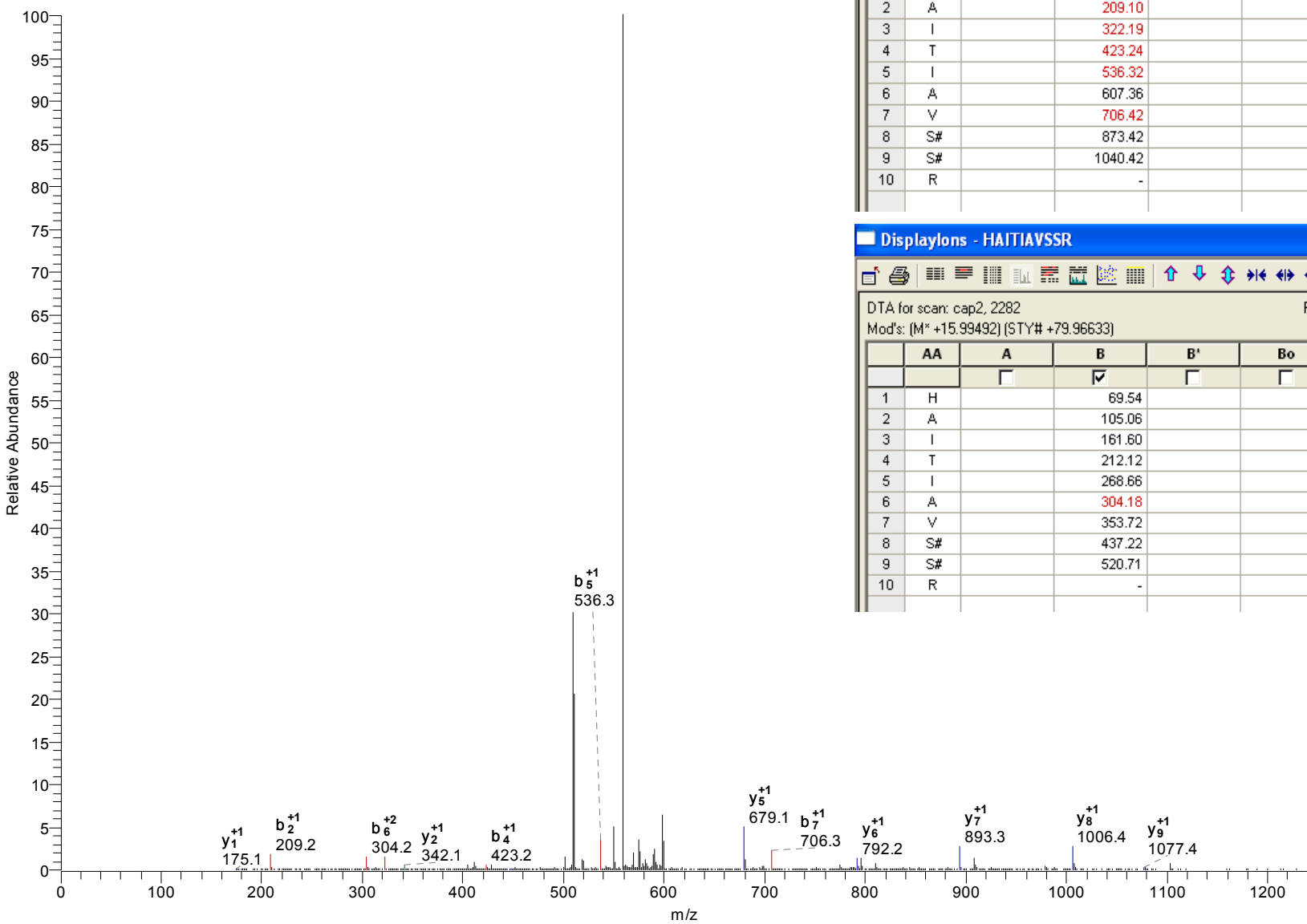


Retinol Dehydrogenase 14

#2282-2282 NL: 8.95E4



Displaylons - HAITIAVSSR

DTA for scan: cap2, 2282
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 608.10

	AA	A	B	B ⁺	Bo	C	Y
1	H		138.07				-
2	A		209.10				1077.47
3	I		322.19				1006.44
4	T		423.24				893.35
5	I		536.32				792.31
6	A		607.36				679.22
7	V		706.42				608.18
8	S#		873.42				509.12
9	S#		1040.42				342.12
10	R		-				175.12

Displaylons - HAITIAVSSR

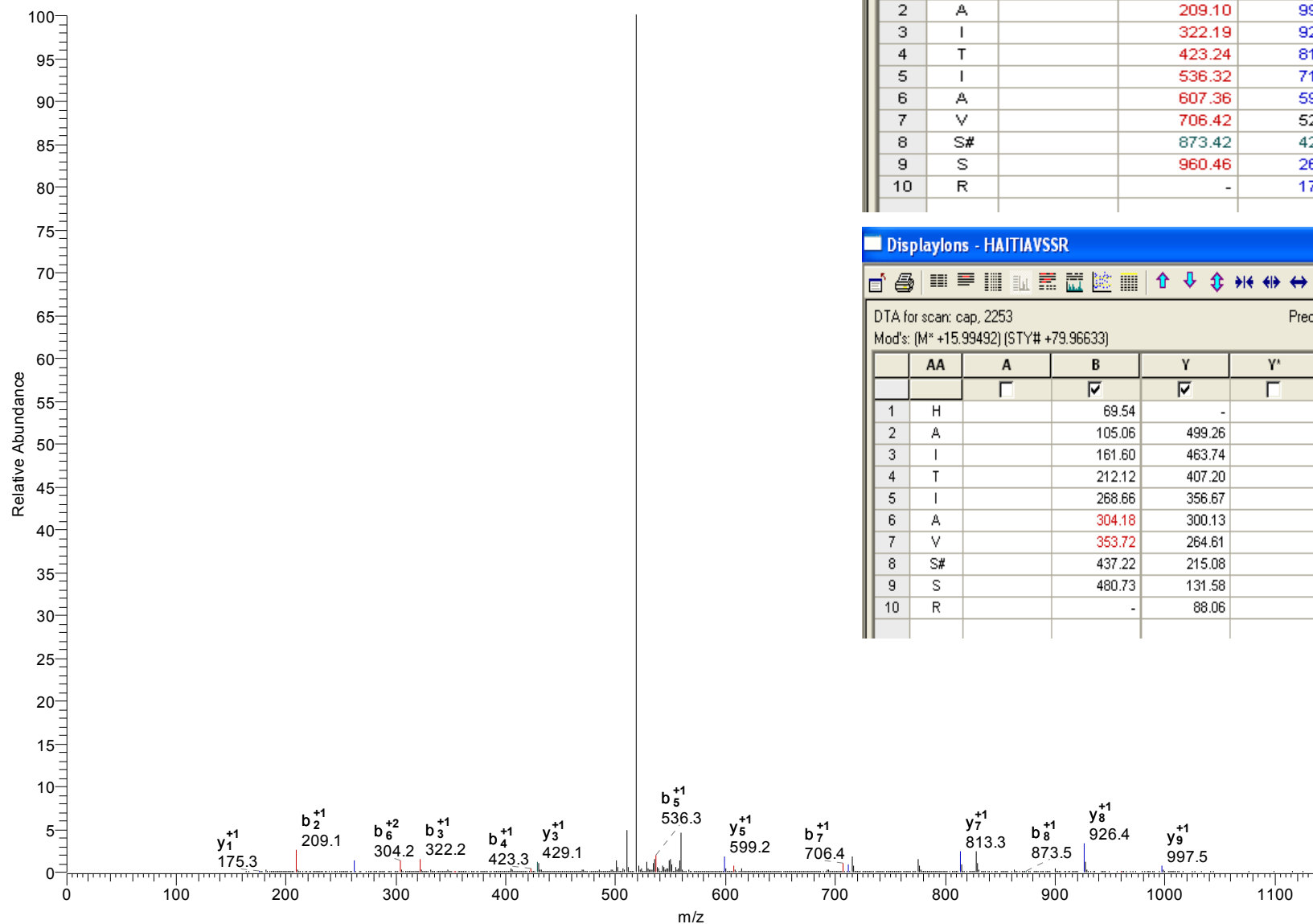
DTA for scan: cap2, 2282
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 608.10

	AA	A	B	B ⁺	Bo	C	Y
1	H		69.54				-
2	A		105.06				539.24
3	I		161.60				503.72
4	T		212.12				447.18
5	I		268.66				396.66
6	A		304.18				340.11
7	V		353.72				304.60
8	S#		437.22				255.06
9	S#		520.71				171.56
10	R		-				88.06

Retinol Dehydrogenase 14

#2253-2253 NL: 7.54E4



Displaylons - HAITIAVSSR

DTA for scan: cap, 2253
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	H		138.07	-		10
2	A		209.10	997.51		9
3	I		322.19	926.47		8
4	T		423.24	813.39		7
5	I		536.32	712.34		6
6	A		607.36	599.25		5
7	V		706.42	528.22		4
8	S#		873.42	429.15		3
9	S		960.46	262.15		2
10	R		-	175.12		1

Displaylons - HAITIAVSSR

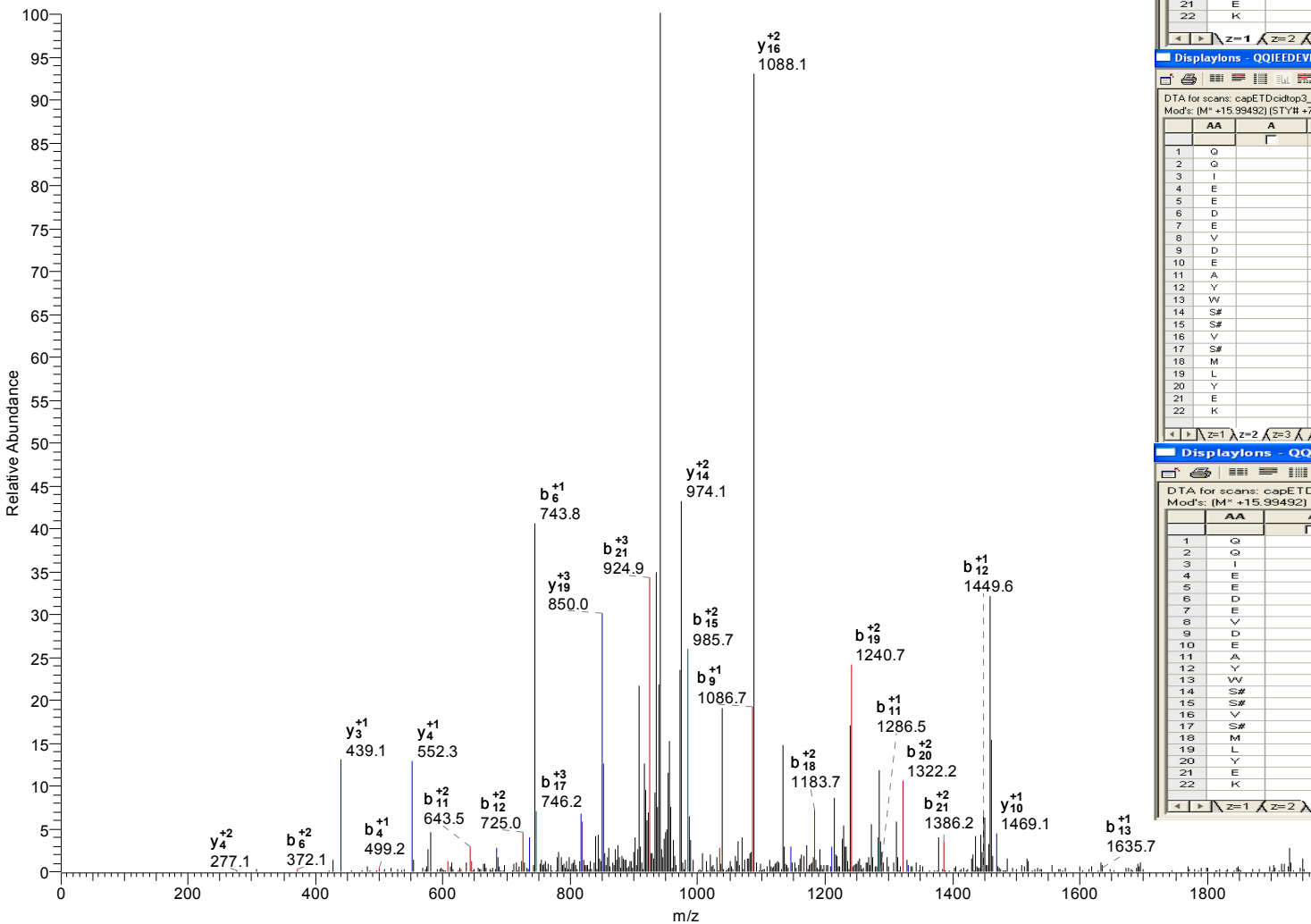
DTA for scan: cap, 2253
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 567.90 Charge: 2

	AA	A	B	Y	Y*	Yo	Z	
1	H		69.54	-				10
2	A		105.06	499.26				9
3	I		161.60	463.74				8
4	T		212.12	407.20				7
5	I		268.66	356.67				6
6	A		304.18	300.13				5
7	V		353.72	264.61				4
8	S#		437.22	215.08				3
9	S		480.73	131.58				2
10	R		-	86.06				1

Retinol Dehydrogenase 14

#2869-2870 NL: 6.23E2



Display ions - QQIEDEVDEAYWSSVSMLEYK

DTA for scans: capETDcidtop3_080419044303, 2869-2870
Mod's: (M⁺+15.99492) (STY# +79.96633)

	AA	A	B	Y	Z
1	Q		129.07	-	22
2	Q		257.12	2790.02	21
3	I		370.21	2661.96	20
4	E		499.25	2548.88	19
5	E		628.29	2419.84	18
6	D		743.32	2290.79	17
7	E		872.36	2175.77	16
8	V		971.43	2046.72	15
9	D		1086.46	1947.66	14
10	E		1215.50	1832.63	13
11	A		1286.54	1703.59	12
12	Y		1449.60	1632.55	11
13	W		1635.66	1469.49	10
14	S#		1802.68	1283.41	9
15	S#		1969.68	1116.41	8
16	V		2068.75	949.41	7
17	S#		2235.74	850.34	6
18	M		2368.78	683.34	5
19	L		2479.67	552.30	4
20	Y		2642.93	439.22	3
21	E		2771.97	276.16	2
22	K		-	147.11	1

z=1 z=2 z=3

Display ions - QQIEDEVDEAYWSSVSMLEYK

DTA for scans: capETDcidtop3_080419044303, 2869-2870
Mod's: (M⁺+15.99492) (STY# +79.96633)

	AA	A	B	Y	Y'	Yo	Z
1	Q		65.04	-	-	-	22
2	Q		129.07	1395.51	-	-	21
3	I		185.61	1331.49	-	-	20
4	E		250.13	1274.94	-	-	19
5	E		314.65	1210.42	-	-	18
6	D		372.16	1145.90	-	-	17
7	E		436.69	1088.39	-	-	16
8	V		486.22	1023.87	-	-	15
9	D		543.73	974.33	-	-	14
10	E		608.25	916.82	-	-	13
11	A		643.77	852.30	-	-	12
12	Y		725.30	816.78	-	-	11
13	W		818.34	735.25	-	-	10
14	S#		901.84	642.21	-	-	9
15	S#		985.34	558.71	-	-	8
16	V		1034.88	475.21	-	-	7
17	S#		1118.38	425.67	-	-	6
18	M		1183.90	342.18	-	-	5
19	L		1240.44	276.66	-	-	4
20	Y		1321.97	220.11	-	-	3
21	E		1386.49	138.58	-	-	2
22	K		-	74.06	-	-	1

z=1 z=2 z=3

Display ions - QQIEDEVDEAYWSSVSMLEYK

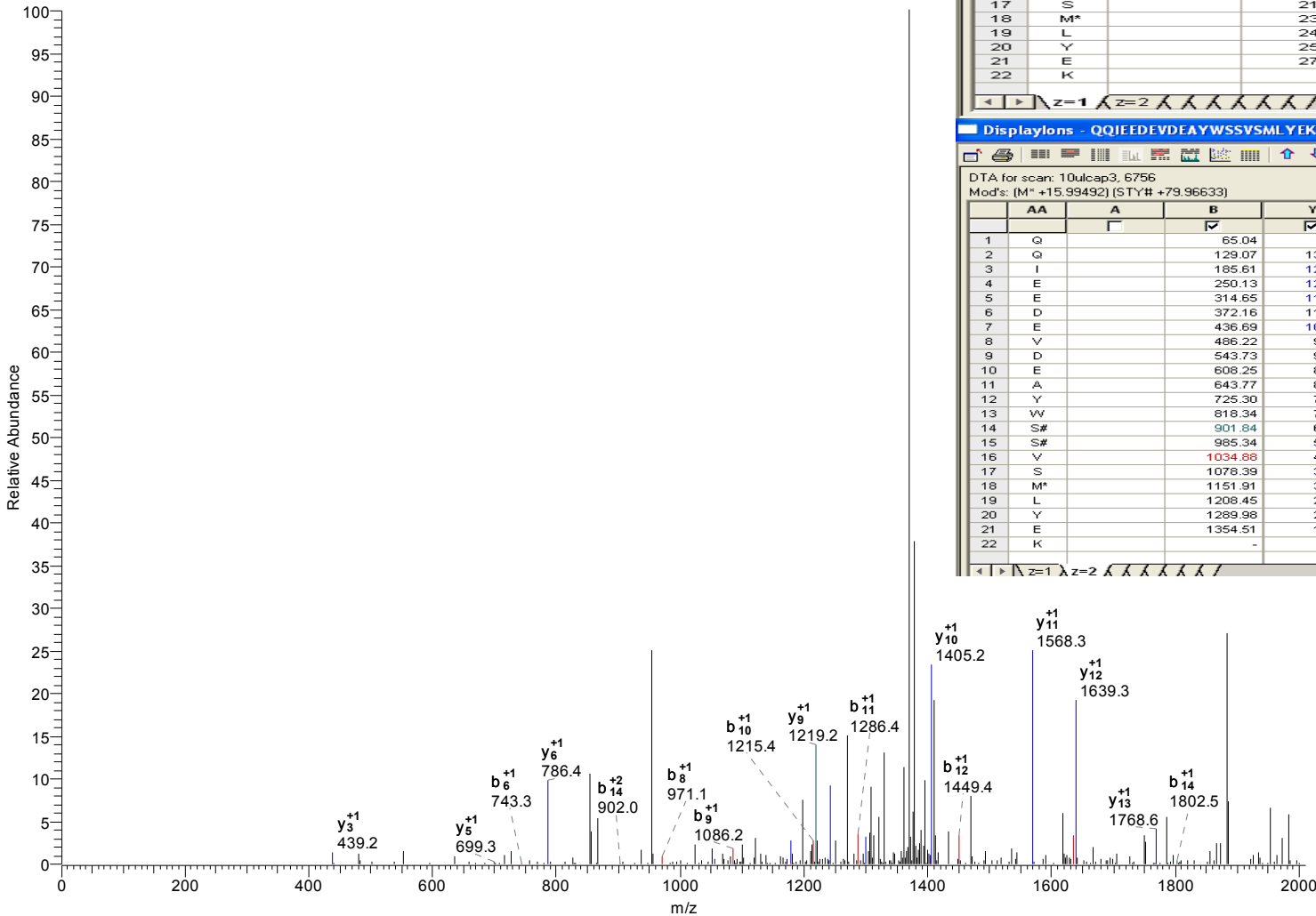
DTA for scans: capETDcidtop3_080419044303, 2869-2870
Mod's: (M⁺+15.99492) (STY# +79.96633)

	AA	A	B	Y	Z
1	Q		43.69	-	22
2	Q		86.36	930.66	21
3	I		124.07	887.99	20
4	E		167.09	850.30	19
5	E		210.10	807.28	18
6	D		248.45	764.27	17
7	E		291.46	725.93	16
8	V		324.48	682.91	15
9	D		362.62	648.89	14
10	E		405.84	611.55	13
11	A		429.52	568.53	12
12	Y		483.87	544.85	11
13	W		545.90	490.50	10
14	S#		601.56	428.47	9
15	S#		657.23	372.81	8
16	V		690.25	317.14	7
17	S#		745.92	284.12	6
18	M		789.60	228.45	5
19	L		827.29	184.77	4
20	Y		881.65	147.06	3
21	E		924.66	92.72	2
22	K		-	49.71	1

z=1 z=2 z=3

Retinol Dehydrogenase 14

#6756-6756 NL: 4.28E2



Displaylons - QQIEEDVDEAYWSSVSMLEYK

DTA for scan: 10ulcap3, 6756
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	Q		129.07			22
2	Q		257.12	2726.05		21
3	I		370.21	2597.99		20
4	E		499.25	2484.91		19
5	E		628.29	2355.87		18
6	D		743.32	2226.82		17
7	E		872.36	2111.80		16
8	V		971.43	1982.75		15
9	D		1086.46	1883.68		14
10	E		1215.50	1768.66		13
11	A		1286.54	1639.62		12
12	Y		1449.60	1568.58		11
13	VW		1635.68	1405.51		10
14	S#		1802.68	1219.44		9
15	S#		1969.68	1052.44		8
16	V		2068.75	885.44		7
17	S		2155.78	786.37		6
18	M*		2302.81	699.34		5
19	L		2415.90	552.30		4
20	Y		2578.96	439.22		3
21	E		2708.00	276.16		2
22	K		-	147.11		1

Displaylons - QQIEEDVDEAYWSSVSMLEYK

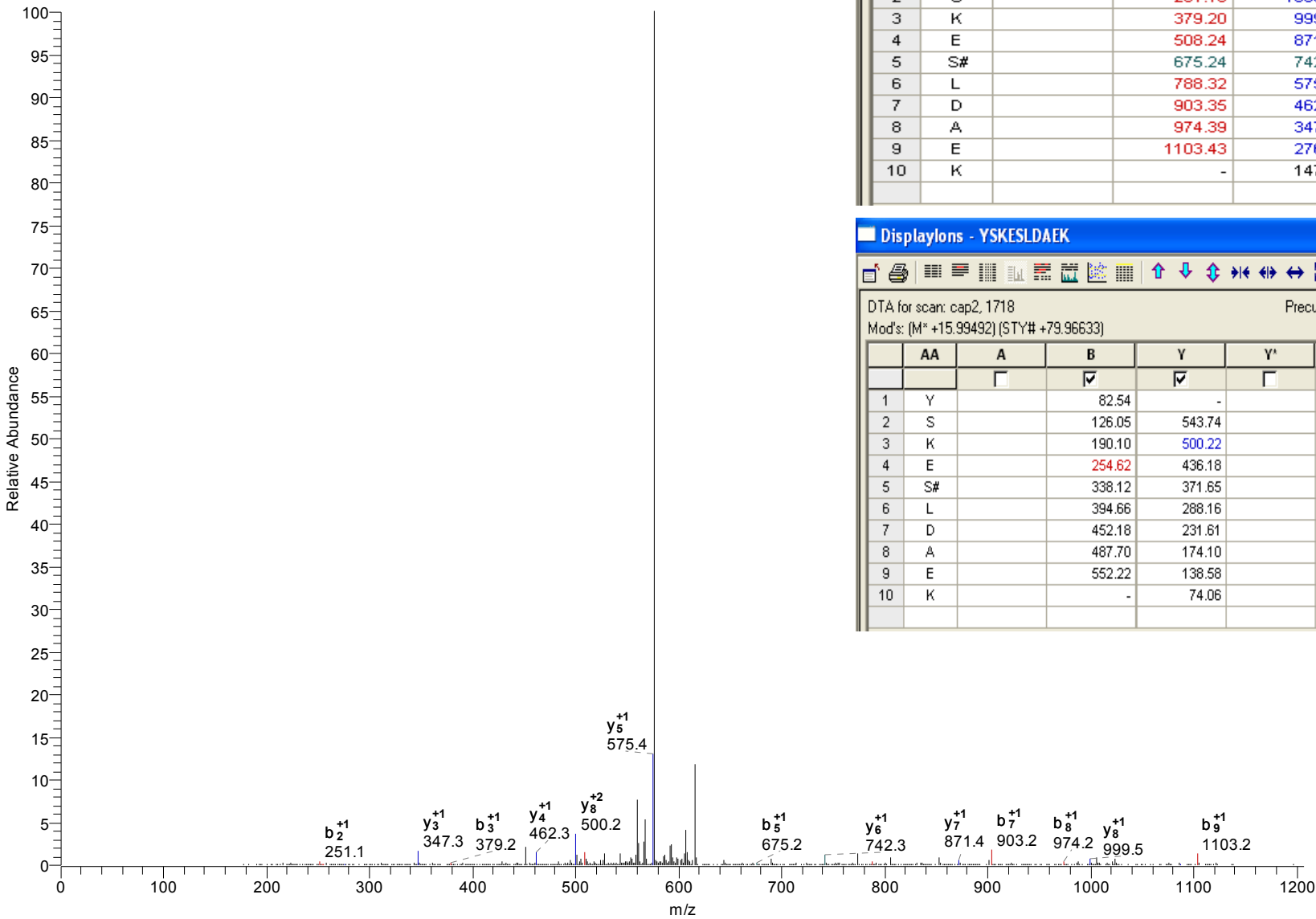
DTA for scan: 10ulcap3, 6756
Mod's: (M⁺ +15.99492) (STY# +79.96633)

Precursor ion: 1428.21 Charge: 2

	AA	A	B	Y	Y*	Y ₀	Z	
1	Q		65.04	-				22
2	Q		129.07	1363.53				21
3	I		185.61	1299.50				20
4	E		250.13	1242.96				19
5	E		314.65	1178.44				18
6	D		372.16	1113.91				17
7	E		436.69	1056.40				16
8	V		486.22	991.88				15
9	D		543.73	942.35				14
10	E		608.25	884.83				13
11	A		643.77	820.31				12
12	Y		725.30	784.79				11
13	VW		818.34	703.26				10
14	S#		901.84	610.22				9
15	S#		985.34	526.72				8
16	V		1034.88	443.22				7
17	S		1078.39	393.69				6
18	M*		1151.91	350.17				5
19	L		1208.45	276.66				4
20	Y		1289.98	220.11				3
21	E		1354.51	138.58				2
22	K		-	74.06				1

Retinol Dehydrogenase 14

#1718-1718 NL: 2.18E4

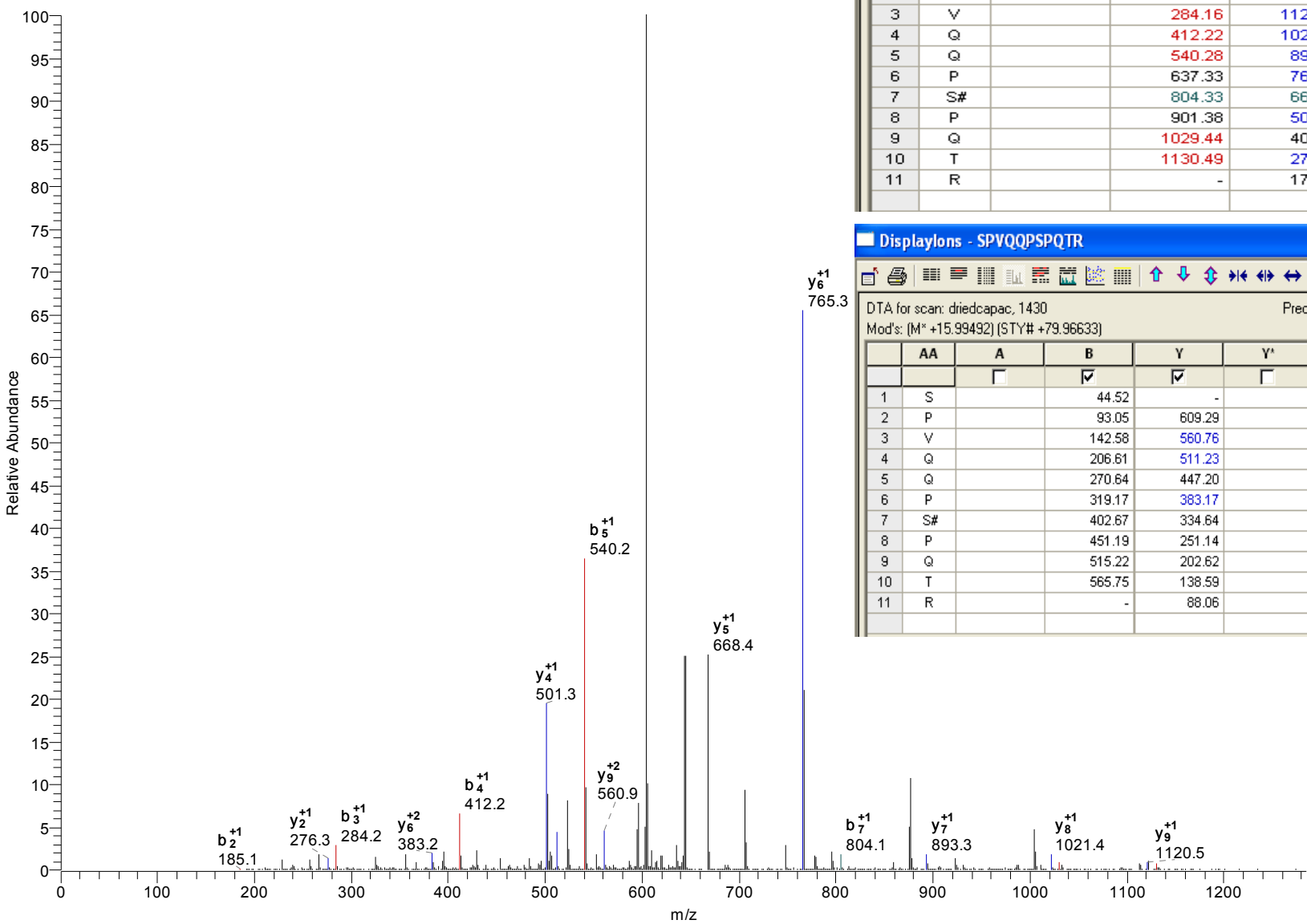


Displaylons - YSKESLDAEK						
DTA for scan: cap2, 1718						
Mod's: (M* +15.99492) (STY# +79.96633)						
	AA	A	B	Y	Z	
1	Y		164.07	-		10
2	S		251.10	1086.47		9
3	K		379.20	999.44		8
4	E		508.24	871.34		7
5	S#		675.24	742.30		6
6	L		788.32	575.30		5
7	D		903.35	462.22		4
8	A		974.39	347.19		3
9	E		1103.43	276.16		2
10	K		-	147.11		1

Displaylons - YSKESLDAEK							
DTA for scan: cap2, 1718							
Mod's: (M* +15.99492) (STY# +79.96633)							
				Precursor ion: 625.66		Charge: 2	
	AA	A	B	Y	Y*	Yo	Z
1	Y		82.54	-			10
2	S		126.05	543.74			9
3	K		190.10	500.22			8
4	E		254.62	436.18			7
5	S#		338.12	371.65			6
6	L		394.66	288.16			5
7	D		452.18	231.61			4
8	A		487.70	174.10			3
9	E		552.22	138.58			2
10	K		-	74.06			1

Retinol Dehydrogenase 14

#1430-1430 NL: 5.58E4



Displaylons - SPVQQPSPQTR

DTA for scan: driedcapac, 1430
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
		☐	☒	☒	☐	
1	S		88.04	-		11
2	P		185.09	1217.57		10
3	V		284.16	1120.51		9
4	Q		412.22	1021.45		8
5	Q		540.28	893.39		7
6	P		637.33	765.33		6
7	S#		804.33	668.28		5
8	P		901.38	501.28		4
9	Q		1029.44	404.23		3
10	T		1130.49	276.17		2
11	R		-	175.12		1

Displaylons - SPVQQPSPQTR

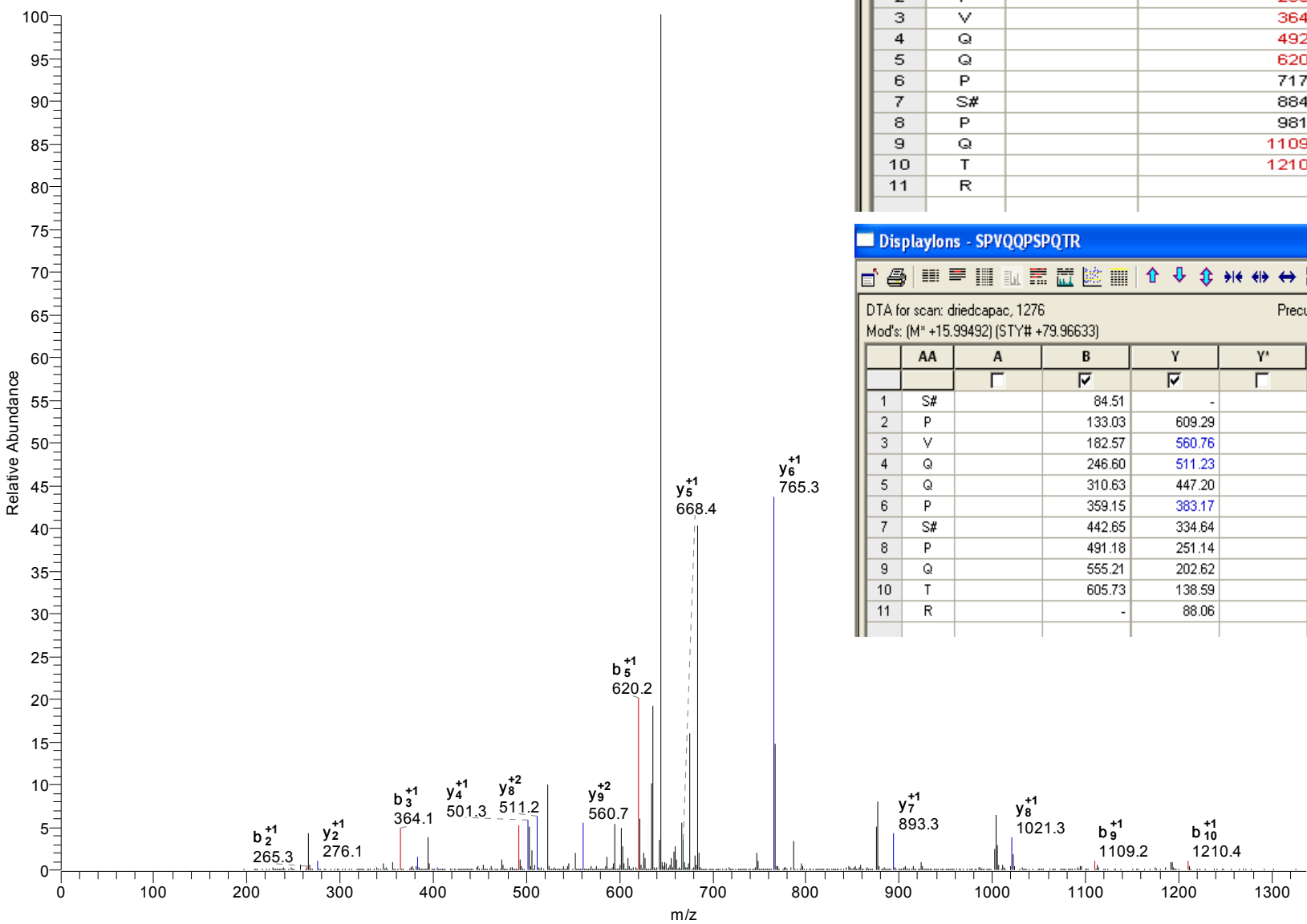
DTA for scan: driedcapac, 1430
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 652.86 Charge: 2

	AA	A	B	Y	Y*	Yo	Z	
		☐	☒	☒	☐	☐	☐	
1	S		44.52	-				11
2	P		93.05	609.29				10
3	V		142.58	560.76				9
4	Q		206.61	511.23				8
5	Q		270.64	447.20				7
6	P		319.17	383.17				6
7	S#		402.67	334.64				5
8	P		451.19	251.14				4
9	Q		515.22	202.62				3
10	T		565.75	138.59				2
11	R		-	88.06				1

Retinol Dehydrogenase 14

#1276-1276 NL: 3.94E4

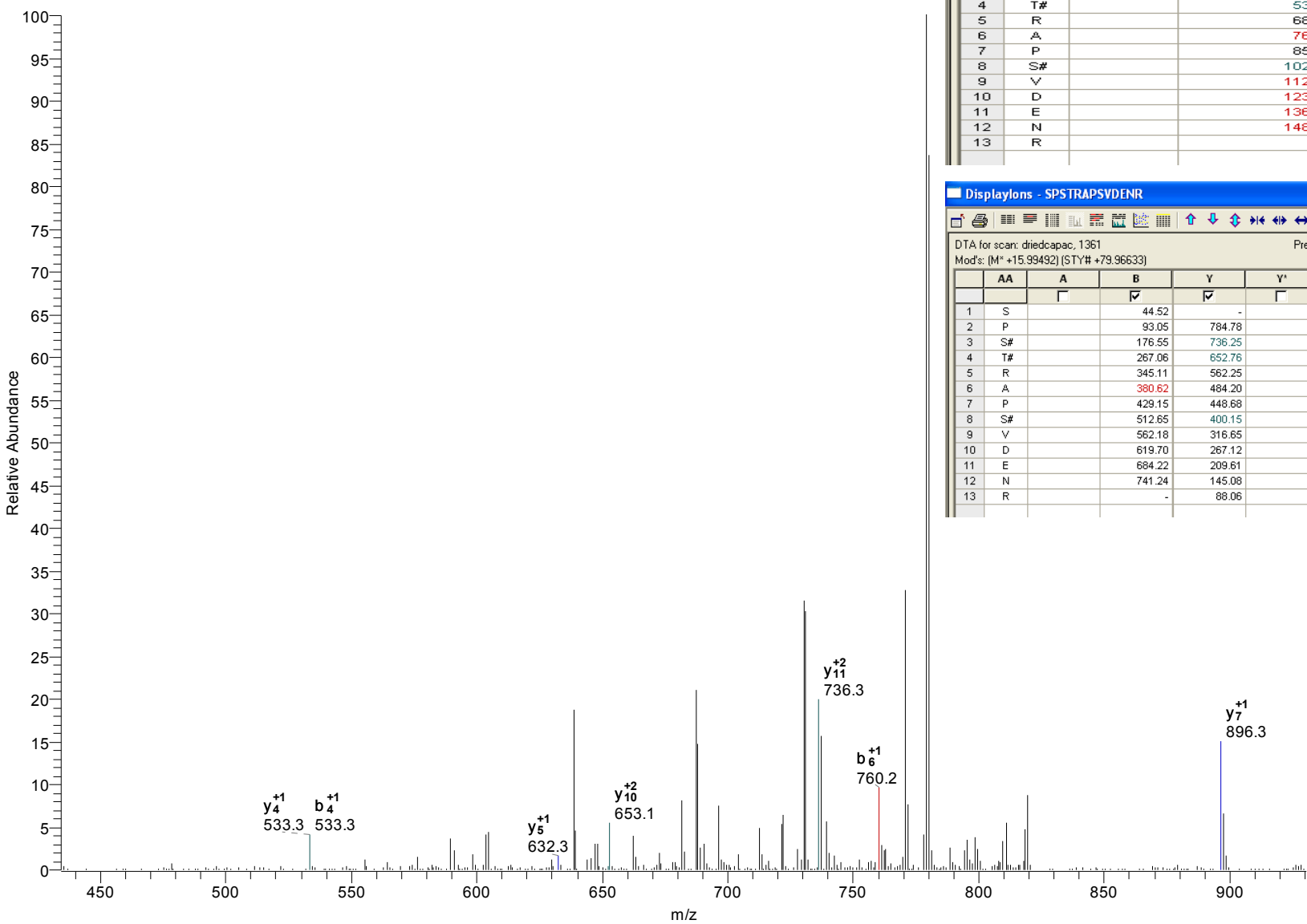


Displaylons - SPVQQPSPQTR					
DTA for scan: driedcapac, 1276					
Mod's: (M* +15.99492) (STY# +79.96633)					
	AA	A	B	Y	
		☐	☒	☒	
1	S#		168.01	-	11
2	P		265.06	1217.57	10
3	V		364.13	1120.51	9
4	Q		492.19	1021.45	8
5	Q		620.24	893.39	7
6	P		717.30	765.33	6
7	S#		884.30	668.28	5
8	P		981.35	501.28	4
9	Q		1109.41	404.23	3
10	T		1210.45	276.17	2
11	R		-	175.12	1

Displaylons - SPVQQPSPQTR							
DTA for scan: driedcapac, 1276							
Mod's: (M* +15.99492) (STY# +79.96633)							
Precursor ion: 692.80 Charge: 2							
	AA	A	B	Y	Y'	Yo	Z
		☐	☒	☒	☐	☐	☐
1	S#		84.51	-			11
2	P		133.03	609.29			10
3	V		182.57	560.76			9
4	Q		246.60	511.23			8
5	Q		310.63	447.20			7
6	P		359.15	383.17			6
7	S#		442.65	334.64			5
8	P		491.18	251.14			4
9	Q		555.21	202.62			3
10	T		605.73	138.59			2
11	R		-	88.06			1

Retinol Dehydrogenase 14

#1361-1361 NL: 6.40E3

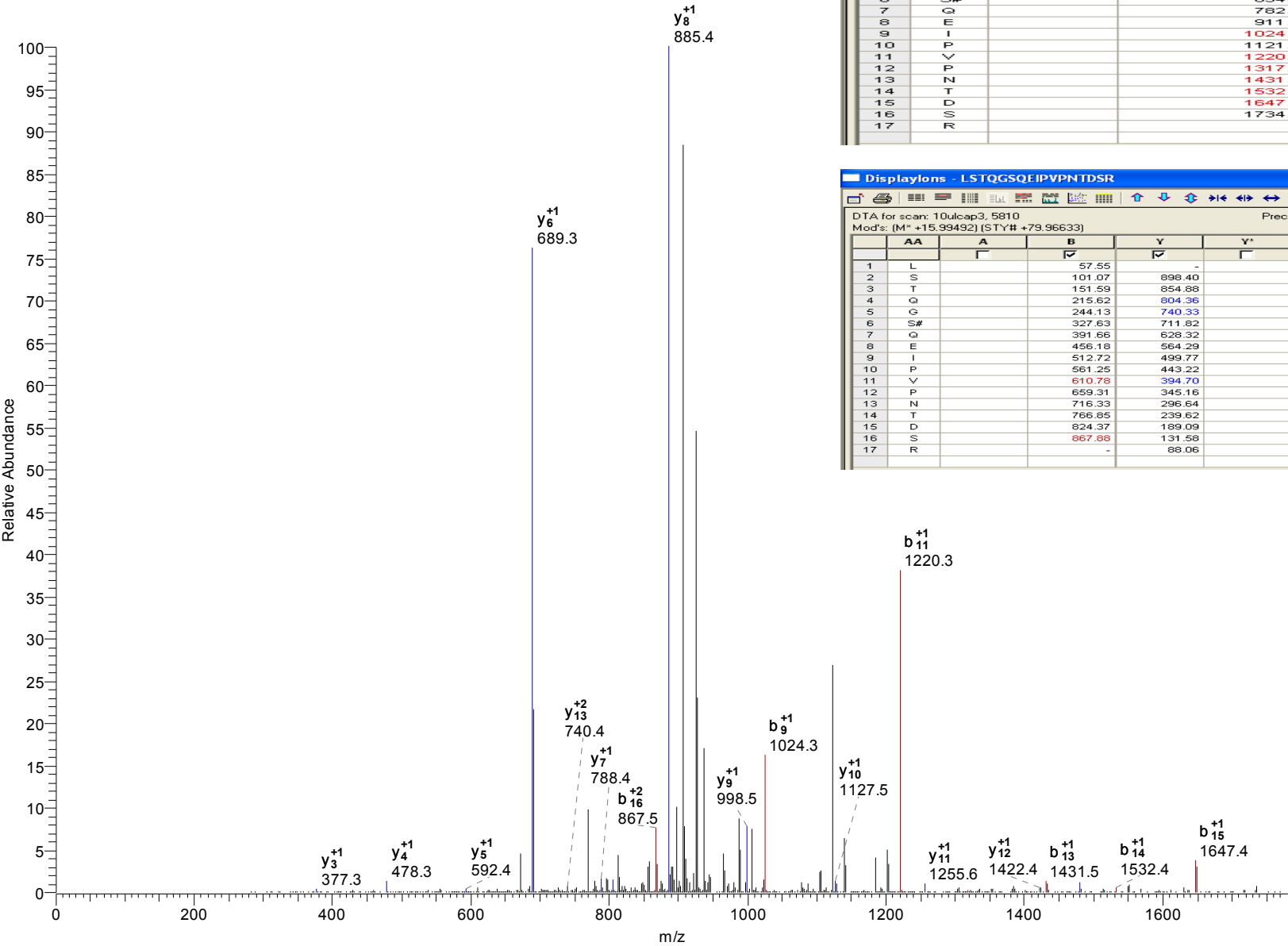


DisplayIons - SPSTRAPSVDENR						
DTA for scan: driedcapac, 1361						
Mod's: (M* +15.99492) (STY# +79.96633)						
	AA	A	B	Y		
1	S		88.04	-	13	
2	P		185.09	1568.55	12	
3	S#		352.09	1471.50	11	
4	T#		533.10	1304.50	10	
5	R		689.21	1123.49	9	
6	A		760.24	967.39	8	
7	P		857.30	896.35	7	
8	S#		1024.29	799.30	6	
9	V		1123.36	632.30	5	
10	D		1238.39	533.23	4	
11	E		1367.43	418.20	3	
12	N		1481.47	289.16	2	
13	R		-	175.12	1	

DisplayIons - SPSTRAPSVDENR						
DTA for scan: driedcapac, 1361						
Mod's: (M* +15.99492) (STY# +79.96633)						
Precursor ion: 828.53 Charge: 2						
	AA	A	B	Y	Y*	Yo
1	S		44.52	-		
2	P		93.05	784.78		
3	S#		176.55	736.25		
4	T#		267.06	652.76		
5	R		345.11	562.25		
6	A		380.62	484.20		
7	P		429.15	448.68		
8	S#		512.65	400.15		
9	V		562.18	316.65		
10	D		619.70	267.12		
11	E		684.22	209.61		
12	N		741.24	145.08		
13	R		-	88.06		

Retinol Dehydrogenase 14

#5810-5810 NL: 9.52E3



Displaylons - LSTQGSQEIPVPNTDSR

DTA for scan: 10ulcap3, 5810
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	L			114.09	-
2	S			201.12	1795.79
3	T			302.17	1708.75
4	Q			430.23	1607.71
5	G			487.25	1479.65
6	S#			654.25	1422.63
7	Q			782.31	1255.63
8	E			911.35	1127.57
9	I			1024.43	998.53
10	P			1121.49	885.44
11	V			1220.56	788.39
12	P			1317.61	689.32
13	N			1431.65	592.27
14	T			1532.70	478.23
15	D			1647.73	377.18
16	S			1734.76	262.15
17	R			-	175.12

Displaylons - LSTQGSQEIPVPNTDSR

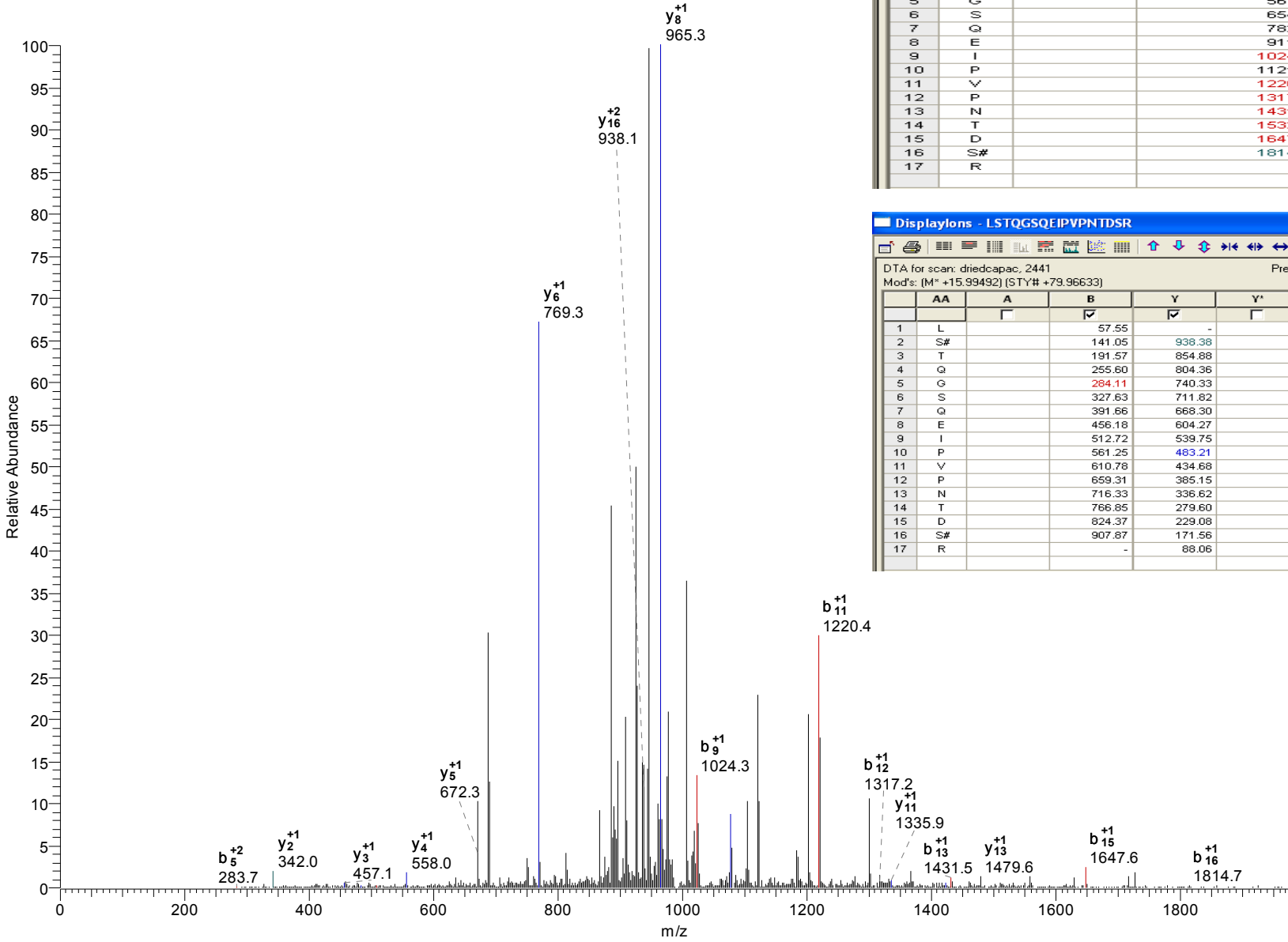
DTA for scan: 10ulcap3, 5810
Mod's: [M⁺ +15.99492] (STY# +79.96633)

Precursor ion: 955.25 Charge: 2

	AA	A	B	Y	Y*	Yo	Z	
1	L		57.55		-			17
2	S		101.07	898.40				16
3	T		151.59	854.88				15
4	Q		215.62	804.36				14
5	G		244.13	740.33				13
6	S#		327.63	711.82				12
7	Q		391.86	628.32				11
8	E		456.18	564.29				10
9	I		512.72	499.77				9
10	P		561.25	443.22				8
11	V		610.78	394.70				7
12	P		659.31	345.16				6
13	N		716.33	296.64				5
14	T		766.85	239.62				4
15	D		824.37	189.09				3
16	S		867.88	131.58				2
17	R		-	88.06				1

Retinol Dehydrogenase 14

#2441-2441 NL: 1.03E4



Displaylons - LSTQGSQEIPVPNTDSR

DTA for scan: driedcapac, 2441
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	A	B	Y	
1	L			114.09	-
2	S#			281.09	1875.75
3	T			382.14	1708.75
4	Q			510.20	1607.71
5	Q			567.22	1479.65
6	S			654.25	1422.63
7	Q			782.31	1335.59
8	E			911.35	1207.54
9	I			1024.43	1078.49
10	P			1121.49	965.41
11	V			1220.56	868.36
12	P			1317.61	769.29
13	N			1431.65	672.23
14	T			1532.70	558.19
15	D			1647.73	457.14
16	S#			1814.72	342.12
17	R			-	175.12

Displaylons - LSTQGSQEIPVPNTDSR

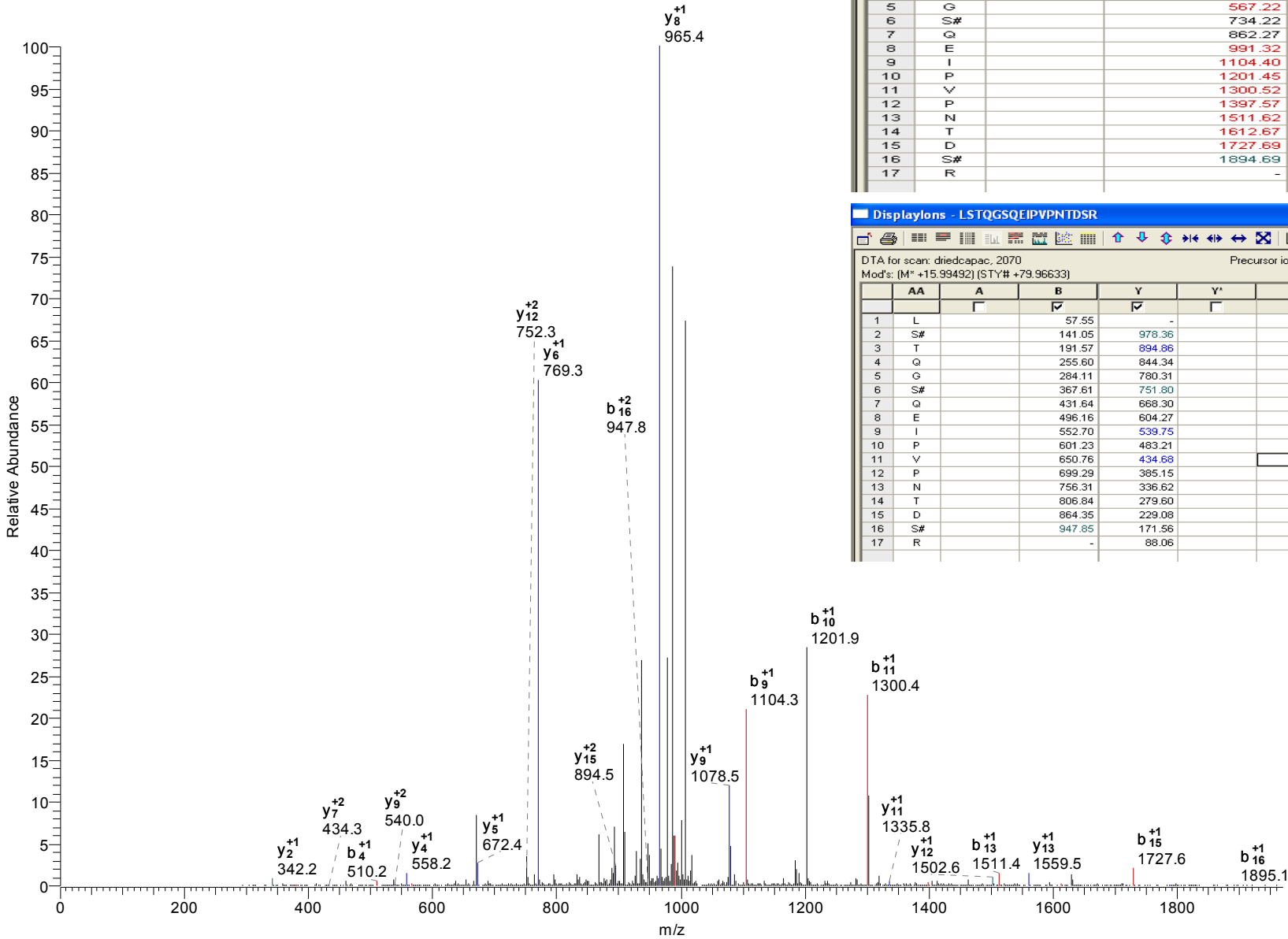
DTA for scan: driedcapac, 2441
Mod's: [M⁺ +15.99492] [STY# +79.96633]

Precursor ion: 995.10 Charge: 2

	AA	A	B	Y	Y'	Yo	Z	
1	L		57.55					17
2	S#		141.05	938.38				16
3	T		191.57	854.88				15
4	Q		255.60	804.36				14
5	Q		284.11	740.33				13
6	S		327.63	711.82				12
7	Q		391.66	668.30				11
8	E		456.18	604.27				10
9	I		512.72	539.75				9
10	P		561.25	483.21				8
11	V		610.78	434.68				7
12	P		659.31	385.15				6
13	N		716.33	336.62				5
14	T		766.85	279.60				4
15	D		824.37	229.08				3
16	S#		907.87	171.56				2
17	R		-	88.06				1

Retinol Dehydrogenase +1

#2070-2070 NL: 2.27E4



Displaylons - LSTQGSQEIPVPNTDSR

DTA for scan: driedcapac, 2070
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	A	B	Y	
1	L		114.09	-	17
2	S#		281.09	1955.72	16
3	T		382.14	1788.72	15
4	Q		510.20	1687.67	14
5	G		567.22	1559.61	13
6	S#		734.22	1502.59	12
7	Q		862.27	1335.59	11
8	E		991.32	1207.54	10
9	I		1104.40	1078.49	9
10	P		1201.45	965.41	8
11	V		1300.52	868.36	7
12	P		1397.57	769.29	6
13	N		1511.62	672.23	5
14	T		1612.67	558.19	4
15	D		1727.69	457.14	3
16	S#		1894.69	342.12	2
17	R		-	175.12	1

Displaylons - LSTQGSQEIPVPNTDSR

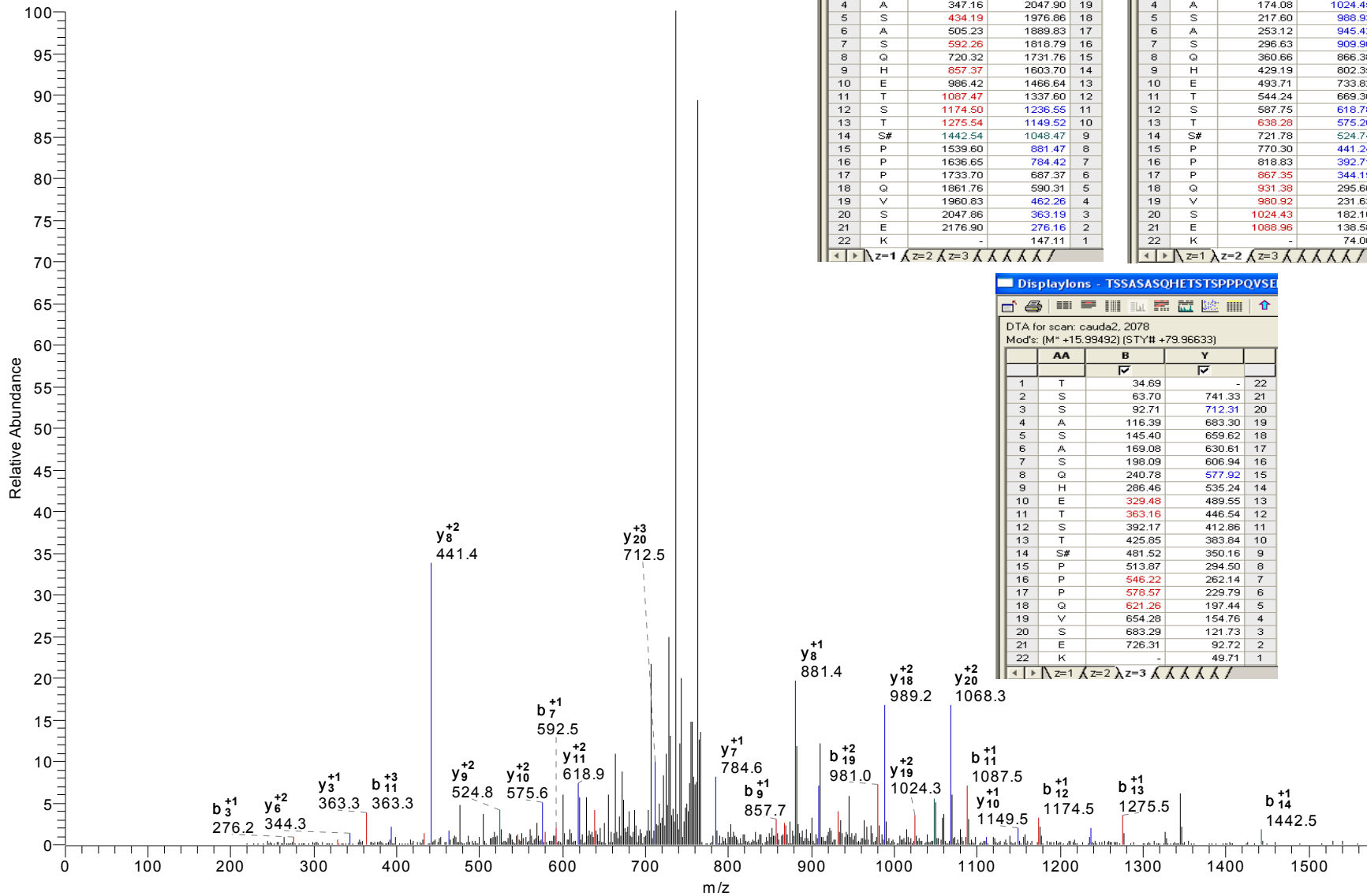
DTA for scan: driedcapac, 2070
Mod's: [M⁺ +15.99492] [STY# +79.96633]

Precursor ion: 1034.79 Charge: 2

	AA	A	B	Y	Y'	Yo	Z	
1	L		57.55	-				17
2	S#		141.05	978.36				16
3	T		191.57	894.86				15
4	Q		255.60	844.34				14
5	G		284.11	780.31				13
6	S#		367.61	751.80				12
7	Q		431.64	668.30				11
8	E		496.16	604.27				10
9	I		552.70	539.75				9
10	P		601.23	483.21				8
11	V		650.76	434.68				7
12	P		699.29	385.15				6
13	N		756.31	336.62				5
14	T		806.84	279.60				4
15	D		864.35	229.08				3
16	S#		947.85	171.56				2
17	R		-	88.06				1

Retinol dehydrogenase 14

#2078-2078 NL: 3.18E3



Displaylons - TSSASAQHETSTSPPPQVSE

DTA for scan: cauda2, 2078
Mod's: [M⁺+15.99492] (STY# +79.96633)

	AA	B	Y	
1	T	102.05	-	22
2	S	189.09	2221.96	21
3	S	276.12	2134.93	20
4	A	347.16	2047.90	19
5	S	434.19	1976.86	18
6	A	505.23	1889.83	17
7	S	592.26	1818.79	16
8	Q	720.32	1731.76	15
9	H	857.37	1603.70	14
10	E	986.42	1466.64	13
11	T	1087.47	1337.60	12
12	S	1174.50	1236.55	11
13	T	1275.54	1149.52	10
14	S#	1442.54	1048.47	9
15	P	1539.60	881.47	8
16	P	1636.65	784.42	7
17	P	1733.70	687.37	6
18	Q	1861.76	590.31	5
19	V	1960.83	462.26	4
20	S	2047.86	363.19	3
21	E	2176.90	276.16	2
22	K	-	147.11	1

Displaylons - TSSASAQHETSTSPPPQVSE

DTA for scan: cauda2, 2078
Mod's: [M⁺+15.99492] (STY# +79.96633)

	AA	B	Y	
1	T	51.53	-	22
2	S	95.05	1111.48	21
3	S	138.56	1067.97	20
4	A	174.08	1024.45	19
5	S	217.60	988.93	18
6	A	253.12	945.42	17
7	S	296.63	909.90	16
8	Q	360.66	866.38	15
9	H	429.19	802.35	14
10	E	493.71	733.82	13
11	T	544.24	669.30	12
12	S	587.75	618.78	11
13	T	638.28	575.26	10
14	S#	721.78	524.74	9
15	P	770.30	441.24	8
16	P	818.83	392.71	7
17	P	867.35	344.19	6
18	Q	931.38	295.66	5
19	V	980.92	231.63	4
20	S	1024.43	182.10	3
21	E	1088.96	138.58	2
22	K	-	74.06	1

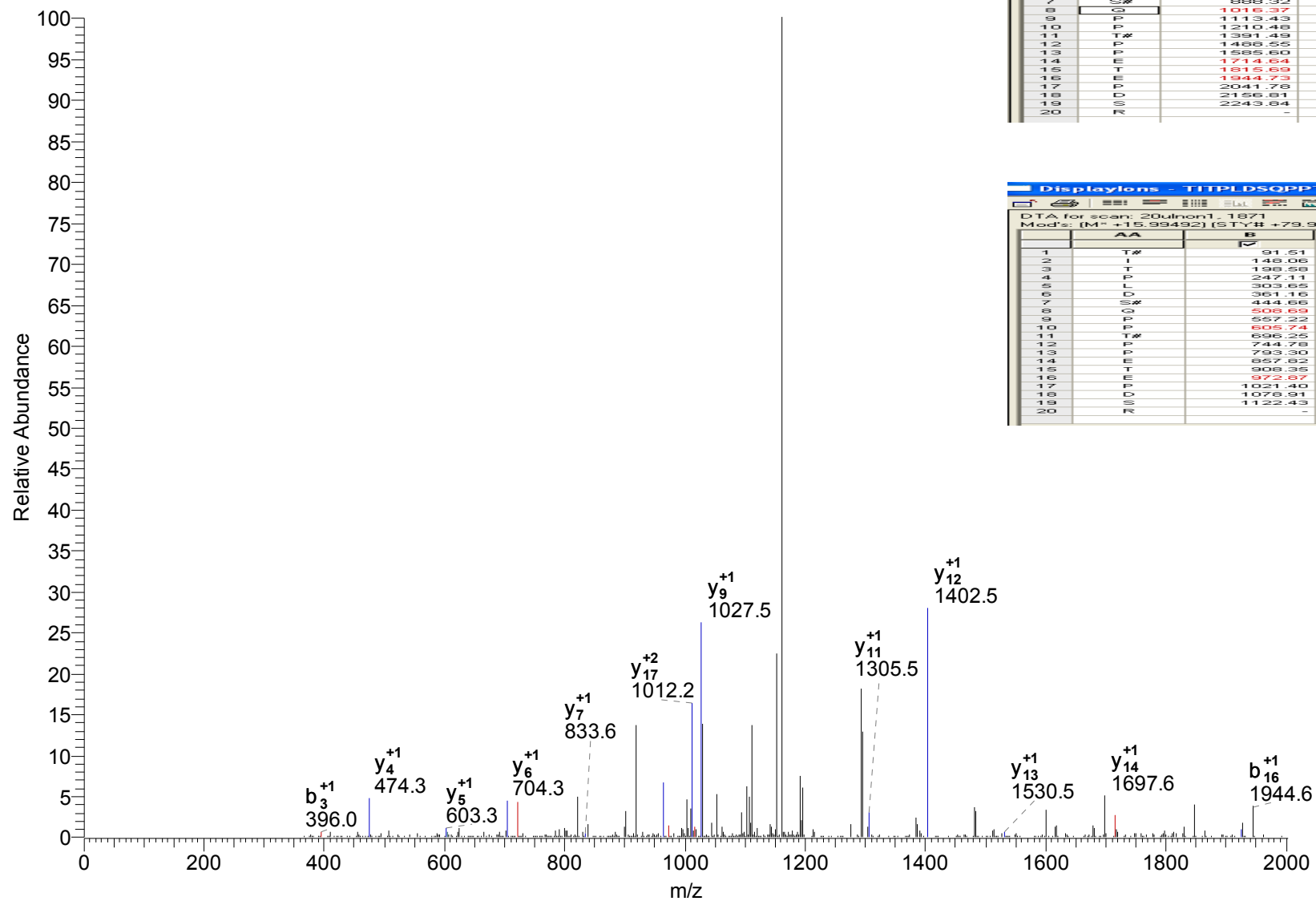
Displaylons - TSSASAQHETSTSPPPQVSE

DTA for scan: cauda2, 2078
Mod's: [M⁺+15.99492] (STY# +79.96633)

	AA	B	Y	
1	T	34.69	-	22
2	S	63.70	741.33	21
3	S	92.71	712.31	20
4	A	116.39	683.30	19
5	S	145.40	659.62	18
6	A	169.08	630.61	17
7	S	198.09	606.94	16
8	Q	240.78	577.92	15
9	H	286.46	535.24	14
10	E	329.48	489.55	13
11	T	363.16	446.54	12
12	S	392.17	412.86	11
13	T	425.85	383.84	10
14	S#	481.52	350.16	9
15	P	513.87	294.50	8
16	P	546.22	262.14	7
17	P	578.57	229.79	6
18	Q	621.26	197.44	5
19	V	654.28	154.76	4
20	S	683.29	121.73	3
21	E	726.31	92.72	2
22	K	-	49.71	1

Rdh14 Retinol dehydrogenase 14

#1871-1871 NL: 6.16E3



Displays - TITPLDSQPP TPPETPDPSR

DTA for scan: 20ulnon1_1871
Mod's: (M⁺ +15.99492) (S⁺Y⁺ +79.96633)

	AA	B	Y	
1	T#	182.02	-	20
2	I	295.11	2236.94	19
3	T	396.15	2123.86	18
4	P	493.21	2022.61	17
5	L	506.29	1925.76	16
6	D	721.32	1812.67	15
7	S#	888.32	1697.65	14
8	Q	1016.37	1530.65	13
9	P	1113.43	1402.59	12
10	P	1210.48	1305.54	11
11	T#	1391.49	1208.48	10
12	P	1488.55	1027.47	9
13	P	1585.60	930.42	8
14	E	1714.64	833.36	7
15	T	1815.69	704.32	6
16	E	1944.73	603.27	5
17	P	2041.78	474.23	4
18	D	2156.81	377.18	3
19	S	2243.84	262.15	2
20	R	-	175.12	1

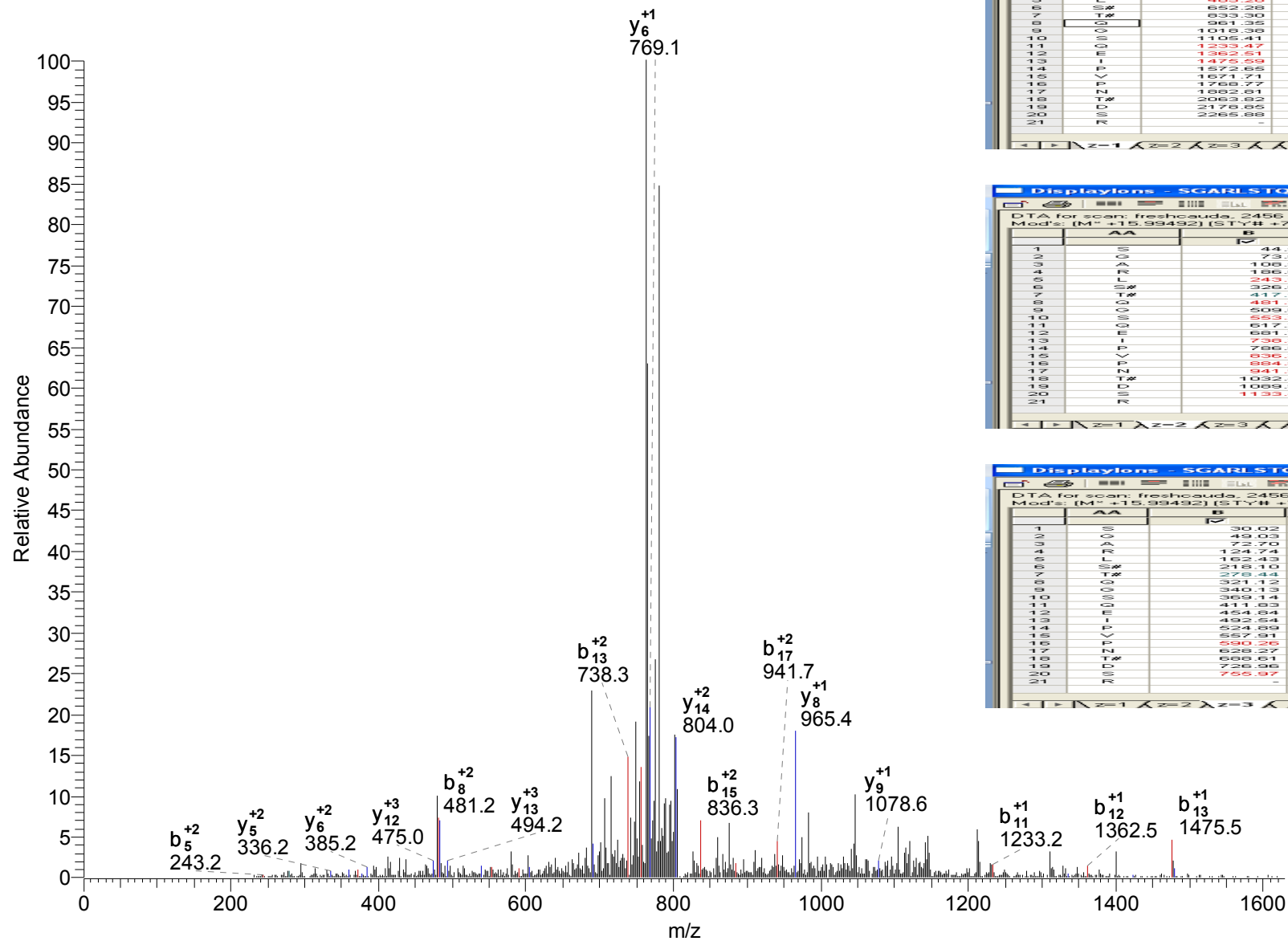
Displays - TITPLDSQPP TPPETPDPSR

DTA for scan: 20ulnon1_1871
Mod's: (M⁺ +15.99492) (S⁺Y⁺ +79.96633)

	AA	B	Y	
1	T#	91.51	-	20
2	I	148.06	1118.97	19
3	T	198.58	1062.43	18
4	P	247.11	1011.31	17
5	L	303.65	963.38	16
6	D	351.16	906.64	15
7	S#	444.66	849.33	14
8	Q	506.69	785.83	13
9	P	557.22	701.60	12
10	P	605.74	653.27	11
11	T#	696.25	604.75	10
12	P	744.78	514.24	9
13	P	793.30	465.71	8
14	E	857.82	417.19	7
15	T	908.35	352.66	6
16	E	972.87	302.14	5
17	P	1021.40	237.62	4
18	D	1076.91	189.09	3
19	S	1122.43	131.58	2
20	R	-	88.06	1

Rdh14 Retinol dehydrogenase 14

#2456-2456 NL: 6.07E3



Displays - SCARLS TQGSQEIPVPNTDSR

DTA for scan: freshcauda, 2456
Mod: (M⁺ +15.93432) (S Ty# +79.96633)

	AA	B	Y	
1	S	68.04	-	21
2	O	145.06	2352.96	20
3	A	216.10	2295.94	19
4	R	372.20	2224.90	18
5	L	465.28	2068.60	17
6	S#	662.28	1955.72	16
7	T#	833.30	1766.72	15
8	O	981.35	1607.71	14
9	O	1018.38	1479.65	13
10	S	1105.41	1422.63	12
11	O	1233.47	1336.59	11
12	E	1362.51	1207.54	10
13	I	1475.59	1076.49	9
14	P	1572.65	965.41	8
15	V	1671.71	868.36	7
16	N	1768.77	769.29	6
17	N	1862.81	672.23	5
18	T#	2063.82	558.19	4
19	D	2178.85	377.18	3
20	R	2265.88	262.15	2
21	R	-	175.12	1

Displays - SCARLS TQGSQEIPVPNTDSR

DTA for scan: freshcauda, 2456
Mod: (M⁺ +15.93432) (S Ty# +79.96633)

	AA	B	Y	
1	S	44.52	-	21
2	O	73.03	1176.98	20
3	A	106.55	1148.47	19
4	R	186.60	1112.96	18
5	L	243.15	1034.90	17
6	S#	326.64	978.36	16
7	T#	417.15	894.66	15
8	O	481.18	804.36	14
9	O	509.69	740.33	13
10	S	553.21	711.82	12
11	O	517.24	659.30	11
12	E	681.76	604.27	10
13	I	738.30	539.75	9
14	P	786.83	483.21	8
15	V	836.36	434.68	7
16	N	884.89	385.15	6
17	N	941.91	336.62	5
18	T#	1032.42	279.60	4
19	D	1089.93	189.09	3
20	R	1133.44	131.58	2
21	R	-	85.05	1

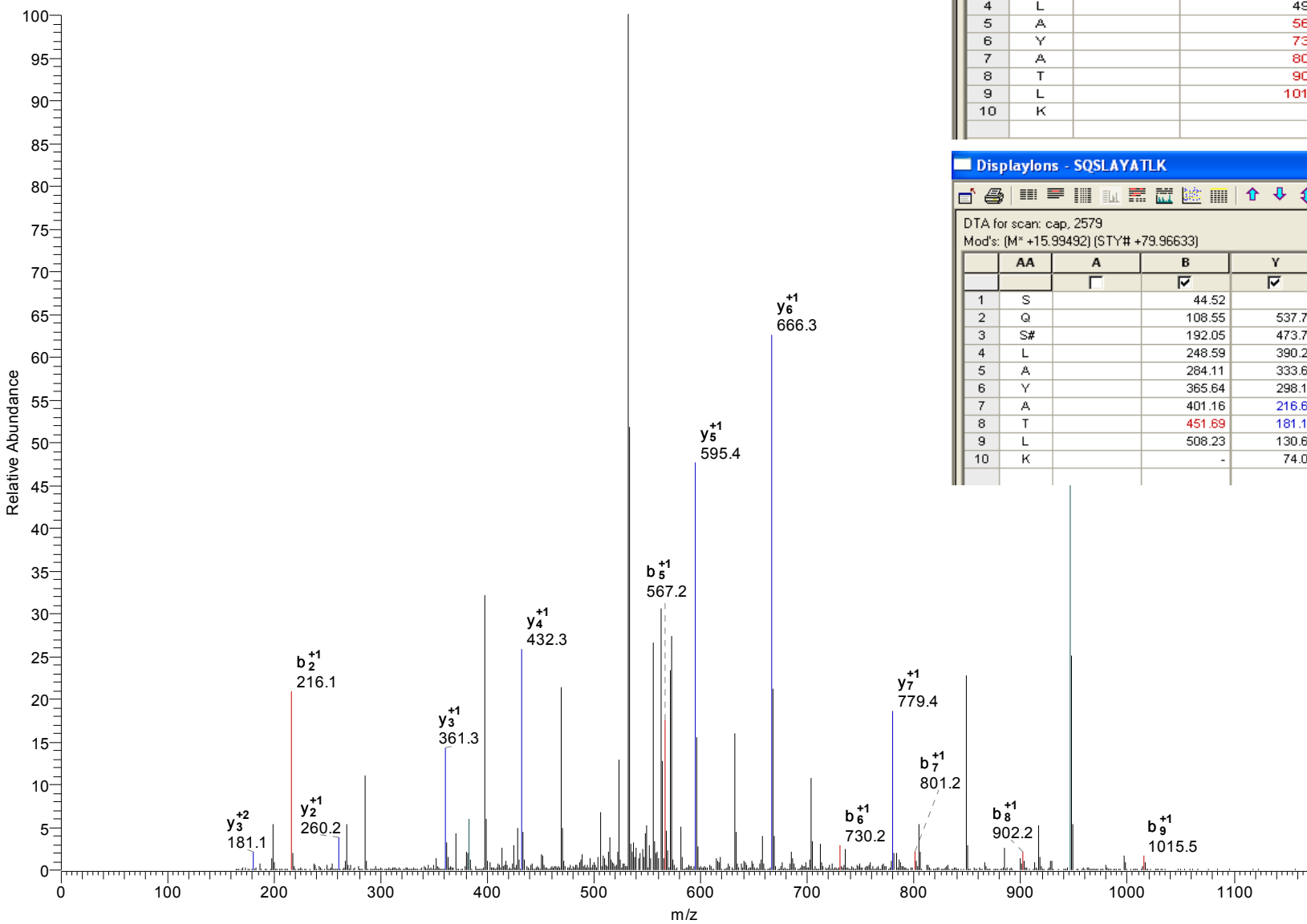
Displays - SCARLS TQGSQEIPVPNTDSR

DTA for scan: freshcauda, 2456
Mod: (M⁺ +15.93432) (S Ty# +79.96633)

	AA	B	Y	
1	S	30.02	-	21
2	O	49.03	784.99	20
3	A	72.70	765.99	19
4	R	124.74	742.31	18
5	L	162.43	690.27	17
6	S#	216.10	652.56	16
7	T#	278.44	596.91	15
8	O	321.12	536.57	14
9	O	340.13	493.89	13
10	S	369.14	474.88	12
11	O	411.83	445.87	11
12	E	454.84	403.18	10
13	I	492.64	360.17	9
14	P	524.69	322.47	8
15	V	567.91	290.12	7
16	N	590.26	257.10	6
17	N	628.27	224.75	5
18	T#	668.61	186.74	4
19	D	726.96	126.40	3
20	R	766.97	86.06	2
21	R	-	59.04	1

Akap4 A-kinase anchor protein 4

#2579-2579 NL: 1.71E4

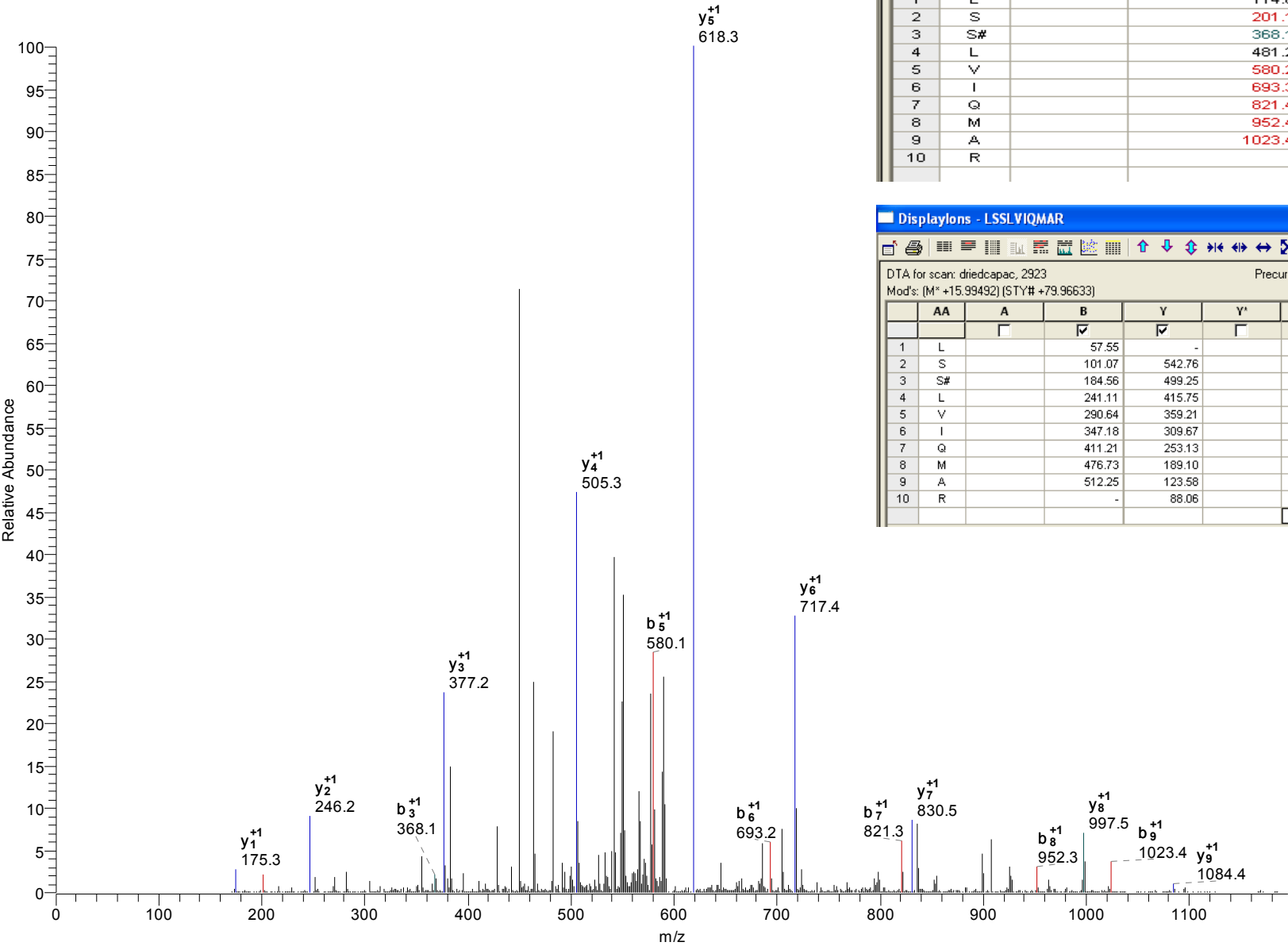


Displaylons - SSQLAYATLK					
DTA for scan: cap, 2579					
Mod's: (M* +15.99492) (STY# +79.96633)					
	AA	A	B	Y	
1	S		88.04	-	10
2	Q		216.10	1074.52	9
3	S#		383.10	946.46	8
4	L		496.18	779.47	7
5	A		567.22	666.38	6
6	Y		730.28	595.34	5
7	A		801.32	432.28	4
8	T		902.37	361.24	3
9	L		1015.45	260.20	2
10	K		-	147.11	1

Displaylons - SSQLAYATLK						
DTA for scan: cap, 2579						
Mod's: (M* +15.99492) (STY# +79.96633)						
Precursor ion: 581.63						
	AA	A	B	Y	Y'	Yo
1	S		44.52	-		
2	Q		108.55	537.77		
3	S#		192.05	473.74		
4	L		248.59	390.24		
5	A		284.11	333.69		
6	Y		365.64	298.18		
7	A		401.16	216.64		
8	T		451.69	181.13		
9	L		508.23	130.60		
10	K		-	74.06		

Akap4 A-kinase anchor protein 4

#2923-2923 NL: 1.86E4



Displaylons - LSSLVIQMAR

DTA for scan: driedcapac, 2923
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L		114.09	-	10
2	S		201.12	1084.52	9
3	S#		368.12	997.49	8
4	L		481.21	830.49	7
5	V		580.27	717.41	6
6	I		693.36	618.34	5
7	Q		821.42	505.26	4
8	M		952.46	377.20	3
9	A		1023.49	246.16	2
10	R		-	175.12	1

Displaylons - LSSLVIQMAR

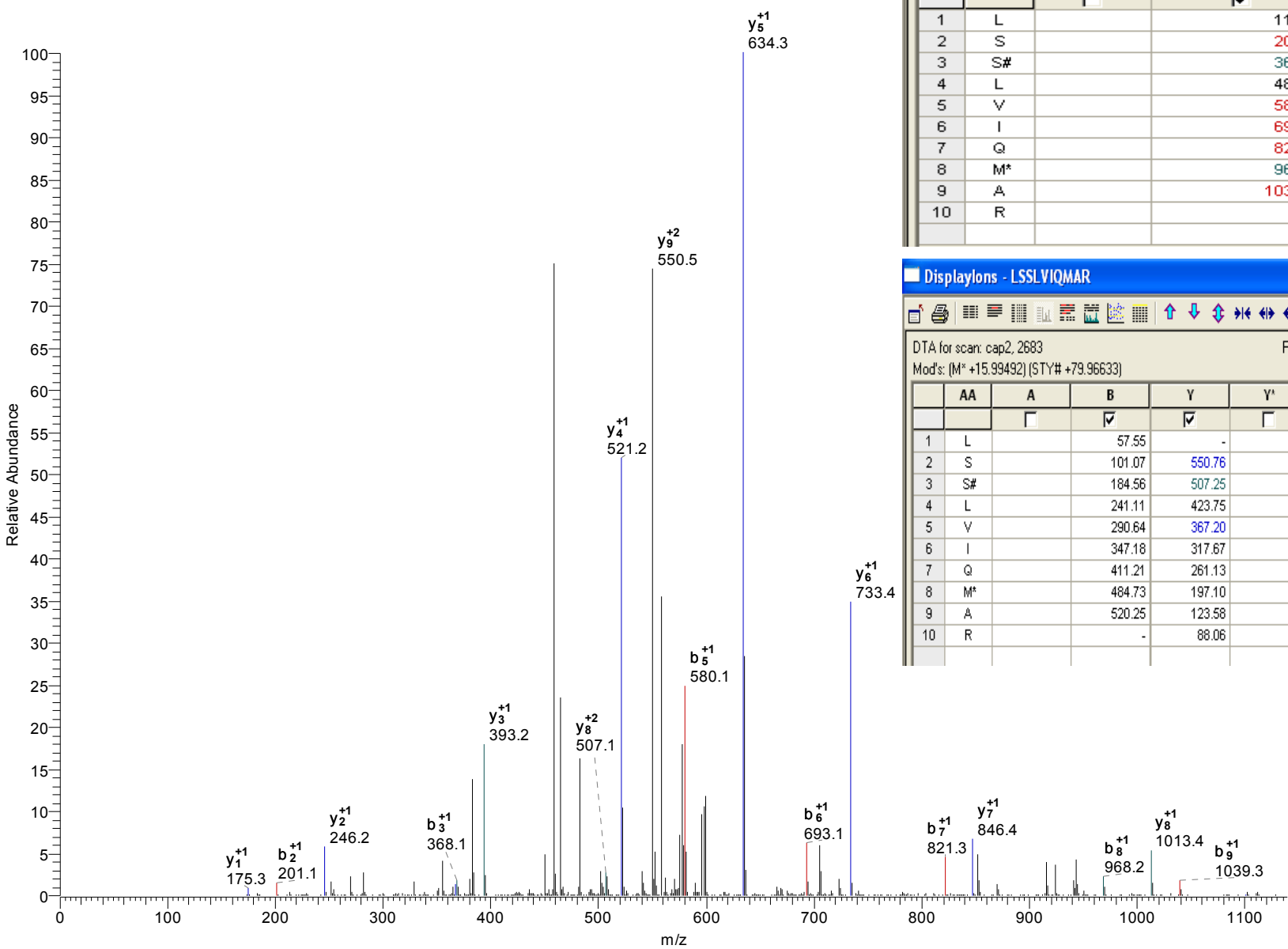
DTA for scan: driedcapac, 2923
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 599.19 Charge: 2

	AA	A	B	Y	Y'	Yo	Z	
1	L		57.55	-				10
2	S		101.07	542.76				9
3	S#		184.56	499.25				8
4	L		241.11	415.75				7
5	V		290.64	359.21				6
6	I		347.18	309.67				5
7	Q		411.21	253.13				4
8	M		476.73	189.10				3
9	A		512.25	123.58				2
10	R		-	88.06				1

Akap4 A-kinase anchor protein 4

#2683-2683 NL: 2.41E5



Displaylons - LSSLVIQMAR

DTA for scan: cap2, 2683
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	L		114.09	-	10
2	S		201.12	1100.52	9
3	S#		368.12	1013.48	8
4	L		481.21	846.49	7
5	V		580.27	733.40	6
6	I		693.36	634.33	5
7	Q		821.42	521.25	4
8	M*		968.45	393.19	3
9	A		1039.49	246.16	2
10	R		-	175.12	1

Displaylons - LSSLVIQMAR

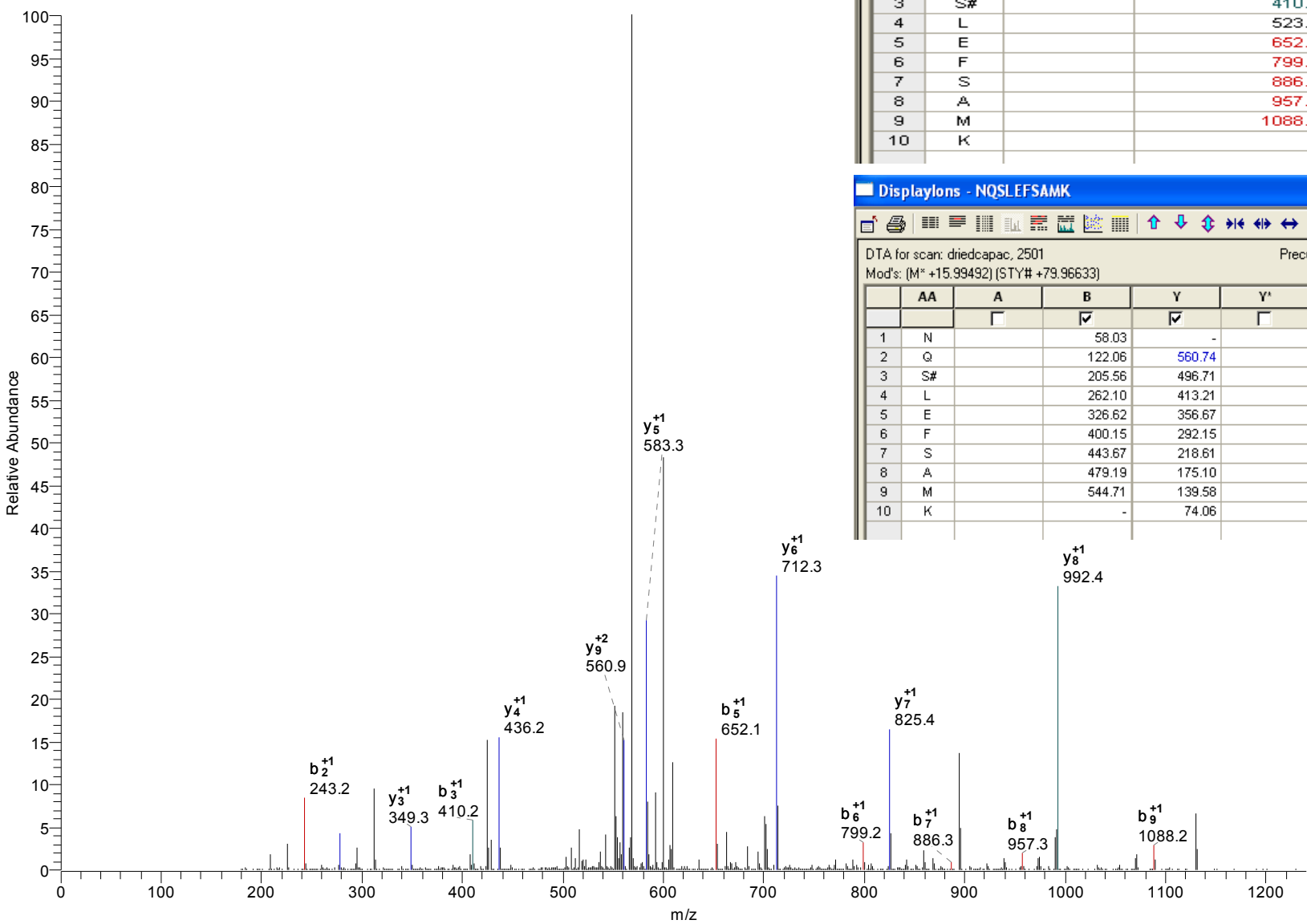
DTA for scan: cap2, 2683
Mod's: [M* +15.99492] (STY# +79.96633)

Precursor ion: 607.35 Charge: 2

	AA	A	B	Y	Y'	Y0	Z	
1	L		57.55	-				10
2	S		101.07	550.76				9
3	S#		184.56	507.25				8
4	L		241.11	423.75				7
5	V		290.64	367.20				6
6	I		347.18	317.67				5
7	Q		411.21	261.13				4
8	M*		484.73	197.10				3
9	A		520.25	123.58				2
10	R		-	88.06				1

Akap4 A-kinase anchor protein 4

#2501-2501 NL: 1.07E5

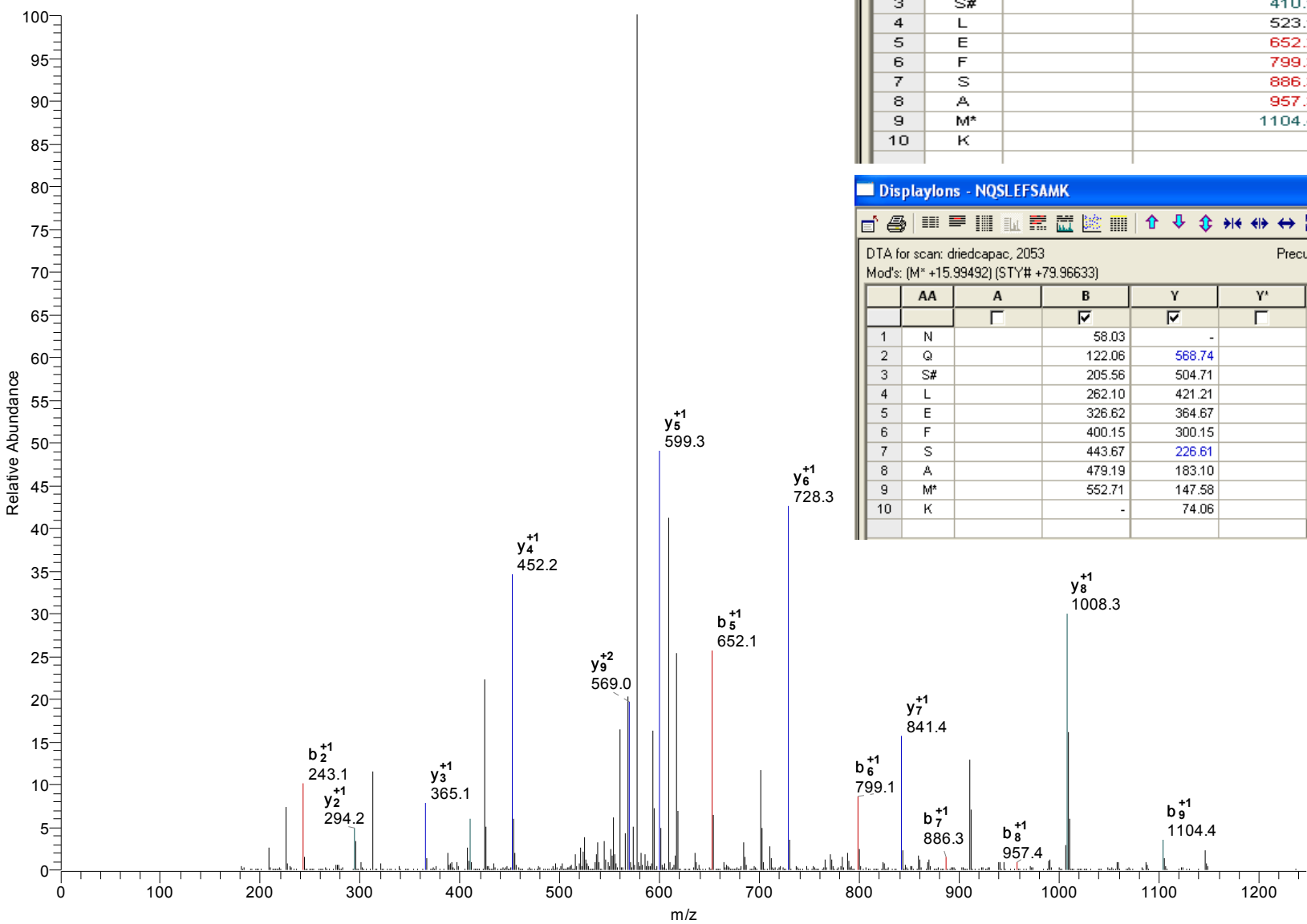


Displaylons - NQSLEFSAMK					
DTA for scan: driedcapac, 2501					
Mod's: [M* +15.99492] (STY# +79.96633)					
	AA	A	B	Y	
1	N		115.05	-	10
2	Q		243.11	1120.47	9
3	S#		410.11	992.42	8
4	L		523.19	825.42	7
5	E		652.23	712.33	6
6	F		799.30	583.29	5
7	S		886.33	436.22	4
8	A		957.37	349.19	3
9	M		1088.41	278.15	2
10	K		-	147.11	1

Displaylons - NQSLEFSAMK							
DTA for scan: driedcapac, 2501							
Mod's: [M* +15.99492] (STY# +79.96633)							
Precursor ion: 617.33 Charge: 2							
	AA	A	B	Y	Y'	Yo	Z
1	N		58.03	-			10
2	Q		122.06	560.74			9
3	S#		205.56	496.71			8
4	L		262.10	413.21			7
5	E		326.62	356.67			6
6	F		400.15	292.15			5
7	S		443.67	218.61			4
8	A		479.19	175.10			3
9	M		544.71	139.58			2
10	K		-	74.06			1

Akap4 A-kinase anchor protein 4

#2053-2053 NL: 2.78E5



Displaylons - NQSLEFSAMK

DTA for scan: driedcapac, 2053
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	10
2	Q		243.11	1136.47	9
3	S#		410.11	1008.41	8
4	L		523.19	841.41	7
5	E		652.23	728.33	6
6	F		799.30	599.29	5
7	S		886.33	452.22	4
8	A		957.37	365.19	3
9	M*		1104.41	294.15	2
10	K		-	147.11	1

Displaylons - NQSLEFSAMK

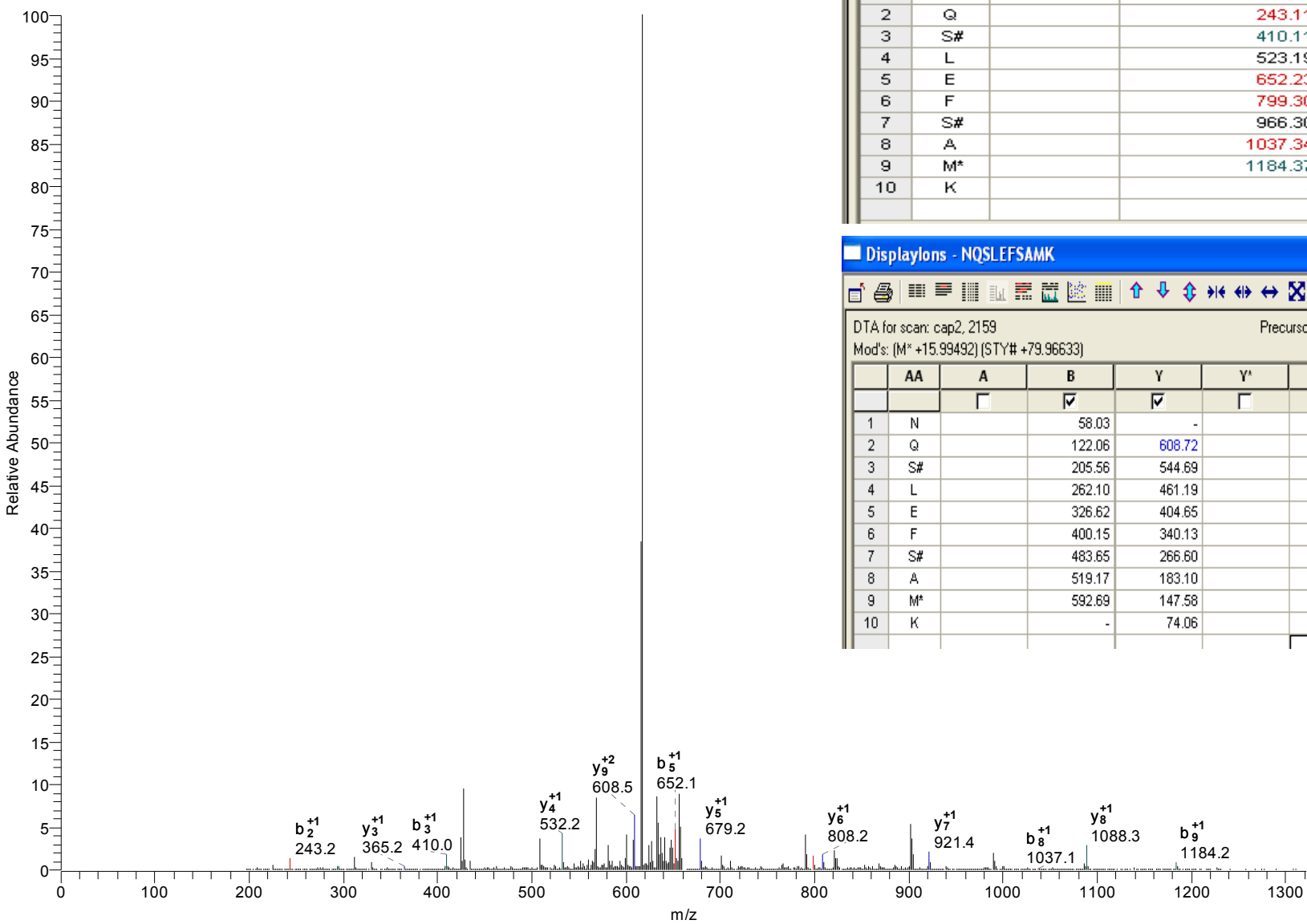
DTA for scan: driedcapac, 2053
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 626.05 Charge: 2

	AA	A	B	Y	Y'	Yo	Z	
1	N		58.03	-				10
2	Q		122.06	568.74				9
3	S#		205.56	504.71				8
4	L		262.10	421.21				7
5	E		326.62	364.67				6
6	F		400.15	300.15				5
7	S		443.67	226.61				4
8	A		479.19	183.10				3
9	M*		552.71	147.58				2
10	K		-	74.06				1

Akap4 A-kinase anchor protein 4

#2159-2159 NL: 3.98E4



Displaylons - NQSLEFSAMK

DTA for scan: cap2, 2159
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	10
2	Q		243.11	1216.44	9
3	S#		410.11	1088.38	8
4	L		523.19	921.38	7
5	E		652.23	808.29	6
6	F		799.30	679.25	5
7	S#		966.30	532.18	4
8	A		1037.34	365.19	3
9	M*		1184.37	294.15	2
10	K		-	147.11	1

Displaylons - NQSLEFSAMK

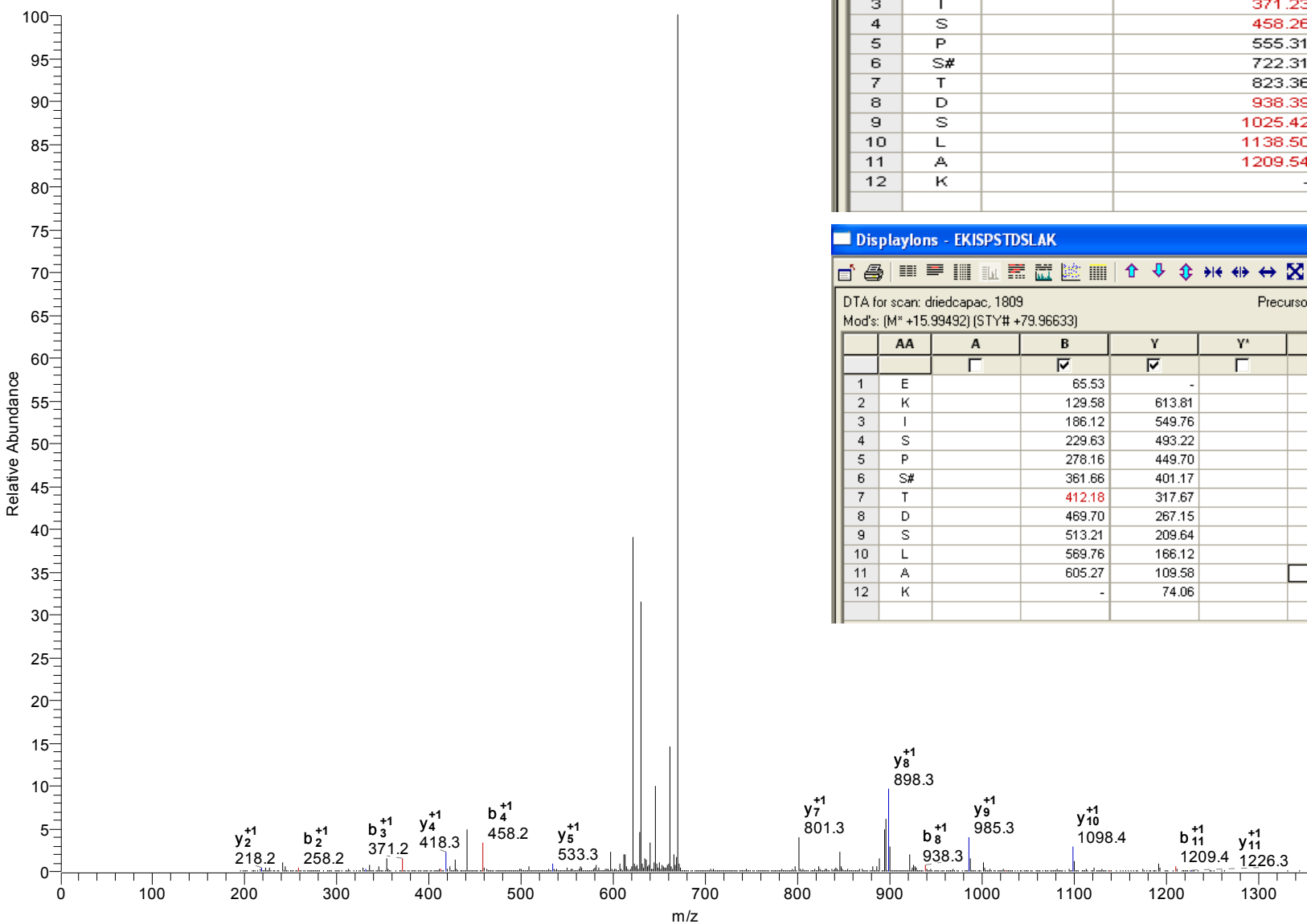
DTA for scan: cap2, 2159
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 666.22 Charge: 2

	AA	A	B	Y	Y'	Yo	Z	
1	N		58.03	-				10
2	Q		122.06	608.72				9
3	S#		205.56	544.69				8
4	L		262.10	461.19				7
5	E		326.62	404.65				6
6	F		400.15	340.13				5
7	S#		483.65	266.60				4
8	A		519.17	183.10				3
9	M*		592.69	147.58				2
10	K		-	74.06				1

Akap4 A-kinase anchor protein 4

#1809-1809 NL: 7.99E4

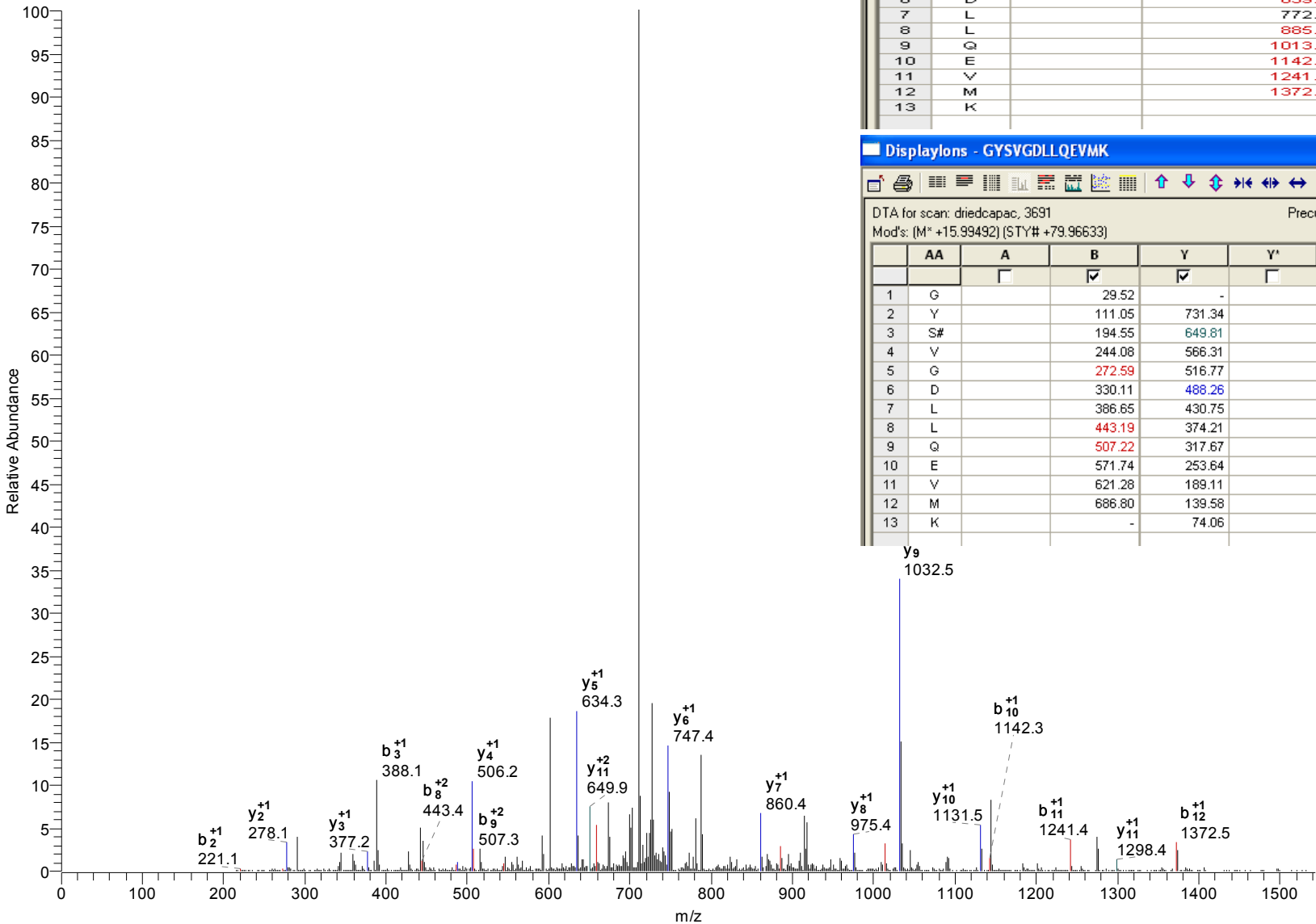


Displaylons - EKISPSTD SLAK					
DTA for scan: driedcapac, 1809					
Mod's: [M* +15.99492] (STY# +79.96633)					
	AA	A	B	Y	
1	E		130.05	-	12
2	K		258.14	1226.60	11
3	I		371.23	1098.51	10
4	S		458.26	985.42	9
5	P		555.31	898.39	8
6	S#		722.31	801.34	7
7	T		823.36	634.34	6
8	D		938.39	533.29	5
9	S		1025.42	418.27	4
10	L		1138.50	331.23	3
11	A		1209.54	218.15	2
12	K		-	147.11	1

Displaylons - EKISPSTD SLAK							
DTA for scan: driedcapac, 1809							
Mod's: [M* +15.99492] (STY# +79.96633)							
Precursor ion: 677.87 Charge: 2							
	AA	A	B	Y	Y*	Yo	Z
1	E		65.53	-			
2	K		129.58	613.81			
3	I		186.12	549.76			
4	S		229.63	493.22			
5	P		278.16	449.70			
6	S#		361.66	401.17			
7	T		412.18	317.67			
8	D		469.70	267.15			
9	S		513.21	209.64			
10	L		569.76	166.12			
11	A		605.27	109.58			
12	K		-	74.06			

Akap4 A-kinase anchor protein 4

#3691-3691 NL: 1.66E4

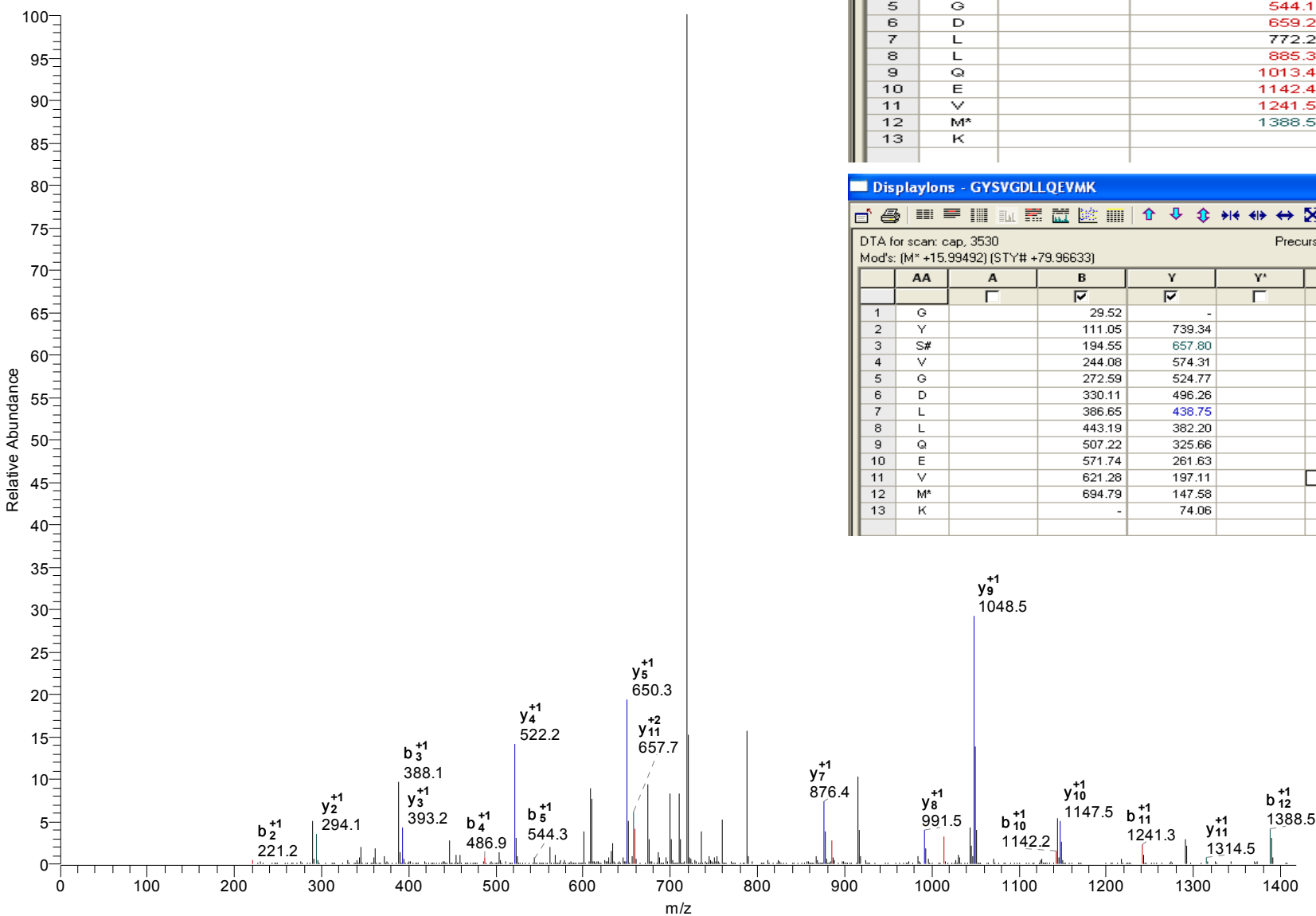


DisplayIons - GYSVGDLLQEV MK							
DTA for scan: driedcapac, 3691							
Mod's: [M* +15.99492] (STY# +79.96633)							
	AA	A	B	Y			
1	G			58.03	-		13
2	Y			221.09	1461.67		12
3	S#			388.09	1298.61		11
4	V			487.16	1131.61		10
5	G			544.18	1032.54		9
6	D			659.21	975.52		8
7	L			772.29	860.49		7
8	L			885.38	747.41		6
9	Q			1013.43	634.32		5
10	E			1142.48	506.26		4
11	V			1241.54	377.22		3
12	M			1372.59	278.15		2
13	K			-	147.11		1

DisplayIons - GYSVGDLLQEV MK							
DTA for scan: driedcapac, 3691							
Mod's: [M* +15.99492] (STY# +79.96633)							
Precursor ion: 760.22 Charge: 2							
	AA	A	B	Y	Y'	Yo	Z
1	G		29.52	-			13
2	Y		111.05	731.34			12
3	S#		194.55	649.81			11
4	V		244.08	566.31			10
5	G		272.59	516.77			9
6	D		330.11	488.26			8
7	L		386.65	430.75			7
8	L		443.19	374.21			6
9	Q		507.22	317.67			5
10	E		571.74	253.64			4
11	V		621.28	189.11			3
12	M		686.80	139.58			2
13	K		-	74.06			1

Akap4 A-kinase anchor protein 4

#3530-3530 NL: 1.21E6



DisplayIons - GYSVGDLLQEV MK

DTA for scan: cap, 3530
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	A	B	Y	
1	G			58.03	- 13
2	Y			221.09	1477.66 12
3	S#			388.09	1314.60 11
4	V			487.16	1147.60 10
5	G			544.18	1048.53 9
6	D			659.21	991.51 8
7	L			772.29	876.49 7
8	L			885.38	763.40 6
9	Q			1013.43	650.32 5
10	E			1142.48	522.26 4
11	V			1241.54	393.22 3
12	M*			1388.58	294.15 2
13	K			-	147.11 1

DisplayIons - GYSVGDLLQEV MK

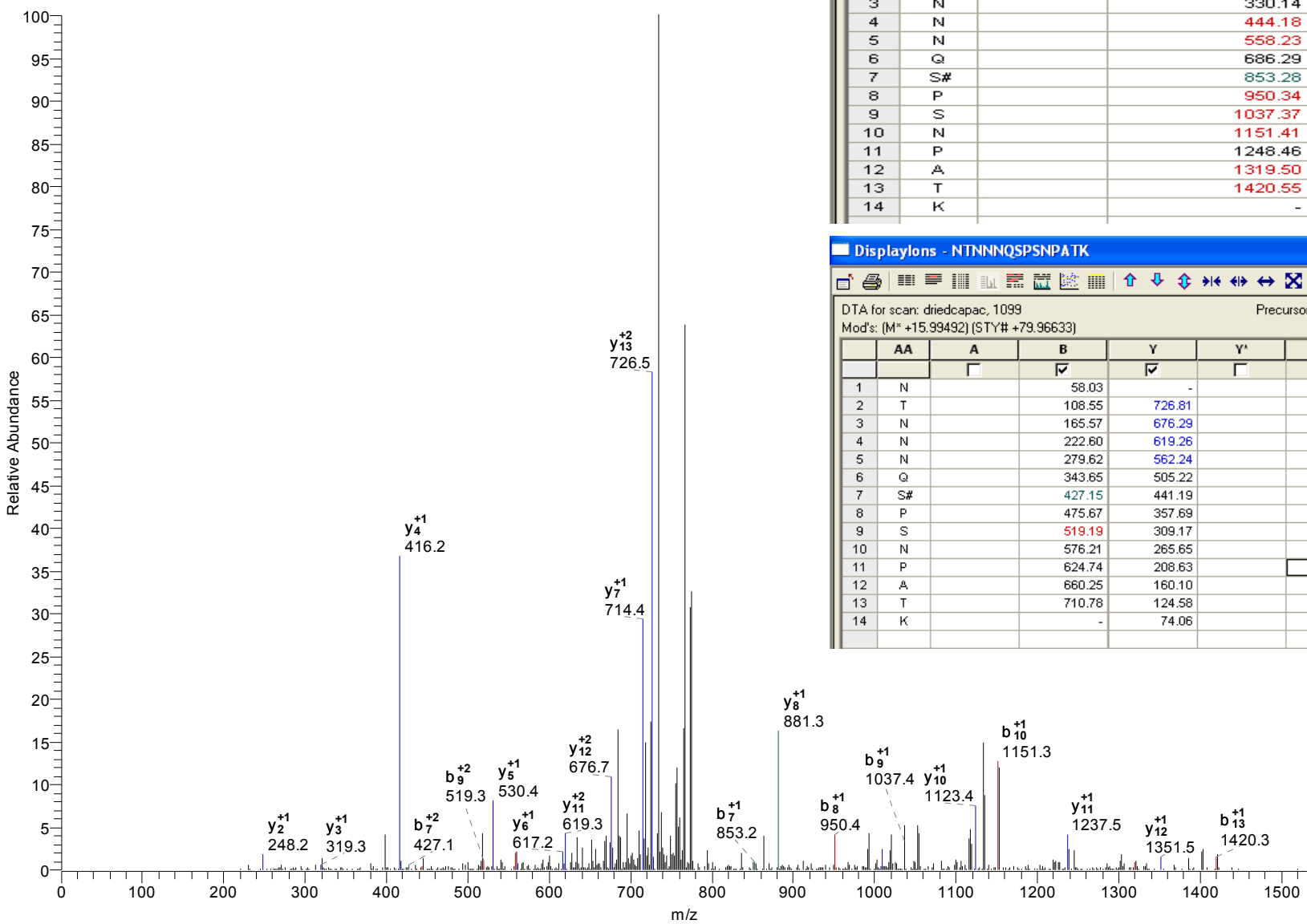
DTA for scan: cap, 3530
Mod's: [M⁺ +15.99492] [STY# +79.96633]

Precursor ion: 768.14 Charge: 2

	AA	A	B	Y	Y*	Yo	Z	
1	G			29.52	-			13
2	Y			111.05	739.34			12
3	S#			194.55	657.80			11
4	V			244.08	574.31			10
5	G			272.59	524.77			9
6	D			330.11	496.26			8
7	L			386.65	438.75			7
8	L			443.19	382.20			6
9	Q			507.22	325.66			5
10	E			571.74	261.63			4
11	V			621.28	197.11			3
12	M*			694.79	147.58			2
13	K			-	74.06			1

Akap4 A-kinase anchor protein 4

#1099-1099 NL: 4.05E3



Displaylons - NTNNNQSPSNPATK

DTA for scan: driedcapac, 1099
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	14
2	T		216.10	1452.61	13
3	N		330.14	1351.56	12
4	N		444.18	1237.52	11
5	N		558.23	1123.48	10
6	Q		686.29	1009.44	9
7	S#		853.28	881.38	8
8	P		950.34	714.38	7
9	S		1037.37	617.33	6
10	N		1151.41	530.29	5
11	P		1248.46	416.25	4
12	A		1319.50	319.20	3
13	T		1420.55	248.16	2
14	K		-	147.11	1

Displaylons - NTNNNQSPSNPATK

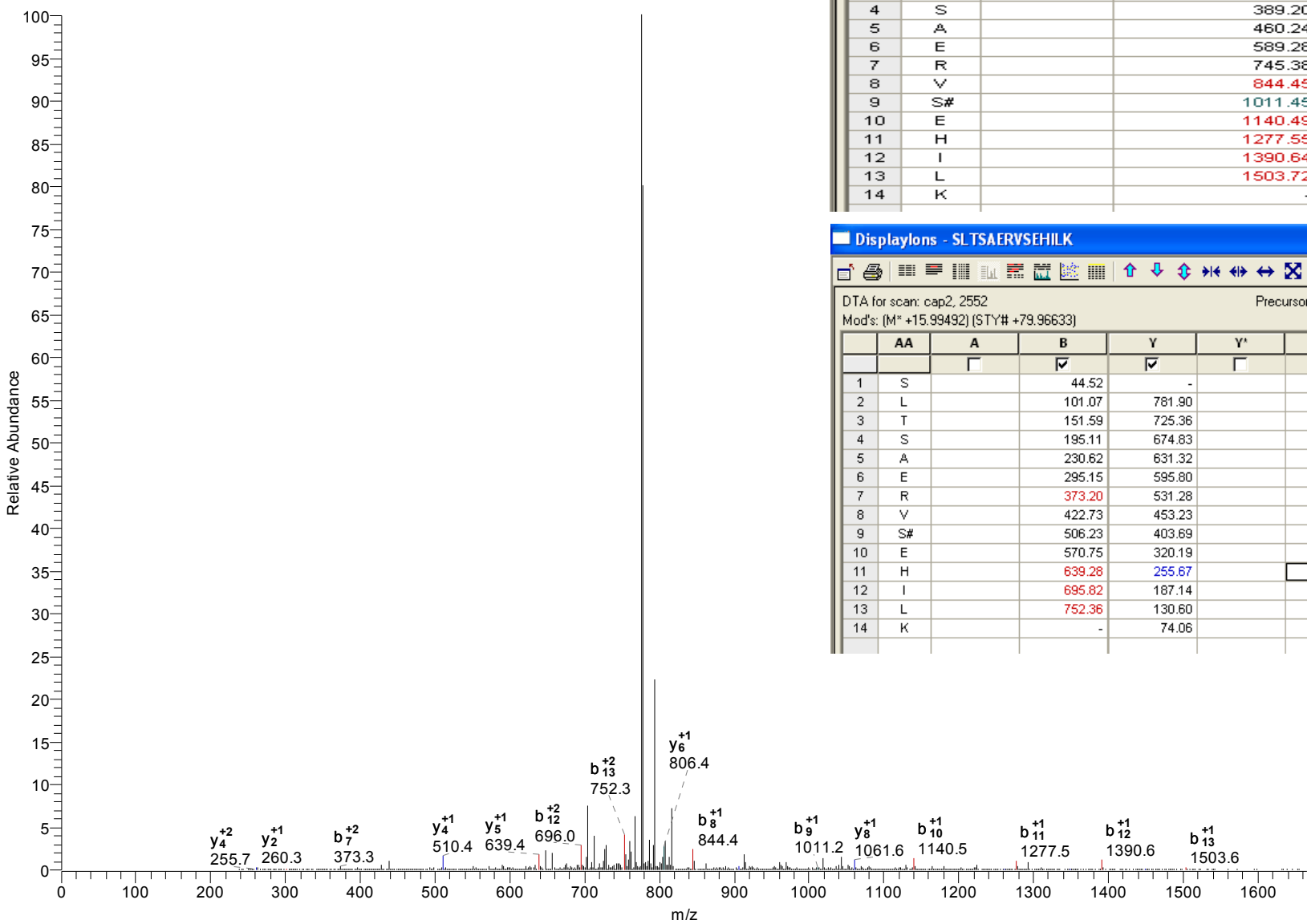
DTA for scan: driedcapac, 1099
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 783.20 Charge: 2

	AA	A	B	Y	Y*	Yo	Z	
1	N		58.03	-				14
2	T		108.55	726.81				13
3	N		165.57	676.29				12
4	N		222.60	619.26				11
5	N		279.62	562.24				10
6	Q		343.65	505.22				9
7	S#		427.15	441.19				8
8	P		475.67	357.69				7
9	S		519.19	309.17				6
10	N		576.21	265.65				5
11	P		624.74	208.63				4
12	A		660.25	160.10				3
13	T		710.78	124.58				2
14	K		-	74.06				1

Akap4 A-kinase anchor protein 4

#2552-2552 NL: 7.05E4



Displaylons - SLTSAERVSEHILK

DTA for scan: cap2, 2552
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	14
2	L		201.12	1562.79	13
3	T		302.17	1449.71	12
4	S		389.20	1348.66	11
5	A		460.24	1261.63	10
6	E		589.28	1190.59	9
7	R		745.38	1061.55	8
8	V		844.45	905.45	7
9	S#		1011.45	806.38	6
10	E		1140.49	639.38	5
11	H		1277.55	510.34	4
12	I		1390.64	373.28	3
13	L		1503.72	260.20	2
14	K		-	147.11	1

Displaylons - SLTSAERVSEHILK

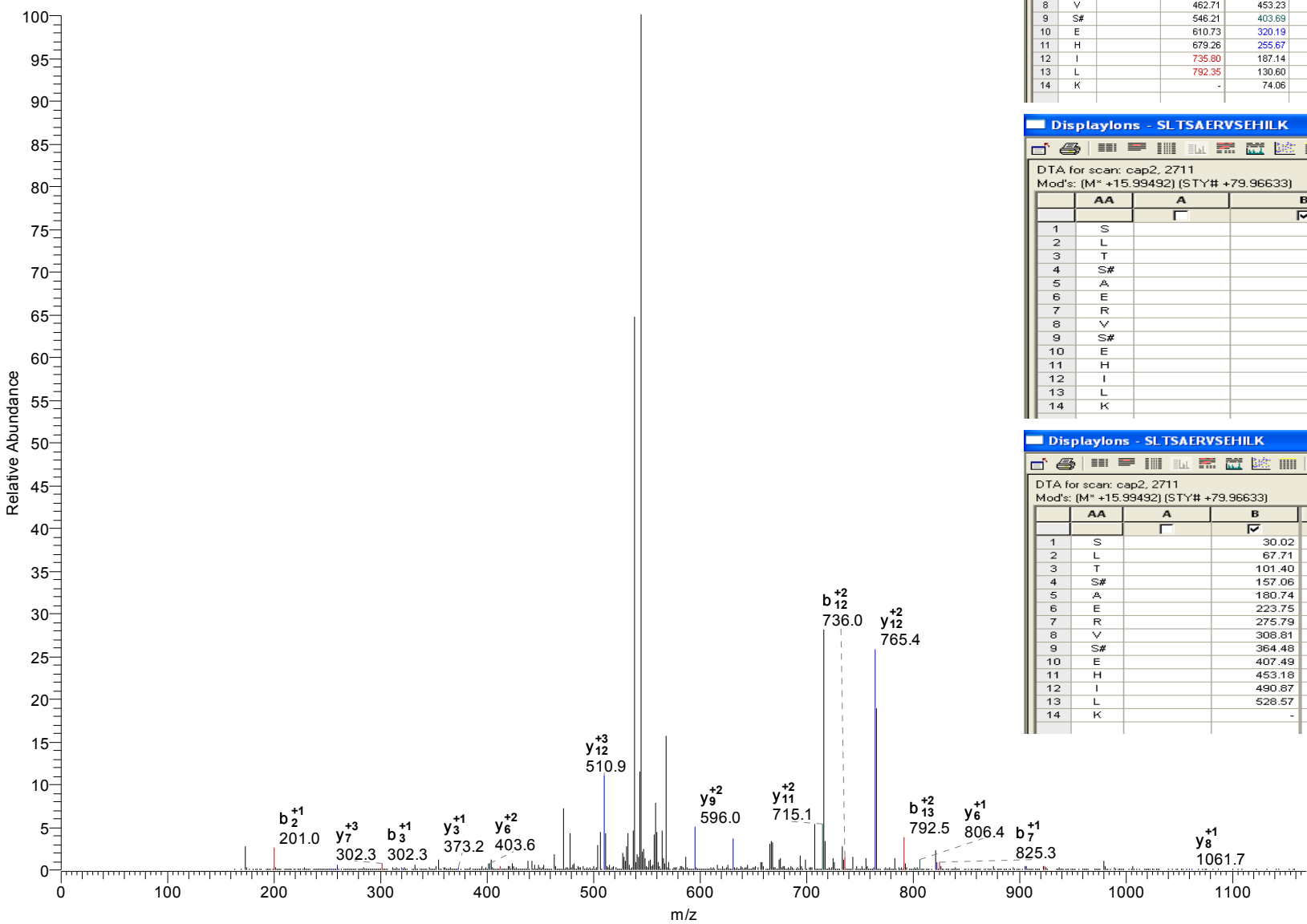
DTA for scan: cap2, 2552
Mod's: (M* +15.99492) (STY# +79.96633)

Precursor ion: 825.81 Charge: 2

	AA	A	B	Y	Y'	Y0	Z	
1	S		44.52	-				14
2	L		101.07	781.90				13
3	T		151.59	725.36				12
4	S		195.11	674.83				11
5	A		230.62	631.32				10
6	E		295.15	585.80				9
7	R		373.20	531.28				8
8	V		422.73	453.23				7
9	S#		506.23	403.69				6
10	E		570.75	320.19				5
11	H		639.28	255.67				4
12	I		695.82	187.14				3
13	L		752.36	130.60				2
14	K		-	74.06				1

Akap4 A-kinase anchor protein 4

#2711-2711 NL: 7.13E4



Displaylons - SLTSAERVSEHILK

DTA for scan: cap2, 2711
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Y'	Yo	Z	
1	S		44.52	-				14
2	L		101.07	821.88				13
3	T		151.59	765.34				12
4	S#		235.09	714.82				11
5	A		270.81	631.32				10
6	E		335.13	595.80				9
7	R		413.18	531.28				8
8	V		462.71	453.23				7
9	S#		546.21	403.69				6
10	E		610.73	320.19				5
11	H		679.26	255.67				4
12	I		735.80	187.14				3
13	L		792.35	130.60				2
14	K		-	74.06				1

Displaylons - SLTSAERVSEHILK

DTA for scan: cap2, 2711
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	14
2	L		201.12	1642.76	13
3	T		302.17	1529.68	12
4	S#		469.17	1428.63	11
5	A		540.21	1261.63	10
6	E		669.25	1190.59	9
7	R		825.35	1061.55	8
8	V		924.42	905.45	7
9	S#		1091.42	806.38	6
10	E		1220.46	639.38	5
11	H		1357.52	510.34	4
12	I		1470.60	373.28	3
13	L		1583.69	260.20	2
14	K		-	147.11	1

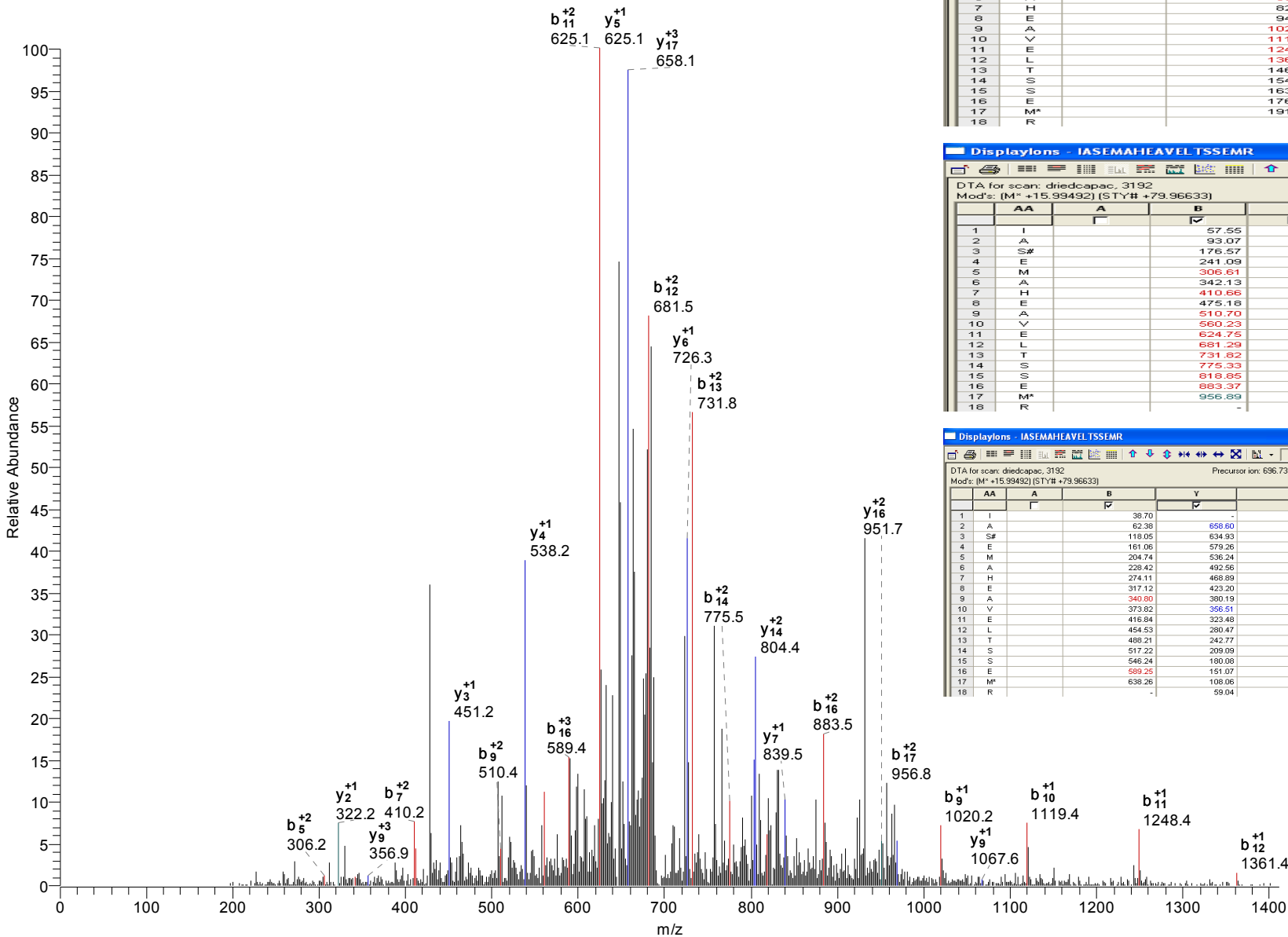
Displaylons - SLTSAERVSEHILK

DTA for scan: cap2, 2711
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S		30.02	-		14
2	L		67.71	548.26		13
3	T		101.40	510.56		12
4	S#		157.06	476.88		11
5	A		180.74	421.21		10
6	E		223.75	397.54		9
7	R		275.79	354.52		8
8	V		308.81	302.49		7
9	S#		364.48	269.47		6
10	E		407.49	213.80		5
11	H		453.18	170.78		4
12	I		490.87	125.10		3
13	L		528.57	87.40		2
14	K		-	49.71		1

Akap4 A-kinase anchor protein 4

#3192-3192 NL: 2.83E3



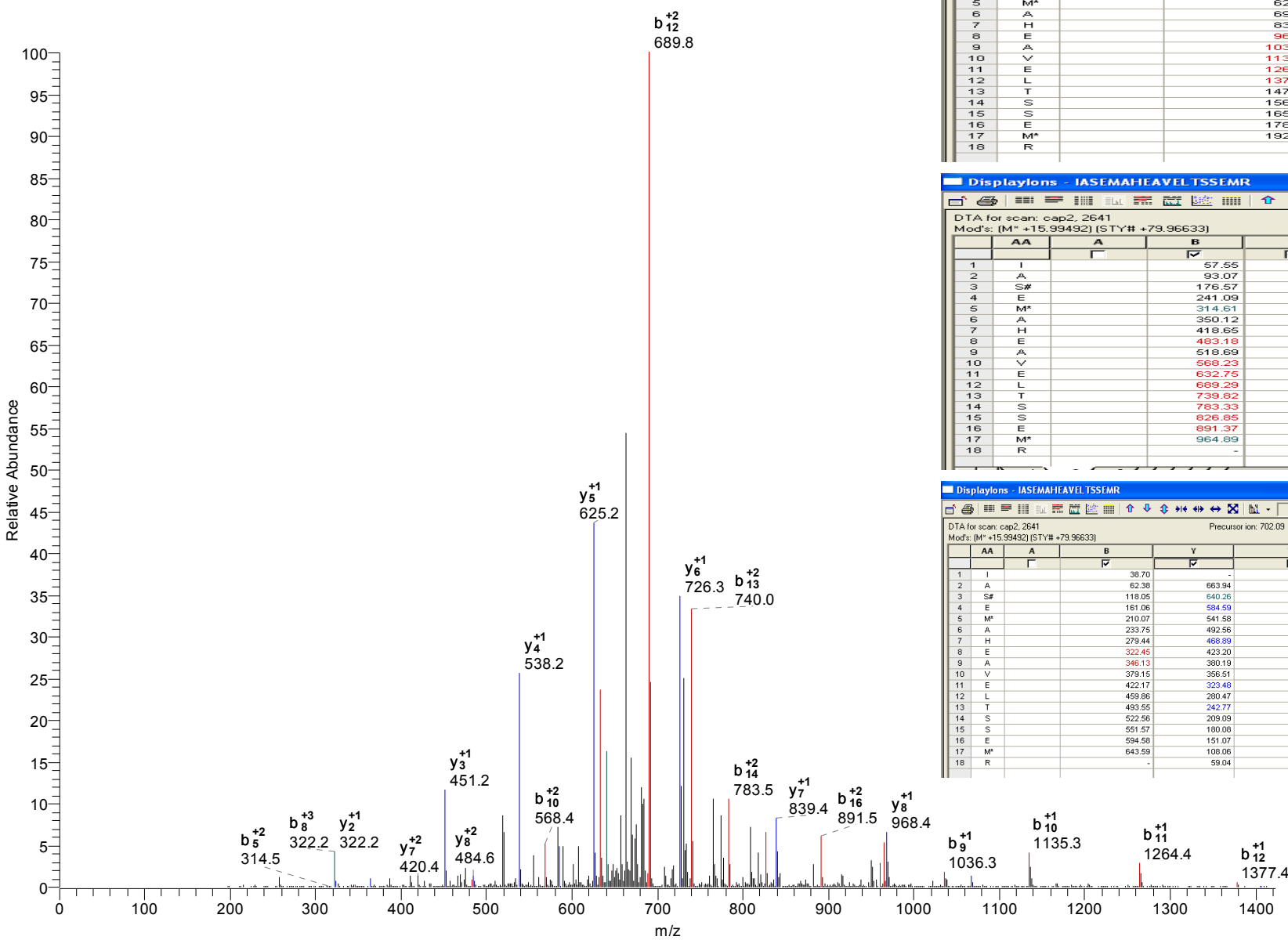
Displaylons - IASEMAHEVELTSSEMR					
DTA for scan: driedcapac, 3192					
Mod's: (M ⁺ +15.99492) (STY# +79.96633)					
	AA	A	B	Y	
1	I		114.09	-	18
2	A		185.13	1973.80	17
3	S#		352.13	1902.76	16
4	E		481.17	1735.76	15
5	M		612.21	1606.72	14
6	A		683.25	1475.68	13
7	H		820.31	1404.64	12
8	E		949.35	1267.58	11
9	A		1020.39	1138.54	10
10	V		1119.45	1067.50	9
11	E		1248.50	968.44	8
12	L		1361.58	839.39	7
13	T		1482.63	726.31	6
14	S		1549.66	626.26	5
15	S		1638.69	538.23	4
16	E		1765.74	451.20	3
17	M*		1912.77	322.15	2
18	R		-	175.12	1

Displaylons - IASEMAHEVELTSSEMR					
DTA for scan: driedcapac, 3192					
Mod's: (M ⁺ +15.99492) (STY# +79.96633)					
	AA	A	B	Y	Z
1	I		57.55	-	18
2	A		93.07	987.40	17
3	S#		176.57	951.88	16
4	E		241.09	868.38	15
5	M		306.61	803.86	14
6	A		342.13	738.34	13
7	H		410.66	702.82	12
8	E		475.18	634.30	11
9	A		510.70	569.77	10
10	V		560.23	534.26	9
11	E		624.75	484.72	8
12	L		681.29	420.20	7
13	T		731.82	363.66	6
14	S		775.33	313.13	5
15	S		818.85	269.62	4
16	E		883.37	226.10	3
17	M*		956.89	161.58	2
18	R		-	88.06	1

Displaylons - IASEMAHEVELTSSEMR					
DTA for scan: driedcapac, 3192					
Mod's: (M ⁺ +15.99492) (STY# +79.96633)					
	AA	A	B	Y	Y*
1	I		38.70	-	-
2	A		62.38	658.60	-
3	S#		118.05	634.93	-
4	E		161.06	579.26	-
5	M		204.74	535.24	-
6	A		228.42	492.56	-
7	H		274.11	468.89	-
8	E		317.12	423.20	-
9	A		340.80	380.19	-
10	V		373.82	356.51	-
11	E		416.84	323.49	-
12	L		454.53	290.47	-
13	T		488.21	242.77	-
14	S		517.22	209.09	-
15	S		546.24	180.08	-
16	E		589.25	151.07	-
17	M*		638.26	108.06	-
18	R		-	59.04	-

Akap4 A-kinase anchor protein 4

#2641-2641 NL: 2.06E5



Displaylons - IASEMAHEAVELTSSEMR

DTA for scan: cap2, 2641
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	I		114.09	-	18
2	A		185.13	1989.79	17
3	S#		352.13	1918.76	16
4	E		481.17	1751.76	15
5	M*		628.20	1622.71	14
6	A		699.24	1475.68	13
7	H		836.30	1404.64	12
8	E		965.34	1267.58	11
9	A		1036.38	1138.54	10
10	V		1135.45	1067.50	9
11	E		1264.49	968.44	8
12	L		1377.58	839.39	7
13	T		1478.62	726.31	6
14	S		1565.66	625.26	5
15	S		1652.69	538.23	4
16	E		1781.73	451.20	3
17	M*		1928.77	322.15	2
18	R		-	175.12	1

Displaylons - IASEMAHEAVELTSSEMR

DTA for scan: cap2, 2641
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	I		57.55	-	-	18
2	A		93.07	995.40	-	17
3	S#		176.57	959.88	-	16
4	E		241.09	876.38	-	15
5	M*		314.61	811.86	-	14
6	A		350.12	738.34	-	13
7	H		418.65	702.82	-	12
8	E		483.18	634.30	-	11
9	A		518.69	569.77	-	10
10	V		568.23	534.26	-	9
11	E		632.75	484.72	-	8
12	L		689.29	420.20	-	7
13	T		739.82	363.66	-	6
14	S		763.33	313.13	-	5
15	S		826.85	269.62	-	4
16	E		891.37	226.10	-	3
17	M*		964.89	161.58	-	2
18	R		-	88.06	-	1

Displaylons - IASEMAHEAVELTSSEMR

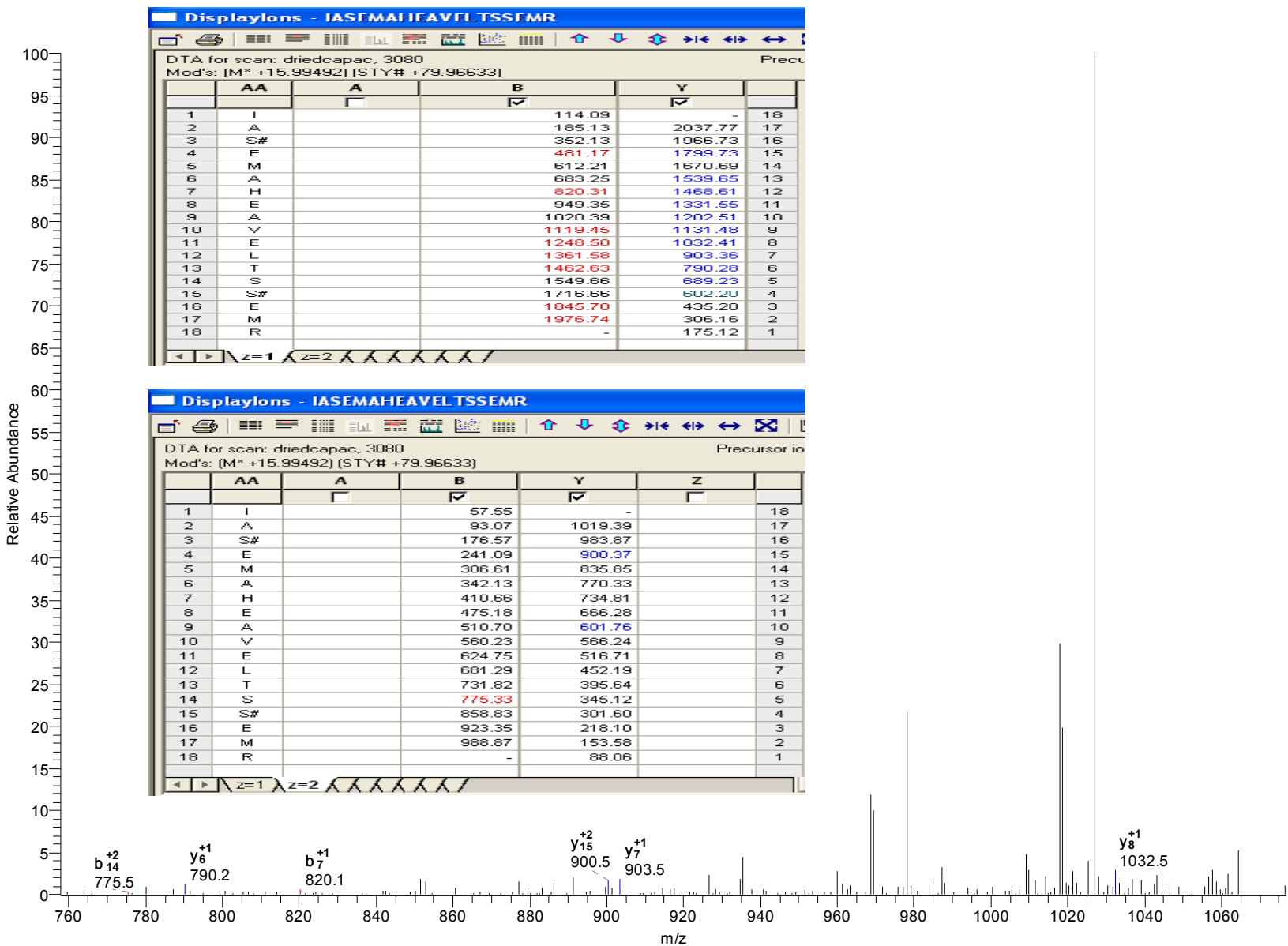
DTA for scan: cap2, 2641
Mod's: (M⁺ +15.99492) (STY# +79.96633)

Precursor ion: 702.09 Charge: 3 Activation type: CID Mass

	AA	A	B	Y	Y*	Yo	Z	
1	I		38.70	-	-	-	-	19
2	A		62.36	663.94	-	-	-	17
3	S#		118.05	640.26	-	-	-	16
4	E		161.06	584.59	-	-	-	15
5	M*		210.07	541.58	-	-	-	14
6	A		233.75	492.56	-	-	-	13
7	H		279.44	468.89	-	-	-	12
8	E		322.45	423.20	-	-	-	11
9	A		346.13	380.19	-	-	-	10
10	V		379.15	355.51	-	-	-	9
11	E		422.17	323.49	-	-	-	8
12	L		459.86	280.47	-	-	-	7
13	T		493.55	242.77	-	-	-	6
14	S		522.56	209.09	-	-	-	5
15	S		551.57	180.08	-	-	-	4
16	E		594.58	151.07	-	-	-	3
17	M*		643.59	108.06	-	-	-	2
18	R		-	59.04	-	-	-	1

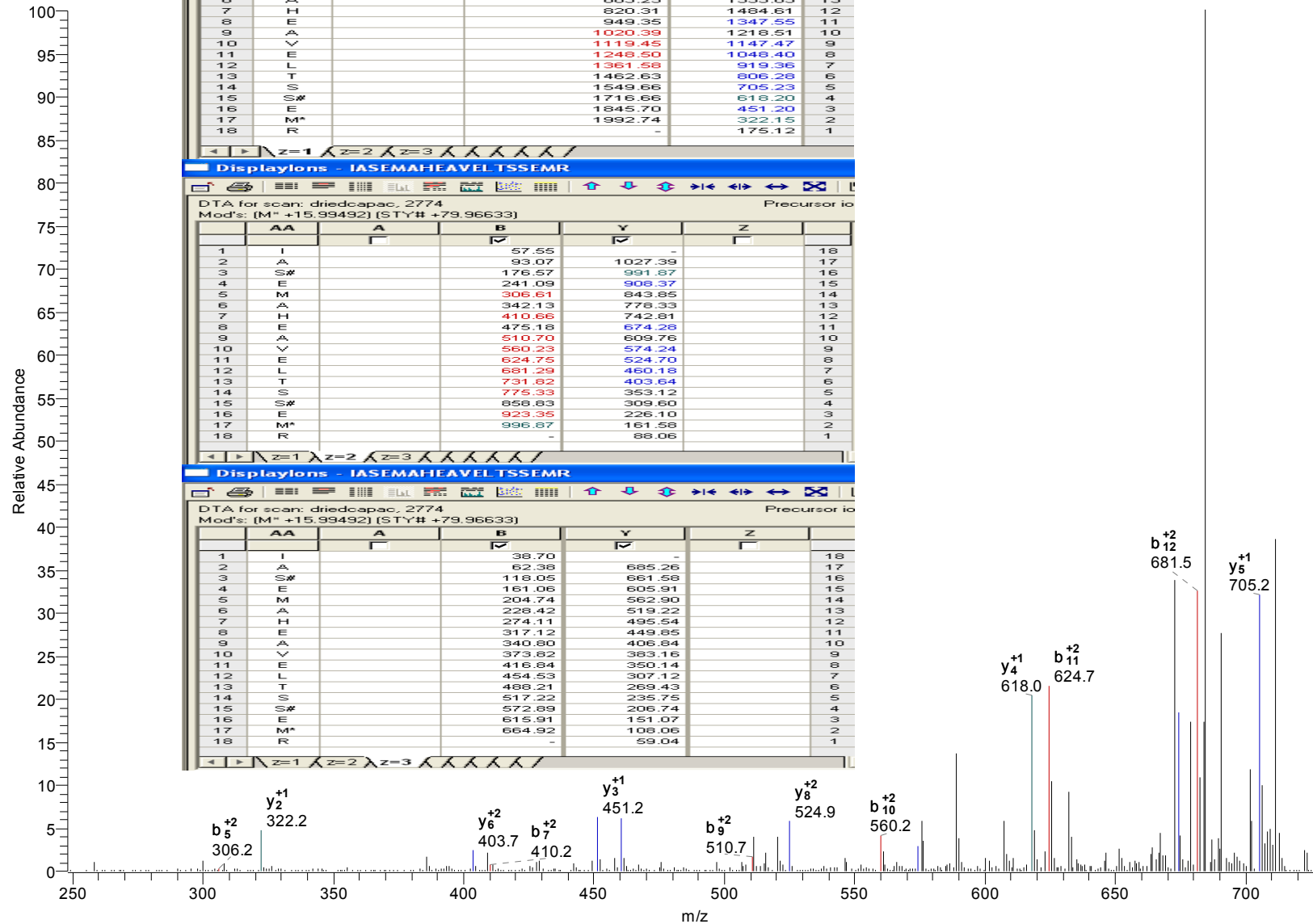
Akap4 A-kinase anchor protein 4

#3080-3080 NL: 2.98E3



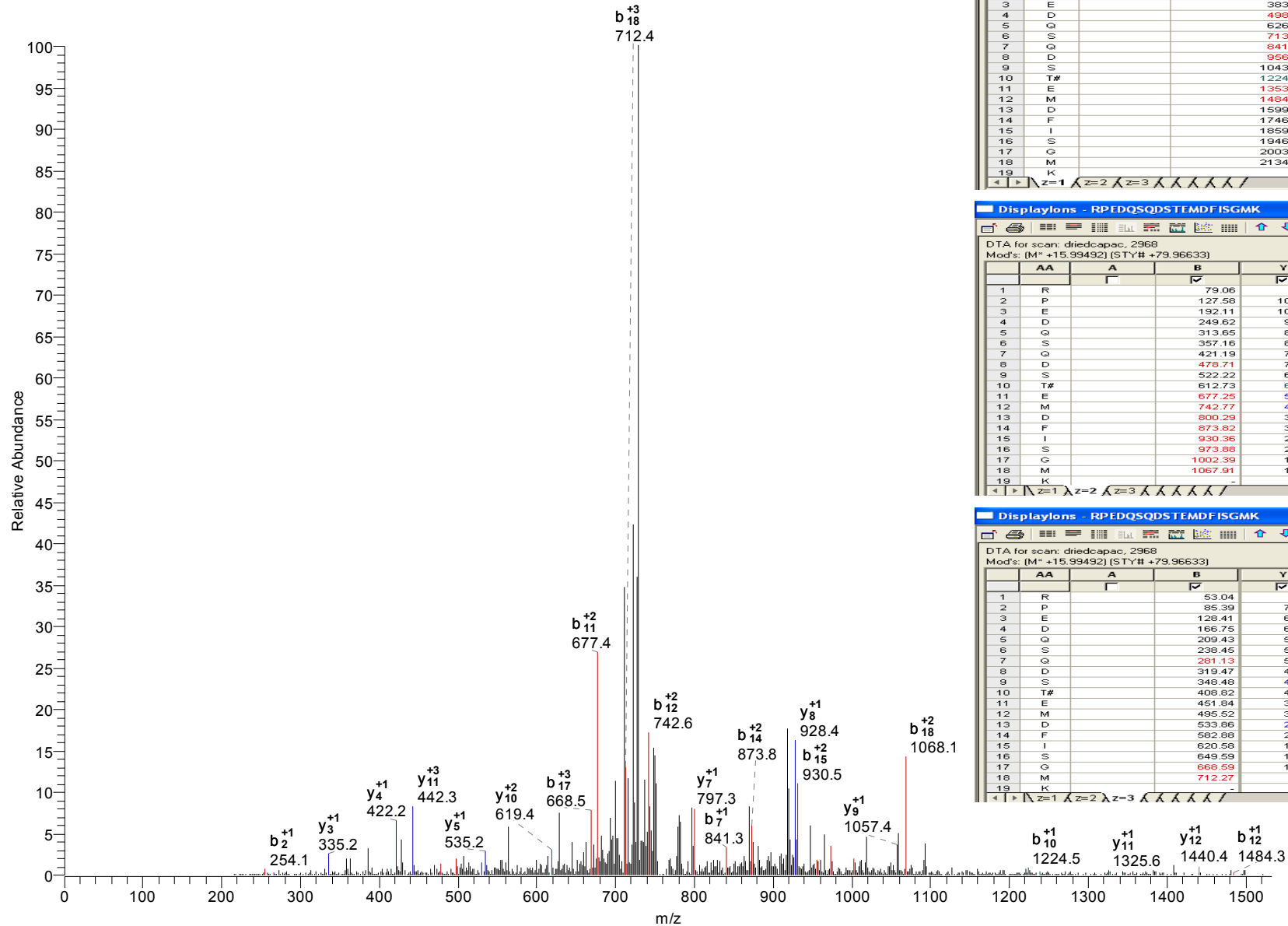
Akap4 A-kinase anchor protein 4

#2774-2774 NL: 7.53E4



Akap4 A-kinase anchor protein 4

#2968-2968 NL: 5.14E3



Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: driedcapac, 2968
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	R		157.11		19
2	P		254.16		18
3	E		383.20		17
4	D		498.23		16
5	Q		626.29		15
6	S		713.32		14
7	Q		841.38		13
8	D		956.41		12
9	S		1043.44		11
10	T#		1224.45		10
11	E		1353.50		9
12	M		1484.54		8
13	D		1599.56		7
14	F		1746.63		6
15	I		1859.72		5
16	S		1946.75		4
17	G		2003.77		3
18	M		2134.81		2
19	K		-	147.11	1

Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: driedcapac, 2968
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	R		79.06			19
2	P		127.58	1062.91		18
3	E		192.11	1014.38		17
4	D		249.62	949.86		16
5	Q		313.65	892.35		15
6	S		357.16	828.32		14
7	Q		421.19	784.80		13
8	D		478.71	729.77		12
9	S		522.22	663.26		11
10	T#		612.73	619.75		10
11	E		677.25	529.24		9
12	M		742.77	464.72		8
13	D		800.29	399.20		7
14	F		873.82	341.68		6
15	I		930.36	268.15		5
16	S		973.88	211.61		4
17	G		1002.39	168.09		3
18	M		1067.91	139.58		2
19	K		-	74.06		1

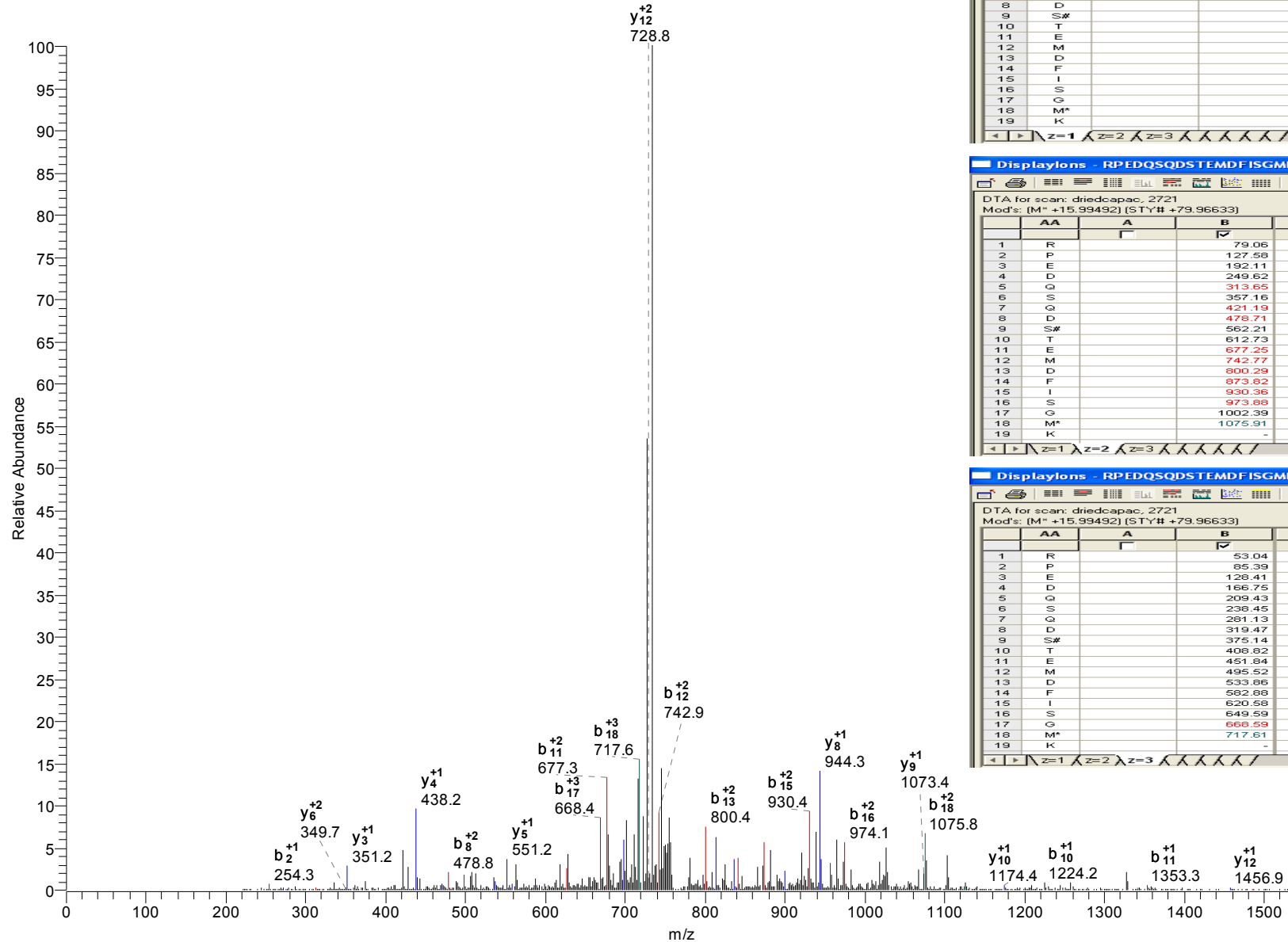
Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: driedcapac, 2968
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	R		53.04			19
2	P		85.39	708.94		18
3	E		128.41	676.59		17
4	D		166.75	633.58		16
5	Q		209.43	595.24		15
6	S		236.45	552.55		14
7	Q		281.13	523.54		13
8	D		319.47	480.85		12
9	S		348.48	442.51		11
10	T#		408.82	413.50		10
11	E		451.84	353.16		9
12	M		495.52	310.15		8
13	D		533.66	266.47		7
14	F		582.88	228.12		6
15	I		620.58	179.10		5
16	S		649.59	141.41		4
17	G		668.59	112.40		3
18	M		712.27	93.39		2
19	K		-	49.71		1

Akap4 A-kinase anchor protein 4

#2721-2721 NL: 9.32E3



Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: driedcapac, 2721
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	R		157.11		19
2	P		254.16		18
3	E		383.20		17
4	D		498.23		16
5	Q		626.29		15
6	S		713.32		14
7	Q		841.38		13
8	D		958.41		12
9	S#		1123.41		11
10	T		1224.45		10
11	E		1353.50		9
12	M		1484.54		8
13	D		1599.56		7
14	F		1746.63		6
15	I		1859.72		5
16	S		1946.75		4
17	G		2003.77		3
18	M*		2150.80		2
19	K		-	147.11	1

Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: driedcapac, 2721
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	R		79.06			19
2	P		127.58	1070.91		18
3	E		192.11	1022.38		17
4	D		249.62	957.86		16
5	Q		313.65	900.35		15
6	S		357.16	836.32		14
7	Q		421.19	792.80		13
8	D		478.71	728.77		12
9	S#		562.21	671.26		11
10	T		612.73	587.76		10
11	E		677.25	537.24		9
12	M		742.77	472.71		8
13	D		800.29	407.19		7
14	F		873.82	349.68		6
15	I		930.36	276.15		5
16	S		973.88	219.60		4
17	G		1002.39	176.09		3
18	M*		1075.91	147.58		2
19	K		-	74.06		1

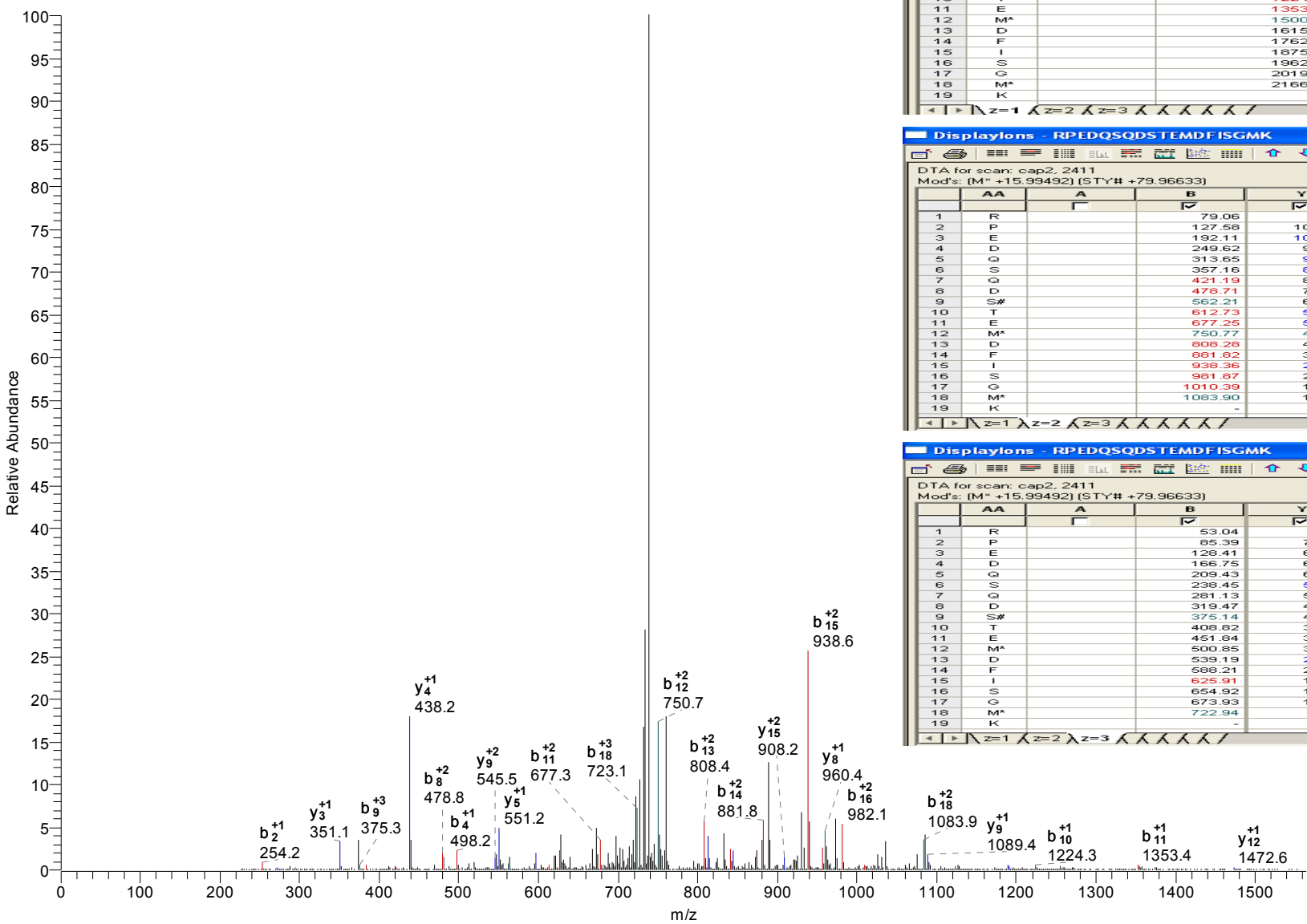
Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: driedcapac, 2721
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	R		53.04			19
2	P		85.39	714.27		18
3	E		128.41	681.92		17
4	D		166.75	638.91		16
5	Q		209.43	600.57		15
6	S		238.45	557.88		14
7	Q		281.13	528.67		13
8	D		319.47	486.18		12
9	S#		375.14	447.84		11
10	T		408.82	392.18		10
11	E		451.84	358.49		9
12	M		495.52	315.48		8
13	D		533.86	271.80		7
14	F		582.88	233.46		6
15	I		620.58	184.43		5
16	S		649.59	146.74		4
17	G		668.59	117.73		3
18	M*		717.61	98.72		2
19	K		-	49.71		1

Akap4 A-kinase anchor protein 4

#2411-2411 NL: 1.20E5



Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: cap2, 2411
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	R		157.11		19
2	P		254.16		18
3	E		383.20		17
4	D		498.23		16
5	Q		626.29		15
6	S		713.32		14
7	Q		841.38		13
8	D		956.41		12
9	S#		1123.41		11
10	T		1224.45		10
11	E		1353.50		9
12	M*		1500.53		8
13	D		1615.56		7
14	F		1762.63		6
15	I		1875.71		5
16	S		1962.74		4
17	G		2019.76		3
18	M*		2166.80		2
19	K		-	147.11	1

Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: cap2, 2411
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	R		79.06			19
2	P		127.58	1078.91		18
3	E		192.11	1030.38		17
4	D		249.62	965.86		16
5	Q		313.65	908.34		15
6	S		357.16	844.31		14
7	Q		421.19	800.80		13
8	D		478.71	736.77		12
9	S#		562.21	679.26		11
10	T		612.73	595.76		10
11	E		677.25	545.23		9
12	M*		750.77	480.71		8
13	D		806.28	407.19		7
14	F		881.82	349.68		6
15	I		938.36	276.15		5
16	S		981.87	219.60		4
17	G		1010.39	176.09		3
18	M*		1083.90	147.58		2
19	K		-	74.06		1

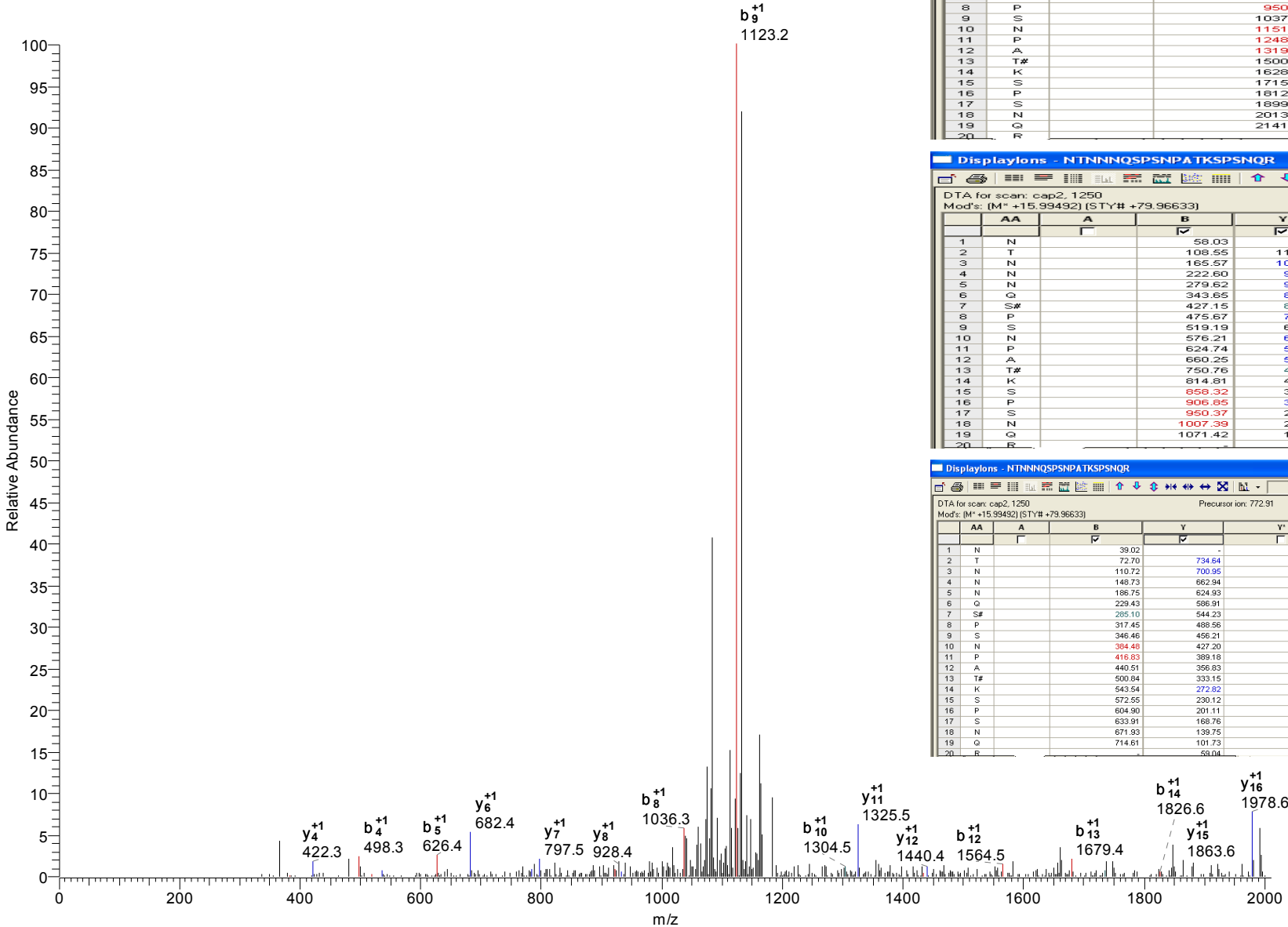
Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: cap2, 2411
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	R		53.04			19
2	P		85.39	719.61		18
3	E		128.41	687.26		17
4	D		166.75	644.24		16
5	Q		209.43	605.90		15
6	S		238.46	563.21		14
7	Q		281.13	534.20		13
8	D		319.47	491.52		12
9	S#		375.14	453.17		11
10	T		408.82	397.51		10
11	E		451.84	363.82		9
12	M*		500.85	320.81		8
13	D		539.19	271.80		7
14	F		588.21	233.46		6
15	I		625.91	184.43		5
16	S		654.92	146.74		4
17	G		673.93	117.73		3
18	M*		722.94	96.72		2
19	K		-	49.71		1

Akap4 A-kinase anchor protein 4

#2851-2851 NL: 1.73E3



Display ions - NTNNNQSPSPATKSPSNQR

DTA for scan: cap2, 1250
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	20
2	T		216.10	2201.90	19
3	N		330.14	2100.85	18
4	N		444.18	1986.81	17
5	N		558.23	1872.76	16
6	Q		686.29	1758.72	15
7	S#		853.28	1630.66	14
8	P		950.34	1463.66	13
9	S		1037.37	1366.61	12
10	N		1151.41	1279.58	11
11	P		1248.46	1155.54	10
12	A		1319.50	1066.48	9
13	T#		1500.52	997.45	8
14	K		1628.61	816.43	7
15	S		1715.64	688.34	6
16	P		1812.69	601.31	5
17	S		1899.73	504.25	4
18	N		2013.77	417.22	3
19	Q		2141.83	303.18	2
20	R			175.12	1

Display ions - NTNNNQSPSPATKSPSNQR

DTA for scan: cap2, 1250
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	N		58.03	-		20
2	T		108.55	1101.45		19
3	N		165.57	1050.93		18
4	N		222.60	993.91		17
5	N		279.62	936.89		16
6	Q		343.65	879.86		15
7	S#		427.15	815.83		14
8	P		475.67	732.34		13
9	S		519.19	683.81		12
10	N		576.21	640.29		11
11	P		624.74	583.27		10
12	A		660.25	534.75		9
13	T#		750.76	499.23		8
14	K		814.81	408.72		7
15	S		858.32	344.67		6
16	P		906.85	301.16		5
17	S		950.37	252.63		4
18	N		1007.39	209.11		3
19	Q		1071.42	152.09		2
20	R			88.06		1

