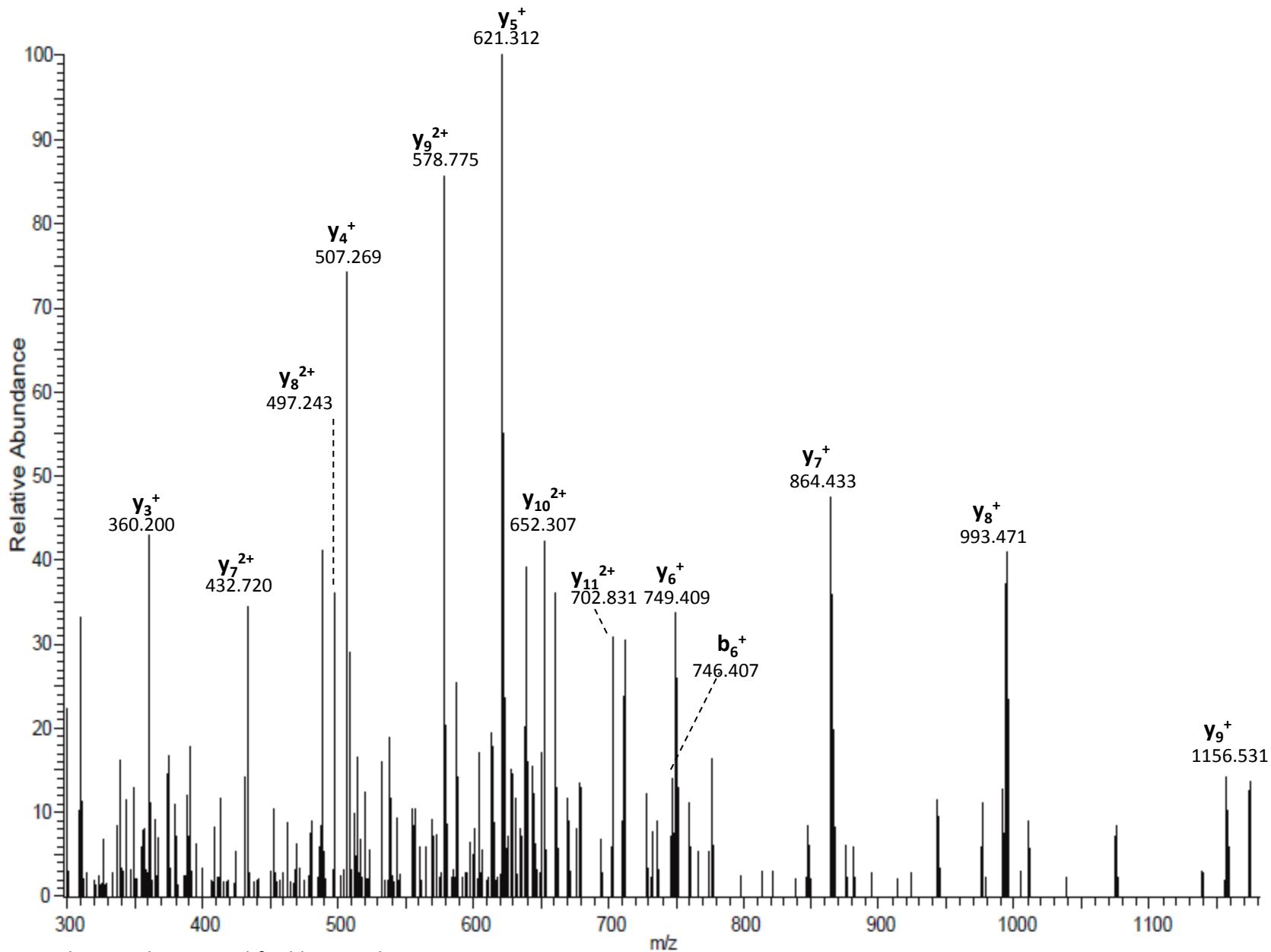


Tandem Mass Spectrum for γ S: TGTK*ITFYEDKNFQGR (QE data)

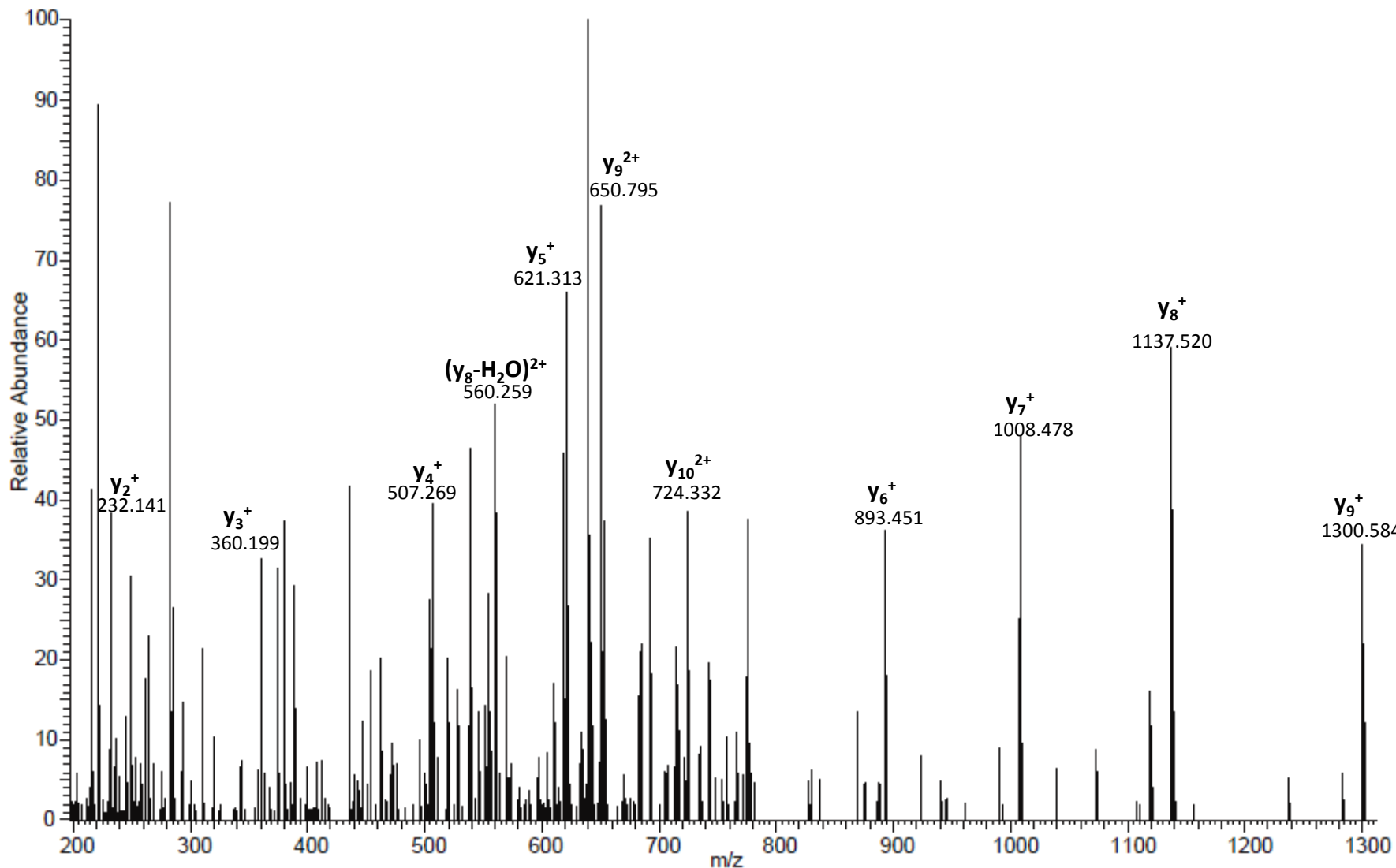


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for γ S:TGTK*ITFYEDKNFQGR (QE data)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	159.0764	80.0418	159.077		1	175.119	88.063138	175.1197	
3	260.1241	130.5657			2	232.1404	116.573838	232.1411	
4	532.2726	266.6399			3	360.199	180.603138	360.2001	
5	645.3566	323.1819		323.1782	4	507.2674	254.137338	507.2691	
6	746.4043	373.7058	746.4071		5	621.3103	311.158788	621.3123	
7	893.4727	447.2400			6	749.4053	375.206288	749.4092	
8	1056.536	528.7716			7	864.4322	432.719738	864.4332	432.7201
9	1185.5786	593.2929			8	993.4748	497.241038	993.4714	497.243
10	1300.6056	650.8064			9	1156.5382	578.772738	1156.5312	578.7751
11	1428.7005	714.8539			10	1303.6066	652.306938		652.307
12	1542.7435	771.8754			11	1404.6543	702.830788		702.8311
13	1689.8119	845.4096			12	1517.7383	759.372788		759.3711
14	1817.8705	909.4389			13	1789.8868	895.447038		
15	1874.8919	937.9496			14	1890.9345	945.970888		
					15	1947.9559	974.481588		

Tandem Mass Spectrum for γ S: ITFYEDK*NFQGR (QE Data)

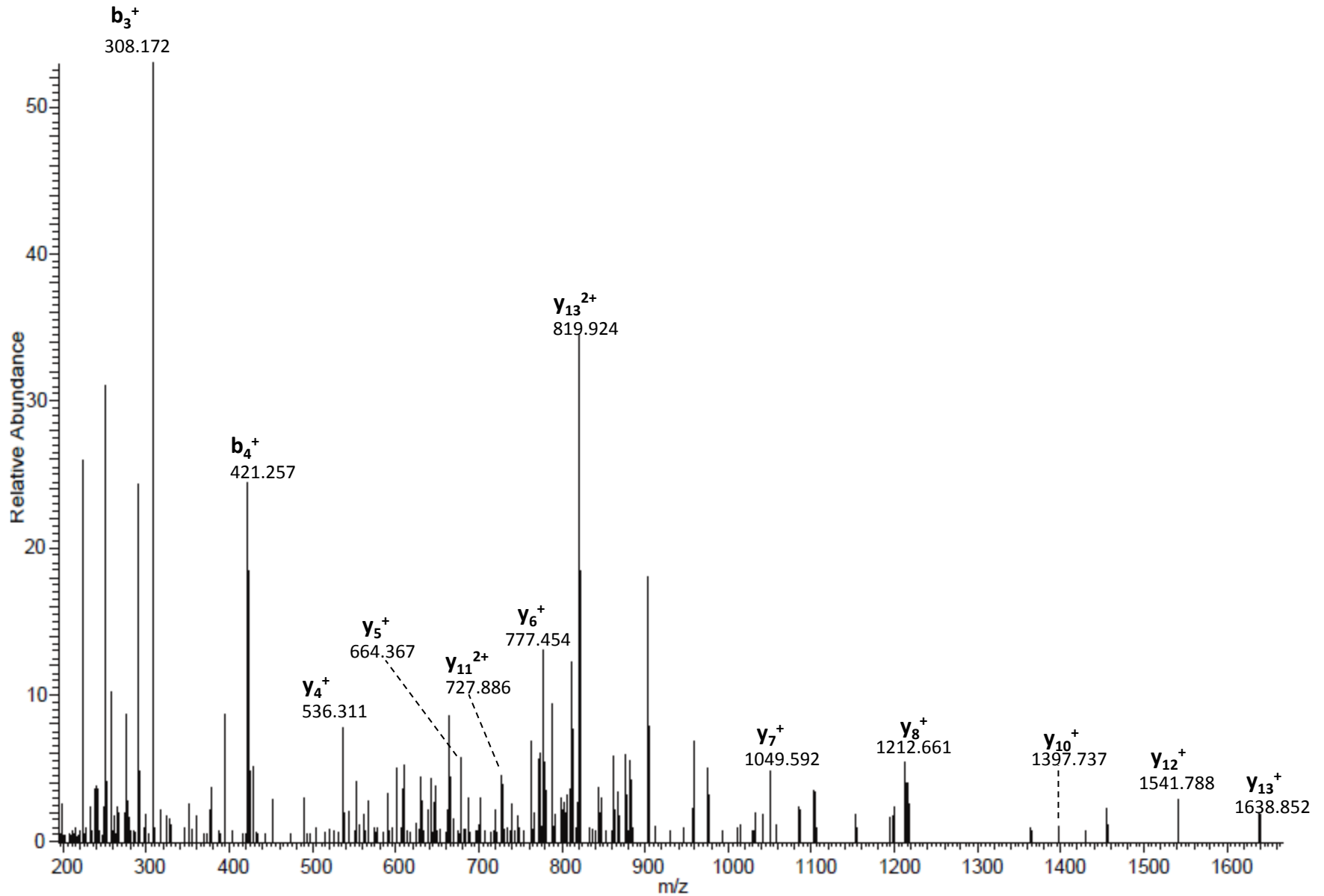


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for γ S: ITFYEDK*NFQGR (QE data)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	215.139	108.0731	215.1393		1	175.119	88.063138	175.1194	
3	362.2074	181.6073			2	232.1404	116.573838	232.1409	
4	525.2708	263.1390			3	360.199	180.603138	360.1993	
5	654.3134	327.6603			4	507.2674	254.137338	507.2689	
6	769.3403	385.1738			5	621.3103	311.158788	621.3132	
7	1041.4888	521.2480			6	893.4588	447.233038	893.4512	447.2306
8	1155.5317	578.2695			7	1008.4857	504.746488	1008.4776	
9	1302.6001	651.8037			8	1137.5283	569.267788	1137.5197	
10	1430.6587	715.8330			9	1300.5917	650.799488	1300.5836	650.7946
11	1487.6801	744.3437		744.3485	10	1447.6601	724.333688		724.3319
					11	1548.7078	774.857538		774.8545

Tandem Mass Spectrum for γ S: AVHLPSGGQYK*IQIFEK (QE data)

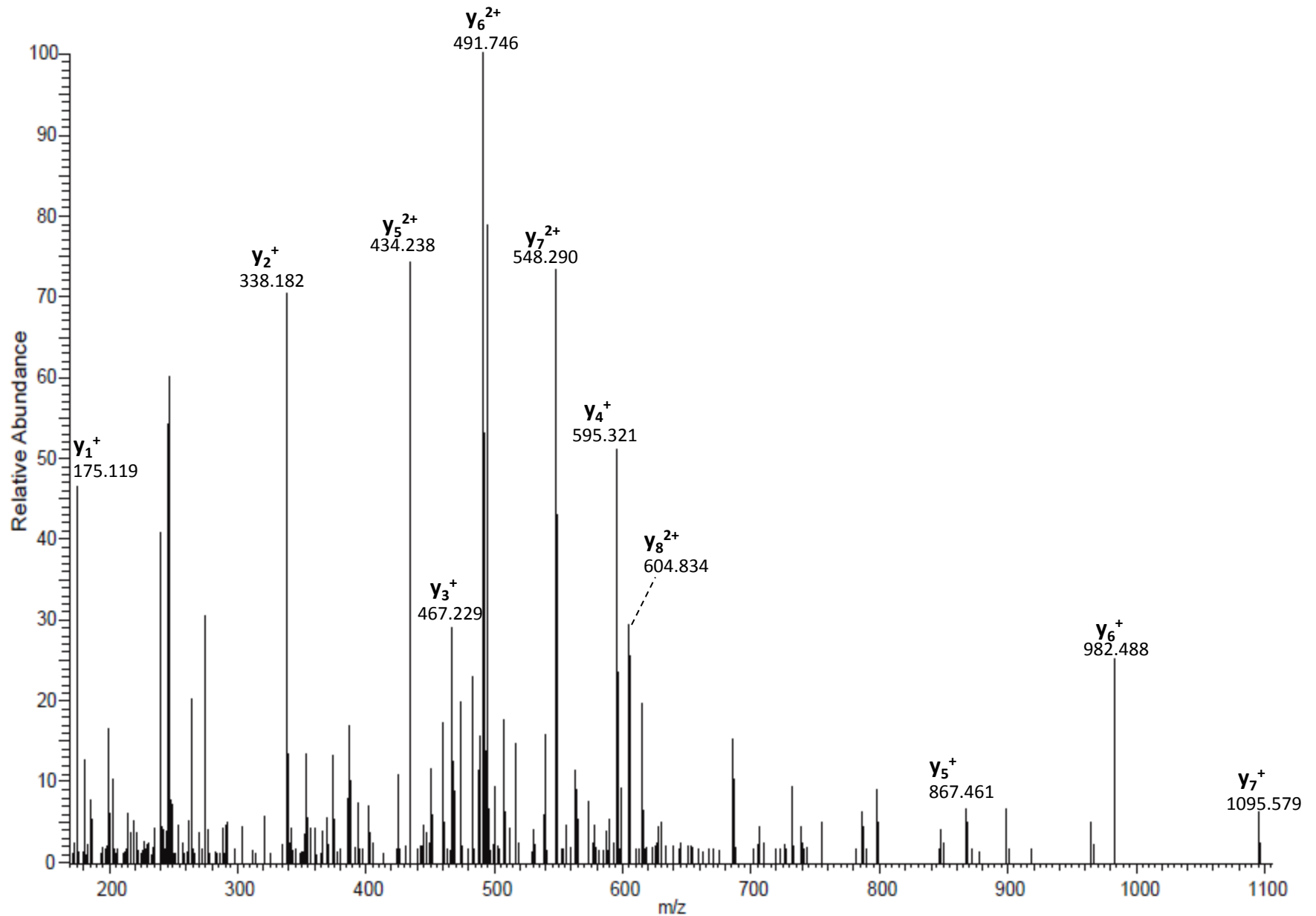


* Indicates the site that is modified by CysGly

b- and y- ions table for γ S: AVHLPSGGQYK*IQIFEK

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	171.112886	0.0600	171.1133		1	147.1128	74.060038	147.1133	
3	308.1717154	5.5895	307.1725		2	276.1554	138.581338	276.1573	
4	421.2558211	1.1315	421.2567		3	423.2238	212.115538	423.224	
5	518.3085259	6.579			4	536.3079	268.657588	536.3107	
6	605.3406303	1.739			5	664.3665	332.686888	664.3672	
7	662.362331	6.846	662.3585		6	777.4505	389.228888	777.4536	
8	719.3835360	1.954	719.3804		7	1049.599	525.303138	1049.5918	
9	847.4421424	2.247	847.4405	424.2276	8	1212.6623	606.834788	1212.6607	606.8325
10	1010.5054505	7.563	1010.5087		9	1340.7209	670.864088		
11	1282.6539641	8.306		641.8301	10	1397.7423	699.374788	1397.7373	
12	1395.7379698	3.726		698.3721	11	1454.7638	727.885538	1454.7733	727.8794
13	1523.7965762	4.019		762.3975	12	1541.7958	771.401538	1541.7882	771.4
14	1636.8806818	9.439		818.9512	13	1638.8486	819.927938	1638.852	819.9237
15	1783.949892	4.781			14	1751.9327	876.469988		876.4658
16	1912.9916956	9.994			15	1888.9916	944.999438		
					16	1988.06	994.533638		

Tandem Mass Spectrum for γ S: QYLLDK*KEYR (QE data)

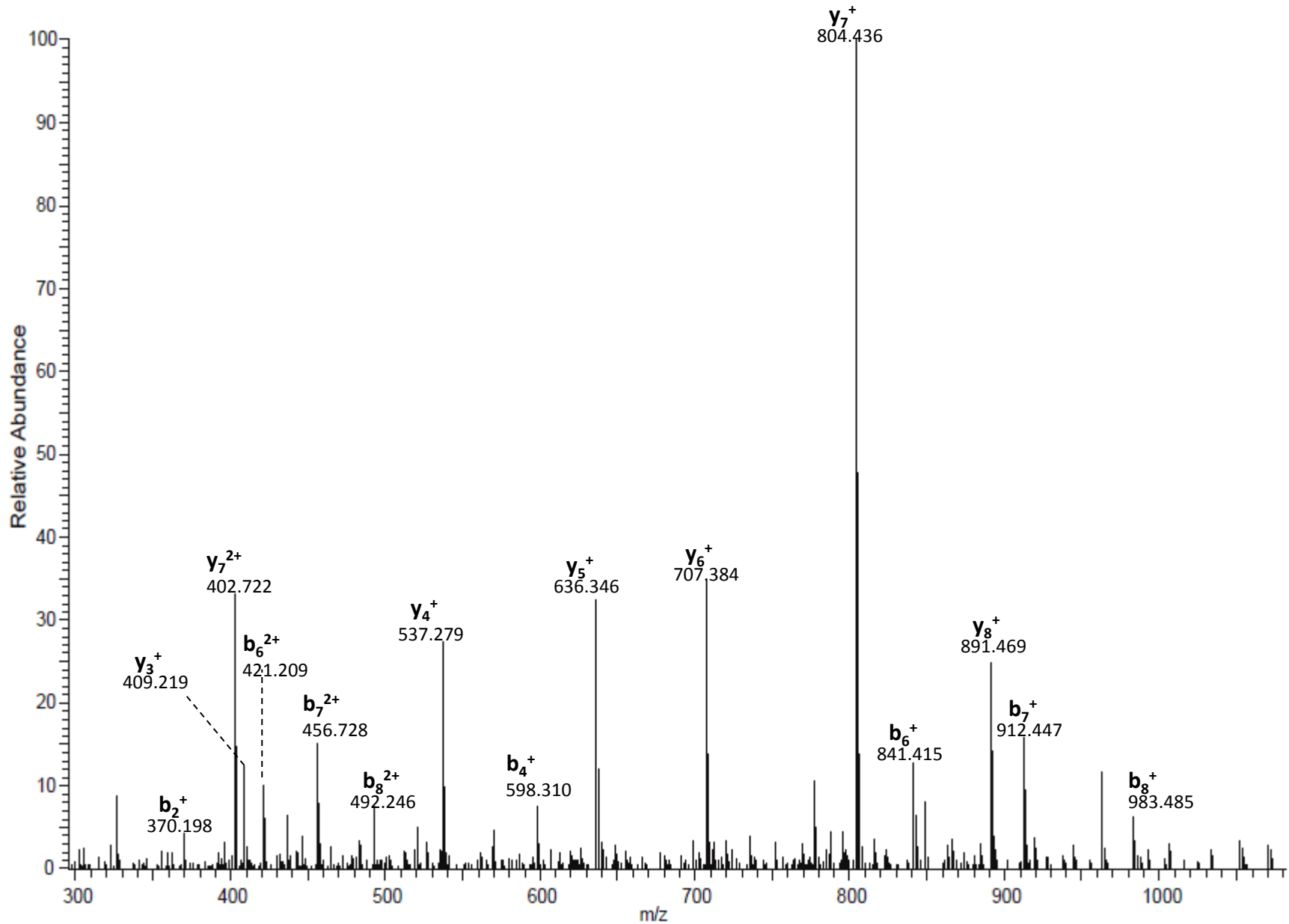


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for γ S: QYLLDK*KEYR (QE data)

b ions					y ions				
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	292.1292	146.5682	292.1298		1	175.119	88.063138	175.1194	
3	405.2132	203.1102			2	338.1823	169.594788	338.183	
4	518.2973	259.6523			3	467.2249	234.116088	467.2294	
5	633.3243	317.1658			4	595.3198	298.163538	595.3214	298.1655
6	905.4727	453.2400		453.2421	5	867.4683	434.237788	867.4605	434.2331
7	1033.5677	517.2875			6	982.4952	491.751238	982.4883	491.7457
8	1162.6103	581.8088			7	1095.5793	548.293288	1095.5786	548.2893
9	1325.6736	663.3404			8	1208.6634	604.835338		604.8344
10					9	1371.7267	686.366988		

Tandem Mass Spectrum for γ S: K*PIDWGAASPAVQSFR (QE data)

