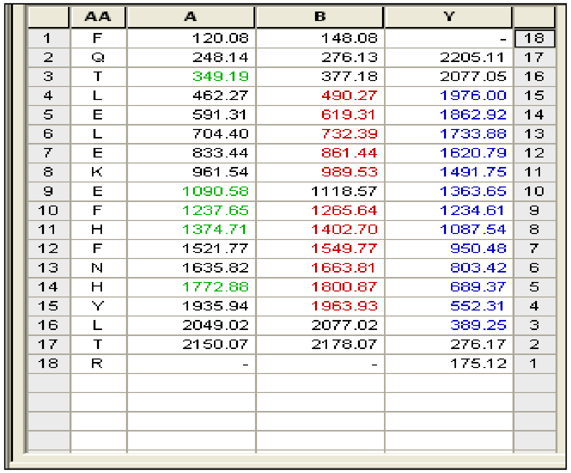
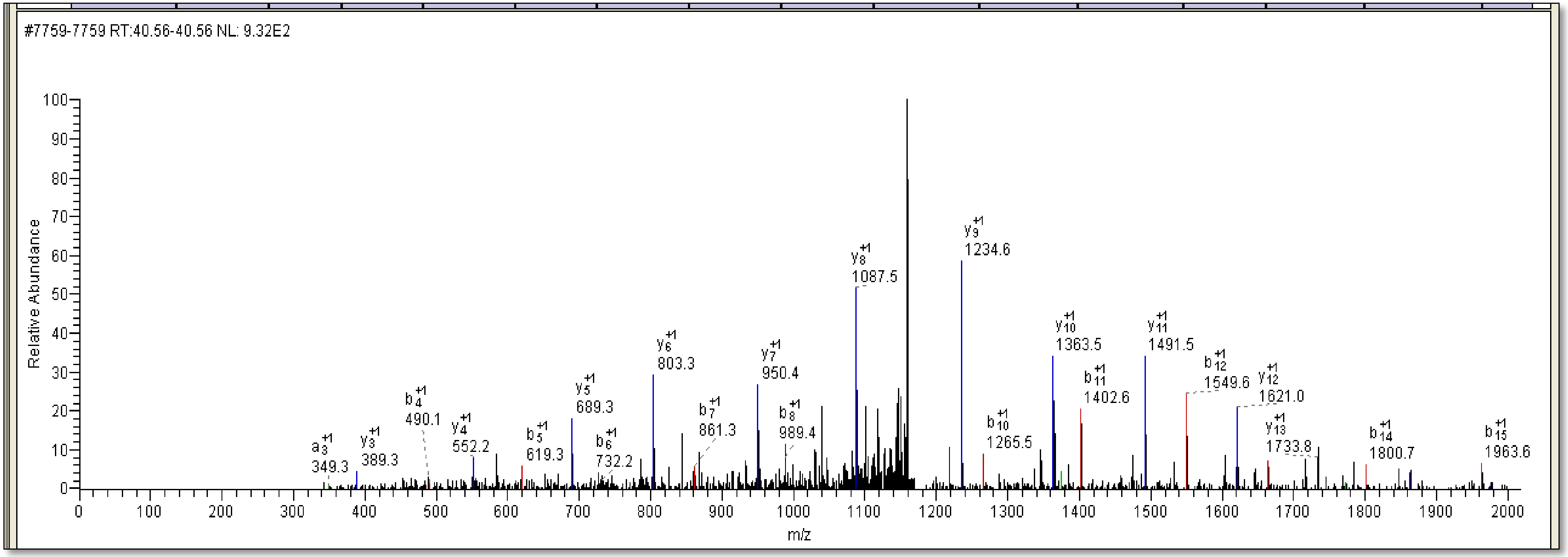
abd-A NP_732176.1 abdominal A CG10325-PB

R.FQTLELEKEFHFNHYLTR.R

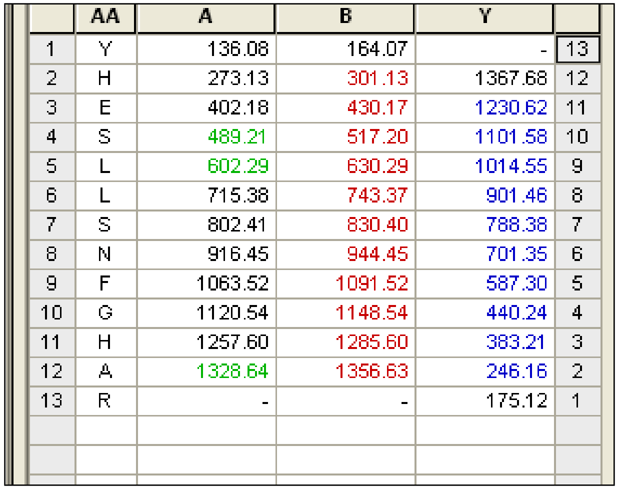


	AA	A	B	Y	
1	F	120.08	148.08	-	18
2	Q	248.14	276.13	2205.11	17
3	T	349.19	377.18	2077.05	16
4	L	462.27	490.27	1976.00	15
5	E	591.31	619.31	1862.92	14
6	L	704.40	732.39	1733.88	13
7	E	833.44	861.44	1620.79	12
8	K	961.54	989.53	1491.75	11
9	E	1090.58	1118.57	1363.65	10
10	F	1237.65	1265.64	1234.61	9
11	H	1374.71	1402.70	1087.54	8
12	F	1521.77	1549.77	950.48	7
13	N	1635.82	1663.81	803.42	6
14	H	1772.88	1800.87	689.37	5
15	Y	1935.94	1963.93	552.31	4
16	L	2049.02	2077.02	389.25	3
17	T	2150.07	2178.07	276.17	2
18	R	-	-	175.12	1

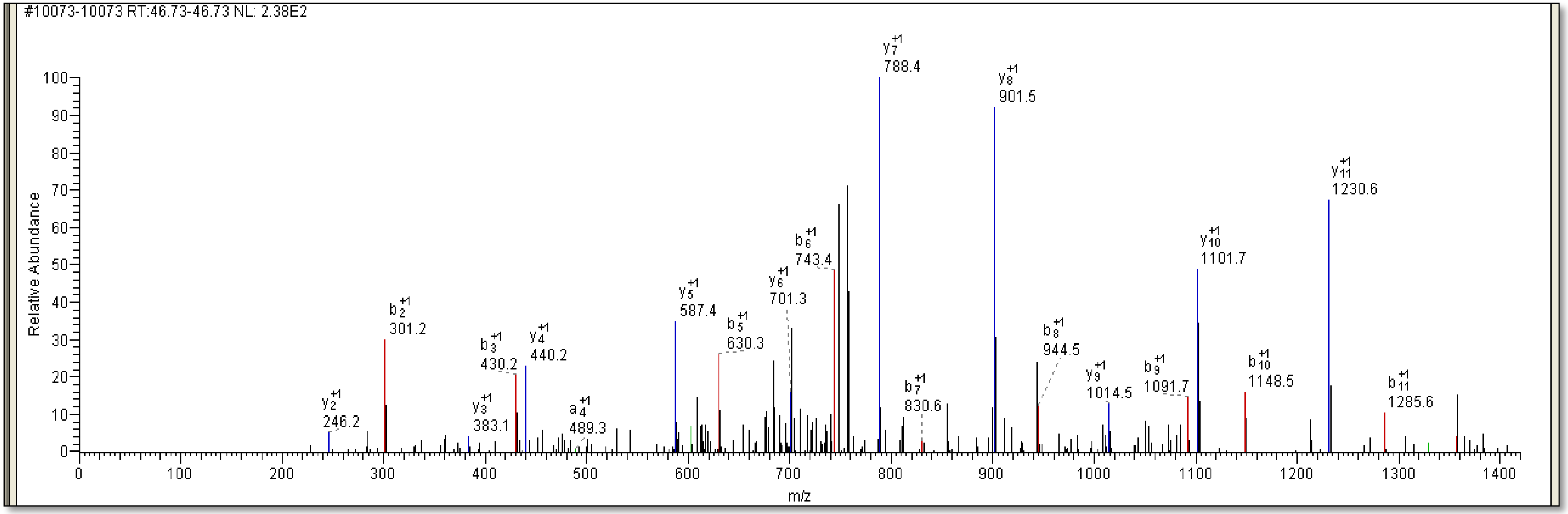


ab NP_476562.1 abrupt CG4807-PA

R.YHESLLSNFGHAR.M

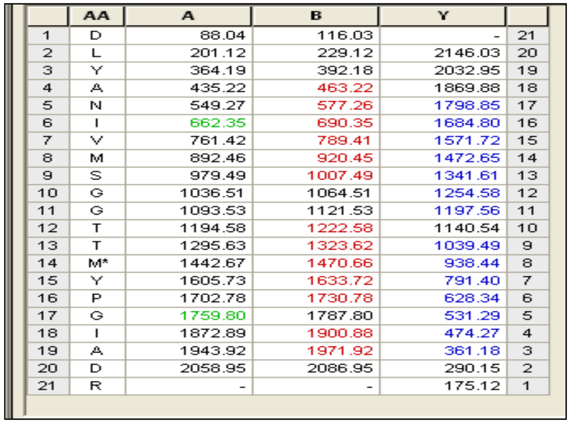


	AA	A	B	Y	
1	Y	136.08	164.07	-	13
2	H	273.13	301.13	1367.68	12
3	E	402.18	430.17	1230.62	11
4	S	489.21	517.20	1101.58	10
5	L	602.29	630.29	1014.55	9
6	L	715.38	743.37	901.46	8
7	S	802.41	830.40	788.38	7
8	N	916.45	944.45	701.35	6
9	F	1063.52	1091.52	587.30	5
10	G	1120.54	1148.54	440.24	4
11	H	1257.60	1285.60	383.21	3
12	A	1328.64	1356.63	246.16	2
13	R	-	-	175.12	1

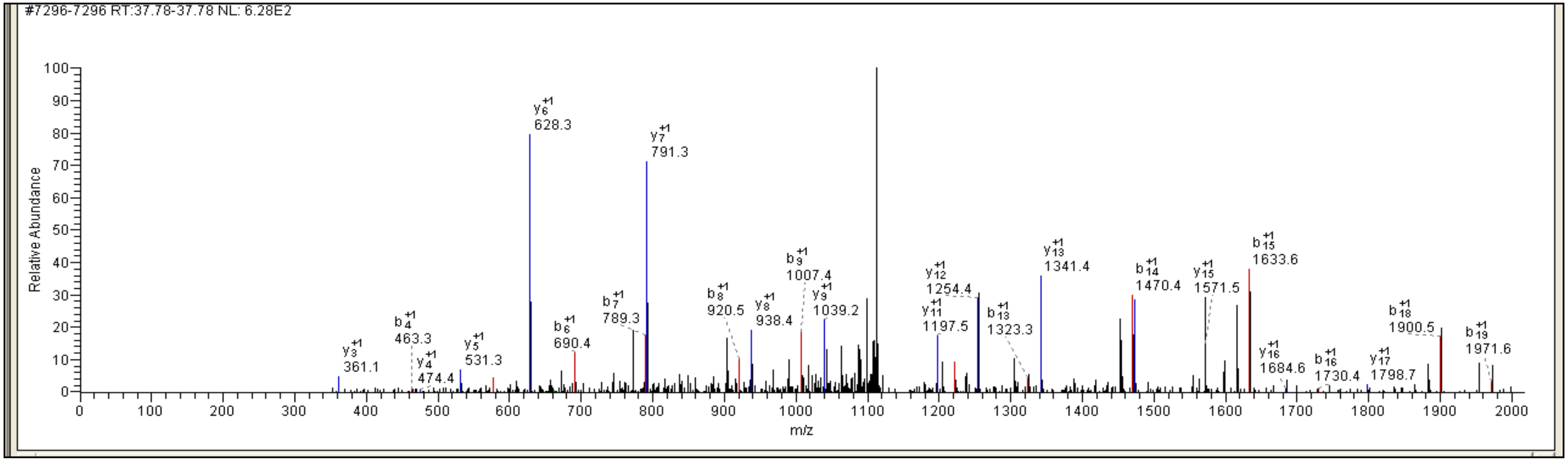


Act87E NP_477091.1 Actin 87E CG18290-PA

K.DLYANIVMSGGTTMYPGIADR.M



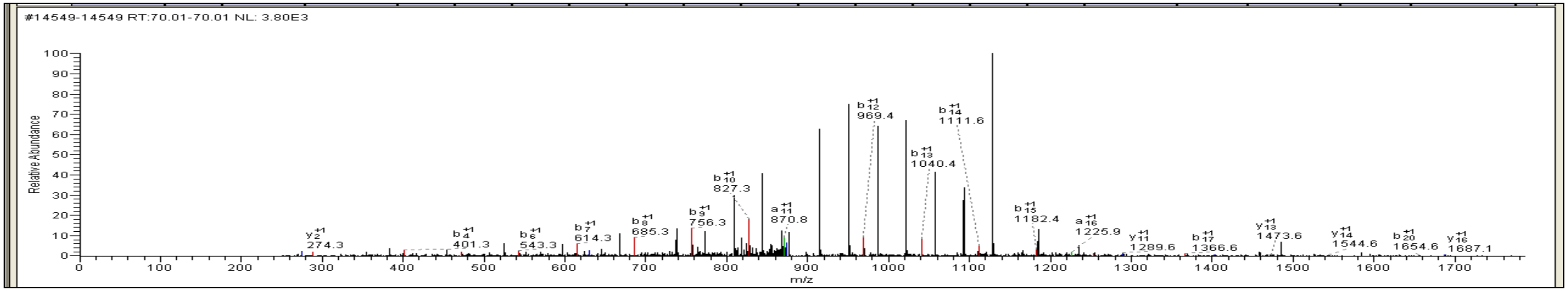
	AA	A	B	Y	
1	D	88.04	116.03	-	21
2	L	201.12	229.12	2146.03	20
3	Y	364.19	392.18	2032.95	19
4	A	435.22	463.22	1869.88	18
5	N	549.27	577.26	1798.85	17
6	I	662.35	690.35	1684.80	16
7	V	761.42	789.41	1571.72	15
8	M	892.46	920.45	1472.65	14
9	S	979.49	1007.49	1341.61	13
10	G	1036.51	1064.51	1254.58	12
11	G	1093.53	1121.53	1197.56	11
12	T	1194.58	1222.58	1140.54	10
13	T	1295.63	1323.62	1039.49	9
14	M*	1442.67	1470.66	938.44	8
15	Y	1605.73	1633.72	791.40	7
16	P	1702.78	1730.78	628.34	6
17	G	1759.80	1787.80	531.29	5
18	I	1872.89	1900.88	474.27	4
19	A	1943.92	1971.92	361.18	3
20	D	2058.95	2086.95	290.15	2
21	R	-	-	175.12	1



Alh NP_001097697.1 Alhambra CG1070-PE

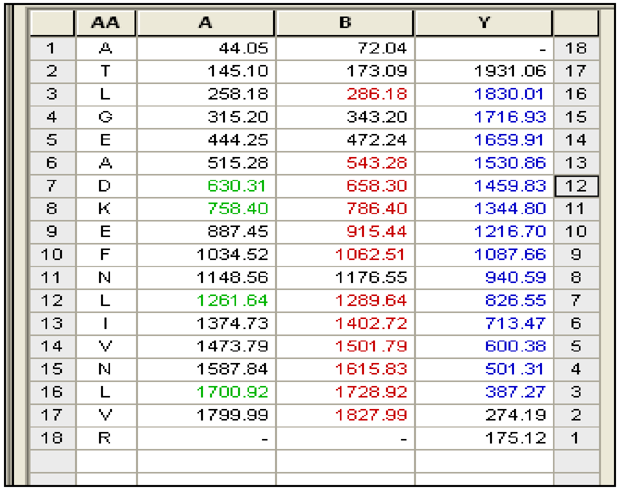
K.DATIAAAAAAAAAAAALSNSQQDLKDVR.I

S no	AA	A	B	Y	
1	D	88.04	116.03	-	28
2	A	159.08	187.07	2540.34	27
3	T	260.12	288.12	2469.31	26
4	I	373.21	401.2	2368.26	25
5	A	444.25	472.24	2255.17	24
6	A	515.28	543.28	2184.14	23
7	A	586.32	614.31	2113.1	22
8	A	657.36	685.35	2042.06	21
9	A	728.39	756.39	1971.03	20
10	A	799.43	827.43	1899.99	19
11	A	870.47	898.46	1828.95	18
12	A	941.51	969.5	1757.91	17
13	A	1012.54	1040.54	1686.88	16
14	A	1083.58	1111.57	1615.84	15
15	A	1154.62	1182.61	1544.8	14
16	A	1225.65	1253.65	1473.77	13
17	L	1338.74	1366.73	1402.73	12
18	S	1425.77	1453.76	1289.64	11
19	N	1539.81	1567.81	1202.61	10
20	S	1626.84	1654.84	1088.57	9
21	Q	1754.9	1782.9	1001.54	8
22	Q	1882.96	1910.96	873.48	7
23	D	1997.99	2025.98	745.42	6
24	L	2111.07	2139.07	630.39	5
25	K	2239.17	2267.16	517.31	4
26	D	2354.19	2382.19	389.21	3
27	V	2453.26	2481.26	274.19	2
28	R	-	-	175.12	1

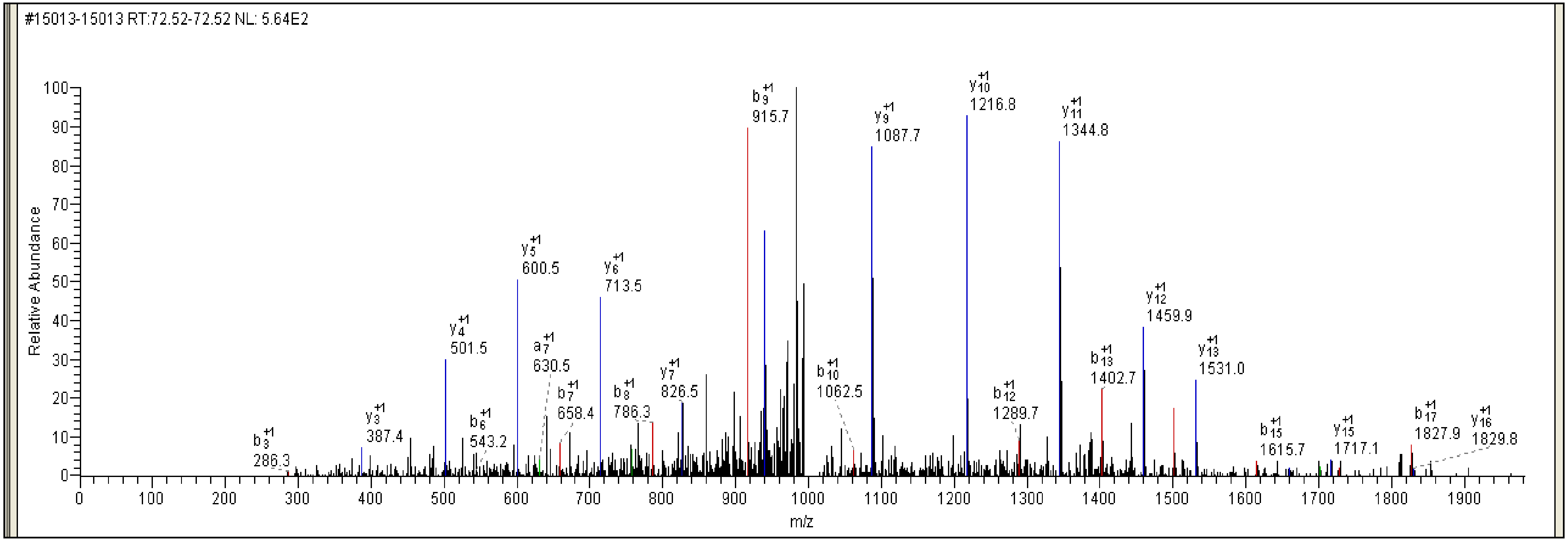


Actn NP_477484.2 alpha actinin CG4376-PA

K.ATLGEADKEFNLIVNLVR.E



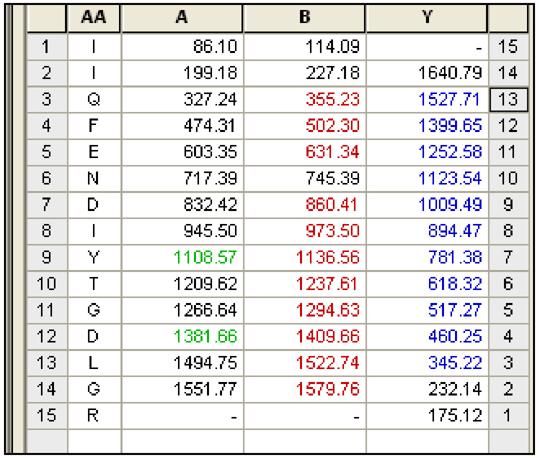
	AA	A	B	Y	
1	A	44.05	72.04	-	18
2	T	145.10	173.09	1931.06	17
3	L	258.18	286.18	1830.01	16
4	G	315.20	343.20	1716.93	15
5	E	444.25	472.24	1659.91	14
6	A	515.28	543.28	1530.86	13
7	D	630.31	658.30	1459.83	12
8	K	758.40	786.40	1344.80	11
9	E	887.45	915.44	1216.70	10
10	F	1034.52	1062.51	1087.66	9
11	N	1148.56	1176.55	940.59	8
12	L	1261.64	1289.64	826.55	7
13	I	1374.73	1402.72	713.47	6
14	V	1473.79	1501.79	600.38	5
15	N	1587.84	1615.83	501.31	4
16	L	1700.92	1728.92	387.27	3
17	V	1799.99	1827.99	274.19	2
18	R	-	-	175.12	1



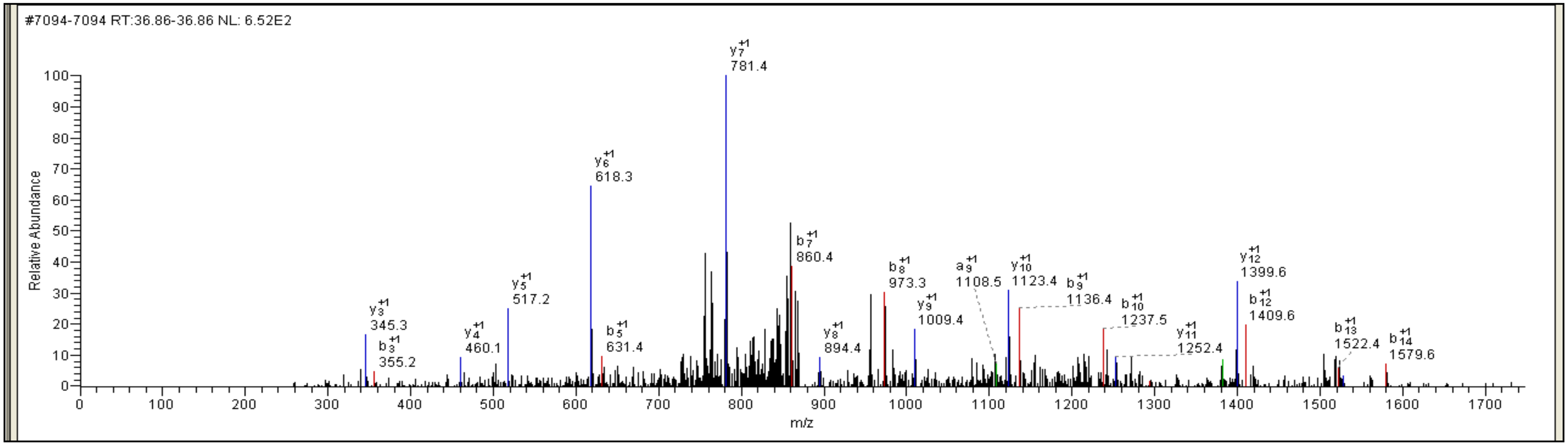
Acf1 NP_536734.2

ATP-dependent chromatin assembly factor large subunit CG1966-PA

R.IIQFENDIYTGDLGR.L

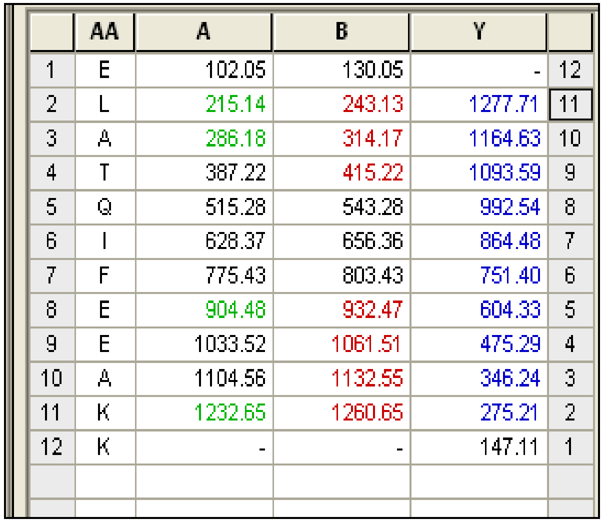


	AA	A	B	Y	
1	I	86.10	114.09	-	15
2	I	199.18	227.18	1640.79	14
3	Q	327.24	355.23	1527.71	13
4	F	474.31	502.30	1399.65	12
5	E	603.35	631.34	1252.58	11
6	N	717.39	745.39	1123.54	10
7	D	832.42	860.41	1009.49	9
8	I	945.50	973.50	894.47	8
9	Y	1108.57	1136.56	781.38	7
10	T	1209.62	1237.61	618.32	6
11	G	1266.64	1294.63	517.27	5
12	D	1381.66	1409.66	460.25	4
13	L	1494.75	1522.74	345.22	3
14	G	1551.77	1579.76	232.14	2
15	R	-	-	175.12	1