Display ions - NTNNNQSPSPATKSPSNQR

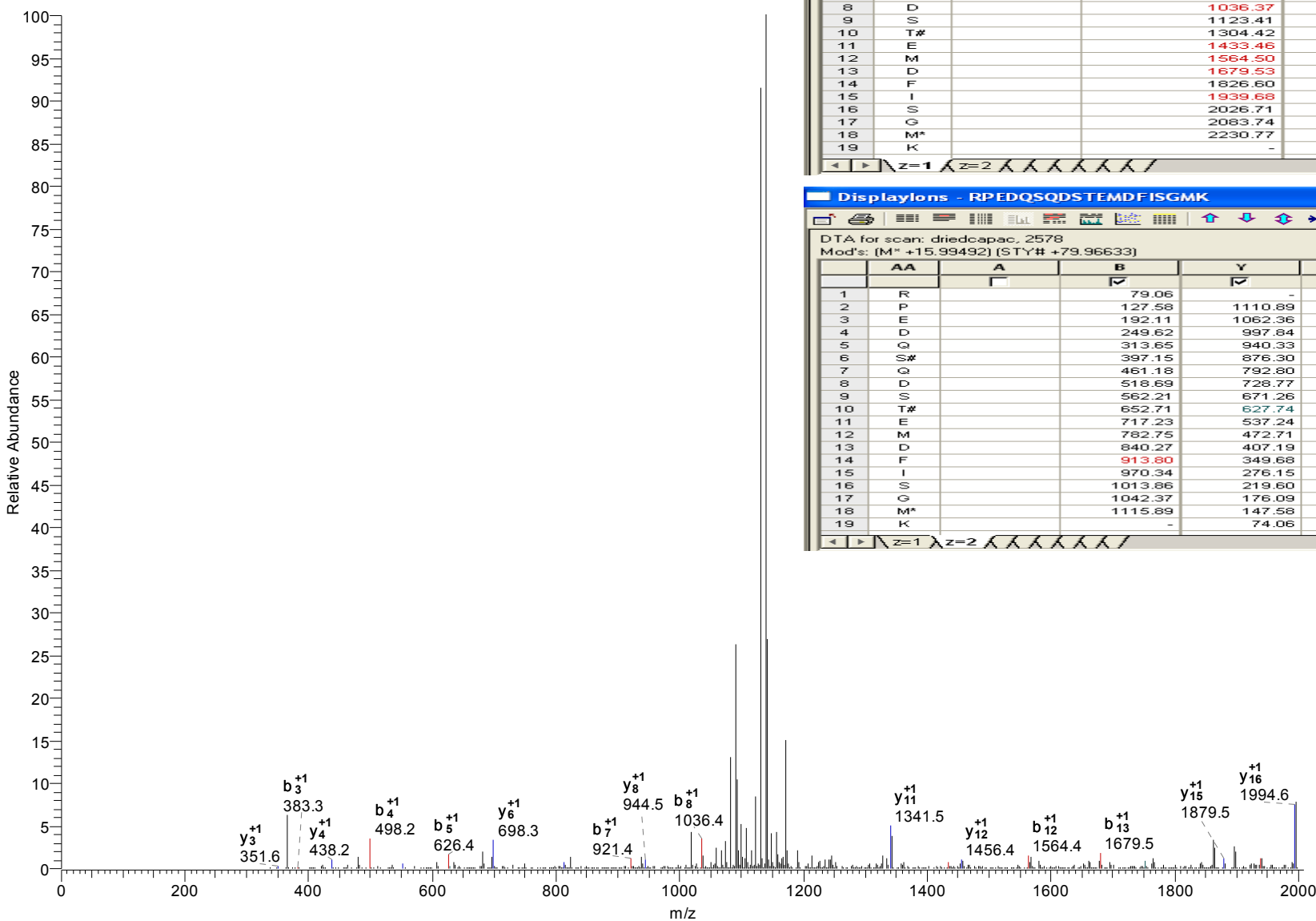
DTA for scan: cap2, 1250
Mod's: (M⁺ +15.99492) (STY# +79.96633)

Precursor ion: 772.91 Charge: 3 Activation type: CID Mass

	AA	A	B	Y	Y'	Y ₀	Z	
1	N		39.02	-				20
2	T		72.70	734.84				19
3	N		110.72	700.95				18
4	N		148.73	662.94				17
5	N		186.75	624.93				16
6	Q		229.43	586.91				15
7	S#		285.10	544.23				14
8	P		317.45	488.58				13
9	S		346.46	456.21				12
10	N		384.48	427.20				11
11	P		416.83	389.18				10
12	A		440.51	356.83				9
13	T#		500.84	333.15				8
14	K		543.54	272.82				7
15	S		572.56	230.12				6
16	P		604.90	201.11				5
17	S		633.91	168.76				4
18	N		671.93	139.75				3
19	Q		714.61	101.73				2
20	R			59.04				1

Akap4 A-kinase anchor protein 4

#2578-2578 NL: 9.85E3



Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: driedcapac, 2578
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	R		157.11	-	19
2	P		254.16	2220.77	18
3	E		383.20	2123.72	17
4	D		498.23	1994.68	16
5	Q		626.29	1879.65	15
6	S#		793.29	1751.59	14
7	Q		921.35	1584.60	13
8	D		1036.37	1456.54	12
9	S		1123.41	1341.51	11
10	T#		1304.42	1254.48	10
11	E		1433.46	1073.46	9
12	M		1564.50	944.42	8
13	D		1679.53	813.38	7
14	F		1826.60	698.35	6
15	I		1939.68	551.29	5
16	S		2026.71	438.20	4
17	Q		2083.74	351.17	3
18	M*		2230.77	294.15	2
19	K		-	147.11	1

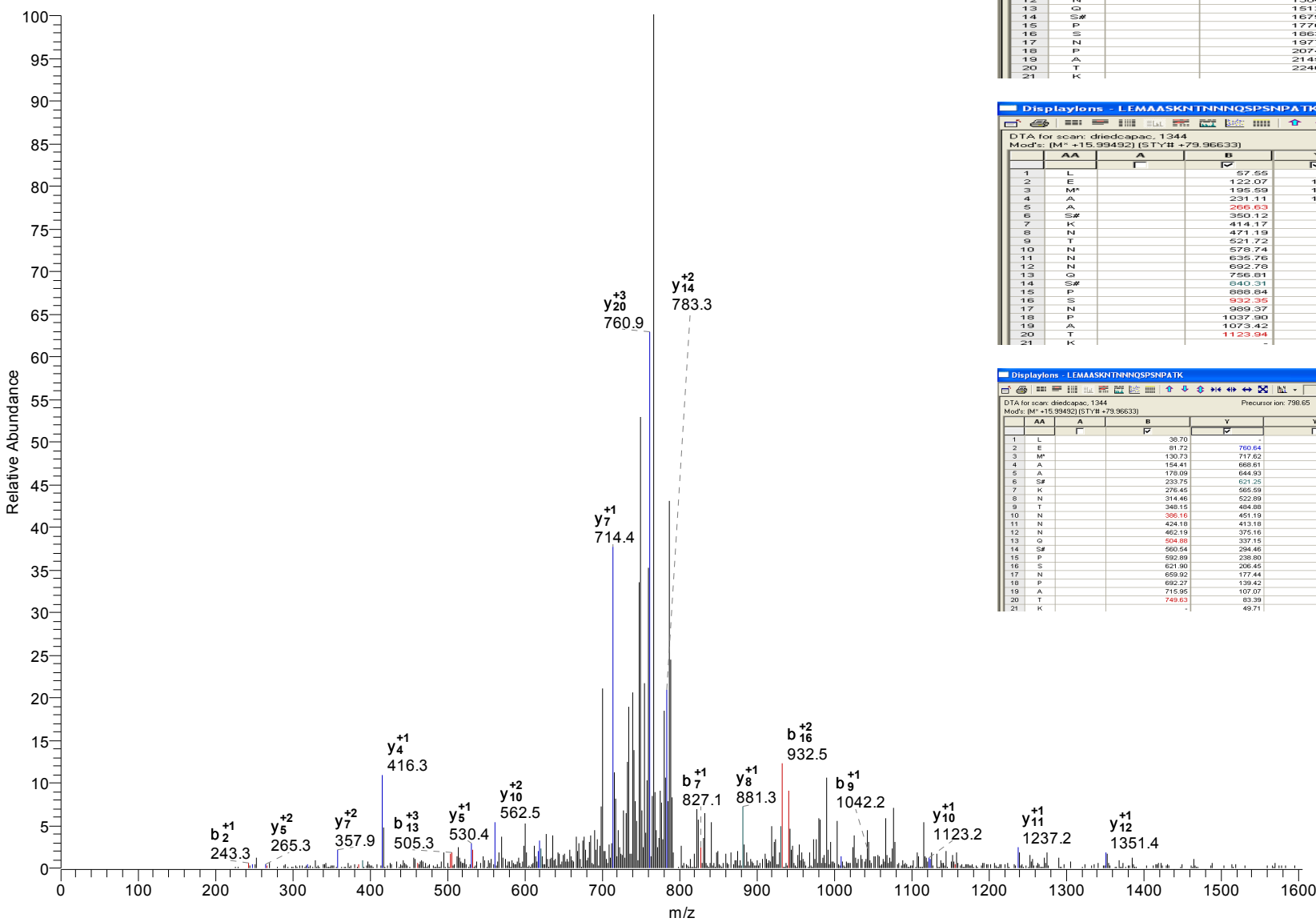
Displaylons - RPEDQSQDSTEMDFISGMK

DTA for scan: driedcapac, 2578
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	R		79.06	-		19
2	P		127.58	1110.89		18
3	E		192.11	1062.36		17
4	D		249.62	997.84		16
5	Q		313.65	940.33		15
6	S#		397.15	876.30		14
7	Q		461.18	792.80		13
8	D		518.69	728.77		12
9	S		562.21	671.26		11
10	T#		652.71	627.74		10
11	E		717.23	537.24		9
12	M		782.75	472.71		8
13	D		840.27	407.19		7
14	F		913.80	349.68		6
15	I		970.34	276.15		5
16	S		1013.86	219.60		4
17	Q		1042.37	176.09		3
18	M*		1115.89	147.58		2
19	K		-	74.06		1

Akap4 A-kinase anchor protein 4

#1344-1344 NL: 2.20E3



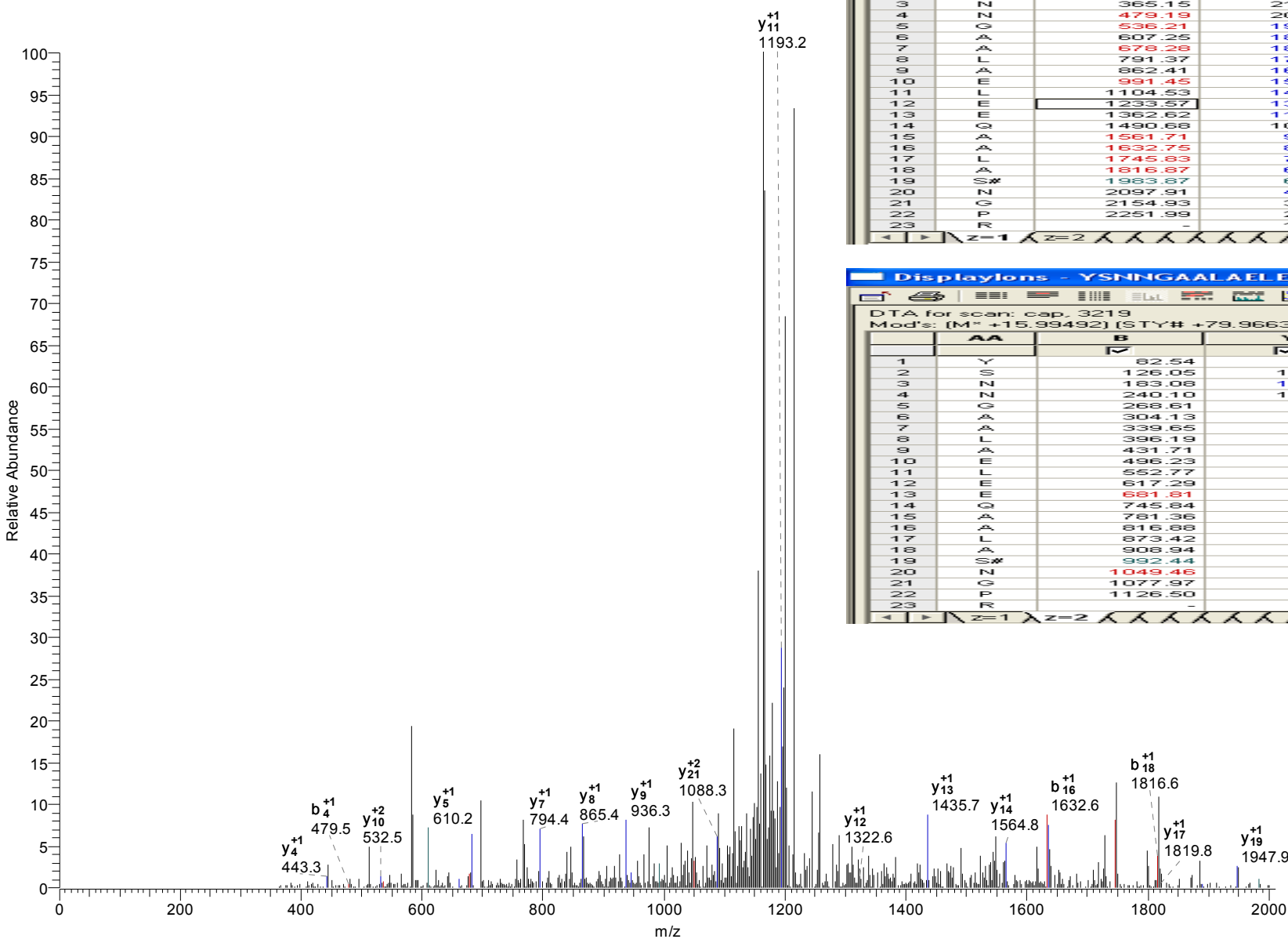
Displaylons - LEMAASKNTNNNQSPSPNPA TK						
DTA for scan: driedcapac. 1344						
Mod's: (M ⁺ +15.99492) (STY# +79.96633)						
	AA	A	B	Y		
1	L		114.09	-		21
2	E		243.13	2279.90		20
3	M*		390.17	2150.86		19
4	A		461.21	2003.82		18
5	A		532.24	1932.78		17
6	S#		699.24	1881.75		16
7	K		827.34	1694.75		15
8	N		941.38	1566.65		14
9	T		1042.43	1452.61		13
10	N		1156.47	1351.56		12
11	N		1270.51	1237.52		11
12	N		1394.56	1123.48		10
13	Q		1512.61	1009.44		9
14	S#		1679.61	881.38		8
15	P		1776.67	714.38		7
16	S		1863.70	617.33		6
17	N		1977.74	530.29		5
18	P		2074.79	415.25		4
19	A		2145.83	319.20		3
20	T		2246.88	249.16		2
21	K		-	147.11		1

Displaylons - LEMAASKNTNNNQSPSPNPA TK						
DTA for scan: driedcapac. 1344						
Mod's: (M ⁺ +15.99492) (STY# +79.96633)						
	AA	A	B	Y	Z	
1	L		57.55	-		21
2	E		122.07	1140.45		20
3	M*		196.59	1075.93		19
4	A		231.11	1002.41		18
5	A		266.63	966.90		17
6	S#		350.12	931.38		16
7	K		414.17	847.88		15
8	N		471.19	783.83		14
9	T		521.72	726.81		13
10	N		578.74	676.29		12
11	N		635.76	619.26		11
12	N		692.78	562.24		10
13	Q		756.81	505.22		9
14	S#		840.31	441.19		8
15	P		888.84	357.69		7
16	S		932.36	309.17		6
17	N		989.37	265.65		5
18	P		1037.90	208.63		4
19	A		1073.42	160.10		3
20	T		1123.94	124.58		2
21	K		-	74.06		1

Displaylons - LEMAASKNTNNNQSPSPNPA TK						
DTA for scan: driedcapac. 1344						
Mod's: (M ⁺ +15.99492) (STY# +79.96633)						
	AA	A	B	Y	Y'	Y''
1	L		36.70	-		21
2	E		81.72	760.84		20
3	M*		130.73	717.62		19
4	A		154.41	666.61		18
5	A		176.09	644.93		17
6	S#		233.75	621.25		16
7	K		276.45	565.59		15
8	N		314.46	522.89		14
9	T		348.15	484.88		13
10	N		386.16	451.19		12
11	N		424.18	413.18		11
12	N		462.19	375.16		10
13	Q		504.88	337.15		9
14	S#		560.54	294.46		8
15	P		592.89	238.60		7
16	S		621.90	206.45		6
17	N		659.92	177.44		5
18	P		692.27	139.42		4
19	A		715.95	107.07		3
20	T		749.63	83.39		2
21	K		-	49.71		1

Akap4 A-kinase anchor protein 4

#3219-3219 NL: 1.37E3



Displaylons - YSNNGAALAELEEQAALASNG

DTA for scan: cap. 3219
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	Y	164.07	-	23
2	S	251.10	2263.04	22
3	N	365.15	2176.00	21
4	N	479.19	2061.96	20
5	Q	536.21	1947.92	19
6	A	607.25	1890.90	18
7	A	676.26	1819.86	17
8	L	791.37	1748.82	16
9	A	862.41	1635.74	15
10	E	991.45	1564.70	14
11	L	1104.53	1435.66	13
12	E	1233.57	1322.57	12
13	E	1362.62	1193.53	11
14	Q	1490.68	1064.49	10
15	A	1561.71	936.43	9
16	A	1632.75	865.39	8
17	L	1745.83	794.36	7
18	A	1816.87	681.27	6
19	S#	1983.87	610.23	5
20	N	2097.91	443.24	4
21	G	2154.93	329.19	3
22	P	2251.99	272.17	2
23	R	-	175.12	1

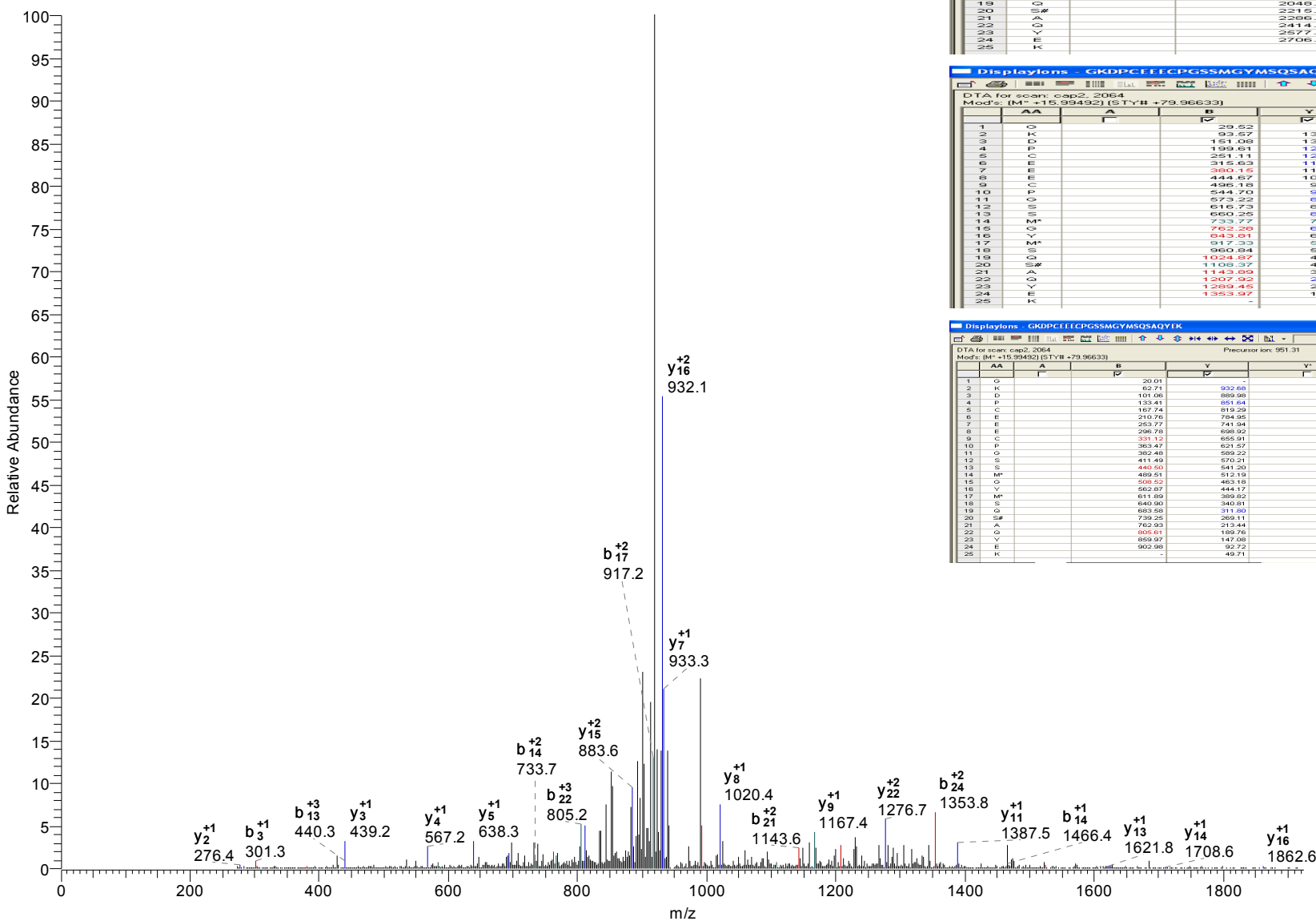
Displaylons - YSNNGAALAELEEQAALASNG

DTA for scan: cap. 3219
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	Y	82.54	-	23
2	S	126.05	1132.02	22
3	N	183.08	1088.51	21
4	N	240.10	1031.48	20
5	Q	268.61	974.46	19
6	A	304.13	945.95	18
7	A	339.65	910.43	17
8	L	396.19	874.91	16
9	A	431.71	818.37	15
10	E	496.23	762.85	14
11	L	552.77	718.33	13
12	E	617.29	661.79	12
13	E	681.81	597.27	11
14	Q	745.84	532.75	10
15	A	781.36	468.72	9
16	A	816.88	433.20	8
17	L	873.42	397.68	7
18	A	908.94	341.14	6
19	S#	992.44	305.62	5
20	N	1049.46	222.12	4
21	G	1077.97	165.10	3
22	P	1126.50	136.59	2
23	R	-	88.06	1

Akap4 A-kinase anchor protein 4

#2064-2064 NL: 1.26E4



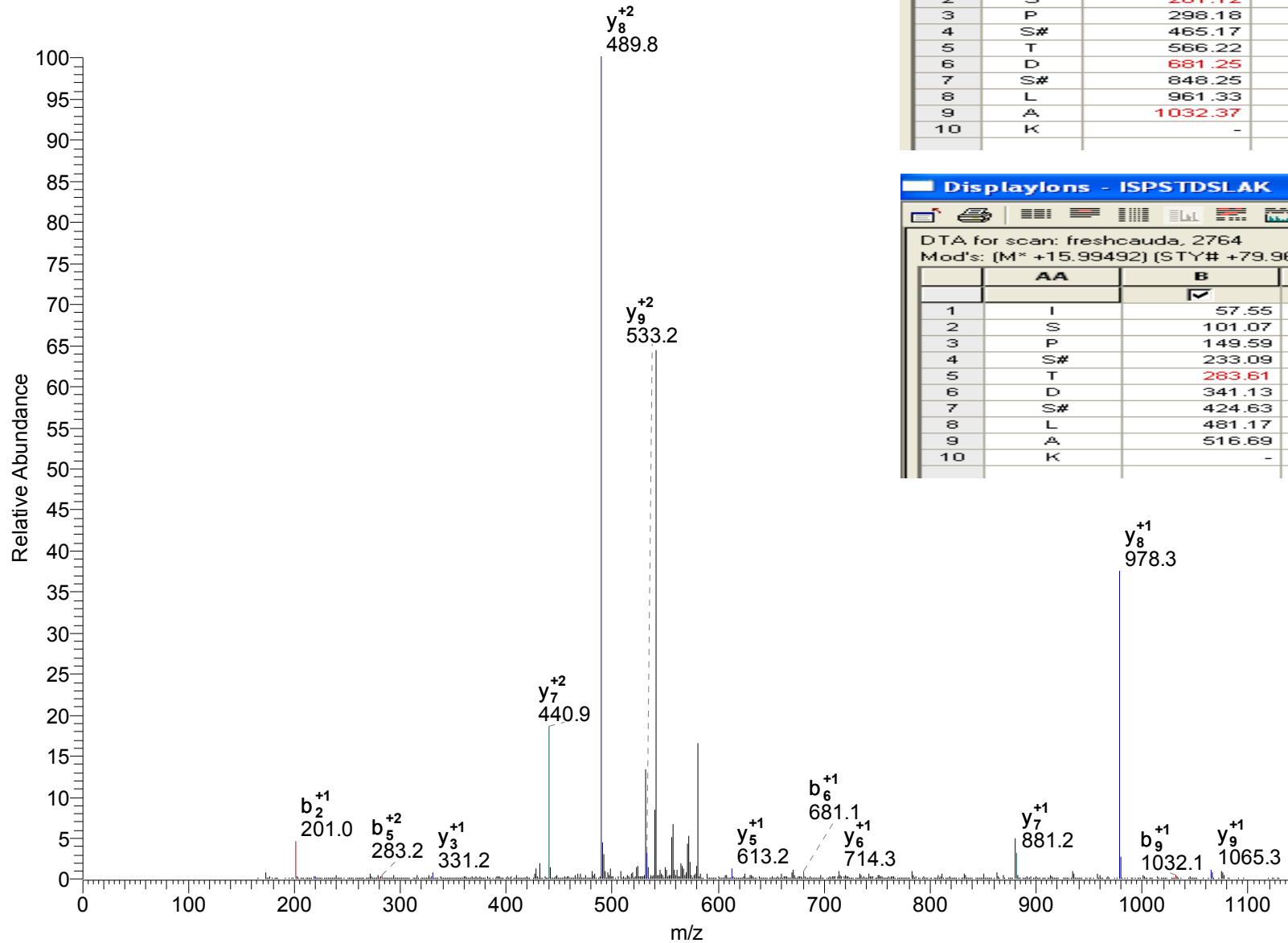
Displays - GKDPCEEECPGSSMGYMSQSAQYEK									
DTA for scan: cap2, 2064									
Mod's: (M ⁺ +15.99492) (S ⁺ Y ⁺ +79.96633)									
1	AA	A	B	Y	Z	1	2	3	4
1	G	-	58.03	-	-	25	-	-	-
2	K	-	186.12	2796.02	24	-	-	-	-
3	D	-	301.15	2687.92	23	-	-	-	-
4	P	-	398.20	2552.90	22	-	-	-	-
5	C	-	501.21	2455.84	21	-	-	-	-
6	E	-	630.26	2352.83	20	-	-	-	-
7	E	-	759.30	2223.79	19	-	-	-	-
8	E	-	888.34	2094.75	18	-	-	-	-
9	C	-	981.36	1965.71	17	-	-	-	-
10	P	-	1088.40	1862.70	16	-	-	-	-
11	G	-	1145.42	1765.64	15	-	-	-	-
12	S	-	1232.46	1708.62	14	-	-	-	-
13	S	-	1319.49	1621.59	13	-	-	-	-
14	M*	-	1465.52	1534.56	12	-	-	-	-
15	G	-	1523.54	1387.52	11	-	-	-	-
16	Y	-	1686.61	1330.50	10	-	-	-	-
17	M*	-	1833.64	1187.44	9	-	-	-	-
18	S	-	1920.68	1050.40	8	-	-	-	-
19	G	-	2049.73	933.37	7	-	-	-	-
20	S#	-	2215.73	805.31	6	-	-	-	-
21	A	-	2286.77	638.31	5	-	-	-	-
22	G	-	2414.83	567.26	4	-	-	-	-
23	Y	-	2577.89	439.22	3	-	-	-	-
24	E	-	2706.93	276.16	2	-	-	-	-
25	K	-	-	147.11	1	-	-	-	-

Displays - GKDPCEEECPGSSMGYMSQSAQYEK									
DTA for scan: cap2, 2064									
Mod's: (M ⁺ +15.99492) (S ⁺ Y ⁺ +79.96633)									
1	AA	A	B	Y	Z	1	2	3	4
1	G	-	29.52	-	-	25	-	-	-
2	K	-	93.57	1398.51	24	-	-	-	-
3	D	-	151.08	1334.47	23	-	-	-	-
4	P	-	195.61	1276.86	22	-	-	-	-
5	C	-	251.11	1258.43	21	-	-	-	-
6	E	-	315.63	1176.92	20	-	-	-	-
7	E	-	380.15	1112.40	19	-	-	-	-
8	E	-	444.67	1047.88	18	-	-	-	-
9	C	-	495.18	983.36	17	-	-	-	-
10	P	-	544.70	931.85	16	-	-	-	-
11	G	-	573.22	883.33	15	-	-	-	-
12	S	-	616.73	854.82	14	-	-	-	-
13	S	-	660.26	811.30	13	-	-	-	-
14	M*	-	733.77	767.79	12	-	-	-	-
15	G	-	762.20	694.27	11	-	-	-	-
16	Y	-	843.61	665.75	10	-	-	-	-
17	M*	-	917.33	584.22	9	-	-	-	-
18	S	-	960.84	510.71	8	-	-	-	-
19	G	-	1024.87	467.19	7	-	-	-	-
20	S#	-	1105.37	403.16	6	-	-	-	-
21	A	-	1143.69	319.66	5	-	-	-	-
22	G	-	1207.92	284.14	4	-	-	-	-
23	Y	-	1289.45	220.11	3	-	-	-	-
24	E	-	1353.97	136.58	2	-	-	-	-
25	K	-	-	74.06	1	-	-	-	-

Displays - GKDPCEEECPGSSMGYMSQSAQYEK									
DTA for scan: cap2, 2064									
Mod's: (M ⁺ +15.99492) (S ⁺ Y ⁺ +79.96633)									
1	AA	A	B	Y	Y*	Yo	Z	1	2
1	G	-	20.01	-	-	-	-	25	-
2	K	-	62.71	932.58	-	-	-	24	-
3	D	-	101.06	889.98	-	-	-	23	-
4	P	-	133.41	851.84	-	-	-	22	-
5	C	-	167.74	819.29	-	-	-	21	-
6	E	-	210.76	784.95	-	-	-	20	-
7	E	-	253.77	741.94	-	-	-	19	-
8	E	-	296.78	698.92	-	-	-	18	-
9	C	-	331.12	655.91	-	-	-	17	-
10	P	-	363.47	621.87	-	-	-	16	-
11	G	-	382.48	589.22	-	-	-	15	-
12	S	-	411.49	570.21	-	-	-	14	-
13	S	-	440.50	541.20	-	-	-	13	-
14	M*	-	469.51	512.19	-	-	-	12	-
15	G	-	498.52	483.18	-	-	-	11	-
16	Y	-	562.87	444.17	-	-	-	10	-
17	M*	-	611.89	399.92	-	-	-	9	-
18	S	-	640.90	340.81	-	-	-	8	-
19	G	-	683.58	311.80	-	-	-	7	-
20	S#	-	736.26	260.11	-	-	-	6	-
21	A	-	762.93	213.44	-	-	-	5	-
22	G	-	805.81	189.76	-	-	-	4	-
23	Y	-	859.97	147.08	-	-	-	3	-
24	E	-	902.98	92.72	-	-	-	2	-
25	K	-	-	49.71	-	-	-	1	-

Akap4 A-kinase anchor protein 4

#2764-2764 NL: 7.00E4



Displaylons - ISPSTD LAK

DTA for scan: freshcauda, 2764
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	I	114.09	-	10
2	S	201.12	1065.39	9
3	P	298.18	978.36	8
4	S#	465.17	881.31	7
5	T	566.22	714.31	6
6	D	681.25	613.26	5
7	S#	848.25	498.23	4
8	L	961.33	331.23	3
9	A	1032.37	218.15	2
10	K	-	147.11	1

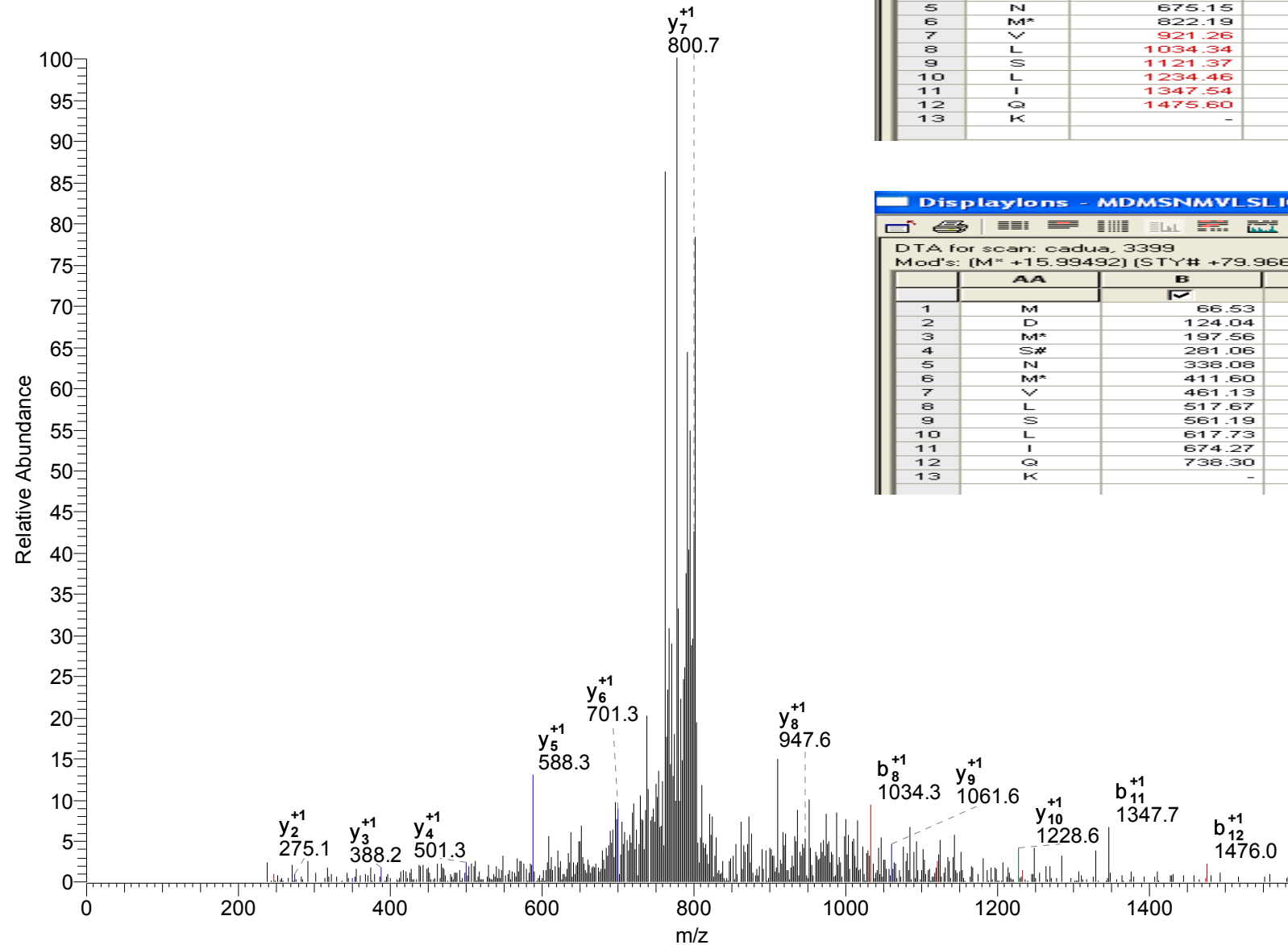
Displaylons - ISPSTD LAK

DTA for scan: freshcauda, 2764
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	I	57.55	-	10
2	S	101.07	533.20	9
3	P	149.59	489.68	8
4	S#	233.09	441.16	7
5	T	283.61	357.66	6
6	D	341.13	307.13	5
7	S#	424.63	249.62	4
8	L	481.17	166.12	3
9	A	516.69	109.58	2
10	K	-	74.06	1

Akap4 A-kinase anchor protein 4

#3399-3399 NL: 7.18E2



Displaylons - MDMSNMVLSLIQK

DTA for scan: cadua, 3399
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	M	132.05	-	13
2	D	247.07	1490.66	12
3	M*	394.11	1375.64	11
4	S#	561.11	1228.60	10
5	N	675.15	1061.60	9
6	M*	822.19	947.56	8
7	V	921.26	800.52	7
8	L	1034.34	701.46	6
9	S	1121.37	588.37	5
10	L	1234.46	501.34	4
11	I	1347.54	388.26	3
12	Q	1475.60	275.17	2
13	K	-	147.11	1

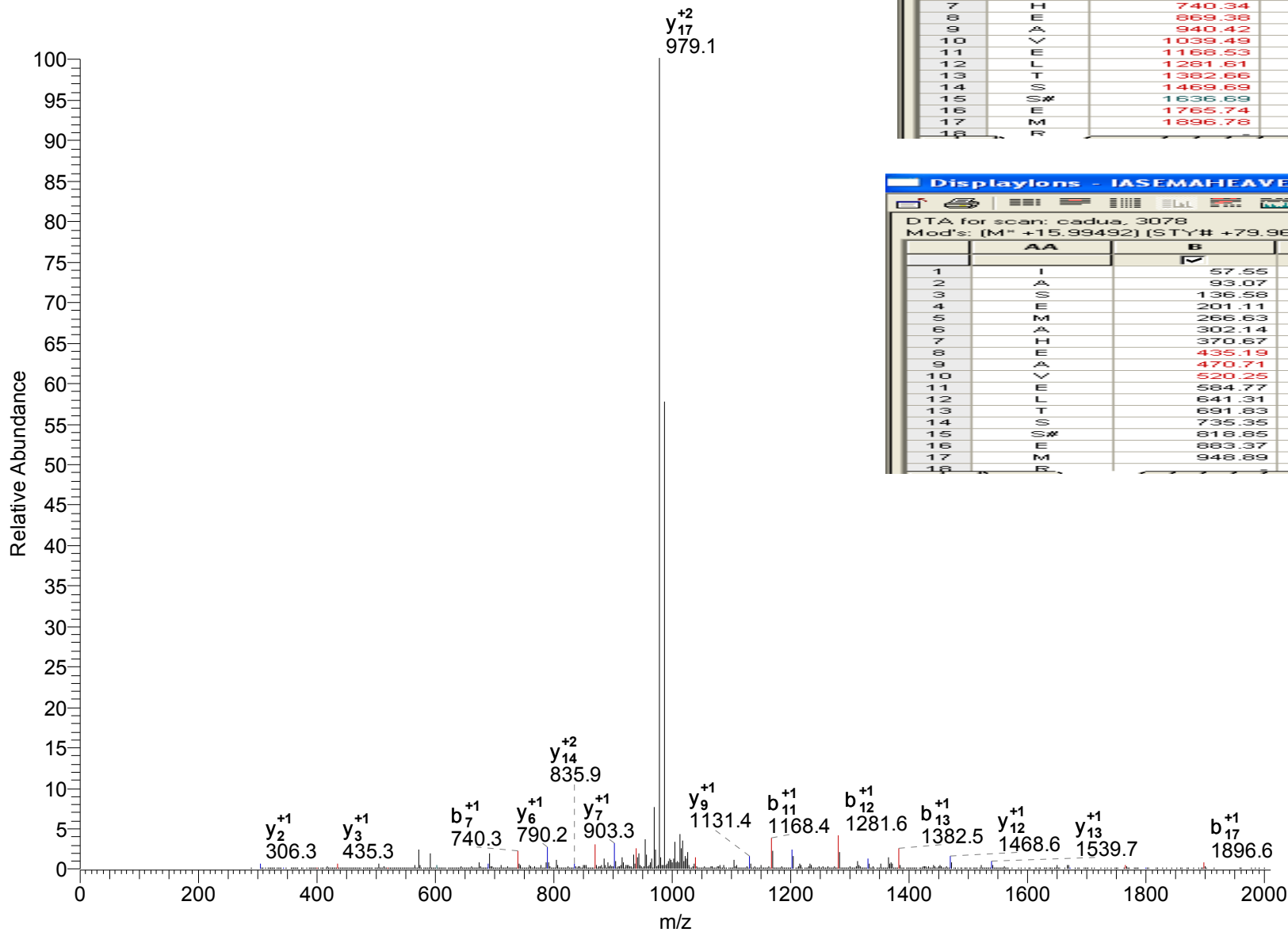
Displaylons - MDMSNMVLSLIQK

DTA for scan: cadua, 3399
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	M	66.53	-	13
2	D	124.04	745.84	12
3	M*	197.56	688.32	11
4	S#	281.06	614.80	10
5	N	338.08	531.30	9
6	M*	411.60	474.28	8
7	V	461.13	400.77	7
8	L	517.67	351.23	6
9	S	561.19	294.69	5
10	L	617.73	251.17	4
11	I	674.27	194.63	3
12	Q	738.30	138.09	2
13	K	-	74.06	1

Akap4 A-kinase anchor protein 4

#3078-3078 NL: 3.12E4



Displaylons - IASEMAHEAVELTSSEMR

DTA for scan: cadua, 3078
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	I	114.09	-	18
2	A	185.13	1957.80	17
3	S	272.16	1886.77	16
4	E	401.20	1799.73	15
5	M	532.24	1670.69	14
6	A	603.28	1539.65	13
7	H	740.34	1468.61	12
8	E	869.38	1331.55	11
9	A	940.42	1202.51	10
10	V	1039.49	1131.48	9
11	E	1168.53	1032.41	8
12	L	1291.61	903.36	7
13	T	1382.66	790.28	6
14	S	1469.69	689.23	5
15	S#	1636.69	602.20	4
16	E	1765.74	435.20	3
17	M	1896.78	306.16	2
18	R		175.12	1

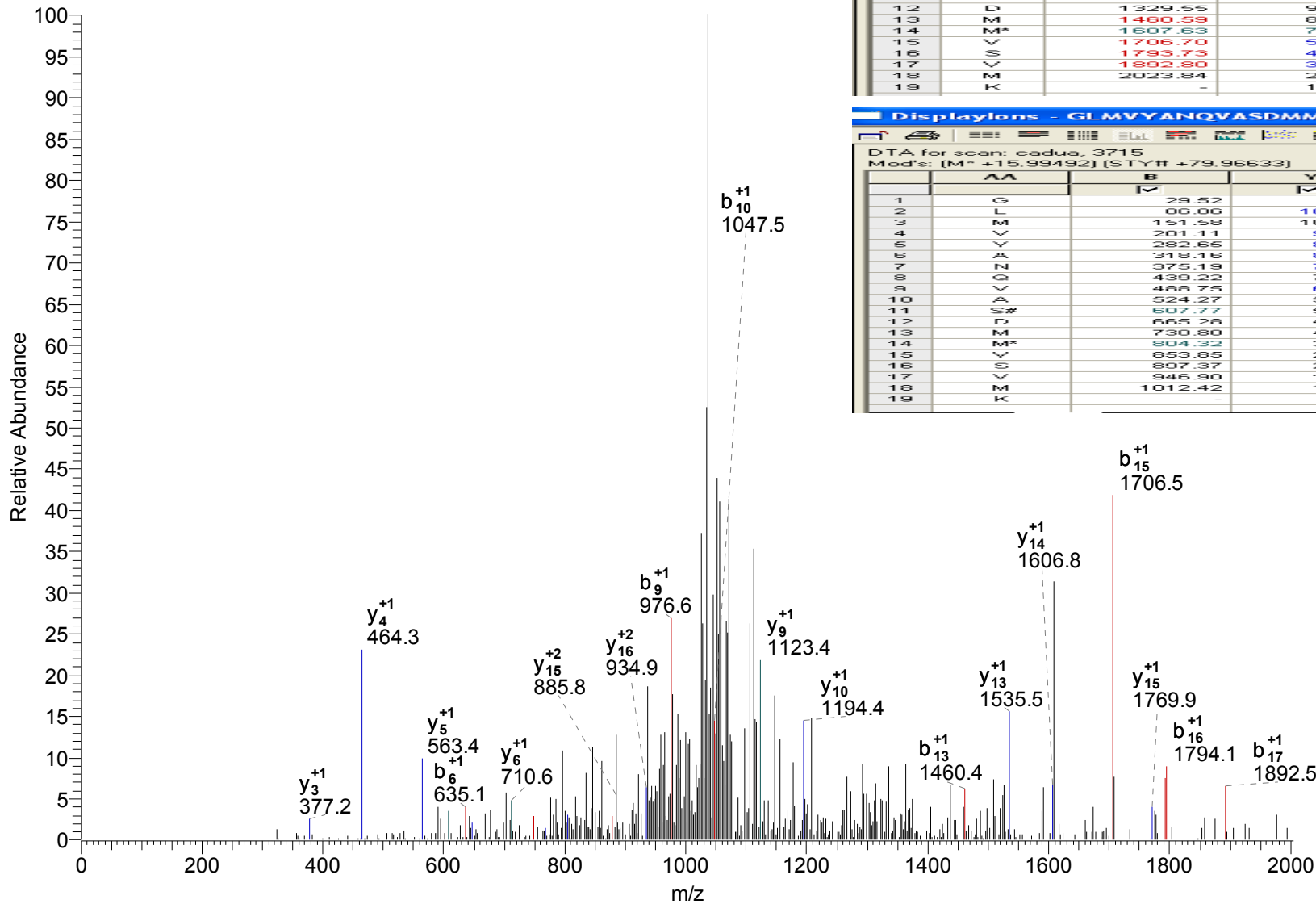
Displaylons - IASEMAHEAVELTSSEMR

DTA for scan: cadua, 3078
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	I	57.55	-	18
2	A	93.07	979.41	17
3	S	136.58	943.89	16
4	E	201.11	900.37	15
5	M	266.63	835.85	14
6	A	302.14	770.33	13
7	H	370.67	734.81	12
8	E	435.19	666.28	11
9	A	470.71	601.76	10
10	V	520.25	566.24	9
11	E	584.77	516.71	8
12	L	641.31	452.19	7
13	T	691.83	395.64	6
14	S	735.35	345.12	5
15	S#	818.85	301.60	4
16	E	883.37	218.10	3
17	M	948.89	153.58	2
18	R		88.06	1

Akap4 A-kinase anchor protein 4

#3715-3715 NL: 4.63E2



Displaylens - GLMVYANQVASDMMVSVMK

DTA for scan: cadua. 3715
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	G	58.03	-	19
2	L	171.11	2112.92	18
3	M	302.15	1999.84	17
4	V	401.22	1868.80	16
5	Y	564.29	1769.73	15
6	A	635.32	1606.67	14
7	N	749.37	1535.63	13
8	Q	877.42	1421.59	12
9	V	976.49	1293.53	11
10	A	1047.53	1194.46	10
11	S#	1214.53	1123.42	9
12	D	1329.55	956.42	8
13	M	1460.59	841.40	7
14	M*	1507.63	710.36	6
15	V	1706.70	563.32	5
16	S	1793.73	464.25	4
17	V	1892.80	377.22	3
18	M	2023.84	278.15	2
19	K	-	147.11	1

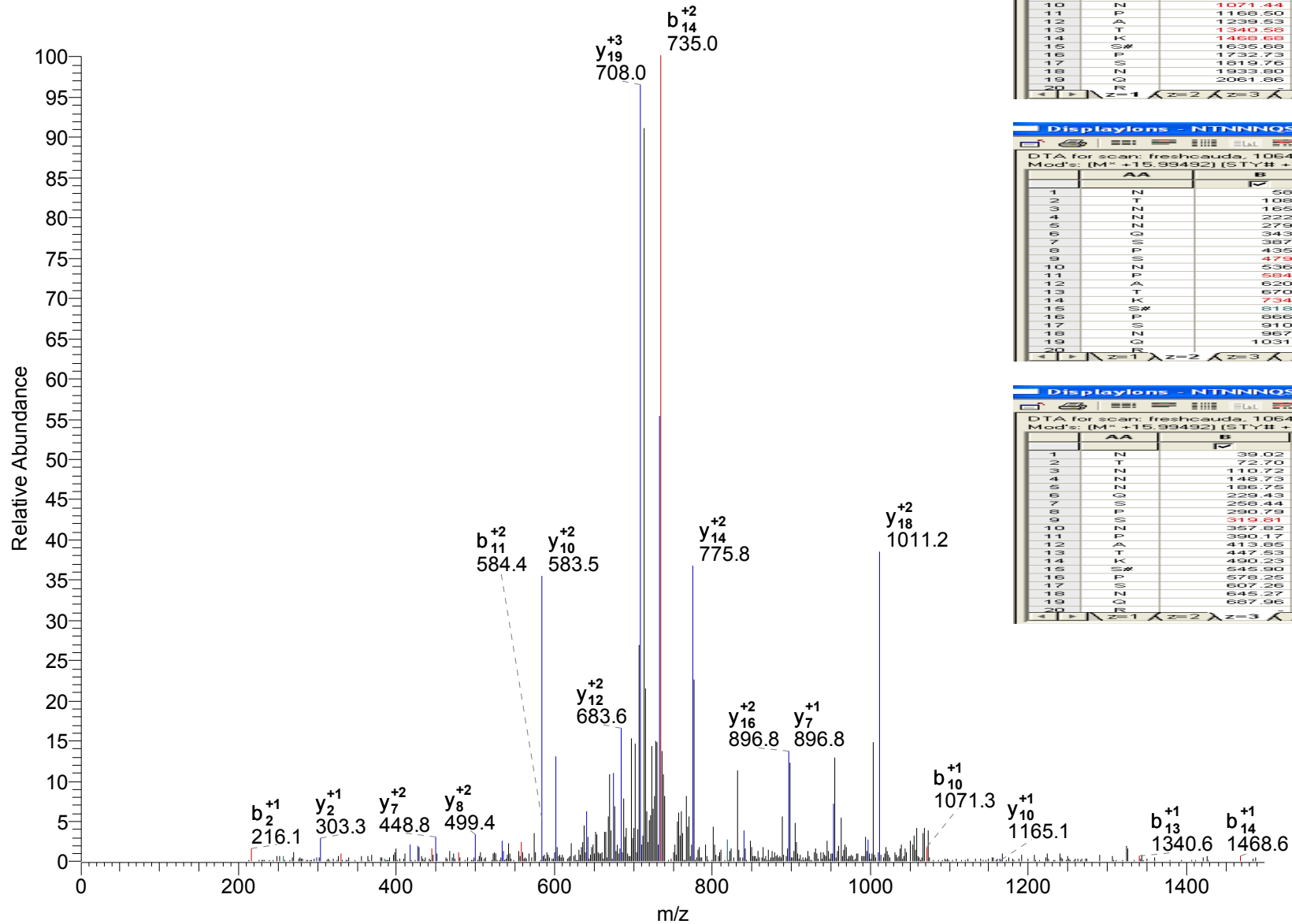
Displaylens - GLMVYANQVASDMMVSVMK

DTA for scan: cadua. 3715
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	G	29.52	-	19
2	L	96.06	1056.97	18
3	M	151.58	1000.42	17
4	V	201.11	934.90	16
5	Y	282.65	885.37	15
6	A	318.16	803.84	14
7	N	375.19	768.32	13
8	Q	439.22	711.30	12
9	V	488.75	647.27	11
10	A	524.27	597.73	10
11	S#	607.77	562.22	9
12	D	665.28	478.72	8
13	M	730.80	421.20	7
14	M*	804.32	355.68	6
15	V	853.85	282.16	5
16	S	897.37	232.63	4
17	V	946.90	189.11	3
18	M	1012.42	139.58	2
19	K	-	74.06	1

Akap4 A-kinase anchor protein 4

#1064-1064 NL: 2.37E3



Displayions - NTNNNQSPSNPA TKSPSNQR

DTA for scan: freshcauda, 1064
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	N	115.05	-	20
2	T	216.10	2121.93	19
3	N	330.14	2020.68	18
4	N	444.18	1906.84	17
5	N	558.23	1792.60	16
6	Q	686.28	1678.75	15
7	S	773.32	1550.70	14
8	P	870.37	1463.66	13
9	S	957.40	1366.61	12
10	N	1071.44	1279.58	11
11	P	1168.50	1165.54	10
12	A	1239.53	1068.48	9
13	T	1340.58	997.45	8
14	K	1468.68	896.40	7
15	SW	1535.68	769.30	6
16	P	1732.73	601.31	5
17	N	1819.76	504.25	4
18	N	1933.80	417.22	3
19	Q	2061.86	303.18	2
20	R		175.12	1

Displayions - NTNNNQSPSNPA TKSPSNQR

DTA for scan: freshcauda, 1064
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	N	58.03	-	
2	T	108.55	1061.47	
3	N	165.57	1010.35	
4	N	222.60	953.92	
5	N	279.62	896.90	
6	Q	343.65	839.86	
7	S	387.16	775.85	
8	P	435.69	732.34	
9	SW	479.20	683.81	
10	N	536.23	640.29	
11	P	584.75	593.27	
12	A	620.27	534.75	
13	T	670.79	499.23	
14	K	734.84	448.70	
15	SW	816.34	394.66	
16	P	866.87	301.16	
17	N	910.38	252.63	
18	N	967.41	209.11	
19	Q	1031.43	152.09	
20	R		88.06	

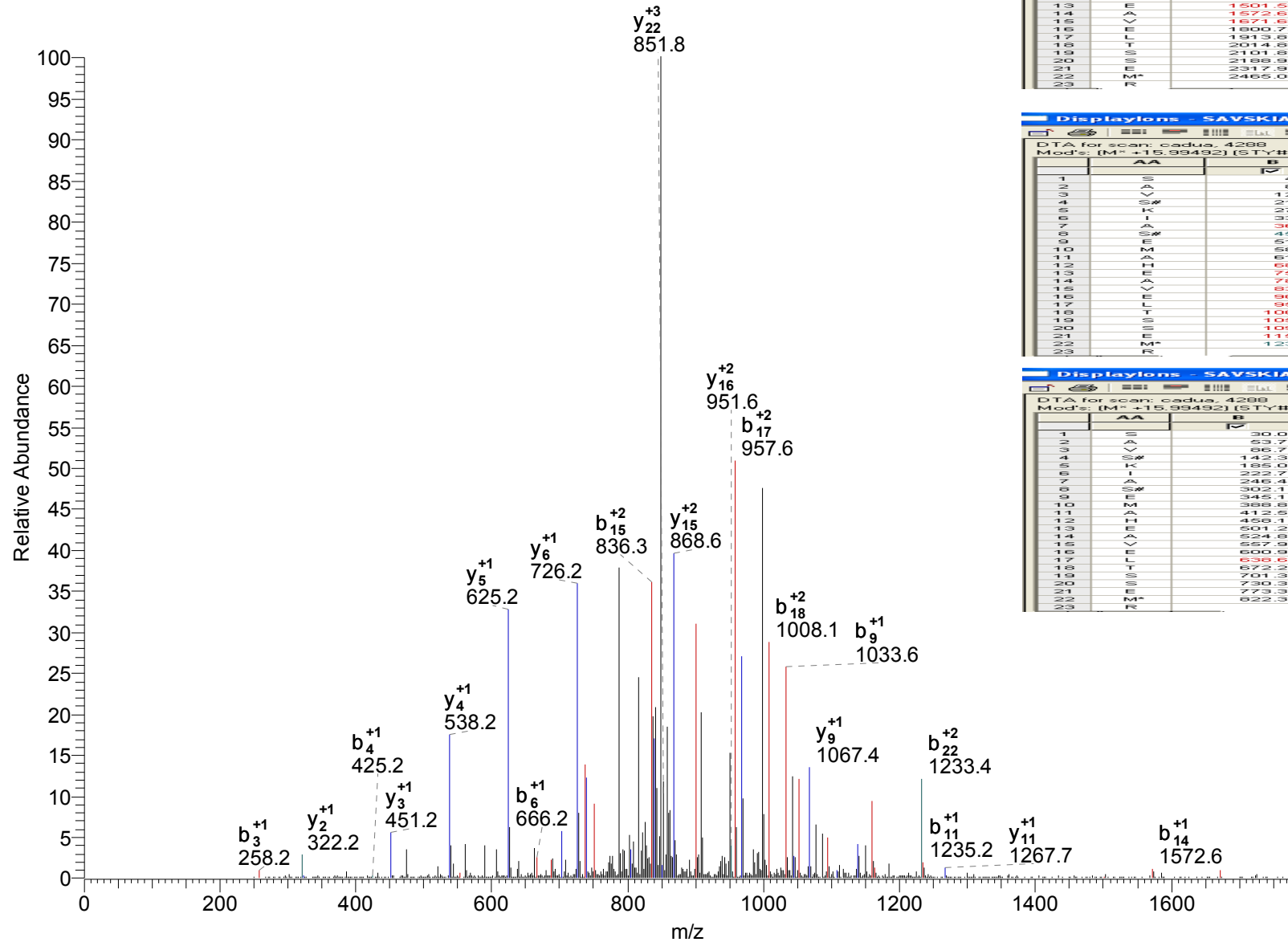
Displayions - NTNNNQSPSNPA TKSPSNQR

DTA for scan: freshcauda, 1064
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	N	39.02	-	20
2	T	72.70	707.99	19
3	N	110.72	674.30	18
4	N	148.73	636.26	17
5	N	186.75	598.27	16
6	Q	229.43	560.26	15
7	S	268.44	517.57	14
8	P	290.79	488.56	13
9	S	319.61	456.21	12
10	N	357.62	427.20	11
11	P	390.17	389.18	10
12	A	413.65	356.63	9
13	T	447.53	333.15	8
14	K	490.23	299.47	7
15	SW	545.90	256.77	6
16	P	578.25	201.11	5
17	N	607.26	166.76	4
18	N	645.27	139.75	3
19	Q	687.96	101.73	2
20	R		59.14	1

Akap4 A-kinase anchor protein 4

#4288-4288 NL: 1.27E4



Displays SAVSKIASEMAHEAVELTSEM

DTA for scan: cadua. 4288
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	88.04	-	23
2	A	159.08	2552.08	22
3	V	258.14	2481.04	21
4	SW	425.14	2381.98	20
5	K	553.24	2214.98	19
6	I	666.32	2086.88	18
7	A	737.36	1973.80	17
8	SW	904.36	1902.76	16
9	E	1033.40	1735.76	15
10	M	1164.44	1606.72	14
11	A	1235.48	1475.68	13
12	H	1372.54	1404.64	12
13	E	1501.58	1267.58	11
14	V	1572.62	1138.54	10
15	V	1671.68	1067.50	9
16	E	1800.73	958.44	8
17	L	1913.81	839.39	7
18	T	2014.86	726.31	6
19	S	2101.89	625.26	5
20	S	2188.92	538.23	4
21	E	2317.97	451.20	3
22	M ⁺	2465.00	322.15	2
23	R	-	88.06	1

Displays SAVSKIASEMAHEAVELTSEM

DTA for scan: cadua. 4288
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	44.52	-	23
2	A	60.04	1276.54	22
3	V	129.56	1241.03	21
4	SW	213.08	1191.49	20
5	K	277.12	1107.99	19
6	I	333.66	1043.94	18
7	A	369.18	967.40	17
8	SW	452.66	951.86	16
9	E	517.20	868.38	15
10	M	582.72	803.86	14
11	A	618.24	738.34	13
12	H	686.77	702.82	12
13	E	751.29	634.30	11
14	V	786.81	565.77	10
15	V	836.36	534.26	9
16	E	900.67	484.72	8
17	L	957.41	420.20	7
18	T	1007.93	363.66	6
19	S	1051.45	313.13	5
20	S	1094.97	268.62	4
21	E	1159.49	226.10	3
22	M ⁺	1233.00	161.58	2
23	R	-	58.06	1

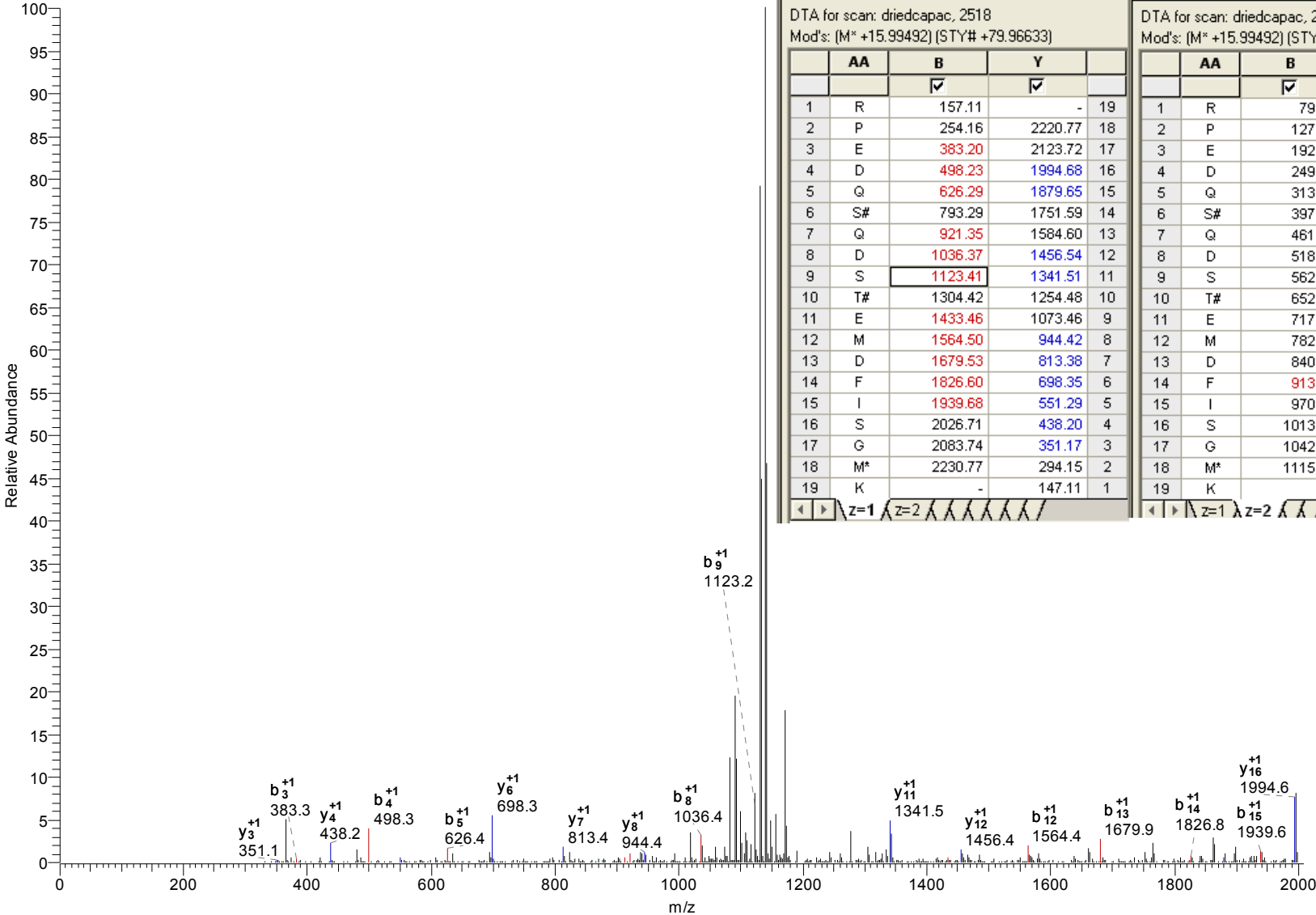
Displays SAVSKIASEMAHEAVELTSEM

DTA for scan: cadua. 4288
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	30.02	-	23
2	A	63.70	851.37	22
3	V	66.72	627.69	21
4	SW	142.38	794.66	20
5	K	185.08	739.00	19
6	I	222.78	696.30	18
7	A	246.46	659.60	17
8	SW	302.12	634.93	16
9	E	345.14	579.26	15
10	M	368.62	536.24	14
11	A	412.50	492.56	13
12	H	456.18	458.89	12
13	E	501.20	423.20	11
14	V	524.88	380.19	10
15	V	567.90	356.51	9
16	E	600.91	323.48	8
17	L	636.61	280.47	7
18	T	672.29	242.77	6
19	S	701.30	209.09	5
20	S	730.31	180.08	4
21	E	773.33	151.07	3
22	M ⁺	822.34	108.06	2
23	R	-	59.04	1

Akap4 A-kinase anchor protein 4

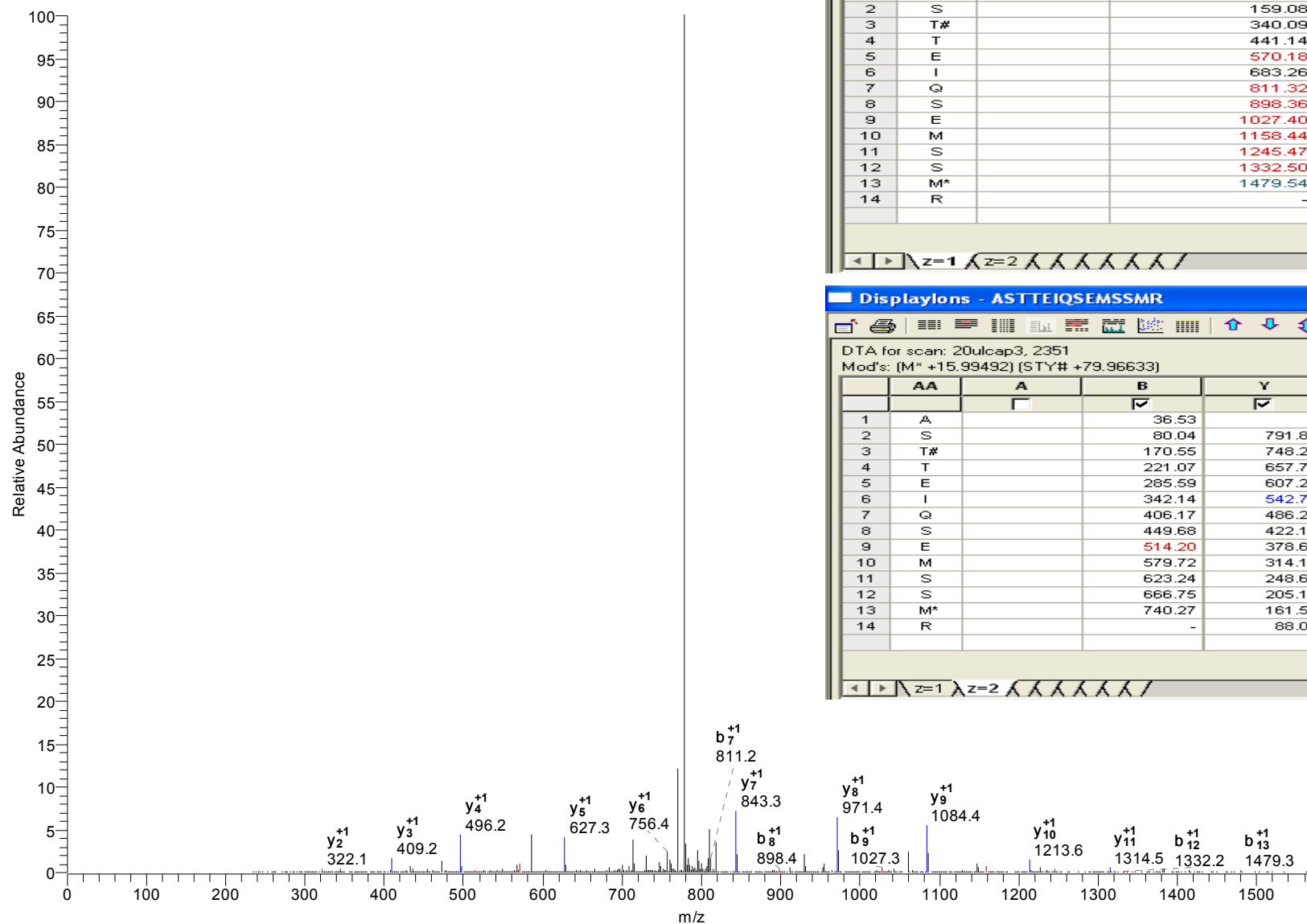
#2518-2518 NL: 5.49E3



Displaylons - RPEDQSQDSTEMDFISGMK					Displaylons - RPEDQSQDSTEMDFISGMK				
DTA for scan: driedcapac, 2518 Mod's: (M* +15.99492) (STY# +79.96633)					DTA for scan: driedcapac, 2518 Mod's: (M* +15.99492) (STY# +79.96633)				
	AA	B	Y			AA	B	Y	
		✓	✓				✓	✓	
1	R	157.11	-	19	1	R	79.06	-	19
2	P	254.16	2220.77	18	2	P	127.58	1110.89	18
3	E	383.20	2123.72	17	3	E	192.11	1062.36	17
4	D	498.23	1994.68	16	4	D	249.62	997.84	16
5	Q	626.29	1879.65	15	5	Q	313.65	940.33	15
6	S#	793.29	1751.59	14	6	S#	397.15	876.30	14
7	Q	921.35	1584.60	13	7	Q	461.18	792.80	13
8	D	1036.37	1456.54	12	8	D	518.69	728.77	12
9	S	1123.41	1341.51	11	9	S	562.21	671.26	11
10	T#	1304.42	1254.48	10	10	T#	652.71	627.74	10
11	E	1433.46	1073.46	9	11	E	717.23	537.24	9
12	M	1564.50	944.42	8	12	M	782.75	472.71	8
13	D	1679.53	813.38	7	13	D	840.27	407.19	7
14	F	1826.60	698.35	6	14	F	913.80	349.68	6
15	I	1939.68	551.29	5	15	I	970.34	276.15	5
16	S	2026.71	438.20	4	16	S	1013.86	219.60	4
17	G	2083.74	351.17	3	17	G	1042.37	176.09	3
18	M*	2230.77	294.15	2	18	M*	1115.89	147.58	2
19	K	-	147.11	1	19	K	-	74.06	1

predicted similar to sperm acrosome
associated 1

#2351-2351 NL: 2.06E4



Displays - ASTTEIQSEMSSMR

DTA for scan: 20ulcap3, 2351
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	A		72.04	-	14
2	S		159.08	1582.61	13
3	T#		340.09	1495.58	12
4	T		441.14	1314.57	11
5	E		570.18	1213.52	10
6	I		683.26	1084.48	9
7	Q		811.32	971.39	8
8	S		898.36	843.33	7
9	E		1027.40	756.30	6
10	M		1158.44	627.26	5
11	S		1245.47	496.22	4
12	S		1332.50	409.19	3
13	M*		1479.54	322.15	2
14	R		-	175.12	1

z=1 z=2

Displays - ASTTEIQSEMSSMR

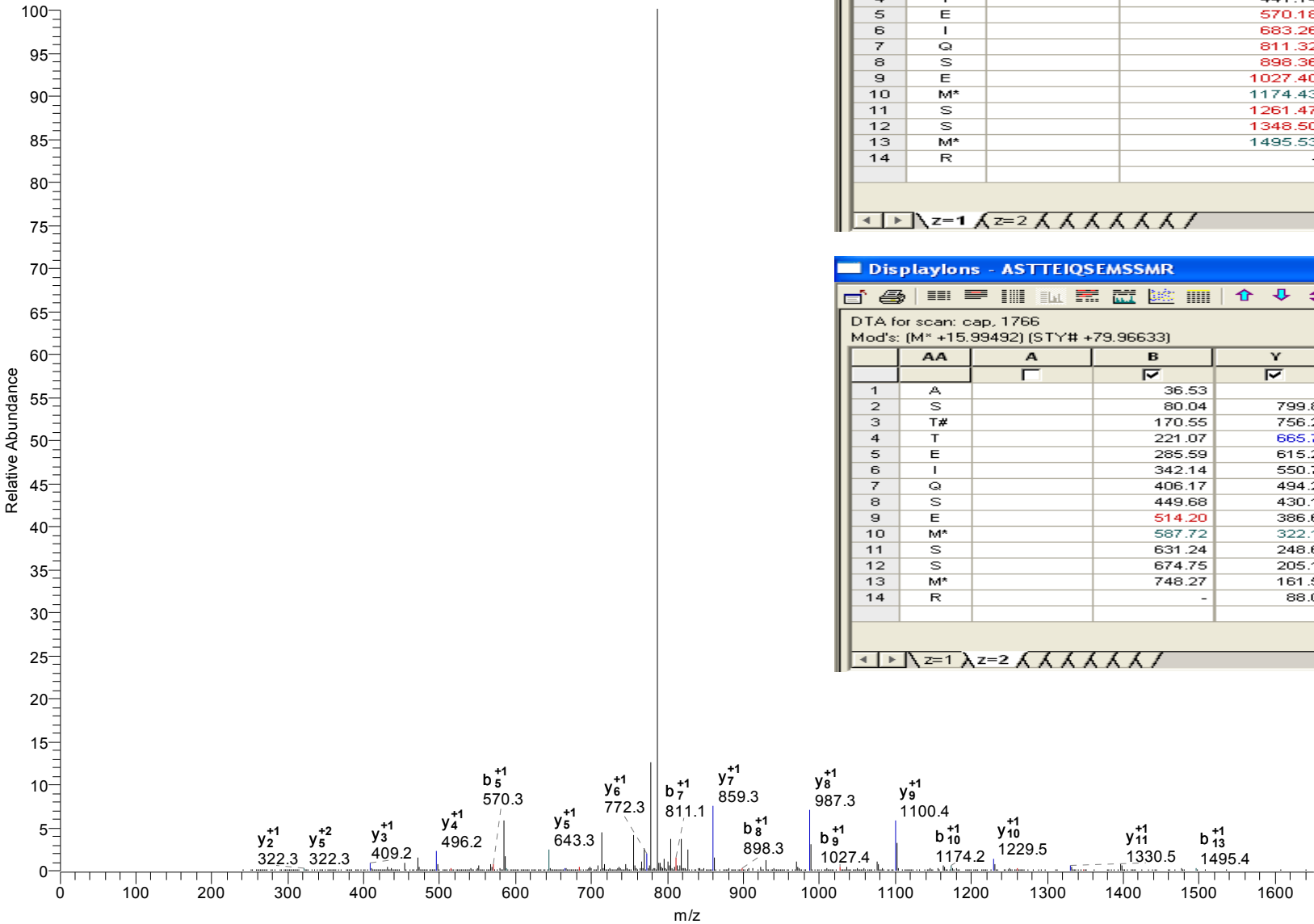
DTA for scan: 20ulcap3, 2351
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	A		36.53	-		14
2	S		80.04	791.81		13
3	T#		170.55	748.29		12
4	T		221.07	657.79		11
5	E		285.59	607.26		10
6	I		342.14	542.74		9
7	Q		406.17	486.20		8
8	S		449.68	422.17		7
9	E		514.20	378.65		6
10	M		579.72	314.13		5
11	S		623.24	248.61		4
12	S		666.75	205.10		3
13	M*		740.27	161.58		2
14	R		-	88.06		1

z=1 z=2

predicted similar to sperm acrosome associated 1

#1766-1766 NL: 2.82E4



Displaylons - ASTTEIQSEMSSMR

DTA for scan: cap. 1766
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	A		72.04	-	14
2	S		159.08	1598.61	13
3	T#		340.09	1511.58	12
4	T		441.14	1330.56	11
5	E		570.18	1229.51	10
6	I		683.26	1100.47	9
7	Q		811.32	987.39	8
8	S		898.36	859.33	7
9	E		1027.40	772.30	6
10	M*		1174.43	643.25	5
11	S		1261.47	496.22	4
12	S		1348.50	409.19	3
13	M*		1495.53	322.15	2
14	R		-	175.12	1

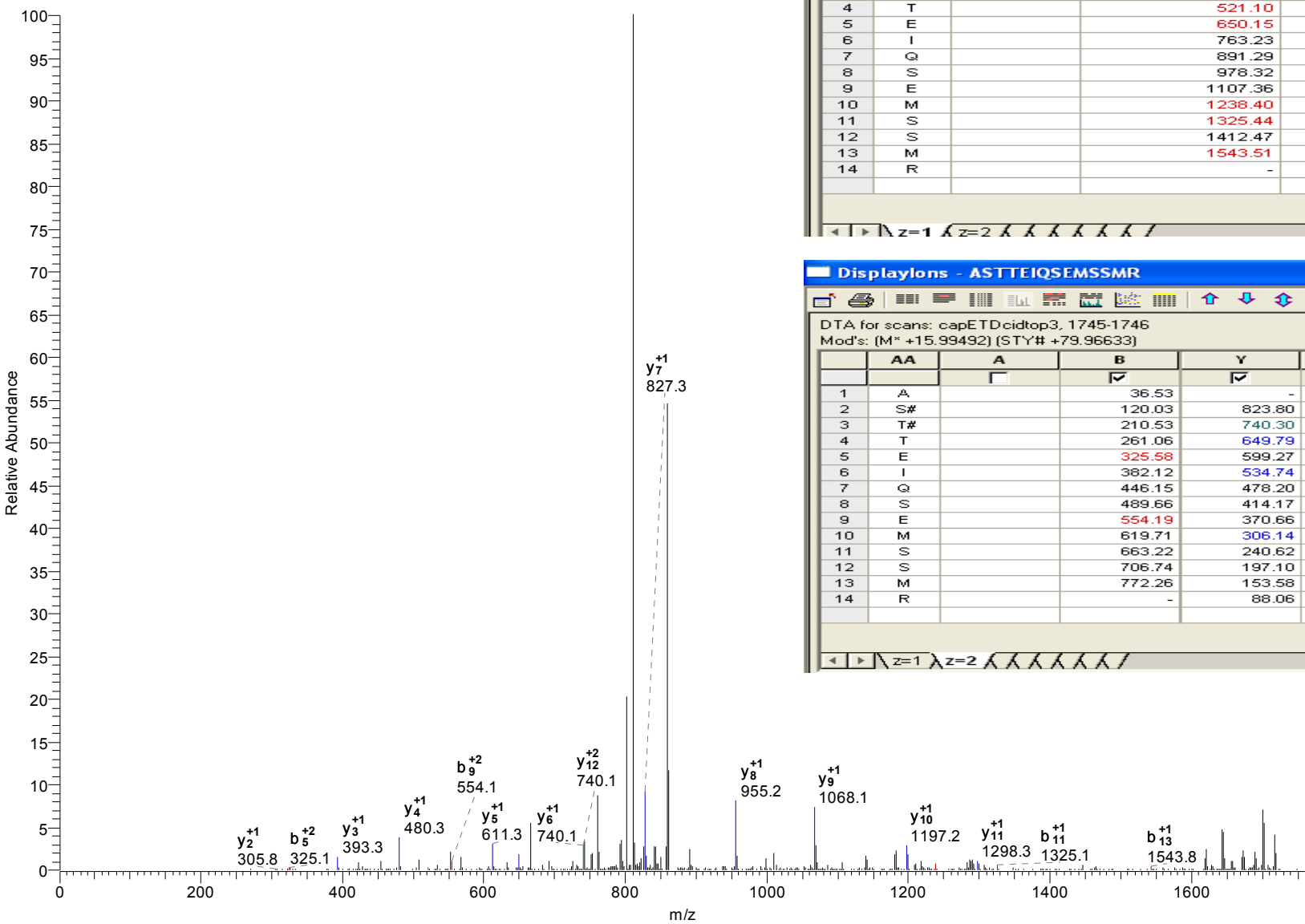
Displaylons - ASTTEIQSEMSSMR

DTA for scan: cap. 1766
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	A		36.53	-		14
2	S		80.04	799.81		13
3	T#		170.55	756.29		12
4	T		221.07	665.78		11
5	E		285.59	615.26		10
6	I		342.14	550.74		9
7	Q		406.17	494.20		8
8	S		449.68	430.17		7
9	E		514.20	386.65		6
10	M*		587.72	322.13		5
11	S		631.24	248.61		4
12	S		674.75	205.10		3
13	M*		748.27	161.58		2
14	R		-	88.06		1

predicted similar to sperm acrosome associated 1

#1745-1746 NL: 4.85E3



Displaylons - ASTTEIQSEMSSMR

DTA for scans: capETDcidtop3, 1745-1746
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	A		72.04	-	14
2	S#		239.04	1646.58	13
3	T#		420.06	1479.59	12
4	T		521.10	1298.57	11
5	E		650.15	1197.52	10
6	I		763.23	1068.48	9
7	Q		891.29	955.40	8
8	S		978.32	827.34	7
9	E		1107.36	740.31	6
10	M		1238.40	611.26	5
11	S		1325.44	480.22	4
12	S		1412.47	393.19	3
13	M		1543.51	306.16	2
14	R		-	175.12	1

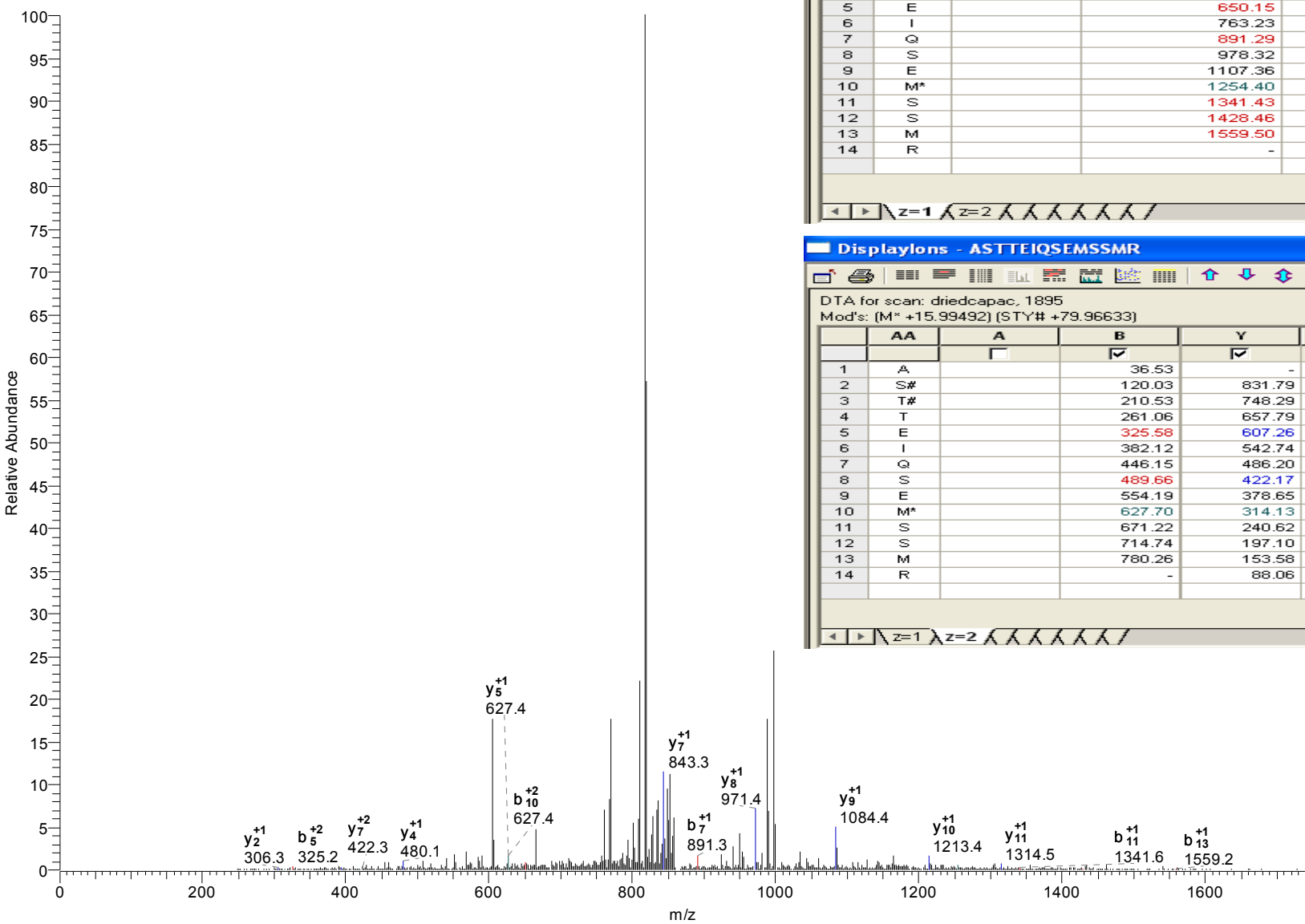
Displaylons - ASTTEIQSEMSSMR

DTA for scans: capETDcidtop3, 1745-1746
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	A		36.53	-		14
2	S#		120.03	823.80		13
3	T#		210.53	740.30		12
4	T		261.06	649.79		11
5	E		325.58	599.27		10
6	I		382.12	534.74		9
7	Q		446.15	478.20		8
8	S		489.66	414.17		7
9	E		554.19	370.66		6
10	M		619.71	306.14		5
11	S		663.22	240.62		4
12	S		706.74	197.10		3
13	M		772.26	153.58		2
14	R		-	88.06		1

predicted similar to sperm acrosome associated 1

#1895-1895 NL: 8.90E3



Displaylons - ASTTEIQSEMSSMR

DTA for scan: driedcapac, 1895
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	A		72.04	-	14
2	S#		239.04	1662.58	13
3	T#		420.06	1495.58	12
4	T		521.10	1314.57	11
5	E		650.15	1213.52	10
6	I		763.23	1084.48	9
7	Q		891.29	971.39	8
8	S		978.32	843.33	7
9	E		1107.36	756.30	6
10	M*		1254.40	627.26	5
11	S		1341.43	480.22	4
12	S		1428.46	393.19	3
13	M		1559.50	306.16	2
14	R		-	175.12	1

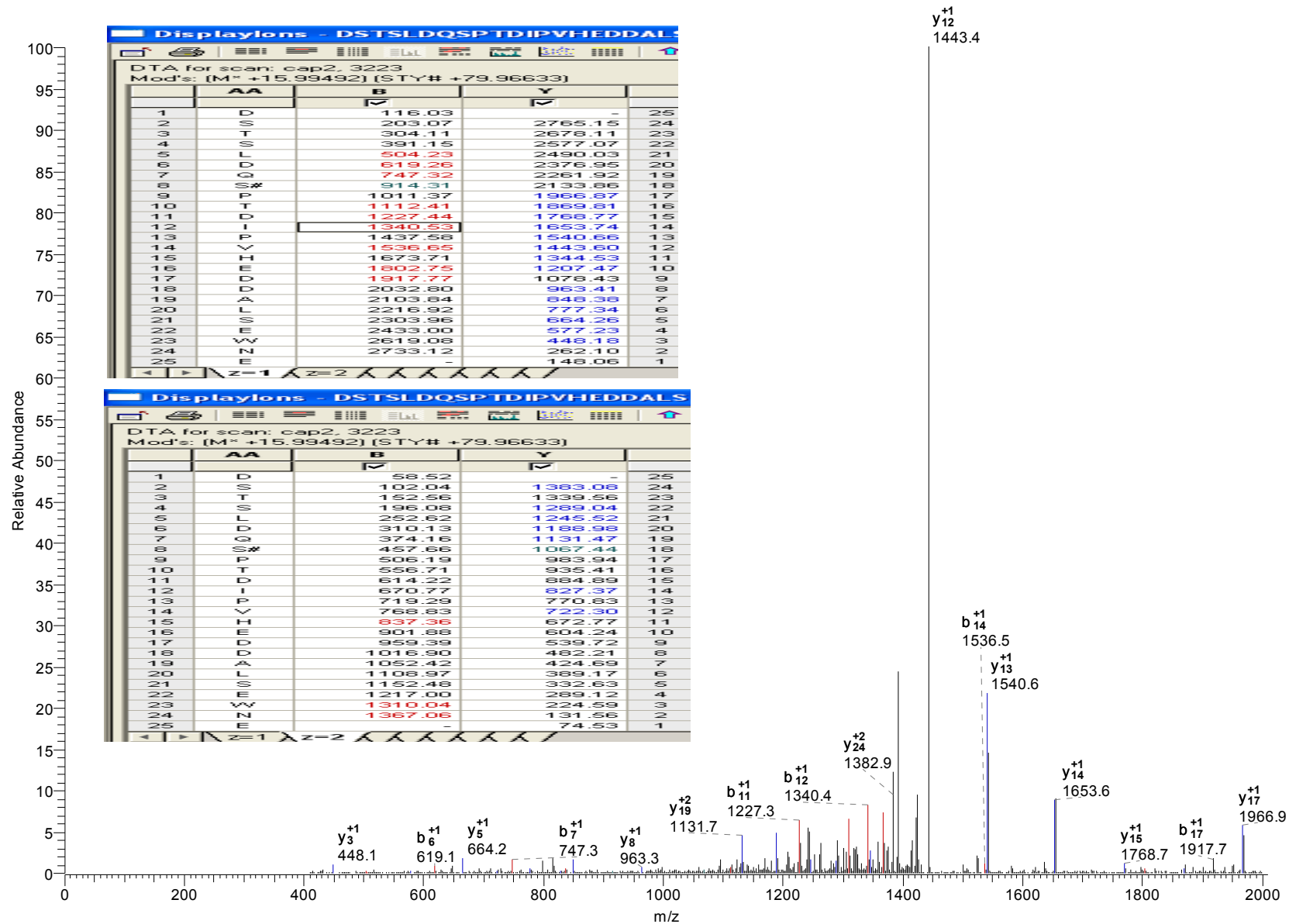
Displaylons - ASTTEIQSEMSSMR

DTA for scan: driedcapac, 1895
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	A		36.53	-		14
2	S#		120.03	831.79		13
3	T#		210.53	748.29		12
4	T		261.06	657.79		11
5	E		325.58	607.26		10
6	I		382.12	542.74		9
7	Q		446.15	486.20		8
8	S		489.66	422.17		7
9	E		554.19	378.65		6
10	M*		627.70	314.13		5
11	S		671.22	240.62		4
12	S		714.74	197.10		3
13	M		780.26	153.58		2
14	R		-	88.06		1

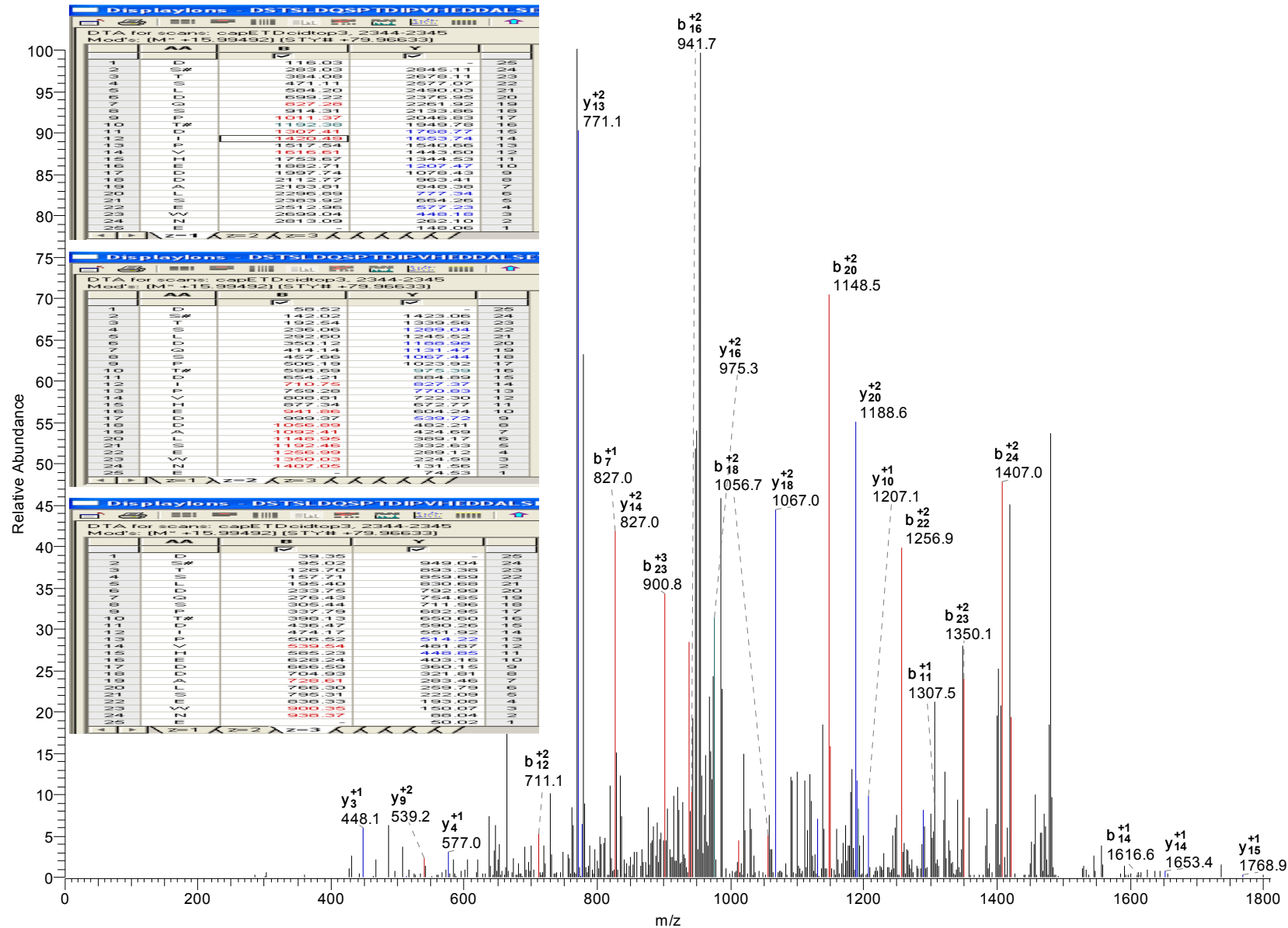
predicted similar to sperm acrosome
associated 1

#3223-3223 NL: 1.00E4



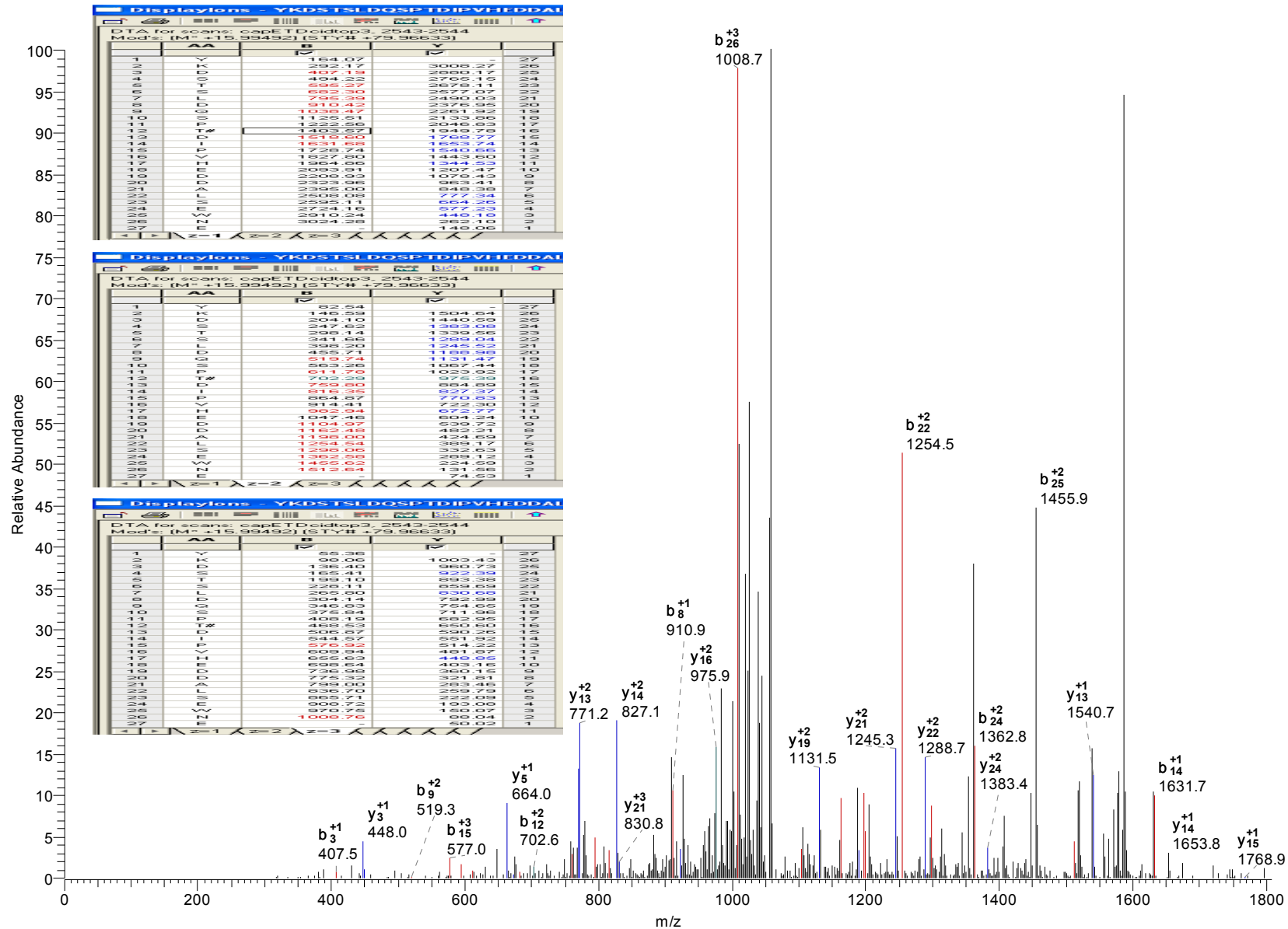
predicted similar to sperm acrosome associated 1

#2344-2345 NL: 3.91E2



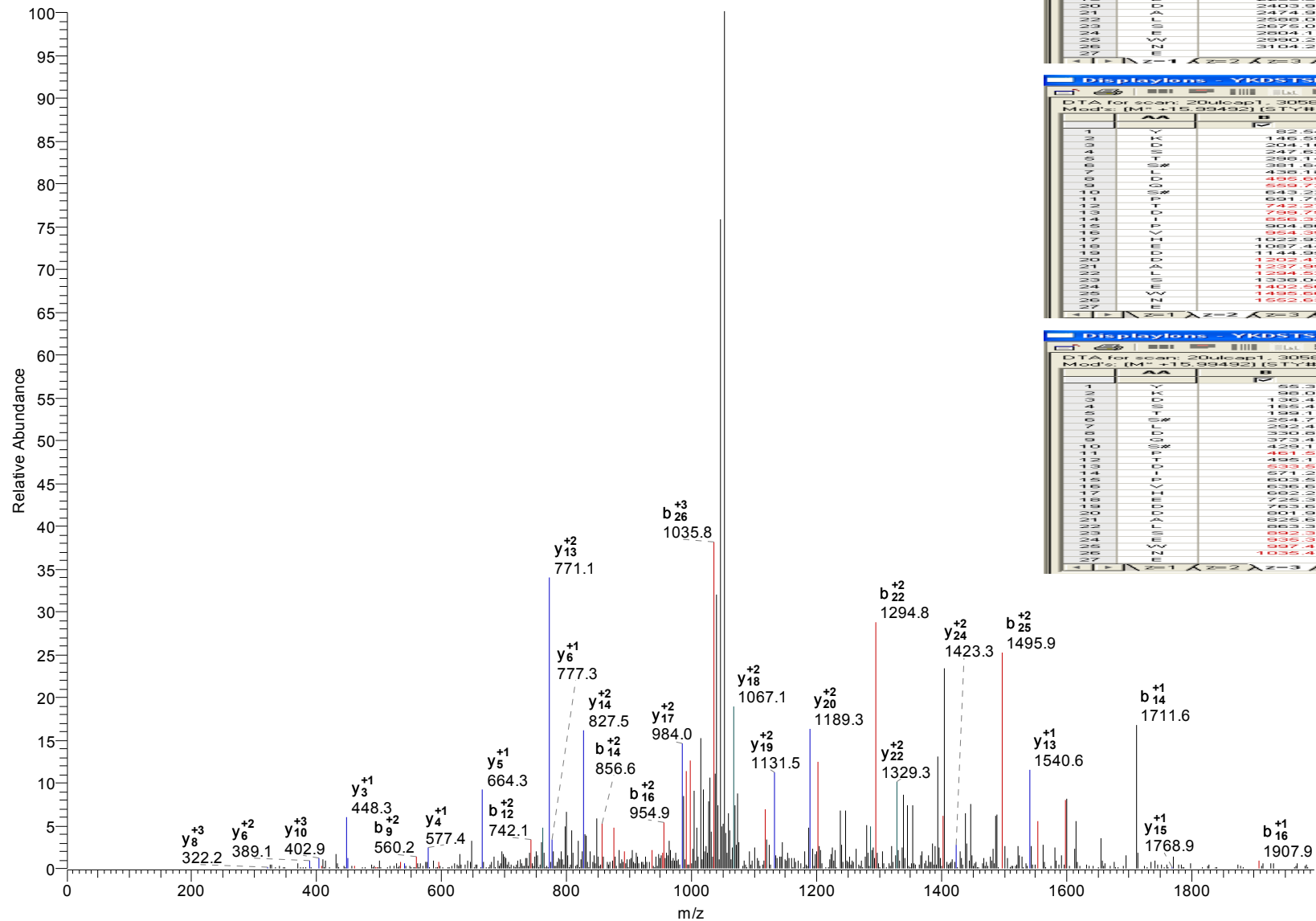
predicted similar to sperm acrosome
associated 1

#2543-2544 NL: 5.64E2



predicted similar to sperm acrosome
associated 1

#3058-3058 NL: 1.34E3



Displays - YKDTSLDQSPFDIEVHEDDAI

DTA for scan: 20ulcap1_3058
Mod: (M: -15.95492) (S: TyH: +79.96633)

AA	B	Y	
1	164.07	3088.23	27
2	293.17	3050.14	26
3	407.15	2945.11	25
4	494.23	2758.08	24
5	595.35	2557.03	23
6	676.37	2450.93	22
7	990.38	2375.95	20
8	1118.44	2351.92	19
9	1265.44	2133.86	18
10	1393.49	1966.87	17
11	1598.57	1869.81	16
12	1711.65	1768.77	15
13	1808.72	1653.74	14
14	1907.77	1443.60	12
15	2044.88	1344.53	11
16	2173.87	1207.47	10
17	2288.90	1078.43	9
18	2403.93	963.41	8
19	2474.96	848.38	7
20	2588.05	727.35	6
21	2675.08	654.26	5
22	2804.12	577.23	4
23	2990.20	448.18	3
24	3104.24	362.10	2
25		146.06	1

Displays - YKDTSLDQSPFDIEVHEDDAI

DTA for scan: 20ulcap1_3058
Mod: (M: -15.95492) (S: TyH: +79.96633)

AA	B	Y	
1	52.54	1544.6	27
2	146.59	1460.67	26
3	204.10	1423.04	25
4	247.52	1378.54	24
5	298.14	1329.02	23
6	391.64	1188.96	20
7	436.18	1131.47	19
8	495.69	1067.44	18
9	559.72	963.04	17
10	643.22	855.41	16
11	691.75	804.88	15
12	742.27	770.63	14
13	799.70	722.30	12
14	856.33	672.77	11
15	904.86	604.24	10
16	954.39	482.21	8
17	1032.92	424.69	7
18	1087.44	389.17	6
19	1202.47	332.53	5
20	1237.90	269.12	4
21	1294.53	224.59	3
22	1336.04	131.66	2
23	1402.58		1
24	1495.60		
25	1552.63		

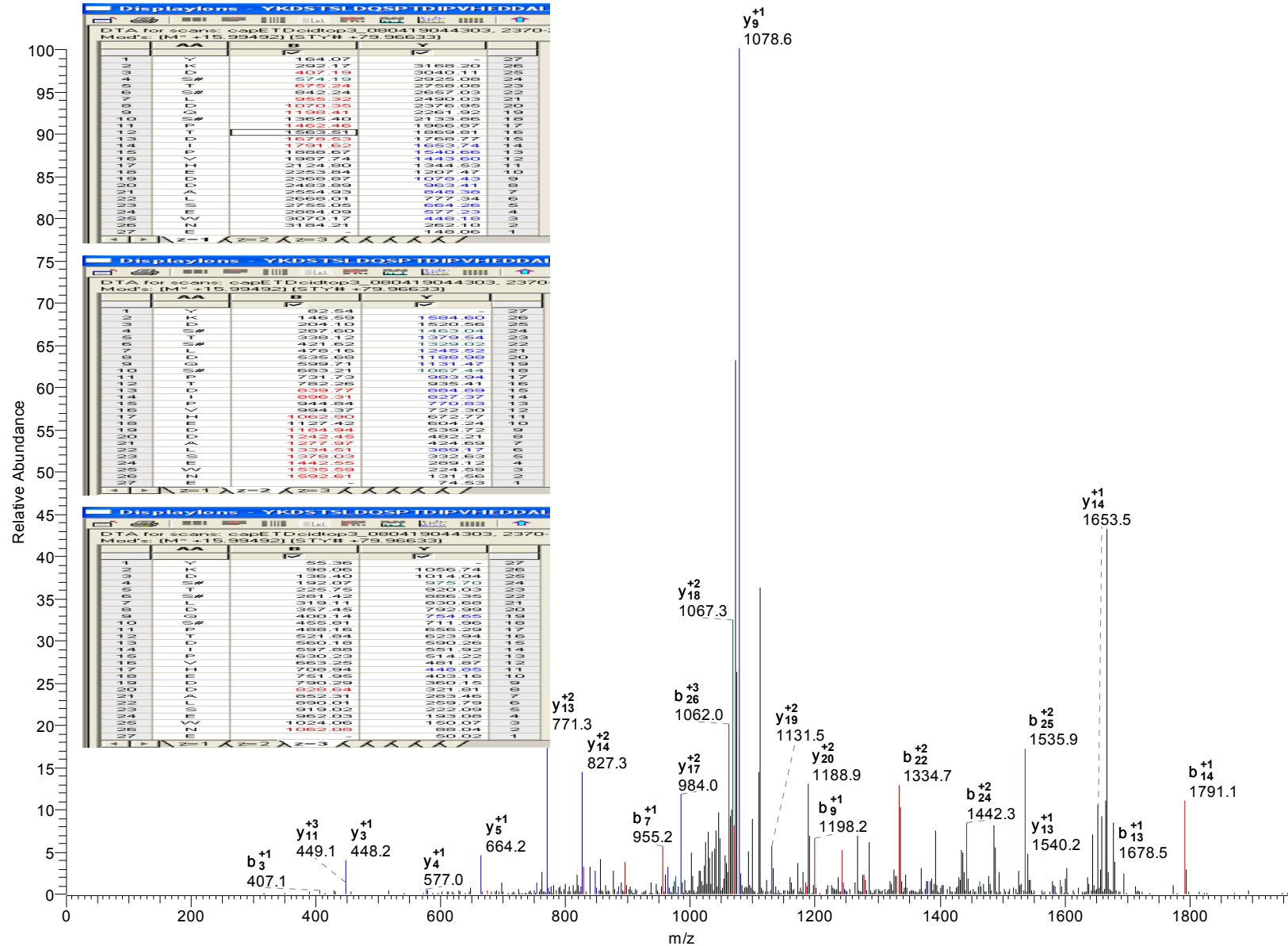
Displays - YKDTSLDQSPFDIEVHEDDAI

DTA for scan: 20ulcap1_3058
Mod: (M: -15.95492) (S: TyH: +79.96633)

AA	B	Y	
1	55.36	1030.05	27
2	98.05	987.36	26
3	136.40	949.04	25
4	159.10	920.03	24
5	200.46	866.38	23
6	250.48	830.68	22
7	330.80	792.59	20
8	373.48	754.65	19
9	429.16	711.96	18
10	461.60	666.29	17
11	495.18	623.94	16
12	533.63	590.26	15
13	571.22	551.92	14
14	603.67	514.23	13
15	636.60	461.67	12
16	662.28	448.95	11
17	725.30	403.16	10
18	763.64	360.15	9
19	801.88	321.61	8
20	825.65	283.46	7
21	863.35	255.79	6
22	892.36	222.08	5
23	936.38	193.06	4
24	997.47	150.07	3
25	1036.42	66.04	2
26		0.02	1

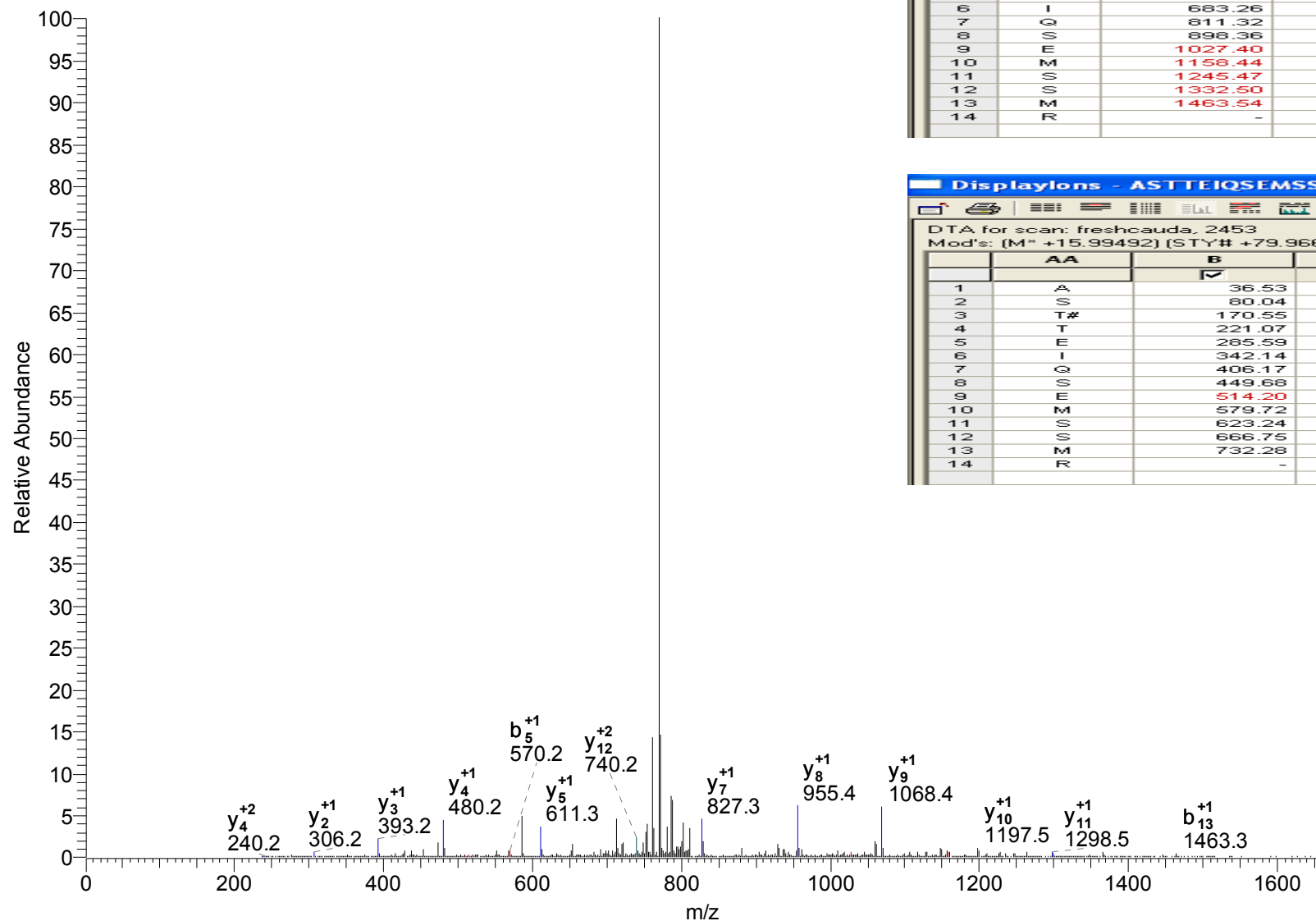
predicted similar to sperm acrosome
associated 1

#2370-2371 NL: 3.15E3



predicted similar to sperm acrosome associated 1

#2453-2453 NL: 6.05E4



Displaylons - ASTTEIQSEMSSMR

DTA for scan: freshcauda, 2453
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	A	72.04	-	14
2	S	159.08	1566.62	13
3	T#	340.09	1479.59	12
4	T	441.14	1298.57	11
5	E	570.18	1197.52	10
6	I	683.26	1068.48	9
7	Q	811.32	955.40	8
8	S	898.36	827.34	7
9	E	1027.40	740.31	6
10	M	1158.44	611.26	5
11	S	1245.47	480.22	4
12	S	1332.50	393.19	3
13	M	1463.54	306.16	2
14	R	-	175.12	1

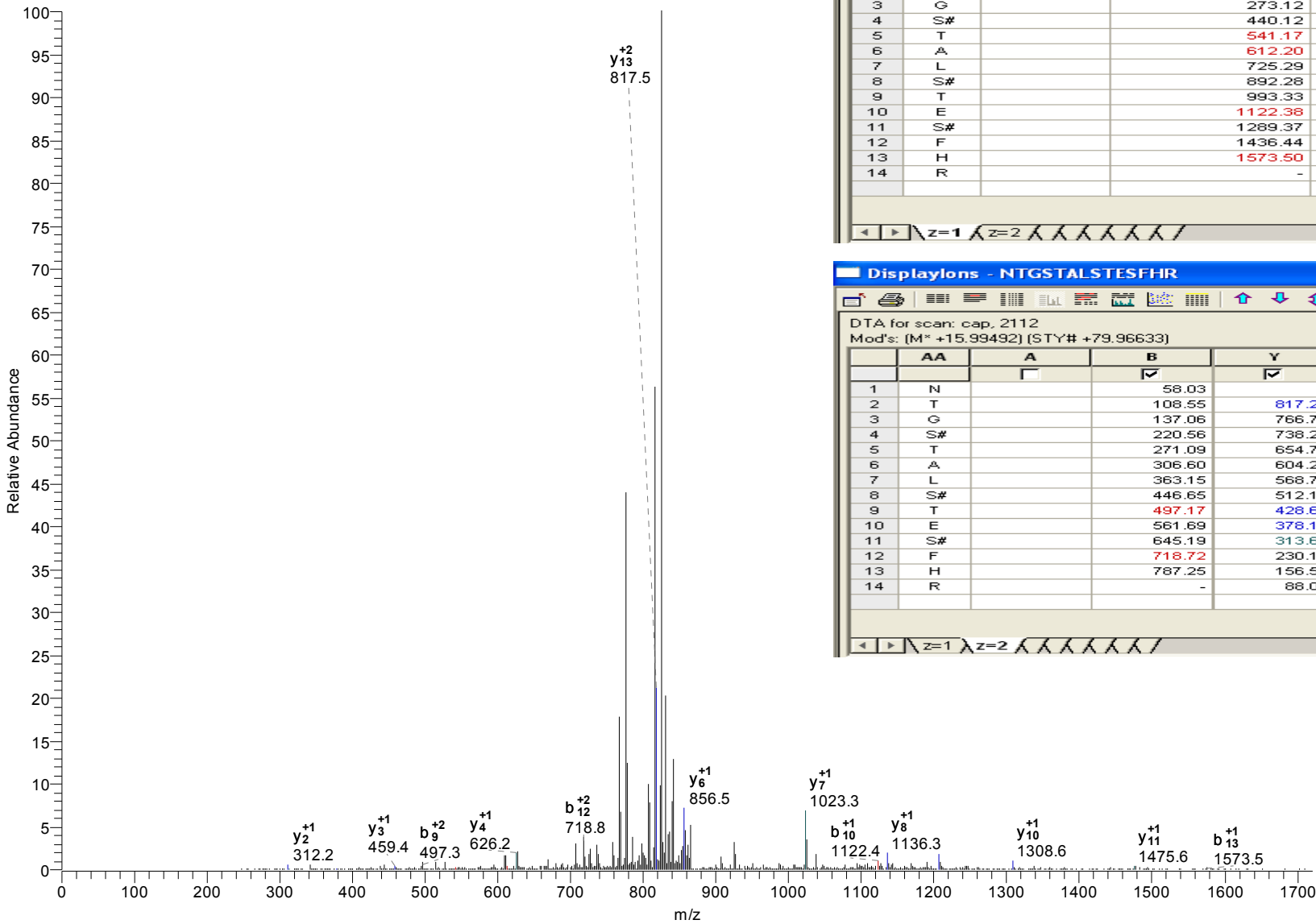
Displaylons - ASTTEIQSEMSSMR

DTA for scan: freshcauda, 2453
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	A	36.53	-	14
2	S	80.04	783.81	13
3	T#	170.55	740.30	12
4	T	221.07	649.79	11
5	E	285.59	599.27	10
6	I	342.14	534.74	9
7	Q	406.17	478.20	8
8	S	449.68	414.17	7
9	E	514.20	370.66	6
10	M	579.72	306.14	5
11	S	623.24	240.62	4
12	S	666.75	197.10	3
13	M	732.28	153.58	2
14	R	-	88.06	1

predicted similar to sarcolemma associated protein

#2112-2112 NL: 1.14E4



Displaylons - NTGSTALSTESFHR

DTA for scan: cap. 2112
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	14
2	T		216.10	1633.57	13
3	G		273.12	1532.52	12
4	S#		440.12	1475.50	11
5	T		541.17	1308.50	10
6	A		612.20	1207.45	9
7	L		725.29	1136.42	8
8	S#		892.28	1023.33	7
9	T		993.33	856.33	6
10	E		1122.38	755.29	5
11	S#		1289.37	626.24	4
12	F		1436.44	459.25	3
13	H		1573.50	312.18	2
14	R		-	175.12	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14

Displaylons - NTGSTALSTESFHR

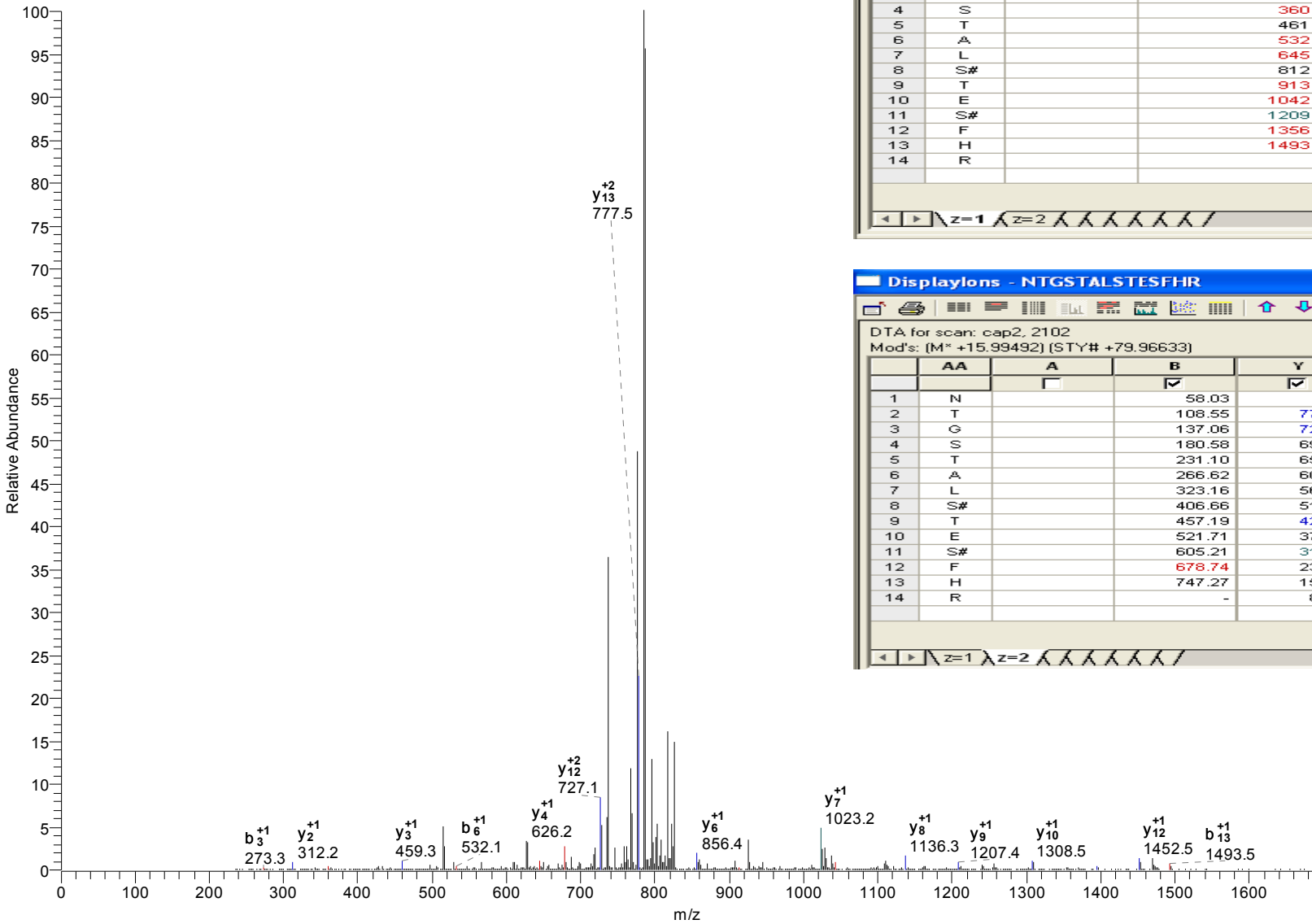
DTA for scan: cap. 2112
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	N		58.03	-	-	14
2	T		108.55	817.29	-	13
3	G		137.06	766.76	-	12
4	S#		220.56	738.25	-	11
5	T		271.09	654.75	-	10
6	A		306.60	604.23	-	9
7	L		363.15	568.71	-	8
8	S#		446.65	512.17	-	7
9	T		497.17	428.67	-	6
10	E		561.69	378.15	-	5
11	S#		645.19	313.63	-	4
12	F		718.72	230.13	-	3
13	H		787.25	156.59	-	2
14	R		-	88.06	-	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14

predicted similar to sarcolemma associated protein

#2102-2102 NL: 1.09E5



Displaylons - NTGSTALSTESFHR

DTA for scan: cap2, 2102
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05		14
2	T		216.10	1553.60	13
3	G		273.12	1452.56	12
4	S		360.15	1395.53	11
5	T		461.20	1308.50	10
6	A		532.24	1207.45	9
7	L		645.32	1136.42	8
8	S#		812.32	1023.33	7
9	T		913.37	856.33	6
10	E		1042.41	755.29	5
11	S#		1209.41	626.24	4
12	F		1356.48	459.25	3
13	H		1493.53	312.18	2
14	R		-	175.12	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14

Displaylons - NTGSTALSTESFHR

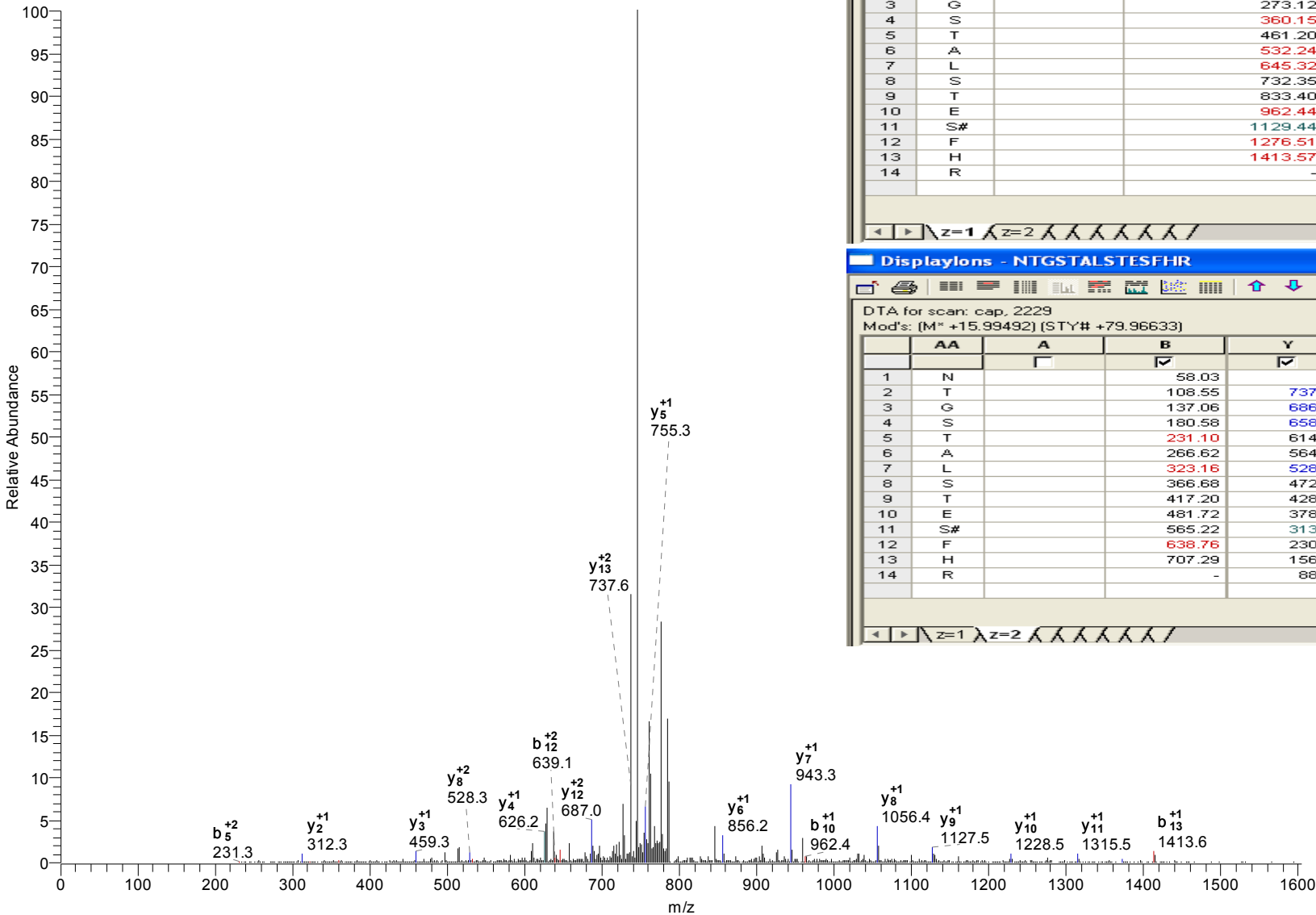
DTA for scan: cap2, 2102
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	N		58.03			14
2	T		108.55	777.31		13
3	G		137.06	726.78		12
4	S		180.58	698.27		11
5	T		231.10	654.75		10
6	A		266.62	604.23		9
7	L		323.16	568.71		8
8	S#		406.66	512.17		7
9	T		457.19	428.67		6
10	E		521.71	378.15		5
11	S#		605.21	313.63		4
12	F		678.74	230.13		3
13	H		747.27	156.59		2
14	R		-	88.06		1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14

predicted similar to sarcolemma associated protein

#2229-2229 NL: 1.53E4



Displaylons - NTGSTALSTESFHR

DTA for scan: cap. 2229
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	14
2	T		216.10	1473.64	13
3	G		273.12	1372.59	12
4	S		360.15	1315.57	11
5	T		461.20	1228.54	10
6	A		532.24	1127.49	9
7	L		645.32	1056.45	8
8	S		732.35	943.37	7
9	T		833.40	856.33	6
10	E		962.44	755.29	5
11	S#		1129.44	626.24	4
12	F		1276.51	459.25	3
13	H		1413.57	312.18	2
14	R		-	175.12	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14

Displaylons - NTGSTALSTESFHR

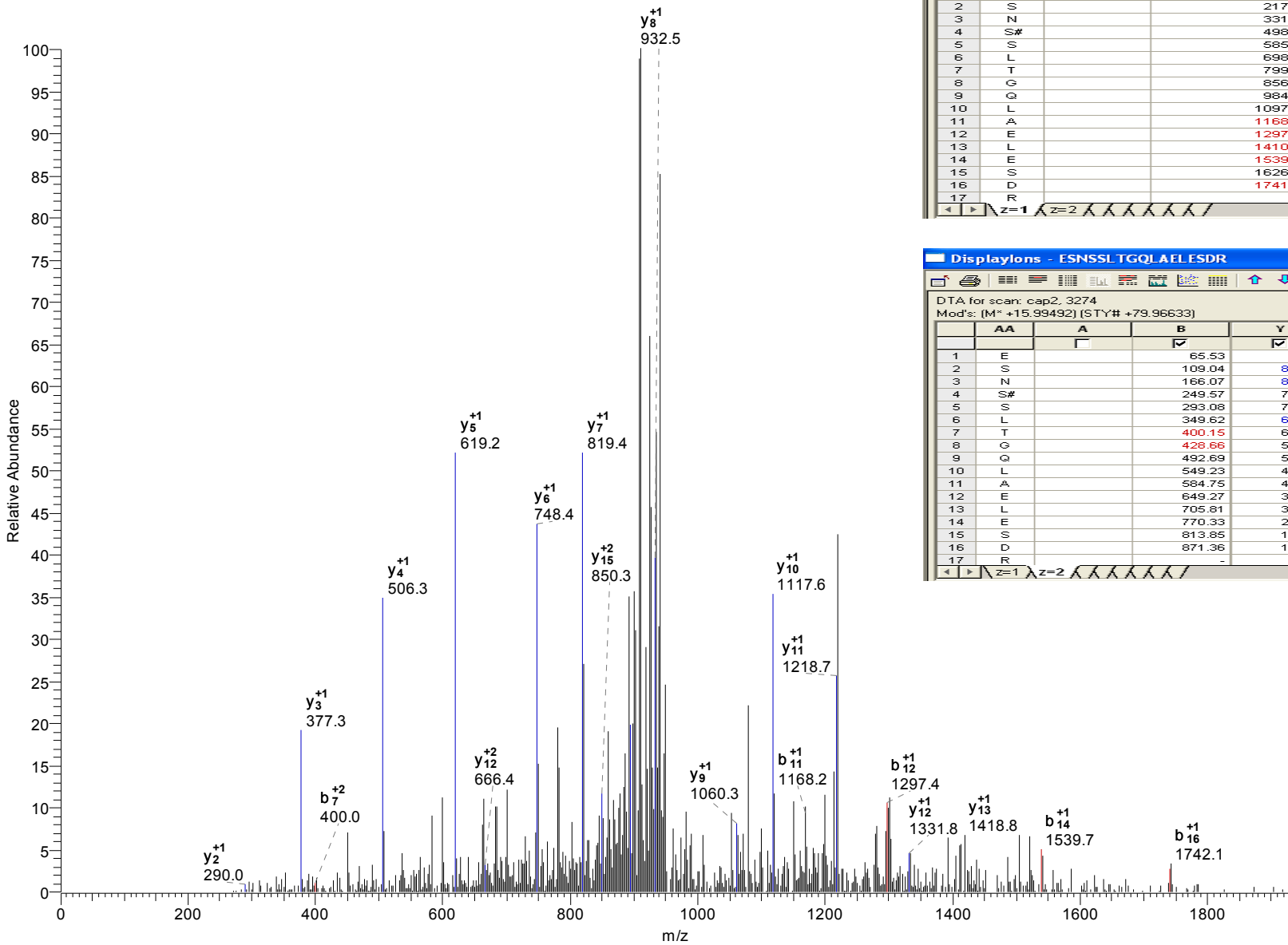
DTA for scan: cap. 2229
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	N		58.03	-	-	14
2	T		108.55	737.32	-	13
3	G		137.06	686.80	-	12
4	S		180.58	658.29	-	11
5	T		231.10	614.77	-	10
6	A		266.62	564.25	-	9
7	L		323.16	528.73	-	8
8	S		366.68	472.19	-	7
9	T		417.20	428.67	-	6
10	E		481.72	378.15	-	5
11	S#		565.22	313.63	-	4
12	F		638.76	230.13	-	3
13	H		707.29	156.59	-	2
14	R		-	88.06	-	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14

predicted similar to sarcolemma associated protein

#3274-3274 NL: 6.79E2



Displaylons - ESNSSLTGQLAELESDR

DTA for scan: cap2, 3274
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	E		130.05	-	17
2	S		217.08	1786.79	16
3	N		331.12	1699.75	15
4	S#		498.12	1585.71	14
5	S		585.16	1418.71	13
6	L		698.24	1331.68	12
7	T		799.29	1218.60	11
8	G		856.31	1117.55	10
9	Q		984.37	1060.53	9
10	L		1097.45	932.47	8
11	A		1168.49	819.38	7
12	E		1297.53	748.35	6
13	L		1410.61	619.30	5
14	E		1539.66	506.22	4
15	S		1626.69	377.18	3
16	D		1741.72	290.15	2
17	R		-	175.12	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17

Displaylons - ESNSSLTGQLAELESDR

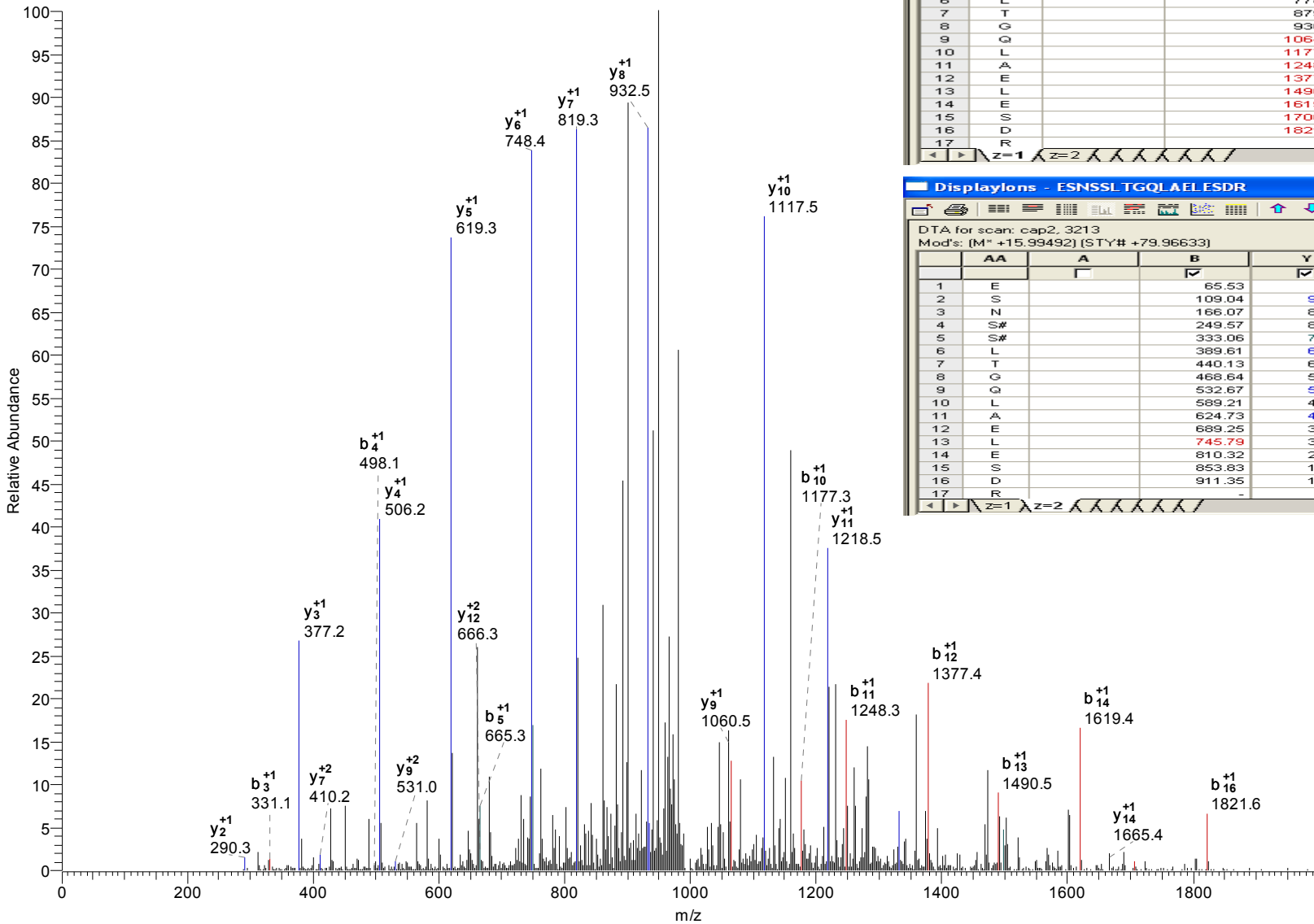
DTA for scan: cap2, 3274
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	E		65.53	-	-	17
2	S		109.04	893.90	-	16
3	N		166.07	850.38	-	15
4	S#		249.57	793.36	-	14
5	S		293.08	709.86	-	13
6	L		349.62	666.34	-	12
7	T		400.15	609.80	-	11
8	G		428.66	559.28	-	10
9	Q		492.69	530.77	-	9
10	L		549.23	466.74	-	8
11	A		584.75	410.20	-	7
12	E		649.27	374.68	-	6
13	L		705.81	310.16	-	5
14	E		770.33	253.61	-	4
15	S		813.85	189.09	-	3
16	D		871.36	145.58	-	2
17	R		-	88.06	-	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17

predicted similar to sarcolemma associated protein

#3213-3213 NL: 4.13E3



Displaylons - ESNSSLTGQLAELESDR

DTA for scan: cap2, 3213
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	E		130.05	-	17
2	S		217.08	1866.75	16
3	N		331.12	1779.72	15
4	S#		498.12	1665.68	14
5	S#		665.12	1498.68	13
6	L		778.21	1331.68	12
7	T		879.25	1218.60	11
8	G		936.27	1117.55	10
9	Q		1064.33	1060.53	9
10	L		1177.42	932.47	8
11	A		1248.45	819.38	7
12	E		1377.50	748.35	6
13	L		1490.58	619.30	5
14	E		1619.62	506.22	4
15	S		1706.66	377.18	3
16	D		1821.68	290.15	2
17	R		-	175.12	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17

Displaylons - ESNSSLTGQLAELESDR

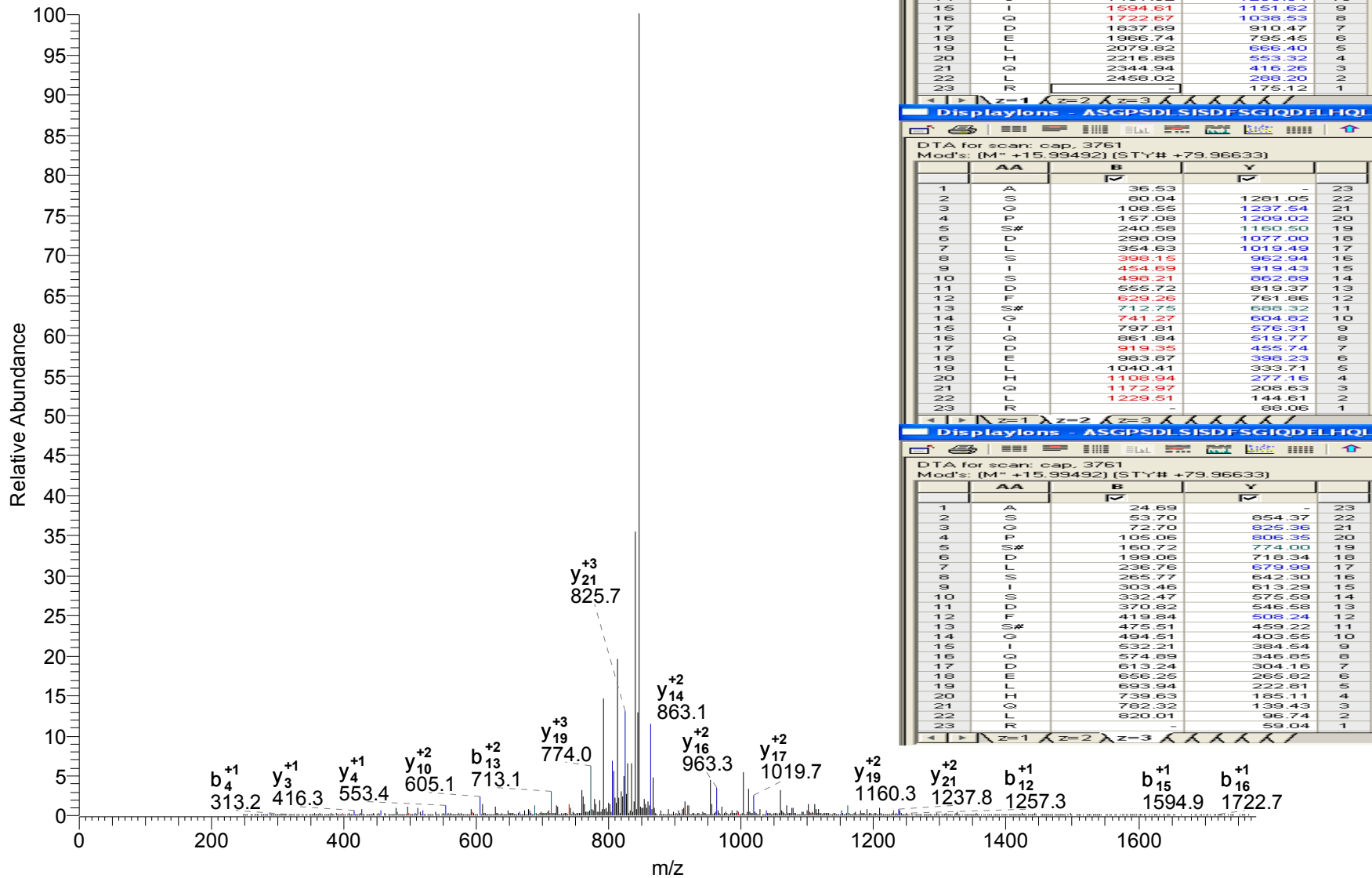
DTA for scan: cap2, 3213
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	E		65.53	-	-	17
2	S		109.04	933.88	-	16
3	N		166.07	890.36	-	15
4	S#		249.57	833.34	-	14
5	S#		333.06	749.84	-	13
6	L		389.61	666.34	-	12
7	T		440.13	609.80	-	11
8	G		468.64	559.28	-	10
9	Q		532.67	530.77	-	9
10	L		589.21	466.74	-	8
11	A		624.73	410.20	-	7
12	E		689.25	374.68	-	6
13	L		745.79	310.16	-	5
14	E		810.32	253.61	-	4
15	S		853.83	189.09	-	3
16	D		911.35	145.58	-	2
17	R		-	88.06	-	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17

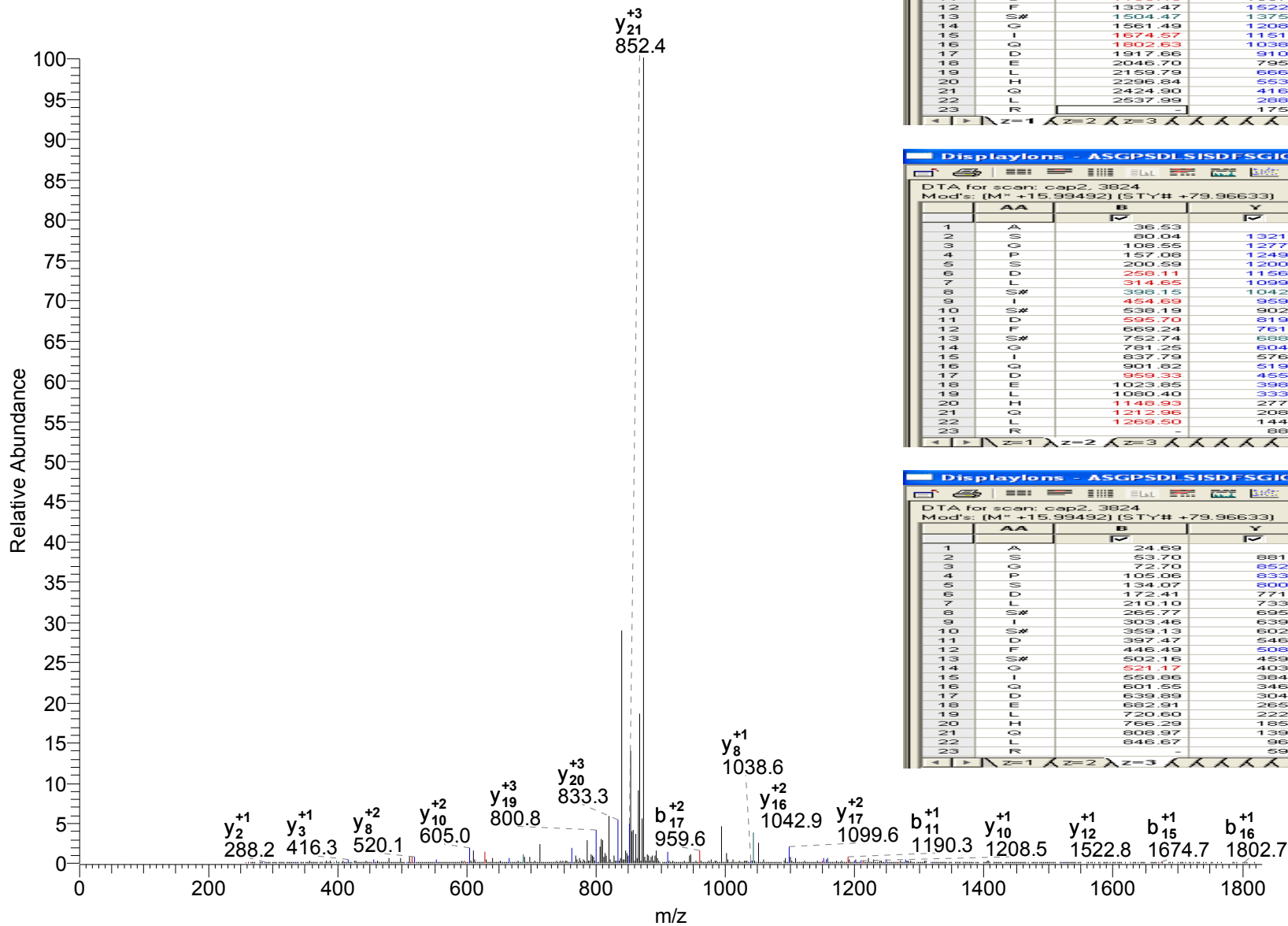
predicted similar to sarcolemma associated protein

#3761-3761 NL: 2.73E4



predicted similar to sarcolemma associated protein

#3824-3824 NL: 6.56E4



Displaylons - ASGPSDLISIDFSGIQDELHQL

DTA for scan: cap2: 3824
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	A	72.04	-	23
2	S	159.08	2641.06	22
3	Q	216.10	2554.03	21
4	P	313.15	2497.01	20
5	S	400.18	2399.96	19
6	D	515.21	2312.92	18
7	L	628.29	2197.90	17
8	S#	795.29	2084.81	16
9	I	908.38	1917.81	15
10	S#	1075.37	1804.73	14
11	D	1190.40	1637.73	13
12	F	1337.47	1522.70	12
13	S#	1504.47	1375.64	11
14	Q	1561.49	1208.64	10
15	I	1674.57	1151.62	9
16	Q	1802.63	1038.53	8
17	D	1917.66	910.47	7
18	E	2046.70	795.45	6
19	L	2159.79	666.40	5
20	H	2296.84	553.32	4
21	Q	2424.90	416.26	3
22	L	2537.99	269.20	2
23	R	-	175.12	1

Displaylons - ASGPSDLISIDFSGIQDELHQL

DTA for scan: cap2: 3824
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	A	36.53	-	23
2	S	80.04	1321.03	22
3	Q	108.55	1277.52	21
4	P	157.08	1249.01	20
5	S	200.59	1200.48	19
6	D	258.11	1156.97	18
7	L	314.65	1099.45	17
8	S#	398.15	1042.91	16
9	I	454.69	959.41	15
10	S#	538.19	902.87	14
11	D	595.70	819.37	13
12	F	659.24	761.86	12
13	S#	752.74	688.32	11
14	Q	781.25	604.82	10
15	I	837.79	576.31	9
16	Q	901.82	519.77	8
17	D	959.33	455.74	7
18	E	1023.85	398.23	6
19	L	1080.40	333.71	5
20	H	1148.93	277.16	4
21	Q	1212.96	208.63	3
22	L	1269.50	144.61	2
23	R	-	88.06	1

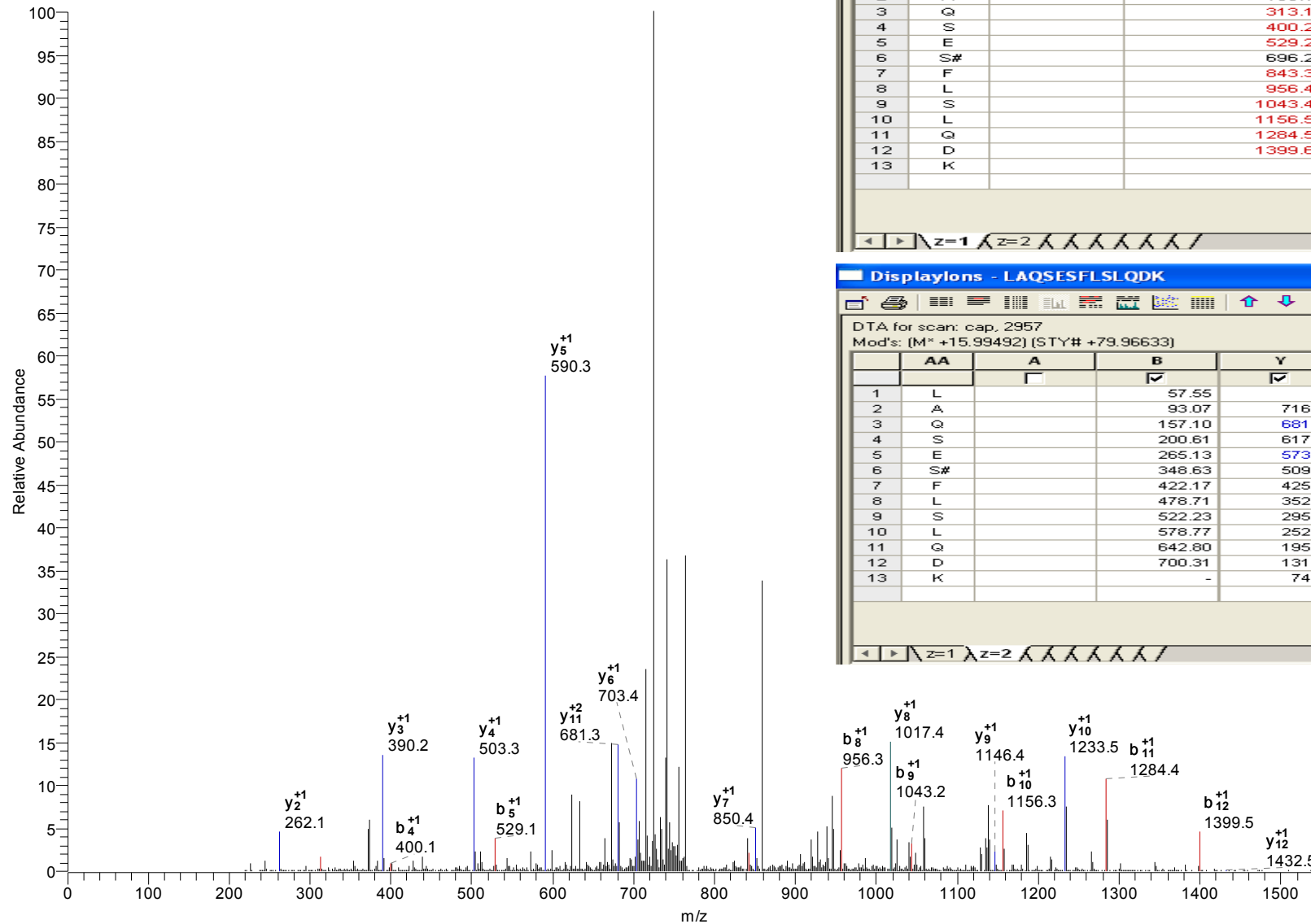
Displaylons - ASGPSDLISIDFSGIQDELHQL

DTA for scan: cap2: 3824
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	A	24.69	-	23
2	S	53.70	881.03	22
3	Q	72.70	852.01	21
4	P	105.06	833.01	20
5	S	134.07	800.66	19
6	D	172.41	771.65	18
7	L	210.10	733.30	17
8	S#	265.77	695.61	16
9	I	303.46	639.94	15
10	S#	359.13	602.25	14
11	D	397.47	546.58	13
12	F	446.49	508.24	12
13	S#	502.16	459.22	11
14	Q	521.17	403.55	10
15	I	558.86	384.54	9
16	Q	601.55	346.65	8
17	D	639.89	304.16	7
18	E	682.91	265.82	6
19	L	720.60	222.81	5
20	H	766.29	185.11	4
21	Q	808.97	139.43	3
22	L	846.67	96.74	2
23	R	-	59.04	1

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#2957-2957 NL: 3.12E4



Displaylons - LAQSESFLSLQDK

DTA for scan: cap, 2957
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L		114.09	-	13
2	A		185.13	1432.64	12
3	Q		313.19	1361.60	11
4	S		400.22	1233.54	10
5	E		529.26	1146.51	9
6	S#		696.26	1017.47	8
7	F		843.33	850.47	7
8	L		956.41	703.40	6
9	S		1043.44	590.31	5
10	L		1156.53	503.28	4
11	Q		1284.59	390.20	3
12	D		1399.61	262.14	2
13	K		-	147.11	1

z=1 z=2

Displaylons - LAQSESFLSLQDK

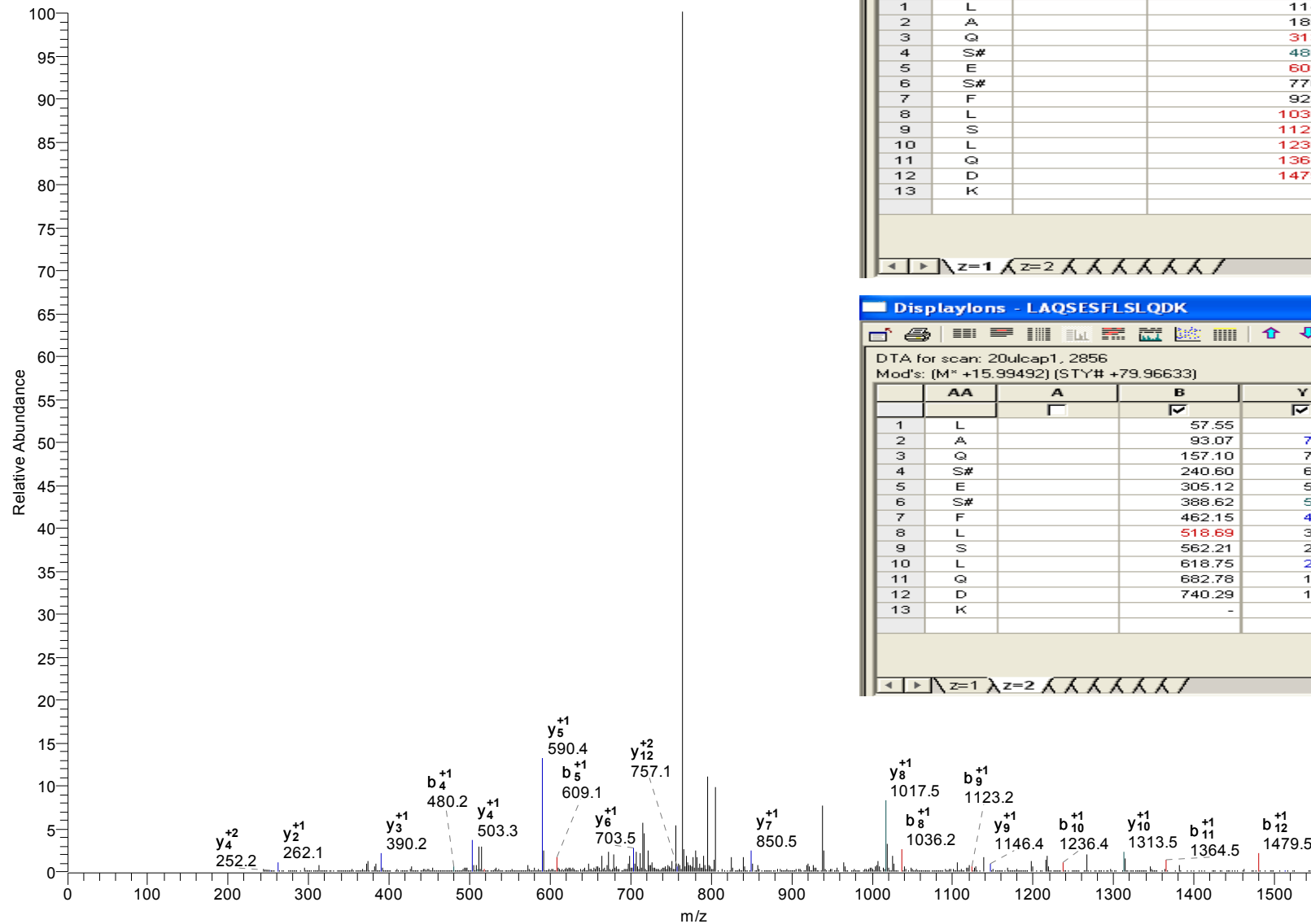
DTA for scan: cap, 2957
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L		57.55	-	-	13
2	A		93.07	716.82	-	12
3	Q		157.10	681.30	-	11
4	S		200.61	617.27	-	10
5	E		265.13	573.76	-	9
6	S#		348.63	509.24	-	8
7	F		422.17	425.74	-	7
8	L		478.71	352.20	-	6
9	S		522.23	295.66	-	5
10	L		578.77	252.14	-	4
11	Q		642.80	195.60	-	3
12	D		700.31	131.57	-	2
13	K		-	74.06	-	1

z=1 z=2

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#2856-2856 NL: 1.28E4



Displaylons - LAQSESFLSLQDK

DTA for scan: 20ulcap1, 2856
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	L		114.09	-	13
2	A		185.13	1512.60	12
3	Q		313.19	1441.56	11
4	S#		480.19	1313.51	10
5	E		609.23	1146.51	9
6	S#		776.23	1017.47	8
7	F		923.29	850.47	7
8	L		1036.38	703.40	6
9	S		1123.41	590.31	5
10	L		1236.49	503.28	4
11	Q		1364.55	390.20	3
12	D		1479.58	262.14	2
13	K		-	147.11	1

z=1 z=2

Displaylons - LAQSESFLSLQDK

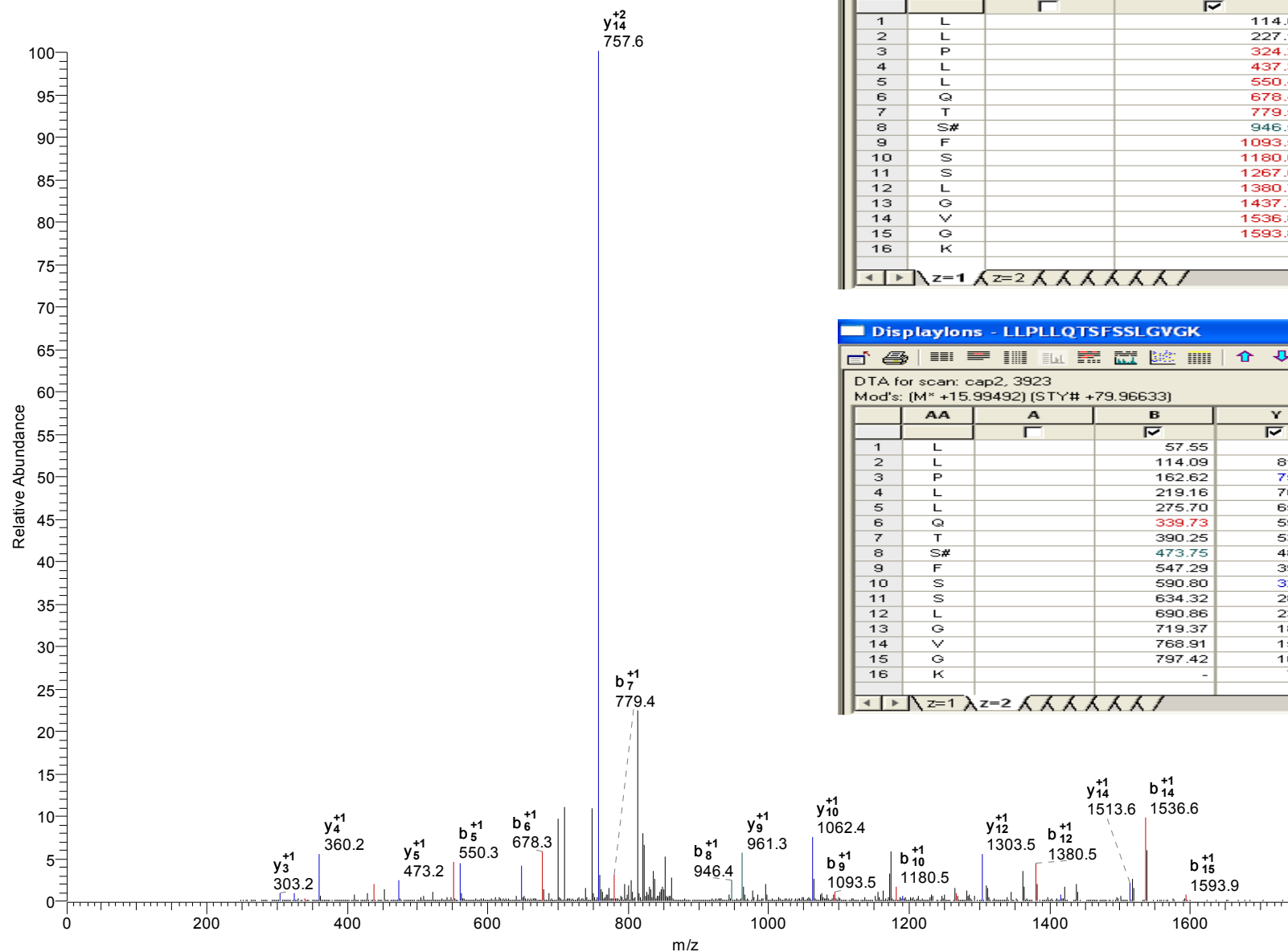
DTA for scan: 20ulcap1, 2856
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	L		57.55	-	-	13
2	A		93.07	756.80	-	12
3	Q		157.10	721.29	-	11
4	S#		240.60	657.26	-	10
5	E		305.12	573.76	-	9
6	S#		388.62	509.24	-	8
7	F		462.15	425.74	-	7
8	L		518.69	352.20	-	6
9	S		562.21	295.66	-	5
10	L		618.75	252.14	-	4
11	Q		682.78	195.60	-	3
12	D		740.29	131.57	-	2
13	K		-	74.06	-	1

z=1 z=2

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3923-3923 NL: 3.16E4



Displaylons - LLPLLQTSFSSLGVGK

DTA for scan: cap2, 3923
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	L		114.09	-	16
2	L		227.18	1626.85	15
3	P		324.23	1513.77	14
4	L		437.31	1416.71	13
5	L		550.40	1303.63	12
6	Q		678.45	1190.55	11
7	T		779.50	1062.49	10
8	S#		946.50	961.44	9
9	F		1093.57	794.44	8
10	S		1180.60	647.37	7
11	S		1267.63	560.34	6
12	L		1380.72	473.31	5
13	G		1437.74	360.22	4
14	V		1536.81	303.20	3
15	G		1593.83	204.13	2
16	K		-	147.11	1

z=1 z=2

Displaylons - LLPLLQTSFSSLGVGK

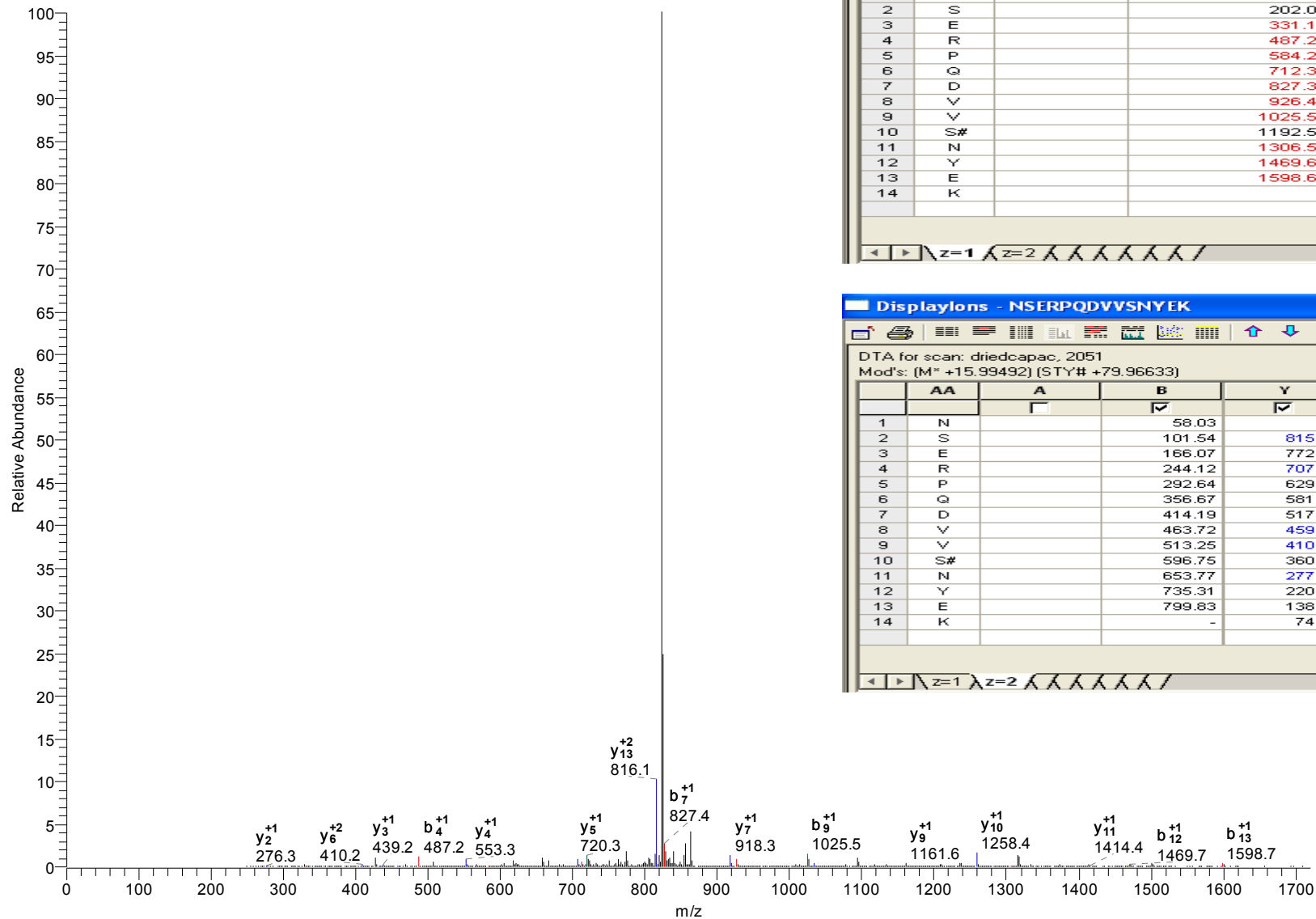
DTA for scan: cap2, 3923
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	L		57.55	-	-	16
2	L		114.09	813.93	-	15
3	P		162.62	757.39	-	14
4	L		219.16	708.86	-	13
5	L		275.70	652.32	-	12
6	Q		339.73	595.78	-	11
7	T		390.25	531.75	-	10
8	S#		473.75	481.22	-	9
9	F		547.29	397.72	-	8
10	S		590.80	324.19	-	7
11	S		634.32	280.67	-	6
12	L		690.86	237.16	-	5
13	G		719.37	180.62	-	4
14	V		768.91	152.10	-	3
15	G		797.42	102.57	-	2
16	K		-	74.06	-	1

z=1 z=2

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#2051-2051 NL: 5.26E4



Displaylons - NSERPQDVVSNEYK

DTA for scan: driedcapac, 2051
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	N			115.05	-
2	S			202.08	1630.71
3	E			331.12	1543.68
4	R			487.23	1414.64
5	P			584.28	1258.54
6	Q			712.34	1161.48
7	D			827.36	1033.42
8	V			926.43	918.40
9	V			1025.50	819.33
10	S#			1192.50	720.26
11	N			1306.54	553.26
12	Y			1469.61	439.22
13	E			1598.65	276.16
14	K			-	147.11

z=1 z=2

Displaylons - NSERPQDVVSNEYK

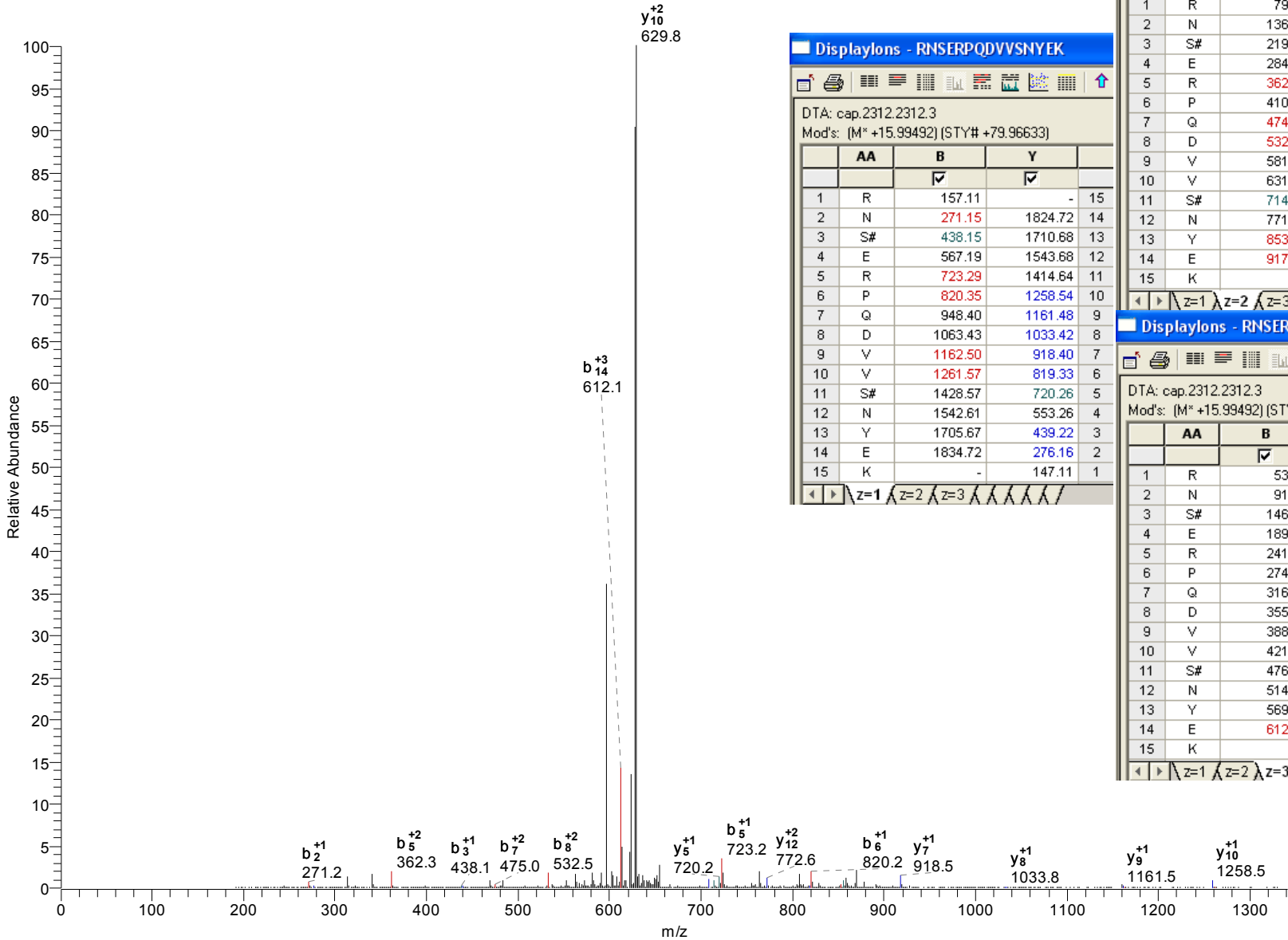
DTA for scan: driedcapac, 2051
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	N			58.03	-	14
2	S			101.54	815.86	13
3	E			166.07	772.34	12
4	R			244.12	707.82	11
5	P			292.64	629.77	10
6	Q			356.67	581.24	9
7	D			414.19	517.22	8
8	V			463.72	459.70	7
9	V			513.25	410.17	6
10	S#			596.75	360.63	5
11	N			653.77	277.13	4
12	Y			735.31	220.11	3
13	E			799.83	138.58	2
14	K			-	74.06	1

z=1 z=2

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#2312-2312 RT:38.00-38.00 NL: 1.14E5



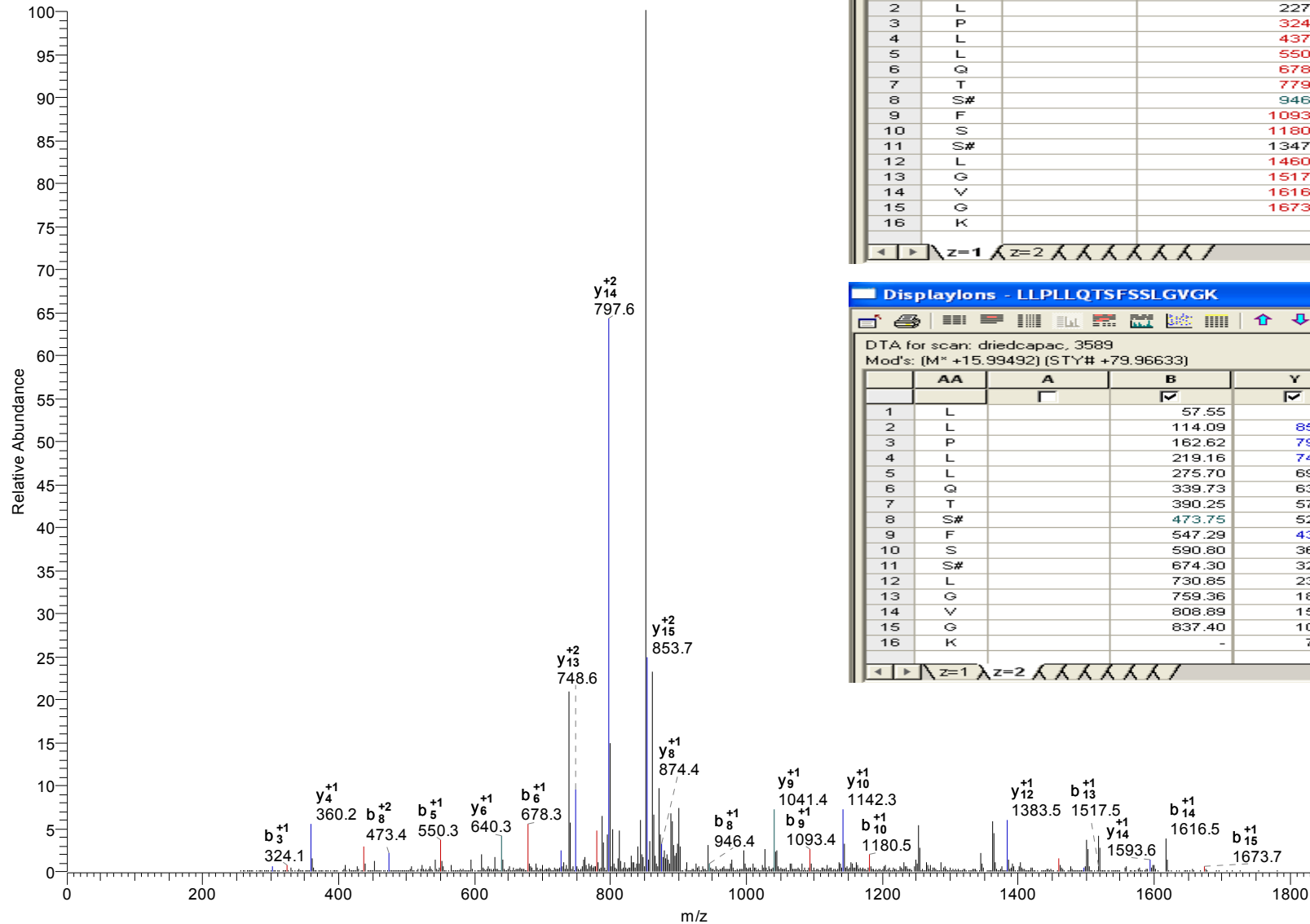
Displaylons - RNSERPQDVVSNYEK				
DTA: cap.2312.2312.3				
Mod's: (M* +15.99492) (STY# +79.96633)				
	AA	B	Y	
1	R	157.11	-	15
2	N	271.15	1824.72	14
3	S#	438.15	1710.68	13
4	E	567.19	1543.68	12
5	R	723.29	1414.64	11
6	P	820.35	1258.54	10
7	Q	948.40	1161.48	9
8	D	1063.43	1033.42	8
9	V	1162.50	918.40	7
10	V	1261.57	819.33	6
11	S#	1428.57	720.26	5
12	N	1542.61	553.26	4
13	Y	1705.67	439.22	3
14	E	1834.72	276.16	2
15	K	-	147.11	1

Displaylons - RNSERPQDVVSNYEK				
DTA: cap.2312.2312.3				
Mod's: (M* +15.99492) (STY# +79.96633)				
	AA	B	Y	
1	R	79.06	-	15
2	N	136.08	912.86	14
3	S#	219.58	855.84	13
4	E	284.10	772.34	12
5	R	362.15	707.82	11
6	P	410.68	629.77	10
7	Q	474.71	581.24	9
8	D	532.22	517.22	8
9	V	581.75	459.70	7
10	V	631.29	410.17	6
11	S#	714.79	360.63	5
12	N	771.81	277.13	4
13	Y	853.34	220.11	3
14	E	917.86	138.58	2
15	K	-	74.06	1

	AA	B	Y	
1	R	53.04	-	15
2	N	91.06	608.91	14
3	S#	146.72	570.90	13
4	E	189.74	515.23	12
5	R	241.77	472.22	11
6	P	274.12	420.18	10
7	Q	316.81	387.83	9
8	D	355.15	345.15	8
9	V	388.17	306.80	7
10	V	421.19	273.78	6
11	S#	476.86	240.76	5
12	N	514.87	185.09	4
13	Y	569.23	147.08	3
14	E	612.24	92.72	2
15	K	-	49.71	1

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3589-3589 NL: 1.49E4



Displaylons - LLPLLQTSFSSLGVGK

DTA for scan: driedcapac, 3589
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L			114.09	-
2	L			227.18	1706.82
3	P			324.23	1593.73
4	L			437.31	1496.68
5	L			550.40	1383.60
6	Q			678.45	1270.51
7	T			779.50	1142.45
8	S#			946.50	1041.41
9	F			1093.57	874.41
10	S			1180.60	727.34
11	S#			1347.60	640.31
12	L			1460.68	473.31
13	G			1517.71	360.22
14	V			1616.77	303.20
15	G			1673.80	204.13
16	K			-	147.11

z=1 z=2

Displaylons - LLPLLQTSFSSLGVGK

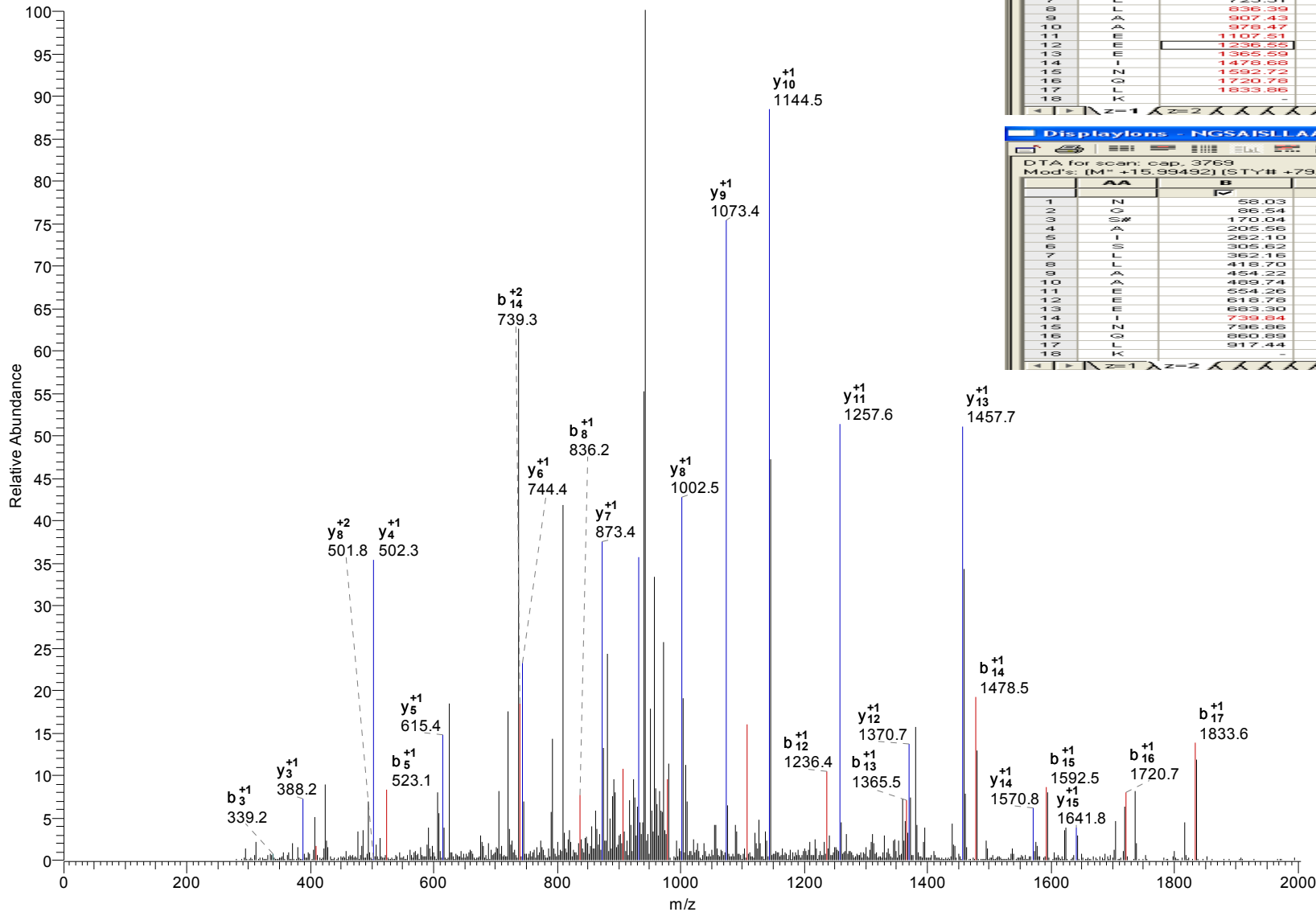
DTA for scan: driedcapac, 3589
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L			57.55	-	16
2	L			114.09	853.91	15
3	P			162.62	797.37	14
4	L			219.16	748.84	13
5	L			275.70	692.30	12
6	Q			339.73	635.76	11
7	T			390.25	571.73	10
8	S#			473.75	521.21	9
9	F			547.29	437.71	8
10	S			590.80	364.17	7
11	S#			674.30	320.66	6
12	L			730.85	237.16	5
13	G			759.36	180.62	4
14	V			808.89	152.10	3
15	G			837.40	102.57	2
16	K			-	74.06	1

z=1 z=2

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3769-3769 NL: 4.20E3



Displaylons - NGS AISLLAAEEFINQLK

DTA for scan: cap. 3769
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	N	115.05	-	18
2	Q	172.07	1865.93	17
3	S#	339.07	1808.90	16
4	A	410.11	1641.91	15
5	I	523.19	1570.87	14
6	S	610.22	1457.78	13
7	L	723.31	1370.75	12
8	L	836.39	1257.67	11
9	A	907.43	1144.58	10
10	A	978.47	1073.55	9
11	E	1107.51	1002.51	8
12	E	1236.55	873.47	7
13	E	1365.59	744.43	6
14	I	1478.66	615.38	5
15	N	1592.72	502.30	4
16	Q	1720.78	388.26	3
17	L	1833.86	260.20	2
18	K	-	147.11	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18