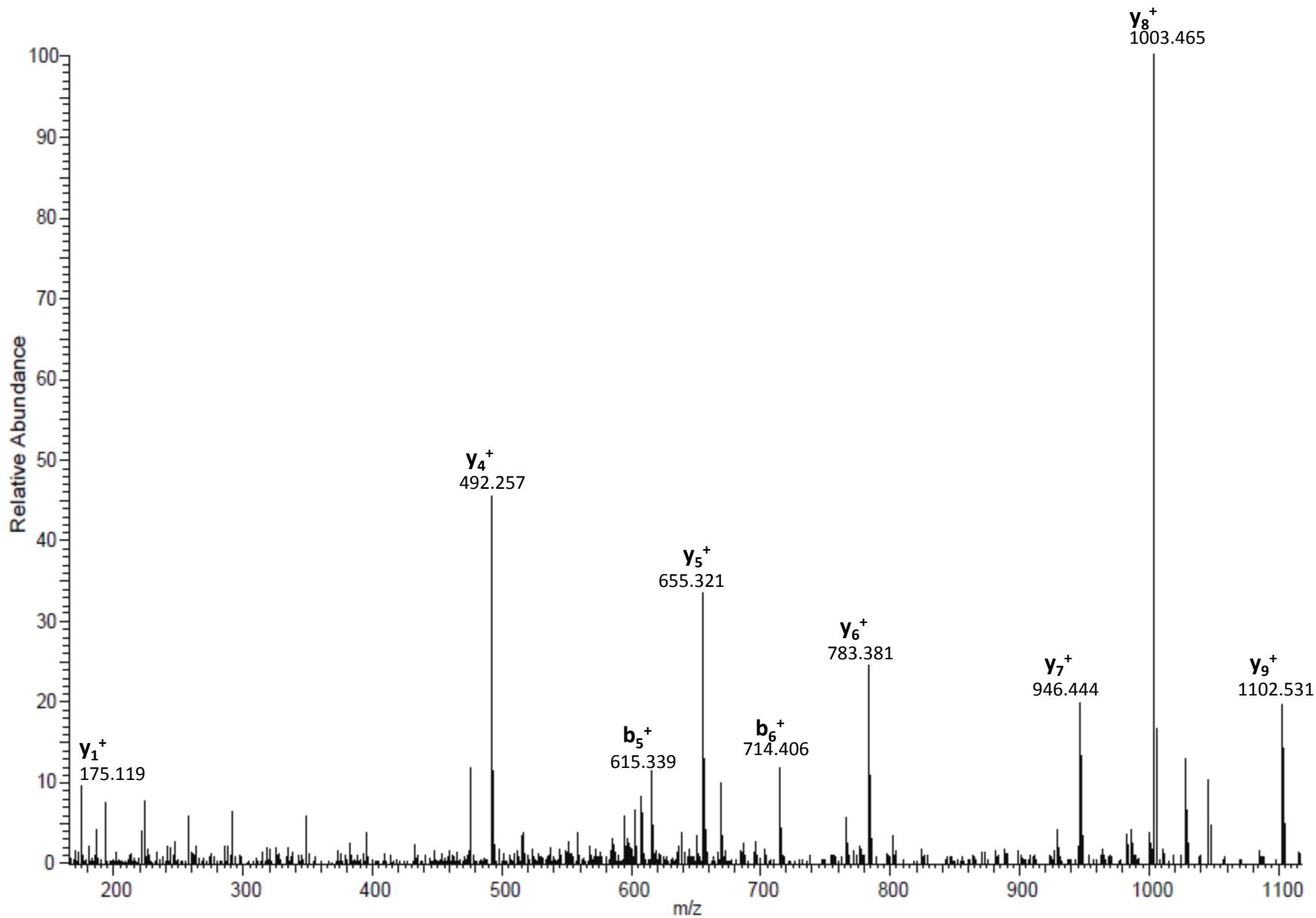


* Indicates the site that is modified by CysGly

Predicated and detected b- and γ - ions for γ S: K*PIDWGAASPAVQSFR (QE data)

b ions					y ions				
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	370.2085	185.6079	370.198		1	175.119	88.063138	175.1195	
3	483.2926	242.1499			2	322.1874	161.597338	322.1832	
4	598.3195	299.6634	598.3101		3	409.2194	205.113338	409.2194	
5	784.3988	392.7030			4	537.278	269.142638	537.2793	
6	841.4203	421.2138	841.4152	421.2087	5	636.3464	318.676838	636.3472	
7	912.4574	456.7323	912.4468	456.7275	6	707.3835	354.195388	707.3844	
8	983.4945	492.2509	983.4852	492.2456	7	804.4363	402.721788	804.4369	402.7221
9	1070.5265	535.7669	1070.5166	535.7625	8	891.4683	446.237788	891.4687	446.2373
10	1167.5793	584.2933			9	962.5054	481.756338	962.5075	
11	1238.6164	619.8118			10	1033.5425	517.274888	1033.5398	
12	1337.6848	669.3460		669.347	11	1090.564	545.785638	1090.5655	
13	1465.7434	733.3753			12	1276.6433	638.825288		
14	1552.7754	776.8913			13	1391.6702	696.338738		696.34
15	1699.8439	850.4256			14	1504.7543	752.880788		
					15	1601.8071	801.407188		

Tandem Mass Spectrum for β B1: VGSVK*VSSGTWVGYPGYR (QE data)

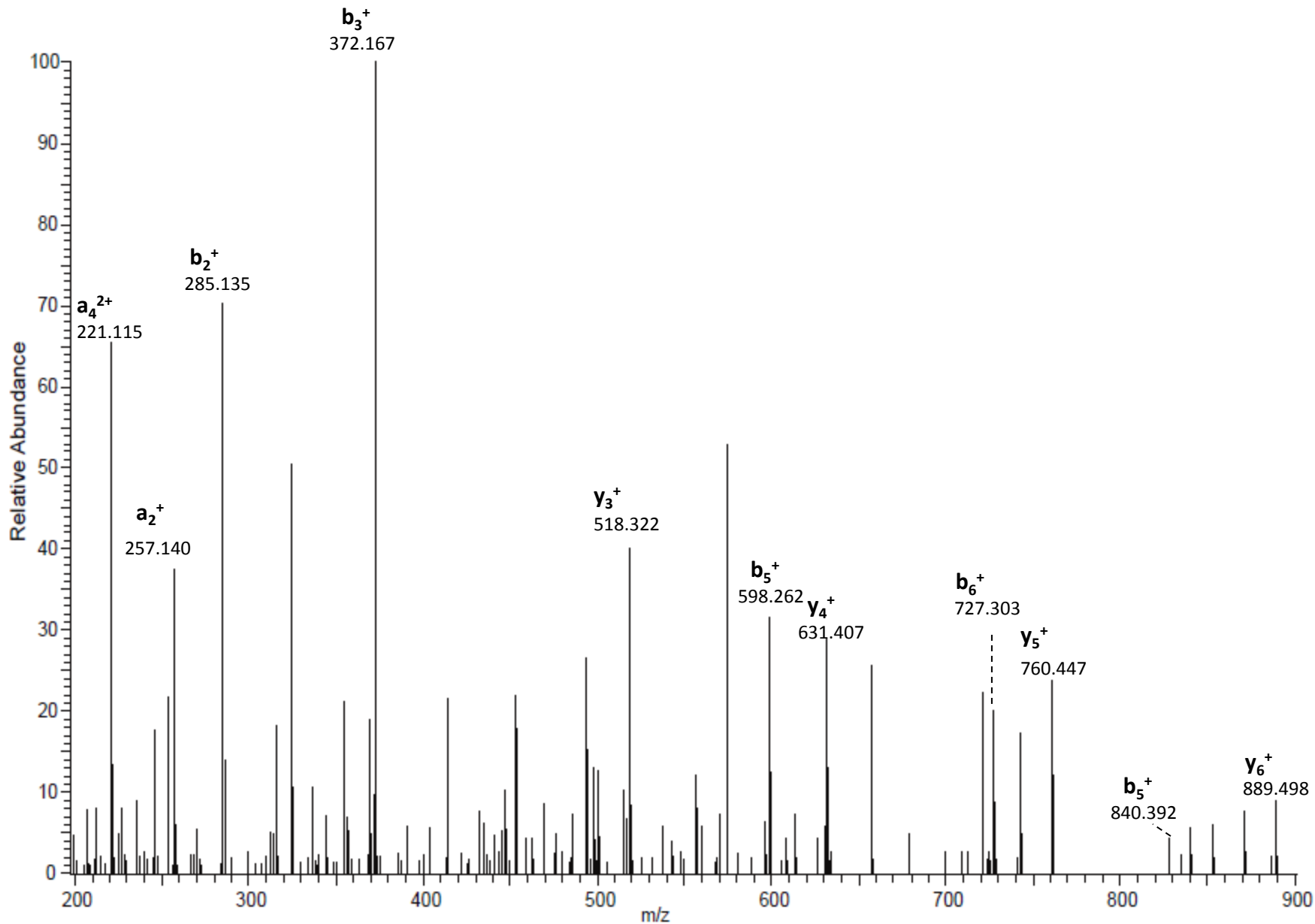


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for β B1: VGSVK*VSSGTWVG YQYPGYR (QE data)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	157.0972	79.0522	157.0974		1	175.119	88.063138	175.1194	
3	244.1292	122.5682	244.1305		2	338.1823	169.594788		
4	343.1976	172.1024			3	395.2037	198.105488		
5	615.3461	308.1767	615.3388	308.1721	4	492.2565	246.631888	492.2581	246.6323
6	714.4145	357.7109	714.4055		5	655.3198	328.163538	655.3214	
7	801.4465	401.2269	801.4365		6	783.3784	392.192838	783.3814	
8	888.4785	444.7429	888.4739		7	946.4417	473.724488	946.4445	
9	945.5	473.2536			8	1003.4632	502.235238	1003.4654	
10	1046.5477	523.7775	1046.5403	523.77	9	1102.5316	551.769438	1102.5306	
11	1232.627	616.8171	1232.635	616.8126	10	1288.6109	644.809088	1288.613	
12	1331.6954	666.3513			11	1389.6586	695.332938		
13	1388.7169	694.8621			12	1446.6801	723.843688		
14	1551.7802	776.3937		776.4099	13	1533.7121	767.359688		
15	1679.8388	840.4230			14	1620.7441	810.875688		
16	1842.9021	921.9547			15	1719.8125	860.409888		
17	1939.9549	970.4811			16	1991.961	996.484138		
18	1996.9763	998.9918			17	2091.0294	1046.018338		
19	2160.0397	1080.5235			18	2178.0615	1089.534388		
					19	2235.0829	1118.045088		

Tandem Mass Spectrum for α B: HFSPEELK*VK (QE data)

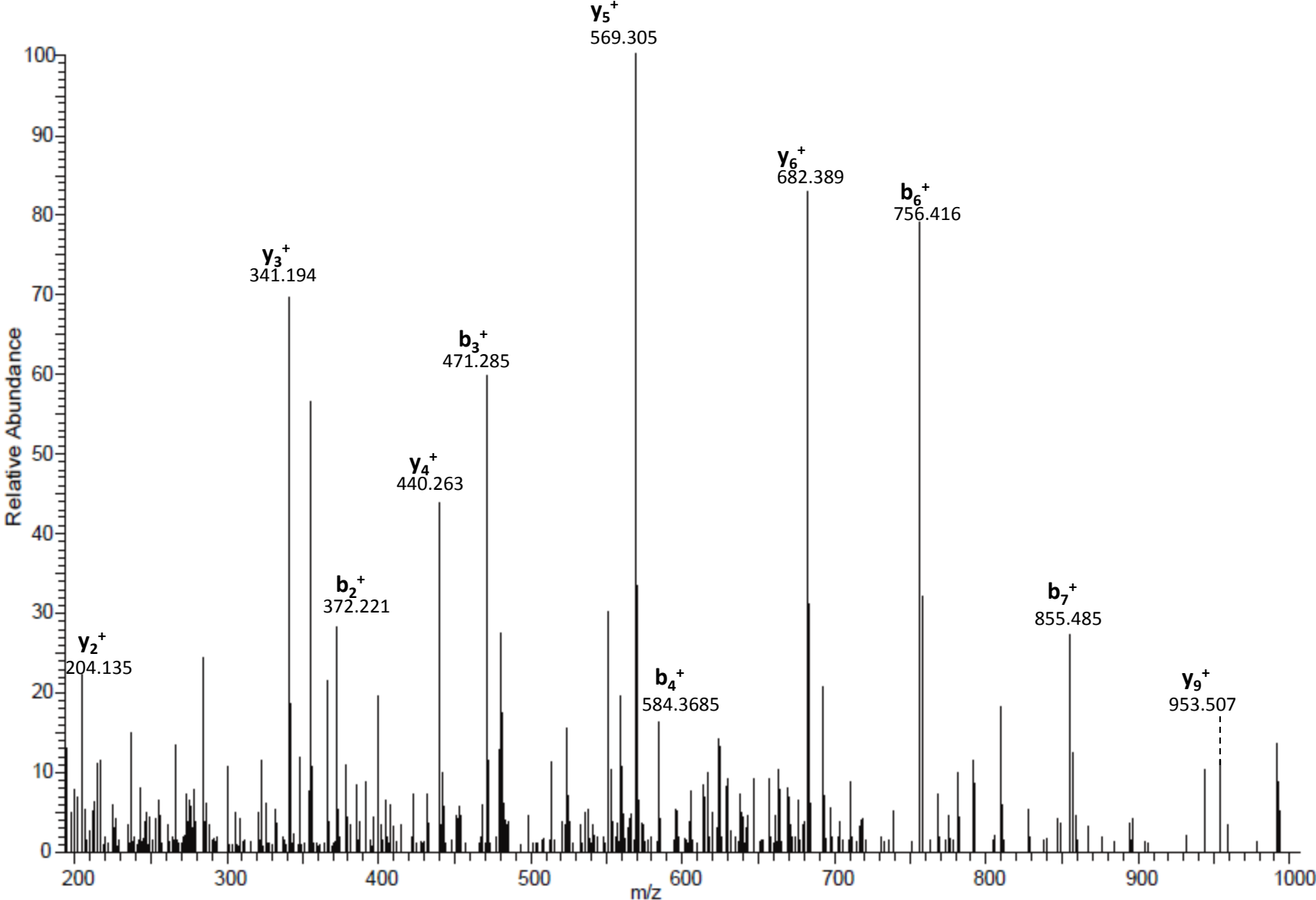


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for α B: HFSPEELK*VK (QE data)

b ions					y ions				
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	285.1346	143.0709	285.1353		1	147.1128	74.060038	147.1133	
3	372.1666	186.5869	372.1675		2	246.1812	123.594238	246.1815	
4	469.2194	235.1133	469.2256	235.1114	3	518.3297	259.668488	518.322	
5	598.262	299.6346	598.2619	299.6361	4	631.4137	316.210488	631.4065	316.2056
6	727.3046	364.1559	727.3033	364.1601	5	760.4563	380.731788	760.4467	380.7266
7	840.3886	420.6979	840.392		6	889.4989	445.253088	889.4975	445.258
8	1112.5371	556.7722		556.7664	7	986.5517	493.779488	986.544	493.775
9	1211.6055	606.3064		606.3015	8	1073.5837	537.295488		537.2955
10					9	1220.6521	610.829688		

Tandem Mass Spectrum for α B: VK*VLGDVIEVHGK (QE data)

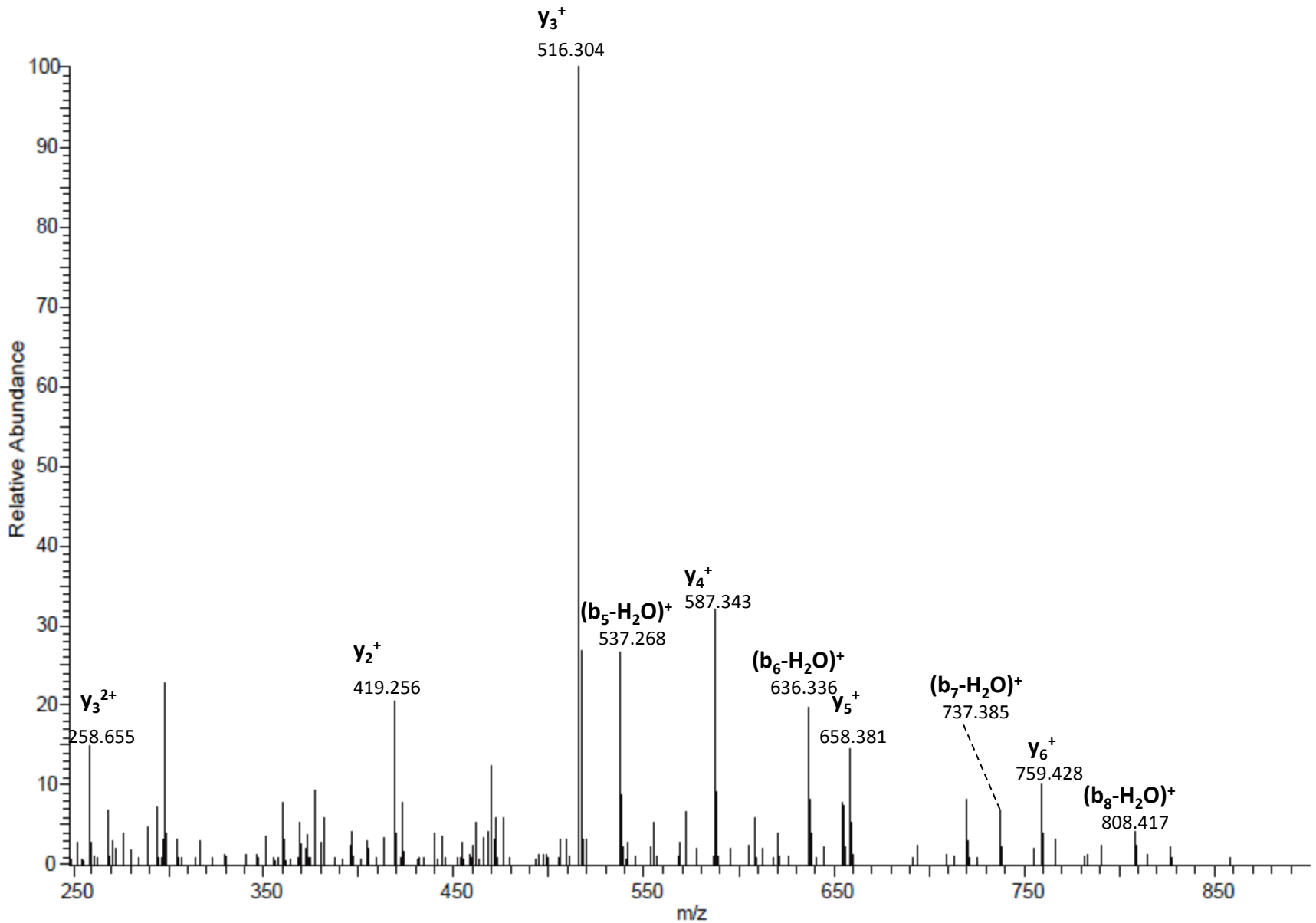


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for α B: VK*VLGDVIEVHGK (QE data)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	372.2242	186.6157	372.221		1	147.1128	74.060038	147.1133	
3	471.2926	236.1499	471.285		2	204.1343	102.570788	204.1348	
4	584.3766	292.6919	584.3685		3	341.1932	171.100238	341.1939	
5	641.3981	321.2027	641.3991		4	440.2616	220.634438	440.2631	
6	756.425	378.7161	756.4155	378.7103	5	569.3042	285.155738	569.3054	
7	855.4935	428.2504	855.4849		6	682.3883	341.697788	682.3894	
8	968.5775	484.7924			7	781.4567	391.231988	781.4567	
9	1097.6201	549.3137			8	896.4836	448.745438	896.4794	
10	1196.6885	598.8479			9	953.5051	477.256188	953.5071	
11	1333.7474	667.3773			10	1066.5891	533.798188		
12	1390.7689	695.8881			11	1165.6575	583.332388		
					12	1437.806	719.406638		

Tandem Mass Spectrum for α B: EEKPAVTAAPK*K (QE data)

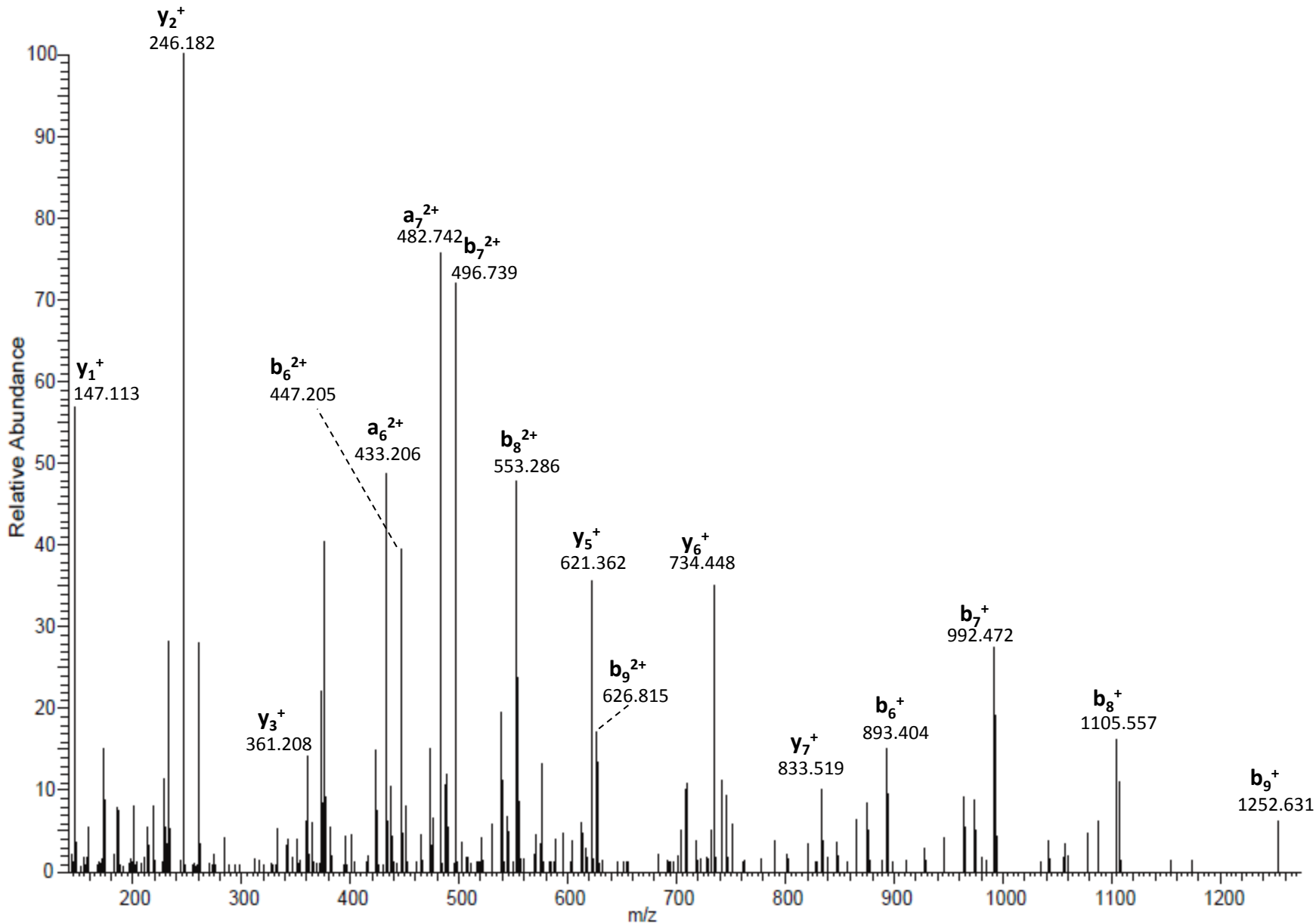


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for α B: EEKPAVTAAPK*K (QE data)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	259.0925	130.0499			1	147.1128	74.060038	147.1132	
3	387.1874	194.0973			2	419.2613	210.134288	419.2557	
4	484.2402	242.6237			3	516.314	258.660638	516.304	258.6553
5	555.2773	278.1423	555.2789		4	587.3511	294.179188	587.3433	294.1748
6	654.3457	327.6765	654.3439		5	658.3883	329.697788	658.3811	329.693
7	755.3934	378.2003	755.4014		6	759.4359	380.221588	759.4275	380.2175
8	826.4305	413.7189	826.4253		7	858.5044	429.755838	858.4985	
9	897.4676	449.2374			8	929.5415	465.274388		
10	994.5204	497.7638			9	1026.5942	513.800738		
11	1266.6689	633.8381			10	1154.6892	577.848238		577.8478
					11	1283.7318	642.369538		

Tandem Mass Spectrum for α A: SDRDK*FVIFLDVK (QE data)

