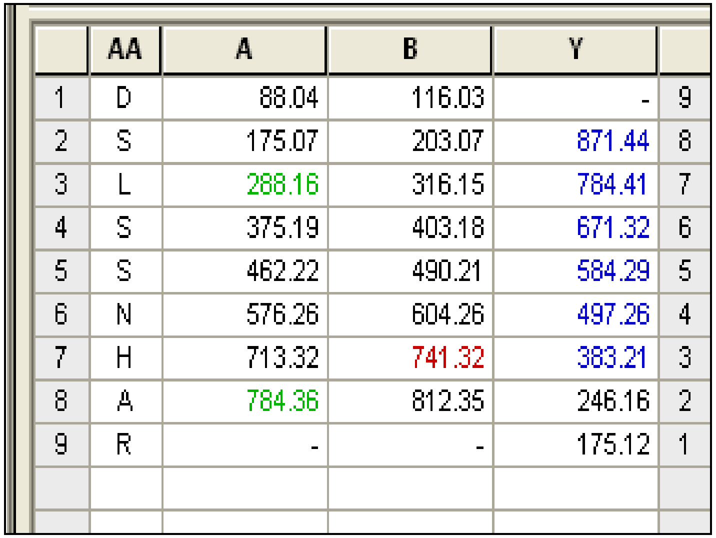
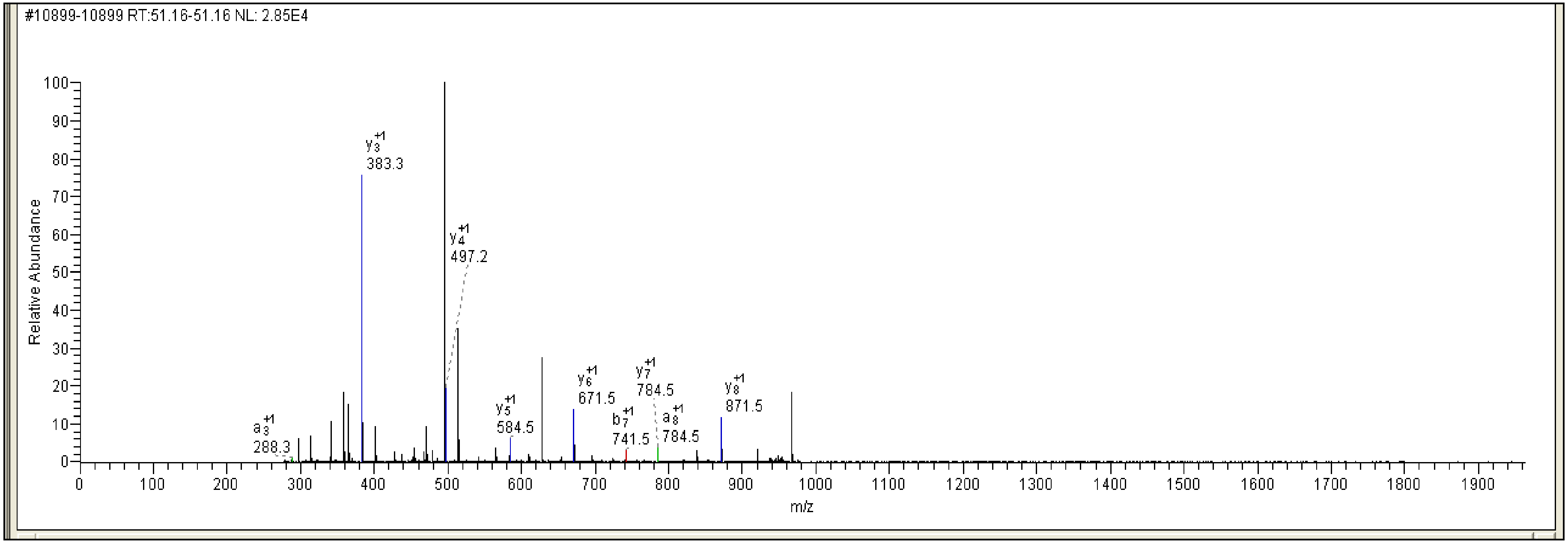
CG4554 NP_611676.1 CG4554 CG4554-PA

K.DSLSSNHAR.T

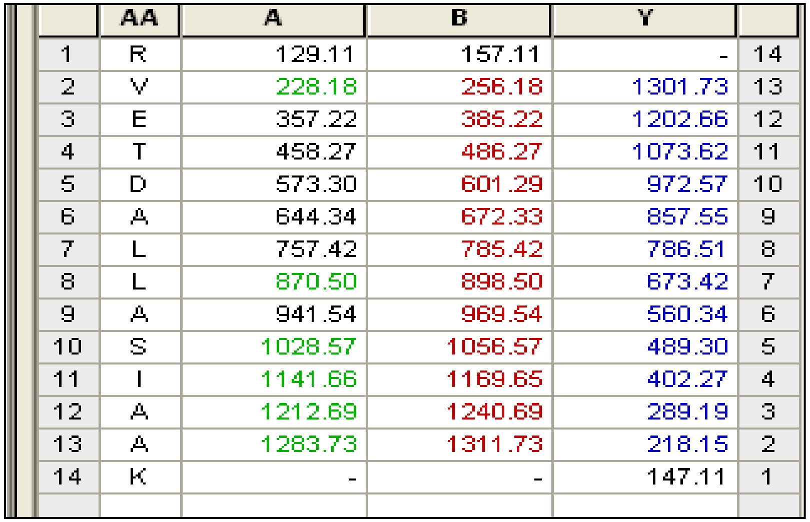


	AA	A	B	Y	
1	D	88.04	116.03	-	9
2	S	175.07	203.07	871.44	8
3	L	288.16	316.15	784.41	7
4	S	375.19	403.18	671.32	6
5	S	462.22	490.21	584.29	5
6	N	576.26	604.26	497.26	4
7	H	713.32	741.32	383.21	3
8	A	784.36	812.35	246.16	2
9	R	-	-	175.12	1

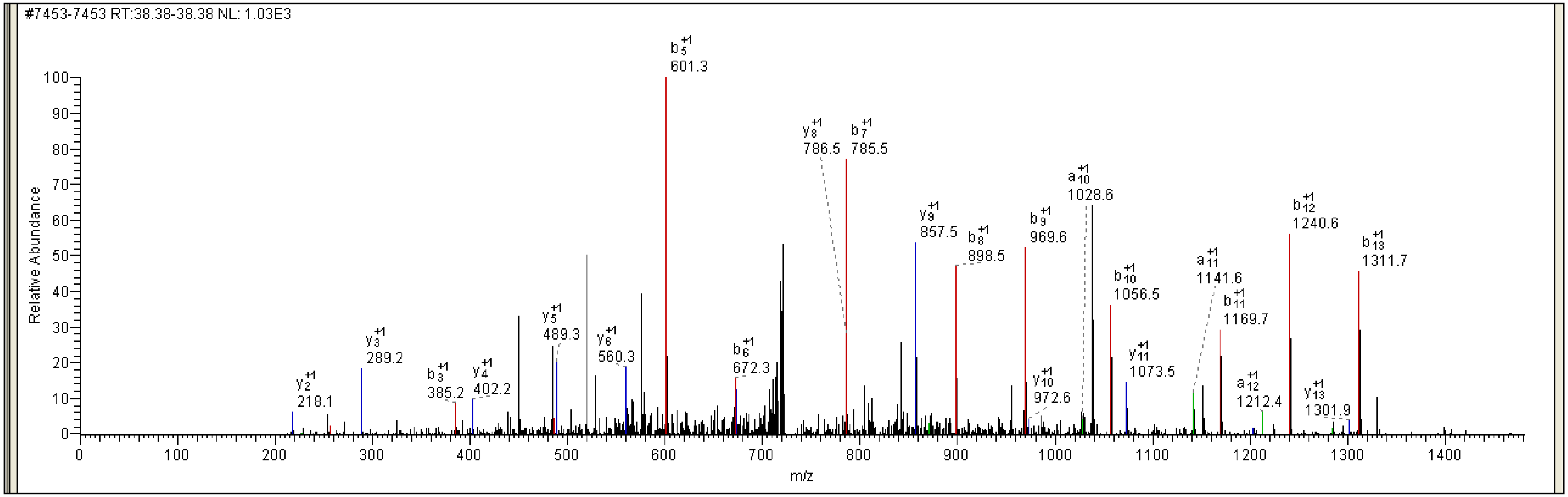


CG4747 NP_609336.3 CG4747 CG4747-PA

R.RVETDALLASIAAK.R



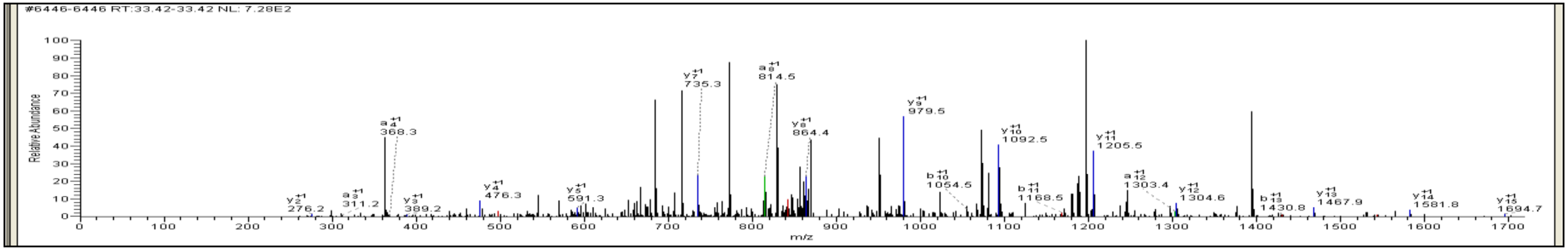
	AA	A	B	Y	
1	R	129.11	157.11	-	14
2	V	228.18	256.18	1301.73	13
3	E	357.22	385.22	1202.66	12
4	T	458.27	486.27	1073.62	11
5	D	573.30	601.29	972.57	10
6	A	644.34	672.33	857.55	9
7	L	757.42	785.42	786.51	8
8	L	870.50	898.50	673.42	7
9	A	941.54	969.54	560.34	6
10	S	1028.57	1056.57	489.30	5
11	I	1141.66	1169.65	402.27	4
12	A	1212.69	1240.69	289.19	3
13	A	1283.73	1311.73	218.15	2
14	K	-	-	147.11	1



NP_609499.1 CG4788 CG4788-PA

R.IKPGTHAHVINYVIIDEGSDSLEK.A

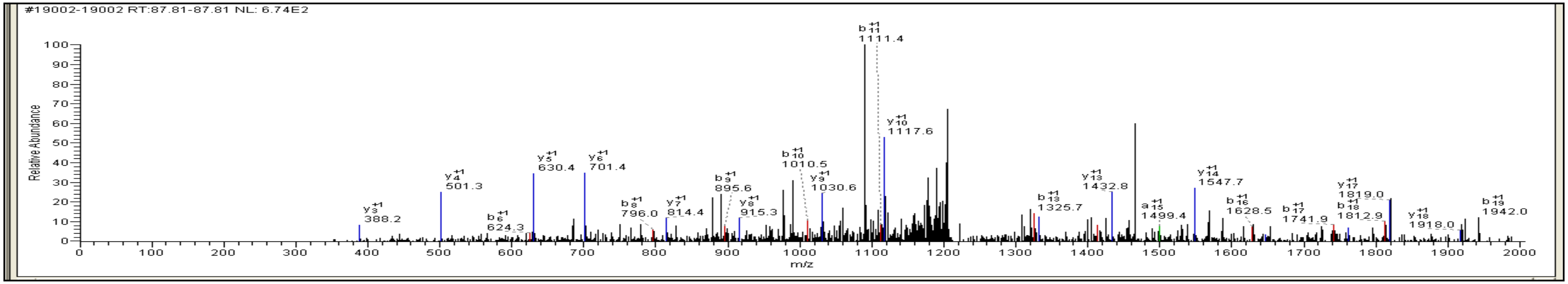
S no	AA	A	B	Y	
1	I	86.1	114.09	-	24
2	K	214.19	242.19	2522.29	23
3	P	311.24	339.24	2394.19	22
4	G	368.27	396.26	2297.14	21
5	T	469.31	497.31	2240.12	20
6	H	606.37	634.37	2139.07	19
7	A	677.41	705.4	2002.01	18
8	H	814.47	842.46	1930.98	17
9	V	913.54	941.53	1793.92	16
10	I	1026.62	1054.62	1694.85	15
11	N	1140.66	1168.66	1581.76	14
12	Y	1303.73	1331.72	1467.72	13
13	V	1402.8	1430.79	1304.66	12
14	I	1515.88	1543.87	1205.59	11
15	I	1628.96	1656.96	1092.51	10
16	D	1743.99	1771.99	979.42	9
17	E	1873.03	1901.03	864.39	8
18	G	1930.05	1958.05	735.35	7
19	S	2017.09	2045.08	678.33	6
20	D	2132.11	2160.11	591.3	5
21	S	2219.15	2247.14	476.27	4
22	L	2332.23	2360.22	389.24	3
23	E	2461.27	2489.27	276.16	2
24	K	-	-	147.11	1



CG4849 NP_651605.1 CG4849 CG4849-PA

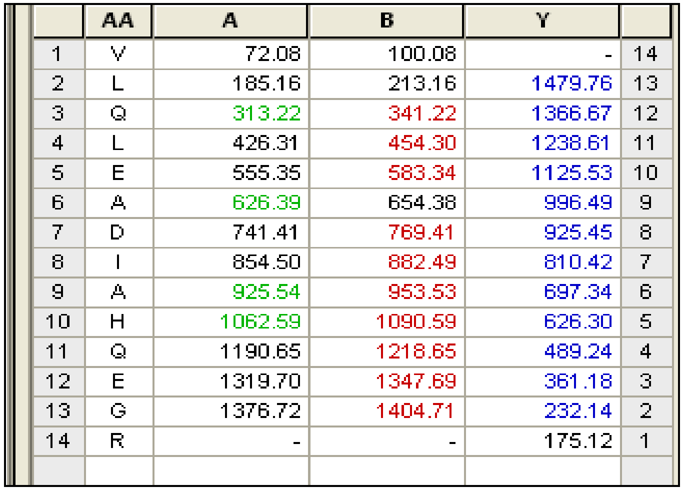
K.LIAQVVGDVDTTLSDTLAELNVR.V

S no	AA	A	B	Y	
1	L	86.1	114.09	-	23
2	I	199.18	227.18	2329.22	22
3	A	270.22	298.21	2216.14	21
4	Q	398.28	426.27	2145.1	20
5	V	497.34	525.34	2017.04	19
6	V	596.41	624.41	1917.98	18
7	G	653.43	681.43	1818.91	17
8	D	768.46	796.46	1761.89	16
9	V	867.53	895.52	1646.86	15
10	D	982.56	1010.55	1547.79	14
11	T	1083.6	1111.6	1432.76	13
12	T	1184.65	1212.65	1331.72	12
13	L	1297.74	1325.73	1230.67	11
14	S	1384.77	1412.76	1117.58	10
15	D	1499.8	1527.79	1030.55	9
16	T	1600.84	1628.84	915.53	8
17	L	1713.93	1741.92	814.48	7
18	A	1784.96	1812.96	701.39	6
19	E	1914.01	1942	630.36	5
20	L	2027.09	2055.09	501.31	4
21	N	2141.13	2169.13	388.23	3
22	V	2240.2	2268.2	274.19	2
23	R	-	-	175.12	1

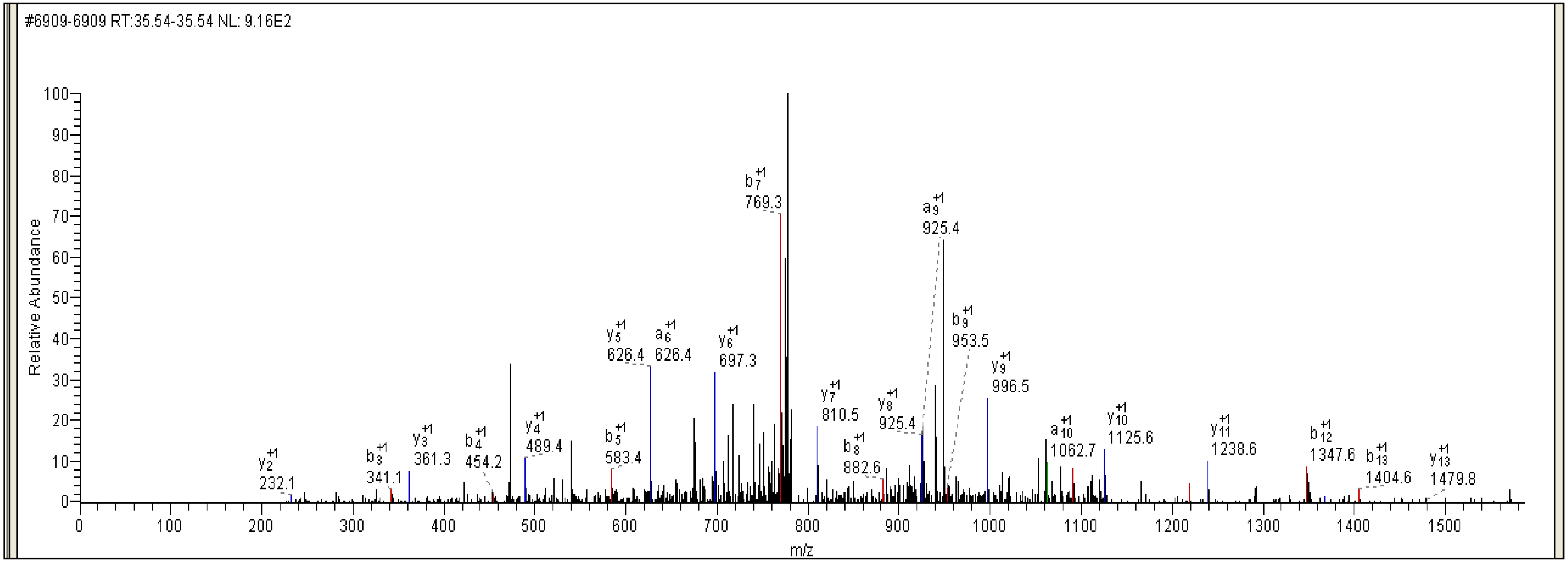


CG5190 NP_611335.1 CG5190 CG5190-PA

K.VLQLEADIAHQEGR.R

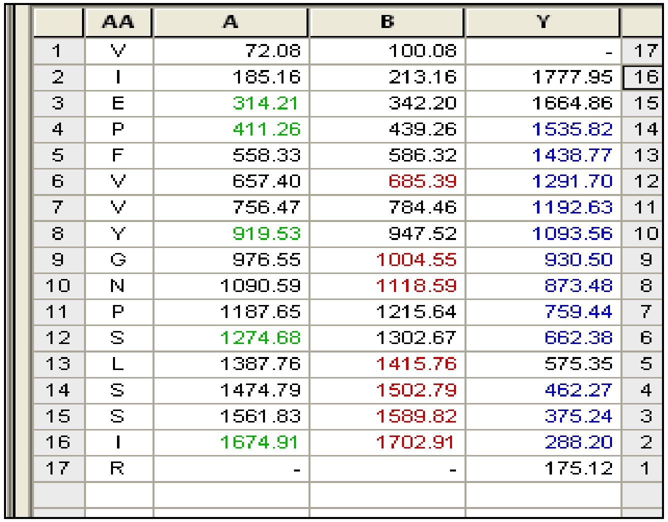


	AA	A	B	Y	
1	V	72.08	100.08	-	14
2	L	185.16	213.16	1479.76	13
3	Q	313.22	341.22	1366.67	12
4	L	426.31	454.30	1238.61	11
5	E	555.35	583.34	1125.53	10
6	A	626.39	654.38	996.49	9
7	D	741.41	769.41	925.45	8
8	I	854.50	882.49	810.42	7
9	A	925.54	953.53	697.34	6
10	H	1062.59	1090.59	626.30	5
11	Q	1190.65	1218.65	489.24	4
12	E	1319.70	1347.69	361.18	3
13	G	1376.72	1404.71	232.14	2
14	R	-	-	175.12	1

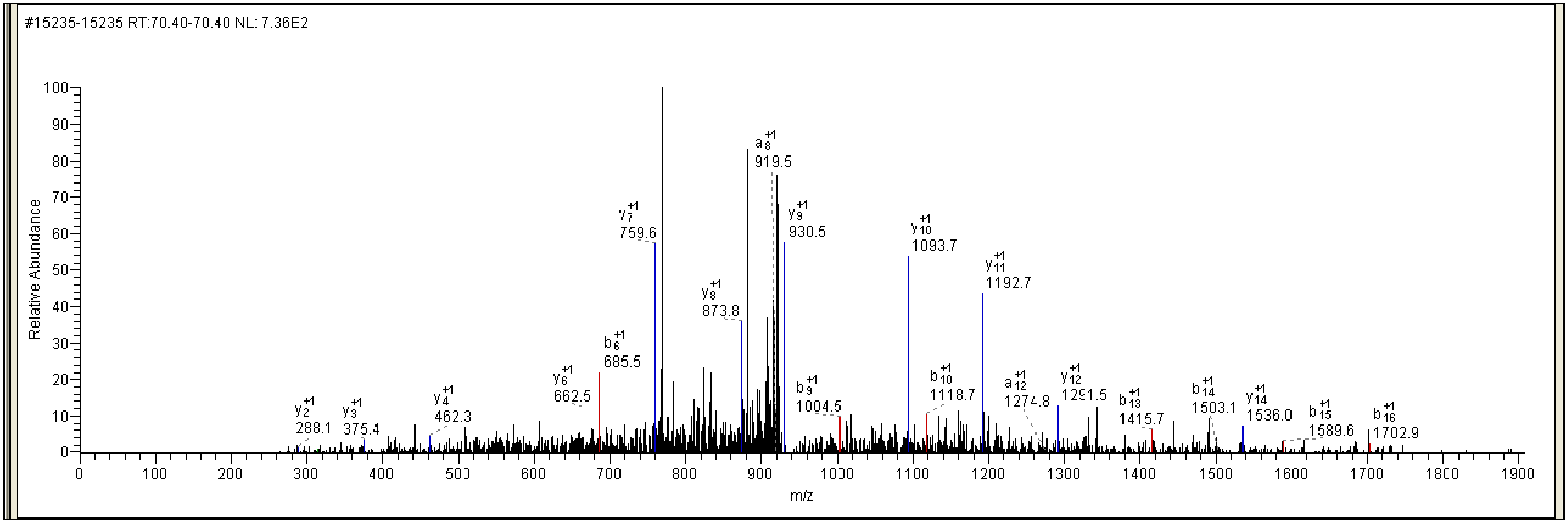


CG5317 NP_609543.2 CG5317 CG5317-PA

R.VIEPFVVYGNPSLSSIR.E

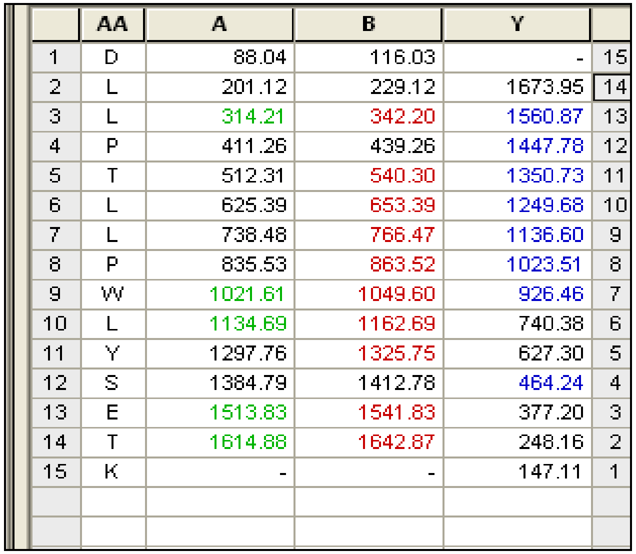


	AA	A	B	Y	
1	V	72.08	100.08	-	17
2	I	185.16	213.16	1777.95	16
3	E	314.21	342.20	1664.86	15
4	P	411.26	439.26	1535.82	14
5	F	558.33	586.32	1438.77	13
6	V	657.40	685.39	1291.70	12
7	V	756.47	784.46	1192.63	11
8	Y	919.53	947.52	1093.56	10
9	G	976.55	1004.55	930.50	9
10	N	1090.59	1118.59	873.48	8
11	P	1187.65	1215.64	759.44	7
12	S	1274.68	1302.67	662.38	6
13	L	1387.76	1415.76	575.35	5
14	S	1474.79	1502.79	462.27	4
15	S	1561.83	1589.82	375.24	3
16	I	1674.91	1702.91	288.20	2
17	R	-	-	175.12	1

