-5, 5460	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	3.27E-05	0.95	4.66	-	1516.6
AHQ-10-6, 5552 - 5567	R.SRPSQVLDSPFPTGSAFGFSLR.G	2354.60606	3	6.58E-05	0.98	6.56	-	1868.4
AHQ-10-4, 3700	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	2	6.71E-08	0.87	4.13	-	415.9
AHQ-10-4, 3695 - 3719	K.TEEAEKTPVGSCFLAQPESGR.R	2295.46902	3	8.48E-07	0.89	4.57	-	805.8
AHQ-10-4, 5224 - 5295	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	8.83E-06	0.90	4.23	-	523.9
AHQ-10-4, 5351 - 5384	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.66E-06	0.96	4.90	-	983.5
AHQ-10-9, 4996	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	1.65E-04	0.70	3.19	-	510.2
AHQ-10-7, 5216 - 5218	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	4.38E-07	0.95	4.79	-	789.8
AHQ-10-6, 5208 - 5257	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	2.10E-06	0.95	5.47	-	696.6
AHQ-10-13-, 5228 - 5240	R.TLGPSQEETGGVFLCPWR.A	2036.25364	2	3.75E-06	0.90	4.15	-	753.3
AHQ-10-5, 3684	K.TPVGSCFLAQPESGR.R	1607.76993	2	2.61E-07	0.90	3.95	-	619.0
AHQ-10-4, 3833	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.74E-05	0.84	3.59	-	843.8
AHQ-10-7, 3573 - 3613	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.12E-04	0.72	3.23	-	453.1
AHQ-10-11, 3570 - 3598	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.35E-05	0.75	2.97	-	593.1
AHQ-10-6, 3619	K.TPVGSCFLAQPESGR.R	1607.76993	2	3.29E-06	0.81	3.14	-	679.6
AHQ-10-4, 3677 - 3699	K.TPVGSCFLAQPESGR.R	1607.76993	2	1.74E-07	0.91	3.86	-	771.7
AHQ-10-4, 4408 - 4411	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	1.78E-04	0.96	4.78	-	2023.3
AHQ-10-5, 4388 - 4393	K.TPVSCFNIQM*CVGATGHNIPQK.L	2478.81062	3	5.64E-04	0.92	4.02	-	1455.0
AHQ-10-4, 2683	R.VAIVVGAPR.T	882.08560	2	6.02E-06	0.94	3.47	-	1381.3
AHQ-10-7, 2657	R.VAIVVGAPR.T	882.08560	2	6.69E-04	0.94	3.27	-	1463.7
AHQ-10-4, 6548	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	1.22E-04	0.88	3.82	-	625.3
AHQ-10-4, 5967 - 6044	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	4.96E-04	0.80	3.65	-	448.0
AHQ-10-4, 5308 - 5367	R.VLLLGSQQAGTTLNLDLGGK.H	1999.29783	2	5.34E-08	0.97	6.19	-	1395.6
AHQ-10-4, 3347	R.VVLCELGNPM*K.K	1277.53632	2	1.32E-05	0.91	3.50	-	1205.1
AHQ-10-4, 4035 - 4052	R.VVLCELGNPMK.K	1261.53692	2	1.69E-06	0.97	4.57	-	1552.8
AHQ-10-6, 3293	R.VVLCELGNPM*K.K	1277.53632	2	3.99E-05	0.84	3.04	-	875.0
AHQ-10-4, 3635 - 3641	R.VVLCELGNPMKK.N	1389.70984	2	7.39E-09	0.89	3.23	-	959.7
AHQ-10-6, 4101	R.VYLFLQPR.G	1036.25129	2	2.97E-04	0.93	3.23	-	1212.3
gi|4503715|ref|NP_000500.1| fibrinogen, gamma chain isoform gamma-A precursor [Homo sapiens]				1.07E-11	16.02	190.30	62.90	49481.2
AHQ-10-7, 4497	K.AIQLTYNPDESSKPNMIDAATLK.S	2521.82886	2	2.89E-04	0.80	4.01	-	475.2
AHQ-10-7, 3933 - 4012	K.AIQLTYNPDESSKPNM*IDAATLK.S	2537.82826	3	2.69E-05	0.68	3.20	-	583.4
AHQ-10-7, 6017 - 6076	K.ANQQFLVYCEIDGSGNGWTVFQK.R	2663.90221	3	3.31E-04	0.54	3.39	-	542.4
AHQ-10-7, 5997 - 6074	K.ANQQFLVYCEIDGSGNGWTVFQK.R	2663.90221	2	1.07E-11	0.91	3.97	-	758.4
AHQ-10-7, 5890 - 5905	K.ANQQFLVYCEIDGSGNGWTVFQK.R	2663.90221	2	5.48E-07	0.89	4.05	-	643.2
AHQ-10-7, 5180 - 5240	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	7.44E-10	0.88	3.55	-	706.3
AHQ-10-13-, 5158	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	9.03E-06	0.85	3.31	-	695.3
AHQ-10-7, 5296 - 5306	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	7.72E-06	0.74	3.06	-	454.3
AHQ-10-14-, 5150 - 5205	K.ASTPNGYDNGIIWATWK.T	1895.06358	2	1.18E-07	0.81	3.29	-	667.1
AHQ-10-7, 2756 - 2825	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	1.26E-08	0.98	5.90	-	1449.6
AHQ-10-9, 2675	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	2	2.06E-04	0.60	2.82	-	328.2
AHQ-10-7, 2690 - 2758	K.CHAGHLNGVYYQGGTYSK.A	2014.16662	3	9.57E-08	0.97	5.03	-	2353.4
AHQ-10-7, 3072 - 3133	R.DNCCILDER.F	1197.27847	2	9.25E-05	0.78	3.01	-	618.7
AHQ-10-9, 2972 - 3036	R.DNCCILDER.F	1197.27847	2	3.18E-05	0.87	3.12	-	853.2
AHQ-10-9, 4783 - 4852	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	3.76E-07	0.92	4.50	-	712.4
AHQ-10-7, 5060	K.EGFGHLSPTGTTEFWLGNEK.I	2208.37146	2	8.80E-04	0.90	4.16	-	710.2
AHQ-10-7, 5904 - 5914	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	4.14E-05	0.70	3.34	-	377.1
AHQ-10-7, 6094 - 6158	R.FGSYCPTTCGIADFLSTYQTK.V	2420.65656	2	6.81E-08	0.86	3.74	-	516.0
AHQ-10-7, 4366 - 4425	K.IHLISTQSAIPYALR.V	1683.97576	2	8.18E-05	0.91	3.56	-	1073.5
AHQ-10-6, 4436	K.IHLISTQSAIPYALR.V	1683.97576	2	6.42E-05	0.74	3.16	-	599.4
AHQ-10-7, 2137	R.LDGSVDFKK.N	1009.13788	2	5.55E-04	0.68	2.59	-	614.2
AHQ-10-14-, 2254	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	6.15E-05	0.57	2.58	-	797.9
AHQ-10-8, 2205	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	4.59E-07	0.69	2.63	-	650.4
AHQ-10-7, 2173 - 2228	R.LTIGEGQQHHLGGAK.Q	1546.71290	2	7.71E-08	0.88	3.69	-	889.4
AHQ-10-7, 5970 - 6037	R.LTYAYFAGGDAGDAFDGFDFGDDPSDK.F	2835.88415	2	3.54E-05	0.86	3.85	-	720.1
AHQ-10-7, 3820	K.QSGLYFIKPLK.A	1294.56665	2	5.79E-05	0.77	3.03	-	394.6
AHQ-10-7, 2337	K.RLDGSVDFK.K	1037.15132	2	1.72E-04	0.81	3.17	-	461.1
AHQ-10-7, 3788	K.VAQLEAQCQEPCKDTVQIHDITGK.D	2772.06211	3	6.14E-06	0.89	4.21	-	710.3
AHQ-10-9, 3811	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	6.30E-04	0.82	3.77	-	835.8
AHQ-10-7, 3902 - 3960	K.VAQLEAQCQEPCKDTVQIHDITGKDCQDIANK.G	3718.05993	3	7.86E-05	0.94	4.93	-	966.5

AHQ-10-7, 3220 - 3276	R.VELEDWNGR.T	1118.18129	2	4.86E-05	0.83	2.94	-	919.4
AHQ-10-7, 3136	R.VELEDWNGR.T	1118.18129	2	1.12E-04	0.84	3.04	-	1007.2
AHQ-10-4, 3139 - 3217	K.YEASILTHDSSIR.Y	1492.61564	2	5.73E-07	0.59	3.15	-	603.4
AHQ-10-7, 3032 - 3100	K.YEASILTHDSSIR.Y	1492.61564	2	1.92E-08	0.81	3.13	-	604.3
AHQ-10-11, 3078	K.YEASILTHDSSIR.Y	1492.61564	2	4.09E-06	0.81	3.04	-	610.1
AHQ-10-8, 2990 - 2999	K.YEASILTHDSSIR.Y	1492.61564	2	2.27E-06	0.89	3.79	-	702.6
AHQ-10-9, 2940 - 2951	K.YEASILTHDSSIR.Y	1492.61564	3	9.67E-05	0.80	3.25	-	694.3
AHQ-10-11, 2759 - 2816	R.YLQEIYNSNNQK.I	1514.62131	2	7.40E-04	0.91	4.04	-	870.2
AHQ-10-9, 2708 - 2721	R.YLQEIYNSNNQK.I	1514.62131	2	2.44E-04	0.91	3.68	-	1284.1
gi|4557703|ref|NP_000414.1| keratin 2a [Homo sapiens]				1.11E-11	17.63	200.31	37.10	65864.9
AHQ-10-7, 2212	K.AQYEEIAQR.S	1108.18640	2	8.30E-05	0.64	2.80	-	664.2
AHQ-10-3, 3466	R.DYQELMNVK.L	1140.29181	2	2.27E-04	0.85	3.27	-	791.4
AHQ-10-6, 6160	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	3.48E-04	0.86	4.46	-	571.2
AHQ-10-4, 6292	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	1.08E-04	0.88	4.34	-	766.9
AHQ-10-3, 6210	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	1.98E-04	0.94	5.59	-	909.1
AHQ-10-7, 6205	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	2.00E-10	0.95	5.54	-	1241.1
AHQ-10-5, 6295	R.FGGFGGPGGVGGLGGPGGFGPGGYPGGIHEVSVNQSLLQPLNVK.V	4094.54151	3	1.58E-04	0.94	5.45	-	878.6
AHQ-10-6, 3016	R.FLEQQNQVLQTK.W	1476.65935	2	6.62E-07	0.97	4.72	-	2231.6
AHQ-10-13, 3455 - 3467	R.FLEQQNQVLQTK.W	1476.65935	2	6.69E-06	0.96	4.36	-	1871.8
AHQ-10-2, 3295	R.FLEQQNQVLQTK.W	1476.65935	2	2.08E-04	0.91	4.22	-	1478.2
AHQ-10-13-, 3073 - 3084	R.FLEQQNQVLQTK.W	1476.65935	2	9.52E-07	0.97	4.73	-	1888.0
AHQ-10-7, 2984 - 3062	R.FLEQQNQVLQTK.W	1476.65935	2	5.48E-08	0.97	4.75	-	2030.7
AHQ-10-12, 3088 - 3100	R.FLEQQNQVLQTK.W	1476.65935	2	4.61E-06	0.96	4.94	-	1649.9
AHQ-10-8, 2973	R.FLEQQNQVLQTK.W	1476.65935	2	5.66E-06	0.96	3.94	-	2081.8
AHQ-10-3, 3065	R.FLEQQNQVLQTK.W	1476.65935	2	1.09E-06	0.97	5.09	-	2063.3
AHQ-10-11, 3156	R.FLEQQNQVLQTK.W	1476.65935	2	6.71E-05	0.92	3.52	-	1259.8
AHQ-10-5, 3048 - 3124	R.FLEQQNQVLQTK.W	1476.65935	2	2.27E-08	0.98	5.55	-	2519.0
AHQ-10-2, 3127	R.FLEQQNQVLQTK.W	1476.65935	2	5.77E-07	0.98	4.66	-	2661.7
AHQ-10-3, 3226	R.FLEQQNQVLQTK.W	1476.65935	2	2.29E-06	0.97	5.03	-	2070.0
AHQ-10-14-, 3048 - 3056	R.FLEQQNQVLQTK.W	1476.65935	2	1.63E-08	0.97	5.12	-	2265.2
AHQ-10-4, 3065 - 3068	R.FLEQQNQVLQTK.W	1476.65935	2	8.47E-08	0.98	6.15	-	2403.9
AHQ-10-5, 3212 - 3221	R.FLEQQNQVLQTK.W	1476.65935	2	2.85E-04	0.94	3.83	-	1611.9
AHQ-10-9, 2891 - 2892	R.FLEQQNQVLQTK.W	1476.65935	2	1.78E-07	0.96	4.98	-	1718.0
AHQ-10-1, 3179 - 3253	R.FLEQQNQVLQTK.W	1476.65935	2	2.51E-06	0.97	4.54	-	2401.5
AHQ-10-3, 2335	R.GFSSGSAVVSGGSR.R	1255.31950	2	1.59E-04	0.95	4.22	-	1321.6
AHQ-10-3, 2247	R.HGGGGGGFGGGGFGSR.S	1321.34296	2	6.04E-06	0.95	4.11	-	1097.4
AHQ-10-5, 2915	K.IEISELNR.V	974.09353	2	1.38E-04	0.78	2.74	-	672.4
AHQ-10-10, 2862	K.IEISELNR.V	974.09353	2	4.34E-04	0.81	2.78	-	759.3
AHQ-10-11, 2878	K.IEISELNR.V	974.09353	2	7.72E-04	0.76	2.83	-	606.2
AHQ-10-7, 4016	K.LNDLEEALQQAK.E	1372.50630	2	1.36E-04	0.96	4.53	-	1554.8
AHQ-10-8, 4039 - 4071	K.LNDLEEALQQAK.E	1372.50630	2	1.91E-06	0.94	3.73	-	1638.0
AHQ-10-3, 4103	K.LNDLEEALQQAK.E	1372.50630	2	2.50E-05	0.97	5.12	-	1674.6
AHQ-10-6, 4043	K.LNDLEEALQQAK.E	1372.50630	2	3.18E-06	0.96	4.94	-	1372.6
AHQ-10-3, 4474	R.NKLNDLEEALQQAK.E	1614.78232	2	1.56E-05	0.93	3.42	-	1373.4
AHQ-10-11, 5556 - 5562	R.NLDLDSIIAEVK.A	1330.50933	2	5.38E-07	0.95	4.24	-	1146.1
AHQ-10-8, 5715	R.NLDLDSIIAEVK.A	1330.50933	2	3.65E-05	0.96	4.67	-	1237.4
AHQ-10-5, 5759	R.NLDLDSIIAEVK.A	1330.50933	2	3.43E-06	0.96	4.70	-	1159.2
AHQ-10-2, 5783	R.NLDLDSIIAEVK.A	1330.50933	2	2.04E-07	0.96	4.57	-	1256.0
AHQ-10-7, 5658 - 5665	R.NLDLDSIIAEVK.A	1330.50933	2	5.58E-07	0.97	4.76	-	1495.9
AHQ-10-13, 5925	R.NLDLDSIIAEVK.A	1330.50933	2	1.59E-06	0.95	4.29	-	1260.2
AHQ-10-4, 5780	R.NLDLDSIIAEVK.A	1330.50933	2	2.76E-06	0.95	4.20	-	1100.9
AHQ-10-13-, 5644 - 5648	R.NLDLDSIIAEVK.A	1330.50933	2	4.23E-06	0.97	5.37	-	1362.6
AHQ-10-3, 5678	R.NLDLDSIIAEVK.A	1330.50933	2	6.44E-08	0.94	4.19	-	1115.8
AHQ-10-14-, 5652	R.NLDLDSIIAEVK.A	1330.50933	2	5.12E-06	0.97	4.75	-	1557.0
AHQ-10-1, 5805	R.NLDLDSIIAEVK.A	1330.50933	2	1.06E-04	0.94	4.16	-	1015.5
AHQ-10-6, 5636 - 5656	R.NLDLDSIIAEVK.A	1330.50933	2	9.26E-07	0.94	4.10	-	1131.4
AHQ-10-9, 5435	R.NLDLDSIIAEVK.A	1330.50933	2	5.18E-04	0.92	3.55	-	1116.3
AHQ-10-14-, 3168	K.NVQDAIADAEQR.G	1330.38637	2	2.85E-08	0.96	4.04	-	1807.9
AHQ-10-6, 3140	K.NVQDAIADAEQR.G	1330.38637	2	1.94E-07	0.94	3.84	-	1468.6
AHQ-10-2, 3246	K.NVQDAIADAEQR.G	1330.38637	2	4.47E-08	0.93	3.93	-	948.5
AHQ-10-7, 3130 - 3204	K.NVQDAIADAEQR.G	1330.38637	2	3.79E-04	0.85	2.86	-	1143.3
AHQ-10-11, 3118	K.NVQDAIADAEQR.G	1330.38637	2	9.75E-07	0.90	3.11	-	1267.7
AHQ-10-3, 3179 - 3198	K.NVQDAIADAEQR.G	1330.38637	2	1.42E-07	0.94	4.32	-	1150.7
AHQ-10-13-, 3180	K.NVQDAIADAEQR.G	1330.38637	2	1.73E-05	0.79	3.19	-	784.9
AHQ-10-8, 3141	K.NVQDAIADAEQR.G	1330.38637	2	6.03E-04	0.90	3.70	-	901.0
AHQ-10-5, 3179	K.NVQDAIADAEQR.G	1330.38637	2	6.53E-07	0.88	3.60	-	1069.4
AHQ-10-2, 3271	R.TAAENDFVTLK.K	1209.33064	2	2.08E-04	0.82	2.77	-	929.3
AHQ-10-3, 2734	R.TAAENDFVTLKK.D	1337.50356	2	3.14E-06	0.72	2.77	-	845.7
AHQ-10-14-, 4888	R.TSQNSELNNMQDLVEDYK.K	2129.24808	2	1.32E-07	0.88	3.86	-	843.7
AHQ-10-14-, 4465	R.TSQNSELNNMQDLVEDYKK.K	2257.42100	3	2.05E-04	0.84	3.45	-	1028.1
AHQ-10-3, 4513 - 4519	R.TSQNSELNNMQDLVEDYKK.K	2257.42100	3	5.99E-09	0.83	3.50	-	958.3
AHQ-10-3, 3185	R.TSQNSELNNM*QDLVEDYKK.K	2273.42040	3	3.59E-07	0.81	3.12	-	955.7
AHQ-10-3, 5561 - 5610	K.VDLLNQEIEFLK.V	1461.68459	2	2.18E-08	0.95	5.08	-	1026.2
AHQ-10-7, 5533	K.VDLLNQEIEFLK.V	1461.68459	2	1.20E-05	0.95	4.39	-	1177.2
AHQ-10-8, 5586	K.VDLLNQEIEFLK.V	1461.68459	2	1.96E-06	0.92	4.10	-	903.6
AHQ-10-1, 5694	K.VDLLNQEIEFLK.V	1461.68459	2	1.17E-06	0.90	3.87	-	832.3
AHQ-10-11, 5375 - 5434	K.VDLLNQEIEFLK.V	1461.68459	2	1.25E-04	0.84	3.43	-	734.5
AHQ-10-14-, 5529 - 5532	K.VDLLNQEIEFLK.V	1461.68459	2	1.10E-06	0.93	4.50	-	803.2
AHQ-10-4, 5656	K.VDLLNQEIEFLK.V	1461.68459	2	9.04E-04	0.78	2.66	-	957.2
AHQ-10-2, 5663 - 5666	K.VDLLNQEIEFLK.V	1461.68459	2	3.75E-09	0.94	4.61	-	915.7
AHQ-10-13, 5799	K.VDLLNQEIEFLK.V	1461.68459	2	7.41E-06	0.79	3.35	-	696.4
AHQ-10-13-, 5514 - 5525	K.VDLLNQEIEFLK.V	1461.68459	2	2.66E-05	0.92	3.62	-	1268.8
AHQ-10-5, 5645 - 5651	K.VDLLNQEIEFLK.V	1461.68459	2	1.67E-06	0.92	4.18	-	777.6
AHQ-10-6, 5515	K.VDLLNQEIEFLK.V	1461.68459	2	2.48E-07	0.90	4.17	-	670.6
AHQ-10-3, 5389 - 5445	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	4.39E-04	0.84	4.23	-	661.5
AHQ-10-13-, 5334	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	9.42E-05	0.92	4.29	-	1141.5
AHQ-10-2, 5482	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	6.33E-04	0.87	3.97	-	863.3
AHQ-10-14-, 5301 - 5341	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	1.11E-11	0.89	3.77	-	979.5
AHQ-10-6, 5344	K.VLYDAEISQIHQSVTDTNVILSM*DNSR.N	3066.34680	3	4.91E-06	0.85	3.73	-	954.8
AHQ-10-3, 3169	K.YEELQVTVGR.H	1194.31920	2	1.59E-06	0.97	3.68	-	2167.5
AHQ-10-13-, 3170	K.YEELQVTVGR.H	1194.31920	2	9.55E-06	0.93	3.58	-	1309.2
AHQ-10-6, 3124	K.YEELQVTVGR.H	1194.31920	2	7.54E-06	0.97	4.02	-	2042.2
AHQ-10-7, 3113 - 3181	K.YEELQVTVGR.H	1194.31920	2	5.35E-05	0.91	2.82	-	1523.7
AHQ-10-14-, 3148	K.YEELQVTVGR.H	1194.31920	2	1.04E-05	0.95	3.48	-	1599.4
AHQ-10-3, 3002	R.YLDGLTAER.T	1038.13608	2	7.28E-06	0.91	3.32	-	831.2
AHQ-10-6, 2947	R.YLDGLTAER.T	1038.13608	2	3.40E-04	0.89	3.01	-	1032.4
gi|4507877|ref|NP_003364.1| vinculin isoform VCL [Homo sapiens]				1.44E-11	34.35	400.32	42.00	116721.6
AHQ-10-4, 2644 - 2659	K.AGEVINQPM*MM*AAR.Q	1551.83812	2	4.71E-05	0.68	4.01	-	458.6
AHQ-10-2, 6511	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.74E-09	0.95	4.70	-	950.2
AHQ-10-12, 6308	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.93E-06	0.92	3.38	-	951.9
AHQ-10-11, 6275	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.75E-08	0.97	4.62	-	1302.1
AHQ-10-10, 6247	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.51E-08	0.96	4.41	-	1198.1
AHQ-10-9, 6081 - 6166	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	8.37E-07	0.90	3.43	-	865.8
AHQ-10-4, 6472	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	3.41E-11	0.96	5.20	-	1014.3
AHQ-10-5, 6488 - 6544	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.44E-11	0.95	4.52	-	1005.1
AHQ-10-8, 6398 - 6463	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	5.29E-07	0.93	4.47	-	832.8
AHQ-10-3, 6399	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	1.88E-04	0.91	3.61	-	968.7

AHQ-10-7, 6416 - 6432	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	7.77E-08	0.97	5.33	-	1116.4
AHQ-10-6, 6364	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	4.16E-11	0.96	5.00	-	1012.6
AHQ-10-14-, 6380 - 6381	K.AIPDLTAPVAAVQAAVSNLVR.V	2077.41342	2	9.91E-07	0.94	4.16	-	945.7
AHQ-10-6, 3331	R.ALASQLQDSLK.D	1174.32943	2	2.43E-04	0.89	3.36	-	1033.4
AHQ-10-3, 3405 - 3406	R.ALASQLQDSLK.D	1174.32943	2	4.58E-05	0.86	3.53	-	697.2
AHQ-10-4, 3363 - 3397	R.ALASQLQDSLK.D	1174.32943	2	9.73E-04	0.85	2.94	-	712.0
AHQ-10-5, 3383 - 3396	R.ALASQLQDSLK.D	1174.32943	2	8.80E-05	0.95	3.55	-	1526.9
AHQ-10-9, 3361 - 3365	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.06E-05	0.94	3.55	-	1271.0
AHQ-10-6, 3519 - 3579	K.AQQVSQGLDVLTAK.V	1458.64233	2	1.12E-07	0.96	4.70	-	1397.9
AHQ-10-4, 3591	K.AQQVSQGLDVLTAK.V	1458.64233	2	6.76E-10	0.96	4.57	-	1346.4
AHQ-10-4, 3453 - 3535	K.AQQVSQGLDVLTAK.V	1458.64233	2	3.51E-05	0.94	3.98	-	1325.7
AHQ-10-1, 3763	K.AQQVSQGLDVLTAK.V	1458.64233	2	4.77E-04	0.88	2.77	-	1016.2
AHQ-10-5, 3575 - 3637	K.AQQVSQGLDVLTAK.V	1458.64233	2	8.08E-11	0.95	4.02	-	1253.1
AHQ-10-5, 2539	K.AVAGNISDPGLQK.S	1270.41721	2	2.08E-05	0.81	3.33	-	628.3
AHQ-10-3, 2577	K.AVAGNISDPGLQK.S	1270.41721	2	3.15E-06	0.88	3.15	-	855.8
AHQ-10-4, 2552	K.AVAGNISDPGLQK.S	1270.41721	2	1.66E-06	0.91	3.90	-	801.1
AHQ-10-4, 2467 - 2535	K.AVAGNISDPGLQK.S	1270.41721	2	5.86E-04	0.83	3.11	-	739.2
AHQ-10-8, 2501	K.AVAGNISDPGLQK.S	1270.41721	2	6.90E-04	0.85	3.63	-	607.5
AHQ-10-5, 5553	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	8.41E-06	0.87	3.78	-	1158.5
AHQ-10-4, 5553	K.CDRVDQLTAQLADLAAR.G	1918.12182	3	9.20E-06	0.94	5.25	-	1129.0
AHQ-10-3, 2387	R.DPSASPGDAGEQAIR.Q	1471.51169	2	3.96E-07	0.84	3.38	-	582.5
AHQ-10-6, 2339	R.DPSASPGDAGEQAIR.Q	1471.51169	2	4.39E-09	0.81	2.99	-	607.0
AHQ-10-4, 2359	R.DPSASPGDAGEQAIR.Q	1471.51169	2	5.74E-08	0.89	3.72	-	662.9
AHQ-10-5, 2347 - 2348	R.DPSASPGDAGEQAIR.Q	1471.51169	2	3.83E-08	0.95	4.47	-	846.9
AHQ-10-4, 5419 - 5475	R.EAFQPQEPDFPPPPPDLEQLR.L	2448.67149	3	5.03E-04	0.63	3.02	-	1004.8
AHQ-10-4, 5297 - 5363	R.EAFQPQEPDFPPPPPDLEQLR.L	2448.67149	3	6.45E-07	0.83	3.94	-	884.3
AHQ-10-8, 2707 - 2775	R.ELTPQVVSAAR.I	1171.32878	2	1.20E-04	0.84	2.61	-	991.5
AHQ-10-5, 3085	K.ETVQTTEDQILKR.D	1561.71942	2	1.03E-04	0.78	2.82	-	612.4
AHQ-10-7, 3014	K.ETVQTTEDQILKR.D	1561.71942	2	3.49E-04	0.52	2.79	-	624.9
AHQ-10-7, 6222 - 6293	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	9.83E-08	0.97	5.23	-	1142.3
AHQ-10-5, 6303 - 6368	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	6.66E-08	0.95	5.10	-	953.0
AHQ-10-3, 6222 - 6281	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	1.68E-05	0.88	4.15	-	648.3
AHQ-10-4, 6303 - 6368	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	4.95E-08	0.98	6.44	-	1256.4
AHQ-10-11, 6152	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	3.08E-04	0.90	4.01	-	701.9
AHQ-10-6, 6175 - 6243	R.GILSGTSDLLLTFDEAEVR.K	2037.25656	2	6.58E-05	0.92	4.76	-	683.0
AHQ-10-4, 3561	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	3	1.28E-06	0.96	4.69	-	1661.2
AHQ-10-4, 3568	K.GWLRDPSASPGDAGEQAIR.Q	1984.11876	2	1.88E-04	0.87	4.14	-	577.1
AHQ-10-4, 2315	K.IAELCDDPKER.D	1347.47690	2	7.05E-06	0.69	2.94	-	594.7
AHQ-10-10, 3098	R.IPTISTQLK.I	1001.20202	2	1.91E-05	0.86	2.62	-	1045.6
AHQ-10-6, 4091 - 4169	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	3.05E-06	0.94	5.33	-	1117.6
AHQ-10-5, 4171 - 4233	K.KIDAAQNWLADPNGGPEGEEQIR.G	2509.67332	3	1.44E-07	0.95	5.58	-	1017.5
AHQ-10-5, 2313	R.LANVM*M*GPYR.Q	1184.41440	2	1.47E-04	0.89	3.59	-	809.2
AHQ-10-4, 3459	R.LANVMMGPYR.Q	1152.41560	2	5.27E-05	0.94	3.55	-	1098.7
AHQ-10-5, 2963	R.LANVMM*GPYR.Q	1168.41500	2	7.82E-06	0.59	2.76	-	528.5
AHQ-10-6, 2308	R.LANVM*M*GPYR.Q	1184.41440	2	1.67E-04	0.90	3.49	-	761.4
AHQ-10-4, 4200 - 4265	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	1.09E-06	0.83	3.91	-	616.9
AHQ-10-6, 4083 - 4161	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	1.70E-05	0.73	3.36	-	688.1
AHQ-10-4, 4112 - 4171	K.LLAVAATAPPDAPNREEVFDER.A	2382.61458	3	6.84E-08	0.84	3.77	-	743.1
AHQ-10-4, 3655	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	2	5.70E-04	0.87	3.47	-	825.1
AHQ-10-4, 3661 - 3667	K.LVQAAQM*LQSDPYSVPAR.D	1991.25773	3	1.38E-06	0.98	5.40	-	2820.3
AHQ-10-4, 2944	K.M*LGQM*TDQVADLR.A	1510.71935	2	2.39E-06	0.93	3.41	-	1569.7
AHQ-10-6, 3639	K.M*LGQMTDQVADLR.A	1494.71995	2	2.02E-05	0.92	3.49	-	1323.4
AHQ-10-5, 3692 - 3704	K.M*LGQMTDQVADLR.A	1494.71995	2	1.76E-05	0.97	4.09	-	2198.1
AHQ-10-4, 3717	K.M*LGQMTDQVADLR.A	1494.71995	2	3.15E-04	0.90	3.48	-	1069.2
AHQ-10-5, 2939	K.M*LGQM*TDQVADLR.A	1510.71935	2	6.29E-06	0.95	3.36	-	1784.5
AHQ-10-7, 3632	K.M*LGQMTDQVADLR.A	1494.71995	2	4.01E-05	0.65	2.71	-	833.1
AHQ-10-4, 3311	K.MLGQM*TDQVADLR.A	1494.71995	2	4.15E-06	0.91	3.56	-	1181.6
AHQ-10-5, 3245 - 3255	K.M*SAEINEIIR.V	1192.36823	2	9.88E-07	0.91	3.03	-	1044.7
AHQ-10-6, 3213	K.M*SAEINEIIR.V	1192.36823	2	3.03E-06	0.83	2.54	-	896.7
AHQ-10-6, 3115	K.M*TGLVDEAIDTK.S	1309.46876	2	9.10E-05	0.90	3.16	-	1233.8
AHQ-10-4, 3563 - 3567	K.MTGLVDEAIDTK.S	1293.46936	2	7.20E-08	0.97	4.30	-	1666.3
AHQ-10-4, 3145	K.M*TGLVDEAIDTK.S	1309.46876	2	2.32E-07	0.88	2.92	-	971.3
AHQ-10-4, 3012	K.NQWIDNVEK.M	1146.23464	1	5.07E-04	0.26	2.00	-	292.1
AHQ-10-5, 2965	K.QVATALQNLQTK.T	1315.50112	2	2.04E-06	0.91	3.31	-	776.2
AHQ-10-4, 2908 - 2972	K.QVATALQNLQTK.T	1315.50112	2	5.11E-05	0.86	3.69	-	528.9
AHQ-10-7, 2934	K.QVATALQNLQTK.T	1315.50112	2	6.53E-04	0.55	2.77	-	365.3
AHQ-10-4, 2991	K.SFLDSGYR.I	945.01074	2	1.72E-04	0.78	2.71	-	607.5
AHQ-10-4, 3420 - 3489	R.SLGEISALTSK.L	1106.25186	2	3.89E-08	0.95	3.96	-	1060.6
AHQ-10-7, 3412	R.SLGEISALTSK.L	1106.25186	2	1.01E-05	0.88	3.47	-	787.5
AHQ-10-8, 3349 - 3370	K.SLLDASEEAIKK.D	1304.47187	2	2.87E-04	0.82	3.00	-	996.2
AHQ-10-5, 3351 - 3411	K.SLLDASEEAIKK.D	1304.47187	2	1.25E-06	0.77	2.83	-	690.6
AHQ-10-3, 2515	K.STVEGIQASVK.T	1119.25064	2	5.00E-05	0.89	3.12	-	879.6
AHQ-10-5, 6219 - 6283	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	4.95E-05	0.43	3.04	-	467.0
AHQ-10-4, 6263	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	8.76E-04	0.78	3.88	-	575.6
AHQ-10-4, 5636 - 5691	R.TNISDEESEQATEM*LVHNAQNLMQSVK.E	3064.30957	3	2.15E-05	0.72	4.34	-	537.3
AHQ-10-5, 3308	R.TNLLQVCER.I	1134.28859	2	1.29E-04	0.84	2.80	-	904.5
AHQ-10-4, 4740	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	1.79E-04	0.97	5.40	-	2210.9
AHQ-10-4, 4732	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	2	2.04E-07	0.85	4.24	-	482.8
AHQ-10-6, 5020	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	2	4.96E-04	0.82	3.88	-	604.3
AHQ-10-4, 5145	K.VAM*ANIQPQMLVAGATSIAR.R	2059.44338	3	1.54E-04	0.91	4.29	-	1997.7
AHQ-10-5, 4720	K.VAM*ANIQPQM*LVAGATSIAR.R	2075.44278	3	2.49E-04	0.85	3.51	-	1208.3
AHQ-10-4, 4839	R.VDQLTAQLADLAAR.G	1485.66778	2	3.97E-08	0.98	4.28	-	3396.1
AHQ-10-6, 4732 - 4735	R.VDQLTAQLADLAAR.G	1485.66778	2	2.07E-07	0.97	4.99	-	1890.2
AHQ-10-5, 4819 - 4820	R.VDQLTAQLADLAAR.G	1485.66778	2	6.62E-08	0.99	5.66	-	3520.4
AHQ-10-4, 3256	R.VGKETVQTTEDQILK.R	1689.88910	2	2.86E-04	0.87	3.35	-	1056.4
AHQ-10-5, 5101 - 5155	R.VLQLTSWDEDAWASK.D	1749.90156	2	9.06E-08	0.95	4.53	-	971.7
AHQ-10-4, 5073	R.VLQLTSWDEDAWASK.D	1749.90156	2	1.28E-05	0.92	3.42	-	1072.7
AHQ-10-4, 5179	R.VLQLTSWDEDAWASK.D	1749.90156	2	6.14E-07	0.96	4.39	-	1517.1
AHQ-10-3, 5114	R.VLQLTSWDEDAWASK.D	1749.90156	2	7.30E-06	0.69	2.65	-	618.7
AHQ-10-6, 5055 - 5056	R.VLQLTSWDEDAWASK.D	1749.90156	2	5.16E-07	0.96	4.57	-	1255.0
AHQ-10-7, 5056 - 5130	R.VLQLTSWDEDAWASK.D	1749.90156	2	2.12E-04	0.91	3.75	-	973.3
AHQ-10-5, 2884 - 2929	R.WIDNPTVDDR.G	1231.29640	2	1.01E-04	0.94	3.58	-	1491.6
AHQ-10-6, 2872 - 2879	R.WIDNPTVDDR.G	1231.29640	2	4.93E-04	0.94	3.66	-	1275.5
AHQ-10-4, 2907 - 2931	R.WIDNPTVDDR.G	1231.29640	2	4.02E-06	0.93	4.05	-	1042.9
AHQ-10-7, 2881	R.WIDNPTVDDR.G	1231.29640	2	1.06E-04	0.90	3.14	-	954.5
AHQ-10-3, 2942	R.WIDNPTVDDR.G	1231.29640	2	1.19E-04	0.89	3.24	-	876.1
gi|4502549|ref|NP_001734.1| calmodulin 2 (phosphorylase kinase, delta); phosphorylase kinase delta				1.51E-11	1.85	30.22	30.90	16837.5
AHQ-10-12, 3542 - 3596	K.DTDSEEEIREAFR.V	1597.62234	2	1.43E-06	0.42	2.75	-	299.0
AHQ-10-12, 4084 - 4149	K.EAFSLFDKDGDGTITTK.E	1845.98441	3	5.70E-05	0.87	3.82	-	884.0
AHQ-10-12, 4077 - 4132	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	1.59E-04	0.68	3.14	-	406.0
AHQ-10-11, 4023 - 4058	K.EAFSLFDKDGDGTITTK.E	1845.98441	2	5.08E-05	0.51	2.62	-	475.0
AHQ-10-12, 3776 - 3832	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.51E-11	0.93	4.35	-	857.8
AHQ-10-12, 3649	R.VFDKDGNGYISAAELR.H	1755.90933	2	1.79E-06	0.77	2.70	-	749.2
gi|4503971|ref|NP_001484.1| GDP dissociation inhibitor 1; mental retardation, X-linked 41; mental r				1.90E-11	2.68	30.26	14.50	50582.4
AHQ-10-7, 4982 - 5009	R.NPYYGGESSSITPLEELYK.R	2148.31110	2	1.48E-07	0.88	4.26	-	636.1
AHQ-10-7, 4070 - 4136	R.TDDYLDQPCLETVNR.I	1840.94632	2	9.56E-08	0.86	3.86	-	518.6
AHQ-10-7, 6244 - 6246	K.YIAIASTTVETTDPEKEVEPALELLEPIDQK.F	3444.82460	3	1.90E-11	0.94	5.15	-	771.8

gi|4758086|ref|NP_004069.1| cysteine and glycine-rich protein 1; cysteine-rich protein; LIM-domain				1.99E-11	3.60	40.23	37.80	20567.3
AHQ-10-11, 3279 - 3314	K.GLESTTLADKDGEIYCK.G	1902.06957	2	1.79E-05	0.95	4.67	-	1141.0
AHQ-10-11, 3522	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	2	5.65E-10	0.90	4.07	-	733.8
AHQ-10-11, 3464 - 3520	K.GYGYGQGAGTLSTDKGESLGIK.H	2160.32665	3	1.99E-11	0.85	3.84	-	723.7
AHQ-10-11, 3470	K.NLDSTTVAVHGEEIYCK.S	1938.10514	2	1.11E-07	0.95	4.24	-	1074.5
AHQ-10-11, 4075	K.TVYFAEEVQCEGNSFHK.S	2047.19015	2	5.50E-08	0.85	3.73	-	664.2
gi|4504345|ref|NP_000508.1| alpha 2 globin [Homo sapiens]				2.16E-11	3.80	40.33	50.70	15257.4
AHQ-10-13-, 4213	K.FLASVSTVLTSK.Y	1253.46970	2	1.41E-07	0.94	3.37	-	1440.8
AHQ-10-13, 4572 - 4576	K.FLASVSTVLTSK.Y	1253.46970	2	5.73E-08	0.94	3.45	-	1667.3
AHQ-10-13, 4360 - 4417	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	1.46E-08	0.81	3.06	-	701.1
AHQ-10-13-, 3992 - 4048	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	3.35E-11	0.95	4.34	-	1211.9
AHQ-10-13-, 3982 - 4040	K.TYFPHFDLSHGSAQVK.G	1835.01138	3	1.07E-08	0.90	4.23	-	638.3
AHQ-10-14-, 3982	K.TYFPHFDLSHGSAQVK.G	1835.01138	2	1.98E-09	0.81	3.36	-	587.7
AHQ-10-13-, 4750 - 4793	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	4.51E-09	0.94	5.20	-	1259.8
AHQ-10-13-, 5269	K.VADALTNAVAHVDDM*PNALSALSDLHAHK.L	3014.31995	3	9.03E-08	0.97	6.69	-	1243.4
AHQ-10-13, 3100 - 3163	K.VGAHAGEYGAEALER.M	1530.62397	3	3.63E-05	0.95	5.03	-	2060.2
AHQ-10-13, 3187 - 3244	K.VGAHAGEYGAEALER.M	1530.62397	2	1.24E-04	0.95	4.24	-	1327.5
AHQ-10-13-, 2665 - 2725	K.VGAHAGEYGAEALER.M	1530.62397	3	2.64E-04	0.95	5.51	-	1477.3
AHQ-10-14-, 2561 - 2638	K.VGAHAGEYGAEALER.M	1530.62397	2	8.40E-11	0.97	4.24	-	1601.4
AHQ-10-13, 3076 - 3131	K.VGAHAGEYGAEALER.M	1530.62397	2	3.58E-07	0.96	4.08	-	1538.7
AHQ-10-13-, 2666 - 2724	K.VGAHAGEYGAEALER.M	1530.62397	2	2.16E-11	0.96	4.49	-	1476.4
gi|4505839|ref|NP_002645.1| pyruvate kinase, muscle; Pyruvate kinase-3; Thyroid hormone-binding pro				2.49E-11	12.51	140.31	36.00	57913.6
AHQ-10-7, 5540	R.EAEAAIYHLQLFEELR.R	1933.15326	2	1.50E-07	0.91	3.87	-	799.2
AHQ-10-7, 6376	K.FGVEQDVDM*VFASFIR.K	1877.10995	2	1.68E-08	0.98	5.40	-	1762.5
AHQ-10-7, 4518 - 4524	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	1.62E-06	0.96	4.99	-	1375.3
AHQ-10-7, 4617	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.21E-06	0.96	4.51	-	1612.6
AHQ-10-9, 4097 - 4163	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	2.55E-04	0.18	2.55	-	419.3
AHQ-10-7, 4314 - 4381	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	3.62E-05	0.92	4.09	-	1062.1
AHQ-10-8, 4382	K.GADFLVTEVENGGSLGSK.K	1780.91396	2	7.13E-05	0.76	3.04	-	804.7
AHQ-10-7, 6141 - 6156	R.GIFPVLCKDPVQEAWAEDVDLR.V	2559.87857	3	2.49E-11	0.98	6.15	-	2445.0
AHQ-10-7, 4392 - 4406	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	2.69E-07	0.87	3.97	-	598.2
AHQ-10-8, 4465	K.GVNLPGAAVDLPAVSEK.D	1637.85902	2	7.34E-06	0.86	3.63	-	517.7
AHQ-10-7, 4017	K.KGVNLPGAAVDLPAVSEK.D	1766.03194	2	2.35E-05	0.94	4.50	-	976.8
AHQ-10-11, 5303	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	3.28E-04	0.85	3.40	-	495.9
AHQ-10-7, 5382 - 5396	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	3	6.04E-04	0.90	4.28	-	1070.4
AHQ-10-7, 5113 - 5177	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	6.11E-04	0.89	3.31	-	813.1
AHQ-10-7, 5356 - 5414	R.LAPITSDPTEATAVGAVEASFK.C	2176.40912	2	7.37E-06	0.97	5.72	-	1278.8
AHQ-10-7, 3285 - 3356	R.LDIDSPPITAR.N	1198.35099	2	6.10E-06	0.90	3.39	-	1022.5
AHQ-10-7, 3378	R.LDIDSPPITAR.N	1198.35099	2	6.61E-05	0.90	3.12	-	1048.6
AHQ-10-7, 2512	R.LNFSHGTHEYHAETIK.N	1885.02879	2	3.16E-05	0.90	4.04	-	816.8
AHQ-10-7, 2516	R.LNFSHGTHEYHAETIK.N	1885.02879	3	2.13E-08	0.95	5.01	-	1255.9
AHQ-10-7, 3742 - 3760	R.NTGIICTIGPASR.S	1361.54994	2	2.66E-04	0.91	3.49	-	1049.1
AHQ-10-13-, 3472 - 3485	R.NTGIICTIGPASR.S	1361.54994	2	1.59E-06	0.93	3.82	-	1243.1
AHQ-10-7, 3368 - 3370	R.NTGIICTIGPASR.S	1361.54994	2	7.66E-06	0.94	4.38	-	986.7
AHQ-10-7, 4360	R.RFDEILEASDGIM*VAR.G	1839.06325	2	1.01E-04	0.75	3.18	-	405.7
AHQ-10-7, 4844	R.RFDEILEASDGIMVAR.G	1823.06385	2	2.57E-10	0.97	5.91	-	1282.8
AHQ-10-7, 4856	R.RFDEILEASDGIMVAR.G	1823.06385	3	8.37E-05	0.88	3.73	-	1529.4
AHQ-10-7, 3993 - 4018	R.TATESFASDPILYR.P	1571.71277	2	3.82E-04	0.66	2.75	-	545.1
AHQ-10-7, 2968	R.VNFAMNVGK.A	980.16641	2	5.93E-04	0.74	2.74	-	587.5
gi|4505667|ref|NP_001074.1| phosphodiesterase 5A isoform 1; cGMP-binding cGMP-specific 3',5'-cyclic				3.50E-11	0.94	10.19	1.70	100012.4
AHQ-10-5, 5233 - 5291	R.IAELVATEFFDQGDR.E	1711.85332	2	3.50E-11	0.94	3.87	-	1188.6
gi|5729877|ref|NP_006588.1| heat shock 70kDa protein 8 isoform 1; heat shock cognate protein, 71-kD				4.02E-11	10.46	120.23	23.80	70897.6
AHQ-10-6, 4295	R.ARFEELNADLFR.G	1481.63768	2	2.79E-09	0.96	4.62	-	1267.2
AHQ-10-6, 4303	R.ARFEELNADLFR.G	1481.63768	3	5.50E-05	0.90	4.01	-	1039.2
AHQ-10-6, 4501	R.FEELNADLFR.G	1254.37310	2	2.37E-05	0.92	3.56	-	1214.7
AHQ-10-6, 5009	K.GPAVGIDLGTTYSCVGVFQHGK.V	2265.53088	3	4.02E-11	0.89	4.37	-	780.2
AHQ-10-6, 5299	K.ILDKCNEIINWLDK.N	1776.04688	2	2.99E-07	0.95	4.26	-	1286.0
AHQ-10-6, 2624	K.M*KEIAEAYLGK.T	1269.49260	2	9.17E-05	0.93	3.64	-	1259.2
AHQ-10-6, 2811	K.NQVAM*NPTNTVFDAK.R	1666.83756	2	5.55E-09	0.90	3.62	-	846.0
AHQ-10-6, 3351 - 3388	K.NSLESYAFNM*K.A	1320.45333	2	1.12E-04	0.72	2.69	-	574.4
AHQ-10-6, 4019	K.NSLESYAFNMK.A	1304.45393	2	5.27E-04	0.75	3.23	-	608.5
AHQ-10-6, 4940 - 4943	K.SFYPEEVSSMVLTK.M	1617.84485	2	7.63E-10	0.86	3.20	-	556.4
AHQ-10-6, 6159 - 6237	K.SINPDEAVAYGAAVQAAILSGDK.S	2261.47411	2	1.03E-04	0.87	4.22	-	532.6
AHQ-10-6, 3156	K.SQIHDIVLVGGSTR.I	1482.66712	2	2.22E-06	0.96	4.39	-	1726.9
AHQ-10-7, 3125 - 3150	K.SQIHDIVLVGGSTR.I	1482.66712	2	1.22E-06	0.94	4.10	-	1149.5
AHQ-10-6, 4375 - 4431	K.TVTNAVVTVPAYFNDSQR.Q	1983.17068	2	1.54E-04	0.77	3.41	-	370.9
gi|4557419|ref|NP_000063.1| CD36 antigen (collagen type I receptor, thrombospondin receptor); CD36				4.17E-11	2.73	30.24	10.20	53052.1
AHQ-10-5, 4496	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	3.08E-06	0.81	3.30	-	529.4
AHQ-10-4, 4551	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	2.73E-05	0.75	3.42	-	483.7
AHQ-10-6, 4423	K.AFASPVENPDNYCFCTEK.I	2152.30319	2	1.49E-04	0.84	3.51	-	605.5
AHQ-10-7, 5217	K.SQVLQFFSSDICR.S	1588.76661	2	1.56E-04	0.95	3.75	-	1589.1
AHQ-10-2, 5343	K.SQVLQFFSSDICR.S	1588.76661	2	3.05E-07	0.94	4.03	-	1025.6
AHQ-10-5, 5295	K.SQVLQFFSSDICR.S	1588.76661	2	3.62E-06	0.95	3.97	-	1365.4
AHQ-10-6, 6247 - 6248	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.75E-10	0.94	4.10	-	1009.1
AHQ-10-1, 6319 - 6390	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	1.89E-07	0.85	3.50	-	677.7
AHQ-10-5, 6371	R.TYLDIQPITGFTLQFAK.R	1957.25787	2	4.17E-11	0.97	4.74	-	1766.9
gi|13129150|ref|NP_005339.1| heat shock 90kDa protein 1, alpha; heat shock 90kD protein 1, alpha [H				4.52E-11	1.55	20.24	3.00	84659.1
AHQ-10-5, 2547	K.FYEQFSK.N	949.04099	1	1.21E-04	0.59	2.32	-	587.3
AHQ-10-6, 3884	R.NPDDITNEEYGEFYK.S	1834.87381	2	1.49E-06	0.95	4.55	-	1212.7
AHQ-10-7, 3862 - 3925	R.NPDDITNEEYGEFYK.S	1834.87381	2	7.01E-05	0.85	3.61	-	644.5
AHQ-10-8, 3930	R.NPDDITNEEYGEFYK.S	1834.87381	2	1.80E-04	0.91	3.41	-	1142.5
AHQ-10-5, 3865 - 3943	R.NPDDITNEEYGEFYK.S	1834.87381	2	4.52E-11	0.95	4.84	-	892.0
gi|24119203|ref|NP_705935.1| tropomyosin 3 [Homo sapiens]				4.81E-11	4.35	50.31	14.50	29032.5
AHQ-10-9, 3408 - 3463	R.IQLVEEELDR.A	1244.37653	2	3.56E-05	0.93	3.75	-	1098.1
AHQ-10-10, 2818	K.IQVLQQQADDAEER.A	1643.73738	2	1.94E-08	0.92	3.05	-	1556.8
AHQ-10-9, 2723 - 2724	K.IQVLQQQADDAEER.A	1643.73738	2	1.58E-06	0.97	4.47	-	1730.6
AHQ-10-9, 2519	R.KIQVLQQQADDAEER.A	1771.91030	2	4.81E-11	0.98	6.11	-	1735.2
AHQ-10-9, 3196	R.RIQLVEEELDR.A	1400.56288	2	2.12E-07	0.97	4.49	-	1517.4
AHQ-10-9, 3019	K.TIDDLEDKLK.C	1190.32563	2	6.43E-05	0.56	2.64	-	341.0
gi|4557361|ref|NP_001187.1| BH3 interacting domain death agonist; BH3-interacting domain death agon				6.00E-11	1.57	20.18	21.00	21994.6
AHQ-10-11, 5779	R.ELDALGHELPVLAPQWEGYDELQTDGNR.S	3167.38790	3	2.63E-05	0.62	3.09	-	510.1
AHQ-10-11, 2800	R.IEADSESQEDIIR.N	1505.56635	2	6.00E-11	0.96	3.66	-	2016.9
gi|4505733|ref|NP_002610.1| platelet factor 4 (chemokine (C-X-C motif) ligand 4); platelet factor 4				8.34E-11	6.44	70.26	39.60	10844.9
AHQ-10-14-, 4052	K.AGPHCPTAQLIATLK.N	1579.84600	2	2.13E-09	0.91	3.60	-	881.6
AHQ-10-13-, 4133	K.AGPHCPTAQLIATLK.N	1579.84600	3	5.75E-04	0.87	4.31	-	1128.4
AHQ-10-13, 4492 - 4551	K.AGPHCPTAQLIATLK.N	1579.84600	2	4.03E-04	0.55	2.70	-	454.8
AHQ-10-14, 5087	K.AGPHCPTAQLIATLK.N	1579.84600	2	5.03E-04	0.66	2.98	-	474.5
AHQ-10-14-, 3970	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	5.81E-06	0.89	3.20	-	877.7
AHQ-10-14-, 3973 - 4036	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	8.34E-11	0.97	5.12	-	2321.7
AHQ-10-14, 4728	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	9.98E-06	0.70	3.32	-	397.0
AHQ-10-14, 4863	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	7.59E-06	0.89	3.85	-	668.6
AHQ-10-14-, 3856	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.77E-08	0.98	4.70	-	2857.3
AHQ-10-14-, 3861	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	2.15E-09	0.91	4.24	-	782.2
AHQ-10-13-, 4017	K.AGPHCPTAQLIATLKNGR.K	1907.18700	3	1.01E-05	0.90	3.54	-	1452.8
AHQ-10-13-, 3906	K.AGPHCPTAQLIATLKNGR.K	1907.18700	2	9.75E-09	0.86	3.44	-	872.5
AHQ-10-14, 3511 - 3567	R.HITSLEVIK.A	1040.23825	2	5.39E-05	0.85	3.00	-	614.8
AHQ-10-14, 3623 - 3679	R.HITSLEVIK.A	1040.23825	2	4.40E-05	0.74	2.84	-	455.1

