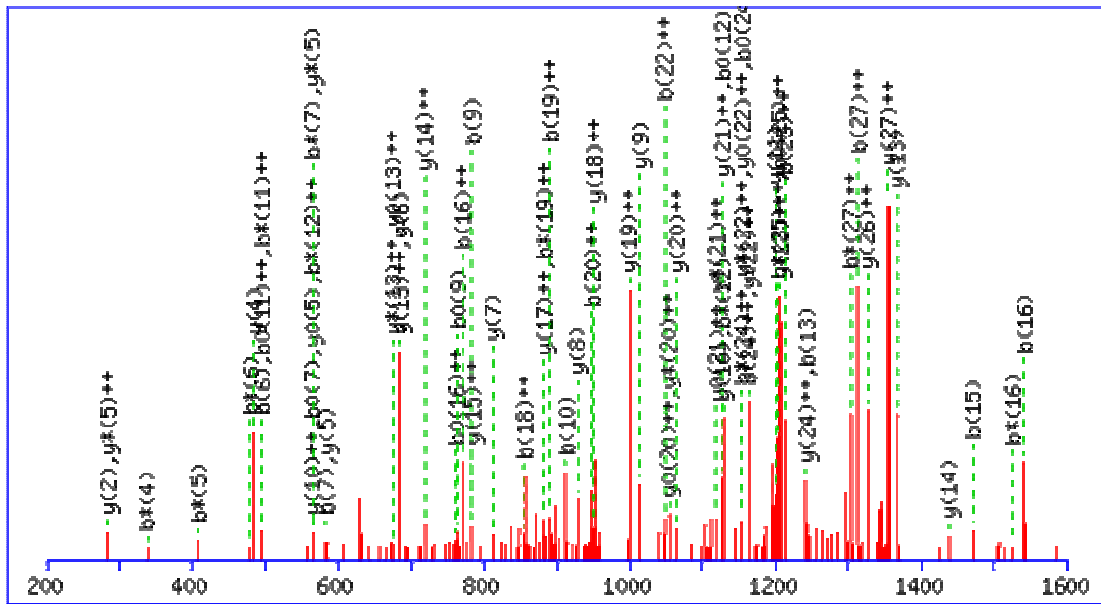


Figure S1. Representative tandem mass spectra annotated with masses observed and fragment assignments for the quantitated proteins which were identified with only one peptide.

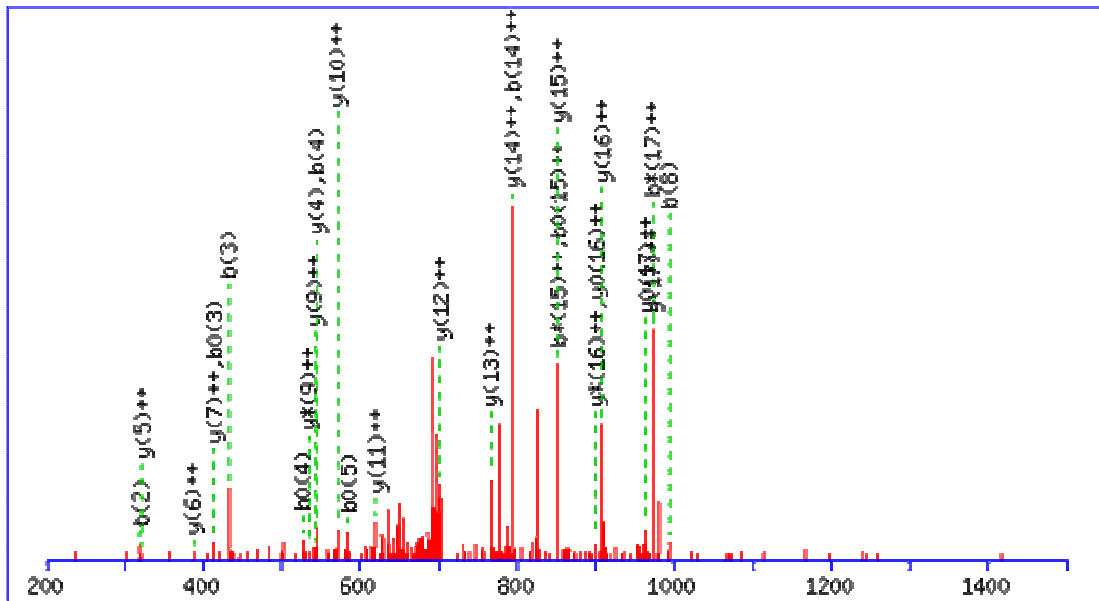
Gene Symbol	Sequences	m/z	Charge	Ion score	Expect
BASP1	AQGPAASAEEPKPVEAPAANSQTQVTVKE	970.155	3+	79	1.6e-06
(IPI00299024 Brain acid soluble protein 1)					



K12, K28: Lysine (K-full)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.04	36.53					A							29
2	200.10	100.56	183.08	92.04			Q	2837.41	1419.21	2820.39	1410.70	2819.40	1410.21	28
3	257.12	129.07	240.10	120.55			G	2709.35	1355.18	2692.33	1346.67	2691.34	1346.18	27
4	354.18	177.59	337.15	169.08			P	2652.33	1326.67	2635.31	1318.16	2634.32	1317.67	26
5	425.21	213.11	408.19	204.60			A	2555.28	1278.14	2538.25	1269.63	2537.27	1269.14	25
6	496.25	248.63	479.22	240.12			A	2484.24	1242.63	2467.22	1234.11	2466.23	1233.62	24
7	583.28	292.15	566.26	283.63	565.27	283.14	S	2413.21	1207.11	2396.18	1198.59	2395.20	1198.10	23
8	654.32	327.66	637.29	319.15	636.31	318.66	A	2326.17	1163.59	2309.15	1155.08	2308.16	1154.59	22
9	783.36	392.19	766.34	383.67	765.35	383.18	E	2255.14	1128.07	2238.11	1119.56	2237.13	1119.07	21
10	912.41	456.71	895.38	448.19	894.40	447.70	E	2126.09	1063.55	2109.07	1055.04	2108.08	1054.55	20
11	1009.46	505.23	992.43	496.72	991.45	496.23	P	1997.05	999.03	1980.03	990.52	1979.04	990.02	19
12	1145.57	573.29	1128.54	564.77	1127.56	564.28	K	1900.00	950.50	1882.97	941.99	1881.99	941.50	18
13	1242.62	621.81	1225.59	613.30	1224.61	612.81	P	1763.89	882.45	1746.86	873.94	1745.88	873.44	17
14	1341.69	671.35	1324.66	662.83	1323.68	662.34	V	1666.84	833.92	1649.81	825.41	1648.83	824.92	16
15	1470.73	735.87	1453.70	727.36	1452.72	726.86	E	1567.77	784.39	1550.74	775.87	1549.76	775.38	15
16	1541.77	771.39	1524.74	762.87	1523.76	762.38	A	1438.73	719.87	1421.70	711.35	1420.72	710.86	14
17	1638.82	819.91	1621.79	811.40	1620.81	810.91	P	1367.69	684.35	1350.66	675.83	1349.68	675.34	13
18	1709.86	855.43	1692.83	846.92	1691.85	846.43	A	1270.64	635.82	1253.61	627.31	1252.63	626.82	12
19	1780.90	890.95	1763.87	882.44	1762.88	881.95	A	1199.60	600.30	1182.57	591.79	1181.59	591.30	11
20	1894.94	947.97	1877.91	939.46	1876.93	938.97	N	1128.56	564.78	1111.54	556.27	1110.55	555.78	10
21	1981.97	991.49	1964.94	982.98	1963.96	982.48	S	1014.52	507.76	997.49	499.25	996.51	498.76	9
22	2097.00	1049.00	2079.97	1040.49	2078.99	1040.00	D	927.49	464.25	910.46	455.73	909.48	455.24	8
23	2225.06	1113.03	2208.03	1104.52	2207.05	1104.03	Q	812.46	406.73	795.43	398.22	794.45	397.73	7
24	2326.10	1163.56	2309.08	1155.04	2308.09	1154.55	T	684.40	342.70	667.38	334.19	666.39	333.70	6
25	2425.17	1213.09	2408.15	1204.58	2407.16	1204.08	V	583.35	292.18	566.33	283.67	565.34	283.18	5
26	2526.22	1263.61	2509.19	1255.10	2508.21	1254.61	T	484.29	242.65	467.26	234.13	466.28	233.64	4
27	2625.29	1313.15	2608.26	1304.63	2607.28	1304.14	V	383.24	192.12	366.21	183.61	365.23	183.12	3
28	2761.40	1381.20	2744.37	1372.69	2743.39	1372.20	K	284.17	142.59	267.14	134.08	266.16	133.58	2
29							E	148.06	74.53			130.05	65.53	1

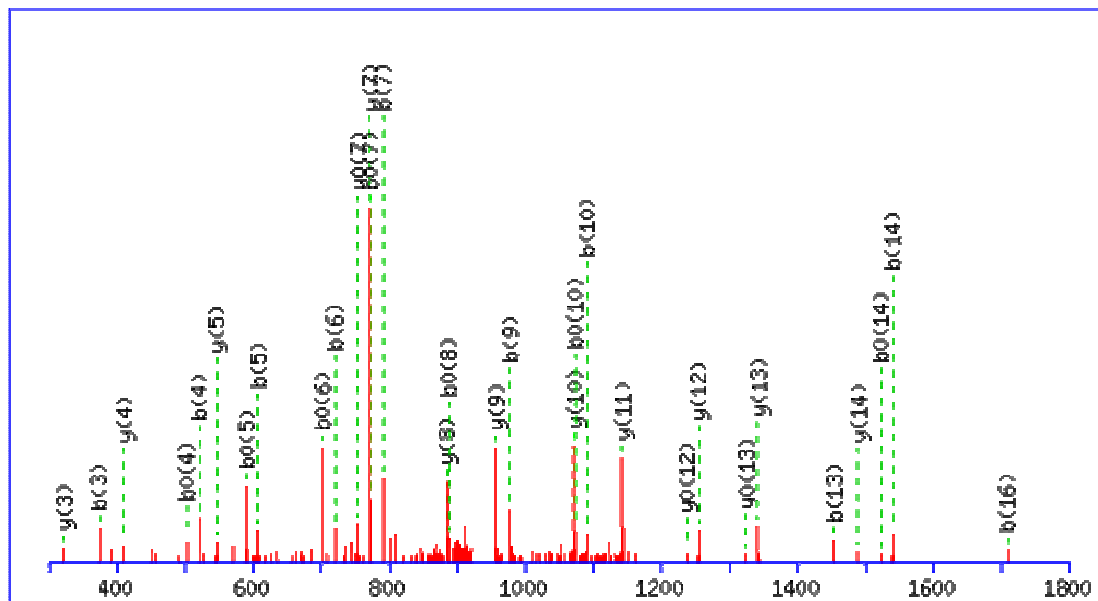
Gene Symbol Sequences m/z Charge Ion score Expect
 C14orf142 MELLGEYVQGEGKPQKLR 712.037 3+ 45 0.0048
 (IPI00646167 hypothetical protein LOC84520)



N-term: N-Acetyl (Protein)
 M1: Oxidation (M)
 Q15: Deamidation (NQ)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	190.05	95.53					M							18
2	319.10	160.05			301.09	151.05	E	1945.04	973.02	1928.01	964.51	1927.03	964.02	17
3	432.18	216.59			414.17	207.59	L	1816.00	908.50	1798.97	899.99	1797.99	899.50	16
4	545.26	273.14			527.25	264.13	L	1702.91	851.96	1685.89	843.45	1684.90	842.95	15
5	602.29	301.65			584.27	292.64	G	1589.83	795.42	1572.80	786.90	1571.82	786.41	14
6	731.33	366.17			713.32	357.16	E	1532.81	766.91	1515.78	758.39	1514.80	757.90	13
7	894.39	447.70			876.38	438.69	Y	1403.76	702.39	1386.74	693.87	1385.75	693.38	12
8	993.46	497.23			975.45	488.23	V	1240.70	620.85	1223.67	612.34	1222.69	611.85	11
9	1050.48	525.74			1032.47	516.74	G	1141.63	571.32	1124.61	562.81	1123.62	562.31	10
10	1178.54	589.77	1161.51	581.26	1160.53	580.77	Q	1084.61	542.81	1067.58	534.30	1066.60	533.80	9
11	1307.58	654.29	1290.56	645.78	1289.57	645.29	E	956.55	478.78	939.53	470.27	938.54	469.77	8
12	1364.60	682.81	1347.58	674.29	1346.59	673.80	G	827.51	414.26	810.48	405.75			7
13	1492.70	746.85	1475.67	738.34	1474.69	737.85	K	770.49	385.75	753.46	377.23			6
14	1589.75	795.38	1572.72	786.87	1571.74	786.37	P	642.39	321.70	625.37	313.19			5
15	1718.79	859.90	1701.77	851.39	1700.78	850.90	Q	545.34	273.17	528.31	264.66			4
16	1846.89	923.95	1829.86	915.43	1828.88	914.94	K	416.30	208.65	399.27	200.14			3
17	1959.97	980.49	1942.95	971.98	1941.96	971.48	L	288.20	144.61	271.18	136.09			2
18							R	175.12	88.06	158.09	79.55			1

Gene Symbol **Sequences** **m/z** **Charge** **Ion score** **Expect**
 C14orf32 SDEFSLADALPEHSPAK 932.450 2+ 91 1.2e-07
 (IPI00171527 Uncharacterized protein C14orf32)

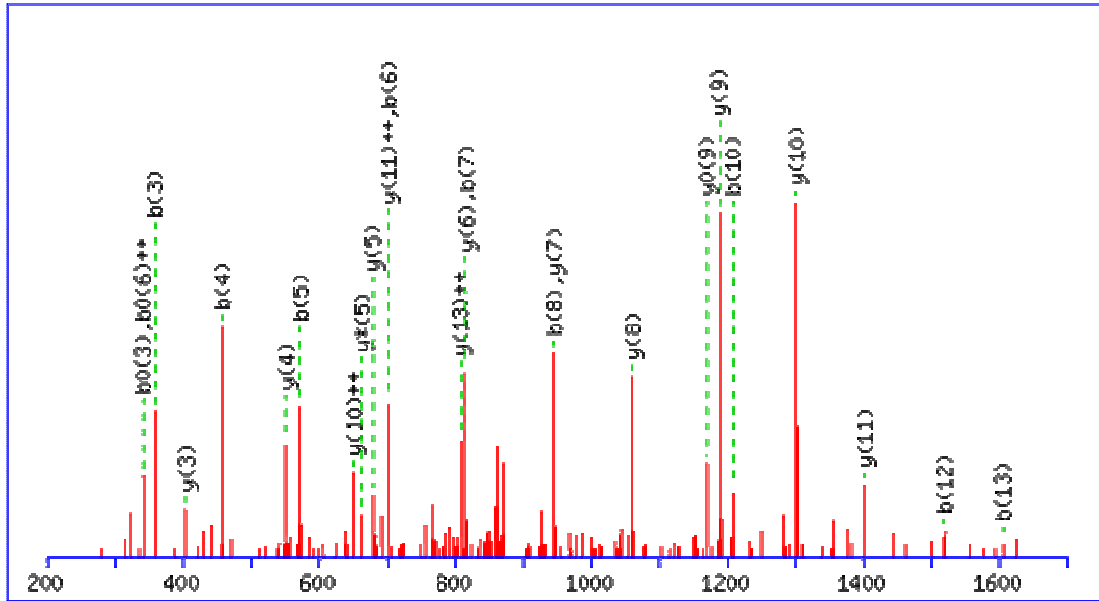


N-term : N-Acetyl (Protein)

K17: Lysine (K-full)

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	130.05	65.53	112.04	56.52	S							17
2	245.08	123.04	227.07	114.04	D	1734.84	867.92	1717.82	859.41	1716.83	858.92	16
3	374.12	187.56	356.11	178.56	E	1619.82	810.41	1602.79	801.90	1601.80	801.41	15
4	521.19	261.10	503.18	252.09	F	1490.77	745.89	1473.75	737.38	1472.76	736.88	14
5	608.22	304.61	590.21	295.61	S	1343.70	672.36	1326.68	663.84	1325.69	663.35	13
6	721.30	361.16	703.29	352.15	L	1256.67	628.84	1239.65	620.33	1238.66	619.83	12
7	792.34	396.67	774.33	387.67	A	1143.59	572.30	1126.56	563.78	1125.58	563.29	11
8	907.37	454.19	889.36	445.18	D	1072.55	536.78	1055.52	528.27	1054.54	527.77	10
9	978.41	489.71	960.39	480.70	A	957.52	479.27	940.50	470.75	939.51	470.26	9
10	1091.49	546.25	1073.48	537.24	L	886.49	443.75	869.46	435.23	868.48	434.74	8
11	1188.54	594.77	1170.53	585.77	P	773.40	387.21	756.38	378.69	755.39	378.20	7
12	1317.58	659.30	1299.57	650.29	E	676.35	338.68	659.32	330.17	658.34	329.67	6
13	1454.64	727.83	1436.63	718.82	H	547.31	274.16	530.28	265.64	529.30	265.15	5
14	1541.68	771.34	1523.66	762.34	S	410.25	205.63	393.22	197.11	392.24	196.62	4
15	1638.73	819.87	1620.72	810.86	P	323.22	162.11	306.19	153.60			3
16	1709.77	855.39	1691.75	846.38	A	226.16	113.59	209.14	105.07			2
17					K	155.13	78.07	138.10	69.55			1

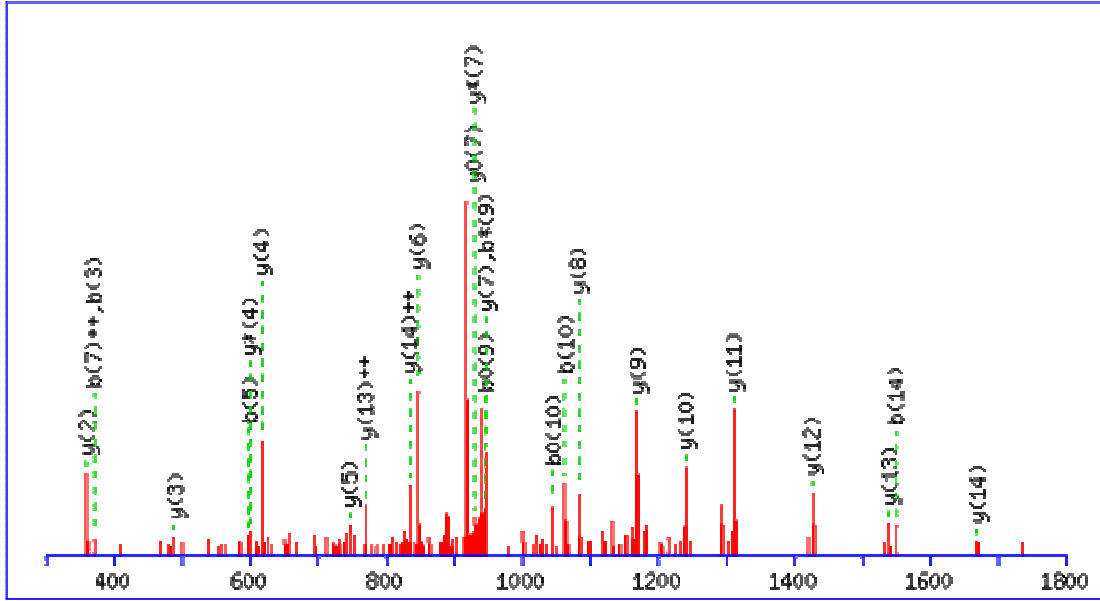
Gene Symbol Sequences m/z Charge Ion score Expect
 C9orf32 TSEVIEDEKQFYSK 880.933 2+ 83 8.5e-07
 (IPI00515040 Chromosome 9 open reading frame 32)