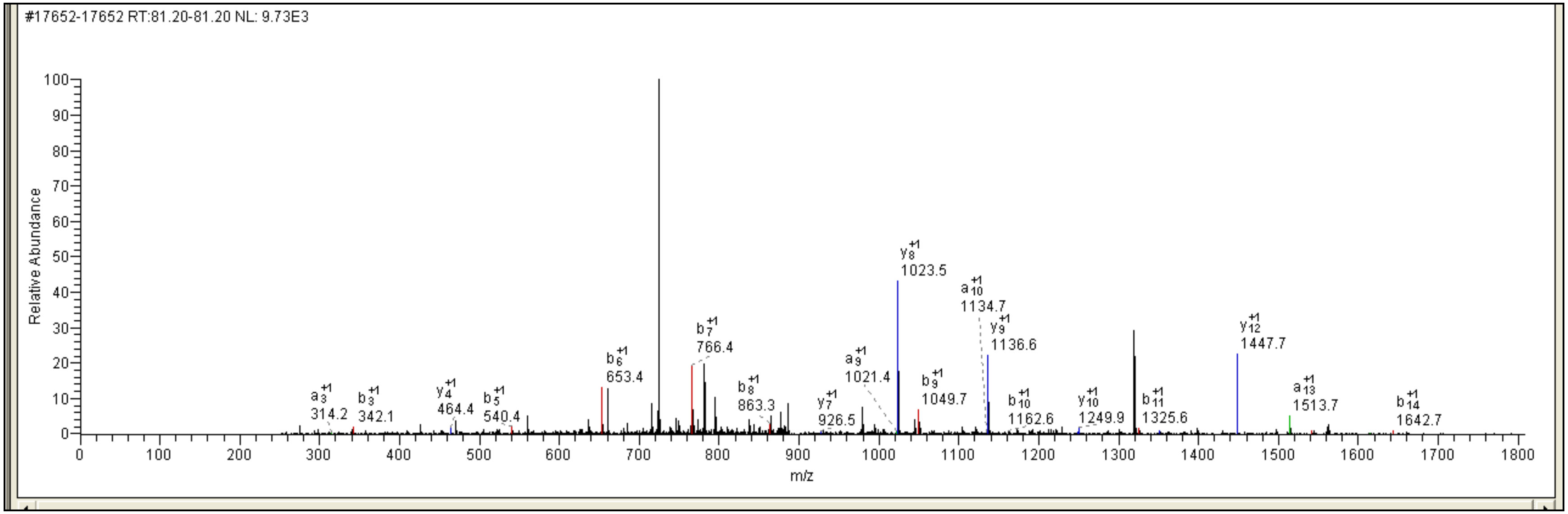


CG5366 NP_609389.1 CG5366 CG5366-PA

R.DLLPTLLPWLYSETK.V

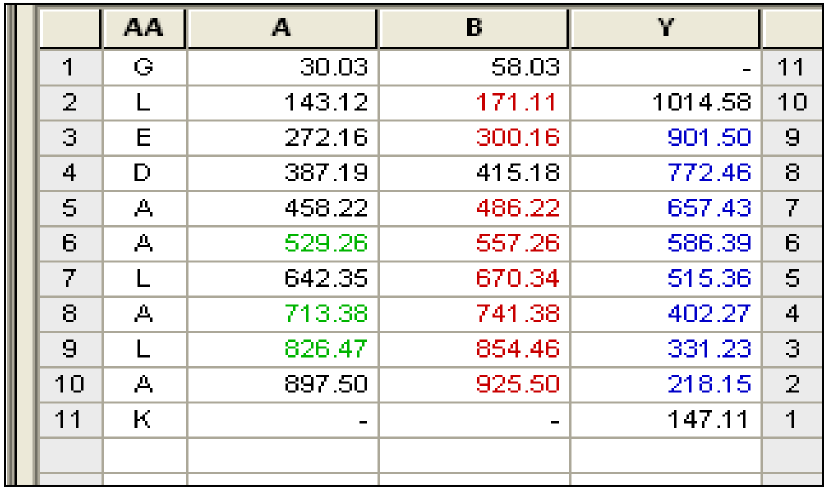


	AA	A	B	Y	
1	D	88.04	116.03	-	15
2	L	201.12	229.12	1673.95	14
3	L	314.21	342.20	1560.87	13
4	P	411.26	439.26	1447.78	12
5	T	512.31	540.30	1350.73	11
6	L	625.39	653.39	1249.68	10
7	L	738.48	766.47	1136.60	9
8	P	835.53	863.52	1023.51	8
9	W	1021.61	1049.60	926.46	7
10	L	1134.69	1162.69	740.38	6
11	Y	1297.76	1325.75	627.30	5
12	S	1384.79	1412.78	464.24	4
13	E	1513.83	1541.83	377.20	3
14	T	1614.88	1642.87	248.16	2
15	K	-	-	147.11	1

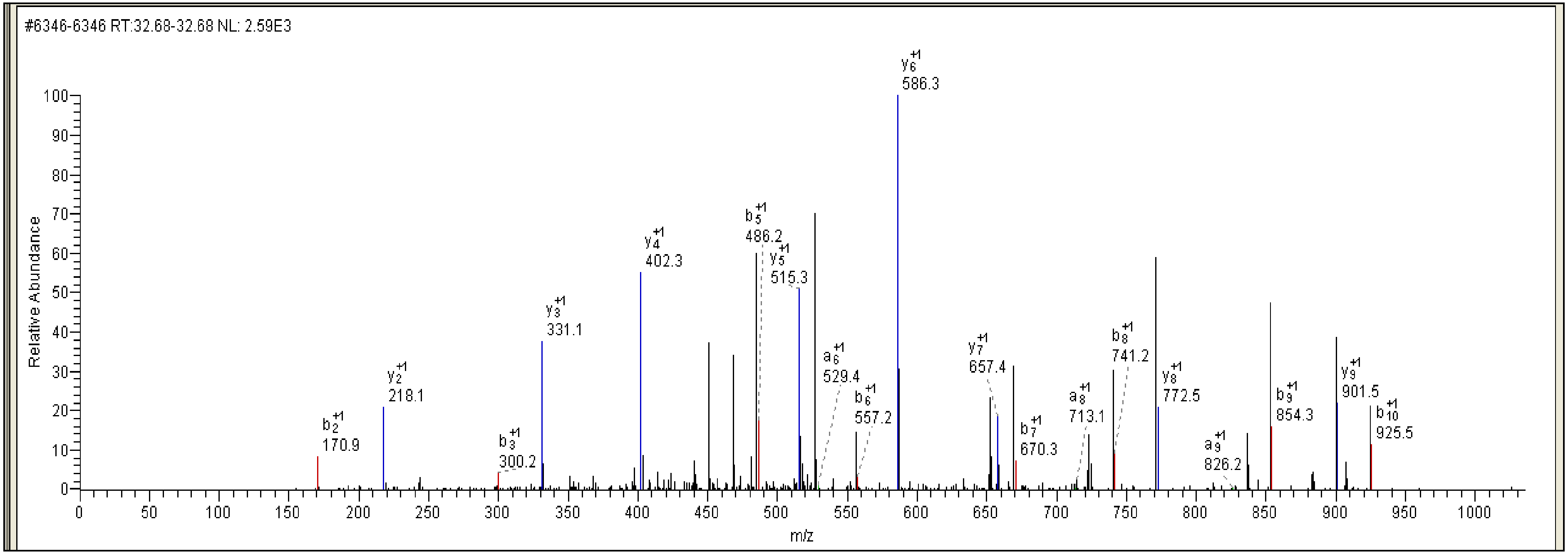


TwdlJ NP_651489.1 CG5471 CG5471-PA

R.GLEDAALALAK.Q

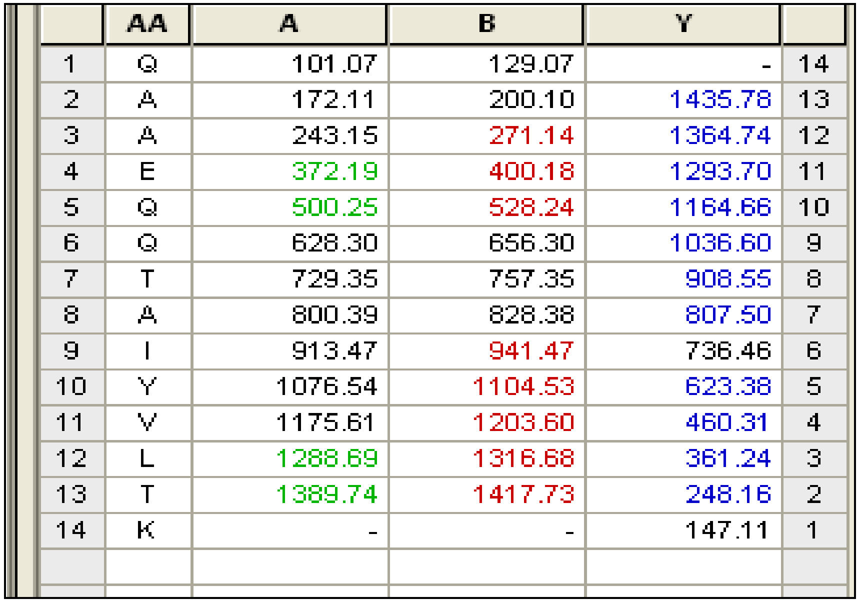


	AA	A	B	Y	
1	G	30.03	58.03	-	11
2	L	143.12	171.11	1014.58	10
3	E	272.16	300.16	901.50	9
4	D	387.19	415.18	772.46	8
5	A	458.22	486.22	657.43	7
6	A	529.26	557.26	586.39	6
7	L	642.35	670.34	515.36	5
8	A	713.38	741.38	402.27	4
9	L	826.47	854.46	331.23	3
10	A	897.50	925.50	218.15	2
11	K	-	-	147.11	1

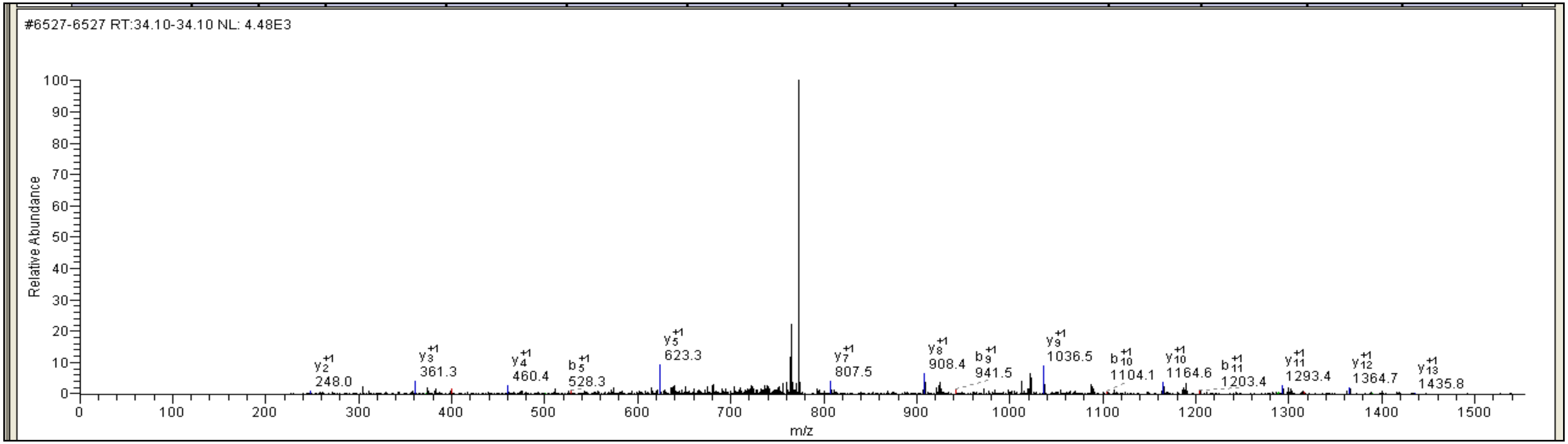


Tb NP_651494.1 CG5480 CG5480-PA

K.QAAEQQTAIYVLTK.Q

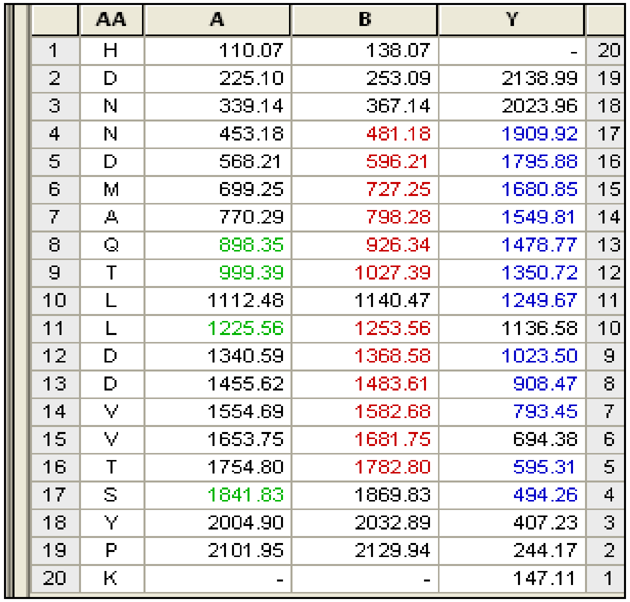


	AA	A	B	Y	
1	Q	101.07	129.07	-	14
2	A	172.11	200.10	1435.78	13
3	A	243.15	271.14	1364.74	12
4	E	372.19	400.18	1293.70	11
5	Q	500.25	528.24	1164.66	10
6	Q	628.30	656.30	1036.60	9
7	T	729.35	757.35	908.55	8
8	A	800.39	828.38	807.50	7
9	I	913.47	941.47	736.46	6
10	Y	1076.54	1104.53	623.38	5
11	V	1175.61	1203.60	460.31	4
12	L	1288.69	1316.68	361.24	3
13	T	1389.74	1417.73	248.16	2
14	K	-	-	147.11	1

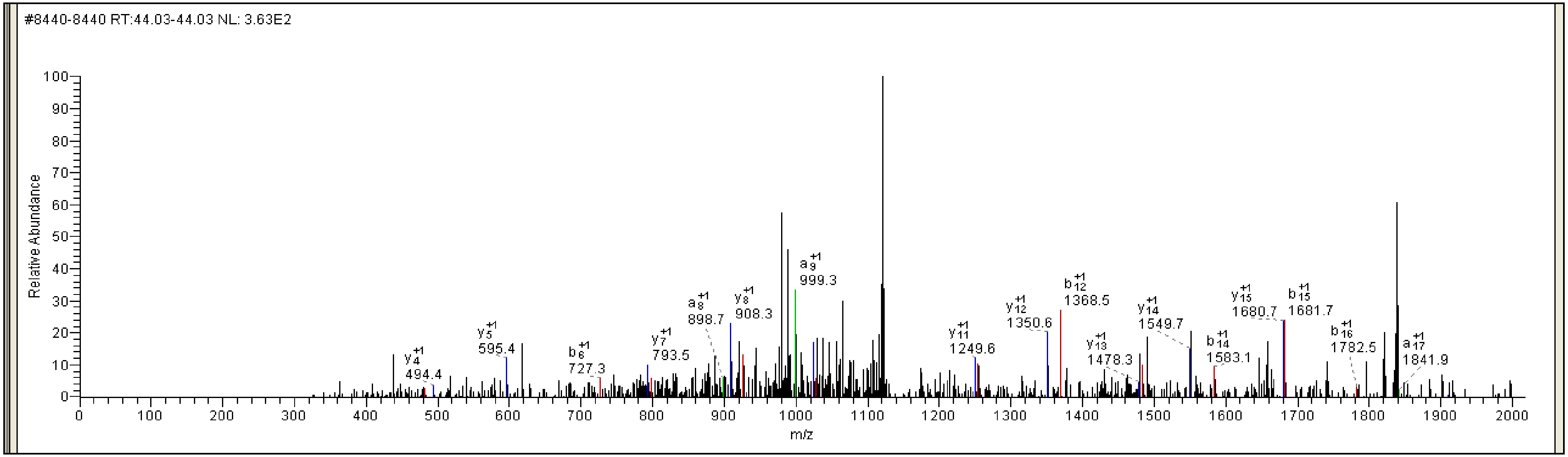


CG5728 NP_651245.1 CG5728 CG5728-PA

K.HDNNDMAQTLLDDVVTSYPK.R

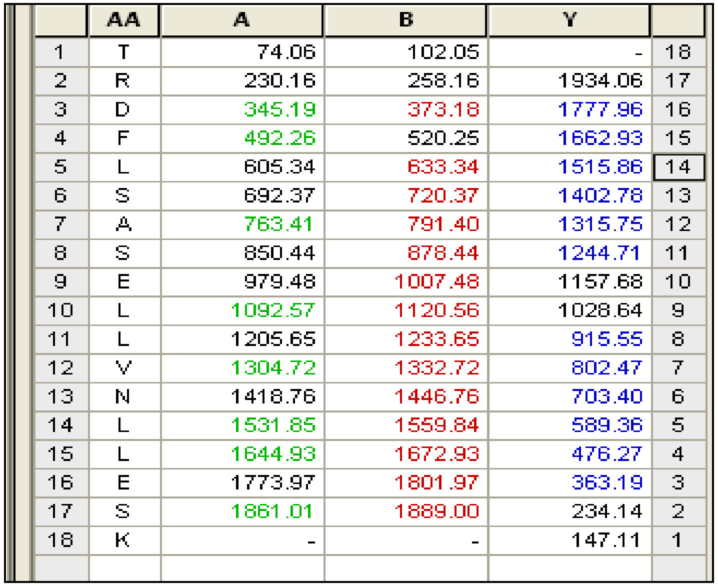


	AA	A	B	Y	
1	H	110.07	138.07	-	20
2	D	225.10	253.09	2138.99	19
3	N	339.14	367.14	2023.96	18
4	N	453.18	481.18	1909.92	17
5	D	568.21	596.21	1795.88	16
6	M	699.25	727.25	1680.85	15
7	A	770.29	798.28	1549.81	14
8	Q	898.35	926.34	1478.77	13
9	T	999.39	1027.39	1350.72	12
10	L	1112.48	1140.47	1249.67	11
11	L	1225.56	1253.56	1136.58	10
12	D	1340.59	1368.58	1023.50	9
13	D	1455.62	1483.61	908.47	8
14	V	1554.69	1582.68	793.45	7
15	V	1653.75	1681.75	694.38	6
16	T	1754.80	1782.80	595.31	5
17	S	1841.83	1869.83	494.26	4
18	Y	2004.90	2032.89	407.23	3
19	P	2101.95	2129.94	244.17	2
20	K	-	-	147.11	1

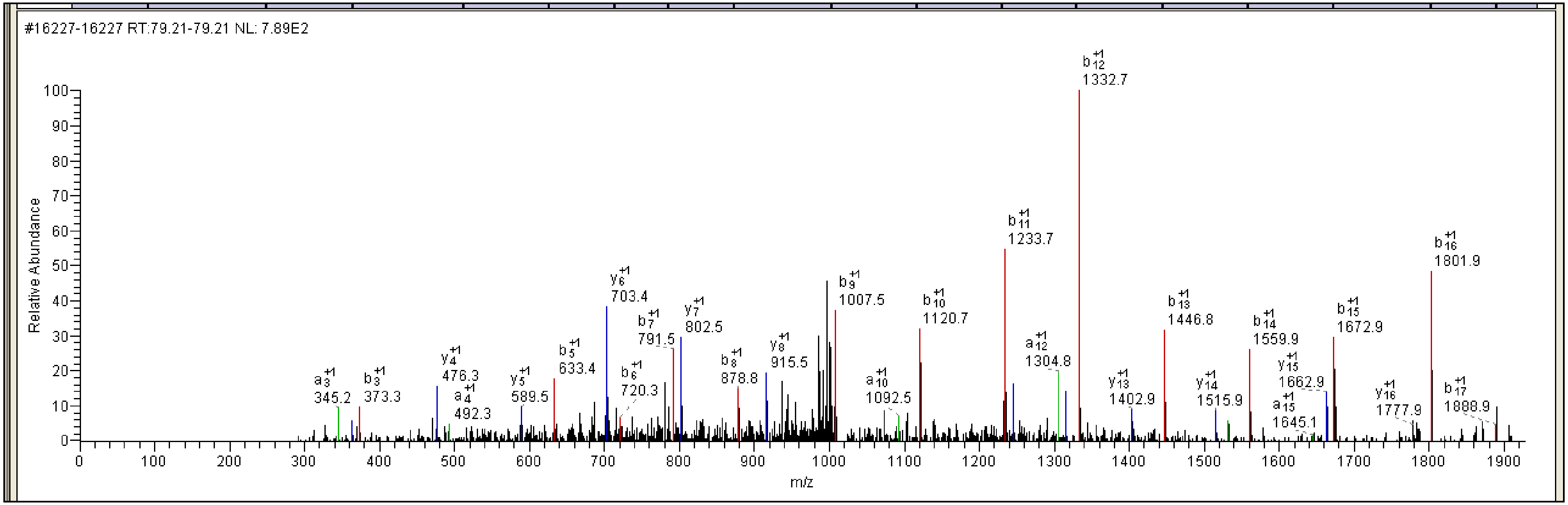


Nup75 NP_611300.2 CG5733 CG5733-PA

R.TRDFLSASELLVNLLESK.I

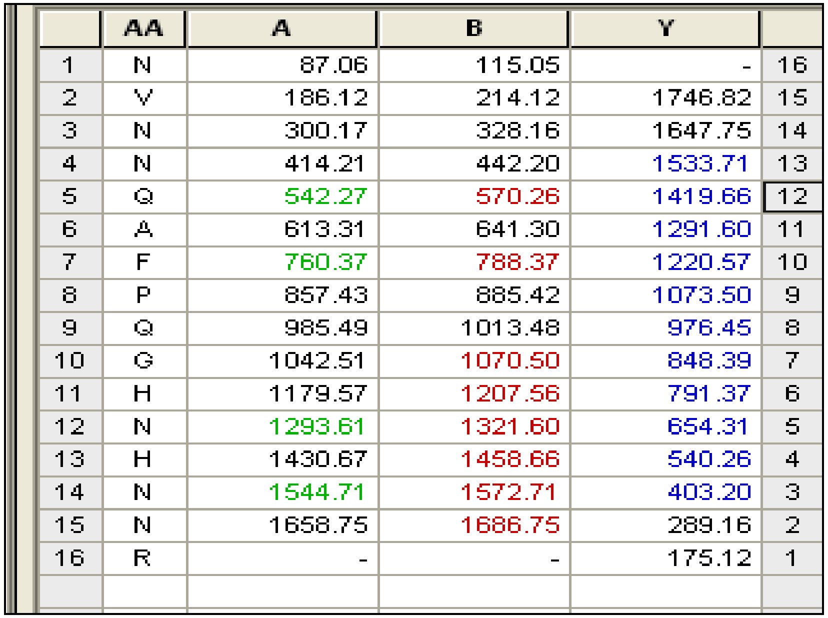


	AA	A	B	Y	
1	T	74.06	102.05	-	18
2	R	230.16	258.16	1934.06	17
3	D	345.19	373.18	1777.96	16
4	F	492.26	520.25	1662.93	15
5	L	605.34	633.34	1515.86	14
6	S	692.37	720.37	1402.78	13
7	A	763.41	791.40	1315.75	12
8	S	850.44	878.44	1244.71	11
9	E	979.48	1007.48	1157.68	10
10	L	1092.57	1120.56	1028.64	9
11	L	1205.65	1233.65	915.55	8
12	V	1304.72	1332.72	802.47	7
13	N	1418.76	1446.76	703.40	6
14	L	1531.85	1559.84	589.36	5
15	L	1644.93	1672.93	476.27	4
16	E	1773.97	1801.97	363.19	3
17	S	1861.01	1889.00	234.14	2
18	K	-	-	147.11	1

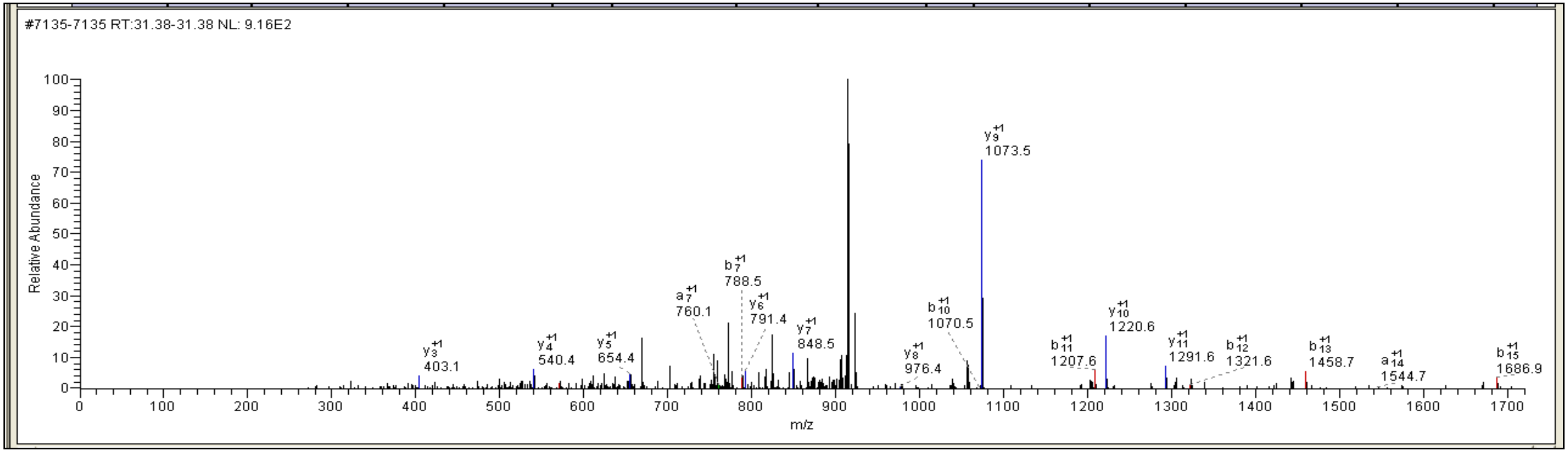


CG5792 NP_723771.2 CG5792 CG5792-PB

R.NVNNQAFPQGHNHNNR.N

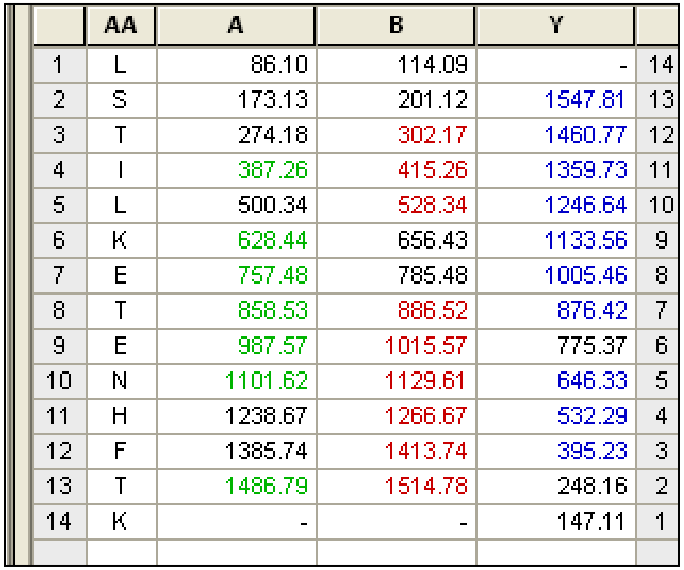


	AA	A	B	Y	
1	N	87.06	115.05	-	16
2	V	186.12	214.12	1746.82	15
3	N	300.17	328.16	1647.75	14
4	N	414.21	442.20	1533.71	13
5	Q	542.27	570.26	1419.66	12
6	A	613.31	641.30	1291.60	11
7	F	760.37	788.37	1220.57	10
8	P	857.43	885.42	1073.50	9
9	Q	985.49	1013.48	976.45	8
10	G	1042.51	1070.50	848.39	7
11	H	1179.57	1207.56	791.37	6
12	N	1293.61	1321.60	654.31	5
13	H	1430.67	1458.66	540.26	4
14	N	1544.71	1572.71	403.20	3
15	N	1658.75	1686.75	289.16	2
16	R	-	-	175.12	1

