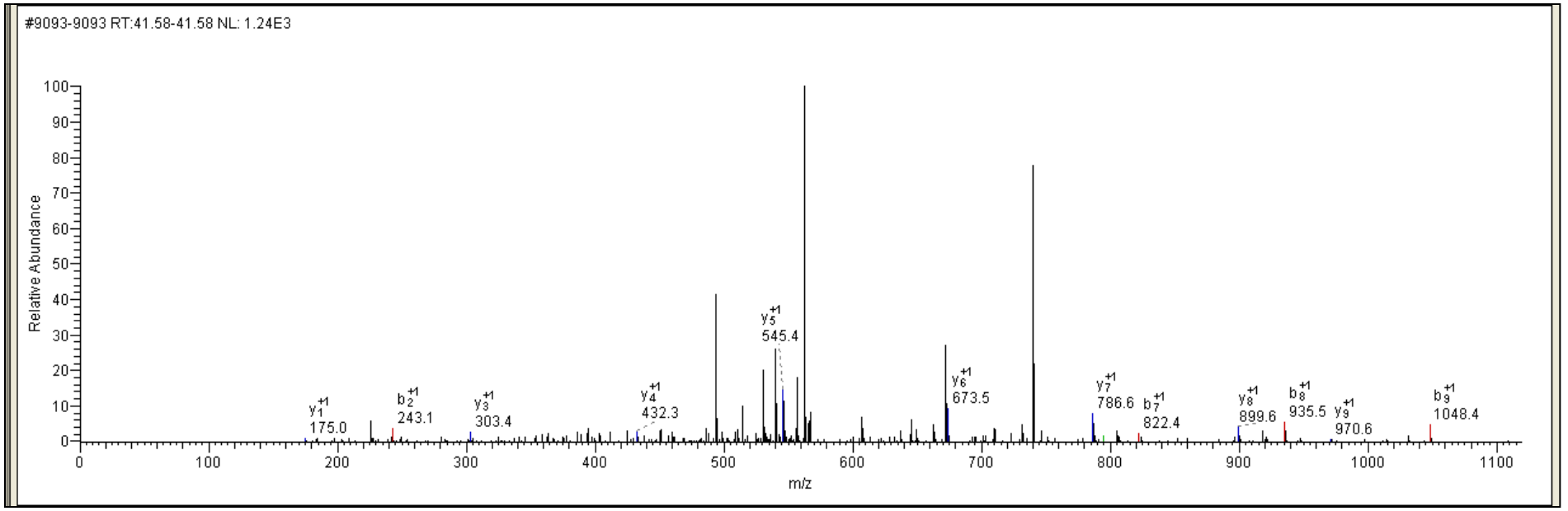
RpL35A NP_649539.1 Ribosomal protein L35A CG2099-PA

R.NQHENQAILKIEGAR.R

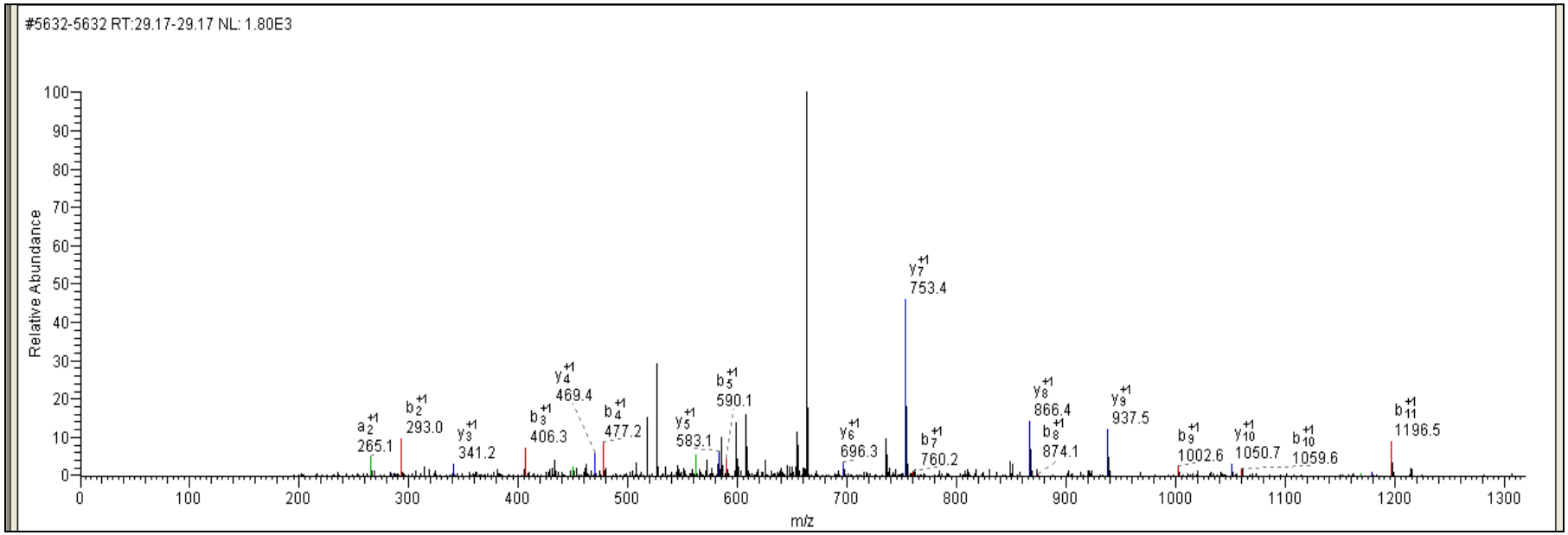
	AA	A	B	Y	
1	N	87.06	115.05	-	15
2	Q	215.11	243.11	1606.87	14
3	H	352.17	380.17	1478.81	13
4	E	481.22	509.21	1341.75	12
5	N	595.26	623.25	1212.71	11
6	Q	723.32	751.31	1098.66	10
7	A	794.35	822.35	970.60	9
8	I	907.44	935.43	899.57	8
9	L	1020.52	1048.52	786.48	7
10	K	1148.62	1176.61	673.40	6
11	I	1261.70	1289.70	545.30	5
12	E	1390.74	1418.74	432.22	4
13	G	1447.77	1475.76	303.18	3
14	A	1518.80	1546.80	246.16	2
15	R	-	-	175.12	1



RpL36 NP_476629.1 Ribosomal protein L36 CG7622-PA

R.YELAIGLNKGHK.T

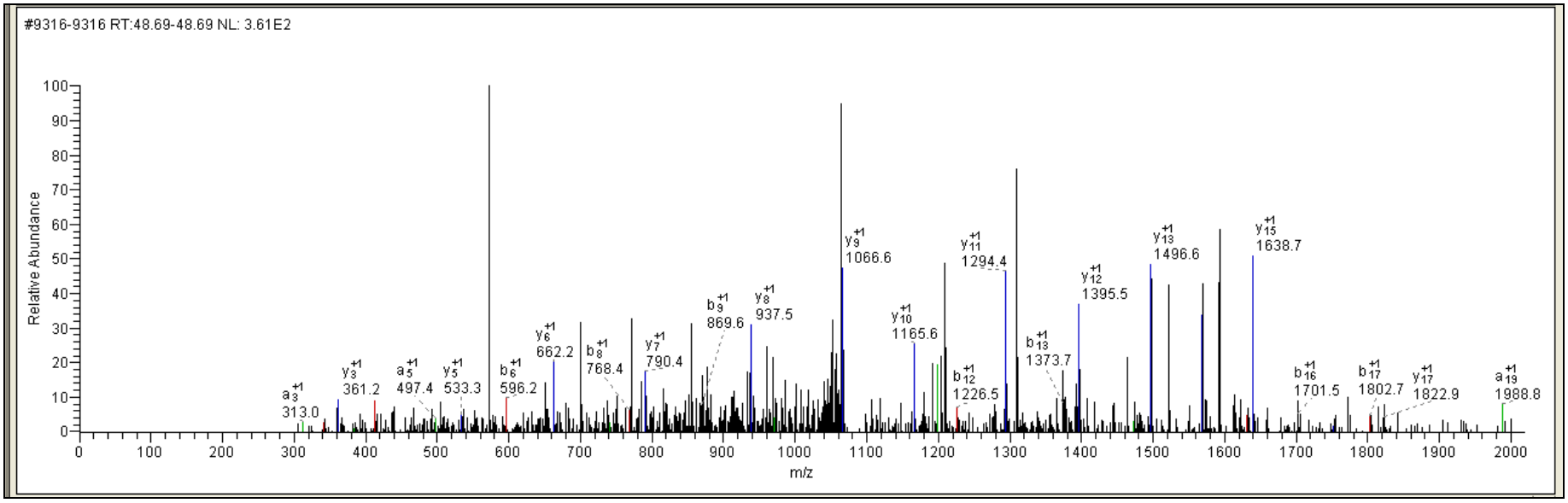
	AA	A	B	Y	
1	Y	136.08	164.07	-	12
2	E	265.12	293.11	1179.68	11
3	L	378.20	406.20	1050.64	10
4	A	449.24	477.23	937.56	9
5	I	562.32	590.32	866.52	8
6	G	619.34	647.34	753.44	7
7	L	732.43	760.42	696.42	6
8	N	846.47	874.47	583.33	5
9	K	974.57	1002.56	469.29	4
10	G	1031.59	1059.58	341.19	3
11	H	1168.65	1196.64	284.17	2
12	K	-	-	147.11	1



RpLP0 NP_524211.1 Ribosomal protein LP0 CG7490-PA

K.NLLAIAATTEVEFKEATTIK.E

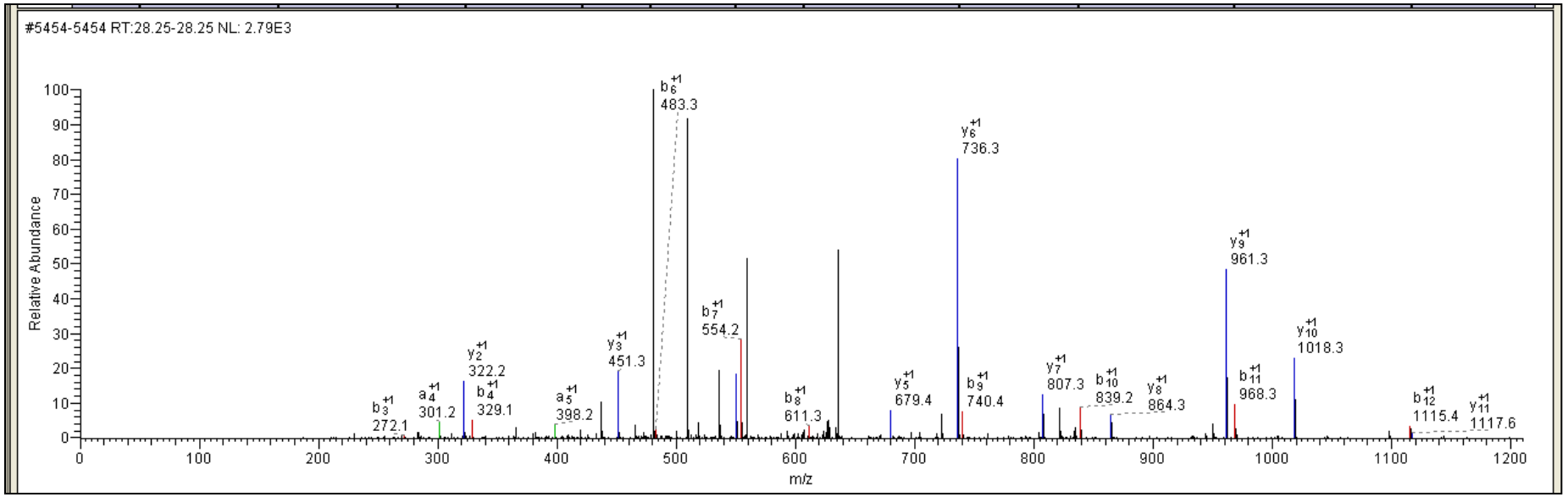
	AA	A	B	Y	
1	N	87.06	115.05	-	20
2	L	200.14	228.13	2049.15	19
3	L	313.22	341.22	1936.06	18
4	A	384.26	412.26	1822.98	17
5	I	497.34	525.34	1751.94	16
6	A	568.38	596.38	1638.86	15
7	A	639.42	667.41	1567.82	14
8	T	740.47	768.46	1496.78	13
9	T	841.51	869.51	1395.74	12
10	E	970.56	998.55	1294.69	11
11	V	1069.63	1097.62	1165.65	10
12	E	1198.67	1226.66	1066.58	9
13	F	1345.74	1373.73	937.54	8
14	K	1473.83	1501.83	790.47	7
15	E	1602.87	1630.87	662.37	6
16	A	1673.91	1701.91	533.33	5
17	T	1774.96	1802.95	462.29	4
18	T	1876.01	1904.00	361.24	3
19	I	1989.09	2017.09	260.20	2
20	K	-	-	147.11	1



RpS10b NP_728273.1 Ribosomal protein S10b CG14206-PB

K.GDVGPGAGEVEFR.G

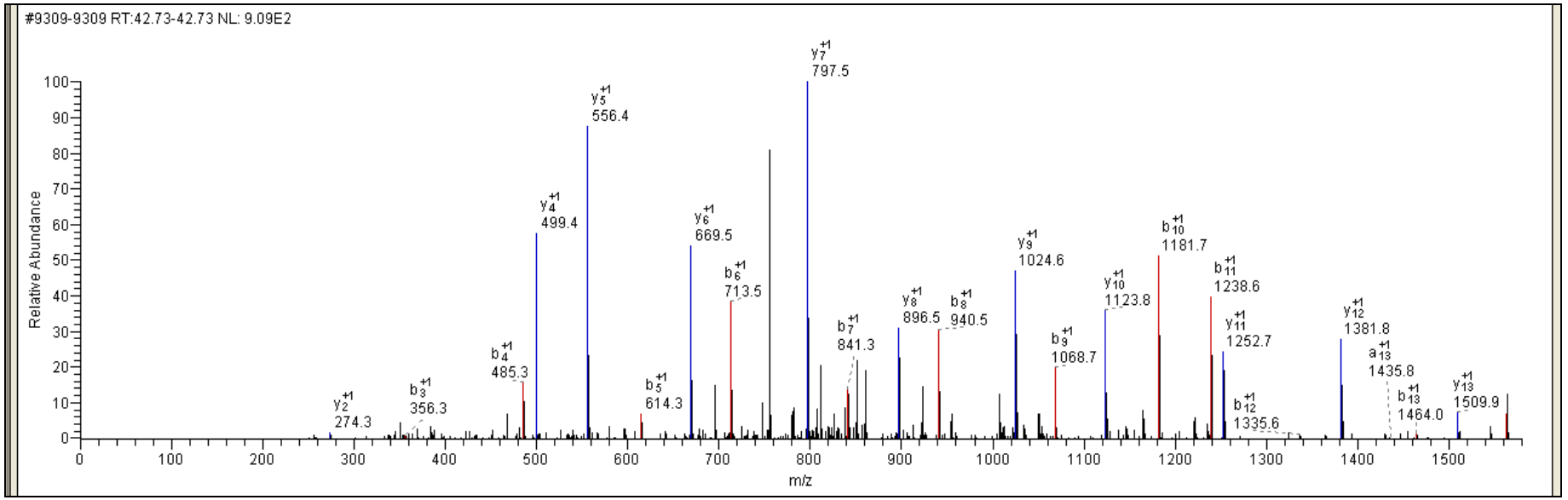
	AA	A	B	Y	
1	G	30.03	58.03	-	13
2	D	145.06	173.06	1232.59	12
3	V	244.13	272.12	1117.56	11
4	G	301.15	329.15	1018.50	10
5	P	398.20	426.20	961.47	9
6	G	455.22	483.22	864.42	8
7	A	526.26	554.26	807.40	7
8	G	583.28	611.28	736.36	6
9	E	712.33	740.32	679.34	5
10	V	811.39	839.39	550.30	4
11	E	940.44	968.43	451.23	3
12	F	1087.51	1115.50	322.19	2
13	R	-	-	175.12	1