AHQ-10-14-, 2776 - 2832	R.HITSLEVIK.A	1040.23825	2	4.25E-04	0.83	3.11	-	524.0
AHQ-10-14-, 2660 - 2720	R.HITSLEVIK.A	1040.23825	2	2.63E-08	0.94	3.95	-	912.9
AHQ-10-13, 3228 - 3275	R.HITSLEVIK.A	1040.23825	2	3.89E-05	0.65	2.54	-	578.9
AHQ-10-13, 5077	K.ICLDLQAPLYK.K	1335.59400	2	7.65E-06	0.94	3.60	-	1455.9
AHQ-10-14-, 4716 - 4718	K.ICLDLQAPLYK.K	1335.59400	2	9.39E-07	0.98	4.96	-	2262.2
AHQ-10-14, 5428	K.ICLDLQAPLYK.K	1335.59400	2	9.62E-08	0.95	3.55	-	1940.8
AHQ-10-13-, 4724	K.ICLDLQAPLYK.K	1335.59400	2	6.25E-06	0.96	4.05	-	1666.2
AHQ-10-9, 4491	K.ICLDLQAPLYK.K	1335.59400	2	9.31E-04	0.94	3.68	-	1468.6
AHQ-10-14-, 4729	K.ICLDLQAPLYK.K	1335.59400	1	2.24E-07	0.70	3.21	-	484.2
AHQ-10-14-, 4262 - 4328	K.ICLDLQAPLYKK.I	1463.76691	2	3.05E-04	0.84	3.15	-	1258.2
AHQ-10-14-, 4396 - 4472	R.KICLDLQAPLYK.K	1463.76691	2	8.43E-05	0.97	4.89	-	1425.9
AHQ-10-14-, 4401 - 4428	R.KICLDLQAPLYK.K	1463.76691	3	3.44E-06	0.91	3.77	-	1542.5
AHQ-10-13, 4693 - 4759	R.KICLDLQAPLYK.K	1463.76691	2	6.66E-04	0.91	4.34	-	539.6
AHQ-10-14-, 3992 - 4005	R.KICLDLQAPLYKK.I	1591.93982	3	7.41E-07	0.91	4.56	-	1002.8
AHQ-10-14-, 3998	R.KICLDLQAPLYKK.I	1591.93982	2	8.70E-05	0.93	4.06	-	1233.6
gi|4503689|ref|NP_000499.1| fibrinogen, alpha chain isoform alpha-E preproprotein [Homo sapiens] [M				9.47E-11	11.56	150.23	19.10	94972.5
AHQ-10-7, 5329	K.DSDWPFCSDEDWNYK.C	1965.98609	2	1.27E-05	0.93	3.86	-	705.6
AHQ-10-6, 4731 - 4795	K.DSHSLTTNIM*EILR.G	1646.84779	2	5.88E-04	0.91	3.74	-	1034.6
AHQ-10-5, 2692	R.EVDLKDYEDQQK.Q	1510.58460	2	2.79E-07	0.61	2.58	-	607.1
AHQ-10-7, 2652	R.EVDLKDYEDQQK.Q	1510.58460	2	7.24E-05	0.71	2.95	-	498.7
AHQ-10-8, 2665	R.EVDLKDYEDQQK.Q	1510.58460	2	2.32E-08	0.91	3.53	-	930.7
AHQ-10-9, 2557	R.EVDLKDYEDQQK.Q	1510.58460	2	1.10E-04	0.54	2.61	-	504.9
AHQ-10-6, 2651	R.EVDLKDYEDQQK.Q	1510.58460	2	4.86E-06	0.84	3.21	-	697.5
AHQ-10-10, 2642 - 2704	R.EVDLKDYEDQQK.Q	1510.58460	2	2.83E-07	0.84	3.19	-	648.0
AHQ-10-6, 1888 - 1924	R.GGSTSYGTGSETESPR.N	1573.55765	2	4.72E-06	0.55	2.70	-	481.9
AHQ-10-8, 1897	R.GGSTSYGTGSETESPR.N	1573.55765	2	1.35E-05	0.66	2.94	-	485.6
AHQ-10-6, 3895 - 3897	K.GLIDEVNQDFTNR.I	1521.61384	2	1.89E-05	0.75	3.19	-	537.5
AHQ-10-9, 4305 - 4365	K.GLIDEVNQDFTNR.I	1521.61384	2	2.48E-04	0.91	3.42	-	1269.7
AHQ-10-9, 4175 - 4247	K.GLIDEVNQDFTNR.I	1521.61384	2	1.48E-06	0.91	3.59	-	963.2
AHQ-10-9, 3692 - 3748	K.GLIDEVNQDFTNR.I	1521.61384	2	4.61E-05	0.87	3.63	-	561.8
AHQ-10-10, 4338	K.GLIDEVNQDFTNR.I	1521.61384	2	8.36E-04	0.78	3.39	-	627.3
AHQ-10-11, 4384 - 4387	K.GLIDEVNQDFTNR.I	1521.61384	2	6.30E-06	0.85	3.64	-	629.0
AHQ-10-8, 4481	K.GLIDEVNQDFTNR.I	1521.61384	2	4.07E-07	0.94	4.17	-	1080.6
AHQ-10-7, 4420 - 4421	K.GLIDEVNQDFTNR.I	1521.61384	2	3.23E-07	0.96	4.68	-	1144.1
AHQ-10-13, 4828	K.GLIDEVNQDFTNR.I	1521.61384	2	5.43E-05	0.89	3.30	-	970.9
AHQ-10-3, 4427 - 4505	K.GLIDEVNQDFTNR.I	1521.61384	2	5.33E-05	0.88	3.40	-	988.5
AHQ-10-14-, 4460 - 4469	K.GLIDEVNQDFTNR.I	1521.61384	2	6.42E-08	0.94	4.23	-	1054.3
AHQ-10-1, 4642	K.GLIDEVNQDFTNR.I	1521.61384	2	4.40E-06	0.81	2.83	-	826.4
AHQ-10-6, 3179	R.HPDEAAFFDTASTGK.T	1594.66329	2	7.45E-05	0.83	3.38	-	543.9
AHQ-10-7, 3166	R.HPDEAAFFDTASTGK.T	1594.66329	2	4.33E-05	0.63	2.65	-	369.0
AHQ-10-6, 2709 - 2772	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	8.16E-05	0.97	4.56	-	2086.8
AHQ-10-9, 2632	R.HRHPDEAAFFDTASTGK.T	1887.98954	3	7.83E-05	0.83	3.22	-	1134.9
AHQ-10-7, 3912	K.MKPVPDLVPGNFK.S	1442.75114	2	9.13E-06	0.62	2.53	-	405.4
AHQ-10-7, 2238	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	4.43E-08	0.90	4.04	-	776.3
AHQ-10-6, 2231	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	4.31E-09	0.96	4.50	-	1391.1
AHQ-10-8, 2255	R.NPSSAGSWNSGSSGPGSTGNR.N	1964.94443	2	9.47E-11	0.94	4.36	-	1100.7
AHQ-10-6, 2867	K.NSLFEYQK.N	1029.12765	2	7.69E-04	0.67	2.73	-	576.1
AHQ-10-6, 2291	R.PGSTGTWNPGSSER.G	1433.46515	2	4.13E-06	0.65	2.89	-	454.6
AHQ-10-7, 4433 - 4504	R.PNNPDWGTFEEVSGNVSPGTR.R	2261.34962	2	2.45E-04	0.79	3.84	-	386.9
AHQ-10-12, 6077 - 6120	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.57E-04	0.86	3.78	-	301.0
AHQ-10-11, 6094	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	3.97E-04	0.61	2.88	-	262.2
AHQ-10-7, 6385	K.TFPGFFSPMLGEFVSETESR.G	2266.51432	2	7.51E-05	0.81	3.60	-	337.1
AHQ-10-7, 6236	K.TFPGFFSPM*LGEFVSETESR.G	2282.51372	2	1.41E-05	0.56	2.90	-	190.5
AHQ-10-9, 2399	K.VQHIQLLQK.N	1107.33106	2	4.06E-04	0.82	2.70	-	764.6
AHQ-10-8, 2459	K.VQHIQLLQK.N	1107.33106	2	2.25E-04	0.81	2.70	-	823.4
AHQ-10-7, 2484	K.VQHIQLLQK.N	1107.33106	1	4.51E-04	0.44	2.19	-	610.7
AHQ-10-9, 2401	K.VQHIQLLQK.N	1107.33106	1	2.52E-04	0.38	2.47	-	529.5
gi|20070158|ref|NP_003567.2| serine/threonine kinase 24 (STE20 homolog, yeast); STE20-like kinase 3				9.66E-11	0.88	10.15	3.40	49307.6
AHQ-10-7, 3754	K.SQACGGNLGSIEELR.G	1592.71366	2	9.66E-11	0.88	2.96	-	1562.9
gi|5902128|ref|NP_008880.1| syntaxin binding protein 2; Hunc18b [Homo sapiens]				9.86E-11	6.00	70.28	20.90	66438.1
AHQ-10-6, 6319	R.AADPVSPLLHELTFQAM*AYDLLDIEQDTYR.Y	3453.81998	3	2.04E-05	0.85	4.06	-	667.7
AHQ-10-6, 5991	R.EPIPSLEAIYLLSPTEK.S	1901.18939	2	3.03E-07	0.77	2.87	-	557.4
AHQ-10-6, 3355	R.KGPEDTAQLAHAVLAK.L	1649.87303	3	2.20E-07	0.95	4.80	-	1641.7
AHQ-10-6, 6256	K.M*SDILAEGITIVEDINKR.R	2034.32082	3	9.86E-11	0.84	3.43	-	855.4
AHQ-10-6, 3244 - 3248	R.NLEQLGGTVTNPGGSGTSSR.L	1933.02693	2	6.15E-05	0.96	5.23	-	956.0
AHQ-10-6, 5149	R.NLWPFVSDPAPTASSQAAVSAR.F	2273.48981	2	1.78E-04	0.65	3.10	-	306.5
AHQ-10-6, 5592	R.REPIPSLEAIYLLSPTEK.S	2057.37574	2	7.51E-09	0.97	5.54	-	1415.6
AHQ-10-6, 5585	R.REPIPSLEAIYLLSPTEK.S	2057.37574	3	8.93E-07	0.75	3.46	-	852.8
gi|5031973|ref|NP_005733.1| protein disulfide isomerase-related protein [Homo sapiens]				1.01E-10	4.12	50.24	16.10	48121.0
AHQ-10-7, 6280	R.DGELPVEDDIDLSDVELDDLGKDEL	2759.86565	2	1.01E-10	0.95	4.87	-	1008.9
AHQ-10-7, 3908	R.GSTAPVGGGAFPTIVER.E	1616.79990	2	2.41E-05	0.70	2.81	-	904.8
AHQ-10-7, 4580	K.LAAVDATVNQVLASR.Y	1528.73579	2	4.72E-07	0.96	4.22	-	1536.3
AHQ-10-7, 4222	K.NLEPEWAAAASEVK.E	1515.64921	2	8.89E-05	0.59	2.84	-	280.4
AHQ-10-7, 5724	R.TGEAIVDAALSALR.Q	1387.56411	2	5.46E-05	0.92	2.59	-	1990.9
gi|5031635|ref|NP_005498.1| cofilin 1 (non-muscle) [Homo sapiens]				1.08E-10	5.56	60.28	42.80	18502.4
AHQ-10-12, 3572 - 3597	K.AVLFCLSEDKK.N	1311.52930	2	4.79E-04	0.78	3.08	-	730.1
AHQ-10-13-, 5320 - 5324	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	1.08E-10	0.97	5.65	-	1115.3
AHQ-10-11, 5266	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	5.71E-04	0.61	2.71	-	479.2
AHQ-10-12, 5241 - 5296	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	4.08E-09	0.97	5.58	-	1363.5
AHQ-10-14-, 5344	K.EILVGDVGQTVDDPYATFVK.M	2167.40069	2	3.02E-07	0.96	4.78	-	1242.3
AHQ-10-12, 2640 - 2641	K.HELQANCYEEVKDR.C	1792.90812	3	5.69E-05	0.97	5.38	-	1455.3
AHQ-10-12, 3206	K.KAVLFCLSEDKK.N	1439.70221	3	3.67E-05	0.91	3.66	-	1212.7
AHQ-10-11, 4255	K.LGGSAVISLEGKPL	1341.57848	2	6.82E-04	0.83	3.09	-	838.1
AHQ-10-12, 4296 - 4369	K.LGGSAVISLEGKPL	1341.57848	2	3.29E-08	0.97	4.94	-	1568.2
AHQ-10-14-, 4324 - 4332	K.LGGSAVISLEGKPL	1341.57848	2	2.51E-05	0.92	3.82	-	1214.7
AHQ-10-13-, 4329 - 4342	K.LGGSAVISLEGKPL	1341.57848	2	4.10E-05	0.95	4.49	-	1138.0
AHQ-10-12, 3305	R.YALYDATYETK.E	1338.44364	1	4.28E-05	0.70	2.96	-	458.9
AHQ-10-12, 3253 - 3312	R.YALYDATYETK.E	1338.44364	2	2.59E-07	0.97	4.52	-	1304.9
AHQ-10-13-, 3304	R.YALYDATYETK.E	1338.44364	2	1.43E-04	0.95	3.72	-	1124.6
AHQ-10-11, 3230	R.YALYDATYETK.E	1338.44364	2	1.09E-06	0.93	3.11	-	1334.0
gi|17921989|ref|NP_005991.1| tubulin, alpha 1; testis-specific alpha tubulin; tubulin alpha-1 chain				1.08E-10	10.97	140.27	40.00	49924.1
AHQ-10-7, 4946 - 4952	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	2.82E-09	0.97	4.78	-	1885.9
AHQ-10-7, 5636	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	4.19E-09	0.92	3.79	-	1049.3
AHQ-10-14-, 5644	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	3.18E-04	0.83	3.35	-	987.2
AHQ-10-13-, 5629	R.AVCMLSNTTAIAEAWAR.L	1867.13992	2	8.44E-07	0.92	3.80	-	1391.5
AHQ-10-11, 4876	R.AVCM*LSNTTAIAEAWAR.L	1883.13932	2	1.55E-06	0.92	3.62	-	1147.9
AHQ-10-13, 5833 - 5904	R.AVFVDLEPTVIDEIR.N	1716.95615	2	2.85E-06	0.66	2.88	-	744.9
AHQ-10-7, 5653 - 5660	R.AVFVDLEPTVIDEIR.N	1716.95615	2	4.09E-09	0.91	3.90	-	1256.3
AHQ-10-7, 5118	K.AYHEQLSVAEITNACFEPANQMVK.C	2753.06070	3	6.73E-04	0.83	3.56	-	707.4
AHQ-10-7, 3345	K.DVNAAIAAIK.T	986.14745	1	3.16E-04	0.28	2.06	-	547.1
AHQ-10-7, 3444	K.EIIDPVLDR.I	1070.22122	2	2.72E-05	0.70	2.77	-	478.7
AHQ-10-8, 4918 - 4935	R.IHFPLATYAPVISAEK.A	1758.05310	2	3.51E-05	0.92	3.85	-	656.6
AHQ-10-14-, 4985	R.IHFPLATYAPVISAEK.A	1758.05310	2	4.02E-05	0.86	3.05	-	726.1
AHQ-10-10, 4744 - 4823	R.IHFPLATYAPVISAEK.A	1758.05310	2	1.25E-04	0.79	3.42	-	425.2
AHQ-10-11, 6127	R.LISQIVSSITASLR.F	1488.75471	2	1.58E-05	0.89	3.04	-	1043.0
AHQ-10-7, 5558	R.LISQIVSSITASLR.F	1488.75471	2	4.93E-04	0.79	2.74	-	910.4
AHQ-10-8, 6303	R.LISQIVSSITASLR.F	1488.75471	2	1.16E-06	0.95	4.14	-	974.4

AHQ-10-7, 6258	R.LISQIVSSITASLR.F	1488.75471	2	2.18E-07	0.94	3.84	-	1179.3
AHQ-10-13-, 6185	R.LISQIVSSITASLR.F	1488.75471	2	2.57E-08	0.91	3.62	-	938.5
AHQ-10-14-, 6224	R.LISQIVSSITASLR.F	1488.75471	2	3.26E-05	0.95	3.72	-	1318.8
AHQ-10-8, 3421 - 3422	R.NLDIERPTYTNLNR.L	1719.88022	2	6.46E-07	0.45	2.83	-	303.4
AHQ-10-13-, 3501 - 3512	R.NLDIERPTYTNLNR.L	1719.88022	2	4.56E-05	0.75	3.26	-	498.4
AHQ-10-14-, 5388	R.SIQFVDWCPTGFK.V	1586.79232	2	6.17E-04	0.73	2.71	-	699.4
AHQ-10-11, 5290 - 5298	R.SIQFVDWCPTGFK.V	1586.79232	2	9.16E-07	0.88	3.66	-	771.9
AHQ-10-7, 5380	R.SIQFVDWCPTGFK.V	1586.79232	2	2.47E-04	0.73	3.01	-	632.6
AHQ-10-13-, 5385	R.SIQFVDWCPTGFK.V	1586.79232	2	5.84E-07	0.85	3.33	-	845.7
AHQ-10-13, 5619	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.08E-10	0.57	2.95	-	360.6
AHQ-10-12, 5274	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.38E-06	0.31	2.72	-	287.6
AHQ-10-14-, 5256 - 5312	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	5.24E-07	0.83	3.45	-	555.0
AHQ-10-13-, 5312	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	8.69E-08	0.89	3.99	-	711.7
AHQ-10-11, 5215 - 5218	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	3.80E-10	0.87	4.04	-	583.9
AHQ-10-7, 5260 - 5316	K.TIGGGDDSFTTFFCETGAGK.H	2070.17889	2	1.15E-09	0.90	4.05	-	633.3
AHQ-10-7, 4237	K.VGINYQPPTVVPGGDLAK.V	1826.08584	3	1.58E-04	0.81	4.00	-	678.6
AHQ-10-13-, 4253 - 4273	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.95E-04	0.74	2.95	-	408.8
AHQ-10-12, 4210 - 4280	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	3.59E-07	0.91	4.13	-	520.3
AHQ-10-6, 4259	K.VGINYQPPTVVPGGDLAK.V	1826.08584	2	1.25E-05	0.73	3.13	-	352.1
AHQ-10-7, 3832	K.YM*ACCLLYR.G	1268.50804	2	5.98E-04	0.84	2.63	-	704.2
AHQ-10-7, 4257	K.YMACCLLYR.G	1252.50864	2	4.38E-05	0.92	2.96	-	951.7
gi|20535366|ref|XP_053177.4|	similar to Tubulin alpha-3/alpha-7 chain (Alpha-tubulin 3/7) [Homo sap			1.22E-10	2.65	30.26	9.60	49858.2
AHQ-10-7, 3081	K.DVNAAIATIK.T	1016.17355	2	6.96E-05	0.90	3.65	-	954.9
AHQ-10-7, 3086	K.DVNAAIATIK.T	1016.17355	1	3.77E-04	0.28	2.32	-	231.3
AHQ-10-13-, 3162 - 3165	K.DVNAAIATIK.T	1016.17355	2	4.06E-04	0.86	3.75	-	763.7
AHQ-10-11, 3102	K.DVNAAIATIK.T	1016.17355	2	4.65E-04	0.82	3.22	-	813.5
AHQ-10-7, 5086	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.07E-08	0.88	4.07	-	563.1
AHQ-10-7, 4860 - 4917	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.23E-07	0.89	3.41	-	936.0
AHQ-10-11, 4811 - 4880	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.41E-05	0.69	3.22	-	430.9
AHQ-10-12, 4900	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	5.48E-04	0.58	2.99	-	397.0
AHQ-10-13, 5268	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.41E-05	0.82	3.60	-	546.5
AHQ-10-14, 5511 - 5579	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.58E-07	0.74	3.45	-	373.1
AHQ-10-7, 4521	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.29E-07	0.87	4.09	-	507.3
AHQ-10-13-, 4569	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.42E-04	0.75	3.33	-	380.2
AHQ-10-13-, 4882 - 4941	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.10E-07	0.69	3.21	-	460.6
AHQ-10-14-, 5100	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.22E-10	0.90	3.95	-	722.0
AHQ-10-14-, 4554	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	2.12E-10	0.89	4.36	-	488.9
AHQ-10-14-, 4817 - 4890	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.34E-07	0.89	4.00	-	658.6
AHQ-10-14-, 4916 - 4948	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	1.74E-10	0.96	5.20	-	1000.5
AHQ-10-14-, 4953	K.TIGGGDDSFNTFFSETGAGK.H	2009.07549	2	7.42E-04	0.74	3.35	-	447.7
AHQ-10-14-, 5420 - 5492	R.TIQFVDWCPTGFK.V	1600.81899	2	3.13E-04	0.49	2.62	-	385.6
AHQ-10-13-, 5420	R.TIQFVDWCPTGFK.V	1600.81899	2	1.08E-04	0.85	3.05	-	845.9
gi|29741246|ref|XP_294070.1|	similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho			1.31E-10	2.84	30.27	11.80	35032.0
AHQ-10-9, 5203 - 5205	K.LVINGNPITIFQER.D	1614.87029	2	1.66E-09	0.94	3.96	-	1011.3
AHQ-10-13-, 5436	K.LVINGNPITIFQER.D	1614.87029	2	3.21E-06	0.92	3.45	-	931.6
AHQ-10-13-, 5309 - 5376	K.LVINGNPITIFQER.D	1614.87029	2	1.31E-10	0.92	3.92	-	912.9
AHQ-10-11, 5192 - 5248	K.LVINGNPITIFQER.D	1614.87029	2	4.64E-04	0.81	2.86	-	780.0
AHQ-10-13, 5607 - 5664	K.LVINGNPITIFQER.D	1614.87029	2	4.79E-06	0.91	3.04	-	1057.3
AHQ-10-14, 5923	K.LVINGNPITIFQER.D	1614.87029	2	1.03E-04	0.58	2.51	-	493.5
AHQ-10-14-, 5333	K.LVINGNPITIFQER.D	1614.87029	2	4.69E-08	0.89	3.30	-	750.7
AHQ-10-9, 5719 - 5783	K.VLHDNFGIVKGLM*TTVHAITATQK.T	2612.04471	3	4.10E-04	0.97	5.40	-	2071.1
AHQ-10-9, 6057 - 6069	K.VLHDNFGIVKGLMTTVHAITATQK.T	2596.04531	3	3.71E-09	0.94	4.62	-	1190.5
gi|29568101|ref|NP_006467.3|	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g; AT			1.54E-10	0.97	10.27	14.60	11400.3
AHQ-10-14-, 3668	K.TPALVNAAVTYSKPR.L	1588.83283	3	1.54E-10	0.97	5.31	-	2005.8
gi|13124879|ref|NP_002465.1|	smooth muscle myosin heavy chain 11 isoform SM1 [Homo sapiens]			1.69E-10	6.20	80.36	4.20	227336.7
AHQ-10-5, 2763	R.EDQSILCTGESGAGK.T	1553.63107	2	3.79E-04	0.70	2.87	-	614.7
AHQ-10-5, 2941	K.FDQLLAEEK.N	1093.21165	2	1.87E-06	0.88	2.87	-	1188.4
AHQ-10-2, 3016	K.FDQLLAEEK.N	1093.21165	2	3.87E-06	0.90	3.07	-	1327.7
AHQ-10-3, 2962	K.FDQLLAEEK.N	1093.21165	2	3.16E-05	0.91	2.94	-	1479.8
AHQ-10-2, 2988 - 2992	R.KFDQLLAEEK.N	1221.38456	1	8.73E-06	0.37	2.91	-	510.1
AHQ-10-2, 2984	R.KFDQLLAEEK.N	1221.38456	3	9.01E-06	0.73	3.30	-	792.3
AHQ-10-6, 2827 - 2875	R.KFDQLLAEEK.N	1221.38456	2	2.55E-05	0.86	3.29	-	946.1
AHQ-10-2, 5644	K.LQQLFNHTMFILEQEEYQR.E	2468.77258	3	9.65E-04	0.90	3.62	-	1479.5
AHQ-10-2, 5054 - 5115	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	6.79E-09	0.98	7.19	-	2314.4
AHQ-10-2, 5234	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	5.03E-08	0.95	4.45	-	1923.7
AHQ-10-3, 4989	K.LQQLFNHTM*FILEQEEYQR.E	2484.77198	3	2.14E-05	0.92	4.41	-	1219.9
AHQ-10-2, 4546	R.NWQWWR.L	976.07459	1	1.65E-04	0.44	2.02	-	250.1
AHQ-10-2, 5714 - 5770	K.QLLQANPILEAFGNAK.T	1727.98540	2	3.24E-08	0.96	4.54	-	1171.9
AHQ-10-2, 5826	K.QLLQANPILEAFGNAK.T	1727.98540	2	6.40E-05	0.95	4.51	-	1015.9
AHQ-10-2, 5914	K.QLLQANPILEAFGNAK.T	1727.98540	2	6.87E-04	0.82	3.28	-	563.3
AHQ-10-1, 5789 - 5849	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.17E-04	0.90	3.93	-	545.3
AHQ-10-5, 5739 - 5795	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.69E-10	0.97	5.17	-	1065.9
AHQ-10-10, 5495 - 5554	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.48E-04	0.76	2.81	-	695.9
AHQ-10-4, 5927	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.92E-06	0.84	3.35	-	662.9
AHQ-10-4, 5752 - 5820	K.QLLQANPILEAFGNAK.T	1727.98540	2	2.00E-07	0.96	4.27	-	1583.0
AHQ-10-3, 5657 - 5730	K.QLLQANPILEAFGNAK.T	1727.98540	2	4.30E-09	0.96	4.78	-	1089.0
AHQ-10-6, 5613 - 5673	K.QLLQANPILEAFGNAK.T	1727.98540	2	1.90E-08	0.97	4.83	-	1214.1
AHQ-10-4, 5371	K.TQLEELEDELQATEDAK.L	1963.04334	3	6.45E-07	0.97	5.99	-	1480.7
AHQ-10-3, 5277 - 5289	K.TQLEELEDELQATEDAK.L	1963.04334	3	7.44E-07	0.97	5.60	-	1792.8
AHQ-10-3, 5275	K.TQLEELEDELQATEDAK.L	1963.04334	2	3.52E-06	0.98	5.33	-	2240.0
AHQ-10-2, 5362	K.TQLEELEDELQATEDAK.L	1963.04334	3	4.68E-08	0.96	5.39	-	1425.1
AHQ-10-2, 5358 - 5418	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.16E-06	0.95	4.90	-	1209.0
AHQ-10-5, 5263 - 5335	K.TQLEELEDELQATEDAK.L	1963.04334	2	5.29E-04	0.89	3.93	-	614.3
AHQ-10-5, 5347	K.TQLEELEDELQATEDAK.L	1963.04334	2	1.00E-08	0.98	6.59	-	2244.5
AHQ-10-2, 3930	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.61E-07	0.96	4.95	-	1114.7
AHQ-10-1, 5406	K.TQLEELEDELQATEDAK.L	1963.04334	3	9.28E-05	0.93	4.00	-	1510.3
AHQ-10-6, 5235 - 5315	K.TQLEELEDELQATEDAK.L	1963.04334	2	7.01E-06	0.97	5.26	-	1707.9
AHQ-10-6, 5241	K.TQLEELEDELQATEDAK.L	1963.04334	3	5.86E-04	0.86	4.13	-	711.1
AHQ-10-4, 5361	K.TQLEELEDELQATEDAK.L	1963.04334	2	2.47E-09	0.98	5.89	-	1844.8
AHQ-10-7, 5226 - 5252	K.TQLEELEDELQATEDAK.L	1963.04334	2	4.40E-08	0.97	5.49	-	1589.3
AHQ-10-1, 5401	K.TQLEELEDELQATEDAK.L	1963.04334	2	7.83E-10	0.97	4.83	-	1834.9
gi|27498267|ref|XP_209737.1|	similar to tyrosine 3/tryptophan 5 -monooxygenase activation protein,			1.83E-10	1.90	20.35	31.60	11063.6
AHQ-10-10, 5434	R.DICNDVLSLLEK.F	1420.61093	2	3.16E-06	0.94	3.53	-	1597.1
AHQ-10-11, 6196	R.DICNDVLSLLEK.F	1420.61093	2	6.02E-07	0.92	3.49	-	1431.6
AHQ-10-10, 4714 - 4787	K.GIVDQSQQAYQEAFEISK.K	2042.19176	3	4.27E-10	0.98	6.95	-	2302.6
AHQ-10-10, 4710 - 4766	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.83E-10	0.98	4.94	-	2029.1
AHQ-10-11, 4547	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.87E-04	0.71	3.13	-	466.4
AHQ-10-11, 4758	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	6.42E-06	0.94	4.69	-	867.3
AHQ-10-10, 4491	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	9.76E-04	0.57	2.63	-	483.3
AHQ-10-9, 4640 - 4688	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	9.92E-08	0.96	4.67	-	1263.4
AHQ-10-12, 4840	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	3.44E-04	0.97	5.33	-	1715.3
AHQ-10-13, 5183	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	2.58E-06	0.96	4.41	-	1487.2
AHQ-10-13-, 4857	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	1.98E-10	0.97	5.64	-	1410.3
AHQ-10-14-, 4860	K.GIVDQSQQAYQEAFEISK.K	2042.19176	2	5.13E-09	0.97	5.01	-	1541.0
gi|4759212|ref|NP_004598.1|	beta-tubulin cofactor A [Homo sapiens]			2.26E-10	1.94	20.29	25.90	12854.8
AHQ-10-13-, 3394	R.ILENEKDLEEAEEYKEAR.L	2209.35284	2	5.84E-07	0.95	4.57	-	1180.7
AHQ-10-13-, 3386	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	2.26E-10	0.97	5.69	-	1997.0

AHQ-10-13, 3719 - 3775	R.ILENEKDLEEAEEYKEAR.L	2209.35284	3	4.84E-09	0.96	5.77	-	1310.1
AHQ-10-13-, 3648 - 3705	R.LEAAYLDLQR.I	1192.34645	2	3.60E-06	0.96	4.02	-	1557.4
AHQ-10-13, 4096	R.LEAAYLDLQR.I	1192.34645	2	5.50E-05	0.95	3.20	-	1720.6
gi|29739414|ref|XP_294015.1| similar to Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH) [Ho				2.30E-10	1.52	20.25	12.80	26916.7
AHQ-10-9, 3711 - 3779	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.31E-05	0.91	4.30	-	1209.2
AHQ-10-11, 4064	K.IISNASCTTNCLAPLAK.V	1837.10868	2	3.92E-05	0.51	2.76	-	657.3
AHQ-10-11, 3759	K.IISNASCTTNCLAPLAK.V	1837.10868	2	2.21E-07	0.58	2.95	-	837.5
AHQ-10-10, 3800 - 3858	K.IISNASCTTNCLAPLAK.V	1837.10868	2	3.80E-07	0.85	3.82	-	1222.7
AHQ-10-9, 4493 - 4551	K.LISWYDNEFGYSNR.V	1764.87478	2	5.68E-09	0.96	4.95	-	1187.8
AHQ-10-11, 4683	K.LISWYDNEFGYSNR.V	1764.87478	2	3.84E-09	0.97	4.82	-	1420.6
AHQ-10-13, 5155	K.LISWYDNEFGYSNR.V	1764.87478	2	3.26E-07	0.95	4.24	-	1277.3
AHQ-10-13-, 4817 - 4873	K.LISWYDNEFGYSNR.V	1764.87478	2	2.12E-06	0.75	3.28	-	523.1
AHQ-10-14-, 4705 - 4784	K.LISWYDNEFGYSNR.V	1764.87478	2	2.30E-10	0.95	4.45	-	1033.3
AHQ-10-9, 4608 - 4663	K.LISWYDNEFGYSNR.V	1764.87478	2	8.00E-08	0.91	4.06	-	646.0
gi|4827056|ref|NP_005103.1| WD repeat-containing protein 1 isoform 2 [Homo sapiens]				2.39E-10	11.15	130.33	41.60	58001.9
AHQ-10-6, 4769 - 4832	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	1.80E-07	0.96	5.44	-	1682.5
AHQ-10-7, 4773	K.AHDGGIYAISWSPDSTHLLSASGDK.T	2586.75455	3	1.37E-04	0.96	4.89	-	1883.3
AHQ-10-6, 5217	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	1.53E-09	0.84	3.86	-	742.6
AHQ-10-7, 5166 - 5236	K.CFSIDNPGYEPEVVAVHPGGDTVAIGGVDGNVR.L	3400.67708	3	5.33E-04	0.74	3.22	-	734.9
AHQ-10-6, 3793 - 3865	R.FATASADGQIYIYDGK.T	1720.86021	2	1.29E-07	0.91	3.76	-	969.5
AHQ-10-6, 3688	R.FATASADGQIYIYDGK.T	1720.86021	2	2.56E-04	0.82	3.05	-	760.4
AHQ-10-6, 4001 - 4060	R.FATASADGQIYIYDGK.T	1720.86021	2	2.98E-08	0.87	3.69	-	849.4
AHQ-10-6, 4405 - 4483	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	3	1.81E-04	0.95	4.56	-	1515.9
AHQ-10-6, 4432 - 4492	K.GPVTDVAYSHDGAFLAVCDASK.V	2282.47194	2	9.38E-05	0.97	5.17	-	1448.5
AHQ-10-6, 2697	K.IKDIAWTEDSK.R	1306.44632	2	4.08E-05	0.94	3.72	-	1290.9
AHQ-10-6, 2460 - 2513	K.IKDIAWTEDSKR.I	1462.63267	2	6.52E-04	0.83	3.18	-	793.1
AHQ-10-6, 2465	K.IKDIAWTEDSKR.I	1462.63267	3	1.38E-04	0.77	3.61	-	681.0
AHQ-10-7, 5189	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	4.27E-04	0.77	3.25	-	634.2
AHQ-10-6, 5104 - 5175	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	2.39E-10	0.94	4.99	-	1020.8
AHQ-10-6, 5229 - 5309	R.LATGSDDNCAAFFEGPPFK.F	2046.20216	2	6.52E-10	0.96	5.24	-	1278.1
AHQ-10-6, 4147	R.M*TVDESGQLISCSMDDTVR.Y	2162.36305	2	8.55E-09	0.93	4.44	-	571.5
AHQ-10-6, 2152	K.SIQCLTVHKNGGK.S	1443.65418	2	3.86E-04	0.53	2.71	-	676.3
AHQ-10-6, 4071	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	6.31E-07	0.98	6.66	-	2136.3
AHQ-10-6, 4157	K.SYIYSGSHDGHINYWDSETGENDSFAGK.G	3138.17570	3	1.77E-06	0.97	6.19	-	1343.3
AHQ-10-6, 3539 - 3541	K.VFASLPQVER.G	1146.32091	2	9.64E-04	0.81	2.86	-	587.5
AHQ-10-9, 3668	K.YAPSGFYIASGDVSGK.L	1619.75589	2	1.30E-04	0.74	2.76	-	496.6
AHQ-10-6, 2900 - 2965	K.YEYQPFAGK.I	1103.20822	2	5.19E-05	0.87	2.70	-	694.2
gi|28626504|ref|NP_113659.3| UNC-112 related protein 2 [Homo sapiens]				2.49E-10	20.10	230.31	55.70	75429.7
AHQ-10-6, 3347	K.AGDALWLR.F	902.03223	2	1.70E-04	0.89	3.33	-	1211.1
AHQ-10-6, 6235	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.18E-10	0.82	3.30	-	704.6
AHQ-10-3, 6189 - 6194	R.ASFSQPLFQAVAAICR.L	1768.02967	2	4.68E-05	0.94	4.03	-	903.8
AHQ-10-7, 6176	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.19E-05	0.95	4.29	-	1056.6
AHQ-10-11, 6046 - 6050	R.ASFSQPLFQAVAAICR.L	1768.02967	2	2.05E-06	0.89	3.60	-	747.1
AHQ-10-8, 6207 - 6221	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.55E-06	0.93	4.27	-	792.1
AHQ-10-6, 6052 - 6112	R.ASFSQPLFQAVAAICR.L	1768.02967	2	8.58E-09	0.95	4.23	-	908.1
AHQ-10-5, 6259	R.ASFSQPLFQAVAAICR.L	1768.02967	2	5.92E-04	0.77	2.78	-	491.5
AHQ-10-9, 5910 - 5916	R.ASFSQPLFQAVAAICR.L	1768.02967	2	1.43E-04	0.85	3.08	-	798.9
AHQ-10-6, 6116 - 6120	R.ASFSQPLFQAVAAICR.L	1768.02967	3	1.22E-07	0.96	5.45	-	1186.2
AHQ-10-6, 3545 - 3617	K.EKEPEEELYDLSK.V	1609.71294	2	7.69E-07	0.70	2.96	-	416.2
AHQ-10-6, 6217	R.FIQAWQSLPDFGISYVM*VR.F	2274.62593	3	3.69E-06	0.89	4.09	-	987.0
AHQ-10-6, 3147 - 3207	K.GCEVVPDVNVSGQK.F	1489.63335	2	8.86E-10	0.91	3.03	-	1019.0
AHQ-10-11, 3190 - 3195	K.GCEVVPDVNVSGQK.F	1489.63335	2	4.93E-06	0.76	3.03	-	592.9
AHQ-10-6, 6251	R.GEELDEDLFLQLTGGHEAF	2121.24574	2	1.95E-07	0.88	3.88	-	761.4
AHQ-10-6, 3177	R.GM*PAHFSDSAQTEACYHM*LSR.P	2430.63997	3	4.88E-09	0.96	4.87	-	1747.7
AHQ-10-6, 3765	R.IDLAVGDVVK.T	1029.21223	1	2.74E-05	0.58	2.93	-	460.3
AHQ-10-9, 3599 - 3600	R.IDLAVGDVVK.T	1029.21223	2	1.89E-04	0.91	3.37	-	1260.5
AHQ-10-12, 4358	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	5.76E-05	0.97	5.12	-	1603.0
AHQ-10-9, 4145	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	7.83E-10	0.98	5.47	-	1851.3
AHQ-10-6, 4319	R.ILEAHQNVAQLSLAEAQLR.F	2105.38372	2	4.12E-07	0.98	6.22	-	1645.2
AHQ-10-9, 2615	R.KDEILGIANNR.L	1243.39499	2	4.61E-04	0.84	2.65	-	980.5
AHQ-10-6, 2703 - 2760	R.KDEILGIANNR.L	1243.39499	2	2.72E-07	0.95	4.39	-	1457.0
AHQ-10-6, 3996	R.KQDWSDHAIWWEQK.R	1858.00504	3	4.76E-08	0.96	5.10	-	1452.0
AHQ-10-6, 6044 - 6099	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.12E-06	0.95	5.13	-	808.6
AHQ-10-6, 5947	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	6.01E-04	0.92	3.94	-	977.0
AHQ-10-6, 5684 - 5737	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	1.79E-04	0.86	3.82	-	601.2
AHQ-10-7, 6089	K.LEGSAPTDVLDSLTTIPELK.D	2100.35256	2	5.31E-07	0.92	4.38	-	746.3
AHQ-10-6, 2645 - 2647	R.LFFGPQHR.P	1002.15349	2	4.05E-04	0.54	2.64	-	485.9
AHQ-10-6, 4528 - 4596	K.LLVPSPEGM*SEIYLR.C	1721.01141	2	1.51E-06	0.75	3.01	-	325.1
AHQ-10-6, 5707 - 5715	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	1.29E-05	0.94	4.88	-	1299.1
AHQ-10-8, 6285 - 6287	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.68E-06	0.90	4.03	-	1463.0
AHQ-10-7, 6241	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	3.72E-08	0.96	5.51	-	1693.9
AHQ-10-3, 6237 - 6293	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.21E-04	0.87	4.54	-	781.6
AHQ-10-9, 5974	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	6.65E-05	0.89	3.80	-	1288.8
AHQ-10-2, 6343	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	5.86E-05	0.90	4.08	-	1075.3
AHQ-10-6, 6191	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L	3027.24073	3	2.24E-09	0.90	4.33	-	1092.9
AHQ-10-7, 2442	R.LTQLYEQAR.W	1122.25622	2	5.62E-06	0.93	3.44	-	1543.1
AHQ-10-6, 2435 - 2455	R.LTQLYEQAR.W	1122.25622	2	1.16E-06	0.91	3.66	-	915.0
AHQ-10-11, 3922	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	6.07E-06	0.46	3.18	-	346.2
AHQ-10-6, 3892 - 3947	K.SQDEAPGDPIQQLNLK.G	1753.89174	2	3.15E-09	0.89	3.96	-	517.4
AHQ-10-6, 4075 - 4092	K.TASGDYIDSSWELR.V	1600.66783	2	1.61E-06	0.83	3.00	-	695.4
AHQ-10-9, 4024 - 4025	K.TASGDYIDSSWELR.V	1600.66783	2	2.78E-09	0.91	3.45	-	1168.2
AHQ-10-7, 4172	K.TASGDYIDSSWELR.V	1600.66783	2	4.08E-06	0.93	3.84	-	1000.5
AHQ-10-6, 4191 - 4255	K.TASGDYIDSSWELR.V	1600.66783	2	1.09E-09	0.95	3.87	-	1306.4
AHQ-10-6, 3928 - 3985	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	2.22E-05	0.95	5.90	-	1069.1
AHQ-10-6, 3824	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	3	1.37E-08	0.97	5.68	-	1776.9
AHQ-10-6, 3828	R.TGSGGPGNHPHGPDASAEGLNPYGLVAPR.F	2783.95312	2	1.55E-06	0.93	4.86	-	566.7
AHQ-10-6, 6367	R.TM*ADSSYTSEVQAILAFLSLQR.T	2448.73471	3	2.04E-07	0.95	4.92	-	1561.4
AHQ-10-6, 3867	R.VFVGEEDPEAESVTLR.V	1777.91007	3	1.74E-04	0.93	3.99	-	1483.8
AHQ-10-6, 3844	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.93E-05	0.92	3.65	-	1348.5
AHQ-10-14-, 3896 - 3938	R.VFVGEEDPEAESVTLR.V	1777.91007	2	6.59E-09	0.93	4.03	-	1031.9
AHQ-10-11, 3844	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.21E-06	0.85	3.84	-	786.0
AHQ-10-5, 3947	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.65E-08	0.94	4.35	-	1174.7
AHQ-10-12, 3909	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.88E-06	0.74	2.75	-	782.5
AHQ-10-9, 3705	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.09E-05	0.85	3.38	-	954.9
AHQ-10-7, 3850 - 3856	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.49E-10	0.96	4.72	-	1372.0
AHQ-10-8, 3914	R.VFVGEEDPEAESVTLR.V	1777.91007	2	1.79E-05	0.90	3.27	-	1482.7
AHQ-10-3, 3935	R.VFVGEEDPEAESVTLR.V	1777.91007	2	5.25E-08	0.86	3.23	-	1041.7
AHQ-10-4, 3965	R.VFVGEEDPEAESVTLR.V	1777.91007	2	2.97E-09	0.92	4.02	-	1111.4
AHQ-10-9, 2811	R.VTGESHIGGVLLK.I	1310.52448	2	2.17E-07	0.88	3.02	-	1391.4
AHQ-10-14-, 2998	R.VTGESHIGGVLLK.I	1310.52448	2	1.58E-04	0.75	2.81	-	949.5
AHQ-10-7, 2902	R.VTGESHIGGVLLK.I	1310.52448	2	1.56E-06	0.91	3.19	-	1583.8
AHQ-10-6, 2935	R.VTGESHIGGVLLK.I	1310.52448	1	6.76E-04	0.74	2.82	-	820.7
AHQ-10-6, 2915 - 2972	R.VTGESHIGGVLLK.I	1310.52448	2	5.13E-06	0.94	3.97	-	1419.2
AHQ-10-5, 4733	K.VVLAGGVAPALFR.G	1270.54832	2	1.03E-07	0.97	4.60	-	2080.9
AHQ-10-9, 4420	K.VVLAGGVAPALFR.G	1270.54832	2	4.66E-06	0.93	4.01	-	1359.2
AHQ-10-7, 4626	K.VVLAGGVAPALFR.G	1270.54832	2	8.79E-07	0.96	4.46	-	1499.3
AHQ-10-6, 4623 - 4624	K.VVLAGGVAPALFR.G	1270.54832	2	3.26E-07	0.97	4.85	-	1473.3