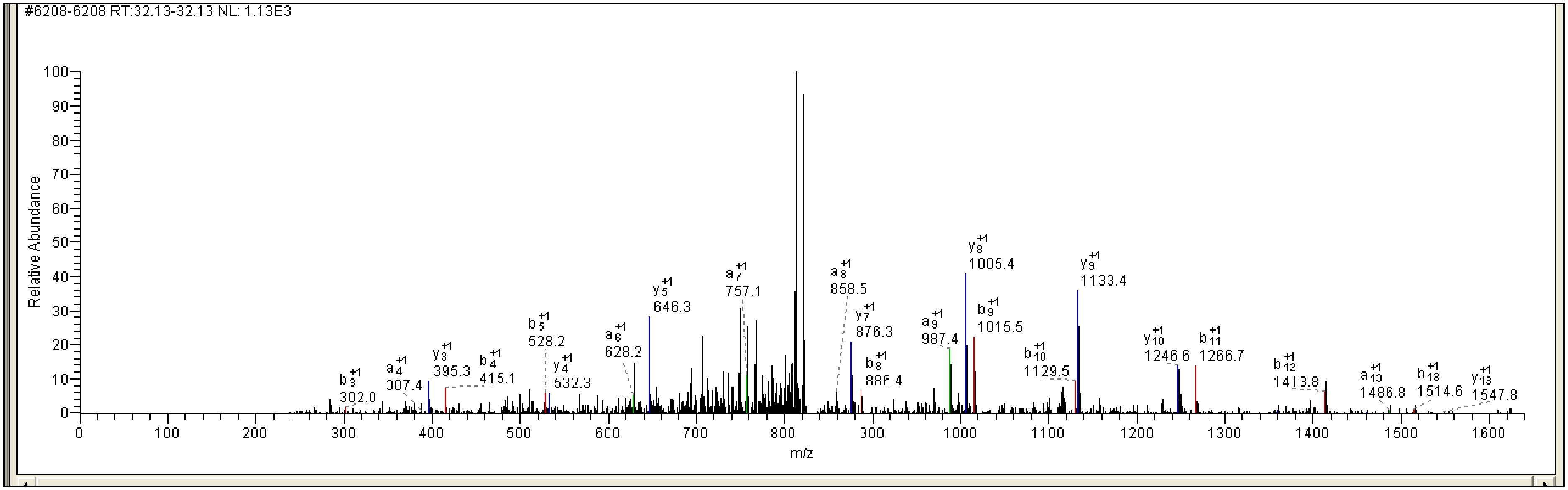


CG6129 NP_651216.2 CG6129 CG6129-PB

R.LSTILKETENHFTK.T

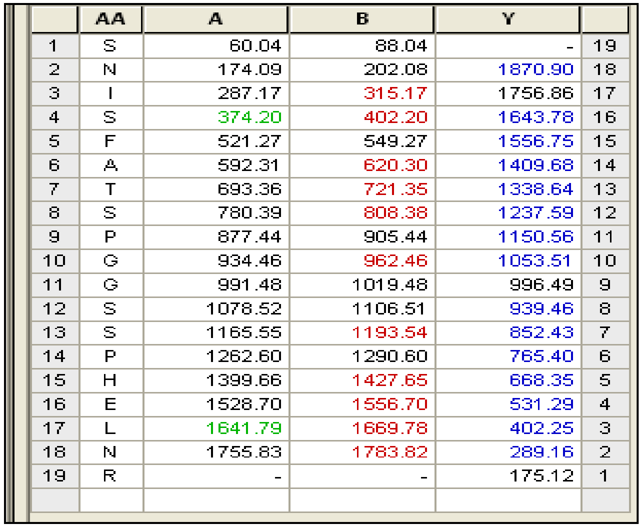


	AA	A	B	Y	
1	L	86.10	114.09	-	14
2	S	173.13	201.12	1547.81	13
3	T	274.18	302.17	1460.77	12
4	I	387.26	415.26	1359.73	11
5	L	500.34	528.34	1246.64	10
6	K	628.44	656.43	1133.56	9
7	E	757.48	785.48	1005.46	8
8	T	858.53	886.52	876.42	7
9	E	987.57	1015.57	775.37	6
10	N	1101.62	1129.61	646.33	5
11	H	1238.67	1266.67	532.29	4
12	F	1385.74	1413.74	395.23	3
13	T	1486.79	1514.78	248.16	2
14	K	-	-	147.11	1

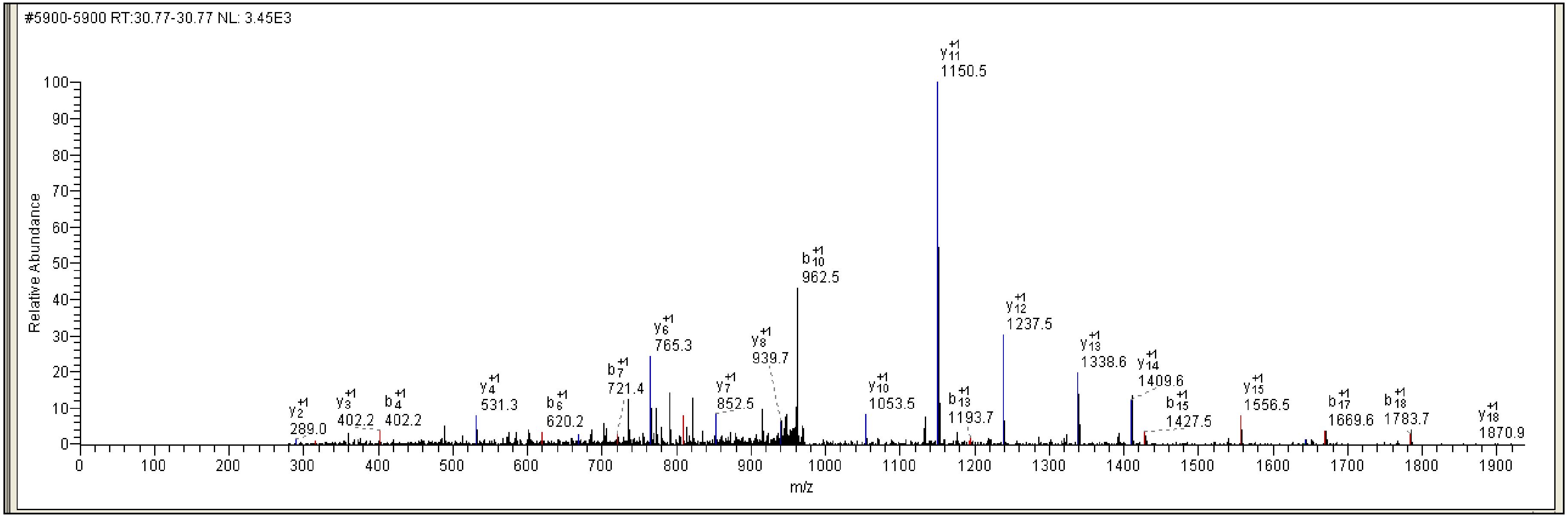


CG6540 NP_573314.1 CG6540 CG6540-PA

R.SNISFATSPGGSSPHELNR.S

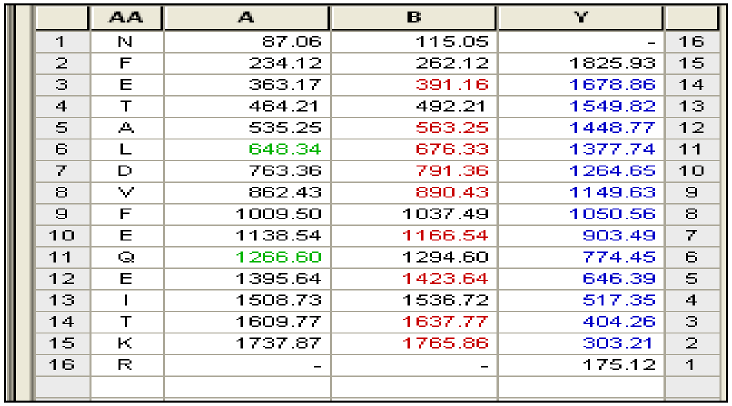


	AA	A	B	Y	
1	S	60.04	88.04	-	19
2	N	174.09	202.08	1870.90	18
3	I	287.17	315.17	1756.86	17
4	S	374.20	402.20	1643.78	16
5	F	521.27	549.27	1556.75	15
6	A	592.31	620.30	1409.68	14
7	T	693.36	721.35	1338.64	13
8	S	780.39	808.38	1237.59	12
9	P	877.44	905.44	1150.56	11
10	G	934.46	962.46	1053.51	10
11	G	991.48	1019.48	996.49	9
12	S	1078.52	1106.51	939.46	8
13	S	1165.55	1193.54	852.43	7
14	P	1262.60	1290.60	765.40	6
15	H	1399.66	1427.65	668.35	5
16	E	1528.70	1556.70	531.29	4
17	L	1641.79	1669.78	402.25	3
18	N	1755.83	1783.82	289.16	2
19	R	-	-	175.12	1

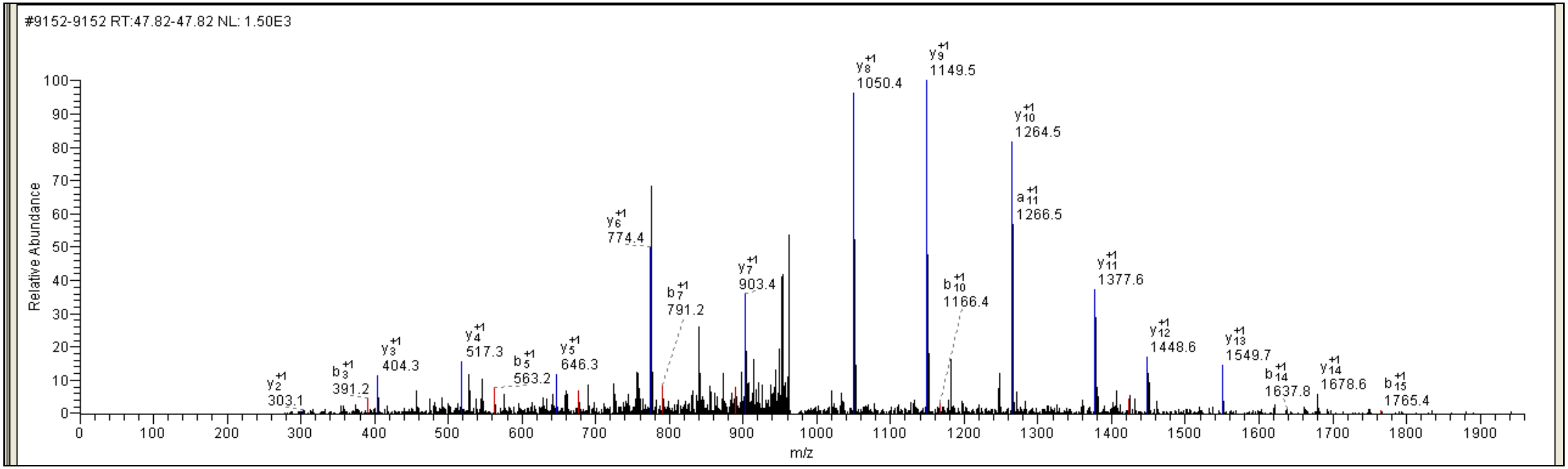


NP_648236.1 CG6673 CG6673-PB

K.NFETALDVFEQEITKR.G

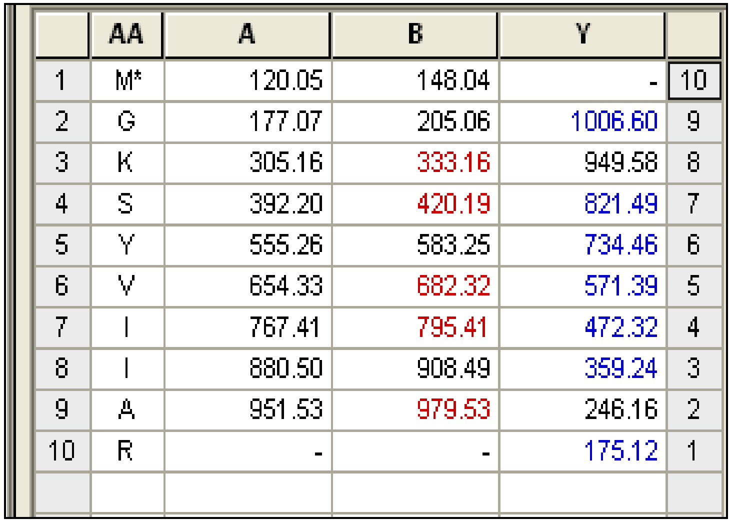


	AA	A	B	Y	
1	N	87.06	115.05	-	16
2	F	234.12	262.12	1825.93	15
3	E	363.17	391.16	1678.86	14
4	T	464.21	492.21	1549.82	13
5	A	535.25	563.25	1448.77	12
6	L	648.34	676.33	1377.74	11
7	D	763.36	791.36	1264.65	10
8	V	862.43	890.43	1149.63	9
9	F	1009.50	1037.49	1050.56	8
10	E	1138.54	1166.54	903.49	7
11	Q	1266.60	1294.60	774.45	6
12	E	1395.64	1423.64	646.39	5
13	I	1508.73	1536.72	517.35	4
14	T	1609.77	1637.77	404.26	3
15	K	1737.87	1765.86	303.21	2
16	R	-	-	175.12	1

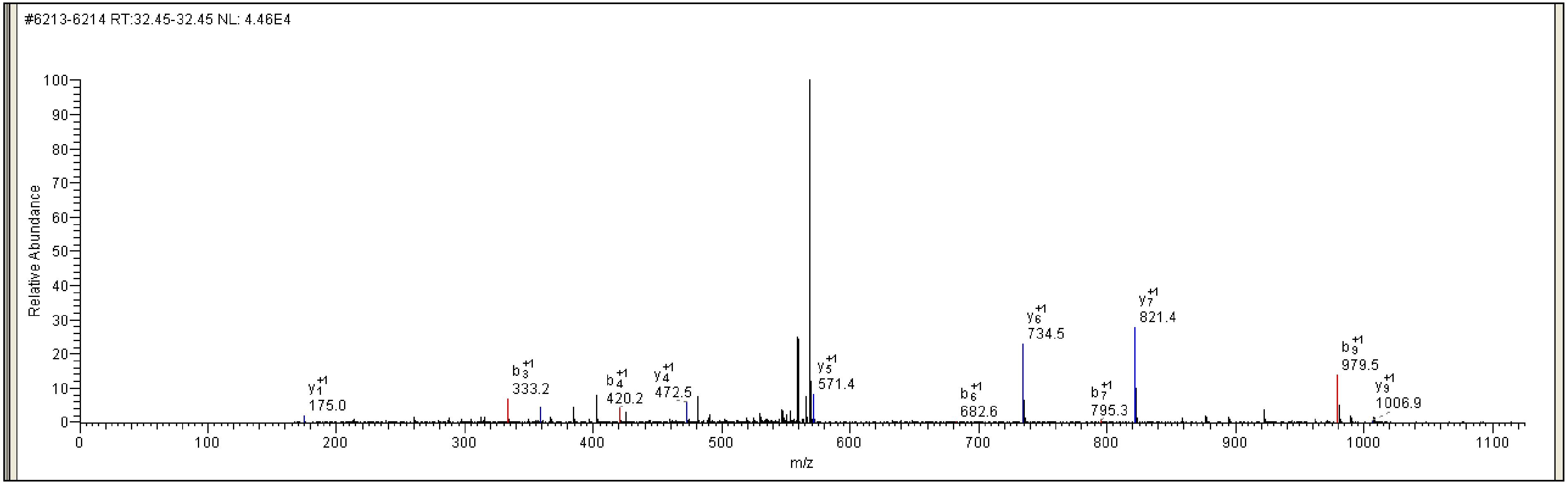


CG6766 NP_609537.1 CG6766 CG6766-PA

-.MGKSYVIIAR.I

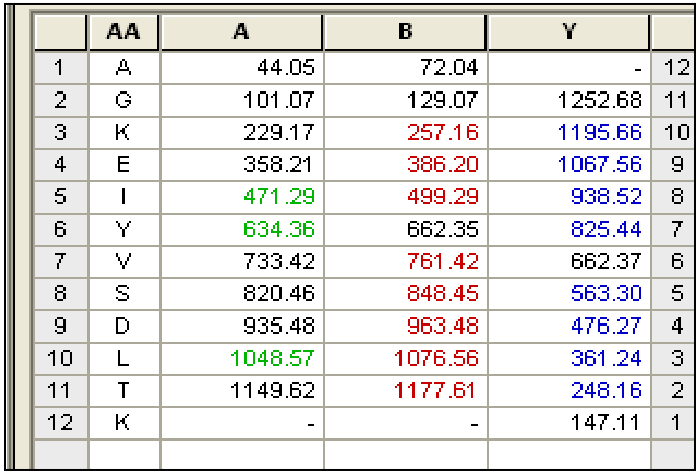


	AA	A	B	Y	
1	M*	120.05	148.04	-	10
2	G	177.07	205.06	1006.60	9
3	K	305.16	333.16	949.58	8
4	S	392.20	420.19	821.49	7
5	Y	555.26	583.25	734.46	6
6	V	654.33	682.32	571.39	5
7	I	767.41	795.41	472.32	4
8	I	880.50	908.49	359.24	3
9	A	951.53	979.53	246.16	2
10	R	-	-	175.12	1

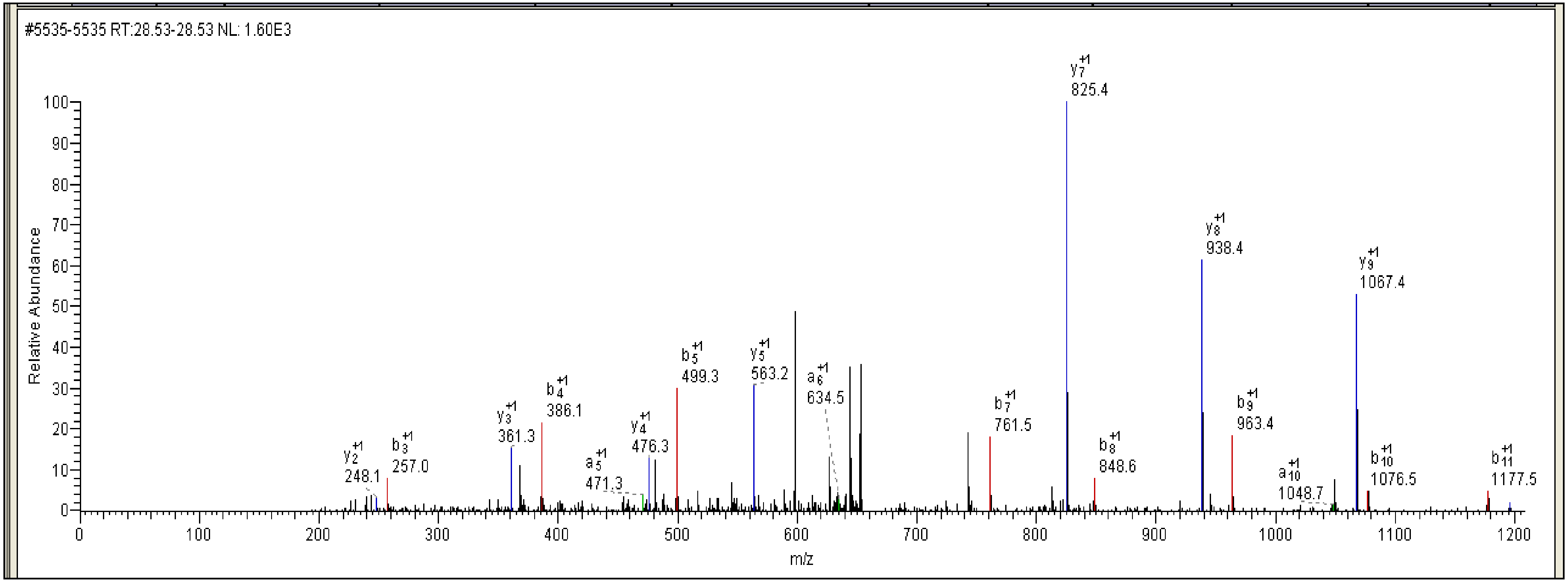


CG6937 NP_651066.2 CG6937 CG6937-PA

K.AGKEIYVSDLTK.A

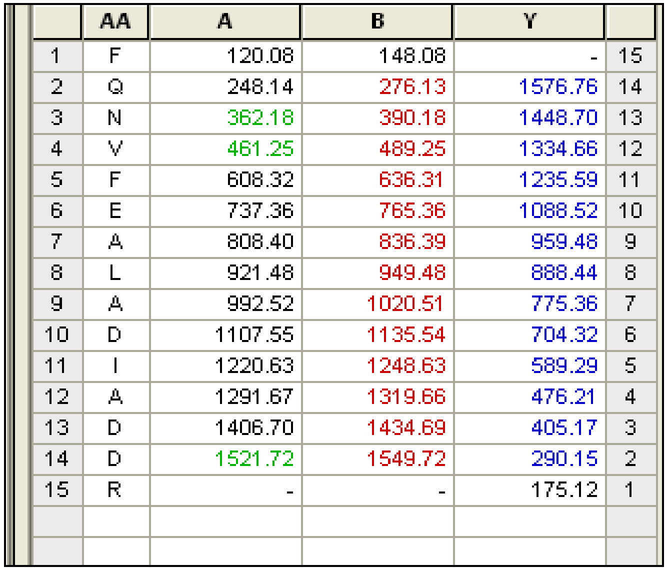


	AA	A	B	Y	
1	A	44.05	72.04	-	12
2	G	101.07	129.07	1252.68	11
3	K	229.17	257.16	1195.66	10
4	E	358.21	386.20	1067.56	9
5	I	471.29	499.29	938.52	8
6	Y	634.36	662.35	825.44	7
7	V	733.42	761.42	662.37	6
8	S	820.46	848.45	563.30	5
9	D	935.48	963.48	476.27	4
10	L	1048.57	1076.56	361.24	3
11	T	1149.62	1177.61	248.16	2
12	K	-	-	147.11	1

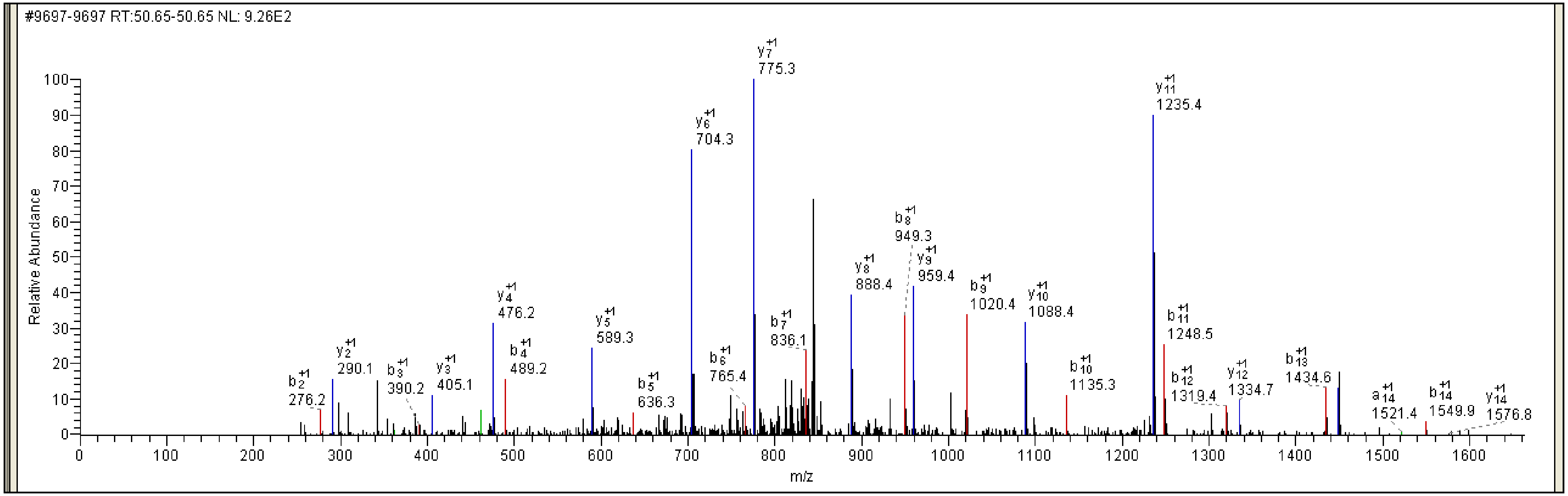


Nup133 NP_651080.2 CG6958 CG6958-PA

R.FQNVFEALADIADDR.I

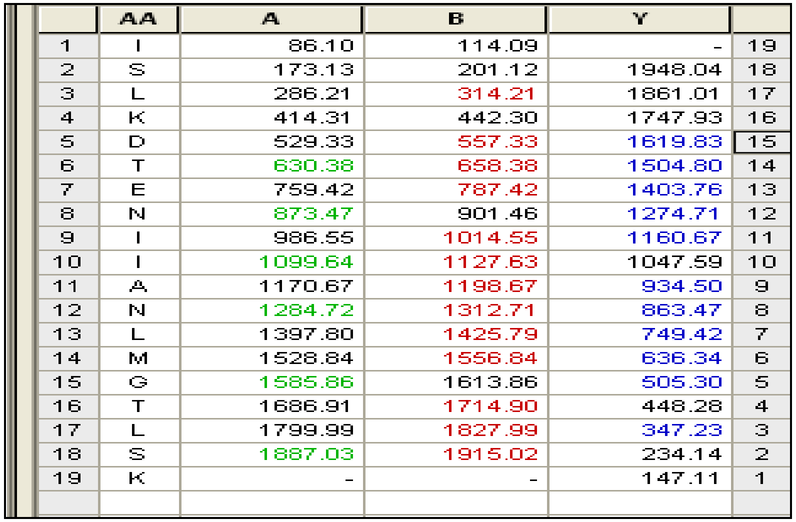


	AA	A	B	Y	
1	F	120.08	148.08	-	15
2	Q	248.14	276.13	1576.76	14
3	N	362.18	390.18	1448.70	13
4	V	461.25	489.25	1334.66	12
5	F	608.32	636.31	1235.59	11
6	E	737.36	765.36	1088.52	10
7	A	808.40	836.39	959.48	9
8	L	921.48	949.48	888.44	8
9	A	992.52	1020.51	775.36	7
10	D	1107.55	1135.54	704.32	6
11	I	1220.63	1248.63	589.29	5
12	A	1291.67	1319.66	476.21	4
13	D	1406.70	1434.69	405.17	3
14	D	1521.72	1549.72	290.15	2
15	R	-	-	175.12	1