RpS14a NP_524884.1 Ribosomal protein S14a CG1524-PB

K.VQKEEVQVQLGPQVR.D

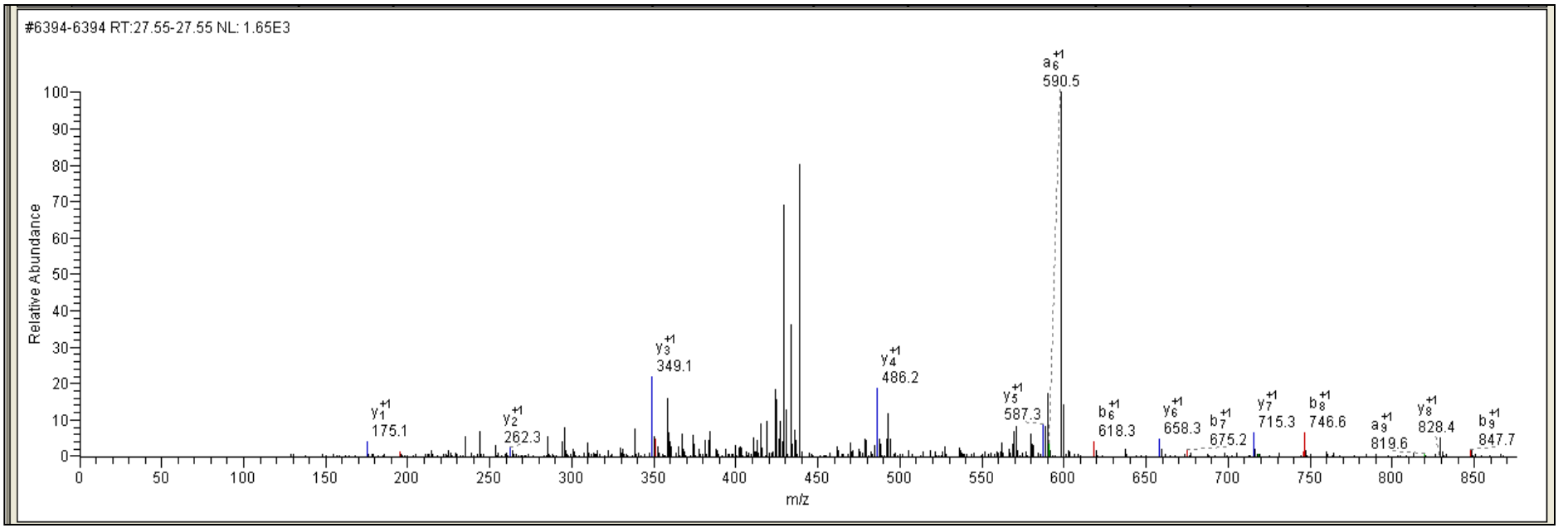
	AA	A	B	Y	
1	V	72.08	100.08	-	15
2	Q	200.14	228.13	1637.90	14
3	K	328.23	356.23	1509.84	13
4	E	457.28	485.27	1381.74	12
5	E	586.32	614.31	1252.70	11
6	V	685.39	713.38	1123.66	10
7	Q	813.45	841.44	1024.59	9
8	V	912.51	940.51	896.53	8
9	Q	1040.57	1068.57	797.46	7
10	L	1153.66	1181.65	669.40	6
11	G	1210.68	1238.67	556.32	5
12	P	1307.73	1335.73	499.30	4
13	Q	1435.79	1463.79	402.25	3
14	V	1534.86	1562.85	274.19	2
15	R	-	-	175.12	1



RpS15 NP_611136.1 Ribosomal protein S15 CG8332-PA

K.HGRPGIGATHSSR.F

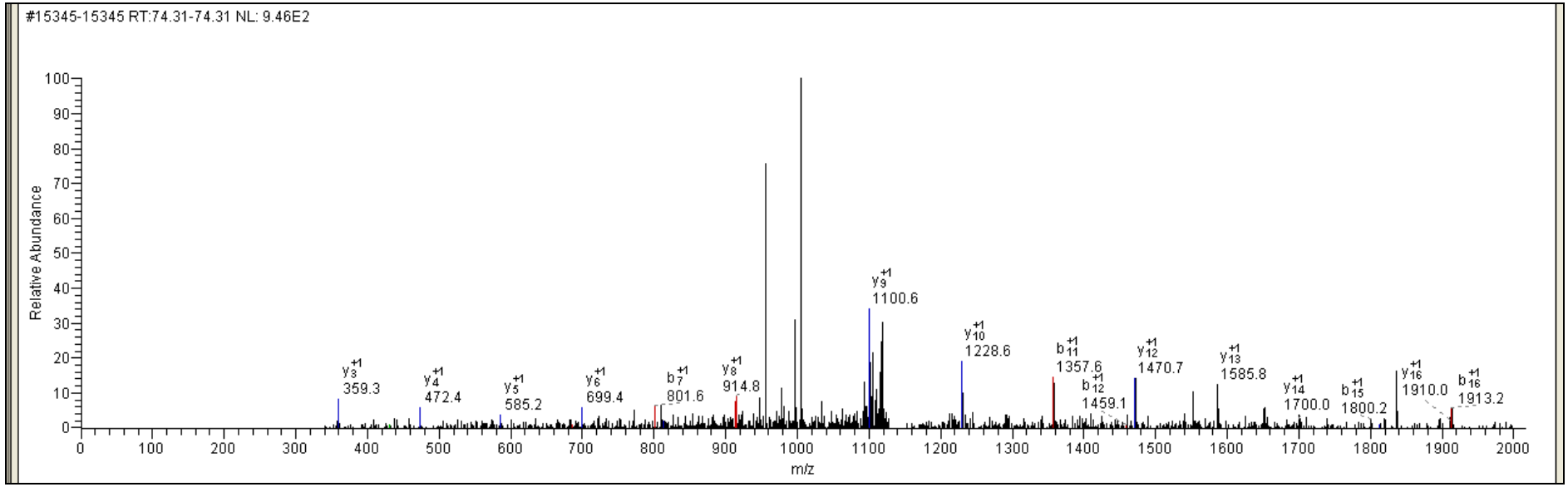
	AA	A	B	Y	
1	H	110.07	138.07	-	13
2	G	167.09	195.09	1195.63	12
3	R	323.19	351.19	1138.61	11
4	P	420.25	448.24	982.51	10
5	G	477.27	505.26	885.45	9
6	I	590.35	618.35	828.43	8
7	G	647.37	675.37	715.35	7
8	A	718.41	746.41	658.33	6
9	T	819.46	847.45	587.29	5
10	H	956.52	984.51	486.24	4
11	S	1043.55	1071.54	349.18	3
12	S	1130.58	1158.58	262.15	2
13	R	-	-	175.12	1



RpS15Aa NP_727692.1 Ribosomal protein S15Aa CG2033-PC

R.FDVPINDIEKWTNNLLPSR.Q

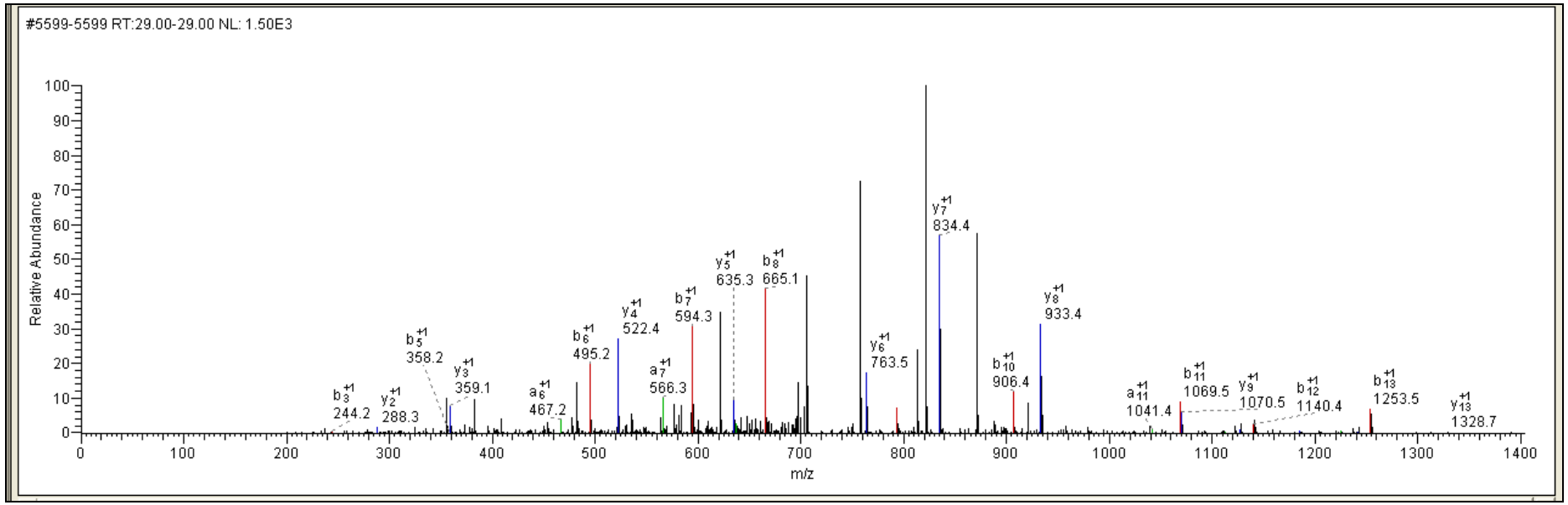
	AA	A	B	Y	
1	F	120.08	148.08	-	19
2	D	235.11	263.10	2124.11	18
3	V	334.18	362.17	2009.08	17
4	P	431.23	459.22	1910.01	16
5	I	544.31	572.31	1812.96	15
6	N	658.36	686.35	1699.88	14
7	D	773.38	801.38	1585.83	13
8	I	886.47	914.46	1470.81	12
9	E	1015.51	1043.50	1357.72	11
10	K	1143.60	1171.60	1228.68	10
11	W	1329.68	1357.68	1100.58	9
12	T	1430.73	1458.73	914.51	8
13	N	1544.77	1572.77	813.46	7
14	N	1658.82	1686.81	699.41	6
15	L	1771.90	1799.90	585.37	5
16	L	1884.99	1912.98	472.29	4
17	P	1982.04	2010.03	359.20	3
18	S	2069.07	2097.07	262.15	2
19	R	-	-	175.12	1



RpS16 NP_611685.1 Ribosomal protein S16 CG4046-PA

R.VSGGGHVAQIYAIR.Q

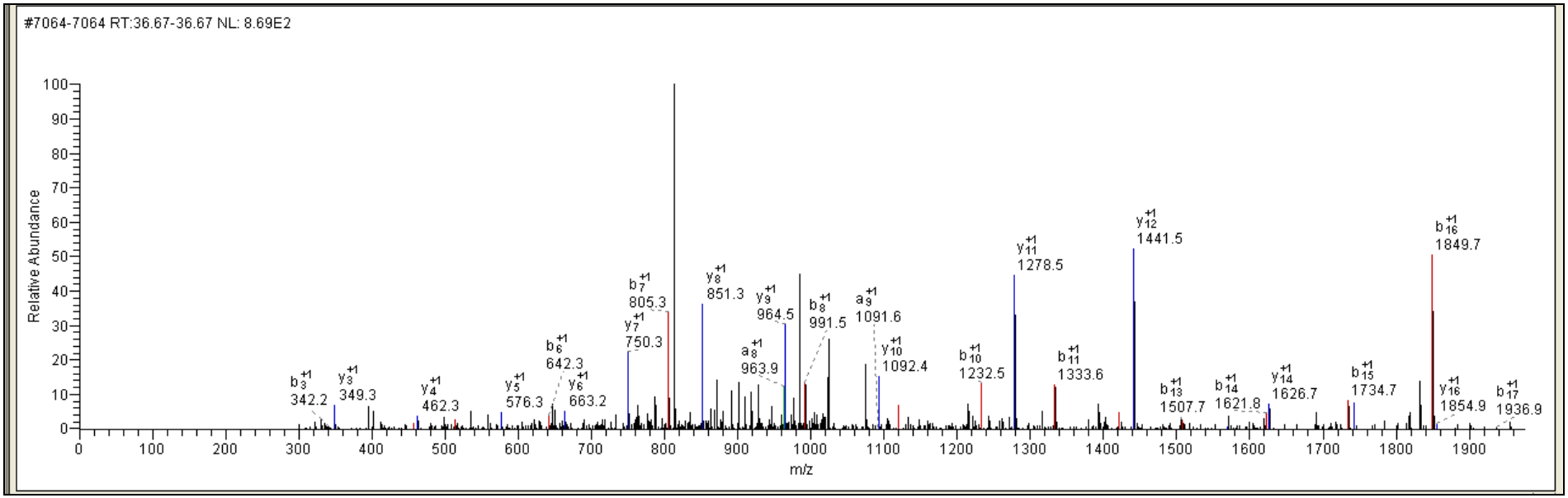
	AA	A	B	Y	
1	V	72.08	100.08	-	14
2	S	159.11	187.11	1328.71	13
3	G	216.13	244.13	1241.67	12
4	G	273.16	301.15	1184.65	11
5	G	330.18	358.17	1127.63	10
6	H	467.24	495.23	1070.61	9
7	V	566.30	594.30	933.55	8
8	A	637.34	665.34	834.48	7
9	Q	765.40	793.40	763.45	6
10	I	878.48	906.48	635.39	5
11	Y	1041.55	1069.54	522.30	4
12	A	1112.58	1140.58	359.24	3
13	I	1225.67	1253.66	288.20	2
14	R	-	-	175.12	1