AHQ-10-11, 4527 - 4596	K.VVLAGGVAPALFR.G	1270.54832	2	4.13E-07	0.94	3.67	-	1402.2
gi|11761631|ref|NP_005132.1| fibrinogen, beta chain preproprotein [Homo sapiens]				2.63E-10	21.69	250.29	44.60	55901.8
AHQ-10-6, 2464 - 2481	K.AHYGGFTVQNEANK.Y	1536.63020	2	3.87E-10	0.91	3.73	-	1022.3
AHQ-10-11, 2483	K.AHYGGFTVQNEANK.Y	1536.63020	2	1.60E-06	0.85	3.23	-	788.2
AHQ-10-7, 3126	R.DNDGWLTSDPR.K	1276.29403	2	4.54E-04	0.87	3.12	-	1026.9
AHQ-10-11, 3263	K.DNENVVNEYSSELEK.H	1769.80167	2	3.14E-06	0.66	2.78	-	386.4
AHQ-10-9, 3801	K.DNENVVNEYSSELEK.H	1769.80167	2	5.32E-05	0.90	3.54	-	979.9
AHQ-10-6, 3279	K.DNENVVNEYSSELEK.H	1769.80167	2	4.82E-07	0.77	3.08	-	565.5
AHQ-10-7, 3872 - 3936	K.DNENVVNEYSSELEK.H	1769.80167	2	4.32E-07	0.87	3.75	-	714.1
AHQ-10-7, 3538	K.DNENVVNEYSSELEK.H	1769.80167	2	1.66E-05	0.87	3.64	-	797.3
AHQ-10-11, 3918	K.DNENVVNEYSSELEK.H	1769.80167	2	3.51E-07	0.75	3.04	-	595.4
AHQ-10-7, 4068 - 4140	K.DNENVVNEYSSELEK.H	1769.80167	2	1.25E-05	0.84	3.74	-	556.7
AHQ-10-8, 3302 - 3305	K.DNENVVNEYSSELEK.H	1769.80167	2	8.41E-04	0.75	3.47	-	411.8
AHQ-10-7, 3360	K.DNENVVNEYSSELEK.H	1769.80167	2	3.03E-08	0.89	3.46	-	1022.7
AHQ-10-7, 3268	K.DNENVVNEYSSELEK.H	1769.80167	2	2.70E-06	0.86	4.03	-	467.9
AHQ-10-6, 4085 - 4116	K.DNENVVNEYSSELEK.H	1769.80167	2	1.05E-08	0.88	4.28	-	644.5
AHQ-10-6, 3576	K.EDGGGWWYNR.C	1240.26508	2	9.84E-04	0.81	3.30	-	476.7
AHQ-10-7, 3565 - 3568	K.EDGGGWWYNR.C	1240.26508	2	1.12E-04	0.64	2.87	-	409.7
AHQ-10-6, 3385	R.EEAPSLRPAPPPISGGGYR.A	1952.15981	2	6.86E-04	0.35	2.65	-	209.5
AHQ-10-6, 3991 - 4007	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	1.08E-05	0.88	3.91	-	841.4
AHQ-10-8, 4017	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	1.77E-04	0.89	3.62	-	1243.2
AHQ-10-6, 3591	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	3	1.79E-07	0.87	4.08	-	1034.3
AHQ-10-7, 3965 - 3969	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	1.83E-06	0.92	4.67	-	641.3
AHQ-10-7, 3964	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	3	1.13E-07	0.93	5.17	-	1102.3
AHQ-10-8, 4018	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	5.75E-05	0.82	4.00	-	412.6
AHQ-10-6, 4004	K.GGETSEMYLIQPDSSVKPYR.V	2258.49373	2	2.98E-06	0.84	3.83	-	579.3
AHQ-10-7, 3578	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	1.71E-04	0.78	3.46	-	349.4
AHQ-10-6, 3604	K.GGETSEM*YLIQPDSSVKPYR.V	2274.49313	2	9.12E-06	0.36	2.58	-	309.3
AHQ-10-7, 4124 - 4193	K.HGTDDGVVWMNWK.G	1545.70374	2	1.61E-04	0.94	3.78	-	1277.8
AHQ-10-7, 3518 - 3584	K.HGTDDGVVWM*NWK.G	1561.70314	2	1.52E-04	0.94	3.98	-	1160.9
AHQ-10-6, 3320	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	1.01E-04	0.70	3.40	-	657.3
AHQ-10-8, 3657	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	1.55E-05	0.90	4.06	-	865.6
AHQ-10-7, 3238 - 3292	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	1.21E-05	0.91	4.72	-	716.7
AHQ-10-6, 3703	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	5.21E-06	0.69	2.99	-	607.5
AHQ-10-8, 3651	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	6.25E-06	0.93	5.18	-	751.0
AHQ-10-9, 3171	R.KGGETSEM*YLIQPDSSVKPYR.V	2402.66604	3	4.21E-04	0.82	3.43	-	1059.5
AHQ-10-7, 3668	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	2	1.45E-05	0.92	4.44	-	844.5
AHQ-10-7, 3629 - 3684	R.KGGETSEMYLIQPDSSVKPYR.V	2386.66664	3	2.66E-07	0.95	5.87	-	804.4
AHQ-10-7, 3232 - 3298	K.LESDVSAQMEYCR.T	1589.73005	2	6.85E-07	0.91	3.71	-	987.7
AHQ-10-7, 3109 - 3176	K.LESDVSAQMEYCR.T	1589.73005	2	1.41E-08	0.91	3.56	-	1101.0
AHQ-10-6, 2583 - 2591	K.LESDVSAQM*EYCR.T	1605.72945	2	8.15E-08	0.94	4.33	-	818.7
AHQ-10-7, 2584	K.LESDVSAQM*EYCR.T	1605.72945	2	3.47E-08	0.94	4.49	-	990.5
AHQ-10-6, 3259	K.LESDVSAQMEYCR.T	1589.73005	2	6.97E-07	0.84	2.87	-	954.3
AHQ-10-8, 5942	R.M*GPTELLIEMEDWK.G	1708.97776	2	4.06E-06	0.76	2.77	-	858.0
AHQ-10-7, 5885	R.M*GPTELLIEMEDWK.G	1708.97776	2	6.47E-10	0.95	4.21	-	1315.2
AHQ-10-6, 5856 - 5869	R.M*GPTELLIEMEDWK.G	1708.97776	2	1.99E-04	0.94	4.27	-	1035.6
AHQ-10-6, 4891 - 4967	K.NYCGLPGEYWLGNDK.I	1787.92994	2	2.39E-07	0.88	4.16	-	386.0
AHQ-10-7, 4948 - 4981	K.NYCGLPGEYWLGNDK.I	1787.92994	2	4.07E-04	0.67	3.06	-	307.2
AHQ-10-8, 4951	K.NYCGLPGEYWLGNDK.I	1787.92994	2	6.72E-05	0.84	3.65	-	325.7
AHQ-10-6, 2267	K.QGFGNVATNTDGK.N	1309.36716	2	5.99E-04	0.73	2.79	-	472.5
AHQ-10-7, 2224 - 2282	K.QGFGNVATNTDGK.N	1309.36716	2	1.23E-05	0.76	3.14	-	543.6
AHQ-10-8, 3147	K.REEAPSLRPAPPPISGGGYR.A	2108.34617	3	8.31E-06	0.95	4.33	-	1742.5
AHQ-10-7, 3092 - 3148	K.REEAPSLRPAPPPISGGGYR.A	2108.34617	3	2.93E-05	0.94	5.09	-	1388.2
AHQ-10-6, 3108 - 3167	K.REEAPSLRPAPPPISGGGYR.A	2108.34617	3	1.67E-04	0.96	5.15	-	1716.1
AHQ-10-8, 3685	R.TPCTVSCNIPVVSGK.E	1621.85811	2	2.37E-04	0.68	2.80	-	445.7
AHQ-10-7, 3625 - 3680	R.TPCTVSCNIPVVSGK.E	1621.85811	2	2.21E-05	0.80	3.59	-	516.3
AHQ-10-6, 4672	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	2	4.31E-08	0.73	3.36	-	254.5
AHQ-10-6, 4573	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	2.32E-04	0.92	4.56	-	1205.7
AHQ-10-7, 4553 - 4608	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	7.73E-04	0.87	3.97	-	793.8
AHQ-10-6, 4659	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	6.43E-08	0.95	5.24	-	1043.7
AHQ-10-7, 4664	R.TPCTVSCNIPVVSGKECEEIIR.K	2552.88440	3	1.74E-09	0.96	5.63	-	1294.3
AHQ-10-7, 4317 - 4320	R.TPCTVSCNIPVVSGKECEEIIRK.G	2681.05731	3	2.19E-05	0.79	3.92	-	525.7
AHQ-10-6, 4276 - 4277	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	1.61E-06	0.68	3.16	-	427.7
AHQ-10-7, 4250 - 4258	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	6.23E-04	0.80	2.92	-	948.8
AHQ-10-7, 3806 - 3877	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	4.42E-07	0.93	4.53	-	745.1
AHQ-10-7, 4244 - 4304	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	2.63E-10	0.97	5.53	-	1105.8
AHQ-10-7, 4345	R.VYCDMNTENGGWTVIQNR.Q	2159.34553	2	6.75E-05	0.87	3.66	-	951.3
AHQ-10-6, 3816 - 3887	R.VYCDM*NTENGGWTVIQNR.Q	2175.34493	2	3.55E-08	0.94	4.19	-	1167.9
AHQ-10-6, 2209	K.YQISVNK.Y	851.96999	2	2.33E-04	0.78	2.57	-	682.4
AHQ-10-6, 4335	R.YYWGGQYTWDM*AK.H	1685.83949	2	1.05E-06	0.90	3.07	-	862.7
AHQ-10-11, 4286	R.YYWGGQYTWDM*AK.H	1685.83949	2	6.71E-05	0.94	4.16	-	936.9
AHQ-10-14-, 4353 - 4381	R.YYWGGQYTWDM*AK.H	1685.83949	2	1.67E-04	0.83	2.81	-	746.2
AHQ-10-7, 4800 - 4804	R.YYWGGQYTWDMAK.H	1669.84009	2	5.53E-05	0.94	3.58	-	1268.1
gi|28178832|ref|NP_002159.2| isocitrate dehydrogenase 2 (NADP+), mitochondrial precursor; isocitrat				2.71E-10	5.03	60.24	17.90	50909.0
AHQ-10-8, 4034 - 4038	K.DLAGCIHGLSNVK.L	1385.57150	2	2.71E-10	0.97	4.70	-	1999.3
AHQ-10-8, 5770	K.GRPTSTNPIASIFAWTR.G	1876.10817	2	7.44E-05	0.45	2.52	-	467.0
AHQ-10-8, 5358 - 5415	K.LNEHFLNTTDFLDTIK.S	1922.12725	2	2.37E-05	0.92	3.95	-	971.8
AHQ-10-8, 2169 - 2215	K.TIEAEAAHGTVTR.H	1356.46696	2	7.38E-05	0.85	2.99	-	895.3
AHQ-10-8, 3105	K.VCVETVESGAMTK.D	1412.61230	2	1.99E-05	0.97	4.03	-	1794.3
AHQ-10-8, 4133	K.YFDLGLPNR.D	1095.23246	2	3.67E-05	0.87	2.86	-	820.6
gi|4507869|ref|NP_003361.1| vasodilator-stimulated phosphoprotein [Homo sapiens]				3.15E-10	1.52	20.30	10.30	39829.4
AHQ-10-8, 3273	K.SSSSVTTSETQPCTPSSSDYSDLQR.V	2709.75011	2	8.96E-04	0.54	3.03	-	230.3
AHQ-10-8, 5859	K.VKEEIIEAFVQELR.K	1703.96061	3	6.36E-06	0.93	4.52	-	1150.1
AHQ-10-8, 5850 - 5857	K.VKEEIIEAFVQELR.K	1703.96061	2	3.15E-10	0.98	5.93	-	1670.2
gi|18104989|ref|NP_002822.2| protein tyrosine phosphatase, non-receptor type 6 isoform 1; protein-t				3.16E-10	2.61	30.22	7.10	67560.7
AHQ-10-6, 5536	K.AGFWEEFESLQK.Q	1471.59489	2	1.90E-04	0.84	3.31	-	1005.9
AHQ-10-6, 3227 - 3245	K.GLDCDIDIQK.T	1178.29500	2	6.62E-06	0.87	2.95	-	1078.1
AHQ-10-6, 6307	R.YTVGGLETFDSLTDLVEHFK.K	2272.49536	3	3.16E-10	0.90	4.35	-	582.9
gi|7656991|ref|NP_055140.1| coronin, actin binding protein, 1C; coronin, actin-binding protein, 1C;				3.51E-10	7.52	90.28	32.10	53248.7
AHQ-10-6, 5545	R.AIFLADGNVFTTGFSR.M	1716.91793	2	1.61E-04	0.93	4.00	-	987.7
AHQ-10-6, 5421 - 5487	R.AIFLADGNVFTTGFSR.M	1716.91793	2	3.51E-10	0.97	5.38	-	1691.8
AHQ-10-6, 3171	R.HVFGQAVKNDQCYDDIR.V	2067.22783	3	2.48E-05	0.76	3.00	-	592.7
AHQ-10-6, 3405	R.KCEPIIMTVPR.K	1345.65706	2	5.91E-04	0.74	2.98	-	477.6
AHQ-10-7, 6313	R.KSDLFQDDLYPDTAGPEAALEAEEWFEGK.N	3273.46087	3	1.88E-04	0.95	5.64	-	934.6
AHQ-10-6, 2287 - 2349	K.NDQCYDDIR.V	1200.21762	2	1.00E-04	0.81	2.93	-	1081.7
AHQ-10-6, 6239 - 6320	K.NM*QEPIALHEM*DTSNGVLLPFYDPDTSIIYLCGK.G	3917.39141	3	5.64E-07	0.77	3.79	-	392.3
AHQ-10-6, 2385 - 2436	K.SIKDTICNQDER.I	1480.58332	2	1.58E-05	0.85	2.71	-	1217.6
AHQ-10-7, 4165	R.VTWDSSFCAVNPR.F	1540.68205	2	1.58E-05	0.87	3.07	-	975.1
AHQ-10-6, 4192	R.VTWDSSFCAVNPR.F	1540.68205	2	1.95E-08	0.95	3.59	-	1496.8
AHQ-10-6, 5505 - 5584	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	3	1.95E-04	0.91	3.94	-	827.3
AHQ-10-6, 5593	R.YFEITDESPYVHYLNTFSSK.E	2441.63258	2	5.41E-06	0.72	3.07	-	597.8
gi|17986258|ref|NP_066299.2| smooth muscle and non-muscle myosin alkali light chain isoform 1 [Homo				3.78E-10	5.25	60.26	37.10	16930.0
AHQ-10-13-, 4136	K.DQGTYEDYVEGLR.V	1545.58904	2	1.52E-04	0.95	3.68	-	1392.3
AHQ-10-12, 2604 - 2636	R.HVLVTLGEK.M	996.18547	2	6.46E-04	0.87	2.77	-	704.7
AHQ-10-12, 2501 - 2556	R.HVLVTLGEK.M	996.18547	2	2.34E-05	0.88	3.34	-	698.8
AHQ-10-12, 3697 - 3760	K.NKDQGTYEDYVEGLR.V	1787.86505	3	2.72E-06	0.87	3.77	-	1067.4
AHQ-10-12, 3853	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.24E-06	0.75	3.28	-	538.5

AHQ-10-12, 3949 - 3961	K.NKDQGTYEDYVEGLR.V	1787.86505	2	1.78E-05	0.79	3.17	-	702.6
AHQ-10-12, 3696	K.NKDQGTYEDYVEGLR.V	1787.86505	2	3.68E-06	0.71	2.70	-	678.2
AHQ-10-14, 4519 - 4524	K.NKDQGTYEDYVEGLR.V	1787.86505	2	5.00E-05	0.62	2.96	-	551.1
AHQ-10-14-, 3670 - 3721	K.NKDQGTYEDYVEGLR.V	1787.86505	2	2.28E-05	0.90	3.80	-	905.1
AHQ-10-13-, 3745	K.NKDQGTYEDYVEGLR.V	1787.86505	2	4.49E-05	0.93	4.25	-	1219.6
AHQ-10-13-, 3753	K.NKDQGTYEDYVEGLR.V	1787.86505	3	3.18E-05	0.94	4.41	-	1472.9
AHQ-10-14-, 3716	K.NKDQGTYEDYVEGLR.V	1787.86505	3	1.00E-04	0.94	4.12	-	1601.3
AHQ-10-13-, 3366	R.VFDKEGNGTVMGAEIR.H	1723.93228	2	3.78E-10	0.84	3.43	-	766.8
AHQ-10-14-, 5922 - 5924	K.VLDFEHFLPM*LQTVAK.N	1905.24957	3	2.20E-07	0.88	4.19	-	784.8
AHQ-10-12, 6096 - 6177	K.VLDFEHFLPMLQTVAK.N	1889.25017	2	1.67E-09	0.95	5.26	-	897.7
gi|4504183|ref|NP_000843.1| glutathione transferase; deafness, X-linked 7; fatty acid ethyl ester s				4.18E-10	3.23	40.25	30.50	23355.7
AHQ-10-11, 5059	K.ALPGQLKPFETLLSQNQGGK.T	2127.42930	2	2.49E-05	0.83	3.72	-	385.4
AHQ-10-11, 3238	K.ASCLYGQLPK.F	1138.31884	2	1.19E-04	0.84	2.95	-	777.1
AHQ-10-10, 3207	K.ASCLYGQLPK.F	1138.31884	2	1.37E-05	0.76	2.64	-	579.0
AHQ-10-11, 4558 - 4615	K.FQDGDLTLYQSNTILR.H	1885.06701	2	1.87E-04	0.68	3.60	-	369.1
AHQ-10-11, 4382	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	4.18E-10	0.95	5.00	-	828.1
AHQ-10-10, 4336	K.YISLIYTNYEAGKDDYVK.A	2156.37637	2	2.54E-04	0.65	2.90	-	419.7
gi|4885165|ref|NP_005204.1| cystatin A; stefin A; cystatin AS [Homo sapiens]				4.37E-10	3.23	40.20	57.10	11006.4
AHQ-10-14-, 3673 - 3682	K.PATPEIQEIVDK.V	1340.50421	2	2.07E-06	0.77	2.76	-	519.1
AHQ-10-14-, 4458	K.SLPGQNEDLVLTGYQVDK.N	1977.16121	2	1.22E-09	0.56	3.03	-	167.2
AHQ-10-14-, 4306 - 4364	K.SLPGQNEDLVLTGYQVDK.N	1977.16121	2	2.66E-06	0.88	3.94	-	326.0
AHQ-10-14, 5115	K.SLPGQNEDLVLTGYQVDK.N	1977.16121	2	4.37E-10	0.70	3.13	-	274.2
AHQ-10-3, 4418	K.SLPGQNEDLVLTGYQVDK.N	1977.16121	2	1.51E-04	0.66	3.35	-	199.7
AHQ-10-14-, 2982	K.TNETYGKLEAVQYK.T	1644.80688	2	3.56E-06	0.85	3.09	-	1015.8
AHQ-10-13-, 3160	K.TQVVAGTNYYIK.V	1357.53647	2	1.47E-05	0.90	3.51	-	1203.9
gi|4758606|ref|NP_004508.1| integrin-linked kinase [Homo sapiens]				4.55E-10	8.28	100.23	19.70	51418.9
AHQ-10-7, 4878	R.EVPFADLSNMEIGM*K.V	1697.95498	2	1.05E-04	0.53	2.77	-	374.9
AHQ-10-7, 4112 - 4122	R.EVPFADLSNM*EIGM*K.V	1713.95438	2	2.06E-04	0.80	3.23	-	587.7
AHQ-10-7, 4328	K.FDM*IVPILEK.M	1221.49108	2	2.55E-04	0.89	3.29	-	762.4
AHQ-10-7, 5317	K.FDMIVPILEK.M	1205.49168	2	1.37E-04	0.87	3.19	-	724.7
AHQ-10-7, 2253	R.GDDTPLHLAASHGHR.D	1584.67809	2	4.55E-10	0.92	3.30	-	1389.0
AHQ-10-7, 5610	R.GMAFLHTLEPLIPR.H	1595.93361	3	1.09E-05	0.88	3.46	-	1165.1
AHQ-10-7, 5608	R.GMAFLHTLEPLIPR.H	1595.93361	2	1.93E-04	0.85	3.36	-	781.3
AHQ-10-7, 4148	R.M*YAPAWVAPEALQK.K	1591.85542	2	8.33E-04	0.87	3.52	-	547.7
AHQ-10-7, 4533 - 4610	R.MYAPAWVAPEALQK.K	1575.85602	2	8.16E-07	0.91	3.57	-	999.2
AHQ-10-13-, 4248	R.M*YAPAWVAPEALQK.K	1591.85542	2	6.82E-04	0.90	3.10	-	871.6
AHQ-10-7, 4105	R.SAVVEMLIM*R.G	1165.45256	2	4.91E-06	0.88	2.68	-	1324.4
AHQ-10-7, 3008	R.SVMIDEDMTAR.I	1268.44340	2	4.22E-04	0.71	2.90	-	677.7
gi|21361122|ref|NP_001440.2| four and a half LIM domains 1; Four-and-a-half LIM domains 1 [Homo sap				4.72E-10	2.74	30.23	14.30	31894.7
AHQ-10-9, 2423 - 2425	K.AIVAGDQNVEYK.G	1307.43431	2	3.00E-09	0.95	4.58	-	1180.5
AHQ-10-9, 3552 - 3565	R.FVFHQEQVYCPDCAK.K	1931.13758	3	2.61E-04	0.80	3.49	-	993.0
AHQ-10-9, 3553	R.FVFHQEQVYCPDCAK.K	1931.13758	2	7.87E-06	0.93	3.39	-	1390.3
AHQ-10-13-, 3784	R.FVFHQEQVYCPDCAK.K	1931.13758	2	5.85E-05	0.97	4.64	-	1673.6
AHQ-10-9, 2931 - 3012	K.GEDFYCVTCHETK.F	1648.75260	2	4.72E-10	0.85	3.10	-	806.7
gi|4758018|ref|NP_004359.1| calponin 2; Calonin 2 [Homo sapiens]				4.85E-10	0.94	10.20	5.50	33696.9
AHQ-10-12, 5868 - 5872	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	1.13E-04	0.85	3.27	-	818.3
AHQ-10-13-, 5838 - 5918	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	4.85E-10	0.94	4.07	-	1185.6
AHQ-10-11, 5762 - 5842	R.TWIEGLTGLSIGPDFQK.G	1863.10294	2	6.11E-06	0.58	2.78	-	528.9
gi|21956645|ref|NP_665807.1| myotrophin; granule cell differentiation protein [Homo sapiens]				6.92E-10	1.91	20.31	25.40	12894.7
AHQ-10-13, 4228 - 4295	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.99E-04	0.83	3.16	-	832.1
AHQ-10-13, 4352 - 4419	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.33E-05	0.95	4.48	-	1081.3
AHQ-10-13-, 4066	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.16E-06	0.97	4.71	-	1824.6
AHQ-10-13-, 3928 - 4008	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	1.27E-08	0.98	6.27	-	1233.2
AHQ-10-14-, 3870 - 3924	K.GPDGLTAFEATDNQAIK.A	1748.87196	2	3.65E-05	0.97	4.68	-	1907.6
AHQ-10-14-, 3558	K.NGDLDEVKDYVAK.G	1466.57496	2	6.92E-10	0.93	4.09	-	1054.5
AHQ-10-13-, 3558 - 3636	K.NGDLDEVKDYVAK.G	1466.57496	2	9.77E-08	0.91	3.28	-	1317.5
AHQ-10-13, 3948 - 4029	K.NGDLDEVKDYVAK.G	1466.57496	2	1.32E-05	0.78	2.99	-	713.5
gi|4502027|ref|NP_000468.1| albumin precursor; PRO0883 protein [Homo sapiens]				6.99E-10	37.46	430.35	63.70	69366.4
AHQ-10-6, 2539 - 2569	K.AAFTECCQAADK.A	1374.47927	2	1.67E-05	0.92	3.36	-	1277.1
AHQ-10-5, 2557 - 2628	K.AAFTECCQAADK.A	1374.47927	2	4.87E-06	0.89	3.55	-	883.5
AHQ-10-5, 2577	K.AAFTECCQAADK.A	1374.47927	1	3.05E-06	0.80	3.34	-	612.6
AHQ-10-6, 1923 - 2003	K.ADDKETCFAEEGKK.L	1629.72754	2	4.54E-04	0.36	2.58	-	534.4
AHQ-10-5, 1817 - 1888	K.ADDKETCFAEEGKK.L	1629.72754	2	6.96E-05	0.93	3.87	-	1148.8
AHQ-10-5, 1860 - 1916	K.ADDKETCFAEEGKK.L	1629.72754	3	2.23E-04	0.88	4.13	-	967.7
AHQ-10-7, 2025	K.AEFAEVSK.L	880.96496	1	7.58E-05	0.10	1.86	-	293.4
AHQ-10-6, 2009 - 2085	K.AEFAEVSK.L	880.96496	2	5.61E-04	0.58	2.69	-	328.5
AHQ-10-5, 5189	K.AEFAEVSKLVTDLTK.V	1651.88247	2	1.26E-05	0.81	3.01	-	819.9
AHQ-10-13-, 5170	K.AVMDDFAAFVEK.C	1343.53006	2	2.00E-07	0.94	3.81	-	1272.9
AHQ-10-5, 4419 - 4480	K.AVM*DDFAAFVEK.C	1359.52946	2	5.82E-04	0.92	3.39	-	900.5
AHQ-10-6, 5099 - 5161	K.AVMDDFAAFVEK.C	1343.53006	2	5.46E-07	0.95	3.64	-	1325.2
AHQ-10-14-, 5160 - 5161	K.AVMDDFAAFVEK.C	1343.53006	2	1.27E-09	0.95	4.18	-	1358.8
AHQ-10-5, 5228 - 5232	K.AVMDDFAAFVEK.C	1343.53006	2	1.31E-08	0.96	4.55	-	1344.0
AHQ-10-10, 5026	K.AVMDDFAAFVEK.C	1343.53006	2	1.54E-05	0.91	3.24	-	1086.9
AHQ-10-5, 2196 - 2204	K.CCAAADPHECYAK.V	1556.67999	2	2.60E-08	0.82	3.12	-	773.9
AHQ-10-5, 2152	K.CCKADDKETCFAEEGKK.L	2080.26010	3	7.73E-06	0.92	3.89	-	1336.9
AHQ-10-5, 2411 - 2489	K.CCTESLVNR.R	1141.25805	2	9.84E-08	0.92	3.05	-	1645.5
AHQ-10-3, 6193	K.DVFLGM*FLYEYAR.R	1640.88331	2	1.75E-04	0.92	3.51	-	950.0
AHQ-10-7, 6217	K.DVFLGM*FLYEYAR.R	1640.88331	2	7.22E-04	0.91	3.21	-	872.4
AHQ-10-1, 6294 - 6301	K.DVFLGM*FLYEYAR.R	1640.88331	2	9.42E-04	0.96	4.17	-	1383.7
AHQ-10-6, 6136 - 6143	K.DVFLGM*FLYEYAR.R	1640.88331	2	6.32E-04	0.84	3.15	-	804.0
AHQ-10-2, 6288	K.DVFLGM*FLYEYAR.R	1640.88331	2	3.05E-05	0.90	3.43	-	808.8
AHQ-10-5, 6268 - 6269	K.DVFLGM*FLYEYAR.R	1640.88331	2	7.24E-06	0.96	4.49	-	1320.6
AHQ-10-6, 2757 - 2819	R.FKDLGEENFK.A	1227.34766	2	1.10E-05	0.85	3.06	-	796.3
AHQ-10-13-, 2844	R.FKDLGEENFK.A	1227.34766	2	3.87E-07	0.90	3.10	-	887.1
AHQ-10-5, 2737 - 2801	R.FKDLGEENFK.A	1227.34766	2	6.63E-05	0.82	3.40	-	607.1
AHQ-10-14-, 2813	R.FKDLGEENFK.A	1227.34766	2	2.50E-07	0.81	3.10	-	745.7
AHQ-10-10, 3054	K.FQNALLVR.Y	961.14282	2	5.09E-05	0.80	2.81	-	812.1
AHQ-10-5, 4569	R.HPDYSVVLLLR.L	1312.54206	2	1.97E-06	0.56	2.63	-	331.3
AHQ-10-6, 6047	R.HPYFYAPELLFFAK.R	1744.02658	3	1.35E-09	0.93	4.33	-	1104.7
AHQ-10-5, 6175 - 6199	R.HPYFYAPELLFFAK.R	1744.02658	3	1.09E-08	0.96	5.16	-	1427.0
AHQ-10-5, 3703	K.KLVAASQAALGL	1142.37371	2	1.46E-04	0.90	3.22	-	917.2
AHQ-10-5, 2855 - 2916	K.KQTALVELVK.H	1129.37494	2	5.43E-05	0.89	3.32	-	978.4
AHQ-10-2, 3680 - 3748	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.76E-08	0.83	2.79	-	750.4
AHQ-10-7, 3514	K.KVPQVSTPTLVEVSR.N	1640.90605	3	3.23E-08	0.93	4.72	-	1294.0
AHQ-10-7, 3508	K.KVPQVSTPTLVEVSR.N	1640.90605	2	7.81E-09	0.92	3.83	-	781.6
AHQ-10-3, 3601 - 3677	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.57E-05	0.81	3.06	-	506.7
AHQ-10-5, 3615 - 3681	K.KVPQVSTPTLVEVSR.N	1640.90605	2	6.43E-09	0.88	3.21	-	747.5
AHQ-10-5, 3563 - 3620	K.KVPQVSTPTLVEVSR.N	1640.90605	3	7.09E-08	0.94	4.48	-	1418.8
AHQ-10-6, 3305	K.KVPQVSTPTLVEVSR.N	1640.90605	2	3.55E-08	0.83	3.36	-	527.7
AHQ-10-11, 3519 - 3584	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.28E-04	0.68	3.05	-	603.2
AHQ-10-6, 3511 - 3585	K.KVPQVSTPTLVEVSR.N	1640.90605	2	2.11E-06	0.76	2.97	-	444.7
AHQ-10-5, 3964 - 4009	K.KVPQVSTPTLVEVSRNLGK.V	2053.39186	3	2.94E-05	0.89	4.06	-	831.0
AHQ-10-5, 3815	K.KVPQVSTPTLVEVSRNLGK.V	2053.39186	3	7.22E-07	0.76	3.60	-	665.3
AHQ-10-5, 2808	K.KYLYEIAR.R	1056.23937	2	3.34E-04	0.88	2.61	-	767.1
AHQ-10-5, 2447 - 2511	K.LKECCEKPLLEK.S	1549.83503	3	5.73E-04	0.92	4.56	-	1043.4
AHQ-10-6, 2476 - 2488	K.LKECCEKPLLEK.S	1549.83503	3	3.85E-04	0.91	4.05	-	1159.8
AHQ-10-5, 4053	K.LVAASQAALGL	1014.20080	2	8.86E-05	0.94	3.19	-	1568.9

AHQ-10-11, 3300 - 3303	K.LVNEVTEFAK.T	1150.30633	2	6.05E-06	0.93	3.89	-	788.3
AHQ-10-5, 3211	K.LVNEVTEFAK.T	1150.30633	1	6.55E-05	0.75	2.58	-	584.9
AHQ-10-5, 3339 - 3352	K.LVNEVTEFAK.T	1150.30633	2	1.05E-06	0.81	3.34	-	577.6
AHQ-10-6, 3300	K.LVNEVTEFAK.T	1150.30633	2	2.96E-05	0.87	3.09	-	670.3
AHQ-10-3, 3375	K.LVNEVTEFAK.T	1150.30633	2	1.04E-06	0.83	3.22	-	612.6
AHQ-10-5, 3525 - 3540	K.LVNEVTEFAK.T	1150.30633	2	2.66E-05	0.86	3.33	-	546.7
AHQ-10-5, 3537	K.LVNEVTEFAK.T	1150.30633	1	4.38E-05	0.82	2.94	-	870.2
AHQ-10-5, 4688	R.LVRPEVDVM*CTAFHDNEETFLK.K	2668.98368	3	4.75E-06	0.96	4.97	-	1703.9
AHQ-10-6, 4620 - 4621	R.LVRPEVDVM*CTAFHDNEETFLK.K	2668.98368	3	5.61E-09	0.96	5.78	-	1222.0
AHQ-10-5, 5501	R.LVRPEVDVMCTAFHDNEETFLK.K	2652.98428	3	8.21E-06	0.98	7.02	-	2190.5
AHQ-10-6, 4244 - 4308	R.LVRPEVDVM*CTAFHDNEETFLKK.Y	2797.15659	3	5.40E-05	0.89	4.40	-	954.2
AHQ-10-5, 5241	R.LVRPEVDVMCTAFHDNEETFLKK.Y	2781.15719	3	9.18E-09	0.98	6.57	-	1908.3
AHQ-10-5, 6435	R.M*PCAEDYLSVVLNQLCVLHEK.T	2537.91475	3	3.90E-07	0.94	4.85	-	1079.7
AHQ-10-5, 3083	R.NECFLQHKDDNPNLPR.L	1999.15349	3	6.49E-06	0.80	3.86	-	687.7
AHQ-10-6, 4095	R.RHPDYSVVLLLR.L	1468.72842	3	5.31E-04	0.97	5.09	-	2057.6
AHQ-10-5, 4163 - 4220	R.RHPDYSVVLLLR.L	1468.72842	3	2.15E-05	0.95	4.68	-	1902.9
AHQ-10-5, 5796	R.RHPYFYAPELLFFAK.R	1900.21293	2	1.11E-04	0.97	4.76	-	1545.9
AHQ-10-5, 5787 - 5848	R.RHPYFYAPELLFFAK.R	1900.21293	3	1.15E-07	0.97	5.82	-	1838.1
AHQ-10-6, 5683 - 5687	R.RHPYFYAPELLFFAK.R	1900.21293	3	8.76E-10	0.97	5.53	-	2052.5
AHQ-10-6, 6283	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	1.78E-04	0.95	5.13	-	1312.8
AHQ-10-5, 6407	K.RM*PCAEDYLSVVLNQLCVLHEK.T	2694.10110	3	2.16E-05	0.94	5.41	-	1071.8
AHQ-10-6, 4384	R.RPCFSALEVDETYVPK.E	1913.14041	2	4.42E-04	0.84	4.24	-	451.4
AHQ-10-6, 4381	R.RPCFSALEVDETYVPK.E	1913.14041	3	1.50E-07	0.67	3.29	-	688.9
AHQ-10-6, 4479 - 4487	R.RPCFSALEVDETYVPK.E	1913.14041	3	3.30E-06	0.91	4.85	-	798.5
AHQ-10-5, 4460	R.RPCFSALEVDETYVPK.E	1913.14041	3	2.65E-04	0.56	3.13	-	619.9
AHQ-10-5, 4611	R.RPCFSALEVDETYVPK.E	1913.14041	2	3.00E-06	0.94	4.55	-	724.1
AHQ-10-5, 4555 - 4580	R.RPCFSALEVDETYVPK.E	1913.14041	3	3.32E-07	0.93	4.65	-	1044.0
AHQ-10-6, 4480 - 4499	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.21E-04	0.94	4.50	-	869.8
AHQ-10-5, 4476 - 4553	R.RPCFSALEVDETYVPK.E	1913.14041	2	1.98E-05	0.94	4.44	-	881.2
AHQ-10-7, 5797	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	6.00E-04	0.92	4.91	-	690.7
AHQ-10-7, 6229	K.SHCIAEVENDEMPADLPSLAADFVESK.D	2977.22697	3	5.30E-04	0.93	5.07	-	803.8
AHQ-10-5, 5919 - 5975	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	1.83E-07	0.95	5.77	-	794.9
AHQ-10-6, 5739 - 5795	K.SHCIAEVENDEM*PADLPSLAADFVESK.D	2993.22637	3	2.28E-05	0.89	5.07	-	568.3
AHQ-10-5, 4948 - 5005	K.SLHTLFGDKLCTVATLR.E	1934.24913	2	6.64E-04	0.93	4.15	-	994.0
AHQ-10-5, 1897	K.TCVADESAENCDK.S	1501.53308	2	6.99E-10	0.96	4.11	-	1597.5
AHQ-10-6, 1964 - 1976	K.TCVADESAENCDK.S	1501.53308	2	3.70E-06	0.98	5.03	-	2782.0
AHQ-10-5, 4391	K.TCVADESAENCDKSLHTLFGDK.L	2500.65848	3	8.04E-09	0.90	4.89	-	600.9
AHQ-10-5, 3783	K.TYETTLEKCCAAADPHECYAK.V	2522.72734	3	2.86E-05	0.87	4.41	-	534.6
AHQ-10-9, 5171	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.28E-04	0.77	2.87	-	460.8
AHQ-10-9, 5169	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.12E-06	0.74	3.13	-	633.3
AHQ-10-6, 5375	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.28E-04	0.90	4.47	-	414.3
AHQ-10-5, 5212 - 5225	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	2.57E-07	0.88	3.90	-	463.6
AHQ-10-5, 5369	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	1.79E-06	0.74	3.38	-	340.2
AHQ-10-5, 5375	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.75E-05	0.89	4.07	-	990.5
AHQ-10-5, 5572	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	1.35E-06	0.93	4.75	-	846.1
AHQ-10-5, 5480 - 5493	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.90E-06	0.96	4.88	-	1432.7
AHQ-10-4, 5515	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	4.58E-08	0.95	4.75	-	1461.4
AHQ-10-3, 5435 - 5443	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	9.49E-07	0.92	4.77	-	946.4
AHQ-10-2, 5530	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	9.14E-06	0.92	4.48	-	541.2
AHQ-10-2, 5506 - 5532	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.70E-05	0.90	3.79	-	1088.9
AHQ-10-5, 5492	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	2	3.50E-05	0.89	4.17	-	405.4
AHQ-10-7, 5386	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	6.34E-06	0.94	4.80	-	1063.7
AHQ-10-1, 5565	K.VFDEFKPLVEEPQNLIK.Q	2046.35142	3	2.15E-07	0.85	3.98	-	729.6
AHQ-10-5, 3144	K.VHTECCHGDLLECADDR.A	2091.20307	2	2.78E-07	0.97	4.84	-	2108.7
AHQ-10-6, 3109	K.VHTECCHGDLLECADDR.A	2091.20307	2	1.58E-08	0.97	5.28	-	1584.9
AHQ-10-5, 3713	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	5.46E-04	0.90	4.78	-	647.6
AHQ-10-7, 3645	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	1.24E-04	0.86	4.10	-	801.6
AHQ-10-5, 3728	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	2	7.71E-04	0.81	3.17	-	746.1
AHQ-10-5, 3824	K.VHTECCHGDLLECADDRADLAK.Y	2589.77855	3	1.61E-04	0.75	3.58	-	543.9
AHQ-10-6, 3787	K.VPQVSTPTLVEVSR.N	1512.73313	2	1.97E-05	0.87	2.98	-	863.2
AHQ-10-7, 3782	K.VPQVSTPTLVEVSR.N	1512.73313	2	1.05E-06	0.90	3.12	-	944.4
AHQ-10-5, 2479 - 2540	K.YICENQDSISSK.L	1445.53420	2	1.39E-06	0.93	4.05	-	794.1
AHQ-10-5, 2383	K.YICENQDSISSK.L	1445.53420	2	2.23E-06	0.92	3.91	-	677.5
AHQ-10-3, 2431	K.YICENQDSISSK.L	1445.53420	2	1.08E-04	0.80	3.01	-	540.2
AHQ-10-7, 2386	K.YICENQDSISSK.L	1445.53420	2	1.59E-08	0.92	3.85	-	767.2
AHQ-10-6, 2472	K.YICENQDSISSK.L	1445.53420	2	8.13E-05	0.90	3.48	-	865.1
gi|29730023|ref|XP_291482.1| similar to 78 kDa glucose-regulated protein precursor (GRP 78) (Immuno				7.18E-10	5.81	70.24	13.10	63563.0
AHQ-10-6, 4271 - 4272	K.ELEEIVQPIISK.L	1398.62680	2	9.59E-05	0.93	4.01	-	973.6
AHQ-10-5, 4621	R.IINKPTAAAIAYGLDK.R	1659.95097	2	7.18E-10	0.84	4.05	-	913.4
AHQ-10-7, 4537	R.IINKPTAAAIAYGLDK.R	1659.95097	2	8.60E-07	0.84	3.95	-	924.7
AHQ-10-6, 4329	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	3.19E-07	0.82	4.01	-	915.2
AHQ-10-5, 4417 - 4485	R.IINKPTAAAIAYGLDKR.E	1816.13732	2	2.50E-06	0.80	4.14	-	727.4
AHQ-10-5, 3503 - 3531	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	7.69E-05	0.81	3.92	-	394.5
AHQ-10-6, 3448 - 3503	K.LYGSAGPPPTGEEDTAEKDEL	2177.26447	2	2.77E-06	0.94	4.71	-	835.6
AHQ-10-6, 3940	R.NELESYAYSLK.N	1317.42597	2	7.17E-04	0.83	3.41	-	774.6
AHQ-10-6, 4567 - 4641	K.TFAPKEISAM*VLTK.M	1552.86064	2	4.93E-07	0.84	2.96	-	1108.0
AHQ-10-5, 5421 - 5436	K.TFAPKEISAMVLTK.M	1536.86124	2	2.08E-04	0.61	2.64	-	845.8
gi|5453603|ref|NP_006422.1| chaperonin containing TCP1, subunit 2 (beta); chaperonin containing t-c				7.33E-10	1.74	20.24	7.10	57487.9
AHQ-10-7, 3174	R.EALLSSAVDHGSDEVK.F	1657.76083	2	4.60E-04	0.78	3.25	-	786.0
AHQ-10-7, 6270	R.VQDDEVGDGTTSVTVLAAELLR.E	2289.48263	2	7.33E-10	0.96	4.71	-	1238.3
gi|27500274|ref|XP_113950.3| similar to Munc13-4 protein [Homo sapiens]				7.98E-10	3.23	40.20	6.10	123281.1
AHQ-10-4, 4620	K.HSTSAVDLSTCFAQISHTAR.Q	2191.36726	3	1.08E-04	0.86	3.33	-	1000.6
AHQ-10-4, 5159 - 5236	K.LPAQLAWEALEQR.V	1525.73360	2	9.79E-04	0.62	2.55	-	557.1
AHQ-10-4, 6423	R.LPLTYPAPNGDPILQLLEGR.K	2178.51621	2	7.98E-10	0.89	4.09	-	587.7
AHQ-10-4, 4047	R.SVFPLSVSDSPAR.L	1362.51311	2	1.10E-05	0.86	2.98	-	1050.7
gi|4503327|ref|NP_000389.1| cytochrome b5 reductase membrane-bound isoform; diaphorase (NADH) [Homo				9.09E-10	1.45	20.23	12.00	34234.6
AHQ-10-9, 4287 - 4292	R.STPAITLESPDIKYPLR.L	1902.18061	2	9.09E-10	0.93	4.54	-	706.0
AHQ-10-9, 4636	K.SVGMIAGGTGITPM*LQVIR.A	1918.31483	2	7.42E-06	0.51	2.56	-	530.4
gi|4757952|ref|NP_001782.1| cell division cycle 42 isoform 1; cell division cycle 42 (GTP-binding p				9.68E-10	1.85	20.25	14.70	21258.5
AHQ-10-11, 2390 - 2412	K.CVVVGDGAVGK.T	1062.22237	2	1.18E-04	0.91	3.13	-	1249.7
AHQ-10-11, 6136	K.NVFDEAILAALEPPEPK.K	1854.09282	3	9.68E-10	0.94	5.04	-	960.0
gi|10863977|ref|NP_067000.1| LSM2 homolog, U6 small nuclear RNA associated; U6 snRNA-associated Sm-				9.86E-10	0.97	10.25	20.00	10834.5
AHQ-10-14-, 5154	R.YVQLPADEVDTQLLQDAAR.K	2146.34311	2	9.86E-10	0.97	5.08	-	1505.7
gi|4505735|ref|NP_002611.1| platelet factor 4 variant 1; Platelet factor 4, variant 1 (PF4-like) [H				1.16E-09	1.86	20.25	25.00	11552.6
AHQ-10-14-, 3678 - 3750	R.AEAEEDGDLQCLCVK.T	1739.86036	2	1.16E-09	0.95	4.40	-	1098.6
AHQ-10-14-, 3809	R.AEAEEDGDLQCLCVK.T	1739.86036	2	2.56E-06	0.93	3.42	-	1314.6
AHQ-10-14, 4571 - 4575	R.AEAEEDGDLQCLCVK.T	1739.86036	2	4.24E-06	0.96	4.93	-	1339.9
AHQ-10-14-, 5894	K.ICLDLQALLYK.K	1351.63656	2	2.97E-05	0.91	3.32	-	990.0
gi|29732955|ref|XP_291603.1| similar to glyceraldehyde 3-phosphate dehydrogenase [Homo sapiens] [MA				1.17E-09	0.86	10.20	16.80	11173.0
AHQ-10-9, 3837 - 3915	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.17E-09	0.86	3.91	-	1116.9
AHQ-10-9, 3923 - 3988	K.NISNASCTTNCIAPLAK.M	1838.05353	2	1.04E-07	0.81	3.97	-	987.0
AHQ-10-10, 3719	K.NISNASCTTNCIAPLAK.M	1838.05353	2	4.11E-07	0.61	2.81	-	935.1
AHQ-10-10, 4015 - 4016	K.NISNASCTTNCIAPLAK.M	1838.05353	2	6.21E-09	0.44	3.08	-	565.8
AHQ-10-11, 3848	K.NISNASCTTNCIAPLAK.M	1838.05353	2	6.62E-05	0.74	3.31	-	621.6
AHQ-10-9, 3612 - 3673	K.NISNASCTTNCIAPLAK.M	1838.05353	2	3.22E-07	0.73	3.62	-	912.3
gi|30159310|ref|XP_301899.1| similar to beta-actin [Homo sapiens]				1.28E-09	1.51	20.20	9.20	32376.4
AHQ-10-8, 1566 - 1943	K.DSYVGNEAQSK.R	1198.22158	1	1.28E-09	0.58	2.80	-	321.0

AHQ-10-8, 4913 - 4965	K.SYKLLDGQVITIGNER.F	1807.04092	2	4.29E-04	0.82	3.28	-	626.1
AHQ-10-8, 4358 - 4413	K.SYKLLDGQVITIGNER.F	1807.04092	2	2.01E-06	0.93	4.04	-	968.0
gi|4507171|ref|NP_003109.1| secreted protein, acidic, cysteine-rich (osteonectin); Osteonectin (sec				1.43E-09	1.79	20.20	7.60	34632.0
AHQ-10-8, 3198	R.LEAGDHPVELLAR.D	1420.59579	2	1.43E-09	0.95	3.96	-	1205.5
AHQ-10-8, 3385	K.LHLDYIGPCK.Y	1217.41920	2	1.98E-04	0.83	3.00	-	670.7
gi|30160191|ref|XP_294035.2| similar to Pyruvate kinase, M1 isozyme (Pyruvate kinase muscle isozyme				1.43E-09	0.96	10.25	2.80	50222.2
AHQ-10-7, 4828	K.IYVDDGLISLQVK.Q	1463.70048	2	5.73E-09	0.98	4.98	-	2325.2
AHQ-10-7, 4836	K.IYVDDGLISLQVK.Q	1463.70048	1	6.03E-05	0.76	3.15	-	758.4
AHQ-10-11, 4798	K.IYVDDGLISLQVK.Q	1463.70048	2	3.16E-04	0.88	3.46	-	1001.0
AHQ-10-7, 4717	K.IYVDDGLISLQVK.Q	1463.70048	2	1.43E-09	0.96	4.15	-	2038.5
gi|4501893|ref|NP_001094.1| actinin, alpha 2 [Homo sapiens]				1.49E-09	7.55	90.23	10.50	103853.1
AHQ-10-5, 4389	K.AGTQIENIEEDFR.N	1522.59861	2	1.90E-05	0.82	3.35	-	623.0
AHQ-10-6, 5085	K.AGTQIENIEEDFRNGLK.L	1935.08442	2	4.19E-07	0.35	3.32	-	424.7
AHQ-10-4, 4903	K.CQLEINFNTLQTK.L	1610.81373	2	2.16E-07	0.93	4.01	-	1044.3
AHQ-10-6, 4644 - 4660	K.CQLEINFNTLQTK.L	1610.81373	2	2.73E-04	0.93	4.30	-	889.7
AHQ-10-4, 4747 - 4760	K.CQLEINFNTLQTK.L	1610.81373	2	5.26E-07	0.95	3.96	-	1131.7
AHQ-10-4, 4615	K.CQLEINFNTLQTK.L	1610.81373	2	1.50E-08	0.93	3.80	-	1102.3
AHQ-10-5, 4732 - 4751	K.CQLEINFNTLQTK.L	1610.81373	2	1.13E-04	0.94	4.25	-	958.8
AHQ-10-4, 4749	K.EGLLLWCQR.K	1176.37031	2	9.62E-06	0.93	3.30	-	1151.7
AHQ-10-5, 4711	K.EGLLLWCQR.K	1176.37031	2	1.08E-05	0.89	3.40	-	738.7
AHQ-10-8, 4065 - 4067	R.FAIQDISVEETSAK.E	1538.68108	2	1.35E-06	0.86	3.50	-	708.1
AHQ-10-4, 4123 - 4156	R.FAIQDISVEETSAK.E	1538.68108	2	4.82E-04	0.95	3.79	-	1367.8
AHQ-10-3, 4113	R.FAIQDISVEETSAK.E	1538.68108	2	3.09E-05	0.62	2.63	-	501.6
AHQ-10-6, 4045 - 4109	R.FAIQDISVEETSAK.E	1538.68108	2	1.27E-05	0.74	2.73	-	666.2
AHQ-10-5, 4120	R.FAIQDISVEETSAK.E	1538.68108	2	1.03E-08	0.96	4.33	-	1357.7
AHQ-10-10, 3974 - 3978	R.FAIQDISVEETSAK.E	1538.68108	2	1.01E-07	0.84	3.56	-	660.1
AHQ-10-4, 5663 - 5676	K.GYEEWLLNEIR.R	1422.56701	2	3.34E-04	0.95	4.03	-	1326.8
AHQ-10-4, 5235	K.GYEEWLLNEIR.R	1422.56701	2	4.23E-06	0.89	2.92	-	1280.4
AHQ-10-6, 5525 - 5527	K.GYEEWLLNEIR.R	1422.56701	2	4.90E-06	0.95	4.57	-	1169.9
AHQ-10-5, 5647 - 5648	K.GYEEWLLNEIR.R	1422.56701	2	8.94E-06	0.90	3.69	-	1007.3
AHQ-10-6, 5107	K.GYEEWLLNEIR.R	1422.56701	2	5.09E-05	0.90	2.86	-	1192.5
AHQ-10-7, 5548	K.GYEEWLLNEIR.R	1422.56701	2	3.98E-04	0.87	2.94	-	1289.2
AHQ-10-4, 2216 - 2280	R.KHEAFESDLAAHQDR.V	1754.84152	2	1.49E-09	0.96	4.19	-	1363.6
AHQ-10-4, 4287 - 4367	K.LVSIGAEEIVDGNVK.M	1543.74400	2	1.32E-04	0.92	3.86	-	1112.8
AHQ-10-4, 4436 - 4508	K.LVSIGAEEIVDGNVK.M	1543.74400	2	6.63E-07	0.86	3.35	-	932.1
AHQ-10-6, 4168	K.LVSIGAEEIVDGNVK.M	1543.74400	2	7.95E-05	0.90	3.81	-	1109.3
AHQ-10-4, 4005 - 4067	K.LVSIGAEEIVDGNVK.M	1543.74400	2	4.36E-06	0.94	3.91	-	1094.7
AHQ-10-5, 3999 - 4075	K.LVSIGAEEIVDGNVK.M	1543.74400	2	3.11E-04	0.92	4.04	-	874.2
AHQ-10-4, 3627 - 3632	K.TFTAWCNSHLR.K	1394.54018	2	4.28E-05	0.86	2.91	-	804.1
gi|29742827|ref|XP_294099.1| similar to myosin:SUBUNIT=regulatory light chain [Homo sapiens]				1.56E-09	0.96	10.22	7.40	17094.0
AHQ-10-11, 3719 - 3724	R.FTDEEVDELYR.E	1416.47127	2	3.39E-09	0.97	4.39	-	1576.9
AHQ-10-12, 3726 - 3802	R.FTDEEVDELYR.E	1416.47127	2	7.23E-07	0.94	3.09	-	1688.6
AHQ-10-13, 4203 - 4212	R.FTDEEVDELYR.E	1416.47127	2	4.10E-06	0.96	3.80	-	1776.3
AHQ-10-13-, 3828 - 3900	R.FTDEEVDELYR.E	1416.47127	2	4.92E-09	0.97	4.25	-	1714.0
AHQ-10-14-, 3805	R.FTDEEVDELYR.E	1416.47127	2	1.56E-09	0.96	3.56	-	1733.4
AHQ-10-11, 3536	R.FTDEEVDELYR.E	1416.47127	2	3.81E-05	0.76	2.61	-	696.4
gi|4503571|ref|NP_001419.1| enolase 1; phosphopyruvate hydratase; MYC promoter-binding protein 1; n				1.83E-09	7.02	80.28	23.30	47168.7
AHQ-10-9, 4833	R.AAVPSGASTGIYEALELR.D	1806.00979	2	9.73E-04	0.66	2.72	-	277.4
AHQ-10-13-, 5060	R.AAVPSGASTGIYEALELR.D	1806.00979	2	3.43E-05	0.93	4.36	-	515.3
AHQ-10-14-, 5057 - 5076	R.AAVPSGASTGIYEALELR.D	1806.00979	2	2.70E-09	0.96	5.60	-	626.1
AHQ-10-8, 4137	R.GNPTVEVDLFTSK.G	1407.55065	2	8.43E-04	0.67	3.11	-	538.7
AHQ-10-8, 5637	R.HIADLAGNSEVILPVPAFNVINGGSHAGNK.L	3013.35654	3	2.94E-08	0.88	4.44	-	785.5
AHQ-10-8, 2409	R.IGAEVYHNLK.N	1144.30502	2	2.36E-05	0.95	4.28	-	1161.9
AHQ-10-8, 5694	K.LAM*QEFMILPVGAANFR.E	1925.30752	2	2.42E-05	0.86	3.55	-	834.7
AHQ-10-8, 5866 - 5870	K.LAMQEFM*ILPVGAANFR.E	1925.30752	2	4.26E-04	0.93	4.88	-	817.0
AHQ-10-10, 4682	K.VVIGM*DVAASEFFR.S	1557.79584	2	9.65E-05	0.84	2.79	-	942.0
AHQ-10-11, 4591	R.YISPDQLADLYK.S	1426.59557	2	9.89E-06	0.86	2.69	-	833.4
AHQ-10-8, 4629	R.YISPDQLADLYK.S	1426.59557	2	1.83E-09	0.94	4.01	-	787.6
AHQ-10-9, 4440	R.YISPDQLADLYK.S	1426.59557	2	6.15E-08	0.90	3.37	-	889.1
AHQ-10-10, 4530 - 4532	R.YISPDQLADLYK.S	1426.59557	2	5.65E-05	0.79	3.00	-	581.4
gi|4557871|ref|NP_001054.1| transferrin [Homo sapiens]				1.84E-09	5.31	60.23	12.90	77049.5
AHQ-10-5, 3604	K.EGYYGYTGAFR.C	1284.35776	2	6.20E-04	0.69	2.60	-	521.2
AHQ-10-5, 4035 - 4044	R.FDEFFSEGCAPGSK.K	1579.66868	2	1.84E-09	0.97	4.64	-	1437.2
AHQ-10-5, 3371 - 3372	K.IECVSAETTEDCIAK.I	1728.87748	2	7.15E-07	0.94	4.29	-	908.6
AHQ-10-5, 4515 - 4565	K.M*YLGYEYVTAIR.N	1495.72451	2	1.16E-06	0.92	3.48	-	1117.7
AHQ-10-5, 6335 - 6404	R.SAGWNIPIGLLYCDLPEPR.K	2173.47658	2	8.51E-06	0.90	4.25	-	455.7
AHQ-10-5, 4700	K.SDNCEDTPEAGYFAVAVVK.K	2074.21067	2	8.10E-09	0.91	4.42	-	427.0
gi|4506413|ref|NP_002875.1| RAP1A, member of RAS oncogene family; RAS-related protein RAP1A [Homo s				1.92E-09	5.72	70.25	42.90	20987.1
AHQ-10-11, 6204	R.DLYM*KNGQGFALVYSITAQSTFNDLQDLR.E	3326.68143	3	2.60E-04	0.90	4.31	-	930.4
AHQ-10-11, 6150 - 6151	K.INVNEIFYDLVR.Q	1495.70427	2	3.88E-08	0.97	4.99	-	1661.3
AHQ-10-14-, 6260	K.INVNEIFYDLVR.Q	1495.70427	2	3.35E-08	0.94	4.13	-	1079.9
AHQ-10-14-, 5557	K.INVNEIFYDLVR.Q	1495.70427	2	9.02E-05	0.79	3.01	-	629.7
AHQ-10-13-, 6224 - 6244	K.INVNEIFYDLVR.Q	1495.70427	2	6.19E-05	0.84	3.59	-	612.6
AHQ-10-11, 6051	K.INVNEIFYDLVR.Q	1495.70427	2	9.99E-05	0.88	3.42	-	1009.1
AHQ-10-13-, 2897	K.LVVLGSGGVGK.S	986.19059	1	4.68E-04	0.74	2.43	-	972.4
AHQ-10-11, 2810 - 2874	K.LVVLGSGGVGK.S	986.19059	2	3.76E-04	0.92	3.67	-	1038.1
AHQ-10-14-, 5745	K.SALTVQFVQGIFVEK.Y	1666.94196	2	5.79E-06	0.91	3.30	-	1174.7
AHQ-10-11, 5870 - 5935	K.SALTVQFVQGIFVEK.Y	1666.94196	2	1.54E-06	0.64	2.88	-	601.6
AHQ-10-11, 5996 - 6052	K.SALTVQFVQGIFVEK.Y	1666.94196	2	7.86E-04	0.54	2.55	-	736.3
AHQ-10-13-, 5718 - 5726	K.SALTVQFVQGIFVEK.Y	1666.94196	2	8.26E-04	0.96	4.34	-	1690.7
AHQ-10-11, 5426 - 5443	K.SALTVQFVQGIFVEK.Y	1666.94196	2	2.11E-06	0.84	3.59	-	643.7
AHQ-10-11, 5852 - 5928	K.SKINVNEIFYDLVR.Q	1710.95483	2	9.28E-08	0.93	4.39	-	911.7
AHQ-10-11, 5847	K.SKINVNEIFYDLVR.Q	1710.95483	3	6.60E-07	0.95	4.44	-	1608.1
AHQ-10-11, 5000 - 5004	K.SKINVNEIFYDLVR.Q	1710.95483	2	6.80E-06	0.90	3.53	-	1002.7
AHQ-10-11, 5707 - 5714	K.SKINVNEIFYDLVR.Q	1710.95483	3	1.72E-08	0.95	4.51	-	1605.7
AHQ-10-11, 5706	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.92E-09	0.94	4.31	-	953.0
AHQ-10-11, 5202	K.SKINVNEIFYDLVR.Q	1710.95483	2	1.46E-05	0.78	3.45	-	547.6
AHQ-10-13-, 2846 - 2901	K.YDPTIEDSYR.K	1259.30338	2	8.04E-06	0.79	2.73	-	426.6
AHQ-10-11, 2794 - 2862	K.YDPTIEDSYR.K	1259.30338	2	3.73E-04	0.60	2.72	-	277.4
AHQ-10-14-, 2866 - 2877	K.YDPTIEDSYR.K	1259.30338	2	2.01E-07	0.79	2.73	-	466.0
AHQ-10-11, 2471	K.YDPTIEDSYRK.Q	1387.47629	2	9.57E-05	0.59	2.58	-	318.1
gi|4506877|ref|NP_002996.1| selectin P precursor; Selectin P (granulocyte membrane protein, 140kD;				2.18E-09	1.88	20.24	3.40	90844.7
AHQ-10-2, 4670	K.STCQFICDEGYSLSGPER.L	2109.23671	2	2.18E-09	0.93	4.10	-	902.3
AHQ-10-4, 4655	K.STCQFICDEGYSLSGPER.L	2109.23671	2	1.28E-07	0.92	4.20	-	905.5
AHQ-10-3, 4586	K.STCQFICDEGYSLSGPER.L	2109.23671	2	4.86E-09	0.95	4.48	-	1061.1
AHQ-10-5, 4620	K.STCQFICDEGYSLSGPER.L	2109.23671	2	7.77E-09	0.95	4.71	-	966.5
AHQ-10-3, 2977 - 2991	R.YTDLVAIQNK.N	1165.32100	2	5.25E-07	0.95	3.78	-	1191.4
AHQ-10-2, 3040	R.YTDLVAIQNK.N	1165.32100	2	2.29E-06	0.95	3.79	-	1424.3
gi|5031571|ref|NP_005713.1| actin-related protein 2; ARP2 (actin-related protein 2, yeast) homolog				2.31E-09	4.46	50.21	12.70	44760.5
AHQ-10-8, 3650	K.DLMVGDEASELR.S	1335.46633	2	2.56E-07	0.96	4.23	-	1321.1
AHQ-10-8, 3317	K.DLM*VGDEASELR.S	1351.46573	2	7.41E-08	0.89	3.06	-	1165.6
AHQ-10-8, 3365 - 3435	R.GYAFNHSADFETVR.M	1614.69943	2	2.31E-09	0.94	4.17	-	1251.4
AHQ-10-8, 4113	K.HLWDYTFGPEK.L	1393.52736	2	3.55E-07	0.90	3.64	-	715.2
AHQ-10-9, 3932	K.HLWDYTFGPEK.L	1393.52736	2	1.37E-05	0.69	2.77	-	442.2
AHQ-10-9, 3543	K.LCYVGYNIEQEQK.L	1645.81494	2	1.27E-06	0.78	2.72	-	535.0
AHQ-10-8, 3681	K.LCYVGYNIEQEQK.L	1645.81494	2	1.08E-05	0.94	3.58	-	1353.6
gi|16751921|ref|NP_444513.1| dermcidin precursor; AIDD protein [Homo sapiens]				2.31E-09	1.71	20.20	12.70	11283.8