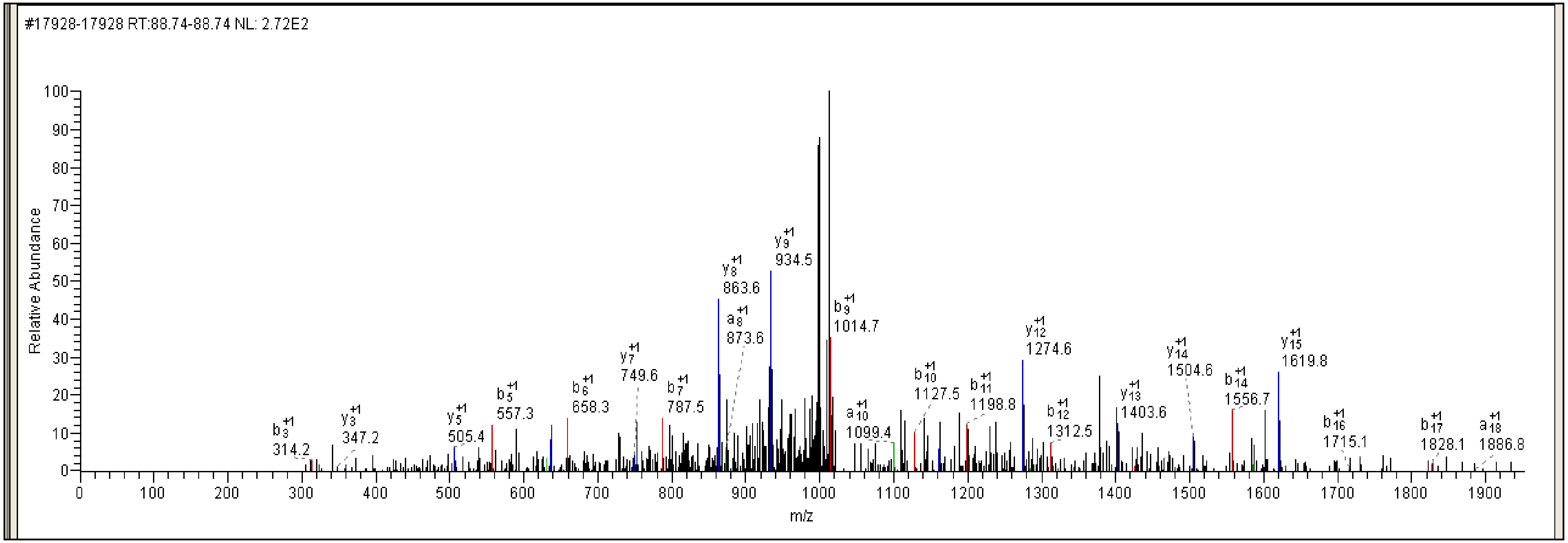


CG7065 NP_572529.2 CG7065 CG7065-PA

K.ISLKDTENIIANLMGTLSK.N

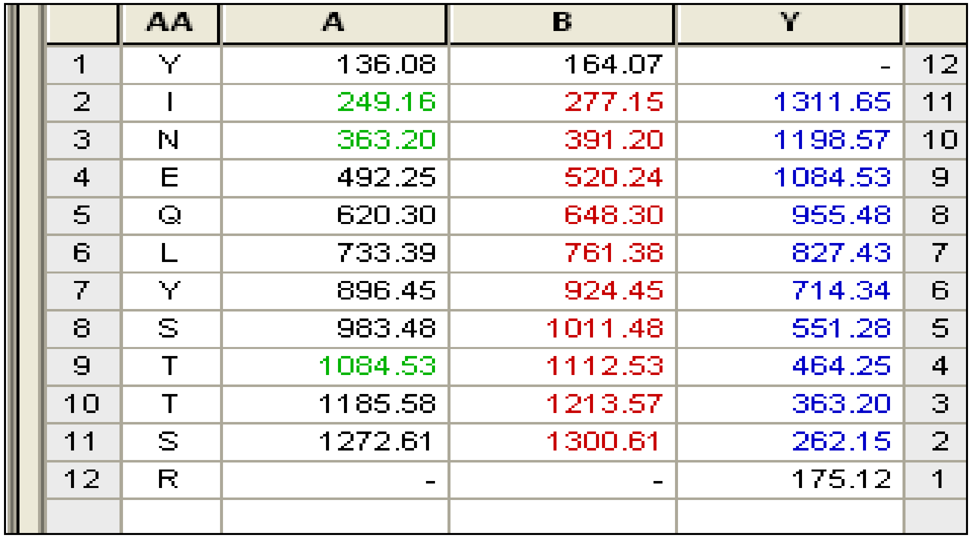


	AA	A	B	Y	
1	I	86.10	114.09	-	19
2	S	173.13	201.12	1948.04	18
3	L	286.21	314.21	1861.01	17
4	K	414.31	442.30	1747.93	16
5	D	529.33	557.33	1619.83	15
6	T	630.38	658.38	1504.80	14
7	E	759.42	787.42	1403.76	13
8	N	873.47	901.46	1274.71	12
9	I	986.55	1014.55	1160.67	11
10	I	1099.64	1127.63	1047.59	10
11	A	1170.67	1198.67	934.50	9
12	N	1284.72	1312.71	863.47	8
13	L	1397.80	1425.79	749.42	7
14	M	1528.84	1556.84	636.34	6
15	G	1585.86	1613.86	505.30	5
16	T	1686.91	1714.90	448.28	4
17	L	1799.99	1827.99	347.23	3
18	S	1887.03	1915.02	234.14	2
19	K	-	-	147.11	1

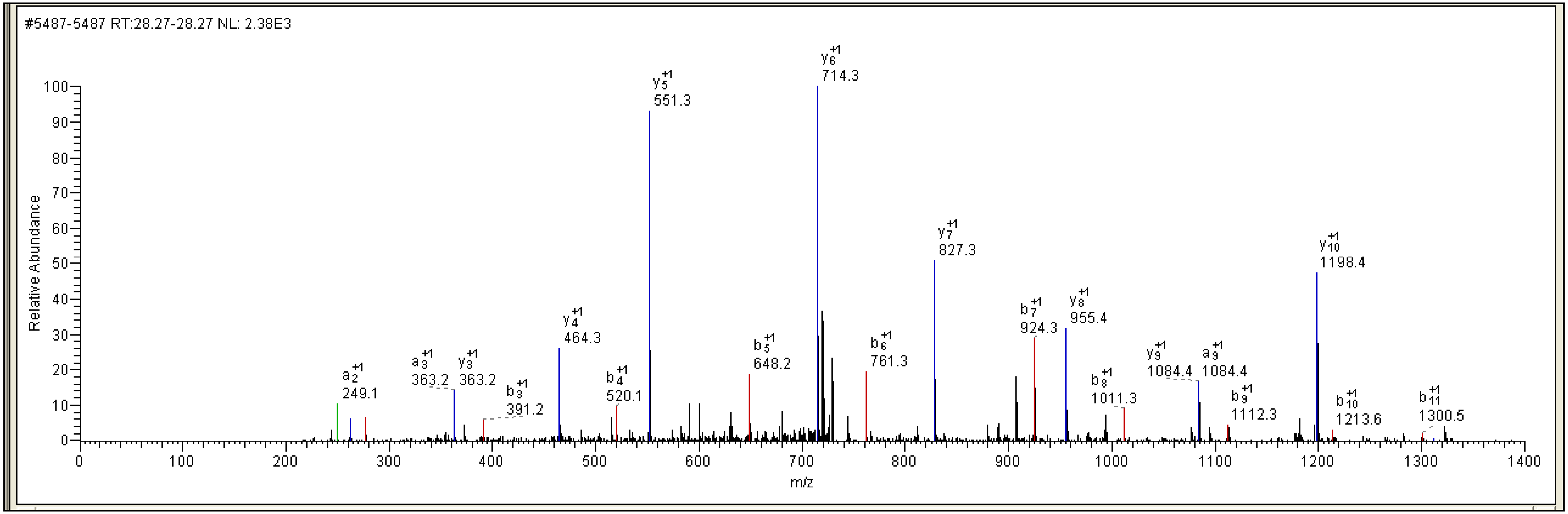


CG7137 NP_611400.1 CG7137 CG7137-PA

R.YINEQLYSTTSR.K



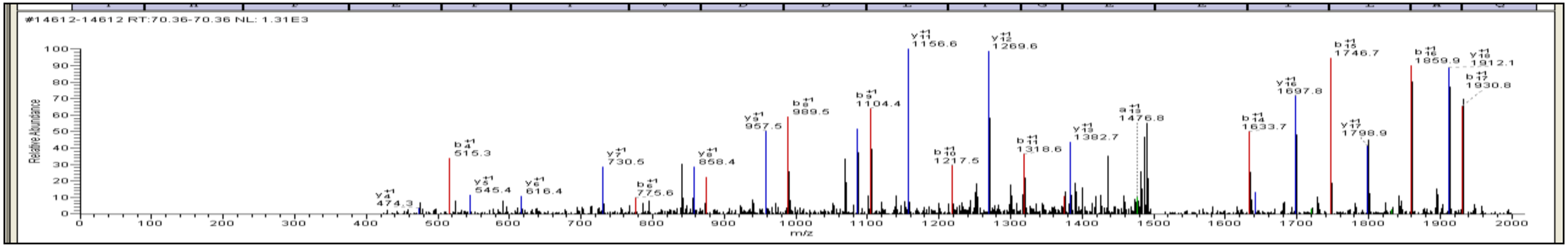
	AA	A	B	Y	
1	Y	136.08	164.07	-	12
2	I	249.16	277.15	1311.65	11
3	N	363.20	391.20	1198.57	10
4	E	492.25	520.24	1084.53	9
5	Q	620.30	648.30	955.48	8
6	L	733.39	761.38	827.43	7
7	Y	896.45	924.45	714.34	6
8	S	983.48	1011.48	551.28	5
9	T	1084.53	1112.53	464.25	4
10	T	1185.58	1213.57	363.20	3
11	S	1272.61	1300.61	262.15	2
12	R	-	-	175.12	1



CG7154 NP_609148.1 CG7154 CG7154-PA

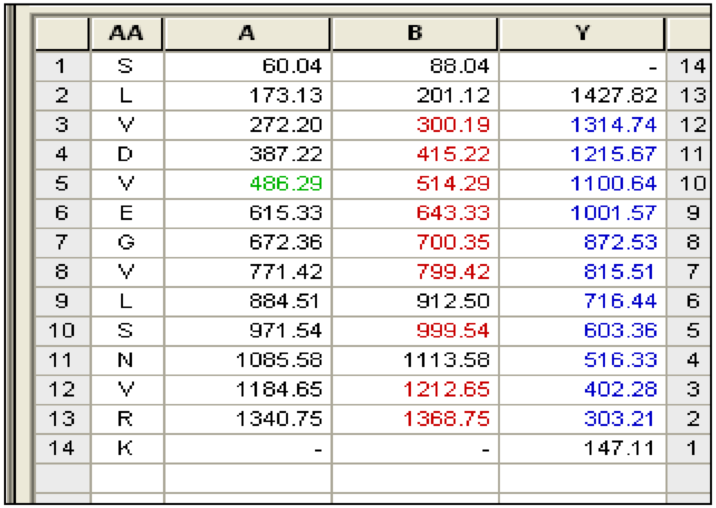
K.THFEPYVDDLTGEEILAQVQNAAQQAK.Q

S no	AA	A	B	Y	
1	T	74.06	102.05	-	27
2	H	211.12	239.11	2914.42	26
3	F	358.19	386.18	2777.36	25
4	E	487.23	515.22	2630.29	24
5	P	584.28	612.28	2501.25	23
6	Y	747.35	775.34	2404.2	22
7	V	846.41	874.41	2241.14	21
8	D	961.44	989.44	2142.07	20
9	D	1076.47	1104.46	2027.04	19
10	L	1189.55	1217.55	1912.01	18
11	T	1290.6	1318.6	1798.93	17
12	G	1347.62	1375.62	1697.88	16
13	E	1476.66	1504.66	1640.86	15
14	E	1605.71	1633.7	1511.82	14
15	I	1718.79	1746.79	1382.78	13
16	L	1831.87	1859.87	1269.69	12
17	A	1902.91	1930.91	1156.61	11
18	Q	2030.97	2058.97	1085.57	10
19	V	2130.04	2158.03	957.51	9
20	Q	2258.1	2286.09	858.44	8
21	N	2372.14	2400.14	730.38	7
22	A	2443.18	2471.17	616.34	6
23	A	2514.21	2542.21	545.3	5
24	Q	2642.27	2670.27	474.27	4
25	Q	2770.33	2798.33	346.21	3
26	A	2841.37	2869.36	218.15	2
27	K	-	-	147.11	1

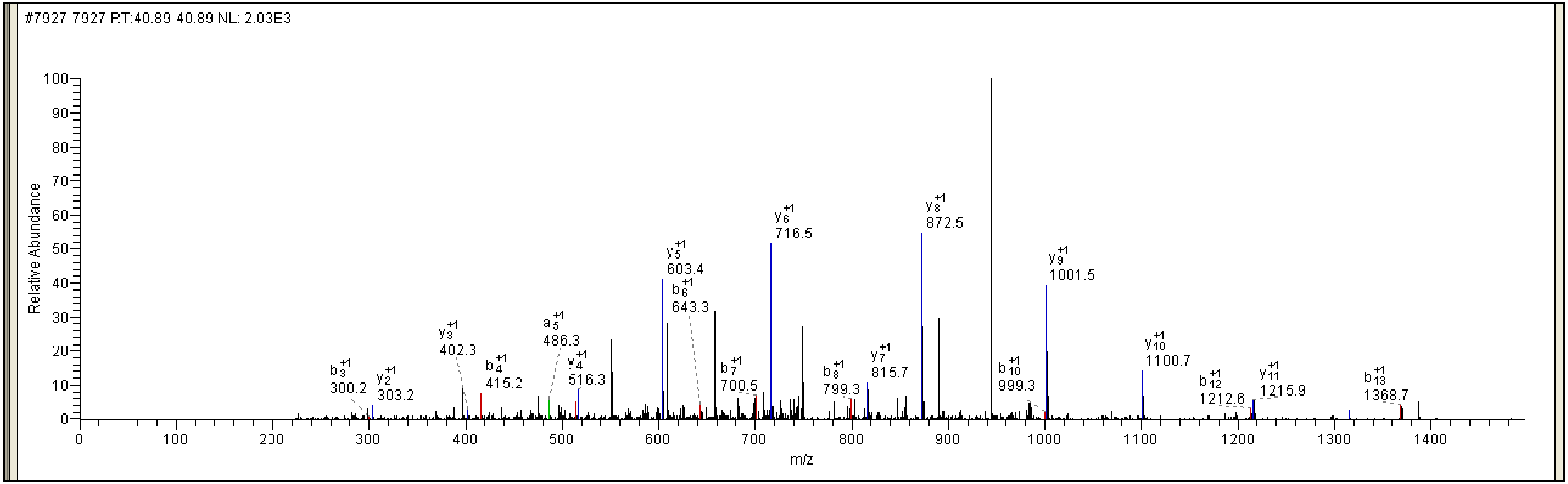


CG7671 NP_650716.2 CG7671 CG7671-PA

R.SLVDVEGVLSNVRK.S

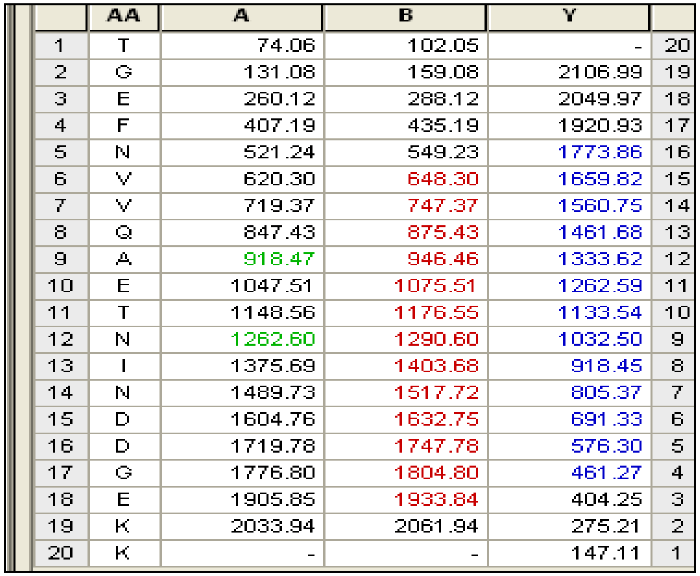


	AA	A	B	Y	
1	S	60.04	88.04	-	14
2	L	173.13	201.12	1427.82	13
3	V	272.20	300.19	1314.74	12
4	D	387.22	415.22	1215.67	11
5	V	486.29	514.29	1100.64	10
6	E	615.33	643.33	1001.57	9
7	G	672.36	700.35	872.53	8
8	V	771.42	799.42	815.51	7
9	L	884.51	912.50	716.44	6
10	S	971.54	999.54	603.36	5
11	N	1085.58	1113.58	516.33	4
12	V	1184.65	1212.65	402.28	3
13	R	1340.75	1368.75	303.21	2
14	K	-	-	147.11	1

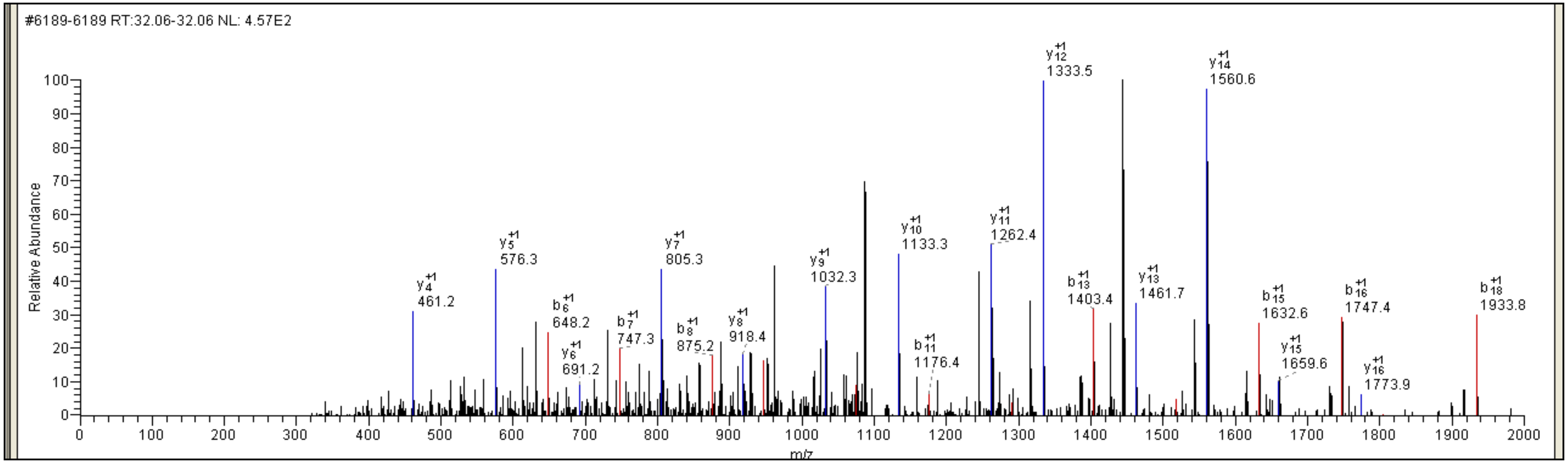


NP_651760.1 CG7911 CG7911-PA

K.TGEFNVVQAETNINDDGEKK.T

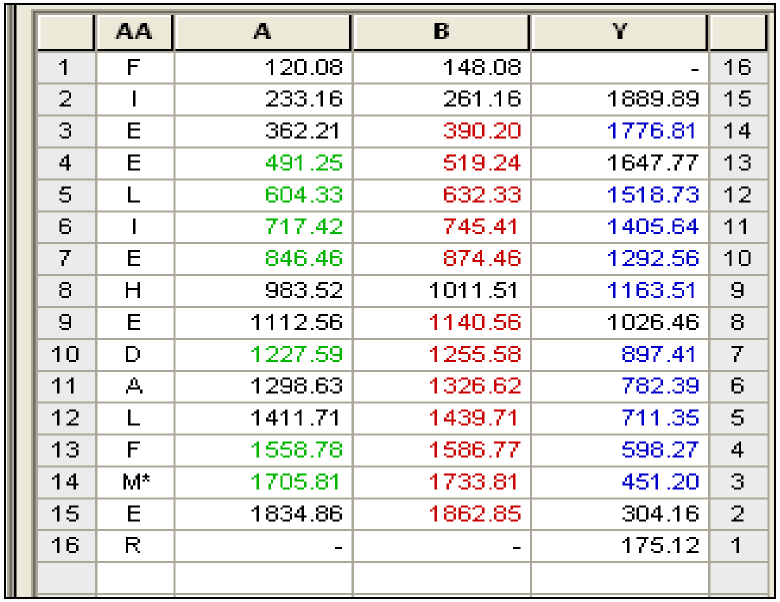


	AA	A	B	Y	
1	T	74.06	102.05	-	20
2	G	131.08	159.08	2106.99	19
3	E	260.12	288.12	2049.97	18
4	F	407.19	435.19	1920.93	17
5	N	521.24	549.23	1773.86	16
6	V	620.30	648.30	1659.82	15
7	V	719.37	747.37	1560.75	14
8	Q	847.43	875.43	1461.68	13
9	A	918.47	946.46	1333.62	12
10	E	1047.51	1075.51	1262.59	11
11	T	1148.56	1176.55	1133.54	10
12	N	1262.60	1290.60	1032.50	9
13	I	1375.69	1403.68	918.45	8
14	N	1489.73	1517.72	805.37	7
15	D	1604.76	1632.75	691.33	6
16	D	1719.78	1747.78	576.30	5
17	G	1776.80	1804.80	461.27	4
18	E	1905.85	1933.84	404.25	3
19	K	2033.94	2061.94	275.21	2
20	K	-	-	147.11	1

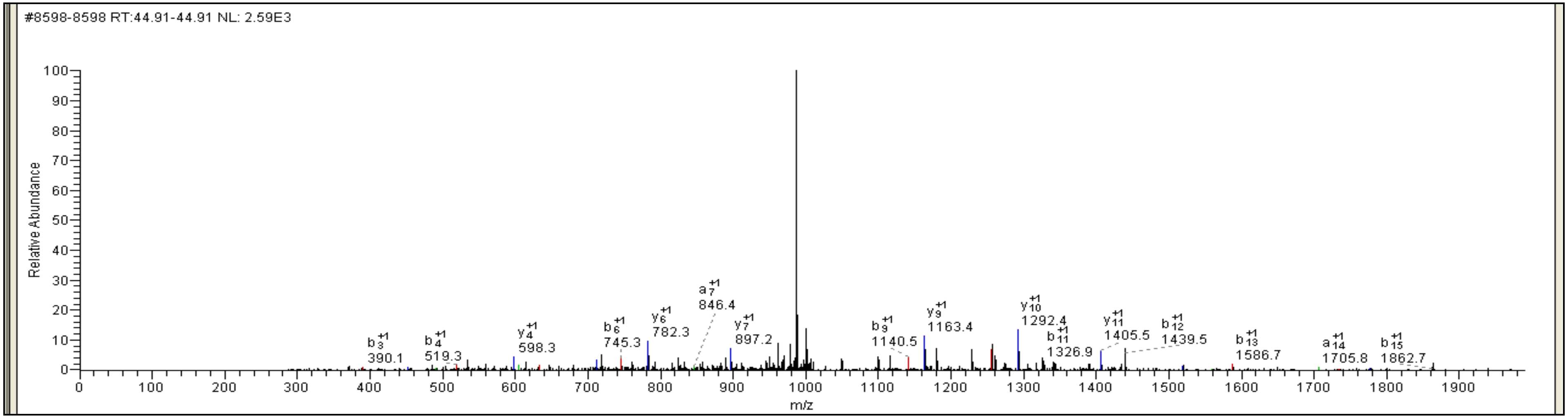


NP_651768.1CG7946 CG7946-PA

R.FIEELIEHEDALFMER.D



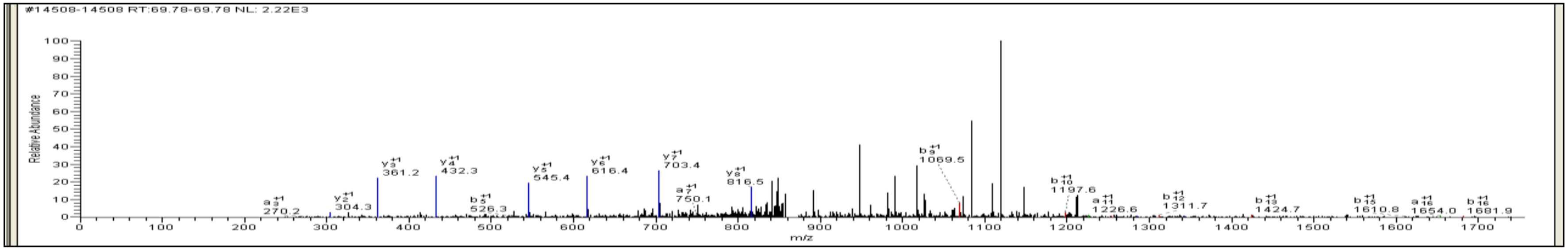
	AA	A	B	Y	
1	F	120.08	148.08	-	16
2	I	233.16	261.16	1889.89	15
3	E	362.21	390.20	1776.81	14
4	E	491.25	519.24	1647.77	13
5	L	604.33	632.33	1518.73	12
6	I	717.42	745.41	1405.64	11
7	E	846.46	874.46	1292.56	10
8	H	983.52	1011.51	1163.51	9
9	E	1112.56	1140.56	1026.46	8
10	D	1227.59	1255.58	897.41	7
11	A	1298.63	1326.62	782.39	6
12	L	1411.71	1439.71	711.35	5
13	F	1558.78	1586.77	598.27	4
14	M*	1705.81	1733.81	451.20	3
15	E	1834.86	1862.85	304.16	2
16	R	-	-	175.12	1



CG8036 NP_649812.2 CG8036 CG8036-PB

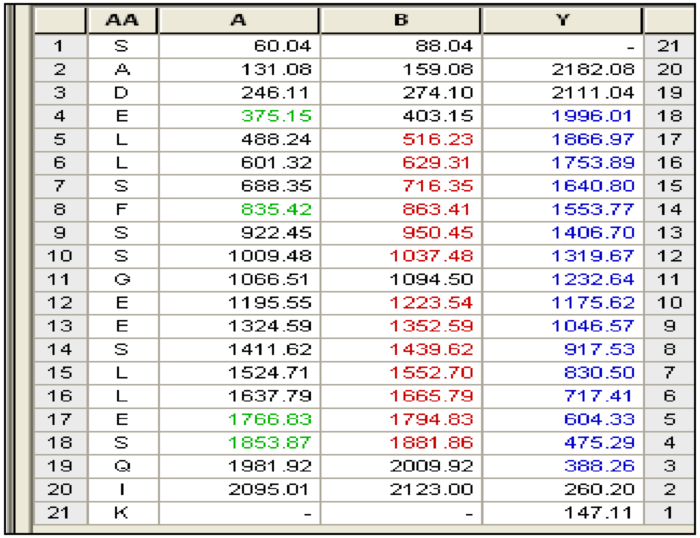
R.VVVVEDHYQQGGLGEAVLSALAGER.N

S no	AA	A	B	Y	
1	V	72.08	100.08	-	25
2	V	171.15	199.14	2497.27	24
3	V	270.22	298.21	2398.2	23
4	V	369.29	397.28	2299.13	22
5	E	498.33	526.32	2200.06	21
6	D	613.36	641.35	2071.02	20
7	H	750.41	778.41	1955.99	19
8	Y	913.48	941.47	1818.93	18
9	Q	1041.54	1069.53	1655.87	17
10	Q	1169.59	1197.59	1527.81	16
11	G	1226.62	1254.61	1399.75	15
12	G	1283.64	1311.63	1342.73	14
13	L	1396.72	1424.72	1285.71	13
14	G	1453.74	1481.74	1172.63	12
15	E	1582.79	1610.78	1115.61	11
16	A	1653.82	1681.82	986.56	10
17	V	1752.89	1780.89	915.53	9
18	L	1865.98	1893.97	816.46	8
19	S	1953.01	1981	703.37	7
20	A	2024.04	2052.04	616.34	6
21	L	2137.13	2165.12	545.3	5
22	A	2208.17	2236.16	432.22	4
23	G	2265.19	2293.18	361.18	3
24	E	2394.23	2422.22	304.16	2
25	R	-	-	175.12	1

