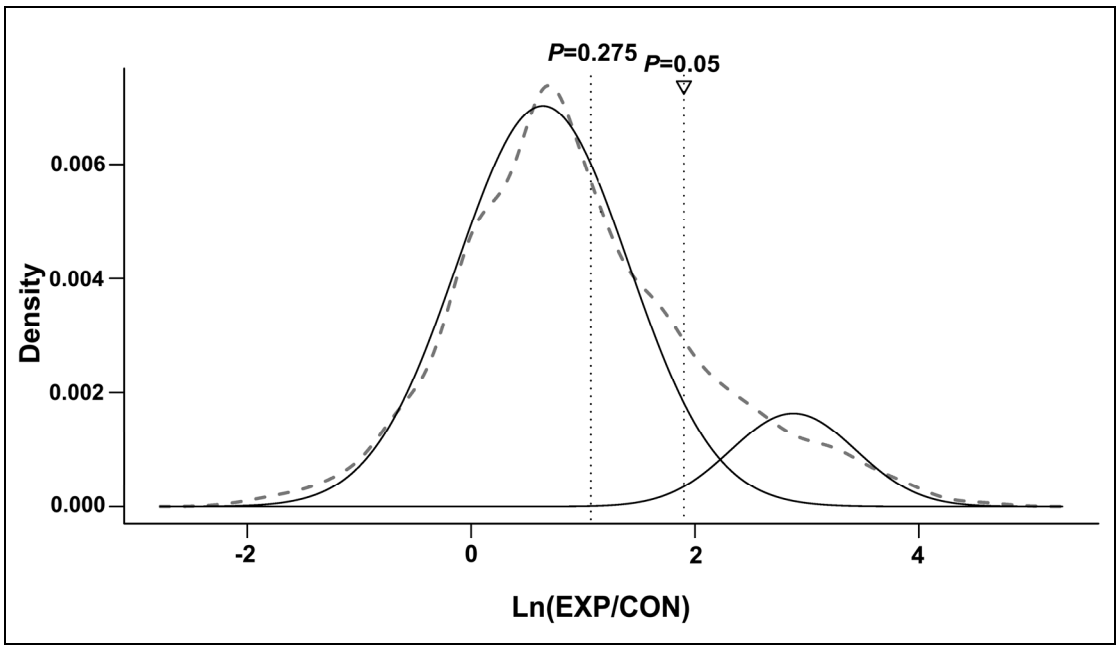


Figure S1. Gaussian distribution of the log-ratios ln(EXP/CON) of proteins identified using the protein-based procedure. The spectral counts were merged over all biological replicates and membrane domains prior to the imputation of missing values. Bayesian Information Criterion-based Gaussian Mixture modeling (ref. 26) suggested that the distribution of log-ratios (dashed line) comprises two Gaussian components (solid lines). The left Gaussian represents the log-ratio distribution of most contaminating proteins and some S-acylated proteins while the right Gaussian represents the log-ratio distribution of most S-acylated proteins and a small number of contaminants. The mean (standard deviation) values for the left and the right Gaussians are 0.64 (0.76) and 2.88 (0.56), respectively. To distinguish S-acylated proteins from contaminating proteins, *p*-values were calculated based on the distribution of the left Gaussian. Proteins with $p<0.05$ (corresponding to EXP/CON>6.7) were treated as significant and accepted as high-confidence S-acylated protein candidates while those with *p* values between 0.275 and 0.05 (corresponding to $3.0 \leq$ EXP/CON ≤ 6.7) were considered as medium-confidence S-acylated protein candidates.

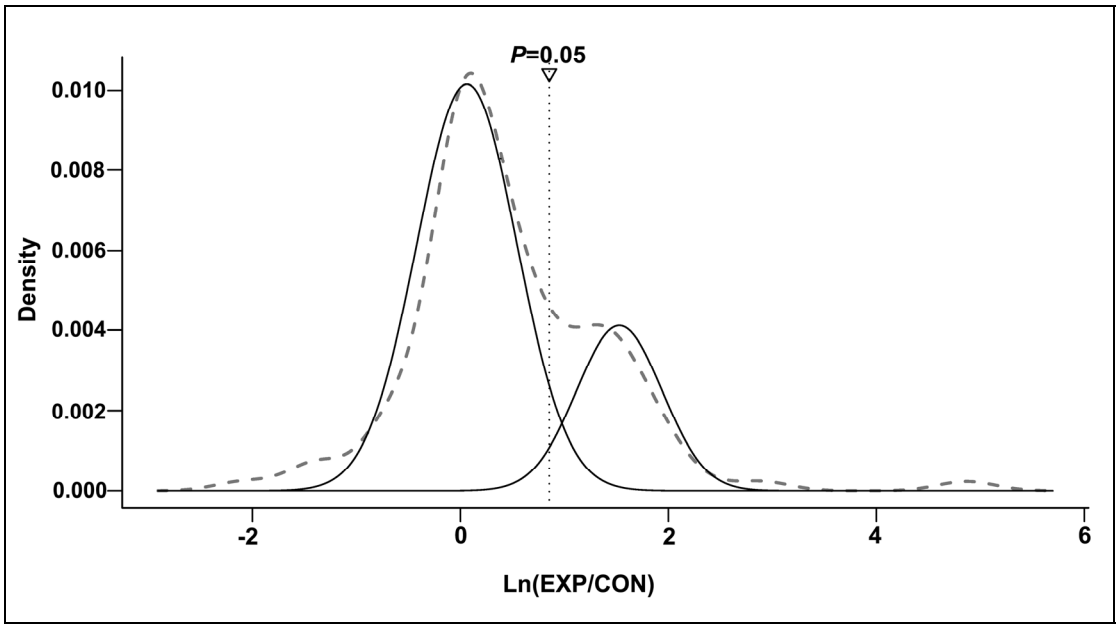
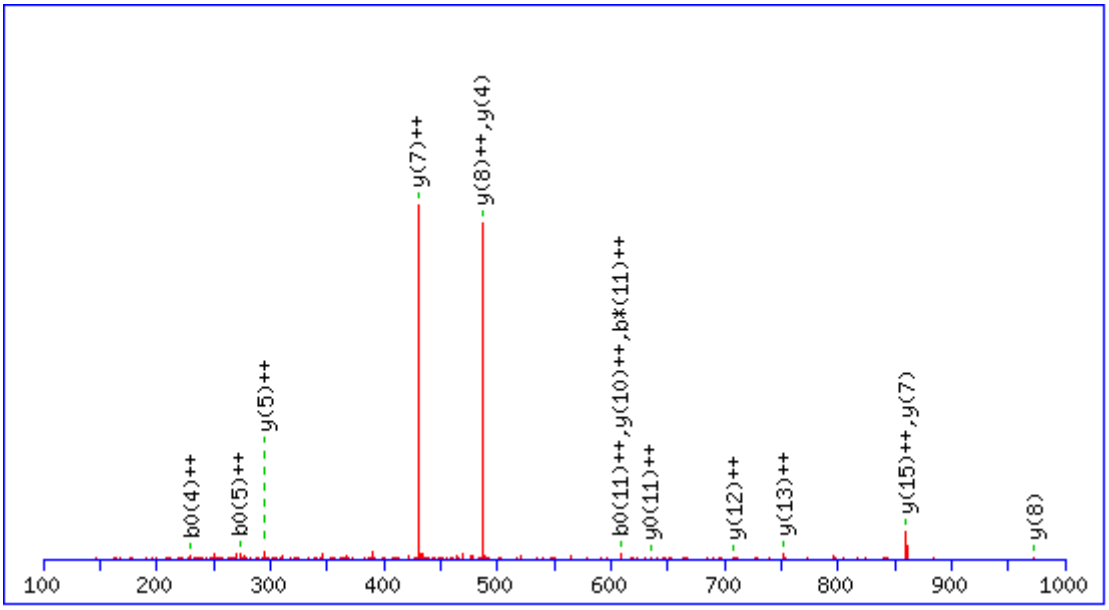


Figure S2. Gaussian distribution of the log-ratios ln(EXP/CON) of peptides identified using the peptide-based procedure. The spectral counts were merged over all biological and technical replicates as well as membrane domains. Bayesian Information Criterion-based Gaussian Mixture modeling (ref. 26) for the peptides with EXP and CON measurements (*i.e.*, spectral count ≥ 1 in both groups) suggested that the distribution of log-ratios (dashed line) comprises two Gaussian components (solid lines). The left Gaussian represents the log-ratio distribution of most contaminating peptides and some S-acylated peptides while the right Gaussian represents the log-ratio distribution of most S-acylated peptides and a small number of contaminants. To distinguish S-acylated peptides from contaminating peptides, *p*-values were calculated based on the distribution of the left Gaussian. Peptides with $p<0.05$ (corresponding to EXP/CON>2.4) were treated as significant and accepted as high-confidence S-acylated peptide candidates. The free cysteines on these candidates were considered as high-confidence candidate S-acylation sites.

Figure S3. Representative tandem mass spectra for candidate S-acylated peptides. See Table S5~S7 for more details about the identified peptides.

Gene Symbol	Sequences	m/z	Charge	Ion score
-	MLITSQAMDILRCNPQK	495.28	4+	59.3

(**IPI00022913** PRO1575)

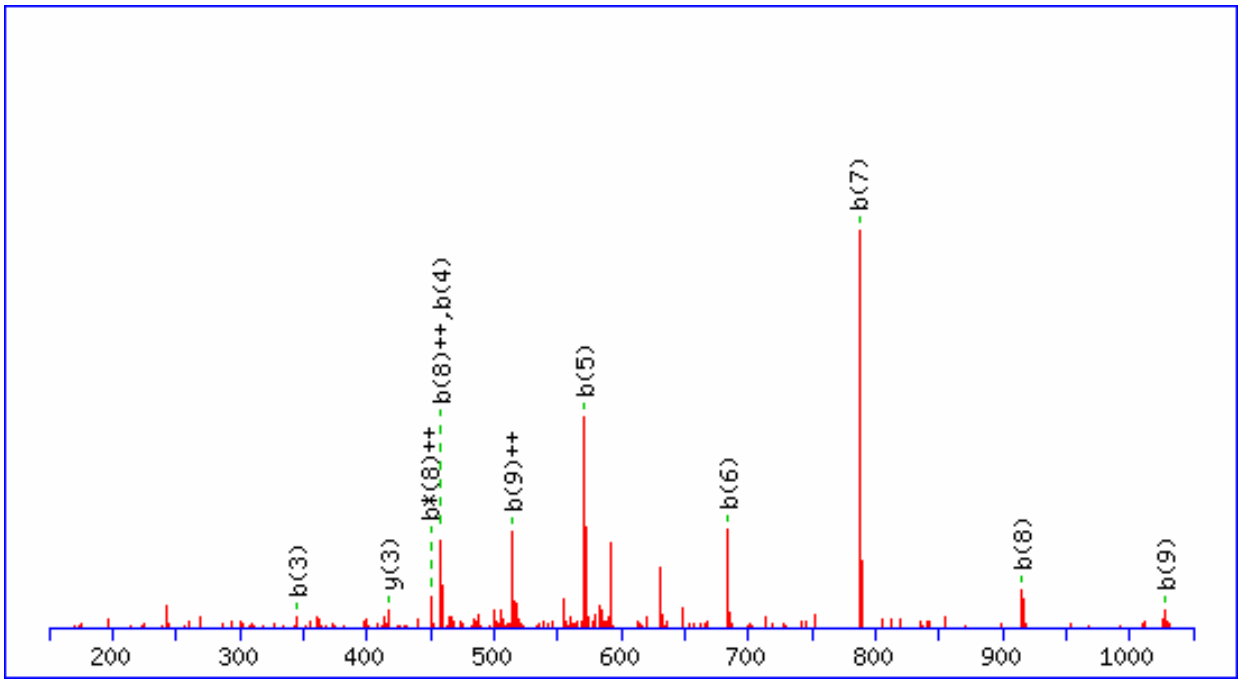


M1 **:** Oxidation (M)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.20	74.61					M							17
2	261.36	131.18					L	1832.17	916.59	1815.14	908.08	1814.16	907.58	16
3	374.52	187.76					I	1719.02	860.01	1701.99	851.50	1701.00	851.00	15
4	475.62	238.32			457.61	229.31	T	1605.86	803.43	1588.83	794.92	1587.84	794.43	14
5	562.70	281.85			544.68	272.85	S	1504.75	752.88	1487.72	744.37	1486.74	743.87	13
6	690.83	345.92	673.80	337.40	672.81	336.91	Q	1417.68	709.34	1400.65	700.83	1399.66	700.33	12
7	761.91	381.46	744.88	372.94	743.89	372.45	A	1289.55	645.28	1272.52	636.76	1271.53	636.27	11
8	893.10	447.06	876.07	438.54	875.09	438.05	M	1218.47	609.74	1201.44	601.22	1200.45	600.73	10
9	1008.19	504.60	991.16	496.08	990.18	495.59	D	1087.27	544.14	1070.24	535.63	1069.26	535.13	9
10	1121.35	561.18	1104.32	552.66	1103.33	552.17	I	972.19	486.60	955.16	478.08			8
11	1234.51	617.76	1217.48	609.24	1216.49	608.75	L	859.03	430.02	842.00	421.50			7
12	1390.69	695.85	1373.66	687.33	1372.68	686.84	R	745.87	373.44	728.84	364.92			6
13	1493.83	747.42	1476.80	738.91	1475.82	738.41	C	589.69	295.35	572.65	286.83			5
14	1607.94	804.47	1590.91	795.96	1589.92	795.46	N	486.54	243.78	469.51	235.26			4
15	1705.05	853.03	1688.02	844.51	1687.04	844.02	P	372.44	186.72	355.41	178.21			3
16	1833.18	917.09	1816.15	908.58	1815.17	908.09	Q	275.32	138.17	258.29	129.65			2
17							K	147.20	74.10	130.16	65.59			1

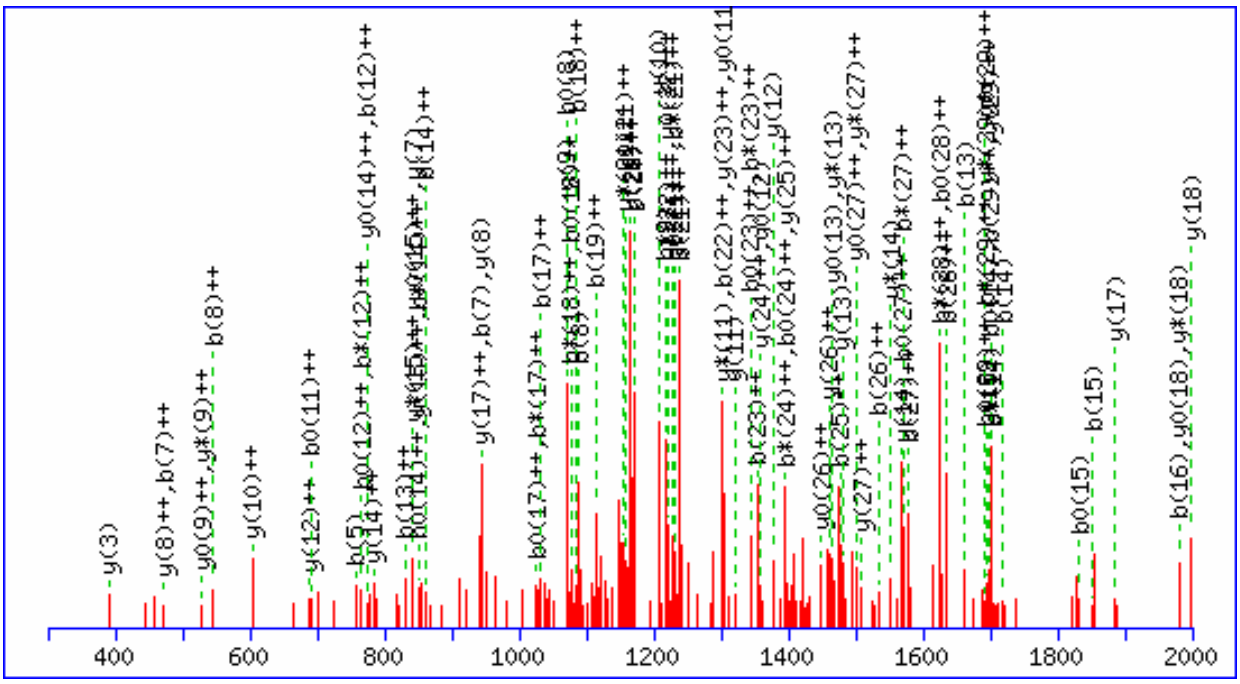
Gene Symbol	Sequences	m/z	Charge	Ion score
-	KCLLLLCQLR	601.63	2+	65.5

(**IPI00747966** Conserved hypothetical protein)



#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.18	65.09	112.15	56.58	K					10
2	232.32	116.67	215.29	108.15	C	1075.41	538.21	1058.38	529.69	9
3	345.48	173.24	328.45	164.73	L	972.27	486.64	955.24	478.12	8
4	458.64	229.82	441.61	221.31	L	859.11	430.06	842.08	421.54	7
5	571.80	286.40	554.77	277.89	L	745.95	373.48	728.92	364.97	6
6	684.95	342.98	667.92	334.47	L	632.80	316.90	615.77	308.39	5
7	788.10	394.55	771.07	386.04	C	519.64	260.32	502.61	251.81	4
8	916.23	458.62	899.20	450.10	Q	416.50	208.75	399.47	200.24	3
9	1029.38	515.20	1012.35	506.68	L	288.37	144.69	271.34	136.17	2
10					R	175.21	88.11	158.18	79.59	1

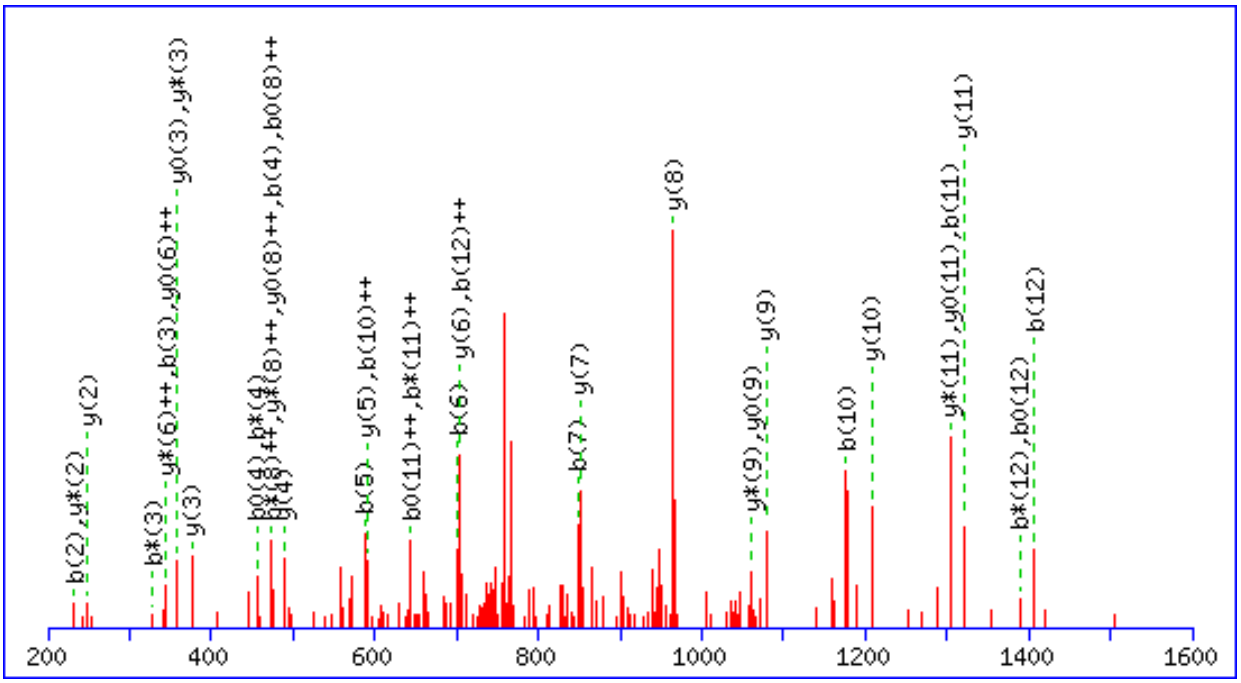
Gene Symbol	Sequences	m/z	Charge	Ion score
ACTB/ACTG1	FRCPEALFQPSFLGMESCGIHETTFNSIMK	1183.39	3+	115.6



C3 : NEM (C)

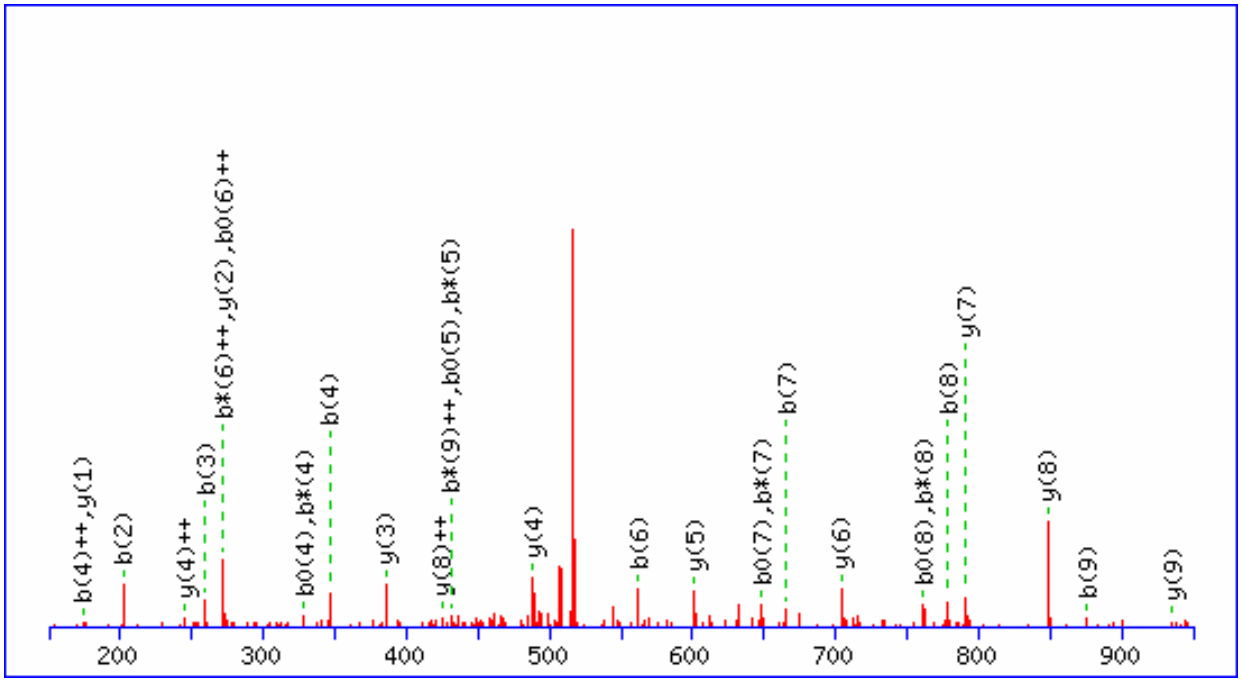
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.18	74.59					F							30
2	304.37	152.69	287.34	144.17			R	3400.90	1700.95	3383.87	1692.44	3382.89	1691.95	29
3	532.64	266.82	515.61	258.31			C	3244.71	1622.86	3227.68	1614.35	3226.70	1613.85	28
4	629.75	315.38	612.72	306.86			P	3016.45	1508.73	2999.42	1500.21	2998.43	1499.72	27
5	758.86	379.94	741.83	371.42	740.85	370.93	E	2919.33	1460.17	2902.30	1451.65	2901.32	1451.16	26
6	829.94	415.48	812.91	406.96	811.93	406.47	A	2790.22	1395.61	2773.19	1387.10	2772.20	1386.60	25
7	943.10	472.05	926.07	463.54	925.09	463.05	L	2719.14	1360.07	2702.11	1351.56	2701.12	1351.07	24
8	1090.27	545.64	1073.24	537.13	1072.26	536.63	F	2605.98	1303.49	2588.95	1294.98	2587.97	1294.49	23
9	1218.40	609.71	1201.37	601.19	1200.39	600.70	Q	2458.81	1229.91	2441.78	1221.39	2440.79	1220.90	22
10	1315.52	658.26	1298.49	649.75	1297.50	649.26	P	2330.68	1165.84	2313.65	1157.33	2312.66	1156.84	21
11	1402.60	701.80	1385.57	693.29	1384.58	692.79	S	2233.56	1117.29	2216.53	1108.77	2215.55	1108.28	20
12	1549.77	775.39	1532.74	766.87	1531.75	766.38	F	2146.49	1073.75	2129.46	1065.23	2128.47	1064.74	19
13	1662.93	831.97	1645.90	823.45	1644.91	822.96	L	1999.31	1000.16	1982.28	991.64	1981.30	991.15	18
14	1719.98	860.49	1702.95	851.98	1701.96	851.49	G	1886.15	943.58	1869.12	935.07	1868.14	934.57	17
15	1851.17	926.09	1834.14	917.58	1833.16	917.08	M	1829.10	915.06	1812.07	906.54	1811.09	906.05	16
16	1980.29	990.65	1963.26	982.13	1962.27	981.64	E	1697.91	849.46	1680.88	840.94	1679.89	840.45	15
17	2067.37	1034.19	2050.34	1025.67	2049.35	1025.18	S	1568.79	784.90	1551.76	776.39	1550.78	775.89	14
18	2170.51	1085.76	2153.48	1077.24	2152.49	1076.75	C	1481.72	741.36	1464.69	732.85	1463.70	732.35	13
19	2227.56	1114.28	2210.53	1105.77	2209.55	1105.28	G	1378.57	689.79	1361.54	681.28	1360.56	680.78	12
20	2340.72	1170.86	2323.69	1162.35	2322.70	1161.86	I	1321.52	661.26	1304.49	652.75	1303.51	652.26	11
21	2477.86	1239.43	2460.83	1230.92	2459.84	1230.43	H	1208.36	604.69	1191.33	596.17	1190.35	595.68	10
22	2606.97	1303.99	2589.94	1295.47	2588.96	1294.98	E	1071.22	536.12	1054.19	527.60	1053.21	527.11	9
23	2708.08	1354.54	2691.04	1346.03	2690.06	1345.53	T	942.11	471.56	925.08	463.04	924.10	462.55	8
24	2809.18	1405.09	2792.15	1396.58	2791.16	1396.09	T	841.01	421.01	823.98	412.49	822.99	412.00	7
25	2956.35	1478.68	2939.32	1470.17	2938.34	1469.67	F	739.90	370.46	722.87	361.94	721.89	361.45	6
26	3070.46	1535.73	3053.43	1527.22	3052.44	1526.72	N	592.73	296.87	575.70	288.35	574.71	287.86	5
27	3157.53	1579.27	3140.50	1570.76	3139.52	1570.26	S	478.63	239.82	461.60	231.30	460.61	230.81	4
28	3270.69	1635.85	3253.66	1627.33	3252.68	1626.84	I	391.55	196.28	374.52	187.76			3
29	3401.89	1701.45	3384.86	1692.93	3383.87	1692.44	M	278.39	139.70	261.36	131.18			2
30							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ACTN4	CQLEINFNTLQTK	776.70	2+	97.1



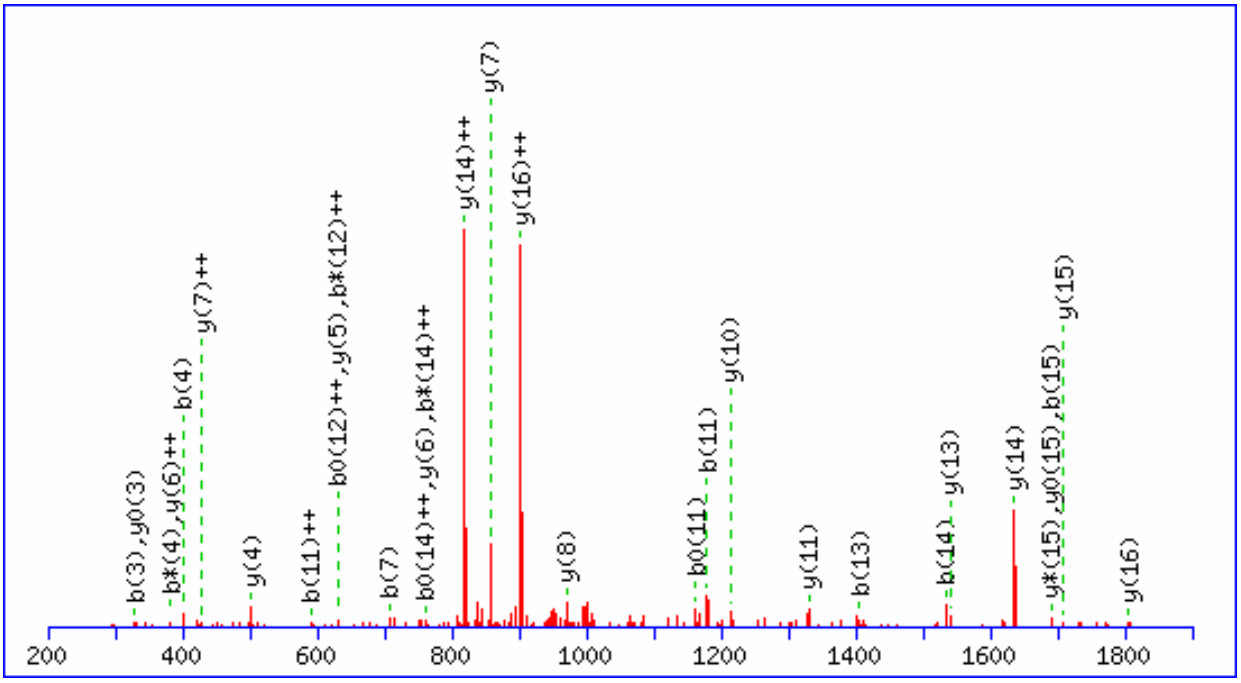
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	104.15	52.58					C							13
2	232.28	116.64	215.25	108.13			Q	1449.63	725.32	1432.60	716.80	1431.61	716.31	12
3	345.44	173.22	328.41	164.71			L	1321.50	661.25	1304.47	652.74	1303.48	652.25	11
4	474.55	237.78	457.52	229.26	456.54	228.77	E	1208.34	604.67	1191.31	596.16	1190.33	595.67	10
5	587.71	294.36	570.68	285.84	569.69	285.35	I	1079.23	540.12	1062.20	531.60	1061.21	531.11	9
6	701.81	351.41	684.78	342.89	683.80	342.40	N	966.07	483.54	949.04	475.02	948.05	474.53	8
7	848.99	425.00	831.96	416.48	830.97	415.99	F	851.97	426.49	834.94	417.97	833.95	417.48	7
8	963.09	482.05	946.06	473.53	945.07	473.04	N	704.79	352.90	687.76	344.39	686.78	343.89	6
9	1064.19	532.60	1047.16	524.08	1046.18	523.59	T	590.69	295.85	573.66	287.33	572.67	286.84	5
10	1177.35	589.18	1160.32	580.66	1159.33	580.17	L	489.59	245.30	472.56	236.78	471.57	236.29	4
11	1305.48	653.24	1288.45	644.73	1287.46	644.24	Q	376.43	188.72	359.40	180.20	358.41	179.71	3
12	1406.58	703.80	1389.55	695.28	1388.57	694.79	T	248.30	124.65	231.27	116.14	230.28	115.65	2
13							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ADCY3	NSGSCLCLPR	525.54	2+	75.1



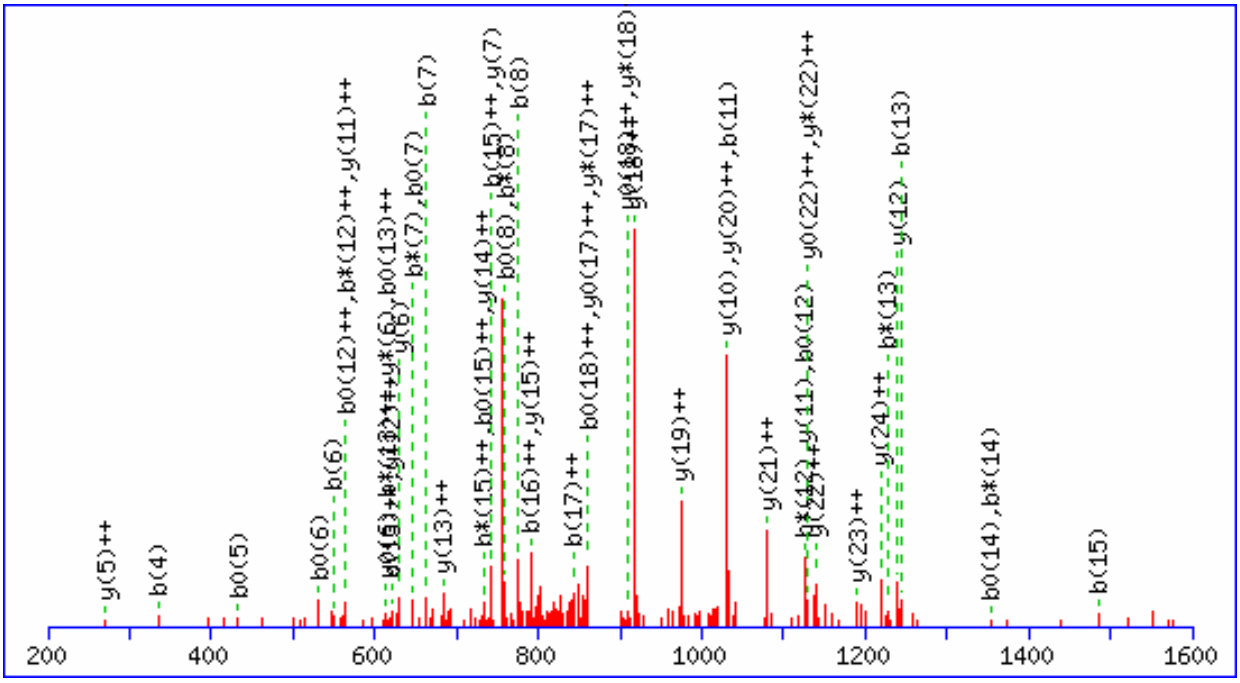
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.11	58.06	98.08	49.54			N							10
2	202.19	101.60	185.16	93.08	184.17	92.59	S	936.13	468.57	919.10	460.05	918.12	459.56	9
3	259.24	130.12	242.21	121.61	241.22	121.12	G	849.05	425.03	832.02	416.52	831.04	416.02	8
4	346.32	173.66	329.29	165.15	328.30	164.65	S	792.00	396.51	774.97	387.99	773.99	387.50	7
5	449.46	225.23	432.43	216.72	431.44	216.23	C	704.93	352.97	687.89	344.45			6
6	562.62	281.81	545.59	273.30	544.60	272.80	L	601.78	301.40	584.75	292.88			5
7	665.76	333.38	648.73	324.87	647.74	324.38	C	488.62	244.82	471.59	236.30			4
8	778.92	389.96	761.89	381.45	760.90	380.96	L	385.48	193.24	368.45	184.73			3
9	876.03	438.52	859.00	430.01	858.02	429.51	P	272.32	136.67	255.29	128.15			2
10							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ADORA1	CQPAPPIDEDLPEERPDD	1019.08	2+	74.7



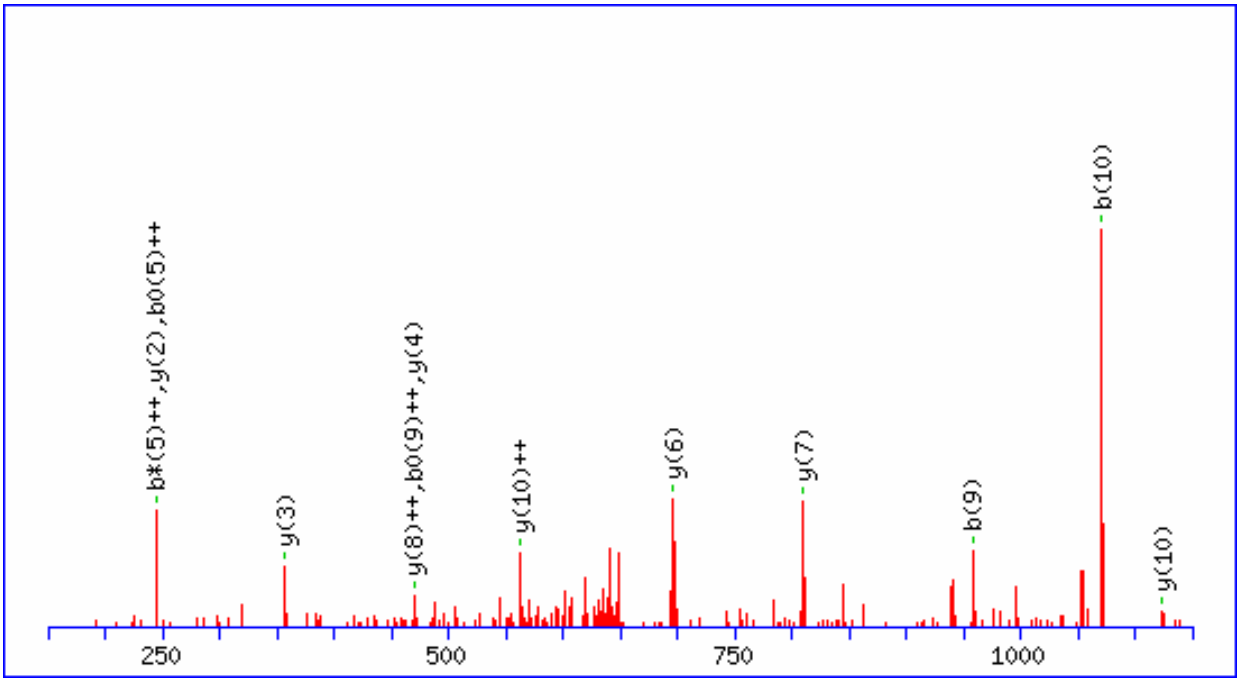
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	104.15	52.58					C							18
2	232.28	116.64	215.25	108.13			Q	1934.00	967.50	1916.97	958.99	1915.98	958.50	17
3	329.40	165.20	312.36	156.69			P	1805.87	903.44	1788.84	894.92	1787.85	894.43	16
4	400.47	200.74	383.44	192.23			A	1708.75	854.88	1691.72	846.37	1690.74	845.87	15
5	497.59	249.30	480.56	240.78			P	1637.68	819.34	1620.65	810.83	1619.66	810.33	14
6	594.70	297.86	577.67	289.34			P	1540.56	770.78	1523.53	762.27	1522.55	761.78	13
7	707.86	354.43	690.83	345.92			I	1443.45	722.23	1426.42	713.71	1425.43	713.22	12
8	822.95	411.98	805.92	403.46	804.93	402.97	D	1330.29	665.65	1313.26	657.13	1312.27	656.64	11
9	952.06	476.54	935.03	468.02	934.05	467.53	E	1215.20	608.10	1198.17	599.59	1197.19	599.10	10
10	1067.15	534.08	1050.12	525.56	1049.13	525.07	D	1086.09	543.55	1069.06	535.03	1068.07	534.54	9
11	1180.31	590.66	1163.28	582.14	1162.29	581.65	L	971.00	486.00	953.97	477.49	952.98	477.00	8
12	1277.42	639.22	1260.39	630.70	1259.41	630.21	P	857.84	429.43	840.81	420.91	839.83	420.42	7
13	1406.54	703.77	1389.51	695.26	1388.52	694.76	E	760.73	380.87	743.70	372.35	742.71	371.86	6
14	1535.65	768.33	1518.62	759.81	1517.64	759.32	E	631.61	316.31	614.58	307.80	613.60	307.30	5
15	1691.84	846.42	1674.81	837.91	1673.82	837.41	R	502.50	251.75	485.47	243.24	484.48	242.75	4
16	1788.95	894.98	1771.92	886.46	1770.94	885.97	P	346.31	173.66			328.30	164.65	3
17	1904.04	952.52	1887.01	944.01	1886.02	943.52	D	249.20	125.10			231.18	116.10	2
18							D	134.11	67.56			116.10	58.55	1

Gene Symbol	Sequences	m/z	Charge	Ion score
AHNAK	SSGCDVNLPGVNVKLPTGQISGPEIK	870.72	3+	66.1



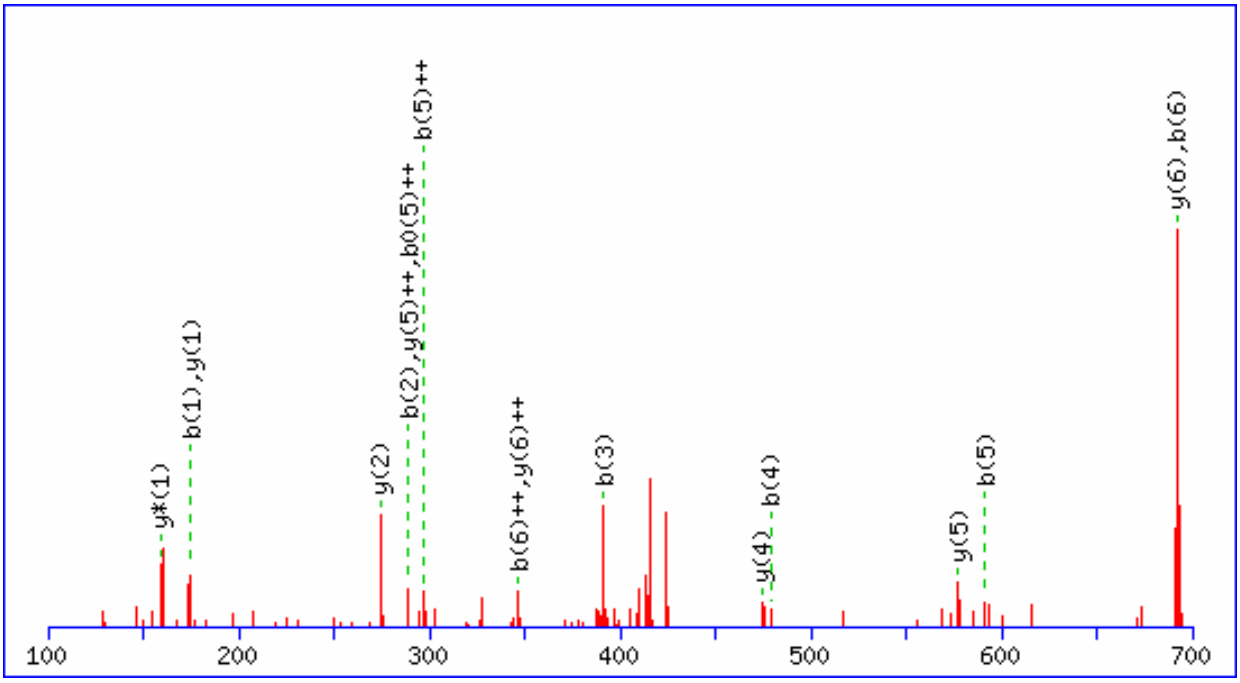
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							26
2	175.16	88.09			157.15	79.08	S	2523.88	1262.44	2506.85	1253.93	2505.86	1253.44	25
3	232.21	116.61			214.20	107.60	G	2436.80	1218.91	2419.77	1210.39	2418.79	1209.90	24
4	335.36	168.18			317.34	159.17	C	2379.75	1190.38	2362.72	1181.86	2361.74	1181.37	23
5	450.44	225.73			432.43	216.72	D	2276.61	1138.81	2259.58	1130.29	2258.59	1129.80	22
6	549.58	275.29			531.56	266.28	V	2161.52	1081.26	2144.49	1072.75	2143.51	1072.26	21
7	663.68	332.34	646.65	323.83	645.66	323.34	N	2062.39	1031.70	2045.36	1023.18	2044.37	1022.69	20
8	776.84	388.92	759.80	380.41	758.82	379.91	L	1948.29	974.65	1931.26	966.13	1930.27	965.64	19
9	873.95	437.48	856.92	428.96	855.94	428.47	P	1835.13	918.07	1818.10	909.55	1817.11	909.06	18
10	931.00	466.00	913.97	457.49	912.99	457.00	G	1738.01	869.51	1720.98	861.00	1720.00	860.50	17
11	1030.13	515.57	1013.10	507.06	1012.12	506.56	V	1680.96	840.99	1663.93	832.47	1662.95	831.98	16
12	1144.24	572.62	1127.21	564.11	1126.22	563.61	N	1581.83	791.42	1564.80	782.90	1563.82	782.41	15
13	1243.37	622.19	1226.34	613.67	1225.35	613.18	V	1467.73	734.37	1450.70	725.85	1449.71	725.36	14
14	1371.54	686.27	1354.51	677.76	1353.52	677.27	K	1368.60	684.80	1351.57	676.29	1350.58	675.80	13
15	1484.70	742.85	1467.67	734.34	1466.68	733.84	L	1240.43	620.72	1223.40	612.20	1222.41	611.71	12
16	1581.81	791.41	1564.78	782.89	1563.80	782.40	P	1127.27	564.14	1110.24	555.62	1109.25	555.13	11
17	1682.92	841.96	1665.89	833.45	1664.90	832.95	T	1030.15	515.58	1013.12	507.07	1012.14	506.57	10
18	1739.97	870.49	1722.94	861.97	1721.95	861.48	G	929.05	465.03	912.02	456.51	911.03	456.02	9
19	1868.10	934.55	1851.07	926.04	1850.08	925.54	Q	872.00	436.50	854.97	427.99	853.98	427.50	8
20	1981.25	991.13	1964.22	982.62	1963.24	982.12	I	743.87	372.44	726.84	363.92	725.85	363.43	7
21	2068.33	1034.67	2051.30	1026.15	2050.32	1025.66	S	630.71	315.86	613.68	307.34	612.70	306.85	6
22	2125.38	1063.20	2108.35	1054.68	2107.37	1054.19	G	543.63	272.32	526.60	263.81	525.62	263.31	5
23	2222.50	1111.75	2205.47	1103.24	2204.48	1102.75	P	486.58	243.80	469.55	235.28	468.57	234.79	4
24	2351.61	1176.31	2334.58	1167.79	2333.60	1167.30	E	389.47	195.24	372.44	186.72	371.45	186.23	3
25	2464.77	1232.89	2447.74	1224.37	2446.75	1223.88	I	260.35	130.68	243.32	122.17			2
26							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ANLN	SCEGQNPELLPK	657.95	2+	56.0



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							12
2	191.23	96.12			173.21	87.11	C	1228.40	614.70	1211.36	606.19	1210.38	605.69	11
3	320.34	160.68			302.33	151.67	E	1125.25	563.13	1108.22	554.61	1107.24	554.12	10
4	377.39	189.20			359.38	180.19	G	996.14	498.57	979.11	490.06	978.12	489.57	9
5	505.52	253.27	488.49	244.75	487.51	244.26	Q	939.09	470.05	922.06	461.53	921.07	461.04	8
6	619.63	310.32	602.59	301.80	601.61	301.31	N	810.96	405.98	793.93	397.47	792.94	396.98	7
7	716.74	358.87	699.71	350.36	698.73	349.87	P	696.86	348.93	679.82	340.42	678.84	339.92	6
8	845.85	423.43	828.82	414.92	827.84	414.42	E	599.74	300.37	582.71	291.86	581.72	291.37	5
9	959.01	480.01	941.98	471.49	941.00	471.00	L	470.63	235.82	453.60	227.30			4
10	1072.17	536.59	1055.14	528.07	1054.15	527.58	L	357.47	179.24	340.44	170.72			3
11	1169.28	585.15	1152.25	576.63	1151.27	576.14	P	244.31	122.66	227.28	114.14			2
12							K	147.20	74.10	130.16	65.59			1

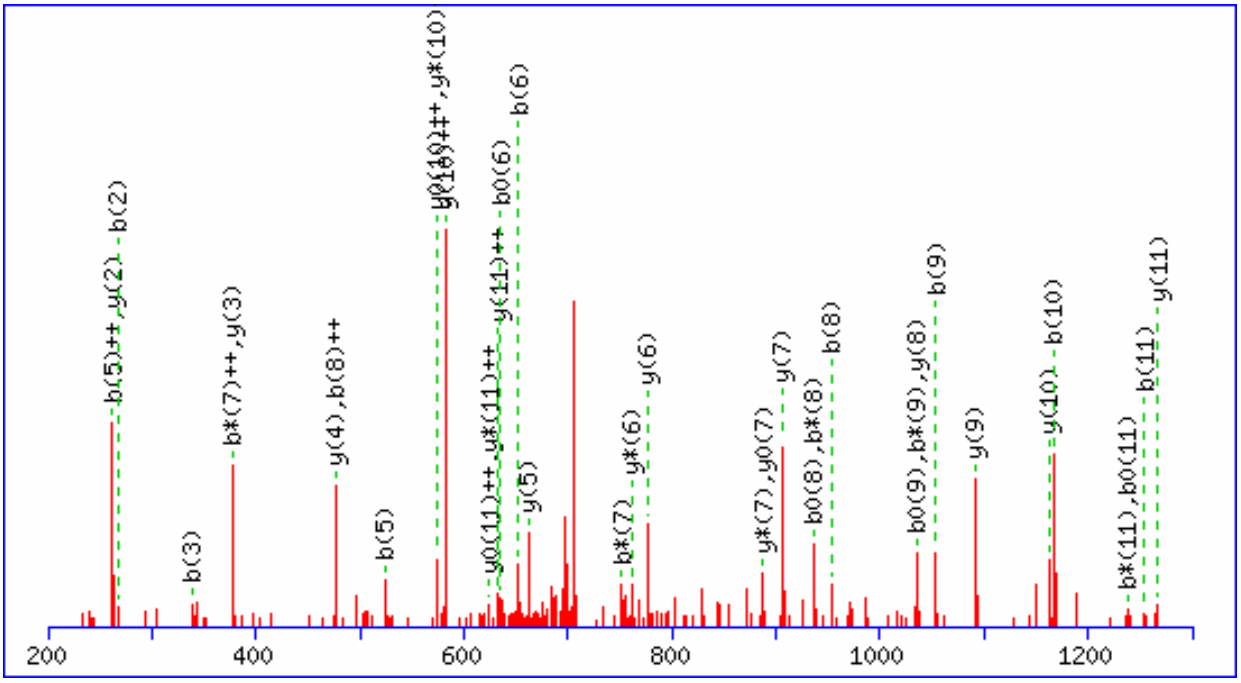
Gene Symbol	Sequences	m/z	Charge	Ion score
ATP11A	MDCSLVR	433.33	2+	57.4



N-term : N-Acetyl (Protein)

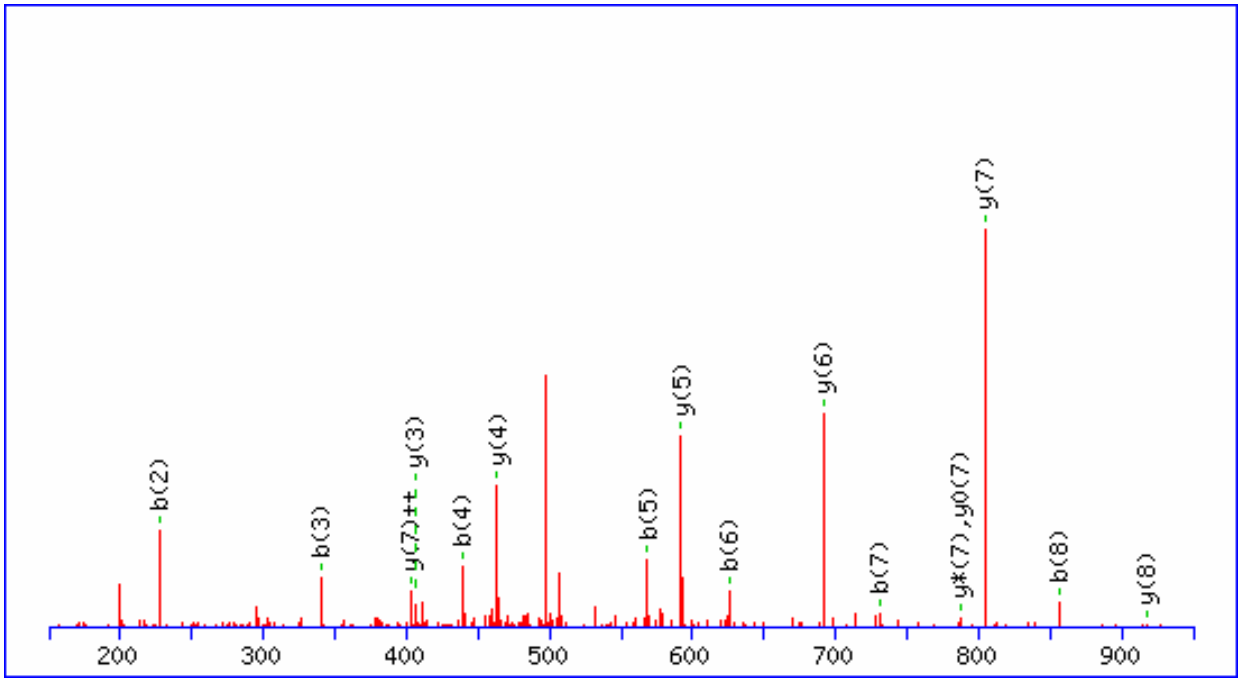
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	174.24	87.62			M							7
2	289.33	145.17	271.31	136.16	D	692.81	346.91	675.77	338.39	674.79	337.90	6
3	392.47	196.74	374.46	187.73	C	577.72	289.36	560.69	280.85	559.70	280.36	5
4	479.55	240.28	461.53	231.27	S	474.57	237.79	457.54	229.28	456.56	228.78	4
5	592.71	296.86	574.69	287.85	L	387.50	194.25	370.47	185.74			3
6	691.84	346.42	673.82	337.41	V	274.34	137.67	257.31	129.16			2
7					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ATP11A	YCAGEENWVDSR	715.10	2+	84.6



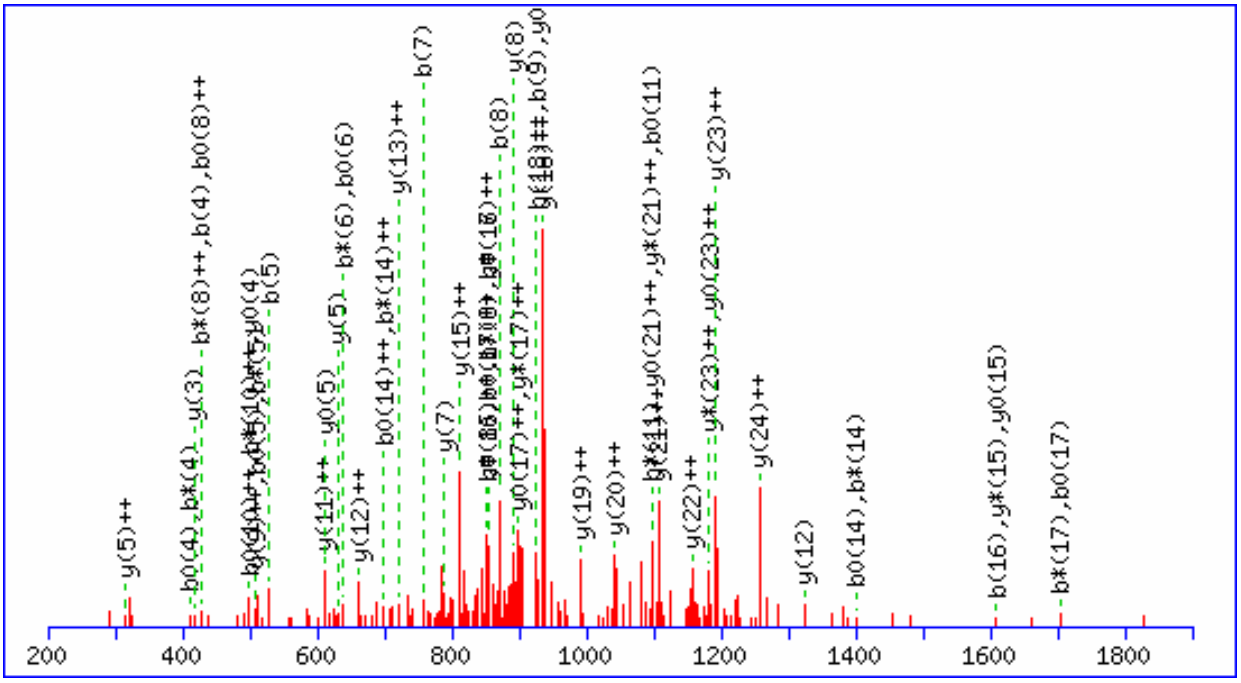
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.18	82.59					Y							12
2	267.32	134.17					C	1266.32	633.66	1249.29	625.15	1248.30	624.65	11
3	338.40	169.70					A	1163.17	582.09	1146.14	573.58	1145.16	573.08	10
4	395.45	198.23					G	1092.10	546.55	1075.07	538.04	1074.08	537.54	9
5	524.57	262.79			506.55	253.78	E	1035.05	518.03	1018.01	509.51	1017.03	509.02	8
6	653.68	327.34			635.67	318.34	E	905.93	453.47	888.90	444.95	887.92	444.46	7
7	767.78	384.40	750.75	375.88	749.77	375.39	N	776.82	388.91	759.79	380.40	758.80	379.90	6
8	953.99	477.50	936.96	468.99	935.98	468.49	W	662.71	331.86	645.68	323.35	644.70	322.85	5
9	1053.12	527.07	1036.09	518.55	1035.11	518.06	V	476.50	238.76	459.47	230.24	458.49	229.75	4
10	1168.21	584.61	1151.18	576.09	1150.20	575.60	D	377.37	189.19	360.34	180.68	359.36	180.18	3
11	1255.29	628.15	1238.26	619.63	1237.27	619.14	S	262.29	131.65	245.26	123.13	244.27	122.64	2
12							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ATP1A1	LIIVEGCQR	515.61	2+	52.8



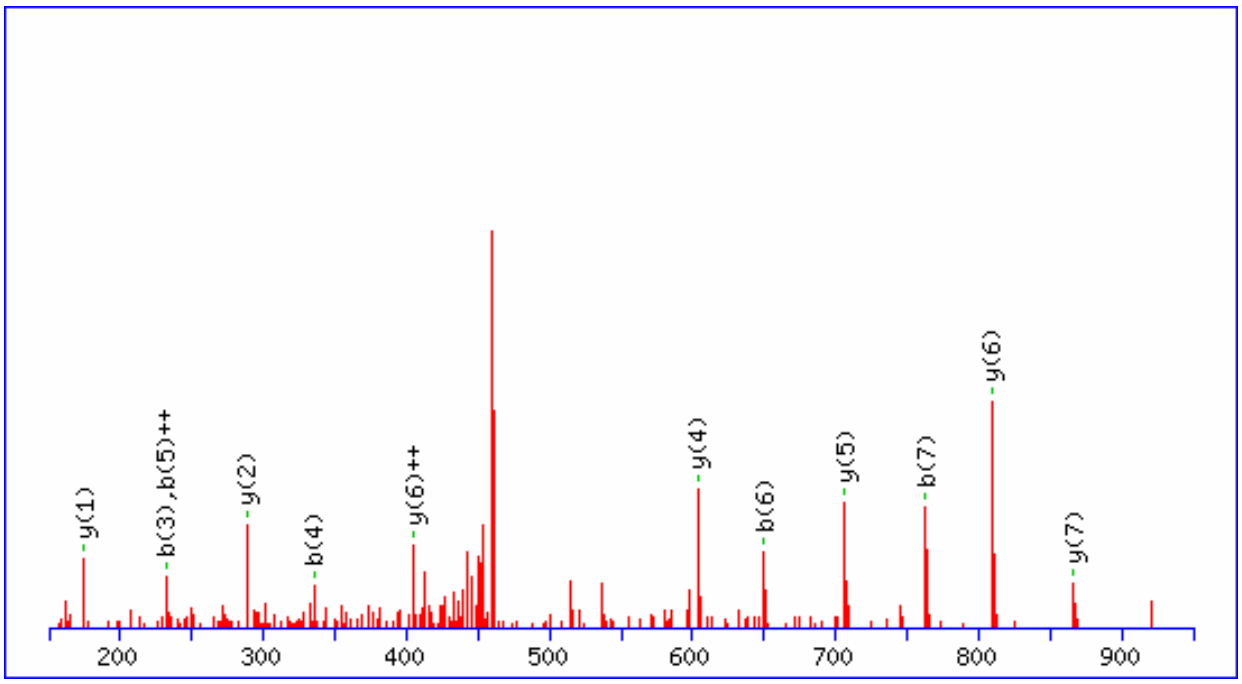
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					L							9
2	227.32	114.17					I	918.09	459.55	901.06	451.04	900.08	450.54	8
3	340.48	170.74					I	804.94	402.97	787.90	394.46	786.92	393.96	7
4	439.61	220.31					V	691.78	346.39	674.75	337.88	673.76	337.39	6
5	568.73	284.87			550.71	275.86	E	592.65	296.83	575.62	288.31	574.63	287.82	5
6	625.78	313.39			607.76	304.38	G	463.53	232.27	446.50	223.75			4
7	728.92	364.96			710.90	355.96	C	406.48	203.74	389.45	195.23			3
8	857.05	429.03	840.02	420.51	839.03	420.02	Q	303.34	152.17	286.31	143.66			2
9							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ATP1A1	NLEAVETLGSTSTI**C**SDKTGTLTQNR	914.46	3+	64.9



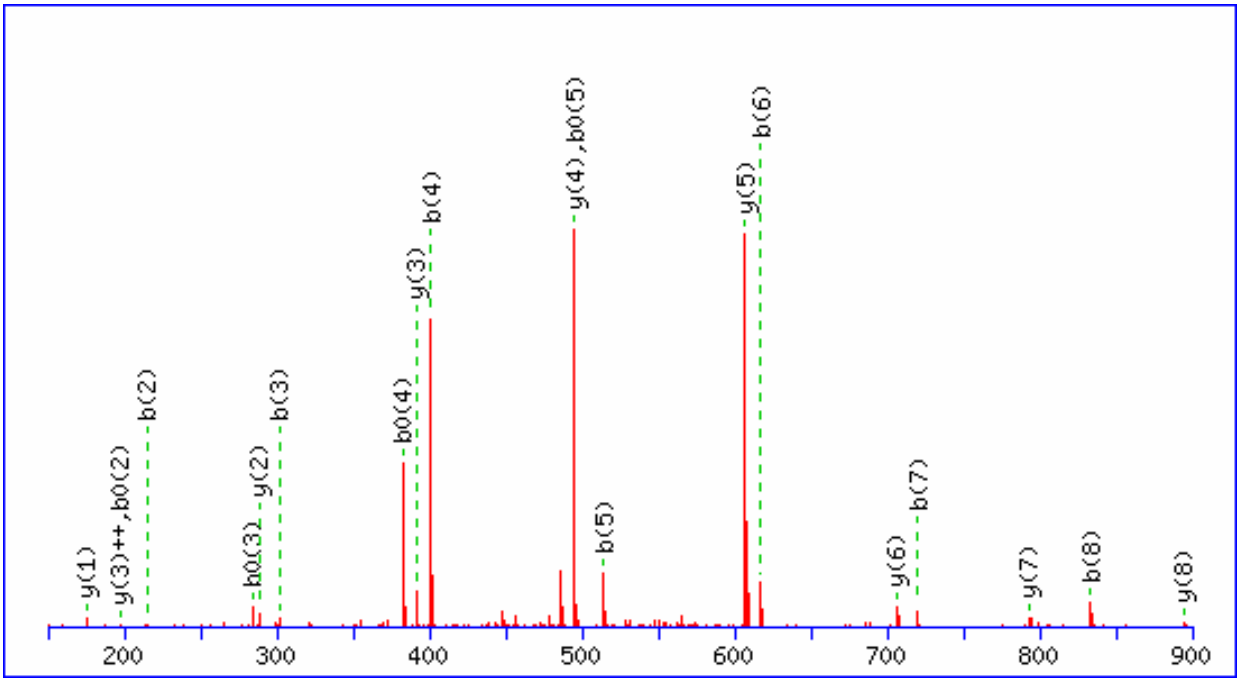
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	115.11	58.06	98.08	49.54			N							26
2	228.27	114.64	211.24	106.12			L	2626.87	1313.94	2609.84	1305.42	2608.85	1304.93	25
3	357.38	179.20	340.35	170.68	339.37	170.19	E	2513.71	1257.36	2496.68	1248.84	2495.70	1248.35	24
4	428.46	214.73	411.43	206.22	410.44	205.73	A	2384.60	1192.80	2367.57	1184.29	2366.58	1183.79	23
5	527.59	264.30	510.56	255.78	509.58	255.29	V	2313.52	1157.26	2296.49	1148.75	2295.50	1148.26	22
6	656.71	328.86	639.67	320.34	638.69	319.85	E	2214.39	1107.70	2197.36	1099.18	2196.37	1098.69	21
7	757.81	379.41	740.78	370.89	739.79	370.40	T	2085.27	1043.14	2068.24	1034.63	2067.26	1034.13	20
8	870.97	435.99	853.94	427.47	852.95	426.98	L	1984.17	992.59	1967.14	984.07	1966.15	983.58	19
9	928.02	464.51	910.99	456.00	910.00	455.51	G	1871.01	936.01	1853.98	927.49	1853.00	927.00	18
10	1015.10	508.05	998.06	499.54	997.08	499.04	S	1813.96	907.48	1796.93	898.97	1795.95	898.48	17
11	1116.20	558.60	1099.17	550.09	1098.18	549.60	T	1726.88	863.95	1709.85	855.43	1708.87	854.94	16
12	1203.28	602.14	1186.25	593.63	1185.26	593.13	S	1625.78	813.39	1608.75	804.88	1607.76	804.39	15
13	1304.38	652.69	1287.35	644.18	1286.37	643.69	T	1538.70	769.86	1521.67	761.34	1520.69	760.85	14
14	1417.54	709.27	1400.51	700.76	1399.52	700.27	I	1437.60	719.30	1420.57	710.79	1419.58	710.30	13
15	1520.68	760.84	1503.65	752.33	1502.67	751.84	C	1324.44	662.72	1307.41	654.21	1306.43	653.72	12
16	1607.76	804.38	1590.73	795.87	1589.74	795.38	S	1221.30	611.15	1204.27	602.64	1203.28	602.15	11
17	1722.85	861.93	1705.82	853.41	1704.83	852.92	D	1134.22	567.61	1117.19	559.10	1116.21	558.61	10
18	1851.02	926.01	1833.99	917.50	1833.00	917.01	K	1019.13	510.07	1002.10	501.56	1001.12	501.06	9
19	1952.12	976.56	1935.09	968.05	1934.11	967.56	T	890.96	445.98	873.93	437.47	872.95	436.98	8
20	2009.17	1005.09	1992.14	996.58	1991.16	996.08	G	789.86	395.43	772.83	386.92	771.84	386.43	7
21	2110.28	1055.64	2093.25	1047.13	2092.26	1046.63	T	732.81	366.91	715.78	358.39	714.79	357.90	6
22	2223.43	1112.22	2206.40	1103.71	2205.42	1103.21	L	631.70	316.36	614.67	307.84	613.69	307.35	5
23	2324.54	1162.77	2307.51	1154.26	2306.52	1153.77	T	518.54	259.78	501.51	251.26	500.53	250.77	4
24	2452.67	1226.84	2435.64	1218.32	2434.65	1217.83	Q	417.44	209.22	400.41	200.71			3
25	2566.77	1283.89	2549.74	1275.37	2548.75	1274.88	N	289.31	145.16	272.28	136.64			2
26							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ATP9A	AGCCEWLR	469.63	2+	58.1



#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55			A							8
2	129.14	65.07			G	867.03	434.02	850.00	425.50	849.01	425.01	7
3	232.28	116.64			C	809.98	405.49	792.95	396.98	791.96	396.48	6
4	335.42	168.22			C	706.83	353.92	689.80	345.41	688.82	344.91	5
5	464.54	232.77	446.52	223.76	E	603.69	302.35	586.66	293.83	585.68	293.34	4
6	650.75	325.88	632.73	316.87	W	474.58	237.79	457.55	229.28			3
7	763.90	382.46	745.89	373.45	L	288.37	144.69	271.34	136.17			2
8					R	175.21	88.11	158.18	79.59			1

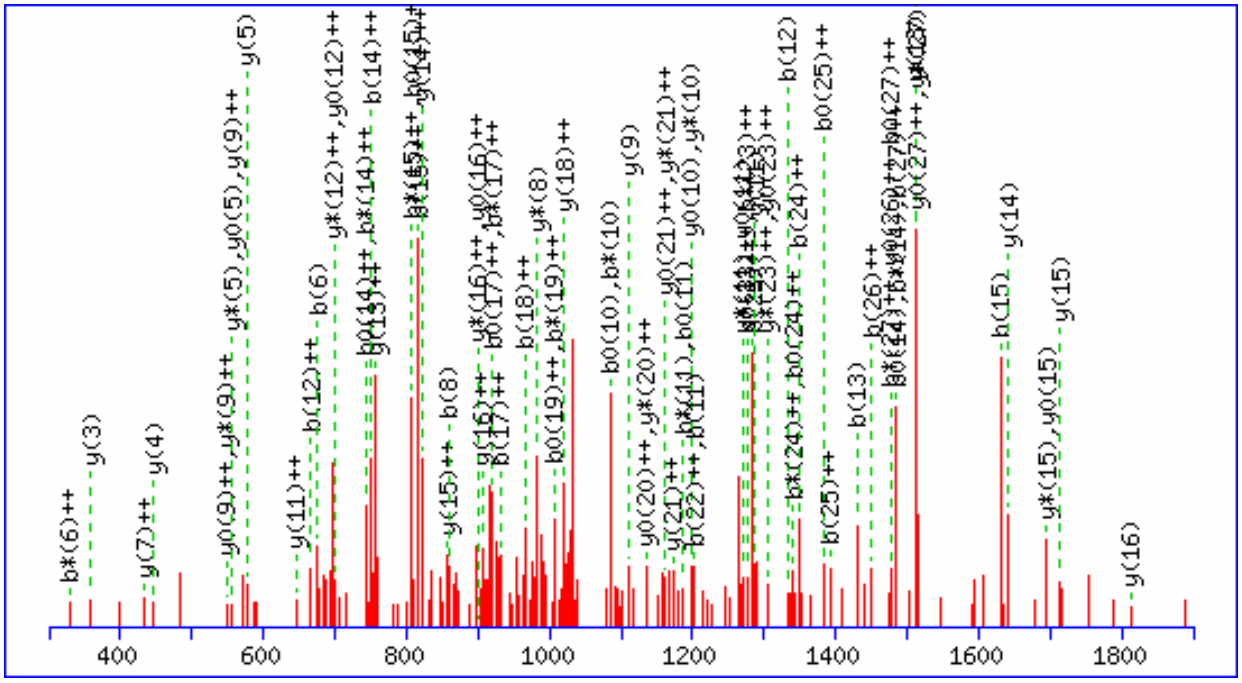
Gene Symbol	Sequences	m/z	Charge	Ion score
C13orf1	ATSVLCCLR	504.58	2+	78.8



N-term : N-Acetyl (Protein)

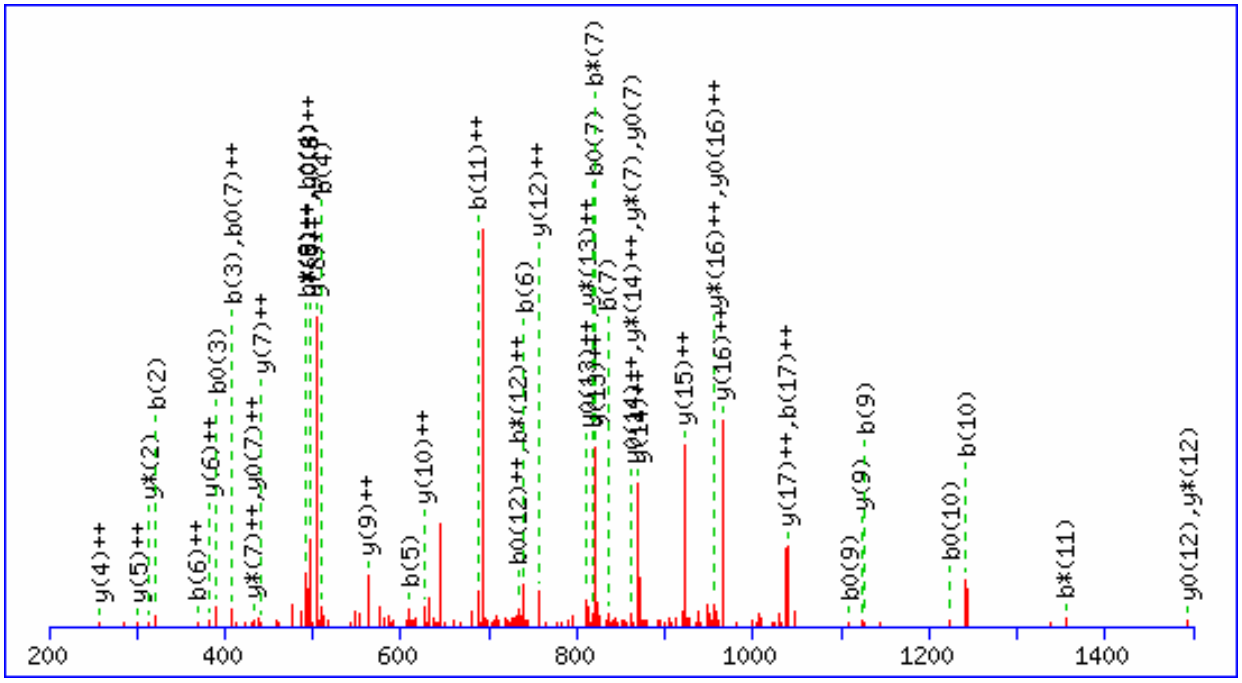
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.12	57.57			A							9
2	215.23	108.12	197.21	99.11	T	895.12	448.07	878.09	439.55	877.11	439.06	8
3	302.30	151.66	284.29	142.65	S	794.02	397.51	776.99	389.00	776.00	388.51	7
4	401.43	201.22	383.42	192.21	V	706.94	353.97	689.91	345.46			6
5	514.59	257.80	496.58	248.79	L	607.81	304.41	590.78	295.89			5
6	617.74	309.37	599.72	300.36	C	494.65	247.83	477.62	239.31			4
7	720.88	360.94	702.86	351.94	C	391.51	196.26	374.48	187.74			3
8	834.04	417.52	816.02	408.51	L	288.37	144.69	271.34	136.17			2
9					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
C6orf125	VAQAFREGENTQVAEPEACDQMYESLAR	1048.57	3+	50.1



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							28
2	171.22	86.11					A	3045.25	1523.13	3028.22	1514.62	3027.24	1514.12	27
3	299.35	150.18	282.32	141.66			Q	2974.18	1487.59	2957.15	1479.08	2956.16	1478.58	26
4	370.42	185.72	353.39	177.20			A	2846.05	1423.53	2829.02	1415.01	2828.03	1414.52	25
5	517.60	259.30	500.57	250.79			F	2774.97	1387.99	2757.94	1379.47	2756.95	1378.98	24
6	673.78	337.40	656.75	328.88			R	2627.80	1314.40	2610.76	1305.89	2609.78	1305.39	23
7	802.90	401.95	785.87	393.44	784.88	392.95	E	2471.61	1236.31	2454.58	1227.79	2453.59	1227.30	22
8	859.95	430.48	842.92	421.96	841.93	421.47	G	2342.50	1171.75	2325.47	1163.24	2324.48	1162.74	21
9	989.06	495.04	972.03	486.52	971.05	486.03	E	2285.44	1143.23	2268.41	1134.71	2267.43	1134.22	20
10	1103.17	552.09	1086.14	543.57	1085.15	543.08	N	2156.33	1078.67	2139.30	1070.15	2138.32	1069.66	19
11	1204.27	602.64	1187.24	594.12	1186.25	593.63	T	2042.23	1021.62	2025.20	1013.10	2024.21	1012.61	18
12	1332.40	666.70	1315.37	658.19	1314.38	657.70	Q	1941.12	971.07	1924.09	962.55	1923.11	962.06	17
13	1431.53	716.27	1414.50	707.75	1413.51	707.26	V	1812.99	907.00	1795.96	898.49	1794.98	897.99	16
14	1502.61	751.81	1485.58	743.29	1484.59	742.80	A	1713.86	857.44	1696.83	848.92	1695.85	848.43	15
15	1631.72	816.36	1614.69	807.85	1613.71	807.36	E	1642.79	821.90	1625.76	813.38	1624.77	812.89	14
16	1728.84	864.92	1711.81	856.41	1710.82	855.91	P	1513.67	757.34	1496.64	748.82	1495.66	748.33	13
17	1857.95	929.48	1840.92	920.96	1839.94	920.47	E	1416.56	708.78	1399.53	700.27	1398.54	699.77	12
18	1929.03	965.02	1912.00	956.50	1911.01	956.01	A	1287.44	644.23	1270.41	635.71	1269.43	635.22	11
19	2032.17	1016.59	2015.14	1008.07	2014.16	1007.58	C	1216.36	608.69	1199.33	600.17	1198.35	599.68	10
20	2147.26	1074.13	2130.23	1065.62	2129.24	1065.13	D	1113.22	557.11	1096.19	548.60	1095.21	548.11	9
21	2275.39	1138.20	2258.36	1129.68	2257.37	1129.19	Q	998.13	499.57	981.10	491.06	980.12	490.56	8
22	2406.58	1203.80	2389.55	1195.28	2388.57	1194.79	M	870.01	435.51	852.97	426.99	851.99	426.50	7
23	2569.76	1285.38	2552.73	1276.87	2551.74	1276.38	Y	738.81	369.91	721.78	361.39	720.79	360.90	6
24	2698.87	1349.94	2681.84	1341.42	2680.86	1340.93	E	575.64	288.32	558.61	279.81	557.62	279.31	5
25	2785.95	1393.48	2768.92	1384.96	2767.93	1384.47	S	446.52	223.76	429.49	215.25	428.51	214.76	4
26	2899.11	1450.06	2882.08	1441.54	2881.09	1441.05	L	359.44	180.23	342.41	171.71			3
27	2970.18	1485.60	2953.15	1477.08	2952.17	1476.59	A	246.29	123.65	229.26	115.13			2
28							R	175.21	88.11	158.18	79.59			1

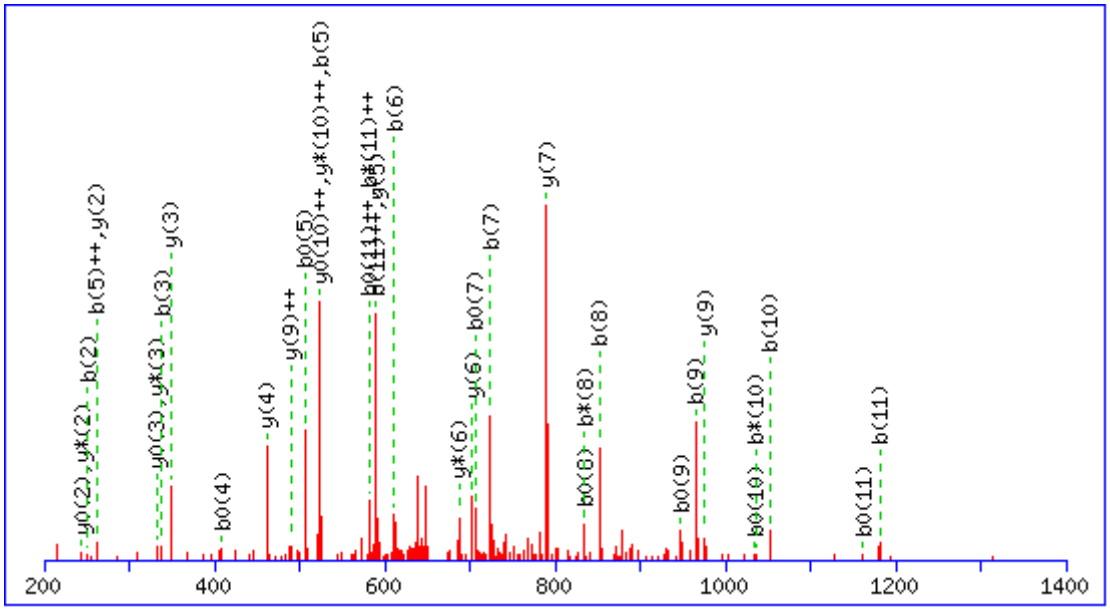
Gene Symbol	Sequences	m/z	Charge	Ion score
CAPN5	MFSCVKPYEDQNYSALR	750.93	3+	76.3



N-term : N-Acetyl (Protein)

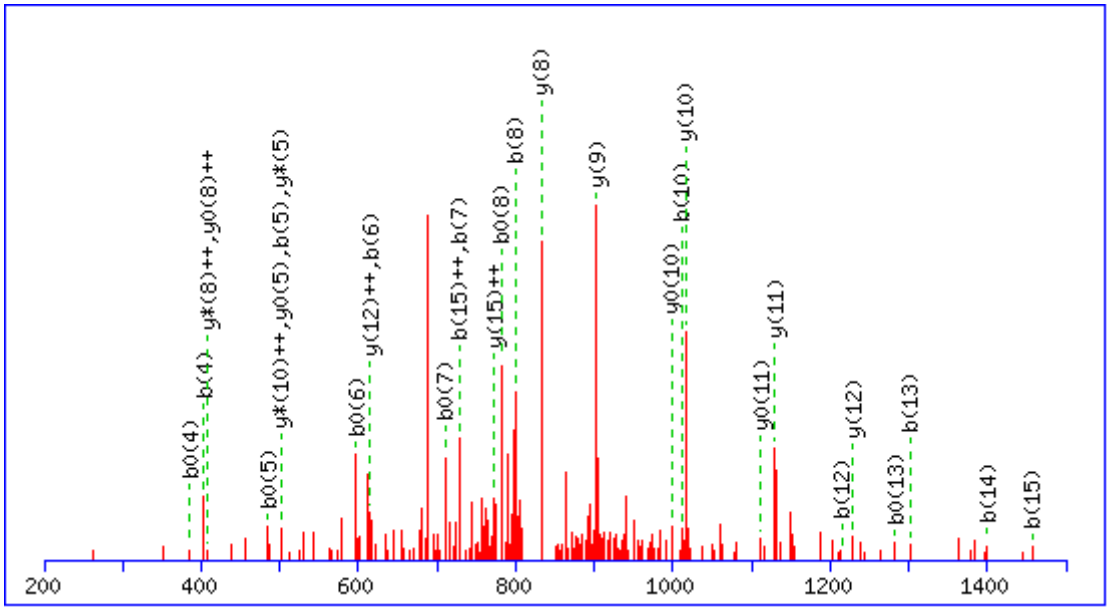
#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	174.24	87.62					M							18
2	321.41	161.21					F	2077.30	1039.15	2060.27	1030.64	2059.28	1030.15	17
3	408.49	204.75			390.48	195.74	S	1930.13	965.57	1913.10	957.05	1912.11	956.56	16
4	511.63	256.32			493.62	247.31	C	1843.05	922.03	1826.02	913.51	1825.03	913.02	15
5	610.77	305.89			592.75	296.88	V	1739.91	870.46	1722.88	861.94	1721.89	861.45	14
6	738.94	369.97	721.91	361.46	720.92	360.97	K	1640.77	820.89	1623.74	812.38	1622.76	811.88	13
7	836.05	418.53	819.02	410.02	818.04	409.52	P	1512.60	756.81	1495.57	748.29	1494.59	747.80	12
8	999.23	500.12	982.20	491.60	981.21	491.11	Y	1415.49	708.25	1398.46	699.73	1397.47	699.24	11
9	1128.34	564.67	1111.31	556.16	1110.33	555.67	E	1252.31	626.66	1235.28	618.15	1234.30	617.65	10
10	1243.43	622.22	1226.40	613.70	1225.41	613.21	D	1123.20	562.10	1106.17	553.59	1105.18	553.10	9
11	1371.56	686.28	1354.53	677.77	1353.54	677.27	Q	1008.11	504.56	991.08	496.04	990.10	495.55	8
12	1485.66	743.33	1468.63	734.82	1467.64	734.33	N	879.98	440.50	862.95	431.98	861.97	431.49	7
13	1648.83	824.92	1631.80	816.41	1630.82	815.91	Y	765.88	383.44	748.85	374.93	747.87	374.44	6
14	1735.91	868.46	1718.88	859.94	1717.90	859.45	S	602.71	301.86	585.68	293.34	584.69	292.85	5
15	1806.99	904.00	1789.96	895.48	1788.97	894.99	A	515.63	258.32	498.60	249.80			4
16	1920.15	960.58	1903.12	952.06	1902.13	951.57	L	444.55	222.78	427.52	214.26			3
17	2076.33	1038.67	2059.30	1030.15	2058.32	1029.66	R	331.39	166.20	314.36	157.69			2
18							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
CAV2	CFSSVSLQLSQD	658.01	2+	77.5



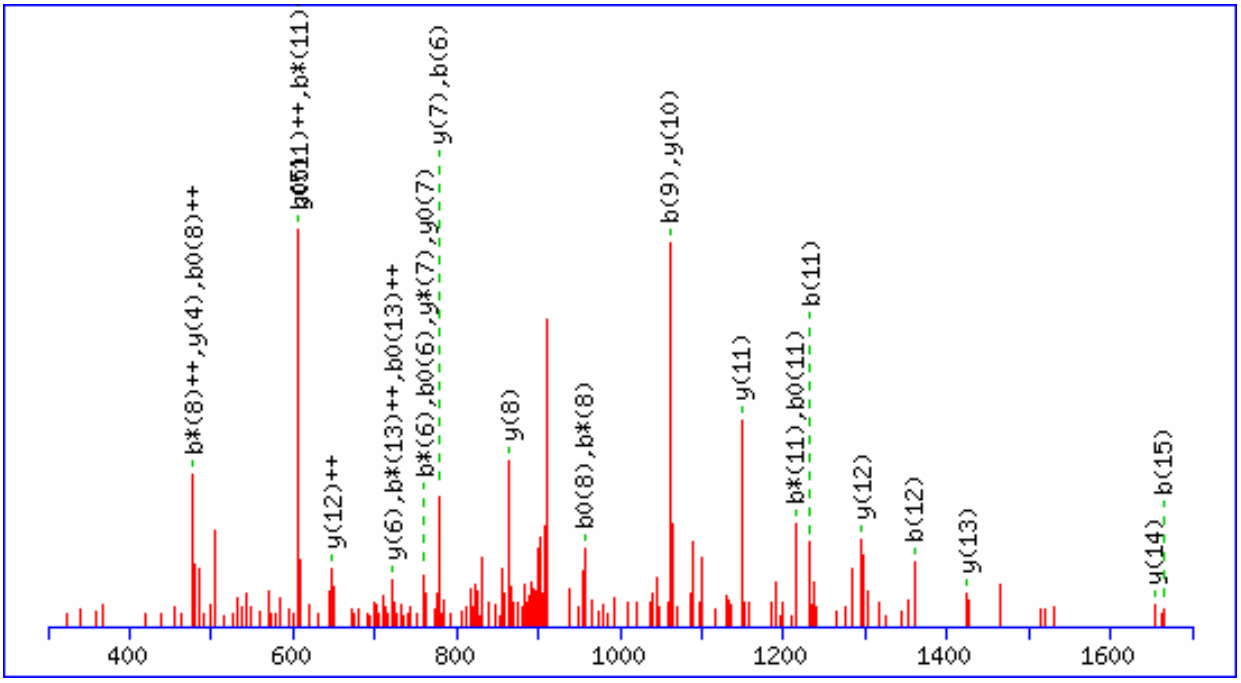
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	104.15	52.58					C							12
2	251.32	126.17					F	1211.30	606.15	1194.27	597.64	1193.28	597.15	11
3	338.40	169.70			320.39	160.70	S	1064.12	532.57	1047.09	524.05	1046.11	523.56	10
4	425.48	213.24			407.46	204.24	S	977.05	489.03	960.02	480.51	959.03	480.02	9
5	524.61	262.81			506.60	253.80	V	889.97	445.49	872.94	436.97	871.95	436.48	8
6	611.69	306.35			593.67	297.34	S	790.84	395.92	773.81	387.41	772.82	386.92	7
7	724.85	362.93			706.83	353.92	L	703.76	352.38	686.73	343.87	685.75	343.38	6
8	852.97	426.99	835.94	418.48	834.96	417.98	Q	590.60	295.81	573.57	287.29	572.59	286.80	5
9	966.13	483.57	949.10	475.05	948.12	474.56	L	462.47	231.74	445.44	223.23	444.46	222.73	4
10	1053.21	527.11	1036.18	518.59	1035.19	518.10	S	349.32	175.16	332.29	166.65	331.30	166.15	3
11	1181.34	591.17	1164.31	582.66	1163.32	582.17	Q	262.24	131.62	245.21	123.11	244.22	122.62	2
12							D	134.11	67.56			116.10	58.55	1