RpS18 NP_725943.1 Ribosomal protein S18 CG8900-PB

K.DIIDGKYWQLTSSNLDSK.L

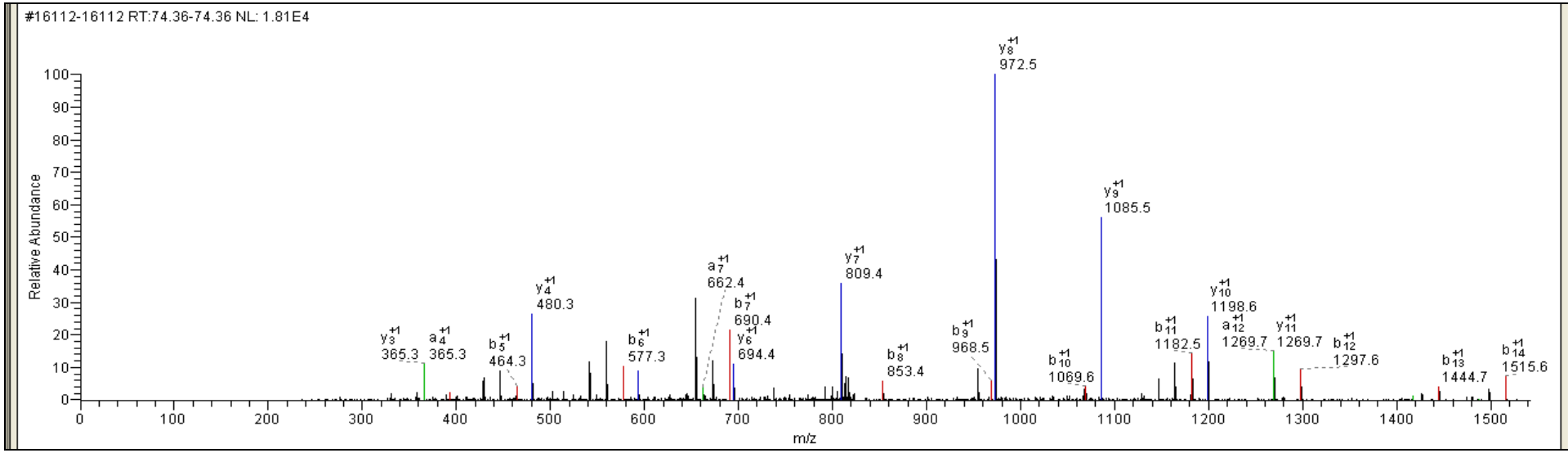
	AA	A	B	Y	
1	D	88.04	116.03	-	18
2	I	201.12	229.12	1968.01	17
3	I	314.21	342.20	1854.92	16
4	D	429.23	457.23	1741.84	15
5	G	486.26	514.25	1626.81	14
6	K	614.35	642.35	1569.79	13
7	Y	777.41	805.41	1441.70	12
8	W	963.49	991.49	1278.63	11
9	Q	1091.55	1119.55	1092.55	10
10	L	1204.64	1232.63	964.49	9
11	T	1305.68	1333.68	851.41	8
12	S	1392.72	1420.71	750.36	7
13	S	1479.75	1507.74	663.33	6
14	N	1593.79	1621.79	576.30	5
15	L	1706.87	1734.87	462.26	4
16	D	1821.90	1849.90	349.17	3
17	S	1908.93	1936.93	234.14	2
18	K	-	-	147.11	1



RpS24 NP_611693.1 Ribosomal protein S24 CG3751-PA

R.STGFALIYDTLDFAK.K

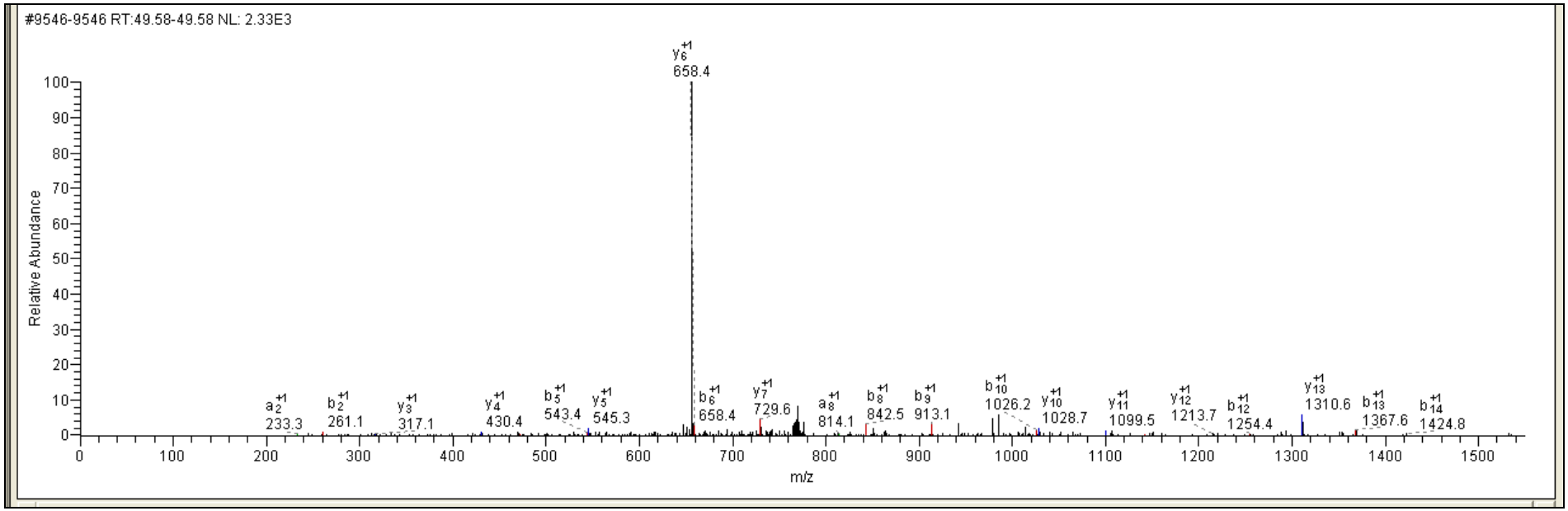
	AA	A	B	Y	
1	S	60.04	88.04	-	15
2	T	161.09	189.09	1574.81	14
3	G	218.11	246.11	1473.76	13
4	F	365.18	393.18	1416.74	12
5	A	436.22	464.21	1269.67	11
6	L	549.30	577.30	1198.64	10
7	I	662.39	690.38	1085.55	9
8	Y	825.45	853.45	972.47	8
9	D	940.48	968.47	809.40	7
10	T	1041.53	1069.52	694.38	6
11	L	1154.61	1182.60	593.33	5
12	D	1269.64	1297.63	480.25	4
13	F	1416.70	1444.70	365.22	3
14	A	1487.74	1515.74	218.15	2
15	K	-	-	147.11	1



rl NP_001015122.1 rolled CG12559-PC

K.LFPNADALALDLLGK.M

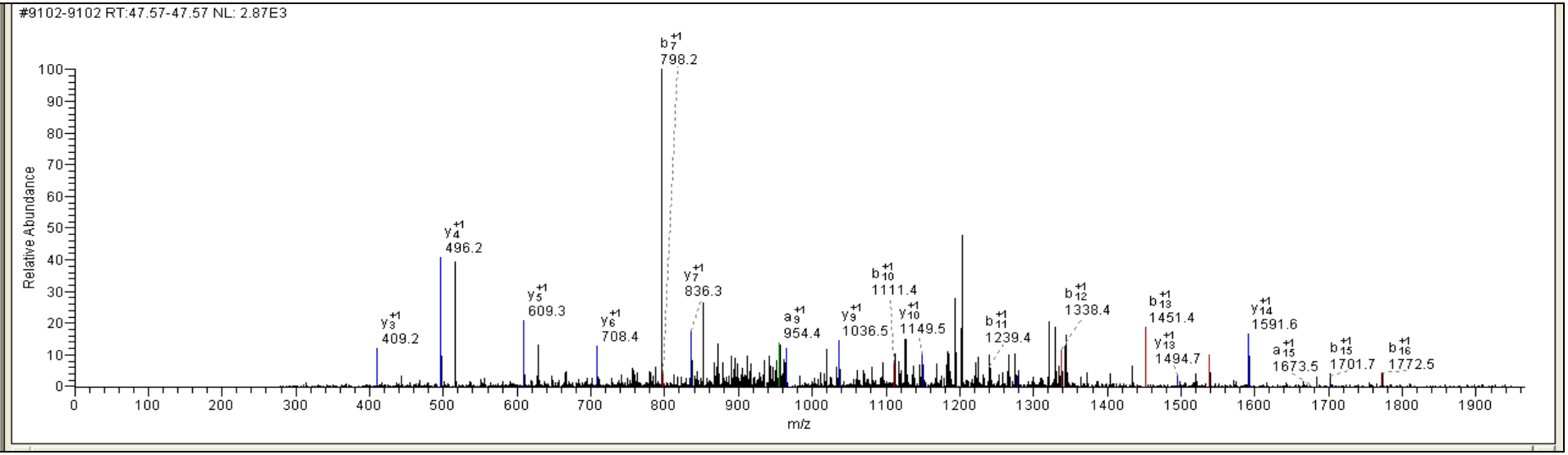
	AA	A	B	Y	
1	L	86.10	114.09	-	15
2	F	233.16	261.16	1457.80	14
3	P	330.22	358.21	1310.73	13
4	N	444.26	472.26	1213.68	12
5	A	515.30	543.29	1099.64	11
6	D	630.32	658.32	1028.60	10
7	A	701.36	729.36	913.57	9
8	L	814.45	842.44	842.53	8
9	A	885.48	913.48	729.45	7
10	L	998.57	1026.56	658.41	6
11	D	1113.59	1141.59	545.33	5
12	L	1226.68	1254.67	430.30	4
13	L	1339.76	1367.76	317.22	3
14	G	1396.78	1424.78	204.13	2
15	K	-	-	147.11	1



Rpn12 NP_648904.1 Rpn12 CG4157-PA

K.ELLPSEELAEQVLSYAR.D

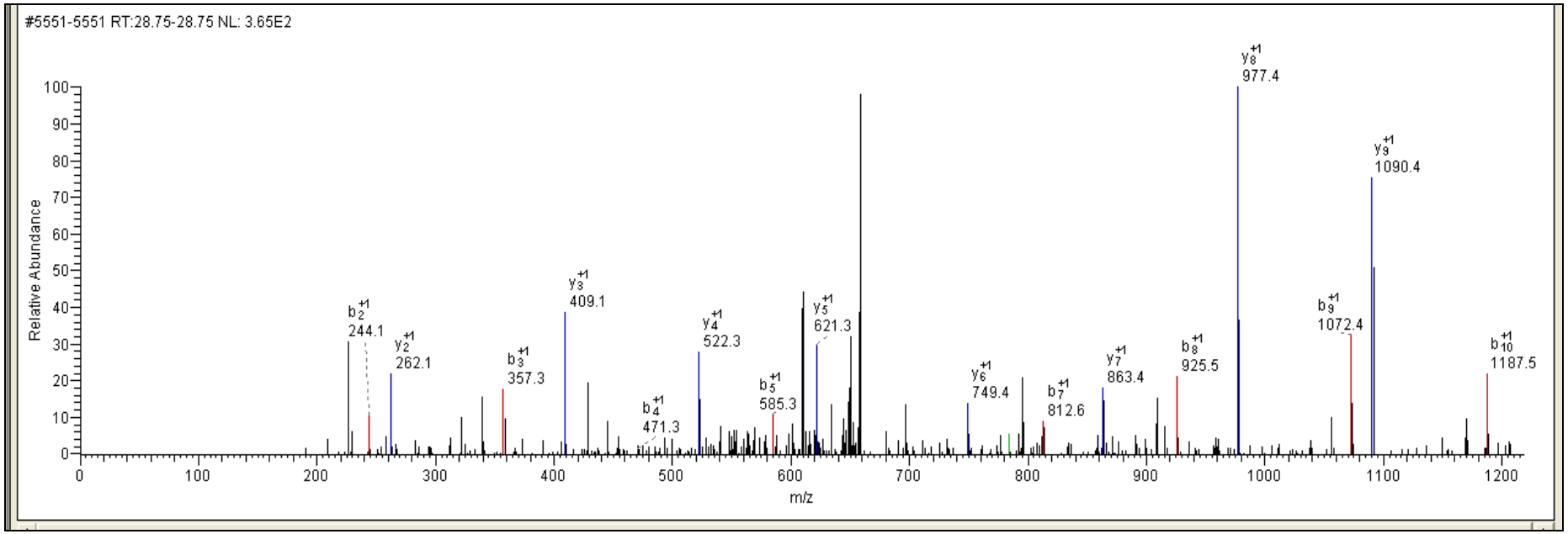
	AA	A	B	Y	
1	E	102.05	130.05	-	17
2	L	215.14	243.13	1817.96	16
3	L	328.22	356.22	1704.88	15
4	P	425.28	453.27	1591.80	14
5	S	512.31	540.30	1494.74	13
6	E	641.35	669.35	1407.71	12
7	E	770.39	798.39	1278.67	11
8	L	883.48	911.47	1149.63	10
9	A	954.51	982.51	1036.54	9
10	E	1083.56	1111.55	965.51	8
11	Q	1211.62	1239.61	836.46	7
12	V	1310.68	1338.68	708.40	6
13	L	1423.77	1451.76	609.34	5
14	S	1510.80	1538.79	496.25	4
15	Y	1673.86	1701.86	409.22	3
16	A	1744.90	1772.90	246.16	2
17	R	-	-	175.12	1



RpS25 NP_524315.2 RpS25 CG6684-PA

R.DKLNNQVLFDK.A

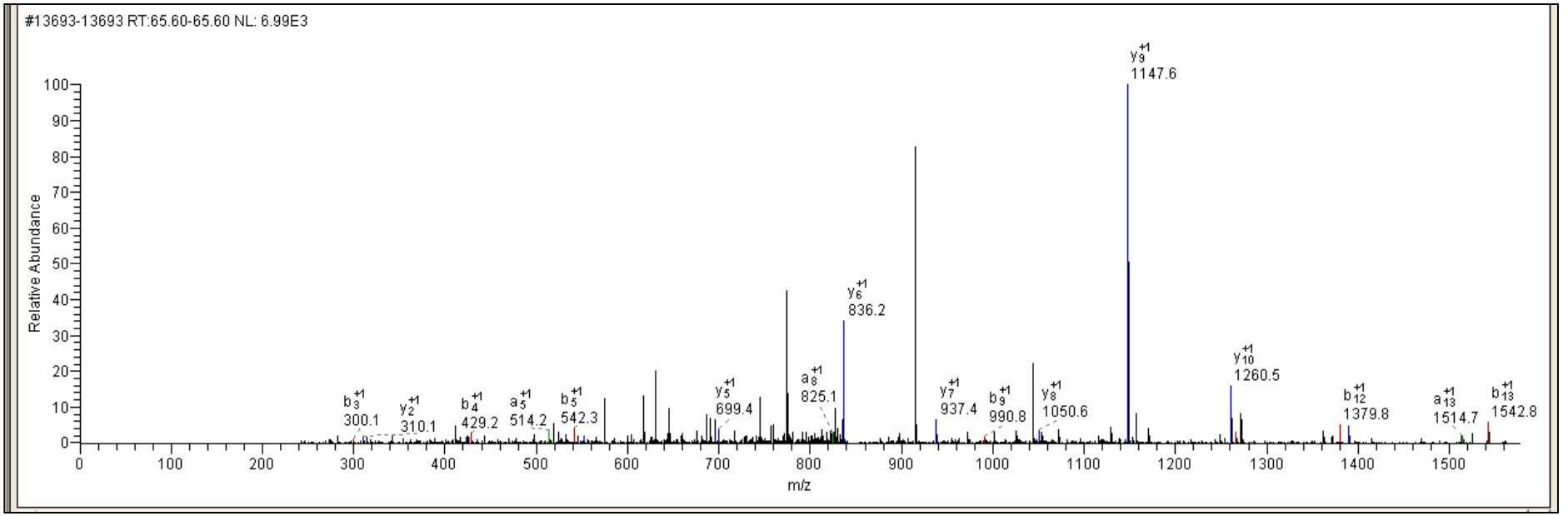
	AA	A	B	Y	
1	D	88.04	116.03	-	11
2	K	216.13	244.13	1218.68	10
3	L	329.22	357.21	1090.59	9
4	N	443.26	471.26	977.51	8
5	N	557.30	585.30	863.46	7
6	Q	685.36	713.36	749.42	6
7	V	784.43	812.43	621.36	5
8	L	897.52	925.51	522.29	4
9	F	1044.58	1072.58	409.21	3
10	D	1159.61	1187.61	262.14	2
11	K	-	-	147.11	1