N-term : N-Acetyl (Protein)
 K9, K14: Lysine (K-full)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	144.07	72.54			126.05	63.53	T							14
2	231.10	116.05			213.09	107.05	S	1617.80	809.40	1600.77	800.89	1599.79	800.40	13
3	360.14	180.57			342.13	171.57	E	1530.77	765.89	1513.74	757.37	1512.76	756.88	12
4	459.21	230.11			441.20	221.10	V	1401.72	701.37	1384.70	692.85	1383.71	692.36	11
5	572.29	286.65			554.28	277.64	I	1302.65	651.83	1285.63	643.32	1284.64	642.83	10
6	701.34	351.17			683.32	342.17	E	1189.57	595.29	1172.54	586.78	1171.56	586.28	9
7	816.36	408.68			798.35	399.68	D	1060.53	530.77	1043.50	522.25	1042.52	521.76	8
8	945.40	473.21			927.39	464.20	E	945.50	473.25	928.47	464.74	927.49	464.25	7
9	1081.51	541.26	1064.49	532.75	1063.50	532.26	K	816.46	408.73	799.43	400.22	798.45	399.73	6
10	1209.57	605.29	1192.55	596.78	1191.56	596.28	Q	680.35	340.68	663.32	332.17	662.34	331.67	5
11	1356.64	678.82	1339.61	670.31	1338.63	669.82	F	552.29	276.65	535.26	268.14	534.28	267.64	4
12	1519.70	760.36	1502.68	751.84	1501.69	751.35	Y	405.22	203.11	388.20	194.60	387.21	194.11	3
13	1606.74	803.87	1589.71	795.36	1588.73	794.87	S	242.16	121.58	225.13	113.07	224.15	112.58	2
14							K	155.13	78.07	138.10	69.55			1

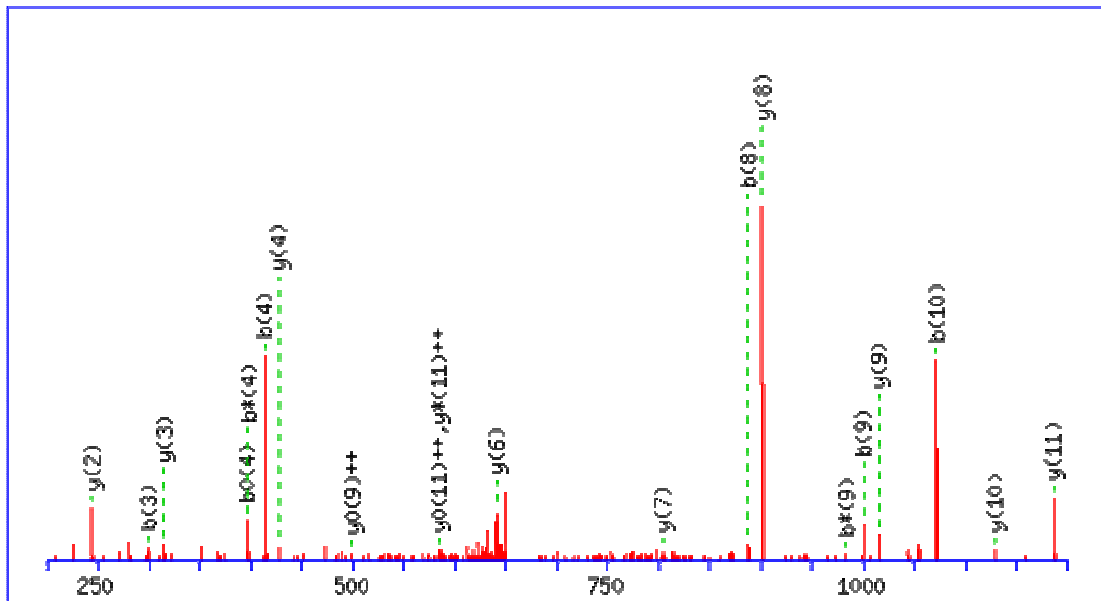
Gene Symbol Sequences m/z Charge Ion score Expect
 CLTB LQELDAASKVTEQEWK 955.994 2+ 89 1.9e-07
 (IPI00014589 Isoform Brain of Clathrin light chain B)



K9: Lysine (K-full)

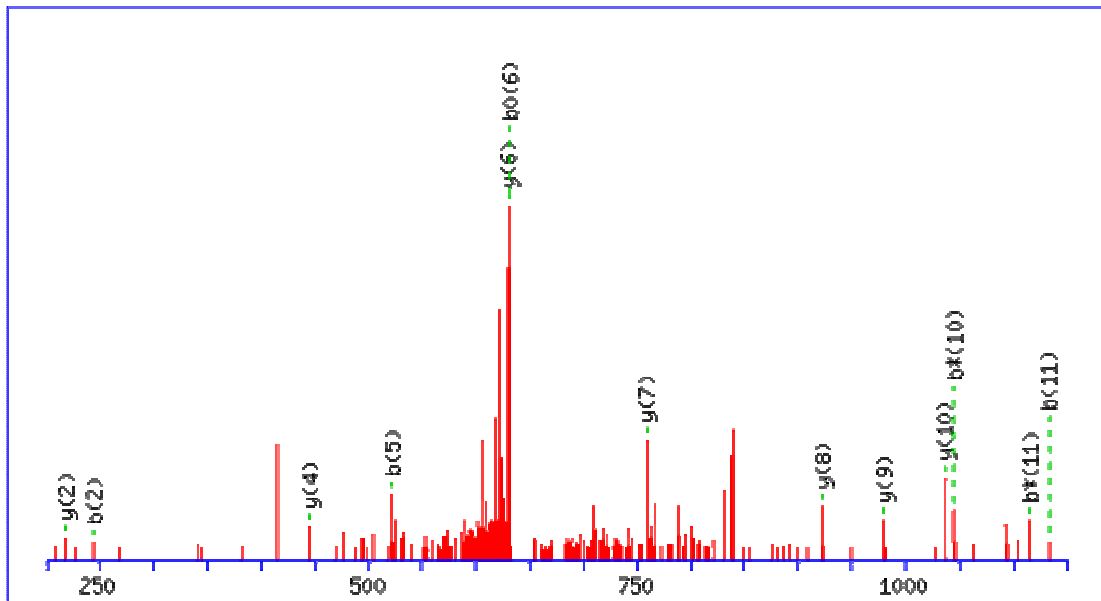
#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.09	57.55					L							16
2	242.15	121.58	225.12	113.07			Q	1797.89	899.45	1780.86	890.93	1779.88	890.44	15
3	371.19	186.10	354.17	177.59	353.18	177.09	E	1669.83	835.42	1652.80	826.90	1651.82	826.41	14
4	484.28	242.64	467.25	234.13	466.27	233.64	L	1540.78	770.90	1523.76	762.38	1522.77	761.89	13
5	599.30	300.16	582.28	291.64	581.29	291.15	D	1427.70	714.35	1410.67	705.84	1409.69	705.35	12
6	670.34	335.67	653.31	327.16	652.33	326.67	A	1312.67	656.84	1295.65	648.33	1294.66	647.84	11
7	741.38	371.19	724.35	362.68	723.37	362.19	A	1241.64	621.32	1224.61	612.81	1223.63	612.32	10
8	828.41	414.71	811.38	406.20	810.40	405.70	S	1170.60	585.80	1153.57	577.29	1152.59	576.80	9
9	964.52	482.76	947.49	474.25	946.51	473.76	K	1083.57	542.29	1066.54	533.77	1065.56	533.28	8
10	1063.59	532.30	1046.56	523.78	1045.58	523.29	V	947.46	474.23	930.43	465.72	929.45	465.23	7
11	1164.64	582.82	1147.61	574.31	1146.62	573.82	T	848.39	424.70	831.36	416.19	830.38	415.69	6
12	1293.68	647.34	1276.65	638.83	1275.67	638.34	E	747.34	374.17	730.32	365.66	729.33	365.17	5
13	1421.74	711.37	1404.71	702.86	1403.73	702.37	Q	618.30	309.65	601.27	301.14	600.29	300.65	4
14	1550.78	775.89	1533.75	767.38	1532.77	766.89	E	490.24	245.62	473.21	237.11	472.23	236.62	3
15	1736.86	868.93	1719.83	860.42	1718.85	859.93	W	361.20	181.10	344.17	172.59			2
16							R	175.12	88.06	158.09	79.55			1

Gene Symbol **Sequences** **m/z** **Charge** **Ion score** **Expect**
 COX5B KGLDPYNVLPK 657.871 2+ 56 0.00023
 (IPI00021785 Cytochrome c oxidase subunit 5B, mitochondrial precursor)



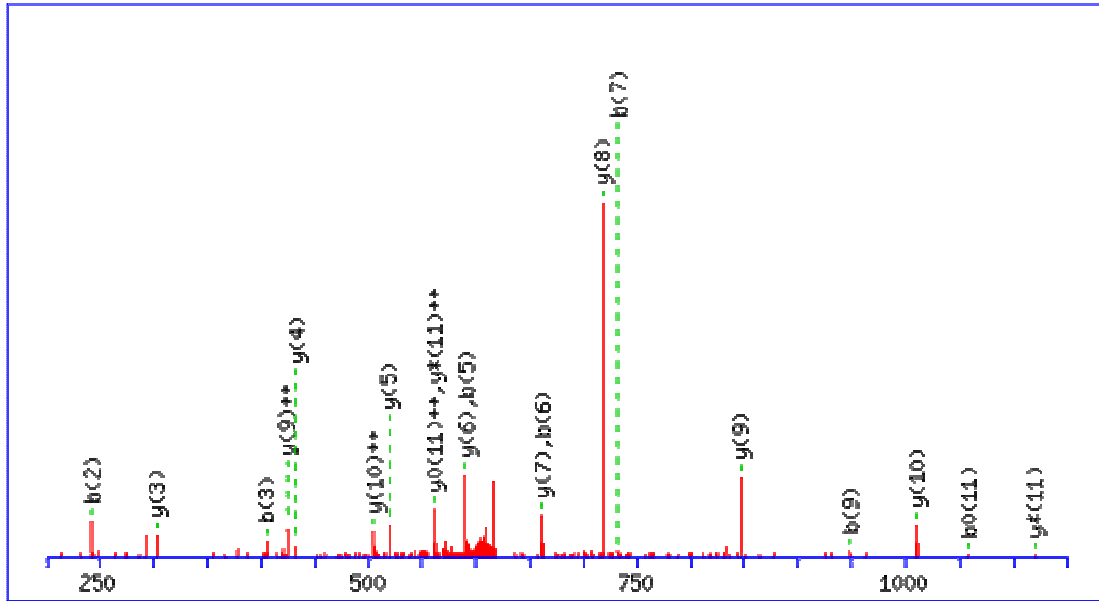
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.10	65.05	112.08	56.54			K							12
2	186.12	93.57	169.10	85.05			G	1186.65	593.83	1169.62	585.31	1168.64	584.82	11
3	299.21	150.11	282.18	141.59			L	1129.63	565.32	1112.60	556.80	1111.61	556.31	10
4	414.23	207.62	397.21	199.11	396.22	198.62	D	1016.54	508.77	999.51	500.26	998.53	499.77	9
5	511.29	256.15	494.26	247.63	493.28	247.14	P	901.51	451.26	884.49	442.75			8
6	674.35	337.68	657.32	329.17	656.34	328.67	Y	804.46	402.73	787.43	394.22			7
7	788.39	394.70	771.37	386.19	770.38	385.70	N	641.40	321.20	624.37	312.69			6
8	887.46	444.23	870.44	435.72	869.45	435.23	V	527.36	264.18	510.33	255.67			5
9	1000.55	500.78	983.52	492.26	982.54	491.77	L	428.29	214.65	411.26	206.13			4
10	1071.58	536.30	1054.56	527.78	1053.57	527.29	A	315.20	158.10	298.18	149.59			3
11	1168.64	584.82	1151.61	576.31	1150.63	575.82	P	244.17	122.59	227.14	114.07			2
12							K	147.11	74.06	130.09	65.55			1

Gene Symbol **Sequences** **m/z** **Charge** **Ion score** **Expect**
 DGKA WGGGYEGQNLAK 640.306 2+ 48 0.0018
 (IPI00333143 Diacylglycerol kinase alpha)



#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	187.09	94.05					W							12
2	244.11	122.56					G	1093.53	547.27	1076.50	538.75	1075.52	538.26	11
3	301.13	151.07					G	1036.51	518.76	1019.48	510.24	1018.50	509.75	10
4	358.15	179.58					G	979.48	490.25	962.46	481.73	961.47	481.24	9
5	521.21	261.11					Y	922.46	461.74	905.44	453.22	904.45	452.73	8
6	650.26	325.63			632.25	316.63	E	759.40	380.20	742.37	371.69	741.39	371.20	7
7	707.28	354.14			689.27	345.14	G	630.36	315.68	613.33	307.17			6
8	835.34	418.17	818.31	409.66	817.33	409.17	Q	573.34	287.17	556.31	278.66			5
9	949.38	475.19	932.35	466.68	931.37	466.19	N	445.28	223.14	428.25	214.63			4
10	1062.46	531.74	1045.44	523.22	1044.45	522.73	L	331.23	166.12	314.21	157.61			3
11	1133.50	567.25	1116.47	558.74	1115.49	558.25	A	218.15	109.58	201.12	101.07			2
12							K	147.11	74.06	130.09	65.55			1

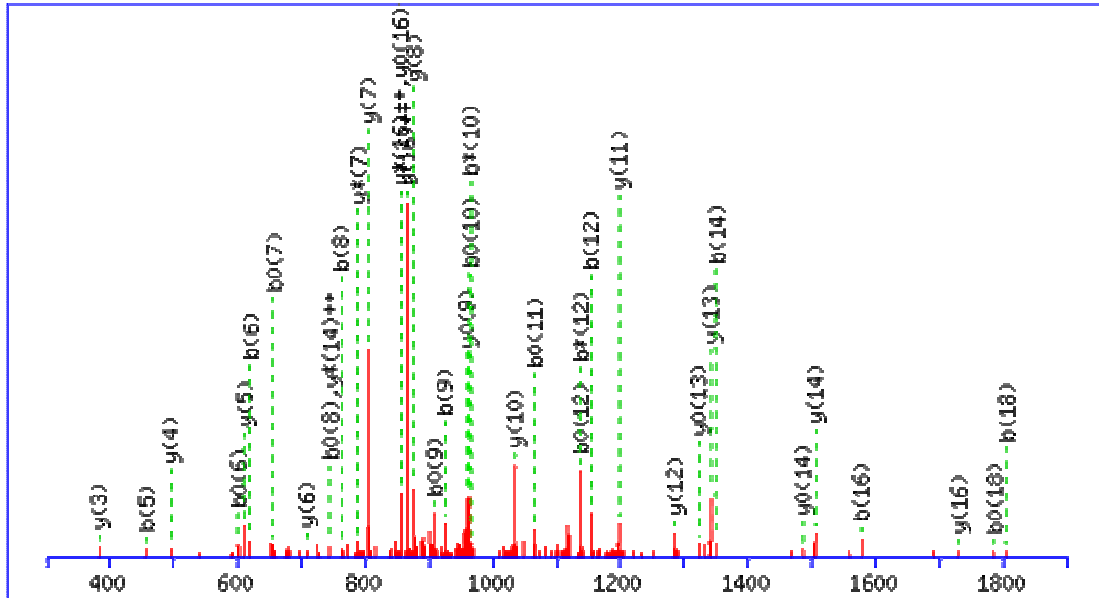
Gene Symbol Sequences m/z Charge Ion score Expect
 FAM50A AQYKGAASEAGR 625.812 2+ 60 0.00013
 (IPI00030098 Protein FAM50A)



N-term : N-Acetyl (Protein)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.05	57.53					A							12
2	242.11	121.56	225.09	113.05			Q	1137.56	569.29	1120.54	560.77	1119.55	560.28	11
3	405.18	203.09	388.15	194.58			Y	1009.51	505.26	992.48	496.74	991.50	496.25	10
4	533.27	267.14	516.25	258.63			K	846.44	423.73	829.42	415.21	828.43	414.72	9
5	590.29	295.65	573.27	287.14			G	718.35	359.68	701.32	351.16	700.34	350.67	8
6	661.33	331.17	644.30	322.66			A	661.33	331.17	644.30	322.65	643.32	322.16	7
7	732.37	366.69	715.34	358.17			A	590.29	295.65	573.26	287.13	572.28	286.64	6
8	819.40	410.20	802.37	401.69	801.39	401.20	S	519.25	260.13	502.23	251.62	501.24	251.12	5
9	948.44	474.72	931.42	466.21	930.43	465.72	E	432.22	216.61	415.19	208.10	414.21	207.61	4
10	1019.48	510.24	1002.45	501.73	1001.47	501.24	A	303.18	152.09	286.15	143.58			3
11	1076.50	538.75	1059.47	530.24	1058.49	529.75	G	232.14	116.57	215.11	108.06			2
12							R	175.12	88.06	158.09	79.55			1

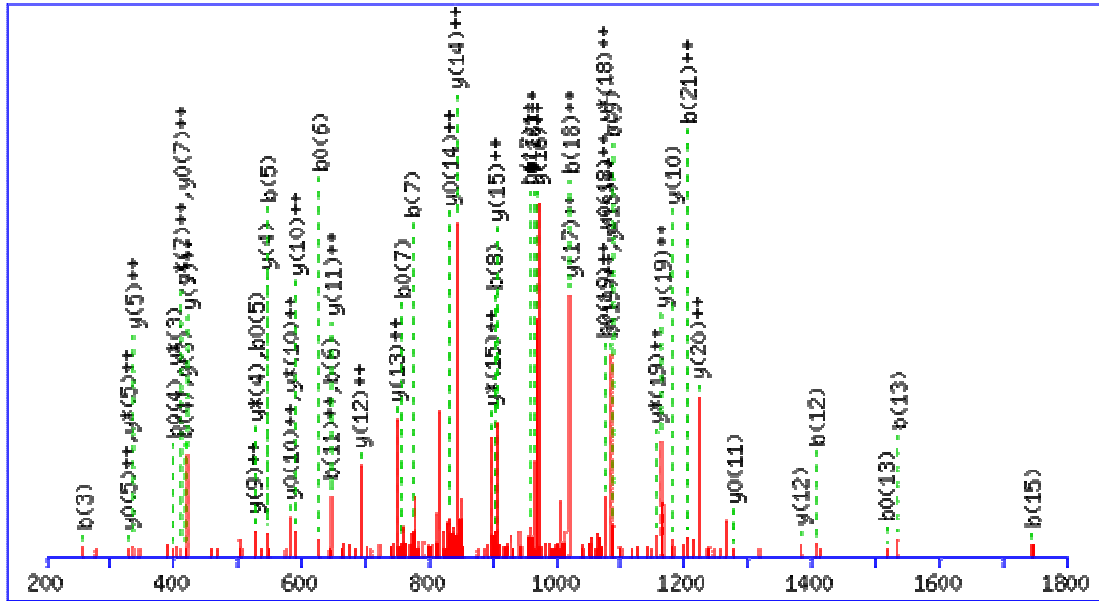
Gene Symbol Sequences m/z Charge Ion score Expect
 FIP1L1 TGAPQYGSYGTAPVNLNIK 980.008 2+ 79 1.7e-06
 (IPI00008449 Isoform 3 of Pre-mRNA 3'-end-processing factor FIP1)