Gene Symbol	Sequences	m/z	Charge	Ion score
CAV2	SVTDVIIAPLCTSVGR	816.144	2+	53.6



#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55	70.07	35.54	S							16
2	187.22	94.11	169.20	85.10	V	1544.83	772.92	1527.80	764.41	1526.82	763.91	15
3	288.32	144.66	270.30	135.66	T	1445.70	723.36	1428.67	714.84	1427.69	714.35	14
4	403.41	202.21	385.39	193.20	D	1344.60	672.80	1327.57	664.29	1326.58	663.80	13
5	502.54	251.77	484.52	242.77	V	1229.51	615.26	1212.48	606.74	1211.50	606.25	12
6	615.70	308.35	597.68	299.34	I	1130.38	565.69	1113.35	557.18	1112.37	556.69	11
7	728.85	364.93	710.84	355.92	I	1017.22	509.12	1000.19	500.60	999.21	500.11	10
8	799.93	400.47	781.92	391.46	A	904.07	452.54	887.04	444.02	886.05	443.53	9
9	897.05	449.03	879.03	440.02	P	832.99	417.00	815.96	408.48	814.97	407.99	8
10	1010.20	505.61	992.19	496.60	L	735.87	368.44	718.84	359.93	717.86	359.43	7
11	1113.35	557.18	1095.33	548.17	C	622.72	311.86	605.68	303.35	604.70	302.85	6
12	1214.45	607.73	1196.44	598.72	T	519.57	260.29	502.54	251.77	501.56	251.28	5
13	1301.53	651.27	1283.51	642.26	S	418.47	209.74	401.44	201.22	400.45	200.73	4
14	1400.66	700.83	1382.64	691.83	V	331.39	166.20	314.36	157.68			3
15	1457.71	729.36	1439.70	720.35	G	232.26	116.63	215.23	108.12			2
16					R	175.21	88.11	158.18	79.59			1

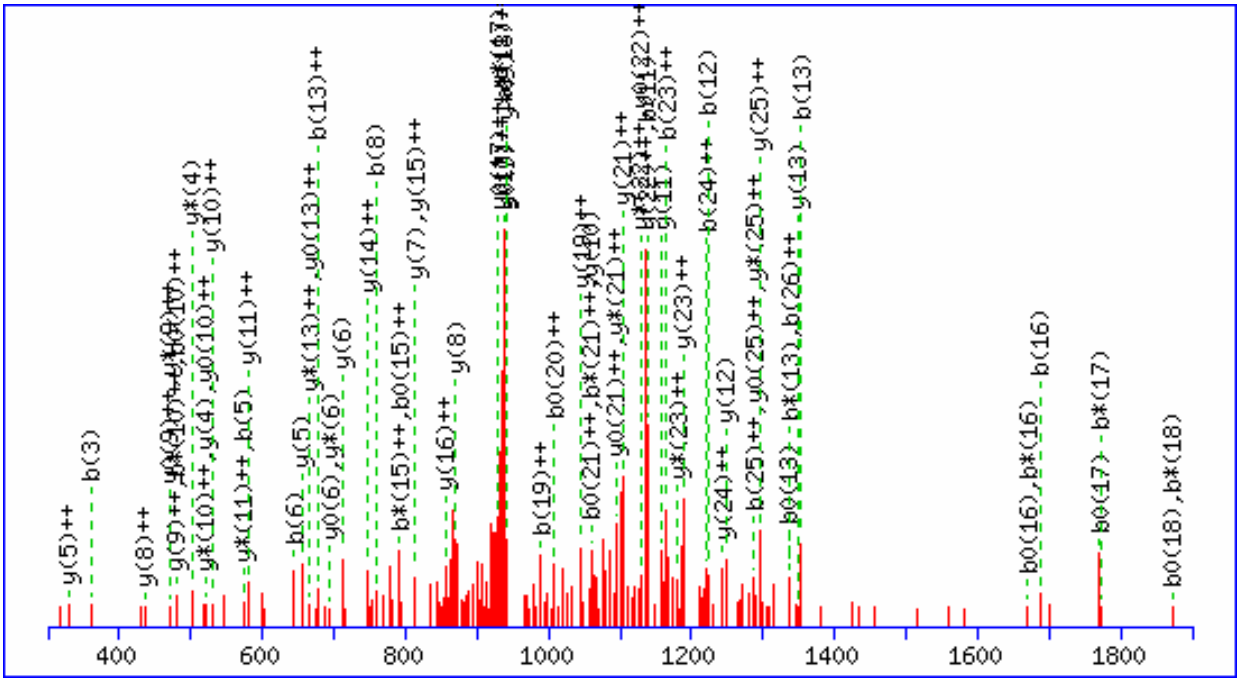
Gene Symbol	Sequences	m/z	Charge	Ion score
CD38	ANCEFSPVSGDKPCCR	919.70	2+	73.8



C3 : NEM (C)

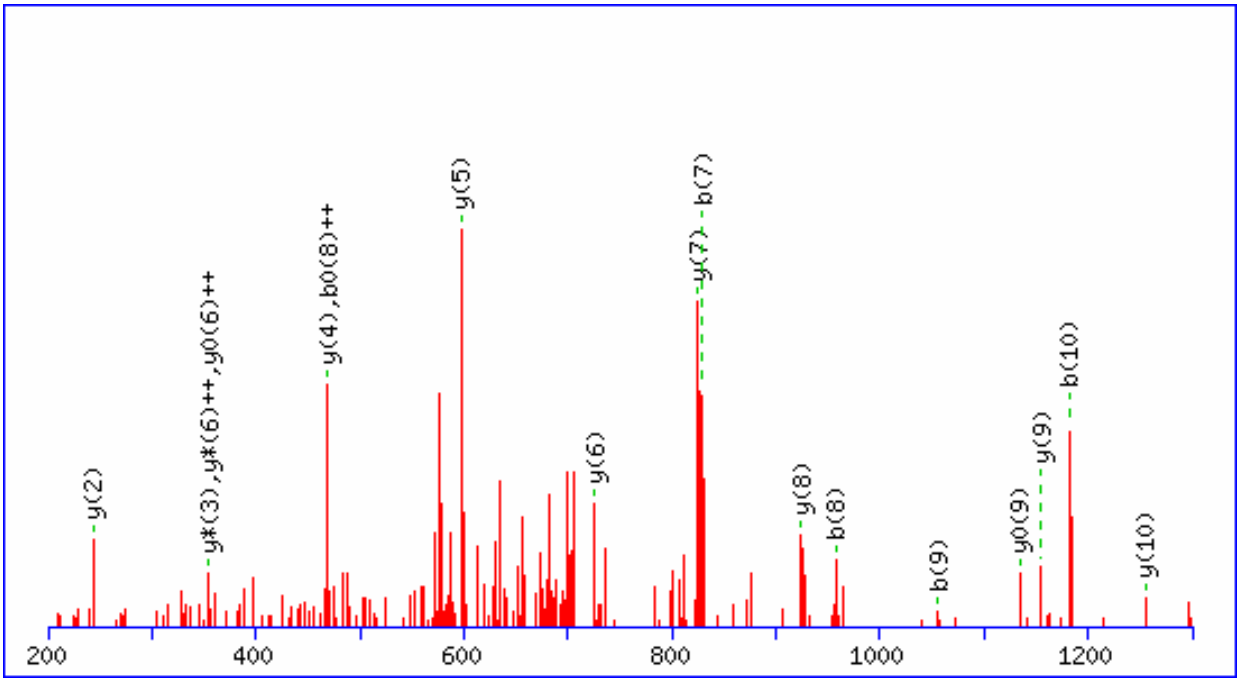
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							16
2	186.19	93.60	169.16	85.08			N	1767.98	884.49	1750.95	875.98	1749.97	875.49	15
3	414.46	207.73	397.43	199.22			C	1653.88	827.44	1636.85	818.93	1635.86	818.44	14
4	543.57	272.29	526.54	263.77	525.56	263.28	E	1425.61	713.31	1408.58	704.79	1407.59	704.30	13
5	690.74	345.88	673.71	337.36	672.73	336.87	F	1296.50	648.75	1279.47	640.24	1278.48	639.74	12
6	777.82	389.41	760.79	380.90	759.81	380.41	S	1149.32	575.16	1132.29	566.65	1131.31	566.16	11
7	874.94	437.97	857.91	429.46	856.92	428.96	P	1062.24	531.63	1045.21	523.11	1044.23	522.62	10
8	974.07	487.54	957.04	479.02	956.05	478.53	V	965.13	483.07	948.10	474.55	947.11	474.06	9
9	1061.15	531.08	1044.11	522.56	1043.13	522.07	S	866.00	433.50	848.97	424.99	847.98	424.50	8
10	1118.20	559.60	1101.17	551.09	1100.18	550.59	G	778.92	389.96	761.89	381.45	760.91	380.96	7
11	1233.28	617.15	1216.25	608.63	1215.27	608.14	D	721.87	361.44	704.84	352.92	703.85	352.43	6
12	1361.46	681.23	1344.43	672.72	1343.44	672.22	K	606.78	303.90	589.75	295.38			5
13	1458.57	729.79	1441.54	721.27	1440.56	720.78	P	478.61	239.81	461.58	231.29			4
14	1561.71	781.36	1544.68	772.85	1543.70	772.35	C	381.49	191.25	364.46	182.74			3
15	1664.86	832.93	1647.83	824.42	1646.84	823.93	C	278.35	139.68	261.32	131.16			2
16							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
CD97	WACLVAGGSKYSEFTSTTSGTGHNQTR	950.09	3+	74.6



#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	187.22	94.11					W							27
2	258.30	129.65					A	2661.83	1331.42	2644.80	1322.91	2643.82	1322.41	26
3	361.44	181.22					C	2590.76	1295.88	2573.73	1287.37	2572.74	1286.87	25
4	474.60	237.80					L	2487.61	1244.31	2470.58	1235.80	2469.60	1235.30	24
5	573.73	287.37					V	2374.46	1187.73	2357.43	1179.22	2356.44	1178.72	23
6	644.81	322.91					A	2275.33	1138.17	2258.29	1129.65	2257.31	1129.16	22
7	701.86	351.43					G	2204.25	1102.63	2187.22	1094.11	2186.23	1093.62	21
8	758.91	379.96					G	2147.20	1074.10	2130.17	1065.59	2129.18	1065.09	20
9	845.99	423.50			827.97	414.49	S	2090.14	1045.58	2073.11	1037.06	2072.13	1036.57	19
10	974.16	487.58	957.13	479.07	956.14	478.58	K	2003.07	1002.04	1986.04	993.52	1985.05	993.03	18
11	1137.33	569.17	1120.30	560.65	1119.32	560.16	Y	1874.90	937.95	1857.86	929.44	1856.88	928.94	17
12	1224.41	612.71	1207.38	604.19	1206.39	603.70	S	1711.72	856.36	1694.69	847.85	1693.71	847.36	16
13	1353.52	677.26	1336.49	668.75	1335.51	668.26	E	1624.64	812.83	1607.61	804.31	1606.63	803.82	15
14	1500.70	750.85	1483.67	742.34	1482.68	741.84	F	1495.53	748.27	1478.50	739.75	1477.52	739.26	14
15	1601.80	801.40	1584.77	792.89	1583.78	792.40	T	1348.36	674.68	1331.33	666.17	1330.34	665.67	13
16	1688.88	844.94	1671.85	836.43	1670.86	835.93	S	1247.25	624.13	1230.22	615.62	1229.24	615.12	12
17	1789.98	895.49	1772.95	886.98	1771.97	886.49	T	1160.18	580.59	1143.14	572.08	1142.16	571.58	11
18	1891.08	946.05	1874.05	937.53	1873.07	937.04	T	1059.07	530.04	1042.04	521.52	1041.06	521.03	10
19	1978.16	989.59	1961.13	981.07	1960.15	980.58	S	957.97	479.49	940.94	470.97	939.95	470.48	9
20	2035.21	1018.11	2018.18	1009.60	2017.20	1009.10	G	870.89	435.95	853.86	427.43	852.88	426.94	8
21	2136.32	1068.66	2119.29	1060.15	2118.30	1059.66	T	813.84	407.42	796.81	398.91	795.82	398.42	7
22	2193.37	1097.19	2176.34	1088.67	2175.35	1088.18	G	712.74	356.87	695.70	348.36	694.72	347.86	6
23	2330.51	1165.76	2313.48	1157.24	2312.49	1156.75	H	655.68	328.35	638.65	319.83	637.67	319.34	5
24	2444.61	1222.81	2427.58	1214.29	2426.60	1213.80	N	518.54	259.78	501.51	251.26	500.53	250.77	4
25	2572.74	1286.87	2555.71	1278.36	2554.72	1277.87	Q	404.44	202.72	387.41	194.21	386.43	193.72	3
26	2673.84	1337.43	2656.81	1328.91	2655.83	1328.42	T	276.31	138.66	259.28	130.15	258.30	129.65	2
27							R	175.21	88.11	158.18	79.59			1

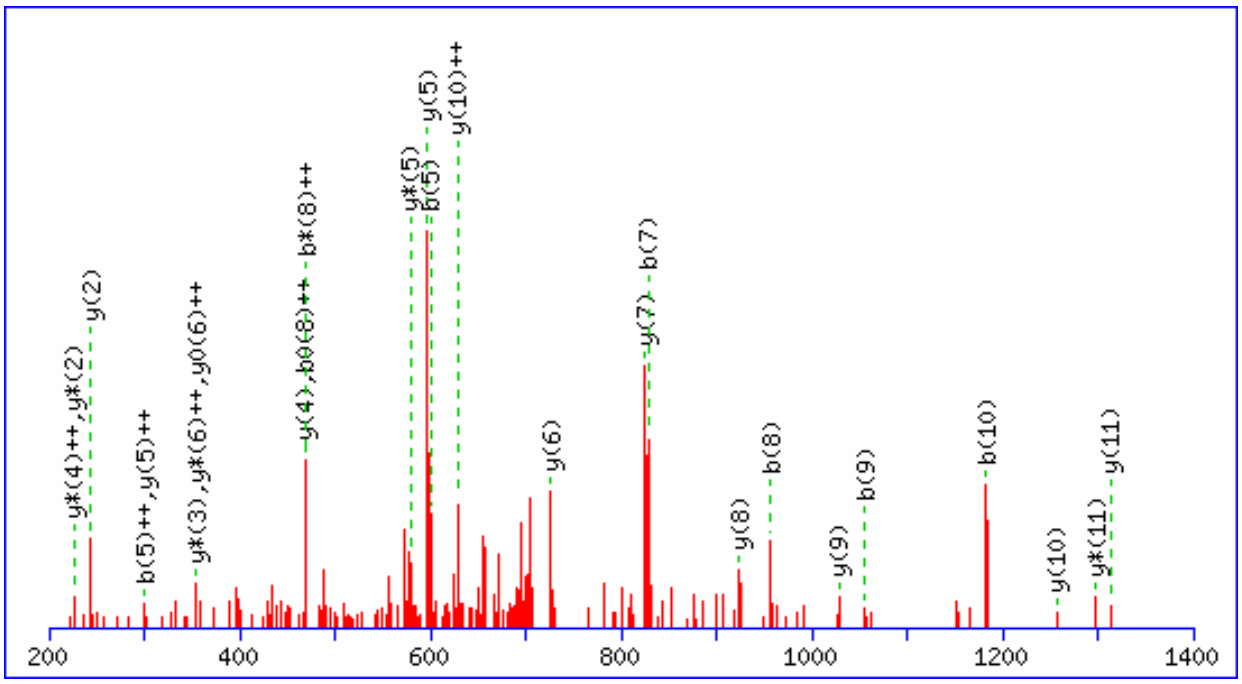
Gene Symbol	Sequences	m/z	Charge	Ion score
CDC42SE1	LGCCVVEKPQPK	713.55	2+	66.0



C4 **:** NEM (C)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					L							12
2	171.22	86.11					G	1313.57	657.29	1296.54	648.77	1295.55	648.28	11
3	274.36	137.68					C	1256.51	628.76	1239.48	620.25	1238.50	619.75	10
4	502.63	251.82					C	1153.37	577.19	1136.34	568.67	1135.36	568.18	9
5	601.76	301.38					V	925.10	463.06	908.07	454.54	907.09	454.05	8
6	700.89	350.95					V	825.97	413.49	808.94	404.97	807.96	404.48	7
7	830.00	415.51			811.99	406.50	E	726.84	363.92	709.81	355.41	708.83	354.92	6
8	958.18	479.59	941.15	471.08	940.16	470.58	K	597.73	299.37	580.70	290.85			5
9	1055.29	528.15	1038.26	519.63	1037.28	519.14	P	469.56	235.28	452.52	226.77			4
10	1183.42	592.21	1166.39	583.70	1165.41	583.21	Q	372.44	186.72	355.41	178.21			3
11	1280.54	640.77	1263.51	632.26	1262.52	631.76	P	244.31	122.66	227.28	114.14			2
12							K	147.20	74.10	130.16	65.59			1

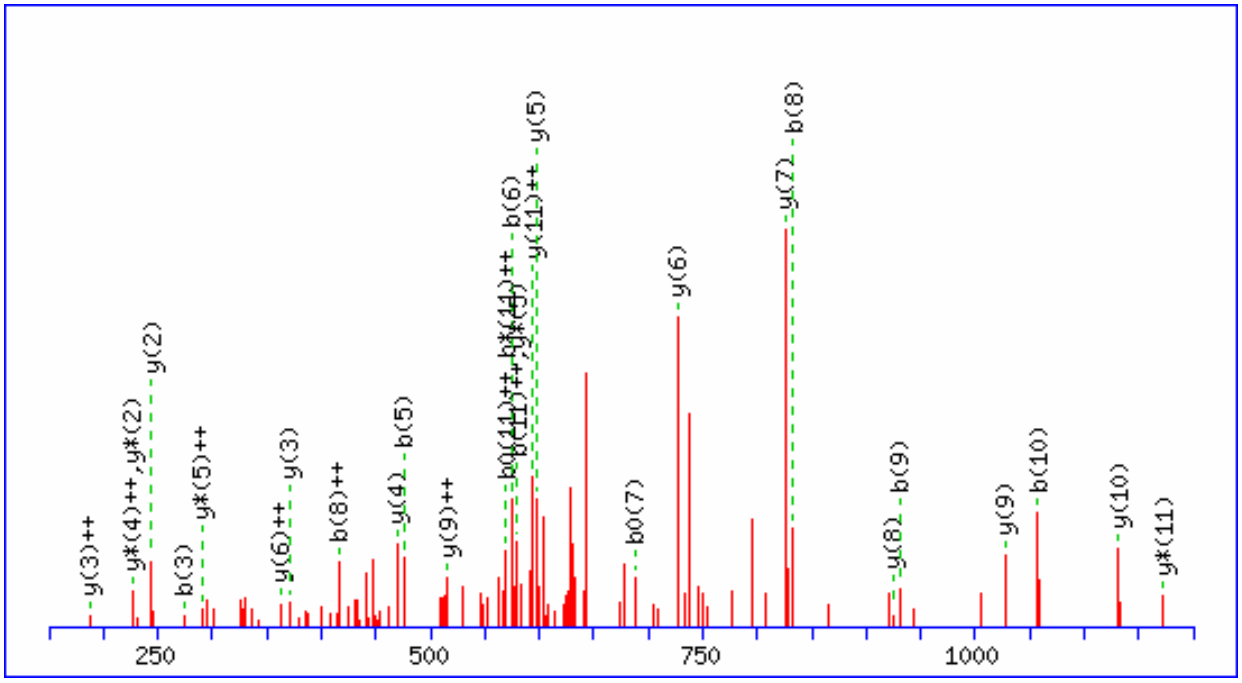
Gene Symbol	Sequences	m/z	Charge	Ion score
CDC42SE1	LGCCVVEKPQPK	713.62	2+	74.3



C3 : NEM (C)

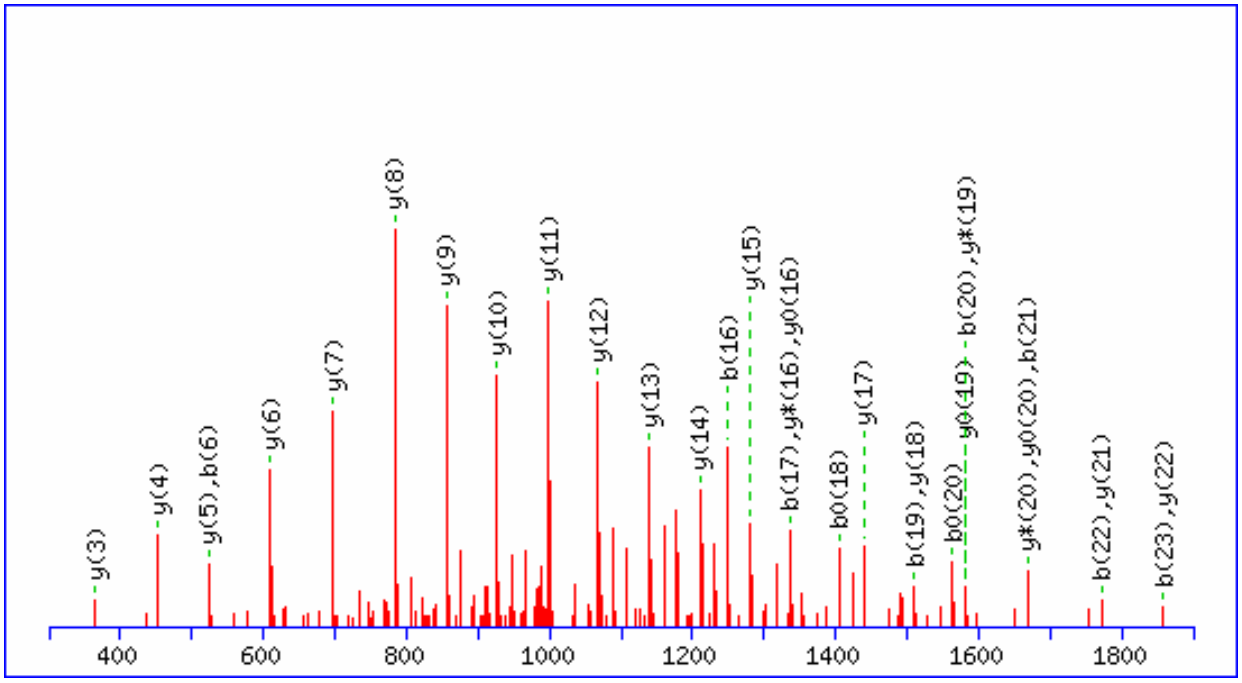
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					L							12
2	171.22	86.11					G	1313.57	657.29	1296.54	648.77	1295.55	648.28	11
3	399.49	200.25					C	1256.51	628.76	1239.48	620.25	1238.50	619.75	10
4	502.63	251.82					C	1028.25	514.63	1011.22	506.11	1010.23	505.62	9
5	601.76	301.38					V	925.10	463.06	908.07	454.54	907.09	454.05	8
6	700.89	350.95					V	825.97	413.49	808.94	404.97	807.96	404.48	7
7	830.00	415.51			811.99	406.50	E	726.84	363.92	709.81	355.41	708.83	354.92	6
8	958.18	479.59	941.15	471.08	940.16	470.58	K	597.73	299.37	580.70	290.85			5
9	1055.29	528.15	1038.26	519.63	1037.28	519.14	P	469.56	235.28	452.52	226.77			4
10	1183.42	592.21	1166.39	583.70	1165.41	583.21	Q	372.44	186.72	355.41	178.21			3
11	1280.54	640.77	1263.51	632.26	1262.52	631.76	P	244.31	122.66	227.28	114.14			2
12							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
CDC42SE1	LGCCVVEKPQPK	650.96	2+	59.6



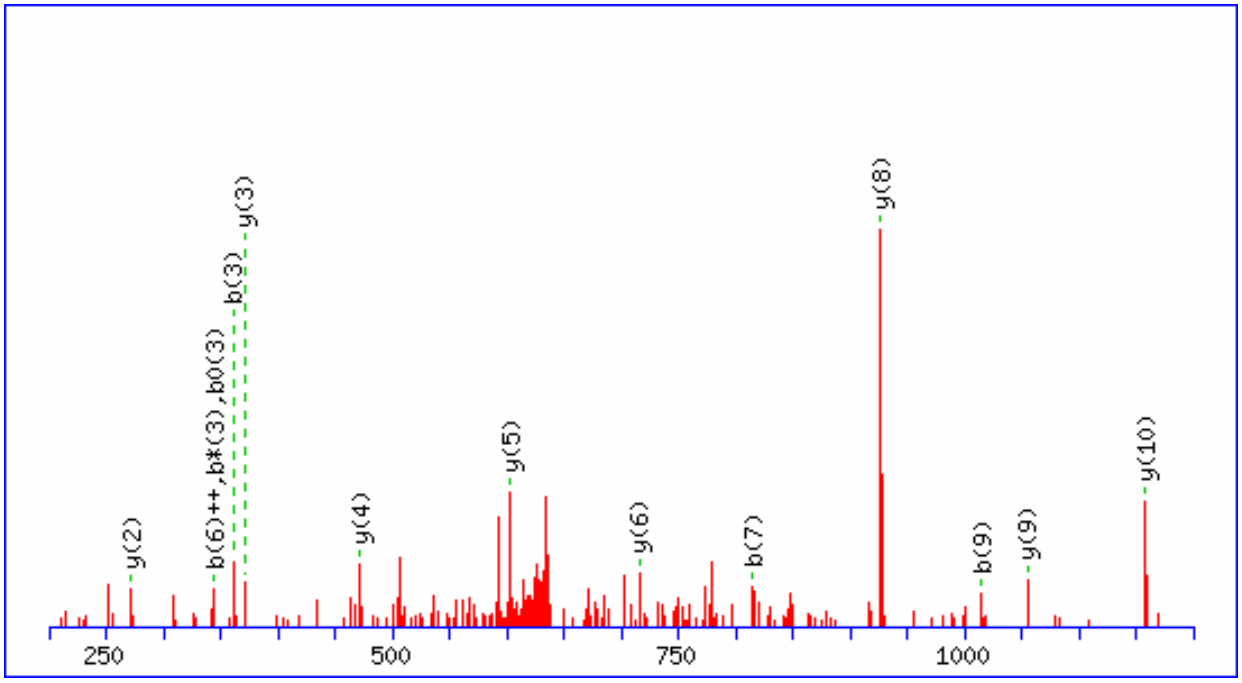
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					L							12
2	171.22	86.11					G	1188.44	594.72	1171.41	586.21	1170.43	585.72	11
3	274.36	137.68					C	1131.39	566.20	1114.36	557.68	1113.37	557.19	10
4	377.50	189.26					C	1028.25	514.63	1011.22	506.11	1010.23	505.62	9
5	476.63	238.82					V	925.10	463.06	908.07	454.54	907.09	454.05	8
6	575.76	288.39					V	825.97	413.49	808.94	404.97	807.96	404.48	7
7	704.88	352.94			686.86	343.94	E	726.84	363.92	709.81	355.41	708.83	354.92	6
8	833.05	417.03	816.02	408.51	815.04	408.02	K	597.73	299.37	580.70	290.85			5
9	930.17	465.59	913.14	457.07	912.15	456.58	P	469.56	235.28	452.52	226.77			4
10	1058.30	529.65	1041.27	521.14	1040.28	520.64	Q	372.44	186.72	355.41	178.21			3
11	1155.41	578.21	1138.38	569.69	1137.40	569.20	P	244.31	122.66	227.28	114.14			2
12							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
CKAP4	SSSSSSASAAAAAAAASSSASCSR	1017.10	2+	182.1



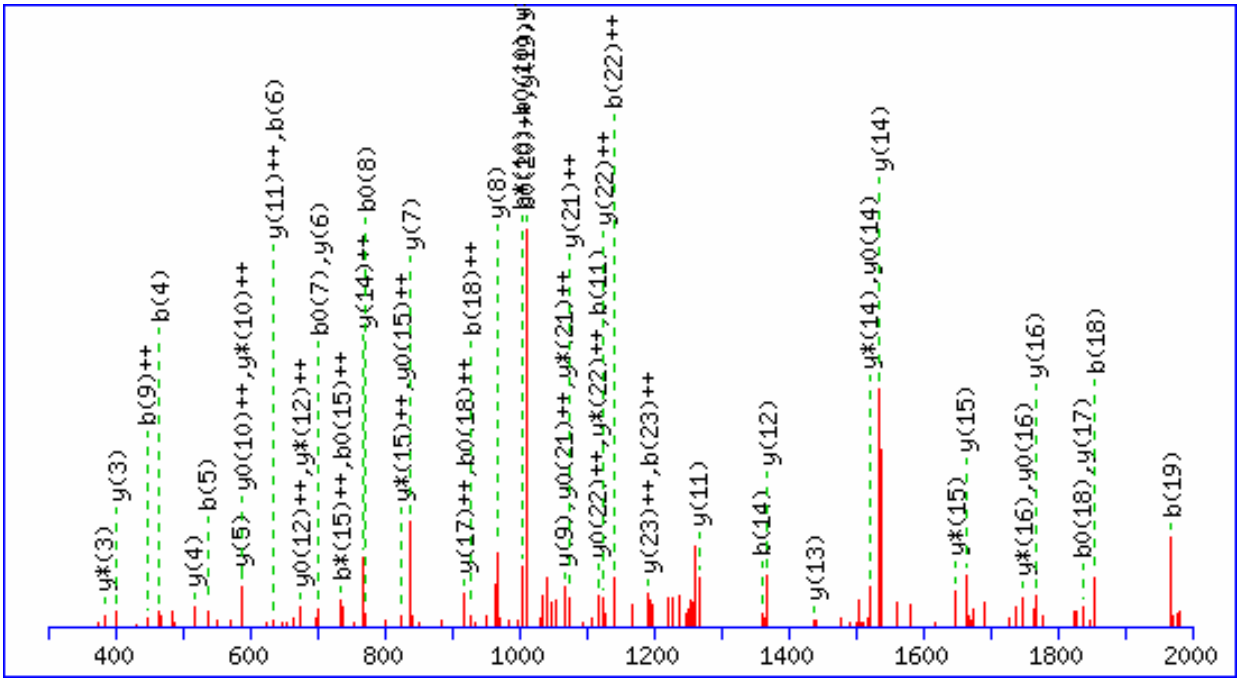
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55	70.07	35.54	S							24
2	175.16	88.09	157.15	79.08	S	1946.98	973.99	1929.95	965.48	1928.97	964.99	23
3	262.24	131.62	244.22	122.62	S	1859.90	930.46	1842.87	921.94	1841.89	921.45	22
4	349.32	175.16	331.30	166.15	S	1772.83	886.92	1755.80	878.40	1754.81	877.91	21
5	436.39	218.70	418.38	209.69	S	1685.75	843.38	1668.72	834.86	1667.73	834.37	20
6	523.47	262.24	505.46	253.23	S	1598.67	799.84	1581.64	791.32	1580.66	790.83	19
7	594.55	297.78	576.53	288.77	A	1511.59	756.30	1494.56	747.79	1493.58	747.29	18
8	681.63	341.32	663.61	332.31	S	1440.52	720.76	1423.49	712.25	1422.50	711.75	17
9	752.70	376.86	734.69	367.85	A	1353.44	677.22	1336.41	668.71	1335.42	668.22	16
10	823.78	412.40	805.77	403.39	A	1282.36	641.68	1265.33	633.17	1264.35	632.68	15
11	894.86	447.93	876.85	438.93	A	1211.28	606.15	1194.25	597.63	1193.27	597.14	14
12	965.94	483.47	947.92	474.47	A	1140.21	570.61	1123.18	562.09	1122.19	561.60	13
13	1037.02	519.01	1019.00	510.00	A	1069.13	535.07	1052.10	526.55	1051.11	526.06	12
14	1108.09	554.55	1090.08	545.54	A	998.05	499.53	981.02	491.01	980.03	490.52	11
15	1179.17	590.09	1161.16	581.08	A	926.97	463.99	909.94	455.47	908.96	454.98	10
16	1250.25	625.63	1232.23	616.62	A	855.89	428.45	838.86	419.94	837.88	419.44	9
17	1337.33	669.17	1319.31	660.16	S	784.82	392.91	767.79	384.40	766.80	383.90	8
18	1424.40	712.71	1406.39	703.70	S	697.74	349.37	680.71	340.86	679.72	340.37	7
19	1511.48	756.24	1493.47	747.24	S	610.66	305.83	593.63	297.32	592.65	296.83	6
20	1582.56	791.78	1564.54	782.78	A	523.58	262.30	506.55	253.78	505.57	253.29	5
21	1669.64	835.32	1651.62	826.31	S	452.51	226.76	435.48	218.24	434.49	217.75	4
22	1772.78	886.89	1754.76	877.89	C	365.43	183.22	348.40	174.70	347.41	174.21	3
23	1859.86	930.43	1841.84	921.43	S	262.29	131.65	245.26	123.13	244.27	122.64	2
24					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
CORO1C	KCEPIIMTVPR	643.99	2+	66.3



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.18	65.09	112.15	56.58			K							11
2	232.32	116.67	215.29	108.15			C	1159.44	580.23	1142.41	571.71	1141.43	571.22	10
3	361.44	181.22	344.41	172.71	343.42	172.21	E	1056.30	528.65	1039.27	520.14	1038.28	519.65	9
4	458.55	229.78	441.52	221.26	440.54	220.77	P	927.19	464.10	910.16	455.58	909.17	455.09	8
5	571.71	286.36	554.68	277.84	553.69	277.35	I	830.07	415.54	813.04	407.02	812.06	406.53	7
6	684.87	342.94	667.84	334.42	666.85	333.93	I	716.91	358.96	699.88	350.45	698.90	349.95	6
7	816.06	408.54	799.03	400.02	798.05	399.53	M	603.76	302.38	586.72	293.87	585.74	293.37	5
8	917.17	459.09	900.14	450.57	899.15	450.08	T	472.56	236.78	455.53	228.27	454.54	227.78	4
9	1016.30	508.65	999.27	500.14	998.28	499.65	V	371.46	186.23	354.42	177.72			3
10	1113.41	557.21	1096.38	548.70	1095.40	548.20	P	272.32	136.67	255.29	128.15			2
11							R	175.21	88.11	158.18	79.59			1

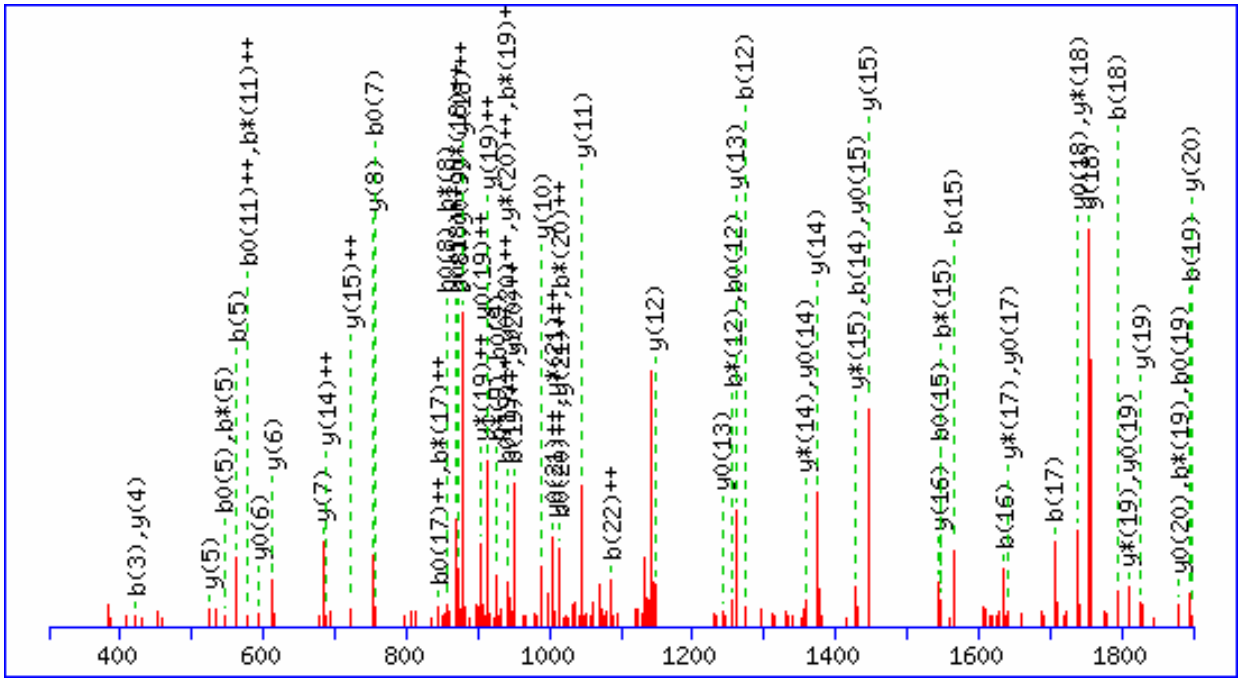
Gene Symbol	Sequences	m/z	Charge	Ion score
CSTB	MMCGAPSATQPATAETQHIADQVR	1278.82	2+	83.5



N-term : N-Acetyl (Protein)

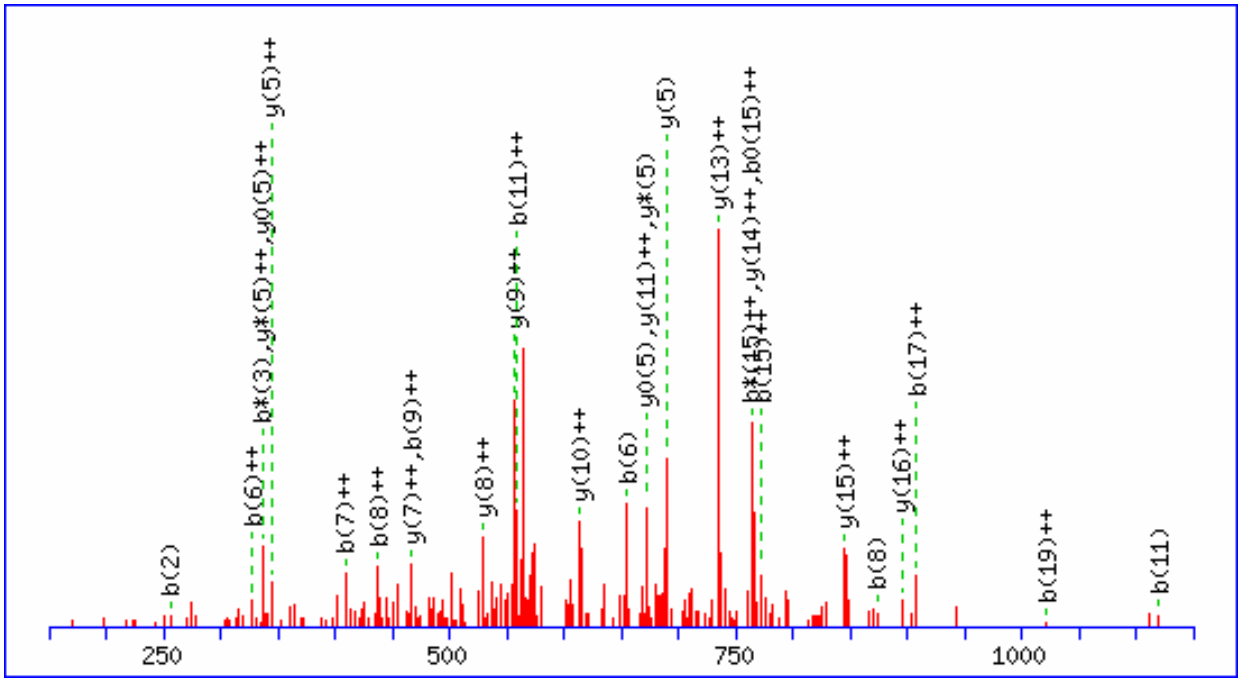
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	174.24	87.62					M							24
2	305.44	153.22					M	2384.63	1192.82	2367.59	1184.30	2366.61	1183.81	23
3	408.58	204.79					C	2253.43	1127.22	2236.40	1118.70	2235.41	1118.21	22
4	465.63	233.32					G	2150.29	1075.65	2133.26	1067.13	2132.27	1066.64	21
5	536.71	268.86					A	2093.23	1047.12	2076.20	1038.61	2075.22	1038.11	20
6	633.82	317.42					P	2022.16	1011.58	2005.13	1003.07	2004.14	1002.57	19
7	720.90	360.95			702.89	351.95	S	1925.04	963.02	1908.01	954.51	1907.03	954.02	18
8	791.98	396.49			773.96	387.49	A	1837.96	919.49	1820.93	910.97	1819.95	910.48	17
9	893.08	447.05			875.07	438.04	T	1766.89	883.95	1749.86	875.43	1748.87	874.94	16
10	1021.21	511.11	1004.18	502.59	1003.20	502.10	Q	1665.78	833.40	1648.75	824.88	1647.77	824.39	15
11	1118.33	559.67	1101.30	551.15	1100.31	550.66	P	1537.65	769.33	1520.62	760.82	1519.64	760.32	14
12	1189.41	595.21	1172.37	586.69	1171.39	586.20	A	1440.54	720.77	1423.51	712.26	1422.52	711.77	13
13	1290.51	645.76	1273.48	637.24	1272.49	636.75	T	1369.46	685.23	1352.43	676.72	1351.45	676.23	12
14	1361.59	681.30	1344.56	672.78	1343.57	672.29	A	1268.36	634.68	1251.33	626.17	1250.34	625.67	11
15	1490.70	745.85	1473.67	737.34	1472.69	736.85	E	1197.28	599.14	1180.25	590.63	1179.26	590.14	10
16	1591.81	796.41	1574.77	787.89	1573.79	787.40	T	1068.16	534.59	1051.13	526.07	1050.15	525.58	9
17	1719.93	860.47	1702.90	851.96	1701.92	851.46	Q	967.06	484.03	950.03	475.52	949.05	475.03	8
18	1857.07	929.04	1840.04	920.53	1839.06	920.03	H	838.93	419.97	821.90	411.45	820.92	410.96	7
19	1970.23	985.62	1953.20	977.10	1952.22	976.61	I	701.79	351.40	684.76	342.88	683.78	342.39	6
20	2041.31	1021.16	2024.28	1012.64	2023.29	1012.15	A	588.63	294.82	571.60	286.31	570.62	285.81	5
21	2156.40	1078.70	2139.37	1070.19	2138.38	1069.69	D	517.56	259.28	500.53	250.77	499.54	250.27	4
22	2284.53	1142.77	2267.50	1134.25	2266.51	1133.76	Q	402.47	201.74	385.44	193.22			3
23	2383.66	1192.33	2366.63	1183.82	2365.64	1183.32	V	274.34	137.67	257.31	129.16			2
24							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
CTNND1	YQEAAPNVANNTGPHAASCFGAK	1159.80	2+	113.9



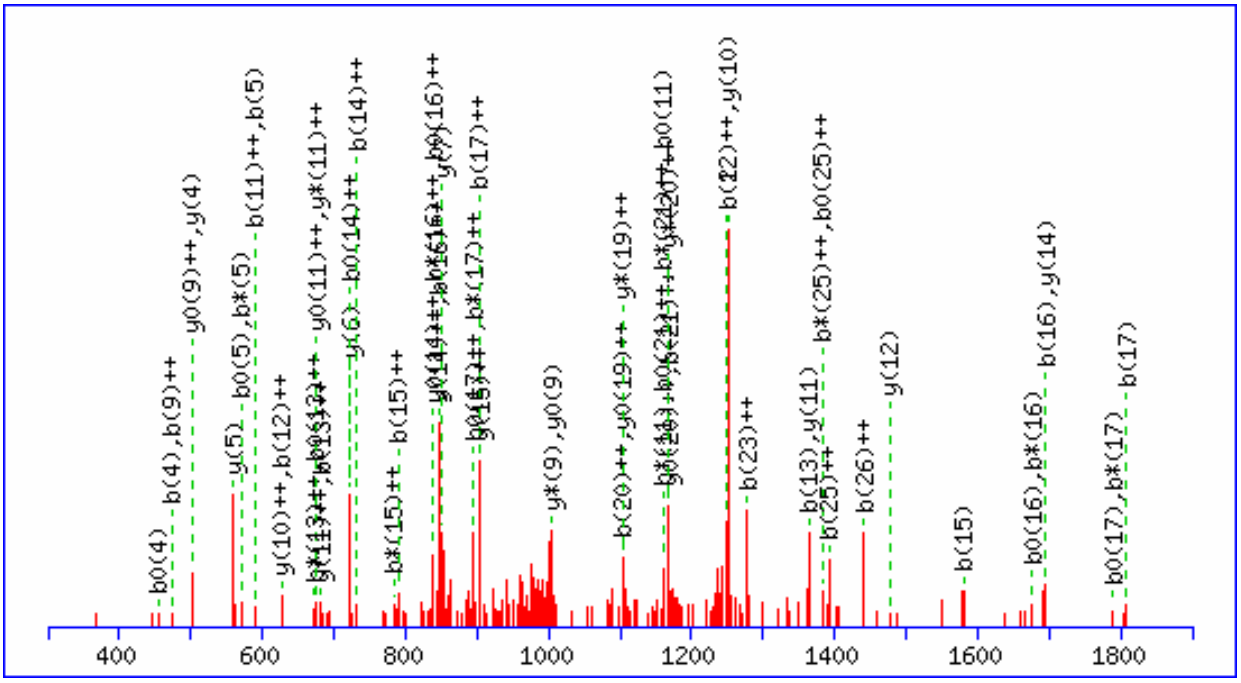
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.18	82.59					Y							23
2	292.31	146.66	275.28	138.14			Q	2156.32	1078.66	2139.28	1070.15	2138.30	1069.65	22
3	421.42	211.22	404.39	202.70	403.41	202.21	E	2028.19	1014.60	2011.16	1006.08	2010.17	1005.59	21
4	492.50	246.76	475.47	238.24	474.49	237.75	A	1899.07	950.04	1882.04	941.52	1881.06	941.03	20
5	563.58	282.29	546.55	273.78	545.56	273.29	A	1827.99	914.50	1810.96	905.99	1809.98	905.49	19
6	660.70	330.85	643.66	322.34	642.68	321.84	P	1756.92	878.96	1739.89	870.45	1738.90	869.95	18
7	774.80	387.90	757.77	379.39	756.78	378.90	N	1659.80	830.40	1642.77	821.89	1641.79	821.40	17
8	873.93	437.47	856.90	428.95	855.91	428.46	V	1545.70	773.35	1528.67	764.84	1527.68	764.35	16
9	945.01	473.01	927.98	464.49	926.99	464.00	A	1446.57	723.79	1429.54	715.27	1428.55	714.78	15
10	1059.11	530.06	1042.08	521.54	1041.09	521.05	N	1375.49	688.25	1358.46	679.73	1357.47	679.24	14
11	1173.21	587.11	1156.18	578.59	1155.20	578.10	N	1261.39	631.20	1244.36	622.68	1243.37	622.19	13
12	1274.32	637.66	1257.29	629.15	1256.30	628.65	T	1147.28	574.15	1130.25	565.63	1129.27	565.14	12
13	1331.37	666.19	1314.34	657.67	1313.35	657.18	G	1046.18	523.59	1029.15	515.08	1028.17	514.59	11
14	1428.48	714.75	1411.45	706.23	1410.47	705.74	P	989.13	495.07	972.10	486.55	971.11	486.06	10
15	1565.62	783.31	1548.59	774.80	1547.61	774.31	H	892.01	446.51	874.98	438.00	874.00	437.50	9
16	1636.70	818.85	1619.67	810.34	1618.68	809.85	A	754.87	377.94	737.84	369.43	736.86	368.93	8
17	1707.78	854.39	1690.75	845.88	1689.76	845.39	A	683.80	342.40	666.77	333.89	665.78	333.39	7
18	1794.86	897.93	1777.82	889.42	1776.84	888.92	S	612.72	306.86	595.69	298.35	594.70	297.86	6
19	1898.00	949.50	1880.97	940.99	1879.98	940.50	C	525.64	263.32	508.61	254.81			5
20	2045.17	1023.09	2028.14	1014.57	2027.16	1014.08	F	422.50	211.75	405.47	203.24			4
21	2102.22	1051.62	2085.19	1043.10	2084.21	1042.61	G	275.32	138.17	258.29	129.65			3
22	2173.30	1087.15	2156.27	1078.64	2155.29	1078.15	A	218.27	109.64	201.24	101.13			2
23							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
DDX3X	VRPCVVYGGADIGQQIRDLER	587.02	4+	70.5



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							21
2	256.32	128.67	239.29	120.15			R	2246.53	1123.77	2229.50	1115.25	2228.51	1114.76	20
3	353.44	177.22	336.41	168.71			P	2090.34	1045.67	2073.31	1037.16	2072.32	1036.67	19
4	456.58	228.80	439.55	220.28			C	1993.22	997.12	1976.19	988.60	1975.21	988.11	18
5	555.71	278.36	538.68	269.85			V	1890.08	945.54	1873.05	937.03	1872.07	936.54	17
6	654.85	327.93	637.81	319.41			V	1790.95	895.98	1773.92	887.46	1772.94	886.97	16
7	818.02	409.51	800.99	401.00			Y	1691.82	846.41	1674.79	837.90	1673.80	837.41	15
8	875.07	438.04	858.04	429.52			G	1528.65	764.83	1511.62	756.31	1510.63	755.82	14
9	932.12	466.56	915.09	458.05			G	1471.60	736.30	1454.56	727.79	1453.58	727.29	13
10	1003.20	502.10	986.17	493.59			A	1414.54	707.78	1397.51	699.26	1396.53	698.77	12
11	1118.29	559.65	1101.26	551.13	1100.27	550.64	D	1343.47	672.24	1326.44	663.72	1325.45	663.23	11
12	1231.44	616.23	1214.41	607.71	1213.43	607.22	I	1228.38	614.69	1211.35	606.18	1210.36	605.69	10
13	1288.50	644.75	1271.46	636.24	1270.48	635.74	G	1115.22	558.11	1098.19	549.60	1097.21	549.11	9
14	1416.62	708.82	1399.59	700.30	1398.61	699.81	Q	1058.17	529.59	1041.14	521.07	1040.15	520.58	8
15	1544.75	772.88	1527.72	764.37	1526.74	763.87	Q	930.04	465.52	913.01	457.01	912.03	456.52	7
16	1657.91	829.46	1640.88	820.94	1639.90	820.45	I	801.91	401.46	784.88	392.94	783.90	392.45	6
17	1814.10	907.55	1797.07	899.04	1796.08	898.54	R	688.75	344.88	671.72	336.37	670.74	335.87	5
18	1929.18	965.10	1912.15	956.58	1911.17	956.09	D	532.57	266.79	515.54	258.27	514.55	257.78	4
19	2042.34	1021.67	2025.31	1013.16	2024.33	1012.67	L	417.48	209.24	400.45	200.73	399.47	200.24	3
20	2171.46	1086.23	2154.43	1077.72	2153.44	1077.22	E	304.32	152.67	287.29	144.15	286.31	143.66	2
21							R	175.21	88.11	158.18	79.59			1

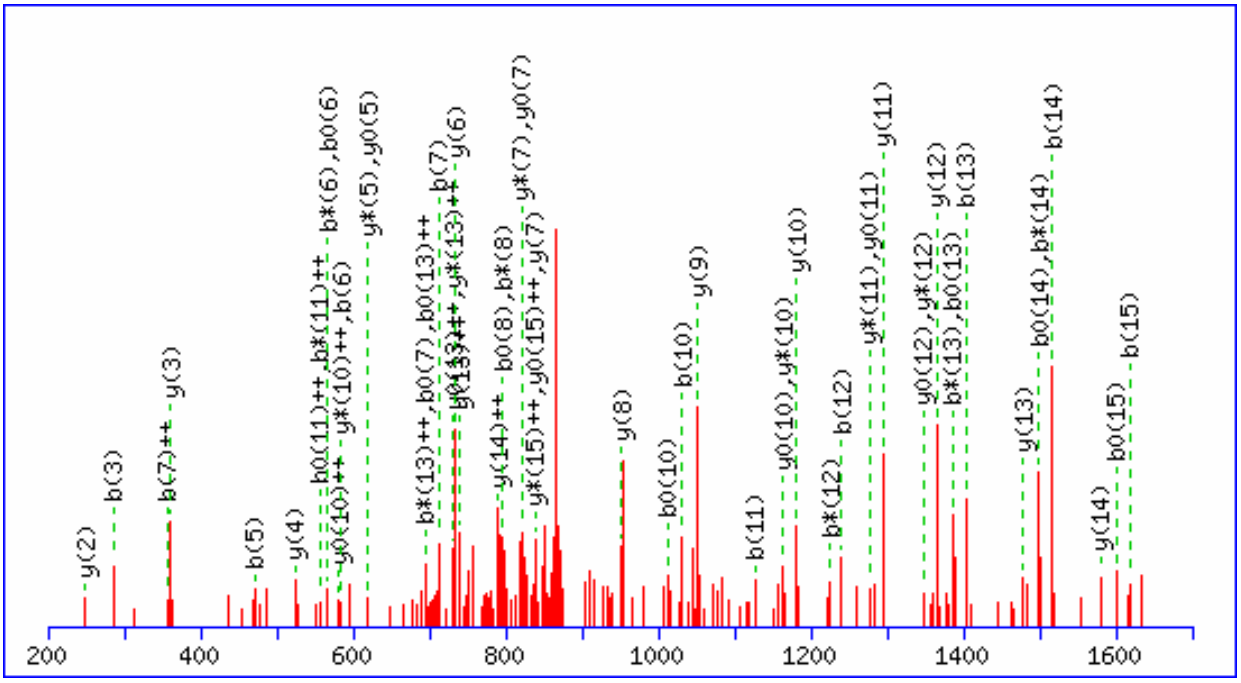
Gene Symbol	Sequences	m/z	Charge	Ion score
DHX9	DKDDDGGEDDDANCNLICGDEYGPETR	1019.59	3+	75.0



C18 : NEM (C)

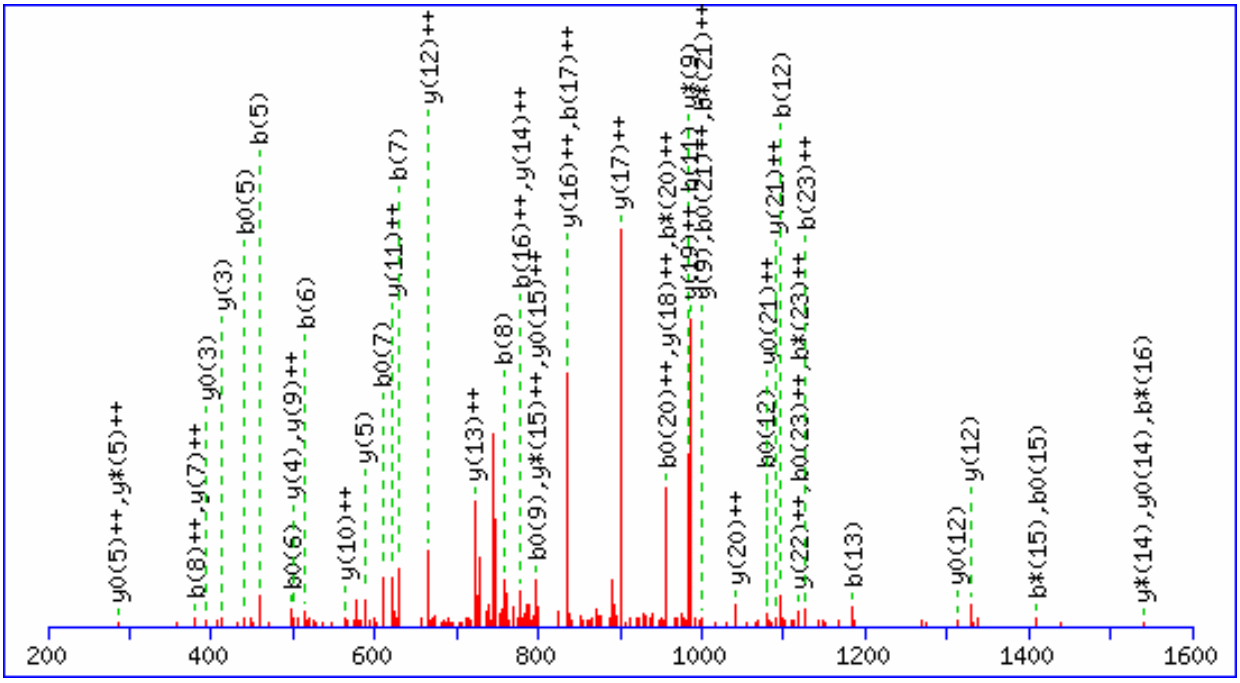
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.10	58.55			98.08	49.54	D							27
2	244.27	122.64	227.24	114.12	226.25	113.63	K	2942.94	1471.97	2925.91	1463.46	2924.93	1462.97	26
3	359.36	180.18	342.32	171.67	341.34	171.17	D	2814.77	1407.89	2797.74	1399.37	2796.75	1398.88	25
4	474.44	237.73	457.41	229.21	456.43	228.72	D	2699.68	1350.35	2682.65	1341.83	2681.67	1341.34	24
5	589.53	295.27	572.50	286.75	571.51	286.26	D	2584.59	1292.80	2567.56	1284.29	2566.58	1283.79	23
6	646.58	323.79	629.55	315.28	628.57	314.79	G	2469.51	1235.26	2452.48	1226.74	2451.49	1226.25	22
7	703.63	352.32	686.60	343.80	685.62	343.31	G	2412.46	1206.73	2395.43	1198.22	2394.44	1197.72	21
8	832.75	416.88	815.72	408.36	814.73	407.87	E	2355.40	1178.21	2338.37	1169.69	2337.39	1169.20	20
9	947.83	474.42	930.80	465.91	929.82	465.41	D	2226.29	1113.65	2209.26	1105.13	2208.28	1104.64	19
10	1062.92	531.96	1045.89	523.45	1044.91	522.96	D	2111.20	1056.11	2094.17	1047.59	2093.19	1047.10	18
11	1178.01	589.51	1160.98	580.99	1159.99	580.50	D	1996.12	998.56	1979.09	990.05	1978.10	989.55	17
12	1249.09	625.05	1232.06	616.53	1231.07	616.04	A	1881.03	941.02	1864.00	932.50	1863.01	932.01	16
13	1363.19	682.10	1346.16	673.58	1345.17	673.09	N	1809.95	905.48	1792.92	896.96	1791.94	896.47	15
14	1466.33	733.67	1449.30	725.15	1448.32	724.66	C	1695.85	848.43	1678.82	839.91	1677.83	839.42	14
15	1580.43	790.72	1563.40	782.21	1562.42	781.71	N	1592.71	796.86	1575.67	788.34	1574.69	787.85	13
16	1693.59	847.30	1676.56	838.78	1675.58	838.29	L	1478.60	739.81	1461.57	731.29	1460.59	730.80	12
17	1806.75	903.88	1789.72	895.36	1788.73	894.87	I	1365.45	683.23	1348.41	674.71	1347.43	674.22	11
18	2035.02	1018.01	2017.99	1009.50	2017.00	1009.01	C	1252.29	626.65	1235.26	618.13	1234.27	617.64	10
19	2092.07	1046.54	2075.04	1038.02	2074.05	1037.53	G	1024.02	512.51	1006.99	504.00	1006.00	503.51	9
20	2207.16	1104.08	2190.13	1095.57	2189.14	1095.07	D	966.97	483.99	949.94	475.47	948.95	474.98	8
21	2336.27	1168.64	2319.24	1160.12	2318.26	1159.63	E	851.88	426.44	834.85	417.93	833.87	417.44	7
22	2499.44	1250.23	2482.41	1241.71	2481.43	1241.22	Y	722.77	361.89	705.74	353.37	704.75	352.88	6
23	2556.50	1278.75	2539.46	1270.24	2538.48	1269.74	G	559.59	280.30	542.56	271.79	541.58	271.29	5
24	2653.61	1327.31	2636.58	1318.79	2635.60	1318.30	P	502.54	251.77	485.51	243.26	484.53	242.77	4
25	2782.72	1391.87	2765.69	1383.35	2764.71	1382.86	E	405.43	203.22	388.40	194.70	387.41	194.21	3
26	2883.83	1442.42	2866.80	1433.90	2865.81	1433.41	T	276.31	138.66	259.28	130.15	258.30	129.65	2
27							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
DPYSL2	AITIANQTNCPLYITK	882.60	2+	79.1



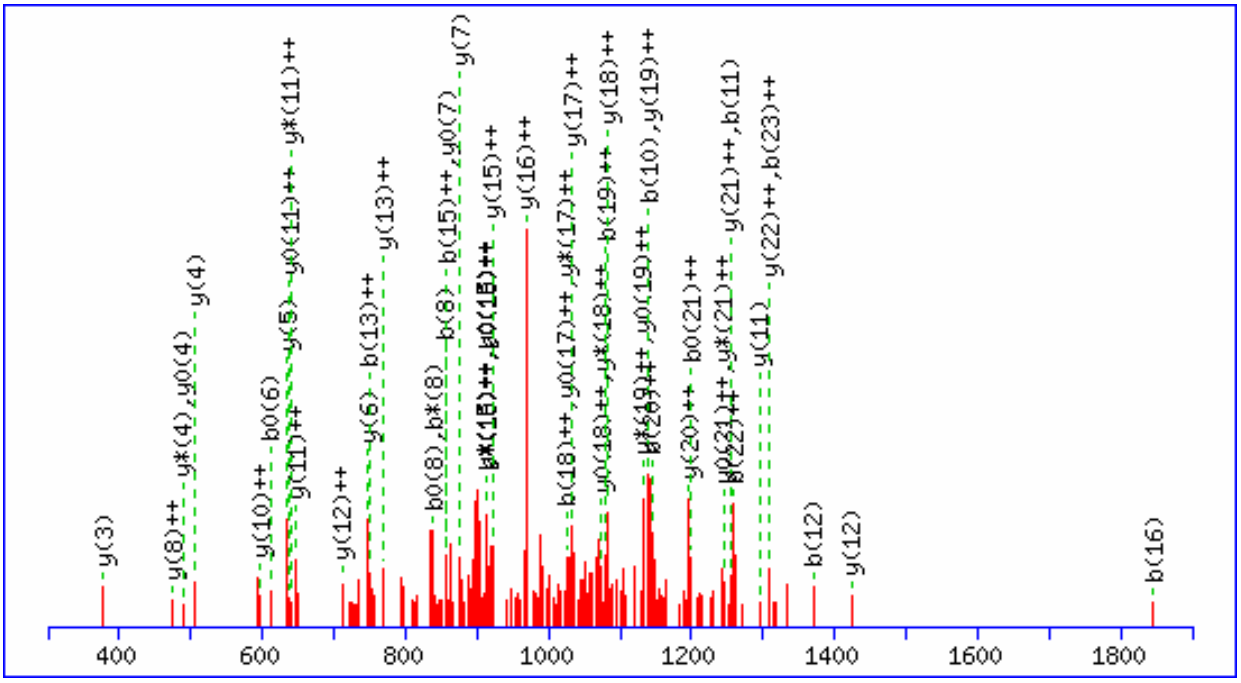
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							16
2	185.24	93.13					I	1693.98	847.49	1676.95	838.98	1675.97	838.49	15
3	286.35	143.68			268.33	134.67	T	1580.82	790.92	1563.79	782.40	1562.81	781.91	14
4	399.50	200.26			381.49	191.25	I	1479.72	740.36	1462.69	731.85	1461.70	731.36	13
5	470.58	235.80			452.57	226.79	A	1366.56	683.79	1349.53	675.27	1348.55	674.78	12
6	584.69	292.85	567.65	284.33	566.67	283.84	N	1295.48	648.25	1278.45	639.73	1277.47	639.24	11
7	712.81	356.91	695.78	348.40	694.80	347.90	Q	1181.38	591.19	1164.35	582.68	1163.37	582.19	10
8	813.92	407.46	796.89	398.95	795.90	398.46	T	1053.25	527.13	1036.22	518.61	1035.24	518.12	9
9	928.02	464.51	910.99	456.00	910.01	455.51	N	952.15	476.58	935.12	468.06	934.13	467.57	8
10	1031.16	516.09	1014.13	507.57	1013.15	507.08	C	838.05	419.53	821.02	411.01	820.03	410.52	7
11	1128.28	564.64	1111.25	556.13	1110.26	555.64	P	734.90	367.96	717.87	359.44	716.89	358.95	6
12	1241.44	621.22	1224.41	612.71	1223.42	612.21	L	637.79	319.40	620.76	310.88	619.77	310.39	5
13	1404.61	702.81	1387.58	694.29	1386.59	693.80	Y	524.63	262.82	507.60	254.30	506.62	253.81	4
14	1517.77	759.39	1500.74	750.87	1499.75	750.38	I	361.46	181.23	344.43	172.72	343.44	172.22	3
15	1618.87	809.94	1601.84	801.42	1600.86	800.93	T	248.30	124.65	231.27	116.14	230.28	115.65	2
16							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
EDIL3	CSGPLGIEGGIISNQQITASSTHR	809.61	3+	99.1



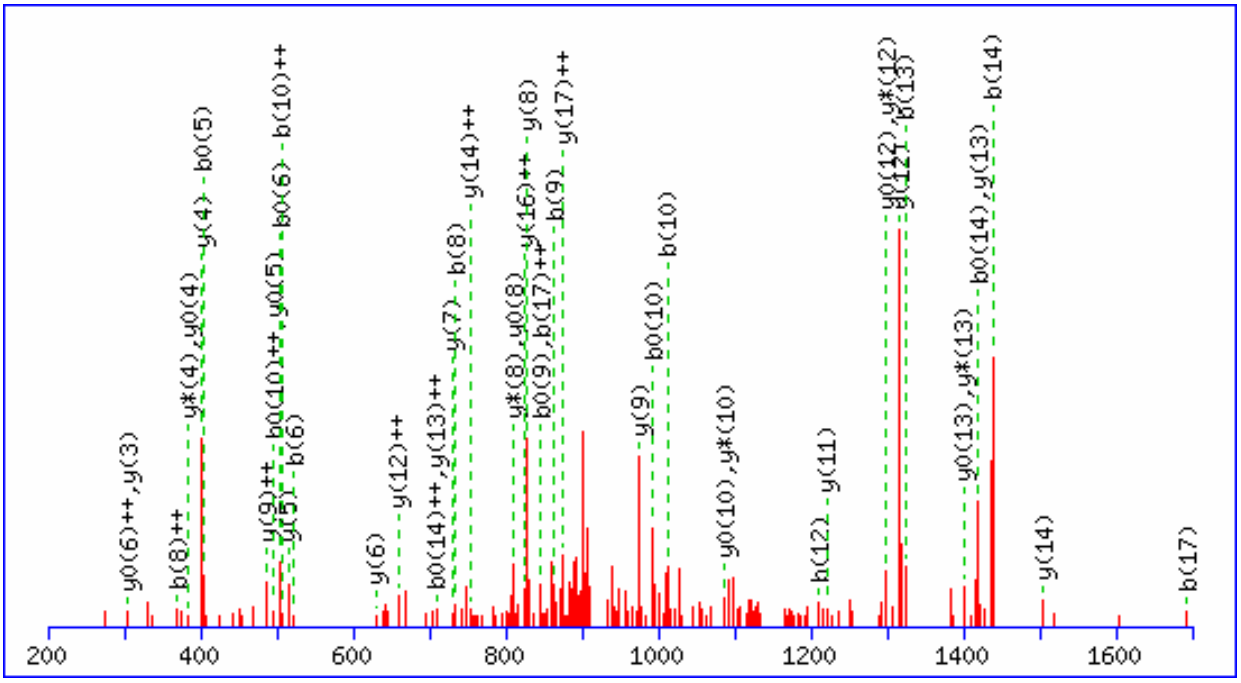
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	104.15	52.58					C							24
2	191.23	96.12			173.21	87.11	S	2324.53	1162.77	2307.50	1154.25	2306.51	1153.76	23
3	248.28	124.64			230.26	115.64	G	2237.45	1119.23	2220.42	1110.71	2219.43	1110.22	22
4	345.39	173.20			327.38	164.19	P	2180.40	1090.70	2163.37	1082.19	2162.38	1081.70	21
5	458.55	229.78			440.54	220.77	L	2083.28	1042.15	2066.25	1033.63	2065.27	1033.14	20
6	515.60	258.31			497.59	249.30	G	1970.13	985.57	1953.09	977.05	1952.11	976.56	19
7	628.76	314.88			610.75	305.88	I	1913.07	957.04	1896.04	948.53	1895.06	948.03	18
8	757.88	379.44			739.86	370.43	E	1799.92	900.46	1782.89	891.95	1781.90	891.45	17
9	814.93	407.97			796.91	398.96	G	1670.80	835.91	1653.77	827.39	1652.79	826.90	16
10	871.98	436.49			853.96	427.49	G	1613.75	807.38	1596.72	798.86	1595.74	798.37	15
11	985.14	493.07			967.12	484.06	I	1556.70	778.85	1539.67	770.34	1538.68	769.85	14
12	1098.29	549.65			1080.28	540.64	I	1443.54	722.27	1426.51	713.76	1425.53	713.27	13
13	1185.37	593.19			1167.35	584.18	S	1330.38	665.70	1313.35	657.18	1312.37	656.69	12
14	1299.47	650.24	1282.44	641.73	1281.46	641.23	N	1243.31	622.16	1226.28	613.64	1225.29	613.15	11
15	1427.60	714.30	1410.57	705.79	1409.59	705.30	Q	1129.20	565.11	1112.17	556.59	1111.19	556.10	10
16	1555.73	778.37	1538.70	769.85	1537.72	769.36	Q	1001.08	501.04	984.04	492.53	983.06	492.03	9
17	1668.89	834.95	1651.86	826.43	1650.87	825.94	I	872.95	436.98	855.92	428.46	854.93	427.97	8
18	1769.99	885.50	1752.96	876.99	1751.98	876.49	T	759.79	380.40	742.76	371.88	741.77	371.39	7
19	1841.07	921.04	1824.04	912.52	1823.06	912.03	A	658.68	329.85	641.65	321.33	640.67	320.84	6
20	1928.15	964.58	1911.12	956.06	1910.13	955.57	S	587.61	294.31	570.58	285.79	569.59	285.30	5
21	2015.23	1008.12	1998.19	999.60	1997.21	999.11	S	500.53	250.77	483.50	242.25	482.51	241.76	4
22	2116.33	1058.67	2099.30	1050.15	2098.31	1049.66	T	413.45	207.23	396.42	198.71	395.44	198.22	3
23	2253.47	1127.24	2236.44	1118.72	2235.45	1118.23	H	312.35	156.68	295.32	148.16			2
24							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
EEF1B2	SSILLDVKPWDDETDMAKLEE**C**VR	932.10	3+	73.4



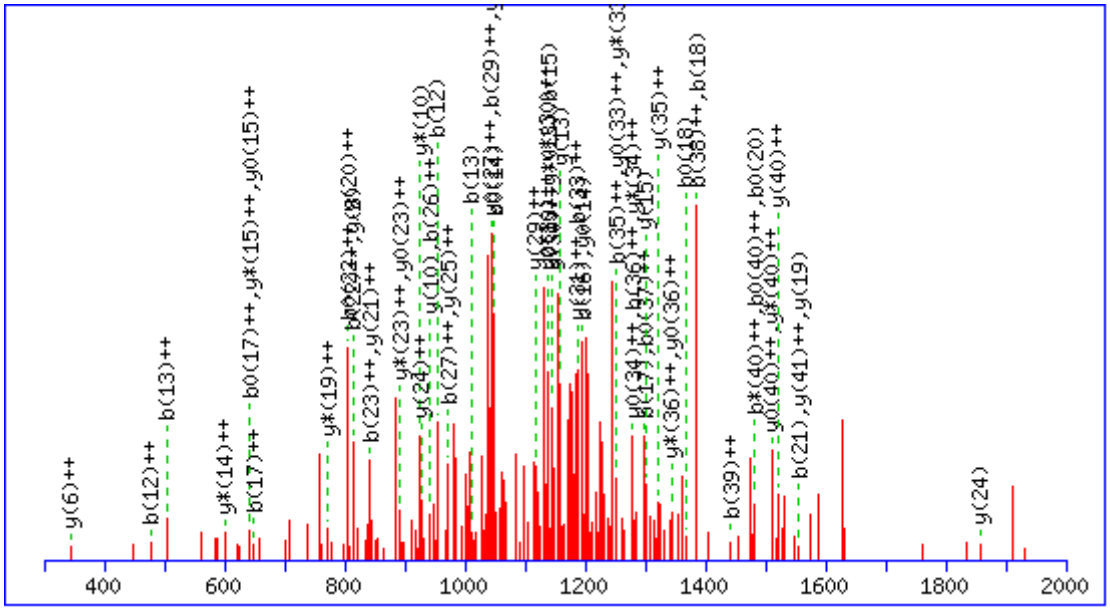
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							24
2	175.16	88.09			157.15	79.08	S	2707.06	1354.03	2690.03	1345.52	2689.05	1345.03	23
3	288.32	144.66			270.30	135.66	I	2619.98	1310.50	2602.95	1301.98	2601.97	1301.49	22
4	401.48	201.24			383.46	192.24	L	2506.83	1253.92	2489.80	1245.40	2488.81	1244.91	21
5	514.64	257.82			496.62	248.81	L	2393.67	1197.34	2376.64	1188.82	2375.65	1188.33	20
6	629.72	315.37			611.71	306.36	D	2280.51	1140.76	2263.48	1132.24	2262.50	1131.75	19
7	728.85	364.93			710.84	355.92	V	2165.42	1083.22	2148.39	1074.70	2147.41	1074.21	18
8	857.03	429.02	840.00	420.50	839.01	420.01	K	2066.29	1033.65	2049.26	1025.13	2048.28	1024.64	17
9	954.14	477.57	937.11	469.06	936.13	468.57	P	1938.12	969.56	1921.09	961.05	1920.10	960.56	16
10	1140.35	570.68	1123.32	562.16	1122.34	561.67	W	1841.00	921.01	1823.97	912.49	1822.99	912.00	15
11	1255.44	628.22	1238.41	619.71	1237.42	619.22	D	1654.79	827.90	1637.76	819.39	1636.78	818.89	14
12	1370.53	685.77	1353.50	677.25	1352.51	676.76	D	1539.71	770.36	1522.68	761.84	1521.69	761.35	13
13	1499.64	750.32	1482.61	741.81	1481.62	741.32	E	1424.62	712.81	1407.59	704.30	1406.60	703.81	12
14	1600.74	800.88	1583.71	792.36	1582.73	791.87	T	1295.51	648.26	1278.48	639.74	1277.49	639.25	11
15	1715.83	858.42	1698.80	849.90	1697.82	849.41	D	1194.40	597.71	1177.37	589.19	1176.39	588.70	10
16	1847.03	924.02	1830.00	915.50	1829.01	915.01	M	1079.31	540.16	1062.28	531.65	1061.30	531.15	9
17	1918.11	959.56	1901.07	951.04	1900.09	950.55	A	948.12	474.56	931.09	466.05	930.10	465.56	8
18	2046.28	1023.64	2029.25	1015.13	2028.26	1014.64	K	877.04	439.02	860.01	430.51	859.03	430.02	7
19	2159.44	1080.22	2142.40	1071.71	2141.42	1071.21	L	748.87	374.94	731.84	366.42	730.85	365.93	6
20	2288.55	1144.78	2271.52	1136.26	2270.53	1135.77	E	635.71	318.36	618.68	309.84	617.70	309.35	5
21	2417.66	1209.34	2400.63	1200.82	2399.65	1200.33	E	506.60	253.80	489.57	245.29	488.58	244.79	4
22	2520.81	1260.91	2503.78	1252.39	2502.79	1251.90	C	377.48	189.25	360.45	180.73			3
23	2619.94	1310.47	2602.91	1301.96	2601.92	1301.46	V	274.34	137.67	257.31	129.16			2
24							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
EIF2S3	SCGSSTPDEFPTDIPGTK	920.15	2+	50.8



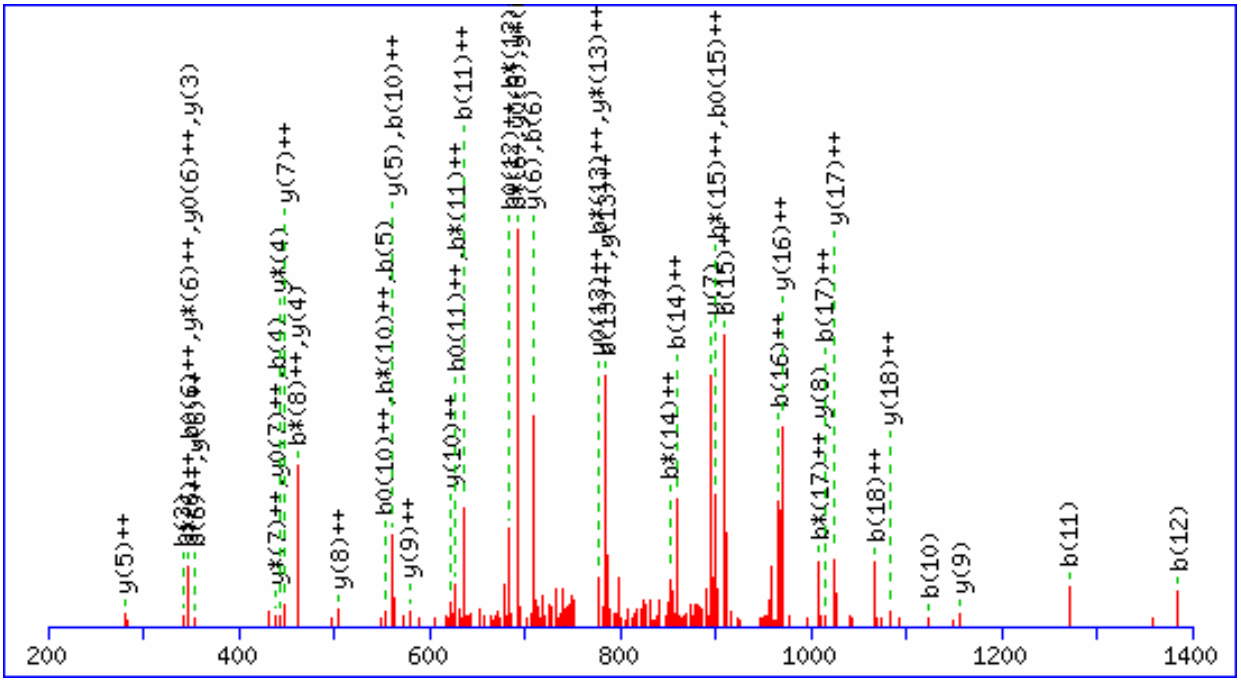
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55	70.07	35.54	S							18
2	191.23	96.12	173.21	87.11	C	1752.87	876.94	1735.84	868.43	1734.86	867.93	17
3	248.28	124.64	230.26	115.64	G	1649.73	825.37	1632.70	816.85	1631.72	816.36	16
4	335.36	168.18	317.34	159.17	S	1592.68	796.84	1575.65	788.33	1574.66	787.84	15
5	422.43	211.72	404.42	202.71	S	1505.60	753.30	1488.57	744.79	1487.59	744.30	14
6	523.54	262.27	505.52	253.27	T	1418.52	709.77	1401.49	701.25	1400.51	700.76	13
7	620.65	310.83	602.64	301.82	P	1317.42	659.21	1300.39	650.70	1299.41	650.21	12
8	735.74	368.37	717.73	359.37	D	1220.31	610.66	1203.27	602.14	1202.29	601.65	11
9	864.85	432.93	846.84	423.92	E	1105.22	553.11	1088.19	544.60	1087.20	544.11	10
10	1012.03	506.52	994.01	497.51	F	976.10	488.56	959.07	480.04	958.09	479.55	9
11	1109.14	555.08	1091.13	546.07	P	828.93	414.97	811.90	406.45	810.91	405.96	8
12	1210.25	605.63	1192.23	596.62	T	731.81	366.41	714.78	357.90	713.80	357.40	7
13	1325.33	663.17	1307.32	654.16	D	630.71	315.86	613.68	307.34	612.70	306.85	6
14	1438.49	719.75	1420.48	710.74	I	515.62	258.32	498.59	249.80	497.61	249.31	5
15	1535.61	768.31	1517.59	759.30	P	402.47	201.74	385.44	193.22	384.45	192.73	4
16	1592.66	796.83	1574.64	787.83	G	305.35	153.18	288.32	144.66	287.34	144.17	3
17	1693.76	847.39	1675.75	838.38	T	248.30	124.65	231.27	116.14	230.28	115.65	2
18					K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FBXO45	MAAPAPGAGAASGGAGCSGGGAGAGAGSGSGAAGAGGRLPSR	1081.69	3+	44.7



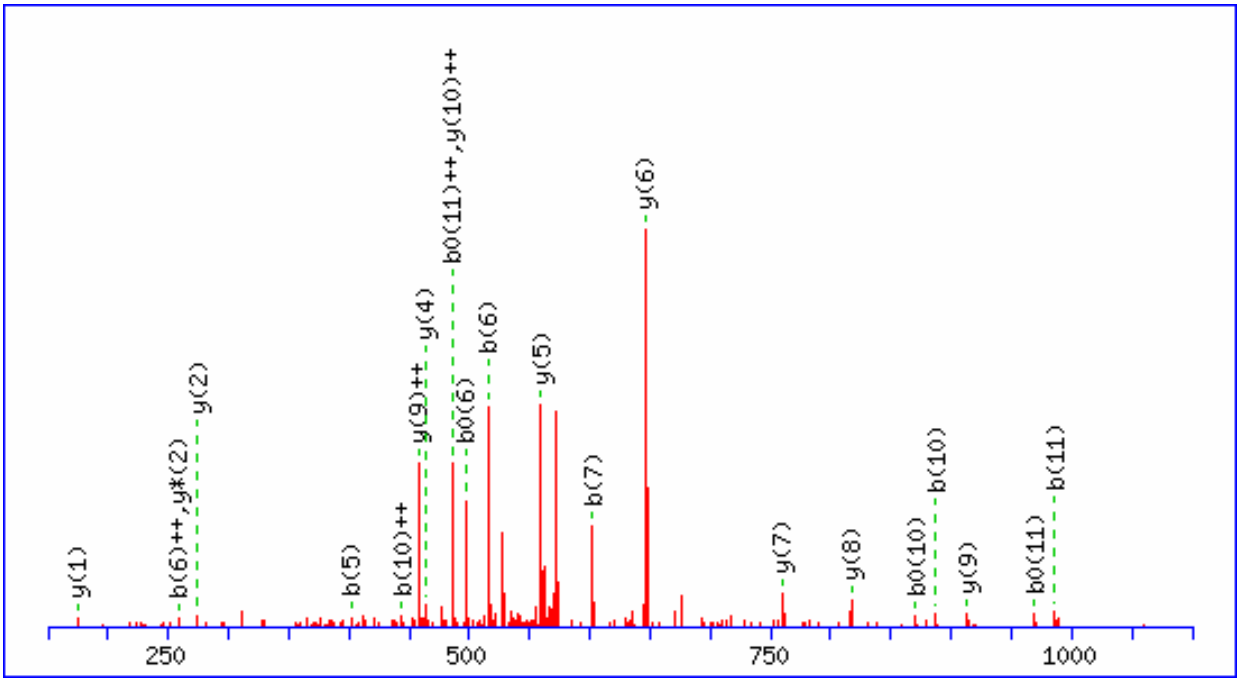
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.20	66.61					M							42
2	203.28	102.14					A	3111.26	1556.13	3094.23	1547.62	3093.25	1547.13	41
3	274.36	137.68					A	3040.18	1520.60	3023.15	1512.08	3022.17	1511.59	40
4	371.48	186.24					P	2969.10	1485.06	2952.07	1476.54	2951.09	1476.05	39
5	442.55	221.78					A	2871.99	1436.50	2854.96	1427.98	2853.97	1427.49	38
6	539.67	270.34					P	2800.91	1400.96	2783.88	1392.44	2782.90	1391.95	37
7	596.72	298.86					G	2703.80	1352.40	2686.77	1343.89	2685.78	1343.39	36
8	667.80	334.40					A	2646.75	1323.88	2629.71	1315.36	2628.73	1314.87	35
9	724.85	362.93					G	2575.67	1288.34	2558.64	1279.82	2557.65	1279.33	34
10	795.93	398.47					A	2518.62	1259.81	2501.59	1251.30	2500.60	1250.80	33
11	867.00	434.01					A	2447.54	1224.27	2430.51	1215.76	2429.52	1215.27	32
12	954.08	477.54			936.07	468.54	S	2376.46	1188.73	2359.43	1180.22	2358.45	1179.73	31
13	1011.13	506.07			993.12	497.06	G	2289.38	1145.20	2272.35	1136.68	2271.37	1136.19	30
14	1068.18	534.60			1050.17	525.59	G	2232.33	1116.67	2215.30	1108.15	2214.32	1107.66	29
15	1139.26	570.14			1121.25	561.13	A	2175.28	1088.14	2158.25	1079.63	2157.27	1079.14	28
16	1196.31	598.66			1178.30	589.65	G	2104.20	1052.61	2087.17	1044.09	2086.19	1043.60	27
17	1299.46	650.23			1281.44	641.22	C	2047.15	1024.08	2030.12	1015.56	2029.14	1015.07	26
18	1386.53	693.77			1368.52	684.76	S	1944.01	972.51	1926.98	963.99	1925.99	963.50	25
19	1443.59	722.30			1425.57	713.29	G	1856.93	928.97	1839.90	920.45	1838.92	919.96	24
20	1500.64	750.82			1482.62	741.81	G	1799.88	900.44	1782.85	891.93	1781.86	891.44	23
21	1557.69	779.35			1539.67	770.34	G	1742.83	871.92	1725.80	863.40	1724.81	862.91	22
22	1628.77	814.89			1610.75	805.88	A	1685.78	843.39	1668.75	834.88	1667.76	834.38	21
23	1685.82	843.41			1667.80	834.40	G	1614.70	807.85	1597.67	799.34	1596.68	798.85	20
24	1756.89	878.95			1738.88	869.94	A	1557.65	779.33	1540.62	770.81	1539.63	770.32	19
25	1813.95	907.48			1795.93	898.47	G	1486.57	743.79	1469.54	735.27	1468.55	734.78	18
26	1885.02	943.02			1867.01	934.01	A	1429.52	715.26	1412.49	706.75	1411.50	706.26	17
27	1942.08	971.54			1924.06	962.53	G	1358.44	679.72	1341.41	671.21	1340.43	670.72	16
28	2029.15	1015.08			2011.14	1006.07	S	1301.39	651.20	1284.36	642.68	1283.37	642.19	15
29	2086.20	1043.61			2068.19	1034.60	G	1214.31	607.66	1197.28	599.14	1196.30	598.65	14
30	2173.28	1087.14			2155.27	1078.14	S	1157.26	579.13	1140.23	570.62	1139.25	570.13	13
31	2230.33	1115.67			2212.32	1106.66	G	1070.18	535.60	1053.15	527.08	1052.17	526.59	12
32	2301.41	1151.21			2283.40	1142.20	A	1013.13	507.07	996.10	498.55	995.12	498.06	11
33	2372.49	1186.75			2354.47	1177.74	A	942.05	471.53	925.02	463.02	924.04	462.52	10
34	2429.54	1215.27			2411.52	1206.27	G	870.98	435.99	853.95	427.48	852.96	426.98	9
35	2500.62	1250.81			2482.60	1241.81	A	813.93	407.47	796.89	398.95	795.91	398.46	8
36	2557.67	1279.34			2539.65	1270.33	G	742.85	371.93	725.82	363.41	724.83	362.92	7
37	2614.72	1307.86			2596.70	1298.86	G	685.80	343.40	668.77	334.89	667.78	334.39	6
38	2770.91	1385.96	2753.88	1377.44	2752.89	1376.95	R	628.74	314.88	611.71	306.36	610.73	305.87	5
39	2884.06	1442.54	2867.03	1434.02	2866.05	1433.53	L	472.56	236.78	455.53	228.27	454.54	227.78	4
40	2981.18	1491.09	2964.15	1482.58	2963.16	1482.09	P	359.40	180.20	342.37	171.69	341.39	171.20	3
41	3068.26	1534.63	3051.23	1526.12	3050.24	1525.62	S	262.29	131.65	245.26	123.13	244.27	122.64	2
42							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FER1L3	LDLPNRPETSFLWFTNPCK	760.70	3+	87.5



