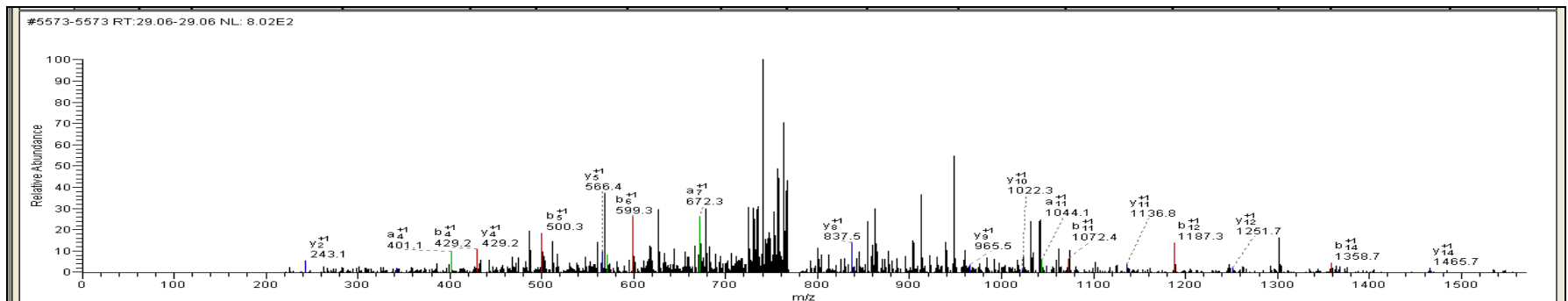


NP_724177.1 fondue CG15825-PA

R.AGYHAVTASVDDNGKIGTHSVHS

S no	AA	A	B	Y	
1	A	44.05	72.04	-	23
2	G	101.07	129.07	2252.07	22
3	Y	264.13	292.13	2195.05	21
4	H	401.19	429.19	2031.98	20
5	A	472.23	500.23	1894.93	19
6	V	571.3	599.29	1823.89	18
7	T	672.35	700.34	1724.82	17
8	A	743.38	771.38	1623.77	16
9	S	830.42	858.41	1552.74	15
10	V	929.48	957.48	1465.7	14
11	D	1044.51	1072.51	1366.63	13
12	D	1159.54	1187.53	1251.61	12
13	N	1273.58	1301.58	1136.58	11
14	G	1330.6	1358.6	1022.54	10
15	K	1458.7	1486.69	965.52	9
16	I	1571.78	1599.78	837.42	8
17	G	1628.8	1656.8	724.34	7
18	T	1729.85	1757.85	667.32	6
19	H	1866.91	1894.9	566.27	5
20	S	1953.94	1981.94	429.21	4
21	V	2053.01	2081	342.18	3
22	H	2190.07	2218.06	243.11	2
23	S	-	-	106.05	1

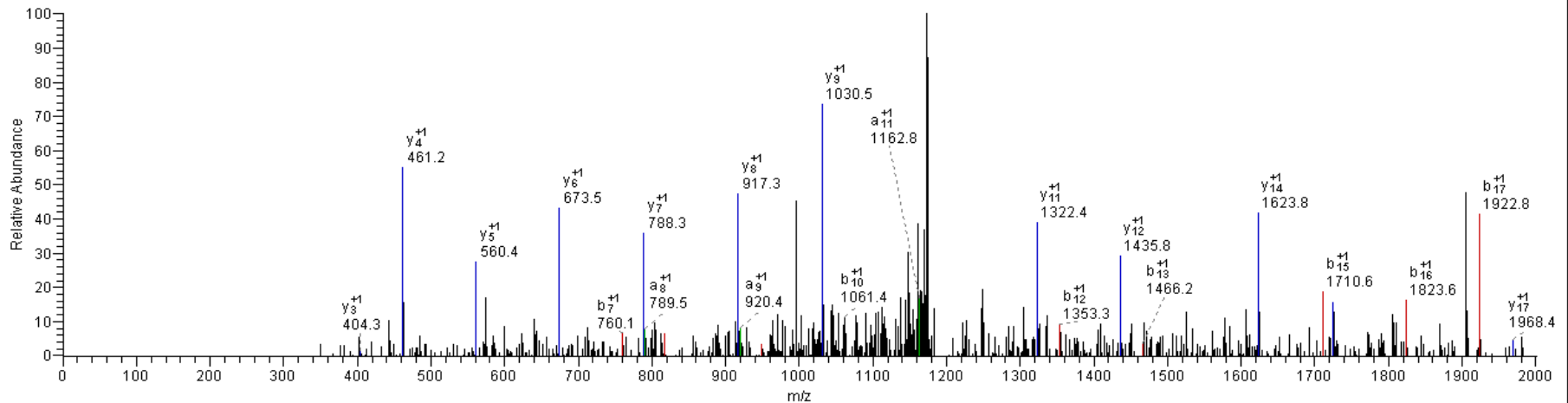


glu NP_723996.1 gluon CG11397-PA

K.GQTENETGMLEYLEDIVGTQR.Y

	AA	A	B	Y	
1	G	30.03	58.03	-	21
2	Q	158.09	186.09	2326.09	20
3	T	259.14	287.13	2198.03	19
4	E	388.18	416.18	2096.98	18
5	N	502.23	530.22	1967.94	17
6	E	631.27	659.26	1853.89	16
7	T	732.32	760.31	1724.85	15
8	G	789.34	817.33	1623.80	14
9	M	920.38	948.37	1566.78	13
10	L	1033.46	1061.46	1435.74	12
11	E	1162.50	1190.50	1322.66	11
12	Y	1325.57	1353.56	1193.62	10
13	L	1438.65	1466.65	1030.55	9
14	E	1567.69	1595.69	917.47	8
15	D	1682.72	1710.72	788.43	7
16	I	1795.81	1823.80	673.40	6
17	V	1894.87	1922.87	560.32	5
18	G	1951.90	1979.89	461.25	4
19	T	2052.94	2080.94	404.23	3
20	Q	2181.00	2209.00	303.18	2
21	R	-	-	175.12	1

#9119-9119 RT:47.58-47.58 NL: 2.35E2

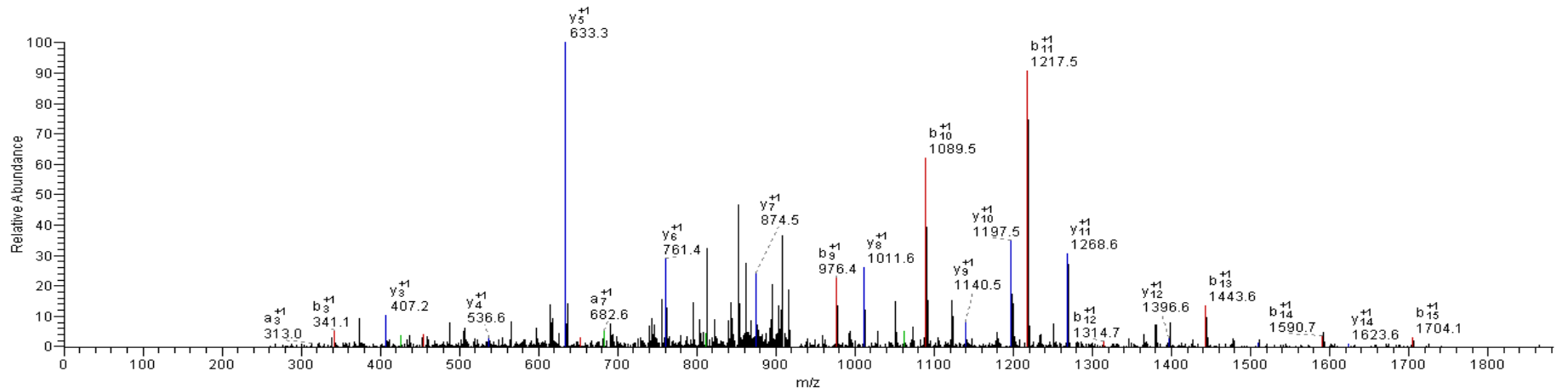


GstD1 NP_524326.1 Glutathione S transferase D1 CG10045-PA

K.LLNLQAGEHLKPEFLK.I

	AA	A	B	Y	
1	L	86.10	114.09	-	16
2	L	199.18	227.18	1736.97	15
3	N	313.22	341.22	1623.89	14
4	L	426.31	454.30	1509.84	13
5	Q	554.37	582.36	1396.76	12
6	A	625.40	653.40	1268.70	11
7	G	682.42	710.42	1197.66	10
8	E	811.47	839.46	1140.64	9
9	H	948.53	976.52	1011.60	8
10	L	1061.61	1089.61	874.54	7
11	K	1189.71	1217.70	761.46	6
12	P	1286.76	1314.75	633.36	5
13	E	1415.80	1443.80	536.31	4
14	F	1562.87	1590.86	407.27	3
15	L	1675.95	1703.95	260.20	2
16	K	-	-	147.11	1

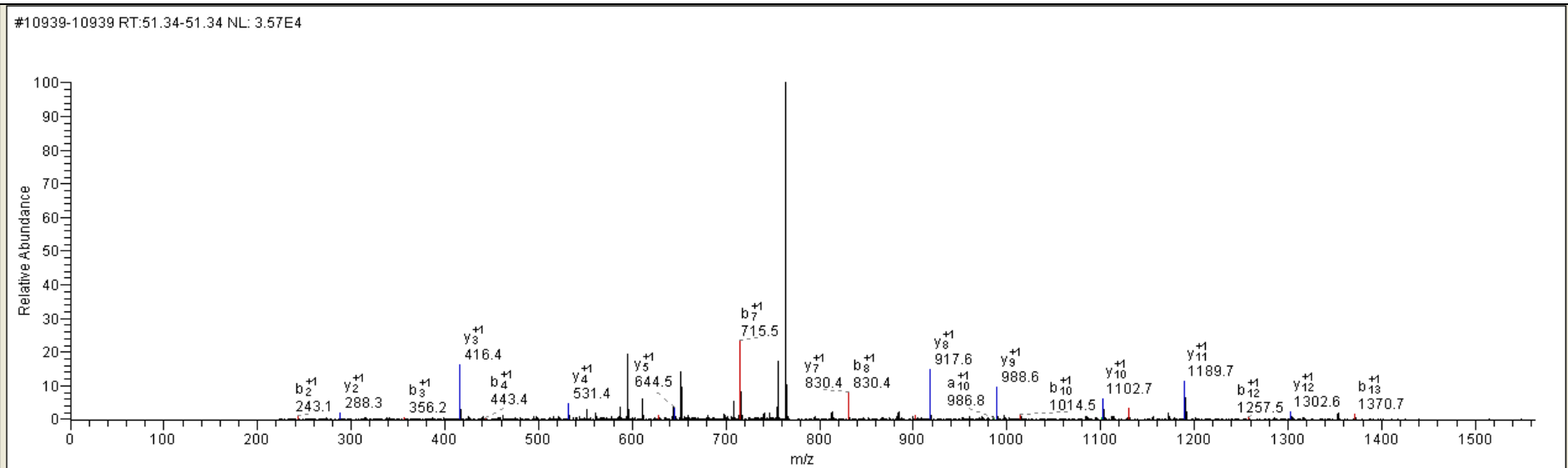
#6958-6958 RT:36.15-36.15 NL: 1.37E3



Gp93 NP_651601.1 Glycoprotein 93 CG5520-PA

R.ELISNASDAIDKIR.L

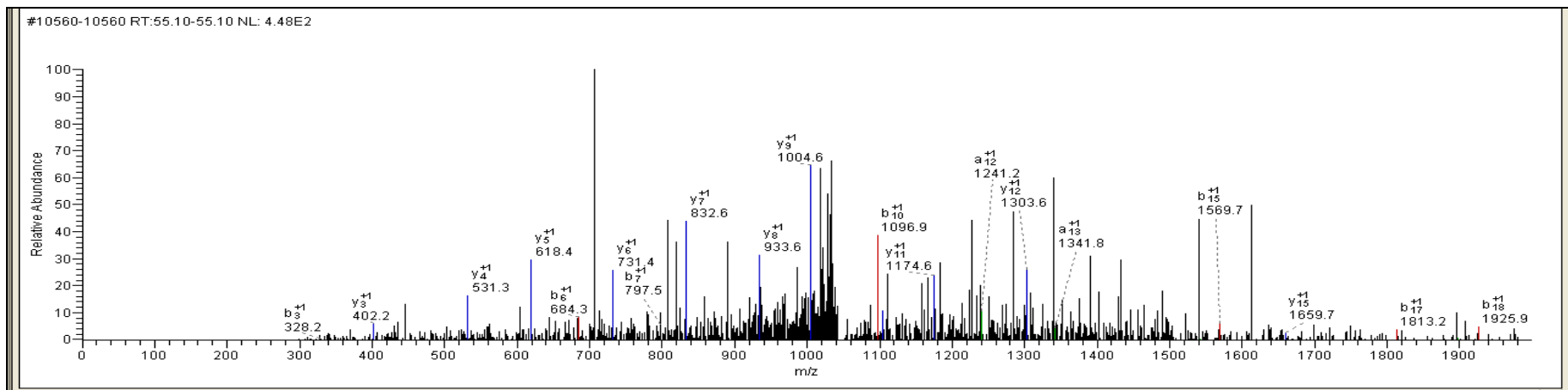
	AA	A	B	Y	
1	E	102.05	130.05	-	14
2	L	215.14	243.13	1415.79	13
3	I	328.22	356.22	1302.70	12
4	S	415.26	443.25	1189.62	11
5	N	529.30	557.29	1102.59	10
6	A	600.34	628.33	988.54	9
7	S	687.37	715.36	917.51	8
8	D	802.39	830.39	830.47	7
9	A	873.43	901.43	715.45	6
10	I	986.52	1014.51	644.41	5
11	D	1101.54	1129.54	531.32	4
12	K	1229.64	1257.63	416.30	3
13	I	1342.72	1370.72	288.20	2
14	R	-	-	175.12	1



Hel89B NP_732097.1 Helicase 89B CG4261-PA

K.ILTLDQIEAVATTLSENLR.S

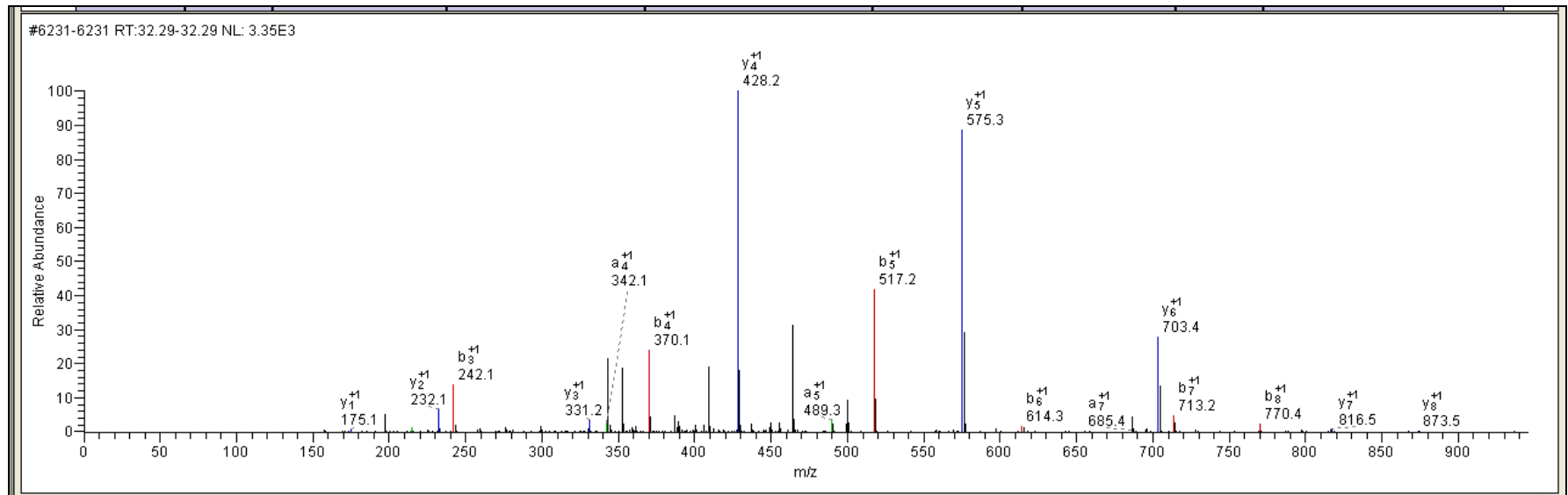
	AA	A	B	Y	
1	I	86.10	114.09	-	19
2	L	199.18	227.18	1987.07	18
3	T	300.23	328.22	1873.99	17
4	L	413.31	441.31	1772.94	16
5	D	528.34	556.33	1659.85	15
6	Q	656.40	684.39	1544.83	14
7	I	769.48	797.48	1416.77	13
8	E	898.52	926.52	1303.69	12
9	A	969.56	997.56	1174.64	11
10	V	1068.63	1096.62	1103.61	10
11	A	1139.67	1167.66	1004.54	9
12	T	1240.71	1268.71	933.50	8
13	T	1341.76	1369.76	832.45	7
14	L	1454.85	1482.84	731.40	6
15	S	1541.88	1569.87	618.32	5
16	E	1670.92	1698.92	531.29	4
17	N	1784.96	1812.96	402.25	3
18	L	1898.05	1926.04	288.20	2
19	R	-	-	175.12	1



His2Av NP_524519.1 Histone H2A variant CG5499-PA

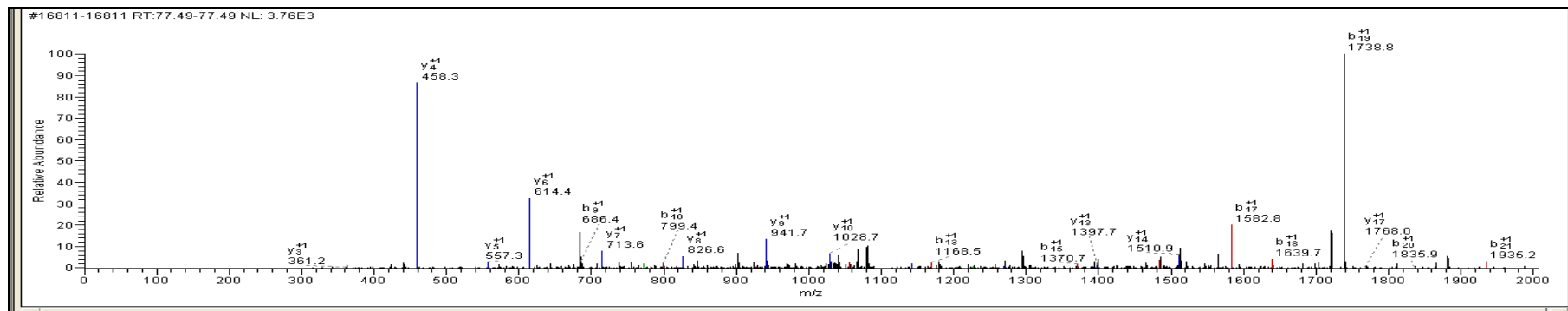
R.AGLQFPVGR.I

	AA	A	B	Y	
1	A	44.05	72.04	-	9
2	G	101.07	129.07	873.49	8
3	L	214.16	242.15	816.47	7
4	Q	342.21	370.21	703.39	6
5	F	489.28	517.28	575.33	5
6	P	586.33	614.33	428.26	4
7	V	685.40	713.40	331.21	3
8	G	742.42	770.42	232.14	2
9	R	-	-	175.12	1