Displaylons - NGS AISLLAAEEFINQLK

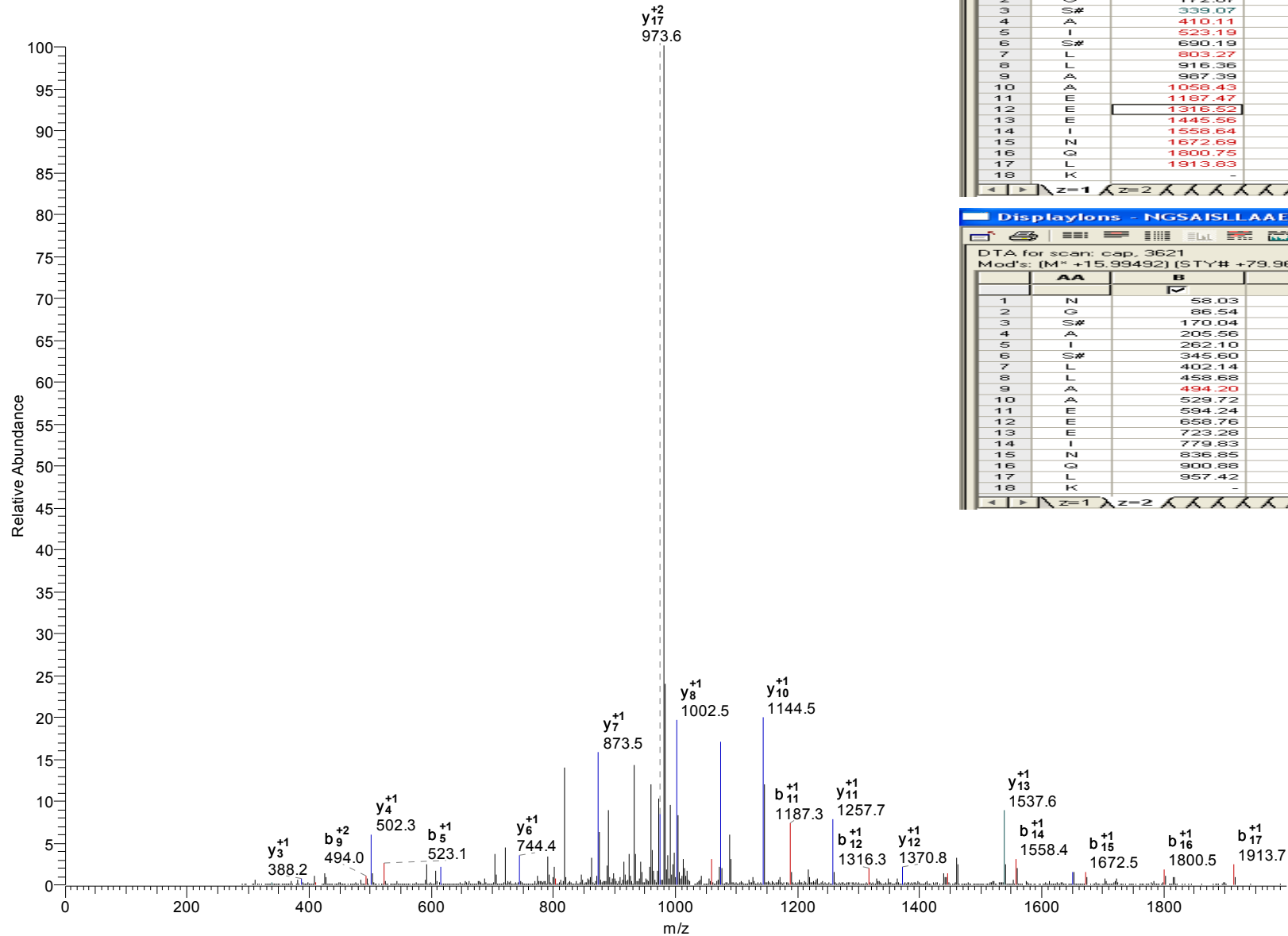
DTA for scan: cap. 3769
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	N	58.03	-	18
2	Q	86.54	933.47	17
3	S#	170.04	904.96	16
4	A	205.56	821.46	15
5	I	262.10	785.94	14
6	S	305.62	729.40	13
7	L	362.16	685.88	12
8	L	418.70	629.34	11
9	A	454.22	572.80	10
10	A	489.74	537.28	9
11	E	564.26	501.76	8
12	E	618.78	437.24	7
13	E	683.30	372.72	6
14	I	739.84	308.19	5
15	N	796.86	251.65	4
16	Q	860.89	194.63	3
17	L	917.44	130.60	2
18	K	-	74.06	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3621-3621 NL: 1.98E4



Displaylens - NGSAISLLAAEEEEINQLK

DTA for scan: cap. 3621
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	115.05	-	18
2	Q	172.07	1945.89	17
3	S#	339.07	1888.87	16
4	A	410.11	1721.87	15
5	I	523.19	1650.83	14
6	S#	690.19	1537.75	13
7	L	803.27	1370.75	12
8	L	916.36	1257.67	11
9	A	987.39	1144.58	10
10	A	1058.43	1073.55	9
11	E	1187.47	1002.51	8
12	E	1316.52	873.47	7
13	E	1445.56	744.43	6
14	I	1558.64	615.38	5
15	N	1672.69	502.30	4
16	Q	1800.75	388.26	3
17	L	1913.83	260.20	2
18	K	-	147.11	1

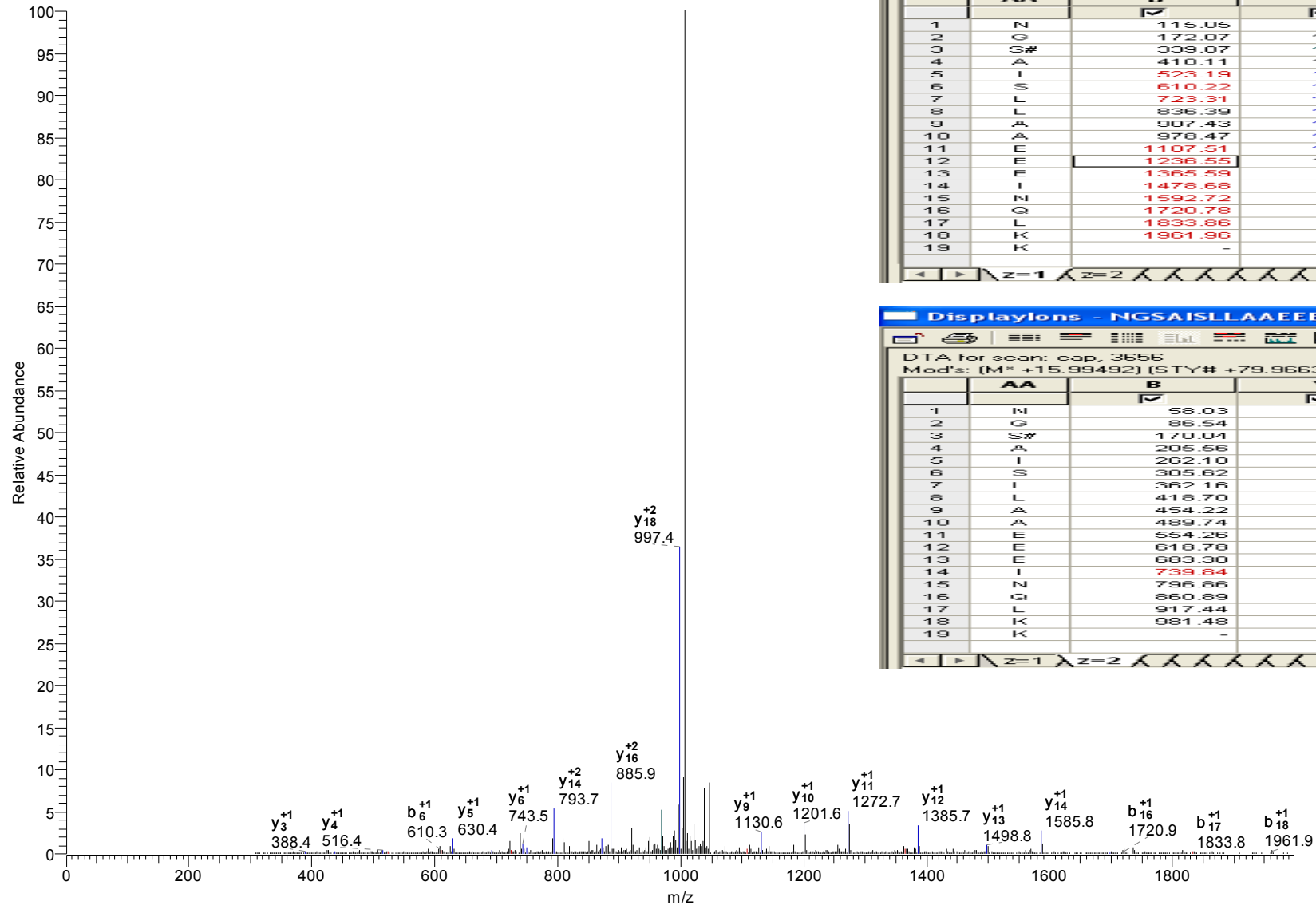
Displaylens - NGSAISLLAAEEEEINQLK

DTA for scan: cap. 3621
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	58.03	-	18
2	Q	86.54	973.45	17
3	S#	170.04	944.94	16
4	A	205.56	861.44	15
5	I	262.10	825.92	14
6	S#	345.60	769.38	13
7	L	402.14	685.88	12
8	L	458.68	629.34	11
9	A	494.20	572.80	10
10	A	529.72	537.28	9
11	E	594.24	501.76	8
12	E	658.76	437.24	7
13	E	723.28	372.72	6
14	I	779.83	308.19	5
15	N	836.85	251.65	4
16	Q	900.88	194.63	3
17	L	957.42	130.60	2
18	K	-	74.06	1

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3656-3656 NL: 2.52E4



Displaylens - NGS AISLLAAEEEEINQLKK

DTA for scan: cap. 3656
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	N	115.05	-	19
2	G	172.07	1994.02	18
3	S#	339.07	1937.00	17
4	A	410.11	1770.00	16
5	I	523.19	1698.96	15
6	S	610.22	1585.88	14
7	L	723.31	1498.85	13
8	L	836.39	1385.76	12
9	A	907.43	1272.68	11
10	A	978.47	1201.64	10
11	E	1107.51	1130.61	9
12	E	1236.55	1001.56	8
13	E	1365.59	872.52	7
14	I	1478.68	743.48	6
15	N	1592.72	630.39	5
16	Q	1720.78	516.35	4
17	L	1833.86	388.29	3
18	K	1961.96	275.21	2
19	K	-	147.11	1

Navigation: < > z=1 z=2

Displaylens - NGS AISLLAAEEEEINQLKK

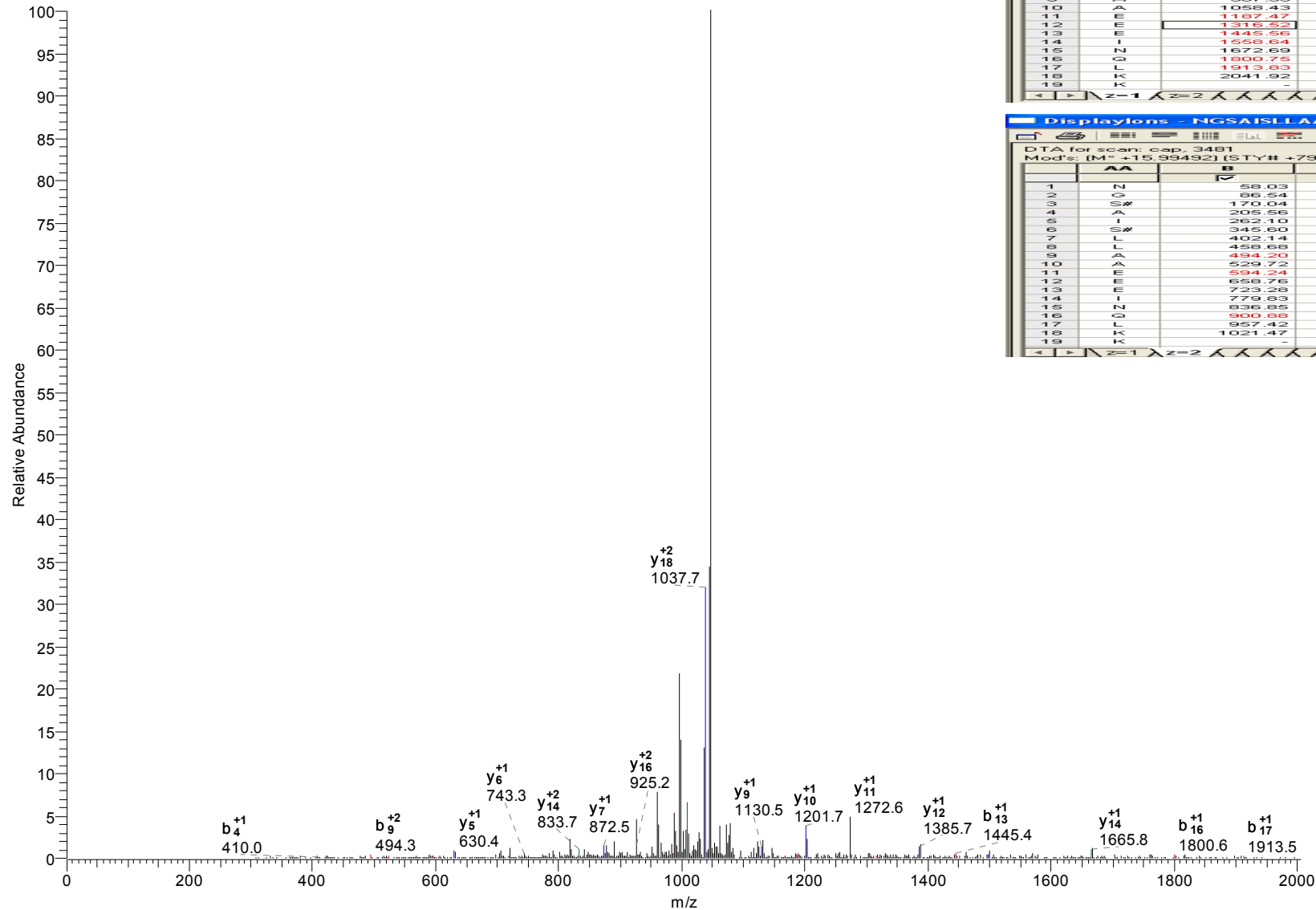
DTA for scan: cap. 3656
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	N	58.03	-	19
2	G	86.54	997.51	18
3	S#	170.04	969.00	17
4	A	205.56	885.50	16
5	I	262.10	849.99	15
6	S	305.62	793.44	14
7	L	362.16	749.93	13
8	L	418.70	693.39	12
9	A	454.22	636.84	11
10	A	489.74	601.32	10
11	E	554.26	565.81	9
12	E	618.78	501.28	8
13	E	683.30	436.76	7
14	I	739.84	372.24	6
15	N	796.86	315.70	5
16	Q	860.89	259.68	4
17	L	917.44	194.65	3
18	K	981.48	138.11	2
19	K	-	74.06	1

Navigation: < > z=1 z=2

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3481-3481 NL: 7.82E3



Displaylens - NGSAILLAAEEIEINOLKK

DTA for scan: cap. 3481
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	115.05	-	19
2	Q	172.07	2073.99	18
3	S#	339.07	2016.97	17
4	A	410.11	1849.97	16
5	I	523.19	1778.93	15
6	S#	690.19	1665.85	14
7	L	803.27	1498.85	13
8	L	916.36	1385.76	12
9	A	967.39	1272.68	11
10	A	1058.43	1201.64	10
11	E	1187.47	1130.61	9
12	E	1316.52	1001.56	8
13	E	1445.56	872.52	7
14	I	1555.64	743.48	6
15	N	1672.69	630.39	5
16	Q	1800.75	516.35	4
17	L	1913.83	388.29	3
18	K	2041.92	275.21	2
19	K	-	147.11	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18 z=19

Displaylens - NGSAILLAAEEIEINOLKK

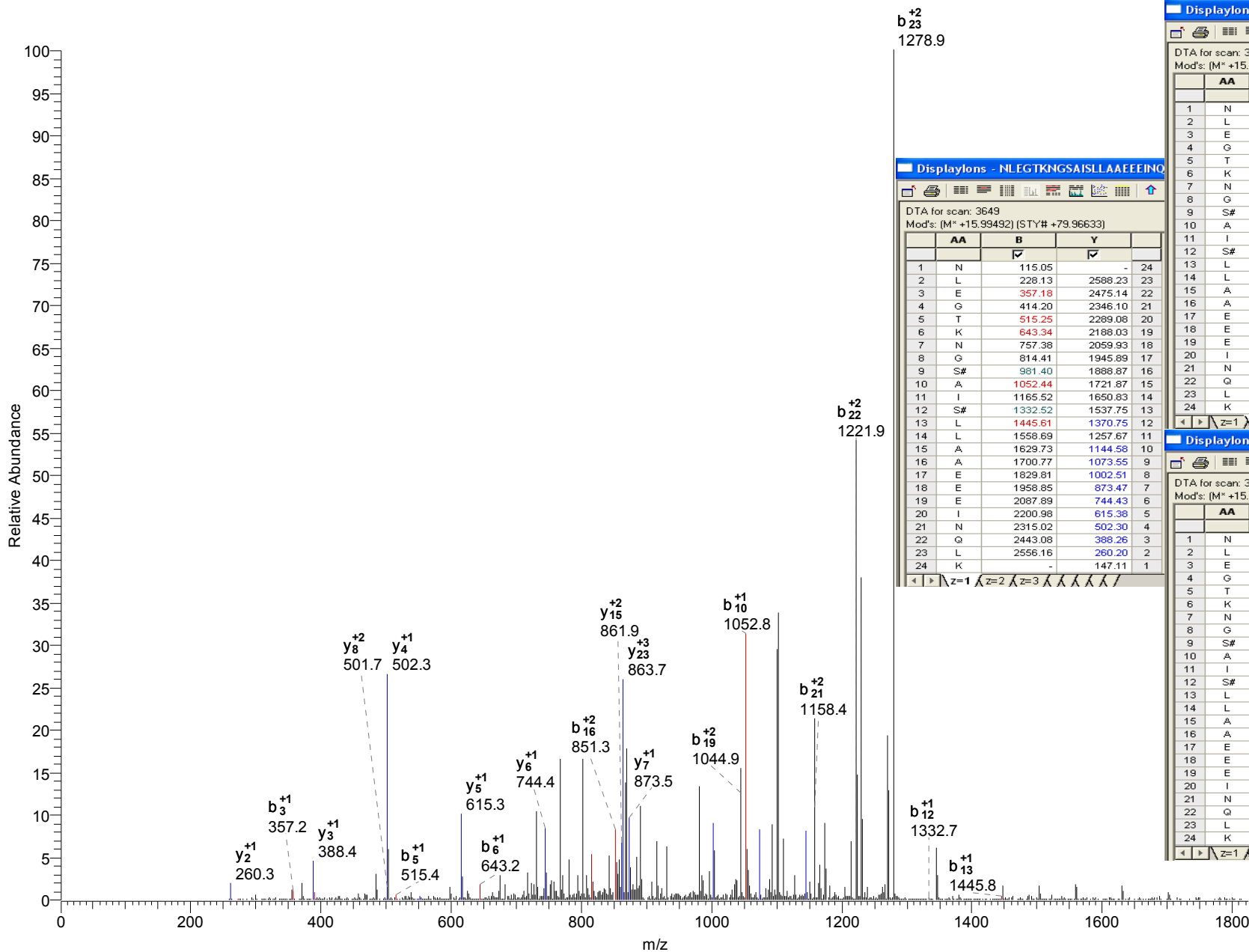
DTA for scan: cap. 3481
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	58.03	-	19
2	Q	86.54	1037.50	18
3	S#	170.04	1006.39	17
4	A	205.56	925.49	16
5	I	262.10	889.57	15
6	S#	345.60	833.43	14
7	L	402.14	749.93	13
8	L	458.68	693.39	12
9	A	494.20	636.84	11
10	A	529.72	601.32	10
11	E	594.24	555.81	9
12	E	658.76	501.28	8
13	E	723.28	436.76	7
14	I	779.83	372.24	6
15	N	836.85	315.70	5
16	Q	900.88	258.68	4
17	L	957.42	194.65	3
18	K	1021.47	136.11	2
19	K	-	74.06	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18 z=19

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3649-3649 RT:54.18-54.18 NL:3.58E4



Displaylons - NLEGTKNGSAISLLAAEEFIHQ

DTA for scan: 3649
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	58.03	-	24
2	L	114.57	1294.62	23
3	E	179.09	1238.07	22
4	G	207.60	1173.55	21
5	T	258.13	1145.04	20
6	K	322.17	1094.52	19
7	N	379.20	1030.47	18
8	G	407.71	973.45	17
9	S#	491.21	944.94	16
10	A	526.72	861.44	15
11	I	583.27	825.92	14
12	S#	666.77	769.38	13
13	L	723.31	685.88	12
14	L	779.85	629.34	11
15	A	815.37	572.80	10
16	A	850.89	537.28	9
17	E	915.41	501.76	8
18	E	979.93	437.24	7
19	E	1044.45	372.72	6
20	I	1100.99	308.19	5
21	N	1158.01	251.65	4
22	Q	1222.04	194.63	3
23	L	1278.59	130.60	2
24	K	-	74.06	1

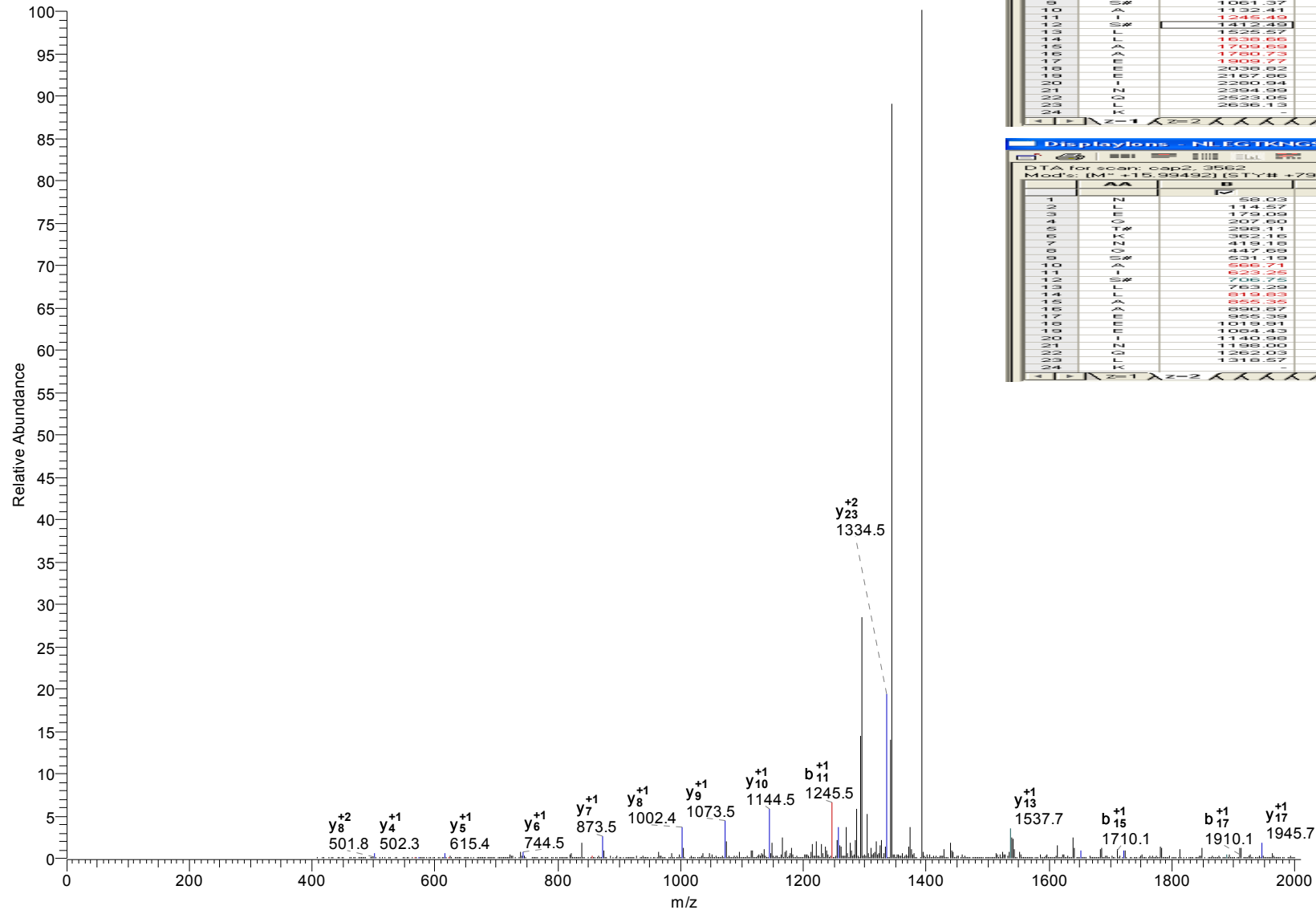
Displaylons - NLEGTKNGSAISLLAAEEFIHQ

DTA for scan: 3649
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	39.02	-	24
2	L	76.72	863.41	23
3	E	119.73	825.72	22
4	G	138.74	782.70	21
5	T	172.42	763.70	20
6	K	215.12	730.01	19
7	N	253.13	687.32	18
8	G	272.14	649.30	17
9	S#	327.81	630.30	16
10	A	351.49	574.63	15
11	I	389.18	550.95	14
12	S#	444.85	513.26	13
13	L	482.54	457.59	12
14	L	520.24	419.89	11
15	A	543.91	382.20	10
16	A	567.59	358.52	9
17	E	610.61	334.84	8
18	E	653.62	291.83	7
19	E	696.64	248.81	6
20	I	734.33	205.80	5
21	N	772.34	168.10	4
22	Q	815.03	130.09	3
23	L	852.73	87.40	2
24	K	-	49.71	1

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3562-3562 NL: 2.19E4



Display ions - NLIGTKNGSAISLLAAEEINQ

DTA for scan: cap2_3562
Mod#s: (M+ +15.39492) (S TY# +79.96633)

	AA	B	Y	
1	N	115.05	-	24
2	L	226.13	2668.19	23
3	E	367.18	2555.11	22
4	G	414.20	2426.07	21
5	T#	595.21	2389.04	20
6	K	723.31	2186.03	19
7	N	837.35	2059.93	18
8	G	894.37	1945.89	17
9	S#	1061.37	1888.87	16
10	A	1132.41	1721.87	15
11	I	1245.49	1650.93	14
12	S#	1412.49	1537.75	13
13	L	1525.57	1370.75	12
14	L	1638.65	1257.67	11
15	A	1709.69	1144.58	10
16	A	1780.73	1073.55	9
17	E	1809.77	1002.51	8
18	E	2036.82	973.47	7
19	E	2167.86	744.43	6
20	I	2280.94	615.38	5
21	N	2394.99	502.30	4
22	G	2523.05	388.26	3
23	L	2636.13	250.20	2
24	K	-	147.11	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18 z=19 z=20 z=21 z=22 z=23 z=24

Display ions - NLIGTKNGSAISLLAAEEINQ

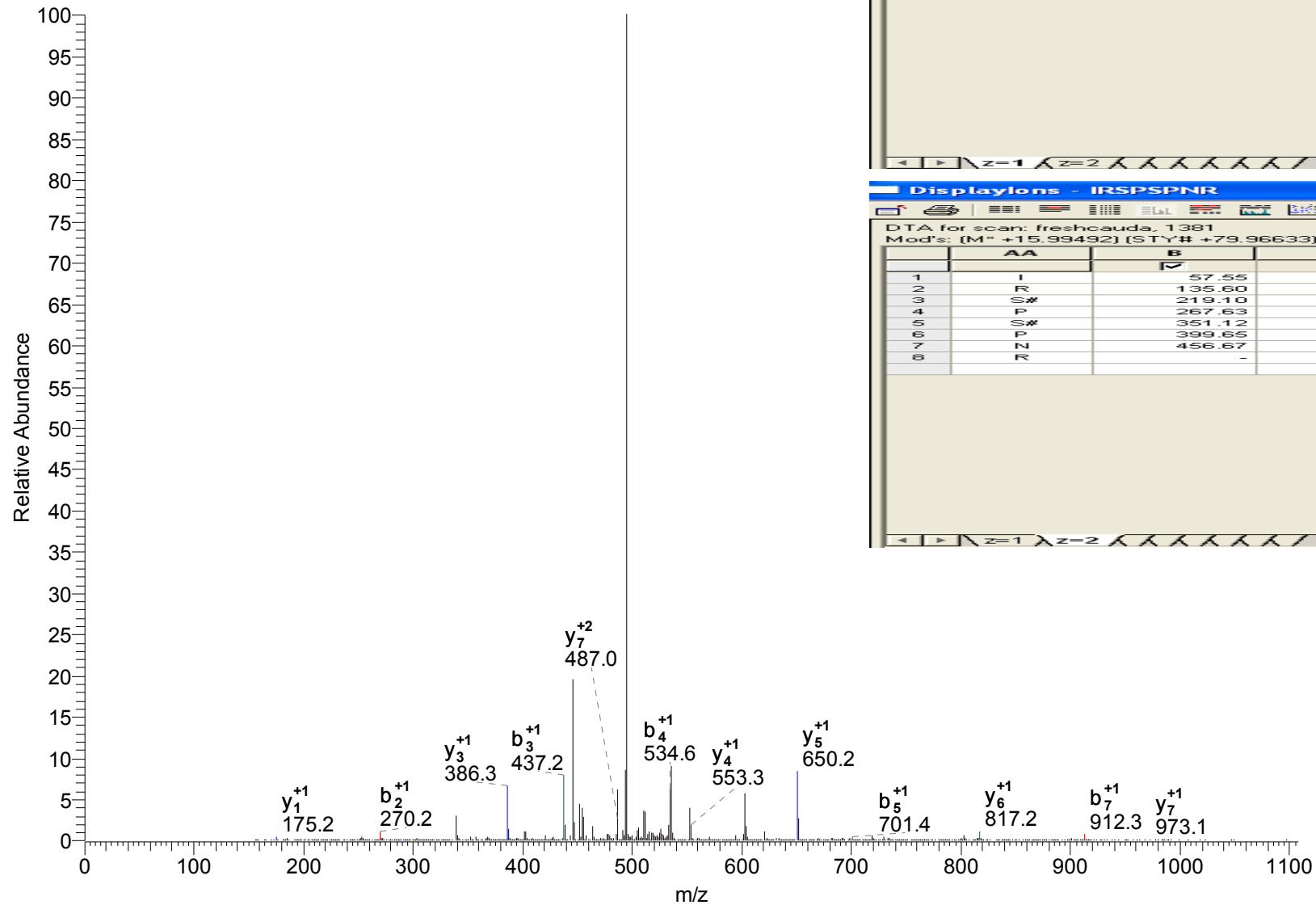
DTA for scan: cap2_3562
Mod#s: (M+ +15.39492) (S TY# +79.96633)

	AA	B	Y	
1	N	58.03	-	24
2	L	114.57	1334.60	23
3	E	179.09	1276.06	22
4	G	207.60	1213.54	21
5	T#	298.11	1185.03	20
6	K	362.16	1094.52	19
7	N	419.16	1030.47	18
8	G	447.69	973.45	17
9	S#	531.19	944.94	16
10	A	606.71	861.44	15
11	I	623.25	825.92	14
12	S#	706.75	769.38	13
13	L	763.29	685.88	12
14	L	819.83	629.34	11
15	A	855.35	572.80	10
16	A	890.87	537.28	9
17	E	955.39	501.76	8
18	E	1019.91	437.24	7
19	E	1094.43	372.72	6
20	I	1140.98	308.19	5
21	N	1195.00	251.65	4
22	G	1262.03	194.63	3
23	L	1318.57	130.60	2
24	K	-	74.05	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18 z=19 z=20 z=21 z=22 z=23 z=24

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#1381-1381 NL: 5.68E4



Displaylons - IRSPSPNR

DTA for scan: freshcauda, 1381
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	I	114.09	-	8
2	R	270.19	973.37	7
3	S#	437.19	817.26	6
4	P	534.24	650.27	5
5	S#	701.24	553.21	4
6	P	798.29	386.21	3
7	N	912.34	289.16	2
8	R	-	175.12	1

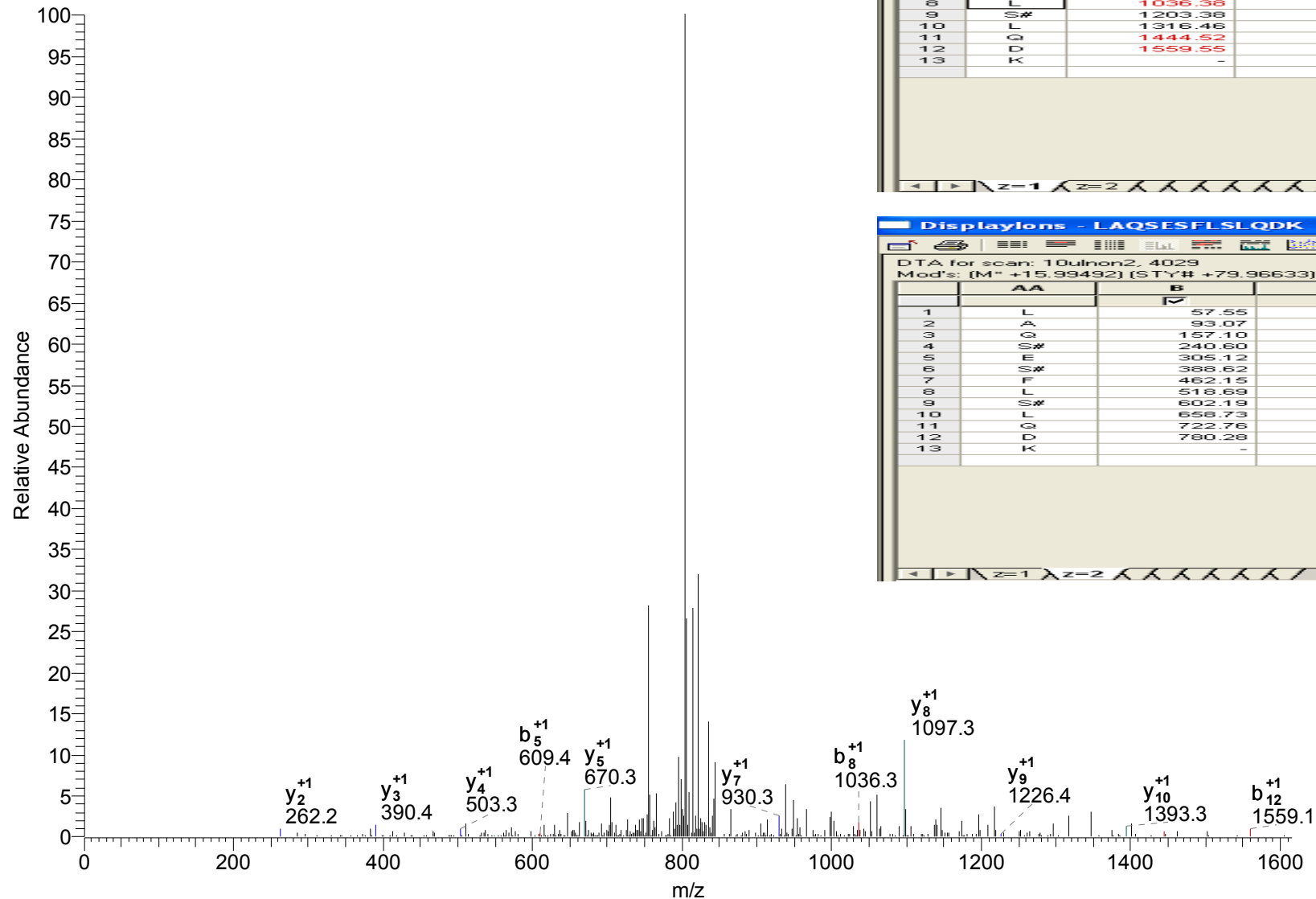
Displaylons - IRSPSPNR

DTA for scan: freshcauda, 1381
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	I	57.55	-	8
2	R	135.60	487.19	7
3	S#	219.10	409.14	6
4	P	267.63	325.64	5
5	S#	351.12	277.11	4
6	P	399.65	193.61	3
7	N	456.67	145.08	2
8	R	-	88.06	1

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#4029-4029 NL: 8.28E2



Displaylons - LAQSESFLSLQDK

DTA for scan: 10ulnon2, 4029
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	L	114.09	-	13
2	A	185.13	1592.57	12
3	Q	313.19	1521.53	11
4	S#	480.19	1393.47	10
5	E	509.23	1226.47	9
6	S#	776.23	1097.43	8
7	F	923.29	930.43	7
8	L	1036.38	783.36	6
9	S#	1203.38	670.28	5
10	L	1316.46	503.28	4
11	Q	1444.52	390.20	3
12	D	1559.55	262.14	2
13	K	-	147.11	1

z=1 z=2

Displaylons - LAQSESFLSLQDK

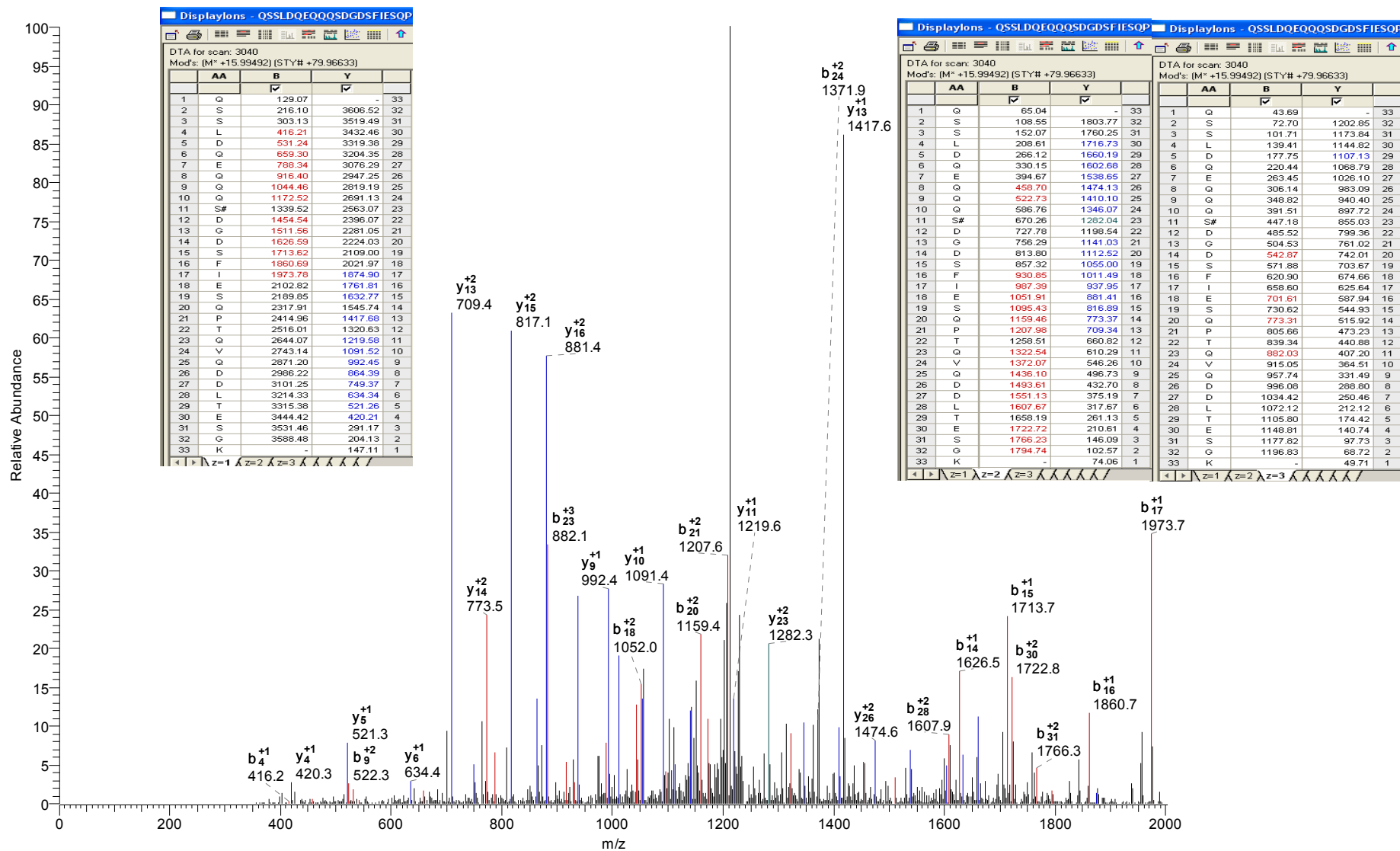
DTA for scan: 10ulnon2, 4029
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	L	57.55	-	13
2	A	93.07	796.79	12
3	Q	157.10	761.27	11
4	S#	240.60	697.24	10
5	E	305.12	613.74	9
6	S#	388.62	549.22	8
7	F	462.15	465.72	7
8	L	518.69	392.19	6
9	S#	602.19	335.64	5
10	L	658.73	252.14	4
11	Q	722.76	195.60	3
12	D	780.28	131.57	2
13	K	-	74.06	1

z=1 z=2

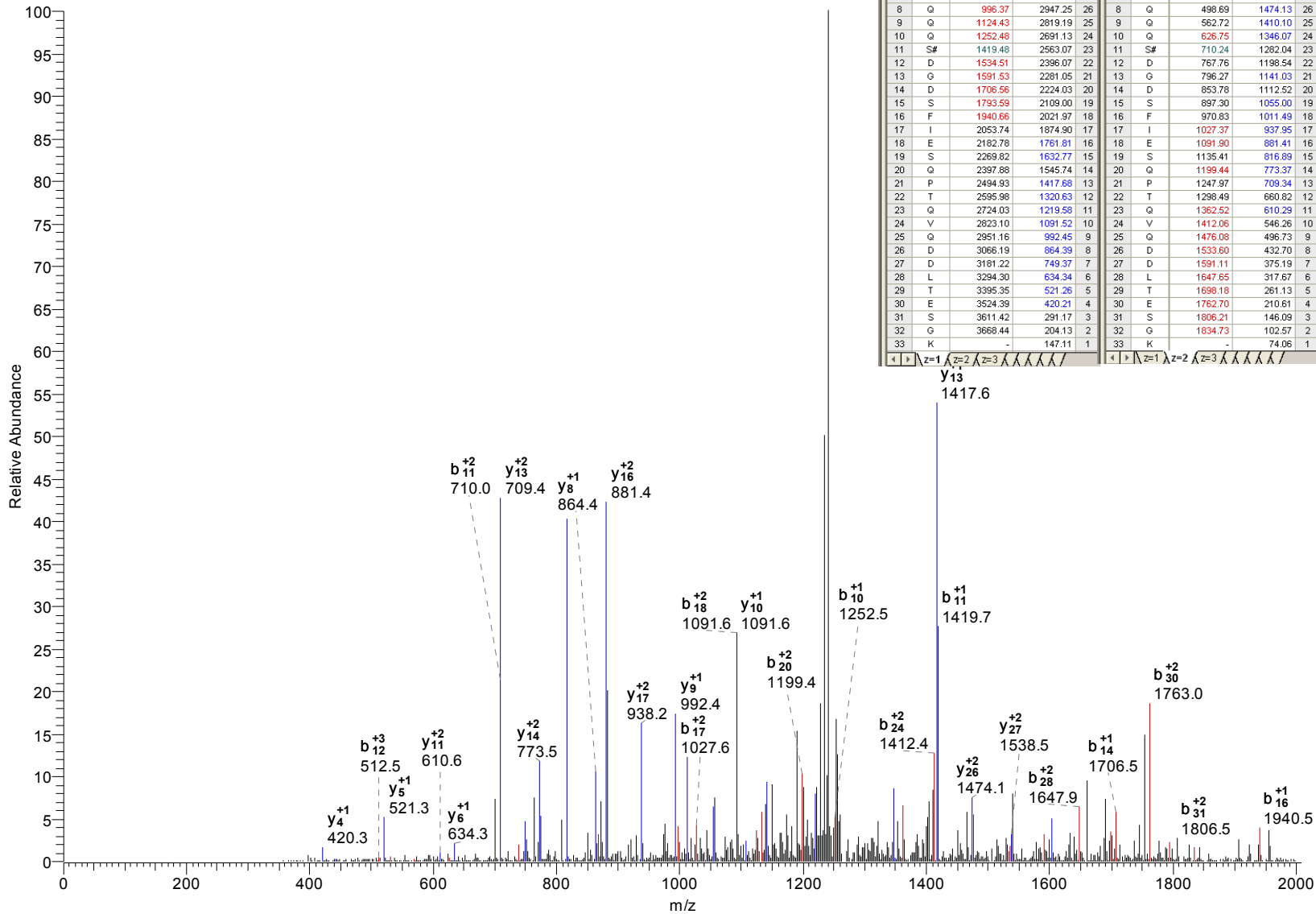
Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#3040-3040 RT:46.71-46.71 NL: 3.93E3



Spata18 Isoform 1 of Spermatogenesis-associated protein 18

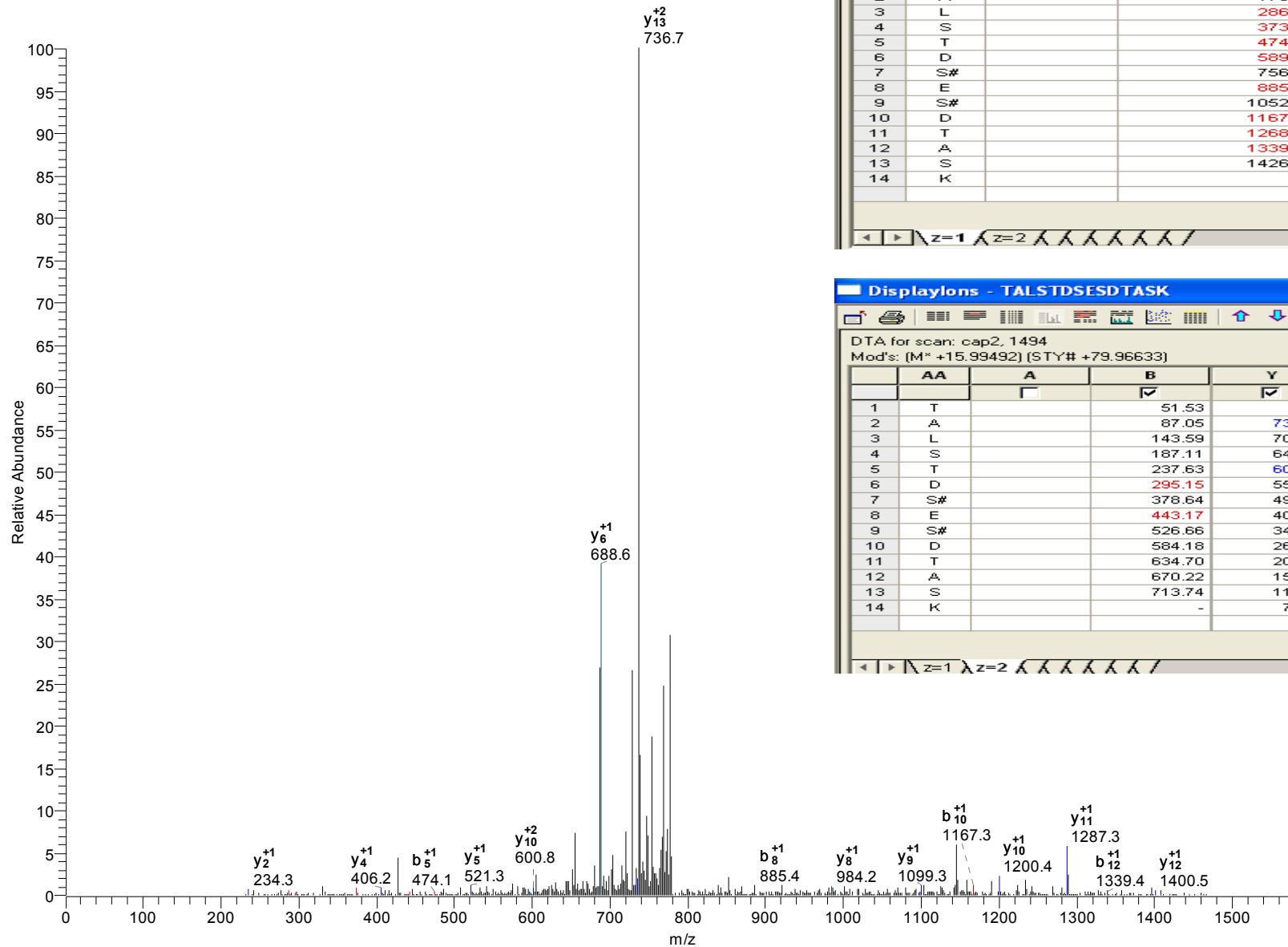
#3006-3006 RT:46.30-46.30 NL: 5.59E3



Displaylons - QSSLDQEQQSDGDSFIESQ									
DTA for scan: 3006									
Mod's: (M* +15.99492) (STY# +79.96633)									
	AA	B	Y						
1	Q	129.07	-	33	Q	65.04	-	33	
2	S	216.10	3696.49	32	S	108.55	1943.75	32	
3	S#	383.10	3599.46	31	S#	192.05	1800.23	31	
4	L	496.18	3432.46	30	L	248.59	1716.73	30	
5	D	611.21	3319.38	29	D	306.11	1660.19	29	
6	Q	739.27	3204.35	28	Q	370.14	1602.68	28	
7	E	868.31	3076.29	27	E	434.66	1538.65	27	
8	Q	996.37	2947.25	26	Q	498.69	1474.13	26	
9	Q	1124.43	2819.19	25	Q	562.72	1410.10	25	
10	Q	1252.48	2691.13	24	Q	626.75	1346.07	24	
11	S#	1419.48	2563.07	23	S#	710.24	1282.04	23	
12	D	1534.51	2396.07	22	D	767.76	1198.54	22	
13	G	1591.53	2281.05	21	G	796.27	1141.03	21	
14	D	1706.56	2224.03	20	D	853.78	1112.52	20	
15	S	1793.59	2109.00	19	S	897.30	1055.00	19	
16	F	1940.66	2021.97	18	F	970.83	1011.49	18	
17	I	2053.74	1874.90	17	I	1027.37	937.95	17	
18	E	2182.78	1761.81	16	E	1091.90	881.41	16	
19	S	2269.82	1632.77	15	S	1135.41	816.89	15	
20	Q	2397.88	1545.74	14	Q	1199.44	773.37	14	
21	P	2494.93	1417.68	13	P	1247.97	709.34	13	
22	T	2595.98	1320.63	12	T	1298.49	660.82	12	
23	Q	2724.03	1219.58	11	Q	1362.52	610.29	11	
24	V	2823.10	1091.52	10	V	1412.06	546.26	10	
25	Q	2951.16	992.45	9	Q	1476.08	496.73	9	
26	D	3066.19	864.39	8	D	1533.60	432.70	8	
27	D	3181.22	749.37	7	D	1591.11	375.19	7	
28	L	3294.30	634.34	6	L	1647.65	317.67	6	
29	T	3395.35	521.26	5	T	1698.18	261.13	5	
30	E	3524.39	420.21	4	E	1762.70	210.61	4	
31	S	3611.42	291.17	3	S	1806.21	146.09	3	
32	G	3668.44	204.13	2	G	1834.73	102.57	2	
33	K	-	147.11	1	K	-	74.06	1	

68 kDa protein

#1494-1494 NL: 4.08E3



Displaylons - TALSTDSESDTASK

DTA for scan: cap2, 1494
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	T		102.05	-	14
2	A		173.09	1471.52	13
3	L		286.18	1400.49	12
4	S		373.21	1287.40	11
5	T		474.26	1200.37	10
6	D		589.28	1099.32	9
7	S#		756.28	984.30	8
8	E		885.32	817.30	7
9	S#		1052.32	688.25	6
10	D		1167.35	521.26	5
11	T		1268.40	406.23	4
12	A		1339.43	305.18	3
13	S		1426.47	234.14	2
14	K		-	147.11	1

z=1 z=2

Displaylons - TALSTDSESDTASK

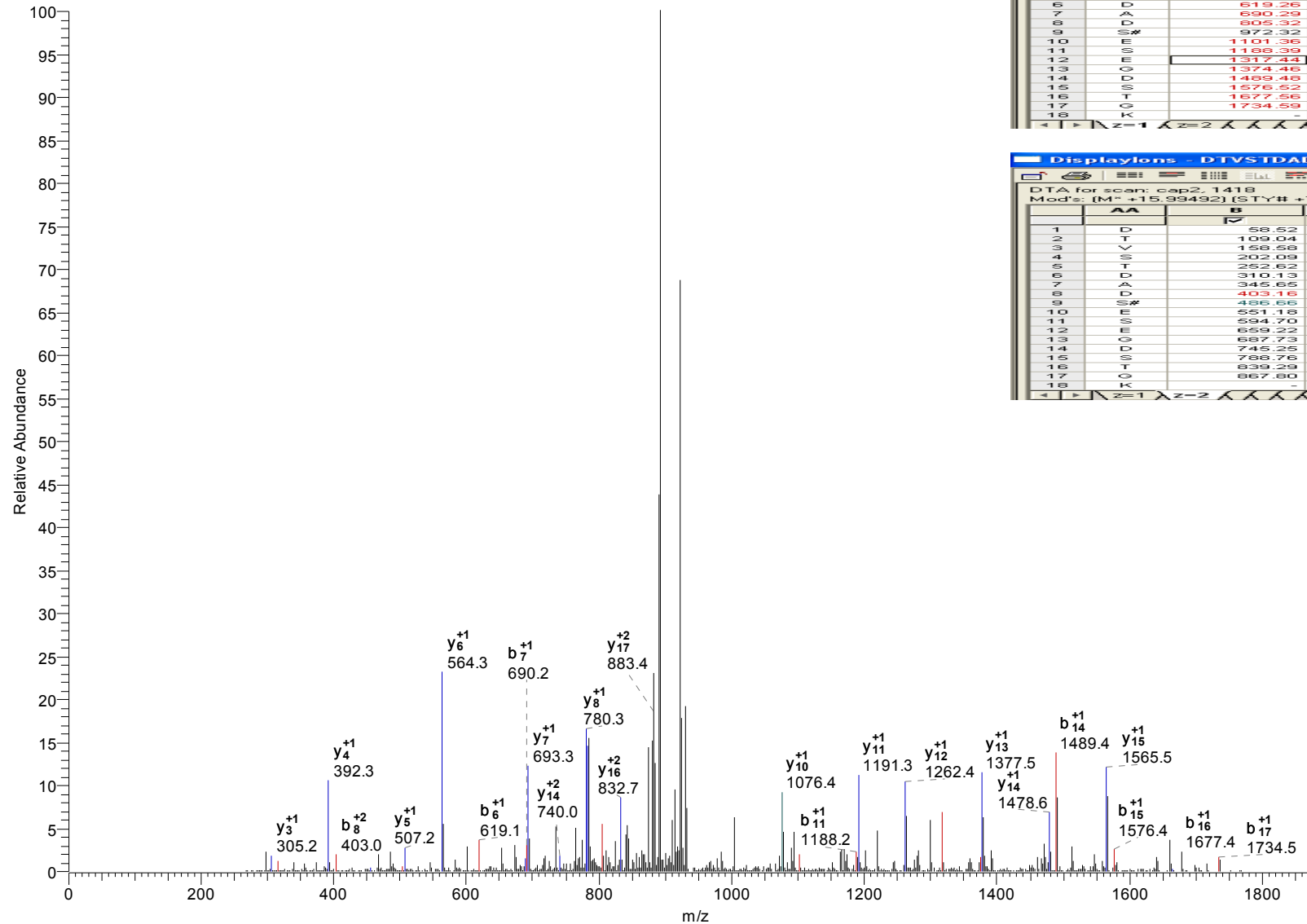
DTA for scan: cap2, 1494
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	T		51.53	-		14
2	A		87.05	736.27		13
3	L		143.59	700.75		12
4	S		187.11	644.20		11
5	T		237.63	600.69		10
6	D		295.15	550.17		9
7	S#		378.64	492.65		8
8	E		443.17	409.15		7
9	S#		526.66	344.63		6
10	D		584.18	261.13		5
11	T		634.70	203.62		4
12	A		670.22	153.09		3
13	S		713.74	117.58		2
14	K		-	74.06		1

z=1 z=2

68 kDa protein

#1418-1418 NL: 7.26E3



Displaylens - DTVSTADSESEGDSTGK

DTA for scan: cap2_1418
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	D	116.03	-	18
2	T	217.08	1765.66	17
3	V	316.15	1664.62	16
4	S	403.18	1565.66	15
5	T	504.23	1478.52	14
6	D	619.26	1377.47	13
7	A	690.29	1262.44	12
8	D	805.32	1191.40	11
9	S#	972.32	1076.38	10
10	E	1101.36	909.38	9
11	S	1166.39	780.34	8
12	E	1317.44	693.30	7
13	G	1374.46	564.26	6
14	D	1489.48	507.24	5
15	S	1576.52	392.21	4
16	T	1677.56	305.18	3
17	G	1734.59	204.13	2
18	K	-	147.11	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18

Displaylens - DTVSTADSESEGDSTGK

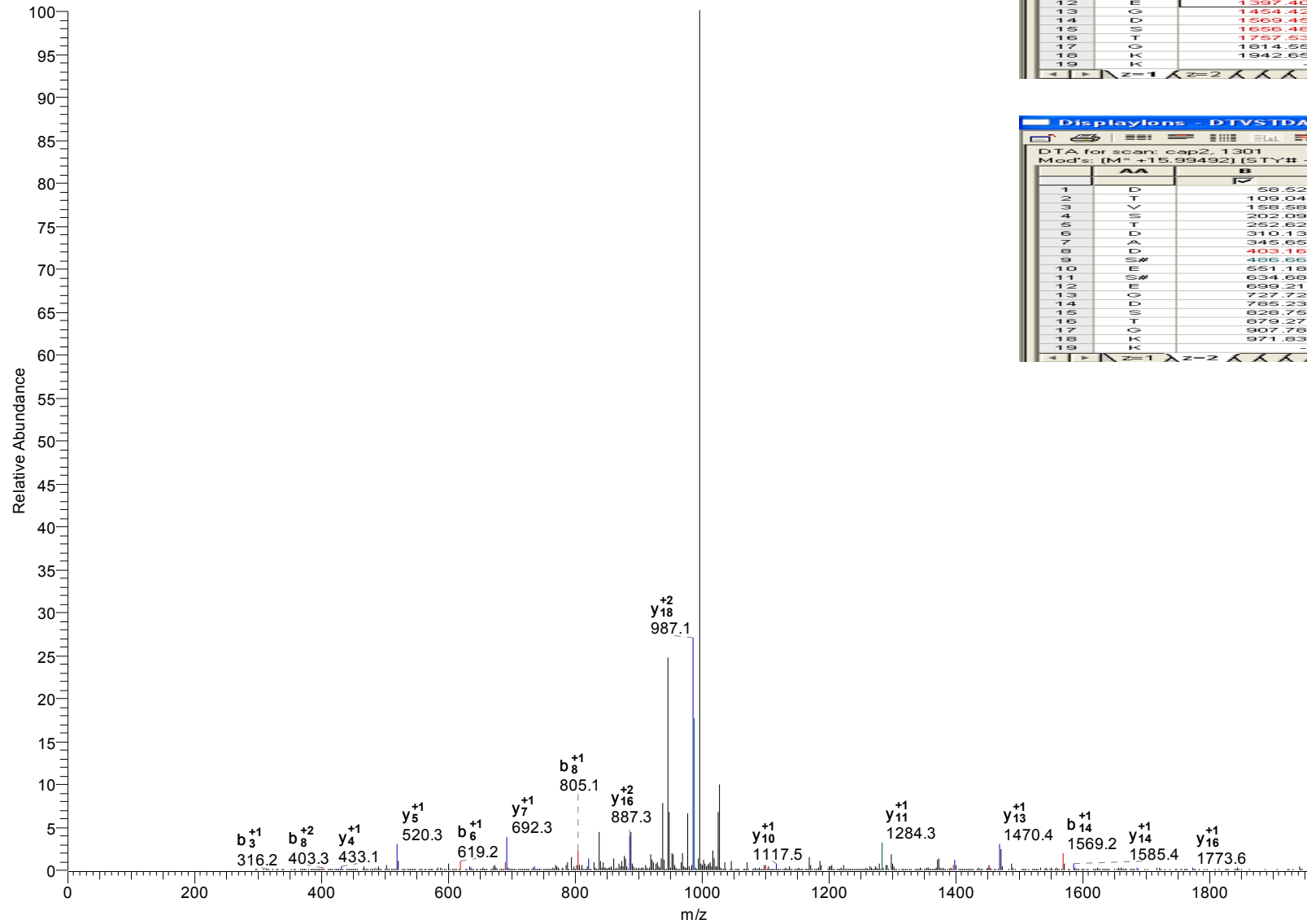
DTA for scan: cap2_1418
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	D	58.52	-	18
2	T	109.04	863.34	17
3	V	158.58	832.61	16
4	S	202.09	783.28	15
5	T	252.62	739.76	14
6	D	310.13	689.24	13
7	A	345.65	631.72	12
8	D	403.16	596.21	11
9	S#	486.66	538.69	10
10	E	551.18	485.19	9
11	S	624.70	390.67	8
12	E	659.22	347.16	7
13	G	687.73	282.63	6
14	D	745.25	254.12	5
15	S	788.76	196.61	4
16	T	839.29	153.09	3
17	G	867.80	102.57	2
18	K	-	74.06	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18

68 kDa protein

#1301-1301 NL: 1.67E4



Displaylens - DTVSTDADSESEGDSTGKK

DTA for scan: cap2. 1301
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	D	116.03	-	19
2	T	217.08	1973.73	18
3	V	316.15	1872.68	17
4	S	403.18	1773.61	16
5	T	504.23	1686.58	15
6	D	619.28	1585.53	14
7	A	690.29	1470.50	13
8	D	805.32	1399.47	12
9	S#	972.32	1284.44	11
10	E	1101.36	1117.44	10
11	S#	1268.36	988.40	9
12	E	1397.40	821.40	8
13	G	1454.42	692.36	7
14	D	1569.45	635.34	6
15	S	1656.48	520.31	5
16	T	1767.53	433.26	4
17	G	1814.55	332.23	3
18	K	1942.65	275.21	2
19	K		147.11	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18 z=19

Displaylens - DTVSTDADSESEGDSTGKK

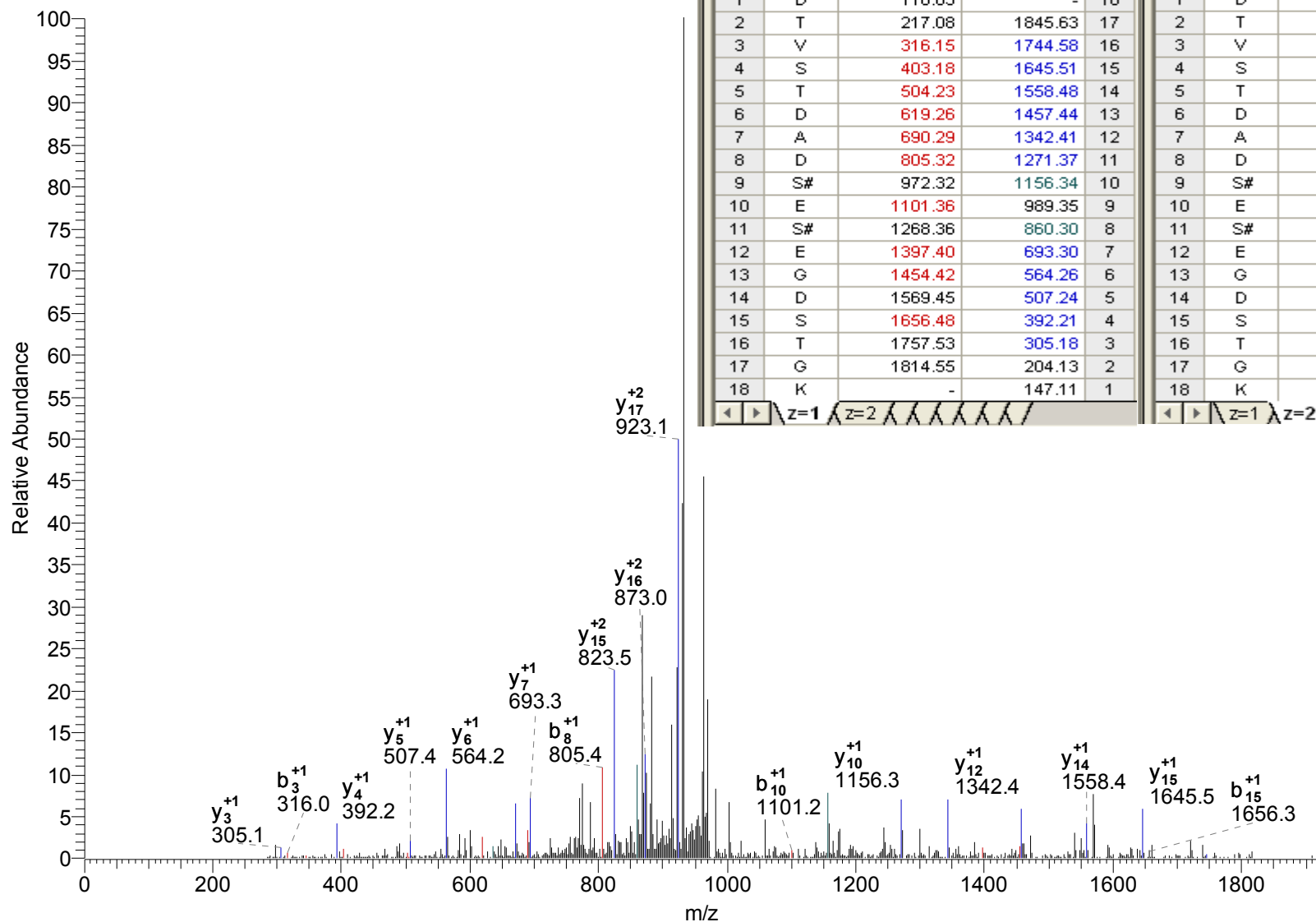
DTA for scan: cap2. 1301
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	D	58.52	-	19
2	T	109.04	987.37	18
3	V	158.58	936.84	17
4	S	202.09	887.31	16
5	T	252.62	843.79	15
6	D	310.13	793.27	14
7	A	345.65	735.76	13
8	D	403.16	700.24	12
9	S#	486.66	642.72	11
10	E	561.18	589.22	10
11	S#	634.68	494.70	9
12	E	699.21	411.20	8
13	G	727.72	345.68	7
14	D	785.23	318.17	6
15	S	828.75	260.66	5
16	T	879.27	217.14	4
17	G	907.78	166.62	3
18	K	971.83	138.11	2
19	K		74.06	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13 z=14 z=15 z=16 z=17 z=18 z=19

68 kDa protein

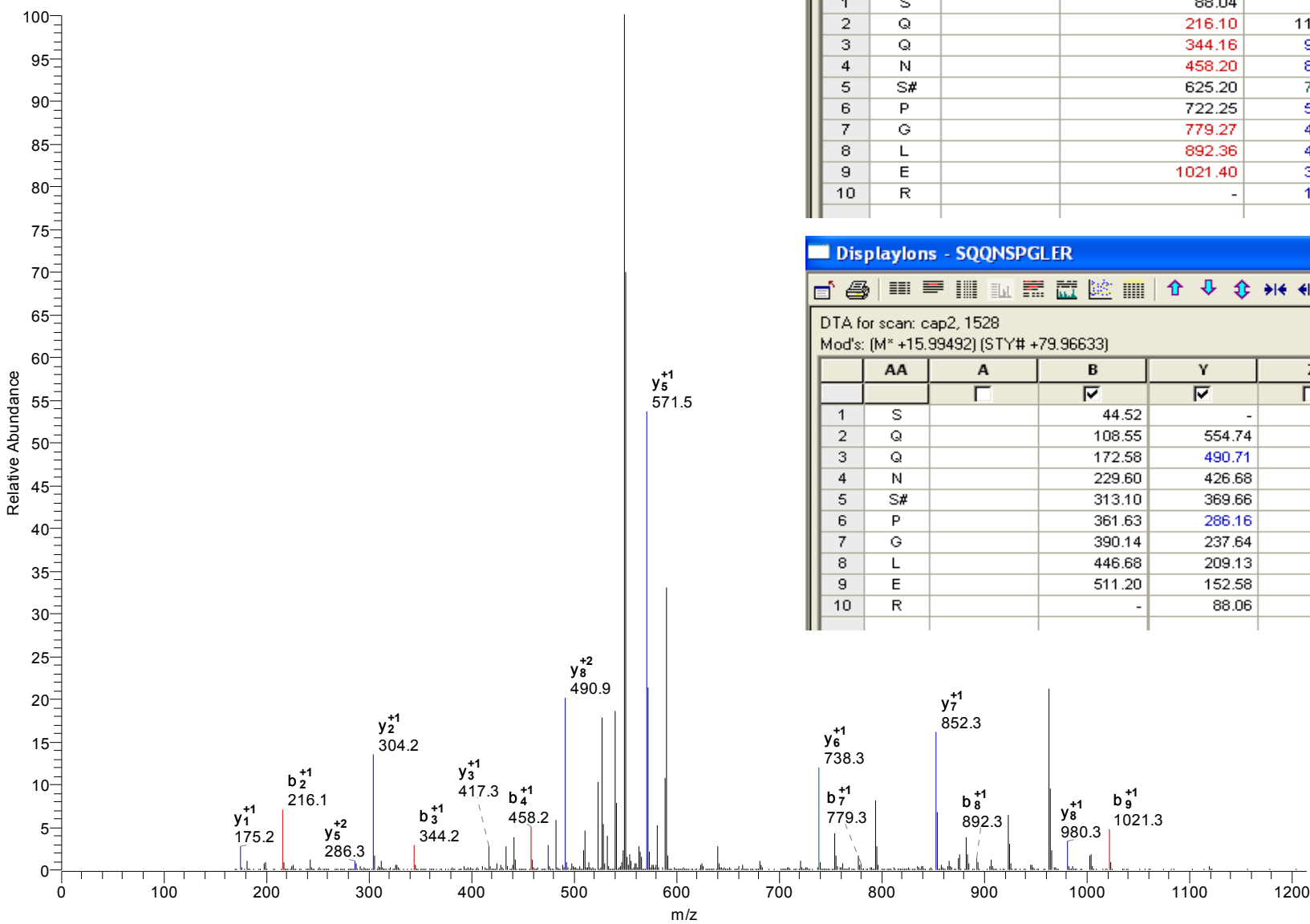
#1412-1412 NL: 2.91E3



Displaylons - DTVSTDADSESEGDSTGK					Displaylons - DTVSTDADSESEGDSTGK				
DTA for scan: cap2, 1412					DTA for scan: cap2, 1412				
Mod's: (M* +15.99492) (STY# +79.96633)					Mod's: (M* +15.99492) (STY# +79.96633)				
	AA	B	Y			AA	B	Y	
		✓	✓				✓	✓	
1	D	116.03	-	18	1	D	58.52	-	18
2	T	217.08	1845.63	17	2	T	109.04	923.32	17
3	V	316.15	1744.58	16	3	V	158.58	872.80	16
4	S	403.18	1645.51	15	4	S	202.09	823.26	15
5	T	504.23	1558.48	14	5	T	252.62	779.75	14
6	D	619.26	1457.44	13	6	D	310.13	729.22	13
7	A	690.29	1342.41	12	7	A	345.65	671.71	12
8	D	805.32	1271.37	11	8	D	403.16	636.19	11
9	S#	972.32	1156.34	10	9	S#	486.66	578.68	10
10	E	1101.36	989.35	9	10	E	551.18	495.18	9
11	S#	1268.36	860.30	8	11	S#	634.68	430.66	8
12	E	1397.40	693.30	7	12	E	699.21	347.16	7
13	G	1454.42	564.26	6	13	G	727.72	282.63	6
14	D	1569.45	507.24	5	14	D	785.23	254.12	5
15	S	1656.48	392.21	4	15	S	828.75	196.61	4
16	T	1757.53	305.18	3	16	T	879.27	153.09	3
17	G	1814.55	204.13	2	17	G	907.78	102.57	2
18	K	-	147.11	1	18	K	-	74.06	1

Akap3 A kinase (PRKA) anchor protein 3

#1528-1528 NL: 9.23E4

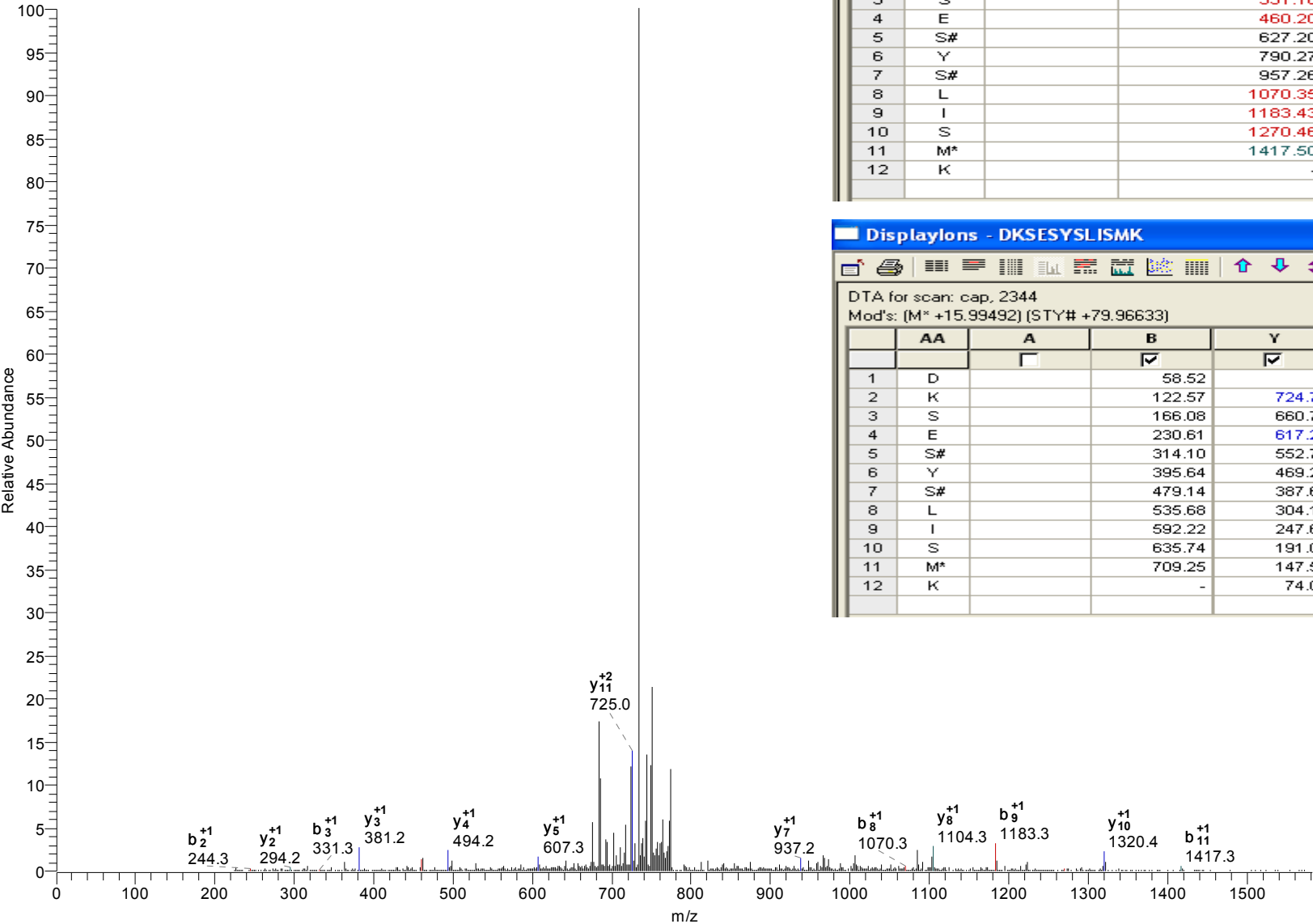


Displaylons - SQQNSPGLER					
DTA for scan: cap2, 1528					
Mod's: [M* +15.99492] (STY# +79.96633)					
	AA	A	B	Y	
1	S		88.04	-	10
2	Q		216.10	1108.48	9
3	Q		344.16	980.42	8
4	N		458.20	852.36	7
5	S#		625.20	738.32	6
6	P		722.25	571.32	5
7	G		779.27	474.27	4
8	L		892.36	417.25	3
9	E		1021.40	304.16	2
10	R		-	175.12	1

Displaylons - SQQNSPGLER					
DTA for scan: cap2, 1528					
Mod's: [M* +15.99492] (STY# +79.96633)					
	AA	A	B	Y	Z
1	S		44.52	-	10
2	Q		108.55	554.74	9
3	Q		172.58	490.71	8
4	N		229.60	426.68	7
5	S#		313.10	369.66	6
6	P		361.63	286.16	5
7	G		390.14	237.64	4
8	L		446.68	209.13	3
9	E		511.20	152.58	2
10	R		-	88.06	1

Akap3 A kinase (PRKA) anchor protein 3

#2344-2344 NL: 1.24E4



Displaylons - DKSESYSLISMK

DTA for scan: cap. 2344
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	D		116.03	-	12
2	K		244.13	1448.58	11
3	S		331.16	1320.48	10
4	E		460.20	1233.45	9
5	S#		627.20	1104.41	8
6	Y		790.27	937.41	7
7	S#		957.26	774.35	6
8	L		1070.35	607.35	5
9	I		1183.43	494.26	4
10	S		1270.46	381.18	3
11	M*		1417.50	294.15	2
12	K		-	147.11	1

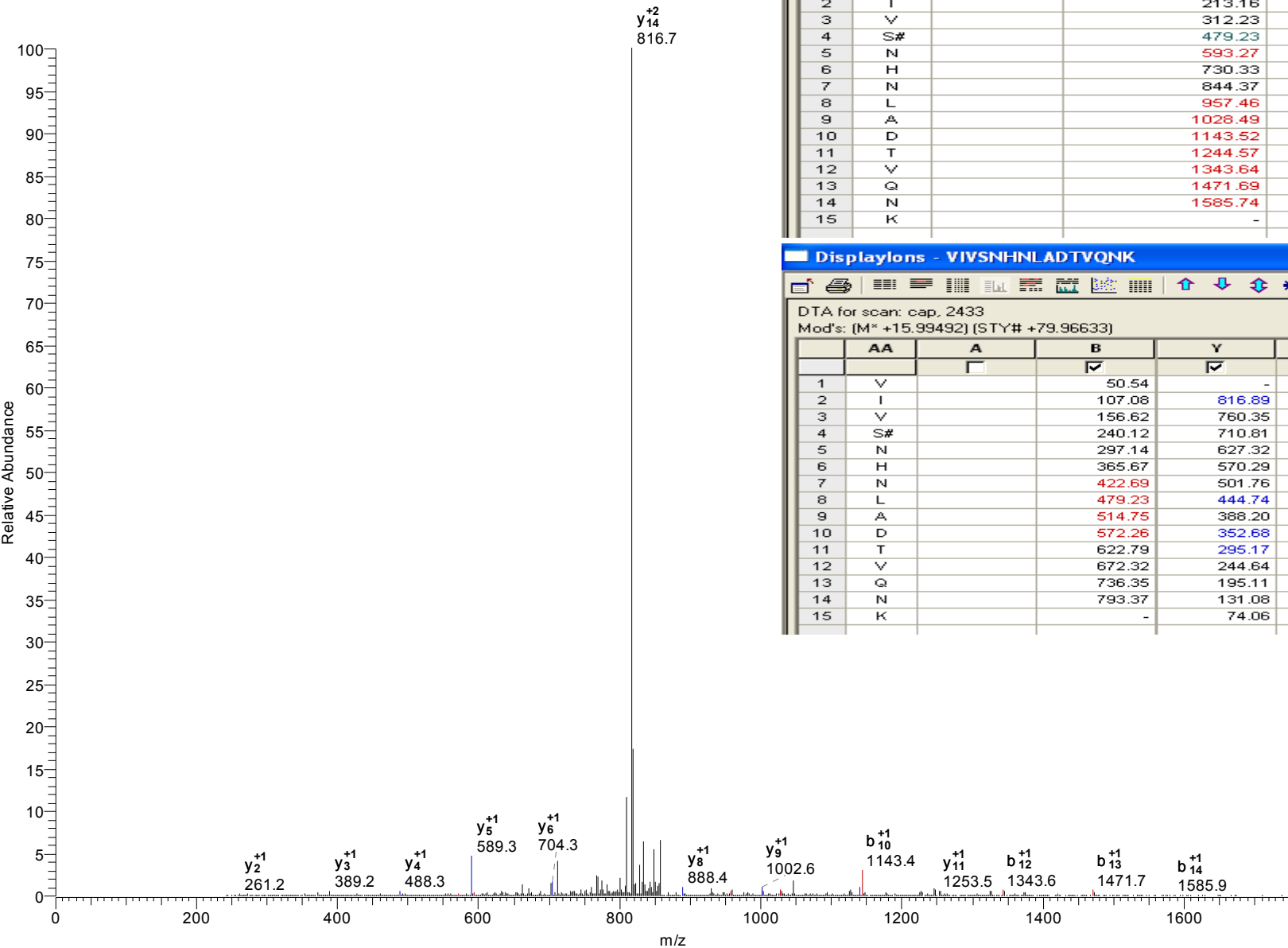
Displaylons - DKSESYSLISMK

DTA for scan: cap. 2344
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	D		58.52	-		12
2	K		122.57	724.79		11
3	S		166.08	660.75		10
4	E		230.61	617.23		9
5	S#		314.10	552.71		8
6	Y		395.64	469.21		7
7	S#		479.14	387.68		6
8	L		535.68	304.18		5
9	I		592.22	247.64		4
10	S		635.74	191.09		3
11	M*		709.25	147.58		2
12	K		-	74.06		1

Akap3 A kinase (PRKA) anchor protein 3

#2433-2433 NL: 4.83E4



Displaylons - VIVSNHNLADTVQNK

DTA for scan: cap, 2433
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	V		100.08	-	15
2	I		213.16	1632.77	14
3	V		312.23	1519.69	13
4	S#		479.23	1420.62	12
5	N		593.27	1253.62	11
6	H		730.33	1139.58	10
7	N		844.37	1002.52	9
8	L		957.46	888.48	8
9	A		1028.49	775.39	7
10	D		1143.52	704.36	6
11	T		1244.57	589.33	5
12	V		1343.64	488.28	4
13	Q		1471.69	389.21	3
14	N		1585.74	261.16	2
15	K		-	147.11	1

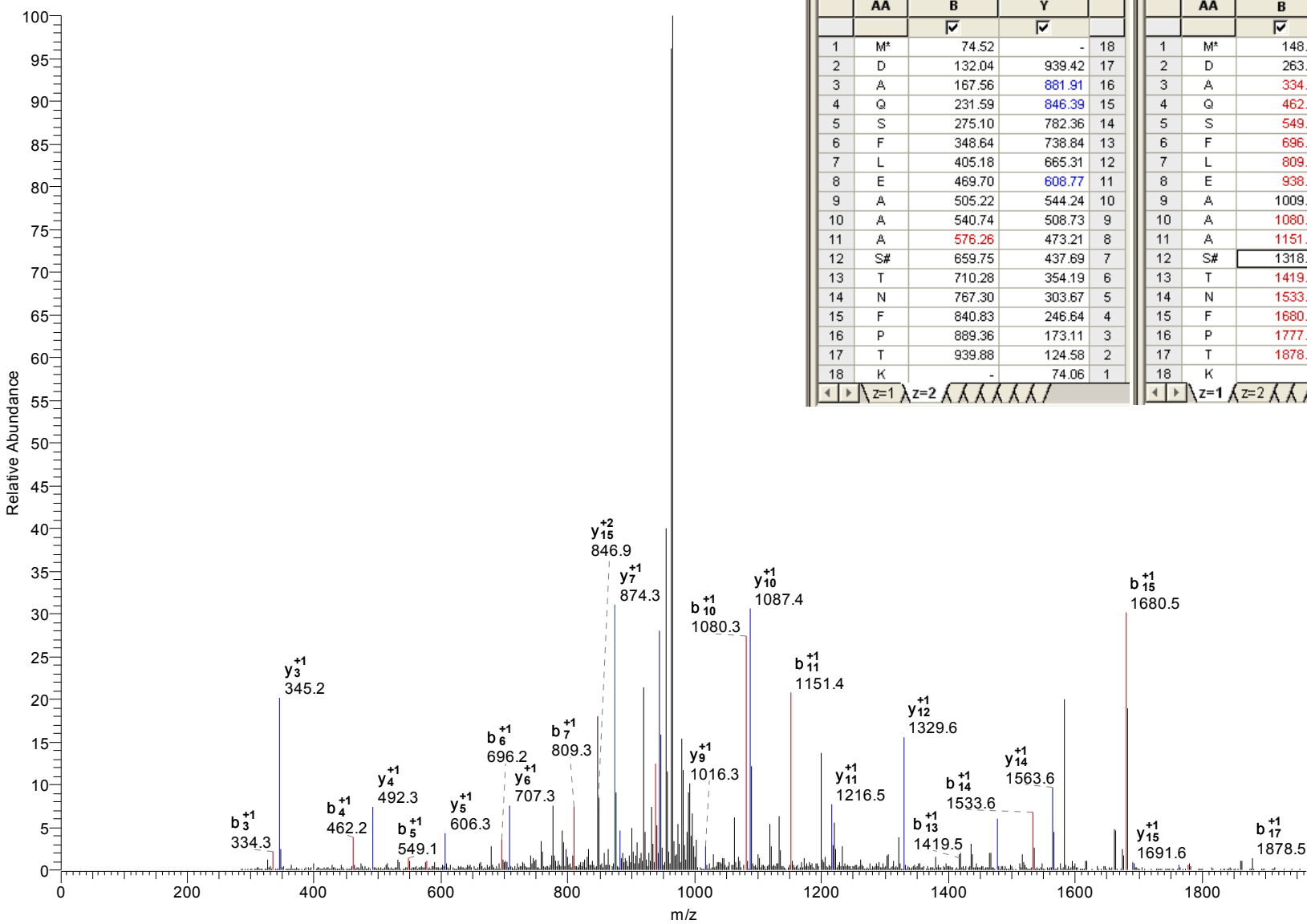
Displaylons - VIVSNHNLADTVQNK

DTA for scan: cap, 2433
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	V		50.54	-		15
2	I		107.08	816.89		14
3	V		156.62	760.35		13
4	S#		240.12	710.81		12
5	N		297.14	627.32		11
6	H		365.67	570.29		10
7	N		422.69	501.76		9
8	L		479.23	444.74		8
9	A		514.75	388.20		7
10	D		572.26	352.68		6
11	T		622.79	295.17		5
12	V		672.32	244.64		4
13	Q		736.35	195.11		3
14	N		793.37	131.08		2
15	K		-	74.06		1

Akap3 A kinase (PRKA) anchor protein 3

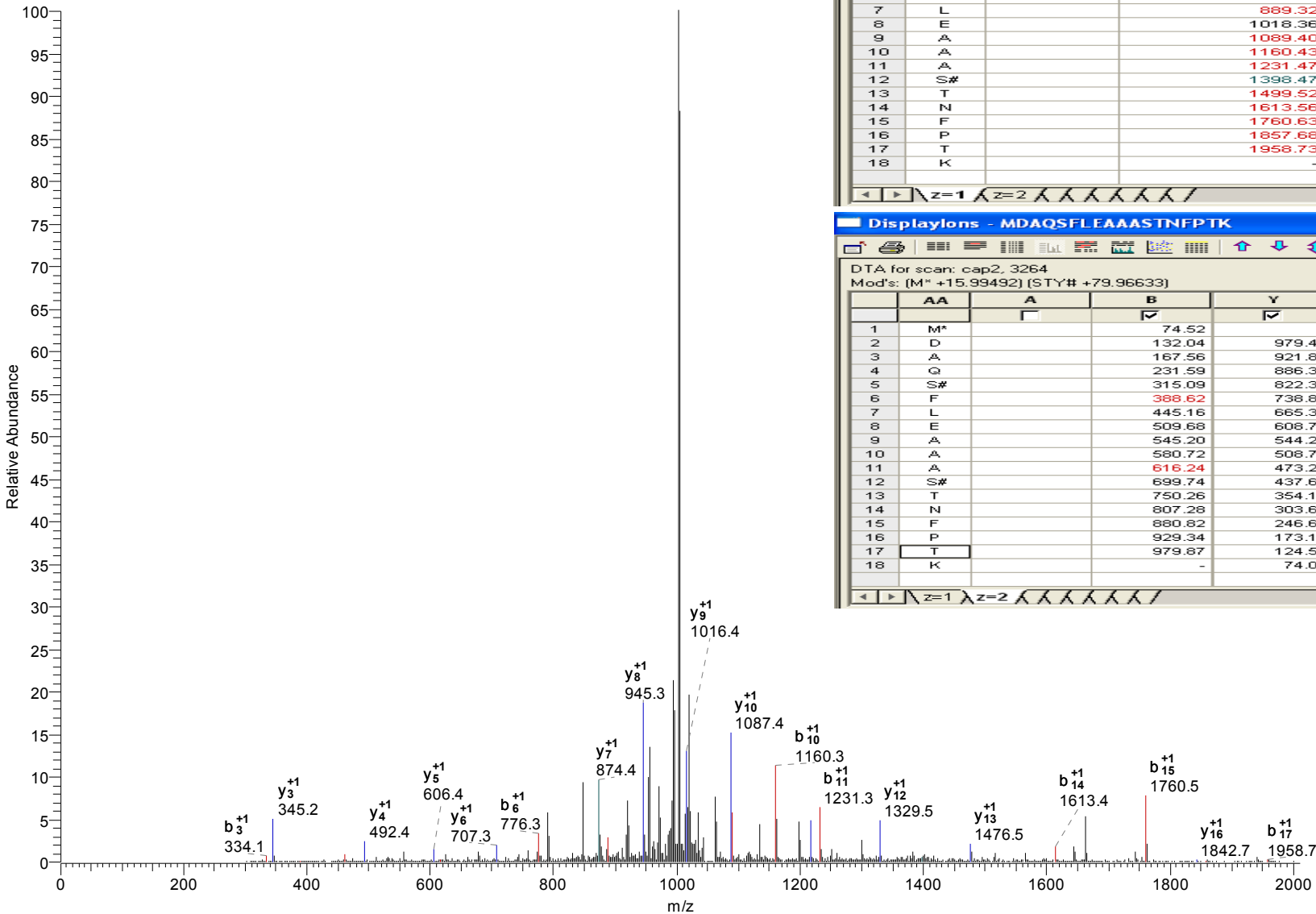
#3294-3294 NL: 1.02E4



Displaylons - MDAQSFLEAAASTNFPTK					Displaylons - MDAQSFLEAAASTNFPTK				
DTA for scan: cap, 3294					DTA for scan: cap, 3294				
Mod's: (M* +15.99492) (STY# +79.96633)					Mod's: (M* +15.99492) (STY# +79.96633)				
	AA	B	Y			AA	B	Y	
1	M*	74.52	-	18	1	M*	148.04	-	18
2	D	132.04	939.42	17	2	D	263.07	1877.83	17
3	A	167.56	881.91	16	3	A	334.11	1762.80	16
4	Q	231.59	846.39	15	4	Q	462.17	1691.77	15
5	S	275.10	782.36	14	5	S	549.20	1563.71	14
6	F	348.64	738.84	13	6	F	696.27	1476.68	13
7	L	405.18	665.31	12	7	L	809.35	1329.61	12
8	E	469.70	608.77	11	8	E	938.39	1216.52	11
9	A	505.22	544.24	10	9	A	1009.43	1087.48	10
10	A	540.74	508.73	9	10	A	1080.47	1016.44	9
11	A	576.26	473.21	8	11	A	1151.50	945.41	8
12	S#	659.75	437.69	7	12	S#	1318.50	874.37	7
13	T	710.28	354.19	6	13	T	1419.55	707.37	6
14	N	767.30	303.67	5	14	N	1533.59	606.32	5
15	F	840.83	246.64	4	15	F	1680.66	492.28	4
16	P	889.36	173.11	3	16	P	1777.71	345.21	3
17	T	939.88	124.58	2	17	T	1878.76	248.16	2
18	K	-	74.06	1	18	K	-	147.11	1

Akap3 A kinase (PRKA) anchor protein 3

#3264-3264 NL: 1.76E4



Displaylons - MDAQSFLEAAASTNFP TK

DTA for scan: cap2, 3264
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	A	B	Y	
1	M*		148.04	-	18
2	D		263.07	1957.80	17
3	A		334.11	1842.77	16
4	Q		462.17	1771.73	15
5	S#		629.16	1643.68	14
6	F		776.23	1476.68	13
7	L		889.32	1329.61	12
8	E		1018.36	1216.52	11
9	A		1089.40	1087.48	10
10	A		1160.43	1016.44	9
11	A		1231.47	945.41	8
12	S#		1398.47	874.37	7
13	T		1499.52	707.37	6
14	N		1613.56	606.32	5
15	F		1760.63	492.28	4
16	P		1857.68	345.21	3
17	T		1958.73	248.16	2
18	K		-	147.11	1

z=1 z=2

Displaylons - MDAQSFLEAAASTNFP TK

DTA for scan: cap2, 3264
Mod's: [M⁺ +15.99492] [STY# +79.96633]

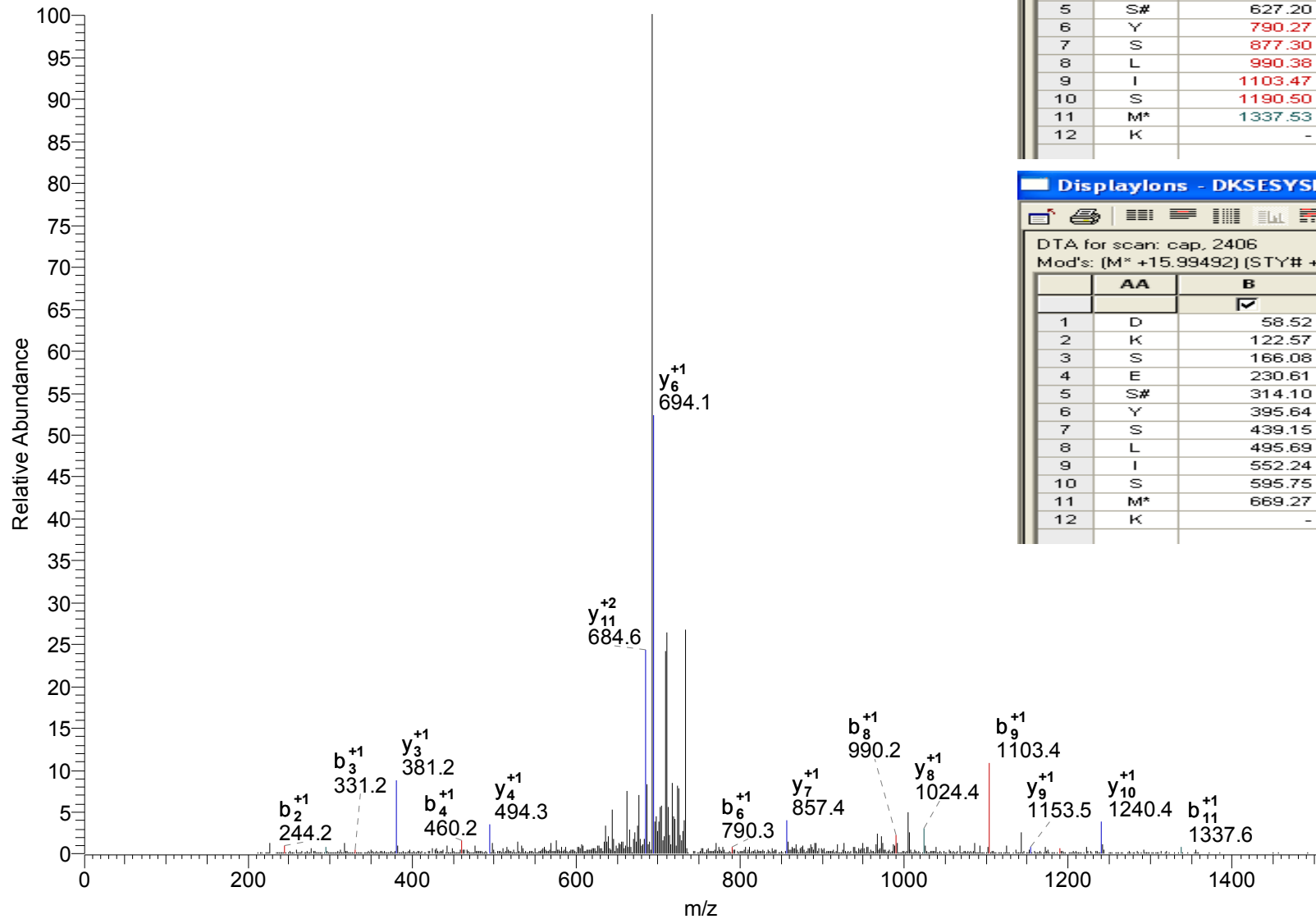
Precursor ion

	AA	A	B	Y	Z	
1	M*		74.52	-		18
2	D		132.04	979.40		17
3	A		167.56	921.89		16
4	Q		231.59	886.37		15
5	S#		315.09	822.34		14
6	F		388.62	738.84		13
7	L		445.16	665.31		12
8	E		509.68	608.77		11
9	A		545.20	544.24		10
10	A		580.72	508.73		9
11	A		616.24	473.21		8
12	S#		699.74	437.69		7
13	T		750.26	354.19		6
14	N		807.28	303.67		5
15	F		880.82	246.64		4
16	P		929.34	173.11		3
17	T		979.87	124.58		2
18	K		-	74.06		1

z=1 z=2

Akap3A kinase (PRKA) anchor protein 3

#2406-2406 NL: 1.13E4



Displaylons - DKSESYSLISMK

DTA for scan: cap. 2406
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	D	116.03	-	12
2	K	244.13	1368.61	11
3	S	331.16	1240.52	10
4	E	460.20	1153.48	9
5	S#	627.20	1024.44	8
6	Y	790.27	857.44	7
7	S	877.30	694.38	6
8	L	990.38	607.35	5
9	I	1103.47	494.26	4
10	S	1190.50	381.18	3
11	M*	1337.53	294.15	2
12	K	-	147.11	1

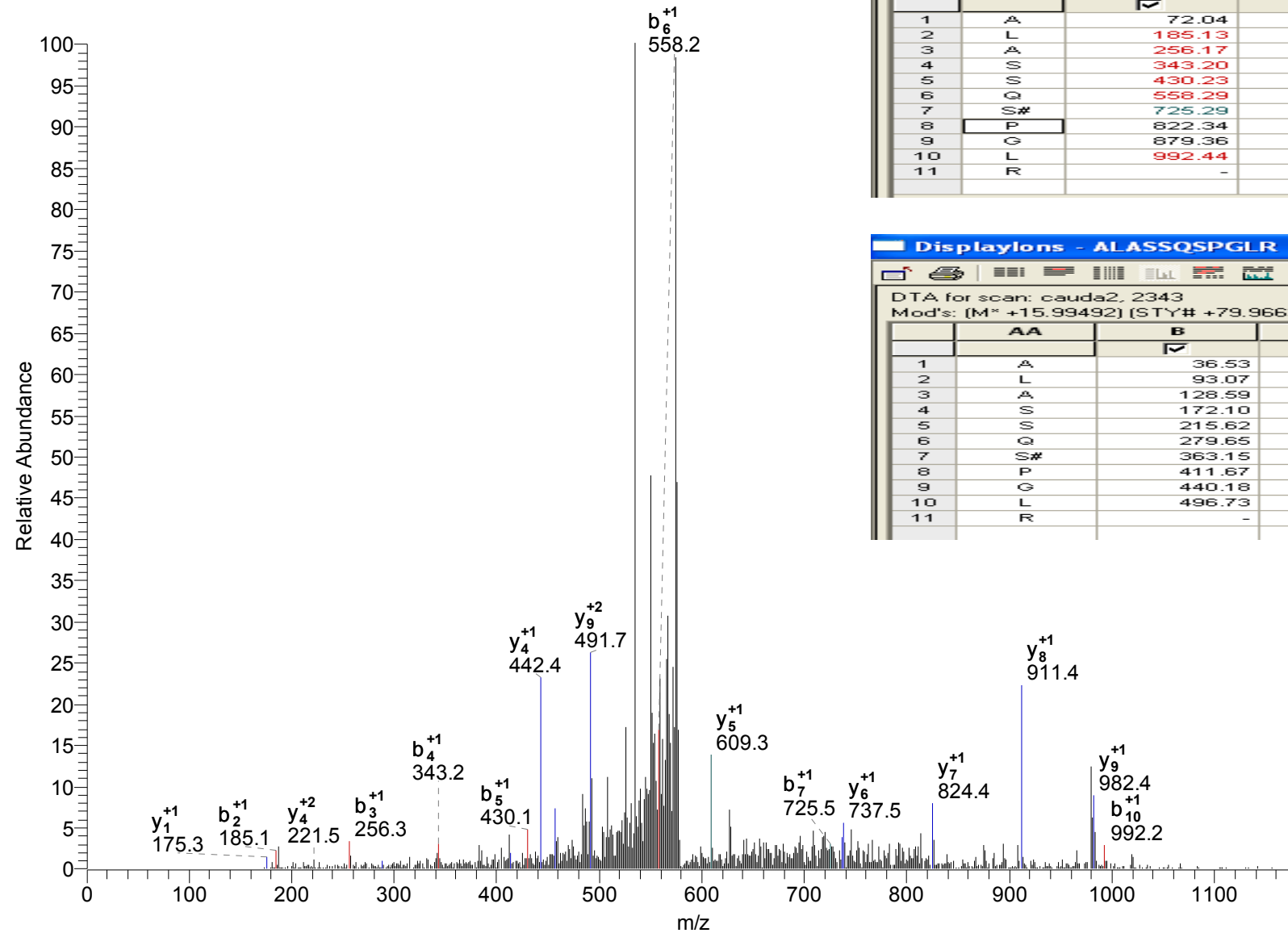
Displaylons - DKSESYSLISMK

DTA for scan: cap. 2406
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	D	58.52	-	12
2	K	122.57	684.81	11
3	S	166.08	620.76	10
4	E	230.61	577.25	9
5	S#	314.10	512.72	8
6	Y	395.64	429.23	7
7	S	439.15	347.69	6
8	L	495.69	304.18	5
9	I	552.24	247.64	4
10	S	595.75	191.09	3
11	M*	669.27	147.58	2
12	K	-	74.06	1

Akap3 A kinase (PRKA) anchor protein 3

#2343-2343 NL: 2.97E3



Displaylons - ALASSQSPGLR

DTA for scan: cauda2, 2343
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	A	72.04	-	11
2	L	185.13	1095.52	10
3	A	256.17	982.44	9
4	S	343.20	911.40	8
5	S	430.23	824.37	7
6	Q	558.29	737.33	6
7	S#	725.29	609.28	5
8	P	822.34	442.28	4
9	G	879.36	345.22	3
10	L	992.44	288.20	2
11	R	-	175.12	1

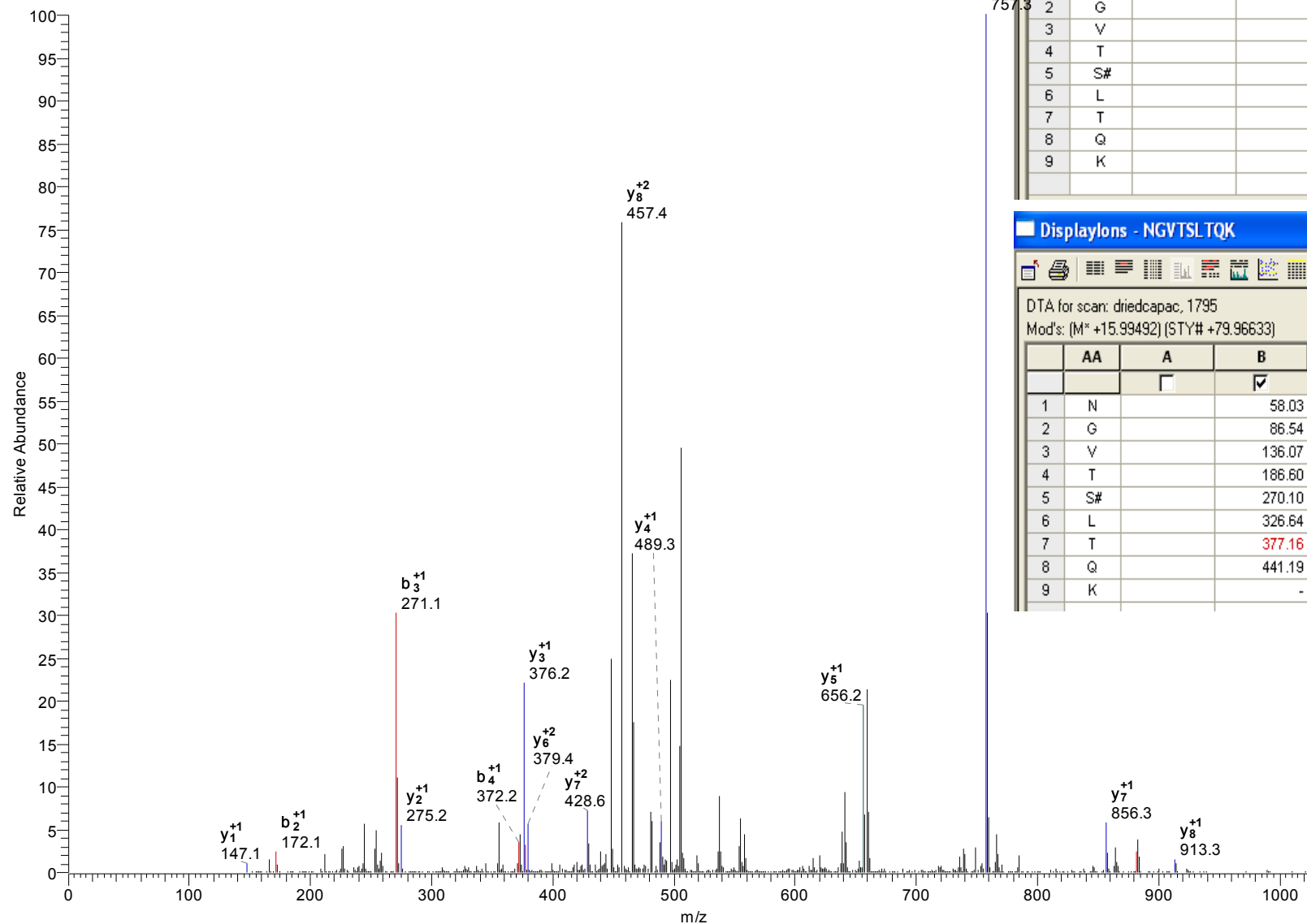
Displaylons - ALASSQSPGLR

DTA for scan: cauda2, 2343
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	A	36.53	-	11
2	L	93.07	548.26	10
3	A	128.59	491.72	9
4	S	172.10	456.20	8
5	S	215.62	412.69	7
6	Q	279.65	369.17	6
7	S#	363.15	305.14	5
8	P	411.67	221.64	4
9	G	440.18	173.12	3
10	L	496.73	144.61	2
11	R	-	88.06	1

Odf2 Isoform 3 of Outer dense fiber protein 2

#1795-1795 NL: 3.47E4



Displaylons - NGVTSLTQK

DTA for scan: driedcapac, 1795
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	9
2	G		172.07	913.44	8
3	V		271.14	856.42	7
4	T		372.19	757.35	6
5	S#		539.19	656.30	5
6	L		652.27	489.30	4
7	T		753.32	376.22	3
8	Q		881.38	275.17	2
9	K		-	147.11	1

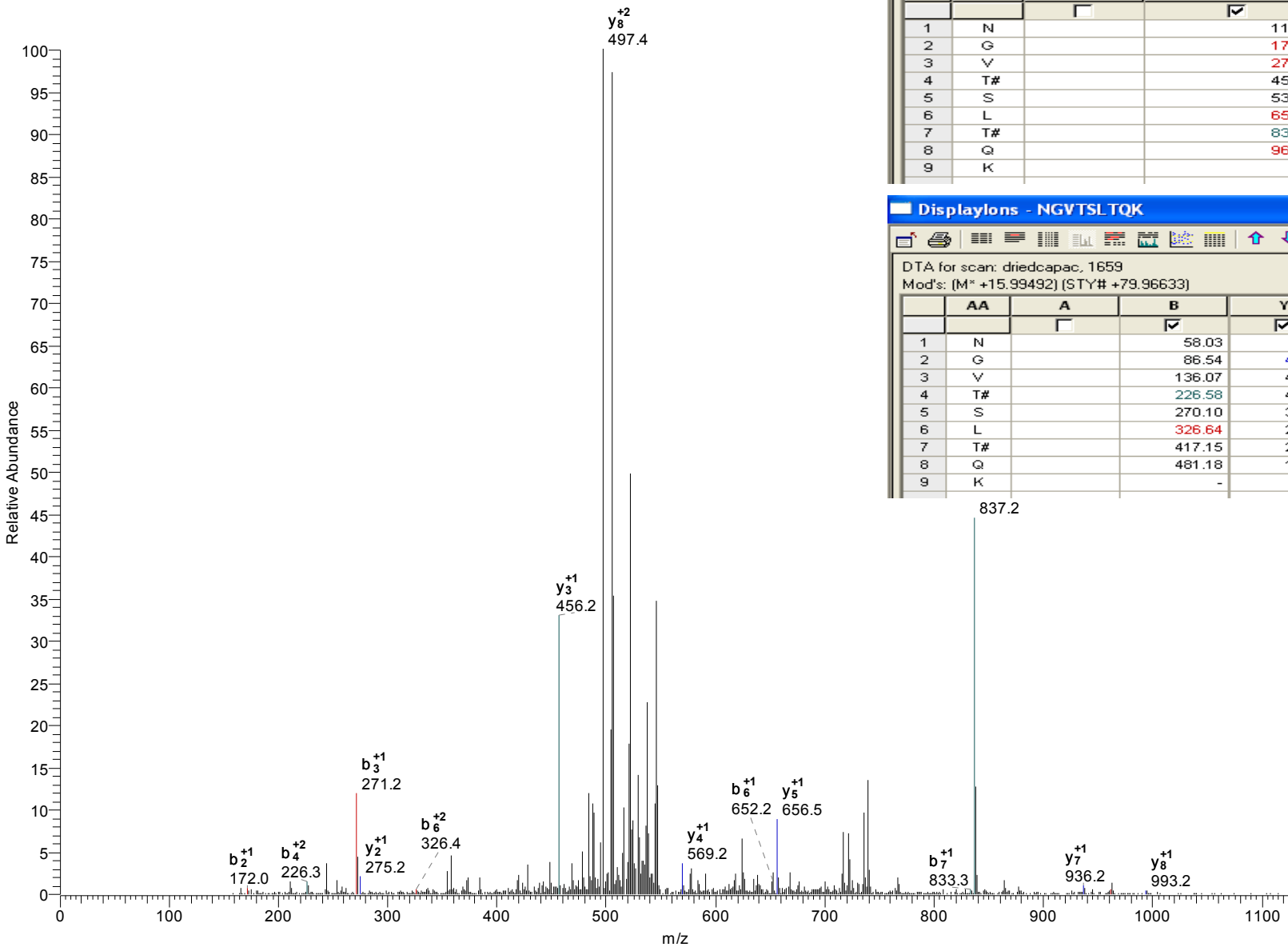
Displaylons - NGVTSLTQK

DTA for scan: driedcapac, 1795
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	N		58.03	-		9
2	G		86.54	457.22		8
3	V		136.07	428.71		7
4	T		186.60	379.18		6
5	S#		270.10	328.65		5
6	L		326.64	245.16		4
7	T		377.16	188.61		3
8	Q		441.19	138.09		2
9	K		-	74.06		1

Odf2 Isoform 3 of Outer dense fiber protein 2

#1659-1659 NL: 9.16E3



Displaylons - NGVTSLTQK

DTA for scan: driedcapac, 1659
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	9
2	G		172.07	993.41	8
3	V		271.14	936.38	7
4	T#		452.15	837.32	6
5	S		539.19	656.30	5
6	L		652.27	569.27	4
7	T#		833.28	456.19	3
8	Q		961.34	275.17	2
9	K		-	147.11	1

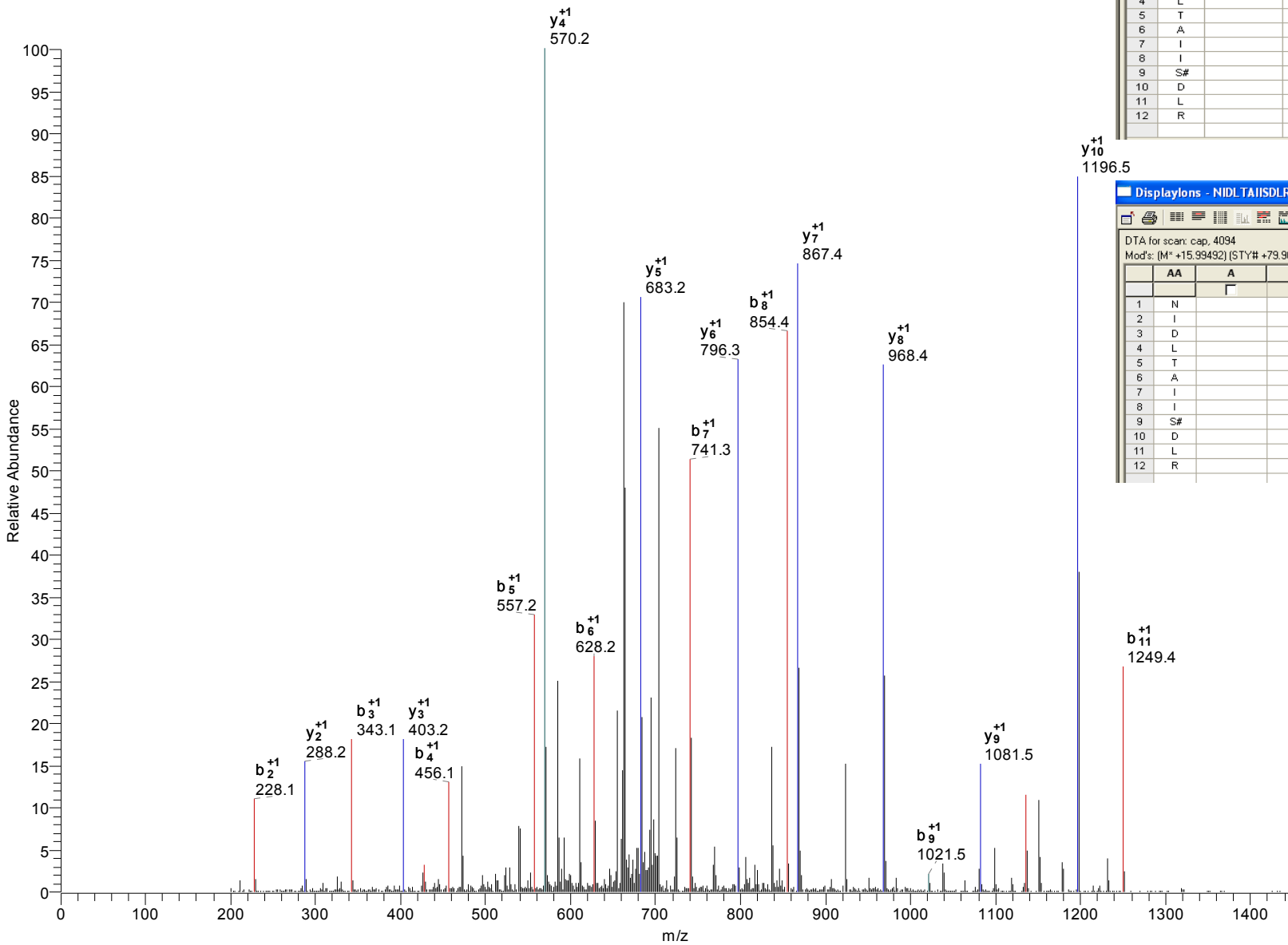
Displaylons - NGVTSLTQK

DTA for scan: driedcapac, 1659
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	N		58.03	-		9
2	G		86.54	497.21		8
3	V		136.07	468.70		7
4	T#		226.58	419.16		6
5	S		270.10	328.65		5
6	L		326.64	285.14		4
7	T#		417.15	228.60		3
8	Q		481.18	138.09		2
9	K		-	74.06		1

Odf2 Isoform 3 of Outer dense fiber protein 2

#4094-4094 NL: 1.32E4



Displaylons - NIDLTAIISDLR

DTA for scan: cap. 4094
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	12
2	I		228.13	1309.68	11
3	D		343.16	1196.59	10
4	L		456.25	1081.57	9
5	T		557.29	968.48	8
6	A		628.33	867.43	7
7	I		741.41	796.40	6
8	I		854.50	683.31	5
9	S#		1021.50	570.23	4
10	D		1136.52	403.23	3
11	L		1249.61	288.20	2
12	R		-	175.12	1

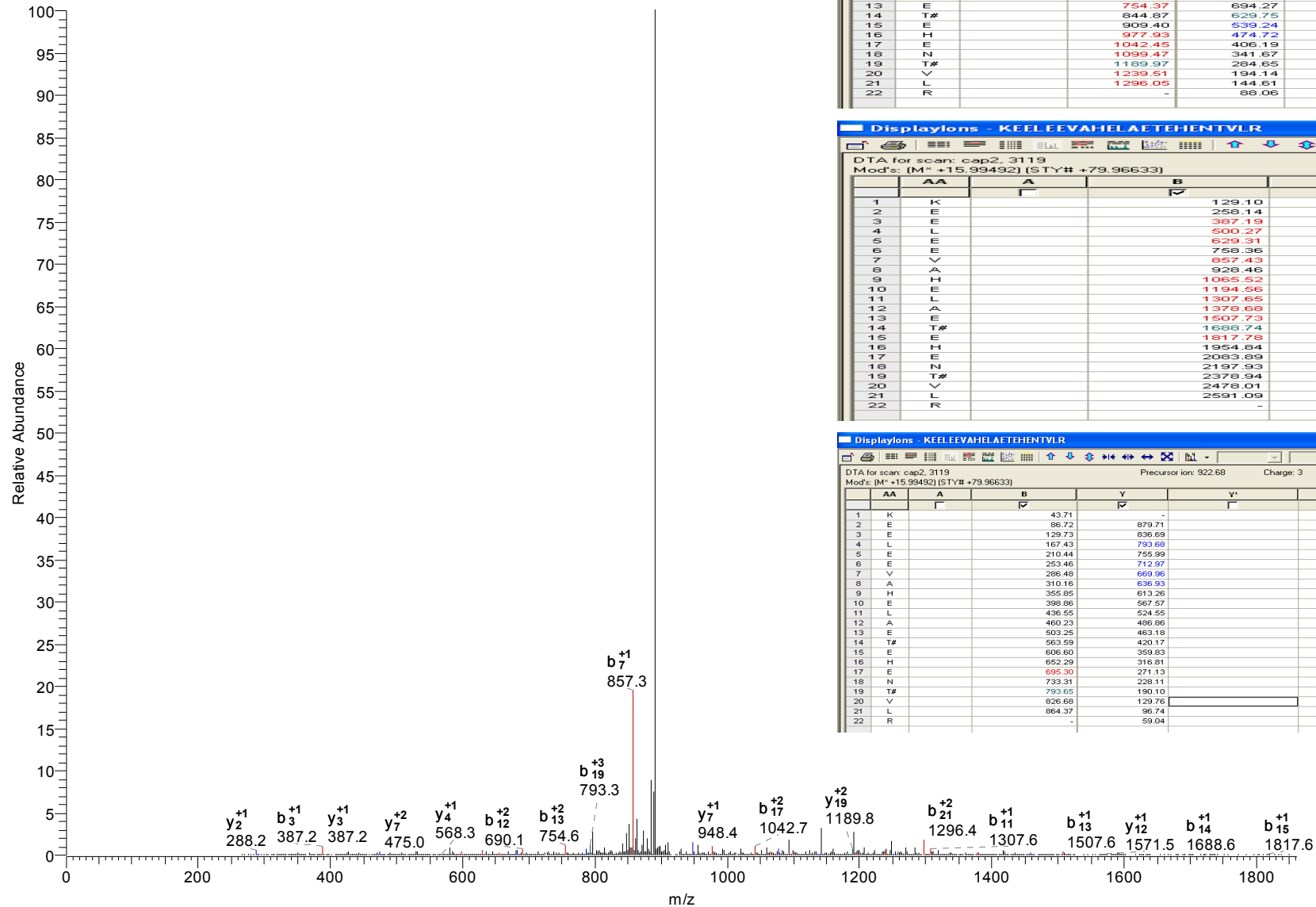
Displaylons - NIDLTAIISDLR

DTA for scan: cap. 4094
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	N		58.03	-		12
2	I		114.57	655.34		11
3	D		172.08	598.80		10
4	L		228.63	541.29		9
5	T		279.15	484.74		8
6	A		314.67	434.22		7
7	I		371.21	398.70		6
8	I		427.75	342.16		5
9	S#		511.25	285.62		4
10	D		568.77	202.12		3
11	L		625.31	144.61		2
12	R		-	88.06		1

Odf2 Isoform 3 of Outer dense fiber protein 2

#3119-3119 NL: 1.26E5



Displayions - KEEL E V A H E L A E T H E N T V L R

DTA for scan: cap2. 3119
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	K		65.05	-		22
2	E		129.58	1319.06		21
3	L		194.10	1254.54		20
4	L		250.64	1190.02		19
5	E		315.16	1133.47		18
6	E		379.68	1068.95		17
7	V		429.22	1004.43		16
8	A		484.73	954.90		15
9	H		533.26	919.38		14
10	E		597.79	850.85		13
11	L		654.33	786.33		12
12	A		689.85	729.79		11
13	E		754.37	694.27		10
14	T#		844.87	629.75		9
15	E		909.40	539.24		8
16	H		977.93	474.72		7
17	E		1042.46	406.19		6
18	N		1099.47	341.67		5
19	T#		1189.97	284.65		4
20	V		1239.51	194.14		3
21	L		1296.05	144.61		2
22	R		-	86.06		1

Displayions - KEEL E V A H E L A E T H E N T V L R

DTA for scan: cap2. 3119
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y		
1	K			129.10	-	22
2	E			258.14	2637.11	21
3	E			387.19	2509.07	20
4	L			500.27	2379.03	19
5	E			629.31	2265.94	18
6	E			758.36	2136.90	17
7	V			857.43	2007.86	16
8	A			926.46	1908.79	15
9	H			1065.52	1837.75	14
10	E			1194.56	1700.69	13
11	L			1307.65	1571.65	12
12	A			1375.68	1458.57	11
13	E			1507.73	1387.53	10
14	T#			1688.74	1258.49	9
15	H			1817.78	1077.47	8
16	H			1954.84	948.43	7
17	E			2083.89	811.37	6
18	N			2197.93	682.33	5
19	T#			2378.94	568.29	4
20	V			2478.01	387.27	3
21	L			2591.09	288.20	2
22	R			-	175.12	1

Displayions - KEEL E V A H E L A E T H E N T V L R

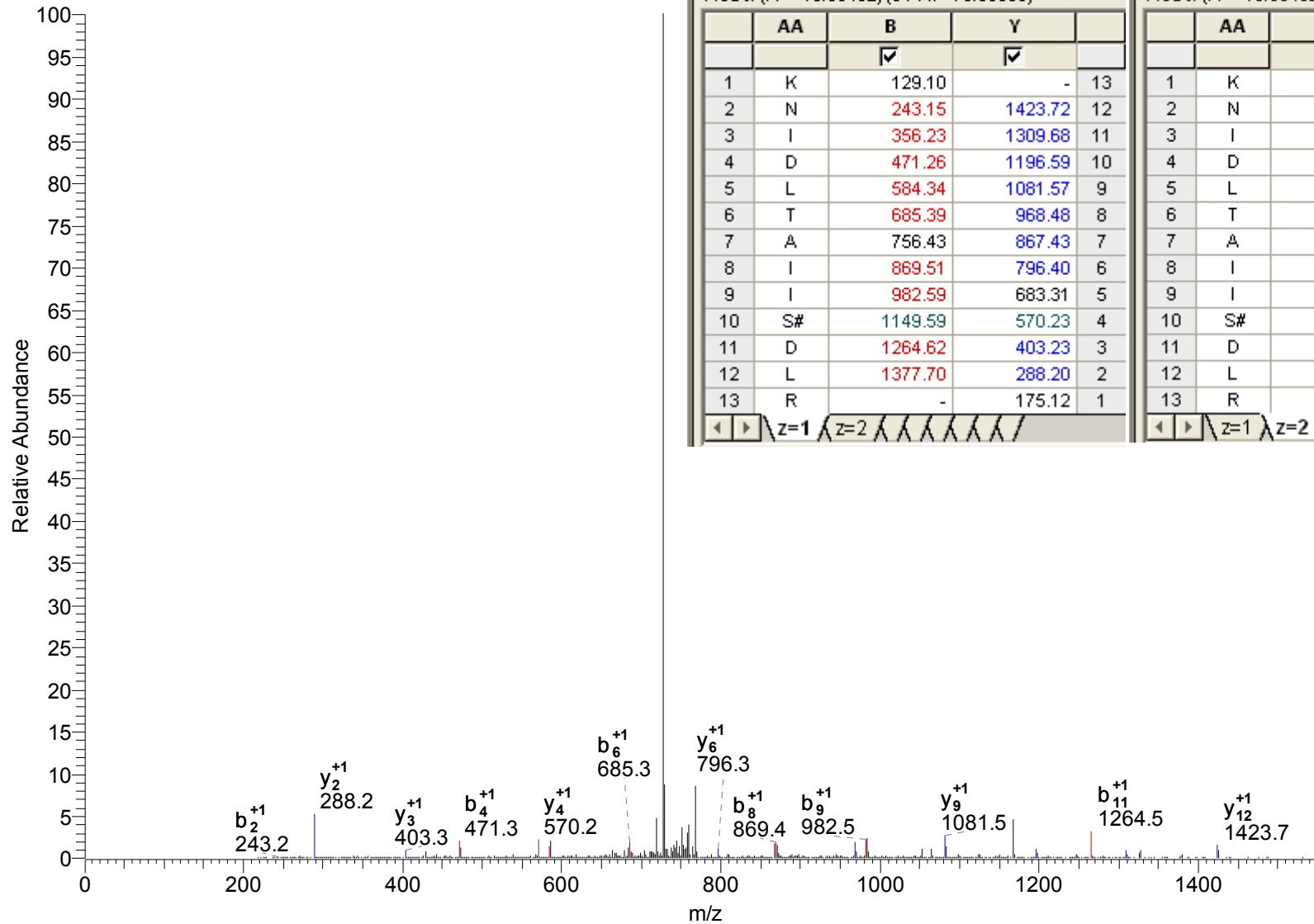
DTA for scan: cap2. 3119
Mod's: (M⁺ +15.99492) (STY# +79.96633)

Precursor ion: 922.68 Charge: 3 Activation type: CID

	AA	A	B	Y	Y*	Yo	Z	
1	K		43.71	-				22
2	E		86.72	879.71				21
3	E		129.73	836.69				20
4	L		167.43	793.68				19
5	E		210.44	755.99				18
6	E		253.46	712.97				17
7	V		286.48	669.96				16
8	A		310.16	636.93				15
9	H		355.65	613.26				14
10	E		398.86	567.57				13
11	L		436.55	524.55				12
12	A		460.23	486.86				11
13	E		503.25	463.18				10
14	T#		563.59	420.17				9
15	E		606.60	359.83				8
16	H		652.29	316.81				7
17	E		695.30	271.13				6
18	N		733.31	228.11				5
19	T#		793.65	190.10				4
20	V		826.68	129.78				3
21	L		864.37	96.74				2
22	R		-	59.04				1

Odf2 Isoform 3 of Outer dense fiber protein 2

#3934-3934 NL: 1.86E4

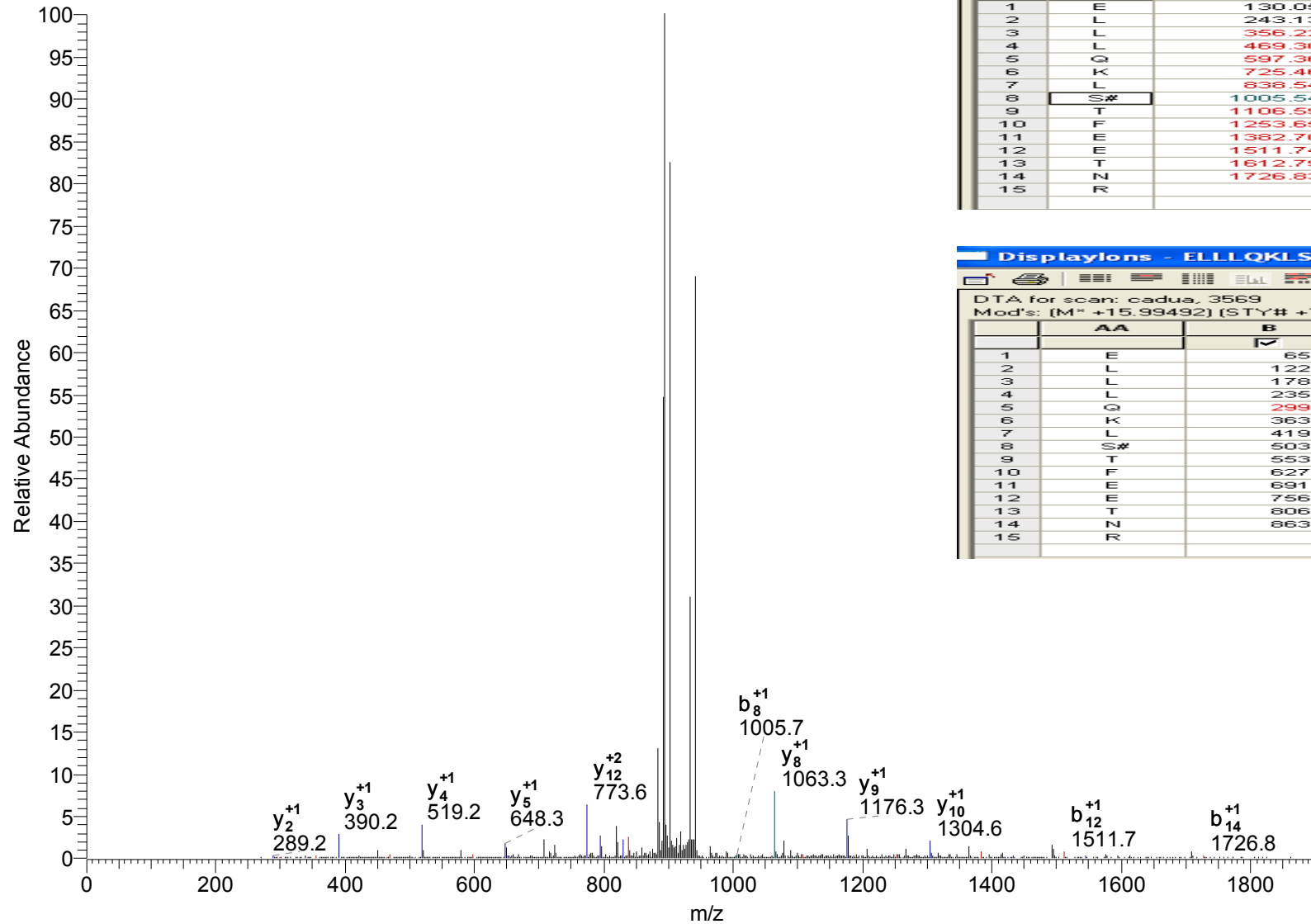


Displaylons - KNIDLTAISDLR				
DTA for scan: cap, 3934				
Mod's: (M* +15.99492) (STY# +79.96633)				
	AA	B	Y	
		☒	☒	
1	K	129.10	-	13
2	N	243.15	1423.72	12
3	I	356.23	1309.68	11
4	D	471.26	1196.59	10
5	L	584.34	1081.57	9
6	T	685.39	968.48	8
7	A	756.43	867.43	7
8	I	869.51	796.40	6
9	I	982.59	683.31	5
10	S#	1149.59	570.23	4
11	D	1264.62	403.23	3
12	L	1377.70	288.20	2
13	R	-	175.12	1
z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13				

Displaylons - KNIDLTAISDLR				
DTA for scan: cap, 3934				
Mod's: (M* +15.99492) (STY# +79.96633)				
	AA	B	Y	
		☒	☒	
1	K	65.05	-	13
2	N	122.08	712.36	12
3	I	178.62	655.34	11
4	D	236.13	598.80	10
5	L	292.67	541.29	9
6	T	343.20	484.74	8
7	A	378.72	434.22	7
8	I	435.26	398.70	6
9	I	491.80	342.16	5
10	S#	575.30	285.62	4
11	D	632.81	202.12	3
12	L	689.35	144.61	2
13	R	-	88.06	1
z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13				

Odf2 Isoform 3 of Outer dense fiber protein 2

#3569-3569 NL: 2.65E4



Displaylons - ELLQKLSTFEETNR

DTA for scan: cadua, 3569
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	E	130.05	-	15
2	L	243.13	1771.90	14
3	L	356.22	1658.81	13
4	L	469.30	1545.73	12
5	Q	582.36	1432.65	11
6	K	695.44	1304.59	10
7	L	808.52	1176.49	9
8	S#	921.60	1063.41	8
9	T	1034.68	896.41	7
10	F	1147.76	795.36	6
11	E	1260.84	648.29	5
12	E	1373.92	519.25	4
13	T	1487.00	390.21	3
14	N	1600.08	289.16	2
15	R	1713.16	175.12	1

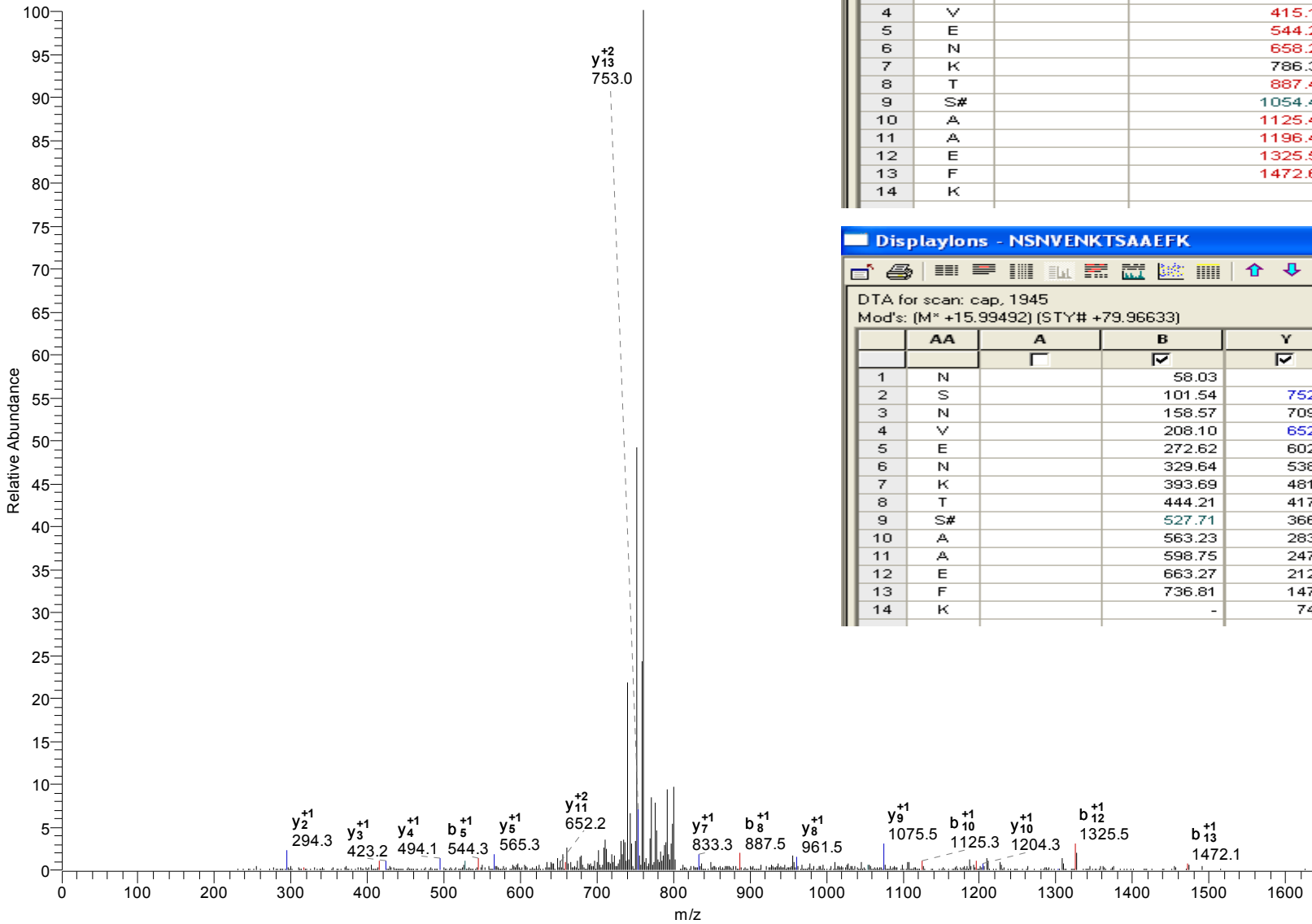
Displaylons - ELLQKLSTFEETNR

DTA for scan: cadua, 3569
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	E	65.53	-	15
2	L	122.07	886.45	14
3	L	178.61	829.91	13
4	L	235.15	773.37	12
5	Q	291.69	716.83	11
6	K	348.23	652.80	10
7	L	404.77	588.75	9
8	S#	461.31	532.21	8
9	T	517.85	448.71	7
10	F	574.39	398.19	6
11	E	630.93	324.65	5
12	E	687.47	260.13	4
13	T	744.01	195.61	3
14	N	800.55	145.08	2
15	R	857.09	88.06	1

Izumo sperm-egg fusion protein 1 precursor

#1945-1945 NL: 5.65E3

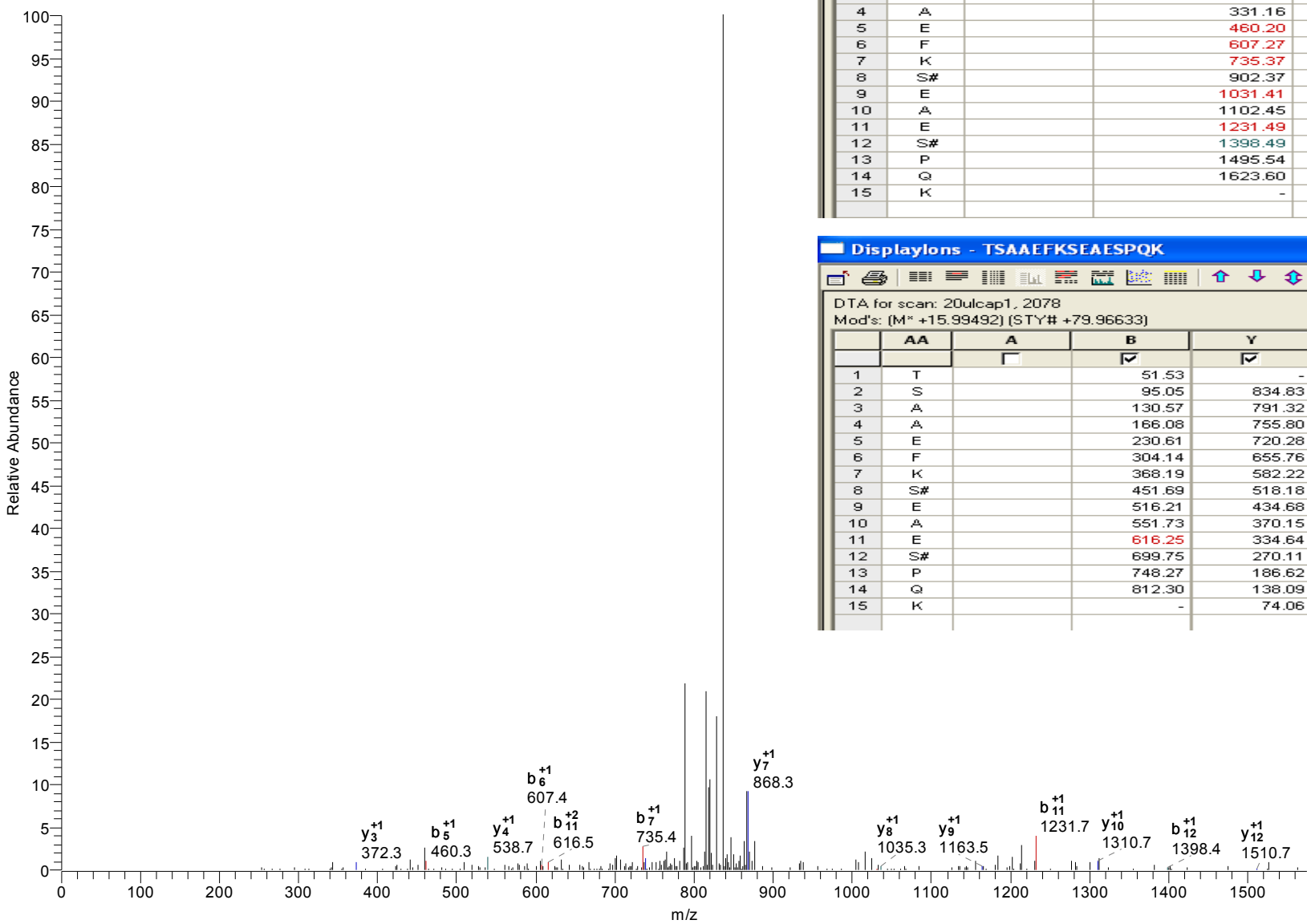


Displaylons - NSNVENKTSAAEFK						
DTA for scan: cap. 1945						
Mod's: (M* +15.99492) (STY# +79.96633)						
	AA	A	B	Y		
1	N		115.05	-	14	
2	S		202.08	1504.67	13	
3	N		316.13	1417.64	12	
4	V		415.19	1303.59	11	
5	E		544.24	1204.52	10	
6	N		658.28	1075.48	9	
7	K		786.37	961.44	8	
8	T		887.42	833.34	7	
9	S#		1054.42	732.30	6	
10	A		1125.46	565.30	5	
11	A		1196.49	494.26	4	
12	E		1325.54	423.22	3	
13	F		1472.61	294.18	2	
14	K		-	147.11	1	

Displaylons - NSNVENKTSAAEFK						
DTA for scan: cap. 1945						
Mod's: (M* +15.99492) (STY# +79.96633)						
	AA	A	B	Y	Z	
1	N		58.03	-		14
2	S		101.54	752.84		13
3	N		158.57	709.32		12
4	V		208.10	652.30		11
5	E		272.62	602.77		10
6	N		329.64	538.24		9
7	K		393.69	481.22		8
8	T		444.21	417.18		7
9	S#		527.71	366.65		6
10	A		563.23	283.15		5
11	A		598.75	247.63		4
12	E		663.27	212.12		3
13	F		736.81	147.59		2
14	K		-	74.06		1

Izumo sperm-egg fusion protein 1 precursor

#2078-2078 NL: 1.02E3

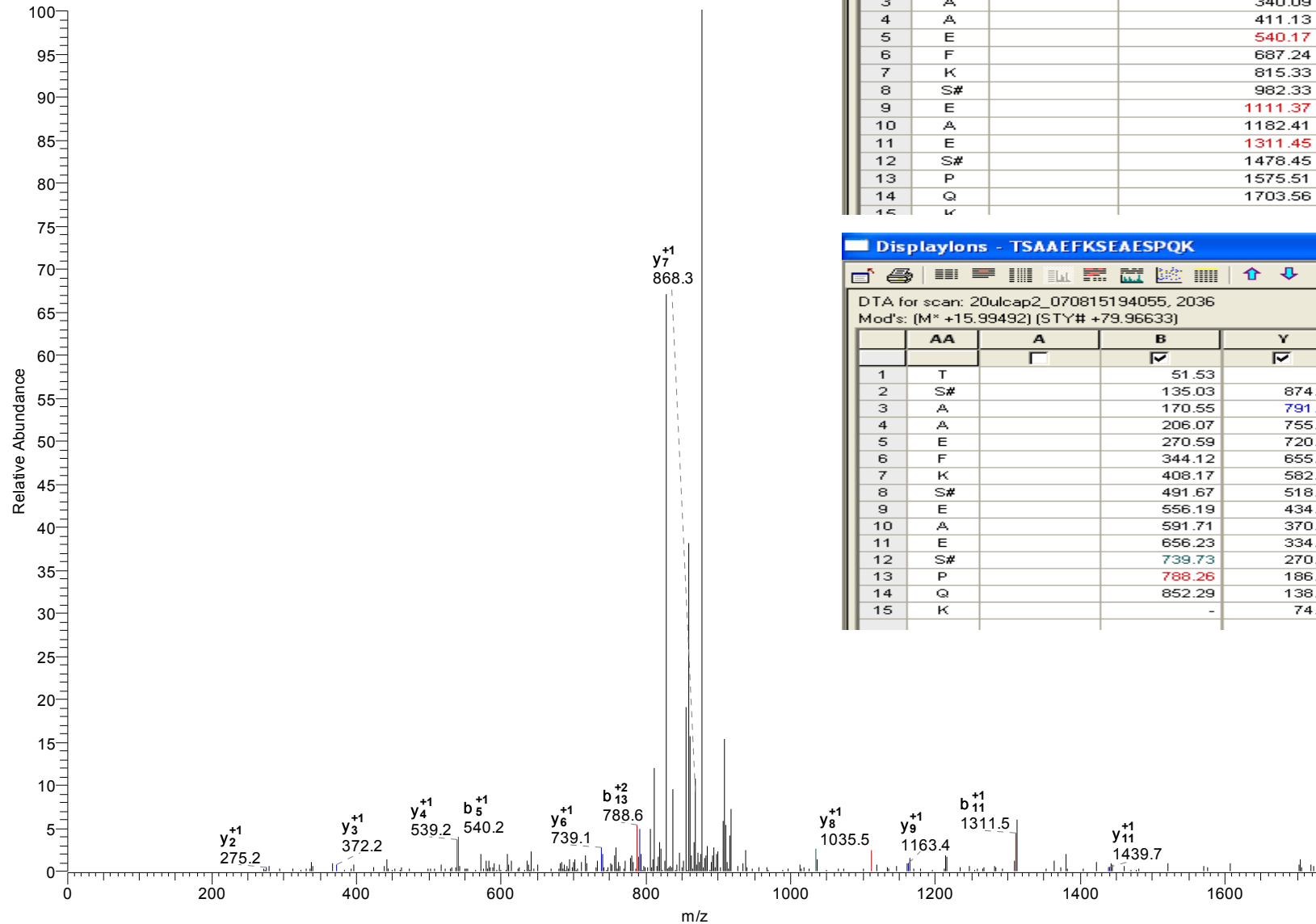


Displaylons - TSAAEFKSEAESPQK					
DTA for scan: 20ulcap1, 2078					
Mod's: (M* +15.99492) (STY# +79.96633)					
	AA	A	B	Y	
1	T		102.05	-	15
2	S		189.09	1668.66	14
3	A		260.12	1581.62	13
4	A		331.16	1510.59	12
5	E		460.20	1439.55	11
6	F		607.27	1310.51	10
7	K		735.37	1163.44	9
8	S#		902.37	1035.34	8
9	E		1031.41	868.34	7
10	A		1102.45	739.30	6
11	E		1231.49	668.27	5
12	S#		1398.49	539.22	4
13	P		1495.54	372.22	3
14	Q		1623.60	275.17	2
15	K		-	147.11	1

Displaylons - TSAAEFKSEAESPQK					
DTA for scan: 20ulcap1, 2078					
Mod's: (M* +15.99492) (STY# +79.96633)					
	AA	A	B	Y	Z
1	T		51.53	-	15
2	S		95.05	834.83	14
3	A		130.57	791.32	13
4	A		166.08	755.80	12
5	E		230.61	720.28	11
6	F		304.14	655.76	10
7	K		368.19	582.22	9
8	S#		451.69	518.18	8
9	E		516.21	434.68	7
10	A		551.73	370.15	6
11	E		616.25	334.64	5
12	S#		699.75	270.11	4
13	P		748.27	186.62	3
14	Q		812.30	138.09	2
15	K		-	74.06	1

Izumo sperm-egg fusion protein 1 precursor

#2036-2036 NL: 8.37E2



DisplayIons - TSAAEFKSEAESPQK

DTA for scan: 20ulcap2_070815194055_2036
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	T		102.05	-	15
2	S#		269.05	1748.62	14
3	A		340.09	1581.62	13
4	A		411.13	1510.59	12
5	E		540.17	1439.55	11
6	F		687.24	1310.51	10
7	K		815.33	1163.44	9
8	S#		982.33	1035.34	8
9	E		1111.37	868.34	7
10	A		1182.41	739.30	6
11	E		1311.45	668.27	5
12	S#		1478.45	539.22	4
13	P		1575.51	372.22	3
14	Q		1703.56	275.17	2
15	K			147.11	1

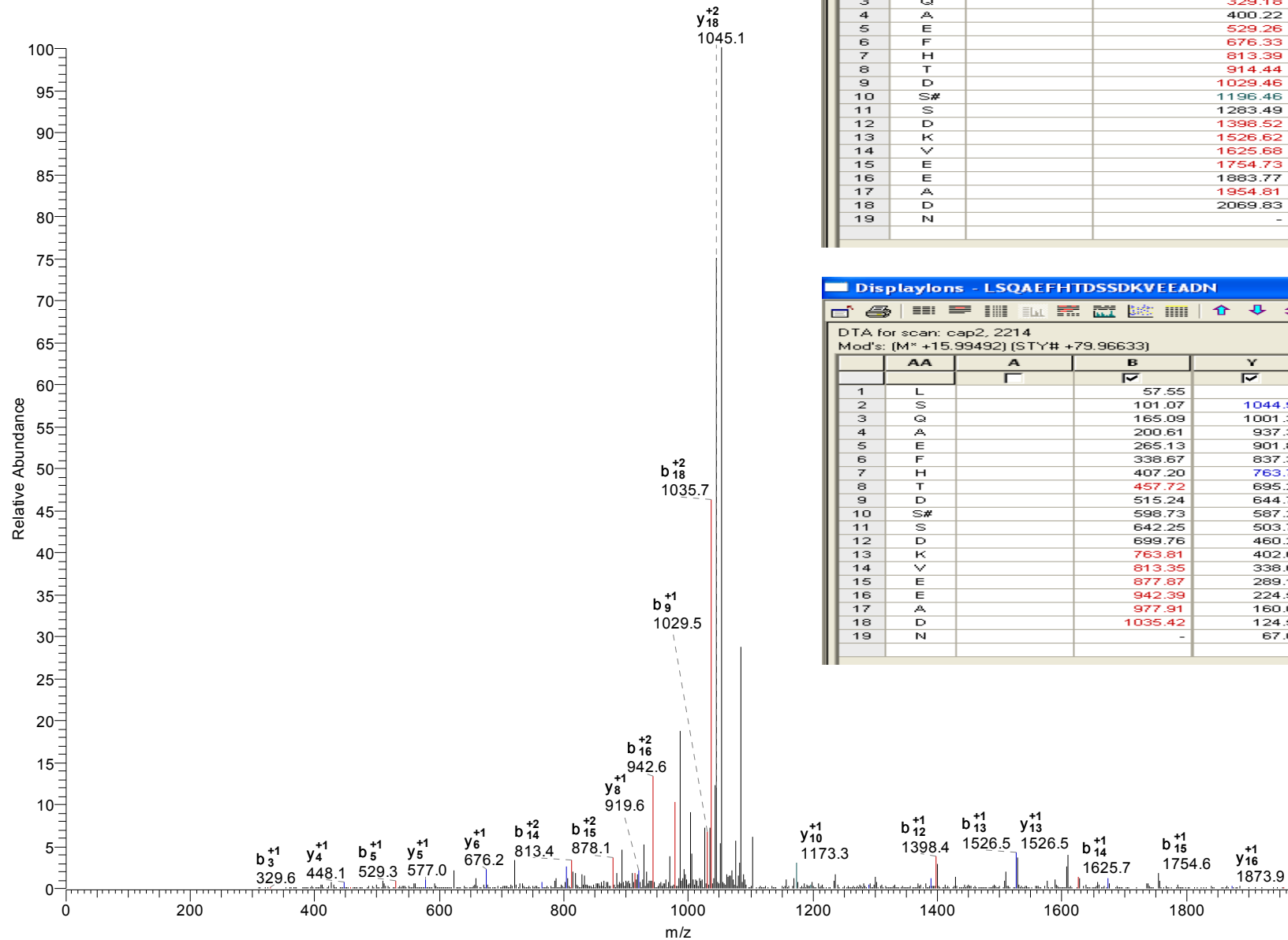
DisplayIons - TSAAEFKSEAESPQK

DTA for scan: 20ulcap2_070815194055_2036
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	T		51.53	-		15
2	S#		135.03	874.81		14
3	A		170.55	791.32		13
4	A		206.07	755.80		12
5	E		270.59	720.28		11
6	F		344.12	655.76		10
7	K		408.17	582.22		9
8	S#		491.67	518.18		8
9	E		556.19	434.68		7
10	A		591.71	370.15		6
11	E		656.23	334.64		5
12	S#		739.73	270.11		4
13	P		788.26	186.62		3
14	Q		852.29	138.09		2
15	K		-	74.06		1

Izumo sperm-egg fusion protein 1 precursor

#2214-2214 NL: 7.54E3



Displaylons - LSQAEFHTDSSDKVEEADN

DTA for scan: cap2, 2214
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L		114.09	-	19
2	S		201.12	2088.80	18
3	Q		329.18	2001.77	17
4	A		400.22	1873.71	16
5	E		529.26	1802.68	15
6	F		676.33	1673.63	14
7	H		813.39	1526.56	13
8	T		914.44	1389.51	12
9	D		1029.46	1288.46	11
10	S#		1196.46	1173.43	10
11	S		1283.49	1006.43	9
12	D		1398.52	919.40	8
13	K		1526.62	804.37	7
14	V		1625.68	676.28	6
15	E		1754.73	577.21	5
16	E		1883.77	448.17	4
17	A		1954.81	319.12	3
18	D		2069.83	248.09	2
19	N		-	133.06	1

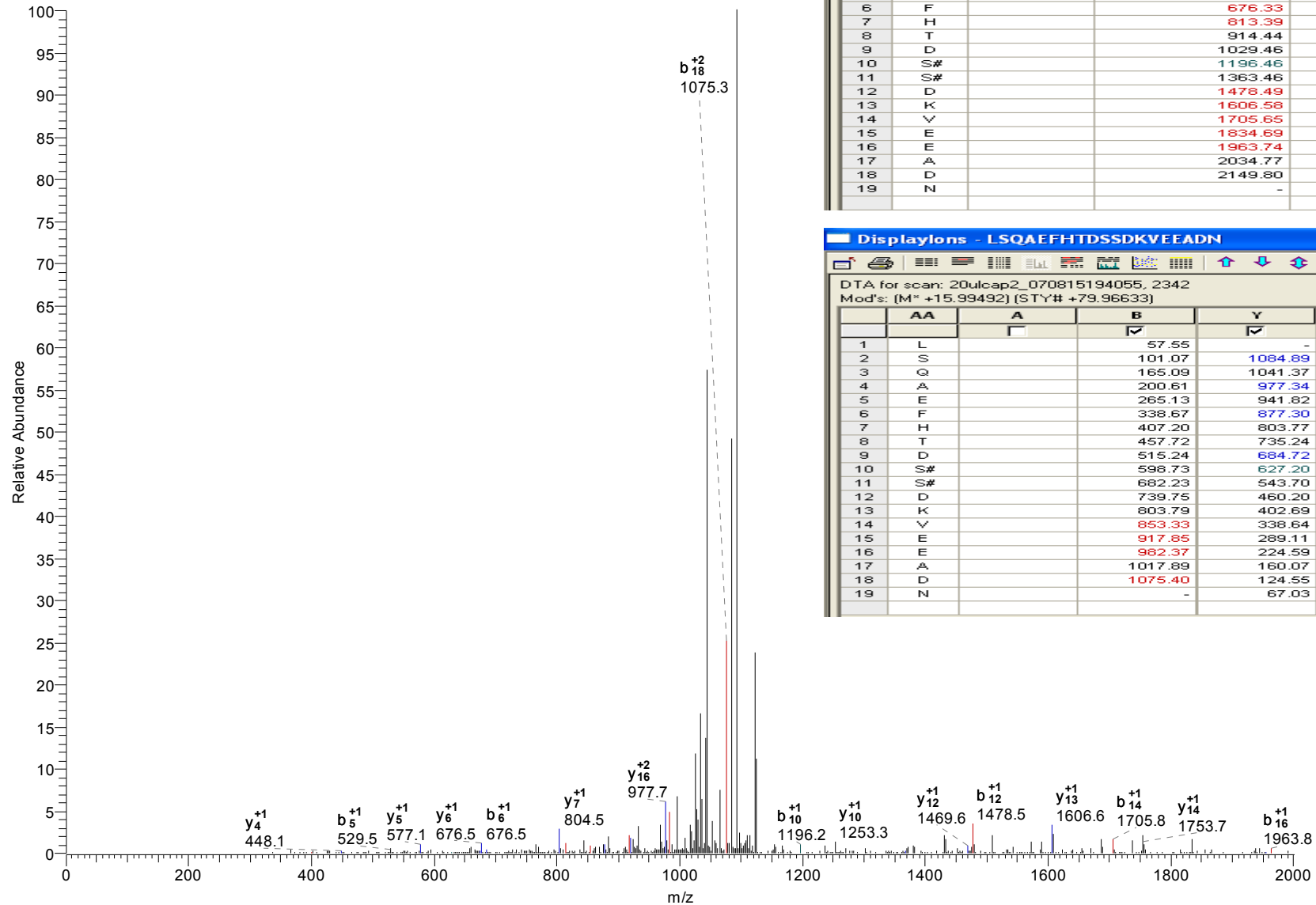
Displaylons - LSQAEFHTDSSDKVEEADN

DTA for scan: cap2, 2214
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L		57.55	-	-	19
2	S		101.07	1044.91	-	18
3	Q		165.09	1001.39	-	17
4	A		200.61	937.36	-	16
5	E		265.13	901.84	-	15
6	F		338.67	837.32	-	14
7	H		407.20	763.79	-	13
8	T		457.72	695.26	-	12
9	D		515.24	644.73	-	11
10	S#		598.73	587.22	-	10
11	S		642.25	503.72	-	9
12	D		699.76	460.20	-	8
13	K		763.81	402.69	-	7
14	V		813.35	338.64	-	6
15	E		877.87	289.11	-	5
16	E		942.39	224.59	-	4
17	A		977.91	160.07	-	3
18	D		1035.42	124.55	-	2
19	N		-	67.03	-	1

Izumo sperm-egg fusion protein 1 precursor

#2342-2342 NL: 3.42E3



Displaylons - LSQAEFHTDSSDKVEEADN

DTA for scan: 20ulcap2_070815194055_2342
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L			114.09	-
2	S			201.12	2168.77
3	Q			329.18	2081.74
4	A			400.22	1953.68
5	E			529.26	1882.64
6	F			676.33	1753.60
7	H			813.39	1606.53
8	T			914.44	1469.47
9	D			1029.46	1368.42
10	S#			1196.46	1253.40
11	S#			1363.46	1086.40
12	D			1478.49	919.40
13	K			1606.58	804.37
14	V			1705.65	676.28
15	E			1834.69	577.21
16	E			1963.74	448.17
17	A			2034.77	319.12
18	D			2149.80	248.09
19	N			-	133.06

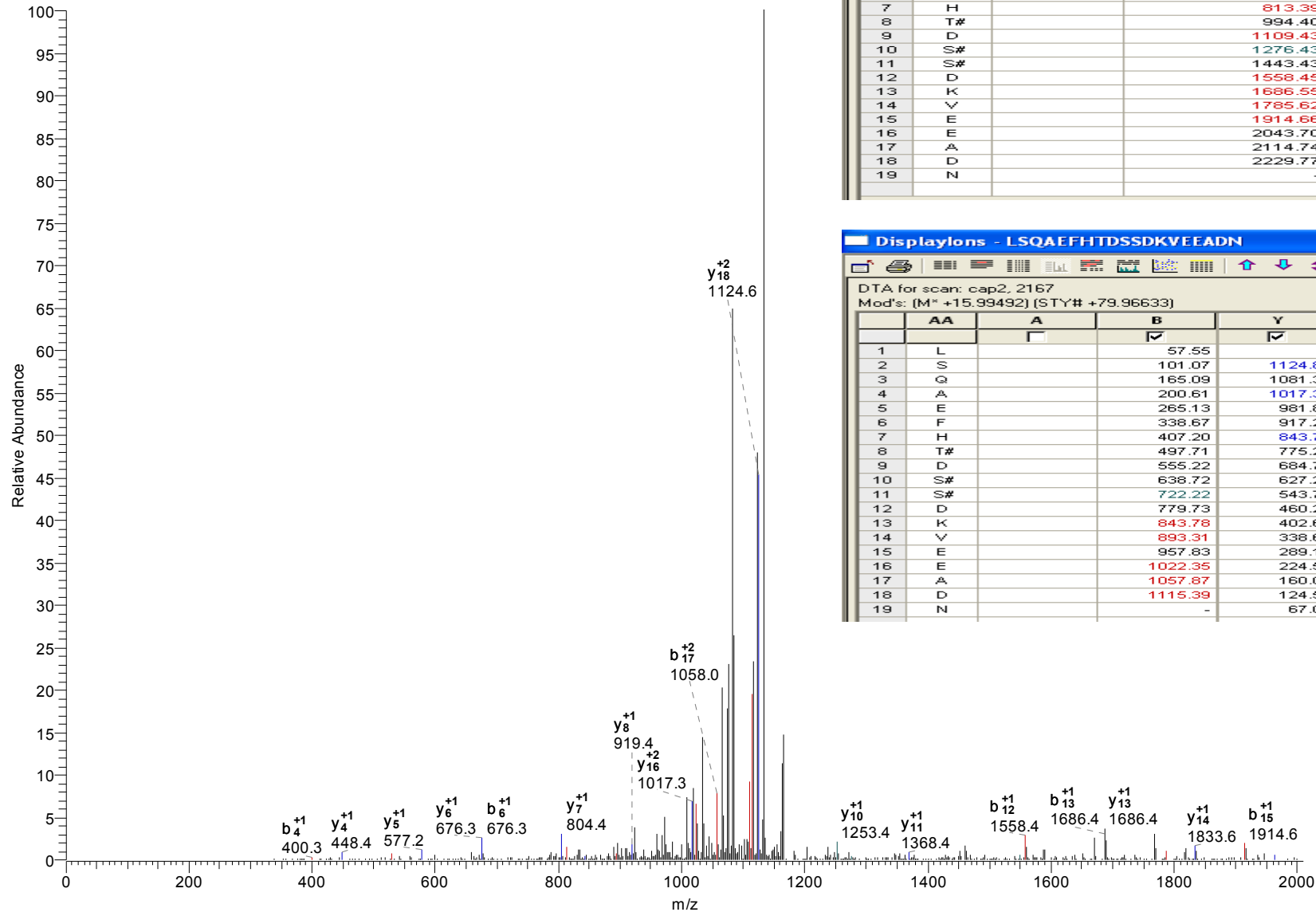
Displaylons - LSQAEFHTDSSDKVEEADN

DTA for scan: 20ulcap2_070815194055_2342
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z
1	L			57.55	-
2	S			101.07	1084.89
3	Q			165.09	1041.37
4	A			200.61	977.34
5	E			265.13	941.82
6	F			338.67	877.30
7	H			407.20	803.77
8	T			457.72	735.24
9	D			515.24	684.72
10	S#			598.73	627.20
11	S#			682.23	543.70
12	D			739.75	460.20
13	K			803.79	402.69
14	V			853.33	338.64
15	E			917.85	289.11
16	E			982.37	224.59
17	A			1017.89	160.07
18	D			1075.40	124.55
19	N			-	67.03

Izumo sperm-egg fusion protein 1 precursor

#2167-2167 NL: 4.37E3



Displaylons - LSQAEFHTDSSDKVEEADN

DTA for scan: cap2, 2167
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	L		114.09	-	19
2	S		201.12	2248.74	18
3	Q		329.18	2161.70	17
4	A		400.22	2033.65	16
5	E		529.26	1962.61	15
6	F		676.33	1833.57	14
7	H		813.39	1686.50	13
8	T#		994.40	1549.44	12
9	D		1109.43	1368.42	11
10	S#		1276.43	1253.40	10
11	S#		1443.43	1086.40	9
12	D		1558.45	919.40	8
13	K		1686.55	804.37	7
14	V		1785.62	676.28	6
15	E		1914.66	577.21	5
16	E		2043.70	448.17	4
17	A		2114.74	319.12	3
18	D		2229.77	248.09	2
19	N		-	133.06	1

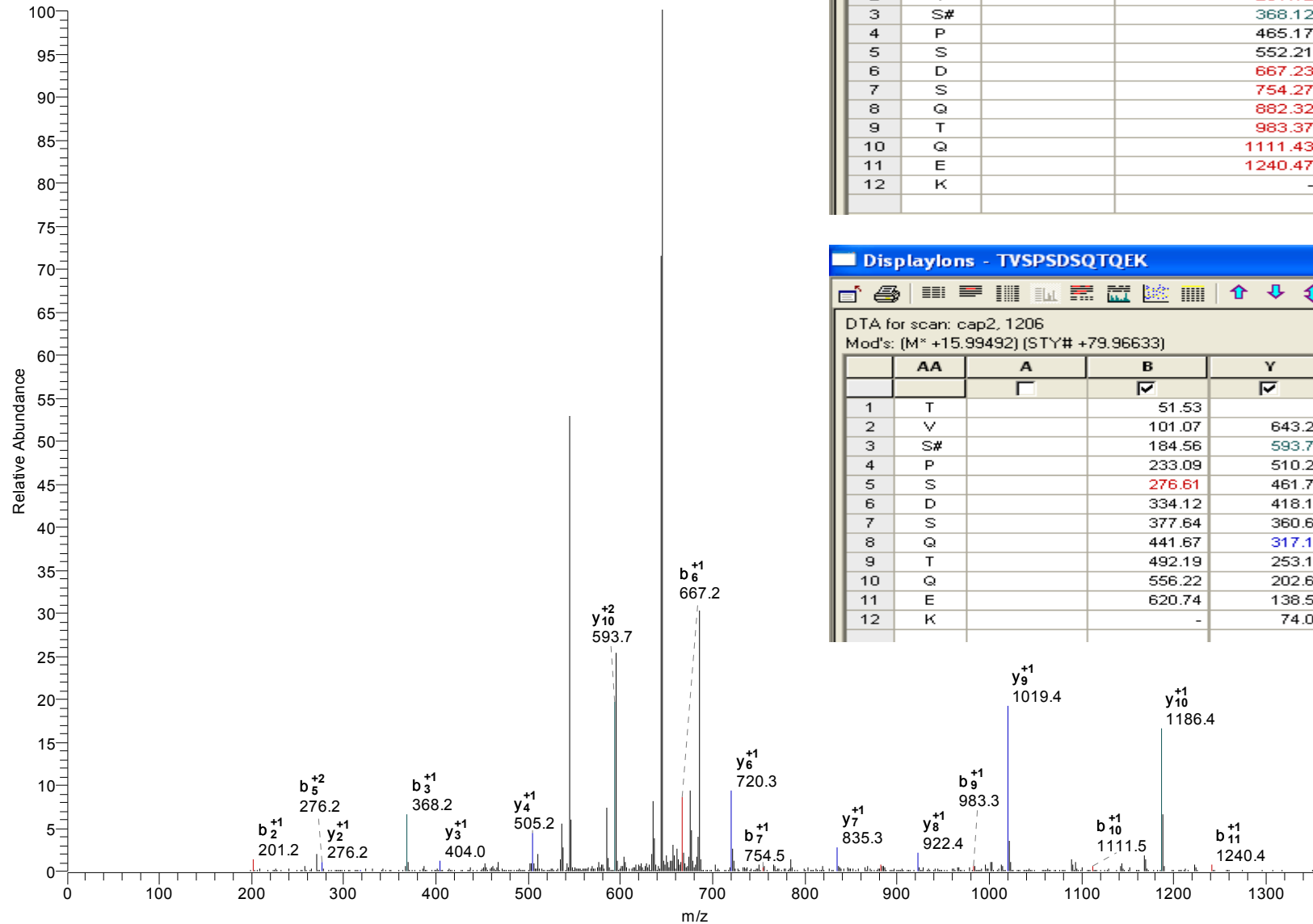
Displaylons - LSQAEFHTDSSDKVEEADN

DTA for scan: cap2, 2167
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	L		57.55	-		19
2	S		101.07	1124.87		18
3	Q		165.09	1081.36		17
4	A		200.61	1017.33		16
5	E		265.13	981.81		15
6	F		338.67	917.29		14
7	H		407.20	843.75		13
8	T#		497.71	775.22		12
9	D		555.22	684.72		11
10	S#		638.72	627.20		10
11	S#		722.22	543.70		9
12	D		779.73	460.20		8
13	K		843.78	402.69		7
14	V		893.31	338.64		6
15	E		957.83	289.11		5
16	E		1022.35	224.59		4
17	A		1057.87	160.07		3
18	D		1115.39	124.55		2
19	N		-	67.03		1

Uncharacterized protein C2orf57 homolog

#1206-1206 NL: 6.02E3



Displaylons - TVSPSDSQTQEK

DTA for scan: cap2, 1206
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	T		102.05	-	12
2	V		201.12	1285.53	11
3	S#		368.12	1186.46	10
4	P		465.17	1019.46	9
5	S		552.21	922.41	8
6	D		667.23	835.38	7
7	S		754.27	720.35	6
8	Q		882.32	633.32	5
9	T		983.37	505.26	4
10	Q		1111.43	404.21	3
11	E		1240.47	276.16	2
12	K		-	147.11	1

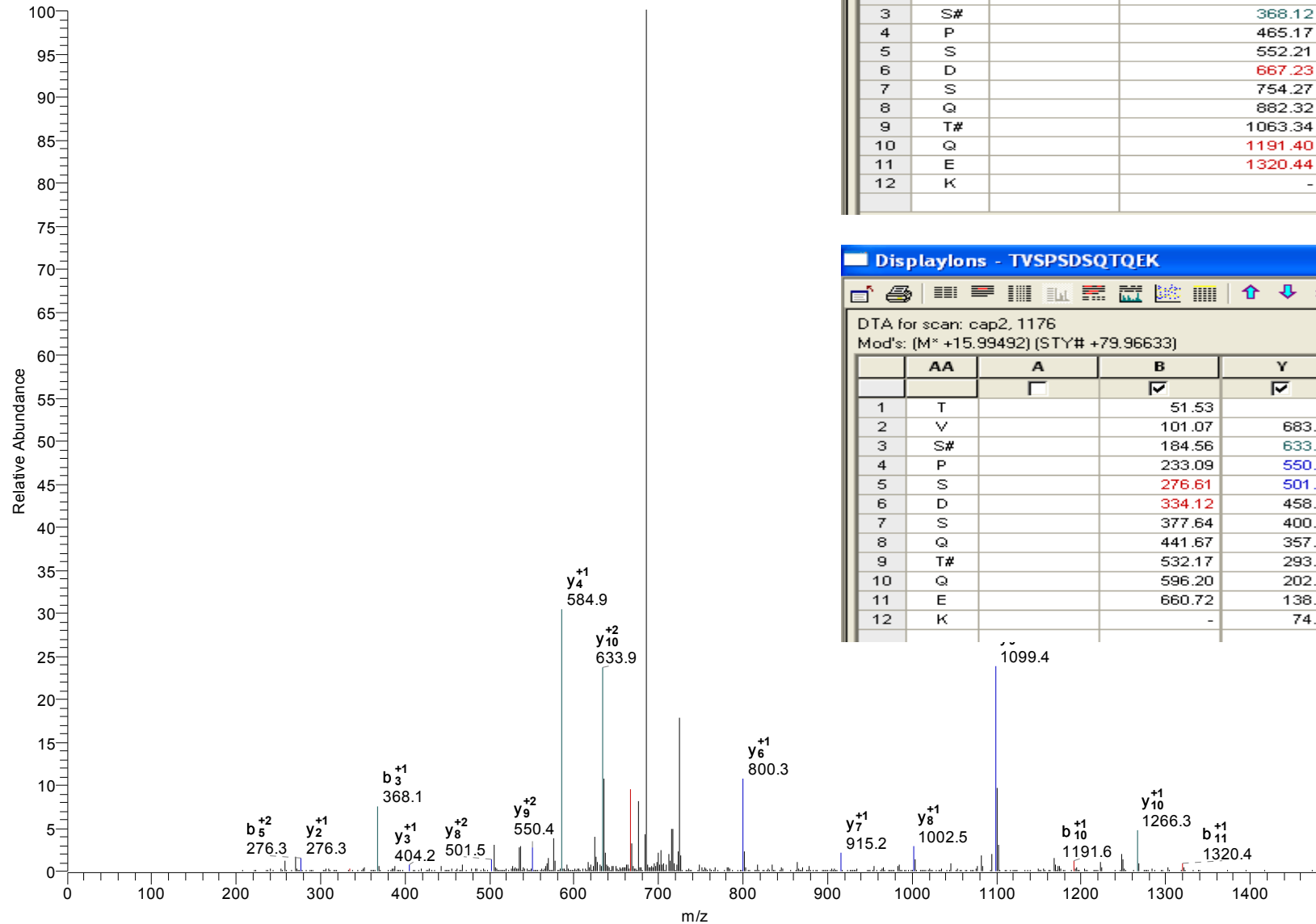
Displaylons - TVSPSDSQTQEK

DTA for scan: cap2, 1206
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	T		51.53	-		12
2	V		101.07	643.27		11
3	S#		184.56	593.73		10
4	P		233.09	510.24		9
5	S		276.61	461.71		8
6	D		334.12	418.19		7
7	S		377.64	360.68		6
8	Q		441.67	317.16		5
9	T		492.19	253.13		4
10	Q		556.22	202.61		3
11	E		620.74	138.58		2
12	K		-	74.06		1

Uncharacterized protein C2orf57 homolog

#1176-1176 NL: 6.29E3



Displaylons - TVSPSDSQTQEK

DTA for scan: cap2, 1176
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	T		102.05	-	12
2	V		201.12	1365.50	11
3	S#		368.12	1266.43	10
4	P		465.17	1099.43	9
5	S		552.21	1002.38	8
6	D		667.23	915.35	7
7	S		754.27	800.32	6
8	Q		882.32	713.29	5
9	T#		1063.34	585.23	4
10	Q		1191.40	404.21	3
11	E		1320.44	276.16	2
12	K		-	147.11	1

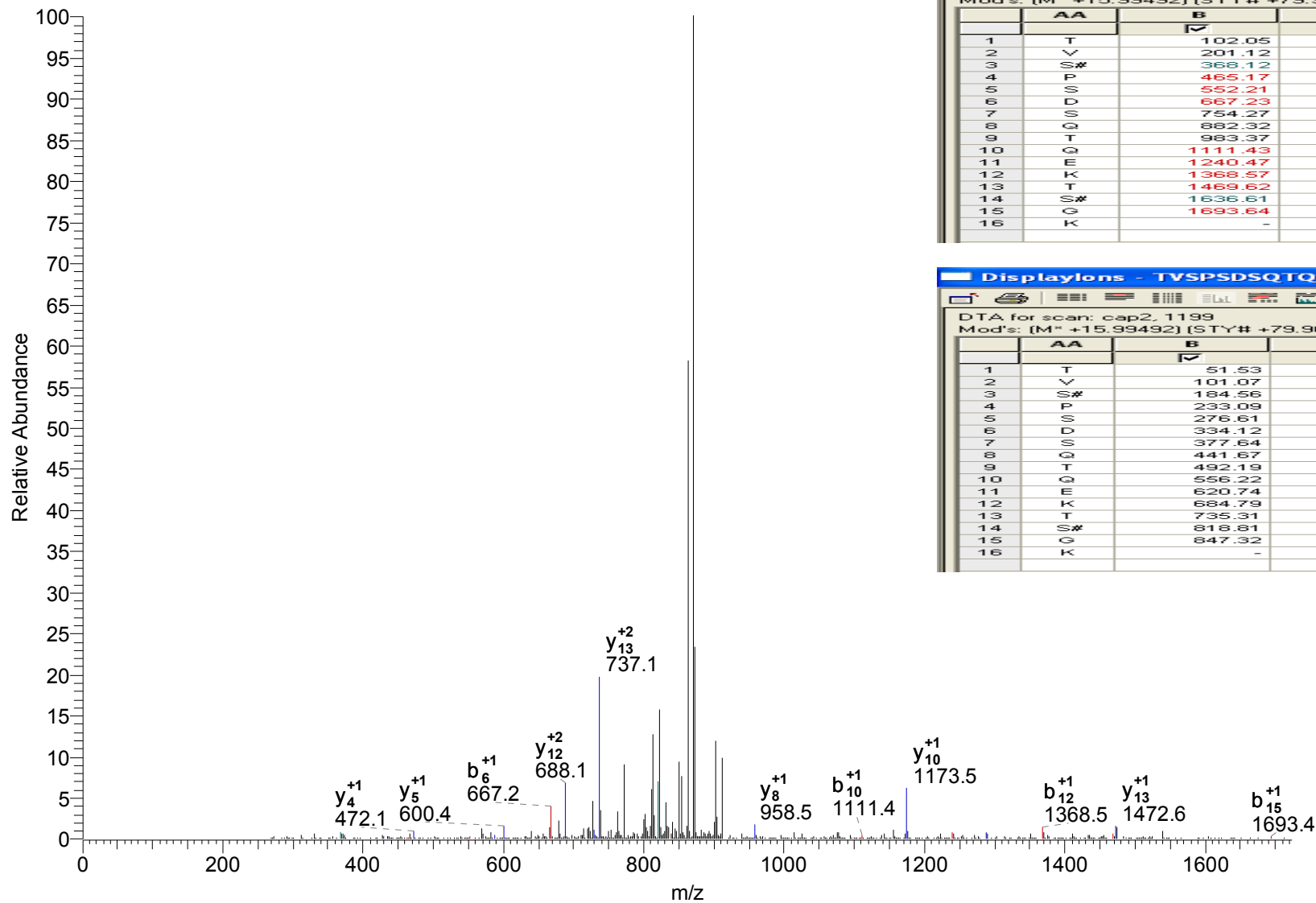
Displaylons - TVSPSDSQTQEK

DTA for scan: cap2, 1176
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	T		51.53	-		12
2	V		101.07	683.25		11
3	S#		184.56	633.72		10
4	P		233.09	550.22		9
5	S		276.61	501.69		8
6	D		334.12	458.18		7
7	S		377.64	400.66		6
8	Q		441.67	357.15		5
9	T#		532.17	293.12		4
10	Q		596.20	202.61		3
11	E		660.72	138.58		2
12	K		-	74.06		1

Uncharacterised protein C2orf57 homolog

#1199-1199 NL: 1.02E4



Displaylons - TVSPSDSQTQEKTSQK

DTA for scan: cap2, 1199
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	T	102.05	-	16
2	V	201.12	1738.69	15
3	S#	368.12	1639.62	14
4	P	465.17	1472.63	13
5	S	552.21	1375.57	12
6	D	667.23	1288.54	11
7	S	754.27	1173.51	10
8	Q	882.32	1086.48	9
9	T	983.37	958.42	8
10	Q	1111.43	857.38	7
11	E	1240.47	729.32	6
12	K	1368.57	600.28	5
13	T	1469.62	472.18	4
14	S#	1636.61	371.13	3
15	G	1693.64	204.13	2
16	K	-	147.11	1