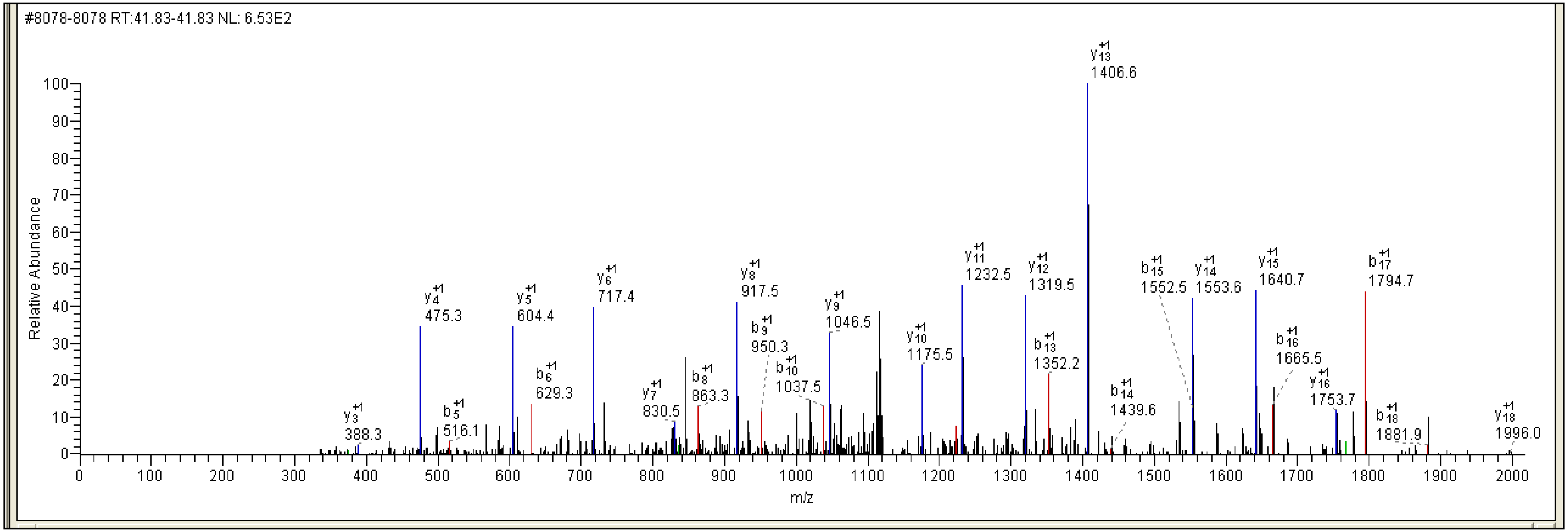


CG8258 NP_610418.1 CG8258 CG8258-PA

K.SADELLSFSSGEESLLESQIK.A



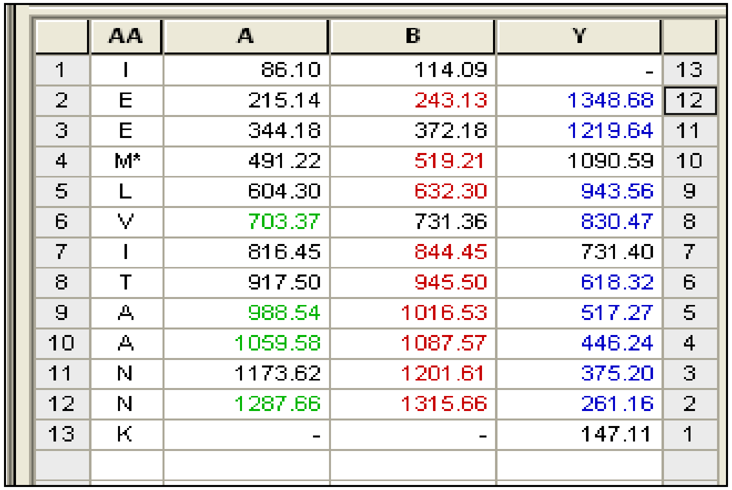
	AA	A	B	Y	
1	S	60.04	88.04	-	21
2	A	131.08	159.08	2182.08	20
3	D	246.11	274.10	2111.04	19
4	E	375.15	403.15	1996.01	18
5	L	488.24	516.23	1866.97	17
6	L	601.32	629.31	1753.89	16
7	S	688.35	716.35	1640.80	15
8	F	835.42	863.41	1553.77	14
9	S	922.45	950.45	1406.70	13
10	S	1009.48	1037.48	1319.67	12
11	G	1066.51	1094.50	1232.64	11
12	E	1195.55	1223.54	1175.62	10
13	E	1324.59	1352.59	1046.57	9
14	S	1411.62	1439.62	917.53	8
15	L	1524.71	1552.70	830.50	7
16	L	1637.79	1665.79	717.41	6
17	E	1766.83	1794.83	604.33	5
18	S	1853.87	1881.86	475.29	4
19	Q	1981.92	2009.92	388.26	3
20	I	2095.01	2123.00	260.20	2
21	K	-	-	147.11	1



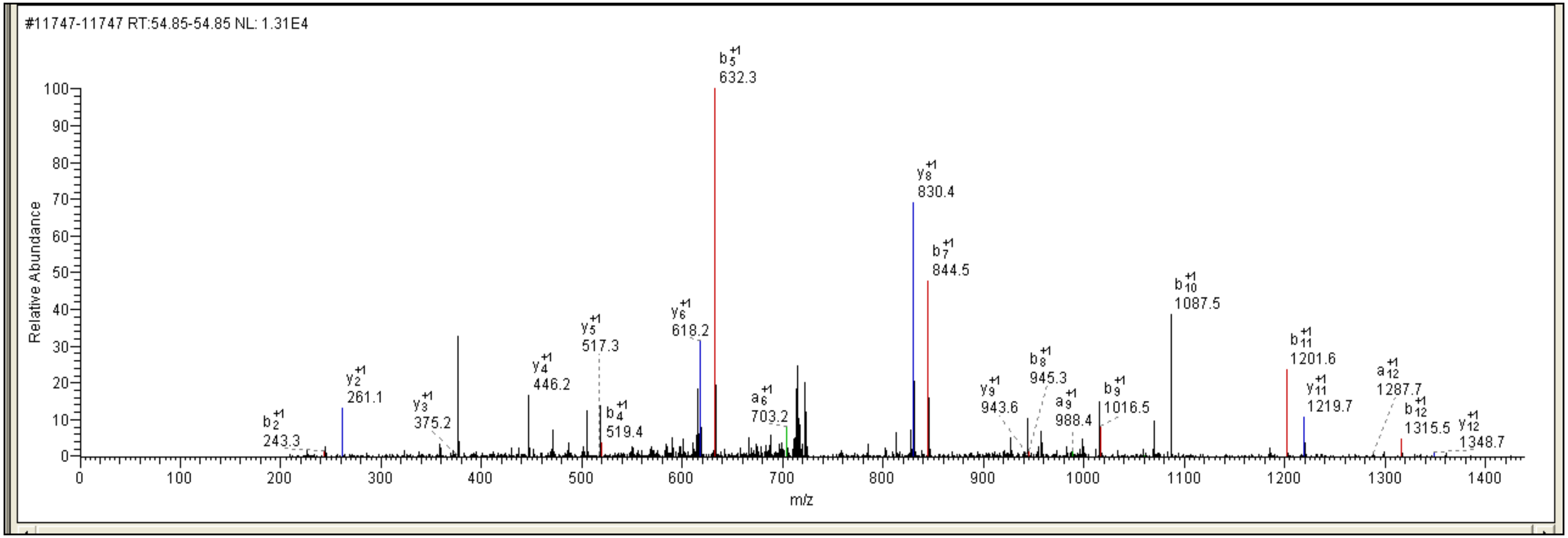
#8078-8078 RT:41.83-41.83 NL: 6.53E2

CG8793 NP_649135.2 CG8793 CG8793-PA

K.IEEMLVITAANNK.P

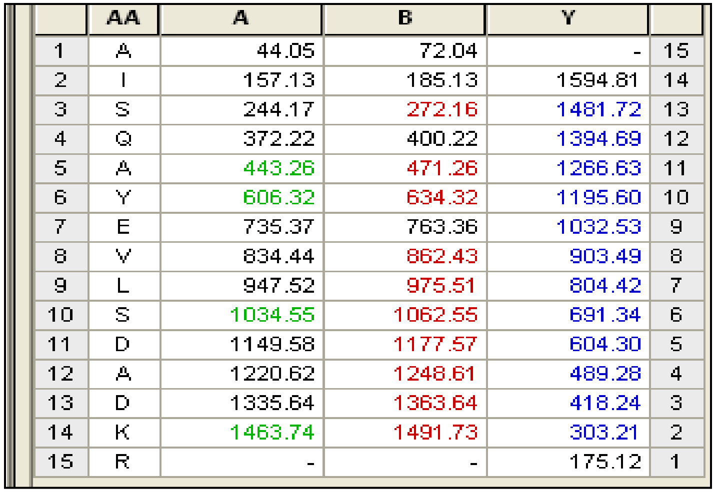


	AA	A	B	Y	
1	I	86.10	114.09	-	13
2	E	215.14	243.13	1348.68	12
3	E	344.18	372.18	1219.64	11
4	M*	491.22	519.21	1090.59	10
5	L	604.30	632.30	943.56	9
6	V	703.37	731.36	830.47	8
7	I	816.45	844.45	731.40	7
8	T	917.50	945.50	618.32	6
9	A	988.54	1016.53	517.27	5
10	A	1059.58	1087.57	446.24	4
11	N	1173.62	1201.61	375.20	3
12	N	1287.66	1315.66	261.16	2
13	K	-	-	147.11	1

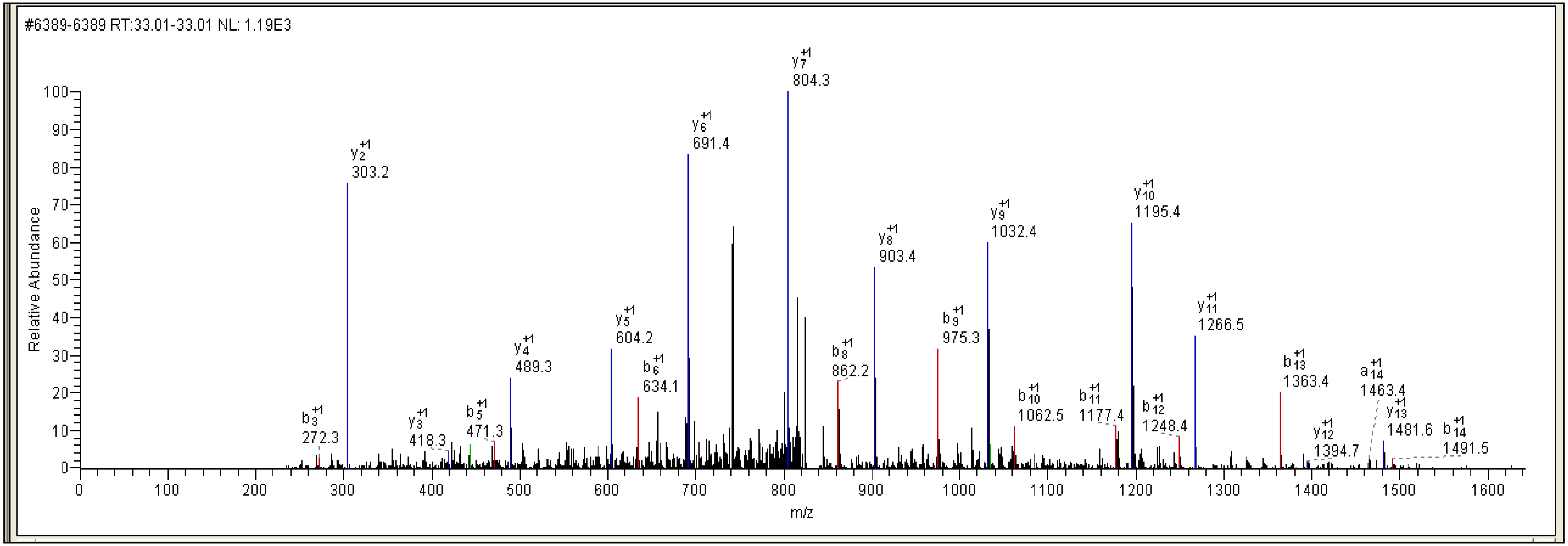


Droj2 NP_650283.1 CG8863 CG8863-PA

K.AISQAYEVLSDADKR.Q

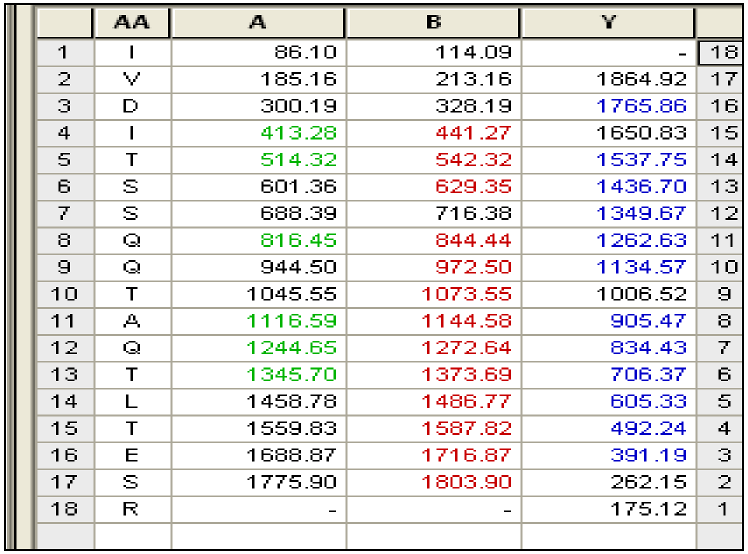


	AA	A	B	Y	
1	A	44.05	72.04	-	15
2	I	157.13	185.13	1594.81	14
3	S	244.17	272.16	1481.72	13
4	Q	372.22	400.22	1394.69	12
5	A	443.26	471.26	1266.63	11
6	Y	606.32	634.32	1195.60	10
7	E	735.37	763.36	1032.53	9
8	V	834.44	862.43	903.49	8
9	L	947.52	975.51	804.42	7
10	S	1034.55	1062.55	691.34	6
11	D	1149.58	1177.57	604.30	5
12	A	1220.62	1248.61	489.28	4
13	D	1335.64	1363.64	418.24	3
14	K	1463.74	1491.73	303.21	2
15	R	-	-	175.12	1

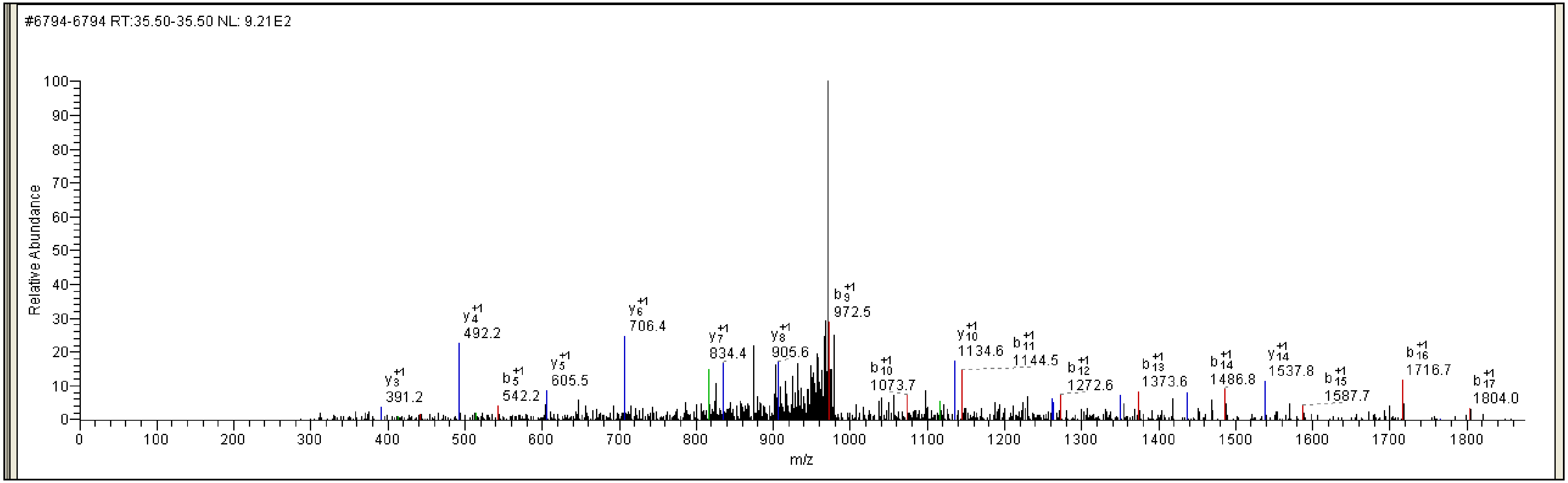


CG9143 NP_611467.1 CG9143 CG9143-PA

K.IVDITSSQQTAQTLTESR.L

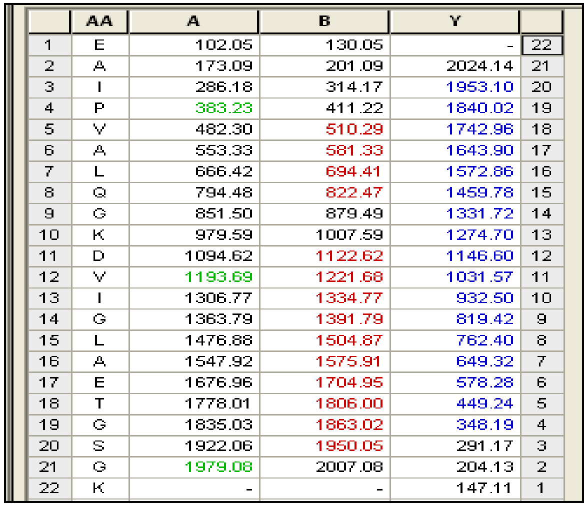


	AA	A	B	Y	
1	I	86.10	114.09	-	18
2	V	185.16	213.16	1864.92	17
3	D	300.19	328.19	1765.86	16
4	I	413.28	441.27	1650.83	15
5	T	514.32	542.32	1537.75	14
6	S	601.36	629.35	1436.70	13
7	S	688.39	716.38	1349.67	12
8	Q	816.45	844.44	1262.63	11
9	Q	944.50	972.50	1134.57	10
10	T	1045.55	1073.55	1006.52	9
11	A	1116.59	1144.58	905.47	8
12	Q	1244.65	1272.64	834.43	7
13	T	1345.70	1373.69	706.37	6
14	L	1458.78	1486.77	605.33	5
15	T	1559.83	1587.82	492.24	4
16	E	1688.87	1716.87	391.19	3
17	S	1775.90	1803.90	262.15	2
18	R	-	-	175.12	1

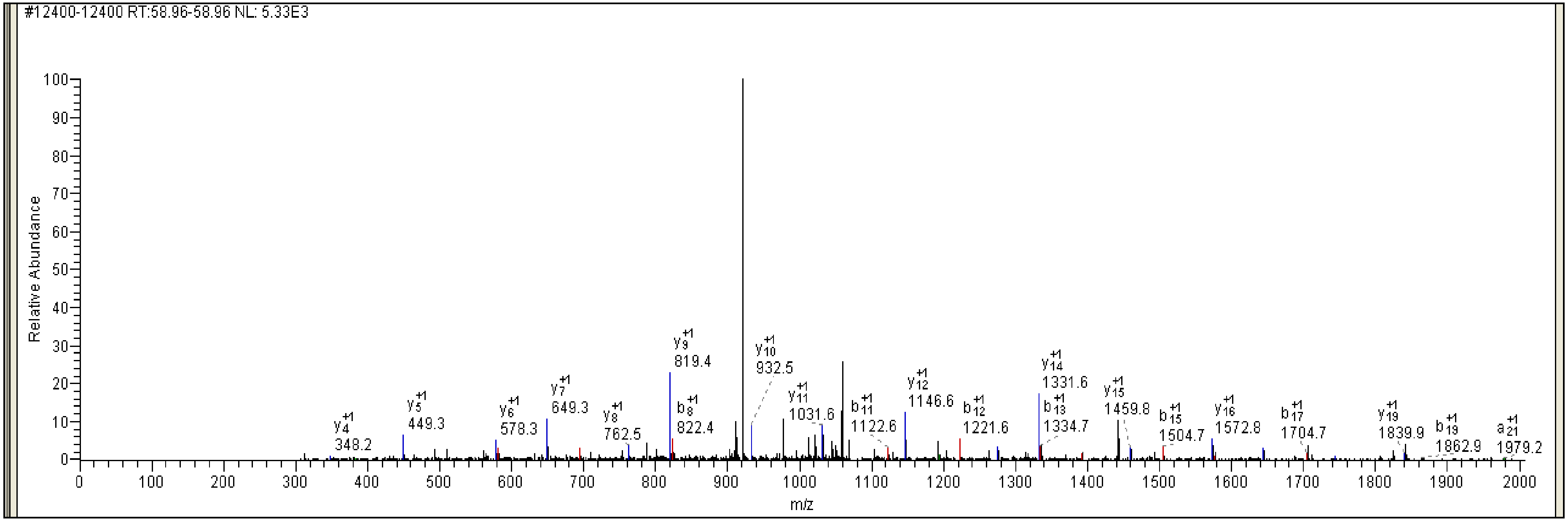


CG9253 NP_610090.1 CG9253 CG9253-PA

R.EAIPVALQGKDVIGLAETGSGK.T

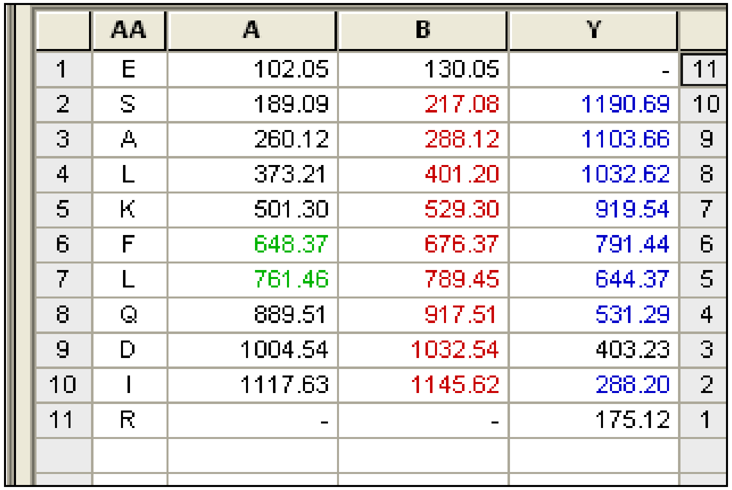


	AA	A	B	Y	
1	E	102.05	130.05	-	22
2	A	173.09	201.09	2024.14	21
3	I	286.18	314.17	1953.10	20
4	P	383.23	411.22	1840.02	19
5	V	482.30	510.29	1742.96	18
6	A	553.33	581.33	1643.90	17
7	L	666.42	694.41	1572.86	16
8	Q	794.48	822.47	1459.78	15
9	G	851.50	879.49	1331.72	14
10	K	979.59	1007.59	1274.70	13
11	D	1094.62	1122.62	1146.60	12
12	V	1193.69	1221.68	1031.57	11
13	I	1306.77	1334.77	932.50	10
14	G	1363.79	1391.79	819.42	9
15	L	1476.88	1504.87	762.40	8
16	A	1547.92	1575.91	649.32	7
17	E	1676.96	1704.95	578.28	6
18	T	1778.01	1806.00	449.24	5
19	G	1835.03	1863.02	348.19	4
20	S	1922.06	1950.05	291.17	3
21	G	1979.08	2007.08	204.13	2
22	K	-	-	147.11	1

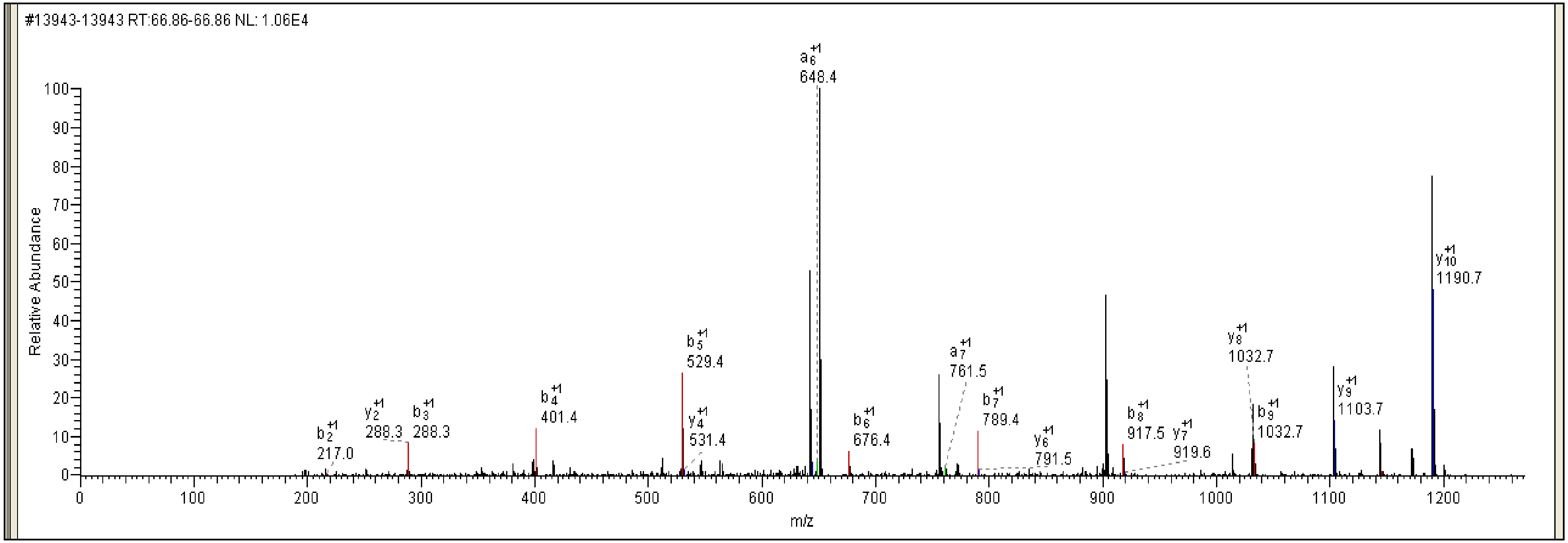


NP_731797.1 CG9813 CG9813-PF

R.ESALKFLQDIR.L

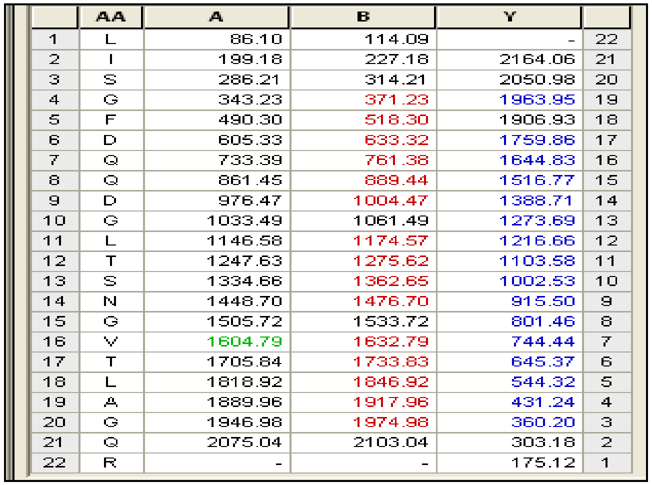


	AA	A	B	Y	
1	E	102.05	130.05	-	11
2	S	189.09	217.08	1190.69	10
3	A	260.12	288.12	1103.66	9
4	L	373.21	401.20	1032.62	8
5	K	501.30	529.30	919.54	7
6	F	648.37	676.37	791.44	6
7	L	761.46	789.45	644.37	5
8	Q	889.51	917.51	531.29	4
9	D	1004.54	1032.54	403.23	3
10	I	1117.63	1145.62	288.20	2
11	R	-	-	175.12	1