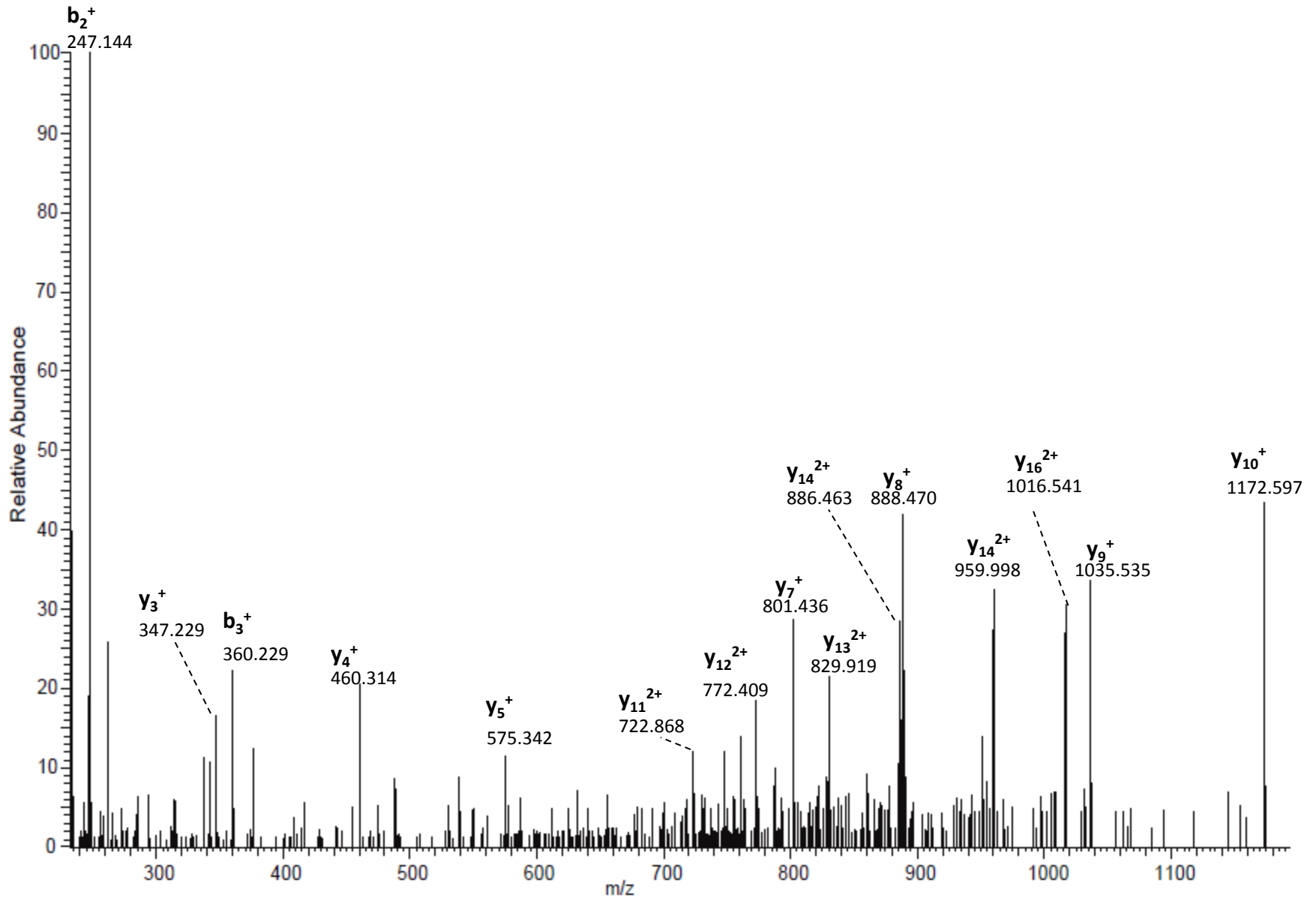


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for α A: SDRDK*FVIFLDVK (QE data)

b ions					y ions				
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	203.0662	102.0367			1	147.1128	74.060038	147.1133	
3	359.1674	180.0873	359.1682		2	246.1812	123.594238	246.1818	
4	474.1943	237.6008	474.194		3	361.2082	181.107738	361.2087	
5	746.3428	373.6750	746.3381	373.67	4	474.2922	237.649738	474.2931	
6	893.4112	447.2092	893.4036	447.2049	5	621.3606	311.183938	621.3624	
7	992.4796	496.7434	992.472	496.7393	6	734.4447	367.725988	734.4483	
8	1105.5637	553.2855	1105.557	553.2822	7	833.5131	417.260188	833.5189	
9	1252.6321	626.8197	1252.6306	626.8151	8	980.5815	490.794388		
10	1365.7161	683.3617		683.3623	9	1252.73	626.868638	1252.6306	
11	1480.7431	740.8752		740.872	10	1367.7569	684.382088		
12	1579.8115	790.4094		790.4042	11	1523.858	762.432638		
					12	1638.885	819.946138		

Tandem Mass Spectrum for α A: FVIFLDVK*HFSPEDLTVK (QE data)

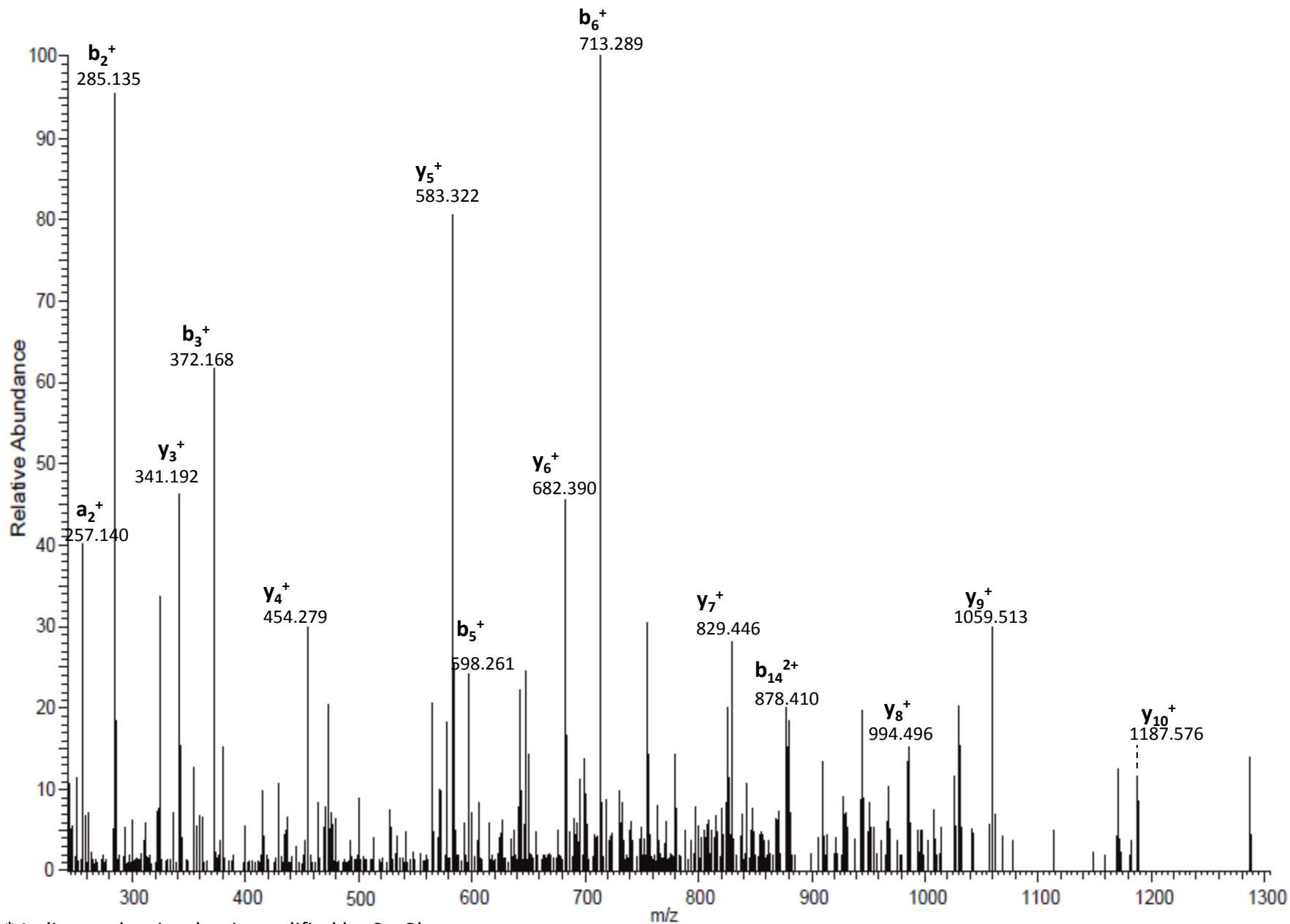


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for α A: FVIFLDVK*HFSPEDLTVK (QE data)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	247.1441	124.0757			1	147.1128	74.060038	147.1133	
3	360.2282	180.6177	360.2296		2	246.1812	123.594238		
4	507.2966	254.1519	507.2971		3	347.2289	174.118088	347.2291	
5	620.3806	310.6939			4	460.313	230.660138	460.3143	
6	735.4076	368.2074			5	575.3399	288.173588	575.3423	
7	834.476	417.7416			6	704.3825	352.694888		
8	1106.6245	553.8159			7	801.4353	401.221288	801.4364	401.2228
9	1243.6834	622.3453			8	888.4673	444.737288	888.4704	
10	1390.7518	695.8795			9	1035.5357	518.271488	1035.5351	
11	1477.7838	739.3955			10	1172.5946	586.800938	1172.597	586.8029
12	1574.8366	787.9219			11	1444.7431	722.875188		722.868
13	1703.8792	852.4432			12	1543.8115	772.409388		772.4094
14	1818.9061	909.9567			13	1658.8384	829.922838		829.9188
15	1931.9902	966.4987			14	1771.9225	886.464888		886.4633
16	2033.0379	1017.0226			15	1918.9909	959.999088		959.9975
17	2132.1063	1066.5568			16	2032.075	1016.541138		1016.5414
					17	2131.1434	1066.075338		

Tandem Mass Spectrum for α A: HFSPEDLTVK*VQDDFVEIHGK (QE data)

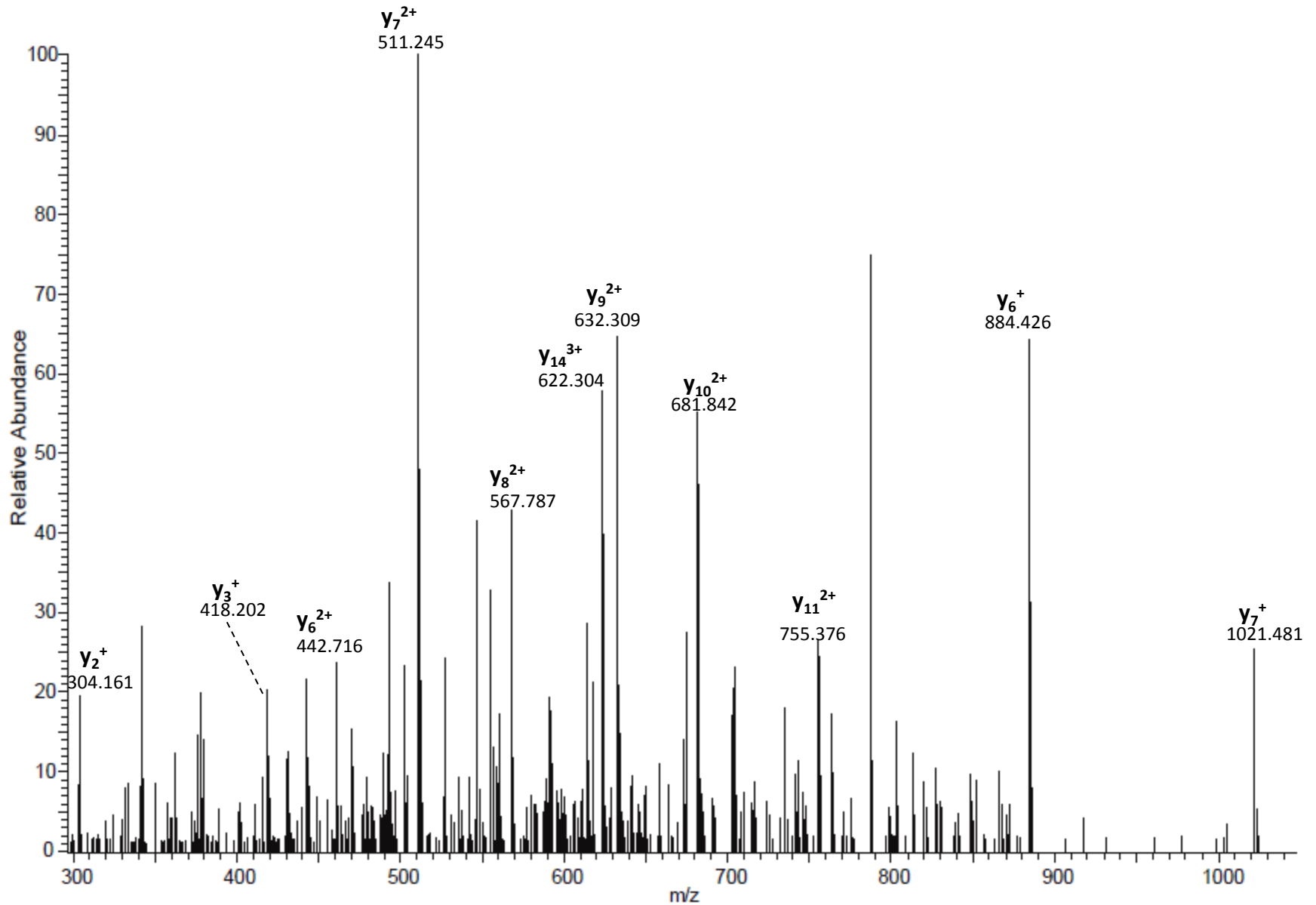


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for α A: HFSPEDLTVK*VQDDFVEIHGK (QE data)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	285.1346	143.0709	285.1354		1	147.1128	74.060038	147.1134	
3	372.1666	186.5869	372.1682		2	204.1343	102.570788	204.135	
4	469.2194	235.1133			3	341.1932	171.100238	341.1924	
5	598.262	299.6346	598.2613	299.636	4	454.2772	227.642238	454.2794	
6	713.2889	357.1481	713.2895	357.1491	5	583.3198	292.163538	583.3217	
7	826.373	413.6901	826.3729	413.6919	6	682.3883	341.697788	682.3899	
8	927.4207	464.2140	927.429	464.2111	7	829.4567	415.231988	829.4461	415.2353
9	1026.4891	513.7482	1026.4999		8	944.4836	472.745438	944.4966	
10	1298.6375	649.8224		649.8165	9	1059.5106	530.258938	1059.5133	530.254
11	1397.706	699.3566		699.3572	10	1187.5691	594.288188	1187.5757	
12	1525.7645	763.3859		763.3801	11	1286.6375	643.822388		
13	1640.7915	820.8994			12	1558.786	779.896638		779.8908
14	1755.8184	878.4128		878.4095	13	1657.8544	829.430838		829.4451
15	1902.8868	951.9470		951.9451	14	1758.9021	879.954688		879.9469
16	2001.9553	1001.4813			15	1871.9862	936.496738		
17	2130.9978	1066.0025			16	1987.0131	994.010188		
18	2244.0819	1122.5446			17	2116.0557	1058.531488		
19	2381.1408	1191.0740			18	2213.1085	1107.057888		
20	2438.1623	1219.5848			19	2300.1405	1150.573888		
					20	2447.2089	1224.108088		

Tandem Mass Spectrum for α A: VQDDFVEIHGK*HNER (QE data)

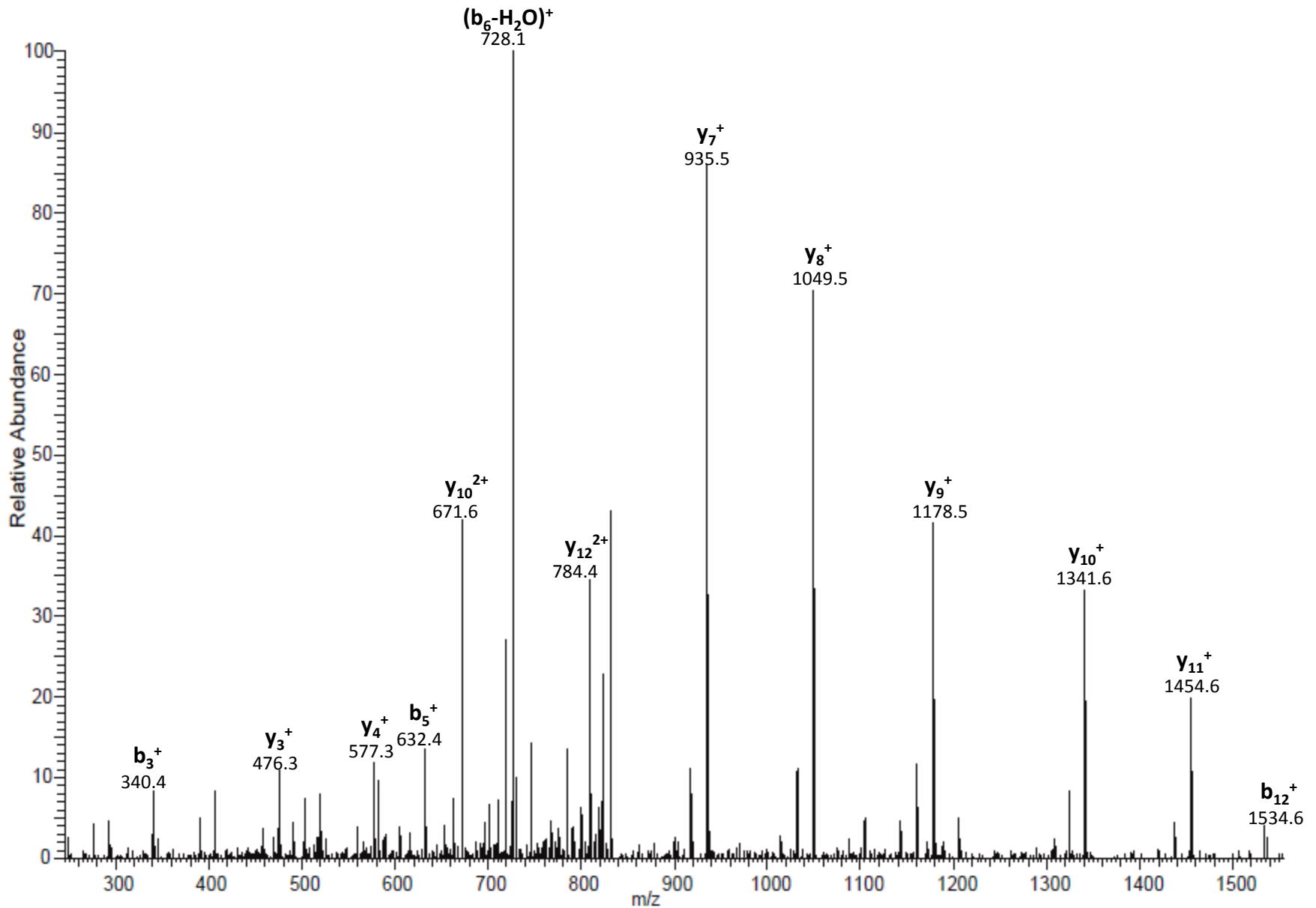


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for α A: VQDDFVEIHGK*HNER (QE data)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	228.1343	114.5708	228.1347		1	175.119	88.063138	175.1192	
3	343.1612	172.0842	343.1657		2	304.1615	152.584388	304.1611	
4	458.1882	229.5977	458.1812		3	418.2045	209.605888	418.2018	
5	605.2566	303.1319			4	555.2634	278.135338	555.2623	
6	704.325	352.6661			5	827.4118	414.209538	827.4014	
7	833.3676	417.1874			6	884.4333	442.720288	884.4255	442.7157
8	946.4516	473.7294			7	1021.4922	511.249738	1021.481	511.2445
9	1083.5106	542.2589			8	1134.5763	567.791788	1134.5675	567.7867
10	1140.532	570.7696			9	1263.6189	632.313088	1263.6154	632.3091
11	1412.6805	706.8439			10	1362.6873	681.847288		681.8416
12	1549.7394	775.3733			11	1509.7557	755.381488		755.3756
13	1663.7823	832.3948			12	1624.7827	812.894988		812.8878
14	1792.8249	896.9161			13	1739.8096	870.408438		870.4103
15					14	1867.8682	934.437738		

Tandem Mass Spectrum for β B2: IILYENPNFTGK*K (Orbitrap Velos)

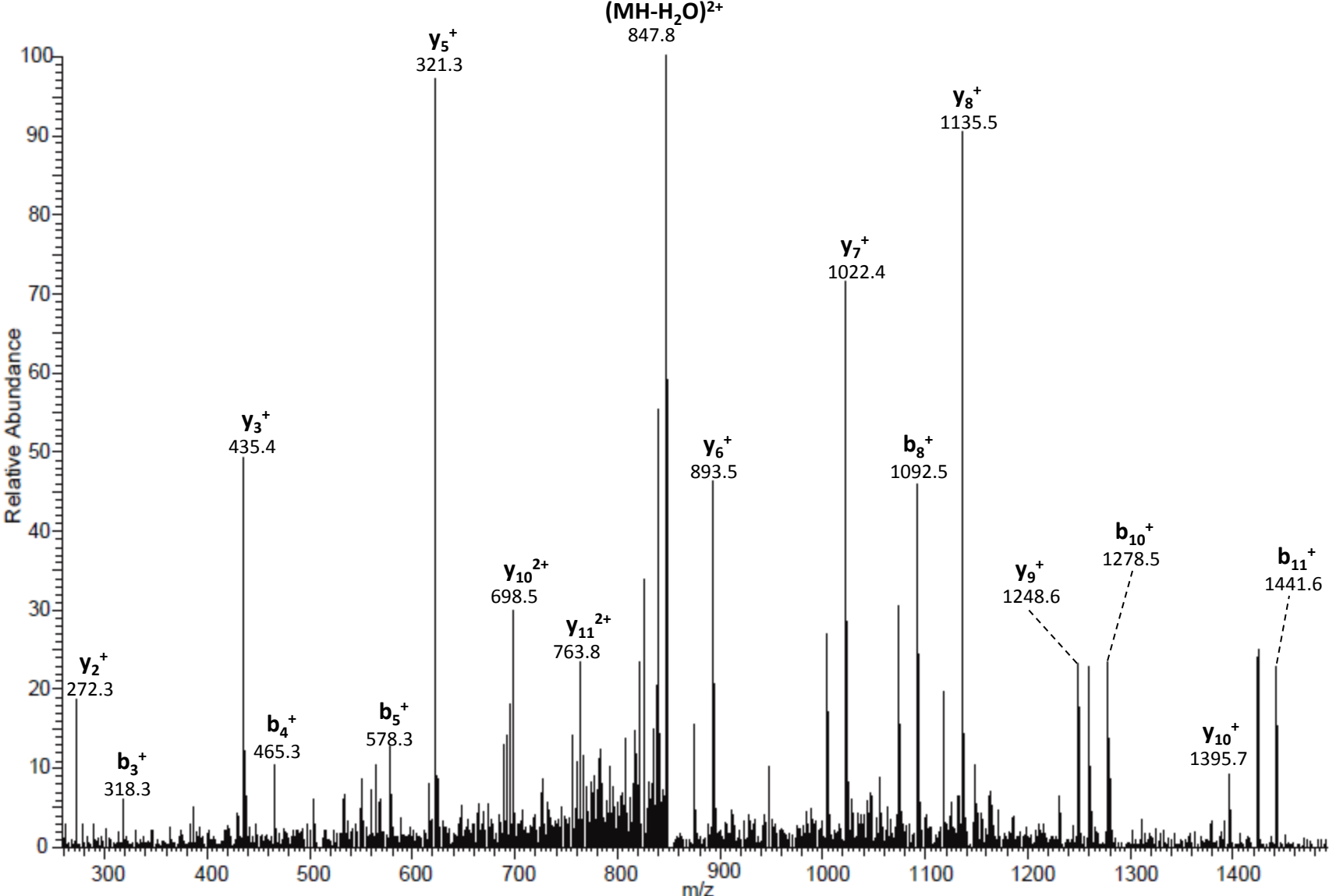


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for β B2: IILYENPNFTGK*K (Orbitrap Velos)

b ions					y ions				
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	227.1754	114.0913			1	147.1128	74.060038		
3	340.2595	170.6334	340.4		2	419.2613	210.134288	419.3	
4	503.3228	252.1650	503.3		3	476.2827	238.644988	476.3	
5	632.3654	316.6863	632.4		4	577.3304	289.168838	577.3	
6	746.4083	373.7078	746.4		5	724.3988	362.703038	724.5	
7	843.4611	422.2342			6	838.4418	419.724538		
8	957.504	479.2556			7	935.4945	468.250888	935.5	
9	1104.5724	552.7898			8	1049.5374	525.272338	1049.5	
10	1205.6201	603.3137	1205.5		9	1178.58	589.793638	1178.5	
11	1262.6416	631.8244			10	1341.6434	671.325338	1341.6	671.5
12	1534.79	767.8986	1534.6		11	1454.7274	727.867338	1454.6	
						1567.8115	784.409388		784.4

Tandem Mass Spectrum for β B1: GEMFILEK*GEYPR (Orbitrap Velos)