R.DGGAGASGILQQLSDIVGVPVSR.V

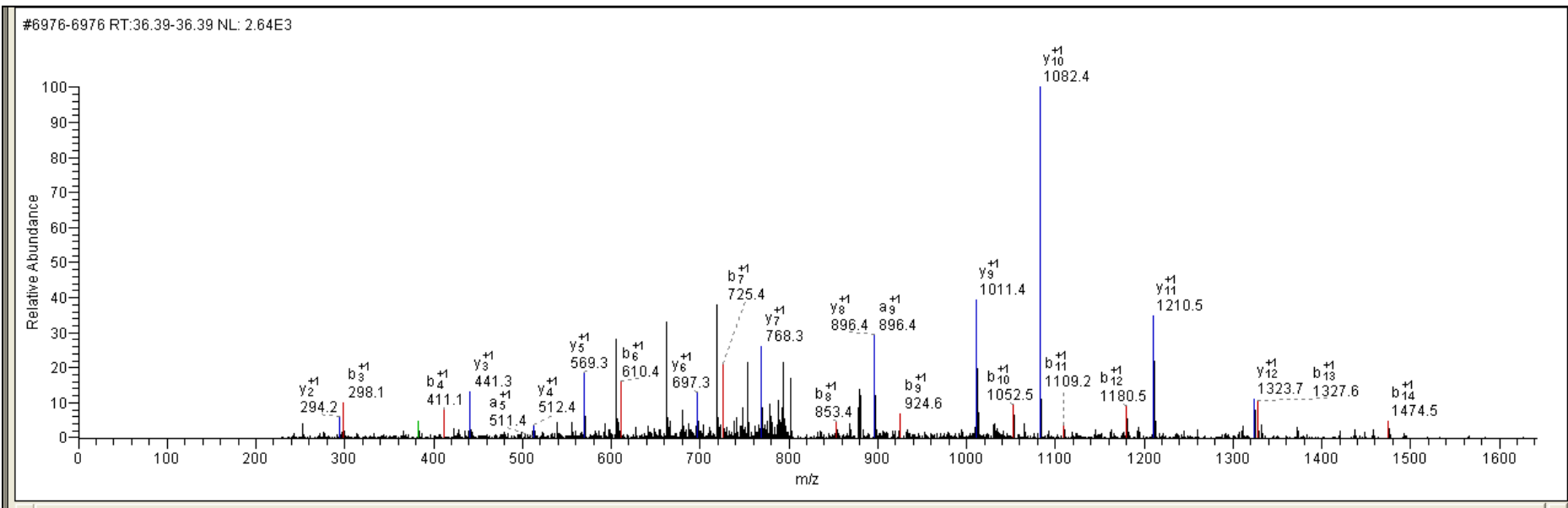
S no	AA	A	B	Y	
1	D	88.04	116.03	-	23
2	G	145.06	173.06	2081.13	22
3	G	202.08	230.08	2024.11	21
4	A	273.12	301.11	1967.09	20
5	G	330.14	358.14	1896.05	19
6	A	401.18	429.17	1839.03	18
7	S	488.21	516.2	1768	17
8	G	545.23	573.23	1680.96	16
9	I	658.32	686.31	1623.94	15
10	L	771.4	799.39	1510.86	14
11	Q	899.46	927.45	1397.77	13
12	Q	1027.52	1055.51	1269.72	12
13	L	1140.6	1168.6	1141.66	11
14	S	1227.63	1255.63	1028.57	10
15	D	1342.66	1370.65	941.54	9
16	I	1455.74	1483.74	826.51	8
17	V	1554.81	1582.81	713.43	7
18	G	1611.83	1639.83	614.36	6
19	V	1710.9	1738.9	557.34	5
20	P	1807.95	1835.95	458.27	4
21	V	1907.02	1935.02	361.22	3
22	S	1994.06	2022.05	262.15	2
23	R	-	-	175.12	1



NP_572614.1 Interaction partner of Dnmt2 CG2961-PA

K.AILKADQAQGAFFK.S

	AA	A	B	Y	
1	A	44.05	72.04	-	15
2	I	157.13	185.13	1549.87	14
3	I	270.22	298.21	1436.79	13
4	L	383.30	411.30	1323.71	12
5	K	511.40	539.39	1210.62	11
6	A	582.43	610.43	1082.53	10
7	D	697.46	725.46	1011.49	9
8	Q	825.52	853.51	896.46	8
9	A	896.56	924.55	768.40	7
10	Q	1024.81	1052.61	697.37	6
11	G	1081.64	1109.63	569.31	5
12	A	1152.67	1180.67	512.29	4
13	F	1299.74	1327.74	441.25	3
14	F	1446.81	1474.81	294.18	2
15	K	-	-	147.11	1

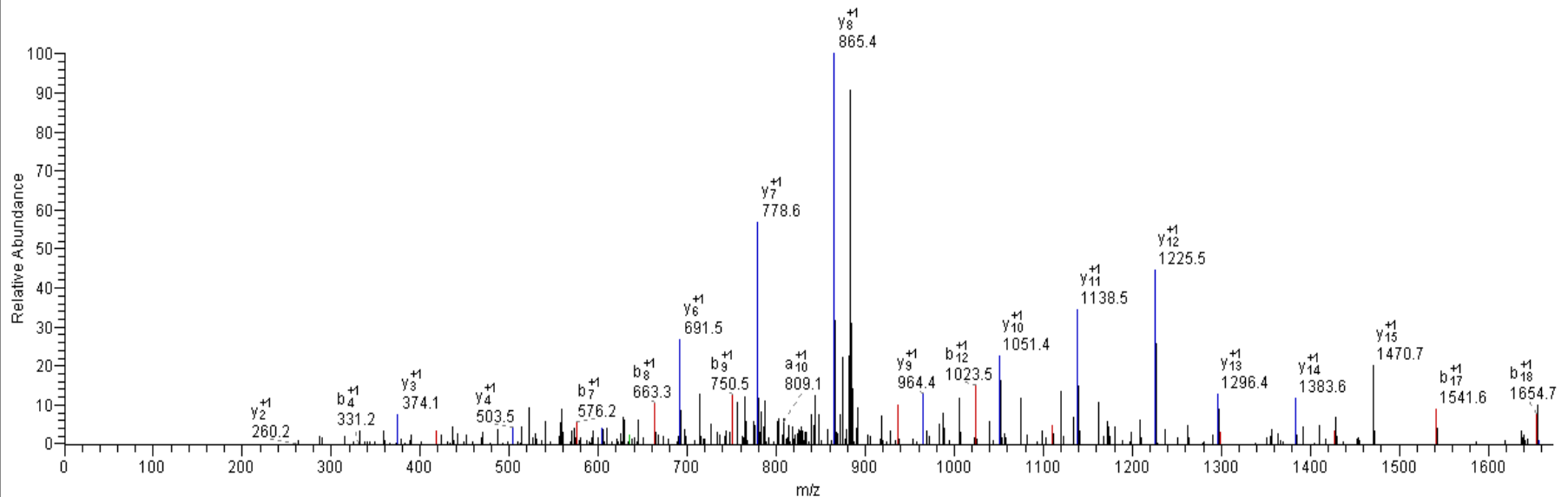


Jupiter NP_731595.1 Jupiter CG31363-PD

K.SGSVSSASSSVSSSTENLK.M

	AA	A	B	Y	
1	S	60.04	88.04	-	19
2	G	117.07	145.06	1713.81	18
3	S	204.10	232.09	1656.79	17
4	V	303.17	331.16	1569.76	16
5	S	390.20	418.19	1470.69	15
6	S	477.23	505.23	1383.66	14
7	A	548.27	576.26	1296.63	13
8	S	635.30	663.29	1225.59	12
9	S	722.33	750.33	1138.56	11
10	S	809.36	837.36	1051.53	10
11	V	908.43	936.43	964.49	9
12	S	995.46	1023.46	865.43	8
13	S	1082.50	1110.49	778.39	7
14	S	1169.53	1197.52	691.36	6
15	T	1270.58	1298.57	604.33	5
16	E	1399.62	1427.61	503.28	4
17	N	1513.66	1541.66	374.24	3
18	L	1626.75	1654.74	260.20	2
19	K	-	-	147.11	1

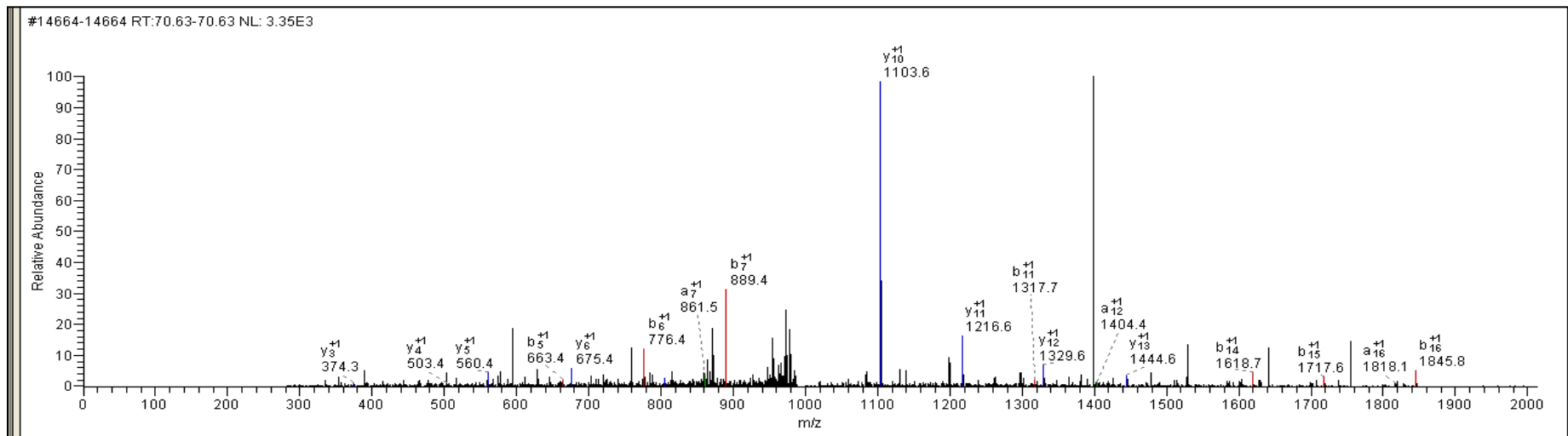
#5675-5675 RT:29.31-29.31 NL: 3.05E2



kis NP_523441.1 kismet CG3696-PA

K.TFIWDLITPTEDGEVQK.I

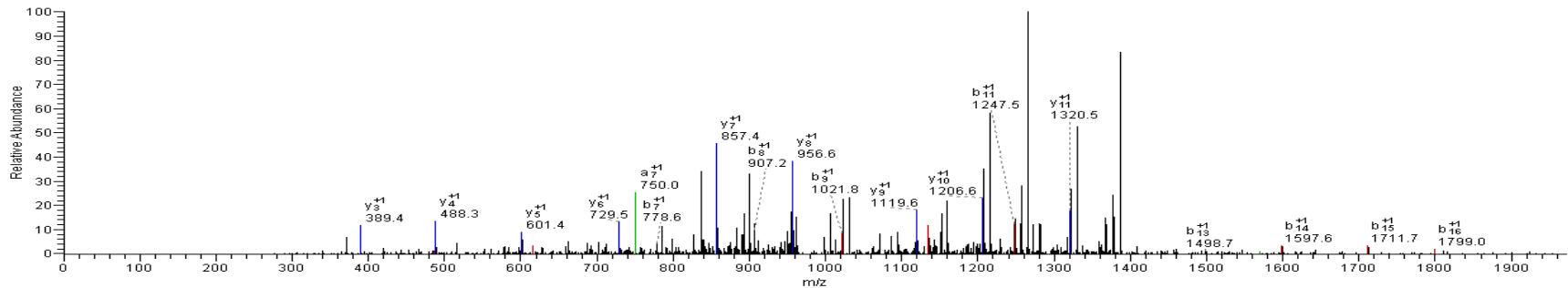
	AA	A	B	Y	
1	T	74.06	102.05	-	17
2	F	221.13	249.12	1890.95	16
3	I	334.21	362.21	1743.88	15
4	W	520.29	548.29	1630.80	14
5	D	635.32	663.31	1444.72	13
6	L	748.40	776.40	1329.69	12
7	I	861.49	889.48	1216.61	11
8	T	962.53	990.53	1103.52	10
9	P	1059.59	1087.58	1002.47	9
10	T	1160.64	1188.63	905.42	8
11	E	1289.68	1317.67	804.37	7
12	D	1404.70	1432.70	675.33	6
13	G	1461.73	1489.72	560.30	5
14	E	1590.77	1618.76	503.28	4
15	V	1689.84	1717.83	374.24	3
16	Q	1817.90	1845.89	275.17	2
17	K	-	-	147.11	1



K.ALTAEEYENILNHVNSYVQQLVELK.M

S no	AA	A	B	Y	
1	A	44.05	72.04	-	25
2	L	157.13	185.13	2846.46	24
3	T	258.18	286.18	2733.37	23
4	A	329.22	357.21	2632.33	22
5	E	458.26	486.26	2561.29	21
6	E	587.3	615.3	2432.25	20
7	Y	750.37	778.36	2303.2	19
8	E	879.41	907.4	2140.14	18
9	N	993.45	1021.45	2011.1	17
10	I	1106.54	1134.53	1897.05	16
11	L	1219.62	1247.62	1783.97	15
12	N	1333.66	1361.66	1670.89	14
13	H	1470.72	1498.72	1556.84	13
14	V	1569.79	1597.79	1419.78	12
15	N	1683.83	1711.83	1320.72	11
16	S	1770.87	1798.86	1206.67	10
17	Y	1933.93	1961.92	1119.64	9
18	V	2033	2060.99	956.58	8
19	Q	2161.06	2189.05	857.51	7
20	Q	2289.11	2317.11	729.45	6
21	L	2402.2	2430.19	601.39	5
22	V	2501.27	2529.26	488.31	4
23	E	2630.31	2658.3	389.24	3
24	L	2743.39	2771.39	260.2	2
25	K	-	-	147.11	1

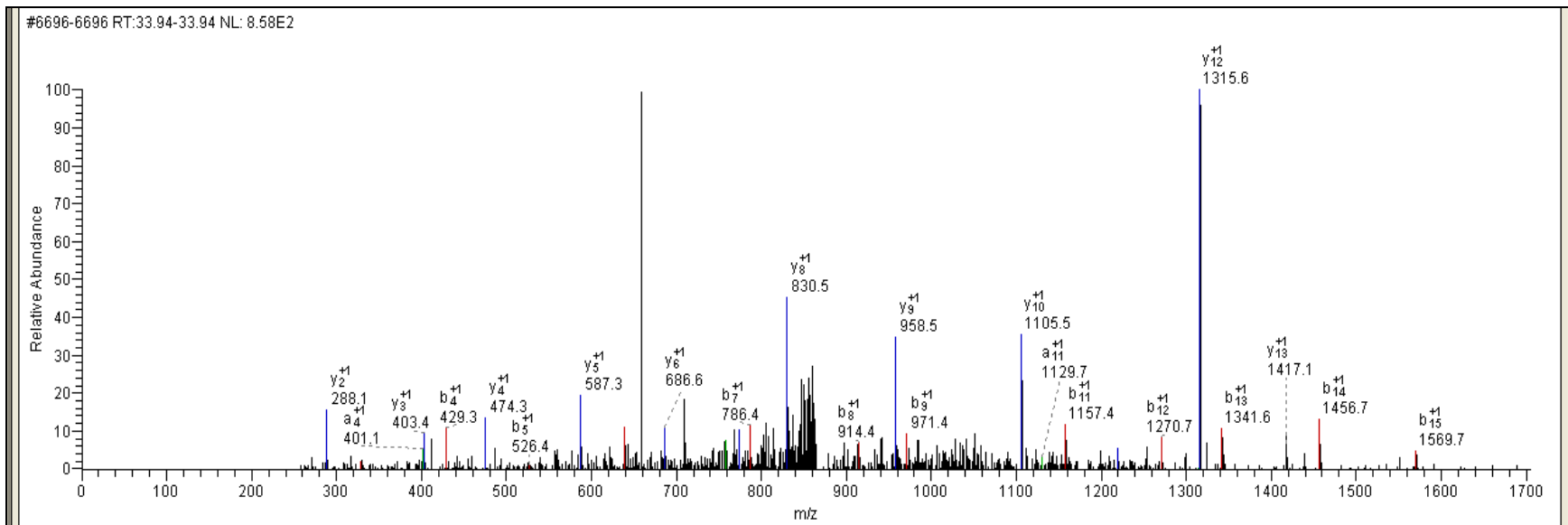
#17187-17187 RT:84.59-84.59 NL: 2.26E3



LanB1 NP_476618.1 Laminin B1 CG7123-PA

R.IDVTPIFQGSVLDIR.K

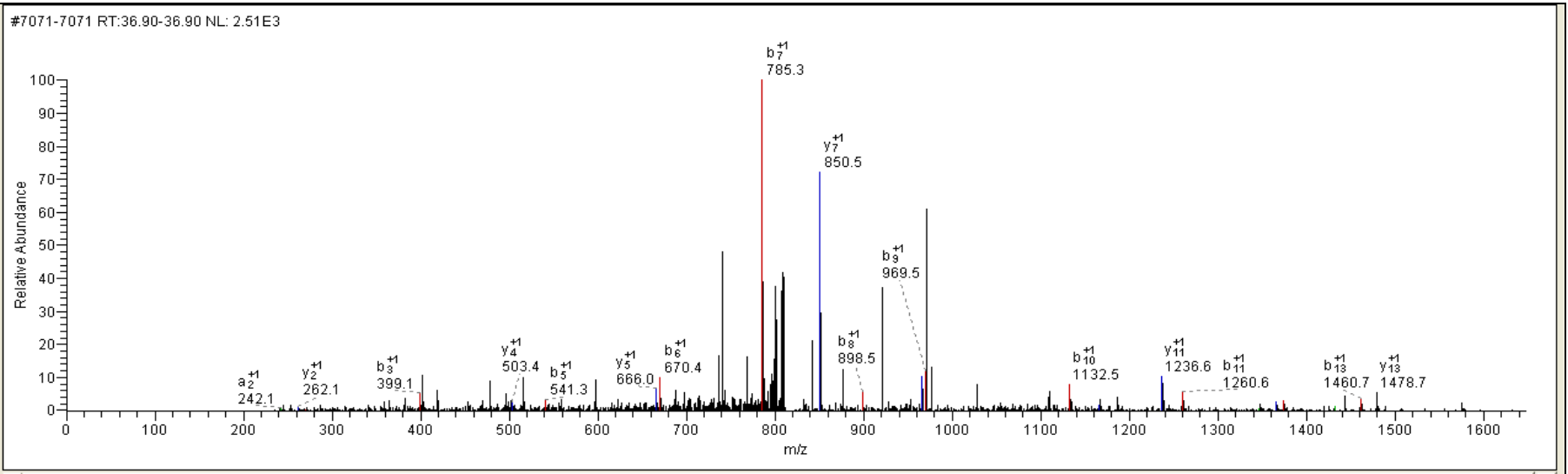
	AA	A	B	Y	
1	I	86.10	114.09	-	16
2	D	201.12	229.12	1630.88	15
3	V	300.19	328.19	1515.85	14
4	T	401.24	429.23	1416.78	13
5	P	498.29	526.29	1315.74	12
6	I	611.38	639.37	1218.68	11
7	F	758.44	786.44	1105.60	10
8	Q	886.50	914.50	958.53	9
9	G	943.52	971.52	830.47	8
10	S	1030.56	1058.55	773.45	7
11	V	1129.63	1157.62	686.42	6
12	L	1242.71	1270.70	587.35	5
13	A	1313.75	1341.74	474.27	4
14	D	1428.77	1456.77	403.23	3
15	I	1541.86	1569.85	288.20	2
16	R	-	-	175.12	1



I(2)37Cc NP_476607.2 lethal (2) 37Cc CG10691-PB

R.RIEAAEDIAYQLSR.S

	AA	A	B	Y	
1	R	129.11	157.11	-	14
2	I	242.20	270.19	1478.75	13
3	E	371.24	399.24	1365.66	12
4	A	442.28	470.27	1236.62	11
5	A	513.31	541.31	1165.58	10
6	E	642.36	670.35	1094.55	9
7	D	757.38	785.38	965.51	8
8	I	870.47	898.46	850.48	7
9	A	941.51	969.50	737.39	6
10	Y	1104.57	1132.56	666.36	5
11	Q	1232.63	1260.62	503.29	4
12	L	1345.71	1373.71	375.24	3
13	S	1432.74	1460.74	262.15	2
14	R	-	-	175.12	1