K19: Lysine (K-full)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.05	51.53			84.04	42.53	T							19
2	159.08	80.04			141.07	71.04	G	1857.96	929.48	1840.93	920.97	1839.95	920.48	18
3	230.11	115.56			212.10	106.56	A	1800.94	900.97	1783.91	892.46	1782.93	891.97	17
4	327.17	164.09			309.16	155.08	P	1729.90	865.45	1712.87	856.94	1711.89	856.45	16
5	455.22	228.12	438.20	219.60	437.21	219.11	Q	1632.85	816.93	1615.82	808.41	1614.84	807.92	15
6	618.29	309.65	601.26	301.13	600.28	300.64	Y	1504.79	752.90	1487.76	744.38	1486.78	743.89	14
7	675.31	338.16	658.28	329.65	657.30	329.15	G	1341.73	671.37	1324.70	662.85	1323.71	662.36	13
8	762.34	381.67	745.32	373.16	744.33	372.67	S	1284.70	642.86	1267.68	634.34	1266.69	633.85	12
9	925.41	463.21	908.38	454.69	907.39	454.20	Y	1197.67	599.34	1180.65	590.83	1179.66	590.33	11
10	982.43	491.72	965.40	483.20	964.42	482.71	G	1034.61	517.81	1017.58	509.29	1016.60	508.80	10
11	1083.47	542.24	1066.45	533.73	1065.46	533.24	T	977.59	489.30	960.56	480.78	959.58	480.29	9
12	1154.51	577.76	1137.48	569.25	1136.50	568.75	A	876.54	438.77	859.51	430.26			8
13	1251.56	626.29	1234.54	617.77	1233.55	617.28	P	805.50	403.25	788.48	394.74			7
14	1350.63	675.82	1333.61	667.31	1332.62	666.81	V	708.45	354.73	691.42	346.22			6
15	1464.68	732.84	1447.65	724.33	1446.66	723.84	N	609.38	305.19	592.35	296.68			5
16	1577.76	789.38	1560.73	780.87	1559.75	780.38	L	495.34	248.17	478.31	239.66			4
17	1691.80	846.40	1674.78	837.89	1673.79	837.40	N	382.25	191.63	365.23	183.12			3
18	1804.89	902.95	1787.86	894.43	1786.88	893.94	I	268.21	134.61	251.18	126.10			2
19							K	155.13	78.07	138.10	69.55			1

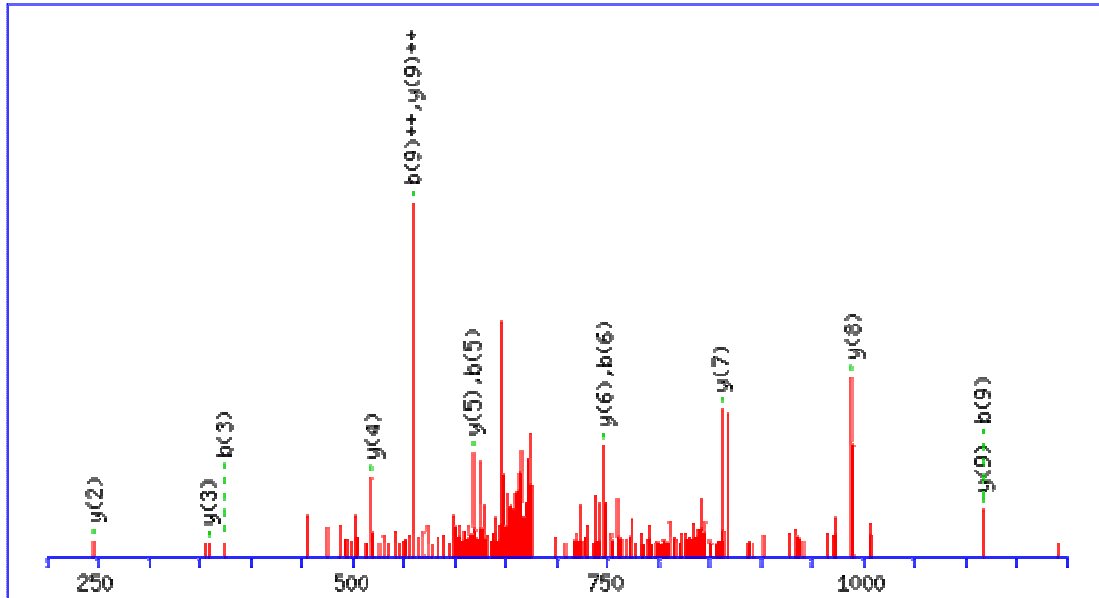
Gene Symbol Sequences m/z Charge Ion score Expect
 GRHPR AADCEVEQWDSDEPIPAKELER 863.060 3+ 84 4e-07
 (IPI00037448 Glyoxylate reductase/hydroxypyruvate reductase)



C4: Carbamidomethylated

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.04	36.53					A							22
2	143.08	72.04					A	2516.12	1258.57	2499.10	1250.05	2498.11	1249.56	21
3	258.11	129.56			240.10	120.55	D	2445.09	1223.05	2428.06	1214.53	2427.08	1214.04	20
4	418.14	209.57			400.13	200.57	C	2330.06	1165.53	2313.03	1157.02	2312.05	1156.53	19
5	547.18	274.09			529.17	265.09	E	2170.03	1085.52	2153.00	1077.01	2152.02	1076.51	18
6	646.25	323.63			628.24	314.62	V	2040.99	1021.00	2023.96	1012.48	2022.98	1011.99	17
7	775.29	388.15			757.28	379.14	E	1941.92	971.46	1924.89	962.95	1923.91	962.46	16
8	903.35	452.18	886.32	443.67	885.34	443.17	Q	1812.88	906.94	1795.85	898.43	1794.87	897.94	15
9	1089.43	545.22	1072.40	536.71	1071.42	536.21	W	1684.82	842.91	1667.79	834.40	1666.81	833.91	14
10	1204.46	602.73	1187.43	594.22	1186.45	593.73	D	1498.74	749.87	1481.71	741.36	1480.73	740.87	13
11	1291.49	646.25	1274.46	637.74	1273.48	637.24	S	1383.71	692.36	1366.68	683.85	1365.70	683.35	12
12	1406.52	703.76	1389.49	695.25	1388.51	694.76	D	1296.68	648.84	1279.65	640.33	1278.67	639.84	11
13	1535.56	768.28	1518.53	759.77	1517.55	759.28	E	1181.65	591.33	1164.63	582.82	1163.64	582.32	10
14	1632.61	816.81	1615.59	808.30	1614.60	807.80	P	1052.61	526.81	1035.58	518.30	1034.60	517.80	9
15	1745.70	873.35	1728.67	864.84	1727.69	864.35	I	955.56	478.28	938.53	469.77	937.55	469.28	8
16	1842.75	921.88	1825.72	913.36	1824.74	912.87	P	842.47	421.74	825.45	413.23	824.46	412.73	7
17	1913.79	957.40	1896.76	948.88	1895.78	948.39	A	745.42	373.21	728.39	364.70	727.41	364.21	6
18	2041.88	1021.44	2024.85	1012.93	2023.87	1012.44	K	674.38	337.70	657.36	329.18	656.37	328.69	5
19	2170.92	1085.97	2153.90	1077.45	2152.91	1076.96	E	546.29	273.65	529.26	265.13	528.28	264.64	4
20	2284.01	1142.51	2266.98	1133.99	2266.00	1133.50	L	417.25	209.13	400.22	200.61	399.24	200.12	3
21	2413.05	1207.03	2396.02	1198.52	2395.04	1198.02	E	304.16	152.58	287.13	144.07	286.15	143.58	2
22							R	175.12	88.06	158.09	79.55			1

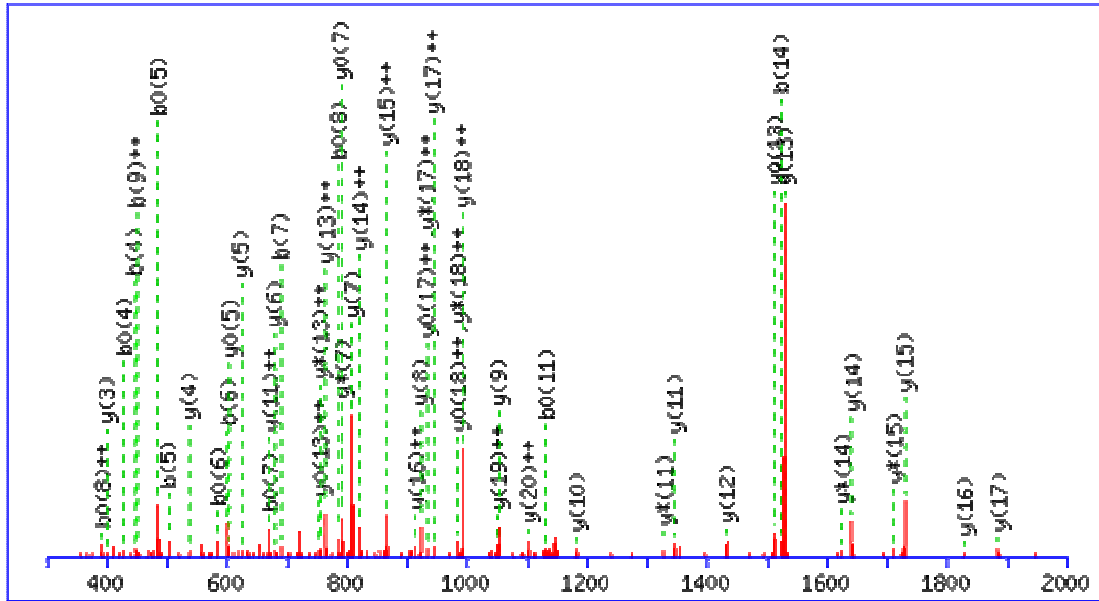
Gene Symbol Sequences m/z Charge Ion score Expect
 GSPT1 FVKQDQVCIAR 682.361 2+ 57 0.00027
 (IPI00218829 G1 to S phase transition protein 1 homolog)



C8: Carbamidomethylated

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.08	74.54					F							11
2	247.14	124.08					V	1216.65	608.83	1199.62	600.31	1198.64	599.82	10
3	375.24	188.12	358.21	179.61			K	1117.58	559.29	1100.55	550.78	1099.57	550.29	9
4	503.30	252.15	486.27	243.64			Q	989.48	495.25	972.46	486.73	971.47	486.24	8
5	618.32	309.67	601.30	301.15	600.31	300.66	D	861.42	431.22	844.40	422.70	843.41	422.21	7
6	746.38	373.70	729.36	365.18	728.37	364.69	Q	746.40	373.70	729.37	365.19			6
7	845.45	423.23	828.43	414.72	827.44	414.22	V	618.34	309.67	601.31	301.16			5
8	1005.48	503.24	988.46	494.73	987.47	494.24	C	519.27	260.14	502.24	251.63			4
9	1118.57	559.79	1101.54	551.27	1100.56	550.78	I	359.24	180.12	342.21	171.61			3
10	1189.60	595.31	1172.58	586.79	1171.59	586.30	A	246.16	123.58	229.13	115.07			2
11							R	175.12	88.06	158.09	79.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
 HIGD1A STDTGVSLPSYEEDQGSKLIR 1166.573 2+ 80 1.5e-06
 (IPI00295621 HIG1 domain family member 1A)

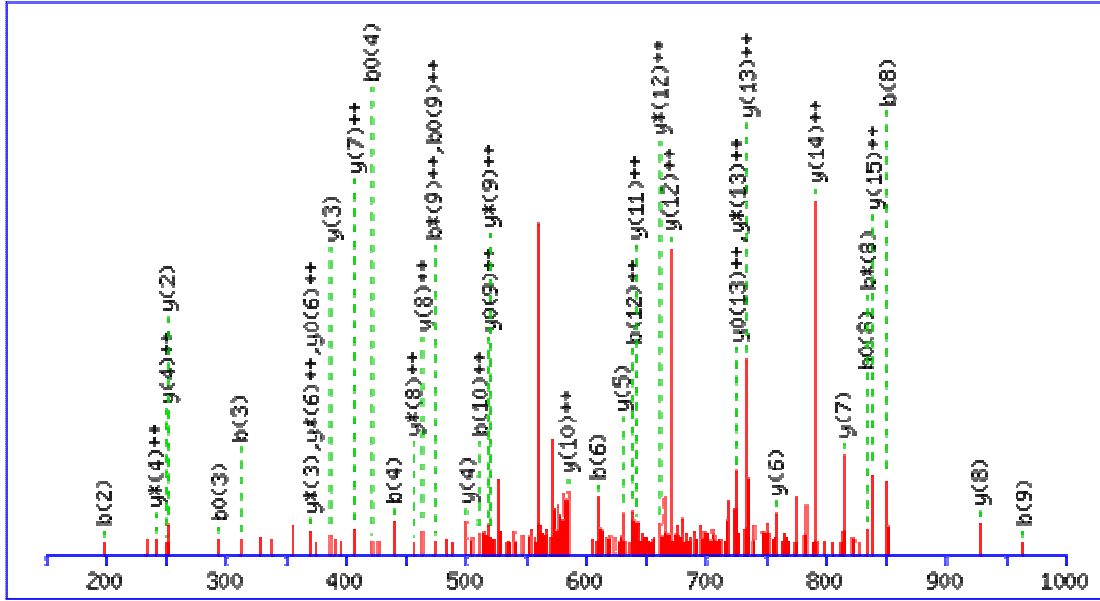


N-term : N-Acetyl (Protein)

K18: Lysine (K-full)

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	130.05	65.53			112.04	56.52	S							21
2	231.10	116.05			213.09	107.05	T	2203.10	1102.05	2186.07	1093.54	2185.09	1093.05	20
3	346.12	173.57			328.11	164.56	D	2102.05	1051.53	2085.02	1043.01	2084.04	1042.52	19
4	447.17	224.09			429.16	215.08	T	1987.02	994.01	1970.00	985.50	1969.01	985.01	18
5	504.19	252.60			486.18	243.60	G	1885.97	943.49	1868.95	934.98	1867.96	934.49	17
6	603.26	302.13			585.25	293.13	V	1828.95	914.98	1811.93	906.47	1810.94	905.97	16
7	690.29	345.65			672.28	336.65	S	1729.88	865.45	1712.86	856.93	1711.87	856.44	15
8	803.38	402.19			785.37	393.19	L	1642.85	821.93	1625.83	813.42	1624.84	812.92	14
9	900.43	450.72			882.42	441.71	P	1529.77	765.39	1512.74	756.87	1511.76	756.38	13
10	987.46	494.24			969.45	485.23	S	1432.72	716.86	1415.69	708.35	1414.71	707.86	12
11	1150.53	575.77			1132.52	566.76	Y	1345.68	673.35	1328.66	664.83	1327.67	664.34	11
12	1279.57	640.29			1261.56	631.28	E	1182.62	591.81	1165.59	583.30	1164.61	582.81	10
13	1408.61	704.81			1390.60	695.80	E	1053.58	527.29	1036.55	518.78	1035.57	518.29	9
14	1523.64	762.32			1505.63	753.32	D	924.54	462.77	907.51	454.26	906.52	453.77	8
15	1651.70	826.35	1634.67	817.84	1633.69	817.35	Q	809.51	405.26	792.48	396.74	791.50	396.25	7
16	1708.72	854.86	1691.69	846.35	1690.71	845.86	G	681.45	341.23	664.42	332.72	663.44	332.22	6
17	1795.75	898.38	1778.72	889.87	1777.74	889.37	S	624.43	312.72	607.40	304.20	606.42	303.71	5
18	1931.86	966.43	1914.83	957.92	1913.85	957.43	K	537.40	269.20	520.37	260.69			4
19	2044.94	1022.98	2027.92	1014.46	2026.93	1013.97	L	401.29	201.15	384.26	192.63			3
20	2158.03	1079.52	2141.00	1071.00	2140.02	1070.51	I	288.20	144.61	271.18	136.09			2
21							R	175.12	88.06	158.09	79.55			1

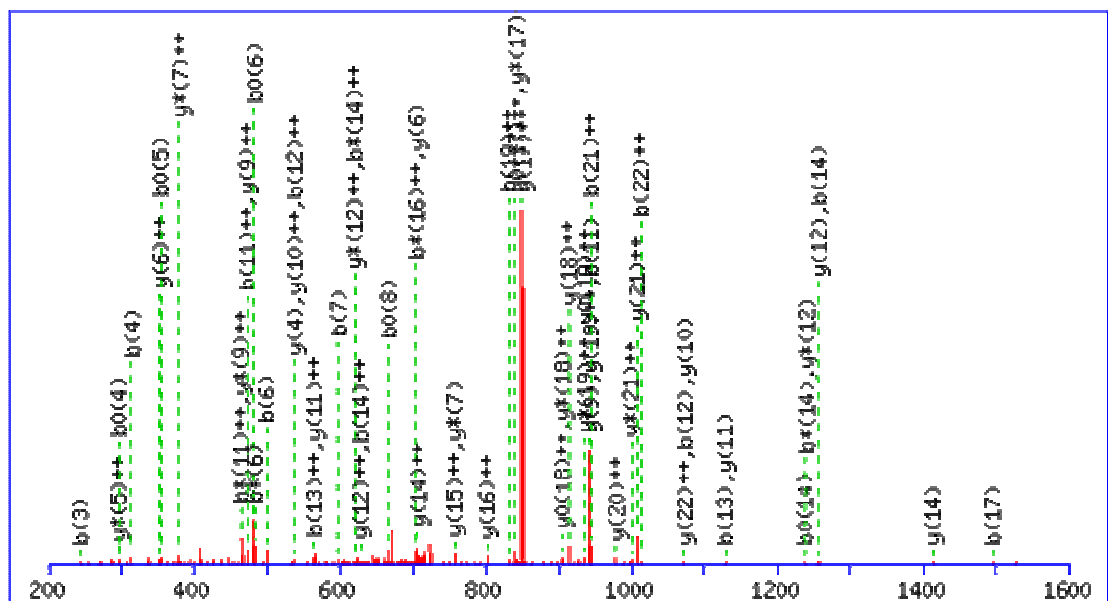
Gene Symbol Sequences m/z Charge Ion score Expect
 HIP1R TPLQGILQLGQELKPK 593.697 3+ 47 0.00015
 (IPI00024417 Huntingtin-interacting protein 1-related protein)



K14, K16: Lysine (K-full)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	102.05	51.53			84.04	42.53	T							16
2	199.11	100.06			181.10	91.05	P	1678.02	839.52	1661.00	831.00	1660.01	830.51	15
3	312.19	156.60			294.18	147.59	L	1580.97	790.99	1563.94	782.48	1562.96	781.98	14
4	440.25	220.63	423.22	212.12	422.24	211.62	Q	1467.89	734.45	1450.86	725.93	1449.88	725.44	13
5	497.27	249.14	480.25	240.63	479.26	240.13	G	1339.83	670.42	1322.80	661.90	1321.82	661.41	12
6	610.36	305.68	593.33	297.17	592.35	296.68	I	1282.81	641.91	1265.78	633.39	1264.80	632.90	11
7	723.44	362.22	706.41	353.71	705.43	353.22	L	1169.72	585.36	1152.70	576.85	1151.71	576.36	10
8	851.50	426.25	834.47	417.74	833.49	417.25	Q	1056.64	528.82	1039.61	520.31	1038.63	519.82	9
9	964.58	482.79	947.56	474.28	946.57	473.79	L	928.58	464.79	911.55	456.28	910.57	455.79	8
10	1021.60	511.31	1004.58	502.79	1003.59	502.30	G	815.50	408.25	798.47	399.74	797.49	399.25	7
11	1149.66	575.33	1132.64	566.82	1131.65	566.33	Q	758.47	379.74	741.45	371.23	740.46	370.74	6
12	1278.71	639.86	1261.68	631.34	1260.69	630.85	E	630.42	315.71	613.39	307.20	612.41	306.71	5
13	1391.79	696.40	1374.76	687.88	1373.78	687.39	L	501.37	251.19	484.35	242.68			4
14	1527.90	764.45	1510.87	755.94	1509.89	755.45	K	388.29	194.65	371.26	186.13			3
15	1624.95	812.98	1607.92	804.47	1606.94	803.97	P	252.18	126.59	235.15	118.08			2
16							K	155.13	78.07	138.10	69.55			1