AHQ-10-14-, 3608	K.DAVEDLESVGK.G	1162.22915	2	4.14E-05	0.77	3.21	-	703.3
AHQ-10-6, 3575	K.DAVEDLESVGK.G	1162.22915	2	4.01E-06	0.79	2.79	-	926.6
AHQ-10-13-, 3626	K.DAVEDLESVGK.G	1162.22915	2	6.09E-04	0.73	2.84	-	738.4
AHQ-10-2, 3692	K.DAVEDLESVGK.G	1162.22915	2	5.76E-05	0.76	2.73	-	824.4
AHQ-10-13, 4108	K.LGKDAVEDLESVGK.G	1460.61186	3	3.52E-05	0.85	3.40	-	1475.8
AHQ-10-14-, 3714	K.LGKDAVEDLESVGK.G	1460.61186	2	2.31E-09	0.93	3.95	-	1225.3
AHQ-10-14-, 3720	K.LGKDAVEDLESVGK.G	1460.61186	3	5.33E-05	0.95	3.90	-	2428.0
AHQ-10-3, 3725	K.LGKDAVEDLESVGK.G	1460.61186	2	8.54E-07	0.90	3.78	-	1114.8
gi|16507237|ref|NP_005338.1| heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa); BiP; he				2.33E-09	8.05	90.27	19.00	72332.5
AHQ-10-6, 4105	R.AKFEELNM*DLFR.S	1529.74249	2	9.29E-06	0.90	3.67	-	840.6
AHQ-10-6, 4817	R.AKFEELNMDLFR.S	1513.74309	2	2.33E-09	0.83	2.91	-	656.9
AHQ-10-6, 5460 - 5533	R.IEIESFYEGEDFSETLTR.A	2166.28328	2	5.13E-06	0.92	4.03	-	904.7
AHQ-10-6, 4523	K.IEWLESHQDADIEDFK.A	1976.08864	2	1.87E-06	0.96	5.39	-	1122.5
AHQ-10-6, 3791	R.ITPSYVAFTPEGER.L	1567.72412	2	8.45E-09	0.83	3.36	-	521.1
AHQ-10-5, 3859 - 3867	R.ITPSYVAFTPEGER.L	1567.72412	2	1.43E-05	0.82	3.32	-	546.9
AHQ-10-6, 3743	K.KSDIDEIVLVGGSTR.I	1589.77277	3	1.25E-04	0.80	3.51	-	1024.4
AHQ-10-6, 3689 - 3740	K.KSDIDEIVLVGGSTR.I	1589.77277	2	6.72E-06	0.90	3.30	-	1188.2
AHQ-10-5, 3811	K.KSDIDEIVLVGGSTR.I	1589.77277	2	1.26E-08	0.97	4.93	-	1921.0
AHQ-10-5, 3679 - 3739	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	8.62E-06	0.88	3.51	-	810.9
AHQ-10-6, 3675	K.SQIFSTASDNQPTVTIK.V	1838.00865	2	2.41E-08	0.94	4.40	-	1080.9
AHQ-10-6, 3103	K.TKPYIQVDIGGGQTK.T	1605.81703	2	7.97E-07	0.79	2.74	-	770.2
AHQ-10-5, 3948	K.VTHAVVTVPAYFNDAQR.Q	1889.10372	3	2.60E-04	0.91	4.55	-	848.7
gi|4503105|ref|NP_001313.1| cystatin SA precursor; cystatin 2; cystatin S5; salivary cysteine (thio				2.37E-09	1.89	20.25	18.40	16444.6
AHQ-10-13-, 3620 - 3690	R.ALHFVISEYNK.A	1321.50582	2	7.68E-04	0.92	3.43	-	1073.4
AHQ-10-13-, 3752	R.IIEGGIYDADLNDER.V	1693.79317	2	2.37E-09	0.97	4.76	-	1354.2
AHQ-10-13, 4127 - 4207	R.IIEGGIYDADLNDER.V	1693.79317	2	9.31E-08	0.95	4.90	-	990.7
gi|10716563|ref|NP_001737.1| calnexin [Homo sapiens]				2.52E-09	3.58	40.24	10.00	67567.8
AHQ-10-5, 2416 - 2456	K.AEEDEILNR.S	1089.13826	2	5.34E-05	0.89	3.27	-	1192.7
AHQ-10-7, 4692	K.APVPTGEVYFADSFDR.G	1771.90722	2	4.70E-09	0.82	2.91	-	802.6
AHQ-10-5, 4759	K.APVPTGEVYFADSFDR.G	1771.90722	2	3.58E-06	0.91	3.56	-	1085.4
AHQ-10-12, 4685	K.APVPTGEVYFADSFDR.G	1771.90722	2	4.82E-05	0.38	2.60	-	656.5
AHQ-10-11, 4624	K.APVPTGEVYFADSFDR.G	1771.90722	2	2.52E-09	0.84	2.95	-	816.9
AHQ-10-5, 3891	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	2	4.46E-06	0.91	4.36	-	579.3
AHQ-10-5, 3889	K.IPDPEAVKPDDWDEDAPAK.I	2109.23496	3	1.57E-07	0.89	3.88	-	878.7
AHQ-10-5, 5868	R.KIPNPDFFEDLEPFR.M	1865.07739	3	3.46E-06	0.96	4.75	-	2134.5
gi|14149734|ref|NP_065174.1| coronin, actin binding protein, 1B [Homo sapiens]				2.70E-09	0.92	10.24	5.90	54234.4
AHQ-10-6, 6204	R.KSDLFQDDLYPDTAGPEAALEAEEWVSGR.D	3211.39431	3	2.70E-09	0.92	4.72	-	915.9
gi|13994151|ref|NP_066272.1| PDZ and LIM domain 1 (elfin); carboxy terminal LIM domain protein 1 [H				2.78E-09	9.25	110.23	34.70	36071.5
AHQ-10-13-, 4381	K.CGTGIVGVFVK.L	1138.36198	2	1.46E-05	0.92	3.15	-	1235.0
AHQ-10-13-, 3577	K.DFEQPLAISR.V	1176.30388	2	6.24E-05	0.85	2.62	-	1049.9
AHQ-10-11, 3523	K.DFEQPLAISR.V	1176.30388	2	7.94E-07	0.93	3.63	-	1128.8
AHQ-10-13, 3992	K.DFEQPLAISR.V	1176.30388	2	1.36E-05	0.92	3.48	-	923.7
AHQ-10-14-, 3594 - 3606	K.DFEQPLAISR.V	1176.30388	2	1.51E-04	0.92	3.56	-	930.0
AHQ-10-13-, 3370	K.GCTDNLTLTVAR.S	1322.47058	2	5.61E-04	0.80	3.01	-	742.1
AHQ-10-9, 3769	K.GHFFVEDQIYCEK.H	1673.82684	2	1.12E-05	0.82	3.08	-	610.3
AHQ-10-14-, 3913 - 3956	K.GHFFVEDQIYCEK.H	1673.82684	2	7.40E-06	0.93	3.88	-	902.9
AHQ-10-11, 3894	K.GHFFVEDQIYCEK.H	1673.82684	2	8.06E-04	0.73	3.25	-	400.4
AHQ-10-12, 3964 - 3969	K.GHFFVEDQIYCEK.H	1673.82684	2	6.29E-06	0.95	4.27	-	1159.7
AHQ-10-14-, 3248	R.IKGCTDNLTLTVAR.S	1563.80174	2	5.18E-09	0.91	4.07	-	877.8
AHQ-10-13-, 3276	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.73E-08	0.94	4.05	-	1000.2
AHQ-10-13, 3676	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.78E-09	0.95	4.52	-	1081.0
AHQ-10-12, 3278 - 3281	R.IKGCTDNLTLTVAR.S	1563.80174	2	2.93E-07	0.93	4.08	-	821.1
AHQ-10-9, 3009 - 3076	R.IKGCTDNLTLTVAR.S	1563.80174	2	1.73E-05	0.82	3.42	-	693.4
AHQ-10-14-, 4613	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	2	5.26E-04	0.76	2.80	-	649.1
AHQ-10-14-, 4622	K.LPM*CDKCGTGIVGVFVK.L	1900.27298	3	3.25E-04	0.85	3.51	-	895.4
AHQ-10-14-, 3752	R.LVGGKDFEQPLAISR.V	1630.86972	2	6.93E-06	0.94	4.33	-	1115.6
AHQ-10-13, 4119	R.LVGGKDFEQPLAISR.V	1630.86972	2	8.16E-05	0.79	3.49	-	621.8
AHQ-10-13-, 3760	R.LVGGKDFEQPLAISR.V	1630.86972	2	6.30E-06	0.95	4.38	-	1265.2
AHQ-10-12, 6100	K.QSTSFLVLQEILESEEK.G	1981.18977	2	1.45E-04	0.82	3.11	-	815.9
AHQ-10-13-, 5770 - 5782	K.QSTSFLVLQEILESEEKGDPNKPSGFR.S	3037.32681	3	2.17E-07	0.76	3.55	-	590.1
AHQ-10-13-, 2521	R.SAM*PFTASPASSTTAR.V	1599.74799	2	2.61E-05	0.53	2.72	-	606.8
AHQ-10-13-, 3281	K.VWSPLVTEEGKR.H	1401.59247	2	1.80E-04	0.90	3.13	-	1007.7
AHQ-10-11, 3214 - 3215	K.VWSPLVTEEGKR.H	1401.59247	2	5.50E-06	0.78	2.80	-	617.6
gi|5123454|ref|NP_005336.2| heat shock 70kDa protein 1A; heat shock 70kD protein 1A; heat shock-ind				3.24E-09	4.42	50.28	14.80	70037.7
AHQ-10-6, 3328 - 3391	K.AQIHDLVLVGGSTR.I	1466.66769	2	1.38E-08	0.97	4.86	-	1548.6
AHQ-10-6, 4563 - 4564	K.DAGVIAGLNVLR.I	1198.39736	2	3.63E-06	0.97	4.56	-	1873.0
AHQ-10-6, 5648 - 5716	K.ELEQVCNPIISGLYQGAGGPGPGGFGAQGPK.G	3058.37100	3	4.12E-04	0.97	5.55	-	2053.5
AHQ-10-6, 3987	K.NQVALNPQNTVFDAK.R	1659.82478	2	3.24E-09	0.88	3.46	-	771.8
AHQ-10-6, 3687	K.NQVALNPQNTVFDAK.R	1659.82478	2	2.86E-07	0.95	4.29	-	856.6
AHQ-10-6, 6139 - 6180	K.SINPDEAVAYGAAVQAAILM*GDK.S	2321.59293	2	5.36E-06	0.64	2.99	-	565.8
gi|21314617|ref|NP_000433.2| platelet/endothelial cell adhesion molecule (CD31 antigen); platelet/e				4.16E-09	4.68	60.20	11.80	82449.6
AHQ-10-4, 5959	K.CTIQVTHLAQEFPEIIIQK.D	2270.63371	3	2.21E-06	0.90	3.72	-	1168.5
AHQ-10-3, 5655 - 5723	R.DQNFVILEFPVEEQDR.V	1979.13566	2	2.57E-04	0.81	3.38	-	738.2
AHQ-10-1, 5779	R.DQNFVILEFPVEEQDR.V	1979.13566	2	4.25E-05	0.71	3.01	-	808.9
AHQ-10-4, 5868	R.DQNFVILEFPVEEQDR.V	1979.13566	2	3.48E-05	0.46	2.63	-	401.4
AHQ-10-4, 5745	R.DQNFVILEFPVEEQDR.V	1979.13566	3	6.80E-05	0.87	4.05	-	858.7
AHQ-10-4, 5731	R.DQNFVILEFPVEEQDR.V	1979.13566	2	7.46E-04	0.74	3.23	-	629.6
AHQ-10-5, 5723 - 5736	R.DQNFVILEFPVEEQDR.V	1979.13566	2	7.91E-08	0.78	3.94	-	594.0
AHQ-10-4, 4092	R.ISYDAQFEVIK.G	1313.48046	2	1.61E-08	0.94	3.37	-	1322.9
AHQ-10-5, 4084	R.ISYDAQFEVIK.G	1313.48046	2	4.16E-09	0.82	3.09	-	765.0
AHQ-10-4, 4204 - 4205	K.SELVTVTESFSTPK.F	1525.68231	2	9.22E-04	0.64	2.94	-	491.2
AHQ-10-4, 4072	K.STESYFIPEVR.I	1328.45199	2	7.49E-04	0.86	2.89	-	696.0
AHQ-10-4, 5227 - 5276	K.VIAPVDEVQISILSSK.V	1698.98227	2	2.57E-05	0.68	2.88	-	329.7
gi|15723376|ref|NP_277050.1| MacGAP protein [Homo sapiens]				4.45E-09	0.95	10.20	2.10	70163.1
AHQ-10-5, 3331	R.FLSQESGVAQTLK.K	1408.58178	2	4.45E-09	0.95	3.68	-	1726.8
gi|19743813|ref|NP_002202.2| integrin beta 1 isoform 1A precursor; integrin VLA-4 beta subunit; fib				4.59E-09	1.67	20.23	4.80	88414.9
AHQ-10-3, 4919	K.LKPEDITQIQPQQLVLR.L	2020.36187	2	4.59E-09	0.92	4.50	-	701.5
AHQ-10-3, 4917	K.LKPEDITQIQPQQLVLR.L	2020.36187	3	5.20E-05	0.80	3.89	-	703.7
AHQ-10-3, 6294 - 6329	K.LSENNIQTIFAVTEEFQPVYK.E	2471.74650	2	3.60E-07	0.75	2.89	-	518.5
AHQ-10-3, 6226 - 6295	K.LSENNIQTIFAVTEEFQPVYK.E	2471.74650	3	1.83E-05	0.86	3.60	-	1131.9
gi|4507109|ref|NP_000336.1| alpha-synuclein isoform NACP140; non A4 component of amyloid precursor				4.97E-09	1.61	20.18	27.10	14460.1
AHQ-10-12, 4181	K.TKEQVTNVGGAVVTGVTAVAQK.T	2158.44170	2	7.35E-06	0.88	3.68	-	867.8
AHQ-10-13-, 4106	K.TVEGAGSIAAATGFVK.K	1479.66001	2	4.97E-09	0.72	2.92	-	676.8
gi|13562114|ref|NP_110400.1| beta tubulin 1, class VI [Homo sapiens]				5.79E-09	11.77	140.34	40.80	50326.6
AHQ-10-8, 5879 - 5951	R.ALSVAELTQQMFDAR.N	1680.90740	2	2.61E-04	0.73	2.85	-	848.7
AHQ-10-7, 5749 - 5829	R.ALSVAELTQQMFDAR.N	1680.90740	2	4.69E-06	0.94	4.54	-	1307.3
AHQ-10-7, 5830	R.ALSVAELTQQMFDAR.N	1680.90740	2	8.87E-04	0.83	3.03	-	1175.6
AHQ-10-14-, 4037	R.AVLVDLEPGTM*DSIR.S	1632.86102	2	1.79E-04	0.65	2.54	-	647.2
AHQ-10-14-, 4636 - 4692	R.AVLVDLEPGTMDSIR.S	1616.86162	2	4.59E-07	0.90	4.12	-	597.3
AHQ-10-8, 6306	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	1.58E-07	0.98	6.84	-	2565.7
AHQ-10-11, 6063 - 6132	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.50E-05	0.89	3.82	-	1072.7
AHQ-10-13-, 6192	K.GHYTEGAELIENVLEVVR.H	2029.23935	3	2.50E-04	0.89	4.01	-	1689.2
AHQ-10-13-, 6193 - 6194	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	2.20E-05	0.98	6.58	-	2258.7
AHQ-10-7, 6272	K.GHYTEGAELIENVLEVVR.H	2029.23935	2	5.79E-09	0.98	6.67	-	2169.2
AHQ-10-14-, 6002 - 6036	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	1.83E-04	0.94	4.66	-	827.3
AHQ-10-7, 6012	R.GLSM*AATFIGNNTAIQEIFNR.V	2285.56551	2	7.21E-04	0.69	2.80	-	535.4
AHQ-10-7, 3834 - 3906	R.IMNSFSVMPSPK.V	1338.62160	2	1.37E-04	0.46	2.53	-	505.3

AHQ-10-7, 3168 - 3172	R.ISVYYNEAYGR.K	1335.44622	2	3.32E-07	0.92	3.37	-	939.6
AHQ-10-10, 3154	R.ISVYYNEAYGR.K	1335.44622	2	3.63E-05	0.82	2.62	-	888.4
AHQ-10-13-, 3248 - 3300	R.ISVYYNEAYGR.K	1335.44622	2	7.17E-06	0.94	3.53	-	1211.0
AHQ-10-7, 4954	K.LGALFQPDSFVHGNSGAGNNWAK.G	2388.58260	3	3.98E-08	0.80	3.78	-	647.4
AHQ-10-7, 5553	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	2	5.27E-06	0.82	3.41	-	510.8
AHQ-10-7, 4944	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	3	5.62E-04	0.77	3.29	-	1233.3
AHQ-10-7, 4953	R.LHFFM*PGFAPLTAQGSQQYR.A	2313.62224	2	2.35E-04	0.93	4.08	-	839.5
AHQ-10-11, 5446	R.LHFFMPGFAPLTAQGSQQYR.A	2297.62284	3	4.22E-05	0.87	3.55	-	1511.7
AHQ-10-7, 6194	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	2.97E-05	0.91	4.58	-	946.1
AHQ-10-12, 6080 - 6082	K.LTTPTYGDLNHLVSLTM*SGITTSLR.F	2709.06919	3	4.54E-05	0.61	3.02	-	721.3
AHQ-10-7, 6213 - 6278	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	8.21E-04	0.81	3.17	-	1069.2
AHQ-10-8, 6409	K.LTTPTYGDLNHLVSLTMSGITTSLR.F	2693.06979	3	1.09E-06	0.91	4.01	-	1172.7
AHQ-10-9, 4817 - 4879	R.NSSCFVEWIPNNVK.V	1695.87718	2	3.58E-04	0.79	3.42	-	576.2
AHQ-10-7, 3161	R.VSEHFSAMFK.R	1183.36152	2	3.06E-04	0.82	2.61	-	924.0
gi|7669492|ref|NP_002037.2| glyceraldehyde-3-phosphate dehydrogenase [Homo sapiens]				7.29E-09	1.80	20.21	10.70	36053.0
AHQ-10-9, 3912 - 3989	K.RVIISAPSADAPMFVM*GVNHEK.Y	2386.77962	3	7.32E-04	0.86	4.15	-	1044.9
AHQ-10-9, 3820	R.VPTANVSVVDLTCR.L	1532.74450	3	3.86E-05	0.87	3.82	-	1228.9
AHQ-10-9, 3887 - 3943	R.VPTANVSVVDLTCR.L	1532.74450	2	1.00E-06	0.95	3.79	-	1434.4
AHQ-10-9, 3783 - 3843	R.VPTANVSVVDLTCR.L	1532.74450	2	1.42E-08	0.92	4.05	-	849.5
AHQ-10-6, 4005	R.VPTANVSVVDLTCR.L	1532.74450	2	9.37E-06	0.84	3.38	-	628.1
AHQ-10-10, 3919 - 3984	R.VPTANVSVVDLTCR.L	1532.74450	2	1.67E-07	0.93	3.34	-	1136.3
AHQ-10-11, 3962 - 3968	R.VPTANVSVVDLTCR.L	1532.74450	2	7.29E-09	0.93	4.01	-	1030.5
AHQ-10-13, 4391 - 4451	R.VPTANVSVVDLTCR.L	1532.74450	2	5.37E-04	0.54	2.57	-	505.8
AHQ-10-14, 4819	R.VPTANVSVVDLTCR.L	1532.74450	2	6.60E-05	0.73	2.74	-	601.2
AHQ-10-13-, 4041	R.VPTANVSVVDLTCR.L	1532.74450	2	3.40E-08	0.91	3.80	-	793.5
AHQ-10-14-, 4028 - 4030	R.VPTANVSVVDLTCR.L	1532.74450	2	9.58E-08	0.96	4.21	-	1270.6
gi|10863927|ref|NP_066953.1| peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens]				7.76E-09	3.79	50.26	30.90	18012.4
AHQ-10-12, 3929	K.FEDENFILK.H	1155.28144	2	2.95E-04	0.65	3.10	-	503.0
AHQ-10-14-, 3332	K.KITIADCGQLE	1249.41637	2	5.59E-04	0.87	3.79	-	1091.1
AHQ-10-12, 4512	K.SIYGEKFEDENFILK.H	1833.03047	2	7.76E-09	0.97	5.20	-	1612.1
AHQ-10-13-, 4565	K.SIYGEKFEDENFILK.H	1833.03047	2	1.38E-05	0.92	4.28	-	883.6
AHQ-10-14-, 4557	K.SIYGEKFEDENFILK.H	1833.03047	2	3.40E-07	0.95	4.71	-	1101.0
AHQ-10-12, 2649 - 2717	K.VKEGMNIVEAM*ER.F	1522.77330	2	7.88E-04	0.78	2.76	-	950.4
AHQ-10-14-, 4525	R.VSFELFADKVPK.T	1380.61317	2	1.24E-04	0.81	2.97	-	814.2
AHQ-10-12, 4484	R.VSFELFADKVPK.T	1380.61317	2	4.38E-06	0.89	3.57	-	905.0
AHQ-10-12, 4493	R.VSFELFADKVPK.T	1380.61317	3	1.82E-07	0.51	3.19	-	335.0
gi|4506925|ref|NP_003013.1| SH3 domain binding glutamic acid-rich protein like; SH3-binding domain				7.79E-09	2.78	30.26	50.00	12774.2
AHQ-10-13-, 5840 - 5896	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	1.19E-05	0.95	4.73	-	1111.0
AHQ-10-13, 5895 - 5953	R.ENNAVYAFLGLTAPPGSK.E	1850.06426	2	2.01E-04	0.90	4.36	-	653.7
AHQ-10-13-, 4872 - 4948	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	2.89E-07	0.90	4.58	-	679.0
AHQ-10-13-, 4748 - 4814	R.ENVPENSRPATGYPLPPQIFNESQYR.G	3005.24660	3	7.79E-09	0.92	5.20	-	869.0
AHQ-10-13-, 2422 - 2485	R.VYIASSSGSTAIK.K	1284.44065	2	4.72E-05	0.91	3.55	-	1596.5
gi|27498332|ref|XP_212565.1| similar to tubulin, beta 5 [Homo sapiens]				8.27E-09	3.20	40.26	9.90	49670.5
AHQ-10-8, 5401	R.ALTVPELTQQVFDAK.N	1660.89259	2	4.14E-05	0.72	2.92	-	377.6
AHQ-10-11, 5250	R.ALTVPELTQQVFDAK.N	1660.89259	2	9.05E-04	0.70	2.89	-	543.7
AHQ-10-8, 3382	R.IM*NTFSVVPSPK.V	1336.58217	2	1.19E-04	0.87	3.36	-	979.9
AHQ-10-9, 3588 - 3641	R.IMNTFSVVPSPK.V	1320.58277	2	3.15E-06	0.69	2.62	-	983.6
AHQ-10-7, 3358	R.IM*NTFSVVPSPK.V	1336.58217	2	1.32E-04	0.61	2.54	-	718.1
AHQ-10-8, 5999	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	7.54E-06	0.92	3.84	-	774.5
AHQ-10-8, 6226	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	3.36E-04	0.75	3.06	-	567.2
AHQ-10-7, 6180	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	4.77E-08	0.96	5.23	-	855.6
AHQ-10-7, 5866 - 5937	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.92E-04	0.96	4.85	-	1346.3
AHQ-10-11, 6060 - 6131	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	4.89E-04	0.33	2.71	-	318.0
AHQ-10-12, 6084	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	8.30E-04	0.71	3.08	-	458.7
AHQ-10-13, 6175 - 6247	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.90E-05	0.93	4.12	-	984.1
AHQ-10-13, 6312	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.78E-05	0.94	4.47	-	868.6
AHQ-10-13-, 5990 - 6056	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	4.65E-04	0.70	3.52	-	478.2
AHQ-10-14-, 5921	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	1.79E-08	0.90	3.59	-	881.9
AHQ-10-14-, 6101 - 6169	K.M*AVTFIGNSTAIQELFK.R	1887.18942	2	8.27E-09	0.92	4.32	-	701.6
gi|4557385|ref|NP_000055.1| complement component 3 precursor; acylation-stimulating protein cleavag				8.45E-09	2.84	30.28	3.10	187162.3
AHQ-10-6, 5560	K.EYVLPSFEVIVEPTEK.F	1880.12704	2	2.89E-06	0.94	4.59	-	889.2
AHQ-10-6, 3573	R.IPIEDGSGEVVLSR.K	1471.63788	2	8.45E-09	0.93	3.34	-	1199.3
AHQ-10-6, 4365	R.VPVAVQGEDTVQSLTQGDGVAK.L	2199.40432	2	2.75E-04	0.97	5.65	-	949.9
gi|4503631|ref|NP_000120.1| coagulation factor XIII A1 subunit precursor; Coagulation factor XIII,				8.73E-09	14.74	170.29	24.60	83232.8
AHQ-10-6, 2635	K.DGTHVVENVDATHIGK.L	1692.81163	2	3.66E-04	0.75	2.93	-	803.9
AHQ-10-5, 2663	K.DGTHVVENVDATHIGK.L	1692.81163	2	1.08E-05	0.93	4.20	-	968.3
AHQ-10-7, 2637	K.DGTHVVENVDATHIGK.L	1692.81163	3	1.02E-05	0.91	3.55	-	1349.6
AHQ-10-5, 2659 - 2661	K.DGTHVVENVDATHIGK.L	1692.81163	3	1.72E-08	0.95	4.66	-	1301.2
AHQ-10-5, 6495 - 6565	K.EAVLIQAGEYM*GQLLEQASLHFFVTAR.I	3039.45415	3	7.26E-06	0.91	4.82	-	841.2
AHQ-10-7, 5349	K.ETFDVTLEPLSFK.K	1526.71190	2	7.69E-06	0.87	3.52	-	767.8
AHQ-10-5, 4804	R.GTQVVGSDM*TVTVQFTNPLK.E	2139.41549	2	1.07E-06	0.93	4.62	-	767.1
AHQ-10-6, 5271 - 5351	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.67E-05	0.58	2.83	-	247.1
AHQ-10-11, 5196 - 5198	K.GTYIPVPIVSELQSGK.W	1688.94594	2	6.45E-05	0.71	3.58	-	243.8
AHQ-10-5, 5473 - 5475	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.17E-04	0.67	3.37	-	258.4
AHQ-10-5, 5383 - 5415	K.GTYIPVPIVSELQSGK.W	1688.94594	2	2.33E-08	0.83	3.01	-	543.1
AHQ-10-11, 6146	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	6.08E-06	0.92	3.70	-	1008.7
AHQ-10-7, 6292 - 6350	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	3.72E-06	0.88	4.04	-	749.0
AHQ-10-6, 6241	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	8.73E-09	0.94	4.53	-	1038.2
AHQ-10-5, 6364	R.GVNLQEFLNVTSVHLFK.E	1946.23831	2	5.74E-07	0.97	5.34	-	1272.1
AHQ-10-7, 2328	K.KDGTHVVENVDATHIGK.L	1820.98455	3	1.28E-05	0.94	4.75	-	1270.0
AHQ-10-5, 2340	K.KDGTHVVENVDATHIGK.L	1820.98455	3	6.90E-08	0.98	5.72	-	2264.5
AHQ-10-5, 2525	K.KDGTHVVENVDATHIGK.L	1820.98455	2	2.73E-04	0.77	2.77	-	871.4
AHQ-10-5, 2853	R.KLIASMSSDSLR.H	1308.53039	2	6.97E-05	0.94	3.73	-	1322.5
AHQ-10-5, 4581	R.LALETALMYGAK.K	1281.54655	2	6.99E-07	0.96	4.23	-	1687.3
AHQ-10-7, 4488	R.LALETALMYGAK.K	1281.54655	2	2.41E-06	0.96	4.10	-	1388.6
AHQ-10-7, 4085	R.LALETALM*YGAK.K	1297.54595	2	6.37E-04	0.87	3.36	-	750.9
AHQ-10-6, 4504 - 4505	R.LALETALMYGAK.K	1281.54655	2	1.88E-08	0.88	3.25	-	1047.3
AHQ-10-5, 4183 - 4217	R.LALETALM*YGAK.K	1297.54595	2	2.55E-08	0.94	4.00	-	1081.1
AHQ-10-5, 2304	K.LIASM*SSDSLR.H	1196.35688	2	4.92E-05	0.93	3.57	-	846.6
AHQ-10-5, 1917 - 1933	R.LSIQSSPK.C	859.99043	2	6.96E-04	0.63	2.73	-	567.5
AHQ-10-5, 3463	K.QIGGDGM*MDITDTYK.F	1661.83636	2	4.20E-04	0.40	2.69	-	481.0
AHQ-10-5, 2891 - 2893	K.QIGGDGM*M*DITDTYK.F	1677.83576	2	2.68E-07	0.84	3.90	-	479.9
AHQ-10-5, 5063	R.SNVDMDFEVENAVLGK.D	1767.93869	2	2.83E-08	0.97	5.50	-	1934.8
AHQ-10-5, 4433 - 4499	R.SNVDM*DFEVENAVLGK.D	1783.93809	2	2.20E-07	0.97	4.76	-	2017.6
AHQ-10-6, 4975 - 4983	R.SNVDMDFEVENAVLGK.D	1767.93869	2	8.71E-07	0.92	4.04	-	1188.4
AHQ-10-5, 2423	R.VEYVIGR.Y	835.97056	2	4.78E-04	0.83	2.51	-	766.4
gi|5803011|ref|NP_001966.1| enolase 2; enolase-2, gamma, neuronal; neurone-specific enolase; neuron				8.75E-09	1.67	20.19	7.10	47268.3
AHQ-10-8, 3991	K.VNQIGSVTEAIQACK.L	1619.82216	2	8.75E-09	0.78	3.00	-	658.2
AHQ-10-8, 6094 - 6105	R.YITGDQLGALYQDFVR.D	1860.05915	2	4.05E-07	0.89	3.77	-	941.9
gi|4507521|ref|NP_001055.1| transketolase [Homo sapiens]				8.82E-09	2.41	30.23	7.20	67877.3
AHQ-10-6, 4429	K.ILATPPQEDAPSVDIANIR.M	2021.26036	3	7.72E-08	0.96	4.60	-	1595.1
AHQ-10-6, 4419	K.ILATPPQEDAPSVDIANIR.M	2021.26036	2	8.82E-09	0.86	3.51	-	556.9
AHQ-10-6, 5480	K.LDNLVAILDINR.L	1369.59192	2	9.38E-07	0.91	3.60	-	953.6
AHQ-10-6, 6279	R.TVPFCSTFAAFFTR.A	1653.88190	2	9.05E-08	0.64	2.59	-	352.9
gi|4507487|ref|NP_003238.1| thrombospondin 2 [Homo sapiens]				8.99E-09	1.72	20.20	2.60	129954.5
AHQ-10-2, 4915 - 4971	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.14E-08	0.95	4.07	-	1228.7
AHQ-10-7, 4764	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	3.84E-08	0.88	3.46	-	762.6

AHQ-10-3, 4842 - 4901	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	7.85E-04	0.91	3.74	-	1040.1
AHQ-10-4, 4899 - 4961	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	8.99E-09	0.89	3.06	-	1240.1
AHQ-10-1, 4955	R.DDDYAGFVFGYQSSSR.F	1814.84582	2	1.50E-04	0.89	2.97	-	1165.4
AHQ-10-7, 2945	R.NALWHTGNTPGQVR.T	1551.69124	2	4.14E-06	0.83	2.78	-	912.9
AHQ-10-4, 2732 - 2807	R.NALWHTGNTPGQVR.T	1551.69124	2	1.93E-04	0.70	2.69	-	825.1
AHQ-10-3, 2838	R.NALWHTGNTPGQVR.T	1551.69124	2	9.14E-06	0.85	2.72	-	1164.5
AHQ-10-13-, 2866	R.NALWHTGNTPGQVR.T	1551.69124	2	2.84E-05	0.59	2.61	-	631.3
gi|4885609|ref|NP_005408.1| v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog; Protooncogen				9.11E-09	3.45	40.23	10.40	59834.4
AHQ-10-7, 2316	R.EVLDQVER.G	988.07707	2	8.88E-04	0.82	2.64	-	985.6
AHQ-10-7, 3878	K.LFGGFNSSDTVTSPQR.A	1713.82931	2	9.27E-07	0.83	3.49	-	744.4
AHQ-10-7, 2640 - 2648	R.LTTVCPTSKPQTQGLAK.D	1832.11198	2	3.10E-05	0.84	3.31	-	601.0
AHQ-10-7, 5889	R.TQFNSLQQLVAYYSK.H	1790.99681	2	9.11E-09	0.96	4.51	-	1334.8
gi|29737978|ref|XP_290747.1| similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy				1.02E-08	3.56	40.25	1.50	191380.7
AHQ-10-1, 4073	K.ADFCIIHYAGK.V	1296.47641	2	1.16E-07	0.90	3.30	-	992.8
AHQ-10-3, 3909 - 3951	K.ADFCIIHYAGK.V	1296.47641	2	5.11E-06	0.91	3.46	-	837.7
AHQ-10-5, 3909 - 3911	K.ADFCIIHYAGK.V	1296.47641	2	2.51E-07	0.93	3.58	-	1040.7
AHQ-10-6, 3820 - 3847	K.ADFCIIHYAGK.V	1296.47641	2	1.24E-06	0.92	3.90	-	954.6
AHQ-10-2, 3975 - 3988	K.ADFCIIHYAGK.V	1296.47641	2	3.48E-06	0.96	3.48	-	1750.4
AHQ-10-4, 3931	K.ADFCIIHYAGK.V	1296.47641	2	2.05E-06	0.94	4.06	-	1007.3
AHQ-10-3, 3098	R.AGVLAHLEEER.D	1224.34854	2	4.24E-08	0.94	3.91	-	1371.0
AHQ-10-2, 3146 - 3166	R.AGVLAHLEEER.D	1224.34854	2	6.67E-07	0.96	4.61	-	1448.2
AHQ-10-4, 3096	R.AGVLAHLEEER.D	1224.34854	2	2.38E-06	0.93	3.81	-	1368.0
AHQ-10-2, 3155	R.AGVLAHLEEER.D	1224.34854	3	1.47E-05	0.60	3.03	-	429.9
AHQ-10-6, 3056	R.AGVLAHLEEER.D	1224.34854	2	1.02E-08	0.96	4.37	-	1786.7
AHQ-10-5, 3071	R.AGVLAHLEEER.D	1224.34854	2	2.35E-07	0.86	3.72	-	884.9
AHQ-10-6, 3640	K.DKADFCIIHYAGK.V	1539.73719	2	4.62E-07	0.94	3.78	-	1418.9
AHQ-10-2, 3784	K.DKADFCIIHYAGK.V	1539.73719	2	2.35E-05	0.97	5.00	-	1945.0
AHQ-10-2, 3775	K.DKADFCIIHYAGK.V	1539.73719	3	1.67E-06	0.94	4.33	-	1410.9
AHQ-10-5, 4539	K.LDPHLVLDQLR.C	1319.53460	2	5.32E-06	0.76	2.76	-	597.2
AHQ-10-2, 4618	K.LDPHLVLDQLR.C	1319.53460	3	1.32E-05	0.89	3.43	-	969.3
AHQ-10-6, 4457	K.LDPHLVLDQLR.C	1319.53460	2	6.97E-04	0.69	2.73	-	545.9
AHQ-10-4, 4584	K.LDPHLVLDQLR.C	1319.53460	2	9.12E-05	0.75	2.74	-	391.2
gi|4757810|ref|NP_004037.1| ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit,				1.06E-08	8.10	90.22	17.90	59750.3
AHQ-10-7, 3560	K.GIRPAINVGLSVSR.V	1439.68861	2	9.34E-05	0.95	4.45	-	958.1
AHQ-10-7, 5174	K.GM*SLNLEPDNVGVVVFGNDK.L	2121.35703	2	2.02E-07	0.92	4.47	-	439.9
AHQ-10-7, 5581	K.GMSLNLEPDNVGVVVFGNDK.L	2105.35763	2	5.61E-06	0.69	2.96	-	493.1
AHQ-10-7, 2946	R.GYLDKLEPSK.I	1150.30633	2	1.92E-05	0.87	3.14	-	1019.4
AHQ-10-7, 3536 - 3537	K.HALIIYDDLSK.Q	1288.47413	2	1.06E-08	0.95	3.24	-	1332.4
AHQ-10-7, 3624 - 3686	R.ILGADTSVDLEETGR.V	1576.68772	2	3.10E-07	0.95	3.75	-	1616.1
AHQ-10-7, 5008	R.TGAIVDVPVGEELLGR.V	1625.84824	2	5.50E-04	0.92	3.94	-	823.5
AHQ-10-7, 2680	K.TGTAEM*SSILEER.I	1440.55928	2	8.75E-06	0.94	3.69	-	1528.2
AHQ-10-7, 3729	K.TGTAEMSSILEER.I	1424.55988	2	4.33E-05	0.92	3.34	-	1466.6
gi|5453740|ref|NP_006462.1| myosin regulatory light chain MRCL3; myosin, light polypeptide, regulat				1.07E-08	4.49	50.27	26.90	19794.0
AHQ-10-14-, 5777 - 5778	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	1.04E-04	0.98	5.39	-	1865.5
AHQ-10-13-, 5769	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	7.54E-06	0.97	4.25	-	1981.6
AHQ-10-13-, 5180	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.07E-07	0.97	5.03	-	1569.9
AHQ-10-11, 4994 - 5058	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	6.41E-07	0.97	5.05	-	1331.8
AHQ-10-11, 5176 - 5254	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.07E-08	0.96	4.91	-	1161.6
AHQ-10-14, 5743 - 5748	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	1.59E-05	0.95	4.61	-	1324.9
AHQ-10-13, 5472 - 5527	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.12E-05	0.74	2.92	-	762.9
AHQ-10-11, 5538 - 5595	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	6.68E-04	0.82	3.72	-	461.2
AHQ-10-11, 5655	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	3.63E-06	0.93	3.39	-	1358.8
AHQ-10-14-, 5169	R.ATSNVFAM*FDQSQIQEFK.E	2108.31681	2	2.05E-07	0.97	4.96	-	1581.9
AHQ-10-12, 5637 - 5704	R.ATSNVFAMFDQSQIQEFK.E	2092.31741	2	9.15E-06	0.77	2.90	-	709.5
AHQ-10-11, 5459	R.DGFIDKEDLHDMLASLGK.N	2005.23806	2	1.89E-05	0.91	3.40	-	1258.7
AHQ-10-11, 5454 - 5455	R.DGFIDKEDLHDMLASLGK.N	2005.23806	3	3.32E-08	0.96	4.51	-	1620.3
AHQ-10-11, 4346	R.DGFIDKEDLHDM*LASLGK.N	2021.23746	2	1.10E-05	0.84	3.38	-	845.1
AHQ-10-11, 4212	K.GNFNYIEFTR.I	1261.36733	2	1.64E-04	0.82	2.86	-	899.2
AHQ-10-14-, 4102 - 4165	K.GNFNYIEFTR.I	1261.36733	2	1.18E-05	0.80	3.23	-	672.4
AHQ-10-12, 4137 - 4140	K.GNFNYIEFTR.I	1261.36733	2	9.96E-05	0.83	3.05	-	835.0
AHQ-10-13, 4555	K.GNFNYIEFTR.I	1261.36733	2	1.94E-04	0.85	2.75	-	1145.7
AHQ-10-11, 4043 - 4059	K.GNFNYIEFTR.I	1261.36733	2	7.79E-04	0.74	3.16	-	699.3
gi|4503725|ref|NP_000792.1| FK506-binding protein 1A; FK506-binding protein 1; FK506-binding protei				1.10E-08	1.87	20.27	13.00	11950.6
AHQ-10-13-, 3077	R.GWEEGVAQM*SVGQR.A	1550.67866	2	1.76E-07	0.90	3.62	-	948.3
AHQ-10-13-, 3860	R.GWEEGVAQMSVGQR.A	1534.67926	2	1.10E-08	0.98	5.33	-	1657.9
AHQ-10-14-, 3838	R.GWEEGVAQMSVGQR.A	1534.67926	2	3.83E-07	0.94	3.94	-	1177.8
AHQ-10-13, 3476 - 3488	R.GWEEGVAQM*SVGQR.A	1550.67866	2	1.10E-04	0.80	3.04	-	900.7
gi|4758460|ref|NP_004479.1| glycoprotein V (platelet) [Homo sapiens]				1.13E-08	4.51	50.23	10.20	60958.9
AHQ-10-5, 3851	R.GVLQSQSFSGM*TVLQR.L	1754.98948	2	3.53E-06	0.96	4.62	-	1372.1
AHQ-10-6, 3783	R.GVLQSQSFSGM*TVLQR.L	1754.98948	2	1.13E-08	0.80	3.20	-	784.6
AHQ-10-6, 4472	R.GVLQSQSFSGMTVLQR.L	1738.99008	2	2.06E-07	0.92	3.52	-	1330.9
AHQ-10-5, 5323	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	2	5.51E-06	0.95	4.54	-	1105.4
AHQ-10-5, 5313 - 5321	R.LM*ISDSHISAVAPGTFSDLIK.L	2219.54375	3	1.47E-05	0.89	4.30	-	995.1
AHQ-10-5, 4525	R.LPNLSSLTLSR.N	1201.39802	2	3.46E-05	0.92	3.40	-	1441.2
AHQ-10-5, 3447	R.YLGVTLSPR.L	1006.18036	2	1.58E-04	0.92	3.83	-	1168.6
gi|6005942|ref|NP_009057.1| valosin-containing protein; yeast Cdc48p homolog; transitional endoplas				1.14E-08	4.32	50.27	10.00	89321.3
AHQ-10-5, 4481	K.DVDLEFLAK.M	1050.18677	2	7.69E-05	0.86	3.23	-	866.0
AHQ-10-5, 4707 - 4781	R.LIVDEAINEDNSVVSLSQPK.M	2171.39088	2	1.14E-08	0.96	5.31	-	1256.3
AHQ-10-5, 6447	K.NAPAIIFIDELDAIAPK.R	1812.09907	2	1.93E-05	0.96	4.56	-	1507.0
AHQ-10-5, 6451 - 6521	K.NAPAIIFIDELDAIAPK.R	1812.09907	3	4.00E-06	0.92	3.99	-	1442.3
AHQ-10-5, 5496	K.NVFIIGATNRPDIIDPAILRPGR.L	2519.93026	3	9.40E-04	0.69	3.73	-	419.8
AHQ-10-5, 3553	R.WALSQSNPSALR.E	1330.47434	2	5.72E-04	0.88	3.06	-	1245.6
gi|4557731|ref|NP_000618.1| latent transforming growth factor beta binding protein 1 precursor [Hom				1.22E-08	6.27	80.27	8.40	152790.9
AHQ-10-2, 3639	R.ASGLGDHCEDINECLEDK.S	2065.13910	3	1.54E-08	0.95	4.77	-	1392.7
AHQ-10-3, 3569	R.ASGLGDHCEDINECLEDK.S	2065.13910	3	1.35E-05	0.88	4.30	-	909.6
AHQ-10-3, 3501 - 3566	R.ASGLGDHCEDINECLEDK.S	2065.13910	2	1.04E-05	0.97	5.39	-	1708.7
AHQ-10-3, 3942	K.CVDIDECTQVQHLCSQGR.C	2209.38110	2	2.49E-06	0.87	3.79	-	763.9
AHQ-10-4, 2173	K.DQCEDIDECQHR.H	1607.61898	2	2.74E-04	0.48	2.57	-	499.7
AHQ-10-14-, 3164	K.EAQPGQSQVSYQGLPVQK.T	1945.12244	2	1.51E-04	0.84	3.40	-	561.6
AHQ-10-2, 5531	K.IGFGPDPTFSSCVPDPPVISEEKGPCYR.L	3112.43550	3	1.53E-04	0.79	3.77	-	381.9
AHQ-10-4, 2889	R.TSTDLDVDVDQPK.E	1433.50014	2	2.51E-05	0.84	2.97	-	835.3
AHQ-10-4, 2720	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.12E-07	0.90	3.80	-	1137.2
AHQ-10-2, 2802	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	6.90E-06	0.90	3.66	-	1227.9
AHQ-10-5, 2733	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	1.22E-08	0.63	2.83	-	729.8
AHQ-10-3, 2746 - 2747	R.TSTDLDVDVDQPKEEK.K	1819.90213	2	7.08E-06	0.88	3.64	-	1189.7
AHQ-10-5, 3491	R.YTCICYEGYR.F	1387.51964	2	1.09E-04	0.75	2.69	-	599.5
AHQ-10-4, 3520	R.YTCICYEGYR.F	1387.51964	2	3.94E-05	0.87	2.93	-	721.8
gi|20539300|ref|XP_088391.4| similar to tropomyosin 4 [Homo sapiens]				1.22E-08	2.53	30.23	9.40	18592.1
AHQ-10-9, 3483 - 3485	R.KLVILEGELER.A	1299.54160	3	3.50E-05	0.96	4.63	-	2054.2
AHQ-10-11, 3668	R.KLVILEGELER.A	1299.54160	2	9.49E-07	0.94	4.00	-	1246.5
AHQ-10-9, 3475 - 3548	R.KLVILEGELER.A	1299.54160	2	1.22E-08	0.97	4.47	-	1812.1
AHQ-10-9, 3791	R.KLVILEGELERAEER.A	1785.03525	2	5.38E-04	0.78	3.35	-	695.8
AHQ-10-9, 3787 - 3788	R.KLVILEGELERAEER.A	1785.03525	3	7.19E-07	0.63	3.34	-	521.7
AHQ-10-9, 3793	K.LVILEGELER.A	1171.36868	2	2.78E-05	0.93	3.00	-	1585.8
gi|5729997|ref|NP_004154.2| RAB27B, member RAS oncogene family [Homo sapiens]				1.23E-08	2.62	30.19	19.30	24607.7
AHQ-10-11, 5392	K.AVETLLDLIM*K.R	1262.54151	2	1.84E-04	0.78	3.09	-	626.1
AHQ-10-13-, 3786	K.VHLQLWDTAGQER.F	1553.70390	2	9.42E-04	0.90	3.25	-	889.7