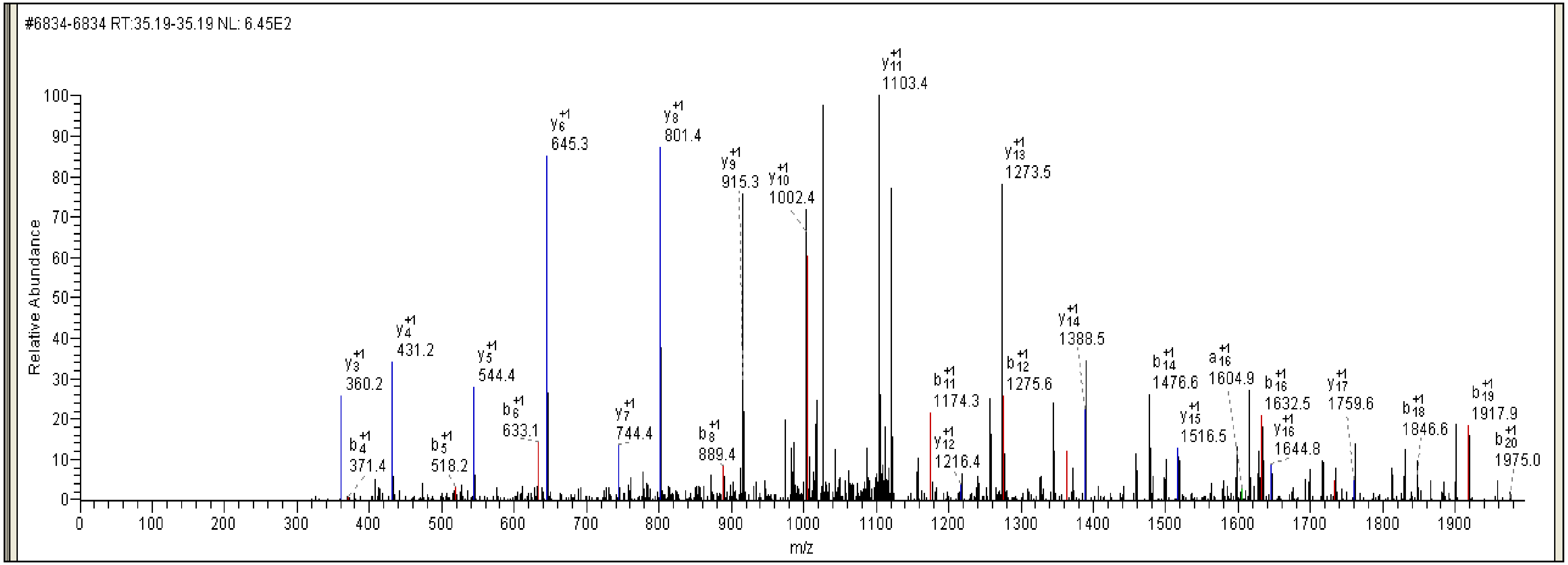


chic NP_477016.1 chickadee CG9553-PA

K.LISGFDQQDGLTSNGVTLAGQR.Y

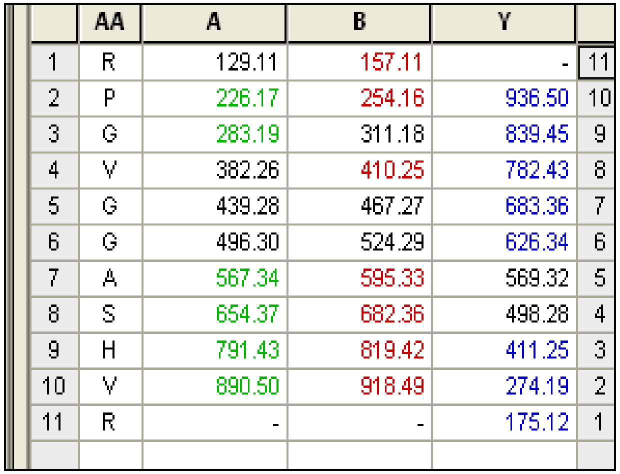


	AA	A	B	Y	
1	L	86.10	114.09	-	22
2	I	199.18	227.18	2164.06	21
3	S	286.21	314.21	2050.98	20
4	G	343.23	371.23	1963.95	19
5	F	490.30	518.30	1906.93	18
6	D	605.33	633.32	1759.86	17
7	Q	733.39	761.38	1644.83	16
8	Q	861.45	889.44	1516.77	15
9	D	976.47	1004.47	1388.71	14
10	G	1033.49	1061.49	1273.69	13
11	L	1146.58	1174.57	1216.66	12
12	T	1247.63	1275.62	1103.58	11
13	S	1334.66	1362.65	1002.53	10
14	N	1448.70	1476.70	915.50	9
15	G	1505.72	1533.72	801.46	8
16	V	1604.79	1632.79	744.44	7
17	T	1705.84	1733.83	645.37	6
18	L	1818.92	1846.92	544.32	5
19	A	1889.96	1917.96	431.24	4
20	G	1946.98	1974.98	360.20	3
21	Q	2075.04	2103.04	303.18	2
22	R	-	-	175.12	1

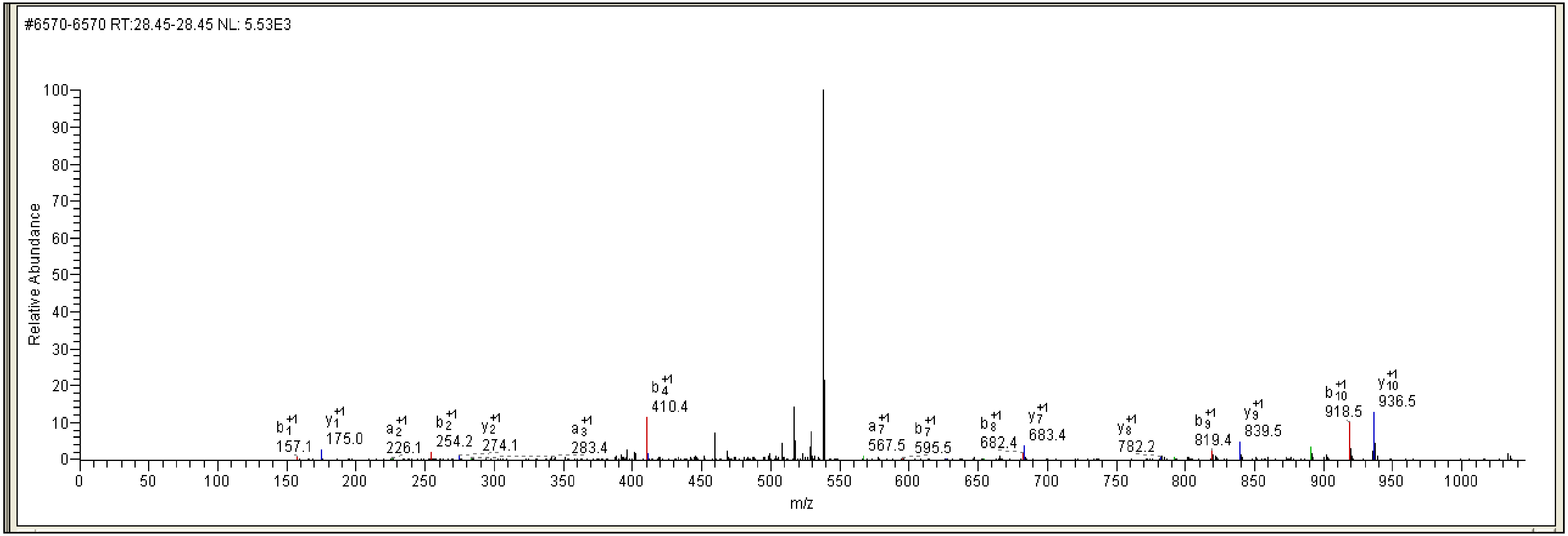


Chro NP_730762.2 Chromator CG10712-PB

R.RPGVGGASHVR.Q

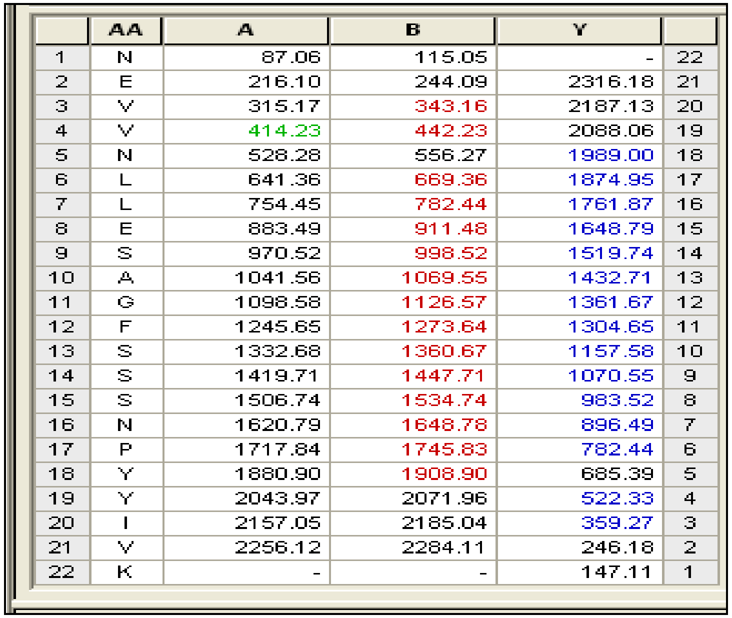


	AA	A	B	Y	
1	R	129.11	157.11	-	11
2	P	226.17	254.16	936.50	10
3	G	283.19	311.18	839.45	9
4	V	382.26	410.25	782.43	8
5	G	439.28	467.27	683.36	7
6	G	496.30	524.29	626.34	6
7	A	567.34	595.33	569.32	5
8	S	654.37	682.36	498.28	4
9	H	791.43	819.42	411.25	3
10	V	890.50	918.49	274.19	2
11	R	-	-	175.12	1

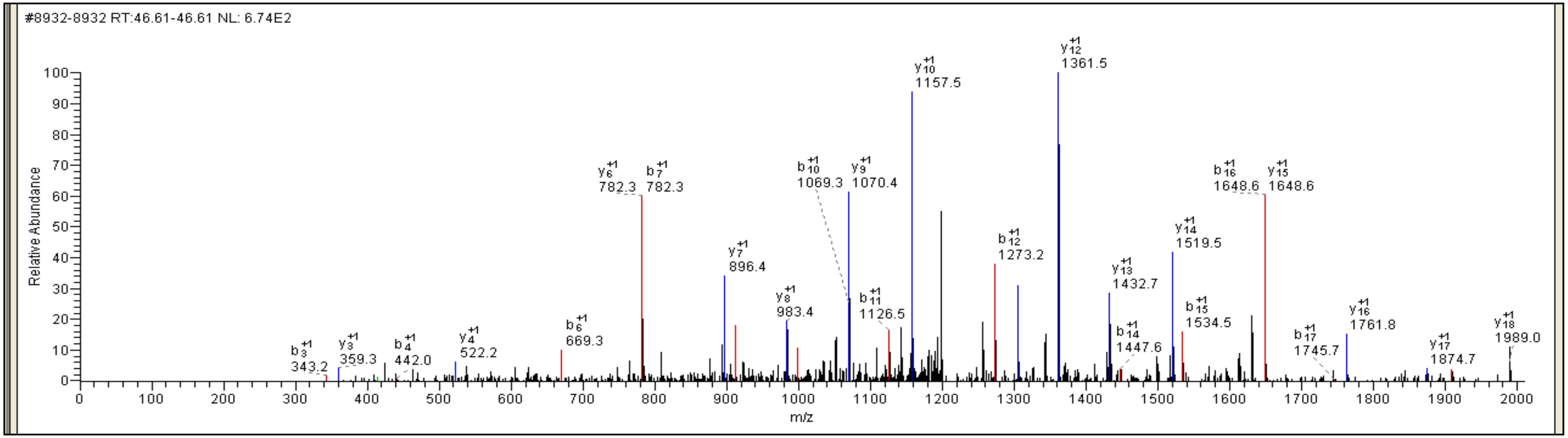


Cap NP_523374.2 Chromosome-associated protein CG9802-PA

R.NEVVNLLESAGFSSSNPYYIVK.Q

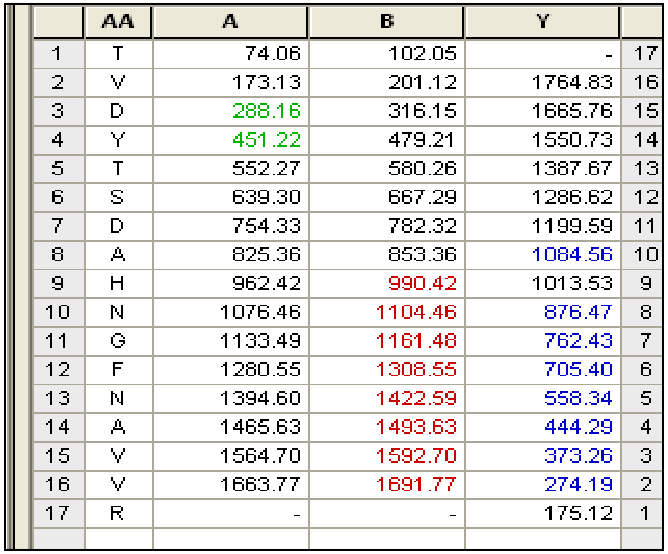


	AA	A	B	Y	
1	N	87.06	115.05	-	22
2	E	216.10	244.09	2316.18	21
3	V	315.17	343.16	2187.13	20
4	V	414.23	442.23	2088.06	19
5	N	528.28	556.27	1989.00	18
6	L	641.36	669.36	1874.95	17
7	L	754.45	782.44	1761.87	16
8	E	883.49	911.48	1648.79	15
9	S	970.52	998.52	1519.74	14
10	A	1041.56	1069.55	1432.71	13
11	G	1098.58	1126.57	1361.67	12
12	F	1245.65	1273.64	1304.65	11
13	S	1332.68	1360.67	1157.58	10
14	S	1419.71	1447.71	1070.55	9
15	S	1506.74	1534.74	983.52	8
16	N	1620.79	1648.78	896.49	7
17	P	1717.84	1745.83	782.44	6
18	Y	1880.90	1908.90	685.39	5
19	Y	2043.97	2071.96	522.33	4
20	I	2157.05	2185.04	359.27	3
21	V	2256.12	2284.11	246.18	2
22	K	-	-	147.11	1

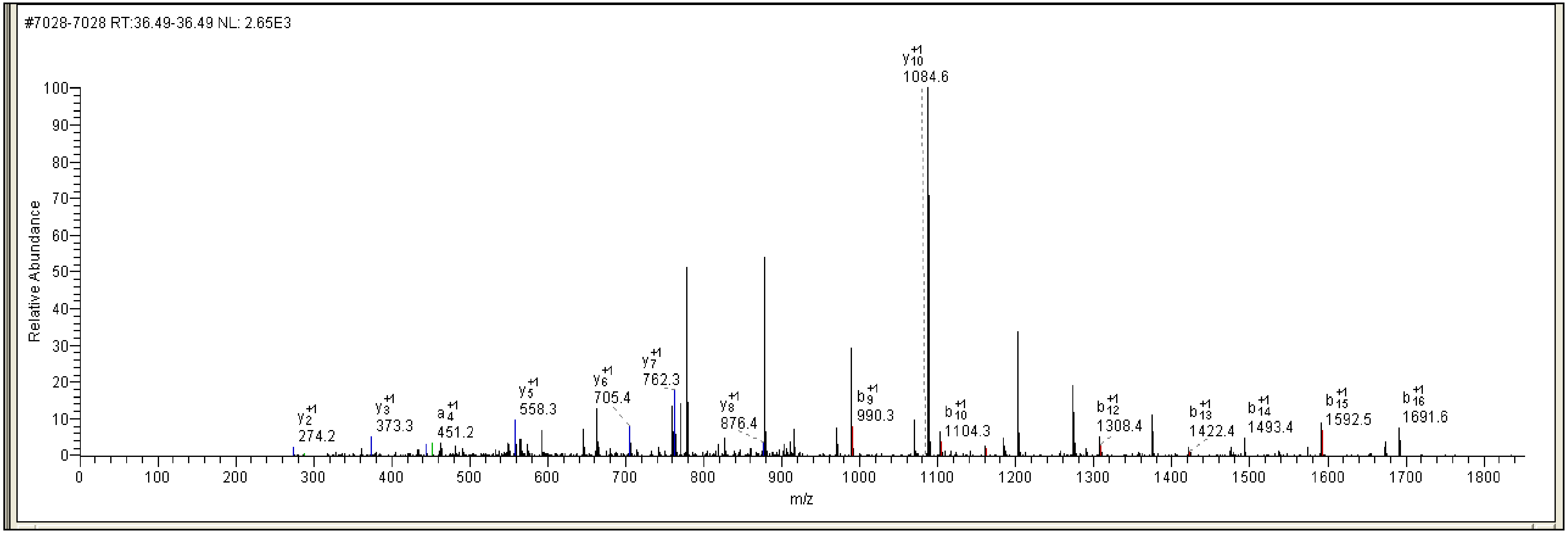


NP_723504.1 Cuticular protein 30F CG31876-PA

R.TVDYTSDAHNGFNAVVR.R

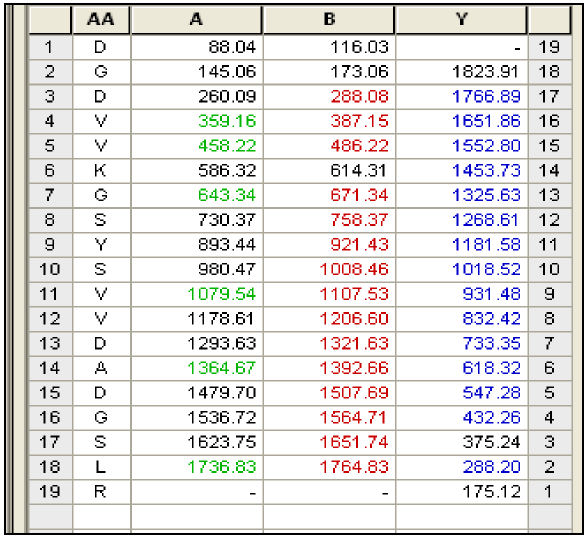


	AA	A	B	Y	
1	T	74.06	102.05	-	17
2	V	173.13	201.12	1764.83	16
3	D	288.16	316.15	1665.76	15
4	Y	451.22	479.21	1550.73	14
5	T	552.27	580.26	1387.67	13
6	S	639.30	667.29	1286.62	12
7	D	754.33	782.32	1199.59	11
8	A	825.36	853.36	1084.56	10
9	H	962.42	990.42	1013.53	9
10	N	1076.46	1104.46	876.47	8
11	G	1133.49	1161.48	762.43	7
12	F	1280.55	1308.55	705.40	6
13	N	1394.60	1422.59	558.34	5
14	A	1465.63	1493.63	444.29	4
15	V	1564.70	1592.70	373.26	3
16	V	1663.77	1691.77	274.19	2
17	R	-	-	175.12	1

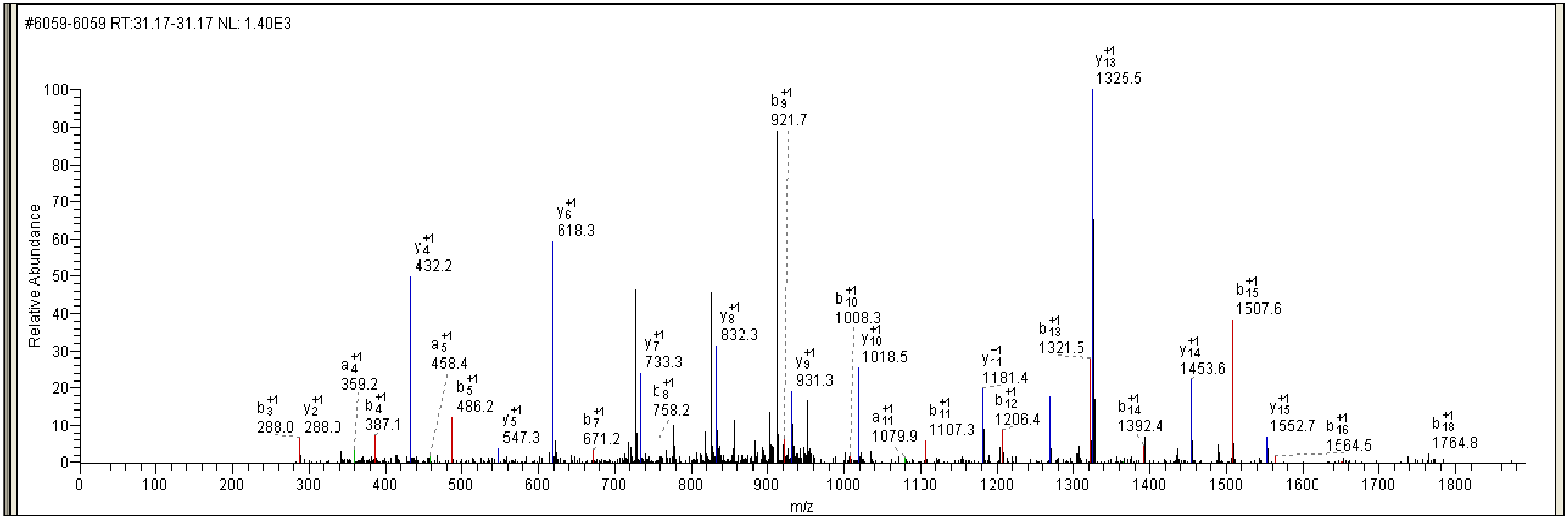


Cpr64Ab NP_647873.2 Cuticular protein 64Ab CG15007-PA

R.DGDVVKGSYSVVDADGSLR.T

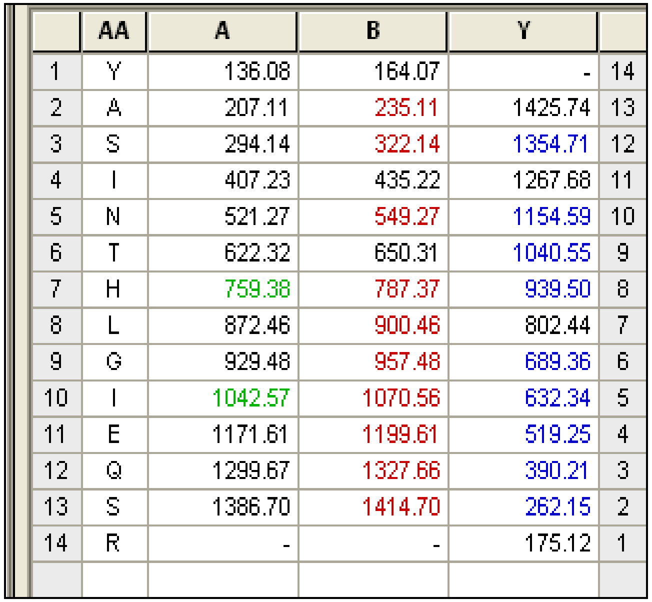


	AA	A	B	Y	
1	D	88.04	116.03	-	19
2	G	145.06	173.06	1823.91	18
3	D	260.09	288.08	1766.89	17
4	V	359.16	387.15	1651.86	16
5	V	458.22	486.22	1552.80	15
6	K	586.32	614.31	1453.73	14
7	G	643.34	671.34	1325.63	13
8	S	730.37	758.37	1268.61	12
9	Y	893.44	921.43	1181.58	11
10	S	980.47	1008.46	1018.52	10
11	V	1079.54	1107.53	931.48	9
12	V	1178.61	1206.60	832.42	8
13	D	1293.63	1321.63	733.35	7
14	A	1364.67	1392.66	618.32	6
15	D	1479.70	1507.69	547.28	5
16	G	1536.72	1564.71	432.26	4
17	S	1623.75	1651.74	375.24	3
18	L	1736.83	1764.83	288.20	2
19	R	-	-	175.12	1