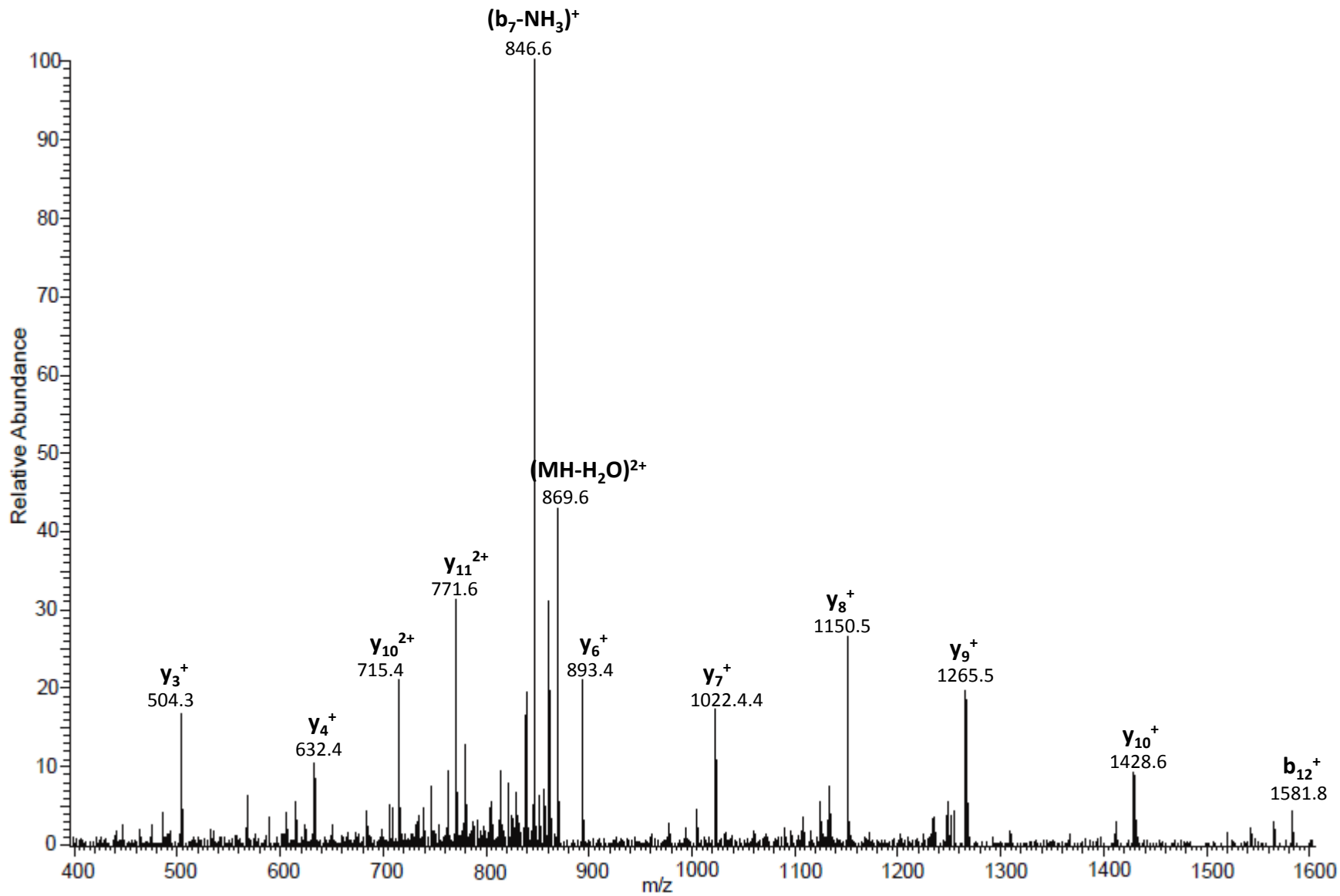


* Indicates the site that is modified by CysGly

Predicated and detected b- and γ - ions for β B1: GEMFILEK*GEYPR (Orbitrap Velos)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	187.0713	94.0393			1	175.119	88.063138		
3	318.1118	159.5595	318.3		2	272.1717	136.589488	272.2	
4	465.1802	233.0937	465.3		3	435.235	218.121138	435.3	
5	578.2643	289.6358	578.3		4	564.2776	282.642438	564.3	
6	691.3484	346.1778	691.3		5	621.2991	311.153188	621.3	
7	820.391	410.6991	820.4		6	893.4476	447.227438	893.5	
8	1092.5394	546.7733	1092.5		7	1022.4902	511.748738	1022.4	
9	1149.5609	575.2841	1149.3		8	1135.5742	568.290738	1135.5	
10	1278.6035	639.8054	1278.5		9	1248.6583	624.832788	1248.6	
11	1441.6668	721.3370	1441.6		10	1395.7267	698.366988	1395.7	698.5
12	1538.7196	769.8634			11	1526.7672	763.887238		763.7
					12	1655.8098	828.408538		

Tandem Mass Spectrum for β A3: ITIYDQENFQGK*R (Orbitrap Velos)

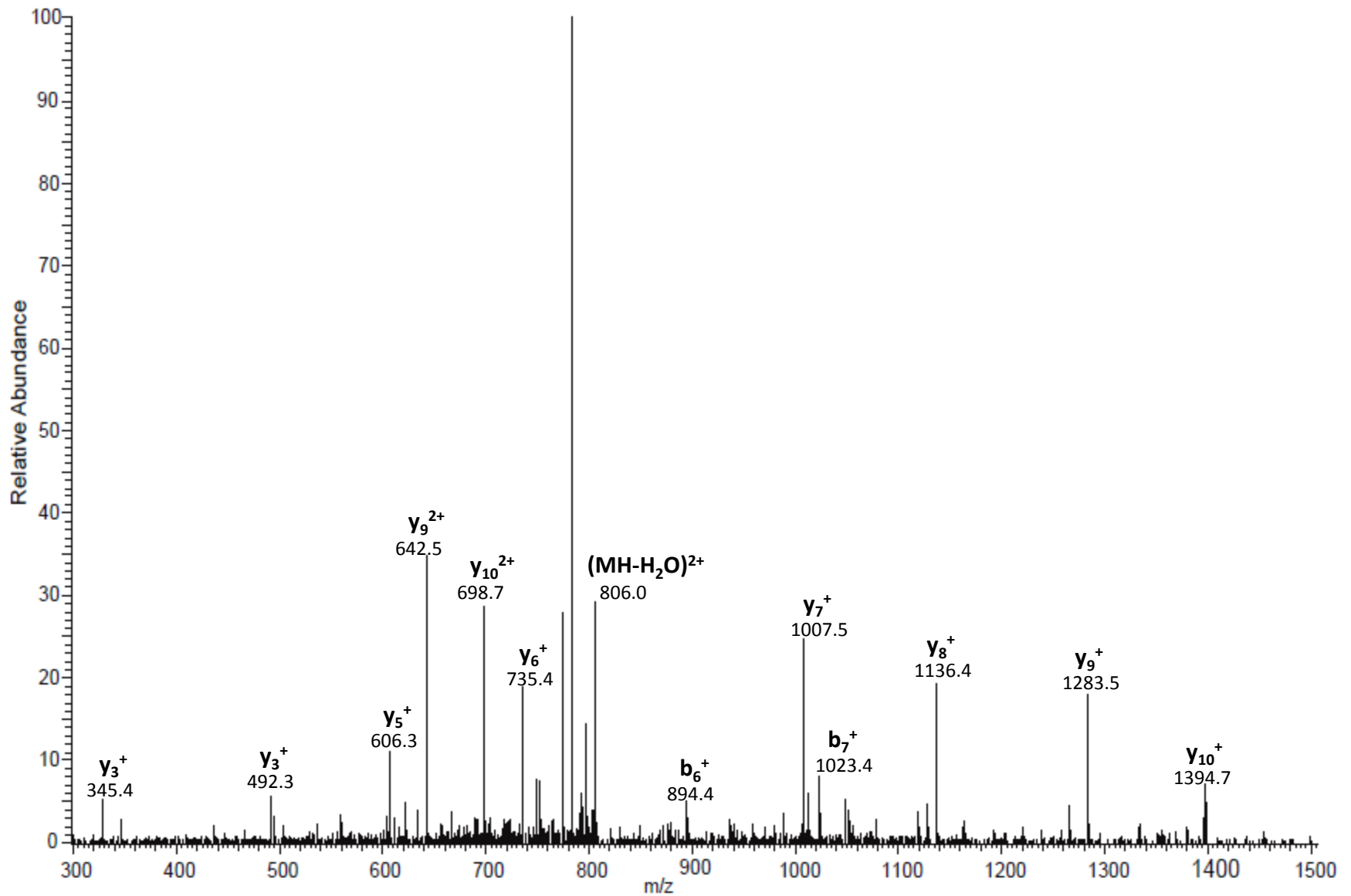


* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for β A3: ITIYDQENFQGK*R (Orbitrap Velos)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	215.139	108.0731			1	175.119	88.063138		
3	328.2231	164.6152	328.3		2	447.2674	224.137338	447.5	
4	491.2864	246.1468	491.2		3	504.2889	252.648088	504.3	
5	606.3134	303.6603	606.4		4	632.3475	316.677388	632.4	
6	734.3719	367.6896	734.4		5	779.4159	390.211588	779.4	
7	863.4145	432.2109			6	893.4588	447.233038	893.4	
8	977.4575	489.2324	977.5		7	1022.5014	511.754338	1022.4	
9	1124.5259	562.7666	1124.5		8	1150.56	575.783638	1150.5	
10	1252.5844	626.7958	1252.6		9	1265.5869	633.297088	1265.5	
11	1309.6059	655.3066	1309.4		10	1428.6502	714.828738	1428.6	715.4
12	1581.7544	791.3808			11	1541.7343	771.370788	1581.8	771.5
					12	1642.782	821.894638		

Tandem Mass Spectrum for β A3: MTIFEK*ENFIGR (Orbitrap Velos)

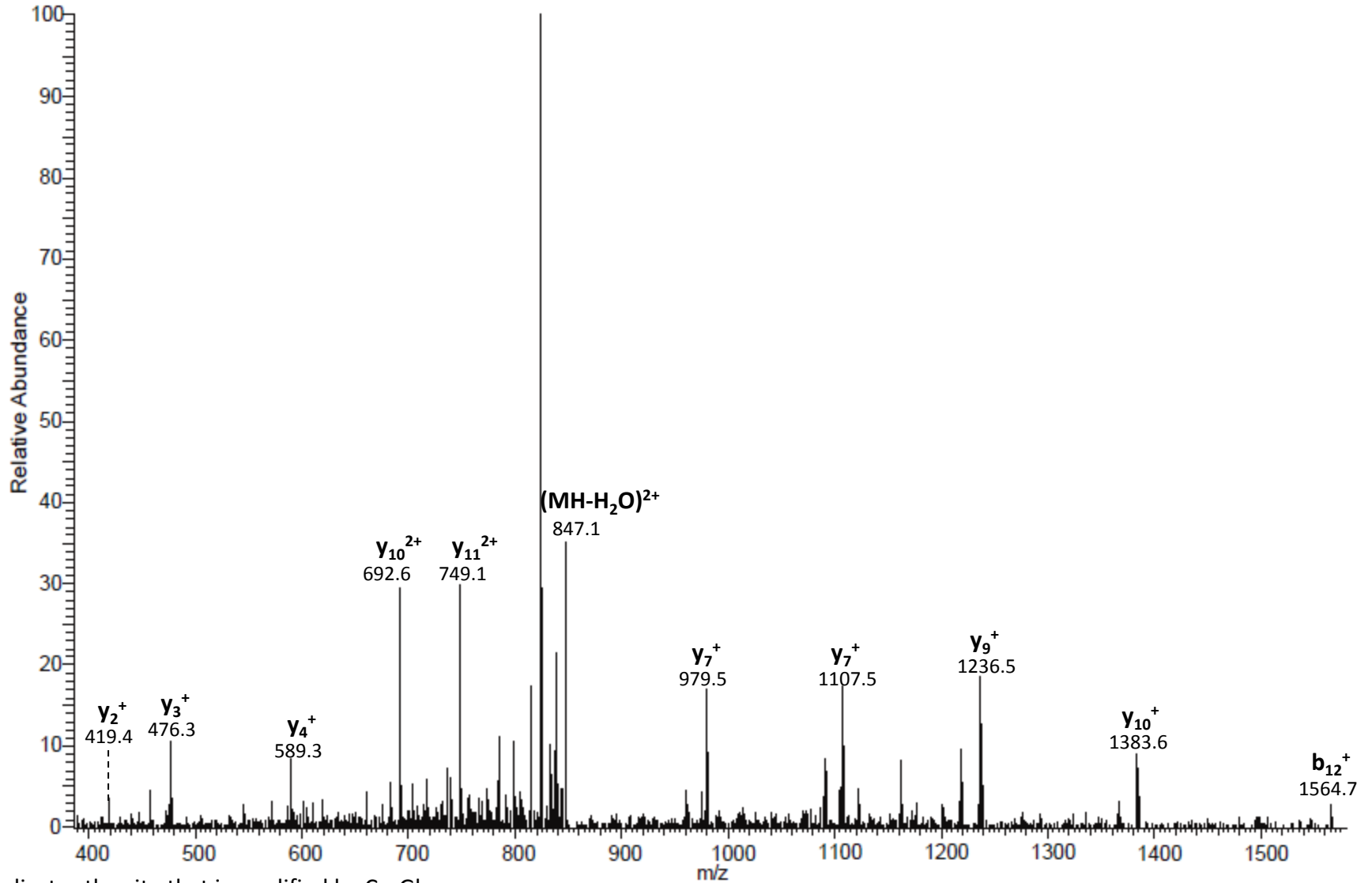


* Indicates the site that is modified by CysGly

Predicated and detected b- and γ - ions for β A3: MTIFEK*ENFIGR (Orbitrap Velos)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	233.0954	117.0513			1	175.119	88.063138		
3	346.1795	173.5934			2	232.1404	116.573838	232.2	
4	493.2479	247.1276			3	345.2245	173.115888	345.3	
5	622.2905	311.6489			4	492.2929	246.650088	492.3	
6	894.439	447.7231		894.4	5	606.3358	303.671538	606.3	
7	1023.4816	512.2444		1023.4	6	735.3784	368.192838	735.4	
8	1137.5245	569.2659			7	1007.5269	504.267088	1007.5	
9	1284.5929	642.8001			8	1136.5695	568.788388	1136.4	
10	1397.677	699.3421			9	1283.6379	642.322588	1283.5	642.5
11	1454.6984	727.8528		1454.7	10	1396.7219	698.864588	1397.7	698.7
12					11	1497.7696	749.388438		

Tandem Mass Spectrum for β A4: LTIFEQENFLGK*K (Orbitrap Velos)



* Indicates the site that is modified by CysGly

Predicated and detected b- and y- ions for β A4: LTIFEQENFLGK*K (Orbitrap Velos)

b ions				y ions					
	Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)		Theoretical (+1)	Theoretical (+2)	Experimental (+1)	Experimental(+2)
2	215.139	108.0731			1	147.1128	74.060038		
3	328.2231	164.6152	328.3		2	419.2613	210.134288	419.4	
4	475.2915	238.1494	475.5		3	476.2827	238.644988	476.3	
5	604.3341	302.6707	604.4		4	589.3668	295.187038	589.3	
6	732.3927	366.7000			5	736.4352	368.721238	736.4	
7	861.4353	431.2213			6	850.4781	425.742688	979.5	
8	975.4782	488.2427			7	979.5207	490.263988	1107.5	
9	1122.5466	561.7769			8	1107.5793	554.293288	1236.5	
10	1235.6307	618.3190			9	1236.6219	618.814588	1383.6	
11	1292.6521	646.8297			10	1383.6903	692.348788		692.6
12	1564.8006	782.9039	1564.7		11	1496.7744	748.890838		749.1
						1597.8221	799.414688		

Supplemental Table 1: Demographics of lens donors, age, cause of death, cataract status and application of tissue.

Donor age	Sex	Cause of death	Normal/diseased	Application
22	Female	pneumonia	Normal	1D-LC-MS/MS on QE
53	Male	end-stage COPD	Normal	1D-LC-MS/MS on QE
50	Male	myocardial Infarction	Cataract	1D-LC-MS/MS on QE
37	Unknown	Unknown	Normal	MudPIT
58	Unknown	Unknown	Normal	MudPIT

Supplemental Table 2: Lys residues of lens proteins that are modified by (DHA)Gly in the different fractions obtained from different aged lenses.

Crystallins	Site	Lenses											
		22 year-old Normal			53 year-old Normal			50 year-old Cataract			37 year-old Normal (MudPIT)	58 year-old Normal (MudPIT)	
		WSF	USF	UIF	WSF	USF	UIF	WSF	USF	UIF	UIF	UIF	
γ S	K7				X			X					X
	K14							X				X	X
	K95					X			X	X		X	
	K145				X			X				X	X
	K159				X			X					X
β B1	K118												X
	K187				X	X		X	X			X	X
β B2	K120										X	X	
β A4	K118										X	X	
β A3	K44												X
	K131												X
α B	K90					X				X			X
	K92					X							X
	K174							X			X		X
α A	K70					X	X		X	X			
	K78					X			X	X			
	K88					X			X				
	K99		X										

X indicates modification was detected.

Proteins Identified in different aged lens samples

Accession #	Gene Name	Description	Total Spectral Count (SC)	22 year-old			53 year-old			50 year-old		
				WSF (SC)	USF (SC)	UIF (SC)	WSF (SC)	USF (SC)	UIF (SC)	WSF (SC)	USF (SC)	UIF (SC)
Q13813	SPTAN1	Isoform 2 of Spectrin alpha chain, non-erythrocytic 1	1221	191	316	171	84	100	90	101	99	69
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	1010	124	244	225	46	70	98	45	101	57
O15020	SPTBN2	Spectrin beta chain, non-erythrocytic 2	80	4	17	16	5	9	11	1	11	6
P11277	SPTB	Spectrin beta chain, erythrocytic	48	2	15	15	0	2	4	0	6	4
Q15149	PLEC	Plectin	381	24	157	57	12	44	36	8	33	10
Q12934	BFSP1	Filensin	4366	93	1611	248	51	939	448	53	711	212
P07315	CRYGC	Gamma-crystallin C	3572	314	229	69	902	411	367	775	357	148
P07316	CRYGB	Gamma-crystallin B	1286	139	85	23	250	158	106	295	179	51
P11844	CRYGA	Gamma-crystallin A	55	7	7	2	2	10	8	7	12	0
Q13515	BFSP2	Phakinin	3808	127	1544	178	49	783	333	65	597	132
P04264	KRT1	Keratin, type II cytoskeletal 1	688	22	31	166	62	67	112	32	34	162
P35908	KRT2	Keratin, type II cytoskeletal 2 epidermal	181	4	4	36	20	15	39	11	8	44
P13647	KRT5	Keratin, type II cytoskeletal 5	78	3	3	29	7	5	9	3	6	13
P02538	KRT6A	Keratin, type II cytoskeletal 6A	77	3	3	27	9	5	9	3	5	13
Q6KB66	KRT80	Keratin, type II cytoskeletal 80	25	0	1	3	5	5	5	1	1	4
P35527	KRT9	Keratin, type I cytoskeletal 9	312	12	16	94	17	22	46	14	19	72
P13645	KRT10	Keratin, type I cytoskeletal 10	281	3	6	66	24	26	65	9	15	67
P02533	KRT14	Keratin, type I cytoskeletal 14	42	0	0	24	3	0	3	0	2	10
P08779	KRT16	Keratin, type I cytoskeletal 16	36	0	0	16	7	2	4	0	1	6
Q2M215	KRT24	Keratin, type I cytoskeletal 24	10	0	0	6	0	1	3	0	0	0
Q92764	KRT35	Keratin, type I cuticular Ha5	5	0	0	1	0	0	1	0	0	3
P22914	CRYGS	Beta-crystallin S	6728	653	379	100	1637	677	702	1737	595	248
Q9UFA7	DKFZp434A0627	Crystallin, gamma S, isoform CRA_a	4441	439	247	79	1067	443	478	1066	441	181
P60709	ACTB	Actin, cytoplasmic 1	986	159	307	50	32	114	67	48	178	31
Q53G76		Beta actin variant (Fragment)	845	121	257	50	32	105	67	46	136	31
Q53GK6		Beta actin variant (Fragment)	844	122	256	50	32	105	67	45	136	31
P68032	ACTC1	Actin, alpha cardiac muscle 1	433	77	113	35	15	48	37	25	69	14
Q658J3	POTEE	POTE ankyrin domain family member E	276	37	103	21	13	28	22	13	29	10
Q562R1	ACTBL2	Beta-actin-like protein 2	246	48	58	16	5	27	20	11	52	9
Q562Z4	ACT	Actin-like protein (Fragment)	154	27	53	10	5	14	8	5	25	7
Q562U2	ACT	Actin-like protein (Fragment)	114	16	36	14	5	9	10	5	12	7
P53674	CRYBB1	Beta-crystallin B1	14144	1220	803	304	3231	1815	1433	2993	1896	449
A0A097	CRYBA1	Beta crystallin A3 chain transcript CN (Fragment)	9065	1239	825	252	1456	1011	636	1922	1388	336
A0A0H3	CRYBA1	Crystallin beta A3/A1 (Fragment)	2086	403	122	37	195	129	105	655	350	90
P04075	ALDOA	Fructose-bisphosphate aldolase A	653	120	131	33	89	81	42	73	58	26
B7Z3K9		Fructose-bisphosphate aldolase	323	75	61	20	36	38	21	27	35	10
B7Z1Z9		Fructose-bisphosphate aldolase	254	53	46	14	27	33	21	20	30	10
P00352	ALDH1A1	Retinal dehydrogenase 1	2259	389	337	157	243	302	241	195	279	116
Q53FB6		Mitochondrial aldehyde dehydrogenase 2 variant (Fragment)	67	10	7	8	5	10	13	2	8	4
P11171	EPB41	Protein 4.1	175	0	18	74	0	1	40	0	1	41
O43491	EPB41L2	Band 4.1-like protein 2	170	0	13	68	0	3	43	0	4	39
Q9H4G0	EPB41L1	Band 4.1-like protein 1	30	0	3	14	0	0	4	0	0	9
Q9Y2J2	EPB41L3	Band 4.1-like protein 3	22	0	2	9	0	0	4	0	0	7
P02489	CRYAA	Alpha-crystallin A chain	11571	1365	2953	338	652	2042	1118	639	1995	469
A0A0H3	CRYBB2	Beta-crystallin B2 (Fragment)	4283	831	607	282	636	431	339	531	407	219
A0A0H3	CRYBB2	Beta-crystallin B2	3852	723	508	257	546	392	301	515	397	213
P08670	VIM	Vimentin	308	14	165	43	3	46	8	1	24	4
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	1330	284	246	64	135	160	94	120	169	58
P63104	YWHAZ	14-3-3 protein zeta/delta	133	27	16	10	13	13	25	10	15	4
P62258	YWHAE	14-3-3 protein epsilon	97	27	25	4	10	6	3	6	13	3

P61981	YWHAG	14-3-3 protein gamma	74	22	22	1	7	5	2	4	11	0
P31946	YWHAB	14-3-3 protein beta/alpha	37	14	9	1	2	0	1	3	7	0
Q04917	YWHAH	14-3-3 protein eta	31	9	10	1	2	0	1	2	6	0
P07320	CRYGD	Gamma-crystallin D	3249	165	236	34	530	599	423	597	507	158
P14618	PKM	Pyruvate kinase PKM	388	75	102	33	39	54	29	19	29	8
P14618	PKM	Isoform M1 of Pyruvate kinase PKM	362	71	98	34	38	46	27	16	25	7
P06733	ENO1	Alpha-enolase	331	81	44	21	67	20	36	38	9	15
P09104	ENO2	Gamma-enolase	97	25	6	2	20	8	13	14	4	5
P48637	GSS	Glutathione synthetase	639	96	89	31	62	103	81	59	85	33
Q99497	PARK7	Protein deglycase DJ-1	737	147	24	4	221	72	53	158	46	12
P02511	CRYAB	Alpha-crystallin B chain	16304	2170	4054	404	1336	2603	1648	951	2399	739
P80723	BASP1	Brain acid soluble protein 1	1847	164	173	641	59	42	306	99	27	336
V9HW89	HEL-S-95n	Epididymis secretory sperm binding protein Li 95n	801	166	155	52	50	95	74	57	114	38
Q00796	SORD	Sorbitol dehydrogenase	740	150	142	52	50	95	77	52	92	30
P00558	PGK1	Phosphoglycerate kinase 1	619	98	44	36	79	87	99	58	55	63
P26038	MSN	Moesin	100	3	15	44	0	3	14	2	5	14
P35241	RDX	Radixin	100	1	8	37	0	3	24	2	2	23
P53673	CRYBA4	Beta-crystallin A4	5656	851	744	123	953	776	409	895	763	142
P48163	ME1	NADP-dependent malic enzyme	246	59	43	6	39	28	19	25	18	9
B4DX99		Malic enzyme	169	41	28	3	30	19	15	20	6	7
P07900	HSP90AA1	Heat shock protein HSP 90-alpha	217	47	83	23	16	15	6	13	10	4
P08238	HSP90AB1	Heat shock protein HSP 90-beta	103	20	47	11	3	4	2	8	6	2
Q6UWM7	LCTL	Lactase-like protein	365	0	30	164	0	3	83	0	3	82
I6L894	ANK2	Ankyrin-2	95	5	30	33	0	2	11	1	7	6
Q12955	ANK3	Ankyrin-3	18	1	4	9	0	0	1	0	2	1
P21333	FLNA	Filamin-A	112	13	33	22	5	9	10	6	10	4
P29401	TKT	Transketolase	404	27	6	2	112	43	51	90	46	27
P98160	HSPG2	Basement membrane-specific heparan sulfate proteoglycan	68	0	1	33	0	0	27	0	0	7
O00410	IPO5	Importin-5	225	14	60	28	6	30	39	5	35	8
B7Z670		cDNA FLJ61703, highly similar to Neuronal cell adhesion mo	153	0	31	57	0	2	33	0	6	24
Q9BXM0	PRX	Periaxin	113	0	7	79	0	1	17	0	0	9
P35237	SERPINB6	Serpin B6	414	67	28	5	105	39	22	94	41	13
P30041	PRDX6	Peroxiredoxin-6	267	73	53	45	9	7	36	20	5	19
P30301	MIP	Lens fiber major intrinsic protein	353	2	151	4	0	31	89	0	38	38
P11216	PYGB	Glycogen phosphorylase, brain form	144	15	51	13	6	25	12	2	16	4
O75955	FLOT1	Flotillin-1	120	0	1	56	0	0	32	0	0	31
Q14254	FLOT2	Flotillin-2	112	0	1	59	0	0	32	0	0	20
P09936	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1	379	123	34	24	46	35	45	42	15	15
P00338	LDHA	L-lactate dehydrogenase A chain	246	45	45	13	22	31	29	21	29	11
P07195	LDHB	L-lactate dehydrogenase B chain	43	8	9	6	2	4	4	3	4	3
P05023	ATP1A1	Sodium/potassium-transporting ATPase subunit alpha-1	97	0	0	60	0	0	24	0	0	13
P35555	FBN1	Fibrillin-1	58	0	0	49	0	0	0	0	0	9
Q14974	KPNB1	Importin subunit beta-1	217	25	69	17	12	24	30	13	21	6
B9EH95	ARVCF	Armadillo repeat gene deletes in velocardiofacial syndrome	141	1	24	39	0	5	38	0	9	25
P18669	PGAM1	Phosphoglycerate mutase 1	285	46	13	7	80	34	34	47	12	12
P16152	CBR1	Carbonyl reductase [NADPH] 1	627	98	74	40	40	82	100	46	77	70
P31150	GDI1	Rab GDP dissociation inhibitor alpha	283	37	56	3	17	46	49	14	46	15
P50395	GDI2	Rab GDP dissociation inhibitor beta	266	33	37	2	15	44	54	15	48	18
Q01469	FABP5	Fatty acid-binding protein, epidermal	231	35	26	17	30	37	23	22	34	7
Q71U36	TUBA1A	Tubulin alpha-1A chain	348	45	89	16	14	55	44	10	51	24
P68363	TUBA1B	Tubulin alpha-1B chain	306	44	75	14	11	47	40	9	46	20
P35222	CTNNB1	Catenin beta-1	115	0	31	37	1	4	19	2	9	12
A0A024	CRYBB3	Crystallin, beta B3, isoform CRA_a	538	110	68	37	72	58	52	45	71	25
P48165	GJA8	Gap junction alpha-8 protein	364	0	6	182	0	0	71	0	0	105