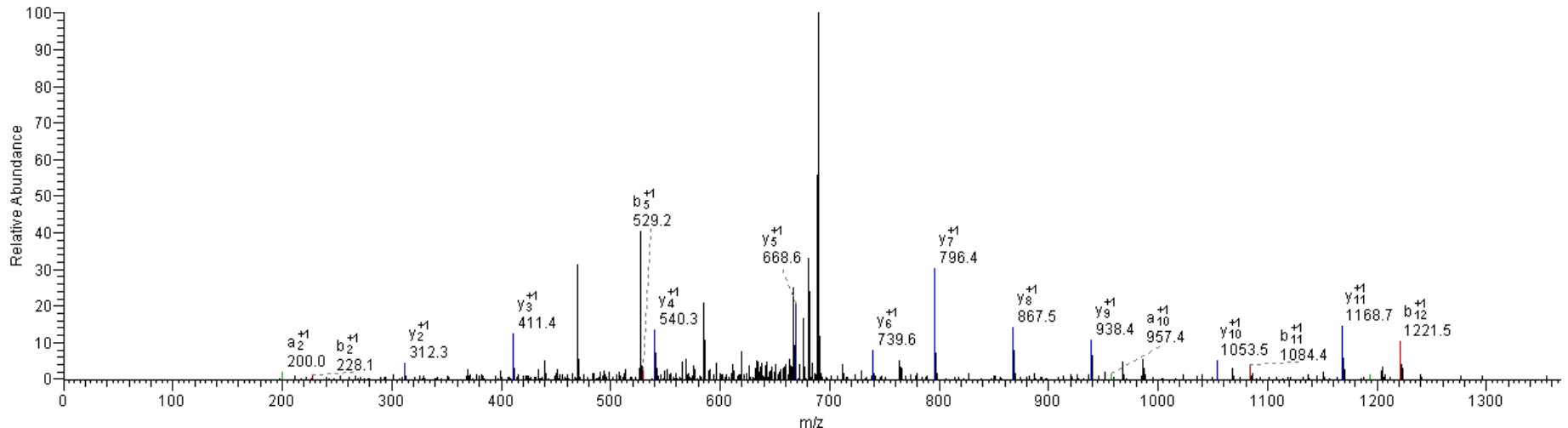


NP_648545.1 lethal (3) j2D3 CG6801-PA

R.NIDDAAGAKEVHR.S

	AA	A	B	Y	
1	N	87.06	115.05	-	13
2	I	200.14	228.13	1281.65	12
3	D	315.17	343.16	1168.57	11
4	D	430.19	458.19	1053.54	10
5	A	501.23	529.23	938.52	9
6	A	572.27	600.26	867.48	8
7	G	629.29	657.28	796.44	7
8	A	700.33	728.32	739.42	6
9	K	828.42	856.42	668.38	5
10	E	957.46	985.46	540.29	4
11	V	1056.53	1084.53	411.25	3
12	H	1193.59	1221.59	312.18	2
13	R	-	-	175.12	1

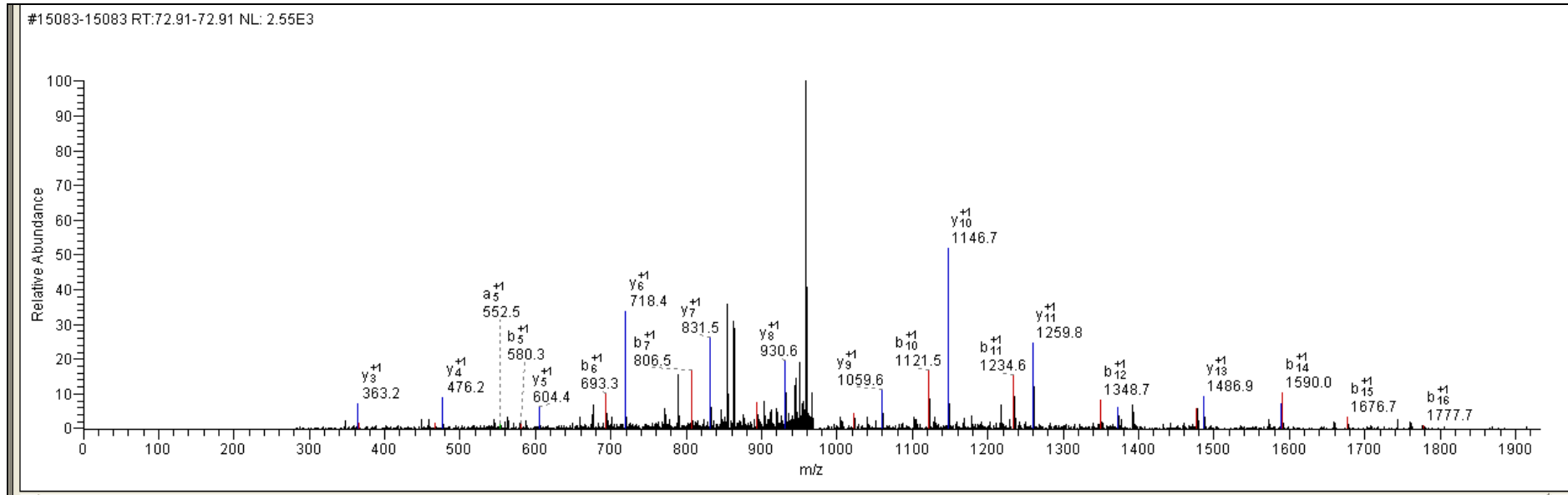
#7452-7452 RT:33.03-33.03 NL: 9.42E2



lin19 NP_724623.1 lin-19-like CG1877-PC

R.LNHTNLISEVLNQLSTR.F

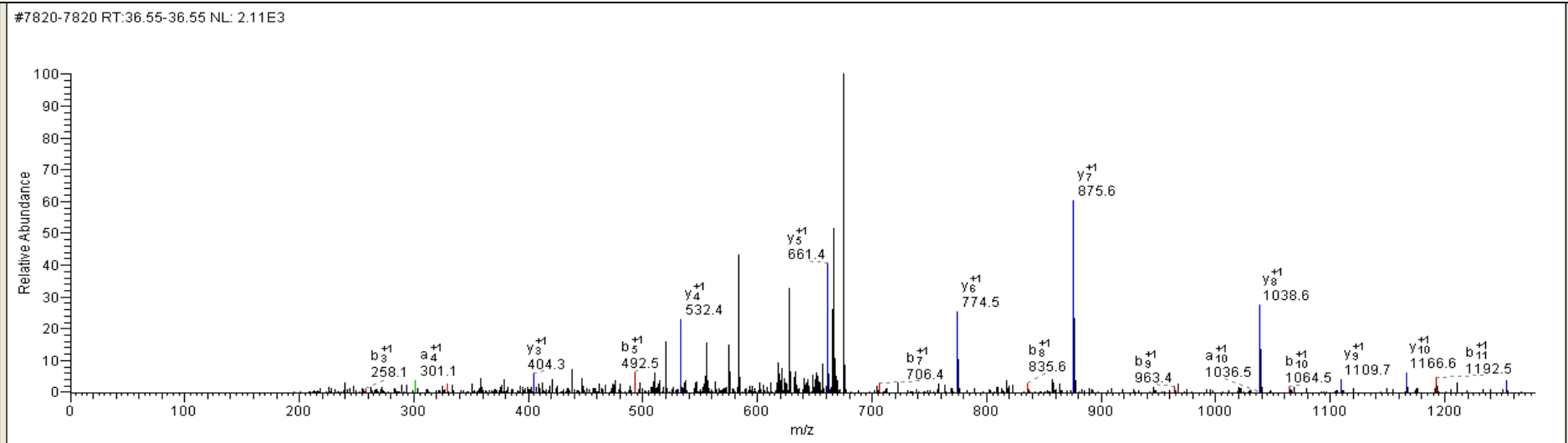
	AA	A	B	Y	
1	L	86.10	114.09	-	17
2	N	200.14	228.13	1838.97	16
3	H	337.20	365.19	1724.93	15
4	T	438.25	466.24	1587.87	14
5	N	552.29	580.28	1486.82	13
6	L	665.37	693.37	1372.78	12
7	I	778.46	806.45	1259.70	11
8	S	865.49	893.48	1146.61	10
9	E	994.53	1022.53	1059.58	9
10	V	1093.60	1121.59	930.54	8
11	L	1206.68	1234.68	831.47	7
12	N	1320.73	1348.72	718.38	6
13	Q	1448.79	1476.78	604.34	5
14	L	1561.87	1589.86	476.28	4
15	S	1648.90	1676.90	363.20	3
16	T	1749.95	1777.94	276.17	2
17	R	-	-	175.12	1



Iola NP_524766.2 longitudinals lacking CG12052-PG

K.LSGAYTLEQTKR.A

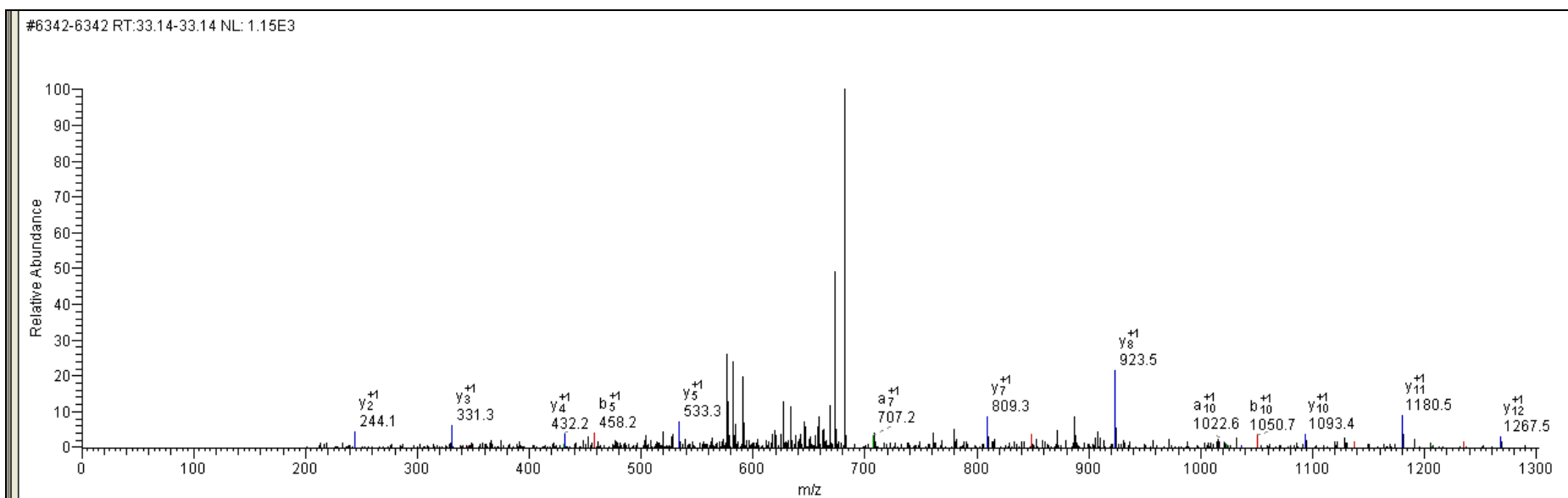
	AA	A	B	Y	
1	L	86.10	114.09	-	12
2	S	173.13	201.12	1253.65	11
3	G	230.15	258.14	1166.62	10
4	A	301.19	329.18	1109.59	9
5	Y	464.25	492.25	1038.56	8
6	T	565.30	593.29	875.49	7
7	L	678.38	706.38	774.45	6
8	E	807.42	835.42	661.36	5
9	Q	935.48	963.48	532.32	4
10	T	1036.53	1064.53	404.26	3
11	K	1164.63	1192.62	303.21	2
12	R	-	-	175.12	1



Mapmodulin NP_523780.1 Mapmodulin CG5784-PB

R.ISSGLNYLTTSPK.L

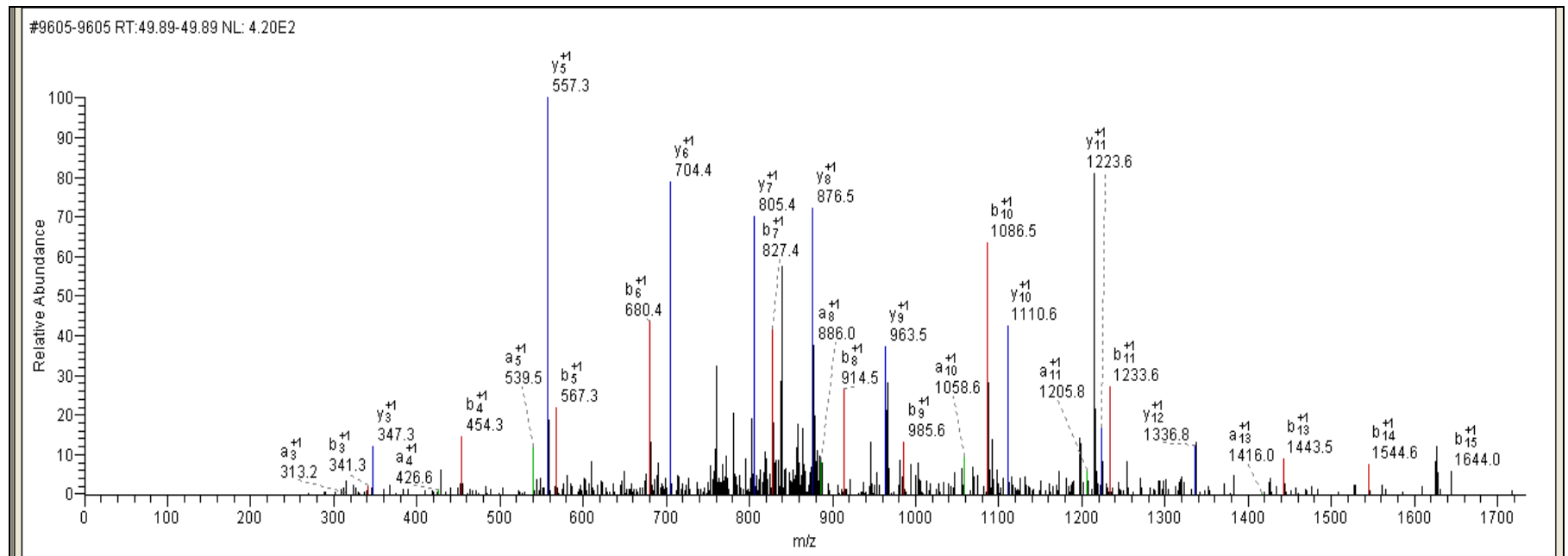
	AA	A	B	Y	
1	I	86.10	114.09	-	13
2	S	173.13	201.12	1267.65	12
3	S	260.16	288.16	1180.62	11
4	G	317.18	345.18	1093.59	10
5	L	430.27	458.26	1036.57	9
6	N	544.31	572.30	923.48	8
7	Y	707.37	735.37	809.44	7
8	L	820.46	848.45	646.38	6
9	T	921.50	949.50	533.29	5
10	T	1022.55	1050.55	432.25	4
11	S	1109.58	1137.58	331.20	3
12	P	1206.64	1234.63	244.17	2
13	K	-	-	147.11	1



me31B NP_523533.2 maternal expression at 31B CG4916-PA

K.DPQILLFSATFPLTVK.N

	AA	A	B	Y	
1	D	88.04	116.03	-	16
2	P	185.09	213.09	1674.98	15
3	Q	313.15	341.15	1577.93	14
4	I	426.23	454.23	1449.87	13
5	L	539.32	567.31	1336.79	12
6	L	652.40	680.40	1223.70	11
7	F	799.47	827.47	1110.62	10
8	S	886.50	914.50	963.55	9
9	A	957.54	985.54	876.52	8
10	T	1058.59	1086.58	805.48	7
11	F	1205.66	1233.65	704.43	6
12	P	1302.71	1330.70	557.37	5
13	L	1415.79	1443.79	460.31	4
14	T	1516.84	1544.84	347.23	3
15	V	1615.91	1643.90	246.18	2
16	K	-	-	147.11	1

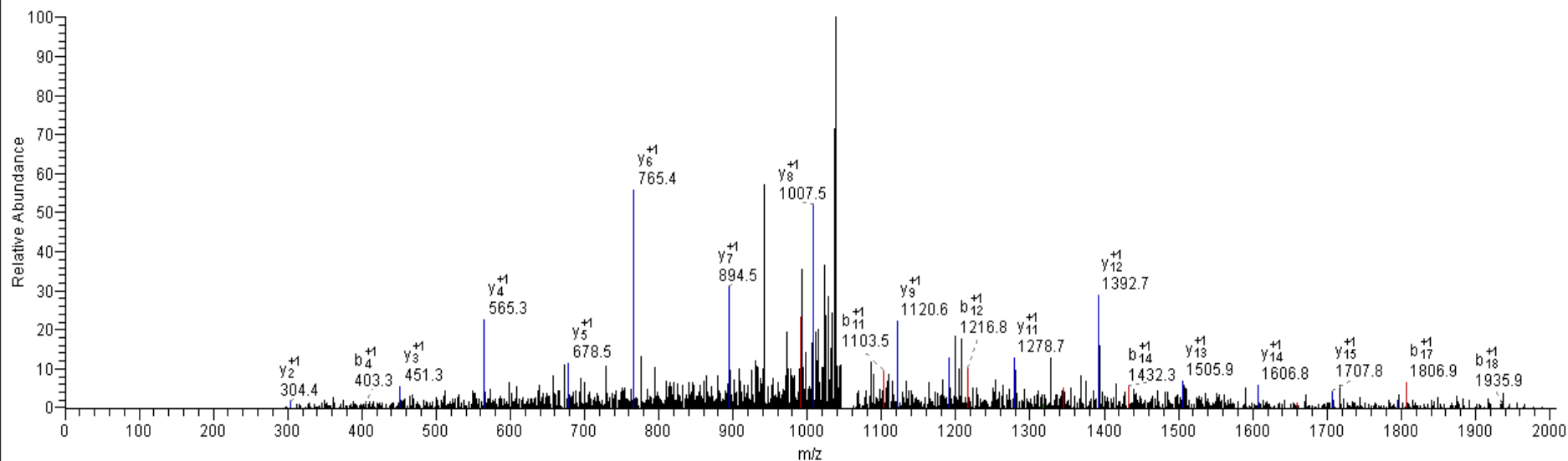


CG42236 NP_001033938.1 midlife-crisis CG11763-PD

R.ESVSTTLNSAILESINFER.R

	AA	A	B	Y	
1	E	102.05	130.05	-	19
2	S	189.09	217.08	1981.02	18
3	V	288.16	316.15	1893.99	17
4	S	375.19	403.18	1794.92	16
5	T	476.24	504.23	1707.89	15
6	T	577.28	605.28	1606.84	14
7	L	690.37	718.36	1505.80	13
8	N	804.41	832.40	1392.71	12
9	S	891.44	919.44	1278.67	11
10	A	962.48	990.47	1191.64	10
11	I	1075.56	1103.56	1120.60	9
12	L	1188.65	1216.64	1007.52	8
13	E	1317.69	1345.68	894.43	7
14	S	1404.72	1432.72	765.39	6
15	L	1517.81	1545.80	678.36	5
16	N	1631.85	1659.84	565.27	4
17	F	1778.92	1806.91	451.23	3
18	E	1907.96	1935.95	304.16	2
19	R	-	-	175.12	1