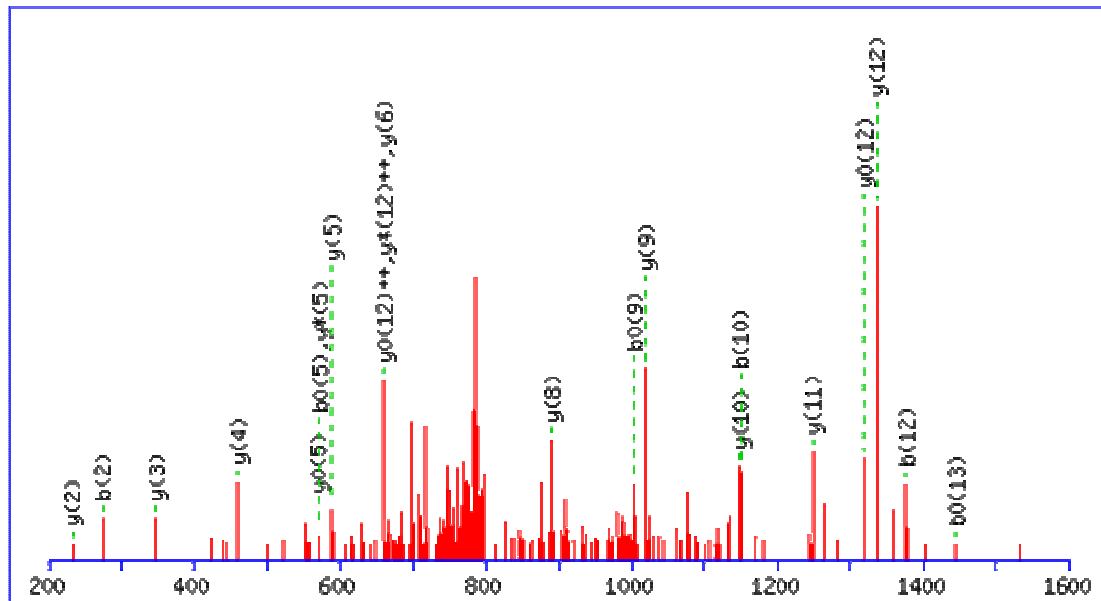
Gene Symbol Sequences m/z Charge Ion score Expect
HMGA2 GEGAGQPSTSAQGQPAAPAPQKR 733.707 3+ 73 7.8e-06
(IPI00005996 High mobility group protein HMGI-C)



K22: Lysine (K-full)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.03	29.52					G							23
2	187.07	94.04			169.06	85.03	E	2142.08	1071.54	2125.05	1063.03	2124.07	1062.54	22
3	244.09	122.55			226.08	113.54	G	2013.04	1007.02	1996.01	998.51	1995.02	998.02	21
4	315.13	158.07			297.12	149.06	A	1956.01	978.51	1938.99	970.00	1938.00	969.51	20
5	372.15	186.58			354.14	177.57	G	1884.98	942.99	1867.95	934.48	1866.97	933.99	19
6	500.21	250.61	483.18	242.10	482.20	241.60	Q	1827.96	914.48	1810.93	905.97	1809.94	905.48	18
7	597.26	299.13	580.24	290.62	579.25	290.13	P	1699.90	850.45	1682.87	841.94	1681.89	841.45	17
8	684.29	342.65	667.27	334.14	666.28	333.65	S	1602.84	801.93	1585.82	793.41	1584.83	792.92	16
9	785.34	393.17	768.32	384.66	767.33	384.17	T	1515.81	758.41	1498.79	749.90	1497.80	749.40	15
10	872.37	436.69	855.35	428.18	854.36	427.69	S	1414.76	707.89	1397.74	699.37	1396.75	698.88	14
11	943.41	472.21	926.38	463.70	925.40	463.20	A	1327.73	664.37	1310.71	655.86			13
12	1071.47	536.24	1054.44	527.73	1053.46	527.23	Q	1256.69	628.85	1239.67	620.34			12
13	1128.49	564.75	1111.47	556.24	1110.48	555.74	G	1128.64	564.82	1111.61	556.31			11
14	1256.55	628.78	1239.52	620.27	1238.54	619.77	Q	1071.61	536.31	1054.59	527.80			10
15	1353.60	677.31	1336.58	668.79	1335.59	668.30	P	943.56	472.28	926.53	463.77			9
16	1424.64	712.82	1407.61	704.31	1406.63	703.82	A	846.50	423.76	829.48	415.24			8
17	1495.68	748.34	1478.65	739.83	1477.67	739.34	A	775.47	388.24	758.44	379.72			7
18	1592.73	796.87	1575.70	788.36	1574.72	787.86	P	704.43	352.72	687.40	344.21			6
19	1663.77	832.39	1646.74	823.87	1645.76	823.38	A	607.38	304.19	590.35	295.68			5
20	1760.82	880.91	1743.79	872.40	1742.81	871.91	P	536.34	268.67	519.31	260.16			4
21	1888.88	944.94	1871.85	936.43	1870.87	935.94	Q	439.29	220.15	422.26	211.63			3
22	2024.99	1013.00	2007.96	1004.48	2006.98	1003.99	K	311.23	156.12	294.20	147.60			2
23							R	175.12	88.06	158.09	79.55			1

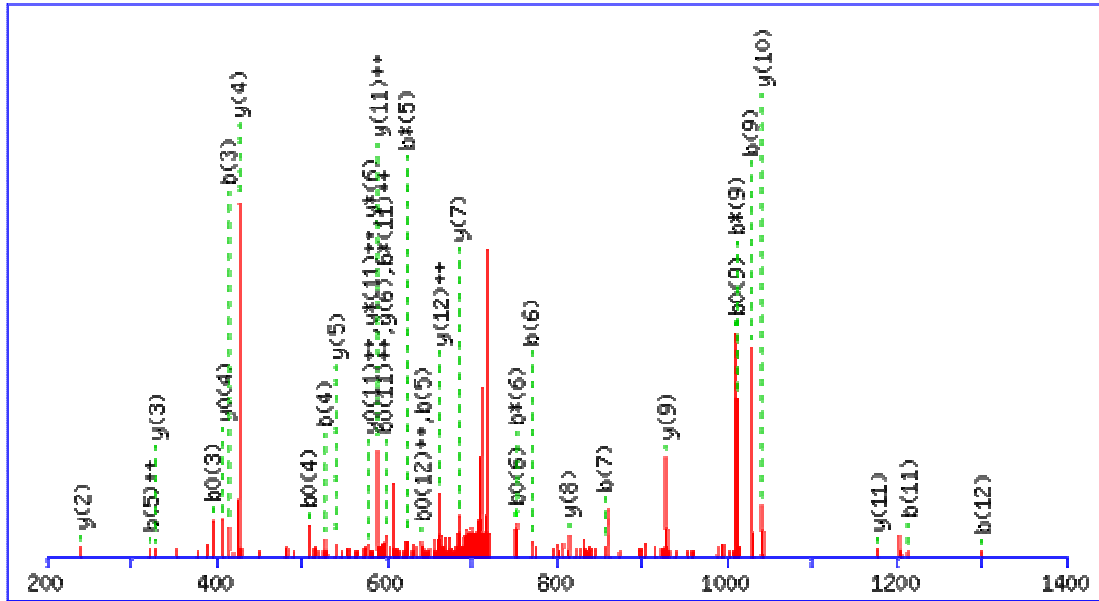
Gene Symbol Sequences m/z Charge Ion score Expect
 INPP1 LCSTEEETAELLSK 805.387 2+ 75 4.2e-06
 (IPI00027139 Inositol polyphosphate 1-phosphatase)



C2: Carbamidomethylated

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.09	57.55			L							14
2	274.12	137.56			C	1496.68	748.84	1479.65	740.33	1478.67	739.84	13
3	361.15	181.08	343.14	172.08	S	1336.65	668.83	1319.62	660.31	1318.64	659.82	12
4	462.20	231.60	444.19	222.60	T	1249.62	625.31	1232.59	616.80	1231.61	616.31	11
5	591.24	296.13	573.23	287.12	E	1148.57	574.79	1131.54	566.27	1130.56	565.78	10
6	720.29	360.65	702.28	351.64	E	1019.53	510.27	1002.50	501.75	1001.51	501.26	9
7	849.33	425.17	831.32	416.16	E	890.48	445.75	873.46	437.23	872.47	436.74	8
8	950.38	475.69	932.37	466.69	T	761.44	381.22	744.41	372.71	743.43	372.22	7
9	1021.41	511.21	1003.40	502.21	A	660.39	330.70	643.37	322.19	642.38	321.69	6
10	1150.46	575.73	1132.45	566.73	E	589.36	295.18	572.33	286.67	571.34	286.18	5
11	1263.54	632.27	1245.53	623.27	L	460.31	230.66	443.29	222.15	442.30	221.65	4
12	1376.62	688.82	1358.61	679.81	L	347.23	174.12	330.20	165.60	329.22	165.11	3
13	1463.66	732.33	1445.65	723.33	S	234.14	117.58	217.12	109.06	216.13	108.57	2
14					K	147.11	74.06	130.09	65.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
 LOC389217 EFHNLNESGNPSSK 727.838 2+ 58 0.00016
 (IPI00398010 similar to Protein SET)

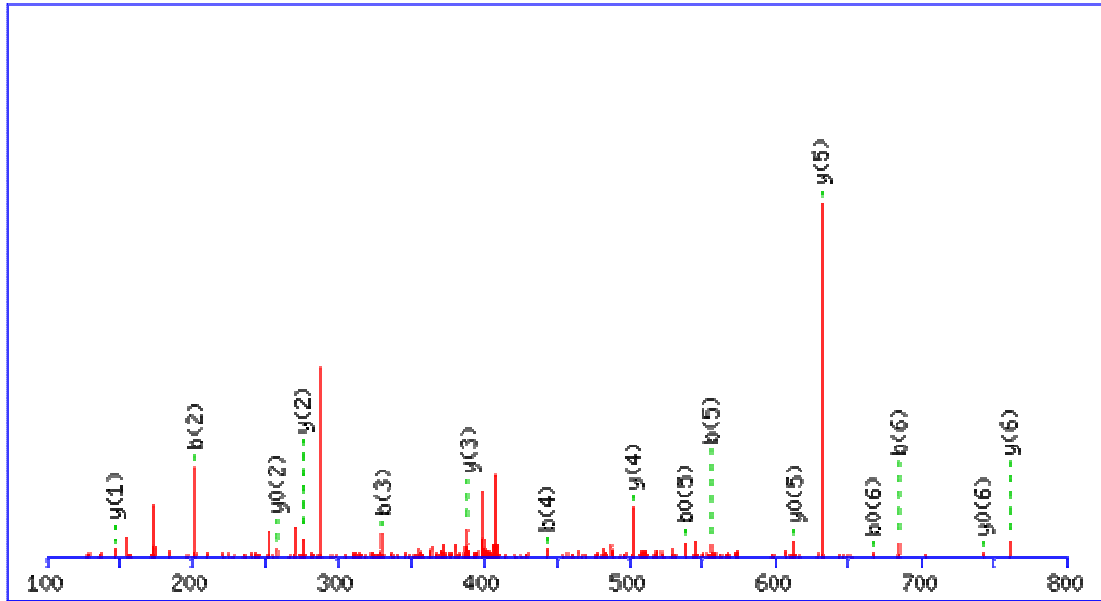


N9: Deamidation (NQ)

K13: Lysine (K-full)

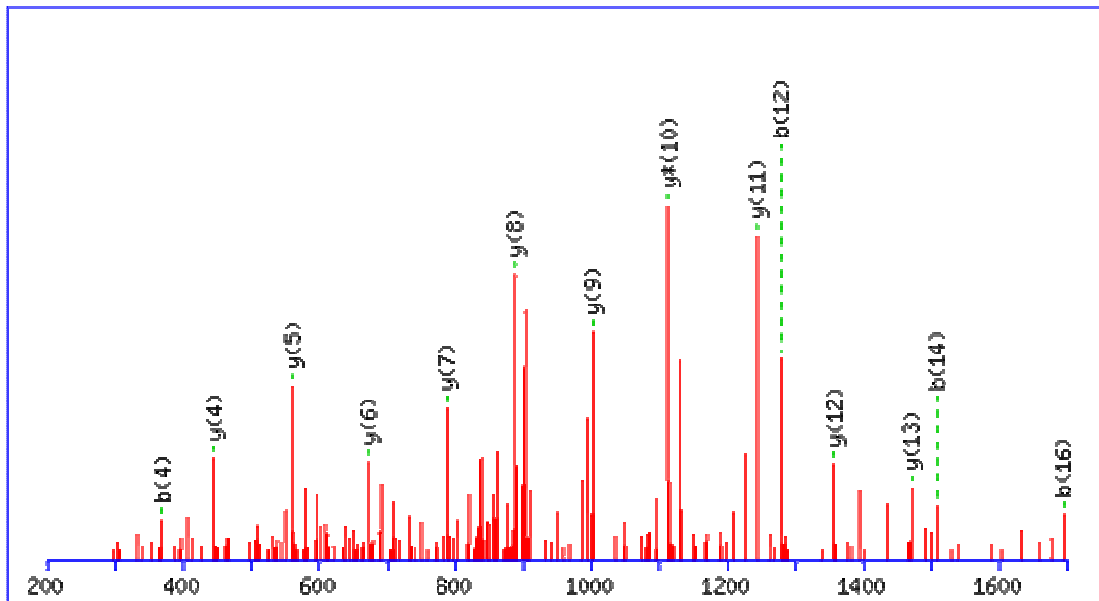
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.05	65.53			112.04	56.52	E							13
2	277.12	139.06			259.11	130.06	F	1325.62	663.31	1308.59	654.80	1307.61	654.31	12
3	414.18	207.59			396.17	198.59	H	1178.55	589.78	1161.53	581.27	1160.54	580.77	11
4	527.26	264.13			509.25	255.13	L	1041.49	521.25	1024.47	512.74	1023.48	512.25	10
5	641.30	321.16	624.28	312.64	623.29	312.15	N	928.41	464.71	911.38	456.20	910.40	455.70	9
6	770.35	385.68	753.32	377.16	752.34	376.67	E	814.37	407.69	797.34	399.17	796.36	398.68	8
7	857.38	429.19	840.35	420.68	839.37	420.19	S	685.32	343.17	668.30	334.65	667.31	334.16	7
8	914.40	457.70	897.37	449.19	896.39	448.70	G	598.29	299.65	581.27	291.14	580.28	290.64	6
9	1029.43	515.22	1012.40	506.70	1011.42	506.21	N	541.27	271.14	524.24	262.63	523.26	262.13	5
10	1126.48	563.74	1109.45	555.23	1108.47	554.74	P	426.24	213.63	409.22	205.11	408.23	204.62	4
11	1213.51	607.26	1196.49	598.75	1195.50	598.25	S	329.19	165.10	312.16	156.59	311.18	156.09	3
12	1300.54	650.78	1283.52	642.26	1282.53	641.77	S	242.16	121.58	225.13	113.07	224.15	112.58	2
13							K	155.13	78.07	138.10	69.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
 LOC645877 AEELIEK 416.227 2+ 41 0.014
 (IPI00161095 Uncharacterized protein ENSP00000267785)



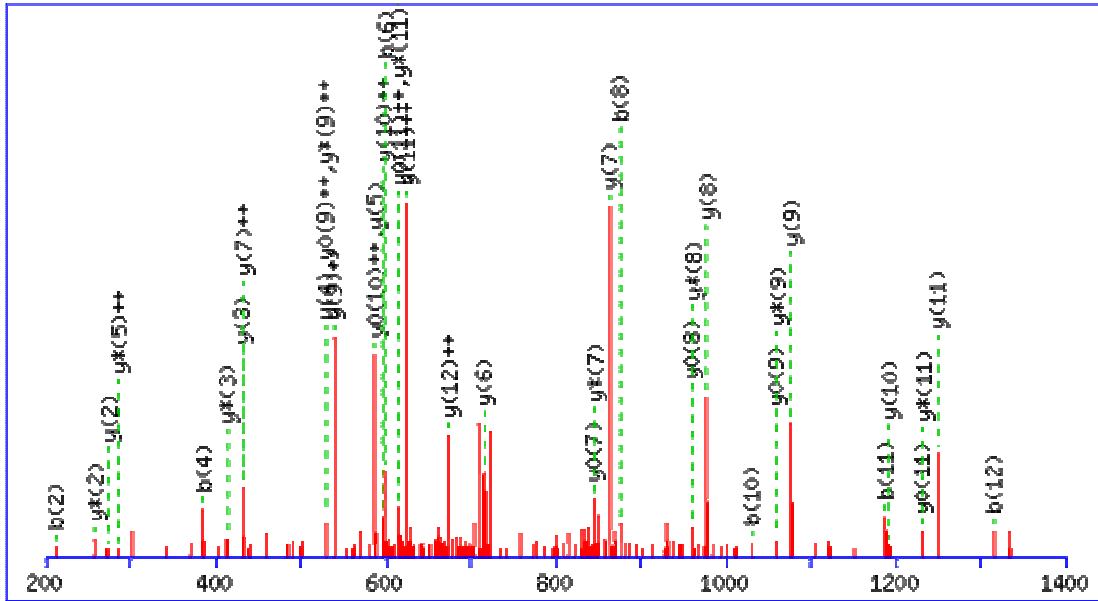
#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.04	36.53			A							7
2	201.09	101.05	183.08	92.04	E	760.41	380.71	743.38	372.19	742.40	371.70	6
3	330.13	165.57	312.12	156.56	E	631.37	316.19	614.34	307.67	613.36	307.18	5
4	443.21	222.11	425.20	213.11	L	502.32	251.67	485.30	243.15	484.31	242.66	4
5	556.30	278.65	538.29	269.65	I	389.24	195.12	372.21	186.61	371.23	186.12	3
6	685.34	343.17	667.33	334.17	E	276.16	138.58	259.13	130.07	258.14	129.58	2
7					K	147.11	74.06	130.09	65.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
 MED29 VAAQNLIQNTNIDNGQK 920.983 2+ 90 1.2e-07
 (IPI00032780 mediator complex subunit 29)