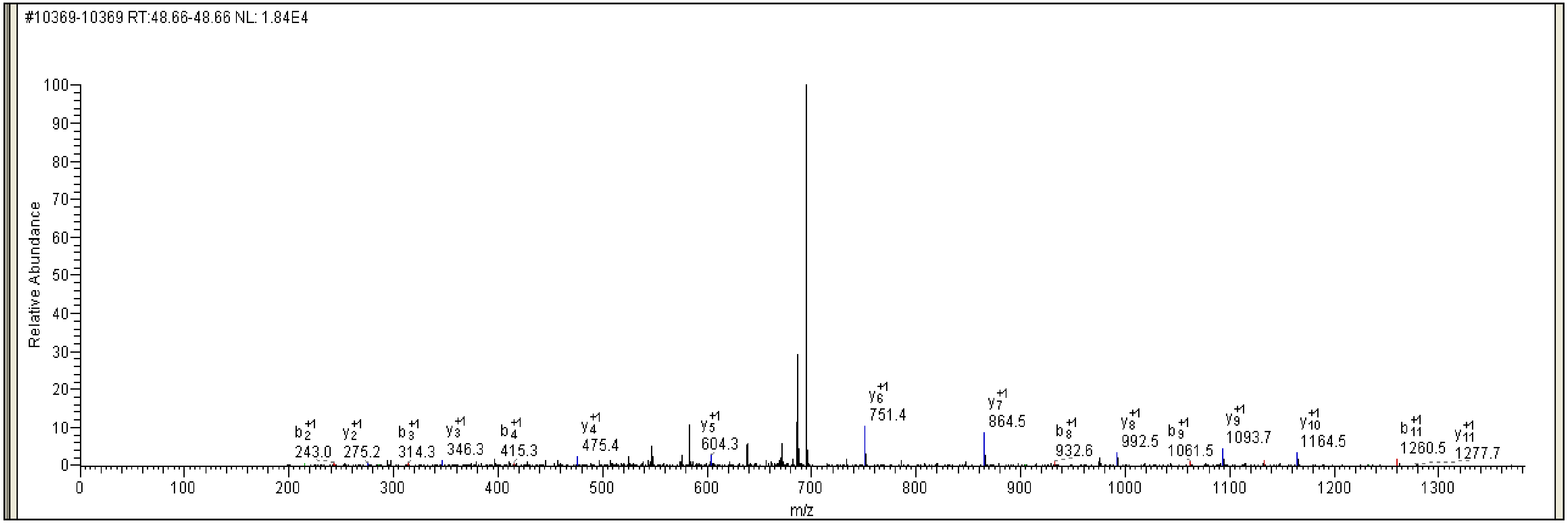


bel NP_536783.1 belle CG9748-PA

R.ELATQIFEEAKK.F



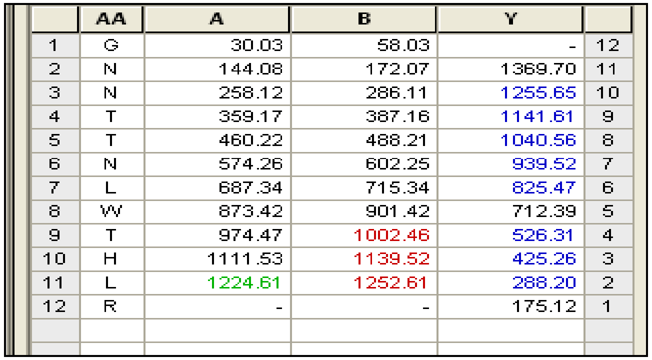
	AA	A	B	Y	
1	E	102.05	130.05	-	12
2	L	215.14	243.13	1277.71	11
3	A	286.18	314.17	1164.63	10
4	T	387.22	415.22	1093.59	9
5	Q	515.28	543.28	992.54	8
6	I	628.37	656.36	864.48	7
7	F	775.43	803.43	751.40	6
8	E	904.48	932.47	604.33	5
9	E	1033.52	1061.51	475.29	4
10	A	1104.56	1132.55	346.24	3
11	K	1232.65	1260.65	275.21	2
12	K	-	-	147.11	1



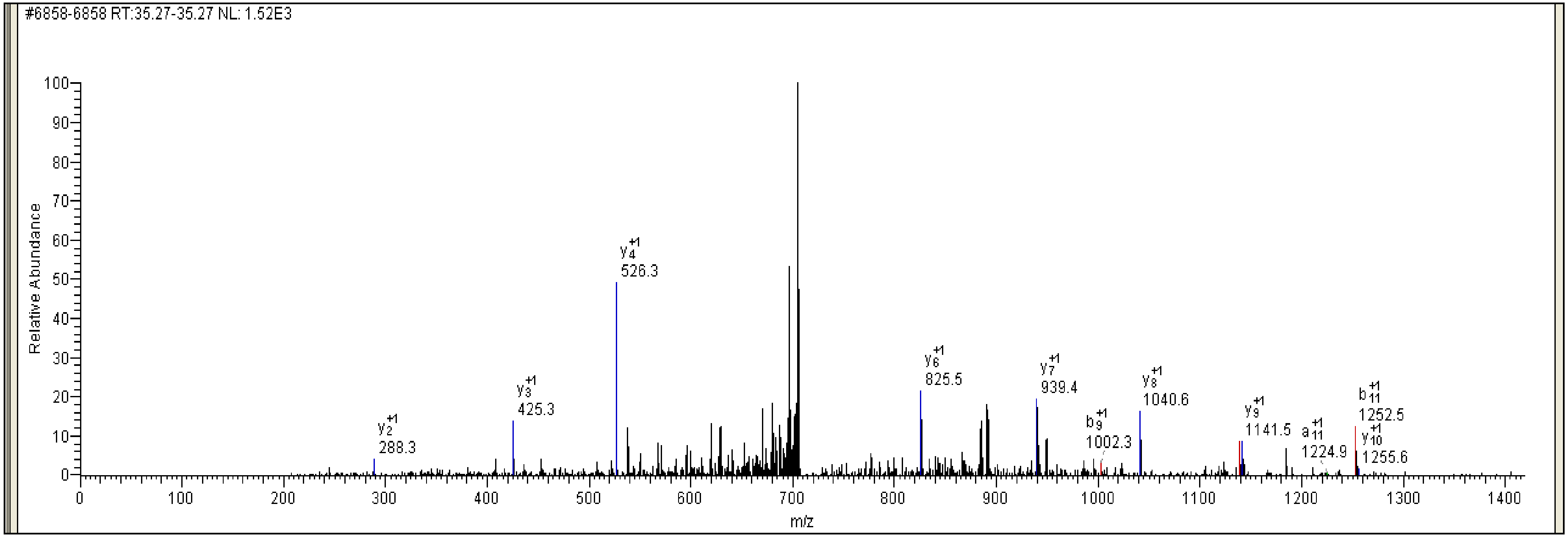
NP_725418.1

Boundary element-associated factor of 32kD CG10159-PB

K.GNNTTNLWTHLR.H



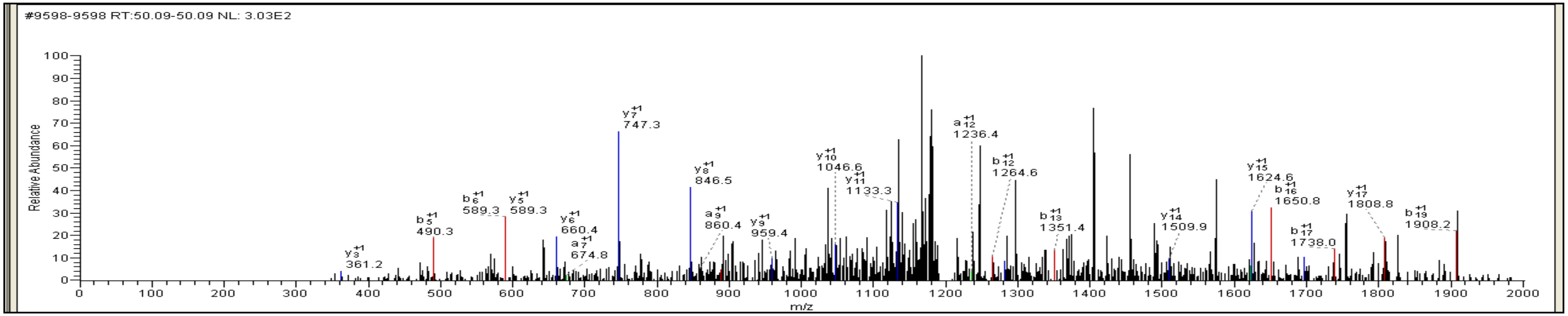
	AA	A	B	Y	
1	G	30.03	58.03	-	12
2	N	144.08	172.07	1369.70	11
3	N	258.12	286.11	1255.65	10
4	T	359.17	387.16	1141.61	9
5	T	460.22	488.21	1040.56	8
6	N	574.26	602.25	939.52	7
7	L	687.34	715.34	825.47	6
8	W	873.42	901.42	712.39	5
9	T	974.47	1002.46	526.31	4
10	H	1111.53	1139.52	425.26	3
11	L	1224.61	1252.61	288.20	2
12	R	-	-	175.12	1



Ca-P60A NP_476832.1 Calcium ATPase at 60A CG3725-PA

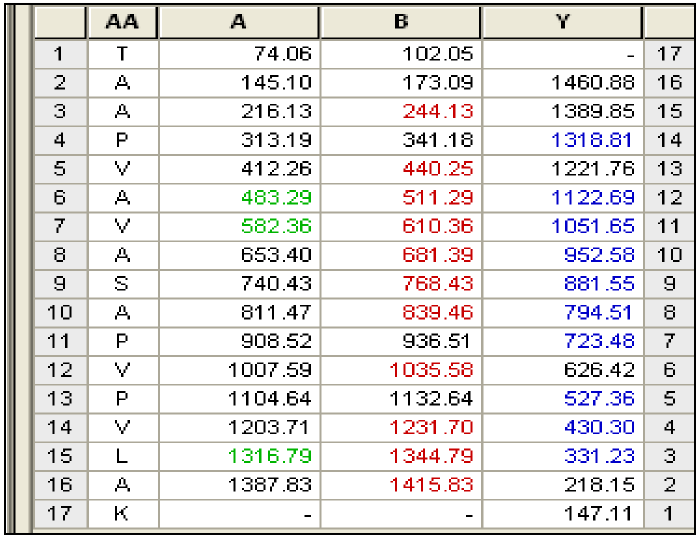
K.SAAEMVLADDNFSSIVSAVEEGR.A

S no	AA	A	B	Y	
1	S	60.04	88.04	-	23
2	A	131.08	159.08	2310.09	22
3	A	202.12	230.11	2239.05	21
4	E	331.16	359.16	2168.02	20
5	M	462.2	490.2	2038.97	19
6	V	561.27	589.27	1907.93	18
7	L	674.35	702.35	1808.87	17
8	A	745.39	773.39	1695.78	16
9	D	860.42	888.41	1624.74	15
10	D	975.45	1003.44	1509.72	14
11	N	1089.49	1117.48	1394.69	13
12	F	1236.56	1264.55	1280.65	12
13	S	1323.59	1351.58	1133.58	11
14	S	1410.62	1438.62	1046.55	10
15	I	1523.7	1551.7	959.52	9
16	V	1622.77	1650.77	846.43	8
17	S	1709.81	1737.8	747.36	7
18	A	1780.84	1808.84	660.33	6
19	V	1879.91	1907.91	589.29	5
20	E	2008.95	2036.95	490.23	4
21	E	2138	2165.99	361.18	3
22	G	2195.02	2223.01	232.14	2
23	R	-	-	175.12	1

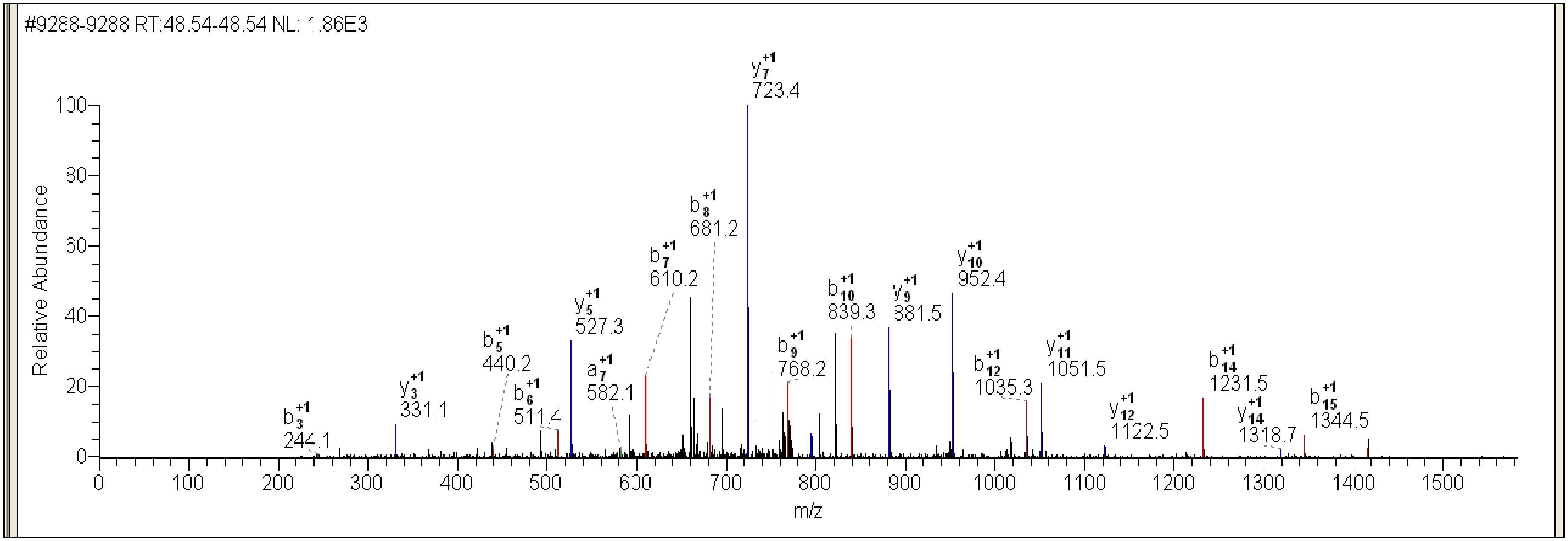


Ccp84Ae NP_649679.1 Ccp84Ae CG1330-PA

R.TAAPVAVASAPVPVLAK.T

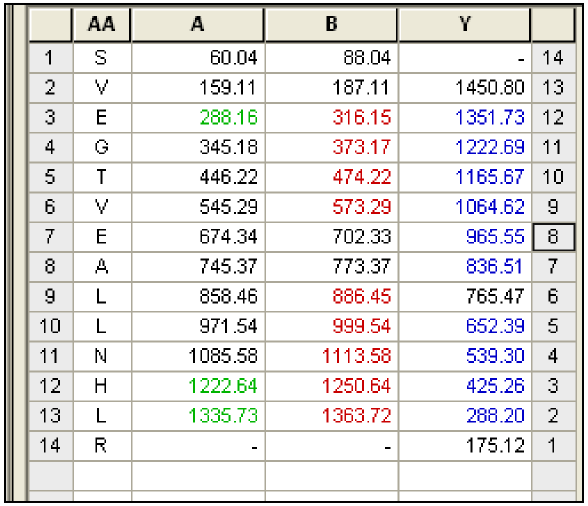


	AA	A	B	Y	
1	T	74.06	102.05	-	17
2	A	145.10	173.09	1460.88	16
3	A	216.13	244.13	1389.85	15
4	P	313.19	341.18	1318.81	14
5	V	412.26	440.25	1221.76	13
6	A	483.29	511.29	1122.69	12
7	V	582.36	610.36	1051.65	11
8	A	653.40	681.39	952.58	10
9	S	740.43	768.43	881.55	9
10	A	811.47	839.46	794.51	8
11	P	908.52	936.51	723.48	7
12	V	1007.59	1035.58	626.42	6
13	P	1104.64	1132.64	527.36	5
14	V	1203.71	1231.70	430.30	4
15	L	1316.79	1344.79	331.23	3
16	A	1387.83	1415.83	218.15	2
17	K	-	-	147.11	1

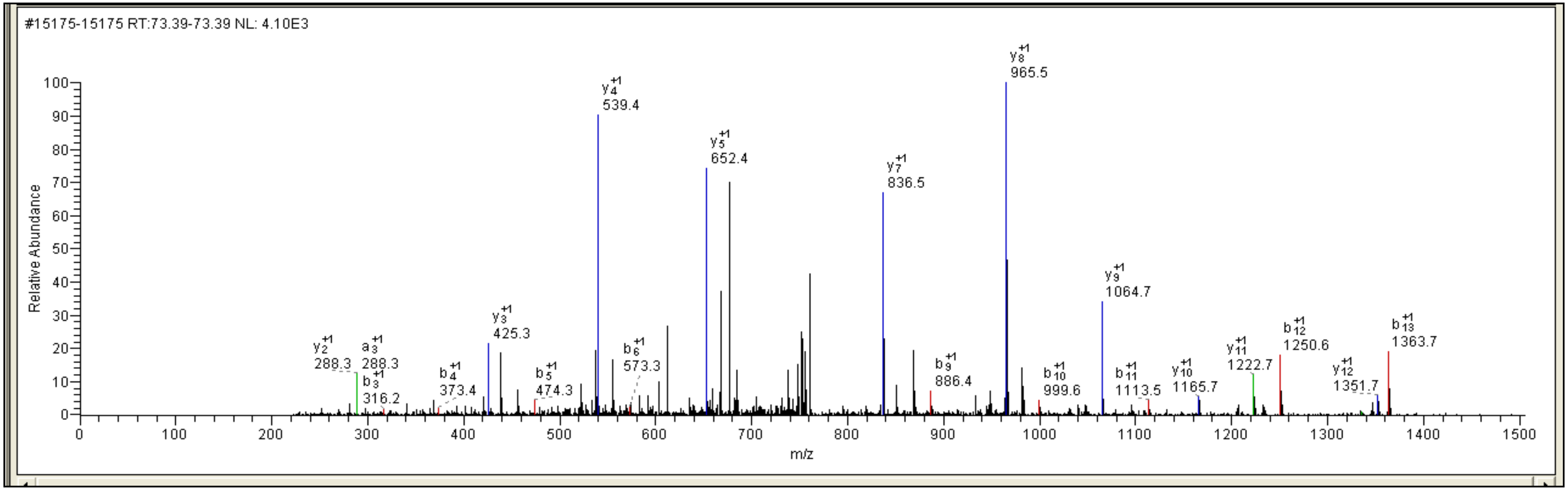


NP_649652.3 CG1024 CG1024-PA

K.SVEGTVEALLNHLR.E

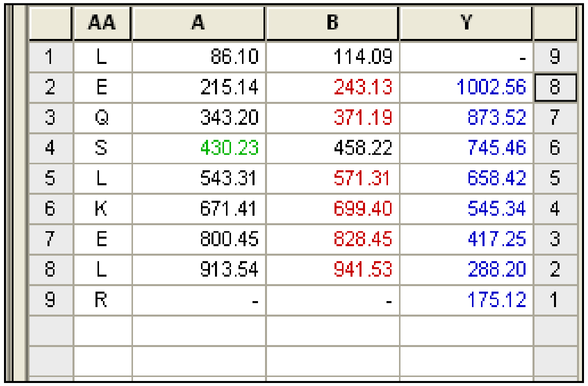


	AA	A	B	Y	
1	S	60.04	88.04	-	14
2	V	159.11	187.11	1450.80	13
3	E	288.16	316.15	1351.73	12
4	G	345.18	373.17	1222.69	11
5	T	446.22	474.22	1165.67	10
6	V	545.29	573.29	1064.62	9
7	E	674.34	702.33	965.55	8
8	A	745.37	773.37	836.51	7
9	L	858.46	886.45	765.47	6
10	L	971.54	999.54	652.39	5
11	N	1085.58	1113.58	539.30	4
12	H	1222.64	1250.64	425.26	3
13	L	1335.73	1363.72	288.20	2
14	R	-	-	175.12	1

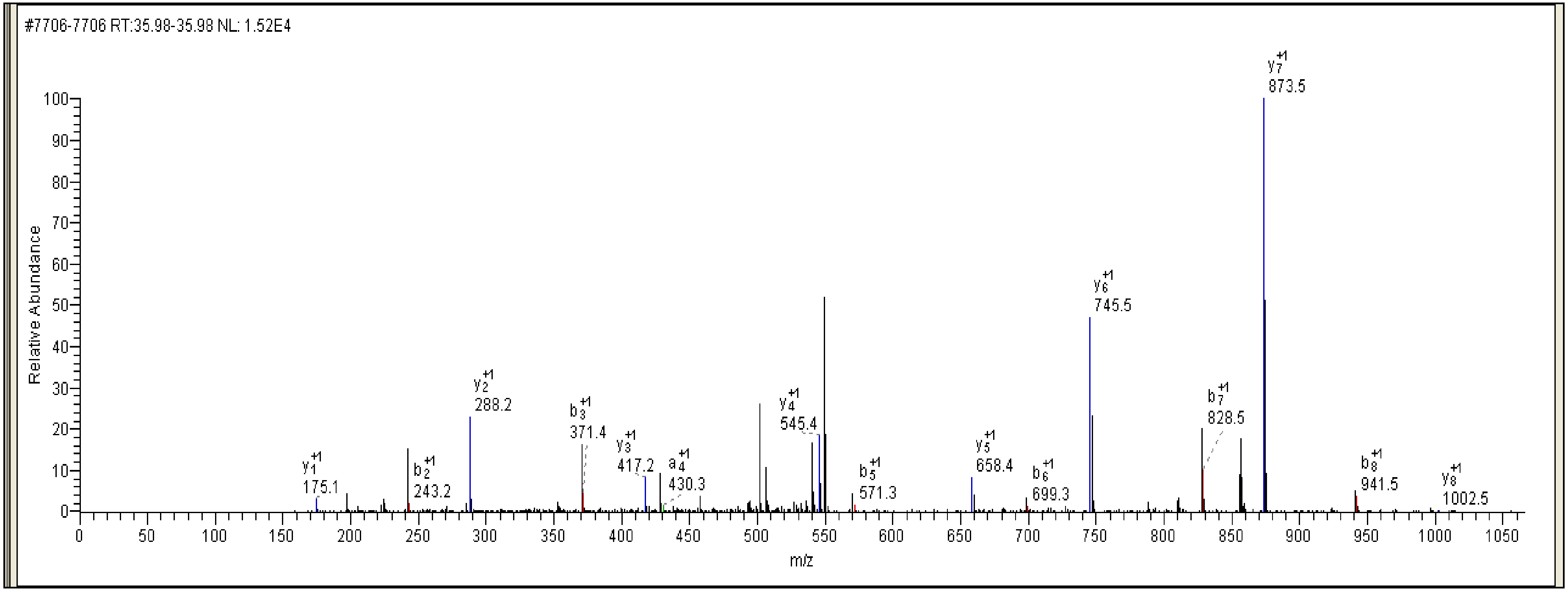


CG10413 NP_609887.1 CG10413 CG10413-PA

K.LEQSLKELR.I

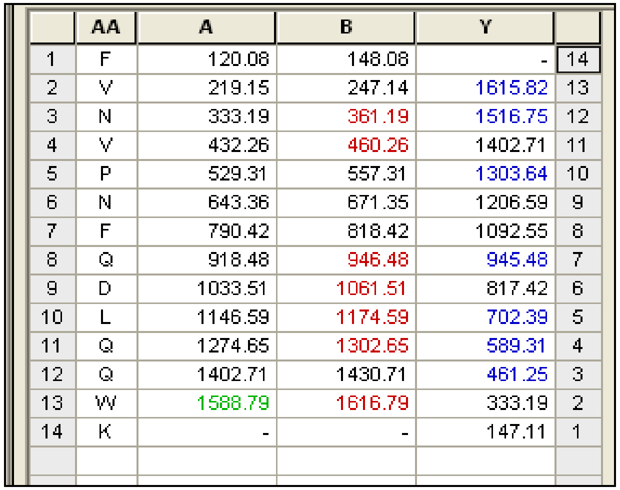


	AA	A	B	Y	
1	L	86.10	114.09	-	9
2	E	215.14	243.13	1002.56	8
3	Q	343.20	371.19	873.52	7
4	S	430.23	458.22	745.46	6
5	L	543.31	571.31	658.42	5
6	K	671.41	699.40	545.34	4
7	E	800.45	828.45	417.25	3
8	L	913.54	941.53	288.20	2
9	R	-	-	175.12	1

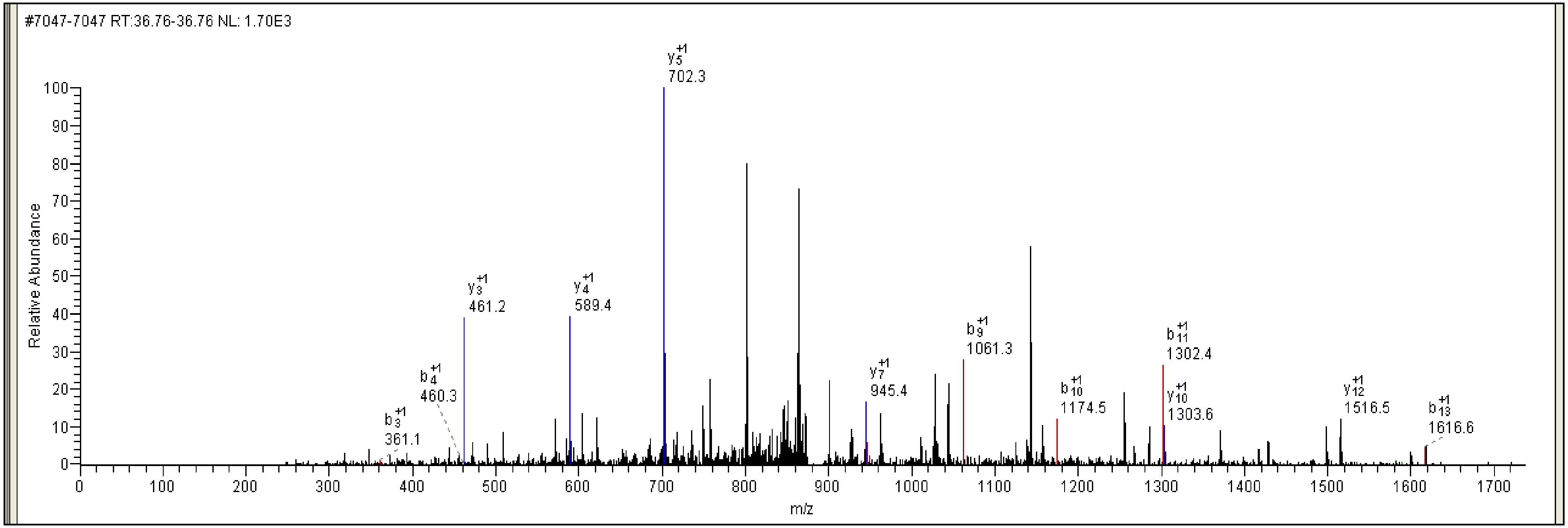


NP_649751.1 CG10445 CG10445-PA

R.FVNVPNFQDLQQWK.K

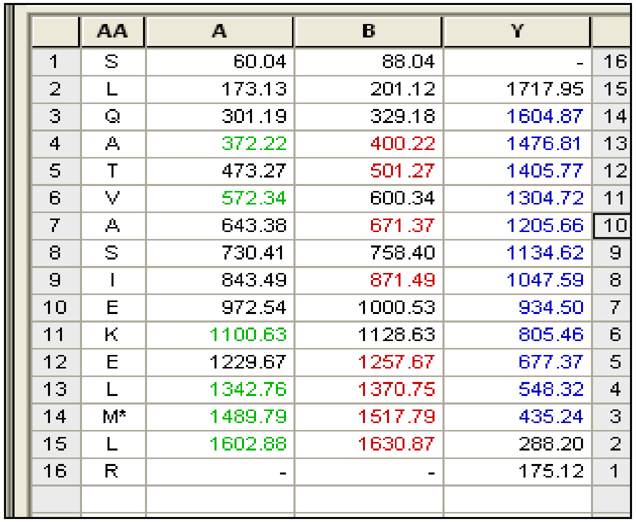


	AA	A	B	Y	
1	F	120.08	148.08	-	14
2	V	219.15	247.14	1615.82	13
3	N	333.19	361.19	1516.75	12
4	V	432.26	460.26	1402.71	11
5	P	529.31	557.31	1303.64	10
6	N	643.36	671.35	1206.59	9
7	F	790.42	818.42	1092.55	8
8	Q	918.48	946.48	945.48	7
9	D	1033.51	1061.51	817.42	6
10	L	1146.59	1174.59	702.39	5
11	Q	1274.65	1302.65	589.31	4
12	Q	1402.71	1430.71	461.25	3
13	W	1588.79	1616.79	333.19	2
14	K	-	-	147.11	1