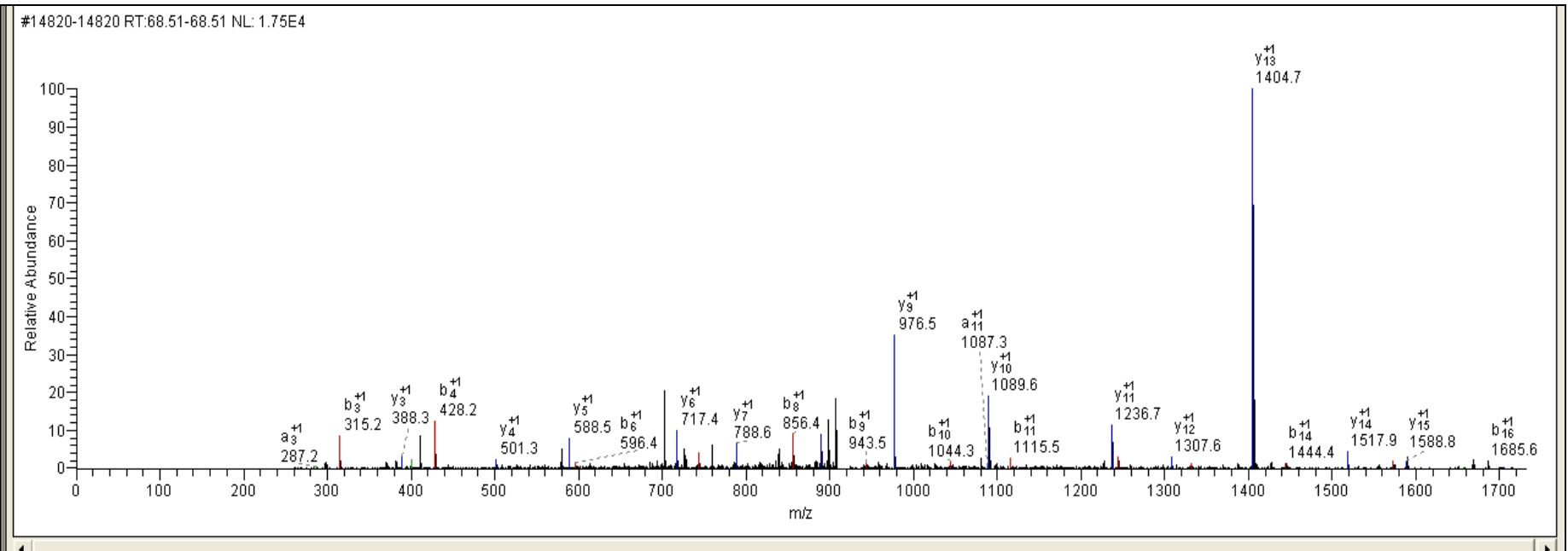
#15399-15399 RT:71.16-71.16 NL: 8.13E2



NP_732619.1 modifier of mdg4 CG32491-PR

K.QDALPAFISTAESLQIK.G

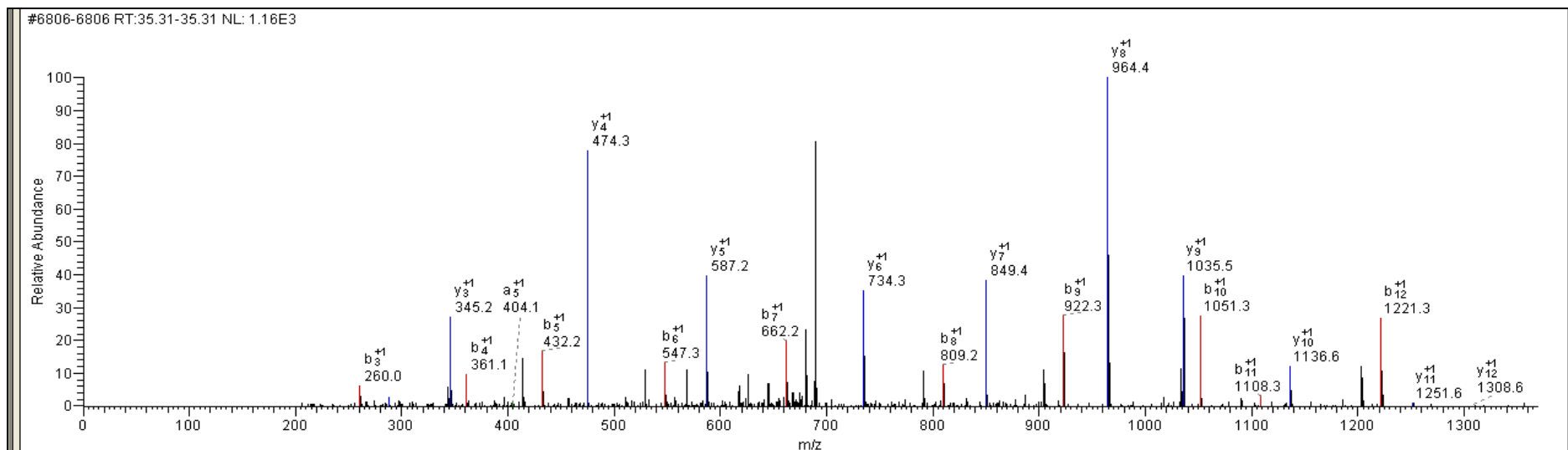
	AA	A	B	Y	
1	Q	101.07	129.07	-	17
2	D	216.10	244.09	1703.92	16
3	A	287.13	315.13	1588.89	15
4	L	400.22	428.21	1517.86	14
5	P	497.27	525.27	1404.77	13
6	A	568.31	596.30	1307.72	12
7	F	715.38	743.37	1236.68	11
8	I	828.46	856.46	1089.62	10
9	S	915.49	943.49	976.53	9
10	T	1016.54	1044.54	889.50	8
11	A	1087.58	1115.57	788.45	7
12	E	1216.62	1244.62	717.41	6
13	S	1303.65	1331.65	588.37	5
14	L	1416.74	1444.73	501.34	4
15	Q	1544.80	1572.79	388.26	3
16	I	1657.88	1685.87	260.20	2
17	K	-	-	147.11	1



Mlc-c NP_511049.1 Myosin light chain cytoplasmic CG3201-PA

R.SGDTADDFIEGLR.H

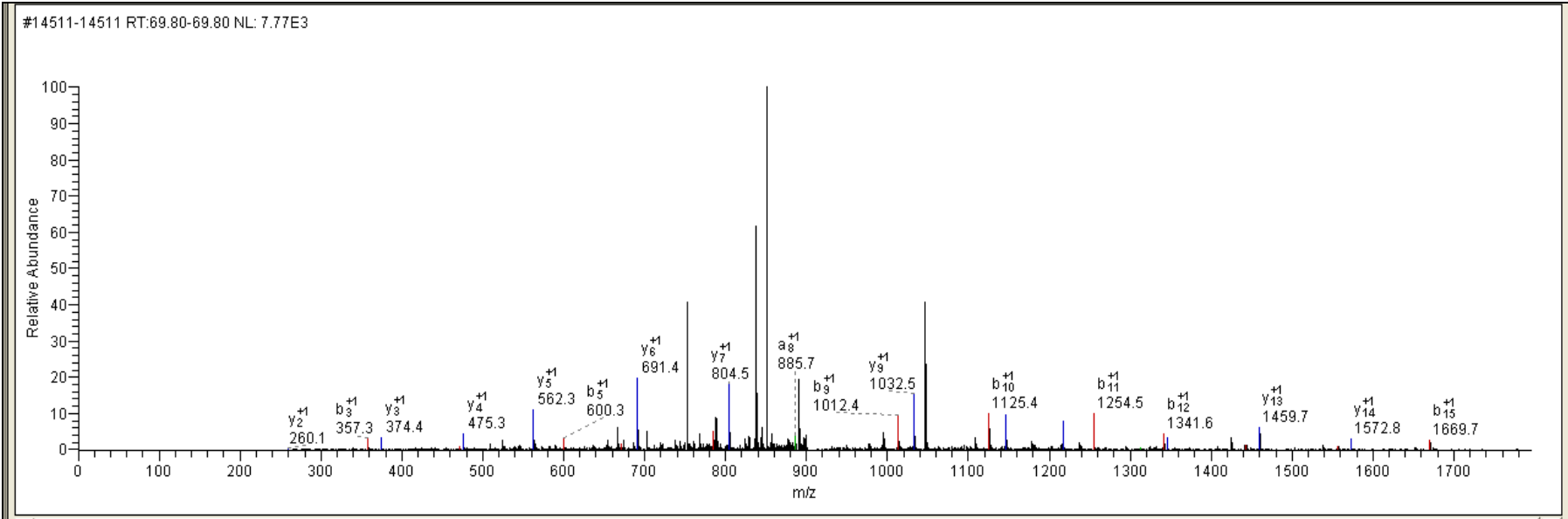
	AA	A	B	Y	
1	S	60.04	88.04	-	13
2	G	117.07	145.06	1308.61	12
3	D	232.09	260.09	1251.59	11
4	T	333.14	361.14	1136.56	10
5	A	404.18	432.17	1035.51	9
6	D	519.20	547.20	964.47	8
7	D	634.23	662.23	849.45	7
8	F	781.30	809.29	734.42	6
9	I	894.38	922.38	587.35	5
10	E	1023.43	1051.42	474.27	4
11	G	1080.45	1108.44	345.22	3
12	L	1193.53	1221.53	288.20	2
13	R	-	-	175.12	1



Nipped-A NP_001097192.1 Nipped-A CG33554-PD

K.NEINEALEVIESTNLK.Y

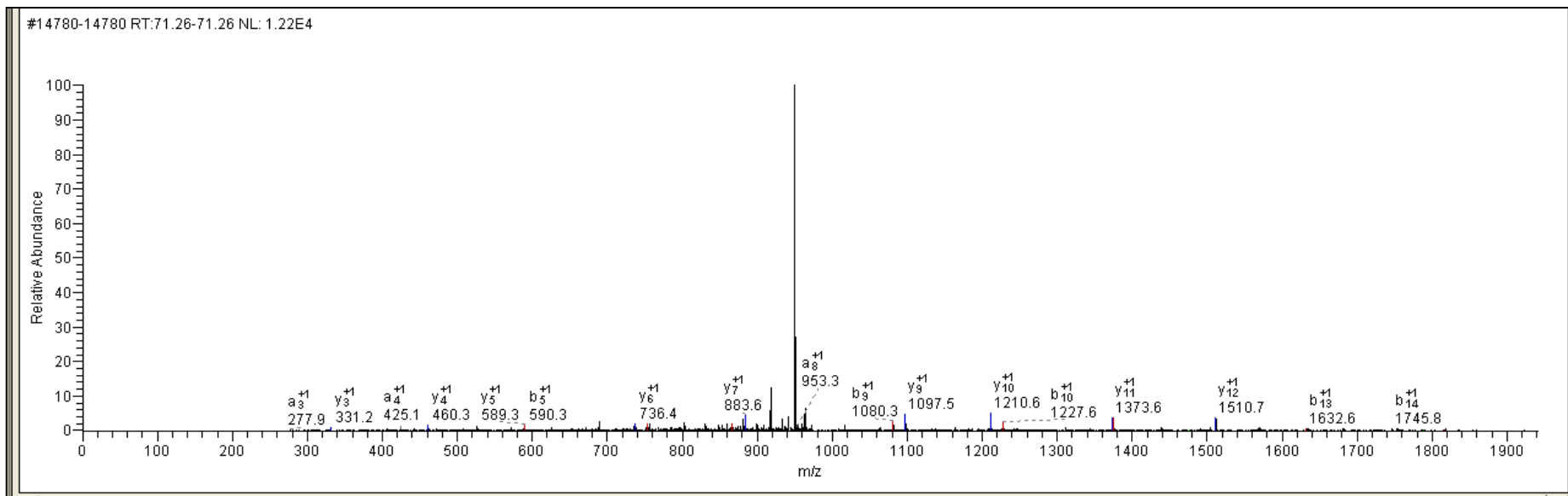
	AA	A	B	Y	
1	N	87.06	115.05	-	16
2	E	216.10	244.09	1701.89	15
3	I	329.18	357.18	1572.85	14
4	N	443.22	471.22	1459.76	13
5	E	572.27	600.26	1345.72	12
6	A	643.30	671.30	1216.68	11
7	L	756.39	784.38	1145.64	10
8	E	885.43	913.43	1032.56	9
9	V	984.50	1012.49	903.51	8
10	I	1097.58	1125.58	804.45	7
11	E	1226.63	1254.62	691.36	6
12	S	1313.66	1341.65	562.32	5
13	T	1414.71	1442.70	475.29	4
14	N	1528.75	1556.74	374.24	3
15	L	1641.83	1669.83	260.20	2
16	K	-	-	147.11	1



Nnp-1 NP_651976.1 Nnp-1 CG12396-PA

R.GMTMHYLDVFFFEELAK.A

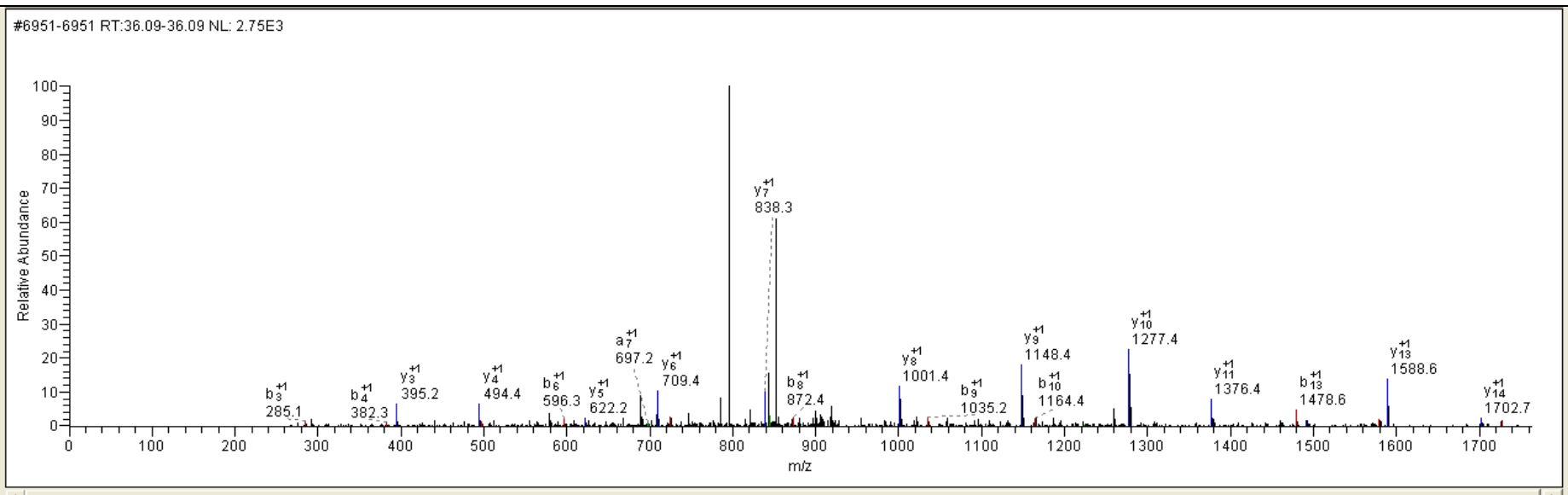
	AA	A	B	Y	
1	G	30.03	58.03	-	16
2	M*	177.07	205.06	1905.88	15
3	T	278.12	306.11	1758.84	14
4	M*	425.15	453.15	1657.79	13
5	H	562.21	590.21	1510.76	12
6	Y	725.27	753.27	1373.70	11
7	L	838.36	866.35	1210.64	10
8	D	953.39	981.38	1097.55	9
9	V	1052.45	1080.45	982.52	8
10	F	1199.52	1227.52	883.46	7
11	F	1346.59	1374.59	736.39	6
12	E	1475.63	1503.63	589.32	5
13	E	1604.68	1632.67	460.28	4
14	L	1717.76	1745.75	331.23	3
15	A	1788.80	1816.79	218.15	2
16	K	-	-	147.11	1



Nlp NP_524557.1 Nucleoplasmin CG7917-PA

R.AVNPDVEFYESKVTFK.L

	AA	A	B	Y	
1	A	44.05	72.04	-	16
2	V	143.12	171.11	1801.90	15
3	N	257.16	285.16	1702.83	14
4	P	354.21	382.21	1588.79	13
5	D	469.24	497.24	1491.74	12
6	V	568.31	596.30	1376.71	11
7	E	697.35	725.35	1277.64	10
8	F	844.42	872.41	1148.60	9
9	Y	1007.48	1035.48	1001.53	8
10	E	1136.53	1164.52	838.47	7
11	S	1223.56	1251.55	709.42	6
12	K	1351.65	1379.65	622.39	5
13	V	1450.72	1478.72	494.30	4
14	T	1551.77	1579.76	395.23	3
15	F	1698.84	1726.83	294.18	2
16	K	-	-	147.11	1

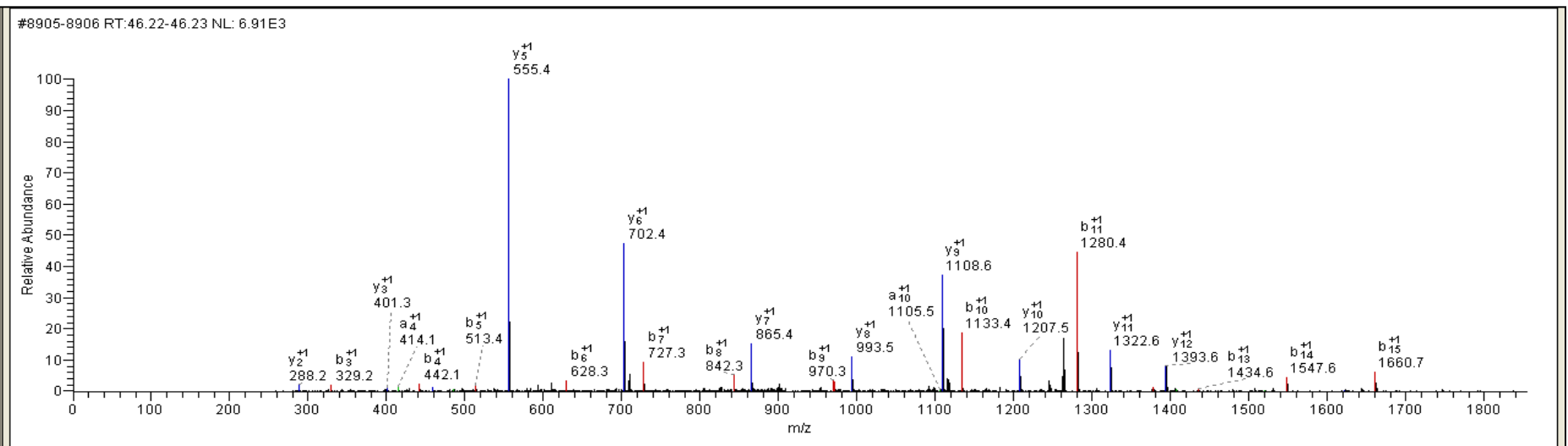


Nurf-38 NP_523849.3

Nucleosome remodeling factor - 38kD CG4634-PA

K.VNDIADVDQYFPGLLR.A

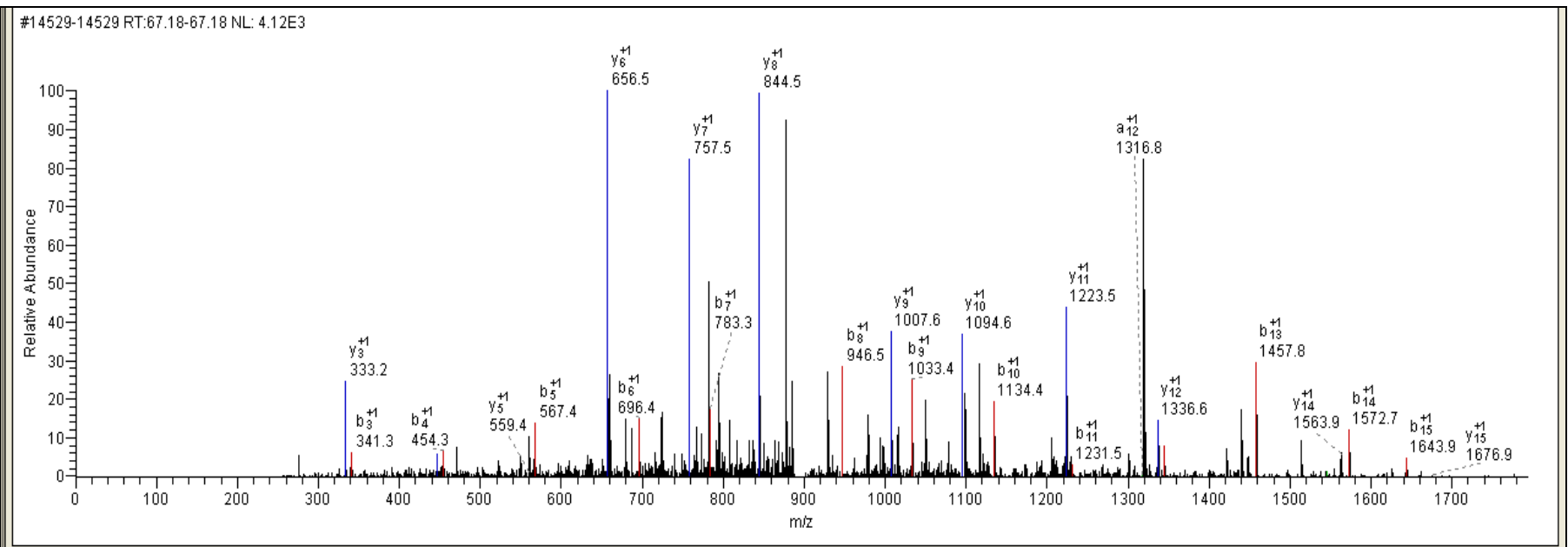
	AA	A	B	Y	
1	V	72.08	100.08	-	16
2	N	186.12	214.12	1735.86	15
3	D	301.15	329.15	1621.82	14
4	I	414.23	442.23	1506.80	13
5	A	485.27	513.27	1393.71	12
6	D	600.30	628.29	1322.67	11
7	V	699.37	727.36	1207.65	10
8	D	814.39	842.39	1108.58	9
9	Q	942.45	970.45	993.55	8
10	Y	1105.52	1133.51	865.49	7
11	F	1252.58	1280.58	702.43	6
12	P	1349.64	1377.63	555.36	5
13	G	1406.66	1434.65	458.31	4
14	L	1519.74	1547.74	401.29	3
15	L	1632.83	1660.82	288.20	2
16	R	-	-	175.12	1