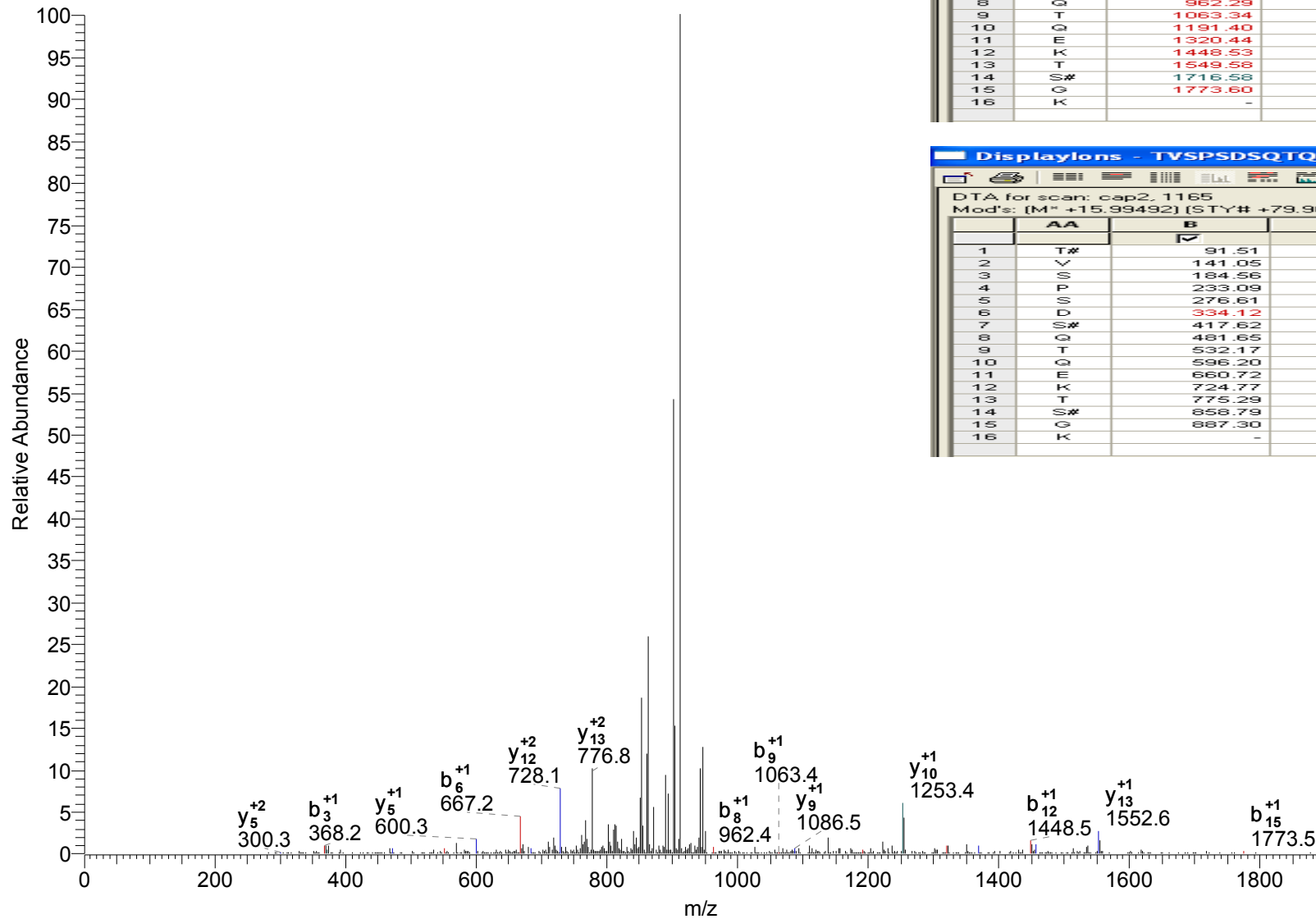
Displaylons - TVSPSDSQTQEKTSQK

DTA for scan: cap2, 1199
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	T	51.53	-	16
2	V	101.07	869.85	15
3	S#	184.56	820.32	14
4	P	233.09	736.82	13
5	S	276.61	688.29	12
6	D	334.12	644.77	11
7	S	377.64	587.26	10
8	Q	441.67	543.74	9
9	T	492.19	479.72	8
10	Q	556.22	429.19	7
11	E	620.74	365.16	6
12	K	684.79	300.64	5
13	T	735.31	236.59	4
14	S#	818.81	186.07	3
15	G	847.32	102.57	2
16	K	-	74.06	1

Uncharacterised protein C2orf57 homolog

#1165-1165 NL: 6.16E3

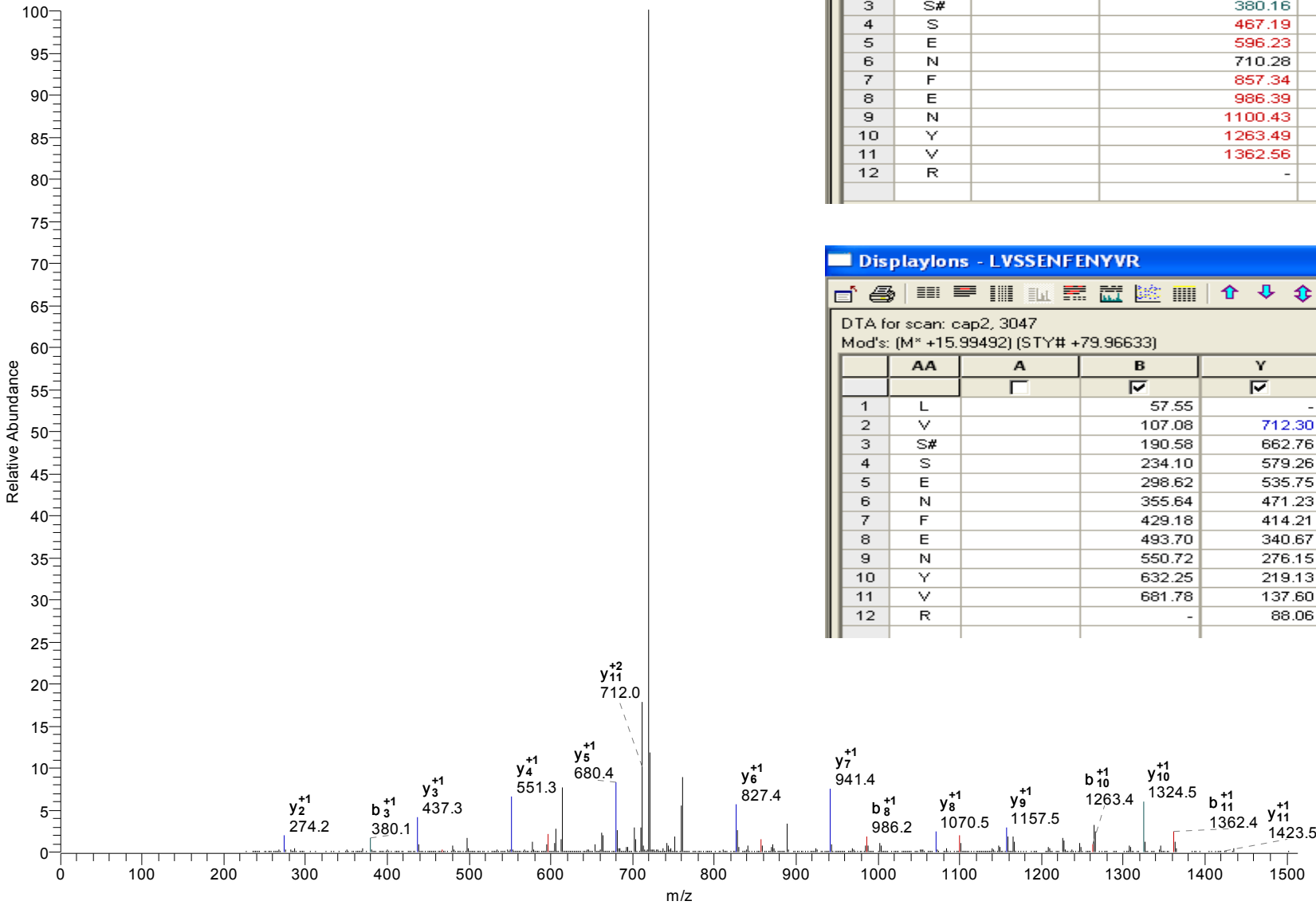


Displaylons - TVSPSDSQTQEKTSQK				
DTA for scan: cap2, 1165				
Mod's: [M ⁺ +15.99492] [STY# +79.96633]				
	AA	B	Y	
1	T#	182.02	-	16
2	V	281.09	1738.69	15
3	S	368.12	1639.62	14
4	P	465.17	1552.59	13
5	S	552.21	1455.54	12
6	D	667.23	1368.51	11
7	S#	834.23	1253.48	10
8	Q	962.29	1086.48	9
9	T	1063.34	958.42	8
10	Q	1191.40	857.38	7
11	E	1320.44	729.32	6
12	K	1448.53	600.28	5
13	T	1549.58	472.18	4
14	S#	1716.58	371.13	3
15	G	1773.60	204.13	2
16	K	-	147.11	1

Displaylons - TVSPSDSQTQEKTSQK				
DTA for scan: cap2, 1165				
Mod's: [M ⁺ +15.99492] [STY# +79.96633]				
	AA	B	Y	
1	T#	91.51	-	16
2	V	141.05	869.85	15
3	S	184.56	820.32	14
4	P	233.09	776.80	13
5	S	276.61	728.27	12
6	D	334.12	684.76	11
7	S#	417.62	627.24	10
8	Q	481.65	543.74	9
9	T	532.17	479.72	8
10	Q	596.20	429.19	7
11	E	660.72	365.16	6
12	K	724.77	300.64	5
13	T	775.29	236.59	4
14	S#	858.79	186.07	3
15	G	887.30	102.57	2
16	K	-	74.06	1

Fabp9 Testis lipid-binding protein

#3047-3047 NL: 5.80E5

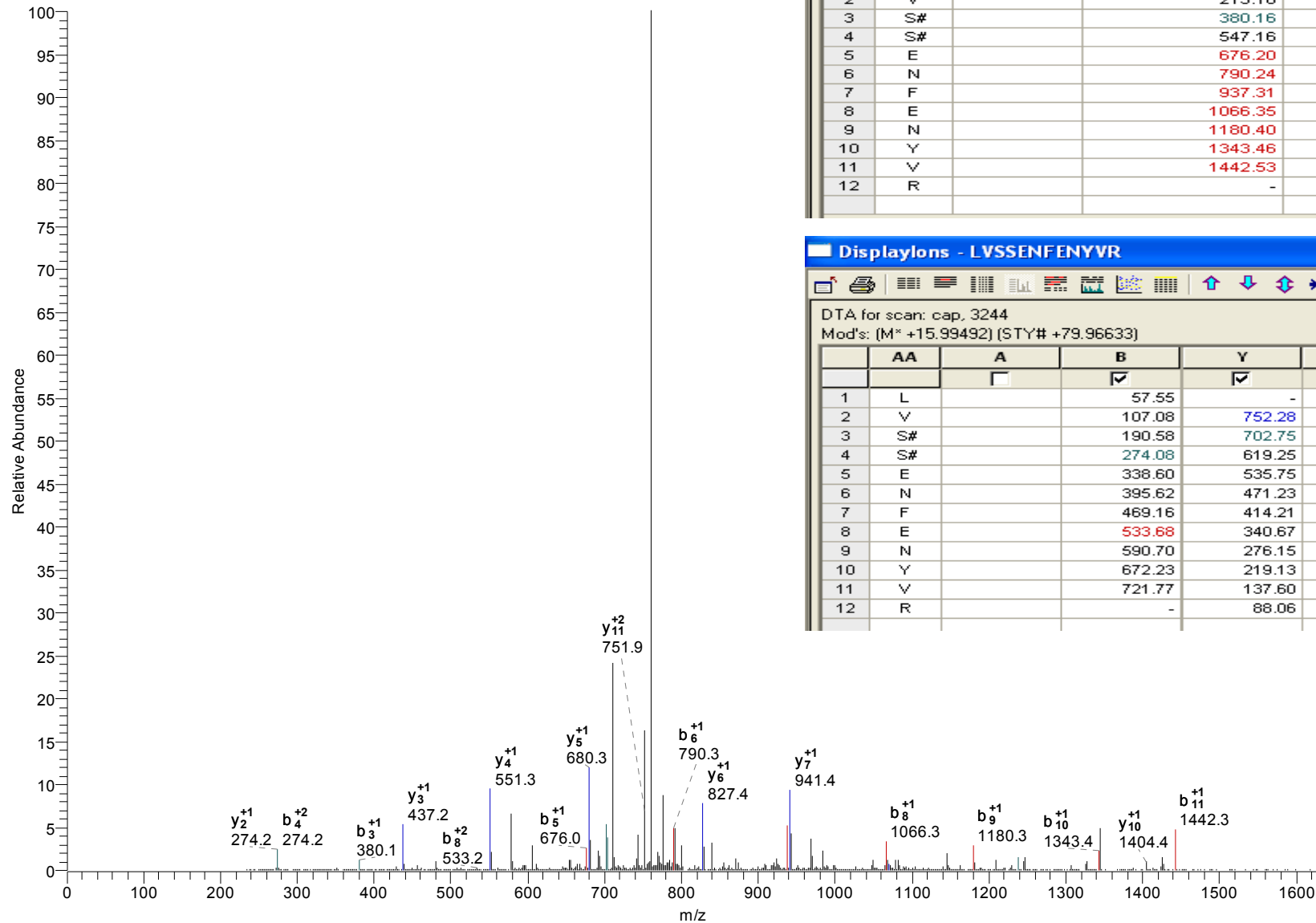


Displaylons - LVSSSENFENYVR					
DTA for scan: cap2, 3047					
Mod's: (M* +15.99492) (STY# +79.96633)					
	AA	A	B	Y	
1	L		114.09	-	12
2	V		213.16	1423.59	11
3	S#		380.16	1324.52	10
4	S		467.19	1157.52	9
5	E		596.23	1070.49	8
6	N		710.28	941.45	7
7	F		857.34	827.40	6
8	E		986.39	680.34	5
9	N		1100.43	551.29	4
10	Y		1263.49	437.25	3
11	V		1362.56	274.19	2
12	R		-	175.12	1

Displaylons - LVSSSENFENYVR					
DTA for scan: cap2, 3047					
Mod's: (M* +15.99492) (STY# +79.96633)					
	AA	A	B	Y	Z
1	L		57.55	-	
2	V		107.08	712.30	
3	S#		190.58	662.76	
4	S		234.10	579.26	
5	E		298.62	535.75	
6	N		355.64	471.23	
7	F		429.18	414.21	
8	E		493.70	340.67	
9	N		550.72	276.15	
10	Y		632.25	219.13	
11	V		681.78	137.60	
12	R		-	88.06	

Fabp9 Testis lipid-binding protein

#3244-3244 NL: 5.78E4



Displaylons - LVSSSENFENYVR

DTA for scan: cap. 3244
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L		114.09	-	12
2	V		213.16	1503.56	11
3	S#		380.16	1404.49	10
4	S#		547.16	1237.49	9
5	E		676.20	1070.49	8
6	N		790.24	941.45	7
7	F		937.31	827.40	6
8	E		1066.35	680.34	5
9	N		1180.40	551.29	4
10	Y		1343.46	437.25	3
11	V		1442.53	274.19	2
12	R		-	175.12	1

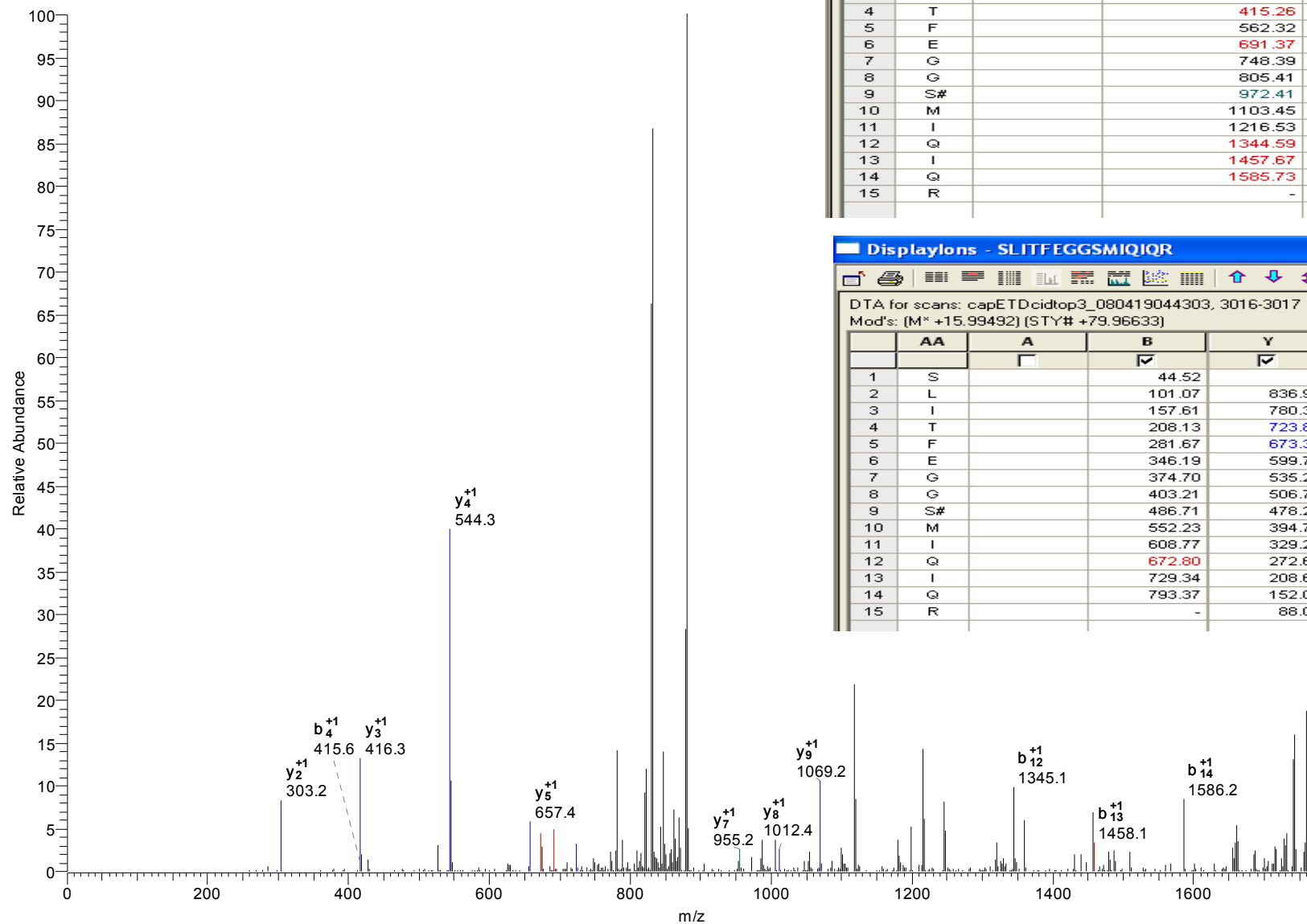
Displaylons - LVSSSENFENYVR

DTA for scan: cap. 3244
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L		57.55	-		12
2	V		107.08	752.28		11
3	S#		190.58	702.75		10
4	S#		274.08	619.25		9
5	E		338.60	535.75		8
6	N		395.62	471.23		7
7	F		469.16	414.21		6
8	E		533.68	340.67		5
9	N		590.70	276.15		4
10	Y		672.23	219.13		3
11	V		721.77	137.60		2
12	R		-	88.06		1

Fabp9 Testis lipid-binding protein

#3016-3017 NL: 1.04E3



Displaylons - SLITFEGGSMIIQQR

DTA for scans: capETDcidtop3_080419044303, 3016-3017
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	15
2	L		201.12	1672.81	14
3	I		314.21	1559.73	13
4	T		415.26	1446.64	12
5	F		562.32	1345.60	11
6	E		691.37	1198.53	10
7	G		748.39	1069.49	9
8	G		805.41	1012.46	8
9	S#		972.41	955.44	7
10	M		1103.45	788.44	6
11	I		1216.53	657.40	5
12	Q		1344.59	544.32	4
13	I		1457.67	416.26	3
14	Q		1585.73	303.18	2
15	R		-	175.12	1

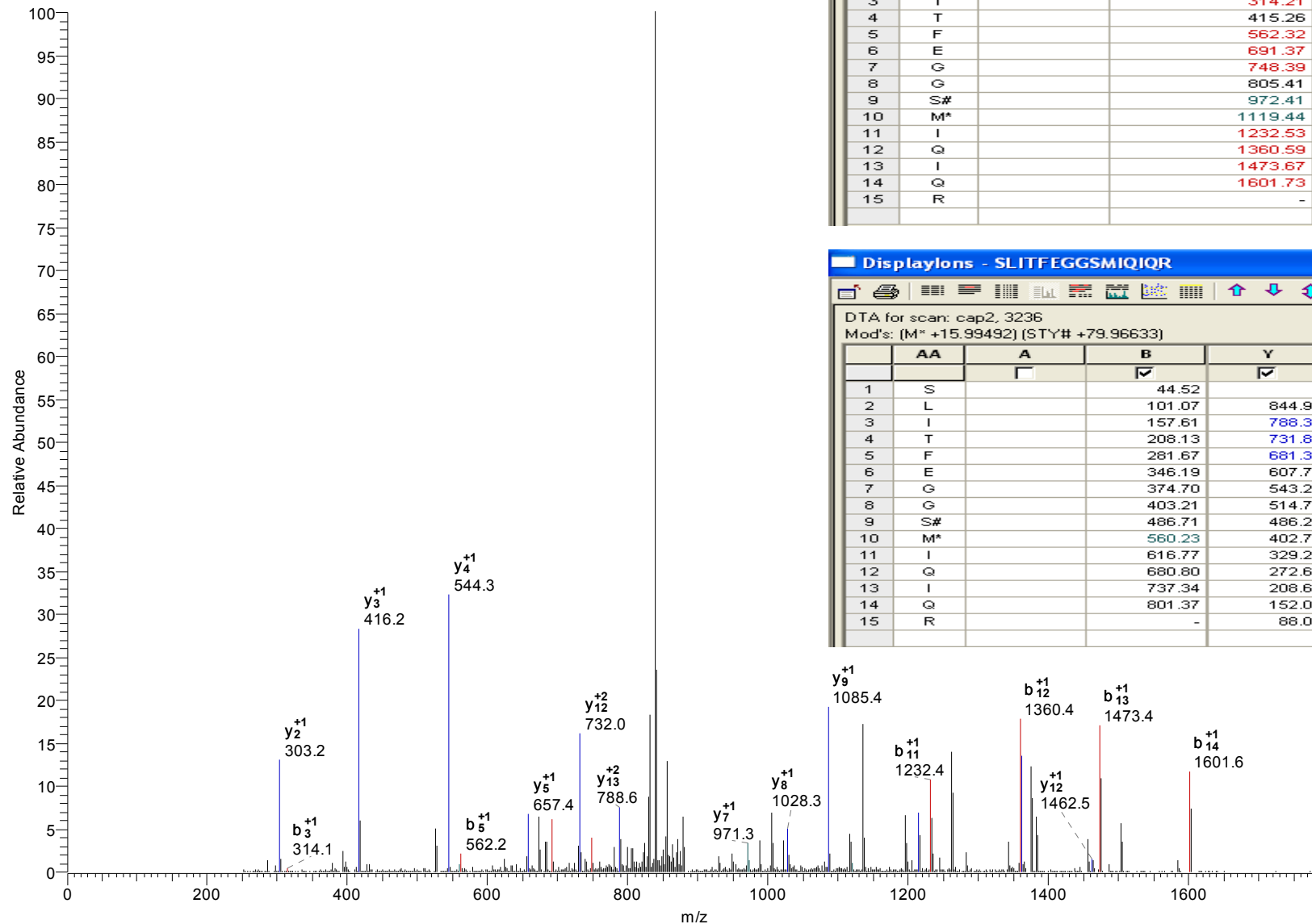
Displaylons - SLITFEGGSMIIQQR

DTA for scans: capETDcidtop3_080419044303, 3016-3017
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S		44.52	-		15
2	L		101.07	836.91		14
3	I		157.61	780.37		13
4	T		208.13	723.83		12
5	F		281.67	673.30		11
6	E		346.19	599.77		10
7	G		374.70	535.25		9
8	G		403.21	506.74		8
9	S#		486.71	478.23		7
10	M		552.23	394.73		6
11	I		608.77	329.21		5
12	Q		672.80	272.66		4
13	I		729.34	208.63		3
14	Q		793.37	152.09		2
15	R		-	88.06		1

Fabp9 Testis lipid-binding protein

#3236-3236 NL: 2.98E4



Displaylons - SLITFEGGSMIIQIR

DTA for scan: cap2, 3236
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	15
2	L		201.12	1688.81	14
3	I		314.21	1575.72	13
4	T		415.26	1462.64	12
5	F		562.32	1361.59	11
6	E		691.37	1214.52	10
7	G		748.39	1085.48	9
8	G		805.41	1028.46	8
9	S#		972.41	971.44	7
10	M*		1119.44	804.44	6
11	I		1232.53	657.40	5
12	Q		1360.59	544.32	4
13	I		1473.67	416.26	3
14	Q		1601.73	303.18	2
15	R		-	175.12	1

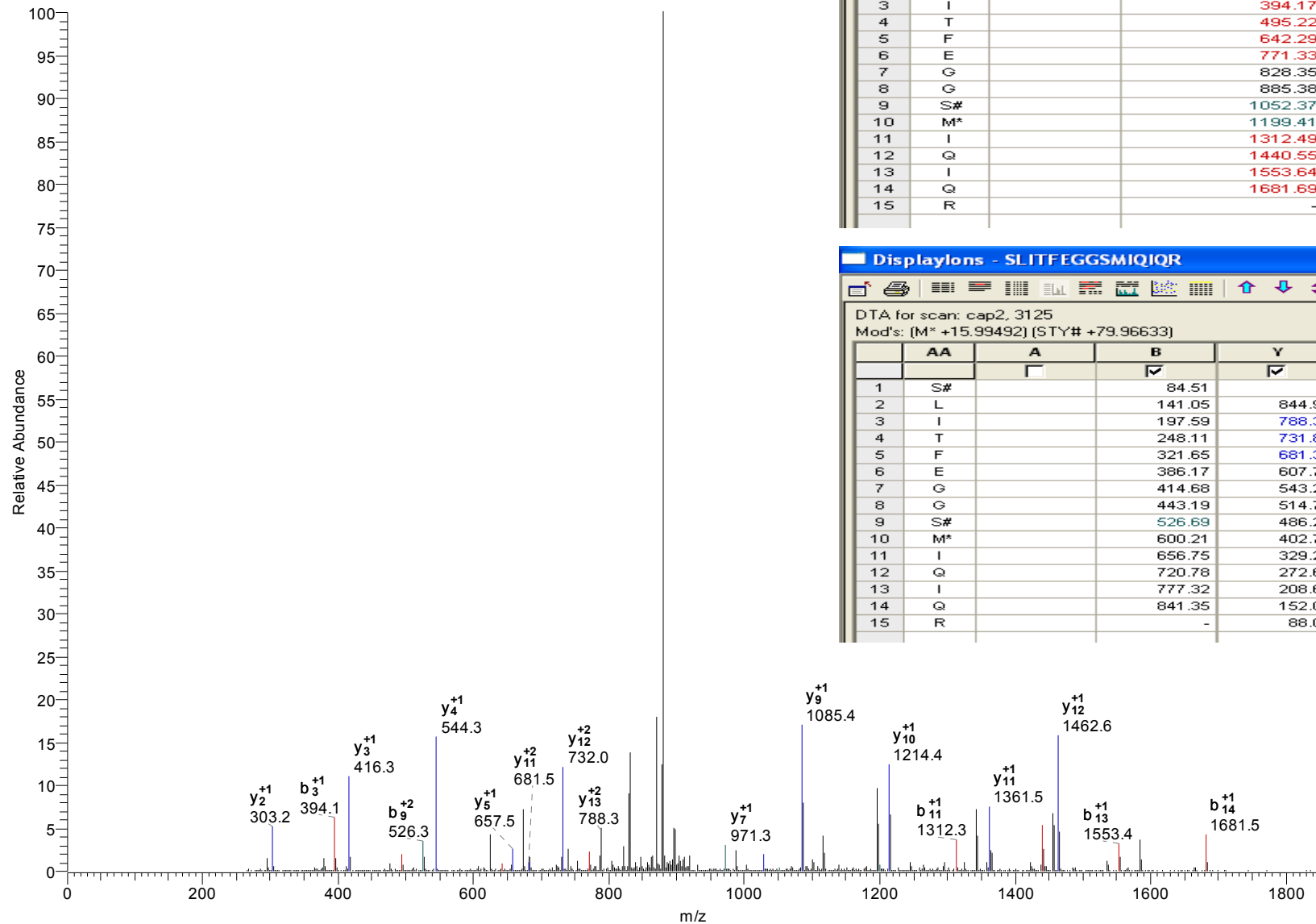
Displaylons - SLITFEGGSMIIQIR

DTA for scan: cap2, 3236
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	S		44.52	-	-	15
2	L		101.07	844.91	-	14
3	I		157.61	788.37	-	13
4	T		208.13	731.82	-	12
5	F		281.67	681.30	-	11
6	E		346.19	607.77	-	10
7	G		374.70	543.24	-	9
8	G		403.21	514.73	-	8
9	S#		486.71	486.22	-	7
10	M*		560.23	402.72	-	6
11	I		616.77	329.21	-	5
12	Q		680.80	272.66	-	4
13	I		737.34	208.63	-	3
14	Q		801.37	152.09	-	2
15	R		-	88.06	-	1

Fabp9 Testis lipid-binding protein

#3125-3125 NL: 6.59E4



Displaylons - SLITFEGGSMIQR

DTA for scan: cap2, 3125
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	S#		168.01	-	15
2	L		281.09	1688.81	14
3	I		394.17	1575.72	13
4	T		495.22	1462.64	12
5	F		642.29	1361.59	11
6	E		771.33	1214.52	10
7	G		828.35	1085.48	9
8	G		885.38	1028.46	8
9	S#		1052.37	971.44	7
10	M*		1199.41	804.44	6
11	I		1312.49	657.40	5
12	Q		1440.55	544.32	4
13	I		1553.64	416.26	3
14	Q		1681.69	303.18	2
15	R		-	175.12	1

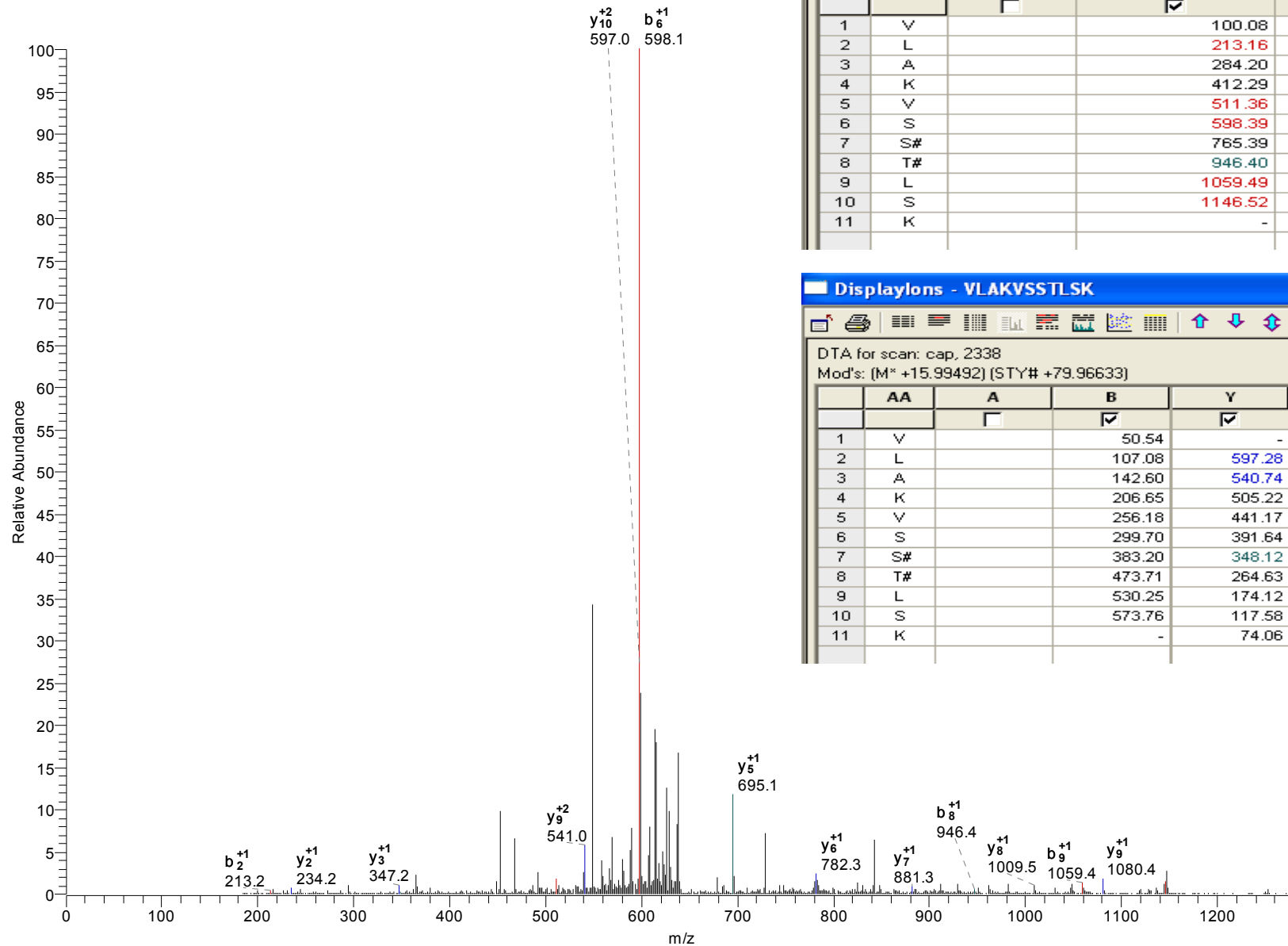
Displaylons - SLITFEGGSMIQR

DTA for scan: cap2, 3125
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	S#		84.51	-		15
2	L		141.05	844.91		14
3	I		197.59	788.37		13
4	T		248.11	731.82		12
5	F		321.65	681.30		11
6	E		386.17	607.77		10
7	G		414.68	543.24		9
8	G		443.19	514.73		8
9	S#		526.69	486.22		7
10	M*		600.21	402.72		6
11	I		656.75	329.21		5
12	Q		720.78	272.66		4
13	I		777.32	208.63		3
14	Q		841.35	152.09		2
15	R		-	88.06		1

predicted similar to FLJ44048 protein

#2338-2338 NL: 2.22E4



Displaylons - VLAKVSSTLSK

DTA for scan: cap, 2338
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	V		100.08	-	11
2	L		213.16	1193.56	10
3	A		284.20	1080.47	9
4	K		412.29	1009.44	8
5	V		511.36	881.34	7
6	S		598.39	782.27	6
7	S#		765.39	695.24	5
8	T#		946.40	528.24	4
9	L		1059.49	347.23	3
10	S		1146.52	234.14	2
11	K		-	147.11	1

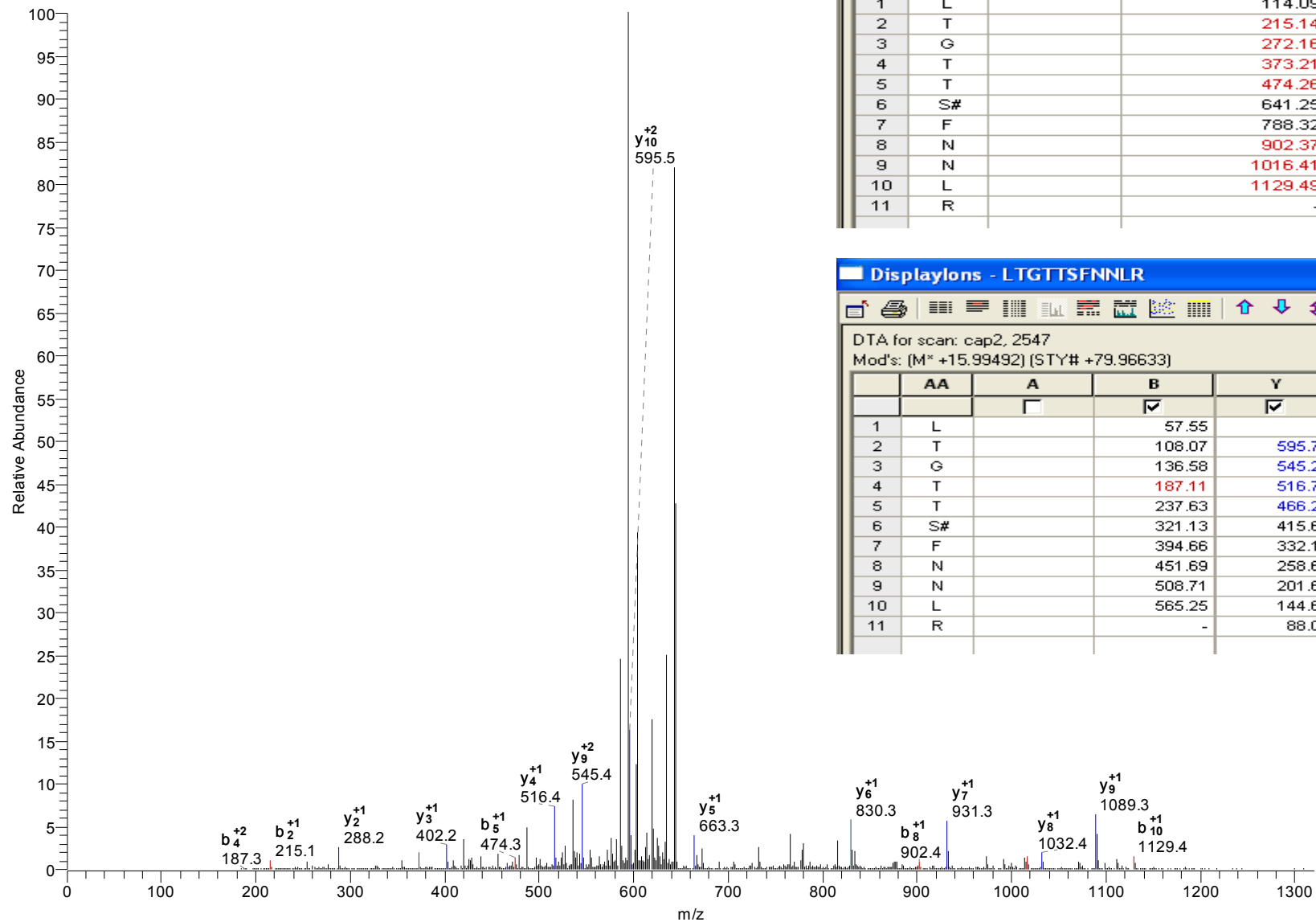
Displaylons - VLAKVSSTLSK

DTA for scan: cap, 2338
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	V		50.54	-		11
2	L		107.08	597.28		10
3	A		142.60	540.74		9
4	K		206.65	505.22		8
5	V		256.18	441.17		7
6	S		299.70	391.64		6
7	S#		383.20	348.12		5
8	T#		473.71	264.63		4
9	L		530.25	174.12		3
10	S		573.76	117.58		2
11	K		-	74.06		1

predicted similar to FLJ44048 protein

#2547-2547 NL: 3.86E4



Displaylons - LTGTTSFNNLR

DTA for scan: cap2, 2547
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L	☐	☒	114.09	-
2	T			215.14	1190.52
3	G			272.16	1089.47
4	T			373.21	1032.45
5	T			474.26	931.40
6	S#			641.25	830.36
7	F			788.32	663.36
8	N			902.37	516.29
9	N			1016.41	402.25
10	L			1129.49	288.20
11	R			-	175.12

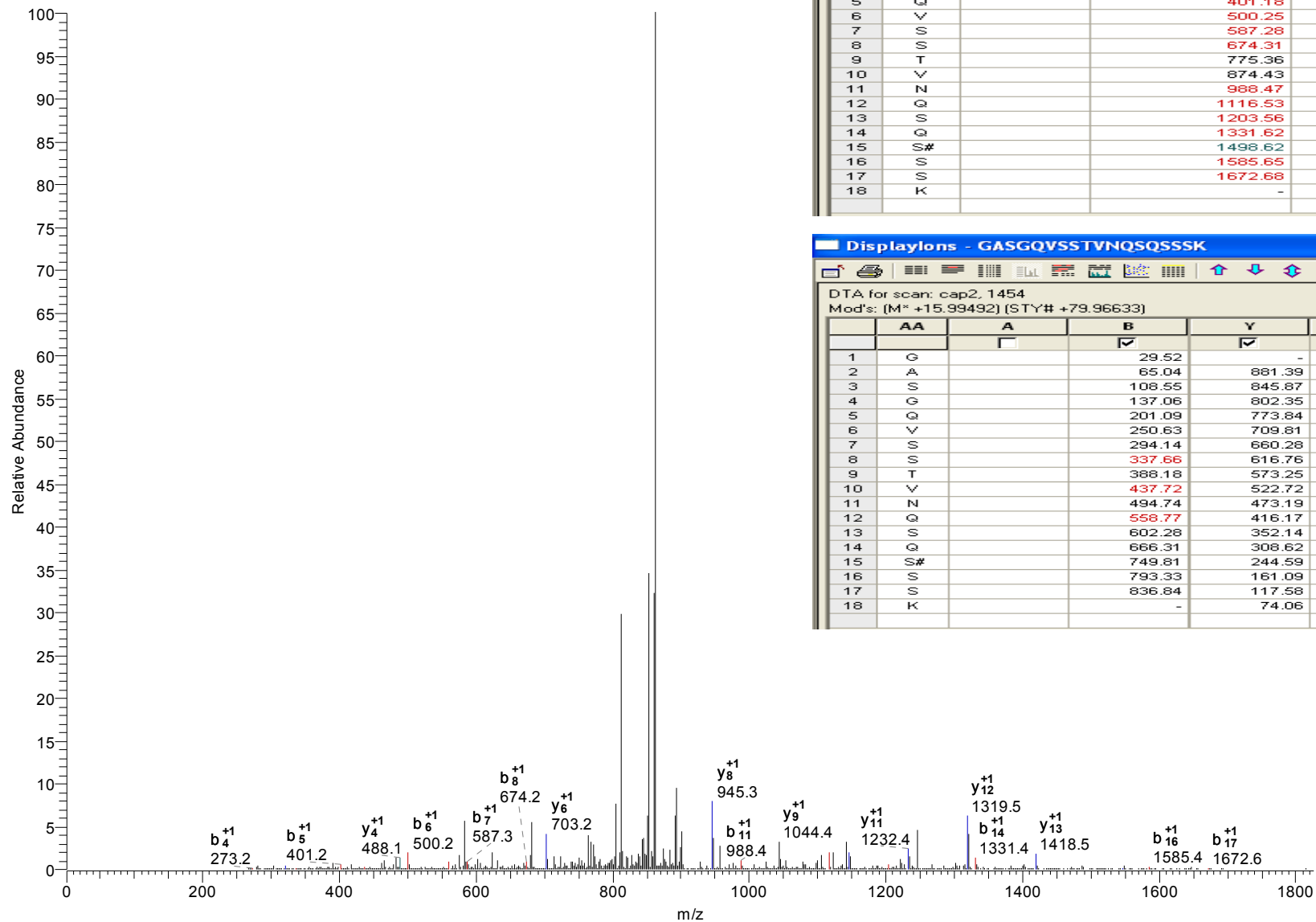
Displaylons - LTGTTSFNNLR

DTA for scan: cap2, 2547
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L	☐	☒	☒	☐	11
2	T			57.55	-	10
3	G			108.07	595.76	9
4	T			136.58	545.24	8
5	T			187.11	516.73	7
6	S#			237.63	466.21	6
7	F			321.13	415.68	5
8	N			394.66	332.18	4
9	N			451.69	258.65	3
10	L			508.71	201.63	2
11	R			565.25	144.61	1

predicted similar to FLJ44048 protein

#1454-1454 NL: 2.19E4



Displaylons - GASGQVSS TVNQSQSSSK

DTA for scan: cap2, 1454
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	G		58.03	-	18
2	A		129.07	1761.77	17
3	S		216.10	1690.73	16
4	G		273.12	1603.70	15
5	Q		401.18	1546.67	14
6	V		500.25	1418.62	13
7	S		587.28	1319.55	12
8	S		674.31	1232.52	11
9	T		775.36	1145.48	10
10	V		874.43	1044.44	9
11	N		988.47	945.37	8
12	Q		1116.53	831.32	7
13	S		1203.56	703.27	6
14	Q		1331.62	616.23	5
15	S#		1498.62	488.18	4
16	S		1585.65	321.18	3
17	S		1672.68	234.14	2
18	K		-	147.11	1

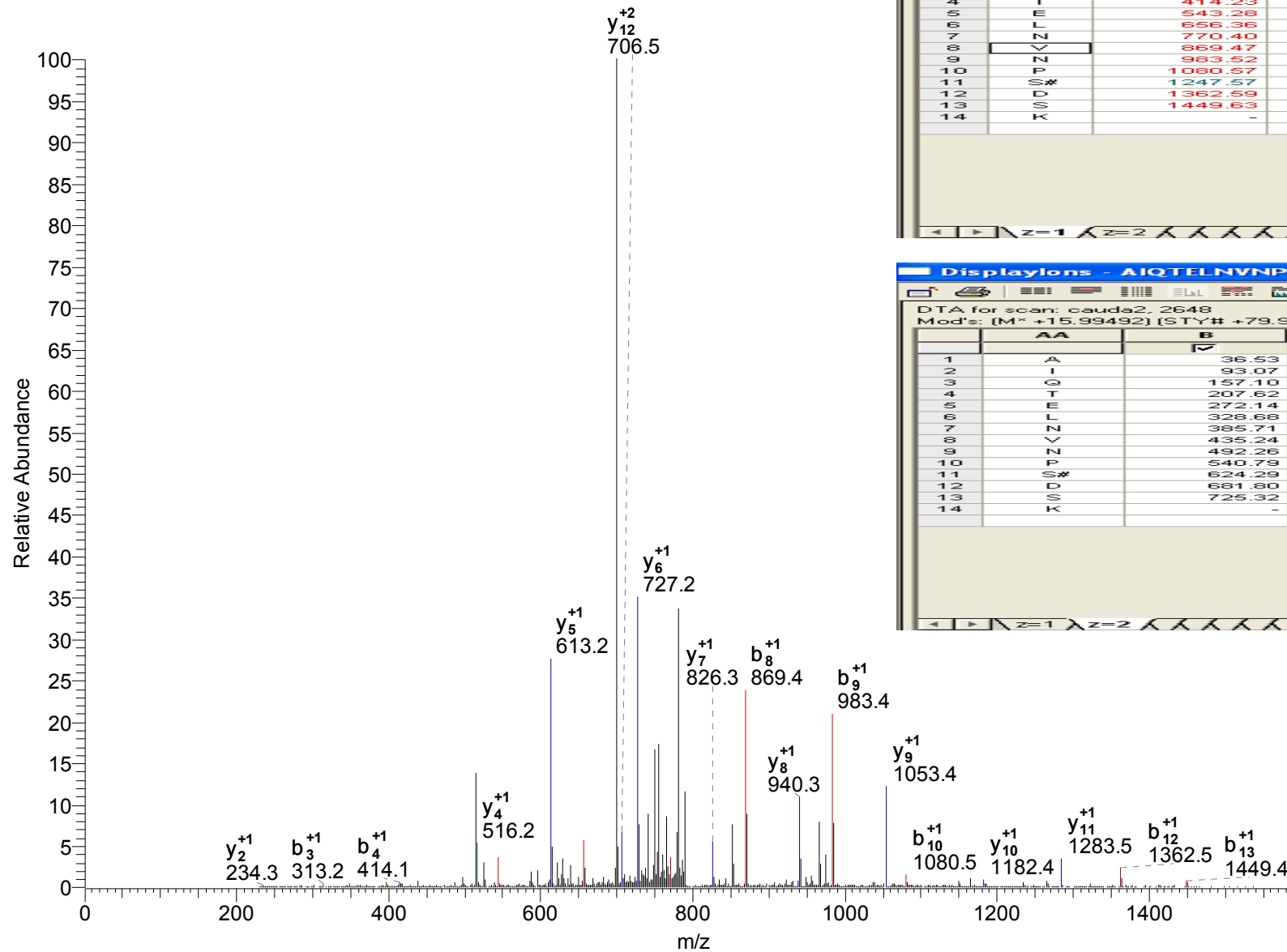
Displaylons - GASGQVSS TVNQSQSSSK

DTA for scan: cap2, 1454
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	G		29.52	-		18
2	A		65.04	881.39		17
3	S		108.55	845.87		16
4	G		137.06	802.35		15
5	Q		201.09	773.84		14
6	V		250.63	709.81		13
7	S		294.14	660.28		12
8	S		337.66	616.76		11
9	T		388.18	573.25		10
10	V		437.72	522.72		9
11	N		494.74	473.19		8
12	Q		558.77	416.17		7
13	S		602.28	352.14		6
14	Q		666.31	308.62		5
15	S#		749.81	244.59		4
16	S		793.33	161.09		3
17	S		836.84	117.58		2
18	K		-	74.06		1

predicted similar to FLJ44048 protein

#2648-2648 NL: 2.12E4



Displaylons - AIQTELVNPNPSDK

DTA for scan: cauda2, 2648
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	A	72.04	-	14
2	I	185.13	1524.69	13
3	Q	313.19	1411.61	12
4	T	414.23	1283.55	11
5	E	543.28	1182.50	10
6	L	656.36	1053.46	9
7	N	770.40	940.38	8
8	V	869.47	826.33	7
9	N	983.52	727.27	6
10	P	1080.57	613.22	5
11	S#	1247.57	516.17	4
12	D	1362.59	349.17	3
13	S	1449.63	234.14	2
14	K	-	147.11	1

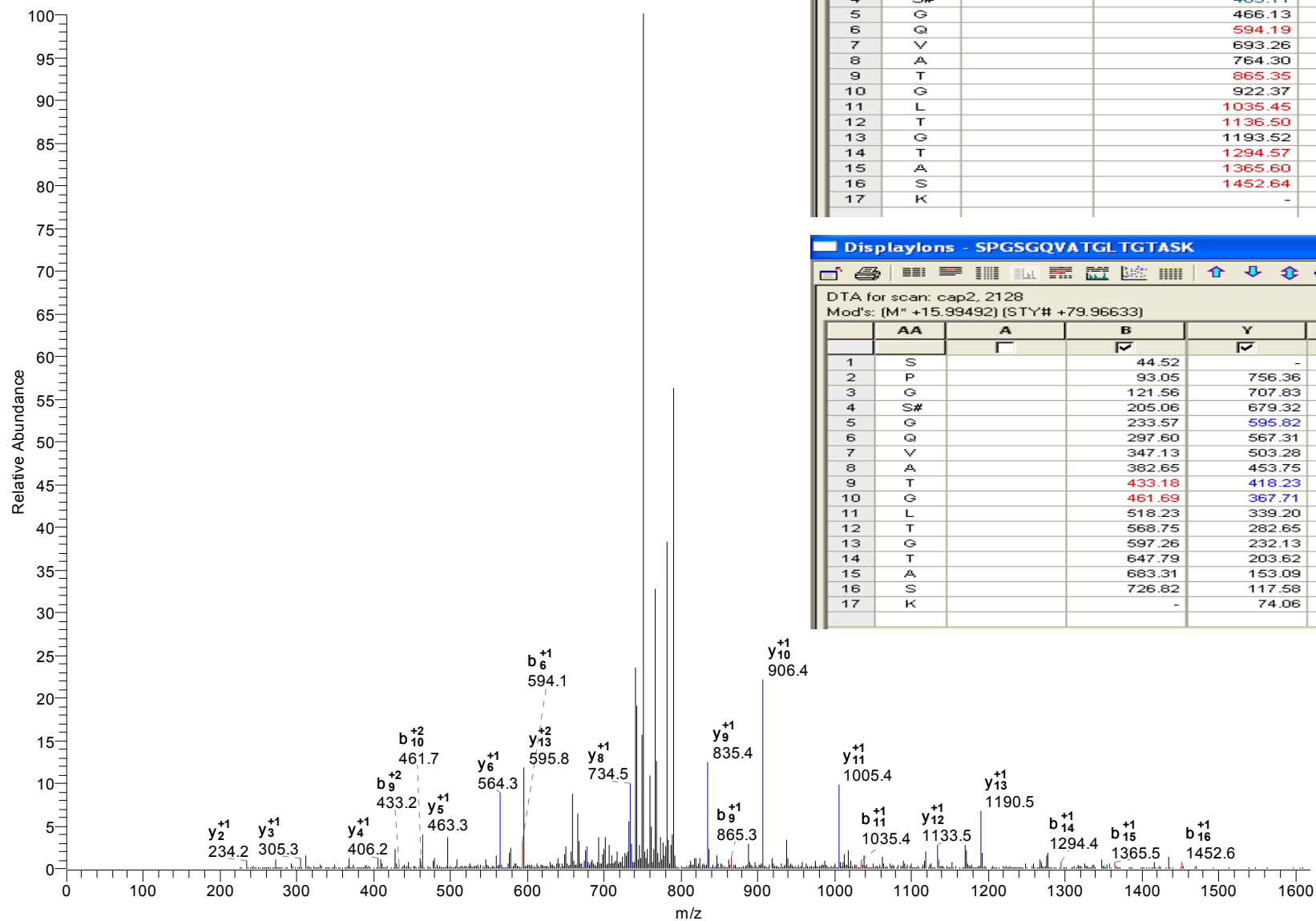
Displaylons - AIQTELVNPNPSDK

DTA for scan: cauda2, 2648
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	A	36.53	-	14
2	I	93.07	762.85	13
3	Q	157.10	706.31	12
4	T	207.62	642.28	11
5	E	272.14	591.76	10
6	L	328.68	527.23	9
7	N	385.71	470.69	8
8	V	435.24	413.67	7
9	N	492.26	364.14	6
10	P	540.79	307.12	5
11	S#	624.29	258.59	4
12	D	681.80	175.09	3
13	S	725.32	117.58	2
14	K	-	74.06	1

Protein FAM71B

#2128-2128 NL: 1.15E4



Displaylons - SPGSGQVATGLTGTASK

DTA for scan: cap2, 2128
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	17
2	P		185.09	1511.71	16
3	G		242.11	1414.66	15
4	S#		409.11	1357.64	14
5	G		466.13	1190.64	13
6	Q		594.19	1133.62	12
7	V		693.26	1005.56	11
8	A		764.30	906.49	10
9	T		865.35	835.45	9
10	G		922.37	734.40	8
11	L		1035.45	677.38	7
12	T		1136.50	564.30	6
13	G		1193.52	463.25	5
14	T		1294.57	406.23	4
15	A		1365.60	305.18	3
16	S		1452.64	234.14	2
17	K		-	147.11	1

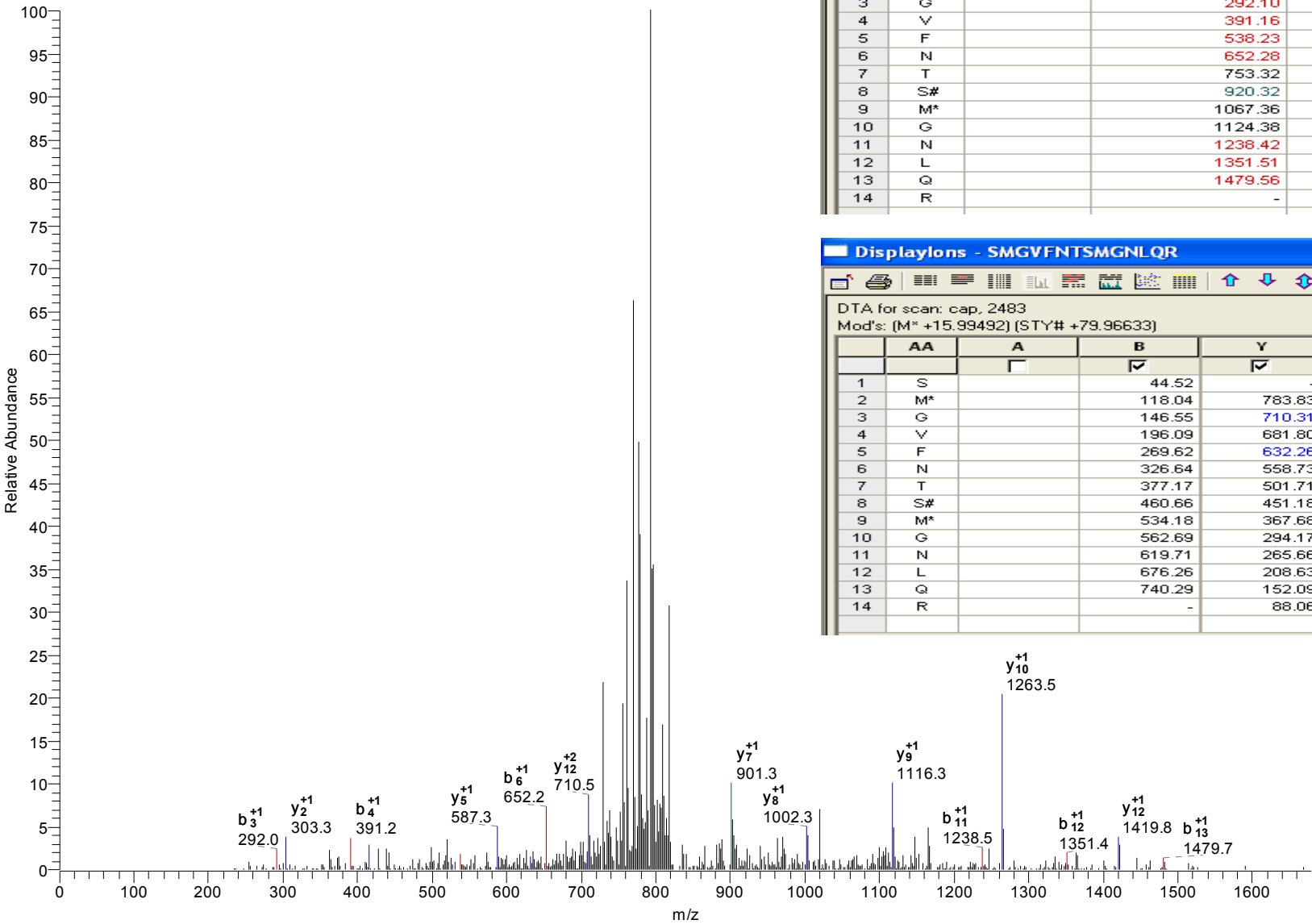
Displaylons - SPGSGQVATGLTGTASK

DTA for scan: cap2, 2128
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	S		44.52	-	-	17
2	P		93.05	756.36	-	16
3	G		121.56	707.83	-	15
4	S#		205.06	679.32	-	14
5	G		233.57	595.82	-	13
6	Q		297.60	567.31	-	12
7	V		347.13	503.28	-	11
8	A		382.65	453.75	-	10
9	T		433.18	418.23	-	9
10	G		461.69	367.71	-	8
11	L		518.23	339.20	-	7
12	T		568.75	282.65	-	6
13	G		597.26	232.13	-	5
14	T		647.79	203.62	-	4
15	A		683.31	153.09	-	3
16	S		726.82	117.58	-	2
17	K		-	74.06	-	1

Protein FAM71B

#2483-2483 NL: 2.03E3



Displaylons - SMGVFNTSMGNLQR

DTA for scan: cap. 2483
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	14
2	M*		235.07	1566.64	13
3	G		292.10	1419.61	12
4	V		391.16	1362.59	11
5	F		538.23	1263.52	10
6	N		652.28	1116.45	9
7	T		753.32	1002.41	8
8	S#		920.32	901.36	7
9	M*		1067.36	734.36	6
10	G		1124.38	587.33	5
11	N		1238.42	530.30	4
12	L		1351.51	416.26	3
13	Q		1479.56	303.18	2
14	R		-	175.12	1

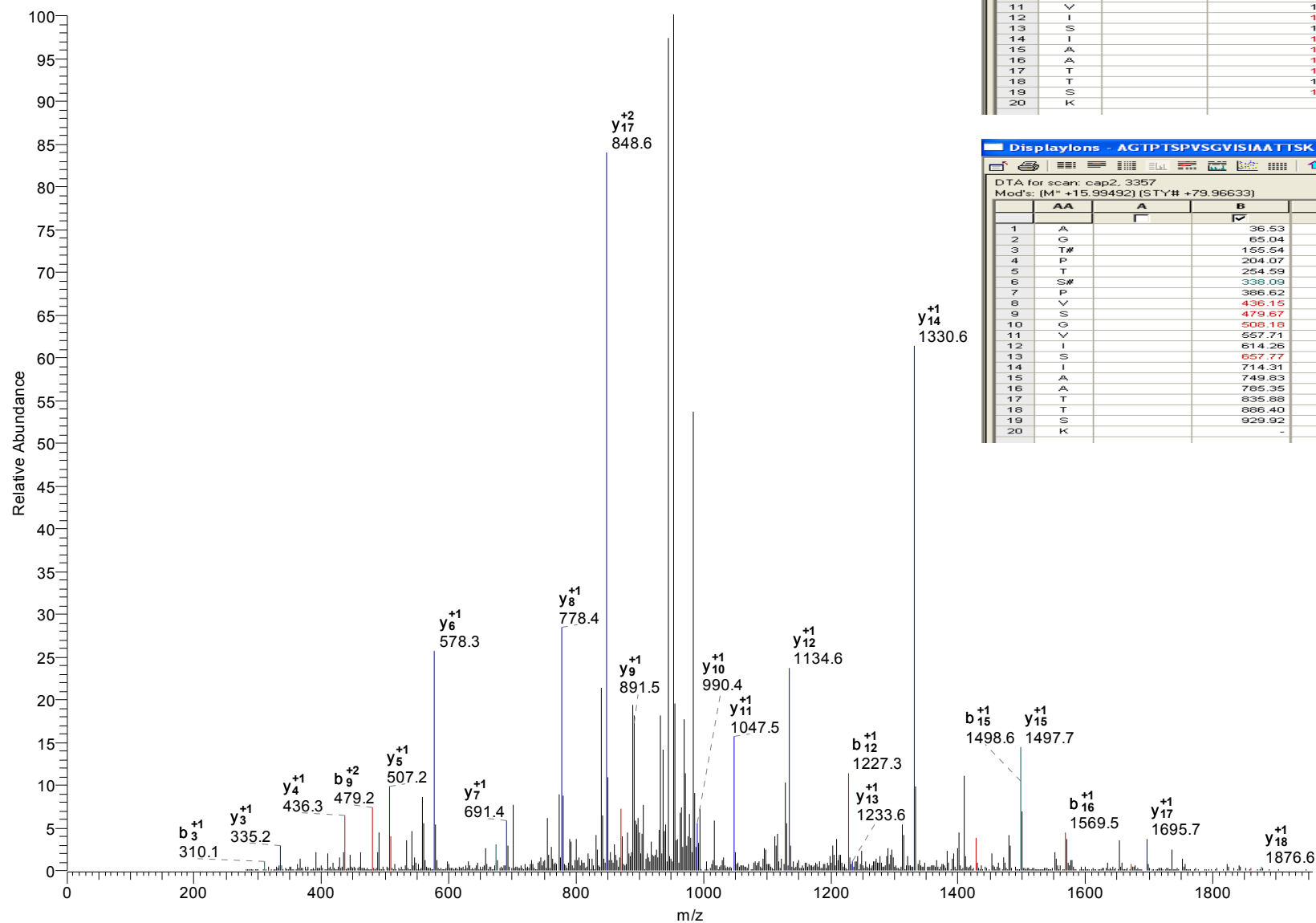
Displaylons - SMGVFNTSMGNLQR

DTA for scan: cap. 2483
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S		44.52	-		14
2	M*		118.04	783.83		13
3	G		146.55	710.31		12
4	V		196.09	681.80		11
5	F		269.62	632.26		10
6	N		326.64	558.73		9
7	T		377.17	501.71		8
8	S#		460.66	451.18		7
9	M*		534.18	367.68		6
10	G		562.69	294.17		5
11	N		619.71	265.66		4
12	L		676.26	208.63		3
13	Q		740.29	152.09		2
14	R		-	88.06		1

Protein FAM71B

#3357-3357 NL: 7.74E3



Displaylons - AGTPTSPVSGVISIAATTSK

DTA for scan: cap2, 3357
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	A		72.04		20
2	G		129.07	1933.89	19
3	T#		310.08	1876.87	18
4	P		407.13	1695.86	17
5	T		508.18	1598.80	16
6	S#		675.18	1497.76	15
7	P		772.23	1330.76	14
8	V		871.30	1233.70	13
9	S		958.33	1134.64	12
10	G		1015.35	1047.60	11
11	V		1114.42	990.58	10
12	I		1227.51	891.51	9
13	S		1314.54	778.43	8
14	I		1427.62	691.40	7
15	A		1498.66	578.31	6
16	A		1569.70	507.28	5
17	T		1670.74	436.24	4
18	T		1771.79	335.19	3
19	S		1858.82	234.14	2
20	K		-	147.11	1

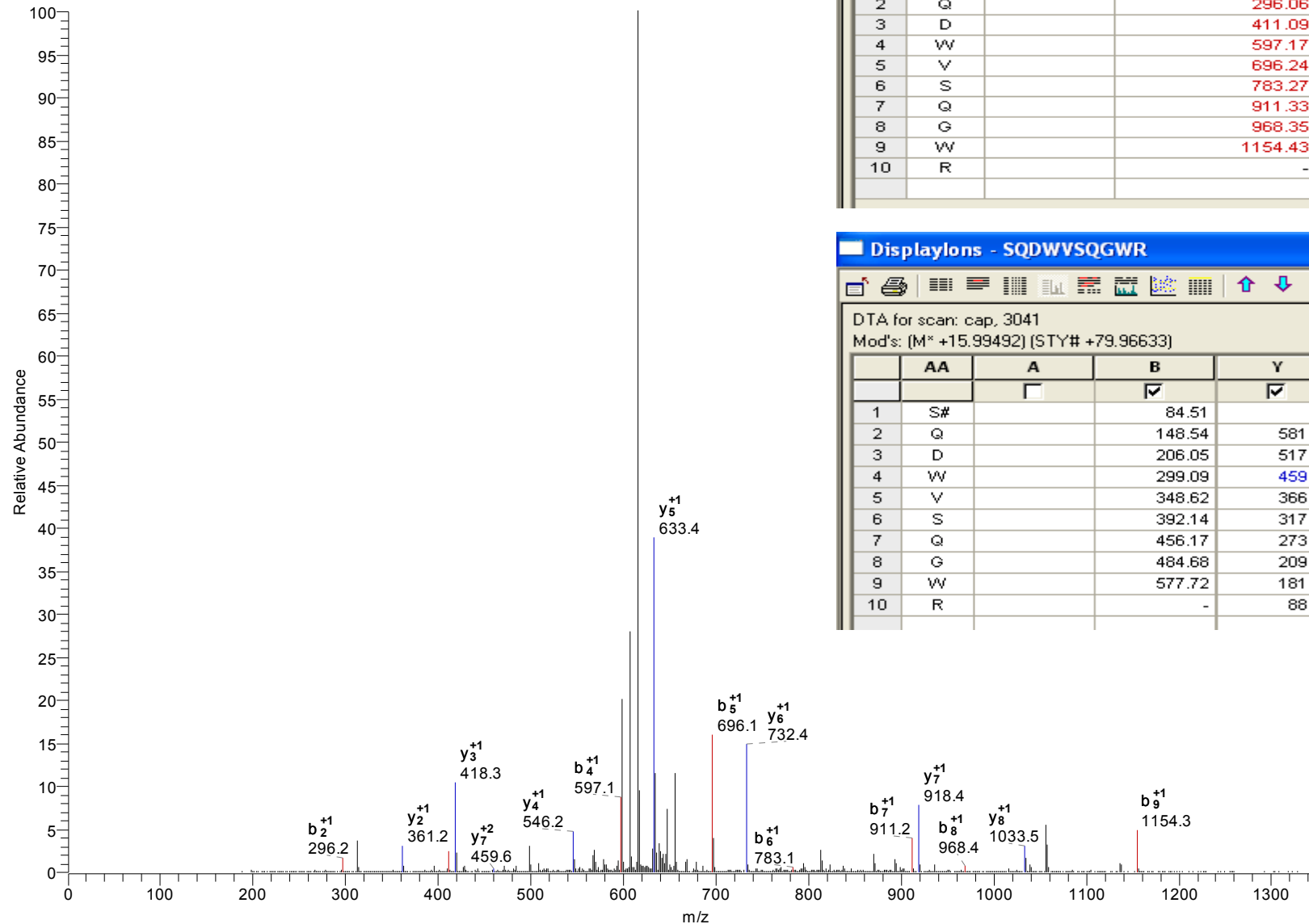
Displaylons - AGTPTSPVSGVISIAATTSK

DTA for scan: cap2, 3357
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	A		36.53			20
2	G		65.04	967.45		19
3	T#		155.54	938.94		18
4	P		204.07	848.43		17
5	T		254.59	799.91		16
6	S#		338.09	749.38		15
7	P		386.62	665.88		14
8	V		436.15	617.36		13
9	S		479.67	567.82		12
10	G		508.18	524.31		11
11	V		557.71	495.80		10
12	I		614.26	446.26		9
13	S		657.77	389.72		8
14	I		714.31	346.20		7
15	A		749.83	289.66		6
16	A		785.35	254.14		5
17	T		835.88	218.62		4
18	T		886.40	168.10		3
19	S		929.92	117.58		2
20	K		-	74.06		1

Sp3111 Sperm protein SSP3111

#3041-3041 NL: 5.27E4



Displaylons - SQDWVSQGWR

DTA for scan: cap. 3041
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S#		168.01	-	10
2	Q		296.06	1161.54	9
3	D		411.09	1033.49	8
4	W		597.17	918.46	7
5	V		696.24	732.38	6
6	S		783.27	633.31	5
7	Q		911.33	546.28	4
8	G		968.35	418.22	3
9	W		1154.43	361.20	2
10	R		-	175.12	1

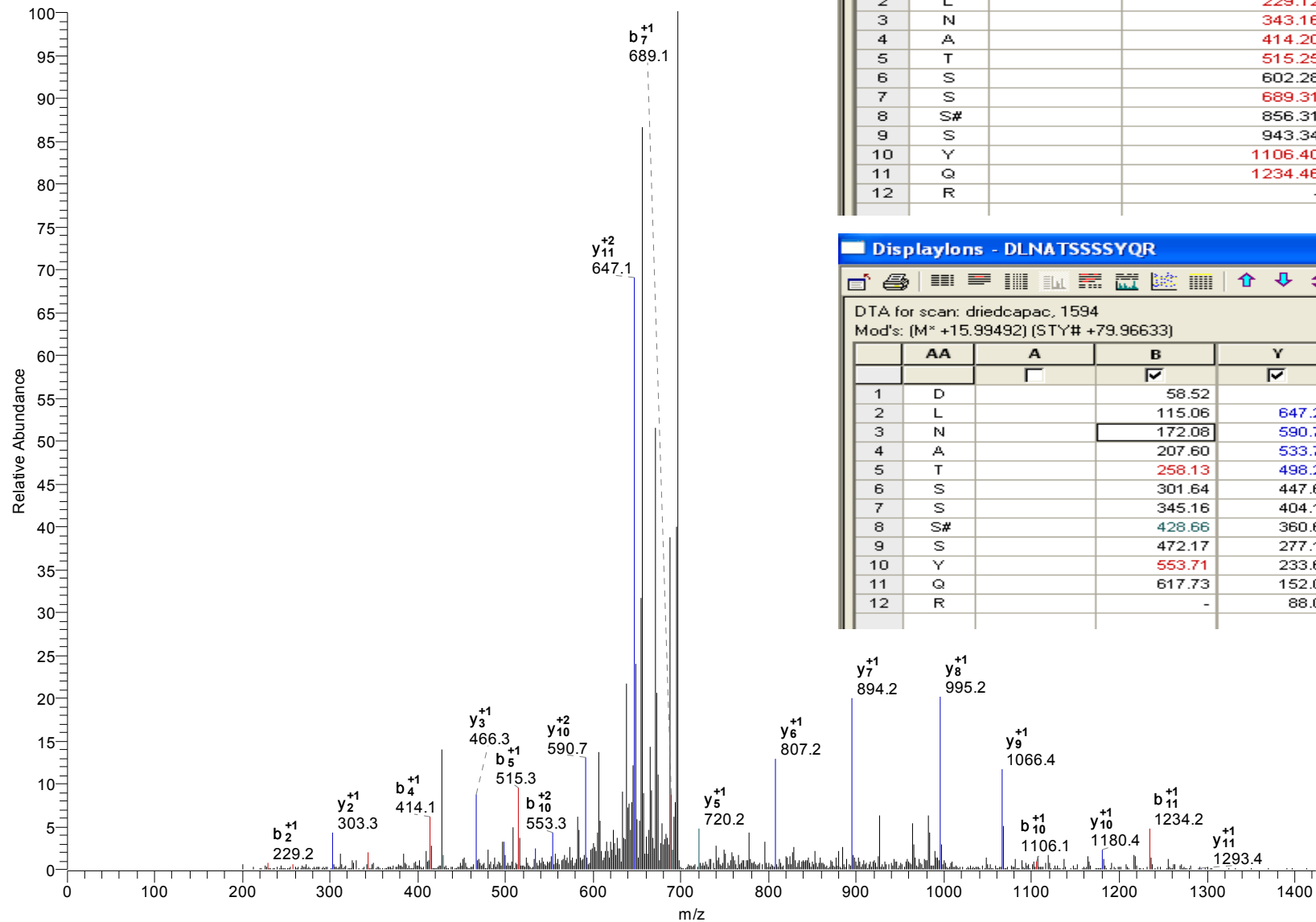
Displaylons - SQDWVSQGWR

DTA for scan: cap. 3041
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S#		84.51	-		10
2	Q		148.54	581.28		9
3	D		206.05	517.25		8
4	W		299.09	459.73		7
5	V		348.62	366.69		6
6	S		392.14	317.16		5
7	Q		456.17	273.64		4
8	G		484.68	209.61		3
9	W		577.72	181.10		2
10	R		-	88.06		1

Sp3111 Sperm protein SSP3111

#1594-1594 NL: 4.67E3



Displaylons - DLNATSSSSYQR

DTA for scan: driedcapac, 1594
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	D		116.03	-	12
2	L		229.12	1293.55	11
3	N		343.16	1180.46	10
4	A		414.20	1066.42	9
5	T		515.25	995.38	8
6	S		602.28	894.34	7
7	S		689.31	807.30	6
8	S#		856.31	720.27	5
9	S		943.34	553.27	4
10	Y		1106.40	466.24	3
11	Q		1234.46	303.18	2
12	R		-	175.12	1

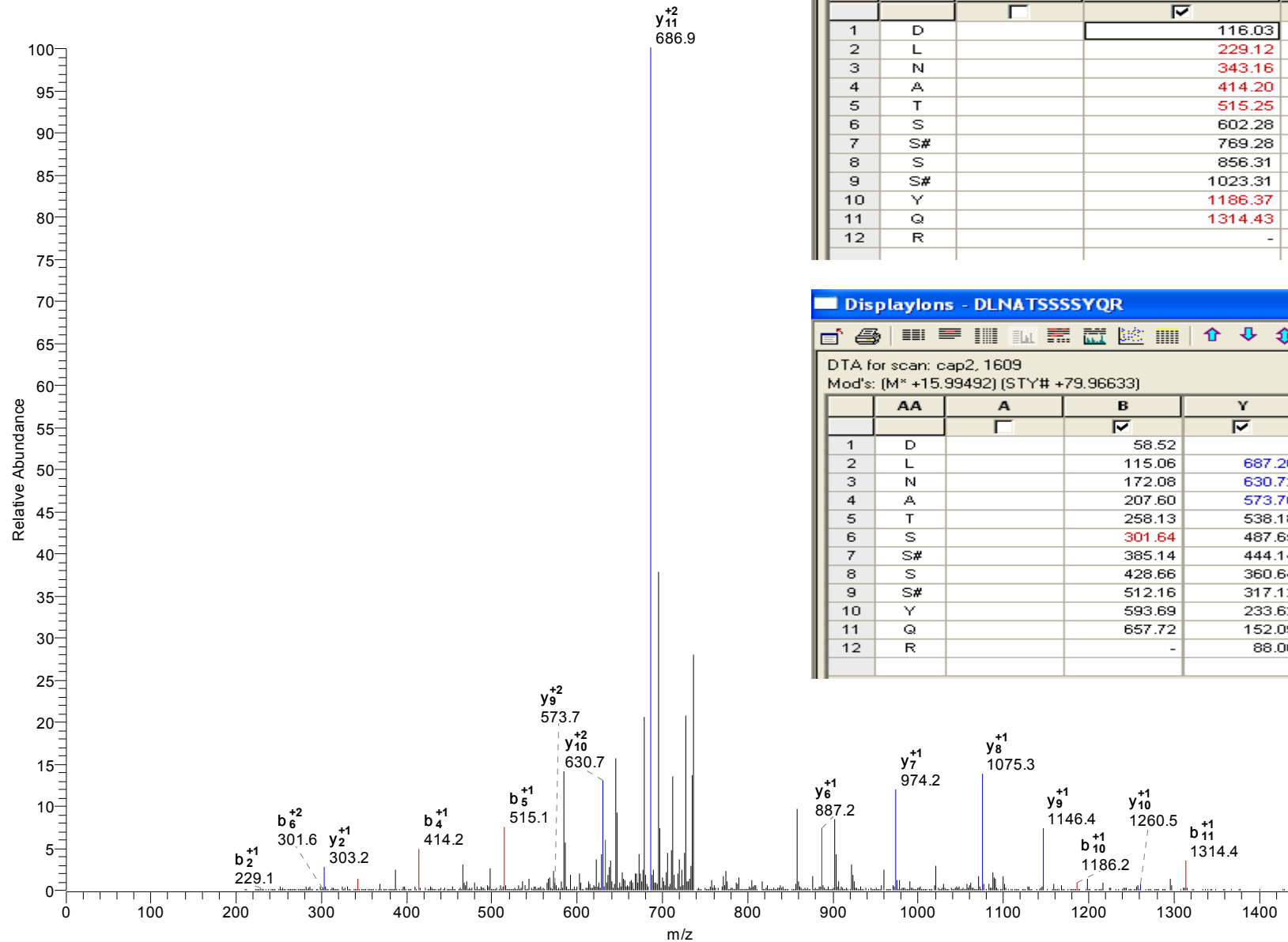
Displaylons - DLNATSSSSYQR

DTA for scan: driedcapac, 1594
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	D		58.52	-		12
2	L		115.06	647.28		11
3	N		172.08	590.74		10
4	A		207.60	533.71		9
5	T		258.13	498.20		8
6	S		301.64	447.67		7
7	S		345.16	404.16		6
8	S#		428.66	360.64		5
9	S		472.17	277.14		4
10	Y		553.71	233.62		3
11	Q		617.73	152.09		2
12	R		-	88.06		1

Sp3111 Sperm protein SSP3111

#1609-1609 NL: 1.04E4



Displaylons - DLNATSSSSYQR

DTA for scan: cap2, 1609
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	D		116.03	-	12
2	L		229.12	1373.51	11
3	N		343.16	1260.43	10
4	A		414.20	1146.39	9
5	T		515.25	1075.35	8
6	S		602.28	974.30	7
7	S#		769.28	887.27	6
8	S		856.31	720.27	5
9	S#		1023.31	633.24	4
10	Y		1186.37	466.24	3
11	Q		1314.43	303.18	2
12	R		-	175.12	1

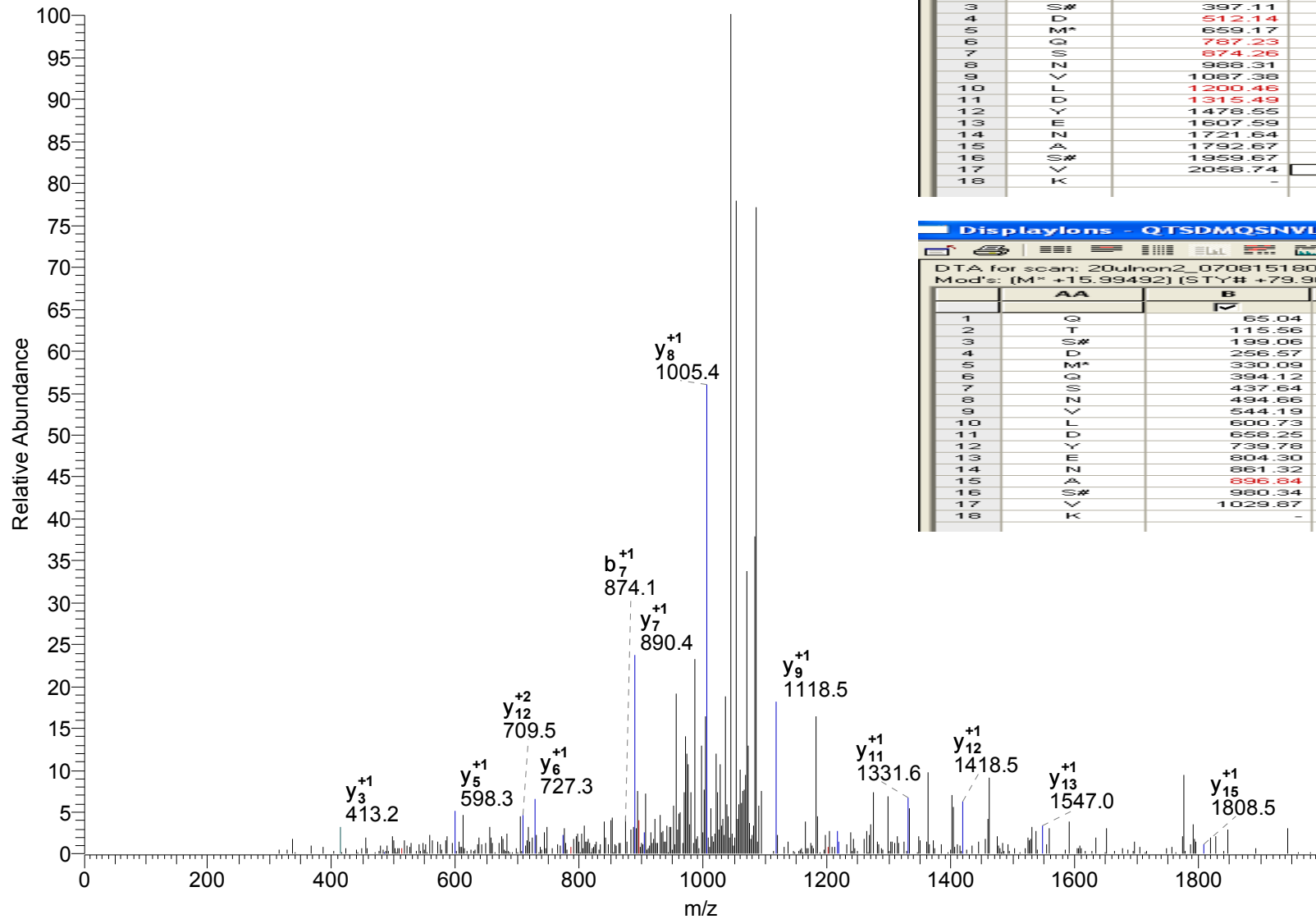
Displaylons - DLNATSSSSYQR

DTA for scan: cap2, 1609
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	D		58.52	-		12
2	L		115.06	687.26		11
3	N		172.08	630.72		10
4	A		207.60	573.70		9
5	T		258.13	538.18		8
6	S		301.64	487.65		7
7	S#		385.14	444.14		6
8	S		428.66	360.64		5
9	S#		512.16	317.12		4
10	Y		593.69	233.62		3
11	Q		657.72	152.09		2
12	R		-	88.06		1

Sp3111 Sperm protein SSP3111

#1730-1730 NL: 4.40E2



Displaylens - QTSDMQSNVLDYENASVK

DTA for scan: 20ulnon2_070815180655_1730
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	Q	129.07	-	18
2	T	230.11	2076.79	17
3	S#	397.11	1975.74	16
4	D	512.14	1808.74	15
5	M*	659.17	1693.71	14
6	Q	787.23	1546.68	13
7	S	874.26	1418.62	12
8	N	988.31	1331.59	11
9	V	1087.38	1217.54	10
10	L	1200.46	1118.48	9
11	D	1315.49	1005.39	8
12	Y	1478.55	890.37	7
13	E	1607.59	727.30	6
14	N	1721.64	598.26	5
15	A	1792.67	484.22	4
16	S#	1959.67	413.18	3
17	V	2058.74	246.18	2
18	K	-	147.11	1

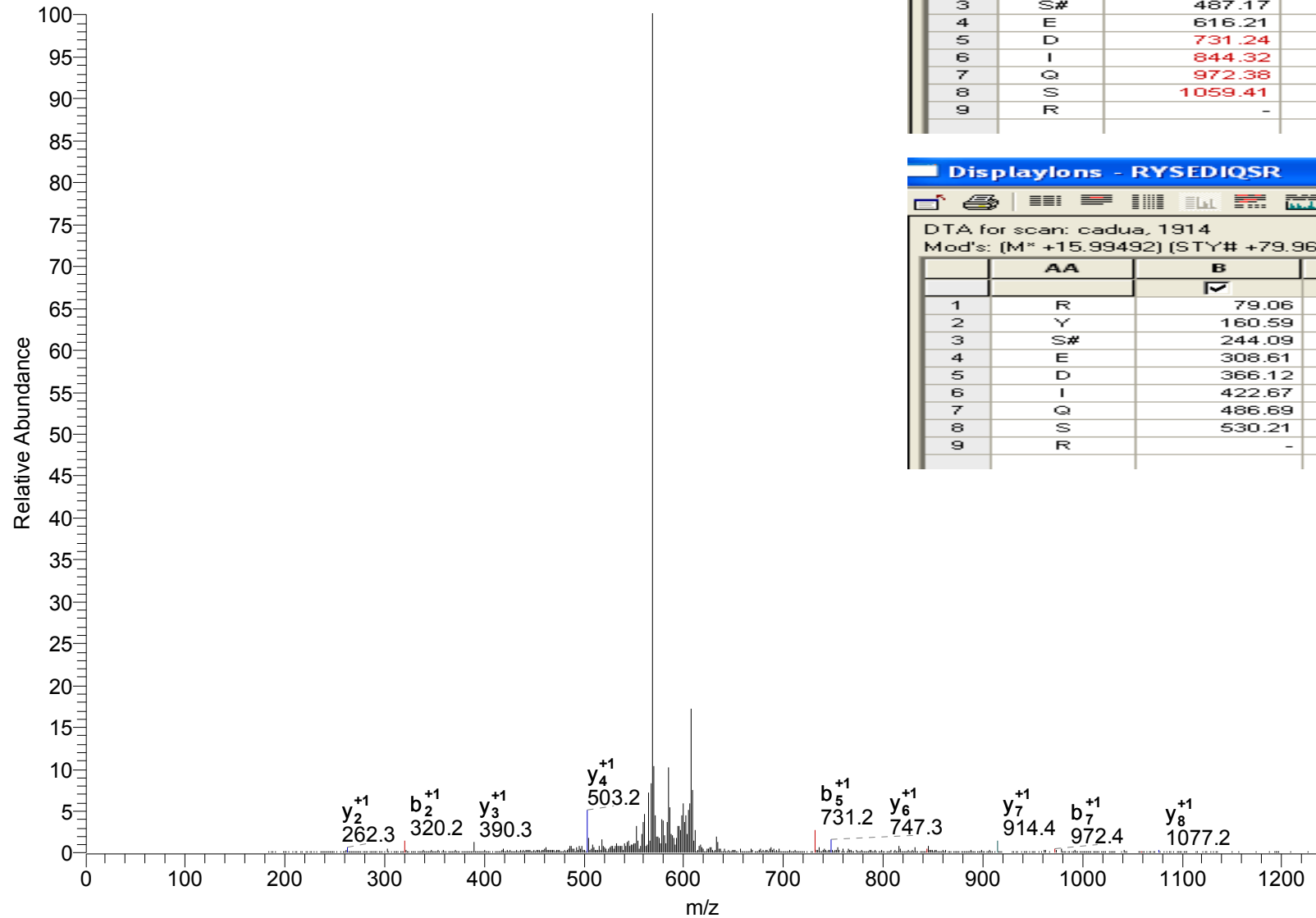
Displaylens - QTSDMQSNVLDYENASVK

DTA for scan: 20ulnon2_070815180655_1730
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	Q	65.04	-	18
2	T	115.56	1038.90	17
3	S#	199.06	988.37	16
4	D	256.57	904.87	15
5	M*	330.09	847.36	14
6	Q	394.12	773.84	13
7	S	437.64	709.81	12
8	N	494.66	666.30	11
9	V	544.19	609.28	10
10	L	600.73	559.74	9
11	D	658.25	503.20	8
12	Y	739.78	445.69	7
13	E	804.30	364.15	6
14	N	861.32	299.63	5
15	A	896.84	242.61	4
16	S#	980.34	207.09	3
17	V	1029.87	123.59	2
18	K	-	74.06	1

Sp3111 Sperm protein SSP3111

#1914-1914 NL: 1.72E4



Displaylons - RYSEDIQSR

DTA for scan: cadua, 1914
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	R	157.11	-	9
2	Y	320.17	1077.42	8
3	S#	487.17	914.36	7
4	E	616.21	747.36	6
5	D	731.24	618.32	5
6	I	844.32	503.29	4
7	Q	972.38	390.21	3
8	S	1059.41	262.15	2
9	R	-	175.12	1

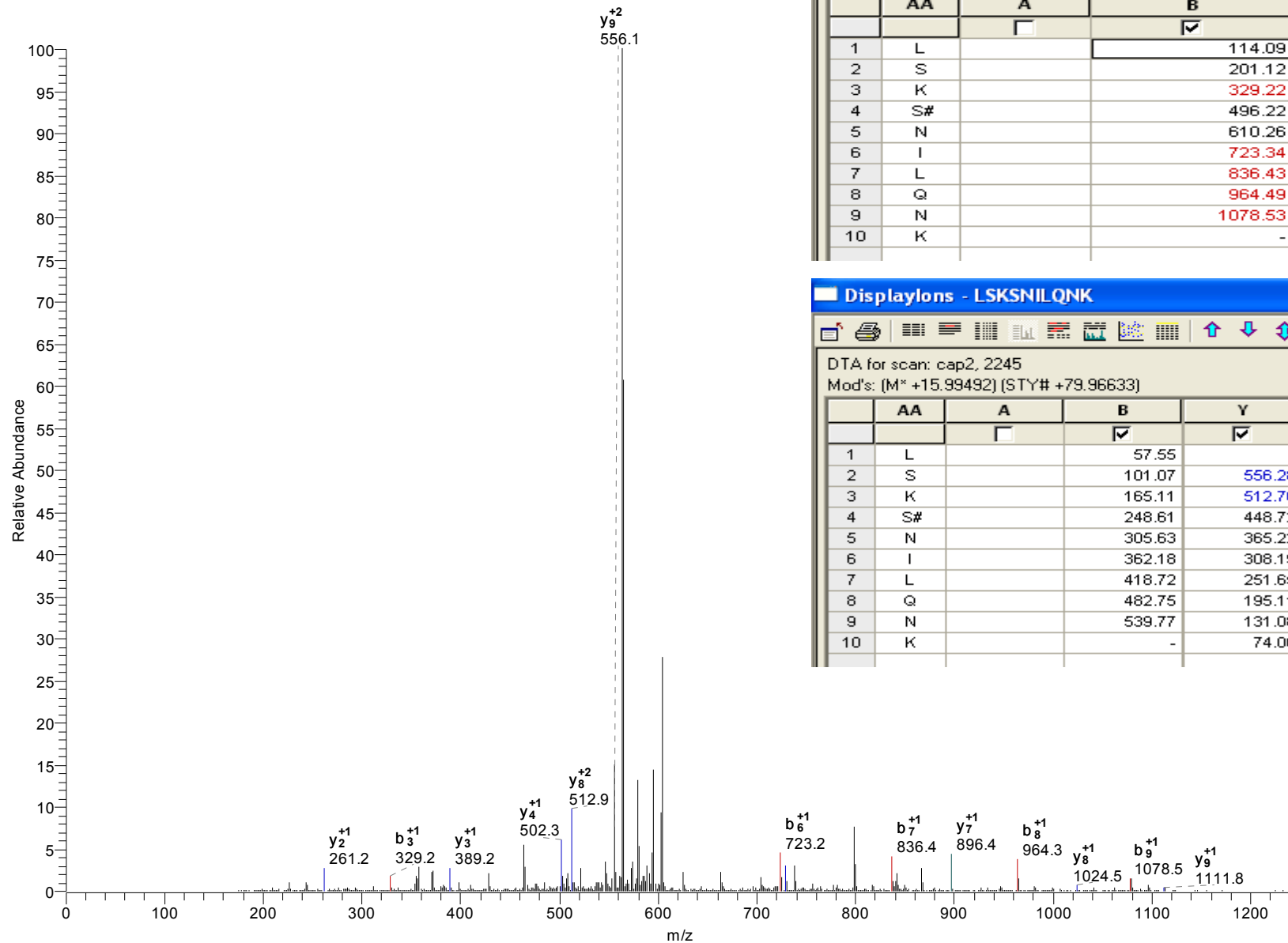
Displaylons - RYSEDIQSR

DTA for scan: cadua, 1914
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	R	79.06	-	9
2	Y	160.59	539.22	8
3	S#	244.09	457.68	7
4	E	308.61	374.19	6
5	D	366.12	309.66	5
6	I	422.67	252.15	4
7	Q	486.69	195.61	3
8	S	530.21	131.58	2
9	R	-	88.06	1

Uncharacterized protein C7orf31 homolog

#2245-2245 NL: 2.21E4



Displaylons - LSKSNILQNK

DTA for scan: cap2, 2245
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L	☐	☒	☒	10
2	S		114.09	-	9
3	K		201.12	1111.55	8
4	S#		329.22	1024.52	7
5	N		496.22	896.42	6
6	I		610.26	729.43	5
7	L		723.34	615.38	4
8	Q		836.43	502.30	3
9	N		964.49	389.21	2
10	K		1078.53	261.16	1
			-	147.11	

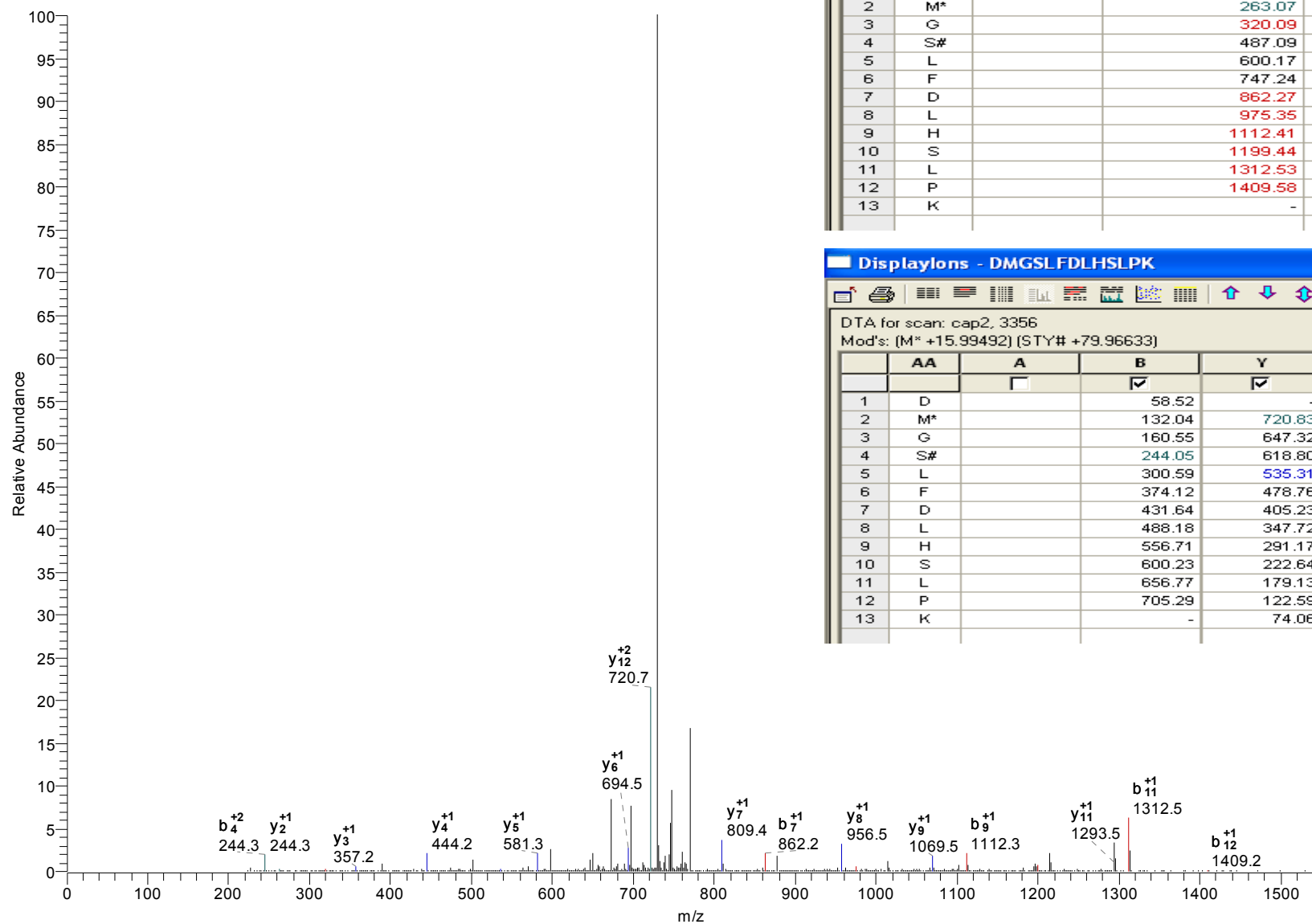
Displaylons - LSKSNILQNK

DTA for scan: cap2, 2245
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L	☐	☒	☒	☐	10
2	S		57.55	-		9
3	K		101.07	556.28		8
4	S#		165.11	512.76		7
5	N		248.61	448.72		6
6	I		305.63	365.22		5
7	L		362.18	308.19		4
8	Q		418.72	251.65		3
9	N		482.75	195.11		2
10	K		539.77	131.08		1
			-	74.06		

Uncharacterized protein C7orf31 homolog

#3356-3356 NL: 4.55E4



Displaylons - DMGSLFDLHSLPK

DTA for scan: cap2, 3356
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	A	B	Y	
1	D		116.03	-	13
2	M*		263.07	1440.66	12
3	G		320.09	1293.62	11
4	S#		487.09	1236.60	10
5	L		600.17	1069.60	9
6	F		747.24	956.52	8
7	D		862.27	809.45	7
8	L		975.35	694.42	6
9	H		1112.41	581.34	5
10	S		1199.44	444.28	4
11	L		1312.53	357.25	3
12	P		1409.58	244.17	2
13	K		-	147.11	1

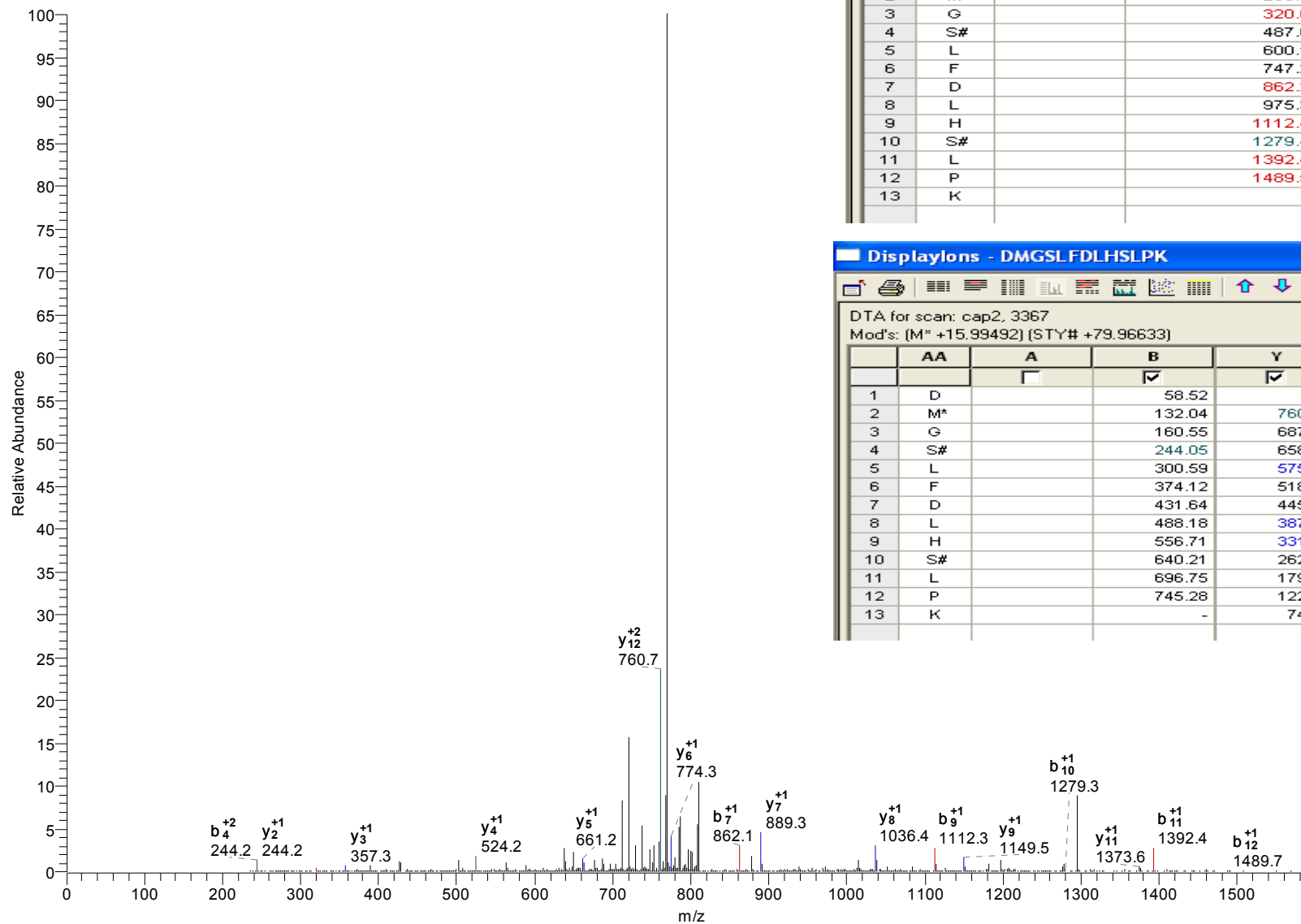
Displaylons - DMGSLFDLHSLPK

DTA for scan: cap2, 3356
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	A	B	Y	Z	
1	D		58.52	-		13
2	M*		132.04	720.83		12
3	G		160.55	647.32		11
4	S#		244.05	618.80		10
5	L		300.59	535.31		9
6	F		374.12	478.76		8
7	D		431.64	405.23		7
8	L		488.18	347.72		6
9	H		556.71	291.17		5
10	S		600.23	222.64		4
11	L		656.77	179.13		3
12	P		705.29	122.59		2
13	K		-	74.06		1

Uncharacterized protein C7orf31 homolog

#3367-3367 NL: 2.35E4



Displaylons - DMGSLFDLHSLPK

DTA for scan: cap2, 3367
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	D		116.03	-	13
2	M*		263.07	1520.63	12
3	G		320.09	1373.59	11
4	S#		487.09	1316.57	10
5	L		600.17	1149.57	9
6	F		747.24	1036.49	8
7	D		862.27	889.42	7
8	L		975.35	774.39	6
9	H		1112.41	661.31	5
10	S#		1279.41	524.25	4
11	L		1392.49	357.25	3
12	P		1489.55	244.17	2
13	K		-	147.11	1

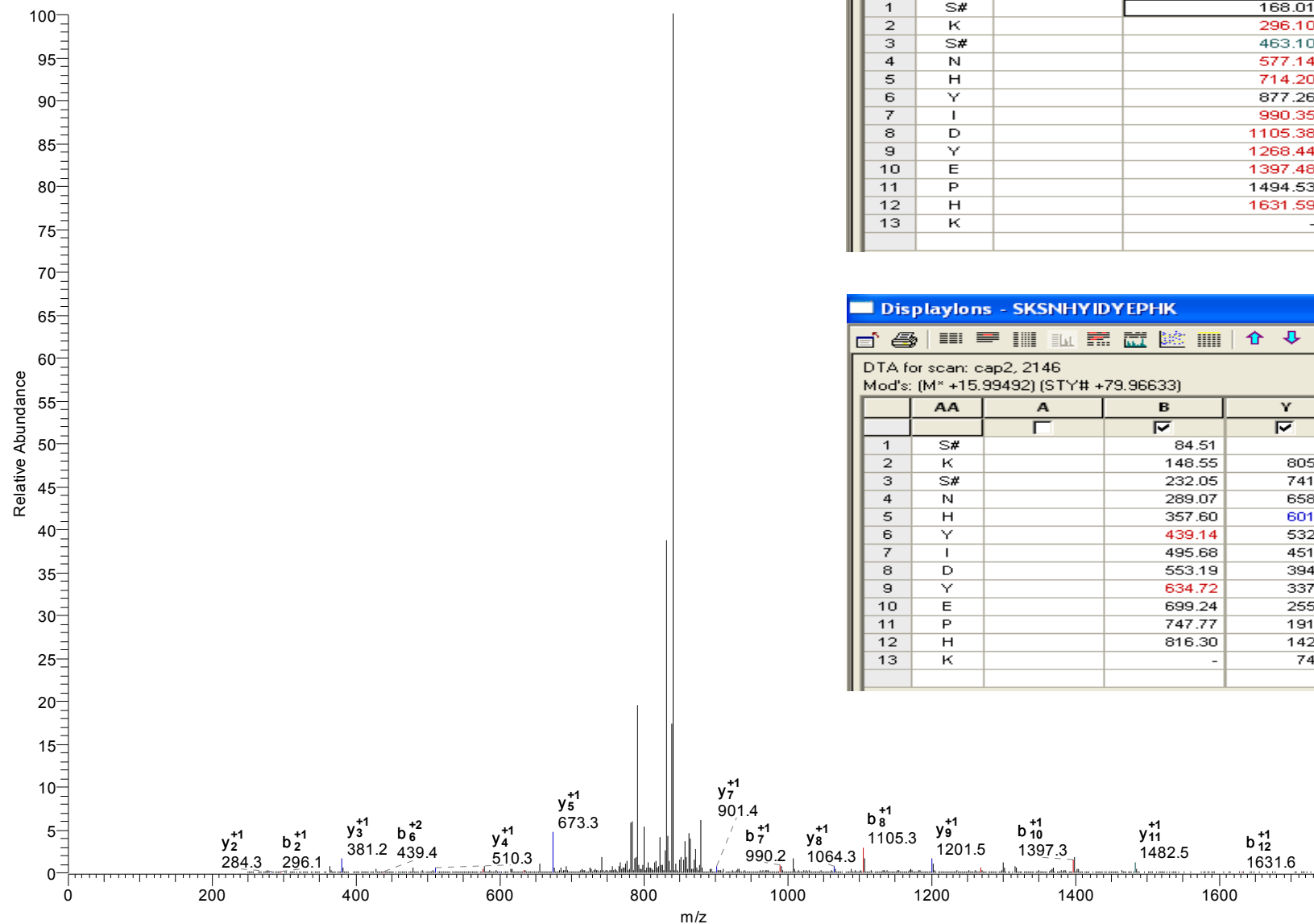
Displaylons - DMGSLFDLHSLPK

DTA for scan: cap2, 3367
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	D		58.52	-		13
2	M*		132.04	760.82		12
3	G		160.55	687.30		11
4	S#		244.05	658.79		10
5	L		300.59	575.29		9
6	F		374.12	518.75		8
7	D		431.64	445.21		7
8	L		488.18	387.70		6
9	H		556.71	331.16		5
10	S#		640.21	262.63		4
11	L		696.75	179.13		3
12	P		745.28	122.59		2
13	K		-	74.06		1

Uncharacterized protein C7orf31 homolog

#2146-2146 NL: 4.95E4



Displaylons - SKSNHYIDYEPHK

DTA for scan: cap2, 2146
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S#		168.01	-	13
2	K		296.10	1610.70	12
3	S#		463.10	1482.60	11
4	N		577.14	1315.61	10
5	H		714.20	1201.56	9
6	Y		877.26	1064.50	8
7	I		990.35	901.44	7
8	D		1105.38	788.36	6
9	Y		1268.44	673.33	5
10	E		1397.48	510.27	4
11	P		1494.53	381.22	3
12	H		1631.59	284.17	2
13	K		-	147.11	1

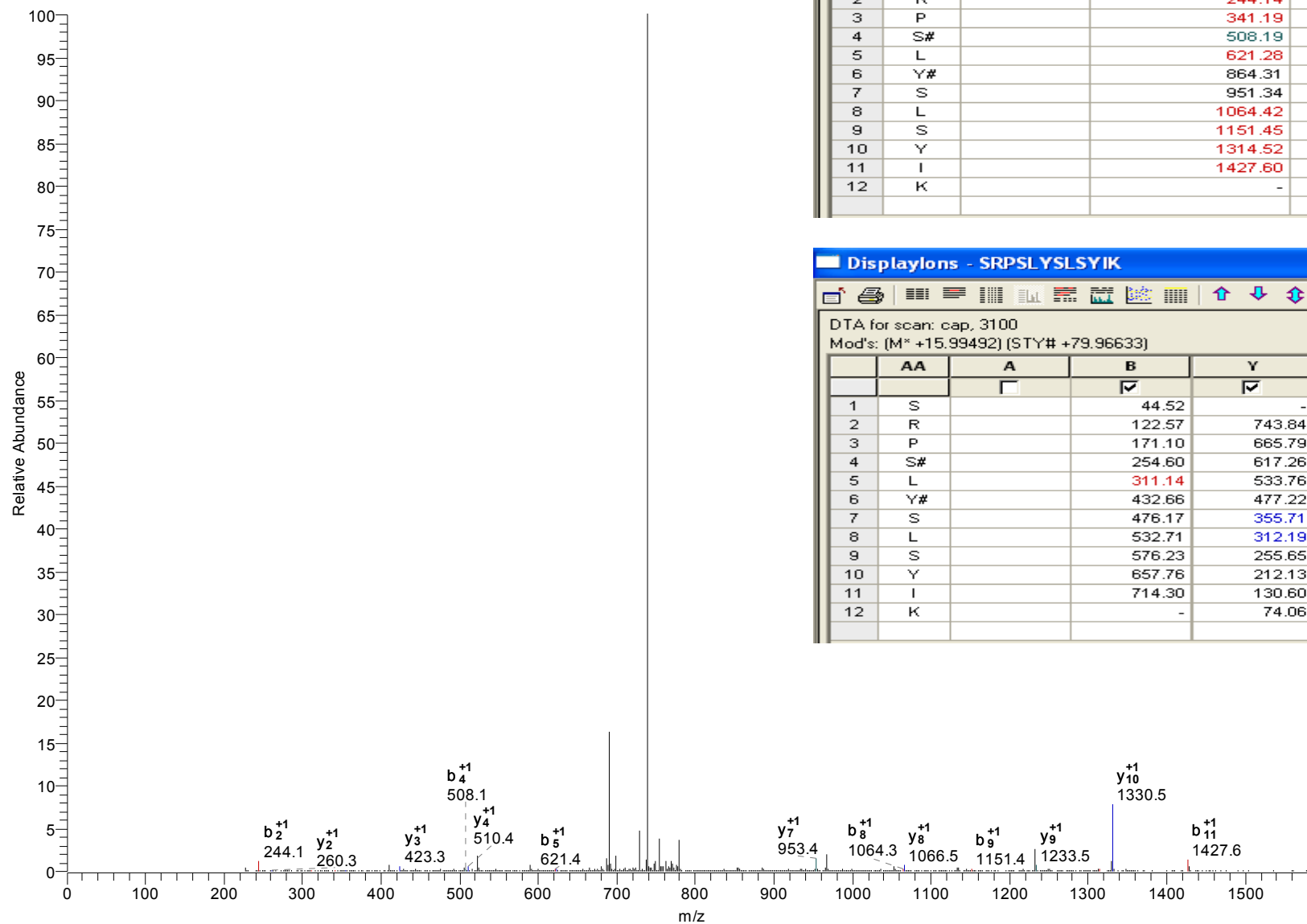
Displaylons - SKSNHYIDYEPHK

DTA for scan: cap2, 2146
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S#		84.51	-		13
2	K		148.55	805.85		12
3	S#		232.05	741.81		11
4	N		289.07	658.31		10
5	H		357.60	601.29		9
6	Y		439.14	532.76		8
7	I		495.68	451.22		7
8	D		553.19	394.68		6
9	Y		634.72	337.17		5
10	E		699.24	255.64		4
11	P		747.77	191.12		3
12	H		816.30	142.59		2
13	K		-	74.06		1

Oaz3 ornithine decarboxylase antizyme 3

#3100-3100 NL: 5.93E4



Displaylons - SRPSLYSLSYIK

DTA for scan: cap, 3100
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	12
2	R		244.14	1486.67	11
3	P		341.19	1330.57	10
4	S#		508.19	1233.52	9
5	L		621.28	1066.52	8
6	Y#		864.31	953.44	7
7	S		951.34	710.41	6
8	L		1064.42	623.38	5
9	S		1151.45	510.29	4
10	Y		1314.52	423.26	3
11	I		1427.60	260.20	2
12	K		-	147.11	1

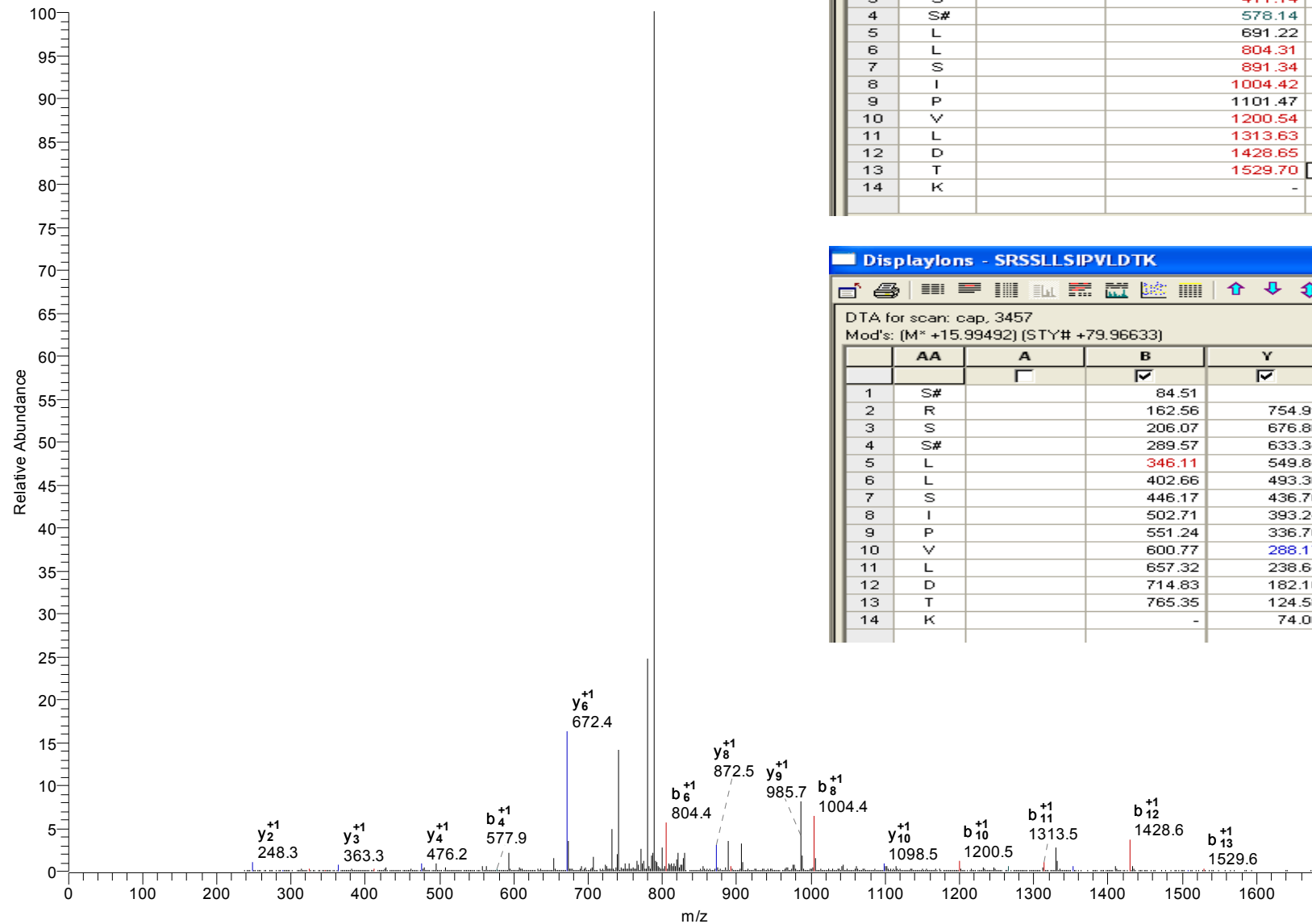
Displaylons - SRPSLYSLSYIK

DTA for scan: cap, 3100
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	S		44.52	-		12
2	R		122.57	743.84		11
3	P		171.10	665.79		10
4	S#		254.60	617.26		9
5	L		311.14	533.76		8
6	Y#		432.66	477.22		7
7	S		476.17	355.71		6
8	L		532.71	312.19		5
9	S		576.23	255.65		4
10	Y		657.76	212.13		3
11	I		714.30	130.60		2
12	K		-	74.06		1

Theg Isoform 2 of Testicular haploid expressed gene protein

#3457-3457 NL: 4.60E4



Displaylons - SRSSLISIPVLDTK

DTA for scan: cap. 3457
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	S#		168.01	-	14
2	R		324.11	1508.81	13
3	S		411.14	1352.71	12
4	S#		578.14	1265.68	11
5	L		691.22	1098.68	10
6	L		804.31	985.59	9
7	S		891.34	872.51	8
8	I		1004.42	785.48	7
9	P		1101.47	672.39	6
10	V		1200.54	575.34	5
11	L		1313.63	476.27	4
12	D		1428.65	363.19	3
13	T		1529.70	248.16	2
14	K		-	147.11	1

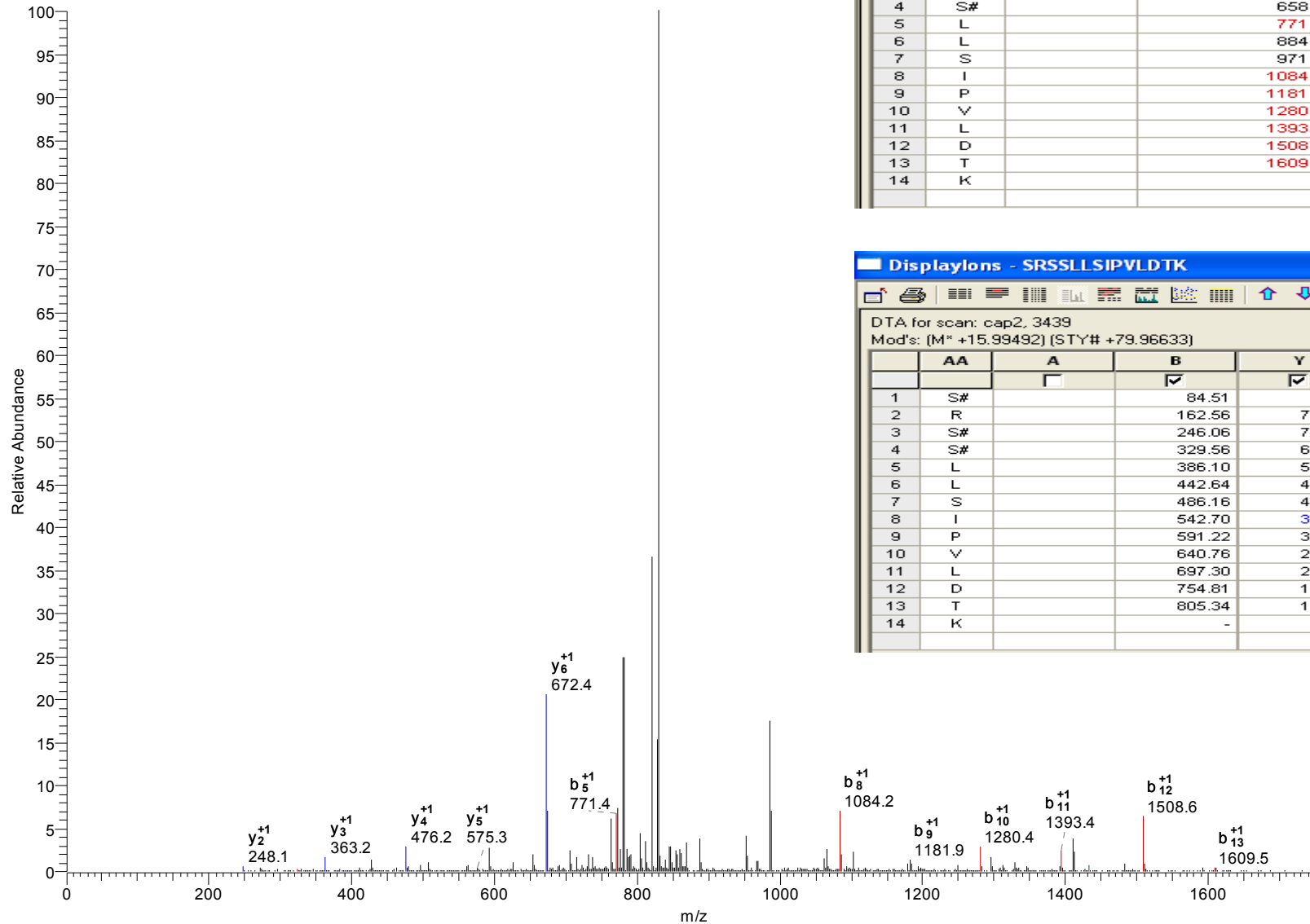
Displaylons - SRSSLISIPVLDTK

DTA for scan: cap. 3457
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	S#		84.51	-		14
2	R		162.56	754.91		13
3	S		206.07	676.86		12
4	S#		289.57	633.34		11
5	L		346.11	549.84		10
6	L		402.66	493.30		9
7	S		446.17	436.76		8
8	I		502.71	393.24		7
9	P		551.24	336.70		6
10	V		600.77	288.17		5
11	L		657.32	238.64		4
12	D		714.83	182.10		3
13	T		765.35	124.58		2
14	K		-	74.06		1

Theg Isoform 2 of Testicular haploid expressed gene protein

#3439-3439 NL: 3.47E4



Displaylons - SRSSLLSIPVLDTK

DTA for scan: cap2, 3439
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	S#	☐	☒	☒	
2	R		168.01	-	14
3	S#		324.11	1588.77	13
4	S#		491.11	1432.67	12
5	L		658.10	1265.68	11
6	L		771.19	1098.68	10
7	S		884.27	985.59	9
8	I		971.30	872.51	8
9	P		1084.39	785.48	7
10	V		1181.44	672.39	6
11	L		1280.51	575.34	5
12	D		1393.59	476.27	4
13	T		1508.62	363.19	3
14	K		1609.67	248.16	2
			-	147.11	1

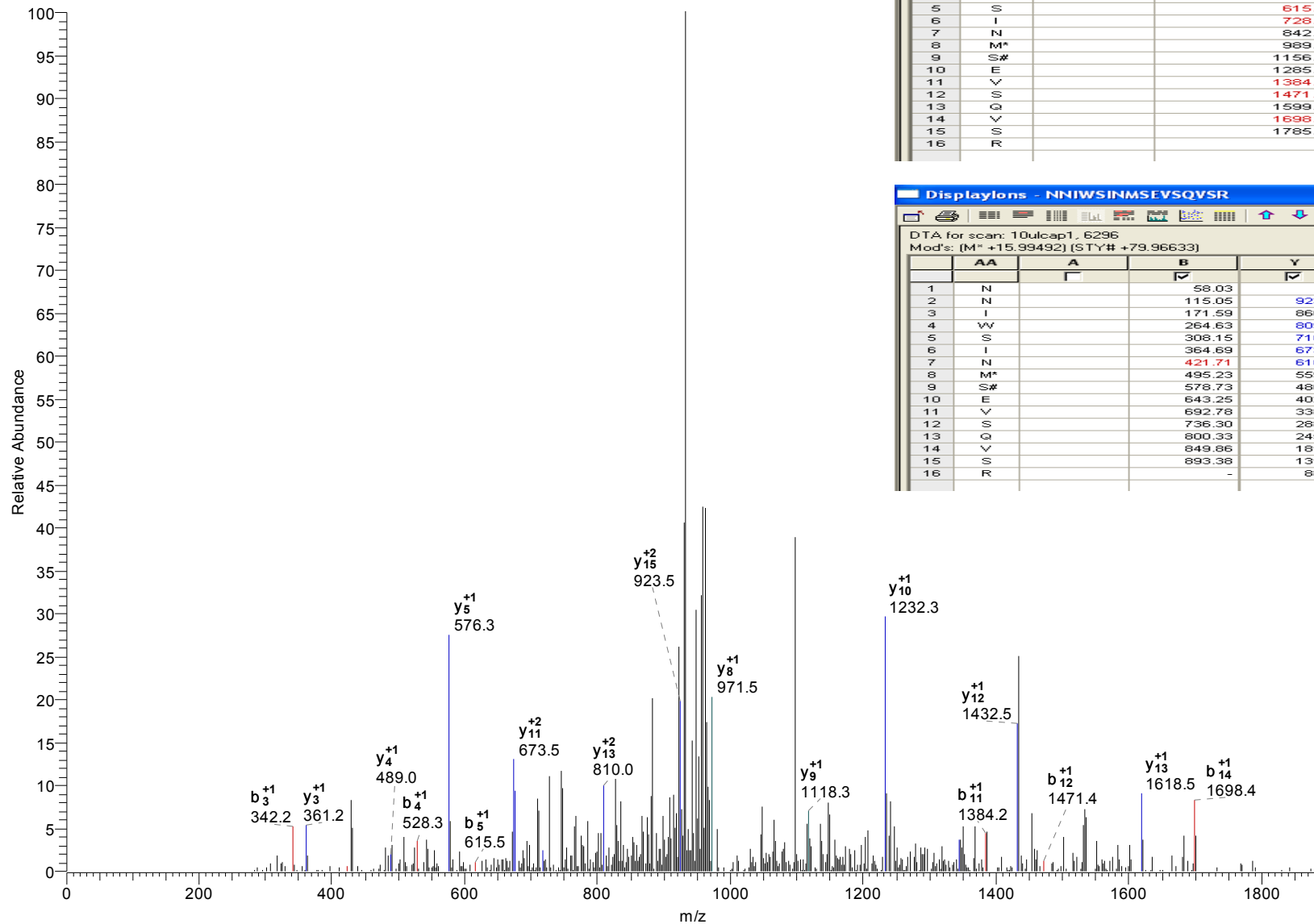
Displaylons - SRSSLLSIPVLDTK

DTA for scan: cap2, 3439
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	S#	☐	☒	☒	☐	
2	R		84.51	-		14
3	S#		162.56	794.89		13
4	S#		246.06	716.84		12
5	L		329.56	633.34		11
6	L		386.10	549.84		10
7	S		442.64	493.30		9
8	I		486.16	436.76		8
9	P		542.70	393.24		7
10	V		591.22	336.70		6
11	L		640.76	288.17		5
12	D		697.30	238.64		4
13	T		754.81	182.10		3
14	K		805.34	124.58		2
			-	74.06		1

Theg Isoform 2 of Testicular haploid expressed gene protein

#6296-6296 NL: 3.25E2



Displaylons - NNIWSINMSEVSQVSR

DTA for scan: 10ulcap1, 6296
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N		115.05	-	16
2	N		229.09	1845.82	15
3	I		342.18	1731.78	14
4	W		528.26	1618.69	13
5	S		615.29	1432.61	12
6	I		728.37	1345.58	11
7	N		842.42	1232.50	10
8	M*		989.45	1118.45	9
9	S#		1156.45	971.42	8
10	E		1285.49	804.42	7
11	V		1384.56	675.38	6
12	S		1471.59	576.31	5
13	Q		1599.65	489.28	4
14	V		1698.72	361.22	3
15	S		1785.75	262.15	2
16	R		-	175.12	1

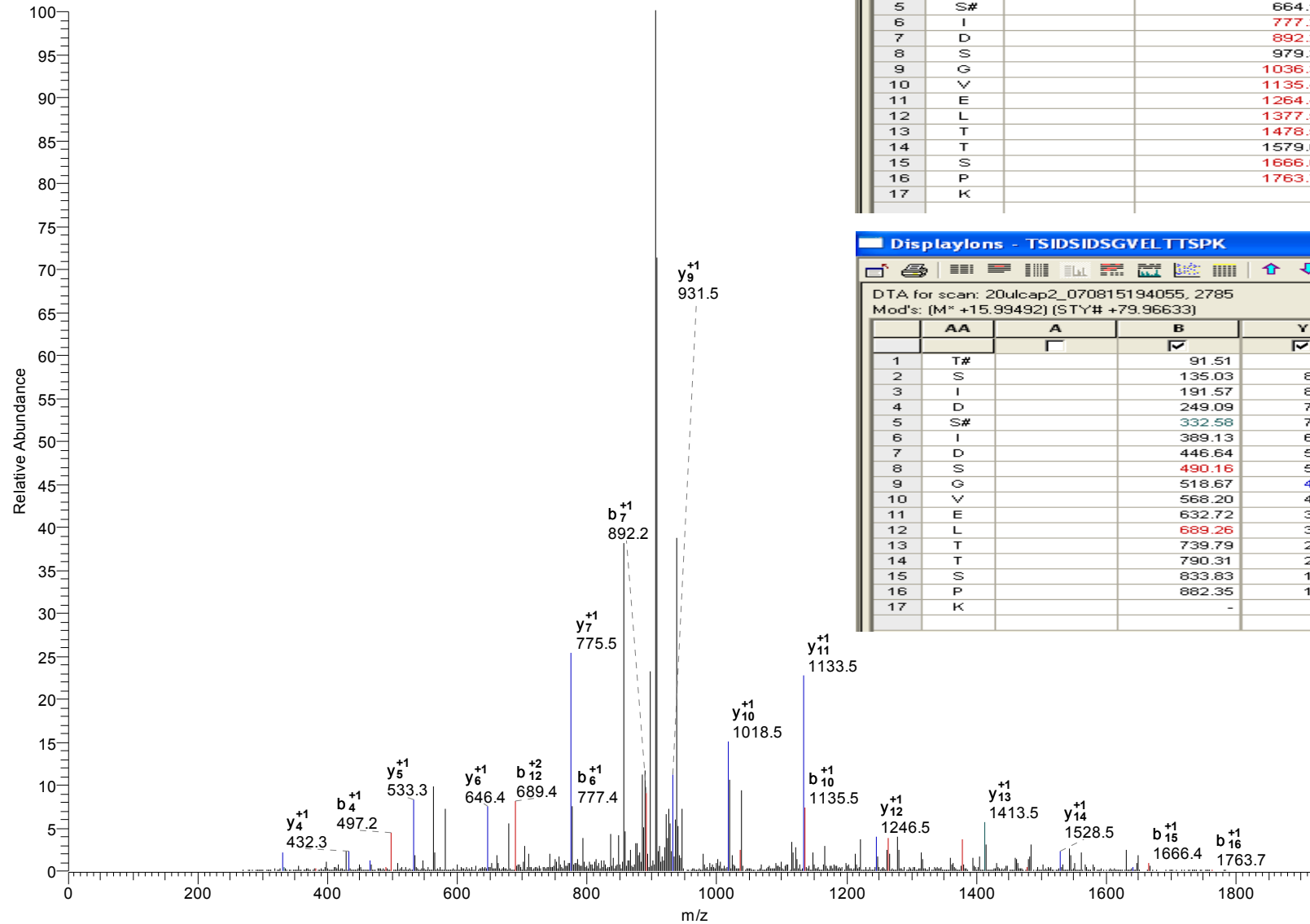
Displaylons - NNIWSINMSEVSQVSR

DTA for scan: 10ulcap1, 6296
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	N		58.03	-	-	16
2	N		115.05	923.41	-	15
3	I		171.59	866.39	-	14
4	W		264.63	809.85	-	13
5	S		308.15	716.81	-	12
6	I		364.69	673.29	-	11
7	N		421.71	616.75	-	10
8	M*		495.23	559.73	-	9
9	S#		578.73	486.21	-	8
10	E		643.25	402.71	-	7
11	V		692.78	338.19	-	6
12	S		736.30	288.66	-	5
13	Q		800.33	245.14	-	4
14	V		849.86	181.11	-	3
15	S		893.38	131.58	-	2
16	R		-	88.06	-	1

Slc16a6 66 kDa protein

#2785-2785 NL: 8.54E3



Displaylons - TSIDSIDSGVELTTSPK

DTA for scan: 20ulcap2_070815194055, 2785
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	T#		182.02	-	17
2	S		269.05	1728.79	16
3	I		382.14	1641.76	15
4	D		497.16	1528.68	14
5	S#		664.16	1413.65	13
6	I		777.25	1246.65	12
7	D		892.27	1133.57	11
8	S		979.31	1018.54	10
9	G		1036.33	931.51	9
10	V		1135.40	874.49	8
11	E		1264.44	775.42	7
12	L		1377.52	646.38	6
13	T		1478.57	533.29	5
14	T		1579.62	432.25	4
15	S		1666.65	331.20	3
16	P		1763.70	244.17	2
17	K		-	147.11	1

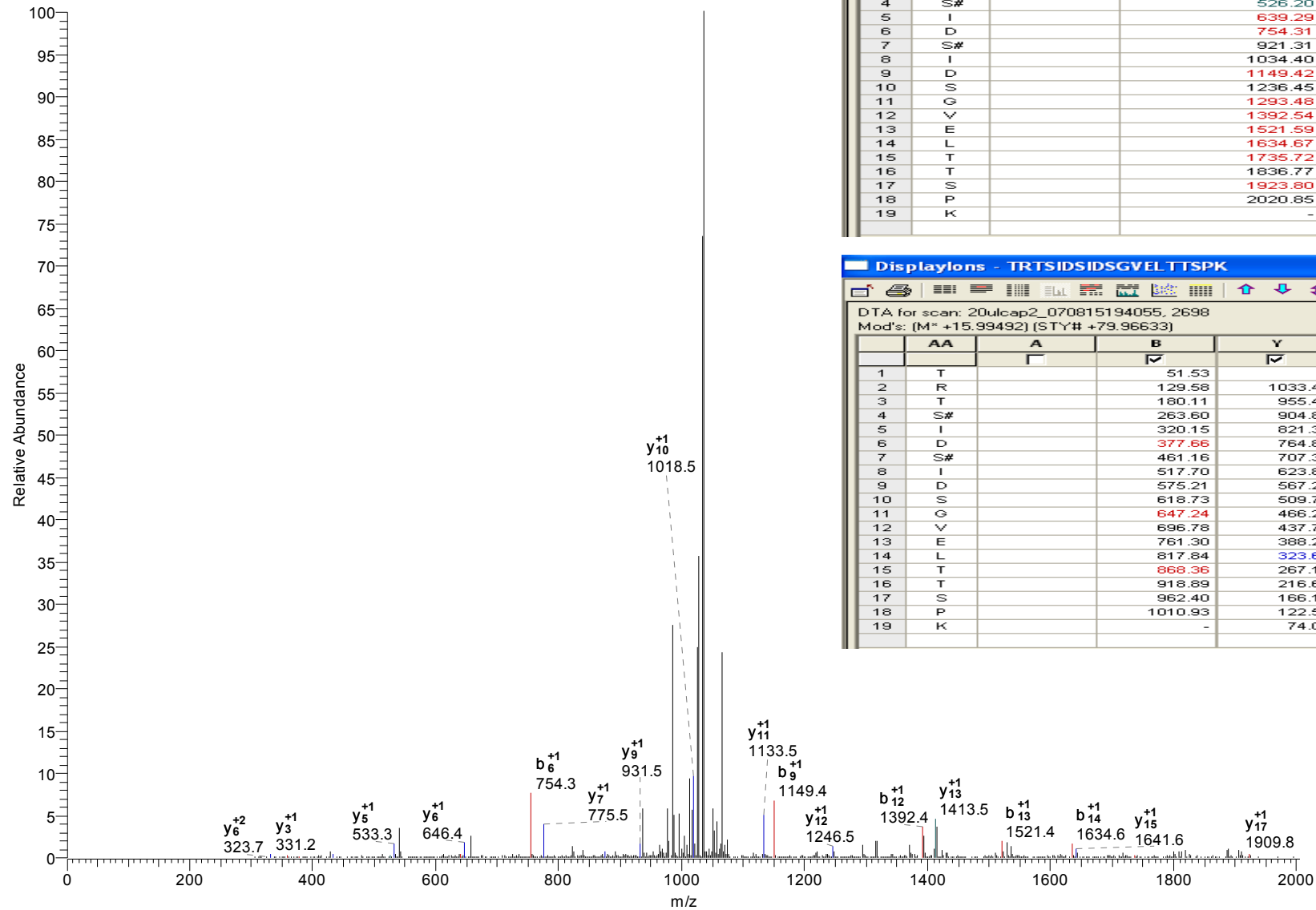
Displaylons - TSIDSIDSGVELTTSPK

DTA for scan: 20ulcap2_070815194055, 2785
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z
1	T#		91.51	-	17
2	S		135.03	864.90	16
3	I		191.57	821.38	15
4	D		249.09	764.84	14
5	S#		332.58	707.33	13
6	I		389.13	623.83	12
7	D		446.64	567.29	11
8	S		490.16	509.77	10
9	G		518.67	466.26	9
10	V		568.20	437.75	8
11	E		632.72	388.21	7
12	L		689.26	323.69	6
13	T		739.79	267.15	5
14	T		790.31	216.63	4
15	S		833.83	166.10	3
16	P		882.35	122.59	2
17	K		-	74.06	1

Slc16a6 66 kDa protein

#2698-2698 NL: 1.14E4



Displaylons - TRTSIDSGVELTTSPK

DTA for scan: 20ulcap2_070815194055_2698
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	T		102.05	-	19
2	R		258.16	2065.91	18
3	T		359.20	1909.81	17
4	S#		526.20	1808.76	16
5	I		639.29	1641.76	15
6	D		754.31	1528.68	14
7	S#		921.31	1413.65	13
8	I		1034.40	1246.65	12
9	D		1149.42	1133.57	11
10	S		1236.45	1018.54	10
11	G		1293.48	931.51	9
12	V		1392.54	874.49	8
13	E		1521.59	775.42	7
14	L		1634.67	646.38	6
15	T		1735.72	533.29	5
16	T		1836.77	432.25	4
17	S		1923.80	331.20	3
18	P		2020.85	244.17	2
19	K		-	147.11	1

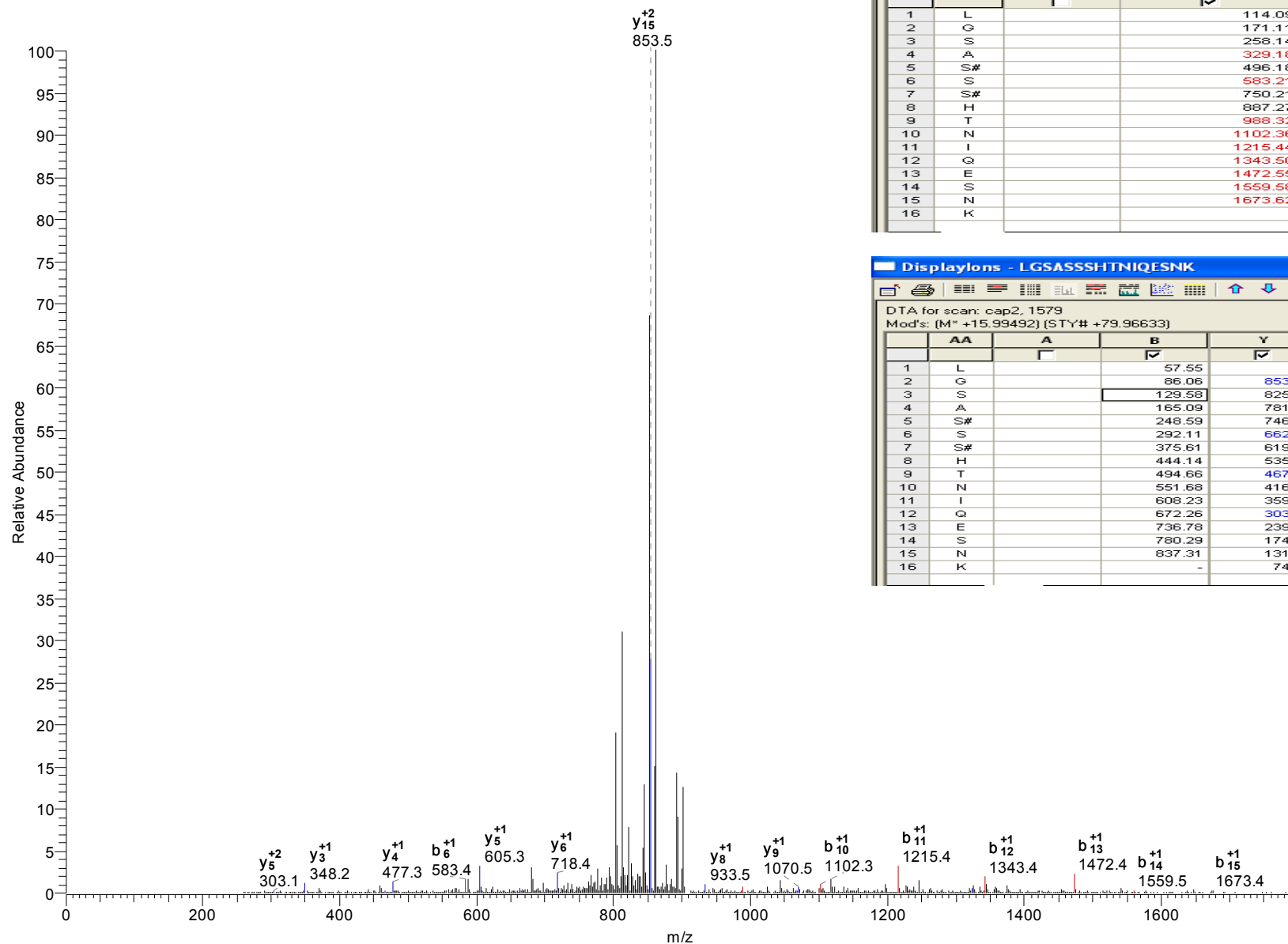
Displaylons - TRTSIDSGVELTTSPK

DTA for scan: 20ulcap2_070815194055_2698
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	T		51.53	-		19
2	R		129.58	1033.46		18
3	T		180.11	955.41		17
4	S#		263.60	904.88		16
5	I		320.15	821.38		15
6	D		377.66	764.84		14
7	S#		461.16	707.33		13
8	I		517.70	623.83		12
9	D		575.21	567.29		11
10	S		618.73	509.77		10
11	G		647.24	466.26		9
12	V		696.78	437.75		8
13	E		761.30	388.21		7
14	L		817.84	323.69		6
15	T		868.36	267.15		5
16	T		918.89	216.63		4
17	S		962.40	166.10		3
18	P		1010.93	122.59		2
19	K		-	74.06		1

Camk4 Isoform 2 of Calcium/calmodulin-dependent protein kinase type IV

#1579-1579 NL: 1.65E4



Displaylons - LGSASSHTNIQESNK

DTA for scan: cap2, 1579
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L			114.09	-
2	G			171.11	1706.64
3	S			258.14	1649.62
4	A			329.18	1562.59
5	S#			496.18	1491.55
6	S			583.21	1324.55
7	S#			750.21	1237.52
8	H			887.27	1070.52
9	T			988.32	933.46
10	N			1102.36	832.42
11	I			1215.44	718.37
12	Q			1343.50	605.29
13	E			1472.55	477.23
14	S			1559.58	348.19
15	N			1673.62	261.16
16	K			-	147.11

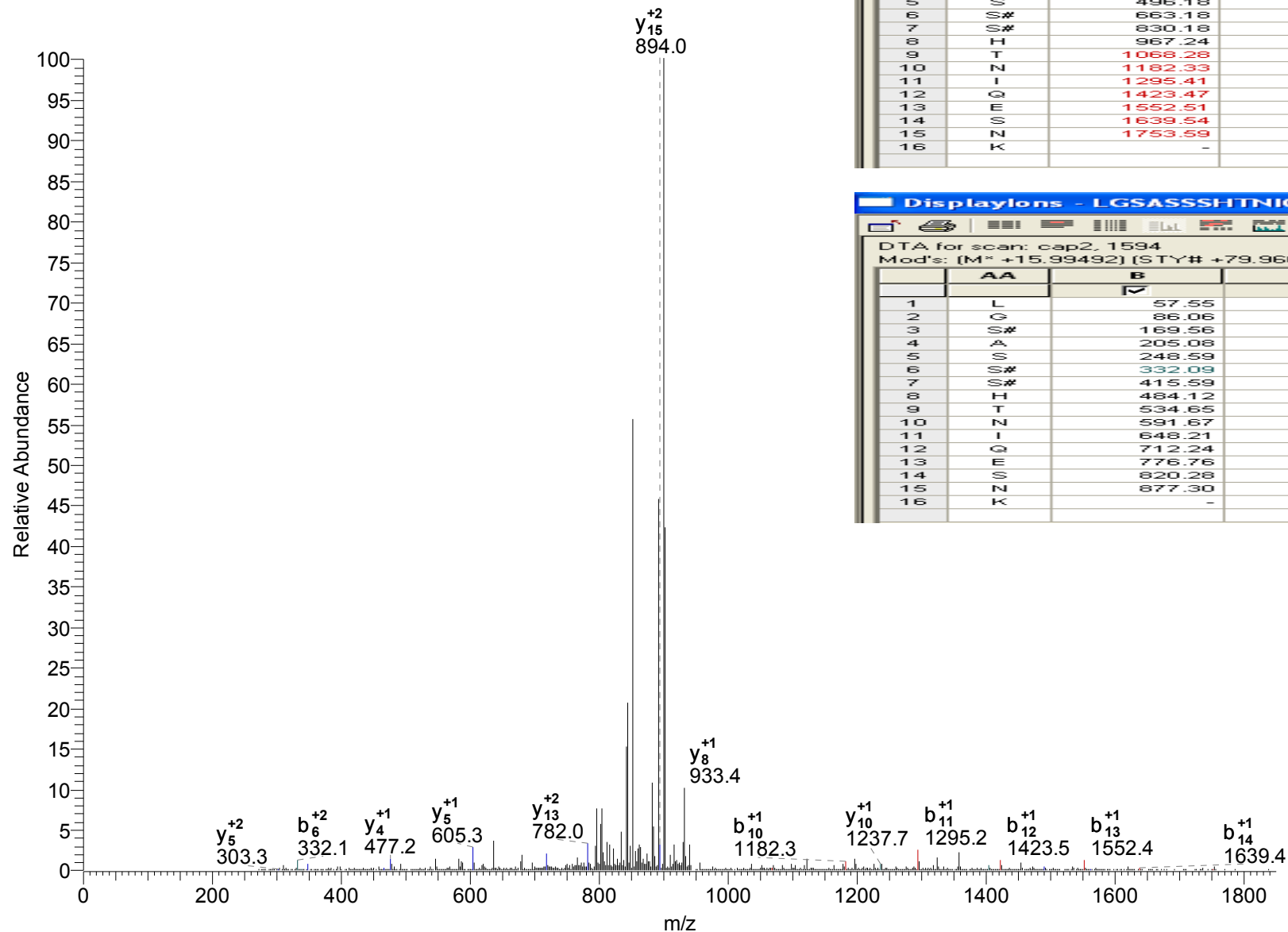
Displaylons - LGSASSHTNIQESNK

DTA for scan: cap2, 1579
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z
1	L			57.55	-
2	G			86.06	853.82
3	S			129.58	825.31
4	A			165.09	781.80
5	S#			248.59	746.28
6	S			292.11	662.78
7	S#			375.61	619.26
8	H			444.14	535.76
9	T			494.66	467.24
10	N			551.68	416.71
11	I			608.23	359.69
12	Q			672.26	303.15
13	E			736.78	239.12
14	S			780.29	174.60
15	N			837.31	131.08
16	K			-	74.06

Camk4 Isoform 2 of Calcium/Calmodulin-dependent protein kinase type IV

#1594-1594 NL: 1.57E4



Displaylons - LGSASSHTNIQESNK

DTA for scan: cap2, 1594
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	L	114.09	-	16
2	Q	171.11	1786.61	15
3	S#	338.11	1729.59	14
4	A	409.15	1562.59	13
5	S	496.18	1491.55	12
6	S#	563.18	1404.52	11
7	S#	830.18	1237.52	10
8	H	967.24	1070.52	9
9	T	1068.28	933.46	8
10	N	1182.33	832.42	7
11	I	1295.41	718.37	6
12	Q	1423.47	605.29	5
13	E	1552.51	477.23	4
14	S	1639.54	348.19	3
15	N	1753.59	261.16	2
16	K	-	147.11	1

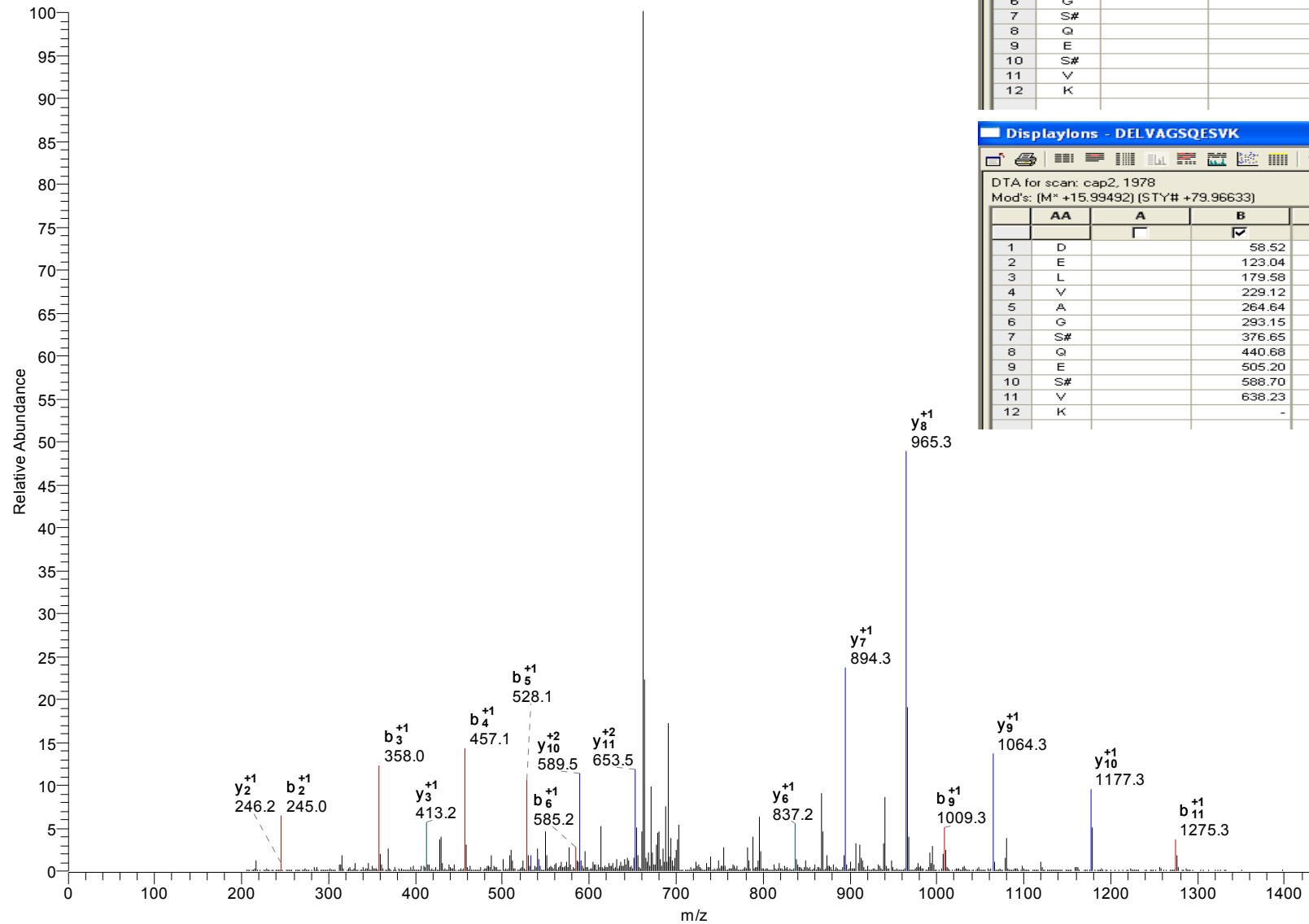
Displaylons - LGSASSHTNIQESNK

DTA for scan: cap2, 1594
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	L	57.55	-	16
2	Q	86.06	893.81	15
3	S#	169.56	865.30	14
4	A	205.08	781.80	13
5	S	248.59	746.28	12
6	S#	332.09	702.76	11
7	S#	415.59	619.26	10
8	H	484.12	535.76	9
9	T	534.65	467.24	8
10	N	591.67	416.71	7
11	I	648.21	359.69	6
12	Q	712.24	303.15	5
13	E	776.76	239.12	4
14	S	820.28	174.60	3
15	N	877.30	131.08	2
16	K	-	74.06	1

Dynein intermediate chain 1, axonemal

#1978-1978 NL: 3.94E4



Displaylons - DELVAGSQSVK

DTA for scan: cap2, 1978
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	D			116.03	-
2	E			245.08	1306.53
3	L			358.16	1177.49
4	V			457.23	1064.41
5	A			528.27	965.34
6	G			585.29	894.30
7	S#			752.29	837.28
8	Q			880.34	670.28
9	E			1009.39	542.22
10	S#			1176.39	413.18
11	V			1275.45	246.18
12	K			-	147.11

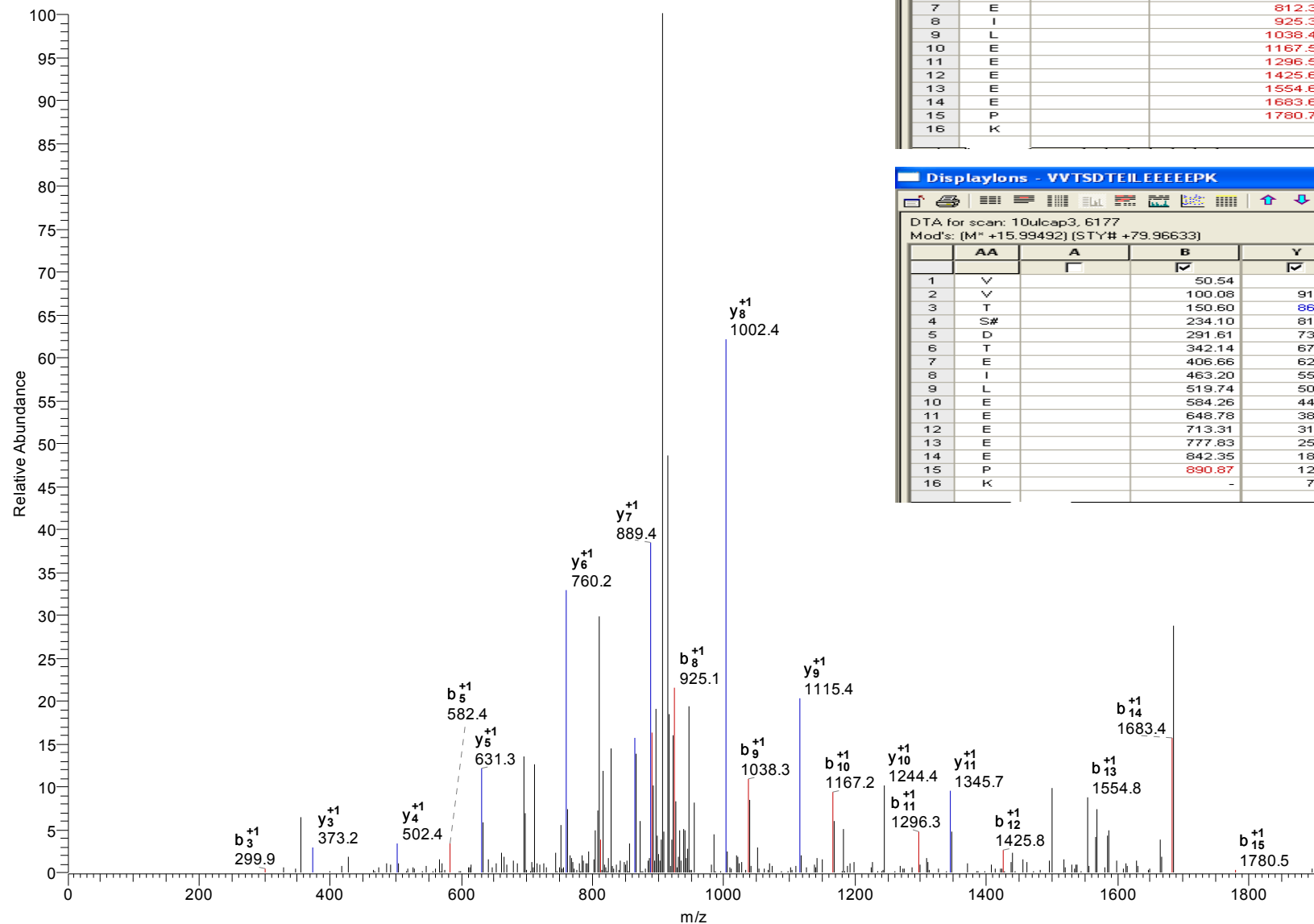
Displaylons - DELVAGSQSVK

DTA for scan: cap2, 1978
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z
1	D			58.52	-
2	E			123.04	653.77
3	L			179.58	589.25
4	V			229.12	532.71
5	A			264.64	483.17
6	G			293.15	447.65
7	S#			376.65	419.14
8	Q			440.68	335.64
9	E			505.20	271.61
10	S#			588.70	207.09
11	V			638.23	123.59
12	K			-	74.06

Dynein intermediate chain 1, axonemal

#6177-6177 NL: 3.10E2



Displaylons - VVTSDEILEEEEEPK

DTA for scan: 10ulcap3, 6177
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	V		100.08	-	16
2	V		199.14	1827.78	15
3	T		300.19	1728.71	14
4	S#		487.19	1627.66	13
5	D		582.22	1460.66	12
6	T		683.26	1345.64	11
7	E		812.31	1244.59	10
8	I		925.39	1115.55	9
9	L		1038.48	1002.46	8
10	E		1167.52	889.38	7
11	E		1296.56	760.34	6
12	E		1425.60	631.29	5
13	E		1554.65	502.25	4
14	E		1683.69	373.21	3
15	P		1780.74	244.17	2
16	K		-	147.11	1

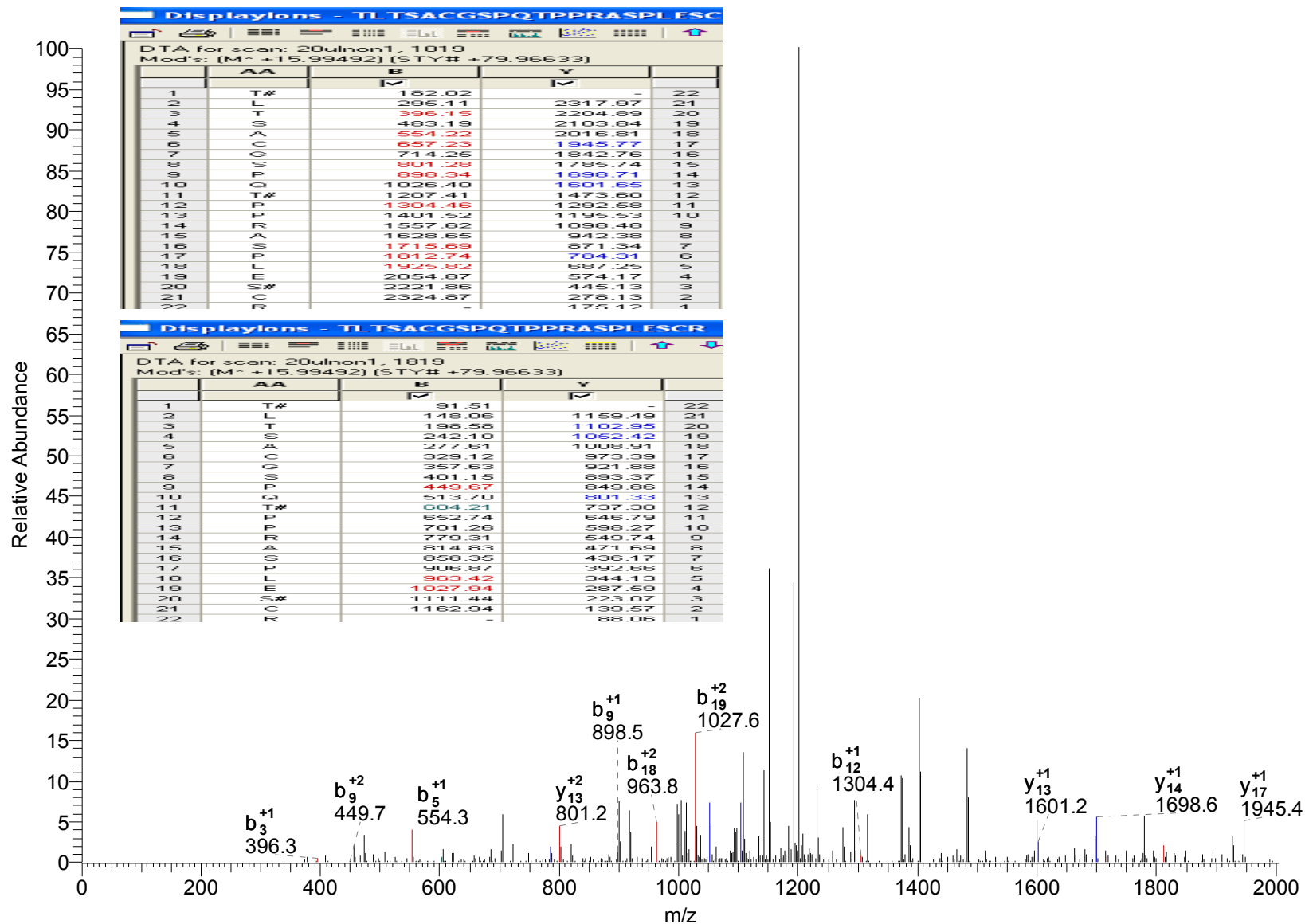
Displaylons - VVTSDEILEEEEEPK

DTA for scan: 10ulcap3, 6177
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	V		50.54	-	-	16
2	V		100.08	914.39	-	15
3	T		150.60	864.86	-	14
4	S#		234.10	814.33	-	13
5	D		291.61	730.84	-	12
6	T		342.14	673.32	-	11
7	E		406.66	622.80	-	10
8	I		463.20	558.28	-	9
9	L		519.74	501.73	-	8
10	E		584.26	445.19	-	7
11	E		648.78	380.67	-	6
12	E		713.31	316.15	-	5
13	E		777.83	251.63	-	4
14	E		842.35	187.11	-	3
15	P		890.87	122.59	-	2
16	K		-	74.06	-	1

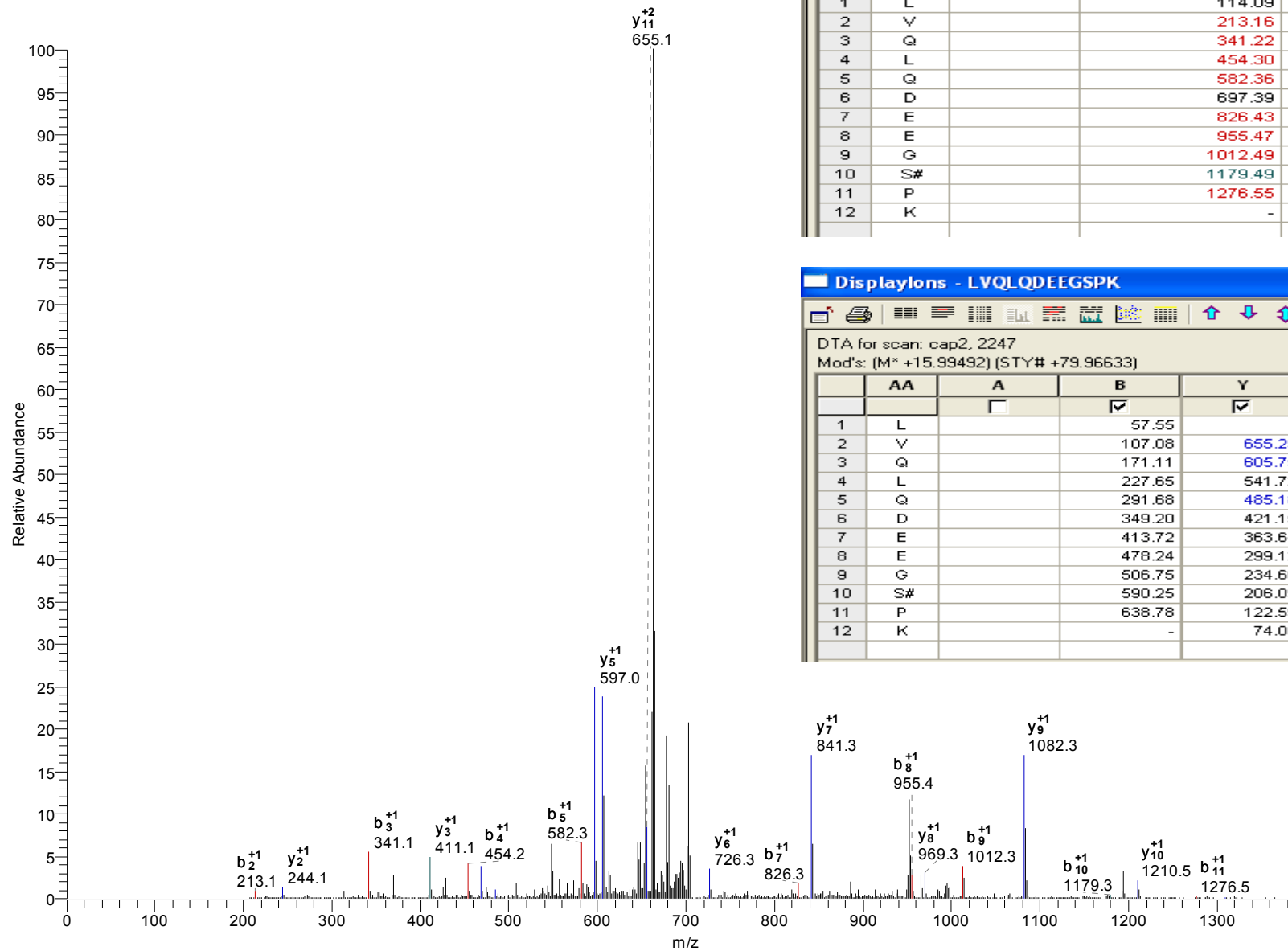
Dynein intermediate chain 1, axonemal

#1819-1819 NL: 1.42E3



predicted similar to kinectin 1

#2247-2247 NL: 2.60E4



Displaylons - LVQLQDEEGSPK

DTA for scan: cap2, 2247
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L	☐	☒	114.09	-
2	V			213.16	1309.57
3	Q			341.22	1210.50
4	L			454.30	1082.44
5	Q			582.36	969.36
6	D			697.39	841.30
7	E			826.43	726.27
8	E			955.47	597.23
9	G			1012.49	468.19
10	S#			1179.49	411.16
11	P			1276.55	244.17
12	K			-	147.11

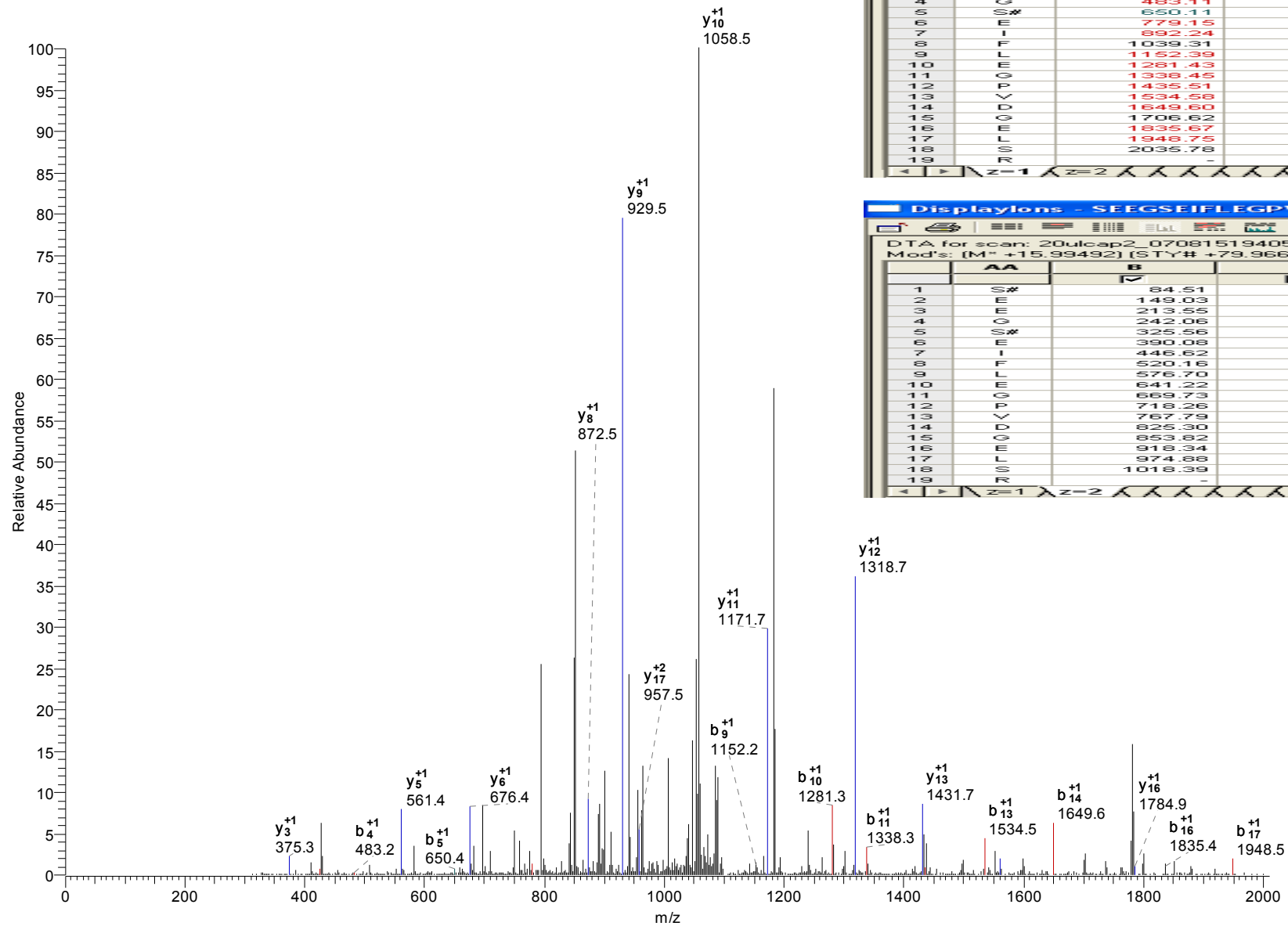
Displaylons - LVQLQDEEGSPK

DTA for scan: cap2, 2247
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L	☐	☒	☒	☐	12
2	V		57.55	-		11
3	Q		107.08	655.29		10
4	L		171.11	605.75		9
5	Q		227.65	541.72		8
6	D		291.68	485.18		7
7	E		349.20	421.15		6
8	E		413.72	363.64		5
9	E		478.24	299.12		4
10	G		506.75	234.60		3
11	S#		590.25	206.09		2
12	P		638.78	122.59		1
12	K		-	74.06		

predicted similar to kinectin 1

#3107-3107 NL: 6.13E3



Displaylons - SEEGSEIFLEGPDVDELRS

DTA for scan: 20Dulcap2_070815194055_3107
Mod's: [M⁺+15.99492] (STY# +79.96633)

	AA	B	Y	
1	S#	168.01	-	19
2	E	297.05	2042.90	18
3	E	426.09	1913.85	17
4	G	483.11	1784.81	16
5	S#	650.11	1727.79	15
6	E	779.15	1560.79	14
7	I	892.24	1431.75	13
8	F	1039.31	1318.66	12
9	L	1152.39	1171.60	11
10	E	1281.43	1058.51	10
11	G	1338.45	929.47	9
12	P	1435.51	872.45	8
13	V	1534.58	775.39	7
14	D	1649.60	676.33	6
15	G	1706.62	561.30	5
16	E	1835.67	504.28	4
17	L	1948.75	375.24	3
18	S	2035.78	262.15	2
19	R	-	175.12	1

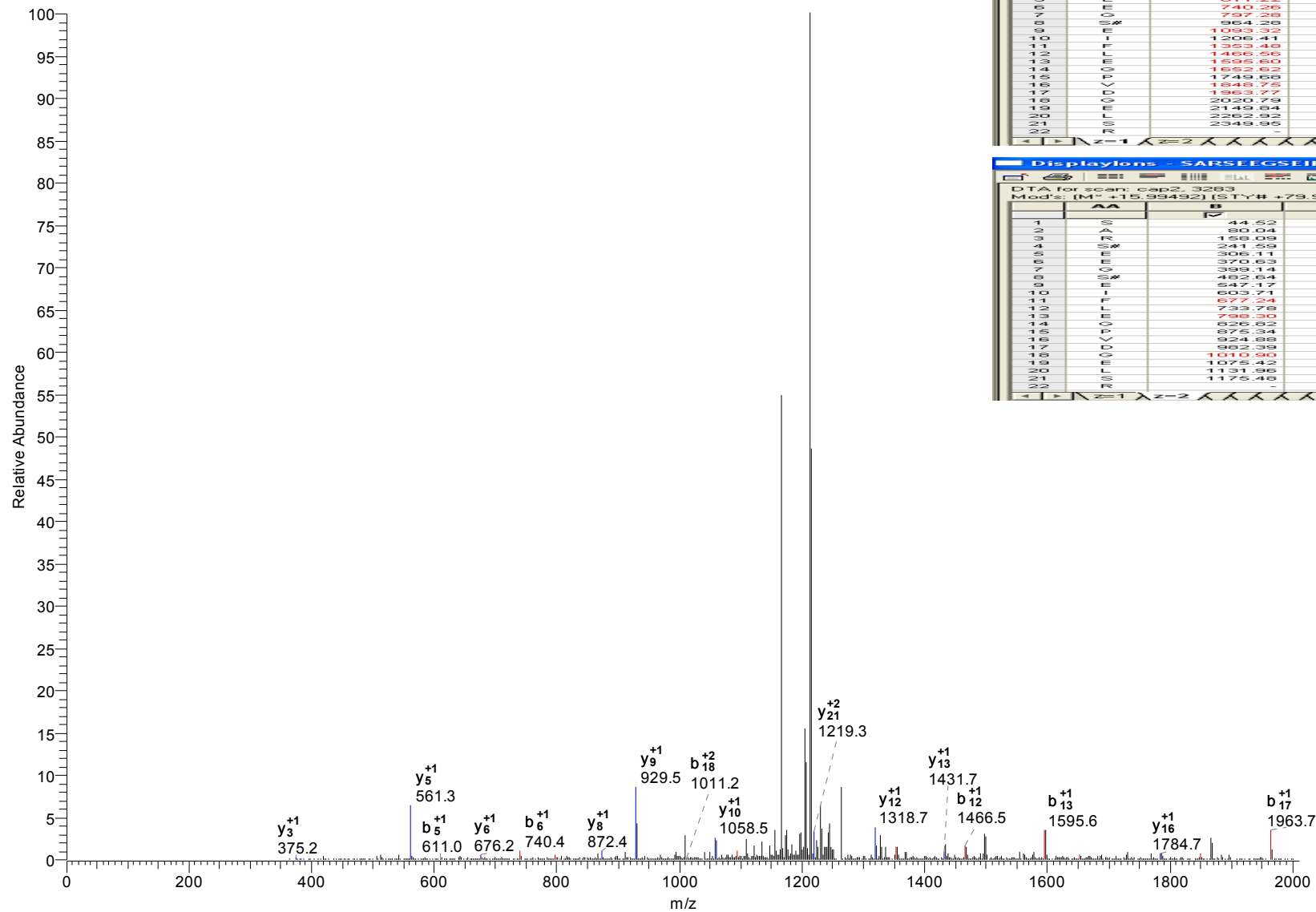
Displaylons - SEEGSEIFLEGPDVDELRS

DTA for scan: 20Dulcap2_070815194055_3107
Mod's: [M⁺+15.99492] (STY# +79.96633)

	AA	B	Y	
1	S#	84.51	-	19
2	E	149.03	1021.95	18
3	E	213.55	957.43	17
4	G	242.06	892.91	16
5	S#	325.56	864.40	15
6	E	390.08	790.90	14
7	I	445.62	715.38	13
8	F	520.16	659.84	12
9	L	576.70	586.30	11
10	E	641.22	529.76	10
11	G	669.73	465.24	9
12	P	718.26	436.73	8
13	V	767.79	388.20	7
14	D	825.30	338.67	6
15	G	853.82	281.15	5
16	E	918.34	252.64	4
17	L	974.88	188.12	3
18	S	1018.39	131.58	2
19	R	-	68.06	1

predicted similar to kinectin 1

#3283-3283 NL: 1.16E4



Displaylens - SARSEEGSEIFLEGPDGELSI

DTA for scan: cap2_3283
Mod# (M⁺ +15.93432) (S⁺TY# +79.96633)

	AA	B	Y	
1	S	88.04	-	22
2	A	159.08	2437.03	21
3	R	315.18	2385.39	20
4	S#	452.18	2209.89	19
5	E	611.22	2042.90	18
6	E	740.26	1913.85	17
7	G	797.28	1784.81	16
8	S#	964.28	1727.79	15
9	E	1095.32	1560.79	14
10	I	1206.41	1431.75	13
11	F	1353.43	1318.66	12
12	L	1466.56	1171.60	11
13	E	1595.60	1058.51	10
14	G	1662.62	929.47	9
15	P	1749.68	872.45	8
16	V	1848.75	775.39	7
17	D	1963.77	676.33	6
18	G	2020.79	561.30	5
19	E	2149.84	504.26	4
20	L	2262.92	375.24	3
21	S	2349.95	262.15	2
22	R	-	175.12	1

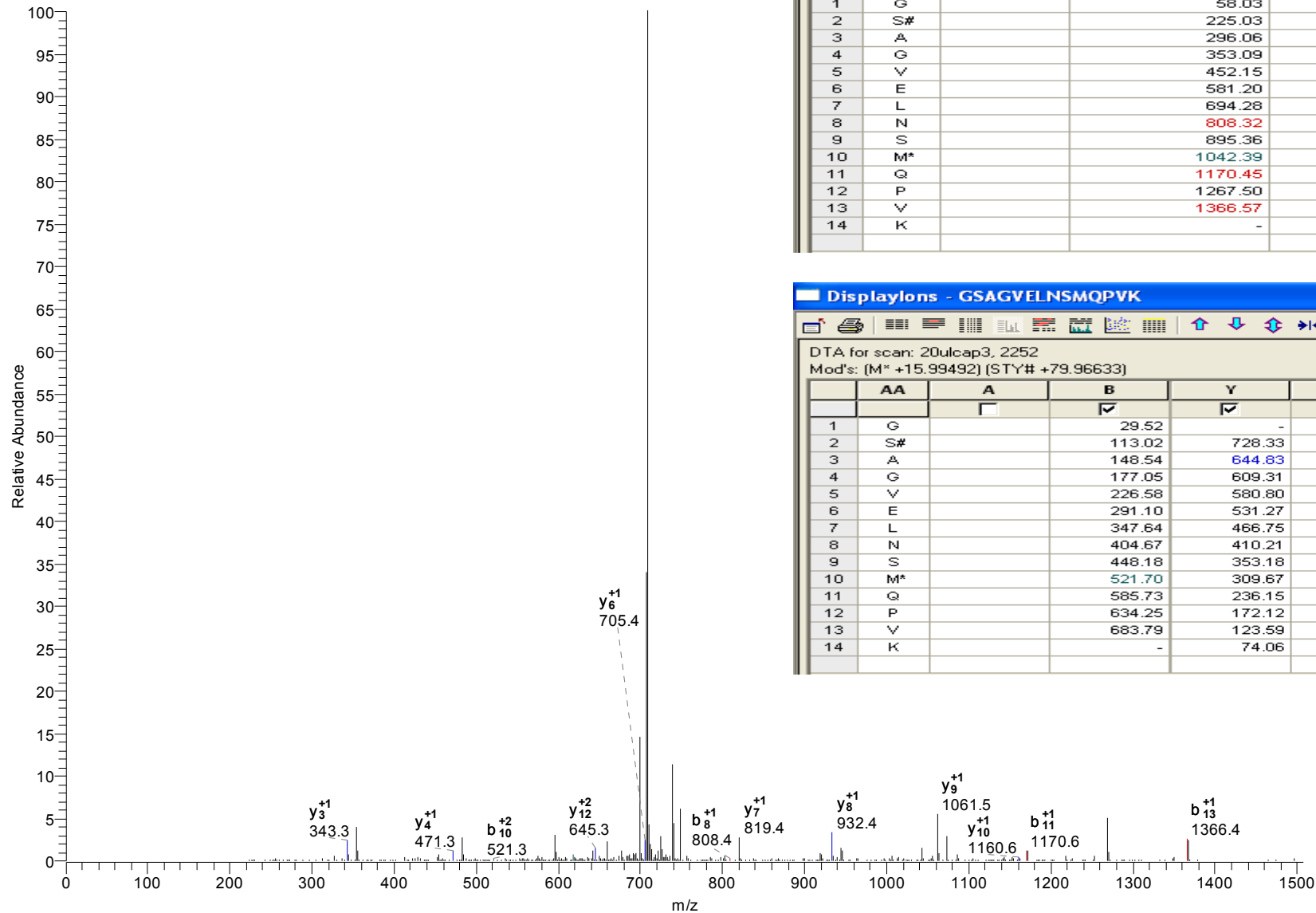
Displaylens - SARSEEGSEIFLEGPDGELSI

DTA for scan: cap2_3283
Mod# (M⁺ +15.93432) (S⁺TY# +79.96633)