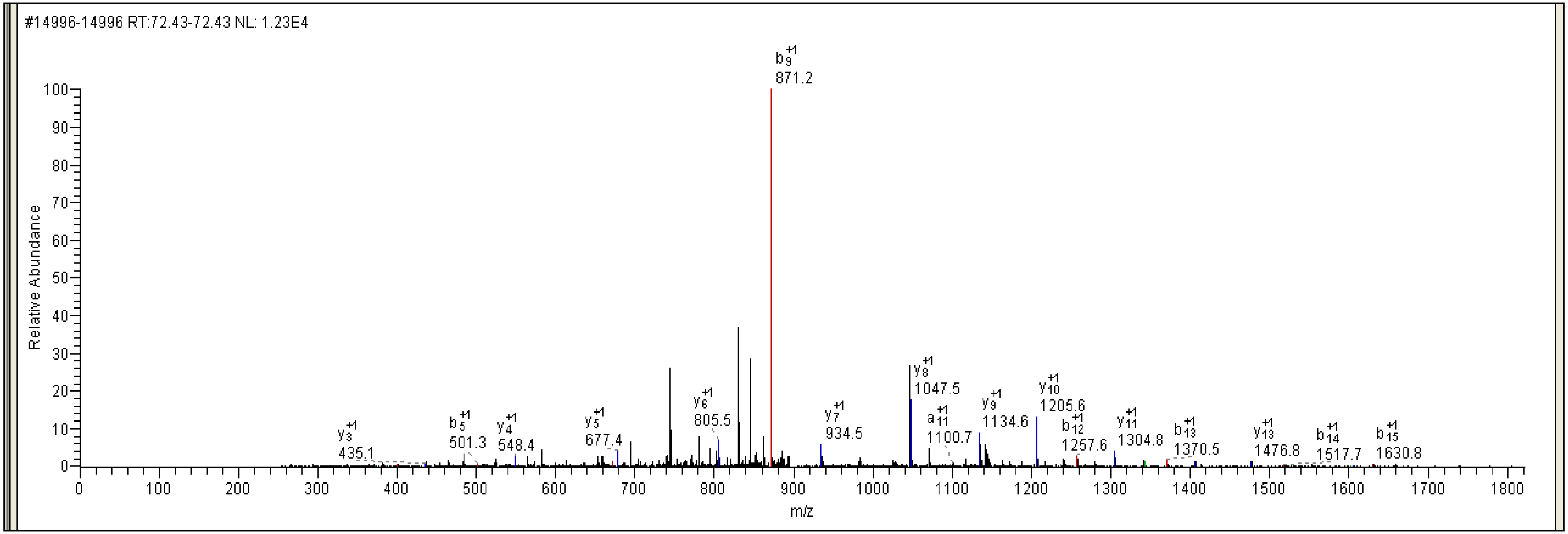


Bre1 NP_647989.2 CG10542 CG10542-PA

R.SLQATVASIEKELMLR.Q

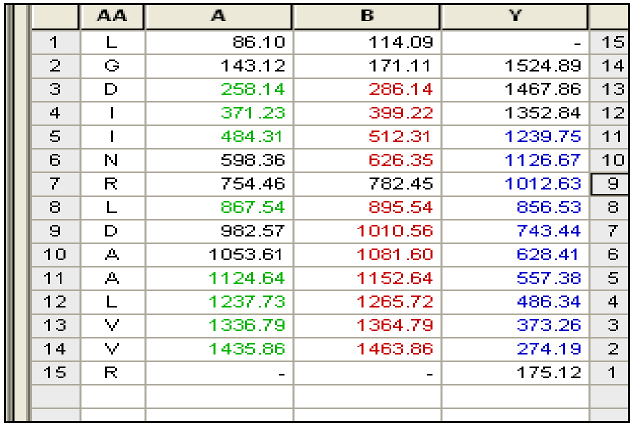


	AA	A	B	Y	
1	S	60.04	88.04	-	16
2	L	173.13	201.12	1717.95	15
3	Q	301.19	329.18	1604.87	14
4	A	372.22	400.22	1476.81	13
5	T	473.27	501.27	1405.77	12
6	V	572.34	600.34	1304.72	11
7	A	643.38	671.37	1205.66	10
8	S	730.41	758.40	1134.62	9
9	I	843.49	871.49	1047.59	8
10	E	972.54	1000.53	934.50	7
11	K	1100.63	1128.63	805.46	6
12	E	1229.67	1257.67	677.37	5
13	L	1342.76	1370.75	548.32	4
14	M*	1489.79	1517.79	435.24	3
15	L	1602.88	1630.87	288.20	2
16	R	-	-	175.12	1

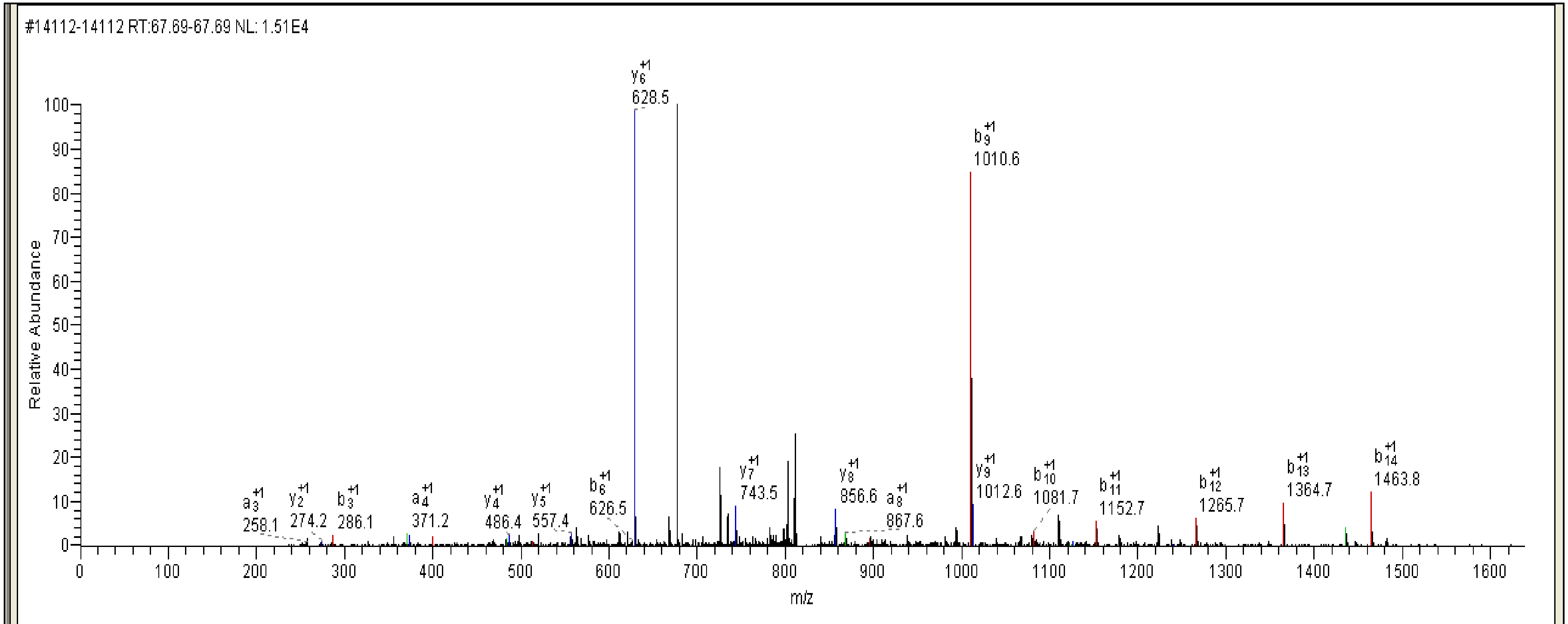


NP_572929.1 CG11092 CG11092-PA

R.LGDIINRLDAALVVR.K

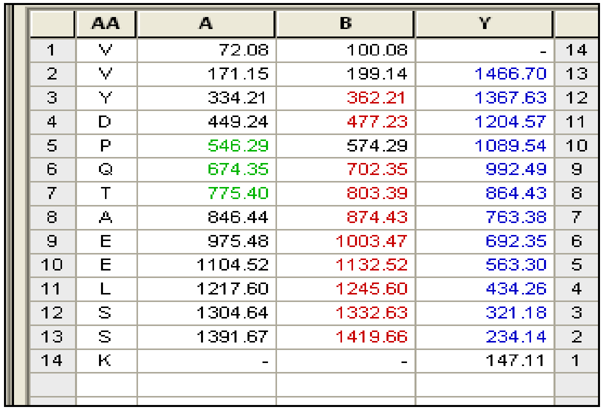


	AA	A	B	Y	
1	L	86.10	114.09	-	15
2	G	143.12	171.11	1524.89	14
3	D	258.14	286.14	1467.86	13
4	I	371.23	399.22	1352.84	12
5	I	484.31	512.31	1239.75	11
6	N	598.36	626.35	1126.67	10
7	R	754.46	782.45	1012.63	9
8	L	867.54	895.54	856.53	8
9	D	982.57	1010.56	743.44	7
10	A	1053.61	1081.60	628.41	6
11	A	1124.64	1152.64	557.38	5
12	L	1237.73	1265.72	486.34	4
13	V	1336.79	1364.79	373.26	3
14	V	1435.86	1463.86	274.19	2
15	R	-	-	175.12	1

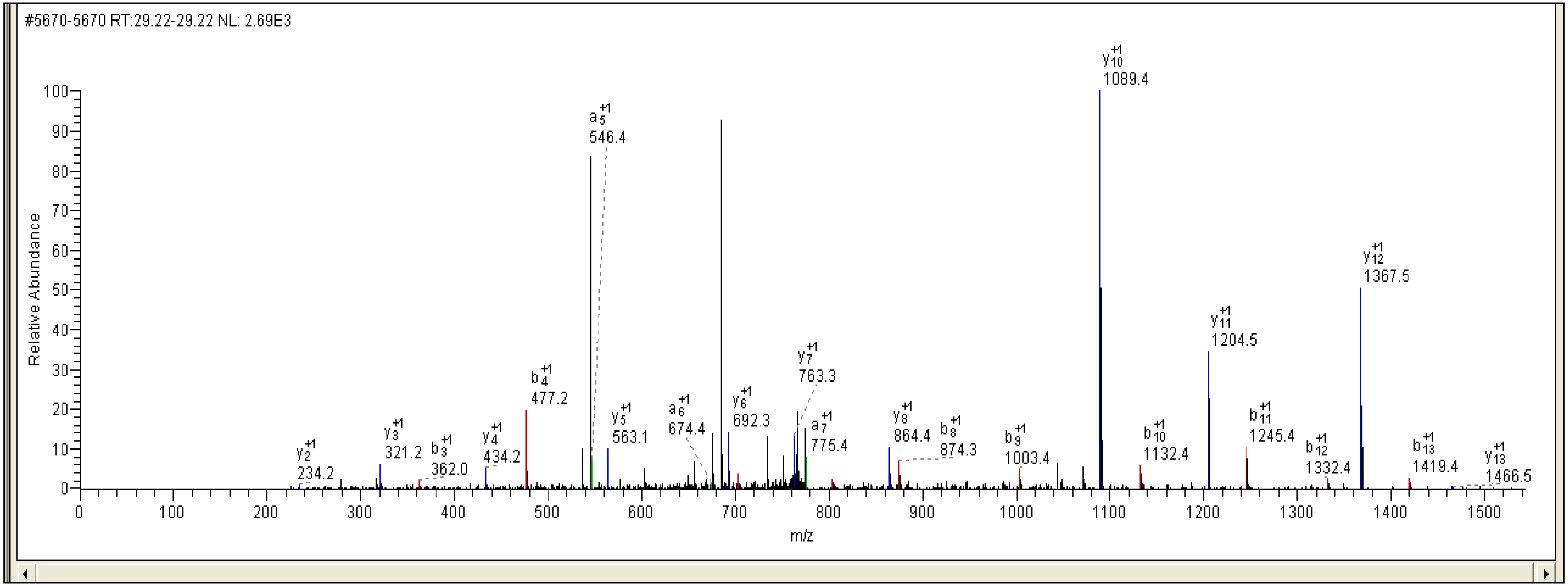


CG11963 NP_649846.2 CG11963 CG11963-PA

R.VVYDPQTAEELSSK.M

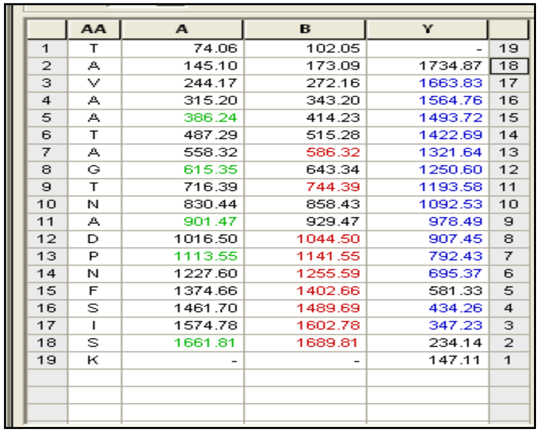


	AA	A	B	Y	
1	V	72.08	100.08	-	14
2	V	171.15	199.14	1466.70	13
3	Y	334.21	362.21	1367.63	12
4	D	449.24	477.23	1204.57	11
5	P	546.29	574.29	1089.54	10
6	Q	674.35	702.35	992.49	9
7	T	775.40	803.39	864.43	8
8	A	846.44	874.43	763.38	7
9	E	975.48	1003.47	692.35	6
10	E	1104.52	1132.52	563.30	5
11	L	1217.60	1245.60	434.26	4
12	S	1304.64	1332.63	321.18	3
13	S	1391.67	1419.66	234.14	2
14	K	-	-	147.11	1

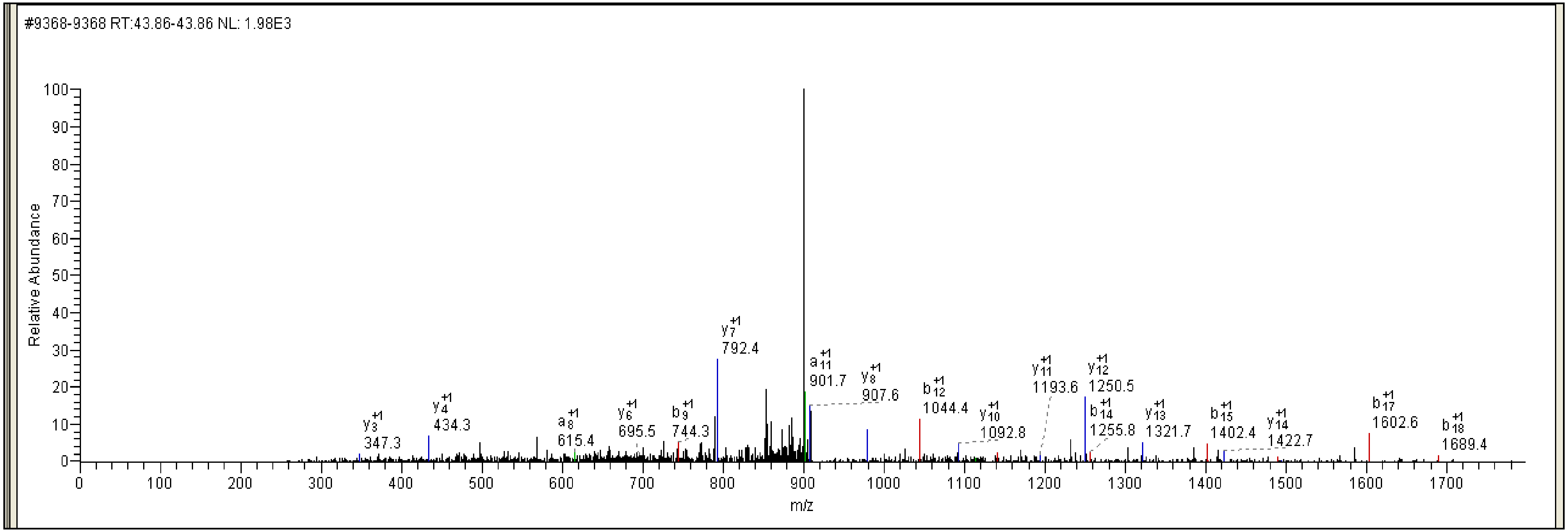


NP_572548.1 CG12124 CG12124-PA

R.TAVAATAGTNADPNFSISK.L



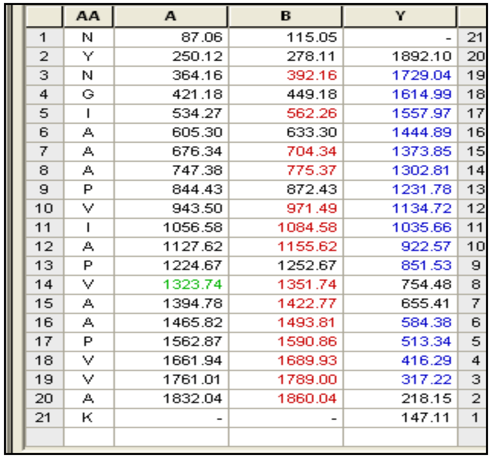
	AA	A	B	Y	
1	T	74.06	102.05	-	19
2	A	145.10	173.09	1734.87	18
3	V	244.17	272.16	1663.83	17
4	A	315.20	343.20	1564.76	16
5	A	386.24	414.23	1493.72	15
6	T	487.29	515.28	1422.69	14
7	A	558.32	586.32	1321.64	13
8	G	615.35	643.34	1250.60	12
9	T	716.39	744.39	1193.58	11
10	N	830.44	858.43	1092.53	10
11	A	901.47	929.47	978.49	9
12	D	1016.50	1044.50	907.45	8
13	P	1113.55	1141.55	792.43	7
14	N	1227.60	1255.59	695.37	6
15	F	1374.66	1402.66	581.33	5
16	S	1461.70	1489.69	434.26	4
17	I	1574.78	1602.78	347.23	3
18	S	1661.81	1689.81	234.14	2
19	K	-	-	147.11	1



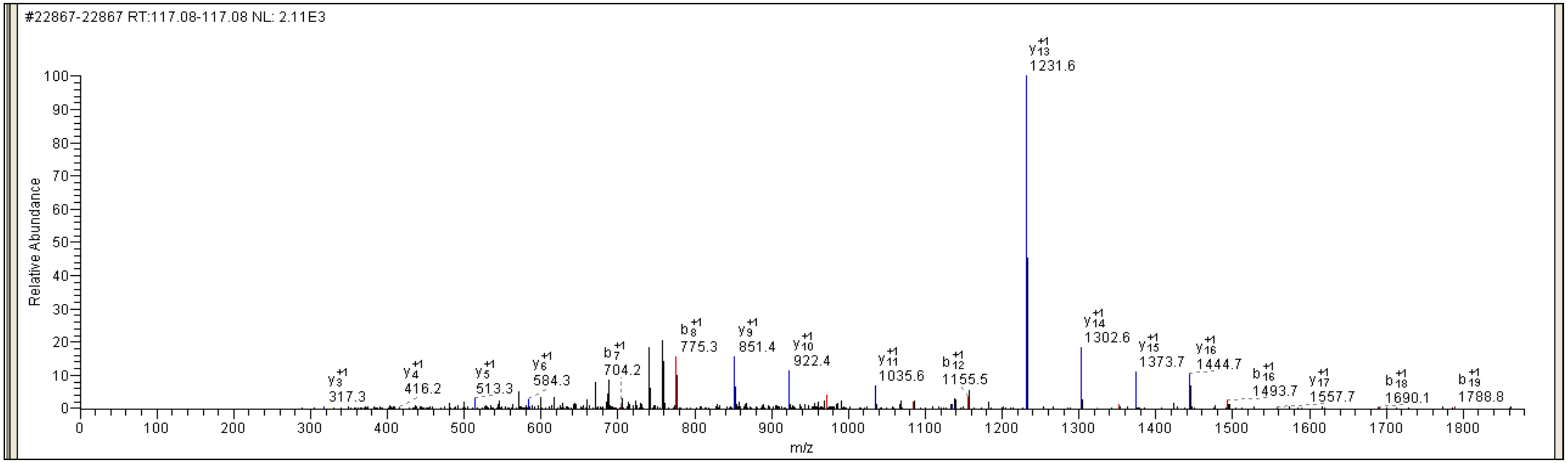
CG12519 NP_649114.2

CG12519 CG12519-PA

R.NYNGIAAAPVIAPVAAPVVAK.Y



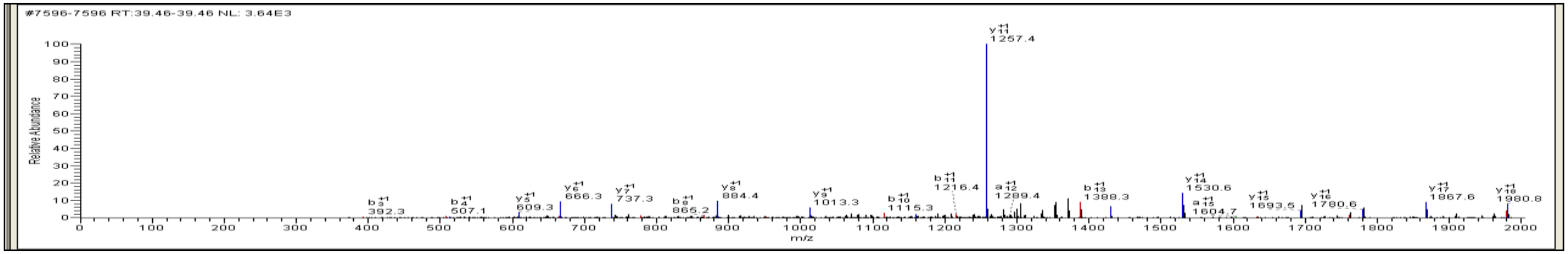
	AA	A	B	Y	
1	N	87.06	115.05	-	21
2	Y	250.12	278.11	1892.10	20
3	N	364.16	392.16	1729.04	19
4	G	421.18	449.18	1614.99	18
5	I	534.27	562.26	1557.97	17
6	A	605.30	633.30	1444.89	16
7	A	676.34	704.34	1373.85	15
8	A	747.38	775.37	1302.81	14
9	P	844.43	872.43	1231.78	13
10	V	943.50	971.49	1134.72	12
11	I	1056.58	1084.58	1035.66	11
12	A	1127.62	1155.62	922.57	10
13	P	1224.67	1252.67	851.53	9
14	V	1323.74	1351.74	754.48	8
15	A	1394.78	1422.77	655.41	7
16	A	1465.82	1493.81	584.38	6
17	P	1562.87	1590.86	513.34	5
18	V	1661.94	1689.93	416.29	4
19	V	1761.01	1789.00	317.22	3
20	A	1832.04	1860.04	218.15	2
21	K	-	-	147.11	1



CG13047 NP_648862.1 CG13047 CG13047-PA

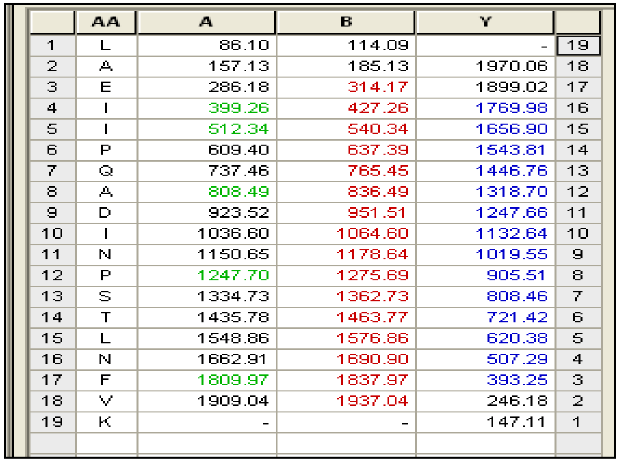
R.NNYDGTLSSYTTAPFEFAGPYSSR.Y

S no	AA	A	B	Y	
1	N	87.06	115.05	-	24
2	N	201.1	229.09	2531.14	23
3	Y	364.16	392.16	2417.09	22
4	D	479.19	507.18	2254.03	21
5	G	536.21	564.2	2139	20
6	T	637.26	665.25	2081.98	19
7	L	750.34	778.34	1980.93	18
8	S	837.37	865.37	1867.85	17
9	S	924.41	952.4	1780.82	16
10	Y	1087.47	1115.46	1693.79	15
11	T	1188.52	1216.51	1530.72	14
12	T	1289.56	1317.56	1429.67	13
13	A	1360.6	1388.6	1328.63	12
14	P	1457.65	1485.65	1257.59	11
15	F	1604.72	1632.72	1160.54	10
16	E	1733.77	1761.76	1013.47	9
17	F	1880.83	1908.83	884.43	8
18	A	1951.87	1979.87	737.36	7
19	G	2008.89	2036.89	666.32	6
20	P	2105.95	2133.94	609.3	5
21	Y	2269.01	2297	512.25	4
22	S	2356.04	2384.04	349.18	3
23	S	2443.07	2471.07	262.15	2
24	R	-	-	175.12	1