Nup153 NP_001097002.1 Nup153 CG4453-PB

R.ILNLLESYSTPLIDAK.R

	AA	A	B	Y	
1	I	86.10	114.09	-	16
2	L	199.18	227.18	1676.91	15
3	N	313.22	341.22	1563.83	14
4	L	426.31	454.30	1449.78	13
5	L	539.39	567.39	1336.70	12
6	E	668.43	696.43	1223.62	11
7	S	755.47	783.46	1094.57	10
8	Y	918.53	946.52	1007.54	9
9	S	1005.56	1033.56	844.48	8
10	T	1106.61	1134.60	757.45	7
11	P	1203.66	1231.66	656.40	6
12	L	1316.75	1344.74	559.34	5
13	I	1429.83	1457.83	446.26	4
14	D	1544.86	1572.85	333.18	3
15	A	1615.89	1643.89	218.15	2
16	K	-	-	147.11	1

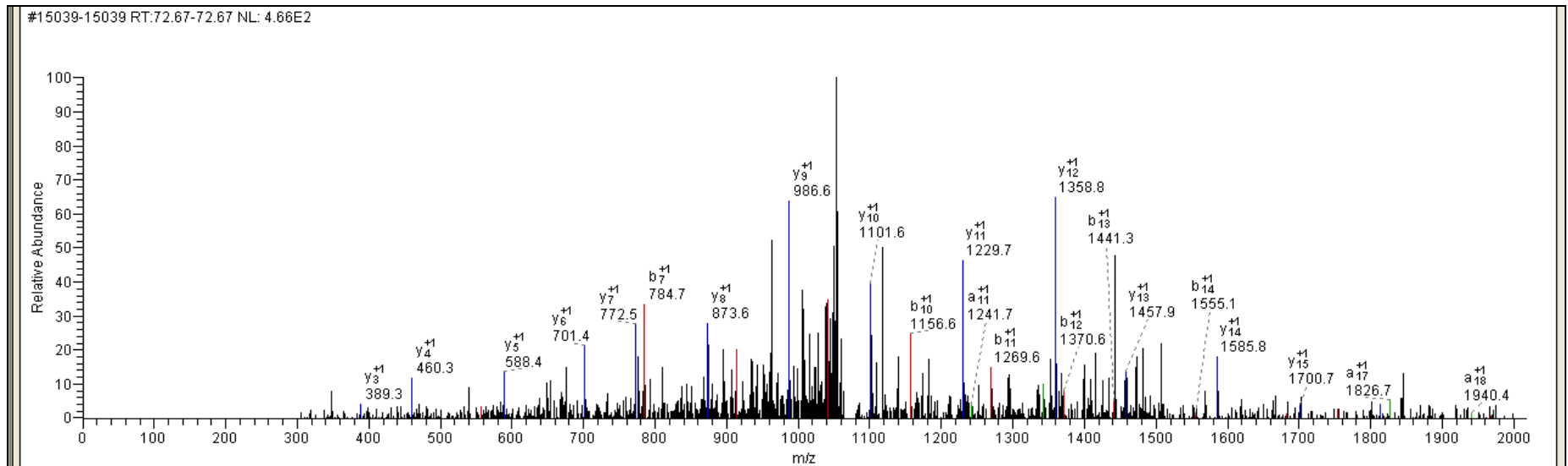


Oscp NP_524358.2

Oligomycin sensitivity-conferring protein CG4307-PA

K.LSQLDQVEKDLTALQATIR.S

	AA	A	B	Y	
1	L	86.10	114.09	-	19
2	S	173.13	201.12	2029.09	18
3	Q	301.19	329.18	1942.06	17
4	L	414.27	442.27	1814.00	16
5	D	529.30	557.29	1700.92	15
6	Q	657.36	685.35	1585.89	14
7	V	756.43	784.42	1457.83	13
8	E	885.47	913.46	1358.76	12
9	K	1013.56	1041.56	1229.72	11
10	D	1128.59	1156.58	1101.63	10
11	L	1241.67	1269.67	986.60	9
12	T	1342.72	1370.72	873.52	8
13	A	1413.76	1441.75	772.47	7
14	L	1526.84	1554.84	701.43	6
15	Q	1654.90	1682.90	588.35	5
16	A	1725.94	1753.93	460.29	4
17	T	1826.99	1854.98	389.25	3
18	I	1940.07	1968.06	288.20	2
19	R	-	-	175.12	1

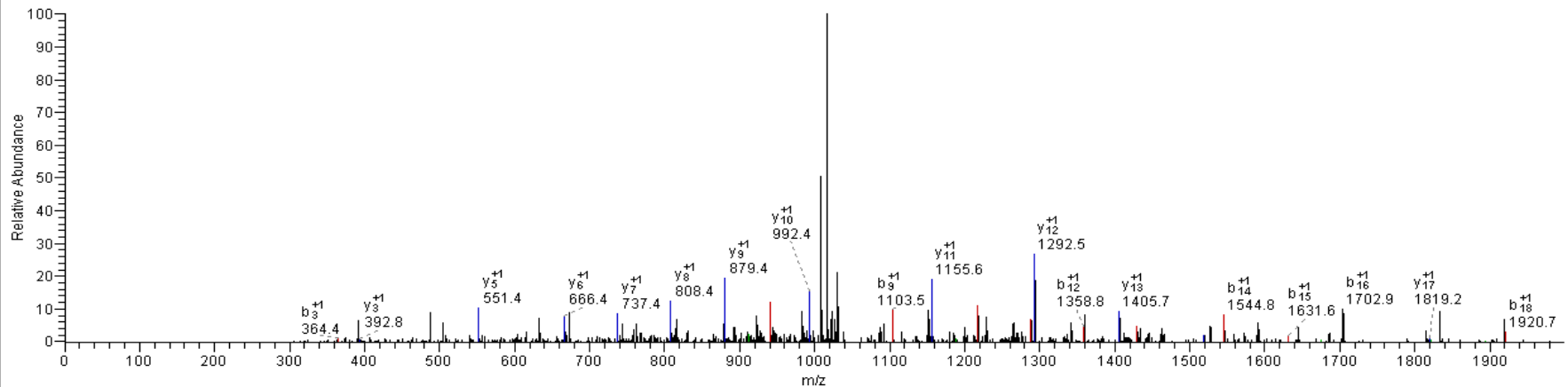


osa NP_996228.1 osa CG7467-PC

R.EFSVNLLHYLAAADSAMAR.T

	AA	A	B	Y	
1	E	102.05	130.05	-	19
2	F	249.12	277.12	1965.99	18
3	S	336.16	364.15	1818.92	17
4	V	435.22	463.22	1731.88	16
5	N	549.27	577.26	1632.82	15
6	L	662.35	690.35	1518.77	14
7	L	775.43	803.43	1405.69	13
8	H	912.49	940.49	1292.61	12
9	Y	1075.56	1103.55	1155.55	11
10	L	1188.64	1216.64	992.48	10
11	A	1259.68	1287.67	879.40	9
12	A	1330.72	1358.71	808.36	8
13	A	1401.75	1429.75	737.32	7
14	D	1516.78	1544.77	666.29	6
15	S	1603.81	1631.81	551.26	5
16	A	1674.85	1702.84	464.23	4
17	M*	1821.88	1849.88	393.19	3
18	A	1892.92	1920.92	246.16	2
19	R	-	-	175.12	1

#14396-14396 RT:69.16-69.16 NL: 1.03E3

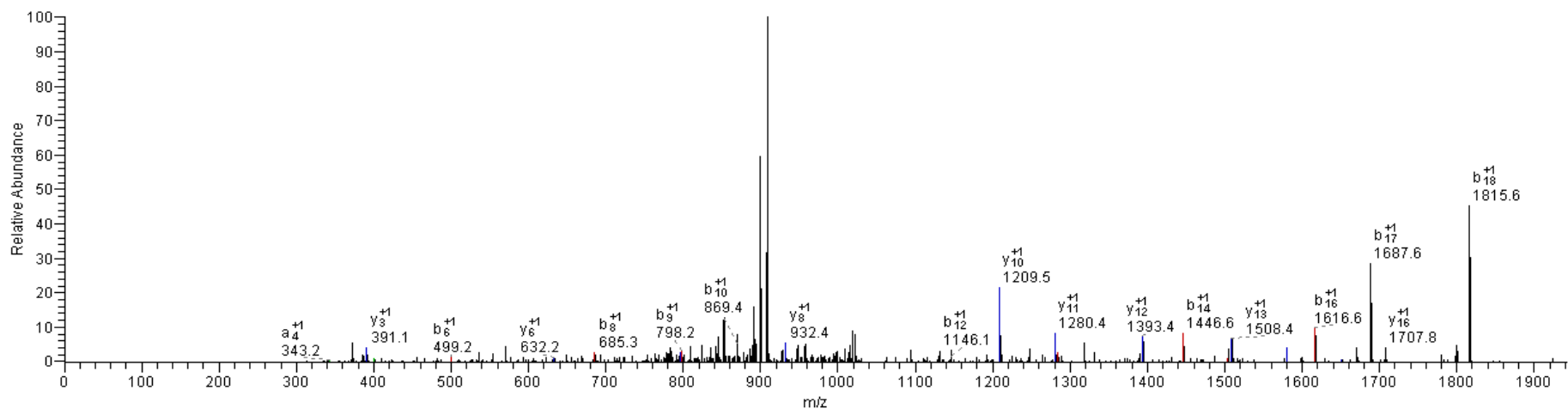


Osi15 NP_649636.1 Osiris 15 CG1157-PA

R.NGQAGAADLAYNHYGLAQPF

	AA	A	B	Y	
1	N	87.06	115.05	-	20
2	G	144.08	172.07	1963.93	19
3	Q	272.14	300.13	1906.91	18
4	A	343.17	371.17	1778.85	17
5	G	400.19	428.19	1707.81	16
6	A	471.23	499.23	1650.79	15
7	A	542.27	570.26	1579.75	14
8	D	657.30	685.29	1508.72	13
9	L	770.38	798.37	1393.69	12
10	A	841.42	869.41	1280.61	11
11	Y	1004.48	1032.47	1209.57	10
12	N	1118.52	1146.52	1046.51	9
13	H	1255.58	1283.58	932.46	8
14	Y	1418.64	1446.64	795.40	7
15	G	1475.67	1503.66	632.34	6
16	L	1588.75	1616.75	575.32	5
17	A	1659.79	1687.78	462.23	4
18	Q	1787.85	1815.84	391.20	3
19	P	1884.90	1912.89	263.14	2
20	F	-	-	166.09	1

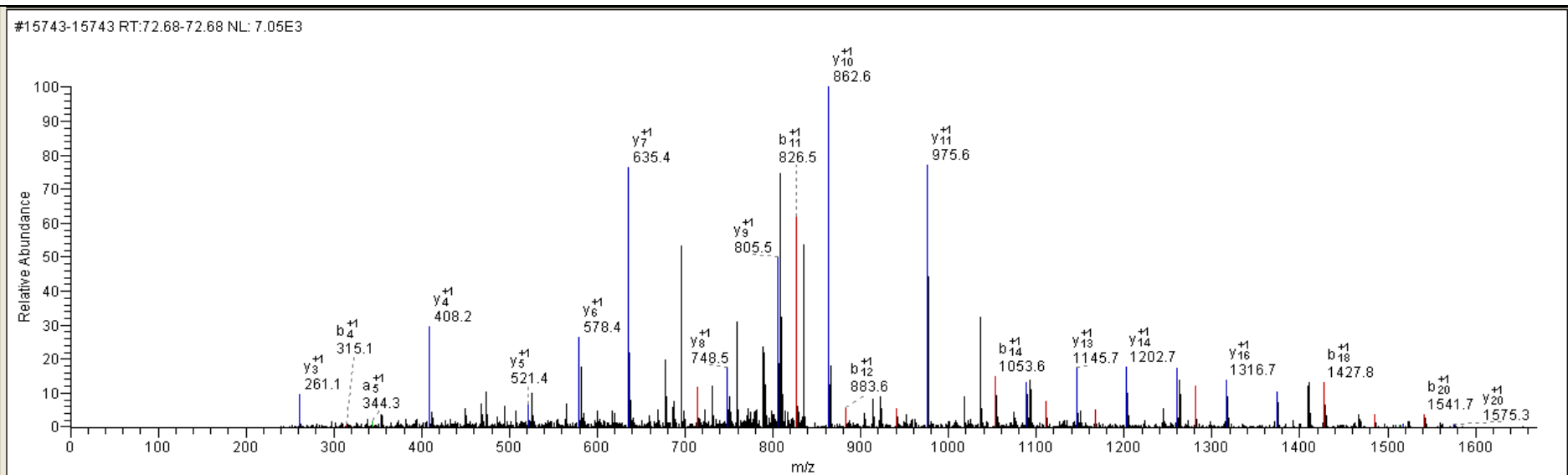
#7190-7190 RT:37.34-37.34 NL: 1.18E3



Osi6 NP_649625.2 Osiris 6 CG1151-PA

R.IGGSGGGGGLLGGLGGLFGGK.N

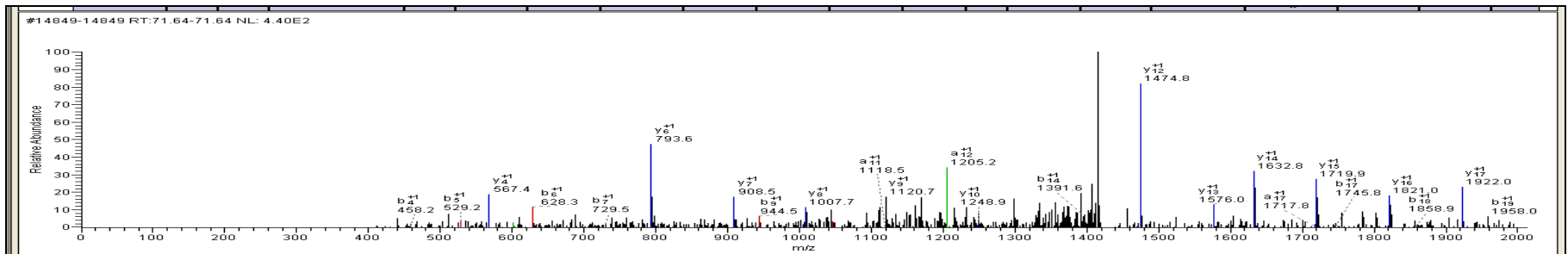
	AA	A	B	Y	
1	I	86.10	114.09	-	21
2	G	143.12	171.11	1574.83	20
3	G	200.14	228.13	1517.81	19
4	S	287.17	315.17	1460.79	18
5	G	344.19	372.19	1373.75	17
6	G	401.21	429.21	1316.73	16
7	G	458.24	486.23	1259.71	15
8	G	515.26	543.25	1202.69	14
9	G	572.28	600.27	1145.67	13
10	L	685.36	713.36	1088.65	12
11	L	798.45	826.44	975.56	11
12	G	855.47	883.46	862.48	10
13	G	912.49	940.48	805.46	9
14	L	1025.57	1053.57	748.44	8
15	G	1082.60	1110.59	635.35	7
16	G	1139.62	1167.61	578.33	6
17	L	1252.70	1280.70	521.31	5
18	F	1399.77	1427.76	408.22	4
19	G	1456.79	1484.79	261.16	3
20	G	1513.81	1541.81	204.13	2
21	K	-	-	147.11	1