Rpt3 NP_572686.1 Rpt3 CG16916-PA

R.EAVELPLTHFELYK.Q

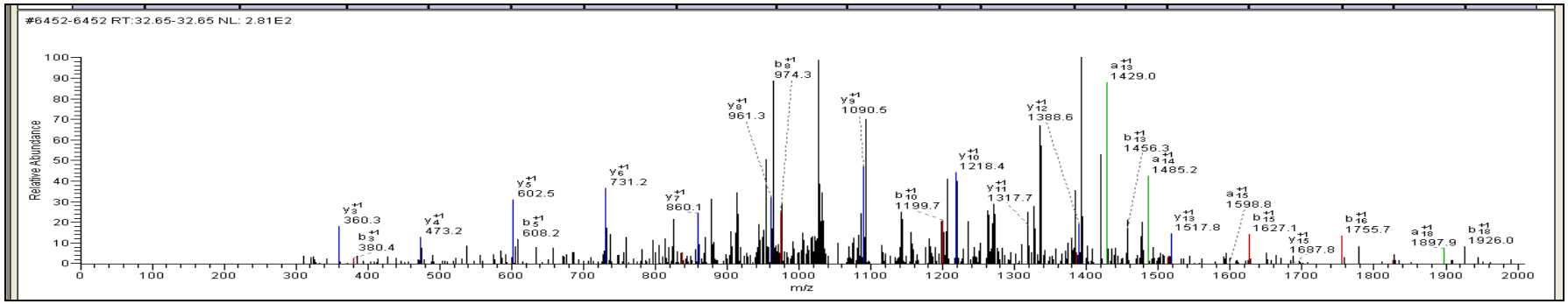
	AA	A	B	Y	
1	E	102.05	130.05	-	14
2	A	173.09	201.09	1559.85	13
3	V	272.16	300.16	1488.81	12
4	E	401.20	429.20	1389.74	11
5	L	514.29	542.28	1260.70	10
6	P	611.34	639.33	1147.61	9
7	L	724.42	752.42	1050.56	8
8	T	825.47	853.47	937.48	7
9	H	962.53	990.53	836.43	6
10	F	1109.60	1137.59	699.37	5
11	E	1238.64	1266.64	552.30	4
12	L	1351.73	1379.72	423.26	3
13	Y	1514.79	1542.78	310.18	2
14	K	-	-	147.11	1



sls NP_652705.2 sallimus CG1915-PC

K.TMFLDTQHPQGEAGLEAVQETEEELANR.Y

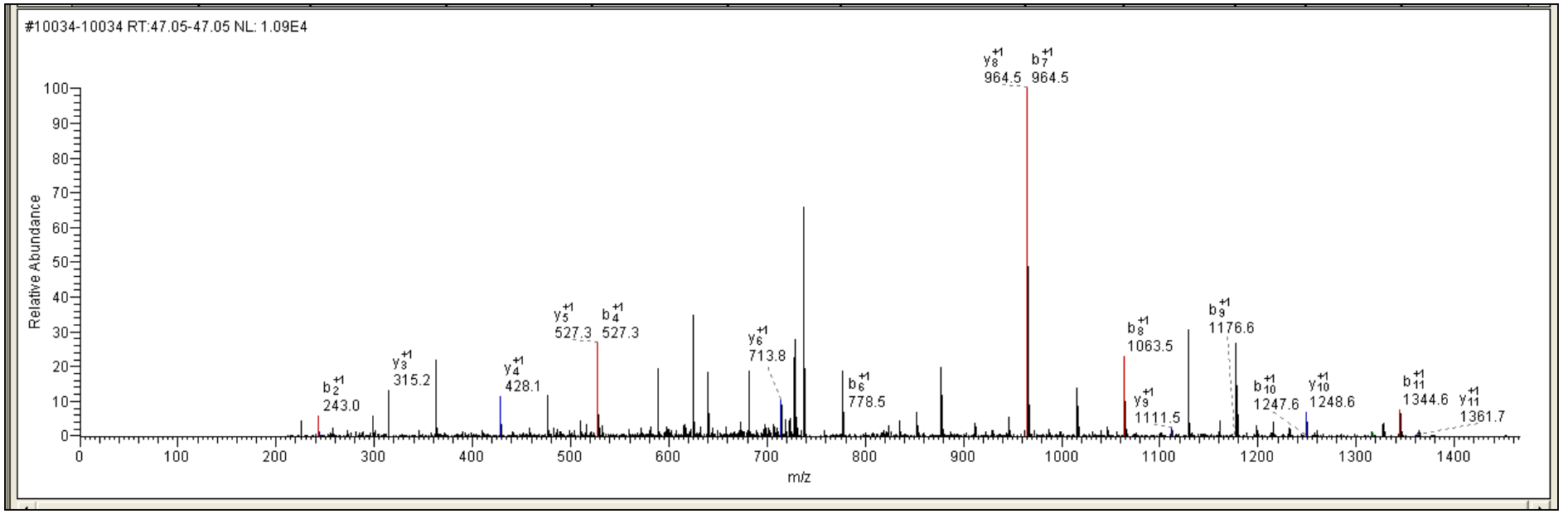
S no	AA	A	B	Y	
1	T	74.06	102.05	-	28
2	M	205.1	233.1	3042.41	27
3	F	352.17	380.16	2911.37	26
4	L	465.25	493.25	2764.3	25
5	D	580.28	608.27	2651.22	24
6	T	681.33	709.32	2536.19	23
7	Q	809.39	837.38	2435.14	22
8	H	946.45	974.44	2307.08	21
9	P	1043.5	1071.49	2170.03	20
10	Q	1171.56	1199.55	2072.97	19
11	G	1228.58	1256.57	1944.91	18
12	E	1357.62	1385.62	1887.89	17
13	A	1428.66	1456.65	1758.85	16
14	G	1485.68	1513.67	1687.81	15
15	L	1598.76	1626.76	1630.79	14
16	E	1727.81	1755.8	1517.71	13
17	A	1798.84	1826.84	1388.67	12
18	V	1897.91	1925.91	1317.63	11
19	Q	2025.97	2053.96	1218.56	10
20	E	2155.01	2183.01	1090.5	9
21	T	2256.06	2284.06	961.46	8
22	E	2385.1	2413.1	860.41	7
23	E	2514.15	2542.14	731.37	6
24	E	2643.19	2671.18	602.33	5
25	L	2756.27	2784.27	473.28	4
26	A	2827.31	2855.3	360.2	3
27	N	2941.35	2969.35	289.16	2
28	R	-	-	175.12	1



NP_524863.3 screw CG31695-PA

K.ELHMHNWVIAPK.K

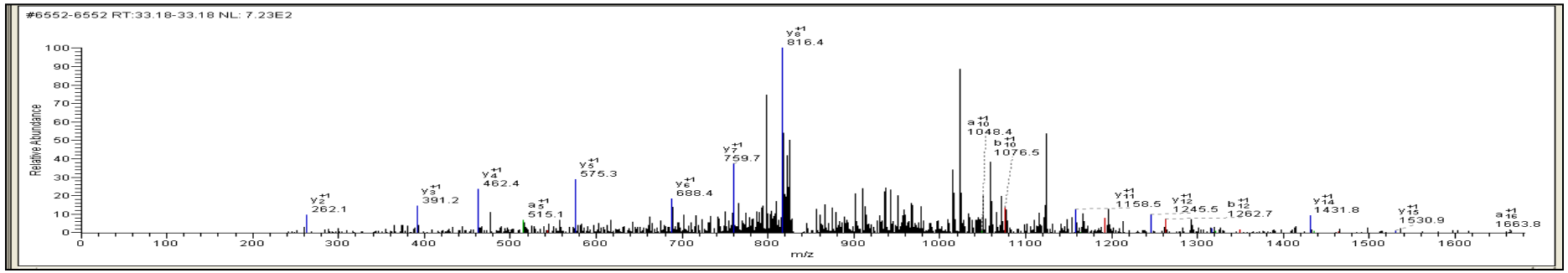
	AA	A	B	Y	
1	E	102.05	130.05	-	12
2	L	215.14	243.13	1361.71	11
3	H	352.20	380.19	1248.63	10
4	M*	499.23	527.23	1111.57	9
5	H	636.29	664.29	964.54	8
6	N	750.34	778.33	827.48	7
7	W	936.41	964.41	713.43	6
8	V	1035.48	1063.48	527.36	5
9	I	1148.57	1176.56	428.29	4
10	A	1219.60	1247.60	315.20	3
11	P	1316.66	1344.65	244.17	2
12	K	-	-	147.11	1



shot NP_725335.1 short stop CG18076-PG

R.GVTERYTGLVDASDNIGALLAESR.Q

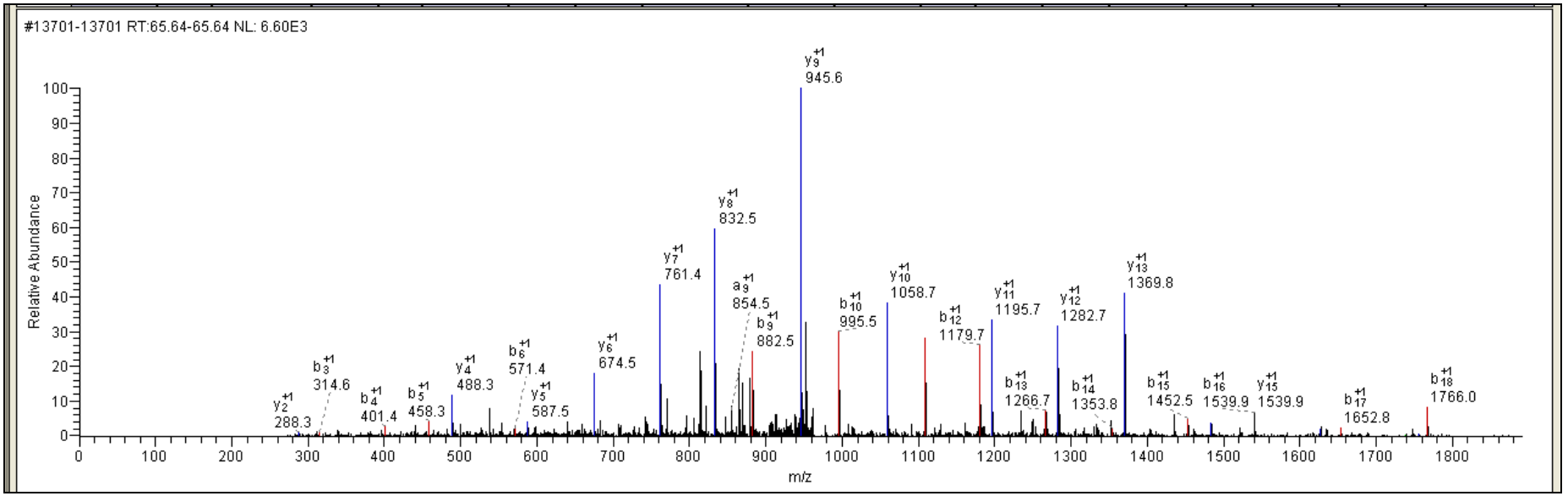
S no	AA	A	B	Y	
1	G	30.03	58.03	-	24
2	V	129.1	157.1	2450.25	23
3	T	230.15	258.14	2351.18	22
4	E	359.19	387.19	2250.14	21
5	R	515.29	543.29	2121.09	20
6	Y	678.36	706.35	1964.99	19
7	T	779.4	807.4	1801.93	18
8	G	836.43	864.42	1700.88	17
9	L	949.51	977.51	1643.86	16
10	V	1048.58	1076.57	1530.78	15
11	D	1163.61	1191.6	1431.71	14
12	A	1234.64	1262.64	1316.68	13
13	S	1321.67	1349.67	1245.64	12
14	D	1436.7	1464.7	1158.61	11
15	N	1550.74	1578.74	1043.58	10
16	I	1663.83	1691.82	929.54	9
17	G	1720.85	1748.84	816.46	8
18	A	1791.89	1819.88	759.44	7
19	L	1904.97	1932.97	688.4	6
20	L	2018.06	2046.05	575.31	5
21	A	2089.09	2117.09	462.23	4
22	E	2218.14	2246.13	391.19	3
23	S	2305.17	2333.16	262.15	2
24	R	-	-	175.12	1



Snr1 NP_730935.1 Snf5-related 1 CG1064-PA

R.LAESGLSSHILASSVSLLR.A

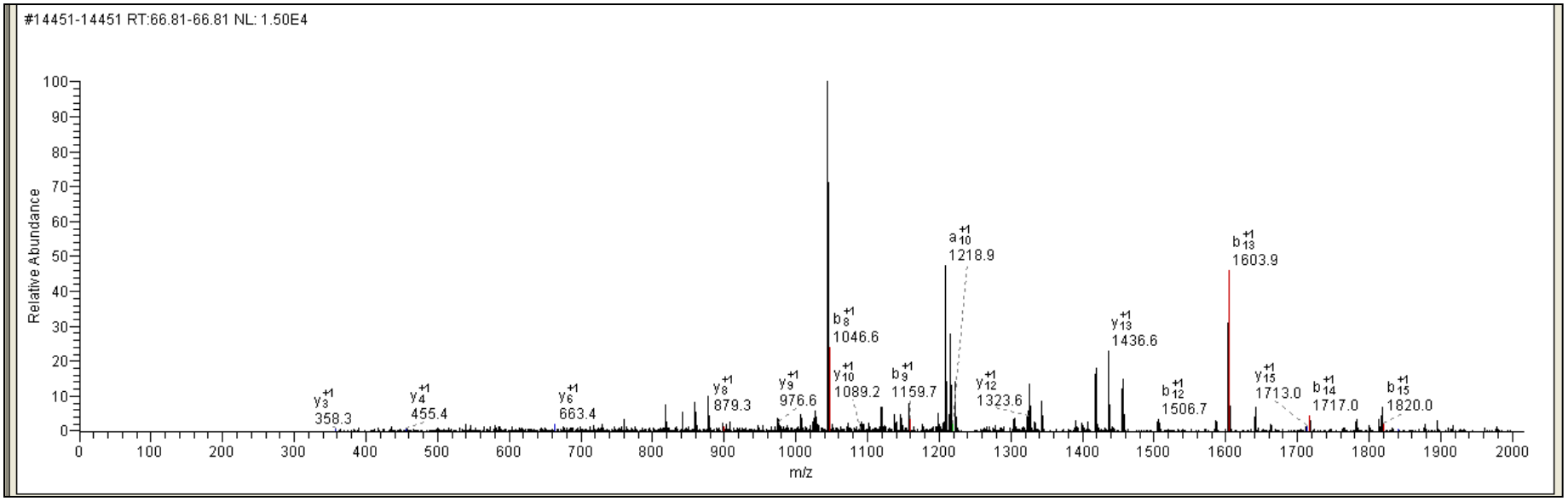
	AA	A	B	Y	
1	L	86.10	114.09	-	19
2	A	157.13	185.13	1827.00	18
3	E	286.18	314.17	1755.96	17
4	S	373.21	401.20	1626.92	16
5	G	430.23	458.22	1539.89	15
6	L	543.31	571.31	1482.86	14
7	S	630.35	658.34	1369.78	13
8	S	717.38	745.37	1282.75	12
9	H	854.44	882.43	1195.72	11
10	I	967.52	995.52	1058.66	10
11	L	1080.60	1108.60	945.57	9
12	A	1151.64	1179.64	832.49	8
13	S	1238.67	1266.67	761.45	7
14	S	1325.71	1353.70	674.42	6
15	V	1424.77	1452.77	587.39	5
16	S	1511.81	1539.80	488.32	4
17	L	1624.89	1652.89	401.29	3
18	L	1737.97	1765.97	288.20	2
19	R	-	-	175.12	1