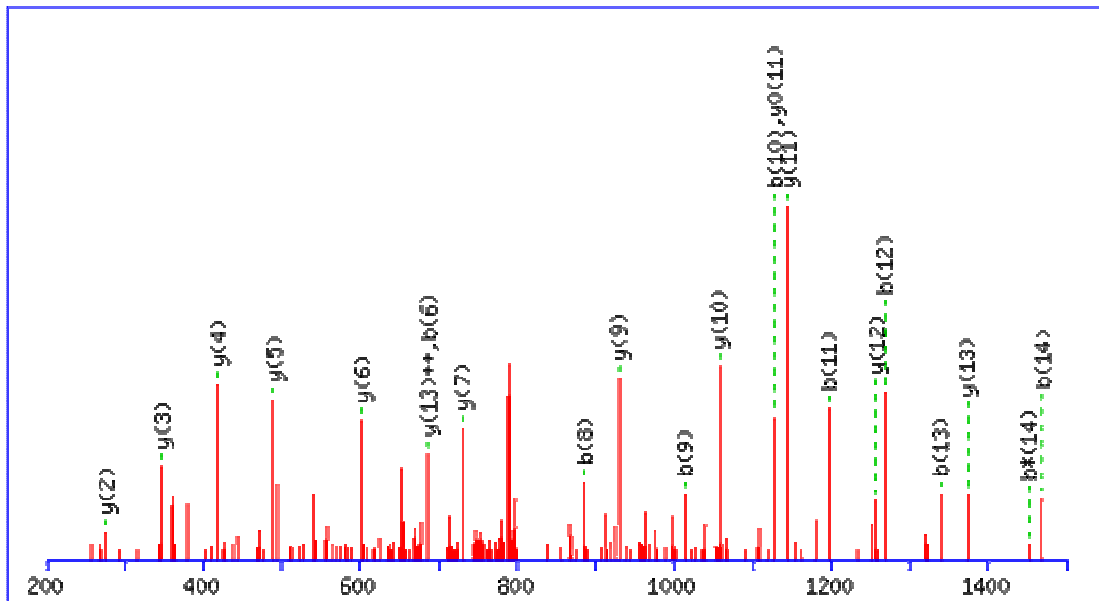
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.08	50.54					V							17
2	171.11	86.06					A	1741.88	871.45	1724.86	862.93	1723.87	862.44	16
3	242.15	121.58					A	1670.85	835.93	1653.82	827.41	1652.84	826.92	15
4	370.21	185.61	353.18	177.09			Q	1599.81	800.41	1582.78	791.89	1581.80	791.40	14
5	484.25	242.63	467.22	234.12			N	1471.75	736.38	1454.72	727.87	1453.74	727.37	13
6	597.34	299.17	580.31	290.66			L	1357.71	679.36	1340.68	670.84	1339.70	670.35	12
7	710.42	355.71	693.39	347.20			I	1244.62	622.82	1227.60	614.30	1226.61	613.81	11
8	838.48	419.74	821.45	411.23			Q	1131.54	566.27	1114.51	557.76	1113.53	557.27	10
9	952.52	476.76	935.49	468.25			N	1003.48	502.24	986.45	493.73	985.47	493.24	9
10	1053.57	527.29	1036.54	518.77	1035.56	518.28	T	889.44	445.22	872.41	436.71	871.43	436.22	8
11	1167.61	584.31	1150.59	575.80	1149.60	575.30	N	788.39	394.70	771.36	386.19	770.38	385.69	7
12	1280.70	640.85	1263.67	632.34	1262.69	631.85	I	674.35	337.68	657.32	329.16	656.34	328.67	6
13	1395.72	698.36	1378.70	689.85	1377.71	689.36	D	561.26	281.13	544.24	272.62	543.25	272.13	5
14	1509.77	755.39	1492.74	746.87	1491.76	746.38	N	446.24	223.62	429.21	215.11			4
15	1566.79	783.90	1549.76	775.38	1548.78	774.89	G	332.19	166.60	315.17	158.09			3
16	1694.85	847.93	1677.82	839.41	1676.84	838.92	Q	275.17	138.09	258.14	129.58			2
17							K	147.11	74.06	130.09	65.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
MTHFD2 LVGDVDFEGVRQK 731.392 2+ 58 0.0002
(IPI00011307 Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase)



#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.09	57.55					L							13
2	213.16	107.08					V	1348.69	674.85	1331.66	666.33	1330.67	665.84	12
3	270.18	135.59					G	1249.62	625.31	1232.59	616.80	1231.61	616.31	11
4	385.21	193.11			367.20	184.10	D	1192.60	596.80	1175.57	588.29	1174.59	587.80	10
5	484.28	242.64			466.27	233.64	V	1077.57	539.29	1060.54	530.77	1059.56	530.28	9
6	599.30	300.16			581.29	291.15	D	978.50	489.75	961.47	481.24	960.49	480.75	8
7	746.37	373.69			728.36	364.68	F	863.47	432.24	846.45	423.73	845.46	423.24	7
8	875.41	438.21			857.40	429.21	E	716.40	358.71	699.38	350.19	698.39	349.70	6
9	932.44	466.72			914.43	457.72	G	587.36	294.18	570.34	285.67			5
10	1031.50	516.26			1013.49	507.25	V	530.34	265.67	513.31	257.16			4
11	1187.61	594.31	1170.58	585.79	1169.59	585.30	R	431.27	216.14	414.25	207.63			3
12	1315.66	658.34	1298.64	649.82	1297.65	649.33	Q	275.17	138.09	258.14	129.58			2
13							K	147.11	74.06	130.09	65.55			1

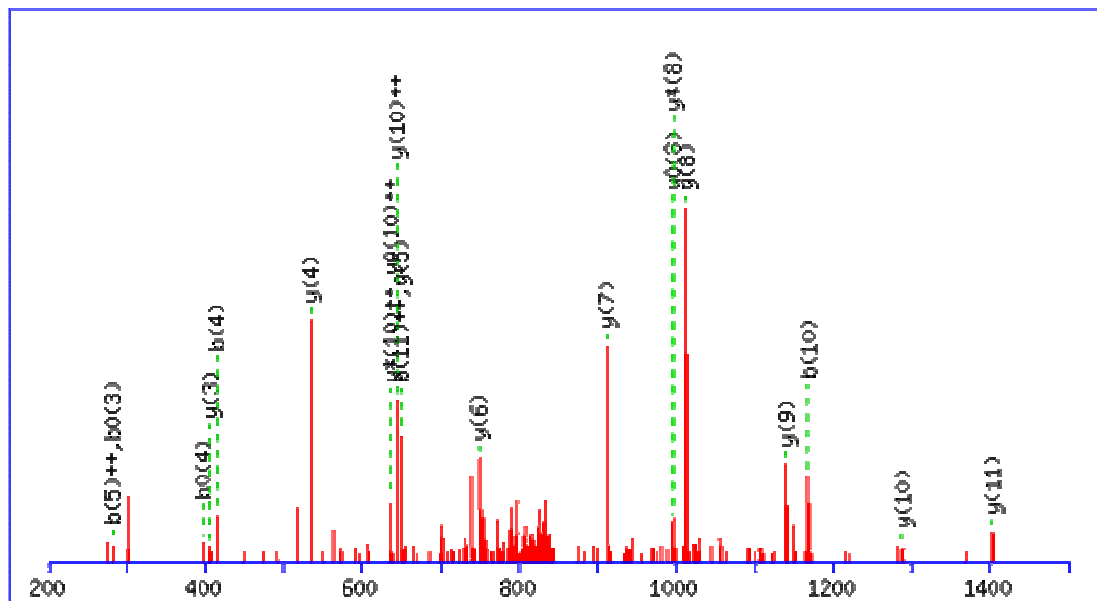
Gene Symbol Sequences m/z Charge Ion score Expect
 NACA2 IQDLSQQAQLAAAEK 807.923 2+ 105 5.1e-09
 (IPI00007471 Nascent polypeptide-associated complex subunit alpha-2)



Q2: Deamidation (NQ)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.09	57.55					I							15
2	243.13	122.07	226.11	113.56			Q	1501.75	751.38	1484.72	742.86	1483.74	742.37	14
3	358.16	179.58	341.13	171.07	340.15	170.58	D	1372.71	686.86	1355.68	678.34	1354.70	677.85	13
4	471.24	236.13	454.22	227.61	453.23	227.12	L	1257.68	629.34	1240.65	620.83	1239.67	620.34	12
5	558.28	279.64	541.25	271.13	540.27	270.64	S	1144.60	572.80	1127.57	564.29	1126.59	563.80	11
6	686.34	343.67	669.31	335.16	668.32	334.67	Q	1057.56	529.29	1040.54	520.77	1039.55	520.28	10
7	814.39	407.70	797.37	399.19	796.38	398.70	Q	929.51	465.26	912.48	456.74	911.49	456.25	9
8	885.43	443.22	868.40	434.71	867.42	434.21	A	801.45	401.23	784.42	392.71	783.44	392.22	8
9	1013.49	507.25	996.46	498.74	995.48	498.24	Q	730.41	365.71	713.38	357.20	712.40	356.70	7
10	1126.57	563.79	1109.55	555.28	1108.56	554.79	L	602.35	301.68	585.32	293.17	584.34	292.67	6
11	1197.61	599.31	1180.58	590.80	1179.60	590.30	A	489.27	245.14	472.24	236.62	471.26	236.13	5
12	1268.65	634.83	1251.62	626.31	1250.64	625.82	A	418.23	209.62	401.20	201.11	400.22	200.61	4
13	1339.69	670.35	1322.66	661.83	1321.67	661.34	A	347.19	174.10	330.17	165.59	329.18	165.09	3
14	1468.73	734.87	1451.70	726.35	1450.72	725.86	E	276.16	138.58	259.13	130.07	258.14	129.58	2
15							K	147.11	74.06	130.09	65.55			1

Gene Symbol **Sequences** **m/z** **Charge** **Ion score** **Expect**
 NXT1 ASVDFKTYVDQACR 851.400 2+ 46 0.0029
 (IPI00007605 NTF2-related export protein 1)

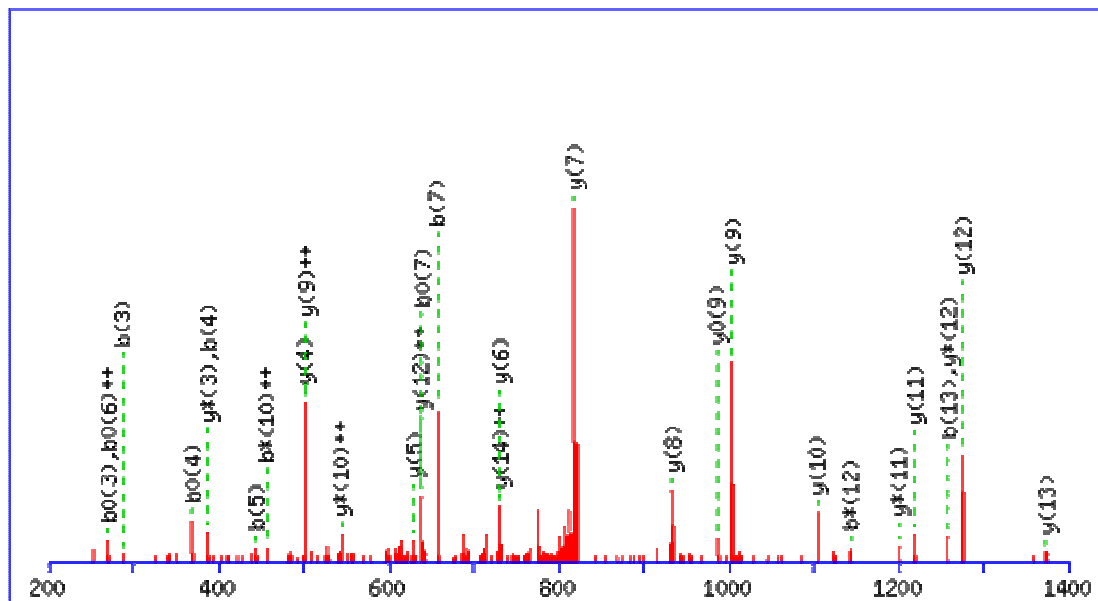


N-term : N-Acetyl (Protein)

C13: Carbamidomethylated

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.05	57.53					A							14
2	201.09	101.05			183.08	92.04	S	1588.74	794.87	1571.72	786.36	1570.73	785.87	13
3	300.16	150.58			282.14	141.58	V	1501.71	751.36	1484.68	742.85	1483.70	742.35	12
4	415.18	208.09			397.17	199.09	D	1402.64	701.82	1385.62	693.31	1384.63	692.82	11
5	562.25	281.63			544.24	272.62	F	1287.62	644.31	1270.59	635.80	1269.60	635.31	10
6	690.35	345.68	673.32	337.16	672.34	336.67	K	1140.55	570.78	1123.52	562.26	1122.54	561.77	9
7	791.39	396.20	774.37	387.69	773.38	387.20	T	1012.45	506.73	995.43	498.22	994.44	497.72	8
8	954.46	477.73	937.43	469.22	936.45	468.73	Y	911.40	456.21	894.38	447.69	893.39	447.20	7
9	1053.53	527.27	1036.50	518.75	1035.51	518.26	V	748.34	374.67	731.31	366.16	730.33	365.67	6
10	1168.55	584.78	1151.53	576.27	1150.54	575.77	D	649.27	325.14	632.25	316.63	631.26	316.13	5
11	1296.61	648.81	1279.58	640.30	1278.60	639.80	Q	534.25	267.63	517.22	259.11			4
12	1367.65	684.33	1350.62	675.81	1349.64	675.32	A	406.19	203.60	389.16	195.08			3
13	1527.68	764.34	1510.65	755.83	1509.67	755.34	C	335.15	168.08	318.12	159.57			2
14							R	175.12	88.06	158.09	79.55			1

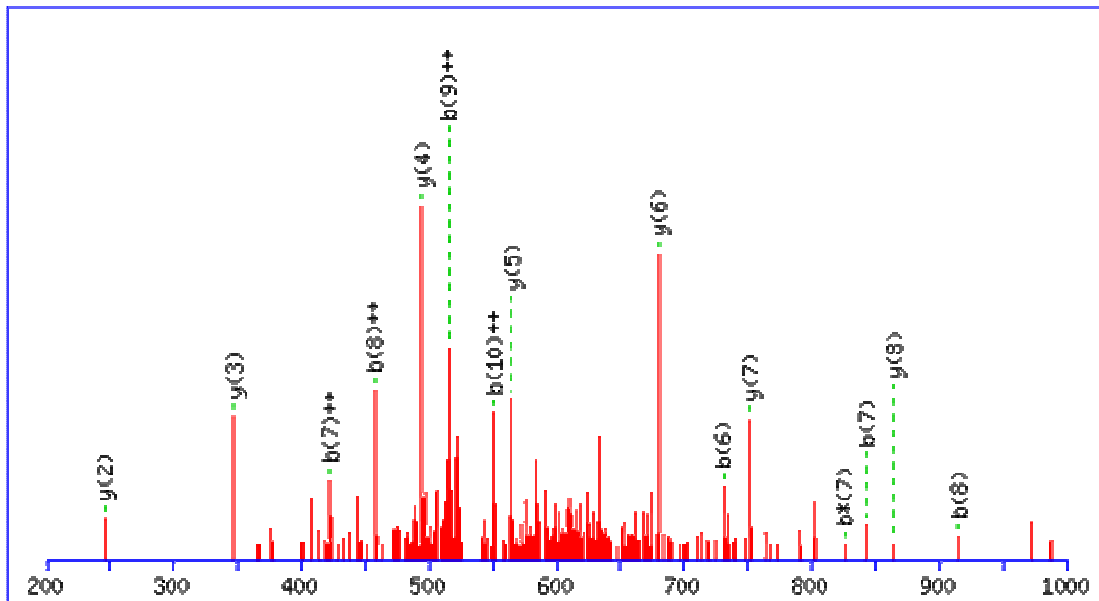
Gene Symbol **Sequences** **m/z** **Charge** **Ion score** **Expect**
 OGT ASSVGNVADSTEPTKR 830.912 2+ 76 4.3e-06
(IPI00005780 Isoform 3 of UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltrans)



N-term : N-Acetyl (Protein)

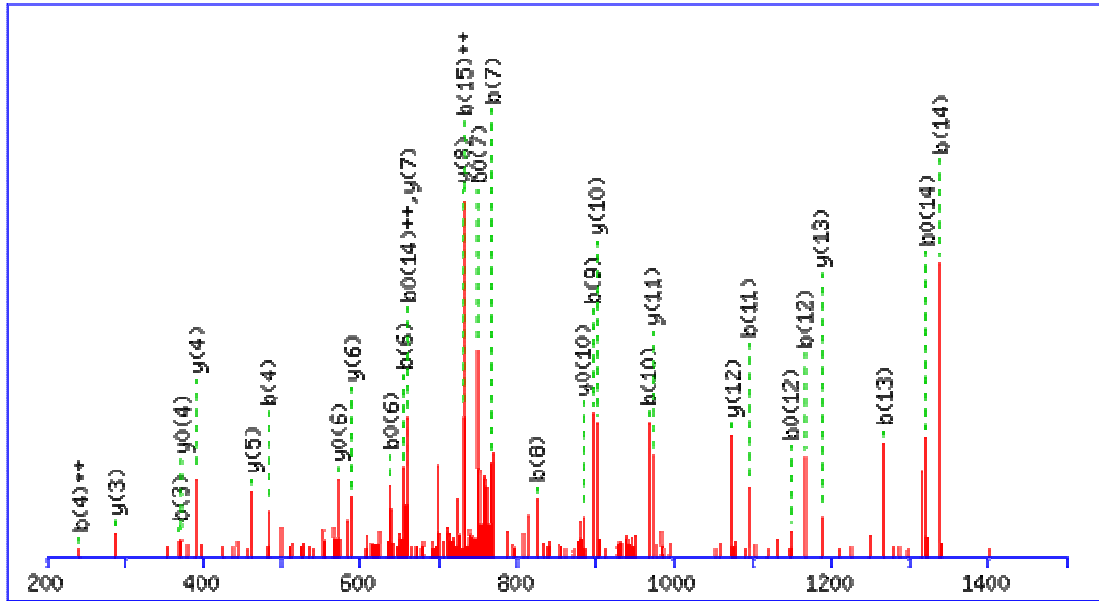
#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.05	57.53					A							16
2	201.09	101.05			183.08	92.04	S	1547.77	774.39	1530.74	765.87	1529.76	765.38	15
3	288.12	144.56			270.11	135.56	S	1460.73	730.87	1443.71	722.36	1442.72	721.87	14
4	387.19	194.10			369.18	185.09	V	1373.70	687.35	1356.68	678.84	1355.69	678.35	13
5	444.21	222.61			426.20	213.60	G	1274.63	637.82	1257.61	629.31	1256.62	628.82	12
6	558.25	279.63	541.23	271.12	540.24	270.62	N	1217.61	609.31	1200.59	600.80	1199.60	600.30	11
7	657.32	329.16	640.29	320.65	639.31	320.16	V	1103.57	552.29	1086.54	543.77	1085.56	543.28	10
8	728.36	364.68	711.33	356.17	710.35	355.68	A	1004.50	502.75	987.47	494.24	986.49	493.75	9
9	843.38	422.20	826.36	413.68	825.37	413.19	D	933.46	467.24	916.44	458.72	915.45	458.23	8
10	930.42	465.71	913.39	457.20	912.41	456.71	S	818.44	409.72	801.41	401.21	800.43	400.72	7
11	1031.46	516.24	1014.44	507.72	1013.45	507.23	T	731.40	366.21	714.38	357.69	713.39	357.20	6
12	1160.51	580.76	1143.48	572.24	1142.50	571.75	E	630.36	315.68	613.33	307.17	612.35	306.68	5
13	1257.56	629.28	1240.53	620.77	1239.55	620.28	P	501.31	251.16	484.29	242.65	483.30	242.16	4
14	1358.61	679.81	1341.58	671.29	1340.60	670.80	T	404.26	202.63	387.24	194.12	386.25	193.63	3
15	1486.70	743.85	1469.68	735.34	1468.69	734.85	K	303.21	152.11	286.19	143.60			2
16							R	175.12	88.06	158.09	79.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
PBLD MKLPIFIADAFTAR 531.968 3+ 55 0.00021
(IPI00024896 Phenazine biosynthesis-like domain-containing protein)