P63000	RAC1	Ras-related C3 botulinum toxin substrate 1	277	0	16	99	2	12	63	1	3	81
P60953	CDC42	Cell division control protein 42 homolog	84	0	3	19	1	4	21	0	1	35
Q8TCT0	CERK	Ceramide kinase	116	0	6	54	0	0	29	0	1	26
P26232	CTNNA2	Isoform 2 of Catenin alpha-2	39	0	7	20	0	0	11	0	0	1
P04792	HSPB1	Heat shock protein beta-1	327	53	61	21	43	45	25	35	37	7
Q93088	BHMT	Betaine--homocysteine S-methyltransferase 1	188	15	9	5	15	32	51	17	36	8
P60174	TP11	Triosephosphate isomerase	87	30	7	9	18	3	4	12	0	4
P07738	BPGM	Bisphosphoglycerate mutase	289	50	24	14	57	20	15	66	27	16
Q5TDP6	LGSN	Lengsin	207	10	51	33	8	18	22	5	39	21
P09488	GSTM1	Glutathione S-transferase Mu 1	35	7	8	5	0	0	0	3	4	8
P28161	GSTM2	Glutathione S-transferase Mu 2	33	9	7	1	4	1	1	3	2	5
P21266	GSTM3	Glutathione S-transferase Mu 3	12	2	4	0	0	0	0	1	5	0
P17858	PFKL	ATP-dependent 6-phosphofructokinase, liver type	118	17	25	7	3	16	10	5	29	6
P61026	RAB10	Ras-related protein Rab-10	40	1	3	16	1	2	7	0	3	7
Q9H0U4	RAB1B	Ras-related protein Rab-1B	40	1	1	19	0	0	9	0	1	9
P62820	RAB1A	Ras-related protein Rab-1A	39	1	1	20	0	0	10	0	1	6
Q15286	RAB35	Ras-related protein Rab-35	18	1	1	8	0	0	5	0	1	2
Q6BCY4	CYB5R2	NADH-cytochrome b5 reductase 2	97	36	2	0	23	5	7	16	6	2
P49368	CCT3	T-complex protein 1 subunit gamma	56	8	22	1	1	10	3	1	9	1
P08572	COL4A2	Collagen alpha-2(IV) chain	51	0	0	26	0	0	16	0	0	9
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate)-O-methyltransferase	137	24	17	6	23	11	12	24	12	8
Q13449	LSAMP	Limbic system-associated membrane protein	132	0	20	46	0	1	32	0	2	31
P61586	RHOA	Transforming protein RhoA	115	1	5	37	0	2	33	1	1	35
Q9NT12	ATP8A2	Phospholipid-transporting ATPase 1B	58	0	0	35	0	0	10	0	0	13
P07437	TUBB	Tubulin beta chain	47	4	24	6	0	2	5	1	3	2
Q8N3J6	CADM2	Cell adhesion molecule 2	122	0	9	55	0	0	29	0	1	28
P30086	PEBP1	Phosphatidyethanolamine-binding protein 1	119	44	7	4	21	6	13	17	5	2
P13639	EEF2	Elongation factor 2	91	2	26	6	1	11	20	2	19	4
P19022	CDH2	Cadherin-2	83	4	7	46	0	0	17	0	0	9
P36969	GPX4	Phospholipid hydroperoxide glutathione peroxidase, mitoch	67	0	0	21	0	0	20	1	0	25
P32754	HPD	4-hydroxyphenylpyruvate dioxygenase	59	21	0	0	6	0	0	17	10	5
P78371	CCT2	T-complex protein 1 subunit beta	46	2	25	0	1	7	1	1	7	2
O75781	PALM	Paralemmin-1	35	0	3	19	0	0	7	0	0	6
O94856	NFASC	Isoform 12 of Neurofascin	35	0	1	20	0	0	10	0	0	4
P53672	CRYBA2	Beta-crystallin A2	152	31	51	6	11	16	6	9	21	1
Q9ULX7	CA14	Carbonic anhydrase 14	119	0	12	48	0	3	31	0	1	24
P60842	EIF4A1	Eukaryotic initiation factor 4A-I	79	5	22	4	1	9	10	0	24	4
Q14240	EIF4A2	Eukaryotic initiation factor 4A-II	79	7	24	4	1	8	12	0	19	4
P32119	PRDX2	Peroxiredoxin-2	74	23	11	2	9	5	9	7	3	5
Q06830	PRDX1	Peroxiredoxin-1	17	6	4	1	2	1	1	1	0	1
P51149	RAB7A	Ras-related protein Rab-7a	75	0	0	41	0	0	18	0	0	16
P00390	GSR	Glutathione reductase, mitochondrial	74	15	4	3	7	8	7	15	11	4
P62937	PPIA	Peptidyl-prolyl cis-trans isomerase A	62	16	1	4	13	3	6	16	2	1
P50453	SERPINB9	Serpin B9	47	14	3	0	14	4	4	7	1	0
P30740	SERPINB1	Leukocyte elastase inhibitor	17	1	0	0	8	1	1	5	1	0
Q53FA7	TP53I3	Quinone oxidoreductase PIG3	74	27	10	16	7	1	6	3	3	1
Q14764	MVP	Major vault protein	64	6	20	0	2	12	7	6	10	1
P20340	RAB6A	Ras-related protein Rab-6A	64	0	1	38	0	0	17	0	0	8
P00387	CYB5R3	NADH-cytochrome b5 reductase 3	46	0	2	25	0	0	11	0	0	8
P55786	NPEPPS	Puromycin-sensitive aminopeptidase	44	7	9	8	1	10	3	1	3	2
Q14204	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	40	0	11	0	0	9	11	0	5	4
P63092	GNAS	Guanine nucleotide-binding protein G(s) subunit alpha isofo	29	0	2	12	0	0	10	0	0	5
P08754	GNAI3	Guanine nucleotide-binding protein G(k) subunit alpha	25	0	2	15	0	0	6	0	0	2
P02792	FTL	Ferritin light chain	117	8	2	0	28	7	1	48	14	9

P06744	GPI	Glucose-6-phosphate isomerase	100	16	12	6	7	15	18	7	16	3
Q9Y6H8	GJA3	Gap junction alpha-3 protein	86	0	0	31	0	0	27	0	2	26
P48643	CCT5	T-complex protein 1 subunit epsilon	55	0	16	0	0	11	13	0	13	2
P50991	CCT4	T-complex protein 1 subunit delta	26	1	8	0	0	4	2	1	8	2
P22392	NME2	Isoform 3 of Nucleoside diphosphate kinase B	51	25	0	1	6	0	0	14	3	2
P13591	NCAM1	Neural cell adhesion molecule 1	41	0	1	28	0	0	8	0	0	4
P38606	ATP6V1A	V-type proton ATPase catalytic subunit A	40	8	21	0	3	4	1	0	3	0
Q9BY67	CADM1	Cell adhesion molecule 1	29	0	0	7	0	0	10	0	0	12
Q00610	CLTC	Clathrin heavy chain 1	18	1	10	3	0	1	2	0	1	0
P00441	SOD1	Superoxide dismutase [Cu-Zn]	140	58	9	5	26	0	0	39	1	2
P09382	LGALS1	Galectin-1	115	18	21	17	9	14	16	5	6	9
P00918	CA2	Carbonic anhydrase 2	106	19	21	2	8	17	14	5	9	11
P15121	AKR1B1	Aldose reductase	103	23	18	5	6	8	14	7	16	6
P11166	SLC2A1	Solute carrier family 2, facilitated glucose transporter memt	78	0	0	37	0	0	14	0	0	27
P52209	PGD	6-phosphogluconate dehydrogenase, decarboxylating	68	11	9	5	7	9	12	5	6	4
B4DL86		6-phosphogluconate dehydrogenase, decarboxylating	62	7	8	5	6	9	11	6	6	4
P61204	ARF3	ADP-ribosylation factor 3	63	5	10	12	6	3	14	6	3	4
P16930	FAH	Fumarylacetoacetase	61	7	1	0	21	6	3	19	1	3
P23141	CES1	Liver carboxylesterase 1	53	8	1	2	12	3	8	11	2	6
Q9HCJ1	ANKH	Progressive ankylosis protein homolog	52	0	0	3	0	0	33	0	0	16
Q8N126	CADM3	Cell adhesion molecule 3	51	0	6	27	0	1	10	0	1	6
Q86VP6	CAND1	Cullin-associated NEDD8-dissociated protein 1	50	3	7	1	1	9	16	2	5	6
P11233	RALA	Ras-related protein Ral-A	48	0	0	25	0	0	14	0	0	9
Q5T9C9	PIP5KL1	Phosphatidylinositol 4-phosphate 5-kinase-like protein 1	42	0	2	22	0	0	13	0	0	5
Q9BX67	JAM3	Junctional adhesion molecule C	22	0	0	14	0	0	8	0	0	0
Q03135	CAV1	Caveolin-1	89	0	5	36	0	1	34	0	0	13
Q14019	COTL1	Coactosin-like protein	74	14	11	0	4	15	16	3	8	3
P02462	COL4A1	Collagen alpha-1(IV) chain	62	0	0	24	0	1	24	0	0	13
A2RU48	SMCO3	Single-pass membrane and coiled-coil domain-containing pr	44	0	6	13	0	0	12	0	2	11
P30566	ADSL	Adenylosuccinate lyase	34	7	2	3	2	3	7	3	3	4
P13489	RNH1	Ribonuclease inhibitor	30	2	14	0	3	3	4	0	4	0
P17987	TCP1	T-complex protein 1 subunit alpha	28	1	12	0	1	6	4	1	3	0
P07355	ANXA2	Annexin A2	24	4	5	8	3	0	3	1	0	0
Q8IXS6	PALM2	Paralemmin-2	18	0	0	13	0	0	4	0	0	1
P23526	AHCY	Adenosylhomocysteinase	98	25	9	6	14	4	7	15	6	12
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	73	7	25	0	4	13	9	3	10	2
P40227	CCT6A	T-complex protein 1 subunit zeta	69	4	23	1	2	17	10	1	9	2
P58546	MTPN	Myotrophin	62	14	10	1	10	6	8	7	6	0
P40925	MDH1	Malate dehydrogenase, cytoplasmic	51	24	2	6	8	1	1	6	0	3
P68104	EEF1A1	Elongation factor 1-alpha 1	47	3	15	7	0	8	6	0	8	0
P32320	CDA	Cytidine deaminase	47	9	4	1	20	6	4	2	0	1
P22748	CA4	Carbonic anhydrase 4	38	0	4	18	0	0	8	0	0	8
P13798	APEH	Acylamino-acid-releasing enzyme	30	5	0	2	11	0	1	8	0	3
P61019	RAB2A	Ras-related protein Rab-2A	28	0	0	18	0	0	4	0	0	6
Q9NUQ9	FAM49B	Protein FAM49B	21	2	1	10	0	0	1	0	0	7
Q96KP4	CNDP2	Cytosolic non-specific dipeptidase	21	9	6	0	3	0	0	2	0	1
P10768	ESD	S-formylglutathione hydrolase	20	8	0	0	5	0	1	4	1	1
Q9GZM7	TINAGL1	Tubulointerstitial nephritis antigen-like	15	0	1	12	0	0	2	0	0	0
P34913	EPHX2	Bifunctional epoxide hydrolase 2	73	8	6	5	8	6	33	3	1	3
P54920	NAPA	Alpha-soluble NSF attachment protein	57	4	21	7	1	6	5	3	5	5
Q15907	RAB11B	Ras-related protein Rab-11B	56	2	2	22	1	1	13	0	5	10
P60891	PRPS1	Ribose-phosphate pyrophosphokinase 1	44	4	15	0	1	8	4	3	8	1
P01034	CST3	Cystatin-C	41	0	1	2	0	1	23	0	0	14
Q15124	PGM5	Phosphoglucomutase-like protein 5	33	3	5	2	2	4	7	0	8	2

P61020	RAB5B	Ras-related protein Rab-5B	29	0	1	16	1	0	7	0	0	4
P08758	ANXA5	Annexin A5	28	5	11	3	0	2	2	1	1	3
Q6NZ12	PTRF	Polymerase I and transcript release factor	28	0	10	8	0	3	1	0	5	1
O15498	YKT6	Synaptobrevin homolog YKT6	22	0	2	14	0	0	2	0	0	4
P62834	RAP1A	Ras-related protein Rap-1A	19	0	1	3	0	1	9	0	0	5
O60664	PLIN3	Perilipin-3	9	1	7	1	0	0	0	0	0	0
P55344	LIM2	Lens fiber membrane intrinsic protein	125	0	16	51	0	3	21	0	1	33
P55344	LIM2	Isoform 2 of Lens fiber membrane intrinsic protein	123	0	16	47	0	3	21	0	1	35
P55064	AQP5	Aquaporin-5	75	0	0	41	0	0	23	0	0	11
Q99426	TBCB	Tubulin-folding cofactor B	34	6	15	2	1	3	2	1	3	1
O94760	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	34	2	2	10	0	0	12	1	0	7
Q9UL25	RAB21	Ras-related protein Rab-21	30	0	2	17	0	0	6	0	0	5
P10909	CLU	Clusterin	28	0	2	9	0	1	10	0	0	6
P05026	ATP1B1	Sodium/potassium-transporting ATPase subunit beta-1	27	0	0	15	0	0	6	0	0	6
Q01518	CAP1	Adenylyl cyclase-associated protein 1	25	0	7	0	2	8	4	0	4	0
P01116	KRAS	Isoform 2B of GTPase KRas	19	0	0	14	0	0	1	0	0	4
P01112	HRAS	GTPase HRas	12	0	0	10	0	0	0	0	0	2
P62805	HIST1H4A	Histone H4	21	0	0	16	0	0	5	0	0	0
Q08257	CRYZ	Quinone oxidoreductase	20	3	5	2	4	1	0	2	3	0
P11142	HSPA8	Heat shock cognate 71 kDa protein	13	3	5	1	1	1	0	2	0	0
O15230	LAMA5	Laminin subunit alpha-5	7	0	0	3	0	0	3	0	0	1
O60437	PPL	Periplakin	6	0	5	0	0	1	0	0	0	0
P04271	S100B	Protein S100-B	131	43	11	12	20	6	7	20	6	6
POC870	JMJ7	JmjC domain-containing protein 7	50	7	12	0	3	12	5	3	7	1
P61163	ACTR1A	Alpha-centractin	43	6	17	0	2	5	2	2	9	0
P62826	RAN	GTP-binding nuclear protein Ran	40	8	8	10	3	2	3	2	1	3
P23528	CFL1	Cofilin-1	36	4	18	1	0	3	3	1	6	0
P61626	LYZ	Lysozyme C	26	0	3	7	0	1	9	0	1	5
P61160	ACTR2	Actin-related protein 2	21	3	12	0	1	2	0	0	3	0
Q9Y2S2	CRYL1	Lambda-crystallin homolog	18	3	9	1	0	0	0	1	2	2
O76054	SEC14L2	SEC14-like protein 2	18	0	11	0	1	2	2	0	1	1
O60814	HIST1H2BK	Histone H2B type 1-K	15	0	0	9	0	0	5	0	0	1
P37837	TALDO1	Transaldolase	12	4	0	0	3	1	2	1	1	0
P22234	PAICS	Multifunctional protein ADE2	12	0	3	0	1	2	3	1	1	1
O75083	WDR1	WD repeat-containing protein 1	11	3	6	0	0	1	0	0	1	0
O76024	WFS1	Wolframin	11	0	0	4	0	0	6	0	0	1
P78310	CXADR	Coxsackievirus and adenovirus receptor	10	0	0	8	0	0	2	0	0	0
P04083	ANXA1	Annexin A1	9	1	4	2	1	0	0	1	0	0
Q9BT78	COPS4	COP9 signalosome complex subunit 4	7	1	6	0	0	0	0	0	0	0
P62873	GNB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit t	7	0	5	1	0	0	0	0	1	0
Q8NHU6	TDRD7	Tudor domain-containing protein 7	6	0	3	1	0	0	0	0	2	0
POCG47	UBB	Polyubiquitin-B	51	14	2	1	8	3	5	10	1	7
P14174	MIF	Macrophage migration inhibitory factor	43	10	7	4	8	3	3	6	2	0
P60981	DSTN	Dextrin	37	1	13	0	2	7	7	1	6	0
B3SHH9	TMEM114	Transmembrane protein 114	32	0	1	22	0	0	6	0	0	3
P49327	FASN	Fatty acid synthase	28	2	6	0	4	5	4	2	4	1
P12814	ACTN1	Alpha-actinin-1	27	1	4	3	3	1	5	4	3	3
P09417	QDPR	Dihydropteridine reductase	24	8	2	0	1	2	2	3	5	1
P04908	HIST1H2AB	Histone H2A type 1-B/E	21	0	0	9	0	0	6	3	2	1
P12955	PEPD	Xaa-Pro dipeptidase	17	5	0	0	4	0	0	7	0	1
P04216	THY1	Thy-1 membrane glycoprotein	14	0	0	5	0	0	2	0	2	5
Q15257	PPP2R4	Serine/threonine-protein phosphatase 2A activator	12	2	1	3	0	1	2	0	1	2
O75131	CPNE3	Copine-3	11	0	4	1	1	0	4	1	0	0
P14324	FDPS	Farnesyl pyrophosphate synthase	10	1	5	1	0	0	2	0	1	0

Q9NV96	TMEM30A	Cell cycle control protein 50A	10	0	0	8	0	0	2	0	0	0
Q8IW45	NAXD	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	9	2	1	0	2	1	1	2	0	0
P02786	TFRC	Transferrin receptor protein 1	9	0	0	9	0	0	0	0	0	0
P01857	IGHG1	Ig gamma-1 chain C region	7	0	1	2	0	0	1	0	0	3
P36871	PGM1	Phosphoglucomutase-1	7	1	3	0	1	0	1	0	1	0
Q92542	NCSTN	Nicastrin	7	0	0	0	0	0	4	0	0	3
Q02790	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	7	0	3	0	0	3	0	0	1	0
Q92597	NDRG1	Protein NDRG1	7	2	5	0	0	0	0	0	0	0
P12268	IMPDH2	Inosine-5'-monophosphate dehydrogenase 2	6	2	0	0	2	1	0	1	0	0
P06753	TPM3	Isoform 6 of Tropomyosin alpha-3 chain	5	1	0	0	2	0	0	2	0	0
Q99536	VAT1	Synaptic vesicle membrane protein VAT-1 homolog	5	0	1	1	0	0	1	0	0	2
P55268	LAMB2	Laminin subunit beta-2	5	0	0	2	0	0	3	0	0	0
Q14203	DCTN1	Dynactin subunit 1	4	0	4	0	0	0	0	0	0	0
Q9POJ0	NDUFA13	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub	66	6	11	0	3	15	13	2	11	5
P61457	PCBD1	Pterin-4-alpha-carbinolamine dehydratase	38	6	2	1	8	5	2	9	5	0
Q99832	CCT7	T-complex protein 1 subunit eta	18	0	10	0	1	2	0	0	5	0
Q86Y23	HRNR	Hornerin	15	0	0	4	1	1	2	1	1	5
P36405	ARL3	ADP-ribosylation factor-like protein 3	14	4	4	6	0	0	0	0	0	0
Q9BWD1	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	14	6	0	0	2	0	0	6	0	0
P13987	CD59	CD59 glycoprotein	13	0	0	10	0	0	3	0	0	0
P21695	GPD1	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	11	2	4	0	0	1	1	1	2	0
Q9UI40	SLC24A2	Isoform 2 of Sodium/potassium/calcium exchanger 2	11	0	0	7	0	0	4	0	0	0
Q16775	HAGH	Hydroxyacylglutathione hydrolase, mitochondrial	10	7	0	0	1	0	0	1	1	0
P48029	SLC6A8	Sodium- and chloride-dependent creatine transporter 1	10	0	0	6	0	0	2	0	0	2
P61106	RAB14	Ras-related protein Rab-14	9	0	0	8	0	0	0	0	0	1
O95336	PGLS	6-phosphogluconolactonase	9	1	0	1	0	0	2	0	0	5
P29218	IMPA1	Inositol monophosphatase 1	8	4	4	0	0	0	0	0	0	0
P10599	TXN	Thioredoxin	8	3	0	0	1	0	0	4	0	0
O75695	RP2	Protein XRP2	8	0	0	7	0	0	1	0	0	0
Q9BWS9	CHID1	Chitinase domain-containing protein 1	8	0	0	1	0	0	3	0	0	4
P30153	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory	7	3	2	2	0	0	0	0	0	0
Q16555	DPYSL2	Dihydropyrimidinase-related protein 2	7	1	5	0	0	0	0	0	1	0
O75874	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	7	1	3	0	0	0	1	0	2	0
Q96NU7	AMDHD1	Probable imidazolonepropionase	6	1	4	0	0	0	0	0	1	0
P02794	FTH1	Ferritin heavy chain	6	1	0	0	0	0	0	5	0	0
Q96IU4	ABHD14B	Protein ABHD14B	6	4	0	0	2	0	0	0	0	0
Q99733	NAP1L4	Nucleosome assembly protein 1-like 4	6	3	0	2	0	0	0	1	0	0
P31939	ATIC	Bifunctional purine biosynthesis protein PURH	5	0	5	0	0	0	0	0	0	0
P55011	SLC12A2	Solute carrier family 12 member 2	5	0	0	4	0	0	0	0	0	1
O75663	TIPRL	TIP41-like protein	5	1	3	0	0	0	0	0	1	0
P21399	ACO1	Cytoplasmic aconitate hydratase	5	1	2	0	0	1	0	0	1	0
P43007	SLC1A4	Neutral amino acid transporter A	4	0	0	3	0	0	1	0	0	0
P05198	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	4	0	3	0	0	0	0	0	1	0
P78324	SIRPA	Tyrosine-protein phosphatase non-receptor type substrate :	3	0	0	3	0	0	0	0	0	0
P49189	ALDH9A1	4-trimethylaminobutyraldehyde dehydrogenase	3	2	1	0	0	0	0	0	0	0
P27824	CANX	Calnexin	3	0	0	3	0	0	0	0	0	0
Q92530	PSMF1	Proteasome inhibitor PI31 subunit	3	0	3	0	0	0	0	0	0	0
Q8TD20	SLC2A12	Solute carrier family 2, facilitated glucose transporter memt	3	0	0	2	0	0	1	0	0	0
Q04760	GLO1	Lactoylglutathione lyase	3	3	0	0	0	0	0	0	0	0
P31948	STIP1	Stress-induced-phosphoprotein 1	3	3	0	0	0	0	0	0	0	0
Q14653	IRF3	Isoform 4 of Interferon regulatory factor 3	24	2	13	0	0	1	0	1	6	1
Q9HD40	SEPSECS	O-phosphoseryl-tRNA(Sec) selenium transferase	24	6	3	0	0	2	3	5	4	1
Q9Y5L5	LENEP	Lens epithelial cell protein LEP503	17	0	0	6	0	0	5	0	0	6
O60888	CUTA	Protein CutA	16	4	1	0	5	1	2	1	1	1