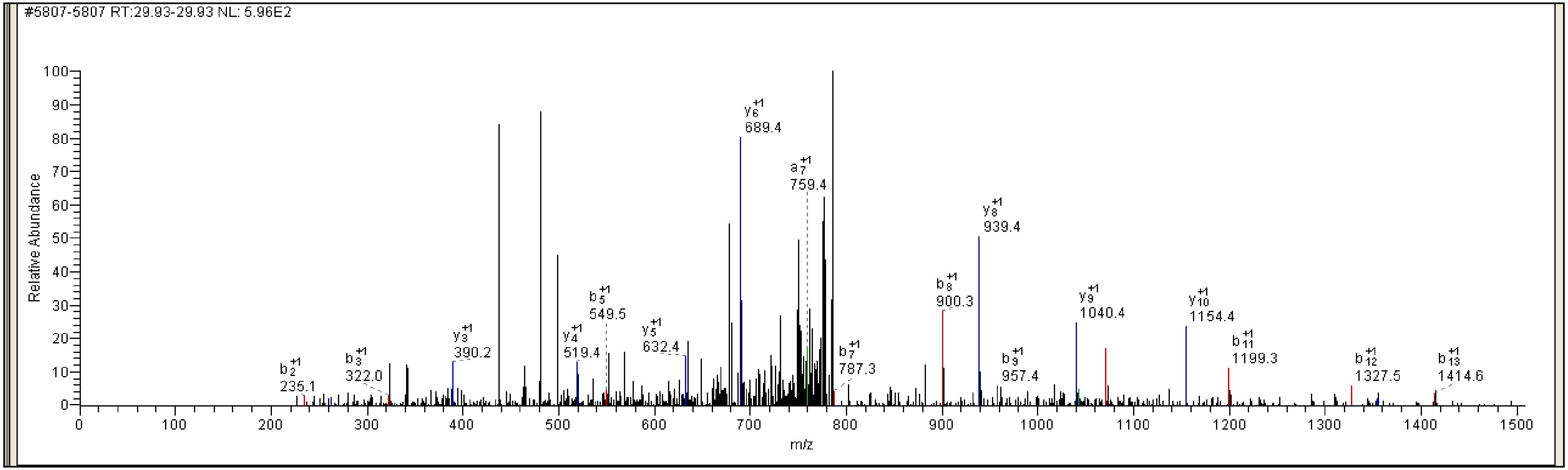


dco NP_733414.1 discs overgrown CG2048-PA

R.YASINTHLGIEQSR.R



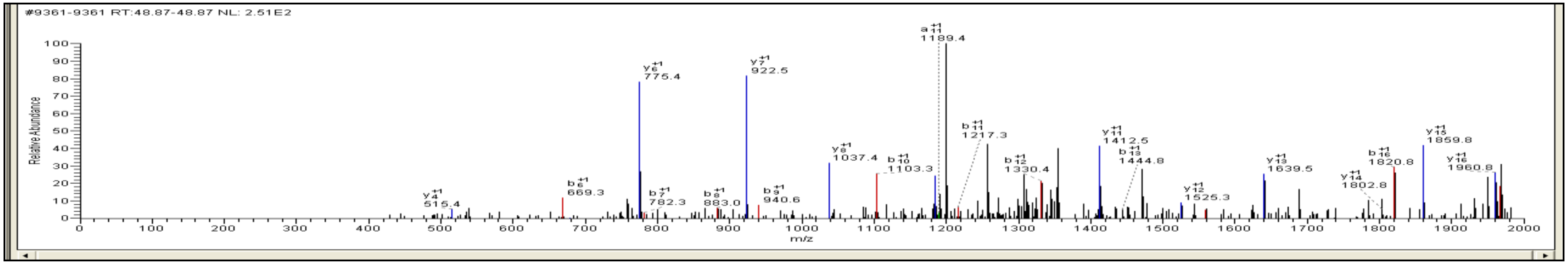
	AA	A	B	Y	
1	Y	136.08	164.07	-	14
2	A	207.11	235.11	1425.74	13
3	S	294.14	322.14	1354.71	12
4	I	407.23	435.22	1267.68	11
5	N	521.27	549.27	1154.59	10
6	T	622.32	650.31	1040.55	9
7	H	759.38	787.37	939.50	8
8	L	872.46	900.46	802.44	7
9	G	929.48	957.48	689.36	6
10	I	1042.57	1070.56	632.34	5
11	E	1171.61	1199.61	519.25	4
12	Q	1299.67	1327.66	390.21	3
13	S	1386.70	1414.70	262.15	2
14	R	-	-	175.12	1



DNApol-delta NP_524099.2 DNA-polymerase-delta CG5949-PA

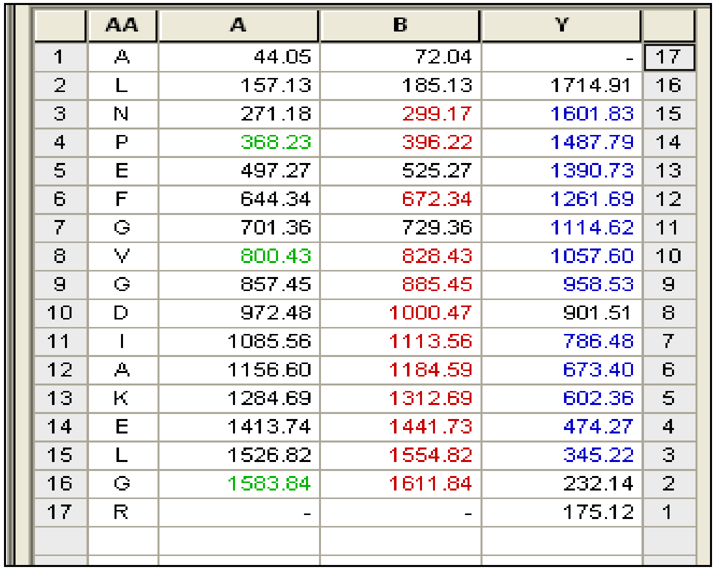
R.EVDPDILTGYNINNFDFPYLLNR.A

S no	AA	A	B	Y	
1	E	102.05	130.05	-	23
2	V	201.12	229.12	2613.3	22
3	D	316.15	344.15	2514.23	21
4	P	413.2	441.2	2399.2	20
5	D	528.23	556.22	2302.15	19
6	I	641.31	669.31	2187.12	18
7	L	754.4	782.39	2074.04	17
8	T	855.45	883.44	1960.96	16
9	G	912.47	940.46	1859.91	15
10	Y	1075.53	1103.53	1802.89	14
11	N	1189.57	1217.57	1639.82	13
12	I	1302.66	1330.65	1525.78	12
13	N	1416.7	1444.7	1412.7	11
14	N	1530.74	1558.74	1298.65	10
15	F	1677.81	1705.81	1184.61	9
16	D	1792.84	1820.83	1037.54	8
17	F	1939.91	1967.9	922.51	7
18	P	2036.96	2064.95	775.45	6
19	Y	2200.02	2228.02	678.39	5
20	L	2313.11	2341.1	515.33	4
21	L	2426.19	2454.19	402.25	3
22	N	2540.23	2568.23	289.16	2
23	R	-	-	175.12	1

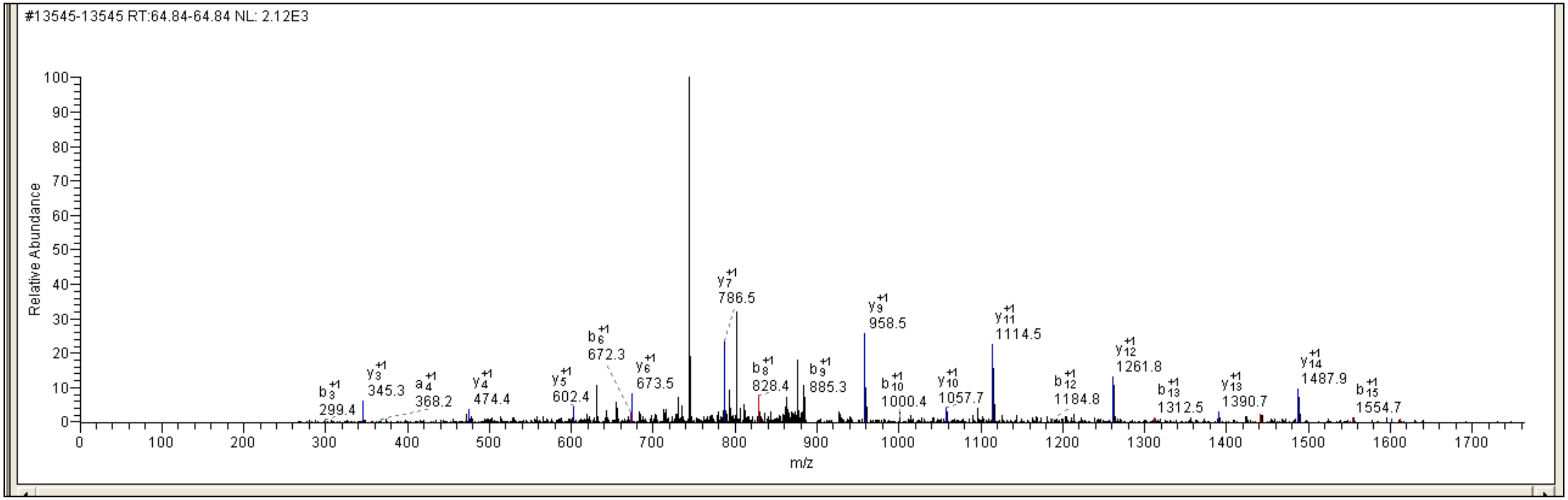


Dsp1 NP_996485.1 Dorsal switch protein 1 CG12223-PE

K.ALNPEFGVGDIAKELGR.K

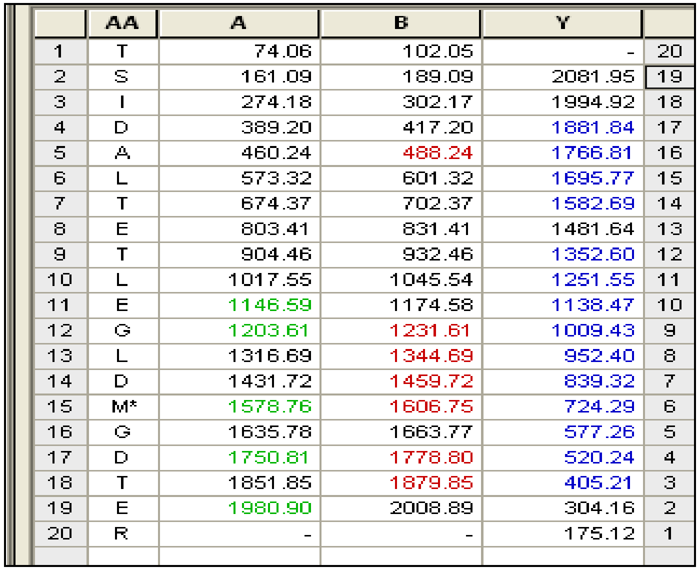


	AA	A	B	Y	
1	A	44.05	72.04	-	17
2	L	157.13	185.13	1714.91	16
3	N	271.18	299.17	1601.83	15
4	P	368.23	396.22	1487.79	14
5	E	497.27	525.27	1390.73	13
6	F	644.34	672.34	1261.69	12
7	G	701.36	729.36	1114.62	11
8	V	800.43	828.43	1057.60	10
9	G	857.45	885.45	958.53	9
10	D	972.48	1000.47	901.51	8
11	I	1085.56	1113.56	786.48	7
12	A	1156.60	1184.59	673.40	6
13	K	1284.69	1312.69	602.36	5
14	E	1413.74	1441.73	474.27	4
15	L	1526.82	1554.82	345.22	3
16	G	1583.84	1611.84	232.14	2
17	R	-	-	175.12	1

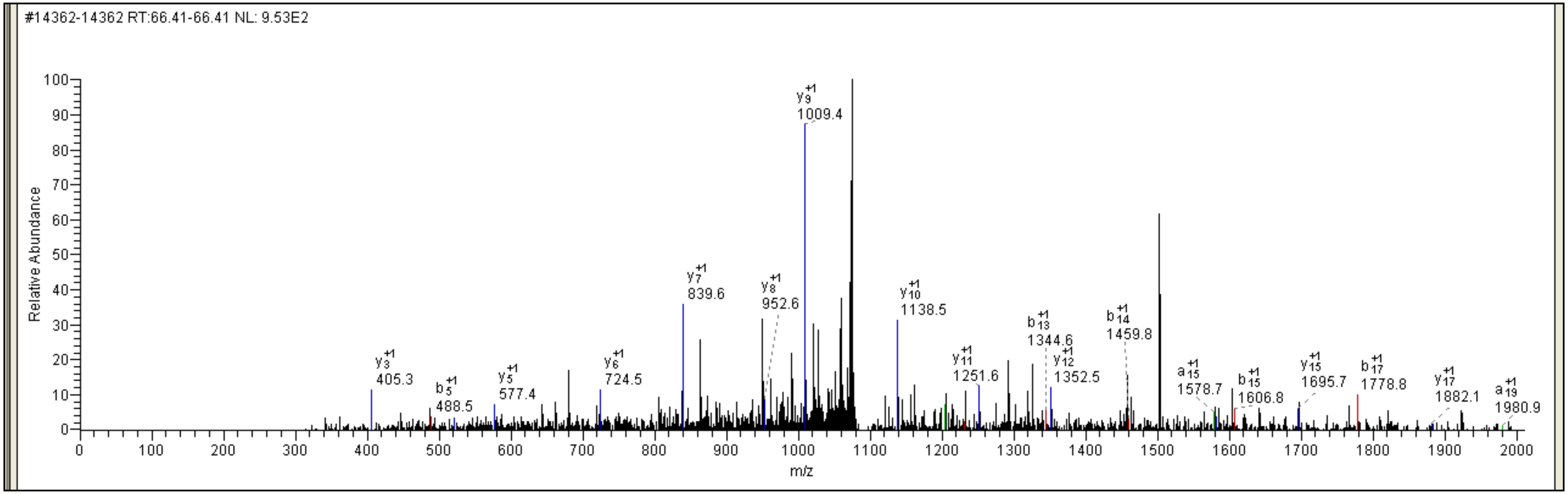


Dsor1 NP_511098.1 Downstream of raf1 CG15793-PA

K.TSIDALTETLEGLDMGDTER.K

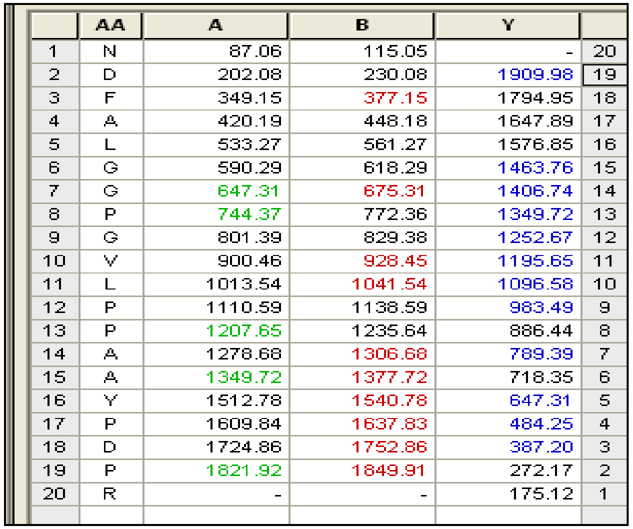


	AA	A	B	Y	
1	T	74.06	102.05	-	20
2	S	161.09	189.09	2081.95	19
3	I	274.18	302.17	1994.92	18
4	D	389.20	417.20	1881.84	17
5	A	460.24	488.24	1766.81	16
6	L	573.32	601.32	1695.77	15
7	T	674.37	702.37	1582.69	14
8	E	803.41	831.41	1481.64	13
9	T	904.46	932.46	1352.60	12
10	L	1017.55	1045.54	1251.55	11
11	E	1146.59	1174.58	1138.47	10
12	G	1203.61	1231.61	1009.43	9
13	L	1316.69	1344.69	952.40	8
14	D	1431.72	1459.72	839.32	7
15	M*	1578.76	1606.75	724.29	6
16	G	1635.78	1663.77	577.26	5
17	D	1750.81	1778.80	520.24	4
18	T	1851.85	1879.85	405.21	3
19	E	1980.90	2008.89	304.16	2
20	R	-	-	175.12	1

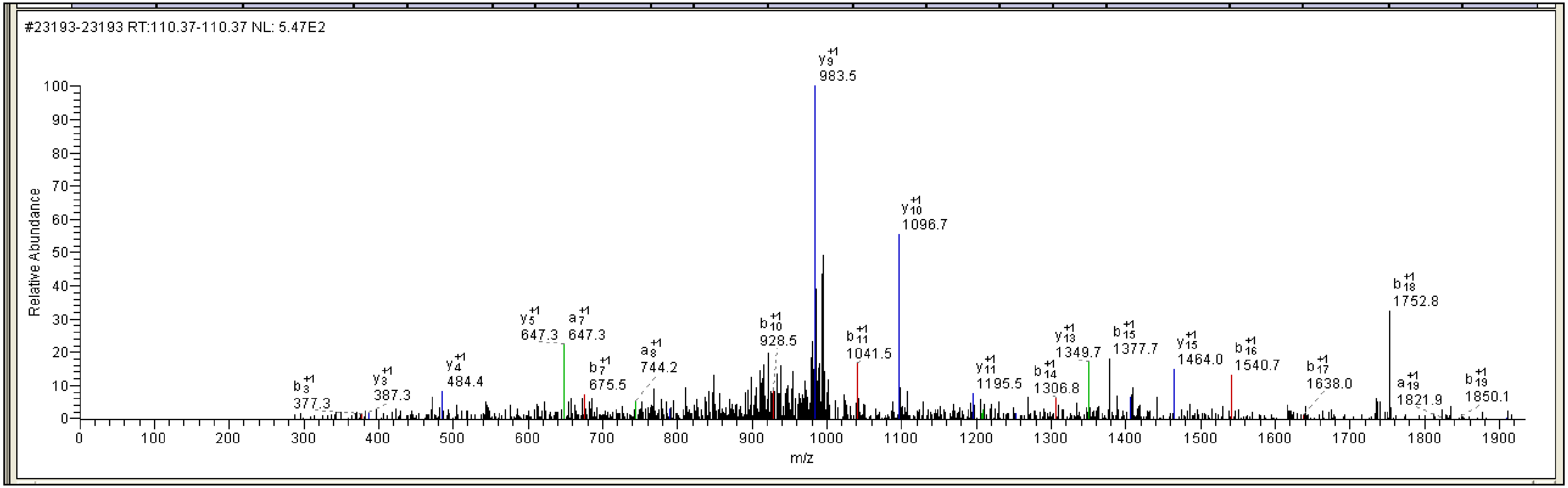


dyl NP_728979.1 dusky-like CG15013-PB

R.NDFALGGPGVLPPAAYPDPR.H

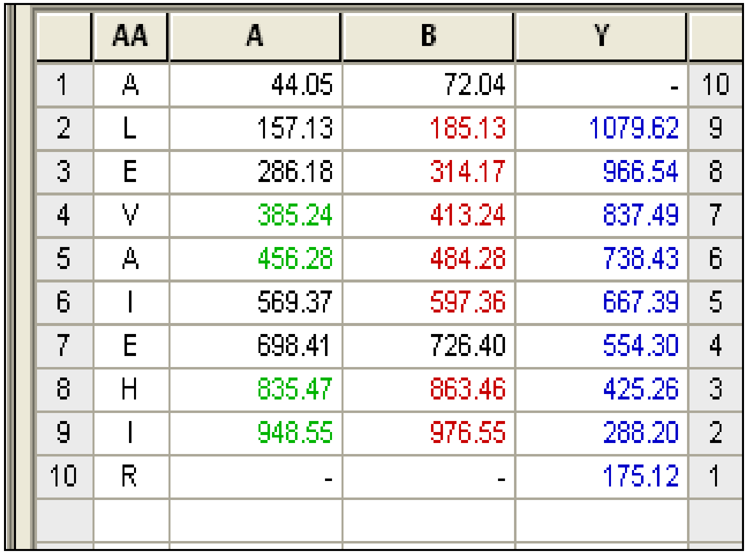


	AA	A	B	Y	
1	N	87.06	115.05	-	20
2	D	202.08	230.08	1909.98	19
3	F	349.15	377.15	1794.95	18
4	A	420.19	448.18	1647.89	17
5	L	533.27	561.27	1576.85	16
6	G	590.29	618.29	1463.76	15
7	G	647.31	675.31	1406.74	14
8	P	744.37	772.36	1349.72	13
9	G	801.39	829.38	1252.67	12
10	V	900.46	928.45	1195.65	11
11	L	1013.54	1041.54	1096.58	10
12	P	1110.59	1138.59	983.49	9
13	P	1207.65	1235.64	886.44	8
14	A	1278.68	1306.68	789.39	7
15	A	1349.72	1377.72	718.35	6
16	Y	1512.78	1540.78	647.31	5
17	P	1609.84	1637.83	484.25	4
18	D	1724.86	1752.86	387.20	3
19	P	1821.92	1849.91	272.17	2
20	R	-	-	175.12	1

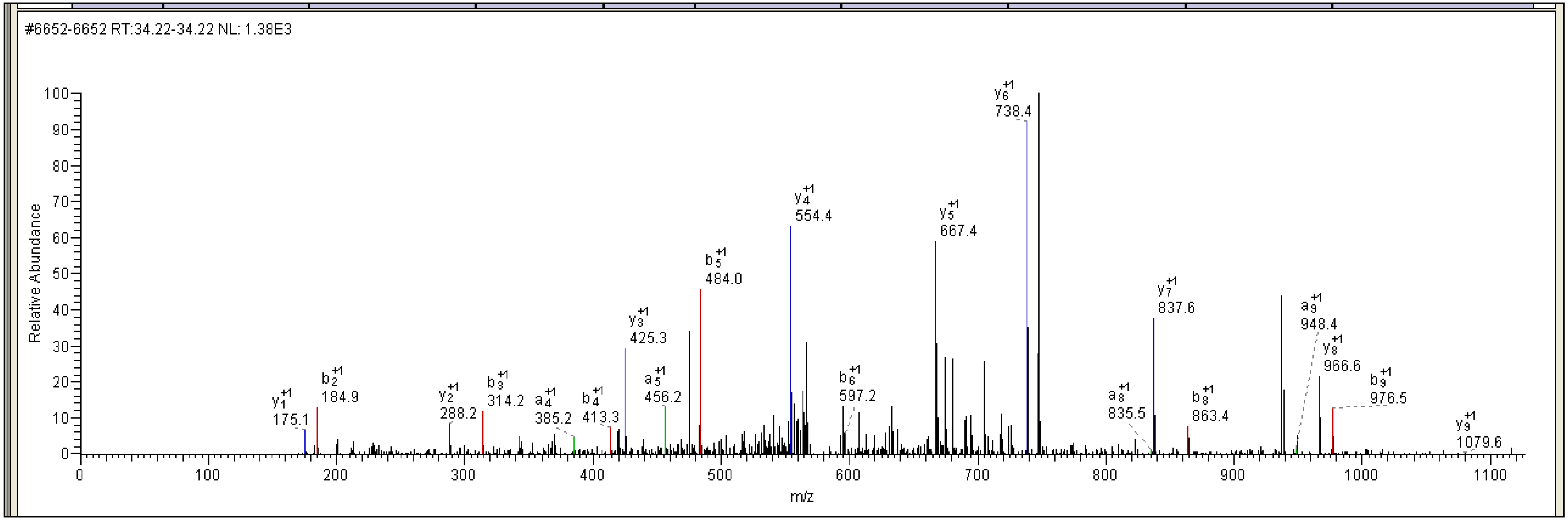


eIF-2alpha NP_573130.1 eIF-2alpha CG9946-PA

K.ALEVAIEHIR.A



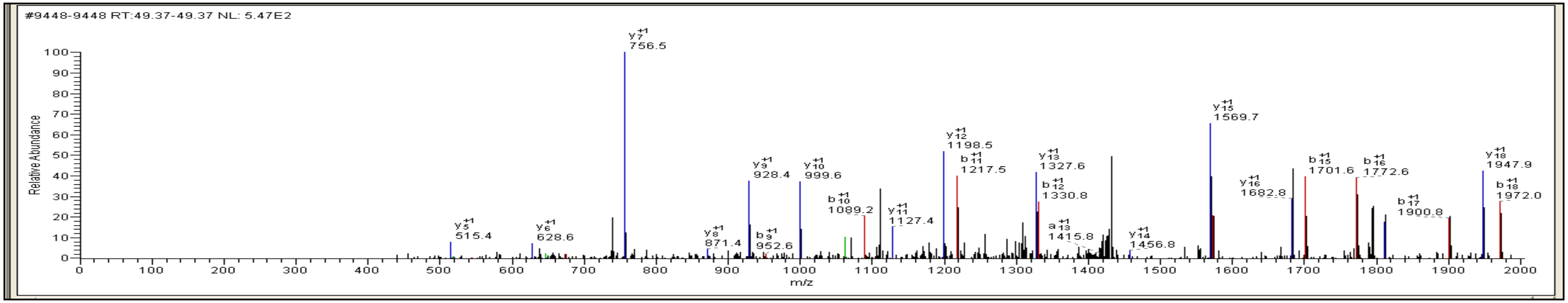
	AA	A	B	Y	
1	A	44.05	72.04	-	10
2	L	157.13	185.13	1079.62	9
3	E	286.18	314.17	966.54	8
4	V	385.24	413.24	837.49	7
5	A	456.28	484.28	738.43	6
6	I	569.37	597.36	667.39	5
7	E	698.41	726.40	554.30	4
8	H	835.47	863.46	425.26	3
9	I	948.55	976.55	288.20	2
10	R	-	-	175.12	1



EfTuM NP_524752.1 Elongation factor Tu mitochondrial CG6050-PA

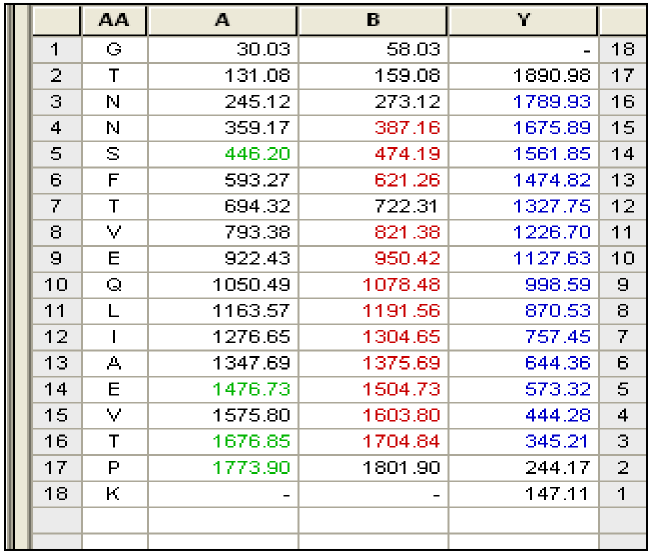
K.STVTGVEMFHQILEEAQAGDQLGALVR.G

S no	AA	A	B	Y	
1	S	60.04	88.04	-	27
2	T	161.09	189.09	2812.43	26
3	V	260.16	288.16	2711.38	25
4	T	361.21	389.2	2612.31	24
5	G	418.23	446.22	2511.27	23
6	V	517.3	545.29	2454.24	22
7	E	646.34	674.34	2355.18	21
8	M	777.38	805.38	2226.13	20
9	F	924.45	952.44	2095.09	19
10	H	1061.51	1089.5	1948.02	18
11	Q	1189.57	1217.56	1810.97	17
12	I	1302.65	1330.65	1682.91	16
13	L	1415.74	1443.73	1569.82	15
14	E	1544.78	1572.77	1456.74	14
15	E	1673.82	1701.82	1327.7	13
16	A	1744.86	1772.85	1198.65	12
17	Q	1872.92	1900.91	1127.62	11
18	A	1943.95	1971.95	999.56	10
19	G	2000.97	2028.97	928.52	9
20	D	2116	2144	871.5	8
21	Q	2244.06	2272.06	756.47	7
22	L	2357.14	2385.14	628.41	6
23	G	2414.17	2442.16	515.33	5
24	A	2485.2	2513.2	458.31	4
25	L	2598.29	2626.28	387.27	3
26	V	2697.36	2725.35	274.19	2
27	R	-	-	175.12	1