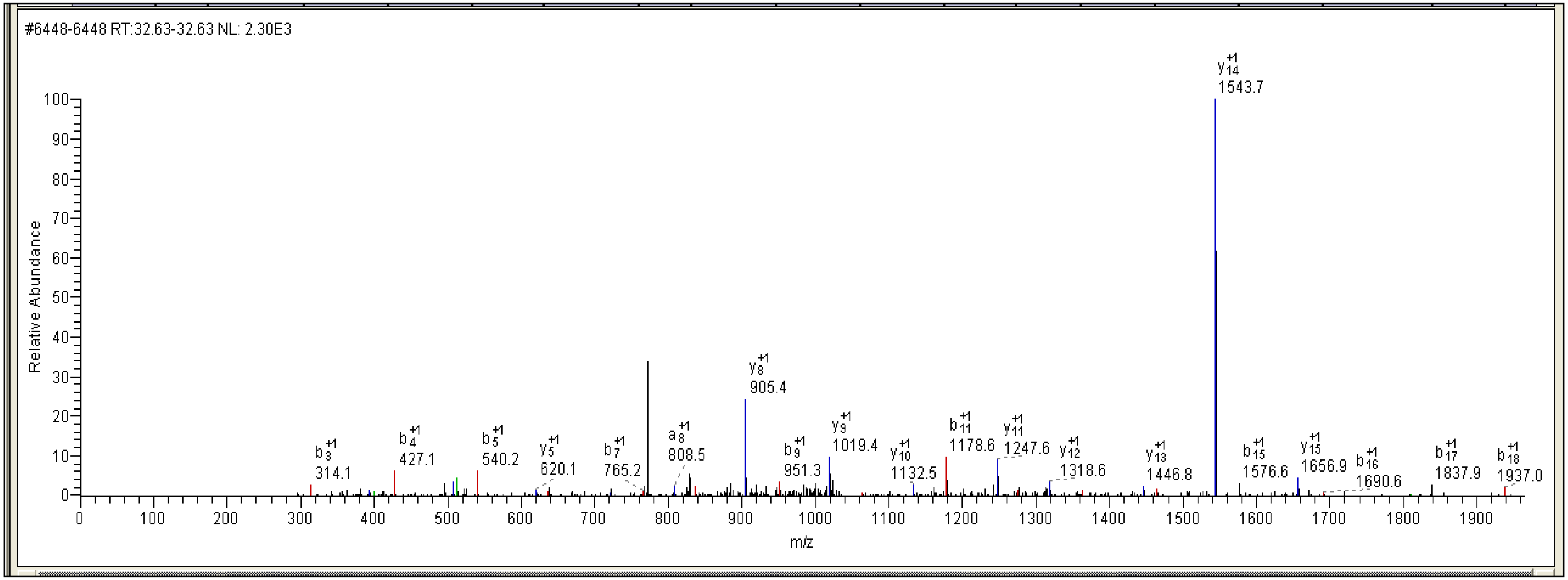


CG13185 NP_001097279.1 CG13185 CG13185-PC

K.LAEIIPQADINPSTLNFVK.S

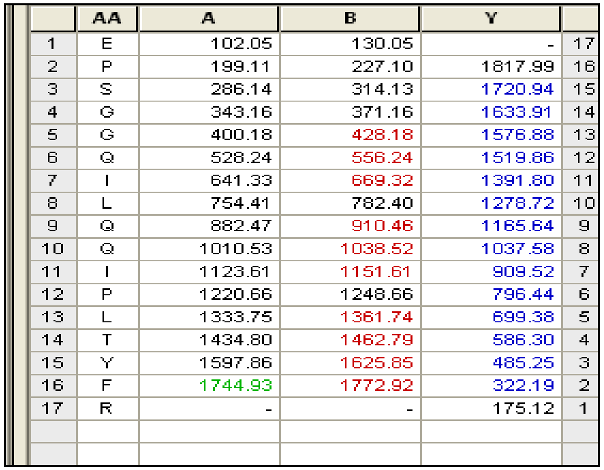


	AA	A	B	Y	
1	L	86.10	114.09	-	19
2	A	157.13	185.13	1970.06	18
3	E	286.18	314.17	1899.02	17
4	I	399.26	427.26	1769.98	16
5	I	512.34	540.34	1656.90	15
6	P	609.40	637.39	1543.81	14
7	Q	737.46	765.45	1446.76	13
8	A	808.49	836.49	1318.70	12
9	D	923.52	951.51	1247.66	11
10	I	1036.60	1064.60	1132.64	10
11	N	1150.65	1178.64	1019.55	9
12	P	1247.70	1275.69	905.51	8
13	S	1334.73	1362.73	808.46	7
14	T	1435.78	1463.77	721.42	6
15	L	1548.86	1576.86	620.38	5
16	N	1662.91	1690.90	507.29	4
17	F	1809.97	1837.97	393.25	3
18	V	1909.04	1937.04	246.18	2
19	K	-	-	147.11	1

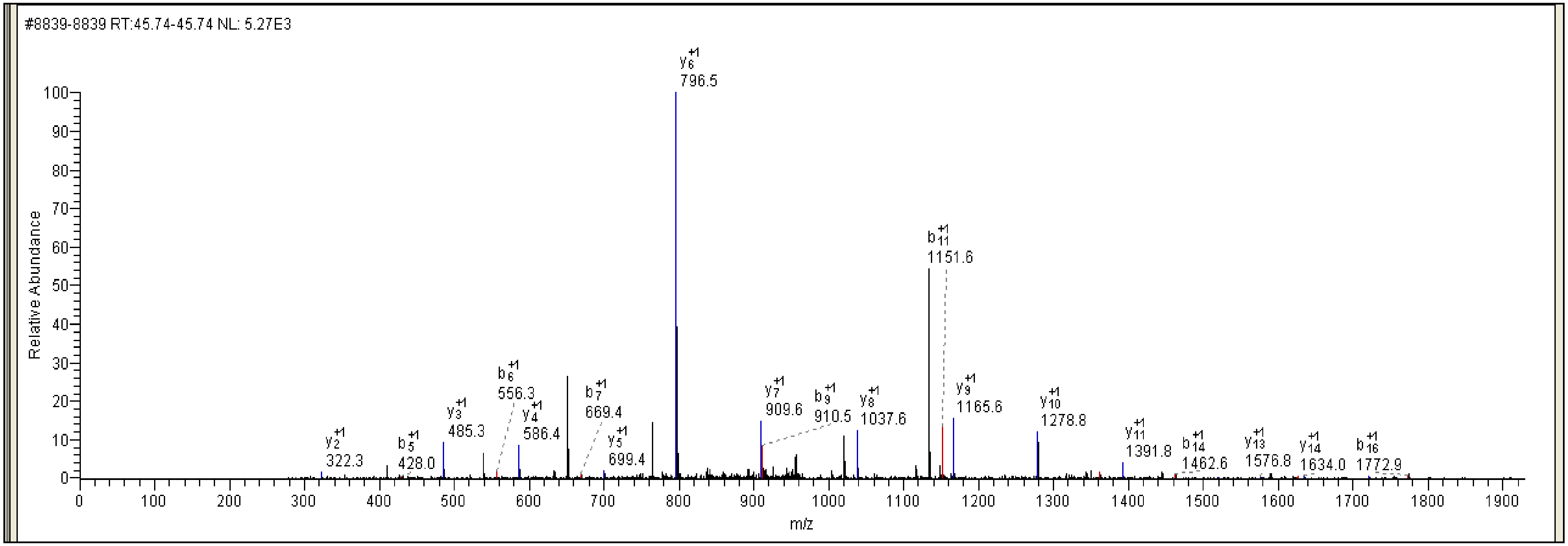


NP_569854.1 CG13362 CG13362-PA

R.EPSGGQILQQIPLTYFR.T

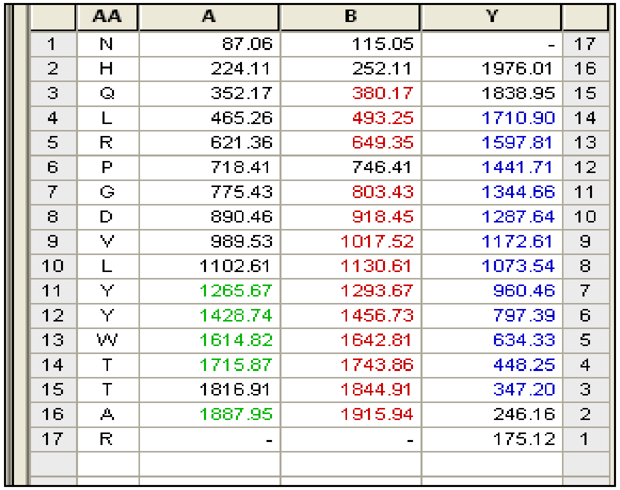


	AA	A	B	Y	
1	E	102.05	130.05	-	17
2	P	199.11	227.10	1817.99	16
3	S	286.14	314.13	1720.94	15
4	G	343.16	371.16	1633.91	14
5	G	400.18	428.18	1576.88	13
6	Q	528.24	556.24	1519.86	12
7	I	641.33	669.32	1391.80	11
8	L	754.41	782.40	1278.72	10
9	Q	882.47	910.46	1165.64	9
10	Q	1010.53	1038.52	1037.58	8
11	I	1123.61	1151.61	909.52	7
12	P	1220.66	1248.66	796.44	6
13	L	1333.75	1361.74	699.38	5
14	T	1434.80	1462.79	586.30	4
15	Y	1597.86	1625.85	485.25	3
16	F	1744.93	1772.92	322.19	2
17	R	-	-	175.12	1

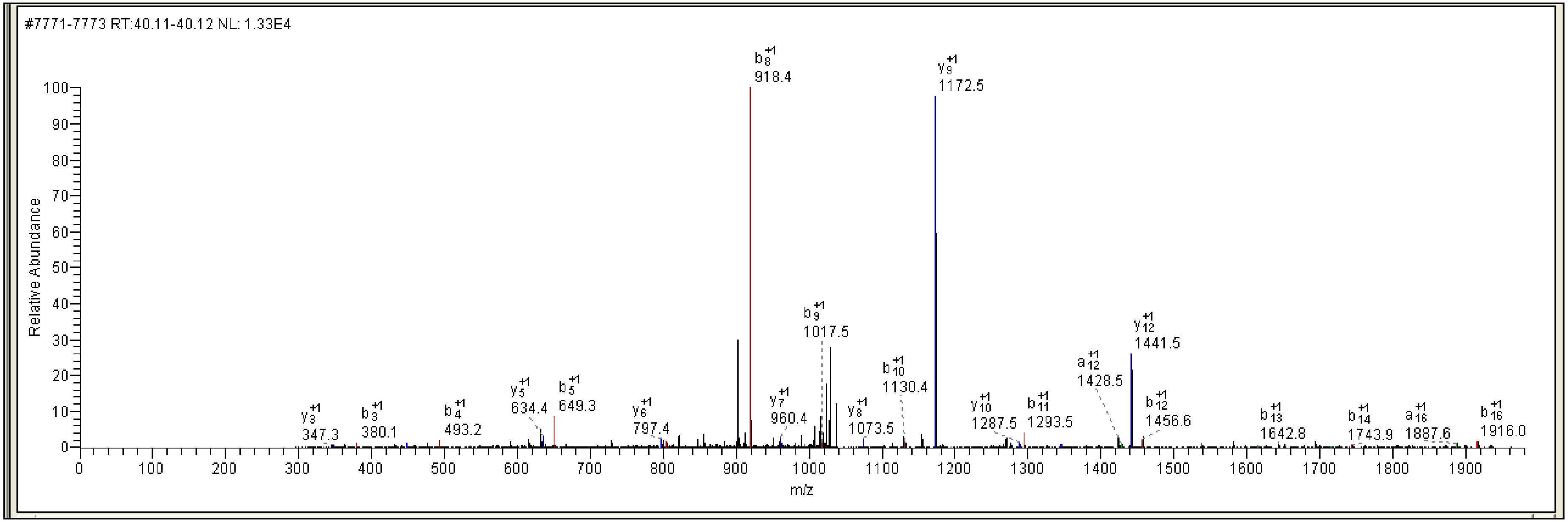


CG13422 NP_611483.1 CG13422 CG13422-PA

R.NHQLRPGDVLYYWTTAR.Y

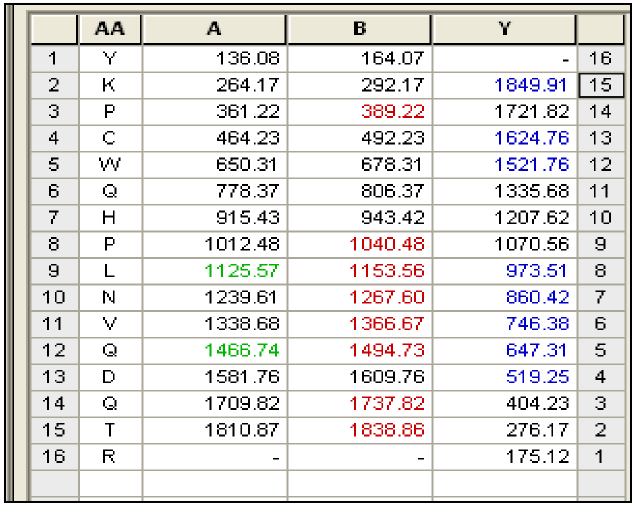


	AA	A	B	Y	
1	N	87.06	115.05	-	17
2	H	224.11	252.11	1976.01	16
3	Q	352.17	380.17	1838.95	15
4	L	465.26	493.25	1710.90	14
5	R	621.36	649.35	1597.81	13
6	P	718.41	746.41	1441.71	12
7	G	775.43	803.43	1344.66	11
8	D	890.46	918.45	1287.64	10
9	V	989.53	1017.52	1172.61	9
10	L	1102.61	1130.61	1073.54	8
11	Y	1265.67	1293.67	960.46	7
12	Y	1428.74	1456.73	797.39	6
13	W	1614.82	1642.81	634.33	5
14	T	1715.87	1743.86	448.25	4
15	T	1816.91	1844.91	347.20	3
16	A	1887.95	1915.94	246.16	2
17	R	-	-	175.12	1

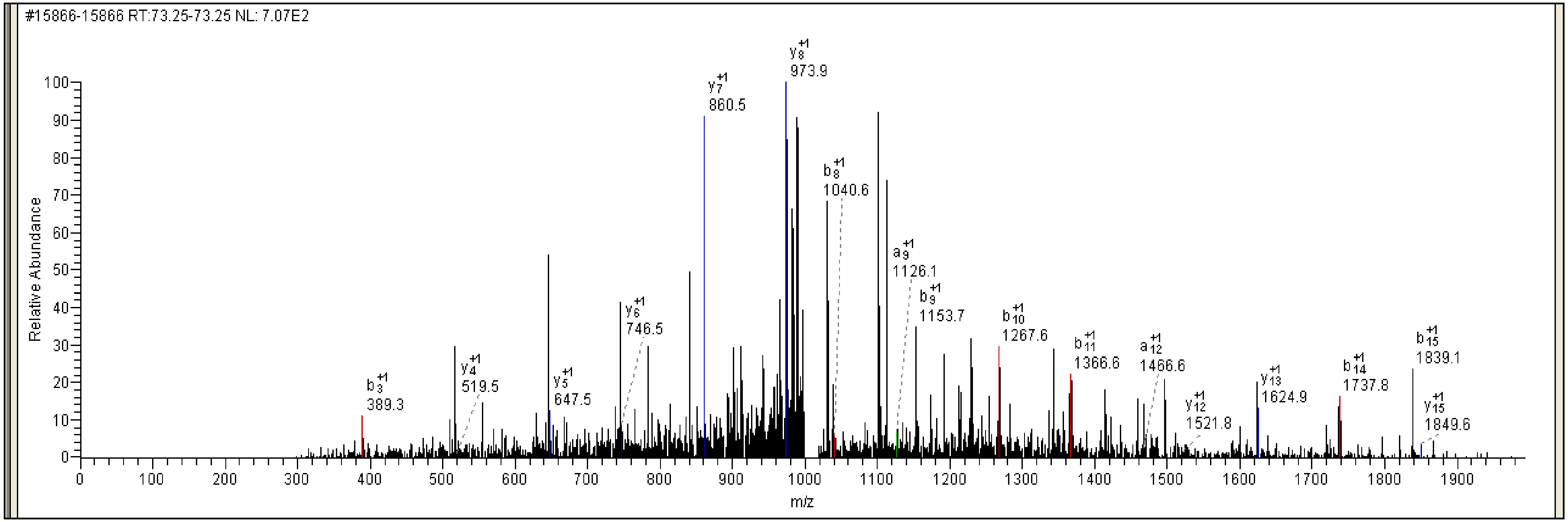


NP_651069.1 CG13843 CG13843-PA

K.YKPCWQHPLNVQDQTR.F

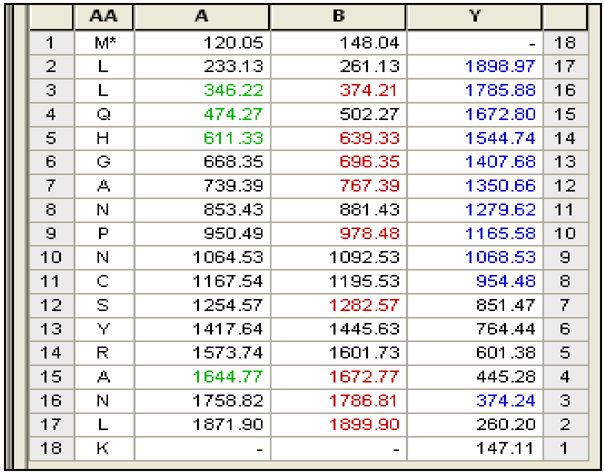


	AA	A	B	Y	
1	Y	136.08	164.07	-	16
2	K	264.17	292.17	1849.91	15
3	P	361.22	389.22	1721.82	14
4	C	464.23	492.23	1624.76	13
5	W	650.31	678.31	1521.76	12
6	Q	778.37	806.37	1335.68	11
7	H	915.43	943.42	1207.62	10
8	P	1012.48	1040.48	1070.56	9
9	L	1125.57	1153.56	973.51	8
10	N	1239.61	1267.60	860.42	7
11	V	1338.68	1366.67	746.38	6
12	Q	1466.74	1494.73	647.31	5
13	D	1581.76	1609.76	519.25	4
14	Q	1709.82	1737.82	404.23	3
15	T	1810.87	1838.86	276.17	2
16	R	-	-	175.12	1

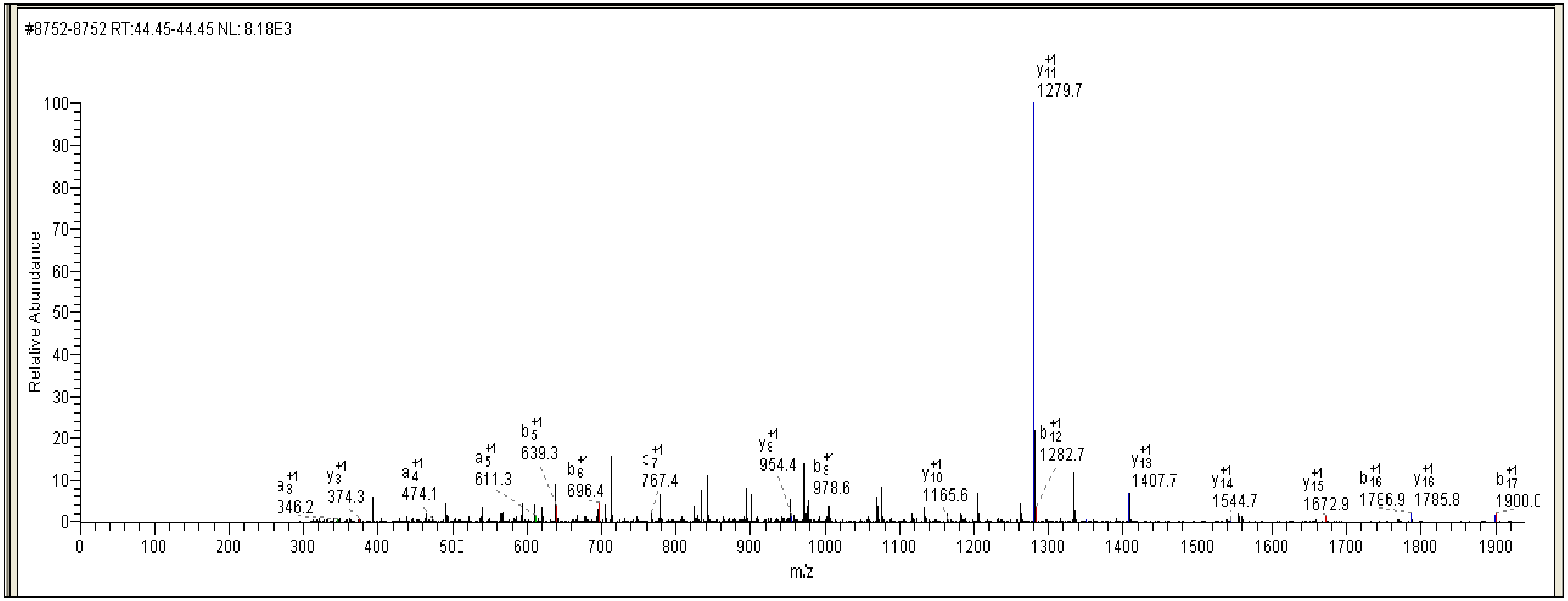


CG13933 NP_647658.1 CG13933 CG13933-PA

R.MLLQHGANPNCSYRANLK.P



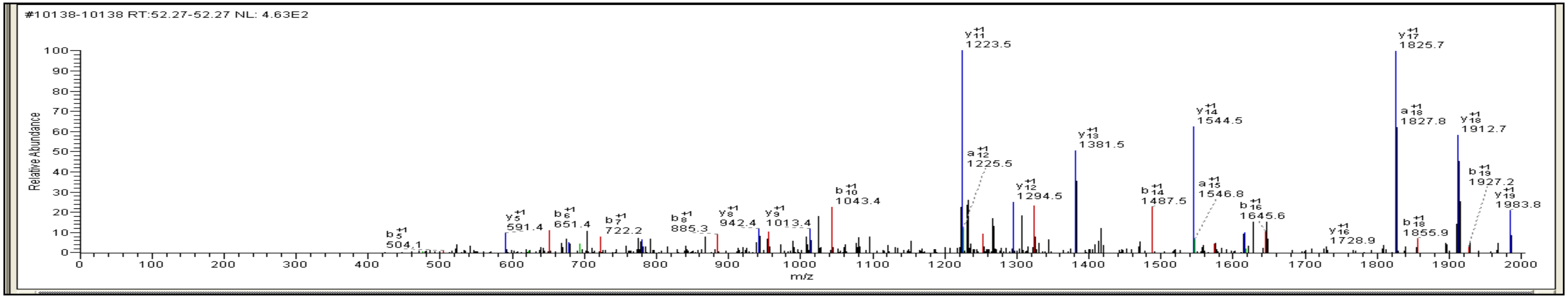
	AA	A	B	Y	
1	M*	120.05	148.04	-	18
2	L	233.13	261.13	1898.97	17
3	L	346.22	374.21	1785.88	16
4	Q	474.27	502.27	1672.80	15
5	H	611.33	639.33	1544.74	14
6	G	668.35	696.35	1407.68	13
7	A	739.39	767.39	1350.66	12
8	N	853.43	881.43	1279.62	11
9	P	950.49	978.48	1165.58	10
10	N	1064.53	1092.53	1068.53	9
11	C	1167.54	1195.53	954.48	8
12	S	1254.57	1282.57	851.47	7
13	Y	1417.64	1445.63	764.44	6
14	R	1573.74	1601.73	601.38	5
15	A	1644.77	1672.77	445.28	4
16	N	1758.82	1786.81	374.24	3
17	L	1871.90	1899.90	260.20	2
18	K	-	-	147.11	1



CG14096 NP_649113.1 CG14096 CG14096-PA

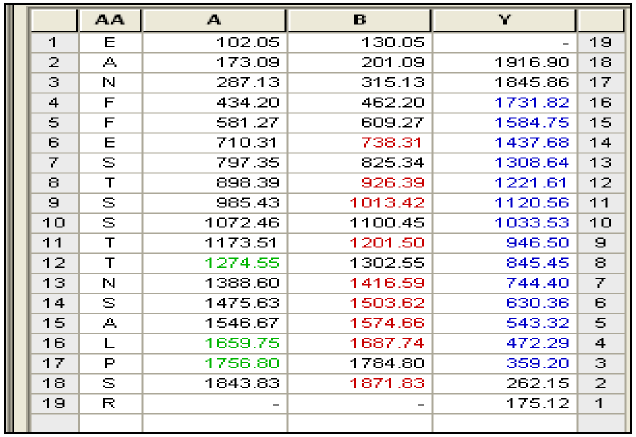
K.YTAAPFAYASPLAYSAPLAYTSPLAYK.T

S no	AA	A	B	Y	
1	Y	136.08	164.07	-	27
2	T	237.12	265.12	2705.39	26
3	A	308.16	336.16	2604.34	25
4	A	379.2	407.19	2533.3	24
5	P	476.25	504.25	2462.26	23
6	F	623.32	651.31	2365.21	22
7	A	694.36	722.35	2218.14	21
8	Y	857.42	885.41	2147.11	20
9	A	928.46	956.45	1984.04	19
10	S	1015.49	1043.48	1913.01	18
11	P	1112.54	1140.54	1825.97	17
12	L	1225.63	1253.62	1728.92	16
13	A	1296.66	1324.66	1615.84	15
14	Y	1459.73	1487.72	1544.8	14
15	S	1546.76	1574.75	1381.74	13
16	A	1617.79	1645.79	1294.7	12
17	P	1714.85	1742.84	1223.67	11
18	L	1827.93	1855.93	1126.61	10
19	A	1898.97	1926.96	1013.53	9
20	Y	2062.03	2090.03	942.49	8
21	T	2163.08	2191.07	779.43	7
22	S	2250.11	2278.11	678.38	6
23	P	2347.16	2375.16	591.35	5
24	L	2460.25	2488.24	494.3	4
25	A	2531.29	2559.28	381.21	3
26	Y	2694.35	2722.34	310.18	2
27	K	-	-	147.11	1