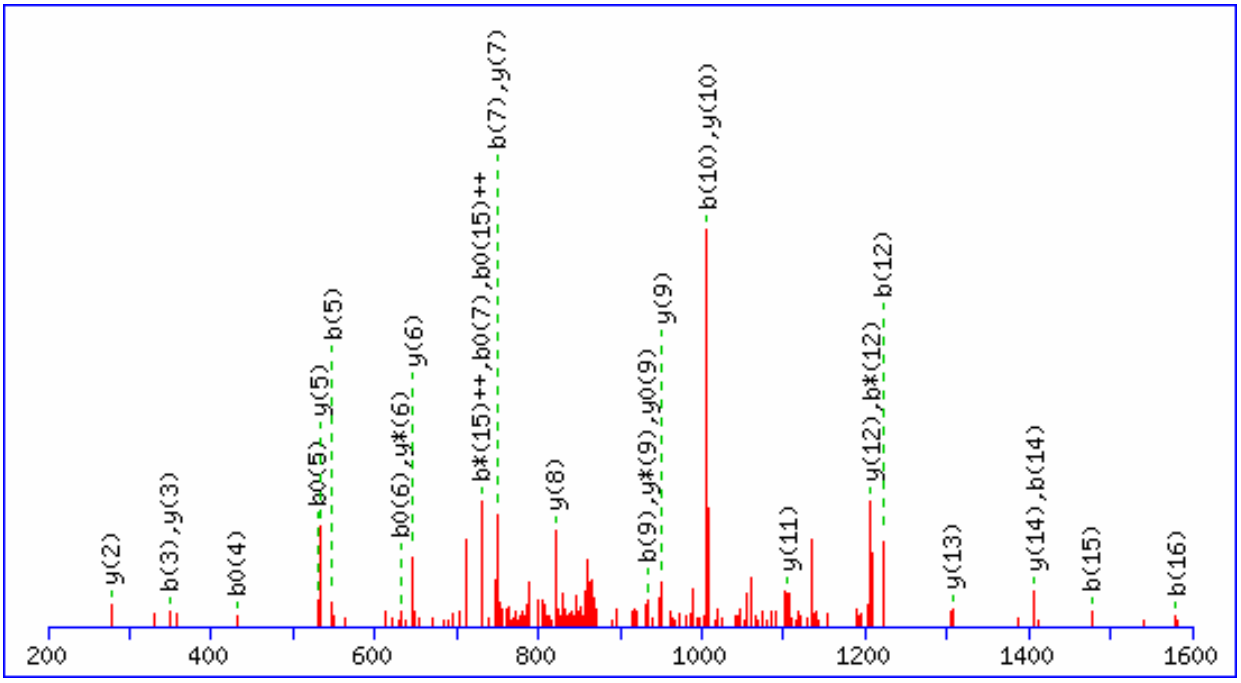
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					L							19
2	229.25	115.13			211.24	106.12	D	2166.43	1083.72	2149.40	1075.21	2148.42	1074.71	18
3	342.41	171.71			324.40	162.70	L	2051.35	1026.18	2034.32	1017.66	2033.33	1017.17	17
4	439.53	220.27			421.51	211.26	P	1938.19	969.60	1921.16	961.08	1920.17	960.59	16
5	553.63	277.32	536.60	268.80	535.61	268.31	N	1841.07	921.04	1824.04	912.53	1823.06	912.03	15
6	709.81	355.41	692.78	346.90	691.80	346.40	R	1726.97	863.99	1709.94	855.47	1708.96	854.98	14
7	806.93	403.97	789.90	395.45	788.91	394.96	P	1570.79	785.90	1553.76	777.38	1552.77	776.89	13
8	936.04	468.53	919.01	460.01	918.03	459.52	E	1473.67	737.34	1456.64	728.82	1455.66	728.33	12
9	1037.15	519.08	1020.12	510.56	1019.13	510.07	T	1344.56	672.78	1327.53	664.27	1326.54	663.77	11
10	1124.22	562.62	1107.19	554.10	1106.21	553.61	S	1243.45	622.23	1226.42	613.72	1225.44	613.22	10
11	1271.40	636.20	1254.37	627.69	1253.38	627.20	F	1156.38	578.69	1139.34	570.18	1138.36	569.68	9
12	1384.56	692.78	1367.53	684.27	1366.54	683.77	L	1009.20	505.10	992.17	496.59	991.19	496.10	8
13	1570.77	785.89	1553.74	777.37	1552.75	776.88	W	896.04	448.53	879.01	440.01	878.03	439.52	7
14	1717.94	859.47	1700.91	850.96	1699.92	850.47	F	709.83	355.42	692.80	346.91	691.82	346.41	6
15	1819.04	910.03	1802.01	901.51	1801.03	901.02	T	562.66	281.83	545.63	273.32	544.64	272.83	5
16	1933.15	967.08	1916.12	958.56	1915.13	958.07	N	461.56	231.28	444.53	222.77			4
17	2030.26	1015.63	2013.23	1007.12	2012.25	1006.63	P	347.45	174.23	330.42	165.72			3
18	2133.40	1067.21	2116.37	1058.69	2115.39	1058.20	C	250.34	125.67	233.31	117.16			2
19							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNA	CSGPGLSPGMVR	580.56	2+	61.4



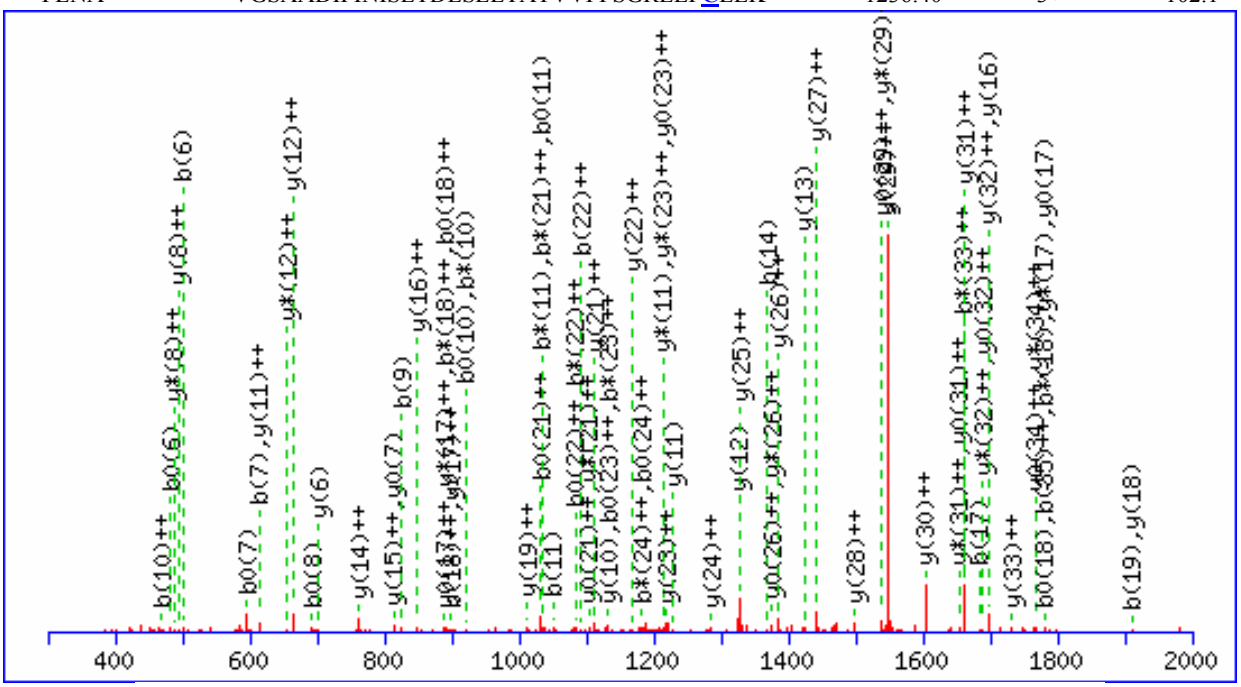
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	104.15	52.58			C							12
2	191.23	96.12	173.21	87.11	S	1058.23	529.62	1041.20	521.11	1040.22	520.61	11
3	248.28	124.64	230.26	115.64	G	971.16	486.08	954.12	477.57	953.14	477.07	10
4	345.39	173.20	327.38	164.19	P	914.10	457.56	897.07	449.04	896.09	448.55	9
5	402.45	201.73	384.43	192.72	G	816.99	409.00	799.96	400.48	798.97	399.99	8
6	515.60	258.31	497.59	249.30	L	759.94	380.47	742.91	371.96	741.92	371.47	7
7	602.68	301.84	584.67	292.84	S	646.78	323.89	629.75	315.38	628.76	314.89	6
8	699.80	350.40	681.78	341.39	P	559.70	280.36	542.67	271.84			5
9	756.85	378.93	738.83	369.92	G	462.59	231.80	445.56	223.28			4
10	888.04	444.53	870.03	435.52	M	405.54	203.27	388.51	194.76			3
11	987.17	494.09	969.16	485.08	V	274.34	137.67	257.31	129.16			2
12					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNA	SPYTVTVGQACNPSACR	877.67	2+	100.4



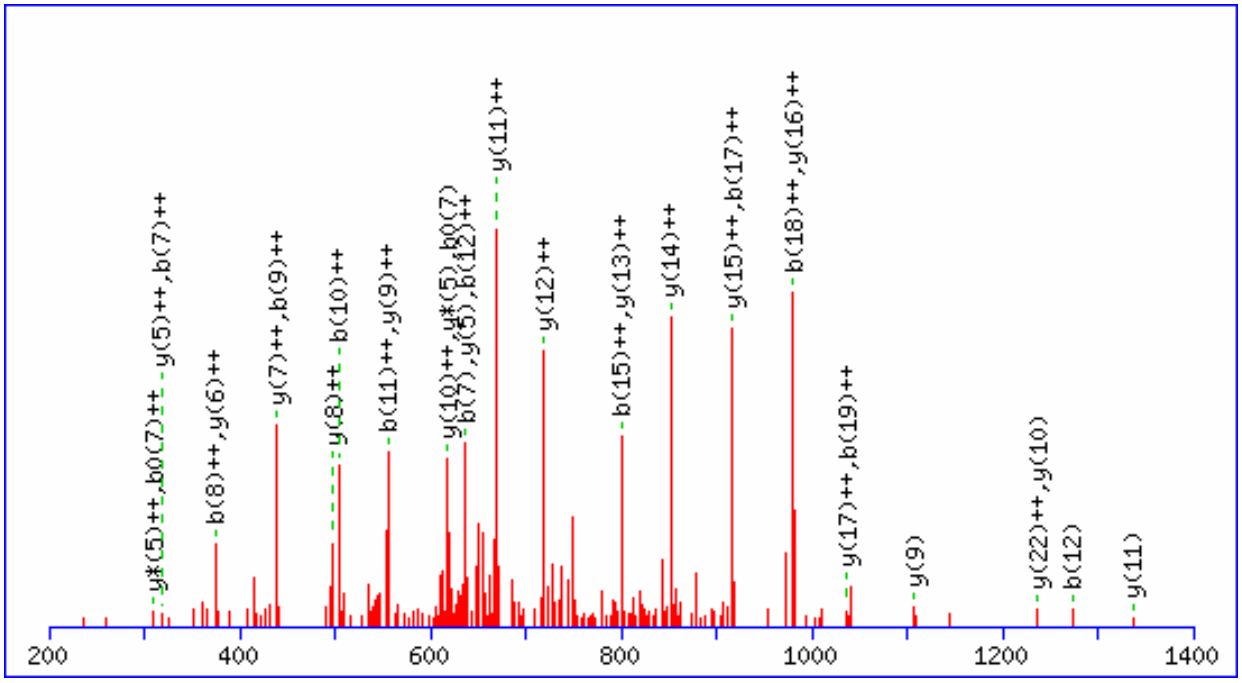
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							17
2	185.20	93.10			167.19	84.10	P	1667.88	834.45	1650.85	825.93	1649.87	825.44	16
3	348.37	174.69			330.36	165.68	Y	1570.77	785.89	1553.74	777.37	1552.75	776.88	15
4	449.48	225.24			431.46	216.24	T	1407.60	704.30	1390.57	695.79	1389.58	695.29	14
5	548.61	274.81			530.59	265.80	V	1306.49	653.75	1289.46	645.23	1288.48	644.74	13
6	649.71	325.36			631.70	316.35	T	1207.36	604.18	1190.33	595.67	1189.35	595.18	12
7	748.84	374.93			730.83	365.92	V	1106.26	553.63	1089.23	545.12	1088.24	544.62	11
8	805.90	403.45			787.88	394.44	G	1007.13	504.07	990.10	495.55	989.11	495.06	10
9	934.02	467.52	916.99	459.00	916.01	458.51	Q	950.07	475.54	933.04	467.03	932.06	466.53	9
10	1005.10	503.06	988.07	494.54	987.09	494.05	A	821.95	411.48	804.92	402.96	803.93	402.47	8
11	1108.25	554.63	1091.21	546.11	1090.23	545.62	C	750.87	375.94	733.84	367.42	732.85	366.93	7
12	1222.35	611.68	1205.32	603.16	1204.33	602.67	N	647.72	324.37	630.69	315.85	629.71	315.36	6
13	1319.46	660.24	1302.43	651.72	1301.45	651.23	P	533.62	267.32	516.59	258.80	515.61	258.31	5
14	1406.54	703.77	1389.51	695.26	1388.52	694.77	S	436.51	218.76	419.48	210.24	418.49	209.75	4
15	1477.62	739.31	1460.59	730.80	1459.60	730.31	A	349.43	175.22	332.40	166.70			3
16	1580.76	790.88	1563.73	782.37	1562.75	781.88	C	278.35	139.68	261.32	131.16			2
17							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNA	VGSAADIPINISETDLSLLTATVVPPSGREEP**C**LLK	1236.40	3+	102.1



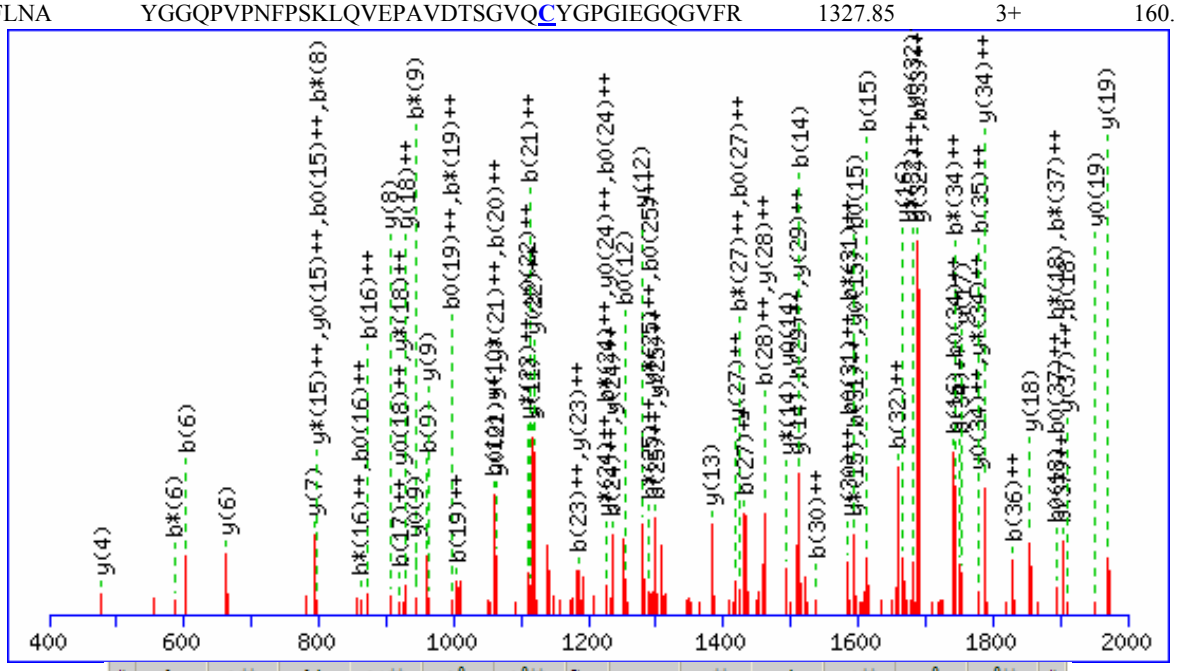
#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	100.14	50.57					V							36
2	157.19	79.10					G	3609.08	1805.05	3592.05	1796.53	3591.07	1796.04	35
3	244.27	122.64			226.25	113.63	S	3552.03	1776.52	3535.00	1768.01	3534.02	1767.51	34
4	315.35	158.18			297.33	149.17	A	3464.96	1732.98	3447.93	1724.47	3446.94	1723.97	33
5	386.42	193.72			368.41	184.71	A	3393.88	1697.44	3376.85	1688.93	3375.86	1688.44	32
6	501.51	251.26			483.50	242.25	D	3322.80	1661.90	3305.77	1653.39	3304.78	1652.90	31
7	614.67	307.84			596.65	298.83	I	3207.71	1604.36	3190.68	1595.85	3189.70	1595.35	30
8	711.78	356.40			693.77	347.39	P	3094.56	1547.78	3077.52	1539.27	3076.54	1538.77	29
9	824.94	412.97			806.93	403.97	I	2997.44	1499.22	2980.41	1490.71	2979.42	1490.22	28
10	939.04	470.03	922.01	461.51	921.03	461.02	N	2884.28	1442.65	2867.25	1434.13	2866.27	1433.64	27
11	1052.20	526.60	1035.17	518.09	1034.19	517.60	I	2770.18	1385.59	2753.15	1377.08	2752.16	1376.59	26
12	1139.28	570.14	1122.25	561.63	1121.26	561.14	S	2657.02	1329.02	2639.99	1320.50	2639.01	1320.01	25
13	1268.39	634.70	1251.36	626.19	1250.38	625.69	E	2569.94	1285.48	2552.91	1276.96	2551.93	1276.47	24
14	1369.50	685.25	1352.47	676.74	1351.48	676.24	T	2440.83	1220.92	2423.80	1212.40	2422.82	1211.91	23
15	1484.58	742.80	1467.55	734.28	1466.57	733.79	D	2339.73	1170.37	2322.70	1161.85	2321.71	1161.36	22
16	1597.74	799.37	1580.71	790.86	1579.73	790.37	L	2224.64	1112.82	2207.61	1104.31	2206.62	1103.82	21
17	1684.82	842.91	1667.79	834.40	1666.80	833.91	S	2111.48	1056.24	2094.45	1047.73	2093.47	1047.24	20
18	1797.98	899.49	1780.95	890.98	1779.96	890.48	L	2024.40	1012.71	2007.37	1004.19	2006.39	1003.70	19
19	1911.13	956.07	1894.10	947.56	1893.12	947.06	L	1911.25	956.13	1894.22	947.61	1893.23	947.12	18
20	2012.24	1006.62	1995.21	998.11	1994.22	997.62	T	1798.09	899.55	1781.06	891.03	1780.07	890.54	17
21	2083.32	1042.16	2066.29	1033.65	2065.30	1033.15	A	1696.99	849.00	1679.96	840.48	1678.97	839.99	16
22	2184.42	1092.71	2167.39	1084.20	2166.40	1083.71	T	1625.91	813.46	1608.88	804.94	1607.89	804.45	15
23	2283.55	1142.28	2266.52	1133.76	2265.54	1133.27	V	1524.80	762.91	1507.77	754.39	1506.79	753.90	14
24	2382.68	1191.84	2365.65	1183.33	2364.67	1182.84	V	1425.67	713.34	1408.64	704.83	1407.66	704.33	13
25	2479.80	1240.40	2462.77	1231.89	2461.78	1231.39	P	1326.54	663.77	1309.51	655.26	1308.53	654.77	12
26	2576.91	1288.96	2559.88	1280.44	2558.90	1279.95	P	1229.43	615.22	1212.40	606.70	1211.41	606.21	11
27	2663.99	1332.50	2646.96	1323.98	2645.97	1323.49	S	1132.31	566.66	1115.28	558.14	1114.30	557.65	10
28	2721.04	1361.02	2704.01	1352.51	2703.03	1352.02	G	1045.23	523.12	1028.20	514.61	1027.22	514.11	9
29	2877.23	1439.12	2860.20	1430.60	2859.21	1430.11	R	988.18	494.60	971.15	486.08	970.17	485.59	8
30	3006.34	1503.67	2989.31	1495.16	2988.33	1494.67	E	832.00	416.50	814.97	407.99	813.98	407.49	7
31	3135.45	1568.23	3118.42	1559.72	3117.44	1559.22	E	702.88	351.95	685.85	343.43	684.87	342.94	6
32	3232.57	1616.79	3215.54	1608.27	3214.55	1607.78	P	573.77	287.39	556.74	278.87			5
33	3335.71	1668.36	3318.68	1659.85	3317.70	1659.35	C	476.65	238.83	459.62	230.32			4
34	3448.87	1724.94	3431.84	1716.42	3430.86	1715.93	L	373.51	187.26	356.48	178.74			3
35	3562.03	1781.52	3545.00	1773.00	3544.01	1772.51	L	260.35	130.68	243.32	122.17			2
36							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNA	VHSPSGALEECYVTEIDQDKYAVR	678.60	4+	115.6



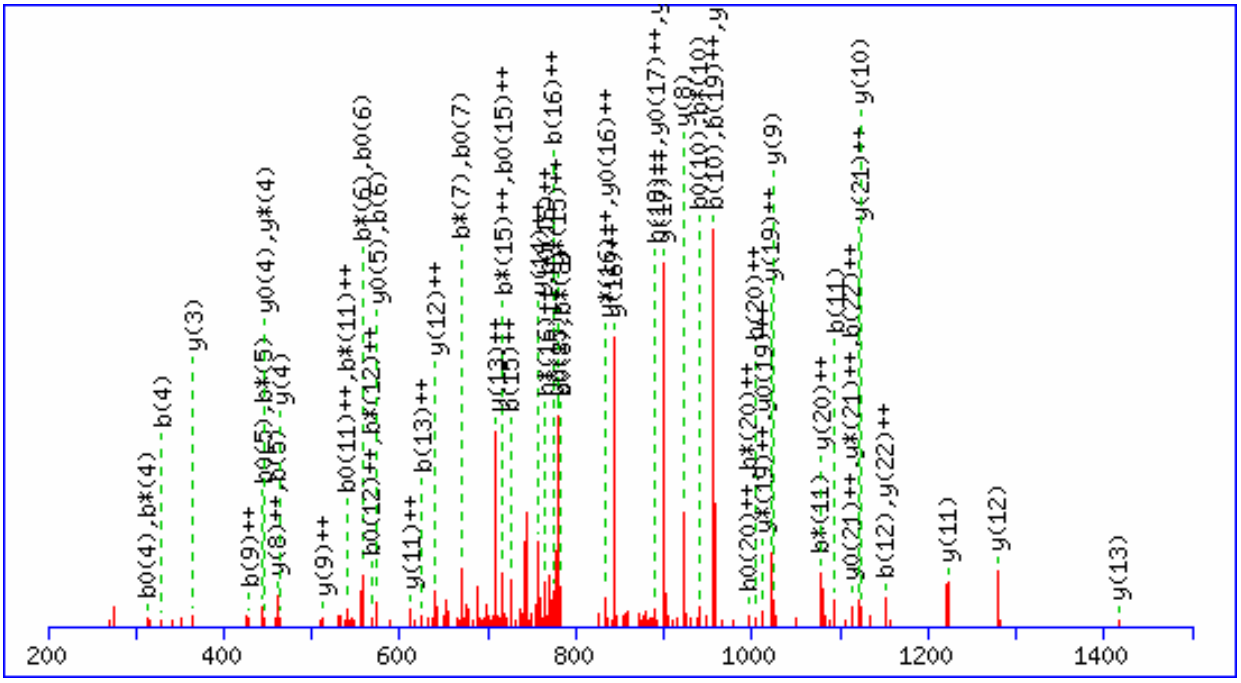
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							24
2	237.28	119.14					H	2611.81	1306.41	2594.78	1297.90	2593.80	1297.40	23
3	324.36	162.68			306.34	153.67	S	2474.67	1237.84	2457.64	1229.33	2456.66	1228.83	22
4	421.47	211.24			403.46	202.23	P	2387.60	1194.30	2370.57	1185.79	2369.58	1185.30	21
5	508.55	254.78			490.53	245.77	S	2290.48	1145.75	2273.45	1137.23	2272.47	1136.74	20
6	565.60	283.30			547.58	274.30	G	2203.41	1102.21	2186.37	1093.69	2185.39	1093.20	19
7	636.68	318.84			618.66	309.83	A	2146.35	1073.68	2129.32	1065.17	2128.34	1064.67	18
8	749.83	375.42			731.82	366.41	L	2075.28	1038.14	2058.25	1029.63	2057.26	1029.13	17
9	878.95	439.98			860.93	430.97	E	1962.12	981.56	1945.09	973.05	1944.10	972.56	16
10	1008.06	504.54			990.05	495.53	E	1833.00	917.01	1815.97	908.49	1814.99	908.00	15
11	1111.21	556.11			1093.19	547.10	C	1703.89	852.45	1686.86	843.93	1685.88	843.44	14
12	1274.38	637.69			1256.36	628.69	Y	1600.75	800.88	1583.72	792.36	1582.73	791.87	13
13	1373.51	687.26			1355.49	678.25	V	1437.57	719.29	1420.54	710.78	1419.56	710.28	12
14	1474.61	737.81			1456.60	728.80	T	1338.44	669.73	1321.41	661.21	1320.43	660.72	11
15	1603.73	802.37			1585.71	793.36	E	1237.34	619.17	1220.31	610.66	1219.32	610.17	10
16	1716.89	858.95			1698.87	849.94	I	1108.23	554.62	1091.19	546.10	1090.21	545.61	9
17	1831.97	916.49			1813.96	907.48	D	995.07	498.04	978.04	489.52	977.05	489.03	8
18	1960.10	980.56	1943.07	972.04	1942.09	971.55	Q	879.98	440.49	862.95	431.98	861.96	431.49	7
19	2075.19	1038.10	2058.16	1029.58	2057.17	1029.09	D	751.85	376.43	734.82	367.91	733.84	367.42	6
20	2203.36	1102.18	2186.33	1093.67	2185.35	1093.18	K	636.76	318.89	619.73	310.37			5
21	2366.54	1183.77	2349.50	1175.26	2348.52	1174.76	Y	508.59	254.80	491.56	246.28			4
22	2437.61	1219.31	2420.58	1210.80	2419.60	1210.30	A	345.42	173.21	328.39	164.70			3
23	2536.74	1268.88	2519.71	1260.36	2518.73	1259.87	V	274.34	137.67	257.31	129.16			2
24							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNA	YGGQPVPNFPSKLQVEPAVDTSGVQCYGPGIEGQGVFR	1327.85	3+	160.1



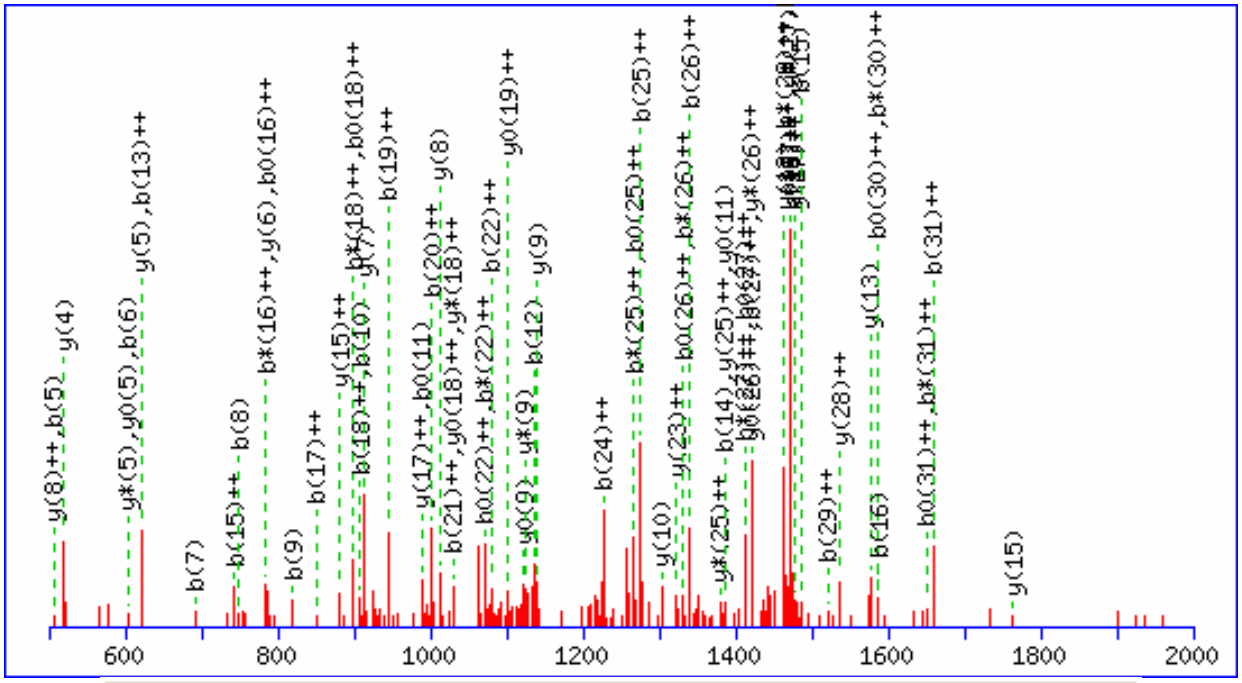
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	164.18	82.59					Y							38
2	221.23	111.12					G	3817.22	1909.12	3800.19	1900.60	3799.21	1900.11	37
3	278.28	139.65					G	3760.17	1880.59	3743.14	1872.07	3742.16	1871.58	36
4	406.41	203.71	389.38	195.20			Q	3703.12	1852.06	3686.09	1843.55	3685.10	1843.06	35
5	503.53	252.27	486.50	243.75			P	3574.99	1788.00	3557.96	1779.48	3556.98	1778.99	34
6	602.66	301.83	585.63	293.32			V	3477.88	1739.44	3460.84	1730.93	3459.86	1730.43	33
7	699.77	350.39	682.74	341.88			P	3378.74	1689.88	3361.71	1681.36	3360.73	1680.87	32
8	813.88	407.44	796.85	398.93			N	3281.63	1641.32	3264.60	1632.80	3263.61	1632.31	31
9	961.05	481.03	944.02	472.51			F	3167.53	1584.27	3150.50	1575.75	3149.51	1575.26	30
10	1058.17	529.59	1041.14	521.07			P	3020.35	1510.68	3003.32	1502.16	3002.34	1501.67	29
11	1145.24	573.13	1128.21	564.61	1127.23	564.12	S	2923.24	1462.12	2906.21	1453.61	2905.22	1453.11	28
12	1273.42	637.21	1256.39	628.70	1255.40	628.20	K	2836.16	1418.58	2819.13	1410.07	2818.14	1409.58	27
13	1386.57	693.79	1369.54	685.28	1368.56	684.78	L	2707.99	1354.50	2690.96	1345.98	2689.97	1345.49	26
14	1514.70	757.86	1497.67	749.34	1496.69	748.85	Q	2594.83	1297.92	2577.80	1289.40	2576.81	1288.91	25
15	1613.83	807.42	1596.80	798.91	1595.82	798.41	V	2466.70	1233.85	2449.67	1225.34	2448.69	1224.85	24
16	1742.95	871.98	1725.92	863.46	1724.93	862.97	E	2367.57	1184.29	2350.54	1175.77	2349.55	1175.28	23
17	1840.06	920.54	1823.03	912.02	1822.05	911.53	P	2238.46	1119.73	2221.43	1111.22	2220.44	1110.72	22
18	1911.14	956.07	1894.11	947.56	1893.13	947.07	A	2141.34	1071.17	2124.31	1062.66	2123.33	1062.17	21
19	2010.27	1005.64	1993.24	997.12	1992.26	996.63	V	2070.26	1035.64	2053.23	1027.12	2052.25	1026.63	20
20	2125.36	1063.18	2108.33	1054.67	2107.34	1054.18	D	1971.13	986.07	1954.10	977.55	1953.12	977.06	19
21	2226.46	1113.74	2209.43	1105.22	2208.45	1104.73	T	1856.04	928.53	1839.01	920.01	1838.03	919.52	18
22	2313.54	1157.27	2296.51	1148.76	2295.53	1148.27	S	1754.94	877.97	1737.91	869.46	1736.92	868.97	17
23	2370.59	1185.80	2353.56	1177.28	2352.58	1176.79	G	1667.86	834.44	1650.83	825.92	1649.85	825.43	16
24	2469.72	1235.37	2452.69	1226.85	2451.71	1226.36	V	1610.81	805.91	1593.78	797.39	1592.80	796.90	15
25	2597.85	1299.43	2580.82	1290.91	2579.84	1290.42	Q	1511.68	756.34	1494.65	747.83	1493.67	747.34	14
26	2701.00	1351.00	2683.96	1342.49	2682.98	1341.99	C	1383.55	692.28	1366.52	683.76	1365.54	683.27	13
27	2864.17	1432.59	2847.14	1424.07	2846.15	1423.58	Y	1280.41	640.71	1263.38	632.19	1262.39	631.70	12
28	2921.22	1461.11	2904.19	1452.60	2903.20	1452.11	G	1117.24	559.12	1100.20	550.61	1099.22	550.11	11
29	3018.33	1509.67	3001.30	1501.16	3000.32	1500.66	P	1060.18	530.60	1043.15	522.08	1042.17	521.59	10
30	3075.39	1538.20	3058.36	1529.68	3057.37	1529.19	G	963.07	482.04	946.04	473.52	945.05	473.03	9
31	3188.54	1594.78	3171.51	1586.26	3170.53	1585.77	I	906.02	453.51	888.99	445.00	888.00	444.50	8
32	3317.66	1659.33	3300.63	1650.82	3299.64	1650.33	E	792.86	396.93	775.83	388.42	774.84	387.93	7
33	3374.71	1687.86	3357.68	1679.34	3356.69	1678.85	G	663.75	332.38	646.72	323.86			6
34	3502.84	1751.92	3485.81	1743.41	3484.82	1742.92	Q	606.69	303.85	589.66	295.34			5
35	3559.89	1780.45	3542.86	1771.93	3541.87	1771.44	G	478.57	239.79	461.53	231.27			4
36	3659.02	1830.01	3641.99	1821.50	3641.01	1821.01	V	421.51	211.26	404.48	202.75			3
37	3806.19	1903.60	3789.16	1895.09	3788.18	1894.59	F	322.38	161.70	305.35	153.18			2
38							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	AGSNMLLIGVHGPTTPCEEVSMK	791.82	3+	96.1



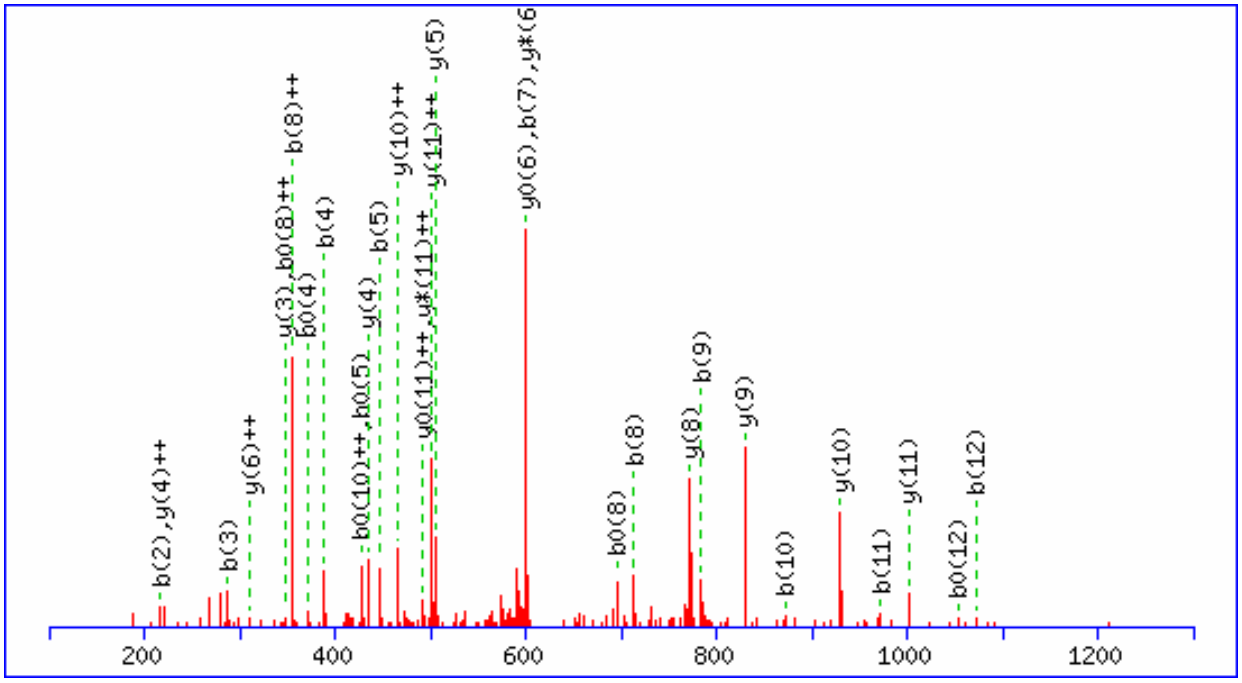
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							23
2	129.14	65.07					G	2301.68	1151.35	2284.65	1142.83	2283.67	1142.34	22
3	216.21	108.61			198.20	99.60	S	2244.63	1122.82	2227.60	1114.30	2226.62	1113.81	21
4	330.32	165.66	313.29	157.15	312.30	156.65	N	2157.55	1079.28	2140.52	1070.77	2139.54	1070.27	20
5	461.51	231.26	444.48	222.75	443.50	222.25	M	2043.45	1022.23	2026.42	1013.71	2025.44	1013.22	19
6	574.67	287.84	557.64	279.32	556.66	278.83	L	1912.25	956.63	1895.22	948.12	1894.24	947.62	18
7	687.83	344.42	670.80	335.90	669.81	335.41	L	1799.10	900.05	1782.07	891.54	1781.08	891.04	17
8	800.99	401.00	783.96	392.48	782.97	391.99	I	1685.94	843.47	1668.91	834.96	1667.92	834.47	16
9	858.04	429.52	841.01	421.01	840.02	420.51	G	1572.78	786.90	1555.75	778.38	1554.77	777.89	15
10	957.17	479.09	940.14	470.57	939.15	470.08	V	1515.73	758.37	1498.70	749.85	1497.72	749.36	14
11	1094.31	547.66	1077.28	539.14	1076.29	538.65	H	1416.60	708.80	1399.57	700.29	1398.58	699.80	13
12	1151.36	576.18	1134.33	567.67	1133.34	567.18	G	1279.46	640.23	1262.43	631.72	1261.45	631.23	12
13	1248.47	624.74	1231.44	616.23	1230.46	615.73	P	1222.41	611.71	1205.38	603.19	1204.39	602.70	11
14	1349.58	675.29	1332.55	666.78	1331.56	666.29	T	1125.29	563.15	1108.26	554.64	1107.28	554.14	10
15	1450.68	725.84	1433.65	717.33	1432.67	716.84	T	1024.19	512.60	1007.16	504.08	1006.17	503.59	9
16	1547.80	774.40	1530.77	765.89	1529.78	765.39	P	923.09	462.05	906.06	453.53	905.07	453.04	8
17	1650.94	825.97	1633.91	817.46	1632.92	816.97	C	825.97	413.49	808.94	404.97	807.96	404.48	7
18	1780.05	890.53	1763.02	882.02	1762.04	881.52	E	722.83	361.92	705.80	353.40	704.81	352.91	6
19	1909.17	955.09	1892.14	946.57	1891.15	946.08	E	593.71	297.36	576.68	288.85	575.70	288.35	5
20	2008.30	1004.65	1991.27	996.14	1990.28	995.65	V	464.60	232.80	447.57	224.29	446.58	223.80	4
21	2095.38	1048.19	2078.35	1039.68	2077.36	1039.18	S	365.47	183.24	348.44	174.72	347.45	174.23	3
22	2226.57	1113.79	2209.54	1105.27	2208.56	1104.78	M	278.39	139.70	261.36	131.18			2
23							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	AHIANPSGASTECFVTDNADGTYQVEYTPFEK	1155.23	3+	109.8



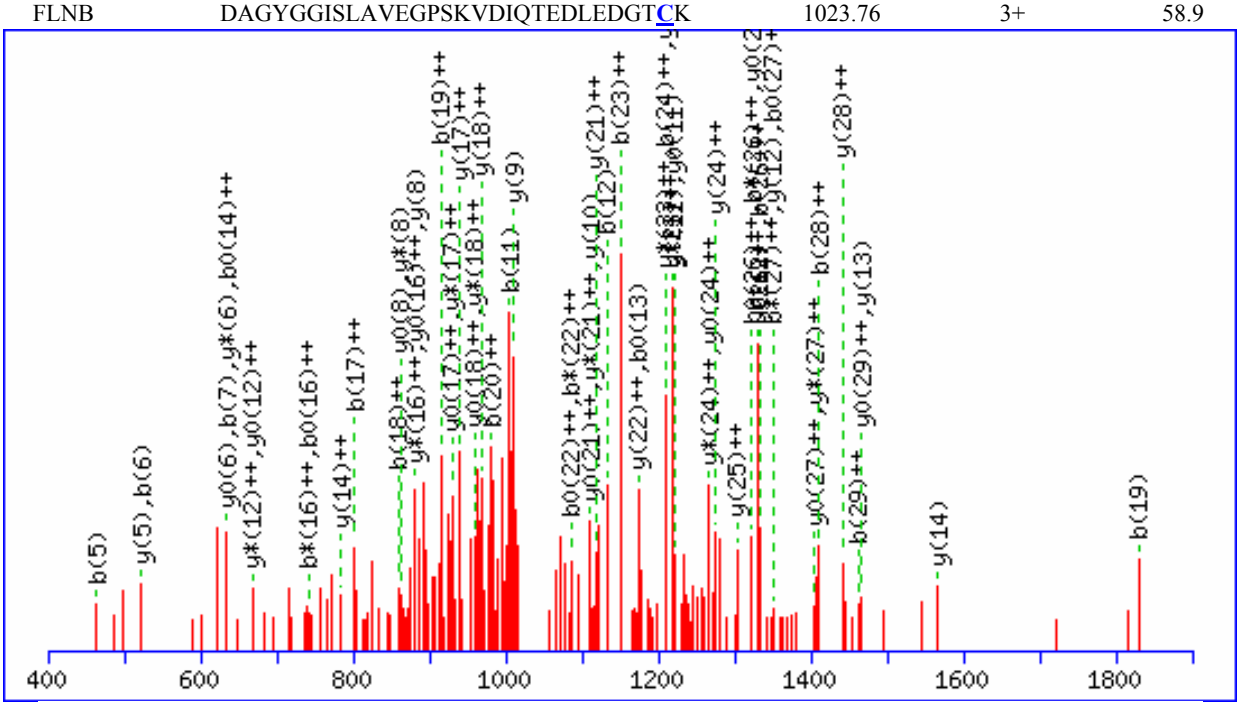
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	72.09	36.55					A							32
2	209.23	105.12					H	3393.58	1697.29	3376.55	1688.78	3375.56	1688.29	31
3	322.38	161.70					I	3256.44	1628.72	3239.41	1620.21	3238.43	1619.72	30
4	393.46	197.23					A	3143.28	1572.15	3126.25	1563.63	3125.27	1563.14	29
5	507.56	254.29	490.53	245.77			N	3072.21	1536.61	3055.17	1528.09	3054.19	1527.60	28
6	604.68	302.84	587.65	294.33			P	2958.10	1479.56	2941.07	1471.04	2940.09	1470.55	27
7	691.76	346.38	674.73	337.87	673.74	337.37	S	2860.99	1431.00	2843.96	1422.48	2842.97	1421.99	26
8	748.81	374.91	731.78	366.39	730.79	365.90	G	2773.91	1387.46	2756.88	1378.94	2755.89	1378.45	25
9	819.88	410.45	802.85	401.93	801.87	401.44	A	2716.86	1358.93	2699.83	1350.42	2698.84	1349.93	24
10	906.96	453.99	889.93	445.47	888.95	444.98	S	2645.78	1323.39	2628.75	1314.88	2627.77	1314.39	23
11	1008.07	504.54	991.04	496.02	990.05	495.53	T	2558.70	1279.86	2541.67	1271.34	2540.69	1270.85	22
12	1137.18	569.09	1120.15	560.58	1119.16	560.09	E	2457.60	1229.30	2440.57	1220.79	2439.58	1220.30	21
13	1240.32	620.67	1223.29	612.15	1222.31	611.66	C	2328.49	1164.75	2311.46	1156.23	2310.47	1155.74	20
14	1387.50	694.25	1370.47	685.74	1369.48	685.24	F	2225.34	1113.18	2208.31	1104.66	2207.33	1104.17	19
15	1486.63	743.82	1469.60	735.30	1468.61	734.81	V	2078.17	1039.59	2061.14	1031.07	2060.15	1030.58	18
16	1587.73	794.37	1570.70	785.85	1569.72	785.36	T	1979.04	990.02	1962.01	981.51	1961.02	981.02	17
17	1702.82	851.91	1685.79	843.40	1684.80	842.91	D	1877.93	939.47	1860.90	930.96	1859.92	930.46	16
18	1816.92	908.96	1799.89	900.45	1798.91	899.96	N	1762.85	881.93	1745.82	873.41	1744.83	872.92	15
19	1888.00	944.50	1870.97	935.99	1869.98	935.50	A	1648.74	824.88	1631.71	816.36	1630.73	815.87	14
20	2003.09	1002.05	1986.06	993.53	1985.07	993.04	D	1577.67	789.34	1560.64	780.82	1559.65	780.33	13
21	2060.14	1030.57	2043.11	1022.06	2042.12	1021.57	G	1462.58	731.79	1445.55	723.28	1444.56	722.79	12
22	2161.24	1081.13	2144.21	1072.61	2143.23	1072.12	T	1405.53	703.27	1388.50	694.75	1387.51	694.26	11
23	2324.42	1162.71	2307.39	1154.20	2306.40	1153.70	Y	1304.42	652.72	1287.39	644.20	1286.41	643.71	10
24	2452.54	1226.78	2435.51	1218.26	2434.53	1217.77	Q	1141.25	571.13	1124.22	562.61	1123.23	562.12	9
25	2551.68	1276.34	2534.65	1267.83	2533.66	1267.33	V	1013.12	507.06	996.09	498.55	995.11	498.06	8
26	2680.79	1340.90	2663.76	1332.38	2662.77	1331.89	E	913.99	457.50	896.96	448.98	895.97	448.49	7
27	2843.96	1422.49	2826.93	1413.97	2825.95	1413.48	Y	784.88	392.94	767.85	384.43	766.86	383.93	6
28	2945.07	1473.04	2928.04	1464.52	2927.05	1464.03	T	621.70	311.36	604.67	302.84	603.69	302.35	5
29	3042.18	1521.60	3025.15	1513.08	3024.17	1512.59	P	520.60	260.80	503.57	252.29	502.58	251.80	4
30	3189.36	1595.18	3172.33	1586.67	3171.34	1586.17	F	423.48	212.25	406.45	203.73	405.47	203.24	3
31	3318.47	1659.74	3301.44	1651.22	3300.46	1650.73	E	276.31	138.66	259.28	130.14	258.29	129.65	2
32							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	CLATGPGIASTVK	610.12	2+	79.3



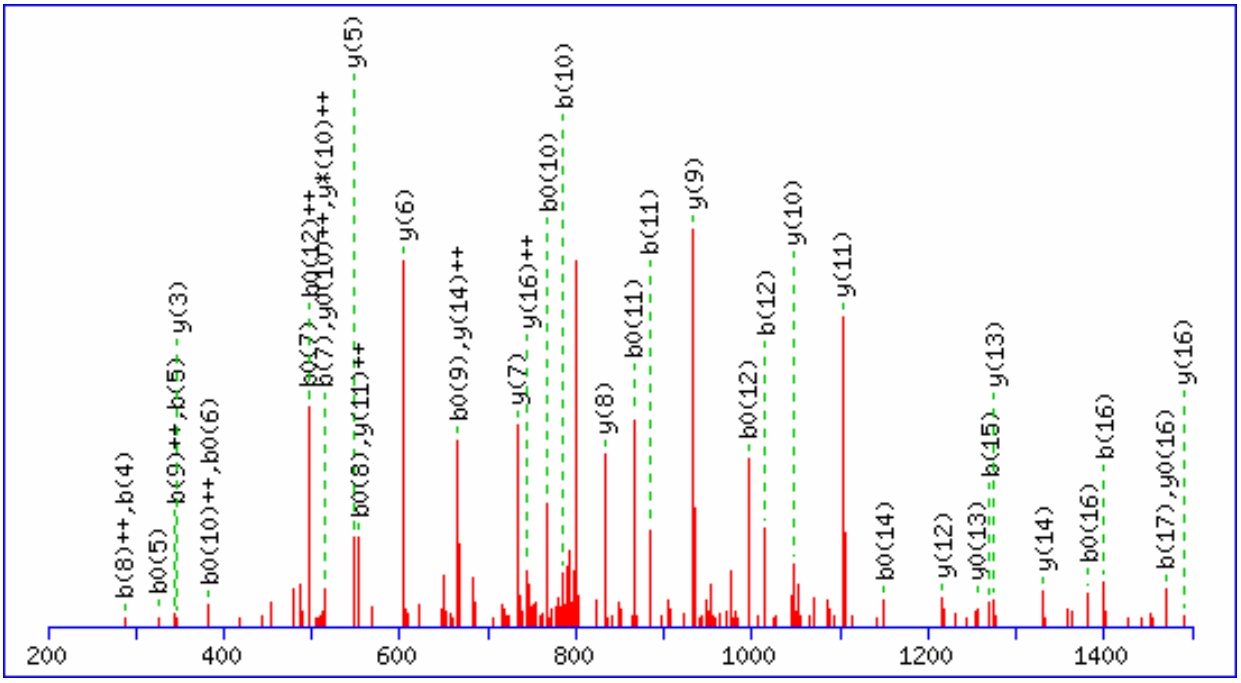
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	104.15	52.58			C							13
2	217.31	109.16			L	1115.30	558.15	1098.27	549.64	1097.29	549.15	12
3	288.39	144.70			A	1002.14	501.58	985.11	493.06	984.13	492.57	11
4	389.49	195.25	371.47	186.24	T	931.07	466.04	914.03	457.52	913.05	457.03	10
5	446.54	223.77	428.53	214.77	G	829.96	415.48	812.93	406.97	811.95	406.48	9
6	543.66	272.33	525.64	263.32	P	772.91	386.96	755.88	378.44	754.89	377.95	8
7	600.71	300.86	582.69	291.85	G	675.79	338.40	658.76	329.89	657.78	329.39	7
8	713.87	357.44	695.85	348.43	I	618.74	309.88	601.71	301.36	600.73	300.87	6
9	784.94	392.98	766.93	383.97	A	505.59	253.30	488.56	244.78	487.57	244.29	5
10	872.02	436.51	854.01	427.51	S	434.51	217.76	417.48	209.24	416.49	208.75	4
11	973.12	487.07	955.11	478.06	T	347.43	174.22	330.40	165.70	329.42	165.21	3
12	1072.26	536.63	1054.24	527.62	V	246.33	123.67	229.30	115.15			2
13					K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	DAGYGGISLAVEGPSKVDIQTEDLEDGTCK	1023.76	3+	58.9



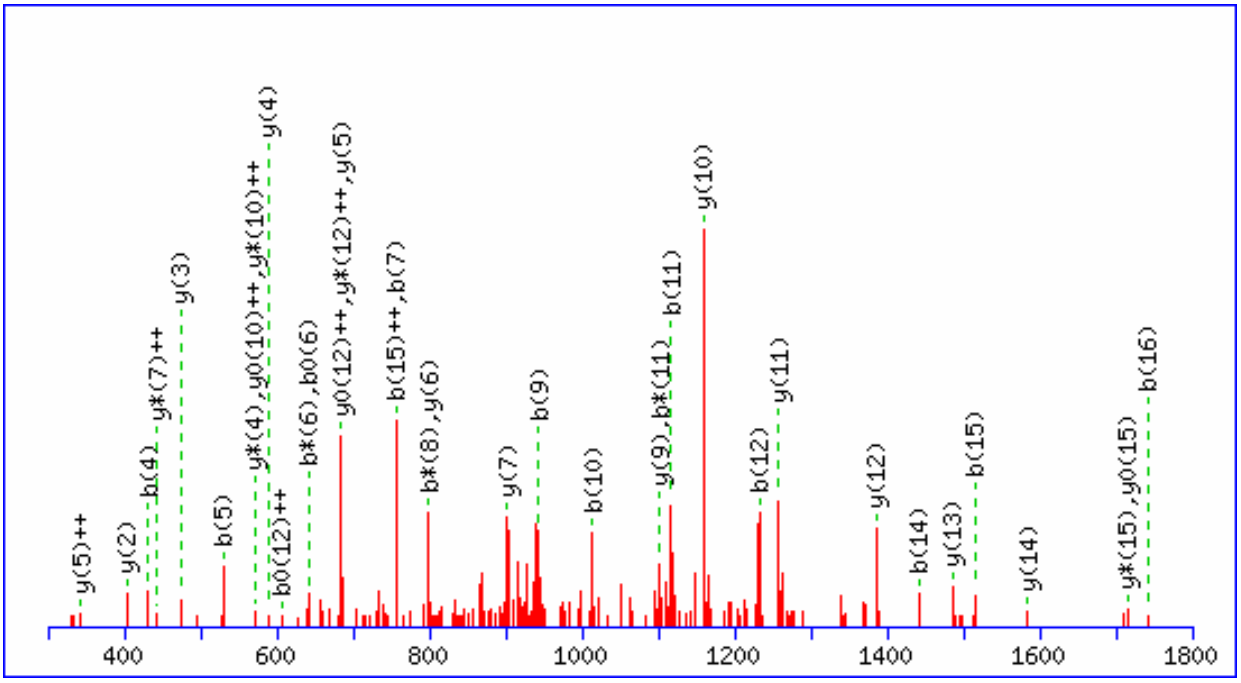
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.10	58.55			98.08	49.54	D							30
2	187.17	94.09			169.16	85.08	A	2954.20	1477.60	2937.17	1469.09	2936.18	1468.60	29
3	244.22	122.62			226.21	113.61	G	2883.12	1442.06	2866.09	1433.55	2865.11	1433.06	28
4	407.40	204.20			389.38	195.20	Y	2826.07	1413.54	2809.04	1405.02	2808.06	1404.53	27
5	464.45	232.73			446.43	223.72	G	2662.90	1331.95	2645.87	1323.44	2644.88	1322.95	26
6	521.50	261.25			503.49	252.25	G	2605.85	1303.43	2588.82	1294.91	2587.83	1294.42	25
7	634.66	317.83			616.64	308.83	I	2548.79	1274.90	2531.76	1266.39	2530.78	1265.89	24
8	721.74	361.37			703.72	352.36	S	2435.64	1218.32	2418.61	1209.81	2417.62	1209.31	23
9	834.89	417.95			816.88	408.94	L	2348.56	1174.78	2331.53	1166.27	2330.54	1165.78	22
10	905.97	453.49			887.96	444.48	A	2235.40	1118.21	2218.37	1109.69	2217.39	1109.20	21
11	1005.10	503.05			987.09	494.05	V	2164.32	1082.67	2147.29	1074.15	2146.31	1073.66	20
12	1134.22	567.61			1116.20	558.60	E	2065.19	1033.10	2048.16	1024.59	2047.18	1024.09	19
13	1191.27	596.14			1173.25	587.13	G	1936.08	968.54	1919.05	960.03	1918.06	959.54	18
14	1288.38	644.70			1270.37	635.69	P	1879.03	940.02	1862.00	931.50	1861.01	931.01	17
15	1375.46	688.23			1357.44	679.23	S	1781.91	891.46	1764.88	882.95	1763.90	882.45	16
16	1503.63	752.32	1486.60	743.80	1485.62	743.31	K	1694.84	847.92	1677.80	839.41	1676.82	838.91	15
17	1602.76	801.89	1585.73	793.37	1584.75	792.88	V	1566.66	783.84	1549.63	775.32	1548.65	774.83	14
18	1717.85	859.43	1700.82	850.91	1699.84	850.42	D	1467.53	734.27	1450.50	725.75	1449.52	725.26	13
19	1831.01	916.01	1813.98	907.49	1812.99	907.00	I	1352.44	676.73	1335.41	668.21	1334.43	667.72	12
20	1959.14	980.07	1942.11	971.56	1941.12	971.06	Q	1239.29	620.15	1222.26	611.63	1221.27	611.14	11
21	2060.24	1030.62	2043.21	1022.11	2042.23	1021.62	T	1111.16	556.08	1094.13	547.57	1093.14	547.08	10
22	2189.36	1095.18	2172.32	1086.67	2171.34	1086.17	E	1010.05	505.53	993.02	497.02	992.04	496.52	9
23	2304.44	1152.73	2287.41	1144.21	2286.43	1143.72	D	880.94	440.97	863.91	432.46	862.92	431.97	8
24	2417.60	1209.30	2400.57	1200.79	2399.58	1200.30	L	765.85	383.43	748.82	374.92	747.84	374.42	7
25	2546.71	1273.86	2529.68	1265.35	2528.70	1264.85	E	652.70	326.85	635.66	318.34	634.68	317.84	6
26	2661.80	1331.40	2644.77	1322.89	2643.79	1322.40	D	523.58	262.29	506.55	253.78	505.57	253.29	5
27	2718.85	1359.93	2701.82	1351.42	2700.84	1350.92	G	408.49	204.75	391.46	196.24	390.48	195.74	4
28	2819.96	1410.48	2802.93	1401.97	2801.94	1401.47	T	351.44	176.23	334.41	167.71	333.43	167.22	3
29	2923.10	1462.05	2906.07	1453.54	2905.08	1453.05	C	250.34	125.67	233.31	117.16			2
30							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	GAGTGGLGLTVEGPCEAK	809.68	2+	89.6



#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.06	29.53			G							18
2	129.14	65.07			A	1560.75	780.88	1543.72	772.36	1542.73	771.87	17
3	186.19	93.60			G	1489.67	745.34	1472.64	736.82	1471.65	736.33	16
4	287.29	144.15	269.28	135.14	T	1432.62	716.81	1415.59	708.30	1414.60	707.81	15
5	344.34	172.68	326.33	163.67	G	1331.51	666.26	1314.48	657.75	1313.50	657.25	14
6	401.39	201.20	383.38	192.19	G	1274.46	637.74	1257.43	629.22	1256.45	628.73	13
7	514.55	257.78	496.54	248.77	L	1217.41	609.21	1200.38	600.69	1199.40	600.20	12
8	571.60	286.31	553.59	277.30	G	1104.25	552.63	1087.22	544.12	1086.24	543.62	11
9	684.76	342.88	666.75	333.88	L	1047.20	524.11	1030.17	515.59	1029.19	515.10	10
10	785.87	393.44	767.85	384.43	T	934.05	467.53	917.02	459.01	916.03	458.52	9
11	885.00	443.00	866.98	433.99	V	832.94	416.97	815.91	408.46	814.93	407.97	8
12	1014.11	507.56	996.10	498.55	E	733.81	367.41	716.78	358.89	715.80	358.40	7
13	1071.16	536.08	1053.15	527.08	G	604.70	302.85	587.67	294.34	586.68	293.84	6
14	1168.28	584.64	1150.26	575.63	P	547.65	274.33	530.62	265.81	529.63	265.32	5
15	1271.42	636.21	1253.40	627.21	C	450.53	225.77	433.50	217.25	432.52	216.76	4
16	1400.53	700.77	1382.52	691.76	E	347.39	174.20	330.36	165.68	329.37	165.19	3
17	1471.61	736.31	1453.60	727.30	A	218.27	109.64	201.24	101.13			2
18					K	147.20	74.10	130.16	65.59			1

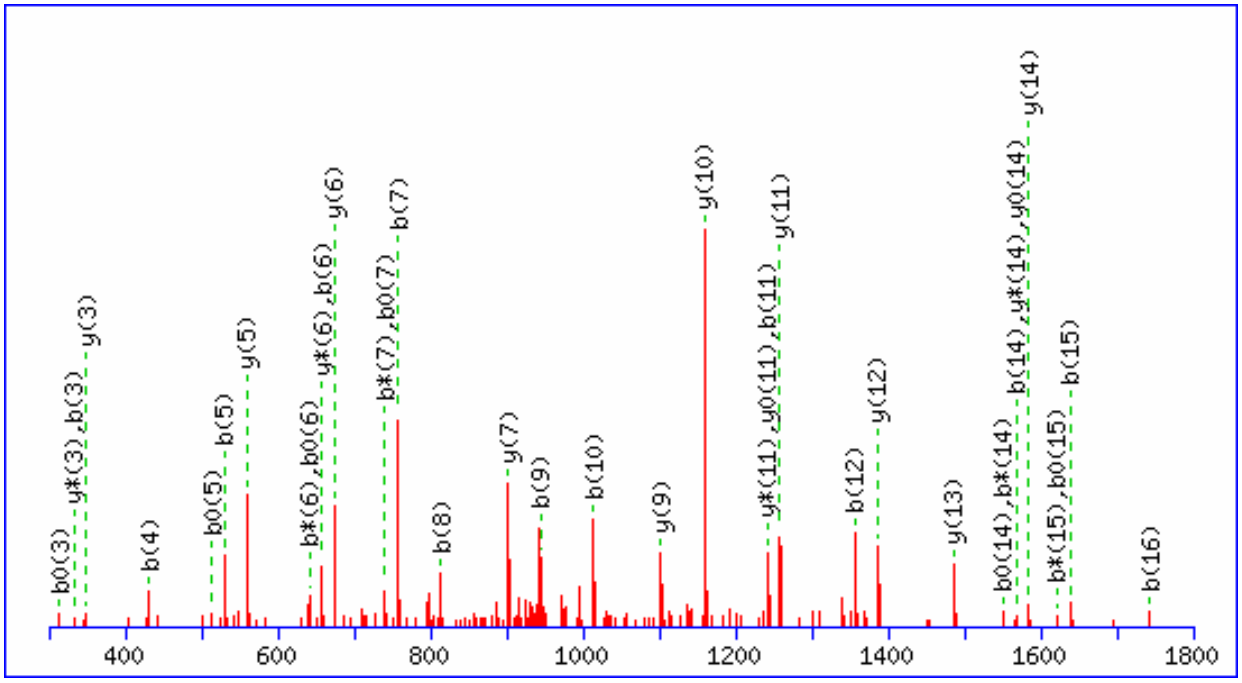
Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	SPFVVQVGEA**C**NPNA**C**R	959.11	2+	106.3



C16 : NEM (C)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							17
2	185.20	93.10			167.19	84.10	P	1830.07	915.54	1813.04	907.03	1812.06	906.53	16
3	332.37	166.69			314.36	157.68	F	1732.96	866.98	1715.93	858.47	1714.94	857.98	15
4	431.51	216.26			413.49	207.25	V	1585.78	793.40	1568.75	784.88	1567.77	784.39	14
5	530.64	265.82			512.62	256.81	V	1486.65	743.83	1469.62	735.32	1468.64	734.82	13
6	658.77	329.89	641.74	321.37	640.75	320.88	Q	1387.52	694.26	1370.49	685.75	1369.51	685.26	12
7	757.90	379.45	740.87	370.94	739.88	370.44	V	1259.39	630.20	1242.36	621.69	1241.38	621.19	11
8	814.95	407.98	797.92	399.46	796.93	398.97	G	1160.26	580.63	1143.23	572.12	1142.25	571.63	10
9	944.06	472.54	927.03	464.02	926.05	463.53	E	1103.21	552.11	1086.18	543.59	1085.19	543.10	9
10	1015.14	508.07	998.11	499.56	997.12	499.07	A	974.10	487.55	957.07	479.04			8
11	1118.28	559.65	1101.25	551.13	1100.27	550.64	C	903.02	452.01	885.99	443.50			7
12	1232.39	616.70	1215.36	608.18	1214.37	607.69	N	799.88	400.44	782.84	391.93			6
13	1329.50	665.25	1312.47	656.74	1311.49	656.25	P	685.77	343.39	668.74	334.88			5
14	1443.60	722.31	1426.57	713.79	1425.59	713.30	N	588.66	294.83	571.63	286.32			4
15	1514.68	757.84	1497.65	749.33	1496.67	748.84	A	474.56	237.78	457.52	229.27			3
16	1742.95	871.98	1725.92	863.46	1724.93	862.97	C	403.48	202.24	386.45	193.73			2
17							R	175.21	88.11	158.18	79.59			1

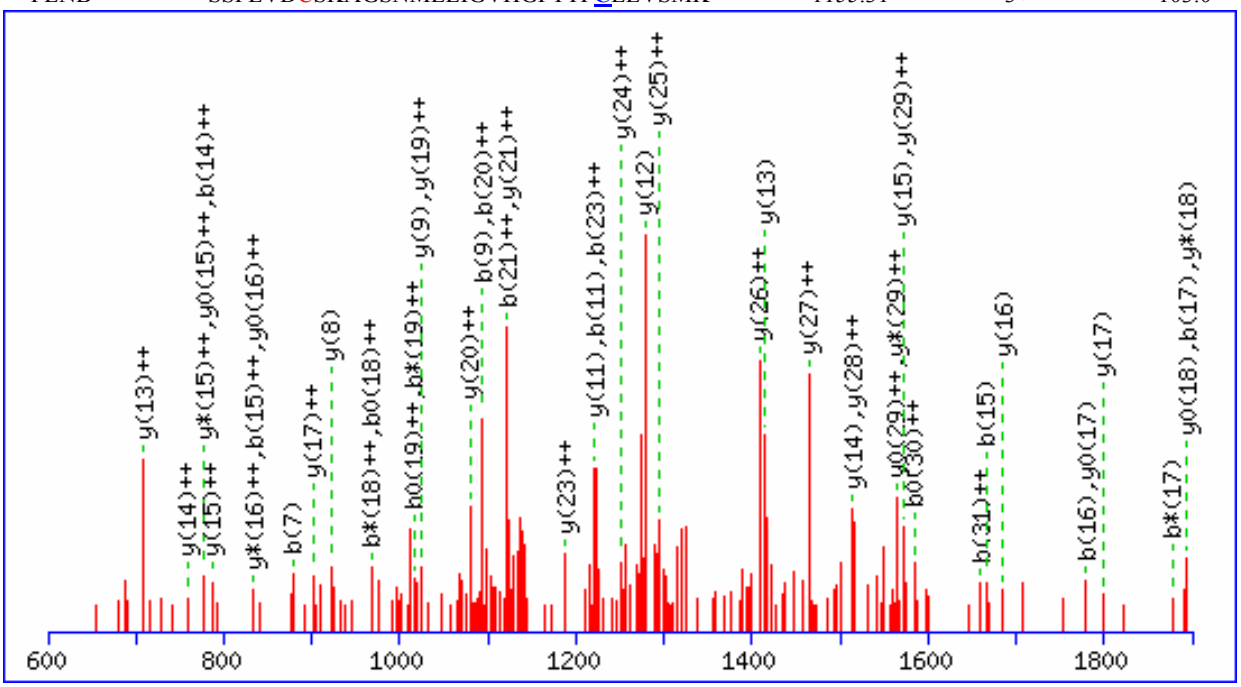
Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	SPFVVQVGEACNPNACR	959.17	2+	130.1



C11 : NEM (C)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							17
2	185.20	93.10			167.19	84.10	P	1830.07	915.54	1813.04	907.03	1812.06	906.53	16
3	332.37	166.69			314.36	157.68	F	1732.96	866.98	1715.93	858.47	1714.94	857.98	15
4	431.51	216.26			413.49	207.25	V	1585.78	793.40	1568.75	784.88	1567.77	784.39	14
5	530.64	265.82			512.62	256.81	V	1486.65	743.83	1469.62	735.32	1468.64	734.82	13
6	658.77	329.89	641.74	321.37	640.75	320.88	Q	1387.52	694.26	1370.49	685.75	1369.51	685.26	12
7	757.90	379.45	740.87	370.94	739.88	370.44	V	1259.39	630.20	1242.36	621.69	1241.38	621.19	11
8	814.95	407.98	797.92	399.46	796.93	398.97	G	1160.26	580.63	1143.23	572.12	1142.25	571.63	10
9	944.06	472.54	927.03	464.02	926.05	463.53	E	1103.21	552.11	1086.18	543.59	1085.19	543.10	9
10	1015.14	508.07	998.11	499.56	997.12	499.07	A	974.10	487.55	957.07	479.04			8
11	1243.41	622.21	1226.38	613.69	1225.39	613.20	C	903.02	452.01	885.99	443.50			7
12	1357.51	679.26	1340.48	670.74	1339.50	670.25	N	674.75	337.88	657.72	329.36			6
13	1454.63	727.82	1437.60	719.30	1436.61	718.81	P	560.65	280.83	543.62	272.31			5
14	1568.73	784.87	1551.70	776.35	1550.71	775.86	N	463.53	232.27	446.50	223.75			4
15	1639.81	820.41	1622.78	811.89	1621.79	811.40	A	349.43	175.22	332.40	166.70			3
16	1742.95	871.98	1725.92	863.46	1724.93	862.97	C	278.35	139.68	261.32	131.16			2
17							R	175.21	88.11	158.18	79.59			1

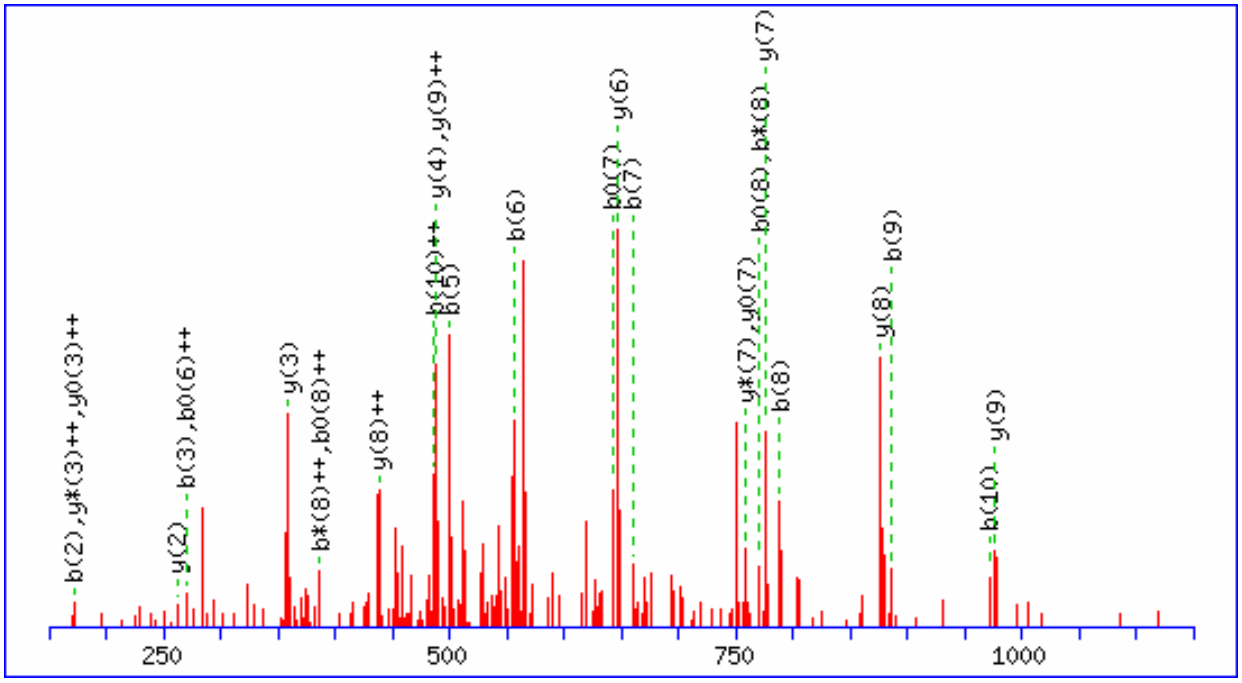
Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	SSFLVDCSKAGSNMLLIGVHGPTTPCEEVSMK	1155.31	3+	103.0



C7 : NEM (C)

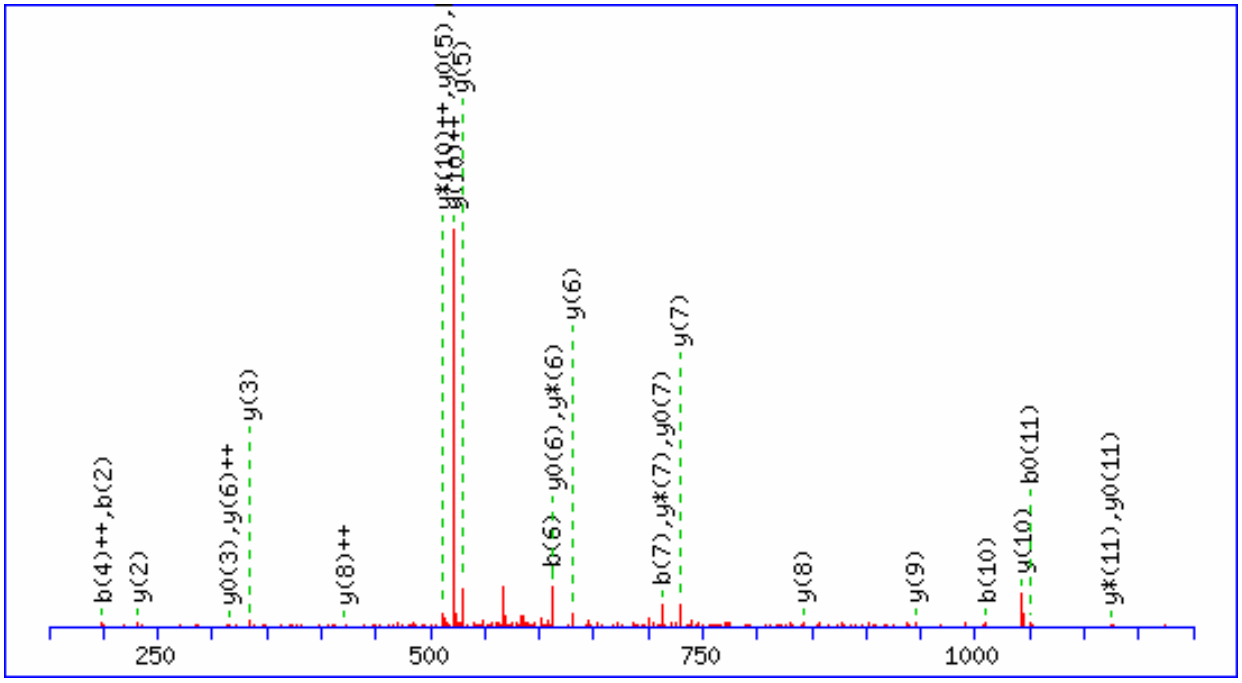
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							32
2	175.16	88.09			157.15	79.08	S	3377.91	1689.46	3360.87	1680.94	3359.89	1680.45	31
3	322.34	161.67			304.32	152.66	F	3290.83	1645.92	3273.80	1637.40	3272.81	1636.91	30
4	435.49	218.25			417.48	209.24	L	3143.65	1572.33	3126.62	1563.82	3125.64	1563.32	29
5	534.63	267.82			516.61	258.81	V	3030.50	1515.75	3013.47	1507.24	3012.48	1506.74	28
6	649.71	325.36			631.70	316.35	D	2931.37	1466.19	2914.33	1457.67	2913.35	1457.18	27
7	877.98	439.49			859.97	430.49	C	2816.28	1408.64	2799.25	1400.13	2798.26	1399.64	26
8	965.06	483.03			947.04	474.03	S	2588.01	1294.51	2570.98	1285.99	2569.99	1285.50	25
9	1093.23	547.12	1076.20	538.60	1075.22	538.11	K	2500.93	1250.97	2483.90	1242.45	2482.92	1241.96	24
10	1164.31	582.66	1147.28	574.14	1146.29	573.65	A	2372.76	1186.88	2355.73	1178.37	2354.74	1177.88	23
11	1221.36	611.18	1204.33	602.67	1203.34	602.18	G	2301.68	1151.35	2284.65	1142.83	2283.67	1142.34	22
12	1308.44	654.72	1291.41	646.21	1290.42	645.71	S	2244.63	1122.82	2227.60	1114.30	2226.62	1113.81	21
13	1422.54	711.77	1405.51	703.26	1404.52	702.77	N	2157.55	1079.28	2140.52	1070.77	2139.54	1070.27	20
14	1553.74	777.37	1536.71	768.86	1535.72	768.36	M	2043.45	1022.23	2026.42	1013.71	2025.44	1013.22	19
15	1666.89	833.95	1649.86	825.44	1648.88	824.94	L	1912.25	956.63	1895.22	948.12	1894.24	947.62	18
16	1780.05	890.53	1763.02	882.01	1762.04	881.52	L	1799.10	900.05	1782.07	891.54	1781.08	891.04	17
17	1893.21	947.11	1876.18	938.59	1875.19	938.10	I	1685.94	843.47	1668.91	834.96	1667.92	834.47	16
18	1950.26	975.63	1933.23	967.12	1932.24	966.63	G	1572.78	786.90	1555.75	778.38	1554.77	777.89	15
19	2049.39	1025.20	2032.36	1016.68	2031.38	1016.19	V	1515.73	758.37	1498.70	749.85	1497.72	749.36	14
20	2186.53	1093.77	2169.50	1085.25	2168.51	1084.76	H	1416.60	708.80	1399.57	700.29	1398.58	699.80	13
21	2243.58	1122.29	2226.55	1113.78	2225.57	1113.29	G	1279.46	640.23	1262.43	631.72	1261.45	631.23	12
22	2340.70	1170.85	2323.67	1162.34	2322.68	1161.84	P	1222.41	611.71	1205.38	603.19	1204.39	602.70	11
23	2441.80	1221.40	2424.77	1212.89	2423.79	1212.40	T	1125.29	563.15	1108.26	554.64	1107.28	554.14	10
24	2542.90	1271.96	2525.87	1263.44	2524.89	1262.95	T	1024.19	512.60	1007.16	504.08	1006.17	503.59	9
25	2640.02	1320.51	2622.99	1312.00	2622.00	1311.51	P	923.09	462.05	906.06	453.53	905.07	453.04	8
26	2743.16	1372.09	2726.13	1363.57	2725.15	1363.08	C	825.97	413.49	808.94	404.97	807.96	404.48	7
27	2872.28	1436.64	2855.25	1428.13	2854.26	1427.63	E	722.83	361.92	705.80	353.40	704.81	352.91	6
28	3001.39	1501.20	2984.36	1492.68	2983.38	1492.19	E	593.71	297.36	576.68	288.85	575.70	288.35	5
29	3100.52	1550.76	3083.49	1542.25	3082.51	1541.76	V	464.60	232.80	447.57	224.29	446.58	223.80	4
30	3187.60	1594.30	3170.57	1585.79	3169.58	1585.30	S	365.47	183.24	348.44	174.72	347.45	174.23	3
31	3318.79	1659.90	3301.76	1651.39	3300.78	1650.89	M	278.39	139.70	261.36	131.18			2
32							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	VAVTEGCQPSR	573.84	2+	53.0



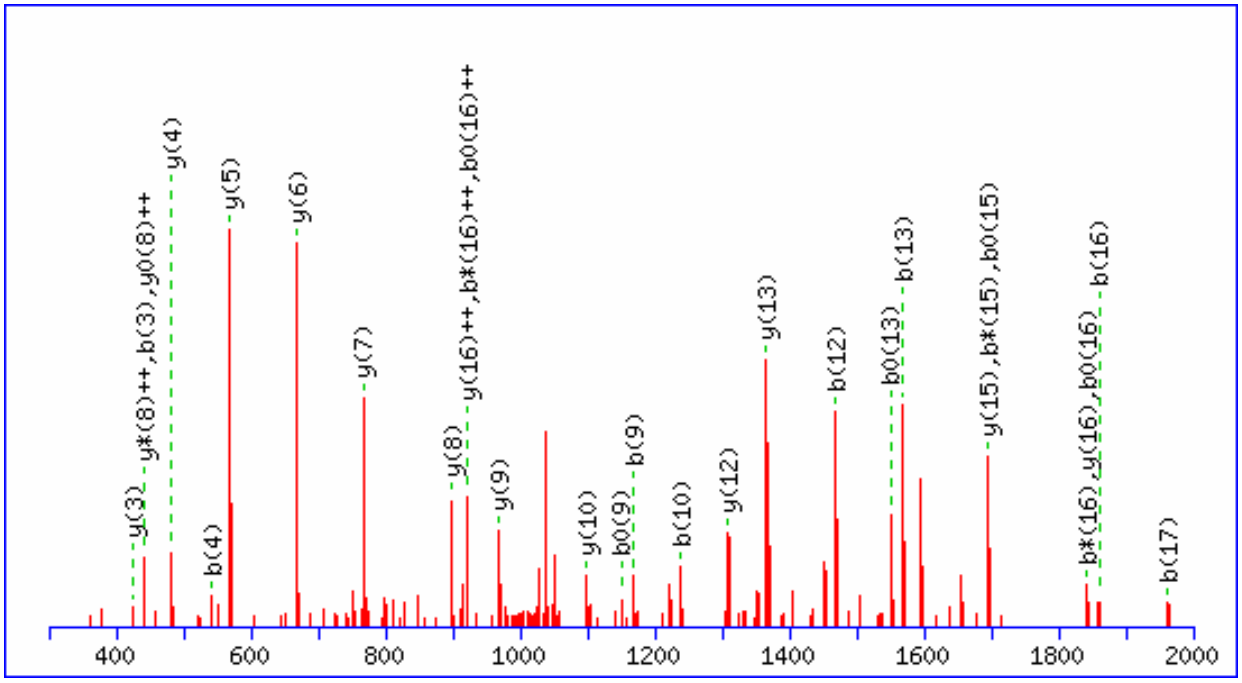
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							11
2	171.22	86.11					A	1048.15	524.58	1031.12	516.06	1030.14	515.57	10
3	270.35	135.68					V	977.07	489.04	960.04	480.53	959.06	480.03	9
4	371.45	186.23			353.44	177.22	T	877.94	439.48	860.91	430.96	859.93	430.47	8
5	500.57	250.79			482.55	241.78	E	776.84	388.92	759.81	380.41	758.82	379.92	7
6	557.62	279.31			539.60	270.30	G	647.72	324.37	630.69	315.85	629.71	315.36	6
7	660.76	330.88			642.74	321.88	C	590.67	295.84	573.64	287.33	572.66	286.83	5
8	788.89	394.95	771.86	386.43	770.87	385.94	Q	487.53	244.27	470.50	235.75	469.52	235.26	4
9	886.00	443.51	868.97	434.99	867.99	434.50	P	359.40	180.20	342.37	171.69	341.39	171.20	3
10	973.08	487.04	956.05	478.53	955.07	478.04	S	262.29	131.65	245.26	123.13	244.27	122.64	2
11							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLNB	VVPCLVTPVTGR	620.58	2+	52.7



#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57			V							12
2	199.27	100.14			V	1142.39	571.70	1125.36	563.18	1124.38	562.69	11
3	296.39	148.70			P	1043.26	522.13	1026.23	513.62	1025.25	513.13	10
4	399.53	200.27			C	946.15	473.58	929.12	465.06	928.13	464.57	9
5	512.69	256.85			L	843.00	422.01	825.97	413.49	824.99	413.00	8
6	611.82	306.41			V	729.85	365.43	712.81	356.91	711.83	356.42	7
7	712.92	356.96	694.91	347.96	T	630.71	315.86	613.68	307.35	612.70	306.85	6
8	810.04	405.52	792.02	396.51	P	529.61	265.31	512.58	256.79	511.60	256.30	5
9	909.17	455.09	891.15	446.08	V	432.50	216.75	415.46	208.24	414.48	207.74	4
10	1010.27	505.64	992.26	496.63	T	333.36	167.19	316.33	158.67	315.35	158.18	3
11	1067.32	534.17	1049.31	525.16	G	232.26	116.63	215.23	108.12			2
12					R	175.21	88.11	158.18	79.59			1

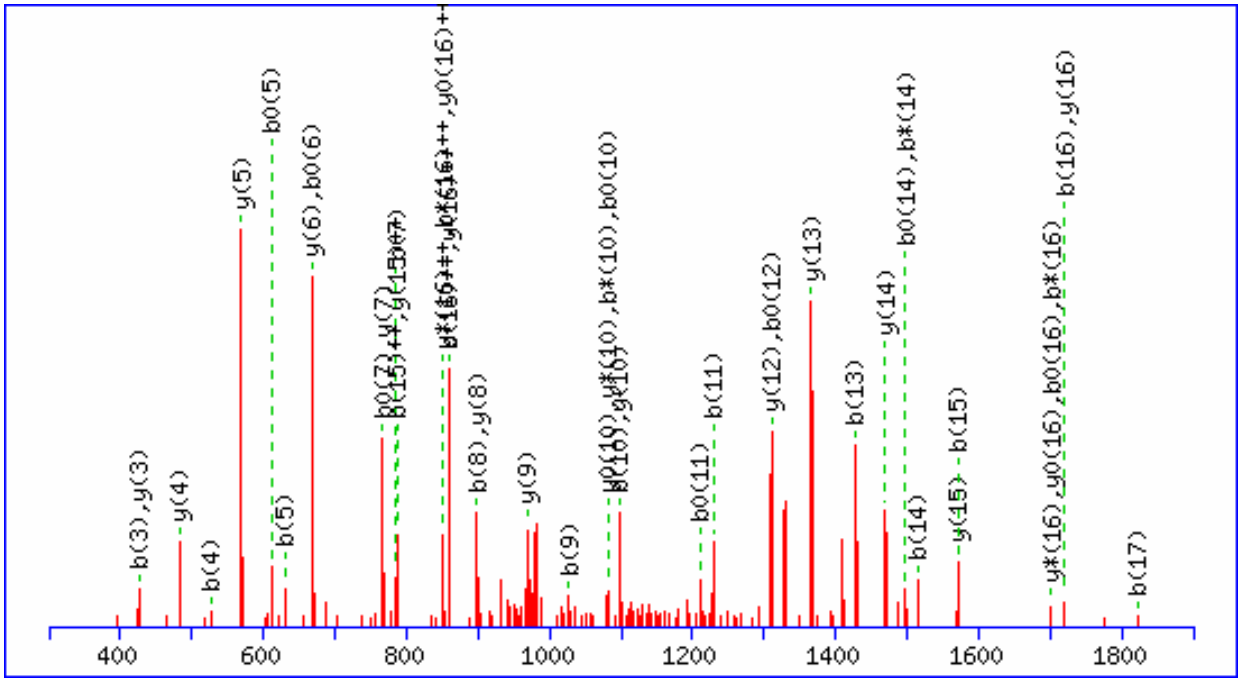
Gene Symbol	Sequences	m/z	Charge	Ion score
FLOT1	MFFTCGPNEAMVVSGFCR	1069.18	2+	121.7



M1 : Oxidation (M)
C5 : NEM (C)

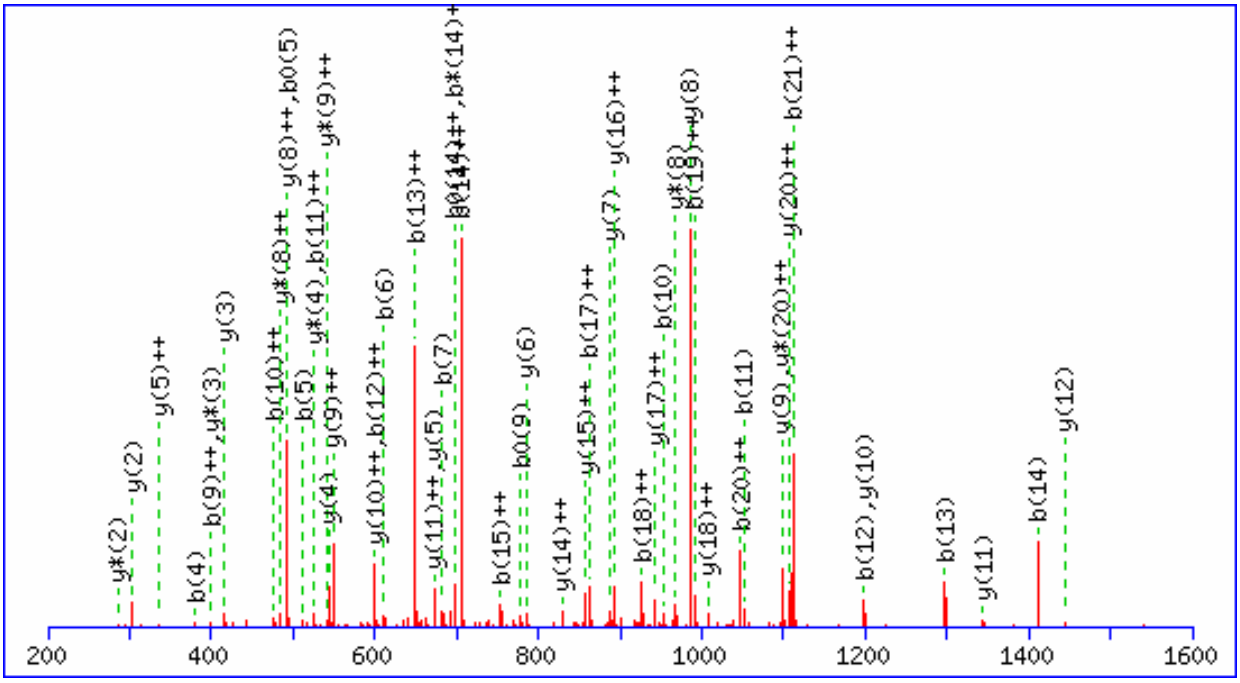
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.20	74.61					M							18
2	295.38	148.19					F	1991.29	996.15	1974.26	987.64	1973.28	987.14	17
3	442.55	221.78					F	1844.12	922.56	1827.09	914.05	1826.10	913.56	16
4	543.66	272.33			525.64	263.32	T	1696.95	848.98	1679.92	840.46	1678.93	839.97	15
5	771.92	386.47			753.91	377.46	C	1595.84	798.42	1578.81	789.91	1577.83	789.42	14
6	828.97	414.99			810.96	405.98	G	1367.57	684.29	1350.54	675.78	1349.56	675.28	13
7	926.09	463.55			908.07	454.54	P	1310.52	655.77	1293.49	647.25	1292.51	646.76	12
8	1040.19	520.60	1023.16	512.08	1022.18	511.59	N	1213.41	607.21	1196.38	598.69	1195.39	598.20	11
9	1169.31	585.16	1152.28	576.64	1151.29	576.15	E	1099.30	550.16	1082.27	541.64	1081.29	541.15	10
10	1240.38	620.70	1223.35	612.18	1222.37	611.69	A	970.19	485.60	953.16	477.08	952.18	476.59	9
11	1371.58	686.29	1354.55	677.78	1353.57	677.29	M	899.11	450.06	882.08	441.55	881.10	441.05	8
12	1470.71	735.86	1453.68	727.34	1452.70	726.85	V	767.92	384.46	750.89	375.95	749.90	375.45	7
13	1569.84	785.43	1552.81	776.91	1551.83	776.42	V	668.79	334.90	651.75	326.38	650.77	325.89	6
14	1656.92	828.96	1639.89	820.45	1638.90	819.96	S	569.65	285.33	552.62	276.82	551.64	276.32	5
15	1713.97	857.49	1696.94	848.97	1695.96	848.48	G	482.58	241.79	465.55	233.28			4
16	1861.15	931.08	1844.11	922.56	1843.13	922.07	F	425.53	213.27	408.50	204.75			3
17	1964.29	982.65	1947.26	974.13	1946.27	973.64	C	278.35	139.68	261.32	131.16			2
18							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLOT1	MFFTCGPNEAMVVSGFCR	998.67	2+	131.0