AHQ-10-11, 4243 - 4318	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	7.48E-07	0.59	2.75	-	549.5
AHQ-10-10, 4212 - 4287	K.YGIPYFETSAATGQNVEK.A	1976.13177	2	1.23E-08	0.94	3.83	-	1074.1
gi|21361370|ref|NP_002853.2| phosphorylase, glycogen; brain [Homo sapiens]				1.33E-08	1.83	20.23	2.80	96695.3
AHQ-10-5, 3788	R.GLAGLGDVAEVR.K	1157.30210	2	1.87E-07	0.97	4.61	-	1848.8
AHQ-10-5, 5567 - 5568	K.LLPLVSDEVFIR.D	1401.67552	2	1.33E-08	0.86	2.93	-	741.1
gi|4503747|ref|NP_001448.1| filamin B, beta (actin binding protein 278); beta filamin; filamin 1 (a				1.35E-08	3.61	40.22	1.30	278191.4
AHQ-10-1, 6035	R.LIALLEVLSQK.R	1227.51852	2	7.09E-07	0.97	4.27	-	1504.0
AHQ-10-9, 5648	R.LIALLEVLSQK.R	1227.51852	2	8.98E-08	0.96	3.74	-	1329.4
AHQ-10-7, 5897	R.LIALLEVLSQK.R	1227.51852	2	6.49E-06	0.96	4.09	-	1294.6
AHQ-10-6, 5864	R.LIALLEVLSQK.R	1227.51852	2	3.96E-08	0.97	4.42	-	1224.5
AHQ-10-5, 5980	R.LIALLEVLSQK.R	1227.51852	2	4.37E-07	0.95	3.88	-	1089.1
AHQ-10-2, 5999	R.LIALLEVLSQK.R	1227.51852	2	1.80E-07	0.96	4.26	-	1403.0
AHQ-10-4, 6004	R.LIALLEVLSQK.R	1227.51852	2	1.35E-08	0.97	4.40	-	1457.4
AHQ-10-3, 5913	R.LIALLEVLSQK.R	1227.51852	2	6.95E-08	0.95	4.13	-	1211.3
AHQ-10-11, 5778 - 5780	R.LIALLEVLSQK.R	1227.51852	2	1.52E-07	0.96	4.19	-	1414.7
AHQ-10-2, 3742 - 3762	R.LLGWIQNK.I	972.16560	2	6.14E-04	0.90	3.84	-	629.3
AHQ-10-5, 3672	R.LLGWIQNK.I	972.16560	2	8.17E-04	0.85	3.16	-	697.9
AHQ-10-2, 5966 - 5967	R.QM*QLENVSVALEFLDR.E	1909.15348	2	7.08E-06	0.89	4.25	-	826.0
AHQ-10-1, 6421 - 6422	R.QMQLENVSVALEFLDR.E	1893.15408	2	5.80E-05	0.85	3.14	-	992.3
AHQ-10-2, 5983	R.QM*QLENVSVALEFLDR.E	1909.15348	3	8.70E-06	0.85	3.28	-	973.4
AHQ-10-3, 5893	R.QM*QLENVSVALEFLDR.E	1909.15348	2	1.24E-05	0.90	3.90	-	837.7
gi|11056061|ref|NP_066932.1| thymosin, beta 4 [Homo sapiens]				1.37E-08	0.75	10.19	29.50	5052.6
AHQ-10-14-, 2522	K.NPLPSKETIEQEK.Q	1513.67476	2	1.37E-08	0.75	3.00	-	425.6
gi|20149594|ref|NP_031381.2| heat shock 90kDa protein 1, beta; heat shock 90kD protein 1, beta; Hea				1.38E-08	5.40	60.25	8.70	83263.6
AHQ-10-5, 2531	K.EDQTEYLEER.R	1312.32145	2	3.05E-04	0.77	2.81	-	482.5
AHQ-10-4, 3165	R.ELISNASDALDK.I	1276.37539	2	2.35E-04	0.86	3.33	-	697.1
AHQ-10-5, 3955 - 4031	R.NPDDITQEEYGEFYK.S	1848.90048	2	2.02E-06	0.97	5.04	-	1345.2
AHQ-10-6, 3955	R.NPDDITQEEYGEFYK.S	1848.90048	2	6.47E-07	0.95	4.70	-	1099.8
AHQ-10-5, 3980	K.SLTNDWEDHLAVK.H	1528.64798	2	1.38E-08	0.93	4.28	-	1028.7
AHQ-10-5, 3897	K.SLTNDWEDHLAVK.H	1528.64798	2	4.95E-07	0.91	3.64	-	948.0
AHQ-10-5, 4192 - 4195	R.TLTLVDTGIGMTK.A	1350.60718	2	3.53E-07	0.95	4.02	-	1046.6
AHQ-10-5, 3632 - 3636	R.TLTLVDTGIGM*TK.A	1366.60658	2	6.42E-05	0.94	3.61	-	1261.0
gi|4758950|ref|NP_000933.1| peptidylprolyl isomerase B (cyclophilin B) [Homo sapiens]				1.44E-08	1.80	20.20	12.50	23742.4
AHQ-10-12, 3145	R.DKPLKDVIIADCGK.I	1573.83653	3	1.19E-04	0.78	3.14	-	962.0
AHQ-10-11, 3068	R.DKPLKDVIIADCGK.I	1573.83653	2	1.44E-08	0.93	3.97	-	939.4
AHQ-10-11, 4098 - 4154	K.DTNGSQFFITTVK.T	1458.59766	2	3.11E-06	0.87	3.46	-	924.1
gi|4502201|ref|NP_001649.1| ADP-ribosylation factor 1 [Homo sapiens]				1.52E-08	1.58	20.26	21.50	20696.6
AHQ-10-13-, 5928	K.LGEIVTTIPTIGFNVETVEYK.N	2324.65485	2	1.24E-05	0.61	3.35	-	207.9
AHQ-10-12, 6202	R.M*LAEDELRDAVLLVFANK.Q	2064.39175	3	1.52E-08	0.97	5.28	-	1956.5
gi|10835002|ref|NP_001166.1| Rho GDP dissociation inhibitor (GDI) beta; Ly-GDI [Homo sapiens]				1.62E-08	0.97	10.27	8.50	22987.8
AHQ-10-10, 2502 - 2503	K.APEPHVEEDDDDELDSK.L	1940.90995	2	1.62E-08	0.97	5.42	-	1380.2
gi|4502167|ref|NP_000475.1| amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disea				1.64E-08	1.81	20.21	3.90	86942.8
AHQ-10-4, 5632 - 5693	R.LALENYITALQAVPPRPR.H	2023.36745	3	1.64E-08	0.87	3.77	-	826.1
AHQ-10-4, 2737 - 2769	K.VESLEQEAANER.Q	1375.42391	2	5.17E-04	0.94	4.25	-	1254.9
gi|4759082|ref|NP_004648.1| serum deprivation response protein; serum deprivation response; phospha				1.73E-08	3.39	40.26	14.60	47172.9
AHQ-10-9, 5671 - 5733	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.54E-05	0.96	4.87	-	1317.0
AHQ-10-13-, 5869	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	5.01E-05	0.95	4.40	-	1214.1
AHQ-10-12, 5788 - 5834	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	3.05E-06	0.96	4.72	-	1397.9
AHQ-10-11, 5728 - 5810	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.41E-06	0.87	3.13	-	974.4
AHQ-10-14-, 5889 - 5958	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	3.84E-04	0.73	3.07	-	605.3
AHQ-10-9, 5559 - 5615	R.DNSQVNAVTVLTLLDK.L	1730.94122	2	2.77E-04	0.64	3.00	-	676.7
AHQ-10-9, 3416	K.LVNMLDAVQENQHK.M	1639.85851	2	4.08E-04	0.88	3.57	-	847.0
AHQ-10-9, 3701	R.QEKPSSPSPM*PSSTPSPSLNLGNTEEAIR.D	3056.30877	3	2.51E-04	0.71	3.06	-	672.7
AHQ-10-11, 5598 - 5606	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	5.24E-05	0.95	5.11	-	938.2
AHQ-10-9, 5405 - 5467	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	1.73E-08	0.93	4.35	-	911.9
AHQ-10-13-, 5692	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	2.20E-05	0.85	3.76	-	567.2
AHQ-10-7, 5704	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	4.94E-05	0.91	4.17	-	643.9
AHQ-10-6, 5685	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.86E-04	0.89	3.44	-	850.0
AHQ-10-9, 5499	K.VLIFQEENEIPASVFVK.Q	1963.26241	2	8.72E-07	0.69	3.05	-	481.4
gi|4557675|ref|NP_000201.1| integrin alpha chain, alpha 6 [Homo sapiens]				1.74E-08	3.48	40.20	5.50	119509.5
AHQ-10-4, 3404	K.FGSCQQGVAATFTK.D	1503.66172	2	4.58E-06	0.93	3.82	-	1153.9
AHQ-10-5, 5581	R.NSYPDVAVGSLSDSVTIFR.S	2028.20822	2	7.29E-07	0.91	4.08	-	666.6
AHQ-10-4, 5423	K.SEDEVGSLIEYEFR.V	1673.75872	2	1.74E-08	0.93	3.58	-	1130.0
AHQ-10-4, 3215 - 3295	R.TGGLYSCDITAR.G	1315.43490	2	5.23E-05	0.72	3.10	-	572.1
gi|5803181|ref|NP_006810.1| stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) [Homo				1.84E-08	1.78	20.21	5.90	62638.9
AHQ-10-6, 5891	K.ALSVGNIDDALQCYSEAIK.L	2069.27871	2	1.84E-08	0.91	4.26	-	644.5
AHQ-10-6, 4369	R.LAYINPDLALEEK.N	1489.69480	2	1.58E-06	0.88	3.76	-	793.2
gi|5453595|ref|NP_006358.1| adenylyl cyclase-associated protein [Homo sapiens]				1.89E-08	5.73	70.26	16.00	51672.7
AHQ-10-8, 2813	R.ALLVTASQCQQPAENK.L	1759.96271	2	3.82E-04	0.93	3.97	-	959.9
AHQ-10-7, 6122 - 6184	R.ALLVTASQCQQPAENKLSDLLAPISEQIK.E	3168.60826	3	1.89E-08	0.78	3.80	-	849.1
AHQ-10-7, 4776 - 4833	K.LSDLLAPISEQIK.E	1427.66814	2	1.48E-04	0.71	2.80	-	684.6
AHQ-10-7, 3362	K.NSLDCEIVSAK.S	1237.36245	1	7.77E-04	0.42	2.21	-	382.0
AHQ-10-7, 3196 - 3252	K.NSLDCEIVSAK.S	1237.36245	2	1.78E-04	0.77	2.62	-	705.0
AHQ-10-7, 3005 - 3068	K.NSLDCEIVSAK.S	1237.36245	2	6.70E-04	0.92	3.35	-	1064.9
AHQ-10-14-, 3132 - 3206	K.NSLDCEIVSAK.S	1237.36245	2	6.17E-04	0.89	3.07	-	844.8
AHQ-10-8, 4598	R.SALFAQINQGESITHALK.H	1929.16615	2	1.07E-06	0.91	4.55	-	667.5
AHQ-10-7, 4756	R.SALFAQINQGESITHALK.H	1929.16615	2	4.10E-06	0.66	3.41	-	471.4
AHQ-10-7, 4530 - 4592	R.SALFAQINQGESITHALK.H	1929.16615	2	2.27E-06	0.94	4.94	-	721.8
AHQ-10-7, 6104	K.SSEMNVLIPTEGGDFNEFPVPEQFK.T	2813.08809	2	5.92E-04	0.72	3.27	-	225.4
AHQ-10-7, 4056 - 4132	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.89E-04	0.82	3.22	-	768.3
AHQ-10-8, 4569	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	4.55E-05	0.89	4.14	-	607.3
AHQ-10-7, 4526	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	1.19E-06	0.93	4.12	-	888.2
AHQ-10-7, 4622 - 4698	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	8.90E-08	0.92	4.41	-	781.2
AHQ-10-9, 4357	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	2.43E-06	0.86	3.16	-	790.5
AHQ-10-11, 4482	R.VENQENVSNLVIEDTELK.Q	2074.23206	2	6.38E-05	0.83	3.47	-	567.3
AHQ-10-7, 4536 - 4540	R.VENQENVSNLVIEDTELK.Q	2074.23206	3	2.49E-06	0.89	4.56	-	831.1
gi|21618359|ref|NP_004095.3| fatty acid synthase [Homo sapiens]				1.99E-08	1.83	20.24	1.70	273262.0
AHQ-10-3, 5531	R.LFDHPESPTPNPTEPLFLAQAEVYK.E	2842.15075	3	8.14E-04	0.86	4.10	-	779.5
AHQ-10-1, 6317	K.LPEDPLLSGLLDSPALK.A	1779.06739	2	1.99E-08	0.97	4.88	-	1774.8
gi|21361755|ref|NP_004090.3| stomatin; erythrocyte membrane protein band 7.2 (stomatin) [Homo sapie				2.08E-08	4.46	50.26	14.90	31708.5
AHQ-10-1, 4214	K.EASM*VITESPAALQLR.Y	1732.98059	2	4.98E-07	0.91	3.94	-	829.5
AHQ-10-10, 4351	K.EASMVITESPAALQLR.Y	1716.98119	2	5.19E-06	0.91	3.18	-	1224.8
AHQ-10-10, 2446	R.LLAQTTLR.N	916.10035	2	8.47E-04	0.80	2.66	-	555.1
AHQ-10-1, 4061	R.VQNATLAVANITNADSATR.L	1931.09731	2	5.72E-05	0.78	3.27	-	508.7
AHQ-10-1, 4438	R.VQNATLAVANITNADSATR.L	1931.09731	2	5.06E-07	0.83	3.56	-	599.4
AHQ-10-2, 3896	R.VQNATLAVANITNADSATR.L	1931.09731	2	5.79E-06	0.94	4.75	-	726.3
AHQ-10-1, 3973	R.VQNATLAVANITNADSATR.L	1931.09731	2	3.61E-06	0.96	4.48	-	1448.5
AHQ-10-1, 3843	R.VQNATLAVANITNADSATR.L	1931.09731	2	7.58E-06	0.95	5.22	-	1029.0
AHQ-10-10, 3568	R.VQNATLAVANITNADSATR.L	1931.09731	2	4.07E-05	0.63	2.56	-	478.0
AHQ-10-10, 3679	R.VQNATLAVANITNADSATR.L	1931.09731	2	2.08E-08	0.90	3.64	-	897.5
AHQ-10-10, 4150	R.VQNATLAVANITNADSATR.L	1931.09731	2	9.48E-05	0.81	2.76	-	797.3
AHQ-10-13-, 3821	R.YLQTLTTIAAEK.N	1352.55813	2	2.30E-04	0.95	3.81	-	1478.2
AHQ-10-1, 3978	R.YLQTLTTIAAEK.N	1352.55813	2	5.08E-04	0.90	3.70	-	964.6
gi|5031573|ref|NP_005712.1| ARP3 actin-related protein 3 homolog; ARP3 (actin-related protein 3, ye				2.09E-08	7.49	90.31	36.60	47370.9
AHQ-10-8, 4818	R.AEPEDHYFLLTEPPLNTPENR.E	2483.67423	2	1.26E-06	0.89	3.51	-	749.8
AHQ-10-8, 6457	R.DITYFIQQLLR.D	1410.64250	2	6.39E-06	0.92	3.16	-	1238.5
AHQ-10-8, 3122	R.DREVGIPPEQSLETAK.A	1769.93431	2	6.38E-04	0.92	3.62	-	817.8

AHQ-10-8, 3450	K.DYEEIGPSICR.H	1340.44122	2	1.86E-06	0.89	3.26	-	976.4
AHQ-10-8, 5498	K.GVDDLDFFIGDEAIEKPTYATK.W	2445.66268	2	2.09E-08	0.71	3.15	-	492.2
AHQ-10-8, 5789	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	8.71E-05	0.58	3.21	-	371.1
AHQ-10-7, 5841	K.LGYAGNTEPQFIIPSCIAIK.E	2194.53570	2	9.13E-05	0.40	2.76	-	425.1
AHQ-10-8, 3910	K.NIVLSGGSTMFR.D	1282.49463	2	4.31E-05	0.83	3.18	-	970.0
AHQ-10-8, 6021 - 6033	R.TLTGTVIDSGDGVTHVIPVAEGYVIGSCIK.H	3061.45302	3	3.81E-04	0.96	6.20	-	1362.2
AHQ-10-8, 3653 - 3698	R.YSYVCPDLVK.E	1245.42618	2	4.29E-04	0.78	2.67	-	883.9
gi|17986001|ref|NP_005505.2| major histocompatibility complex, class I, B; HLA class I histocompati				2.16E-08	1.71	20.19	9.40	40459.8
AHQ-10-8, 2687 - 2765	R.DGEDQTQDTELVETRPAGDR.T	2233.24975	3	1.53E-06	0.78	3.70	-	781.1
AHQ-10-8, 4749	R.FISVGYVDDTQFVR.F	1646.82447	2	2.16E-08	0.94	3.65	-	1394.8
gi|21735621|ref|NP_005909.2| mitochondrial malate dehydrogenase precursor [Homo sapiens]				2.41E-08	3.07	40.19	22.50	35503.0
AHQ-10-9, 5461 - 5531	K.GYLGPEQLPDCLKGCDVVVIPAGVPR.K	2813.24211	3	7.16E-05	0.44	3.00	-	366.7
AHQ-10-9, 4845	K.IFGVTTLDIVR.A	1234.46961	2	3.65E-07	0.88	3.04	-	1050.6
AHQ-10-9, 5183	R.LTLYDIAHTPGVAADLSHIETK.A	2366.65506	3	1.55E-06	0.88	3.71	-	1301.5
AHQ-10-9, 5027 - 5036	K.SQETECTYFSTPLLLGK.K	1976.19328	2	2.41E-08	0.88	3.69	-	765.9
gi|4504351|ref|NP_000510.1| delta globin [Homo sapiens]				2.44E-08	0.94	10.23	8.80	16055.4
AHQ-10-13-, 3186	K.VNVDAVGGEALGR.L	1257.37853	2	2.44E-08	0.94	4.52	-	1063.5
gi|28827809|ref|NP_789797.1| nucleoside diphosphate kinase B-like [Homo sapiens]				2.44E-08	0.74	10.15	12.40	15529.0
AHQ-10-12, 2824 - 2829	R.VM*LGETNPADSKPGTIR.G	1803.03091	3	2.44E-08	0.74	3.04	-	752.2
AHQ-10-12, 2812	R.VM*LGETNPADSKPGTIR.G	1803.03091	2	9.10E-04	0.37	2.67	-	348.8
gi|5901922|ref|NP_008996.1| CDC37 homolog [Homo sapiens]				2.55E-08	0.88	10.17	5.60	44468.0
AHQ-10-8, 6162	R.LGPGGLDPVEVYESLPEELQK.C	2270.52091	2	2.55E-08	0.88	3.38	-	554.8
gi|6598323|ref|NP_001485.2| GDP dissociation inhibitor 2; rab GDP-dissociation inhibitor, beta [Hom				2.66E-08	2.83	30.28	11.90	50662.9
AHQ-10-8, 5101	R.NPYYGGESASITPLEDLYK.R	2118.28499	2	4.70E-04	0.94	4.30	-	1283.4
AHQ-10-8, 6265	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	1.69E-06	0.97	4.96	-	1330.9
AHQ-10-7, 6224 - 6225	K.SPYLYPLYGLGELPQGFAR.L	2142.44089	2	5.08E-07	0.97	5.69	-	1220.6
AHQ-10-8, 3946 - 3947	R.TDDYLDQPCYETINR.I	1904.98887	2	2.66E-08	0.91	4.16	-	560.9
gi|4757812|ref|NP_004880.1| ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, iso				2.74E-08	1.63	20.23	25.50	10917.8
AHQ-10-13-, 5608 - 5616	R.DFSPSGIFGAFQR.G	1429.56124	2	7.57E-07	0.96	4.64	-	1131.8
AHQ-10-14-, 5612	R.DFSPSGIFGAFQR.G	1429.56124	2	2.74E-08	0.81	3.24	-	494.2
AHQ-10-13, 5900	R.DFSPSGIFGAFQR.G	1429.56124	2	8.01E-04	0.75	2.64	-	646.1
AHQ-10-14-, 5268	K.LGELPSWILM*R.D	1331.60876	2	6.45E-05	0.82	3.25	-	477.0
gi|4503531|ref|NP_001958.1| eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens] [				2.79E-08	1.80	20.19	7.40	46393.9
AHQ-10-8, 3639	R.GIYAYGFEKPSAIQQR.A	1829.04828	2	2.79E-08	0.91	3.72	-	751.7
AHQ-10-8, 2842	K.GYDVIAQAQSGTGK.T	1395.49996	2	6.84E-04	0.89	3.13	-	1244.4
gi|4507677|ref|NP_003290.1| tumor rejection antigen (gp96) 1; Tumor rejection antigen-1 (gp96); glu				3.20E-08	5.30	60.27	11.70	92468.2
AHQ-10-5, 3243	K.FAFQAEVNR.M	1082.19378	2	5.15E-04	0.91	3.15	-	1161.0
AHQ-10-4, 3264	K.FAFQAEVNR.M	1082.19378	2	2.04E-04	0.91	3.25	-	1074.8
AHQ-10-4, 3968	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	2.76E-06	0.97	5.49	-	1983.3
AHQ-10-5, 3940	R.FQSSHHPTDITSLDQYVER.M	2261.39276	3	1.09E-07	0.97	5.43	-	1723.6
AHQ-10-4, 3936	K.GVVDSDDLPLNVSR.E	1486.60940	2	6.91E-06	0.94	4.30	-	1036.1
AHQ-10-6, 3857	K.GVVDSDDLPLNVSR.E	1486.60940	2	6.59E-06	0.93	4.60	-	910.8
AHQ-10-5, 6267	K.GYEVIYLTEPVDEYCIQALPEFDGKR.F	3107.43557	3	5.47E-04	0.67	3.11	-	546.0
AHQ-10-5, 4065	K.SILFVPTSAPR.G	1188.40094	2	2.69E-04	0.87	3.46	-	844.7
AHQ-10-5, 6311 - 6316	K.YSQFINFPIYVWSSK.T	1880.13366	2	3.20E-08	0.95	4.71	-	941.5
AHQ-10-4, 6313	K.YSQFINFPIYVWSSK.T	1880.13366	2	1.56E-05	0.96	4.96	-	1123.0
gi|4504073|ref|NP_000398.1| glycoprotein Ib beta polypeptide precursor [Homo sapiens]				3.20E-08	2.44	30.18	15.50	21717.6
AHQ-10-1, 4733	R.LLPYLAEDELR.A	1332.52691	2	4.12E-06	0.82	3.18	-	443.1
AHQ-10-2, 4660	R.LLPYLAEDELR.A	1332.52691	2	1.06E-06	0.72	2.96	-	311.1
AHQ-10-3, 4590	R.LLPYLAEDELR.A	1332.52691	2	8.91E-06	0.84	3.09	-	677.8
AHQ-10-4, 4637	R.LLPYLAEDELR.A	1332.52691	2	7.60E-05	0.73	2.59	-	357.0
AHQ-10-8, 4506 - 4515	R.LLPYLAEDELR.A	1332.52691	2	1.28E-05	0.70	2.52	-	506.3
AHQ-10-13-, 4542 - 4549	R.LLPYLAEDELR.A	1332.52691	2	3.20E-08	0.82	2.91	-	452.4
AHQ-10-10, 4374 - 4390	R.LLPYLAEDELR.A	1332.52691	2	1.89E-06	0.90	3.48	-	597.5
AHQ-10-11, 4430 - 4455	R.LLPYLAEDELR.A	1332.52691	2	1.78E-06	0.87	2.80	-	631.9
AHQ-10-10, 4082 - 4084	R.LSLTDPLVAER.A	1214.39356	2	8.33E-05	0.81	2.83	-	884.6
AHQ-10-11, 4130	R.LSLTDPLVAER.A	1214.39356	2	4.79E-04	0.93	3.57	-	1183.6
AHQ-10-11, 2492 - 2494	R.TAHLGANPWR.C	1123.24913	2	1.25E-05	0.81	3.08	-	542.3
gi|4506365|ref|NP_002856.1| RAB2, member RAS oncogene family [Homo sapiens]				3.40E-08	1.89	20.23	13.70	23545.4
AHQ-10-11, 4048 - 4103	K.IQEGVFDINNEANGIK.I	1761.91387	2	2.48E-06	0.92	3.89	-	920.7
AHQ-10-11, 4250 - 4259	K.LQIWDTAGQESFR.S	1551.68478	2	3.40E-08	0.97	4.50	-	1740.3
gi|17986260|ref|NP_524147.1| smooth muscle and non-muscle myosin alkali light chain isoform 2 [Homo				3.51E-08	0.97	10.27	23.30	12969.7
AHQ-10-14-, 5270	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	3.51E-08	0.97	5.40	-	1773.8
AHQ-10-12, 5220 - 5277	K.M*TEEEVEM*LVAGHEDSNGCINYEELVR.M	3188.42436	3	1.56E-05	0.95	5.40	-	1301.8
gi|4505763|ref|NP_000282.1| phosphoglycerate kinase 1 [Homo sapiens]				3.54E-08	4.52	50.27	18.70	44614.4
AHQ-10-8, 5522	K.ACANPAAGSVILLENLR.F	1771.03187	2	2.69E-06	0.92	4.09	-	877.2
AHQ-10-8, 5310	K.ALESPERPFLAILGGAK.V	1770.06542	2	1.30E-07	0.97	5.40	-	1523.8
AHQ-10-8, 4533	K.DVLFLKDCVGPEVEK.A	1750.00620	2	3.54E-08	0.94	4.18	-	1061.6
AHQ-10-8, 5189 - 5197	K.ITLPVDFVTADKFDENAK.T	2024.25948	2	1.04E-05	0.84	4.01	-	494.2
AHQ-10-8, 4157	K.YSLEPVAVELK.S	1248.44991	2	8.57E-05	0.86	3.26	-	776.6
gi|19913424|ref|NP_001681.2| ATPase, H+ transporting, lysosomal 70kD, V1 subunit A, isoform 1; V-AT				3.54E-08	0.78	10.17	2.80	68303.7
AHQ-10-6, 4115	R.LAEMPADSGYPAYLGAR.L	1782.99819	2	3.54E-08	0.78	3.32	-	591.0
gi|4507649|ref|NP_003280.1| tropomyosin 2 (beta) [Homo sapiens]				3.56E-08	0.90	10.16	4.60	32989.6
AHQ-10-9, 2661	K.ATDAEADVASLNR.R	1333.38703	2	3.56E-08	0.90	3.28	-	1188.6
gi|24430192|ref|NP_005548.2| keratin 16; keratin, type I cytoskeletal 16; cytokeratin 16 [Homo sapi				3.56E-08	2.57	30.32	11.40	51267.5
AHQ-10-5, 2645	R.APSTYGGGLSVSSR.F	1339.43640	2	3.56E-08	0.87	3.33	-	717.9
AHQ-10-5, 3505	R.GQTGGDVNVEM*DAAPGVDLSR.I	2105.22972	2	5.30E-04	0.72	3.99	-	496.8
AHQ-10-5, 5012	K.IIAATIENAQPILQIDNAR.L	2065.35950	3	8.54E-05	0.98	6.35	-	1802.6
gi|5031677|ref|NP_005681.1| dynamin 1-like protein isoform 3; dynamin-like protein [Homo sapiens] [				3.93E-08	3.69	40.21	7.60	78060.6
AHQ-10-13, 4979	K.ALQGASQIIAEIR.E	1370.57991	2	5.42E-04	0.63	2.74	-	753.4
AHQ-10-13-, 4625	K.ALQGASQIIAEIR.E	1370.57991	2	3.93E-08	0.94	3.84	-	1666.6
AHQ-10-5, 4665	K.ALQGASQIIAEIR.E	1370.57991	2	2.61E-06	0.96	3.47	-	2500.6
AHQ-10-6, 5821	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	2.85E-04	0.88	3.94	-	735.8
AHQ-10-5, 6340	K.IFSPNVVNLTLVDLPGMTK.V	2059.45828	2	1.70E-07	0.91	3.54	-	1028.6
AHQ-10-5, 5956	K.IFSPNVVNLTLVDLPGM*TK.V	2075.45768	2	6.88E-05	0.91	3.87	-	925.7
AHQ-10-6, 6311	R.TLESVDPLGGLNTIDILTAIR.N	2212.52928	2	5.73E-04	0.93	4.28	-	903.1
gi|4759300|ref|NP_004772.1| vesicle-associated membrane protein 3 (cellubrevin); vesicle-associated				4.26E-08	1.90	20.24	33.00	11309.0
AHQ-10-13-, 3569	R.ADALQAGASQFETSAAK.L	1666.77095	2	2.67E-05	0.95	4.75	-	987.4
AHQ-10-13-, 3689	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	4.26E-08	0.95	4.09	-	1268.4
AHQ-10-13, 4061	R.LQQTQNQVDEVVDIM*R.V	1933.13344	2	1.98E-04	0.55	2.76	-	413.4
gi|30147623|ref|XP_293669.2| similar to actinin, alpha 4 [Homo sapiens]				4.28E-08	0.91	10.20	3.50	57794.4
AHQ-10-4, 3987	K.LSGSNPYTTVTPQIINSK.W	1921.14079	2	4.28E-08	0.91	3.97	-	1009.3
gi|7657056|ref|NP_055415.1| EH-domain containing 3; EH domain containing 3 [Homo sapiens]				4.43E-08	4.69	50.34	17.60	60886.7
AHQ-10-7, 2889	K.ADQIETQQLMR.V	1333.49681	2	1.55E-04	0.87	3.45	-	1290.1
AHQ-10-7, 6397	R.FVCAQLPNPVLESISVIDTPGILSGEK.Q	2886.30971	2	4.22E-07	0.97	5.51	-	1367.6
AHQ-10-7, 5280	K.GGAFEGTLHGPFGHGYGEGAGEGIDDAEWVVAR.D	3317.48513	3	3.62E-04	0.98	6.87	-	2709.3
AHQ-10-7, 5116	K.LDISDEFSEVIK.A	1395.53664	2	4.43E-08	0.90	3.56	-	998.5
AHQ-10-7, 4624	K.LFEAEEQDLFR.D	1397.51432	2	2.51E-06	0.97	4.34	-	1930.6
gi|5031839|ref|NP_005545.1| keratin 6A; Keratin-6A; keratin, epidermal type II, K6A; cytokeratin 6A				4.79E-08	0.85	10.16	2.10	60044.6
AHQ-10-5, 5125 - 5137	K.ADTLTDEINFLR.A	1408.53864	2	4.79E-08	0.85	3.28	-	932.8
AHQ-10-3, 5086 - 5095	K.ADTLTDEINFLR.A	1408.53864	2	5.17E-06	0.84	3.15	-	1081.4
gi|19923457|ref|NP_057447.2| glycoprotein VI (platelet); platelet glycoprotein VI [Homo sapiens] [M				4.85E-08	1.79	20.23	7.10	67308.6
AHQ-10-7, 5313	K.PSLQALPSSLVPLEKPVTLR.C	2146.55880	3	3.93E-07	0.93	4.54	-	1097.7
AHQ-10-7, 3621	K.PSLSAQPGPAVSSGGDVTLQCQTR.Y	2415.62303	2	4.85E-08	0.87	3.50	-	572.1
gi|18570595|ref|XP_095590.1| similar to myosin regulatory light chain [Homo sapiens]				5.29E-08	0.93	10.20	8.90	13951.5
AHQ-10-12, 3188 - 3189	K.LNGTDPEDVIR.H	1229.32195	2	1.12E-05	0.93	3.96	-	1014.3
AHQ-10-13-, 3086 - 3157	K.LNGTDPEDVIR.H	1229.32195	2	1.88E-04	0.79	3.03	-	815.7

AHQ-10-11, 3038 - 3098	K.LNGTDPEDVIR.H	1229.32195	2	5.29E-08	0.93	3.84	-	1085.6
gi|4507953|ref|NP_003397.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, zeta polypep			5.36E-08	4.45	50.28	27.30	27744.9
AHQ-10-10, 3192 - 3246	K.FLIPNASQAESK.V	1305.46156	2	1.31E-05	0.81	3.09	-	538.3
AHQ-10-10, 2359 - 2427	K.SVTEQGAELSNEER.N	1549.57922	2	1.63E-05	0.83	2.82	-	1095.1
AHQ-10-14-, 2349 - 2404	K.SVTEQGAELSNEER.N	1549.57922	2	4.52E-04	0.80	2.88	-	966.7
AHQ-10-13-, 2404	K.SVTEQGAELSNEER.N	1549.57922	2	5.36E-08	0.88	3.68	-	1040.9
AHQ-10-11, 2376 - 2443	K.SVTEQGAELSNEER.N	1549.57922	2	1.57E-04	0.90	3.31	-	1256.2
AHQ-10-14-, 6280	K.TAFDEAIAELDTLSEESYK.D	2133.25160	2	6.23E-06	0.97	5.51	-	1450.8
AHQ-10-10, 6254 - 6322	K.TAFDEAIAELDTLSEESYKDSTLIM*QLLR.D	3320.66704	3	1.06E-05	0.82	3.53	-	958.0
AHQ-10-10, 2083 - 2138	R.YLAEVAAGDDKK.G	1280.40887	2	1.11E-06	0.96	4.01	-	1721.2
AHQ-10-10, 2119 - 2124	R.YLAEVAAGDDKK.G	1280.40887	3	1.37E-04	0.92	3.44	-	1389.2
gi|4507725|ref|NP_000362.1|	transthyretin (prealbumin, amyloidosis type I); Transthyretin (prealbum			5.43E-08	3.50	40.29	33.30	15886.9
AHQ-10-13-, 3782	K.AADDTWEPFASGK.T	1395.45529	2	1.37E-04	0.88	2.71	-	1039.3
AHQ-10-13, 4189	K.AADDTWEPFASGK.T	1395.45529	2	3.62E-06	0.71	2.82	-	635.7
AHQ-10-13-, 3941 - 4021	R.GSPAINVAVHVFR.K	1367.58095	2	3.30E-04	0.95	4.27	-	1133.5
AHQ-10-13-, 3364	R.KAADDTWEPFASGK.T	1523.62820	2	6.26E-05	0.94	3.62	-	1379.5
AHQ-10-13-, 5268	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	2	5.43E-08	0.89	3.86	-	908.1
AHQ-10-13-, 5266	K.TSESGELHGLTTEEEFVEGIYK.V	2456.60073	3	9.43E-07	0.97	5.77	-	1880.1
gi|13518026|ref|NP_004978.2|	LIM and senescent cell antigen-like domains 1 [Homo sapiens]			5.44E-08	2.78	30.22	11.10	37251.2
AHQ-10-8, 4366	K.CHAIIDEQPLIFK.N	1585.84900	2	7.83E-04	0.89	3.57	-	948.7
AHQ-10-9, 4199	K.CHAIIDEQPLIFK.N	1585.84900	2	6.47E-06	0.94	4.03	-	1293.9
AHQ-10-9, 4204 - 4205	K.CHAIIDEQPLIFK.N	1585.84900	3	3.70E-04	0.79	4.02	-	757.0
AHQ-10-9, 3583 - 3585	K.FVEFDMKPVCK.K	1401.67594	2	6.06E-04	0.88	3.49	-	1266.4
AHQ-10-9, 3324 - 3347	R.VIEGDVVSALNK.A	1244.41966	2	1.78E-06	0.95	4.38	-	1171.3
AHQ-10-11, 3396 - 3466	R.VIEGDVVSALNK.A	1244.41966	2	5.44E-08	0.96	4.11	-	1587.7
AHQ-10-13, 3947	R.VIEGDVVSALNK.A	1244.41966	2	3.56E-07	0.93	3.44	-	1116.7
AHQ-10-8, 3467 - 3490	R.VIEGDVVSALNK.A	1244.41966	2	6.69E-07	0.89	3.49	-	854.2
gi|24797067|ref|NP_002107.3|	major histocompatibility complex, class I, A precursor; HLA-A1 class I			5.59E-08	5.52	60.23	22.70	40840.5
AHQ-10-8, 4810	R.APWIEQEGPEYWDQETR.N	2135.23420	2	7.05E-06	0.92	4.05	-	698.7
AHQ-10-8, 2685	R.DGEDQTQDTELVETR.P	1736.73008	2	2.32E-04	0.94	3.61	-	2124.8
AHQ-10-8, 3391	R.DGEDQTQDTELVETRPAGDGTFQK.W	2638.69666	3	4.90E-05	0.85	3.84	-	801.3
AHQ-10-14-, 4760	R.FIAVGYVDDTQFVR.F	1630.82504	2	2.32E-07	0.96	4.09	-	1607.9
AHQ-10-8, 4770	R.FIAVGYVDDTQFVR.F	1630.82504	2	2.28E-07	0.97	4.54	-	1869.6
AHQ-10-1, 4946	R.FIAVGYVDDTQFVR.F	1630.82504	2	9.94E-05	0.95	3.89	-	1506.9
AHQ-10-8, 2273	R.YLENGKETLQR.T	1351.49032	2	2.94E-06	0.90	3.34	-	1063.0
AHQ-10-8, 3327	R.YTCHVQHEGLPKPLTLR.W	2051.35781	2	5.59E-08	0.95	4.53	-	1442.3
gi|4507383|ref|NP_001052.1|	thromboxane A synthase 1 (platelet, cytochrome P450, family 5, subfamil			5.74E-08	1.89	20.20	5.80	60675.3
AHQ-10-7, 4162	R.FQACPETQVPLQLESK.S	1877.10807	2	1.72E-06	0.95	4.08	-	1109.7
AHQ-10-7, 3978	R.HSASPMGVQDFDIVR.D	1659.84828	2	5.74E-08	0.94	3.97	-	1086.9
gi|13489087|ref|NP_109591.1|	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member			5.85E-08	0.88	10.21	5.00	42741.5
AHQ-10-8, 3969	K.TYGADLASVDFQHASEDAR.K	2054.11949	3	3.93E-07	0.91	4.21	-	716.1
AHQ-10-8, 3922 - 3979	K.TYGADLASVDFQHASEDAR.K	2054.11949	2	5.85E-08	0.88	3.96	-	759.5
gi|30150022|ref|XP_300862.1|	similar to beta-tubulin 4Q [Homo sapiens]			6.25E-08	2.77	30.22	18.50	33545.2
AHQ-10-7, 5716	K.EAESCDCLQGFQLTHSLGGGTGSGMGTLLISK.I	3315.65550	3	1.11E-06	0.91	4.43	-	1242.4
AHQ-10-8, 4350	K.LAVNMVPFPR.L	1144.41480	2	3.95E-05	0.89	3.65	-	679.7
AHQ-10-9, 4171	K.LAVNMVPFPR.L	1144.41480	2	6.25E-08	0.95	4.03	-	895.9
AHQ-10-11, 4322	K.LAVNMVPFPR.L	1144.41480	2	2.15E-04	0.77	2.89	-	580.6
AHQ-10-7, 4324 - 4325	K.LAVNMVPFPR.L	1144.41480	2	1.82E-05	0.87	3.66	-	516.5
AHQ-10-11, 4771	R.LHFFM*PGFAPLTSR.G	1637.92902	3	3.66E-04	0.83	3.25	-	1107.4
AHQ-10-11, 4759	R.LHFFM*PGFAPLTSR.G	1637.92902	2	6.05E-05	0.91	3.21	-	916.7
gi|4758304|ref|NP_004902.1|	protein disulfide isomerase related protein (calcium-binding protein, i			6.36E-08	4.40	50.23	10.10	72931.9
AHQ-10-6, 3715	K.FAM*EPEEFDSDTLR.E	1703.80830	2	9.11E-07	0.73	2.84	-	537.7
AHQ-10-6, 3628	R.FDVSGYPTIK.I	1127.27123	2	8.96E-04	0.94	3.47	-	1251.7
AHQ-10-6, 3811	K.GESDPAYQQYQDAANNLR.E	2041.08081	2	2.05E-05	0.85	3.70	-	729.7
AHQ-10-6, 2911	K.IDATSASVLASR.F	1191.31686	2	6.36E-08	0.96	3.85	-	1833.3
AHQ-10-6, 3409	K.RFDVSGYPTLK.I	1283.45758	2	4.64E-05	0.93	3.54	-	1348.8
gi|12025678|ref|NP_004915.2|	actinin, alpha 4 [Homo sapiens]			6.75E-08	7.60	100.26	17.50	104853.3
AHQ-10-4, 4512	K.AGTQIENIDEDFRDGLK.L	1922.04251	2	6.75E-08	0.63	2.79	-	618.2
AHQ-10-4, 3551	R.DYETATLSDIK.A	1256.34094	2	1.00E-04	0.95	3.61	-	1674.1
AHQ-10-4, 4559	R.ETTDTDTADQVIASFK.V	1742.81936	2	8.59E-07	0.95	4.15	-	1323.9
AHQ-10-4, 3015 - 3083	K.GISQEQMQEFR.A	1353.48658	2	1.86E-06	0.47	2.80	-	458.7
AHQ-10-4, 4683 - 4755	K.ICDQWDALGSLTHSR.R	1760.90926	2	7.99E-06	0.93	3.92	-	1184.7
AHQ-10-4, 4813	R.ISIEM*NGTLEDQLSHLK.Q	1945.18413	3	2.13E-04	0.62	3.14	-	581.2
AHQ-10-4, 3775	K.M*LDAEDIVNTARPDEK.A	1833.99864	2	4.36E-04	0.85	3.41	-	628.5
AHQ-10-4, 4536 - 4541	R.QFASQANVVGPWIQTK.M	1775.00061	2	1.16E-04	0.53	2.97	-	318.1
AHQ-10-6, 5929	R.VEQIAAIAQELNELDYYDSHNVNTR.C	2907.09810	3	2.72E-05	0.96	5.13	-	1317.4
AHQ-10-4, 3923	K.VLAGDKNFITAEELR.R	1676.89525	2	1.84E-04	0.70	3.49	-	607.9
gi|8923579|ref|NP_060377.1|	hypothetical protein FLJ20625 [Homo sapiens]			6.84E-08	0.79	10.17	18.60	17744.7
AHQ-10-14-, 5944	K.LPPLPSLTSQPHQVLASEPIPFSDLQQVSR.I	3283.72259	3	6.84E-08	0.79	3.31	-	627.0
gi|13899317|ref|NP_113657.1|	SH3 domain binding glutamic acid-rich protein like 2 [Homo sapiens] [M			6.92E-08	1.58	20.25	25.20	12326.0
AHQ-10-14-, 5262	K.ESNTVFSFLGLKPR.L	1595.82383	2	6.92E-08	0.60	3.00	-	358.6
AHQ-10-13-, 5270	K.ESNTVFSFLGLKPR.L	1595.82383	2	3.06E-05	0.63	2.58	-	477.8
AHQ-10-13, 5575	K.ESNTVFSFLGLKPR.L	1595.82383	2	4.47E-04	0.36	2.62	-	300.9
AHQ-10-14-, 4300	R.VFIASSSGFVAIK.K	1326.56551	2	3.47E-05	0.98	4.97	-	3082.7
AHQ-10-13-, 4301	R.VFIASSSGFVAIK.K	1326.56551	2	1.36E-05	0.98	4.59	-	3457.4
gi|22042381|ref|XP_065237.3|	similar to FKSG30 [Homo sapiens]			7.43E-08	1.21	20.17	8.30	42016.0
AHQ-10-8, 2866 - 2929	K.QEYDESGPSIVHR.K	1517.58206	2	2.70E-05	0.55	3.07	-	533.4
AHQ-10-14-, 2484	K.QEYDESGPSIVHR.K	1517.58206	2	7.43E-08	0.65	2.74	-	302.6
AHQ-10-8, 2421 - 2483	K.QEYDESGPSIVHR.K	1517.58206	2	2.22E-07	0.70	3.14	-	354.2
AHQ-10-8, 3706 - 3755	R.VAPEEHPILLTEAPLNPK.A	1969.27019	2	9.75E-04	0.56	2.85	-	339.0
gi|4502905|ref|NP_001822.1|	clusterin; complement-associated protein SP-40 [Homo sapiens]			7.54E-08	1.77	20.19	6.00	52494.3
AHQ-10-9, 2863	R.EILSVDCSTNNPSQAK.L	1764.89299	2	7.54E-08	0.90	3.88	-	749.2
AHQ-10-9, 2860 - 2869	R.ELDESLQVAER.L	1289.37416	2	5.86E-04	0.86	3.06	-	1071.8
gi|27482573|ref|XP_208709.1|	similar to Ubiquitin-conjugating enzyme E2-18 kDa UbcH7 (Ubiquitin-pro			7.98E-08	0.94	10.22	14.30	17875.4
AHQ-10-12, 6144	K.TDQVIQSLIALVNDPQPEHPLR.A	2484.79318	3	7.98E-08	0.94	4.43	-	1077.5
gi|6005846|ref|NP_009215.1|	PTK9L protein tyrosine kinase 9-like (A6-related protein); protein tyro			8.32E-08	2.79	30.22	15.80	39547.7
AHQ-10-14-, 6110	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	1.04E-04	0.86	2.95	-	878.4
AHQ-10-12, 6040	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	8.32E-08	0.91	3.97	-	778.2
AHQ-10-13-, 6082	R.AVLPLLDAQQPCYLLYR.L	2035.39506	2	1.62E-06	0.84	3.28	-	821.0
AHQ-10-11, 4030	R.ETIELVHTEPTDVAQLPSR.V	2136.34822	2	1.07E-05	0.92	4.18	-	768.8
AHQ-10-12, 4500	K.VVIEDEQLVLGASQEPVGR.W	2039.27568	2	3.03E-04	0.97	4.32	-	1980.2
gi|4504517|ref|NP_001531.1|	heat shock 27kDa protein 1; heat shock 27kD protein 1 [Homo sapiens] [M			8.89E-08	2.75	30.27	21.00	22782.3
AHQ-10-11, 4516 - 4594	K.LATQSNEITIPVTFESR.A	1907.11412	2	9.06E-06	0.81	3.62	-	349.1
AHQ-10-14-, 4606 - 4678	K.LATQSNEITIPVTFESR.A	1907.11412	2	5.62E-05	0.51	2.98	-	234.9
AHQ-10-10, 4366	R.LFDQAFGLPR.L	1164.33793	2	1.23E-06	0.96	3.43	-	1806.7
AHQ-10-14-, 4526	R.LFDQAFGLPR.L	1164.33793	2	5.15E-05	0.92	3.25	-	1273.9
AHQ-10-11, 4422	R.LFDQAFGLPR.L	1164.33793	2	4.40E-07	0.96	4.39	-	1554.0
AHQ-10-13-, 4680	R.VSLDVNHFAPDELTVK.T	1784.99058	2	2.83E-06	0.92	4.21	-	959.8
AHQ-10-13-, 4462 - 4526	R.VSLDVNHFAPDELTVK.T	1784.99058	2	8.89E-08	0.97	5.42	-	1570.8
AHQ-10-10, 4524	R.VSLDVNHFAPDELTVK.T	1784.99058	2	2.81E-06	0.91	3.04	-	1271.3
AHQ-10-11, 4428	R.VSLDVNHFAPDELTVK.T	1784.99058	2	1.08E-05	0.90	3.67	-	1033.3
gi|4885063|ref|NP_005156.1|	aldolase C, fructose-bisphosphate; Aldolase C, fructose-bisphosphatase			8.95E-08	0.95	10.25	6.30	39455.6
AHQ-10-9, 3904	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	7.23E-05	0.45	2.92	-	564.4
AHQ-10-8, 4399 - 4534	K.GVVPLAGTDGETTTQGLDGLSER.C	2274.42806	2	8.95E-08	0.95	5.10	-	591.5
gi|5453605|ref|NP_006421.1|	chaperonin containing TCP1, subunit 4 (delta); chaperonin containing t-			9.07E-08	0.93	10.18	2.40	57838.8
AHQ-10-7, 3521	K.VIDPATATSVDLR.D	1358.52277	2	9.07E-08	0.93	3.57	-	1130.5
gi|4507907|ref|NP_000543.1|	von Willebrand factor precursor; Coagulation factor VIII VWF (von Wille			9.08E-08	14.74	180.32	8.80	309296.7