Q96C23	GALM	Aldose 1-epimerase	15	2	7	0	0	3	1	0	2	0
Q08357	SLC20A2	Sodium-dependent phosphate transporter 2	15	0	0	2	0	0	7	0	0	6
Q13200	PSMD2	26S proteasome non-ATPase regulatory subunit 2	15	2	5	0	0	4	0	0	4	0
Q2TAA2	IAH1	Isoamyl acetate-hydrolyzing esterase 1 homolog	14	5	0	0	6	0	0	3	0	0
J3KNQ3	PSMD13	26S proteasome non-ATPase regulatory subunit 13	14	1	3	0	0	3	4	0	3	0
Q9HC10	OTOF	Otoferlin	14	1	0	6	0	1	2	2	2	0
P61088	UBE2N	Ubiquitin-conjugating enzyme E2 N	13	4	4	1	1	0	0	2	0	1
O00268	TAF4	Transcription initiation factor TFIID subunit 4	12	4	2	1	2	0	0	2	1	0
Q9Y2V2	CARHSP1	Calcium-regulated heat-stable protein 1	11	5	1	0	2	0	0	3	0	0
P28074	PSMB5	Proteasome subunit beta type-5	11	2	2	0	1	1	1	0	4	0
Q6GMV2	SMYD5	SET and MYND domain-containing protein 5	10	0	2	1	1	0	3	1	2	0
P00450	CP	Ceruloplasmin	9	0	2	0	0	0	4	0	0	3
P15260	IFNGR1	Interferon gamma receptor 1	9	0	0	6	0	0	1	0	0	2
Q9NZH0	GPRC5B	G-protein coupled receptor family C group 5 member B	7	0	0	4	0	0	3	0	0	0
Q04446	GBE1	1,4-alpha-glucan-branching enzyme	7	0	4	0	0	1	1	0	1	0
P11766	ADH5	Alcohol dehydrogenase class-3	7	2	4	0	0	0	0	0	1	0
P26447	S100A4	Protein S100-A4	7	2	0	1	1	0	0	2	1	0
P21926	CD9	CD9 antigen	6	0	0	5	0	0	1	0	0	0
Q9UJ70	NAGK	N-acetyl-D-glucosamine kinase	6	3	0	0	0	0	0	0	2	1
Q8IZ83	ALDH16A1	Aldehyde dehydrogenase family 16 member A1	6	0	0	0	0	0	4	0	1	1
Q08722	CD47	Leukocyte surface antigen CD47	6	0	0	6	0	0	0	0	0	0
O43242	PSMD3	26S proteasome non-ATPase regulatory subunit 3	6	0	2	0	0	0	2	0	1	1
P27361	MAPK3	Mitogen-activated protein kinase 3	6	0	3	0	0	1	1	0	1	0
Q12873	CHD3	Isoform 3 of Chromodomain-helicase-DNA-binding protein :	6	4	0	2	0	0	0	0	0	0
Q99685	MGLL	Monoglyceride lipase	5	0	2	0	0	0	1	0	0	2
A0A075	PDE4DIP	Myomegalin	5	0	0	0	4	1	0	0	0	0
Q01955	COL4A3	Collagen alpha-3(IV) chain	5	0	0	1	0	0	2	0	0	2
Q13057	COASY	Bifunctional coenzyme A synthase	5	0	1	0	0	0	0	1	2	1
A6NKB5	PCNX2	Pecanex-like protein 2	4	0	0	0	0	3	1	0	0	0
P37802	TAGLN2	Transgelin-2	4	1	0	1	1	0	0	1	0	0
Q07283	TCHH	Trichohyalin	4	0	0	3	0	0	1	0	0	0
P21359	NF1	Neurofibromin	4	0	0	0	0	4	0	0	0	0
P17612	PRKACA	cAMP-dependent protein kinase catalytic subunit alpha	4	1	2	0	0	0	0	0	1	0
P54709	ATP1B3	Sodium/potassium-transporting ATPase subunit beta-3	4	0	0	2	0	0	1	0	0	1
Q86Y39	NDUFA11	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex sub	4	2	0	0	0	0	0	0	2	0
P09211	GSTP1	Glutathione S-transferase P	4	2	0	0	1	0	0	1	0	0
Q969T9	WBP2	WW domain-binding protein 2	4	0	3	0	0	0	0	0	0	1
P10114	RAP2A	Ras-related protein Rap-2a	3	0	0	0	0	0	1	0	0	2
Q12765	SCRN1	Secernin-1	3	2	0	0	0	0	0	1	0	0
Q8IVW8	SPNS2	Protein spinster homolog 2	3	0	0	1	0	0	2	0	0	0
Q9H857	NT5DC2	5'-nucleotidase domain-containing protein 2	3	0	0	0	0	2	0	0	0	1
O00519	FAAH	Fatty-acid amide hydrolase 1	3	0	0	2	0	0	1	0	0	0
O95834	EML2	Echinoderm microtubule-associated protein-like 2	3	0	2	0	0	0	0	0	1	0
P29317	EPHA2	Ephrin type-A receptor 2	3	0	0	2	0	0	1	0	0	0
P55072	VCP	Transitional endoplasmic reticulum ATPase	3	0	3	0	0	0	0	0	0	0
P41222	PTGDS	Prostaglandin-H2 D-isomerase	3	0	1	2	0	0	0	0	0	0
P28070	PSMB4	Proteasome subunit beta type-4	3	2	0	0	0	1	0	0	0	0
P10644	PRKAR1A	cAMP-dependent protein kinase type I-alpha regulatory sub	3	0	2	0	0	0	0	1	0	0
P27816	MAP4	Microtubule-associated protein 4	2	0	0	2	0	0	0	0	0	0
Q14767	LTBP2	Latent-transforming growth factor beta-binding protein 2	2	0	0	2	0	0	0	0	0	0
Q86XX4	FRAS1	Extracellular matrix protein FRAS1	2	0	0	0	0	0	0	0	0	2
P37235	HPCAL1	Hippocalcin-like protein 1	2	0	0	0	0	0	2	0	0	0
P46926	GNPDA1	Glucosamine-6-phosphate isomerase 1	2	2	0	0	0	0	0	0	0	0
Q9NQC3	RTN4	Reticulon-4	2	0	0	2	0	0	0	0	0	0

O00764	PDXK	Pyridoxal kinase	2	0	2	0	0	0	0	0	0	0
O60884	DNAJA2	Dnaj homolog subfamily A member 2	2	0	2	0	0	0	0	0	0	0
Q7Z460	CLASP1	CLIP-associating protein 1	2	0	0	0	0	0	0	0	0	2
P55060	CSE1L	Exportin-2	2	0	0	0	0	0	2	0	0	0
P18206	VCL	Vinculin	2	0	2	0	0	0	0	0	0	0
Q9NZU5	LMCD1	LIM and cysteine-rich domains protein 1	2	0	2	0	0	0	0	0	0	0

Proteins identified in MudPIT analysis

Accession Number	Gene Name	Proteins	Coverage	Total Spectral Count	Spectral Count_37yo	Spectral Count_58yo
Q01082	SPTBN1	Spectrin beta chain, non-erythrocytic 1	69	1125	378	747
Q15020	SPTBN2	Spectrin beta chain, non-erythrocytic 2	20	159	68	91
P11277	SPTB	Spectrin beta chain, erythrocytic	12	47	32	15
Q13813	SPTAN1	Spectrin alpha chain, non-erythrocytic 1	65	1032	319	713
Q15149	PLEC	Plectin	37	465	169	296
A0A024	HSPG2	Heparan sulfate proteoglycan 2 (Perlecan), isoform CRA_b	40	767	585	182
P11171	EPB41	Protein 4.1	39	354	234	120
Q43491	EPB41L2	Band 4.1-like protein 2	38	217	141	76
Q9H4G0	EPB41L1	Isoform 2 of Band 4.1-like protein 1	29	80	53	27
Q9Y2J2	EPB41L3	Band 4.1-like protein 3	18	67	50	17
Q8WZ42	TTN	Titin	0	4	4	0
Q9BXM0	PRX	Periaxin	48	594	313	281
P35241	RDX	Radixin	58	353	143	210
P26038	MSN	Moesin	50	310	127	183
P21333	FLNA	Filamin-A	31	238	95	143
Q13515	BFSP2	Phakinin	84	1524	640	884
Q12934	BFSP1	Filesin	69	2498	1158	1340
P35555	FBN1	Fibrillin-1	22	228	214	14
I6L894	ANK2	Ankyrin-2	17	188	117	71
Q12955	ANK3	Ankyrin-3	4	41	24	17
P05023	ATP1A1	Sodium/potassium-transporting ATPase subunit alpha-1	42	400	105	295
B723V1		Sodium/potassium-transporting ATPase subunit alpha (Fragment)	41	379	103	276
B3KW93		Sodium/potassium-transporting ATPase subunit alpha	19	226	41	185
Q14204	DYNC1H1	Cytoplasmic dynein 1 heavy chain 1	14	185	72	113
P60709	ACTB	Actin, cytoplasmic 1	60	815	483	332
Q53G99		Beta actin variant (Fragment)	60	813	481	332
V9HVZ7	HEL-176	Epididymis luminal protein 176	64	556	290	266
P68032	ACTC1	Actin, alpha cardiac muscle 1	54	237	87	150
Q562R1	ACTBL2	Beta-actin-like protein 2	17	106	26	80
P0CG38	POTE1	POTE ankyrin domain family member I	7	79	16	63
P62258	YWHAE	14-3-3 protein epsilon	51	248	100	148
P63104	YWHAZ	14-3-3 protein zeta/delta	60	123	55	68
P61981	YWHAG	14-3-3 protein gamma	51	61	24	37
Q04917	YWHAH	14-3-3 protein eta	24	39	11	28
P07315	CRYGC	Gamma-crystallin C	90	1289	1047	242
P07316	CRYGB	Gamma-crystallin B	74	332	119	213
P11844	CRYGA	Gamma-crystallin A	48	17	14	3
P22914	CRYGS	Beta-crystallin S	96	2635	1627	1008
Q9UFA7	DKFZp434A0627	Crystallin, gamma S, isoform CRA_a	97	1881	1155	726
P00352	ALDH1A1	Retinal dehydrogenase 1	61	1806	657	1149
P47895	ALDH1A3	Aldehyde dehydrogenase family 1 member A3	11	42	27	15
P17858	PFKL	ATP-dependent 6-phosphofructokinase, liver type	34	121	62	59
Q01813	PFKP	ATP-dependent 6-phosphofructokinase, platelet type	20	47	23	24
P08237	PFKM	ATP-dependent 6-phosphofructokinase, muscle type	13	34	13	21
A0A0H3	CRYBB2	Beta-crystallin B2 (Fragment)	99	3620	2603	1017
A0A0H3	CRYBB2	Beta-crystallin B2	90	3245	2218	1027
O75955	FLOT1	Flotillin-1	74	518	129	389
P06733	ENO1	Alpha-enolase	70	362	146	216
P09104	ENO2	Gamma-enolase	53	178	112	66
L0R849	EDARADD	Alternative protein EDARADD	12	21	2	19
P07900	HSP90AA1	Heat shock protein HSP 90-alpha	44	106	51	55
P08238	HSP90AB1	Heat shock protein HSP 90-beta	35	74	26	48
P14625	HSP90B1	Endoplasmin	8	10	5	5
P14618	PKM	Isoform M1 of Pyruvate kinase PKM	69	311	137	174
P53674	CRYBB1	Beta-crystallin B1	92	10243	4221	6022
P00558	PGK1	Phosphoglycerate kinase 1	77	710	225	485
P07205	PGK2	Phosphoglycerate kinase 2	18	126	33	93
Q9H0U4	RAB1B	Ras-related protein Rab-1B	55	223	41	182
P62820	RAB1A	Ras-related protein Rab-1A	61	213	41	110
P61026	RAB10	Ras-related protein Rab-10	44	141	38	103
Q15286	RAB35	Ras-related protein Rab-35	29	70	21	49
P61006	RAB8A	Ras-related protein Rab-8A	28	34	16	18
P04406	GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	88	1638	1011	627
Q92823	NRCAM	Isoform 3 of Neuronal cell adhesion molecule	41	568	161	407
Q14CA1	NRCAM	NRCAM protein	41	563	156	407
P04075	ALDOA	Fructose-bisphosphate aldolase A	71	241	126	115
P09972	ALDOC	Fructose-bisphosphate aldolase C	52	198	64	134
Q14254	FLOT2	Flotillin-2	65	355	118	237
P55268	LAMB2	Laminin subunit beta-2	28	136	88	48
A0A097	CRYBA1	Beta crystallin A3 chain transcript CN (Fragment)	91	7846	4540	3306
A0A0H3	CRYBA1	Crystallin beta A3/A1 (Fragment)	100	640	271	369
Q6UWM7	LCTL	Lactase-like protein	58	435	272	163
O15230	LAMA5	Laminin subunit alpha-5	15	167	91	76
P35222	CTNNB1	Catenin beta-1	42	125	67	58
P14923	JUP	Junction plakoglobin	19	26	24	2
P50395	GDI2	Rab GDP dissociation inhibitor beta	52	273	139	134
P31150	GDI1	Rab GDP dissociation inhibitor alpha	51	235	140	95
P08670	VIM	Vimentin	61	161	44	117
P41219	PRPH	Peripherin	10	19	4	15
P63092	GNAS	Guanine nucleotide-binding protein G(s) subunit alpha isoforms sh	59	104	65	39
P04899	GNAI2	Guanine nucleotide-binding protein G(i) subunit alpha-2	36	69	38	31
P08754	GNAI3	Guanine nucleotide-binding protein G(k) subunit alpha	44	52	31	21
P63096	GNAI1	Guanine nucleotide-binding protein G(i) subunit alpha-1	20	41	28	13
O75781	PALM	Paralemmin-1	71	80	46	34
Q8IX56	PALM2	Paralemmin-2	42	62	23	39
P26232	CTNNA2	Isoform 2 of Catenin alpha-2	44	115	62	53

P35221	CTNNA1	Catenin alpha-1	18	15	11	4
O00410	IPOS	Importin-5	35	284	78	206
P80723	BASP1	Brain acid soluble protein 1	96	994	431	563
P00338	LDHA	L-lactate dehydrogenase A chain	68	169	101	68
P07195	LDHB	L-lactate dehydrogenase B chain	37	37	12	25
P48163	ME1	NADP-dependent malic enzyme	56	195	107	88
P02489	CRYAA	Alpha-crystallin A chain	97	6497	5324	1173
P02511	CRYAB	Alpha-crystallin B chain	85	6351	3607	2744
P08572	COL4A2	Collagen alpha-2(IV) chain	16	1049	769	280
P29401	TKT	Transketolase	65	338	121	217
P02462	COL4A1	Collagen alpha-1(IV) chain	10	1058	1054	4
P29400	COL4A5	Collagen alpha-5(IV) chain	8	114	110	4
P48637	GSS	Glutathione synthetase	61	936	192	744
P35527	KRT9	Keratin, type I cytoskeletal 9	61	219	37	182
P11216	PYGB	Glycogen phosphorylase, brain form	38	133	50	83
P06737	PYGL	Glycogen phosphorylase, liver form	9	18	16	2
P20340	RAB6A	Isoform 2 of Ras-related protein Rab-6A	71	589	76	513
P20340	RAB6A	Ras-related protein Rab-6A	66	541	75	466
Q9NRW1	RAB6B	Ras-related protein Rab-6B	59	370	36	334
O00192	ARVCF	Armadillo repeat protein deleted in velo-cardio-facial syndrome	38	236	141	95
Q00610	CLTC	Clathrin heavy chain 1	20	81	45	36
P07320	CRYGD	Gamma-crystallin D	82	1802	1378	424
A0A097	GJA8	Gap junction protein (Fragment)	54	504	313	191
P19022	CDH2	Cadherin-2	29	368	105	263
P32754	HPD	4-hydroxyphenylpyruvate dioxygenase	65	142	38	104
Q9NTI2	ATP8A2	Phospholipid-transporting ATPase IB	24	123	42	81
P50453	SERPINB9	Serpin B9	47	83	44	39
P30740	SERPINB1	Leukocyte elastase inhibitor	25	50	28	22
P14543	NID1	Nidogen-1	14	32	17	15
Q14112	NID2	Nidogen-2	11	14	10	4
P35237	SERPINB6	Serpin B6	68	395	125	270
P28161	GSTM2	Glutathione S-transferase Mu 2	56	46	41	5
P09488	GSTM1	Glutathione S-transferase Mu 1	47	34	34	0
P21266	GSTM3	Glutathione S-transferase Mu 3	43	25	15	10
P11047	LAMC1	Laminin subunit gamma-1	18	54	26	28
P60953	CDC42	Cell division control protein 42 homolog	46	243	102	141
P63000	RAC1	Ras-related C3 botulinum toxin substrate 1	43	123	62	61
P84095	RHOG	Rho-related GTP-binding protein RhoG	27	12	10	2
P51149	RAB7A	Ras-related protein Rab-7a	75	199	76	123
P52209	PGD	6-phosphogluconate dehydrogenase, decarboxylating	59	149	103	46
Q71U36	TUBA1A	Tubulin alpha-1A chain	43	218	106	112
P68363	TUBA1B	Tubulin alpha-1B chain	43	209	96	113
Q14974	KPNB1	Importin subunit beta-1	38	119	51	68
Q72406	MYH14	Myosin-14	7	23	5	18
P35579	MYH9	Myosin-9	8	17	6	11
P35580	MYH10	Myosin-10	4	7	3	4
P16152	CBR1	Carbonyl reductase [NADPH] 1	78	703	148	555
Q00796	SORD	Sorbitol dehydrogenase	64	505	166	339
P13591	NCAM1	Isoform 2 of Neural cell adhesion molecule 1	28	152	54	98
H7BYX6	NCAM1	Neural cell adhesion molecule 1	32	124	59	65
O94856	NFASC	Isoform 12 of Neurofascin	25	131	51	80
P55786	NPEPPS	Puromycin-sensitive aminopeptidase	30	89	30	59
P32119	PRDX2	Peroxiredoxin-2	59	56	13	43
Q06830	PRDX1	Peroxiredoxin-1	26	19	6	13
Q13162	PRDX4	Peroxiredoxin-4	47	18	14	4
Q99497	PARK7	Protein deglycase DJ-1	83	239	194	45
P09936	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1	74	197	124	73
P36969	GPX4	Phospholipid hydroperoxide glutathione peroxidase, mitochondrial	60	192	56	136
P00390	GSR	Glutathione reductase, mitochondrial	50	87	45	42
P49327	FASN	Fatty acid synthase	10	46	28	18
P18206	VCL	Vinculin	20	42	8	34
O75923	DYSF	Dysferlin	15	34	26	8
A0A1B1	CRYBA4	Beta crystallin A4 chain (Fragment)	89	3781	3283	498
Q8N3J6	CADM2	Cell adhesion molecule 2	59	384	177	207
P61020	RAB5B	Ras-related protein Rab-5B	53	176	31	145
P51148	RAB5C	Ras-related protein Rab-5C	28	40	11	29
P20339	RAB5A	Ras-related protein Rab-5A	53	37	12	25
P26998	CRYBB3	Beta-crystallin B3	83	209	112	97
P48643	CCT5	T-complex protein 1 subunit epsilon	22	82	27	55
P50991	CCT4	T-complex protein 1 subunit delta	19	35	17	18
P23141	CES1	Liver carboxylesterase 1	44	86	47	39
P61586	RHOA	Transforming protein RhoA	79	315	165	150
Q579C9	PIP5KL1	Phosphatidylinositol 4-phosphate 5-kinase-like protein 1	49	177	87	90
Q53FA7	TP53I3	Quinone oxidoreductase PIG3	61	160	63	97
O94760	DDAH1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	71	99	52	47
P23526	AHCY	Adenosylhomocysteinase	43	97	41	56
P21695	GPD1	Glycerol-3-phosphate dehydrogenase [NAD(+)], cytoplasmic	34	51	10	41
Q8N335	GPD1L	Glycerol-3-phosphate dehydrogenase 1-like protein	14	31	6	25
P10114	RAP2A	Ras-related protein Rap-2a	48	50	7	43
P61225	RAP2B	Ras-related protein Rap-2b	56	42	8	34
Q9Y3L5	RAP2C	Ras-related protein Rap-2c	55	28	5	23
P30153	PPP2R1A	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit	34	61	15	46
P49368	CCT3	T-complex protein 1 subunit gamma	37	54	24	30
P22748	CA4	Carbonic anhydrase 4	44	110	60	50
K7ENI8	CA4	Carbonic anhydrase 4 (Fragment)	82	42	25	17
Q01469	FABP5	Fatty acid-binding protein, epidermal	87	76	39	37
Q9Y6H8	GJA3	Gap junction alpha-3 protein	47	310	174	136
P30041	PRDX6	Peroxiredoxin-6	54	163	44	119
P34913	EPHX2	Bifunctional epoxide hydrolase 2	45	141	106	35

P06744	GPI	Glucose-6-phosphate isomerase	39	138	98	40
P22392	NME2	Isoform 3 of Nucleoside diphosphate kinase B	48	102	52	50
P15531	NME1	Nucleoside diphosphate kinase A	69	51	24	27
Q96ZM7	TINAGL1	Tubulointerstitial nephritis antigen-like	52	104	75	29
O15498	YKT6	Synaptobrevin homolog YKT6	79	90	29	61
Q9NQ79	CRTAC1	Cartilage acidic protein 1	31	73	45	28
Q14240	EIF4A2	Eukaryotic initiation factor 4A-II	33	63	24	39
P60842	EIF4A1	Eukaryotic initiation factor 4A-I	31	58	23	35
P13798	APEH	Acylamino-acid-releasing enzyme	33	68	18	50
P78371	CCT2	T-complex protein 1 subunit beta	41	57	38	19
P12814	ACTN1	Alpha-actinin-1	24	47	14	33
P18669	PGAM1	Phosphoglycerate mutase 1	69	143	70	73
P11233	RALA	Ras-related protein Ral-A	43	111	35	76
P11234	RALB	Ras-related protein Ral-B	49	59	31	28
P00387	CYB5R3	NADH-cytochrome b5 reductase 3	51	105	56	49
A2RU48	SMCO3	Single-pass membrane and coiled-coil domain-containing protein 3	73	88	26	62
P13639	EEF2	Elongation factor 2	20	86	39	47
P40925	MDH1	Malate dehydrogenase, cytoplasmic	53	85	34	51
P07437	TUBB	Tubulin beta chain	44	65	28	37
P04350	TUBB4A	Tubulin beta-4A chain	36	59	25	34
Q86VP6	CAND1	Cullin-associated NEDD8-dissociated protein 1	16	67	23	44
P62937	PPIA	Peptidyl-prolyl cis-trans isomerase A	41	39	19	20
P23284	PPIB	Peptidyl-prolyl cis-trans isomerase B	35	13	5	8
P29317	EPHA2	Ephrin type-A receptor 2	20	39	24	15
P54753	EPHB3	Ephrin type-B receptor 3	3	5	2	3
Q8N126	CADM3	Cell adhesion molecule 3	51	170	58	112
Q01955	COL4A3	Collagen alpha-3(IV) chain	9	123	118	5
Q8TCT0	CERK	Ceramide kinase	33	120	77	43
P00450	CP	Ceruloplasmin	16	71	26	45
Q99832	CCT7	T-complex protein 1 subunit eta	36	61	28	33
Q13449	LSAMP	Limbic system-associated membrane protein	43	551	269	282
P11166	SLC2A1	Solute carrier family 2, facilitated glucose transporter member 1	12	280	69	211
Q9ULX7	CA14	Carbonic anhydrase 14	33	216	106	110
P61204	ARF3	ADP-ribosylation factor 3	65	182	53	129
P18085	ARF4	ADP-ribosylation factor 4	40	148	29	119
P62805	HIST1H4A	Histone H4	58	96	67	29
P22061	PCMT1	Protein-L-isoaspartate(D-aspartate) O-methyltransferase	63	96	69	27
P78310	CXADR	Coxsackievirus and adenovirus receptor	36	71	43	28
P11413	G6PD	Glucose-6-phosphate 1-dehydrogenase	26	59	24	35
P17987	TCP1	T-complex protein 1 subunit alpha	30	55	19	36
P01116	KRAS	Isoform 2B of GTPase KRas	73	38	19	19
P01112	HRAS	GTPase HRas	58	25	14	11
P07355	ANXA2	Annexin A2	49	45	17	28
P55011	SLC12A2	Solute carrier family 12 member 2	12	40	19	21
Q14764	MVP	Major vault protein	25	33	15	18
O60437	PPL	Periplakin	10	25	21	4
P09382	LGALS1	Galectin-1	82	289	65	224
P10909	CLU	Clusterin	30	126	27	99
P08758	ANXA5	Annexin A5	36	91	19	72
P61019	RAB2A	Ras-related protein Rab-2A	57	79	22	57
Q5TDP6	LGSN	Lengsin	27	79	43	36
Q969T9	WBP2	WW domain-binding protein 2	46	60	20	40
Q9NUQ9	FAM49B	Protein FAM49B	36	55	21	34
O95428	PAPLN	Papilin	16	45	36	9
P38606	ATP6V1A	V-type proton ATPase catalytic subunit A	25	36	16	20
P13489	RNH1	Ribonuclease inhibitor	48	34	28	6
Q58EX2	SDK2	Isoform 3 of Protein sidekick-2	9	25	14	11
Q14019	COTL1	Coactosin-like protein	79	102	40	62
P07738	BPGM	Bisphosphoglycerate mutase	66	81	41	40
P53420	COL4A4	Collagen alpha-4(IV) chain	8	77	37	40
Q15124	PGM5	Phosphoglucomutase-like protein 5	24	71	21	50
P15121	AKR1B1	Aldose reductase	58	65	41	24
Q08257	CRYZ	Quinone oxidoreductase	49	38	25	13
O76024	WFS1	Wolframlin	17	27	9	18
E9PCT5	CAV1	Caveolin	66	158	99	59
Q9BY67	CADM1	Cell adhesion molecule 1	39	94	56	38
P04792	HSPB1	Heat shock protein beta-1	64	90	57	33
P10768	ESD	S-formylglutathione hydrolase	59	77	32	45
P30086	PEBP1	Phosphatidylethanolamine-binding protein 1	71	73	46	27
P54920	NAPA	Alpha-soluble NSF attachment protein	51	58	10	48
Q93088	BHMT	Betaine--homocysteine S-methyltransferase 1	34	50	24	26
Q9UJ70	NAGK	N-acetyl-D-glucosamine kinase	29	43	17	26
P37235	HPCAL1	Hippocalcin-like protein 1	56	35	4	31
P61601	NCALD	Neurocalcin-delta	30	14	2	12
P60174	TPI1	Triosephosphate isomerase	48	35	9	26
B4DN31		cDNA FLJ55809	34	34	22	12
P22314	UBA1	Ubiquitin-like modifier-activating enzyme 1	16	33	7	26
O76054	SEC14L2	SEC14-like protein 2	32	32	15	17
Q9BRJ7	NUDT16L1	Protein syndesmos	62	30	19	11
P07942	LAMB1	Laminin subunit beta-1	10	29	22	7
P11142	HSPA8	Heat shock cognate 71 kDa protein	24	26	9	17
P16930	FAH	Fumarylacetoacetase	26	83	25	58
P61106	RAB14	Ras-related protein Rab-14	54	50	13	37
Q68CY4	CYB5R2	NADH-cytochrome b5 reductase 2	42	49	23	26
O75695	RP2	Protein XRP2	39	39	17	22
P02649	APOE	Apolipoprotein E	41	37	3	34
S6B291		IgG H chain	27	37	23	14
Q14376	GALE	UDP-glucose 4-epimerase	37	33	12	21
Q9BX67	JAM3	Junctional adhesion molecule C	35	31	14	17