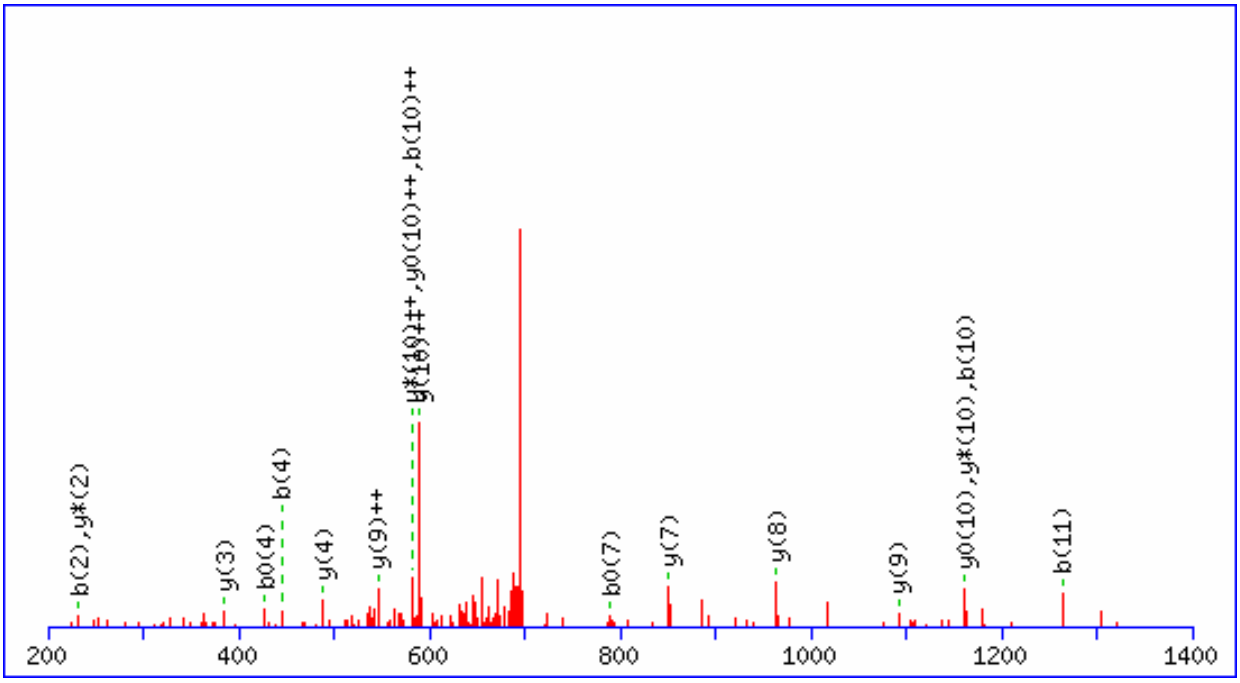
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.20	66.61					M							18
2	279.38	140.19					F	1866.17	933.59	1849.14	925.07	1848.15	924.58	17
3	426.55	213.78					F	1718.99	860.00	1701.96	851.49	1700.98	850.99	16
4	527.66	264.33			509.64	255.32	T	1571.82	786.41	1554.79	777.90	1553.81	777.41	15
5	630.80	315.90			612.78	306.90	C	1470.72	735.86	1453.69	727.35	1452.70	726.85	14
6	687.85	344.43			669.83	335.42	G	1367.57	684.29	1350.54	675.78	1349.56	675.28	13
7	784.97	392.99			766.95	383.98	P	1310.52	655.77	1293.49	647.25	1292.51	646.76	12
8	899.07	450.04	882.04	441.52	881.05	441.03	N	1213.41	607.21	1196.38	598.69	1195.39	598.20	11
9	1028.18	514.59	1011.15	506.08	1010.17	505.59	E	1099.30	550.16	1082.27	541.64	1081.29	541.15	10
10	1099.26	550.13	1082.23	541.62	1081.24	541.13	A	970.19	485.60	953.16	477.08	952.18	476.59	9
11	1230.46	615.73	1213.43	607.22	1212.44	606.72	M	899.11	450.06	882.08	441.55	881.10	441.05	8
12	1329.59	665.30	1312.56	656.78	1311.57	656.29	V	767.92	384.46	750.89	375.95	749.90	375.45	7
13	1428.72	714.86	1411.69	706.35	1410.70	705.86	V	668.79	334.90	651.75	326.38	650.77	325.89	6
14	1515.80	758.40	1498.76	749.89	1497.78	749.39	S	569.65	285.33	552.62	276.82	551.64	276.32	5
15	1572.85	786.93	1555.82	778.41	1554.83	777.92	G	482.58	241.79	465.55	233.28			4
16	1720.02	860.51	1702.99	852.00	1702.01	851.51	F	425.53	213.27	408.50	204.75			3
17	1823.16	912.09	1806.13	903.57	1805.15	903.08	C	278.35	139.68	261.32	131.16			2
18							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
FLOT1	SPPVMVAGGRVFVLPCIQQIQR	799.37	3+	123.2



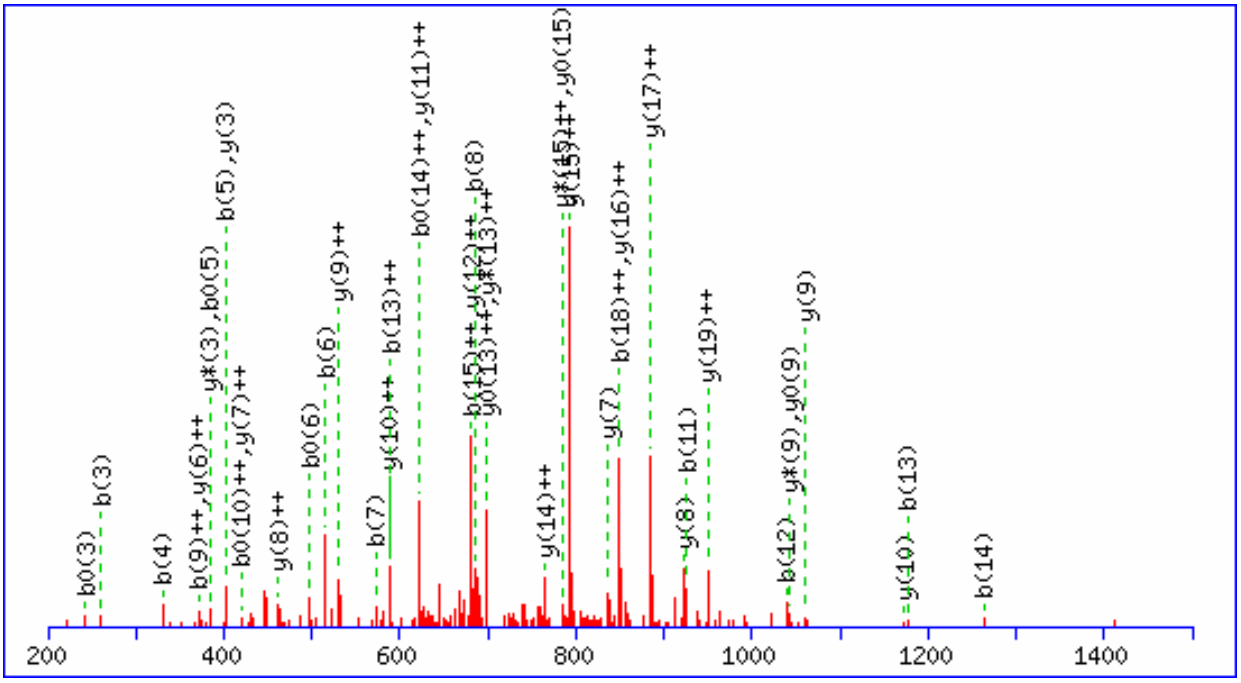
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.09	44.55			70.07	35.54	S					22
2	185.20	93.10			167.19	84.10	P	2309.82	1155.41	2292.79	1146.90	21
3	282.32	141.66			264.30	132.65	P	2212.70	1106.86	2195.67	1098.34	20
4	381.45	191.23			363.43	182.22	V	2115.59	1058.30	2098.56	1049.78	19
5	512.64	256.83			494.63	247.82	M	2016.46	1008.73	1999.43	1000.22	18
6	611.77	306.39			593.76	297.38	V	1885.26	943.13	1868.23	934.62	17
7	682.85	341.93			664.84	332.92	A	1786.13	893.57	1769.10	885.05	16
8	739.90	370.46			721.89	361.45	G	1715.05	858.03	1698.02	849.51	15
9	796.95	398.98			778.94	389.97	G	1658.00	829.50	1640.97	820.99	14
10	953.14	477.07	936.11	468.56	935.12	468.07	R	1600.95	800.98	1583.92	792.46	13
11	1052.27	526.64	1035.24	518.12	1034.26	517.63	V	1444.76	722.89	1427.73	714.37	12
12	1199.45	600.23	1182.41	591.71	1181.43	591.22	F	1345.63	673.32	1328.60	664.80	11
13	1298.58	649.79	1281.55	641.28	1280.56	640.78	V	1198.46	599.73	1181.43	591.22	10
14	1411.73	706.37	1394.70	697.86	1393.72	697.36	L	1099.33	550.17	1082.30	541.65	9
15	1508.85	754.93	1491.82	746.41	1490.83	745.92	P	986.17	493.59	969.14	485.07	8
16	1611.99	806.50	1594.96	797.98	1593.98	797.49	C	889.05	445.03	872.02	436.52	7
17	1725.15	863.08	1708.12	854.56	1707.13	854.07	I	785.91	393.46	768.88	384.94	6
18	1853.28	927.14	1836.25	918.63	1835.26	918.14	Q	672.75	336.88	655.72	328.37	5
19	1981.41	991.21	1964.38	982.69	1963.39	982.20	Q	544.62	272.82	527.59	264.30	4
20	2094.57	1047.79	2077.54	1039.27	2076.55	1038.78	I	416.50	208.75	399.47	200.24	3
21	2222.69	1111.85	2205.66	1103.34	2204.68	1102.84	Q	303.34	152.17	286.31	143.66	2
22							R	175.21	88.11	158.18	79.59	1

Gene Symbol	Sequences	m/z	Charge	Ion score
G3BP1	VMSQNFTNCHTK	705.59	2+	47.5



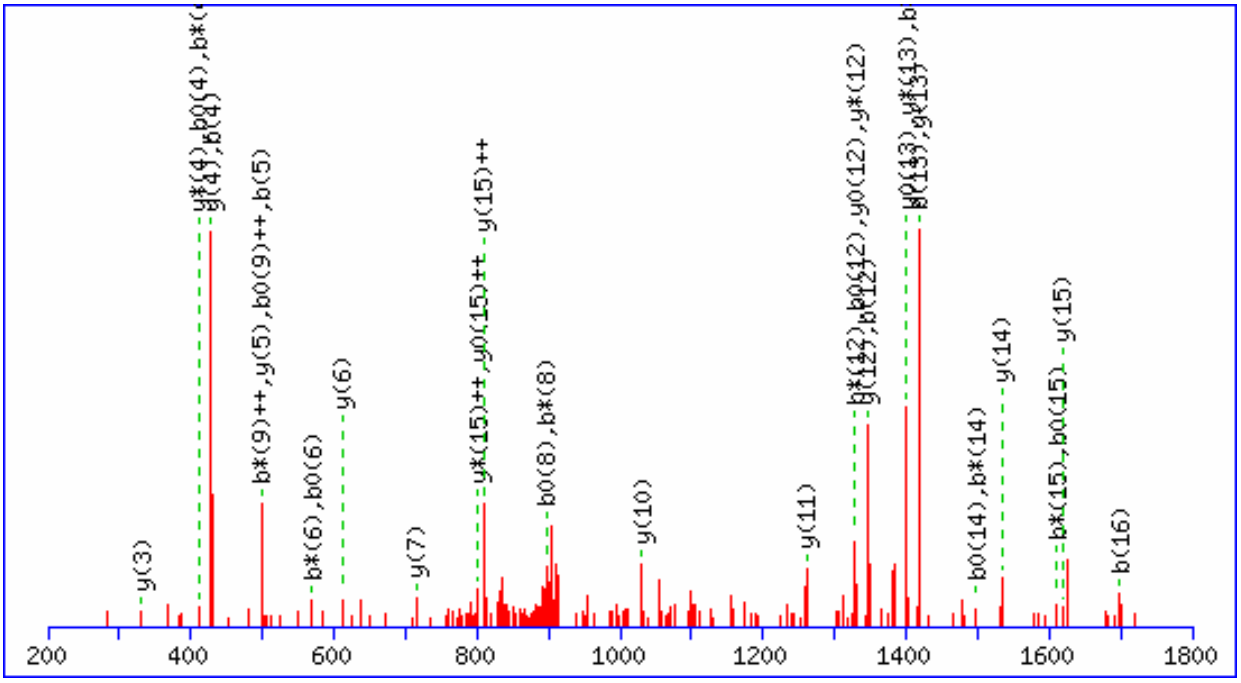
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							12
2	231.34	116.17					M	1311.47	656.24	1294.44	647.72	1293.45	647.23	11
3	318.41	159.71			300.40	150.70	S	1180.27	590.64	1163.24	582.12	1162.26	581.63	10
4	446.54	223.77	429.51	215.26	428.53	214.77	Q	1093.19	547.10	1076.16	538.59	1075.18	538.09	9
5	560.64	280.83	543.61	272.31	542.63	271.82	N	965.06	483.04	948.03	474.52	947.05	474.03	8
6	707.82	354.41	690.79	345.90	689.80	345.41	F	850.96	425.98	833.93	417.47	832.95	416.98	7
7	808.92	404.96	791.89	396.45	790.91	395.96	T	703.79	352.40	686.76	343.88	685.77	343.39	6
8	923.02	462.02	905.99	453.50	905.01	453.01	N	602.68	301.85	585.65	293.33	584.67	292.84	5
9	1026.17	513.59	1009.14	505.07	1008.15	504.58	C	488.58	244.79	471.55	236.28	470.57	235.79	4
10	1163.31	582.16	1146.28	573.64	1145.29	573.15	H	385.44	193.22	368.41	184.71	367.42	184.22	3
11	1264.41	632.71	1247.38	624.19	1246.40	623.70	T	248.30	124.65	231.27	116.14	230.28	115.65	2
12							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
G6PC3	DSGAALGLGIALHSPCYAQVR	700.80	3+	110.2



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.10	58.55			98.08	49.54	D							21
2	203.17	102.09			185.16	93.08	S	1985.29	993.15	1968.26	984.63	1967.28	984.14	20
3	260.22	130.62			242.21	121.61	G	1898.21	949.61	1881.18	941.10	1880.20	940.60	19
4	331.30	166.15			313.29	157.15	A	1841.16	921.08	1824.13	912.57	1823.15	912.08	18
5	402.38	201.69			384.36	192.69	A	1770.08	885.55	1753.05	877.03	1752.07	876.54	17
6	515.54	258.27			497.52	249.26	L	1699.01	850.01	1681.98	841.49	1680.99	841.00	16
7	572.59	286.80			554.57	277.79	G	1585.85	793.43	1568.82	784.91	1567.83	784.42	15
8	685.75	343.38			667.73	334.37	L	1528.80	764.90	1511.77	756.39	1510.78	755.89	14
9	742.80	371.90			724.78	362.90	G	1415.64	708.32	1398.61	699.81	1397.62	699.32	13
10	855.96	428.48			837.94	419.47	I	1358.59	679.80	1341.56	671.28	1340.57	670.79	12
11	927.03	464.02			909.02	455.01	A	1245.43	623.22	1228.40	614.70	1227.42	614.21	11
12	1040.19	520.60			1022.18	511.59	L	1174.35	587.68	1157.32	579.17	1156.34	578.67	10
13	1177.33	589.17			1159.31	580.16	H	1061.20	531.10	1044.16	522.59	1043.18	522.09	9
14	1264.41	632.71			1246.39	623.70	S	924.06	462.53	907.03	454.02	906.04	453.52	8
15	1361.52	681.27			1343.51	672.26	P	836.98	418.99	819.95	410.48			7
16	1464.67	732.84			1446.65	723.83	C	739.86	370.44	722.83	361.92			6
17	1627.84	814.42			1609.82	805.42	Y	636.72	318.86	619.69	310.35			5
18	1698.92	849.96			1680.90	840.95	A	473.55	237.28	456.52	228.76			4
19	1827.05	914.03	1810.02	905.51	1809.03	905.02	Q	402.47	201.74	385.44	193.22			3
20	1926.18	963.59	1909.15	955.08	1908.16	954.58	V	274.34	137.67	257.31	129.16			2
21							R	175.21	88.11	158.18	79.59			1

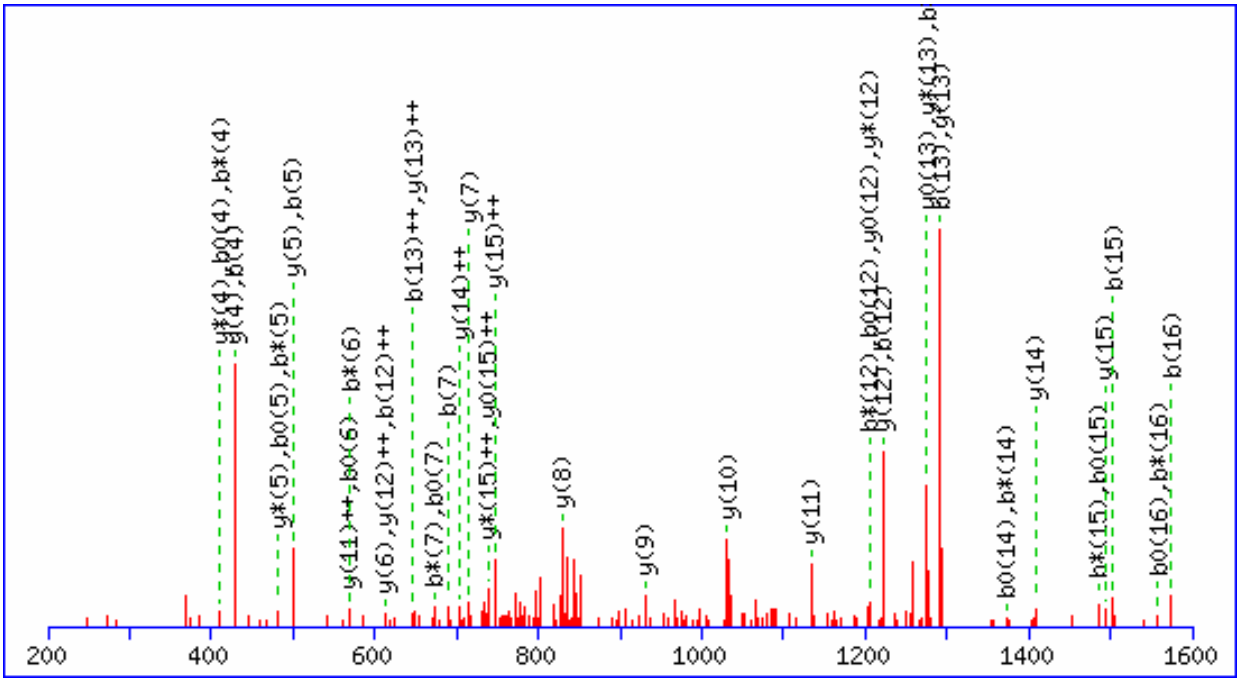
Gene Symbol	Sequences	m/z	Charge	Ion score
GAPDH	IISNASCTTNCLAPLAK	923.52	2+	72.8



C7 : NEM (C)

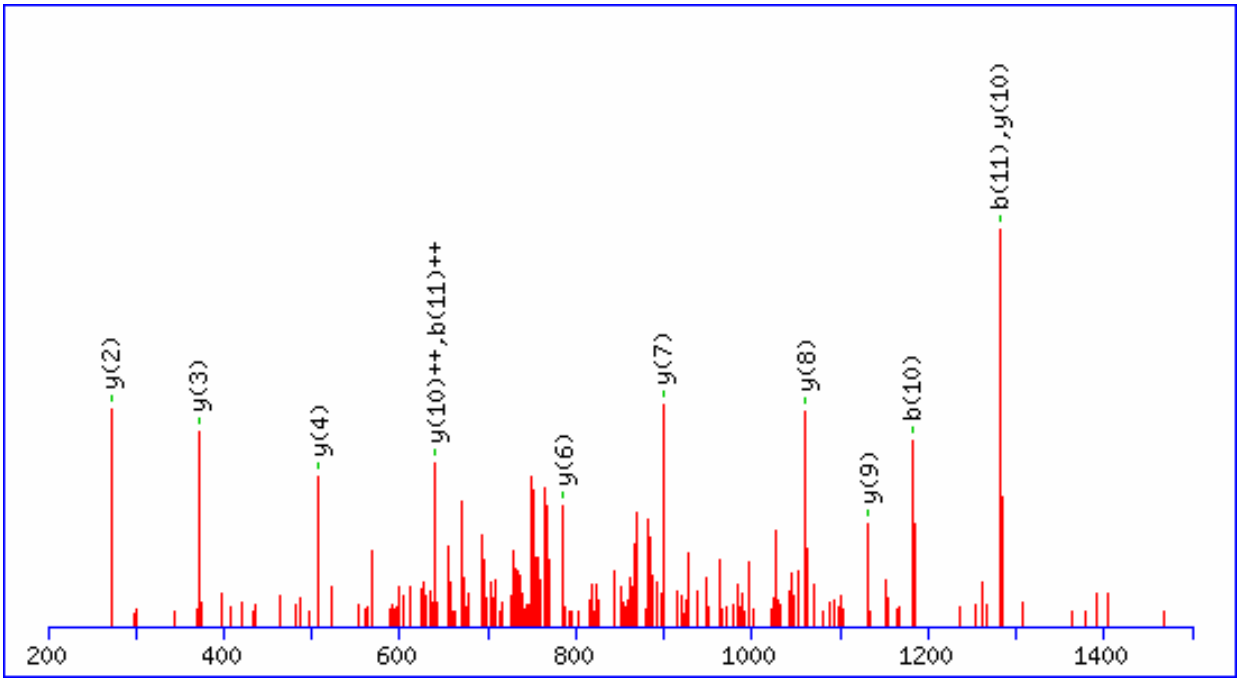
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					I							17
2	227.32	114.17					I	1733.00	867.00	1715.97	858.49	1714.98	857.99	16
3	314.40	157.70			296.39	148.70	S	1619.84	810.42	1602.81	801.91	1601.82	801.42	15
4	428.50	214.76	411.47	206.24	410.49	205.75	N	1532.76	766.88	1515.73	758.37	1514.75	757.88	14
5	499.58	250.29	482.55	241.78	481.57	241.29	A	1418.66	709.83	1401.63	701.32	1400.64	700.83	13
6	586.66	293.83	569.63	285.32	568.64	284.83	S	1347.58	674.29	1330.55	665.78	1329.57	665.29	12
7	814.93	407.97	797.90	399.45	796.91	398.96	C	1260.50	630.76	1243.47	622.24	1242.49	621.75	11
8	916.03	458.52	899.00	450.00	898.02	449.51	T	1032.24	516.62	1015.20	508.11	1014.22	507.61	10
9	1017.13	509.07	1000.10	500.56	999.12	500.06	T	931.13	466.07	914.10	457.55	913.12	457.06	9
10	1131.24	566.12	1114.21	557.61	1113.22	557.11	N	830.03	415.52	813.00	407.00			8
11	1234.38	617.69	1217.35	609.18	1216.36	608.69	C	715.92	358.47	698.89	349.95			7
12	1347.54	674.27	1330.51	665.76	1329.52	665.27	L	612.78	306.89	595.75	298.38			6
13	1418.62	709.81	1401.58	701.30	1400.60	700.80	A	499.62	250.32	482.59	241.80			5
14	1515.73	758.37	1498.70	749.85	1497.72	749.36	P	428.55	214.78	411.52	206.26			4
15	1628.89	814.95	1611.86	806.43	1610.87	805.94	L	331.43	166.22	314.40	157.70			3
16	1699.97	850.49	1682.94	841.97	1681.95	841.48	A	218.27	109.64	201.24	101.13			2
17							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
GAPDH	IISNASCTTNCLAPLAK	860.60	2+	85.0



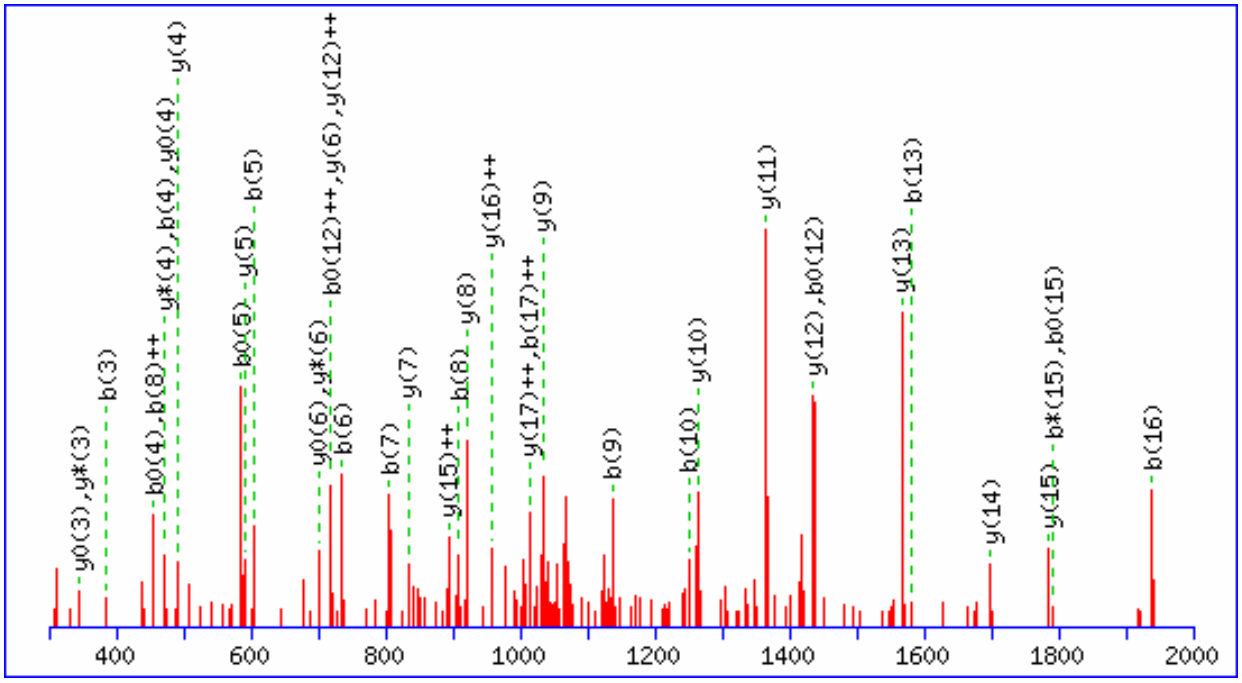
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					I							17
2	227.32	114.17					I	1607.87	804.44	1590.84	795.92	1589.86	795.43	16
3	314.40	157.70			296.39	148.70	S	1494.71	747.86	1477.68	739.35	1476.70	738.85	15
4	428.50	214.76	411.47	206.24	410.49	205.75	N	1407.64	704.32	1390.61	695.81	1389.62	695.31	14
5	499.58	250.29	482.55	241.78	481.57	241.29	A	1293.53	647.27	1276.50	638.76	1275.52	638.26	13
6	586.66	293.83	569.63	285.32	568.64	284.83	S	1222.46	611.73	1205.42	603.22	1204.44	602.72	12
7	689.80	345.40	672.77	336.89	671.79	336.40	C	1135.38	568.19	1118.35	559.68	1117.36	559.19	11
8	790.91	395.96	773.87	387.44	772.89	386.95	T	1032.24	516.62	1015.20	508.11	1014.22	507.61	10
9	892.01	446.51	874.98	437.99	873.99	437.50	T	931.13	466.07	914.10	457.55	913.12	457.06	9
10	1006.11	503.56	989.08	495.04	988.10	494.55	N	830.03	415.52	813.00	407.00			8
11	1109.25	555.13	1092.22	546.62	1091.24	546.12	C	715.92	358.47	698.89	349.95			7
12	1222.41	611.71	1205.38	603.19	1204.40	602.70	L	612.78	306.89	595.75	298.38			6
13	1293.49	647.25	1276.46	638.73	1275.47	638.24	A	499.62	250.32	482.59	241.80			5
14	1390.61	695.81	1373.57	687.29	1372.59	686.80	P	428.55	214.78	411.52	206.26			4
15	1503.76	752.39	1486.73	743.87	1485.75	743.38	L	331.43	166.22	314.40	157.70			3
16	1574.84	787.92	1557.81	779.41	1556.83	778.92	A	218.27	109.64	201.24	101.13			2
17							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
GFPT1	CGIFAYLNYHVPR	777.17	2+	61.8



#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	104.15	52.58			C					13
2	161.20	81.11			G	1450.66	725.83	1433.63	717.32	12
3	274.36	137.68			I	1393.61	697.31	1376.58	688.79	11
4	421.53	211.27			F	1280.45	640.73	1263.42	632.22	10
5	492.61	246.81			A	1133.28	567.14	1116.25	558.63	9
6	655.78	328.40			Y	1062.20	531.60	1045.17	523.09	8
7	768.94	384.98			L	899.03	450.02	882.00	441.50	7
8	883.05	442.03	866.01	433.51	N	785.87	393.44	768.84	384.92	6
9	1046.22	523.61	1029.19	515.10	Y	671.77	336.39	654.74	327.87	5
10	1183.36	592.18	1166.33	583.67	H	508.59	254.80	491.56	246.29	4
11	1282.49	641.75	1265.46	633.23	V	371.46	186.23	354.42	177.72	3
12	1379.60	690.31	1362.57	681.79	P	272.32	136.67	255.29	128.15	2
13					R	175.21	88.11	158.18	79.59	1

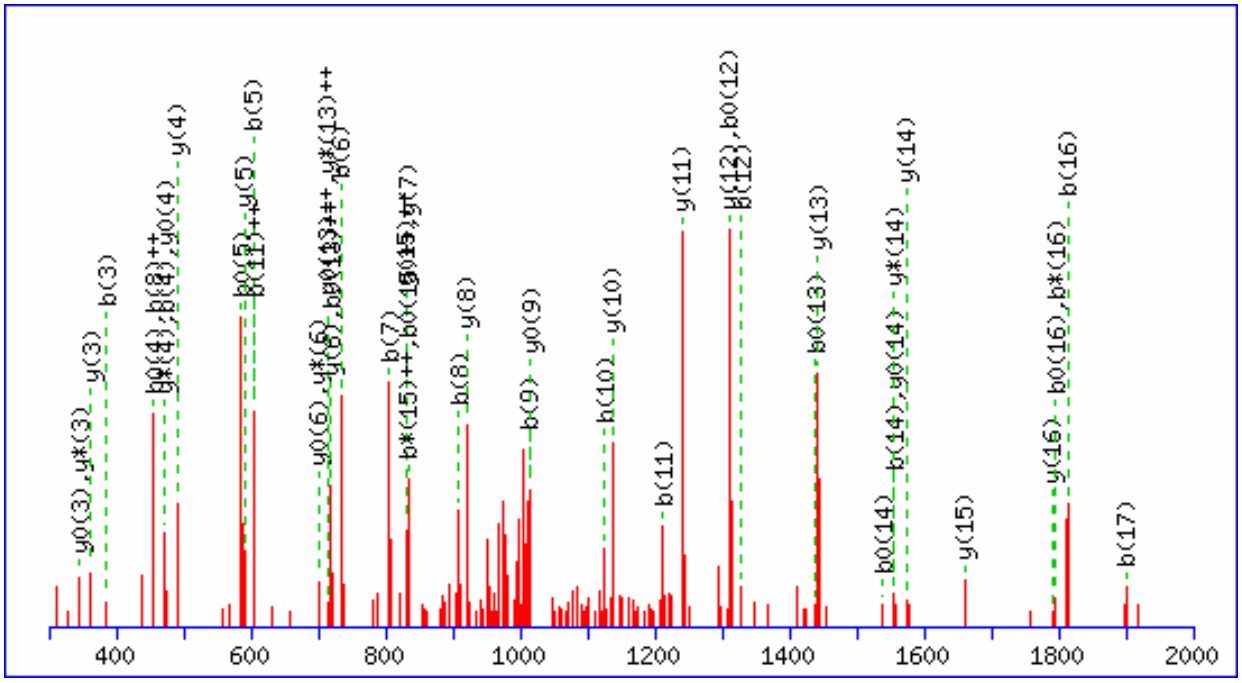
Gene Symbol	Sequences	m/z	Charge	Ion score
GNA11	TLESMMACCLSDEVKESK	1086.37	2+	93.5



N-term : N-Acetyl (Protein)
C9 : NEM (C)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	144.15	72.58			126.13	63.57	T							18
2	257.31	129.16			239.29	120.15	L	2029.36	1015.18	2012.33	1006.67	2011.34	1006.17	17
3	386.42	193.71			368.40	184.71	E	1916.20	958.60	1899.17	950.09	1898.18	949.60	16
4	473.50	237.25			455.48	228.25	S	1787.09	894.05	1770.05	885.53	1769.07	885.04	15
5	604.69	302.85			586.68	293.84	M	1700.01	850.51	1682.98	841.99	1681.99	841.50	14
6	735.89	368.45			717.87	359.44	M	1568.81	784.91	1551.78	776.39	1550.80	775.90	13
7	806.97	403.99			788.95	394.98	A	1437.62	719.31	1420.59	710.80	1419.60	710.30	12
8	910.11	455.56			892.10	446.55	C	1366.54	683.77	1349.51	675.26	1348.52	674.77	11
9	1138.38	569.69			1120.36	560.69	C	1263.39	632.20	1246.36	623.69	1245.38	623.19	10
10	1251.54	626.27			1233.52	617.26	L	1035.13	518.07	1018.10	509.55	1017.11	509.06	9
11	1338.61	669.81			1320.60	660.80	S	921.97	461.49	904.94	452.97	903.95	452.48	8
12	1453.70	727.35			1435.69	718.35	D	834.89	417.95	817.86	409.43	816.88	408.94	7
13	1582.81	791.91			1564.80	782.90	E	719.80	360.41	702.77	351.89	701.79	351.40	6
14	1681.95	841.48			1663.93	832.47	V	590.69	295.85	573.66	287.33	572.67	286.84	5
15	1810.12	905.56	1793.09	897.05	1792.10	896.56	K	491.56	246.28	474.53	237.77	473.54	237.28	4
16	1939.23	970.12	1922.20	961.60	1921.22	961.11	E	363.39	182.20	346.36	173.68	345.37	173.19	3
17	2026.31	1013.66	2009.28	1005.14	2008.29	1004.65	S	234.27	117.64	217.24	109.13	216.26	108.63	2
18							K	147.20	74.10	130.16	65.59			1

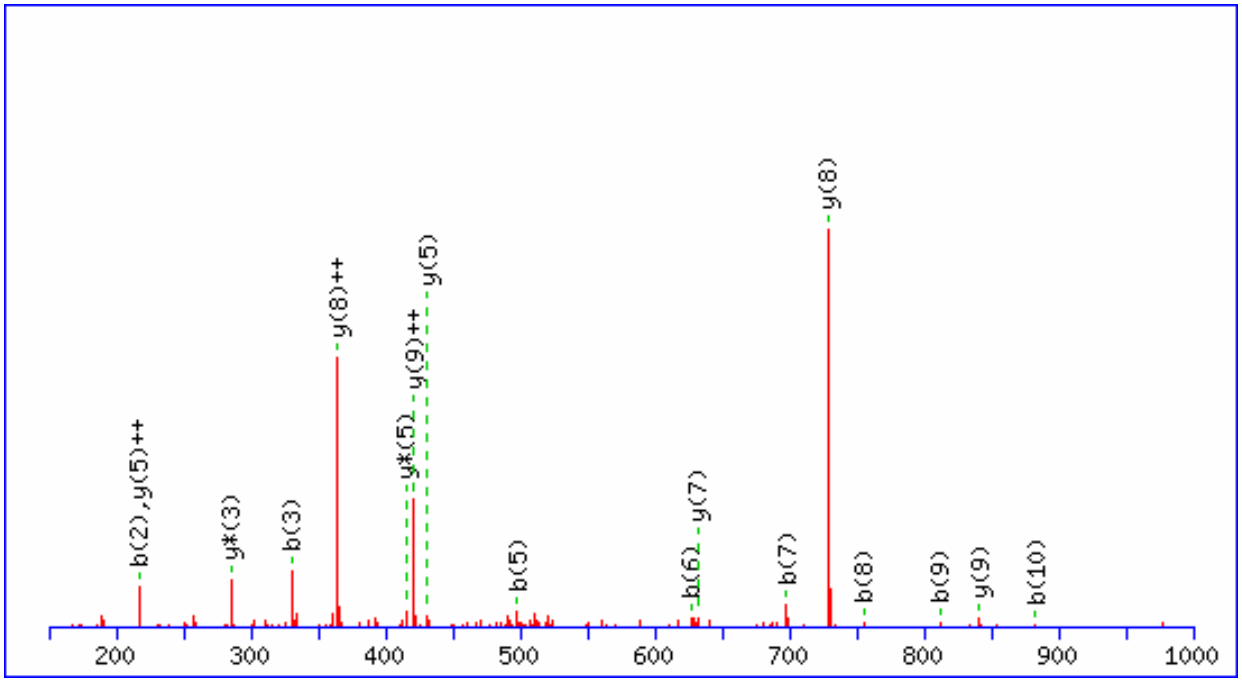
Gene Symbol	Sequences	m/z	Charge	Ion score
GNA11	TLESMMA**CC**LSDEVKESK	1024.24	2+	107.9



N-term : N-Acetyl (Protein)

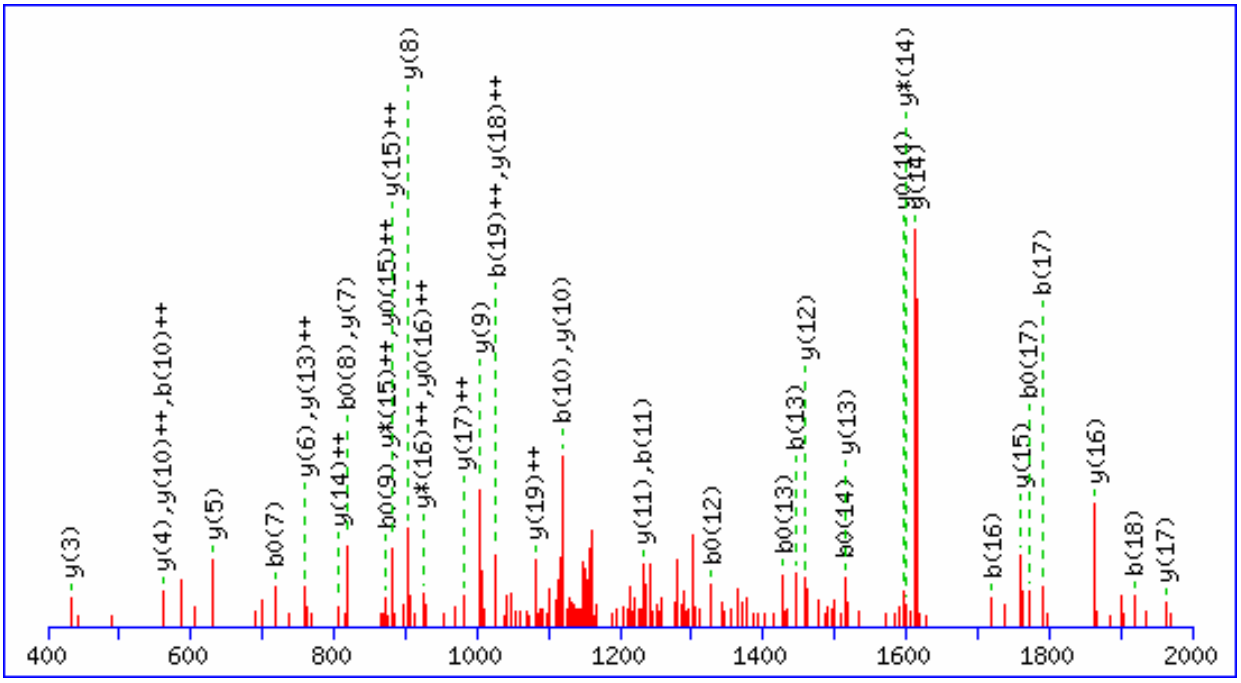
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	144.15	72.58			126.13	63.57	T							18
2	257.31	129.16			239.29	120.15	L	1904.23	952.62	1887.20	944.10	1886.22	943.61	17
3	386.42	193.71			368.40	184.71	E	1791.07	896.04	1774.04	887.53	1773.06	887.03	16
4	473.50	237.25			455.48	228.25	S	1661.96	831.48	1644.93	822.97	1643.94	822.48	15
5	604.69	302.85			586.68	293.84	M	1574.88	787.95	1557.85	779.43	1556.87	778.94	14
6	735.89	368.45			717.87	359.44	M	1443.69	722.35	1426.66	713.83	1425.67	713.34	13
7	806.97	403.99			788.95	394.98	A	1312.49	656.75	1295.46	648.23	1294.47	647.74	12
8	910.11	455.56			892.10	446.55	C	1241.41	621.21	1224.38	612.69	1223.40	612.20	11
9	1013.25	507.13			995.24	498.12	C	1138.27	569.64	1121.24	561.12	1120.25	560.63	10
10	1126.41	563.71			1108.40	554.70	L	1035.13	518.07	1018.10	509.55	1017.11	509.06	9
11	1213.49	607.25			1195.47	598.24	S	921.97	461.49	904.94	452.97	903.95	452.48	8
12	1328.58	664.79			1310.56	655.78	D	834.89	417.95	817.86	409.43	816.88	408.94	7
13	1457.69	729.35			1439.67	720.34	E	719.80	360.41	702.77	351.89	701.79	351.40	6
14	1556.82	778.91			1538.81	769.91	V	590.69	295.85	573.66	287.33	572.67	286.84	5
15	1684.99	843.00	1667.96	834.49	1666.98	833.99	K	491.56	246.28	474.53	237.77	473.54	237.28	4
16	1814.11	907.56	1797.08	899.04	1796.09	898.55	E	363.39	182.20	346.36	173.68	345.37	173.19	3
17	1901.18	951.10	1884.15	942.58	1883.17	942.09	S	234.27	117.64	217.24	109.13	216.26	108.63	2
18							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
GNA12	CLLPAEAGGAR	529.45	2+	53.6



#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	104.15	52.58			C							11
2	217.31	109.16			L	955.09	478.05	938.06	469.53	937.07	469.04	10
3	330.47	165.74			L	841.93	421.47	824.90	412.95	823.92	412.46	9
4	427.58	214.29			P	728.77	364.89	711.74	356.38	710.76	355.88	8
5	498.66	249.83			A	631.66	316.33	614.63	307.82	613.64	307.33	7
6	627.77	314.39	609.76	305.38	E	560.58	280.79	543.55	272.28	542.57	271.79	6
7	698.85	349.93	680.84	340.92	A	431.47	216.24	414.44	207.72			5
8	755.90	378.46	737.89	369.45	G	360.39	180.70	343.36	172.18			4
9	812.95	406.98	794.94	397.97	G	303.34	152.17	286.31	143.66			3
10	884.03	442.52	866.02	433.51	A	246.29	123.65	229.26	115.13			2
11					R	175.21	88.11	158.18	79.59			1

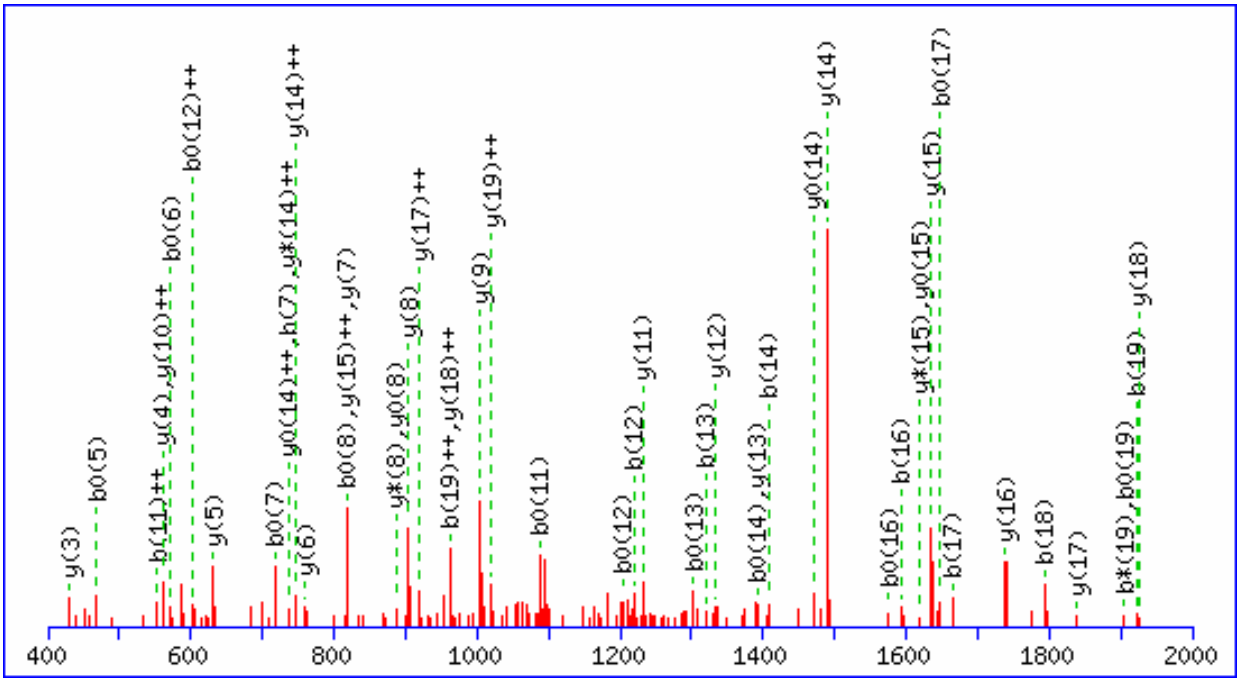
Gene Symbol	Sequences	m/z	Charge	Ion score
GNA13	SVLSVCFPGCLLTSGEAEQQR	1175.93	2+	97.5



C10 : NEM (C)

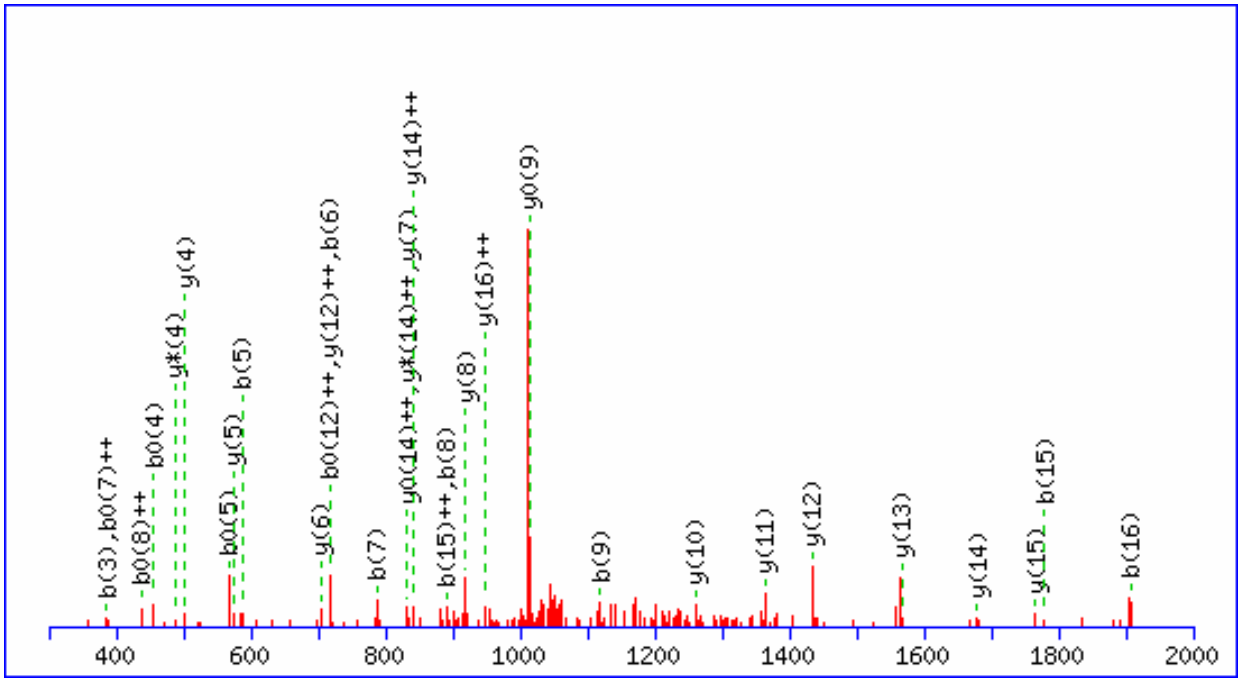
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							21
2	187.22	94.11			169.20	85.10	V	2263.57	1132.29	2246.54	1123.77	2245.55	1123.28	20
3	300.37	150.69			282.36	141.68	L	2164.44	1082.72	2147.41	1074.21	2146.42	1073.72	19
4	387.45	194.23			369.44	185.22	S	2051.28	1026.14	2034.25	1017.63	2033.27	1017.14	18
5	486.58	243.80			468.57	234.79	V	1964.20	982.61	1947.17	974.09	1946.19	973.60	17
6	589.73	295.37			571.71	286.36	C	1865.07	933.04	1848.04	924.52	1847.06	924.03	16
7	736.90	368.95			718.88	359.95	F	1761.93	881.47	1744.90	872.95	1743.91	872.46	15
8	834.01	417.51			816.00	408.50	P	1614.76	807.88	1597.73	799.37	1596.74	798.87	14
9	891.07	446.04			873.05	437.03	G	1517.64	759.32	1500.61	750.81	1499.63	750.32	13
10	1119.33	560.17			1101.32	551.16	C	1460.59	730.80	1443.56	722.28	1442.57	721.79	12
11	1232.49	616.75			1214.48	607.74	L	1232.32	616.66	1215.29	608.15	1214.31	607.66	11
12	1345.65	673.33			1327.63	664.32	L	1119.16	560.09	1102.13	551.57	1101.15	551.08	10
13	1446.75	723.88			1428.74	714.87	T	1006.01	503.51	988.98	494.99	987.99	494.50	9
14	1533.83	767.42			1515.81	758.41	S	904.90	452.95	887.87	444.44	886.89	443.95	8
15	1590.88	795.94			1572.87	786.94	G	817.82	409.42	800.79	400.90	799.81	400.41	7
16	1720.00	860.50			1701.98	851.49	E	760.77	380.89	743.74	372.38	742.76	371.88	6
17	1791.07	896.04			1773.06	887.03	A	631.66	316.33	614.63	307.82	613.64	307.33	5
18	1920.19	960.60			1902.17	951.59	E	560.58	280.79	543.55	272.28	542.57	271.79	4
19	2048.32	1024.66	2031.29	1016.15	2030.30	1015.65	Q	431.47	216.24	414.44	207.72			3
20	2176.45	1088.73	2159.42	1080.21	2158.43	1079.72	Q	303.34	152.17	286.31	143.66			2
21							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
GNA13	SVLSVCFPGCLLTSGEAEQQR	1113.54	2+	114.5



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							21
2	187.22	94.11			169.20	85.10	V	2138.44	1069.73	2121.41	1061.21	2120.43	1060.72	20
3	300.37	150.69			282.36	141.68	L	2039.31	1020.16	2022.28	1011.65	2021.30	1011.15	19
4	387.45	194.23			369.44	185.22	S	1926.16	963.58	1909.13	955.07	1908.14	954.57	18
5	486.58	243.80			468.57	234.79	V	1839.08	920.04	1822.05	911.53	1821.06	911.04	17
6	589.73	295.37			571.71	286.36	C	1739.95	870.48	1722.92	861.96	1721.93	861.47	16
7	736.90	368.95			718.88	359.95	F	1636.80	818.91	1619.77	810.39	1618.79	809.90	15
8	834.01	417.51			816.00	408.50	P	1489.63	745.32	1472.60	736.80	1471.62	736.31	14
9	891.07	446.04			873.05	437.03	G	1392.52	696.76	1375.48	688.25	1374.50	687.75	13
10	994.21	497.61			976.19	488.60	C	1335.46	668.24	1318.43	659.72	1317.45	659.23	12
11	1107.37	554.19			1089.35	545.18	L	1232.32	616.66	1215.29	608.15	1214.31	607.66	11
12	1220.52	610.77			1202.51	601.76	L	1119.16	560.09	1102.13	551.57	1101.15	551.08	10
13	1321.63	661.32			1303.61	652.31	T	1006.01	503.51	988.98	494.99	987.99	494.50	9
14	1408.70	704.86			1390.69	695.85	S	904.90	452.95	887.87	444.44	886.89	443.95	8
15	1465.76	733.38			1447.74	724.37	G	817.82	409.42	800.79	400.90	799.81	400.41	7
16	1594.87	797.94			1576.85	788.93	E	760.77	380.89	743.74	372.38	742.76	371.88	6
17	1665.95	833.48			1647.93	824.47	A	631.66	316.33	614.63	307.82	613.64	307.33	5
18	1795.06	898.04			1777.05	889.03	E	560.58	280.79	543.55	272.28	542.57	271.79	4
19	1923.19	962.10	1906.16	953.58	1905.18	953.09	Q	431.47	216.24	414.44	207.72			3
20	2051.32	1026.16	2034.29	1017.65	2033.31	1017.16	Q	303.34	152.17	286.31	143.66			2
21							R	175.21	88.11	158.18	79.59			1

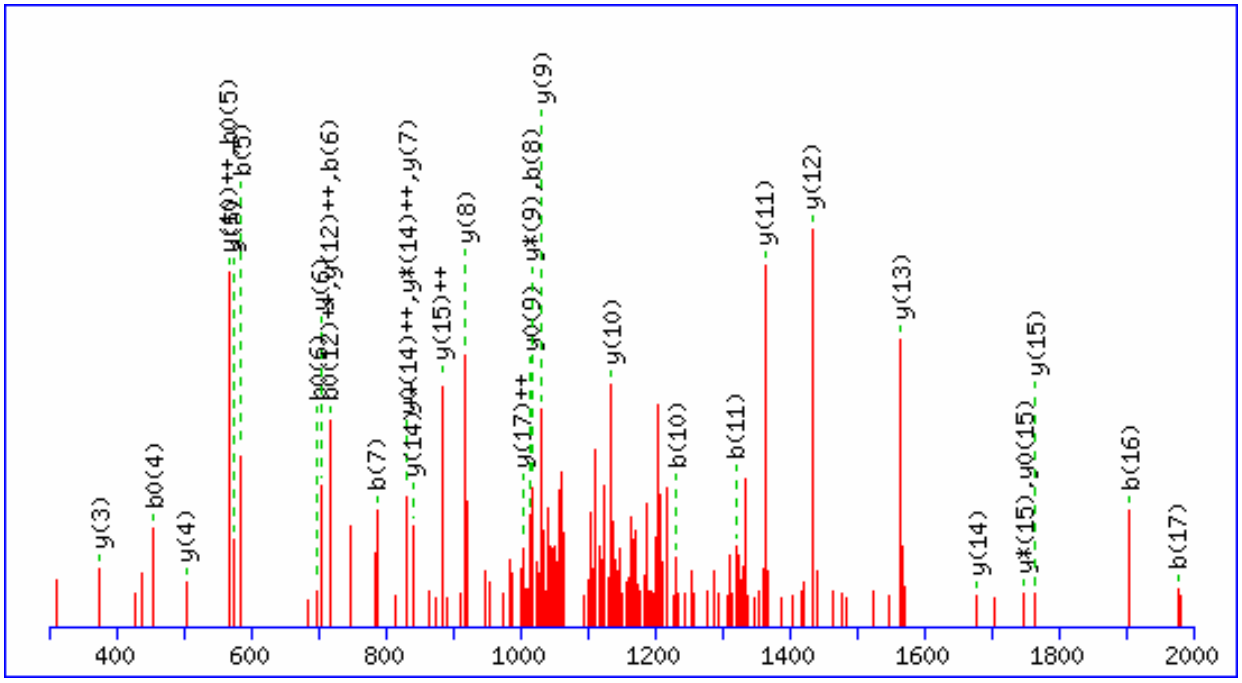
Gene Symbol	Sequences	m/z	Charge	Ion score
GNAQ	TLESIMACCLSEEAKEAR	1076.50	2+	67.7



N-term : N-Acetyl (Protein)
C9 : NEM (C)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	144.15	72.58			126.13	63.57	T							18
2	257.31	129.16			239.29	120.15	L	2009.31	1005.16	1992.28	996.64	1991.29	996.15	17
3	386.42	193.71			368.40	184.71	E	1896.15	948.58	1879.12	940.06	1878.13	939.57	16
4	473.50	237.25			455.48	228.25	S	1767.03	884.02	1750.00	875.51	1749.02	875.01	15
5	586.66	293.83			568.64	284.82	I	1679.96	840.48	1662.93	831.97	1661.94	831.47	14
6	717.85	359.43			699.84	350.42	M	1566.80	783.90	1549.77	775.39	1548.78	774.90	13
7	788.93	394.97			770.91	385.96	A	1435.60	718.31	1418.57	709.79	1417.59	709.30	12
8	892.07	446.54			874.06	437.53	C	1364.53	682.77	1347.49	674.25	1346.51	673.76	11
9	1120.34	560.67			1102.32	551.67	C	1261.38	631.20	1244.35	622.68	1243.37	622.19	10
10	1233.50	617.25			1215.48	608.25	L	1033.11	517.06	1016.08	508.55	1015.10	508.05	9
11	1320.58	660.79			1302.56	651.78	S	919.96	460.48	902.93	451.97	901.94	451.47	8
12	1449.69	725.35			1431.67	716.34	E	832.88	416.94	815.85	408.43	814.86	407.94	7
13	1578.80	789.91			1560.79	780.90	E	703.77	352.39	686.73	343.87	685.75	343.38	6
14	1649.88	825.44			1631.87	816.44	A	574.65	287.83	557.62	279.31	556.64	278.82	5
15	1778.05	889.53	1761.02	881.02	1760.04	880.52	K	503.57	252.29	486.54	243.78	485.56	243.28	4
16	1907.17	954.09	1890.14	945.57	1889.15	945.08	E	375.40	188.20	358.37	179.69	357.39	179.20	3
17	1978.25	989.63	1961.21	981.11	1960.23	980.62	A	246.29	123.65	229.26	115.13			2
18							R	175.21	88.11	158.18	79.59			1

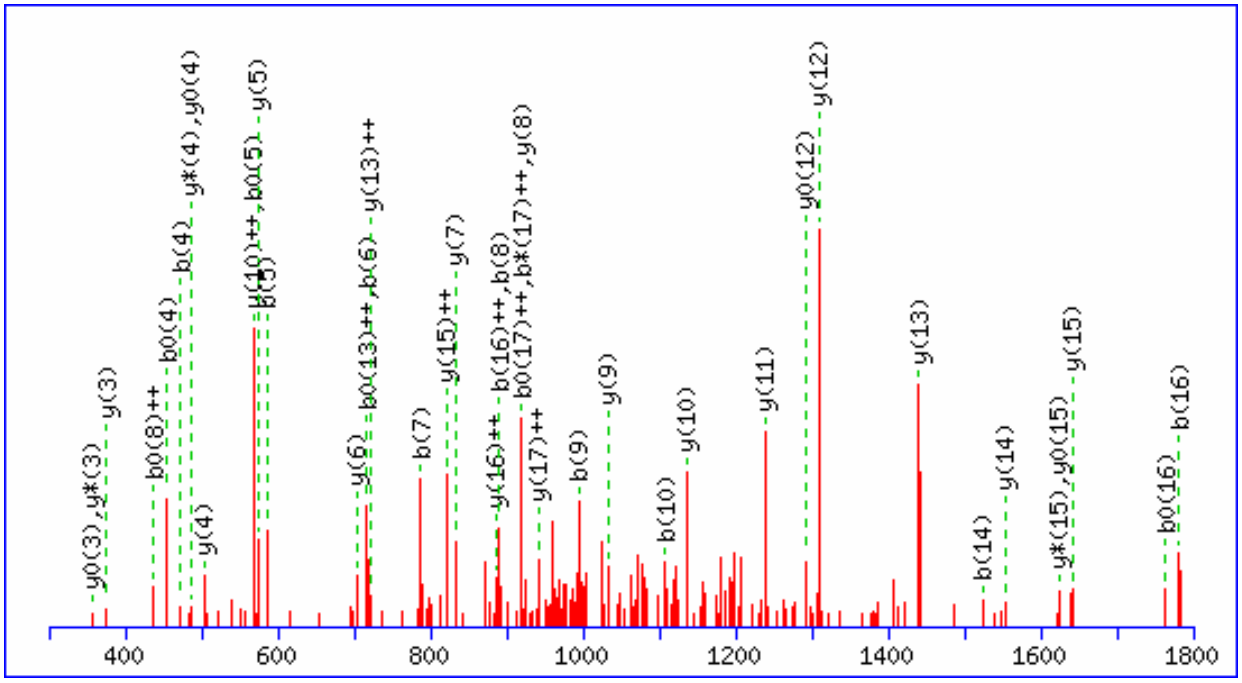
Gene Symbol	Sequences	m/z	Charge	Ion score
GNAQ	TLESIMACCLSEEAKEAR	1076.50	2+	99.9



N-term : N-Acetyl (Protein)
C8 : NEM (C)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	144.15	72.58			126.13	63.57	T							18
2	257.31	129.16			239.29	120.15	L	2009.31	1005.16	1992.28	996.64	1991.29	996.15	17
3	386.42	193.71			368.40	184.71	E	1896.15	948.58	1879.12	940.06	1878.13	939.57	16
4	473.50	237.25			455.48	228.25	S	1767.03	884.02	1750.00	875.51	1749.02	875.01	15
5	586.66	293.83			568.64	284.82	I	1679.96	840.48	1662.93	831.97	1661.94	831.47	14
6	717.85	359.43			699.84	350.42	M	1566.80	783.90	1549.77	775.39	1548.78	774.90	13
7	788.93	394.97			770.91	385.96	A	1435.60	718.31	1418.57	709.79	1417.59	709.30	12
8	1017.20	509.10			999.18	500.09	C	1364.53	682.77	1347.49	674.25	1346.51	673.76	11
9	1120.34	560.67			1102.32	551.67	C	1136.26	568.63	1119.23	560.12	1118.24	559.62	10
10	1233.50	617.25			1215.48	608.25	L	1033.11	517.06	1016.08	508.55	1015.10	508.05	9
11	1320.58	660.79			1302.56	651.78	S	919.96	460.48	902.93	451.97	901.94	451.47	8
12	1449.69	725.35			1431.67	716.34	E	832.88	416.94	815.85	408.43	814.86	407.94	7
13	1578.80	789.91			1560.79	780.90	E	703.77	352.39	686.73	343.87	685.75	343.38	6
14	1649.88	825.44			1631.87	816.44	A	574.65	287.83	557.62	279.31	556.64	278.82	5
15	1778.05	889.53	1761.02	881.02	1760.04	880.52	K	503.57	252.29	486.54	243.78	485.56	243.28	4
16	1907.17	954.09	1890.14	945.57	1889.15	945.08	E	375.40	188.20	358.37	179.69	357.39	179.20	3
17	1978.25	989.63	1961.21	981.11	1960.23	980.62	A	246.29	123.65	229.26	115.13			2
18							R	175.21	88.11	158.18	79.59			1

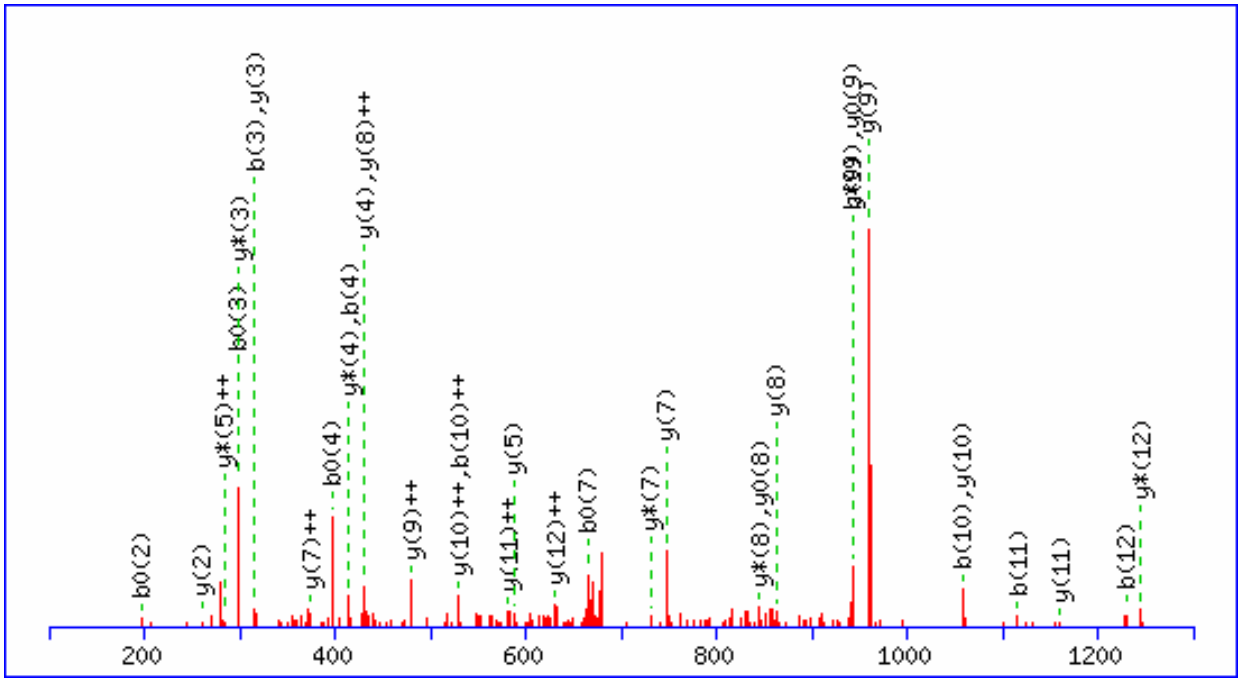
Gene Symbol	Sequences	m/z	Charge	Ion score
GNAQ	TLESIMACCLSEEAKEAR	1013.50	2+	106.5



N-term : N-Acetyl (Protein)

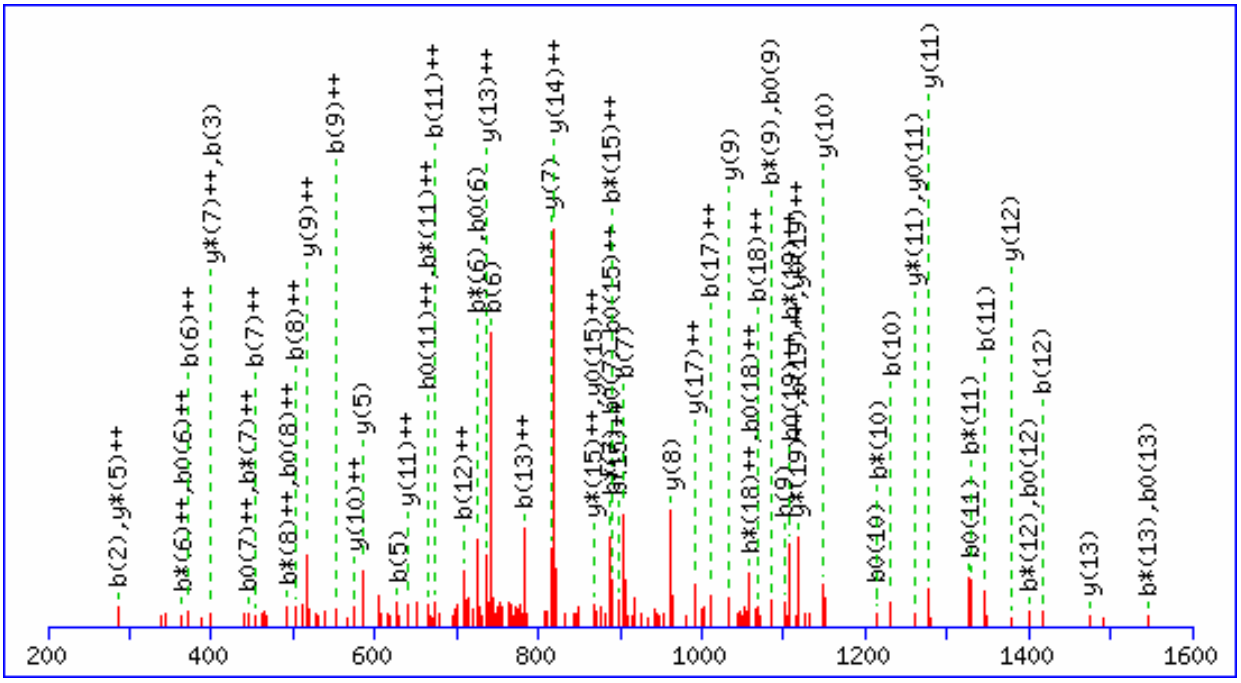
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	144.15	72.58			126.13	63.57	T							18
2	257.31	129.16			239.29	120.15	L	1884.18	942.59	1867.15	934.08	1866.16	933.59	17
3	386.42	193.71			368.40	184.71	E	1771.02	886.02	1753.99	877.50	1753.01	877.01	16
4	473.50	237.25			455.48	228.25	S	1641.91	821.46	1624.88	812.94	1623.89	812.45	15
5	586.66	293.83			568.64	284.82	I	1554.83	777.92	1537.80	769.40	1536.82	768.91	14
6	717.85	359.43			699.84	350.42	M	1441.67	721.34	1424.64	712.83	1423.66	712.33	13
7	788.93	394.97			770.91	385.96	A	1310.48	655.74	1293.45	647.23	1292.46	646.74	12
8	892.07	446.54			874.06	437.53	C	1239.40	620.20	1222.37	611.69	1221.38	611.20	11
9	995.21	498.11			977.20	489.10	C	1136.26	568.63	1119.23	560.12	1118.24	559.62	10
10	1108.37	554.69			1090.36	545.68	L	1033.11	517.06	1016.08	508.55	1015.10	508.05	9
11	1195.45	598.23			1177.43	589.22	S	919.96	460.48	902.93	451.97	901.94	451.47	8
12	1324.56	662.79			1306.55	653.78	E	832.88	416.94	815.85	408.43	814.86	407.94	7
13	1453.68	727.34			1435.66	718.34	E	703.77	352.39	686.73	343.87	685.75	343.38	6
14	1524.76	762.88			1506.74	753.87	A	574.65	287.83	557.62	279.31	556.64	278.82	5
15	1652.93	826.97	1635.90	818.45	1634.91	817.96	K	503.57	252.29	486.54	243.78	485.56	243.28	4
16	1782.04	891.52	1765.01	883.01	1764.03	882.52	E	375.40	188.20	358.37	179.69	357.39	179.20	3
17	1853.12	927.06	1836.09	918.55	1835.10	918.06	A	246.29	123.65	229.26	115.13			2
18							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
GPRC5A	ATTVPDGCRNGLK	687.64	2+	52.8



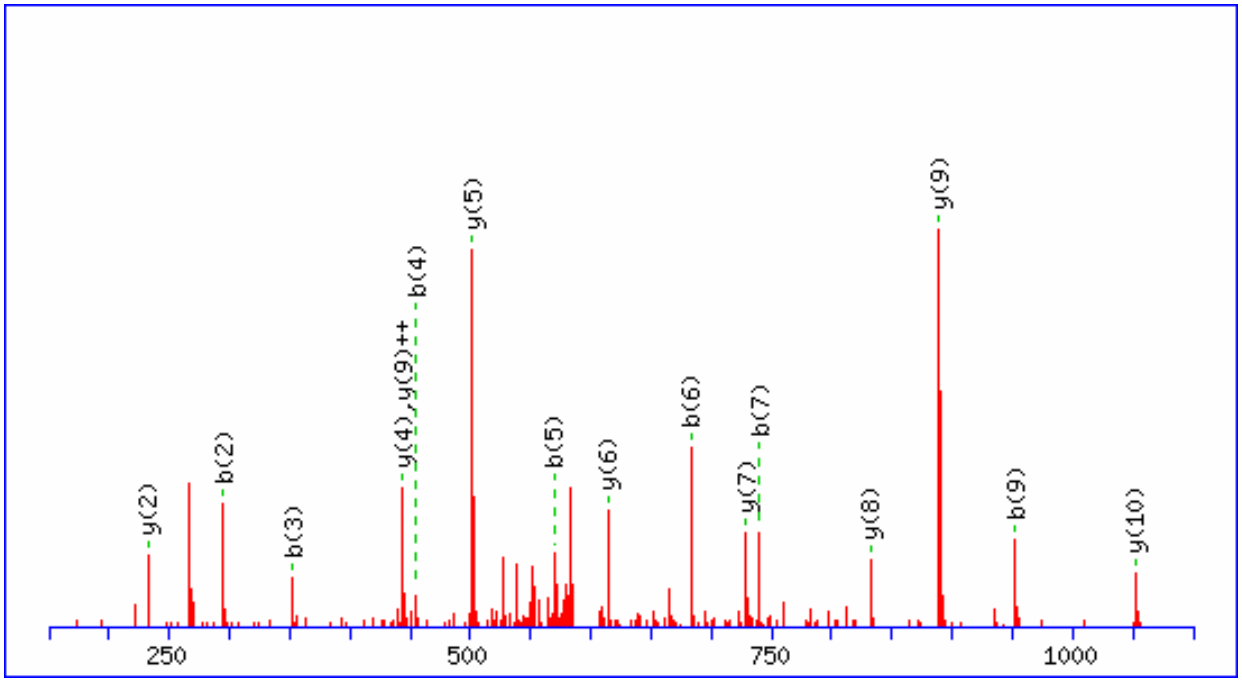
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.12	57.57					A							13
2	215.23	108.12			197.21	99.11	T	1261.43	631.22	1244.40	622.70	1243.41	622.21	12
3	316.33	158.67			298.32	149.66	T	1160.32	580.67	1143.29	572.15	1142.31	571.66	11
4	415.46	208.23			397.45	199.23	V	1059.22	530.11	1042.19	521.60	1041.21	521.11	10
5	512.58	256.79			494.56	247.78	P	960.09	480.55	943.06	472.03	942.07	471.54	9
6	627.66	314.34			609.65	305.33	D	862.97	431.99	845.94	423.48	844.96	422.98	8
7	684.72	342.86			666.70	333.85	G	747.89	374.45	730.86	365.93			7
8	787.86	394.43			769.84	385.43	C	690.84	345.92	673.81	337.41			6
9	944.04	472.53	927.01	464.01	926.03	463.52	R	587.69	294.35	570.66	285.84			5
10	1058.15	529.58	1041.12	521.06	1040.13	520.57	N	431.51	216.26	414.48	207.74			4
11	1115.20	558.10	1098.17	549.59	1097.18	549.10	G	317.40	159.21	300.37	150.69			3
12	1228.36	614.68	1211.32	606.17	1210.34	605.67	L	260.35	130.68	243.32	122.17			2
13							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
GPRC5A	QRNPMDYPVEDAFCKPQLVK	793.58	3+	83.2



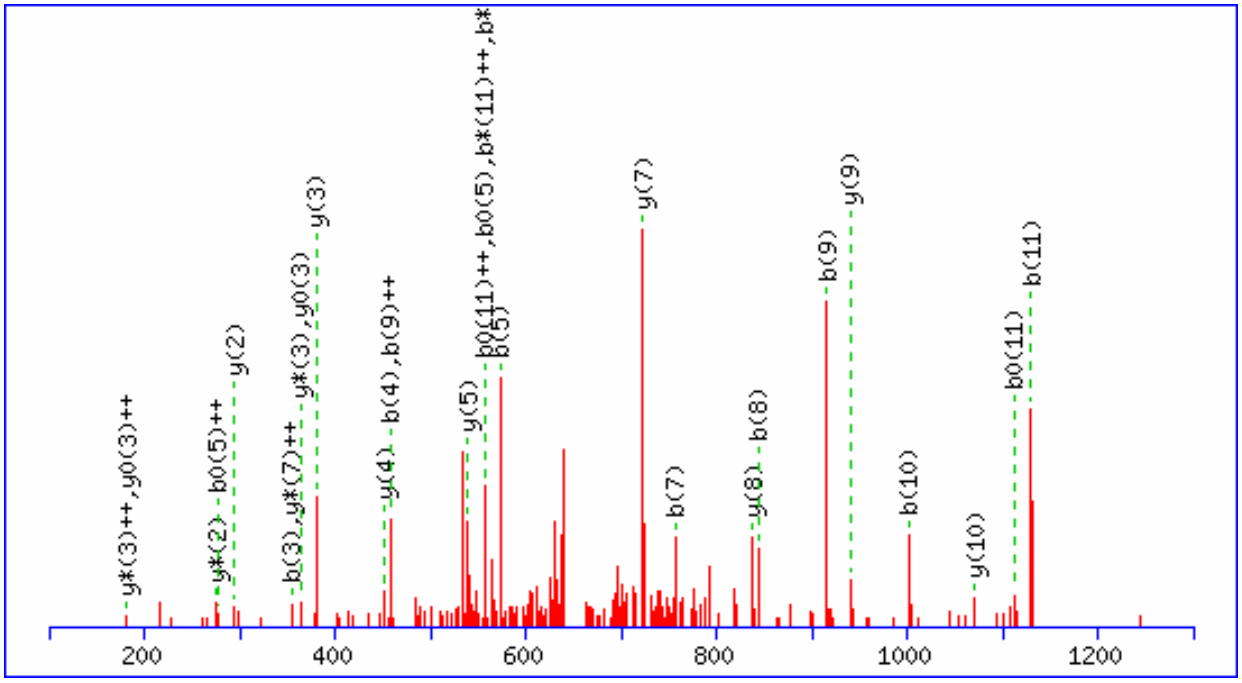
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.14	65.07	112.11	56.56			Q							20
2	285.32	143.17	268.29	134.65			R	2251.60	1126.31	2234.57	1117.79	2233.59	1117.30	19
3	399.43	200.22	382.39	191.70			N	2095.42	1048.21	2078.39	1039.70	2077.40	1039.21	18
4	496.54	248.77	479.51	240.26			P	1981.32	991.16	1964.28	982.65	1963.30	982.15	17
5	627.74	314.37	610.71	305.86			M	1884.20	942.60	1867.17	934.09	1866.18	933.60	16
6	742.82	371.92	725.79	363.40	724.81	362.91	D	1753.00	877.01	1735.97	868.49	1734.99	868.00	15
7	906.00	453.50	888.97	444.99	887.98	444.50	Y	1637.92	819.46	1620.89	810.95	1619.90	810.45	14
8	1003.11	502.06	986.08	493.55	985.10	493.05	P	1474.74	737.88	1457.71	729.36	1456.73	728.87	13
9	1102.24	551.63	1085.21	543.11	1084.23	542.62	V	1377.63	689.32	1360.60	680.80	1359.61	680.31	12
10	1231.36	616.18	1214.33	607.67	1213.34	607.18	E	1278.50	639.75	1261.47	631.24	1260.48	630.74	11
11	1346.45	673.73	1329.41	665.21	1328.43	664.72	D	1149.38	575.20	1132.35	566.68	1131.37	566.19	10
12	1417.52	709.27	1400.49	700.75	1399.51	700.26	A	1034.30	517.65	1017.27	509.14			9
13	1564.70	782.85	1547.67	774.34	1546.68	773.84	F	963.22	482.11	946.19	473.60			8
14	1667.84	834.42	1650.81	825.91	1649.82	825.42	C	816.04	408.53	799.01	400.01			7
15	1796.01	898.51	1778.98	889.99	1778.00	889.50	K	712.90	356.95	695.87	348.44			6
16	1893.13	947.07	1876.10	938.55	1875.11	938.06	P	584.73	292.87	567.70	284.35			5
17	2021.26	1011.13	2004.23	1002.62	2003.24	1002.12	Q	487.61	244.31	470.58	235.80			4
18	2134.41	1067.71	2117.38	1059.20	2116.40	1058.70	L	359.48	180.25	342.45	171.73			3
19	2233.55	1117.28	2216.51	1108.76	2215.53	1108.27	V	246.33	123.67	229.30	115.15			2
20							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
HLA-B/C	MYGCDLGPDGR	593.03	2+	71.4



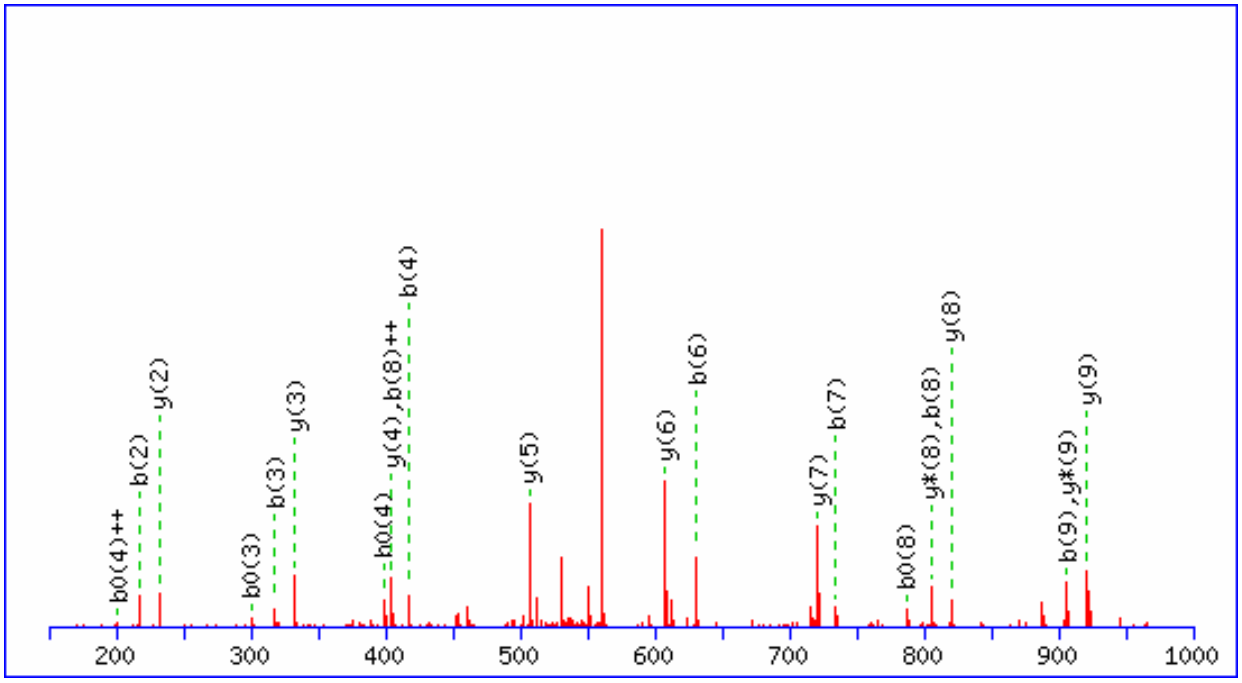
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	132.20	66.61			M							11
2	295.38	148.19			Y	1053.13	527.07	1036.10	518.55	1035.11	518.06	10
3	352.43	176.72			G	889.95	445.48	872.92	436.97	871.94	436.47	9
4	455.57	228.29			C	832.90	416.95	815.87	408.44	814.89	407.95	8
5	570.66	285.83	552.64	276.83	D	729.76	365.38	712.73	356.87	711.74	356.38	7
6	683.82	342.41	665.80	333.40	L	614.67	307.84	597.64	299.32	596.66	298.83	6
7	740.87	370.94	722.85	361.93	G	501.51	251.26	484.48	242.75	483.50	242.25	5
8	837.98	419.50	819.97	410.49	P	444.46	222.74	427.43	214.22	426.45	213.73	4
9	953.07	477.04	935.06	468.03	D	347.35	174.18	330.32	165.66	329.33	165.17	3
10	1010.12	505.56	992.11	496.56	G	232.26	116.63	215.23	108.12			2
11					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
HPCA	LLQCDPSSASQF	648.62	2+	75.9



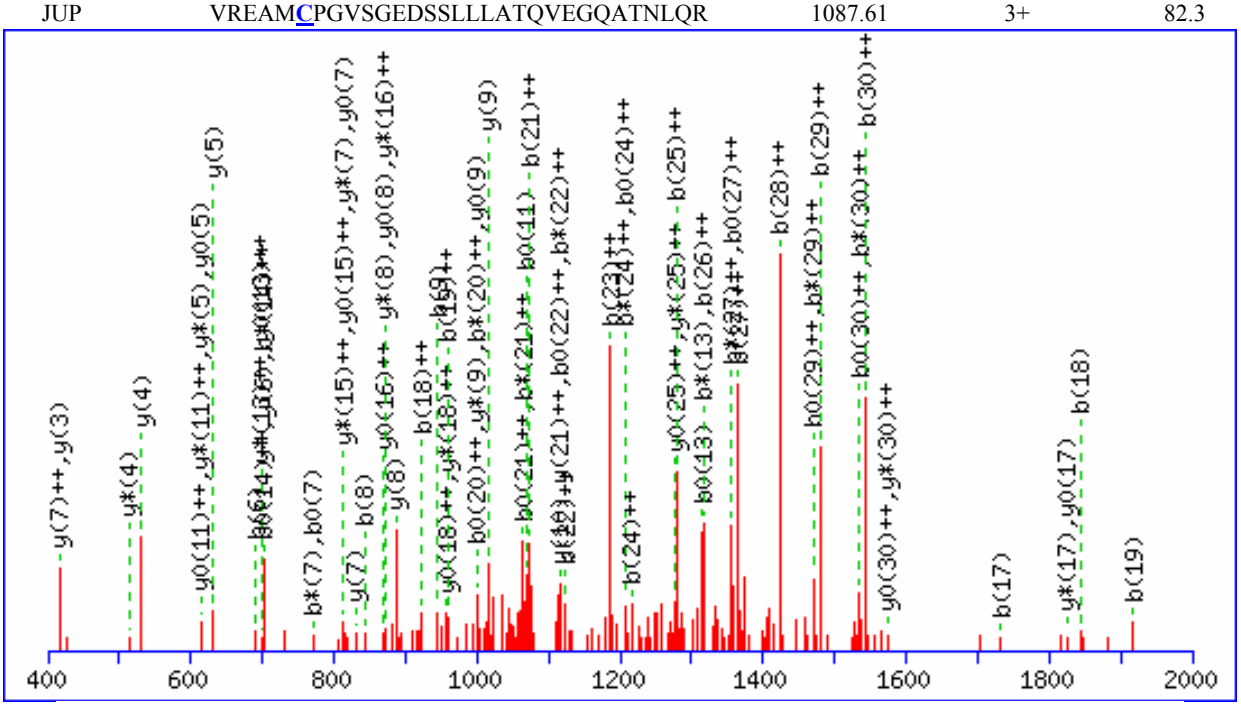
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					L							12
2	227.32	114.17					L	1183.27	592.14	1166.24	583.62	1165.25	583.13	11
3	355.45	178.23	338.42	169.71			Q	1070.11	535.56	1053.08	527.04	1052.10	526.55	10
4	458.60	229.80	441.56	221.29			C	941.98	471.49	924.95	462.98	923.97	462.49	9
5	573.68	287.35	556.65	278.83	555.67	278.34	D	838.84	419.92	821.81	411.41	820.82	410.92	8
6	670.80	335.90	653.77	327.39	652.78	326.90	P	723.75	362.38	706.72	353.86	705.74	353.37	7
7	757.88	379.44	740.84	370.93	739.86	370.43	S	626.64	313.82	609.61	305.31	608.62	304.81	6
8	844.95	422.98	827.92	414.46	826.94	413.97	S	539.56	270.28	522.53	261.77	521.54	261.28	5
9	916.03	458.52	899.00	450.00	898.02	449.51	A	452.48	226.74	435.45	218.23	434.47	217.74	4
10	1003.11	502.06	986.08	493.54	985.09	493.05	S	381.40	191.21	364.37	182.69	363.39	182.20	3
11	1131.24	566.12	1114.21	557.61	1113.22	557.11	Q	294.33	147.67	277.30	139.15			2
12							F	166.20	83.60					1