SpdS NP_731384.1 Spermidine Synthase CG8327-PA

R.DEFSYQEMISFLPLCAHPNPK.K

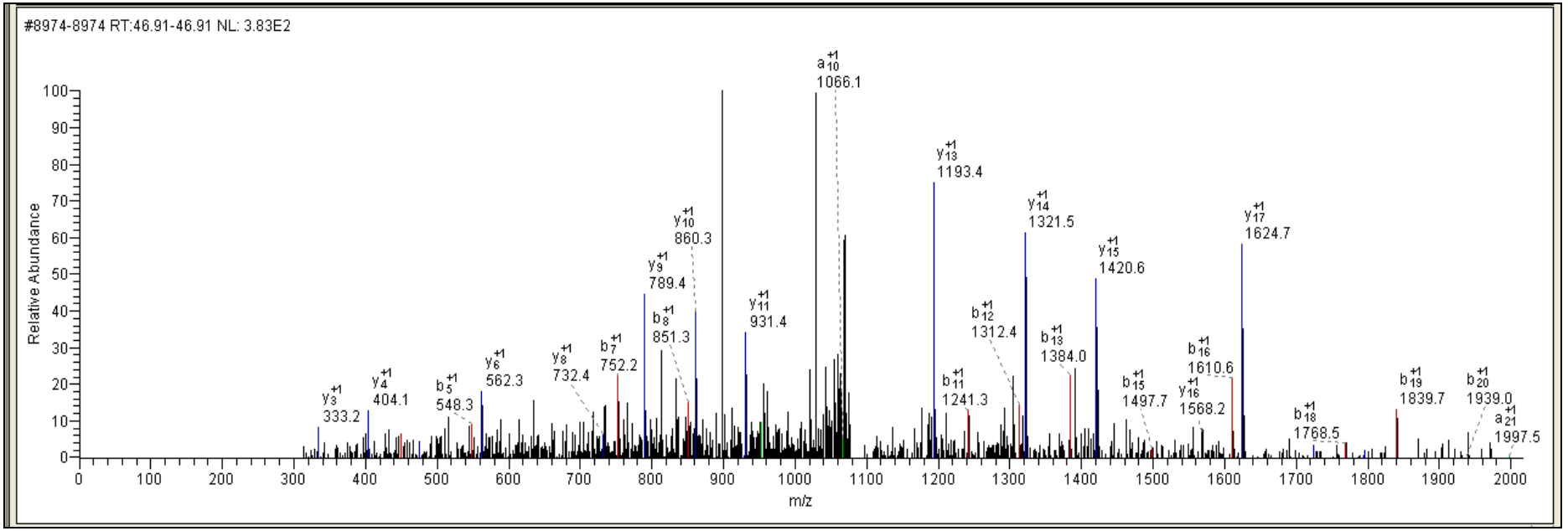
	AA	A	B	Y	
1	D	88.04	116.03	-	21
2	E	217.08	245.08	2367.11	20
3	F	364.15	392.15	2238.07	19
4	S	451.18	479.18	2091.00	18
5	Y	614.25	642.24	2003.97	17
6	Q	742.30	770.30	1840.91	16
7	E	871.35	899.34	1712.85	15
8	M*	1018.38	1046.38	1583.81	14
9	I	1131.47	1159.46	1436.77	13
10	S	1218.50	1246.49	1323.69	12
11	F	1365.57	1393.56	1236.66	11
12	L	1478.65	1506.65	1089.59	10
13	P	1575.70	1603.70	976.50	9
14	L	1688.79	1716.78	879.45	8
15	C	1791.80	1819.79	766.37	7
16	A	1862.83	1890.83	663.36	6
17	H	1999.89	2027.89	592.32	5
18	P	2096.95	2124.94	455.26	4
19	N	2210.99	2238.98	358.21	3
20	P	2308.04	2336.04	244.17	2
21	K	-	-	147.11	1



sesB NP_727448.1 stress-sensitive B CG16944-PC

K.DFDAVGFVKDFAAGGISAAVSK.T

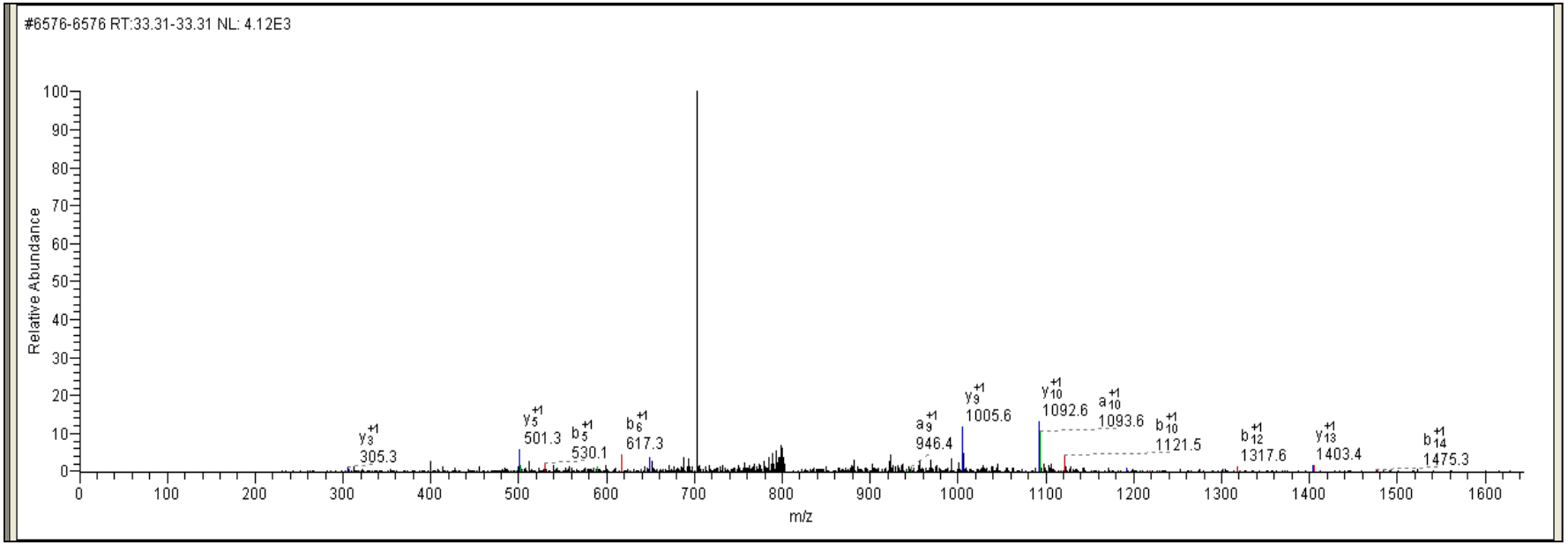
	AA	A	B	Y	
1	D	88.04	116.03	-	22
2	F	235.11	263.10	2057.07	21
3	D	350.13	378.13	1910.00	20
4	A	421.17	449.17	1794.97	19
5	V	520.24	548.24	1723.94	18
6	G	577.26	605.26	1624.87	17
7	F	724.33	752.32	1567.85	16
8	V	823.40	851.39	1420.78	15
9	K	951.49	979.49	1321.71	14
10	D	1066.52	1094.52	1193.62	13
11	F	1213.59	1241.58	1078.59	12
12	A	1284.63	1312.62	931.52	11
13	A	1355.66	1383.66	860.48	10
14	G	1412.68	1440.68	789.45	9
15	G	1469.71	1497.70	732.43	8
16	I	1582.79	1610.78	675.40	7
17	S	1669.82	1697.82	562.32	6
18	A	1740.86	1768.85	475.29	5
19	A	1811.90	1839.89	404.25	4
20	V	1910.96	1938.96	333.21	3
21	S	1998.00	2025.99	234.14	2
22	K	-	-	147.11	1



Taf1 NP_996160.1 TBP-associated factor 1 CG17603-PB

R.SMPDVSPFLFPVSAK.K

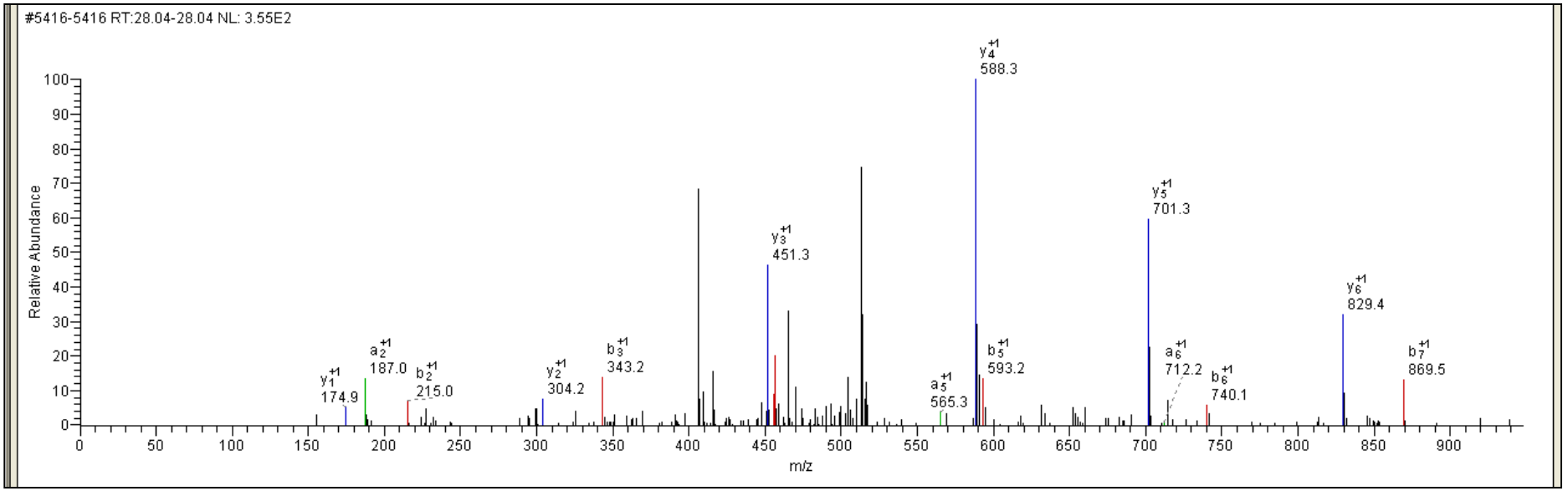
	AA	A	B	Y	
1	S	60.04	88.04	-	15
2	M	191.08	219.08	1534.80	14
3	P	288.14	316.13	1403.76	13
4	D	403.16	431.16	1306.70	12
5	V	502.23	530.23	1191.68	11
6	S	589.27	617.26	1092.61	10
7	P	686.32	714.31	1005.58	9
8	F	833.39	861.38	908.52	8
9	L	946.47	974.47	761.46	7
10	F	1093.54	1121.53	648.37	6
11	P	1190.59	1218.59	501.30	5
12	V	1289.66	1317.65	404.25	4
13	S	1376.69	1404.69	305.18	3
14	A	1447.73	1475.72	218.15	2
15	K	-	-	147.11	1



Taf12 NP_731616.1 TBP-associated factor 12 CG17358-PB

R.DVQLHFER.K

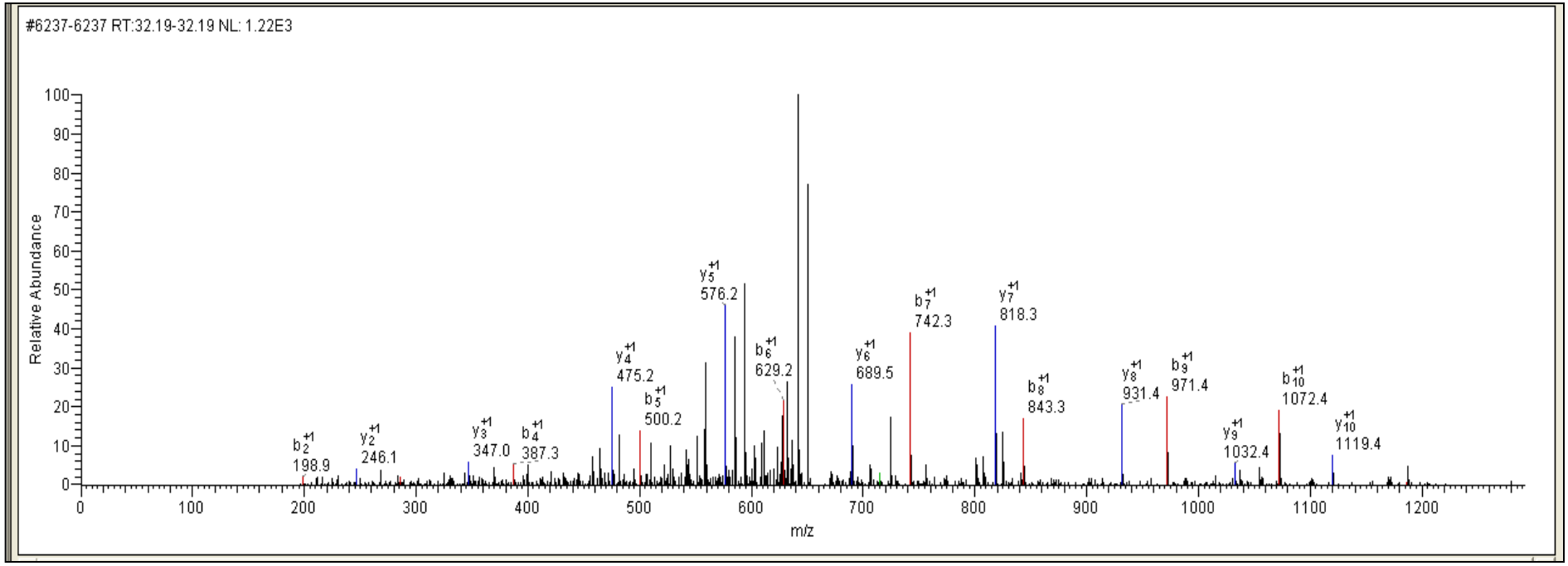
	AA	A	B	Y	
1	D	88.04	116.03	-	8
2	V	187.11	215.10	928.50	7
3	Q	315.17	343.16	829.43	6
4	L	428.25	456.25	701.37	5
5	H	565.31	593.30	588.29	4
6	F	712.38	740.37	451.23	3
7	E	841.42	869.42	304.16	2
8	R	-	-	175.12	1