P37802	TAGLN2	Transgelin-2	58	29	10	19
Q96KP4	CNDP2	Cytosolic non-specific dipeptidase	32	23	7	16
Q9BWD1	ACAT2	Acetyl-CoA acetyltransferase, cytosolic	42	23	16	7
P37837	TALDO1	Transaldolase	31	18	8	10
Q15907	RAB11B	Ras-related protein Rab-11B	47	258	46	212
P23527	HIST1H2BO	Histone H2B type 1-O	49	48	32	16
Q9Y252	CRYL1	Lambda-crystallin homolog	43	48	15	33
P02792	FTL	Ferritin light chain	51	41	8	33
P09417	QDPR	Dihydropteridine reductase	45	37	16	21
O95336	PGLS	6-phosphogluconolactonase	62	33	16	17
P40227	CCT6A	T-complex protein 1 subunit zeta	26	33	9	24
P36871	PGM1	Phosphoglucomutase-1	24	30	11	19
P50990	CCT8	T-complex protein 1 subunit theta	20	26	8	18
P16403	HIST1H1C	Histone H1.2	31	25	15	10
Q93034	CUL5	Cullin-5	16	24	11	13
P36955	SERPINF1	Pigment epithelium-derived factor	29	24	11	13
Q53GN4	WDR1	WD repeat domain 1, isoform CRA_a (Fragment)	21	21	12	9
Q86YZ3	HRNR	Hornerin	5	20	9	11
Q93050	ATP6VOA1	V-type proton ATPase 116 kDa subunit a isoform 1	15	20	5	15
Q8NHU6	TDRD7	Tudor domain-containing protein 7	10	19	11	8
P00918	CA2	Carbonic anhydrase 2	47	141	54	87
Q9HC11	ANKH	Progressive ankylosis protein homolog	25	75	53	22
P68104	EEF1A1	Elongation factor 1-alpha 1	24	55	43	12
Q9UL25	RAB21	Ras-related protein Rab-21	40	47	14	33
P30566	ADSL	Adenylosuccinate lyase	20	37	21	16
P28074	PSMB5	Proteasome subunit beta type-5	27	36	18	18
P62873	GMB1	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	32	35	24	11
Q8IW45	NAXD	ATP-dependent (S)-NAD(P)H-hydrate dehydratase	42	32	22	10
P39060	COL18A1	Collagen alpha-1(XVIII) chain	8	29	17	12
Q6NZ12	PTRF	Polymerase I and transcript release factor	27	29	10	19
O60664	PLIN3	Perilipin-3	27	26	12	14
P02794	FTH1	Ferritin heavy chain	46	25	3	22
Q6IQ22	RAB12	Ras-related protein Rab-12	30	24	11	13
P27824	CANX	Calnexin	18	23	15	8
P17612	PRKACA	cAMP-dependent protein kinase catalytic subunit alpha	26	22	14	8
Q96F27	CHMP6	Charged multivesicular body protein 6	39	22	14	8
Q04760	GLO1	Lactoylglutathione lyase	43	22	10	12
P02786	TFRC	Transferrin receptor protein 1	15	21	10	11
Q99733	NAP1L4	Nucleosome assembly protein 1-like 4	22	17	7	10
P55209	NAP1L1	Nucleosome assembly protein 1-like 1	6	8	3	5
P27361	MAPK3	Mitogen-activated protein kinase 3	26	17	7	10
P28482	MAPK1	Mitogen-activated protein kinase 1	14	12	2	10
P20839	IMPDH1	Inosine 5'-monophosphate dehydrogenase 1	11	9	9	0
P12268	IMPDH2	Inosine 5'-monophosphate dehydrogenase 2	17	8	7	1
P47755	CAPZA2	F-actin-capping protein subunit alpha-2	24	11	7	4
P52907	CAPZA1	F-actin-capping protein subunit alpha-1	30	8	5	3
P63244	RACK1	Receptor of activated protein C kinase 1	32	14	9	5
P31939	ATIC	Bifunctional purine biosynthesis protein PURH	18	12	1	11
P01034	CST3	Cystatin-C	50	146	17	129
P62834	RAP1A	Ras-related protein Rap-1A	42	93	23	70
P53672	CRYBA2	Beta-crystallin A2	58	88	63	25
P0CG47	UBB	Polyubiquitin-B	29	68	39	29
P55344	LIM2	Isoform 2 of Lens fiber membrane intrinsic protein	29	32	22	10
P55344	LIM2	Lens fiber membrane intrinsic protein	19	27	27	0
P35625	TIMP3	Metalloproteinase inhibitor 3	36	56	22	34
Q14031	COL4A6	Collagen alpha-6(IV) chain	5	39	26	13
Q9NZL4	HSPBP1	Hsp70-binding protein 1	24	27	12	15
P36405	ARL3	ADP-ribosylation factor-like protein 3	64	24	10	14
P04083	ANXA1	Annexin A1	28	19	4	15
Q9H857	NT5DC2	5'-nucleotidase domain-containing protein 2	21	19	12	7
O95490	ADGRL2	Adhesion G protein-coupled receptor L2	7	18	6	12
P34932	HSPA4	Heat shock 70 kDa protein 4	13	17	6	11
P27816	MAP4	Microtubule-associated protein 4	9	13	13	0
Q96EF6	FBXO17	F-box only protein 17	34	59	17	42
Q9GZP4	PITHD1	PITH domain-containing protein 1	38	48	15	33
P61163	ACTR1A	Alpha-centractin	27	42	29	13
Q99685	MGLL	Monoglyceride lipase	38	41	16	25
Q15257	PPP2R4	Isoform 1 of Serine/threonine-protein phosphatase 2A activator	29	30	15	15
Q71DI3	HIST2H3A	Histone H3.2	40	27	23	4
Q43592	XPOT	Exportin-T	9	24	4	20
P52565	ARHGDI1	Rho GDP-dissociation inhibitor 1	30	21	4	17
Q99536	VAT1	Synaptic vesicle membrane protein VAT-1 homolog	16	21	6	15
P46926	GNPDA1	Glucosamine-6-phosphate isomerase 1	38	19	12	7
Q8NFZ8	CADM4	Cell adhesion molecule 4	24	19	11	8
Q9H0C3	TMEM117	Transmembrane protein 117	9	19	2	17
P02458	COL2A1	Collagen alpha-1(II) chain	3	18	17	1
Q9NTJ4	MAN2C1	Alpha-mannosidase 2C1	7	16	5	11
P48509	CD151	CD151 antigen	21	16	11	5
P49189	ALDH9A1	4-trimethylaminobutyraldehyde dehydrogenase	16	16	2	14
Q15631	TSN	Translin	36	16	4	12
Q9UHY7	ENOPH1	Enolase-phosphatase E1	30	15	11	4
P61018	RAB4B	Ras-related protein Rab-4B	47	15	2	13
Q43242	PSMD3	26S proteasome non-ATPase regulatory subunit 3	15	14	11	3
Q96F07	CYFIP2	Isoform 2 of Cytoplasmic FMR1-interacting protein 2	5	13	6	7
Q9H4A4	RNPEP	Amino-peptidase B	15	13	7	6
P21964	COMT	Catechol O-methyltransferase	46	13	10	3
P43353	ALDH3B1	Aldehyde dehydrogenase family 3 member B1	12	9	5	4
P51648	ALDH3A2	Fatty aldehyde dehydrogenase	9	4	4	0
P33527	ABCC1	Multidrug resistance-associated protein 1	5	11	3	8

P36578	RPL4	60S ribosomal protein L4	19	10	9	1
Q16851	UGP2	UTP--glucose-1-phosphate uridylyltransferase	14	10	6	4
P06753	TPM3	Isoform 6 of Tropomyosin alpha-3 chain	27	9	4	5
Q13098	GPS1	COP9 signalosome complex subunit 1	15	9	3	6
P05026	ATP1B1	Sodium/potassium-transporting ATPase subunit beta-1	24	53	20	33
P41222	PTGDS	Prostaglandin-H2 D-isomerase	36	40	14	26
Q92542	NCSTN	Nicastrin	12	29	15	14
Q15223	NECTIN1	Nectin-1	18	23	16	7
P08195	SLC3A2	4F2 cell-surface antigen heavy chain	9	22	3	19
Q9NV96	TMEM30A	Cell cycle control protein 50A	12	22	13	9
O00519	FAAH	Fatty-acid amide hydrolase 1	18	21	6	15
Q16270	IGFBP7	Insulin-like growth factor-binding protein 7	26	19	11	8
Q14152	EIF3A	Eukaryotic translation initiation factor 3 subunit A	5	18	6	12
P0C870	JMJD7	JmjC domain-containing protein 7	25	18	7	11
P15260	IFNGR1	Interferon gamma receptor 1	11	18	5	13
Q08357	SLC20A2	Sodium-dependent phosphate transporter 2	9	17	1	16
Q99569	PKP4	Plakophilin-4	5	17	10	7
P09455	RBP1	Retinol-binding protein 1	30	16	2	14
P53007	SLC25A1	Tricarboxylate transport protein, mitochondrial	20	16	11	5
P60891	PRPS1	Ribose-phosphate pyrophosphokinase 1	18	15	7	8
P63010	AP2B1	AP-2 complex subunit beta	7	15	5	10
P61088	UBE2N	Ubiquitin-conjugating enzyme E2 N	47	15	9	6
Q9HAB8	PPCS	Phosphopantothenate--cysteine ligase	14	14	4	11
Q9P0L0	VAPA	Vesicle-associated membrane protein-associated protein A	29	15	10	5
P62826	RAN	GTP-binding nuclear protein Ran	28	15	13	2
P05198	EIF2S1	Eukaryotic translation initiation factor 2 subunit 1	21	15	10	5
P04004	VTN	Vitronectin	11	15	1	14
P13716	ALAD	Delta-aminolevulinic acid dehydratase	20	14	9	5
P06396	GSN	Gelsolin	10	14	4	10
O00534	VWASA	von Willebrand factor A domain-containing protein 5A	9	14	6	8
P26640	VARS	Valine--tRNA ligase	5	14	4	10
P17931	LGALS3	Galectin-3	23	14	7	7
P26639	TARS	Threonine--tRNA ligase, cytoplasmic	11	13	6	7
Q96DA2	RAB39B	Ras-related protein Rab-39B	32	13	3	10
P83731	RPL24	60S ribosomal protein L24	34	13	10	3
Q14767	LTBP2	Latent-transforming growth factor beta-binding protein 2	4	13	3	10
Q9UHN6	TMEM2	Transmembrane protein 2	5	12	5	7
Q96QK1	VPS35	Vacuolar protein sorting-associated protein 35	8	12	5	7
P09960	LTA4H	Leukotriene A-4 hydrolase	13	12	0	12
Q9UIA9	XPO7	Exportin-7	7	12	5	7
P78330	PSPH	Phosphoserine phosphatase	22	11	4	7
P00533	EGFR	Epidermal growth factor receptor	6	11	6	5
P48147	PREP	Prolyl endopeptidase	12	11	5	6
Q14787	TNPO2	Isoform 2 of Transportin-2	6	10	2	8
Q9P2T1	GMPR2	GMP reductase 2	30	10	7	3
Q92729	PTPRU	Receptor-type tyrosine-protein phosphatase U	4	10	6	4
Q86UX2	ITH5	Inter-alpha-trypsin inhibitor heavy chain H5	6	9	9	0
P61247	RPS3A	40S ribosomal protein S3a	20	9	9	0
P60981	DSTN	Destrin	28	7	5	2
Q9Y281	CFL2	Cofilin-2	23	3	0	3
Q92696	RABGGTA	Geranylgeranyl transferase type-2 subunit alpha	17	9	4	5
Q9Y262	EIF3L	Eukaryotic translation initiation factor 3 subunit L	11	8	4	4
P62241	RPS8	40S ribosomal protein S8	25	8	8	0
O95834	EML2	Echinoderm microtubule-associated protein-like 2	11	7	3	4
P54289	CACNA2D1	Voltage-dependent calcium channel subunit alpha-2/delta-1	6	7	2	5
Q9P273	TENM3	Teneurin-3	2	7	3	4
P55064	AQP5	Aquaporin-5	13	71	25	46
Q9UI40	SLC24A2	Isoform 2 of Sodium/potassium/calcium exchanger 2	10	40	21	19
Q96C23	GALM	Aldose 1-epimerase	21	37	2	35
Q8IVW8	SPNS2	Protein spinster homolog 2	12	35	7	28
Q86Y39	NDUFA11	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1:	49	32	15	17
P61457	PCBD1	Pterin-4-alpha-carbinolamine dehydratase	58	25	4	21
P61626	LYZ	Lysozyme C	22	25	18	7
P48029	SLC6A8	Sodium- and chloride-dependent creatine transporter 1	10	24	5	19
P22234	PAICS	Multifunctional protein ADE2	16	23	11	12
P46976	GYG1	Glycogenin-1	12	23	12	11
Q8TD20	SLC2A12	Solute carrier family 2, facilitated glucose transporter member 12	13	23	8	15
Q96FW1	OTUB1	Ubiquitin thioesterase OTUB1	23	20	6	14
Q15435	PPP1R7	Protein phosphatase 1 regulatory subunit 7	19	19	3	16
P61160	ACTR2	Actin-related protein 2	13	18	10	8
O75131	CPNE3	Copine-3	13	16	7	9
Q9P0J0	NDUFA13	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1:	43	16	10	6
O00442	RTCA	RNA 3'-terminal phosphate cyclase	16	15	9	6
P00491	PNP	Purine nucleoside phosphorylase	24	15	7	8
P32320	CDA	Cytidine deaminase	60	15	10	5
Q8NCHO	CHST14	Carbohydrate sulfotransferase 14	15	14	1	13
Q9NQW7	XPNPEP1	Xaa-Pro aminopeptidase 1	9	14	3	11
P21980	TGM2	Protein-glutamine gamma-glutamyltransferase 2	8	14	2	12
Q13867	BLMH	Bleomycin hydrolase	10	13	7	6
Q9Y624	F11R	Junctional adhesion molecule A	14	13	9	4
Q13057	COASY	Bifunctional coenzyme A synthase	7	13	1	12
P49720	PSMB3	Proteasome subunit beta type-3	28	13	5	8
O75874	IDH1	Isocitrate dehydrogenase [NADP] cytoplasmic	14	13	7	6
Q99426	TBCB	Tubulin-folding cofactor B	20	12	11	1
P16435	POR	NADPH--cytochrome P450 reductase	11	12	10	2
Q3LXA3	TKFC	Triokinase/FMN cyclase	13	12	2	10
Q01518	CAP1	Adenylyl cyclase-associated protein 1	13	12	8	4
Q9UQ03	CORO2B	Coronin-2B	11	12	5	7
Q9BZ14	SLC25A39	Solute carrier family 25 member 39	14	11	4	7

Q15008	PSMD6	26S proteasome non-ATPase regulatory subunit 6	13	11	10	1
P61158	ACTR3	Actin-related protein 3	13	11	8	3
P55072	VCP	Transitional endoplasmic reticulum ATPase	8	11	4	7
Q16531	DDB1	DNA damage-binding protein 1	5	10	3	7
Q43813	LANCL1	LanC-like protein 1	16	10	8	2
P09543	CNP	2',3'-cyclic-nucleotide 3'-phosphodiesterase	12	9	5	4
P34896	SHMT1	Serine hydroxymethyltransferase, cytosolic	13	8	3	5
Q43790	KRT86	Keratin, type II cuticular Hb6	9	7	7	0
Q8N2K0	ABHD12	Monoacylglycerol lipase ABHD12	18	7	6	1
P55884	EIF3B	Eukaryotic translation initiation factor 3 subunit B	5	7	2	5
Q9NUU7	DDX19A	ATP-dependent RNA helicase DDX19A	7	7	5	2
Q9H9T3	ELP3	Elongator complex protein 3	9	7	4	3
P62140	PPP1CB	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	23	7	5	2
Q9Y6C2	EMILIN1	EMILIN-1	7	7	0	7
P05556	ITGB1	Integrin beta-1	9	6	3	3
P10301	RRAS	Ras-related protein R-Ras	14	4	0	4
P62070	RRAS2	Ras-related protein R-Ras2	17	4	1	3
P46781	RPS9	40S ribosomal protein S9	20	6	6	0
Q9P265	DIP2B	Disco-interacting protein 2 homolog B	3	6	4	2
P21796	VDAC1	Voltage-dependent anion-selective channel protein 1	12	4	4	0
Q9Y277	VDAC3	Voltage-dependent anion-selective channel protein 3	11	4	4	0
Q9BXW6	OSBPPLA	Oxysterol-binding protein-related protein 1	5	6	5	1
Q43795	MYO1B	Unconventional myosin-Ib	6	6	3	3
P58005	SESN3	Sestrin-3	14	6	3	3
P10599	TXN	Thioredoxin	40	6	2	4
Q9BT78	COPS4	COP9 signalosome complex subunit 4	15	6	3	3
P62269	RPS18	40S ribosomal protein S18	28	5	4	1
Q15530	PDPK1	3-phosphoinositide-dependent protein kinase 1	13	5	4	1
Q6P5S8	IGK@	IGK@ protein	25	43	11	32
Q9NZHO	GPRC5B	G-protein coupled receptor family C group 5 member B	10	40	8	32
P21926	CD9	CD9 antigen	14	25	5	20
P22352	GPX3	Glutathione peroxidase 3	12	18	4	14
P04271	S100B	Protein S100-B	45	18	18	0
P21281	ATP6V1B2	V-type proton ATPase subunit B, brain isoform	10	18	6	12
P08581	MET	Hepatocyte growth factor receptor	3	17	1	16
Q8WUM4	PDCD6IP	Isoform 2 of Programmed cell death 6-interacting protein	5	15	4	11
P41250	GARS	Glycine--tRNA ligase	8	15	2	13
Q6IAA8	LAMTOR1	Ragulator complex protein LAMTOR1	31	14	7	7
P29992	GNA11	Guanine nucleotide-binding protein subunit alpha-11	13	14	11	3
Q724W1	DCXR	L-xylulose reductase	20	14	7	7
Q16775	HAGH	Hydroxyacylglutathione hydrolase, mitochondrial	19	14	3	11
P15151	PVR	Poliovirus receptor	13	13	9	4
P55001	MFAP2	Microfibrillar-associated protein 2	18	13	13	0
Q8N3E9	PLCD3	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase delta-	7	13	3	10
Q96IU4	ABHD14B	Protein ABHD14B	34	13	5	8
P15086	CPB1	Carboxypeptidase B	11	12	5	7
Q5VZM2	RRAGB	Ras-related GTP-binding protein B	13	12	4	8
Q9GZT8	NIF3L1	NIF3-like protein 1	12	12	8	4
Q9BZV2	SLC19A3	Thiamine transporter 2	8	12	4	8
O00232	PSMD12	26S proteasome non-ATPase regulatory subunit 12	10	12	2	10
Q43488	AKR7A2	Aflatoxin B1 aldehyde reductase member 2	15	11	6	5
Q9UI12	ATP6V1H	V-type proton ATPase subunit H	11	11	1	10
P29218	IMPA1	Inositol monophosphatase 1	13	10	4	6
P14324	FDP5	Farnesyl pyrophosphate synthase	19	10	3	7
P46952	HAAO	3-hydroxyanthranilate 3,4-dioxygenase	19	10	0	10
P62266	RPS23	40S ribosomal protein S23	29	10	8	2
Q95373	IPO7	Importin-7	6	10	6	4
P00441	SOD1	Superoxide dismutase [Cu-Zn]	45	10	8	2
Q75915	ARL6IP5	PRA1 family protein 3	20	10	3	7
P21399	ACO1	Cytoplasmic aconitate hydratase	5	10	4	6
B40UF1		cDNA FLJ59760, highly similar to 1,4-alpha-glucan branching enzyn	7	10	6	4
B2RDN1		cDNA, FLJ96690, highly similar to Homo sapiens glutathione transf	32	9	7	2
Q92597	NDRG1	Protein NDRG1	12	9	3	6
Q8IWA5	SLC44A2	Choline transporter-like protein 2	4	9	4	5
P09211	GSTP1	Glutathione S-transferase P	34	9	2	7
Q6UW68	TMEM205	Transmembrane protein 205	22	9	6	3
P12235	SLC25A4	ADP/ATP translocase 1	20	9	9	0
Q07960	ARHGAP1	Rho GTPase-activating protein 1	11	8	2	6
Q96A11	GAL3ST3	Galactose-3-O-sulfotransferase 3	11	8	2	6
Q9BWQ8	FAIM2	Protein lifeguard 2	14	8	5	3
P41091	EIF2S3	Eukaryotic translation initiation factor 2 subunit 3	13	8	4	4
Q9NTK5	OLA1	Obg-like ATPase 1	15	8	4	4
P02787	TF	Serotransferrin	8	8	7	1
P10745	RBP3	Retinol-binding protein 3	4	8	0	8
P47756	CAP2B	F-actin-capping protein subunit beta	12	8	2	6
Q9NZJ7	MTCH1	Mitochondrial carrier homolog 1	11	7	7	0
P51151	RAB9A	Ras-related protein Rab-9A	24	7	1	6
Q9Y2A7	NCKAP1	Nck-associated protein 1	4	7	3	4
P04844	RPN2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase su	10	7	3	4
P14868	DARS	Aspartate--tRNA ligase, cytoplasmic	8	6	2	4
Q13642	FHL1	Isoform 1 of Four and a half LIM domains protein 1	16	6	3	3
Q15582	TGFBI	Transforming growth factor-beta-induced protein ig-h3	7	6	1	5
Q5T457	UBR4	E3 ubiquitin-protein ligase UBR4	1	6	2	4
P31153	MAT2A	S-adenosylmethionine synthase isoform type-2	12	6	2	4
Q8WTV0	SCARB1	Scavenger receptor class B member 1	7	6	2	4
P15374	UCHL3	Ubiquitin carboxyl-terminal hydrolase isozyme L3	23	6	2	4
Q9UQM7	CAMK2A	Calcium/calmodulin-dependent protein kinase type II subunit alph	13	6	2	4
P04156	PRNP	Major prion protein	15	6	3	3
P43007	SLC1A4	Neutral amino acid transporter A	8	6	3	3