	AA	B	Y	
1	S	44.52	-	22
2	A	80.04	1219.02	21
3	R	159.09	1183.50	20
4	S#	241.59	1105.45	19
5	E	306.11	1021.95	18
6	E	370.63	967.43	17
7	G	399.14	892.91	16
8	S#	482.64	864.40	15
9	E	647.17	780.90	14
10	I	603.71	715.38	13
11	F	677.24	659.84	12
12	L	733.78	586.30	11
13	E	798.30	529.76	10
14	G	826.62	465.24	9
15	P	875.34	436.73	8
16	V	924.88	388.20	7
17	D	962.39	338.67	6
18	G	1010.90	281.15	5
19	E	1076.42	252.64	4
20	L	1131.96	188.12	3
21	S	1175.48	131.58	2
22	R	-	88.06	1

Solute carrier family 2, facilitated glucose transporter member 3

#2252-2252 NL: 5.76E3



Displaylons - GSAGVELNSMQPVK

DTA for scan: 20ulcap3, 2252
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	G		58.03	-	14
2	S#		225.03	1455.65	13
3	A		296.06	1288.66	12
4	G		353.09	1217.62	11
5	V		452.15	1160.60	10
6	E		581.20	1061.53	9
7	L		694.28	932.49	8
8	N		808.32	819.40	7
9	S		895.36	705.36	6
10	M*		1042.39	618.33	5
11	Q		1170.45	471.29	4
12	P		1267.50	343.23	3
13	V		1366.57	246.18	2
14	K		-	147.11	1

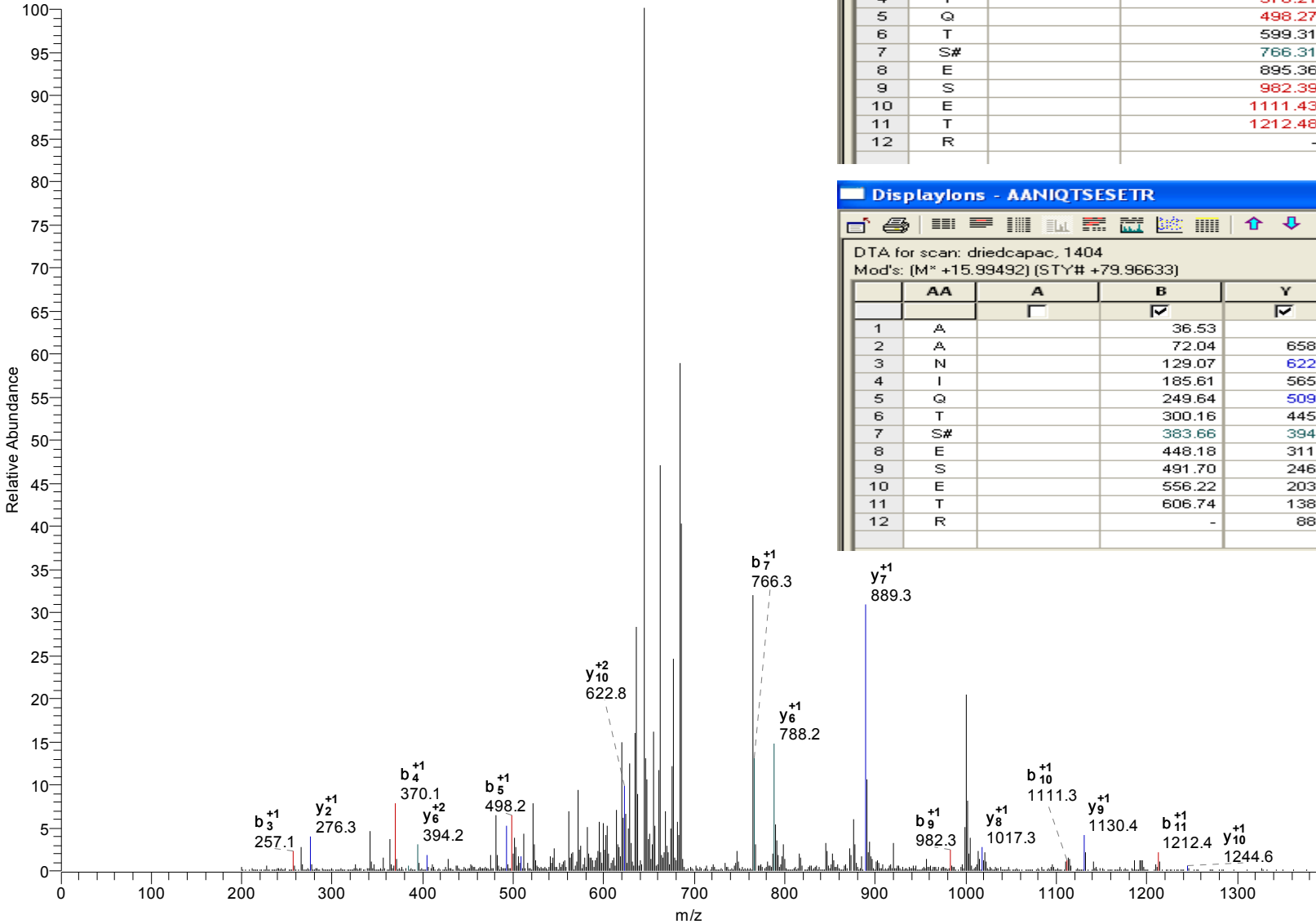
Displaylons - GSAGVELNSMQPVK

DTA for scan: 20ulcap3, 2252
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	G		29.52	-		14
2	S#		113.02	728.33		13
3	A		148.54	644.83		12
4	G		177.05	609.31		11
5	V		226.58	580.80		10
6	E		291.10	531.27		9
7	L		347.64	466.75		8
8	N		404.67	410.21		7
9	S		448.18	353.18		6
10	M*		521.70	309.67		5
11	Q		585.73	236.15		4
12	P		634.25	172.12		3
13	V		683.79	123.59		2
14	K		-	74.06		1

predicted similar to pleckstrin homology domain
containing, family H (with MyTH4 domain)
member 2

#1404-1404 NL: 1.26E4



Displaylons - AANIQTSESETR

DTA for scan: driedcapac, 1404
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	A		72.04	-	12
2	A		143.08	1315.55	11
3	N		257.12	1244.52	10
4	I		370.21	1130.47	9
5	Q		498.27	1017.39	8
6	T		599.31	889.33	7
7	S#		766.31	788.28	6
8	E		895.36	621.28	5
9	S		982.39	492.24	4
10	E		1111.43	405.21	3
11	T		1212.48	276.17	2
12	R		-	175.12	1

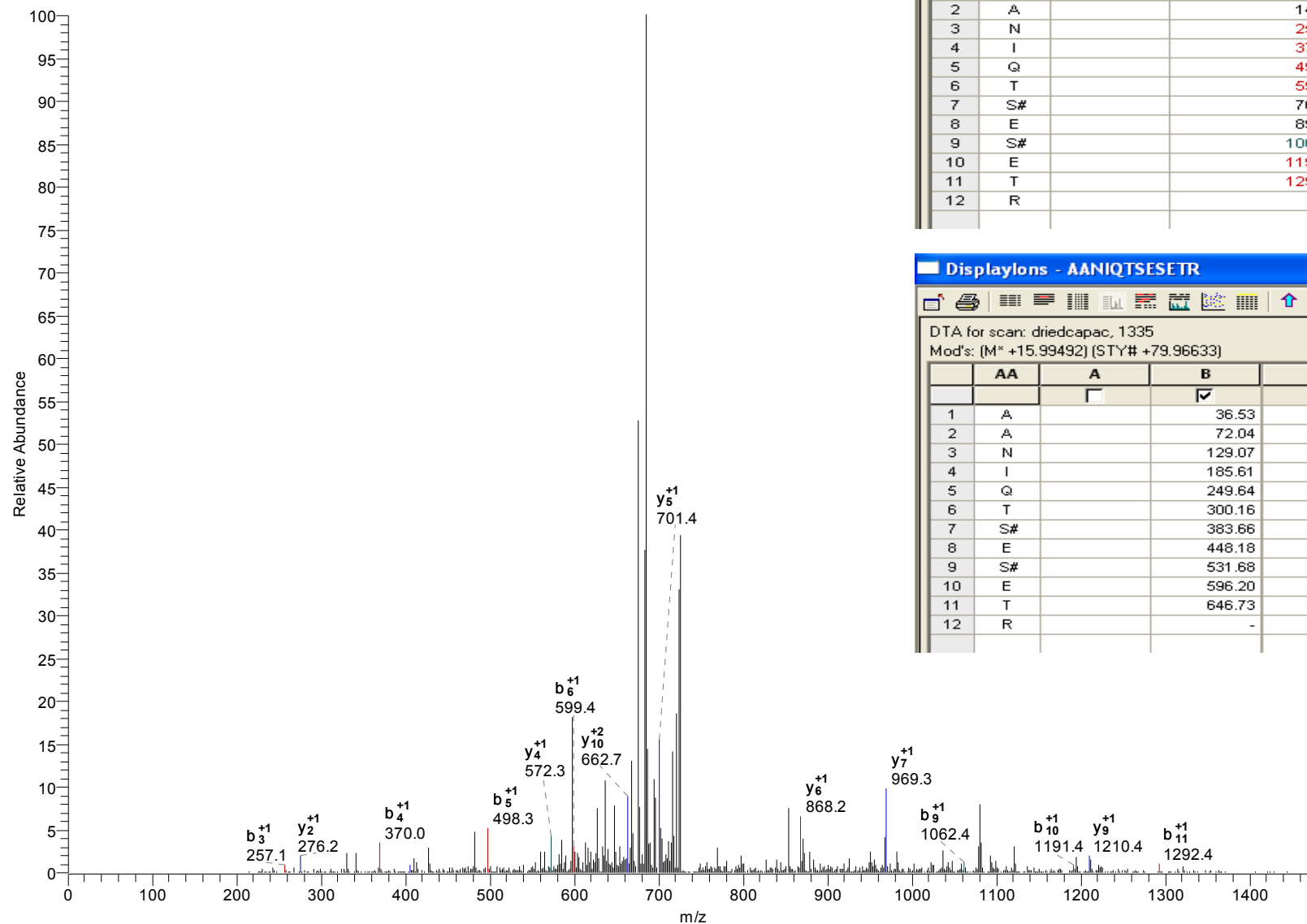
Displaylons - AANIQTSESETR

DTA for scan: driedcapac, 1404
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	A		36.53	-		12
2	A		72.04	658.28		11
3	N		129.07	622.76		10
4	I		185.61	565.74		9
5	Q		249.64	509.20		8
6	T		300.16	445.17		7
7	S#		383.66	394.64		6
8	E		448.18	311.15		5
9	S		491.70	246.62		4
10	E		556.22	203.11		3
11	T		606.74	138.59		2
12	R		-	88.06		1

predicted similar to pleckstrin homology domain
containing, family H (with MyTH4 domain)
member 2

#1335-1335 NL: 4.63E3



Displaylons - AANIQTSESETR

DTA for scan: driedcapac, 1335
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	A		72.04	-	12
2	A		143.08	1395.52	11
3	N		257.12	1324.48	10
4	I		370.21	1210.44	9
5	Q		498.27	1097.35	8
6	T		599.31	969.30	7
7	S#		766.31	868.25	6
8	E		895.36	701.25	5
9	S#		1062.35	572.21	4
10	E		1191.40	405.21	3
11	T		1292.44	276.17	2
12	R		-	175.12	1

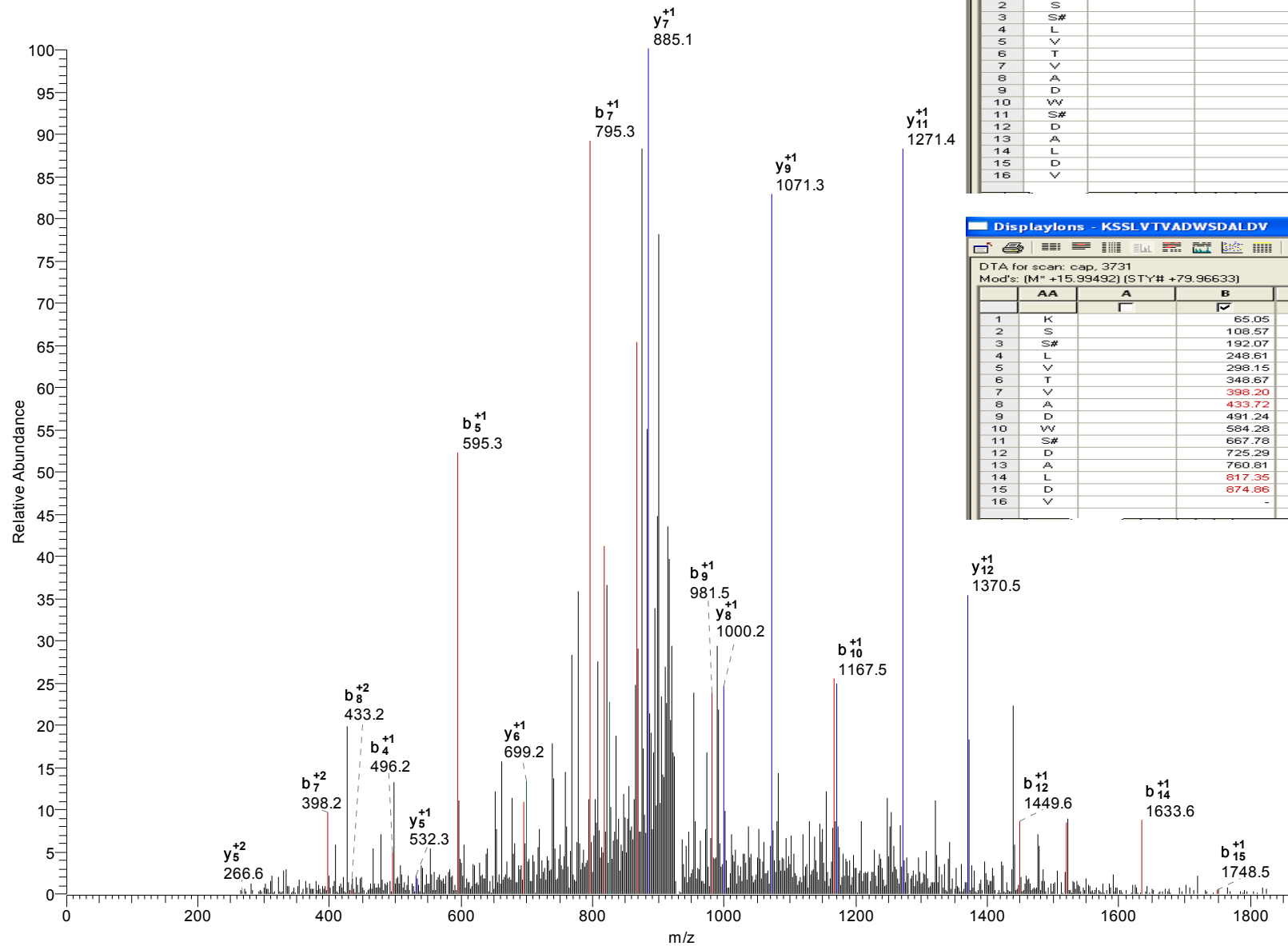
Displaylons - AANIQTSESETR

DTA for scan: driedcapac, 1335
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	A		36.53	-		12
2	A		72.04	698.26		11
3	N		129.07	662.74		10
4	I		185.61	605.72		9
5	Q		249.64	549.18		8
6	T		300.16	485.15		7
7	S#		383.66	434.63		6
8	E		448.18	351.13		5
9	S#		531.68	286.61		4
10	E		596.20	203.11		3
11	T		646.73	138.59		2
12	R		-	88.06		1

Dzip1 similar to DAZ interacting protein 1

#3731-3731 NL: 1.19E3



Displaylons - KSSLVTVADWSDALDV

DTA for scan: cap. 3731
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	K		129.10		16
2	S		216.13	1737.70	15
3	S#		383.13	1650.67	14
4	L		496.22	1483.67	13
5	V		595.29	1370.59	12
6	T		696.33	1271.52	11
7	V		795.40	1170.47	10
8	A		866.44	1071.40	9
9	D		981.47	1000.37	8
10	WV		1167.54	885.34	7
11	S#		1334.54	699.26	6
12	D		1449.57	532.26	5
13	A		1520.61	417.23	4
14	L		1633.69	346.20	3
15	D		1748.72	233.11	2
16	V		-	118.09	1

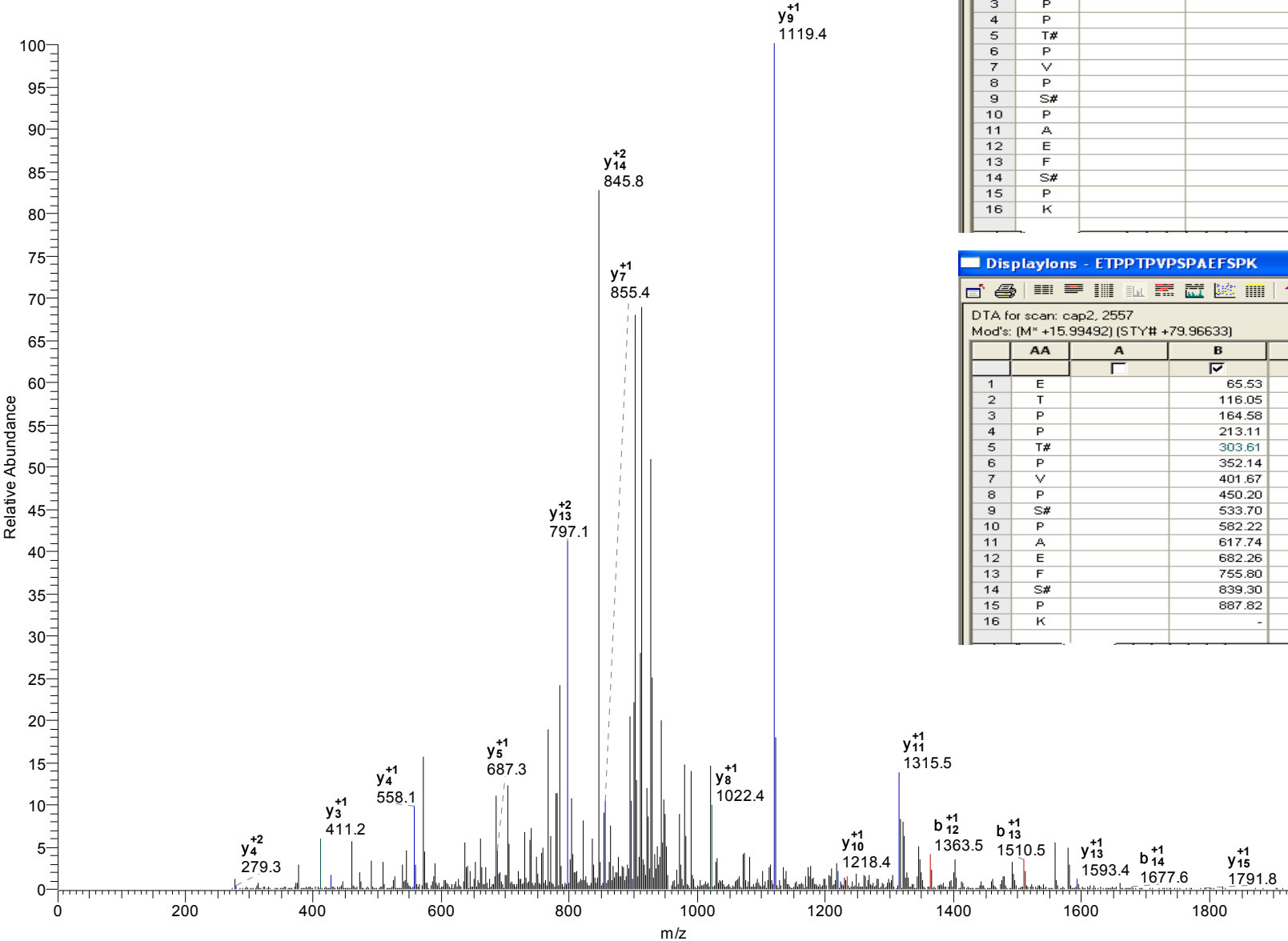
Displaylons - KSSLVTVADWSDALDV

DTA for scan: cap. 3731
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	K		65.05			16
2	S		108.57	869.35		15
3	S#		192.07	825.84		14
4	L		248.61	742.34		13
5	V		298.15	685.80		12
6	T		348.67	636.26		11
7	V		398.20	585.74		10
8	A		433.72	536.21		9
9	D		491.24	500.69		8
10	WV		564.28	443.17		7
11	S#		667.78	350.13		6
12	D		725.29	266.63		5
13	A		760.81	209.12		4
14	L		817.35	173.60		3
15	D		874.86	117.06		2
16	V		-	59.55		1

Testis-specific actin-related protein 3

#2557-2557 NL: 2.47E4



Displaylons - ETPPTVPVSPAEFSPK

DTA for scan: cap2, 2557
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	E		130.05	-	16
2	T		231.10	1791.70	15
3	P		328.15	1690.66	14
4	P		425.20	1593.60	13
5	T#		606.22	1496.55	12
6	P		703.27	1315.54	11
7	V		802.34	1218.48	10
8	P		899.39	1119.42	9
9	S#		1066.39	1022.36	8
10	P		1163.44	855.36	7
11	A		1234.48	758.31	6
12	E		1363.52	687.27	5
13	F		1510.59	558.23	4
14	S#		1677.59	411.16	3
15	P		1774.64	244.17	2
16	K		-	147.11	1

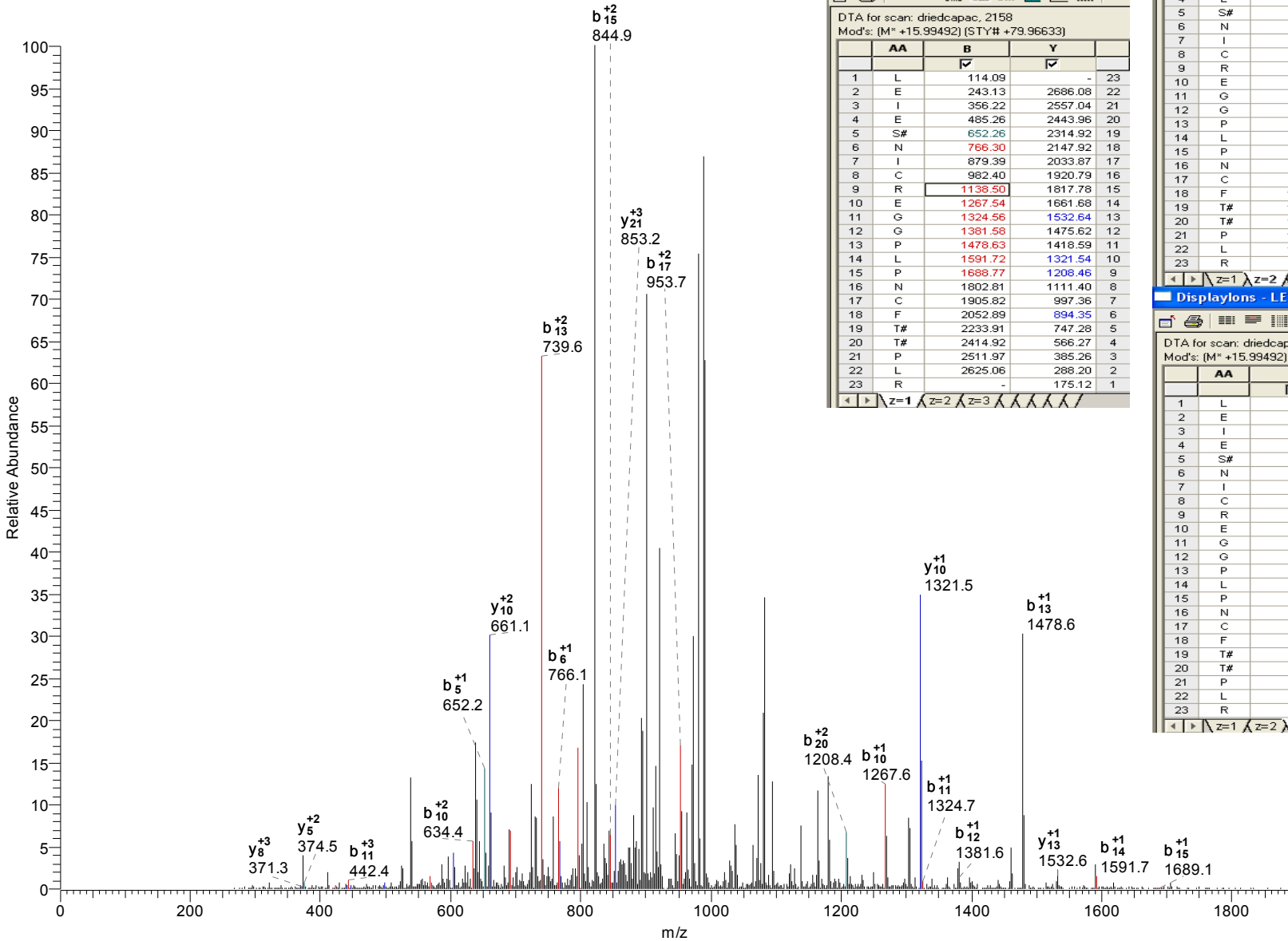
Displaylons - ETPPTVPVSPAEFSPK

DTA for scan: cap2, 2557
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	E		65.53	-		16
2	T		116.05	896.36		15
3	P		164.58	845.83		14
4	P		213.11	797.31		13
5	T#		303.61	748.78		12
6	P		352.14	658.27		11
7	V		401.67	609.75		10
8	P		450.20	560.21		9
9	S#		533.70	511.69		8
10	P		582.22	428.19		7
11	A		617.74	379.66		6
12	E		682.26	344.14		5
13	F		755.80	279.62		4
14	S#		839.30	206.09		3
15	P		887.82	122.59		2
16	K		-	74.06		1

Akap10_ Predicted similar to A kinase (PRKA) anchor protein 10

#2158-2158 NL: 3.17E4



Displaylons - LEIESNICREGGPLNCF TTPL

DTA for scan: driedcapac, 2158
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y
1	L	114.09	-
2	E	243.13	2686.08
3	I	356.22	2557.04
4	E	485.26	2443.96
5	S#	652.26	2314.92
6	N	766.30	2147.92
7	I	879.39	2033.87
8	C	982.40	1920.79
9	R	1138.50	1817.78
10	E	1267.54	1661.68
11	G	1324.56	1532.64
12	G	1381.58	1475.62
13	P	1478.63	1418.59
14	L	1591.72	1321.54
15	P	1688.77	1208.46
16	N	1802.81	1111.40
17	C	1905.82	997.36
18	F	2052.89	894.35
19	T#	2233.91	747.28
20	T#	2414.92	566.27
21	P	2511.97	385.26
22	L	2625.06	289.20
23	R	-	175.12

Displaylons - LEIESNICREGGPLNCF TTPL

DTA for scan: driedcapac, 2158
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y
1	L	57.55	-
2	E	122.07	1343.55
3	I	178.61	1279.02
4	E	243.13	1222.48
5	S#	326.63	1157.96
6	N	383.65	1074.46
7	I	440.20	1017.44
8	C	491.70	960.90
9	R	569.75	909.39
10	E	634.27	831.34
11	G	662.78	766.82
12	G	691.29	738.31
13	P	739.82	709.80
14	L	796.36	661.27
15	P	844.89	604.73
16	N	901.91	556.21
17	C	953.42	499.18
18	F	1026.95	447.68
19	T#	1117.46	374.15
20	T#	1207.96	283.64
21	P	1256.49	193.13
22	L	1313.03	144.61
23	R	-	88.06

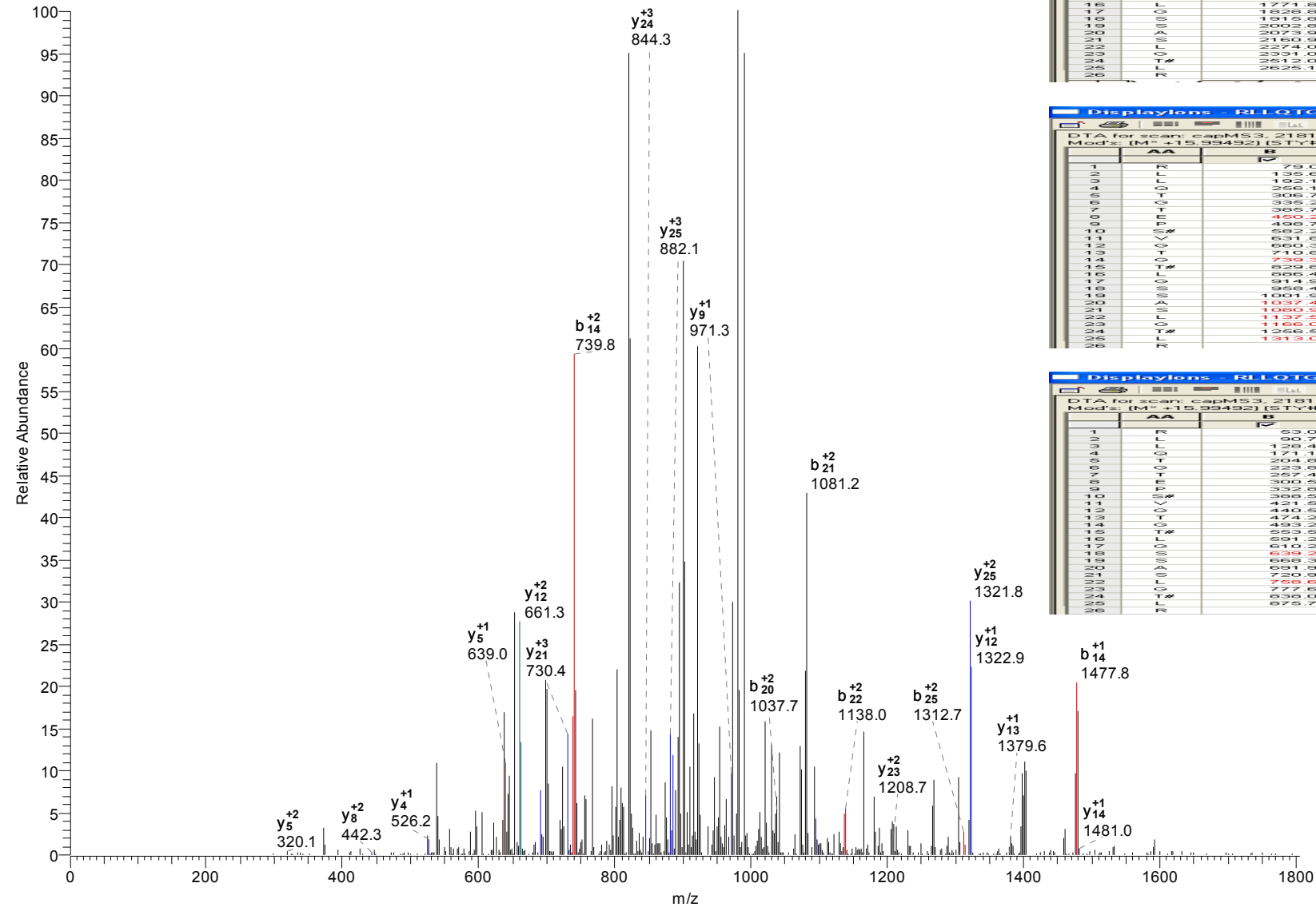
Displaylons - LEIESNICREGGPLNCF TTPL

DTA for scan: driedcapac, 2158
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y
1	L	38.70	-
2	E	81.72	896.03
3	I	119.41	853.02
4	E	162.43	815.32
5	S#	218.09	772.31
6	N	256.11	716.64
7	I	293.80	678.63
8	C	328.14	640.93
9	R	380.17	606.60
10	E	423.18	554.56
11	G	442.19	511.55
12	G	461.20	492.54
13	P	493.55	473.54
14	L	531.24	441.19
15	P	563.60	403.49
16	N	601.61	371.14
17	C	635.95	333.13
18	F	684.97	298.79
19	T#	745.31	249.77
20	T#	805.64	189.43
21	P	838.00	129.09
22	L	875.69	96.74
23	R	-	59.04

RGD1308019_predicted hypothetical protein LOC311795

#2181-2181 NL: 1.99E3



Displays: RLLGTGTPSVGTGTLGSSAS

DTA for scan: capMS3: 2181
Mods: (M: -15.95432) (S: TyH +79.96633)

	AA	B	Y	
1	LR	157.11	2643.17	26
2	LR	270.19	2650.09	25
3	LR	383.26	2656.94	24
4	LR	496.34	2663.86	23
5	LR	609.41	2670.78	22
6	LR	722.49	2677.70	21
7	LR	835.56	2684.62	20
8	LR	948.64	2691.54	19
9	LR	1061.71	2698.46	18
10	LR	1174.79	2705.38	17
11	LR	1287.86	2712.30	16
12	LR	1400.94	2719.22	15
13	LR	1514.01	2726.14	14
14	LR	1627.09	2733.06	13
15	LR	1740.16	2740.00	12
16	LR	1853.24	2746.92	11
17	LR	1966.31	2753.84	10
18	LR	2079.39	2760.76	9
19	LR	2192.46	2767.68	8
20	LR	2305.54	2774.60	7
21	LR	2418.61	2781.52	6
22	LR	2531.69	2788.44	5
23	LR	2644.76	2795.36	4
24	LR	2757.84	2802.28	3
25	LR	2870.91	2809.20	2
26	LR	2984.00	2816.12	1

Displays: RLLGTGTPSVGTGTLGSSAS

DTA for scan: capMS3: 2181
Mods: (M: -15.95432) (S: TyH +79.96633)

	AA	B	Y	
1	LR	79.06	1322.09	26
2	LR	192.14	1265.55	25
3	LR	305.21	1209.01	24
4	LR	418.29	1152.47	23
5	LR	531.36	1095.93	22
6	LR	644.44	1039.39	21
7	LR	757.51	982.85	20
8	LR	870.59	926.31	19
9	LR	983.66	869.77	18
10	LR	1096.74	813.23	17
11	LR	1209.81	756.69	16
12	LR	1322.89	700.15	15
13	LR	1435.96	643.61	14
14	LR	1549.04	587.07	13
15	LR	1662.11	530.53	12
16	LR	1775.19	473.99	11
17	LR	1888.26	417.45	10
18	LR	2001.34	360.91	9
19	LR	2114.41	304.37	8
20	LR	2227.49	247.83	7
21	LR	2340.56	191.29	6
22	LR	2453.64	134.75	5
23	LR	2566.71	78.21	4
24	LR	2679.79	21.67	3
25	LR	2792.86	-	2
26	LR	2905.94	-	1

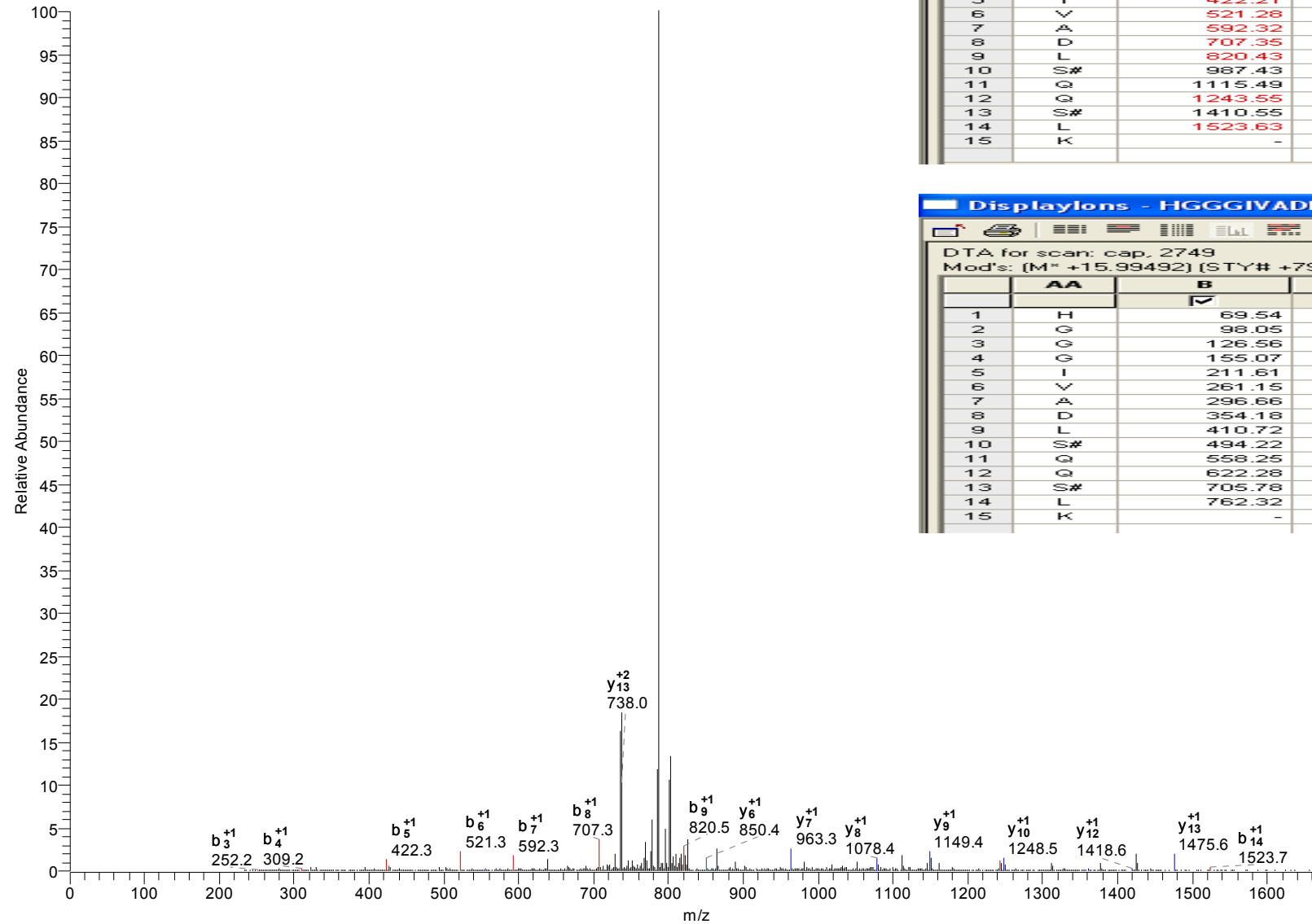
Displays: RLLGTGTPSVGTGTLGSSAS

DTA for scan: capMS3: 2181
Mods: (M: -15.95432) (S: TyH +79.96633)

	AA	B	Y	
1	LR	53.04	561.73	26
2	LR	106.08	544.03	25
3	LR	159.12	526.33	24
4	LR	212.16	508.63	23
5	LR	265.20	490.93	22
6	LR	318.24	473.23	21
7	LR	371.28	455.53	20
8	LR	424.32	437.83	19
9	LR	477.36	420.13	18
10	LR	530.40	402.43	17
11	LR	583.44	384.73	16
12	LR	636.48	367.03	15
13	LR	689.52	349.33	14
14	LR	742.56	331.63	13
15	LR	795.60	313.93	12
16	LR	848.64	296.23	11
17	LR	901.68	278.53	10
18	LR	954.72	260.83	9
19	LR	1007.76	243.13	8
20	LR	1060.80	225.43	7
21	LR	1113.84	207.73	6
22	LR	1166.88	190.03	5
23	LR	1219.92	172.33	4
24	LR	1272.96	154.63	3
25	LR	1326.00	136.93	2
26	LR	1379.04	119.23	1

Ppp1r7 32 kDa protein

#2749-2749 NL: 3.29E4



Displaylons - HGGGIVADLSQQSLK

DTA for scan: cap. 2749
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	H	138.07	-	15
2	G	195.09	1532.68	14
3	G	252.11	1475.65	13
4	G	309.13	1418.63	12
5	I	422.21	1361.61	11
6	V	521.28	1248.53	10
7	A	592.32	1149.46	9
8	D	707.35	1078.42	8
9	L	820.43	963.39	7
10	S#	987.43	850.31	6
11	Q	1115.49	683.31	5
12	Q	1243.55	555.25	4
13	S#	1410.55	427.20	3
14	L	1523.63	260.20	2
15	K	-	147.11	1

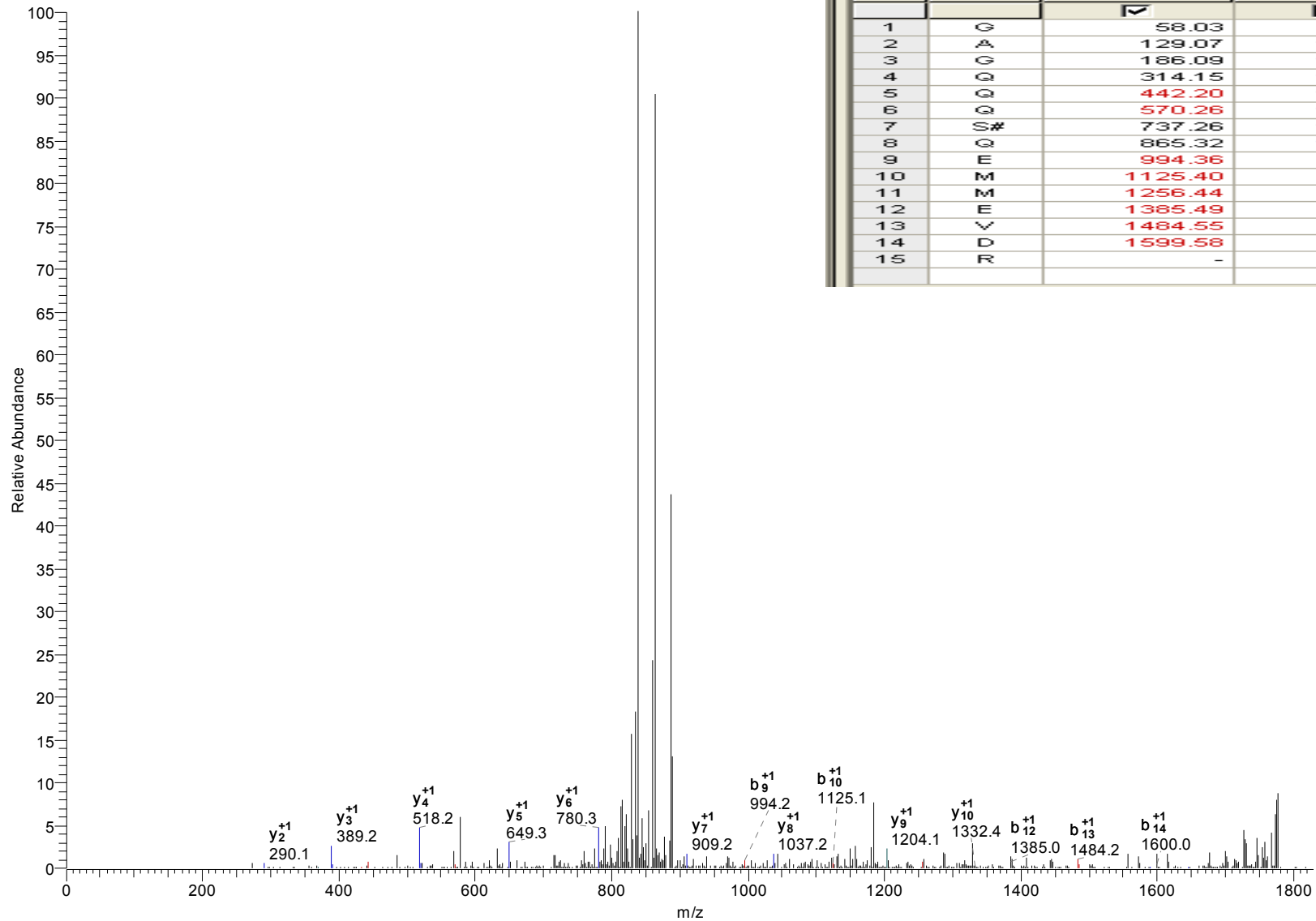
Displaylons - HGGGIVADLSQQSLK

DTA for scan: cap. 2749
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	H	69.54	-	15
2	G	98.05	766.84	14
3	G	126.56	738.33	13
4	G	155.07	709.82	12
5	I	211.61	681.31	11
6	V	261.15	624.77	10
7	A	296.66	575.23	9
8	D	354.18	539.71	8
9	L	410.72	482.20	7
10	S#	494.22	425.66	6
11	Q	558.25	342.16	5
12	Q	622.28	278.13	4
13	S#	705.78	214.10	3
14	L	762.32	130.60	2
15	K	-	74.06	1

Ppp1r7 32 kDa protein

#1138-1139 NL: 1.19E4



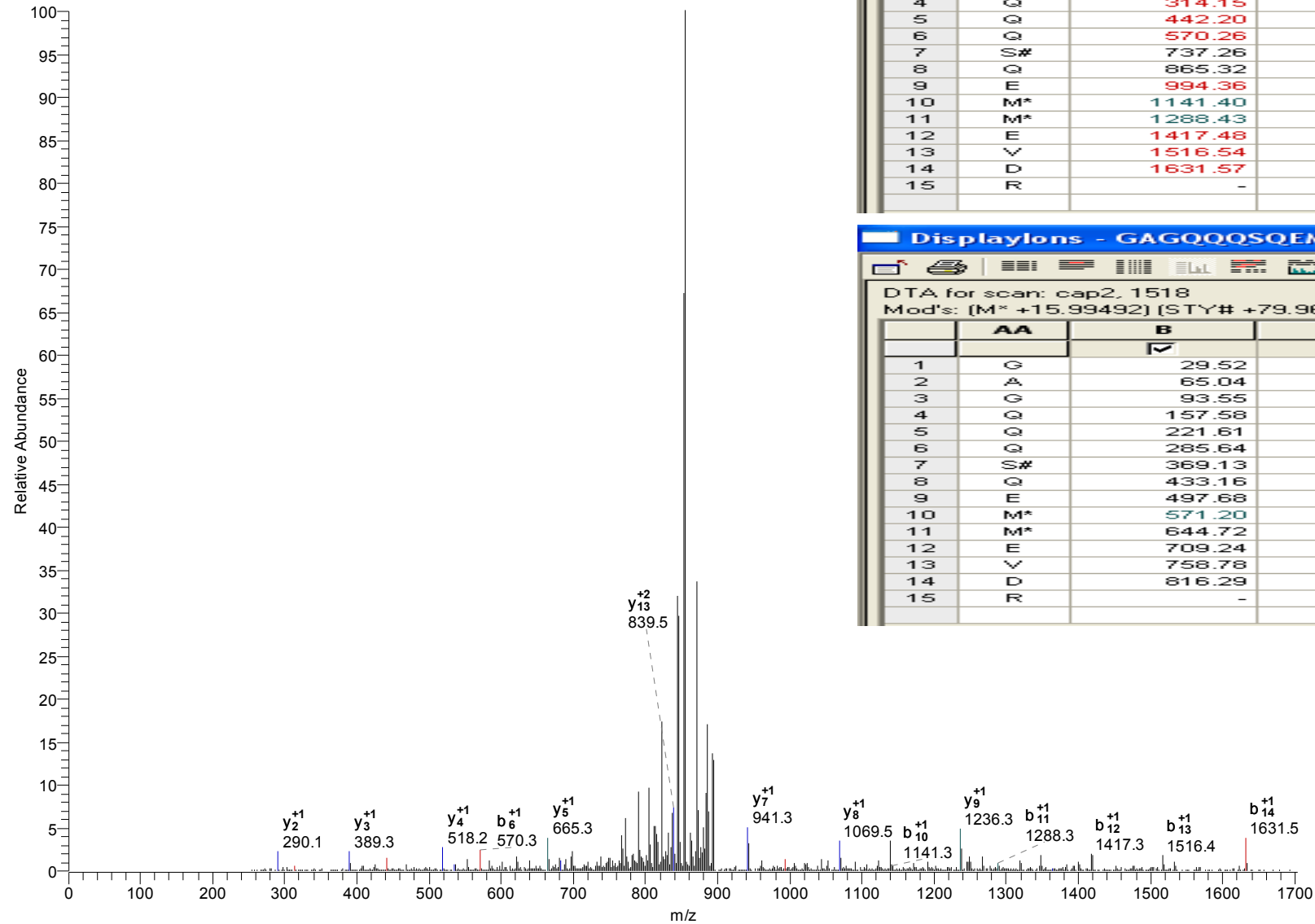
Displaylons - GAGQQQSQEMMEVDR

DTA for scans: capETDcidtop3_080419044303, 1138
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
		✓	✓	
1	G	58.03	-	15
2	A	129.07	1716.67	14
3	G	186.09	1645.63	13
4	Q	314.15	1588.61	12
5	Q	442.20	1460.55	11
6	Q	570.26	1332.50	10
7	S#	737.26	1204.44	9
8	Q	865.32	1037.44	8
9	E	994.36	909.38	7
10	M	1125.40	780.34	6
11	M	1256.44	649.30	5
12	E	1385.49	518.26	4
13	V	1484.55	389.21	3
14	D	1599.58	290.15	2
15	R	-	175.12	1

Ppp1r7 32 kDa protein

#1518-1518 NL: 9.86E3



Displaylons - GAGQQSQEMMEVDR

DTA for scan: cap2, 1518
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	G	58.03	-	15
2	A	129.07	1748.66	14
3	G	186.09	1677.62	13
4	Q	314.15	1620.60	12
5	Q	442.20	1492.54	11
6	Q	570.26	1364.49	10
7	S#	737.26	1236.43	9
8	Q	865.32	1069.43	8
9	E	994.36	941.37	7
10	M*	1141.40	812.33	6
11	M*	1288.43	665.29	5
12	E	1417.48	518.26	4
13	V	1516.54	389.21	3
14	D	1631.57	290.15	2
15	R	-	175.12	1

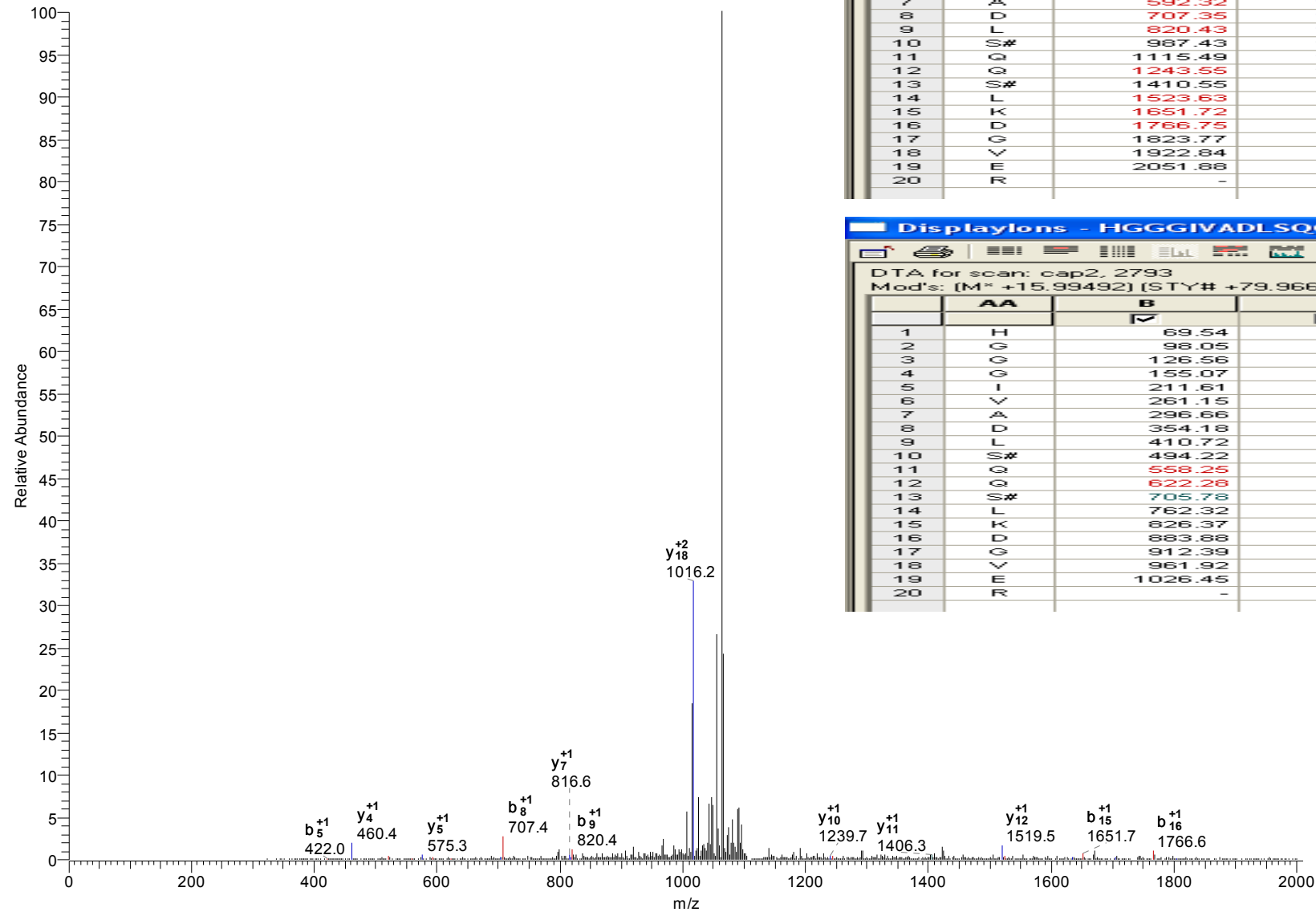
Displaylons - GAGQQSQEMMEVDR

DTA for scan: cap2, 1518
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	G	29.52	-	15
2	A	65.04	874.83	14
3	G	93.55	839.32	13
4	Q	157.58	810.81	12
5	Q	221.61	746.78	11
6	Q	285.64	682.75	10
7	S#	369.13	618.72	9
8	Q	433.16	535.22	8
9	E	497.68	471.19	7
10	M*	571.20	406.67	6
11	M*	644.72	333.15	5
12	E	709.24	259.63	4
13	V	758.78	195.11	3
14	D	816.29	145.58	2
15	R	-	88.06	1

Ppp1r7 32 kDa protein

#2793-2793 NL: 1.26E4



Displaylons - HGGGIVADLSQQSLKDGVER

DTA for scan: cap2, 2793
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	H	138.07	-	20
2	G	195.09	2088.94	19
3	G	252.11	2031.91	18
4	G	309.13	1974.89	17
5	I	422.21	1917.87	16
6	V	521.28	1804.79	15
7	A	592.32	1705.72	14
8	D	707.35	1634.68	13
9	L	820.43	1519.66	12
10	S#	987.43	1406.57	11
11	Q	1115.49	1239.57	10
12	Q	1243.55	1111.51	9
13	S#	1410.55	983.46	8
14	L	1523.63	816.46	7
15	K	1651.72	703.37	6
16	D	1766.75	575.28	5
17	G	1823.77	460.25	4
18	V	1922.84	403.23	3
19	E	2051.88	304.16	2
20	R	-	175.12	1

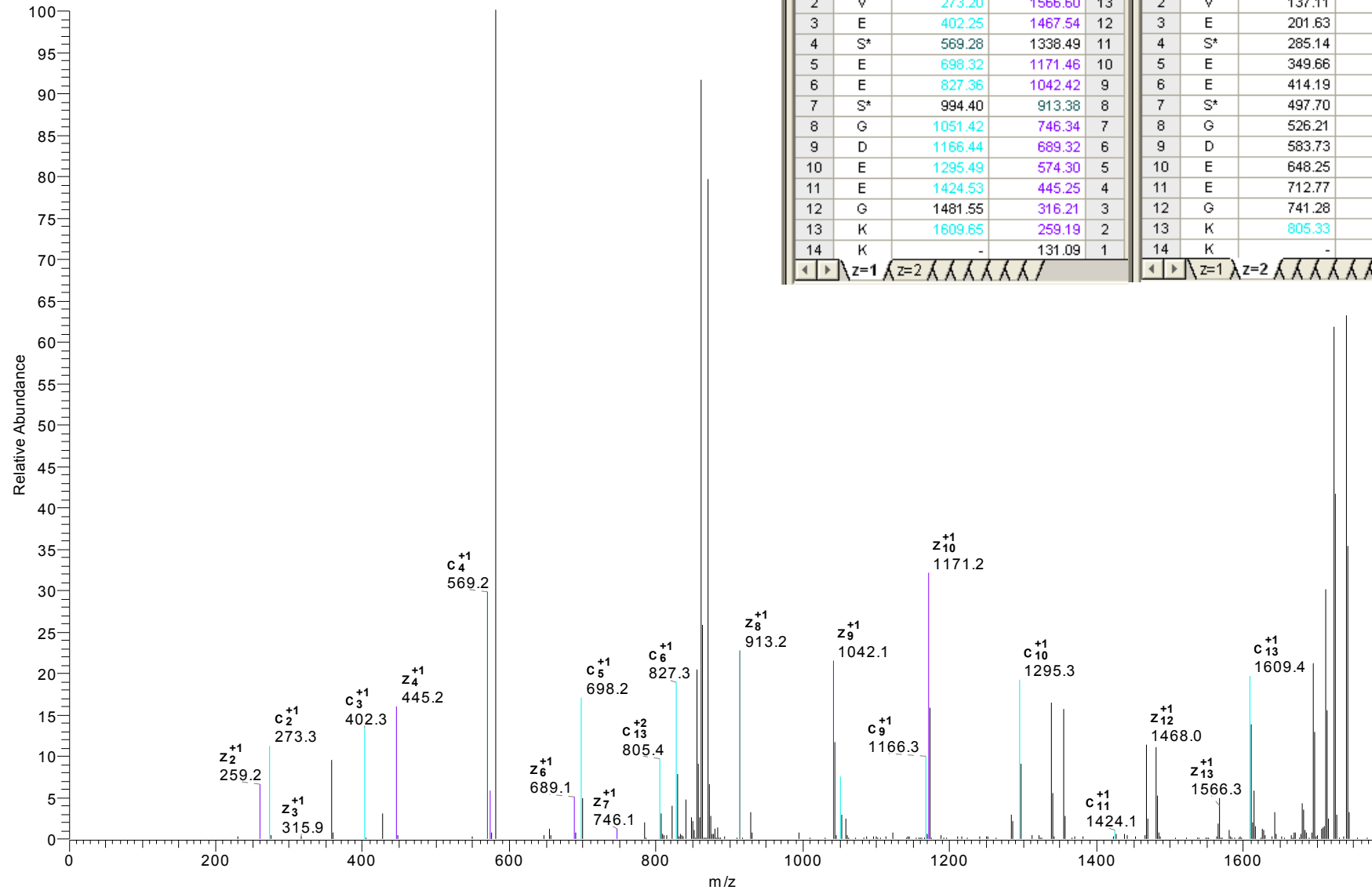
Displaylons - HGGGIVADLSQQSLKDGVER

DTA for scan: cap2, 2793
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	H	69.54	-	20
2	G	98.05	1044.97	19
3	G	126.56	1016.46	18
4	G	155.07	987.95	17
5	I	211.61	959.44	16
6	V	261.15	902.90	15
7	A	296.66	853.36	14
8	D	354.18	817.84	13
9	L	410.72	760.33	12
10	S#	494.22	703.79	11
11	Q	558.25	620.29	10
12	Q	622.28	556.26	9
13	S#	705.78	492.23	8
14	L	762.32	408.73	7
15	K	826.37	352.19	6
16	D	883.88	288.14	5
17	G	912.39	230.63	4
18	V	961.92	202.12	3
19	E	1026.45	152.58	2
20	R	-	88.06	1

Ppp1r7 32 kDa protein

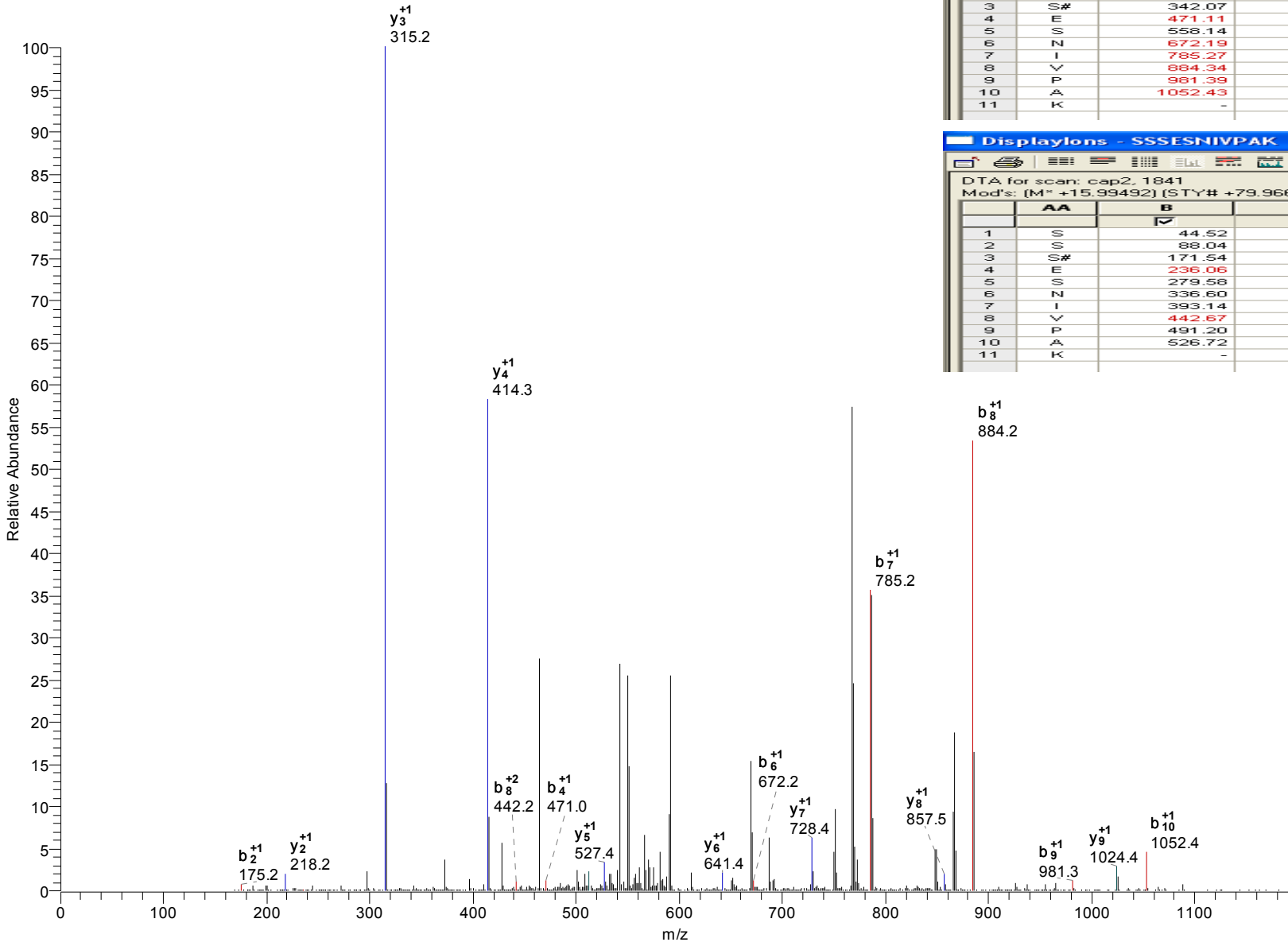
#62-62 NL: 1.26E3



Displaylons - RVESEESGDEEGKK					Displaylons - RVESEESGDEEGKK				
DTA for scan: capETcaD, 62					DTA for scan: capETcaD, 62				
Mod's: (STY* +80.00000)					Mod's: (STY* +80.00000)				
	AA	C	Z			AA	C	Z	
1	R	174.13	-	14	1	R	87.57	-	14
2	V	273.20	1566.60	13	2	V	137.11	783.81	13
3	E	402.25	1467.54	12	3	E	201.63	734.27	12
4	S*	569.28	1338.49	11	4	S*	285.14	669.75	11
5	E	698.32	1171.46	10	5	E	349.66	586.23	10
6	E	827.36	1042.42	9	6	E	414.19	521.71	9
7	S*	994.40	913.38	8	7	S*	497.70	457.19	8
8	G	1051.42	746.34	7	8	G	526.21	373.68	7
9	D	1166.44	689.32	6	9	D	583.73	345.16	6
10	E	1295.49	574.30	5	10	E	648.25	287.65	5
11	E	1424.53	445.25	4	11	E	712.77	223.13	4
12	G	1481.55	316.21	3	12	G	741.28	158.61	3
13	K	1609.65	259.19	2	13	K	805.33	130.10	2
14	K	-	131.09	1	14	K	-	66.05	1

105 kDa protein

#1841-1841 NL: 3.21E4



Displaylens - SSSSNIVPAK

DTA for scan: cap2, 1841
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	S	88.04	-	11
2	S	175.07	1111.50	10
3	S#	342.07	1024.47	9
4	E	471.11	857.47	8
5	S	558.14	728.43	7
6	N	672.19	641.40	6
7	I	785.27	527.36	5
8	V	884.34	414.27	4
9	P	981.39	315.20	3
10	A	1052.43	218.15	2
11	K	-	147.11	1

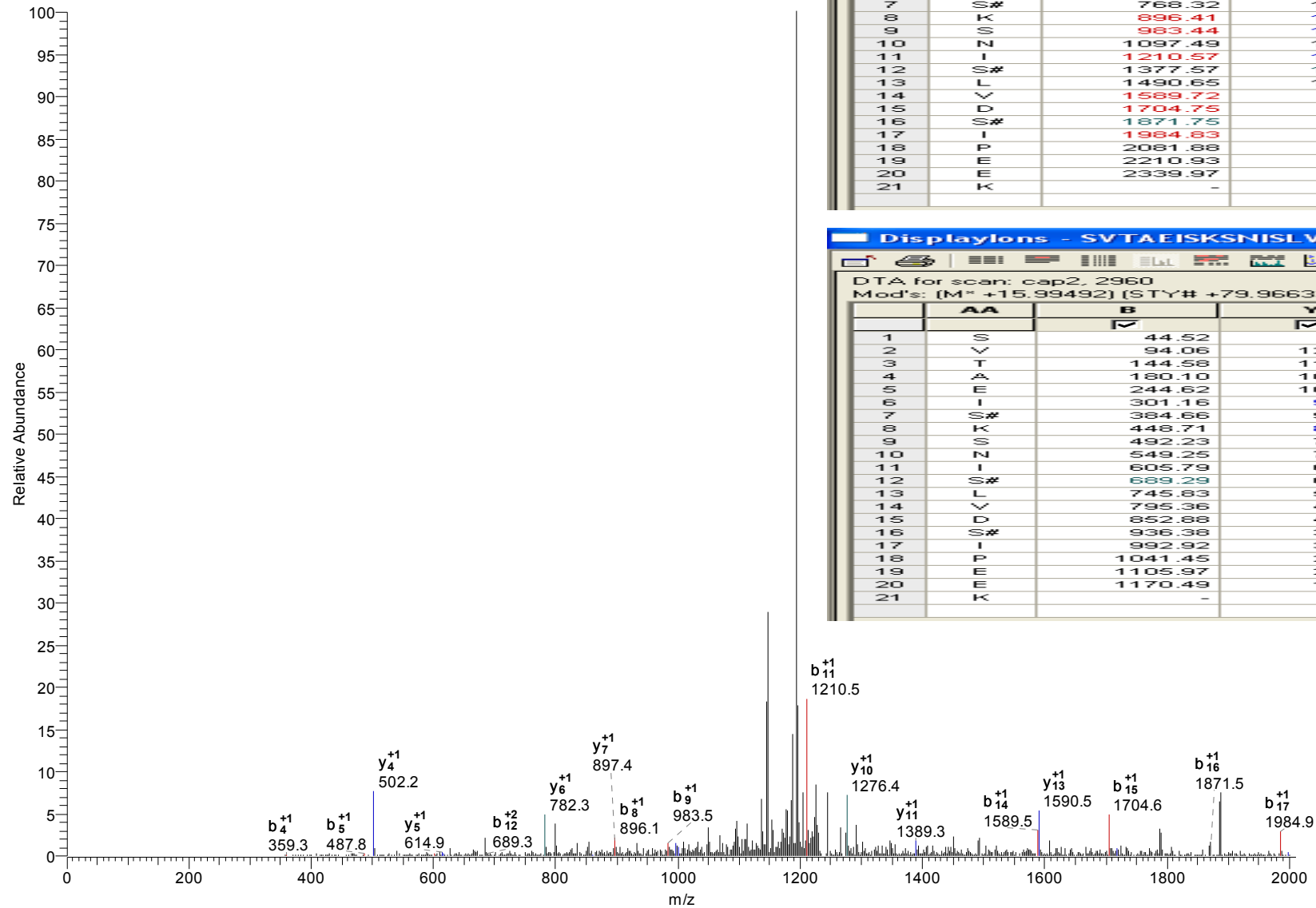
Displaylens - SSSSNIVPAK

DTA for scan: cap2, 1841
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	S	44.52	-	11
2	S	88.04	556.26	10
3	S#	171.54	512.74	9
4	E	236.06	429.24	8
5	S	279.58	364.72	7
6	N	336.60	321.20	6
7	I	393.14	264.18	5
8	V	442.67	207.64	4
9	P	491.20	158.10	3
10	A	526.72	109.58	2
11	K	-	74.06	1

105 kDa protein

#2960-2960 NL: 4.61E3



Displaylons - SVTAEISKSNISLVDSIPEEK

DTA for scan: cap2, 2960
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	S	88.04	-	21
2	V	187.11	2399.04	20
3	T	288.16	2299.97	19
4	A	359.19	2198.93	18
5	E	488.24	2127.89	17
6	I	601.32	1998.85	16
7	S#	768.32	1885.76	15
8	K	896.41	1718.76	14
9	S	983.44	1590.67	13
10	N	1097.49	1503.64	12
11	I	1210.57	1389.60	11
12	S#	1377.57	1276.51	10
13	L	1490.65	1109.51	9
14	V	1589.72	996.43	8
15	D	1704.75	897.36	7
16	S#	1871.75	782.33	6
17	I	1984.83	615.33	5
18	P	2081.88	502.25	4
19	E	2210.93	405.20	3
20	E	2339.97	276.16	2
21	K	-	147.11	1

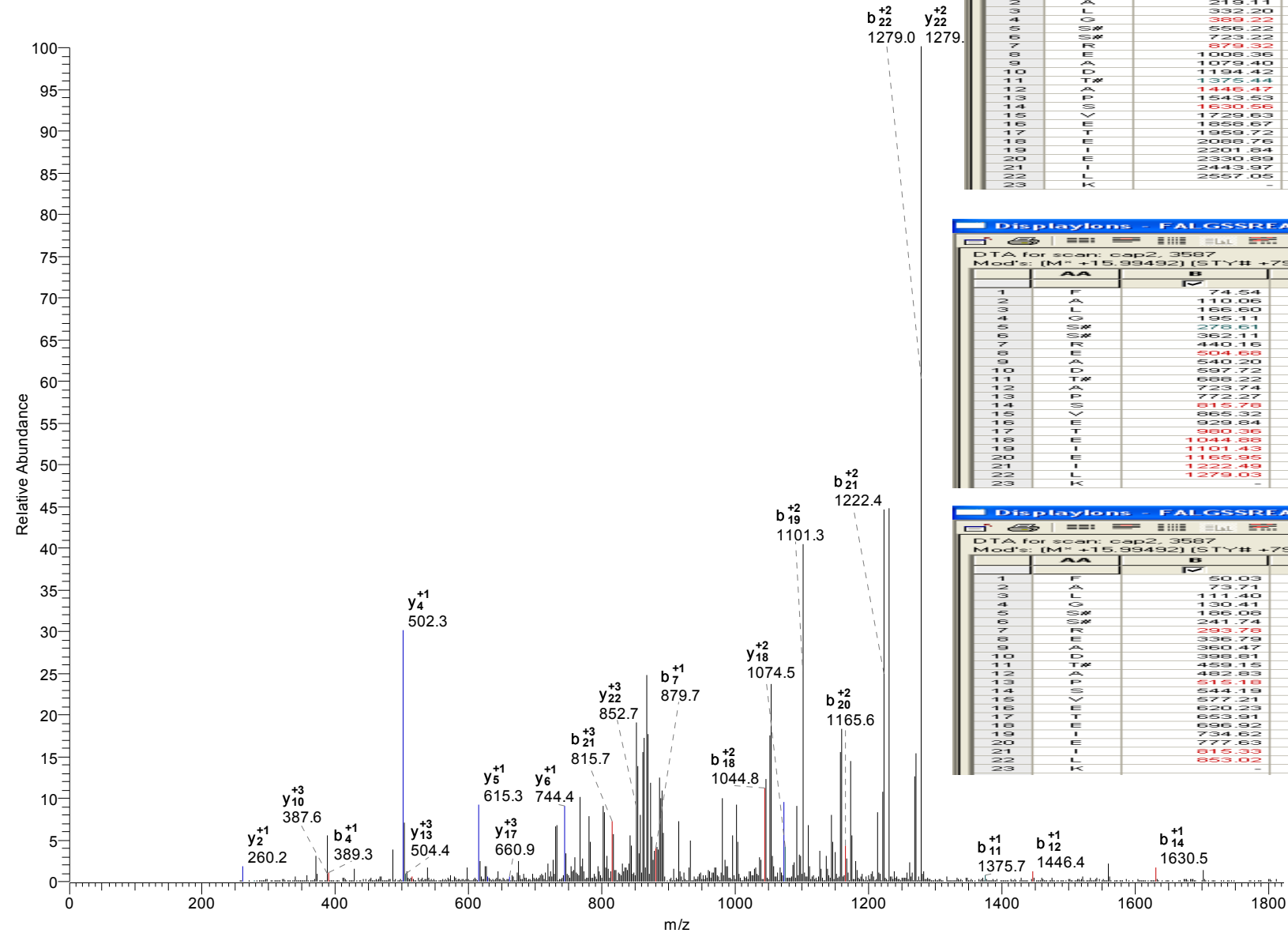
Displaylons - SVTAEISKSNISLVDSIPEEK

DTA for scan: cap2, 2960
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	S	44.52	-	21
2	V	94.06	1200.03	20
3	T	144.58	1150.49	19
4	A	180.10	1099.97	18
5	E	244.62	1064.45	17
6	I	301.16	999.93	16
7	S#	384.66	943.39	15
8	K	448.71	859.89	14
9	S	492.23	795.84	13
10	N	549.25	752.32	12
11	I	605.79	695.30	11
12	S#	689.29	638.76	10
13	L	745.83	555.26	9
14	V	795.36	498.72	8
15	D	852.88	449.18	7
16	S#	936.38	391.67	6
17	I	992.92	308.17	5
18	P	1041.45	251.63	4
19	E	1105.97	203.10	3
20	E	1170.49	138.58	2
21	K	-	74.06	1

Chek2 Checkpoint kinase Chk2

#3587-3587 NL: 1.93E4



Displaylons - FALGSSREADTAPSVETIEILK

DTA for scan: cap2_3587
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	F	148.06	-	23
2	A	219.11	2556.09	22
3	L	332.20	2485.05	21
4	G	389.22	2371.97	20
5	S#	556.22	2314.95	19
6	S#	723.22	2147.95	18
7	R	879.32	1980.95	17
8	E	1005.36	1824.85	16
9	A	1079.40	1695.81	15
10	D	1194.42	1624.77	14
11	T#	1375.44	1509.74	13
12	A	1446.47	1328.73	12
13	P	1543.53	1257.69	11
14	S	1530.56	1160.64	10
15	V	1729.63	1073.61	9
16	E	1858.67	974.54	8
17	T	1959.72	845.50	7
18	E	2088.76	744.45	6
19	I	2201.84	615.41	5
20	E	2330.89	502.32	4
21	I	2443.97	373.28	3
22	L	2557.05	260.20	2
23	K	-	147.11	1

Displaylons - FALGSSREADTAPSVETIEILK

DTA for scan: cap2_3587
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	F	74.54	-	23
2	A	110.06	1278.55	22
3	L	166.60	1243.03	21
4	G	195.11	1186.49	20
5	S#	276.51	1157.98	19
6	S#	352.11	1074.48	18
7	R	440.16	990.98	17
8	E	504.68	912.93	16
9	A	540.20	848.41	15
10	D	597.72	812.89	14
11	T#	666.22	755.36	13
12	A	723.74	664.87	12
13	P	772.27	629.35	11
14	S	815.78	580.82	10
15	V	865.32	537.31	9
16	E	929.84	487.77	8
17	T	980.36	423.25	7
18	E	1044.88	372.73	6
19	I	1101.43	308.21	5
20	E	1165.95	251.67	4
21	I	1222.49	187.14	3
22	L	1279.03	130.60	2
23	K	-	74.06	1

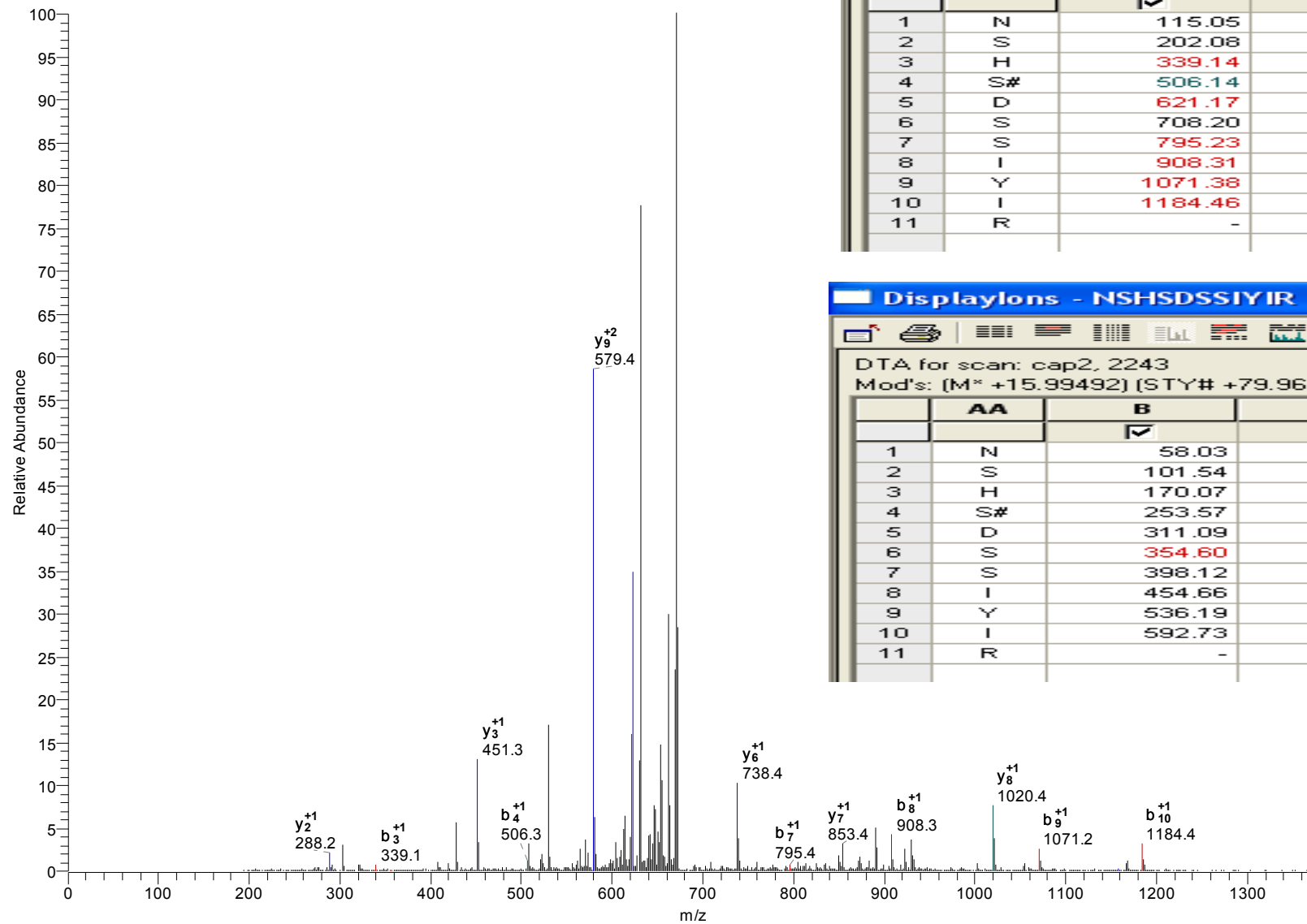
Displaylons - FALGSSREADTAPSVETIEILK

DTA for scan: cap2_3587
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	F	50.03	-	23
2	A	73.71	652.70	22
3	L	111.40	629.02	21
4	G	130.41	791.33	20
5	S#	166.08	772.32	19
6	S#	241.74	716.66	18
7	R	293.76	660.95	17
8	E	336.79	608.96	16
9	A	360.47	565.94	15
10	D	398.81	542.26	14
11	T#	459.15	503.92	13
12	A	482.83	443.58	12
13	P	515.18	419.90	11
14	S	544.19	387.55	10
15	V	577.21	358.54	9
16	E	577.21	325.52	8
17	T	653.91	282.50	7
18	E	696.92	248.62	6
19	I	734.62	205.81	5
20	E	777.63	166.11	4
21	I	815.33	125.10	3
22	L	853.02	87.40	2
23	K	-	49.71	1

Clmn_predicted similar to Calmin

#2243-2243 NL: 2.41E4



Displaylons - NSHSDSSIYIR

DTA for scan: cap2, 2243
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
		☒	☒	
1	N	115.05	-	11
2	S	202.08	1244.53	10
3	H	339.14	1157.50	9
4	S#	506.14	1020.44	8
5	D	621.17	853.44	7
6	S	708.20	738.41	6
7	S	795.23	651.38	5
8	I	908.31	564.35	4
9	Y	1071.38	451.27	3
10	I	1184.46	288.20	2
11	R	-	175.12	1

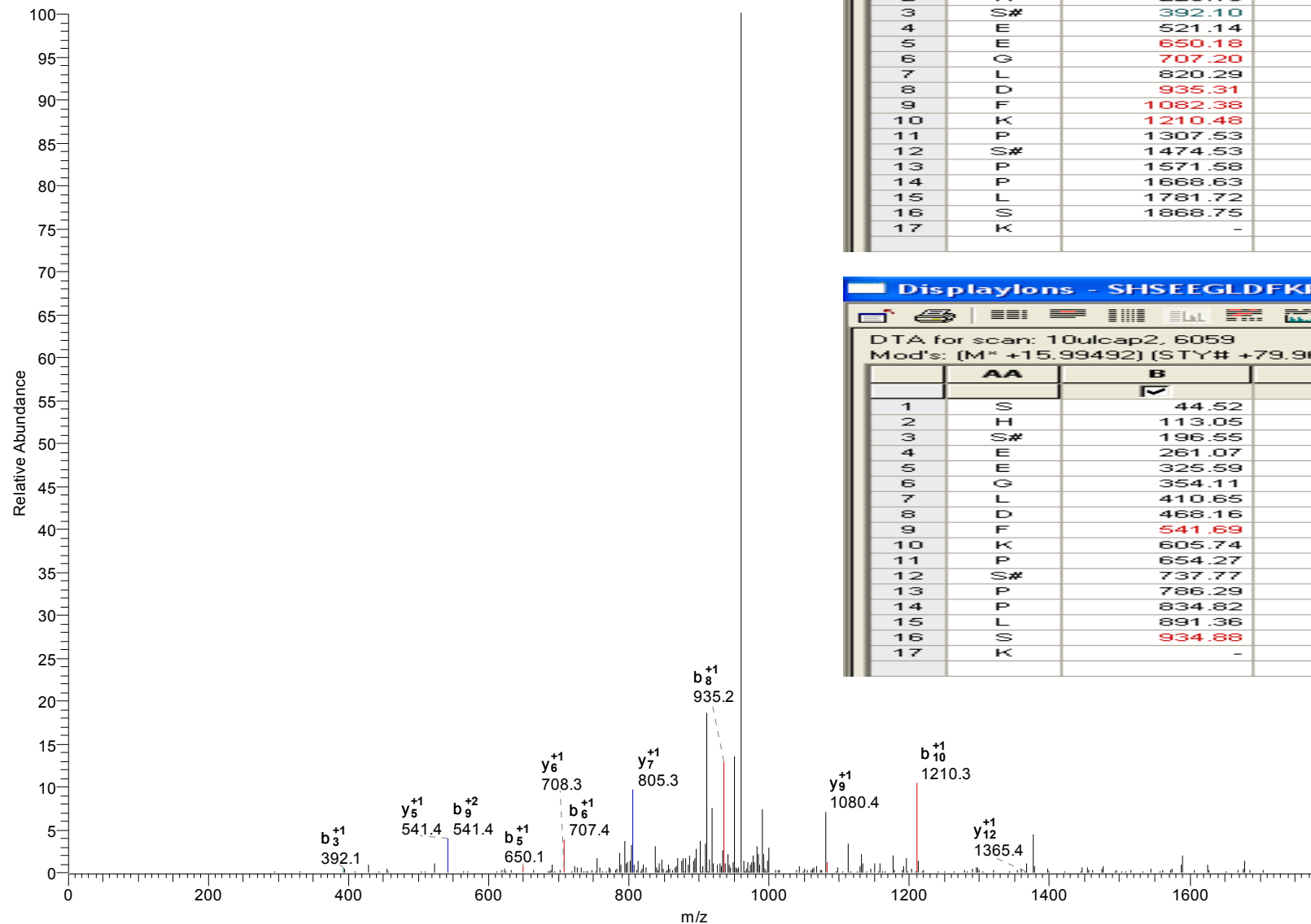
Displaylons - NSHSDSSIYIR

DTA for scan: cap2, 2243
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
		☒	☒	
1	N	58.03	-	11
2	S	101.54	622.77	10
3	H	170.07	579.25	9
4	S#	253.57	510.72	8
5	D	311.09	427.22	7
6	S	354.60	369.71	6
7	S	398.12	326.19	5
8	I	454.66	282.68	4
9	Y	536.19	226.14	3
10	I	592.73	144.61	2
11	R	-	88.06	1

Clmn_predicted similar to Calmin

#6059-6059 NL: 8.99E2



Displaylons - SHSEGLDFKPSPLSK

DTA for scan: 10ulcap2, 6059
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	S	88.04	-	17
2	H	225.10	1927.82	16
3	S#	392.10	1790.76	15
4	E	521.14	1623.77	14
5	E	650.18	1494.72	13
6	G	707.20	1365.68	12
7	L	820.29	1308.66	11
8	D	935.31	1195.58	10
9	F	1082.38	1080.55	9
10	K	1210.48	933.48	8
11	P	1307.53	805.39	7
12	S#	1474.53	708.33	6
13	P	1571.58	541.33	5
14	P	1668.63	444.28	4
15	L	1781.72	347.23	3
16	S	1868.75	234.14	2
17	K	-	147.11	1

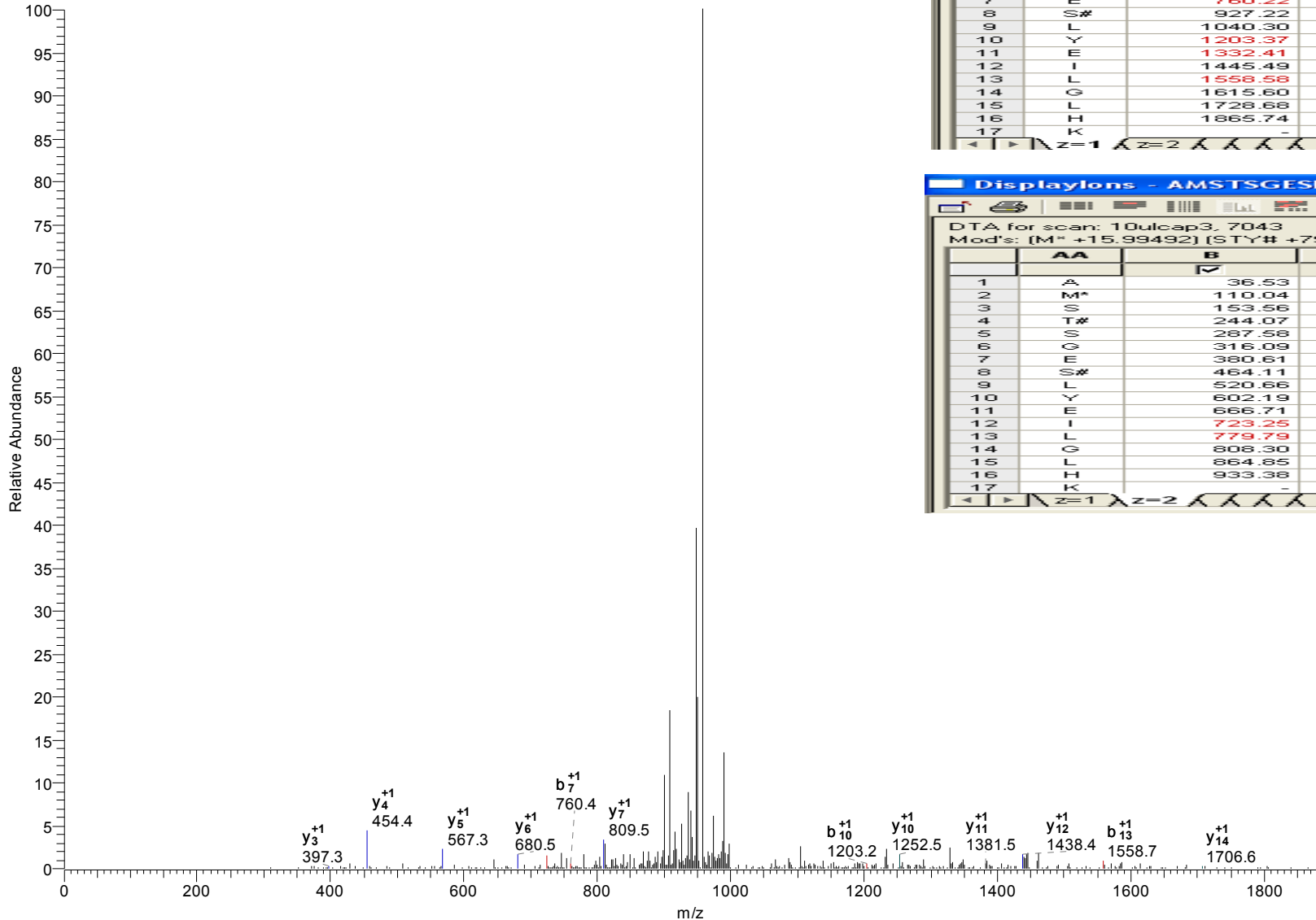
Displaylons - SHSEGLDFKPSPLSK

DTA for scan: 10ulcap2, 6059
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	S	44.52	-	17
2	H	113.05	964.42	16
3	S#	196.55	895.89	15
4	E	261.07	812.39	14
5	E	325.59	747.87	13
6	G	354.11	683.34	12
7	L	410.65	654.83	11
8	D	468.16	598.29	10
9	F	541.69	540.78	9
10	K	605.74	467.24	8
11	P	654.27	403.20	7
12	S#	737.77	354.67	6
13	P	786.29	271.17	5
14	P	834.82	222.64	4
15	L	891.36	174.12	3
16	S	934.88	117.58	2
17	K	-	74.06	1

Hypothetical LOC499579

#7043-7043 NL: 1.30E3

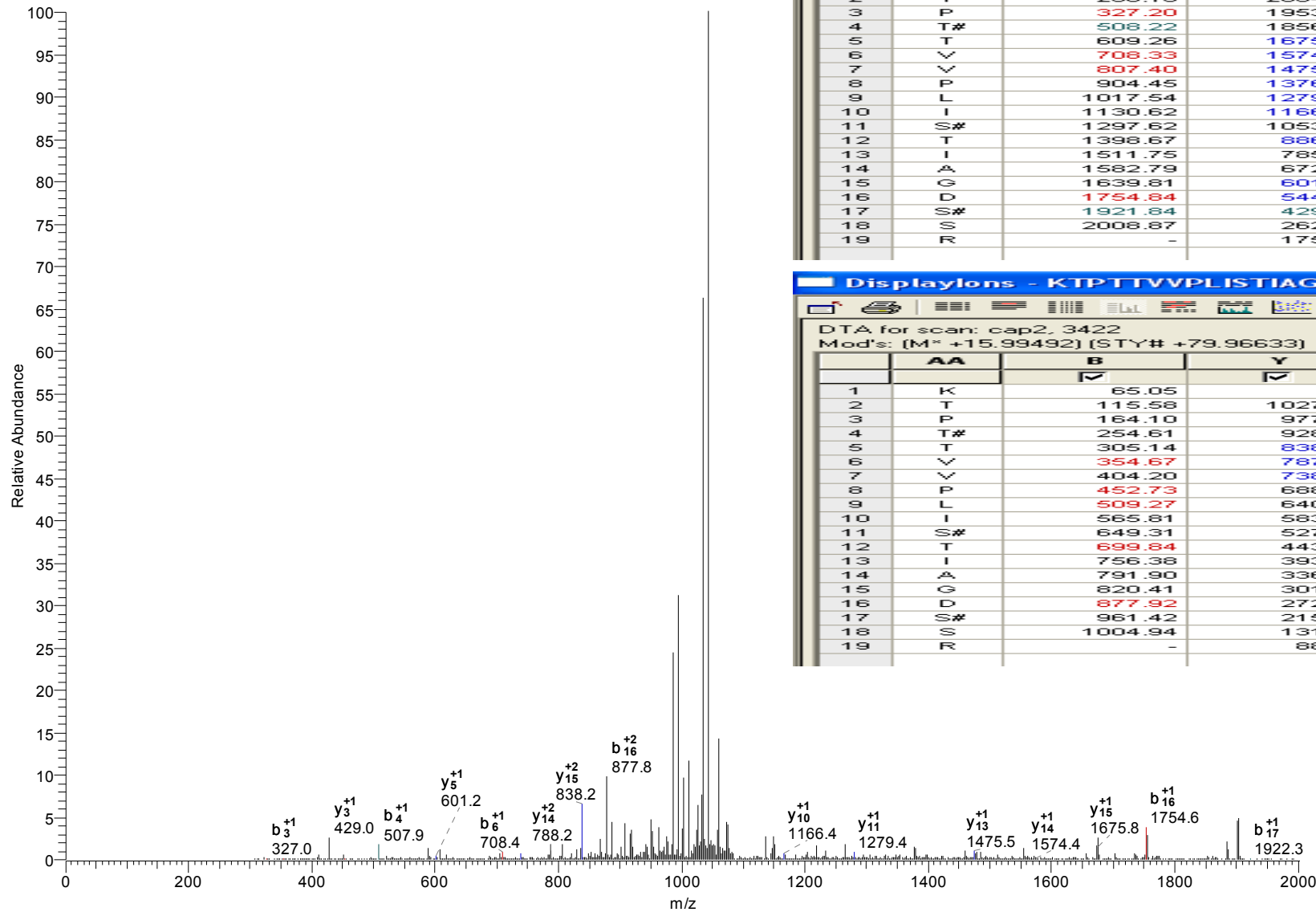


Displaylons - AMSTSGESLYEILGLHK				
DTA for scan: 10ulcap3, 7043				
Mod's: [M* +15.99492] (STY# +79.96633)				
	AA	B	Y	
1	A	72.04	-	17
2	M*	219.08	1940.81	16
3	S	306.11	1793.78	15
4	T#	487.13	1706.74	14
5	S	574.16	1525.73	13
6	G	631.18	1438.70	12
7	E	760.22	1381.68	11
8	S#	927.22	1252.63	10
9	L	1040.30	1085.64	9
10	Y	1203.37	972.55	8
11	E	1332.41	809.49	7
12	I	1445.49	680.45	6
13	L	1558.58	567.36	5
14	G	1615.60	454.28	4
15	L	1728.68	397.26	3
16	H	1865.74	284.17	2
17	K	-	147.11	1

Displaylons - AMSTSGESLYEILGLHK				
DTA for scan: 10ulcap3, 7043				
Mod's: [M* +15.99492] (STY# +79.96633)				
	AA	B	Y	
1	A	36.53	-	17
2	M*	110.04	970.91	16
3	S	153.56	897.39	15
4	T#	244.07	853.88	14
5	S	287.58	763.37	13
6	G	316.09	719.85	12
7	E	380.61	691.34	11
8	S#	464.11	626.82	10
9	L	520.66	543.32	9
10	Y	602.19	486.78	8
11	E	666.71	405.25	7
12	I	723.25	340.73	6
13	L	779.79	284.18	5
14	G	808.30	227.64	4
15	L	864.85	199.13	3
16	H	933.38	142.59	2
17	K	-	74.06	1

Vezf1_predicted similar to vascular endothelial zinc finger 1

#3422-3422 NL: 1.38E4



Displaylons - KTPTTVVPLISTIAGDSSR

DTA for scan: cap2, 3422
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	K	129.10	-	19
2	T	230.15	2054.88	18
3	P	327.20	1953.84	17
4	T#	508.22	1856.78	16
5	T	609.26	1675.77	15
6	V	708.33	1574.72	14
7	V	807.40	1475.65	13
8	P	904.45	1376.59	12
9	L	1017.54	1279.53	11
10	I	1130.62	1166.45	10
11	S#	1297.62	1053.36	9
12	T	1398.67	886.37	8
13	I	1511.75	785.32	7
14	A	1582.79	672.23	6
15	G	1639.81	601.20	5
16	D	1754.84	544.18	4
17	S#	1921.84	429.15	3
18	S	2008.87	262.15	2
19	R	-	175.12	1

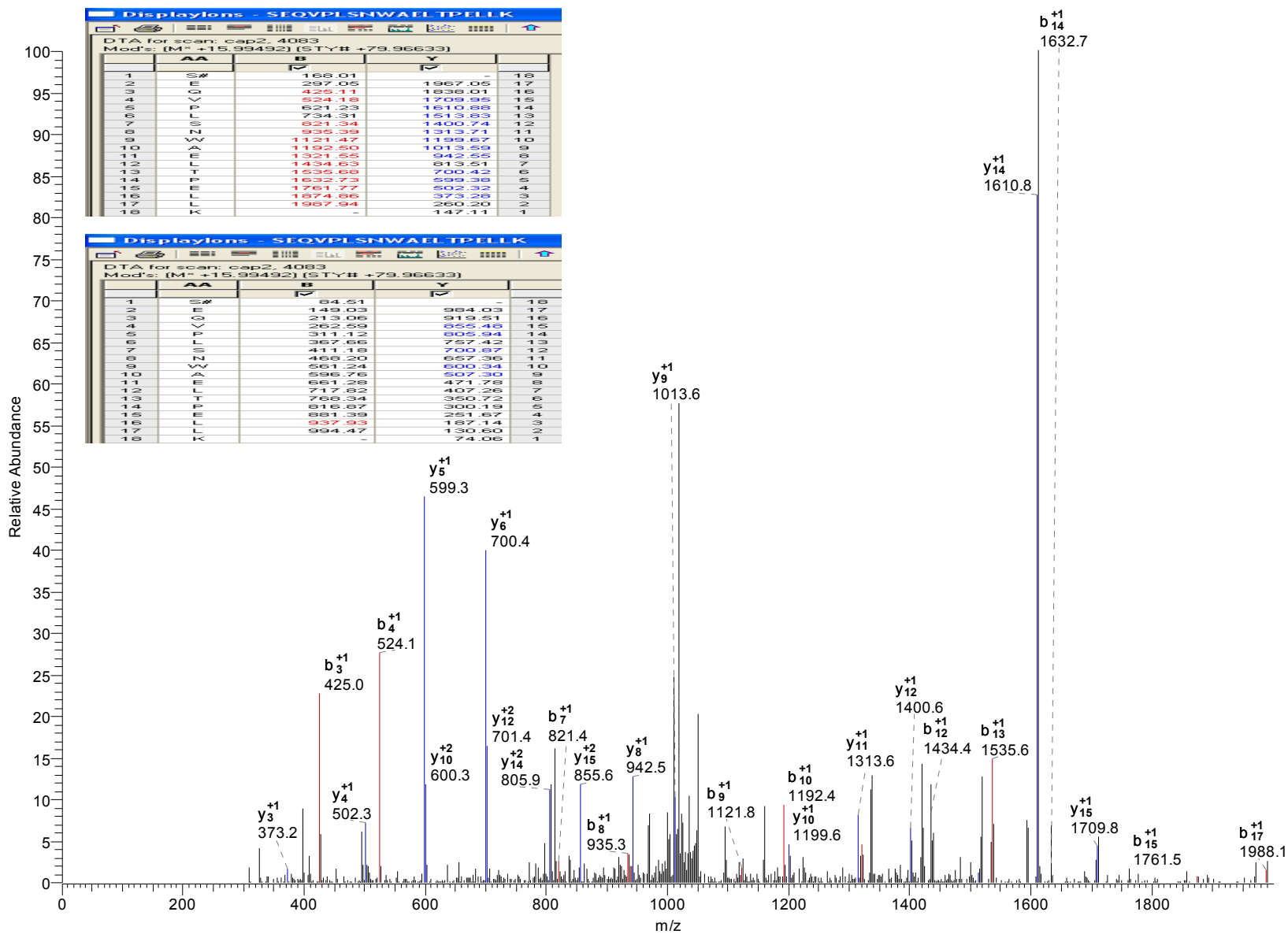
Displaylons - KTPTTVVPLISTIAGDSSR

DTA for scan: cap2, 3422
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	K	65.05	-	19
2	T	115.58	1027.95	18
3	P	164.10	977.42	17
4	T#	254.61	928.90	16
5	T	305.14	838.39	15
6	V	354.67	787.86	14
7	V	404.20	738.33	13
8	P	452.73	688.80	12
9	L	509.27	640.27	11
10	I	565.81	583.73	10
11	S#	649.31	527.19	9
12	T	699.84	443.69	8
13	I	756.38	393.16	7
14	A	791.90	336.62	6
15	G	820.41	301.10	5
16	D	877.92	272.59	4
17	S#	961.42	215.08	3
18	S	1004.94	131.58	2
19	R	-	88.06	1

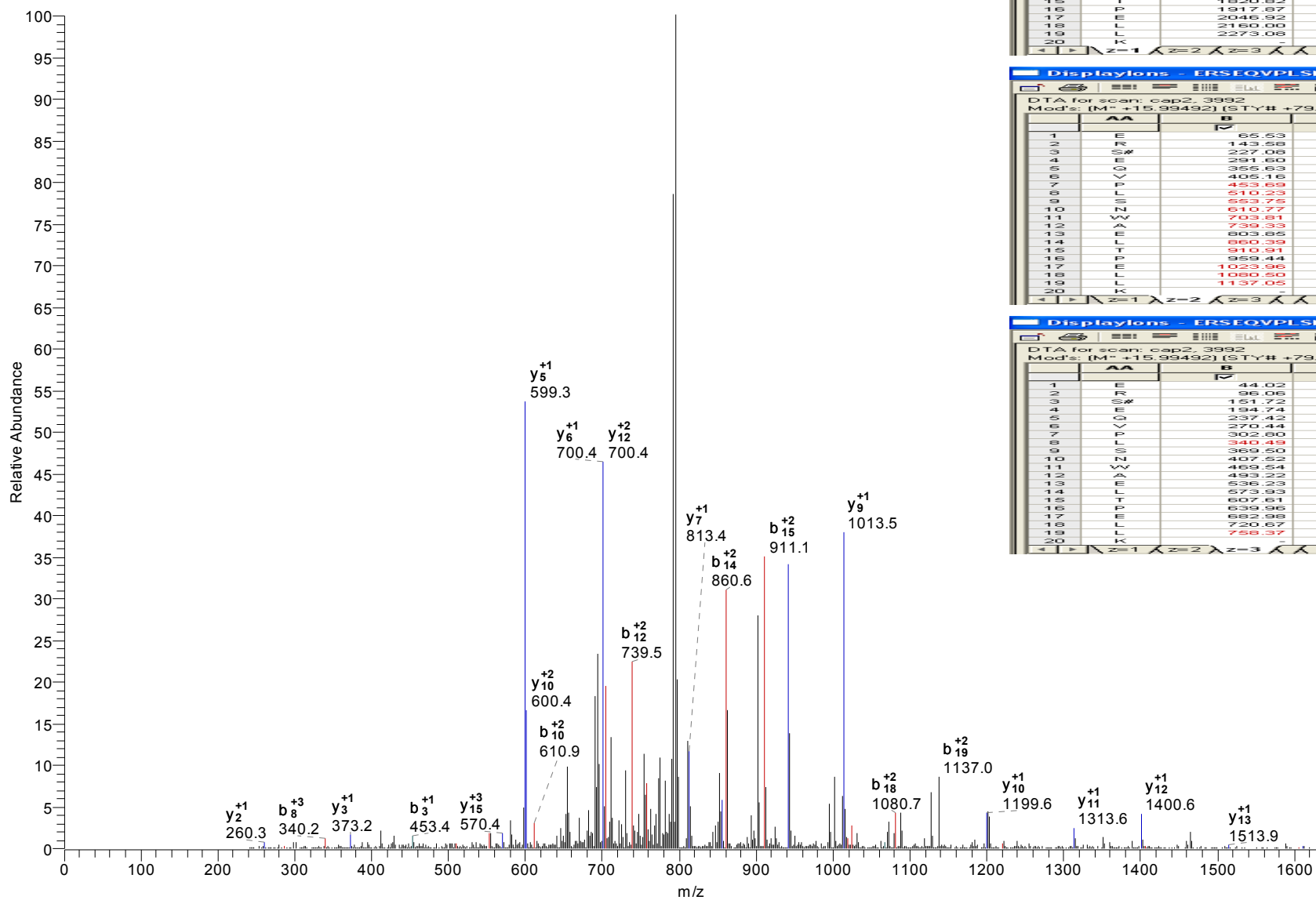
Ropn1 Ropporin-1

#4083-4083 NL: 1.62E3



Ropn1 Ropporin-1

#3992-3992 NL: 2.40E4



Displaylons - ERSEOVPLSNWAEITPELLK

DTA for scan: cap2_3992
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	E	130.05	-	20
2	R	266.15	2290.15	19
3	S#	453.15	2134.03	18
4	E	582.19	1957.05	17
5	Q	710.25	1838.01	16
6	V	809.32	1709.95	15
7	P	906.37	1610.86	14
8	L	1019.46	1513.83	13
9	S	1106.49	1400.74	12
10	N	1220.53	1313.71	11
11	W	1406.61	1199.67	10
12	A	1477.65	1013.59	9
13	E	1606.69	942.55	8
14	L	1719.77	813.51	7
15	T	1820.82	700.42	6
16	P	1917.87	599.38	5
17	E	2046.92	502.32	4
18	L	2160.00	373.28	3
19	L	2273.08	260.20	2
20	K		147.11	1

Displaylons - ERSEOVPLSNWAEITPELLK

DTA for scan: cap2_3992
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	E	65.53	-	20
2	R	143.58	1145.58	19
3	S#	227.08	1067.53	18
4	E	291.60	984.03	17
5	Q	355.63	919.51	16
6	V	405.16	855.48	15
7	P	453.69	805.94	14
8	L	510.23	757.42	13
9	S	563.75	700.87	12
10	N	610.77	657.35	11
11	W	703.81	600.34	10
12	A	739.33	507.30	9
13	E	803.85	471.78	8
14	L	860.39	407.26	7
15	T	910.91	350.72	6
16	P	959.44	300.19	5
17	E	1023.96	251.67	4
18	L	1080.60	187.14	3
19	L	1137.05	130.60	2
20	K		74.06	1

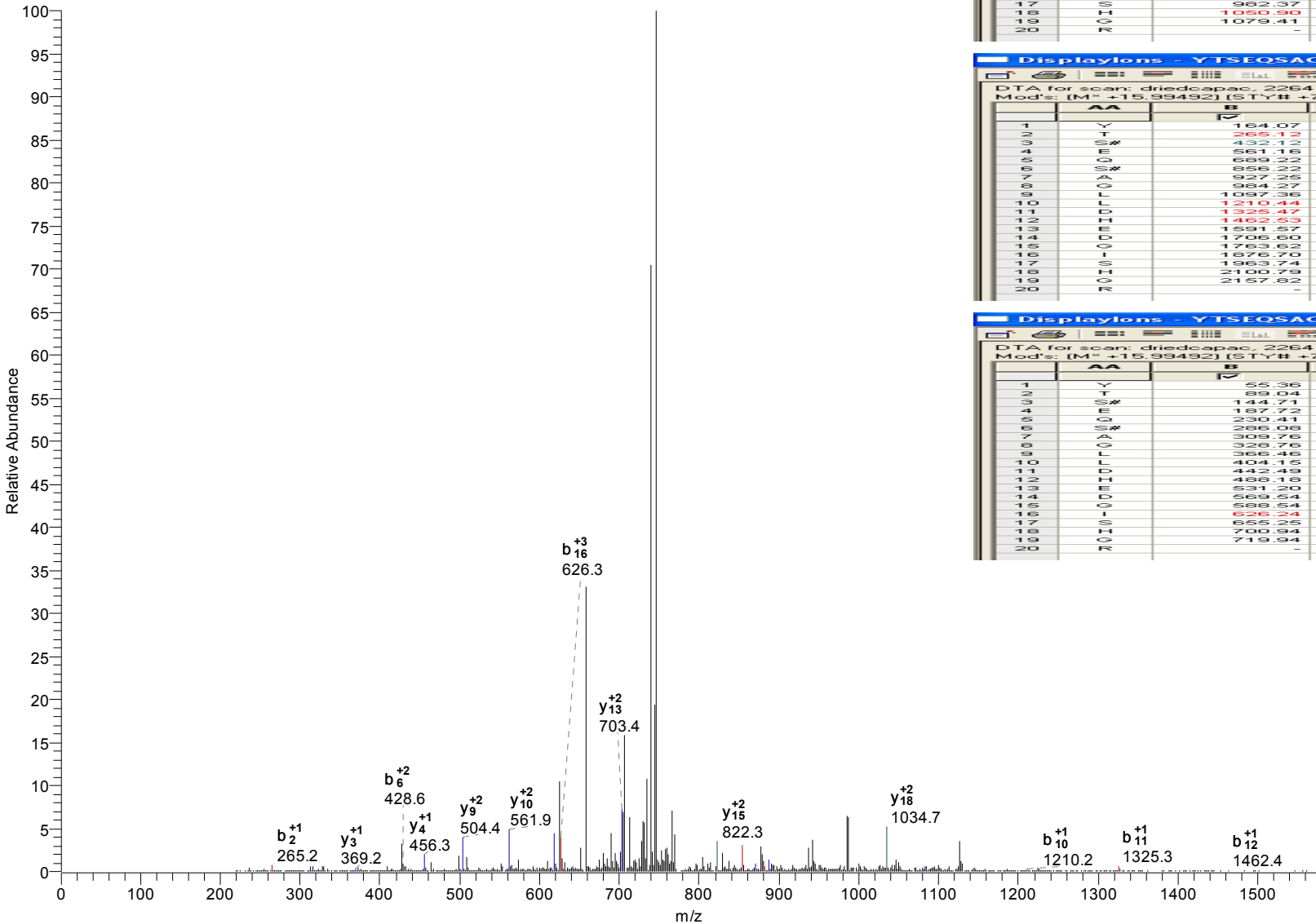
Displaylons - ERSEOVPLSNWAEITPELLK

DTA for scan: cap2_3992
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	E	44.02	-	20
2	R	96.06	764.05	19
3	S#	151.72	712.02	18
4	E	194.74	656.35	17
5	Q	237.42	613.34	16
6	V	270.44	570.85	15
7	P	302.80	537.63	14
8	L	340.49	505.28	13
9	S	369.50	467.59	12
10	N	407.52	438.57	11
11	W	469.54	400.56	10
12	A	493.22	338.53	9
13	E	536.23	314.86	8
14	L	573.93	271.84	7
15	T	607.61	234.15	6
16	P	639.96	200.46	5
17	E	682.98	168.11	4
18	L	720.67	125.10	3
19	L	758.37	87.40	2
20	K		49.71	1

Tesb protein

#2264-2264 NL: 1.88E4



Displayions - YTSEQSAGLLDHEDGISHGR

DTA for scan: driedcapac, 2264
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	Y	82.54	-	20
2	T	133.06	1084.94	19
3	SW	216.56	1034.41	18
4	E	261.06	960.91	17
5	Q	345.11	886.39	16
6	SW	428.61	822.36	15
7	A	464.13	738.86	14
8	Q	492.64	703.34	13
9	L	549.18	674.83	12
10	L	605.73	618.29	11
11	D	663.24	561.75	10
12	H	731.77	504.34	9
13	E	796.29	435.71	8
14	D	863.80	371.19	7
15	Q	882.31	313.67	6
16	I	938.86	285.16	5
17	S	962.37	226.62	4
18	H	1050.90	185.10	3
19	Q	1079.41	116.57	2
20	R	-	88.06	1

Displayions - YTSEQSAGLLDHEDGISHGR

DTA for scan: driedcapac, 2264
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	Y	164.07	-	20
2	T	265.12	2168.86	19
3	SW	432.12	2067.82	18
4	E	561.16	1900.82	17
5	Q	689.22	1771.76	16
6	SW	856.22	1643.72	15
7	A	927.25	1476.72	14
8	Q	984.27	1405.68	13
9	L	1097.36	1348.66	12
10	L	1210.44	1235.56	11
11	D	1325.47	1122.49	10
12	H	1462.53	1007.47	9
13	E	1591.57	870.41	8
14	D	1706.60	741.36	7
15	Q	1763.62	626.34	6
16	I	1876.70	569.32	5
17	S	1963.74	456.23	4
18	H	2100.79	369.20	3
19	Q	2157.82	232.14	2
20	R	-	175.12	1

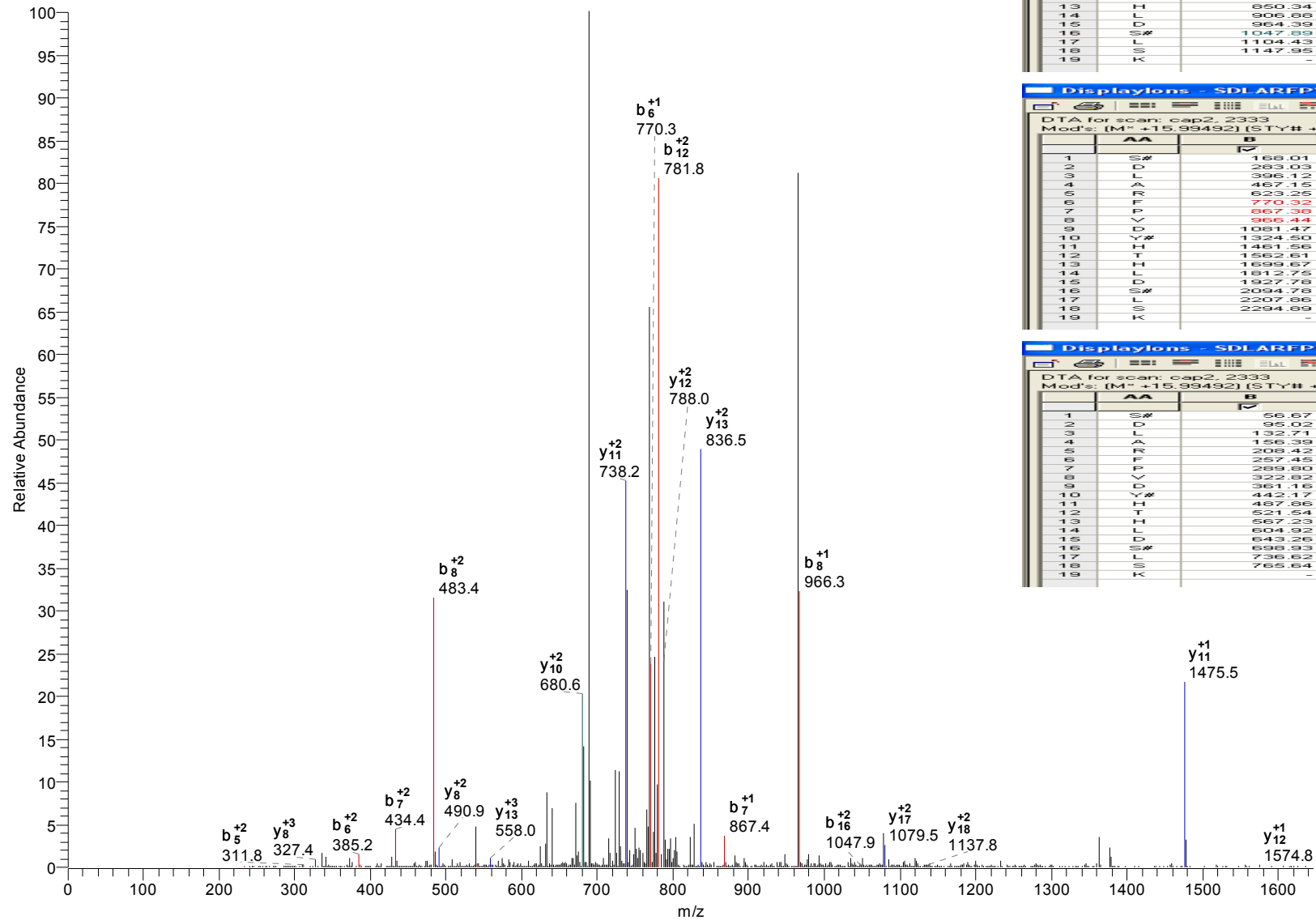
Displayions - YTSEQSAGLLDHEDGISHGR

DTA for scan: driedcapac, 2264
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	Y	55.36	-	20
2	T	89.04	723.63	19
3	SW	144.71	689.94	18
4	E	187.72	634.26	17
5	Q	230.41	591.26	16
6	SW	286.06	548.58	15
7	A	309.76	492.91	14
8	Q	328.76	469.23	13
9	L	365.46	450.22	12
10	L	404.15	412.53	11
11	D	442.49	374.84	10
12	H	488.18	336.49	9
13	E	531.20	290.81	8
14	D	569.54	247.79	7
15	Q	588.54	209.45	6
16	I	626.24	190.44	5
17	S	655.25	152.75	4
18	H	700.94	123.74	3
19	Q	719.94	78.05	2
20	R	-	59.04	1

Pak7_predicted p21 (CDKN1A)-activated kinase 7

#2333-2333 NL: 2.74E4



Displaylens - SDLARFPVDYHHTILDLSLK

DTA for scan: cap2_2333
Mod's: (M⁺ +15.99492) (S^TY# +79.96633)

	AA	B	Y	
1	S#	84.51	-	19
2	D	142.02	1137.50	18
3	L	198.58	1079.99	17
4	A	234.08	1023.46	16
5	R	312.13	987.93	15
6	F	365.67	909.66	14
7	P	434.19	836.34	13
8	V	483.73	787.82	12
9	D	541.24	738.28	11
10	Y#	562.75	680.77	10
11	H	731.28	559.26	9
12	T	781.81	490.73	8
13	H	850.34	440.20	7
14	L	906.88	371.67	6
15	D	964.39	315.13	5
16	S#	1047.89	257.62	4
17	L	1104.43	174.12	3
18	S	1147.95	117.58	2
19	K	-	74.06	1

Displaylens - SDLARFPVDYHHTILDLSLK

DTA for scan: cap2_2333
Mod's: (M⁺ +15.99492) (S^TY# +79.96633)

	AA	B	Y	
1	S#	168.01	-	19
2	D	283.03	2274.00	18
3	L	396.12	2158.97	17
4	A	467.15	2045.89	16
5	R	623.25	1974.85	15
6	F	770.32	1818.75	14
7	P	867.38	1671.68	13
8	V	966.44	1574.63	12
9	D	1081.47	1475.56	11
10	Y#	1324.50	1360.53	10
11	H	1461.56	1117.50	9
12	T	1562.61	980.44	8
13	H	1699.67	879.40	7
14	L	1812.75	742.34	6
15	D	1927.78	629.25	5
16	S#	2094.78	514.23	4
17	L	2207.86	347.23	3
18	S	2294.89	234.14	2
19	K	-	147.11	1

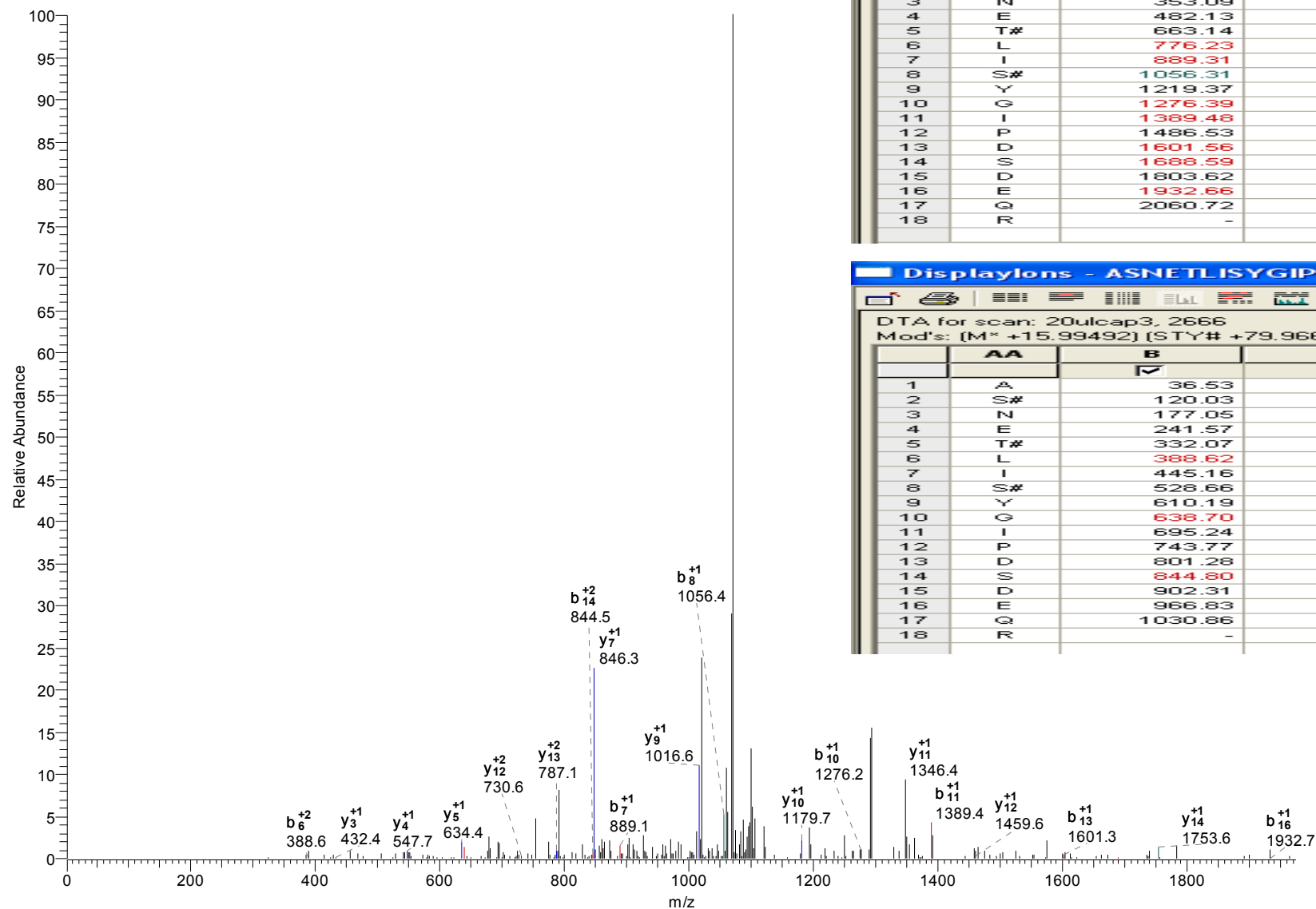
Displaylens - SDLARFPVDYHHTILDLSLK

DTA for scan: cap2_2333
Mod's: (M⁺ +15.99492) (S^TY# +79.96633)

	AA	B	Y	
1	S#	56.67	-	19
2	D	95.02	758.67	18
3	L	132.71	720.33	17
4	A	156.39	682.63	16
5	R	208.42	658.96	15
6	F	257.45	606.92	14
7	P	289.80	557.90	13
8	V	322.82	525.55	12
9	D	361.16	492.52	11
10	Y#	442.17	454.18	10
11	H	487.86	373.17	9
12	T	521.54	327.49	8
13	H	567.23	293.80	7
14	L	604.92	248.12	6
15	D	643.26	210.42	5
16	S#	698.93	172.08	4
17	L	736.52	116.41	3
18	S	765.64	78.72	2
19	K	-	49.71	1

RGD1561507_predicted hypothetical protein LOC292078

#2666-2666 NL: 6.81E2



Displaylons - ASNETLISYGIPDSDEQR

DTA for scan: 20ulcap3, 2666
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	A	72.04	-	18
2	S#	239.04	2163.79	17
3	N	353.09	1996.79	16
4	E	482.13	1882.75	15
5	T#	663.14	1753.71	14
6	L	776.23	1572.69	13
7	I	889.31	1459.61	12
8	S#	1056.31	1346.53	11
9	Y	1219.37	1179.53	10
10	G	1276.39	1016.46	9
11	I	1389.48	959.44	8
12	P	1486.53	846.36	7
13	D	1601.56	749.31	6
14	S	1688.59	634.28	5
15	D	1803.62	547.25	4
16	E	1932.66	432.22	3
17	Q	2060.72	303.18	2
18	R	-	175.12	1

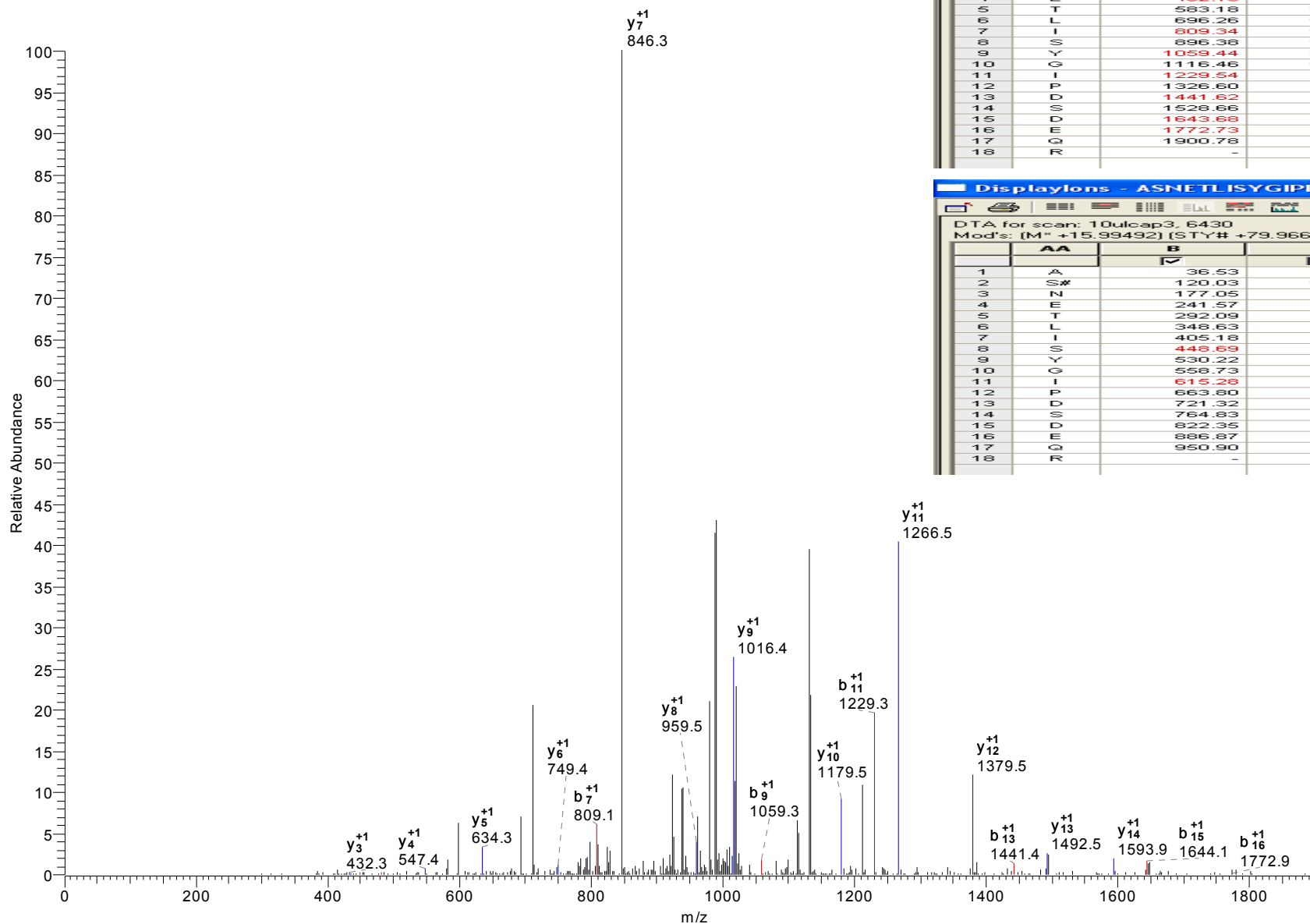
Displaylons - ASNETLISYGIPDSDEQR

DTA for scan: 20ulcap3, 2666
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	A	36.53	-	18
2	S#	120.03	1082.40	17
3	N	177.05	998.90	16
4	E	241.57	941.88	15
5	T#	332.07	877.36	14
6	L	388.62	786.85	13
7	I	445.16	730.31	12
8	S#	528.66	673.77	11
9	Y	610.19	590.27	10
10	G	638.70	508.74	9
11	I	695.24	480.23	8
12	P	743.77	423.68	7
13	D	801.28	375.16	6
14	S	844.80	317.64	5
15	D	902.31	274.13	4
16	E	966.83	216.61	3
17	Q	1030.86	152.09	2
18	R	-	88.06	1

RGD1561507_predicted hypothetical protein LOC292078

#6430-6430 NL: 1.16E3



Displaylons - ASNETLISYGIPDSDEOR

DTA for scan: 10ulcap3, 6430
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	A	72.04	-	18
2	S#	239.04	2003.86	17
3	N	353.09	1836.86	16
4	E	482.13	1722.82	15
5	T	583.18	1593.78	14
6	L	696.26	1492.73	13
7	I	809.34	1379.64	12
8	S	896.38	1266.56	11
9	Y	1059.44	1179.53	10
10	Q	1116.46	1016.46	9
11	I	1229.54	959.44	8
12	P	1326.60	846.36	7
13	D	1441.62	749.31	6
14	S	1526.86	634.26	5
15	D	1643.68	547.25	4
16	E	1772.73	432.22	3
17	Q	1900.78	303.18	2
18	R	-	175.12	1

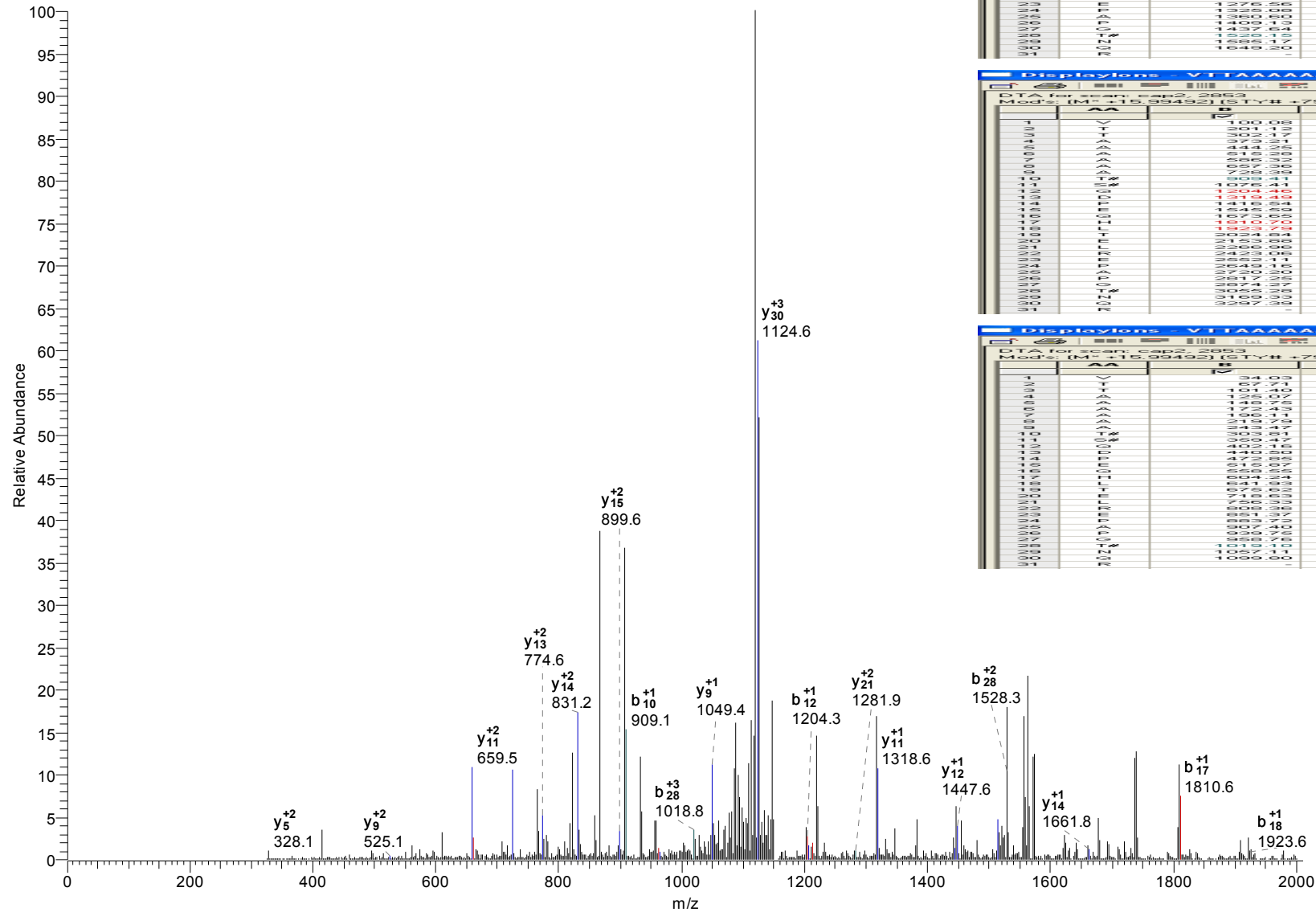
Displaylons - ASNETLISYGIPDSDEOR

DTA for scan: 10ulcap3, 6430
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	A	36.53	-	18
2	S#	120.03	1002.43	17
3	N	177.05	918.93	16
4	E	241.57	861.91	15
5	T	292.09	797.39	14
6	L	348.63	746.87	13
7	I	405.18	690.33	12
8	S	448.69	633.78	11
9	Y	530.22	590.27	10
10	Q	558.73	508.74	9
11	I	615.26	480.23	8
12	P	663.80	423.68	7
13	D	721.32	375.16	6
14	S	764.83	317.64	5
15	D	822.35	274.13	4
16	E	886.87	216.61	3
17	Q	950.90	152.09	2
18	R	-	88.06	1

Cops7a_predicted ZH11 protei

#2853-2853 NL: 9.97E3



Displays V T T A A A A A A T S Q D P L Q H I T E L

OTAs for scan: 2853
Mod% (M⁺ +15.99492) (STY# +79.96633)

AA	IS	N	OT
1	100.00	100.00	100.00
Y	101.02	100.00	100.00
A	102.04	100.00	100.00
A	103.06	100.00	100.00
A	104.08	100.00	100.00
A	105.10	100.00	100.00
T	106.12	100.00	100.00
S	107.14	100.00	100.00
Q	108.16	100.00	100.00
D	109.18	100.00	100.00
P	110.20	100.00	100.00
L	111.22	100.00	100.00
H	112.24	100.00	100.00
I	113.26	100.00	100.00
E	114.28	100.00	100.00
T	115.30	100.00	100.00
S	116.32	100.00	100.00
Q	117.34	100.00	100.00
D	118.36	100.00	100.00
P	119.38	100.00	100.00
L	120.40	100.00	100.00
H	121.42	100.00	100.00
I	122.44	100.00	100.00
E	123.46	100.00	100.00
T	124.48	100.00	100.00
S	125.50	100.00	100.00
Q	126.52	100.00	100.00
D	127.54	100.00	100.00
P	128.56	100.00	100.00
L	129.58	100.00	100.00
H	130.60	100.00	100.00
I	131.62	100.00	100.00
E	132.64	100.00	100.00
T	133.66	100.00	100.00
S	134.68	100.00	100.00
Q	135.70	100.00	100.00
D	136.72	100.00	100.00
P	137.74	100.00	100.00
L	138.76	100.00	100.00
H	139.78	100.00	100.00
I	140.80	100.00	100.00
E	141.82	100.00	100.00
T	142.84	100.00	100.00
S	143.86	100.00	100.00
Q	144.88	100.00	100.00
D	145.90	100.00	100.00
P	146.92	100.00	100.00
L	147.94	100.00	100.00
H	148.96	100.00	100.00
I	149.98	100.00	100.00
E	150.00	100.00	100.00

Displays V T T A A A A A A T S Q D P L Q H I T E L

OTAs for scan: 2853
Mod% (M⁺ +15.99492) (STY# +79.96633)

AA	IS	N	OT
1	100.00	100.00	100.00
Y	101.02	100.00	100.00
A	102.04	100.00	100.00
A	103.06	100.00	100.00
A	104.08	100.00	100.00
A	105.10	100.00	100.00
T	106.12	100.00	100.00
S	107.14	100.00	100.00
Q	108.16	100.00	100.00
D	109.18	100.00	100.00
P	110.20	100.00	100.00
L	111.22	100.00	100.00
H	112.24	100.00	100.00
I	113.26	100.00	100.00
E	114.28	100.00	100.00
T	115.30	100.00	100.00
S	116.32	100.00	100.00
Q	117.34	100.00	100.00
D	118.36	100.00	100.00
P	119.38	100.00	100.00
L	120.40	100.00	100.00
H	121.42	100.00	100.00
I	122.44	100.00	100.00
E	123.46	100.00	100.00
T	124.48	100.00	100.00
S	125.50	100.00	100.00
Q	126.52	100.00	100.00
D	127.54	100.00	100.00
P	128.56	100.00	100.00
L	129.58	100.00	100.00
H	130.60	100.00	100.00
I	131.62	100.00	100.00
E	132.64	100.00	100.00
T	133.66	100.00	100.00
S	134.68	100.00	100.00
Q	135.70	100.00	100.00
D	136.72	100.00	100.00
P	137.74	100.00	100.00
L	138.76	100.00	100.00
H	139.78	100.00	100.00
I	140.80	100.00	100.00
E	141.82	100.00	100.00
T	142.84	100.00	100.00
S	143.86	100.00	100.00
Q	144.88	100.00	100.00
D	145.90	100.00	100.00
P	146.92	100.00	100.00
L	147.94	100.00	100.00
H	148.96	100.00	100.00
I	149.98	100.00	100.00
E	150.00	100.00	100.00

Displays V T T A A A A A A T S Q D P L Q H I T E L

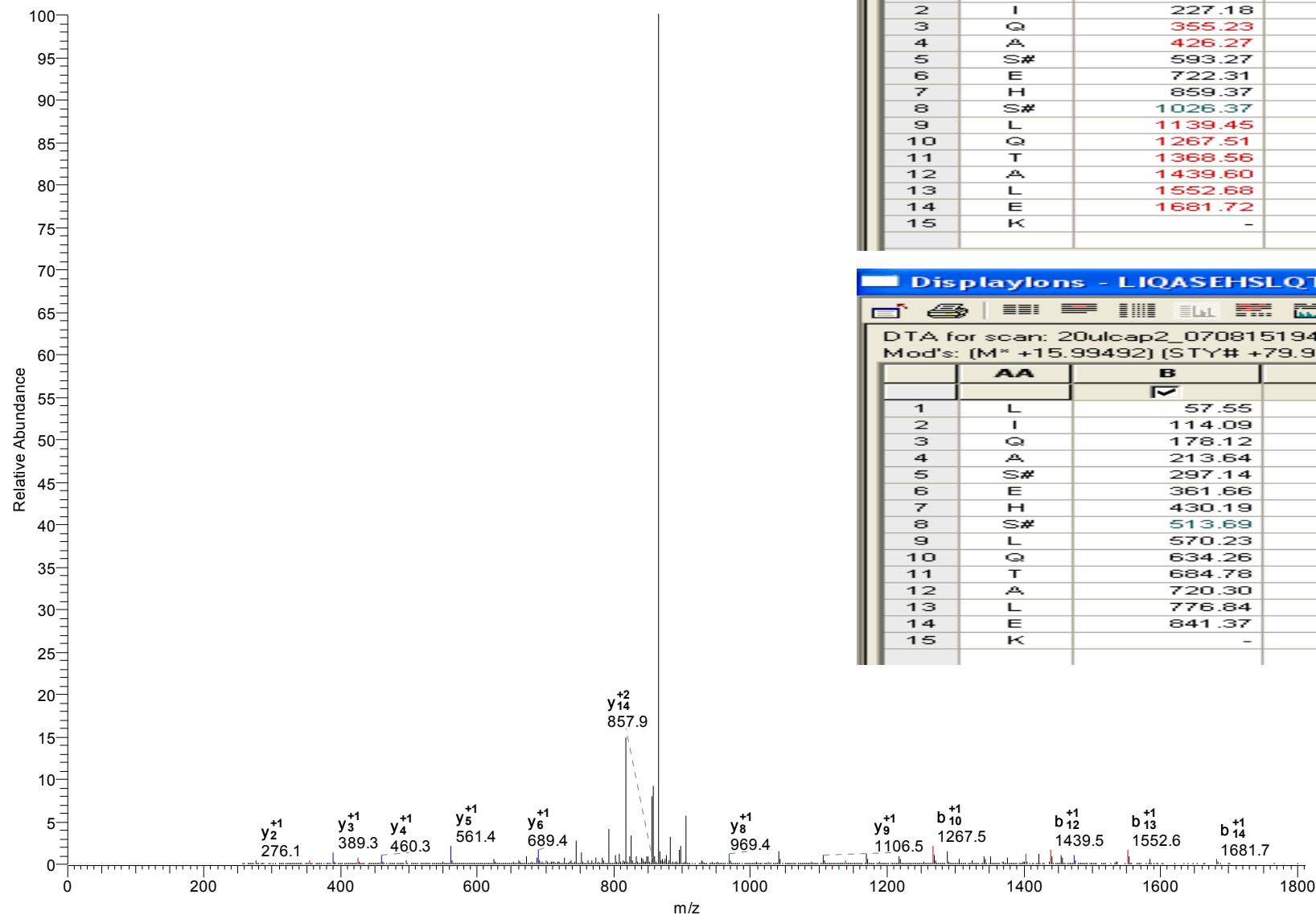
OTAs for scan: 2853
Mod% (M⁺ +15.99492) (STY# +79.96633)

AA	IS	N	OT
1	100.00	100.00	100.00
Y	101.02	100.00	100.00
A	102.04	100.00	100.00
A	103.06	100.00	100.00
A	104.08	100.00	100.00
A	105.10	100.00	100.00
T	106.12	100.00	100.00
S	107.14	100.00	100.00
Q	108.16	100.00	100.00
D	109.18	100.00	100.00
P	110.20	100.00	100.00
L	111.22	100.00	100.00
H	112.24	100.00	100.00
I	113.26	100.00	100.00
E	114.28	100.00	100.00
T	115.30	100.00	100.00
S	116.32	100.00	100.00
Q	117.34	100.00	100.00
D	118.36	100.00	100.00
P	119.38	100.00	100.00
L	120.40	100.00	100.00
H	121.42	100.00	100.00
I	122.44	100.00	100.00
E	123.46	100.00	100.00
T	124.48	100.00	100.00
S	125.50	100.00	100.00
Q	126.52	100.00	100.00
D	127.54	100.00	100.00
P	128.56	100.00	100.00
L	129.58	100.00	100.00
H	130.60	100.00	100.00
I	131.62	100.00	100.00
E	132.64	100.00	100.00
T	133.66	100.00	100.00
S	134.68	100.00	100.00
Q	135.70	100.00	100.00
D	136.72	100.00	100.00
P	137.74	100.00	100.00
L	138.76	100.00	100.00
H	139.78	100.00	100.00
I	140.80	100.00	100.00
E	141.82	100.00	100.00
T	142.84	100.00	100.00
S	143.86	100.00	100.00
Q	144.88	100.00	100.00
D	145.90	100.00	100.00
P	146.92	100.00	100.00
L	147.94	100.00	100.00
H	148.96	100.00	100.00
I	149.98	100.00	100.00
E	150.00	100.00	100.00

RGD1359156 Putative uncharacterized protein

RGD1359156

#2757-2757 NL: 4.95E4



Displaylons - LIQASEHSLQTALEK

DTA for scan: 20ulcap2_070815194055, 2757
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	L	114.09	-	15
2	I	227.18	1714.74	14
3	Q	355.23	1601.66	13
4	A	426.27	1473.60	12
5	S#	593.27	1402.57	11
6	E	722.31	1235.57	10
7	H	859.37	1106.52	9
8	S#	1026.37	969.47	8
9	L	1139.45	802.47	7
10	Q	1267.51	689.38	6
11	T	1368.56	561.32	5
12	A	1439.60	460.28	4
13	L	1552.68	389.24	3
14	E	1681.72	276.16	2
15	K	-	147.11	1

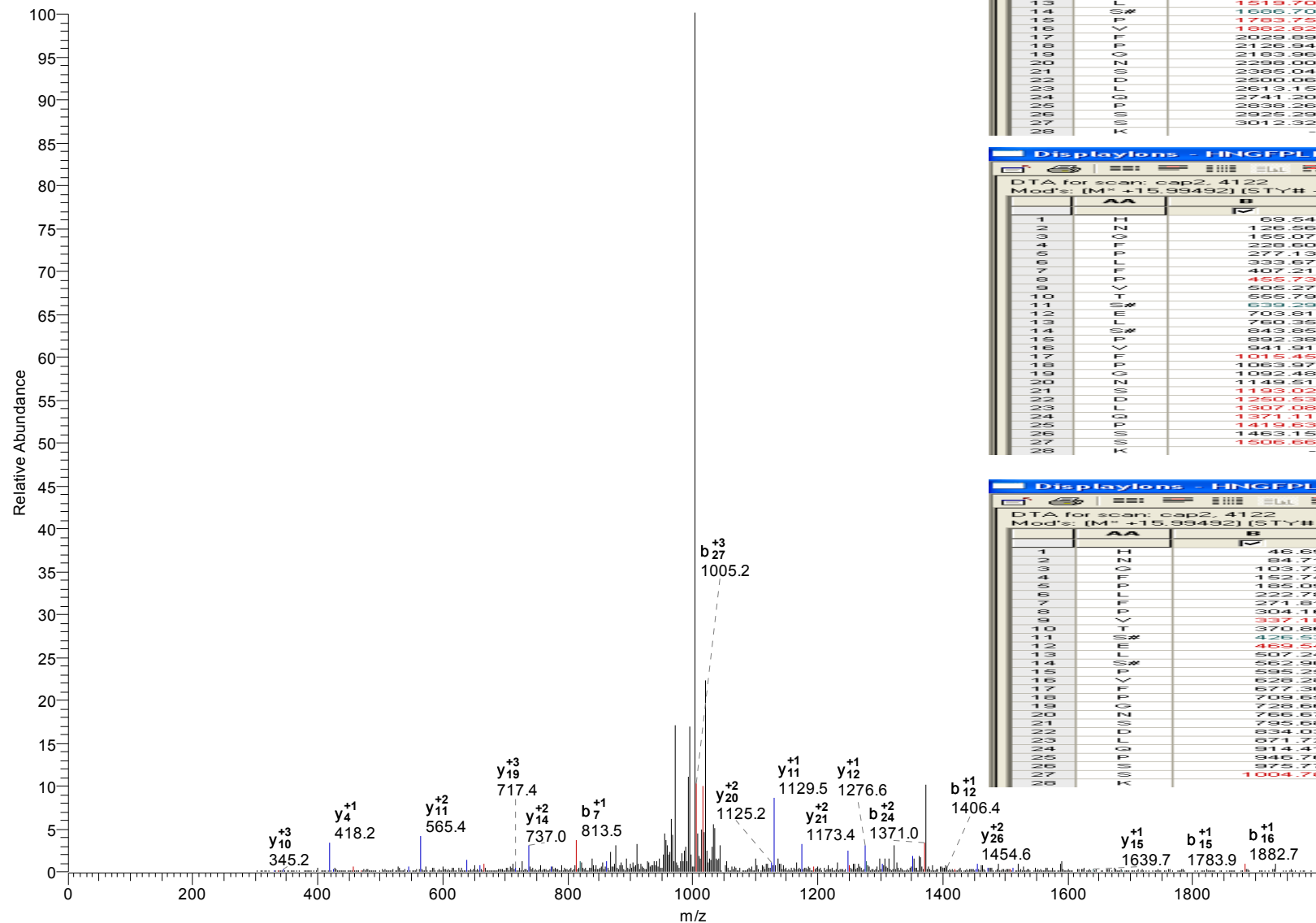
Displaylons - LIQASEHSLQTALEK

DTA for scan: 20ulcap2_070815194055, 2757
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	L	57.55	-	15
2	I	114.09	857.88	14
3	Q	178.12	801.33	13
4	A	213.64	737.30	12
5	S#	297.14	701.79	11
6	E	361.66	618.29	10
7	H	430.19	553.77	9
8	S#	513.69	485.24	8
9	L	570.23	401.74	7
10	Q	634.26	345.20	6
11	T	684.78	281.17	5
12	A	720.30	230.64	4
13	L	776.84	195.12	3
14	E	841.37	138.58	2
15	K	-	74.06	1

Ccdc116 Coiled-coil domain-containing protein 116

#4122-4122 NL: 9.17E3



Displayions - HNGFPLFPVTSLSVPVFGN

DTA for scan: cap2_4122
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	H	138.07	-	28
2	I	252.11	3021.37	27
3	O	309.13	2907.33	26
4	F	456.20	2850.30	25
5	L	553.25	2703.24	24
6	I	586.34	2606.18	23
7	F	613.40	2493.10	22
8	V	910.46	2346.03	21
9	V	1009.53	2245.98	20
10	T	1110.57	2149.91	19
11	E	1277.57	2048.86	18
12	E	1406.61	1881.86	17
13	L	1519.70	1752.82	16
14	S	1586.70	1639.74	15
15	P	1783.75	1472.74	14
16	V	1882.82	1375.69	13
17	P	2029.89	1276.62	12
18	P	2126.94	1129.55	11
19	S	2183.96	1032.50	10
20	I	2298.00	975.47	9
21	S	2365.04	861.43	8
22	D	2500.06	774.40	7
23	O	2613.15	659.37	6
24	L	2741.20	545.29	5
25	P	2838.26	418.23	4
26	S	2925.29	321.18	3
27	S	3012.32	234.14	2
28	K	-	147.11	1

Displayions - HNGFPLFPVTSLSVPVFGN

DTA for scan: cap2_4122
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	H	69.54	-	28
2	I	126.56	1511.19	27
3	O	155.07	1454.17	26
4	F	228.60	1425.65	25
5	L	277.13	1352.12	24
6	I	333.67	1303.59	23
7	F	407.21	1247.05	22
8	V	455.73	1173.52	21
9	V	505.27	1124.99	20
10	T	555.79	1075.46	19
11	E	639.29	1024.93	18
12	E	703.61	941.44	17
13	L	760.35	876.91	16
14	S	843.65	820.37	15
15	P	892.38	736.87	14
16	V	941.91	686.35	13
17	P	1015.45	639.81	12
18	P	1063.97	565.28	11
19	S	1092.48	516.75	10
20	I	1149.51	469.24	9
21	S	1193.02	431.22	8
22	D	1250.53	387.70	7
23	O	1307.06	330.19	6
24	L	1371.11	273.65	5
25	P	1419.63	209.62	4
26	S	1463.15	161.09	3
27	S	1506.66	117.56	2
28	K	-	74.06	1

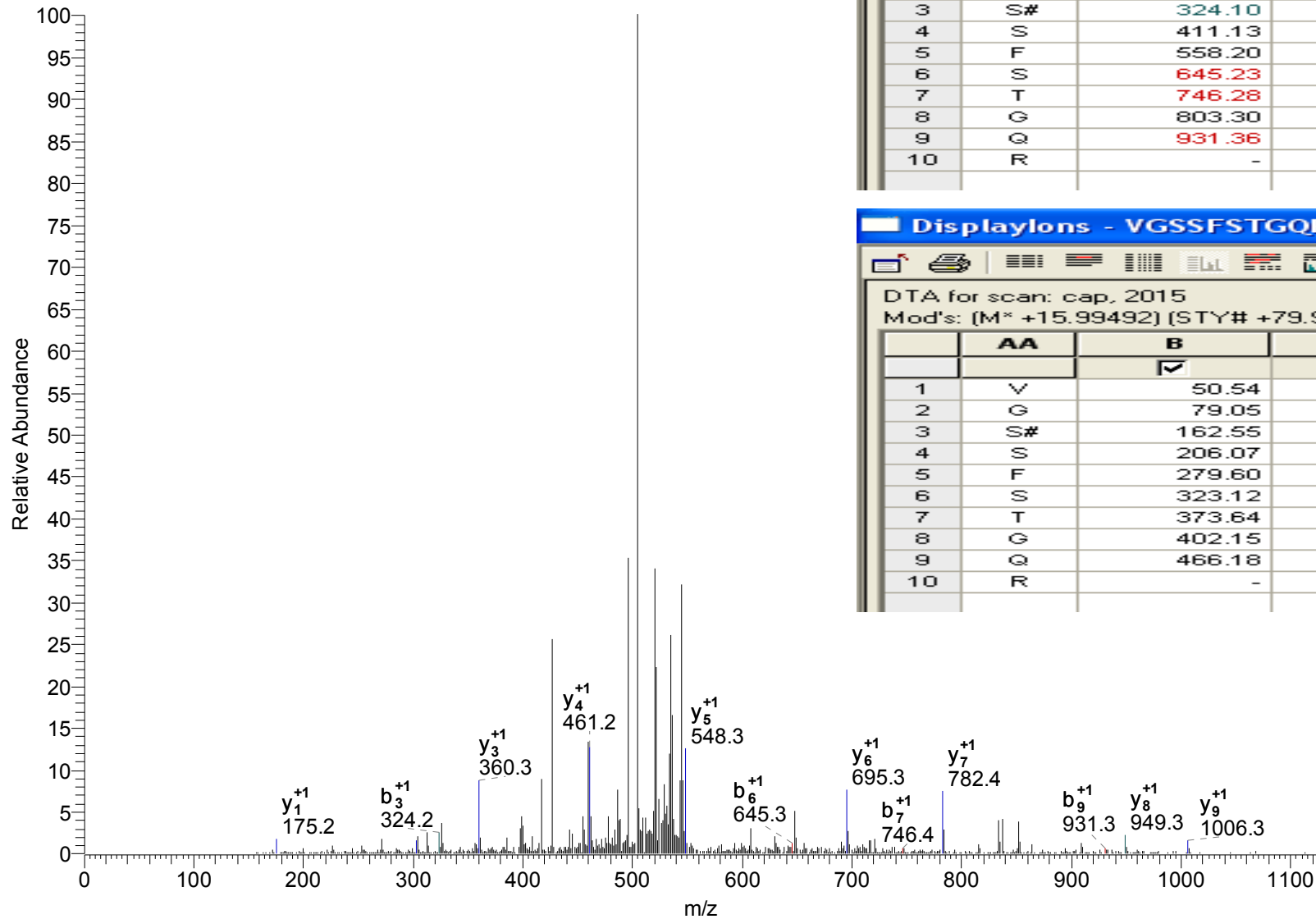
Displayions - HNGFPLFPVTSLSVPVFGN

DTA for scan: cap2_4122
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	H	46.69	-	28
2	I	84.71	1007.79	27
3	O	103.72	969.76	26
4	F	152.74	950.77	25
5	L	155.09	901.75	24
6	I	222.78	869.40	23
7	F	271.61	831.70	22
8	V	304.16	762.68	21
9	V	337.18	750.33	20
10	T	370.86	711.91	19
11	E	426.63	682.63	18
12	E	459.54	627.95	17
13	L	507.34	584.94	16
14	S	552.90	547.25	15
15	P	595.25	491.58	14
16	V	626.28	450.23	13
17	P	677.30	426.21	12
18	P	709.65	377.19	11
19	S	728.69	344.64	10
20	I	765.67	325.53	9
21	S	795.68	287.82	8
22	D	834.03	258.80	7
23	O	871.72	220.46	6
24	L	914.41	182.77	5
25	P	946.76	140.06	4
26	S	975.77	107.73	3
27	S	1004.78	75.72	2
28	K	-	49.71	1

Hspb9_predicted to Heat-shock protein beta-9

#2015-2015 NL: 5.93E3

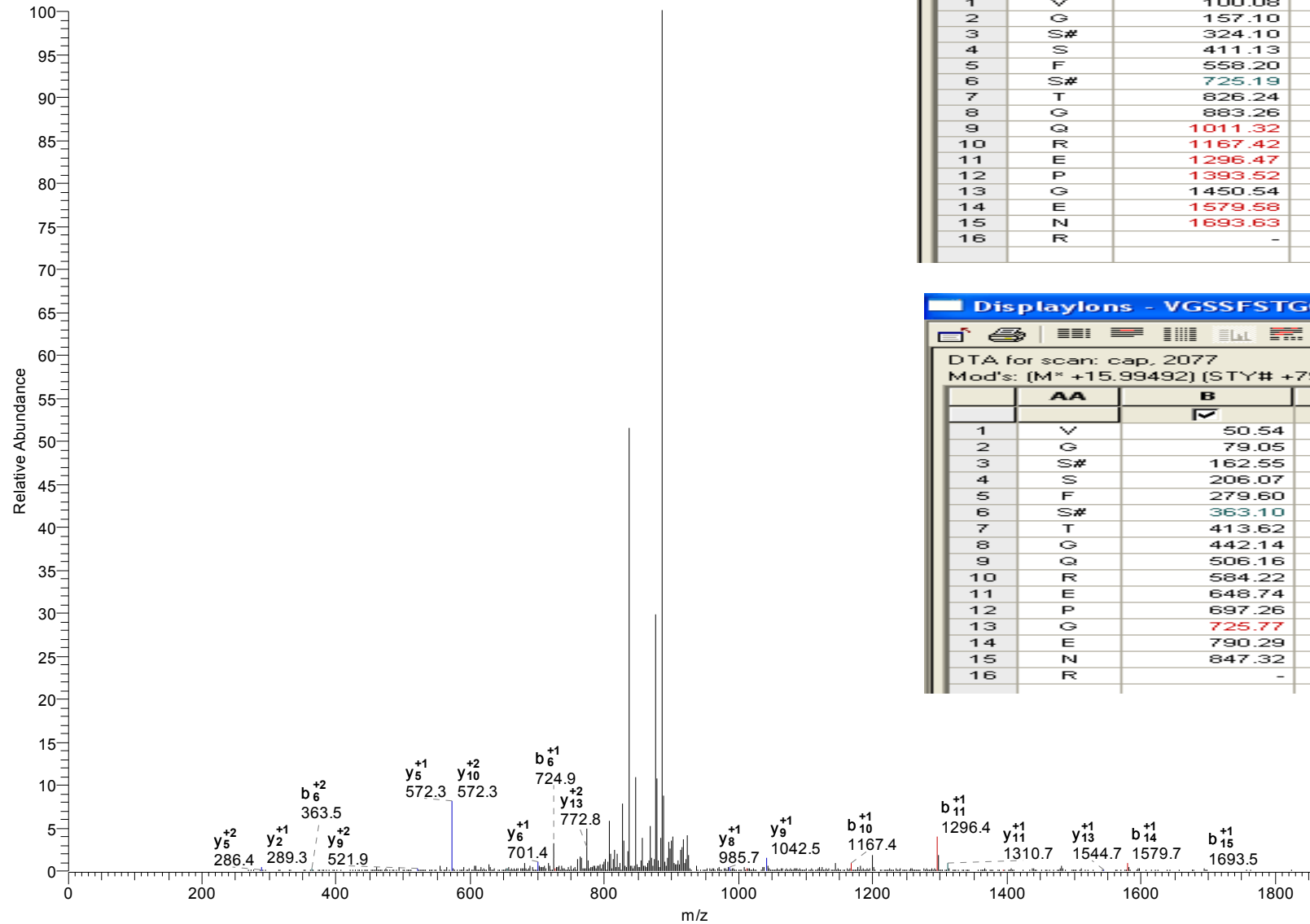


Displaylons - VGSSFSTGQR				
DTA for scan: cap, 2015				
Mod's: [M* +15.99492] [STY# +79.96633]				
	AA	B	Y	
		☒	☒	
1	V	100.08	-	10
2	G	157.10	1006.40	9
3	S#	324.10	949.38	8
4	S	411.13	782.38	7
5	F	558.20	695.35	6
6	S	645.23	548.28	5
7	T	746.28	461.25	4
8	G	803.30	360.20	3
9	Q	931.36	303.18	2
10	R	-	175.12	1

Displaylons - VGSSFSTGQR				
DTA for scan: cap, 2015				
Mod's: [M* +15.99492] [STY# +79.96633]				
	AA	B	Y	
		☒	☒	
1	V	50.54	-	10
2	G	79.05	503.70	9
3	S#	162.55	475.19	8
4	S	206.07	391.69	7
5	F	279.60	348.18	6
6	S	323.12	274.64	5
7	T	373.64	231.13	4
8	G	402.15	180.60	3
9	Q	466.18	152.09	2
10	R	-	88.06	1

Hspb9_predicted similar to Heat-shock protein beta-9

#2077-2077 NL: 8.15E3



Displaylons - VGSSFSTGQREPGENR

DTA for scan: cap. 2077
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	V	100.08	-	16
2	G	157.10	1768.67	15
3	S#	324.10	1711.65	14
4	S	411.13	1544.65	13
5	F	558.20	1457.62	12
6	S#	725.19	1310.55	11
7	T	826.24	1143.55	10
8	G	883.26	1042.50	9
9	Q	1011.32	985.48	8
10	R	1167.42	857.42	7
11	E	1296.47	701.32	6
12	P	1393.52	572.28	5
13	G	1450.54	475.23	4
14	E	1579.58	418.20	3
15	N	1693.63	289.16	2
16	R	-	175.12	1

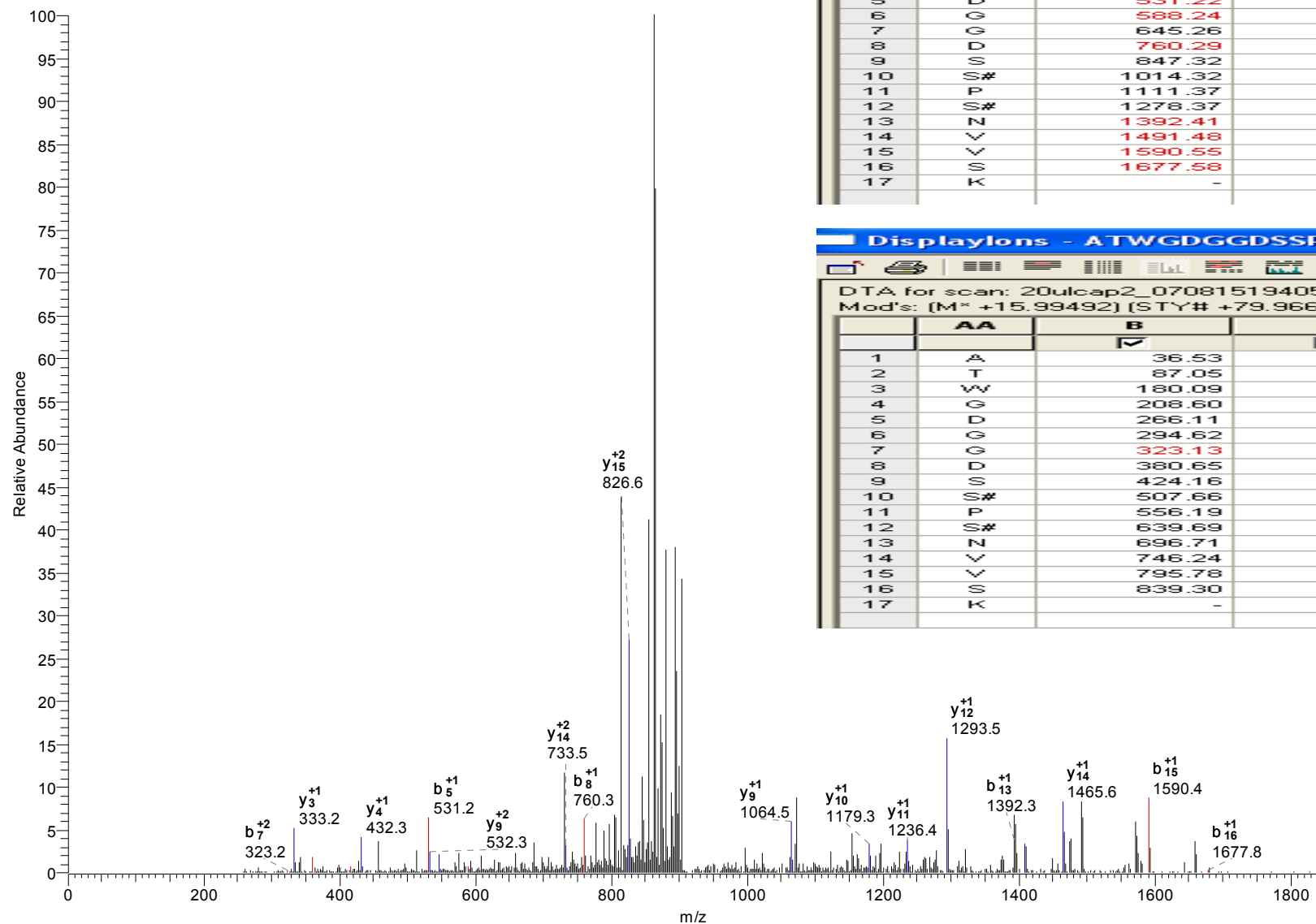
Displaylons - VGSSFSTGQREPGENR

DTA for scan: cap. 2077
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	V	50.54	-	16
2	G	79.05	884.84	15
3	S#	162.55	856.33	14
4	S	206.07	772.83	13
5	F	279.60	729.31	12
6	S#	363.10	655.78	11
7	T	413.62	572.28	10
8	G	442.14	521.75	9
9	Q	506.16	493.24	8
10	R	584.22	429.21	7
11	E	648.74	351.16	6
12	P	697.26	286.64	5
13	G	725.77	238.12	4
14	E	790.29	209.61	3
15	N	847.32	145.08	2
16	R	-	88.06	1

Snap23 Synaptosomal-associated protein 23

#2413-2413 NL: 3.26E3



Displaylons - ATWGDGGDSSPSNVVSK

DTA for scan: 20ulcap2_070815194055, 2413
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	A	72.04	-	17
2	T	173.09	1752.65	16
3	W	359.17	1651.60	15
4	G	416.19	1465.52	14
5	D	531.22	1408.50	13
6	G	588.24	1293.48	12
7	G	645.26	1236.45	11
8	D	760.29	1179.43	10
9	S	847.32	1064.41	9
10	S#	1014.32	977.37	8
11	P	1111.37	810.38	7
12	S#	1278.37	713.32	6
13	N	1392.41	546.32	5
14	V	1491.48	432.28	4
15	V	1590.55	333.21	3
16	S	1677.58	234.14	2
17	K	-	147.11	1

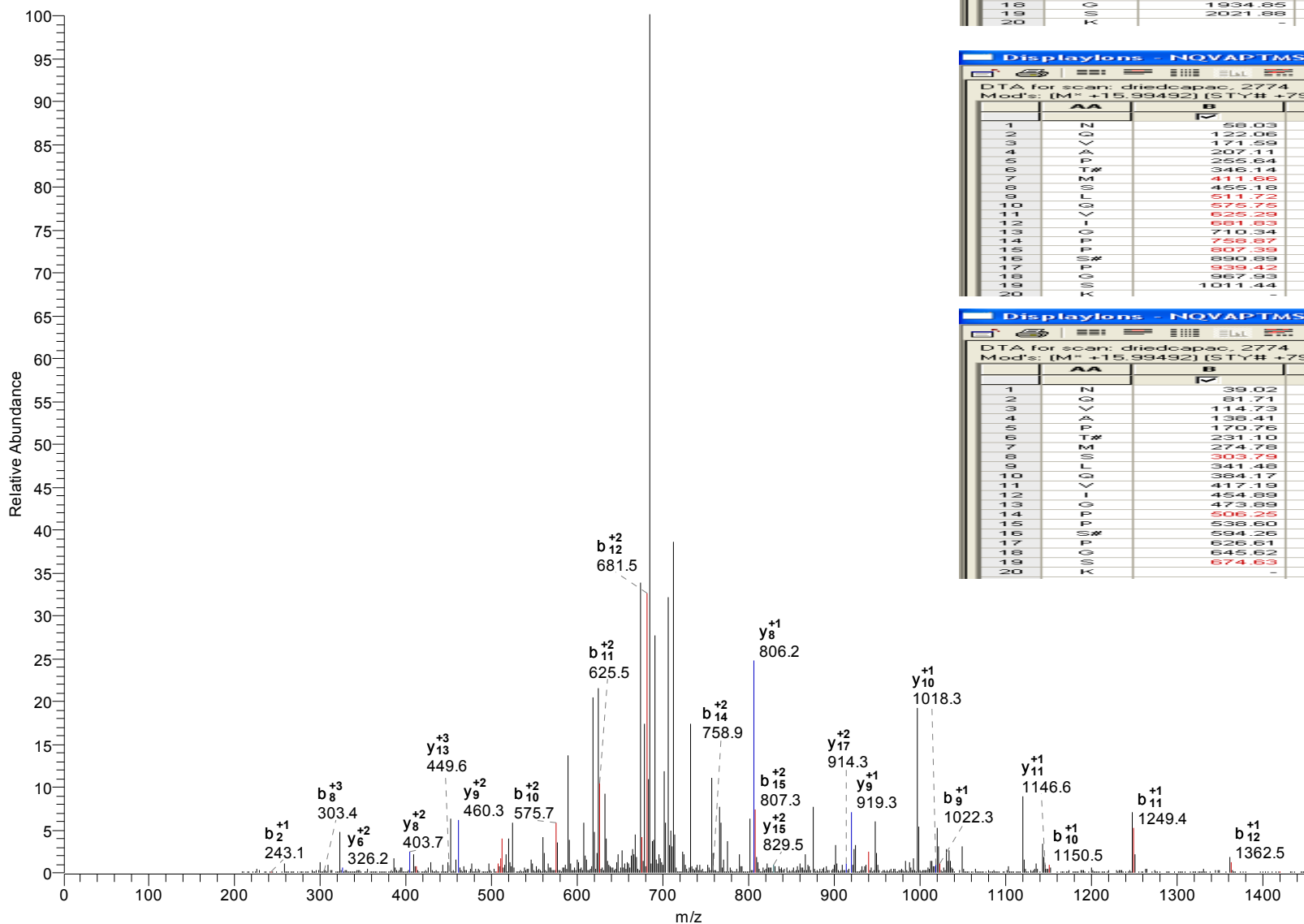
Displaylons - ATWGDGGDSSPSNVVSK

DTA for scan: 20ulcap2_070815194055, 2413
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	A	36.53	-	17
2	T	87.05	876.83	16
3	W	180.09	826.31	15
4	G	208.60	733.27	14
5	D	266.11	704.76	13
6	G	294.62	647.24	12
7	G	323.13	618.73	11
8	D	380.65	590.22	10
9	S	424.16	532.71	9
10	S#	507.66	489.19	8
11	P	556.19	405.69	7
12	S#	639.69	357.17	6
13	N	696.71	273.67	5
14	V	746.24	216.64	4
15	V	795.78	167.11	3
16	S	839.30	117.58	2
17	K	-	74.06	1

Aim1I_predicted similar to absent in melanoma 1

#2774-2774 NL: 7.53E4



Displaylens - NOVAPTMSLOVIGPPSPGSK

DTA for scan: driedcapac, 2774
Mod's: (M⁺ +15.99492) (S⁺ Ty# +79.96633)

	AA	B	Y	
1	N	115.05	-	20
2	Q	243.11	2053.94	19
3	V	342.18	1925.88	18
4	A	413.21	1826.82	17
5	P	510.27	1766.76	16
6	T#	691.28	1658.73	15
7	M	822.32	1477.71	14
8	S	909.35	1346.67	13
9	L	1022.44	1259.64	12
10	Q	1150.50	1146.56	11
11	V	1249.56	1018.50	10
12	I	1362.65	919.43	9
13	O	1419.67	806.34	8
14	P	1516.72	749.32	7
15	P	1613.78	652.27	6
16	S#	1780.77	555.22	5
17	P	1877.83	388.22	4
18	Q	1934.85	291.17	3
19	S	2021.88	234.14	2
20	K	-	147.11	1

Displaylens - NOVAPTMSLOVIGPPSPGSK

DTA for scan: driedcapac, 2774
Mod's: (M⁺ +15.99492) (S⁺ Ty# +79.96633)

	AA	B	Y	
1	N	58.03	-	20
2	Q	122.06	1027.48	19
3	V	171.59	963.45	18
4	A	207.11	913.91	17
5	P	255.64	878.39	16
6	T#	346.14	829.87	15
7	M	411.66	739.36	14
8	S	455.19	673.84	13
9	L	511.72	630.32	12
10	Q	575.75	573.78	11
11	V	625.29	509.75	10
12	I	681.83	460.22	9
13	O	710.34	403.68	8
14	P	758.87	375.17	7
15	P	807.39	326.64	6
16	S#	890.89	278.11	5
17	P	939.42	194.61	4
18	Q	967.93	146.09	3
19	S	1011.44	117.58	2
20	K	-	74.06	1

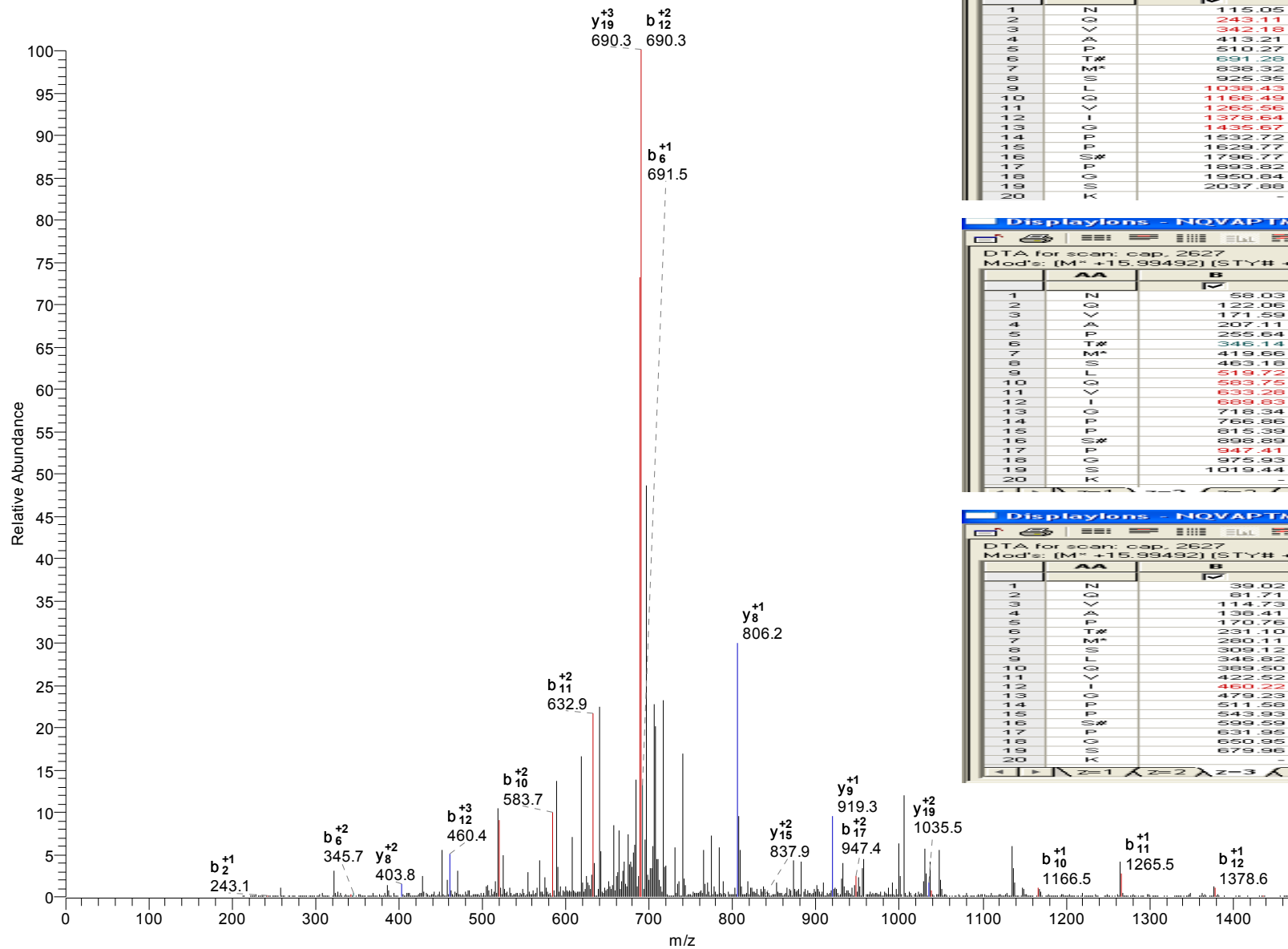
Displaylens - NOVAPTMSLOVIGPPSPGSK

DTA for scan: driedcapac, 2774
Mod's: (M⁺ +15.99492) (S⁺ Ty# +79.96633)

	AA	B	Y	
1	N	39.02	-	20
2	Q	81.71	685.32	19
3	V	114.73	642.83	18
4	A	138.41	609.61	17
5	P	170.76	585.93	16
6	T#	231.10	553.58	15
7	M	274.78	493.24	14
8	S	303.79	449.56	13
9	L	341.48	420.55	12
10	Q	384.17	382.86	11
11	V	417.19	340.17	10
12	I	454.89	307.15	9
13	O	473.89	269.45	8
14	P	508.25	250.45	7
15	P	536.60	218.09	6
16	S#	594.26	185.74	5
17	P	626.61	130.08	4
18	Q	645.62	97.73	3
19	S	674.63	78.72	2
20	K	-	49.71	1

Aim1I_predicted similar to absent in melanoma 1

#2627-2627 NL: 3.84E4



Displaylons - NQVAPTMSLQVIGPPSPGSK

DTA for scan: cap. 2627
Mod's: [M⁺+15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	115.05	-	20
2	Q	243.11	2069.94	19
3	V	342.18	1941.88	18
4	A	413.21	1842.81	17
5	P	510.27	1771.77	16
6	T*	591.26	1674.72	15
7	M*	636.32	1493.71	14
8	S	925.35	1346.67	13
9	L	1038.43	1259.64	12
10	Q	1166.49	1146.56	11
11	V	1265.56	1018.50	10
12	I	1378.64	919.43	9
13	G	1435.67	806.34	8
14	P	1532.72	749.32	7
15	P	1629.77	652.27	6
16	S*	1796.77	555.22	5
17	P	1893.82	388.22	4
18	G	1950.84	291.17	3
19	S	2037.88	234.14	2
20	K	-	147.11	1

Displaylons - NQVAPTMSLQVIGPPSPGSK

DTA for scan: cap. 2627
Mod's: [M⁺+15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	58.03	-	20
2	Q	122.06	1035.47	19
3	V	171.59	971.44	18
4	A	207.11	921.91	17
5	P	255.64	886.39	16
6	T*	346.14	837.66	15
7	M*	419.66	747.35	14
8	S	463.18	673.84	13
9	L	519.72	630.32	12
10	Q	583.75	573.78	11
11	V	633.28	509.75	10
12	I	689.83	460.22	9
13	G	718.34	403.68	8
14	P	766.86	375.17	7
15	P	815.39	326.64	6
16	S*	896.89	278.11	5
17	P	947.41	194.61	4
18	G	975.93	146.09	3
19	S	1019.44	117.58	2
20	K	-	74.06	1