Gene Symbol	Sequences	m/z	Charge	Ion score
ITGA3	SETVLTCATGR	569.49	2+	87.7



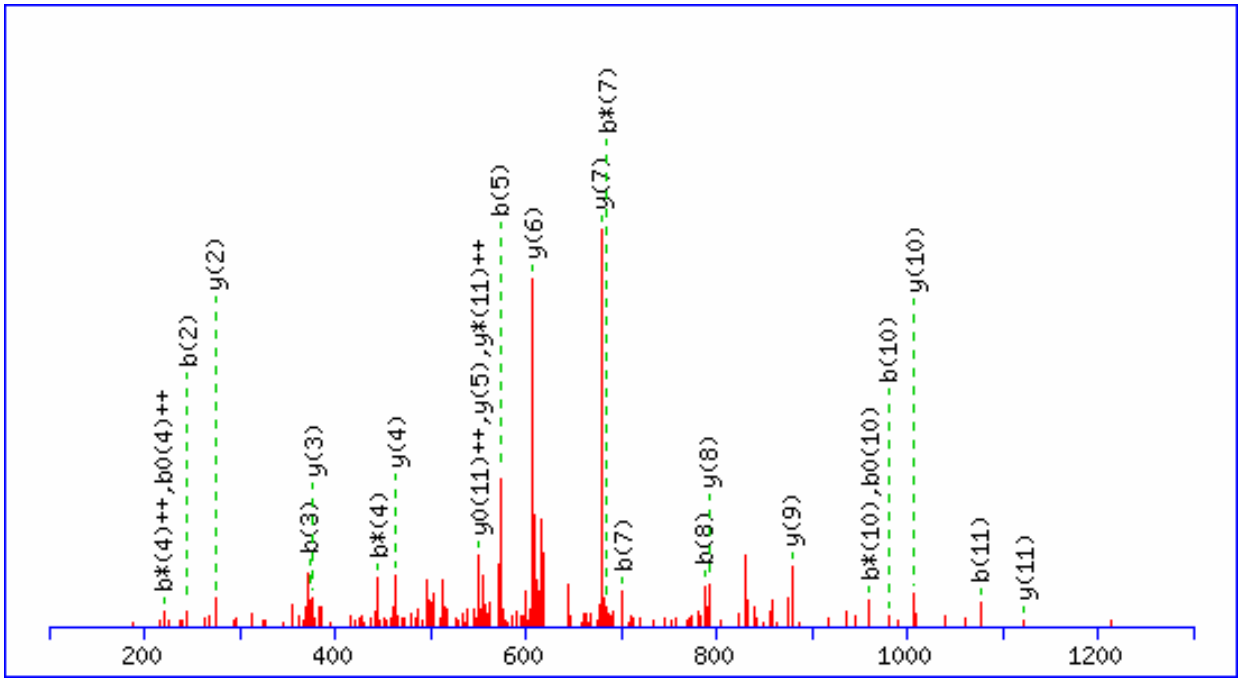
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55	70.07	35.54	S							11
2	217.20	109.10	199.18	100.10	E	1051.20	526.10	1034.16	517.59	1033.18	517.09	10
3	318.30	159.66	300.29	150.65	T	922.08	461.54	905.05	453.03	904.07	452.54	9
4	417.43	209.22	399.42	200.21	V	820.98	410.99	803.95	402.48	802.96	401.99	8
5	530.59	265.80	512.58	256.79	L	721.85	361.43	704.82	352.91	703.83	352.42	7
6	631.70	316.35	613.68	307.34	T	608.69	304.85	591.66	296.33	590.67	295.84	6
7	734.84	367.92	716.82	358.92	C	507.58	254.30	490.55	245.78	489.57	245.29	5
8	805.92	403.46	787.90	394.45	A	404.44	202.72	387.41	194.21	386.43	193.72	4
9	907.02	454.01	889.01	445.01	T	333.36	167.19	316.33	158.67	315.35	158.18	3
10	964.07	482.54	946.06	473.53	G	232.26	116.63	215.23	108.12			2
11					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
JUP	VREAMCPGVSGEDSSLLLATQVEGQATNLQR	1087.61	3+	82.3



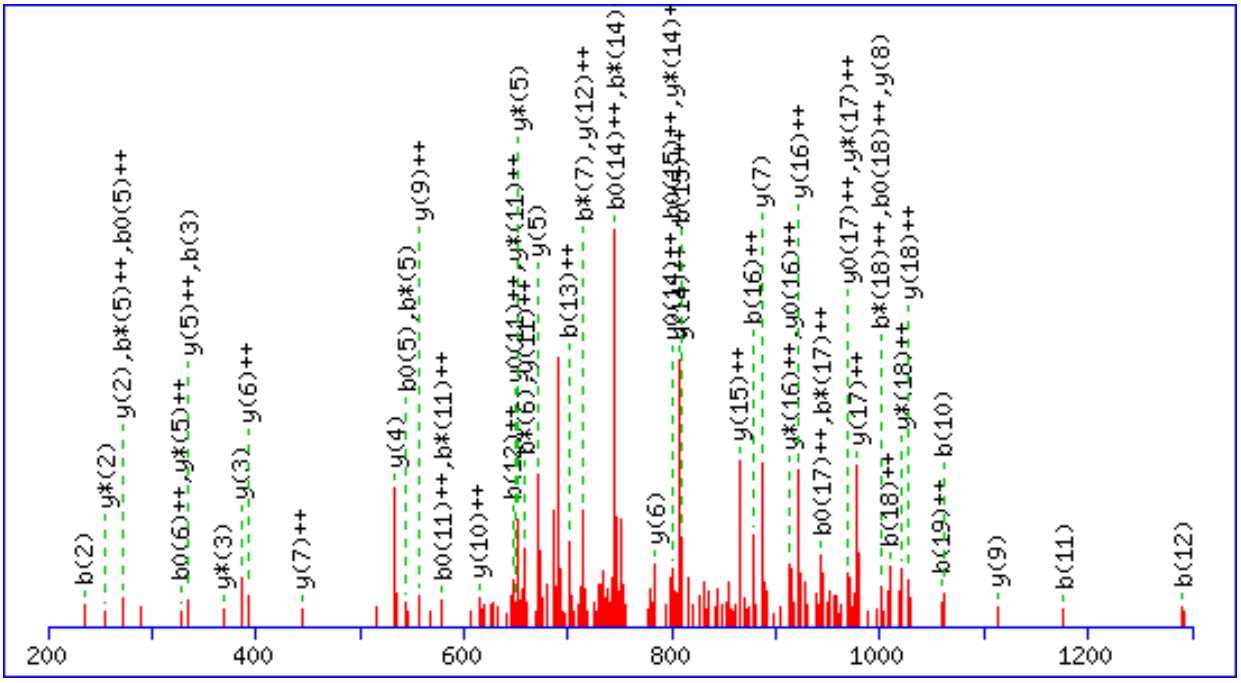
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							31
2	256.32	128.67	239.29	120.15			R	3162.49	1581.75	3145.46	1573.23	3144.47	1572.74	30
3	385.44	193.22	368.41	184.71	367.42	184.22	E	3006.30	1503.66	2989.27	1495.14	2988.29	1494.65	29
4	456.52	228.76	439.49	220.25	438.50	219.75	A	2877.19	1439.10	2860.16	1430.58	2859.17	1430.09	28
5	587.71	294.36	570.68	285.85	569.70	285.35	M	2806.11	1403.56	2789.08	1395.04	2788.10	1394.55	27
6	690.86	345.93	673.83	337.42	672.84	336.92	C	2674.91	1337.96	2657.88	1329.45	2656.90	1328.95	26
7	787.97	394.49	770.94	385.97	769.96	385.48	P	2571.77	1286.39	2554.74	1277.87	2553.76	1277.38	25
8	845.02	423.02	827.99	414.50	827.01	414.01	G	2474.66	1237.83	2457.63	1229.32	2456.64	1228.82	24
9	944.15	472.58	927.12	464.07	926.14	463.57	V	2417.61	1209.31	2400.57	1200.79	2399.59	1200.30	23
10	1031.23	516.12	1014.20	507.60	1013.22	507.11	S	2318.47	1159.74	2301.44	1151.23	2300.46	1150.73	22
11	1088.28	544.64	1071.25	536.13	1070.27	535.64	G	2231.40	1116.20	2214.37	1107.69	2213.38	1107.19	21
12	1217.40	609.20	1200.37	600.69	1199.38	600.19	E	2174.35	1087.68	2157.32	1079.16	2156.33	1078.67	20
13	1332.48	666.75	1315.45	658.23	1314.47	657.74	D	2045.23	1023.12	2028.20	1014.60	2027.22	1014.11	19
14	1419.56	710.28	1402.53	701.77	1401.55	701.28	S	1930.14	965.58	1913.11	957.06	1912.13	956.57	18
15	1506.64	753.82	1489.61	745.31	1488.62	744.82	S	1843.07	922.04	1826.04	913.52	1825.05	913.03	17
16	1619.80	810.40	1602.76	801.89	1601.78	801.39	L	1755.99	878.50	1738.96	869.98	1737.97	869.49	16
17	1732.95	866.98	1715.92	858.47	1714.94	857.97	L	1642.83	821.92	1625.80	813.40	1624.82	812.91	15
18	1846.11	923.56	1829.08	915.04	1828.10	914.55	L	1529.67	765.34	1512.64	756.83	1511.66	756.33	14
19	1917.19	959.10	1900.16	950.58	1899.17	950.09	A	1416.52	708.76	1399.49	700.25	1398.50	699.75	13
20	2018.29	1009.65	2001.26	1001.13	2000.28	1000.64	T	1345.44	673.22	1328.41	664.71	1327.42	664.22	12
21	2146.42	1073.71	2129.39	1065.20	2128.41	1064.71	Q	1244.33	622.67	1227.30	614.16	1226.32	613.66	11
22	2245.55	1123.28	2228.52	1114.77	2227.54	1114.27	V	1116.21	558.61	1099.18	550.09	1098.19	549.60	10
23	2374.67	1187.84	2357.64	1179.32	2356.65	1178.83	E	1017.07	509.04	1000.04	500.53	999.06	500.03	9
24	2431.72	1216.36	2414.69	1207.85	2413.70	1207.36	G	887.96	444.48	870.93	435.97	869.95	435.48	8
25	2559.85	1280.43	2542.82	1271.91	2541.83	1271.42	Q	830.91	415.96	813.88	407.44	812.89	406.95	7
26	2630.93	1315.97	2613.89	1307.45	2612.91	1306.96	A	702.78	351.89	685.75	343.38	684.76	342.89	6
27	2732.03	1366.52	2715.00	1358.00	2714.01	1357.51	T	631.70	316.36	614.67	307.84	613.69	307.35	5
28	2846.13	1423.57	2829.10	1415.05	2828.12	1414.56	N	530.60	265.80	513.57	257.29			4
29	2959.29	1480.15	2942.26	1471.63	2941.27	1471.14	L	416.50	208.75	399.47	200.24			3
30	3087.42	1544.21	3070.39	1535.70	3069.40	1535.21	Q	303.34	152.17	286.31	143.66			2
31							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
KCNK1	MLQSLAGSSCVR	626.47	2+	86.3



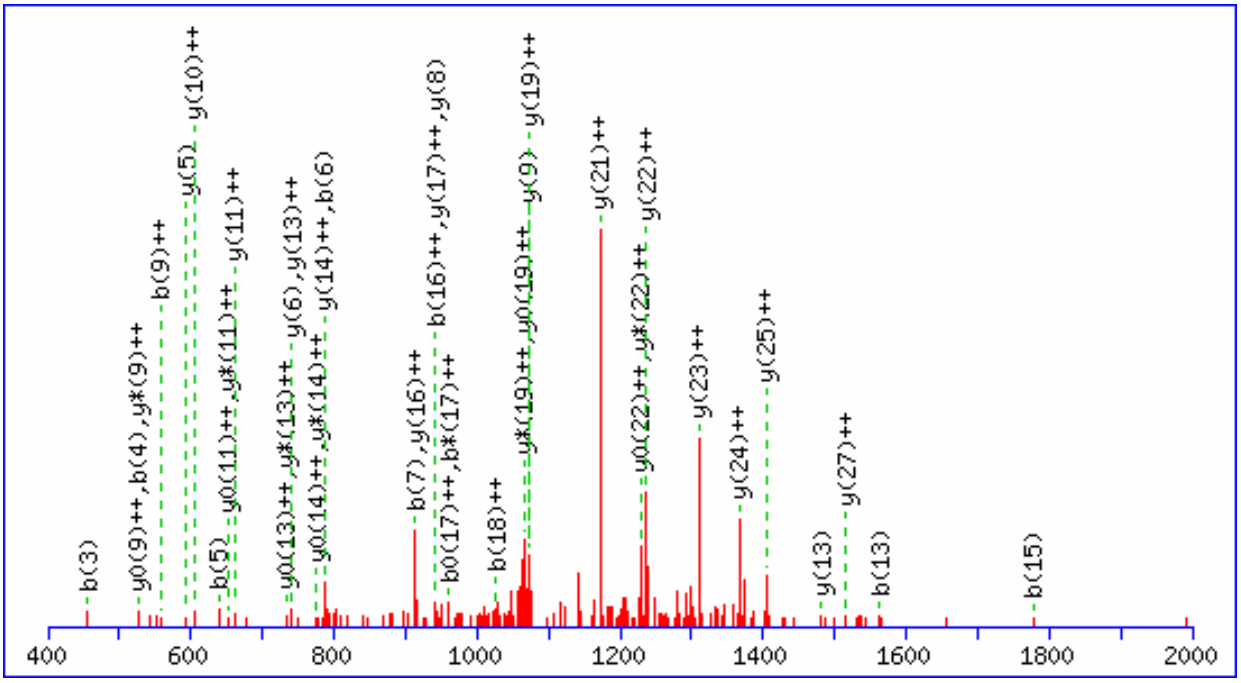
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	132.20	66.61					M							12
2	245.36	123.18					L	1121.29	561.15	1104.26	552.63	1103.27	552.14	11
3	373.49	187.25	356.46	178.73			Q	1008.13	504.57	991.10	496.05	990.12	495.56	10
4	460.57	230.79	443.54	222.27	442.55	221.78	S	880.00	440.50	862.97	431.99	861.99	431.50	9
5	573.73	287.37	556.70	278.85	555.71	278.36	L	792.92	396.97	775.89	388.45	774.91	387.96	8
6	644.80	322.91	627.77	314.39	626.79	313.90	A	679.77	340.39	662.74	331.87	661.75	331.38	7
7	701.85	351.43	684.82	342.92	683.84	342.42	G	608.69	304.85	591.66	296.33	590.67	295.84	6
8	788.93	394.97	771.90	386.45	770.92	385.96	S	551.64	276.32	534.61	267.81	533.62	267.32	5
9	876.01	438.51	858.98	429.99	857.99	429.50	S	464.56	232.78	447.53	224.27	446.54	223.78	4
10	979.15	490.08	962.12	481.56	961.14	481.07	C	377.48	189.25	360.45	180.73			3
11	1078.28	539.65	1061.25	531.13	1060.27	530.64	V	274.34	137.67	257.31	129.16			2
12							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
LGALS1	SFVLNLGKDSNNLCLHFNPR	763.90	3+	90.5



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							20
2	235.26	118.13			217.24	109.13	F	2202.51	1101.76	2185.48	1093.25	2184.50	1092.75	19
3	334.39	167.70			316.37	158.69	V	2055.34	1028.17	2038.31	1019.66	2037.33	1019.17	18
4	447.55	224.28			429.53	215.27	L	1956.21	978.61	1939.18	970.09	1938.19	969.60	17
5	561.65	281.33	544.62	272.81	543.64	272.32	N	1843.05	922.03	1826.02	913.51	1825.04	913.02	16
6	674.81	337.91	657.78	329.39	656.79	328.90	L	1728.95	864.98	1711.92	856.46	1710.93	855.97	15
7	731.86	366.43	714.83	357.92	713.84	357.43	G	1615.79	808.40	1598.76	799.88	1597.78	799.39	14
8	860.03	430.52	843.00	422.00	842.02	421.51	K	1558.74	779.87	1541.71	771.36	1540.72	770.87	13
9	975.12	488.06	958.09	479.55	957.10	479.06	D	1430.57	715.79	1413.54	707.27	1412.55	706.78	12
10	1062.20	531.60	1045.17	523.09	1044.18	522.59	S	1315.48	658.24	1298.45	649.73	1297.47	649.24	11
11	1176.30	588.65	1159.27	580.14	1158.28	579.65	N	1228.40	614.71	1211.37	606.19			10
12	1290.40	645.70	1273.37	637.19	1272.39	636.70	N	1114.30	557.65	1097.27	549.14			9
13	1403.56	702.28	1386.53	693.77	1385.54	693.28	L	1000.20	500.60	983.17	492.09			8
14	1506.70	753.85	1489.67	745.34	1488.69	744.85	C	887.04	444.02	870.01	435.51			7
15	1619.86	810.43	1602.83	801.92	1601.84	801.43	L	783.90	392.45	766.87	383.94			6
16	1757.00	879.00	1739.97	870.49	1738.98	870.00	H	670.74	335.87	653.71	327.36			5
17	1904.17	952.59	1887.14	944.08	1886.16	943.58	F	533.60	267.30	516.57	258.79			4
18	2018.28	1009.64	2001.24	1001.13	2000.26	1000.63	N	386.43	193.72	369.40	185.20			3
19	2115.39	1058.20	2098.36	1049.68	2097.38	1049.19	P	272.32	136.67	255.29	128.15			2
20							R	175.21	88.11	158.18	79.59			1

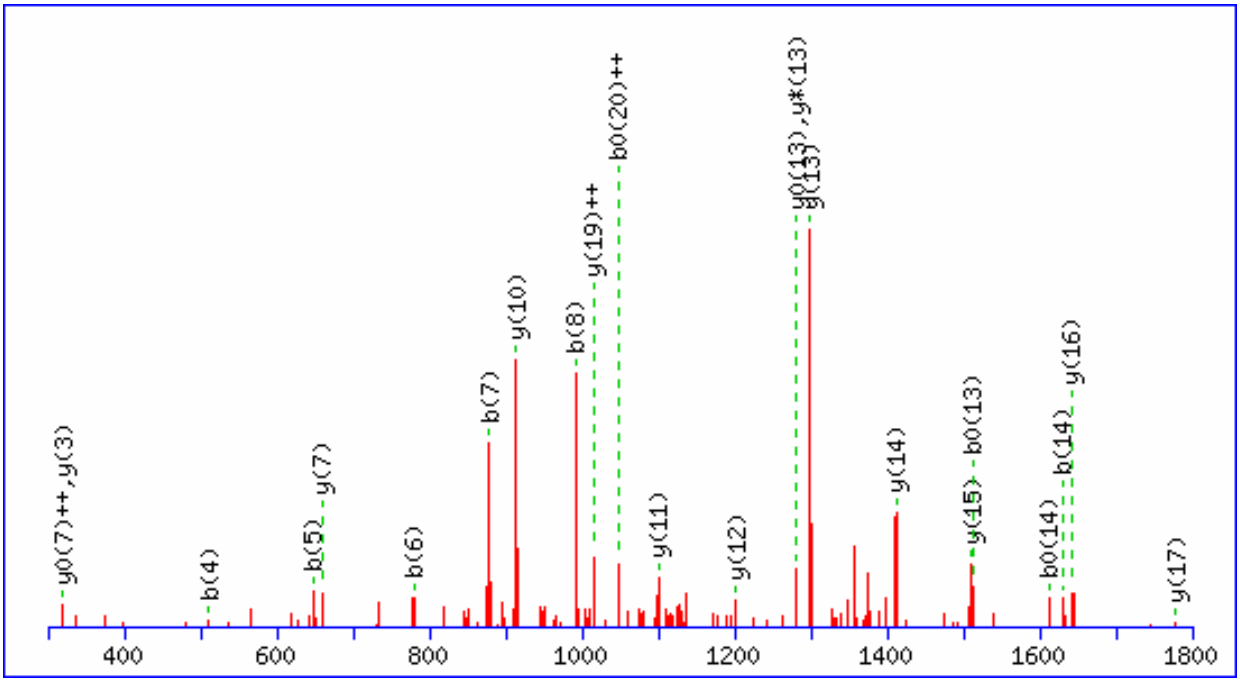
Gene Symbol	Sequences	m/z	Charge	Ion score
LOC653781	CPEALFQPCFLGMESCGIHETTFNSIMK	1088.00	3+	62.2



C1 : NEM (C)

#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	229.28	115.14					C							28
2	326.39	163.70					P	3032.51	1516.76	3015.48	1508.24	3014.50	1507.75	27
3	455.51	228.26			437.49	219.25	E	2935.40	1468.20	2918.37	1459.69	2917.38	1459.19	26
4	526.58	263.80			508.57	254.79	A	2806.28	1403.65	2789.25	1395.13	2788.27	1394.64	25
5	639.74	320.37			621.73	311.37	L	2735.20	1368.11	2718.17	1359.59	2717.19	1359.10	24
6	786.91	393.96			768.90	384.95	F	2622.05	1311.53	2605.02	1303.01	2604.03	1302.52	23
7	915.04	458.03	898.01	449.51	897.03	449.02	Q	2474.87	1237.94	2457.84	1229.43	2456.86	1228.93	22
8	1012.16	506.58	995.13	498.07	994.14	497.58	P	2346.74	1173.88	2329.71	1165.36	2328.73	1164.87	21
9	1115.30	558.15	1098.27	549.64	1097.29	549.15	C	2249.63	1125.32	2232.60	1116.80	2231.61	1116.31	20
10	1262.48	631.74	1245.45	623.23	1244.46	622.73	F	2146.49	1073.75	2129.46	1065.23	2128.47	1064.74	19
11	1375.63	688.32	1358.60	679.81	1357.62	679.31	L	1999.31	1000.16	1982.28	991.64	1981.30	991.15	18
12	1432.68	716.85	1415.65	708.33	1414.67	707.84	G	1886.15	943.58	1869.12	935.07	1868.14	934.57	17
13	1563.88	782.44	1546.85	773.93	1545.87	773.44	M	1829.10	915.06	1812.07	906.54	1811.09	906.05	16
14	1692.99	847.00	1675.96	838.49	1674.98	837.99	E	1697.91	849.46	1680.88	840.94	1679.89	840.45	15
15	1780.07	890.54	1763.04	882.02	1762.06	881.53	S	1568.79	784.90	1551.76	776.39	1550.78	775.89	14
16	1883.22	942.11	1866.18	933.60	1865.20	933.10	C	1481.72	741.36	1464.69	732.85	1463.70	732.35	13
17	1940.27	970.64	1923.24	962.12	1922.25	961.63	G	1378.57	689.79	1361.54	681.28	1360.56	680.78	12
18	2053.42	1027.22	2036.39	1018.70	2035.41	1018.21	I	1321.52	661.26	1304.49	652.75	1303.51	652.26	11
19	2190.56	1095.79	2173.53	1087.27	2172.55	1086.78	H	1208.36	604.69	1191.33	596.17	1190.35	595.68	10
20	2319.68	1160.34	2302.65	1151.83	2301.66	1151.34	E	1071.22	536.12	1054.19	527.60	1053.21	527.11	9
21	2420.78	1210.89	2403.75	1202.38	2402.77	1201.89	T	942.11	471.56	925.08	463.04	924.10	462.55	8
22	2521.89	1261.45	2504.85	1252.93	2503.87	1252.44	T	841.01	421.01	823.98	412.49	822.99	412.00	7
23	2669.06	1335.03	2652.03	1326.52	2651.04	1326.03	F	739.90	370.46	722.87	361.94	721.89	361.45	6
24	2783.16	1392.08	2766.13	1383.57	2765.15	1383.08	N	592.73	296.87	575.70	288.35	574.71	287.86	5
25	2870.24	1435.62	2853.21	1427.11	2852.22	1426.62	S	478.63	239.82	461.60	231.30	460.61	230.81	4
26	2983.40	1492.20	2966.37	1483.69	2965.38	1483.19	I	391.55	196.28	374.52	187.76			3
27	3114.59	1557.80	3097.56	1549.29	3096.58	1548.79	M	278.39	139.70	261.36	131.18			2
28							K	147.20	74.10	130.17	65.59			1

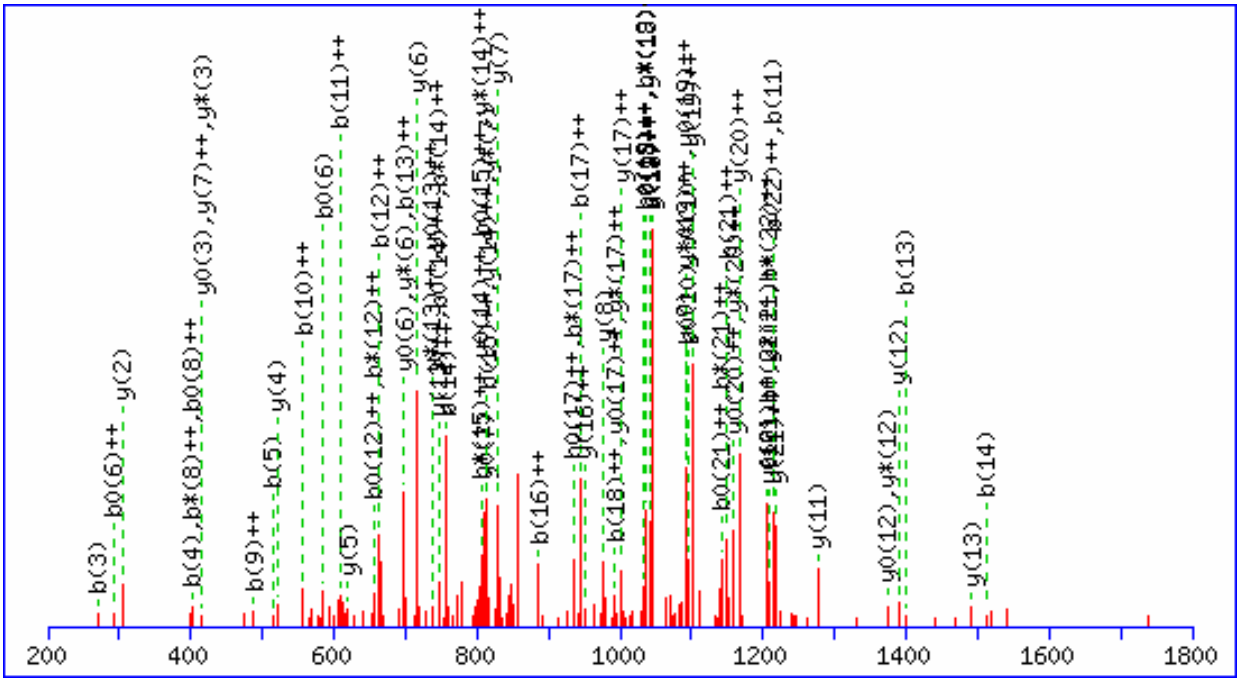
Gene Symbol	Sequences	m/z	Charge	Ion score
LOC730269	CDCFHMVLPTWPGTPGSVSGR	1146.10	2+	72.5



N-term : N-Acetyl (Protein)

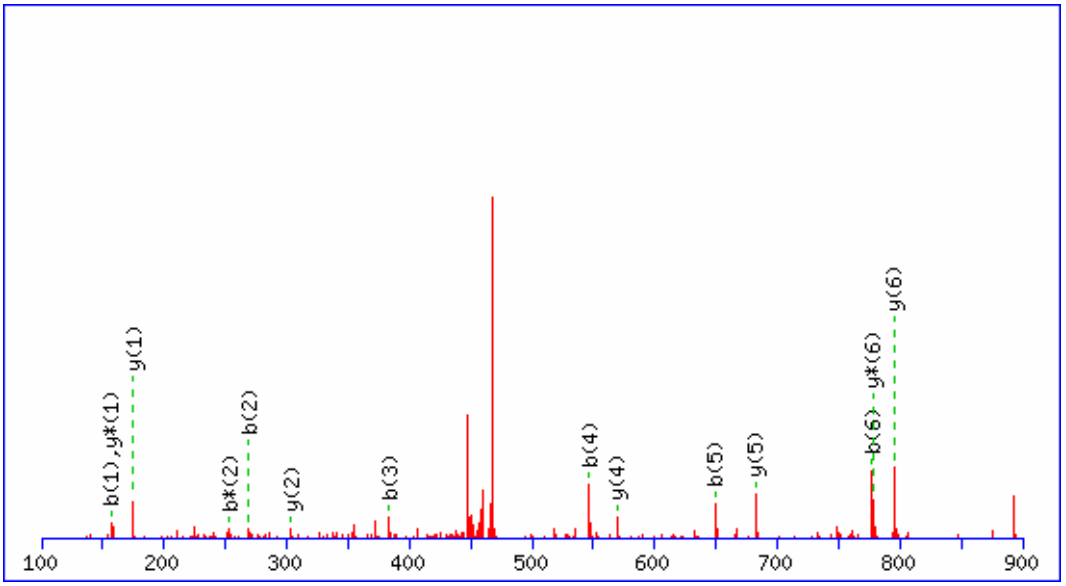
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	146.19	73.60			C							21
2	261.27	131.14	243.26	122.13	D	2145.44	1073.22	2128.41	1064.71	2127.42	1064.22	20
3	364.42	182.71	346.40	173.71	C	2030.35	**1015.68**	2013.32	1007.17	2012.34	1006.67	19
4	**511.59**	256.30	493.58	247.29	F	1927.21	964.11	1910.18	955.59	1909.19	955.10	18
5	**648.73**	324.87	630.72	315.86	H	**1780.04**	890.52	1763.01	882.01	1762.02	881.51	17
6	**779.93**	390.47	761.91	381.46	M	**1642.90**	821.95	1625.87	813.44	1624.88	812.94	16
7	**879.06**	440.03	861.04	431.03	V	**1511.70**	756.35	1494.67	747.84	1493.69	747.35	15
8	**992.22**	496.61	974.20	487.60	L	**1412.57**	706.79	1395.54	698.27	1394.55	697.78	14
9	1089.33	545.17	1071.32	536.16	P	**1299.41**	650.21	**1282.38**	641.69	**1281.40**	641.20	13
10	1190.43	595.72	1172.42	586.71	T	**1202.30**	601.65	1185.27	593.14	1184.28	592.64	12
11	1376.64	688.83	1358.63	679.82	W	**1101.19**	551.10	1084.16	542.59	1083.18	542.09	11
12	1473.76	737.38	1455.74	728.38	P	**914.98**	458.00	897.95	449.48	896.97	448.99	10
13	1530.81	765.91	**1512.80**	756.90	G	817.87	409.44	800.84	400.92	799.85	400.43	9
14	**1631.92**	816.46	**1613.90**	807.45	T	760.82	380.91	743.79	372.40	742.80	371.90	8
15	1729.03	865.02	1711.02	856.01	P	**659.71**	330.36	642.68	321.84	641.70	**321.35**	7
16	1786.08	893.54	1768.07	884.54	G	562.60	281.80	545.57	273.29	544.58	272.79	6
17	1873.16	937.08	1855.14	928.08	S	505.55	253.28	488.52	244.76	487.53	244.27	5
18	1972.29	986.65	1954.27	977.64	V	418.47	209.74	401.44	201.22	400.45	200.73	4
19	2059.37	1030.19	2041.35	1021.18	S	**319.34**	160.17	302.31	151.66	301.32	151.17	3
20	2116.42	1058.71	2098.40	**1049.71**	G	232.26	116.63	215.23	108.12			2
21					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
M6PR	AVVMIS**C**NRHTLADNFNPVSEER	869.04	3+	101.1



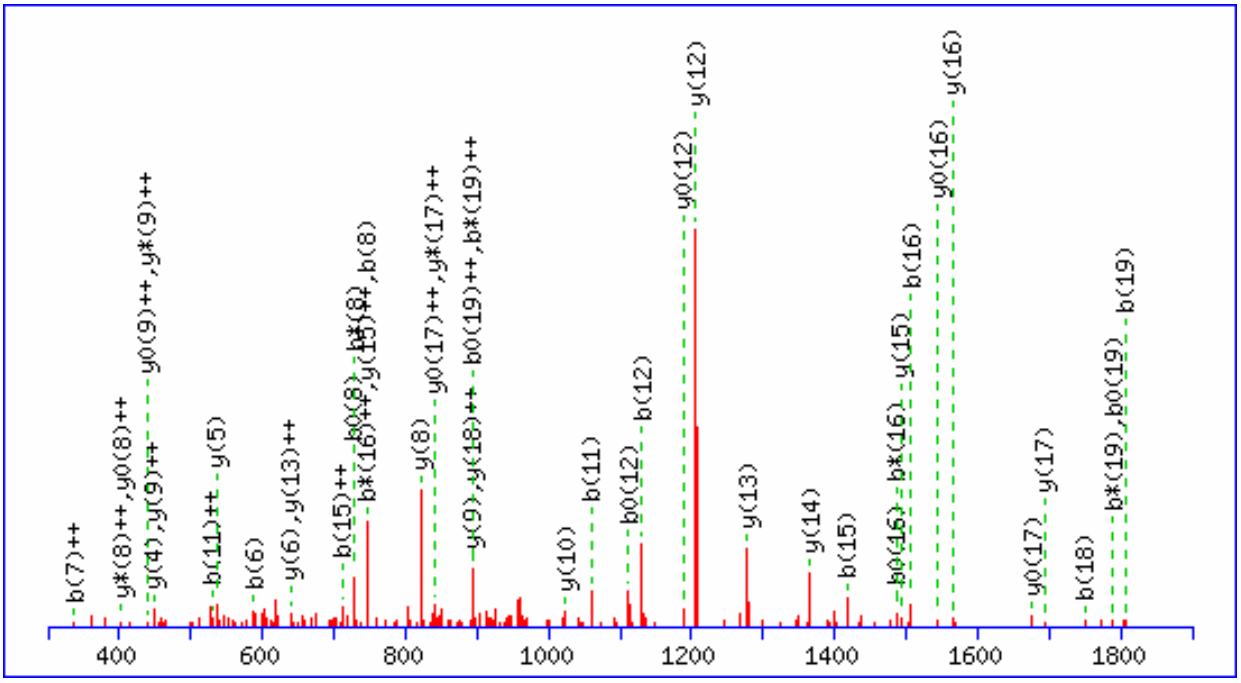
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							23
2	171.22	86.11					V	2532.83	1266.92	2515.80	1258.40	2514.81	1257.91	22
3	270.35	135.68					V	2433.70	1217.35	2416.67	1208.84	2415.68	1208.35	21
4	401.54	201.28					M	2334.57	1167.79	2317.54	1159.27	2316.55	1158.78	20
5	514.70	257.85					I	2203.37	1102.19	2186.34	1093.67	2185.36	1093.18	19
6	601.78	301.39			583.76	292.39	S	2090.21	1045.61	2073.18	1037.10	2072.20	1036.60	18
7	704.92	352.96			686.91	343.96	C	2003.14	1002.07	1986.11	993.56	1985.12	993.06	17
8	819.02	410.02	801.99	401.50	801.01	401.01	N	1899.99	950.50	1882.96	941.99	1881.98	941.49	16
9	975.21	488.11	958.18	479.59	957.19	479.10	R	1785.89	893.45	1768.86	884.93	1767.88	884.44	15
10	1112.35	556.68	1095.32	548.16	1094.33	547.67	H	1629.71	815.36	1612.68	806.84	1611.69	806.35	14
11	1213.45	607.23	1196.42	598.72	1195.44	598.22	T	1492.57	746.79	1475.54	738.27	1474.55	737.78	13
12	1326.61	663.81	1309.58	655.29	1308.60	654.80	L	1391.46	696.24	1374.43	687.72	1373.45	687.23	12
13	1397.69	699.35	1380.66	690.83	1379.67	690.34	A	1278.30	639.66	1261.27	631.14	1260.29	630.65	11
14	1512.78	756.89	1495.75	748.38	1494.76	747.88	D	1207.23	604.12	1190.20	595.60	1189.21	595.11	10
15	1626.88	813.94	1609.85	805.43	1608.86	804.94	N	1092.14	546.57	1075.11	538.06	1074.12	537.57	9
16	1774.05	887.53	1757.02	879.02	1756.04	878.52	F	978.04	489.52	961.01	481.01	960.02	480.51	8
17	1888.16	944.58	1871.12	936.07	1870.14	935.57	N	830.86	415.94	813.83	407.42	812.85	406.93	7
18	1985.27	993.14	1968.24	984.62	1967.26	984.13	P	716.76	358.88	699.73	350.37	698.75	349.88	6
19	2084.40	1042.70	2067.37	1034.19	2066.39	1033.70	V	619.65	310.33	602.61	301.81	601.63	301.32	5
20	2171.48	1086.24	2154.45	1077.73	2153.46	1077.24	S	520.51	260.76	503.48	252.25	502.50	251.75	4
21	2300.59	1150.80	2283.56	1142.29	2282.58	1141.79	E	433.44	217.22	416.41	208.71	415.42	208.21	3
22	2429.71	1215.36	2412.68	1206.84	2411.69	1206.35	E	304.32	152.67	287.29	144.15	286.31	143.66	2
23							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
MMP14	RLLYCQR	476.58	2+	45.6



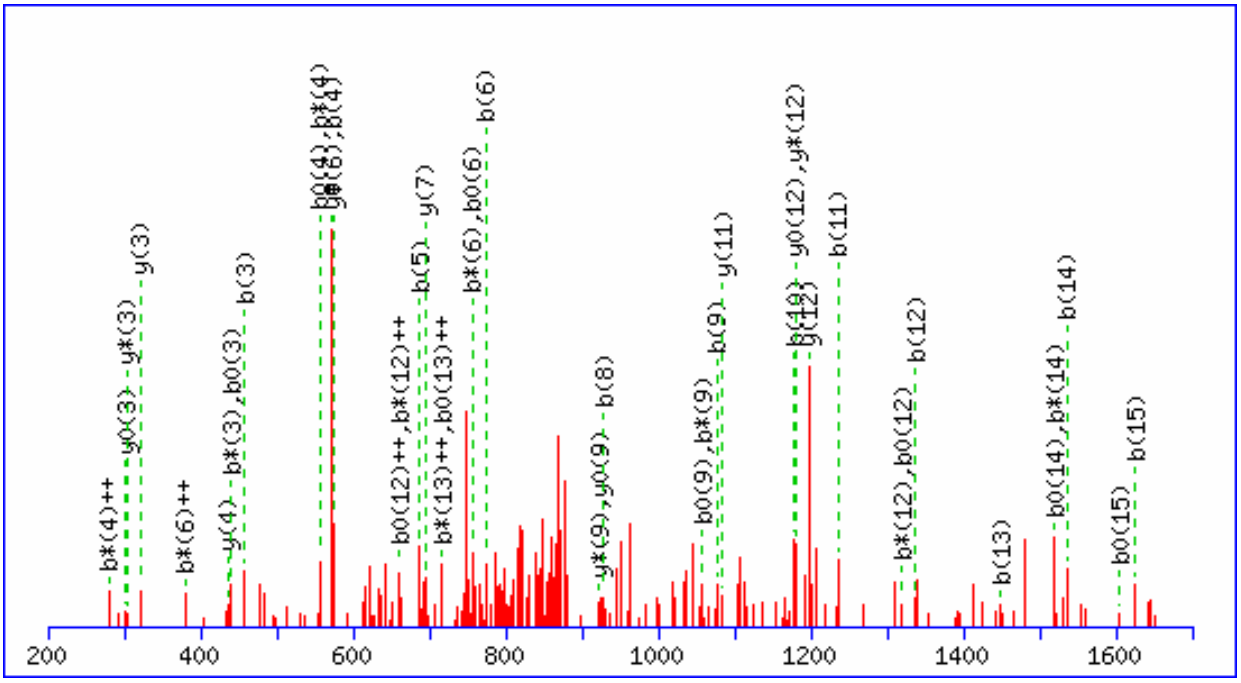
#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	157.19	79.10	140.16	70.59	R					7
2	270.35	135.68	253.32	127.16	L	795.97	398.49	778.94	389.97	6
3	383.51	192.26	366.48	183.74	L	682.81	341.91	665.78	333.39	5
4	546.68	273.85	529.65	265.33	Y	569.65	285.33	552.62	276.82	4
5	649.83	325.42	632.79	316.90	C	406.48	203.74	389.45	195.23	3
6	777.95	389.48	760.92	380.97	Q	303.34	152.17	286.31	143.66	2
7					R	175.21	88.11	158.18	79.59	1

Gene Symbol	Sequences	m/z	Charge	Ion score
MPP1	VASMAQSAPSEAPS**C**SPFGK	976.59	2+	87.3



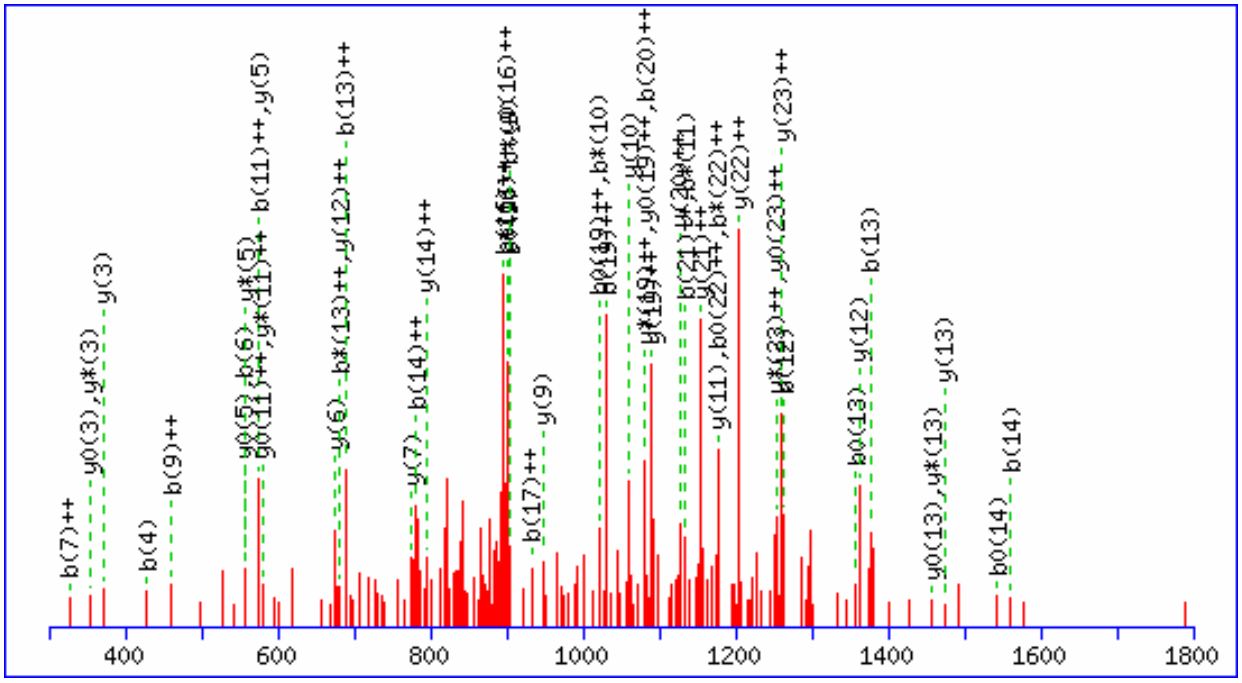
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							20
2	171.22	86.11					A	1854.05	927.53	1837.02	919.01	1836.03	918.52	19
3	258.29	129.65			240.28	120.64	S	1782.97	891.99	1765.94	883.47	1764.95	882.98	18
4	389.49	195.25			371.48	186.24	M	1695.89	848.45	1678.86	839.93	1677.88	839.44	17
5	460.57	230.79			442.55	221.78	A	1564.70	782.85	1547.66	774.34	1546.68	773.84	16
6	588.70	294.85	571.67	286.34	570.68	285.85	Q	1493.62	747.31	1476.59	738.80	1475.60	738.31	15
7	675.77	338.39	658.74	329.88	657.76	329.38	S	1365.49	683.25	1348.46	674.73	1347.47	674.24	14
8	746.85	373.93	729.82	365.42	728.84	364.92	A	1278.41	639.71	1261.38	631.19	1260.40	630.70	13
9	843.97	422.49	826.94	413.97	825.95	413.48	P	1207.33	604.17	1190.30	595.66	1189.32	595.16	12
10	931.05	466.03	914.01	457.51	913.03	457.02	S	1110.22	555.61	1093.19	547.10	1092.20	546.61	11
11	1060.16	530.58	1043.13	522.07	1042.14	521.58	E	1023.14	512.07	1006.11	503.56	1005.13	503.07	10
12	1131.24	566.12	1114.21	557.61	1113.22	557.11	A	894.03	447.52	877.00	439.00	876.01	438.51	9
13	1228.35	614.68	1211.32	606.16	1210.34	605.67	P	822.95	411.98	805.92	403.46	804.93	402.97	8
14	1315.43	658.22	1298.40	649.70	1297.41	649.21	S	725.83	363.42	708.80	354.91	707.82	354.41	7
15	1418.57	709.79	1401.54	701.27	1400.56	700.78	C	638.76	319.88	621.73	311.37	620.74	310.87	6
16	1505.65	753.33	1488.62	744.81	1487.63	744.32	S	535.61	268.31	518.58	259.80	517.60	259.30	5
17	1602.76	801.89	1585.73	793.37	1584.75	792.88	P	448.54	224.77	431.51	216.26			4
18	1749.94	875.47	1732.91	866.96	1731.92	866.47	F	351.42	176.21	334.39	167.70			3
19	1806.99	904.00	1789.96	895.48	1788.97	894.99	G	204.25	102.63	187.22	94.11			2
20							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
MPP6	RDWDNSGPFCGTISSK	885.71	2+	62.4



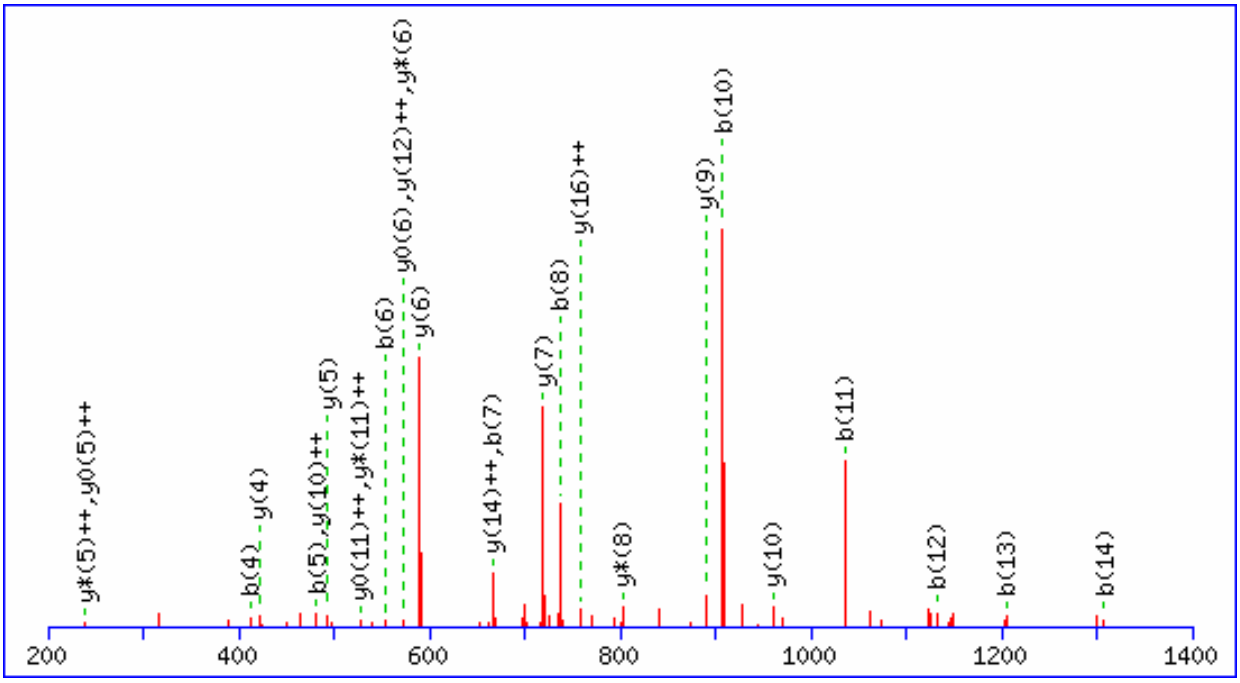
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	157.19	79.10	140.16	70.59			R							16
2	272.28	136.64	255.25	128.13	254.27	127.64	D	1614.71	807.86	1597.68	799.34	1596.70	798.85	15
3	458.49	229.75	441.46	221.23	440.48	220.74	W	1499.62	750.32	1482.59	741.80	1481.61	741.31	14
4	573.58	287.29	556.55	278.78	555.56	278.29	D	1313.41	657.21	1296.38	648.70	1295.40	648.20	13
5	687.68	344.34	670.65	335.83	669.67	335.34	N	1198.33	599.67	1181.30	591.15	1180.31	590.66	12
6	774.76	387.88	757.73	379.37	756.74	378.88	S	1084.22	542.62	1067.19	534.10	1066.21	533.61	11
7	831.81	416.41	814.78	407.89	813.79	407.40	G	997.15	499.08	980.12	490.56	979.13	490.07	10
8	928.92	464.97	911.89	456.45	910.91	455.96	P	940.09	470.55	923.06	462.04	922.08	461.54	9
9	1076.10	538.55	1059.07	530.04	1058.08	529.55	F	842.98	421.99	825.95	413.48	824.96	412.99	8
10	1179.24	590.12	1162.21	581.61	1161.23	581.12	C	695.81	348.41	678.78	339.89	677.79	339.40	7
11	1236.29	618.65	1219.26	610.14	1218.28	609.64	G	592.66	296.84	575.63	288.32	574.65	287.83	6
12	1337.40	669.20	1320.37	660.69	1319.38	660.19	T	535.61	268.31	518.58	259.79	517.60	259.30	5
13	1450.55	725.78	1433.52	717.27	1432.54	716.77	I	434.51	217.76	417.48	209.24	416.49	208.75	4
14	1537.63	769.32	1520.60	760.80	1519.62	760.31	S	321.35	161.18	304.32	152.66	303.33	152.17	3
15	1624.71	812.86	1607.68	804.34	1606.69	803.85	S	234.27	117.64	217.24	109.13	216.26	108.63	2
16							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
MTHFD1	SKIVGAPMHDLLLWNNATVTTCHSK	913.74	3+	78.9



#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							25
2	216.26	108.63	199.23	100.12	198.24	99.63	K	2651.09	1326.05	2634.06	1317.53	2633.08	1317.04	24
3	329.42	165.21	312.38	156.70	311.40	156.20	I	2522.92	1261.96	2505.89	1253.45	2504.90	1252.96	23
4	428.55	214.78	411.52	206.26	410.53	205.77	V	2409.76	1205.38	2392.73	1196.87	2391.75	1196.38	22
5	485.60	243.30	468.57	234.79	467.58	234.30	G	2310.63	1155.82	2293.60	1147.30	2292.62	1146.81	21
6	556.68	278.84	539.64	270.33	538.66	269.83	A	2253.58	1127.29	2236.55	1118.78	2235.56	1118.29	20
7	653.79	327.40	636.76	318.88	635.78	318.39	P	2182.50	1091.75	2165.47	1083.24	2164.49	1082.75	19
8	784.99	393.00	767.96	384.48	766.97	383.99	M	2085.39	1043.20	2068.36	1034.68	2067.37	1034.19	18
9	922.13	461.57	905.10	453.05	904.11	452.56	H	1954.19	977.60	1937.16	969.08	1936.18	968.59	17
10	1037.21	519.11	1020.18	510.60	1019.20	510.10	D	1817.05	909.03	1800.02	900.51	1799.04	900.02	16
11	1150.37	575.69	1133.34	567.17	1132.36	566.68	L	1701.96	851.49	1684.93	842.97	1683.95	842.48	15
12	1263.53	632.27	1246.50	623.75	1245.51	623.26	L	1588.81	794.91	1571.78	786.39	1570.79	785.90	14
13	1376.69	688.85	1359.66	680.33	1358.67	679.84	L	1475.65	738.33	1458.62	729.81	1457.63	729.32	13
14	1562.90	781.95	1545.87	773.44	1544.88	772.94	W	1362.49	681.75	1345.46	673.23	1344.48	672.74	12
15	1677.00	839.00	1659.97	830.49	1658.98	830.00	N	1176.28	588.64	1159.25	580.13	1158.27	579.64	11
16	1791.10	896.05	1774.07	887.54	1773.09	887.05	N	1062.18	531.59	1045.15	523.08	1044.16	522.59	10
17	1862.18	931.59	1845.15	923.08	1844.16	922.59	A	948.08	474.54	931.05	466.03	930.06	465.53	9
18	1963.28	982.15	1946.25	973.63	1945.27	973.14	T	877.00	439.00	859.97	430.49	858.98	430.00	8
19	2062.41	1031.71	2045.38	1023.20	2044.40	1022.70	V	775.89	388.45	758.86	379.94	757.88	379.44	7
20	2163.52	1082.26	2146.49	1073.75	2145.50	1073.26	T	676.76	338.89	659.73	330.37	658.75	329.88	6
21	2264.62	1132.81	2247.59	1124.30	2246.61	1123.81	T	575.66	288.33	558.63	279.82	557.64	279.33	5
22	2367.76	1184.39	2350.73	1175.87	2349.75	1175.38	C	474.56	237.78	457.52	229.27	456.54	228.77	4
23	2504.90	1252.96	2487.87	1244.44	2486.89	1243.95	H	371.41	186.21	354.38	177.69	353.40	177.20	3
24	2591.98	1296.49	2574.95	1287.98	2573.97	1287.49	S	234.27	117.64	217.24	109.13	216.26	108.63	2
25							K	147.20	74.10	130.17	65.59			1

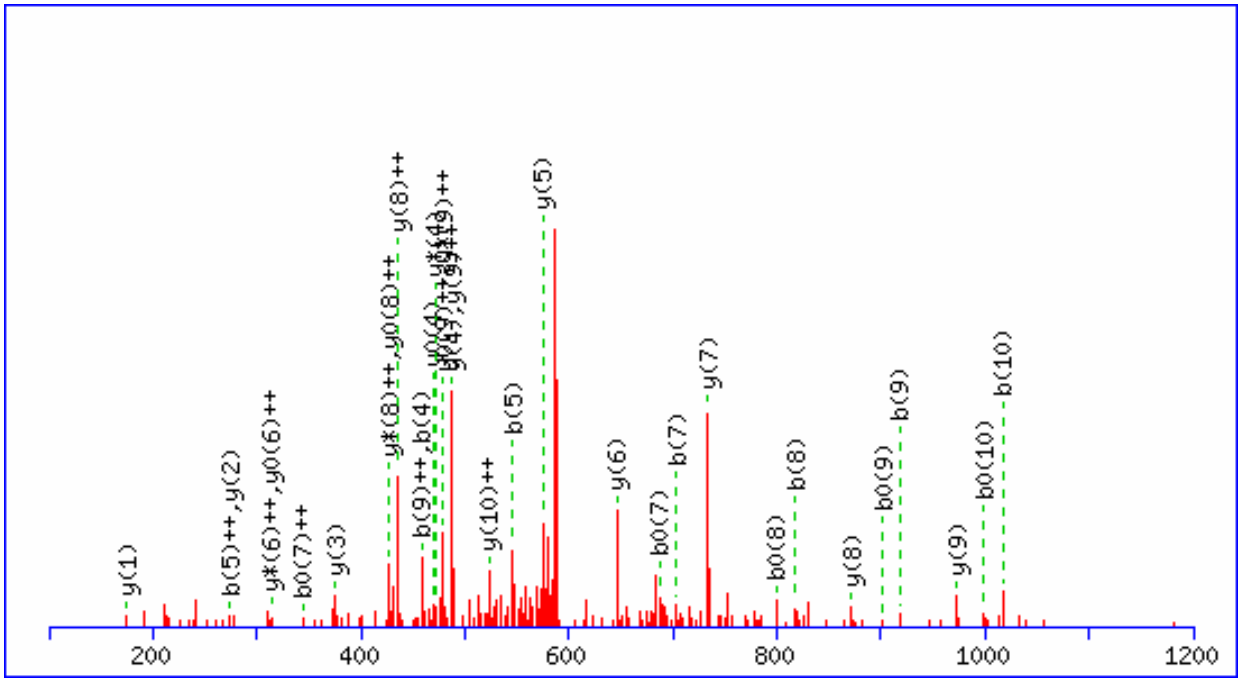
Gene Symbol	Sequences	m/z	Charge	Ion score
NDFIP1	ALALAALAAVEPA**C**GSR	813.55	2+	66.6



N-term : N-Acetyl (Protein)

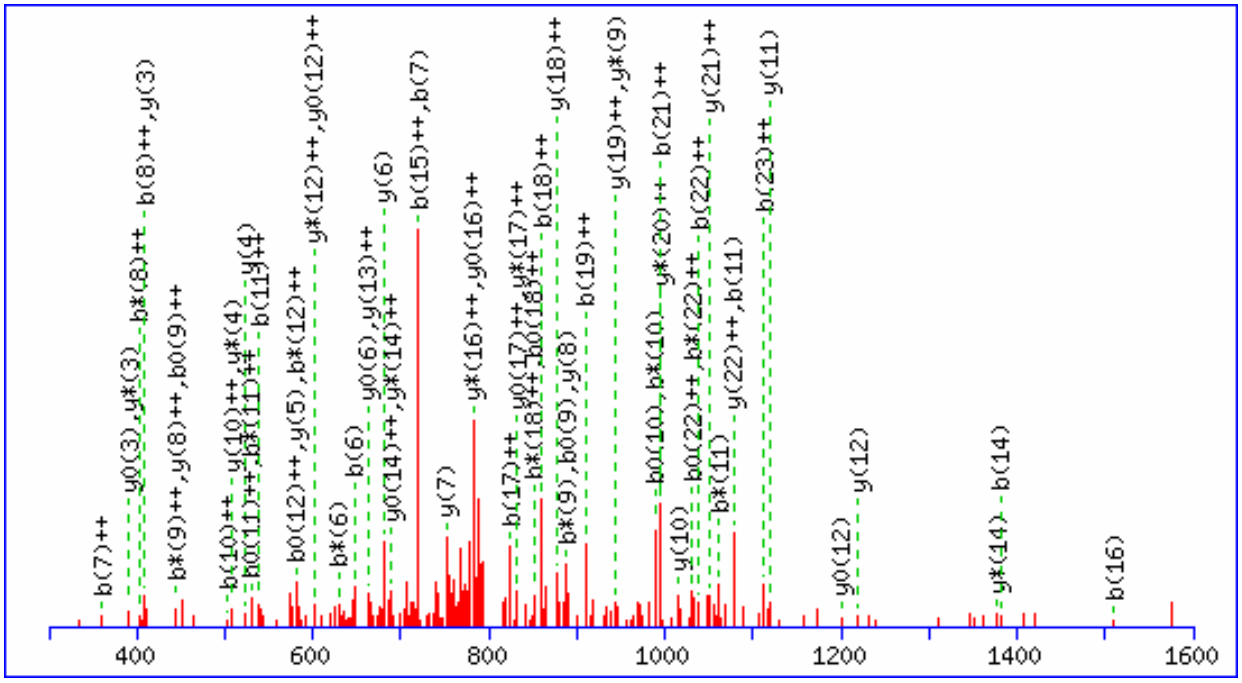
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.12	57.57			A							17
2	227.28	114.14			L	1513.78	757.39	1496.75	748.88	1495.77	748.39	16
3	298.36	149.68			A	1400.62	700.82	1383.59	692.30	1382.61	691.81	15
4	411.52	206.26			L	1329.55	665.28	1312.51	656.76	1311.53	656.27	14
5	482.59	241.80			A	1216.39	608.70	1199.36	600.18	1198.37	599.69	13
6	553.67	277.34			A	1145.31	573.16	1128.28	564.64	1127.29	564.15	12
7	666.83	333.92			L	1074.23	537.62	1057.20	529.10	1056.22	528.61	11
8	737.91	369.46			A	961.07	481.04	944.04	472.53	943.06	472.03	10
9	808.98	405.00			A	890.00	445.50	872.97	436.99	871.98	436.49	9
10	908.12	454.56			V	818.92	409.96	801.89	401.45	800.90	400.96	8
11	1037.23	519.12	1019.21	510.11	E	719.79	360.40	702.76	351.88	701.77	351.39	7
12	1134.35	567.68	1116.33	558.67	P	590.67	295.84	573.64	287.33	572.66	286.83	6
13	1205.42	603.22	1187.41	594.21	A	493.56	247.28	476.53	238.77	475.54	238.28	5
14	1308.57	654.79	1290.55	645.78	C	422.48	211.74	405.45	203.23	404.47	202.74	4
15	1365.62	683.31	1347.60	674.30	G	319.34	160.17	302.31	151.66	301.32	151.17	3
16	1452.69	726.85	1434.68	717.84	S	262.29	131.65	245.26	123.13	244.27	122.64	2
17					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
NONO	FACHSASLTVR	596.56	2+	62.3



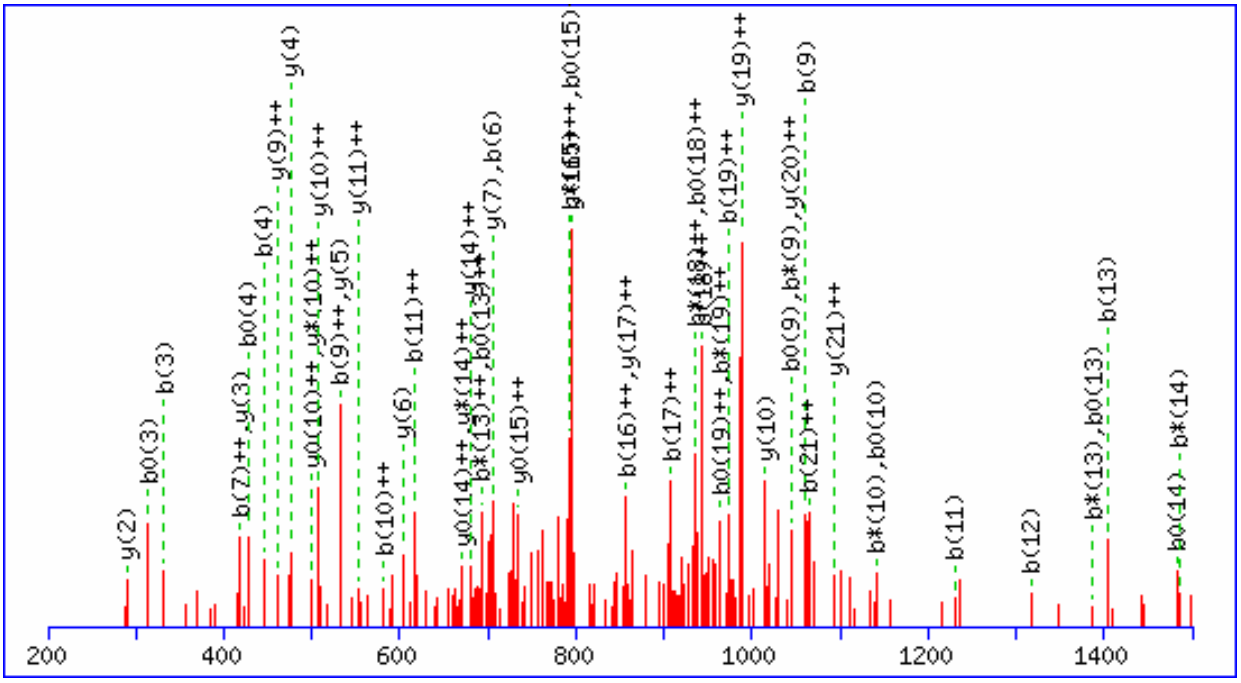
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.18	74.59			F							11
2	219.26	110.13			A	1045.19	523.10	1028.16	514.59	1027.18	514.09	10
3	322.40	161.71			C	974.12	487.56	957.09	479.05	956.10	478.55	9
4	459.54	230.27			H	870.97	435.99	853.94	427.48	852.96	426.98	8
5	546.62	273.81	528.60	264.81	S	733.83	367.42	716.80	358.91	715.82	358.41	7
6	617.70	309.35	599.68	300.34	A	646.76	323.88	629.73	315.37	628.74	314.87	6
7	704.77	352.89	686.76	343.88	S	575.68	288.34	558.65	279.83	557.66	279.34	5
8	817.93	409.47	799.92	400.46	L	488.60	244.80	471.57	236.29	470.59	235.80	4
9	919.04	460.02	901.02	451.01	T	375.44	188.23	358.41	179.71	357.43	179.22	3
10	1018.17	509.59	1000.15	500.58	V	274.34	137.67	257.31	129.16			2
11					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
OXSM	LKGPNHAVSTA**C**TTGAHAVGDSFR	800.04	3+	63.8



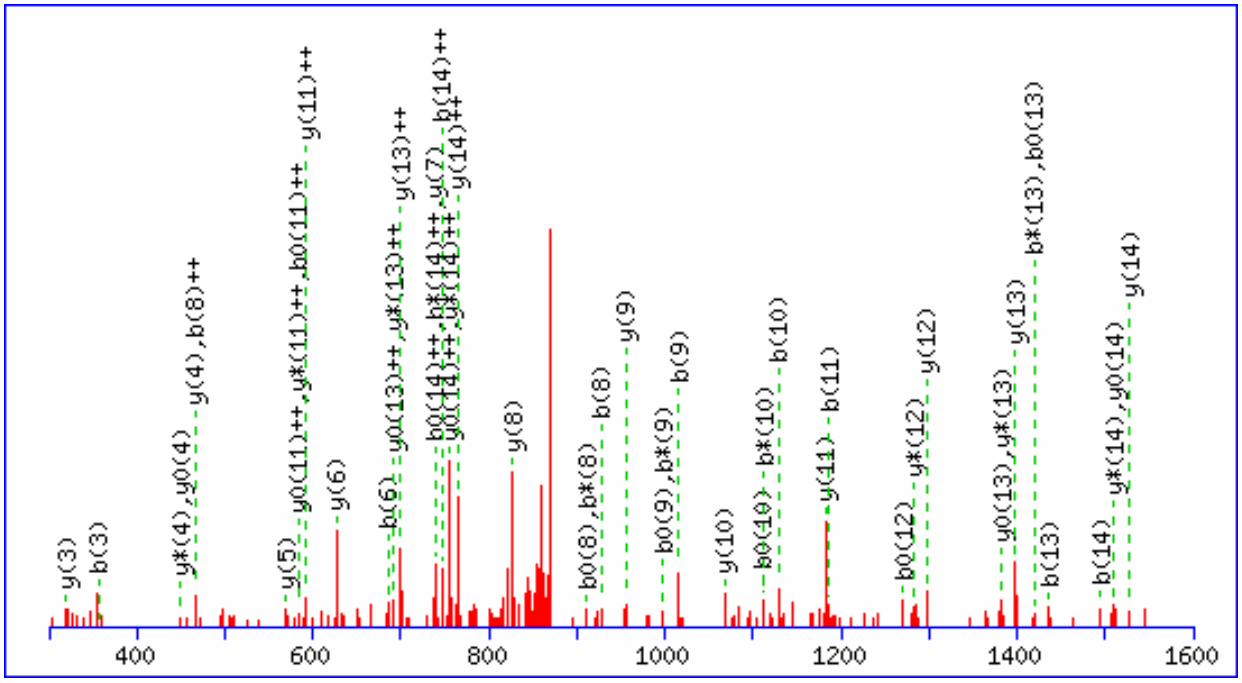
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.17	57.59					L							24
2	242.34	121.67	225.31	113.16			K	2285.48	1143.24	2268.45	1134.73	2267.46	1134.23	23
3	299.39	150.20	282.36	141.68			G	2157.30	1079.16	2140.27	1070.64	2139.29	1070.15	22
4	396.50	198.76	379.47	190.24			P	2100.25	1050.63	2083.22	1042.11	2082.24	1041.62	21
5	510.61	255.81	493.58	247.29			N	2003.14	1002.07	1986.11	993.56	1985.12	993.06	20
6	647.75	324.38	630.72	315.86			H	1889.03	945.02	1872.00	936.51	1871.02	936.01	19
7	718.82	359.92	701.79	351.40			A	1751.90	876.45	1734.86	867.94	1733.88	867.44	18
8	817.96	409.48	800.92	400.97			V	1680.82	840.91	1663.79	832.40	1662.80	831.90	17
9	905.03	453.02	888.00	444.50	887.02	444.01	S	1581.69	791.35	1564.66	782.83	1563.67	782.34	16
10	1006.14	503.57	989.11	495.06	988.12	494.56	T	1494.61	747.81	1477.58	739.29	1476.59	738.80	15
11	1077.21	539.11	1060.18	530.60	1059.20	530.10	A	1393.50	697.26	1376.47	688.74	1375.49	688.25	14
12	1180.36	590.68	1163.33	582.17	1162.34	581.67	C	1322.43	661.72	1305.40	653.20	1304.41	652.71	13
13	1281.46	641.23	1264.43	632.72	1263.45	632.23	T	1219.28	610.15	1202.25	601.63	1201.27	601.14	12
14	1382.57	691.79	1365.53	683.27	1364.55	682.78	T	1118.18	559.59	1101.15	551.08	1100.16	550.59	11
15	1439.62	720.31	1422.59	711.80	1421.60	711.30	G	1017.08	509.04	1000.05	500.53	999.06	500.03	10
16	1510.69	755.85	1493.66	747.34	1492.68	746.84	A	960.03	480.52	942.99	472.00	942.01	471.51	9
17	1647.83	824.42	1630.80	815.91	1629.82	815.41	H	888.95	444.98	871.92	436.46	870.93	435.97	8
18	1718.91	859.96	1701.88	851.44	1700.90	850.95	A	751.81	376.41	734.78	367.89	733.79	367.40	7
19	1818.04	909.53	1801.01	901.01	1800.03	900.52	V	680.73	340.87	663.70	332.35	662.71	331.86	6
20	1875.09	938.05	1858.06	929.54	1857.08	929.04	G	581.60	291.30	564.57	282.79	563.58	282.30	5
21	1990.18	995.59	1973.15	987.08	1972.17	986.59	D	524.55	262.78	507.52	254.26	506.53	253.77	4
22	2077.26	1039.13	2060.23	1030.62	2059.24	1030.13	S	409.46	205.23	392.43	196.72	391.44	196.23	3
23	2224.43	1112.72	2207.40	1104.20	2206.42	1103.71	F	322.38	161.70	305.35	153.18			2
24							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
PCBP1	VMTIPYQPMPASSPVICAGGQDR	807.32	3+	60.7



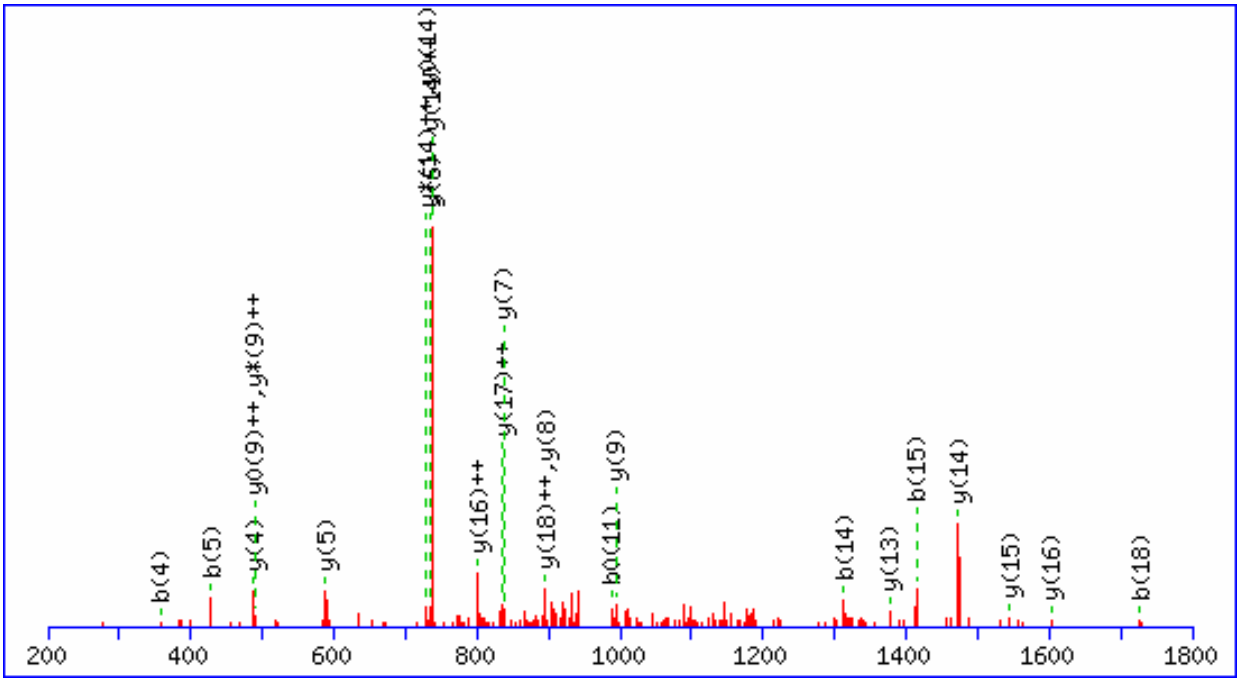
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							23
2	231.34	116.17					M	2320.69	1160.85	2303.66	1152.33	2302.67	1151.84	22
3	332.44	166.72			314.42	157.72	T	2189.49	1095.25	2172.46	1086.73	2171.48	1086.24	21
4	445.60	223.30			427.58	214.29	I	2088.39	1044.70	2071.36	1036.18	2070.37	1035.69	20
5	542.71	271.86			524.70	262.85	P	1975.23	988.12	1958.20	979.60	1957.21	979.11	19
6	705.89	353.45			687.87	344.44	Y	1878.11	939.56	1861.08	931.05	1860.10	930.55	18
7	834.01	417.51	816.98	409.00	816.00	408.50	Q	1714.94	857.97	1697.91	849.46	1696.93	848.97	17
8	931.13	466.07	914.10	457.55	913.11	457.06	P	1586.81	793.91	1569.78	785.39	1568.80	784.90	16
9	1062.33	531.67	1045.30	523.15	1044.31	522.66	M	1489.70	745.35	1472.67	736.84	1471.68	736.34	15
10	1159.44	580.22	1142.41	571.71	1141.43	571.22	P	1358.50	679.75	1341.47	671.24	1340.49	670.75	14
11	1230.52	615.76	1213.49	607.25	1212.50	606.76	A	1261.39	631.20	1244.35	622.68	1243.37	622.19	13
12	1317.60	659.30	1300.57	650.79	1299.58	650.29	S	1190.31	595.66	1173.28	587.14	1172.29	586.65	12
13	1404.67	702.84	1387.64	694.33	1386.66	693.83	S	1103.23	552.12	1086.20	543.60	1085.21	543.11	11
14	1501.79	751.40	1484.76	742.88	1483.77	742.39	P	1016.15	508.58	999.12	500.07	998.14	499.57	10
15	1600.92	800.96	1583.89	792.45	1582.90	791.96	V	919.04	460.02	902.01	451.51	901.02	451.02	9
16	1714.08	857.54	1697.05	849.03	1696.06	848.53	I	819.91	410.46	802.88	401.94	801.89	401.45	8
17	1817.22	909.11	1800.19	900.60	1799.20	900.11	C	706.75	353.88	689.72	345.36	688.73	344.87	7
18	1888.30	944.65	1871.27	936.14	1870.28	935.65	A	603.61	302.31	586.58	293.79	585.59	293.30	6
19	1945.35	973.18	1928.32	964.66	1927.33	964.17	G	532.53	266.77	515.50	258.25	514.51	257.76	5
20	2002.40	1001.70	1985.37	993.19	1984.39	992.70	G	475.48	238.24	458.45	229.73	457.46	229.23	4
21	2130.53	1065.77	2113.50	1057.25	2112.51	1056.76	Q	418.43	209.72	401.39	201.20	400.41	200.71	3
22	2245.62	1123.31	2228.59	1114.80	2227.60	1114.30	D	290.30	145.65	273.27	137.14	272.28	136.64	2
23							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
PKP2	NIQTDNNKSIGCFGSR	877.89	2+	83.6



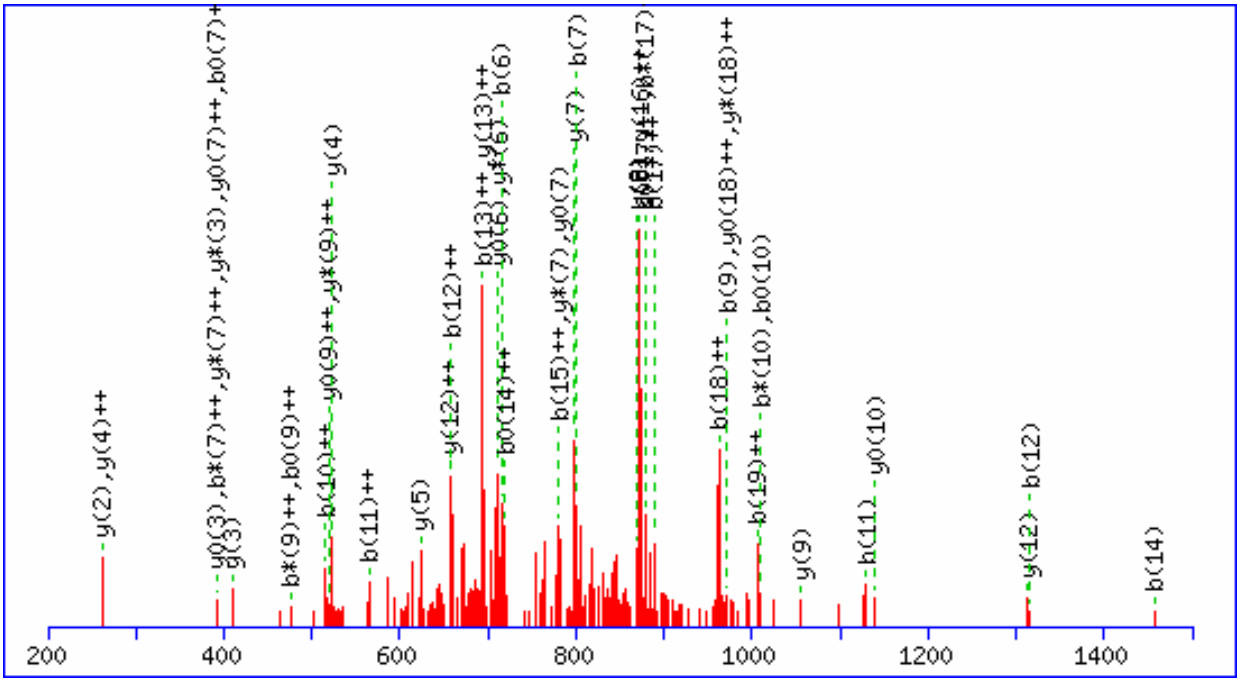
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.11	58.06	98.08	49.54			N							16
2	228.27	114.64	211.24	106.12			I	1640.80	820.90	1623.77	812.39	1622.78	811.89	15
3	356.40	178.70	339.37	170.19			Q	1527.64	764.32	1510.61	755.81	1509.62	755.32	14
4	457.50	229.25	440.47	220.74	439.49	220.25	T	1399.51	700.26	1382.48	691.74	1381.49	691.25	13
5	572.59	286.80	555.56	278.28	554.57	277.79	D	1298.41	649.71	1281.37	641.19	1280.39	640.70	12
6	686.69	343.85	669.66	335.33	668.68	334.84	N	1183.32	592.16	1166.29	583.65	1165.30	583.16	11
7	800.79	400.90	783.76	392.39	782.78	391.89	N	1069.22	535.11	1052.18	526.60	1051.20	526.10	10
8	928.97	464.99	911.94	456.47	910.95	455.98	K	955.11	478.06	938.08	469.55	937.10	469.05	9
9	1016.04	508.53	999.01	500.01	998.03	499.52	S	826.94	413.97	809.91	405.46	808.93	404.97	8
10	1129.20	565.10	1112.17	556.59	1111.19	556.10	I	739.86	370.44	722.83	361.92	721.85	361.43	7
11	1186.25	593.63	1169.22	585.11	1168.24	584.62	G	626.71	313.86	609.68	305.34	608.69	304.85	6
12	1289.40	645.20	1272.36	636.69	1271.38	636.19	C	569.65	285.33	552.62	276.82	551.64	276.32	5
13	1436.57	718.79	1419.54	710.27	1418.55	709.78	F	466.51	233.76	449.48	225.24	448.50	224.75	4
14	1493.62	747.31	1476.59	738.80	1475.61	738.31	G	319.34	160.17	302.31	151.66	301.32	151.17	3
15	1580.70	790.85	1563.67	782.34	1562.68	781.85	S	262.29	131.65	245.26	123.13	244.27	122.64	2
16							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
PKP3	DLAGAPPGEVVGCFTPQSR	951.32	2+	58.7



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.10	58.55			98.08	49.54	D							19
2	229.25	115.13			211.24	106.12	L	1787.03	894.02	1769.99	885.50	1769.01	885.01	18
3	300.33	150.67			282.32	141.66	A	1673.87	837.44	1656.84	828.92	1655.85	828.43	17
4	357.38	179.20			339.37	170.19	G	1602.79	801.90	1585.76	793.38	1584.77	792.89	16
5	428.46	214.73			410.44	205.73	A	1545.74	773.37	1528.71	764.86	1527.72	764.37	15
6	525.58	263.29			507.56	254.28	P	1474.66	737.83	1457.63	729.32	1456.65	728.83	14
7	622.69	311.85			604.68	302.84	P	1377.55	689.28	1360.51	680.76	1359.53	680.27	13
8	679.74	340.37			661.73	331.37	G	1280.43	640.72	1263.40	632.20	1262.41	631.71	12
9	808.86	404.93			790.84	395.92	E	1223.38	612.19	1206.35	603.68	1205.36	603.19	11
10	907.99	454.50			889.97	445.49	V	1094.26	547.64	1077.23	539.12	1076.25	538.63	10
11	1007.12	504.06			989.10	495.06	V	995.13	498.07	978.10	489.56	977.12	489.06	9
12	1064.17	532.59			1046.15	523.58	G	896.00	448.51	878.97	439.99	877.99	439.50	8
13	1167.31	584.16			1149.30	575.15	C	838.95	419.98	821.92	411.46	820.94	410.97	7
14	1314.49	657.75			1296.47	648.74	F	735.81	368.41	718.78	359.89	717.79	359.40	6
15	1415.59	708.30			1397.57	699.29	T	588.63	294.82	571.60	286.31	570.62	285.81	5
16	1512.71	756.86			1494.69	747.85	P	487.53	244.27	470.50	235.75	469.52	235.26	4
17	1640.83	820.92	1623.80	812.41	1622.82	811.91	Q	390.42	195.71	373.38	187.20	372.40	186.70	3
18	1727.91	864.46	1710.88	855.94	1709.90	855.45	S	262.29	131.65	245.26	123.13	244.27	122.64	2
19							R	175.21	88.11	158.18	79.59			1

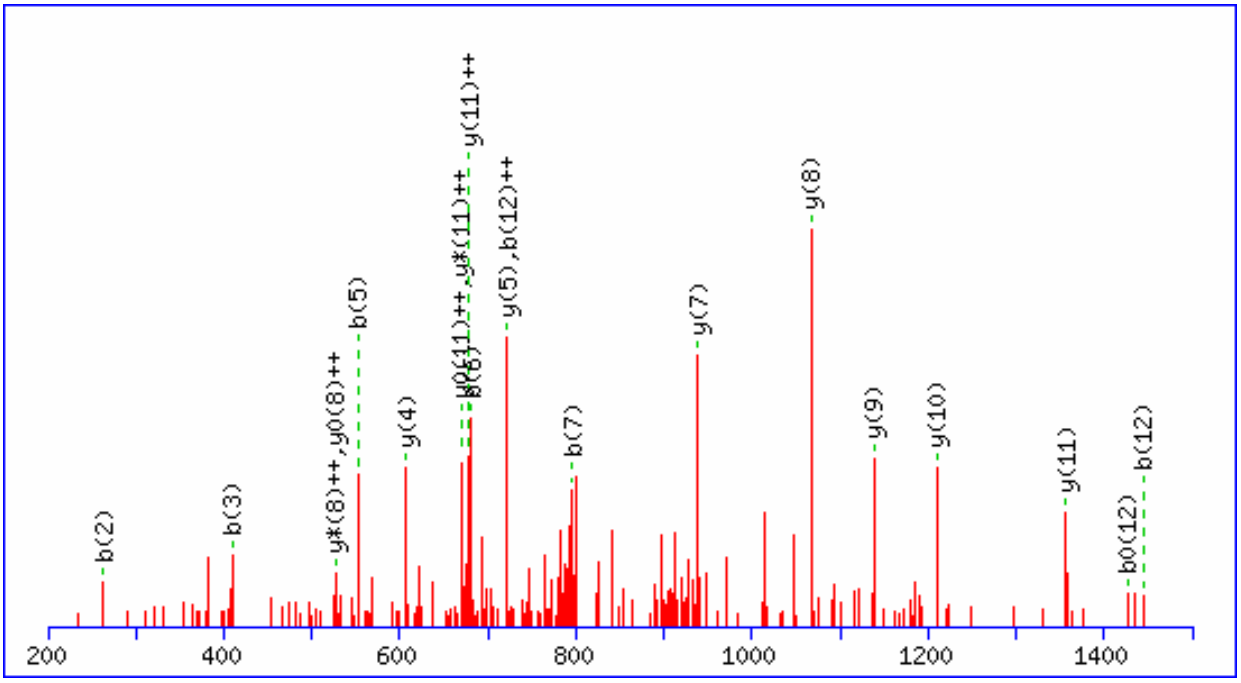
Gene Symbol	Sequences	m/z	Charge	Ion score
PLP2	ADSERLSAPG**C**WAA**C**TNFSR	729.58	3+	62.3



N-term : N-Acetyl (Protein)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.12	57.57					A							20
2	229.21	115.11			211.19	106.10	D	2072.26	1036.63	2055.23	1028.12	2054.25	1027.63	19
3	316.29	158.65			298.27	149.64	S	1957.17	979.09	1940.14	970.58	1939.16	970.08	18
4	445.40	223.20			427.39	214.20	E	1870.10	935.55	1853.07	927.04	1852.08	926.54	17
5	601.59	301.30	584.56	292.78	583.57	292.29	R	1740.98	871.00	1723.95	862.48	1722.97	861.99	16
6	714.74	357.88	697.71	349.36	696.73	348.87	L	1584.80	792.90	1567.77	784.39	1566.78	783.90	15
7	801.82	401.41	784.79	392.90	783.81	392.41	S	1471.64	736.32	1454.61	727.81	1453.62	727.32	14
8	872.90	436.95	855.87	428.44	854.88	427.95	A	1384.56	692.79	1367.53	684.27	1366.55	683.78	13
9	970.01	485.51	952.98	477.00	952.00	476.50	P	1313.48	657.25	1296.45	648.73	1295.47	648.24	12
10	1027.07	514.04	1010.04	505.52	1009.05	505.03	G	1216.37	608.69	1199.34	600.17	1198.35	599.68	11
11	1130.21	565.61	1113.18	557.09	1112.19	556.60	C	1159.32	580.16	1142.29	571.65	1141.30	571.16	10
12	1316.42	658.71	1299.39	650.20	1298.40	649.71	W	1056.18	528.59	1039.14	520.08	1038.16	519.58	9
13	1387.50	694.25	1370.47	685.74	1369.48	685.24	A	869.97	435.49	852.93	426.97	851.95	426.48	8
14	1458.57	729.79	1441.54	721.28	1440.56	720.78	A	798.89	399.95	781.86	391.43	780.87	390.94	7
15	1561.72	781.36	1544.69	772.85	1543.70	772.36	C	727.81	364.41	710.78	355.89	709.79	355.40	6
16	1662.82	831.91	1645.79	823.40	1644.81	822.91	T	624.67	312.84	607.64	304.32	606.65	303.83	5
17	1776.92	888.97	1759.89	880.45	1758.91	879.96	N	523.56	262.29	506.53	253.77	505.55	253.28	4
18	1924.10	962.55	1907.07	954.04	1906.08	953.55	F	409.46	205.23	392.43	196.72	391.44	196.23	3
19	2011.18	1006.09	1994.14	997.58	1993.16	997.08	S	262.29	131.65	245.26	123.13	244.27	122.64	2
20							R	175.21	88.11	158.18	79.59			1