Pen NP_477041.1 Pendulin CG4799-PA

K.EAAWAVTNTTTSGTPEQIVDLIEKYK.I

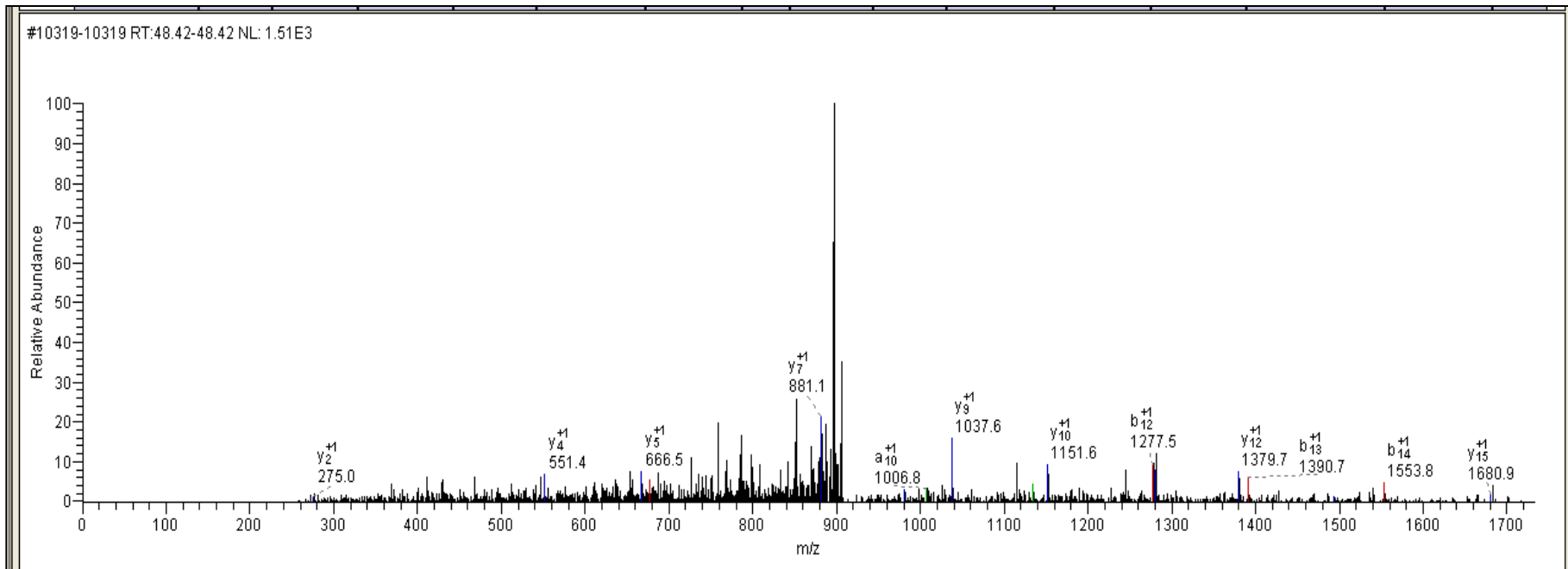
S no	AA	A	B	Y	
1	E	102.05	130.05	-	26
2	A	173.09	201.09	2736.41	25
3	A	244.13	272.12	2665.37	24
4	W	430.21	458.2	2594.33	23
5	A	501.25	529.24	2408.26	22
6	V	600.31	628.31	2337.22	21
7	T	701.36	729.36	2238.15	20
8	N	815.4	843.4	2137.1	19
9	T	916.45	944.45	2023.06	18
10	T	1017.5	1045.49	1922.01	17
11	T	1118.55	1146.54	1820.96	16
12	S	1205.58	1233.57	1719.92	15
13	G	1262.6	1290.6	1632.88	14
14	T	1363.65	1391.64	1575.86	13
15	P	1460.7	1488.7	1474.82	12
16	E	1589.74	1617.74	1377.76	11
17	Q	1717.8	1745.8	1248.72	10
18	I	1830.89	1858.88	1120.66	9
19	V	1929.96	1957.95	1007.58	8
20	D	2044.98	2072.98	908.51	7
21	L	2158.07	2186.06	793.48	6
22	I	2271.15	2299.15	680.4	5
23	E	2400.19	2428.19	567.31	4
24	K	2528.29	2556.28	438.27	3
25	Y	2691.35	2719.35	310.18	2
26	K	-	-	147.11	1



polo NP_524179.2 polo CG12306-PA

R.FSTIVENGVSKDLYQK.I

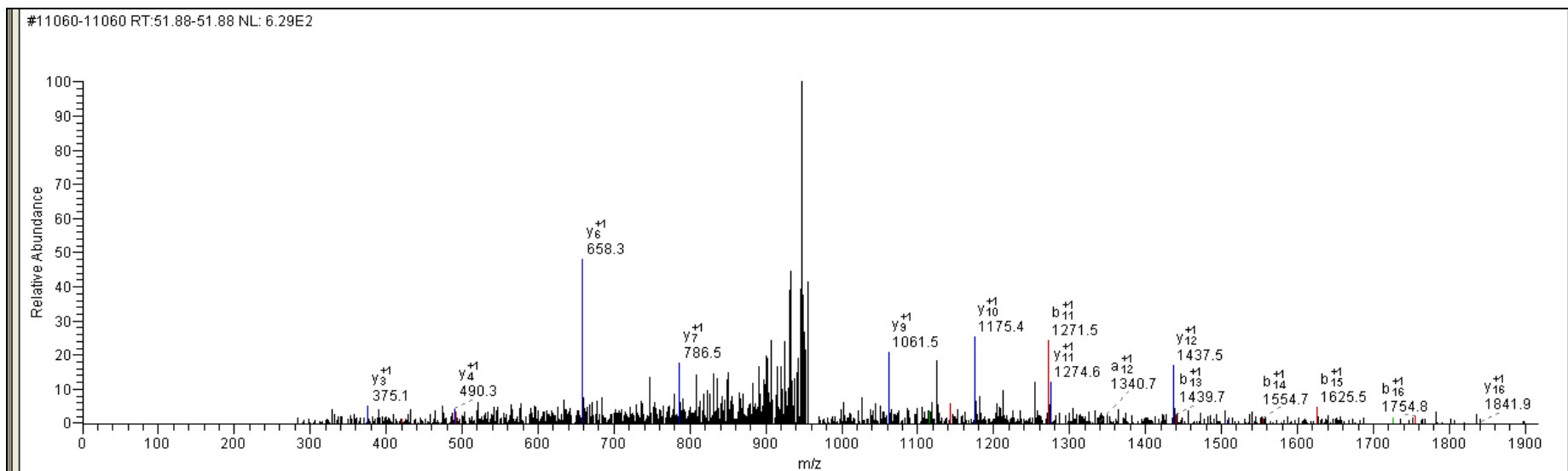
	AA	A	B	Y	
1	F	120.08	148.08	-	16
2	S	207.11	235.11	1680.88	15
3	T	308.16	336.16	1593.85	14
4	I	421.24	449.24	1492.80	13
5	V	520.31	548.31	1379.72	12
6	E	649.36	677.35	1280.65	11
7	N	763.40	791.39	1151.61	10
8	G	820.42	848.41	1037.56	9
9	V	919.49	947.48	980.54	8
10	S	1006.52	1034.52	881.47	7
11	K	1134.62	1162.61	794.44	6
12	D	1249.64	1277.64	666.35	5
13	L	1362.73	1390.72	551.32	4
14	Y	1525.79	1553.78	438.23	3
15	Q	1653.85	1681.84	275.17	2
16	K	-	-	147.11	1



pAbp NP_725752.1 polyA-binding protein CG5119-PE

R.SLGYAYVNFQQPADAER.A

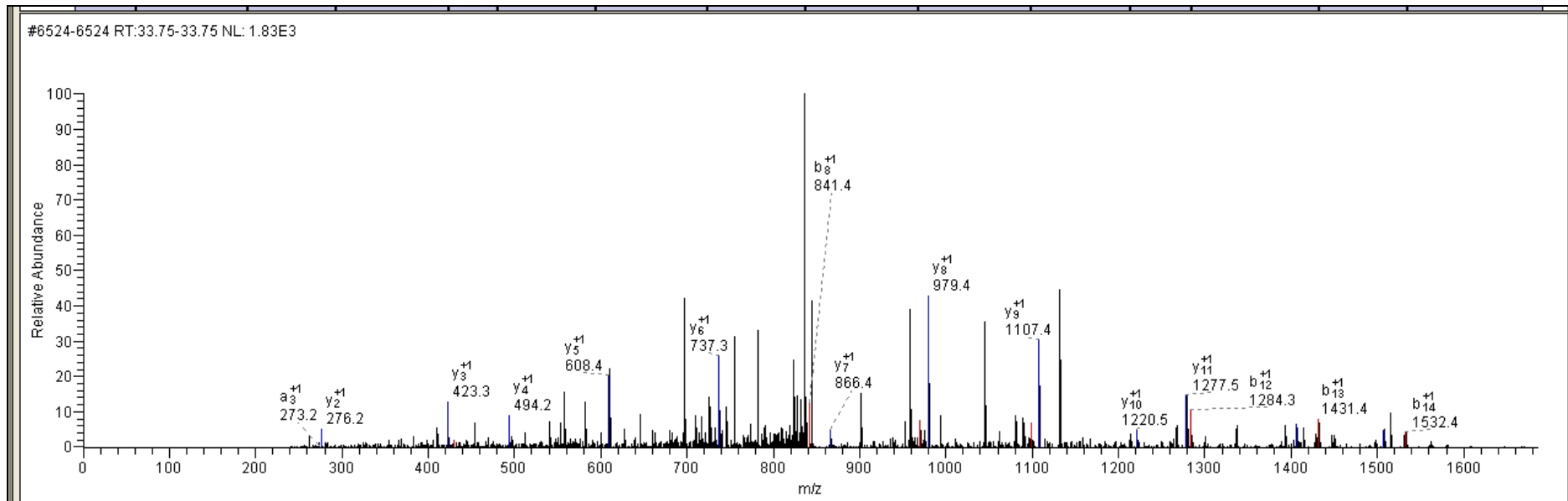
	AA	A	B	Y	
1	S	60.04	88.04	-	17
2	L	173.13	201.12	1841.88	16
3	G	230.15	258.14	1728.80	15
4	Y	393.21	421.21	1671.78	14
5	A	464.25	492.25	1508.71	13
6	Y	627.31	655.31	1437.68	12
7	V	726.38	754.38	1274.61	11
8	N	840.43	868.42	1175.54	10
9	F	987.49	1015.49	1061.50	9
10	Q	1115.55	1143.55	914.43	8
11	Q	1243.61	1271.61	786.37	7
12	P	1340.66	1368.66	658.32	6
13	A	1411.70	1439.70	561.26	5
14	D	1526.73	1554.72	490.23	4
15	A	1597.76	1625.76	375.20	3
16	E	1726.81	1754.80	304.16	2
17	R	-	-	175.12	1



pont NP_652608.1 pontin CG4003-PA

R.AQTEGLQLEENAFTR.L

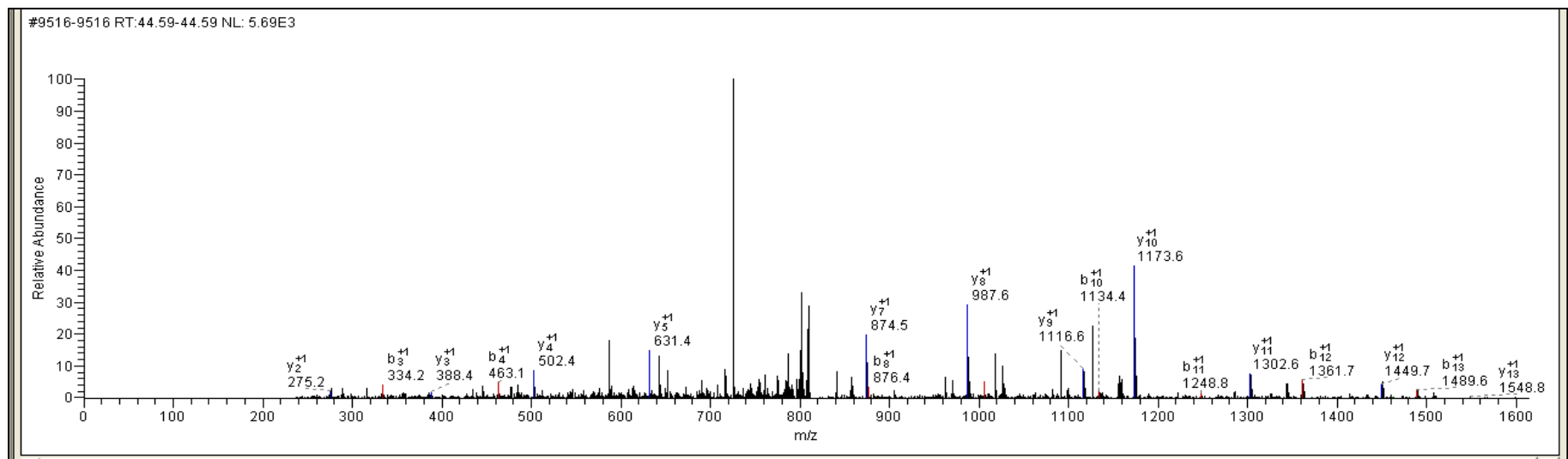
	AA	A	B	Y	
1	A	44.05	72.04	-	15
2	Q	172.11	200.10	1635.80	14
3	T	273.16	301.15	1507.74	13
4	E	402.20	430.19	1406.69	12
5	G	459.22	487.21	1277.65	11
6	L	572.30	600.30	1220.63	10
7	Q	700.36	728.36	1107.54	9
8	L	813.45	841.44	979.48	8
9	E	942.49	970.48	866.40	7
10	E	1071.53	1099.53	737.36	6
11	N	1185.57	1213.57	608.32	5
12	A	1256.61	1284.61	494.27	4
13	F	1403.68	1431.68	423.24	3
14	T	1504.73	1532.72	276.17	2
15	R	-	-	175.12	1



Pdi NP_524079.1 Protein disulfide isomerase CG6988-PA

K.SVFEGELNEENLKK.F

	AA	A	B	Y	
1	S	60.04	88.04	-	14
2	V	159.11	187.11	1548.79	13
3	F	306.18	334.18	1449.72	12
4	E	435.22	463.22	1302.65	11
5	G	492.25	520.24	1173.61	10
6	E	621.29	649.28	1116.59	9
7	L	734.37	762.37	987.55	8
8	N	848.41	876.41	874.46	7
9	E	977.46	1005.45	760.42	6
10	E	1106.50	1134.49	631.38	5
11	N	1220.54	1248.54	502.33	4
12	L	1333.63	1361.62	388.29	3
13	K	1461.72	1489.72	275.21	2
14	K	-	-	147.11	1

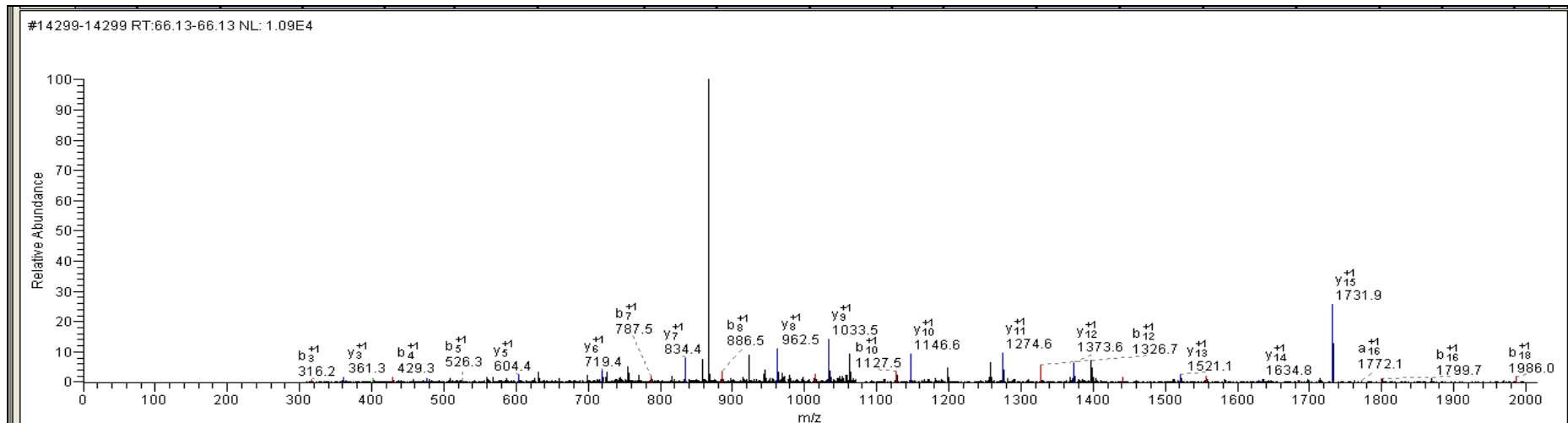


Pp2A-29B NP_001027227.1

Protein phosphatase 2A at 29B CG17291-PA

K.SDLIPNFVQLAQDDQDSVR.L

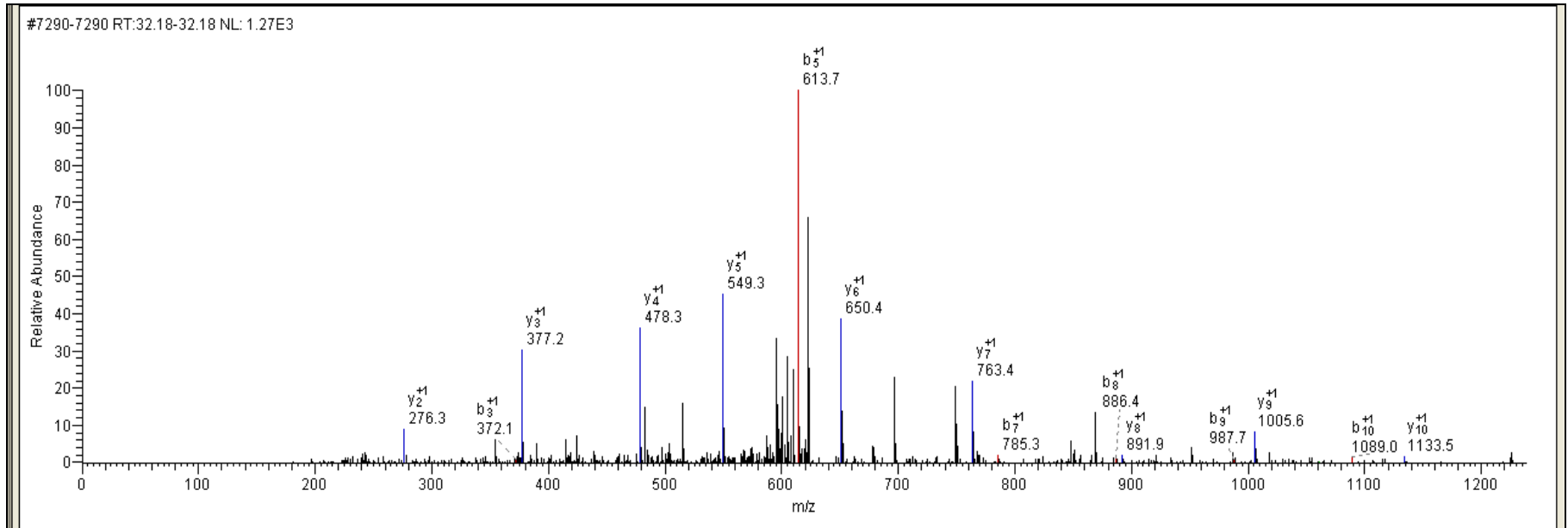
	AA	A	B	Y	
1	S	60.04	88.04	-	19
2	D	175.07	203.07	2073.02	18
3	L	288.16	316.15	1958.00	17
4	I	401.24	429.23	1844.91	16
5	P	498.29	526.29	1731.83	15
6	N	612.34	640.33	1634.78	14
7	F	759.40	787.40	1520.73	13
8	V	858.47	886.47	1373.67	12
9	Q	986.53	1014.53	1274.60	11
10	L	1099.61	1127.61	1146.54	10
11	A	1170.65	1198.65	1033.45	9
12	Q	1298.71	1326.71	962.42	8
13	D	1413.74	1441.73	834.36	7
14	D	1528.76	1556.76	719.33	6
15	Q	1656.82	1684.82	604.30	5
16	D	1771.85	1799.84	476.25	4
17	S	1858.88	1886.88	361.22	3
18	V	1957.95	1985.95	274.19	2
19	R	-	-	175.12	1



prp8 NP_610735.1 prp8 CG8877-PA

K.EQNQLTATTTR.T

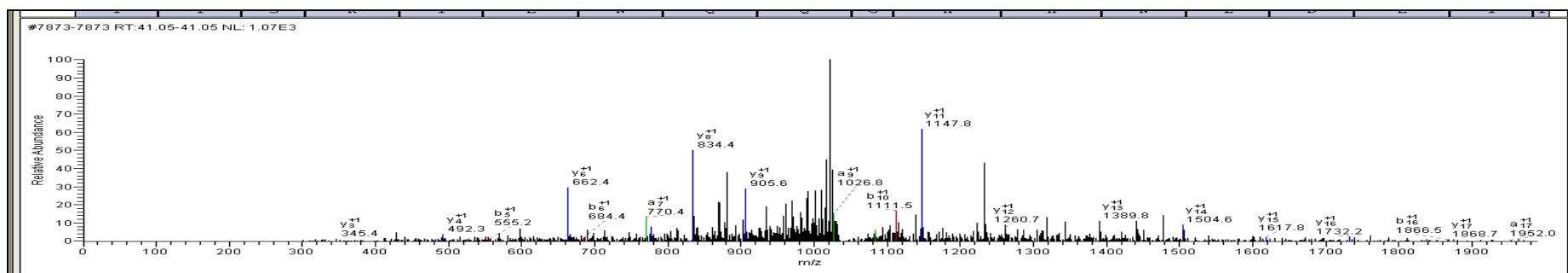
	AA	A	B	Y	
1	E	102.05	130.05	-	11
2	Q	230.11	258.11	1133.59	10
3	N	344.16	372.15	1005.53	9
4	Q	472.22	500.21	891.49	8
5	L	585.30	613.29	763.43	7
6	T	686.35	714.34	650.35	6
7	A	757.38	785.38	549.30	5
8	T	858.43	886.43	478.26	4
9	T	959.48	987.47	377.21	3
10	T	1060.53	1088.52	276.17	2
11	R	-	-	175.12	1