AHQ-10-1, 4141	R.CLPTACTIQLR.G	1335.57568	2	2.22E-06	0.50	2.56	-	393.5
AHQ-10-3, 4779	R.EGGPSQIGDALGFAVR.Y	1574.71988	2	1.98E-05	0.67	3.37	-	379.4
AHQ-10-1, 4082	K.EQDLEVILHNGACSPGAR.Q	1968.13770	2	1.96E-07	0.77	3.17	-	698.7
AHQ-10-2, 3238 - 3243	R.HIVTFDGQNFK.L	1306.45124	2	7.01E-06	0.53	3.04	-	277.3
AHQ-10-1, 4029	R.IALLLM*ASQEPQR.M	1486.76229	2	3.58E-04	0.88	2.93	-	1126.2
AHQ-10-1, 6443	R.IGWPNAPILIQDFETLPR.E	2081.40223	2	4.23E-05	0.61	2.69	-	466.6
AHQ-10-1, 2885	R.ILAGPAGDSNVVK.L	1241.41901	2	3.58E-07	0.94	3.74	-	1343.4
AHQ-10-1, 3806	R.ILTSDVFQDCNK.L	1441.58869	2	9.08E-08	0.90	3.25	-	1010.1
AHQ-10-2, 3723	R.ILTSDVFQDCNK.L	1441.58869	2	1.37E-05	0.84	2.80	-	740.0
AHQ-10-1, 6327 - 6399	R.LLDLVFLLDGSSR.L	1448.68905	2	1.26E-06	0.95	4.08	-	1409.5
AHQ-10-1, 4215	R.LSEAEFEVLK.A	1165.31777	2	1.72E-06	0.86	3.50	-	858.3
AHQ-10-4, 3267	K.LSGEAYGFVAR.I	1170.29934	2	3.16E-07	0.97	4.58	-	1986.7
AHQ-10-1, 4165	K.LTGSCSYVLFQNK.E	1518.71629	2	2.88E-06	0.90	3.93	-	750.9
AHQ-10-2, 4091	K.LTGSCSYVLFQNK.E	1518.71629	2	2.96E-04	0.88	3.60	-	698.0
AHQ-10-1, 5225 - 5283	K.RLPGDIQVVPIGVGPNANVQELER.I	2571.91720	3	3.19E-07	0.98	6.35	-	2215.2
AHQ-10-1, 4791	K.SVGSQWASPENPCLINECVR.V	2306.51832	2	2.35E-05	0.82	3.43	-	400.7
AHQ-10-3, 2523	R.VKEEVFIQQR.N	1276.46658	2	3.43E-04	0.73	2.54	-	735.4
AHQ-10-2, 4492	R.VTVFPIGIGDR.Y	1174.37426	2	2.83E-07	0.94	4.06	-	935.3
AHQ-10-1, 4558	R.VTVFPIGIGDR.Y	1174.37426	2	3.09E-04	0.92	3.22	-	1111.8
AHQ-10-2, 3010	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.23E-04	0.93	4.04	-	925.8
AHQ-10-4, 2941	K.YAGSQVASTSEVLK.Y	1440.58064	2	6.73E-05	0.55	2.57	-	443.3
AHQ-10-3, 2947	K.YAGSQVASTSEVLK.Y	1440.58064	2	3.42E-07	0.92	3.47	-	1020.9
AHQ-10-1, 3129	K.YAGSQVASTSEVLK.Y	1440.58064	2	1.71E-07	0.90	3.08	-	1043.1
AHQ-10-2, 5635	K.YTLFQIFSK.I	1147.34728	2	2.62E-04	0.93	2.85	-	1226.4
AHQ-10-1, 5667	K.YTLFQIFSK.I	1147.34728	2	5.35E-05	0.91	2.67	-	1090.8
gi|11321601|ref|NP_002618.1| phosphofructokinase, platelet; Phosphofructokinase, platelet type [Hom				9.32E-08	5.42	60.24	12.60	85595.6
AHQ-10-5, 4765	K.ASYDVSDSGQLEHVQPWSV	2105.20640	2	7.04E-07	0.89	4.24	-	419.6
AHQ-10-5, 3509	R.DLQSNVEHLTEK.M	1413.51529	2	1.93E-05	0.79	3.16	-	577.7
AHQ-10-5, 5595 - 5596	K.EIGWTDVGGWTGQGGSILGTK.R	2120.30735	2	1.59E-05	0.95	4.83	-	902.5
AHQ-10-5, 3895	K.ELVVTQLGYDTR.V	1394.55511	2	1.51E-07	0.94	3.66	-	1220.6
AHQ-10-5, 4584	K.FTTDDSICVLGISK.R	1557.74760	2	4.10E-07	0.92	3.66	-	913.2
AHQ-10-5, 5923	R.GITNLCVIGGDGSLTGANLFR.K	2137.40264	2	9.32E-08	0.93	4.40	-	764.7
gi|4758012|ref|NP_004850.1| clathrin heavy chain; clathrin, heavy polypeptide-like 2 [Homo sapiens]				9.74E-08	5.22	60.23	5.10	191612.6
AHQ-10-3, 4937 - 5014	R.ISGETIFVTAPHEATAGIIGVNR.K	2354.64751	3	1.16E-07	0.92	4.63	-	923.5
AHQ-10-3, 3606	K.IVLDNSVFSEHR.N	1416.56400	2	4.52E-06	0.59	2.63	-	634.0
AHQ-10-3, 5787	R.NLQNLLILTAIK.A	1354.66353	2	6.12E-06	0.96	4.51	-	1632.1
AHQ-10-3, 4642 - 4707	R.TSIDAYDNFDNISLAQR.L	1944.04818	2	9.74E-08	0.86	3.34	-	1073.3
AHQ-10-3, 3257	K.VANVELYYR.A	1127.27446	2	2.80E-05	0.93	3.42	-	1265.9
AHQ-10-3, 3714	R.VVGAMQLYSVDR.K	1338.55819	2	1.85E-04	0.95	4.44	-	1376.3
gi|8922673|ref|NP_060692.1| parvin, alpha; alpha-parvin; actopaxin [Homo sapiens]				1.00E-07	1.73	20.22	5.60	42243.4
AHQ-10-9, 4197 - 4275	R.DAFDTLFDHAPDK.L	1492.57096	2	1.00E-07	0.96	4.38	-	1299.9
AHQ-10-9, 3849 - 3851	R.VLYNLFTK.Y	998.19983	2	2.03E-04	0.77	2.90	-	374.5
gi|7661818|ref|NP_054900.1| HSPC159 protein [Homo sapiens]				1.03E-07	2.22	30.19	32.00	19011.6
AHQ-10-13-, 6200 - 6201	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.89E-05	0.84	3.76	-	322.9
AHQ-10-11, 6134	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	4.76E-05	0.77	3.27	-	365.7
AHQ-10-12, 6150	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	3.63E-06	0.55	3.27	-	255.5
AHQ-10-14-, 6244	R.GEEQSAIPYFPFIPDQPFR.V	2239.47029	2	2.00E-04	0.49	2.53	-	175.9
AHQ-10-11, 4655 - 4710	K.LDDGHLNNSLSSPVQADVYFPR.L	2445.62923	3	1.27E-04	0.84	3.39	-	1346.5
AHQ-10-11, 4646	R.VFVDGHQLFDFYHR.I	1780.96540	3	1.03E-07	0.83	3.53	-	548.5
gi|17986283|ref|NP_006000.2| tubulin, alpha 3; tubulin, alpha, brain-specific; hum-a-tub1; hum-a-tu				1.03E-07	0.94	10.24	3.30	50135.3
AHQ-10-11, 5270 - 5276	R.AVFVDLEPTVIDEVR.T	1702.92947	2	9.22E-05	0.83	3.55	-	711.5
AHQ-10-14, 5931 - 5935	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.21E-07	0.85	3.54	-	645.3
AHQ-10-14-, 5090	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.14E-04	0.92	4.00	-	807.3
AHQ-10-7, 5344 - 5346	R.AVFVDLEPTVIDEVR.T	1702.92947	2	1.03E-07	0.94	4.77	-	972.5
gi|5729887|ref|NP_006624.1| IQ motif containing GTPase activating protein 2 [Homo sapiens]				1.13E-07	0.97	10.25	1.00	180611.0
AHQ-10-5, 4068	K.VDQVQDIVTGNPTVIK.M	1726.95257	2	1.13E-07	0.97	4.93	-	1642.4
gi|7661948|ref|NP_055545.1| KIAA0152 gene product [Homo sapiens]				1.25E-07	0.92	10.19	4.50	32233.6
AHQ-10-9, 3312 - 3313	R.SNPEDQILYQTER.Y	1593.67683	2	1.25E-07	0.92	3.85	-	848.0
gi|27500115|ref|XP_208901.1| similar to ubiquitin-conjugating enzyme E2M; UBC12 homolog, yeast [Hom				1.26E-07	0.69	10.14	8.70	20964.0
AHQ-10-11, 5596	K.TCDISFSDPDDLLNFK.L	1889.02935	2	1.26E-07	0.69	2.84	-	567.3
gi|18104967|ref|NP_000953.2| prostaglandin-endoperoxide synthase 1 isoform 1 precursor; prostagland				1.29E-07	4.37	50.24	15.90	68686.0
AHQ-10-6, 3927	K.AEHPTWGDEQLFQTTR.L	1917.02765	2	6.03E-06	0.93	3.64	-	982.6
AHQ-10-6, 3852	K.ALGHGVDLGHIYGDNLER.Q	1937.10524	3	2.98E-05	0.88	3.93	-	853.1
AHQ-10-6, 6379	K.IVIEEYVQQLSGYFLQLK.F	2171.52045	3	1.17E-04	0.93	3.78	-	1345.6
AHQ-10-6, 3260	R.VPDASQDDGPAVERPSTEL	1984.06747	2	1.29E-07	0.89	3.84	-	666.3
AHQ-10-6, 5077	K.YQVLDGEMYPPSVEEAPVLM*HYPR.G	2838.20739	3	1.86E-04	0.75	3.27	-	895.4
gi|21281689|ref|NP_079209.1| hypothetical protein FLJ12056 [Homo sapiens]				1.29E-07	0.17	10.15	9.10	23261.9
AHQ-10-6, 2821	R.LPGGQGLERAGAEAAAREAR.R	1981.16278	3	1.29E-07	0.17	3.08	-	421.4
gi|19882251|ref|NP_001889.2| cystatin SN precursor; cystatin 1; cystatin SA-I; cysteine proteinase				1.35E-07	1.62	20.17	20.60	16387.6
AHQ-10-13-, 3465 - 3466	R.ALHFAISEYNK.A	1293.45247	2	2.62E-04	0.89	2.71	-	1171.7
AHQ-10-13-, 4924 - 4929	R.IIPGGIYNADLNDEWVQR.A	2074.28181	3	1.04E-04	0.67	3.27	-	944.7
AHQ-10-13-, 4862 - 4920	R.IIPGGIYNADLNDEWVQR.A	2074.28181	2	1.35E-07	0.73	2.95	-	261.5
gi|4758208|ref|NP_004081.1| dual specificity phosphatase 3; vaccinia virus phosphatase VH1-related;				1.35E-07	1.73	20.18	15.10	20478.2
AHQ-10-11, 5139	K.ANDTQEFNLSAYFER.A	1805.88207	2	1.35E-07	0.86	3.61	-	888.8
AHQ-10-11, 3468	K.LGITHVLNAAEGR.S	1351.53669	3	3.58E-04	0.86	3.48	-	1236.5
gi|7661678|ref|NP_056461.1| RAP1B, member of RAS oncogene family; K-REV; RAS-related protein RAP1B				1.53E-07	4.02	50.26	19.00	20824.7
AHQ-10-11, 3904 - 3966	R.QWNNCAFLESSAK.S	1556.68148	2	2.74E-06	0.67	3.07	-	297.9
AHQ-10-11, 4078 - 4120	R.QWNNCAFLESSAK.S	1556.68148	2	3.11E-04	0.74	2.95	-	368.0
AHQ-10-11, 3720 - 3775	R.VKDTDDVPMILVGNK.C	1644.91497	3	6.77E-06	0.92	4.04	-	1522.5
AHQ-10-11, 3706 - 3767	R.VKDTDDVPMILVGNK.C	1644.91497	2	1.53E-07	0.97	4.75	-	2003.8
AHQ-10-13-, 3450	R.VKDTDDVPM*ILVGNK.C	1660.91437	2	2.81E-04	0.94	4.19	-	1159.7
AHQ-10-11, 3378	R.VKDTDDVPM*ILVGNK.C	1660.91437	3	8.30E-04	0.76	3.75	-	870.0
AHQ-10-11, 3311 - 3366	R.VKDTDDVPM*ILVGNK.C	1660.91437	2	7.49E-04	0.95	4.00	-	1407.0
AHQ-10-11, 4234 - 4295	R.VKDTDDVPMILVGNKCDLEDER.V	2563.84420	3	6.46E-05	0.89	3.93	-	1049.2
AHQ-10-11, 3982 - 4056	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	1.16E-05	0.95	5.25	-	1568.6
AHQ-10-11, 3988	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	2	8.91E-06	0.55	2.63	-	335.9
AHQ-10-13-, 4084 - 4093	R.VKDTDDVPM*ILVGNKCDLEDER.V	2579.84360	3	3.56E-04	0.93	4.99	-	1064.1
gi|20357552|ref|NP_005222.2| cortactin isoform a; oncogene EMS1 [Homo sapiens]				1.54E-07	4.88	60.26	16.20	61585.7
AHQ-10-14-, 4688	K.ASAGHAVSIAQDDAGADDWETDPDFVNDVSEK.E	3334.37643	3	1.61E-07	0.93	5.19	-	858.4
AHQ-10-13-, 3952 - 3954	R.LPSSPVYEDAASFK.A	1511.65733	2	7.52E-06	0.87	3.36	-	606.5
AHQ-10-11, 3850 - 3868	R.LPSSPVYEDAASFK.A	1511.65733	2	1.28E-04	0.71	2.70	-	686.1
AHQ-10-14-, 3841	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	1.54E-07	0.96	4.42	-	1442.6
AHQ-10-14, 4599	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	2.88E-04	0.65	3.01	-	427.6
AHQ-10-13, 4220	K.NASTFEDVTQVSSAYQK.T	1875.97061	2	8.19E-04	0.84	3.09	-	761.6
AHQ-10-11, 2435	K.TQTPPVSPAPQPTEER.L	1735.87642	2	4.88E-04	0.50	2.53	-	421.6
AHQ-10-13-, 2978	K.VDKSAVGFEYQGK.T	1428.57155	2	2.23E-06	0.76	3.07	-	627.2
AHQ-10-14-, 2957	R.VDQSAVGFEYQGK.T	1428.52841	2	1.29E-06	0.86	3.61	-	679.0
gi|29731460|ref|XP_293027.1| similar to ADP,ATP carrier protein, fibroblast isoform (ADP/ATP transl				1.69E-07	0.96	10.17	6.10	23572.2
AHQ-10-10, 4314	K.DFLAGGVAAAISK.M	1220.39980	2	1.69E-07	0.96	3.41	-	2228.0
gi|4504515|ref|NP_002146.1| heat shock 70kDa protein 6 (HSP70B'); heat shock 70kD protein 6 (HSP70B				1.86E-07	2.55	30.19	6.10	70853.4
AHQ-10-6, 4784	R.FEELCSDLFR.S	1317.44926	2	8.91E-06	0.70	2.76	-	601.5
AHQ-10-6, 4653	R.IINEPTAAAIAYGLDR.R	1688.90603	2	1.86E-07	0.92	3.89	-	986.0
AHQ-10-6, 4257	K.LLQDFFNGKELNK.S	1566.78249	2	4.33E-05	0.93	3.75	-	1328.0
gi|24497612|ref|NP_116262.2| nm23-phosphorylated unknown substrate; SH3 domain-containing 70 kDa pr				2.24E-07	1.56	20.18	3.90	72695.6
AHQ-10-6, 5981 - 6037	K.LGCDWVATIFSR.D	1426.62208	2	2.24E-07	0.94	3.51	-	1136.1
AHQ-10-6, 3901	K.LVVSESYDTYISR.S	1532.67654	2	1.70E-06	0.62	2.67	-	649.0
gi|30154095|ref|XP_293967.2| similar to gamma actin-like protein [Homo sapiens]				2.29E-07	1.23	20.18	12.20	19259.0

AHQ-10-9, 4328	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.53E-04	0.31	2.61	-	421.9
AHQ-10-13, 4928 - 5007	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	4.45E-05	0.28	2.65	-	388.3
AHQ-10-14, 5449	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.57E-05	0.62	3.20	-	493.9
AHQ-10-13-, 4528	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.07E-04	0.80	3.68	-	650.4
AHQ-10-13-, 4660	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	2.29E-07	0.48	2.98	-	406.0
AHQ-10-14-, 4617 - 4677	K.DLYTSTVLSGGTTM*YPGIADR.M	2235.45690	2	1.23E-06	0.74	3.54	-	503.4
AHQ-10-8, 4957	K.DLYTSTVLSGGTTMYPGIADR.M	2219.45750	2	2.46E-05	0.75	3.37	-	525.0
gi|4507767|ref|NP_003326.1|	ubiquitin-activating enzyme E1-like; Ubiquitin-activating enzyme-2; ubi			2.35E-07	3.50	40.20	7.60	111719.5
AHQ-10-4, 6363	R.GLNPDLQVIPLTYPLDPTTEHIYGDNFFSR.V	3434.79811	3	6.13E-06	0.84	3.84	-	589.2
AHQ-10-4, 4632	R.VDGVAAALDSFQAR.R	1420.55265	2	2.35E-07	0.94	3.80	-	1488.5
AHQ-10-4, 4124	R.VTELVQQLTGQAPAPGQR.V	1894.12181	2	2.59E-07	0.90	4.05	-	877.7
AHQ-10-4, 4528	R.YDGQIAVFGAGFQEK.L	1630.78190	2	4.12E-04	0.82	2.80	-	751.0
gi|30159830|ref|XP_302246.1|	similar to HSPC280 [Homo sapiens]			2.38E-07	1.85	20.22	3.90	45644.4
AHQ-10-14-, 6325	K.CANLFEALVGTLK.A	1437.68632	2	5.04E-06	0.90	3.57	-	934.6
AHQ-10-14-, 6284 - 6285	R.DDKCANLFEALVGTLK.A	1796.03496	2	2.38E-07	0.96	4.38	-	1448.5
gi|21361547|ref|NP_002930.2|	ribonuclease/angiogenin inhibitor; Placental ribonuclease inhibitor [H			2.43E-07	0.86	10.14	3.30	49973.3
AHQ-10-7, 3480	K.ELSLAGNELGDEGAR.L	1531.60704	2	2.43E-07	0.86	2.81	-	1084.8
gi|4503109|ref|NP_001890.1|	cystatin S precursor; cystatin 4 [Homo sapiens]			2.48E-07	0.79	10.24	12.80	16214.3
AHQ-10-13-, 5098	R.IIPGGIYDADLNDEWVQR.A	2075.26658	2	7.77E-05	0.60	3.30	-	436.4
AHQ-10-13, 5359 - 5428	R.IIPGGIYDADLNDEWVQR.A	2075.26658	2	2.48E-07	0.79	4.75	-	446.7
gi|4557032|ref|NP_002291.1|	lactate dehydrogenase B [Homo sapiens]			2.84E-07	3.66	40.30	10.20	36638.3
AHQ-10-9, 2476	K.IVVVTAGVR.Q	914.12760	2	2.86E-04	0.90	3.13	-	985.1
AHQ-10-9, 3311 - 3371	K.LIAPVAEEEATVPNNK.I	1695.89534	2	8.40E-04	0.92	3.60	-	1160.9
AHQ-10-9, 3456 - 3469	K.SADTLWDIQK.D	1177.28864	2	1.49E-05	0.86	3.33	-	847.1
AHQ-10-13, 6344	K.SLADELALVDVLEDK.L	1630.81843	2	1.21E-06	0.94	3.66	-	1307.8
AHQ-10-13-, 6161 - 6166	K.SLADELALVDVLEDK.L	1630.81843	2	2.84E-07	0.98	5.90	-	2207.1
AHQ-10-14-, 6198	K.SLADELALVDVLEDK.L	1630.81843	2	5.50E-04	0.79	2.69	-	965.4
AHQ-10-11, 6095	K.SLADELALVDVLEDK.L	1630.81843	2	5.81E-05	0.84	2.96	-	1035.4
gi|4557321|ref|NP_000030.1|	apolipoprotein A-I precursor [Homo sapiens]			3.03E-07	1.87	20.23	4.90	30777.6
AHQ-10-10, 4222 - 4226	R.DYVSQFEGSALGK.Q	1401.50297	2	3.03E-07	0.97	4.63	-	1314.8
AHQ-10-14-, 4986	K.LLDNWDSVTSTFSK.L	1613.74965	2	7.85E-04	0.90	3.85	-	819.6
gi|5031857|ref|NP_005557.1|	lactate dehydrogenase A [Homo sapiens]			3.07E-07	2.67	30.25	10.50	36688.5
AHQ-10-14-, 6216	K.DLADELALVDVIEDK.L	1658.82864	2	4.12E-07	0.86	2.55	-	1422.5
AHQ-10-13, 6355	K.DLADELALVDVIEDK.L	1658.82864	2	2.25E-04	0.87	3.14	-	1066.3
AHQ-10-13-, 6176 - 6177	K.DLADELALVDVIEDK.L	1658.82864	2	4.70E-07	0.98	5.00	-	2417.7
AHQ-10-9, 2728 - 2732	K.LVIITAGAR.Q	914.12760	2	2.43E-06	0.85	3.06	-	749.7
AHQ-10-9, 3533	K.QVVESAYEVIK.L	1265.43734	2	3.07E-07	0.96	3.87	-	1625.7
gi|4504071|ref|NP_000164.1|	platelet glycoprotein Ib alpha polypeptide precursor [Homo sapiens] [MA			3.21E-07	6.23	70.25	14.40	68955.0
AHQ-10-4, 3495	K.AM*TSNVASVQCDNSDKFPVYK.Y	2379.60939	3	7.16E-05	0.85	3.82	-	685.0
AHQ-10-4, 3625	K.AM*TSNVASVQCDNSDKFPVYK.Y	2379.60939	3	2.59E-06	0.76	3.09	-	715.4
AHQ-10-3, 4761	R.GLGELQELYLK.G	1263.46458	2	1.00E-05	0.96	4.06	-	1596.6
AHQ-10-12, 4008 - 4022	R.GQDLLSTVSIR.Y	1189.34410	2	8.07E-06	0.96	3.93	-	1266.2
AHQ-10-4, 4055	R.GQDLLSTVSIR.Y	1189.34410	2	3.06E-05	0.94	3.56	-	1316.4
AHQ-10-3, 4037 - 4041	R.GQDLLSTVSIR.Y	1189.34410	2	7.06E-06	0.94	3.43	-	1420.5
AHQ-10-13, 4408	R.GQDLLSTVSIR.Y	1189.34410	2	1.67E-04	0.88	2.95	-	1205.9
AHQ-10-13-, 4037 - 4045	R.GQDLLSTVSIR.Y	1189.34410	2	3.21E-07	0.96	3.75	-	1879.9
AHQ-10-14-, 4009 - 4017	R.GQDLLSTVSIR.Y	1189.34410	2	2.87E-06	0.95	4.04	-	1384.3
AHQ-10-1, 4199	R.GQDLLSTVSIR.Y	1189.34410	2	1.16E-05	0.94	3.54	-	1353.3
AHQ-10-3, 2257 - 2259	R.GVLQGHLESSR.N	1183.29965	2	3.55E-05	0.82	2.78	-	741.8
AHQ-10-3, 3629	R.LTQLNLDRCELTK.L	1605.83862	2	1.50E-05	0.89	3.55	-	873.2
AHQ-10-4, 3601 - 3639	R.LTQLNLDRCELTK.L	1605.83862	2	2.37E-04	0.72	3.36	-	586.8
AHQ-10-3, 4105	R.LTSLPLGALR.G	1041.26938	2	6.90E-05	0.87	3.16	-	853.2
AHQ-10-4, 4713 - 4715	R.WLQDNAENVYVWK.Q	1665.82948	2	5.13E-07	0.97	4.92	-	1815.5
AHQ-10-3, 4662 - 4663	R.WLQDNAENVYVWK.Q	1665.82948	2	1.91E-04	0.97	4.40	-	1775.3
gi|29729616|ref|XP_292963.1|	similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [			3.29E-07	0.86	10.25	16.40	18025.4
AHQ-10-14-, 4696	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	2.48E-04	0.93	4.98	-	898.3
AHQ-10-12, 4606 - 4660	K.HTGPGILSM*ANAGPNTNGSQFFICTAK.S	2810.11545	3	3.29E-07	0.86	4.39	-	776.6
gi|6041669|ref|NP_004538.2|	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa; NADH dehyd			3.30E-07	0.67	10.13	14.00	15208.5
AHQ-10-13-, 4616	R.TLPETLDPAEYNISPETR.R	2047.20831	2	3.30E-07	0.67	2.67	-	539.3
gi|30150448|ref|XP_293066.2|	similar to Stress-70 protein, mitochondrial precursor (75 kDa glucose			3.45E-07	1.72	20.21	5.10	58788.2
AHQ-10-6, 3848	K.DAGQISGLNVLR.V	1243.39499	2	2.79E-05	0.79	3.22	-	670.3
AHQ-10-6, 4392 - 4445	R.VINEPTAAALAYGLDK.S	1646.86592	2	3.45E-07	0.93	4.13	-	727.8
gi|4504973|ref|NP_002292.1|	lactate dehydrogenase C [Homo sapiens]			3.56E-07	0.92	10.20	3.60	36311.0
AHQ-10-9, 2405 - 2417	R.VIGSGCNLDSAR.F	1250.36445	2	3.56E-07	0.92	3.92	-	716.3
gi|4502051|ref|NP_000688.1|	arachidonate 12-lipoxygenase; 12(S)-lipoxygenase [Homo sapiens]			3.97E-07	4.90	60.19	12.10	75721.8
AHQ-10-6, 4589	R.AAAQLTYCSLCPPDDLADR.G	2140.33708	2	3.97E-07	0.73	2.99	-	415.4
AHQ-10-6, 2471	K.AVSTGGGGHVQLLR.R	1352.52468	2	1.46E-06	0.82	3.62	-	701.4
AHQ-10-6, 3127 - 3193	R.EITEVGLCQAQDR.G	1520.64745	2	4.96E-04	0.86	3.29	-	726.9
AHQ-10-6, 5221	R.GLLGLPGALYAHDALR.L	1637.90708	2	1.59E-04	0.71	2.70	-	505.7
AHQ-10-6, 4809	R.ITVQGPGACAEVAFPCYR.W	1999.25659	2	4.75E-05	0.92	3.39	-	1478.3
AHQ-10-6, 4752	R.WVQGEDILSLPEGTAR.L	1771.95190	2	6.12E-04	0.86	3.83	-	828.6
gi|16933567|ref|NP_005361.2|	mel transforming oncogene; ras-associated protein RAB8 [Homo sapiens]			4.08E-07	0.72	10.18	6.80	23668.1
AHQ-10-11, 5411 - 5478	K.ANINVENAFFTLAR.D	1580.76926	2	5.53E-05	0.91	3.53	-	1068.3
AHQ-10-11, 4895	K.ANINVENAFFTLAR.D	1580.76926	2	4.08E-07	0.72	2.71	-	569.7
gi|6005727|ref|NP_006576.1|	chaperonin containing TCP1, subunit 8 (theta); T-complex protein 1, the			4.10E-07	1.64	20.18	4.40	59662.4
AHQ-10-7, 3898	K.FAEAFEAIPR.A	1151.29602	2	4.10E-07	0.95	3.60	-	1383.5
AHQ-10-7, 2952	K.HEKEDGAISTIVLR.G	1568.75678	2	1.17E-05	0.70	3.10	-	513.2
gi|4507951|ref|NP_003396.1|	tyrosine 3/tryptophan 5 -monooxygenase activation protein, eta polypept			4.12E-07	0.91	10.20	5.70	28218.5
AHQ-10-10, 2951 - 3006	K.AVTELNEPLSNEDR.N	1587.67060	2	4.12E-07	0.91	3.92	-	802.8
gi|30154839|ref|XP_301540.1|	similar to keratin 8; cytokeratin 8; keratin, type II cytoskeletal 8 [			4.17E-07	0.86	10.19	3.40	39331.0
AHQ-10-2, 4590 - 4631	K.SLNNKFASFIDK.V	1384.56191	2	2.98E-05	0.54	2.93	-	462.2
AHQ-10-3, 4363	K.SLNNKFASFIDK.V	1384.56191	2	7.07E-05	0.88	3.42	-	777.7
AHQ-10-3, 4527	K.SLNNKFASFIDK.V	1384.56191	2	6.45E-05	0.80	3.03	-	606.7
AHQ-10-3, 4750 - 4759	K.SLNNKFASFIDK.V	1384.56191	2	2.08E-06	0.92	3.83	-	1017.2
AHQ-10-5, 4529 - 4551	K.SLNNKFASFIDK.V	1384.56191	2	4.02E-04	0.86	3.34	-	757.7
AHQ-10-6, 4463 - 4475	K.SLNNKFASFIDK.V	1384.56191	2	7.99E-07	0.79	3.40	-	642.2
AHQ-10-10, 4360	K.SLNNKFASFIDK.V	1384.56191	2	1.20E-06	0.78	2.85	-	695.6
AHQ-10-13, 4873 - 4877	K.SLNNKFASFIDK.V	1384.56191	2	1.63E-05	0.89	3.71	-	679.3
AHQ-10-14, 5295 - 5299	K.SLNNKFASFIDK.V	1384.56191	2	4.17E-07	0.86	3.15	-	808.1
gi|20149545|ref|NP_002717.2|	prolyl endopeptidase [Homo sapiens]			4.43E-07	1.54	20.17	4.80	80733.0
AHQ-10-6, 5121	K.ICDPYAWLEDPDSEQTK.A	2069.19089	2	1.39E-04	0.65	2.99	-	425.7
AHQ-10-6, 5489	R.VFLDPNILSDDGTVALR.G	1846.07392	2	4.43E-07	0.89	3.48	-	1010.8
gi|30149221|ref|XP_291446.2|	similar to Heat shock cognate 71 kDa protein [Homo sapiens]			4.59E-07	0.90	10.18	3.90	45688.5
AHQ-10-6, 2487	R.STAGDTHLGGEDFDNR.M	1692.68222	2	4.59E-07	0.90	3.58	-	1011.9
gi|12408656|ref|NP_005177.2|	calpain 1, large subunit; calpain, large polypeptide L1; calcium-activ			5.16E-07	7.99	100.21	16.10	81889.4
AHQ-10-6, 4899	K.APSDLYQIILK.A	1261.49183	2	5.33E-07	0.84	2.60	-	975.1
AHQ-10-6, 3587	R.DFFLANASR.A	1041.14166	2	4.04E-05	0.86	2.58	-	1223.8
AHQ-10-6, 5573	R.FRLPPGEYVVVPSTFEPNKEGDFVLR.F	2994.39160	3	5.55E-04	0.87	4.22	-	834.2
AHQ-10-6, 4332 - 4352	R.KAPSDLYQIILK.A	1389.66474	2	8.34E-06	0.80	2.93	-	672.8
AHQ-10-6, 6107	K.LGLVEFNILWNR.I	1474.73142	2	5.16E-07	0.78	3.14	-	750.1
AHQ-10-6, 5363	R.LPPGEYVVVPSTFEPNKEGDFVLR.F	2691.03055	3	2.71E-04	0.72	3.23	-	389.2
AHQ-10-6, 5941	K.LVFVHSAEGNEFWSALLEK.A	2177.44364	3	6.18E-04	0.71	3.15	-	582.8
AHQ-10-6, 3908	K.LYELIITR.Y	1021.23493	2	4.54E-04	0.91	3.57	-	1103.1
AHQ-10-6, 4393	K.RPTELLSNPQFIVDGATR.T	2015.25904	3	1.40E-04	0.92	3.97	-	1259.9
AHQ-10-6, 4233	K.WNTTLYEGTWR.R	1427.54534	2	1.85E-04	0.58	2.61	-	520.0
gi|4826657|ref|NP_004333.1|	caldesmon 1 isoform 3; H-CAD; L-CAD [Homo sapiens]			5.33E-07	3.48	40.23	11.30	62662.9
AHQ-10-6, 4652 - 4655	K.EFDPTITDASLSLPSR.R	1749.89986	2	5.33E-07	0.87	3.50	-	771.9

AHQ-10-6, 2628	K.GNVFSSPTAAGTPNK.E	1448.56286	2	2.81E-04	0.88	3.48	-	822.9
AHQ-10-6, 3671 - 3732	K.TTTTNTQVEGDDEAAFLER.L	2099.15534	2	2.74E-06	0.92	4.59	-	590.3
AHQ-10-6, 2739	R.YEIEETETVTK.S	1342.43060	2	3.86E-04	0.81	3.28	-	656.2
gi|10835187|ref|NP_000627.1|	superoxide dismutase 2, mitochondrial [Homo sapiens]			5.54E-07	2.49	30.22	19.40	24733.0
AHQ-10-11, 5684	K.AIWNVINWENVTER.Y	1744.93137	3	1.78E-05	0.93	4.50	-	1159.1
AHQ-10-11, 5616 - 5678	K.AIWNVINWENVTER.Y	1744.93137	2	1.38E-05	0.94	4.39	-	1198.8
AHQ-10-13-, 5780	K.AIWNVINWENVTER.Y	1744.93137	2	5.54E-07	0.85	3.34	-	725.1
AHQ-10-11, 3772 - 3847	K.GDVTAQIALQPALK.F	1425.65548	2	4.21E-05	0.78	3.14	-	812.8
AHQ-10-14-, 3850	K.GDVTAQIALQPALK.F	1425.65548	2	5.97E-04	0.77	2.95	-	922.2
AHQ-10-11, 2527	K.HHAAYVNNLNVTEEK.Y	1739.86999	2	2.07E-06	0.86	3.29	-	699.8
gi|4557597|ref|NP_001449.1|	gamma filamin; filamin 2; filamin C, gamma (actin-binding protein-280);			5.73E-07	0.81	10.24	0.90	288897.4
AHQ-10-5, 4501	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	2	8.90E-07	0.76	3.87	-	263.9
AHQ-10-6, 4407	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	2.64E-05	0.86	4.21	-	476.0
AHQ-10-7, 4372	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	1.92E-06	0.90	4.90	-	550.6
AHQ-10-3, 4466 - 4522	R.GQHVPGSPFQFTVGPLGEGGAHK.V	2305.53673	3	5.73E-07	0.81	3.99	-	417.6
gi|29731857|ref|XP_293042.1|	similar to ribosomal protein S12; 40S ribosomal protein S12 [Homo sapi			6.00E-07	0.95	10.21	8.90	19543.6
AHQ-10-13-, 4457	K.LVEALCAEHQINLIK.V	1753.05645	2	6.00E-07	0.95	4.21	-	1759.3
gi|30149555|ref|XP_301154.1|	similar to heat shock protein 86 [Homo sapiens]			6.27E-07	0.97	10.25	10.60	15781.6
AHQ-10-5, 5620 - 5623	K.HSQFIGYPITLFVEK.E	1780.05877	3	6.27E-07	0.97	5.08	-	2144.3
gi|30147105|ref|XP_210550.2|	similar to Chain , Aldose Reductase (E.C.1.1.1.21) Mutant With Tyr 48			6.38E-07	0.87	10.20	2.20	61339.9
AHQ-10-5, 4151	K.ADLINNLGTIAK.S	1243.43490	2	9.39E-06	0.92	3.93	-	921.7
AHQ-10-5, 4505	K.ADLINNLGTIAK.S	1243.43490	2	6.38E-07	0.87	3.38	-	793.4
AHQ-10-5, 3915	K.ADLINNLGTIAK.S	1243.43490	2	1.81E-04	0.84	3.26	-	486.6
gi|21361657|ref|NP_005304.3|	glucose regulated protein, 58kDa; glucose regulated protein, 58kD [Hom			7.00E-07	6.09	70.25	16.60	56782.0
AHQ-10-13-, 5380	R.ELSDFISYLQR.E	1371.52000	2	1.31E-05	0.97	3.71	-	1937.0
AHQ-10-7, 4484	R.FLQDYFDGNLK.R	1360.49568	2	1.41E-04	0.92	3.50	-	1276.6
AHQ-10-7, 4361	R.FLQDYFDGNLK.R	1360.49568	2	4.37E-05	0.75	3.01	-	717.4
AHQ-10-7, 4440	R.GFPTIYFSPANK.K	1342.52349	2	1.46E-05	0.81	2.78	-	828.8
AHQ-10-7, 5446	R.KTFSHELSDFGLESTAGEIPVVAIR.T	2705.01562	3	7.00E-07	0.82	3.76	-	593.5
AHQ-10-7, 3077	K.M*DATANDVPSPYEVR.G	1681.80586	2	1.27E-06	0.89	3.50	-	600.2
AHQ-10-7, 5785	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	2	2.42E-06	0.97	5.00	-	1698.9
AHQ-10-7, 5776	K.TFSHELSDFGLESTAGEIPVVAIR.T	2576.84271	3	1.42E-04	0.73	3.50	-	609.9
AHQ-10-7, 3149	K.YGVSGYPTLK.I	1085.23435	2	1.76E-06	0.87	2.66	-	734.5
gi|30158489|ref|XP_301421.1|	similar to Chloride intracellular channel protein 1 (Nuclear chloride			7.15E-07	0.32	10.13	6.60	28267.5
AHQ-10-9, 5416 - 5440	K.FLNGNELTLADCNLLPK.L	1934.20276	2	7.15E-07	0.32	2.51	-	531.2
gi|7705704|ref|NP_057001.1|	glutathione S-transferase subunit 13 homolog [Homo sapiens]			7.57E-07	1.60	20.18	13.30	25496.7
AHQ-10-11, 2736	K.AGM*SAEQAQGLLEK.I	1449.61254	2	1.59E-05	0.78	2.55	-	1224.5
AHQ-10-11, 4379	R.NEDITEPQSILAAAEK.A	1729.86695	2	7.57E-07	0.82	3.59	-	405.3
gi|28466991|ref|NP_775771.2|	tau-tubulin kinase [Homo sapiens]			8.59E-07	0.94	10.22	0.70	182465.3
AHQ-10-13-, 4876 - 4885	K.LALDIKIATYR.K	1277.53762	2	8.59E-07	0.94	4.37	-	1747.9
AHQ-10-2, 5028	K.LALDIKIATYR.K	1277.53762	2	2.41E-06	0.91	3.34	-	1750.6
gi|4502219|ref|NP_001656.1|	ras homolog gene family, member G (rho G); RhoG [Homo sapiens]			8.66E-07	0.79	10.18	9.90	21338.4
AHQ-10-11, 4668	K.EYIPTVFDNYSAQSAVDGR.T	2133.25975	2	8.66E-07	0.79	3.55	-	436.8
gi|4503481|ref|NP_001395.1|	eukaryotic translation elongation factor 1 gamma; elongation factor 1-g			8.67E-07	1.81	20.21	6.20	50118.5
AHQ-10-8, 3074	K.ALIAAQYSGAQVR.V	1348.53280	2	1.10E-04	0.97	4.22	-	1761.4
AHQ-10-8, 2718	R.KLDPGSEETQTLVR.E	1573.73020	2	8.67E-07	0.84	3.78	-	375.6
gi|21536452|ref|NP_002762.2|	mesotrypsin preproprotein; trypsin 4, brain; protease, serine, 4; meso			9.20E-07	0.94	10.18	5.30	26697.2
AHQ-10-4, 3244 - 3304	K.VLEGNEQFINAAK.I	1433.59133	2	9.20E-07	0.94	3.67	-	1206.2
gi|13129018|ref|NP_076956.1|	hypothetical protein MGC3077 [Homo sapiens]			9.49E-07	0.83	10.16	5.30	21007.6
AHQ-10-11, 3812	K.VSEEIEDIIK.K	1175.31097	2	9.49E-07	0.83	3.11	-	826.4
gi|16933542|ref|NP_002017.1|	fibronectin 1 isoform 1 preproprotein; cold-insoluble globulin [Homo s			9.52E-07	1.55	20.22	1.60	259222.8
AHQ-10-2, 5684	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	6.82E-05	0.59	3.00	-	320.8
AHQ-10-1, 5713 - 5714	R.NTFAEVTGLSPGVTYYFK.V	1995.21983	2	9.52E-07	0.91	3.61	-	930.7
AHQ-10-2, 4486 - 4558	R.SSPVVIDASTAIDAPSNLR.F	1914.10666	2	7.01E-04	0.64	2.75	-	748.9
gi|5453597|ref|NP_006126.1|	F-actin capping protein alpha-1 subunit; Cap Z [Homo sapiens]			9.85E-07	0.94	10.20	5.60	32922.5
AHQ-10-9, 2685 - 2740	K.DVQDSLTVSNEAQTAK.E	1706.79025	2	9.85E-07	0.94	4.08	-	1197.4
gi|4557801|ref|NP_000261.1|	purine nucleoside phosphorylase [Homo sapiens]			1.03E-06	4.11	50.23	21.50	32147.7
AHQ-10-9, 4164	R.DHINLPGFSGQNPLR.G	1665.83425	2	5.92E-04	0.76	3.40	-	324.6
AHQ-10-9, 4537	K.FEVGDIM*LIR.D	1209.44039	2	1.11E-04	0.82	2.54	-	947.6
AHQ-10-13-, 4109 - 4112	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	9.33E-05	0.95	4.51	-	1155.6
AHQ-10-13, 4459 - 4507	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	2.46E-04	0.82	3.51	-	593.0
AHQ-10-9, 3908 - 3911	K.LGADAVGM*STVPEVIVAR.H	1802.08606	2	4.17E-04	0.95	4.18	-	1239.5
AHQ-10-9, 4652	R.LVFGFLNGR.A	1023.21261	2	3.06E-04	0.72	2.53	-	714.9
AHQ-10-13-, 4860	R.VFGFSLITNK.V	1126.32960	2	5.25E-04	0.74	2.89	-	485.0
AHQ-10-9, 4591	R.VFGFSLITNK.V	1126.32960	2	1.03E-06	0.87	2.98	-	716.5
gi|4504085|ref|NP_000399.1|	glycerol-3-phosphate dehydrogenase 2 (mitochondrial) [Homo sapiens] [MA			1.16E-06	3.88	50.20	7.80	80814.1
AHQ-10-6, 6232	R.ANLLEIAPHLSAPLPIM*LPVYK.W	2417.93800	3	4.89E-05	0.81	3.32	-	848.3
AHQ-10-6, 3343	R.NYLSCDVEVR.R	1256.36746	2	6.89E-05	0.80	3.09	-	803.4
AHQ-10-6, 5725	R.VIFFLPWQK.M	1178.44934	2	1.38E-04	0.90	3.14	-	881.7
AHQ-10-6, 5727 - 5769	R.YGAATANYMEVVSLLK.K	1731.00632	2	1.16E-06	0.81	3.42	-	722.7
AHQ-10-6, 5231 - 5301	R.YGAATANYM*EVVSLLK.K	1747.00572	2	1.62E-06	0.57	2.84	-	466.8
gi|7706497|ref|NP_057392.1|	UMP-CMP kinase [Homo sapiens]			1.22E-06	0.72	10.17	5.70	25854.7
AHQ-10-11, 3810 - 3864	K.YGYTHLSAGELLR.D	1480.64969	2	1.22E-06	0.72	2.61	-	723.0
gi|10834976|ref|NP_000572.1|	glutathione peroxidase 1 [Homo sapiens]			1.22E-06	1.88	20.24	15.40	21909.0
AHQ-10-11, 3826	R.PLAGGEPVSLGSLR.G	1353.54935	2	1.22E-06	0.93	3.89	-	1070.7
AHQ-10-11, 4808 - 4822	K.YVRPGGGFEPNFM*LFEK.C	2005.28455	3	6.54E-06	0.95	4.75	-	1415.5
gi|4507231|ref|NP_003134.1|	single-stranded DNA binding protein; single-stranded DNA-binding protei			1.23E-06	1.63	20.21	22.30	17259.5
AHQ-10-13-, 5677	R.QATTIIADNIIFLSDQTK.E	1993.24692	2	3.57E-06	0.89	3.90	-	710.4
AHQ-10-13-, 3182 - 3242	R.SGDSEVYQLGDVSQK.T	1612.67692	2	1.94E-05	0.93	4.19	-	968.8
AHQ-10-13, 3657	R.SGDSEVYQLGDVSQK.T	1612.67692	2	1.23E-06	0.74	3.12	-	826.6
gi|15431310|ref|NP_000517.2|	keratin 14; cytokeratin 14 [Homo sapiens]			1.23E-06	0.94	10.19	2.50	51621.2
AHQ-10-3, 2941	R.ALEEANADLEVK.I	1302.41284	2	1.23E-06	0.94	3.73	-	1631.9
AHQ-10-5, 2919 - 2997	R.ALEEANADLEVK.I	1302.41284	2	4.34E-06	0.86	3.03	-	979.8
AHQ-10-2, 2996	R.ALEEANADLEVK.I	1302.41284	2	3.37E-04	0.83	2.72	-	1167.7
gi|9507215|ref|NP_061816.1|	tubulin, alpha-like 2; tubulin, alpha 8 [Homo sapiens]			1.26E-06	1.54	20.18	6.90	50093.2
AHQ-10-13, 4983 - 5040	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	1.30E-04	0.73	3.13	-	803.5
AHQ-10-13-, 4708	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	1.26E-06	0.92	3.67	-	1117.9
AHQ-10-14-, 4713	R.AVM*IDLEPTVVDEVR.A	1702.95125	2	4.49E-06	0.75	3.05	-	859.4
AHQ-10-7, 5352	R.IHFPLVTYAPIISAEK.A	1800.13312	2	1.06E-04	0.63	2.79	-	426.0
gi|27481160|ref|XP_208217.1|	similar to elongation factor 1 alpha [Homo sapiens]			1.32E-06	1.46	20.14	4.30	50171.6
AHQ-10-10, 3130	R.LPLQDVYK.I	976.15102	2	4.19E-05	0.75	2.67	-	580.1
AHQ-10-7, 3429 - 3442	K.YYVTIIDAPGHR.D	1405.58282	2	1.32E-06	0.71	2.76	-	578.4
gi|5802966|ref|NP_006861.1|	destrin (actin depolymerizing factor); destrin [Homo sapiens]			1.32E-06	0.90	10.14	6.70	18505.6
AHQ-10-12, 3764	R.YALYDASFETK.E	1308.41754	2	1.32E-06	0.90	2.77	-	1249.5
gi|4504743|ref|NP_002194.1|	integrin alpha 2 precursor; Integrin, alpha-2 (CD49B; alpha-2 subunit o			1.35E-06	1.03	20.14	3.00	129294.4
AHQ-10-3, 3598	K.AGDISCNADINPLK.I	1489.63335	2	1.35E-06	0.72	2.79	-	746.8
AHQ-10-3, 4777	R.VDISLENPGTSPALEAYSETAK.V	2293.46974	2	2.69E-04	0.31	2.59	-	371.3
gi|22060072|ref|XP_088293.2|	similar to cytochrome c [Homo sapiens]			1.39E-06	0.88	10.15	10.50	11887.8
AHQ-10-13-, 3674	K.TGPNLHGLFGR.K	1169.31780	2	1.39E-06	0.88	2.69	-	861.6
gi|4502021|ref|NP_003680.1|	aldo-keto reductase family 7, member A2 (aflatoxin aldehyde reductase);			1.40E-06	1.58	20.22	10.30	36648.3
AHQ-10-9, 3592	K.ALQAAYGASAPSVTSAALR.W	1806.01302	2	1.40E-06	0.63	2.86	-	523.9
AHQ-10-9, 5079 - 5091	R.FYAYNPLAGGLLTGK.Y	1585.82741	2	7.75E-04	0.95	4.40	-	1025.0
gi|11993943|ref|NP_055419.1|	Tax interaction protein 1 [Homo sapiens]			1.42E-06	0.94	10.20	13.70	13734.6
AHQ-10-13-, 4052	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	1.42E-06	0.94	3.93	-	1427.3
AHQ-10-13, 4411	R.VSEGGPAEIAGLQIGDK.I	1641.80454	2	4.40E-05	0.66	2.83	-	669.4
gi|17986273|ref|NP_524144.1|	fast skeletal myosin alkali light chain 1 isoform 1f; A1 catalytic; A2			1.46E-06	0.93	10.21	8.20	21145.0
AHQ-10-12, 3332 - 3388	R.VFDKEGNGTVMGAELR.H	1723.93228	2	1.46E-06	0.93	4.17	-	1343.6