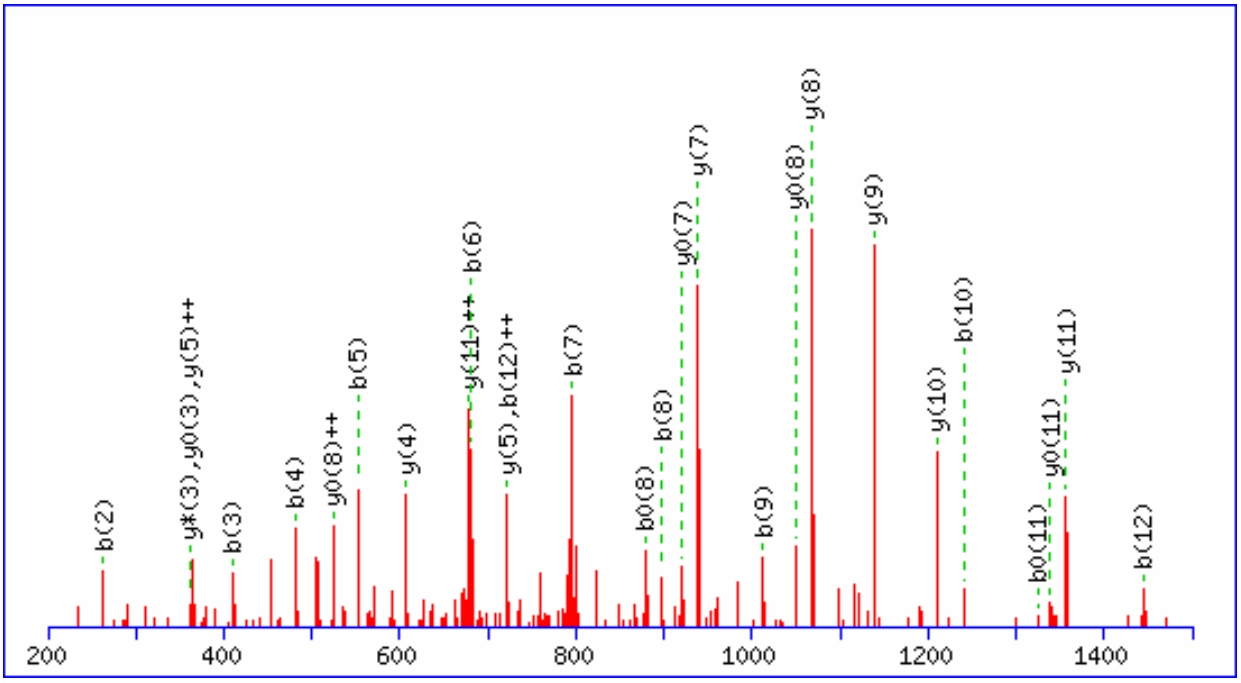
Gene Symbol	Sequences	m/z	Charge	Ion score
PLSCR1	VYFAAEDTDCCTR	809.69	2+	46.0



C11 : NEM (C)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57			V							13
2	263.31	132.16			Y	1520.62	760.81	1503.59	752.30	1502.60	751.81	12
3	410.49	205.75			F	1357.45	679.23	1340.42	670.71	1339.43	670.22	11
4	481.56	241.29			A	1210.27	605.64	1193.24	597.12	1192.26	596.63	10
5	552.64	276.82			A	1139.19	570.10	1122.16	561.59	1121.18	561.09	9
6	681.76	341.38	663.74	332.37	E	1068.12	534.56	1051.09	526.05	1050.10	525.55	8
7	796.84	398.93	778.83	389.92	D	939.00	470.01	921.97	461.49	920.99	461.00	7
8	897.95	449.48	879.93	440.47	T	823.92	412.46	806.88	403.95	805.90	403.45	6
9	1013.03	507.02	995.02	498.01	D	722.81	361.91	705.78	353.39	704.80	352.90	5
10	1116.18	558.59	1098.16	549.59	C	607.72	304.37	590.69	295.85	589.71	295.36	4
11	1344.45	672.73	1326.43	663.72	C	504.58	252.79	487.55	244.28	486.57	243.79	3
12	1445.55	723.28	1427.53	714.27	T	276.31	138.66	259.28	130.15	258.30	129.65	2
13					R	175.21	88.11	158.18	79.59			1

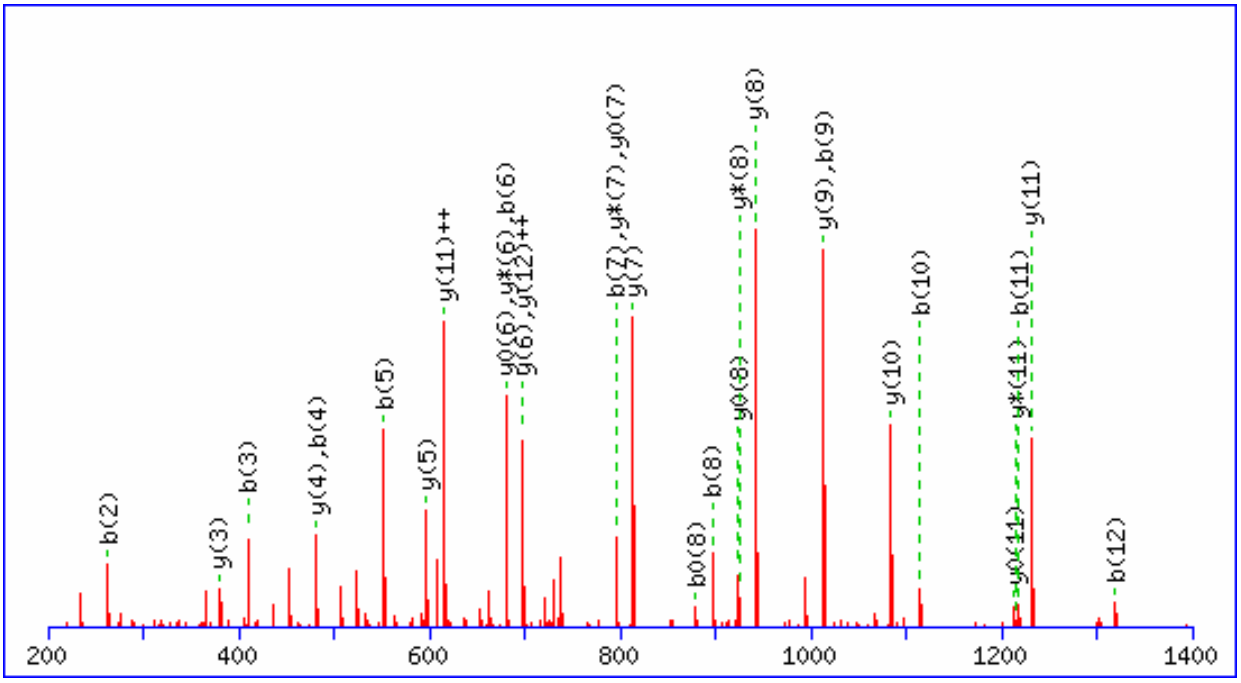
Gene Symbol	Sequences	m/z	Charge	Ion score
PLSCR1	VYFAAEDTDCCTR	810.14	2+	83.6



C10 : NEM (C)

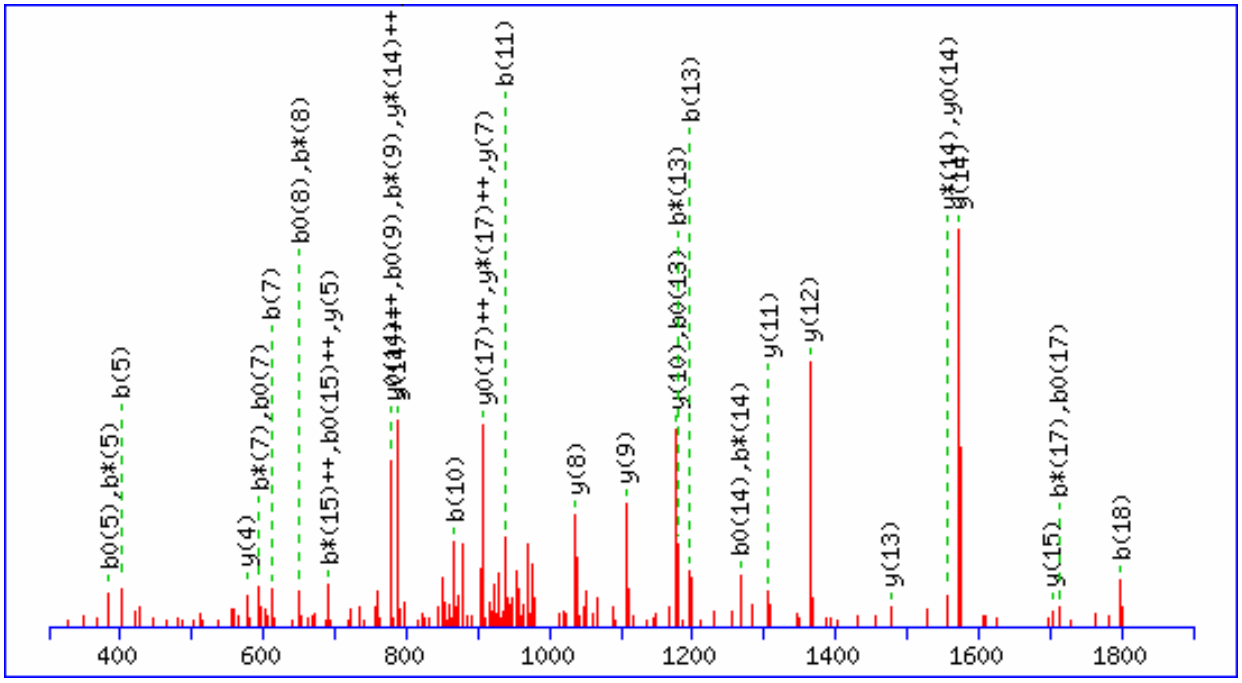
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57			V							13
2	263.31	132.16			Y	1520.62	760.81	1503.59	752.30	1502.60	751.81	12
3	410.49	205.75			F	1357.45	679.23	1340.42	670.71	1339.43	670.22	11
4	481.56	241.29			A	1210.27	605.64	1193.24	597.12	1192.26	596.63	10
5	552.64	276.82			A	1139.19	570.10	1122.16	561.59	1121.18	561.09	9
6	681.76	341.38	663.74	332.37	E	1068.12	534.56	1051.09	526.05	1050.10	525.55	8
7	796.84	398.93	778.83	389.92	D	939.00	470.01	921.97	461.49	920.99	461.00	7
8	897.95	449.48	879.93	440.47	T	823.92	412.46	806.88	403.95	805.90	403.45	6
9	1013.03	507.02	995.02	498.01	D	722.81	361.91	705.78	353.39	704.80	352.90	5
10	1241.30	621.16	1223.29	612.15	C	607.72	304.37	590.69	295.85	589.71	295.36	4
11	1344.45	672.73	1326.43	663.72	C	379.46	190.23	362.43	181.72	361.44	181.22	3
12	1445.55	723.28	1427.53	714.27	T	276.31	138.66	259.28	130.15	258.30	129.65	2
13					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
PLSCR1	VYFAAEDTDCCTR	747.46	2+	105.1



#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57			V							13
2	263.31	132.16			Y	1395.49	698.25	1378.46	689.74	1377.48	689.24	12
3	410.49	205.75			F	1232.32	616.66	1215.29	608.15	1214.31	607.66	11
4	481.56	241.29			A	1085.15	543.08	1068.12	534.56	1067.13	534.07	10
5	552.64	276.82			A	1014.07	507.54	997.04	499.02	996.05	498.53	9
6	681.76	341.38	663.74	332.37	E	942.99	472.00	925.96	463.48	924.98	462.99	8
7	796.84	398.93	778.83	389.92	D	813.88	407.44	796.85	398.93	795.86	398.43	7
8	897.95	449.48	879.93	440.47	T	698.79	349.90	681.76	341.38	680.77	340.89	6
9	1013.03	507.02	995.02	498.01	D	597.69	299.35	580.66	290.83	579.67	290.34	5
10	1116.18	558.59	1098.16	549.59	C	482.60	241.80	465.57	233.29	464.58	232.80	4
11	1219.32	610.16	1201.31	601.16	C	379.46	190.23	362.43	181.72	361.44	181.22	3
12	1320.42	660.72	1302.41	651.71	T	276.31	138.66	259.28	130.15	258.30	129.65	2
13					R	175.21	88.11	158.18	79.59			1

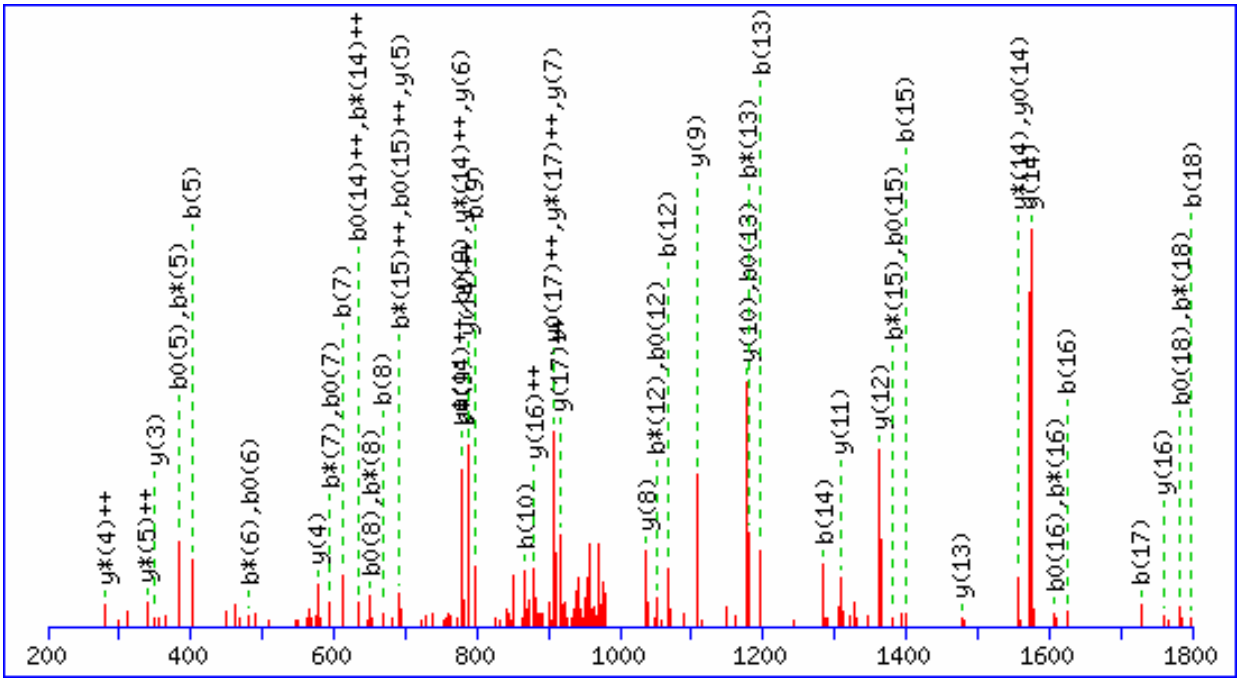
Gene Symbol	Sequences	m/z	Charge	Ion score
PLSCR3	SGAGQPLGQAAEESNCCAR	987.72	2+	95.9



C17 : NEM (C)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							19
2	145.14	73.07			127.12	64.06	G	1888.02	944.52	1870.99	936.00	1870.01	935.51	18
3	216.21	108.61			198.20	99.60	A	1830.97	915.99	1813.94	907.48	1812.96	906.98	17
4	273.27	137.14			255.25	128.13	G	1759.90	880.45	1742.86	871.94	1741.88	871.44	16
5	401.39	201.20	384.36	192.69	383.38	192.19	Q	1702.84	851.93	1685.81	843.41	1684.83	842.92	15
6	498.51	249.76	481.48	241.24	480.49	240.75	P	1574.71	787.86	1557.68	779.35	1556.70	778.85	14
7	611.67	306.34	594.64	297.82	593.65	297.33	L	1477.60	739.30	1460.57	730.79	1459.58	730.30	13
8	668.72	334.86	651.69	326.35	650.70	325.86	G	1364.44	682.73	1347.41	674.21	1346.43	673.72	12
9	796.85	398.93	779.82	390.41	778.83	389.92	Q	1307.39	654.20	1290.36	645.68	1289.38	645.19	11
10	867.93	434.47	850.90	425.95	849.91	425.46	A	1179.26	590.13	1162.23	581.62	1161.25	581.13	10
11	939.00	470.01	921.97	461.49	920.99	461.00	A	1108.18	554.60	1091.15	546.08	1090.17	545.59	9
12	1068.12	534.56	1051.09	526.05	1050.10	525.56	E	1037.11	519.06	1020.08	510.54	1019.09	510.05	8
13	1197.23	599.12	1180.20	590.60	1179.22	590.11	E	907.99	454.50	890.96	445.98	889.98	445.49	7
14	1284.31	642.66	1267.28	634.14	1266.29	633.65	S	778.88	389.94	761.85	381.43	760.86	380.94	6
15	1398.41	699.71	1381.38	691.19	1380.40	690.70	N	691.80	346.40	674.77	337.89			5
16	1501.55	751.28	1484.52	742.77	1483.54	742.27	C	577.70	289.35	560.67	280.84			4
17	1729.82	865.42	1712.79	856.90	1711.81	856.41	C	474.56	237.78	457.52	229.27			3
18	1800.90	900.95	1783.87	892.44	1782.89	891.95	A	246.29	123.65	229.26	115.13			2
19							R	175.21	88.11	158.18	79.59			1

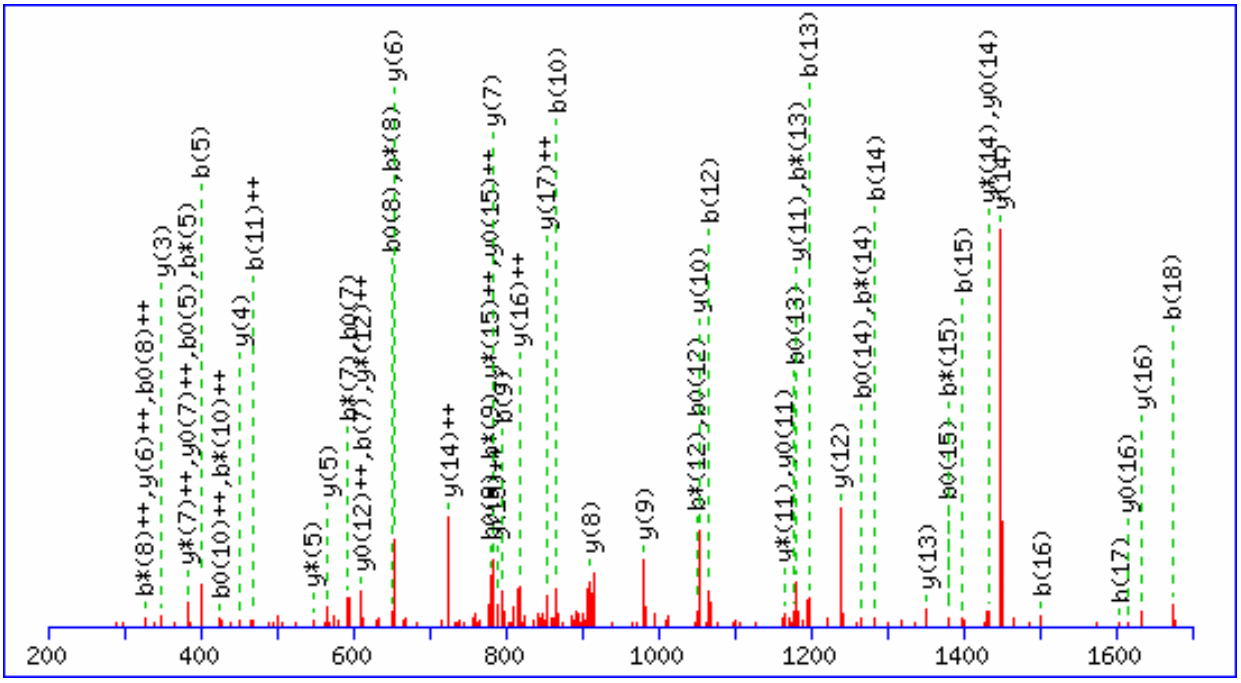
Gene Symbol	Sequences	m/z	Charge	Ion score
PLSCR3	SGAGQPLGQAAEESNCCAR	988.17	2+	96.1



C16 : NEM (C)

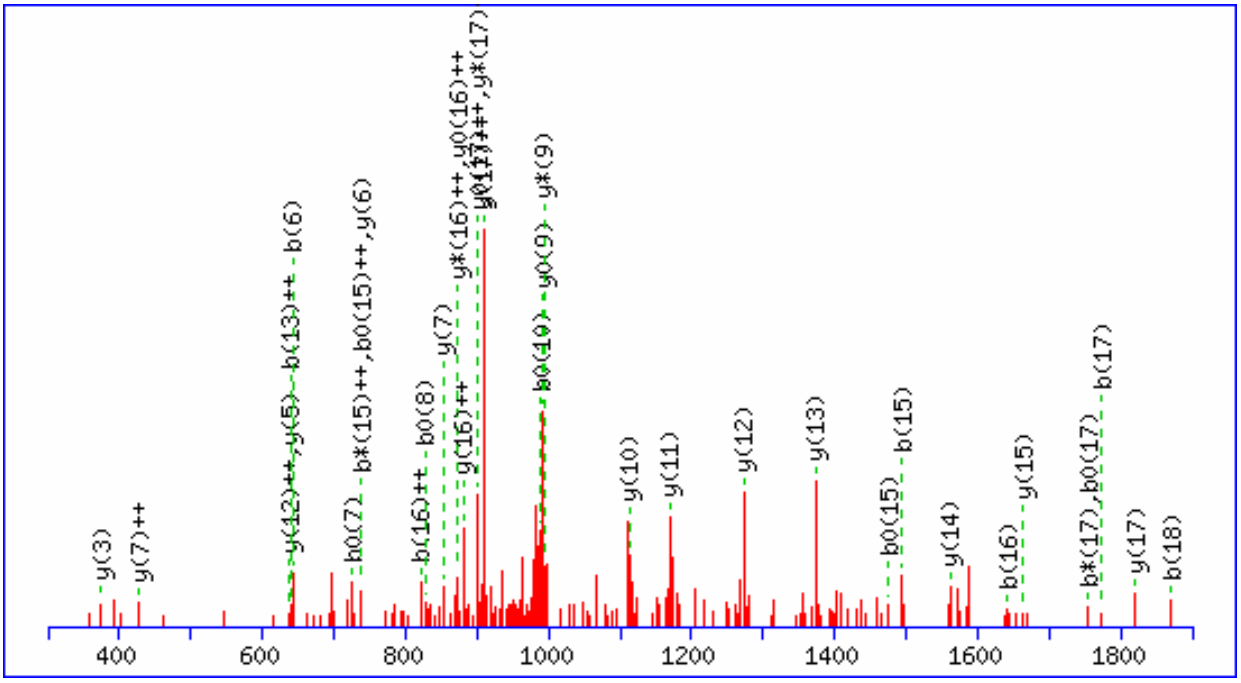
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							19
2	145.14	73.07			127.12	64.06	G	1888.02	944.52	1870.99	936.00	1870.01	935.51	18
3	216.21	108.61			198.20	99.60	A	1830.97	915.99	1813.94	907.48	1812.96	906.98	17
4	273.27	137.14			255.25	128.13	G	1759.90	880.45	1742.86	871.94	1741.88	871.44	16
5	401.39	201.20	384.36	192.69	383.38	192.19	Q	1702.84	851.93	1685.81	843.41	1684.83	842.92	15
6	498.51	249.76	481.48	241.24	480.49	240.75	P	1574.71	787.86	1557.68	779.35	1556.70	778.85	14
7	611.67	306.34	594.64	297.82	593.65	297.33	L	1477.60	739.30	1460.57	730.79	1459.58	730.30	13
8	668.72	334.86	651.69	326.35	650.70	325.86	G	1364.44	682.73	1347.41	674.21	1346.43	673.72	12
9	796.85	398.93	779.82	390.41	778.83	389.92	Q	1307.39	654.20	1290.36	645.68	1289.38	645.19	11
10	867.93	434.47	850.90	425.95	849.91	425.46	A	1179.26	590.13	1162.23	581.62	1161.25	581.13	10
11	939.00	470.01	921.97	461.49	920.99	461.00	A	1108.18	554.60	1091.15	546.08	1090.17	545.59	9
12	1068.12	534.56	1051.09	526.05	1050.10	525.56	E	1037.11	519.06	1020.08	510.54	1019.09	510.05	8
13	1197.23	599.12	1180.20	590.60	1179.22	590.11	E	907.99	454.50	890.96	445.98	889.98	445.49	7
14	1284.31	642.66	1267.28	634.14	1266.29	633.65	S	778.88	389.94	761.85	381.43	760.86	380.94	6
15	1398.41	699.71	1381.38	691.19	1380.40	690.70	N	691.80	346.40	674.77	337.89			5
16	1626.68	813.84	1609.65	805.33	1608.66	804.84	C	577.70	289.35	560.67	280.84			4
17	1729.82	865.42	1712.79	856.90	1711.81	856.41	C	349.43	175.22	332.40	166.70			3
18	1800.90	900.95	1783.87	892.44	1782.89	891.95	A	246.29	123.65	229.26	115.13			2
19							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
PLSCR3	SGAGQPLGQAAEESNCCAR	925.59	2+	105.2



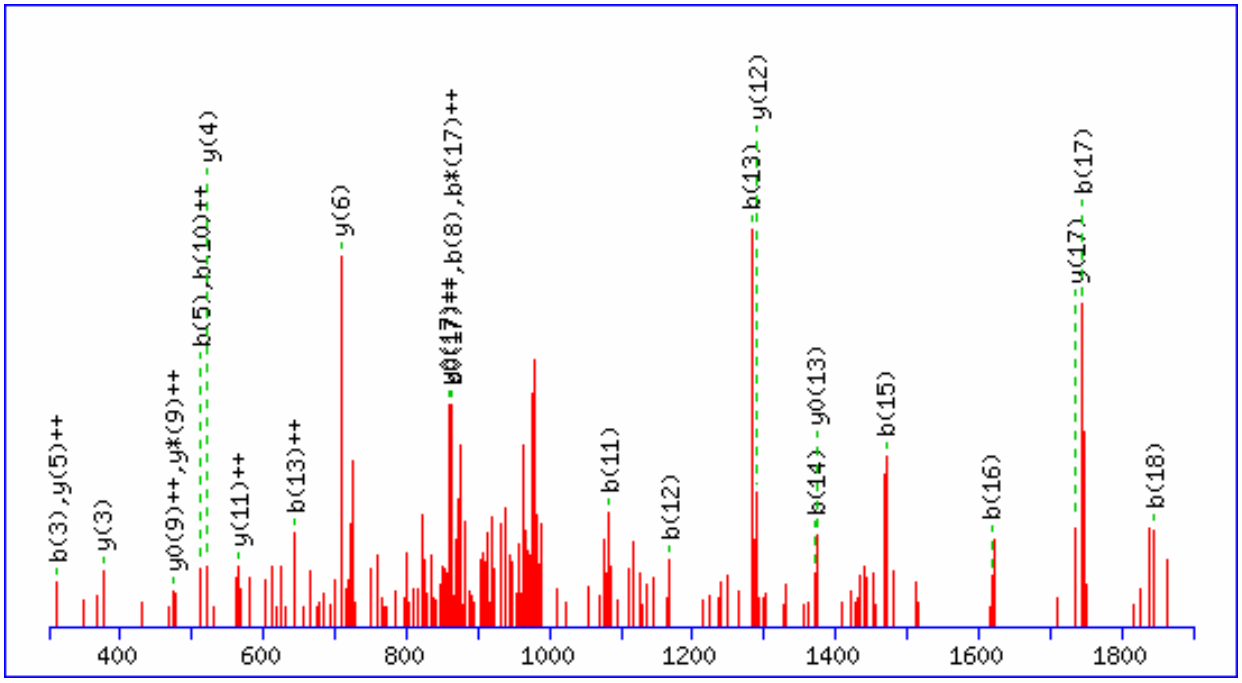
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							19
2	145.14	73.07			127.12	64.06	G	1762.90	881.95	1745.87	873.44	1744.88	872.95	18
3	216.21	108.61			198.20	99.60	A	1705.85	853.43	1688.82	844.91	1687.83	844.42	17
4	273.27	137.14			255.25	128.13	G	1634.77	817.89	1617.74	809.37	1616.75	808.88	16
5	401.39	201.20	384.36	192.69	383.38	192.19	Q	1577.72	789.36	1560.69	780.85	1559.70	780.36	15
6	498.51	249.76	481.48	241.24	480.49	240.75	P	1449.59	725.30	1432.56	716.78	1431.57	716.29	14
7	611.67	306.34	594.64	297.82	593.65	297.33	L	1352.47	676.74	1335.44	668.23	1334.46	667.73	13
8	668.72	334.86	651.69	326.35	650.70	325.86	G	1239.32	620.16	1222.29	611.65	1221.30	611.15	12
9	796.85	398.93	779.82	390.41	778.83	389.92	Q	1182.27	591.64	1165.23	583.12	1164.25	582.63	11
10	867.93	434.47	850.90	425.95	849.91	425.46	A	1054.14	527.57	1037.11	519.06	1036.12	518.56	10
11	939.00	470.01	921.97	461.49	920.99	461.00	A	983.06	492.03	966.03	483.52	965.04	483.03	9
12	1068.12	534.56	1051.09	526.05	1050.10	525.56	E	911.98	456.49	894.95	447.98	893.97	447.49	8
13	1197.23	599.12	1180.20	590.60	1179.22	590.11	E	782.87	391.94	765.84	383.42	764.85	382.93	7
14	1284.31	642.66	1267.28	634.14	1266.29	633.65	S	653.75	327.38	636.72	318.86	635.74	318.37	6
15	1398.41	699.71	1381.38	691.19	1380.40	690.70	N	566.68	283.84	549.64	275.33			5
16	1501.55	751.28	1484.52	742.77	1483.54	742.27	C	452.57	226.79	435.54	218.28			4
17	1604.70	802.85	1587.67	794.34	1586.68	793.85	C	349.43	175.22	332.40	166.70			3
18	1675.78	838.39	1658.75	829.88	1657.76	829.38	A	246.29	123.65	229.26	115.13			2
19							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
PLSCR3	VVGPCWTCGCGTDTNFEVK	1009.18	2+	60.0



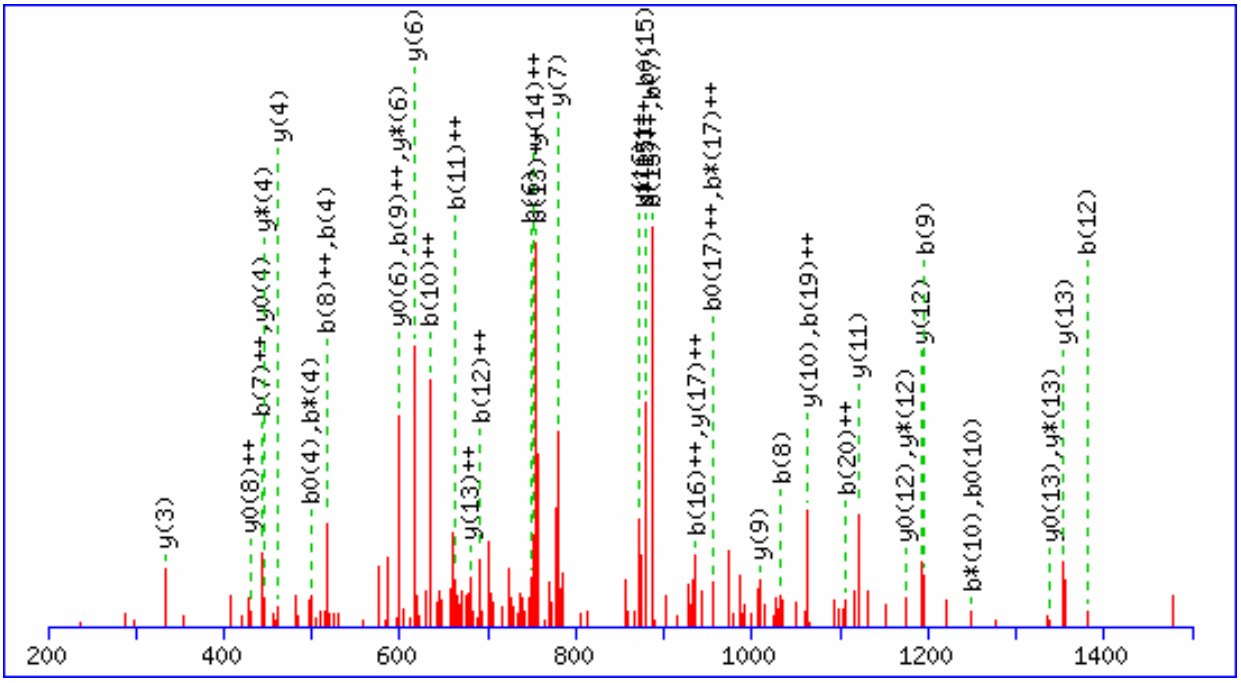
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							19
2	199.27	100.14					V	1918.16	959.58	1901.12	951.07	1900.14	950.57	18
3	256.32	128.66					G	1819.02	910.02	1801.99	901.50	1801.01	901.01	17
4	353.44	177.22					P	1761.97	881.49	1744.94	872.98	1743.96	872.48	16
5	456.58	228.79					C	1664.86	832.93	1647.83	824.42	1646.84	823.93	15
6	642.79	321.90					W	1561.71	781.36	1544.68	772.85	1543.70	772.35	14
7	743.89	372.45			725.88	363.44	T	1375.50	688.26	1358.47	679.74	1357.49	679.25	13
8	847.04	424.02			829.02	415.01	C	1274.40	637.70	1257.37	629.19	1256.39	628.70	12
9	904.09	452.55			886.07	443.54	G	1171.26	586.13	1154.23	577.62	1153.24	577.13	11
10	1007.23	504.12			989.22	495.11	C	1114.21	557.61	1097.18	549.09	1096.19	548.60	10
11	1064.28	532.64			1046.27	523.64	G	1011.06	506.04	994.03	497.52	993.05	497.03	9
12	1165.39	583.20			1147.37	574.19	T	954.01	477.51	936.98	468.99	936.00	468.50	8
13	1280.47	640.74			1262.46	631.73	D	852.91	426.96	835.88	418.44	834.89	417.95	7
14	1381.58	691.29			1363.56	682.28	T	737.82	369.41	720.79	360.90	719.81	360.41	6
15	1495.68	748.34	1478.65	739.83	1477.66	739.34	N	636.72	318.86	619.69	310.35	618.70	309.85	5
16	1642.85	821.93	1625.82	813.42	1624.84	812.92	F	522.61	261.81	505.58	253.30	504.60	252.80	4
17	1771.97	886.49	1754.94	877.97	1753.95	877.48	E	375.44	188.22	358.41	179.71	357.43	179.22	3
18	1871.10	936.05	1854.07	927.54	1853.08	927.05	V	246.33	123.67	229.30	115.15			2
19							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
PLSCR4	VRGPCSTYGCGSDSVFEVK	996.39	2+	61.1



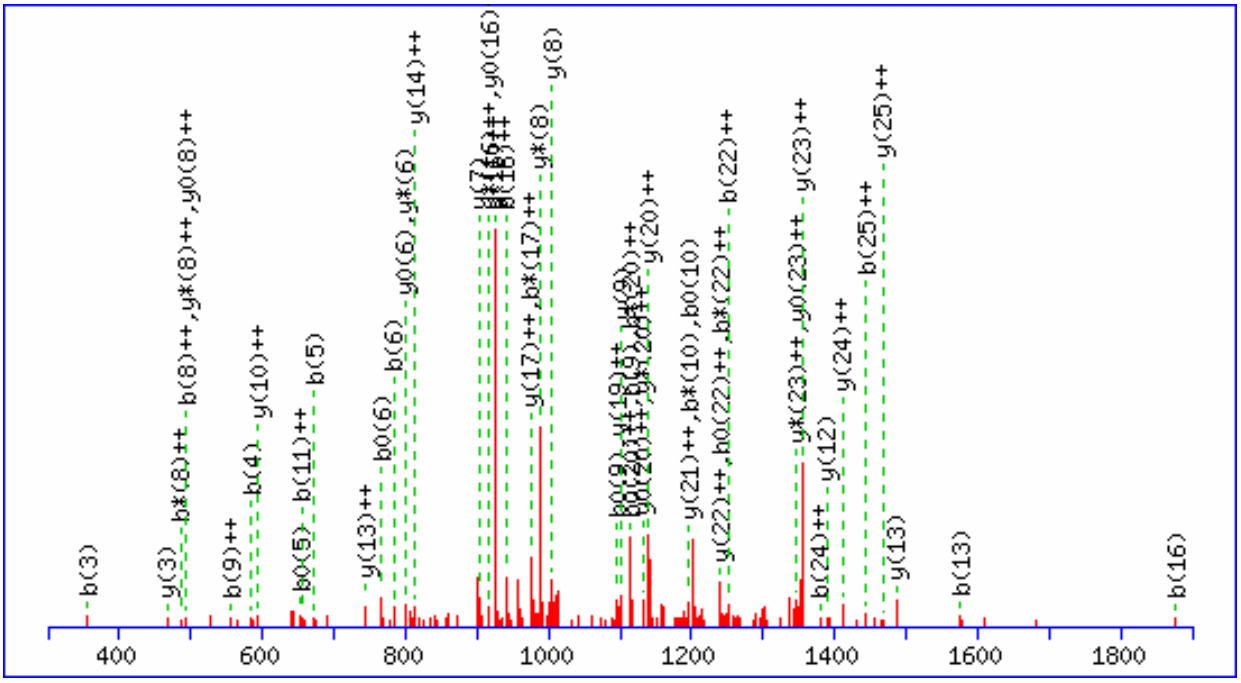
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57					V							19
2	256.32	128.67	239.29	120.15			R	1893.08	947.05	1876.05	938.53	1875.07	938.04	18
3	313.38	157.19	296.35	148.68			G	1736.90	868.95	1719.87	860.44	1718.88	859.94	17
4	410.49	205.75	393.46	197.23			P	1679.85	840.43	1662.82	831.91	1661.83	831.42	16
5	513.63	257.32	496.60	248.81			C	1582.73	791.87	1565.70	783.35	1564.72	782.86	15
6	600.71	300.86	583.68	292.34	582.70	291.85	S	1479.59	740.30	1462.56	731.78	1461.57	731.29	14
7	701.82	351.41	684.78	342.90	683.80	342.40	T	1392.51	696.76	1375.48	688.24	1374.50	687.75	13
8	864.99	433.00	847.96	424.48	846.97	423.99	Y	1291.41	646.21	1274.38	637.69	1273.39	637.20	12
9	922.04	461.52	905.01	453.01	904.02	452.52	G	1128.23	564.62	1111.20	556.11	1110.22	555.61	11
10	1025.18	513.10	1008.15	504.58	1007.17	504.09	C	1071.18	536.09	1054.15	527.58	1053.17	527.09	10
11	1082.23	541.62	1065.20	533.11	1064.22	532.61	G	968.04	484.52	951.01	476.01	950.02	475.52	9
12	1169.31	585.16	1152.28	576.64	1151.30	576.15	S	910.99	456.00	893.96	447.48	892.97	446.99	8
13	1284.40	642.70	1267.37	634.19	1266.38	633.70	D	823.91	412.46	806.88	403.94	805.90	403.45	7
14	1371.48	686.24	1354.45	677.73	1353.46	677.23	S	708.82	354.92	691.79	346.40	690.81	345.91	6
15	1470.61	735.81	1453.58	727.29	1452.59	726.80	V	621.75	311.38	604.72	302.86	603.73	302.37	5
16	1617.78	809.39	1600.75	800.88	1599.77	800.39	F	522.61	261.81	505.58	253.30	504.60	252.80	4
17	1746.90	873.95	1729.86	865.44	1728.88	864.94	E	375.44	188.22	358.41	179.71	357.43	179.22	3
18	1846.03	923.52	1829.00	915.00	1828.01	914.51	V	246.33	123.67	229.30	115.15			2
19							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
PRDX4	TREEE**C**HFYAGGQVYPGEASR	796.40	3+	57.3



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.11	51.56			84.10	42.55	T							21
2	258.30	129.65	241.27	121.14	240.28	120.65	R	2286.42	1143.71	2269.39	1135.20	2268.40	1134.70	20
3	387.41	194.21	370.38	185.69	369.40	185.20	E	2130.23	1065.62	2113.20	1057.10	2112.21	1056.61	19
4	516.53	258.77	499.50	250.25	498.51	249.76	E	2001.12	1001.06	1984.09	992.55	1983.10	992.05	18
5	645.64	323.32	628.61	314.81	627.62	314.32	E	1872.00	936.51	1854.97	927.99	1853.99	927.50	17
6	748.78	374.90	731.75	366.38	730.77	365.89	C	1742.89	871.95	1725.86	863.43	1724.87	862.94	16
7	885.92	443.46	868.89	434.95	867.91	434.46	H	1639.75	820.38	1622.71	811.86	1621.73	811.37	15
8	1033.10	517.05	1016.07	508.54	1015.08	508.04	F	1502.61	751.81	1485.58	743.29	1484.59	742.80	14
9	1196.27	598.64	1179.24	590.12	1178.25	589.63	Y	1355.43	678.22	1338.40	669.70	1337.42	669.21	13
10	1267.35	634.18	1250.32	625.66	1249.33	625.17	A	1192.26	596.63	1175.23	588.12	1174.24	587.63	12
11	1324.40	662.70	1307.37	654.19	1306.38	653.70	G	1121.18	561.09	1104.15	552.58	1103.17	552.09	11
12	1381.45	691.23	1364.42	682.71	1363.43	682.22	G	1064.13	532.57	1047.10	524.05	1046.11	523.56	10
13	1509.58	755.29	1492.55	746.78	1491.56	746.29	Q	1007.08	504.04	990.05	495.53	989.06	495.04	9
14	1608.71	804.86	1591.68	796.34	1590.69	795.85	V	878.95	439.98	861.92	431.46	860.93	430.97	8
15	1771.88	886.45	1754.85	877.93	1753.87	877.44	Y	779.82	390.41	762.79	381.90	761.80	381.41	7
16	1869.00	935.00	1851.97	926.49	1850.98	926.00	P	616.64	308.83	599.61	300.31	598.63	299.82	6
17	1926.05	963.53	1909.02	955.01	1908.03	954.52	G	519.53	260.27	502.50	251.75	501.51	251.26	5
18	2055.16	1028.09	2038.13	1019.57	2037.15	1019.08	E	462.48	231.74	445.45	223.23	444.46	222.74	4
19	2126.24	1063.62	2109.21	1055.11	2108.23	1054.62	A	333.36	167.19	316.33	158.67	315.35	158.18	3
20	2213.32	1107.16	2196.29	1098.65	2195.30	1098.16	S	262.29	131.65	245.26	123.13	244.27	122.64	2
21							R	175.21	88.11	158.18	79.59			1

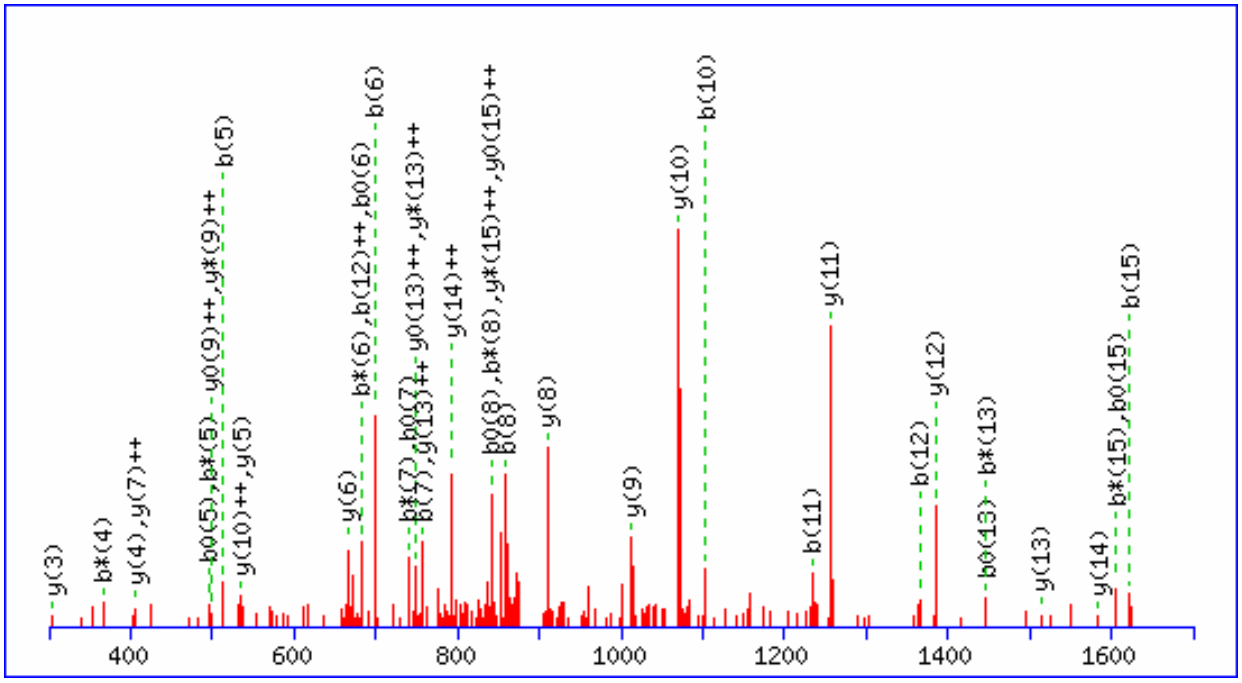
Gene Symbol	Sequences	m/z	Charge	Ion score
PRPF19	SLICSISNEVPEHPCVSPVSNHVYER	1021.73	3+	76.1



N-term : N-Acetyl (Protein)
C4 : NEM (C)

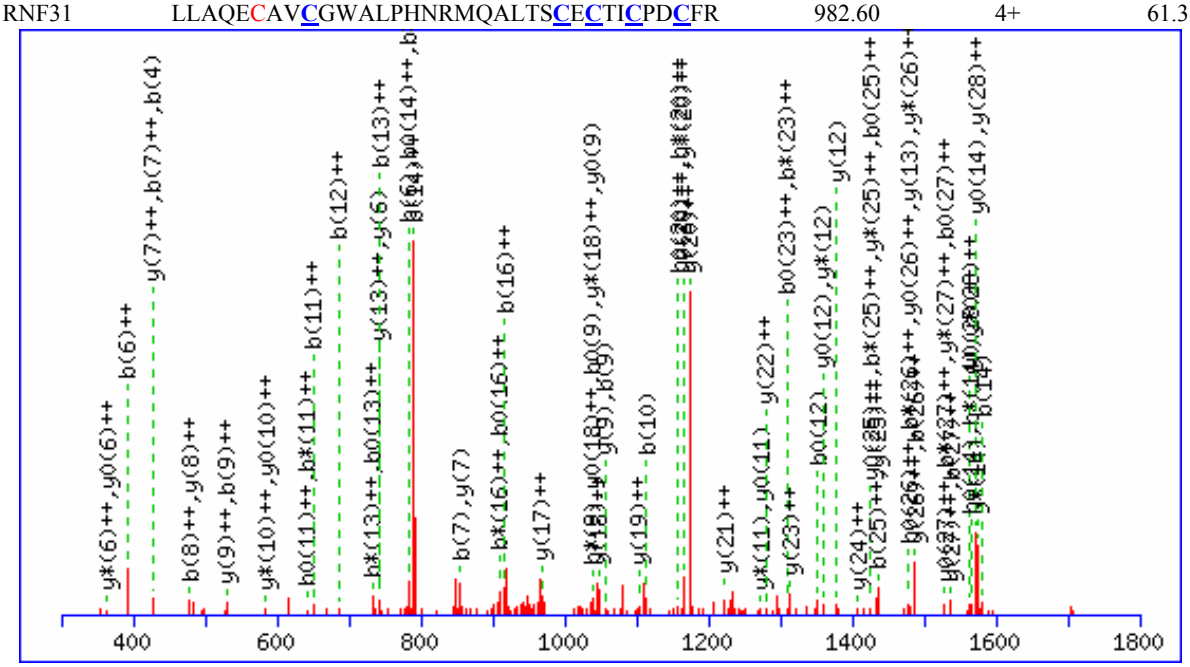
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.12	65.56			112.11	56.56	S							26
2	243.28	122.14			225.26	113.14	L	2935.27	1468.14	2918.24	1459.62	2917.26	1459.13	25
3	356.44	178.72			338.42	169.71	I	2822.11	1411.56	2805.08	1403.05	2804.10	1402.55	24
4	584.71	292.86			566.69	283.85	C	2708.96	1354.98	2691.93	1346.47	2690.94	1345.97	23
5	671.78	336.40			653.77	327.39	S	2480.69	1240.85	2463.66	1232.33	2462.67	1231.84	22
6	784.94	392.97			766.92	383.97	I	2393.61	1197.31	2376.58	1188.79	2375.60	1188.30	21
7	872.02	436.51			854.00	427.51	S	2280.45	1140.73	2263.42	1132.22	2262.44	1131.72	20
8	986.12	493.56	969.09	485.05	968.10	484.56	N	2193.38	1097.19	2176.35	1088.68	2175.36	1088.18	19
9	1115.23	558.12	1098.20	549.61	1097.22	549.11	E	2079.27	1040.14	2062.24	1031.63	2061.26	1031.13	18
10	1214.37	607.69	1197.33	599.17	1196.35	598.68	V	1950.16	975.58	1933.13	967.07	1932.14	966.58	17
11	1311.48	656.24	1294.45	647.73	1293.47	647.24	P	1851.03	926.02	1834.00	917.50	1833.01	917.01	16
12	1440.59	720.80	1423.56	712.29	1422.58	711.79	E	1753.91	877.46	1736.88	868.95	1735.90	868.45	15
13	1577.73	789.37	1560.70	780.86	1559.72	780.36	H	1624.80	812.90	1607.77	804.39	1606.78	803.90	14
14	1674.85	837.93	1657.82	829.41	1656.83	828.92	P	1487.66	744.33	1470.63	735.82	1469.64	735.33	13
15	1777.99	889.50	1760.96	880.98	1759.98	880.49	C	1390.54	695.78	1373.51	687.26	1372.53	686.77	12
16	1877.12	939.07	1860.09	930.55	1859.11	930.06	V	1287.40	644.20	1270.37	635.69	1269.39	635.20	11
17	1964.20	982.60	1947.17	974.09	1946.18	973.60	S	1188.27	594.64	1171.24	586.12	1170.25	585.63	10
18	2061.32	1031.16	2044.28	1022.65	2043.30	1022.15	P	1101.19	551.10	1084.16	542.59	1083.18	542.09	9
19	2160.45	1080.73	2143.42	1072.21	2142.43	1071.72	V	1004.08	502.54	987.05	494.03	986.06	493.54	8
20	2247.52	1124.27	2230.49	1115.75	2229.51	1115.26	S	904.95	452.98	887.92	444.46	886.93	443.97	7
21	2361.63	1181.32	2344.60	1172.80	2343.61	1172.31	N	817.87	409.44	800.84	400.92	799.85	400.43	6
22	2498.77	1249.89	2481.74	1241.37	2480.75	1240.88	H	703.77	352.39	686.74	343.87	685.75	343.38	5
23	2597.90	1299.45	2580.87	1290.94	2579.88	1290.44	V	566.63	283.82	549.60	275.30	548.61	274.81	4
24	2761.07	1381.04	2744.04	1372.52	2743.05	1372.03	Y	467.50	234.25	450.47	225.74	449.48	225.24	3
25	2890.18	1445.60	2873.15	1437.08	2872.17	1436.59	E	304.32	152.67	287.29	144.15	286.31	143.66	2
26							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RAP2C	ALAQEWGCPFMETSAK	884.82	2+	77.8



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							16
2	185.24	93.13					L	1698.94	849.97	1681.91	**841.46**	1680.92	**840.96**	15
3	256.32	128.66					A	**1585.78**	**793.39**	1568.75	784.88	1567.76	784.39	14
4	384.45	192.73	**367.42**	184.21			Q	**1514.70**	**757.85**	1497.67	**749.34**	1496.69	**748.85**	13
5	**513.56**	257.29	**496.53**	248.77	**495.55**	248.28	E	**1386.57**	693.79	1369.54	685.27	1368.56	684.78	12
6	**699.77**	350.39	**682.74**	341.88	**681.76**	341.38	W	**1257.46**	629.23	1240.43	620.72	1239.44	620.23	11
7	**756.83**	378.92	**739.80**	370.40	**738.81**	369.91	G	**1071.25**	**536.13**	1054.22	527.61	1053.23	527.12	10
8	**859.97**	430.49	**842.94**	421.97	**841.95**	421.48	C	**1014.20**	507.60	997.17	**499.09**	996.18	**498.59**	9
9	957.08	479.05	940.05	470.53	939.07	470.04	P	**911.05**	456.03	894.02	447.52	893.04	447.02	8
10	**1104.26**	552.63	1087.23	544.12	1086.24	543.63	F	813.94	**407.47**	796.91	398.96	795.92	398.47	7
11	**1235.45**	618.23	1218.42	609.72	1217.44	609.22	M	**666.76**	333.89	649.73	325.37	648.75	324.88	6
12	**1364.57**	**682.79**	1347.54	674.27	1346.55	673.78	E	**535.57**	268.29	518.54	259.77	517.55	259.28	5
13	1465.67	733.34	**1448.64**	724.82	**1447.66**	724.33	T	**406.45**	203.73	389.42	195.22	388.44	194.72	4
14	1552.75	776.88	1535.72	768.36	1534.73	767.87	S	**305.35**	153.18	288.32	144.66	287.34	144.17	3
15	**1623.83**	812.42	**1606.80**	803.90	**1605.81**	803.41	A	218.27	109.64	201.24	101.13			2
16							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RNF31	LLAQECAVCGWALPHNRMQALTSCECTICPDCFR	982.60	4+	61.3

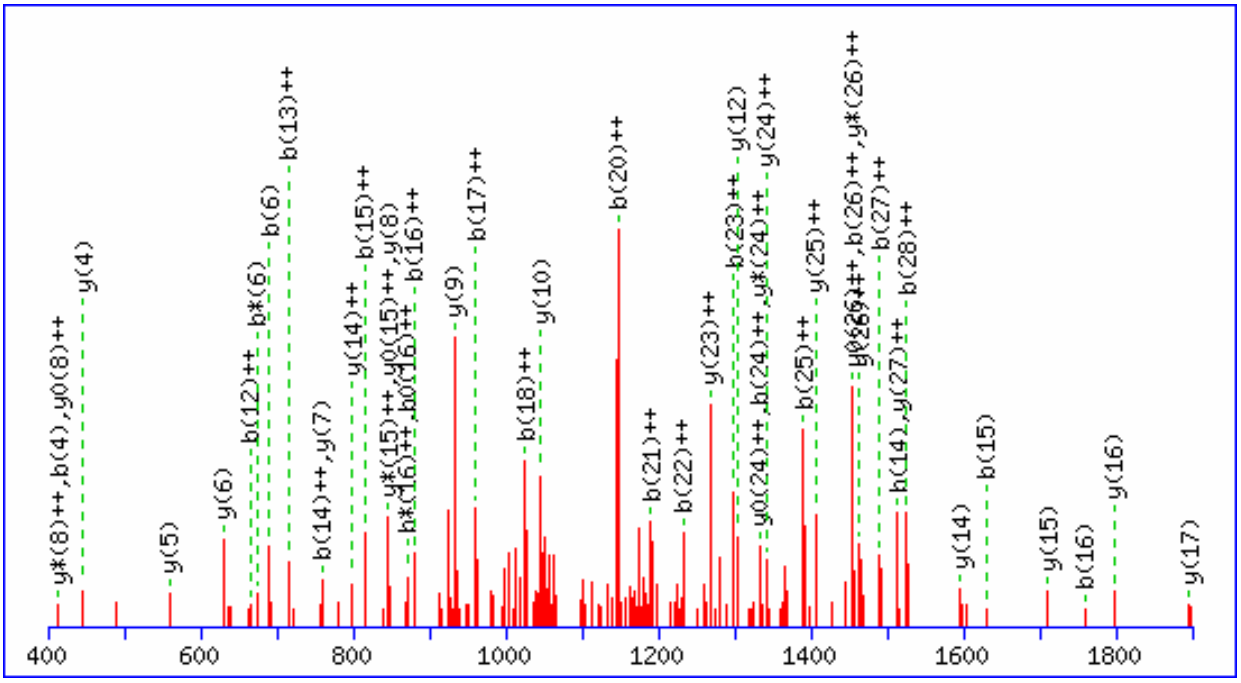


C6 : NEM (C)

M18 : Oxidation (M)

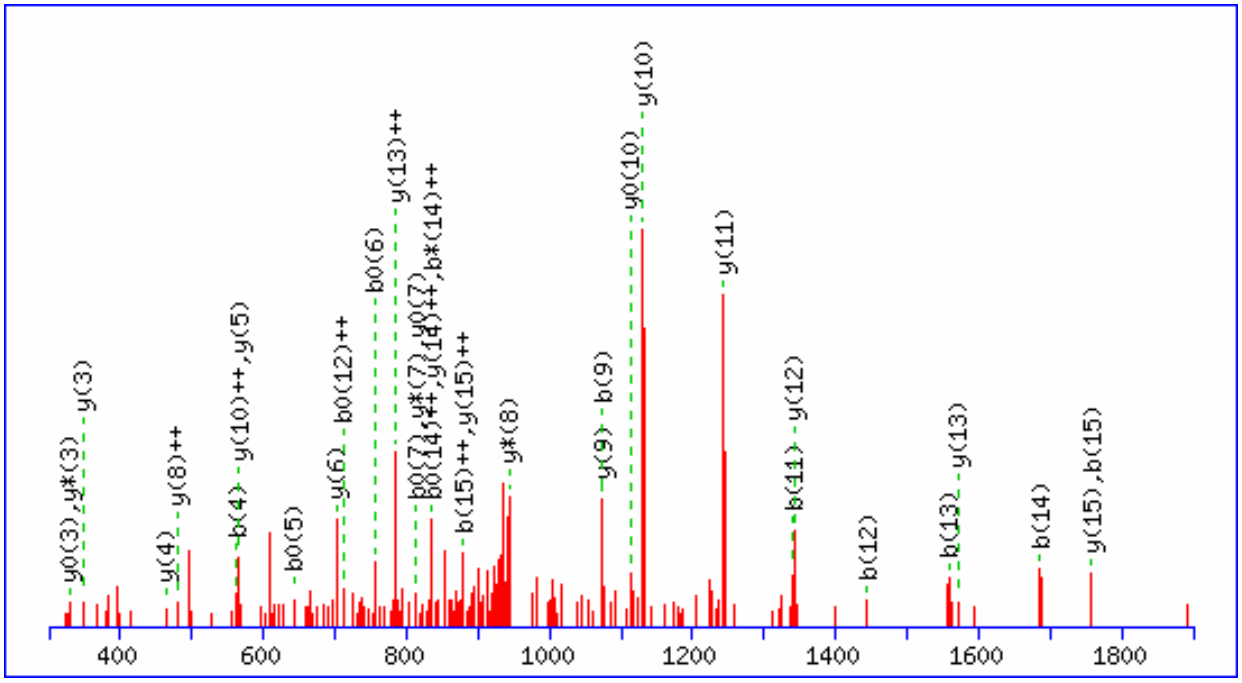
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.17	57.59					L							34
2	227.32	114.17					L	3813.41	1907.21	3796.38	1898.69	3795.40	1898.20	33
3	298.40	149.70					A	3700.25	1850.63	3683.22	1842.12	3682.24	1841.62	32
4	426.53	213.77	409.50	205.25			Q	3629.18	1815.09	3612.15	1806.58	3611.16	1806.08	31
5	555.64	278.33	538.61	269.81	537.63	269.32	E	3501.05	1751.03	3484.02	1742.51	3483.03	1742.02	30
6	783.91	392.46	766.88	383.94	765.90	383.45	C	3371.93	1686.47	3354.90	1677.96	3353.92	1677.46	29
7	854.99	428.00	837.96	419.48	836.98	418.99	A	3143.67	1572.34	3126.63	1563.82	3125.65	1563.33	28
8	954.12	477.56	937.09	469.05	936.11	468.56	V	3072.59	1536.80	3055.56	1528.28	3054.57	1527.79	27
9	1057.26	529.14	1040.23	520.62	1039.25	520.13	C	2973.46	1487.23	2956.43	1478.72	2955.44	1478.22	26
10	1114.32	557.66	1097.29	549.15	1096.30	548.65	G	2870.31	1435.66	2853.28	1427.15	2852.30	1426.65	25
11	1300.53	650.77	1283.50	642.25	1282.51	641.76	W	2813.26	1407.14	2796.23	1398.62	2795.25	1398.13	24
12	1371.60	686.31	1354.57	677.79	1353.59	677.30	A	2627.05	1314.03	2610.02	1305.51	2609.04	1305.02	23
13	1484.76	742.88	1467.73	734.37	1466.75	733.88	L	2555.97	1278.49	2538.94	1269.98	2537.96	1269.48	22
14	1581.88	791.44	1564.85	782.93	1563.86	782.43	P	2442.82	1221.91	2425.79	1213.40	2424.80	1212.90	21
15	1719.02	860.01	1701.99	851.50	1701.00	851.00	H	2345.70	1173.35	2328.67	1164.84	2327.69	1164.35	20
16	1833.12	917.06	1816.09	908.55	1815.10	908.06	N	2208.56	1104.79	2191.53	1096.27	2190.55	1095.78	19
17	1989.30	995.16	1972.27	986.64	1971.29	986.15	R	2094.46	1047.73	2077.43	1039.22	2076.44	1038.73	18
18	2136.50	1068.75	2119.47	1060.24	2118.48	1059.75	M	1938.27	969.64	1921.24	961.13	1920.26	960.63	17
19	2264.63	1132.82	2247.60	1124.30	2246.61	1123.81	Q	1791.08	896.04	1774.05	887.53	1773.06	887.04	16
20	2335.71	1168.36	2318.68	1159.84	2317.69	1159.35	A	1662.95	831.98	1645.92	823.46	1644.93	822.97	15
21	2448.86	1224.94	2431.83	1216.42	2430.85	1215.93	L	1591.87	796.44	1574.84	787.92	1573.86	787.43	14
22	2549.97	1275.49	2532.94	1266.97	2531.95	1266.48	T	1478.71	739.86	1461.68	731.35	1460.70	730.85	13
23	2637.05	1319.03	2620.01	1310.51	2619.03	1310.02	S	1377.61	689.31	1360.58	680.79	1359.59	680.30	12
24	2740.19	1370.60	2723.16	1362.08	2722.17	1361.59	C	1290.53	645.77	1273.50	637.25	1272.52	636.76	11
25	2869.30	1435.16	2852.27	1426.64	2851.29	1426.15	E	1187.39	594.20	1170.36	585.68	1169.37	585.19	10
26	2972.45	1486.73	2955.41	1478.21	2954.43	1477.72	C	1058.28	529.64	1041.25	521.13	1040.26	520.63	9
27	3073.55	1537.28	3056.52	1528.76	3055.53	1528.27	T	955.13	478.07	938.10	469.56	937.12	469.06	8
28	3186.71	1593.86	3169.68	1585.34	3168.69	1584.85	I	854.03	427.52	837.00	419.00	836.01	418.51	7
29	3289.85	1645.43	3272.82	1636.91	3271.83	1636.42	C	740.87	370.94	723.84	362.42	722.86	361.93	6
30	3386.96	1693.99	3369.93	1685.47	3368.95	1684.98	P	637.73	319.37	620.70	310.85	619.71	310.36	5
31	3502.05	1751.53	3485.02	1743.01	3484.04	1742.52	D	540.61	270.81	523.58	262.30	522.60	261.80	4
32	3605.19	1803.10	3588.16	1794.59	3587.18	1794.09	C	425.53	213.27	408.50	204.75			3
33	3752.37	1876.69	3735.34	1868.17	3734.35	1867.68	F	322.38	161.70	305.35	153.18			2
34							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RPL10	AKVDEFPLCGHMVSDEYEQLSSEALEAAR	1076.16	3+	131.6



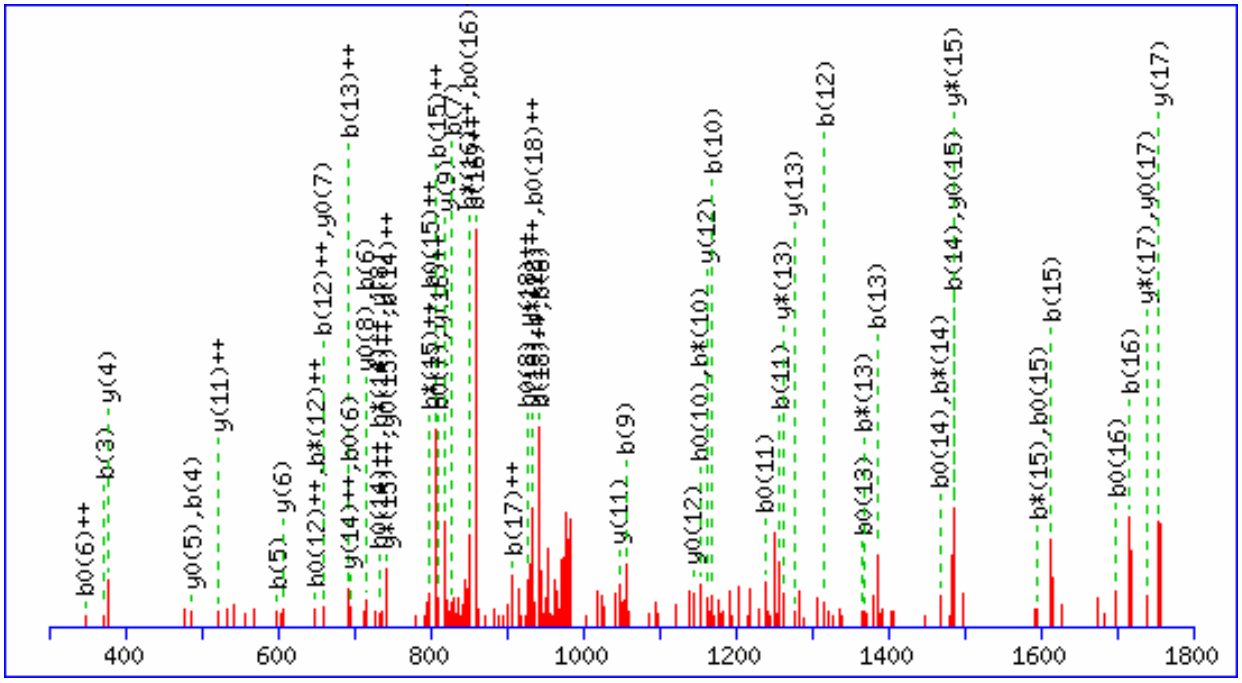
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							29
2	200.26	100.63	183.23	92.12			K	3155.45	1578.23	3138.42	1569.71	3137.43	1569.22	28
3	299.39	150.20	282.36	141.68			V	3027.28	1514.14	3010.25	1505.63	3009.26	1505.13	27
4	414.48	207.74	397.45	199.23	396.46	198.73	D	2928.14	1464.58	2911.11	1456.06	2910.13	1455.57	26
5	543.59	272.30	526.56	263.78	525.58	263.29	E	2813.06	1407.03	2796.03	1398.52	2795.04	1398.02	25
6	690.76	345.89	673.73	337.37	672.75	336.88	F	2683.94	1342.48	2666.91	1333.96	2665.93	1333.47	24
7	787.88	394.44	770.85	385.93	769.86	385.44	P	2536.77	1268.89	2519.74	1260.37	2518.75	1259.88	23
8	901.04	451.02	884.01	442.51	883.02	442.01	L	2439.65	1220.33	2422.62	1211.82	2421.64	1211.32	22
9	1004.18	502.59	987.15	494.08	986.16	493.59	C	2326.50	1163.75	2309.47	1155.24	2308.48	1154.74	21
10	1061.23	531.12	1044.20	522.60	1043.22	522.11	G	2223.35	1112.18	2206.32	1103.67	2205.34	1103.17	20
11	1198.37	599.69	1181.34	591.17	1180.36	590.68	H	2166.30	1083.66	2149.27	1075.14	2148.29	1074.65	19
12	1329.57	665.29	1312.54	656.77	1311.55	656.28	M	2029.16	1015.09	2012.13	1006.57	2011.15	1006.08	18
13	1428.70	714.85	1411.67	706.34	1410.68	705.85	V	1897.97	949.49	1880.94	940.97	1879.95	940.48	17
14	1515.78	758.39	1498.74	749.88	1497.76	749.38	S	1798.84	899.92	1781.81	891.41	1780.82	890.91	16
15	1630.86	815.94	1613.83	807.42	1612.85	806.93	D	1711.76	856.38	1694.73	847.87	1693.74	847.38	15
16	1759.98	880.49	1742.95	871.98	1741.96	871.48	E	1596.67	798.84	1579.64	790.32	1578.66	789.83	14
17	1923.15	962.08	1906.12	953.56	1905.13	953.07	Y	1467.56	734.28	1450.53	725.77	1449.54	725.27	13
18	2052.26	1026.64	2035.23	1018.12	2034.25	1017.63	E	1304.38	652.70	1287.35	644.18	1286.37	643.69	12
19	2180.39	1090.70	2163.36	1082.19	2162.38	1081.69	Q	1175.27	588.14	1158.24	579.62	1157.25	579.13	11
20	2293.55	1147.28	2276.52	1138.76	2275.54	1138.27	L	1047.14	524.07	1030.11	515.56	1029.13	515.07	10
21	2380.63	1190.82	2363.60	1182.30	2362.61	1181.81	S	933.98	467.50	916.95	458.98	915.97	458.49	9
22	2467.71	1234.36	2450.67	1225.84	2449.69	1225.35	S	846.91	423.96	829.88	415.44	828.89	414.95	8
23	2596.82	1298.91	2579.79	1290.40	2578.80	1289.91	E	759.83	380.42	742.80	371.90	741.81	371.41	7
24	2667.90	1334.45	2650.87	1325.94	2649.88	1325.44	A	630.71	315.86	613.68	307.35	612.70	306.85	6
25	2781.05	1391.03	2764.02	1382.52	2763.04	1382.02	L	559.64	280.32	542.61	271.81	541.62	271.31	5
26	2910.17	1455.59	2893.14	1447.07	2892.15	1446.58	E	446.48	223.74	429.45	215.23	428.46	214.74	4
27	2981.25	1491.13	2964.22	1482.61	2963.23	1482.12	A	317.36	159.19	300.33	150.67			3
28	3052.32	1526.67	3035.29	1518.15	3034.31	1517.66	A	246.29	123.65	229.26	115.13			2
29							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RPL10A	FSVCVLGDQQHCDEAK	952.76	2+	69.0



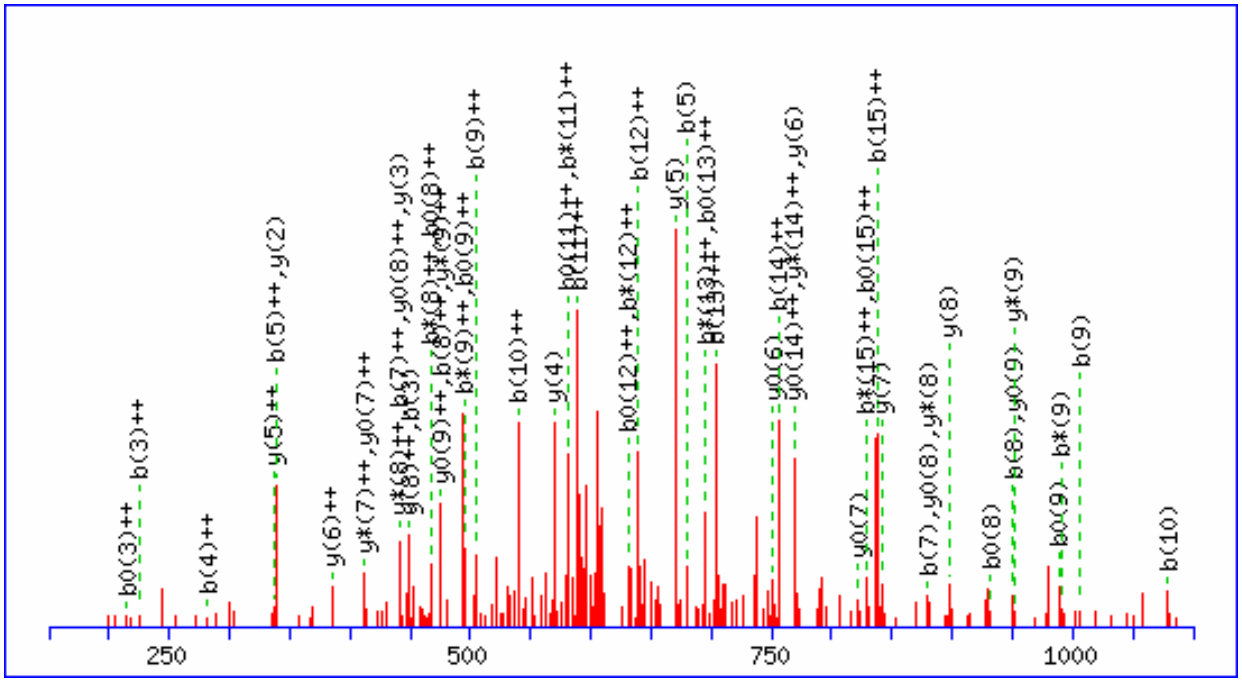
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.18	74.59					F							16
2	235.26	118.13			217.24	109.13	S	1757.92	879.46	1740.89	870.95	1739.90	870.46	15
3	334.39	167.70			316.37	158.69	V	1670.84	835.93	1653.81	827.41	1652.83	826.92	14
4	562.66	281.83			544.64	272.83	C	1571.71	786.36	1554.68	777.84	1553.70	777.35	13
5	661.79	331.40			643.77	322.39	V	1343.44	672.23	1326.41	663.71	1325.43	663.22	12
6	774.95	387.98			756.93	378.97	L	1244.31	622.66	1227.28	614.14	1226.30	613.65	11
7	832.00	416.50			813.98	407.50	G	1131.15	566.08	1114.12	557.57	1113.14	557.07	10
8	947.09	474.05			929.07	465.04	D	1074.10	537.56	1057.07	529.04	1056.09	528.55	9
9	1075.22	538.11	1058.18	529.60	1057.20	529.10	Q	959.02	480.01	941.98	471.50	941.00	471.00	8
10	1203.34	602.18	1186.31	593.66	1185.33	593.17	Q	830.89	415.95	813.86	407.43	812.87	406.94	7
11	1340.48	670.75	1323.45	662.23	1322.47	661.74	H	702.76	351.88	685.73	343.37	684.74	342.87	6
12	1443.63	722.32	1426.60	713.80	1425.61	713.31	C	565.62	283.31	548.59	274.80	547.60	274.31	5
13	1558.71	779.86	1541.68	771.35	1540.70	770.85	D	462.47	231.74	445.44	223.23	444.46	222.73	4
14	1687.83	844.42	1670.80	835.90	1669.81	835.41	E	347.39	174.20	330.36	165.68	329.37	165.19	3
15	1758.91	879.96	1741.88	871.44	1740.89	870.95	A	218.27	109.64	201.24	101.13			2
16							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RPL12	HPHDIIDDINSGAVECPAS	995.55	2+	74.8



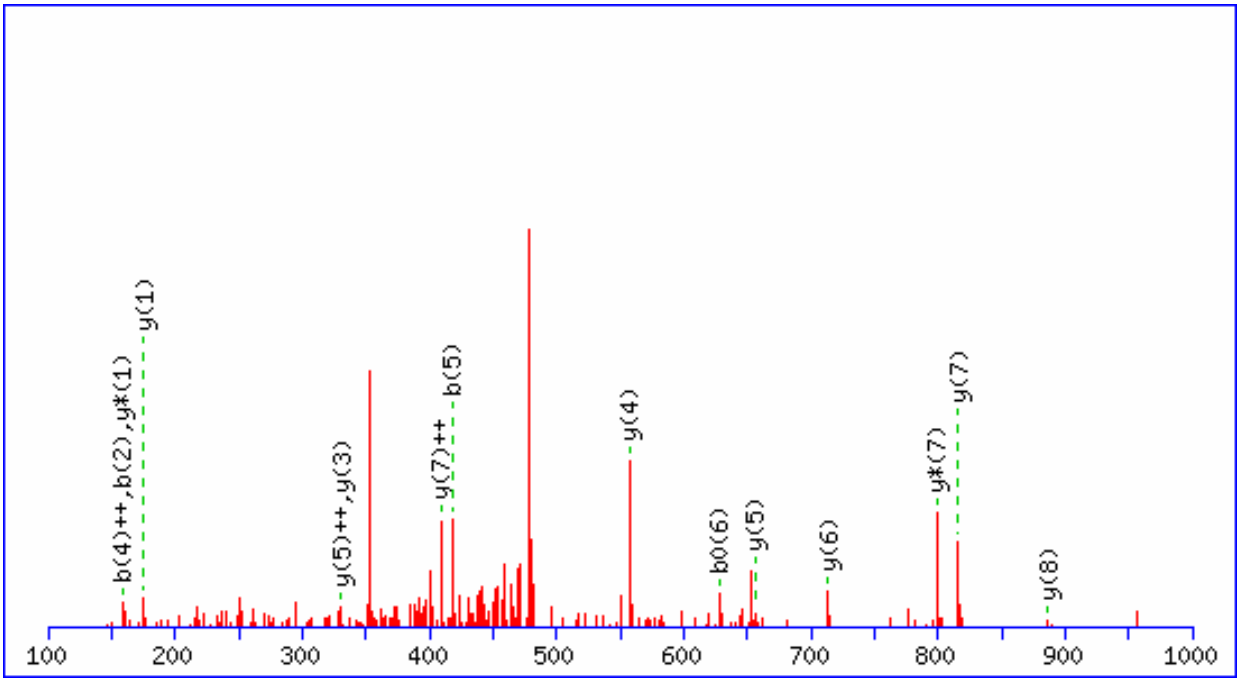
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.15	69.58					H							19
2	235.26	118.14					P	1853.98	927.49	1836.95	918.98	1835.96	918.49	18
3	372.40	186.70					H	1756.87	878.94	1739.83	870.42	1738.85	869.93	17
4	487.49	244.25			469.47	235.24	D	1619.73	810.37	1602.70	801.85	1601.71	801.36	16
5	600.65	300.83			582.63	291.82	I	1504.64	752.82	1487.61	744.31	1486.62	743.82	15
6	713.80	357.41			695.79	348.40	I	1391.48	696.24	1374.45	687.73	1373.47	687.24	14
7	828.89	414.95			810.88	405.94	D	1278.32	639.67	1261.29	631.15	1260.31	630.66	13
8	943.98	472.49			925.96	463.49	D	1163.24	582.12	1146.21	573.61	1145.22	573.11	12
9	1057.14	529.07			1039.12	520.06	I	1048.15	524.58	1031.12	516.06	1030.13	515.57	11
10	1171.24	586.12	1154.21	577.61	1153.22	577.12	N	934.99	468.00	917.96	459.48	916.98	458.99	10
11	1258.32	629.66	1241.29	621.15	1240.30	620.65	S	820.89	410.95			802.87	401.94	9
12	1315.37	658.19	1298.34	649.67	1297.35	649.18	G	733.81	367.41			715.80	358.40	8
13	1386.45	693.73	1369.42	685.21	1368.43	684.72	A	676.76	338.88			658.74	329.88	7
14	1485.58	743.29	1468.55	734.78	1467.56	734.28	V	605.68	303.34			587.67	294.34	6
15	1614.69	807.85	1597.66	799.33	1596.68	798.84	E	506.55	253.78			488.54	244.77	5
16	1717.83	859.42	1700.80	850.91	1699.82	850.41	C	377.44	189.22			359.42	180.21	4
17	1814.95	907.98	1797.92	899.46	1796.93	898.97	P	274.29	137.65			256.28	128.64	3
18	1886.03	943.52	1869.00	935.00	1868.01	934.51	A	177.18	89.09			159.16	80.09	2
19							S	106.10	53.55			88.09	44.55	1

Gene Symbol	Sequences	m/z	Charge	Ion score
RPL18A	EYRDLTTAGAVTQCYR	616.79	3+	67.5



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.12	65.56			112.11	56.56	E							16
2	293.30	147.15			275.28	138.14	Y	1718.91	859.96	1701.88	851.44	1700.89	850.95	15
3	449.48	225.24	432.45	216.73	431.47	216.24	R	1555.73	778.37	1538.70	769.86	1537.72	769.36	14
4	564.57	282.79	547.54	274.27	546.55	273.78	D	1399.55	700.28	1382.52	691.76	1381.53	691.27	13
5	677.73	339.37	660.70	330.85	659.71	330.36	L	1284.46	642.73	1267.43	634.22	1266.45	633.73	12
6	778.83	389.92	761.80	381.40	760.81	380.91	T	1171.30	586.16	1154.27	577.64	1153.29	577.15	11
7	879.93	440.47	862.90	431.96	861.92	431.46	T	1070.20	535.60	1053.17	527.09	1052.19	526.60	10
8	951.01	476.01	933.98	467.49	933.00	467.00	A	969.10	485.05	952.07	476.54	951.08	476.04	9
9	1008.06	504.54	991.03	496.02	990.05	495.53	G	898.02	449.51	880.99	441.00	880.00	440.51	8
10	1079.14	540.07	1062.11	531.56	1061.13	531.07	A	840.97	420.99	823.94	412.47	822.95	411.98	7
11	1178.27	589.64	1161.24	581.12	1160.26	580.63	V	769.89	385.45	752.86	376.93	751.87	376.44	6
12	1279.38	640.19	1262.35	631.68	1261.36	631.18	T	670.76	335.88	653.73	327.37	652.74	326.88	5
13	1407.51	704.26	1390.47	695.74	1389.49	695.25	Q	569.65	285.33	552.62	276.82			4
14	1510.65	755.83	1493.62	747.31	1492.63	746.82	C	441.53	221.27	424.49	212.75			3
15	1673.82	837.41	1656.79	828.90	1655.81	828.41	Y	338.38	169.70	321.35	161.18			2
16							R	175.21	88.11	158.18	79.59			1

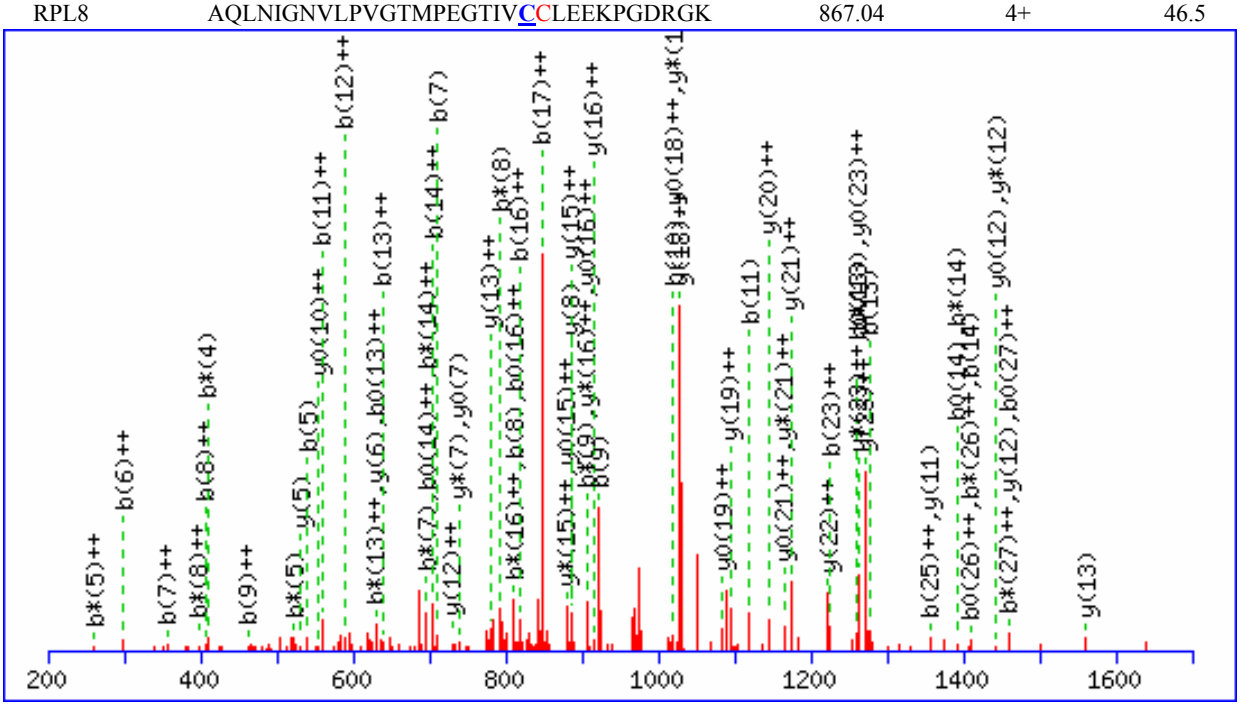
Gene Symbol	Sequences	m/z	Charge	Ion score
RPL34	SACGVCPGR	488.74	2+	52.6



C6 **:** NEM (C)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	88.09	44.55	70.07	35.54	S					9
2	159.16	80.09	141.15	71.08	A	888.05	444.53	871.02	436.01	8
3	262.31	131.66	244.29	122.65	C	816.97	408.99	799.94	400.47	7
4	319.36	160.18	301.34	151.17	G	713.83	357.42	696.80	348.90	6
5	418.49	209.75	400.47	200.74	V	656.77	328.89	639.74	320.38	5
6	646.76	323.88	628.74	314.87	C	557.64	279.33	540.61	270.81	4
7	743.87	372.44	725.86	363.43	P	329.38	165.19	312.34	156.68	3
8	800.92	400.97	782.91	391.96	G	232.26	116.63	215.23	108.12	2
9					R	175.21	88.11	158.18	79.59	1

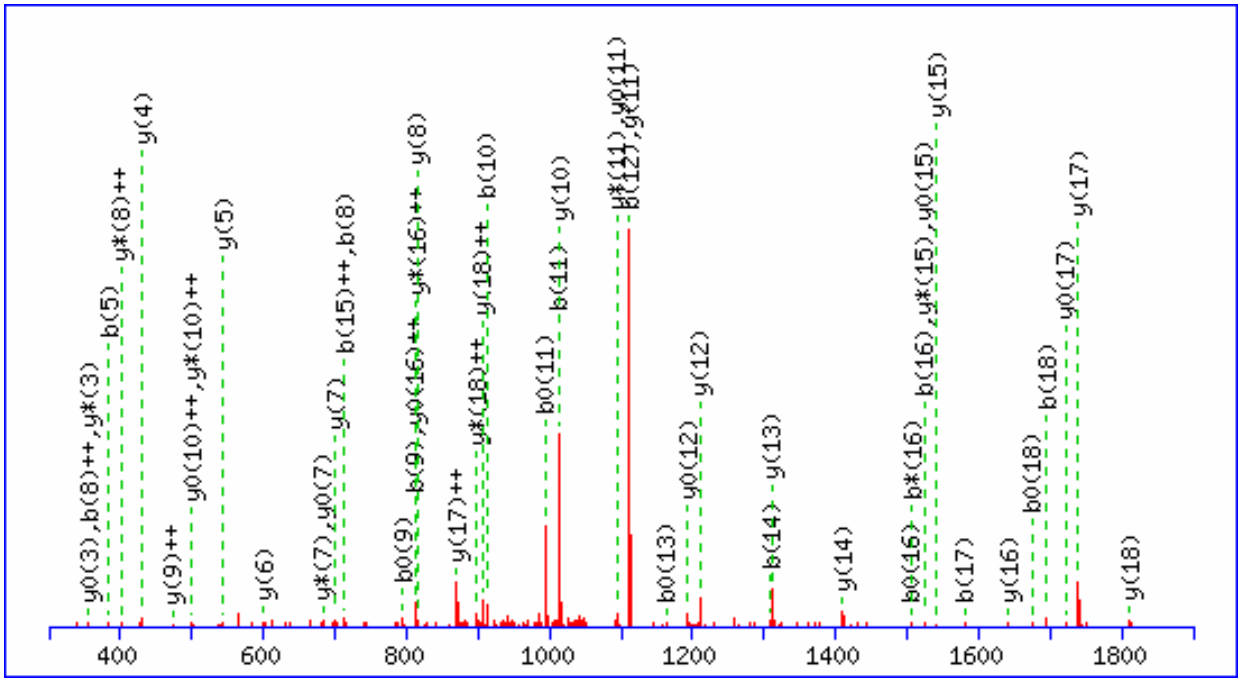
Gene Symbol	Sequences	m/z	Charge	Ion score
RPL8	AQLNIGNVLPVGTMPEGTIVCCLEEKPGDRGK	867.04	4+	46.5



C22 : NEM (C)