Taf8 NP_523397.1 TBP-associated factor 8 CG7128-PA

R.TPSTLEITKTNL

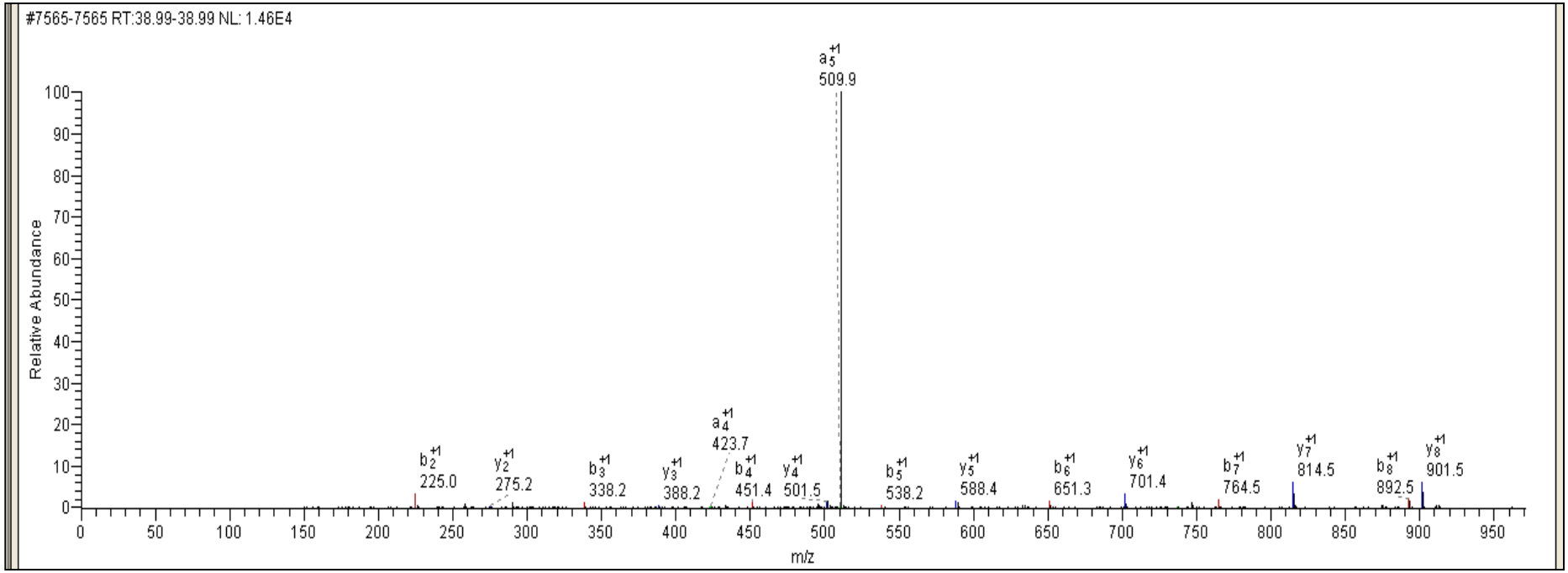
	AA	A	B	Y	
1	T	74.06	102.05	-	12
2	P	171.11	199.11	1216.68	11
3	S	258.14	286.14	1119.63	10
4	T	359.19	387.19	1032.59	9
5	L	472.28	500.27	931.55	8
6	E	601.32	629.31	818.46	7
7	I	714.40	742.40	689.42	6
8	T	815.45	843.45	576.34	5
9	K	943.55	971.54	475.29	4
10	T	1044.59	1072.59	347.19	3
11	N	1158.64	1186.63	246.14	2
12	L	-	-	132.10	1



Thiolase NP_477378.1 Thiolase CG4581-PA

R.HSLLSLLQK.N

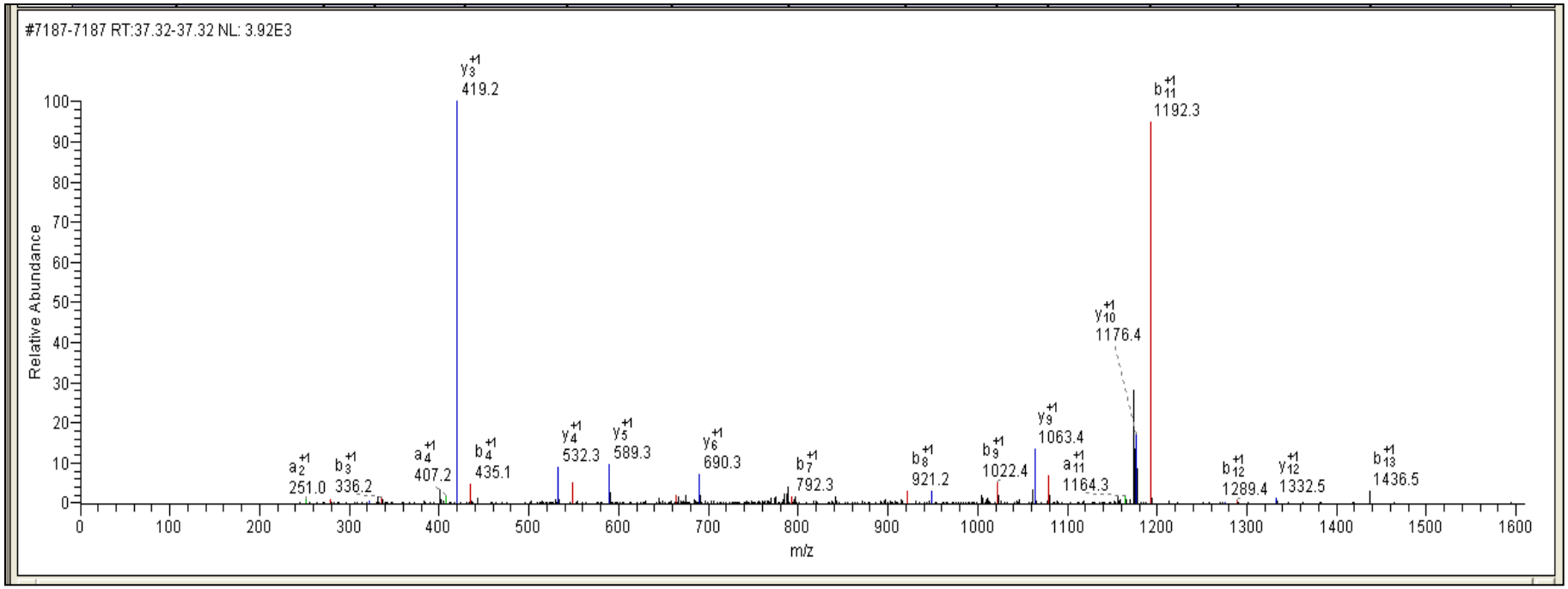
	AA	A	B	Y	
1	H	110.07	138.07	-	9
2	S	197.10	225.10	901.57	8
3	L	310.19	338.18	814.54	7
4	L	423.27	451.27	701.46	6
5	S	510.30	538.30	588.37	5
6	L	623.39	651.38	501.34	4
7	L	736.47	764.47	388.26	3
8	Q	864.53	892.53	275.17	2
9	K	-	-	147.11	1



Jafrac1 NP_727689.1 thioredoxin peroxidase 1 CG1633-PB

R.DYGVLDEETGIPFR.G

	AA	A	B	Y	
1	D	88.04	116.03	-	14
2	Y	251.10	279.10	1495.74	13
3	G	308.12	336.12	1332.68	12
4	V	407.19	435.19	1275.66	11
5	L	520.28	548.27	1176.59	10
6	D	635.30	663.30	1063.51	9
7	E	764.35	792.34	948.48	8
8	E	893.39	921.38	819.44	7
9	T	994.44	1022.43	690.39	6
10	G	1051.46	1079.45	589.35	5
11	I	1164.54	1192.54	532.32	4
12	P	1261.59	1289.59	419.24	3
13	F	1408.66	1436.66	322.19	2
14	R	-	-	175.12	1

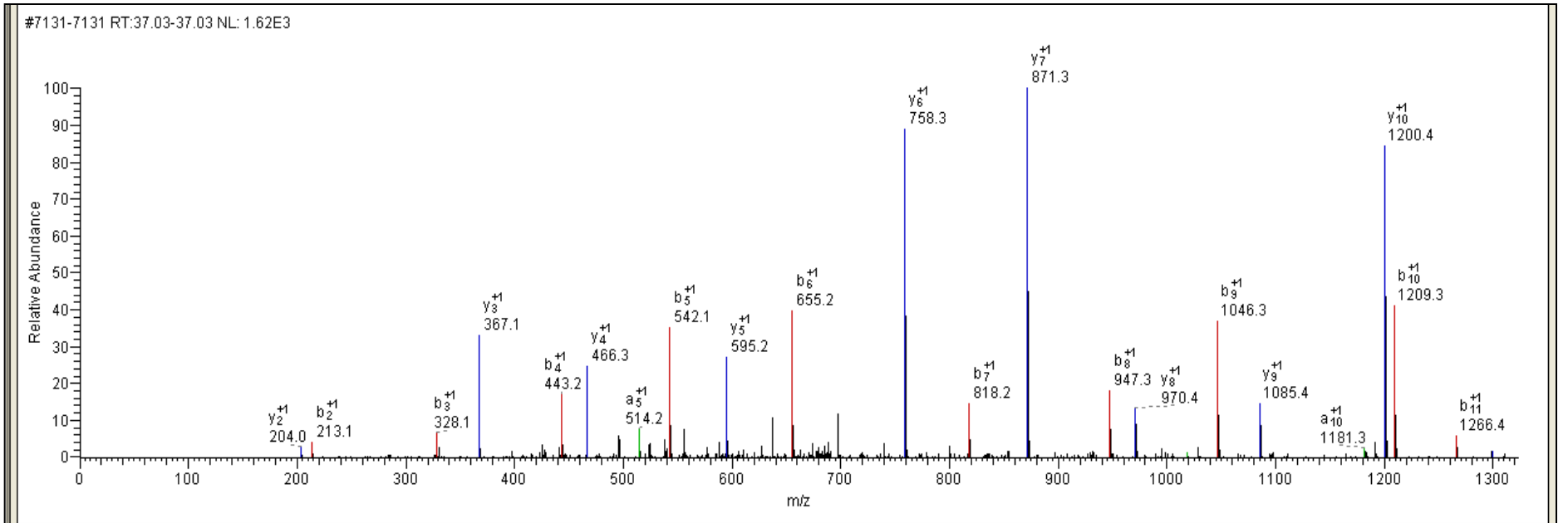


Tctp NP_650048.1

Translationally controlled tumor protein CG4800-PA

K.LVDDVIYEVYGK.L

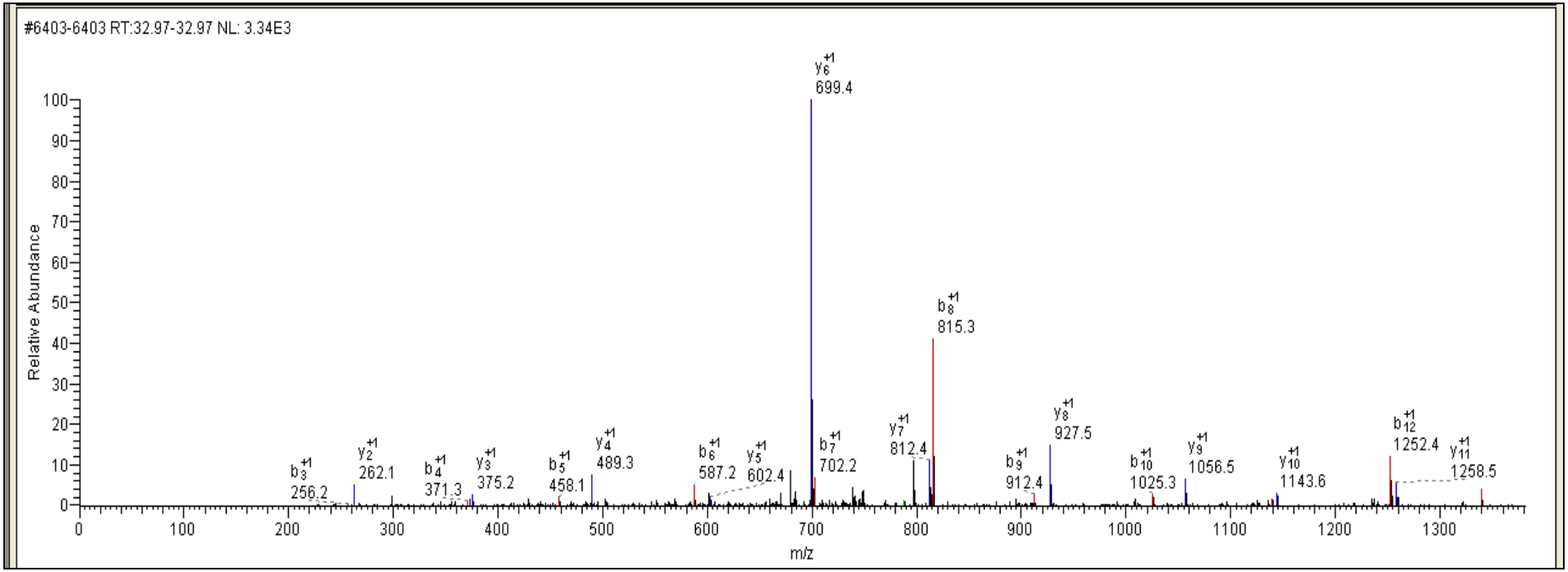
	AA	A	B	Y	
1	L	86.10	114.09	-	12
2	V	185.16	213.16	1299.65	11
3	D	300.19	328.19	1200.58	10
4	D	415.22	443.21	1085.55	9
5	V	514.29	542.28	970.52	8
6	I	627.37	655.37	871.46	7
7	Y	790.43	818.43	758.37	6
8	E	919.48	947.47	595.31	5
9	V	1018.55	1046.54	466.27	4
10	Y	1181.61	1209.60	367.20	3
11	G	1238.63	1266.63	204.13	2
12	K	-	-	147.11	1