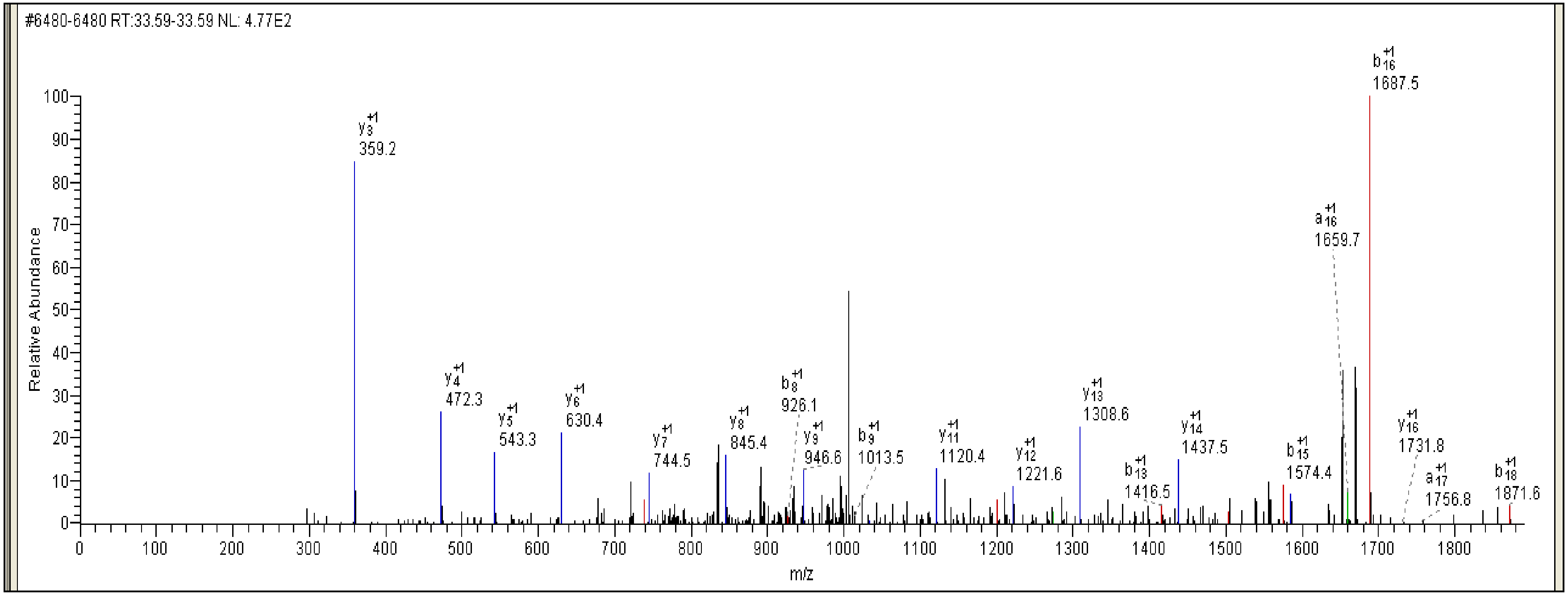


CG14207 NP_608326.1 CG14207 CG14207-PA

R.EANFFESTSSTTNSALPSR.I



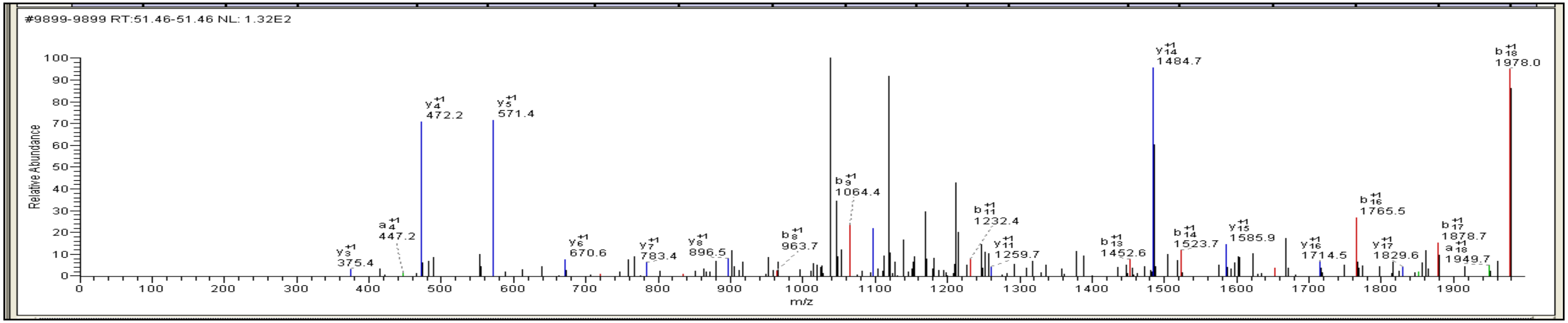
	AA	A	B	Y	
1	E	102.05	130.05	-	19
2	A	173.09	201.09	1916.90	18
3	N	287.13	315.13	1845.86	17
4	F	434.20	462.20	1731.82	16
5	F	581.27	609.27	1584.75	15
6	E	710.31	738.31	1437.68	14
7	S	797.35	825.34	1308.64	13
8	T	898.39	926.39	1221.61	12
9	S	985.43	1013.42	1120.56	11
10	S	1072.46	1100.45	1033.53	10
11	T	1173.51	1201.50	946.50	9
12	T	1274.55	1302.55	845.45	8
13	N	1388.60	1416.59	744.40	7
14	S	1475.63	1503.62	630.36	6
15	A	1546.67	1574.66	543.32	5
16	L	1659.75	1687.74	472.29	4
17	P	1756.80	1784.80	359.20	3
18	S	1843.83	1871.83	262.15	2
19	R	-	-	175.12	1



CG1600 NP_610293.3 CG1600 CG1600-PC

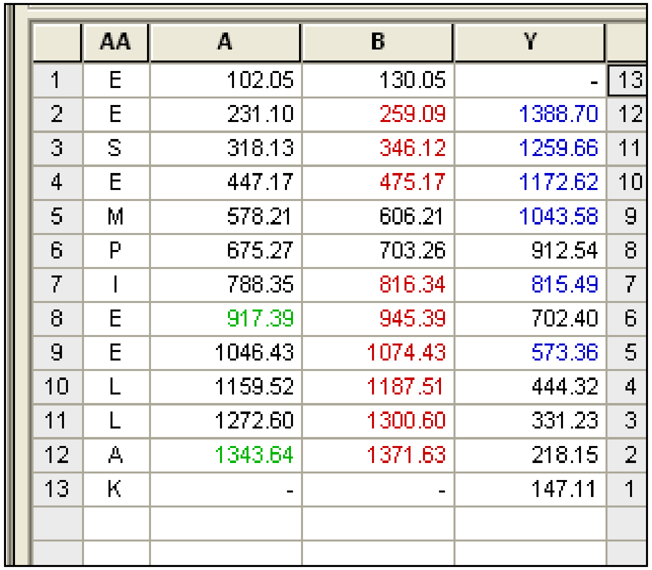
R.VIVYPFDETPAGYAELLVVPDLK.H

S no	AA	A	B	Y	
1	V	72.08	100.08	-	23
2	I	185.16	213.16	2449.29	22
3	V	284.23	312.23	2336.21	21
4	Y	447.3	475.29	2237.14	20
5	P	544.35	572.34	2074.07	19
6	F	691.42	719.41	1977.02	18
7	D	806.44	834.44	1829.95	17
8	E	935.49	963.48	1714.93	16
9	T	1036.53	1064.53	1585.88	15
10	P	1133.59	1161.58	1484.84	14
11	A	1204.62	1232.62	1387.78	13
12	G	1261.65	1289.64	1316.75	12
13	Y	1424.71	1452.7	1259.72	11
14	A	1495.75	1523.74	1096.66	10
15	E	1624.79	1652.78	1025.62	9
16	L	1737.87	1765.87	896.58	8
17	L	1850.96	1878.95	783.5	7
18	V	1950.03	1978.02	670.41	6
19	V	2049.09	2077.09	571.34	5
20	P	2146.15	2174.14	472.28	4
21	D	2261.17	2289.17	375.22	3
22	L	2374.26	2402.25	260.2	2
23	K	-	-	147.11	1

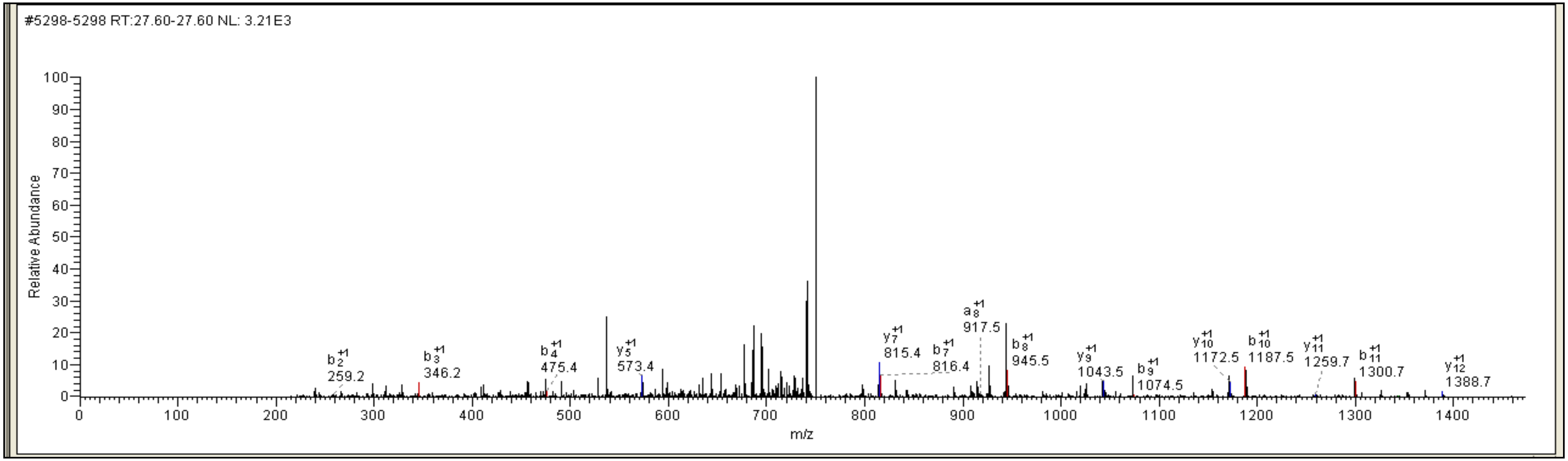


CG1620 NP_610287.2 CG1620 CG1620-PA

R.EESEMPIEELLAK.Y

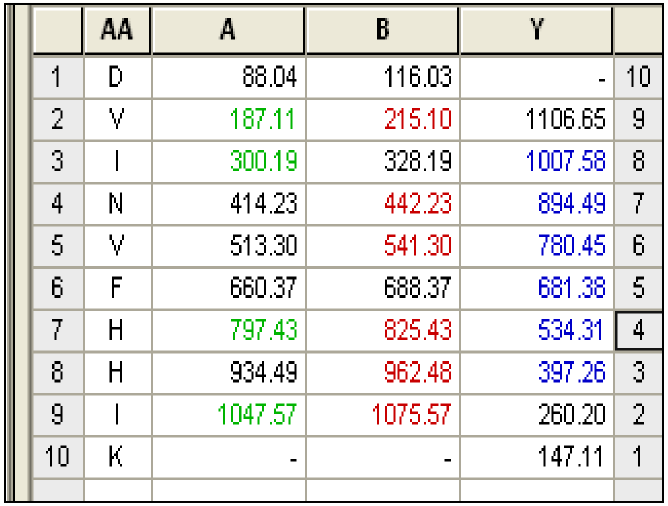


	AA	A	B	Y	
1	E	102.05	130.05	-	13
2	E	231.10	259.09	1388.70	12
3	S	318.13	346.12	1259.66	11
4	E	447.17	475.17	1172.62	10
5	M	578.21	606.21	1043.58	9
6	P	675.27	703.26	912.54	8
7	I	788.35	816.34	815.49	7
8	E	917.39	945.39	702.40	6
9	E	1046.43	1074.43	573.36	5
10	L	1159.52	1187.51	444.32	4
11	L	1272.60	1300.60	331.23	3
12	A	1343.64	1371.63	218.15	2
13	K	-	-	147.11	1

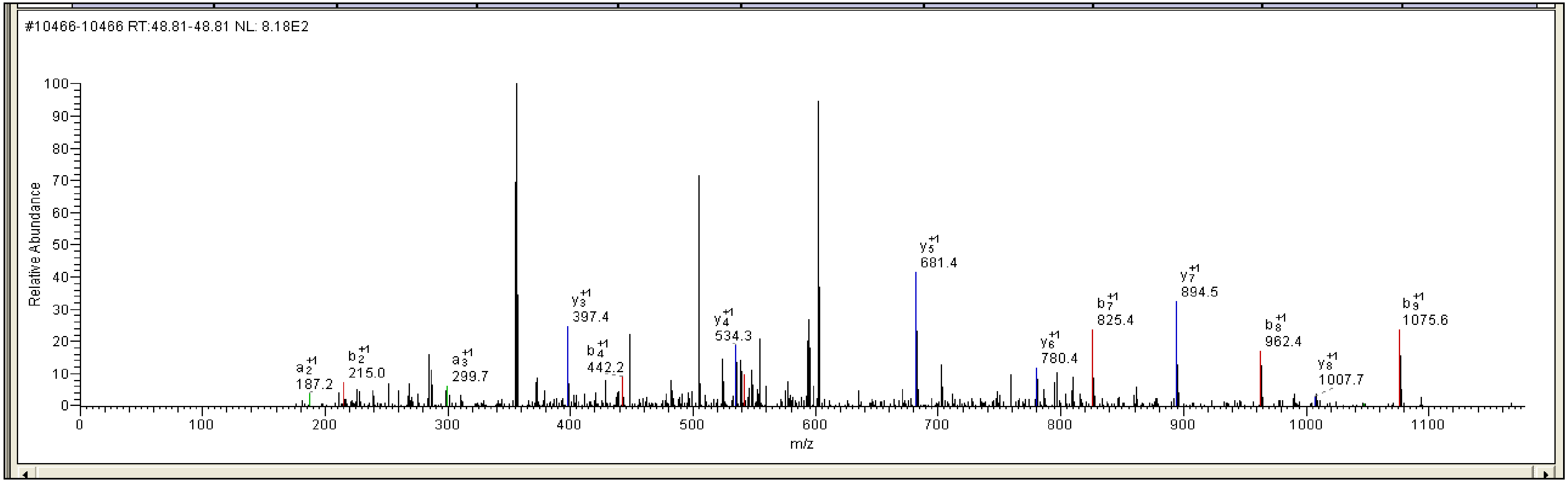


CG16903 NP_569980.1 CG16903 CG16903-PA

R.DVINVFHHIK.Q

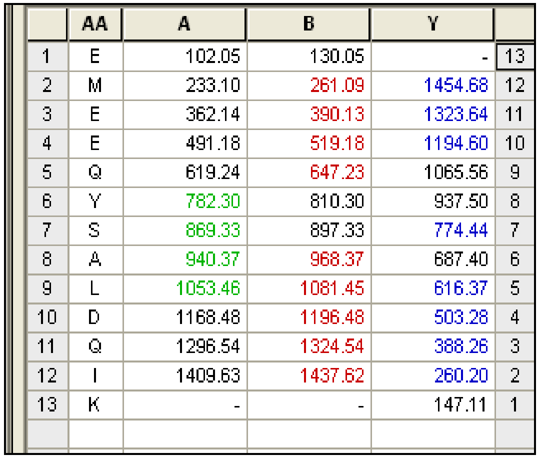


	AA	A	B	Y	
1	D	88.04	116.03	-	10
2	V	187.11	215.10	1106.65	9
3	I	300.19	328.19	1007.58	8
4	N	414.23	442.23	894.49	7
5	V	513.30	541.30	780.45	6
6	F	660.37	688.37	681.38	5
7	H	797.43	825.43	534.31	4
8	H	934.49	962.48	397.26	3
9	I	1047.57	1075.57	260.20	2
10	K	-	-	147.11	1

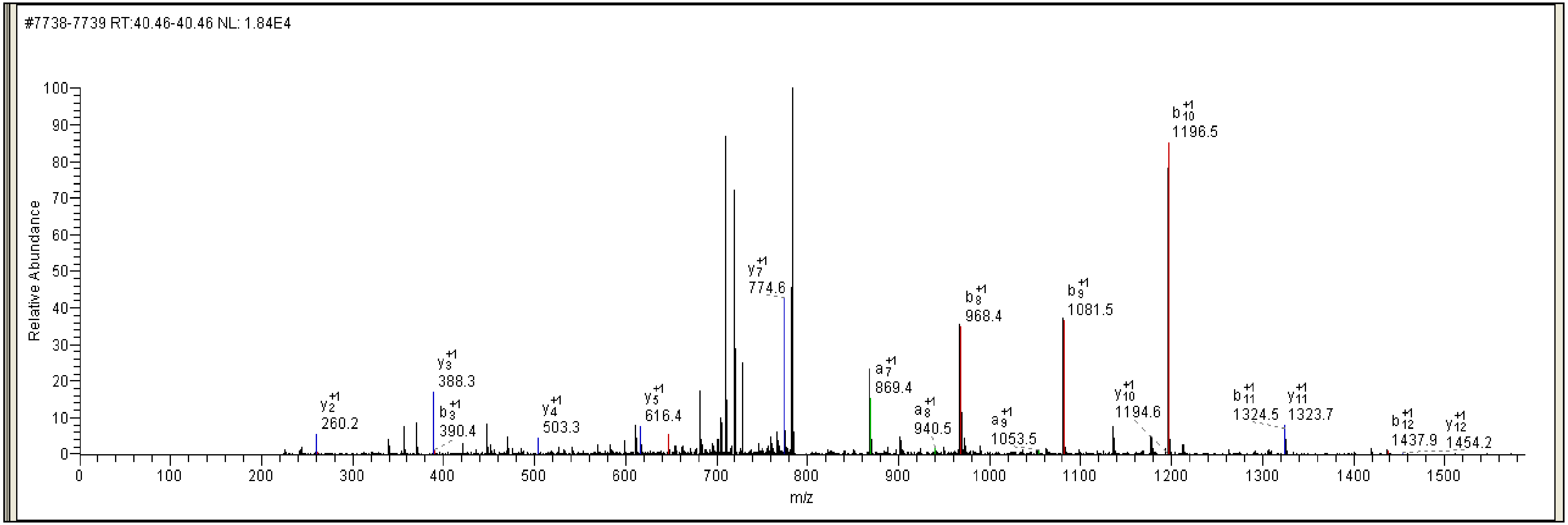


CG17122 NP_730506.1 CG17122 CG17122-PA

K.EMEEQYSALDQIK.N

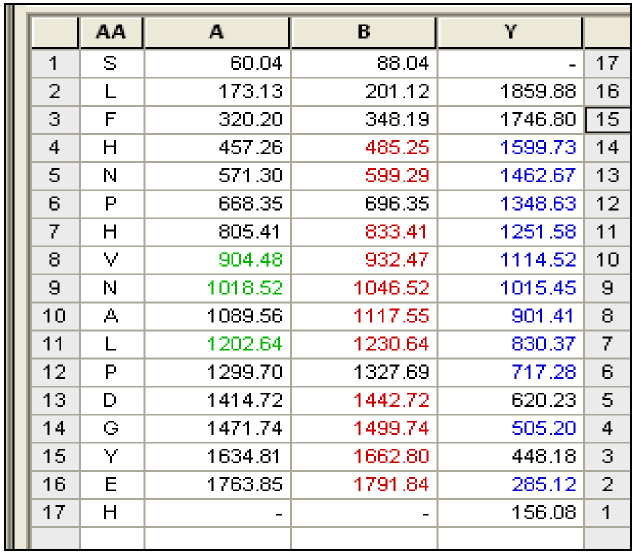


	AA	A	B	Y	
1	E	102.05	130.05	-	13
2	M	233.10	261.09	1454.68	12
3	E	362.14	390.13	1323.64	11
4	E	491.18	519.18	1194.60	10
5	Q	619.24	647.23	1065.56	9
6	Y	782.30	810.30	937.50	8
7	S	869.33	897.33	774.44	7
8	A	940.37	968.37	687.40	6
9	L	1053.46	1081.45	616.37	5
10	D	1168.48	1196.48	503.28	4
11	Q	1296.54	1324.54	388.26	3
12	I	1409.63	1437.62	260.20	2
13	K	-	-	147.11	1

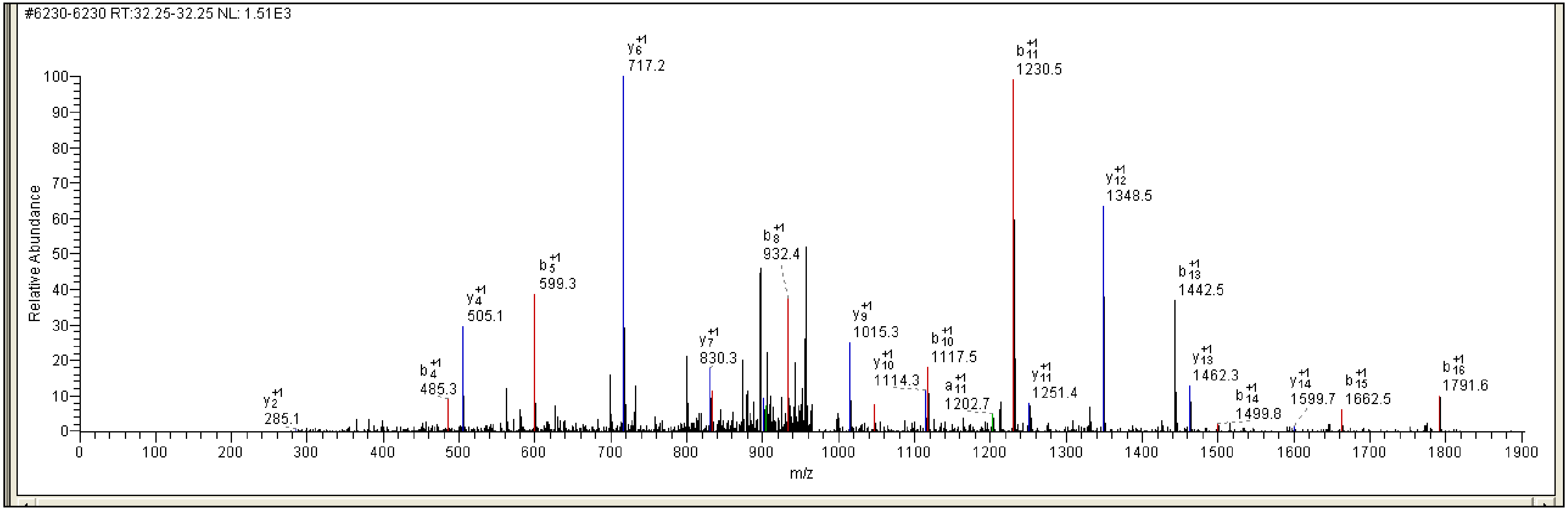


levy NP_611805.1 CG17280 CG17280-PA

K.SLFHNPHVNALPDGYEH

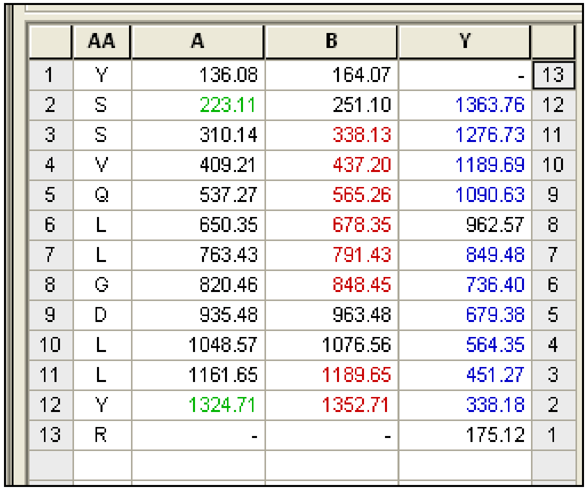


	AA	A	B	Y	
1	S	60.04	88.04	-	17
2	L	173.13	201.12	1859.88	16
3	F	320.20	348.19	1746.80	15
4	H	457.26	485.25	1599.73	14
5	N	571.30	599.29	1462.67	13
6	P	668.35	696.35	1348.63	12
7	H	805.41	833.41	1251.58	11
8	V	904.48	932.47	1114.52	10
9	N	1018.52	1046.52	1015.45	9
10	A	1089.56	1117.55	901.41	8
11	L	1202.64	1230.64	830.37	7
12	P	1299.70	1327.69	717.28	6
13	D	1414.72	1442.72	620.23	5
14	G	1471.74	1499.74	505.20	4
15	Y	1634.81	1662.80	448.18	3
16	E	1763.85	1791.84	285.12	2
17	H	-	-	156.08	1

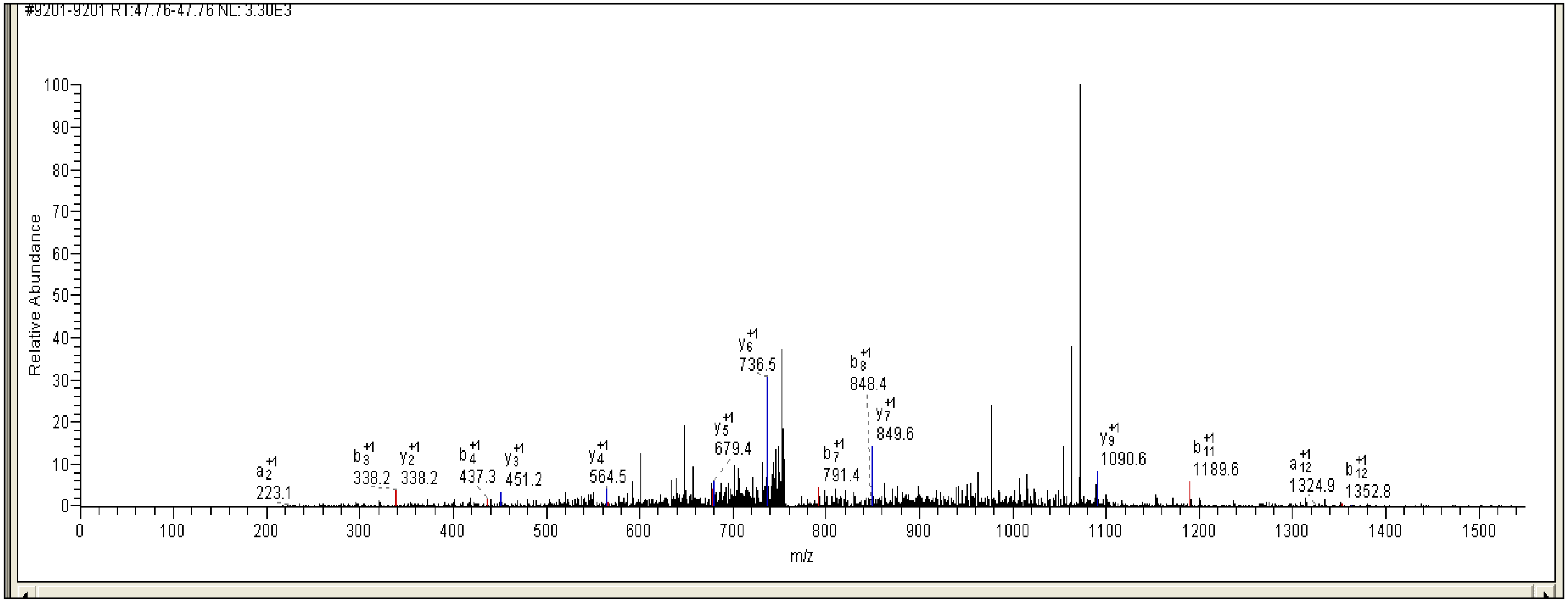


CG17514 NP_001015316.1 CG17514 CG17514-PA

R.YSSVQLLGDLLYR.I

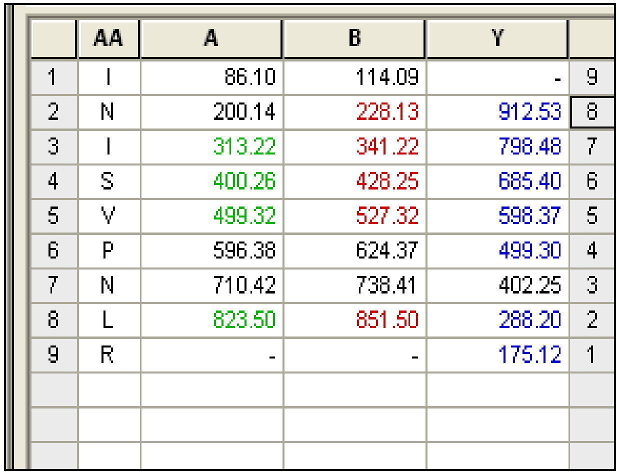


	AA	A	B	Y	
1	Y	136.08	164.07	-	13
2	S	223.11	251.10	1363.76	12
3	S	310.14	338.13	1276.73	11
4	V	409.21	437.20	1189.69	10
5	Q	537.27	565.26	1090.63	9
6	L	650.35	678.35	962.57	8
7	L	763.43	791.43	849.48	7
8	G	820.46	848.45	736.40	6
9	D	935.48	963.48	679.38	5
10	L	1048.57	1076.56	564.35	4
11	L	1161.65	1189.65	451.27	3
12	Y	1324.71	1352.71	338.18	2
13	R	-	-	175.12	1