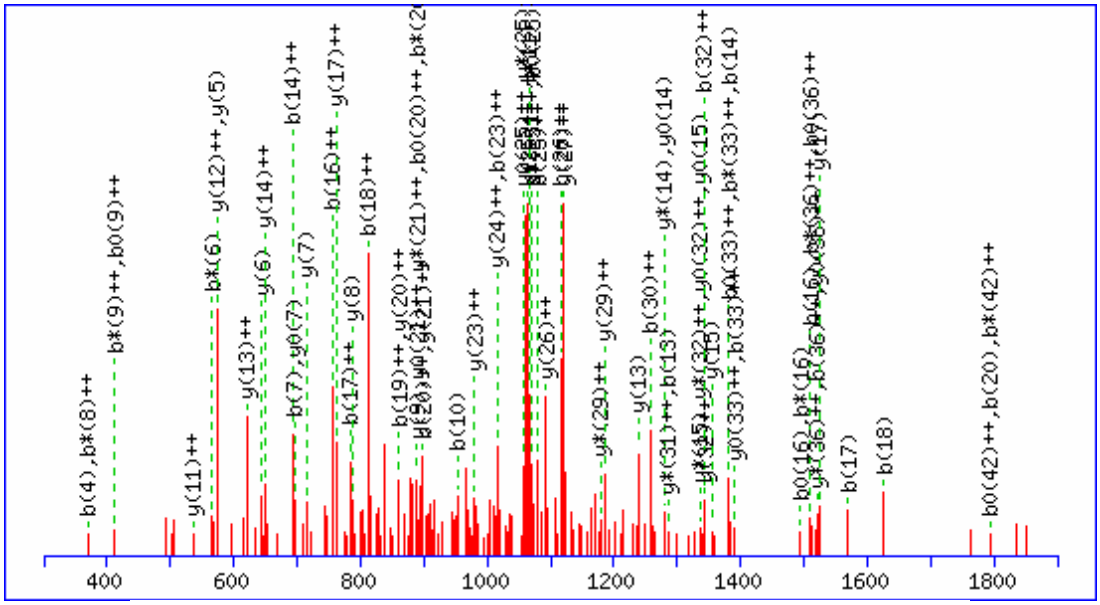
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							32
2	200.22	100.61	183.18	92.10			Q	3394.92	1697.96	3377.89	1689.45	3376.90	1688.95	31
3	313.37	157.19	296.34	148.68			L	3266.79	1633.90	3249.76	1625.38	3248.77	1624.89	30
4	427.48	214.24	410.44	205.73			N	3153.63	1577.32	3136.60	1568.80	3135.61	1568.31	29
5	540.63	270.82	523.60	262.31			I	3039.53	1520.27	3022.50	1511.75	3021.51	1511.26	28
6	597.68	299.35	580.65	290.83			G	2926.37	1463.69	2909.34	1455.17	2908.35	1454.68	27
7	711.79	356.40	694.76	347.88			N	2869.32	1435.16	2852.29	1426.65	2851.30	1426.16	26
8	810.92	405.96	793.89	397.45			V	2755.21	1378.11	2738.18	1369.60	2737.20	1369.10	25
9	924.08	462.54	907.04	454.03			L	2656.08	1328.55	2639.05	1320.03	2638.07	1319.54	24
10	1021.19	511.10	1004.16	502.58			P	2542.93	1271.97	2525.90	1263.45	2524.91	1262.96	23
11	1120.32	560.66	1103.29	552.15			V	2445.81	1223.41	2428.78	1214.89	2427.80	1214.40	22
12	1177.37	589.19	1160.34	580.68			G	2346.68	1173.84	2329.65	1165.33	2328.66	1164.84	21
13	1278.48	639.74	1261.45	631.23	1260.46	630.73	T	2289.63	1145.32	2272.60	1136.80	2271.61	1136.31	20
14	1409.67	705.34	1392.64	696.83	1391.66	696.33	M	2188.52	1094.77	2171.49	1086.25	2170.51	1085.76	19
15	1506.79	753.90	1489.76	745.38	1488.77	744.89	P	2057.33	1029.17	2040.30	1020.65	2039.31	1020.16	18
16	1635.90	818.46	1618.87	809.94	1617.89	809.45	E	1960.21	980.61	1943.18	972.10	1942.20	971.60	17
17	1692.95	846.98	1675.92	838.47	1674.94	837.97	G	1831.10	916.05	1814.07	907.54	1813.08	907.05	16
18	1794.06	897.53	1777.03	889.02	1776.04	888.53	T	1774.05	887.53	1757.02	879.01	1756.03	878.52	15
19	1907.22	954.11	1890.18	945.60	1889.20	945.10	I	1672.94	836.98	1655.91	828.46	1654.93	827.97	14
20	2006.35	1003.68	1989.32	995.16	1988.33	994.67	V	1559.79	780.40	1542.76	771.88	1541.77	771.39	13
21	2109.49	1055.25	2092.46	1046.73	2091.47	1046.24	C	1460.66	730.83	1443.62	722.32	1442.64	721.82	12
22	2337.76	1169.38	2320.73	1160.87	2319.74	1160.37	C	1357.51	679.26	1340.48	670.74	1339.50	670.25	11
23	2450.91	1225.96	2433.88	1217.45	2432.90	1216.95	L	1129.24	565.13	1112.21	556.61	1111.23	556.12	10
24	2580.03	1290.52	2563.00	1282.00	2562.01	1281.51	E	1016.09	508.55	999.06	500.03	998.07	499.54	9
25	2709.14	1355.08	2692.11	1346.56	2691.13	1346.07	E	886.97	443.99	869.94	435.48	868.96	434.98	8
26	2837.32	1419.16	2820.28	1410.65	2819.30	1410.15	K	757.86	379.43	740.83	370.92	739.84	370.43	7
27	2934.43	1467.72	2917.40	1459.20	2916.42	1458.71	P	629.69	315.35	612.66	306.83	611.67	306.34	6
28	2991.48	1496.24	2974.45	1487.73	2973.47	1487.24	G	532.57	266.79	515.54	258.27	514.56	257.78	5
29	3106.57	1553.79	3089.54	1545.27	3088.55	1544.78	D	475.52	238.26	458.49	229.75	457.50	229.26	4
30	3262.75	1631.88	3245.72	1623.37	3244.74	1622.87	R	360.43	180.72	343.40	172.20			3
31	3319.81	1660.41	3302.78	1651.89	3301.79	1651.40	G	204.25	102.63	187.22	94.11			2
32							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RPLP0	AGAIAP**C**EVTVPAQNTGLGPEK	1062.85	2+	90.5



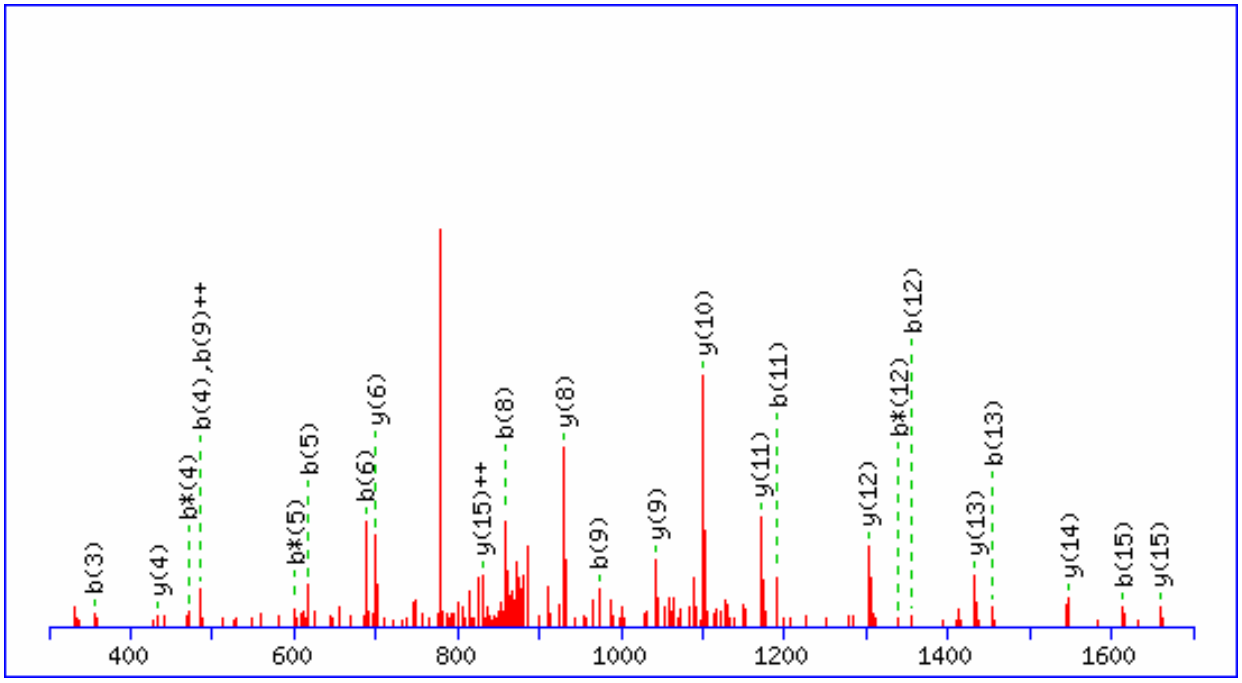
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							22
2	129.14	65.07					G	2053.32	1027.16	2036.29	1018.65	2035.30	1018.15	21
3	200.22	100.61					A	1996.27	998.64	1979.23	990.12	1978.25	989.63	20
4	313.37	157.19					I	1925.19	963.10	1908.16	954.58	1907.17	954.09	19
5	384.45	192.73					A	1812.03	906.52	1795.00	898.00	1794.01	897.51	18
6	481.57	241.29					P	1740.95	870.98	1723.92	862.46	1722.94	861.97	17
7	584.71	292.86					C	1643.84	822.42	1626.81	813.91	1625.82	813.41	16
8	713.82	357.42			695.81	348.41	E	1540.69	770.85	1523.66	762.34	1522.68	761.84	15
9	812.95	406.98			794.94	397.97	V	1411.58	706.29	1394.55	697.78	1393.56	697.29	14
10	914.06	457.53			896.04	448.53	T	1312.45	656.73	1295.42	648.21	1294.43	647.72	13
11	1013.19	507.10			995.17	498.09	V	1211.34	606.18	1194.31	597.66	1193.33	597.17	12
12	1110.30	555.66			1092.29	546.65	P	1112.21	556.61	1095.18	548.10	1094.20	547.60	11
13	1181.38	591.19			1163.37	582.19	A	1015.10	508.05	998.07	499.54	997.08	499.05	10
14	1309.51	655.26	1292.48	646.74	1291.50	646.25	Q	944.02	472.51	926.99	464.00	926.01	463.51	9
15	1423.61	712.31	1406.58	703.80	1405.60	703.30	N	815.89	408.45	798.86	399.93	797.88	399.44	8
16	1524.72	762.86	1507.69	754.35	1506.70	753.86	T	701.79	351.40	684.76	342.88	683.77	342.39	7
17	1581.77	791.39	1564.74	782.87	1563.75	782.38	G	600.68	300.85	583.65	292.33	582.67	291.84	6
18	1694.93	847.97	1677.90	839.45	1676.91	838.96	L	543.63	272.32	526.60	263.81	525.62	263.31	5
19	1751.98	876.49	1734.95	867.98	1733.96	867.49	G	430.48	215.74	413.45	207.23	412.46	206.73	4
20	1849.09	925.05	1832.06	916.54	1831.08	916.04	P	373.42	187.22	356.39	178.70	355.41	178.21	3
21	1978.21	989.61	1961.18	981.09	1960.19	980.60	E	276.31	138.66	259.28	130.14	258.29	129.65	2
22							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RPLP1	ALANVNIGSLICNVGAGGPAPAAGAAPAGGPAPSTAAAPAEEK	939.43	4+	81.9



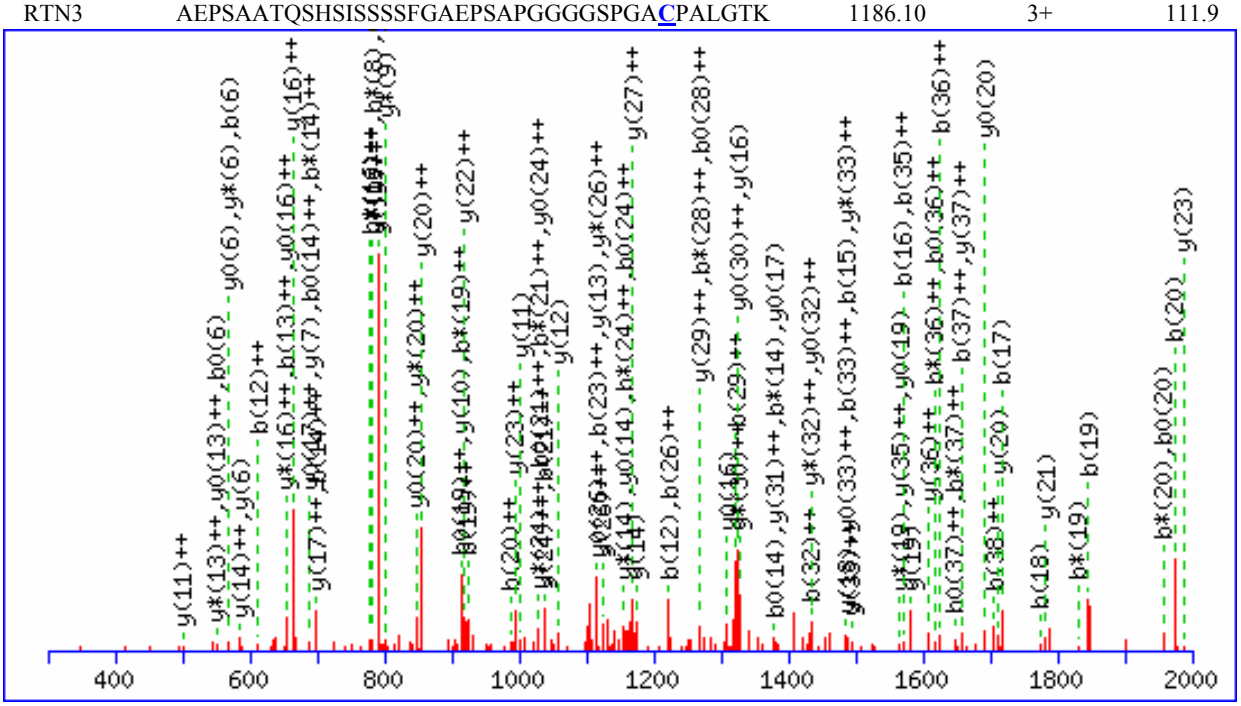
#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	72.09	36.55					A							43
2	185.24	93.13					L	3683.09	1842.05	3666.06	1833.53	3665.07	1833.04	42
3	256.32	128.66					A	3569.93	1785.47	3552.90	1776.95	3551.92	1776.46	41
4	370.42	185.72	353.39	177.20			N	3498.85	1749.93	3481.82	1741.42	3480.84	1740.92	40
5	469.56	235.28	452.52	226.77			V	3384.75	1692.88	3367.72	1684.36	3366.73	1683.87	39
6	583.66	292.33	566.63	283.82			N	3285.62	1643.31	3268.59	1634.80	3267.60	1634.31	38
7	696.82	348.91	679.78	340.40			I	3171.52	1586.26	3154.49	1577.75	3153.50	1577.25	37
8	753.87	377.44	736.84	368.92			G	3058.36	1529.68	3041.33	1521.17	3040.34	1520.68	36
9	840.94	420.98	823.91	412.46	822.93	411.97	S	3001.31	1501.16	2984.28	1492.64	2983.29	1492.15	35
10	954.10	477.55	937.07	469.04	936.09	468.55	L	2914.23	1457.62	2897.20	1449.10	2896.22	1448.61	34
11	1067.26	534.13	1050.23	525.62	1049.24	525.13	I	2801.07	1401.04	2784.04	1392.53	2783.06	1392.03	33
12	1170.40	585.70	1153.37	577.19	1152.39	576.70	C	2687.92	1344.46	2670.88	1335.95	2669.90	1335.45	32
13	1284.50	642.76	1267.47	634.24	1266.49	633.75	N	2584.77	1292.89	2567.74	1284.37	2566.76	1283.88	31
14	1383.64	692.32	1366.61	683.81	1365.62	683.31	V	2470.67	1235.84	2453.64	1227.32	2452.65	1226.83	30
15	1440.69	720.85	1423.66	712.33	1422.67	711.84	G	2371.54	1186.27	2354.51	1177.76	2353.52	1177.27	29
16	1511.76	756.39	1494.73	747.87	1493.75	747.38	A	2314.49	1157.75	2297.46	1149.23	2296.47	1148.74	28
17	1568.82	784.91	1551.79	776.40	1550.80	775.90	G	2243.41	1122.21	2226.38	1113.69	2225.39	1113.20	27
18	1625.87	813.44	1608.84	804.92	1607.85	804.43	G	2186.36	1093.68	2169.33	1085.17	2168.34	1084.68	26
19	1722.98	862.00	1705.95	853.48	1704.97	852.99	P	2129.31	1065.16	2112.28	1056.64	2111.29	1056.15	25
20	1794.06	897.53	1777.03	889.02	1776.05	888.53	A	2032.19	1016.60	2015.16	1008.08	2014.18	1007.59	24
21	1891.18	946.09	1874.15	937.58	1873.16	937.08	P	1961.11	981.06	1944.08	972.55	1943.10	972.05	23
22	1962.25	981.63	1945.22	973.12	1944.24	972.62	A	1864.00	932.50	1846.97	923.99	1845.98	923.50	22
23	2033.33	1017.17	2016.30	1008.65	2015.32	1008.16	A	1792.92	896.96	1775.89	888.45	1774.91	887.96	21
24	2090.38	1045.70	2073.35	1037.18	2072.37	1036.69	G	1721.84	861.43	1704.81	852.91	1703.83	852.42	20
25	2161.46	1081.23	2144.43	1072.72	2143.45	1072.23	A	1664.79	832.90	1647.76	824.38	1646.78	823.89	19
26	2232.54	1116.77	2215.51	1108.26	2214.52	1107.77	A	1593.71	797.36	1576.68	788.85	1575.70	788.35	18
27	2329.65	1165.33	2312.62	1156.82	2311.64	1156.32	P	1522.64	761.82	1505.61	753.31	1504.62	752.81	17
28	2400.73	1200.87	2383.70	1192.35	2382.72	1191.86	A	1425.52	713.26	1408.49	704.75	1407.51	704.26	16
29	2457.78	1229.40	2440.75	1220.88	2439.77	1220.39	G	1354.44	677.73	1337.41	669.21	1336.43	668.72	15
30	2514.83	1257.92	2497.80	1249.41	2496.82	1248.91	G	1297.39	649.20	1280.36	640.68	1279.38	640.19	14
31	2611.95	1306.48	2594.92	1297.96	2593.93	1297.47	P	1240.34	620.67	1223.31	612.16	1222.32	611.67	13
32	2683.03	1342.02	2666.00	1333.50	2665.01	1333.01	A	1143.22	572.12	1126.19	563.60	1125.21	563.11	12
33	2780.14	1390.58	2763.11	1382.06	2762.13	1381.57	P	1072.15	536.58	1055.12	528.06	1054.13	527.57	11
34	2867.22	1434.11	2850.19	1425.60	2849.20	1425.11	S	975.03	488.02	958.00	479.50	957.02	479.01	10
35	2968.32	1484.67	2951.29	1476.15	2950.31	1475.66	T	887.95	444.48	870.92	435.97	869.94	435.47	9
36	3039.40	1520.20	3022.37	1511.69	3021.39	1511.20	A	786.85	393.93	769.82	385.41	768.84	384.92	8
37	3110.48	1555.74	3093.45	1547.23	3092.46	1546.74	A	715.77	358.39	698.74	349.87	697.76	349.38	7
38	3181.56	1591.28	3164.53	1582.77	3163.54	1582.28	A	644.69	322.85	627.66	314.34	626.68	313.84	6
39	3278.67	1639.84	3261.64	1631.33	3260.66	1630.83	P	573.62	287.31	556.59	278.80	555.60	278.30	5
40	3349.75	1675.38	3332.72	1666.86	3331.74	1666.37	A	476.50	238.75	459.47	230.24	458.49	229.75	4
41	3478.86	1739.94	3461.83	1731.42	3460.85	1730.93	E	405.42	203.22	388.39	194.70	387.41	194.21	3
42	3607.98	1804.49	3590.95	1795.98	3589.96	1795.49	E	276.31	138.66	259.28	130.14	258.29	129.65	2
43							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RPS2	KLLMMAGIDDCYTSAR	894.63	2+	86.6



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.18	65.09	112.15	56.58			K							16
2	242.34	121.67	225.31	113.16			L	1660.95	830.98	1643.92	822.47	1642.94	821.97	15
3	355.50	178.25	338.46	169.74			L	1547.80	774.40	1530.77	765.89	1529.78	765.39	14
4	486.69	243.85	469.66	235.33			M	1434.64	717.82	1417.61	709.31	1416.62	708.82	13
5	617.89	309.45	600.86	300.93			M	1303.44	652.22	1286.41	643.71	1285.43	643.22	12
6	688.97	344.99	671.94	336.47			A	1172.25	586.63	1155.22	578.11	1154.23	577.62	11
7	746.02	373.51	728.99	365.00			G	1101.17	551.09	1084.14	542.57	1083.15	542.08	10
8	859.17	430.09	842.14	421.58			I	1044.12	522.56	1027.09	514.05	1026.10	513.55	9
9	974.26	487.63	957.23	479.12	956.25	478.63	D	930.96	465.98	913.93	457.47	912.94	456.98	8
10	1089.35	545.18	1072.32	536.66	1071.33	536.17	D	815.87	408.44	798.84	399.92	797.86	399.43	7
11	1192.49	596.75	1175.46	588.23	1174.48	587.74	C	700.78	350.90	683.75	342.38	682.77	341.89	6
12	1355.67	678.34	1338.63	669.82	1337.65	669.33	Y	597.64	299.32	580.61	290.81	579.63	290.32	5
13	1456.77	728.89	1439.74	720.37	1438.75	719.88	T	434.47	217.74	417.44	209.22	416.45	208.73	4
14	1543.85	772.43	1526.82	763.91	1525.83	763.42	S	333.36	167.19	316.33	158.67	315.35	158.18	3
15	1614.92	807.97	1597.89	799.45	1596.91	798.96	A	246.29	123.65	229.26	115.13			2
16							R	175.21	88.11	158.18	79.59			1

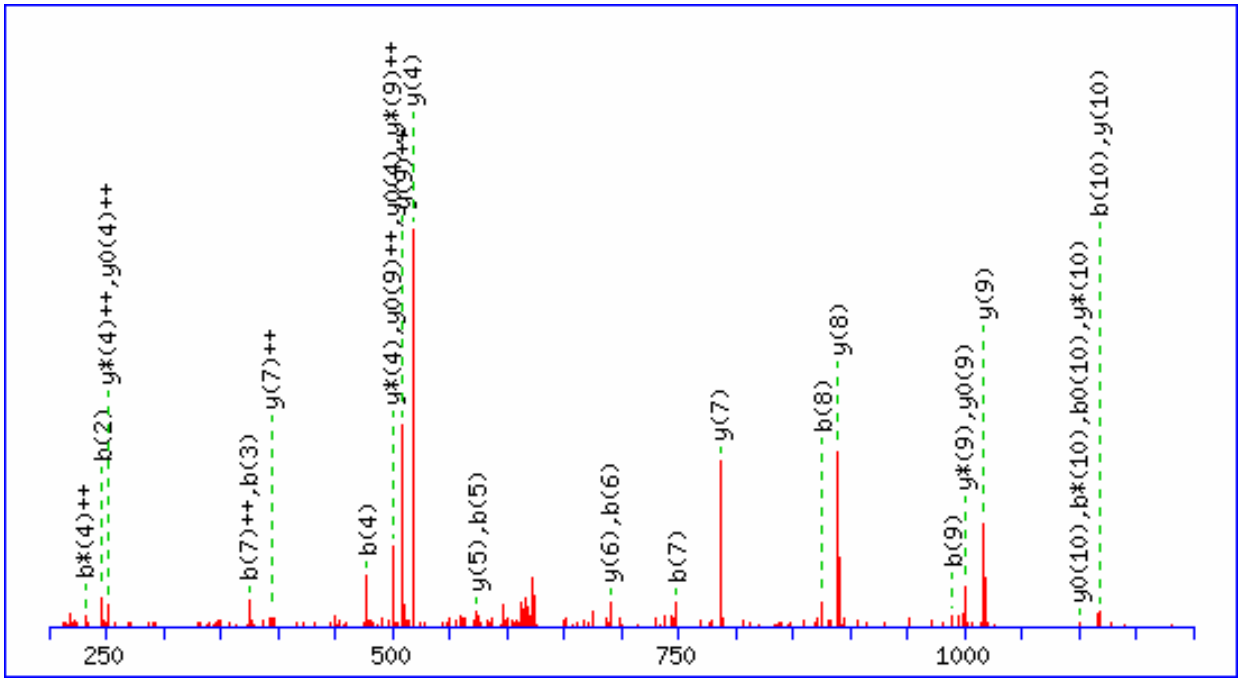
Gene Symbol	Sequences	m/z	Charge	Ion score
RTN3	AEPSAATQSHSISSSSFGAEPSAPGGGGSPGA**C**PALGTK	1186.10	3+	111.9



N-term : N-Acetyl (Protein)

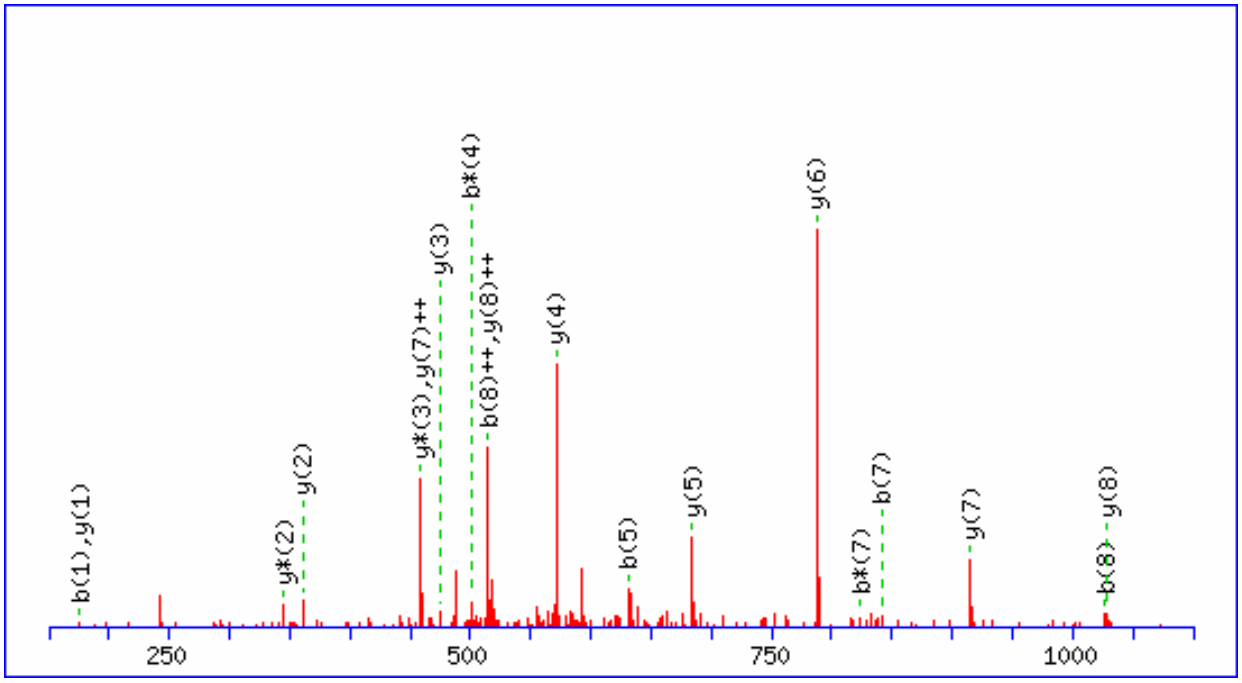
#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	114.12	57.57					A							39
2	243.24	122.12			225.22	113.11	E	3444.63	1722.82	3427.60	1714.30	3426.61	1713.81	38
3	340.35	170.68			322.34	161.67	P	3315.52	1658.26	3298.49	1649.75	3297.50	1649.25	37
4	427.43	214.22			409.41	205.21	S	3218.40	1609.70	3201.37	1601.19	3200.39	1600.70	36
5	498.51	249.76			480.49	240.75	A	3131.32	1566.17	3114.29	1557.65	3113.31	1557.16	35
6	569.58	285.30			551.57	276.29	A	3060.25	1530.63	3043.22	1522.11	3042.23	1521.62	34
7	670.69	335.85			652.67	326.84	T	2989.17	1495.09	2972.14	1486.57	2971.15	1486.08	33
8	798.82	399.91	781.79	391.40	780.80	390.91	Q	2888.06	1444.54	2871.03	1436.02	2870.05	1435.53	32
9	885.90	443.45	868.86	434.94	867.88	434.44	S	2759.93	1380.47	2742.90	1371.96	2741.92	1371.46	31
10	1023.03	512.02	1006.00	503.51	1005.02	503.01	H	2672.86	1336.93	2655.83	1328.42	2654.84	1327.92	30
11	1110.11	555.56	1093.08	547.04	1092.10	546.55	S	2535.72	1268.36	2518.69	1259.85	2517.70	1259.36	29
12	1223.27	612.14	1206.24	603.62	1205.25	603.13	I	2448.64	1224.82	2431.61	1216.31	2430.63	1215.82	28
13	1310.35	655.68	1293.32	647.16	1292.33	646.67	S	2335.48	1168.25	2318.45	1159.73	2317.47	1159.24	27
14	1397.42	699.22	1380.39	690.70	1379.41	690.21	S	2248.41	1124.71	2231.38	1116.19	2230.39	1115.70	26
15	1484.50	742.75	1467.47	734.24	1466.49	733.75	S	2161.33	1081.17	2144.30	1072.65	2143.31	1072.16	25
16	1571.58	786.29	1554.55	777.78	1553.56	777.29	S	2074.25	1037.63	2057.22	1029.11	2056.24	1028.62	24
17	1718.75	859.88	1701.72	851.36	1700.74	850.87	F	1987.17	994.09	1970.14	985.58	1969.16	985.08	23
18	1775.80	888.41	1758.77	879.89	1757.79	879.40	G	1840.00	920.50	1822.97	911.99	1821.98	911.50	22
19	1846.88	923.94	1829.85	915.43	1828.87	914.94	A	1782.95	891.98	1765.92	883.46	1764.93	882.97	21
20	1976.00	988.50	1958.97	979.99	1957.98	979.49	E	1711.87	856.44	1694.84	847.92	1693.86	847.43	20
21	2073.11	1037.06	2056.08	1028.54	2055.10	1028.05	P	1582.76	791.88	1565.73	783.37	1564.74	782.87	19
22	2160.19	1080.60	2143.16	1072.08	2142.17	1071.59	S	1485.64	743.32	1468.61	734.81	1467.63	734.32	18
23	2231.27	1116.14	2214.24	1107.62	2213.25	1107.13	A	1398.56	699.79	1381.53	691.27	1380.55	690.78	17
24	2328.38	1164.69	2311.35	1156.18	2310.37	1155.69	P	1327.49	664.25	1310.46	655.73	1309.47	655.24	16
25	2385.43	1193.22	2368.40	1184.71	2367.42	1184.21	G	1230.37	615.69	1213.34	607.17	1212.36	606.68	15
26	2442.48	1221.75	2425.45	1213.23	2424.47	1212.74	G	1173.32	587.16	1156.29	578.65	1155.30	578.16	14
27	2499.54	1250.27	2482.50	1241.76	2481.52	1241.26	G	1116.27	558.64	1099.24	550.12	1098.25	549.63	13
28	2556.59	1278.80	2539.56	1270.28	2538.57	1269.79	G	1059.22	530.11	1042.19	521.60	1041.20	521.10	12
29	2643.66	1322.34	2626.63	1313.82	2625.65	1313.33	S	1002.17	501.59	985.14	493.07	984.15	492.58	11
30	2740.78	1370.89	2723.75	1362.38	2722.76	1361.89	P	915.09	458.05	898.06	449.53	897.07	449.04	10
31	2797.83	1399.42	2780.80	1390.90	2779.82	1390.41	G	817.97	409.49	800.94	400.98	799.96	400.48	9
32	2868.91	1434.96	2851.88	1426.44	2850.89	1425.95	A	760.92	380.97	743.89	372.45	742.91	371.96	8
33	2972.05	1486.53	2955.02	1478.01	2954.04	1477.52	C	689.84	345.43	672.81	336.91	671.83	336.42	7
34	3069.17	1535.09	3052.14	1526.57	3051.15	1526.08	P	586.70	293.85	569.67	285.34	568.69	284.85	6
35	3140.24	1570.63	3123.21	1562.11	3122.23	1561.62	A	489.59	245.30	472.56	236.78	471.57	236.29	5
36	3253.40	1627.20	3236.37	1618.69	3235.39	1618.20	L	418.51	209.76	401.48	201.24	400.49	200.75	4
37	3310.45	1655.73	3293.42	1647.22	3292.44	1646.72	G	305.35	153.18	288.32	144.66	287.34	144.17	3
38	3411.56	1706.28	3394.53	1697.77	3393.54	1697.27	T	248.30	124.65	231.27	116.14	230.28	115.65	2
39							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
RUVBL2	FVQCPDGELQK	632.55	2+	60.2



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.18	74.59					F							11
2	247.31	124.16					V	1117.25	559.13	1100.22	550.62	1099.24	550.12	10
3	375.44	188.23	358.41	179.71			Q	1018.12	509.57	1001.09	501.05	1000.11	500.56	9
4	478.59	239.80	461.55	231.28			C	889.99	445.50	872.96	436.99	871.98	436.49	8
5	575.70	288.35	558.67	279.84			P	786.85	393.93	769.82	385.41	768.83	384.92	7
6	690.79	345.90	673.76	337.38	672.77	336.89	D	689.74	345.37	672.70	336.86	671.72	336.36	6
7	747.84	374.42	730.81	365.91	729.82	365.42	G	574.65	287.83	557.62	279.31	556.63	278.82	5
8	876.95	438.98	859.92	430.47	858.94	429.97	E	517.60	259.30	500.57	250.79	499.58	250.29	4
9	990.11	495.56	973.08	487.04	972.10	486.55	L	388.48	194.75	371.45	186.23			3
10	1118.24	559.62	1101.21	551.11	1100.22	550.62	Q	275.32	138.17	258.29	129.65			2
11							K	147.20	74.10	130.16	65.59			1

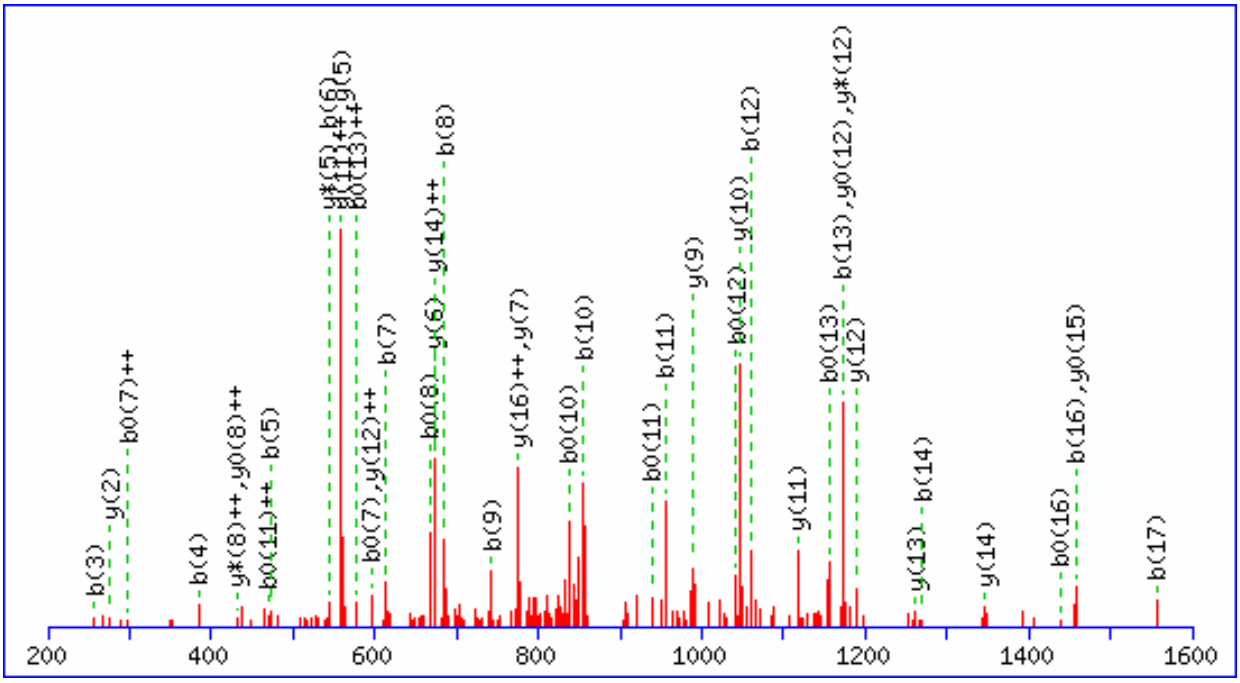
Gene Symbol	Sequences	m/z	Charge	Ion score
SCRIB	MLKCIPLWR	601.51	2+	64.4



N-term : N-Acetyl (Protein)

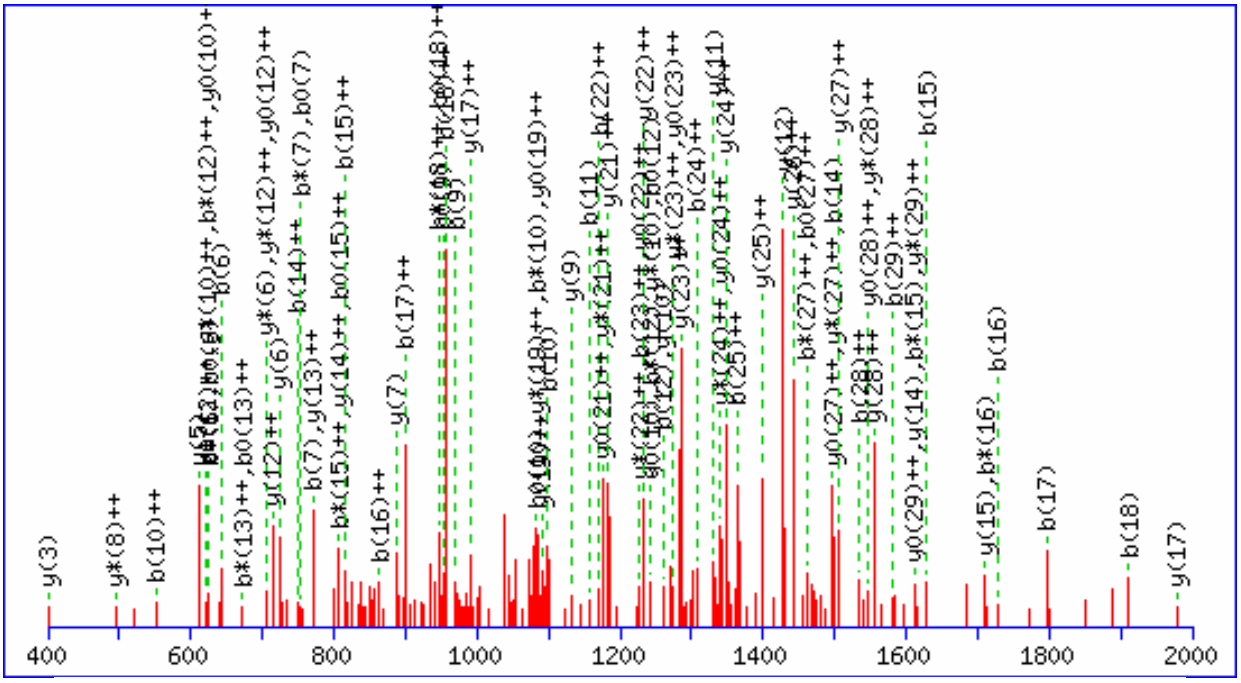
#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	174.24	87.62			M					9
2	287.40	144.20			L	1029.32	515.16	1012.29	506.65	8
3	415.57	208.29	398.54	199.77	K	916.16	458.59	899.13	450.07	7
4	518.71	259.86	501.68	251.35	C	787.99	394.50	770.96	385.98	6
5	631.87	316.44	614.84	307.92	I	684.85	342.93	667.82	334.41	5
6	728.99	365.00	711.96	356.48	P	571.69	286.35	554.66	277.83	4
7	842.14	421.58	825.11	413.06	L	474.58	237.79	457.55	229.28	3
8	1028.35	514.68	1011.32	506.17	W	361.42	181.21	344.39	172.70	2
9					R	175.21	88.11	158.18	79.59	1

Gene Symbol	Sequences	m/z	Charge	Ion score
SFT2D3	SPAESAAAGLTCLPSVTR	866.64	2+	111.7



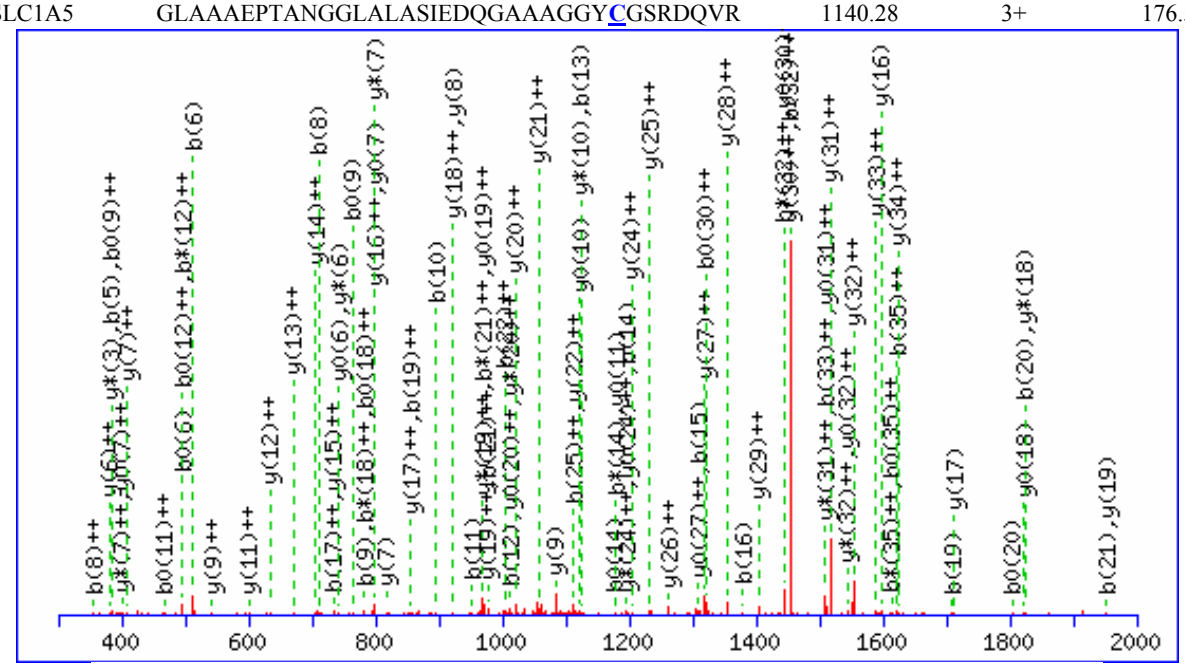
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55	70.07	35.54	S							18
2	185.20	93.10	167.19	84.10	P	1644.87	822.94	1627.84	814.42	1626.85	813.93	17
3	256.28	128.64	238.26	119.64	A	1547.75	774.38	1530.72	765.87	1529.74	765.37	16
4	385.39	193.20	367.38	184.19	E	1476.67	738.84	1459.64	730.33	1458.66	729.83	15
5	472.47	236.74	454.45	227.73	S	1347.56	674.28	1330.53	665.77	1329.55	665.28	14
6	543.55	272.28	525.53	263.27	A	1260.48	630.75	1243.45	622.23	1242.47	621.74	13
7	614.63	307.82	596.61	298.81	A	1189.41	595.21	1172.37	586.69	1171.39	586.20	12
8	685.70	343.36	667.69	334.35	A	1118.33	559.67	1101.30	551.15	1100.31	550.66	11
9	742.75	371.88	724.74	362.87	G	1047.25	524.13	1030.22	515.61	1029.23	515.12	10
10	855.91	428.46	837.90	419.45	L	990.20	495.60	973.17	487.09	972.18	486.60	9
11	957.02	479.01	939.00	470.00	T	877.04	439.02	860.01	430.51	859.03	430.02	8
12	1060.16	530.58	1042.14	521.58	C	775.94	388.47	758.91	379.96	757.92	379.46	7
13	1173.32	587.16	1155.30	578.15	L	672.79	336.90	655.76	328.39	654.78	327.89	6
14	1270.43	635.72	1252.42	626.71	P	559.64	280.32	542.61	271.81	541.62	271.31	5
15	1357.51	679.26	1339.49	670.25	S	462.52	231.76	445.49	223.25	444.51	222.76	4
16	1456.64	728.82	1438.62	719.82	V	375.44	188.23	358.41	179.71	357.43	179.22	3
17	1557.74	779.38	1539.73	770.37	T	276.31	138.66	259.28	130.15	258.30	129.65	2
18					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
SKIV2L2	VKVQSVETVEGCTHEVALPAEEDYLPLKPR	1113.51	3+	109.1



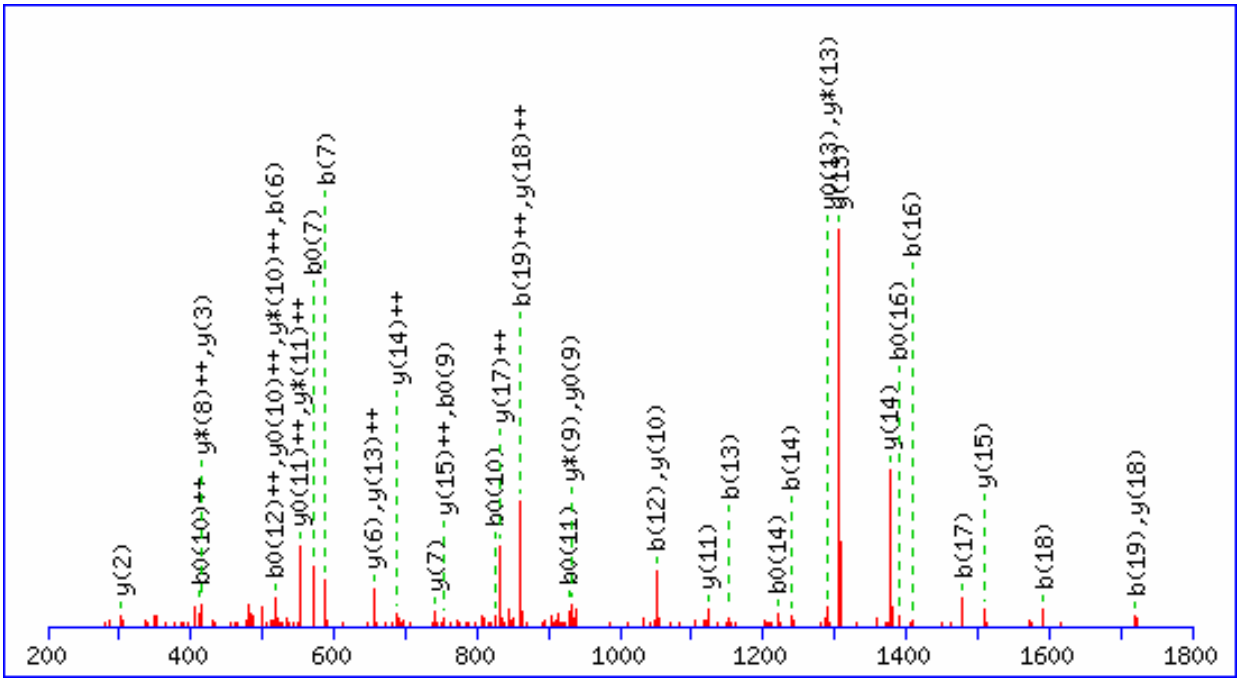
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	100.14	50.57					V							30
2	228.31	114.66	211.28	106.14			K	3239.63	1620.32	3222.60	1611.80	3221.62	1611.31	29
3	327.44	164.23	310.41	155.71			V	3111.46	1556.23	3094.43	1547.72	3093.44	1547.23	28
4	455.57	228.29	438.54	219.77			Q	3012.33	1506.67	2995.30	1498.15	2994.31	1497.66	27
5	542.65	271.83	525.62	263.31	524.63	262.82	S	2884.20	1442.60	2867.17	1434.09	2866.18	1433.60	26
6	641.78	321.39	624.75	312.88	623.76	312.39	V	2797.12	1399.06	2780.09	1390.55	2779.11	1390.06	25
7	770.89	385.95	753.86	377.44	752.88	376.94	E	2697.99	1349.50	2680.96	1340.98	2679.97	1340.49	24
8	872.00	436.50	854.97	427.99	853.98	427.50	T	2568.88	1284.94	2551.85	1276.43	2550.86	1275.93	23
9	971.13	486.07	954.10	477.55	953.11	477.06	V	2467.77	1234.39	2450.74	1225.87	2449.76	1225.38	22
10	1100.24	550.63	1083.21	542.11	1082.23	541.62	E	2368.64	1184.82	2351.61	1176.31	2350.63	1175.82	21
11	1157.29	579.15	1140.26	570.64	1139.28	570.14	G	2239.53	1120.27	2222.50	1111.75	2221.51	1111.26	20
12	1260.44	630.72	1243.41	622.21	1242.42	621.71	C	2182.48	1091.74	2165.44	1083.23	2164.46	1082.73	19
13	1361.54	681.27	1344.51	672.76	1343.53	672.27	T	2079.33	1040.17	2062.30	1031.65	2061.32	1031.16	18
14	1498.68	749.84	1481.65	741.33	1480.67	740.84	H	1978.23	989.62	1961.20	981.10	1960.21	980.61	17
15	1627.79	814.40	1610.76	805.89	1609.78	805.39	E	1841.09	921.05	1824.06	912.53	1823.07	912.04	16
16	1726.93	863.97	1709.90	855.45	1708.91	854.96	V	1711.98	856.49	1694.94	847.98	1693.96	847.48	15
17	1798.00	899.51	1780.97	890.99	1779.99	890.50	A	1612.84	806.93	1595.81	798.41	1594.83	797.92	14
18	1911.16	956.08	1894.13	947.57	1893.15	947.08	L	1541.77	771.39	1524.74	762.87	1523.75	762.38	13
19	2008.28	1004.64	1991.25	996.13	1990.26	995.63	P	1428.61	714.81	1411.58	706.29	1410.59	705.80	12
20	2079.35	1040.18	2062.32	1031.67	2061.34	1031.17	A	1331.49	666.25	1314.46	657.74	1313.48	657.24	11
21	2208.47	1104.74	2191.44	1096.22	2190.45	1095.73	E	1260.42	630.71	1243.39	622.20	1242.40	621.70	10
22	2337.58	1169.30	2320.55	1160.78	2319.57	1160.29	E	1131.30	566.15	1114.27	557.64	1113.29	557.15	9
23	2452.67	1226.84	2435.64	1218.32	2434.65	1217.83	D	1002.19	501.60	985.16	493.08	984.17	492.59	8
24	2615.84	1308.43	2598.81	1299.91	2597.83	1299.42	Y	887.10	444.05	870.07	435.54			7
25	2729.00	1365.00	2711.97	1356.49	2710.99	1356.00	L	723.93	362.47	706.90	353.95			6
26	2826.12	1413.56	2809.09	1405.05	2808.10	1404.55	P	610.77	305.89	593.74	297.37			5
27	2939.27	1470.14	2922.24	1461.63	2921.26	1461.13	L	513.65	257.33	496.62	248.82			4
28	3067.45	1534.23	3050.42	1525.71	3049.43	1525.22	K	400.50	200.75	383.47	192.24			3
29	3164.56	1582.78	3147.53	1574.27	3146.55	1573.78	P	272.32	136.67	255.29	128.15			2
30							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
SLC1A5	GLAAAEPTANGGLALASIEDQGAAAGGYCGSRDQVR	1140.28	3+	176.5



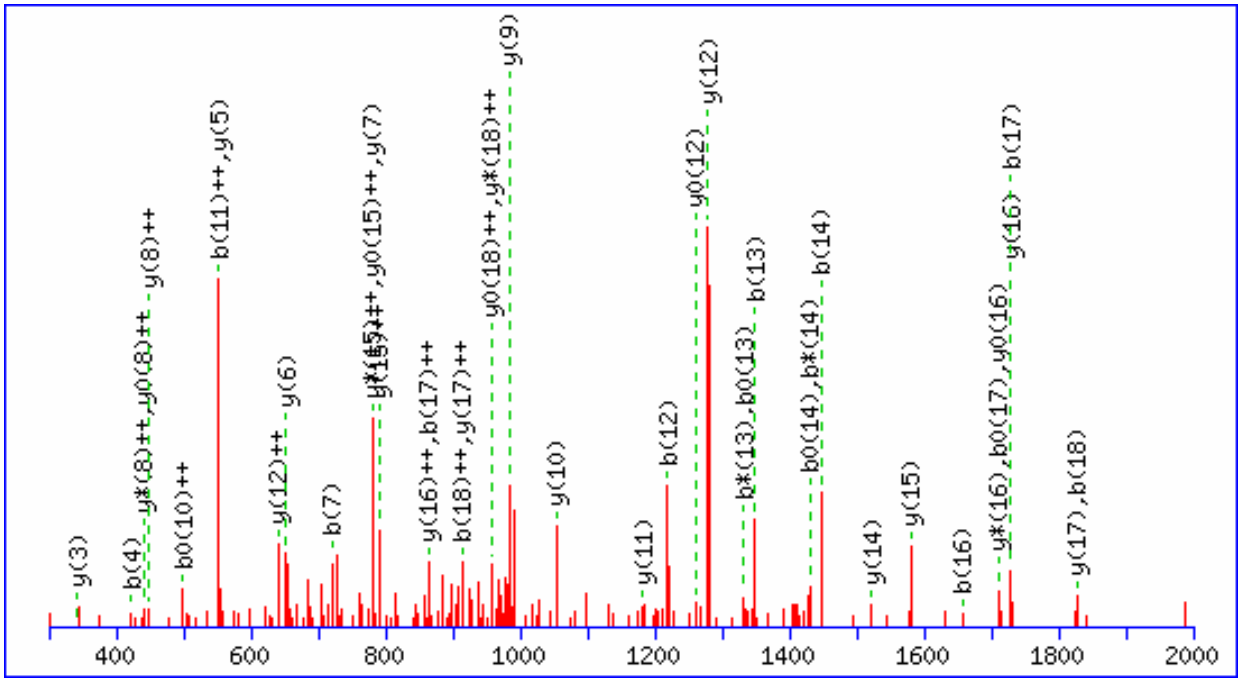
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.06	29.53					G							36
2	171.22	86.11					L	3362.62	1681.81	3345.59	1673.30	3344.60	1672.81	35
3	242.29	121.65					A	3249.46	1625.23	3232.43	1616.72	3231.45	1616.23	34
4	313.37	157.19					A	3178.38	1589.70	3161.35	1581.18	3160.37	1580.69	33
5	384.45	192.73					A	3107.31	1554.16	3090.27	1545.64	3089.29	1545.15	32
6	513.56	257.29			495.55	248.28	E	3036.23	1518.62	3019.20	1510.10	3018.21	1509.61	31
7	610.68	305.84			592.66	296.84	P	2907.11	1454.06	2890.08	1445.55	2889.10	1445.05	30
8	711.78	356.40			693.77	347.39	T	2810.00	1405.50	2792.97	1396.99	2791.98	1396.50	29
9	782.86	391.93			764.85	382.93	A	2708.89	1354.95	2691.86	1346.44	2690.88	1345.94	28
10	896.96	448.99	879.93	440.47	878.95	439.98	N	2637.82	1319.41	2620.79	1310.90	2619.80	1310.40	27
11	954.02	477.51	936.98	469.00	936.00	468.50	G	2523.71	1262.36	2506.68	1253.85	2505.70	1253.35	26
12	1011.07	506.04	994.04	497.52	993.05	497.03	G	2466.66	1233.84	2449.63	1225.32	2448.65	1224.83	25
13	1124.22	562.62	1107.19	554.10	1106.21	553.61	L	2409.61	1205.31	2392.58	1196.79	2391.60	1196.30	24
14	1195.30	598.16	1178.27	589.64	1177.29	589.15	A	2296.45	1148.73	2279.42	1140.22	2278.44	1139.72	23
15	1308.46	654.73	1291.43	646.22	1290.44	645.73	L	2225.38	1113.19	2208.35	1104.68	2207.36	1104.18	22
16	1379.54	690.27	1362.51	681.76	1361.52	681.27	A	2112.22	1056.61	2095.19	1048.10	2094.20	1047.61	21
17	1466.62	733.81	1449.58	725.30	1448.60	724.80	S	2041.14	1021.07	2024.11	1012.56	2023.12	1012.07	20
18	1579.77	790.39	1562.74	781.88	1561.76	781.38	I	1954.06	977.54	1937.03	969.02	1936.05	968.53	19
19	1708.89	854.95	1691.86	846.43	1690.87	845.94	E	1840.91	920.96	1823.87	912.44	1822.89	911.95	18
20	1823.97	912.49	1806.94	903.98	1805.96	903.48	D	1711.79	856.40	1694.76	847.88	1693.78	847.39	17
21	1952.10	976.56	1935.07	968.04	1934.09	967.55	Q	1596.70	798.86	1579.67	790.34	1578.69	789.85	16
22	2009.15	1005.08	1992.12	996.57	1991.14	996.07	G	1468.57	734.79	1451.54	726.28	1450.56	725.78	15
23	2080.23	1040.62	2063.20	1032.10	2062.22	1031.61	A	1411.52	706.27	1394.49	697.75	1393.51	697.26	14
24	2151.31	1076.16	2134.28	1067.64	2133.30	1067.15	A	1340.45	670.73	1323.41	662.21	1322.43	661.72	13
25	2222.39	1111.70	2205.36	1103.18	2204.37	1102.69	A	1269.37	635.19	1252.34	626.67	1251.35	626.18	12
26	2279.44	1140.22	2262.41	1131.71	2261.42	1131.22	G	1198.29	599.65	1181.26	591.13	1180.27	590.64	11
27	2336.49	1168.75	2319.46	1160.23	2318.48	1159.74	G	1141.24	571.12	1124.21	562.61	1123.22	562.12	10
28	2499.66	1250.34	2482.63	1241.82	2481.65	1241.33	Y	1084.19	542.60	1067.16	534.08	1066.17	533.59	9
29	2602.81	1301.91	2585.78	1293.39	2584.79	1292.90	C	921.01	461.01	903.98	452.50	903.00	452.00	8
30	2659.86	1330.43	2642.83	1321.92	2641.84	1321.43	G	817.87	409.44	800.84	400.92	799.86	400.43	7
31	2746.94	1373.97	2729.91	1365.46	2728.92	1364.96	S	760.82	380.91	743.79	372.40	742.80	371.91	6
32	2903.12	1452.06	2886.09	1443.55	2885.11	1443.06	R	673.74	337.38	656.71	328.86	655.73	328.37	5
33	3018.21	1509.61	3001.18	1501.09	3000.19	1500.60	D	517.56	259.28	500.53	250.77	499.54	250.27	4
34	3146.34	1573.67	3129.31	1565.16	3128.32	1564.67	Q	402.47	201.74	385.44	193.22			3
35	3245.47	1623.24	3228.44	1614.72	3227.45	1614.23	V	274.34	137.67	257.31	129.16			2
36							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
SLC26A11	SSGPGMAPSACCCSPAALQR	947.55	2+	77.9



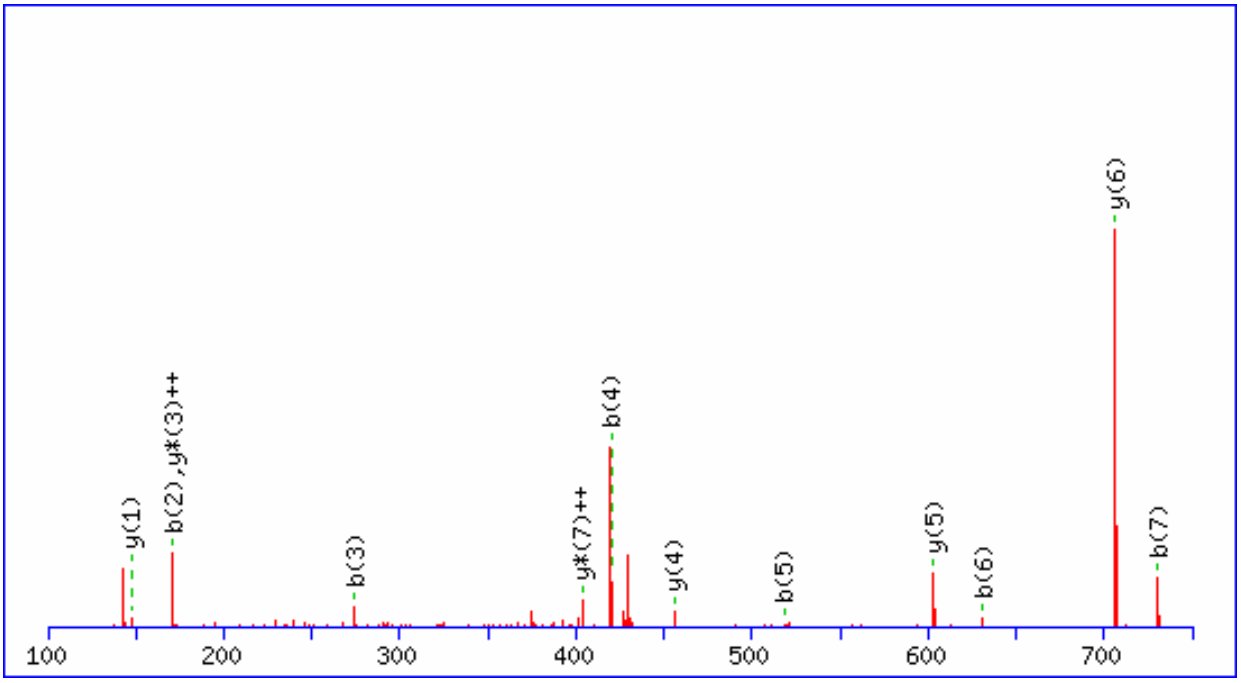
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							20
2	175.16	88.09			157.15	79.08	S	1808.11	904.56	1791.08	896.04	1790.10	895.55	19
3	232.21	116.61			214.20	107.60	G	1721.03	861.02	1704.00	852.51	1703.02	852.01	18
4	329.33	165.17			311.31	156.16	P	1663.98	832.50	1646.95	823.98	1645.97	823.49	17
5	386.38	193.69			368.37	184.69	G	1566.87	783.94	1549.84	775.42	1548.85	774.93	16
6	517.58	259.29			499.56	250.28	M	1509.82	755.41	1492.79	746.90	1491.80	746.40	15
7	588.65	294.83			570.64	285.82	A	1378.62	689.81	1361.59	681.30	1360.61	680.81	14
8	685.77	343.39			667.75	334.38	P	1307.54	654.28	1290.51	645.76	1289.53	645.27	13
9	772.85	386.93			754.83	377.92	S	1210.43	605.72	1193.40	597.20	1192.41	596.71	12
10	843.92	422.47			825.91	413.46	A	1123.35	562.18	1106.32	553.66	1105.34	553.17	11
11	947.07	474.04			929.05	465.03	C	1052.27	526.64	1035.24	518.13	1034.26	517.63	10
12	1050.21	525.61			1032.20	516.60	C	949.13	475.07	932.10	466.55	931.11	466.06	9
13	1153.35	577.18			1135.34	568.17	C	845.99	423.50	828.96	414.98	827.97	414.49	8
14	1240.43	620.72			1222.42	611.71	S	742.84	371.93	725.81	363.41	724.83	362.92	7
15	1337.55	669.28			1319.53	660.27	P	655.77	328.39	638.74	319.87			6
16	1408.62	704.82			1390.61	695.81	A	558.65	279.83	541.62	271.31			5
17	1479.70	740.35			1461.69	731.35	A	487.57	244.29	470.54	235.78			4
18	1592.86	796.93			1574.84	787.93	L	416.50	208.75	399.47	200.24			3
19	1720.99	861.00	1703.96	852.48	1702.97	851.99	Q	303.34	152.17	286.31	143.66			2
20							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
SLC35B2	ACVFGNEPKASDEVPLAPR	1001.13	2+	86.8



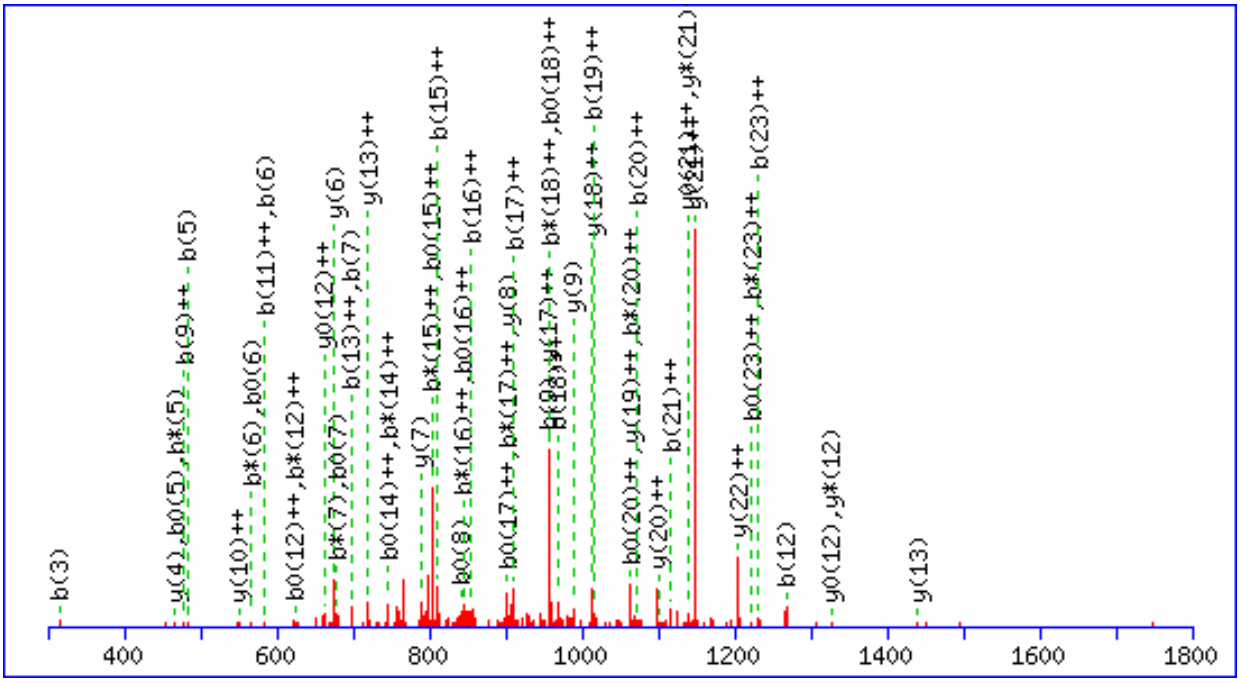
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							19
2	175.23	88.12					C	1930.17	965.59	1913.14	957.07	1912.15	956.58	18
3	274.36	137.68					V	1827.02	914.02	1809.99	905.50	1809.01	905.01	17
4	421.53	211.27					F	1727.89	864.45	1710.86	855.93	1709.88	855.44	16
5	478.59	239.80					G	1580.72	790.86	1563.69	782.35	1562.70	781.86	15
6	592.69	296.85	575.66	288.33			N	1523.67	762.34	1506.64	753.82	1505.65	753.33	14
7	721.80	361.40	704.77	352.89	703.79	352.40	E	1409.56	705.29	1392.53	696.77	1391.55	696.28	13
8	818.92	409.96	801.89	401.45	800.90	400.95	P	1280.45	640.73	1263.42	632.21	1262.43	631.72	12
9	947.09	474.05	930.06	465.53	929.07	465.04	K	1183.33	592.17	1166.30	583.66	1165.32	583.16	11
10	1018.17	509.59	1001.14	501.07	1000.15	500.58	A	1055.16	528.09	1038.13	519.57	1037.15	519.08	10
11	1105.24	553.13	1088.21	544.61	1087.23	544.12	S	984.08	492.55	967.05	484.03	966.07	483.54	9
12	1220.33	610.67	1203.30	602.15	1202.32	601.66	D	897.01	449.01	879.98	440.49	878.99	440.00	8
13	1349.45	675.23	1332.42	666.71	1331.43	666.22	E	781.92	391.46	764.89	382.95	763.90	382.46	7
14	1448.58	724.79	1431.55	716.28	1430.56	715.78	V	652.81	326.91	635.78	318.39			6
15	1545.69	773.35	1528.66	764.83	1527.68	764.34	P	553.67	277.34	536.64	268.83			5
16	1658.85	829.93	1641.82	821.41	1640.83	820.92	L	456.56	228.78	439.53	220.27			4
17	1729.93	865.47	1712.90	856.95	1711.91	856.46	A	343.40	172.20	326.37	163.69			3
18	1827.04	914.03	1810.01	905.51	1809.03	905.02	P	272.32	136.67	255.29	128.15			2
19							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
SLC35B2	GLCFPLVK	438.60	2+	49.2



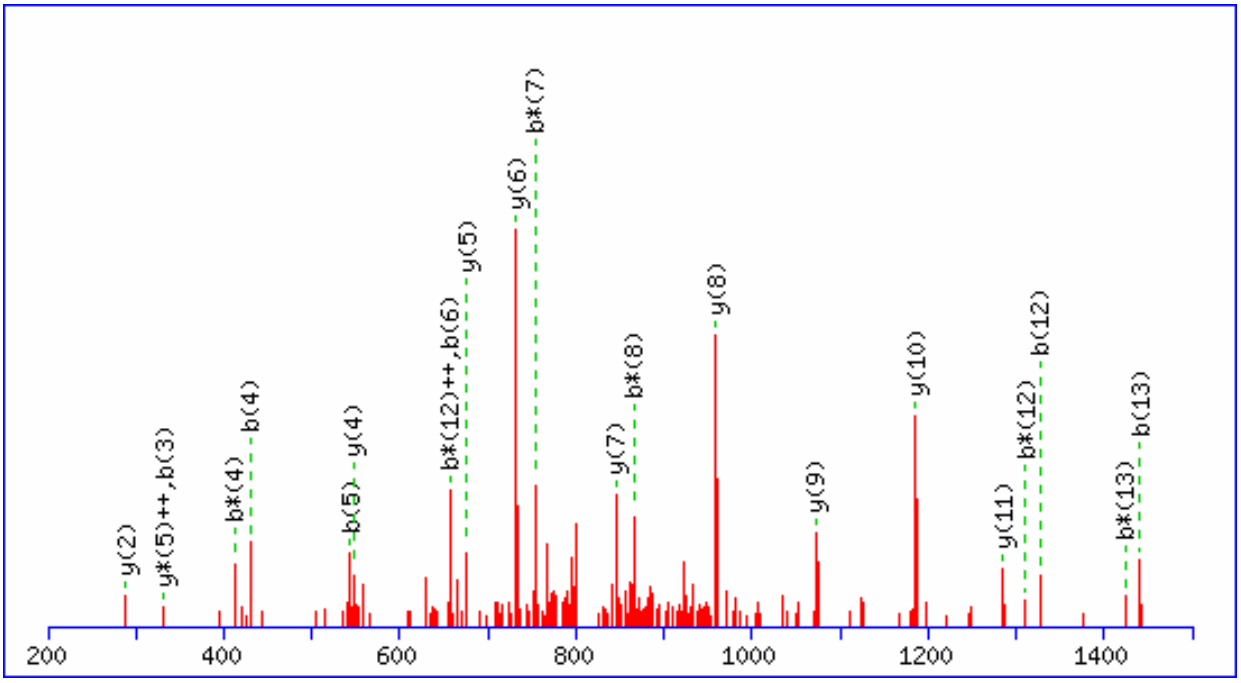
#	b	b^{++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	58.06	29.53	G					8
2	171.22	86.11	L	820.07	410.54	803.04	402.03	7
3	274.36	137.68	C	706.92	353.96	689.89	345.45	6
4	421.53	211.27	F	603.77	302.39	586.74	293.88	5
5	518.65	259.83	P	456.60	228.80	439.57	220.29	4
6	631.81	316.41	L	359.48	180.25	342.45	171.73	3
7	730.94	365.97	V	246.33	123.67	229.30	115.15	2
8			K	147.20	74.10	130.16	65.59	1

Gene Symbol	Sequences	m/z	Charge	Ion score
SLC5A6	SLNPATIYPVLPKLLSLLPLSCQK	870.73	3+	84.6



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.09	44.55			70.07	35.54	S							24
2	201.24	101.13			183.23	92.12	L	2523.10	1262.06	2506.07	1253.54	2505.09	1253.05	23
3	315.35	158.18	298.31	149.66	297.33	149.17	N	2409.95	1205.48	2392.92	1196.96	2391.93	1196.47	22
4	412.46	206.73	395.43	198.22	394.45	197.73	P	2295.84	1148.43	2278.81	1139.91	2277.83	1139.42	21
5	483.54	242.27	466.51	233.76	465.52	233.27	A	2198.73	1099.87	2181.70	1091.35	2180.71	1090.86	20
6	584.64	292.83	567.61	284.31	566.63	283.82	T	2127.65	1064.33	2110.62	1055.81	2109.64	1055.32	19
7	697.80	349.40	680.77	340.89	679.78	340.40	I	2026.55	1013.78	2009.52	1005.26	2008.53	1004.77	18
8	860.97	430.99	843.94	422.48	842.96	421.98	Y	1913.39	957.20	1896.36	948.68	1895.37	948.19	17
9	958.09	479.55	941.06	471.03	940.07	470.54	P	1750.22	875.61	1733.19	867.10	1732.20	866.60	16
10	1057.22	529.11	1040.19	520.60	1039.20	520.11	V	1653.10	827.05	1636.07	818.54	1635.09	818.05	15
11	1170.38	585.69	1153.35	577.18	1152.36	576.68	L	1553.97	777.49	1536.94	768.97	1535.96	768.48	14
12	1267.49	634.25	1250.46	625.73	1249.48	625.24	P	1440.81	720.91	1423.78	712.40	1422.80	711.90	13
13	1395.66	698.34	1378.63	689.82	1377.65	689.33	K	1343.70	672.35	1326.67	663.84	1325.68	663.35	12
14	1508.82	754.92	1491.79	746.40	1490.81	745.91	L	1215.53	608.27	1198.49	599.75	1197.51	599.26	11
15	1621.98	811.49	1604.95	802.98	1603.96	802.49	L	1102.37	551.69	1085.34	543.17	1084.35	542.68	10
16	1709.06	855.03	1692.03	846.52	1691.04	846.02	S	989.21	495.11	972.18	486.59	971.19	486.10	9
17	1822.21	911.61	1805.18	903.10	1804.20	902.60	L	902.13	451.57	885.10	443.06	884.12	442.56	8
18	1935.37	968.19	1918.34	959.67	1917.36	959.18	L	788.98	394.99	771.94	386.48	770.96	385.98	7
19	2032.49	1016.75	2015.46	1008.23	2014.47	1007.74	P	675.82	338.41	658.79	329.90	657.80	329.41	6
20	2145.65	1073.33	2128.61	1064.81	2127.63	1064.32	L	578.70	289.86	561.67	281.34	560.69	280.85	5
21	2232.72	1116.87	2215.69	1108.35	2214.71	1107.86	S	465.54	233.28	448.51	224.76	447.53	224.27	4
22	2335.87	1168.44	2318.83	1159.92	2317.85	1159.43	C	378.47	189.74	361.44	181.22			3
23	2463.99	1232.50	2446.96	1223.99	2445.98	1223.49	Q	275.32	138.17	258.29	129.65			2
24							K	147.20	74.10	130.17	65.59			1

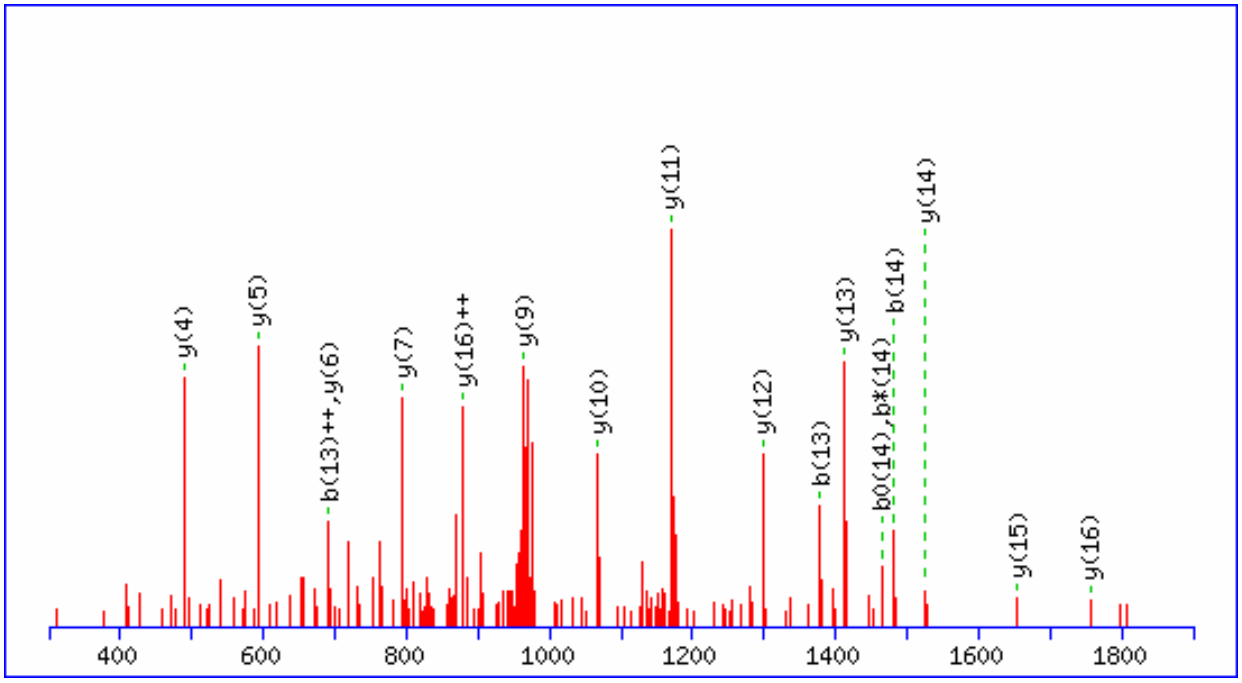
Gene Symbol	Sequences	m/z	Charge	Ion score
SLC7A1	GCKVLLNIGQQMLR	808.44	2+	91.6



N-term : N-Acetyl (Protein)

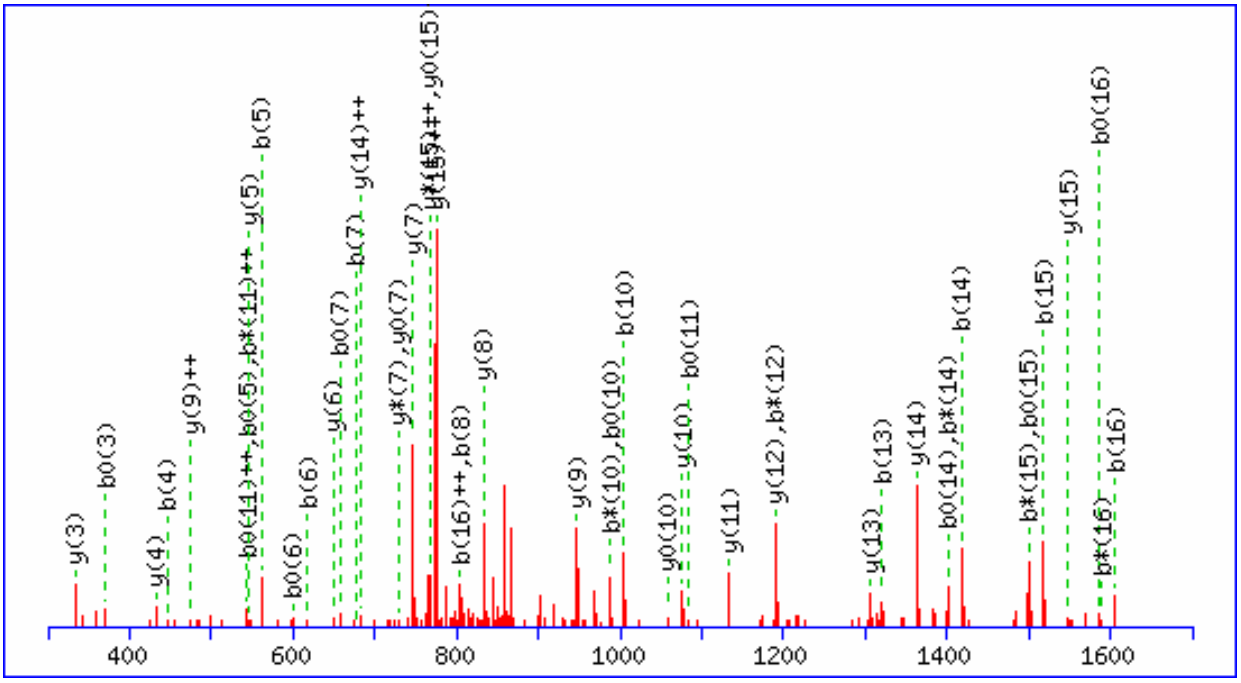
#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	100.10	50.55			G					14
2	203.24	102.12			C	1516.89	758.95	1499.86	750.44	13
3	331.41	166.21	314.38	157.69	K	1413.75	707.38	1396.72	698.86	12
4	430.54	215.78	413.51	207.26	V	1285.58	643.29	1268.55	634.78	11
5	543.70	272.35	526.67	263.84	L	1186.45	593.73	1169.42	585.21	10
6	656.86	328.93	639.83	320.42	L	1073.29	537.15	1056.26	528.63	9
7	770.96	385.98	753.93	377.47	N	960.13	480.57	943.10	472.05	8
8	884.12	442.56	867.09	434.05	I	846.03	423.52	829.00	415.00	7
9	941.17	471.09	924.14	462.57	G	732.87	366.94	715.84	358.42	6
10	1069.30	535.15	1052.27	526.64	Q	675.82	338.41	658.79	329.90	5
11	1197.43	599.22	1180.40	590.70	Q	547.69	274.35	530.66	265.83	4
12	1328.62	664.82	1311.59	656.30	M	419.56	210.29	402.53	201.77	3
13	1441.78	721.39	1424.75	712.88	L	288.37	144.69	271.34	136.17	2
14					R	175.21	88.11	158.18	79.59	1

Gene Symbol	Sequences	m/z	Charge	Ion score
SNAP23	TLTELNKCCGLCVCPCNR	985.76	2+	105.4



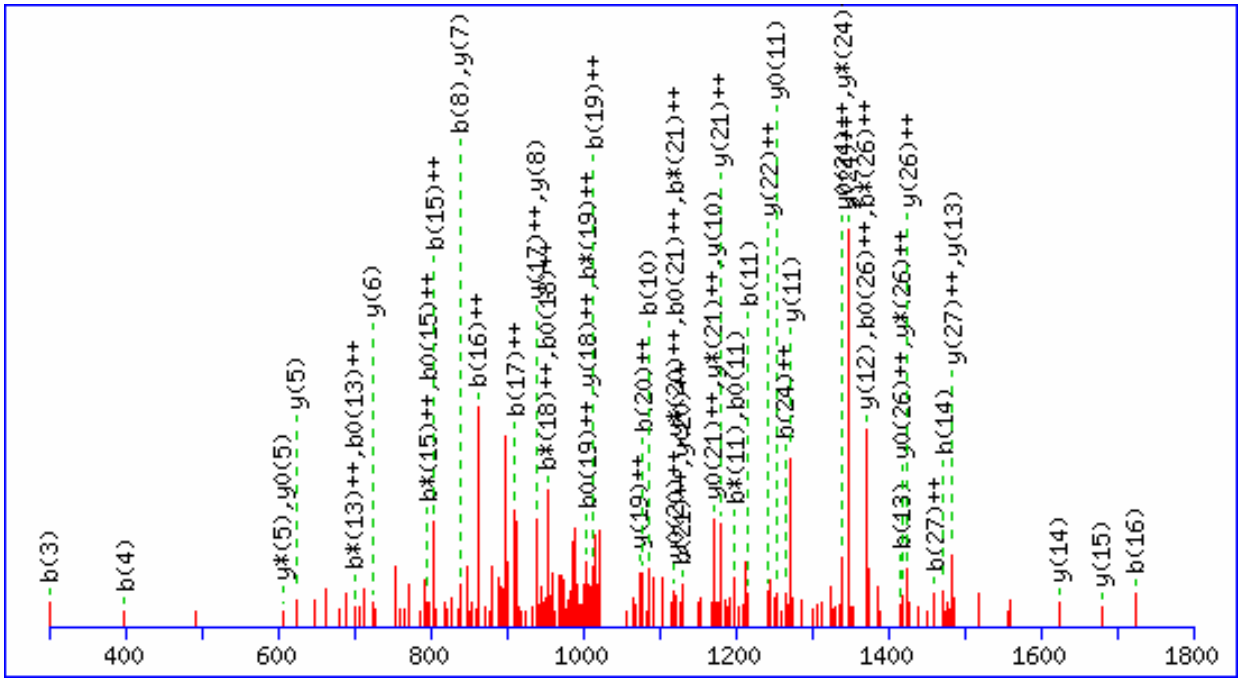
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.11	51.56			84.10	42.55	T							18
2	215.27	108.14			197.25	99.13	L	1870.29	935.65	1853.26	927.13	1852.27	926.64	17
3	316.37	158.69			298.36	149.68	T	1757.13	879.07	1740.10	870.55	1739.12	870.06	16
4	445.49	223.25			427.47	214.24	E	1656.03	828.52	1639.00	820.00	1638.01	819.51	15
5	558.64	279.83			540.63	270.82	L	1526.91	763.96	1509.88	755.45			14
6	672.75	336.88	655.72	328.36	654.73	327.87	N	1413.76	707.38	1396.73	698.87			13
7	800.92	400.96	783.89	392.45	782.90	391.96	K	1299.65	650.33	1282.62	641.82			12
8	904.06	452.54	887.03	444.02	886.05	443.53	C	1171.48	586.24	1154.45	577.73			11
9	1007.21	504.11	990.18	495.59	989.19	495.10	C	1068.34	534.67	1051.31	526.16			10
10	1064.26	532.63	1047.23	524.12	1046.24	523.62	G	965.20	483.10	948.16	474.59			9
11	1177.41	589.21	1160.38	580.70	1159.40	580.20	L	908.14	454.58	891.11	446.06			8
12	1280.56	640.78	1263.53	632.27	1262.54	631.78	C	794.99	398.00	777.96	389.48			7
13	1379.69	690.35	1362.66	681.83	1361.67	681.34	V	691.84	346.43	674.81	337.91			6
14	1482.83	741.92	1465.80	733.40	1464.82	732.91	C	592.71	296.86	575.68	288.34			5
15	1579.95	790.48	1562.92	781.96	1561.93	781.47	P	489.57	245.29	472.54	236.77			4
16	1683.09	842.05	1666.06	833.53	1665.07	833.04	C	392.45	196.73	375.42	188.22			3
17	1797.19	899.10	1780.16	890.58	1779.18	890.09	N	289.31	145.16	272.28	136.64			2
18							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
SNAP23	TTWGDGGENSPCNVVSK	876.74	2+	91.4



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.11	51.56			84.10	42.55	T							17
2	203.22	102.11			185.20	93.10	T	1650.74	825.88	1633.71	817.36	1632.73	816.87	16
3	389.43	195.22			371.41	186.21	W	1549.64	775.32	1532.61	766.81	1531.63	766.32	15
4	446.48	223.74			428.46	214.73	G	1363.43	682.22	1346.40	673.70	1345.42	673.21	14
5	561.56	281.29			543.55	272.28	D	1306.38	653.69	1289.35	645.18	1288.36	644.69	13
6	618.62	309.81			600.60	300.80	G	1191.29	596.15	1174.26	587.63	1173.28	587.14	12
7	675.67	338.34			657.65	329.33	G	1134.24	567.62	1117.21	559.11	1116.23	558.62	11
8	804.78	402.89			786.77	393.89	E	1077.19	539.10	1060.16	530.58	1059.17	530.09	10
9	918.88	459.95	901.85	451.43	900.87	450.94	N	948.08	474.54	931.05	466.03	930.06	465.53	9
10	1005.96	503.48	988.93	494.97	987.95	494.48	S	833.97	417.49	816.94	408.98	815.96	408.48	8
11	1103.08	552.04	1086.05	543.53	1085.06	543.03	P	746.90	373.95	729.87	365.44	728.88	364.94	7
12	1206.22	603.61	1189.19	595.10	1188.20	594.61	C	649.78	325.39	632.75	316.88	631.77	316.39	6
13	1320.32	660.66	1303.29	652.15	1302.31	651.66	N	546.64	273.82	529.61	265.31	528.62	264.82	5
14	1419.45	710.23	1402.42	701.72	1401.44	701.22	V	432.54	216.77	415.50	208.26	414.52	207.76	4
15	1518.58	759.80	1501.55	751.28	1500.57	750.79	V	333.40	167.21	316.37	158.69	315.39	158.20	3
16	1605.66	803.33	1588.63	794.82	1587.65	794.33	S	234.27	117.64	217.24	109.13	216.26	108.63	2
17							K	147.20	74.10	130.16	65.59			1