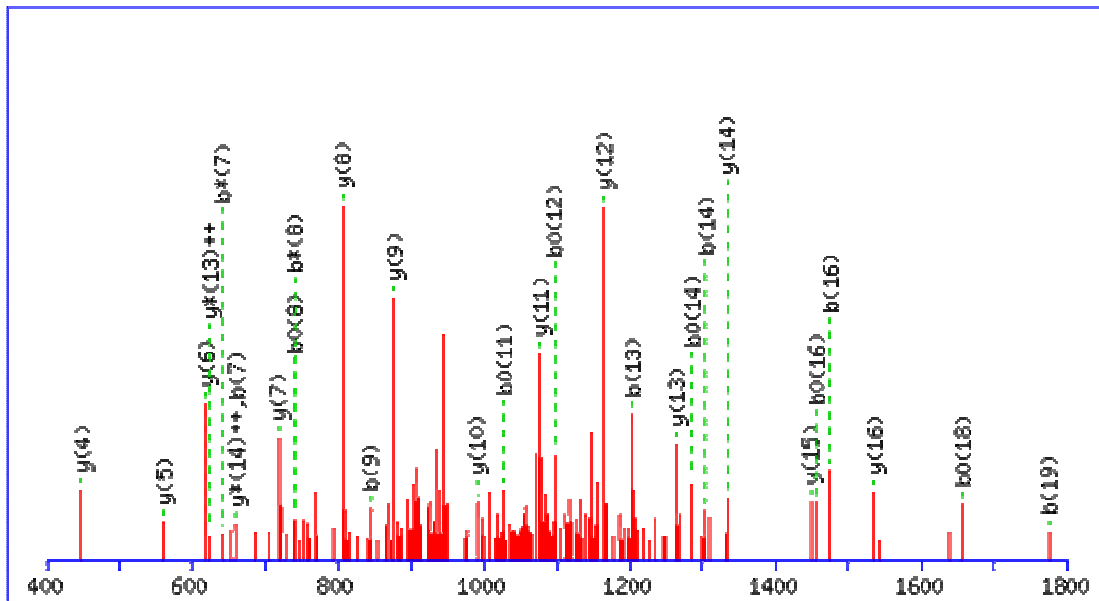
#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	132.05	66.53					M							14
2	260.14	130.57	243.12	122.06			K	1462.84	731.92	1445.82	723.41	1444.83	722.92	13
3	373.23	187.12	356.20	178.60			L	1334.75	667.88	1317.72	659.36	1316.74	658.87	12
4	470.28	235.64	453.25	227.13			P	1221.66	611.33	1204.64	602.82	1203.65	602.33	11
5	583.36	292.19	566.34	283.67			I	1124.61	562.81	1107.58	554.30	1106.60	553.80	10
6	730.43	365.72	713.41	357.21			F	1011.53	506.27	994.50	497.75	993.52	497.26	9
7	843.52	422.26	826.49	413.75			I	864.46	432.73	847.43	424.22	846.45	423.73	8
8	914.55	457.78	897.53	449.27			A	751.37	376.19	734.35	367.68	733.36	367.19	7
9	1029.58	515.29	1012.55	506.78	1011.57	506.29	D	680.34	340.67	663.31	332.16	662.33	331.67	6
10	1100.62	550.81	1083.59	542.30	1082.61	541.81	A	565.31	283.16	548.28	274.64	547.30	274.15	5
11	1247.69	624.35	1230.66	615.83	1229.68	615.34	F	494.27	247.64	477.25	239.13	476.26	238.63	4
12	1348.73	674.87	1331.71	666.36	1330.72	665.87	T	347.20	174.11	330.18	165.59	329.19	165.10	3
13	1419.77	710.39	1402.74	701.88	1401.76	701.38	A	246.16	123.58	229.13	115.07			2
14							R	175.12	88.06	158.09	79.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
 PFDN5 IQQLTALGAAQATAKA 778.445 2+ 105 1.7e-09
 (IPI00015361 Prefoldin subunit 5)



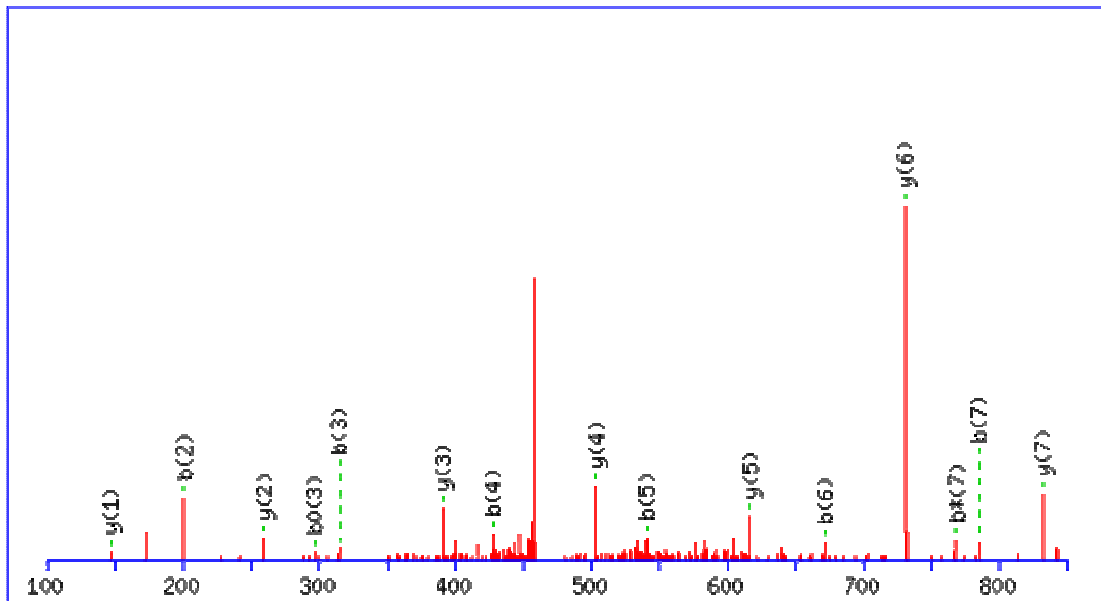
#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.09	57.55					I							16
2	242.15	121.58	225.12	113.07			Q	1442.80	721.90	1425.77	713.39	1424.79	712.90	15
3	370.21	185.61	353.18	177.09			Q	1314.74	657.87	1297.71	649.36	1296.73	648.87	14
4	483.29	242.15	466.27	233.64			L	1186.68	593.84	1169.65	585.33	1168.67	584.84	13
5	584.34	292.67	567.31	284.16	566.33	283.67	T	1073.59	537.30	1056.57	528.79	1055.58	528.30	12
6	655.38	328.19	638.35	319.68	637.37	319.19	A	972.55	486.78	955.52	478.26	954.54	477.77	11
7	768.46	384.73	751.43	376.22	750.45	375.73	L	901.51	451.26	884.48	442.75	883.50	442.25	10
8	825.48	413.25	808.46	404.73	807.47	404.24	G	788.43	394.72	771.40	386.20	770.42	385.71	9
9	896.52	448.76	879.49	440.25	878.51	439.76	A	731.40	366.21	714.38	357.69	713.39	357.20	8
10	967.56	484.28	950.53	475.77	949.55	475.28	A	660.37	330.69	643.34	322.17	642.36	321.68	7
11	1095.62	548.31	1078.59	539.80	1077.61	539.31	Q	589.33	295.17	572.30	286.66	571.32	286.16	6
12	1166.65	583.83	1149.63	575.32	1148.64	574.82	A	461.27	231.14	444.25	222.63	443.26	222.13	5
13	1267.70	634.35	1250.67	625.84	1249.69	625.35	T	390.23	195.62	373.21	187.11	372.22	186.62	4
14	1338.74	669.87	1321.71	661.36	1320.73	660.87	A	289.19	145.10	272.16	136.58			3
15	1466.83	733.92	1449.81	725.41	1448.82	724.91	K	218.15	109.58	201.12	101.07			2
16							A	90.05	45.53					1

Gene Symbol Sequences m/z Charge Ion score Expect
PICALM ATTLNAVSSLASTGLSLTK 961.535 2+ 99 6.8e-09
(IPI00216184 Isoform 2 of Phosphatidylinositol-binding clathrin assembly protein)



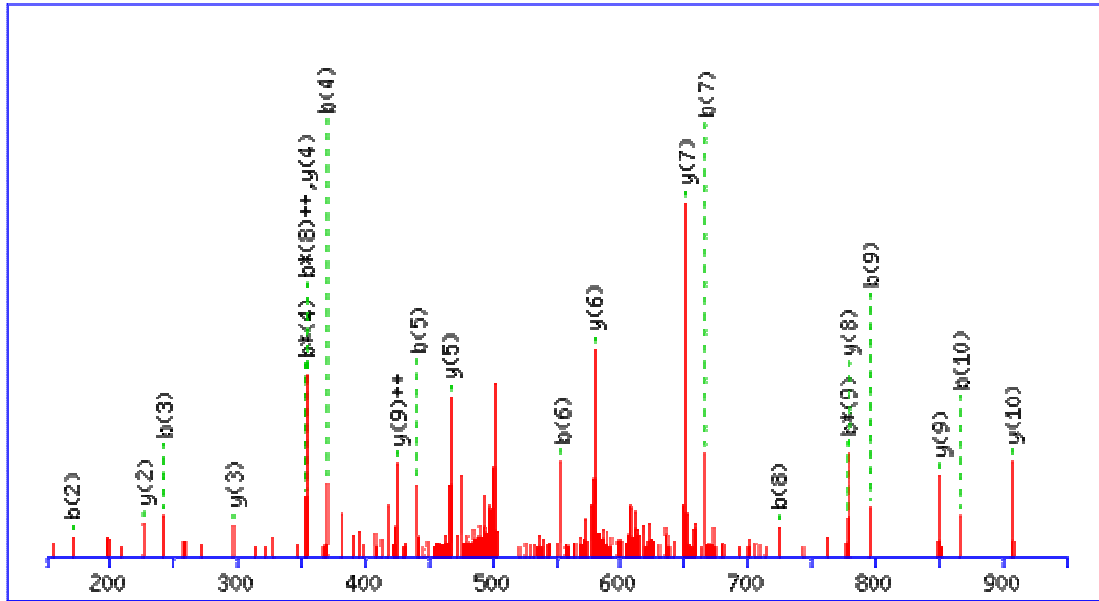
#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.04	36.53					A							20
2	173.09	87.05			155.08	78.04	T	1851.01	926.01	1833.98	917.49	1833.00	917.00	19
3	274.14	137.57			256.13	128.57	T	1749.96	875.48	1732.93	866.97	1731.95	866.48	18
4	387.22	194.12			369.21	185.11	L	1648.91	824.96	1631.89	816.45	1630.90	815.95	17
5	474.26	237.63			456.25	228.63	S	1535.83	768.42	1518.80	759.90	1517.82	759.41	16
6	588.30	294.65	571.27	286.14	570.29	285.65	N	1448.80	724.90	1431.77	716.39	1430.78	715.90	15
7	659.34	330.17	642.31	321.66	641.33	321.17	A	1334.75	667.88	1317.73	659.37	1316.74	658.87	14
8	758.40	379.71	741.38	371.19	740.39	370.70	V	1263.72	632.36	1246.69	623.85	1245.70	623.36	13
9	845.44	423.22	828.41	414.71	827.43	414.22	S	1164.65	582.83	1147.62	574.31	1146.64	573.82	12
10	932.47	466.74	915.44	458.22	914.46	457.73	S	1077.62	539.31	1060.59	530.80	1059.60	530.31	11
11	1045.55	523.28	1028.53	514.77	1027.54	514.27	L	990.58	495.80	973.56	487.28	972.57	486.79	10
12	1116.59	558.80	1099.56	550.29	1098.58	549.79	A	877.50	439.25	860.47	430.74	859.49	430.25	9
13	1203.62	602.31	1186.59	593.80	1185.61	593.31	S	806.46	403.73	789.44	395.22	788.45	394.73	8
14	1304.67	652.84	1287.64	644.32	1286.66	643.83	T	719.43	360.22	702.40	351.71	701.42	351.21	7
15	1361.69	681.35	1344.66	672.84	1343.68	672.34	G	618.38	309.69	601.36	301.18	600.37	300.69	6
16	1474.77	737.89	1457.75	729.38	1456.76	728.89	L	561.36	281.18	544.33	272.67	543.35	272.18	5
17	1561.81	781.41	1544.78	772.89	1543.80	772.40	S	448.28	224.64	431.25	216.13	430.27	215.64	4
18	1674.89	837.95	1657.86	829.44	1656.88	828.94	L	361.24	181.13	344.22	172.61	343.23	172.12	3
19	1775.94	888.47	1758.91	879.96	1757.93	879.47	T	248.16	124.58	231.13	116.07	230.15	115.58	2
20							K	147.11	74.06	130.09	65.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
 PTBP2 VTNILMLK 466.287 2+ 60 4.5e-05
 (IPI00254162 Isoform 3 of Polypyrimidine tract-binding protein 2)



#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.08	50.54					V							8
2	201.12	101.07			183.11	92.06	T	832.50	416.75	815.47	408.24	814.49	407.75	7
3	315.17	158.09	298.14	149.57	297.16	149.08	N	731.45	366.23	714.42	357.71			6
4	428.25	214.63	411.22	206.12	410.24	205.62	I	617.41	309.21	600.38	300.69			5
5	541.33	271.17	524.31	262.66	523.32	262.17	L	504.32	252.66	487.29	244.15			4
6	672.37	336.69	655.35	328.18	654.36	327.69	M	391.24	196.12	374.21	187.61			3
7	785.46	393.23	768.43	384.72	767.45	384.23	L	260.20	130.60	243.17	122.09			2
8							K	147.11	74.06	130.09	65.55			1

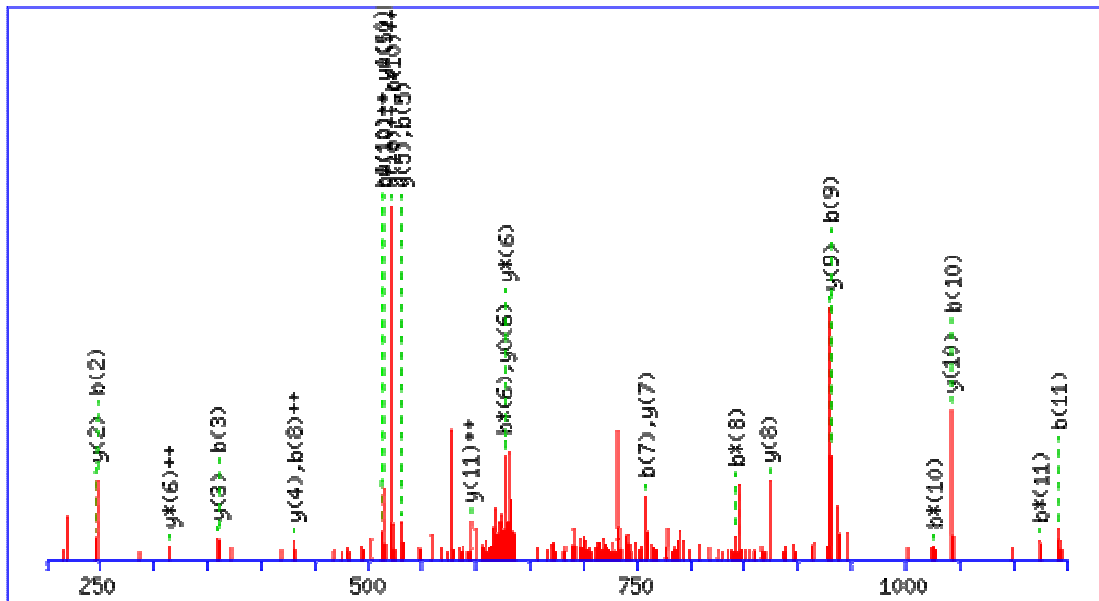
Gene Symbol Sequences m/z Charge Ion score Expect
 PYCR1 LGAQALLGAAK 510.820 2+ 94 9.4e-09
 (IPI00376503 pyrroline-5-carboxylate reductase 1 isoform 2)



K11: Lysine (K-full)

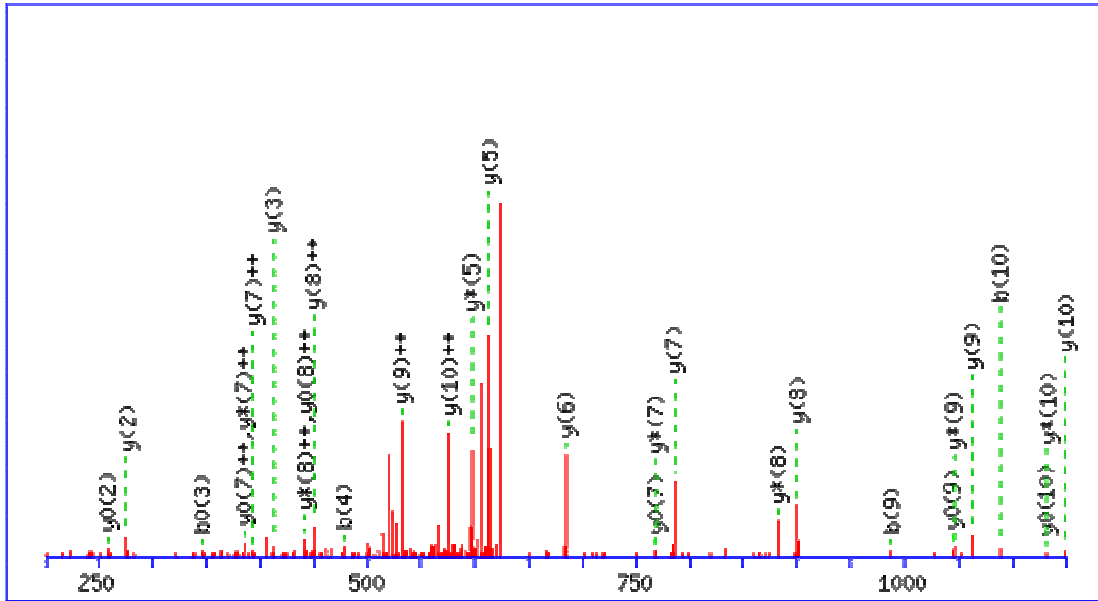
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	#
1	114.09	57.55			L					11
2	171.11	86.06			G	907.55	454.28	890.52	445.76	10
3	242.15	121.58			A	850.52	425.77	833.50	417.25	9
4	370.21	185.61	353.18	177.09	Q	779.49	390.25	762.46	381.73	8
5	441.25	221.13	424.22	212.61	A	651.43	326.22	634.40	317.70	7
6	554.33	277.67	537.30	269.16	L	580.39	290.70	563.36	282.19	6
7	667.41	334.21	650.39	325.70	L	467.31	234.16	450.28	225.64	5
8	724.44	362.72	707.41	354.21	G	354.22	177.61	337.20	169.10	4
9	795.47	398.24	778.45	389.73	A	297.20	149.10	280.17	140.59	3
10	866.51	433.76	849.48	425.25	A	226.16	113.59	209.14	105.07	2
11					K	155.13	78.07	138.10	69.55	1

Gene Symbol Sequences m/z Charge Ion score Expect
 RALYL VFIGNLNTAIVK 644.888 2+ 48 0.0005
 (IPI00166137 Isoform 1 of RNA-binding Raly-like protein)



#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.08	50.54					V							12
2	247.14	124.08					F	1189.69	595.35	1172.67	586.84	1171.68	586.35	11
3	360.23	180.62					I	1042.63	521.82	1025.60	513.30	1024.61	512.81	10
4	417.25	209.13					G	929.54	465.27	912.51	456.76	911.53	456.27	9
5	531.29	266.15	514.27	257.64			N	872.52	436.76	855.49	428.25	854.51	427.76	8
6	644.38	322.69	627.35	314.18			L	758.48	379.74	741.45	371.23	740.47	370.74	7
7	758.42	379.71	741.39	371.20			N	645.39	323.20	628.37	314.69	627.38	314.19	6
8	859.47	430.24	842.44	421.72	841.46	421.23	T	531.35	266.18	514.32	257.67	513.34	257.17	5
9	930.50	465.76	913.48	457.24	912.49	456.75	A	430.30	215.65	413.28	207.14			4
10	1043.59	522.30	1026.56	513.78	1025.58	513.29	I	359.27	180.14	342.24	171.62			3
11	1142.66	571.83	1125.63	563.32	1124.65	562.83	V	246.18	123.59	229.15	115.08			2
12							K	147.11	74.06	130.09	65.55			1