gi|4557395|ref|NP_000058.1| carbonic anhydrase II; carbonate dehydratase II; carbonic dehydratase;				1.46E-06	1.63	20.20	9.60	29245.8
AHQ-10-11, 6187	K.AVQQPDGLAVLGIFLK.V	1669.98899	2	1.46E-06	0.91	4.01	-	651.9
AHQ-10-10, 3703	K.VVDVLDSIK.T	988.16011	2	3.54E-04	0.72	2.60	-	430.4
gi|20127528|ref|NP_037459.2| parvin, beta; CGI-56 protein; beta-parvin [Homo sapiens]				1.47E-06	3.75	50.20	23.40	41714.0
AHQ-10-9, 3297 - 3351	K.ARPEDVVNLDLK.S	1369.54878	2	9.13E-05	0.88	3.57	-	792.6
AHQ-10-9, 4969	R.DAFDTLFDHAPDKLSVVK.K	2019.24293	2	3.46E-05	0.75	3.55	-	377.5
AHQ-10-9, 3427 - 3503	K.LNVAEVTQSEIGQK.Q	1516.67865	2	1.50E-05	0.92	4.00	-	1058.1
AHQ-10-9, 3847	K.NAINSPM*SPALVDVHPEDTQLEENEER.T	3052.23385	3	3.07E-04	0.59	3.29	-	554.4
AHQ-10-9, 3731 - 3768	K.QLEEDLYDGQVLQK.L	1678.82164	2	1.47E-06	0.62	2.96	-	471.8
gi|4758984|ref|NP_004654.1| RAB11A, member RAS oncogene family; RAB 11A, member oncogene family [Ho				1.49E-06	2.83	30.27	18.10	24393.3
AHQ-10-11, 4116	R.DHADSNIVIM*LVGNK.S	1642.85914	2	9.15E-06	0.98	4.95	-	2021.4
AHQ-10-11, 4826 - 4828	R.GAVGALLVYDIAK.H	1290.53317	2	1.49E-06	0.98	5.38	-	2328.4
AHQ-10-11, 2890 - 2898	K.VVLIGDSGVGK.S	1044.22690	2	7.79E-06	0.87	3.26	-	1234.7
gi|6005826|ref|NP_009160.1| protein kinase C and casein kinase substrate in neurons 2; pacsin 2 [Ho				1.50E-06	0.90	10.16	2.30	55904.6
AHQ-10-6, 3900	K.AYAQQLTEWAR.R	1337.46534	2	1.50E-06	0.90	3.14	-	1212.8
gi|27477800|ref|XP_208313.1| similar to tropomyosin 4 [Homo sapiens]				1.56E-06	0.87	10.20	10.10	18426.7
AHQ-10-9, 5103	K.CGDLEEELKNVTNNLK.S	1878.05124	2	4.57E-04	0.61	3.24	-	433.7
AHQ-10-9, 4232	K.CGDLEEELKNVTNNLK.S	1878.05124	2	1.56E-06	0.87	3.64	-	1245.0
gi|4557297|ref|NP_000022.1| delta-aminolevulinic acid dehydratase; porphobilinogen synthase; aminol				1.59E-06	0.94	10.17	3.00	36294.7
AHQ-10-9, 4368	R.CVLIFGVPSR.V	1149.38800	2	1.59E-06	0.94	3.39	-	1826.7
gi|21624607|ref|NP_066972.1| coactosin-like 1 [Homo sapiens]				1.64E-06	3.24	40.29	45.10	15944.9
AHQ-10-13-, 4996	R.DDGSAVIWVTFK.Y	1338.49001	2	1.64E-06	0.89	3.66	-	813.0
AHQ-10-13-, 6242	K.FALITWIGENVSGLQR.A	1805.06986	2	1.67E-04	0.98	5.81	-	2251.5
AHQ-10-13-, 2988	R.KELEEDFIK.S	1151.29110	2	2.30E-04	0.68	2.81	-	608.6
AHQ-10-12, 4988 - 4990	K.YDGSTIVPGEQGAEYQHFIQQCTDDVR.L	3116.27790	3	3.46E-04	0.69	3.42	-	272.2
gi|4506773|ref|NP_002956.1| S100 calcium-binding protein A9; calgranulin B [Homo sapiens]				1.67E-06	1.54	20.21	24.60	13241.9
AHQ-10-13-, 2749	K.LGHPDTLNQGEFK.E	1456.58499	2	1.67E-06	0.81	3.02	-	502.5
AHQ-10-14-, 5409	R.NIETIINTFHQYSVK.L	1808.02738	2	4.88E-04	0.73	2.80	-	752.3
AHQ-10-13-, 5418	R.NIETIINTFHQYSVK.L	1808.02738	2	5.18E-04	0.87	4.14	-	503.3
gi|6715607|ref|NP_000175.1| G-gamma globin [Homo sapiens]				1.94E-06	0.92	10.16	6.80	16126.3
AHQ-10-13-, 4712 - 4716	R.LLVVYPWTQR.F	1275.52342	2	1.94E-06	0.92	3.22	-	1037.9
AHQ-10-13, 5075 - 5091	R.LLVVYPWTQR.F	1275.52342	2	2.58E-05	0.91	3.28	-	1053.0
gi|14251209|ref|NP_001279.2| chloride intracellular channel 1; p64CLCP; chloride channel ABP [Homo				1.94E-06	2.64	30.25	21.60	26922.5
AHQ-10-10, 5270	R.EEFASTCPDDEEIELAYEQVAK.A	2575.69730	3	1.43E-05	0.81	3.11	-	843.0
AHQ-10-13-, 3449	K.GVTFNVTTVDTK.R	1282.42476	2	1.94E-06	0.93	3.81	-	1142.5
AHQ-10-9, 3235	K.GVTFNVTTVDTK.R	1282.42476	2	3.85E-05	0.82	2.75	-	843.4
AHQ-10-13, 5495	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	2.71E-04	0.91	4.08	-	649.9
AHQ-10-14, 5720	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	8.60E-04	0.83	2.81	-	917.7
AHQ-10-10, 5071	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	5.26E-06	0.76	3.17	-	469.5
AHQ-10-9, 4977 - 5039	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	3.33E-06	0.90	4.28	-	692.8
AHQ-10-13-, 5108	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	5.26E-06	0.95	5.07	-	769.9
AHQ-10-14-, 5120 - 5188	K.LAALNPESNTAGLDIFAK.F	1846.07392	2	1.35E-05	0.89	3.95	-	551.8
gi|4502693|ref|NP_001760.1| CD9 antigen; motility related protein; leukocyte antigen MIC3; antigen				2.01E-06	0.92	10.20	4.40	25415.9
AHQ-10-2, 3595	K.KDVLETFTVK.S	1180.37558	2	4.66E-04	0.86	2.91	-	909.0
AHQ-10-11, 3419 - 3422	K.KDVLETFTVK.S	1180.37558	2	2.01E-06	0.92	3.82	-	934.1
AHQ-10-1, 3706	K.KDVLETFTVK.S	1180.37558	2	4.15E-05	0.90	3.92	-	773.4
gi|5031599|ref|NP_005722.1| actin related protein 2/3 complex subunit 2; ARP2/3 protein complex sub				2.05E-06	1.64	20.21	8.30	34332.8
AHQ-10-9, 3777	R.DNTINLIHTFR.D	1344.50101	2	1.60E-04	0.69	2.91	-	505.7
AHQ-10-9, 2737 - 2747	K.YFQFQEEGKEGENR.A	1761.82929	2	2.05E-06	0.94	4.15	-	1348.3
gi|4758756|ref|NP_004528.1| nucleosome assembly protein 1-like 1; HSP22-like protein interacting pr				2.11E-06	2.10	30.20	11.80	45373.8
AHQ-10-7, 6342	K.GIPEFWLTVFK.N	1337.58999	2	2.11E-06	0.57	2.58	-	207.3
AHQ-10-14-, 5249 - 5305	R.LDGLVETPTGYIESLPR.V	1861.08535	2	2.01E-04	0.66	3.16	-	673.2
AHQ-10-7, 5230	K.NVDLLSDMVQEHDEPILK.H	2096.34751	2	3.72E-06	0.87	4.01	-	569.1
gi|21614499|ref|NP_003370.2| villin 2; Villin-2; cytovillin [Homo sapiens]				2.28E-06	1.62	20.18	1.90	69412.3
AHQ-10-6, 4251	K.APDFVFYAPR.L	1183.33971	2	2.28E-06	0.95	3.68	-	1085.4
AHQ-10-6, 3827	K.KAPDFVFYAPR.L	1311.51262	2	4.52E-06	0.67	2.54	-	551.5
gi|22059949|ref|XP_114617.2| similar to tubulin, beta 5 [Homo sapiens]				2.44E-06	1.80	20.33	18.80	22810.8
AHQ-10-7, 5036 - 5044	K.FWEVISDEHGIDPTGTYHGDSDLQLDR.I	3104.24553	3	2.44E-06	0.96	6.55	-	1192.6
AHQ-10-13, 3179 - 3245	R.ISVYYNEATGGK.Y	1302.41453	2	6.78E-05	0.84	3.09	-	815.9
AHQ-10-7, 2724 - 2785	R.ISVYYNEATGGK.Y	1302.41453	2	1.98E-05	0.83	3.18	-	725.8
gi|27480842|ref|XP_208238.1| similar to bA92K2.2 (similar to ubiquitin) [Homo sapiens]				2.46E-06	0.81	10.13	5.80	17966.9
AHQ-10-14-, 3152	K.ESTLHLVLR.L	1068.25169	2	2.46E-06	0.81	2.55	-	571.1
gi|10863873|ref|NP_000651.1| transforming growth factor, beta 1 (Camurati-Engelmann disease); trans				2.47E-06	3.07	40.17	16.60	44422.0
AHQ-10-13-, 3305 - 3360	R.ALDTNYCFSSTEK.N	1537.63010	2	3.61E-04	0.70	3.13	-	498.1
AHQ-10-13-, 5945 - 6025	K.GYHANFCLGPCPYIWSLDTQYSK.V	2781.07085	3	1.08E-04	0.89	3.45	-	1308.7
AHQ-10-8, 3047	R.VAGESAEPEPEPEADYYAK.E	2053.12504	2	3.15E-04	0.57	3.24	-	259.6
AHQ-10-13-, 3564	K.VEQLSNMIVR.S	1189.41074	2	2.47E-06	0.92	3.46	-	1369.2
AHQ-10-13, 3968	K.VEQLSNMIVR.S	1189.41074	2	2.74E-05	0.91	3.00	-	1191.7
gi|13786129|ref|NP_112586.1| RAB33B, member RAS oncogene family; likely ortholog of mouse RAB33b [H				2.55E-06	0.91	10.18	4.80	25717.4
AHQ-10-11, 3542	K.IQLWDTAGQER.F	1317.43243	2	2.62E-05	0.85	3.22	-	820.7
AHQ-10-14-, 3512	K.IQLWDTAGQER.F	1317.43243	2	2.93E-05	0.89	3.53	-	803.2
AHQ-10-11, 3515 - 3538	K.IQLWDTAGQER.F	1317.43243	2	2.55E-06	0.91	3.35	-	950.4
gi|21361198|ref|NP_000286.2| serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiprotei				2.59E-06	0.78	10.16	5.70	46722.2
AHQ-10-7, 5528	R.TLNQPDSQLQLTTGNGLFLSEGLK.L	2575.85625	2	2.59E-06	0.78	3.23	-	573.7
gi|12545410|ref|NP_031394.1| RAS p21 protein activator 3; GTPase activating protein III; Ins(1,3,4,				2.77E-06	2.70	40.17	10.00	95912.5
AHQ-10-5, 4845	R.APSDSAPGCSPCTGGLPANIQLDIDGDRETER.I	3360.54658	3	1.33E-05	0.46	3.49	-	228.9
AHQ-10-5, 5987	R.FFAPAILSPNLFQLTPHHTDPQTSR.T	2837.18380	3	8.02E-04	0.60	3.05	-	420.3
AHQ-10-5, 4656	K.FGDEFLGELR.I	1183.29488	2	2.77E-06	0.94	3.28	-	1529.4
AHQ-10-5, 5815 - 5820	K.SLCPFYGEDFYCEIPR.S	2056.26024	2	4.79E-05	0.69	2.98	-	432.1
gi|4758970|ref|NP_004150.1| proteasome beta 8 subunit isoform E1 proprotein; proteasome subunit, be				2.80E-06	1.60	20.15	4.00	29769.4
AHQ-10-11, 3342 - 3352	R.ASAGSYISALR.V	1096.21876	2	3.07E-06	0.87	3.02	-	901.0
AHQ-10-11, 4047	K.VESTDVSDLLHQYR.E	1662.78230	2	2.80E-06	0.73	2.94	-	723.8
gi|29729345|ref|XP_290995.1| similar to speckle-type POZ protein [Homo sapiens]				2.91E-06	1.61	20.20	10.90	18703.4
AHQ-10-2, 5699 - 5702	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	3.68E-04	0.89	4.04	-	864.4
AHQ-10-3, 5607 - 5611	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	2.91E-06	0.67	3.42	-	787.6
AHQ-10-4, 5711	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	3.80E-06	0.94	3.91	-	1318.2
AHQ-10-5, 5688 - 5700	K.NRVEINDLDPEVFKEMM*R.F	2252.55733	2	4.06E-04	0.59	3.38	-	634.1
AHQ-10-1, 5750	K.NRVEINDLDPEVFKEM*MR.F	2252.55733	2	2.46E-05	0.71	2.99	-	570.8
gi|4507745|ref|NP_003320.1| thioredoxin [Homo sapiens]				3.02E-06	0.90	10.17	12.40	11693.3
AHQ-10-13-, 3836	K.TAFQEALDAAGDK.L	1337.41728	2	4.36E-06	0.91	3.35	-	1295.3
AHQ-10-14-, 3808	K.TAFQEALDAAGDK.L	1337.41728	2	2.01E-05	0.87	2.84	-	1330.0
AHQ-10-13, 4223 - 4225	K.TAFQEALDAAGDK.L	1337.41728	2	3.02E-06	0.90	2.97	-	1454.0
gi|5803121|ref|NP_006801.1| for protein disulfide isomerase-related [Homo sapiens]				3.26E-06	1.57	20.19	8.90	59594.0
AHQ-10-7, 2854	K.DVVHLDSEKDFR.R	1460.57364	2	4.41E-05	0.74	2.65	-	655.7
AHQ-10-7, 6022 - 6038	K.NPQPPQPQVPETPWADEGGSVYHLTDEDFDQFVK.E	3870.10181	3	3.26E-06	0.83	3.77	-	561.8
gi|4505591|ref|NP_002565.1| peroxiredoxin 1; natural killer-enhancing factor A; proliferation-assoc				3.68E-06	1.89	20.25	16.10	22110.2
AHQ-10-11, 3188	K.HGEVCPAGWKPGSDTIKPDVQK.S	2408.67532	3	7.92E-04	0.94	5.06	-	1211.0
AHQ-10-11, 3576 - 3631	R.LVQAFQFTDK.H	1197.36469	2	3.68E-06	0.94	3.61	-	1131.5
gi|5803115|ref|NP_006830.1| inner membrane protein, mitochondrial (mitofilin); motor protein [Homo				3.79E-06	0.87	10.16	1.70	83667.3
AHQ-10-5, 2913	K.VVSQYHELVVQAR.D	1528.73749	2	3.79E-06	0.87	3.15	-	1054.2
gi|16950601|ref|NP_005956.2| myosin light chain kinase isoform 6; myosin light chain kinase [Homo s				3.81E-06	0.95	10.18	1.00	110074.8
AHQ-10-5, 3532 - 3612	K.VSDFYDIEER.L	1273.33005	2	3.81E-06	0.95	3.54	-	1343.0
gi|4505821|ref|NP_002643.1| prolactin-induced protein; prolactin-inducible protein [Homo sapiens] [				4.13E-06	1.61	20.17	17.80	16572.4
AHQ-10-12, 5120	R.FYTIEILKVE	1255.48405	2	4.13E-06	0.93	3.43	-	1327.6
AHQ-10-13-, 5580	K.TYLISSIPLQGAFNYK.Y	1816.08941	2	3.56E-04	0.69	2.80	-	295.3
gi|17149842|ref|NP_004461.2| FK506-binding protein 2 precursor; FK506-binding protein 2 (13kD); pep				4.13E-06	1.56	20.15	18.30	15649.2
AHQ-10-13-, 4094	K.GWDQGLLGM*CEGEK.R	1597.75215	2	2.65E-04	0.78	3.02	-	692.9

AHQ-10-13-, 4124	K.LVIPSELGYGER.G	1333.51491	2	4.13E-06	0.78	2.93	-	408.5
gi|5901944|ref|NP_008977.1|	elastin microfibril interface located protein; TNF? elastin microfibril			4.14E-06	2.42	30.26	6.10	106694.7
AHQ-10-4, 2987	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	9.32E-05	0.66	2.69	-	409.4
AHQ-10-3, 2985	R.GLEEGQAQAGQCPSLEGR.L	1888.99421	2	4.09E-05	0.92	3.73	-	1045.9
AHQ-10-3, 5081	R.LQESCSVCLAGLDGFR.R	1815.01843	2	1.10E-05	0.57	2.63	-	571.2
AHQ-10-3, 3674	R.PARPNLSGSSAGSPLSGLGGEGPGESEK.V	2596.74928	3	4.14E-06	0.94	5.14	-	852.4
gi|4504931|ref|NP_002272.1|	keratin, hair, basic, 1; hard keratin, type II, 1 [Homo sapiens]			4.37E-06	0.90	10.18	2.20	54971.1
AHQ-10-14-, 3288	R.ATAENEFVALK.K	1193.33121	2	4.37E-06	0.90	3.52	-	1556.6
gi|5453832|ref|NP_006380.1|	oxygen regulated protein precursor; oxygen regulated protein (150kD) [H			4.44E-06	1.84	20.23	3.20	111334.8
AHQ-10-3, 5970	R.VEFEELCADLFER.V	1658.81048	2	8.17E-05	0.89	2.86	-	971.4
AHQ-10-3, 5878	K.VLQLINDNTATALSYGVFR.R	2096.37206	2	4.44E-06	0.95	4.60	-	1221.6
gi|5453549|ref|NP_006397.1|	thioredoxin peroxidase; thioredoxin peroxidase (antioxidant enzyme) [Ho			4.48E-06	1.85	20.21	12.90	30539.7
AHQ-10-10, 3624	K.DYGVYLEDSGHTLR.G	1625.72052	2	4.36E-05	0.91	3.20	-	1056.3
AHQ-10-10, 3155 - 3167	R.TREEECHFYAGGQVYPGEASR.V	2445.56624	3	4.48E-06	0.94	4.25	-	1577.7
gi|12707570|ref|NP_004083.2|	mitochondrial short-chain enoyl-coenzyme A hydratase 1 precursor [Homo			4.51E-06	0.88	10.18	6.20	31371.2
AHQ-10-10, 4622 - 4686	K.IFEEDPAVGAIVLTGGDK.A	1832.04401	2	4.51E-06	0.88	3.55	-	1181.2
gi|5902134|ref|NP_009005.1|	coronin, actin binding protein, 1A; coronin, actin-binding, 1A; coronin			4.53E-06	4.18	50.27	17.40	51026.0
AHQ-10-7, 2029 - 2098	R.AAPEASGTPSSDAVSR.L	1503.55369	2	1.53E-04	0.70	2.56	-	810.7
AHQ-10-7, 2122 - 2165	K.ADQCYEDVR.V	1157.19275	2	3.54E-04	0.82	3.11	-	780.4
AHQ-10-7, 2688	R.DGGLICTSCR.D	1141.25805	2	6.70E-06	0.81	2.57	-	849.4
AHQ-10-7, 6253	R.KSDLFQEDLYPPTAGPDPALTAEEWLGGR.D	3175.44994	3	4.53E-06	0.95	5.39	-	819.1
AHQ-10-7, 3968 - 4028	R.VSQTTWDSGFCAVNPK.F	1798.95426	2	8.05E-06	0.91	3.97	-	822.4
gi|4503447|ref|NP_001389.1|	peroxisomal enoyl-coenzyme A hydratase-like protein; delta3,5-delta2,4-			4.58E-06	0.88	10.13	3.40	35994.1
AHQ-10-9, 3944	R.YCAQDAFFQVK.E	1378.53429	2	4.58E-06	0.88	2.68	-	954.0
gi|4557894|ref|NP_000230.1|	lysozyme precursor [Homo sapiens]			4.59E-06	0.87	10.18	8.10	16537.0
AHQ-10-13, 4504	R.STDYGIFQINSR.Y	1401.50620	2	4.59E-06	0.87	3.59	-	607.8
gi|7705849|ref|NP_057215.1|	ras-related GTP-binding protein RAB10; ras-related GTP-binding protein			4.66E-06	0.93	10.19	5.50	22540.8
AHQ-10-13-, 6032	K.AFLTLAEDILR.K	1262.47982	2	4.37E-04	0.95	3.79	-	1800.1
AHQ-10-14-, 6046	K.AFLTLAEDILR.K	1262.47982	2	5.14E-06	0.93	3.41	-	1341.5
AHQ-10-11, 5926	K.AFLTLAEDILR.K	1262.47982	2	4.66E-06	0.93	3.61	-	1249.3
gi|20127408|ref|NP_000173.2|	hydroxyacyl dehydrogenase, subunit A; trifunctional protein, alpha sub			4.73E-06	2.39	30.23	6.30	82999.1
AHQ-10-6, 3572	K.GFYIYQEGVK.R	1204.35569	2	2.02E-04	0.85	2.58	-	685.3
AHQ-10-6, 3100 - 3105	K.TGIEQGSDAGYLCESQK.F	1844.93497	2	4.73E-06	0.95	4.61	-	994.2
AHQ-10-6, 5519 - 5577	K.TVLGTPEVLLGALPGAGGTQR.L	2008.30795	2	7.08E-04	0.59	3.23	-	298.7
gi|4506417|ref|NP_002877.1|	RAP2B, member of RAS oncogene family [Homo sapiens]			4.76E-06	0.83	10.19	14.20	20494.2
AHQ-10-11, 6118	K.EIEVDSSPSVLEILDTAGTEQFASM*R.D	2842.08287	3	4.76E-06	0.83	3.74	-	751.7
gi|20547107|ref|XP_114482.1|	similar to HEAT SHOCK 70 KDA PROTEIN 4 (HEAT SHOCK 70-RELATED PROTEIN			5.01E-06	1.30	20.23	3.90	94330.3
AHQ-10-4, 6236	R.EFSITDVVPYPISLR.W	1736.98906	2	6.20E-06	0.39	2.59	-	192.7
AHQ-10-4, 6053	K.SNLAYDIVQLPTGLTGIK.V	1904.19651	2	5.01E-06	0.91	4.58	-	669.1
gi|21361478|ref|NP_055944.2|	septin 6 isoform B; septin 2 [Homo sapiens]			5.14E-06	0.92	10.24	4.60	49716.3
AHQ-10-7, 4840 - 4868	R.TVPLAGHVGFDSLPDQLVNK.S	2108.38284	2	5.14E-06	0.92	4.88	-	575.6
gi|5174613|ref|NP_005960.1|	nucleosome assembly protein 1-like 4; nucleosome assembly protein 2 [Ho			5.29E-06	0.95	10.18	2.70	42823.1
AHQ-10-7, 2964	K.FYEEVHDLER.K	1337.41897	2	5.29E-06	0.95	3.68	-	1411.7
gi|8922712|ref|NP_060713.1|	hypothetical protein FLJ10849 [Homo sapiens]			5.47E-06	1.33	20.16	9.10	49397.9
AHQ-10-7, 2629	K.AAAQLLQSQAQQSGAQQTK.K	1958.12276	2	1.89E-05	0.83	3.26	-	792.6
AHQ-10-7, 6237	K.STSQGFCFNILCVGETGIGK.S	2178.42845	2	5.47E-06	0.50	3.06	-	380.0
gi|19913441|ref|NP_002140.2|	hippocalcin-like 1; visinin-like protein 3; calcium-binding protein BD			5.66E-06	0.91	10.15	6.70	22313.1
AHQ-10-11, 3648 - 3656	R.TFDTNGDGTIDFR.E	1459.49937	2	5.66E-06	0.91	3.08	-	1039.3
gi|4504521|ref|NP_002147.1|	heat shock 60kDa protein 1 (chaperonin); mitochondrial matrix protein P			5.71E-06	1.80	20.20	5.90	61024.2
AHQ-10-14-, 6272	R.ALM*LQGVDLLADAVAVTM*GPK.G	2146.55768	3	4.48E-04	0.96	4.04	-	2293.9
AHQ-10-7, 5309	K.TLNDELEIIEGMK.F	1505.71604	2	5.71E-06	0.84	3.17	-	759.9
gi|4885183|ref|NP_005210.1|	diaphanous 1; deafness, autosomal dominant 1; hDia1 [Homo sapiens] [MAS			5.79E-06	3.43	40.23	4.70	138977.7
AHQ-10-3, 4490	R.LGLHQVLQDLR.E	1292.51238	2	5.79E-06	0.66	2.67	-	572.7
AHQ-10-3, 4862	K.LVAEDLSQDCFWTK.V	1713.88927	2	1.76E-04	0.87	3.26	-	837.9
AHQ-10-3, 5341	K.QDLEAEVSQLTGEVAK.L	1717.85617	2	1.32E-05	0.95	4.56	-	1193.5
AHQ-10-3, 4678	R.VQLNVFDEQGEEDSYDLK.G	2129.22304	2	6.70E-06	0.95	4.34	-	1497.2
gi|6912238|ref|NP_036226.1|	peroxiredoxin 5; antioxidant enzyme B166 [Homo sapiens]			5.80E-06	0.95	10.24	7.90	22026.2
AHQ-10-12, 6192	K.ETDLLLDDSLVSIFGNR.R	1908.09888	2	5.80E-06	0.95	4.75	-	1058.2
gi|9257257|ref|NP_059830.1|	WD repeat-containing protein 1 isoform 1 [Homo sapiens]			5.82E-06	0.87	10.21	3.80	66193.1
AHQ-10-6, 4873 - 4952	K.VVTVFSVADGYSENNVFYGHHAK.I	2541.75861	3	5.82E-06	0.87	4.15	-	659.0
gi|30158844|ref|XP_292513.2|	similar to KIAA1879 protein [Homo sapiens]			6.14E-06	1.73	20.23	1.20	203894.8
AHQ-10-7, 3329	K.AVDSLVPIGR.G	1027.19957	2	9.87E-06	0.80	2.83	-	685.3
AHQ-10-7, 4034	K.TSIAIDTIINQK.H	1317.51378	2	6.14E-06	0.93	4.51	-	1022.4
gi|5174727|ref|NP_005989.1|	chaperonin containing TCP1, subunit 3 (gamma); TCP1 (t-complex-1) ring			6.14E-06	0.93	10.20	2.00	60330.4
AHQ-10-6, 3789	R.AVAQALEVIPR.T	1167.38326	2	6.14E-06	0.93	4.04	-	1283.3
gi|7705296|ref|NP_057271.1|	bridging integrator 2; bridging integrator-2; breast cancer associated			6.87E-06	3.36	40.24	11.30	61746.8
AHQ-10-5, 5712 - 5755	K.AIVWNNDLLWEDYEEK.L	2038.20157	2	5.65E-04	0.84	3.23	-	863.4
AHQ-10-7, 6157 - 6164	R.IGCYVTIFQNISNLR.D	1800.07167	2	8.19E-06	0.93	4.76	-	851.0
AHQ-10-5, 6241 - 6249	R.IGCYVTIFQNISNLR.D	1800.07167	2	1.55E-04	0.82	3.82	-	647.2
AHQ-10-7, 4073	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	6.87E-06	0.65	2.92	-	442.7
AHQ-10-5, 4185	R.TATVSSPLTSPTSPSTLSLK.S	1976.21467	2	9.09E-06	0.75	3.36	-	596.3
AHQ-10-5, 4445 - 4453	R.TM*EIYVAQFSEIK.E	1575.80793	2	6.60E-05	0.93	4.10	-	933.8
gi|29740132|ref|XP_299177.1|	hypothetical protein XP_299177 [Homo sapiens]			7.09E-06	0.55	10.17	2.70	114488.9
AHQ-10-3, 4919	R.RCHEEKLPLSAGTASHKGQASAQPITPR.Q	3030.36879	3	7.09E-06	0.55	3.44	-	366.2
gi|27481323|ref|XP_208234.1|	similar to unactive progesterone receptor, 23 kD; likely ortholog of m			7.15E-06	0.90	10.14	8.10	18694.3
AHQ-10-11, 4320	K.LTFSCLGGSDNFK.H	1447.59493	2	7.15E-06	0.90	2.88	-	1049.7
gi|4504391|ref|NP_000179.1|	hexokinase 1 isoform HKI; brain form hexokinase [Homo sapiens]			7.22E-06	1.73	20.22	3.50	102502.4
AHQ-10-4, 3381	K.GAALITAVGVR.L	1028.23070	2	7.22E-06	0.97	3.97	-	2311.0
AHQ-10-4, 5624	R.TPDGTENGDFLALDLGGTNFR.V	2211.33051	2	3.94E-05	0.76	3.14	-	880.1
gi|7706675|ref|NP_057661.1|	RAB6B, member RAS oncogene family; small GTPase RAB6B [Homo sapiens] [M			7.40E-06	2.64	30.20	16.30	23461.5
AHQ-10-11, 4554	R.GSDVIIMLVGNK.T	1246.50220	2	7.40E-06	0.95	4.01	-	1856.6
AHQ-10-13-, 3524	R.LQLWDTAGQER.F	1317.43243	2	8.74E-05	0.78	3.03	-	592.4
AHQ-10-11, 3571 - 3628	K.LVFLGEQSVGK.T	1177.37492	2	1.15E-04	0.90	3.29	-	998.2
gi|7657431|ref|NP_055205.1|	EBNA-2 co-activator (100kD) [Homo sapiens]			7.61E-06	0.80	10.18	2.40	99689.7
AHQ-10-5, 5939	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	7.88E-05	0.75	3.23	-	266.0
AHQ-10-4, 5952	R.NLPGLVQEGEPFSEEATLFTK.E	2307.54125	2	7.61E-06	0.80	3.70	-	321.3
gi|4757712|ref|NP_004026.1|	acyl-Coenzyme A oxidase isoform a; acyl-coenzyme A oxidase 1 [Homo sapi			7.62E-06	1.31	20.19	5.80	74745.4
AHQ-10-6, 5839	R.INEGIGQGDLSELPELHALTAGLK.A	2476.76782	3	7.62E-06	0.85	3.87	-	706.3
AHQ-10-6, 5835	R.YDGNVYENLFEWAK.N	1748.87212	2	7.52E-05	0.46	2.64	-	279.7
gi|21614544|ref|NP_002955.2|	S100 calcium-binding protein A8; cystic fibrosis antigen; calgranulin			7.75E-06	0.87	10.15	11.80	10834.4
AHQ-10-14-, 3677	K.ALNSIIDVYHK.Y	1273.46270	2	7.75E-06	0.87	3.07	-	649.7
gi|9966825|ref|NP_065089.1|	HEF like Protein [Homo sapiens]			8.00E-06	0.96	10.26	2.80	86696.2
AHQ-10-13-, 4154	K.AISAFHGSLSSSQPAEIITQSK.L	2260.48935	2	8.00E-06	0.96	5.14	-	1175.0
gi|4557435|ref|NP_001242.1|	CD68 antigen; Macrophage antigen CD68 (microsialin); macrosialin; scave			8.01E-06	0.94	10.24	6.20	37408.0
AHQ-10-5, 4520	R.LQAAQLPHTGVFGQSFSCPSDR.S	2405.63153	3	8.01E-06	0.94	4.72	-	1176.1
gi|5453607|ref|NP_006420.1|	chaperonin containing TCP1, subunit 7 (eta); chaperonin containing t-co			8.52E-06	1.84	20.21	6.60	59366.3
AHQ-10-7, 4805	K.LPIGDVATQYFADR.D	1566.73935	2	3.68E-05	0.93	3.43	-	1042.0
AHQ-10-7, 6281	K.SQDAEVGDGTTSVTLLAAEFLK.Q	2253.44875	2	8.52E-06	0.91	4.24	-	729.4
gi|27480104|ref|XP_208215.1|	similar to triosephosphate isomerase 1 [Homo sapiens]			8.67E-06	3.01	40.19	22.50	26942.6
AHQ-10-10, 3026	R.HVFGESDELIGQK.V	1459.58565	2	6.93E-04	0.80	3.05	-	453.7
AHQ-10-10, 2152 - 2170	K.SNVSDAVAQSTR.I	1235.28659	2	8.67E-06	0.94	3.74	-	1775.6
AHQ-10-11, 4128	K.VTNGAFTGEISPGMIK.D	1622.86786	2	1.76E-04	0.67	2.51	-	704.4
AHQ-10-11, 5106	K.VVLAYEPVWAIGTGK.T	1603.88587	2	1.02E-05	0.61	2.66	-	443.8
gi|4502011|ref|NP_000467.1|	adenylate kinase 1 [Homo sapiens]			8.67E-06	0.80	10.18	10.30	21634.7
AHQ-10-11, 5007	R.IGQPTLLLYVDAGPETM*TQR.L	2220.53174	2	8.67E-06	0.80	3.31	-	677.9
gi|23510338|ref|NP_003325.2|	ubiquitin-activating enzyme E1; A1S9T and BN75 temperature sensitivity			9.58E-06	2.50	30.18	4.60	117848.1
AHQ-10-4, 4472	R.ALPAVQQNNLDEDLIR.K	1810.00167	2	9.58E-06	0.69	3.17	-	342.1

<table>
<tr><td>AHQ-10-4, 5505</td><td>R.NEEDAAELVALAQAVNAR.A</td><td>1885.02541</td><td>2</td><td>8.00E-04</td><td>0.92</td><td>3.64</td><td>-</td><td>1492.1</td></tr>
<tr><td>AHQ-10-4, 3955</td><td>R.YDGQVAVFGSDLQEK.L</td><td>1656.77453</td><td>2</td><td>3.18E-05</td><td>0.90</td><td>3.20</td><td>-</td><td>1105.8</td></tr>
<tr><td colspan="4">gi|4759044|ref|NP_004841.1| Rho-associated, coiled-coil containing protein kinase 2 [Homo sapiens]</td><td>9.76E-06</td><td>1.79</td><td>20.20</td><td>1.90</td><td>160883.4</td></tr>
<tr><td>AHQ-10-3, 5547</td><td>K.ELQDQLEAEQYFSTLYK.T</td><td>2106.27421</td><td>2</td><td>1.63E-05</td><td>0.90</td><td>3.96</td><td>-</td><td>636.3</td></tr>
<tr><td>AHQ-10-3, 5591</td><td>K.NLICAFLTDR.E</td><td>1224.41173</td><td>2</td><td>9.76E-06</td><td>0.89</td><td>3.32</td><td>-</td><td>889.0</td></tr>
<tr><td colspan="4">gi|29568111|ref|NP_006088.2| myosin, light polypeptide 9, regulatory; myosin regulatory light chain</td><td>9.81E-06</td><td>1.68</td><td>20.17</td><td>6.40</td><td>19827.1</td></tr>
<tr><td>AHQ-10-13-, 2837</td><td>R.FTDEEVDEM*YR.E</td><td>1450.50949</td><td>2</td><td>2.67E-05</td><td>0.93</td><td>3.37</td><td>-</td><td>1343.2</td></tr>
<tr><td>AHQ-10-13-, 3897</td><td>K.GNFNYVEFTR.I</td><td>1247.34066</td><td>2</td><td>1.66E-05</td><td>0.46</td><td>2.60</td><td>-</td><td>360.0</td></tr>
<tr><td>AHQ-10-14-, 3877</td><td>K.GNFNYVEFTR.I</td><td>1247.34066</td><td>2</td><td>9.81E-06</td><td>0.75</td><td>2.73</td><td>-</td><td>549.1</td></tr>
<tr><td>AHQ-10-11, 3782</td><td>K.GNFNYVEFTR.I</td><td>1247.34066</td><td>2</td><td>4.45E-05</td><td>0.85</td><td>2.80</td><td>-</td><td>868.9</td></tr>
<tr><td colspan="4">gi|30153966|ref|XP_293932.2| similar to hypothetical protein BC013073 [Homo sapiens]</td><td>9.83E-06</td><td>0.48</td><td>10.19</td><td>9.00</td><td>21711.3</td></tr>
<tr><td>AHQ-10-3, 3602</td><td>R.MIFTLFTINVSKDIRHH</td><td>2073.44997</td><td>3</td><td>9.83E-06</td><td>0.48</td><td>3.04</td><td>-</td><td>626.7</td></tr>
<tr><td>AHQ-10-3, 3957 - 3959</td><td>R.MIFTLFTINVSKDIRHH</td><td>2073.44997</td><td>3</td><td>8.92E-04</td><td>0.73</td><td>3.70</td><td>-</td><td>745.5</td></tr>
<tr><td>AHQ-10-4, 4003 - 4065</td><td>R.MIFTLFTINVSKDIRHH</td><td>2073.44997</td><td>2</td><td>1.58E-04</td><td>0.44</td><td>2.93</td><td>-</td><td>405.2</td></tr>
<tr><td>AHQ-10-8, 3955</td><td>R.MIFTLFTINVSKDIRHH</td><td>2073.44997</td><td>2</td><td>8.30E-04</td><td>0.43</td><td>3.04</td><td>-</td><td>466.1</td></tr>
<tr><td>AHQ-10-2, 4023</td><td>R.MIFTLFTINVSKDIRHH</td><td>2073.44997</td><td>3</td><td>5.34E-04</td><td>0.82</td><td>3.72</td><td>-</td><td>983.5</td></tr>
<tr><td colspan="4">gi|4506713|ref|NP_002945.1| ubiquitin and ribosomal protein S27a precursor; ubiquitin carboxyl exte</td><td>1.03E-05</td><td>0.29</td><td>10.17</td><td>10.30</td><td>17964.8</td></tr>
<tr><td>AHQ-10-14, 4944</td><td>K.TITLEVEPSDTIENVK.A</td><td>1788.97431</td><td>2</td><td>1.03E-05</td><td>0.29</td><td>2.63</td><td>-</td><td>285.9</td></tr>
<tr><td colspan="4">gi|8922804|ref|NP_060760.1| hypothetical protein FLJ10983 [Homo sapiens]</td><td>1.03E-05</td><td>1.62</td><td>20.16</td><td>3.40</td><td>68268.9</td></tr>
<tr><td>AHQ-10-6, 2409</td><td>R.IVLANDPDADR.L</td><td>1199.29585</td><td>2</td><td>1.07E-04</td><td>0.87</td><td>3.12</td><td>-</td><td>1107.4</td></tr>
<tr><td>AHQ-10-6, 3471</td><td>R.LDQETAQWLR.W</td><td>1260.38088</td><td>2</td><td>1.03E-05</td><td>0.74</td><td>2.75</td><td>-</td><td>791.7</td></tr>
<tr><td colspan="4">gi|14149680|ref|NP_056107.1| KIAA0747 protein [Homo sapiens]</td><td>1.07E-05</td><td>0.85</td><td>10.16</td><td>1.20</td><td>122855.6</td></tr>
<tr><td>AHQ-10-4, 5732</td><td>R.ALTLGALTLPLAR.L</td><td>1310.61075</td><td>2</td><td>1.07E-05</td><td>0.85</td><td>2.88</td><td>-</td><td>980.4</td></tr>
<tr><td colspan="4">gi|4757766|ref|NP_004299.1| Rho GTPase activating protein 1; RhoGAP; p50rhoGAP; CDC42 GTPase-activa</td><td>1.08E-05</td><td>2.20</td><td>30.18</td><td>11.40</td><td>50435.4</td></tr>
<tr><td>AHQ-10-7, 5630</td><td>K.FLLDHQGELFPSPDPSGL</td><td>1970.17037</td><td>2</td><td>1.08E-05</td><td>0.67</td><td>3.00</td><td>-</td><td>472.9</td></tr>
<tr><td>AHQ-10-7, 4037 - 4106</td><td>K.NPEQEPIPIVLR.E</td><td>1405.62426</td><td>2</td><td>3.24E-05</td><td>0.67</td><td>2.84</td><td>-</td><td>520.1</td></tr>
<tr><td>AHQ-10-7, 5710</td><td>R.VPATLQVLQTLPEENYQVLR.F</td><td>2312.65053</td><td>2</td><td>4.38E-05</td><td>0.87</td><td>3.62</td><td>-</td><td>800.4</td></tr>
<tr><td colspan="4">gi|9910542|ref|NP_064535.1| SAR1a gene homolog 1; SAR1 protein [Homo sapiens]</td><td>1.14E-05</td><td>0.80</td><td>10.18</td><td>11.60</td><td>22366.6</td></tr>
<tr><td>AHQ-10-11, 6114</td><td>K.VELNALM*TDETISNVPILILGNK.I</td><td>2514.92088</td><td>3</td><td>1.14E-05</td><td>0.80</td><td>3.41</td><td>-</td><td>703.5</td></tr>
<tr><td colspan="4">gi|24308149|ref|NP_060035.1| hypothetical protein DKFZp434F2322 [Homo sapiens]</td><td>1.14E-05</td><td>0.65</td><td>10.14</td><td>2.00</td><td>61404.2</td></tr>
<tr><td>AHQ-10-4, 5595 - 5603</td><td>K.PSGVHLKLVLR.F</td><td>1219.50454</td><td>2</td><td>1.14E-05</td><td>0.65</td><td>2.85</td><td>-</td><td>655.6</td></tr>
<tr><td colspan="4">gi|9845297|ref|NP_063940.1| second mitochondria-derived activator of caspase isoform Smac-alpha, pr</td><td>1.16E-05</td><td>0.91</td><td>10.18</td><td>4.20</td><td>27130.6</td></tr>
<tr><td>AHQ-10-11, 3259</td><td>K.LAEAQIEELR.Q</td><td>1172.31354</td><td>2</td><td>1.16E-05</td><td>0.91</td><td>3.52</td><td>-</td><td>1168.2</td></tr>
<tr><td colspan="4">gi|4757996|ref|NP_004060.1| adaptor-related protein complex 2, sigma 1 subunit isoform AP17; clathr</td><td>1.23E-05</td><td>0.94</td><td>10.21</td><td>10.60</td><td>17017.6</td></tr>
<tr><td>AHQ-10-13-, 5046</td><td>K.VYTVVDEM*FLAGEIR.E</td><td>1759.01650</td><td>2</td><td>1.23E-05</td><td>0.94</td><td>4.13</td><td>-</td><td>1144.1</td></tr>
<tr><td colspan="4">gi|4505813|ref|NP_003737.1| cytoplasmic dynein light polypeptide; dynein, cytoplasmic, light chain</td><td>1.24E-05</td><td>1.54</td><td>20.17</td><td>24.70</td><td>10365.8</td></tr>
<tr><td>AHQ-10-14-, 2441 - 2502</td><td>R.NFGSYVTHETK.H</td><td>1283.37131</td><td>2</td><td>1.24E-05</td><td>0.86</td><td>3.33</td><td>-</td><td>815.7</td></tr>
<tr><td>AHQ-10-14-, 3625</td><td>K.YNPTWHCIVGR.N</td><td>1404.57820</td><td>2</td><td>1.33E-05</td><td>0.68</td><td>2.61</td><td>-</td><td>370.3</td></tr>
<tr><td colspan="4">gi|4506353|ref|NP_002854.1| phosphorylase, glycogen; liver (Hers disease, glycogen storage disease</td><td>1.34E-05</td><td>0.93</td><td>10.17</td><td>1.70</td><td>97147.8</td></tr>
<tr><td>AHQ-10-5, 5215</td><td>K.LVIDQIDNGFFSPK.Q</td><td>1593.80471</td><td>2</td><td>1.34E-05</td><td>0.93</td><td>3.37</td><td>-</td><td>1391.3</td></tr>
<tr><td colspan="4">gi|20543399|ref|XP_116396.1| similar to peptidylprolyl isomerase A (cyclophilin A) [Homo sapiens] [</td><td>1.42E-05</td><td>0.80</td><td>10.14</td><td>5.00</td><td>19852.7</td></tr>
<tr><td>AHQ-10-12, 4361</td><td>R.VSFKLFADK.F</td><td>1055.25138</td><td>2</td><td>1.42E-05</td><td>0.80</td><td>2.78</td><td>-</td><td>908.7</td></tr>
<tr><td colspan="4">gi|25306267|ref|NP_001700.2| brain-derived neurotrophic factor isoform a preproprotein [Homo sapien</td><td>1.44E-05</td><td>0.91</td><td>10.18</td><td>6.10</td><td>27817.8</td></tr>
<tr><td>AHQ-10-13-, 3633</td><td>K.TAVDMSGGTVTVLEK.V</td><td>1508.71993</td><td>2</td><td>1.44E-05</td><td>0.91</td><td>3.69</td><td>-</td><td>1138.3</td></tr>
<tr><td colspan="4">gi|4507789|ref|NP_003338.1| ubiquitin-conjugating enzyme E2L 3 [Homo sapiens]</td><td>1.49E-05</td><td>0.91</td><td>10.18</td><td>9.70</td><td>17861.5</td></tr>
<tr><td>AHQ-10-12, 5014</td><td>R.IEINFPAEYPFKPPK.I</td><td>1791.08155</td><td>2</td><td>1.49E-05</td><td>0.91</td><td>3.67</td><td>-</td><td>960.8</td></tr>
<tr><td colspan="4">gi|4504077|ref|NP_000165.1| glycoprotein IX (platelet) [Homo sapiens]</td><td>1.51E-05</td><td>1.71</td><td>20.17</td><td>7.30</td><td>19046.0</td></tr>
<tr><td>AHQ-10-14-, 2820</td><td>R.CASPSLAAHGPLGR.L</td><td>1395.56962</td><td>2</td><td>2.04E-04</td><td>0.84</td><td>2.90</td><td>-</td><td>906.5</td></tr>
<tr><td>AHQ-10-12, 3553 - 3621</td><td>R.GHGLTALPALPAR.T</td><td>1274.49706</td><td>2</td><td>1.93E-04</td><td>0.79</td><td>2.54</td><td>-</td><td>654.0</td></tr>
<tr><td>AHQ-10-11, 3475</td><td>R.GHGLTALPALPAR.T</td><td>1274.49706</td><td>3</td><td>1.51E-05</td><td>0.88</td><td>3.39</td><td>-</td><td>1049.5</td></tr>
<tr><td>AHQ-10-11, 3471</td><td>R.GHGLTALPALPAR.T</td><td>1274.49706</td><td>2</td><td>1.04E-04</td><td>0.92</td><td>3.29</td><td>-</td><td>813.7</td></tr>
<tr><td colspan="4">gi|9966867|ref|NP_065123.1| eIF-5A2 protein; eIF5AII [Homo sapiens]</td><td>1.58E-05</td><td>0.94</td><td>10.19</td><td>7.80</td><td>16793.1</td></tr>
<tr><td>AHQ-10-12, 4693 - 4696</td><td>K.VHLVGIDIFTGK.K</td><td>1299.54329</td><td>2</td><td>1.58E-05</td><td>0.94</td><td>3.72</td><td>-</td><td>1157.0</td></tr>
<tr><td colspan="4">gi|4758988|ref|NP_004152.1| RAB1A, member RAS oncogene family; RAB1, member RAS oncogene family [Ho</td><td>1.59E-05</td><td>1.52</td><td>20.17</td><td>17.10</td><td>22677.6</td></tr>
<tr><td>AHQ-10-11, 5711 - 5756</td><td>K.EFADSLGIPFLETSAK.N</td><td>1725.91990</td><td>2</td><td>2.09E-05</td><td>0.66</td><td>3.09</td><td>-</td><td>380.3</td></tr>
<tr><td>AHQ-10-14-, 5569</td><td>R.FADDTYTESYISTIGVDFK.I</td><td>2173.31742</td><td>2</td><td>6.93E-04</td><td>0.76</td><td>3.21</td><td>-</td><td>436.8</td></tr>
<tr><td>AHQ-10-11, 5274</td><td>R.FADDTYTESYISTIGVDFK.I</td><td>2173.31742</td><td>2</td><td>1.59E-05</td><td>0.86</td><td>3.38</td><td>-</td><td>874.6</td></tr>
<tr><td colspan="4">gi|4502171|ref|NP_000476.1| adenine phosphoribosyltransferase; AMP pyrophosphorylase; AMP diphospho</td><td>1.60E-05</td><td>0.95</td><td>10.19</td><td>5.60</td><td>19607.6</td></tr>
<tr><td>AHQ-10-11, 3543 - 3563</td><td>R.IDYIAGLDSR.G</td><td>1123.24098</td><td>2</td><td>1.60E-05</td><td>0.95</td><td>3.73</td><td>-</td><td>1475.3</td></tr>
<tr><td colspan="4">gi|6996010|ref|NP_002038.1| glycyl-tRNA synthetase; GlyRS; glycine tRNA ligase [Homo sapiens]</td><td>1.62E-05</td><td>0.86</td><td>10.17</td><td>1.90</td><td>77530.3</td></tr>
<tr><td>AHQ-10-5, 6207</td><td>R.TFFSFPAVVAPFK.C</td><td>1458.72722</td><td>2</td><td>1.62E-05</td><td>0.86</td><td>3.37</td><td>-</td><td>508.0</td></tr>
<tr><td colspan="4">gi|20270259|ref|NP_620061.1| phosphoglycerate kinase 2; phosphoglycerate kinase 1, pseudogene 2 [Ho</td><td>1.62E-05</td><td>0.92</td><td>10.17</td><td>3.60</td><td>44895.0</td></tr>
<tr><td>AHQ-10-8, 3486</td><td>K.LGDVYVNDAFGTAHR.A</td><td>1635.76178</td><td>2</td><td>1.62E-05</td><td>0.92</td><td>3.47</td><td>-</td><td>1058.5</td></tr>
<tr><td colspan="4">gi|4826659|ref|NP_004921.1| F-actin capping protein beta subunit; Cap Z [Homo sapiens]</td><td>1.70E-05</td><td>1.38</td><td>20.16</td><td>8.80</td><td>30628.5</td></tr>
<tr><td>AHQ-10-9, 2819</td><td>K.SGSGTMNLGGSLTR.Q</td><td>1338.47345</td><td>2</td><td>3.08E-04</td><td>0.65</td><td>2.58</td><td>-</td><td>605.9</td></tr>
<tr><td>AHQ-10-9, 3492</td><td>R.STLNEIYFGK.T</td><td>1172.31200</td><td>2</td><td>1.70E-05</td><td>0.73</td><td>2.75</td><td>-</td><td>592.5</td></tr>
<tr><td colspan="4">gi|4757714|ref|NP_004291.1| acid phosphatase 1 isoform c; acid phosphatase of erythrocyte; red cell</td><td>1.76E-05</td><td>0.89</td><td>10.18</td><td>5.70</td><td>18042.4</td></tr>
<tr><td>AHQ-10-11, 3339</td><td>R.SPIAEAVFR.K</td><td>990.13779</td><td>2</td><td>1.76E-05</td><td>0.89</td><td>3.29</td><td>-</td><td>723.6</td></tr>
<tr><td colspan="4">gi|29732170|ref|XP_291550.1| similar to Heat shock protein HSP 90-alpha (HSP 86) [Homo sapiens] [MA</td><td>1.80E-05</td><td>0.96</td><td>10.26</td><td>12.70</td><td>13262.9</td></tr>
<tr><td>AHQ-10-5, 4128</td><td>K.HLEINPDHSIIETLR.Q</td><td>1787.99770</td><td>3</td><td>1.80E-05</td><td>0.96</td><td>5.12</td><td>-</td><td>1709.7</td></tr>
<tr><td colspan="4">gi|4505093|ref|NP_000889.1| monoamine oxidase B [Homo sapiens]</td><td>1.81E-05</td><td>0.58</td><td>10.14</td><td>3.10</td><td>58762.6</td></tr>
<tr><td>AHQ-10-7, 4410</td><td>K.VLGSLEALEPVHYEEK.N</td><td>1814.02869</td><td>2</td><td>1.81E-05</td><td>0.58</td><td>2.80</td><td>-</td><td>456.4</td></tr>
<tr><td colspan="4">gi|29742410|ref|XP_291183.1| similar to TREM-like transcript 1 [Homo sapiens]</td><td>1.83E-05</td><td>0.90</td><td>10.18</td><td>0.00</td><td>32678.3</td></tr>
<tr><td>AHQ-10-13-, 4220</td><td>R.FLPEGCQPLVSSAVDR.R</td><td>1776.99174</td><td>2</td><td>1.83E-05</td><td>0.90</td><td>3.57</td><td>-</td><td>683.5</td></tr>
<tr><td colspan="4">gi|18558709|ref|XP_087572.1| similar to bA291L22.2 (similar to CDC10 (cell division cycle 10, S. ce</td><td>1.87E-05</td><td>0.94</td><td>10.18</td><td>10.90</td><td>9988.5</td></tr>
<tr><td>AHQ-10-8, 3165</td><td>K.FEDYLNAESR.V</td><td>1244.29194</td><td>2</td><td>1.87E-05</td><td>0.94</td><td>3.64</td><td>-</td><td>1339.3</td></tr>
<tr><td colspan="4">gi|5031595|ref|NP_005709.1| actin related protein 2/3 complex subunit 4; Arp2/3 protein complex sub</td><td>1.97E-05</td><td>1.89</td><td>20.17</td><td>11.30</td><td>19666.9</td></tr>
<tr><td>AHQ-10-11, 4292</td><td>R.AENFFILR.R</td><td>1010.17070</td><td>2</td><td>3.50E-04</td><td>0.96</td><td>3.43</td><td>-</td><td>1961.3</td></tr>
<tr><td>AHQ-10-11, 3250</td><td>K.VLIEGSINSVR.V</td><td>1187.37134</td><td>2</td><td>1.97E-05</td><td>0.94</td><td>3.08</td><td>-</td><td>1561.8</td></tr>
<tr><td colspan="4">gi|6005786|ref|NP_009214.1| monoglyceride lipase; lysophospholipase-like [Homo sapiens]</td><td>2.00E-05</td><td>0.77</td><td>10.14</td><td>4.50</td><td>34292.3</td></tr>
<tr><td>AHQ-10-14-, 5729 - 5744</td><td>K.LTVPFLLLQGSADR.L</td><td>1530.79329</td><td>2</td><td>2.00E-05</td><td>0.77</td><td>2.88</td><td>-</td><td>658.5</td></tr>
<tr><td colspan="4">gi|20373153|ref|NP_115997.4| myosin XVIIIB; myosin 18B [Homo sapiens]</td><td>2.01E-05</td><td>0.89</td><td>10.22</td><td>0.70</td><td>285231.7</td></tr>
<tr><td>AHQ-10-8, 6307</td><td>R.ITAAQLQTMLLEKSRVAR.Q</td><td>2030.42494</td><td>2</td><td>2.01E-05</td><td>0.89</td><td>4.33</td><td>-</td><td>1150.2</td></tr>
<tr><td colspan="4">gi|18201905|ref|NP_000166.2| glucose phosphate isomerase; neuroleukin; glucose-6-phosphate isomeras</td><td>2.03E-05</td><td>1.56</td><td>20.22</td><td>7.90</td><td>63146.7</td></tr>
<tr><td>AHQ-10-7, 4790</td><td>K.KIEPELDGSAQVTSHDASTNGLINFIK.Q</td><td>2886.16347</td><td>3</td><td>4.53E-04</td><td>0.66</td><td>3.10</td><td>-</td><td>724.3</td></tr>
<tr><td>AHQ-10-7, 5664</td><td>K.TLAQLNPESSLFIIASK.T</td><td>1833.11828</td><td>2</td><td>2.03E-05</td><td>0.91</td><td>4.32</td><td>-</td><td>480.5</td></tr>
<tr><td colspan="4">gi|10880136|ref|NP_004032.2| arrestin beta 1 isoform A [Homo sapiens]</td><td>2.18E-05</td><td>0.94</td><td>10.24</td><td>4.80</td><td>47065.3</td></tr>
<tr><td>AHQ-10-7, 4129</td><td>K.CPVAMEEADDTVAPSSTFCK.V</td><td>2218.42489</td><td>2</td><td>2.18E-05</td><td>0.94</td><td>4.82</td><td>-</td><td>769.9</td></tr>
<tr><td colspan="4">gi|29736026|ref|XP_085123.3| similar to Ras-related protein Rab-15 [Homo sapiens]</td><td>2.24E-05</td><td>0.90</td><td>10.20</td><td>5.30</td><td>23517.8</td></tr>
<tr><td>AHQ-10-11, 3414 - 3415</td><td>R.IQIWDTAGQER.Y</td><td>1317.43243</td><td>2</td><td>2.24E-05</td><td>0.90</td><td>4.04</td><td>-</td><td>781.6</td></tr>
<tr><td colspan="4">gi|11496885|ref|NP_005442.2| enigma protein; LIM domain protein [Homo sapiens]</td><td>2.28E-05</td><td>0.89</td><td>10.16</td><td>2.60</td><td>49844.4</td></tr>
<tr><td>AHQ-10-13-, 4693 - 4746</td><td>K.VVLEGPAPWGFR.L</td><td>1328.54318</td><td>2</td><td>2.28E-05</td><td>0.89</td><td>3.16</td><td>-</td><td>973.5</td></tr>
<tr><td colspan="4">gi|5031569|ref|NP_005727.1| ARP1 actin-related protein 1 homolog A, centractin alpha; ARP1 (actin-r</td><td>2.34E-05</td><td>0.91</td><td>10.19</td><td>4.30</td><td>42613.4</td></tr>
<tr><td>AHQ-10-8, 6266</td><td>R.TLFSNIVLSGGSTLFK.G</td><td>1684.95729</td><td>2</td><td>2.34E-05</td><td>0.91</td><td>3.67</td><td>-</td><td>908.1</td></tr>
<tr><td colspan="4">gi|14210536|ref|NP_115914.1| similar to chicken tubulin beta 5 [Homo sapiens]</td><td>2.45E-05</td><td>0.65</td><td>10.18</td><td>3.80</td><td>49856.8</td></tr>
<tr><td>AHQ-10-13-, 5857 - 5913</td><td>K.M*ASTFIGNSTAIQELFK.R</td><td>1875.13550</td><td>2</td><td>2.45E-05</td><td>0.65</td><td>3.53</td><td>-</td><td>662.0</td></tr>
<tr><td>AHQ-10-7, 5686</td><td>K.M*ASTFIGNSTAIQELFK.R</td><td>1875.13550</td><td>2</td><td>2.96E-05</td><td>0.72</td><td>3.53</td><td>-</td><td>758.9</td></tr>
<tr><td colspan="4">gi|18426915|ref|NP_004386.2| drebrin 1 isoform a; drebrin E; drebrin-1; drebrin E2 [Homo sapiens] [</td><td>2.46E-05</td><td>0.68</td><td>10.16</td><td>2.80</td><td>71438.9</td></tr>
<tr><td>AHQ-10-8, 2782</td><td>R.SPSDSSTASTPVAEQIER.A</td><td>1862.93023</td><td>2</td><td>2.46E-05</td><td>0.68</td><td>3.23</td><td>-</td><td>303.8</td></tr>
<tr><td colspan="4">gi|4503901|ref|NP_003765.1| polypeptide N-acetylgalactosaminyltransferase 4; UDP-N-acetyl-alpha-D-g</td><td>2.49E-05</td><td>0.61</td><td>10.18</td><td>3.60</td><td>66775.7</td></tr>
<tr><td>AHQ-10-5, 4552</td><td>R.ISRIDPIRSPTM*AGGLFAVSK.K</td><td>2233.62002</td><td>2</td><td>2.49E-05</td><td>0.61</td><td>3.53</td><td>-</td><td>400.8</td></tr>
<tr><td colspan="4">gi|5902016|ref|NP_008939.1| reticulon 4; neuroendocrine-specific protein C like (foocen) [Homo sapi</td><td>2.54E-05</td><td>0.85</td><td>10.18</td><td>8.00</td><td>22395.3</td></tr>
<tr><td>AHQ-10-1, 5229 - 5231</td><td>R.AYLESEVAISEELVQK.Y</td><td>1809.00722</td><td>2</td><td>2.54E-05</td><td>0.85</td><td>3.51</td><td>-</td><td>964.9</td></tr>
<tr><td colspan="4">gi|5454090|ref|NP_006271.1| signal sequence receptor, delta; translocon-associated protein delta [H</td><td>2.62E-05</td><td>0.81</td><td>10.13</td><td>6.40</td><td>18998.5</td></tr>
<tr><td>AHQ-10-12, 4625</td><td>R.FFDEESYSLLR.K</td><td>1406.52121</td><td>2</td><td>2.62E-05</td><td>0.81</td><td>2.67</td><td>-</td><td>675.6</td></tr>
<tr><td colspan="4">gi|4505621|ref|NP_002558.1| prostatic binding protein; phosphatidylethanolamine binding protein [Ho</td><td>2.70E-05</td><td>0.96</td><td>10.22</td><td>10.70</td><td>21056.6</td></tr>
<tr><td>AHQ-10-11, 4199</td><td>K.GNDISSGTVLSDYVGSGPPK.G</td><td>1951.08062</td><td>2</td><td>2.70E-05</td><td>0.96</td><td>4.45</td><td>-</td><td>1409.9</td></tr>
</table>