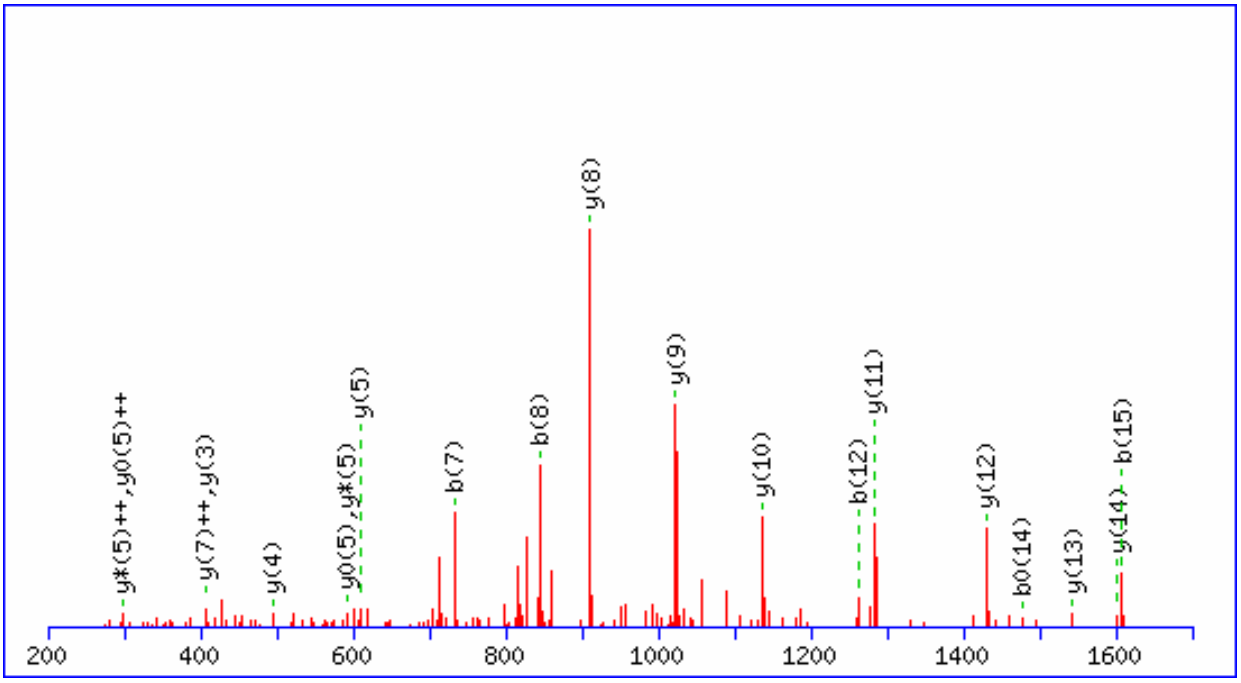
Gene Symbol	Sequences	m/z	Charge	Ion score
SNRPD3	SIGVPIKVLHEAEGHIVTCETNTGEVYR	1032.25	3+	61.4



N-term : N-Acetyl (Protein)

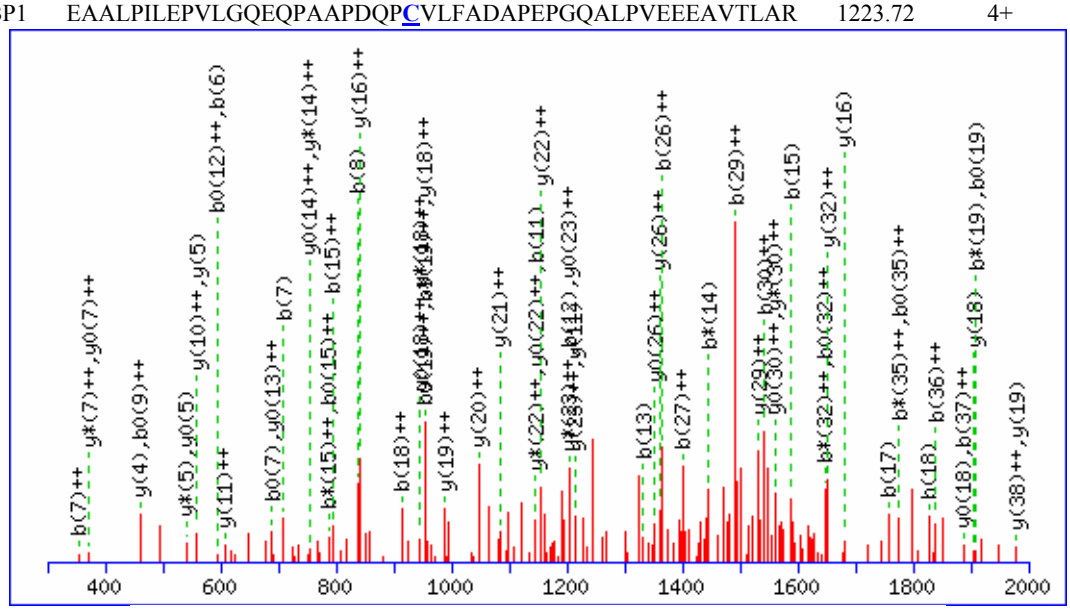
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.12	65.56			112.11	56.56	S							28
2	243.28	122.14			225.26	113.14	I	2966.35	1483.68	2949.32	1475.16	2948.33	1474.67	27
3	300.33	150.67			282.32	141.66	G	2853.19	1427.10	2836.16	1418.58	2835.18	1418.09	26
4	399.46	200.23			381.45	191.23	V	2796.14	1398.57	2779.11	1390.06	2778.12	1389.57	25
5	496.58	248.79			478.56	239.78	P	2697.01	1349.01	2679.98	1340.49	2678.99	1340.00	24
6	609.73	305.37			591.72	296.36	I	2599.89	1300.45	2582.86	1291.94	2581.88	1291.44	23
7	737.91	369.46	720.88	360.94	719.89	360.45	K	2486.74	1243.87	2469.70	1235.36	2468.72	1234.86	22
8	837.04	419.02	820.01	410.51	819.02	410.02	V	2358.56	1179.79	2341.53	1171.27	2340.55	1170.78	21
9	950.20	475.60	933.17	467.09	932.18	466.59	L	2259.43	1130.22	2242.40	1121.70	2241.42	1121.21	20
10	1087.34	544.17	1070.30	535.66	1069.32	535.16	H	2146.27	1073.64	2129.24	1065.13	2128.26	1064.63	19
11	1216.45	608.73	1199.42	600.21	1198.43	599.72	E	2009.14	1005.07	1992.10	996.56	1991.12	996.06	18
12	1287.53	644.27	1270.50	635.75	1269.51	635.26	A	1880.02	940.51	1862.99	932.00	1862.01	931.51	17
13	1416.64	708.82	1399.61	700.31	1398.63	699.82	E	1808.94	904.98	1791.91	896.46	1790.93	895.97	16
14	1473.69	737.35	1456.66	728.83	1455.68	728.34	G	1679.83	840.42	1662.80	831.90	1661.81	831.41	15
15	1610.83	805.92	1593.80	797.40	1592.82	796.91	H	1622.78	811.89	1605.75	803.38	1604.76	802.89	14
16	1723.99	862.50	1706.96	853.98	1705.97	853.49	I	1485.64	743.32	1468.61	734.81	1467.62	734.32	13
17	1823.12	912.06	1806.09	903.55	1805.10	903.06	V	1372.48	686.74	1355.45	678.23	1354.47	677.74	12
18	1924.22	962.62	1907.19	954.10	1906.21	953.61	T	1273.35	637.18	1256.32	628.66	1255.33	628.17	11
19	2027.37	1014.19	2010.34	1005.67	2009.35	1005.18	C	1172.25	586.63	1155.22	578.11	1154.23	577.62	10
20	2156.48	1078.74	2139.45	1070.23	2138.47	1069.74	E	1069.10	535.06	1052.07	526.54	1051.09	526.05	9
21	2257.58	1129.30	2240.55	1120.78	2239.57	1120.29	T	939.99	470.50	922.96	461.98	921.97	461.49	8
22	2371.69	1186.35	2354.66	1177.83	2353.67	1177.34	N	838.89	419.95	821.85	411.43	820.87	410.94	7
23	2472.79	1236.90	2455.76	1228.38	2454.78	1227.89	T	724.78	362.90	707.75	354.38	706.77	353.89	6
24	2529.84	1265.43	2512.81	1256.91	2511.83	1256.42	G	623.68	312.34	606.65	303.83	605.66	303.34	5
25	2658.96	1329.98	2641.93	1321.47	2640.94	1320.97	E	566.63	283.82	549.60	275.30	548.61	274.81	4
26	2758.09	1379.55	2741.06	1371.03	2740.07	1370.54	V	437.51	219.26	420.48	210.75			3
27	2921.26	1461.13	2904.23	1452.62	2903.25	1452.13	Y	338.38	169.70	321.35	161.18			2
28							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
STOM	GPGLFFILP**C**TDSFIK	878.07	2+	79.7



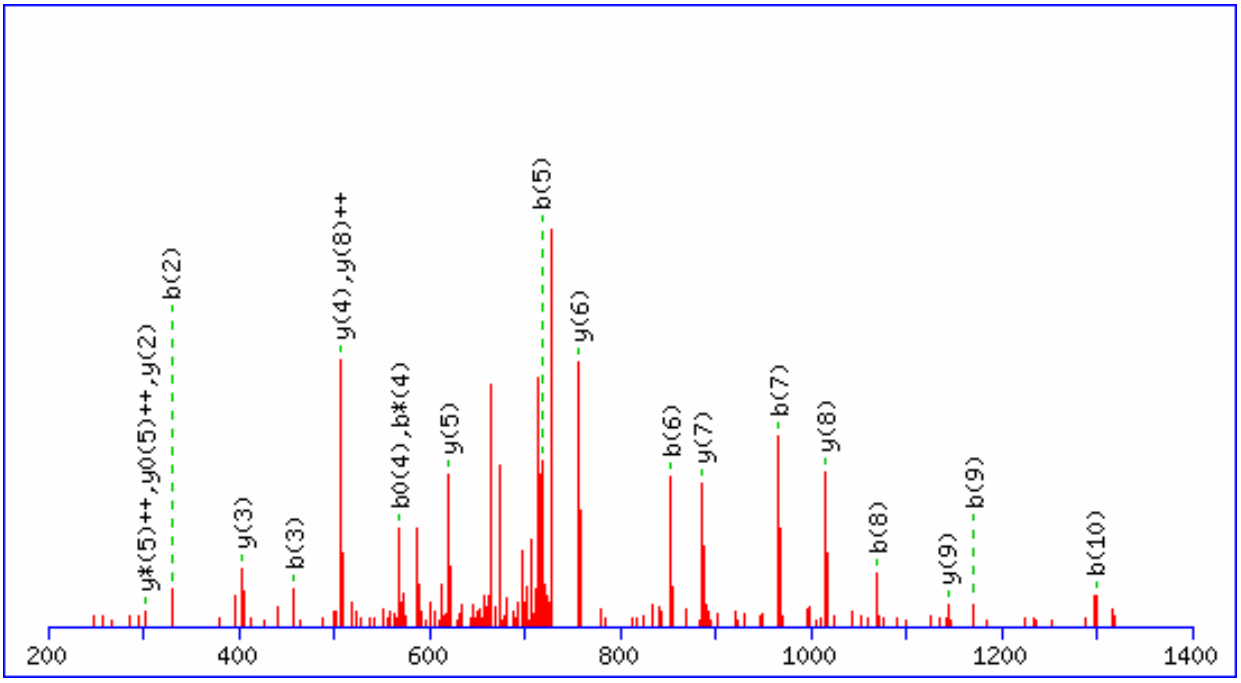
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.06	29.53			G							16
2	155.17	78.09			P	1699.04	850.02	1682.01	841.51	1681.03	841.02	15
3	212.23	106.62			G	1601.93	801.47	1584.90	792.95	1583.91	792.46	14
4	325.38	163.20			L	1544.87	772.94	1527.84	764.43	1526.86	763.93	13
5	472.56	236.78			F	1431.72	716.36	1414.69	707.85	1413.70	707.35	12
6	619.73	310.37			F	1284.54	642.78	1267.51	634.26	1266.53	633.77	11
7	732.89	366.95			I	1137.37	569.19	1120.34	560.67	1119.35	560.18	10
8	846.05	423.53			L	1024.21	512.61	1007.18	504.09	1006.20	503.60	9
9	943.16	472.08			P	911.05	456.03	894.02	447.52	893.04	447.02	8
10	1046.30	523.66			C	813.94	407.47	796.91	398.96	795.92	398.47	7
11	1147.41	574.21	1129.39	565.20	T	710.80	355.90	693.77	347.39	692.78	346.89	6
12	1262.50	631.75	1244.48	622.74	D	609.69	305.35	592.66	296.83	591.68	296.34	5
13	1349.57	675.29	1331.56	666.28	S	494.60	247.81	477.57	239.29	476.59	238.80	4
14	1496.75	748.88	1478.73	739.87	F	407.53	204.27	390.50	195.75			3
15	1609.90	805.46	1591.89	796.45	I	260.35	130.68	243.32	122.17			2
16					K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
TNKS1BP1	EAALPILEPVLGQEQPAAPDQP**C**VLFADAPEPGQALPVEEEAVTLAR	1223.72	4+	48.8



#	b	b++	b*	b*++	b0	b0++	Seq.	y	y++	y*	y*++	y0	y0++	#
1	130.12	65.56			112.11	56.56	E							47
2	201.20	101.10			183.18	92.10	A	4763.36	2382.18	4746.33	2373.67	4745.34	2373.18	46
3	272.28	136.64			254.26	127.64	A	4692.28	2346.64	4675.25	2338.13	4674.26	2337.64	45
4	385.44	193.22			367.42	184.21	L	4621.20	2311.11	4604.17	2302.59	4603.19	2302.10	44
5	482.55	241.78			464.54	232.77	P	4508.04	2254.53	4491.01	2246.01	4490.03	2245.52	43
6	595.71	298.36			577.69	289.35	I	4410.93	2205.97	4393.90	2197.45	4392.91	2196.96	42
7	708.87	354.94			690.85	345.93	L	4297.77	2149.39	4280.74	2140.87	4279.76	2140.38	41
8	837.98	419.49			819.96	410.49	E	4184.61	2092.81	4167.58	2084.30	4166.60	2083.80	40
9	935.09	468.05			917.08	459.04	P	4055.50	2028.25	4038.47	2019.74	4037.49	2019.25	39
10	1034.23	517.62			1016.21	508.61	V	3958.39	1979.70	3941.35	1971.18	3940.37	1970.69	38
11	1147.38	574.20			1129.37	565.19	L	3859.25	1930.13	3842.22	1921.62	3841.24	1921.12	37
12	1204.43	602.72			1186.42	593.71	G	3746.10	1873.55	3729.07	1865.04	3728.08	1864.54	36
13	1332.56	666.79	1315.53	658.27	1314.55	657.78	Q	3689.05	1845.03	3672.01	1836.51	3671.03	1836.02	35
14	1461.68	731.34	1444.65	722.83	1443.66	722.34	E	3560.92	1780.96	3543.89	1772.45	3542.90	1771.95	34
15	1589.81	795.41	1572.78	786.89	1571.79	786.40	Q	3431.80	1716.40	3414.77	1707.89	3413.79	1707.40	33
16	1686.92	843.97	1669.89	835.45	1668.91	834.96	P	3303.67	1652.34	3286.64	1643.83	3285.66	1643.33	32
17	1758.00	879.50	1740.97	870.99	1739.99	870.50	A	3206.56	1603.78	3189.53	1595.27	3188.54	1594.78	31
18	1829.08	915.04	1812.05	906.53	1811.06	906.04	A	3135.48	1568.24	3118.45	1559.73	3117.46	1559.24	30
19	1926.19	963.60	1909.16	955.09	1908.18	954.59	P	3064.40	1532.70	3047.37	1524.19	3046.39	1523.70	29
20	2041.28	1021.14	2024.25	1012.63	2023.27	1012.14	D	2967.29	1484.15	2950.26	1475.63	2949.27	1475.14	28
21	2169.41	1085.21	2152.38	1076.69	2151.39	1076.20	Q	2852.20	1426.60	2835.17	1418.09	2834.18	1417.60	27
22	2266.53	1133.77	2249.49	1125.25	2248.51	1124.76	P	2724.07	1362.54	2707.04	1354.02	2706.05	1353.53	26
23	2369.67	1185.34	2352.64	1176.82	2351.65	1176.33	C	2626.95	1313.98	2609.92	1305.47	2608.94	1304.97	25
24	2468.80	1234.90	2451.77	1226.39	2450.78	1225.90	V	2523.81	1262.41	2506.78	1253.89	2505.80	1253.40	24
25	2581.96	1291.48	2564.93	1282.97	2563.94	1282.47	L	2424.68	1212.84	2407.65	1204.33	2406.67	1203.84	23
26	2729.13	1365.07	2712.10	1356.55	2711.12	1356.06	F	2311.52	1156.27	2294.49	1147.75	2293.51	1147.26	22
27	2800.21	1400.61	2783.18	1392.09	2782.19	1391.60	A	2164.35	1082.68	2147.32	1074.16	2146.33	1073.67	21
28	2915.30	1458.15	2898.27	1449.64	2897.28	1449.14	D	2093.27	1047.14	2076.24	1038.62	2075.26	1038.13	20
29	2986.37	1493.69	2969.34	1485.18	2968.35	1484.68	A	1978.18	989.60	1961.15	981.08	1960.17	980.59	19
30	3083.49	1542.25	3066.46	1533.73	3065.47	1533.24	P	1907.11	954.06	1890.08	945.54	1889.09	945.05	18
31	3212.60	1606.81	3195.57	1598.29	3194.59	1597.80	E	1809.99	905.50	1792.96	896.98	1791.98	896.49	17
32	3309.72	1655.36	3292.69	1646.85	3291.70	1646.36	P	1680.88	840.94	1663.85	832.43	1662.86	831.93	16
33	3366.77	1683.89	3349.74	1675.37	3348.75	1674.88	G	1583.76	792.38	1566.73	783.87	1565.75	783.38	15
34	3494.90	1747.95	3477.87	1739.44	3476.88	1738.95	Q	1526.71	763.86	1509.68	755.34	1508.70	754.85	14
35	3565.98	1783.49	3548.95	1774.98	3547.96	1774.48	A	1398.58	699.79	1381.55	691.28	1380.57	690.79	13
36	3679.13	1840.07	3662.10	1831.56	3661.12	1831.06	L	1327.50	664.26	1310.47	655.74	1309.49	655.25	12
37	3776.25	1888.63	3759.22	1880.11	3758.23	1879.62	P	1214.35	607.68	1197.32	599.16	1196.33	598.67	11
38	3875.38	1938.19	3858.35	1929.68	3857.37	1929.19	V	1117.23	559.12	1100.20	550.60	1099.22	550.11	10
39	4004.49	2002.75	3987.46	1994.24	3986.48	1993.74	E	1018.10	509.55	1001.07	501.04	1000.08	500.55	9
40	4133.61	2067.31	4116.58	2058.79	4115.59	2058.30	E	888.99	445.00	871.95	436.48	870.97	435.99	8
41	4262.72	2131.87	4245.69	2123.35	4244.71	2122.86	E	759.87	380.44	742.84	371.92	741.86	371.43	7
42	4333.80	2167.40	4316.77	2158.89	4315.79	2158.40	A	630.76	315.88	613.73	307.37	612.74	306.87	6
43	4432.93	2216.97	4415.90	2208.45	4414.92	2207.96	V	559.68	280.34	542.65	271.83	541.66	271.34	5
44	4534.04	2267.52	4517.01	2259.01	4516.02	2258.51	T	460.55	230.78	443.52	222.26	442.53	221.77	4
45	4647.19	2324.10	4630.16	2315.59	4629.18	2315.09	L	359.44	180.23	342.41	171.71			3
46	4718.27	2359.64	4701.24	2351.12	4700.26	2350.63	A	246.29	123.65	229.26	115.13			2
47							R	175.21	88.11	158.18	79.59			1

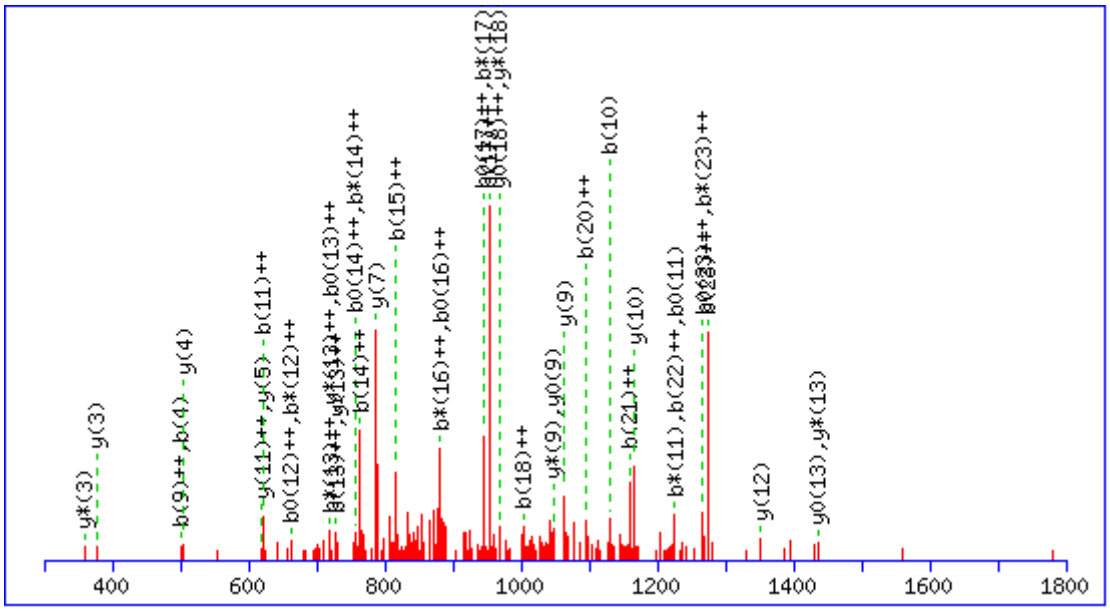
Gene Symbol	Sequences	m/z	Charge	Ion score
TPM3	CTKEEHLCTQR	737.07	2+	75.3



C1 : NEM (C)

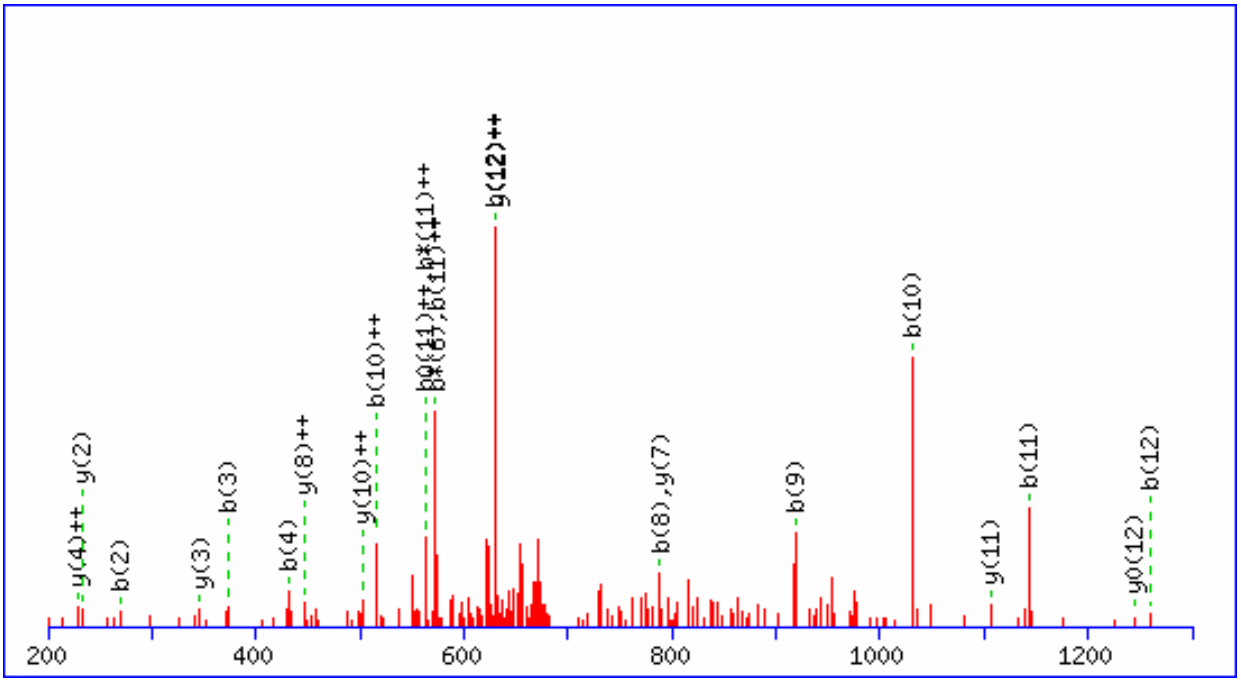
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	229.28	115.14					C							11
2	330.38	165.69			312.36	156.69	T	1245.39	623.20	1228.36	614.68	1227.37	614.19	10
3	458.55	229.78	441.52	221.26	440.54	220.77	K	1144.28	572.65	1127.25	564.13	1126.27	563.64	9
4	587.67	294.34	570.64	285.82	569.65	285.33	E	1016.11	508.56	999.08	500.04	998.09	499.55	8
5	716.78	358.89	699.75	350.38	698.77	349.89	E	887.00	444.00	869.97	435.49	868.98	434.99	7
6	853.92	427.46	836.89	418.95	835.90	418.46	H	757.88	379.44	740.85	370.93	739.87	370.44	6
7	967.08	484.04	950.05	475.53	949.06	475.03	L	620.74	310.88	603.71	302.36	602.73	301.87	5
8	1070.22	535.61	1053.19	527.10	1052.20	526.61	C	507.58	254.30	490.55	245.78	489.57	245.29	4
9	1171.32	586.17	1154.29	577.65	1153.31	577.16	T	404.44	202.72	387.41	194.21	386.43	193.72	3
10	1299.45	650.23	1282.42	641.72	1281.44	641.22	Q	303.34	152.17	286.31	143.66			2
11							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
TUBA4A	AYHEQLSVAEITNA**C**FEPANQMVK	898.89	3+	57.4



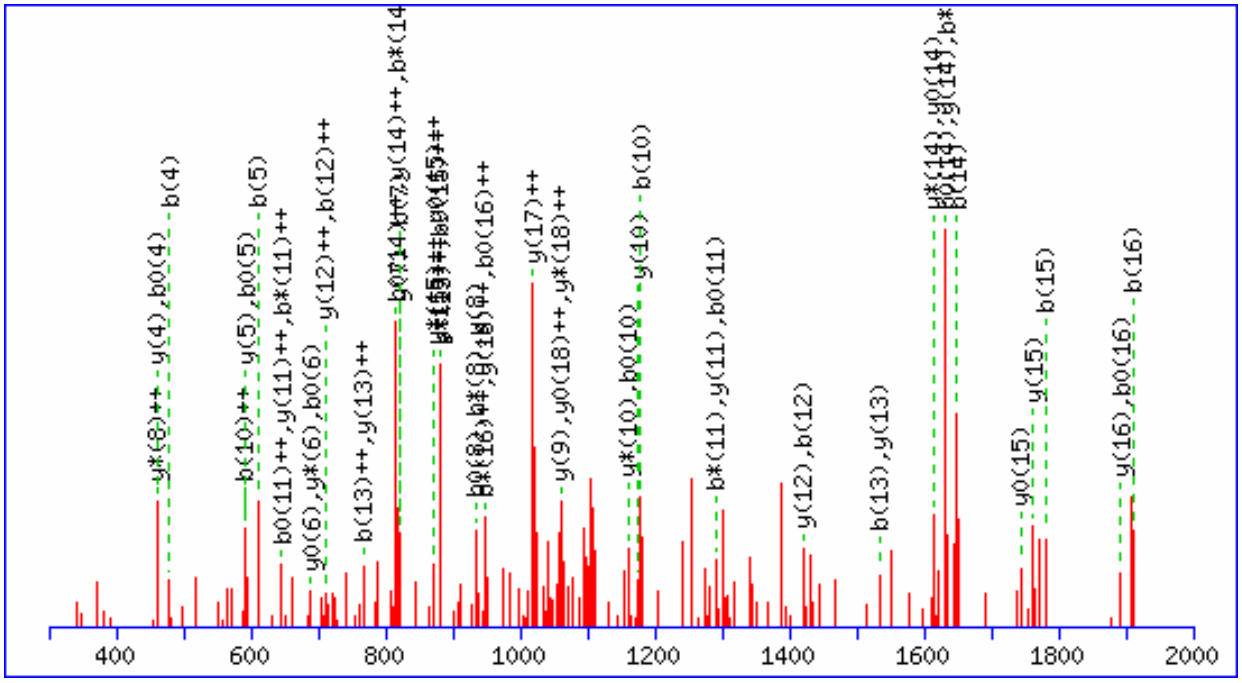
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.09	36.55					A							24
2	235.26	118.13					Y	2623.93	1312.47	2606.90	1303.96	2605.92	1303.46	23
3	372.40	186.70					H	2460.76	1230.88	2443.73	1222.37	2442.75	1221.88	22
4	501.51	251.26			483.50	242.25	E	2323.62	1162.31	2306.59	1153.80	2305.61	1153.31	21
5	629.64	315.32	612.61	306.81	611.63	306.32	Q	2194.51	1097.76	2177.48	1089.24	2176.49	1088.75	20
6	742.80	371.90	725.77	363.39	724.78	362.90	L	2066.38	1033.69	2049.35	1025.18	2048.36	1024.69	19
7	829.88	415.44	812.85	406.93	811.86	406.43	S	1953.22	977.11	1936.19	968.60	1935.21	968.11	18
8	929.01	465.01	911.98	456.49	910.99	456.00	V	1866.14	933.58	1849.11	925.06	1848.13	924.57	17
9	1000.09	500.55	983.06	492.03	982.07	491.54	A	1767.01	884.01	1749.98	875.49	1749.00	875.00	16
10	1129.20	565.10	1112.17	556.59	1111.18	556.10	E	1695.93	848.47	1678.90	839.96	1677.92	839.46	15
11	1242.36	621.68	1225.33	613.17	1224.34	612.67	I	1566.82	783.91	1549.79	775.40	1548.81	774.91	14
12	1343.46	672.23	1326.43	663.72	1325.45	663.23	T	1453.66	727.34	1436.63	718.82	1435.65	718.33	13
13	1457.56	729.29	1440.53	720.77	1439.55	720.28	N	1352.56	676.78	1335.53	668.27	1334.54	667.78	12
14	1528.64	764.82	1511.61	756.31	1510.63	755.82	A	1238.46	619.73	1221.43	611.22	1220.44	610.72	11
15	1631.78	816.40	1614.75	807.88	1613.77	807.39	C	1167.38	584.19	1150.35	575.68	1149.36	575.19	10
16	1778.96	889.98	1761.93	881.47	1760.94	880.98	F	1064.24	532.62	1047.21	524.11	1046.22	523.61	9
17	1908.07	954.54	1891.04	946.02	1890.06	945.53	E	917.06	459.03	900.03	450.52	899.05	450.03	8
18	2005.19	1003.10	1988.16	994.58	1987.17	994.09	P	787.95	394.48	770.92	385.96			7
19	2076.27	1038.64	2059.23	1030.12	2058.25	1029.63	A	690.83	345.92	673.80	337.40			6
20	2190.37	1095.69	2173.34	1087.17	2172.35	1086.68	N	619.75	310.38	602.72	301.87			5
21	2318.50	1159.75	2301.47	1151.24	2300.48	1150.74	Q	505.65	253.33	488.62	244.81			4
22	2449.69	1225.35	2432.66	1216.84	2431.68	1216.34	M	377.52	189.27	360.49	180.75			3
23	2548.82	1274.92	2531.79	1266.40	2530.81	1265.91	V	246.33	123.67	229.30	115.15			2
24							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
UGCG	LRCGGTAEEILDV	688.50	2+	55.8



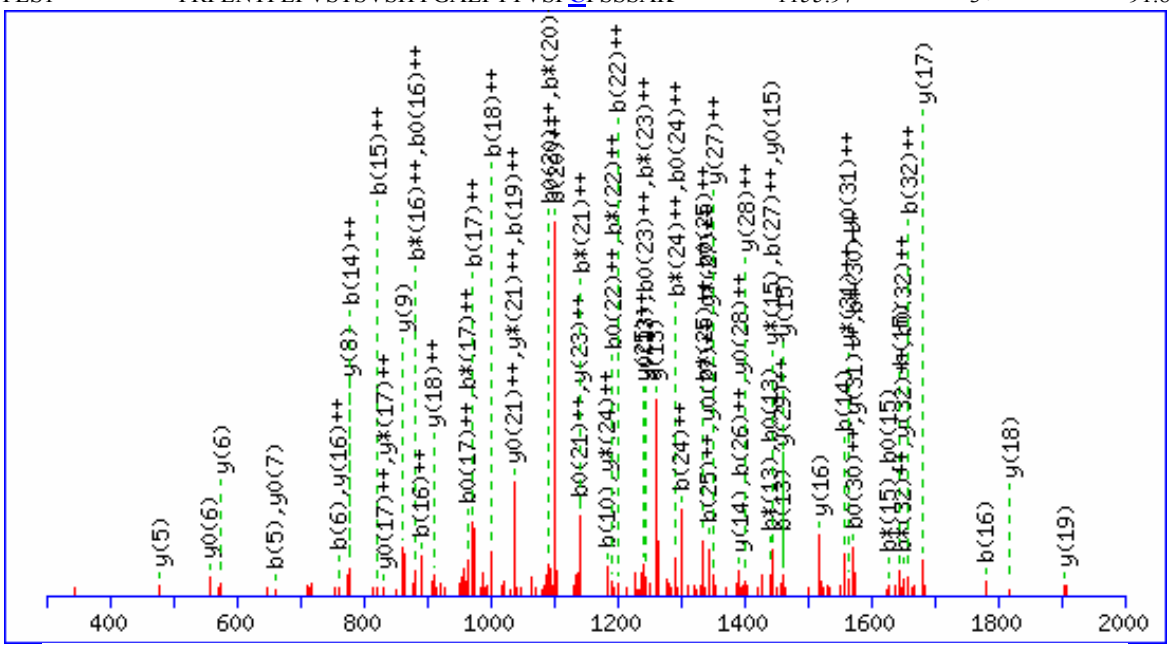
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.17	57.59					L							13
2	270.35	135.68	253.32	127.16			R	1263.40	632.20	1246.37	623.69	1245.38	623.20	12
3	373.49	187.25	356.46	178.74			C	1107.21	554.11			1089.20	545.10	11
4	430.55	215.78	413.51	207.26			G	1004.07	502.54			986.05	493.53	10
5	487.60	244.30	470.57	235.79			G	947.02	474.01			929.00	465.01	9
6	588.70	294.85	571.67	286.34	570.69	285.85	T	889.97	445.49			871.95	436.48	8
7	659.78	330.39	642.75	321.88	641.76	321.39	A	788.86	394.94			770.85	385.93	7
8	788.89	394.95	771.86	386.43	770.88	385.94	E	717.78	359.40			699.77	350.39	6
9	918.01	459.51	900.98	450.99	899.99	450.50	E	588.67	294.84			570.66	285.83	5
10	1031.16	516.09	1014.13	507.57	1013.15	507.08	I	459.56	230.28			441.54	221.27	4
11	1144.32	572.66	1127.29	564.15	1126.31	563.66	L	346.40	173.70			328.38	164.70	3
12	1259.41	630.21	1242.38	621.69	1241.39	621.20	D	233.24	117.12			215.23	108.12	2
13							V	118.15	59.58					1

Gene Symbol	Sequences	m/z	Charge	Ion score
VAPA	CVFEMPNENDKLNDMEPSK	1120.68	2+	51.4



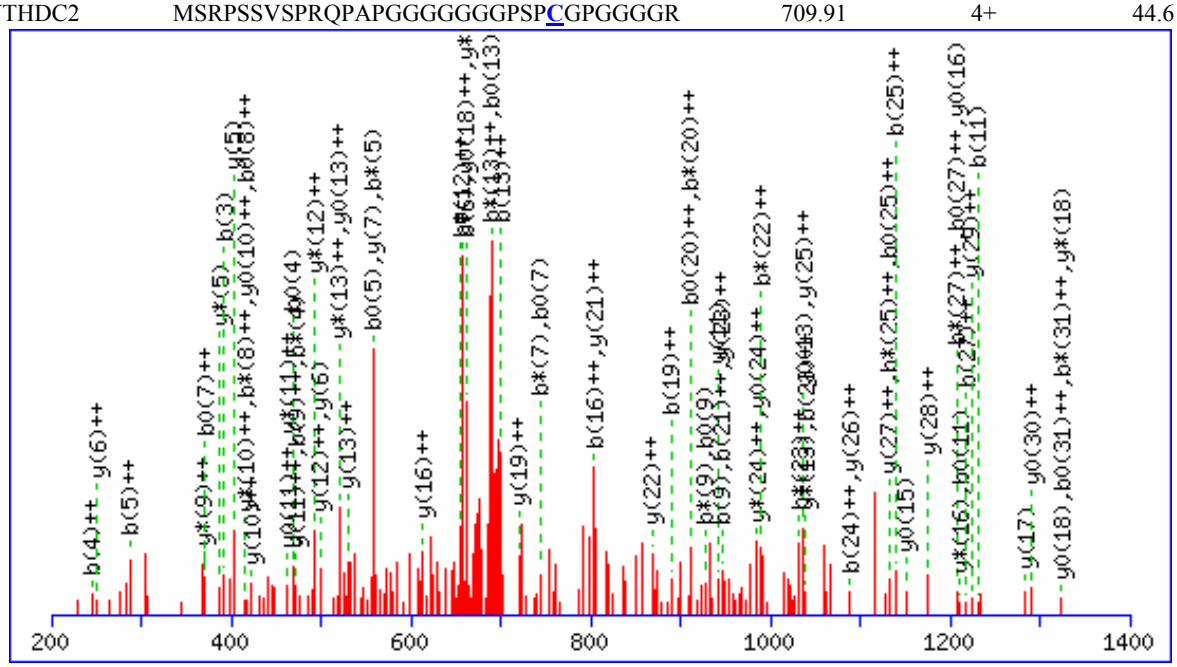
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	104.15	52.58					C							19
2	203.28	102.14					V	2138.35	1069.68	2121.32	1061.17	2120.34	1060.67	18
3	350.46	175.73					F	2039.22	1020.12	2022.19	1011.60	2021.21	1011.11	17
4	479.57	240.29			461.55	231.28	E	1892.05	946.53	1875.02	938.01	1874.03	937.52	16
5	610.77	305.89			592.75	296.88	M	1762.94	881.97	1745.91	873.46	1744.92	872.96	15
6	707.88	354.44			689.87	345.44	P	1631.74	816.37	1614.71	807.86	1613.72	807.37	14
7	821.98	411.50	804.95	402.98	803.97	402.49	N	1534.62	767.82	1517.59	759.30	1516.61	758.81	13
8	951.10	476.05	934.07	467.54	933.08	467.05	E	1420.52	710.76	1403.49	702.25	1402.51	701.76	12
9	1065.20	533.10	1048.17	524.59	1047.19	524.10	N	1291.41	646.21	1274.38	637.69	1273.39	637.20	11
10	1180.29	590.65	1163.26	582.13	1162.27	581.64	D	1177.31	589.16	1160.27	580.64	1159.29	580.15	10
11	1308.46	654.73	1291.43	646.22	1290.44	645.73	K	1062.22	531.61	1045.19	523.10	1044.20	522.61	9
12	1421.62	711.31	1404.59	702.80	1403.60	702.31	L	934.05	467.53	917.02	459.01	916.03	458.52	8
13	1535.72	768.36	1518.69	759.85	1517.70	759.36	N	820.89	410.95	803.86	402.43	802.87	401.94	7
14	1650.81	825.91	1633.78	817.39	1632.79	816.90	D	706.79	353.90	689.76	345.38	688.77	344.89	6
15	1782.00	891.51	1764.97	882.99	1763.99	882.50	M	591.70	296.35	574.67	287.84	573.68	287.35	5
16	1911.12	956.06	1894.09	947.55	1893.10	947.06	E	460.50	230.75	443.47	222.24	442.49	221.75	4
17	2008.23	1004.62	1991.20	996.11	1990.22	995.61	P	331.39	166.20	314.36	157.68	313.37	157.19	3
18	2095.31	1048.16	2078.28	1039.64	2077.29	1039.15	S	234.27	117.64	217.24	109.13	216.26	108.63	2
19							K	147.20	74.10	130.17	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
YES1	YRPENTPEPVSTSVSHYGAEPTTVSPCPSSSAK	1155.97	3+	91.8



#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	164.18	82.59					Y							33
2	320.37	160.69	303.34	152.17			R	3301.53	1651.27	3284.50	1642.75	3283.51	1642.26	32
3	417.48	209.25	400.45	200.73			P	3145.34	1573.18	3128.31	1564.66	3127.33	1564.17	31
4	546.60	273.80	529.57	265.29	528.58	264.79	E	3048.23	1524.62	3031.20	1516.10	3030.21	1515.61	30
5	660.70	330.85	643.67	322.34	642.68	321.85	N	2919.11	1460.06	2902.08	1451.55	2901.10	1451.05	29
6	761.80	381.41	744.77	372.89	743.79	372.40	T	2805.01	1403.01	2787.98	1394.49	2787.00	1394.00	28
7	858.92	429.96	841.89	421.45	840.90	420.96	P	2703.91	1352.46	2686.88	1343.94	2685.89	1343.45	27
8	988.03	494.52	971.00	486.00	970.02	485.51	E	2606.79	1303.90	2589.76	1295.39	2588.78	1294.89	26
9	1085.15	543.08	1068.12	534.56	1067.13	534.07	P	2477.68	1239.34	2460.65	1230.83	2459.66	1230.34	25
10	1184.28	592.64	1167.25	584.13	1166.26	583.64	V	2380.56	1190.79	2363.53	1182.27	2362.55	1181.78	24
11	1271.36	636.18	1254.32	627.67	1253.34	627.17	S	2281.43	1141.22	2264.40	1132.71	2263.42	1132.21	23
12	1372.46	686.73	1355.43	678.22	1354.44	677.73	T	2194.36	1097.68	2177.32	1089.17	2176.34	1088.67	22
13	1459.54	730.27	1442.51	721.76	1441.52	721.26	S	2093.25	1047.13	2076.22	1038.61	2075.24	1038.12	21
14	1558.67	779.84	1541.64	771.32	1540.65	770.83	V	2006.17	1003.59	1989.14	995.08	1988.16	994.58	20
15	1645.75	823.38	1628.71	814.86	1627.73	814.37	S	1907.04	954.03	1890.01	945.51	1889.03	945.02	19
16	1782.88	891.95	1765.85	883.43	1764.87	882.94	H	1819.97	910.49	1802.94	901.97	1801.95	901.48	18
17	1946.06	973.53	1929.03	965.02	1928.04	964.53	Y	1682.83	841.92	1665.80	833.40	1664.81	832.91	17
18	2003.11	1002.06	1986.08	993.54	1985.09	993.05	G	1519.65	760.33	1502.62	751.82	1501.64	751.32	16
19	2074.19	1037.60	2057.16	1029.08	2056.17	1028.59	A	1462.60	731.80	1445.57	723.29	1444.59	722.80	15
20	2203.30	1102.15	2186.27	1093.64	2185.29	1093.15	E	1391.52	696.27	1374.49	687.75	1373.51	687.26	14
21	2300.42	1150.71	2283.39	1142.20	2282.40	1141.70	P	1262.41	631.71	1245.38	623.19	1244.39	622.70	13
22	2401.52	1201.26	2384.49	1192.75	2383.50	1192.26	T	1165.29	583.15	1148.26	574.64	1147.28	574.14	12
23	2502.62	1251.82	2485.59	1243.30	2484.61	1242.81	T	1064.19	532.60	1047.16	524.08	1046.18	523.59	11
24	2601.75	1301.38	2584.72	1292.87	2583.74	1292.37	V	963.09	482.05	946.06	473.53	945.07	473.04	10
25	2688.83	1344.92	2671.80	1336.40	2670.82	1335.91	S	863.96	432.48	846.93	423.97	845.94	423.47	9
26	2785.95	1393.48	2768.92	1384.96	2767.93	1384.47	P	776.88	388.94	759.85	380.43	758.86	379.94	8
27	2889.09	1445.05	2872.06	1436.53	2871.08	1436.04	C	679.76	340.39	662.73	331.87	661.75	331.38	7
28	2986.21	1493.61	2969.18	1485.09	2968.19	1484.60	P	576.62	288.81	559.59	280.30	558.61	279.81	6
29	3073.28	1537.15	3056.25	1528.63	3055.27	1528.14	S	479.51	240.26	462.47	231.74	461.49	231.25	5
30	3160.36	1580.68	3143.33	1572.17	3142.34	1571.68	S	392.43	196.72	375.40	188.20	374.41	187.71	4
31	3247.44	1624.22	3230.41	1615.71	3229.42	1615.22	S	305.35	153.18	288.32	144.66	287.34	144.17	3
32	3318.52	1659.76	3301.48	1651.25	3300.50	1650.75	A	218.27	109.64	201.24	101.13			2
33							K	147.20	74.10	130.17	65.59			1

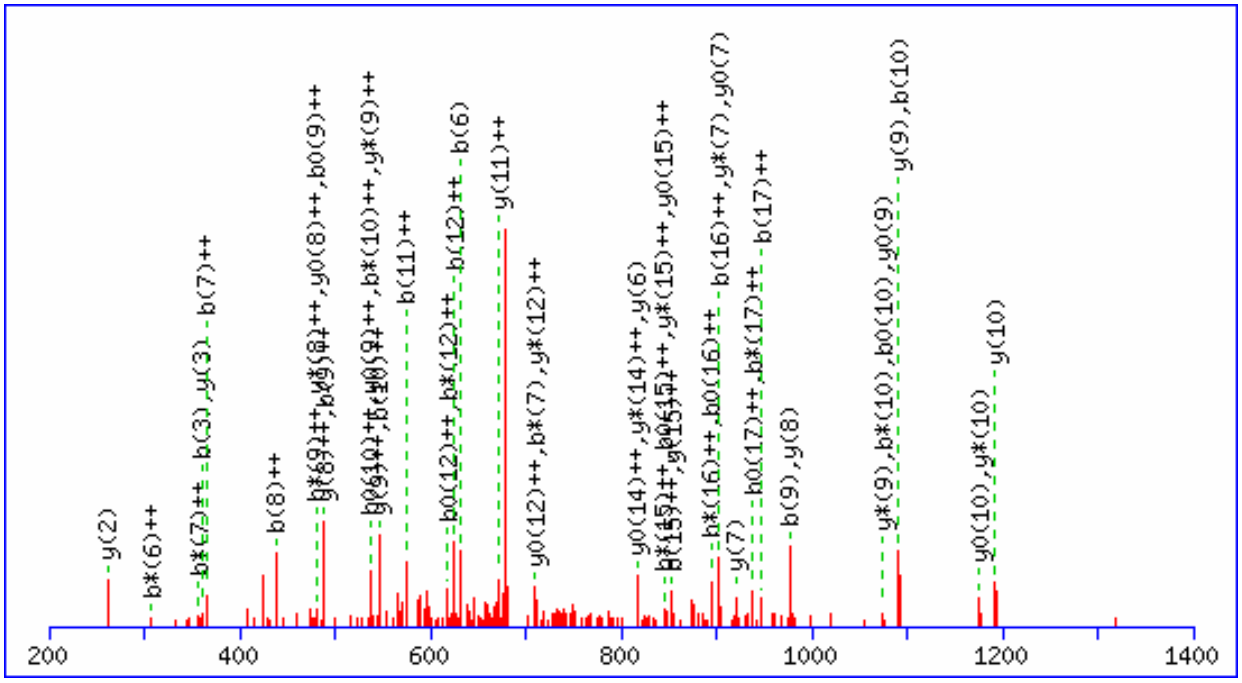
Gene Symbol	Sequences	m/z	Charge	Ion score
YTHDC2	MSRPSSVSPRQPAPGGGGGGGPSPCGPGGGGR	709.91	4+	44.6



M1 : Oxidation (M)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.20	74.61					M							32
2	235.28	118.14			217.27	109.14	S	2688.87	1344.94	2671.84	1336.42	2670.85	1335.93	31
3	391.47	196.24	374.44	187.72	373.45	187.23	R	2601.79	1301.40	2584.76	1292.89	2583.78	1292.39	30
4	488.58	244.79	471.55	236.28	470.57	235.79	P	2445.61	1223.31	2428.58	1214.79	2427.59	1214.30	29
5	575.66	288.33	558.63	279.82	557.64	279.33	S	2348.49	1174.75	2331.46	1166.23	2330.48	1165.74	28
6	662.74	331.87	645.71	323.36	644.72	322.86	S	2261.41	1131.21	2244.38	1122.70	2243.40	1122.20	27
7	761.87	381.44	744.84	372.92	743.85	372.43	V	2174.34	1087.67	2157.31	1079.16	2156.32	1078.66	26
8	848.94	424.98	831.91	416.46	830.93	415.97	S	2075.21	1038.11	2058.18	1029.59	2057.19	1029.10	25
9	946.06	473.53	929.03	465.02	928.04	464.53	P	1988.13	994.57	1971.10	986.05	1970.11	985.56	24
10	1102.25	551.63	1085.22	543.11	1084.23	542.62	R	1891.01	946.01	1873.98	937.50	1873.00	937.00	23
11	1230.37	615.69	1213.34	607.18	1212.36	606.68	Q	1734.83	867.92	1717.80	859.40	1716.81	858.91	22
12	1327.49	664.25	1310.46	655.73	1309.47	655.24	P	1606.70	803.85	1589.67	795.34	1588.68	794.85	21
13	1398.57	699.79	1381.54	691.27	1380.55	690.78	A	1509.58	755.30	1492.55	746.78	1491.57	746.29	20
14	1495.68	748.35	1478.65	739.83	1477.67	739.34	P	1438.51	719.76	1421.48	711.24	1420.49	710.75	19
15	1552.73	776.87	1535.70	768.36	1534.72	767.86	G	1341.39	671.20	1324.36	662.68	1323.38	662.19	18
16	1609.79	805.40	1592.76	796.88	1591.77	796.39	G	1284.34	642.67	1267.31	634.16	1266.32	633.67	17
17	1666.84	833.92	1649.81	825.41	1648.82	824.91	G	1227.29	614.15	1210.26	605.63	1209.27	605.14	16
18	1723.89	862.45	1706.86	853.93	1705.87	853.44	G	1170.24	585.62	1153.21	577.11	1152.22	576.61	15
19	1780.94	890.97	1763.91	882.46	1762.92	881.97	G	1113.19	557.10	1096.15	548.58	1095.17	548.09	14
20	1837.99	919.50	1820.96	910.98	1819.98	910.49	G	1056.13	528.57	1039.10	520.06	1038.12	519.56	13
21	1895.04	948.03	1878.01	939.51	1877.03	939.02	G	999.08	500.05	982.05	491.53	981.07	491.04	12
22	1992.16	996.58	1975.13	988.07	1974.14	987.58	P	942.03	471.52	925.00	463.00	924.02	462.51	11
23	2079.23	1040.12	2062.20	1031.61	2061.22	1031.11	S	844.92	422.96	827.89	414.45	826.90	413.95	10
24	2176.35	1088.68	2159.32	1080.16	2158.33	1079.67	P	757.84	379.42	740.81	370.91			9
25	2279.49	1140.25	2262.46	1131.74	2261.48	1131.24	C	660.72	330.87	643.69	322.35			8
26	2336.54	1168.78	2319.51	1160.26	2318.53	1159.77	G	557.58	279.29	540.55	270.78			7
27	2433.66	1217.33	2416.63	1208.82	2415.64	1208.33	P	500.53	250.77	483.50	242.25			6
28	2490.71	1245.86	2473.68	1237.34	2472.70	1236.85	G	403.41	202.21	386.38	193.70			5
29	2547.76	1274.38	2530.73	1265.87	2529.75	1265.38	G	346.36	173.69	329.33	165.17			4
30	2604.81	1302.91	2587.78	1294.40	2586.80	1293.90	G	289.31	145.16	272.28	136.64			3
31	2661.86	1331.44	2644.83	1322.92	2643.85	1322.43	G	232.26	116.63	215.23	108.12			2
32							R	175.21	88.11	158.18	79.59			1

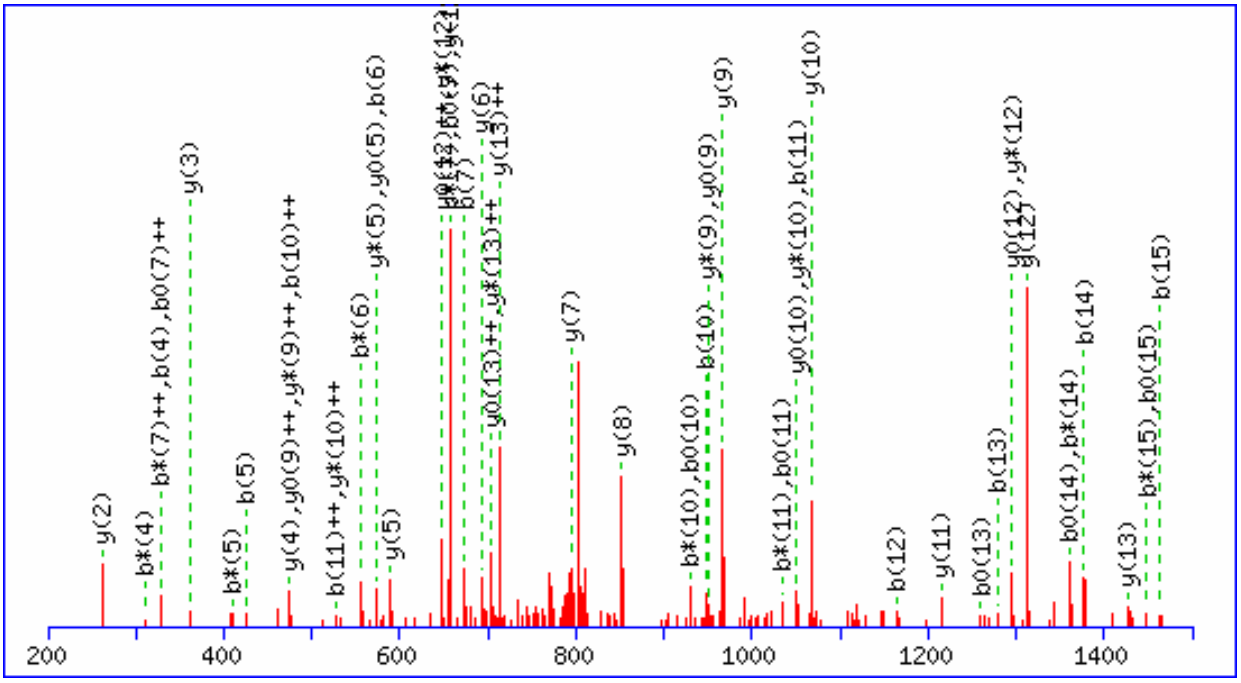
Gene Symbol	Sequences	m/z	Charge	Ion score
ZDHHC5	FRGGVNPFTNGCCNNVSR	689.76	3+	58.4



C13 : NEM (C)

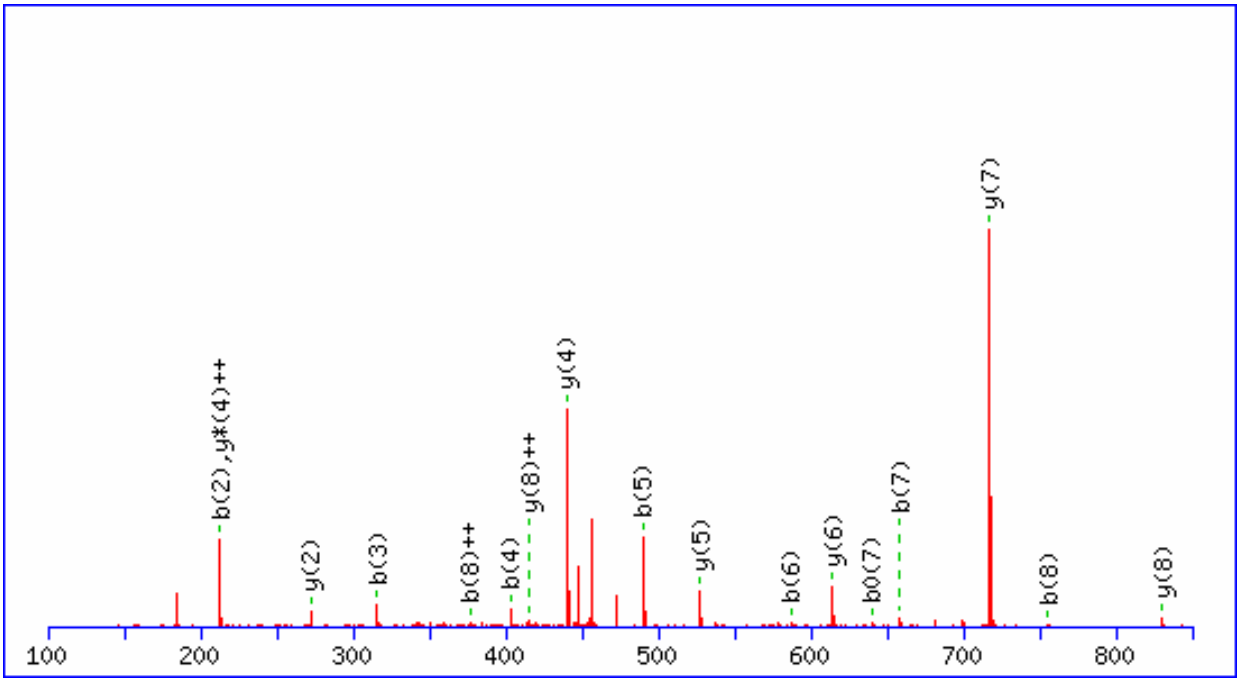
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.18	74.59					F							18
2	304.37	152.69	287.34	144.17			R	1921.10	961.06	1904.07	952.54	1903.09	952.05	17
3	361.42	181.21	344.39	172.70			G	1764.92	882.96	1747.89	874.45	1746.90	873.95	16
4	418.47	209.74	401.44	201.22			G	1707.87	854.44	1690.84	845.92	1689.85	845.43	15
5	517.60	259.30	500.57	250.79			V	1650.81	825.91	1633.78	817.40	1632.80	816.90	14
6	631.70	316.36	614.67	307.84			N	1551.68	776.35	1534.65	767.83	1533.67	767.34	13
7	728.82	364.91	711.79	356.40			P	1437.58	719.29	1420.55	710.78	1419.57	710.29	12
8	875.99	438.50	858.96	429.99			F	1340.47	670.74	1323.43	662.22	1322.45	661.73	11
9	977.10	489.05	960.07	480.54	959.08	480.04	T	1193.29	597.15	1176.26	588.63	1175.28	588.14	10
10	1091.20	546.10	1074.17	537.59	1073.18	537.10	N	1092.19	546.60	1075.16	538.08	1074.17	537.59	9
11	1148.25	574.63	1131.22	566.11	1130.24	565.62	G	978.08	489.55	961.05	481.03	960.07	480.54	8
12	1251.39	626.20	1234.36	617.69	1233.38	617.19	C	921.03	461.02	904.00	452.51	903.02	452.01	7
13	1479.66	740.33	1462.63	731.82	1461.65	731.33	C	817.89	409.45	800.86	400.93	799.88	400.44	6
14	1593.76	797.39	1576.73	788.87	1575.75	788.38	N	589.62	295.32	572.59	286.80	571.61	286.31	5
15	1707.87	854.44	1690.84	845.92	1689.85	845.43	N	475.52	238.26	458.49	229.75	457.50	229.26	4
16	1807.00	904.00	1789.97	895.49	1788.98	895.00	V	361.42	181.21	344.39	172.70	343.40	172.20	3
17	1894.08	947.54	1877.04	939.03	1876.06	938.53	S	262.29	131.65	245.26	123.13	244.27	122.64	2
18							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ZDHHC5	GGVNPFTNGCCNNVSR	820.10	2+	97.5



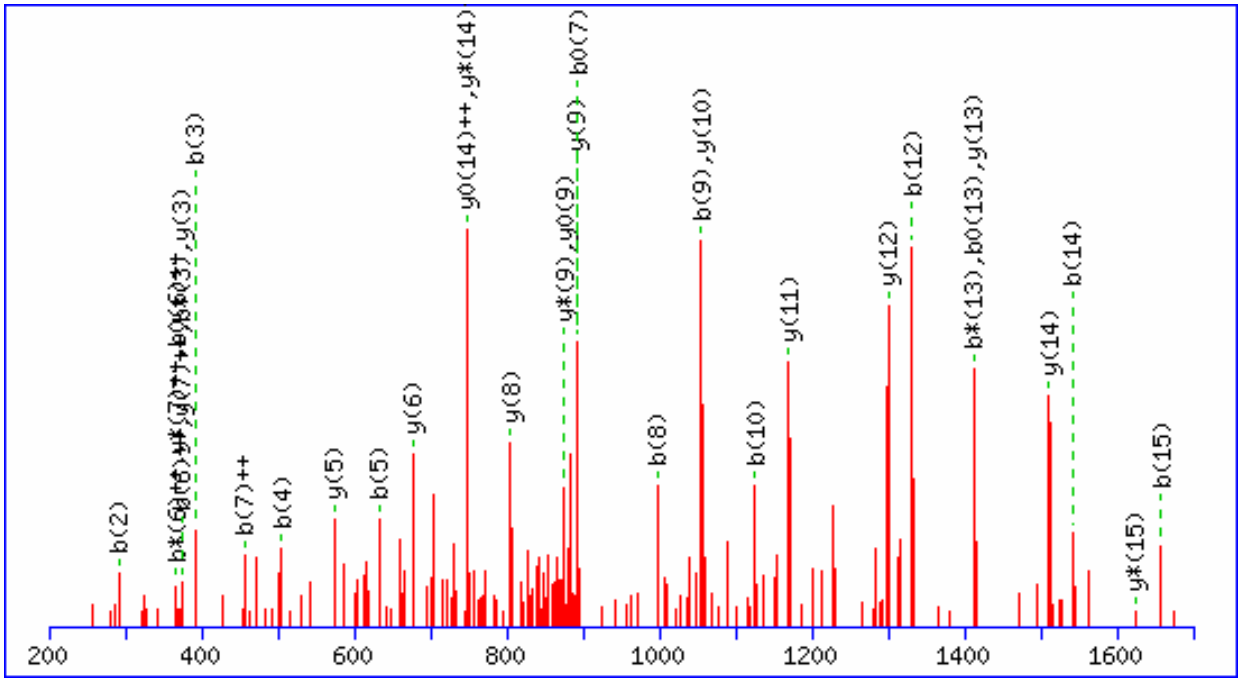
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.06	29.53					G							16
2	115.11	58.06					G	1582.74	791.87	1565.71	783.36	1564.72	782.87	15
3	214.24	107.62					V	1525.69	763.35	1508.66	754.83	1507.67	754.34	14
4	328.34	164.68	311.31	156.16			N	1426.56	713.78	1409.53	705.27	1408.54	704.78	13
5	425.46	213.23	408.43	204.72			P	1312.46	656.73	1295.42	648.22	1294.44	647.72	12
6	572.63	286.82	555.60	278.31			F	1215.34	608.17	1198.31	599.66	1197.32	599.17	11
7	673.74	337.37	656.71	328.86	655.72	328.36	T	1068.17	534.59	1051.14	526.07	1050.15	525.58	10
8	787.84	394.42	770.81	385.91	769.82	385.42	N	967.06	484.04	950.03	475.52	949.05	475.03	9
9	844.89	422.95	827.86	414.43	826.88	413.94	G	852.96	426.98	835.93	418.47	834.94	417.98	8
10	948.03	474.52	931.00	466.01	930.02	465.51	C	795.91	398.46	778.88	389.94	777.89	389.45	7
11	1051.18	526.09	1034.15	517.58	1033.16	517.08	C	692.77	346.89	675.73	338.37	674.75	337.88	6
12	1165.28	583.14	1148.25	574.63	1147.26	574.14	N	589.62	295.32	572.59	286.80	571.61	286.31	5
13	1279.38	640.20	1262.35	631.68	1261.37	631.19	N	475.52	238.26	458.49	229.75	457.50	229.26	4
14	1378.51	689.76	1361.48	681.25	1360.50	680.75	V	361.42	181.21	344.39	172.70	343.40	172.20	3
15	1465.59	733.30	1448.56	724.78	1447.58	724.29	S	262.29	131.65	245.26	123.13	244.27	122.64	2
16							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ZDHHC5	VLCSSPAPR	465.24	2+	66.3



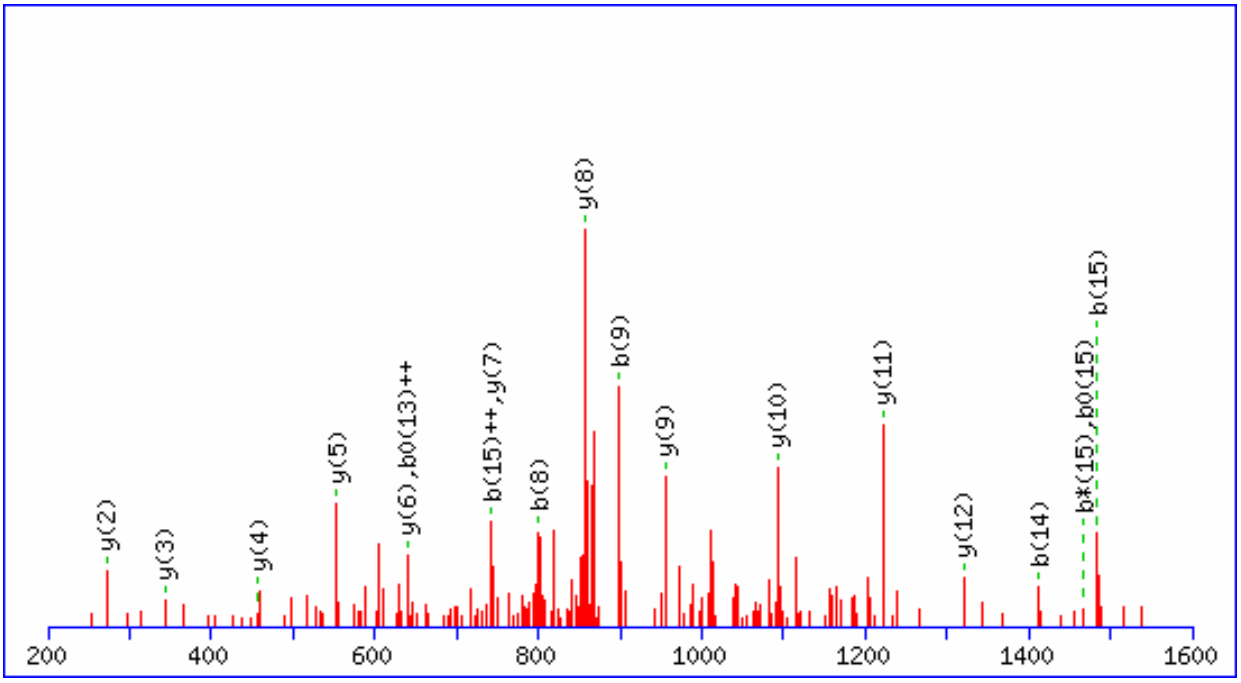
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	100.14	50.57			V							9
2	213.30	107.15			L	830.97	415.99	813.94	407.47	812.96	406.98	8
3	316.44	158.72			C	717.81	359.41	700.78	350.90	699.80	350.40	7
4	403.52	202.26	385.50	193.25	S	614.67	307.84	597.64	299.32	596.66	298.83	6
5	490.59	245.80	472.58	236.79	S	527.59	264.30	510.56	255.79	509.58	255.29	5
6	587.71	294.36	569.69	285.35	P	440.52	220.76	423.49	212.25			4
7	658.79	329.90	640.77	320.89	A	343.40	172.20	326.37	163.69			3
8	755.90	378.46	737.89	369.45	P	272.32	136.67	255.29	128.15			2
9					R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ZDHHC6	YKVIEDYSGACCPLNK	902.30	2+	103.4



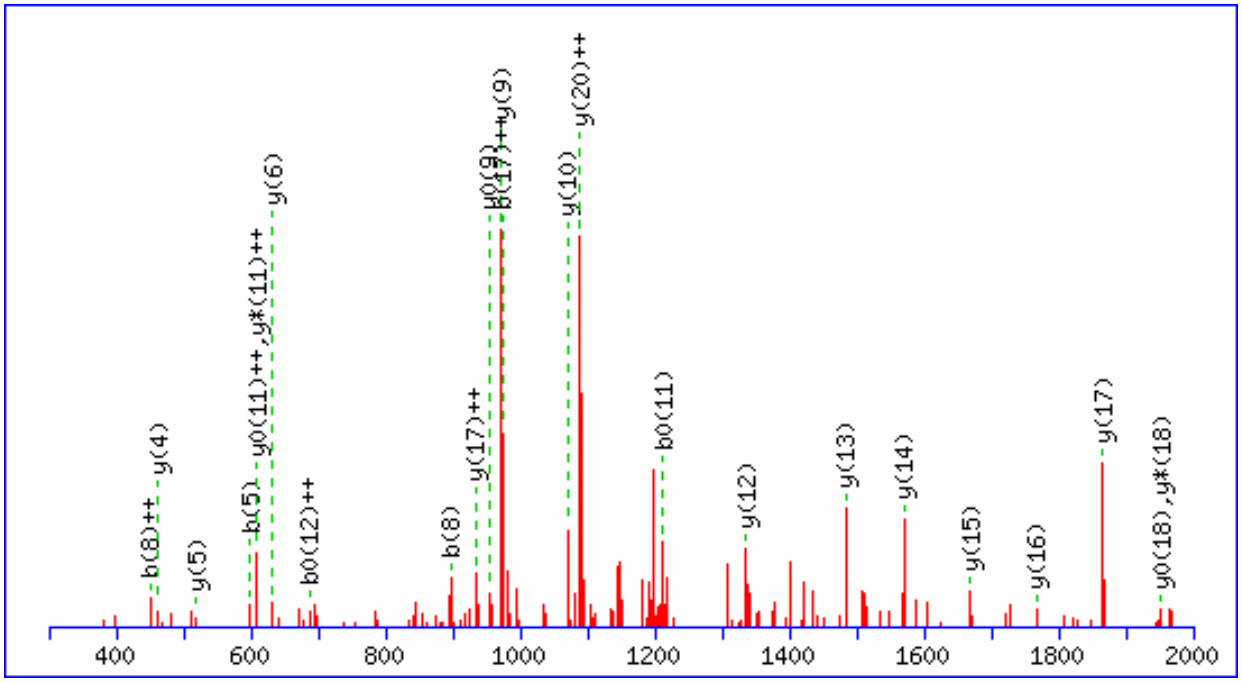
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.18	82.59					Y							16
2	292.35	146.68	275.32	138.17			K	1640.90	820.95	1623.87	812.44	1622.88	811.95	15
3	391.48	196.25	374.45	187.73			V	1512.73	756.87	1495.70	748.35	1494.71	747.86	14
4	504.64	252.83	487.61	244.31			I	1413.60	707.30	1396.56	698.79	1395.58	698.29	13
5	633.76	317.38	616.73	308.87	615.74	308.37	E	1300.44	650.72	1283.41	642.21	1282.42	641.72	12
6	748.84	374.93	731.81	366.41	730.83	365.92	D	1171.32	586.17	1154.29	577.65	1153.31	577.16	11
7	912.02	456.51	894.99	448.00	894.00	447.50	Y	1056.24	528.62	1039.21	520.11	1038.22	519.61	10
8	999.09	500.05	982.06	491.54	981.08	491.04	S	893.06	447.04	876.03	438.52	875.05	438.03	9
9	1056.15	528.58	1039.12	520.06	1038.13	519.57	G	805.99	403.50	788.96	394.98			8
10	1127.22	564.12	1110.19	555.60	1109.21	555.11	A	748.93	374.97	731.90	366.46			7
11	1230.37	615.69	1213.34	607.17	1212.35	606.68	C	677.86	339.43	660.83	330.92			6
12	1333.51	667.26	1316.48	658.74	1315.49	658.25	C	574.71	287.86	557.68	279.35			5
13	1430.62	715.82	1413.59	707.30	1412.61	706.81	P	471.57	236.29	454.54	227.77			4
14	1543.78	772.39	1526.75	763.88	1525.77	763.39	L	374.46	187.73	357.43	179.22			3
15	1657.88	829.45	1640.85	820.93	1639.87	820.44	N	261.30	131.15	244.27	122.64			2
16							K	147.20	74.10	130.16	65.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ZDHHC8	GCCGNVEHVLCSPLAPR	878.57	2+	75.6



#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.06	29.53					G							17
2	161.20	81.11					C	1699.01	850.01	1681.98	841.49	1680.99	841.00	16
3	264.35	132.68					C	1595.86	798.44	1578.83	789.92	1577.85	789.43	15
4	321.40	161.20					G	1492.72	746.86	1475.69	738.35	1474.71	737.86	14
5	435.50	218.25	418.47	209.74			N	1435.67	718.34	1418.64	709.82	1417.66	709.33	13
6	534.63	267.82	517.60	259.30			V	1321.57	661.29	1304.54	652.77	1303.55	652.28	12
7	663.74	332.38	646.71	323.86	645.73	323.37	E	1222.44	611.72	1205.41	603.21	1204.42	602.71	11
8	800.88	400.95	783.85	392.43	782.87	391.94	H	1093.32	547.17	1076.29	538.65	1075.31	538.16	10
9	900.01	450.51	882.98	442.00	882.00	441.50	V	956.18	478.60	939.15	470.08	938.17	469.59	9
10	1013.17	507.09	996.14	498.57	995.16	498.08	L	857.05	429.03	840.02	420.52	839.04	420.02	8
11	1116.31	558.66	1099.28	550.15	1098.30	549.65	C	743.90	372.45	726.86	363.94	725.88	363.44	7
12	1203.39	602.20	1186.36	593.68	1185.38	593.19	S	640.75	320.88	623.72	312.36	622.74	311.87	6
13	1300.51	650.76	1283.48	642.24	1282.49	641.75	P	553.67	277.34	536.64	268.83			5
14	1413.67	707.34	1396.63	698.82	1395.65	698.33	L	456.56	228.78	439.53	220.27			4
15	1484.74	742.88	1467.71	734.36	1466.73	733.87	A	343.40	172.20	326.37	163.69			3
16	1581.86	791.43	1564.83	782.92	1563.84	782.43	P	272.32	136.67	255.29	128.15			2
17							R	175.21	88.11	158.18	79.59			1

Gene Symbol	Sequences	m/z	Charge	Ion score
ZFR	MIPI**C**PVVSFTYVPSRLGEDAK	1232.93	2+	58.6



N-term : N-Acetyl (Protein)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	174.24	87.62					M							22
2	287.40	144.20					I	2292.67	1146.84	2275.64	1138.32	2274.66	1137.83	21
3	384.51	192.76					P	2179.51	1090.26	2162.48	1081.75	2161.50	1081.25	20
4	497.67	249.34					I	2082.40	1041.70	2065.37	1033.19	2064.38	1032.70	19
5	600.81	300.91					C	1969.24	985.12	1952.21	976.61	1951.23	976.12	18
6	697.93	349.47					P	1866.10	933.55	1849.07	925.04	1848.08	924.55	17
7	797.06	399.03					V	1768.98	885.00	1751.95	876.48	1750.97	875.99	16
8	896.19	448.60					V	1669.85	835.43	1652.82	826.91	1651.84	826.42	15
9	983.27	492.14			965.25	483.13	S	1570.72	785.86	1553.69	777.35	1552.71	776.86	14
10	1130.44	565.73			1112.43	556.72	F	1483.64	742.33	1466.61	733.81	1465.63	733.32	13
11	1231.55	616.28			1213.53	607.27	T	1336.47	668.74	1319.44	660.22	1318.45	659.73	12
12	1394.72	697.86			1376.70	688.86	Y	1235.37	618.19	1218.34	609.67	1217.35	609.18	11
13	1493.85	747.43			1475.84	738.42	V	1072.19	536.60	1055.16	528.09	1054.18	527.59	10
14	1590.97	795.99			1572.95	786.98	P	973.06	487.03	956.03	478.52	955.05	478.03	9
15	1678.04	839.53			1660.03	830.52	S	875.95	438.48	858.92	429.96	857.93	429.47	8
16	1834.23	917.62	1817.20	909.10	1816.21	908.61	R	788.87	394.94	771.84	386.42	770.85	385.93	7
17	1947.39	974.20	1930.36	965.68	1929.37	965.19	L	632.68	316.85	615.65	308.33	614.67	307.84	6
18	2004.44	1002.72	1987.41	994.21	1986.42	993.72	G	519.53	260.27	502.50	251.75	501.51	251.26	5
19	2133.55	1067.28	2116.52	1058.76	2115.54	1058.27	E	462.47	231.74	445.44	223.23	444.46	222.73	4
20	2248.64	1124.82	2231.61	1116.31	2230.62	1115.82	D	333.36	167.18	316.33	158.67	315.35	158.18	3
21	2319.72	1160.36	2302.69	1151.85	2301.70	1151.35	A	218.27	109.64	201.24	101.13			2
22							K	147.20	74.10	130.17	65.59			1

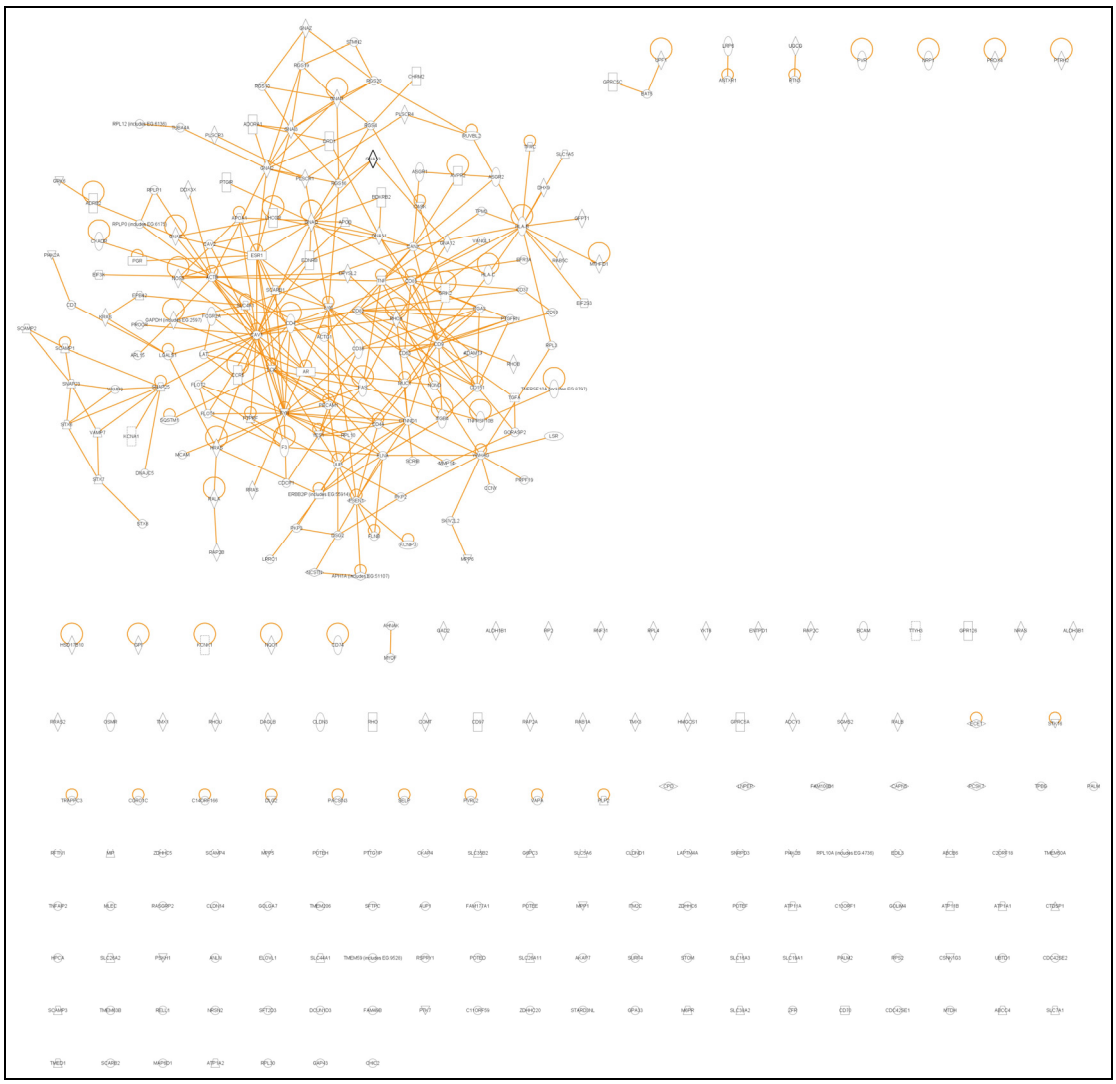


Figure S4. Construction of S-acylated protein network via direct protein-protein interactions. High-confidence candidate S-acylated proteins identified using protein-based procedure and peptide-based procedure in the present study (Table S2 and S6) and all known human S-acylated proteins reported previously in the peer-reviewed literature (Table S8) were merged and analyzed using Ingenuity Pathway Analysis (IPA) software. Only about half of the S-acylated proteins are connected while others hardly have direct interactors.

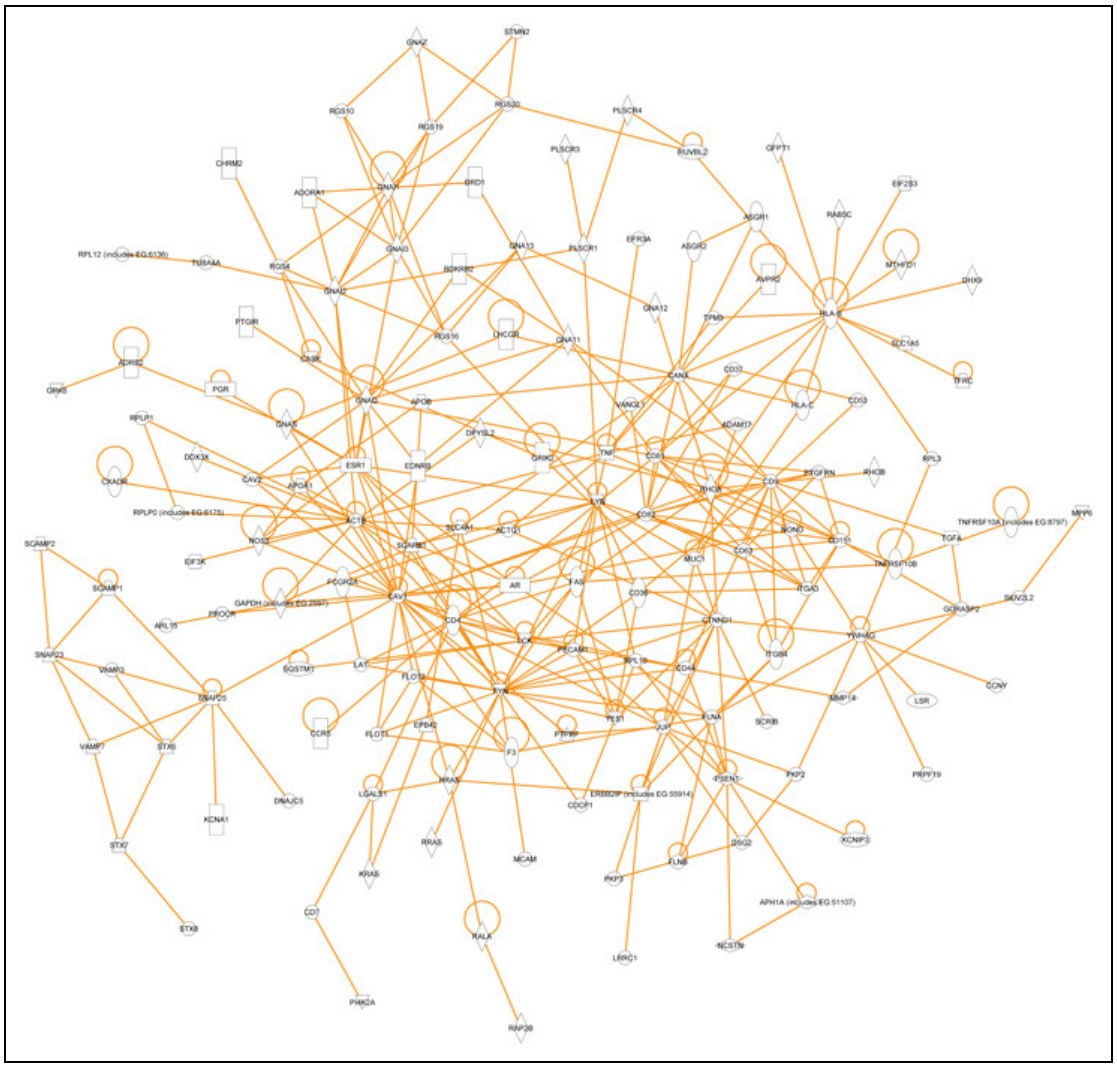


Figure S5. Magnified view of the S-acylated protein network, in which two highly connected subnetworks emerge. See Figure 10 for magnified view of the subnetworks.

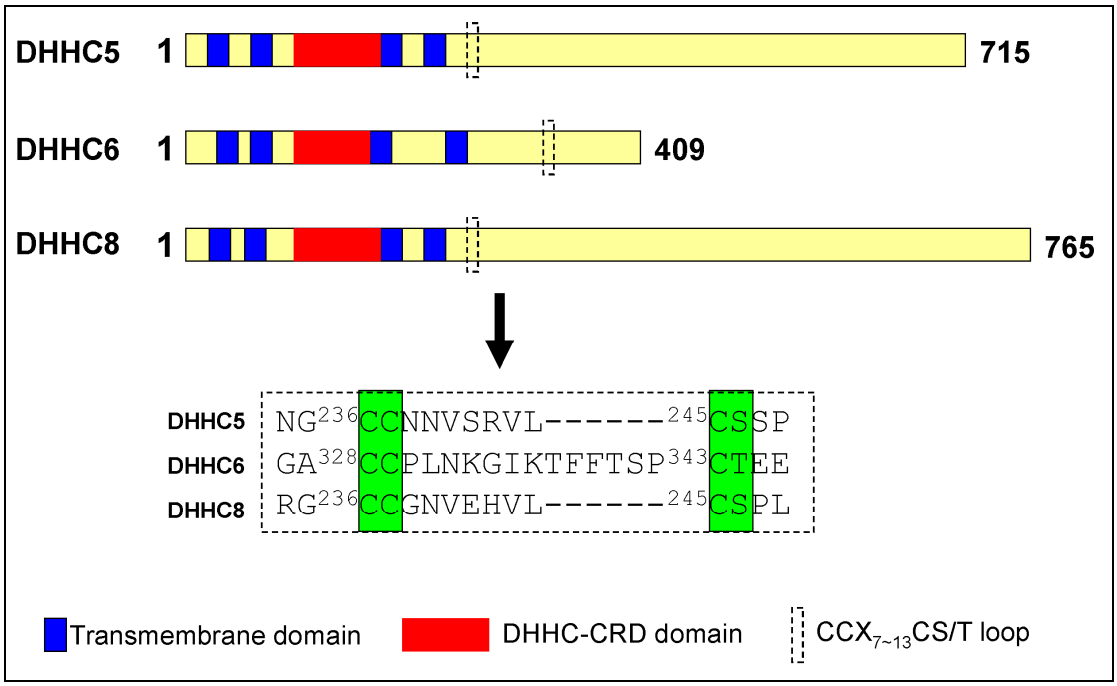


Figure S6. Illustration of the primary structures of DHHC5, DHHC6, and DHHC8 proteins and the alignment of $CCX_{7\sim13}CS/T$ loops. Three putative S-acylated cysteine residues are localized downstream of a conserved DHHC-CRD domain. The alignment analysis of the cysteines revealed a novel $CCX_{7\sim13}CS/T$ motif.

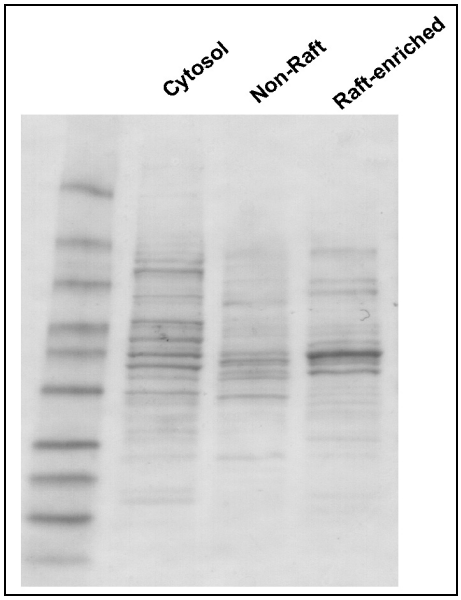


Figure S7. Ponceau S stained blot to confirm equal protein loading. 10 μg proteins from the cytoplasmic, non-raft, and lipid raft-enriched fractions were separated by SDS-PAGE and electrotransferred onto nitrocellulose membrane. Subsequently, the membrane was stained with Ponceau S stain for 5 min and destained with distilled water.