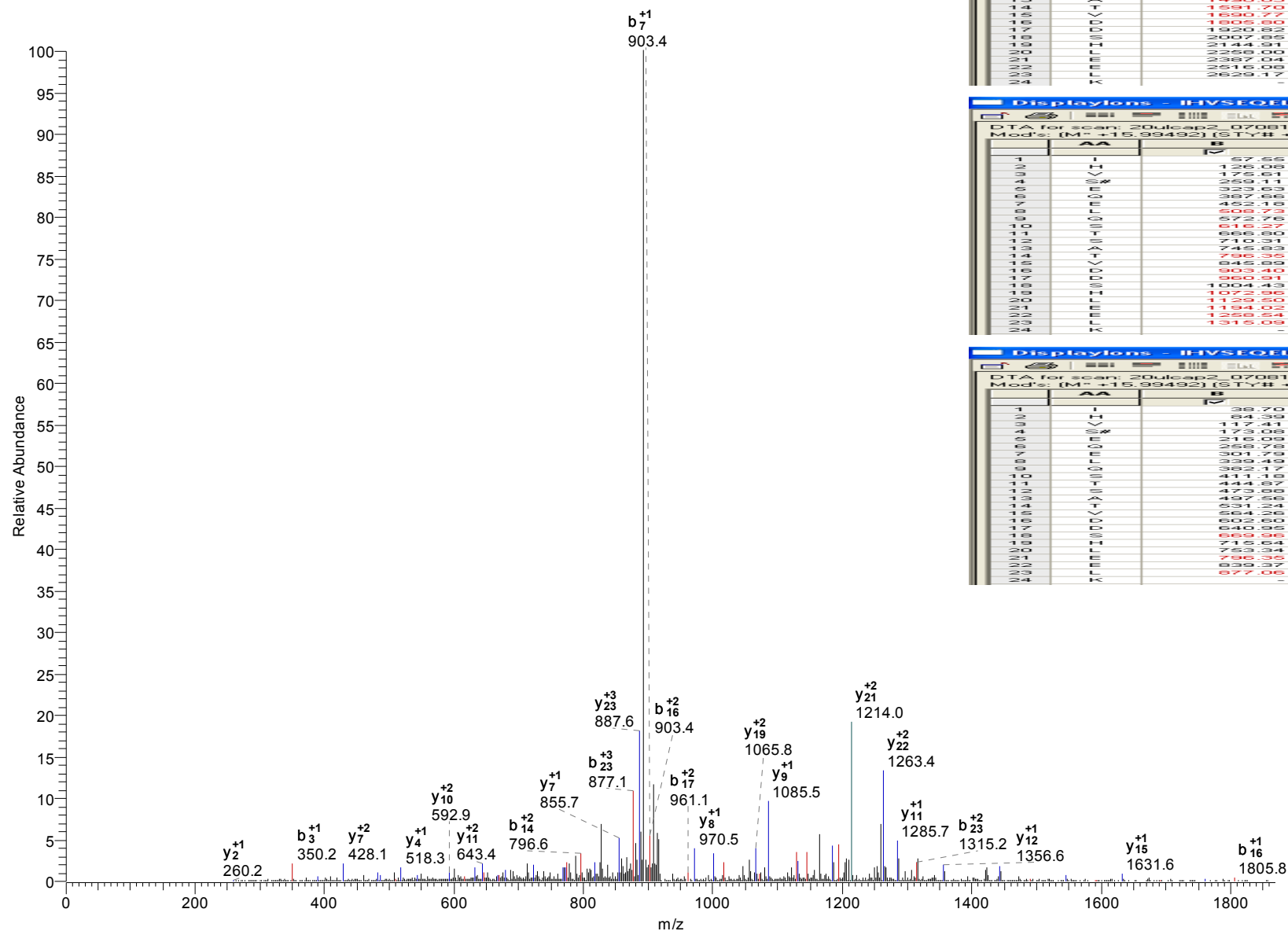
Displaylons - NQVAPTMSLQVIGPPSPGSK

DTA for scan: cap. 2627
Mod's: [M⁺+15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	39.02	-	20
2	Q	81.71	690.65	19
3	V	114.73	647.96	18
4	A	138.41	614.94	17
5	P	170.76	591.25	16
6	T*	231.10	558.91	15
7	M*	280.11	498.57	14
8	S	309.12	449.56	13
9	L	346.82	420.55	12
10	Q	389.50	382.85	11
11	V	422.52	340.17	10
12	I	460.22	307.15	9
13	G	479.23	269.45	8
14	P	511.58	250.45	7
15	P	543.93	218.09	6
16	S*	599.59	185.74	5
17	P	631.95	130.08	4
18	G	650.95	97.73	3
19	S	679.96	78.72	2
20	K	-	49.71	1

Ube1y1 Ubiquitin-activating enzyme E1

#2944-2944 NL: 8.38E3



Displayions - IHVSEGELOSTSA TVDDSHLE

DTA for scan: 20ulcap2_070815194055_2944
Mod's: (M⁺ +15.99492) (STY# +79.96633)

AA	B	Y	
1	I	114.09	-
2	M	251.16	2662.19
3	V	350.22	2525.13
4	S	517.22	2426.06
5	E	646.26	2259.06
6	G	774.32	2130.02
7	D	903.36	2001.96
8	L	1016.44	1872.92
9	Q	1144.50	1759.53
10	S	1231.54	1631.76
11	T	1332.58	1544.74
12	S	1419.62	1443.70
13	A	1490.65	1356.65
14	T	1591.70	1295.63
15	V	1690.77	1184.56
16	D	1805.80	1095.51
17	D	1920.82	970.46
18	S	2007.85	855.45
19	H	2144.91	755.43
20	L	2258.00	631.37
21	L	2387.04	519.24
22	E	2515.06	399.24
23	K	2629.17	260.20
24	-	-	147.11

Displayions - IHVSEGELOSTSA TVDDSHLE

DTA for scan: 20ulcap2_070815194055_2944
Mod's: (M⁺ +15.99492) (STY# +79.96633)

AA	B	Y	
1	I	57.55	-
2	M	126.06	1331.60
3	V	175.61	1263.07
4	S	259.11	1213.53
5	E	323.63	1130.03
6	G	397.66	1055.51
7	D	452.18	1001.46
8	L	508.73	936.95
9	Q	572.75	880.42
10	S	616.27	816.39
11	T	666.80	772.65
12	S	710.31	722.36
13	A	745.83	678.64
14	T	796.36	643.32
15	V	845.89	592.79
16	D	903.40	543.26
17	D	960.91	486.75
18	S	1004.43	428.23
19	H	1072.96	364.72
20	L	1129.50	316.19
21	L	1194.02	259.64
22	E	1258.54	195.12
23	K	1315.09	130.60
24	-	-	74.05

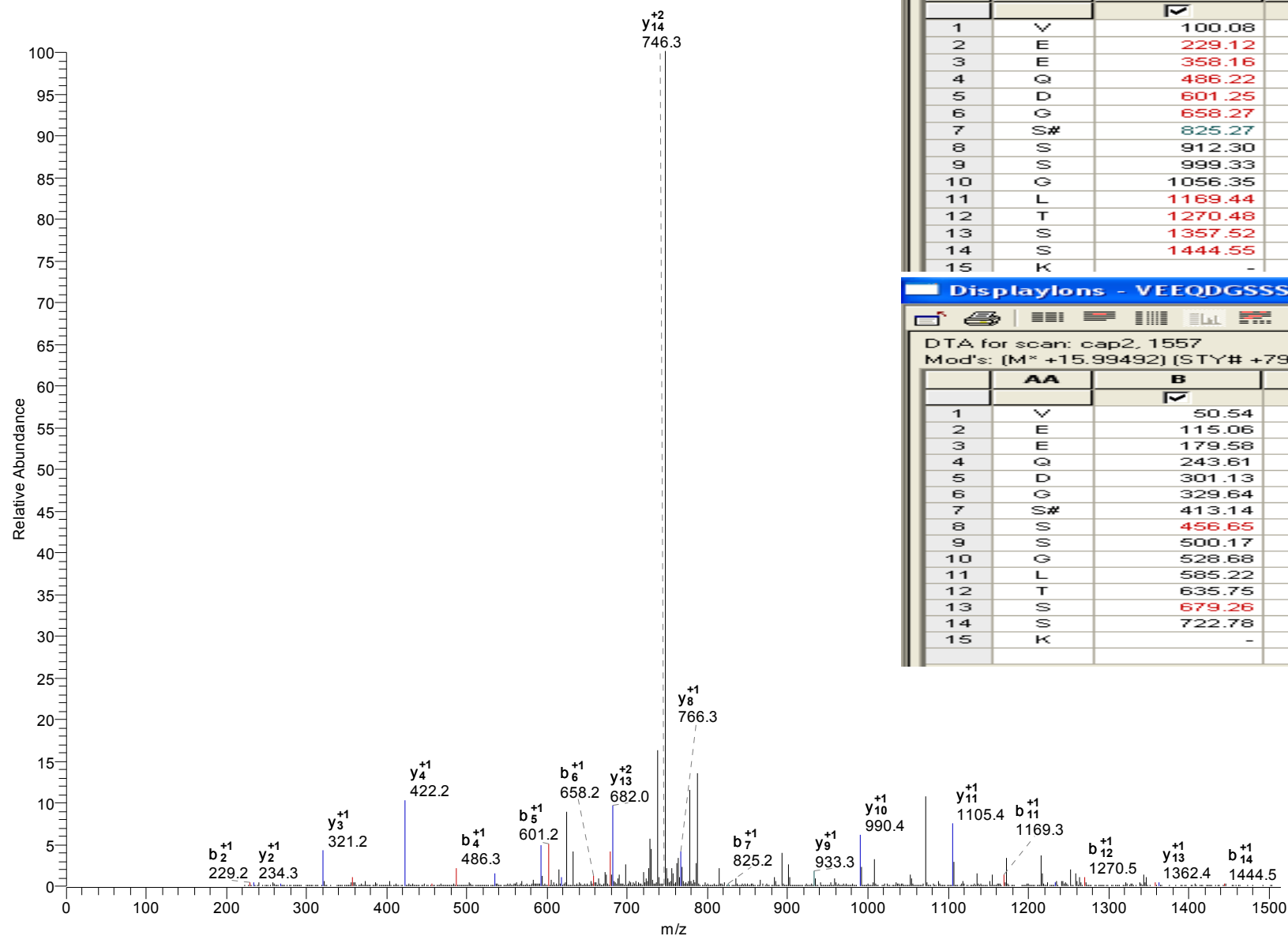
Displayions - IHVSEGELOSTSA TVDDSHLE

DTA for scan: 20ulcap2_070815194055_2944
Mod's: (M⁺ +15.99492) (STY# +79.96633)

AA	B	Y	
1	I	38.70	-
2	M	84.39	866.07
3	V	117.41	842.38
4	S	173.06	809.36
5	E	216.09	753.69
6	G	259.78	710.68
7	D	301.79	667.69
8	L	339.49	624.98
9	Q	382.17	587.26
10	S	411.15	544.60
11	T	444.87	515.59
12	S	473.66	481.90
13	A	497.55	452.89
14	T	531.24	429.21
15	V	564.26	395.53
16	D	602.60	362.51
17	D	640.95	324.17
18	S	659.95	285.82
19	H	715.64	256.01
20	L	753.34	211.13
21	E	796.95	173.43
22	K	839.37	130.42
23	-	877.05	67.40
24	-	-	49.71

RGD1311859_predicted hypothetical protein LOC303534

#1557-1557 NL: 3.02E4



Displaylons - VEEQDGSSSGLTSSK

DTA for scan: cap2, 1557
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	V	100.08	-	15
2	E	229.12	1491.58	14
3	E	358.16	1362.54	13
4	Q	486.22	1233.50	12
5	D	601.25	1105.44	11
6	G	658.27	990.41	10
7	S#	825.27	933.39	9
8	S	912.30	766.39	8
9	S	999.33	679.36	7
10	G	1056.35	592.33	6
11	L	1169.44	535.31	5
12	T	1270.48	422.22	4
13	S	1357.52	321.18	3
14	S	1444.55	234.14	2
15	K	-	147.11	1

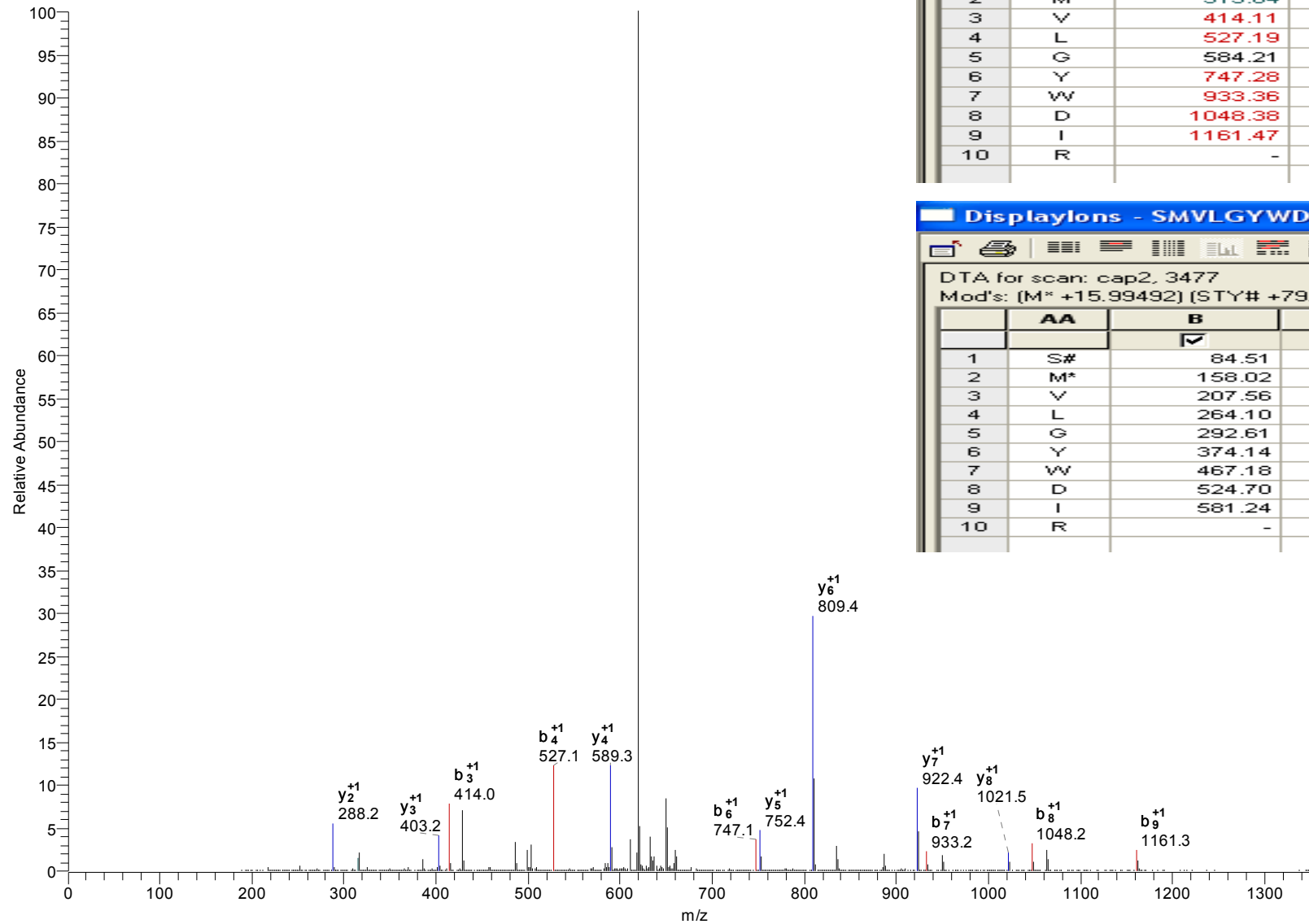
Displaylons - VEEQDGSSSGLTSSK

DTA for scan: cap2, 1557
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	V	50.54	-	15
2	E	115.06	746.30	14
3	E	179.58	681.77	13
4	Q	243.61	617.25	12
5	D	301.13	553.22	11
6	G	329.64	495.71	10
7	S#	413.14	467.20	9
8	S	456.65	383.70	8
9	S	500.17	340.18	7
10	G	528.68	296.67	6
11	L	585.22	268.16	5
12	T	635.75	211.62	4
13	S	679.26	161.09	3
14	S	722.78	117.58	2
15	K	-	74.06	1

Gstm5 Glutathione S-transferase Mu 5

#3477-3477 NL: 8.69E4



Displaylons - SMVLGYWDIR

DTA for scan: cap2, 3477
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	S#	168.01	-	10
2	M*	315.04	1168.58	9
3	V	414.11	1021.55	8
4	L	527.19	922.48	7
5	G	584.21	809.39	6
6	Y	747.28	752.37	5
7	W	933.36	589.31	4
8	D	1048.38	403.23	3
9	I	1161.47	288.20	2
10	R	-	175.12	1

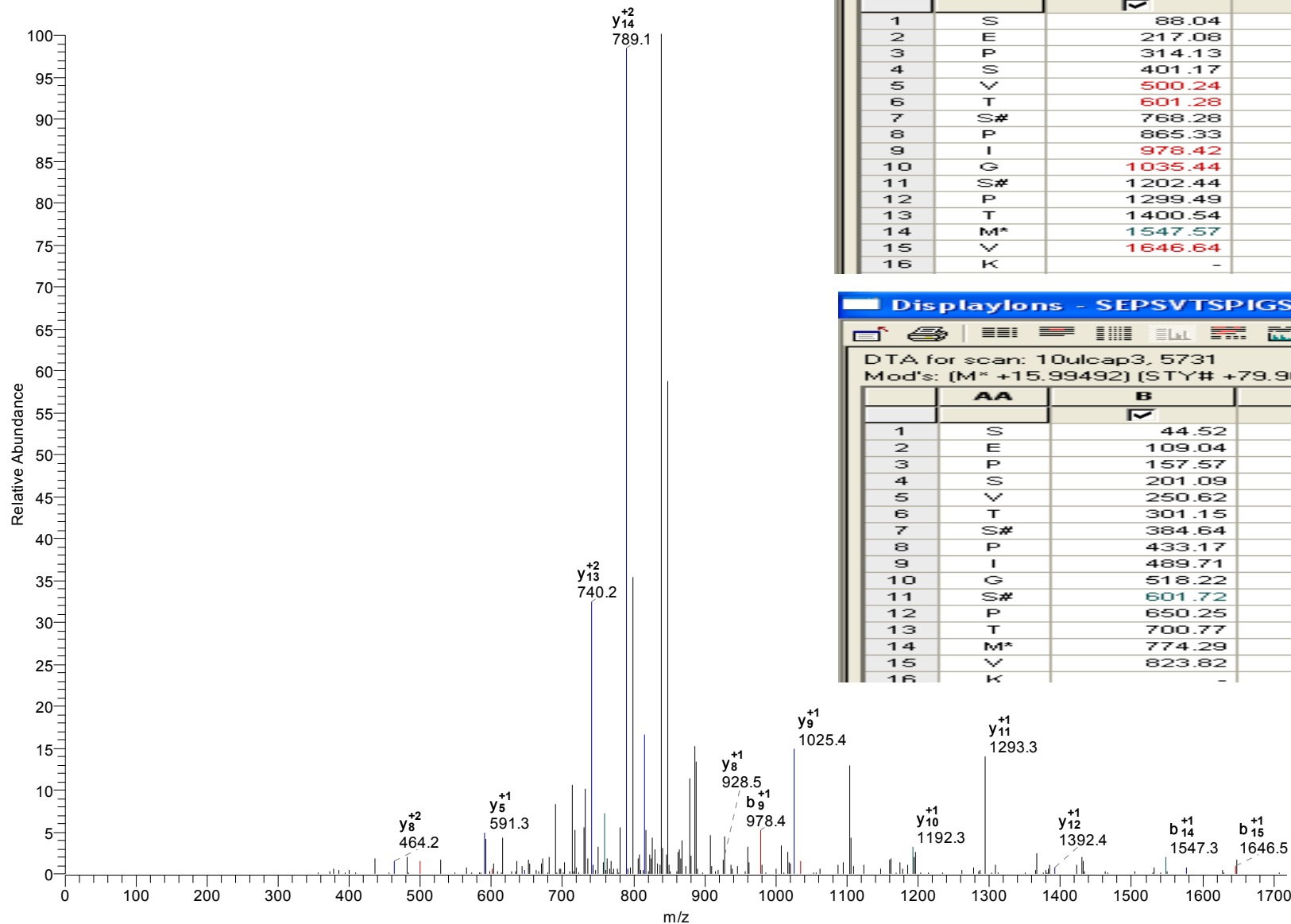
Displaylons - SMVLGYWDIR

DTA for scan: cap2, 3477
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	S#	84.51	-	10
2	M*	158.02	584.79	9
3	V	207.56	511.28	8
4	L	264.10	461.74	7
5	G	292.61	405.20	6
6	Y	374.14	376.69	5
7	W	467.18	295.16	4
8	D	524.70	202.12	3
9	I	581.24	144.61	2
10	R	-	88.06	1

LOC679584;LOC687072 similar to HoloCentric chromosome binding Protein family member

#5731-5731 NL: 3.94E2



Displaylons - SEPSVTSPIGSPTMVK

DTA for scan: 10ulcap3, 5731
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	S	88.04	-	16
2	E	217.08	1705.72	15
3	P	314.13	1576.67	14
4	S	401.17	1479.62	13
5	V	500.24	1392.59	12
6	T	601.28	1293.52	11
7	S#	768.28	1192.47	10
8	P	865.33	1025.47	9
9	I	978.42	928.42	8
10	G	1035.44	815.34	7
11	S#	1202.44	758.32	6
12	P	1299.49	591.32	5
13	T	1400.54	494.26	4
14	M*	1547.57	393.22	3
15	V	1646.64	246.18	2
16	K	-	147.11	1

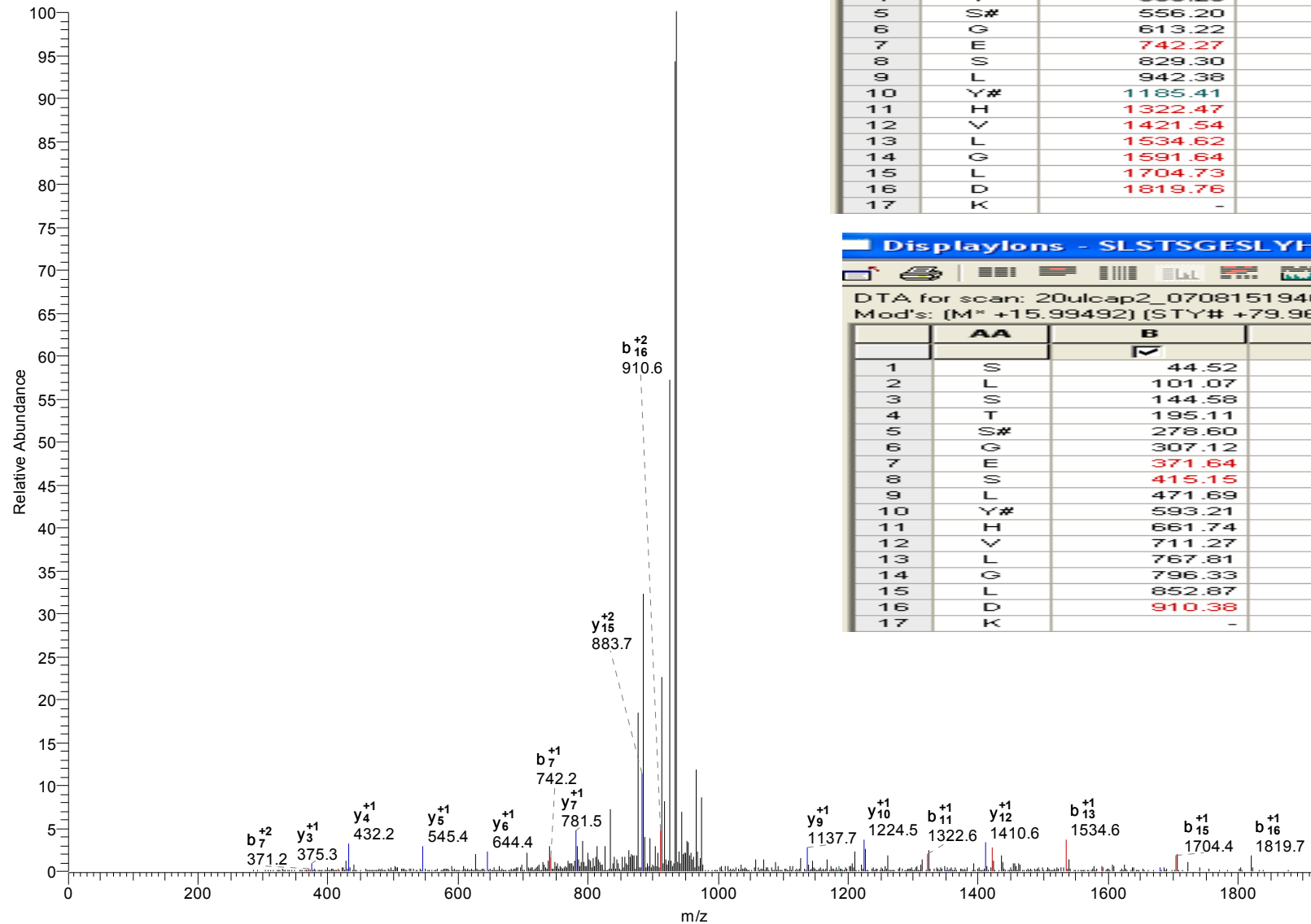
Displaylons - SEPSVTSPIGSPTMVK

DTA for scan: 10ulcap3, 5731
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	S	44.52	-	16
2	E	109.04	853.36	15
3	P	157.57	788.84	14
4	S	201.09	740.31	13
5	V	250.62	696.80	12
6	T	301.15	647.26	11
7	S#	384.64	596.74	10
8	P	433.17	513.24	9
9	I	489.71	464.71	8
10	G	518.22	408.17	7
11	S#	601.72	379.66	6
12	P	650.25	296.16	5
13	T	700.77	247.64	4
14	M*	774.29	197.11	3
15	V	823.82	123.59	2
16	K	-	74.06	1

Dnajc5 DnaJ homolog subfamily C member 5

#3404-3404 NL: 4.81E3



Displaylons - SLSTSGESLYHVLGLDK

DTA for scan: 20ulcap2_070815194055, 3404
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	88.04	-	17
2	L	201.12	1878.83	16
3	S	288.16	1765.74	15
4	T	389.20	1678.71	14
5	S#	556.20	1577.66	13
6	G	613.22	1410.67	12
7	E	742.27	1353.65	11
8	S	829.30	1224.60	10
9	L	942.38	1137.57	9
10	Y#	1185.41	1024.49	8
11	H	1322.47	781.46	7
12	V	1421.54	644.40	6
13	L	1534.62	545.33	5
14	G	1591.64	432.25	4
15	L	1704.73	375.22	3
16	D	1819.76	262.14	2
17	K	-	147.11	1

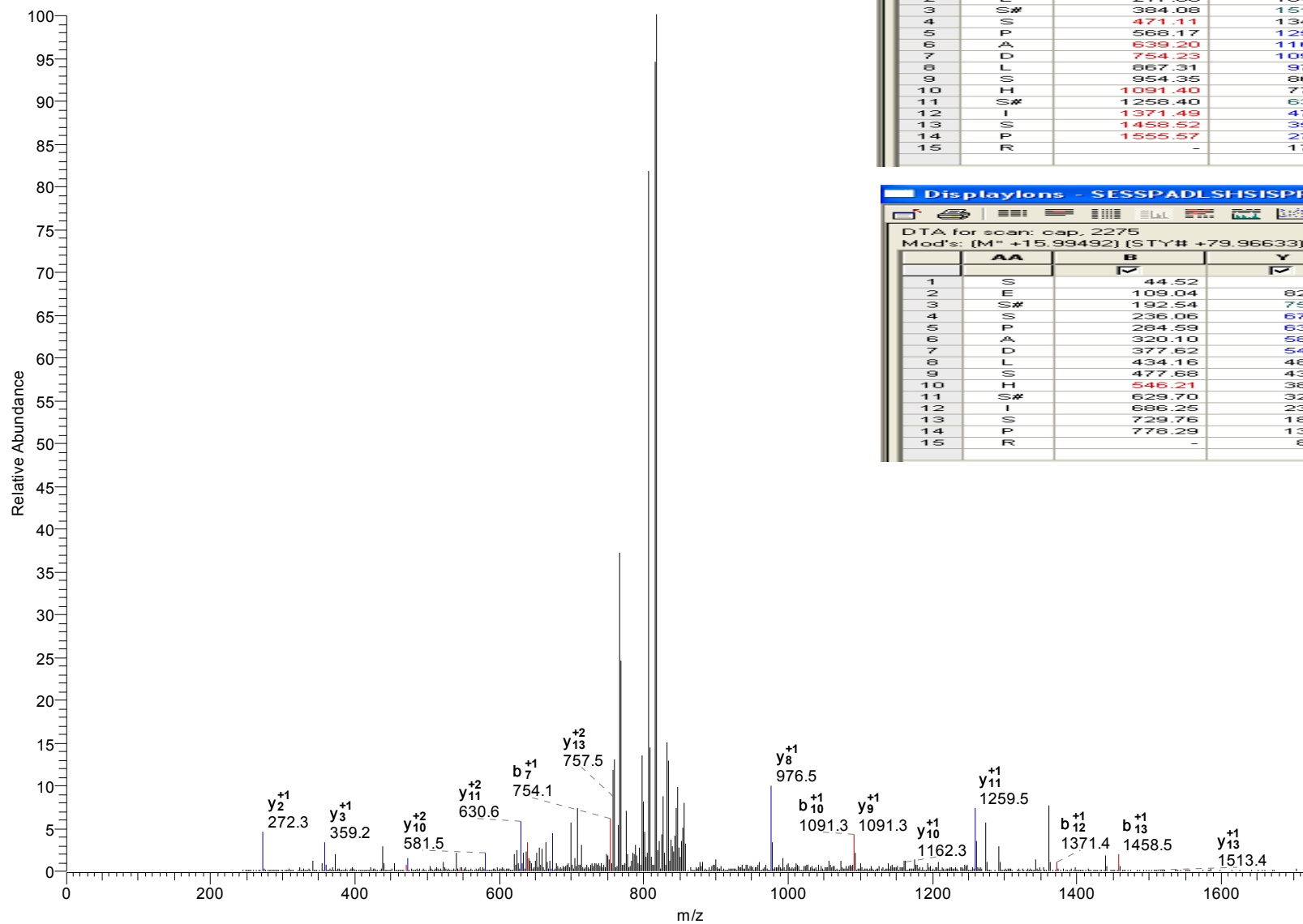
Displaylons - SLSTSGESLYHVLGLDK

DTA for scan: 20ulcap2_070815194055, 3404
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	44.52	-	17
2	L	101.07	939.92	16
3	S	144.58	883.38	15
4	T	195.11	839.86	14
5	S#	278.60	789.34	13
6	G	307.12	705.84	12
7	E	371.64	677.33	11
8	S	415.15	612.80	10
9	L	471.69	569.29	9
10	Y#	593.21	512.75	8
11	H	661.74	391.23	7
12	V	711.27	322.70	6
13	L	767.81	273.17	5
14	G	796.33	216.63	4
15	L	852.87	188.12	3
16	D	910.38	131.57	2
17	K	-	74.06	1

LOC497959 Similar to novel protein

#2275-2275 NL: 9.46E3



Displaylons - SESSPADLSHSISPR

DTA for scan: cap, 2275
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	88.04	-	15
2	E	217.08	1642.65	14
3	S#	384.08	1513.81	13
4	S	471.11	1346.81	12
5	P	568.17	1259.58	11
6	A	639.20	1162.53	10
7	D	754.23	1091.49	9
8	L	867.31	976.46	8
9	S	954.35	863.38	7
10	H	1091.40	776.35	6
11	S#	1258.40	639.29	5
12	I	1371.49	472.29	4
13	S	1458.52	359.20	3
14	P	1555.57	272.17	2
15	R	-	175.12	1

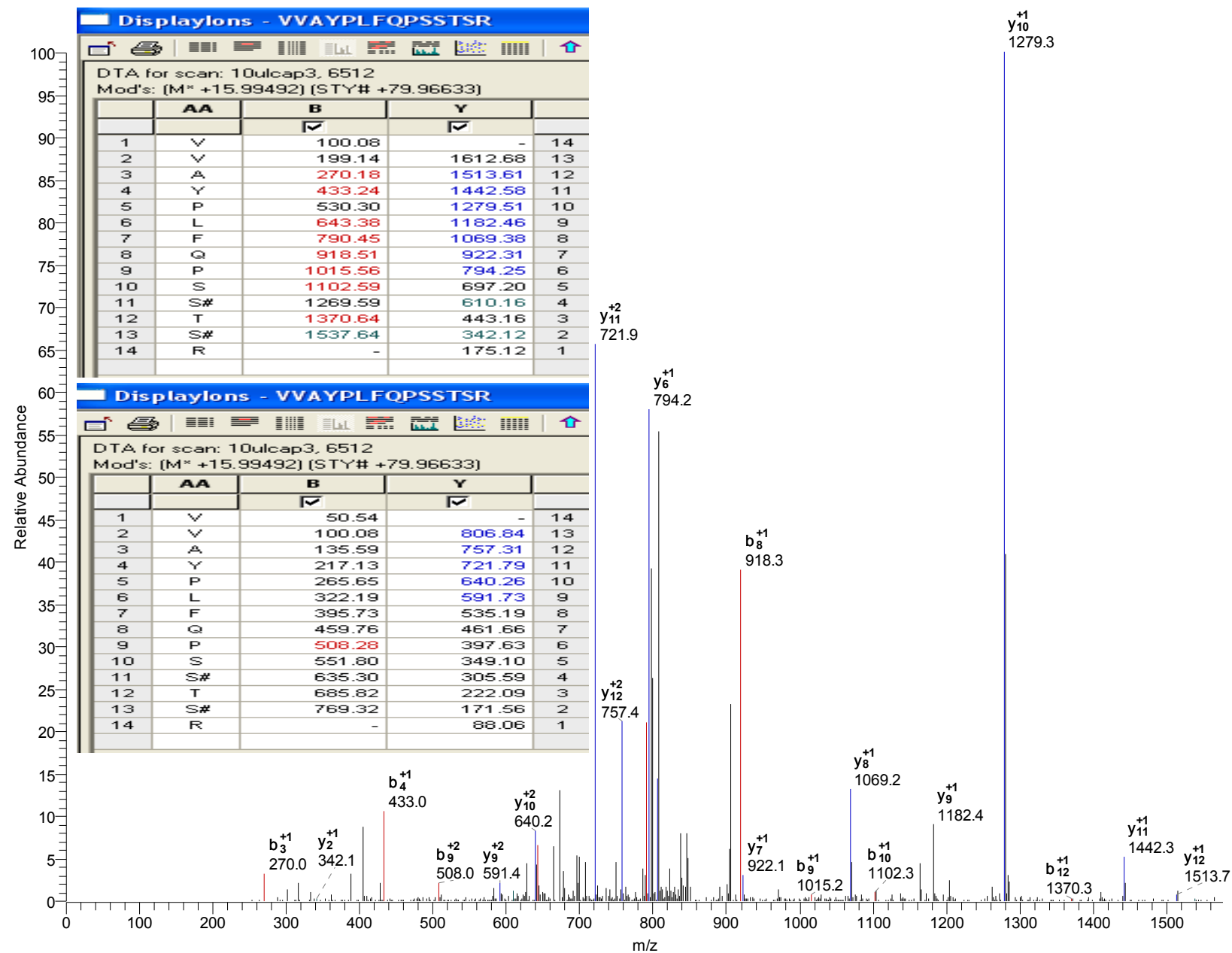
Displaylons - SESSPADLSHSISPR

DTA for scan: cap, 2275
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	44.52	-	15
2	E	109.04	821.83	14
3	S#	192.54	757.31	13
4	S	236.06	673.81	12
5	P	284.59	630.29	11
6	A	320.10	581.77	10
7	D	377.62	546.25	9
8	L	434.16	488.73	8
9	S	477.68	432.19	7
10	H	546.21	388.68	6
11	S#	629.70	320.15	5
12	I	686.25	236.65	4
13	S	729.76	180.11	3
14	P	778.29	136.59	2
15	R	-	88.06	1

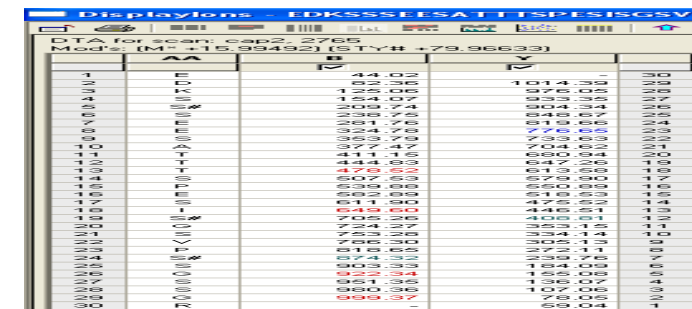
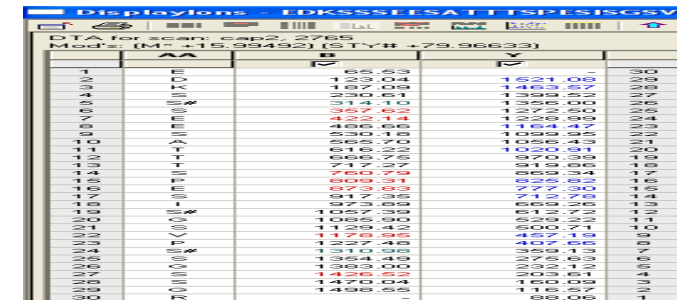
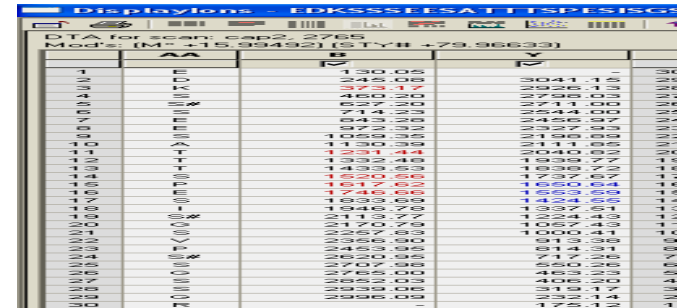
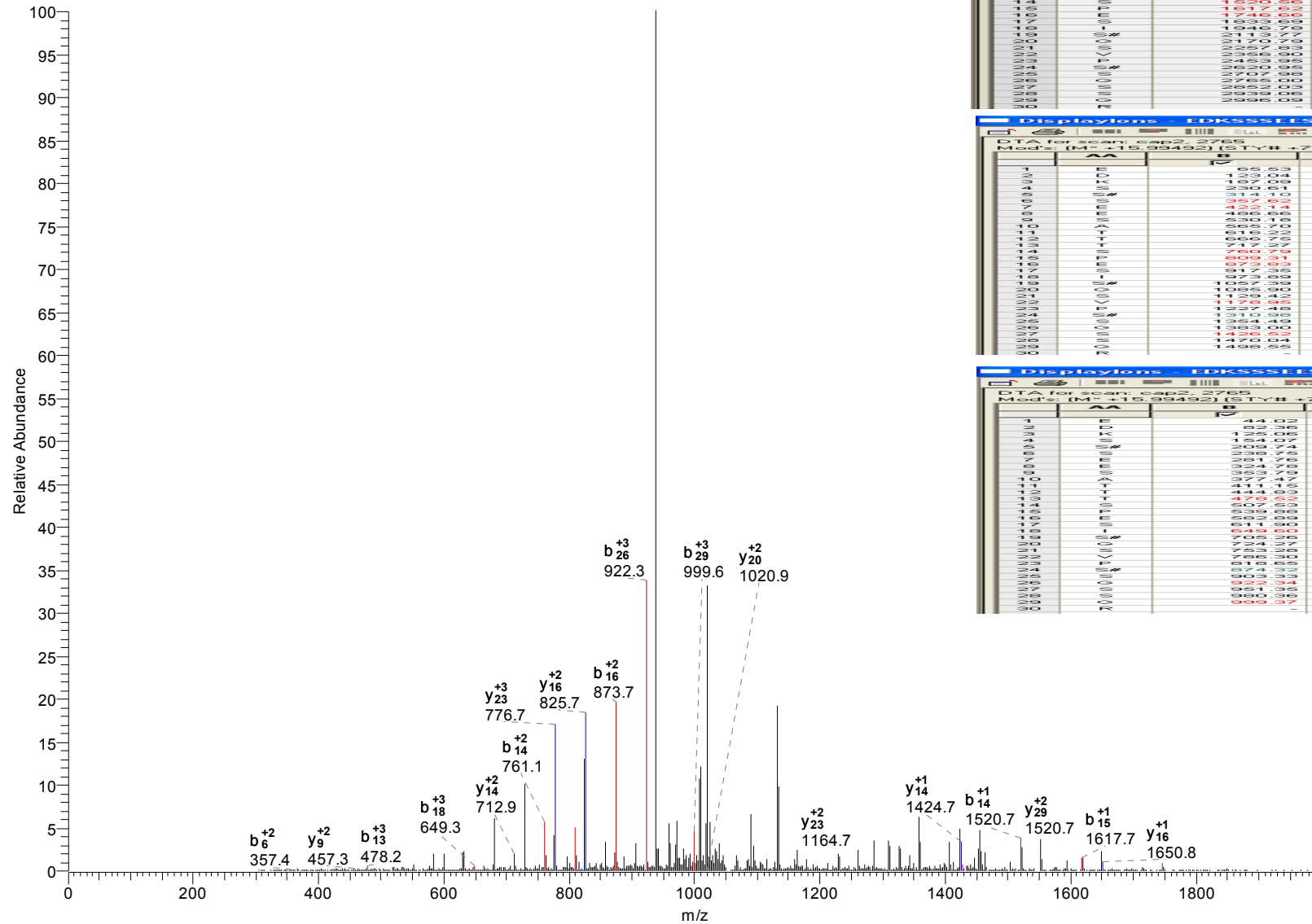
RGD1564067_predicted hypothetical protein

#6512-6512 NL: 1.94E3



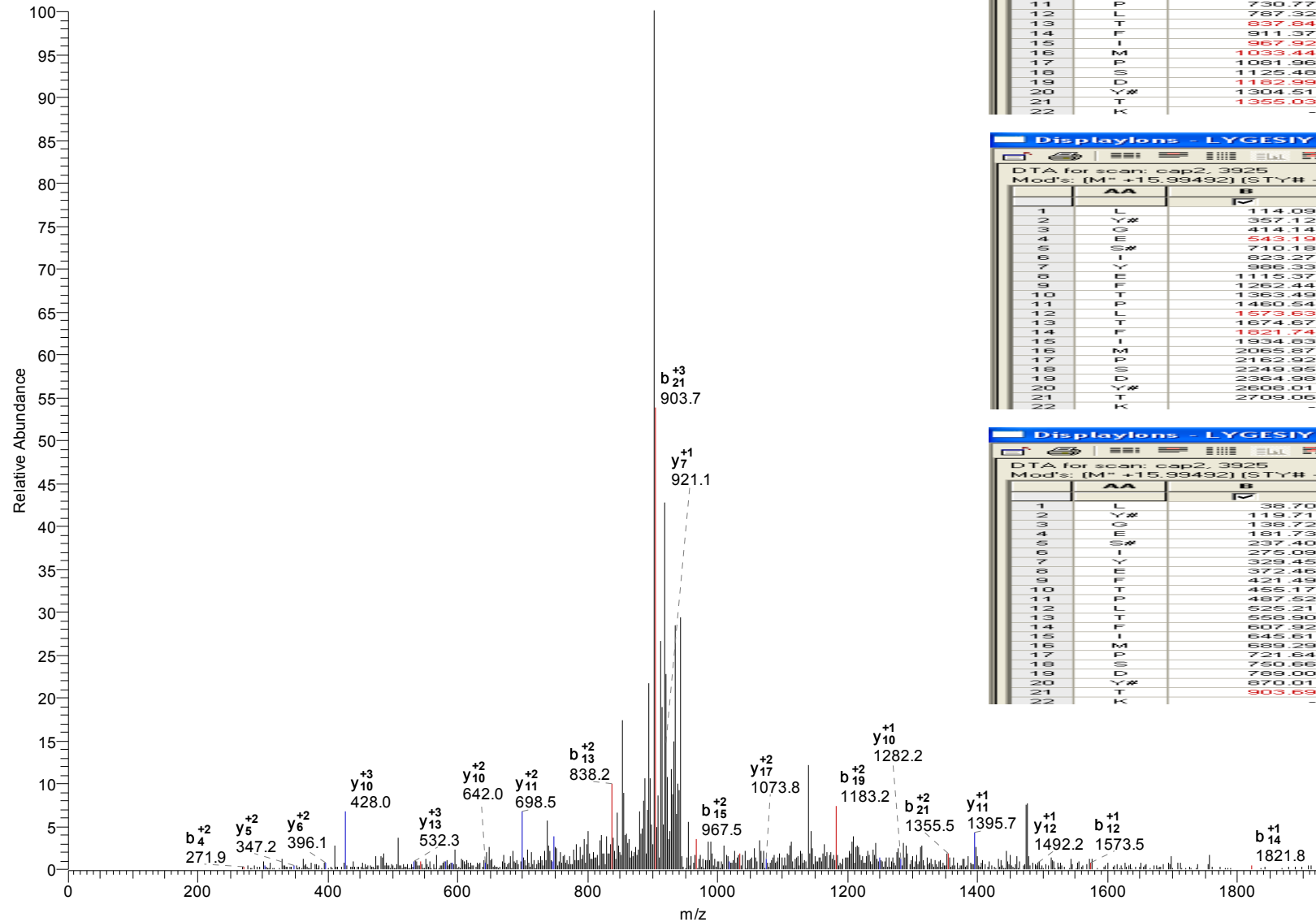
Rad23a RAD23a homolog

#2765-2765 NL: 1.17E4



Ttl2_predicted similar to tubulin tyrosine ligase-like family, member 2

#3925-3925 NL: 2.04E3



DTA for scan: cap2_3925
Mod's: [M⁺+15.99492] [STY# +79.96633]

	AA	B	Y	
1	L	57.55	-	22
2	Y#	179.06	1371.5	21
3	G	207.57	1250.03	20
4	E	272.10	1221.52	19
5	S#	355.60	1157.00	18
6	I	412.14	1073.50	17
7	Y	493.67	1016.95	16
8	E	558.19	935.42	15
9	F	631.72	870.90	14
10	T	682.25	797.37	13
11	P	730.77	746.84	12
12	L	787.32	698.32	11
13	T	837.84	641.77	10
14	F	911.37	591.25	9
15	I	967.92	517.72	8
16	M	1033.44	461.17	7
17	P	1081.96	395.65	6
18	S	1125.48	347.13	5
19	D	1182.99	303.61	4
20	Y#	1304.51	246.10	3
21	T	1355.03	124.58	2
22	K	-	74.06	1

Displays - LYGESIYETPLTFIMPSPDYI
DTA for scan: cap2_3925
Mod's: [M⁺+15.99492] [STY# +79.96633]

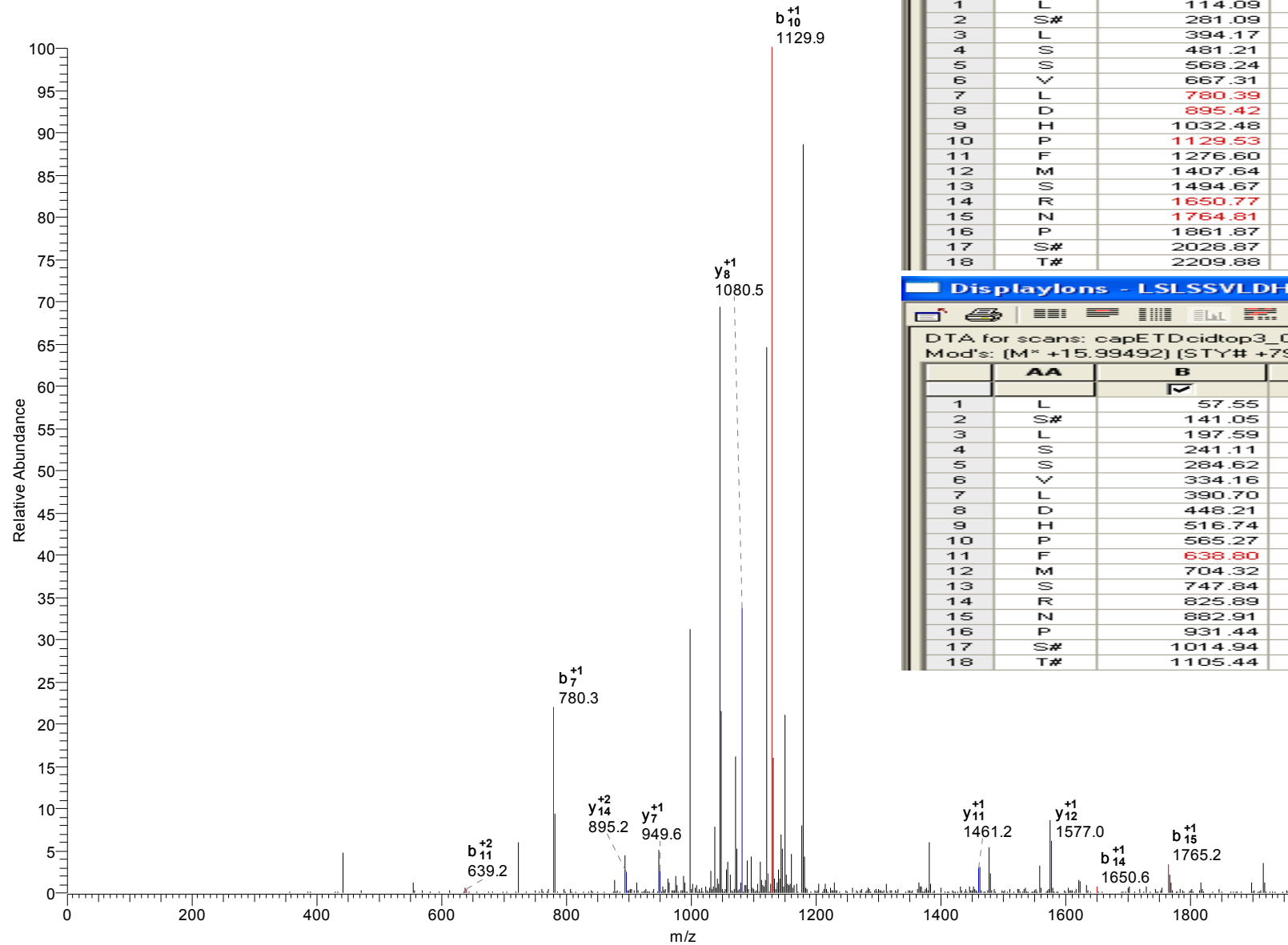
	AA	B	Y	
1	L	114.09	-	22
2	Y#	357.12	2742.06	21
3	G	414.14	2499.05	20
4	E	543.19	2442.03	19
5	S#	710.18	2312.98	18
6	I	823.27	2145.99	17
7	Y	986.33	2032.90	16
8	E	1115.37	1859.84	15
9	F	1262.44	1740.80	14
10	T	1363.49	1593.73	13
11	P	1460.54	1492.68	12
12	L	1573.63	1395.63	11
13	T	1674.67	1282.54	10
14	F	1821.74	1181.49	9
15	I	1934.83	1034.43	8
16	M	2065.87	921.34	7
17	P	2162.92	790.30	6
18	S	2249.95	693.25	5
19	D	2364.96	606.22	4
20	Y#	2608.01	491.19	3
21	T	2709.06	246.16	2
22	K	-	147.11	1

Displays - LYGESIYETPLTFIMPSPDYI
DTA for scan: cap2_3925
Mod's: [M⁺+15.99492] [STY# +79.96633]

	AA	B	Y	
1	L	38.70	-	22
2	Y#	119.71	914.70	21
3	G	138.72	833.69	20
4	E	161.73	814.66	19
5	S#	237.40	771.67	18
6	I	275.09	716.00	17
7	Y	329.45	678.31	16
8	E	372.46	623.95	15
9	F	421.49	580.94	14
10	T	455.17	531.91	13
11	P	497.52	490.23	12
12	L	525.21	465.88	11
13	T	558.90	428.19	10
14	F	607.92	394.50	9
15	I	645.61	345.46	8
16	M	689.29	307.79	7
17	P	721.64	264.11	6
18	S	750.65	231.75	5
19	D	789.00	202.74	4
20	Y#	870.01	164.40	3
21	T	903.69	83.39	2
22	K	-	49.71	1

Plk4_predicted similar to Serine/threonine-protein kinase PLK4

#2624-2625 NL: 1.61E3



Displaylons - LSLSSVLDHPFMSRNPSTK

DTA for scans: capETDcidtop3_080419044303, 2624
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	L	114.09	-	19
2	S#	281.09	2242.90	18
3	L	394.17	2075.90	17
4	S	481.21	1962.82	16
5	S	568.24	1875.79	15
6	V	667.31	1788.75	14
7	L	780.39	1689.69	13
8	D	895.42	1576.60	12
9	H	1032.48	1461.57	11
10	P	1129.53	1324.52	10
11	F	1276.60	1227.46	9
12	M	1407.64	1080.39	8
13	S	1494.67	949.35	7
14	R	1650.77	862.32	6
15	N	1764.81	706.22	5
16	P	1861.87	592.18	4
17	S#	2028.87	495.13	3
18	T#	2209.88	328.13	2

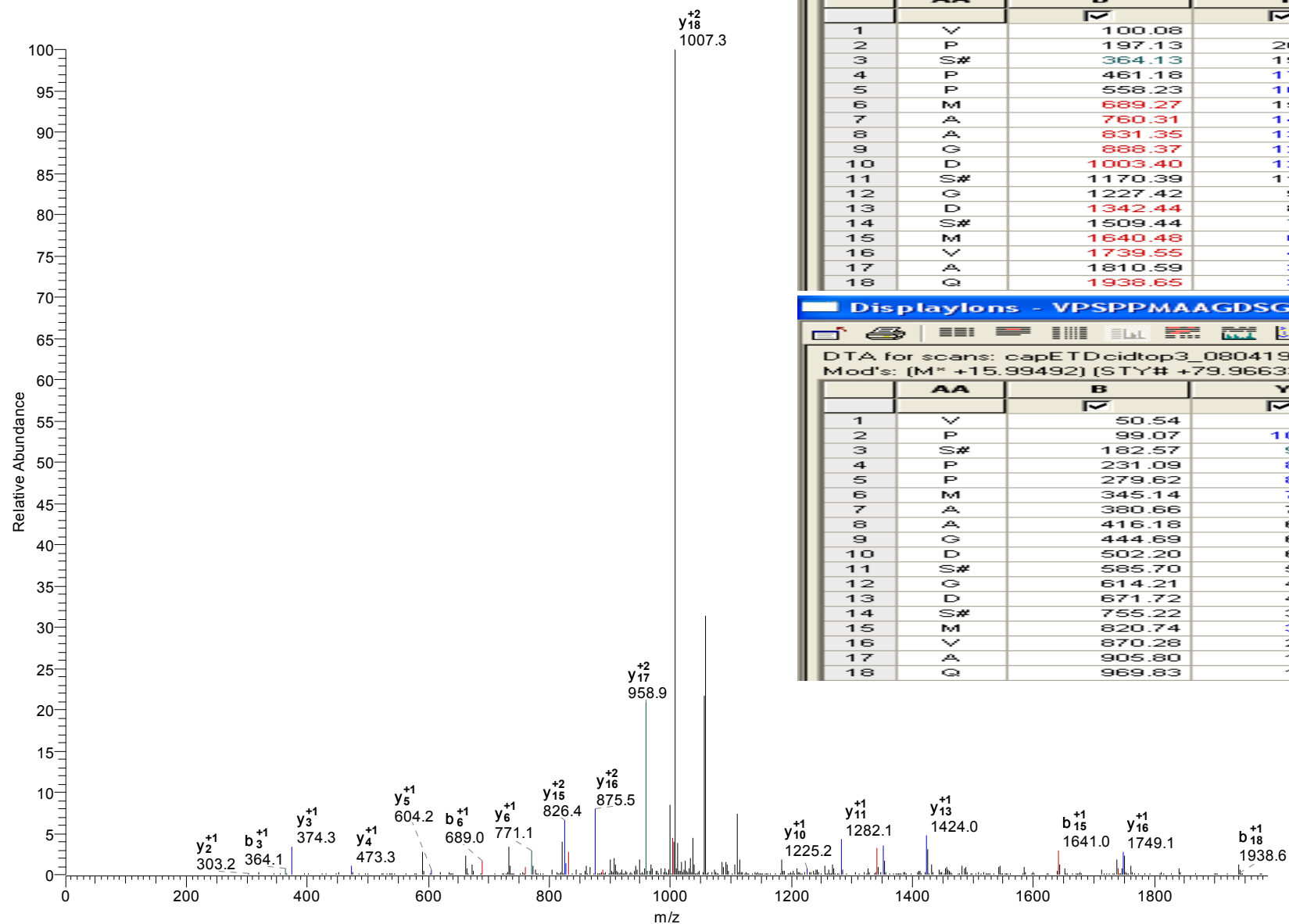
Displaylons - LSLSSVLDHPFMSRNPSTK

DTA for scans: capETDcidtop3_080419044303, 2624
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	L	57.55	-	19
2	S#	141.05	1121.95	18
3	L	197.59	1038.45	17
4	S	241.11	981.91	16
5	S	284.62	938.40	15
6	V	334.16	894.88	14
7	L	390.70	845.35	13
8	D	448.21	788.80	12
9	H	516.74	731.29	11
10	P	565.27	662.76	10
11	F	638.80	614.24	9
12	M	704.32	540.70	8
13	S	747.84	475.18	7
14	R	825.89	431.66	6
15	N	882.91	353.61	5
16	P	931.44	296.59	4
17	S#	1014.94	248.07	3
18	T#	1105.44	164.57	2

RGD1309065_predicted similar to CAP-binding protein complex interacting protein 1

#1175-1176 NL: 4.80E3



Displaylons - VPSPPPMAAGDSGDSMVAQR

DTA for scans: capETDcidtop3_080419044303, 1175
Mod's: [M* +15.99492] (STY# +79.96633)

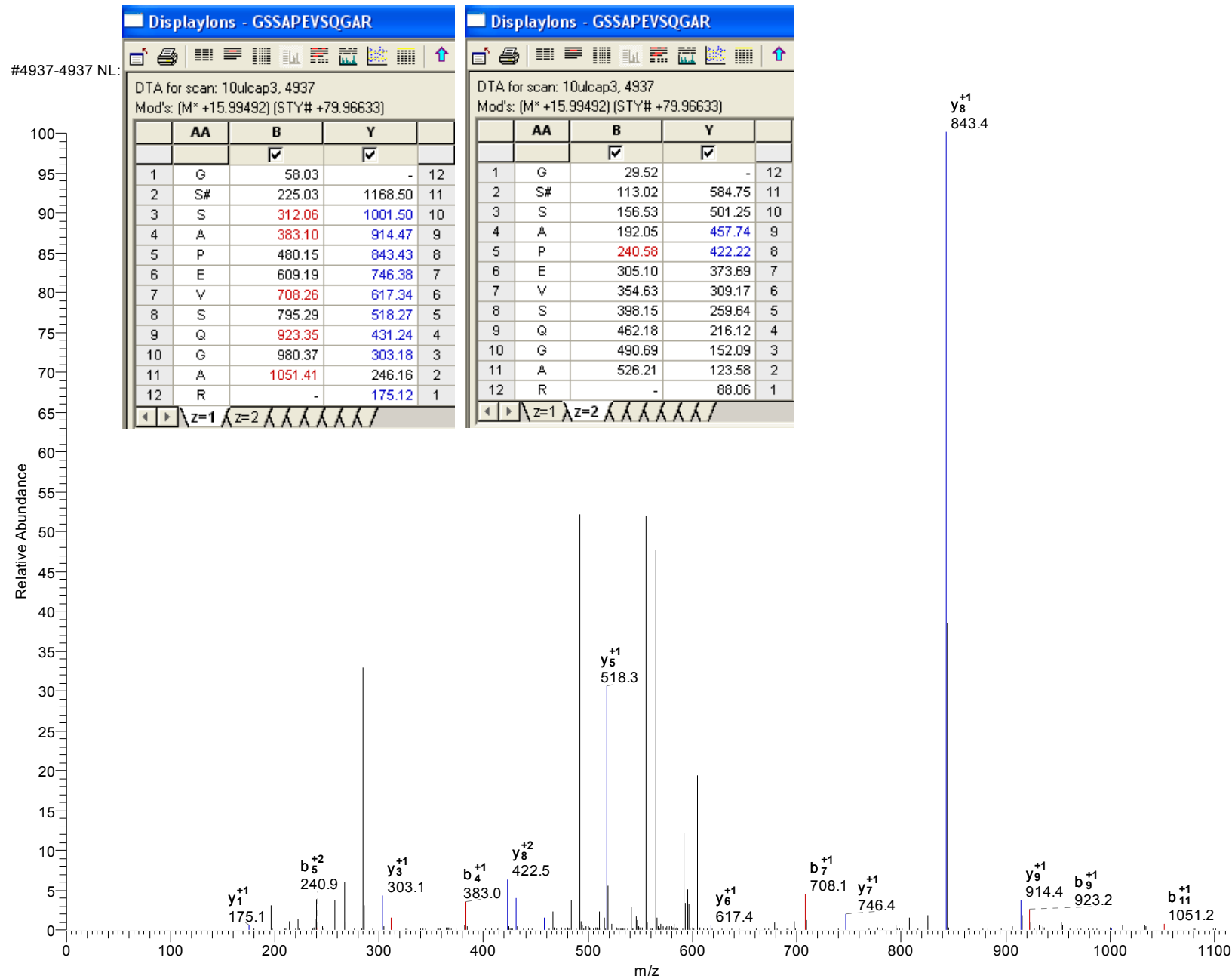
	AA	B	Y	
1	V	100.08	-	19
2	P	197.13	2013.69	18
3	S#	364.13	1916.64	17
4	P	461.18	1749.64	16
5	P	558.23	1652.58	15
6	M	689.27	1555.53	14
7	A	760.31	1424.49	13
8	A	831.35	1353.45	12
9	G	888.37	1282.42	11
10	D	1003.40	1225.40	10
11	S#	1170.39	1110.37	9
12	G	1227.42	943.37	8
13	D	1342.44	886.35	7
14	S#	1509.44	771.32	6
15	M	1640.48	604.32	5
16	V	1739.55	473.28	4
17	A	1810.59	374.21	3
18	Q	1938.65	303.18	2

Displaylons - VPSPPPMAAGDSGDSMVAQR

DTA for scans: capETDcidtop3_080419044303, 1175
Mod's: [M* +15.99492] (STY# +79.96633)

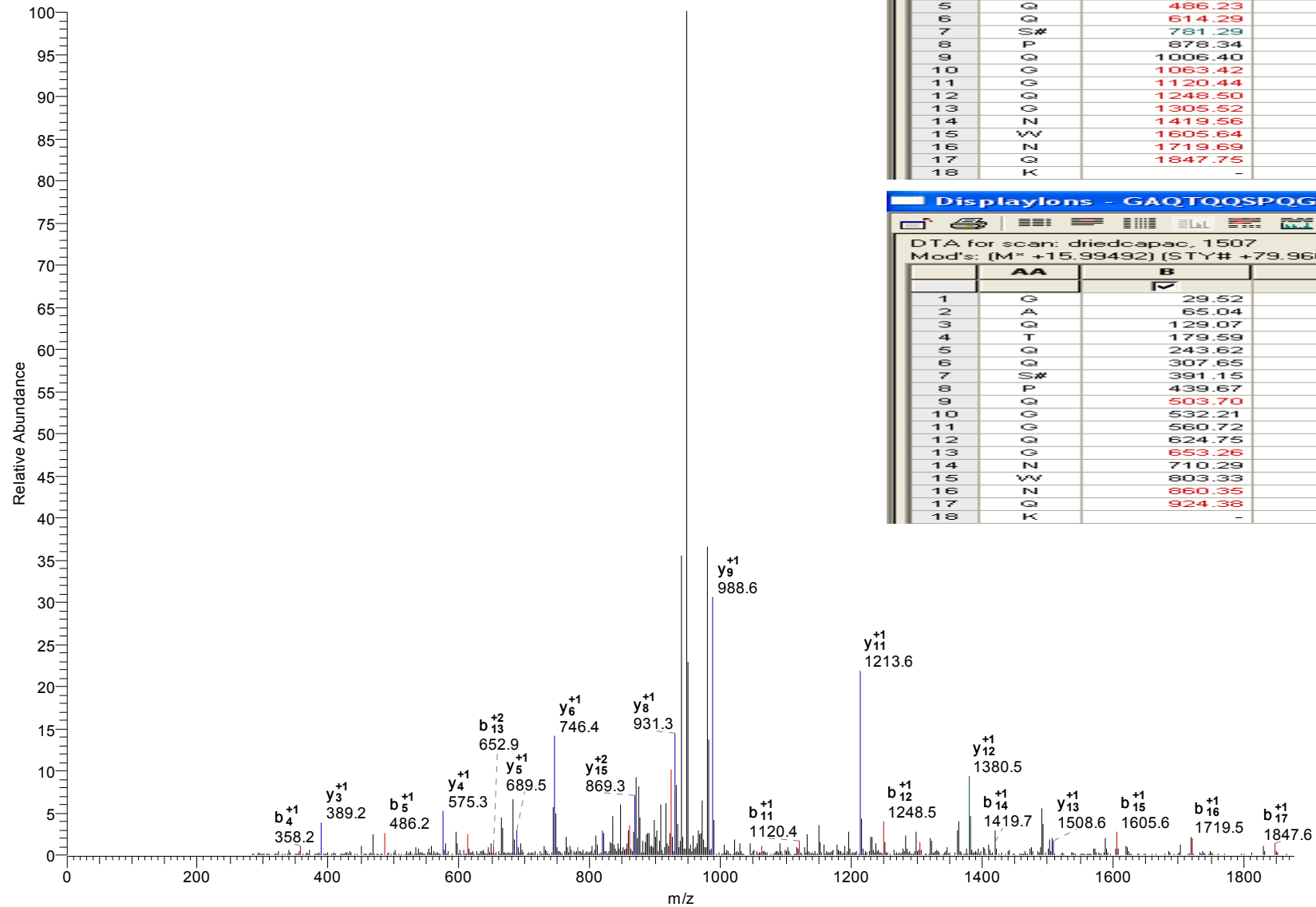
	AA	B	Y	
1	V	50.54	-	19
2	P	99.07	1007.35	18
3	S#	182.57	958.82	17
4	P	231.09	875.32	16
5	P	279.62	826.80	15
6	M	345.14	778.27	14
7	A	380.66	712.75	13
8	A	416.18	677.23	12
9	G	444.69	641.71	11
10	D	502.20	613.20	10
11	S#	585.70	555.69	9
12	G	614.21	472.19	8
13	D	671.72	443.68	7
14	S#	755.22	386.16	6
15	M	820.74	302.67	5
16	V	870.28	237.15	4
17	A	905.80	187.61	3
18	Q	969.83	152.09	2

RGD1309065_predicted similar to CAP-binding protein complex interacting protein 1



Smcp Sperm mitochondrial-associated cysteine-rich protein

#1507-1507 NL: 6.31E3



Displaylons - GAQTQQSPQGGQGNWNQK

DTA for scan: driedcapac, 1507
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	Q	58.03	-	18
2	A	129.07	1936.83	17
3	Q	257.12	1865.79	16
4	T	358.17	1737.73	15
5	Q	486.23	1636.69	14
6	Q	614.29	1508.63	13
7	S#	781.29	1380.57	12
8	P	878.34	1213.57	11
9	Q	1006.40	1116.52	10
10	Q	1063.42	988.46	9
11	Q	1120.44	931.44	8
12	Q	1248.50	874.42	7
13	Q	1305.52	746.36	6
14	N	1419.56	689.34	5
15	W	1605.64	575.29	4
16	N	1719.69	389.21	3
17	Q	1847.75	275.17	2
18	K	-	147.11	1

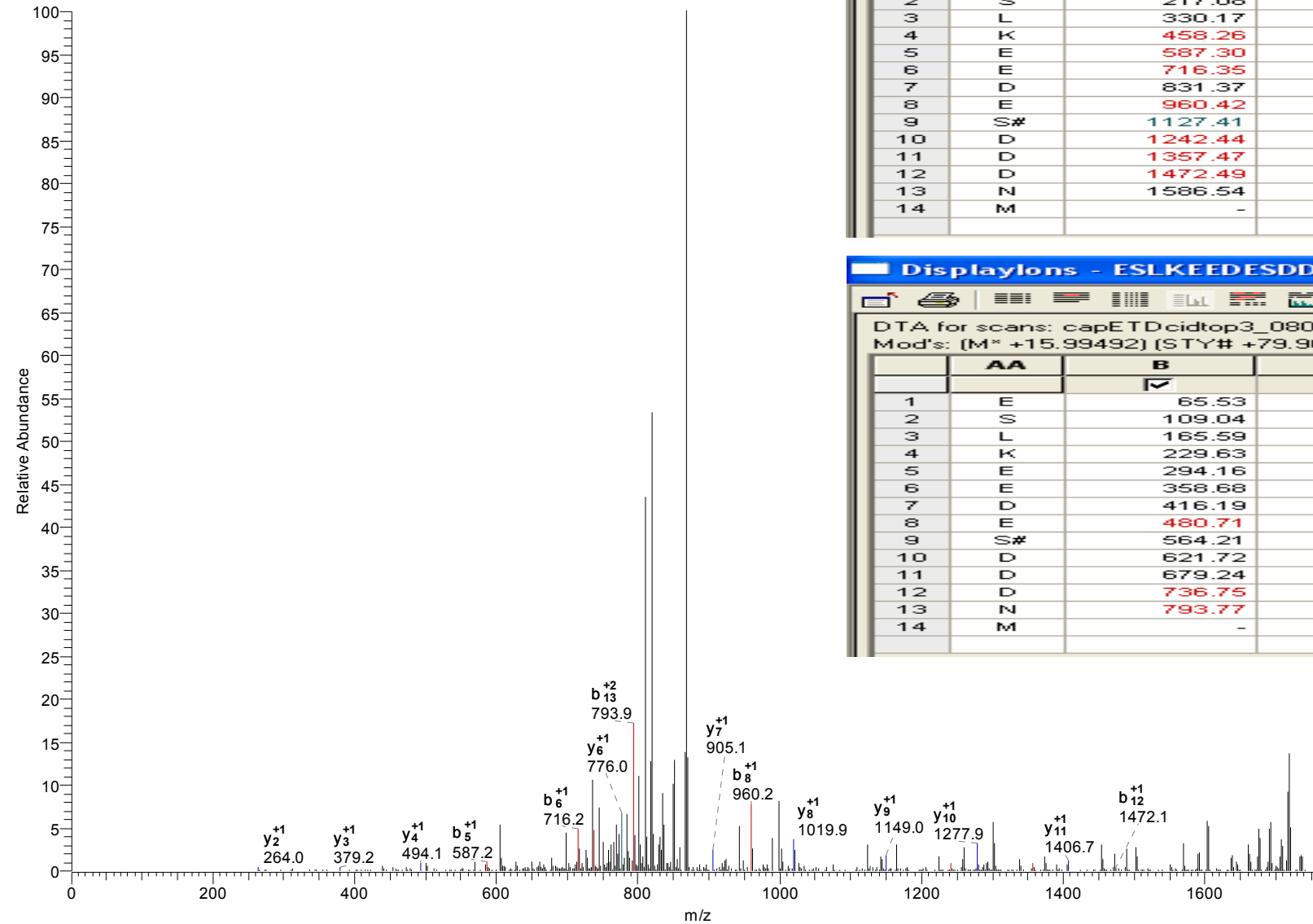
Displaylons - GAQTQQSPQGGQGNWNQK

DTA for scan: driedcapac, 1507
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	Q	29.52	-	18
2	A	65.04	968.92	17
3	Q	129.07	933.40	16
4	T	179.59	869.37	15
5	Q	243.62	818.85	14
6	Q	307.65	754.82	13
7	S#	391.15	690.79	12
8	P	439.67	607.29	11
9	Q	503.70	558.76	10
10	Q	532.21	494.73	9
11	Q	560.72	466.22	8
12	Q	624.75	437.71	7
13	Q	653.26	373.68	6
14	N	710.29	345.17	5
15	W	803.33	288.15	4
16	N	860.35	195.11	3
17	Q	924.38	138.09	2
18	K	-	74.06	1

Psma3I;Psma3 Proteasome subunit alpha type-3

#727-728 NL: 5.20E3



Displaylons - ESLKEEDESDDDNM

DTA for scans: capETDcidtop3_080419044303, 727-
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	E	130.05	-	14
2	S	217.08	1606.55	13
3	L	330.17	1519.51	12
4	K	458.26	1406.43	11
5	E	587.30	1278.34	10
6	E	716.35	1149.29	9
7	D	831.37	1020.25	8
8	E	960.42	905.22	7
9	S#	1127.41	776.18	6
10	D	1242.44	609.18	5
11	D	1357.47	494.16	4
12	D	1472.49	379.13	3
13	N	1586.54	264.10	2
14	M	-	150.06	1

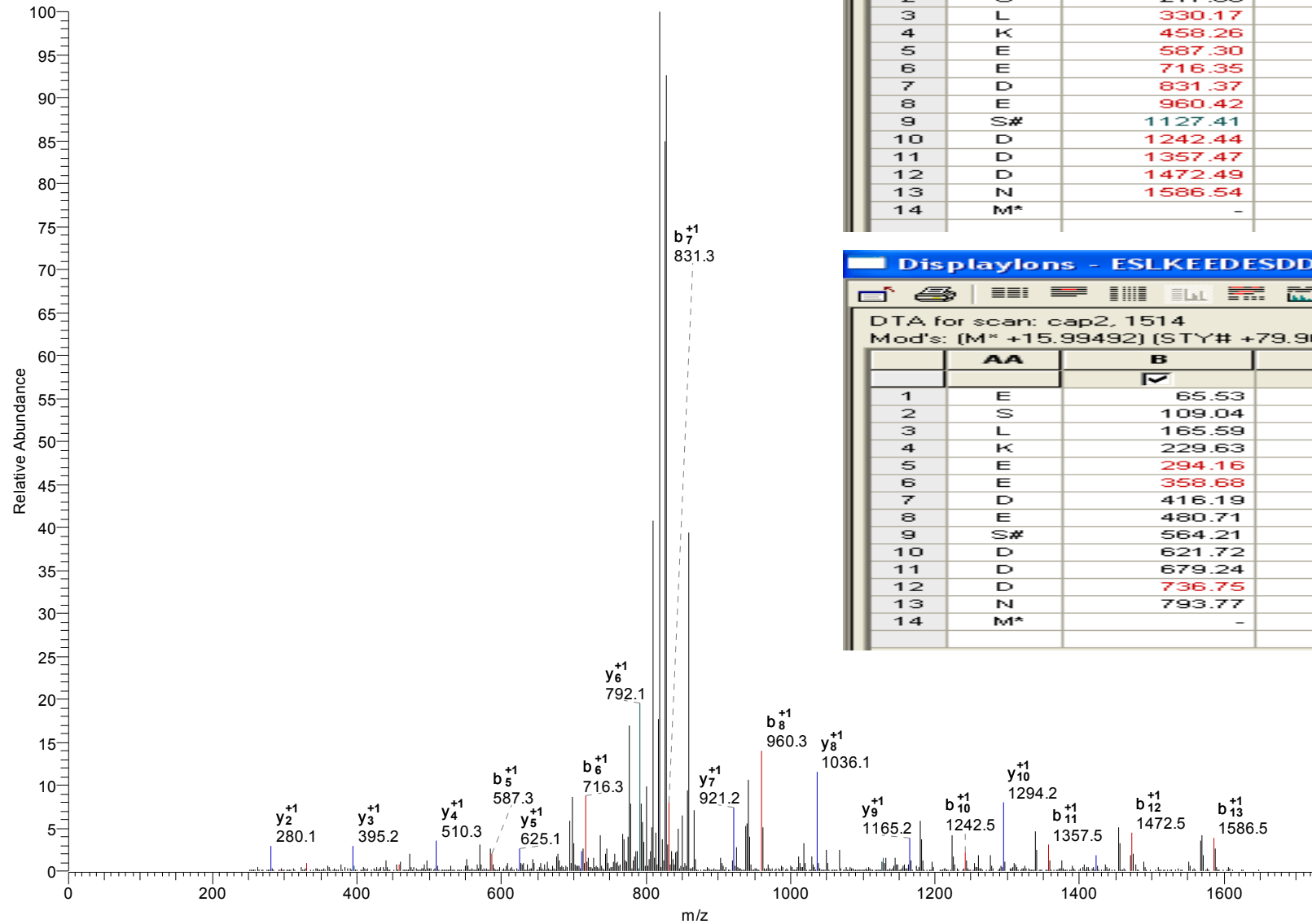
Displaylons - ESLKEEDESDDDNM

DTA for scans: capETDcidtop3_080419044303, 727-
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	E	65.53	-	14
2	S	109.04	803.78	13
3	L	165.59	760.26	12
4	K	229.63	703.72	11
5	E	294.16	639.67	10
6	E	358.68	575.15	9
7	D	416.19	510.63	8
8	E	480.71	453.12	7
9	S#	564.21	388.59	6
10	D	621.72	305.09	5
11	D	679.24	247.58	4
12	D	736.75	190.07	3
13	N	793.77	132.55	2
14	M	-	75.53	1

Psma3I;Psma3 Proteasome subunit alpha type-3

#1514-1514 NL: 2.05E4



Displaylons - ESLKEEDESDDDNM

DTA for scan: cap2, 1514
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	E	130.05	-	14
2	S	217.08	1622.54	13
3	L	330.17	1535.51	12
4	K	458.26	1422.43	11
5	E	587.30	1294.33	10
6	E	716.35	1165.29	9
7	D	831.37	1036.24	8
8	E	960.42	921.22	7
9	S#	1127.41	792.18	6
10	D	1242.44	625.18	5
11	D	1357.47	510.15	4
12	D	1472.49	395.12	3
13	N	1586.54	280.10	2
14	M*	-	166.05	1

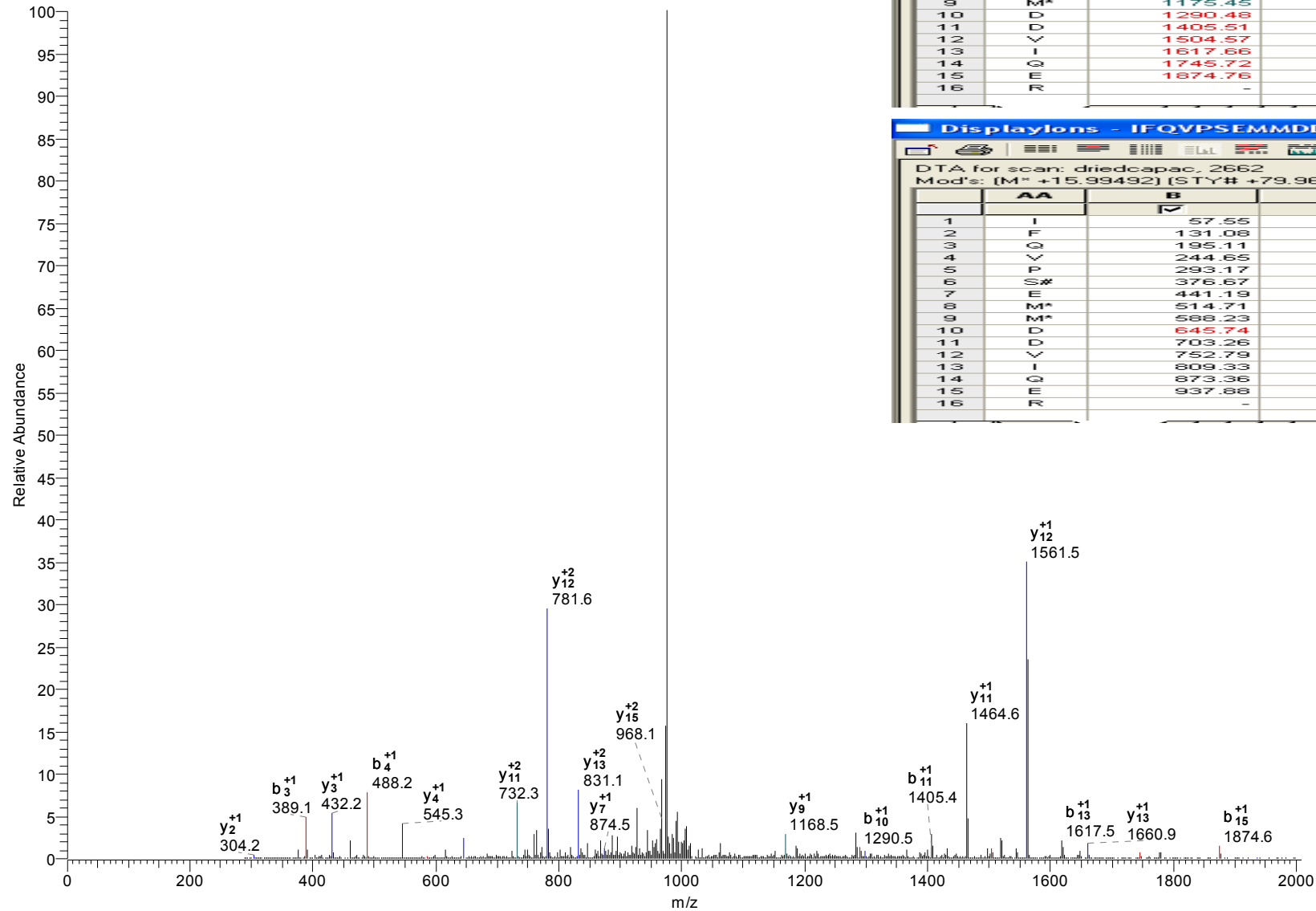
Displaylons - ESLKEEDESDDDNM

DTA for scan: cap2, 1514
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	E	65.53	-	14
2	S	109.04	811.77	13
3	L	165.59	768.26	12
4	K	229.63	711.72	11
5	E	294.16	647.67	10
6	E	358.68	583.15	9
7	D	416.19	518.63	8
8	E	480.71	461.11	7
9	S#	564.21	396.59	6
10	D	621.72	313.09	5
11	D	679.24	255.58	4
12	D	736.75	198.07	3
13	N	793.77	140.55	2
14	M*	-	83.53	1

Spas1 Spermatogenesis-associated protein 19, mitochondrial precursor

#2662-2662 NL: 1.81E4



Displaylons - IFQVPSEMMDDVIER

DTA for scan: driedcapac, 2662
Mod's: [M⁺ +15.99492] [STY# +79.96633]

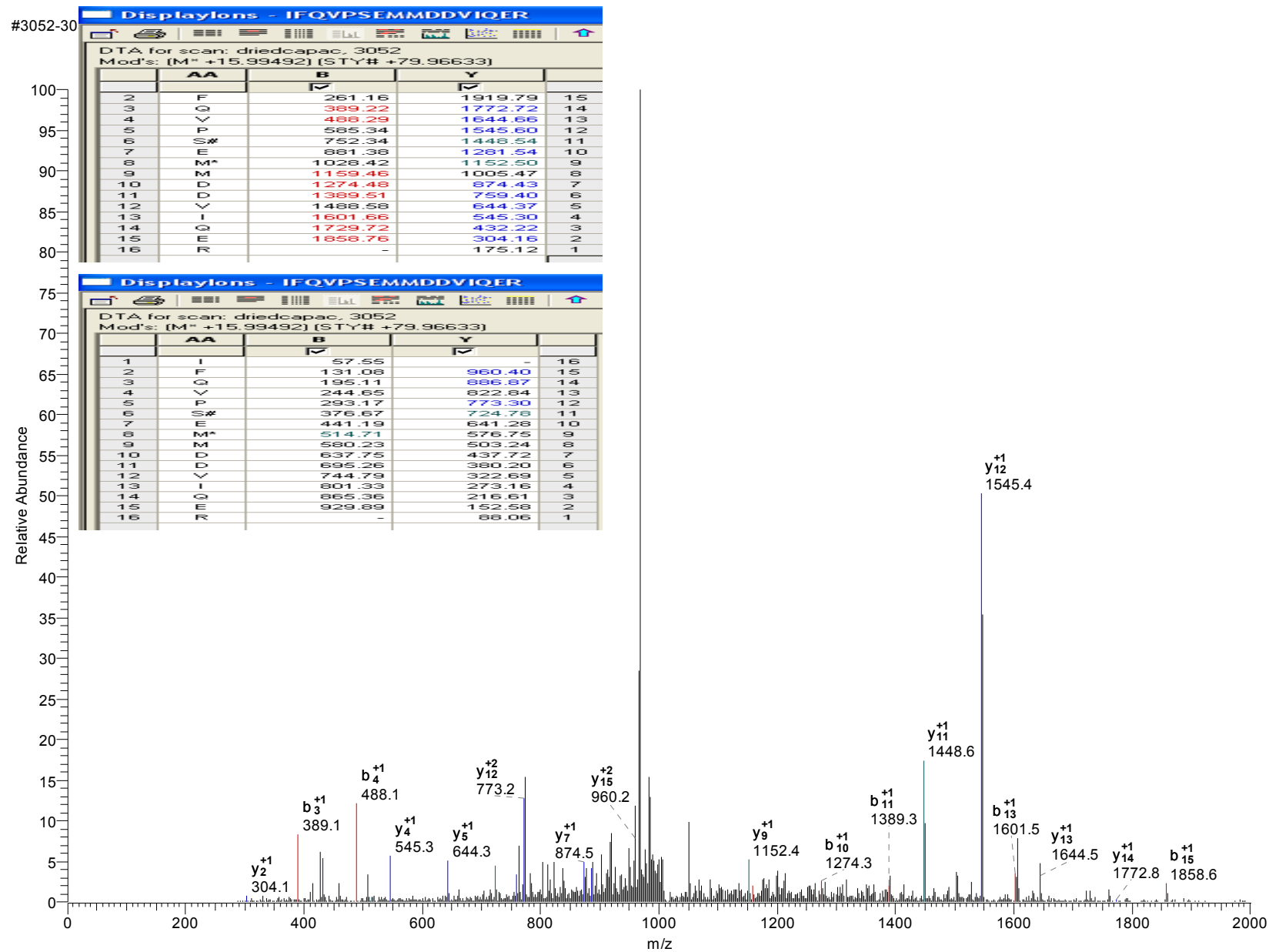
	AA	B	Y	
1	I	114.09	-	16
2	F	261.16	1935.79	15
3	Q	389.22	1789.72	14
4	V	488.29	1660.86	13
5	P	585.34	1561.59	12
6	S#	752.34	1464.54	11
7	E	881.38	1297.54	10
8	M ⁺	1028.42	1168.50	9
9	M ⁺	1175.45	1021.46	8
10	D	1290.48	874.43	7
11	D	1405.51	759.40	6
12	V	1504.57	644.37	5
13	I	1617.66	545.30	4
14	Q	1745.72	432.22	3
15	E	1874.76	304.16	2
16	R	-	175.12	1

Displaylons - IFQVPSEMMDDVIER

DTA for scan: driedcapac, 2662
Mod's: [M⁺ +15.99492] [STY# +79.96633]

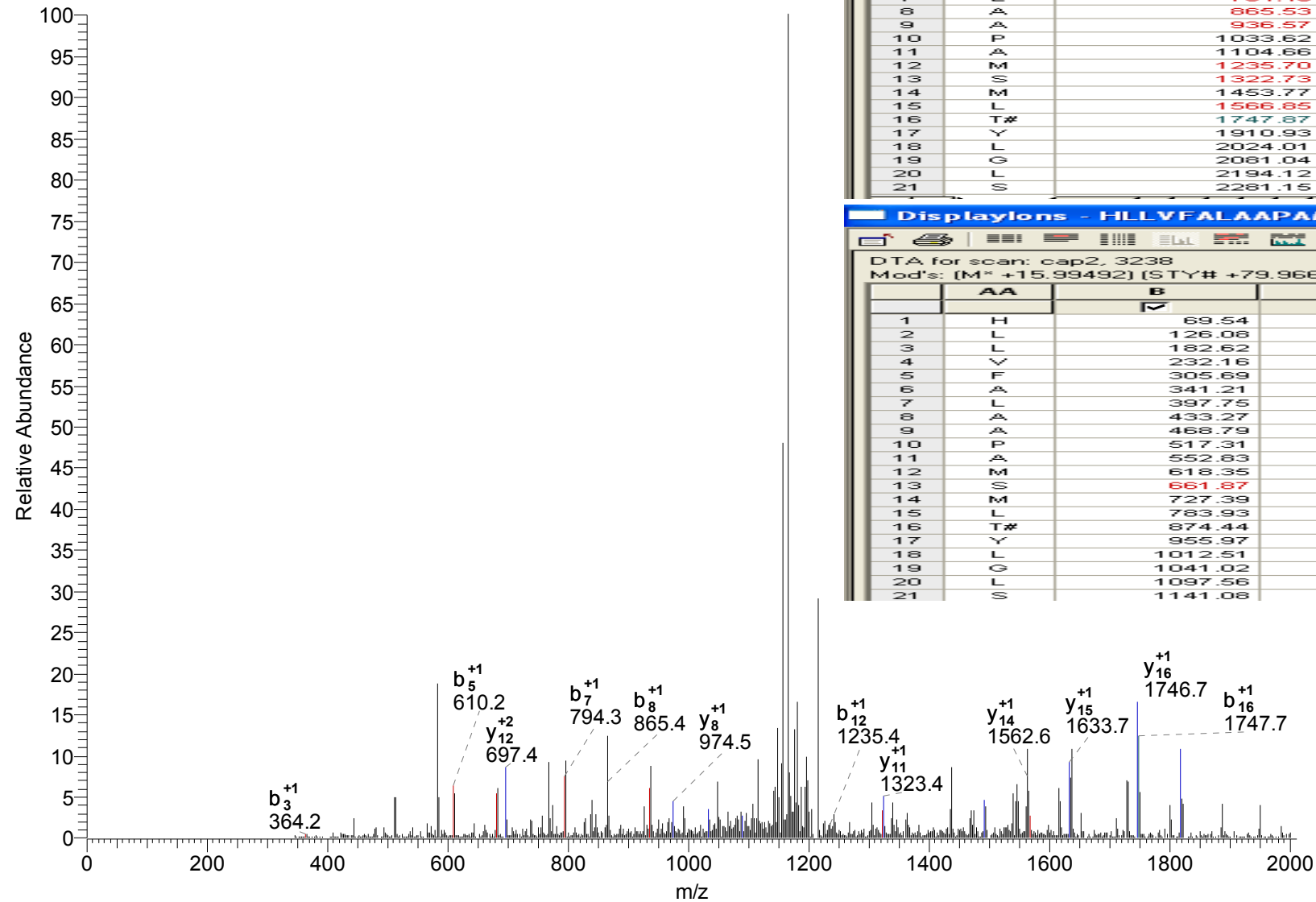
	AA	B	Y	
1	I	57.55	-	16
2	F	131.08	968.40	15
3	Q	195.11	894.86	14
4	V	244.65	830.83	13
5	P	293.17	781.30	12
6	S#	376.67	732.77	11
7	E	441.19	649.27	10
8	M ⁺	514.71	584.75	9
9	M ⁺	588.23	511.23	8
10	D	645.74	437.72	7
11	D	703.26	380.20	6
12	V	752.79	322.69	5
13	I	809.33	273.16	4
14	Q	873.36	216.61	3
15	E	937.88	152.58	2
16	R	-	88.06	1

Spas1 Spermatogenesis-associated protein 19, mitochondrial precursor



Zinc transporter SLC39A9

#3238-3238 NL: 4.21E3



Displaylons - HLLVFALAAPAMSMLTYLGLS

DTA for scan: cap2, 3238
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y
1	H	138.07	-
2	L	251.15	2290.20
3	L	364.23	2177.11
4	V	463.30	2064.03
5	F	610.37	1964.96
6	A	681.41	1817.89
7	L	794.49	1746.86
8	A	865.53	1633.77
9	A	936.57	1562.74
10	P	1033.62	1491.70
11	A	1104.66	1394.65
12	M	1235.70	1323.61
13	S	1322.73	1192.57
14	M	1453.77	1105.54
15	L	1566.85	974.50
16	T#	1747.87	861.41
17	Y	1910.93	680.40
18	L	2024.01	517.33
19	G	2081.04	404.25
20	L	2194.12	347.23
21	S	2281.15	234.14

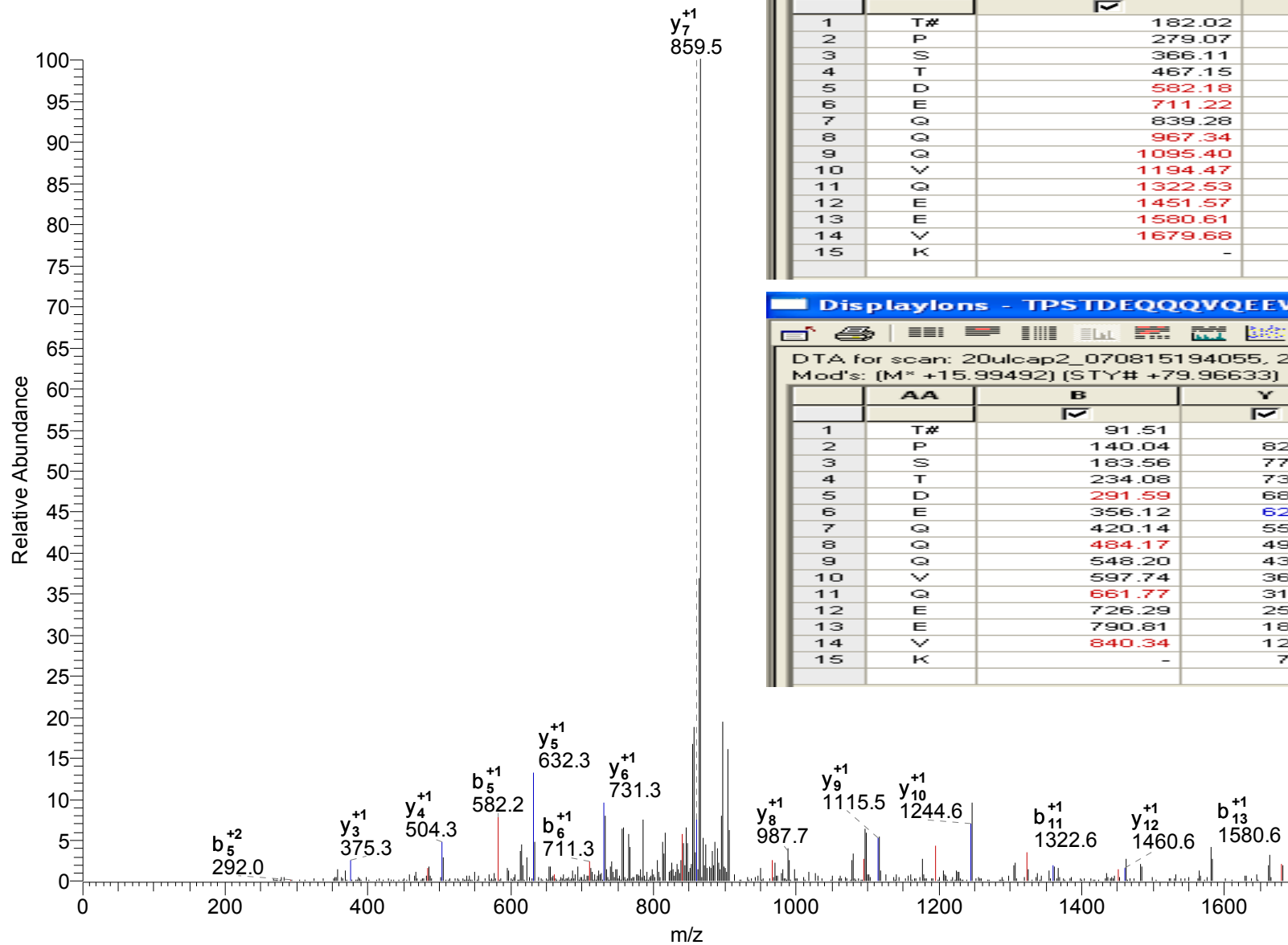
Displaylons - HLLVFALAAPAMSMLTYLGLS

DTA for scan: cap2, 3238
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	H	69.54	-	22
2	L	126.08	1145.60	21
3	L	182.62	1089.06	20
4	V	232.16	1032.52	19
5	F	305.69	982.98	18
6	A	341.21	909.45	17
7	L	397.75	873.93	16
8	A	433.27	817.39	15
9	A	468.79	781.87	14
10	P	517.31	746.35	13
11	A	552.83	697.83	12
12	M	618.35	662.31	11
13	S	661.87	596.79	10
14	M	727.39	553.27	9
15	L	783.93	487.75	8
16	T#	874.44	431.21	7
17	Y	955.97	340.70	6
18	L	1012.51	259.17	5
19	G	1041.02	202.63	4
20	L	1097.56	174.12	3
21	S	1141.08	117.58	2

12 kDa protein

#2149-2149 NL: 1.64E3



Displaylons - TPSTDEQQVQEEVK

DTA for scan: 20ulcap2_070815194055, 2149
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y
1	T#	182.02	-
2	P	279.07	1644.77
3	S	366.11	1547.72
4	T	467.15	1460.69
5	D	582.18	1359.64
6	E	711.22	1244.61
7	Q	839.28	1115.57
8	Q	967.34	987.51
9	Q	1095.40	859.45
10	V	1194.47	731.39
11	Q	1322.53	632.32
12	E	1451.57	504.27
13	E	1580.61	375.22
14	V	1679.68	246.18
15	K	-	147.11

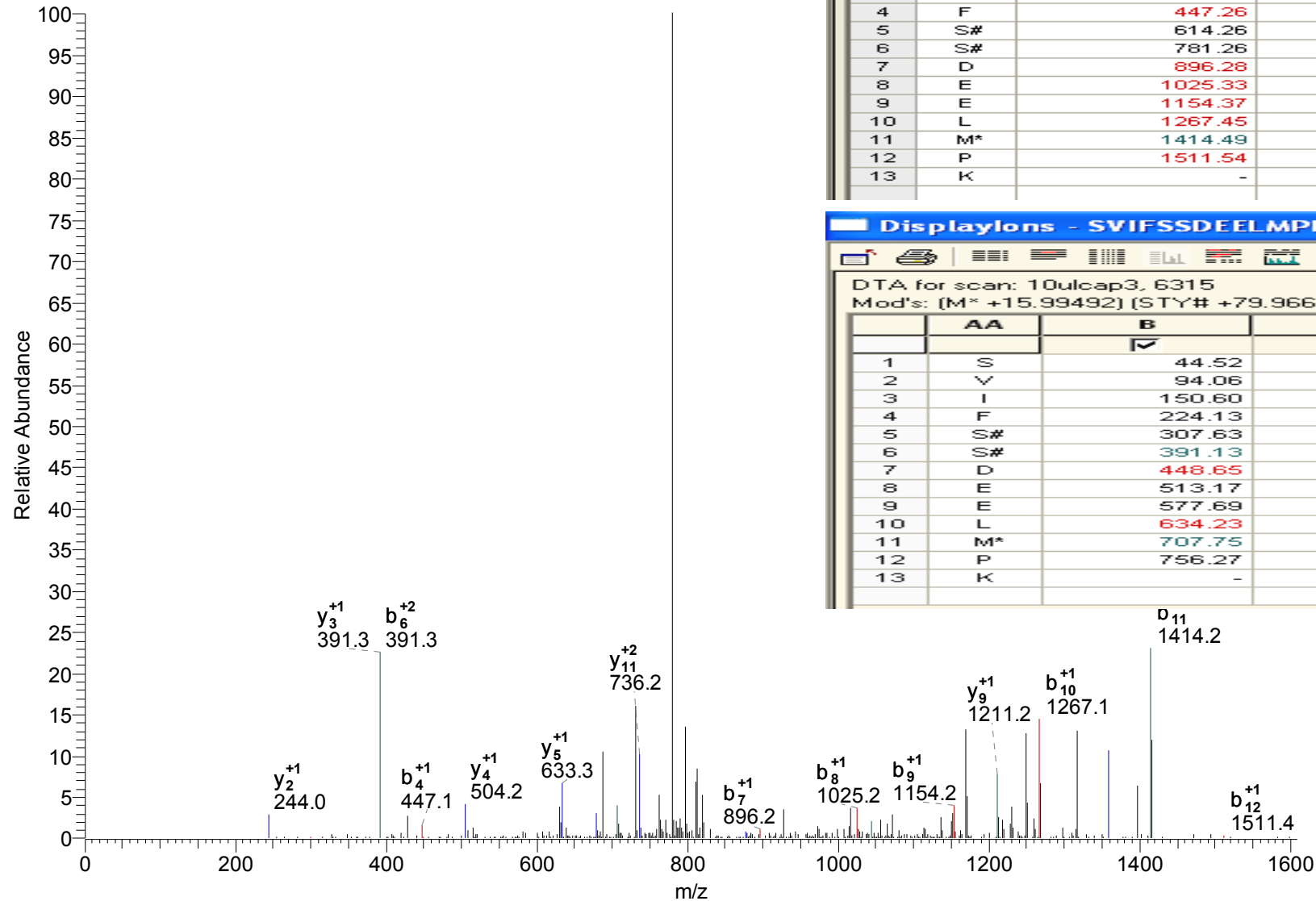
Displaylons - TPSTDEQQVQEEVK

DTA for scan: 20ulcap2_070815194055, 2149
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	T#	91.51	-	15
2	P	140.04	822.89	14
3	S	183.56	774.36	13
4	T	234.08	730.85	12
5	D	291.59	680.32	11
6	E	356.12	622.81	10
7	Q	420.14	558.29	9
8	Q	484.17	494.26	8
9	Q	548.20	430.23	7
10	V	597.74	366.20	6
11	Q	661.77	316.67	5
12	E	726.29	252.64	4
13	E	790.81	188.12	3
14	V	840.34	123.59	2
15	K	-	74.06	1

Similar to RIKEN cDNA 1700052H20

#6315-6315 NL: 1.43E3



Displaylons - SVIFSSDEELMPK

DTA for scan: 10ulcap3, 6315
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	S	88.04	-	13
2	V	187.11	1570.61	12
3	I	300.19	1471.55	11
4	F	447.26	1358.46	10
5	S#	614.26	1211.39	9
6	S#	781.26	1044.40	8
7	D	896.28	877.40	7
8	E	1025.33	762.37	6
9	E	1154.37	633.33	5
10	L	1267.45	504.29	4
11	M*	1414.49	391.20	3
12	P	1511.54	244.17	2
13	K	-	147.11	1

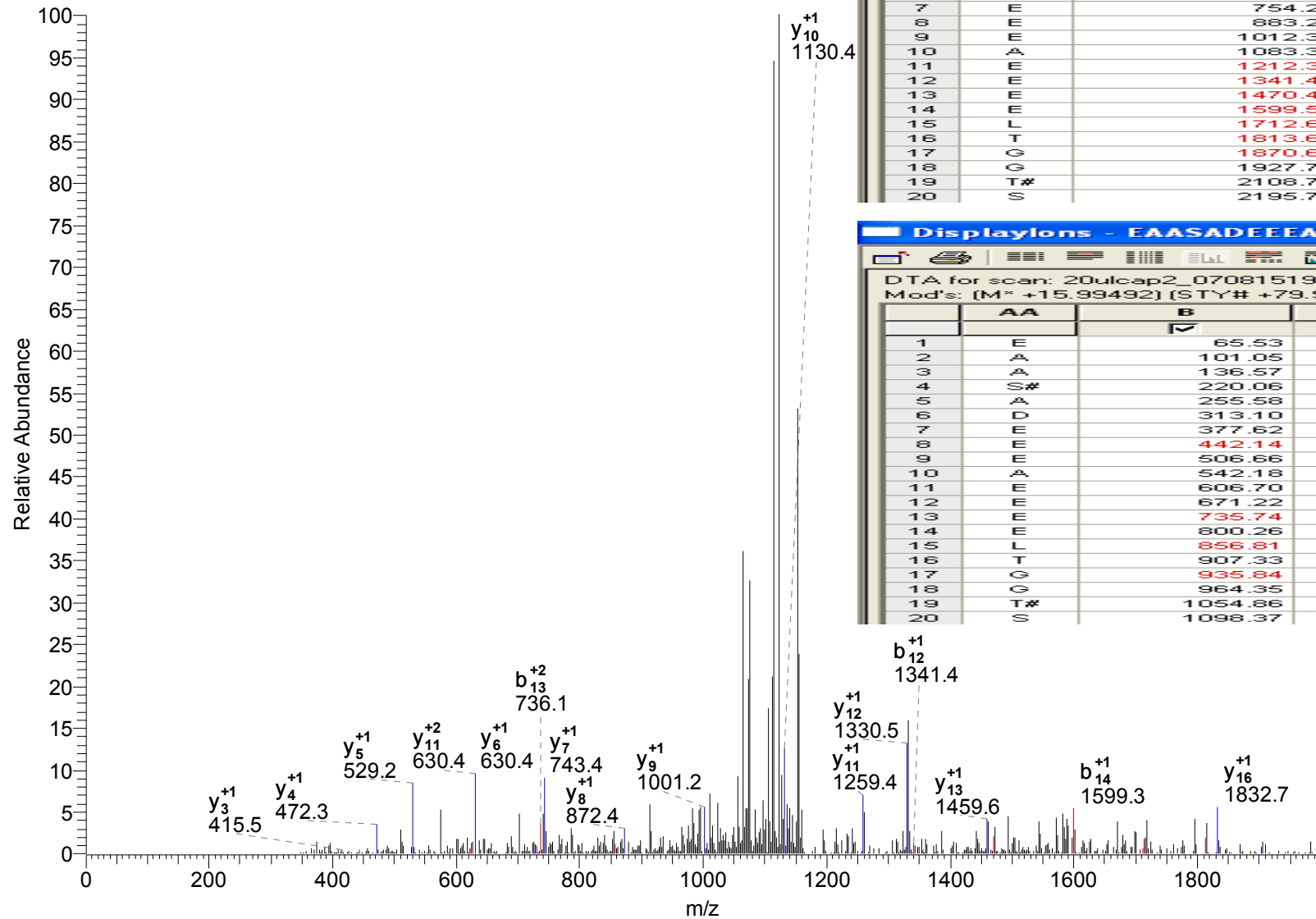
Displaylons - SVIFSSDEELMPK

DTA for scan: 10ulcap3, 6315
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	S	44.52	-	13
2	V	94.06	785.81	12
3	I	150.60	736.28	11
4	F	224.13	679.73	10
5	S#	307.63	606.20	9
6	S#	391.13	522.70	8
7	D	448.65	439.20	7
8	E	513.17	381.69	6
9	E	577.69	317.17	5
10	L	634.23	252.65	4
11	M*	707.75	196.10	3
12	P	756.27	122.59	2
13	K	-	74.06	1

Uncharacterized protein C9orf128 homolog

#2390-2390 NL: 1.24E3



Displaylons - EAASADEEEEEEEELTGGTSK

DTA for scan: 20ulcap2_070815194055, 2390
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y
1	E	130.05	-
2	A	201.09	2212.81
3	A	272.12	2141.77
4	S#	439.12	2070.73
5	A	510.16	1903.73
6	D	625.19	1832.70
7	E	754.23	1717.67
8	E	883.27	1588.63
9	E	1012.31	1459.58
10	A	1083.35	1330.54
11	E	1212.39	1259.50
12	E	1341.44	1130.46
13	E	1470.48	1001.42
14	E	1599.52	872.38
15	L	1712.61	743.33
16	T	1813.65	630.25
17	G	1870.67	529.20
18	G	1927.70	472.18
19	T#	2108.71	415.16
20	S	2195.74	234.14

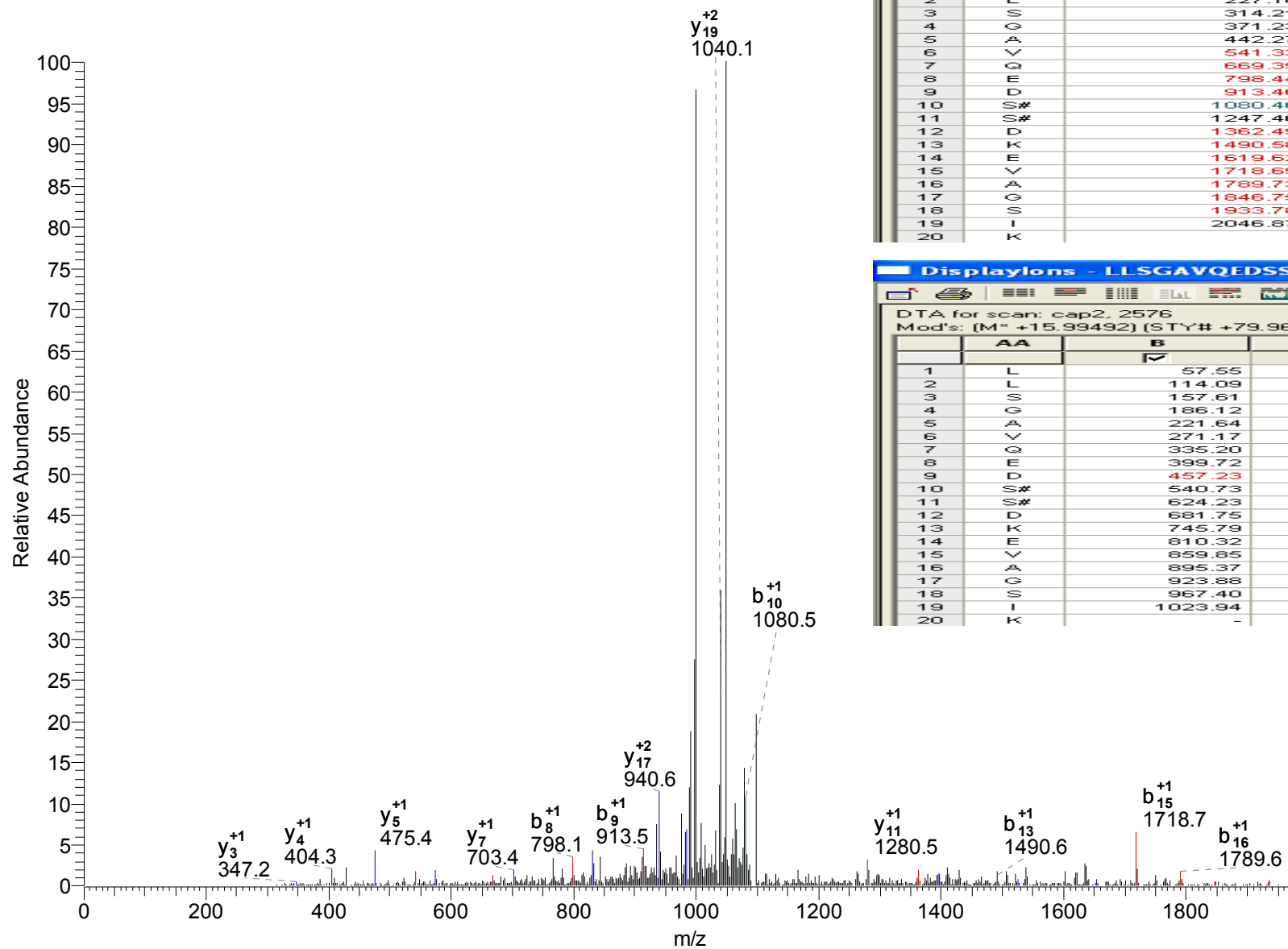
Displaylons - EAASADEEEEEEEELTGGTSK

DTA for scan: 20ulcap2_070815194055, 2390
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	E	65.53	-	21
2	A	101.05	1106.91	20
3	A	136.57	1071.39	19
4	S#	220.06	1035.87	18
5	A	255.58	952.37	17
6	D	313.10	916.85	16
7	E	377.62	859.34	15
8	E	442.14	794.82	14
9	E	506.66	730.30	13
10	A	542.18	665.77	12
11	E	606.70	630.26	11
12	E	671.22	565.73	10
13	E	735.74	501.21	9
14	E	800.26	436.69	8
15	L	856.81	372.17	7
16	T	907.33	315.63	6
17	G	935.84	265.10	5
18	G	964.35	236.59	4
19	T#	1054.86	208.08	3
20	S	1098.37	117.58	2

predicted DDI1 homolog 1

#2576-2576 NL: 4.55E3



Displaylons - LLSGAVQEDSSDKEVAGSIK

DTA for scan: cap2, 2576
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y
1	L	114.09	-
2	L	227.18	2079.89
3	S	314.21	1966.80
4	Q	371.23	1879.77
5	A	442.27	1822.75
6	V	541.33	1751.71
7	Q	669.39	1652.65
8	E	798.44	1524.59
9	D	913.46	1395.54
10	S#	1080.46	1280.52
11	S#	1247.46	1113.52
12	D	1362.49	946.52
13	K	1490.58	831.49
14	E	1619.62	703.40
15	V	1718.69	574.36
16	A	1789.73	475.29
17	Q	1846.75	404.25
18	S	1933.78	347.23
19	I	2046.87	260.20
20	K	-	147.11

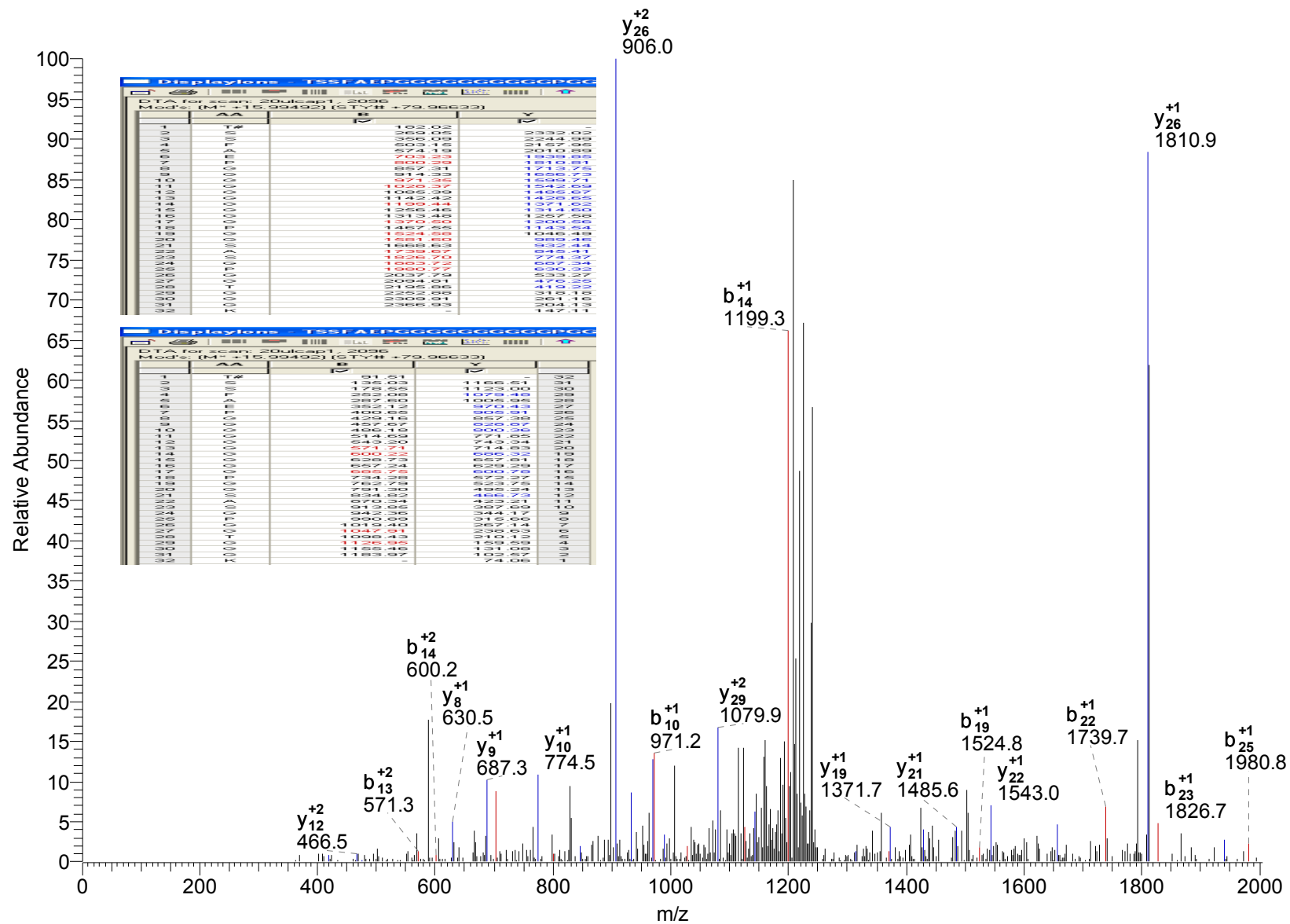
Displaylons - LLSGAVQEDSSDKEVAGSIK

DTA for scan: cap2, 2576
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	L	57.55	-	20
2	L	114.09	1040.45	19
3	S	157.61	983.91	18
4	Q	186.12	940.39	17
5	A	221.64	911.88	16
6	V	271.17	876.36	15
7	Q	335.20	826.83	14
8	E	399.72	762.80	13
9	D	457.23	698.28	12
10	S#	540.73	640.76	11
11	S#	624.23	557.26	10
12	D	681.75	473.76	9
13	K	745.79	416.25	8
14	E	810.32	352.20	7
15	V	859.85	287.68	6
16	A	895.37	238.15	5
17	Q	923.88	202.63	4
18	S	967.40	174.12	3
19	I	1023.94	130.60	2
20	K	-	74.06	1

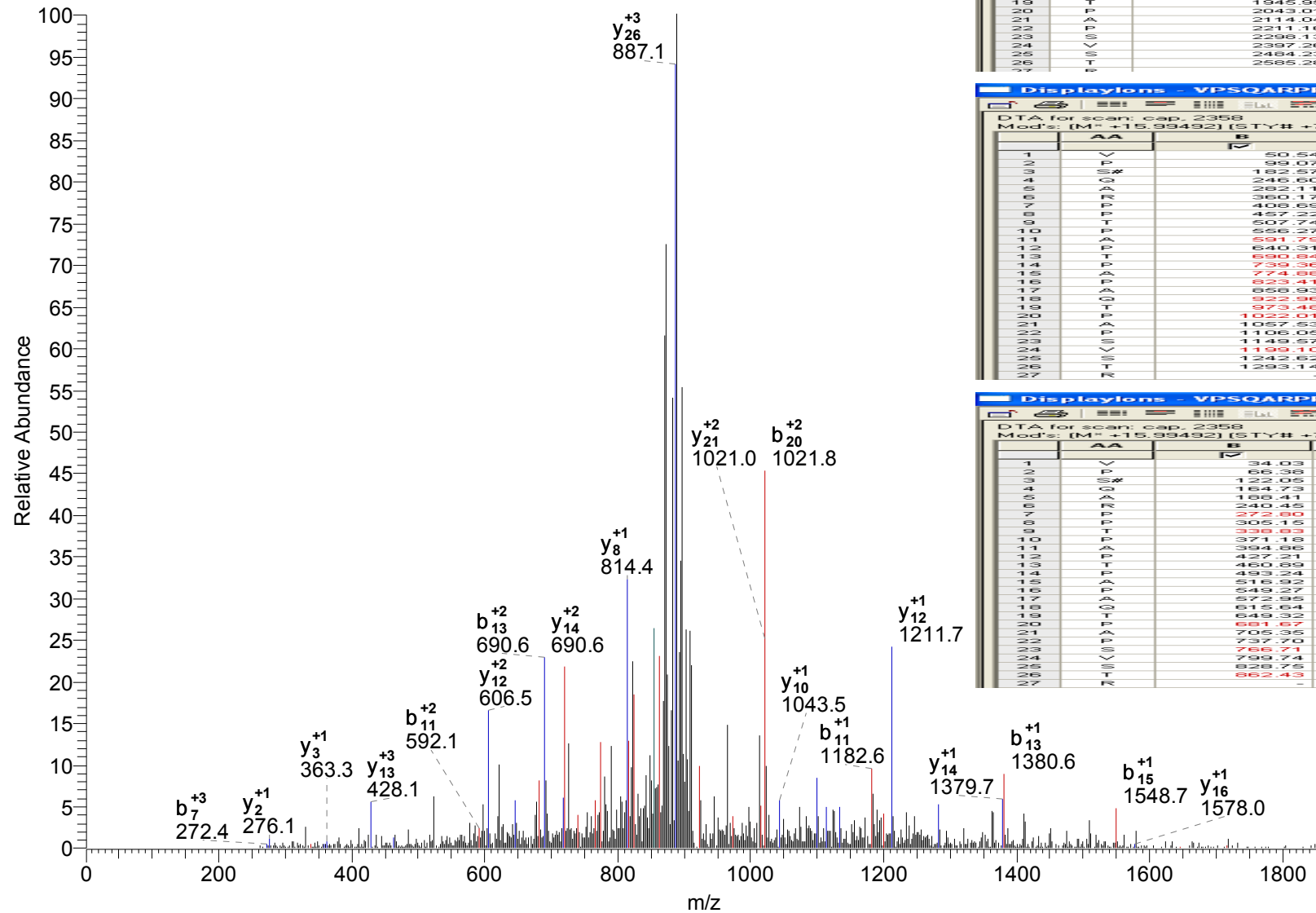
Gsk3a Glycogen synthase kinase-3 alpha

#2096-2096 NL: 5.94E2



Dnajb6 DnaJ homolog subfamily B member 6

#2358-2358 NL: 1.90E3



Displays - VPSQARPP TPAP TPAPQ TPAPS

DTA for scan: cap. 2358
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	V	100.06	-	27
2	P	197.13	2660.32	26
3	S#	364.13	2563.27	25
4	Q	492.19	2396.27	24
5	A	563.22	2266.21	23
6	R	719.32	2197.17	22
7	P	816.36	2041.07	21
8	P	913.43	1944.02	20
9	T	1014.48	1846.97	19
10	P	1111.53	1745.92	18
11	A	1182.57	1648.87	17
12	P	1279.62	1577.83	16
13	T	1360.67	1480.78	15
14	P	1477.72	1379.73	14
15	A	1548.76	1282.67	13
16	P	1645.81	1211.64	12
17	A	1716.85	1114.59	11
18	Q	1844.91	1043.55	10
19	T	1945.95	915.49	9
20	P	2043.01	814.44	8
21	A	2114.04	717.39	7
22	P	2211.10	646.35	6
23	S	2296.13	549.30	5
24	V	2397.20	452.27	4
25	S	2484.23	363.20	3
26	T	2585.28	276.17	2
27	R	-	176.13	1

Displays - VPSQARPP TPAP TPAPQ TPAPS

DTA for scan: cap. 2358
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	V	50.54	-	27
2	P	99.07	1330.66	26
3	S#	182.57	1282.14	25
4	Q	246.80	1198.64	24
5	A	282.11	1134.61	23
6	R	360.17	1099.09	22
7	P	406.69	1021.04	21
8	P	457.23	972.51	20
9	T	507.74	923.99	19
10	P	556.27	873.46	18
11	A	591.79	824.94	17
12	P	640.31	769.42	16
13	T	690.84	740.89	15
14	P	739.36	690.37	14
15	A	774.88	641.84	13
16	V	823.41	606.32	12
17	A	866.93	567.80	11
18	Q	922.96	522.28	10
19	P	973.48	456.25	9
20	P	1022.01	407.72	8
21	A	1057.53	359.20	7
22	P	1106.05	323.68	6
23	S	1149.57	276.15	5
24	V	1199.10	231.64	4
25	S	1242.62	182.10	3
26	T	1293.14	136.59	2
27	R	-	68.06	1

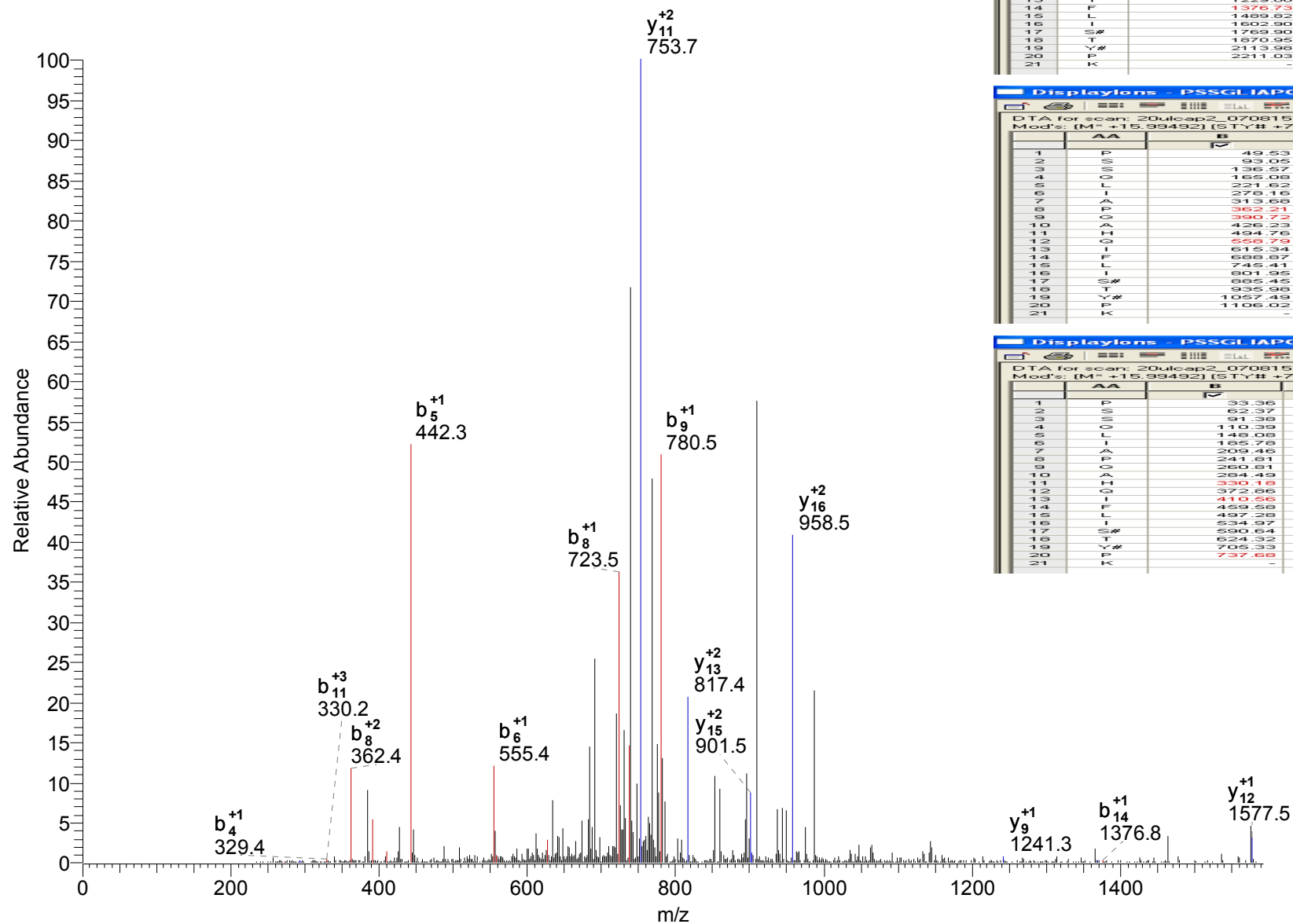
Displays - VPSQARPP TPAP TPAPQ TPAPS

DTA for scan: cap. 2358
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	V	34.03	-	27
2	P	66.38	687.44	26
3	S#	122.05	655.09	25
4	Q	164.73	799.43	24
5	A	186.41	756.74	23
6	R	240.45	733.06	22
7	P	272.80	681.03	21
8	P	306.15	646.68	20
9	T	338.83	616.33	19
10	P	371.18	582.64	18
11	A	394.86	550.29	17
12	P	427.21	526.61	16
13	T	460.69	494.26	15
14	P	493.24	460.66	14
15	A	516.92	428.23	13
16	V	549.27	404.55	12
17	A	572.85	372.80	11
18	Q	615.64	348.52	10
19	T	649.32	305.83	9
20	P	681.67	272.15	8
21	A	705.35	239.80	7
22	P	737.70	216.12	6
23	S	766.71	183.77	5
24	V	799.74	154.76	4
25	S	829.75	121.74	3
26	T	862.43	92.73	2
27	R	-	59.04	1

209 kDa protein

#2830-2830 NL: 4.00E3



Displaylens - PSSGLIAPGAHQIFLISTYPK

DTA for scan: 20ulcap2_070815194055_2830
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	P	98.06	-	21
2	S	185.09	2260.08	20
3	S	272.12	2173.05	19
4	G	329.15	2086.02	18
5	L	442.23	2029.00	17
6	I	666.31	1915.91	16
7	A	626.35	1802.83	15
8	P	723.40	1731.79	14
9	G	760.43	1634.74	13
10	A	851.46	1577.72	12
11	H	989.52	1506.68	11
12	G	1116.58	1369.62	10
13	I	1229.66	1241.56	9
14	F	1376.73	1126.48	8
15	L	1489.82	981.41	7
16	I	1602.90	868.33	6
17	S#	1769.90	755.24	5
18	T	1870.95	588.24	4
19	Y#	2113.98	487.20	3
20	P	2211.03	244.17	2
21	K	-	147.11	1

Displaylens - PSSGLIAPGAHQIFLISTYPK

DTA for scan: 20ulcap2_070815194055_2830
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	P	49.53	-	21
2	S	93.05	1130.54	20
3	S	136.57	1087.03	19
4	G	165.08	1043.51	18
5	L	221.62	1015.00	17
6	I	276.15	958.48	16
7	A	313.68	901.92	15
8	P	362.21	866.40	14
9	G	390.72	817.87	13
10	A	426.23	789.35	12
11	H	494.76	753.84	11
12	G	558.79	685.31	10
13	I	615.34	621.28	9
14	F	688.87	564.74	8
15	L	745.41	491.21	7
16	I	801.95	434.67	6
17	S#	885.45	376.12	5
18	T	935.98	294.63	4
19	Y#	1057.49	244.10	3
20	P	1156.02	122.58	2
21	K	-	74.06	1

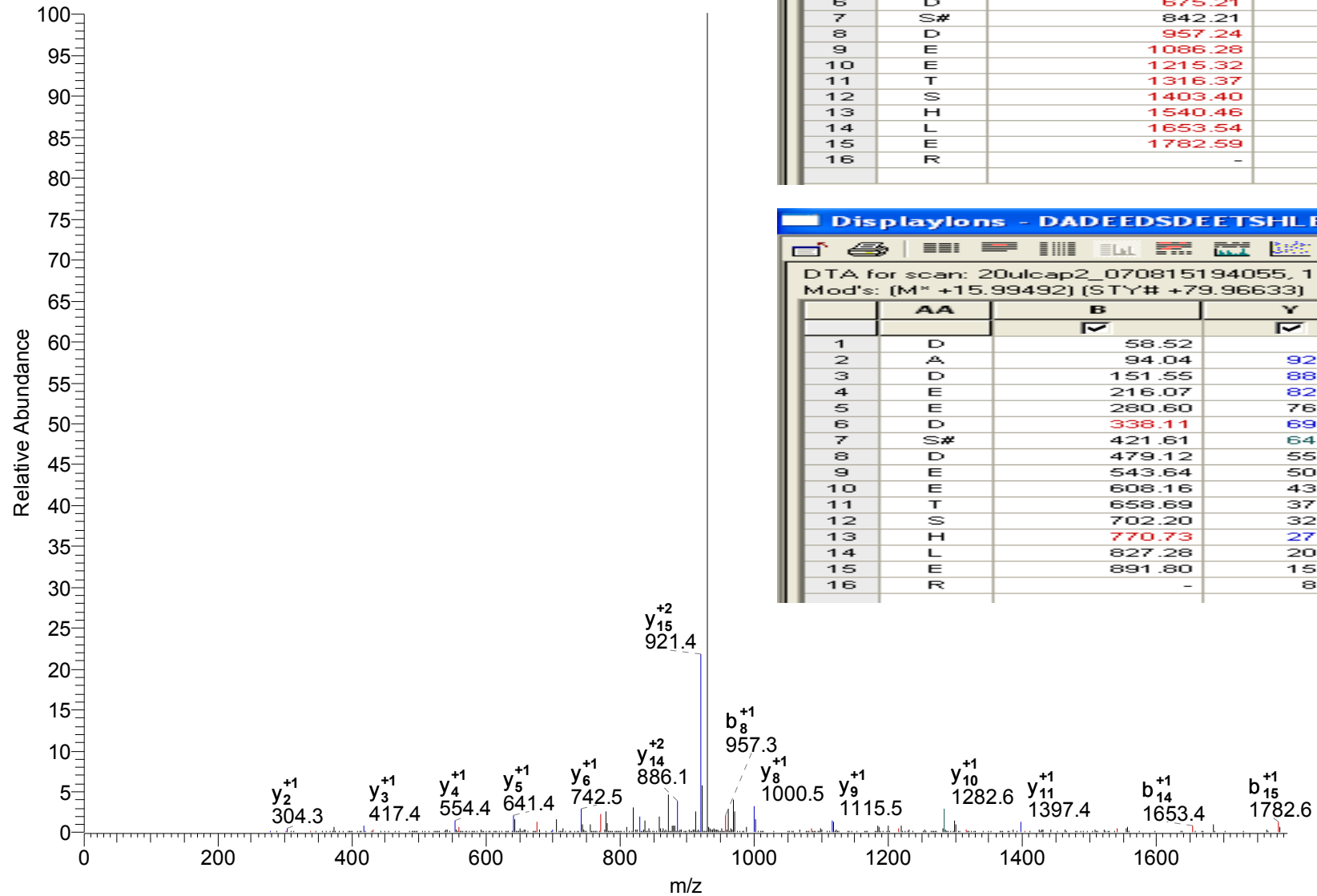
Displaylens - PSSGLIAPGAHQIFLISTYPK

DTA for scan: 20ulcap2_070815194055_2830
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	P	33.36	-	21
2	S	62.37	754.03	20
3	S	91.38	725.02	19
4	G	110.39	696.01	18
5	L	148.08	677.00	17
6	I	165.78	639.31	16
7	A	209.46	601.61	15
8	P	241.81	577.94	14
9	G	260.81	545.58	13
10	A	284.49	526.58	12
11	H	330.18	502.90	11
12	G	372.86	457.21	10
13	I	410.56	414.53	9
14	F	459.58	376.83	8
15	L	497.28	327.81	7
16	I	534.97	290.11	6
17	S#	590.64	262.42	5
18	T	624.32	196.75	4
19	Y#	705.33	163.07	3
20	P	737.68	82.06	2
21	K	-	49.71	1

Similar to Protein C6orf203

#1915-1915 NL: 9.11E3



Displaylons - DADEEDSDEETSHLER

DTA for scan: 20ulcap2_070815194055, 1915
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y
1	D	116.03	-
2	A	187.07	1841.67
3	D	302.10	1770.63
4	E	431.14	1655.61
5	E	560.18	1526.56
6	D	675.21	1397.52
7	S#	842.21	1282.49
8	D	957.24	1115.50
9	E	1086.28	1000.47
10	E	1215.32	871.43
11	T	1316.37	742.38
12	S	1403.40	641.34
13	H	1540.46	554.30
14	L	1653.54	417.25
15	E	1782.59	304.16
16	R	-	175.12

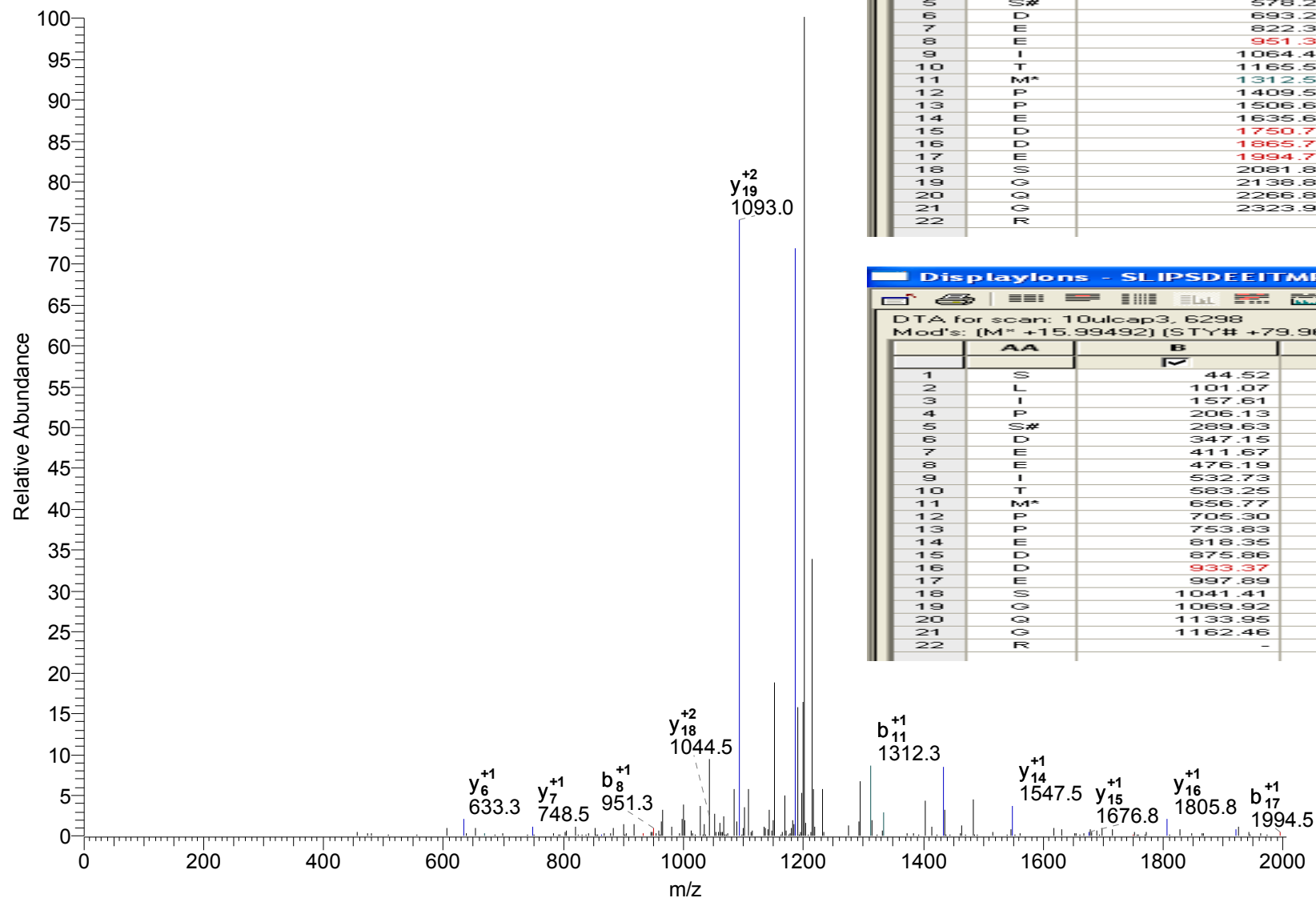
Displaylons - DADEEDSDEETSHLER

DTA for scan: 20ulcap2_070815194055, 1915
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	D	58.52	-	16
2	A	94.04	921.34	15
3	D	151.55	885.82	14
4	E	216.07	828.31	13
5	E	280.60	763.79	12
6	D	338.11	699.26	11
7	S#	421.61	641.75	10
8	D	479.12	558.25	9
9	E	543.64	500.74	8
10	E	608.16	436.22	7
11	T	658.69	371.70	6
12	S	702.20	321.17	5
13	H	770.73	277.66	4
14	L	827.28	209.13	3
15	E	891.80	152.58	2
16	R	-	88.06	1

Dnah8 similar to dynein, axonemal, heavy chain 8

#6298-6298 NL: 6.16E2



Displaylons - SLIPSDEEITMPPEDESQGR

DTA for scan: 10ulcap3, 6298
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y
1	S	88.04	-
2	L	201.12	2411.00
3	I	314.21	2297.91
4	P	411.26	2184.83
5	S#	578.26	2087.77
6	D	693.29	1920.78
7	E	822.33	1805.75
8	E	951.37	1676.71
9	I	1064.45	1547.66
10	T	1165.50	1434.58
11	M*	1312.54	1333.53
12	P	1409.59	1186.50
13	P	1506.64	1089.44
14	E	1635.69	992.39
15	D	1750.71	863.35
16	D	1865.74	748.32
17	E	1994.78	633.30
18	S	2081.81	504.25
19	Q	2138.84	417.22
20	Q	2266.89	360.20
21	Q	2323.92	232.14
22	R	-	175.12

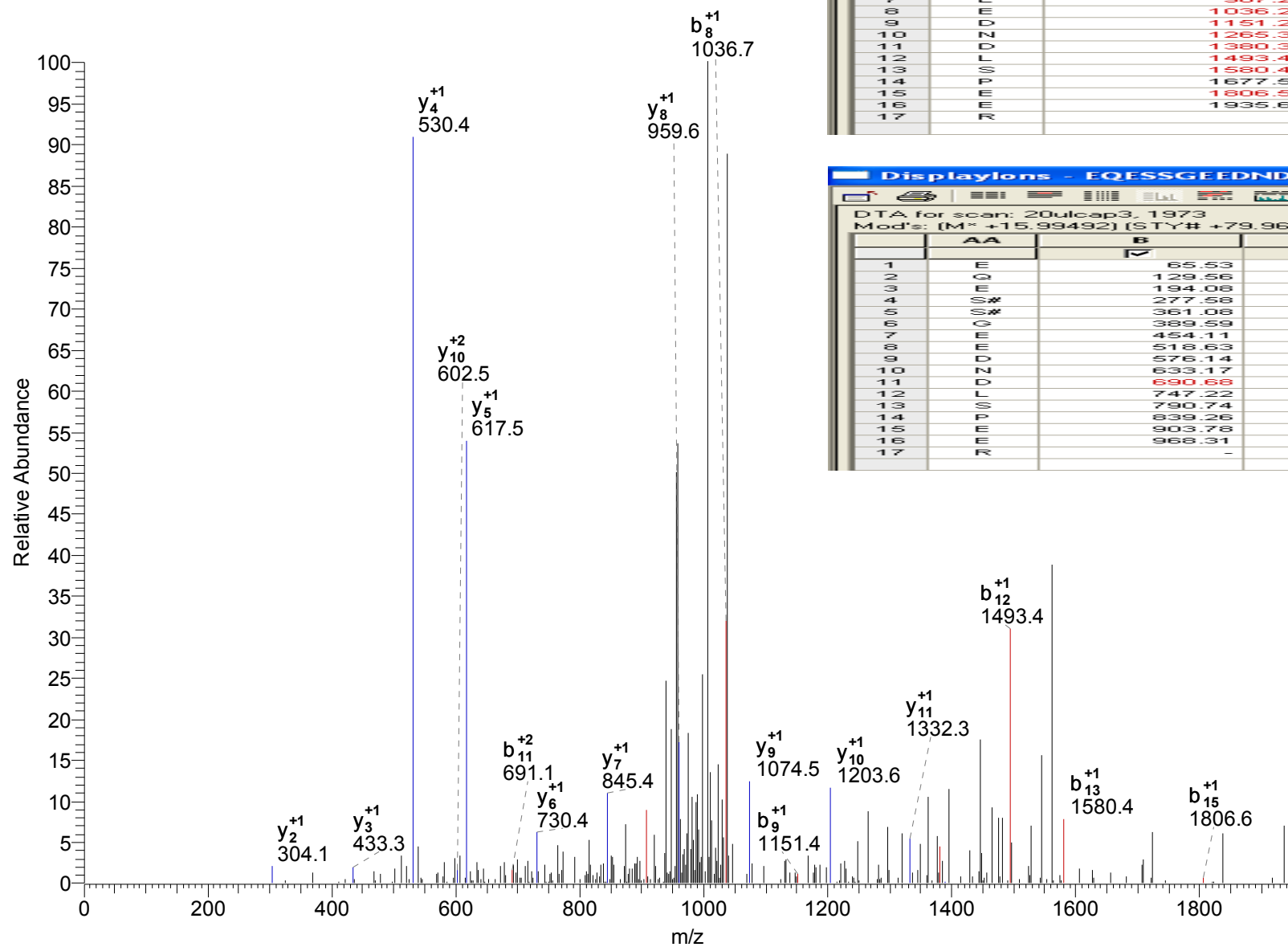
Displaylons - SLIPSDEEITMPPEDESQGR

DTA for scan: 10ulcap3, 6298
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	44.52	-	22
2	L	101.07	1206.00	21
3	I	157.61	1149.46	20
4	P	206.13	1092.92	19
5	S#	289.63	1044.39	18
6	D	347.15	960.89	17
7	E	411.67	903.38	16
8	E	476.19	838.86	15
9	I	532.73	774.34	14
10	T	583.25	717.79	13
11	M*	656.77	667.27	12
12	P	705.30	593.75	11
13	P	753.83	545.23	10
14	E	818.35	496.70	9
15	D	875.86	432.18	8
16	D	933.37	374.66	7
17	E	997.89	317.15	6
18	S	1041.41	252.63	5
19	Q	1069.92	209.11	4
20	Q	1133.95	180.60	3
21	Q	1162.46	116.57	2
22	R	-	88.06	1

Ppp1r2 Protein phosphatase inhibitor 2

#1973-1973 NL: 2.82E2

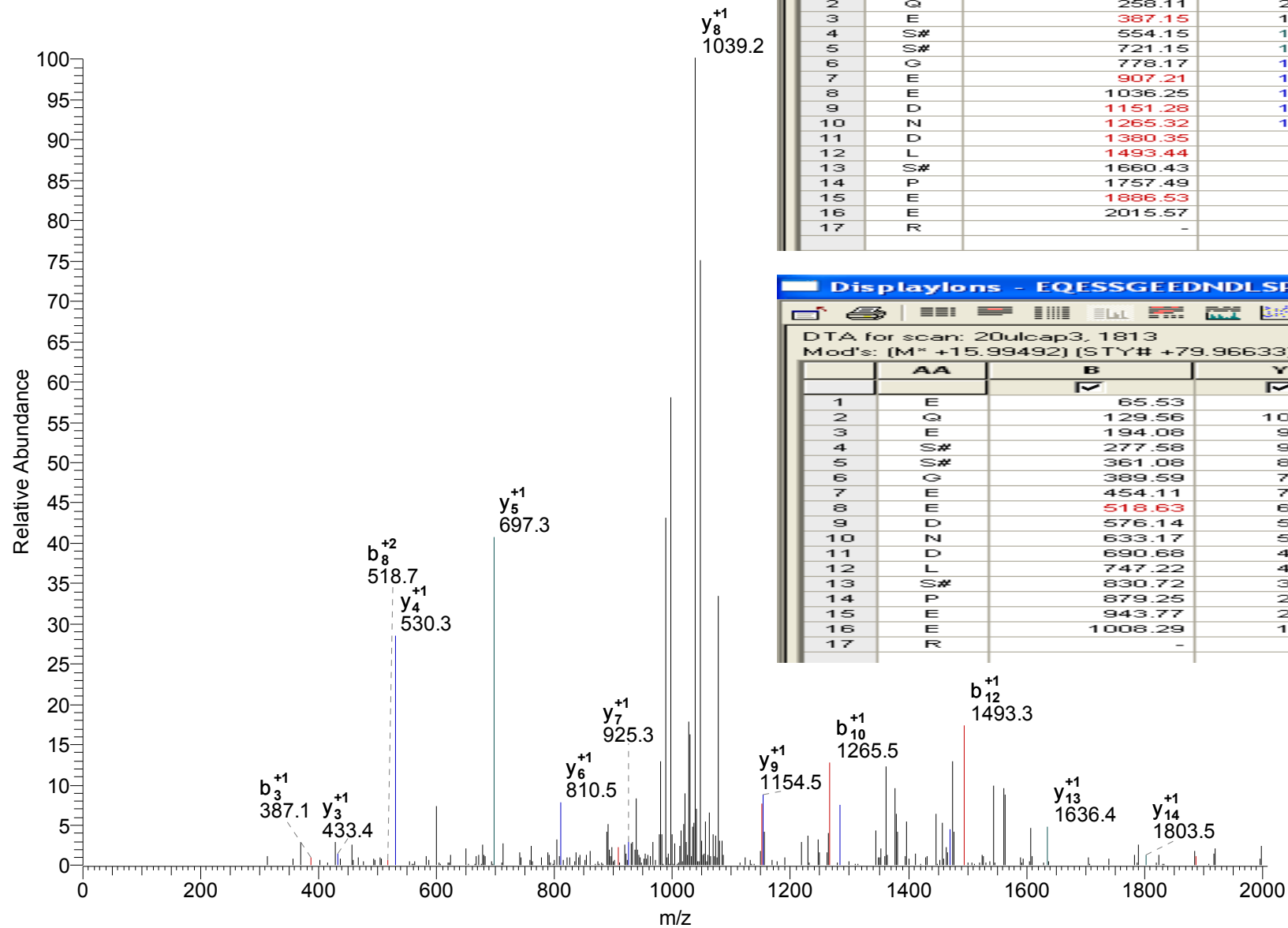


Displays - EQSSGEEDNDLSPEER			
DTA for scan: 20ulcap3, 1973			
Mod's: [M*+15.99492] [STY# +79.96633]			
	AA	B	Y
1	E	130.05	
2	Q	258.11	1980.6
3	E	387.15	1852.6
4	S#	554.15	1723.5
5	S#	721.15	1556.5
6	Q	778.17	1389.5
7	E	907.21	1332.5
8	E	1036.25	1203.5
9	D	1151.28	1074.4
10	D	1265.32	959.4
11	D	1380.35	845.4
12	L	1493.44	730.3
13	S	1580.47	617.2
14	P	1677.52	530.2
15	E	1806.56	433.2
16	E	1935.61	304.1
17	R	-	175.1

Displays - EQESSGEEDNDLSPEER				
DTA for scan: 20ulcap3, 1973				
Mod's: [M* +15.99492] (STY# +79.96633)				
	AA	B	Y	
1	E	65.53	-	17
2	Q	129.56	990.84	16
3	E	194.08	926.81	15
4	S#	277.58	862.29	14
5	S#	351.08	778.79	13
6	Q	389.59	695.29	12
7	E	454.11	666.78	11
8	E	518.63	602.26	10
9	D	576.14	537.74	9
10	N	633.17	480.23	8
11	D	690.68	423.20	7
12	L	747.22	365.69	6
13	S	790.74	309.15	5
14	P	839.26	265.63	4
15	E	903.78	217.11	3
16	E	968.31	152.58	2
17	R	-	88.06	1

Ppp1r2 Protein phosphatase inhibitor 2

#1813-1813 NL: 4.53E2



Displaylons - EQESSGEEDNDLSPEER

DTA for scan: 20ulcap3, 1813
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	E	130.05	-	17
2	Q	258.11	2060.64	16
3	E	387.15	1932.58	15
4	S#	554.15	1803.54	14
5	S#	721.15	1636.54	13
6	G	778.17	1469.54	12
7	E	907.21	1412.52	11
8	E	1036.25	1283.48	10
9	D	1151.28	1154.44	9
10	N	1265.32	1039.41	8
11	D	1380.35	925.37	7
12	L	1493.44	810.34	6
13	S#	1660.43	697.26	5
14	P	1757.49	530.26	4
15	E	1886.53	433.20	3
16	E	2015.57	304.16	2
17	R	-	175.12	1

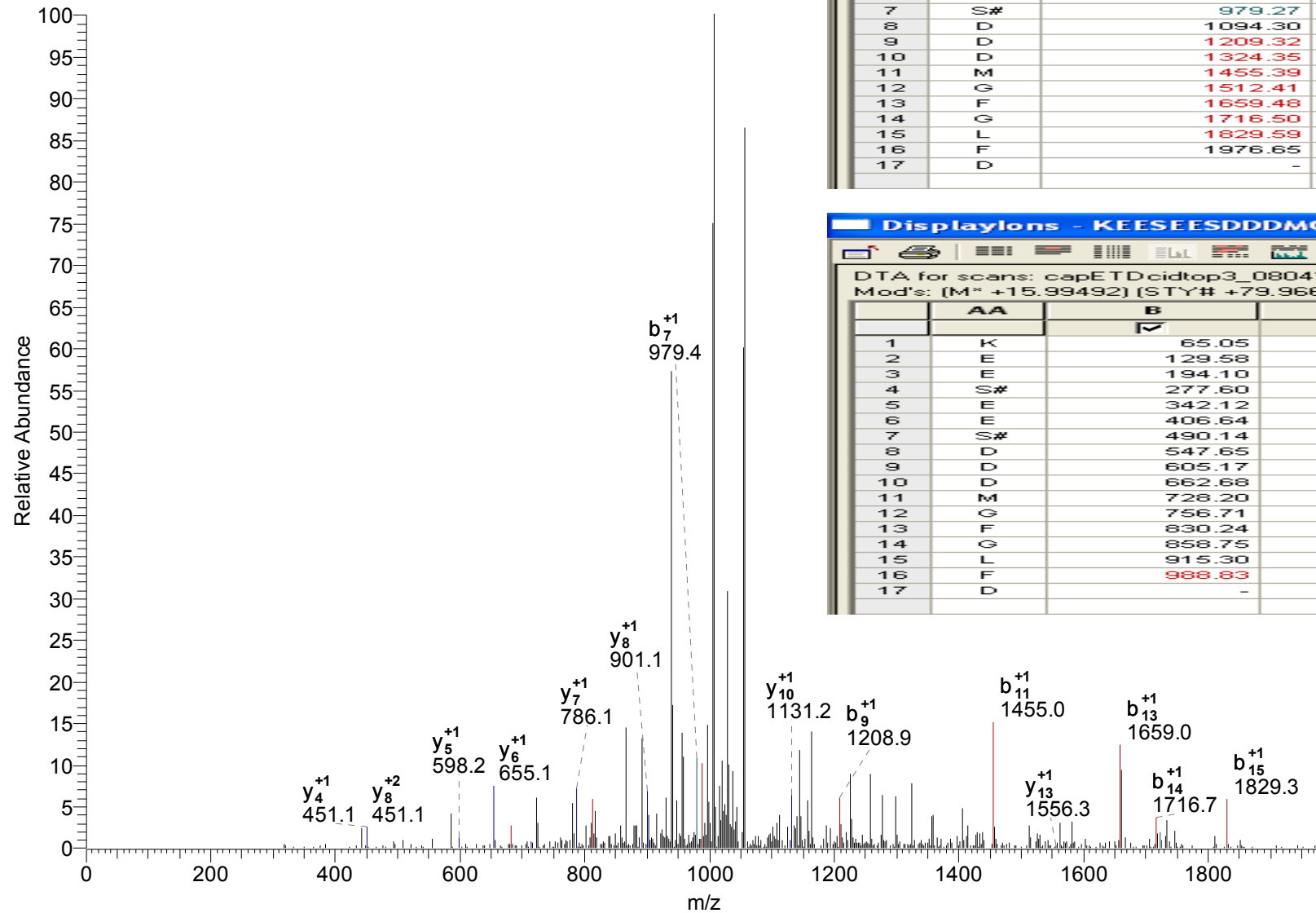
Displaylons - EQESSGEEDNDLSPEER

DTA for scan: 20ulcap3, 1813
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y	
1	E	65.53	-	17
2	Q	129.56	1030.82	16
3	E	194.08	966.79	15
4	S#	277.58	902.27	14
5	S#	361.08	818.77	13
6	G	389.59	735.28	12
7	E	454.11	706.76	11
8	E	518.63	642.24	10
9	D	576.14	577.72	9
10	N	633.17	520.21	8
11	D	690.68	463.19	7
12	L	747.22	405.67	6
13	S#	830.72	349.13	5
14	P	879.25	265.63	4
15	E	943.77	217.11	3
16	E	1008.29	152.58	2
17	R	-	88.06	1

Rplp2 60S acidic ribosomal protein P2

#2888-2889 NL: 6.76E2



Displaylons - KEESEESDDDMGFGLFD

DTA for scans: capETDcidtop3_080419044303, 2888-
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y
1	K	129.10	-
2	E	258.14	1981.60
3	E	387.19	1852.55
4	S#	554.19	1723.51
5	E	683.23	1556.51
6	E	812.27	1427.47
7	S#	979.27	1298.43
8	D	1094.30	1131.43
9	D	1209.32	1016.40
10	D	1324.35	901.38
11	M	1455.39	786.35
12	G	1512.41	655.31
13	F	1659.48	598.29
14	G	1716.50	451.22
15	L	1829.59	394.20
16	F	1976.65	281.11
17	D	-	134.04

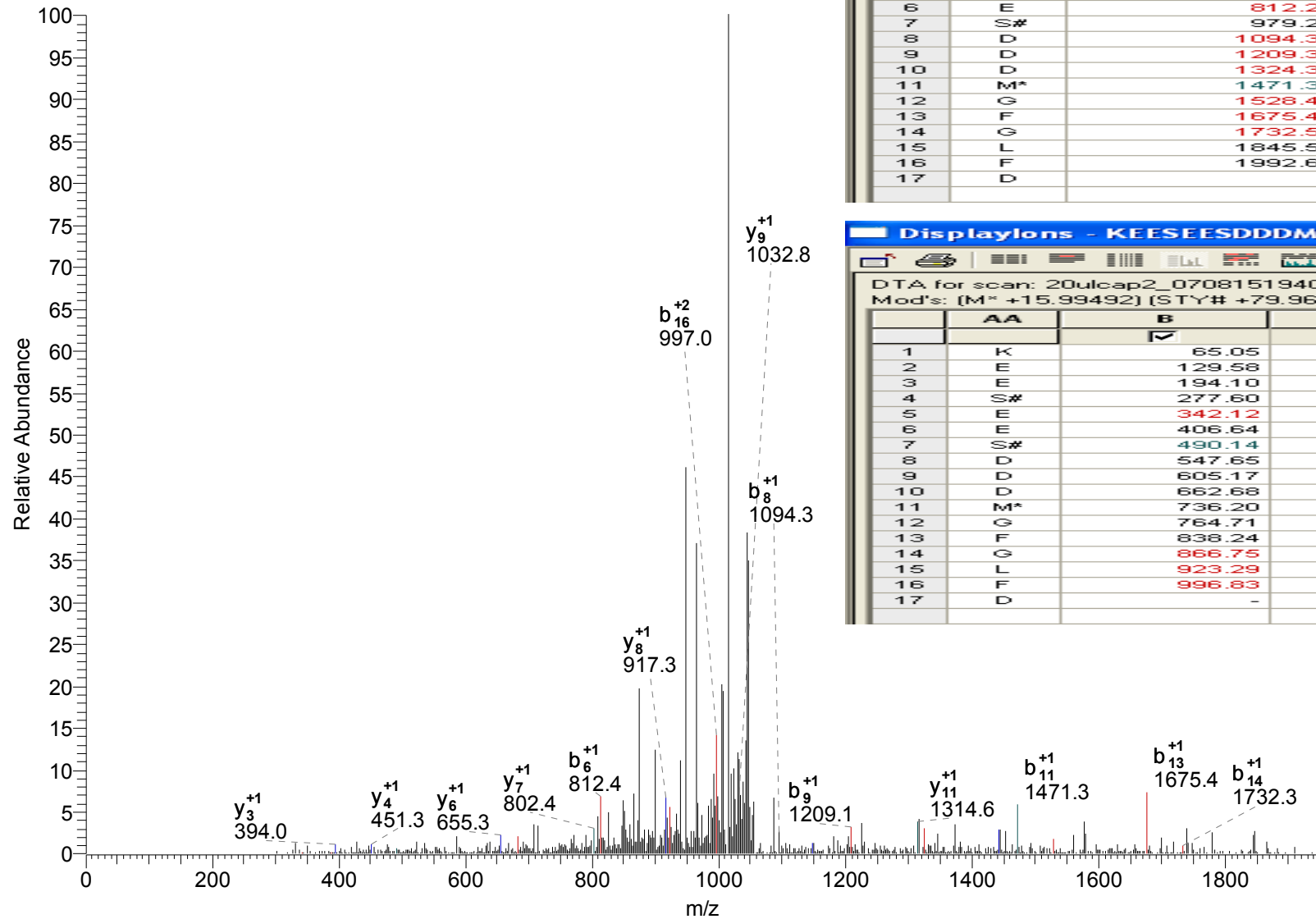
Displaylons - KEESEESDDDMGFGLFD

DTA for scans: capETDcidtop3_080419044303, 2888-
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y
1	K	65.05	-
2	E	129.58	991.30
3	E	194.10	926.78
4	S#	277.60	862.26
5	E	342.12	778.76
6	E	406.64	714.24
7	S#	490.14	649.72
8	D	547.65	566.22
9	D	605.17	508.71
10	D	662.68	451.19
11	M	728.20	393.68
12	G	756.71	328.16
13	F	830.24	299.65
14	G	858.75	226.11
15	L	915.30	197.60
16	F	988.83	141.06
17	D	-	67.53

Rplp2 60S acidic ribosomal protein P2

#3132-3132 NL: 1.74E3



Displaylons - KEESEESDDDMGFGLFD

DTA for scan: 20ulcap2_070815194055, 3132
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y
1	K	129.10	
2	E	258.14	1997.5
3	E	387.19	1868.5
4	S#	554.19	1739.5
5	E	683.23	1572.5
6	E	812.27	1443.4
7	S#	979.27	1314.4
8	D	1094.30	1147.4
9	D	1209.32	1032.4
10	D	1324.35	917.3
11	M*	1471.39	802.3
12	G	1528.41	655.3
13	F	1675.48	598.2
14	G	1732.50	451.2
15	L	1845.58	394.2
16	F	1992.65	281.1
17	D	-	134.0

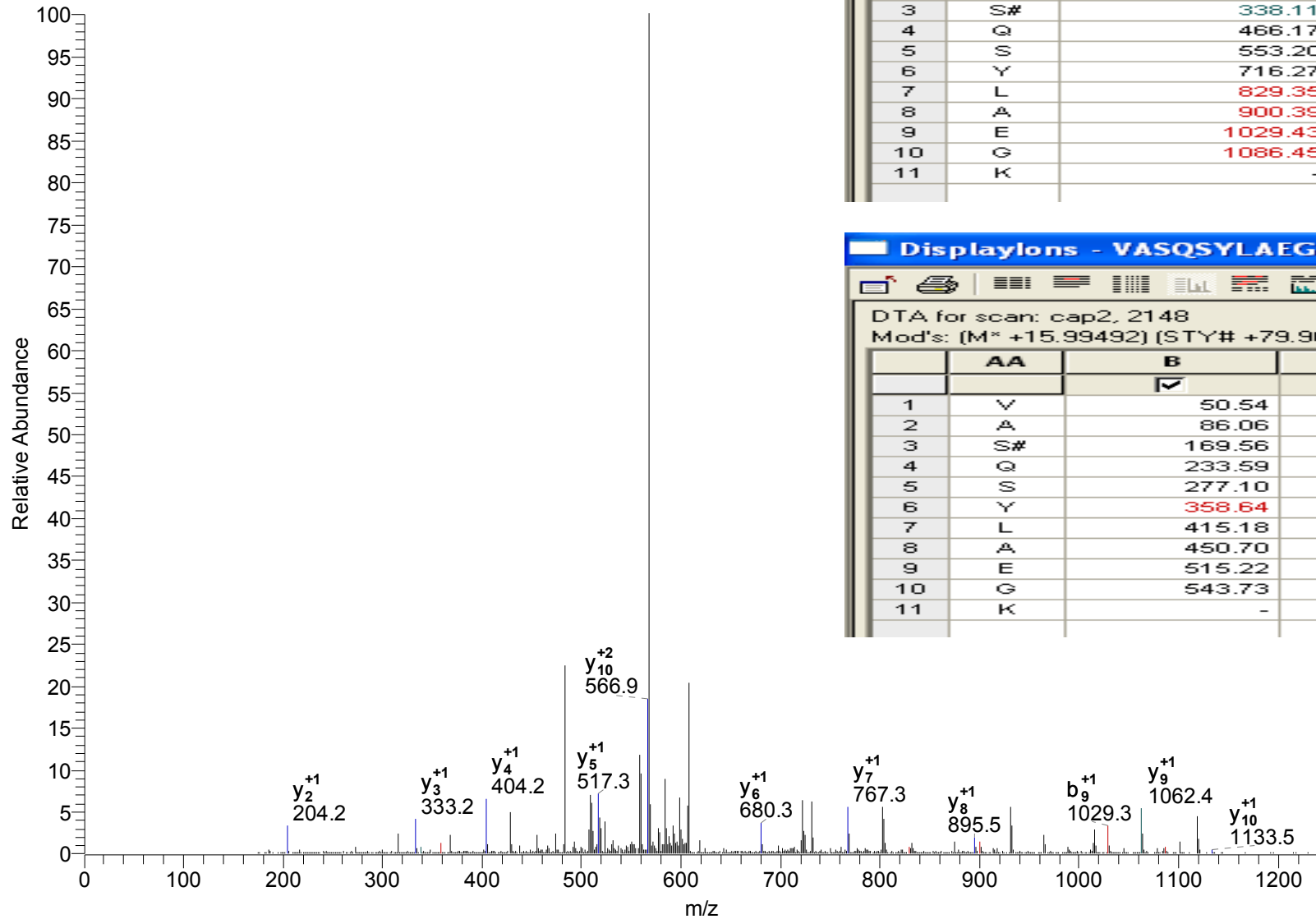
Displaylons - KEESEESDDDMGFGLFD

DTA for scan: 20ulcap2_070815194055, 3132
Mod's: [M* +15.99492] [STY# +79.96633]

	AA	B	Y
1	K	65.05	-
2	E	129.58	999.30
3	E	194.10	934.78
4	S#	277.60	870.26
5	E	342.12	786.76
6	E	406.64	722.24
7	S#	490.14	657.72
8	D	547.65	574.22
9	D	605.17	516.70
10	D	662.68	459.19
11	M*	736.20	401.68
12	G	764.71	328.16
13	F	838.24	299.65
14	G	866.75	226.11
15	L	923.29	197.60
16	F	996.83	141.06
17	D	-	67.53

116 kDa protein

#2148-2148 NL: 2.41E4



Displaylons - VASQSYLAEGK

DTA for scan: cap2, 2148
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y
		☒	☒
1	V	100.08	-
2	A	171.11	1133.49
3	S#	338.11	1062.45
4	Q	466.17	895.45
5	S	553.20	767.39
6	Y	716.27	680.36
7	L	829.35	517.30
8	A	900.39	404.21
9	E	1029.43	333.18
10	G	1086.45	204.13
11	K	-	147.11

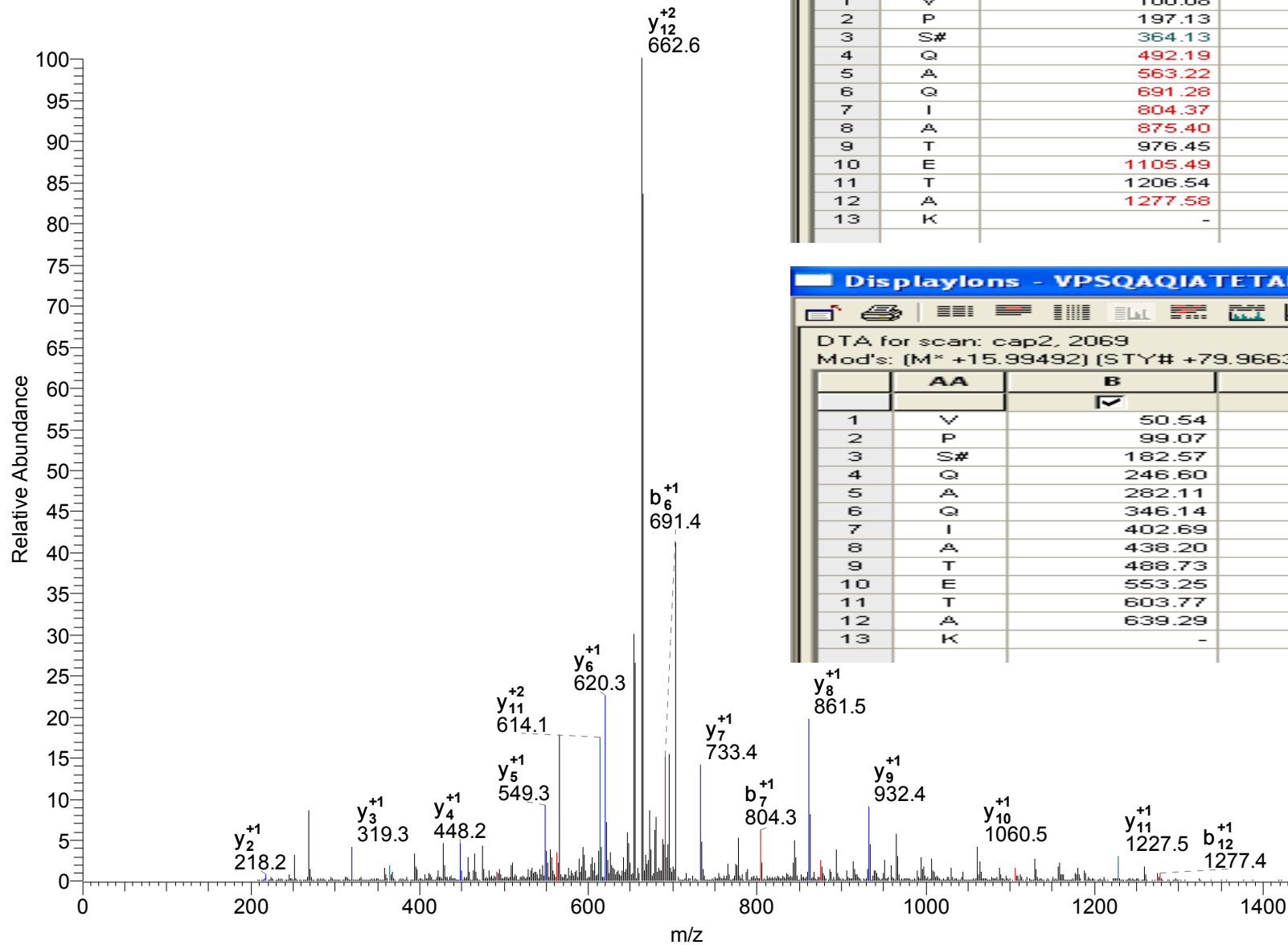
Displaylons - VASQSYLAEGK

DTA for scan: cap2, 2148
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
		☒	☒	
1	V	50.54	-	11
2	A	86.06	567.25	10
3	S#	169.56	531.73	9
4	Q	233.59	448.23	8
5	S	277.10	384.20	7
6	Y	358.64	340.68	6
7	L	415.18	259.15	5
8	A	450.70	202.61	4
9	E	515.22	167.09	3
10	G	543.73	102.57	2
11	K	-	74.06	1

116 kDa protein

#2069-2069 NL: 2.98E4



Displaylons - VPSQAQIATETAK

DTA for scan: cap2, 2069
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	V	100.08	-	13
2	P	197.13	1324.61	12
3	S#	364.13	1227.56	11
4	Q	492.19	1060.56	10
5	A	563.22	932.50	9
6	Q	691.28	861.47	8
7	I	804.37	733.41	7
8	A	875.40	620.32	6
9	T	976.45	549.29	5
10	E	1105.49	448.24	4
11	T	1206.54	319.20	3
12	A	1277.58	218.15	2
13	K	-	147.11	1

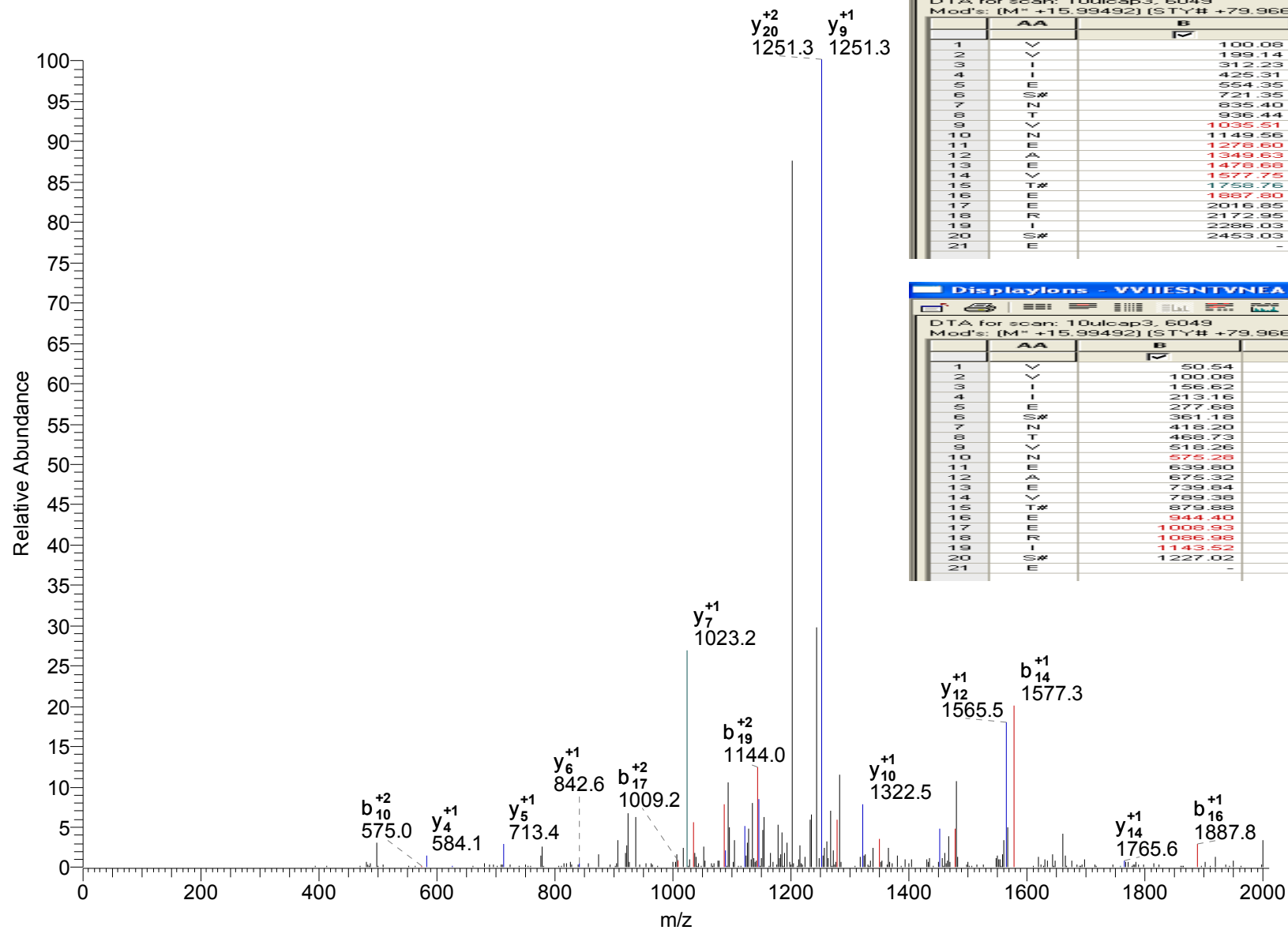
Displaylons - VPSQAQIATETAK

DTA for scan: cap2, 2069
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	V	50.54	-	13
2	P	99.07	662.81	12
3	S#	182.57	614.28	11
4	Q	246.60	530.79	10
5	A	282.11	466.76	9
6	Q	346.14	431.24	8
7	I	402.69	367.21	7
8	A	438.20	310.67	6
9	T	488.73	275.15	5
10	E	553.25	224.62	4
11	T	603.77	160.10	3
12	A	639.29	109.58	2
13	K	-	74.06	1

Acrosome formation-associated factor precursor

#6049-6049 NL: 4.43E2



Displaylons - VVIESNTVNEAEVTEERISE

DTA for scan: 10ulcap3, 6049
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y
1	V	100.08	-
2	V	199.14	2501.01
3	I	312.23	2401.94
4	I	425.31	2288.86
5	E	554.35	2175.78
6	S#	721.35	2046.73
7	N	835.40	1879.74
8	T	936.44	1765.69
9	V	1035.51	1664.65
10	N	1149.56	1565.58
11	E	1278.60	1451.53
12	A	1349.63	1322.49
13	E	1478.68	1251.45
14	V	1577.75	1122.41
15	T#	1758.76	1023.34
16	E	1887.80	842.33
17	E	2016.85	713.29
18	R	2172.95	584.24
19	I	2286.03	428.14
20	S#	2453.03	315.06
21	E	-	148.06

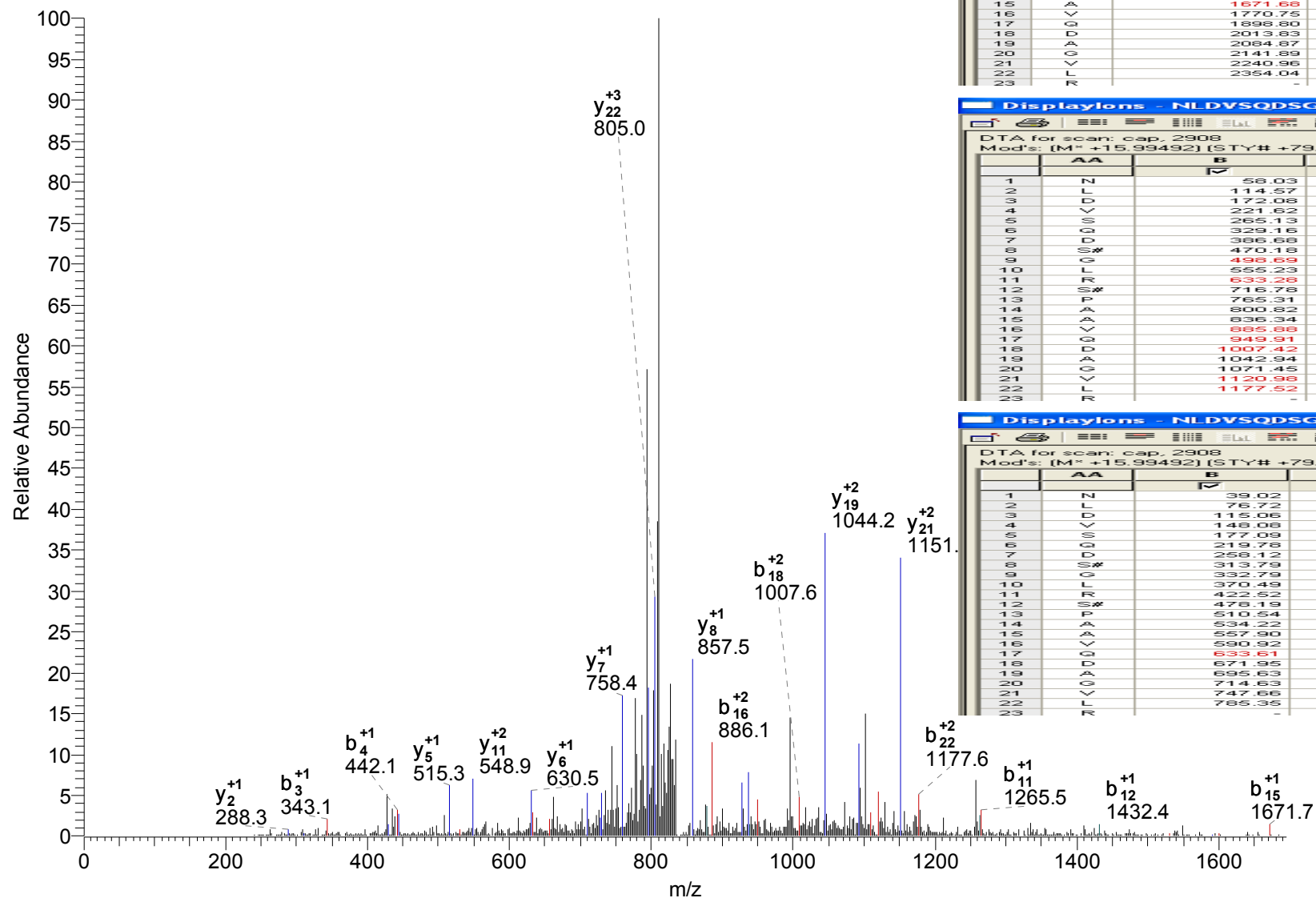
Displaylons - VVIESNTVNEAEVTEERISE

DTA for scan: 10ulcap3, 6049
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	V	50.54	-	21
2	V	100.08	1251.01	20
3	I	156.62	1201.48	19
4	I	213.16	1144.93	18
5	E	277.68	1088.39	17
6	S#	361.18	1023.87	16
7	N	418.20	940.37	15
8	T	468.73	883.35	14
9	V	518.26	832.83	13
10	N	575.28	783.29	12
11	E	639.80	726.27	11
12	A	675.32	661.75	10
13	E	739.84	626.23	9
14	V	789.38	561.71	8
15	T#	879.88	512.18	7
16	E	944.40	421.67	6
17	E	1008.93	357.15	5
18	R	1086.96	292.63	4
19	I	1143.52	214.58	3
20	S#	1227.02	158.03	2
21	E	-	74.53	1

predicted hypothetical protein

#2908-2908 NL: 4.82E3



Displaylens - NLDVSDSGLRSPAAYQDAGVLR

DTA for scan: cap. 2908
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	115.05	-	23
2	L	228.13	2414.11	22
3	D	343.16	2301.03	21
4	V	442.23	2186.00	20
5	S	529.26	2086.93	19
6	Q	657.32	1999.90	18
7	D	772.35	1871.84	17
8	S#	857.35	1756.81	16
9	G	986.37	1589.82	15
10	L	1109.45	1532.79	14
11	R	1265.55	1419.71	13
12	S#	1432.55	1263.61	12
13	P	1529.60	1096.61	11
14	A	1600.64	999.56	10
15	A	1671.68	928.52	9
16	V	1770.75	857.48	8
17	D	1898.80	758.42	7
18	D	2013.83	630.36	6
19	A	2084.87	515.33	5
20	G	2141.89	444.29	4
21	V	2240.96	387.27	3
22	L	2354.04	288.20	2
23	R	-	175.12	1