gi|16753212|ref|NP_003921.2| src family associated phosphoprotein 2; src kinase-associated phosphop				2.71E-05	0.83	10.14	2.80	41216.5
AHQ-10-13-, 3420	K.RGDVIYILSK.E	1164.37938	2	2.71E-05	0.83	2.79	-	930.0
gi|4757900|ref|NP_004334.1| calreticulin precursor; Sicca syndrome antigen A (autoantigen Ro; calre				2.75E-05	2.39	30.21	11.00	48141.1
AHQ-10-7, 4898 - 4969	K.IDNSQVESGSLEDDWDFLPPKK.I	2520.68965	3	2.75E-05	0.76	4.12	-	674.1
AHQ-10-7, 5136	K.KPEDWDEEMDGEWEPPVIQNPEYK.G	2962.14926	3	3.36E-05	0.88	4.20	-	729.3
AHQ-10-7, 4621	K.KPEDWDEEM*DGEWEPPVIQNPEYK.G	2978.14866	3	3.36E-04	0.75	3.55	-	528.8
gi|4557890|ref|NP_000415.1| keratin 5; Keratin-5; 58 kda cytokeratin; keratin, type II cytoskeletal				2.76E-05	0.84	10.16	1.70	62461.1
AHQ-10-5, 3464	K.WTLLQEQGTK.T	1204.35723	2	2.76E-05	0.84	3.23	-	951.8
gi|29743324|ref|XP_293276.1| similar to Heat shock 27 kDa protein (HSP 27) (Stress-responsive prote				2.80E-05	0.89	10.28	16.00	21244.7
AHQ-10-13, 5233 - 5288	R.KYTLPPGVDPTKVSSSLSPEGTLTVEAPM*PK.L	3244.70168	3	2.80E-05	0.89	5.55	-	934.3
gi|4507909|ref|NP_000368.1| Wiskott-Aldrich syndrome protein; Wiskott-Aldrich syndrome (eczema-thro				2.92E-05	0.82	10.16	3.00	52912.3
AHQ-10-7, 2981 - 3052	R.AGISEAQLTDAETSK.L	1521.60892	2	2.92E-05	0.82	3.20	-	744.3
gi|5032009|ref|NP_005600.1| glycogen phosphorylase; phosphorylase, glycogen, muscle; myophosphoryla				2.97E-05	0.83	10.15	1.00	97091.4
AHQ-10-5, 3905	R.VIFLENYR.V	1054.22348	2	2.97E-05	0.83	2.92	-	558.5
gi|4502695|ref|NP_001779.1| cell division cycle 10; cell division cycle 10 (homolog to CDC10 of S.c				3.32E-05	1.36	20.17	9.60	48786.6
AHQ-10-8, 3917	K.IYEFPETDDEEENKLVK.K	2099.23685	2	3.32E-05	0.61	2.98	-	210.4
AHQ-10-8, 6089 - 6169	K.STLINSLFLTDLYSPEYPGPSHR.I	2608.88640	3	3.70E-05	0.74	3.37	-	553.6
gi|5031597|ref|NP_005710.1| actin related protein 2/3 complex subunit 3; ARP2/3 protein complex sub				3.39E-05	1.60	20.20	13.50	20546.5
AHQ-10-11, 5979 - 5991	K.DTDIVDEAIYYFK.A	1592.72721	2	3.39E-05	0.95	4.04	-	1668.3
AHQ-10-14-, 6096 - 6098	K.DTDIVDEAIYYFK.A	1592.72721	2	5.09E-04	0.95	3.92	-	1297.6
AHQ-10-11, 4132	K.LIGNM*ALLPIR.S	1227.54522	2	2.64E-04	0.64	2.73	-	594.0
gi|4501867|ref|NP_001089.1| aconitase 2 [Homo sapiens]				3.40E-05	1.84	20.21	4.00	85424.8
AHQ-10-5, 6240	K.DINQEVYNFLATAGAK.Y	1754.92134	2	3.40E-05	0.92	4.11	-	792.8
AHQ-10-5, 3885	R.WVVIGDENYGEGSSR.E	1668.74540	2	1.14E-04	0.92	3.63	-	1109.3
gi|4506193|ref|NP_002784.1| proteasome beta 1 subunit; proteasome subunit HC5; proteasome component				3.40E-05	0.85	10.14	5.80	26489.2
AHQ-10-11, 3927	K.GAVYSFDPVGSYQR.D	1546.66500	2	3.40E-05	0.85	2.80	-	980.5
gi|15306356|ref|XP_035638.2| similar to interleukin 25; lymphocyte antigen 6 complex, locus E ligan				3.44E-05	0.93	10.15	5.20	18795.1
AHQ-10-13-, 4580	K.SYLYFTQFK.A	1197.36315	2	3.44E-05	0.93	2.96	-	1274.0
gi|4504487|ref|NP_002143.1| histidine-rich calcium-binding protein precursor; histidine-rich calciu				3.56E-05	0.36	10.14	2.60	80243.1
AHQ-10-14-, 4449	R.NNSTGVAGLSEEASAELR.H	1805.88191	2	3.56E-05	0.36	2.77	-	605.6
gi|29788766|ref|NP_064424.2| tubulin, beta polypeptide 4, member Q [Homo sapiens]				3.65E-05	1.14	20.18	3.50	48377.2
AHQ-10-14-, 3865	R.AVLVDLEPGTM*DSVR.S	1618.83435	2	4.09E-05	0.66	2.87	-	436.8
AHQ-10-14-, 4441	R.AVLVDLEPGTMDSVR.S	1602.83495	2	8.55E-04	0.76	3.69	-	429.5
AHQ-10-7, 4364	R.AVLVDLEPGTMDSVR.S	1602.83495	2	3.65E-05	0.48	3.30	-	332.8
gi|30157216|ref|XP_292133.2| similar to genethonin 1 [Homo sapiens]				3.70E-05	0.57	10.19	4.50	39693.8
AHQ-10-13-, 4285	K.TITLEVKPSDTIENVK.A	1788.03268	2	3.59E-04	0.35	2.63	-	383.9
AHQ-10-14-, 4280	K.TITLEVKPSDTIENVK.A	1788.03268	2	2.36E-04	0.73	3.83	-	513.8
AHQ-10-11, 4220	K.TITLEVKPSDTIENVK.A	1788.03268	2	3.70E-05	0.57	3.49	-	322.9
gi|4507149|ref|NP_000445.1| superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult				4.02E-05	0.93	10.18	13.00	15935.7
AHQ-10-11, 5002	K.AVCVLKGDGPVQGIINFEQK.E	2174.50602	3	4.02E-05	0.93	3.62	-	1559.2
gi|10835049|ref|NP_001655.1| ras homolog gene family, member A; Aplysia ras-related homolog 12; Rho				4.11E-05	0.93	10.19	6.20	21768.0
AHQ-10-10, 3670 - 3671	R.IGAFGYMECSAK.T	1335.53122	2	4.11E-05	0.93	3.89	-	972.5
gi|6005886|ref|NP_009200.1| syntaxin binding protein 3; syntaxin 4 binding protein [Homo sapiens] [				4.23E-05	0.94	10.18	1.90	67573.7
AHQ-10-6, 3749	R.HIAVVLEEIPK.L	1248.49628	2	4.23E-05	0.94	3.68	-	1113.4
gi|4557241|ref|NP_001095.1| skeletal muscle specific actinin, alpha 3 [Homo sapiens]				4.25E-05	0.85	10.14	0.90	103293.7
AHQ-10-4, 3057	K.ALDFIASK.G	865.00867	2	4.25E-05	0.85	2.78	-	661.8
gi|19923483|ref|NP_057406.2| GTPase Rab14 [Homo sapiens]				4.28E-05	0.80	10.15	6.00	23896.8
AHQ-10-11, 3736	R.GAAGALM*VYDITR.R	1354.55759	2	4.28E-05	0.80	2.80	-	955.8
gi|14277700|ref|NP_001007.2| ribosomal protein S12; 40S ribosomal protein S12 [Homo sapiens]				4.36E-05	0.87	10.14	6.80	14514.9
AHQ-10-13-, 3938	K.LGEWVGLCK.I	1063.25197	2	4.36E-05	0.87	2.72	-	1046.9
gi|4506675|ref|NP_002941.1| ribophorin I [Homo sapiens]				4.37E-05	1.52	20.14	4.60	68569.0
AHQ-10-1, 5006	R.SEDLLDYGPFR.D	1312.40942	2	4.37E-05	0.82	2.83	-	1105.0
AHQ-10-1, 4225	K.VTAEVVLAHLGGGSTSR.A	1654.84968	2	2.39E-04	0.69	2.81	-	548.6
gi|14211867|ref|NP_115951.1| group XIII secreted phospholipase A2 [Homo sapiens]				4.60E-05	0.26	10.13	7.20	21587.6
AHQ-10-5, 3095	K.VPESMDLGIPAM*TK.C	1505.78265	2	4.60E-05	0.26	2.64	-	206.3
gi|17475428|ref|XP_062849.1| similar to Proteasome subunit alpha type 6 (Proteasome iota chain) (Ma				4.72E-05	0.71	10.13	4.80	30918.3
AHQ-10-10, 2950	K.AINQGGLTSVAVR.K	1286.46301	2	4.72E-05	0.71	2.50	-	695.1
gi|4758638|ref|NP_004896.1| peroxiredoxin 6; antioxidant protein 2; non-selenium glutathione peroxi				5.17E-05	1.50	20.17	11.60	25034.8
AHQ-10-10, 4843 - 4894	R.ELAILLGM*LDPAEKDEK.G	1902.19916	2	2.53E-04	0.61	3.00	-	374.5
AHQ-10-10, 4279 - 4335	K.LPFPIIDDR.N	1086.26548	2	5.17E-05	0.88	3.03	-	900.1
gi|5730118|ref|NP_006514.1| X-prolyl aminopeptidase (aminopeptidase P) 1, soluble; X-prolyl aminope				5.19E-05	1.67	20.17	4.30	69858.4
AHQ-10-6, 5760	R.GSLTFEPLTLVPIQTK.M	1745.05263	2	6.08E-04	0.75	2.84	-	642.7
AHQ-10-6, 4133	R.IENVVLVVPVK.T	1209.50319	2	5.19E-05	0.92	3.33	-	1269.3
gi|4508047|ref|NP_003452.1| zyxin [Homo sapiens]				5.36E-05	0.86	10.22	4.40	61277.0
AHQ-10-8, 3853	K.LGHPEALSAGTGSPQPPSFTYAQQR.E	2598.81170	3	5.36E-05	0.86	4.40	-	679.5
gi|7705827|ref|NP_057187.1| GTP-binding protein Sara [Homo sapiens]				5.37E-05	0.92	10.21	5.60	22409.7
AHQ-10-11, 4323	K.LVFLGLDNAGK.T	1147.34882	2	5.37E-05	0.92	3.07	-	1185.9
AHQ-10-11, 4192 - 4206	K.LVFLGLDNAGK.T	1147.34882	2	7.49E-05	0.96	4.12	-	1472.6
gi|28395033|ref|NP_786886.1| ras homolog gene family, member C; Aplysia RAS-related homolog 9 (onco				5.51E-05	1.77	20.18	16.10	22006.2
AHQ-10-10, 4448	K.HFCPNVPIILVGNK.K	1609.91693	2	5.51E-05	0.86	2.82	-	805.2
AHQ-10-10, 4664 - 4670	K.QVELALWDTAGQEDYDR.L	2010.10662	2	7.06E-05	0.91	3.58	-	1234.6
gi|28373103|ref|NP_005164.2| sarco/endoplasmic reticulum Ca2+ -ATPase isoform a; ATPase, Ca(2+)-tra				5.88E-05	0.93	10.21	1.50	109255.5
AHQ-10-1, 3750 - 3751	R.VDQSILTGESVSVTK.H	1563.73208	2	5.88E-05	0.93	4.15	-	716.2
gi|6912494|ref|NP_036457.1| microtubule-associated protein, RP/EB family, member 1; ADENOMATOUS POL				5.97E-05	0.87	10.20	7.10	29998.9
AHQ-10-9, 4099 - 4155	R.NIELICQENEGENDPVLQR.I	2272.43545	2	5.97E-05	0.87	3.97	-	732.4
gi|28269681|ref|NP_783313.1| NADH-ubiquinone oxidoreductase subunit B14.7 [Homo sapiens]				6.09E-05	0.73	10.16	16.30	14852.0
AHQ-10-13-, 6104	R.EKPDDPLNYFLGGCAGGLTLGAR.T	2423.68676	3	6.09E-05	0.73	3.13	-	731.7
gi|13569962|ref|NP_112243.1| RAB1B, member RAS oncogene family; small GTP-binding protein [Homo sap				6.27E-05	0.83	10.21	8.50	22171.0
AHQ-10-11, 4316	K.NATNVEQAFM*TM*AAEIK.K	1902.13959	2	6.27E-05	0.83	4.11	-	753.0
gi|25188179|ref|NP_005653.3| voltage-dependent anion channel 3 [Homo sapiens]				6.37E-05	1.60	20.16	11.00	30658.4
AHQ-10-10, 3540	K.VCNYGLTFTQK.W	1332.50706	2	6.37E-05	0.87	2.88	-	1054.7
AHQ-10-10, 4244 - 4251	K.VNNASLIGLGYTQTLRPGVK.L	2102.42298	2	7.92E-05	0.73	3.20	-	468.5
gi|11968045|ref|NP_071934.1| hypothetical protein FLJ22056 [Homo sapiens]				6.42E-05	0.60	10.16	9.50	36010.3
AHQ-10-11, 3663	R.GARPPAAGPGGDEDEDEEDTAPESALDTSLDK.S	3214.22226	3	6.42E-05	0.60	3.15	-	393.8
gi|21361456|ref|NP_055425.2| alpha glucosidase II alpha subunit; likely ortholog of mouse G2an alph				6.69E-05	0.95	10.23	1.80	109437.2
AHQ-10-4, 3907	R.VVIIGAGKPAAVVLQTK.G	1665.05702	2	6.69E-05	0.95	4.52	-	1065.8
gi|4504489|ref|NP_000403.1| histidine-rich glycoprotein precursor; histidine-proline rich glycoprot				6.77E-05	0.82	10.14	2.70	59578.0
AHQ-10-5, 6119	K.DSPVLIDFFEDTER.Y	1683.79674	2	6.77E-05	0.82	2.79	-	887.4
gi|28461290|ref|NP_443728.2| TRALPUSH; no opposite paired repeat protein [Homo sapiens]				6.90E-05	0.67	10.13	0.40	240073.5
AHQ-10-7, 3490	K.KKPQVNAK.D	913.09970	1	5.33E-04	0.46	2.38	-	534.7
AHQ-10-8, 3499	K.KKPQVNAK.D	913.09970	1	6.90E-05	0.67	2.52	-	551.3
AHQ-10-6, 3507	K.KKPQVNAK.D	913.09970	1	3.20E-04	0.22	2.18	-	368.8
gi|4506057|ref|NP_002722.1| protein kinase, cAMP-dependent, catalytic, beta [Homo sapiens]				7.23E-05	0.93	10.19	3.40	40622.4
AHQ-10-8, 5778	R.ILQAVNFPFLVR.L	1417.72301	2	7.23E-05	0.93	3.75	-	801.7
gi|17450333|ref|XP_060887.1| similar to peptidyl-Pro cis trans isomerase [Homo sapiens]				7.50E-05	0.89	10.20	11.00	17503.9
AHQ-10-13-, 6141	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	8.52E-05	0.92	3.91	-	976.0
AHQ-10-12, 6112	-.M*VNPTVFDIAVDGKPLGR.V	1946.26009	2	7.50E-05	0.89	3.87	-	821.0
gi|8922940|ref|NP_060830.1| chromosome X open reading frame 15 [Homo sapiens]				7.51E-05	0.30	10.13	2.30	60605.3
AHQ-10-6, 4387	K.YEQMKQQEVQLK.Q	1552.77763	2	7.51E-05	0.30	2.70	-	246.4
gi|4885079|ref|NP_005165.1| ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypept				7.53E-05	0.89	10.17	4.00	32880.7
AHQ-10-9, 4625	R.IYGLGSLALYEK.A	1327.55027	2	7.53E-05	0.89	3.36	-	841.7
gi|6005802|ref|NP_009175.1| proline rich 4 (lacrimal); lacrimal proline rich protein [Homo sapiens]				7.61E-05	0.84	10.15	10.40	15096.6
AHQ-10-1, 5966	R.FPSVSLQEASSFFR.R	1602.77169	2	7.61E-05	0.84	3.03	-	769.0
gi|6005749|ref|NP_009193.1| RNA-binding protein regulatory subunit; oncogene DJ1 [Homo sapiens] [MA				7.68E-05	0.53	10.16	13.80	19846.9
AHQ-10-11, 5064 - 5076	K.EGPYDVVVLPGGNLGAQNLSESAAVK.E	2585.85114	2	7.68E-05	0.53	3.22	-	177.0
gi|5453710|ref|NP_006139.1| LIM and SH3 protein 1; Lasp-1 [Homo sapiens]				7.80E-05	0.68	10.13	0.00	29717.0
AHQ-10-9, 3676	K.GFSVVADTPELQR.I	1419.56466	2	7.80E-05	0.68	2.58	-	704.5

gi|4505303|ref|NP_002466.1|	myosin alkali light chain 1 slow a; myosin light chain 1, slow-twitch m			8.27E-05	1.52	20.17	11.50	22763.8
AHQ-10-12, 2864	R.ALGQNPTNAEVLK.V	1355.52211	1	7.20E-04	0.17	2.54	-	311.7
AHQ-10-12, 2852 - 2909	R.ALGQNPTNAEVLK.V	1355.52211	2	2.98E-04	0.74	3.28	-	507.4
AHQ-10-14-, 2730	K.ILYSQCGDVM*R.A	1359.55429	2	8.27E-05	0.78	2.83	-	706.8
gi|29725607|ref|NP_061141.2|	smooth muscle cell associated protein-1 [Homo sapiens]			9.16E-05	0.89	10.18	1.60	103076.3
AHQ-10-4, 5085	K.LLVLYSGEDDELLQR.A	1763.96968	2	9.16E-05	0.89	3.56	-	915.1
gi|4506381|ref|NP_002863.1|	ras-related C3 botulinum toxin substrate 2; Ras-related C3 botulinum to			9.21E-05	0.90	10.18	7.80	21428.7
AHQ-10-11, 4087	K.KLAPITYPQGLALAK.E	1584.92723	2	9.21E-05	0.90	3.70	-	691.1
gi|4503979|ref|NP_002046.1|	glial fibrillary acidic protein [Homo sapiens]			9.73E-05	0.34	10.14	3.50	49879.9
AHQ-10-14-, 6025	R.QEADEATLARLDLER.K	1730.85818	2	9.73E-05	0.34	2.79	-	419.6
gi|18572267|ref|XP_088476.1|	similar to thioredoxin domain containing 4; endoplasmic reticulum resi			1.04E-04	0.89	10.19	5.70	46970.9
AHQ-10-8, 5734	R.VANILHDDCAFLSAFGDVSKPER.Y	2563.82732	3	1.04E-04	0.89	3.81	-	1128.9
gi|4506405|ref|NP_002872.1|	v-ral simian leukemia viral oncogene homolog B; RAS-like protein B; GTP			1.05E-04	0.76	10.15	7.80	23408.4
AHQ-10-10, 3611	R.SKAEEWGVQYVETSAK.T	1812.95765	2	1.05E-04	0.76	2.92	-	635.2
gi|4506505|ref|NP_002916.1|	regulator of G-protein signaling 10 [Homo sapiens]			1.10E-04	0.73	10.16	6.00	19607.9
AHQ-10-11, 4579	K.LQDQIFNLMK.Y	1250.49254	2	1.10E-04	0.73	3.12	-	490.4
gi|5802974|ref|NP_006784.1|	peroxiredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide			1.16E-04	0.98	10.24	5.50	27692.5
AHQ-10-11, 5047	R.DYGVLLEGSGLALR.G	1463.66058	2	1.16E-04	0.98	4.77	-	2049.8
gi|13259510|ref|NP_004073.2|	dynactin 1 isoform 1; dynactin 1 (p150, Glued (Drosophila) homolog); p			1.19E-04	0.68	10.16	2.00	141693.7
AHQ-10-3, 5417	K.ETVSQRPGATVPTDFATFPSSAFLR.A	2683.95650	3	1.19E-04	0.68	3.28	-	535.4
gi|29734552|ref|XP_291269.1|	similar to KIAA1875 protein [Homo sapiens]			1.28E-04	0.39	10.13	1.70	93320.7
AHQ-10-13-, 4614	R.M*LAPKRSWGTPQLR.L	1657.96500	2	1.28E-04	0.39	2.51	-	505.8
gi|18765729|ref|NP_003816.2|	synaptosomal-associated protein 23 isoform SNAP23A; synaptosomal-assoc			1.35E-04	0.96	10.21	6.60	23353.9
AHQ-10-11, 4287	R.ILGLAIESQDAGIK.T	1428.65614	2	1.35E-04	0.96	4.24	-	1755.8
gi|14211923|ref|NP_115982.1|	PKCI-1-related HIT protein [Homo sapiens]			1.40E-04	1.58	20.18	22.70	17161.6
AHQ-10-13, 6052 - 6055	R.ISQAEEEDQQLLGHLLLVAK.Q	2235.52293	3	1.40E-04	0.68	3.09	-	627.3
AHQ-10-13-, 5778 - 5858	K.SLPADILYEDQQCLVFR.D	2069.32354	2	7.98E-04	0.90	3.63	-	618.2
gi|4506145|ref|NP_002760.1|	protease, serine, 1 preproprotein; cationic trypsinogen; trypsinogen A;			1.45E-04	0.49	10.16	8.10	26557.9
AHQ-10-7, 4472 - 4476	R.LGEHNIEVLEGNEQFINAAK.I	2226.43146	2	1.45E-04	0.49	3.26	-	552.1
gi|27597085|ref|NP_000357.3|	tropomyosin 1 (alpha) [Homo sapiens]			1.45E-04	1.66	20.17	9.50	32865.7
AHQ-10-9, 3179	R.AQKDEEKMEIQEIQLK.E	1961.22673	2	2.40E-04	0.83	3.33	-	778.8
AHQ-10-10, 3283 - 3355	R.KLVIIESDLER.A	1315.54103	2	2.04E-04	0.80	3.19	-	753.4
AHQ-10-9, 3228	R.KLVIIESDLER.A	1315.54103	2	1.45E-04	0.82	2.93	-	1048.3
gi|24234688|ref|NP_004125.3|	heat shock 70kDa protein 9B precursor; heat shock 70kD protein 9; stre			1.49E-04	1.45	20.18	4.60	73680.1
AHQ-10-6, 5260 - 5332	R.AQFEGIVTDLIR.R	1362.55625	2	6.26E-04	0.92	3.54	-	1227.2
AHQ-10-6, 5451	K.STNGDTFLGGEDFDQALLR.H	2057.16328	2	1.49E-04	0.53	2.87	-	301.0
gi|4503291|ref|NP_001346.1|	D-dopachrome tautomerase [Homo sapiens]			1.49E-04	0.75	10.13	9.30	12711.7
AHQ-10-14-, 5342	R.FFPLESWQIGK.I	1352.56151	2	1.49E-04	0.75	2.50	-	427.9
gi|30149013|ref|XP_302138.1|	similar to alpha tubulin [Homo sapiens]			1.52E-04	0.42	10.14	4.60	22444.5
AHQ-10-7, 4724	R.EIINLVLDR.I	1085.27902	1	1.52E-04	0.42	2.24	-	261.4
gi|4557701|ref|NP_000413.1|	keratin 17 [Homo sapiens]			1.57E-04	0.60	10.20	3.00	48105.4
AHQ-10-5, 2169	R.EVATNSELVQSGK.S	1362.46828	2	1.57E-04	0.60	2.65	-	642.0
gi|4505989|ref|NP_000299.1|	protective protein for beta-galactosidase; Protective protein for beta-			1.60E-04	0.89	10.15	2.70	54495.8
AHQ-10-11, 3482	K.YGDSGEQIAGFVK.E	1371.47686	2	1.60E-04	0.89	3.09	-	1183.0
gi|27475985|ref|NP_073565.2|	neurogenic differentiation 6 [Homo sapiens]			1.66E-04	0.77	10.14	3.30	38704.7
AHQ-10-9, 3481	K.QIVLRGKSIKR.A	1298.60643	2	1.66E-04	0.77	2.73	-	917.9
gi|20070125|ref|NP_000909.2|	prolyl 4-hydroxylase, beta subunit; v-erb-a avian erythroblastic leuke			1.67E-04	1.65	20.18	5.50	57115.9
AHQ-10-7, 3657 - 3669	K.VDATEESDLAQQYGVR.G	1781.85882	2	2.93E-04	0.84	3.12	-	1078.7
AHQ-10-7, 3986	K.YQLDKDGVVLFK.K	1425.65394	2	1.67E-04	0.82	3.18	-	995.9
gi|27500008|ref|XP_208872.1|	similar to tropomyosin 3 [Homo sapiens]			1.74E-04	0.85	10.18	6.50	28954.4
AHQ-10-9, 3495 - 3527	R.ALKDEEKM*ELQELQLK.E	1962.25460	2	1.74E-04	0.85	3.63	-	534.4
gi|4557773|ref|NP_000248.1|	myosin, heavy polypeptide 7, cardiac muscle, beta [Homo sapiens]			1.86E-04	1.26	20.15	1.20	223110.8
AHQ-10-3, 3186	R.CNGVLEGIR.I	1019.15759	2	1.86E-04	0.84	2.96	-	730.7
AHQ-10-4, 3124 - 3193	R.CNGVLEGIR.I	1019.15759	2	3.40E-04	0.69	2.55	-	674.5
AHQ-10-2, 4048	R.IEELEEELESERTAR.A	1833.93203	2	8.09E-04	0.42	2.85	-	622.3
gi|4502491|ref|NP_001203.1|	complement component 1, q subcomponent binding protein precursor; hyalu			1.87E-04	0.80	10.17	7.10	31362.0
AHQ-10-9, 5249	K.VEEQEPELTSTPNFVVEVIK.N	2288.53624	2	1.87E-04	0.80	3.34	-	626.2
gi|10835121|ref|NP_000289.1|	pyruvate kinase, liver and RBC; Pyruvate kinase, liver and RBC type [H			1.87E-04	0.75	10.14	1.90	61829.8
AHQ-10-7, 3589	R.GDLGIEIPAEK.V	1142.28420	2	1.87E-04	0.75	2.77	-	761.7
gi|20470897|ref|XP_115995.1|	similar to protease (prosome, macropain) 26S subunit, ATPase 1 [Homo s			1.88E-04	0.65	10.18	14.10	10504.2
AHQ-10-7, 2745 - 2824	K.YEPLVPIIGEEKK.E	1515.77539	2	1.88E-04	0.65	3.62	-	449.0
gi|5031593|ref|NP_005708.1|	actin related protein 2/3 complex subunit 5; Arp2/3 protein complex sub			1.94E-04	1.71	20.19	17.90	16320.3
AHQ-10-14-, 3074 - 3129	K.ALAAGGVGSIVR.V	1071.25558	2	1.94E-04	0.94	3.90	-	1073.9
AHQ-10-12, 3562 - 3632	K.AVQSLDKNGVDLLM*K.Y	1647.91883	2	6.89E-04	0.77	3.46	-	397.6
gi|4757818|ref|NP_004879.1|	ATPase, H+ transporting, lysosomal, V1 subunit G isoform 1; vacuolar H(			1.97E-04	0.72	10.15	9.30	13757.4
AHQ-10-13-, 2865	K.EEAQAEIEQYR.L	1366.41548	2	1.97E-04	0.72	2.94	-	678.9
gi|19913373|ref|NP_079536.2|	G6B protein isoform G6b-A precursor; G6B protein; immunoglobulin recep			2.07E-04	0.62	10.14	4.60	25002.6
AHQ-10-11, 5018	R.WVWAPSFPACK.G	1350.56891	2	2.07E-04	0.62	2.76	-	534.7
gi|21361670|ref|NP_054782.2|	src homology 3 domain-containing protein HIP-55; HIP-55 protein [Homo			2.10E-04	0.81	10.16	3.70	48294.0
AHQ-10-10, 3324 - 3378	R.FQDVGPQAPVGSVYQK.T	1720.90658	2	2.10E-04	0.81	3.23	-	648.1
gi|7705300|ref|NP_057701.1|	hypothetical protein BM-002 [Homo sapiens]			2.18E-04	0.77	10.13	17.60	9117.5
AHQ-10-14-, 5156 - 5220	K.VLSVPESTPFTAVLK.F	1588.86951	2	2.18E-04	0.77	2.65	-	346.6
gi|4504523|ref|NP_002148.1|	heat shock 10kDa protein 1 (chaperonin 10); heat shock 10kD protein 1 (			2.21E-04	0.97	10.23	13.70	10931.6
AHQ-10-14-, 2834 - 2896	K.VLQATVVAVGSGSK.G	1316.52902	2	2.21E-04	0.97	4.57	-	1897.4
gi|16418461|ref|NP_443195.1|	mitochondrial topoisomerase I [Homo sapiens]			2.32E-04	0.29	10.15	2.20	69871.5
AHQ-10-14-, 3890 - 3950	R.WEKEKHEDGVKWR.Q	1727.90404	2	2.32E-04	0.29	2.92	-	302.6
gi|4504137|ref|NP_000830.1|	glutamate receptor, metabotropic 2 precursor [Homo sapiens]			2.33E-04	0.44	10.14	1.50	95507.0
AHQ-10-13, 4607 - 4649	R.LEAM*LFALDRINR.D	1578.86142	2	2.33E-04	0.44	2.78	-	417.9
gi|22748619|ref|NP_689476.1|	tropomyosin 3 [Homo sapiens]			2.39E-04	1.55	20.19	9.90	28222.6
AHQ-10-9, 3265 - 3332	R.KLVIIEGDLER.T	1285.51492	2	2.39E-04	0.67	2.73	-	713.2
AHQ-10-9, 2119 - 2191	K.YSQKEDKYEEEIK.I	1689.80129	2	3.30E-04	0.88	3.80	-	1259.9
gi|4507913|ref|NP_003922.1|	WAS protein family, member 1; WASP family Verprolin-homologous protein;			2.39E-04	0.89	10.15	1.60	61652.0
AHQ-10-11, 2822 - 2880	R.SVLLEAIRK.G	1029.25860	2	2.39E-04	0.89	2.91	-	1364.1
gi|30153852|ref|XP_171113.3|	similar to Moesin (Membrane-organizing extension spike protein) [Homo			2.51E-04	0.94	10.18	9.30	15601.7
AHQ-10-6, 2131	R.RKPDTIEVQQMK.A	1473.72364	2	2.51E-04	0.94	3.51	-	1415.5
gi|20532885|ref|XP_086931.2|	similar to epsilon isoform of 14-3-3 protein [Homo sapiens]			2.53E-04	0.93	10.19	4.70	29380.0
AHQ-10-11, 6102	K.LICCDILDVLDK.H	1479.74157	2	2.53E-04	0.93	3.85	-	800.6
gi|21464101|ref|NP_036611.2|	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein			2.56E-04	0.82	10.20	5.70	28302.4
AHQ-10-10, 3030	K.NVTELNEPLSNEER.N	1644.72215	2	2.56E-04	0.82	3.17	-	691.5
gi|5729991|ref|NP_006494.1|	proteasome 26S ATPase subunit 4 isoform 1; protease 26S subunit 6; Tat-			2.65E-04	0.76	10.13	2.90	47365.9
AHQ-10-5, 3775	R.GVLM*YGPPGCGK.T	1253.47332	2	2.65E-04	0.76	2.54	-	685.8
gi|20553919|ref|XP_033811.2|	similar to hypothetical protein FLJ14775 [Homo sapiens]			2.68E-04	0.48	10.13	9.90	17460.4
AHQ-10-11, 5490 - 5560	R.NGSKEGNHHSTQPKR.N	1677.76352	2	2.68E-04	0.48	2.62	-	719.6
gi|5453599|ref|NP_006127.1|	capping protein (actin filament) muscle Z-line, alpha 2; F-actin cappin			2.70E-04	0.95	10.25	7.00	32948.9
AHQ-10-9, 4573 - 4576	K.KIDGQQTIIACIESHQFQAK.N	2317.60733	3	2.70E-04	0.95	5.10	-	1239.5
gi|5031937|ref|NP_005822.1|	nuclear domain 10 protein [Homo sapiens]			2.74E-04	0.54	10.18	6.10	52253.6
AHQ-10-1, 4674 - 4743	R.EYYTFMWVTLPIDLNNKSAKQQEVQFK.A	3322.77755	3	2.74E-04	0.54	3.63	-	344.1
gi|11321611|ref|NP_006868.1|	guanosine monophosphate reductase; guanine monophosphate reductase [Ho			2.78E-04	0.78	10.18	7.50	37414.6
AHQ-10-9, 3865	K.LFATNHPECLQNVAVSSGSGQNDLEK.M	2818.02614	3	2.78E-04	0.78	3.61	-	782.7
gi|21361619|ref|NP_061882.2|	TOLLIP protein; Toll-interacting protein [Homo sapiens]			2.83E-04	0.71	10.14	5.10	30281.6
AHQ-10-11, 5390	R.GPVYIGELPQDFLR.I	1604.83072	2	2.83E-04	0.71	2.90	-	495.3
gi|5803201|ref|NP_006818.1|	transmembrane trafficking protein [Homo sapiens]			2.93E-04	0.94	10.18	5.00	24975.8
AHQ-10-11, 4802	R.IPDQLVILDMK.H	1285.57833	2	2.93E-04	0.94	3.54	-	1175.0
gi|4757732|ref|NP_004199.1|	programmed cell death 8 isoform 1; apoptosis-inducing factor [Homo sapi			3.03E-04	0.77	10.14	2.10	66900.2
AHQ-10-6, 5105	R.ALGTEVIQLFPEK.G	1445.68516	2	3.03E-04	0.77	2.87	-	847.2
gi|4505185|ref|NP_002406.1|	macrophage migration inhibitory factor (glycosylation-inhibiting factor			3.11E-04	0.93	10.18	7.80	12476.2
AHQ-10-14-, 4436	K.LLCGLLAER.L	1046.26608	2	3.11E-04	0.93	3.55	-	941.4

gi|20149563|ref|NP_004800.2|	stomatin (EPB72)-like 1; stomatin-like 1; stomatin (EBP72)-like 1 [Hom			3.14E-04	0.60	10.16	6.00	42967.8
AHQ-10-13-, 5418	R.LGRIRTPQGPGMVLLLPFIDSFQR.V	2713.24027	3	3.14E-04	0.60	3.21	-	497.6
gi|29736622|ref|XP_293924.1|	similar to cytoplasmic beta-actin [Homo sapiens]			3.18E-04	0.69	10.19	1.90	42002.9
AHQ-10-8, 1767 - 1830	K.CDVDIRK.D	907.02724	2	3.18E-04	0.69	2.57	-	658.5
gi|17999541|ref|NP_060676.2|	vacuolar protein sorting 35; maternal-embryonic 3 [Homo sapiens]			3.51E-04	0.81	10.14	1.30	91706.5
AHQ-10-5, 3567 - 3587	K.LLDEAIQAVK.V	1100.29046	2	3.51E-04	0.81	2.73	-	926.6
gi|21687060|ref|NP_660295.1|	similar to common salivary protein 1 [Homo sapiens]			3.51E-04	0.68	10.18	12.20	18878.5
AHQ-10-3, 4591	K.LGALGGNTQEVTLQPGEYITK.V	2190.43903	2	3.51E-04	0.68	3.08	-	452.0
gi|18105058|ref|NP_061138.2|	vacuolar protein sorting 33B (yeast homolog)) [Homo sapiens]			3.54E-04	0.52	10.16	3.10	70614.9
AHQ-10-14-, 5112	R.GM*DIKQM*KNFVSQELKGLK.Q	2227.63402	2	3.54E-04	0.52	3.13	-	321.7
gi|27481006|ref|XP_117198.2|	hypothetical protein XP_117198 [Homo sapiens]			4.17E-04	0.24	10.13	0.40	251738.6
AHQ-10-6, 3916 - 3924	R.WKPYWM*EGTSCLGATKVM*K.N	2307.69775	3	4.19E-04	0.74	3.08	-	897.3
gi|4504793|ref|NP_002214.1|	inositol 1,4,5-triphosphate receptor, type 2 [Homo sapiens]			4.32E-04	0.68	10.13	0.40	308075.1
AHQ-10-6, 6476	R.GNPQNQVLLHK.H	1248.41647	2	4.32E-04	0.68	2.62	-	1031.4
gi|4506769|ref|NP_002954.1|	S100 calcium-binding protein A7; psoriasin 1 [Homo sapiens]			4.57E-04	0.81	10.15	10.90	11456.9
AHQ-10-13-, 4584	K.GTNYLADVFEK.K	1257.37376	2	4.57E-04	0.81	2.94	-	1066.3
gi|18591697|ref|XP_028966.2|	similar to DnaJ homolog subfamily C member 5 (Cysteine string protein)			4.77E-04	0.75	10.20	10.10	22148.7
AHQ-10-1, 5237 - 5297	K.EINNAHAILTDATKRNIYDK.Y	2301.54470	3	4.77E-04	0.75	4.04	-	885.9
gi|6857820|ref|NP_005019.2|	phosphatidylinositol-4-phosphate 5-kinase type II alpha; 1-phosphatidyl			4.92E-04	0.92	10.18	4.20	46224.3
AHQ-10-7, 2833 - 2857	K.HGAGAEISTVNPEQYSK.R	1788.89618	2	4.92E-04	0.92	3.61	-	1143.2
gi|20149637|ref|NP_057526.2|	type 1 tumor necrosis factor receptor shedding aminopeptidase regulato			4.96E-04	0.57	10.14	1.40	107761.4
AHQ-10-4, 5884	R.NPVGYPLAWQFLR.K	1561.81077	2	4.96E-04	0.57	2.76	-	424.2
gi|15718761|ref|NP_004976.2|	c-K-ras2 protein isoform b; Kirsten rat sarcoma-2 viral (v-Ki-ras2) on			4.98E-04	0.87	10.19	8.00	21424.4
AHQ-10-11, 3764	R.VKDSEDVPM*VLVGNK.C	1646.88770	2	4.98E-04	0.87	3.88	-	944.7
gi|4557377|ref|NP_000052.1|	Bruton agammaglobulinemia tyrosine kinase [Homo sapiens]			5.17E-04	0.65	10.14	2.10	76280.8
AHQ-10-6, 3319 - 3373	R.YVLDDEYTSSVGSK.F	1563.64427	2	5.17E-04	0.65	2.71	-	534.3
gi|4503643|ref|NP_000121.1|	coagulation factor V precursor; labile factor; factor V Leiden [Homo sa			5.26E-04	0.93	10.17	0.60	251716.5
AHQ-10-5, 3177	K.EVIITGIQTQGAK.H	1358.56590	2	5.26E-04	0.93	3.48	-	1246.9
gi|4506765|ref|NP_002952.1|	S100 calcium-binding protein A4; 18A2; 42A; S100 calcium-binding protei			5.41E-04	0.88	10.15	10.90	11728.5
AHQ-10-14-, 3088	K.ALDVM*VSTFHK.Y	1264.47605	2	5.41E-04	0.88	2.87	-	1200.4
gi|4505145|ref|NP_002387.1|	malic enzyme 2, NAD(+)-dependent, mitochondrial; Malic enzyme, mitochon			5.46E-04	0.81	10.17	3.10	65443.3
AHQ-10-6, 5580	R.ILGLGDLGVYGM*GIPVGK.L	1776.13334	2	5.46E-04	0.81	3.40	-	505.6
gi|5031601|ref|NP_005711.1|	actin related protein 2/3 complex subunit 1B; ARP2/3 protein complex su			5.51E-04	0.61	10.19	3.50	40949.5
AHQ-10-9, 3184	K.NSVSQISVLSGGK.A	1276.42175	2	5.51E-04	0.61	2.61	-	694.0
gi|22538814|ref|NP_002976.2|	small inducible cytokine A5 precursor; T-cell specific protein p288; T			5.54E-04	0.60	10.12	8.80	9989.6
AHQ-10-14-, 2464	K.EYFYTSGK.C	995.06653	1	5.54E-04	0.60	2.37	-	275.3
gi|21361427|ref|NP_055182.2|	hypothetical protein, estradiol-induced [Homo sapiens]			5.58E-04	0.45	10.14	8.90	21551.0
AHQ-10-13-, 5294 - 5374	K.EDEIPETVSLEMLDAAK.N	1891.08690	2	5.58E-04	0.45	2.63	-	283.1
gi|14780596|ref|XP_033004.1|	hypothetical protein BC005107 [Homo sapiens]			5.68E-04	0.52	10.13	5.00	18127.9
AHQ-10-2, 2147 - 2223	R.EQIIAKAK.A	901.08569	1	5.68E-04	0.52	2.60	-	351.8
gi|21361322|ref|NP_006078.2|	tubulin, beta, 5 [Homo sapiens]			5.99E-04	0.75	10.16	4.30	49585.5
AHQ-10-13-, 2892	-.M*REIVHLQAGQCGNQIGAK.F	2128.42245	3	5.99E-04	0.75	3.17	-	961.9
gi|4503477|ref|NP_001950.1|	eukaryotic translation elongation factor 1 beta 2; eukaryotic translati			5.99E-04	0.84	10.18	6.70	24763.6
AHQ-10-9, 4956 - 5020	K.SPAGLQVLNDYLADK.S	1604.78589	2	5.99E-04	0.84	3.60	-	580.3
gi|4503141|ref|NP_001805.1|	cathepsin C isoform a preproprotein; dipeptidyl-peptidase I; dipeptidyl			6.15E-04	0.92	10.21	4.10	51841.5
AHQ-10-14-, 5177 - 5178	R.GTDECAIESIAVAATPIPK.L	1945.18072	2	6.15E-04	0.92	4.12	-	1012.4
gi|22065448|ref|XP_084610.2|	similar to tubulin alpha-1 chain - Chinese hamster [Homo sapiens] [MAS			6.18E-04	0.69	10.14	2.40	41009.4
AHQ-10-11, 4666	K.EIIDLVLDR.I	1086.26378	2	6.18E-04	0.69	2.81	-	768.2
gi|4759146|ref|NP_004778.1|	slit homolog 2 [Homo sapiens]			6.38E-04	0.33	10.10	0.50	169868.4
AHQ-10-5, 2151 - 2207	K.GLKVLPK.G	754.98373	1	6.38E-04	0.33	1.98	-	556.2
gi|30149784|ref|XP_291573.2|	similar to elongation factor 1 alpha [Homo sapiens]			6.46E-04	0.95	10.15	2.80	42642.0
AHQ-10-10, 2903 - 2932	K.IGGIGTVPVGR.V	1026.21481	2	6.46E-04	0.95	2.78	-	1783.5
gi|6912638|ref|NP_036557.1|	ras suppressor protein 1 [Homo sapiens]			6.54E-04	2.32	30.19	22.00	31540.1
AHQ-10-10, 6136 - 6227	K.AENNPWVTPIADQFQLGVSHVFEYIR.S	3032.35678	3	8.69E-04	0.56	3.03	-	335.7
AHQ-10-10, 5595 - 5663	R.ALYLSDNDFEILPPDIGK.L	2021.25559	2	6.54E-04	0.83	3.71	-	357.8
AHQ-10-10, 5390	R.LTVLPPELGNLDLTGQK.Q	1809.09672	3	8.44E-04	0.93	3.89	-	1512.1
gi|13376719|ref|NP_079413.1|	hypothetical protein FLJ21439 [Homo sapiens]			6.91E-04	0.81	10.14	2.40	48893.8
AHQ-10-11, 4350	K.GDFNYLEEFK.Q	1262.34887	2	6.91E-04	0.81	2.74	-	714.6
gi|14917115|ref|NP_002268.2|	type I hair keratin 1; Ha-1; hard keratin, type I, 1; keratin, hair, a			6.96E-04	0.48	10.14	3.60	47236.9
AHQ-10-14-, 4012	R.LNVEVDAAPTVDLNR.V	1626.79310	2	6.96E-04	0.48	2.72	-	333.5
gi|22094121|ref|NP_056015.1|	KIAA0648 protein [Homo sapiens]			7.08E-04	0.12	10.11	0.80	146609.2
AHQ-10-13, 4237	K.KYCLHGEAGK.E	1164.31639	1	7.08E-04	0.12	1.89	-	343.5
gi|30153769|ref|XP_301443.1|	similar to eukaryotic translation initiation factor 4A1; initiation fa			7.28E-04	0.63	10.22	8.70	24038.4
AHQ-10-12, 4462 - 4536	R.WFDLKDADINMVTEEDKR.T	2226.45173	3	7.28E-04	0.63	3.08	-	862.1
gi|19913414|ref|NP_055018.2|	adaptor-related protein complex 2, alpha 1 subunit isoform 1; adaptin,			7.45E-04	0.08	10.14	1.10	107545.3
AHQ-10-12, 3732	R.YGGAPQALTLK.L	1119.29547	1	7.45E-04	0.08	1.83	-	340.1
gi|4505759|ref|NP_002622.1|	phosphogluconate dehydrogenase; 6-phosphogluconate dehydrogenase [Homo			7.56E-04	0.94	10.18	2.70	53151.7
AHQ-10-8, 4393 - 4397	R.DYFGAHTYELLAK.P	1528.68958	2	7.56E-04	0.94	3.67	-	1242.7
gi|29733417|ref|XP_294548.1|	similar to hypothetical protein FLJ90396 [Homo sapiens]			7.96E-04	0.26	10.12	2.10	48468.3
AHQ-10-3, 5483	R.DIPFTNLAK.T	1019.17590	1	7.96E-04	0.26	1.84	-	461.6
gi|20546215|ref|XP_115639.1|	similar to leukocyte immunoglobulin-like receptor, subfamily B (with T			8.00E-04	0.41	10.14	0.00	42748.2
AHQ-10-5, 4579 - 4595	R.CSREVNSREDNVLYRVVK.P	2225.47152	2	8.00E-04	0.41	2.82	-	557.3
gi|24307939|ref|NP_036205.1|	chaperonin containing TCP1, subunit 5 (epsilon) [Homo sapiens]			8.19E-04	0.95	10.24	3.00	59670.7
AHQ-10-6, 6085 - 6092	K.LGFAGLVQEISFGTTK.D	1668.91472	2	8.19E-04	0.95	4.81	-	1075.5
gi|8923582|ref|NP_060378.1|	hypothetical protein FLJ20626 [Homo sapiens]			8.40E-04	0.71	10.13	0.00	48956.7
AHQ-10-9, 2789 - 2848	R.AFDWKSQLVIHR.K	1500.72897	2	8.40E-04	0.71	2.69	-	652.8
gi|4507841|ref|NP_003356.1|	ubiquinol-cytochrome c reductase core protein I [Homo sapiens]			8.51E-04	0.61	10.16	6.00	52618.5
AHQ-10-8, 6217 - 6229	R.DVVFNYLHATAFQGTPLAQAVEGPSENVR.K	3132.43152	3	8.51E-04	0.61	3.26	-	611.7
gi|4506045|ref|NP_002718.1|	proteoglycan 1, secretory granule; Proteoglycan 1, secretory granule (p			8.73E-04	0.80	10.16	8.20	17623.6
AHQ-10-1, 4125	K.GPM*FELLPGESNK.I	1435.62747	2	8.73E-04	0.80	2.96	-	759.7
gi|29737116|ref|XP_068464.3|	similar to 60S ribosomal protein L19 [Homo sapiens]			8.86E-04	0.27	10.13	5.20	32149.1
AHQ-10-8, 2690 - 2767	K.LLADQAEARRSKTK.D	1587.80647	2	8.86E-04	0.27	2.55	-	477.8
gi|15147250|ref|NP_150281.1|	protein phosphatase 1, regulatory (inhibitor) subunit 14A; 17-kDa PKC-			9.39E-04	0.71	10.18	10.90	16692.9
AHQ-10-12, 6160 - 6161	K.SCGKPVEDFIQELLAK.L	1836.09909	2	9.39E-04	0.71	3.67	-	434.8
gi|22219462|ref|NP_006359.3|	cAMP responsive element binding protein 3; luman; cyclic AMP response			9.57E-04	0.42	10.15	7.80	41379.0
AHQ-10-1, 4625	K.TSSSSTCILVLLVSFCLLLVPAMYSSDTR.G	3224.75528	3	9.57E-04	0.42	3.03	-	271.3
gi|26638653|ref|NP_004691.2|	potassium voltage-gated channel KQT-like protein 4 isoform a; potassiu			9.60E-04	0.17	10.13	2.60	77100.3
AHQ-10-1, 4379	K.QVQSIEHKLDLLLGFYSR.C	2147.46221	2	9.60E-04	0.17	2.54	-	211.6
gi|4503743|ref|NP_002009.1|	flightless I homolog [Homo sapiens]			9.94E-04	0.32	10.16	1.10	144750.1
AHQ-10-3, 5262 - 5270	R.QLPAMTALQTLHLR.S	1593.91925	2	9.94E-04	0.32	2.78	-	444.5