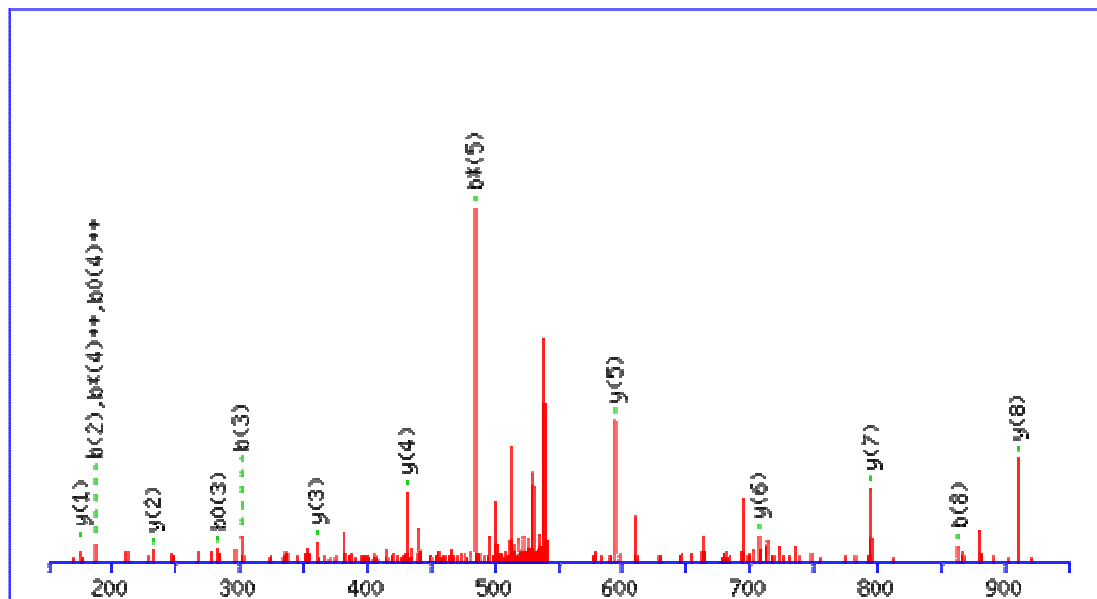
Gene Symbol Sequences m/z Charge Ion score Expect
RPL34 LSYNTASNKTR 631.835 2+ 54 0.00066
(IPI00219160 60S ribosomal protein L34)



K9: Lysine (K-full)

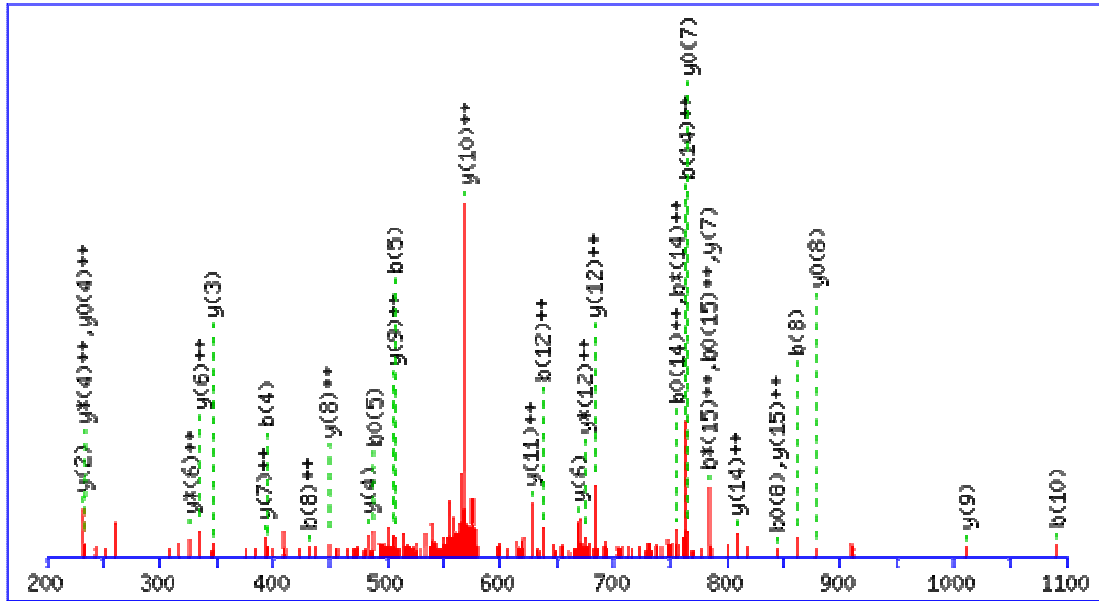
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.09	57.55					L							11
2	201.12	101.07			183.11	92.06	S	1149.57	575.29	1132.55	566.78	1131.56	566.29	10
3	364.19	182.60			346.18	173.59	Y	1062.54	531.77	1045.52	523.26	1044.53	522.77	9
4	478.23	239.62	461.20	231.11	460.22	230.61	N	899.48	450.24	882.45	441.73	881.47	441.24	8
5	579.28	290.14	562.25	281.63	561.27	281.14	T	785.44	393.22	768.41	384.71	767.42	384.22	7
6	650.31	325.66	633.29	317.15	632.30	316.66	A	684.39	342.70	667.36	334.18	666.38	333.69	6
7	737.35	369.18	720.32	360.66	719.34	360.17	S	613.35	307.18	596.32	298.67	595.34	298.17	5
8	851.39	426.20	834.36	417.69	833.38	417.19	N	526.32	263.66	509.29	255.15	508.31	254.66	4
9	987.50	494.25	970.47	485.74	969.49	485.25	K	412.28	206.64	395.25	198.13	394.27	197.64	3
10	1088.55	544.78	1071.52	536.26	1070.54	535.77	T	276.17	138.59	259.14	130.07	258.16	129.58	2
11							R	175.12	88.06	158.09	79.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
RPL36AL GKDSL~~Y~~AQGR 547.784 2+ 58 0.00019
(IPI00056494 60S ribosomal protein L36a-like)



#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.03	29.52					G							10
2	186.12	93.57	169.10	85.05			K	1037.54	519.27	1020.51	510.76	1019.53	510.27	9
3	301.15	151.08	284.12	142.57	283.14	142.07	D	909.44	455.22	892.42	446.71	891.43	446.22	8
4	388.18	194.59	371.16	186.08	370.17	185.59	S	794.42	397.71	777.39	389.20	776.40	388.71	7
5	501.27	251.14	484.24	242.62	483.26	242.13	L	707.38	354.20	690.36	345.68			6
6	664.33	332.67	647.30	324.16	646.32	323.66	Y	594.30	297.65	577.27	289.14			5
7	735.37	368.19	718.34	359.67	717.36	359.18	A	431.24	216.12	414.21	207.61			4
8	863.43	432.22	846.40	423.70	845.42	423.21	Q	360.20	180.60	343.17	172.09			3
9	920.45	460.73	903.42	452.21	902.44	451.72	G	232.14	116.57	215.11	108.06			2
10							R	175.12	88.06	158.09	79.55			1

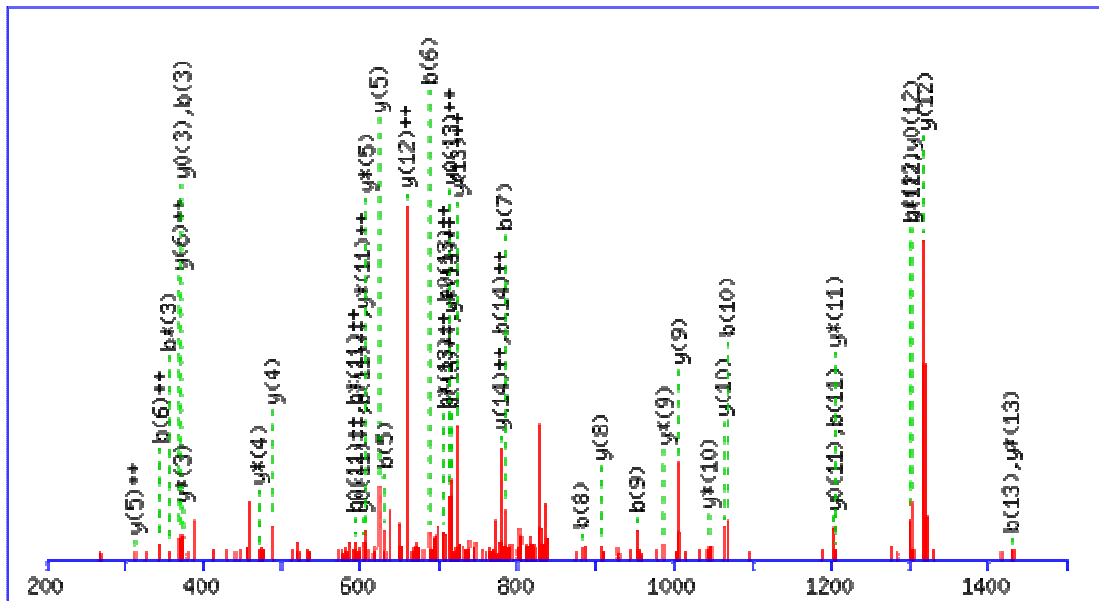
Gene Symbol Sequences m/z Charge Ion score Expect
 S100A16 AADKLIQNLDANHDGR 586.972 3+ 54 0.00054
 (IPI00062120 Protein S100-A16)



K4: Lysine (K-full)

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.04	36.53					A							16
2	143.08	72.04					A	1687.86	844.43	1670.83	835.92	1669.85	835.43	15
3	258.11	129.56			240.10	120.55	D	1616.82	808.92	1599.80	800.40	1598.81	799.91	14
4	394.22	197.61	377.19	189.10	376.21	188.61	K	1501.80	751.40	1484.77	742.89	1483.79	742.40	13
5	507.30	254.15	490.28	245.64	489.29	245.15	L	1365.69	683.35	1348.66	674.83	1347.68	674.34	12
6	620.39	310.70	603.36	302.18	602.38	301.69	I	1252.60	626.81	1235.58	618.29	1234.59	617.80	11
7	748.44	374.73	731.42	366.21	730.43	365.72	Q	1139.52	570.26	1122.49	561.75	1121.51	561.26	10
8	862.49	431.75	845.46	423.23	844.48	422.74	N	1011.46	506.23	994.43	497.72	993.45	497.23	9
9	975.57	488.29	958.54	479.78	957.56	479.28	L	897.42	449.21	880.39	440.70	879.41	440.21	8
10	1090.60	545.80	1073.57	537.29	1072.59	536.80	D	784.33	392.67	767.31	384.16	766.32	383.66	7
11	1161.64	581.32	1144.61	572.81	1143.62	572.32	A	669.31	335.16	652.28	326.64	651.30	326.15	6
12	1275.68	638.34	1258.65	629.83	1257.67	629.34	N	598.27	299.64	581.24	291.12	580.26	290.63	5
13	1412.74	706.87	1395.71	698.36	1394.73	697.87	H	484.23	242.62	467.20	234.10	466.22	233.61	4
14	1527.76	764.39	1510.74	755.87	1509.75	755.38	D	347.17	174.09	330.14	165.57	329.16	165.08	3
15	1584.79	792.90	1567.76	784.38	1566.78	783.89	G	232.14	116.57	215.11	108.06			2
16							R	175.12	88.06	158.09	79.55			1

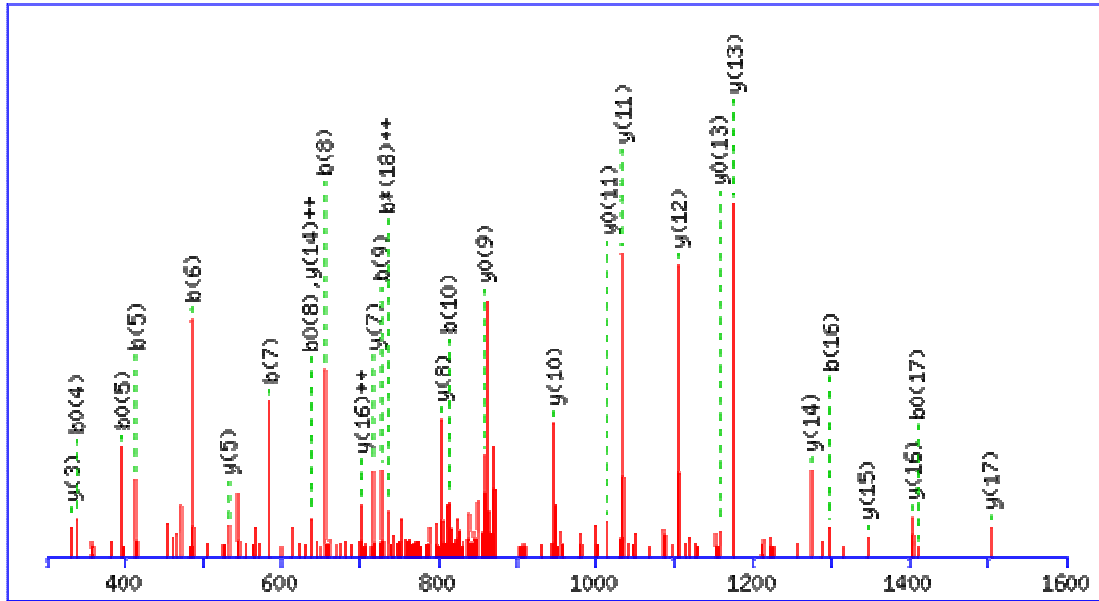
Gene Symbol Sequences m/z Charge Ion score Expect
 SF3B5 MLQPCGPPADKPEEN 845.884 2+ 46 0.0019
 (IPI00010404 Splicing factor 3B subunit 5)



C5: Carbamidomethylated
 K11: Lysine (K-full)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	132.05	66.53					M							15
2	245.13	123.07					L	1559.72	780.37	1542.70	771.85	1541.71	771.36	14
3	373.19	187.10	356.16	178.59			Q	1446.64	723.82	1429.61	715.31	1428.63	714.82	13
4	470.24	235.63	453.22	227.11			P	1318.58	659.79	1301.56	651.28	1300.57	650.79	12
5	630.27	315.64	613.25	307.13			C	1221.53	611.27	1204.50	602.76	1203.52	602.26	11
6	687.30	344.15	670.27	335.64			G	1061.50	531.25	1044.47	522.74	1043.49	522.25	10
7	784.35	392.68	767.32	384.16			P	1004.48	502.74	987.45	494.23	986.47	493.74	9
8	881.40	441.20	864.37	432.69			P	907.42	454.22	890.40	445.70	889.41	445.21	8
9	952.44	476.72	935.41	468.21			A	810.37	405.69	793.35	397.18	792.36	396.68	7
10	1067.46	534.24	1050.44	525.72	1049.45	525.23	D	739.33	370.17	722.31	361.66	721.32	361.17	6
11	1203.57	602.29	1186.55	593.78	1185.56	593.29	K	624.31	312.66	607.28	304.14	606.30	303.65	5
12	1300.63	650.82	1283.60	642.30	1282.62	641.81	P	488.20	244.60	471.17	236.09	470.19	235.60	4
13	1429.67	715.34	1412.64	706.83	1411.66	706.33	E	391.15	196.08	374.12	187.56	373.14	187.07	3
14	1558.71	779.86	1541.69	771.35	1540.70	770.85	E	262.10	131.56	245.08	123.04	244.09	122.55	2
15							N	133.06	67.03	116.03	58.52			1

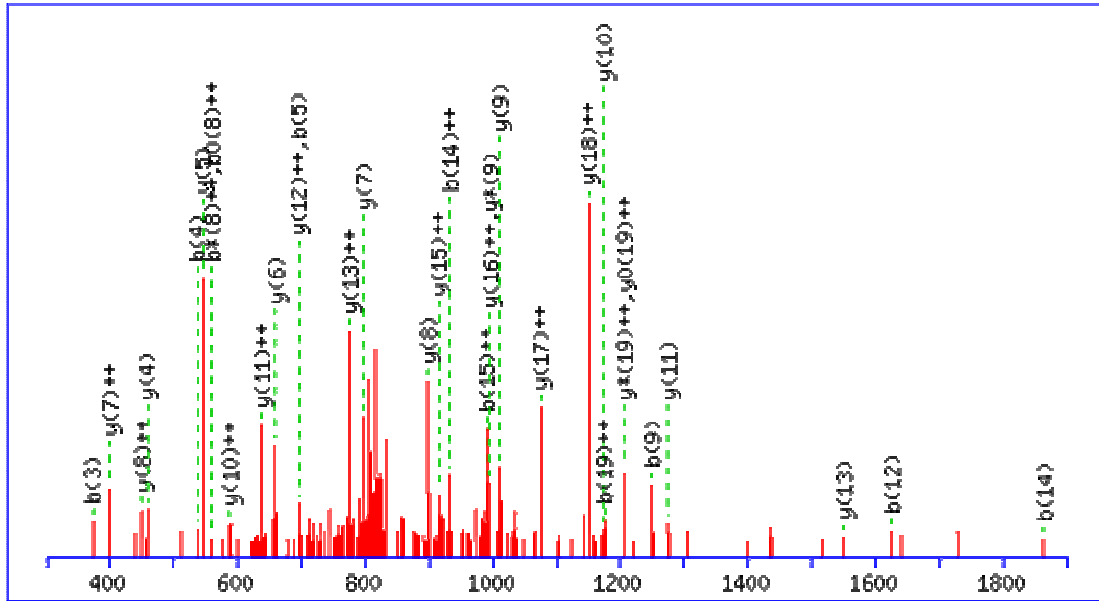
Gene Symbol Sequences m/z Charge Ion score Expect
 SLTM AAATGAVAASAASGQAEK 879.957 2+ 80 1.5e-06
 (IPI00019996 modulator of estrogen induced transcription isoform b)



N-term : N-Acetyl (Protein)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.05	57.53					A							20
2	185.09	93.05					A	1645.85	823.43	1628.82	814.92	1627.84	814.42	19
3	256.13	128.57					A	1574.81	787.91	1557.79	779.40	1556.80	778.90	18
4	357.18	179.09			339.17	170.09	T	1503.78	752.39	1486.75	743.88	1485.77	743.39	17
5	414.20	207.60			396.19	198.60	G	1402.73	701.87	1385.70	693.35	1384.72	692.86	16
6	485.24	243.12			467.22	234.12	A	1345.71	673.36	1328.68	664.84	1327.70	664.35	15
7	584.30	292.66			566.29	283.65	V	1274.67	637.84	1257.64	629.33	1256.66	628.83	14
8	655.34	328.17			637.33	319.17	A	1175.60	588.30	1158.57	579.79	1157.59	579.30	13
9	726.38	363.69			708.37	354.69	A	1104.56	552.79	1087.54	544.27	1086.55	543.78	12
10	813.41	407.21			795.40	398.20	S	1033.53	517.27	1016.50	508.75	1015.52	508.26	11
11	884.45	442.73			866.44	433.72	A	946.50	473.75	929.47	465.24	928.48	464.75	10
12	955.48	478.25			937.47	469.24	A	875.46	438.23	858.43	429.72	857.45	429.23	9
13	1042.52	521.76			1024.51	512.76	S	804.42	402.71	787.39	394.20	786.41	393.71	8
14	1099.54	550.27			1081.53	541.27	G	717.39	359.20	700.36	350.68	699.38	350.19	7
15	1227.60	614.30	1210.57	605.79	1209.59	605.30	Q	660.37	330.69	643.34	322.17	642.36	321.68	6
16	1298.63	649.82	1281.61	641.31	1280.62	640.82	A	532.31	266.66	515.28	258.14	514.30	257.65	5
17	1427.68	714.34	1410.65	705.83	1409.67	705.34	E	461.27	231.14	444.25	222.63	443.26	222.13	4
18	1484.70	742.85	1467.67	734.34	1466.69	733.85	G	332.23	166.62	315.20	158.10			3
19	1612.79	806.90	1595.77	798.39	1594.78	797.89	K	275.21	138.11	258.18	129.59			2
20							K	147.11	74.06	130.09	65.55			1