Trap1 NP_477439.2 Trap1 CG3152-PA

K.GVVDSEDIPLNLSR.E

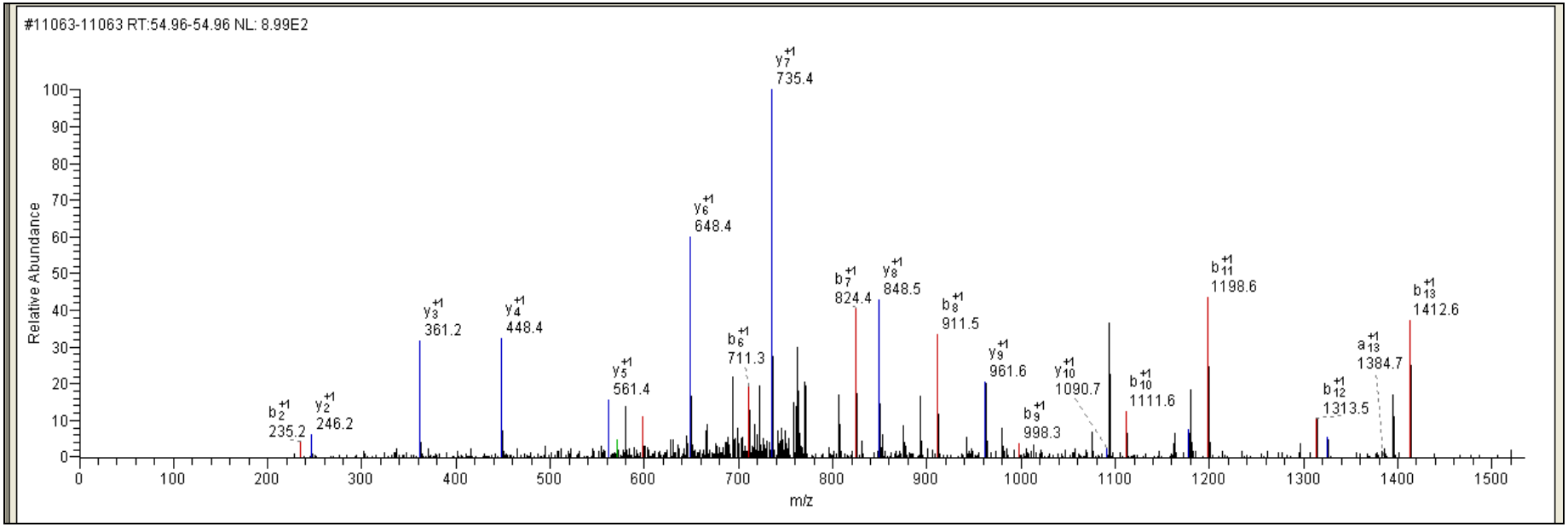
	AA	A	B	Y	
1	G	30.03	58.03	-	14
2	V	129.10	157.10	1456.76	13
3	V	228.17	256.17	1357.70	12
4	D	343.20	371.19	1258.63	11
5	S	430.23	458.22	1143.60	10
6	E	559.27	587.27	1056.57	9
7	D	674.30	702.29	927.53	8
8	I	787.38	815.38	812.50	7
9	P	884.44	912.43	699.41	6
10	L	997.52	1025.51	602.36	5
11	N	1111.56	1139.56	489.28	4
12	L	1224.65	1252.64	375.24	3
13	S	1311.68	1339.67	262.15	2
14	R	-	-	175.12	1



tws NP_476880.1 twins CG6235-PA

R.SFFSEIISSISDVK.L

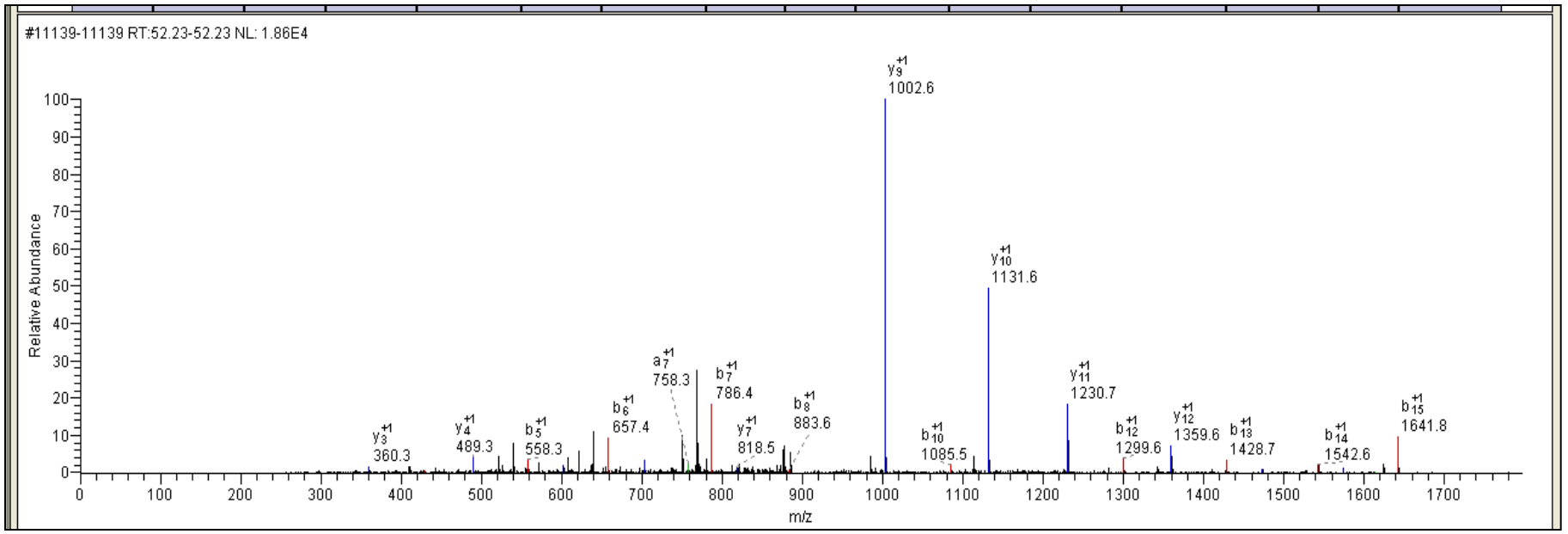
	AA	A	B	Y	
1	S	60.04	88.04	-	14
2	F	207.11	235.11	1471.77	13
3	F	354.18	382.18	1324.70	12
4	S	441.21	469.21	1177.63	11
5	E	570.26	598.25	1090.60	10
6	I	683.34	711.33	961.56	9
7	I	796.42	824.42	848.47	8
8	S	883.46	911.45	735.39	7
9	S	970.49	998.48	648.36	6
10	I	1083.57	1111.57	561.32	5
11	S	1170.60	1198.60	448.24	4
12	D	1285.63	1313.63	361.21	3
13	V	1384.70	1412.69	246.18	2
14	K	-	-	147.11	1



Ubi-p5E NP_727078.1 Ubiquitin-5E CG32744-PA

K.TITLEVEPSDTIENVK.A

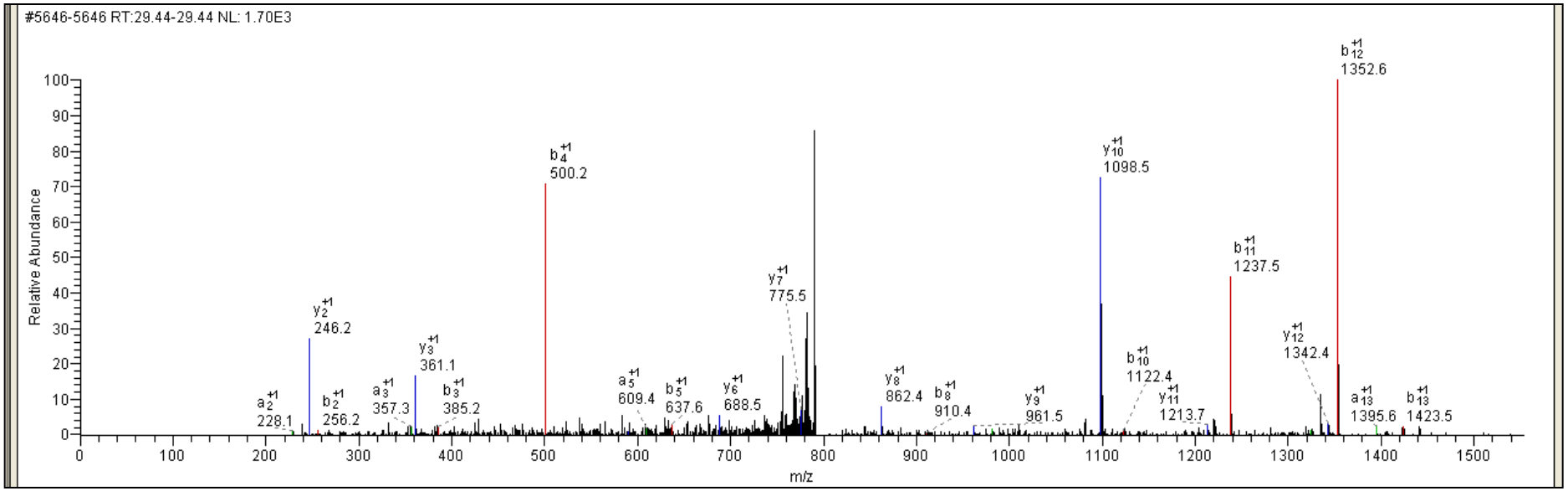
	AA	A	B	Y	
1	T	74.06	102.05	-	16
2	I	187.14	215.14	1686.88	15
3	T	288.19	316.19	1573.80	14
4	L	401.28	429.27	1472.75	13
5	E	530.32	558.31	1359.66	12
6	V	629.39	657.38	1230.62	11
7	E	758.43	786.42	1131.55	10
8	P	855.48	883.48	1002.51	9
9	S	942.51	970.51	905.46	8
10	D	1057.54	1085.54	818.43	7
11	T	1158.59	1186.58	703.40	6
12	I	1271.67	1299.67	602.35	5
13	E	1400.72	1428.71	489.27	4
14	N	1514.76	1542.75	360.22	3
15	V	1613.83	1641.82	246.18	2
16	K	-	-	147.11	1



Vha26 NP_730957.1 Vacuolar H[+]-ATPase 26kD E subunit CG1088-PA

K.VREDHVSSVLDDAR.K

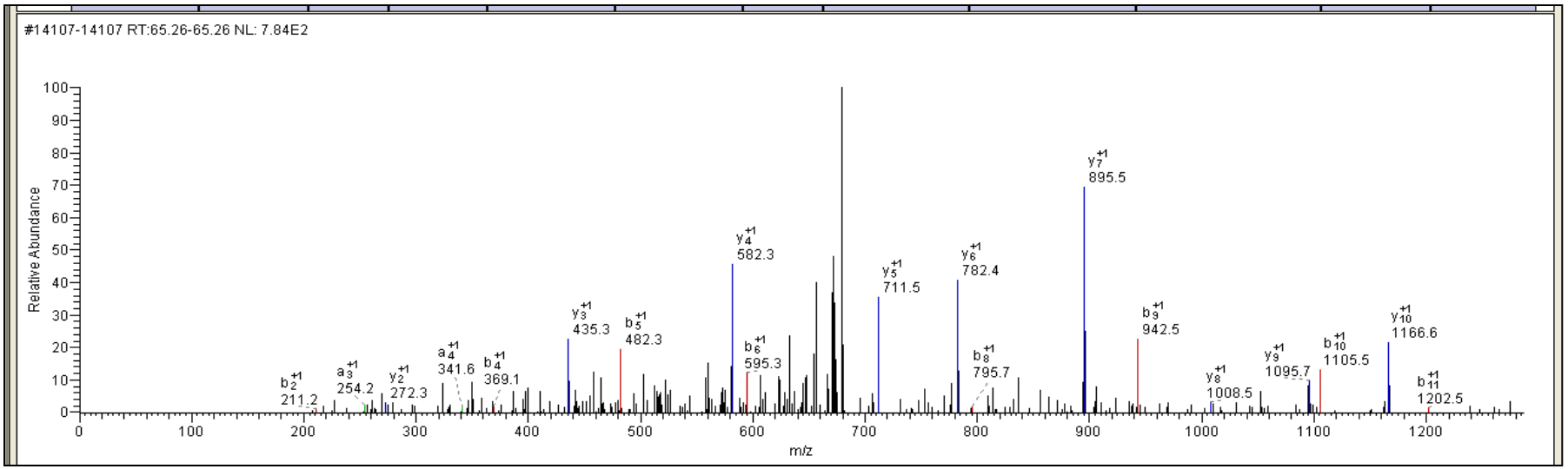
	AA	A	B	Y	
1	V	72.08	100.08	-	14
2	R	228.18	256.18	1498.72	13
3	E	357.22	385.22	1342.62	12
4	D	472.25	500.25	1213.58	11
5	H	609.31	637.31	1098.55	10
6	V	708.38	736.37	961.49	9
7	S	795.41	823.41	862.43	8
8	S	882.44	910.44	775.39	7
9	V	981.51	1009.51	688.36	6
10	L	1094.60	1122.59	589.29	5
11	D	1209.62	1237.62	476.21	4
12	D	1324.65	1352.64	361.18	3
13	A	1395.69	1423.68	246.16	2
14	R	-	-	175.12	1



Vha55 NP_476908.1 Vacuolar H[+]-ATPase 55kD B subunit CG17369-PB

R.IPASILAEFYPR.D

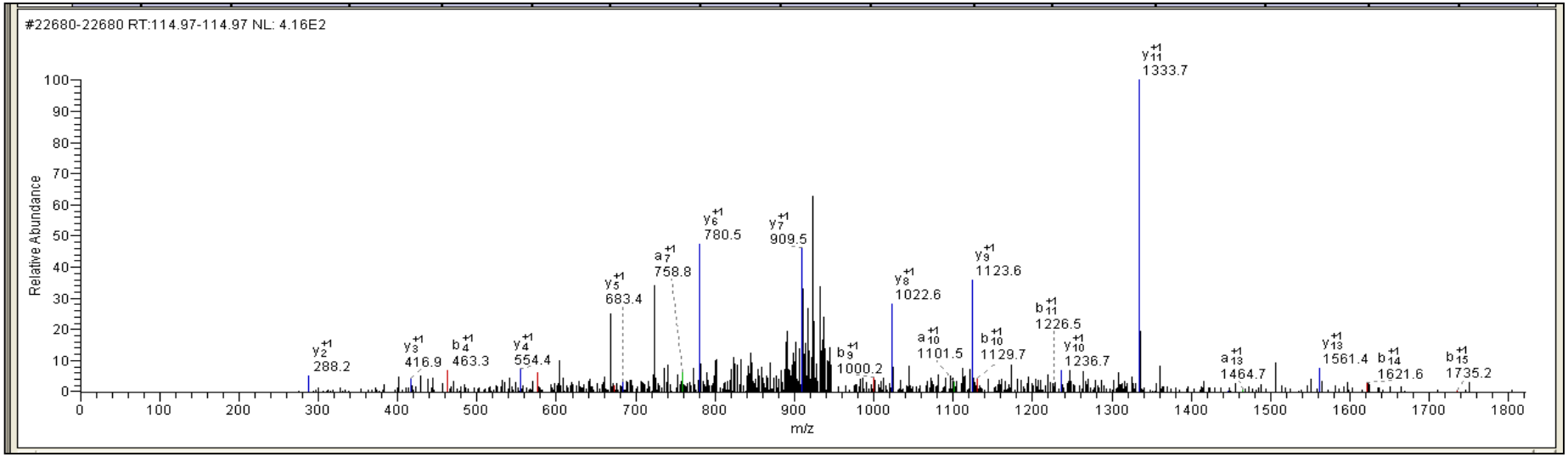
	AA	A	B	Y	
1	I	86.10	114.09	-	12
2	P	183.15	211.14	1263.67	11
3	A	254.19	282.18	1166.62	10
4	S	341.22	369.21	1095.58	9
5	I	454.30	482.30	1008.55	8
6	L	567.39	595.38	895.47	7
7	A	638.42	666.42	782.38	6
8	E	767.47	795.46	711.35	5
9	F	914.53	942.53	582.30	4
10	Y	1077.60	1105.59	435.24	3
11	P	1174.65	1202.65	272.17	2
12	R	-	-	175.12	1