Q9BTW9	TBCD	Tubulin-specific chaperone D	3	6	3	3
P17174	GOT1	Aspartate aminotransferase, cytoplasmic	15	6	2	4
P28070	PSMB4	Proteasome subunit beta type-4	20	5	2	3
P60900	PSMA6	Proteasome subunit alpha type-6	18	5	3	2
Q14203	DCTN1	Dynactin subunit 1	7	5	4	1
Q13214	SEMA3B	Semaphorin-3B	6	5	1	4
Q555J5	HP1BP3	Heterochromatin protein 1-binding protein 3	11	5	5	0
P11766	ADH5	Alcohol dehydrogenase class-3	12	5	4	1
P39023	RPL3	60S ribosomal protein L3	8	5	5	0
O00159	MYO1C	Unconventional myosin-1c	5	5	3	2
P45880	VDAC2	Voltage-dependent anion-selective channel protein 2	15	5	5	0
O00303	EIF3F	Eukaryotic translation initiation factor 3 subunit F	11	5	1	4
Q5VWZ2	LYPLAL1	Lysophospholipase-like protein 1	15	5	3	2
Q12756	KIF1A	Kinesin-like protein KIF1A	3	5	2	3
O00231	PSMD11	26S proteasome non-ATPase regulatory subunit 11	11	5	2	3
P62917	RPL8	60S ribosomal protein L8	14	5	4	1
P55060	CSE1L	Exportin-2	4	5	1	4
P15924	DSP	Desmoplakin	2	5	1	4
Q9Y5L0	TNPO3	Transportin-3	4	4	1	3
P54687	BCAT1	Branched-chain-amino-acid aminotransferase, cytosolic	20	4	4	0
Q9NY33	DPP3	Dipeptidyl peptidase 3	7	4	1	3
A0AVT1	UBA6	Ubiquitin-like modifier-activating enzyme 6	4	4	0	4
P0COL4	C4A	Complement C4-A	3	4	0	4
P40926	MDH2	Malate dehydrogenase, mitochondrial	15	4	3	1
P30301	MIP	Lens fiber major intrinsic protein	14	88	38	50
Q15836	VAMP3	Vesicle-associated membrane protein 3	40	75	3	72
P54709	ATP1B3	Sodium/potassium-transporting ATPase subunit beta-3	14	29	6	23
O60888	CUTA	Protein CutA	33	26	19	7
O75663	TIPRL	TIP41-like protein	18	25	18	7
P04908	HIST1H2AB	Histone H2A type 1-B/E	21	20	9	11
P56134	ATP5J2	ATP synthase subunit f, mitochondrial	26	19	11	8
Q96CN7	ISOC1	Isochorismatase domain-containing protein 1	15	19	5	14
Q9Y5L5	LENEP	Lens epithelial cell protein LEP503	44	18	13	5
Q6DKJ4	NXN	Nucleoredoxin	11	18	4	14
P52758	HRSP12	Ribonuclease UK114	31	17	8	9
P13987	CD59	CD59 glycoprotein	16	16	13	3
Q7L5N1	COPS6	COP9 signalosome complex subunit 6	13	13	8	5
P16035	TIMP2	Metalloproteinase inhibitor 2	17	12	12	0
Q9NP72	RAB18	Ras-related protein Rab-18	17	12	4	8
Q16555	DPYSL2	Dihydropyrimidinase-related protein 2	6	12	8	4
P63218	GNG5	Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma	26	11	4	7
Q9BXM7	PINK1	Serine/threonine-protein kinase PINK1, mitochondrial	8	11	6	5
P46776	RPL27A	60S ribosomal protein L27a	24	11	10	1
P59998	ARPC4	Actin-related protein 2/3 complex subunit 4	18	11	2	9
P14174	MIF	Macrophage migration inhibitory factor	17	10	10	0
Q92905	COPS5	COP9 signalosome complex subunit 5	9	10	3	7
P53004	BLVRA	Biliverdin reductase A	18	10	5	5
P26447	S100A4	Protein S100-A4	20	10	2	8
Q4G0F5	VPS26B	Vacuolar protein sorting-associated protein 26B	7	9	3	6
Q9H0R4	HDHD2	Haloacetal dehalogenase-like hydrolase domain-containing protein 2	15	9	1	8
P10155	TROVE2	60 kDa SS-A/Ro ribonucleoprotein	5	9	6	3
P62191	PSMC1	26S protease regulatory subunit 4	8	9	6	3
Q9Y6M5	SLC30A1	Zinc transporter 1	8	9	4	5
P49419	ALDH7A1	Alpha-aminoacidic semialdehyde dehydrogenase	7	9	5	4
Q8I283	ALDH16A1	Aldehyde dehydrogenase family 16 member A1	5	8	4	4
P18433	PTPRA	Receptor-type tyrosine-protein phosphatase alpha	4	8	5	3
O94973	AP2A2	AP-2 complex subunit alpha-2	3	8	3	5
O75110	ATP9A	Probable phospholipid-transporting ATPase IIA	3	8	0	8
Q969Q5	RAB24	Ras-related protein Rab-24	21	7	1	7
Q9BV20	MRI1	Methylthioribose-1-phosphate isomerase	11	8	3	5
Q9UK39	NOCT	Nocturnin	7	7	3	4
P25787	PSMA2	Proteasome subunit alpha type-2	19	7	5	2
O75144	ICOSLG	ICOS ligand	14	7	4	3
Q13636	RAB31	Ras-related protein Rab-31	20	7	0	7
Q92530	PSMF1	Proteasome inhibitor PI31 subunit	11	7	5	2
P00505	GOT2	Aspartate aminotransferase, mitochondrial	8	7	2	5
O14925	TIMM23	Mitochondrial import inner membrane translocase subunit Tim23	10	7	6	1
O00743	PPP6C	Serine/threonine-protein phosphatase 6 catalytic subunit	10	7	5	2
P31689	DNAJA1	DnaJ homolog subfamily A member 1	10	7	3	4
Q96CW1	AP2M1	AP-2 complex subunit mu	6	7	4	3
Q6PIU2	NCEH1	Neutral cholesterol ester hydrolase 1	10	6	4	2
Q9NRN7	AASDHPTT	L-aminoacidipate-semialdehyde dehydrogenase-phosphopantethein	9	6	2	4
O95433	AHSA1	Activator of 90 kDa heat shock protein ATPase homolog 1	11	4	6	2
Q9BZV1	UBXN6	UBX domain-containing protein 6	9	6	2	4
P26572	MGAT1	Alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltran	6	6	1	5
P42766	RPL35	60S ribosomal protein L35	22	6	5	1
P52306	RAP1GDS1	Rap1 GTPase-GDP dissociation stimulator 1	6	6	1	5
P31213	SRD5A2	3-oxo-5-alpha-steroid 4-dehydrogenase 2	11	6	4	2
Q7LGS6	RRM2B	Ribonucleoside-diphosphate reductase subunit M2 B	10	6	5	1
Q9BZG8	DPH1	Diphthamide biosynthesis protein 1	6	6	0	6
Q13617	CUL2	Cullin-2	3	6	2	4
P12955	PEPD	Xaa-Pro dipeptidase	12	6	4	2
Q9Y230	RUVBL2	RuvB-like 2	7	5	2	3
Q9Y376	CAB39	Calcium-binding protein 39	9	5	0	5
Q96P70	IPO9	Importin-9	4	5	1	4
Q13492	PICALM	Phosphatidylinositol-binding clathrin assembly protein	5	5	2	3
Q9UIC8	LCMT1	Leucine carboxyl methyltransferase 1	8	5	1	4
P04843	RPN1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase su	7	5	5	0
Q02978	SLC25A11	Mitochondrial 2-oxoglutarate/malate carrier protein	12	5	3	2

Q43747	AP1G1	AP-1 complex subunit gamma-1	3	5	3	2
Q9C0E8	LNP	Protein lunapark	8	5	3	2
Q9Y2H2	INPP5F	Phosphatidylinositol phosphatase SAC2	3	5	2	3
P13797	PLS3	Plastin-3	6	5	0	5
P53611	RABGGTB	Geranylgeranyl transferase type-2 subunit beta	10	5	2	3
Q02790	FKBP4	Peptidyl-prolyl cis-trans isomerase FKBP4	10	5	5	0
Q92614	MYO18A	Unconventional myosin-XVIIla	1	5	3	2
P12429	ANXA3	Annexin A3	9	5	1	4
P62750	RPL23A	60S ribosomal protein L23a	15	5	5	0
Q6ZMM2	ADAMTSL5	ADAMTS-like protein 5	12	5	4	1
P49591	SARS	Serine--tRNA ligase, cytoplasmic	6	5	4	1
P0CG29	GSTT2	Glutathione S-transferase theta-2	12	5	1	4
Q12765	SCRN1	Secernin-1	10	5	4	1
Q9NVE7	PANK4	Pantothenate kinase 4	5	5	2	3
Q14558	PRPSAP1	Phosphoribosyl pyrophosphate synthase-associated protein 1	10	5	2	3
Q9UJW0	DCTN4	Dynactin subunit 4	7	5	3	2
Q8TAA9	VANGL1	Vang-like protein 1	7	4	0	4
P0CG05	IGLC2	Ig lambda-2 chain C regions	38	4	1	3
Q9NZL9	MAT2B	Methionine adenosyltransferase 2 subunit beta	11	4	1	3
P25788	PSMA3	Proteasome subunit alpha type-3	14	4	3	1
Q9Y6N5	SQRDL	Sulfide:quinone oxidoreductase, mitochondrial	8	4	1	3
P53794	SLC5A3	Sodium/myo-inositol cotransporter	4	4	1	3
O00391	QSOX1	Sulphydryl oxidase 1	3	4	1	3
Q3SXM5	HSDL1	Inactive hydroxysteroid dehydrogenase-like protein 1	8	4	3	1
Q5TA50	CPTP	Ceramide-1-phosphate transfer protein	15	4	4	0
Q8N336	ELMOD1	ELMODomain-containing protein 1	13	4	4	0
Q14744	PRMT5	Protein arginine N-methyltransferase 5	4	4	3	1
P08574	CYC1	Cytochrome c1, heme protein, mitochondrial	12	4	3	1
P50747	HLCS	Biotin--protein ligase	3	4	2	2
Q9NZ01	TECR	Very-long-chain enoyl-CoA reductase	10	4	3	1
P55290	CDH13	Cadherin-13	7	4	2	2
P49755	TMED10	Transmembrane emp24 domain-containing protein 10	18	4	3	1
Q9UKK9	NUDT5	ADP-sugar pyrophosphatase	16	4	2	2
P43034	PAFAH1B1	Platelet-activating factor acetylhydrolase IB subunit alpha	8	4	4	0
P62753	RPS6	40S ribosomal protein S6	14	4	4	0
Q5T5P2	KIAA1217	Sickle tail protein homolog	2	4	0	4
O95671	ASMTL	N-acetyserotonin O-methyltransferase-like protein	7	4	3	1
Q08722	CD47	Leukocyte surface antigen CD47	9	4	2	2
Q13126	MTAP	S-methyl-5'-thioadenosine phosphorylase	19	4	2	2
O60502	MGEA5	Protein O-GlcNAcase	4	4	1	3
Q9NQE9	HINT3	Histidine triad nucleotide-binding protein 3	15	4	2	2
P23396	RPS3	40S ribosomal protein S3	13	4	2	2
Q6NUI6	CHADL	Chondroadherin-like protein	6	4	0	4
Q9BX55	AP1M1	AP-1 complex subunit mu-1	8	4	1	3
P04920	SLC4A2	Anion exchange protein 2	3	3	1	2
Q9UNM6	PSMD13	26S proteasome non-ATPase regulatory subunit 13	10	3	2	1
P51572	BCAP31	B-cell receptor-associated protein 31	13	3	2	1
P62851	RPS25	40S ribosomal protein S25	22	3	3	0
O00429	DNM1L	Dynamin-1-like protein	5	3	2	1
O75964	ATP5L	ATP synthase subunit g, mitochondrial	36	3	2	3
Q9NZW5	MPP6	MAGUK p55 subfamily member 6	7	3	1	2
Q8Y17	PNPLA6	Neuropathy target esterase	2	3	1	2
P17301	ITGA2	Integrin alpha-2	3	3	2	1
Q99829	CPNE1	Copine-1	8	3	1	2
Q9NQC3	RTN4	Reticulon-4	3	3	1	2
P07737	PFN1	Profilin-1	29	3	2	1
P24539	ATP5F1	ATP synthase F(0) complex subunit B1, mitochondrial	12	3	2	1
P60228	EIF3E	Eukaryotic translation initiation factor 3 subunit E	8	3	2	1
Q9Y450	HBS1L	HBS1-like protein	5	3	1	2
Q9BTU6	PI4K2A	Phosphatidylinositol 4-kinase type 2-alpha	8	3	2	1
A8K7N0		cDNA FLJ75556, highly similar to Homo sapiens ribosomal protein	21	3	2	1
P07305	H1FO	Histone H1.0	14	3	3	0
B3SHH9	TMEM114	Transmembrane protein 114	10	34	21	13
Q96DD7	SHISA4	Protein shisa-4	20	24	0	24
P04216	THY1	Thy-1 membrane glycoprotein	15	22	10	12
Q13200	PSMD2	26S proteasome non-ATPase regulatory subunit 2	3	13	4	9
Q9C0H2	TTYH3	Protein tweety homolog 3	6	10	4	6
Q12805	EFEMP1	EGF-containing fibulin-like extracellular matrix protein 1	3	10	1	9
Q99447	PCYT2	Ethanolamine-phosphate cytidyltransferase	9	8	7	1
Q14CZ7	FASTKD3	FAST kinase domain-containing protein 3, mitochondrial	5	8	4	4
Q9H0X4	FAM234A	Protein FAM234A	6	7	5	2
P26641	EEF1G	Elongation factor 1-gamma	5	7	2	5
O75367	H2AFY	Core histone macro-H2A.1	9	7	7	0
Q99460	PSMD1	26S proteasome non-ATPase regulatory subunit 1	3	7	7	0
P51884	LUM	Lumican	7	7	2	5
P23229	ITGA6	Isoform Alpha-6X1A of Integrin alpha-6	2	7	1	6
Q99969	RARRES2	Retinoic acid receptor responder protein 2	14	7	3	4
O60256	PRPSAP2	Phosphoribosyl pyrophosphate synthase-associated protein 2	8	7	2	5
Q9NPQ8	RIC8A	Synembryn-A	3	7	2	5
Q27AA2	IAH1	Isoamyl acetate-hydrolyzing esterase 1 homolog	9	7	6	1
Q12846	STX4	Syntaxin-4	7	7	2	5
O75340	PDCD6	Programmed cell death protein 6	13	6	1	5
P48449	LSS	Lanosterol synthase	4	6	2	4
P30046	DDT	D-dopachrome decarboxylase	22	6	2	4
P34096	RNASE4	Ribonuclease 4	14	6	6	0
Q15036	SNX17	Sorting nexin-17	7	6	2	4
Q9UN52	COPS3	COP9 signalosome complex subunit 3	8	6	3	3
O00560	SDCBP	Syntenin-1	11	6	6	0
Q9P2J2	IGSF9	Protein turtle homolog A	2	6	4	2

Q95361	TRIM16	Tripartite motif-containing protein 16	4	6	2	4
Q968M9	ARL8A	ADP-ribosylation factor-like protein 8A	12	6	0	6
Q13637	RAB32	Ras-related protein Rab-32	10	5	1	4
Q9NZ53	PODXL2	Podocalyxin-like protein 2	4	5	2	3
Q9BQA1	WDR77	Methylosome protein 50	6	5	2	3
Q9NZU5	LMCD1	LIM and cysteine-rich domains protein 1	8	5	1	4
O75489	NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	8	5	1	4
Q99598	TSNAX	Translin-associated protein X	13	5	5	0
P03950	ANG	Angiogenin	14	5	5	0
P37059	HSD17B2	Estradiol 17-beta-dehydrogenase 2	7	5	4	1
P39656	DDOST	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48	4	5	3	2
P49842	STK19	Serine/threonine-protein kinase 19	3	5	1	4
Q8TEX9	IPO4	Importin-4	2	5	1	4
Q96597	MYADM	Myeloid-associated differentiation marker	10	4	1	3
O75396	SEC22B	Vesicle-trafficking protein SEC22b	10	4	2	2
P23381	WARS	Tryptophan--tRNA ligase, cytoplasmic	5	4	3	1
Q9HB90	RRAGC	Ras-related GTP-binding protein C	5	4	2	2
Q8N0W3	FUK	L-fucose kinase	2	4	0	4
P54136	RARS	Arginine--tRNA ligase, cytoplasmic	4	4	1	3
Q96NU7	AMDHD1	Probable imidazolonepropionase	5	4	2	2
Q9H477	RBKS	Ribokinase	5	4	1	3
P35573	AGL	Glycogen debranching enzyme	1	4	3	1
Q8N7X0	ADGB	Androglobin	1	4	3	1
Q9UBW8	COP57A	COP9 signalosome complex subunit 7a	9	4	4	0
P13073	COX4I1	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial	11	4	4	0
P54851	EMP2	Epithelial membrane protein 2	6	4	4	0
P05388	RPLP0	60S acidic ribosomal protein P0	14	4	4	0
Q9HC38	GLOD4	Glyoxalase domain-containing protein 4	8	4	3	1
P40123	CAP2	Adenylyl cyclase-associated protein 2	7	4	4	0
Q9Y2V2	CARHSP1	Calcium-regulated heat-stable protein 1	18	4	4	0
Q9NX46	ADPRHL2	Poly(ADP-ribose) glycohydrolase ARH3	7	4	2	2
Q8NC56	LEMD2	LEM domain-containing protein 2	5	4	3	1
Q92765	FRZB	Secreted frizzled-related protein 3	6	4	1	3
P35612	ADD2	Beta-adducin	3	4	3	1
A0A068		Ig heavy chain variable region (Fragment)	13	4	0	4
Q15198	PDGFRL	Platelet-derived growth factor receptor-like protein	5	4	0	4
Q9BU40	CHRD1	Chordin-like protein 1	5	4	1	3
P04080	CSTB	Cystatin-B	24	4	2	2
Q96FV2	SCRN2	Secernin-2	13	4	4	0
P20073	ANXA7	Annexin A7	4	4	3	1
P25789	PSMA4	Proteasome subunit alpha type-4	11	4	2	2
Q8N8N7	PTGR2	Prostaglandin reductase 2	6	4	1	3
O95747	OXSR1	Serine/threonine-protein kinase OSR1	5	4	0	4
Q96CC6	RHBDF1	Inactive rhomboid protein 1	4	3	3	0
P53602	MVD	Diphosphomevalonate decarboxylase	5	3	2	1
P02768	ALB	Serum albumin	4	3	1	2
Q9Y5P6	GMPPB	Mannose-1-phosphate guanylyltransferase beta	6	3	0	3
P62829	RPL23	60S ribosomal protein L23	21	3	2	1
Q9UGT4	SUSD2	Sushi domain-containing protein 2	4	3	0	3
Q14697	GANAB	Neutral alpha-glucosidase AB	3	3	3	0
P08174	CD55	Complement decay-accelerating factor	4	3	3	0
Q9HA65	TBC1D17	TBC1 domain family member 17	3	3	0	3
P62701	RPS4X	40S ribosomal protein S4, X isoform	7	3	3	0
Q15628	TRADD	Tumor necrosis factor receptor type 1-associated DEATH domain p	6	3	1	2
P27635	RPL10	60S ribosomal protein L10	10	3	2	1
Q8N4T0	CPA6	Carboxypeptidase A6	6	3	2	1
P48729	CSNK1A1	Casein kinase I isoform alpha	7	3	2	1
Q9BX19	NAA15	N-alpha-acetyltransferase 15, NatA auxiliary subunit	2	3	1	2
O00505	KPNA3	Importin subunit alpha-4	4	3	1	2
B5ME19	EIF3CL	Eukaryotic translation initiation factor 3 subunit C-like protein	2	3	1	2
C9J069	C9orf172	Uncharacterized protein C9orf172	3	3	3	0
P53680	AP2S1	AP-2 complex subunit sigma	11	3	1	2
Q43776	NARS	Asparagine--tRNA ligase, cytoplasmic	3	3	3	0
Q04323	UBXN1	UBX domain-containing protein 1	7	3	1	2
Q13444	ADAM15	Disintegrin and metalloproteinase domain-containing protein 15	3	3	1	2
Q9BQ24	ZFYVE21	Zinc finger FYVE domain-containing protein 21	13	3	2	1
Q9UBX1	CTSF	Cathepsin F	4	3	0	3
Q13630	TSTA3	GDP-L-fucose synthase	8	3	1	2
P61764	STXBP1	Syntaxin-binding protein 1	3	3	2	1
Q96AD5	PNPLA2	Patatin-like phospholipase domain-containing protein 2	5	3	1	2
Q14194	CRMP1	Dihydropyrimidinase-related protein 1	3	3	2	1
P62847	RPS24	40S ribosomal protein S24	20	3	3	0
P25325	MPST	3-mercaptopyruvate sulfurtransferase	10	3	0	3
B4E082		cDNA FLJ51426, highly similar to Adapter-related protein complex	4	3	1	2
Q9HC10	OTOF	Otoferlin	1	3	2	1
Q9NX14	NDUFB11	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 11	12	3	2	1
P07741	APRT	Adenine phosphoribosyltransferase	12	3	0	3
P51665	PSMD7	26S proteasome non-ATPase regulatory subunit 7	6	3	3	0
Q92954	PRG4	Proteoglycan 4	3	3	1	2
Q35Y77	UGT3A2	UDP-glucuronosyltransferase 3A2	6	3	3	0
Q53H96	PYCR1	Pyruvate-5-carboxylate reductase 3	7	3	2	1
Q9Y255	PRELID1	PRELI domain-containing protein 1, mitochondrial	9	3	2	1
Q03154	ACY1	Aminoacylase-1	4	3	2	1
Q43396	TXNL1	Thioredoxin-like protein 1	7	3	0	3
Q95573	ACSL3	Long-chain-fatty-acid--CoA ligase 3	3	2	2	0
Q9UKS6	PACSN3	Protein kinase C and casein kinase substrate in neurons protein 3	5	2	0	2
Q8TAD2	IL17D	Interleukin-17D	6	2	0	2
Q06055	ATP5G2	ATP synthase F(0) complex subunit C2, mitochondrial	11	2	0	2
P61201	COP52	COP9 signalosome complex subunit 2	7	2	2	0

Q96CD0	FBXL8	F-box/LRR-repeat protein 8	8	2	0	2
P07203	GPX1	Glutathione peroxidase 1	12	2	2	0
O14521	SDHD	Succinate dehydrogenase [ubiquinone] cytochrome b small subunit	13	2	2	0
Q9Y5V6	ST14	Suppressor of tumorigenicity 14 protein	7	2	2	0
Q5D862	FLG2	Filaggrin-2	2	2	2	0
P62714	PPP2CB	Serine/threonine-protein phosphatase 2A catalytic subunit beta isoform	9	2	2	0
Q7RTR2	NLR3	Protein NLR3	3	2	2	0
P60880	SNAP25	Synaptosomal-associated protein 25	13	2	2	0
P08648	ITGA5	Integrin alpha-5	2	2	0	2
P34949	MPI	Mannose-6-phosphate isomerase	8	2	0	2
P61769	B2M	Beta-2-microglobulin	17	2	0	2
Q15366	PCBP2	Poly(rC)-binding protein 2	8	2	2	0
Q16773	KYAT1	Kynurenine--oxoglutarate transaminase 1	9	2	2	0
P12081	HARS	Histidine--tRNA ligase, cytoplasmic	3	2	0	2
E9PAV3	NACA	Nascent polypeptide-associated complex subunit alpha, muscle-specific	1	2	0	2
Q8WUA7	TBC1D22A	TBC1 domain family member 22A	4	2	0	2
Q9C0C9	UBE2O	(E3-independent) E2 ubiquitin-conjugating enzyme	2	2	2	0
P06576	ATP5B	ATP synthase subunit beta, mitochondrial	5	2	2	0
Q969X5	ERGIC1	Endoplasmic reticulum-Golgi intermediate compartment protein 1	13	2	2	0
Q7L099	RUFY3	Protein RUFY3	5	2	0	2
Q9BYW1	SLC2A11	Solute carrier family 2, facilitated glucose transporter member 11	7	2	0	2
P55039	DRG2	Developmentally-regulated GTP-binding protein 2	5	2	2	0
Q86UP2	KTN1	Kinectin	1	2	2	0
Q11206	ST3GAL4	CMP-N-acetylneuraminic acid-6-sialyltransferase 4	10	2	2	0
O14980	XPO1	Exportin-1	2	2	0	2
Q03001	DST	Dystonin	0	2	0	2
P84098	RPL19	60S ribosomal protein L19	9	2	2	0
P49721	PSMB2	Proteasome subunit beta type-2	8	2	2	0
P46782	RPS5	40S ribosomal protein S5	11	2	2	0
Q5VYK3	ECM29	Proteasome-associated protein ECM29 homolog	1	2	2	0
Q00839	HNRNPU	Heterogeneous nuclear ribonucleoprotein U	5	2	2	0
O76009	KRT33A	Keratin, type I cuticular Ha3-1	7	2	2	0
P51608	MECP2	Methyl-CpG-binding protein 2	5	2	2	0
Q5T749	KPRP	Keratinocyte proline-rich protein	4	2	2	0
P18621	RPL17	60S ribosomal protein L17	10	2	2	0
O15144	ARPC2	Actin-related protein 2/3 complex subunit 2	7	2	0	2
O00264	PGRMC1	Membrane-associated progesterone receptor component 1	28	2	2	0
Q92520	FAM3C	Protein FAM3C	13	2	2	0
P56192	MARS	Methionine--tRNA ligase, cytoplasmic	3	2	0	2
Q9BV57	ADI1	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	11	2	0	2
Q16799	RTN1	Reticulon-1	3	2	2	0
O95715	CXCL14	C-X-C motif chemokine 14	10	2	0	2
P43490	NAMPT	Nicotinamide phosphoribosyltransferase	10	2	2	0
P63165	SUMO1	Small ubiquitin-related modifier 1	16	2	2	0
P30419	NMT1	Glycylpeptide N-tetradecanoyltransferase 1	4	2	2	0