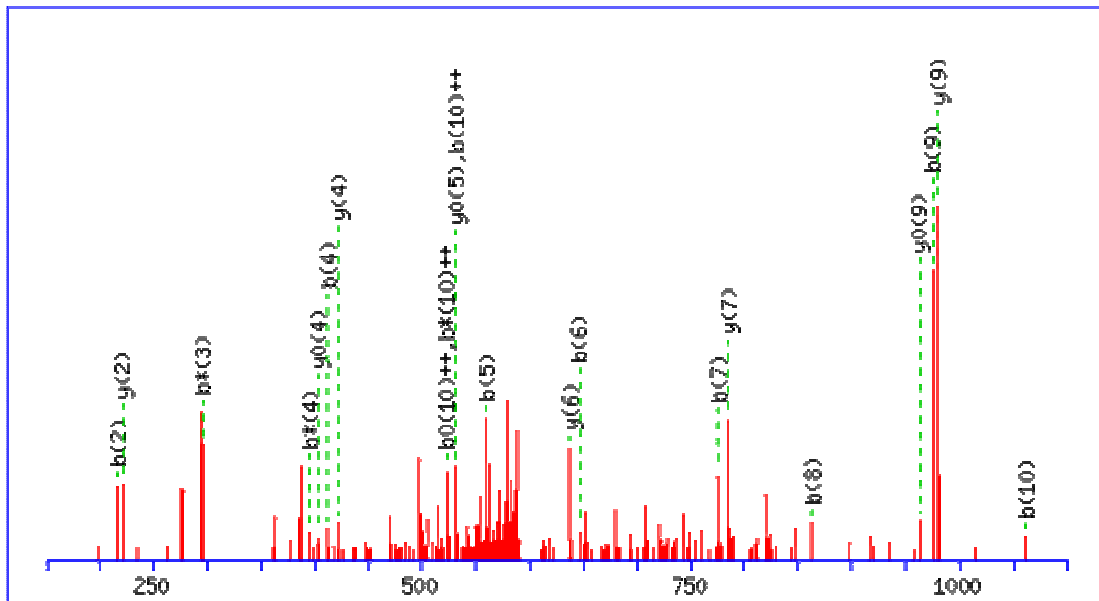
Gene Symbol Sequences m/z Charge Ion score Expect
 SNRPC PKFYCDYCDTYLTHDSPSVR 842.034 3+ 48 0.00088
 (IPI00013396 U1 small nuclear ribonucleoprotein C)



C5, C8: Carbamidomethylated

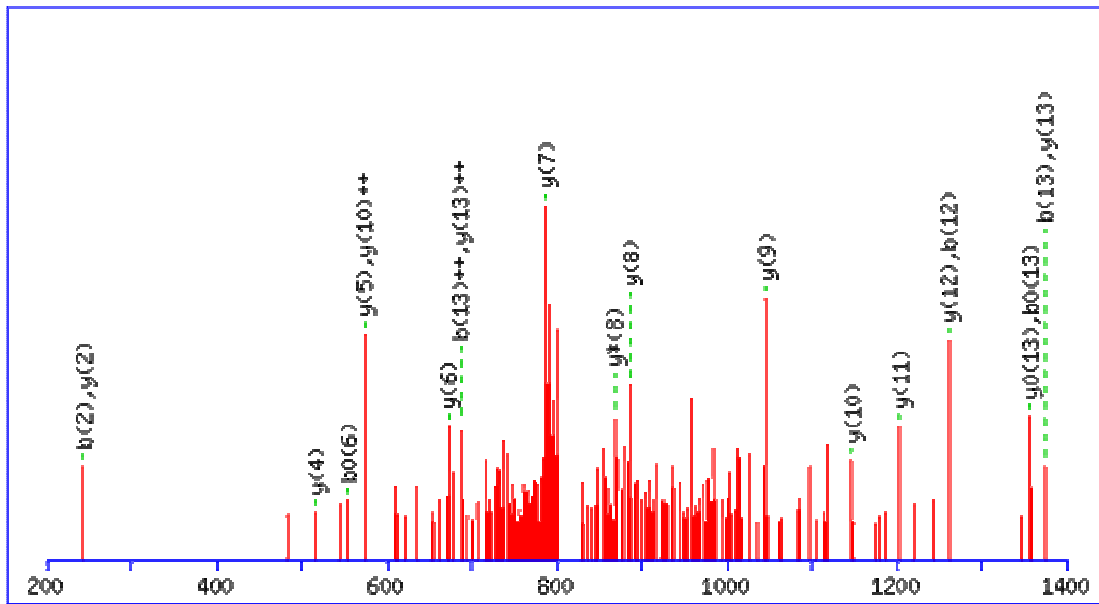
#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	98.06	49.53					P							20
2	226.15	113.58	209.13	105.07			K	2427.04	1214.02	2410.01	1205.51	2409.03	1205.02	19
3	373.22	187.12	356.20	178.60			F	2298.94	1149.98	2281.92	1141.46	2280.93	1140.97	18
4	536.29	268.65	519.26	260.13			Y	2151.87	1076.44	2134.85	1067.93	2133.86	1067.44	17
5	696.32	348.66	679.29	340.15			C	1988.81	994.91	1971.78	986.40	1970.80	985.90	16
6	811.34	406.18	794.32	397.66	793.33	397.17	D	1828.78	914.89	1811.75	906.38	1810.77	905.89	15
7	974.41	487.71	957.38	479.19	956.40	478.70	Y	1713.75	857.38	1696.73	848.87	1695.74	848.38	14
8	1134.44	567.72	1117.41	559.21	1116.43	558.72	C	1550.69	775.85	1533.66	767.34	1532.68	766.84	13
9	1249.47	625.24	1232.44	616.72	1231.45	616.23	D	1390.66	695.83	1373.63	687.32	1372.65	686.83	12
10	1350.51	675.76	1333.49	667.25	1332.50	666.75	T	1275.63	638.32	1258.61	629.81	1257.62	629.31	11
11	1513.58	757.29	1496.55	748.78	1495.57	748.29	Y	1174.59	587.80	1157.56	579.28	1156.57	578.79	10
12	1626.66	813.83	1609.63	805.32	1608.65	804.83	L	1011.52	506.26	994.50	497.75	993.51	497.26	9
13	1727.71	864.36	1710.68	855.84	1709.70	855.35	T	898.44	449.72	881.41	441.21	880.43	440.72	8
14	1864.77	932.89	1847.74	924.37	1846.76	923.88	H	797.39	399.20	780.36	390.69	779.38	390.19	7
15	1979.79	990.40	1962.77	981.89	1961.78	981.40	D	660.33	330.67	643.30	322.16	642.32	321.66	6
16	2066.83	1033.92	2049.80	1025.40	2048.82	1024.91	S	545.30	273.16	528.28	264.64	527.29	264.15	5
17	2163.88	1082.44	2146.85	1073.93	2145.87	1073.44	P	458.27	229.64	441.25	221.13	440.26	220.63	4
18	2250.91	1125.96	2233.88	1117.45	2232.90	1116.95	S	361.22	181.11	344.19	172.60	343.21	172.11	3
19	2349.98	1175.49	2332.95	1166.98	2331.97	1166.49	V	274.19	137.60	257.16	129.08			2
20							R	175.12	88.06	158.09	79.55			1

Gene Symbol **Sequences** **m/z** **Charge** **Ion score** **Expect**
 TIMM8A SKPVFSESLSD 598.299 2+ 51 0.001
 (IPI00028376 Mitochondrial import inner membrane translocase subunit Tim8 A)



#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.04	44.52			70.03	35.52	S							11
2	216.13	108.57	199.11	100.06	198.12	99.57	K	1108.55	554.78	1091.53	546.27	1090.54	545.77	10
3	313.19	157.10	296.16	148.58	295.18	148.09	P	980.46	490.73			962.45	481.73	9
4	412.26	206.63	395.23	198.12	394.24	197.63	V	883.40	442.21			865.39	433.20	8
5	559.32	280.17	542.30	271.65	541.31	271.16	F	784.34	392.67			766.33	383.67	7
6	646.36	323.68	629.33	315.17	628.35	314.68	S	637.27	319.14			619.26	310.13	6
7	775.40	388.20	758.37	379.69	757.39	379.20	E	550.24	275.62			532.22	266.62	5
8	862.43	431.72	845.40	423.21	844.42	422.71	S	421.19	211.10			403.18	202.09	4
9	975.51	488.26	958.49	479.75	957.50	479.26	L	334.16	167.58			316.15	158.58	3
10	1062.55	531.78	1045.52	523.26	1044.54	522.77	S	221.08	111.04			203.07	102.04	2
11							D	134.04	67.53			116.03	58.52	1

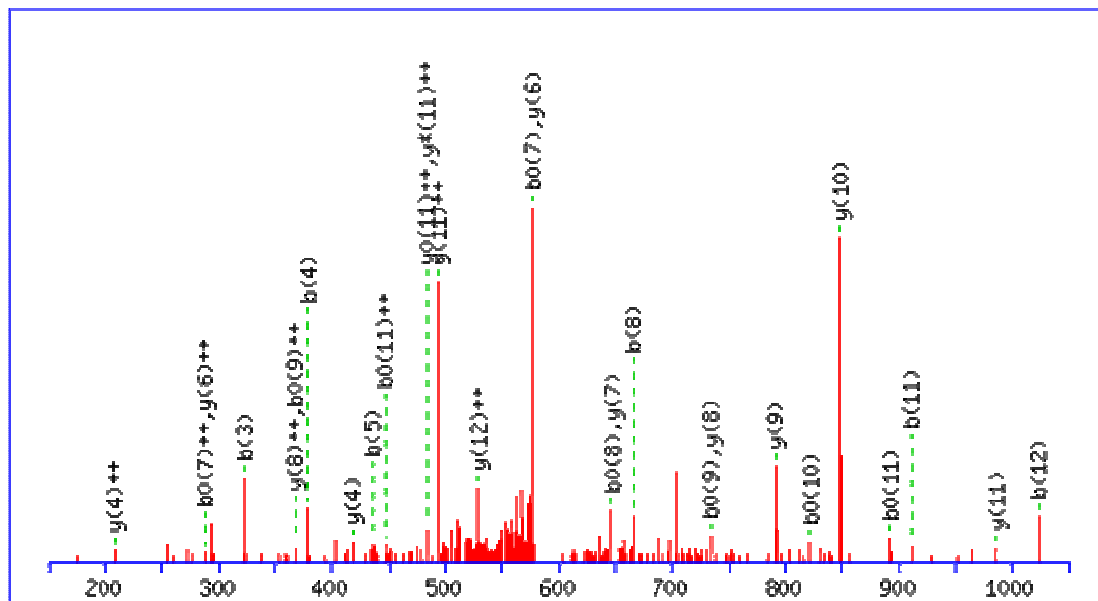
Gene Symbol **Sequences** **m/z** **Charge** **Ion score** **Expect**
 TXNRD2 WLGGGTCVNVGCIPK 809.407 2+ 94 6.2e-08
 (IPI00157820 Thioredoxin reductase 2, mitochondrial precursor (EC 1.8.1.9) (TR3))



C7, C12: Carbamidomethylated

#	b	b ⁺⁺	b ⁺	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁺	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	187.09	94.05					W							15
2	244.11	122.56					G	1431.71	716.36	1414.68	707.84	1413.70	707.35	14
3	357.19	179.10					L	1374.69	687.85	1357.66	679.33	1356.68	678.84	13
4	414.21	207.61					G	1261.60	631.31	1244.58	622.79	1243.59	622.30	12
5	471.24	236.12					G	1204.58	602.79	1187.55	594.28	1186.57	593.79	11
6	572.28	286.64			554.27	277.64	T	1147.56	574.28	1130.53	565.77	1129.55	565.28	10
7	732.31	366.66			714.30	357.66	C	1046.51	523.76	1029.49	515.25			9
8	831.38	416.19			813.37	407.19	V	886.48	443.74	869.45	435.23			8
9	945.42	473.22	928.40	464.70	927.41	464.21	N	787.41	394.21	770.39	385.70			7
10	1044.49	522.75	1027.47	514.24	1026.48	513.74	V	673.37	337.19	656.34	328.68			6
11	1101.51	551.26	1084.49	542.75	1083.50	542.26	G	574.30	287.65	557.28	279.14			5
12	1261.55	631.28	1244.52	622.76	1243.53	622.27	C	517.28	259.14	500.25	250.63			4
13	1374.63	687.82	1357.60	679.31	1356.62	678.81	I	357.25	179.13	340.22	170.62			3
14	1471.68	736.34	1454.66	727.83	1453.67	727.34	P	244.17	122.59	227.14	114.07			2
15							K	147.11	74.06	130.09	65.55			1

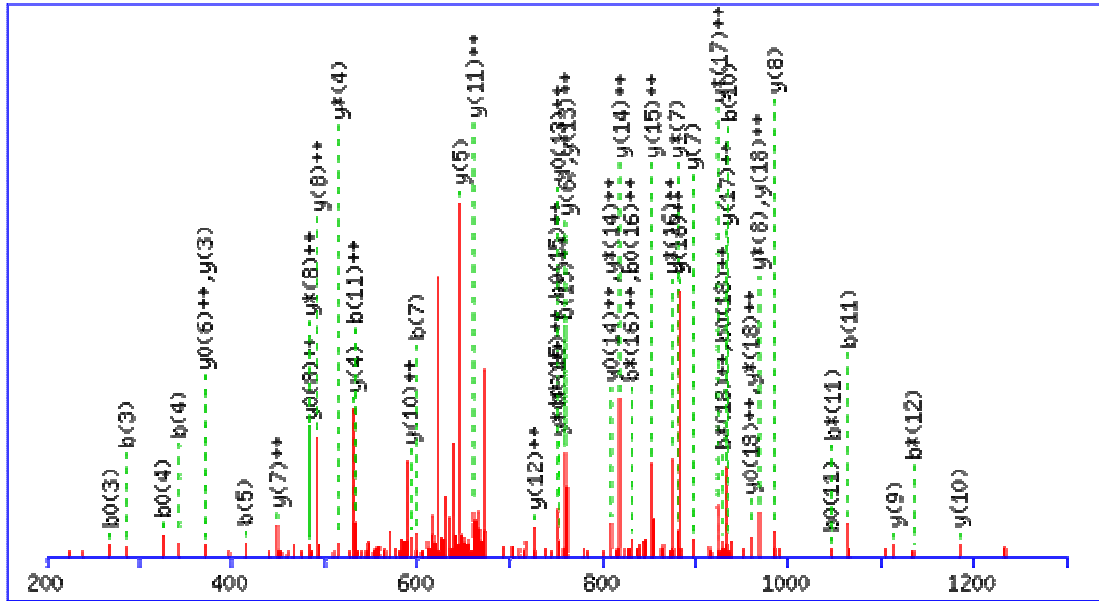
Gene Symbol **Sequences** **m/z** **Charge** **Ion score** **Expect**
 UBXD7 AAHGSAASSALK 585.299 2+ 45 0.0042
 (IPI00642423 Isoform 2 of UBX domain-containing protein 7)



N-term : N-Acetyl (Protein)

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.05	57.53			A							13
2	185.09	93.05			A	1056.54	528.78	1039.52	520.26	1038.53	519.77	12
3	322.15	161.58			H	985.51	493.26	968.48	484.74	967.50	484.25	11
4	379.17	190.09			G	848.45	424.73	831.42	416.21	830.44	415.72	10
5	436.19	218.60			G	791.43	396.22	774.40	387.70	773.42	387.21	9
6	523.23	262.12	505.22	253.11	S	734.40	367.71	717.38	359.19	716.39	358.70	8
7	594.26	297.64	576.25	288.63	A	647.37	324.19	630.35	315.68	629.36	315.18	7
8	665.30	333.15	647.29	324.15	A	576.34	288.67	559.31	280.16	558.32	279.67	6
9	752.33	376.67	734.32	367.66	S	505.30	253.15	488.27	244.64	487.29	244.15	5
10	839.36	420.19	821.35	411.18	S	418.27	209.64	401.24	201.12	400.26	200.63	4
11	910.40	455.70	892.39	446.70	A	331.23	166.12	314.21	157.61			3
12	1023.49	512.25	1005.47	503.24	L	260.20	130.60	243.17	122.09			2
13					K	147.11	74.06	130.09	65.55			1

Gene Symbol Sequences m/z Charge Ion score Expect
 UPP1 AATGANAEKAESHNDPCVR 683.318 3+ 69 1.2e-05
 (IPI00004406 Isoform 1 of Uridine phosphorylase 1)



C16: Carbamidomethylated
 N-term : N-Acetyl (Protein)
 K9: Lysine (K-full)

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.05	57.53					A							19
2	185.09	93.05					A	1934.89	967.95	1917.86	959.43	1916.88	958.94	18
3	286.14	143.57			268.13	134.57	T	1863.85	932.43	1846.82	923.92	1845.84	923.42	17
4	343.16	172.08			325.15	163.08	G	1762.80	881.90	1745.78	873.39	1744.79	872.90	16
5	414.20	207.60			396.19	198.60	A	1705.78	853.39	1688.75	844.88	1687.77	844.39	15
6	528.24	264.62	511.21	256.11	510.23	255.62	N	1634.74	817.88	1617.72	809.36	1616.73	808.87	14
7	599.28	300.14	582.25	291.63	581.27	291.14	A	1520.70	760.85	1503.67	752.34	1502.69	751.85	13
8	728.32	364.66	711.29	356.15	710.31	355.66	E	1449.66	725.34	1432.64	716.82	1431.65	716.33	12
9	864.43	432.72	847.40	424.21	846.42	423.71	K	1320.62	660.81	1303.59	652.30	1302.61	651.81	11
10	935.47	468.24	918.44	459.72	917.46	459.23	A	1184.51	592.76	1167.48	584.25	1166.50	583.75	10
11	1064.51	532.76	1047.48	524.25	1046.50	523.75	E	1113.47	557.24	1096.45	548.73	1095.46	548.24	9
12	1151.54	576.27	1134.52	567.76	1133.53	567.27	S	984.43	492.72	967.41	484.21	966.42	483.71	8
13	1288.60	644.80	1271.57	636.29	1270.59	635.80	H	897.40	449.20	880.37	440.69	879.39	440.20	7
14	1402.64	701.83	1385.62	693.31	1384.63	692.82	N	760.34	380.67	743.31	372.16	742.33	371.67	6
15	1517.67	759.34	1500.64	750.83	1499.66	750.33	D	646.30	323.65	629.27	315.14	628.29	314.65	5
16	1677.70	839.35	1660.67	830.84	1659.69	830.35	C	531.27	266.14	514.24	257.63			4
17	1774.75	887.88	1757.73	879.37	1756.74	878.88	P	371.24	186.12	354.21	177.61			3
18	1873.82	937.41	1856.80	928.90	1855.81	928.41	V	274.19	137.60	257.16	129.08			2
19							R	175.12	88.06	158.09	79.55			1