Displaylens - NLDVSDSGLRSPAAYQDAG

DTA for scan: cap. 2908
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	58.03	-	23
2	L	114.57	1207.56	22
3	D	172.08	1151.02	21
4	V	221.62	1093.50	20
5	S	265.13	1043.97	19
6	Q	329.16	1000.45	18
7	D	386.68	936.42	17
8	S#	470.18	875.91	16
9	G	498.69	795.41	15
10	L	555.23	766.90	14
11	R	633.28	710.36	13
12	S#	716.78	632.31	12
13	P	765.31	548.81	11
14	A	800.82	500.28	10
15	A	836.34	464.76	9
16	V	886.88	429.25	8
17	Q	949.31	379.71	7
18	D	1007.42	315.68	6
19	A	1042.94	258.17	5
20	G	1071.45	222.65	4
21	V	1120.98	194.14	3
22	L	1177.52	144.61	2
23	R	-	88.06	1

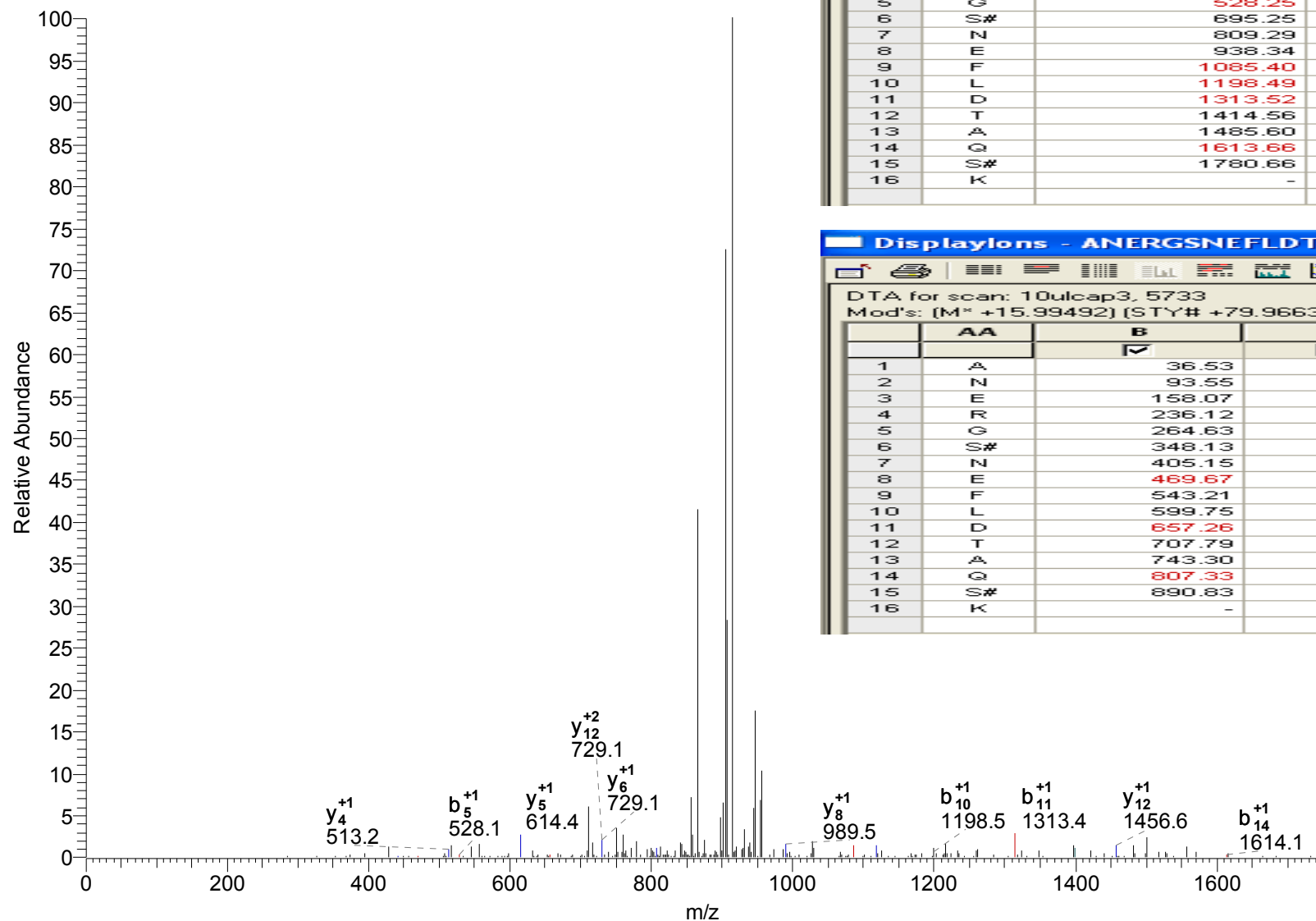
Displaylens - NLDVSDSGLRSPAAYQDAG

DTA for scan: cap. 2908
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	N	39.02	-	23
2	L	76.72	805.38	22
3	D	115.05	767.68	21
4	V	148.08	729.34	20
5	S	177.09	696.32	19
6	Q	219.78	667.30	18
7	D	258.12	624.62	17
8	S#	313.79	586.28	16
9	G	332.79	530.61	15
10	L	370.49	511.60	14
11	R	422.52	473.91	13
12	S#	478.19	421.67	12
13	P	510.54	366.21	11
14	A	534.22	333.86	10
15	A	557.90	310.18	9
16	V	590.92	286.50	8
17	Q	633.61	253.48	7
18	D	671.95	210.79	6
19	A	695.63	172.45	5
20	G	714.63	146.77	4
21	V	747.66	129.76	3
22	L	785.35	96.74	2
23	R	-	59.04	1

Isoform 1 of Thioredoxin domain-containing protein 2

#5733-5733 NL: 8.44E2



Displaylons - ANERGSNEFLDTAQSK

DTA for scan: 10ulcap3, 5733
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y
1	A	72.04	-
2	N	186.09	1855.73
3	E	315.13	1741.68
4	R	471.23	1612.64
5	G	528.25	1456.54
6	S#	695.25	1399.52
7	N	809.29	1232.52
8	E	938.34	1118.48
9	F	1085.40	989.43
10	L	1198.49	842.37
11	D	1313.52	729.28
12	T	1414.56	614.25
13	A	1485.60	513.21
14	Q	1613.66	442.17
15	S#	1780.66	314.11
16	K	-	147.11

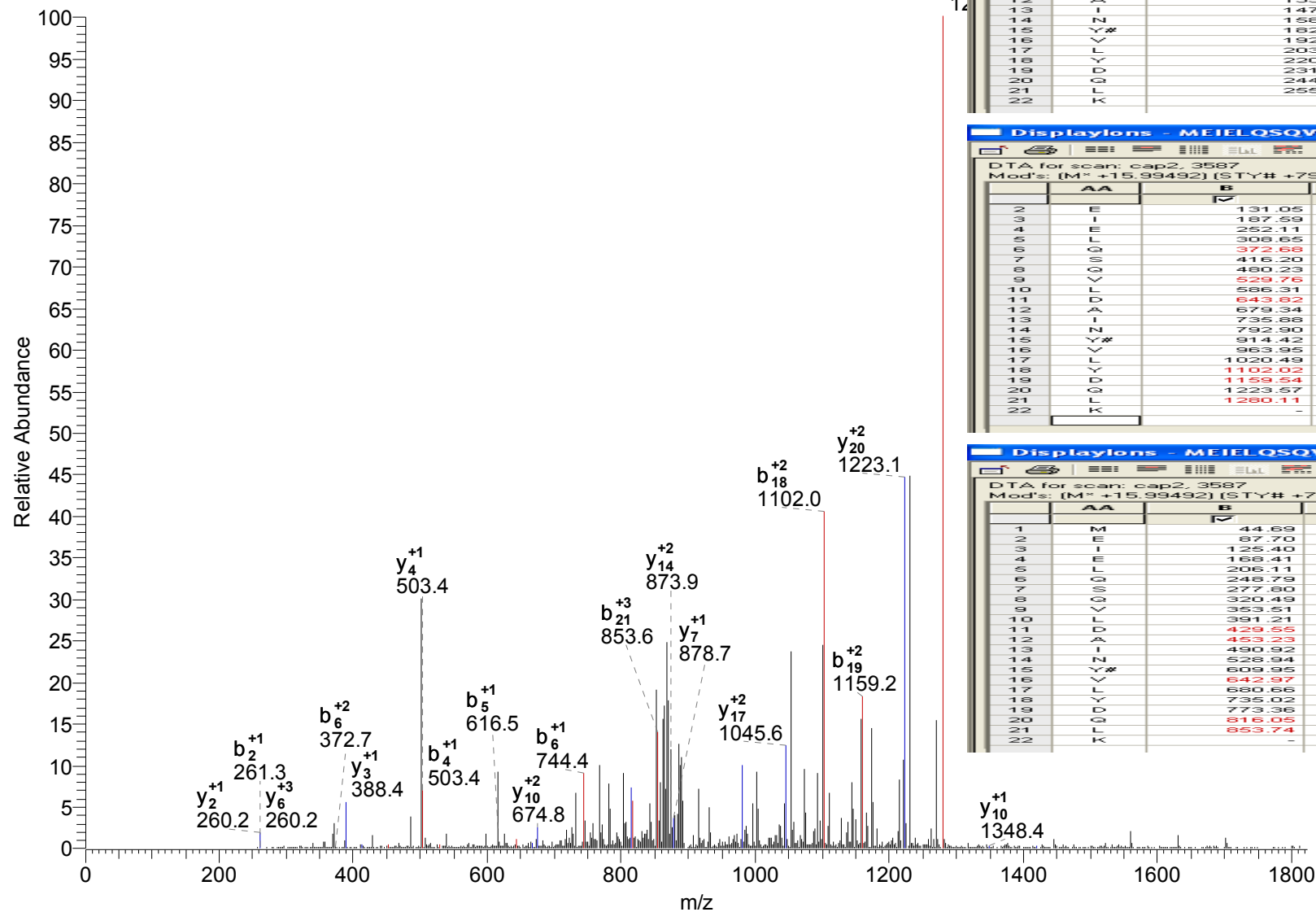
Displaylons - ANERGSNEFLDTAQSK

DTA for scan: 10ulcap3, 5733
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	A	36.53	-	16
2	N	93.55	928.37	15
3	E	158.07	871.35	14
4	R	236.12	806.82	13
5	G	264.63	728.77	12
6	S#	348.13	700.26	11
7	N	405.15	616.76	10
8	E	469.67	559.74	9
9	F	543.21	495.22	8
10	L	599.75	421.69	7
11	D	657.26	365.14	6
12	T	707.79	307.63	5
13	A	743.30	257.11	4
14	Q	807.33	221.59	3
15	S#	890.83	157.56	2
16	K	-	74.06	1

Fbxo21_predicted similar to F-box only protein 21

#3587-3587 NL: 1.93E4



Displaylons - MEIEIQQVQLDAINYVLYDQI

DTA for scan: cap2, 3587
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y
1	M	132.05	
2	E	261.09	2574.2
3	I	374.17	2445.2
4	E	503.22	2332.1
5	L	616.30	2203.1
6	Q	744.36	2090.0
7	S	831.39	1961.9
8	Q	959.45	1874.9
9	V	1058.52	1746.8
10	L	1171.60	1647.8
11	D	1286.63	1534.7
12	A	1357.67	1419.6
13	I	1470.75	1348.6
14	N	1584.79	1235.5
15	Y#	1627.82	1121.5
16	V	1926.89	878.5
17	L	2039.98	779.4
18	Y	2203.04	666.3
19	D	2318.07	503.2
20	Q	2446.12	388.2
21	L	2559.21	260.2
22	K	-	147.1

Displaylons - MEIEIQQVQLDAINYVLYDQIK

DTA for scan: cap2, 3587
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y
2	E	131.05	1287.64
3	I	187.59	1223.12
4	E	252.11	1186.58
5	L	308.65	1102.06
6	Q	372.68	1045.51
7	S	416.20	981.48
8	Q	480.23	937.97
9	V	529.76	873.94
10	L	586.31	824.41
11	D	643.82	767.86
12	A	679.34	710.35
13	I	735.88	674.83
14	N	792.90	618.29
15	Y#	914.42	581.27
16	V	963.95	439.75
17	L	1020.49	390.22
18	Y	1102.02	333.68
19	D	1159.54	252.14
20	Q	1223.57	194.63
21	L	1280.11	130.60
22	K	-	74.06

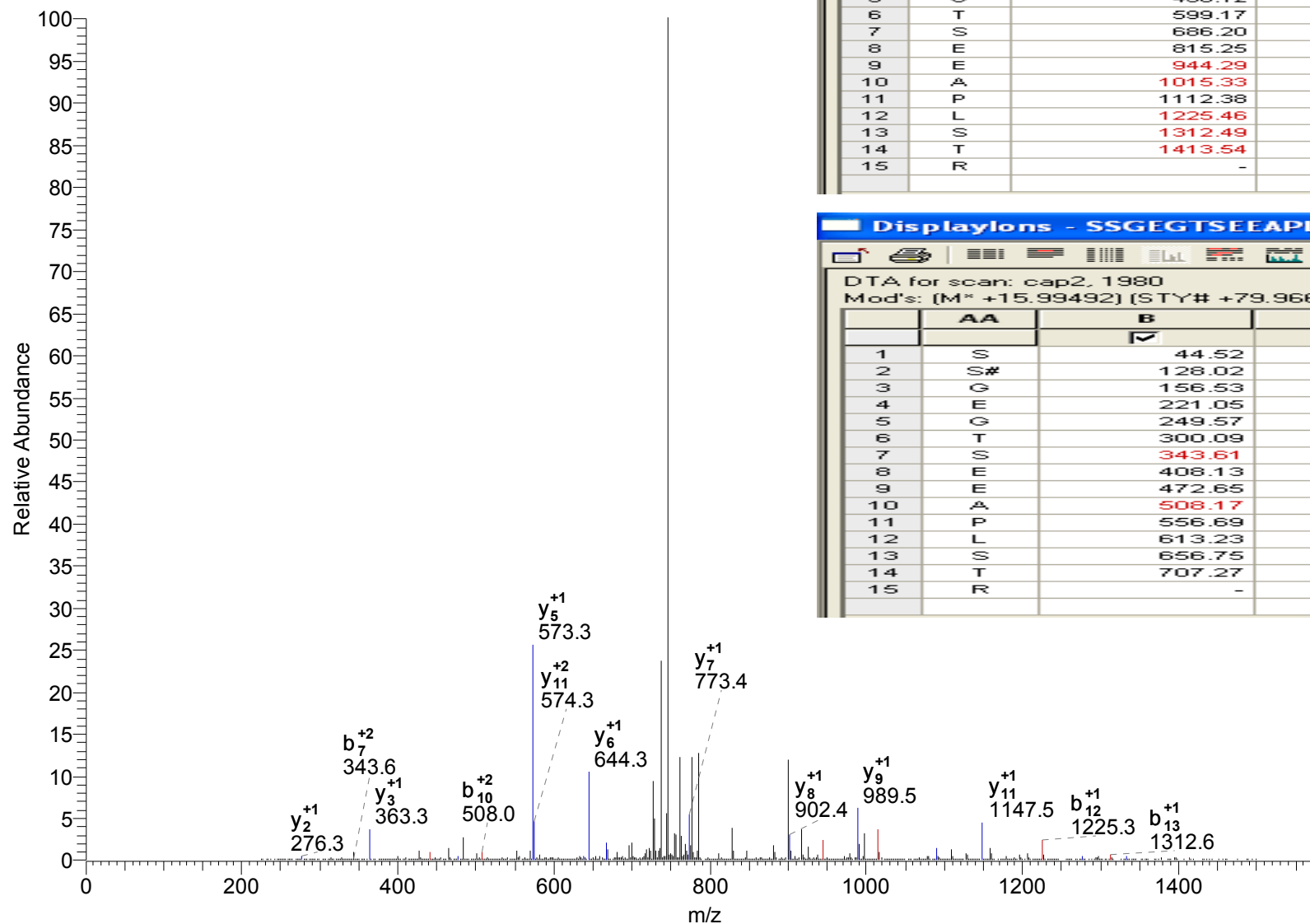
Displaylons - MEIEIQQVQLDAINYVLYDQI

DTA for scan: cap2, 3587
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y
1	M	44.69	-
2	E	67.70	858.76
3	I	125.40	815.75
4	E	168.41	778.05
5	L	206.11	735.04
6	Q	246.79	697.35
7	S	277.60	654.66
8	Q	320.49	625.65
9	V	353.51	582.95
10	L	391.21	549.94
11	D	429.65	512.24
12	A	453.23	473.90
13	I	490.92	450.22
14	N	528.94	412.53
15	V	609.95	374.51
16	Y#	642.97	293.50
17	L	680.66	260.48
18	Y	735.02	222.79
19	D	773.36	168.43
20	Q	816.05	130.09
21	L	853.74	87.40
22	K	-	49.71

Interferon-inducible GTPase 5

#1980-1980 NL: 3.13E4



Displaylons - SSGEGTSEEAPLSTR

DTA for scan: cap2, 1980
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	88.04	-	15
2	S#	255.04	1500.62	14
3	G	312.06	1333.62	13
4	E	441.10	1276.60	12
5	G	498.12	1147.56	11
6	T	599.17	1090.54	10
7	S	686.20	989.49	9
8	E	815.25	902.46	8
9	E	944.29	773.42	7
10	A	1015.33	644.37	6
11	P	1112.38	573.34	5
12	L	1225.46	476.28	4
13	S	1312.49	363.20	3
14	T	1413.54	276.17	2
15	R	-	175.12	1

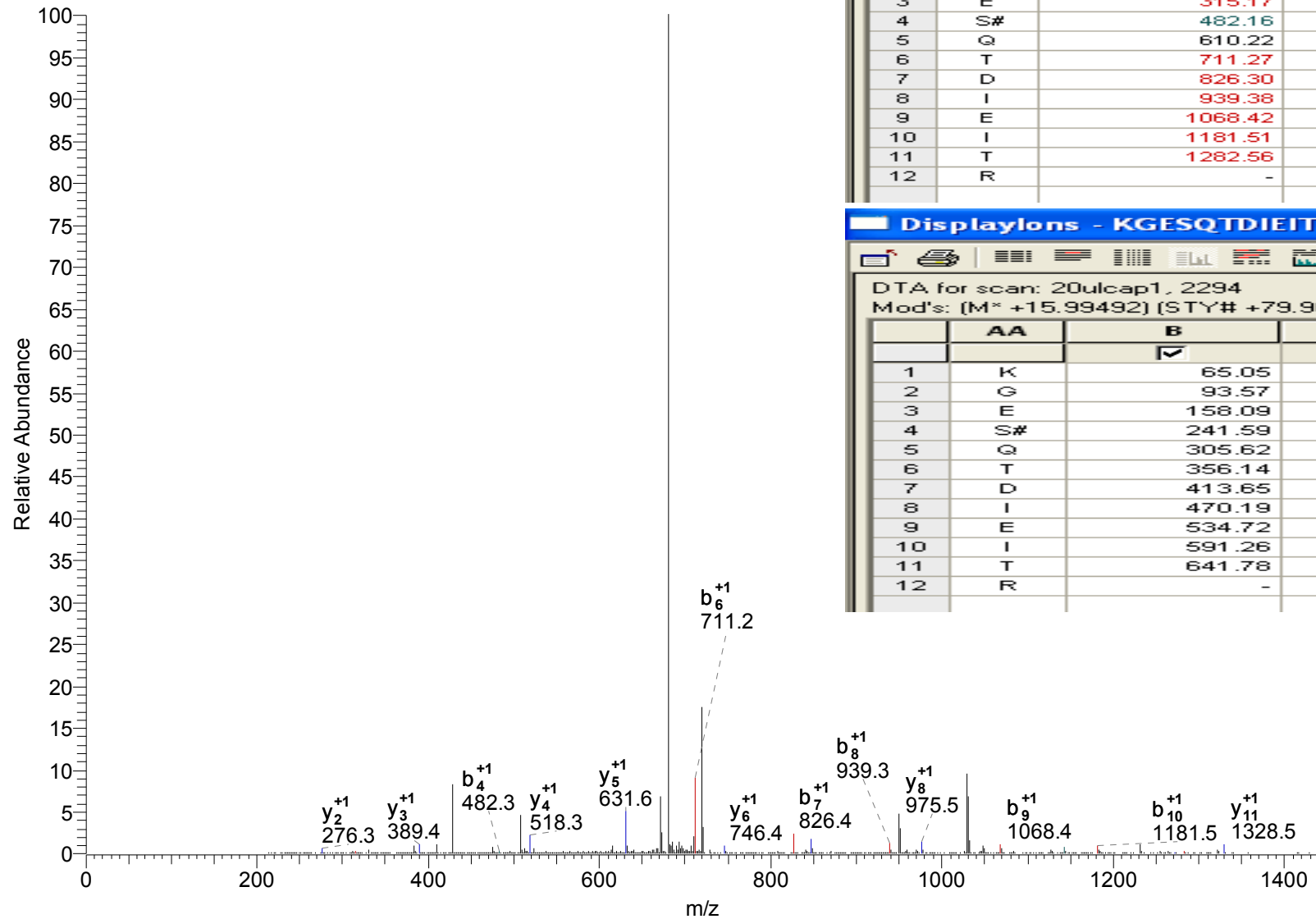
Displaylons - SSGEGTSEEAPLSTR

DTA for scan: cap2, 1980
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	B	Y	
1	S	44.52	-	15
2	S#	128.02	750.81	14
3	G	156.53	667.32	13
4	E	221.05	638.80	12
5	G	249.57	574.28	11
6	T	300.09	545.77	10
7	S	343.61	495.25	9
8	E	408.13	451.73	8
9	E	472.65	387.21	7
10	A	508.17	322.69	6
11	P	556.69	287.17	5
12	L	613.23	238.64	4
13	S	656.75	182.10	3
14	T	707.27	138.59	2
15	R	-	88.06	1

Cct3 T-complex protein 1 subunit gamma

#2294-2294 NL: 2.13E4



Displaylons - KGESQTDIEITR

DTA for scan: 20ulcap1, 2294
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	K	129.10	-	12
2	G	186.12	1328.57	11
3	E	315.17	1271.55	10
4	S#	482.16	1142.51	9
5	Q	610.22	975.51	8
6	T	711.27	847.45	7
7	D	826.30	746.40	6
8	I	939.38	631.38	5
9	E	1068.42	518.29	4
10	I	1181.51	389.25	3
11	T	1282.56	276.17	2
12	R	-	175.12	1

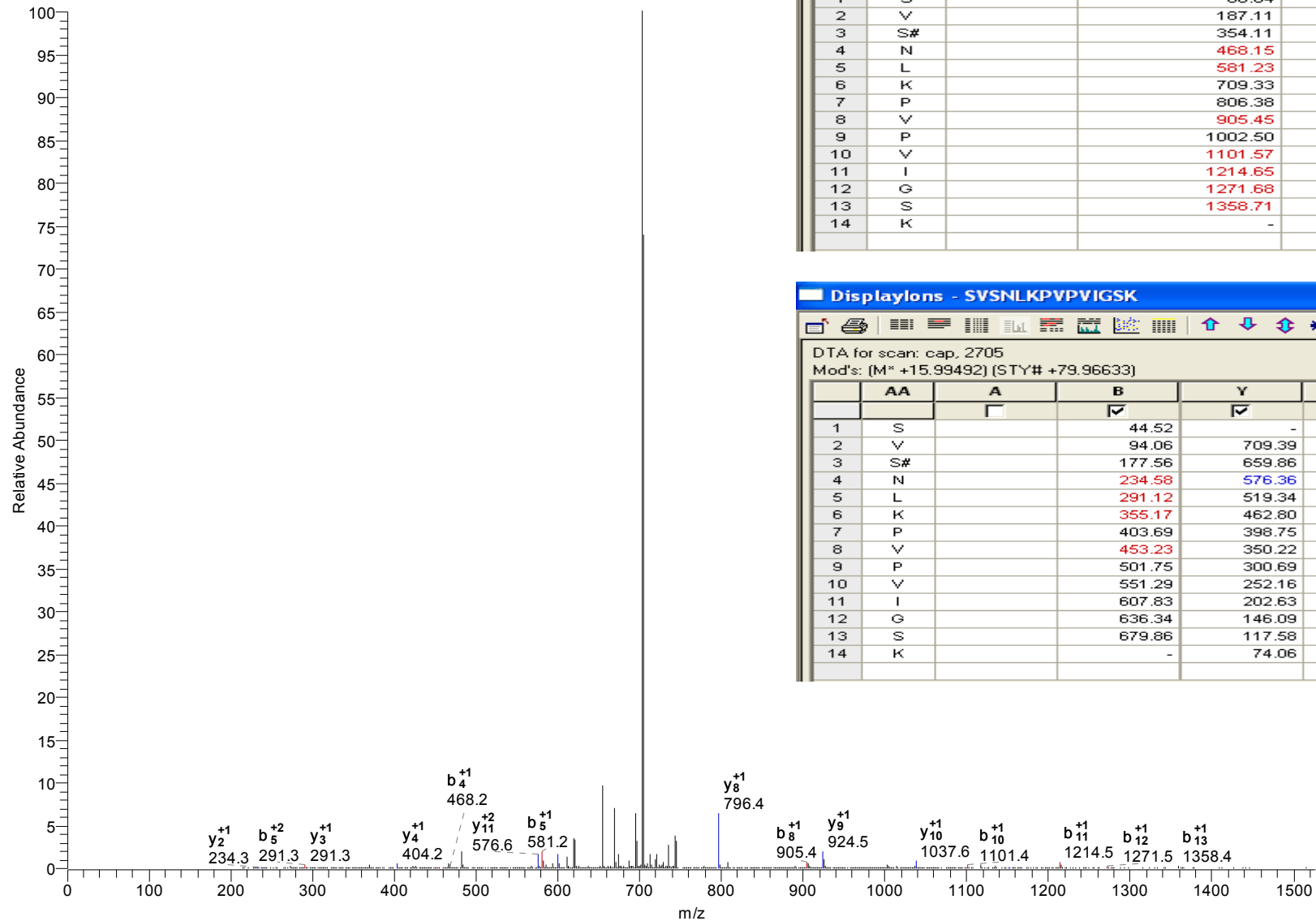
Displaylons - KGESQTDIEITR

DTA for scan: 20ulcap1, 2294
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	K	65.05	-	12
2	G	93.57	664.79	11
3	E	158.09	636.28	10
4	S#	241.59	571.76	9
5	Q	305.62	488.26	8
6	T	356.14	424.23	7
7	D	413.65	373.71	6
8	I	470.19	316.19	5
9	E	534.72	259.65	4
10	I	591.26	195.13	3
11	T	641.78	138.59	2
12	R	-	88.06	1

Sccpdh Probable saccharopine dehydrogenase

#2705-2705 NL: 1.56E5



Displaylons - SVSNLKPVPVIGSK

DTA for scan: cap, 2705
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	14
2	V		187.11	1417.78	13
3	S#		354.11	1318.71	12
4	N		468.15	1151.71	11
5	L		581.23	1037.67	10
6	K		709.33	924.59	9
7	P		806.38	796.49	8
8	V		905.45	699.44	7
9	P		1002.50	600.37	6
10	V		1101.57	503.32	5
11	I		1214.65	404.25	4
12	G		1271.68	291.17	3
13	S		1358.71	234.14	2
14	K		-	147.11	1

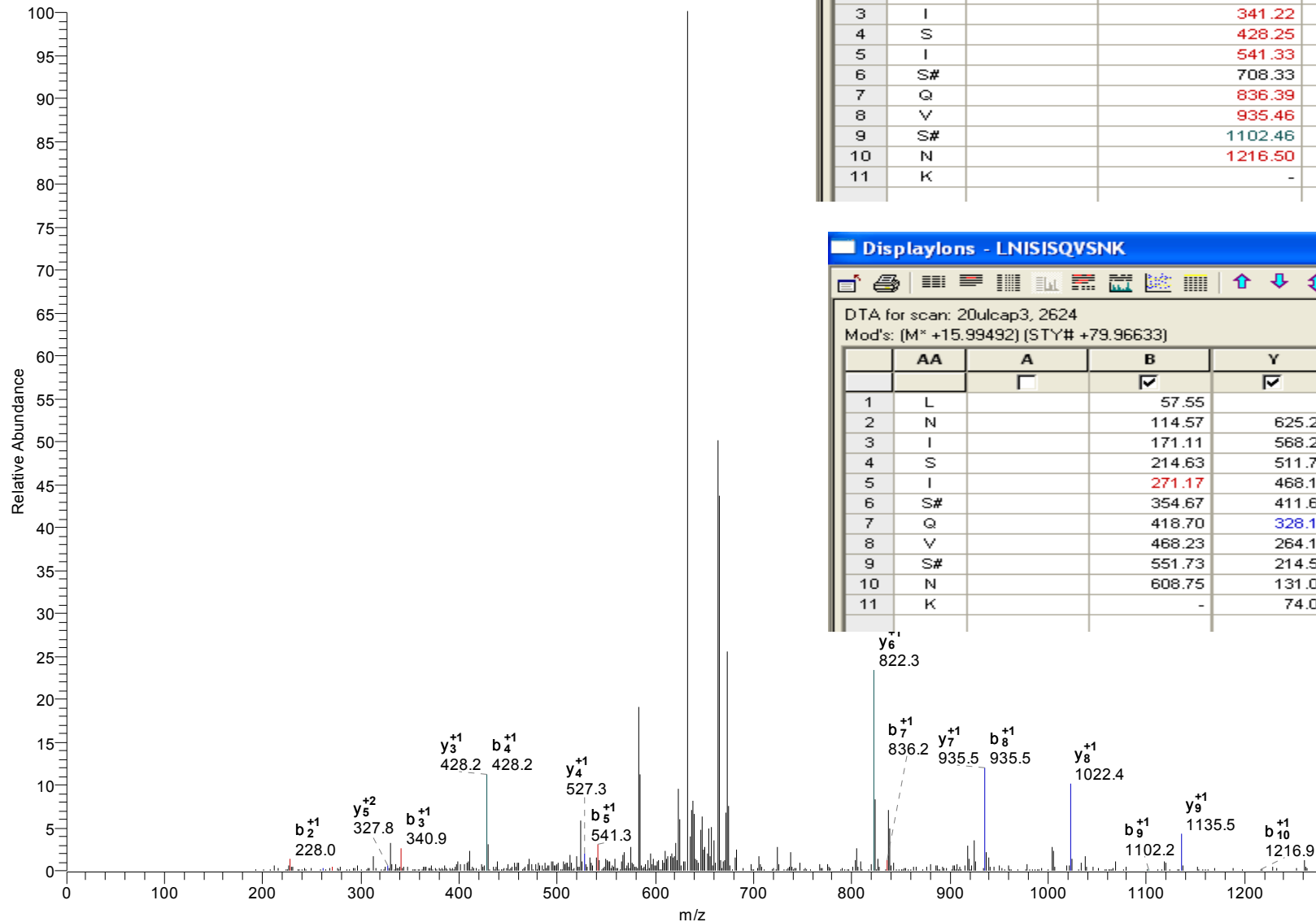
Displaylons - SVSNLKPVPVIGSK

DTA for scan: cap, 2705
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S		44.52	-		14
2	V		94.06	709.39		13
3	S#		177.56	659.86		12
4	N		234.58	576.36		11
5	L		291.12	519.34		10
6	K		355.17	462.80		9
7	P		403.69	398.75		8
8	V		453.23	350.22		7
9	P		501.75	300.69		6
10	V		551.29	252.16		5
11	I		607.83	202.63		4
12	G		636.34	146.09		3
13	S		679.86	117.58		2
14	K		-	74.06		1

Atp1a4 Cation-transporting ATPase

#2624-2624 NL: 1.74E3



Displaylons - LNISISQVSNK

DTA for scan: 20ulcap3, 2624
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L	☐	☒	☒	
2	N		114.09	-	11
3	I		228.13	1249.52	10
4	S		341.22	1135.48	9
5	I		428.25	1022.40	8
6	S#		541.33	935.36	7
7	Q		708.33	822.28	6
8	V		836.39	655.28	5
9	S#		935.46	527.22	4
10	N		1102.46	428.15	3
11	K		1216.50	261.16	2
			-	147.11	1

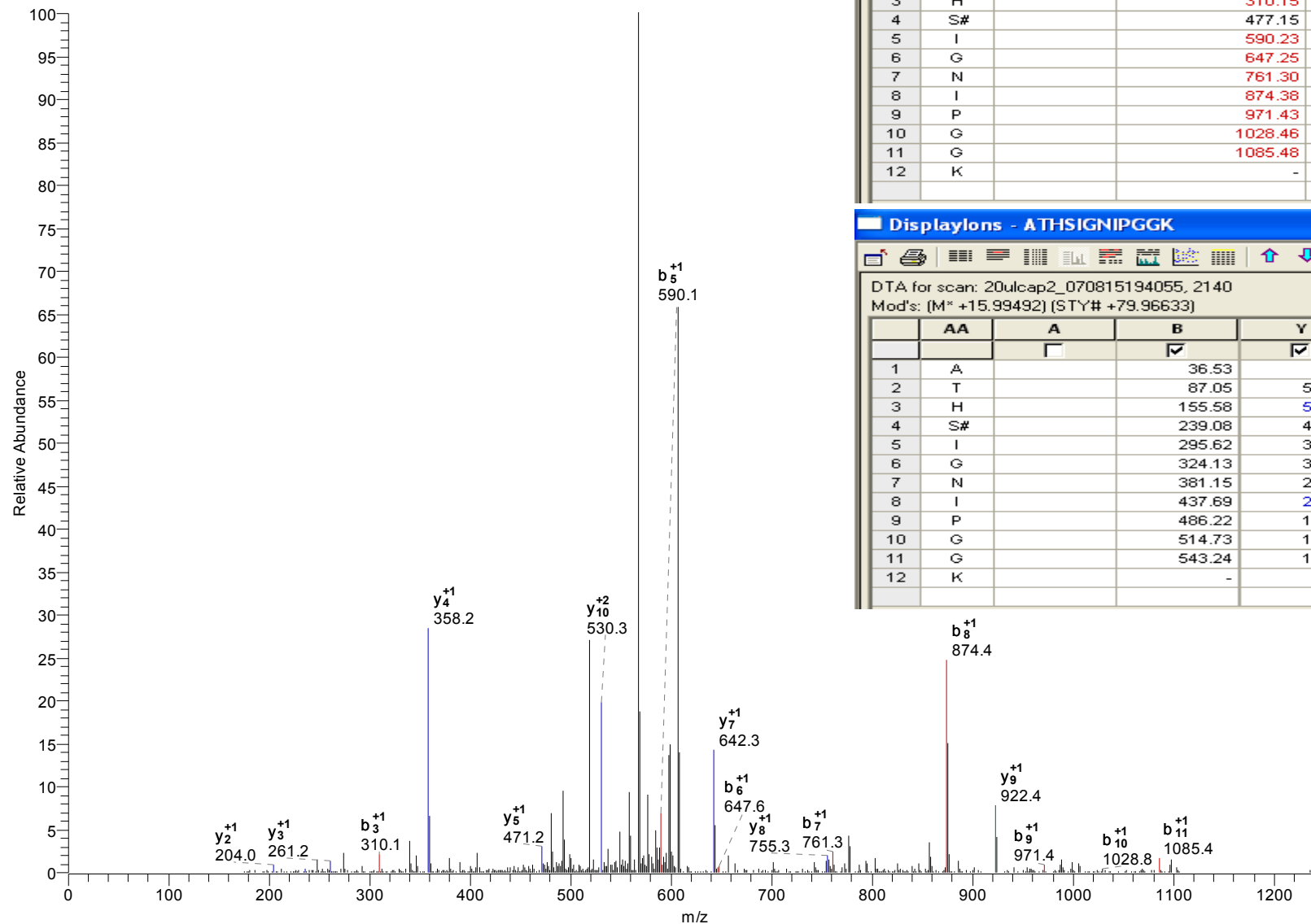
Displaylons - LNISISQVSNK

DTA for scan: 20ulcap3, 2624
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L	☐	☒	☒	☐	
2	N		57.55	-		11
3	I		114.57	625.26		10
4	S		171.11	568.24		9
5	I		214.63	511.70		8
6	S#		271.17	468.19		7
7	Q		354.67	411.64		6
8	V		418.70	328.14		5
9	S#		468.23	264.11		4
10	N		551.73	214.58		3
11	K		608.75	131.08		2
			-	74.06		1

similar to Protein C14orf155

#2140-2140 NL: 3.86E3



Displaylons - ATHSIGNIPGGK

DTA for scan: 20ulcap2_070815194055, 2140
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	A		72.04	-	12
2	T		173.09	1160.55	11
3	H		310.15	1059.50	10
4	S#		477.15	922.44	9
5	I		590.23	755.44	8
6	G		647.25	642.36	7
7	N		761.30	585.34	6
8	I		874.38	471.29	5
9	P		971.43	358.21	4
10	G		1028.46	261.16	3
11	G		1085.48	204.13	2
12	K		-	147.11	1

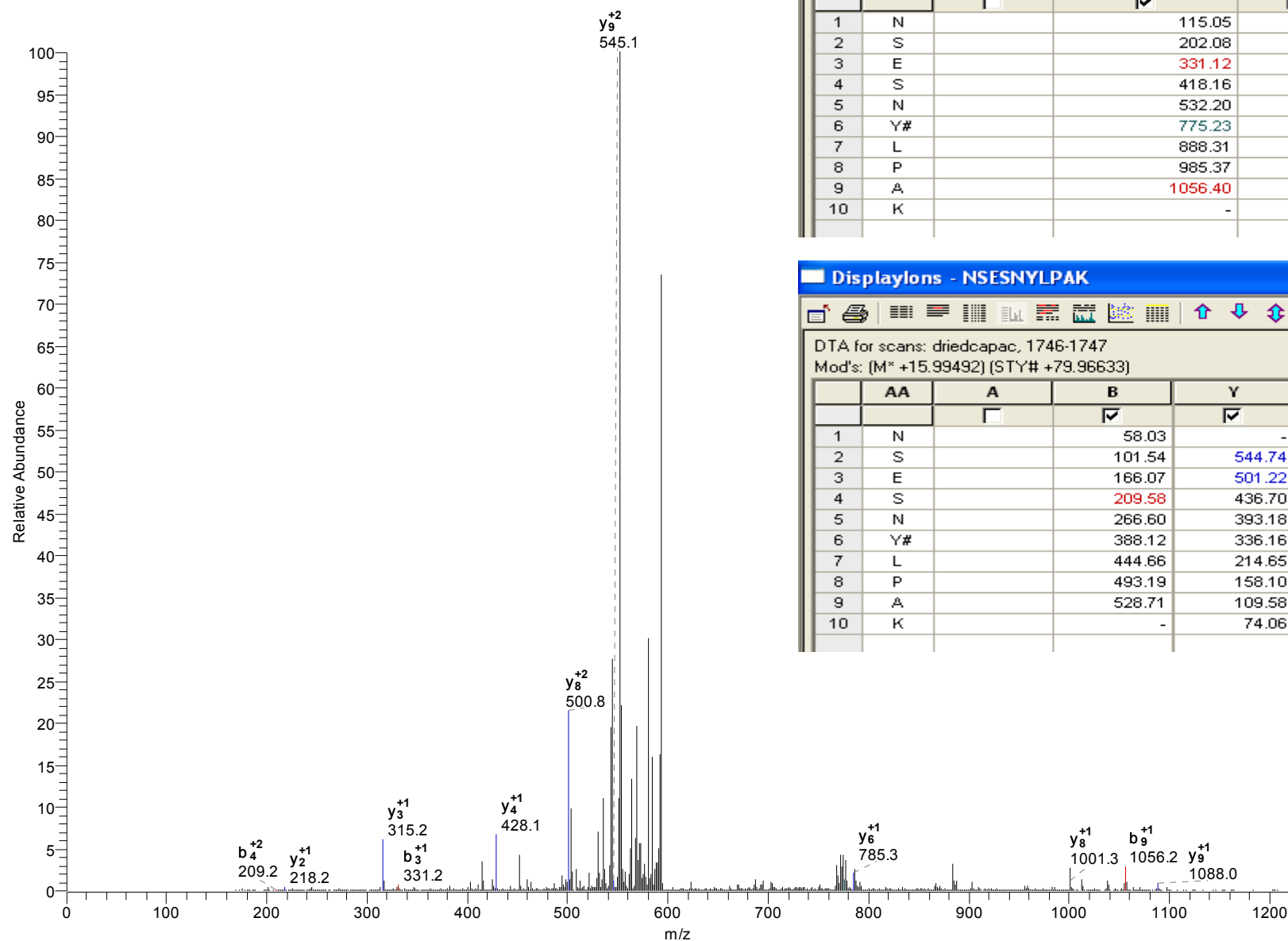
Displaylons - ATHSIGNIPGGK

DTA for scan: 20ulcap2_070815194055, 2140
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	A		36.53	-		12
2	T		87.05	580.78		11
3	H		155.58	530.25		10
4	S#		239.08	461.72		9
5	I		295.62	378.22		8
6	G		324.13	321.68		7
7	N		381.15	293.17		6
8	I		437.69	236.15		5
9	P		486.22	179.61		4
10	G		514.73	131.08		3
11	G		543.24	102.57		2
12	K		-	74.06		1

predicted similar to cancer susceptibility
candidate 5 isoform 1

#1746-1747 NL: 4.46E4



Displays - NSESNYLPAK

DTA for scans: driedcapac, 1746-1747
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	N	☐	☒	☒	10
2	S		115.05	-	9
3	E		202.08	1088.47	8
4	S		331.12	1001.43	7
5	N		418.16	872.39	6
6	Y#		532.20	785.36	5
7	L		775.23	671.32	4
8	P		888.31	428.29	3
9	A		985.37	315.20	2
10	K		1056.40	218.15	1
			-	147.11	

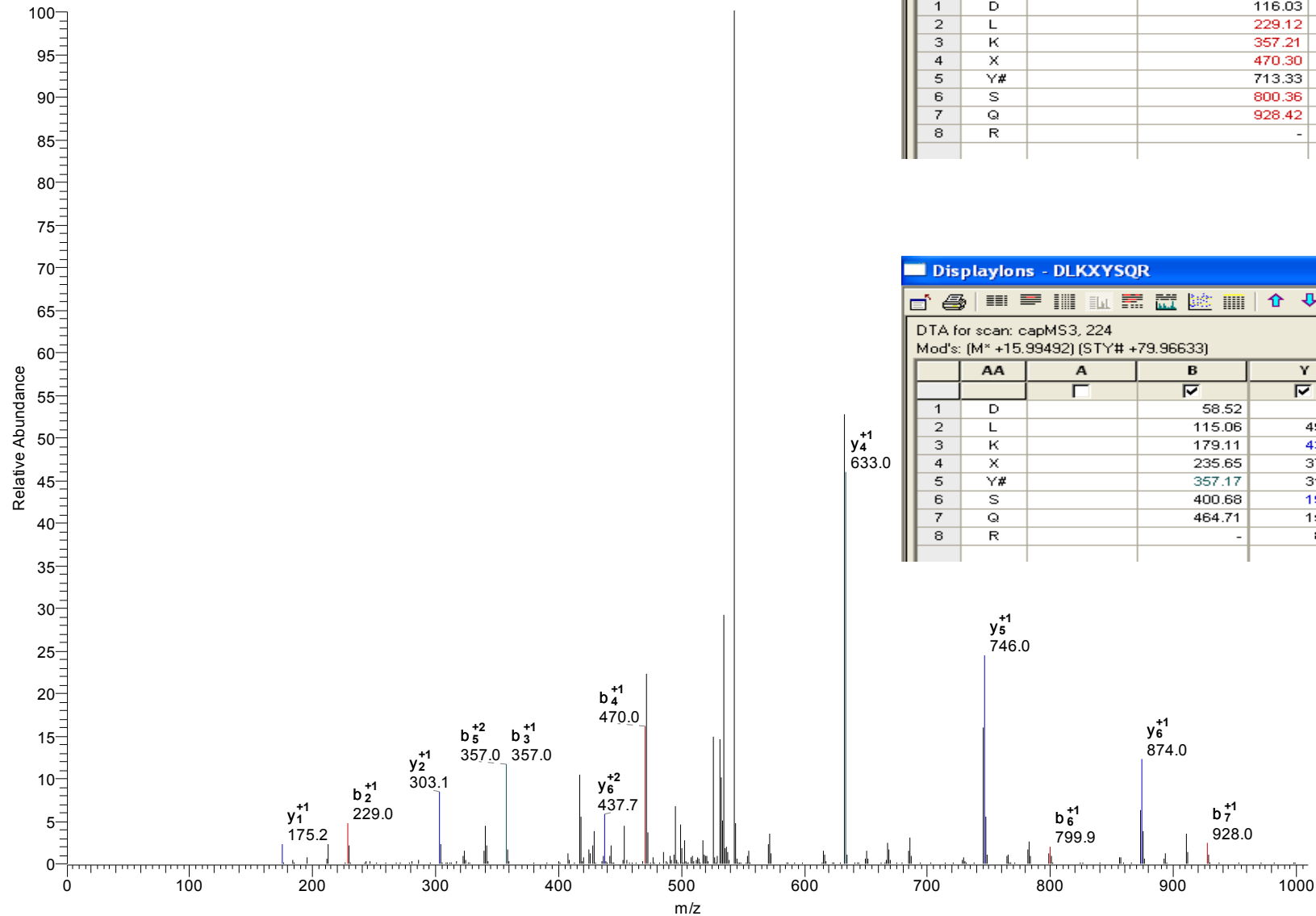
Displays - NSESNYLPAK

DTA for scans: driedcapac, 1746-1747
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	N	☐	☒	☒	☐	10
2	S		58.03	-		9
3	E		101.54	544.74		8
4	S		166.07	501.22		7
5	N		209.58	436.70		6
6	Y#		266.60	393.18		5
7	L		388.12	336.16		4
8	P		444.66	214.65		3
9	A		493.19	158.10		2
10	K		528.71	109.58		1
			-	74.06		

predicted similar to Coiled-coil domain-containing protein 11

#224-224 NL: 3.89E3



Displaylons - DLKXYSQR

DTA for scan: capMS3, 224
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	D		116.03	-	8
2	L		229.12	987.50	7
3	K		357.21	874.42	6
4	X		470.30	746.32	5
5	Y#		713.33	633.24	4
6	S		800.36	390.21	3
7	Q		928.42	303.18	2
8	R		-	175.12	1

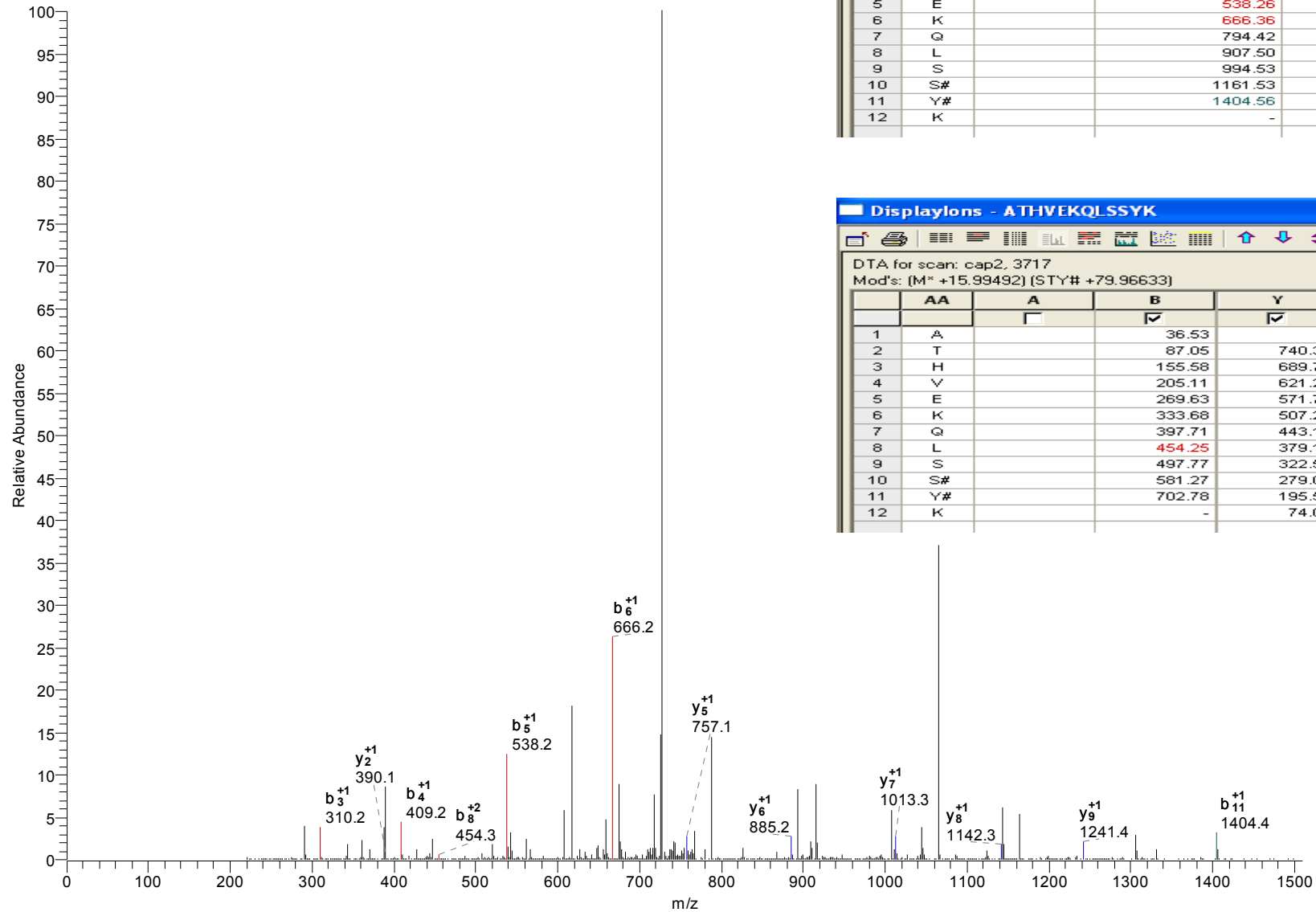
Displaylons - DLKXYSQR

DTA for scan: capMS3, 224
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	D		58.52	-		8
2	L		115.06	494.25		7
3	K		179.11	437.71		6
4	X		235.65	373.67		5
5	Y#		357.17	317.12		4
6	S		400.68	195.61		3
7	Q		464.71	152.09		2
8	R		-	88.06		1

Symbol=Rnf166 RING finger protein 166

#3717-3717 NL: 2.58E4



Displaylons - ATHVEKQLSSYK

DTA for scan: cap2, 3717
Mod's: (M⁺ +15.99492) (S^TY# +79.96633)

	AA	A	B	Y	
1	A	☐	☒	☒	12
2	T				11
3	H				10
4	V				9
5	E				8
6	K				7
7	Q				6
8	L				5
9	S				4
10	S#				3
11	Y#				2
12	K				1

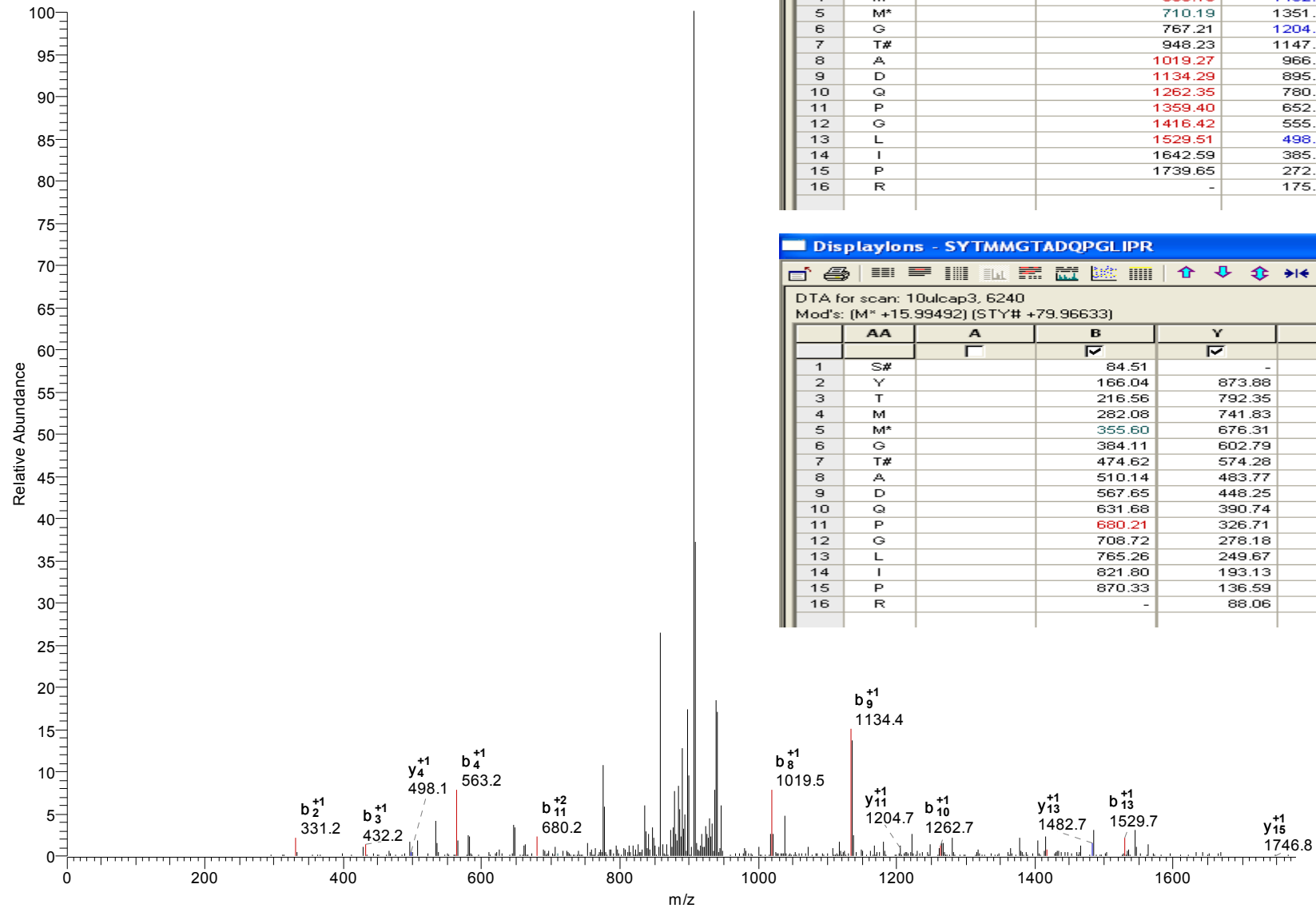
Displaylons - ATHVEKQLSSYK

DTA for scan: cap2, 3717
Mod's: (M⁺ +15.99492) (S^TY# +79.96633)

	AA	A	B	Y	Z	
1	A	☐	☒	☒	☐	12
2	T					11
3	H					10
4	V					9
5	E					8
6	K					7
7	Q					6
8	L					5
9	S					4
10	S#					3
11	Y#					2
12	K					1

kif13B Kinesin 13B

#6240-6240 NL: 1.16E3



Displaylons - SYTMMGTADQPGLIPR

DTA for scan: 10ulcap3, 6240
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S#		168.01	-	16
2	Y		331.07	1746.76	15
3	T		432.12	1583.70	14
4	M		563.16	1482.65	13
5	M*		710.19	1351.61	12
6	G		767.21	1204.57	11
7	T#		948.23	1147.55	10
8	A		1019.27	966.54	9
9	D		1134.29	895.50	8
10	Q		1262.35	780.47	7
11	P		1359.40	652.41	6
12	G		1416.42	555.36	5
13	L		1529.51	498.34	4
14	I		1642.59	385.26	3
15	P		1739.65	272.17	2
16	R		-	175.12	1

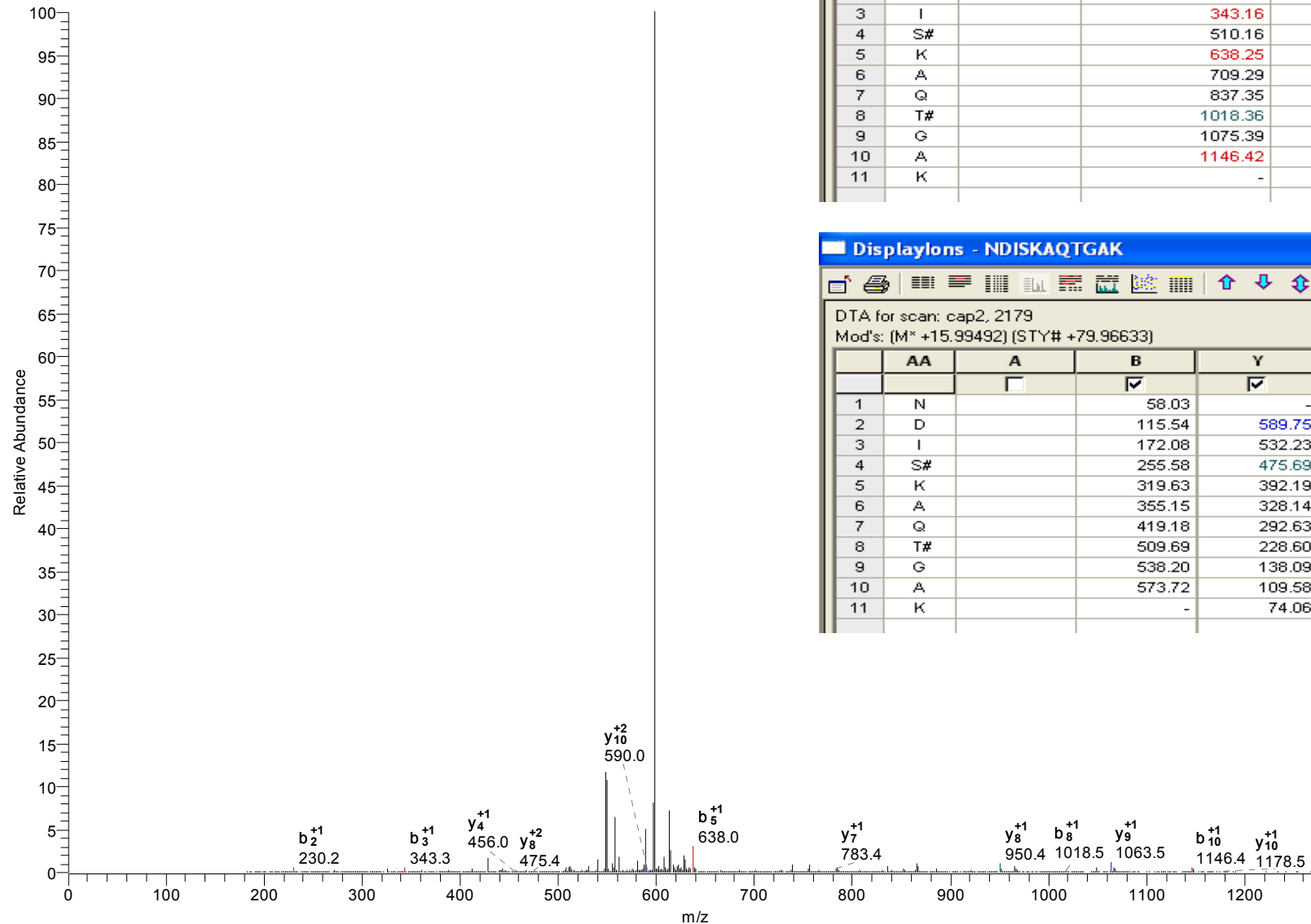
Displaylons - SYTMMGTADQPGLIPR

DTA for scan: 10ulcap3, 6240
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S#		84.51	-		16
2	Y		166.04	873.88		15
3	T		216.56	792.35		14
4	M		282.08	741.83		13
5	M*		355.60	676.31		12
6	G		384.11	602.79		11
7	T#		474.62	574.28		10
8	A		510.14	483.77		9
9	D		567.65	448.25		8
10	Q		631.68	390.74		7
11	P		680.21	326.71		6
12	G		708.72	278.18		5
13	L		765.26	249.67		4
14	I		821.80	193.13		3
15	P		870.33	136.59		2
16	R		-	88.06		1

predicted SMC2 structural maintenance of chromosomes 2-like 1

#2179-2179 NL: 6.64E4



Displaylons - NDISKAQTGAK

DTA for scan: cap2, 2179
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	N	☐	☒	☒	11
2	D		115.05	-	10
3	I		230.08	1178.49	9
4	S#		343.16	1063.46	8
5	K		510.16	950.37	7
6	A		638.25	783.38	6
7	Q		709.29	655.28	5
8	T#		837.35	584.24	4
9	G		1018.36	456.19	3
10	A		1075.39	275.17	2
11	K		1146.42	218.15	1
			-	147.11	

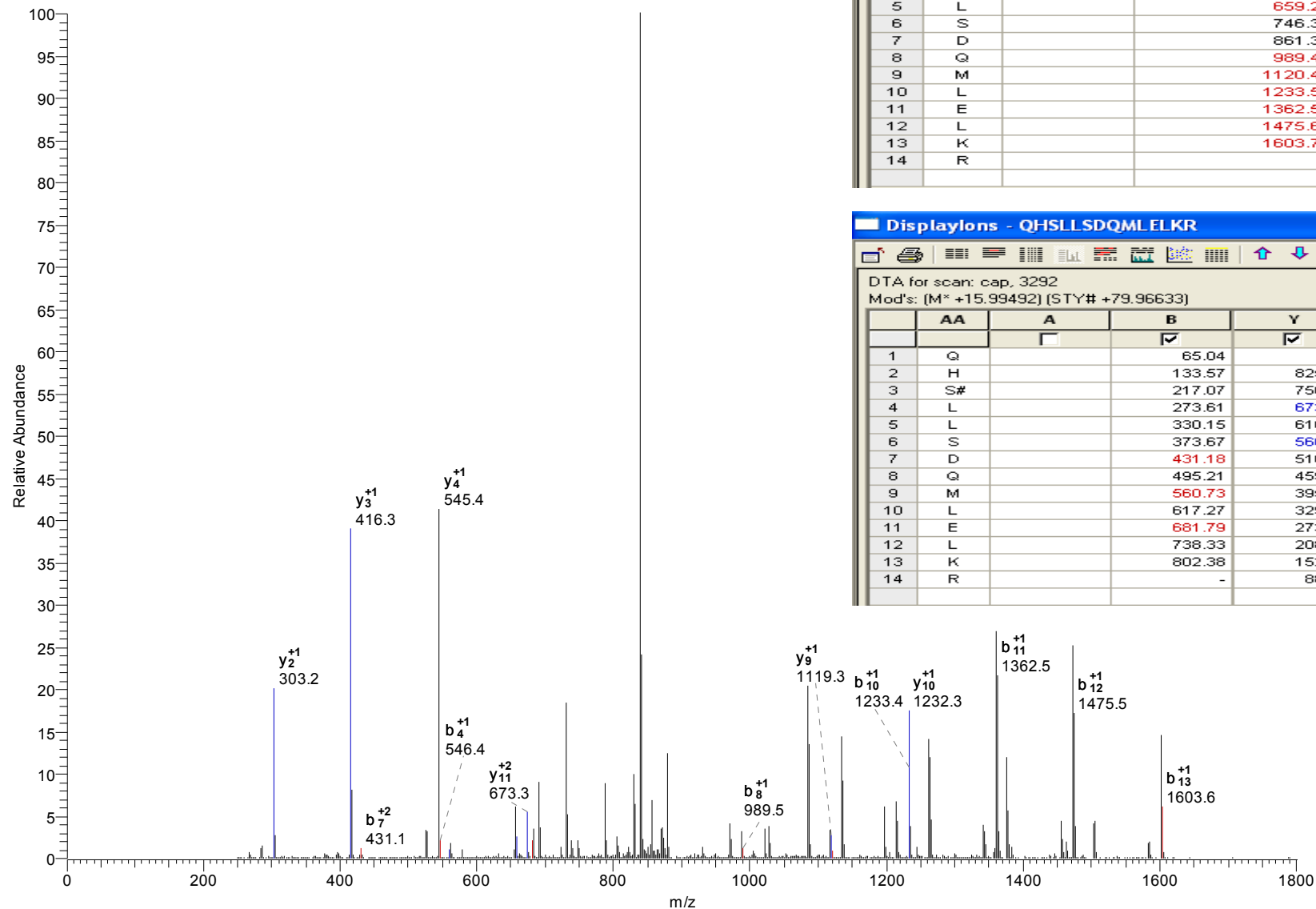
Displaylons - NDISKAQTGAK

DTA for scan: cap2, 2179
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	N	☐	☒	☒	☐	11
2	D		58.03	-		10
3	I		115.54	589.75		9
4	S#		172.08	532.23		8
5	K		255.58	475.69		7
6	A		319.63	392.19		6
7	Q		355.15	328.14		5
8	T#		419.18	292.63		4
9	G		509.69	228.60		3
10	A		538.20	138.09		2
11	K		573.72	109.58		1
			-	74.06		

Nin_predicted similar to Ninein

#3292-3292 NL: 7.51E4



Displaylons - QHSLLSDQMELKR

DTA for scan: cap, 3292
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	Q		129.07	-	14
2	H		266.12	1649.81	13
3	S#		433.12	1512.75	12
4	L		546.21	1345.75	11
5	L		659.29	1232.67	10
6	S		746.32	1119.58	9
7	D		861.35	1032.55	8
8	Q		989.41	917.52	7
9	M		1120.45	789.47	6
10	L		1233.53	658.42	5
11	E		1362.58	545.34	4
12	L		1475.66	416.30	3
13	K		1603.75	303.21	2
14	R		-	175.12	1

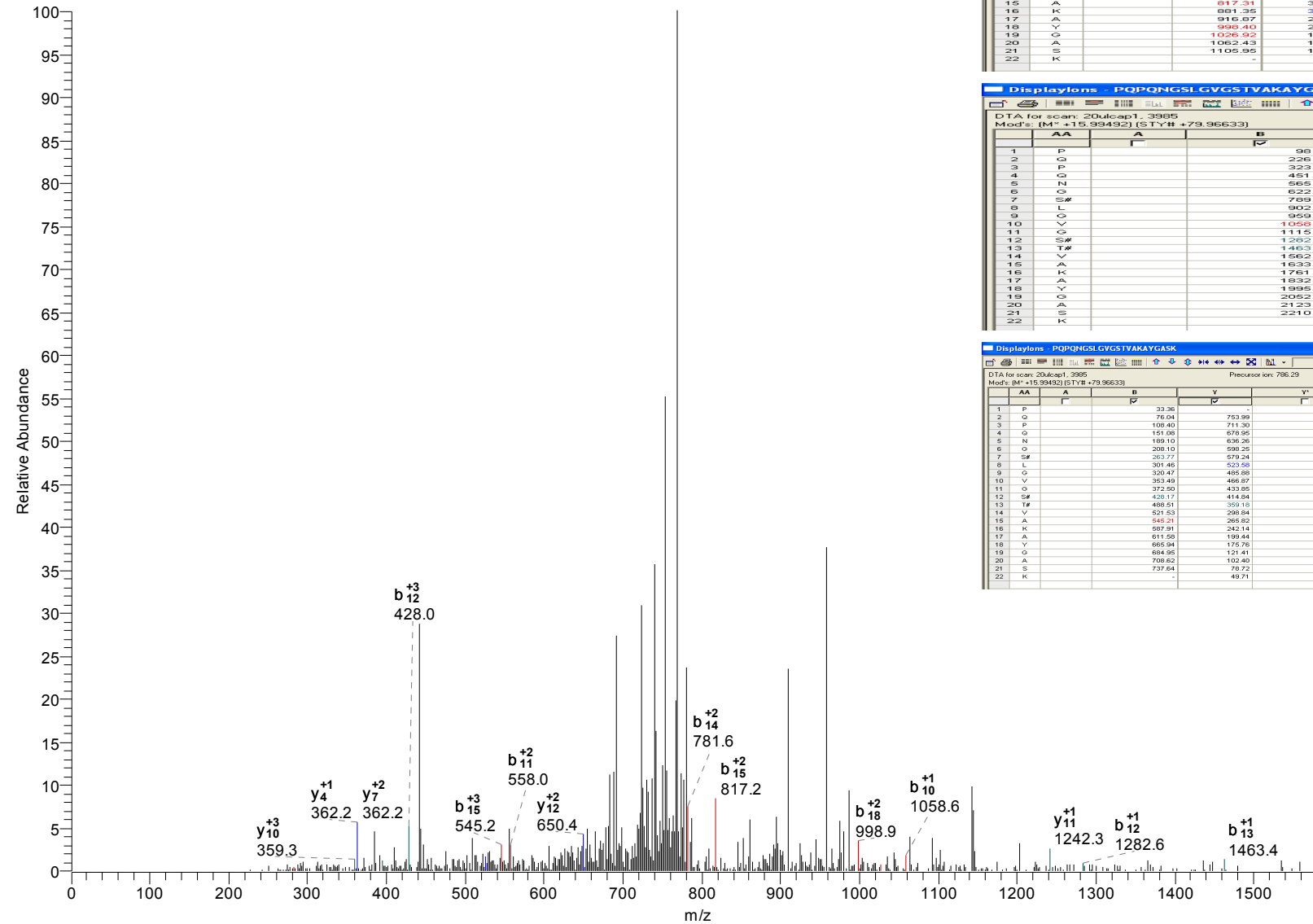
Displaylons - QHSLLSDQMELKR

DTA for scan: cap, 3292
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	Q		65.04	-		14
2	H		133.57	825.41		13
3	S#		217.07	756.88		12
4	L		273.61	673.38		11
5	L		330.15	616.84		10
6	S		373.67	560.29		9
7	D		431.18	516.78		8
8	Q		495.21	459.27		7
9	M		560.73	395.24		6
10	L		617.27	329.72		5
11	E		681.79	273.17		4
12	L		738.33	208.65		3
13	K		802.38	152.11		2
14	R		-	88.06		1

Rpa1 Cb1-727

#3985-3985 NL: 1.18E3



Displays - PQPQNGSLGVGSLVAKAYGASK

DTA for scan: 20ulcap1_3985
Mod's: (M⁺+15.99492) (S Y# +79.96633)

	AA	B	Y	Z	
1	P	49.53	-	-	22
2	G	113.56	1130.46	-	21
3	P	162.09	1066.45	-	20
4	G	226.12	1017.92	-	19
5	N	263.14	953.89	-	18
6	G	311.65	896.67	-	17
7	SW	395.15	866.36	-	16
8	L	451.69	784.86	-	15
9	G	480.20	726.32	-	14
10	V	529.74	689.81	-	13
11	G	558.25	650.27	-	12
12	SW	641.75	621.76	-	11
13	TW	732.25	536.26	-	10
14	V	761.79	447.76	-	9
15	A	817.31	386.22	-	8
16	K	881.35	362.70	-	7
17	A	916.87	296.66	-	6
18	Y	956.40	263.14	-	5
19	G	1026.92	181.61	-	4
20	A	1062.43	153.09	-	3
21	S	1105.95	117.56	-	2
22	K	-	74.06	-	1

Displays - PQPQNGSLGVGSLVAKAYGASK

DTA for scan: 20ulcap1_3985
Mod's: (M⁺+15.99492) (S Y# +79.96633)

	AA	B	Y	Z	
1	P	98.06	-	-	22
2	G	226.12	2259.94	-	21
3	P	323.17	2131.89	-	20
4	G	451.23	2034.83	-	19
5	N	565.27	1906.77	-	18
6	G	622.29	1792.73	-	17
7	SW	789.29	1735.71	-	16
8	L	902.38	1566.71	-	15
9	G	959.40	1455.63	-	14
10	V	1058.47	1396.61	-	13
11	G	1115.49	1299.54	-	12
12	SW	1263.49	1242.52	-	11
13	TW	1463.50	1076.52	-	10
14	V	1562.57	894.50	-	9
15	A	1633.61	795.44	-	8
16	K	1761.70	724.40	-	7
17	A	1832.74	596.30	-	6
18	Y	1995.80	525.27	-	5
19	G	2052.82	362.20	-	4
20	A	2123.86	306.16	-	3
21	S	2210.89	234.14	-	2
22	K	-	147.11	-	1

Displays - PQPQNGSLGVGSLVAKAYGASK

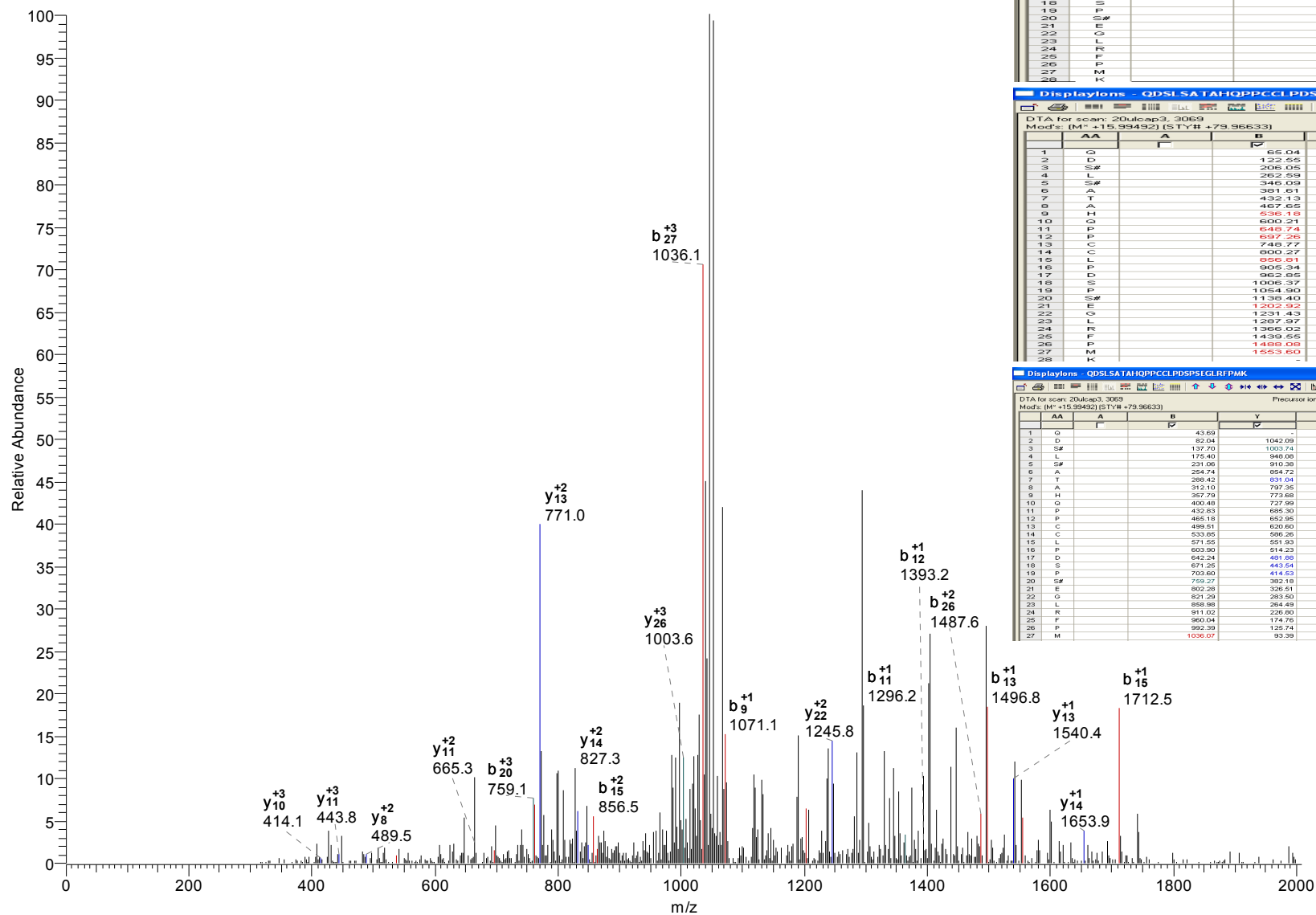
DTA for scan: 20ulcap1_3985
Mod's: (M⁺+15.99492) (S Y# +79.96633)

Precursor ion: 786.29 Charge: 3 Activation type: CID Mass

	AA	B	Y	Y*	Yo	Z	
1	P	33.36	-	-	-	-	22
2	G	76.04	753.99	-	-	-	21
3	P	106.40	711.30	-	-	-	20
4	G	151.26	676.95	-	-	-	19
5	N	189.10	636.26	-	-	-	18
6	G	206.10	596.25	-	-	-	17
7	SW	263.77	576.34	-	-	-	16
8	L	301.46	523.58	-	-	-	15
9	G	320.47	485.88	-	-	-	14
10	V	353.49	466.87	-	-	-	13
11	G	372.50	433.85	-	-	-	12
12	SW	426.17	414.84	-	-	-	11
13	TW	488.51	359.18	-	-	-	10
14	V	521.53	288.84	-	-	-	9
15	A	545.21	265.82	-	-	-	8
16	K	587.91	242.14	-	-	-	7
17	A	611.58	199.44	-	-	-	6
18	Y	665.94	175.76	-	-	-	5
19	G	684.95	121.41	-	-	-	4
20	A	708.62	102.40	-	-	-	3
21	S	737.64	76.72	-	-	-	2
22	K	-	49.71	-	-	-	1

predicted similar to chromosome 17 open reading
frame 27

#3069-3069 NL: 1.01E3



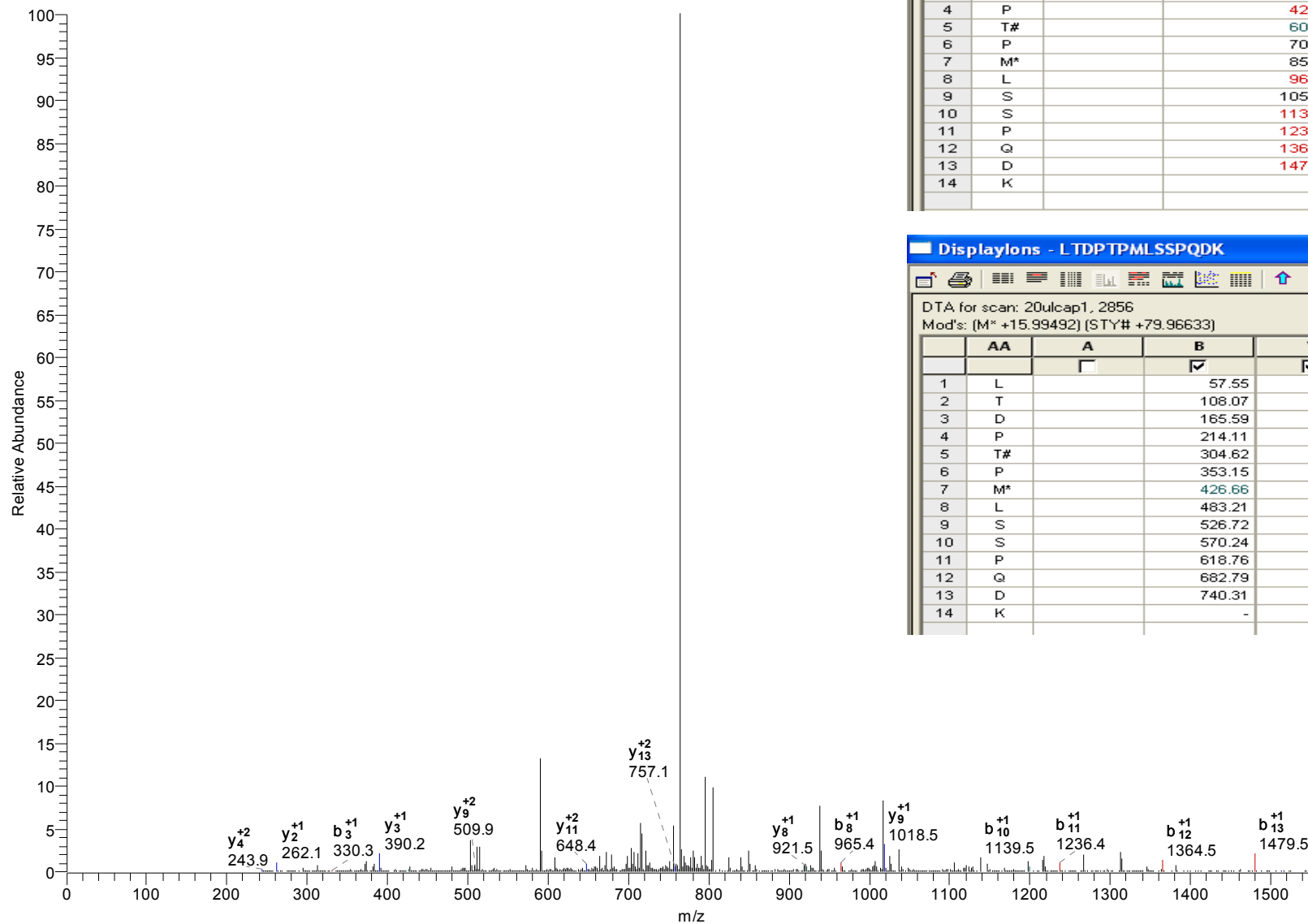
Displays - QDSLSATAHOPPCCLPDSPSEGLRIPMK									
DTA for scan: 20ulcap3, 3069									
Mod's: (M ⁺ +15.99492) (S TY# +79.96633)									
	AA	A	B	Y					
1	G				129.07	-			26
2	D				244.09	3124.24			27
3	SW				411.09	3009.21			26
4	L				524.18	2642.22			25
5	SW				691.17	2729.13			24
6	A				752.21	2562.13			23
7	T				853.26	2491.10			22
8	A				934.30	2380.05			21
9	H				1071.35	2319.01			20
10	G				1189.41	2181.95			19
11	P				1296.47	2053.89			18
12	P				1393.52	1956.84			17
13	C				1486.53	1869.79			16
14	C				1599.54	1756.78			15
15	L				1712.55	1653.77			14
16	P				1809.67	1540.69			13
17	D				1924.70	1443.63			12
18	S				2011.73	1326.61			11
19	P				2108.79	1241.57			10
20	SW				2275.79	1144.52			9
21	E				2404.83	977.52			8
22	G				2461.85	848.46			7
23	L				2574.93	791.46			6
24	R				2731.03	678.38			5
25	F				2878.10	522.27			4
26	P				2975.15	375.21			3
27	M				3106.19	278.15			2
28	K				-	147.11			1

Displays - QDSLSATAHOPPCCLPDSPSEGLRIPMK									
DTA for scan: 20ulcap3, 3069									
Mod's: (M ⁺ +15.99492) (S TY# +79.96633)									
	AA	A	B	Y	Z				
1	G					65.04	-		28
2	D					122.55	1662.62		27
3	SW					206.05	1506.11		26
4	L					262.59	1421.61		25
5	SW					346.09	1336.07		24
6	A					381.61	1261.57		23
7	T					432.13	1246.05		22
8	A					467.65	1196.53		21
9	H					536.16	1150.01		20
10	G					600.21	1091.48		19
11	P					646.74	1027.45		18
12	P					697.26	978.92		17
13	C					748.77	930.40		16
14	C					800.27	878.89		15
15	L					856.81	827.39		14
16	P					905.34	770.85		13
17	D					962.85	722.32		12
18	S					1005.37	664.81		11
19	P					1054.90	621.29		10
20	SW					1136.40	572.76		9
21	E					1202.92	489.27		8
22	G					1231.43	424.74		7
23	L					1267.97	396.23		6
24	R					1366.02	339.69		5
25	F					1439.55	261.64		4
26	P					1488.08	188.11		3
27	M					1553.60	139.58		2
28	K					-	74.05		1

Displays - QDSLSATAHOPPCCLPDSPSEGLRIPMK									
DTA for scan: 20ulcap3, 3069									
Mod's: (M ⁺ +15.99492) (S TY# +79.96633)									
	AA	A	B	Y	Y'	Y''	Y'''	Y''''	
1	G								28
2	D								27
3	SW								26
4	L								25
5	SW								24
6	A								23
7	T								22
8	A								21
9	H								20
10	G								19
11	P								18
12	P								17
13	C								16
14	C								15
15	L								14
16	P								13
17	D								12
18	S								11
19	P								10
20	SW								9
21	E								8
22	G								7
23	L								6
24	R								5
25	F								4
26	P								3
27	M								2
28	K								1

Ssh2_predicted similar to slingshot-like 2

#2856-2856 NL: 1.28E4



DisplayIons - LTDPMLSSPQDK

DTA for scan: 20ulcap1, 2856
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	L	☐	☒	☒	14
2	T		114.09	-	13
3	D		215.14	1512.63	12
4	P		330.17	1411.58	11
5	T#		427.22	1296.55	10
6	P		608.23	1199.50	9
7	M*		705.29	1018.49	8
8	L		852.32	921.43	7
9	S		965.40	774.40	6
10	S		1052.44	661.32	5
11	P		1139.47	574.28	4
12	Q		1236.52	487.25	3
13	D		1364.58	390.20	2
14	K		1479.61	262.14	1

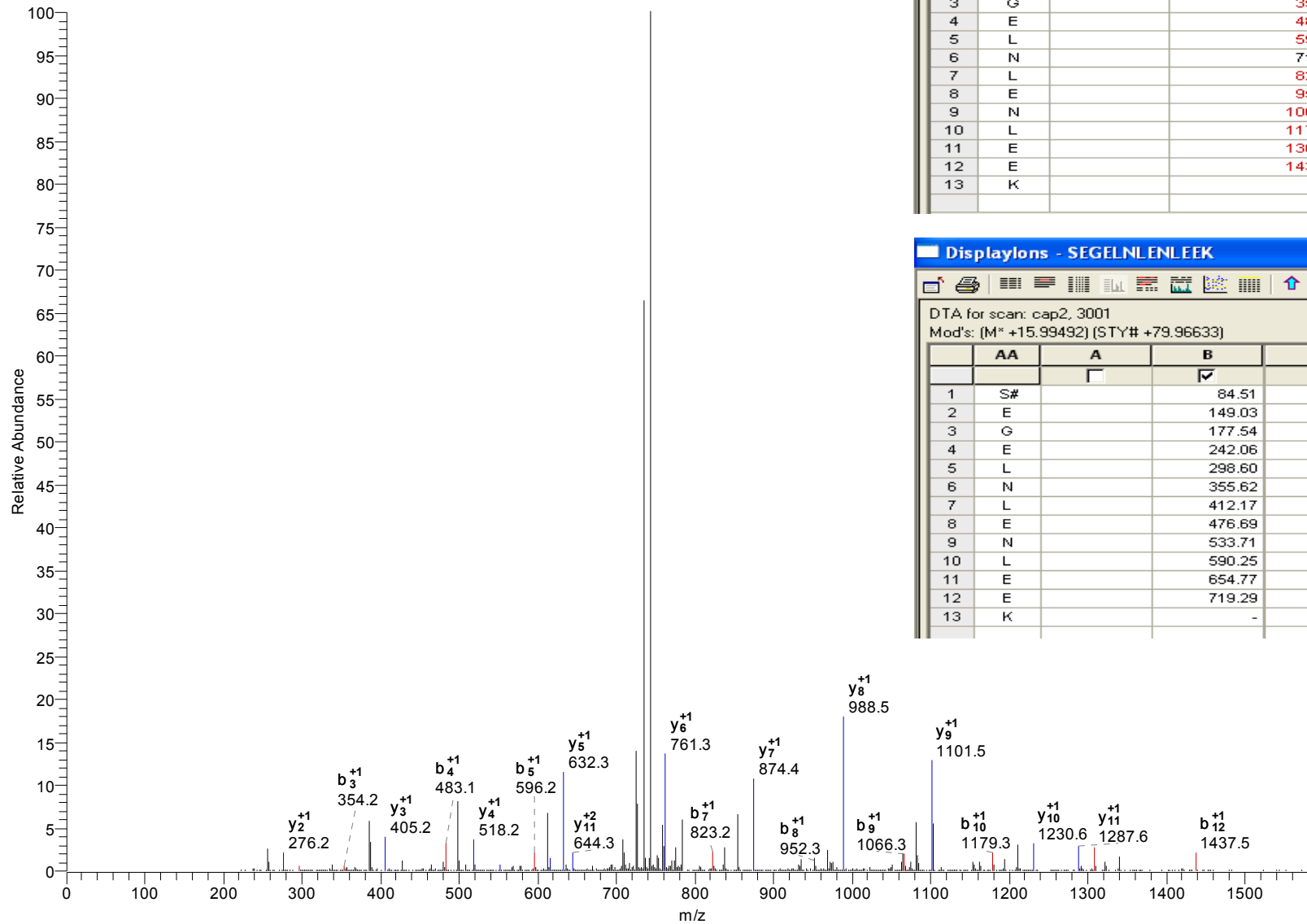
DisplayIons - LTDPMLSSPQDK

DTA for scan: 20ulcap1, 2856
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	L	☐	☒	☒	☐	14
2	T		57.55	-		13
3	D		108.07	756.82		12
4	P		165.59	706.29		11
5	T#		214.11	648.78		10
6	P		304.62	600.25		9
7	M*		353.15	509.75		8
8	L		426.66	461.22		7
9	S		483.21	387.70		6
10	S		526.72	331.16		5
11	P		570.24	287.65		4
12	Q		618.76	244.13		3
13	D		682.79	195.60		2
14	K		740.31	131.57		1

Akap4 83 kDa protein

#3001-3001 NL: 6.71E4



Displaylons - SEGELNLENLEEK

DTA for scan: cap2, 3001
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S#		168.01	-	13
2	E		297.05	1416.69	12
3	G		354.07	1287.64	11
4	E		483.11	1230.62	10
5	L		596.20	1101.58	9
6	N		710.24	988.49	8
7	L		823.32	874.45	7
8	E		952.37	761.37	6
9	N		1066.41	632.32	5
10	L		1179.49	518.28	4
11	E		1308.54	405.20	3
12	E		1437.58	276.16	2
13	K		-	147.11	1

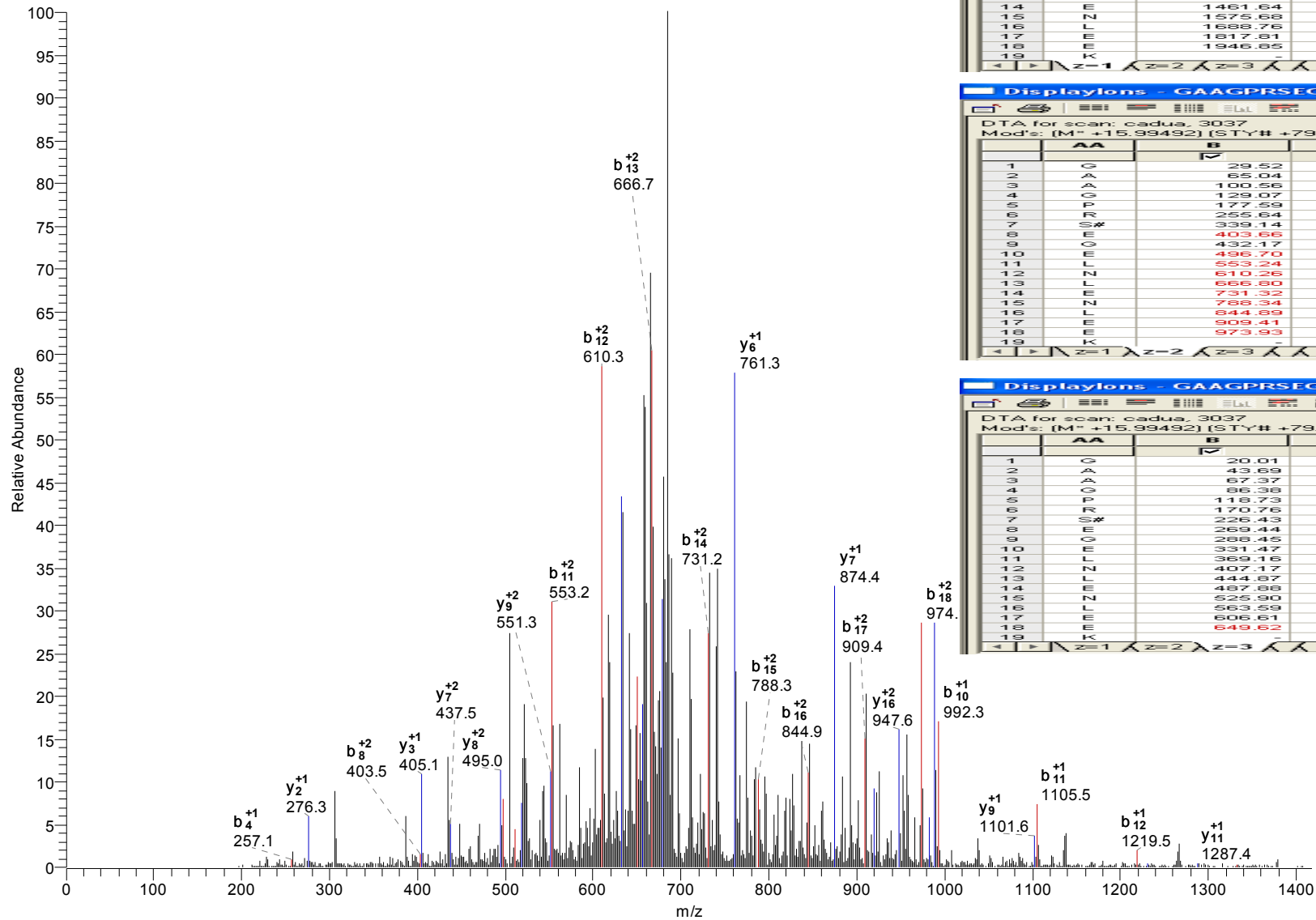
Displaylons - SEGELNLENLEEK

DTA for scan: cap2, 3001
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S#		84.51	-		13
2	E		149.03	708.85		12
3	G		177.54	644.32		11
4	E		242.06	615.81		10
5	L		298.60	551.29		9
6	N		355.62	494.75		8
7	L		412.17	437.73		7
8	E		476.69	381.19		6
9	N		533.71	316.67		5
10	L		590.25	259.64		4
11	E		654.77	203.10		3
12	E		719.29	138.58		2
13	K		-	74.06		1

Akap4 83 kDa protein

#3037-3037 NL: 5.70E3



Displays - GAAGPRSEGEINLENLEEK

DTA for scan: cadua, 3037
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	G	58.03	-	19
2	A	129.07	2035.93	16
3	A	200.10	1964.90	17
4	G	257.12	1893.86	16
5	P	354.18	1936.84	15
6	R	610.28	1739.76	14
7	S	677.28	1583.68	13
8	E	806.32	1416.69	12
9	G	863.34	1287.64	11
10	E	992.35	1230.62	10
11	L	1105.47	1101.58	9
12	N	1219.51	988.49	8
13	L	1332.59	874.45	7
14	E	1461.64	761.37	6
15	N	1575.68	632.32	5
16	L	1688.76	518.28	4
17	E	1817.81	405.20	3
18	E	1946.85	276.16	2
19	K		147.11	1

Displays - GAAGPRSEGEINLENLEEK

DTA for scan: cadua, 3037
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	G	29.52	-	19
2	A	65.04	1018.47	18
3	A	100.56	982.95	17
4	G	129.07	947.43	16
5	P	177.59	918.92	15
6	R	255.64	870.40	14
7	S	339.14	792.35	13
8	E	403.66	708.85	12
9	G	432.17	644.32	11
10	E	496.70	615.81	10
11	L	553.24	551.29	9
12	N	610.26	494.75	8
13	L	666.80	437.73	7
14	E	731.32	381.19	6
15	N	788.34	316.67	5
16	L	844.89	259.64	4
17	E	909.41	203.10	3
18	E	973.93	138.58	2
19	K		74.06	1

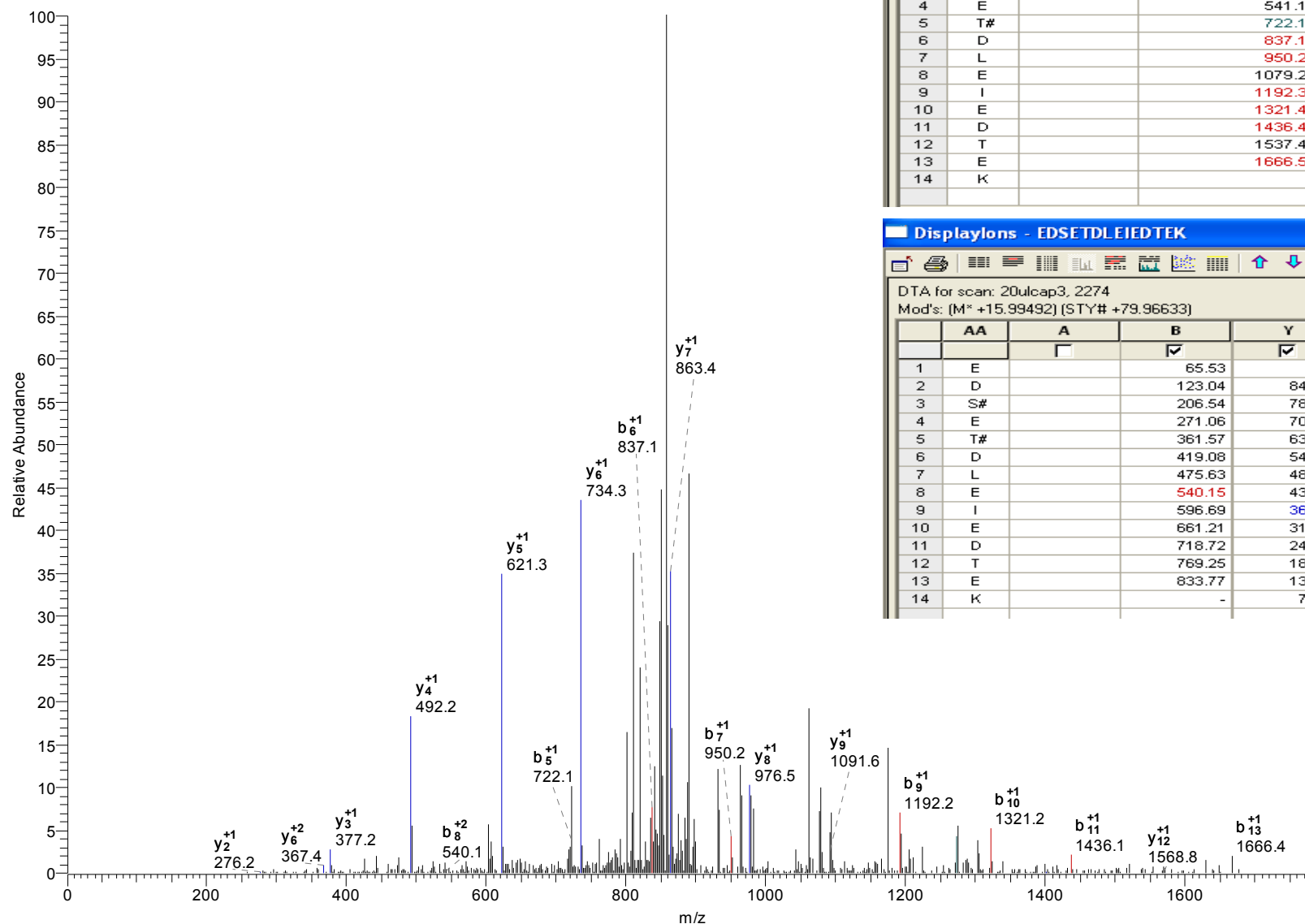
Displays - GAAGPRSEGEINLENLEEK

DTA for scan: cadua, 3037
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	G	20.01	-	19
2	A	43.69	679.32	18
3	A	67.37	655.64	17
4	G	86.38	631.96	16
5	P	118.73	612.95	15
6	R	170.76	580.60	14
7	S	226.43	528.67	13
8	E	269.44	472.90	12
9	G	288.45	429.89	11
10	E	331.47	410.88	10
11	L	369.16	367.86	9
12	N	407.17	330.17	8
13	L	444.87	292.16	7
14	E	487.88	254.46	6
15	N	525.90	211.46	5
16	L	563.59	173.43	4
17	E	606.61	135.74	3
18	E	649.62	92.72	2
19	K		49.71	1

Isoform 1 of Uncharacterized protein C14orf166B homolog

#2274-2274 NL: 1.44E3



Displaylons - EDSETDLEIEDTEK

DTA for scan: 20ulcap3, 2274
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	E		130.05	-	14
2	D		245.08	1683.59	13
3	S#		412.08	1568.57	12
4	E		541.12	1401.57	11
5	T#		722.13	1272.52	10
6	D		837.16	1091.51	9
7	L		950.24	976.48	8
8	E		1079.29	863.40	7
9	I		1192.37	734.36	6
10	E		1321.41	621.27	5
11	D		1436.44	492.23	4
12	T		1537.49	377.20	3
13	E		1666.53	276.16	2
14	K		-	147.11	1

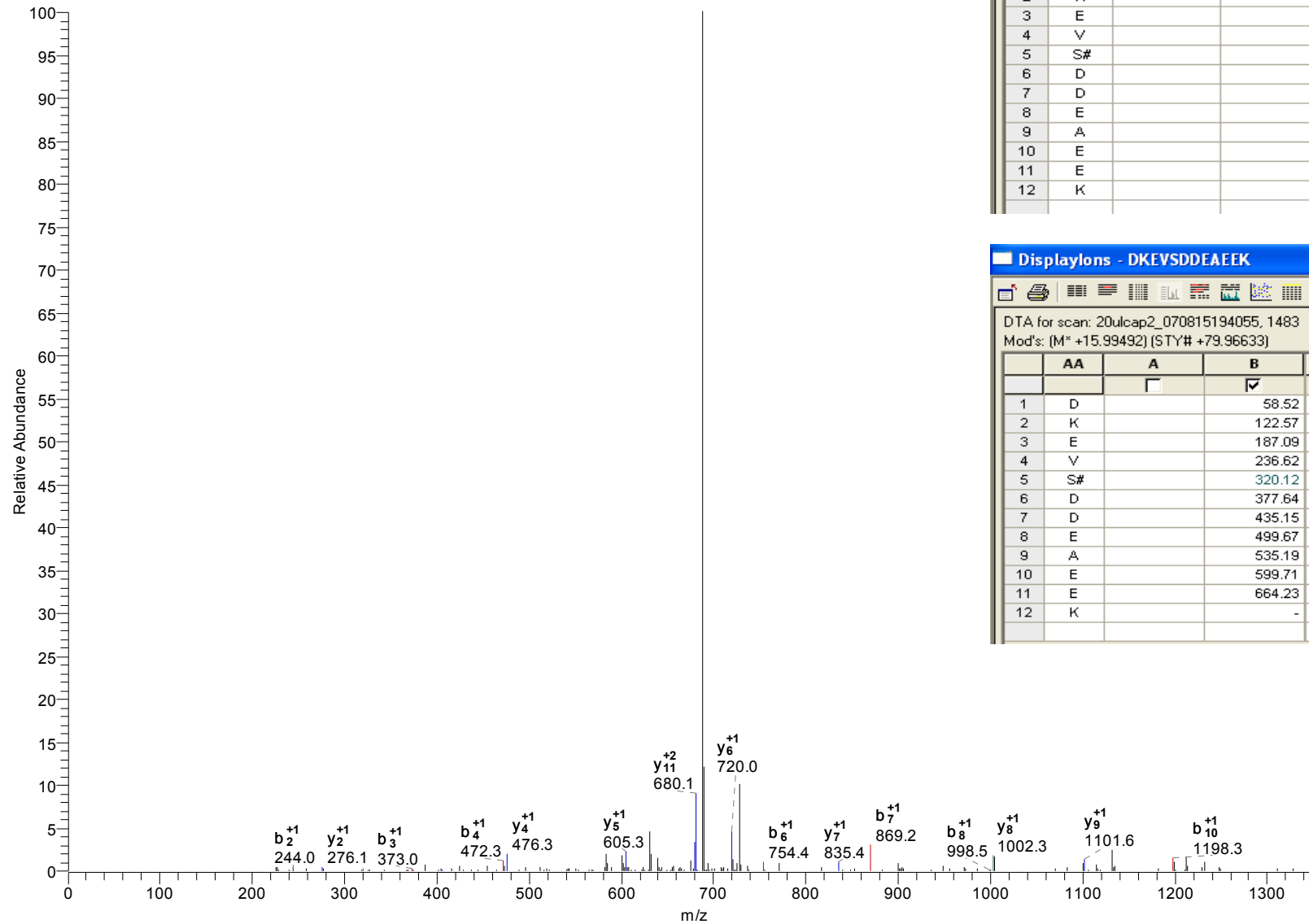
Displaylons - EDSETDLEIEDTEK

DTA for scan: 20ulcap3, 2274
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	E		65.53	-		14
2	D		123.04	842.30		13
3	S#		206.54	784.79		12
4	E		271.06	701.29		11
5	T#		361.57	636.77		10
6	D		419.08	546.26		9
7	L		475.63	488.75		8
8	E		540.15	432.20		7
9	I		596.69	367.68		6
10	E		661.21	311.14		5
11	D		718.72	246.62		4
12	T		769.25	189.11		3
13	E		833.77	138.58		2
14	K		-	74.06		1

Hspca Heat shock protein HSP 90-alpha

#1483-1483 NL: 1.90E3



Displaylons - DKEVSDDEAEEK

DTA for scan: 20ulcap2_070815194055, 1483
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	D		116.03	-	12
2	K		244.13	1358.54	11
3	E		373.17	1230.44	10
4	V		472.24	1101.40	9
5	S#		639.24	1002.33	8
6	D		754.27	835.33	7
7	D		869.29	720.30	6
8	E		998.34	605.28	5
9	A		1069.37	476.24	4
10	E		1198.41	405.20	3
11	E		1327.46	276.16	2
12	K		-	147.11	1

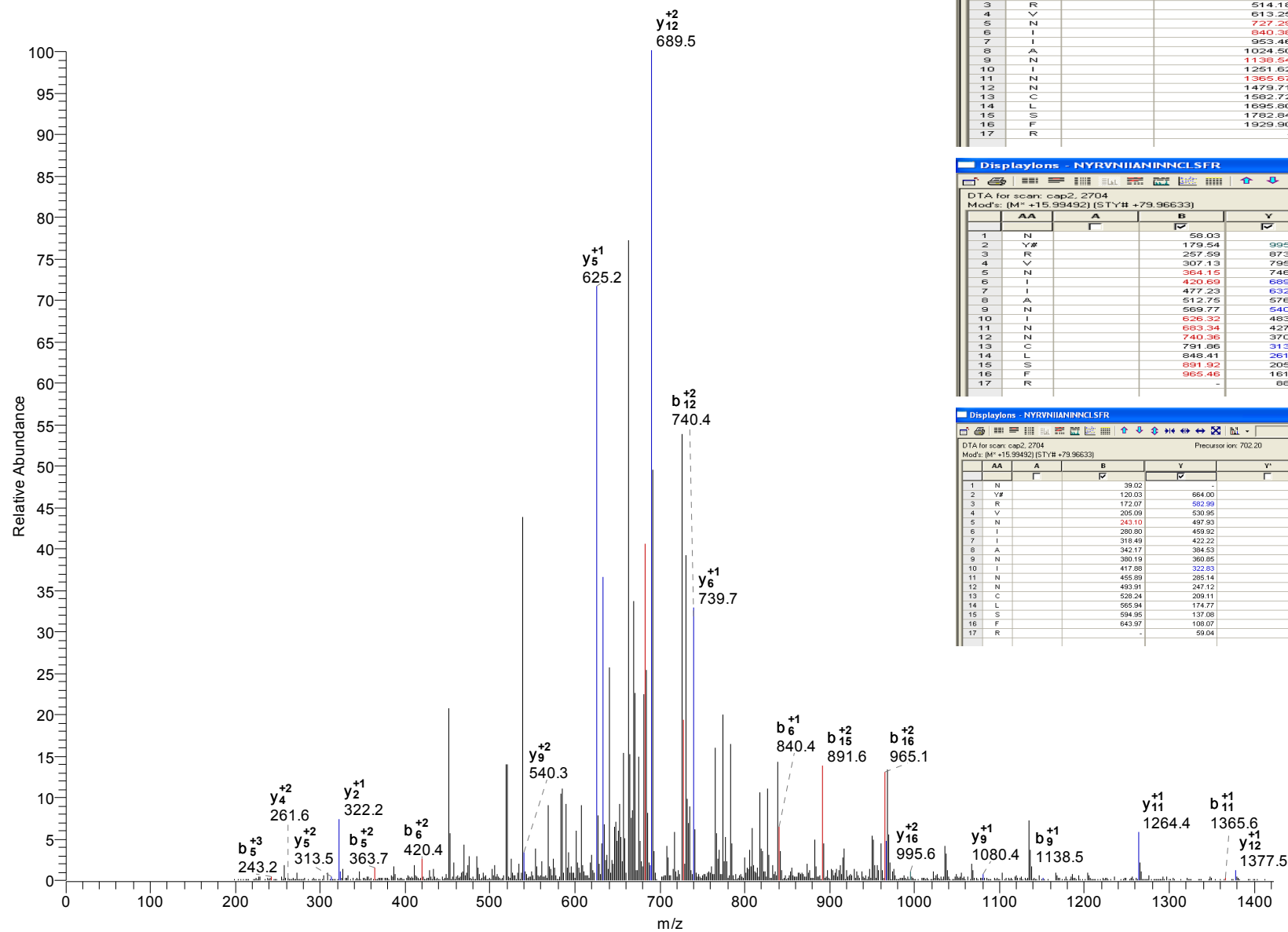
Displaylons - DKEVSDDEAEEK

DTA for scan: 20ulcap2_070815194055, 1483
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	D		58.52	-		12
2	K		122.57	679.77		11
3	E		187.09	615.72		10
4	V		236.62	551.20		9
5	S#		320.12	501.67		8
6	D		377.64	418.17		7
7	D		435.15	360.66		6
8	E		499.67	303.14		5
9	A		535.19	238.62		4
10	E		599.71	203.10		3
11	E		664.23	138.58		2
12	K		-	74.06		1

similar to Tumor necrosis factor, alpha-induced protein 2

#2704-2704 NL: 3.58E4



Displays - NYRVNIININCLSR

DTA for scan: cap2, 2704
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	N			115.05	17
2	Y#			359.06	16
3	R			514.18	15
4	V			613.25	14
5	N			727.29	13
6	I			840.36	12
7	I			953.46	11
8	A			1024.50	10
9	N			1139.54	9
10	I			1251.52	8
11	N			1365.67	7
12	N			1479.71	6
13	C			1582.72	5
14	L			1695.60	4
15	S			1782.84	3
16	F			1929.90	2
17	R			175.12	1

Displays - NYRVNIININCLSR

DTA for scan: cap2, 2704
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z
1	N			58.03	17
2	Y#			179.54	16
3	R			257.59	15
4	V			307.13	14
5	N			364.15	13
6	I			420.69	12
7	I			477.23	11
8	A			512.75	10
9	N			569.77	9
10	I			626.32	8
11	N			683.34	7
12	N			740.36	6
13	C			791.86	5
14	L			848.41	4
15	S			891.92	3
16	F			965.46	2
17	R			88.06	1

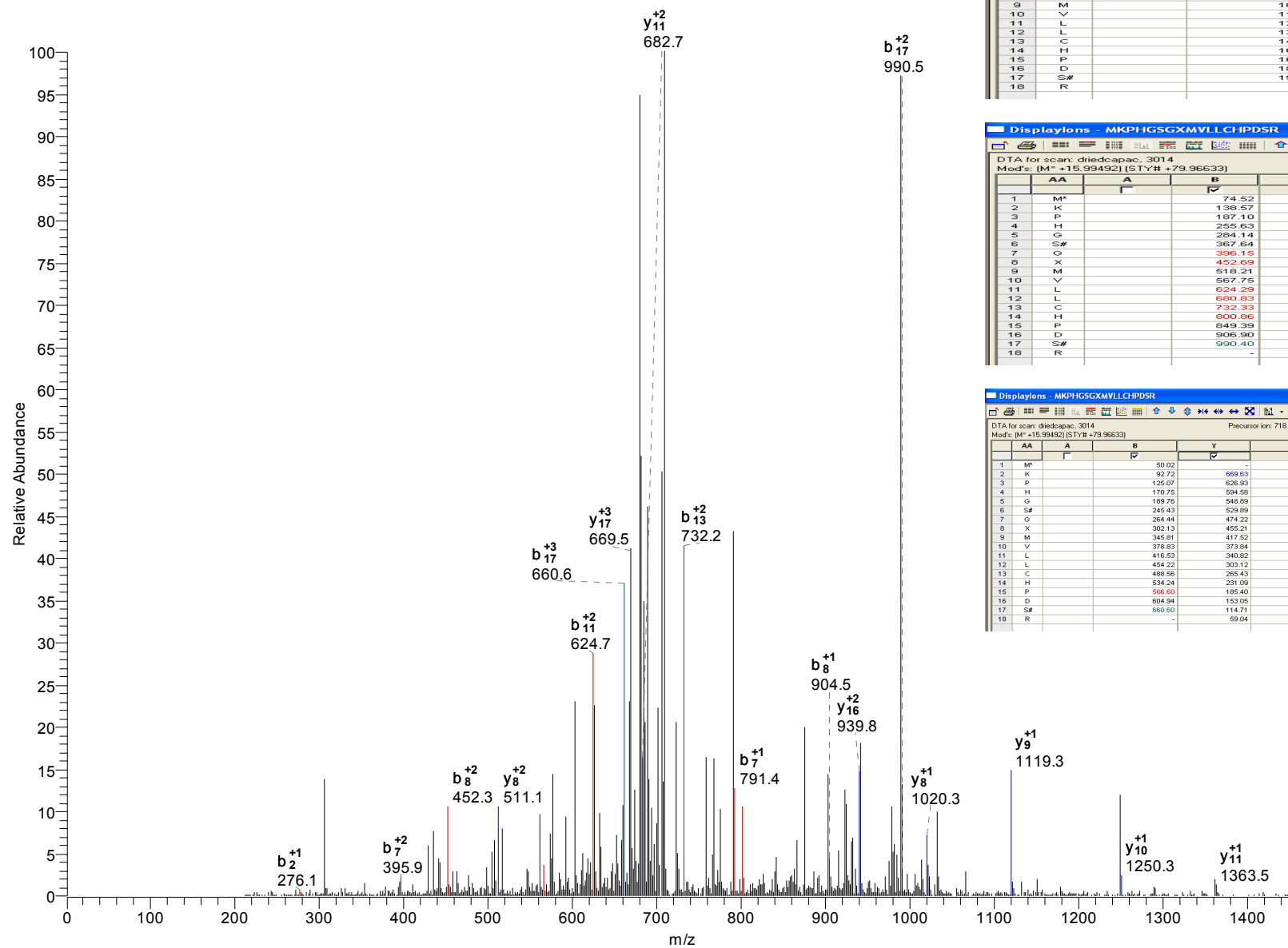
Displays - NYRVNIININCLSR

DTA for scan: cap2, 2704
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Y'	Yo	Z
1	N			39.02			17
2	Y#			120.03	664.00		16
3	R			172.07	582.99		15
4	V			205.09	530.95		14
5	N			243.10	497.93		13
6	I			280.90	459.92		12
7	I			318.49	422.22		11
8	A			342.17	384.53		10
9	N			380.19	350.85		9
10	I			417.88	322.83		8
11	N			455.89	285.14		7
12	N			493.91	247.12		6
13	C			528.24	209.11		5
14	L			565.94	174.77		4
15	S			594.95	137.08		3
16	F			643.97	108.07		2
17	R			59.04			1

Cd209b similar to CD209 antigen-like protein B

#3014-3014 NL: 6.33E3



Displays - MKPHGSGXWVLLCHPDSR

DTA for scan: driedcapac, 3014
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	M*		148.04	-	18
2	K		276.14	2006.67	17
3	P		373.19	1878.78	16
4	H		510.25	1781.73	15
5	G		567.27	1644.67	14
6	S#		734.27	1587.65	13
7	Q		791.29	1420.65	12
8	X		904.37	1363.63	11
9	M		1035.42	1250.54	10
10	V		1134.48	1119.50	9
11	L		1247.57	1020.43	8
12	L		1360.65	907.36	7
13	C		1463.66	794.27	6
14	H		1600.72	691.26	5
15	P		1697.77	554.20	4
16	D		1812.80	457.14	3
17	S#		1979.80	342.12	2
18	R		-	175.12	1

Displays - MKPHGSGXWVLLCHPDSR

DTA for scan: driedcapac, 3014
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z
1	M*		74.52	-	18
2	K		136.57	1003.94	17
3	P		167.10	939.89	16
4	H		255.63	891.37	15
5	G		284.14	822.84	14
6	S#		367.64	794.33	13
7	Q		396.15	710.83	12
8	X		452.69	662.32	11
9	M		516.21	625.77	10
10	V		567.75	560.25	9
11	L		624.29	510.72	8
12	L		680.83	454.18	7
13	C		732.33	397.64	6
14	H		800.66	346.13	5
15	P		849.39	277.60	4
16	D		906.90	229.08	3
17	S#		990.40	171.56	2
18	R		-	88.06	1

Displays - MKPHGSGXWVLLCHPDSR

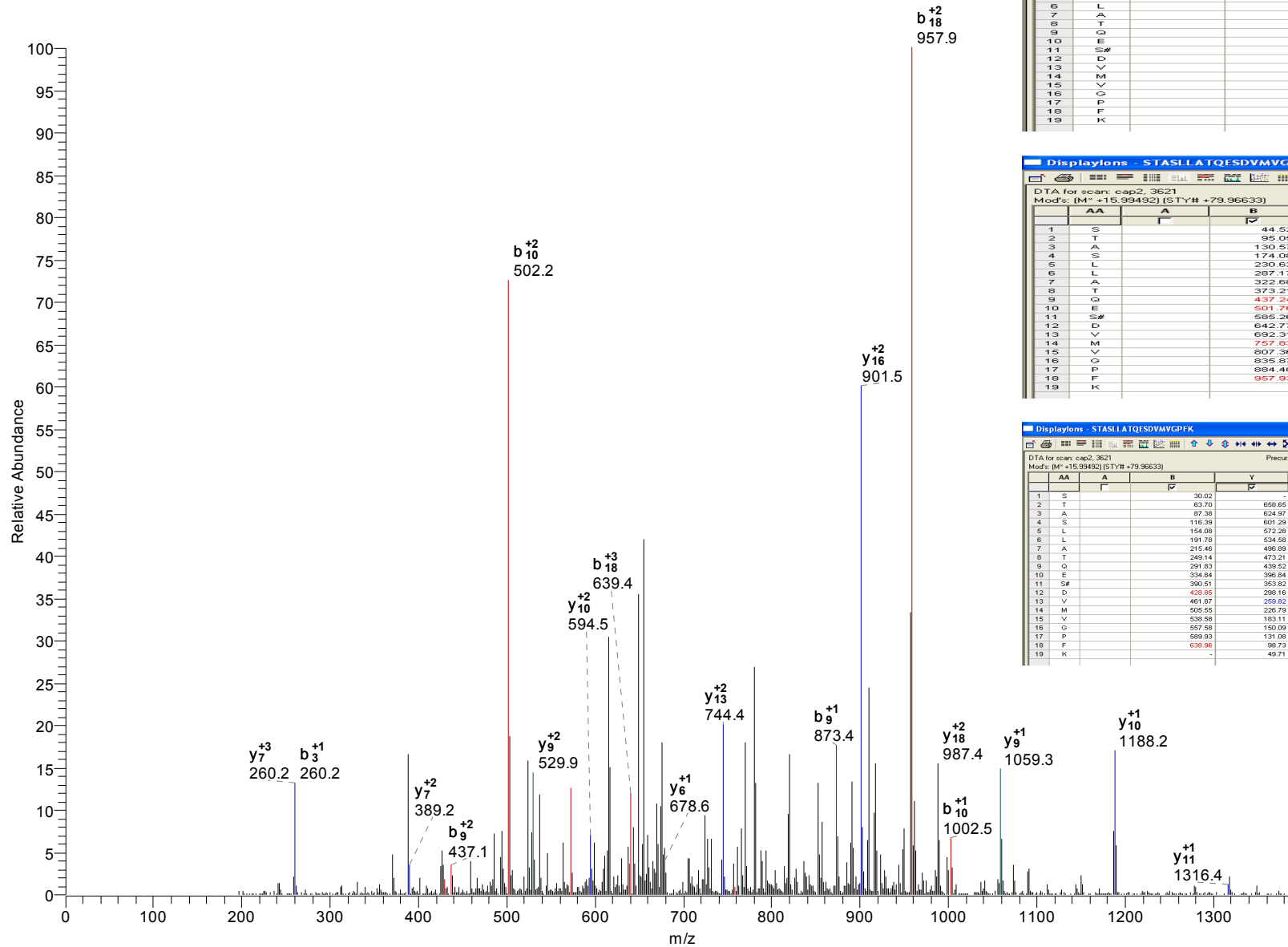
DTA for scan: driedcapac, 3014
Mod's: [M⁺ +15.99492] (STY# +79.96633)

Precursor ion: 718.39 Charge: 3 Activation type: CID Mass

	AA	A	B	Y	Y ⁺	Y ^o	Z
1	M*		50.02	-			18
2	K		92.72	669.63			17
3	P		125.07	626.93			16
4	H		170.75	594.58			15
5	G		199.76	548.89			14
6	S#		245.43	529.89			13
7	Q		264.44	474.22			12
8	X		302.13	455.21			11
9	M		345.81	417.52			10
10	V		378.83	373.84			9
11	L		416.53	340.62			8
12	L		454.22	303.12			7
13	C		488.56	265.43			6
14	H		534.24	231.09			5
15	P		568.60	185.40			4
16	D		604.94	153.05			3
17	S#		660.60	114.71			2
18	R		-	59.04			1

Akap2 A Kinase Anchoring Protein 2

#3621-3621 NL: 1.36E4



Displays - STASLATQESDVMVGPEK

DTA for scan: cap2_3621
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S		68.04		19
2	T		189.09	1973.93	18
3	A		269.12	1872.88	17
4	S		347.16	1801.84	16
5	L		460.24	1714.81	15
6	L		573.32	1601.73	14
7	A		644.36	1488.64	13
8	T		745.41	1417.61	12
9	G		873.47	1316.56	11
10	E		1002.51	1188.50	10
11	S#		1169.51	1059.46	9
12	D		1284.54	892.46	8
13	V		1383.60	777.43	7
14	M		1514.64	678.36	6
15	V		1613.71	547.32	5
16	G		1670.73	448.26	4
17	P		1767.79	391.23	3
18	F		1914.86	294.18	2
19	K		-	147.11	1

Displays - STASLATQESDVMVGPEK

DTA for scan: cap2_3621
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z
1	S		44.52		19
2	T		95.05	987.47	18
3	A		130.57	936.94	17
4	S		174.08	901.43	16
5	L		230.62	857.91	15
6	L		287.17	801.37	14
7	A		322.68	744.83	13
8	T		373.21	709.31	12
9	G		437.24	658.78	11
10	E		501.76	594.76	10
11	S#		565.26	530.23	9
12	D		642.77	446.73	8
13	V		692.31	369.22	7
14	M		757.83	339.69	6
15	V		807.36	274.17	5
16	G		835.87	224.83	4
17	P		884.40	196.12	3
18	F		957.93	147.59	2
19	K		-	74.06	1

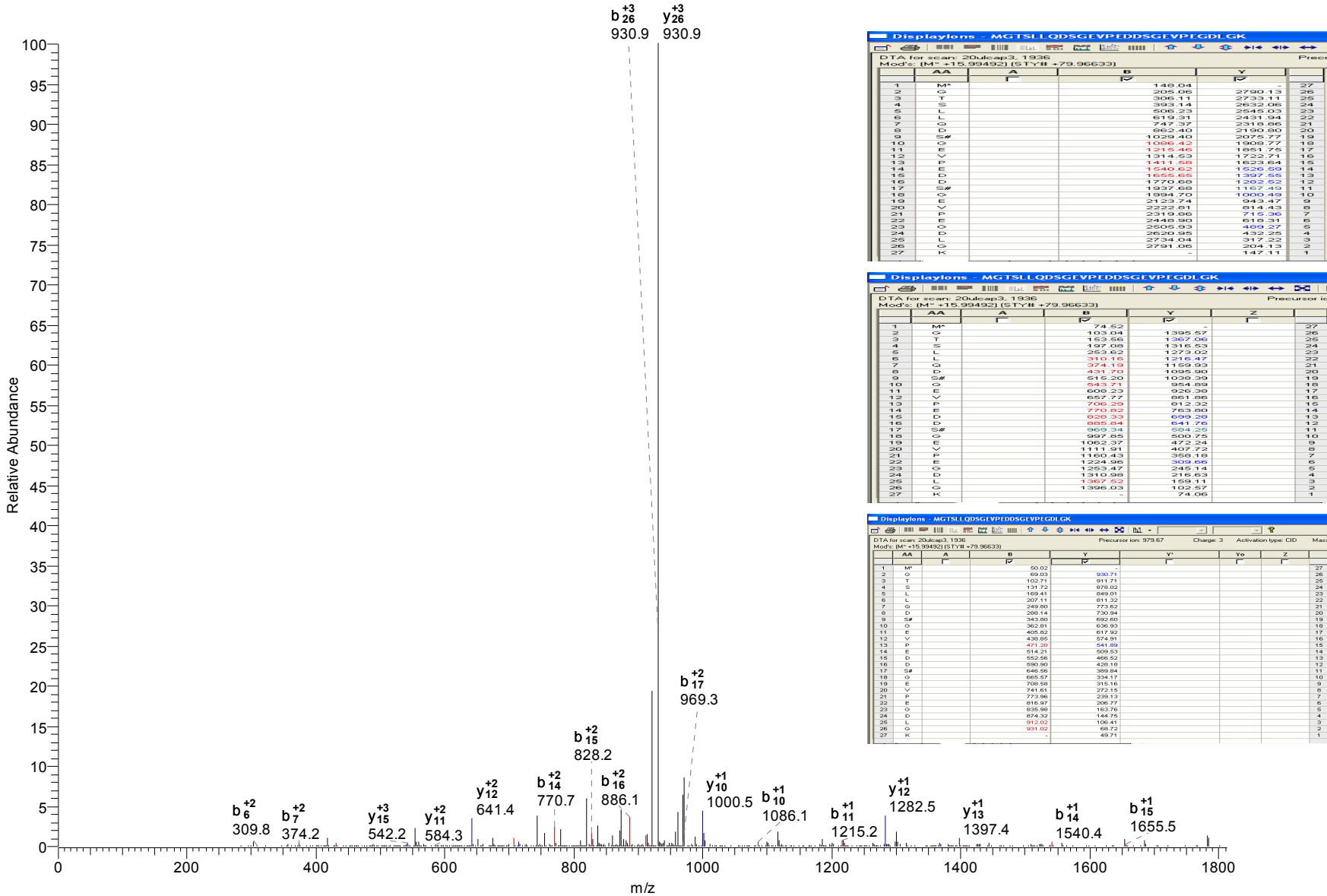
Displays - STASLATQESDVMVGPEK

DTA for scan: cap2_3621
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Y ⁺	Y ^o	Z
1	S		30.02				19
2	T		63.70				18
3	A		87.38				17
4	S		116.39				16
5	L		154.08				15
6	L		191.78				14
7	A		215.46				13
8	T		249.14				12
9	G		291.83				11
10	E		334.04				10
11	S#		390.51				9
12	D		429.85				8
13	V		461.87				7
14	M		505.55				6
15	V		539.58				5
16	G		557.58				4
17	P		589.93				3
18	F		638.96				2
19	K		-				1

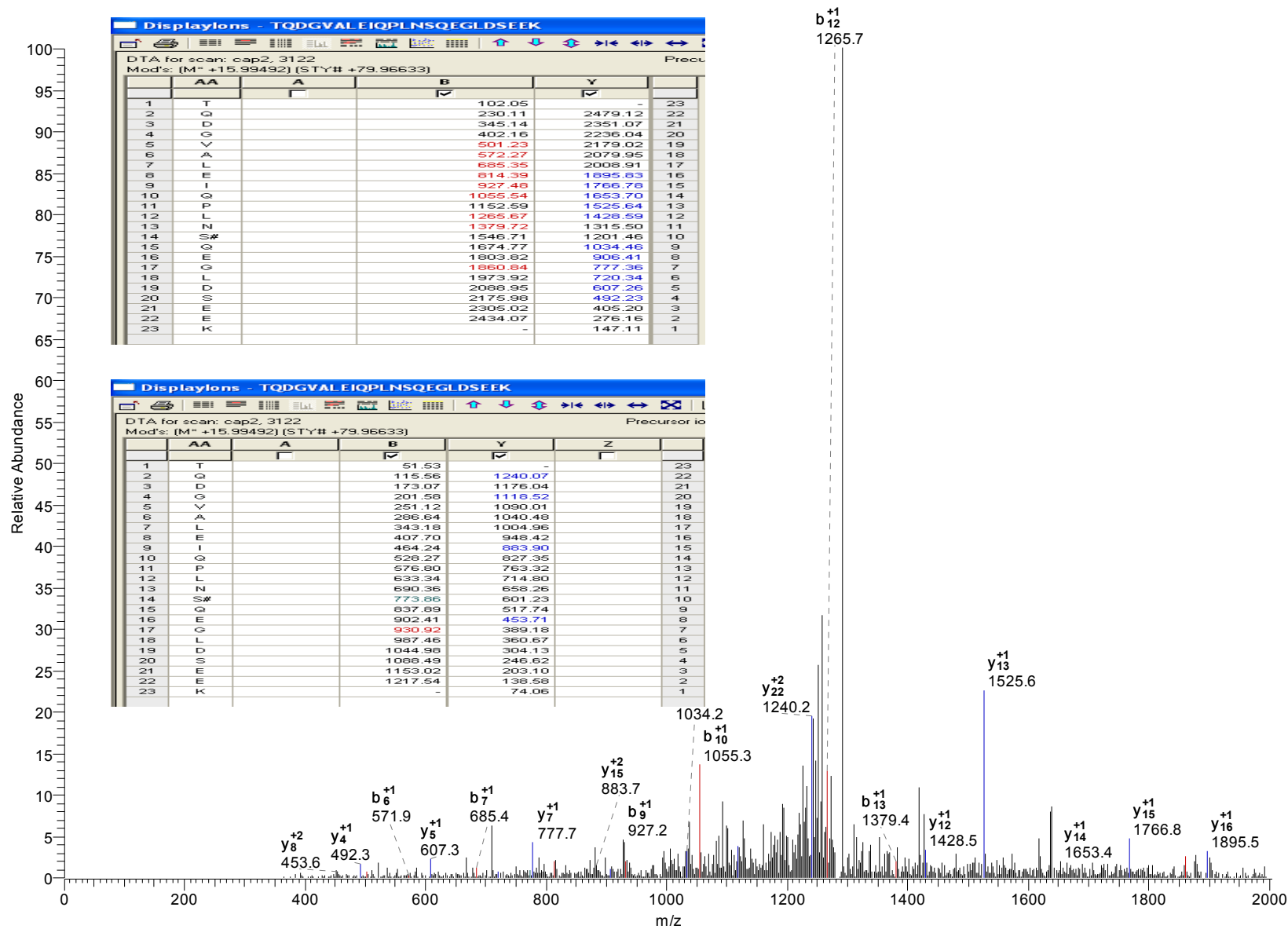
19 kDa protein

#1936-1936 NL: 1.23E4



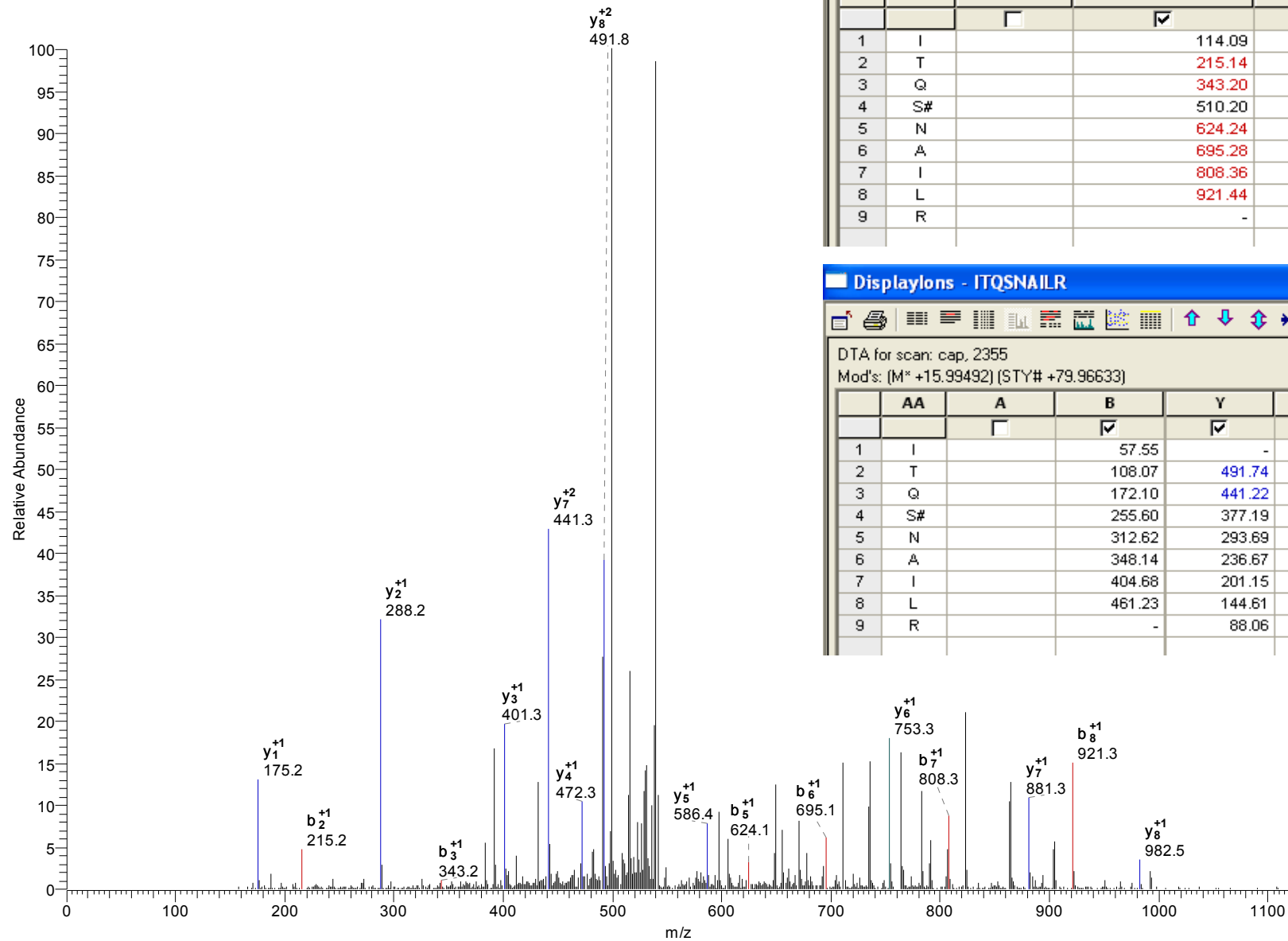
Atp2b4 Isoform XB of Plasma membrane calcium-transporting ATPase 4

#3122-3122 NL: 2.44E3



Similar to glutathione transferase GSTM7-7

#2355-2355 NL: 5.72E3



Displaylons - ITQSNAILR

DTA for scan: cap, 2355
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	I		114.09	-	9
2	T		215.14	982.47	8
3	Q		343.20	881.42	7
4	S#		510.20	753.37	6
5	N		624.24	586.37	5
6	A		695.28	472.32	4
7	I		808.36	401.29	3
8	L		921.44	288.20	2
9	R		-	175.12	1

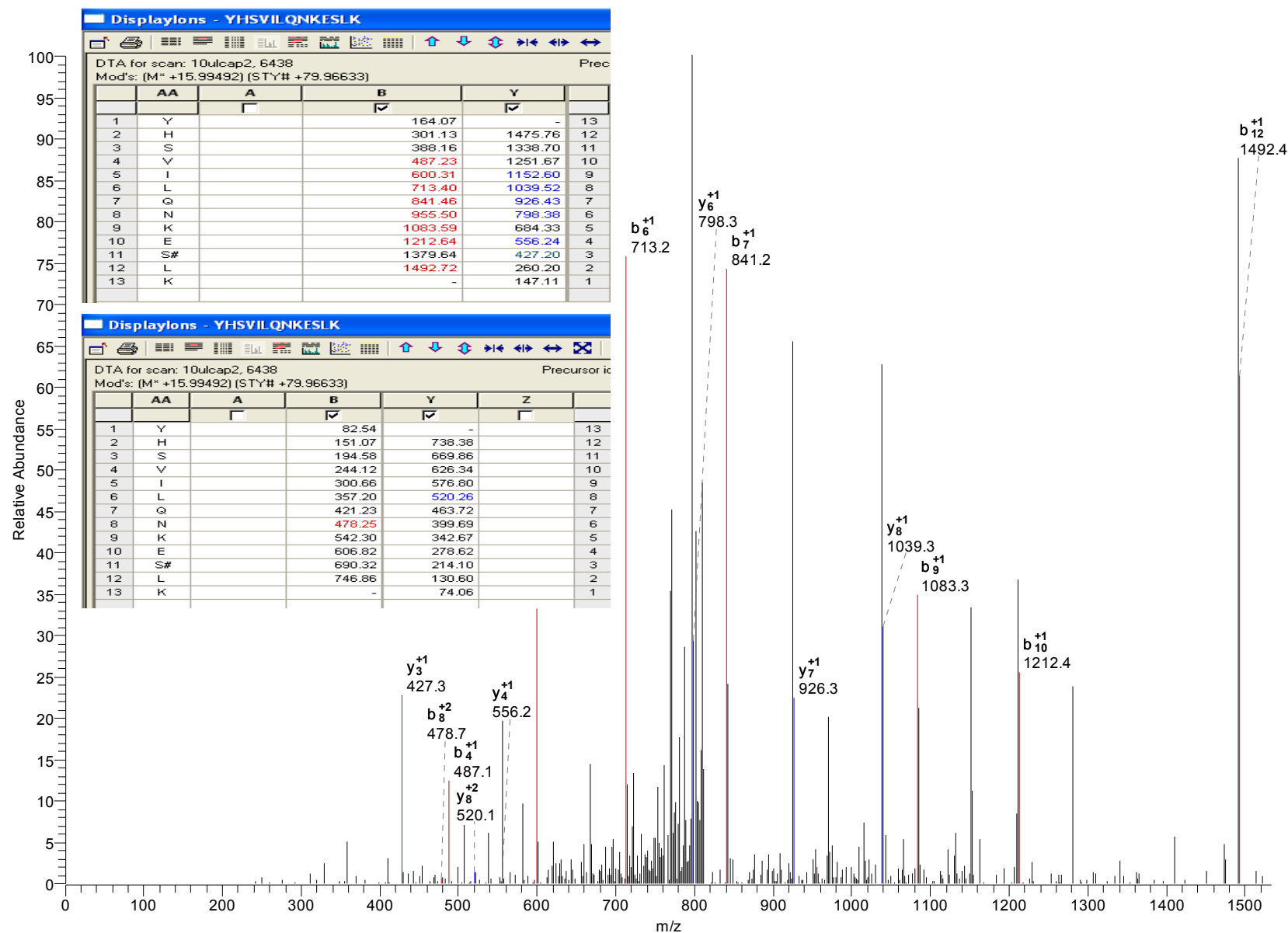
Displaylons - ITQSNAILR

DTA for scan: cap, 2355
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	I		57.55	-		9
2	T		108.07	491.74		8
3	Q		172.10	441.22		7
4	S#		255.60	377.19		6
5	N		312.62	293.69		5
6	A		348.14	236.67		4
7	I		404.68	201.15		3
8	L		461.23	144.61		2
9	R		-	88.06		1

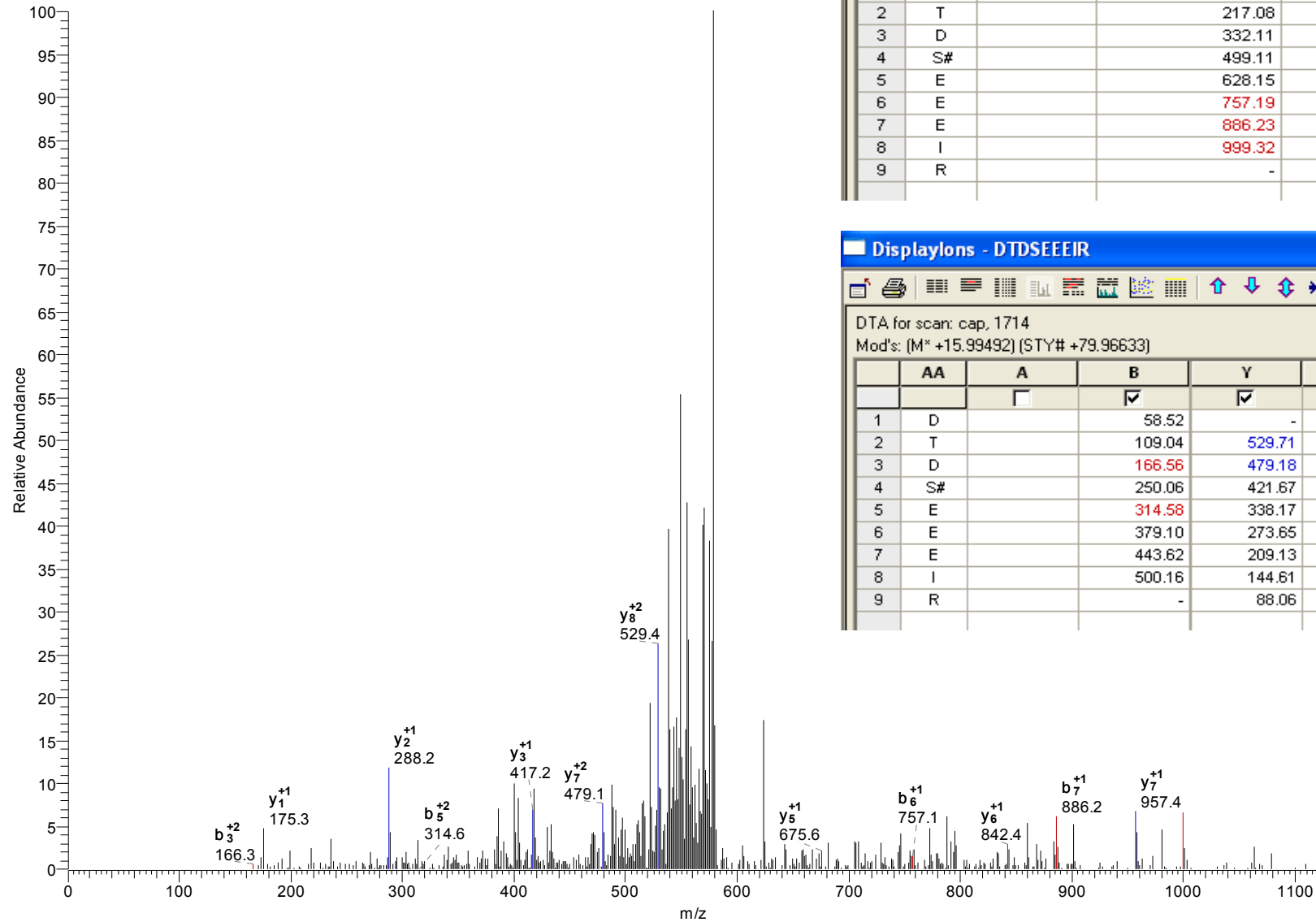
Hrmt1l1 HMT1 hnRNP methyltransferase-like 1

#6438-6438 NL: 2.28E2



Calml3 Calmodulin like protein 3

#1714-1714 NL: 9.02E2



Displaylons - DTDSEEEIR

DTA for scan: cap, 1714
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	D	☐	☒	☒	
2	T		116.03	-	9
3	D		217.08	1058.40	8
4	S#		332.11	957.36	7
5	E		499.11	842.33	6
6	E		628.15	675.33	5
7	E		757.19	546.29	4
8	I		886.23	417.25	3
9	R		999.32	288.20	2
			-	175.12	1

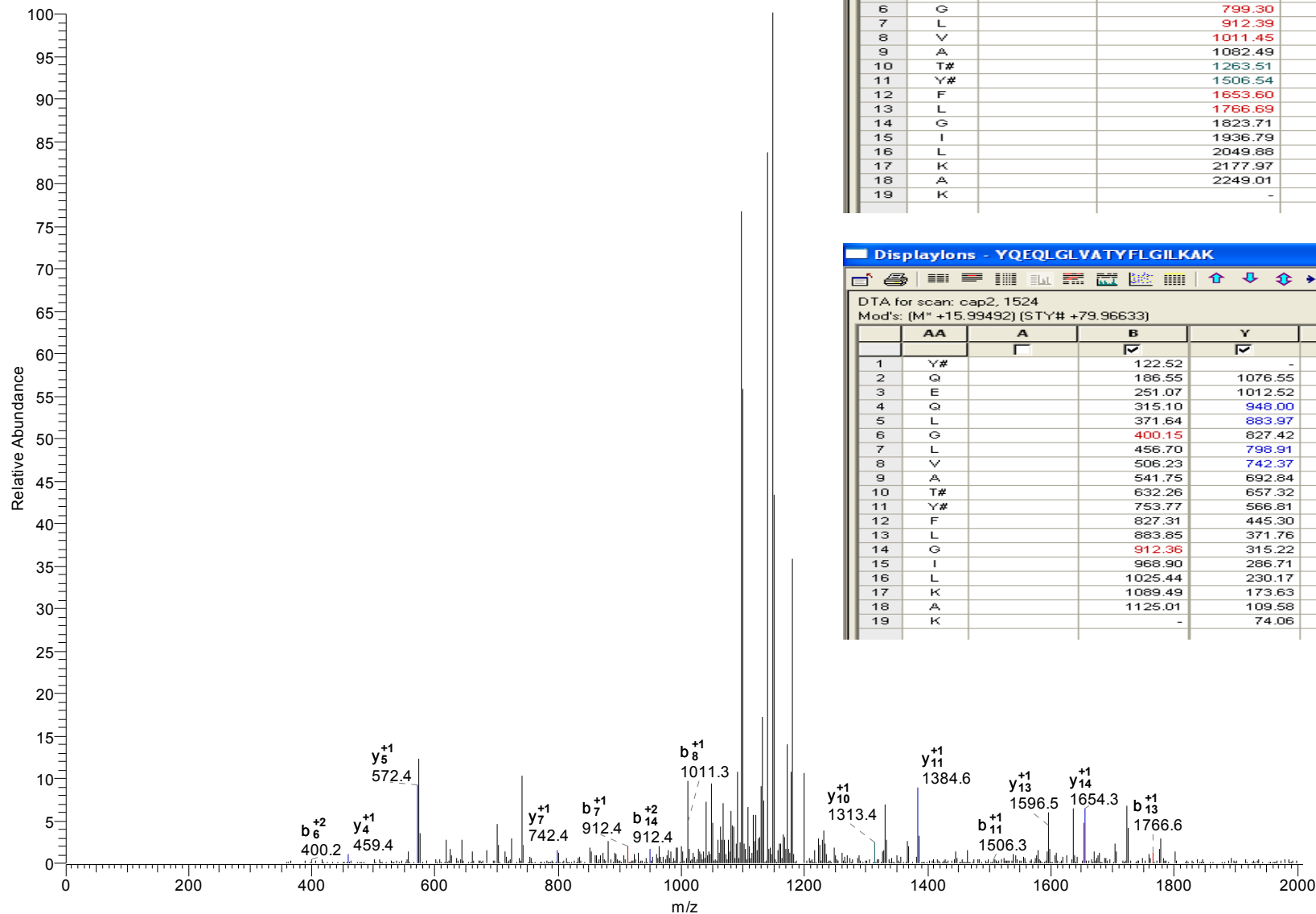
Displaylons - DTDSEEEIR

DTA for scan: cap, 1714
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	D	☐	☒	☒	☐	
2	T		58.52	-		9
3	D		109.04	529.71		8
4	S#		166.56	479.18		7
5	E		250.06	421.67		6
6	E		314.58	338.17		5
7	E		379.10	273.65		4
8	I		443.62	209.13		3
9	R		500.16	144.61		2
			-	88.06		1

predicted similar to RhoGEF4 CG8606-PA,
isoform A

#1524-1524 NL: 2.89E3



Displaylons - YQEQLGLVATYFLGILKAK

DTA for scan: cap2, 1524
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	Y#				19
2	Q		244.04	-	18
3	E		372.10	2152.09	17
4	Q		501.14	2024.03	16
5	L		629.20	1894.98	15
6	G		742.28	1766.93	14
7	L		799.30	1653.84	13
8	V		912.39	1596.82	12
9	A		1011.45	1483.74	11
10	T#		1082.49	1384.67	10
11	Y#		1263.51	1313.63	9
12	F		1506.54	1132.62	8
13	L		1653.60	889.59	7
14	G		1766.69	742.52	6
15	I		1823.71	629.43	5
16	L		1936.79	572.41	4
17	K		2049.88	459.33	3
18	A		2177.97	346.24	2
19	K		2249.01	218.15	1
			-	147.11	

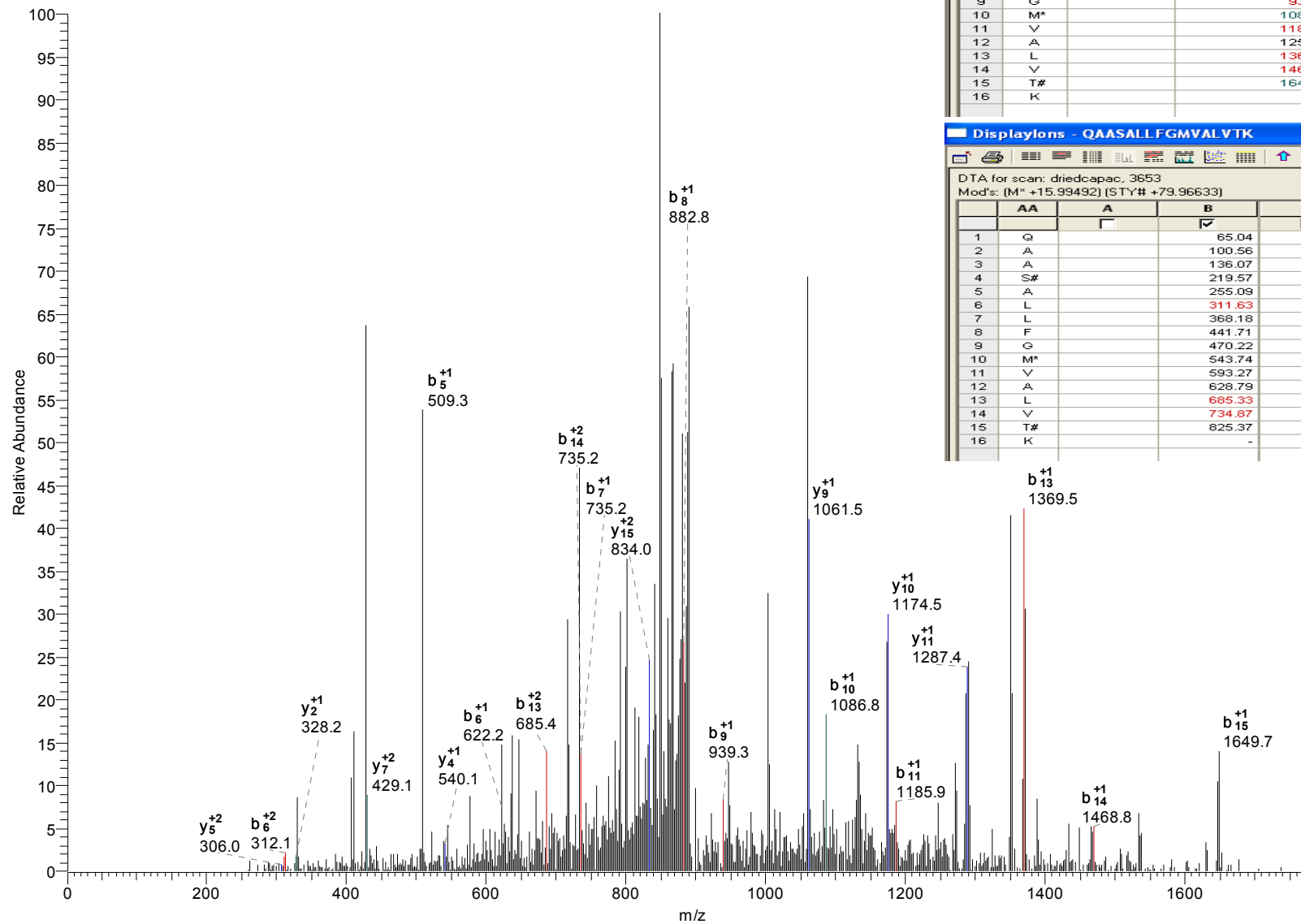
Displaylons - YQEQLGLVATYFLGILKAK

DTA for scan: cap2, 1524
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	Y#					19
2	Q		122.52	-		18
3	E		186.55	1076.55		17
4	Q		251.07	1012.52		16
5	L		315.10	948.00		15
6	L		371.64	883.97		14
7	G		400.15	827.42		13
8	V		456.70	798.91		12
9	A		506.23	742.37		11
10	T#		541.75	692.84		10
11	Y#		632.26	657.32		9
12	F		753.77	566.81		8
13	L		827.31	445.30		7
14	L		883.85	371.76		6
15	G		912.36	315.22		5
16	I		968.90	286.71		4
17	L		1025.44	230.17		3
18	K		1089.49	173.63		2
19	A		1125.01	109.58		1
	K		-	74.06		

58 kDa protein

#3653-3653 NL: 9.14E2



Displaylons - QAASALLFGMVALVTK

DTA for scan: driedcapac, 3653
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	Q				16
2	A		129.07	-	15
3	A		200.10	1667.79	14
4	S#		271.14	1596.75	13
5	A		438.14	1525.71	12
6	L		509.18	1358.72	11
7	L		622.26	1287.68	10
8	F		735.34	1174.59	9
9	G		882.41	1061.51	8
10	M*		939.43	914.44	7
11	V		1086.47	857.42	6
12	A		1185.54	710.38	5
13	L		1256.57	611.32	4
14	V		1369.66	540.28	3
15	T#		1468.73	427.20	2
16	K		1649.74	328.13	1

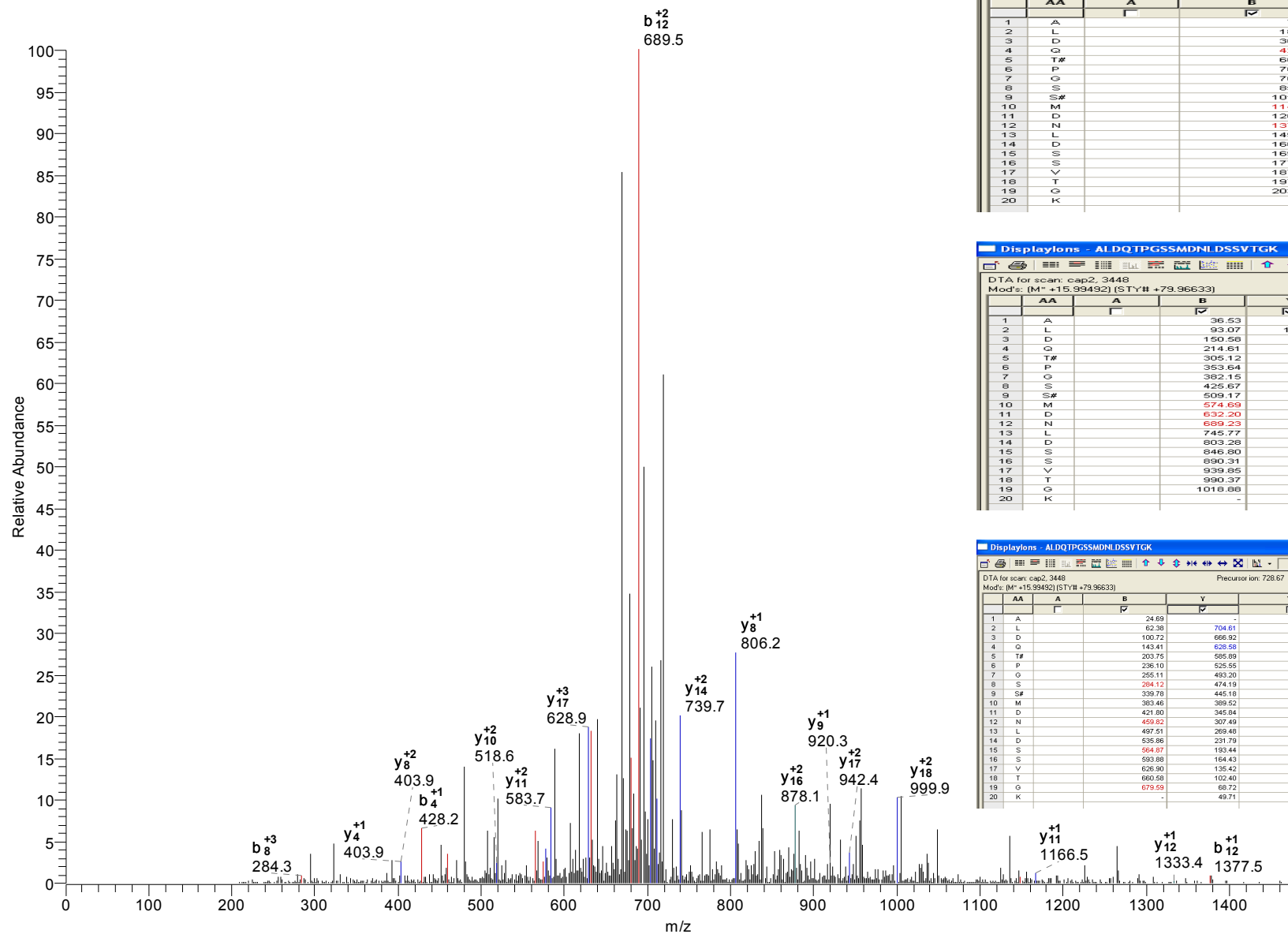
Displaylons - QAASALLFGMVALVTK

DTA for scan: driedcapac, 3653
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z
1	Q				16
2	A		65.04	-	15
3	A		100.56	834.40	14
4	S#		136.07	798.88	13
5	A		219.57	763.36	12
6	L		255.09	679.86	11
7	L		311.63	644.34	10
8	F		366.18	587.80	9
9	G		441.71	531.26	8
10	M*		470.22	457.72	7
11	V		543.74	429.21	6
12	A		593.27	355.70	5
13	L		628.79	306.16	4
14	V		685.33	270.64	3
15	T#		734.87	214.10	2
16	K		825.37	164.57	1

Robo2 similar to Roundabout homolog 2 precursor

#3448-3448 NL: 6.35E3



Displayions - ALDQTPGSSMDNLDSSVTGK

DTA for scan: cap2, 3448
Mod's: (M⁺+15.99492) (S⁺T⁺Y⁺+79.96633)

	AA	A	B	Y	
1	A		72.04		20
2	L		185.13		19
3	D		300.16		18
4	Q		426.21		17
5	T#		609.23		16
6	P		706.28		15
7	G		763.30		14
8	S		850.33		13
9	S#		1017.39		12
10	M		1148.37		11
11	D		1263.40		10
12	N		1377.44		9
13	L		1490.53		8
14	D		1605.55		7
15	S		1692.59		6
16	S		1779.62		5
17	V		1878.69		4
18	T		1979.73		3
19	G		2036.76		2
20	K		-	147.11	1

Displayions - ALDQTPGSSMDNLDSSVTGK

DTA for scan: cap2, 3448
Mod's: (M⁺+15.99492) (S⁺T⁺Y⁺+79.96633)

	AA	A	B	Y	Z	
1	A		36.53			20
2	L		93.07			19
3	D		150.58			18
4	Q		214.51			17
5	T#		305.12			16
6	P		353.64			15
7	G		382.15			14
8	S		425.67			13
9	S#		509.17			12
10	M		574.69			11
11	D		632.20			10
12	N		689.23			9
13	L		745.77			8
14	D		803.28			7
15	S		846.80			6
16	S		890.31			5
17	V		939.85			4
18	T		990.37			3
19	G		1018.88			2
20	K		-	74.06		1

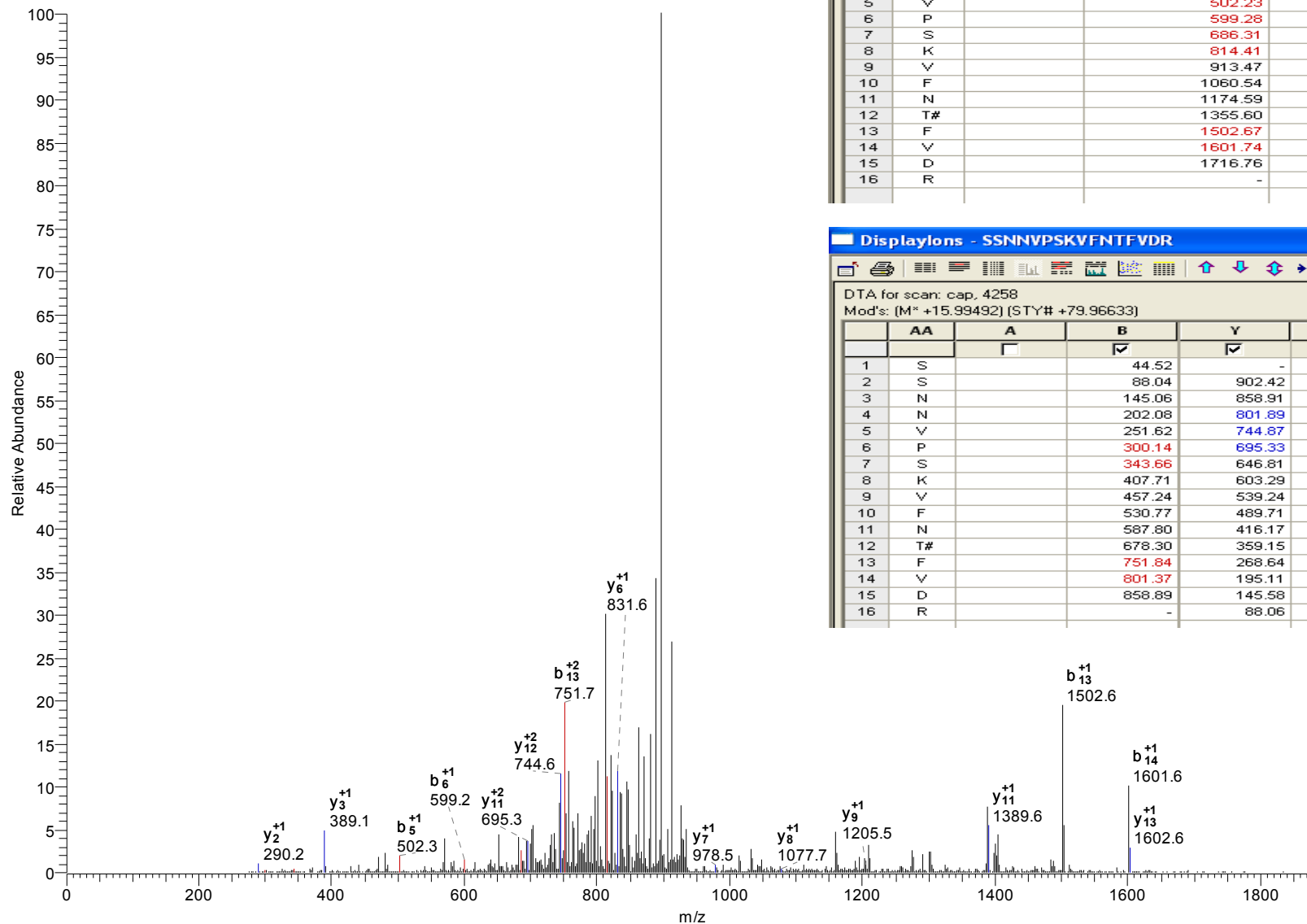
Displayions - ALDQTPGSSMDNLDSSVTGK

DTA for scan: cap2, 3448
Mod's: (M⁺+15.99492) (S⁺T⁺Y⁺+79.96633)

	AA	A	B	Y	Y'	Y''	Z	
1	A		24.69					20
2	L		62.38					19
3	D		100.72					18
4	Q		143.41					17
5	T#		203.75					16
6	P		236.10					15
7	G		255.11					14
8	S		284.12					13
9	S#		339.78					12
10	M		383.46					11
11	D		421.80					10
12	N		459.92					9
13	L		497.51					8
14	D		535.86					7
15	S		564.87					6
16	S		603.88					5
17	V		626.90					4
18	T		660.58					3
19	G		679.59					2
20	K		-	49.71				1

RGD1306520 similar to receptor-interacting factor 1 isoform 1

#4258-4258 NL: 2.31E4



Displaylons - SSNNVPSKVFNTFVDR

DTA for scan: cap. 4258
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	S		88.04	-	16
2	S		175.07	1803.84	15
3	N		289.11	1716.81	14
4	N		403.16	1602.77	13
5	V		502.23	1488.72	12
6	P		599.28	1389.66	11
7	S		686.31	1292.60	10
8	K		814.41	1205.57	9
9	V		913.47	1077.48	8
10	F		1060.54	978.41	7
11	N		1174.59	831.34	6
12	T#		1355.60	717.30	5
13	F		1502.67	536.28	4
14	V		1601.74	389.21	3
15	D		1716.76	290.15	2
16	R		-	175.12	1

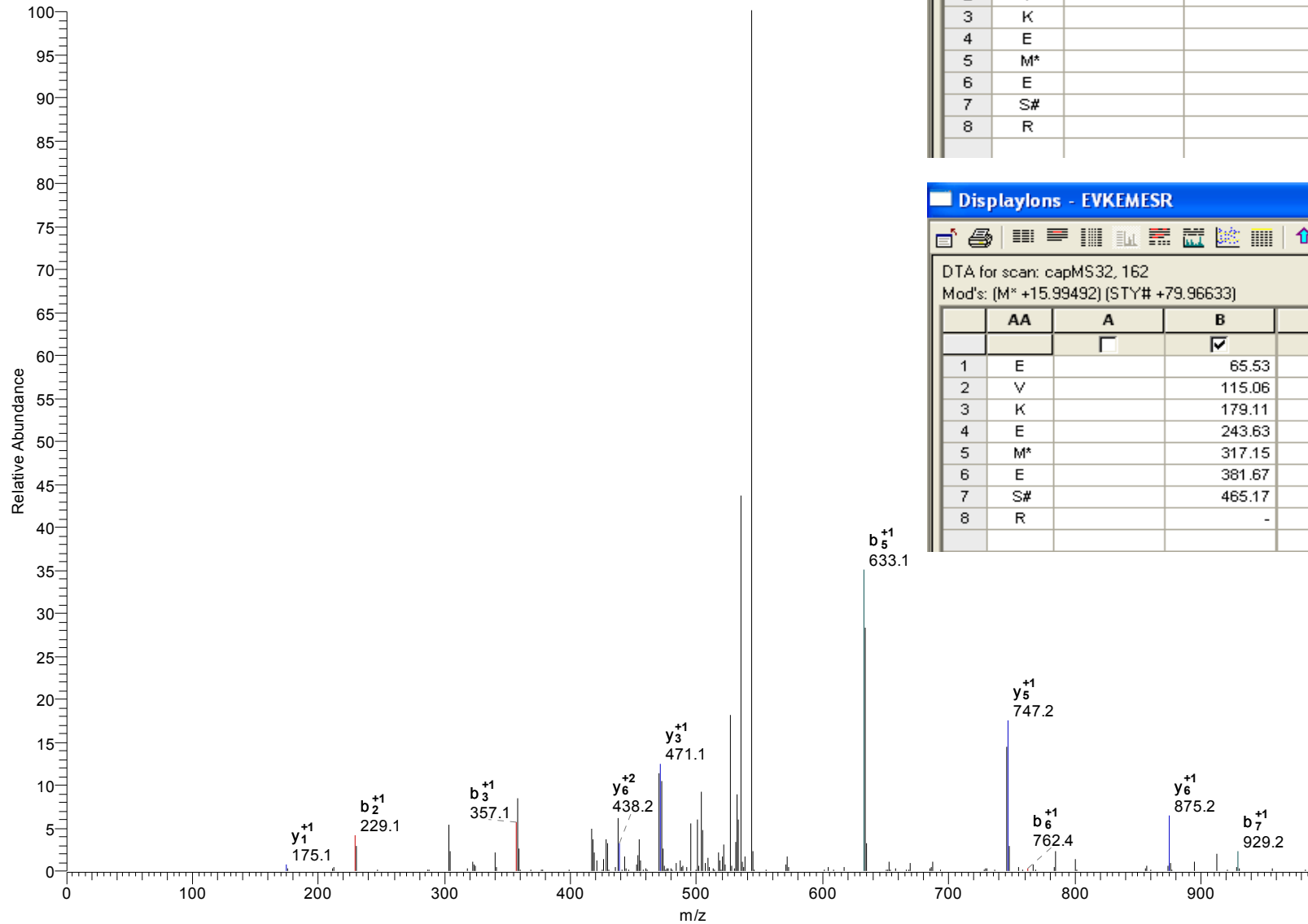
Displaylons - SSNNVPSKVFNTFVDR

DTA for scan: cap. 4258
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	S		44.52	-		16
2	S		88.04	902.42		15
3	N		145.06	858.91		14
4	N		202.08	801.89		13
5	V		251.62	744.87		12
6	P		300.14	695.33		11
7	S		343.66	646.81		10
8	K		407.71	603.29		9
9	V		457.24	539.24		8
10	F		530.77	489.71		7
11	N		587.80	416.17		6
12	T#		678.30	359.15		5
13	F		751.84	268.64		4
14	V		801.37	195.11		3
15	D		858.89	145.58		2
16	R		-	88.06		1

similar to phosphatidylinositol-3-phosphate/phosphatidylinositol 5-kinase, type III isoform 2

#162-162 NL: 7.95E2



Displaylons - EVKEMESR

DTA for scan: capMS32, 162
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
		☐	☒	☒	
1	E		130.05	-	8
2	V		229.12	974.40	7
3	K		357.21	875.33	6
4	E		486.26	747.24	5
5	M*		633.29	618.20	4
6	E		762.33	471.16	3
7	S#		929.33	342.12	2
8	R		-	175.12	1

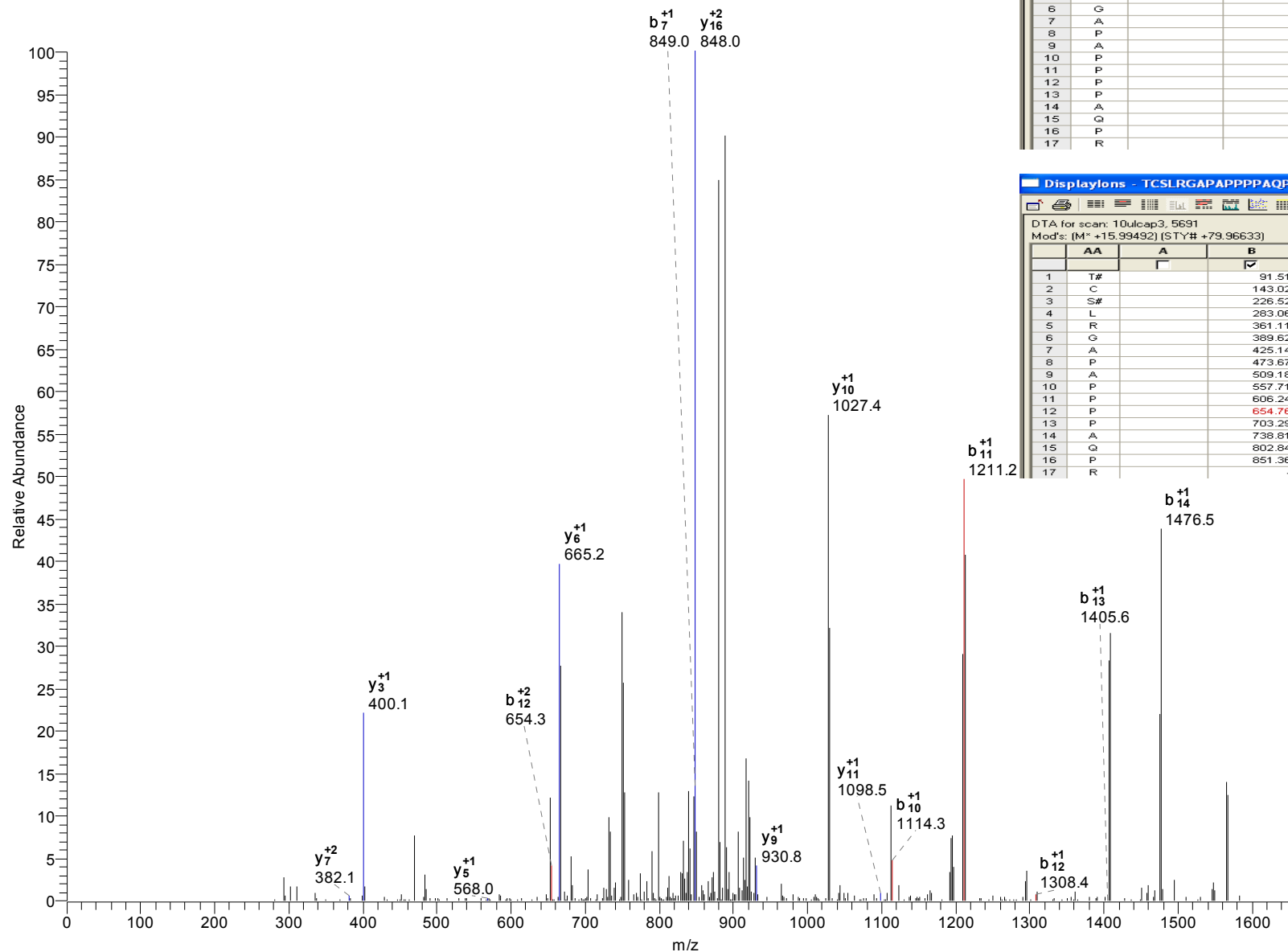
Displaylons - EVKEMESR

DTA for scan: capMS32, 162
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
		☐	☒	☒	☐	
1	E		65.53	-		8
2	V		115.06	487.70		7
3	K		179.11	438.17		6
4	E		243.63	374.12		5
5	M*		317.15	309.60		4
6	E		381.67	236.08		3
7	S#		465.17	171.56		2
8	R		-	88.06		1

RGD1560959 predicted similar to CG8312-PA, Isoform A

#5691-5691 NL:6.61E2



Displaylons - TCSLRGAPAPPPPAQPR

DTA for scan: 10ulcap3, 5691
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	T#		182.02	-	17
2	C		285.03	1694.82	16
3	S#		452.03	1591.81	15
4	L		565.11	1424.81	14
5	R		721.21	1311.73	13
6	G		778.24	1155.63	12
7	A		849.27	1098.61	11
8	P		946.33	1027.57	10
9	A		1017.36	930.52	9
10	P		1114.42	859.48	8
11	P		1211.47	762.43	7
12	P		1308.52	665.37	6
13	P		1405.57	568.32	5
14	A		1476.61	471.27	4
15	Q		1604.67	400.23	3
16	P		1701.72	272.17	2
17	R		-	175.12	1

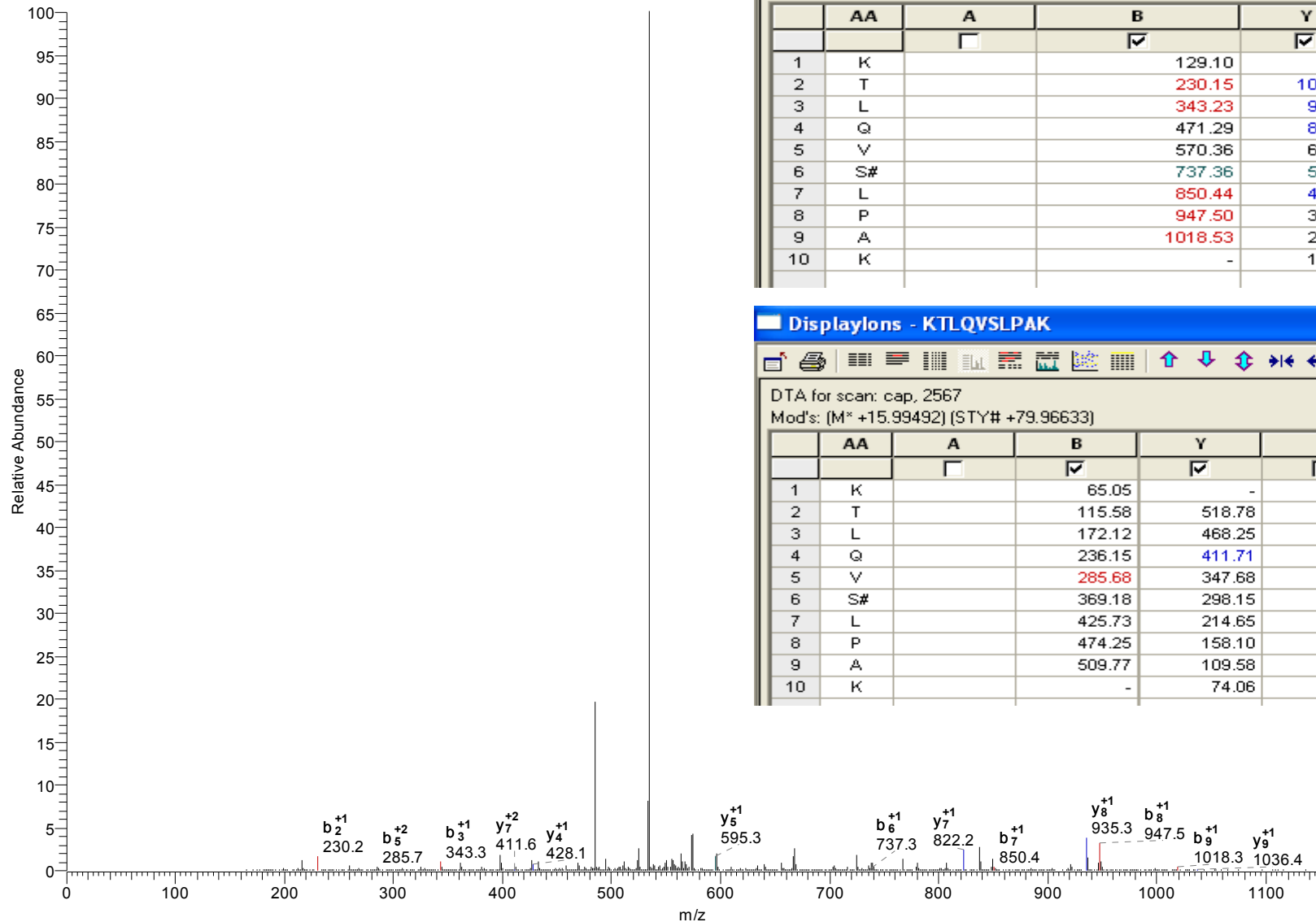
Displaylons - TCSLRGAPAPPPPAQPR

DTA for scan: 10ulcap3, 5691
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	T#		91.51	-		17
2	C		143.02	847.91		16
3	S#		226.52	796.41		15
4	L		283.06	712.91		14
5	R		361.11	656.37		13
6	G		389.62	578.32		12
7	A		425.14	549.81		11
8	P		473.67	514.29		10
9	A		509.18	465.76		9
10	P		557.71	430.24		8
11	P		606.24	381.72		7
12	P		654.76	333.19		6
13	P		703.29	284.66		5
14	A		738.81	236.14		4
15	Q		802.84	200.62		3
16	P		851.36	136.59		2
17	R		-	88.06		1

Tudor domain containing 3

#2567-2567 NL: 1.01E5



Displaylons - KTLQVSLPAK

DTA for scan: cap, 2567
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	K	☐	☒	☒	
2	T		129.10	-	10
3	L		230.15	1036.54	9
4	Q		343.23	935.50	8
5	V		471.29	822.41	7
6	S#		570.36	694.35	6
7	L		737.36	595.29	5
8	P		850.44	428.29	4
9	A		947.50	315.20	3
10	K		1018.53	218.15	2
			-	147.11	1