Vap-33-1 NP_570087.1 Vap-33-1 CG5014-PB

K.SLFDLPLTIEPEHELR.F

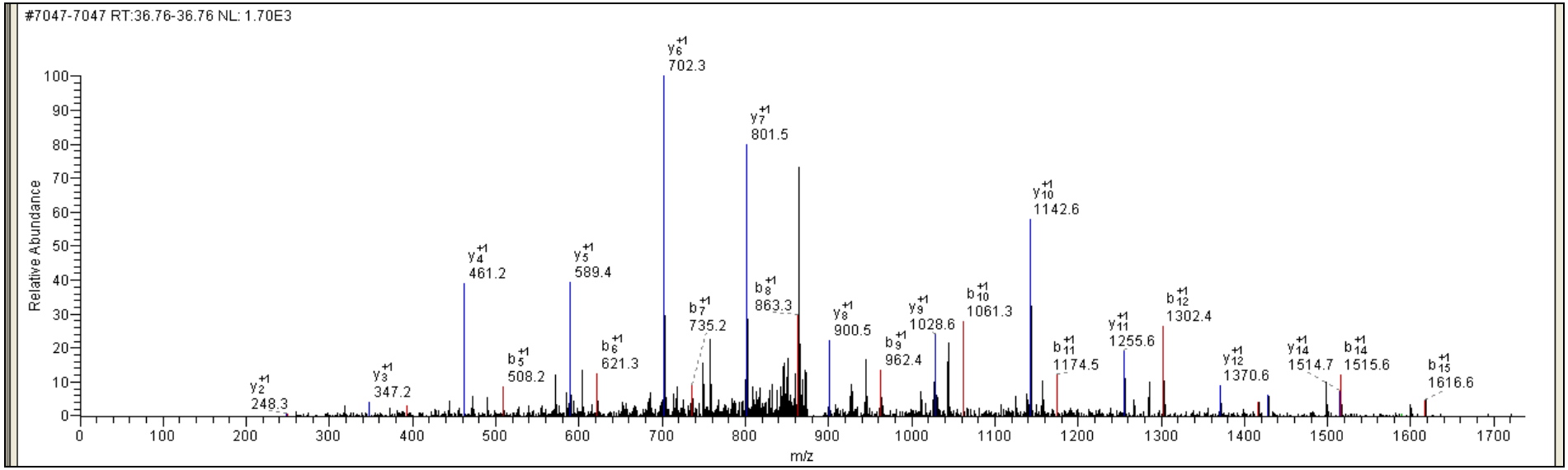
	AA	A	B	Y	
1	S	60.04	88.04	-	16
2	L	173.13	201.12	1821.97	15
3	F	320.20	348.19	1708.89	14
4	D	435.22	463.22	1561.82	13
5	L	548.31	576.30	1446.80	12
6	P	645.36	673.36	1333.71	11
7	L	758.44	786.44	1236.66	10
8	T	859.49	887.49	1123.57	9
9	I	972.58	1000.57	1022.53	8
10	E	1101.62	1129.61	909.44	7
11	P	1198.67	1226.67	780.40	6
12	E	1327.71	1355.71	683.35	5
13	H	1464.77	1492.77	554.30	4
14	E	1593.82	1621.81	417.25	3
15	L	1706.90	1734.89	288.20	2
16	R	-	-	175.12	1



Vha36 NP_651987.1 Vha36 CG8186-PA

K.FTSGDINQVVLQNVTK.A

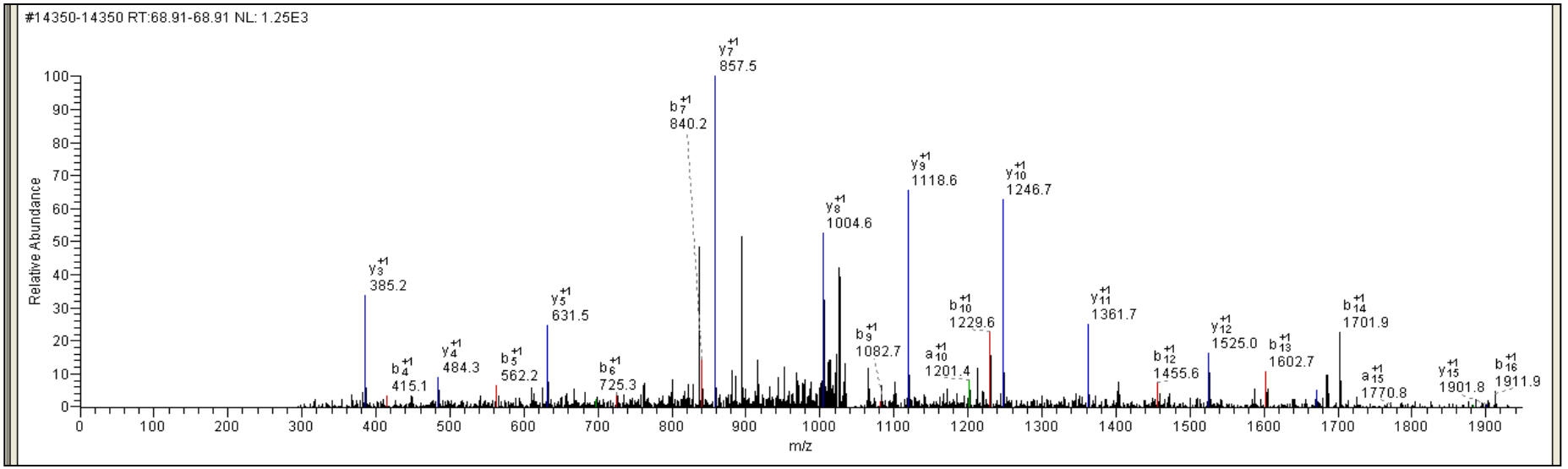
	AA	A	B	Y	
1	F	120.08	148.08	-	16
2	T	221.13	249.12	1615.86	15
3	S	308.16	336.16	1514.82	14
4	G	365.18	393.18	1427.79	13
5	D	480.21	508.20	1370.76	12
6	I	593.29	621.29	1255.74	11
7	N	707.34	735.33	1142.65	10
8	Q	835.39	863.39	1028.61	9
9	V	934.46	962.46	900.55	8
10	V	1033.53	1061.53	801.48	7
11	L	1146.62	1174.61	702.41	6
12	Q	1274.67	1302.67	589.33	5
13	N	1388.72	1416.71	461.27	4
14	V	1487.79	1515.78	347.23	3
15	T	1588.83	1616.83	248.16	2
16	K	-	-	147.11	1



Vha68-2 NP_652004.2 Vha68-2 CG3762-PA

R.ALDDFYDKNFPEFVPLR.T

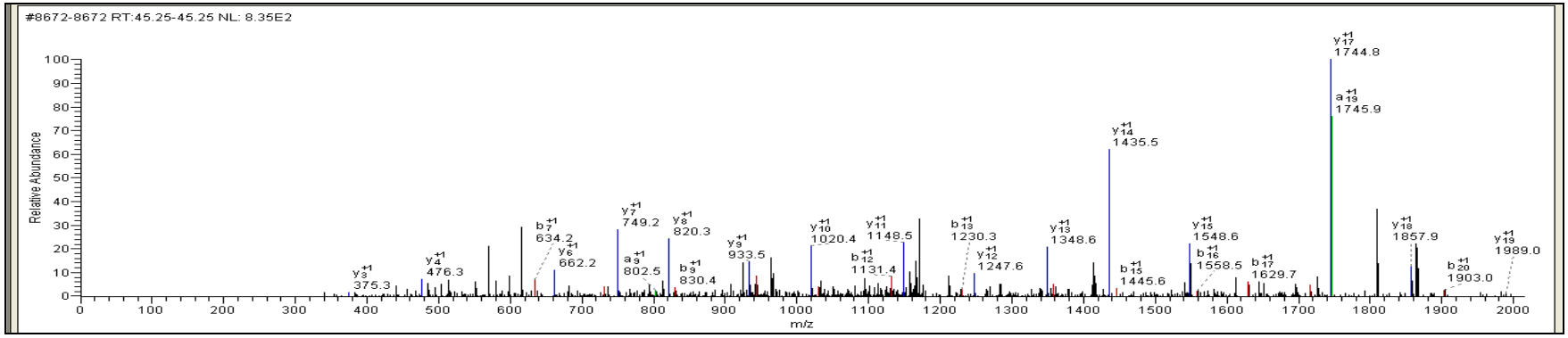
	AA	A	B	Y	
1	A	44.05	72.04	-	17
2	L	157.13	185.13	2014.99	16
3	D	272.16	300.16	1901.91	15
4	D	387.19	415.18	1786.88	14
5	F	534.26	562.25	1671.85	13
6	Y	697.32	725.31	1524.78	12
7	D	812.35	840.34	1361.72	11
8	K	940.44	968.44	1246.69	10
9	N	1054.48	1082.48	1118.60	9
10	F	1201.55	1229.55	1004.56	8
11	P	1298.61	1326.60	857.49	7
12	E	1427.65	1455.64	760.44	6
13	F	1574.72	1602.71	631.39	5
14	V	1673.78	1701.78	484.32	4
15	P	1770.84	1798.83	385.26	3
16	L	1883.92	1911.92	288.20	2
17	R	-	-	175.12	1



woc NP_524886.2 without children CG5965-PA

K.SGSGTMLPVISTVQSLASGETEAR.I

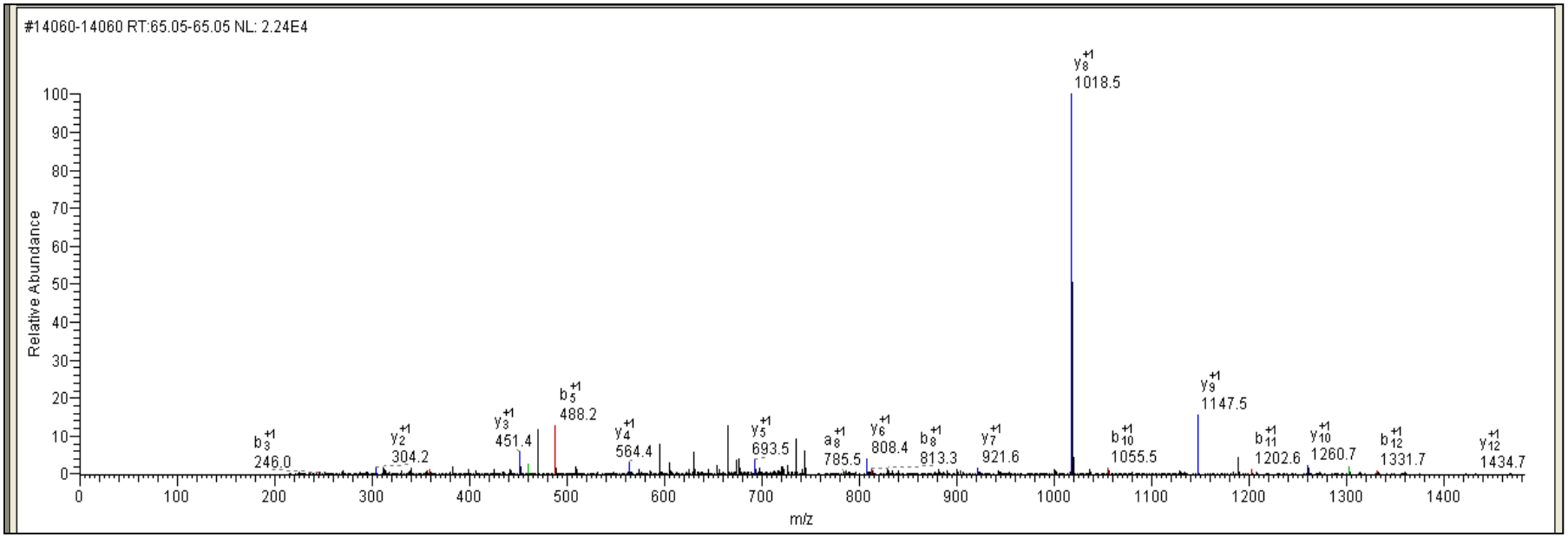
S no	AA	A	B	Y	
1	S	60.04	88.04	-	24
2	G	117.07	145.06	2291.15	23
3	S	204.1	232.09	2234.13	22
4	G	261.12	289.11	2147.1	21
5	T	362.17	390.16	2090.08	20
6	M	493.21	521.2	1989.03	19
7	L	606.29	634.29	1857.99	18
8	P	703.34	731.34	1744.91	17
9	V	802.41	830.41	1647.85	16
10	I	915.5	943.49	1548.79	15
11	S	1002.53	1030.52	1435.7	14
12	T	1103.58	1131.57	1348.67	13
13	V	1202.64	1230.64	1247.62	12
14	Q	1330.7	1358.7	1148.55	11
15	S	1417.74	1445.73	1020.5	10
16	L	1530.82	1558.81	933.46	9
17	A	1601.86	1629.85	820.38	8
18	S	1688.89	1716.88	749.34	7
19	G	1745.91	1773.91	662.31	6
20	E	1874.95	1902.95	605.29	5
21	T	1976	2004	476.25	4
22	E	2105.04	2133.04	375.2	3
23	A	2176.08	2204.08	246.16	2
24	R	-	-	175.12	1



Mf NP_731970.1 Zeelin1 CG6803-PD

R.ASSLEPLDELFER.L

	AA	A	B	Y	
1	A	44.05	72.04	-	13
2	S	131.08	159.08	1434.71	12
3	S	218.11	246.11	1347.68	11
4	L	331.20	359.19	1260.65	10
5	E	460.24	488.24	1147.56	9
6	P	557.29	585.29	1018.52	8
7	L	670.38	698.37	921.47	7
8	D	785.40	813.40	808.38	6
9	E	914.45	942.44	693.36	5
10	L	1027.53	1055.53	564.31	4
11	F	1174.60	1202.59	451.23	3
12	E	1303.64	1331.64	304.16	2
13	R	-	-	175.12	1



zormin NP_001036578.1 zormin CG33484-PC

R.DSVEAGNLVNDIENYVTSR.E

	AA	A	B	Y	
1	D	88.04	116.03	-	19
2	S	175.07	203.07	1979.97	18
3	V	274.14	302.13	1892.93	17
4	E	403.18	431.18	1793.87	16
5	A	474.22	502.21	1664.82	15
6	G	531.24	559.24	1593.79	14
7	N	645.28	673.28	1536.77	13
8	L	758.37	786.36	1422.72	12
9	V	857.44	885.43	1309.64	11
10	N	971.48	999.47	1210.57	10
11	D	1086.51	1114.50	1096.53	9
12	I	1199.59	1227.59	981.50	8
13	E	1328.63	1356.63	868.42	7
14	N	1442.68	1470.67	739.37	6
15	Y	1605.74	1633.73	625.33	5
16	V	1704.81	1732.80	462.27	4
17	T	1805.86	1833.85	363.20	3
18	S	1892.89	1920.88	262.15	2
19	R	-	-	175.12	1