PyK NP_524448.3 Pyruvate kinase CG7070-PA

K.IISKIENQQGMHNLDEIIEAGDGIMVAR.G

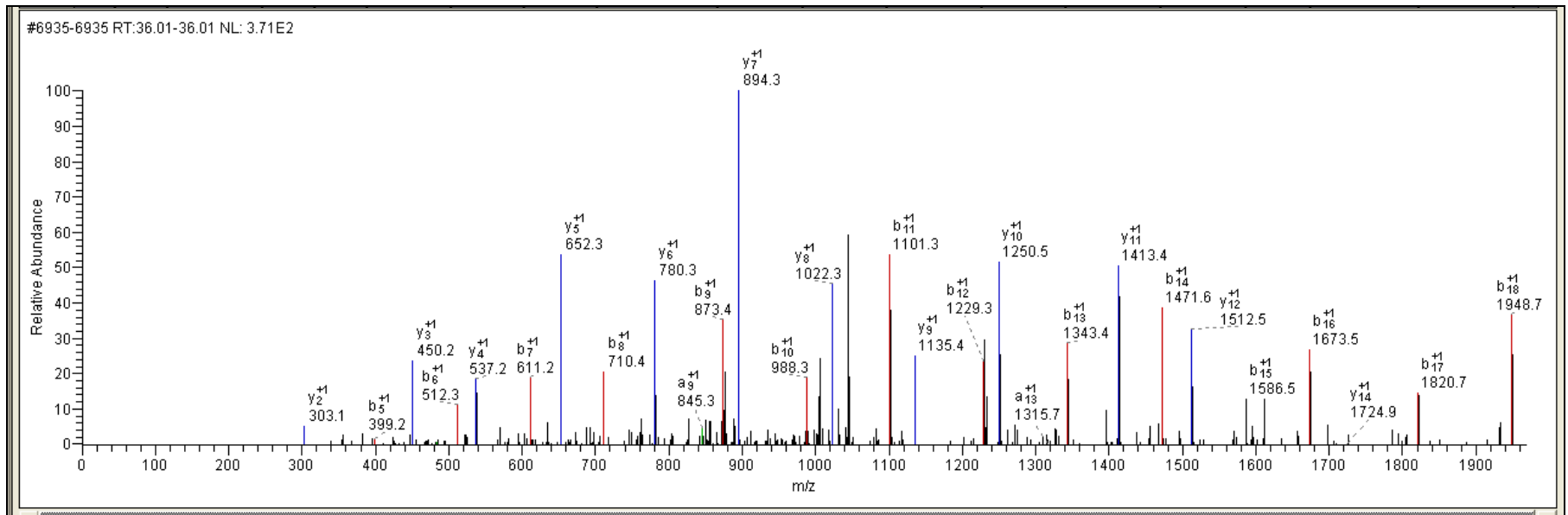
S no	AA	A	B	Y	
1	I	86.1	114.09	-	28
2	I	199.18	227.18	3013.47	27
3	S	286.21	314.21	2900.39	26
4	K	414.31	442.3	2813.36	25
5	I	527.39	555.39	2685.26	24
6	E	656.43	684.43	2572.18	23
7	N	770.48	798.47	2443.13	22
8	Q	898.54	926.53	2329.09	21
9	Q	1026.59	1054.59	2201.03	20
10	G	1083.62	1111.61	2072.97	19
11	M*	1230.65	1258.65	2015.95	18
12	H	1367.71	1395.7	1868.92	17
13	N	1481.75	1509.75	1731.86	16
14	L	1594.84	1622.83	1617.82	15
15	D	1709.86	1737.86	1504.73	14
16	E	1838.91	1866.9	1389.7	13
17	I	1951.99	1979.99	1260.66	12
18	I	2065.07	2093.07	1147.58	11
19	E	2194.12	2222.11	1034.49	10
20	A	2265.15	2293.15	905.45	9
21	G	2322.18	2350.17	834.41	8
22	D	2437.2	2465.2	777.39	7
23	G	2494.22	2522.22	662.37	6
24	I	2607.31	2635.3	605.34	5
25	M*	2754.34	2782.34	492.26	4
26	V	2853.41	2881.41	345.22	3
27	A	2924.45	2952.44	246.16	2
28	R	-	-	175.12	1



Rab5 NP_722795.1 Rab-protein 5 CG3664-PA

R.GAQAAIVVYDIQNQDSFQR.A

	AA	A	B	Y	
1	G	30.03	58.03	-	19
2	A	101.07	129.07	2066.03	18
3	Q	229.13	257.12	1994.99	17
4	A	300.17	328.16	1866.93	16
5	A	371.20	399.20	1795.90	15
6	I	484.29	512.28	1724.86	14
7	V	583.36	611.35	1611.78	13
8	V	682.42	710.42	1512.71	12
9	Y	845.49	873.48	1413.64	11
10	D	960.51	988.51	1250.58	10
11	I	1073.60	1101.59	1135.55	9
12	Q	1201.66	1229.65	1022.46	8
13	N	1315.70	1343.70	894.41	7
14	Q	1443.76	1471.75	780.36	6
15	D	1558.79	1586.78	652.30	5
16	S	1645.82	1673.81	537.28	4
17	F	1792.89	1820.88	450.25	3
18	Q	1920.95	1948.94	303.18	2
19	R	-	-	175.12	1

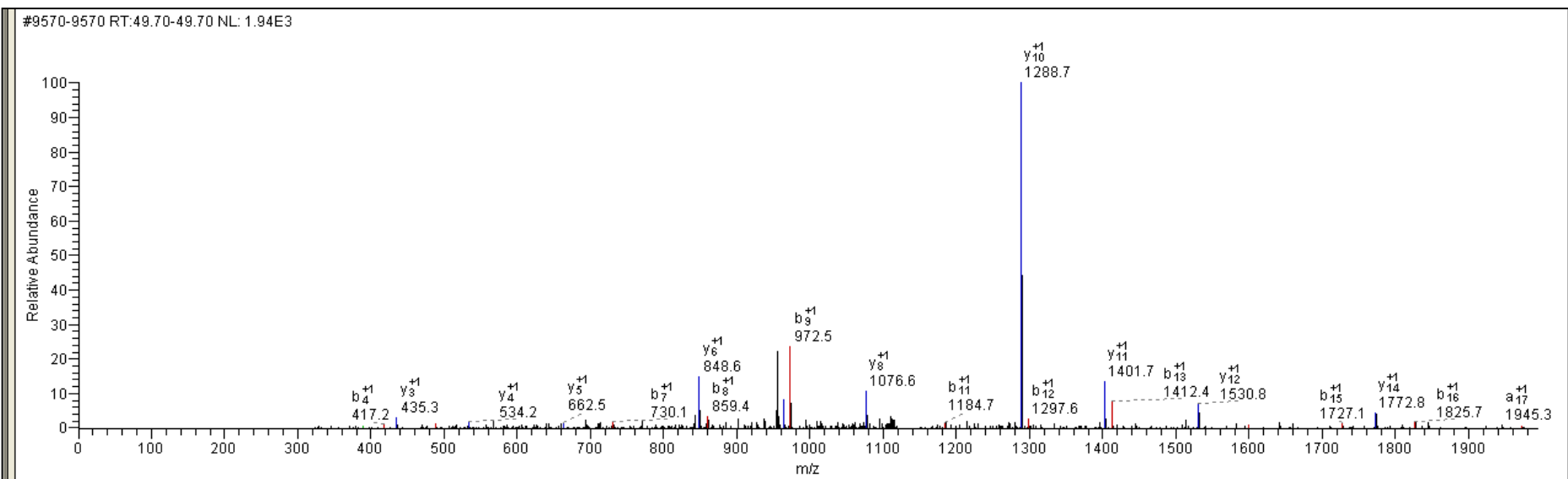


RfC38 NP_609494.1

Replication factor C 38kD subunit CG6258-PA

K.APFTANQEIPDLDWQVFLR.E

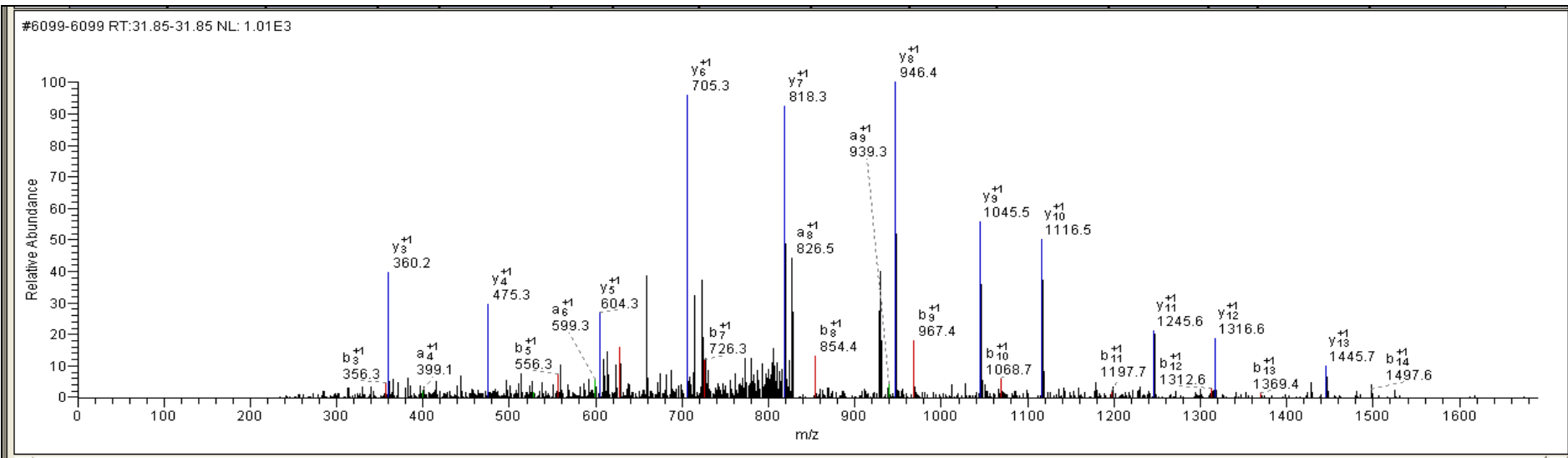
	AA	A	B	Y	
1	A	44.05	72.04	-	19
2	P	141.10	169.10	2189.10	18
3	F	288.17	316.17	2092.05	17
4	T	389.22	417.21	1944.98	16
5	A	460.26	488.25	1843.93	15
6	N	574.30	602.29	1772.90	14
7	Q	702.36	730.35	1658.85	13
8	E	831.40	859.39	1530.80	12
9	I	944.48	972.48	1401.75	11
10	P	1041.54	1069.53	1288.67	10
11	D	1156.56	1184.56	1191.62	9
12	L	1269.65	1297.64	1076.59	8
13	D	1384.67	1412.67	963.50	7
14	W	1570.75	1598.75	848.48	6
15	Q	1698.81	1726.81	662.40	5
16	V	1797.88	1825.88	534.34	4
17	F	1944.95	1972.94	435.27	3
18	L	2058.03	2086.03	288.20	2
19	R	-	-	175.12	1



RfC3 NP_609399.1 RfC3 CG5313-PA

K.IIEAEAVQITEDGKR.A

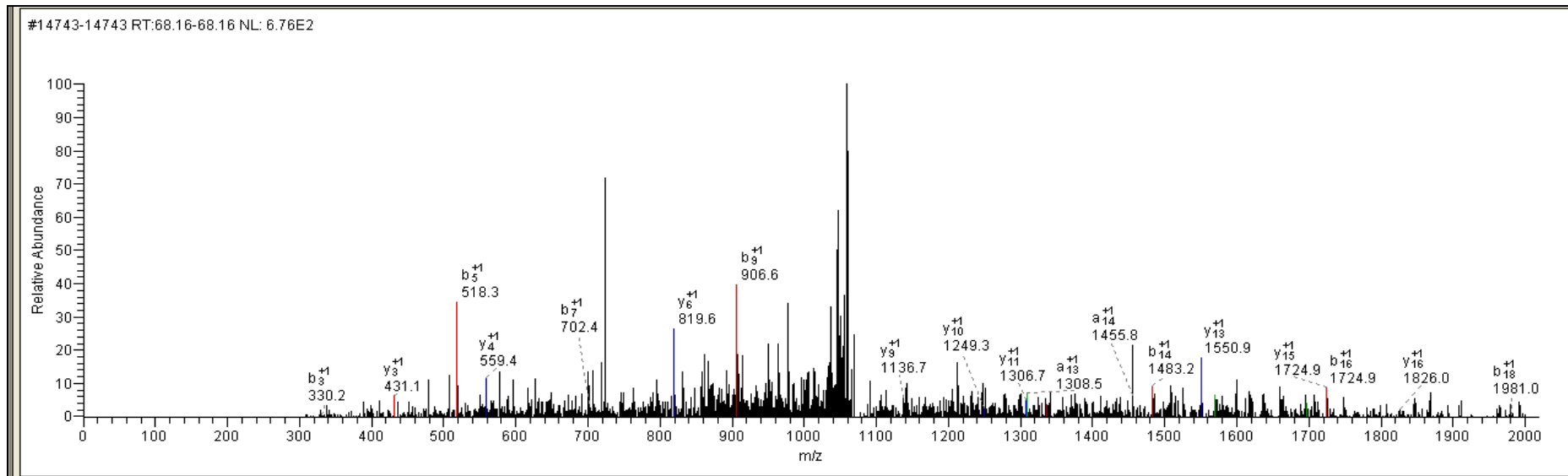
	AA	A	B	Y	
1	I	86.10	114.09	-	15
2	I	199.18	227.18	1558.81	14
3	E	328.22	356.22	1445.72	13
4	A	399.26	427.26	1316.68	12
5	E	528.30	556.30	1245.64	11
6	A	599.34	627.33	1116.60	10
7	V	698.41	726.40	1045.56	9
8	Q	826.47	854.46	946.50	8
9	I	939.55	967.55	818.44	7
10	T	1040.60	1068.59	705.35	6
11	E	1169.64	1197.64	604.30	5
12	D	1284.67	1312.66	475.26	4
13	G	1341.69	1369.68	360.24	3
14	K	1469.78	1497.78	303.21	2
15	R	-	-	175.12	1



RhoGEF2 NP_995868.1 RhoGEF2 CG9635-PF

K.DLTTSSPFGLTTDFLQQQR.M

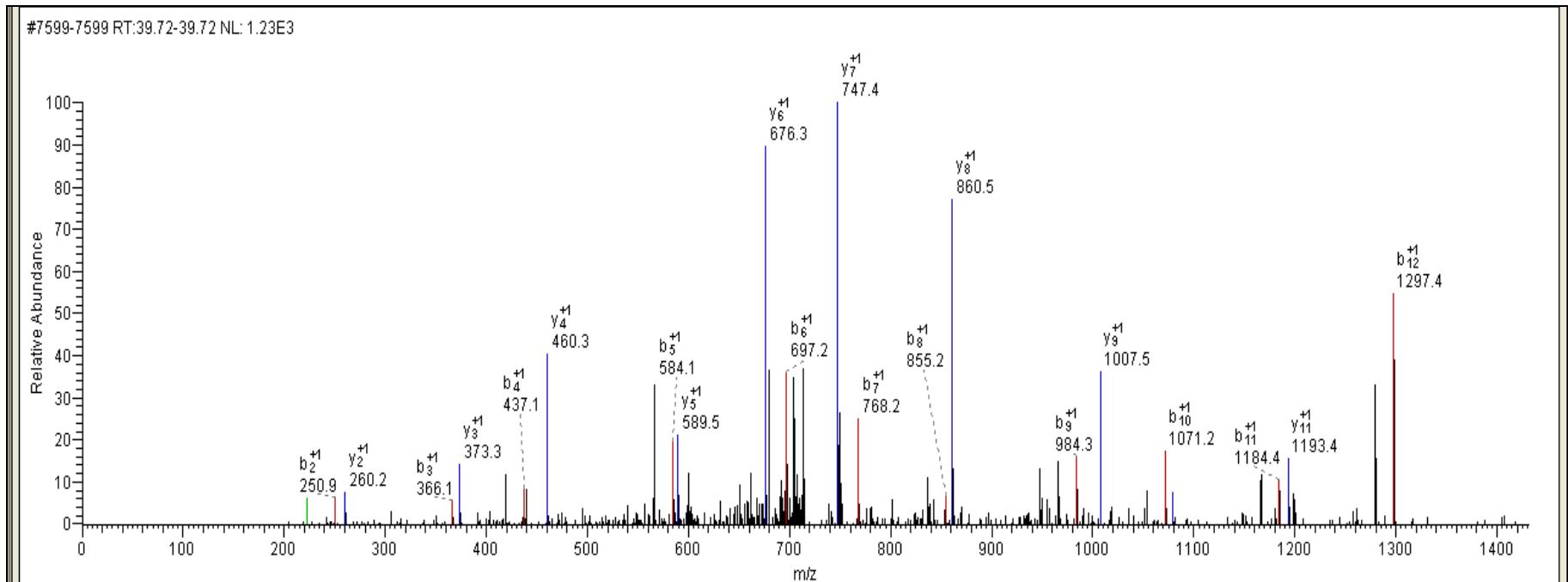
	AA	A	B	Y	
1	D	88.04	116.03	-	19
2	L	201.12	229.12	2040.04	18
3	T	302.17	330.17	1926.96	17
4	T	403.22	431.21	1825.91	16
5	S	490.25	518.25	1724.86	15
6	S	577.28	605.28	1637.83	14
7	P	674.34	702.33	1550.80	13
8	F	821.40	849.40	1453.74	12
9	G	878.43	906.42	1306.67	11
10	L	991.51	1019.50	1249.65	10
11	T	1092.56	1120.55	1136.57	9
12	T	1193.60	1221.60	1035.52	8
13	D	1308.63	1336.63	934.47	7
14	F	1455.70	1483.70	819.45	6
15	L	1568.78	1596.78	672.38	5
16	Q	1696.84	1724.84	559.29	4
17	Q	1824.90	1852.90	431.24	3
18	Q	1952.96	1980.95	303.18	2
19	R	-	-	175.12	1