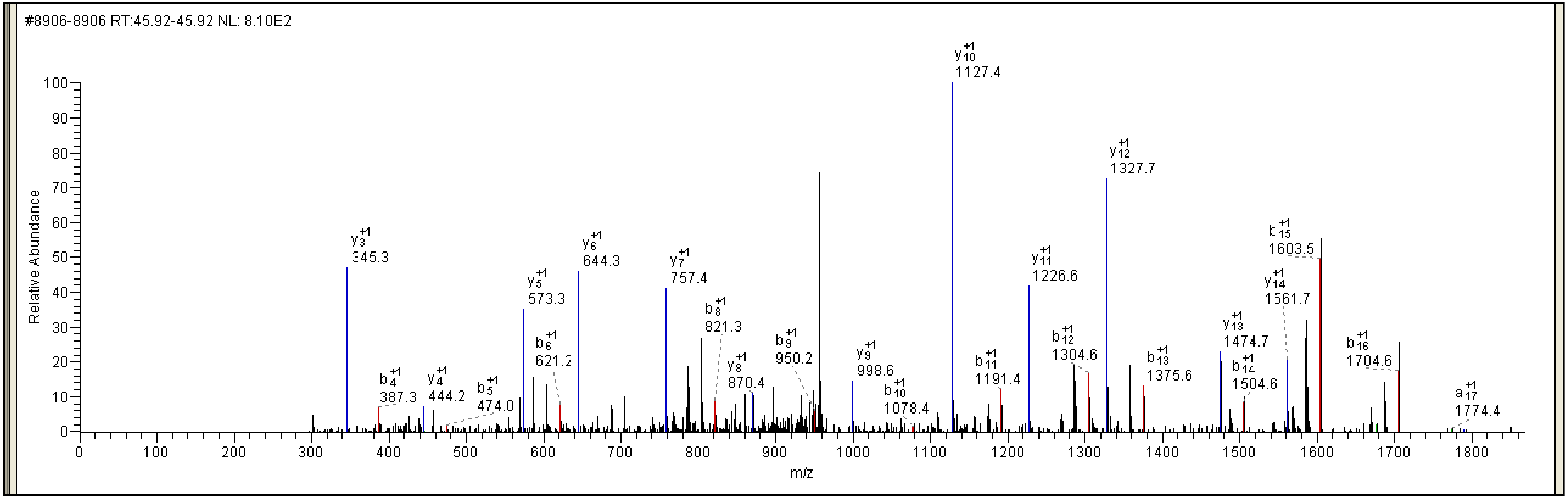


NP_524846.1 enhancer of yellow 2 CG15191-PA

K.GTNNSFTVEQLIAEVTPK.A

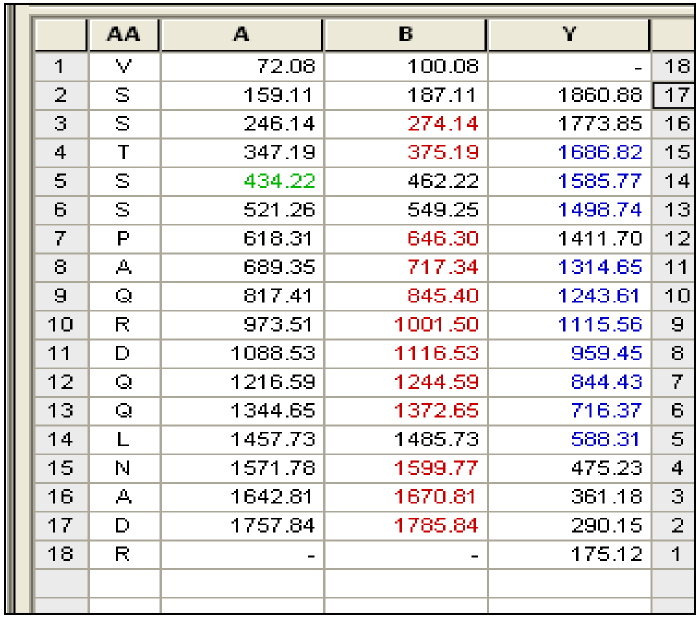


	AA	A	B	Y	
1	G	30.03	58.03	-	18
2	T	131.08	159.08	1890.98	17
3	N	245.12	273.12	1789.93	16
4	N	359.17	387.16	1675.89	15
5	S	446.20	474.19	1561.85	14
6	F	593.27	621.26	1474.82	13
7	T	694.32	722.31	1327.75	12
8	V	793.38	821.38	1226.70	11
9	E	922.43	950.42	1127.63	10
10	Q	1050.49	1078.48	998.59	9
11	L	1163.57	1191.56	870.53	8
12	I	1276.65	1304.65	757.45	7
13	A	1347.69	1375.69	644.36	6
14	E	1476.73	1504.73	573.32	5
15	V	1575.80	1603.80	444.28	4
16	T	1676.85	1704.84	345.21	3
17	P	1773.90	1801.90	244.17	2
18	K	-	-	147.11	1

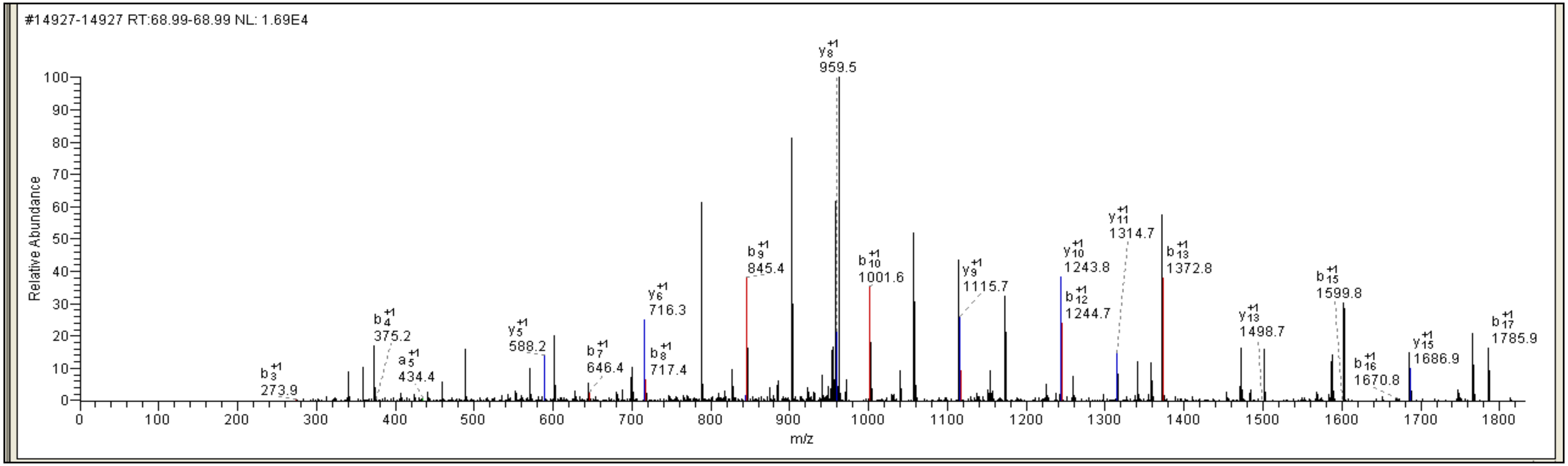


e(y)3 NP_608334.3 enhancer of yellow 3 CG12238-PA

R.VSSTSSPAQRDQQLNADR.D

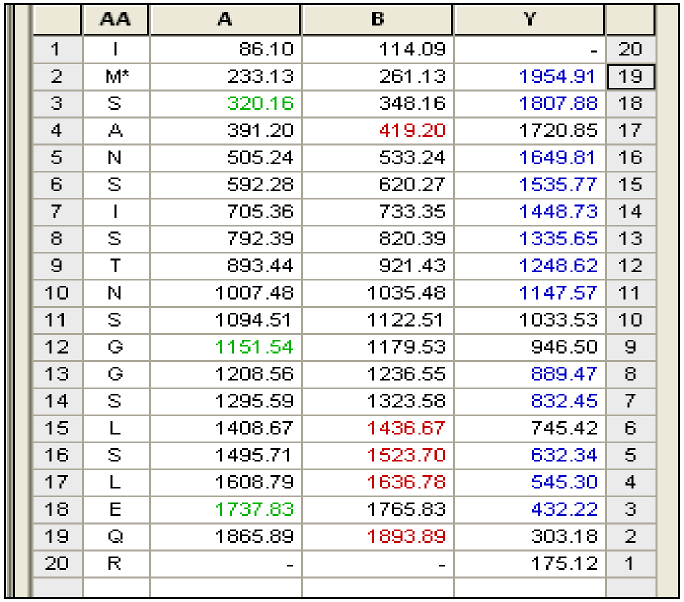


	AA	A	B	Y	
1	V	72.08	100.08	-	18
2	S	159.11	187.11	1860.88	17
3	S	246.14	274.14	1773.85	16
4	T	347.19	375.19	1686.82	15
5	S	434.22	462.22	1585.77	14
6	S	521.26	549.25	1498.74	13
7	P	618.31	646.30	1411.70	12
8	A	689.35	717.34	1314.65	11
9	Q	817.41	845.40	1243.61	10
10	R	973.51	1001.50	1115.56	9
11	D	1088.53	1116.53	959.45	8
12	Q	1216.59	1244.59	844.43	7
13	Q	1344.65	1372.65	716.37	6
14	L	1457.73	1485.73	588.31	5
15	N	1571.78	1599.77	475.23	4
16	A	1642.81	1670.81	361.18	3
17	D	1757.84	1785.84	290.15	2
18	R	-	-	175.12	1

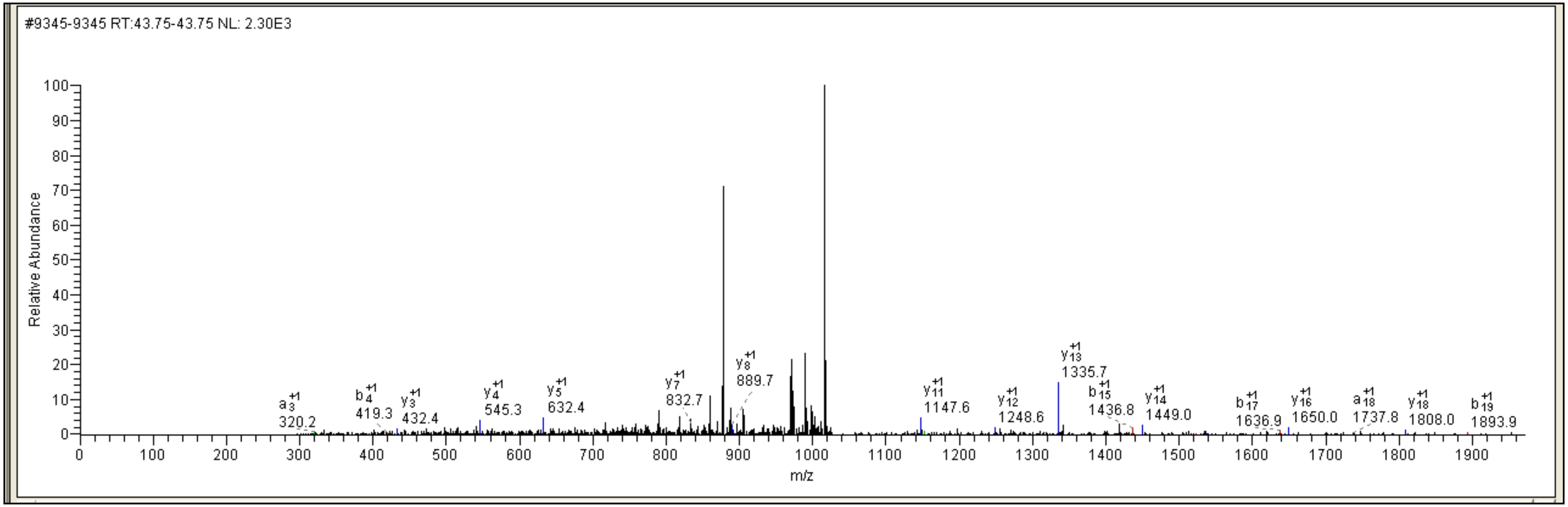


Ets97D NP_524523.2 Ets at 97D CG6338-PA

R.IMSANSISTNSGGSLSLEQR.I



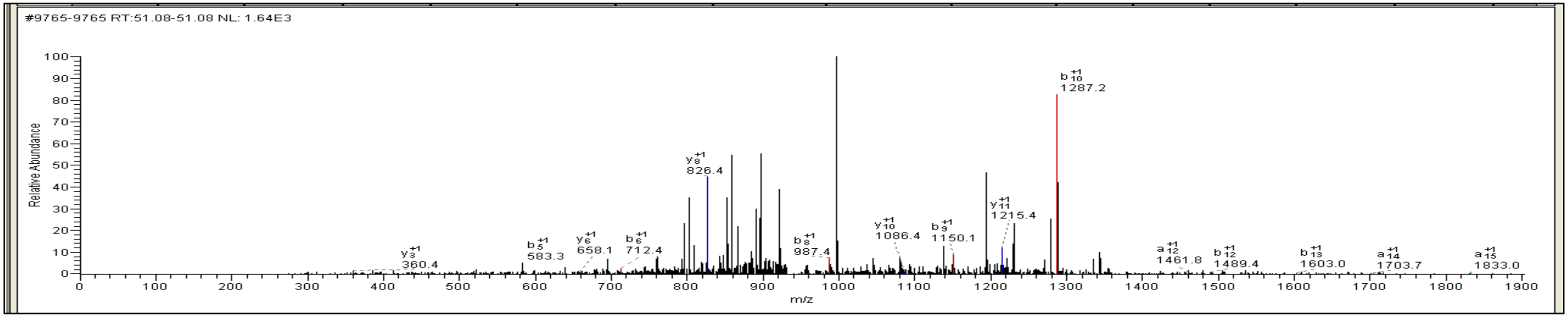
	AA	A	B	Y	
1	I	86.10	114.09	-	20
2	M*	233.13	261.13	1954.91	19
3	S	320.16	348.16	1807.88	18
4	A	391.20	419.20	1720.85	17
5	N	505.24	533.24	1649.81	16
6	S	592.28	620.27	1535.77	15
7	I	705.36	733.35	1448.73	14
8	S	792.39	820.39	1335.65	13
9	T	893.44	921.43	1248.62	12
10	N	1007.48	1035.48	1147.57	11
11	S	1094.51	1122.51	1033.53	10
12	G	1151.54	1179.53	946.50	9
13	G	1208.56	1236.55	889.47	8
14	S	1295.59	1323.58	832.45	7
15	L	1408.67	1436.67	745.42	6
16	S	1495.71	1523.70	632.34	5
17	L	1608.79	1636.78	545.30	4
18	E	1737.83	1765.83	432.22	3
19	Q	1865.89	1893.89	303.18	2
20	R	-	-	175.12	1



eIF-4a NP_723137.1 Eukaryotic initiation factor 4a CG9075-PA

R.ILKDIEQFYHTTIEEMPANIADLI

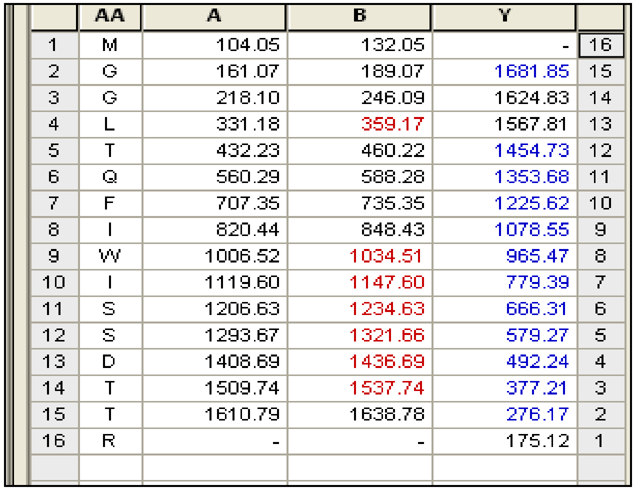
S no	AA	A	B	Y	
1	I	86.1	114.09	-	24
2	L	199.18	227.18	2704.35	23
3	K	327.28	355.27	2591.27	22
4	D	442.3	470.3	2463.17	21
5	I	555.39	583.38	2348.15	20
6	E	684.43	712.42	2235.06	19
7	Q	812.49	840.48	2106.02	18
8	F	959.56	987.55	1977.96	17
9	Y	1122.62	1150.61	1830.89	16
10	H	1259.68	1287.67	1667.83	15
11	T	1360.73	1388.72	1530.77	14
12	T	1461.77	1489.77	1429.72	13
13	I	1574.86	1602.85	1328.68	12
14	E	1703.9	1731.9	1215.59	11
15	E	1832.94	1860.94	1086.55	10
16	M	1963.98	1991.98	957.51	9
17	P	2061.04	2089.03	826.47	8
18	A	2132.07	2160.07	729.41	7
19	N	2246.12	2274.11	658.38	6
20	I	2359.2	2387.2	544.33	5
21	A	2430.24	2458.23	431.25	4
22	D	2545.26	2573.26	360.21	3
23	L	2658.35	2686.34	245.19	2
24	I	-	-	132.1	1



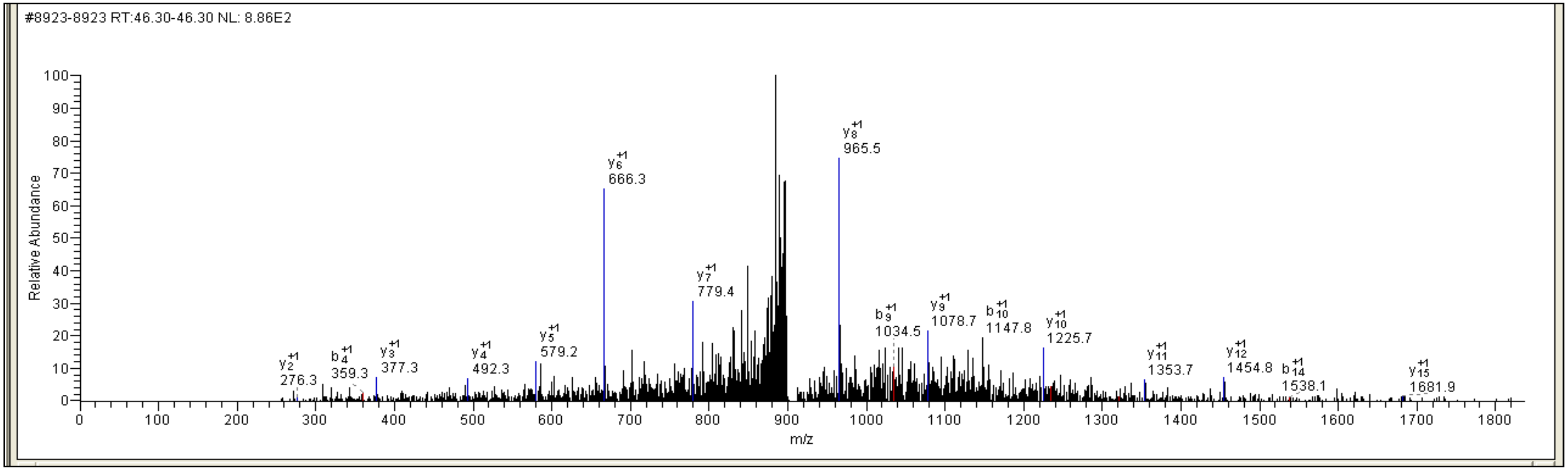
eIF4G NP_524640.3

Eukaryotic-initiation-factor-4G CG10811-PA

K.MGGLTQFIWISSDTTR.L



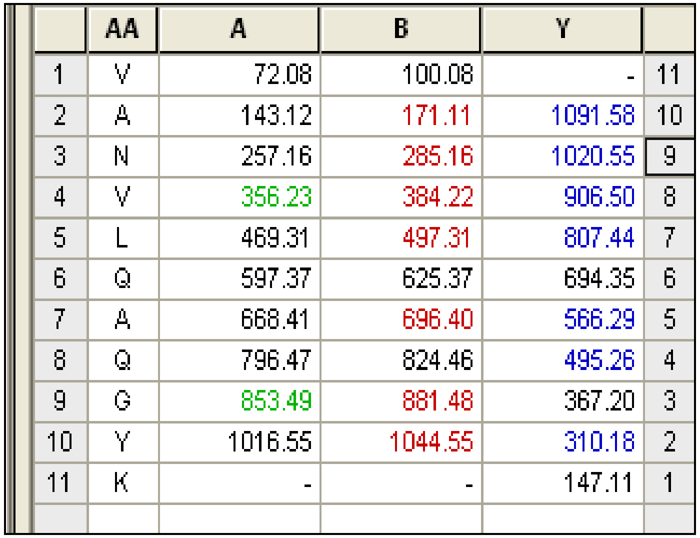
	AA	A	B	Y	
1	M	104.05	132.05	-	16
2	G	161.07	189.07	1681.85	15
3	G	218.10	246.09	1624.83	14
4	L	331.18	359.17	1567.81	13
5	T	432.23	460.22	1454.73	12
6	Q	560.29	588.28	1353.68	11
7	F	707.35	735.35	1225.62	10
8	I	820.44	848.43	1078.55	9
9	W	1006.52	1034.51	965.47	8
10	I	1119.60	1147.60	779.39	7
11	S	1206.63	1234.63	666.31	6
12	S	1293.67	1321.66	579.27	5
13	D	1408.69	1436.69	492.24	4
14	T	1509.74	1537.74	377.21	3
15	T	1610.79	1638.78	276.17	2
16	R	-	-	175.12	1



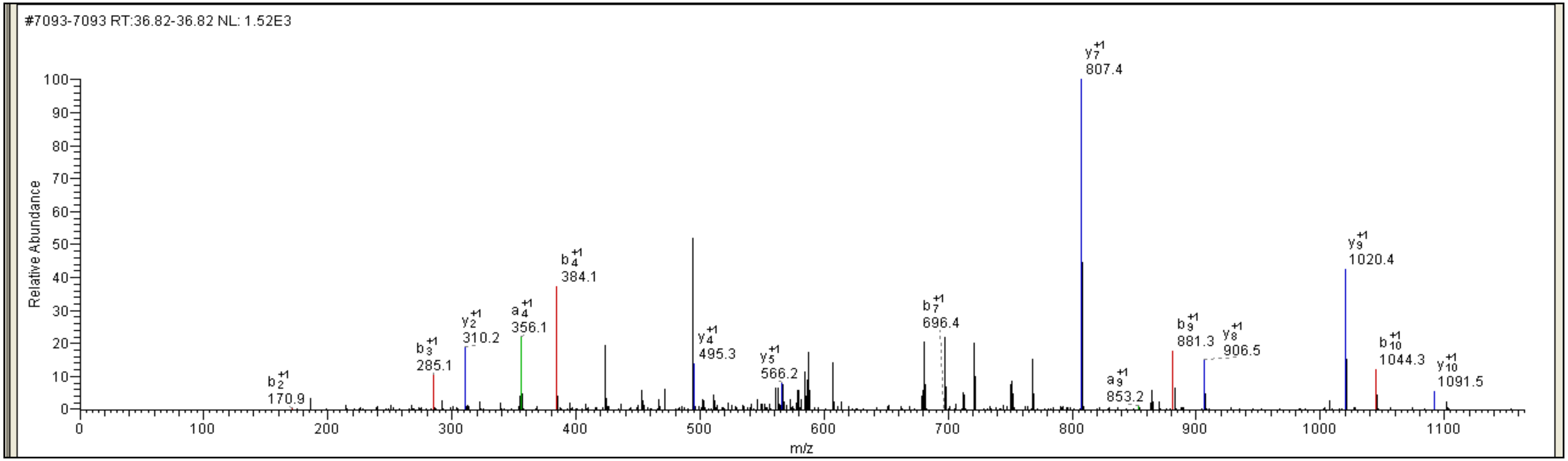
Fatp NP_524723.2

Fatty acid (long chain) transport protein CG7400-PA

K.VANVLQAQGYK.K

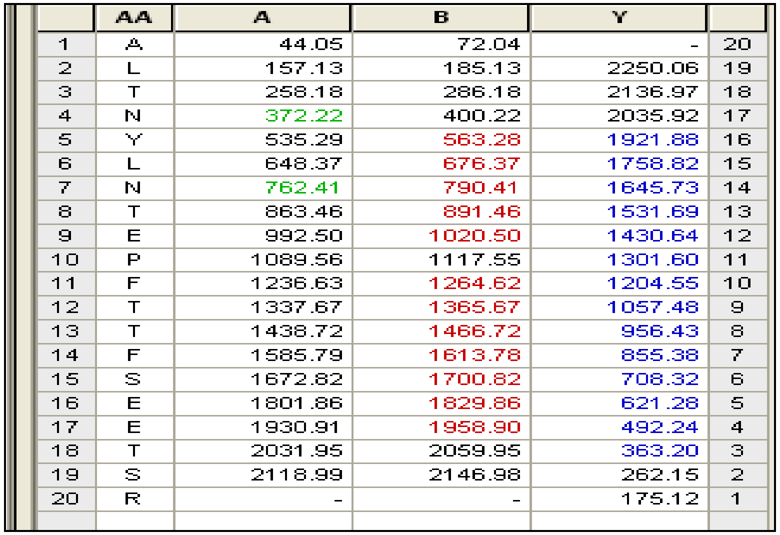


	AA	A	B	Y	
1	V	72.08	100.08	-	11
2	A	143.12	171.11	1091.58	10
3	N	257.16	285.16	1020.55	9
4	V	356.23	384.22	906.50	8
5	L	469.31	497.31	807.44	7
6	Q	597.37	625.37	694.35	6
7	A	668.41	696.40	566.29	5
8	Q	796.47	824.46	495.26	4
9	G	853.49	881.48	367.20	3
10	Y	1016.55	1044.55	310.18	2
11	K	-	-	147.11	1



fau NP_650015.3 fau CG6544-PA

R.ALTNYLNTEPFTTFSEETSR.I



	AA	A	B	Y	
1	A	44.05	72.04	-	20
2	L	157.13	185.13	2250.06	19
3	T	258.18	286.18	2136.97	18
4	N	372.22	400.22	2035.92	17
5	Y	535.29	563.28	1921.88	16
6	L	648.37	676.37	1758.82	15
7	N	762.41	790.41	1645.73	14
8	T	863.46	891.46	1531.69	13
9	E	992.50	1020.50	1430.64	12
10	P	1089.56	1117.55	1301.60	11
11	F	1236.63	1264.62	1204.55	10
12	T	1337.67	1365.67	1057.48	9
13	T	1438.72	1466.72	956.43	8
14	F	1585.79	1613.78	855.38	7
15	S	1672.82	1700.82	708.32	6
16	E	1801.86	1829.86	621.28	5
17	E	1930.91	1958.90	492.24	4
18	T	2031.95	2059.95	363.20	3
19	S	2118.99	2146.98	262.15	2
20	R	-	-	175.12	1