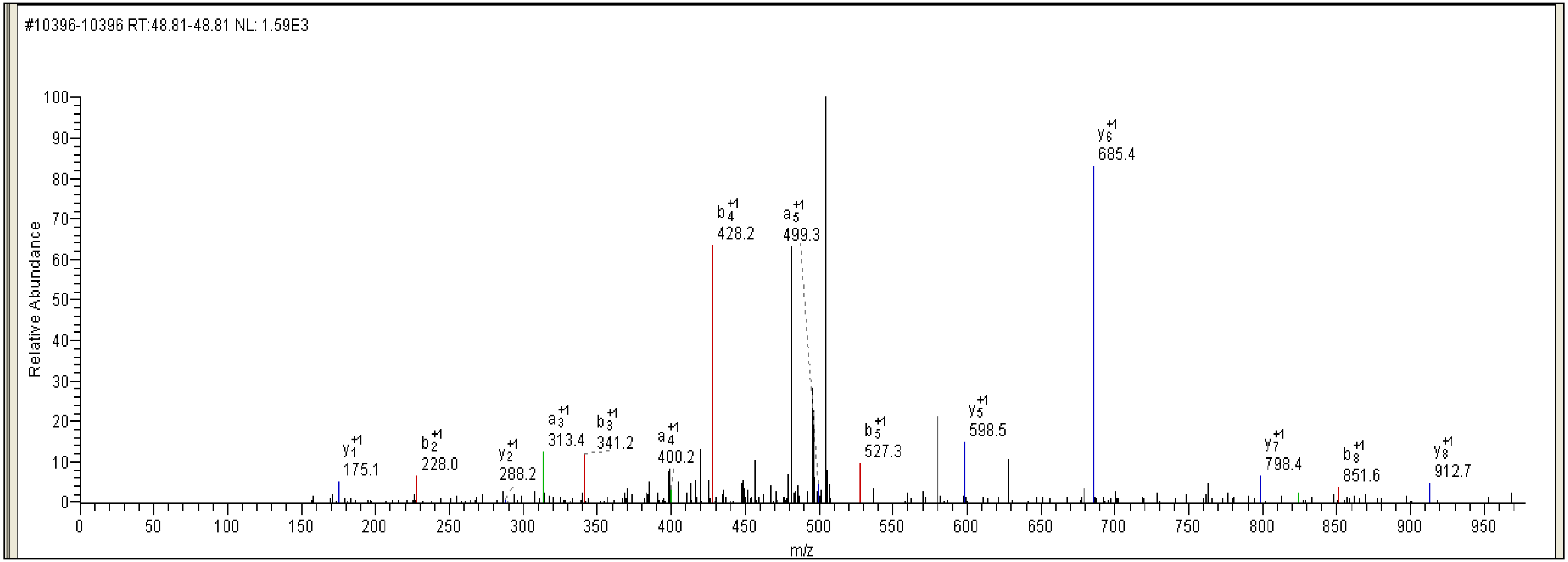


CG17838 NP_732557.2 CG17838 CG17838-PA

K.INISVPNLR.L

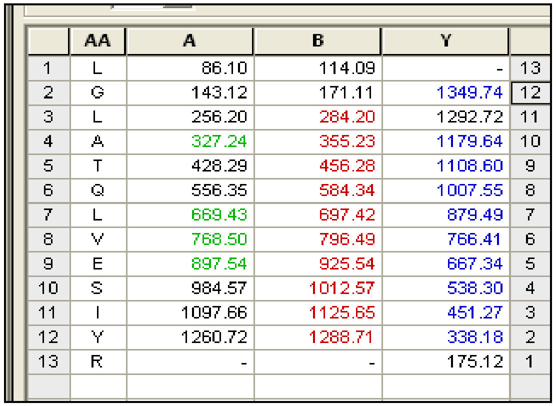


	AA	A	B	Y	
1	I	86.10	114.09	-	9
2	N	200.14	228.13	912.53	8
3	I	313.22	341.22	798.48	7
4	S	400.26	428.25	685.40	6
5	V	499.32	527.32	598.37	5
6	P	596.38	624.37	499.30	4
7	N	710.42	738.41	402.25	3
8	L	823.50	851.50	288.20	2
9	R	-	-	175.12	1

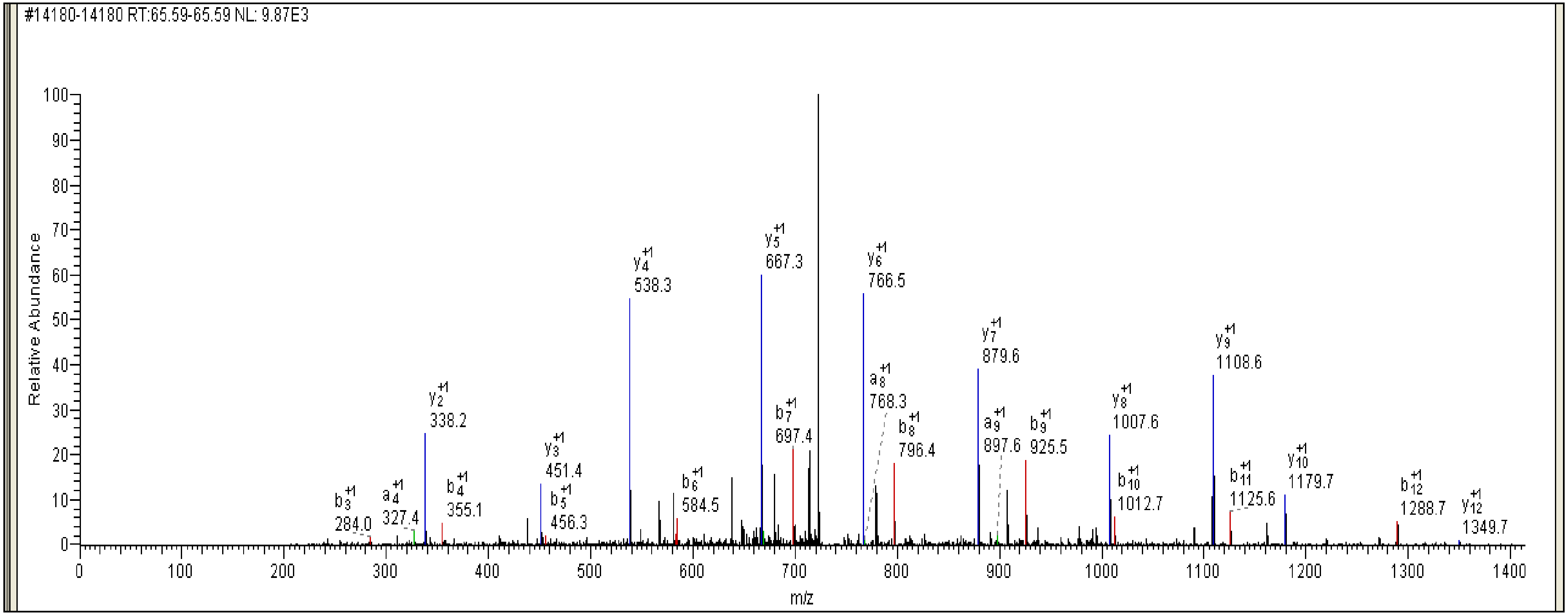


CG2051 NP_731006.1 CG2051 CG2051-PB

K.LGLATQLVESIYR.F

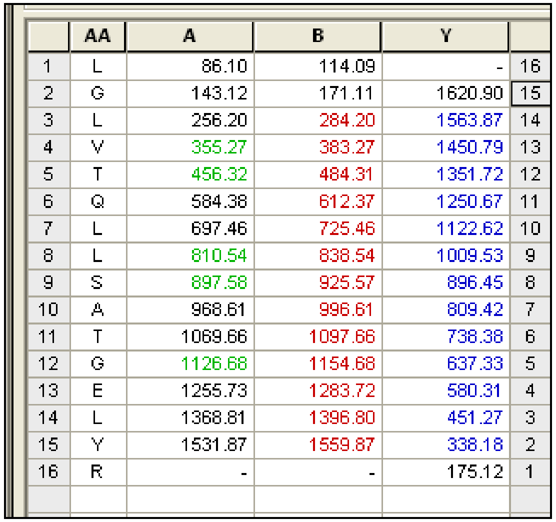


	AA	A	B	Y	
1	L	86.10	114.09	-	13
2	G	143.12	171.11	1349.74	12
3	L	256.20	284.20	1292.72	11
4	A	327.24	355.23	1179.64	10
5	T	428.29	456.28	1108.60	9
6	Q	556.35	584.34	1007.55	8
7	L	669.43	697.42	879.49	7
8	V	768.50	796.49	766.41	6
9	E	897.54	925.54	667.34	5
10	S	984.57	1012.57	538.30	4
11	I	1097.66	1125.65	451.27	3
12	Y	1260.72	1288.71	338.18	2
13	R	-	-	175.12	1

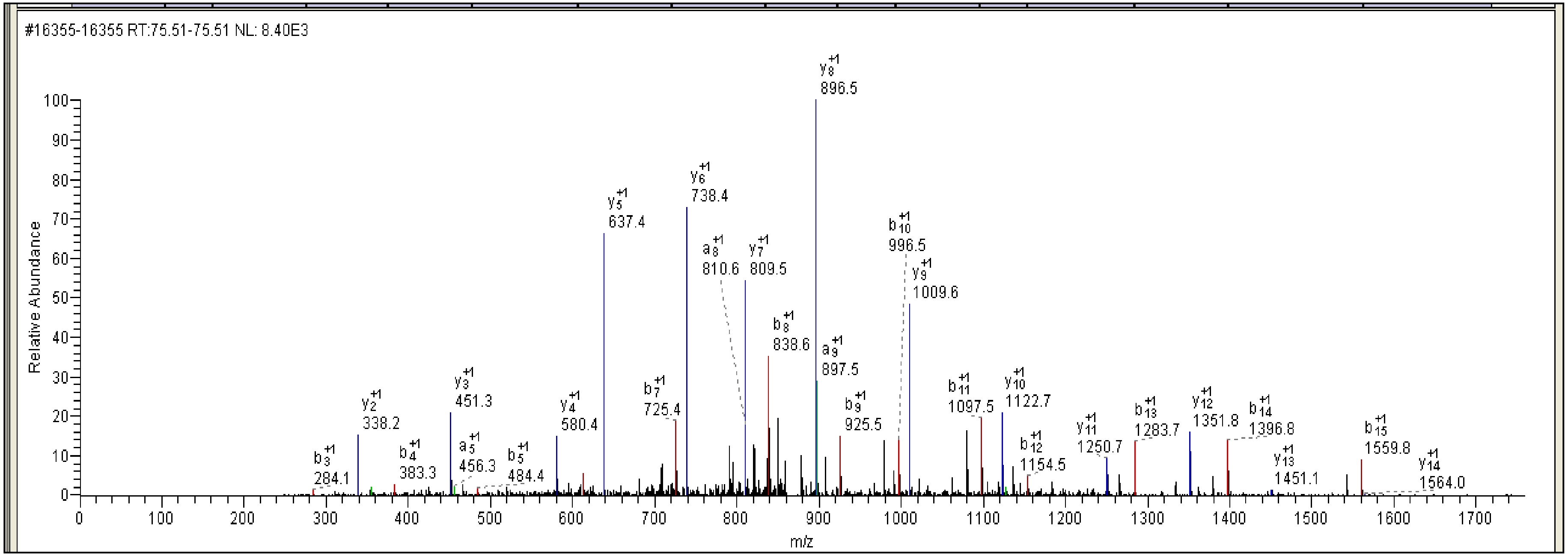


NP_572735.1 CG2247 CG2247-PA

R.LGLVTQLLSATGELYR.G

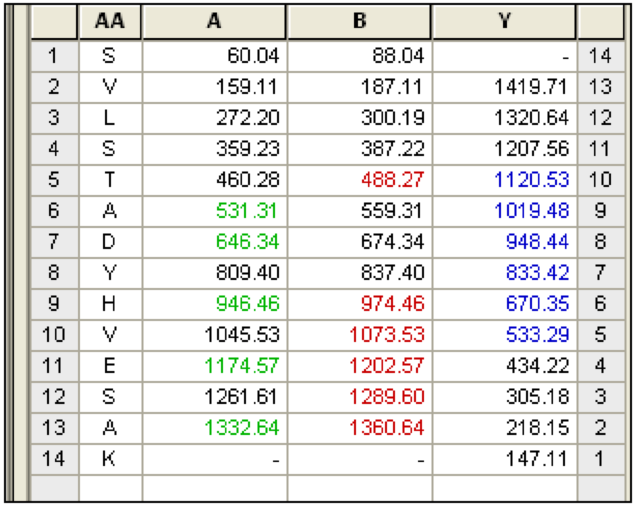


	AA	A	B	Y	
1	L	86.10	114.09	-	16
2	G	143.12	171.11	1620.90	15
3	L	256.20	284.20	1563.87	14
4	V	355.27	383.27	1450.79	13
5	T	456.32	484.31	1351.72	12
6	Q	584.38	612.37	1250.67	11
7	L	697.46	725.46	1122.62	10
8	L	810.54	838.54	1009.53	9
9	S	897.58	925.57	896.45	8
10	A	968.61	996.61	809.42	7
11	T	1069.66	1097.66	738.38	6
12	G	1126.68	1154.68	637.33	5
13	E	1255.73	1283.72	580.31	4
14	L	1368.81	1396.80	451.27	3
15	Y	1531.87	1559.87	338.18	2
16	R	-	-	175.12	1

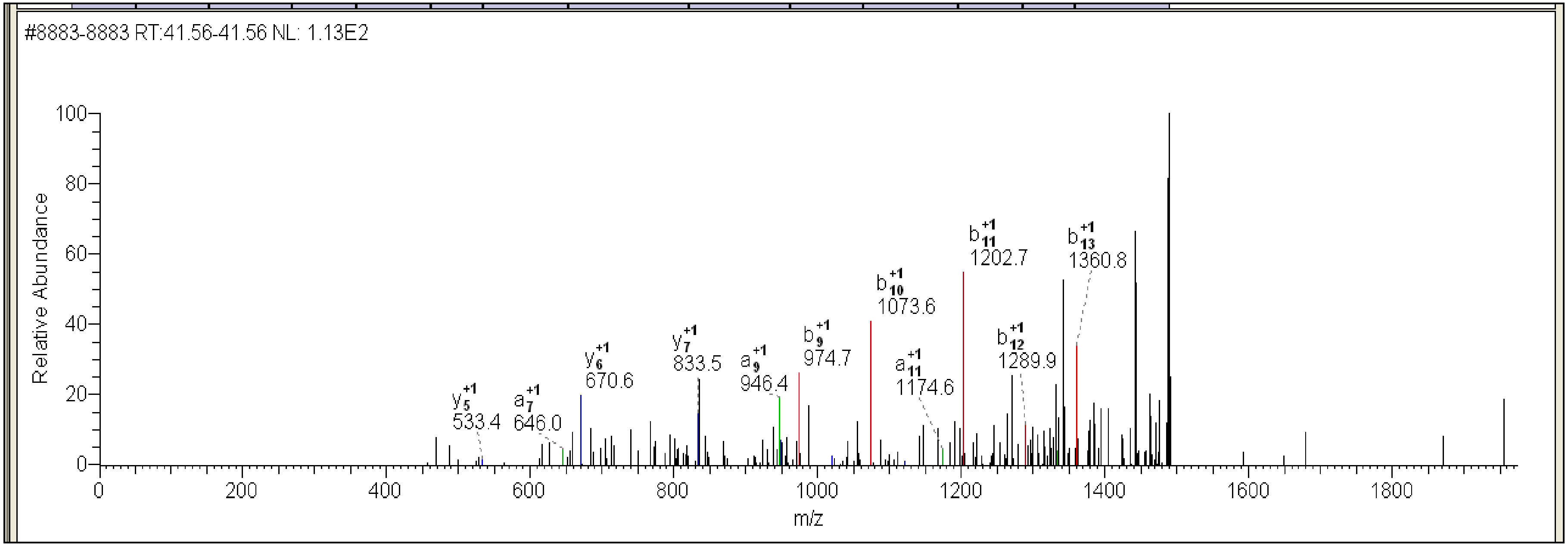


CG2875 NP_570069.1 CG2875 CG2875-PA

K.SVLSTADYHVESAK.K

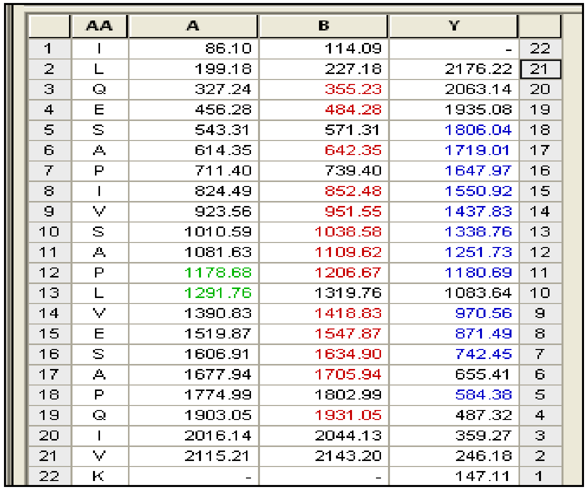


	AA	A	B	Y	
1	S	60.04	88.04	-	14
2	V	159.11	187.11	1419.71	13
3	L	272.20	300.19	1320.64	12
4	S	359.23	387.22	1207.56	11
5	T	460.28	488.27	1120.53	10
6	A	531.31	559.31	1019.48	9
7	D	646.34	674.34	948.44	8
8	Y	809.40	837.40	833.42	7
9	H	946.46	974.46	670.35	6
10	V	1045.53	1073.53	533.29	5
11	E	1174.57	1202.57	434.22	4
12	S	1261.61	1289.60	305.18	3
13	A	1332.64	1360.64	218.15	2
14	K	-	-	147.11	1

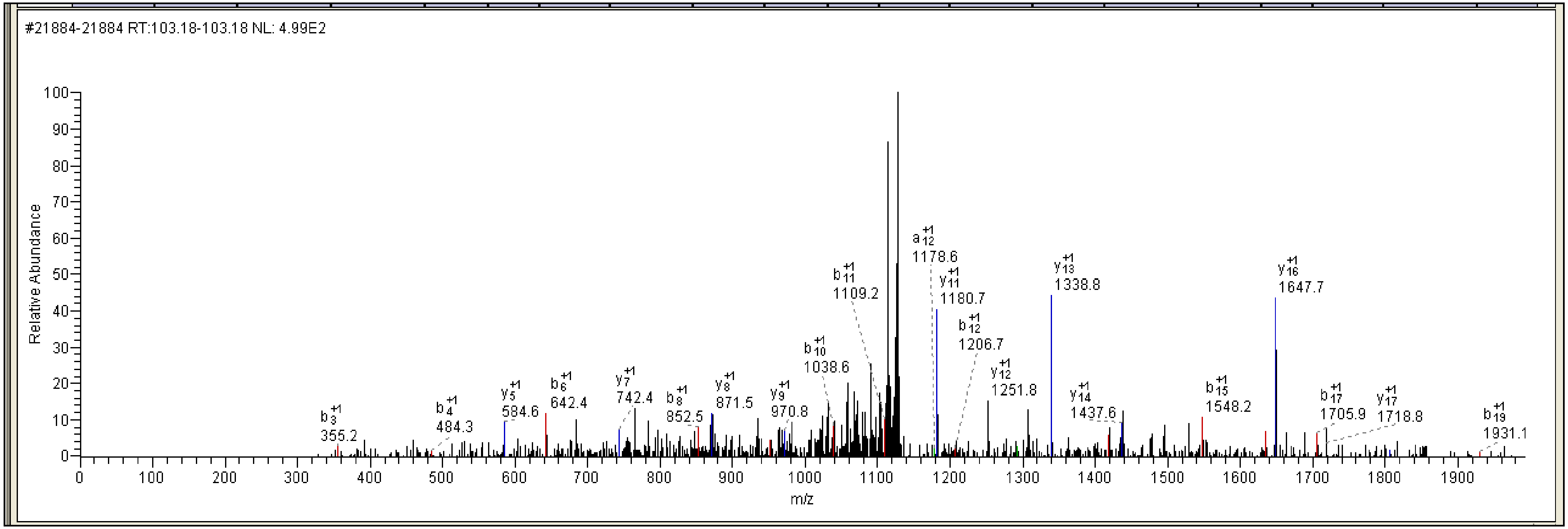


CG2962 NP_572612.2 CG2962 CG2962-PA

K.ILQESAPIVSAPLVESAPQIVK.V

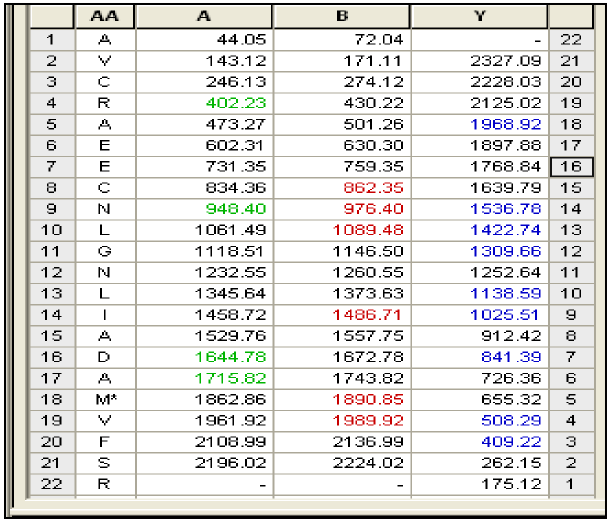


	AA	A	B	Y	
1	I	86.10	114.09	-	22
2	L	199.18	227.18	2176.22	21
3	Q	327.24	355.23	2063.14	20
4	E	456.28	484.28	1935.08	19
5	S	543.31	571.31	1806.04	18
6	A	614.35	642.35	1719.01	17
7	P	711.40	739.40	1647.97	16
8	I	824.49	852.48	1550.92	15
9	V	923.56	951.55	1437.83	14
10	S	1010.59	1038.58	1338.76	13
11	A	1081.63	1109.62	1251.73	12
12	P	1178.68	1206.67	1180.69	11
13	L	1291.76	1319.76	1083.64	10
14	V	1390.83	1418.83	970.56	9
15	E	1519.87	1547.87	871.49	8
16	S	1606.91	1634.90	742.45	7
17	A	1677.94	1705.94	655.41	6
18	P	1774.99	1802.99	584.38	5
19	Q	1903.05	1931.05	487.32	4
20	I	2016.14	2044.13	359.27	3
21	V	2115.21	2143.20	246.18	2
22	K	-	-	147.11	1