RpL10Ab NP_648514.1 Ribosomal protein L10Ab CG7283-PA

K.SYDAFLASESLIK.Q

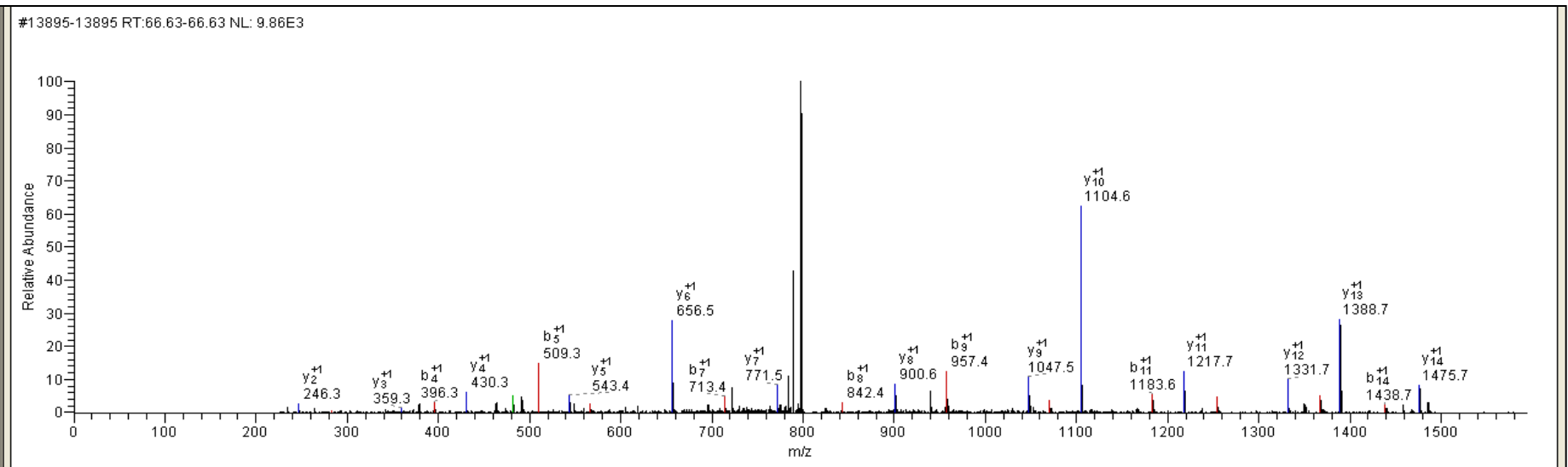
	AA	A	B	Y	
1	S	60.04	88.04	-	13
2	Y	223.11	251.10	1356.70	12
3	D	338.13	366.13	1193.64	11
4	A	409.17	437.17	1078.61	10
5	F	556.24	584.24	1007.58	9
6	L	669.32	697.32	860.51	8
7	A	740.36	768.36	747.42	7
8	S	827.39	855.39	676.39	6
9	E	956.44	984.43	589.36	5
10	S	1043.47	1071.46	460.31	4
11	L	1156.55	1184.55	373.28	3
12	I	1269.64	1297.63	260.20	2
13	K	-	-	147.11	1



RpL12 NP_524819.1 Ribosomal protein L12 CG3195-PA

K.HSGNIGFEDILAIAR.V

	AA	A	B	Y	
1	H	110.07	138.07	-	15
2	S	197.10	225.10	1475.79	14
3	G	254.12	282.12	1388.75	13
4	N	368.17	396.16	1331.73	12
5	I	481.25	509.25	1217.69	11
6	G	538.27	566.27	1104.60	10
7	F	685.34	713.34	1047.58	9
8	E	814.38	842.38	900.51	8
9	D	929.41	957.41	771.47	7
10	I	1042.50	1070.49	656.45	6
11	L	1155.58	1183.57	543.36	5
12	A	1226.62	1254.61	430.28	4
13	I	1339.70	1367.70	359.24	3
14	A	1410.74	1438.73	246.16	2
15	R	-	-	175.12	1

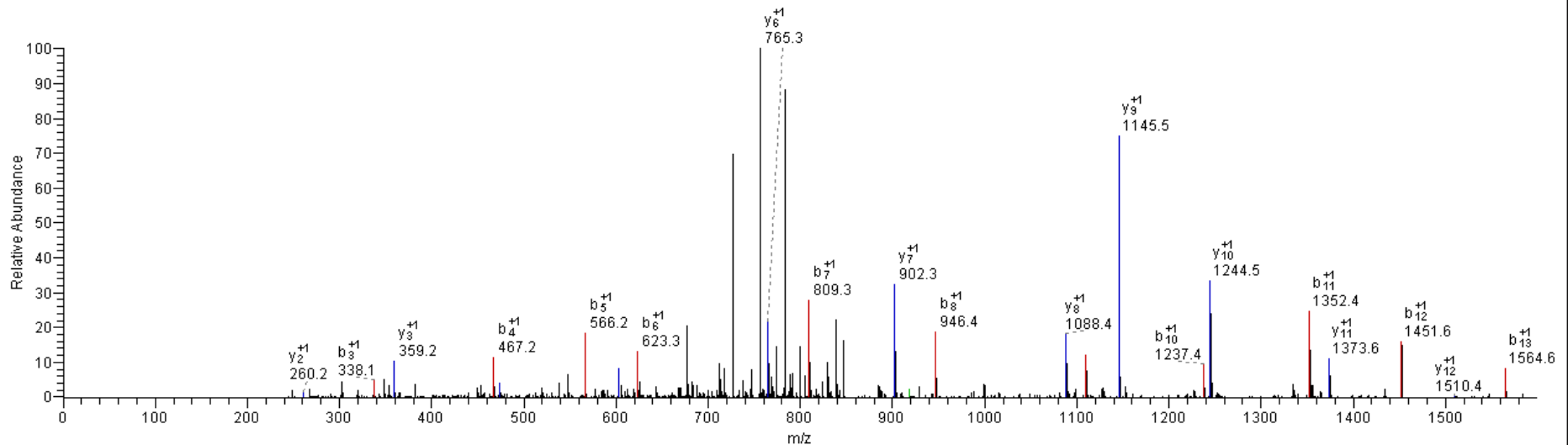


RpL13A NP_649560.1 Ribosomal protein L13A CG1475-PB

R.LSHEVGWHYQDVIK.S

	AA	A	B	Y	
1	L	86.10	114.09	-	14
2	S	173.13	201.12	1597.78	13
3	H	310.19	338.18	1510.74	12
4	E	439.23	467.22	1373.68	11
5	V	538.30	566.29	1244.64	10
6	G	595.32	623.31	1145.57	9
7	W	781.40	809.39	1088.55	8
8	H	918.46	946.45	902.47	7
9	Y	1081.52	1109.52	765.41	6
10	Q	1209.58	1237.57	602.35	5
11	D	1324.61	1352.60	474.29	4
12	V	1423.68	1451.67	359.27	3
13	I	1536.76	1564.75	260.20	2
14	K	-	-	147.11	1

#6293-6293 RT:32.61-32.61 NL: 2.59E3

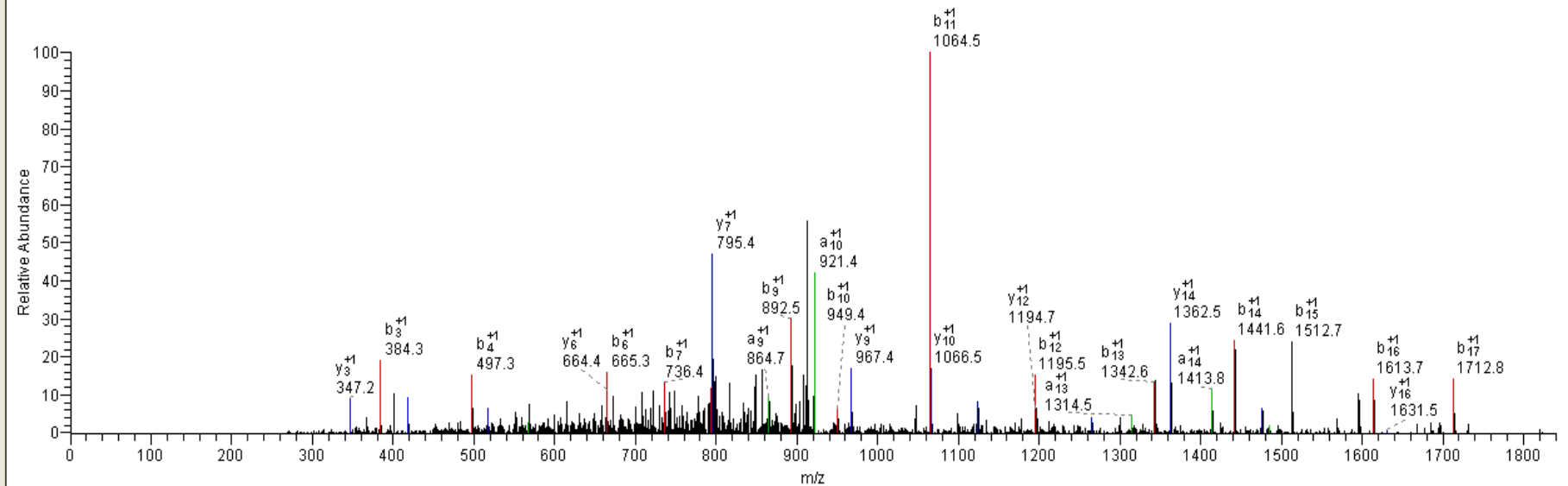


RpL23 NP_523813.1 Ribosomal protein L23 CG3661-PA

R.LNRLPAAGVGDMFVATVK.K

	AA	A	B	Y	
1	L	86.10	114.09	-	18
2	N	200.14	228.13	1745.94	17
3	R	356.24	384.24	1631.89	16
4	L	469.32	497.32	1475.79	15
5	P	566.38	594.37	1362.71	14
6	A	637.41	665.41	1265.66	13
7	A	708.45	736.45	1194.62	12
8	G	765.47	793.47	1123.58	11
9	V	864.54	892.54	1066.56	10
10	G	921.56	949.56	967.49	9
11	D	1036.59	1064.58	910.47	8
12	M	1167.63	1195.63	795.44	7
13	F	1314.70	1342.69	664.40	6
14	V	1413.77	1441.76	517.33	5
15	A	1484.80	1512.80	418.27	4
16	T	1585.85	1613.85	347.23	3
17	V	1684.92	1712.92	246.18	2
18	K	-	-	147.11	1

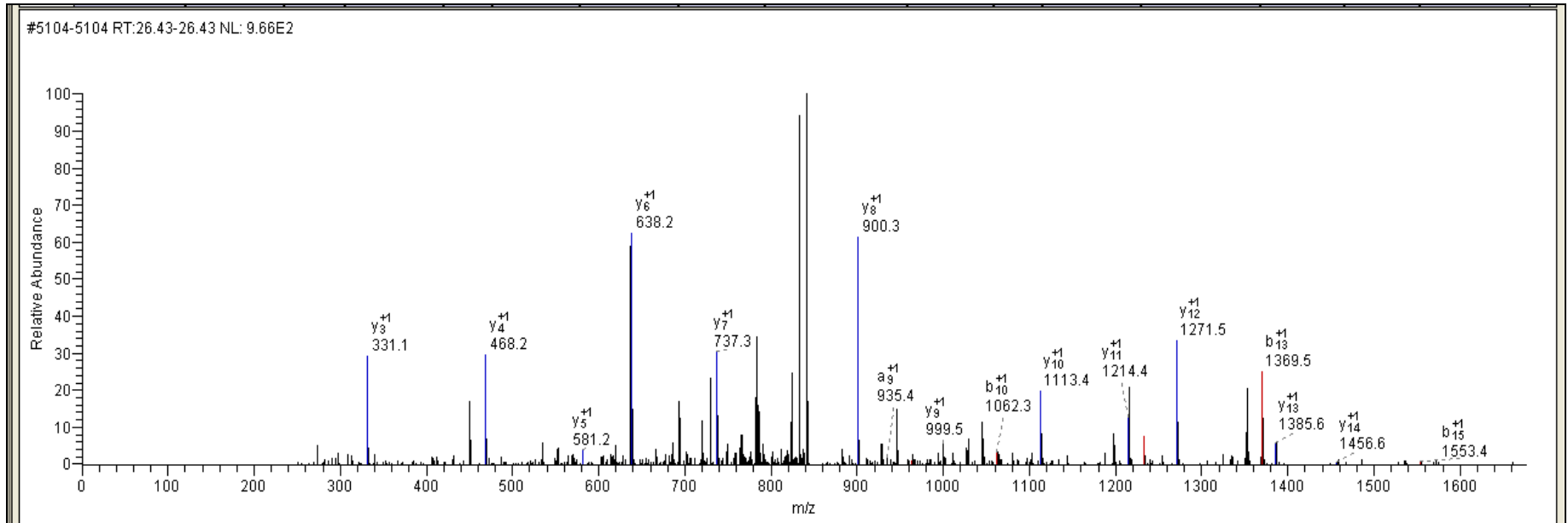
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RpL26 NP_649070.1 Ribosomal protein L26 CG6846-PA

R.ENANGTNVYVGIHPSK.V

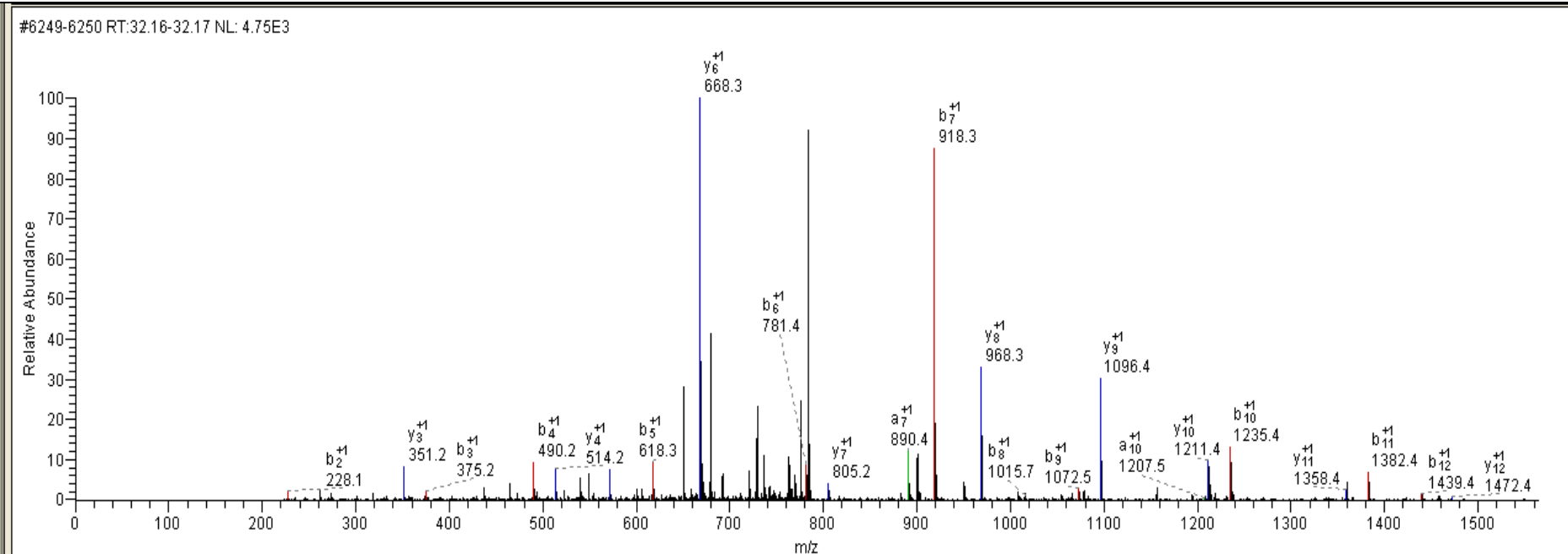
	AA	A	B	Y	
1	E	102.05	130.05	-	16
2	N	216.10	244.09	1570.80	15
3	A	287.13	315.13	1456.75	14
4	N	401.18	429.17	1385.72	13
5	G	458.20	486.19	1271.67	12
6	T	559.25	587.24	1214.65	11
7	N	673.29	701.28	1113.61	10
8	V	772.36	800.35	999.56	9
9	Y	935.42	963.42	900.49	8
10	V	1034.49	1062.49	737.43	7
11	G	1091.51	1119.51	638.36	6
12	I	1204.60	1232.59	581.34	5
13	H	1341.65	1369.65	468.26	4
14	P	1438.71	1466.70	331.20	3
15	S	1525.74	1553.73	234.14	2
16	K	-	-	147.11	1



RpL27A NP_476963.1 Ribosomal protein L27A CG15442-PA

R.INFDKYHPGYFGK.V

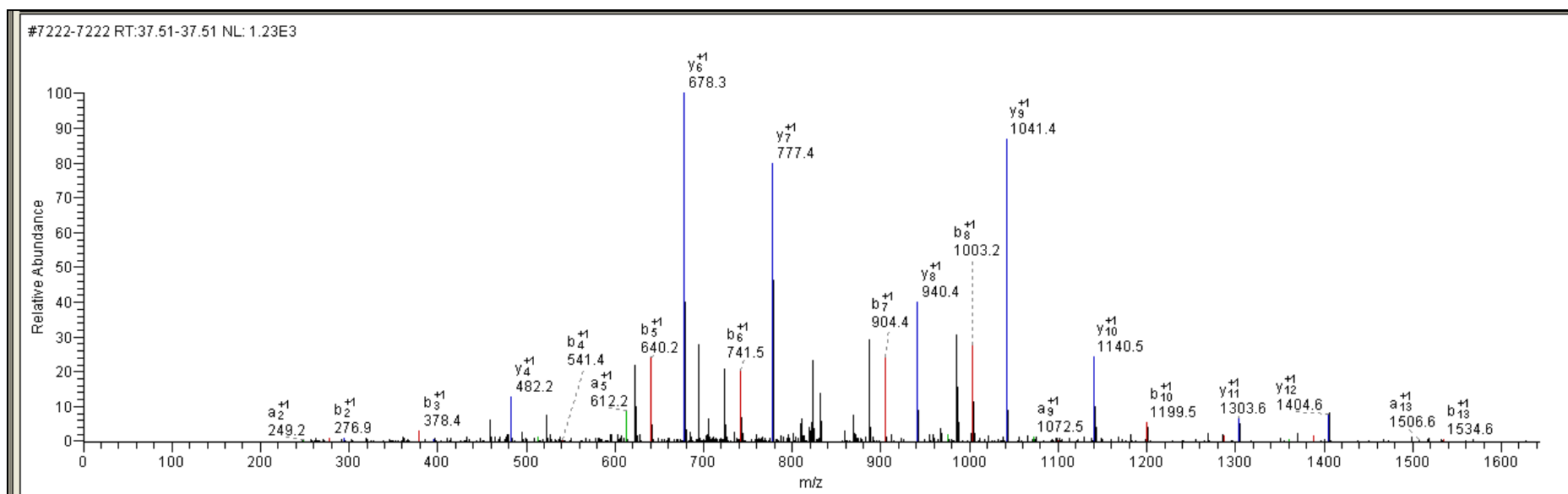
	AA	A	B	Y	
1	I	86.10	114.09	-	13
2	N	200.14	228.13	1472.70	12
3	F	347.21	375.20	1358.65	11
4	D	462.23	490.23	1211.58	10
5	K	590.33	618.32	1096.56	9
6	Y	753.39	781.39	968.46	8
7	H	890.45	918.45	805.40	7
8	P	987.50	1015.50	668.34	6
9	G	1044.53	1072.52	571.29	5
10	Y	1207.59	1235.58	514.27	4
11	F	1354.66	1382.65	351.20	3
12	G	1411.68	1439.67	204.13	2
13	K	-	-	147.11	1



RpL31 NP_724805.1 Ribosomal protein L31 CG1821-PC

K.LYTYVTYVPVSTFK.N

	AA	A	B	Y	
1	L	86.10	114.09	-	14
2	Y	249.16	277.15	1567.80	13
3	T	350.21	378.20	1404.74	12
4	Y	513.27	541.27	1303.69	11
5	V	612.34	640.33	1140.63	10
6	T	713.39	741.38	1041.56	9
7	Y	876.45	904.45	940.51	8
8	V	975.52	1003.51	777.45	7
9	P	1072.57	1100.57	678.38	6
10	V	1171.64	1199.63	581.33	5
11	S	1258.67	1286.67	482.26	4
12	T	1359.72	1387.71	395.23	3
13	F	1506.79	1534.78	294.18	2
14	K	-	-	147.11	1



RpL35 NP_572243.1 Ribosomal protein L35 CG4111-PB

K.QLDELKNELLSLR.V

	AA	A	B	Y	
1	Q	101.07	129.07	-	13
2	L	214.16	242.15	1442.82	12
3	D	329.18	357.18	1329.74	11
4	E	458.22	486.22	1214.71	10
5	L	571.31	599.30	1085.67	9
6	K	699.40	727.40	972.58	8
7	N	813.45	841.44	844.49	7
8	E	942.49	970.48	730.45	6
9	L	1055.57	1083.57	601.40	5
10	L	1168.66	1196.65	488.32	4
11	S	1255.69	1283.68	375.24	3
12	L	1368.77	1396.77	288.20	2
13	R	-	-	175.12	1