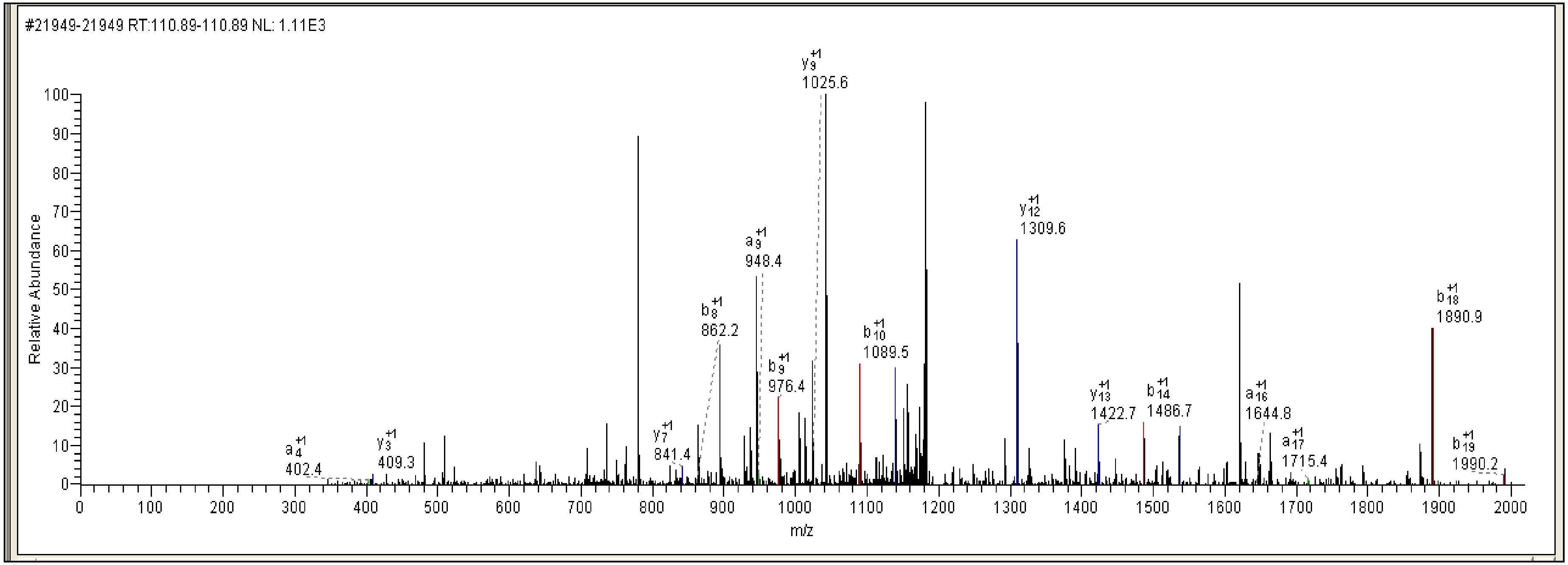


CG30104 NP_725681.1 CG30104 CG30104-PB

K.AVCRAEECNLGNLIADAMVFSR.L

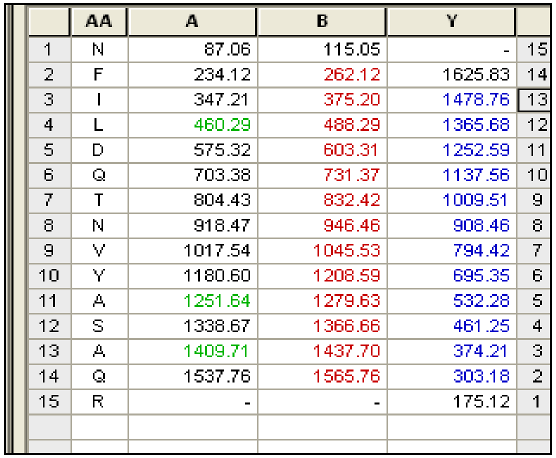


	AA	A	B	Y	
1	A	44.05	72.04	-	22
2	V	143.12	171.11	2327.09	21
3	C	246.13	274.12	2228.03	20
4	R	402.23	430.22	2125.02	19
5	A	473.27	501.26	1968.92	18
6	E	602.31	630.30	1897.88	17
7	E	731.35	759.35	1768.84	16
8	C	834.36	862.35	1639.79	15
9	N	948.40	976.40	1536.78	14
10	L	1061.49	1089.48	1422.74	13
11	G	1118.51	1146.50	1309.66	12
12	N	1232.55	1260.55	1252.64	11
13	L	1345.64	1373.63	1138.59	10
14	I	1458.72	1486.71	1025.51	9
15	A	1529.76	1557.75	912.42	8
16	D	1644.78	1672.78	841.39	7
17	A	1715.82	1743.82	726.36	6
18	M*	1862.86	1890.85	655.32	5
19	V	1961.92	1989.92	508.29	4
20	F	2108.99	2136.99	409.22	3
21	S	2196.02	2224.02	262.15	2
22	R	-	-	175.12	1

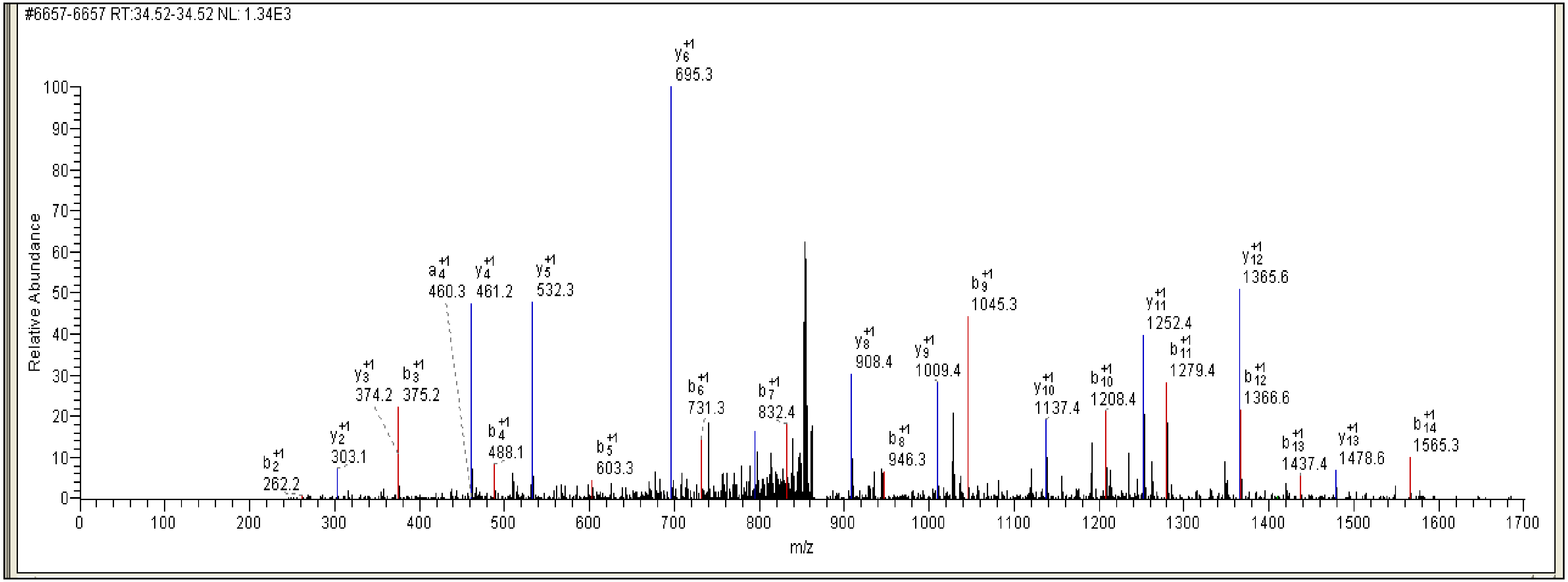


CG30122 NP_611354.2 CG30122 CG30122-PB

R.NFILDQTNVYASAQR.R

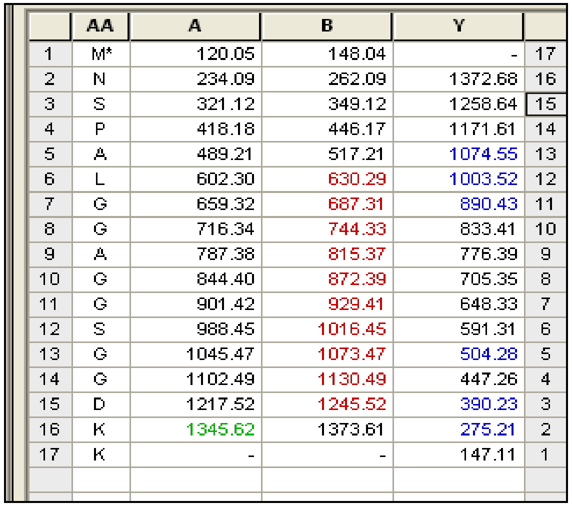


	AA	A	B	Y	
1	N	87.06	115.05	-	15
2	F	234.12	262.12	1625.83	14
3	I	347.21	375.20	1478.76	13
4	L	460.29	488.29	1365.68	12
5	D	575.32	603.31	1252.59	11
6	Q	703.38	731.37	1137.56	10
7	T	804.43	832.42	1009.51	9
8	N	918.47	946.46	908.46	8
9	V	1017.54	1045.53	794.42	7
10	Y	1180.60	1208.59	695.35	6
11	A	1251.64	1279.63	532.28	5
12	S	1338.67	1366.66	461.25	4
13	A	1409.71	1437.70	374.21	3
14	Q	1537.76	1565.76	303.18	2
15	R	-	-	175.12	1

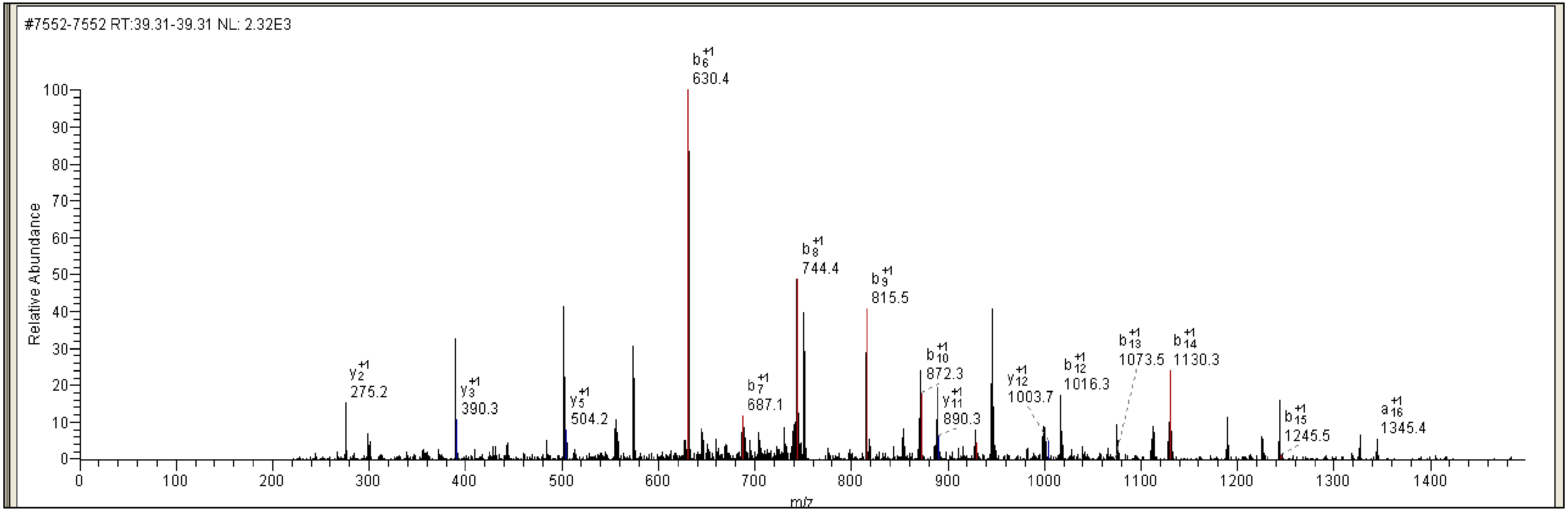


CG30158 NP_652315.2 CG30158 CG30158-PA

R.MNSPALGGAGGSGGDKK.G

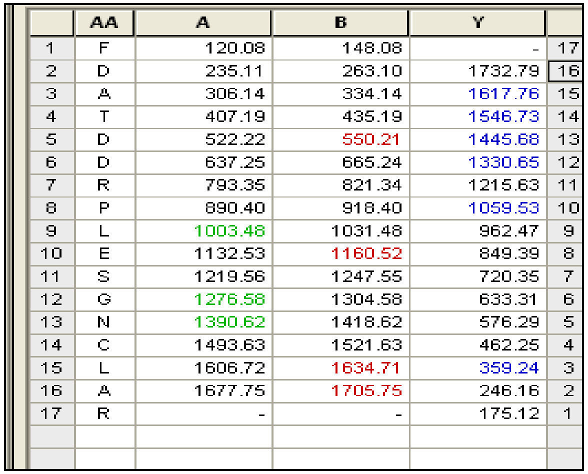


	AA	A	B	Y	
1	M*	120.05	148.04	-	17
2	N	234.09	262.09	1372.68	16
3	S	321.12	349.12	1258.64	15
4	P	418.18	446.17	1171.61	14
5	A	489.21	517.21	1074.55	13
6	L	602.30	630.29	1003.52	12
7	G	659.32	687.31	890.43	11
8	G	716.34	744.33	833.41	10
9	A	787.38	815.37	776.39	9
10	G	844.40	872.39	705.35	8
11	G	901.42	929.41	648.33	7
12	S	988.45	1016.45	591.31	6
13	G	1045.47	1073.47	504.28	5
14	G	1102.49	1130.49	447.26	4
15	D	1217.52	1245.52	390.23	3
16	K	1345.62	1373.61	275.21	2
17	K	-	-	147.11	1

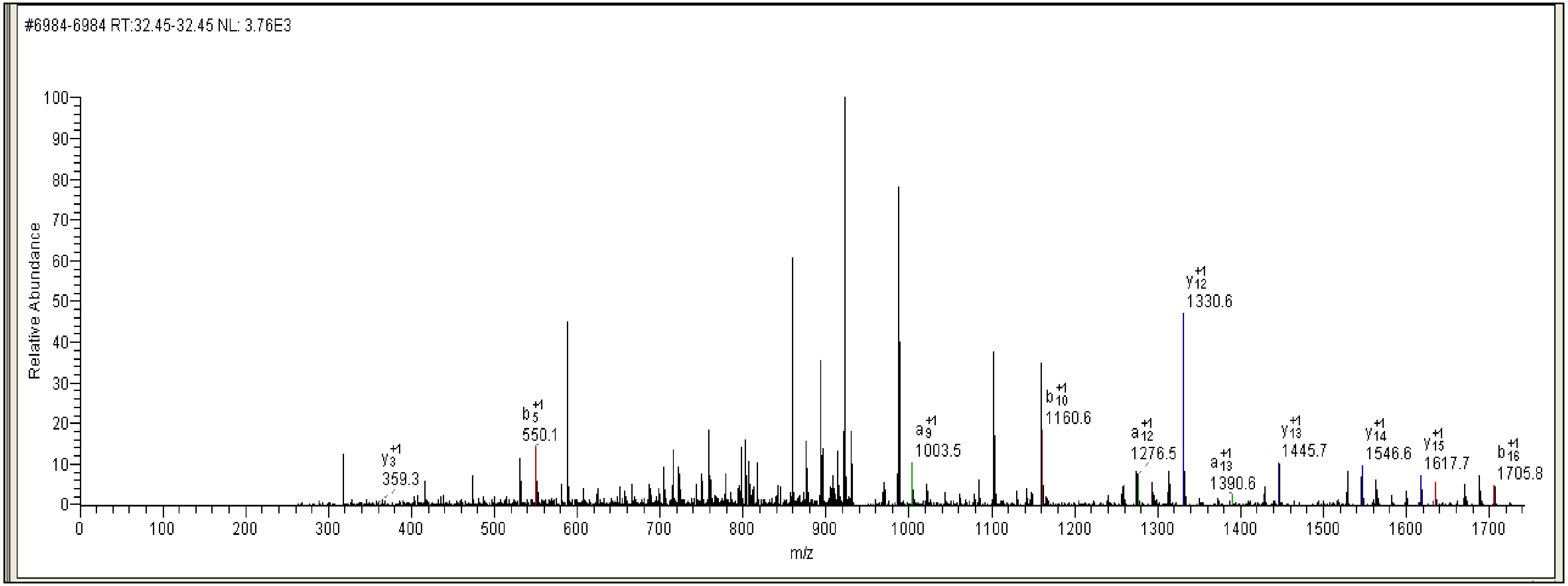


NP_732682.1 CG31465 CG31465-PA

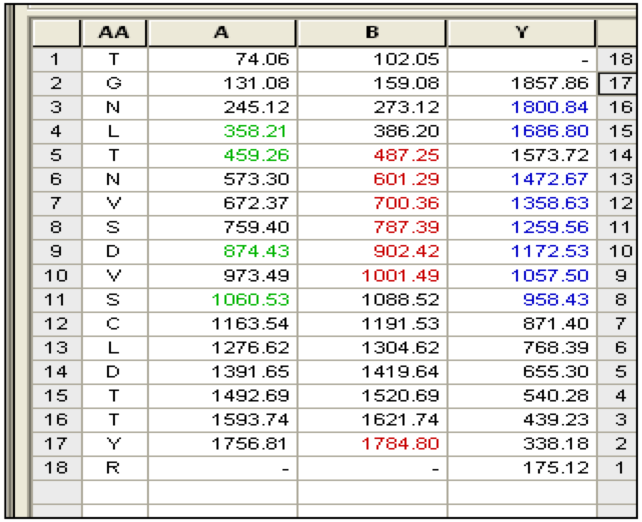
K.FDATDDRPLESGNCLAR.L



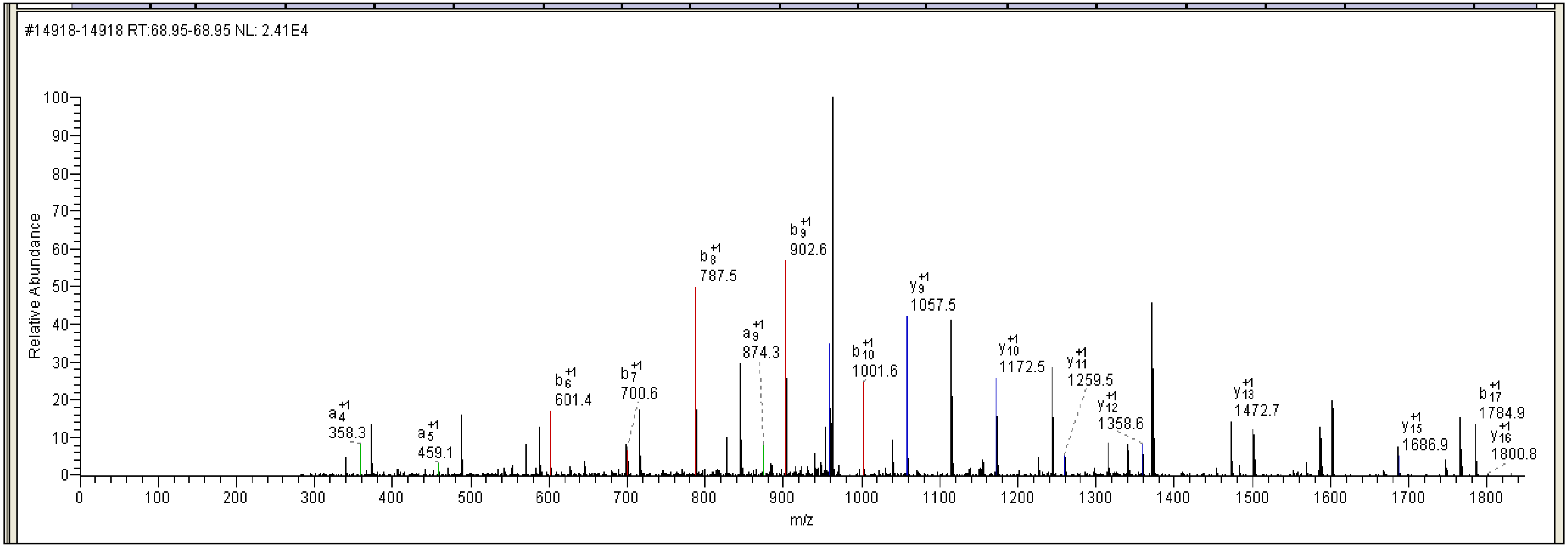
	AA	A	B	Y	
1	F	120.08	148.08	-	17
2	D	235.11	263.10	1732.79	16
3	A	306.14	334.14	1617.76	15
4	T	407.19	435.19	1546.73	14
5	D	522.22	550.21	1445.68	13
6	D	637.25	665.24	1330.65	12
7	R	793.35	821.34	1215.63	11
8	P	890.40	918.40	1059.53	10
9	L	1003.48	1031.48	962.47	9
10	E	1132.53	1160.52	849.39	8
11	S	1219.56	1247.55	720.35	7
12	G	1276.58	1304.58	633.31	6
13	N	1390.62	1418.62	576.29	5
14	C	1493.63	1521.63	462.25	4
15	L	1606.72	1634.71	359.24	3
16	A	1677.75	1705.75	246.16	2
17	R	-	-	175.12	1



CG32086 NP_729720.1 CG32086 CG32086-PA
K.TGNLTNVSDVSCLDTTYR.L



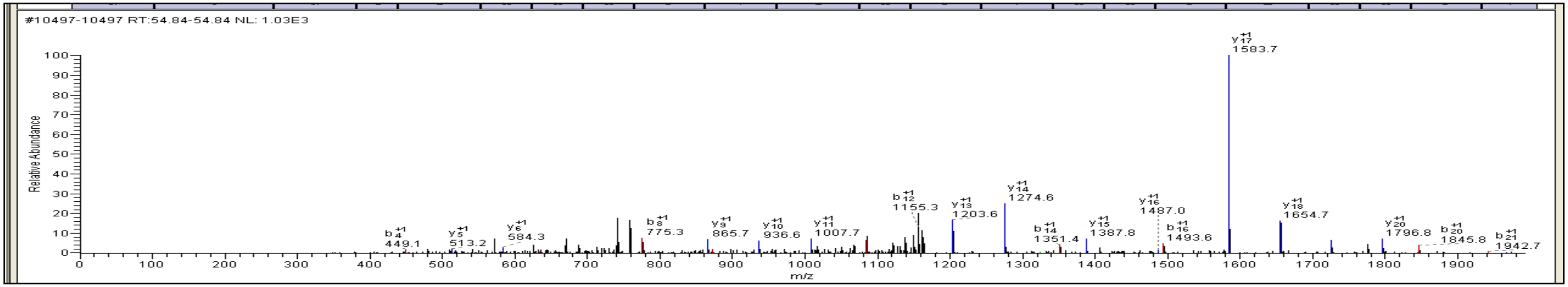
	AA	A	B	Y	
1	T	74.06	102.05	-	18
2	G	131.08	159.08	1857.86	17
3	N	245.12	273.12	1800.84	16
4	L	358.21	386.20	1686.80	15
5	T	459.26	487.25	1573.72	14
6	N	573.30	601.29	1472.67	13
7	V	672.37	700.36	1358.63	12
8	S	759.40	787.39	1259.56	11
9	D	874.43	902.42	1172.53	10
10	V	973.49	1001.49	1057.50	9
11	S	1060.53	1088.52	958.43	8
12	C	1163.54	1191.53	871.40	7
13	L	1276.62	1304.62	768.39	6
14	D	1391.65	1419.64	655.30	5
15	T	1492.69	1520.69	540.28	4
16	T	1593.74	1621.74	439.23	3
17	Y	1756.81	1784.80	338.18	2
18	R	-	-	175.12	1



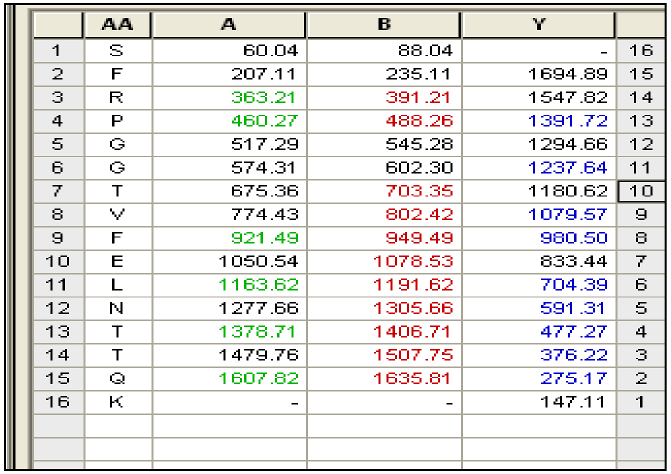
CG32214 NP_730409.1 CG32214 CG32214-PA

R.NYNGIAAAPVIAPVAAPLAAPVVAK.Y

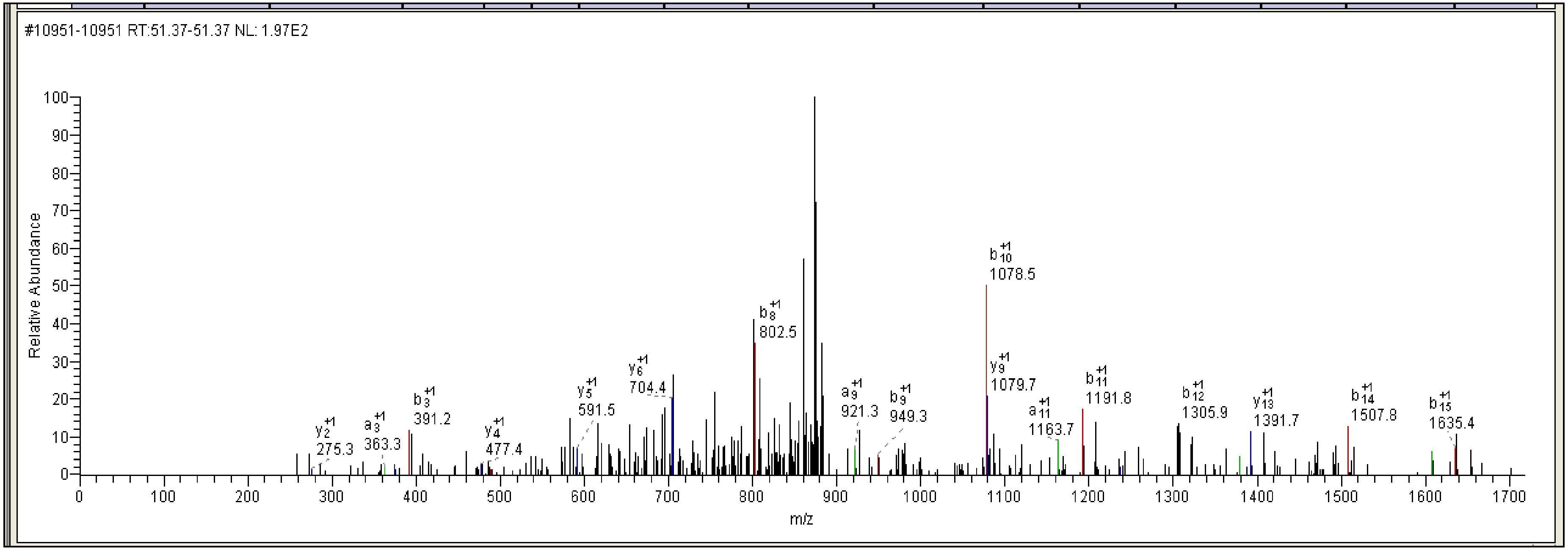
S no	AA	A	B	Y	
1	N	87.06	115.05	-	25
2	Y	250.12	278.11	2244.31	24
3	N	364.16	392.16	2081.25	23
4	G	421.18	449.18	1967.21	22
5	I	534.27	562.26	1910.18	21
6	A	605.3	633.3	1797.1	20
7	A	676.34	704.34	1726.06	19
8	A	747.38	775.37	1655.03	18
9	P	844.43	872.43	1583.99	17
10	V	943.5	971.49	1486.94	16
11	I	1056.58	1084.58	1387.87	15
12	A	1127.62	1155.62	1274.78	14
13	P	1224.67	1252.67	1203.75	13
14	V	1323.74	1351.74	1106.69	12
15	A	1394.78	1422.77	1007.62	11
16	A	1465.82	1493.81	936.59	10
17	P	1562.87	1590.86	865.55	9
18	L	1675.95	1703.95	768.5	8
19	A	1746.99	1774.99	655.41	7
20	A	1818.03	1846.02	584.38	6
21	P	1915.08	1943.07	513.34	5
22	V	2014.15	2042.14	416.29	4
23	V	2113.22	2141.21	317.22	3
24	A	2184.25	2212.25	218.15	2
25	K	-	-	147.11	1



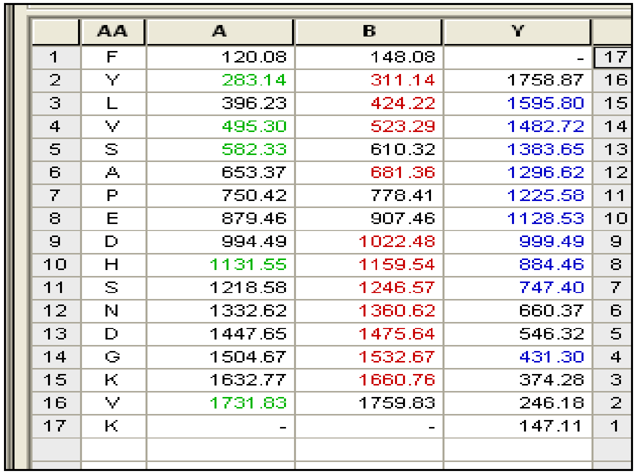
CG32344 NP_612028.4 CG32344 CG32344-PA
R.SFRPGGTVFELNTTQK.S



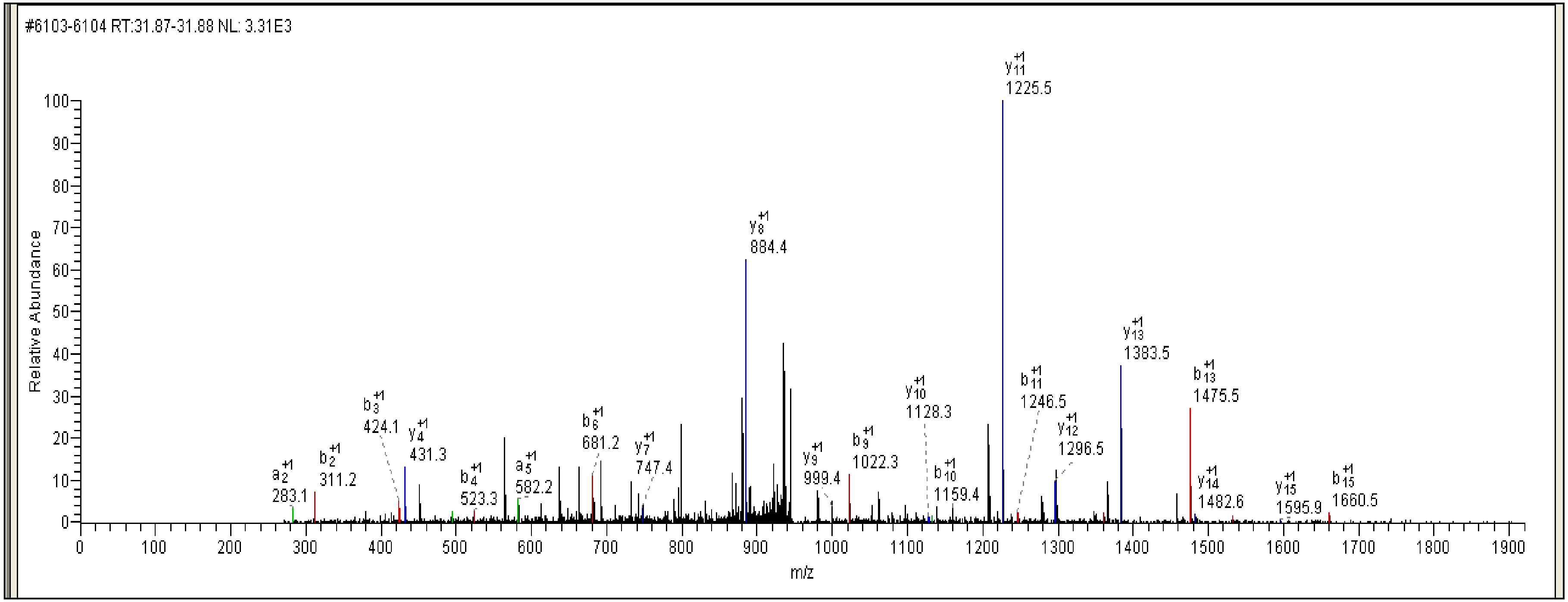
	AA	A	B	Y	
1	S	60.04	88.04	-	16
2	F	207.11	235.11	1694.89	15
3	R	363.21	391.21	1547.82	14
4	P	460.27	488.26	1391.72	13
5	G	517.29	545.28	1294.66	12
6	G	574.31	602.30	1237.64	11
7	T	675.36	703.35	1180.62	10
8	V	774.43	802.42	1079.57	9
9	F	921.49	949.49	980.50	8
10	E	1050.54	1078.53	833.44	7
11	L	1163.62	1191.62	704.39	6
12	N	1277.66	1305.66	591.31	5
13	T	1378.71	1406.71	477.27	4
14	T	1479.76	1507.75	376.22	3
15	Q	1607.82	1635.81	275.17	2
16	K	-	-	147.11	1



TwdlY NP_728017.1 CG32570 CG32570-PA
K.FYLVSAPEDHSNDGKVK.H

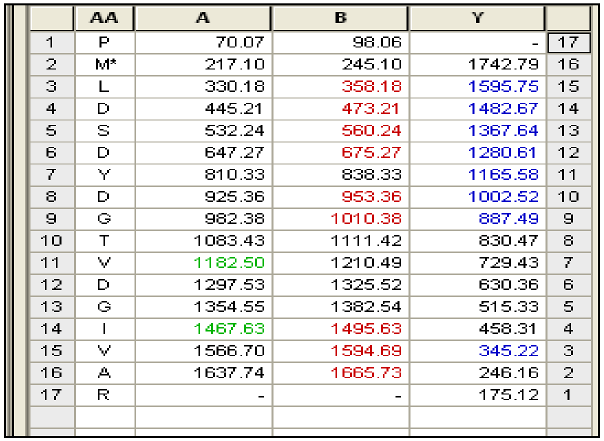


	AA	A	B	Y	
1	F	120.08	148.08	-	17
2	Y	283.14	311.14	1758.87	16
3	L	396.23	424.22	1595.80	15
4	V	495.30	523.29	1482.72	14
5	S	582.33	610.32	1383.65	13
6	A	653.37	681.36	1296.62	12
7	P	750.42	778.41	1225.58	11
8	E	879.46	907.46	1128.53	10
9	D	994.49	1022.48	999.49	9
10	H	1131.55	1159.54	884.46	8
11	S	1218.58	1246.57	747.40	7
12	N	1332.62	1360.62	660.37	6
13	D	1447.65	1475.64	546.32	5
14	G	1504.67	1532.67	431.30	4
15	K	1632.77	1660.76	374.28	3
16	V	1731.83	1759.83	246.18	2
17	K	-	-	147.11	1

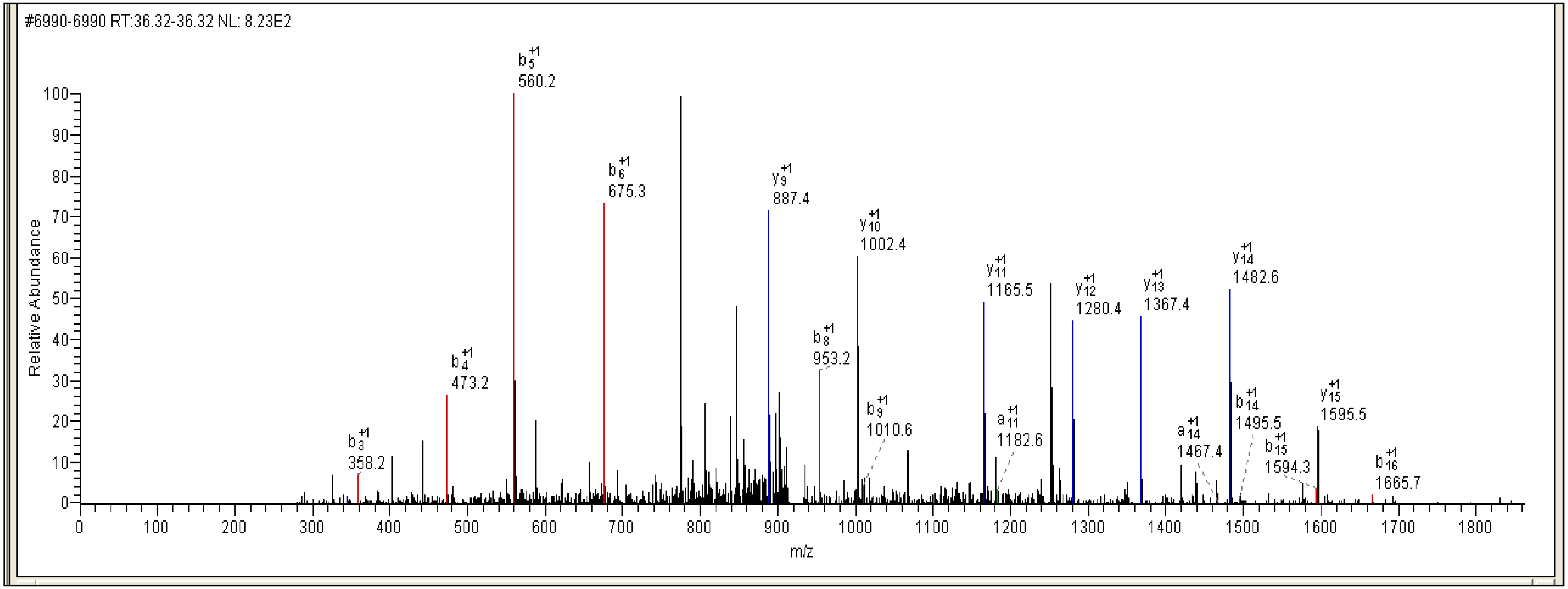


NP_001036688.1 CG34135 CG34135-PA

R.PMLDSDYDGTVDGIVAR.P

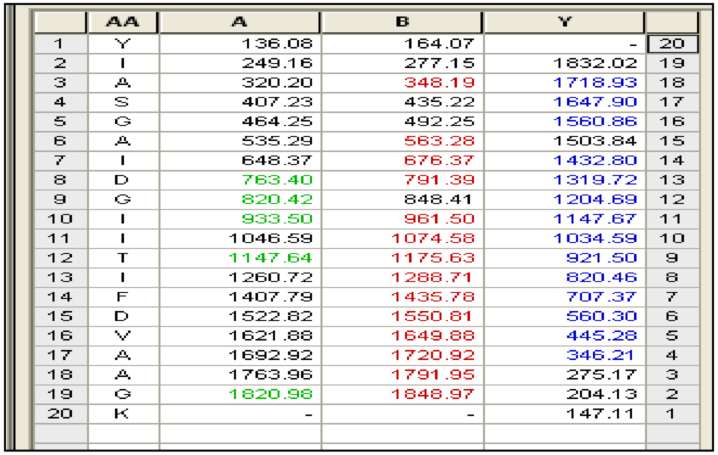


	AA	A	B	Y	
1	P	70.07	98.06	-	17
2	M*	217.10	245.10	1742.79	16
3	L	330.18	358.18	1595.75	15
4	D	445.21	473.21	1482.67	14
5	S	532.24	560.24	1367.64	13
6	D	647.27	675.27	1280.61	12
7	Y	810.33	838.33	1165.58	11
8	D	925.36	953.36	1002.52	10
9	G	982.38	1010.38	887.49	9
10	T	1083.43	1111.42	830.47	8
11	V	1182.50	1210.49	729.43	7
12	D	1297.53	1325.52	630.36	6
13	G	1354.55	1382.54	515.33	5
14	I	1467.63	1495.63	458.31	4
15	V	1566.70	1594.69	345.22	3
16	A	1637.74	1665.73	246.16	2
17	R	-	-	175.12	1

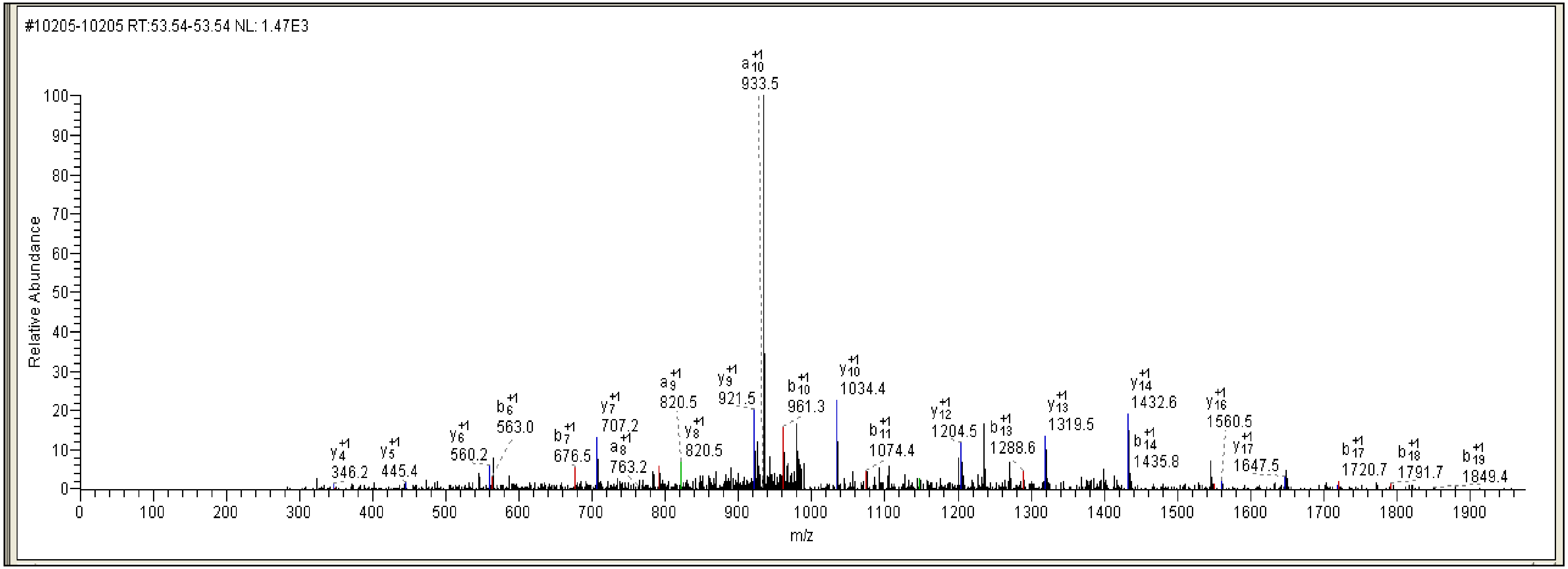


CG3909 NP_649969.1 CG3909 CG3909-PA

K.YIASGAIDGIITIFDVAAGK.V

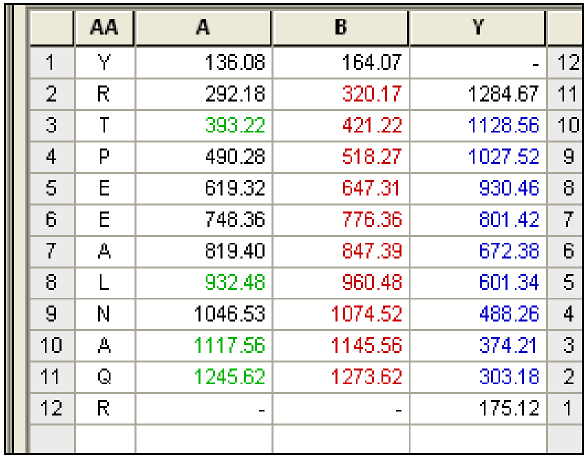


	AA	A	B	Y	
1	Y	136.08	164.07	-	20
2	I	249.16	277.15	1832.02	19
3	A	320.20	348.19	1718.93	18
4	S	407.23	435.22	1647.90	17
5	G	464.25	492.25	1560.86	16
6	A	535.29	563.28	1503.84	15
7	I	648.37	676.37	1432.80	14
8	D	763.40	791.39	1319.72	13
9	G	820.42	848.41	1204.69	12
10	I	933.50	961.50	1147.67	11
11	I	1046.59	1074.58	1034.59	10
12	T	1147.64	1175.63	921.50	9
13	I	1260.72	1288.71	820.46	8
14	F	1407.79	1435.78	707.37	7
15	D	1522.82	1550.81	560.30	6
16	V	1621.88	1649.88	445.28	5
17	A	1692.92	1720.92	346.21	4
18	A	1763.96	1791.95	275.17	3
19	G	1820.98	1848.97	204.13	2
20	K	-	-	147.11	1

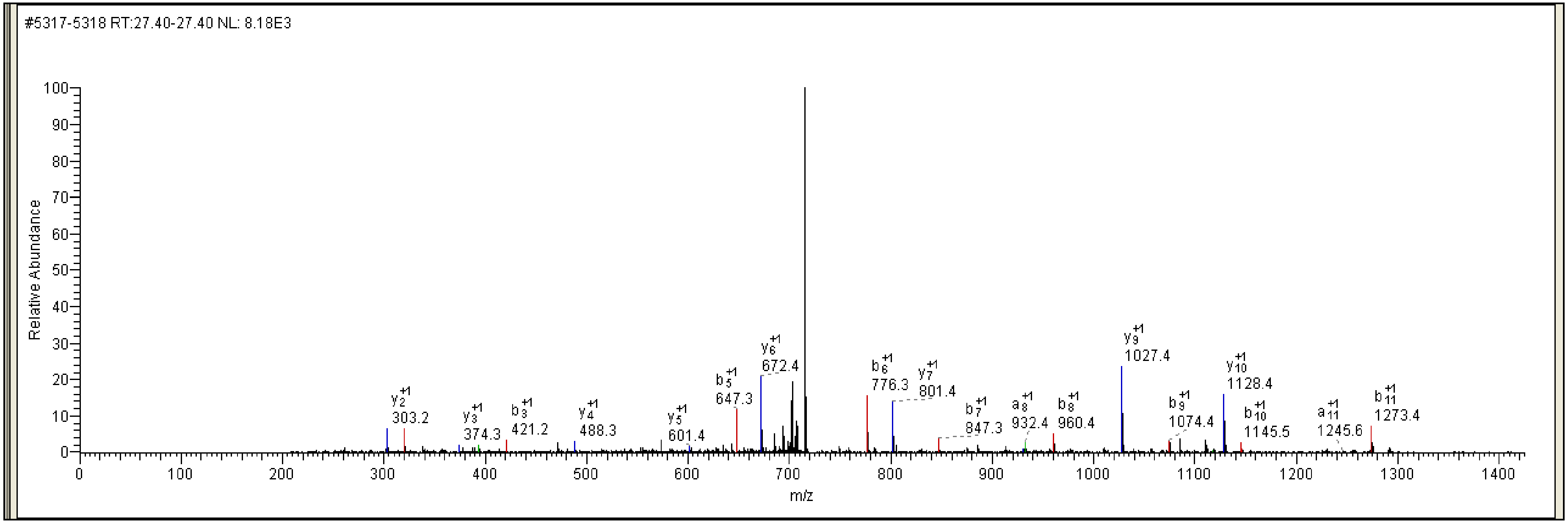


TwdlW NP_650606.2 CG4060 CG4060-PA

K.YRTPEEALNAQR.Q

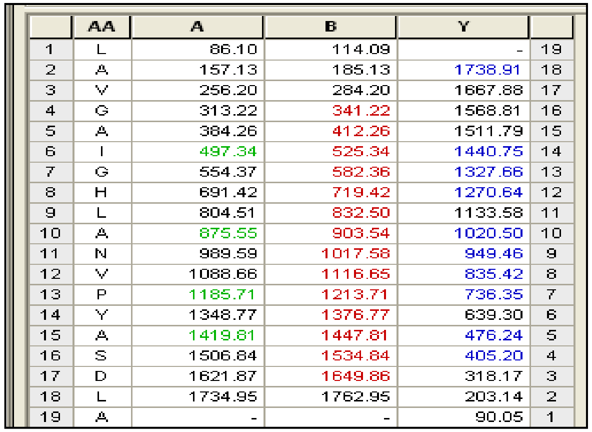


	AA	A	B	Y	
1	Y	136.08	164.07	-	12
2	R	292.18	320.17	1284.67	11
3	T	393.22	421.22	1128.56	10
4	P	490.28	518.27	1027.52	9
5	E	619.32	647.31	930.46	8
6	E	748.36	776.36	801.42	7
7	A	819.40	847.39	672.38	6
8	L	932.48	960.48	601.34	5
9	N	1046.53	1074.52	488.26	4
10	A	1117.56	1145.56	374.21	3
11	Q	1245.62	1273.62	303.18	2
12	R	-	-	175.12	1

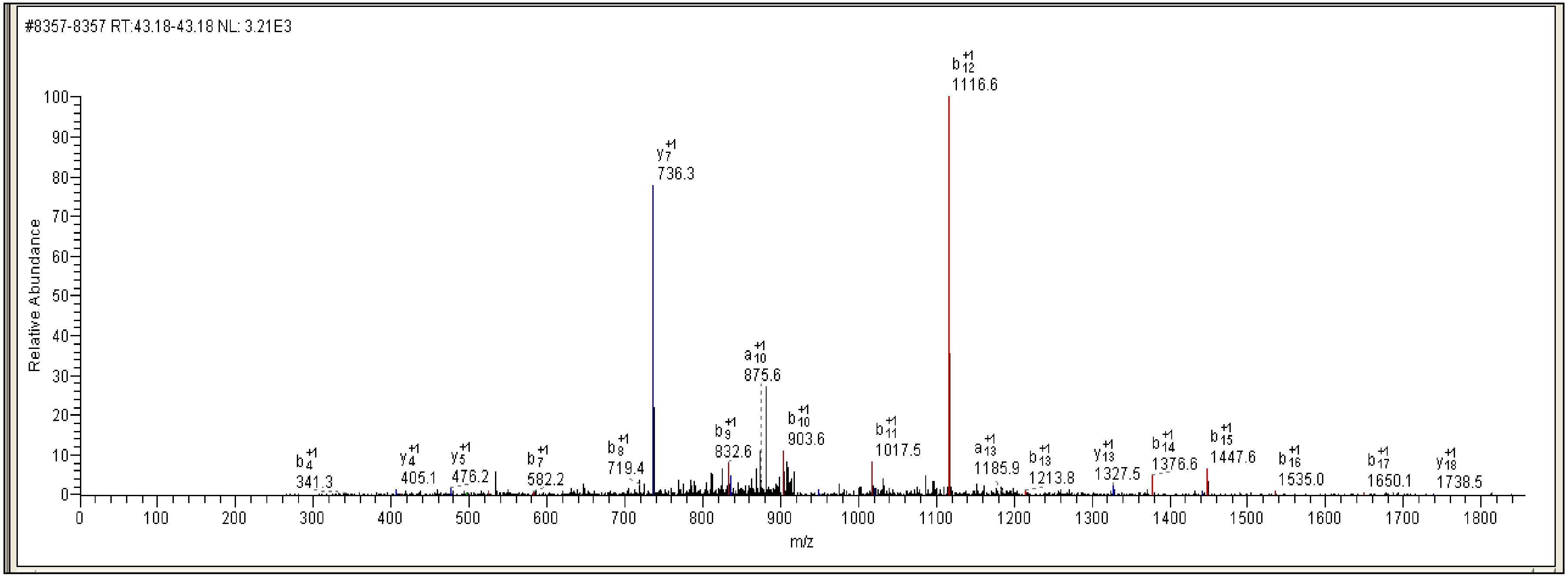


CG4169 NP_648905.1 CG4169 CG4169-PA

K.LAVGAIGHLANVPYASDLA

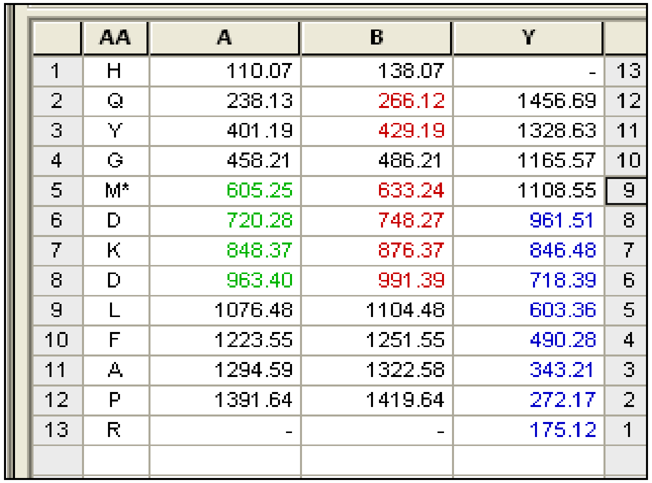


	AA	A	B	Y	
1	L	86.10	114.09	-	19
2	A	157.13	185.13	1738.91	18
3	V	256.20	284.20	1667.88	17
4	G	313.22	341.22	1568.81	16
5	A	384.26	412.26	1511.79	15
6	I	497.34	525.34	1440.75	14
7	G	554.37	582.36	1327.66	13
8	H	691.42	719.42	1270.64	12
9	L	804.51	832.50	1133.58	11
10	A	875.55	903.54	1020.50	10
11	N	989.59	1017.58	949.46	9
12	V	1088.66	1116.65	835.42	8
13	P	1185.71	1213.71	736.35	7
14	Y	1348.77	1376.77	639.30	6
15	A	1419.81	1447.81	476.24	5
16	S	1506.84	1534.84	405.20	4
17	D	1621.87	1649.86	318.17	3
18	L	1734.95	1762.95	203.14	2
19	A	-	-	90.05	1



CG4266 NP_611557.2 CG4266 CG4266-PA

R.HQYGMDKDLFAPR.F



	AA	A	B	Y	
1	H	110.07	138.07	-	13
2	Q	238.13	266.12	1456.69	12
3	Y	401.19	429.19	1328.63	11
4	G	458.21	486.21	1165.57	10
5	M*	605.25	633.24	1108.55	9
6	D	720.28	748.27	961.51	8
7	K	848.37	876.37	846.48	7
8	D	963.40	991.39	718.39	6
9	L	1076.48	1104.48	603.36	5
10	F	1223.55	1251.55	490.28	4
11	A	1294.59	1322.58	343.21	3
12	P	1391.64	1419.64	272.17	2
13	R	-	-	175.12	1