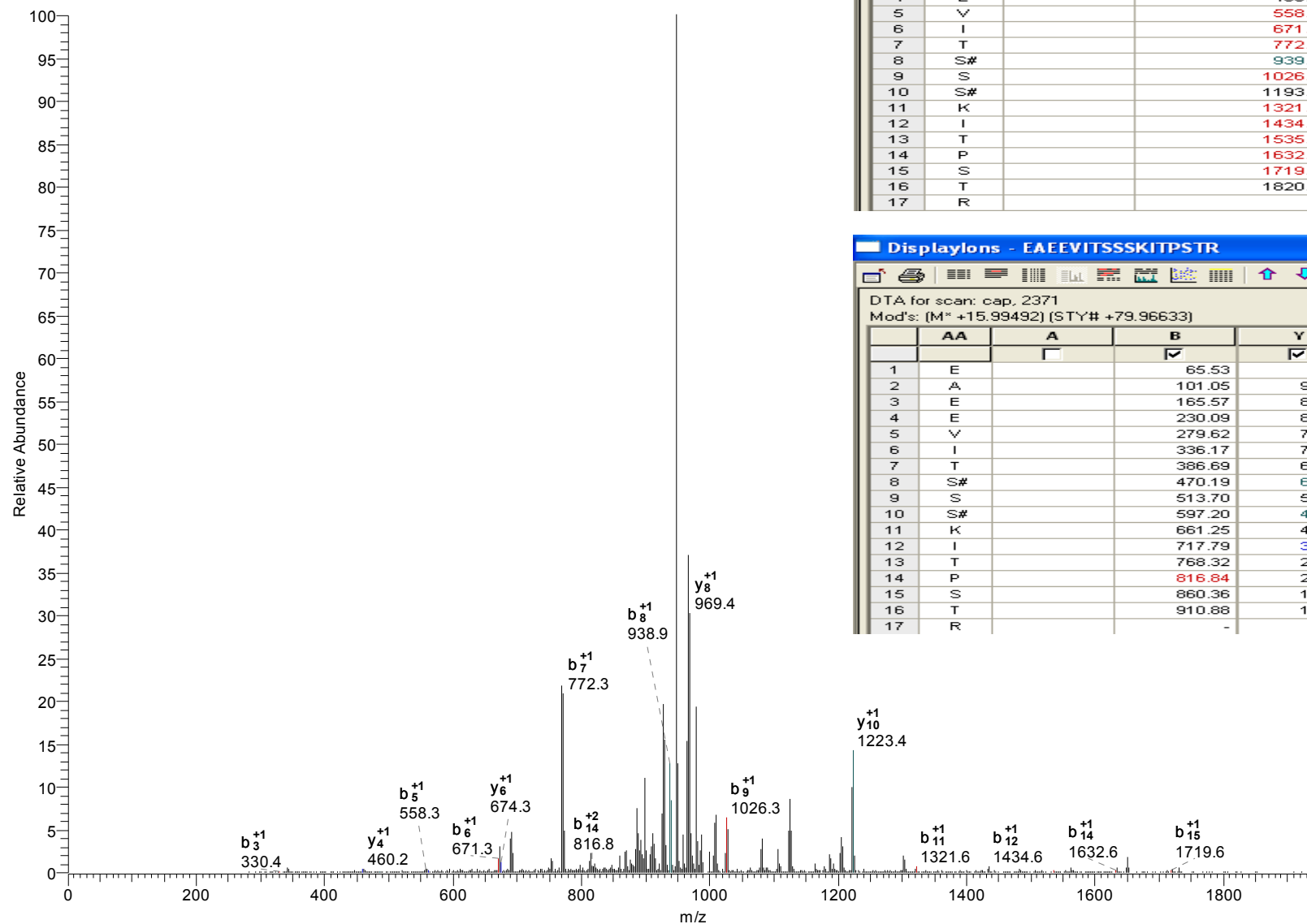
Displaylons - KTLQVSLPAK

DTA for scan: cap, 2567
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	K	☐	☒	☒	☐	
2	T		65.05	-		10
3	L		115.58	518.78		9
4	Q		172.12	468.25		8
5	V		236.15	411.71		7
6	S#		285.68	347.68		6
7	L		369.18	298.15		5
8	P		425.73	214.65		4
9	A		474.25	158.10		3
10	K		509.77	109.58		2
			-	74.06		1

Protein FAM70A

#2371-2371 NL: 1.33E4



Displaylons - EAEVITSSSKITPSTR

DTA for scan: cap. 2371
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	
1	E		130.05	-	17
2	A		201.09	1865.83	16
3	E		330.13	1794.79	15
4	E		459.17	1665.75	14
5	V		558.24	1536.71	13
6	I		671.32	1437.64	12
7	T		772.37	1324.55	11
8	S#		939.37	1223.51	10
9	S		1026.40	1056.51	9
10	S#		1193.40	969.48	8
11	K		1321.50	802.48	7
12	I		1434.58	674.38	6
13	T		1535.63	561.30	5
14	P		1632.68	460.25	4
15	S		1719.71	363.20	3
16	T		1820.76	276.17	2
17	R		-	175.12	1

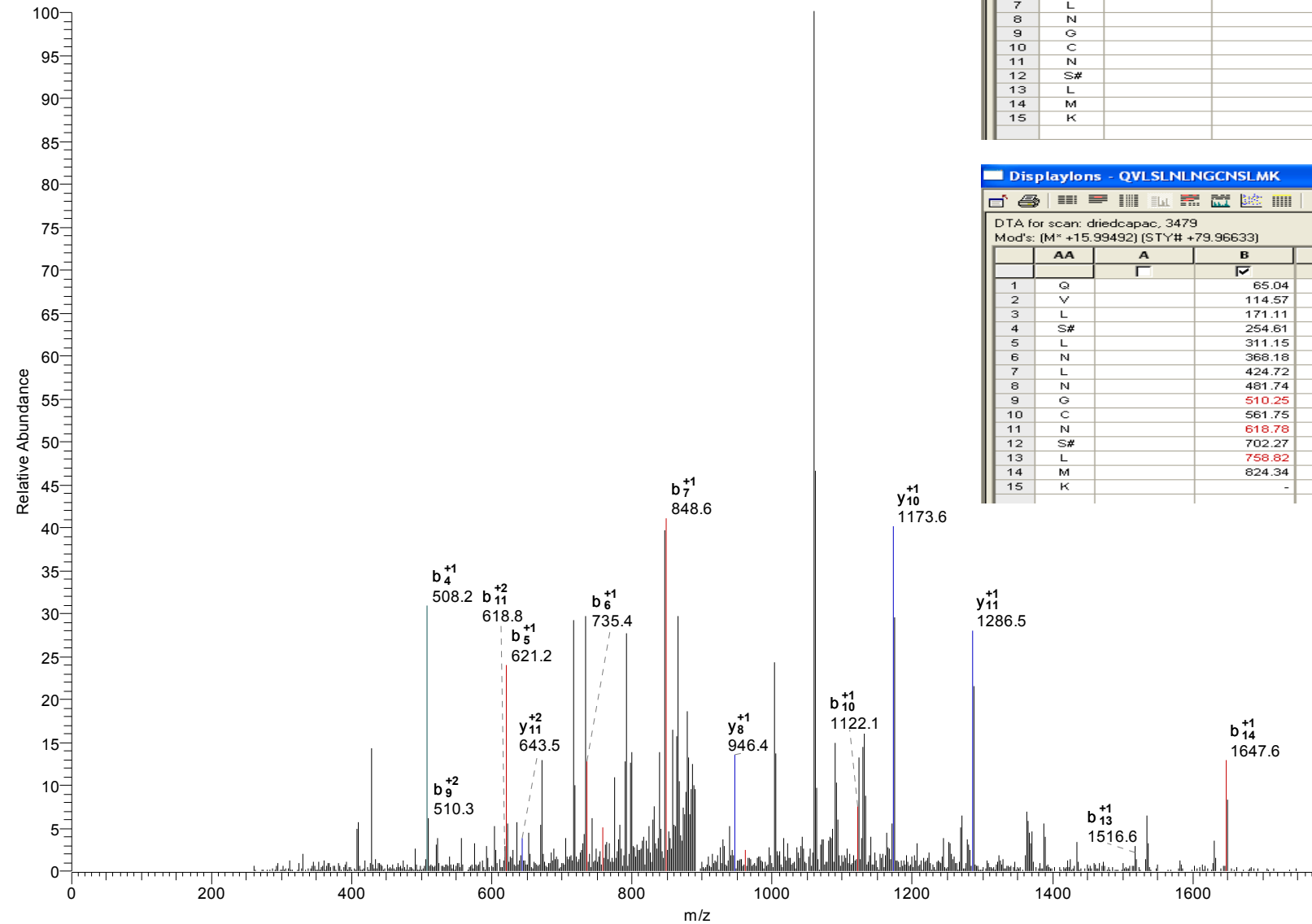
Displaylons - EAEVITSSSKITPSTR

DTA for scan: cap. 2371
Mod's: [M* +15.99492] (STY# +79.96633)

	AA	A	B	Y	Z	
1	E		65.53	-		17
2	A		101.05	933.42		16
3	E		165.57	897.90		15
4	E		230.09	833.38		14
5	V		279.62	768.86		13
6	I		336.17	719.32		12
7	T		386.69	662.78		11
8	S#		470.19	612.26		10
9	S		513.70	528.76		9
10	S#		597.20	485.24		8
11	K		661.25	401.74		7
12	I		717.79	337.70		6
13	T		768.32	281.15		5
14	P		816.84	230.63		4
15	S		860.36	182.10		3
16	T		910.88	138.59		2
17	R		-	88.06		1

Usp38_predicted similar to ubiquitin specific protease 38

#3479-3479 NL: 2.38E3



Displaylons - QVLSLNLCNSLMK

DTA for scan: driedcapac, 3479
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	
1	Q		129.07	-	15
2	V		228.13	1665.71	14
3	L		341.22	1566.65	13
4	S#		508.22	1453.56	12
5	L		621.30	1286.56	11
6	N		735.34	1173.48	10
7	L		848.43	1059.44	9
8	N		962.47	946.35	8
9	G		1019.49	832.31	7
10	C		1122.50	775.29	6
11	N		1236.54	672.28	5
12	S#		1403.54	558.24	4
13	L		1516.63	391.24	3
14	M		1647.67	278.15	2
15	K		-	147.11	1

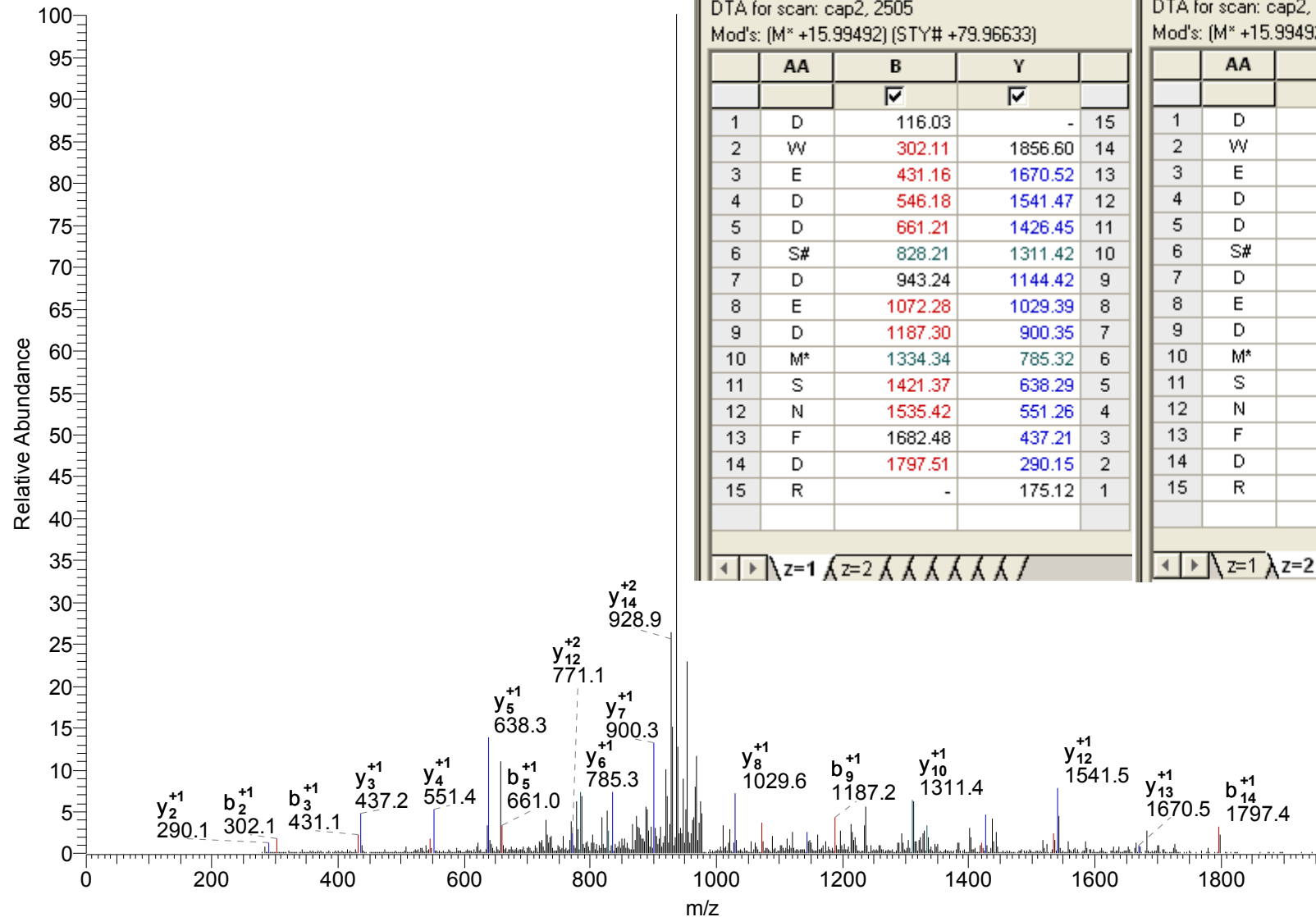
Displaylons - QVLSLNLCNSLMK

DTA for scan: driedcapac, 3479
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	A	B	Y	Z	
1	Q		65.04	-		15
2	V		114.57	833.36		14
3	L		171.11	783.83		13
4	S#		254.61	727.28		12
5	L		311.15	643.79		11
6	N		368.18	587.24		10
7	L		424.72	530.22		9
8	N		481.74	473.68		8
9	G		510.25	416.66		7
10	C		561.75	388.15		6
11	N		618.78	336.64		5
12	S#		702.27	279.62		4
13	L		758.82	196.12		3
14	M		824.34	139.58		2
15	K		-	74.06		1

Ptges3 Predicted prostaglandin E synthase 3

#2505-2505 NL: 1.84E4



Displaylons - DWEDDSDEMSNFDR

DTA for scan: cap2, 2505
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	D	116.03	-	15
2	W	302.11	1856.60	14
3	E	431.16	1670.52	13
4	D	546.18	1541.47	12
5	D	661.21	1426.45	11
6	S#	828.21	1311.42	10
7	D	943.24	1144.42	9
8	E	1072.28	1029.39	8
9	D	1187.30	900.35	7
10	M*	1334.34	785.32	6
11	S	1421.37	638.29	5
12	N	1535.42	551.26	4
13	F	1682.48	437.21	3
14	D	1797.51	290.15	2
15	R	-	175.12	1

z=1 z=2

Displaylons - DWEDDSDEMSNFDR

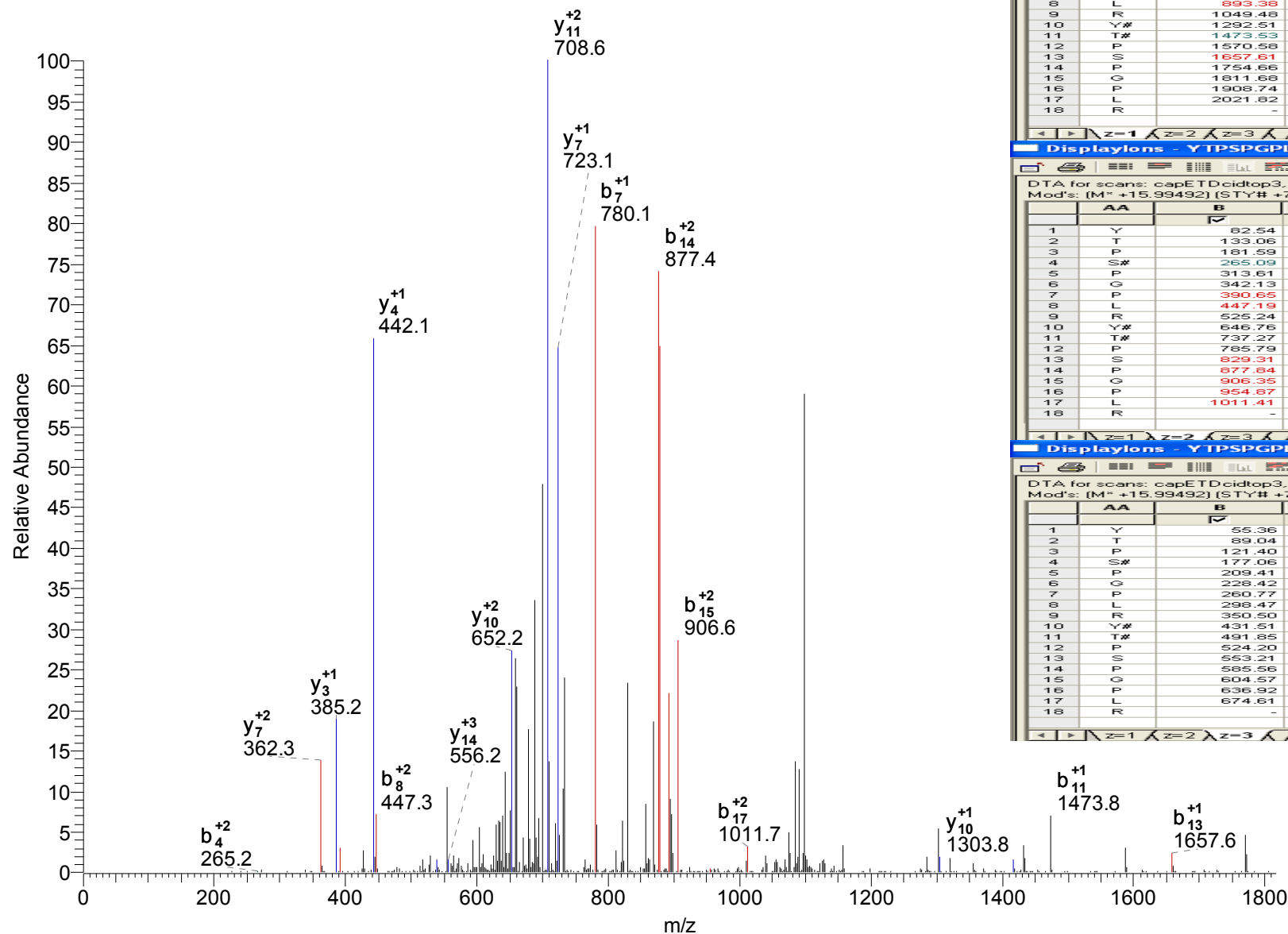
DTA for scan: cap2, 2505
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	D	58.52	-	15
2	W	151.56	928.80	14
3	E	216.08	835.76	13
4	D	273.60	771.24	12
5	D	331.11	713.73	11
6	S#	414.61	656.21	10
7	D	472.12	572.71	9
8	E	536.64	515.20	8
9	D	594.16	450.68	7
10	M*	667.67	393.17	6
11	S	711.19	319.65	5
12	N	768.21	276.13	4
13	F	841.75	219.11	3
14	D	899.26	145.58	2
15	R	-	88.06	1

z=1 z=2

59 kDa Protein

#2417-2418 NL: 5.35E4



Displays - YTPSPGPLYTPSPGPLY

DTA for scans: capETDcidtop3, 2417-2418
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	Y	164.07	-	18
2	T	265.12	2032.87	17
3	P	362.17	1931.82	16
4	S#	529.17	1834.77	15
5	P	626.22	1667.77	14
6	G	683.24	1570.72	13
7	P	780.30	1513.70	12
8	L	893.38	1416.64	11
9	R	1049.48	1303.56	10
10	Y#	1292.51	1147.46	9
11	T#	1473.53	904.43	8
12	P	1570.58	723.41	7
13	S	1657.61	626.36	6
14	P	1754.66	539.33	5
15	G	1811.68	442.28	4
16	P	1908.74	385.26	3
17	L	2021.82	288.20	2
18	R	-	175.12	1

Displays - YTPSPGPLYTPSPGPLY

DTA for scans: capETDcidtop3, 2417-2418
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	Y	82.54	-	18
2	T	133.06	1016.94	17
3	P	181.59	966.41	16
4	S#	265.09	917.89	15
5	P	313.61	834.39	14
6	G	342.13	785.86	13
7	P	390.65	757.35	12
8	L	447.19	708.83	11
9	R	525.24	652.28	10
10	Y#	646.76	574.23	9
11	T#	737.27	452.72	8
12	P	785.79	362.21	7
13	S	829.31	313.68	6
14	P	877.84	270.17	5
15	G	906.35	221.64	4
16	P	954.87	193.13	3
17	L	1011.41	144.61	2
18	R	-	88.06	1

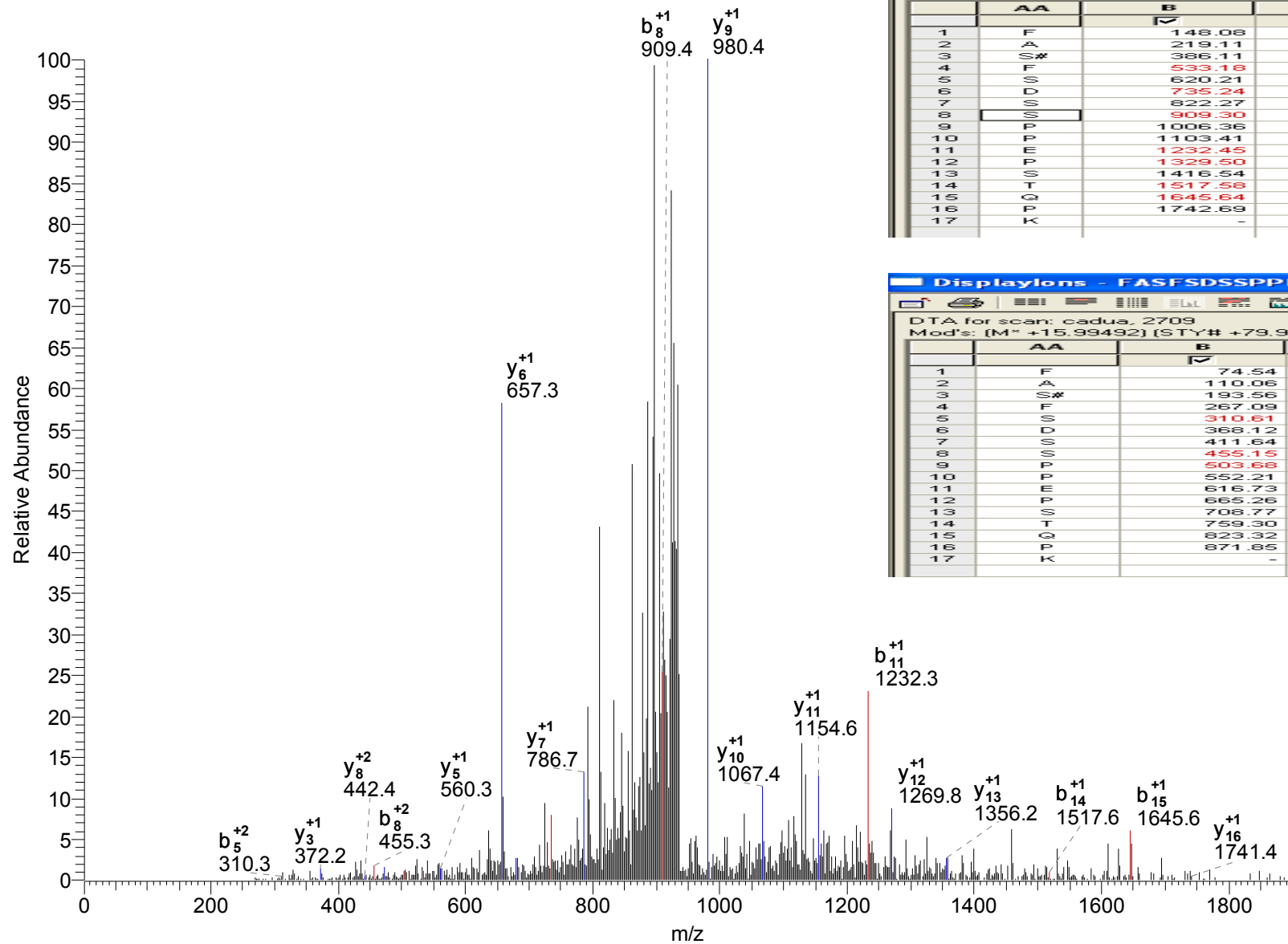
Displays - YTPSPGPLYTPSPGPLY

DTA for scans: capETDcidtop3, 2417-2418
Mod's: [M⁺ +15.99492] (STY# +79.96633)

	AA	B	Y	
1	Y	55.36	-	18
2	T	89.04	678.29	17
3	P	121.40	644.61	16
4	S#	177.06	612.26	15
5	P	209.41	566.60	14
6	G	228.42	524.24	13
7	P	260.77	505.24	12
8	L	298.47	472.89	11
9	R	350.50	435.19	10
10	Y#	431.51	383.16	9
11	T#	491.85	302.15	8
12	P	524.20	241.61	7
13	S	553.21	209.46	6
14	P	585.56	180.45	5
15	G	604.57	148.10	4
16	P	636.92	129.09	3
17	L	674.61	96.74	2
18	R	-	59.04	1

predicted hypothetical protein LOC305476

#2709-2709 NL: 1.38E3



Displaylons - FASFSDSSPPEPSTQPK

DTA for scan: cadua, 2709
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	F	148.08	-	17
2	A	219.11	1741.73	16
3	S#	386.11	1670.69	15
4	F	533.18	1503.70	14
5	S	620.21	1356.63	13
6	D	735.24	1269.60	12
7	S	822.27	1154.57	11
8	S	909.30	1067.54	10
9	P	1006.36	980.50	9
10	P	1103.41	883.45	8
11	E	1232.45	786.40	7
12	P	1329.50	657.36	6
13	S	1416.54	560.30	5
14	T	1517.58	473.27	4
15	Q	1645.64	372.22	3
16	P	1742.69	244.17	2
17	K	-	147.11	1

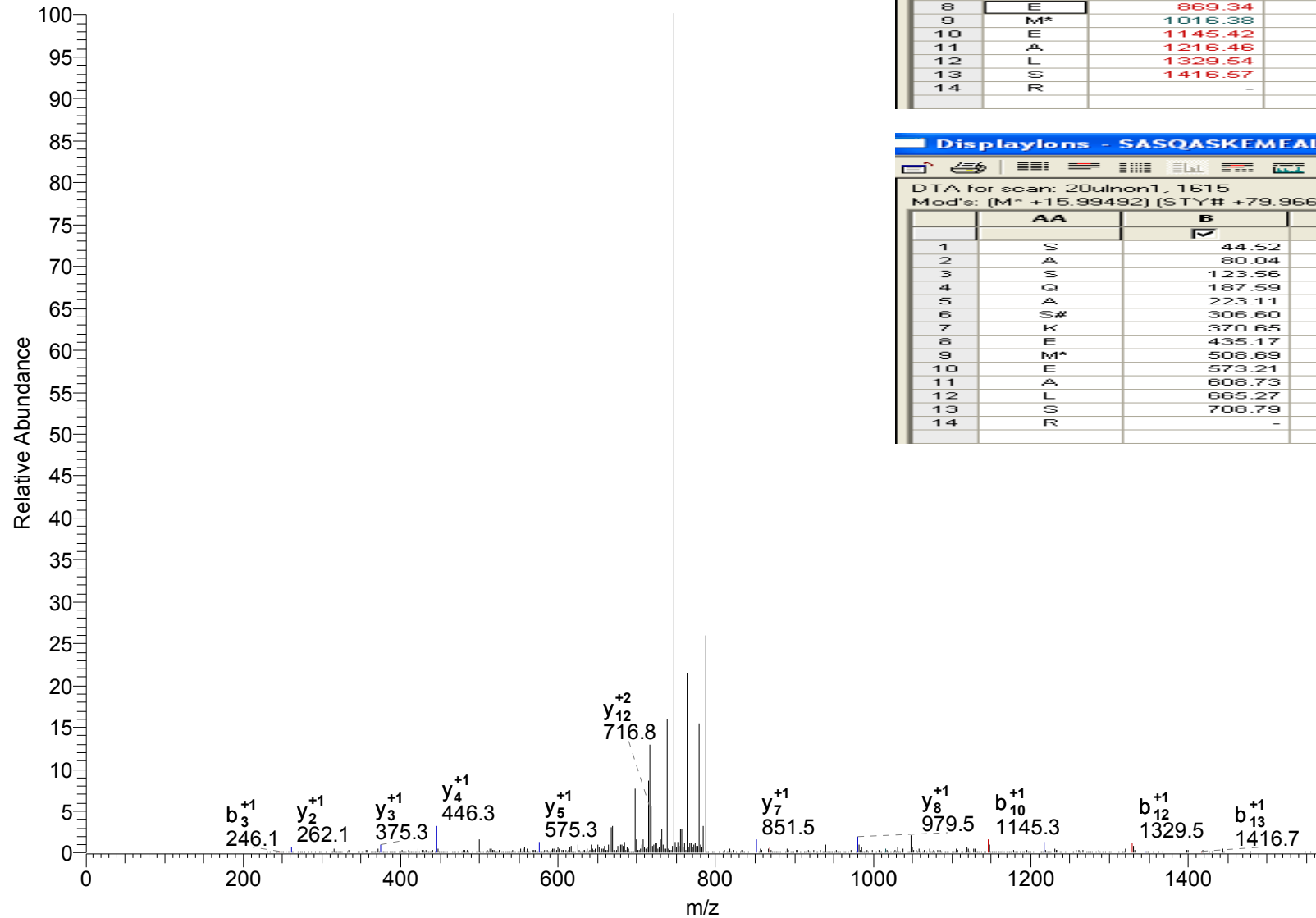
Displaylons - FASFSDSSPPEPSTQPK

DTA for scan: cadua, 2709
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	F	74.54	-	17
2	A	110.06	871.37	16
3	S#	193.56	835.85	15
4	F	267.09	752.35	14
5	S	310.61	678.82	13
6	D	368.12	635.30	12
7	S	411.64	577.79	11
8	S	455.15	534.27	10
9	P	503.68	490.76	9
10	P	552.21	442.23	8
11	E	616.73	393.70	7
12	P	665.26	329.18	6
13	S	708.77	280.65	5
14	T	759.30	237.14	4
15	Q	823.32	186.62	3
16	P	871.85	122.59	2
17	K	-	74.06	1

Monocarboxylate transporter 2

#1615-1615 NL: 7.51E3



Displaylons - SASQASKEMEALSR

DTA for scan: 20ulnon1, 1615
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	S	88.04	-	14
2	A	159.08	1503.65	13
3	S	246.11	1432.61	12
4	Q	374.17	1345.58	11
5	A	445.20	1217.52	10
6	S#	612.20	1146.49	9
7	K	740.30	979.49	8
8	E	869.34	851.39	7
9	M*	1016.38	722.35	6
10	E	1145.42	575.31	5
11	A	1216.46	446.27	4
12	L	1329.54	375.24	3
13	S	1416.57	262.15	2
14	R	-	175.12	1

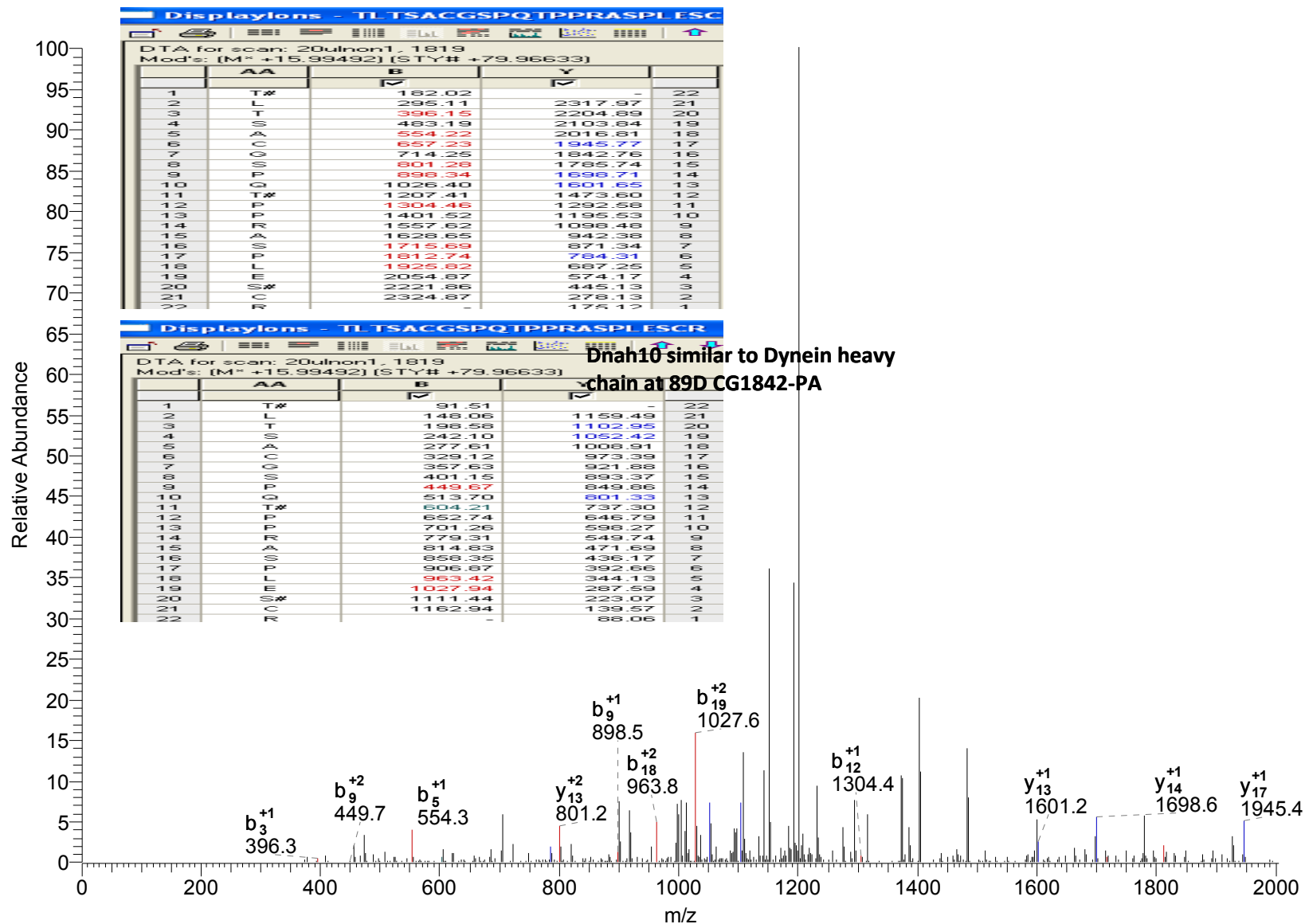
Displaylons - SASQASKEMEALSR

DTA for scan: 20ulnon1, 1615
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	S	44.52	-	14
2	A	80.04	752.33	13
3	S	123.56	716.81	12
4	Q	187.59	673.29	11
5	A	223.11	609.27	10
6	S#	306.60	573.75	9
7	K	370.65	490.25	8
8	E	435.17	426.20	7
9	M*	508.69	361.68	6
10	E	573.21	288.16	5
11	A	608.73	223.64	4
12	L	665.27	188.12	3
13	S	708.79	131.58	2
14	R	-	88.06	1

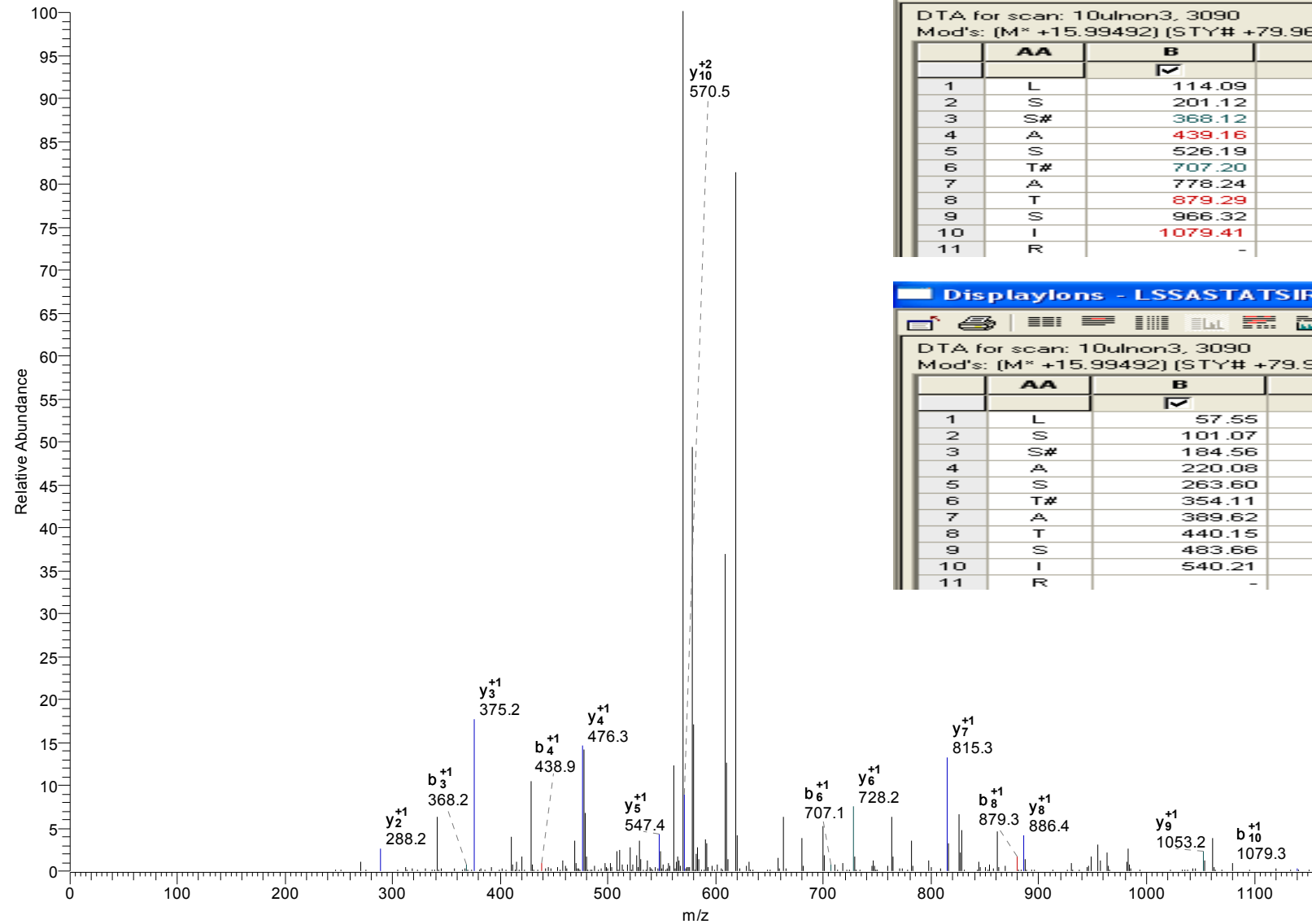
Dnah10 similar to Dynein heavy chain at 89D CG1842-PA

#1819-1819 NL: 1.42E3



predicted similar to CG5435-PA

#3090-3090 NL: 1.23E3



Displaylons - LSSASTATSIR

DTA for scan: 10ulnon3, 3090
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	L	114.09	-	11
2	S	201.12	1140.43	10
3	S#	368.12	1053.40	9
4	A	439.16	886.40	8
5	S	526.19	815.37	7
6	T#	707.20	728.33	6
7	A	778.24	547.32	5
8	T	879.29	476.28	4
9	S	966.32	375.24	3
10	I	1079.41	288.20	2
11	R	-	175.12	1

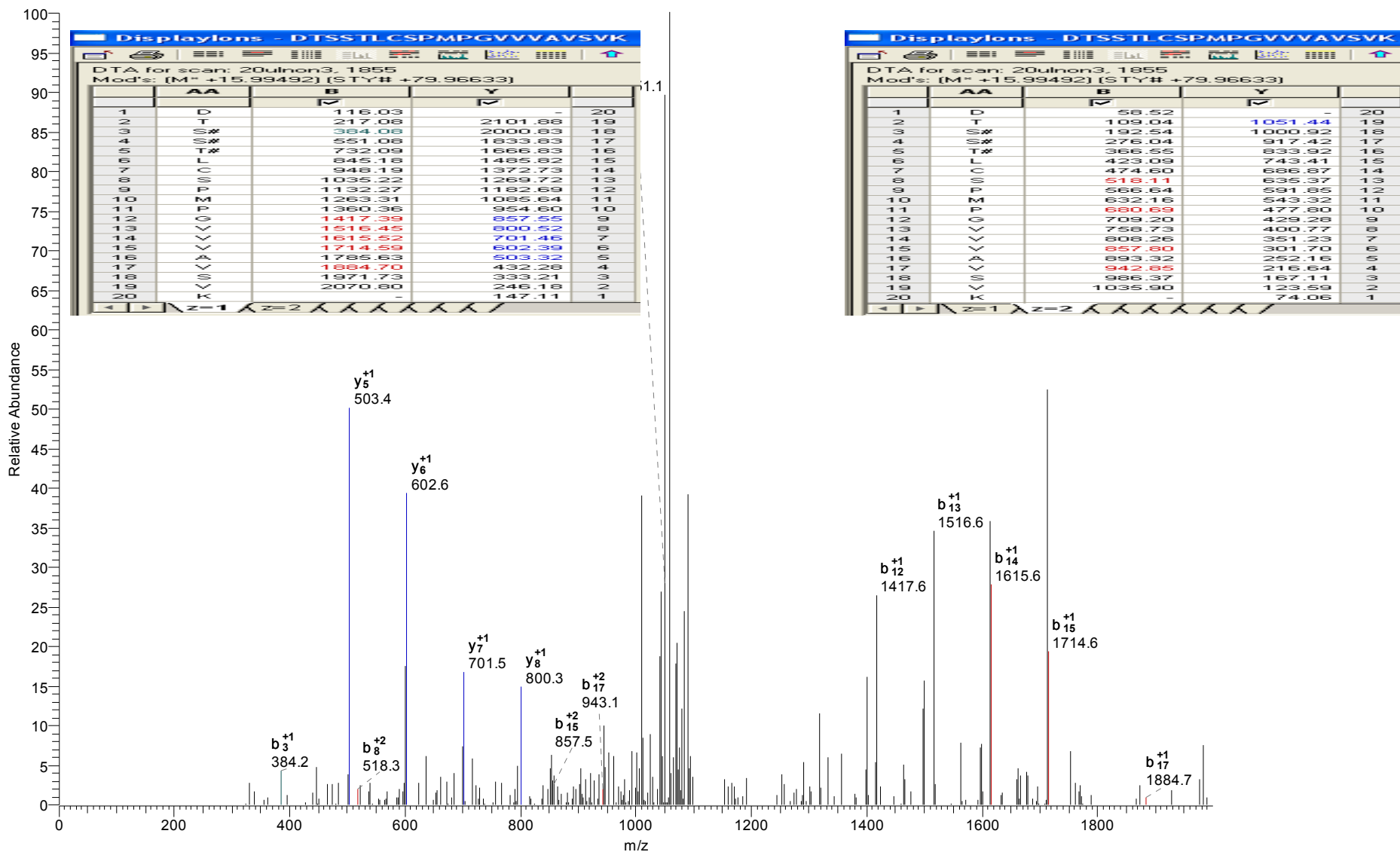
Displaylons - LSSASTATSIR

DTA for scan: 10ulnon3, 3090
Mod's: (M* +15.99492) (STY# +79.96633)

	AA	B	Y	
1	L	57.55	-	11
2	S	101.07	570.72	10
3	S#	184.56	527.20	9
4	A	220.08	443.71	8
5	S	263.60	408.19	7
6	T#	354.11	364.67	6
7	A	389.62	274.16	5
8	T	440.15	238.64	4
9	S	483.66	188.12	3
10	I	540.21	144.61	2
11	R	-	88.06	1

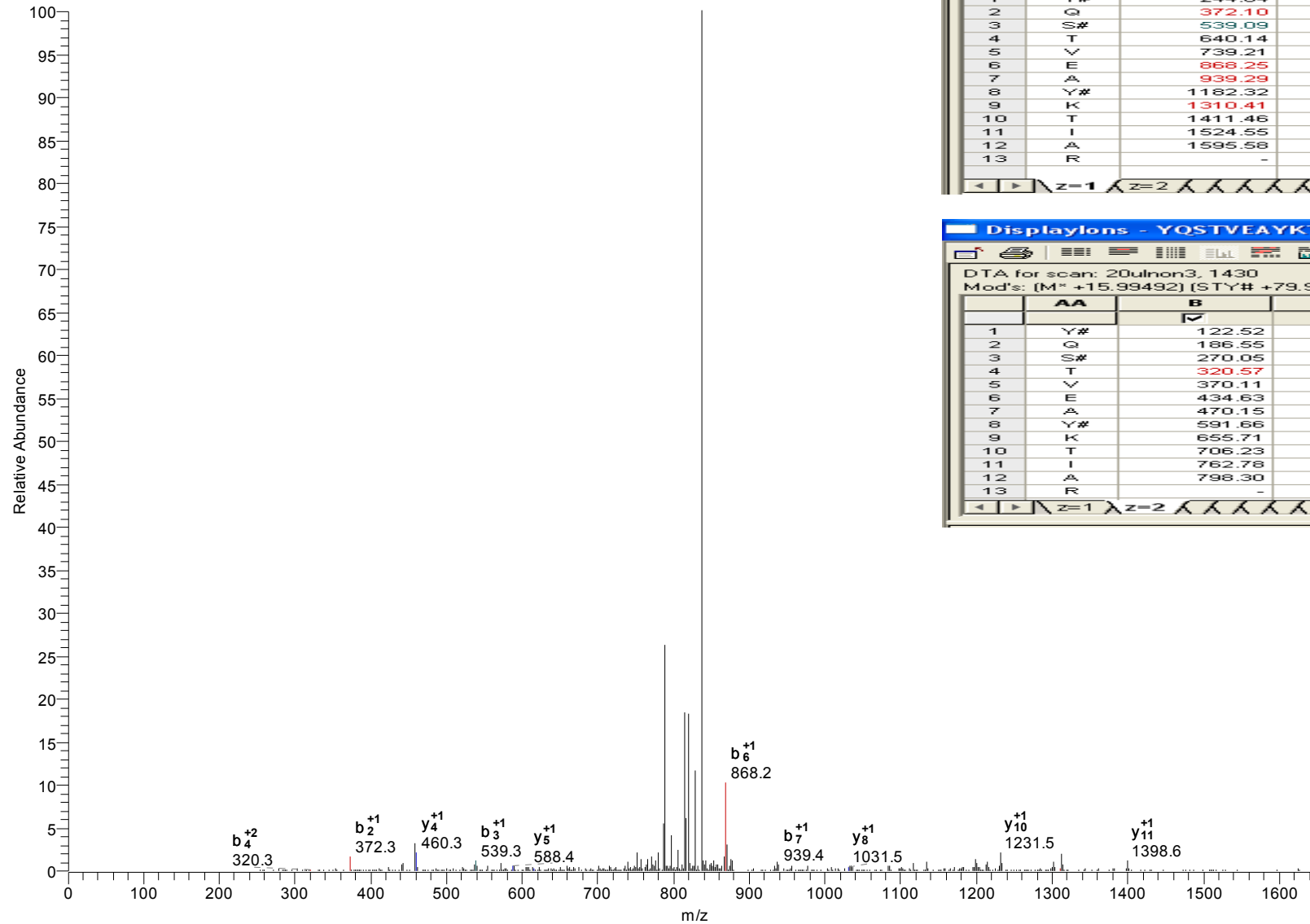
Pcca similar to Propionyl-CoA carboxylase alpha chain, mitochondrial precursor

#1855-1855 NL: 1.81E2



Ucp2 Mitochondrial uncoupling protein

#1430-1430 NL: 6.49E3



Displaylens - YQSTVEAYKTIAR

DTA for scan: 20ulnon3. 1430
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	Y#	244.04	-	13
2	Q	372.10	1526.67	12
3	S#	539.09	1398.61	11
4	T	640.14	1231.61	10
5	V	739.21	1130.56	9
6	E	868.25	1031.49	8
7	A	939.29	902.45	7
8	Y#	1182.32	831.41	6
9	K	1310.41	588.38	5
10	T	1411.46	460.29	4
11	I	1524.55	359.24	3
12	A	1595.58	246.16	2
13	R	-	175.12	1

z=1 z=2

Displaylens - YQSTVEAYKTIAR

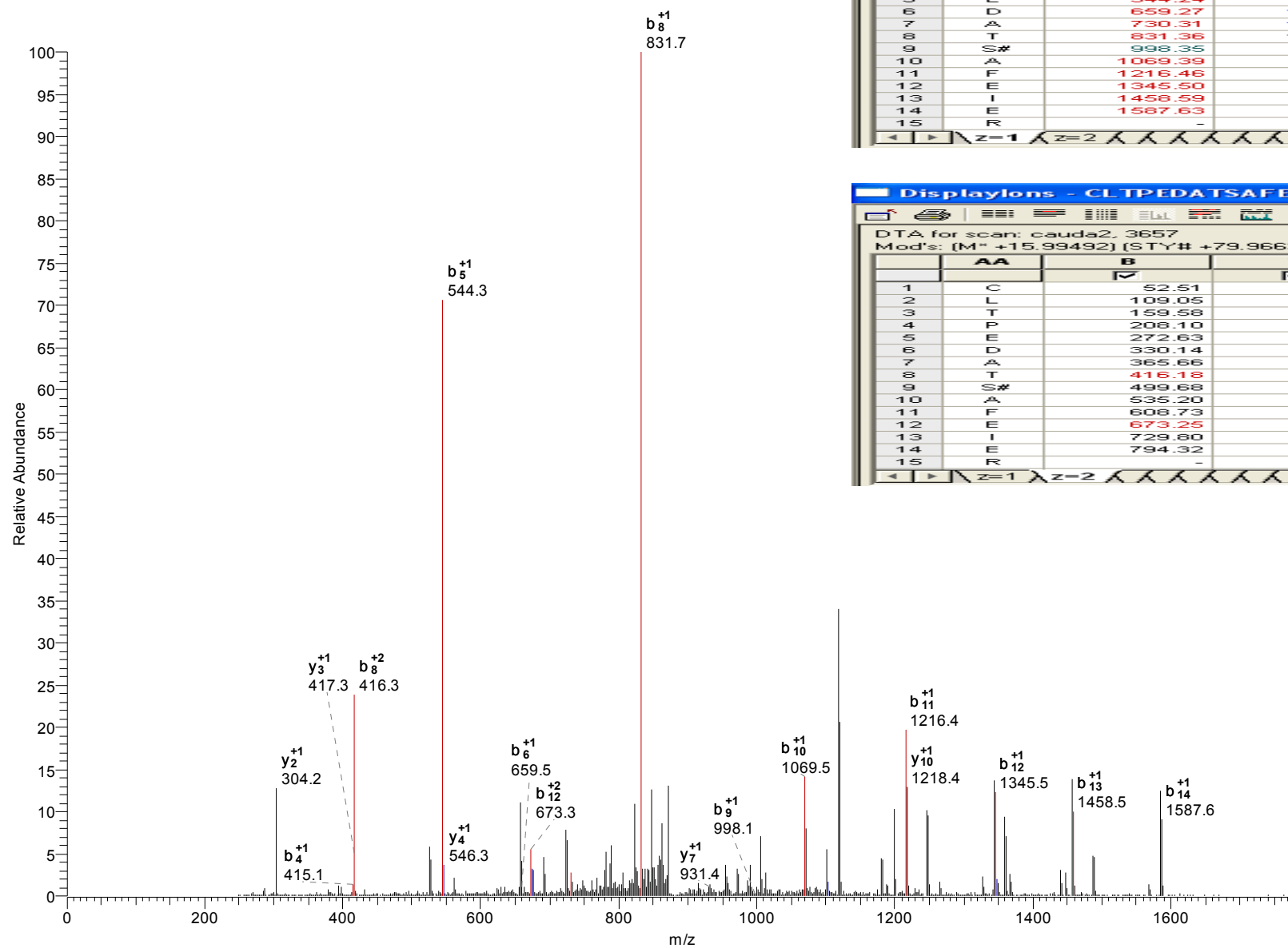
DTA for scan: 20ulnon3. 1430
Mod's: [M⁺ +15.99492] [STY# +79.96633]

	AA	B	Y	
1	Y#	122.52	-	13
2	Q	186.55	763.84	12
3	S#	270.05	699.81	11
4	T	320.57	616.31	10
5	V	370.11	565.78	9
6	E	434.63	516.25	8
7	A	470.15	451.73	7
8	Y#	591.66	416.21	6
9	K	655.71	294.70	5
10	T	706.23	230.65	4
11	I	762.78	180.12	3
12	A	798.30	123.58	2
13	R	-	88.06	1

z=1 z=2

anat Serotonin N-acetyltransferase

#3657-3657 NL: 2.04E4



Displaylons - CLTPEDATSAFEIER

DTA for scan: cauda2, 3657
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	C	104.02	-	15
2	L	217.10	1658.73	14
3	T	318.15	1545.65	13
4	P	415.20	1444.60	12
5	E	544.24	1347.55	11
6	D	659.27	1218.50	10
7	A	730.31	1103.48	9
8	T	831.36	1032.44	8
9	S#	998.35	931.39	7
10	A	1069.39	764.39	6
11	F	1216.46	693.36	5
12	E	1345.50	546.29	4
13	I	1458.59	417.25	3
14	E	1587.63	304.16	2
15	R	-	175.12	1

Navigation: < > Z=1 Z=2

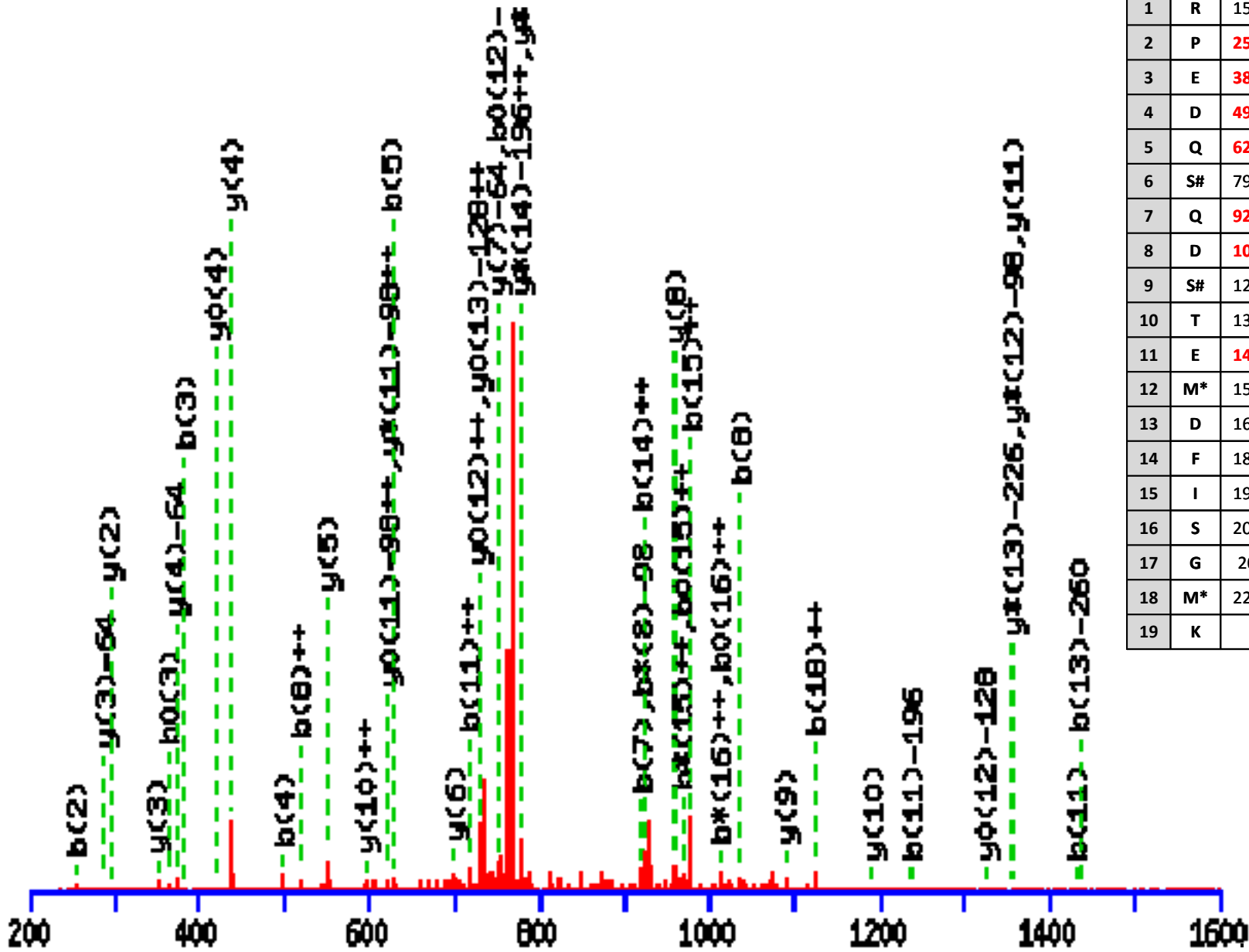
Displaylons - CLTPEDATSAFEIER

DTA for scan: cauda2, 3657
Mod's: (M⁺ +15.99492) (STY# +79.96633)

	AA	B	Y	
1	C	52.51	-	15
2	L	109.05	829.87	14
3	T	159.58	773.33	13
4	P	208.10	722.80	12
5	E	272.63	674.28	11
6	D	330.14	609.76	10
7	A	365.66	552.24	9
8	T	416.18	516.72	8
9	S#	499.68	466.20	7
10	A	535.20	382.70	6
11	F	608.73	347.18	5
12	E	673.25	273.65	4
13	I	729.80	209.13	3
14	E	794.32	152.58	2
15	R	-	88.06	1

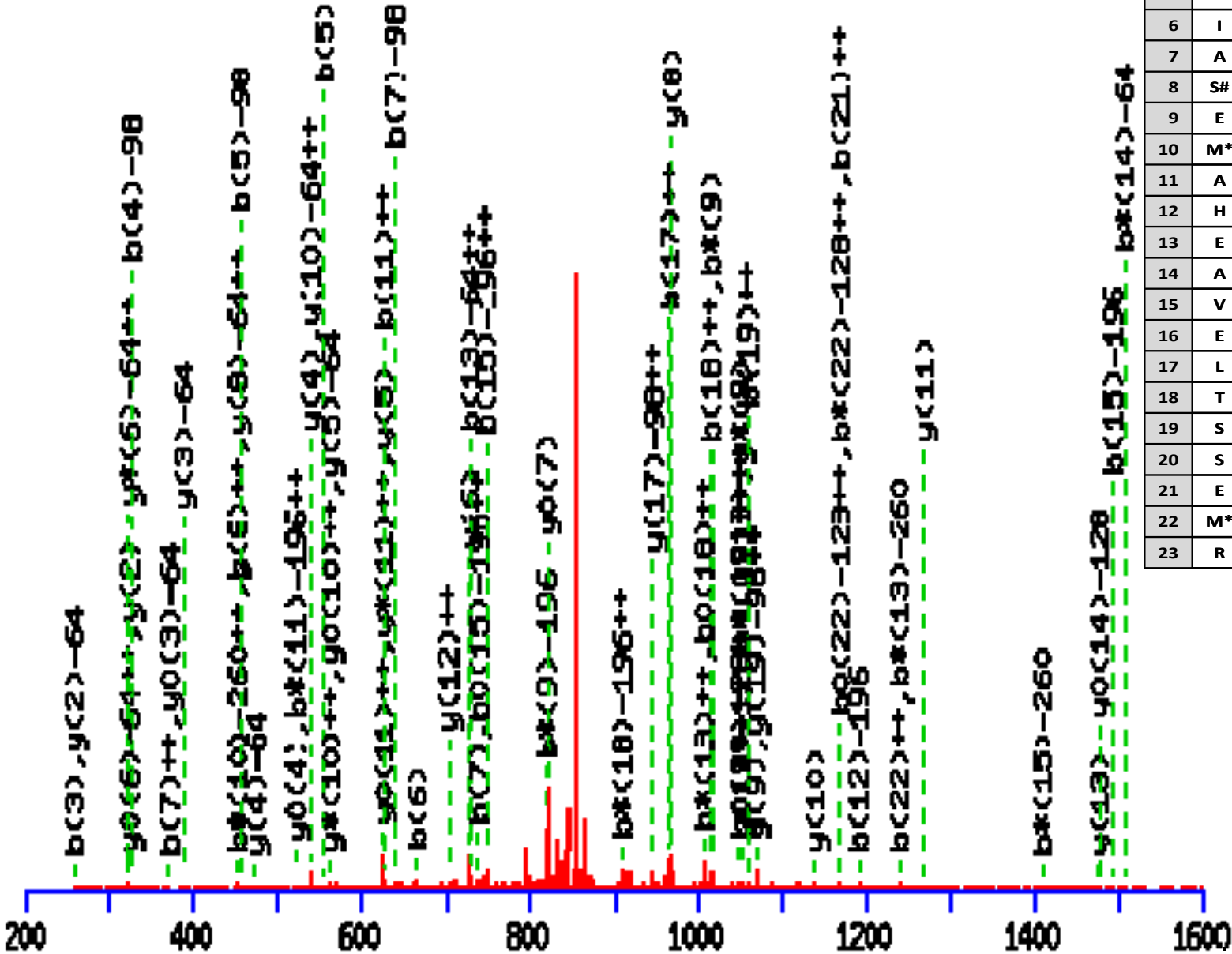
Navigation: < > Z=1 Z=2

AKAP4



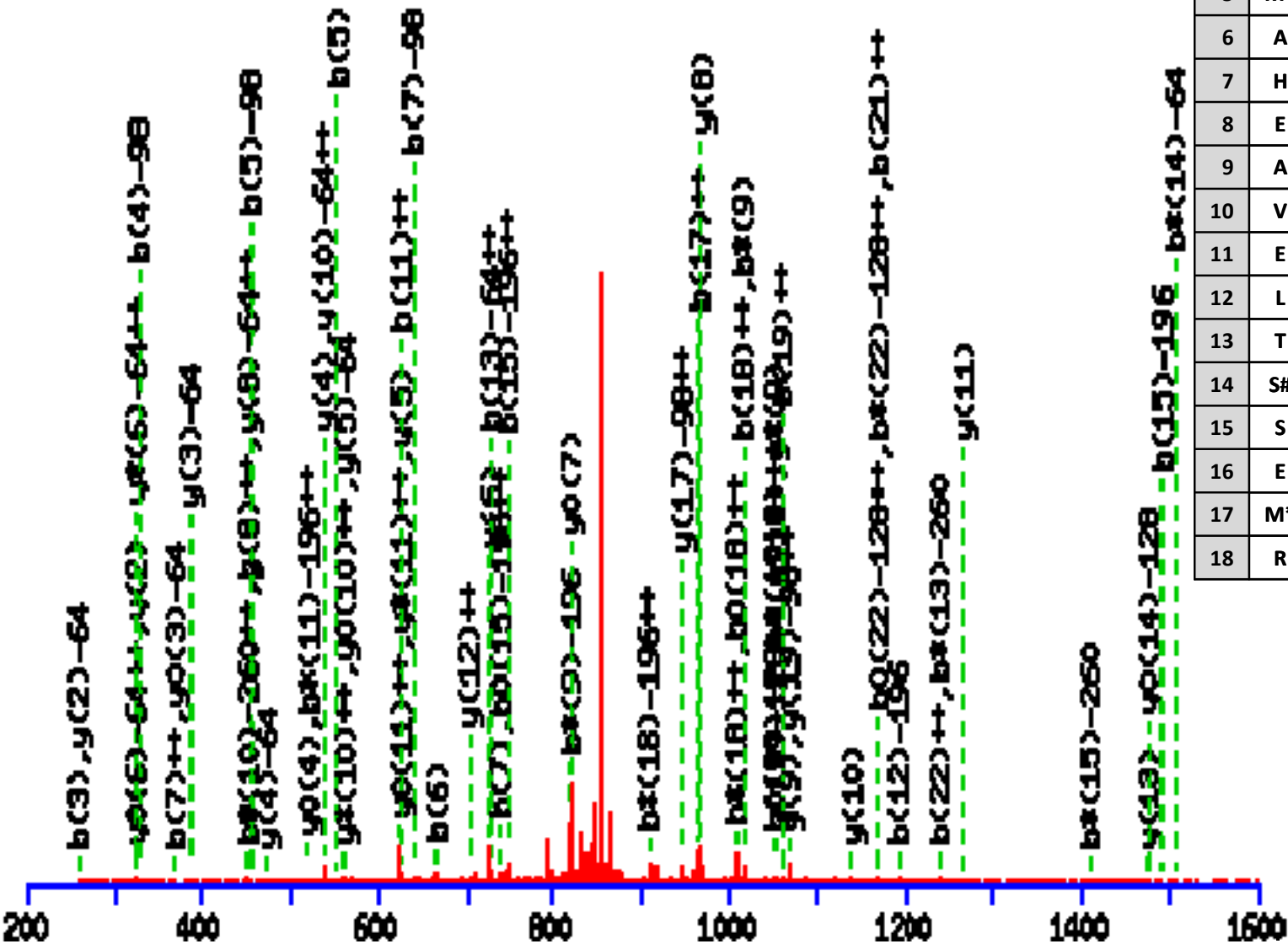
	AA	b	y	
1	R	157.1084		19
2	P	254.1612	2236.77	18
3	E	383.2037	2139.717	17
4	D	498.2307	2010.675	16
5	Q	626.2893	1895.648	15
6	S#	793.2876	1767.589	14
7	Q	921.3462	1600.591	13
8	D	1036.373	1472.532	12
9	S#	1203.372	1357.505	11
10	T	1304.419	1190.507	10
11	E	1433.462	1089.459	9
12	M*	1580.497	960.4165	8
13	D	1695.524	813.3811	7
14	F	1842.593	698.3542	6
15	I	1955.677	551.2858	5
16	S	2042.709	438.2017	4
17	G	2099.73	351.1697	3
18	M*	2246.766	294.1482	2
19	K		147.1128	1

Akap4 A-kinase anchor protein 4



	AA	b	y	
1	S	88.0393		23
2	A	159.0764	2568.076	22
3	V	258.1448	2497.039	21
4	S#	425.1432	2397.97	20
5	K	553.2381	2230.972	19
6	I	666.3222	2102.877	18
7	A	737.3593	1989.793	17
8	S#	904.3577	1918.756	16
9	E	1033.4	1751.758	15
10	M*	1180.436	1622.715	14
11	A	1251.473	1475.68	13
12	H	1388.532	1404.642	12
13	E	1517.574	1267.584	11
14	A	1588.611	1138.541	10
15	V	1687.68	1067.504	9
16	E	1816.722	968.4353	8
17	L	1929.807	839.3927	7
18	T	2030.854	726.3087	6
19	S	2117.886	625.261	5
20	S	2204.918	538.229	4
21	E	2333.961	451.1969	3
22	M*	2480.996	322.1544	2
23	R		175.119	

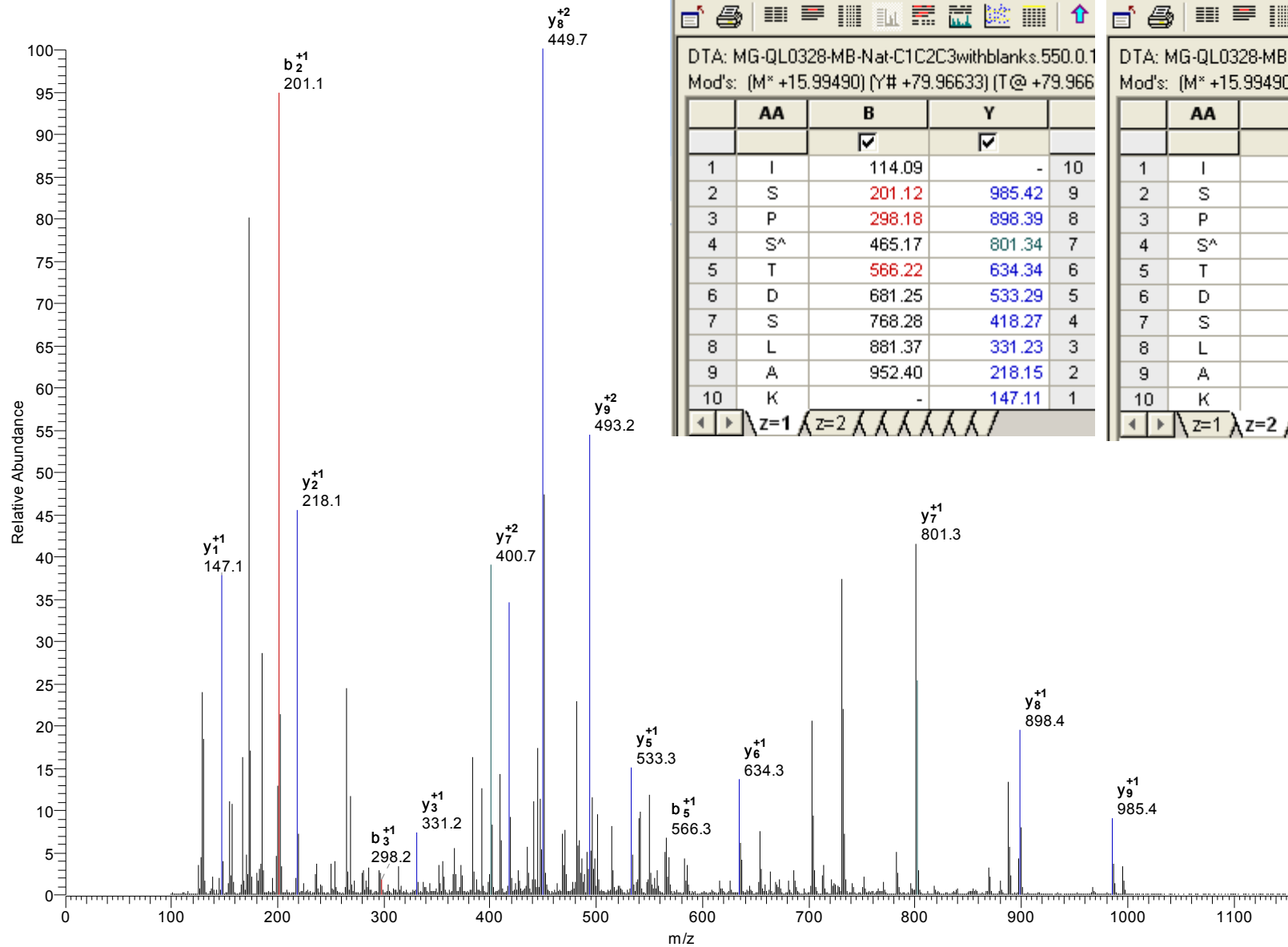
Akap4 A-kinase anchor protein 4



#	AA	b	y	#
1	I	114.0913		18
2	A	185.1285	2069.759	17
3	S#	352.1268	1998.722	16
4	E	481.1694	1831.724	15
5	M*	628.2048	1702.681	14
6	A	699.2419	1555.646	13
7	H	836.3008	1484.609	12
8	E	965.3434	1347.55	11
9	A	1036.381	1218.507	10
10	V	1135.449	1147.47	9
11	E	1264.492	1048.402	8
12	L	1377.576	919.3591	7
13	T	1478.623	806.275	6
14	S#	1565.655	705.2273	5
15	S	1732.654	618.1953	4
16	E	1861.696	451.1969	3
17	M*	2008.732	322.1544	2
18	R		175.119	1

Akap4 A-kinase anchor protein 4

#1563-1563 NL: 1.81E3



Displaylons - ISPSTD SLAK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.550.0.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	I	114.09	-	10
2	S	201.12	985.42	9
3	P	298.18	898.39	8
4	S^	465.17	801.34	7
5	T	566.22	634.34	6
6	D	681.25	533.29	5
7	S	768.28	418.27	4
8	L	881.37	331.23	3
9	A	952.40	218.15	2
10	K	-	147.11	1

z=1 z=2

Displaylons - ISPSTD SLAK

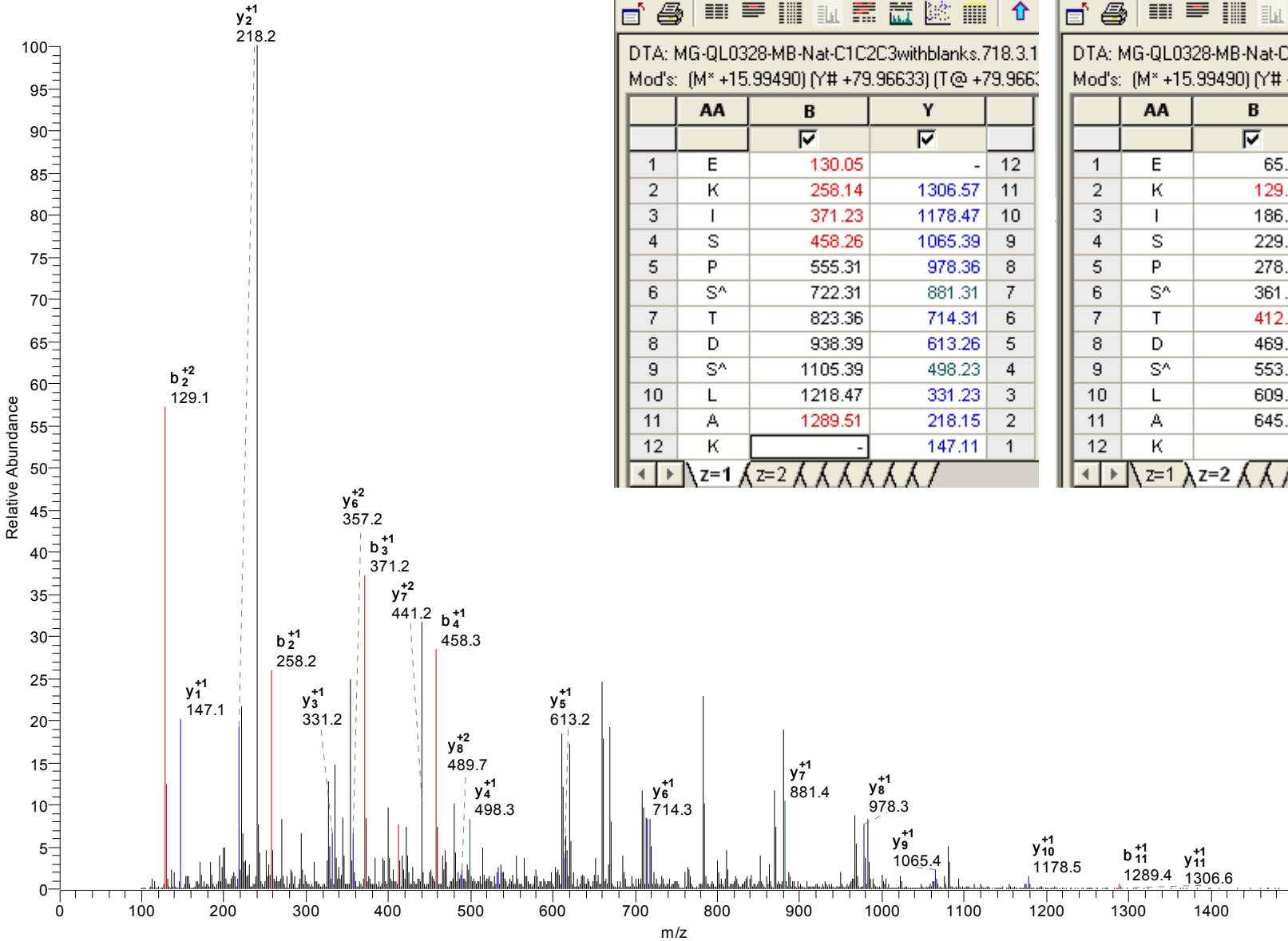
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.550.0.15
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	I	57.55	-	10
2	S	101.07	493.22	9
3	P	149.59	449.70	8
4	S^	233.09	401.17	7
5	T	283.61	317.67	6
6	D	341.13	267.15	5
7	S	384.64	209.64	4
8	L	441.19	166.12	3
9	A	476.70	109.58	2
10	K	-	74.06	1

z=1 z=2

Akap4 A-kinase anchor protein 4

#1568-1568 NL: 3.56E2



Displaylons - EKISPSTD SLAK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.718.3.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	E	130.05	-	12
2	K	258.14	1306.57	11
3	I	371.23	1178.47	10
4	S	458.26	1065.39	9
5	P	555.31	978.36	8
6	S^	722.31	881.31	7
7	T	823.36	714.31	6
8	D	938.39	613.26	5
9	S^	1105.39	498.23	4
10	L	1218.47	331.23	3
11	A	1289.51	218.15	2
12	K	-	147.11	1

z=1 z=2

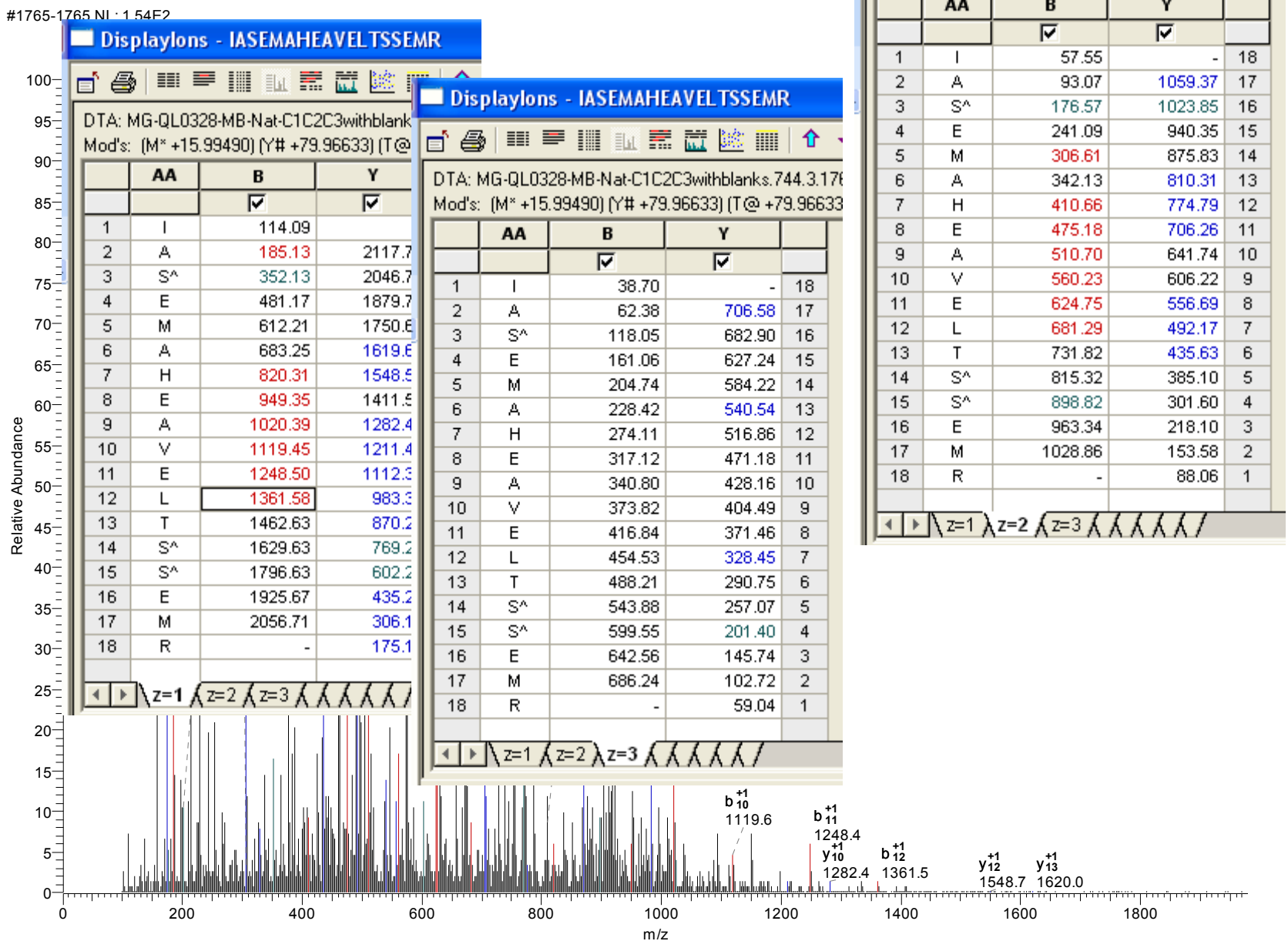
Displaylons - EKISPSTD SLAK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.718.3.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	E	65.53	-	12
2	K	129.58	653.79	11
3	I	186.12	589.74	10
4	S	229.63	533.20	9
5	P	278.16	489.68	8
6	S^	361.66	441.16	7
7	T	412.18	357.66	6
8	D	469.70	307.13	5
9	S^	553.20	249.62	4
10	L	609.74	166.12	3
11	A	645.26	109.58	2
12	K	-	74.06	1

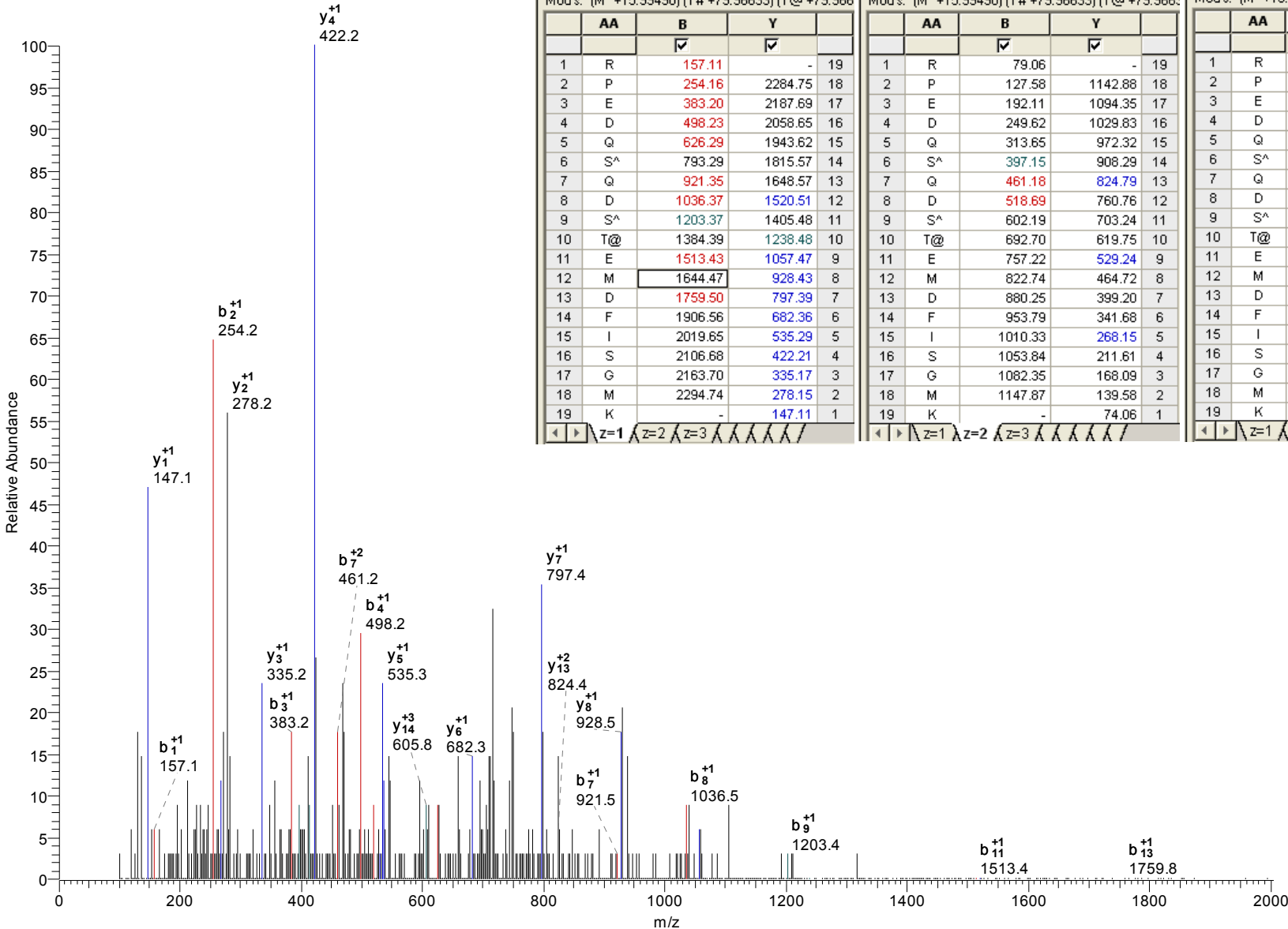
z=1 z=2

#1765-1765 NI · 1.54E2



Akap4 A-kinase anchor protein 4

#1617-1617 NL: 3.50E1



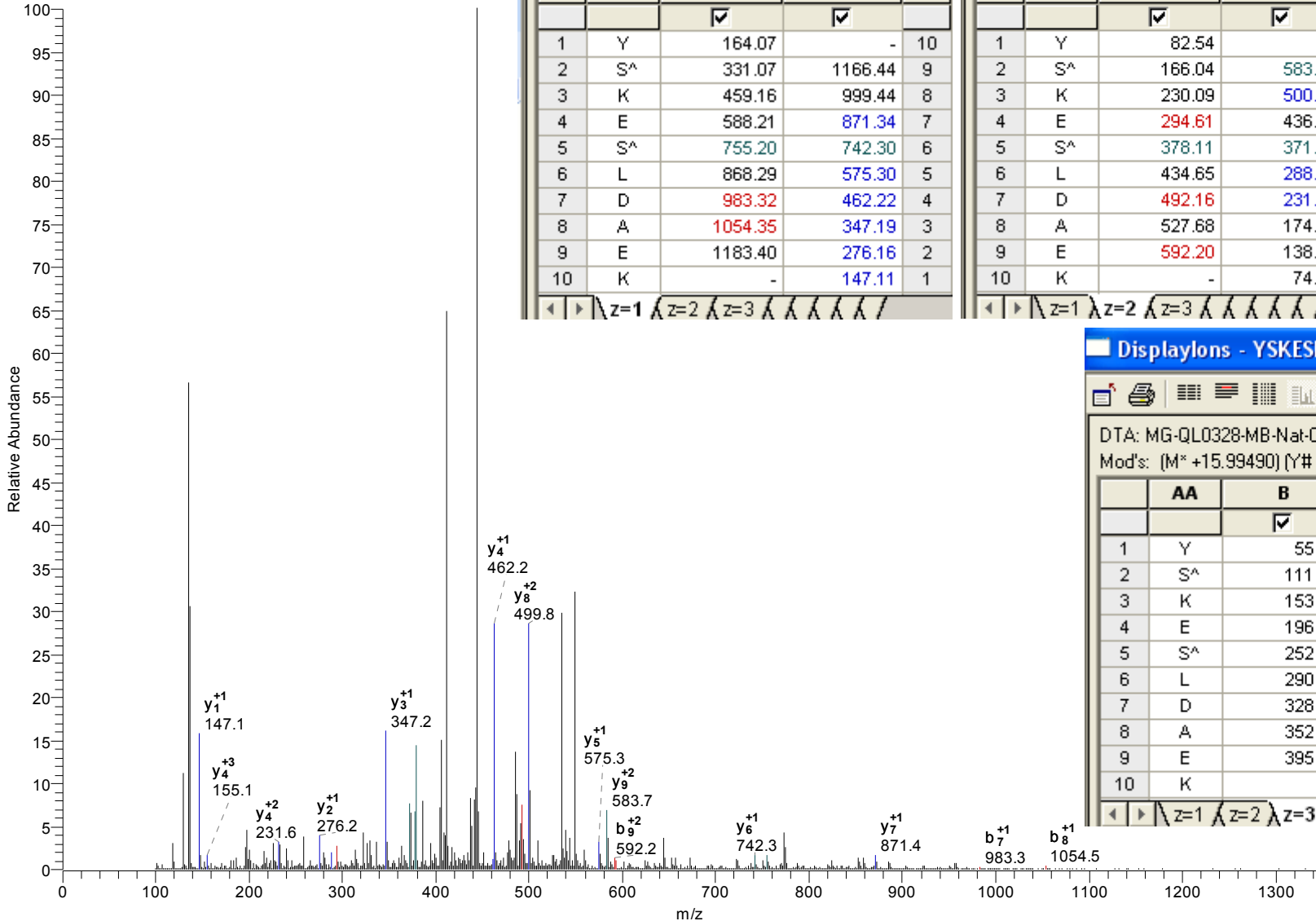
Displaylons - RPEDQSQDSTEMDFISGMK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.814.3.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	R	157.11	-	19
2	P	254.16	2284.75	18
3	E	383.20	2187.69	17
4	D	498.23	2058.65	16
5	Q	626.29	1943.62	15
6	S^	793.29	1815.57	14
7	Q	921.35	1648.57	13
8	D	1036.37	1520.51	12
9	S^	1203.37	1405.48	11
10	T@	1384.39	1238.48	10
11	E	1513.43	1057.47	9
12	M	1644.47	928.43	8
13	D	1759.50	797.39	7
14	F	1906.56	682.36	6
15	I	2019.65	535.29	5
16	S	2106.68	422.21	4
17	G	2163.70	335.17	3
18	M	2294.74	278.15	2
19	K	-	147.11	1

Displaylons - RPEDQSQDSTEMDFISGMK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.814.3.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	R	79.06	-	19
2	P	127.58	1142.88	18
3	E	192.11	1094.35	17
4	D	249.62	1029.83	16
5	Q	313.65	972.32	15
6	S^	397.15	908.29	14
7	Q	461.18	824.79	13
8	D	518.69	760.76	12
9	S^	602.19	703.24	11
10	T@	692.70	619.75	10
11	E	757.22	529.24	9
12	M	822.74	464.72	8
13	D	880.25	399.20	7
14	F	953.79	341.68	6
15	I	1010.33	268.15	5
16	S	1053.84	211.61	4
17	G	1082.35	168.09	3
18	M	1147.87	139.58	2
19	K	-	74.06	1

Displaylons - RPEDQSQDSTEMDFISGMK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.814.3.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	R	53.04	-	19
2	P	85.39	762.25	18
3	E	128.41	729.90	17
4	D	166.75	686.89	16
5	Q	209.43	648.55	15
6	S^	265.10	605.86	14
7	Q	307.79	550.19	13
8	D	346.13	507.51	12
9	S^	401.80	469.17	11
10	T@	462.13	413.50	10
11	E	505.15	353.16	9
12	M	548.83	310.15	8
13	D	587.17	266.47	7
14	F	636.19	228.12	6
15	I	673.89	179.10	5
16	S	702.90	141.41	4
17	G	721.91	112.40	3
18	M	765.59	93.39	2
19	K	-	49.71	1

Retinol Dehydrogenase 14

#1540-1540 NL: 9.56E2



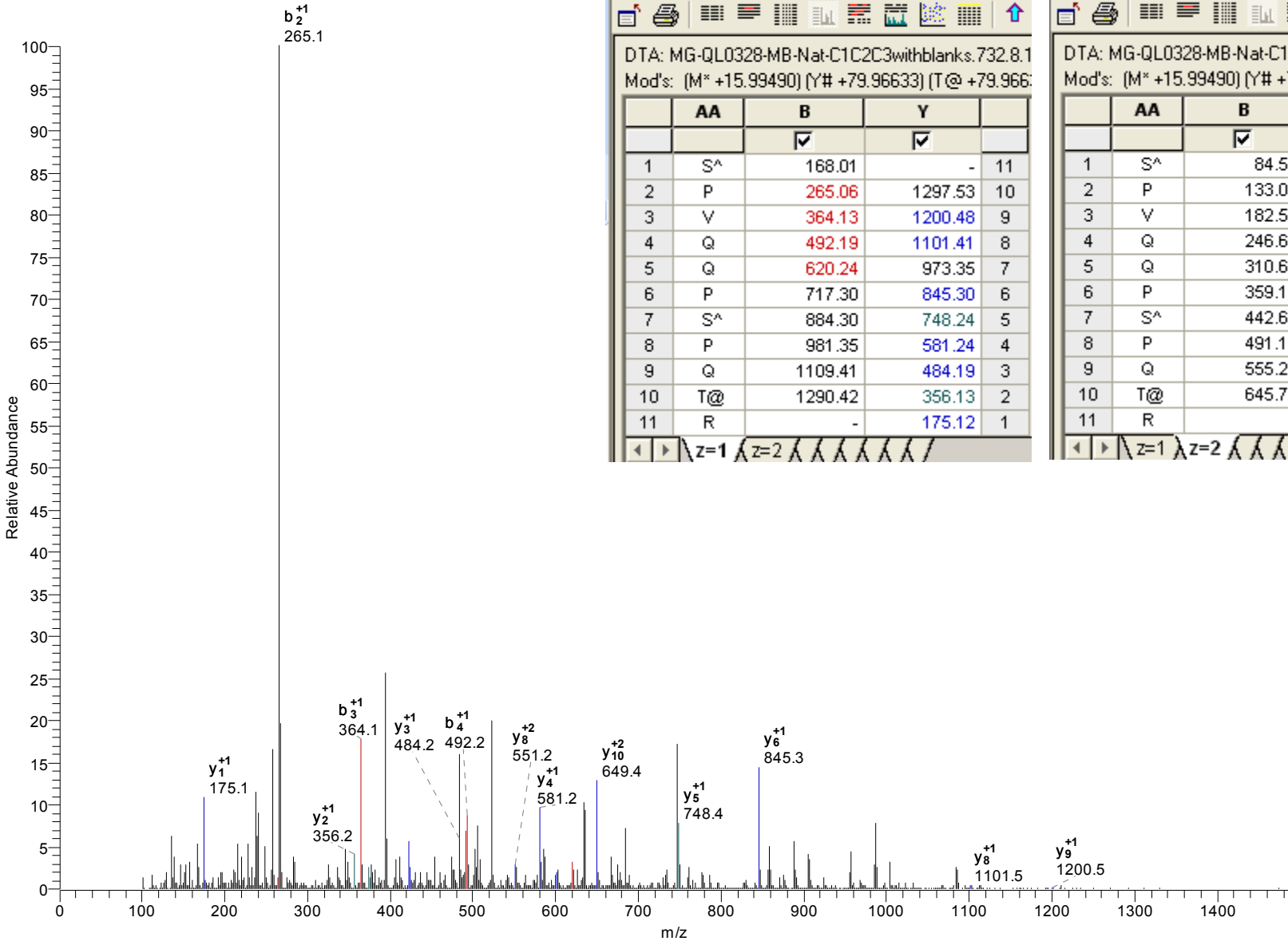
Displaylons - YSKESLDAEK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.443.8.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.966				
	AA	B	Y	
		☒	☒	
1	Y	164.07	-	10
2	S^	331.07	1166.44	9
3	K	459.16	999.44	8
4	E	588.21	871.34	7
5	S^	755.20	742.30	6
6	L	868.29	575.30	5
7	D	983.32	462.22	4
8	A	1054.35	347.19	3
9	E	1183.40	276.16	2
10	K	-	147.11	1

Displaylons - YSKESLDAEK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.443.8.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.966				
	AA	B	Y	
		☒	☒	
1	Y	82.54	-	10
2	S^	166.04	583.72	9
3	K	230.09	500.22	8
4	E	294.61	436.18	7
5	S^	378.11	371.65	6
6	L	434.65	288.16	5
7	D	492.16	231.61	4
8	A	527.68	174.10	3
9	E	592.20	138.58	2
10	K	-	74.06	1

Displaylons - YSKESLDAEK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.443.8.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.966				
	AA	B	Y	
		☒	☒	
1	Y	55.36	-	10
2	S^	111.03	389.48	9
3	K	153.73	333.82	8
4	E	196.74	291.12	7
5	S^	252.41	248.11	6
6	L	290.10	192.44	5
7	D	328.44	154.74	4
8	A	352.12	116.40	3
9	E	395.14	92.72	2
10	K	-	49.71	1

Retinol Dehydrogenase 14

#1507-1507 NL: 3.22E2



Displaylons - SPVQQPSPQTR

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.732.8.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	S^	168.01	-	11
2	P	265.06	1297.53	10
3	V	364.13	1200.48	9
4	Q	492.19	1101.41	8
5	Q	620.24	973.35	7
6	P	717.30	845.30	6
7	S^	884.30	748.24	5
8	P	981.35	581.24	4
9	Q	1109.41	484.19	3
10	T@	1290.42	356.13	2
11	R	-	175.12	1

z=1 z=2

Displaylons - SPVQQPSPQTR

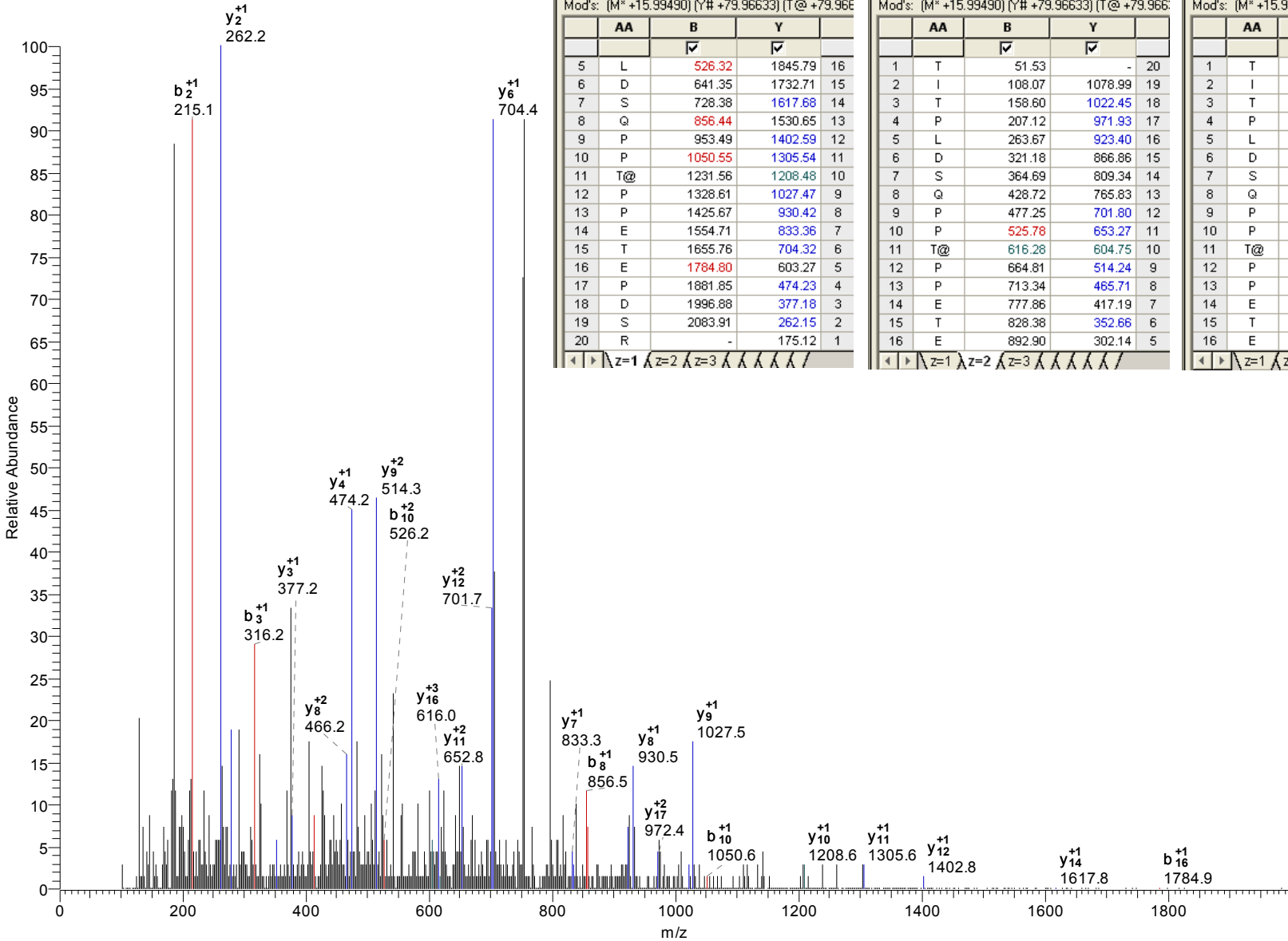
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.732.8.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	S^	84.51	-	11
2	P	133.03	649.27	10
3	V	182.57	600.74	9
4	Q	246.60	551.21	8
5	Q	310.63	487.18	7
6	P	359.15	423.15	6
7	S^	442.65	374.62	5
8	P	491.18	291.13	4
9	Q	555.21	242.60	3
10	T@	645.71	178.57	2
11	R	-	88.06	1

z=1 z=2

Retinol Dehydrogenase 14

#1653-1653 NL: 7.00E1



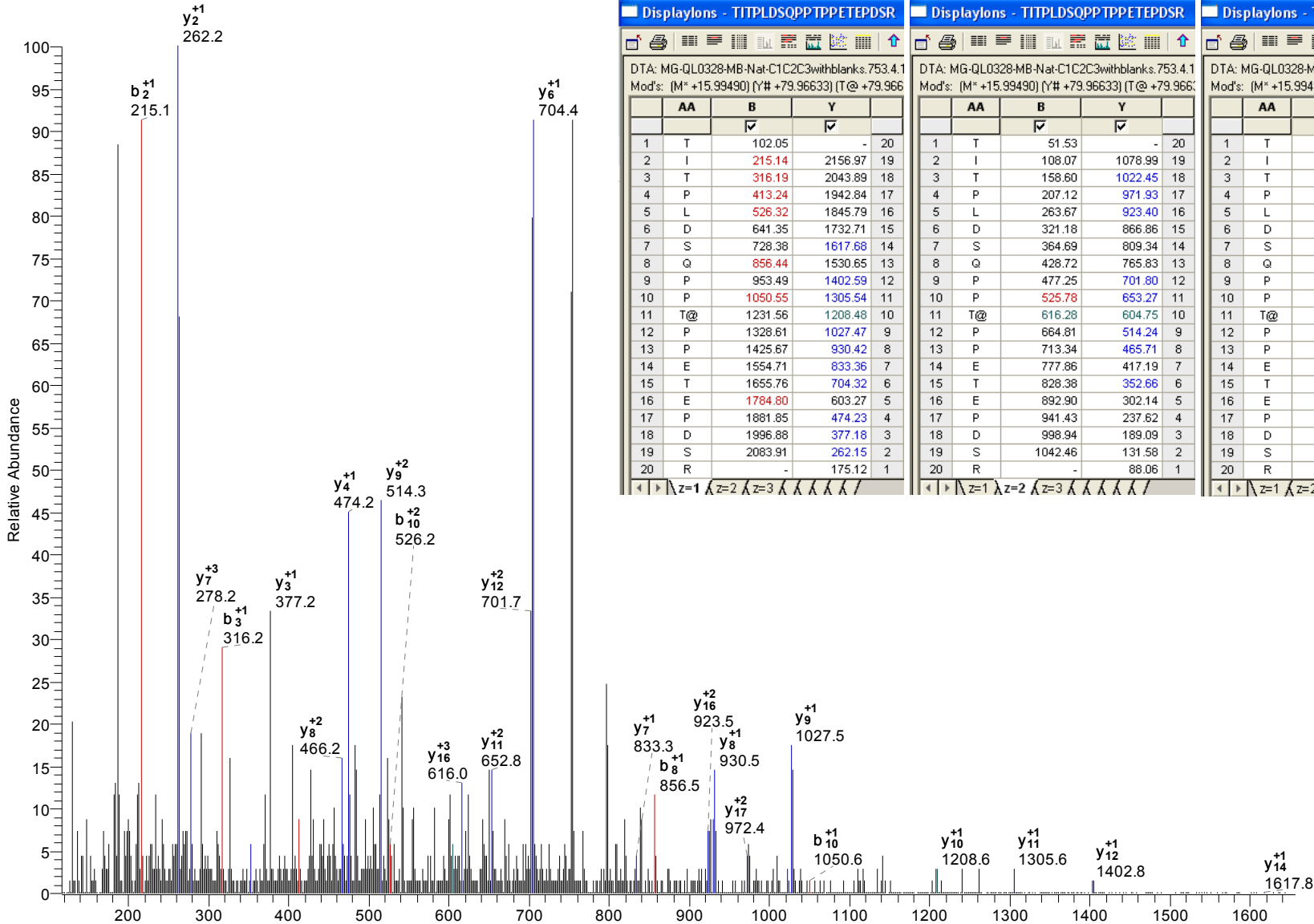
Displaylons - TITPLDSQPPTTPPETEDSR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.753.4.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
5	L	526.32	1845.79	16
6	D	641.35	1732.71	15
7	S	728.38	1617.68	14
8	Q	856.44	1530.65	13
9	P	953.49	1402.59	12
10	P	1050.55	1305.54	11
11	T@	1231.56	1208.48	10
12	P	1328.61	1027.47	9
13	P	1425.67	930.42	8
14	E	1554.71	833.36	7
15	T	1655.76	704.32	6
16	E	1784.80	603.27	5
17	P	1881.85	474.23	4
18	D	1996.88	377.18	3
19	S	2083.91	262.15	2
20	R	-	175.12	1

Displaylons - TITPLDSQPPTTPPETEDSR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.753.4.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	T	51.53	-	20
2	I	108.07	1078.99	19
3	T	158.60	1022.45	18
4	P	207.12	971.93	17
5	L	263.67	923.40	16
6	D	321.18	866.86	15
7	S	364.69	809.34	14
8	Q	428.72	765.83	13
9	P	477.25	701.80	12
10	P	525.78	653.27	11
11	T@	616.28	604.75	10
12	P	664.81	514.24	9
13	P	713.34	465.71	8
14	E	777.86	417.19	7
15	T	828.38	352.66	6
16	E	892.90	302.14	5

Displaylons - TITPLDSQPPTTPPETEDSR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.753.4.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	T	34.69	-	20
2	I	72.38	719.66	19
3	T	106.07	681.97	18
4	P	138.42	648.29	17
5	L	176.11	615.93	16
6	D	214.46	578.24	15
7	S	243.47	539.90	14
8	Q	286.15	510.89	13
9	P	318.50	468.20	12
10	P	350.85	435.85	11
11	T@	411.19	403.50	10
12	P	443.54	343.16	9
13	P	475.89	310.81	8
14	E	518.91	278.46	7
15	T	552.59	235.45	6
16	E	595.60	201.76	5

Retinol Dehydrogenase 14

#1653-1653 NL: 7.00E1



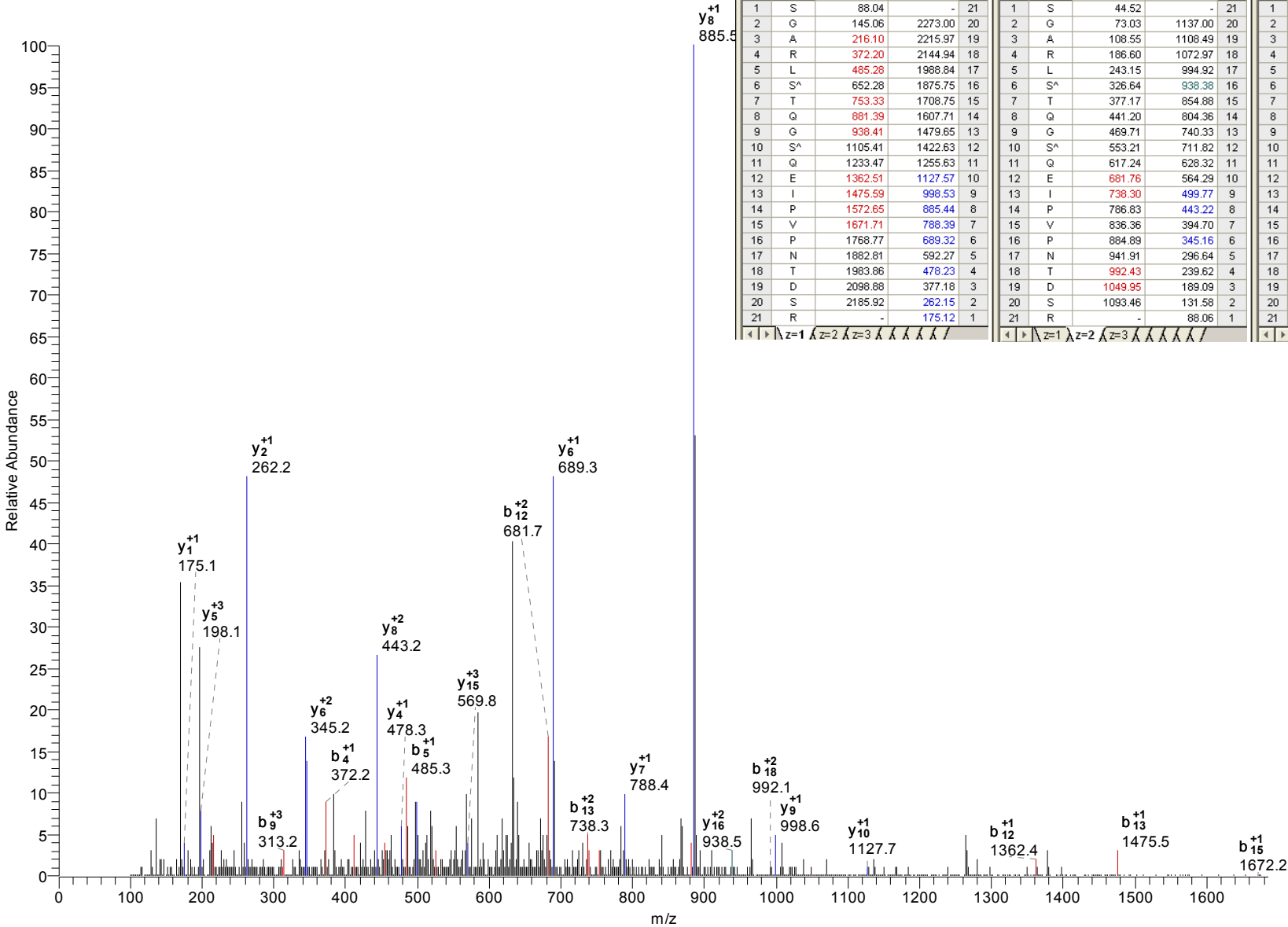
Displaylons - TITPLDSQPPTPPETEDSR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.753.4.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	T	102.05	-	20
2	I	215.14	2156.97	19
3	T	316.19	2043.89	18
4	P	413.24	1942.84	17
5	L	526.32	1845.79	16
6	D	641.35	1732.71	15
7	S	728.38	1617.68	14
8	Q	856.44	1530.65	13
9	P	953.49	1402.59	12
10	P	1050.55	1305.54	11
11	T@	1231.56	1208.48	10
12	P	1328.61	1027.47	9
13	P	1425.67	930.42	8
14	E	1554.71	833.36	7
15	T	1655.76	704.32	6
16	E	1784.80	603.27	5
17	P	1881.85	474.23	4
18	D	1996.88	377.18	3
19	S	2083.91	262.15	2
20	R	-	175.12	1

Displaylons - TITPLDSQPPTPPETEDSR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.753.4.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	T	51.53	-	20
2	I	108.07	1078.99	19
3	T	158.60	1022.45	18
4	P	207.12	971.93	17
5	L	263.67	923.40	16
6	D	321.18	866.86	15
7	S	364.69	809.34	14
8	Q	428.72	765.83	13
9	P	477.25	701.80	12
10	P	525.78	653.27	11
11	T@	616.28	604.75	10
12	P	664.81	514.24	9
13	P	713.34	465.71	8
14	E	777.86	417.19	7
15	T	828.38	352.66	6
16	E	892.90	302.14	5
17	P	941.43	237.62	4
18	D	998.94	189.09	3
19	S	1042.46	131.58	2
20	R	-	88.06	1

Displaylons - TITPLDSQPPTPPETEDSR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.753.4.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	T	34.69	-	20
2	I	72.38	719.66	19
3	T	106.07	681.97	18
4	P	138.42	648.29	17
5	L	176.11	615.93	16
6	D	214.46	578.24	15
7	S	243.47	539.90	14
8	Q	286.15	510.89	13
9	P	318.50	468.20	12
10	P	350.85	435.85	11
11	T@	411.19	403.50	10
12	P	443.54	343.16	9
13	P	475.89	310.81	8
14	E	518.91	278.46	7
15	T	552.59	235.45	6
16	E	595.60	201.76	5
17	P	627.96	158.75	4
18	D	666.30	126.40	3
19	S	695.31	88.06	2
20	R	-	59.04	1

Retinol Dehydrogenase 14

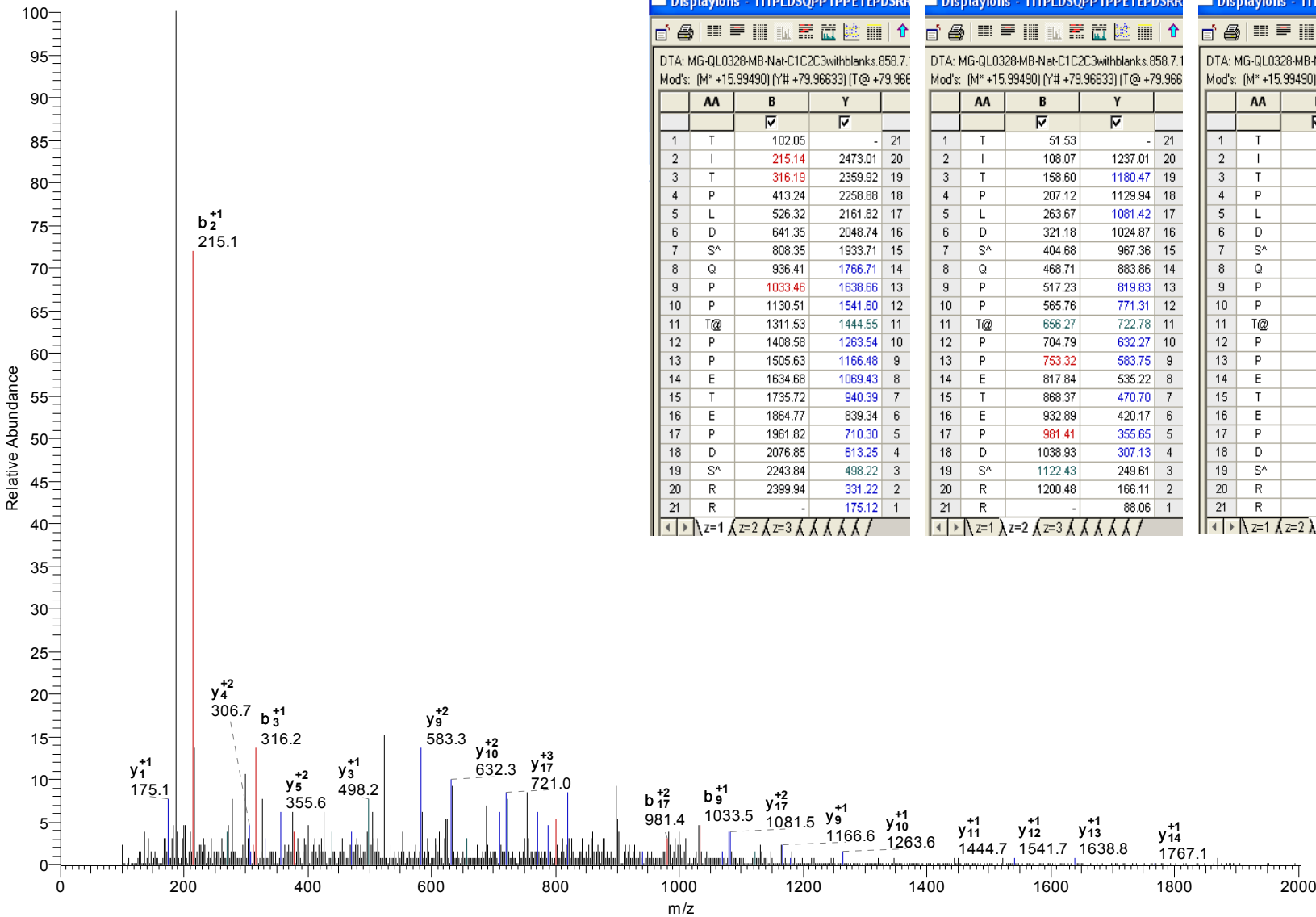
#1489-1489 NL: 1.03E2



Displaylons - SGARLSTQGSQEIPVPNTDSF					Displaylons - SGARLSTQGSQEIPVPNTDSR					Displaylons - SGARLSTQGSQEIPVPNTDSF				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.787.4.1					DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.787.4.1					DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.787.4.1				
Mod's: [M ⁺ +15.99490] [Y# +79.96633] [T@ +79.966]					Mod's: [M ⁺ +15.99490] [Y# +79.96633] [T@ +79.966]					Mod's: [M ⁺ +15.99490] [Y# +79.96633] [T@ +79.966]				
AA	B	Y			AA	B	Y			AA	B	Y		
1	S	88.04	-	21	1	S	44.52	-	21	1	S	30.02	-	21
2	G	145.06	2273.00	20	2	G	73.03	1137.00	20	2	G	49.03	758.34	20
3	A	216.10	2215.97	19	3	A	108.55	1108.49	19	3	A	72.70	739.33	19
4	R	372.20	2144.94	18	4	R	186.60	1072.97	18	4	R	124.74	715.65	18
5	L	485.28	1988.84	17	5	L	243.15	994.92	17	5	L	162.43	663.62	17
6	S ⁺	652.28	1875.75	16	6	S ⁺	326.64	938.38	16	6	S ⁺	218.10	625.92	16
7	T	753.33	1708.75	15	7	T	377.17	854.88	15	7	T	251.78	570.26	15
8	Q	881.39	1607.71	14	8	Q	441.20	804.36	14	8	Q	294.47	536.57	14
9	G	938.41	1479.65	13	9	G	469.71	740.33	13	9	G	313.47	493.89	13
10	S ⁺	1105.41	1422.63	12	10	S ⁺	553.21	711.82	12	10	S ⁺	369.14	474.88	12
11	Q	1233.47	1255.63	11	11	Q	617.24	628.32	11	11	Q	411.83	419.21	11
12	E	1362.51	1127.57	10	12	E	681.76	564.29	10	12	E	454.84	376.53	10
13	I	1475.59	998.53	9	13	I	738.30	499.77	9	13	I	492.54	333.51	9
14	P	1572.65	885.44	8	14	P	786.83	443.22	8	14	P	524.89	295.82	8
15	V	1671.71	788.39	7	15	V	836.36	394.70	7	15	V	557.91	263.47	7
16	P	1768.77	689.32	6	16	P	884.89	345.16	6	16	P	590.26	230.45	6
17	N	1882.81	592.27	5	17	N	941.91	296.64	5	17	N	628.27	198.09	5
18	T	1983.86	478.23	4	18	T	992.43	239.62	4	18	T	661.96	160.08	4
19	D	2098.88	377.18	3	19	D	1049.95	189.09	3	19	D	700.30	126.40	3
20	S	2185.92	262.15	2	20	S	1093.46	131.58	2	20	S	729.31	88.06	2
21	R	-	175.12	1	21	R	-	88.06	1	21	R	-	59.04	1

Retinol Dehydrogenase 14

#1642-1642 NL: 1.33E2



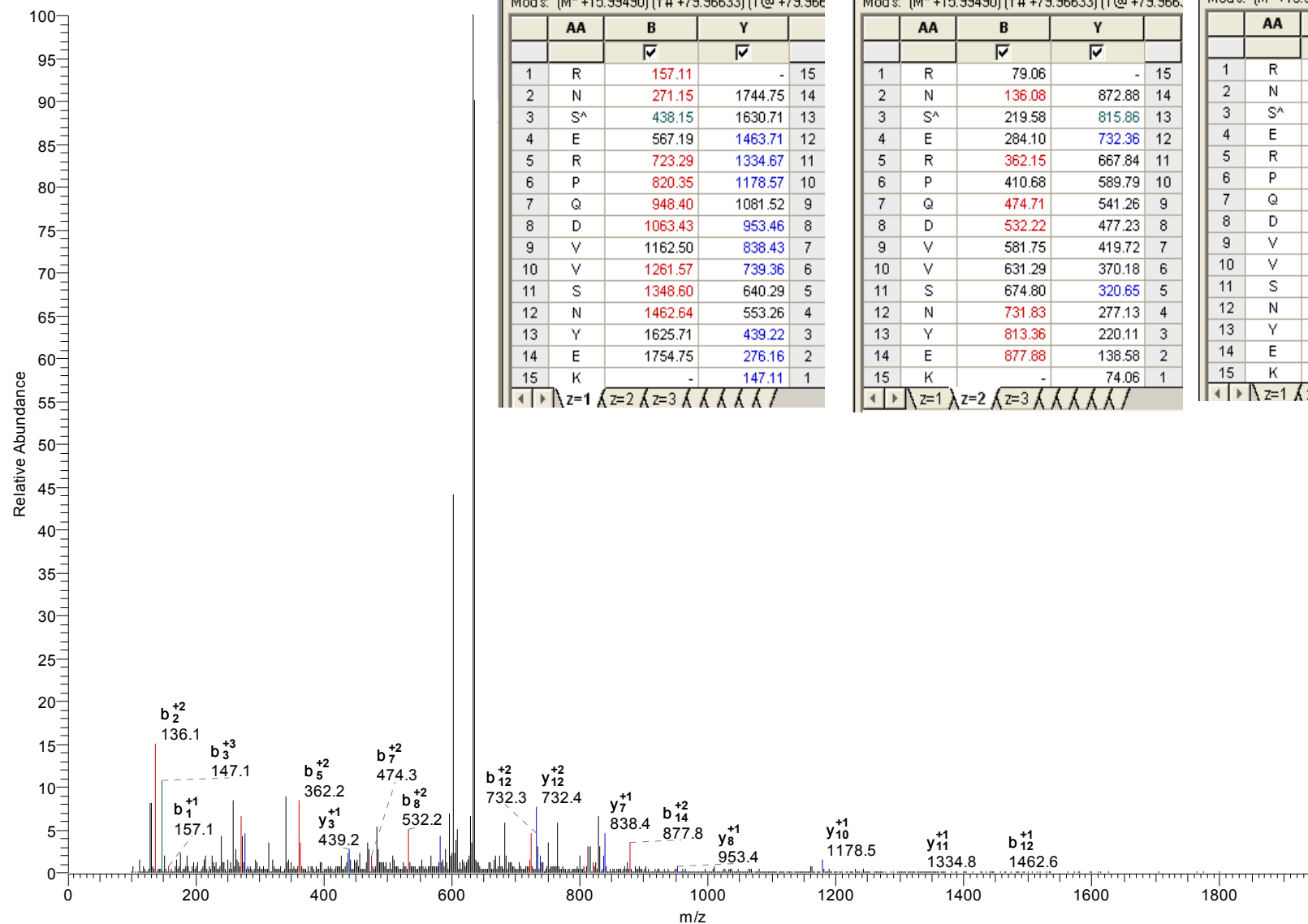
Displaylons - TITPLDSQPPTPPETEPSRR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.858.7.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	T	102.05	-	21
2	I	215.14	2473.01	20
3	T	316.19	2359.92	19
4	P	413.24	2258.88	18
5	L	526.32	2161.82	17
6	D	641.35	2048.74	16
7	S^	808.35	1933.71	15
8	Q	936.41	1766.71	14
9	P	1033.46	1638.66	13
10	P	1130.51	1541.60	12
11	T@	1311.53	1444.55	11
12	P	1408.58	1263.54	10
13	P	1505.63	1166.48	9
14	E	1634.68	1069.43	8
15	T	1735.72	940.39	7
16	E	1864.77	839.34	6
17	P	1961.82	710.30	5
18	D	2076.85	613.25	4
19	S^	2243.84	498.22	3
20	R	2399.94	331.22	2
21	R	-	175.12	1

Displaylons - TITPLDSQPPTPPETEPSRR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.858.7.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	T	51.53	-	21
2	I	108.07	1237.01	20
3	T	158.60	1180.47	19
4	P	207.12	1129.94	18
5	L	263.67	1081.42	17
6	D	321.18	1024.87	16
7	S^	404.68	967.36	15
8	Q	468.71	883.86	14
9	P	517.23	819.83	13
10	P	565.76	771.31	12
11	T@	656.27	722.78	11
12	P	704.79	632.27	10
13	P	753.32	583.75	9
14	E	817.84	535.22	8
15	T	868.37	470.70	7
16	E	932.89	420.17	6
17	P	981.41	355.65	5
18	D	1038.93	307.13	4
19	S^	1122.43	249.61	3
20	R	1200.48	166.11	2
21	R	-	88.06	1

Displaylons - TITPLDSQPPTPPETEPSRR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.858.7.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	T	34.69	-	21
2	I	72.38	825.01	20
3	T	106.07	787.31	19
4	P	138.42	753.63	18
5	L	176.11	721.28	17
6	D	214.46	683.58	16
7	S^	270.12	645.24	15
8	Q	312.81	589.58	14
9	P	345.16	546.89	13
10	P	377.51	514.54	12
11	T@	437.85	482.19	11
12	P	470.20	421.85	10
13	P	502.55	389.50	9
14	E	545.56	357.15	8
15	T	579.25	314.13	7
16	E	622.26	280.45	6
17	P	654.61	237.44	5
18	D	692.95	205.09	4
19	S^	748.62	166.74	3
20	R	800.65	111.08	2
21	R	-	59.04	1

Spata18 Isoform 1 of Spermatogenesis-associated protein 18

#1635-1635 NL: 2.62E2



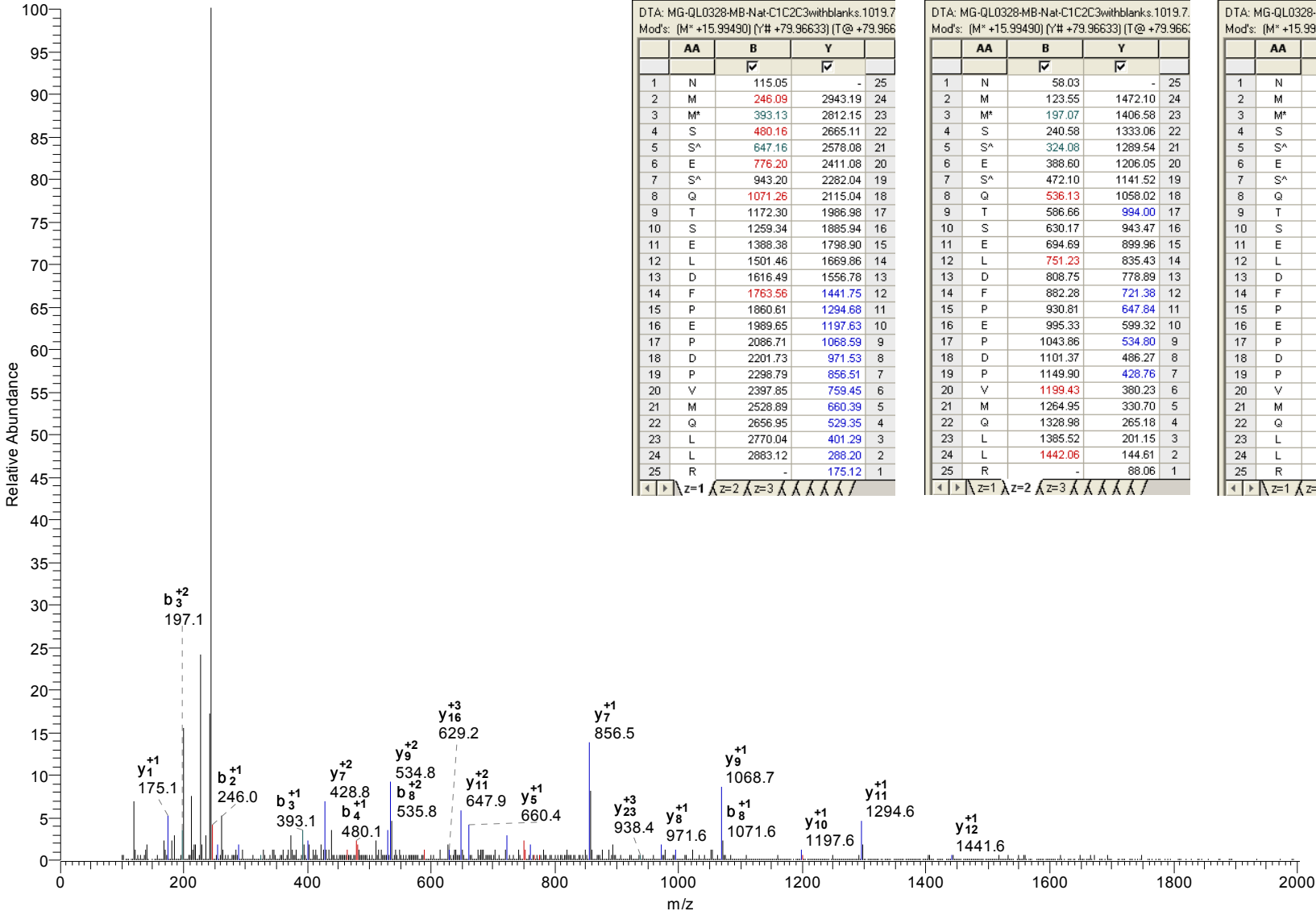
Displaylons - RNSERPQDVVSNEYK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.634.3.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	R	157.11	-	15
2	N	271.15	1744.75	14
3	S [^]	438.15	1630.71	13
4	E	567.19	1463.71	12
5	R	723.29	1334.67	11
6	P	820.35	1178.57	10
7	Q	948.40	1081.52	9
8	D	1063.43	953.46	8
9	V	1162.50	838.43	7
10	V	1261.57	739.36	6
11	S	1348.60	640.29	5
12	N	1462.64	553.26	4
13	Y	1625.71	439.22	3
14	E	1754.75	276.16	2
15	K	-	147.11	1

Displaylons - RNSERPQDVVSNEYK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.634.3.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	R	79.06	-	15
2	N	136.08	872.88	14
3	S [^]	219.58	815.86	13
4	E	284.10	732.36	12
5	R	362.15	667.84	11
6	P	410.68	589.79	10
7	Q	474.71	541.26	9
8	D	532.22	477.23	8
9	V	581.75	419.72	7
10	V	631.29	370.18	6
11	S	674.80	320.65	5
12	N	731.83	277.13	4
13	Y	813.36	220.11	3
14	E	877.88	138.58	2
15	K	-	74.06	1

Displaylons - RNSERPQDVVSNEYK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.634.3.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	R	53.04	-	15
2	N	91.06	582.26	14
3	S [^]	146.72	544.24	13
4	E	189.74	488.58	12
5	R	241.77	445.56	11
6	P	274.12	393.53	10
7	Q	316.81	361.18	9
8	D	355.15	318.49	8
9	V	388.17	280.15	7
10	V	421.19	247.13	6
11	S	450.21	214.10	5
12	N	488.22	185.09	4
13	Y	542.57	147.08	3
14	E	585.59	92.72	2
15	K	-	49.71	1

predicted similar to sarcolemma associated protein

#1994-1994 NL: 1.76E2



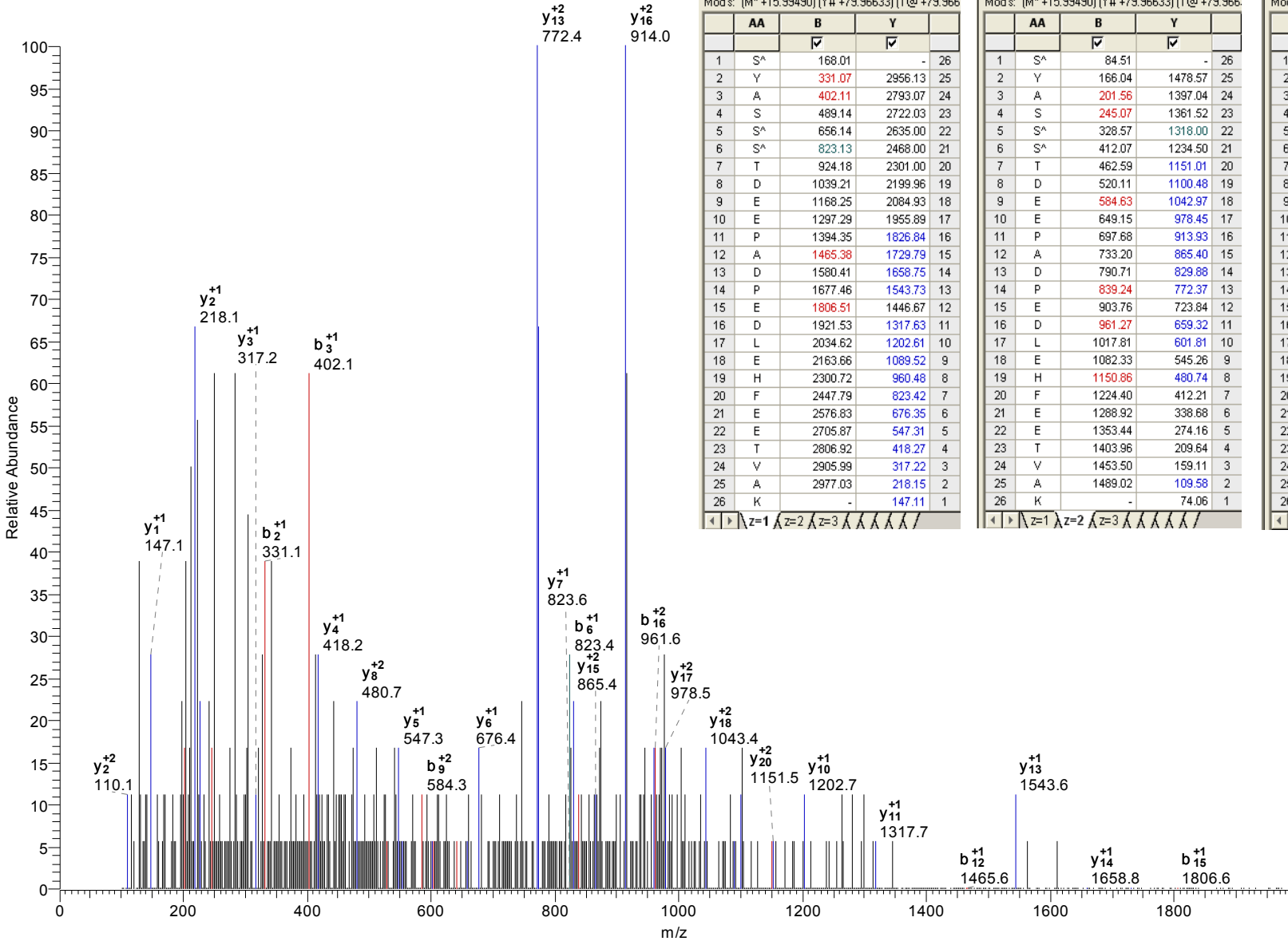
Displaylons - NMMSSSQTSSELDFFEPPDPV				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.1019.7				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	N	115.05	-	25
2	M	246.09	2943.19	24
3	M*	393.13	2812.15	23
4	S	480.16	2665.11	22
5	S^	647.16	2578.08	21
6	E	776.20	2411.08	20
7	S^	943.20	2282.04	19
8	Q	1071.26	2115.04	18
9	T	1172.30	1986.98	17
10	S	1259.34	1885.94	16
11	E	1388.38	1798.90	15
12	L	1501.46	1669.86	14
13	D	1616.49	1556.78	13
14	F	1763.56	1441.75	12
15	P	1860.61	1294.68	11
16	E	1989.65	1197.63	10
17	P	2086.71	1068.59	9
18	D	2201.73	971.53	8
19	P	2298.79	856.51	7
20	V	2397.85	759.45	6
21	M	2528.89	660.39	5
22	Q	2656.95	529.35	4
23	L	2770.04	401.29	3
24	L	2883.12	288.20	2
25	R	-	175.12	1

Displaylons - NMMSSSQTSSELDFFEPPDPV				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.1019.7				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	N	58.03	-	25
2	M	123.55	1472.10	24
3	M*	197.07	1406.58	23
4	S	240.58	1333.06	22
5	S^	324.08	1289.54	21
6	E	388.60	1206.05	20
7	S^	472.10	1141.52	19
8	Q	536.13	1058.02	18
9	T	586.66	994.00	17
10	S	630.17	943.47	16
11	E	694.69	899.96	15
12	L	751.23	835.43	14
13	D	808.75	778.89	13
14	F	882.28	721.38	12
15	P	930.81	647.84	11
16	E	995.33	599.32	10
17	P	1043.86	534.80	9
18	D	1101.37	486.27	8
19	P	1149.90	428.76	7
20	V	1199.43	380.23	6
21	M	1264.95	330.70	5
22	Q	1328.98	265.18	4
23	L	1385.52	201.15	3
24	L	1442.06	144.61	2
25	R	-	88.06	1

Displaylons - NMMSSSQTSSELDFFEPPDPV				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.1019.7				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	N	39.02	-	25
2	M	82.70	981.73	24
3	M*	131.71	938.05	23
4	S	160.72	889.04	22
5	S^	216.39	860.03	21
6	E	259.40	804.37	20
7	S^	315.07	761.35	19
8	Q	357.76	705.69	18
9	T	391.44	663.00	17
10	S	420.45	629.32	16
11	E	463.46	600.31	15
12	L	501.16	557.29	14
13	D	539.50	519.60	13
14	F	588.52	481.26	12
15	P	620.88	432.23	11
16	E	663.89	399.88	10
17	P	696.24	356.87	9
18	D	734.58	324.52	8
19	P	766.93	286.17	7
20	V	799.96	253.82	6
21	M	843.64	220.80	5
22	Q	886.32	177.12	4
23	L	924.02	134.43	3
24	L	961.71	96.74	2
25	R	-	59.04	1

predicted similar to sarcolemma associated protein

#1822-1822 NL: 1.90E1



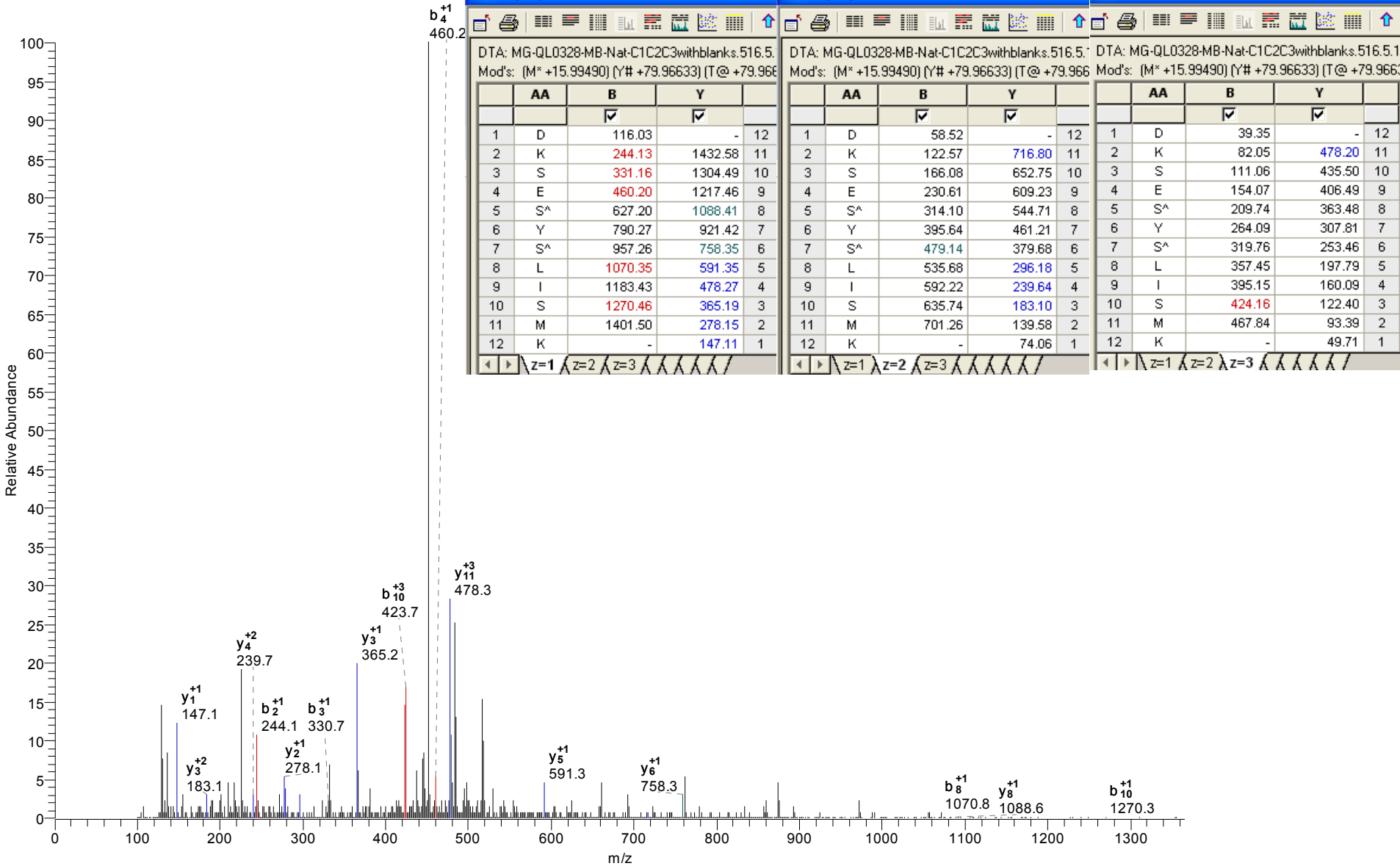
Displaylons - SYASSTDEEPADPEDLEHFE				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.1041.7				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.966)				
	AA	B	Y	
1	S ⁺	168.01	-	26
2	Y	331.07	2956.13	25
3	A	402.11	2793.07	24
4	S	489.14	2722.03	23
5	S ⁺	656.14	2635.00	22
6	S ⁺	823.13	2468.00	21
7	T	924.18	2301.00	20
8	D	1039.21	2199.96	19
9	E	1168.25	2084.93	18
10	E	1297.29	1955.89	17
11	P	1394.35	1826.84	16
12	A	1465.38	1729.79	15
13	D	1580.41	1658.75	14
14	P	1677.46	1543.73	13
15	E	1806.51	1446.67	12
16	D	1921.53	1317.63	11
17	L	2034.62	1202.61	10
18	E	2163.66	1089.52	9
19	H	2300.72	960.48	8
20	F	2447.79	823.42	7
21	E	2576.83	676.35	6
22	E	2705.87	547.31	5
23	T	2806.92	418.27	4
24	V	2905.99	317.22	3
25	A	2977.03	218.15	2
26	K	-	147.11	1

Displaylons - SYASSTDEEPADPEDLEHFE				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.1041.7				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.966)				
	AA	B	Y	
1	S ⁺	84.51	-	26
2	Y	166.04	1478.57	25
3	A	201.56	1397.04	24
4	S	245.07	1361.52	23
5	S ⁺	328.57	1318.00	22
6	S ⁺	412.07	1234.50	21
7	T	462.59	1151.01	20
8	D	520.11	1100.48	19
9	E	584.63	1042.97	18
10	E	649.15	978.45	17
11	P	697.68	913.93	16
12	A	733.20	865.40	15
13	D	790.71	829.88	14
14	P	839.24	772.37	13
15	E	903.76	723.84	12
16	D	961.27	659.32	11
17	L	1017.81	601.81	10
18	E	1082.33	545.26	9
19	H	1150.86	480.74	8
20	F	1224.40	412.21	7
21	E	1288.92	338.68	6
22	E	1353.44	274.16	5
23	T	1403.96	209.64	4
24	V	1453.50	159.11	3
25	A	1489.02	109.58	2
26	K	-	74.06	1

Displaylons - SYASSTDEEPADPEDLEHFE				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.1041.7				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.966)				
	AA	B	Y	
1	S ⁺	56.67	-	26
2	Y	111.03	986.05	25
3	A	134.71	931.69	24
4	S	163.72	908.02	23
5	S ⁺	219.38	879.01	22
6	S ⁺	275.05	823.34	21
7	T	308.73	767.67	20
8	D	347.07	733.99	19
9	E	390.09	695.65	18
10	E	433.10	652.63	17
11	P	465.45	609.62	16
12	A	489.13	577.27	15
13	D	527.48	553.59	14
14	P	559.83	515.25	13
15	E	602.84	482.90	12
16	D	641.18	439.88	11
17	L	678.88	401.54	10
18	E	721.89	363.85	9
19	H	767.58	320.83	8
20	F	816.60	275.14	7
21	E	859.61	226.12	6
22	E	902.63	183.11	5
23	T	936.31	140.09	4
24	V	969.33	106.41	3
25	A	993.01	73.39	2
26	K	-	49.71	1

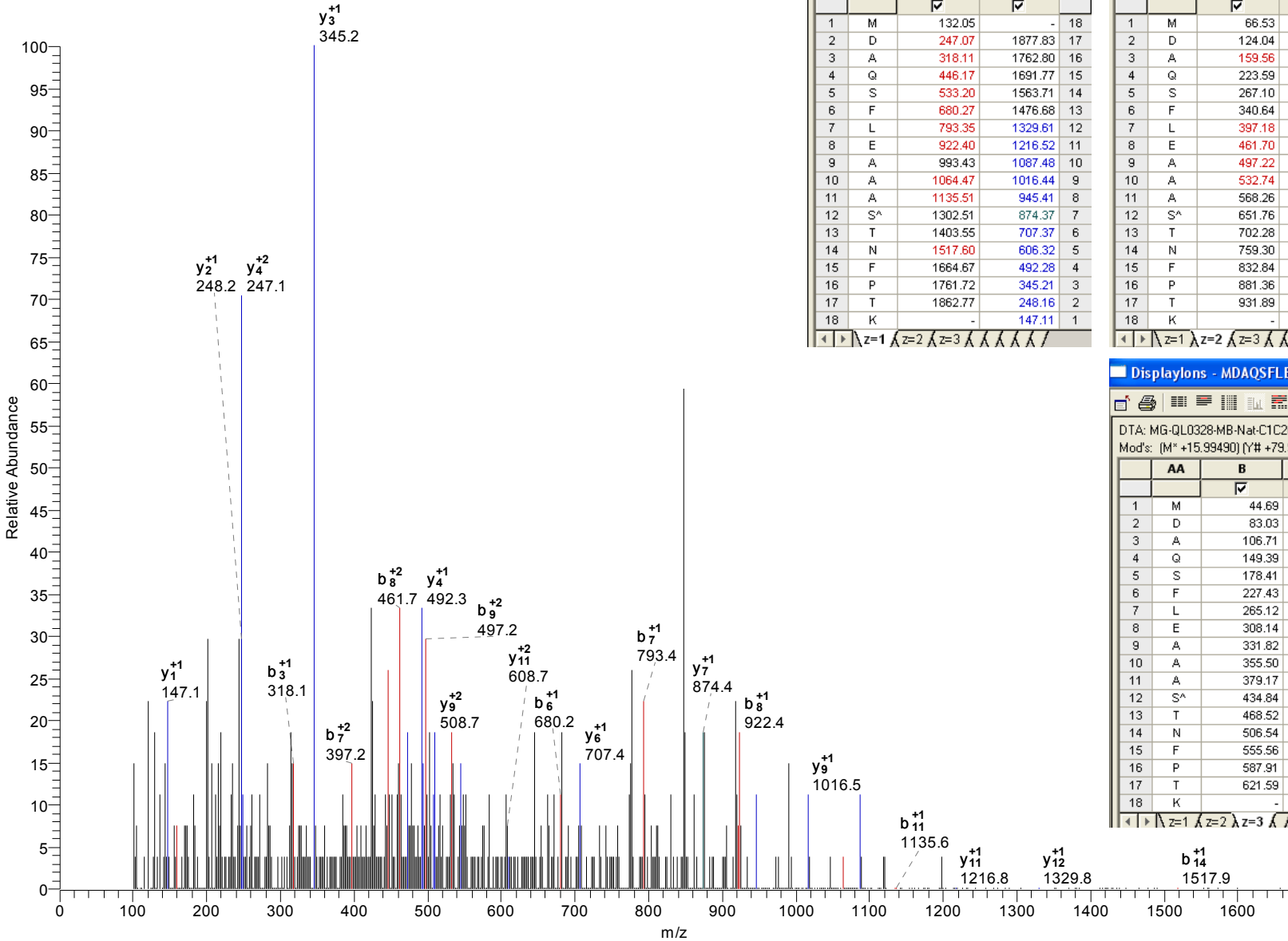
Akap3 A kinase (PRKA) anchor protein 3

#1675-1675 NL: 1.32E2



Akap3 A kinase (PRKA) anchor protein 3

#1828-1828 NL: 2.80E1



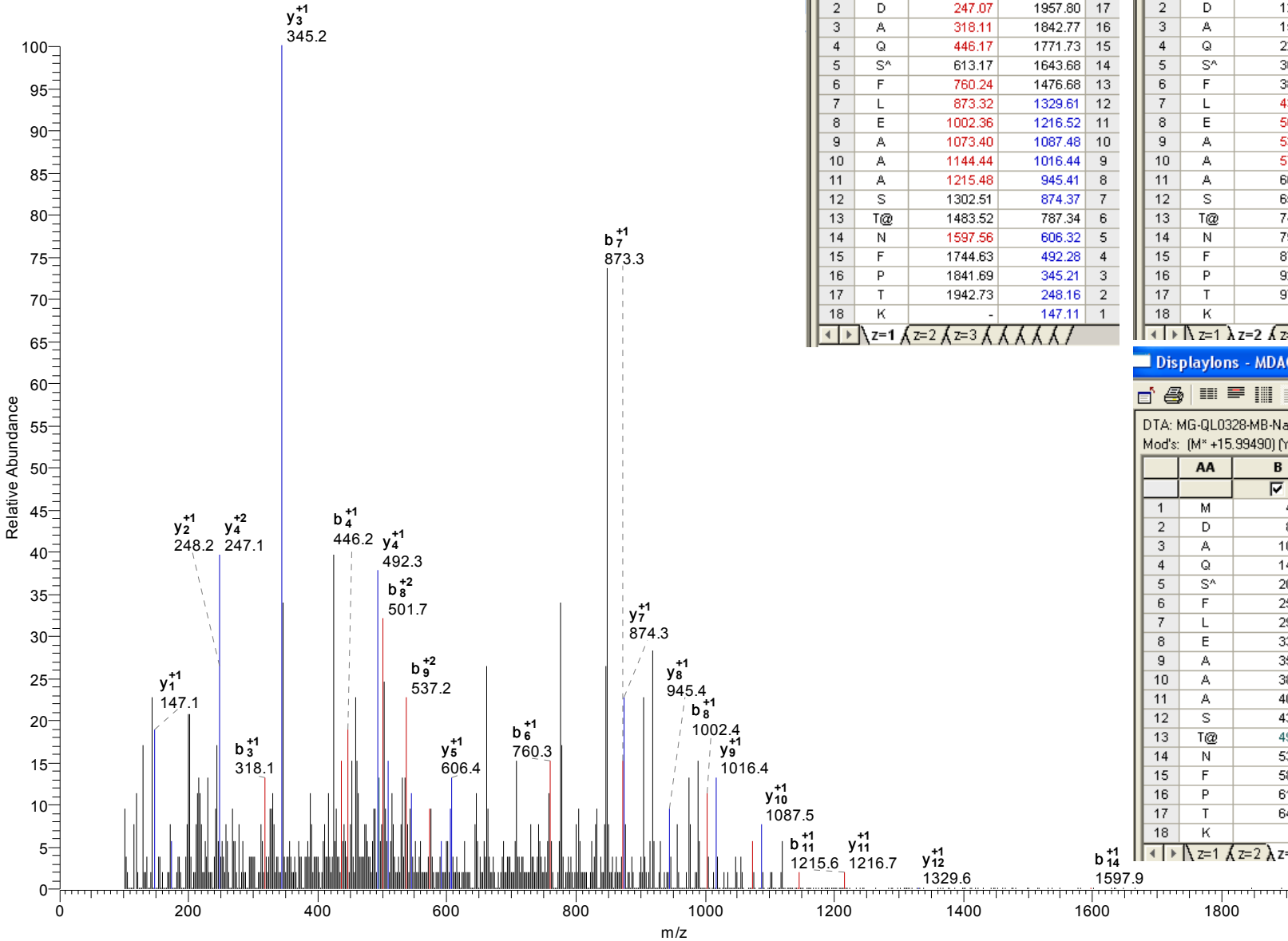
Displaylons - MDAQSFLEAAASTNFPTK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.670.3.1				
Mod's: [M* +15.99490] [Y# +79.96633] [T@ +79.96633]				
	AA	B	Y	
1	M	132.05	-	18
2	D	247.07	1877.83	17
3	A	318.11	1762.80	16
4	Q	446.17	1691.77	15
5	S	533.20	1563.71	14
6	F	680.27	1476.68	13
7	L	793.35	1329.61	12
8	E	922.40	1216.52	11
9	A	993.43	1087.48	10
10	A	1064.47	1016.44	9
11	A	1135.51	945.41	8
12	S^	1302.51	874.37	7
13	T	1403.55	707.37	6
14	N	1517.60	606.32	5
15	F	1664.67	492.28	4
16	P	1761.72	345.21	3
17	T	1862.77	248.16	2
18	K	-	147.11	1

Displaylons - MDAQSFLEAAASTNFPTK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.670.3.1				
Mod's: [M* +15.99490] [Y# +79.96633] [T@ +79.96633]				
	AA	B	Y	
1	M	66.53	-	18
2	D	124.04	939.42	17
3	A	159.56	881.91	16
4	Q	223.59	846.39	15
5	S	267.10	782.36	14
6	F	340.64	738.84	13
7	L	397.18	665.31	12
8	E	461.70	608.77	11
9	A	497.22	544.24	10
10	A	532.74	508.73	9
11	A	568.26	473.21	8
12	S^	651.76	437.69	7
13	T	702.28	354.19	6
14	N	759.30	303.67	5
15	F	832.84	246.64	4
16	P	881.36	173.11	3
17	T	931.89	124.58	2
18	K	-	74.06	1

Displaylons - MDAQSFLEAAASTNFPTK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.670.3.1				
Mod's: [M* +15.99490] [Y# +79.96633] [T@ +79.96633]				
	AA	B	Y	
1	M	44.69	-	18
2	D	83.03	626.62	17
3	A	106.71	588.27	16
4	Q	149.39	564.59	15
5	S	178.41	521.91	14
6	F	227.43	492.90	13
7	L	265.12	443.67	12
8	E	308.14	406.18	11
9	A	331.82	363.17	10
10	A	355.50	339.49	9
11	A	379.17	315.81	8
12	S^	434.84	292.13	7
13	T	468.52	236.46	6
14	N	506.54	202.78	5
15	F	555.56	164.77	4
16	P	587.91	115.74	3
17	T	621.59	83.39	2
18	K	-	49.71	1

Akap3 A kinase (PRKA) anchor protein 3

#1886-1886 NL: 5.40E1



Displaylons - MDAQSFLEAAASTNFP TK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.696.9.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	M	132.05	-	18
2	D	247.07	1957.80	17
3	A	318.11	1842.77	16
4	Q	446.17	1771.73	15
5	S^	613.17	1643.68	14
6	F	760.24	1476.68	13
7	L	873.32	1329.61	12
8	E	1002.36	1216.52	11
9	A	1073.40	1087.48	10
10	A	1144.44	1016.44	9
11	A	1215.48	945.41	8
12	S	1302.51	874.37	7
13	T@	1483.52	787.34	6
14	N	1597.56	606.32	5
15	F	1744.63	492.28	4
16	P	1841.69	345.21	3
17	T	1942.73	248.16	2
18	K	-	147.11	1

Displaylons - MDAQSFLEAAASTNFP TK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.696.9.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	M	66.53	-	18
2	D	124.04	979.40	17
3	A	159.56	921.89	16
4	Q	223.59	886.37	15
5	S^	307.09	822.34	14
6	F	380.62	738.84	13
7	L	437.16	665.31	12
8	E	501.69	608.77	11
9	A	537.20	544.24	10
10	A	572.72	508.73	9
11	A	608.24	473.21	8
12	S	651.76	437.69	7
13	T@	742.26	394.17	6
14	N	799.29	303.67	5
15	F	872.82	246.64	4
16	P	921.35	173.11	3
17	T	971.87	124.58	2
18	K	-	74.06	1

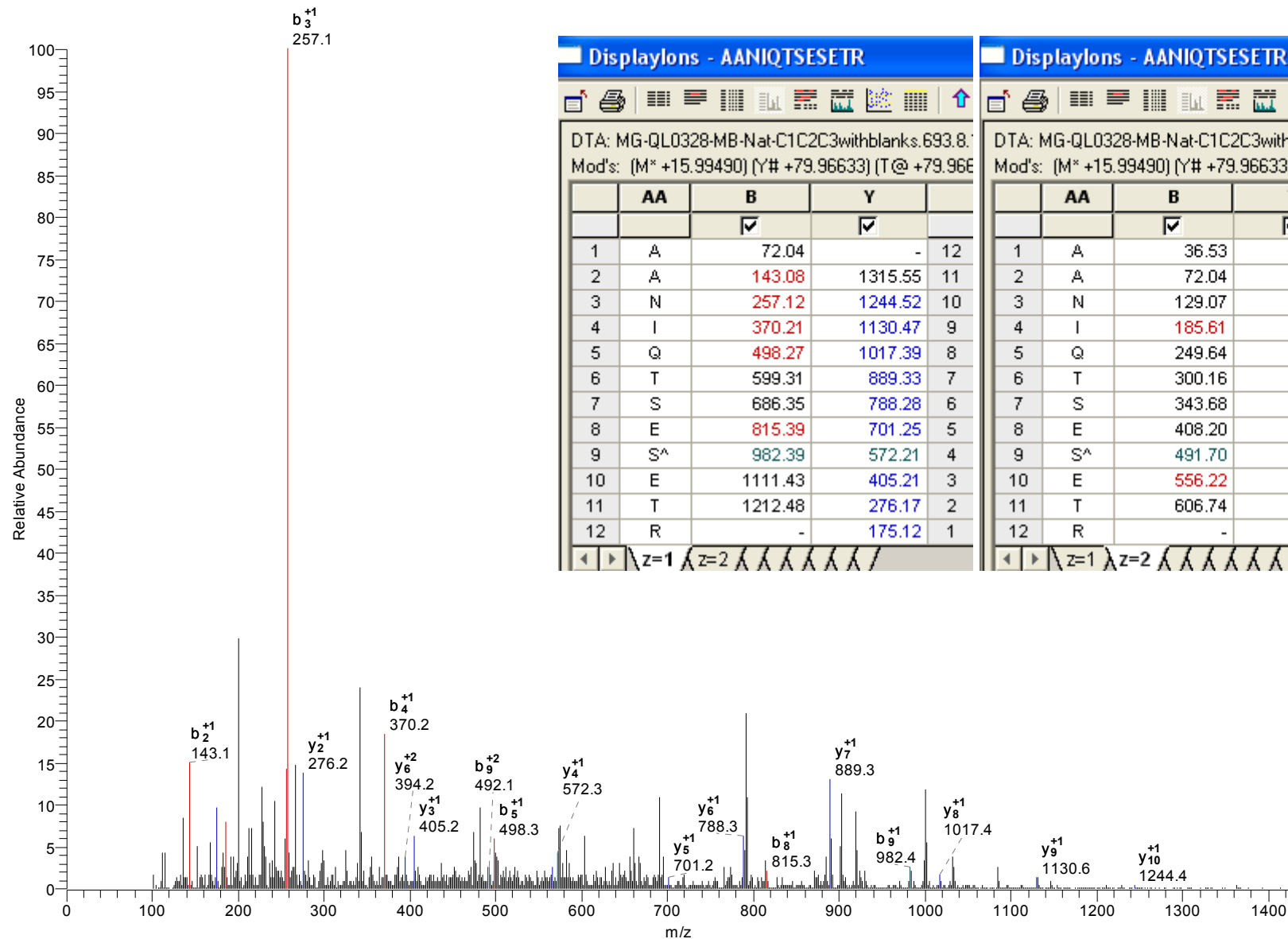
Displaylons - MDAQSFLEAAASTNFP TK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.696.9.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	M	44.69	-	18
2	D	83.03	653.27	17
3	A	106.71	614.93	16
4	Q	149.39	591.25	15
5	S^	205.06	548.56	14
6	F	254.08	492.90	13
7	L	291.78	443.87	12
8	E	334.79	406.18	11
9	A	358.47	363.17	10
10	A	382.15	339.49	9
11	A	405.83	315.81	8
12	S	434.84	292.13	7
13	T@	495.18	263.12	6
14	N	533.19	202.78	5
15	F	582.22	164.77	4
16	P	614.57	115.74	3
17	T	648.25	83.39	2
18	K	-	49.71	1

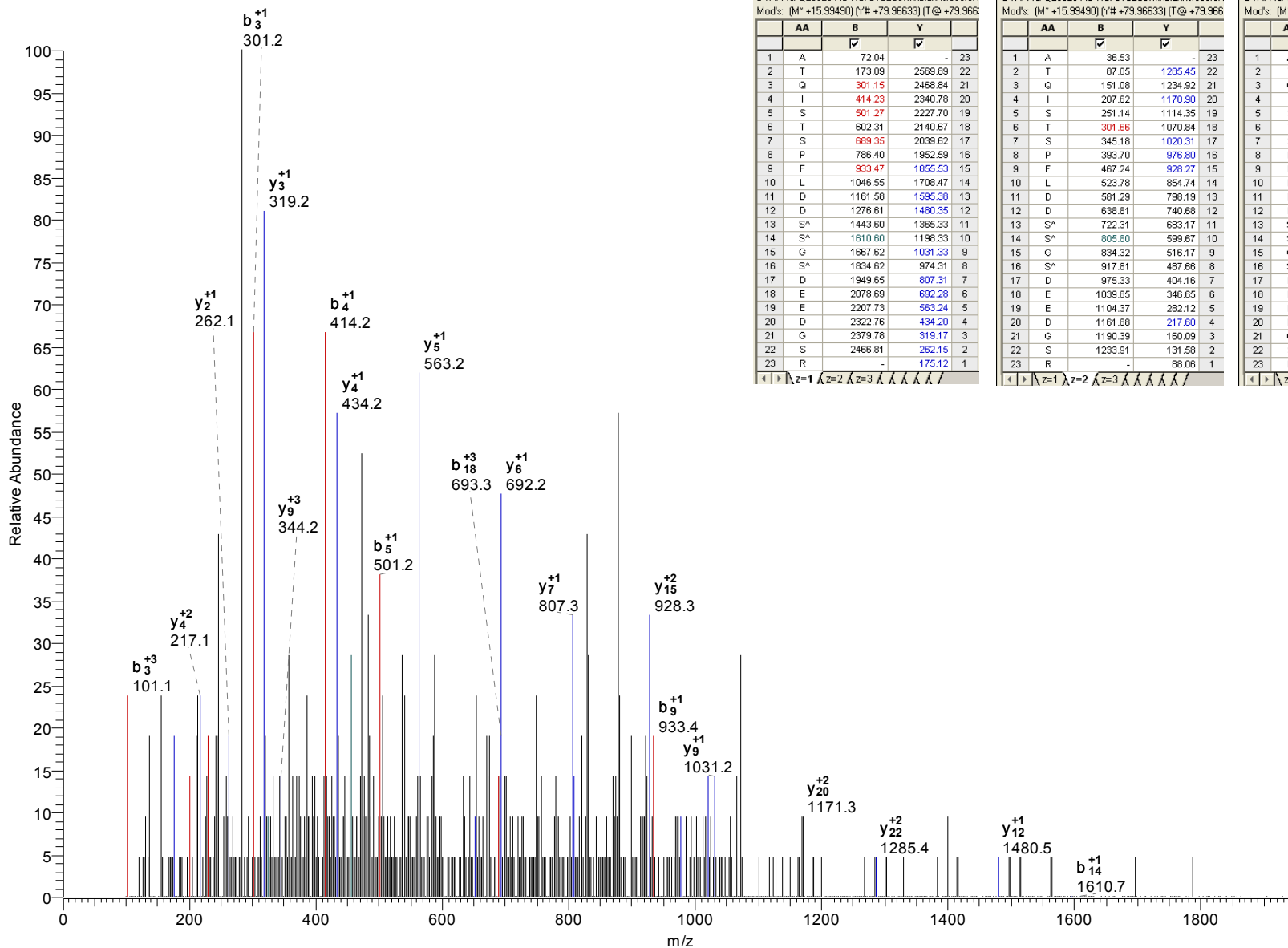
RGD1304935_predicted similar to pleckstrin homology domain containing, family H (with MyTH4 domain) member 2

#1525-1525 NL: 2.40E2



RGD1304935_predicted similar to pleckstrin homology domain containing, family H (with MyTH4 domain) member 2

#1727-1727 NL: 2.20E1



Displaylons - ATQJSTSPFLDDSSGSDFEEDG

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.880.9.1
Mod's: [M* +15.99490] [YH +79.96633] [T@ +79.96633]

	AA	B	Y	
1	A	72.04	-	23
2	T	173.09	2569.89	22
3	Q	301.15	2468.84	21
4	I	414.23	2340.78	20
5	S	501.27	2227.70	19
6	T	602.31	2140.67	18
7	S	689.35	2039.62	17
8	P	786.40	1952.59	16
9	F	933.47	1855.53	15
10	L	1046.55	1708.47	14
11	D	1161.58	1595.38	13
12	D	1276.61	1480.35	12
13	S^	1443.60	1365.33	11
14	S^	1610.60	1198.33	10
15	G	1667.62	1031.33	9
16	S^	1834.62	974.31	8
17	D	1949.65	807.31	7
18	E	2078.69	692.28	6
19	E	2207.73	563.24	5
20	D	2322.76	434.20	4
21	G	2379.78	319.17	3
22	S	2466.81	262.15	2
23	R	-	175.12	1

Displaylons - ATQJSTSPFLDDSSGSDFEEDG

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.880.9.1
Mod's: [M* +15.99490] [YH +79.96633] [T@ +79.96633]

	AA	B	Y	
1	A	36.53	-	23
2	T	67.05	1285.45	22
3	Q	151.08	1234.92	21
4	I	207.62	1170.90	20
5	S	251.14	1114.35	19
6	T	301.66	1070.84	18
7	S	345.18	1020.31	17
8	P	393.70	976.80	16
9	F	467.24	928.27	15
10	L	523.78	854.74	14
11	D	581.29	798.19	13
12	D	638.81	740.68	12
13	S^	722.31	683.17	11
14	S^	805.80	599.67	10
15	G	834.32	516.17	9
16	S^	917.81	487.66	8
17	D	975.33	404.16	7
18	E	1039.85	346.65	6
19	E	1104.37	282.12	5
20	D	1161.88	217.60	4
21	G	1190.39	160.09	3
22	S	1233.91	131.58	2
23	R	-	88.06	1

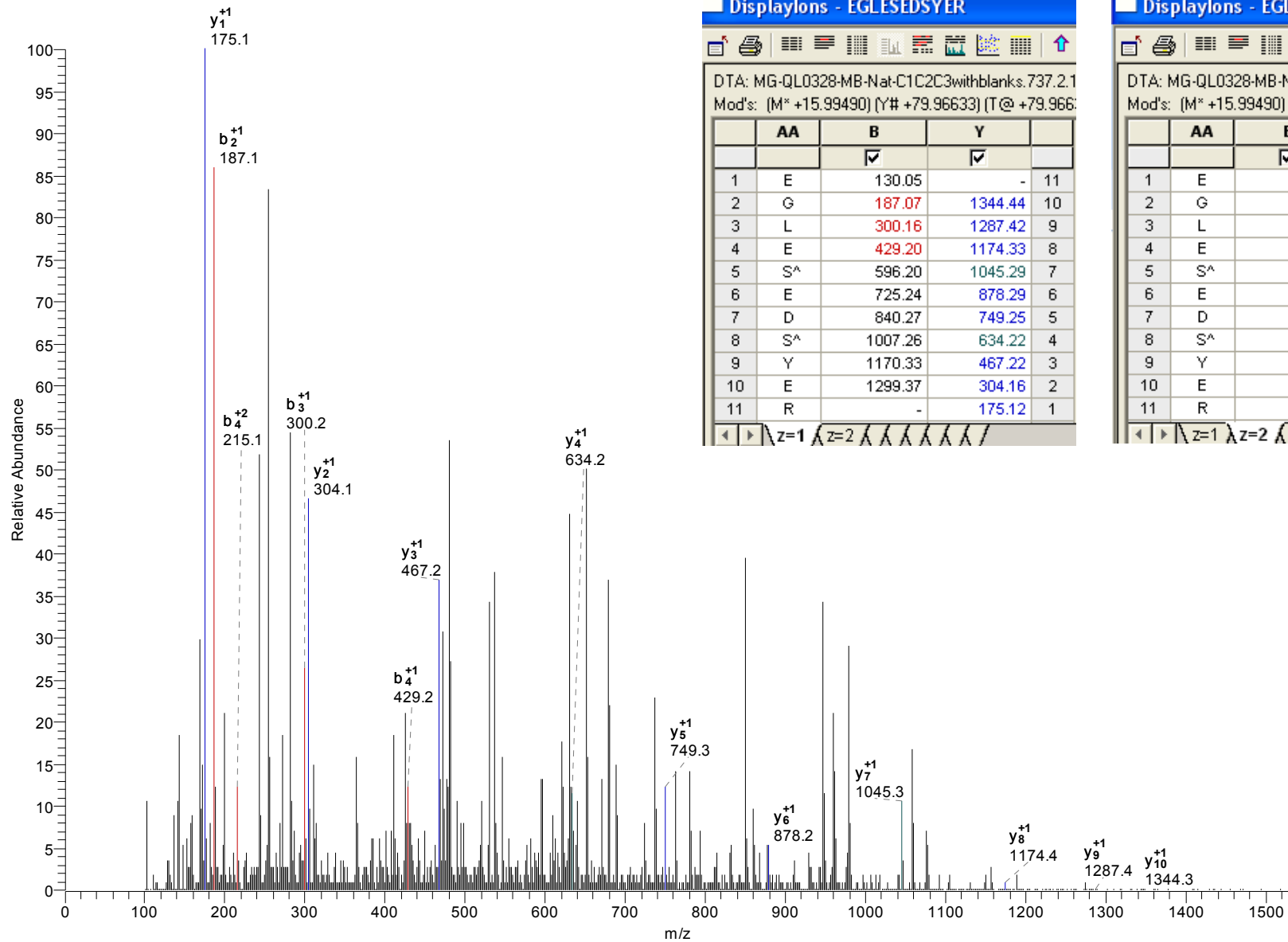
Displaylons - ATQJSTSPFLDDSSGSDFEEDG

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.880.9.1
Mod's: [M* +15.99490] [YH +79.96633] [T@ +79.96633]

	AA	B	Y	
1	A	24.69	-	23
2	T	58.37	857.30	22
3	Q	101.06	823.62	21
4	I	138.75	780.93	20
5	S	167.76	743.24	19
6	T	201.44	714.23	18
7	S	230.45	680.54	17
8	P	262.80	651.53	16
9	F	311.83	619.18	15
10	L	349.52	570.16	14
11	D	387.86	532.47	13
12	D	426.21	494.12	12
13	S^	481.87	455.78	11
14	S^	537.54	400.11	10
15	G	556.55	344.45	9
16	S^	612.21	325.44	8
17	D	650.55	269.78	7
18	E	693.57	231.43	6
19	E	736.58	188.42	5
20	D	774.93	145.40	4
21	G	793.93	107.06	3
22	S	822.94	88.06	2
23	R	-	59.04	1

LOC497959 Similar to novel protein

#1583-1583 NL: 1.15E2



Displaylons - EGLESDSYER

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.737.2.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	E	130.05	-	11
2	G	187.07	1344.44	10
3	L	300.16	1287.42	9
4	E	429.20	1174.33	8
5	S^	596.20	1045.29	7
6	E	725.24	878.29	6
7	D	840.27	749.25	5
8	S^	1007.26	634.22	4
9	Y	1170.33	467.22	3
10	E	1299.37	304.16	2
11	R	-	175.12	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11

Displaylons - EGLESDSYER

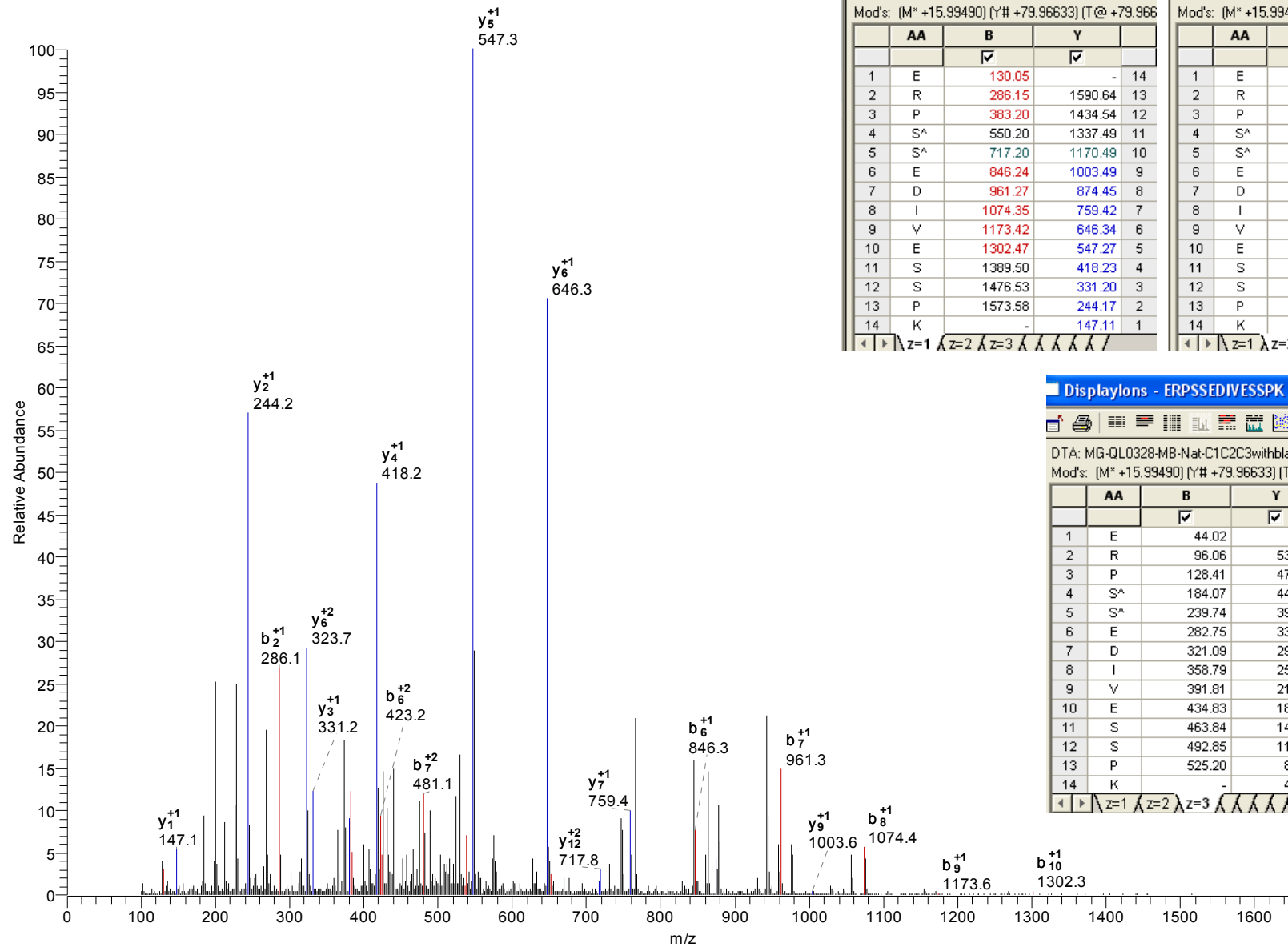
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.737.2.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	E	65.53	-	11
2	G	94.04	672.72	10
3	L	150.58	644.21	9
4	E	215.10	587.67	8
5	S^	298.60	523.15	7
6	E	363.12	439.65	6
7	D	420.64	375.13	5
8	S^	504.14	317.62	4
9	Y	585.67	234.12	3
10	E	650.19	152.58	2
11	R	-	88.06	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11

LOC497959 Similar to novel protein

#1567-1567 NL: 3.03E2



Displaylons - ERPSSDIVESSPK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.573.9.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	E	130.05	-	14
2	R	286.15	1590.64	13
3	P	383.20	1434.54	12
4	S^A	550.20	1337.49	11
5	S^A	717.20	1170.49	10
6	E	846.24	1003.49	9
7	D	961.27	874.45	8
8	I	1074.35	759.42	7
9	V	1173.42	646.34	6
10	E	1302.47	547.27	5
11	S	1389.50	418.23	4
12	S	1476.53	331.20	3
13	P	1573.58	244.17	2
14	K	-	147.11	1

z=1 z=2 z=3

Displaylons - ERPSSDIVESSPK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.573.9.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	E	65.53	-	14
2	R	143.58	795.83	13
3	P	192.11	717.78	12
4	S^A	275.60	669.25	11
5	S^A	359.10	585.75	10
6	E	423.63	502.25	9
7	D	481.14	437.73	8
8	I	537.68	380.22	7
9	V	587.21	323.67	6
10	E	651.74	274.14	5
11	S	695.25	209.62	4
12	S	738.77	166.10	3
13	P	787.29	122.59	2
14	K	-	74.06	1

z=1 z=2 z=3

Displaylons - ERPSSDIVESSPK

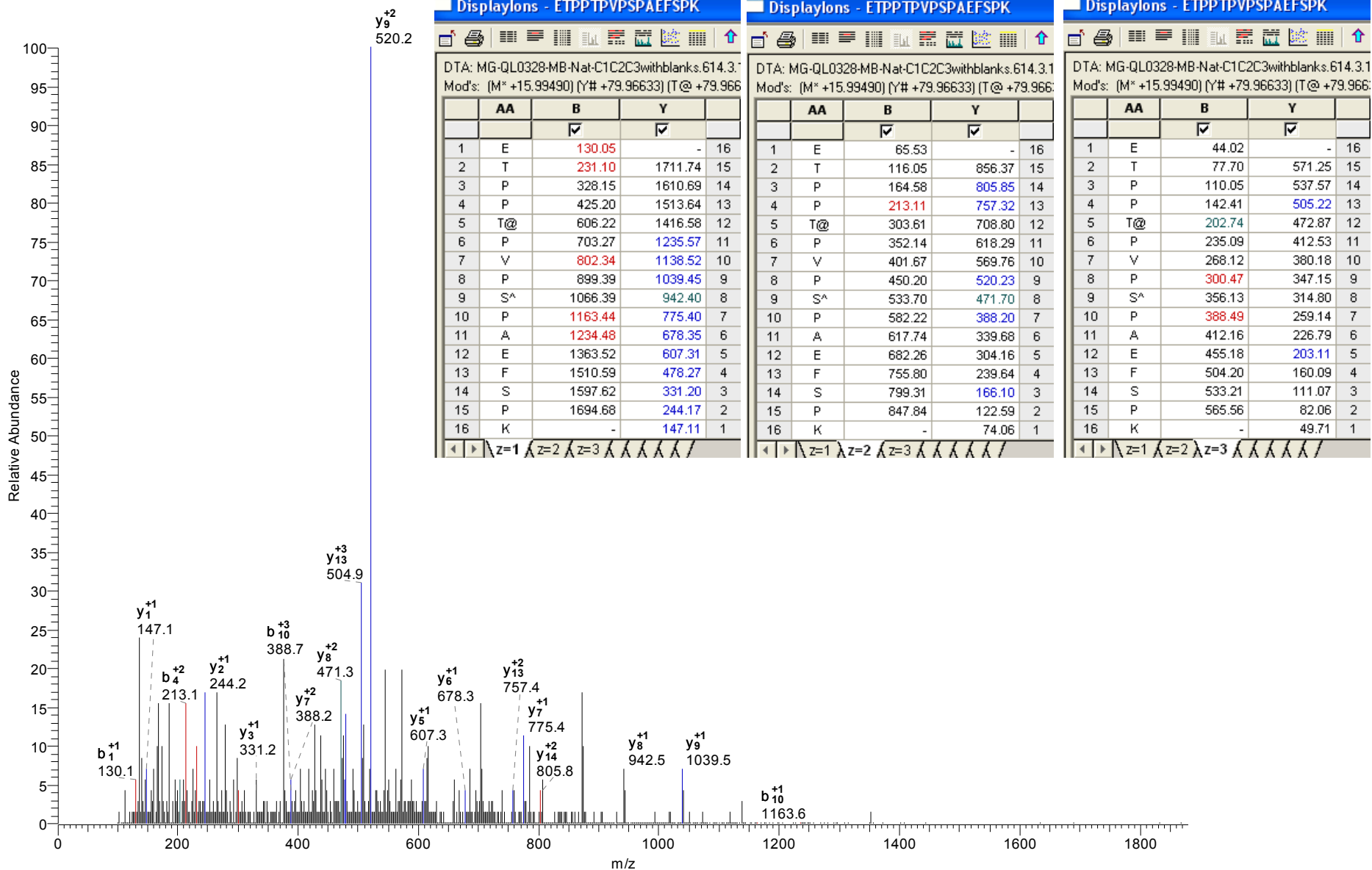
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.573.9.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	E	44.02	-	14
2	R	96.06	530.89	13
3	P	128.41	478.85	12
4	S^A	184.07	446.50	11
5	S^A	239.74	390.84	10
6	E	282.75	335.17	9
7	D	321.09	292.16	8
8	I	358.79	253.81	7
9	V	391.81	216.12	6
10	E	434.83	183.10	5
11	S	463.84	140.08	4
12	S	492.85	111.07	3
13	P	525.20	82.06	2
14	K	-	49.71	1

z=1 z=2 z=3

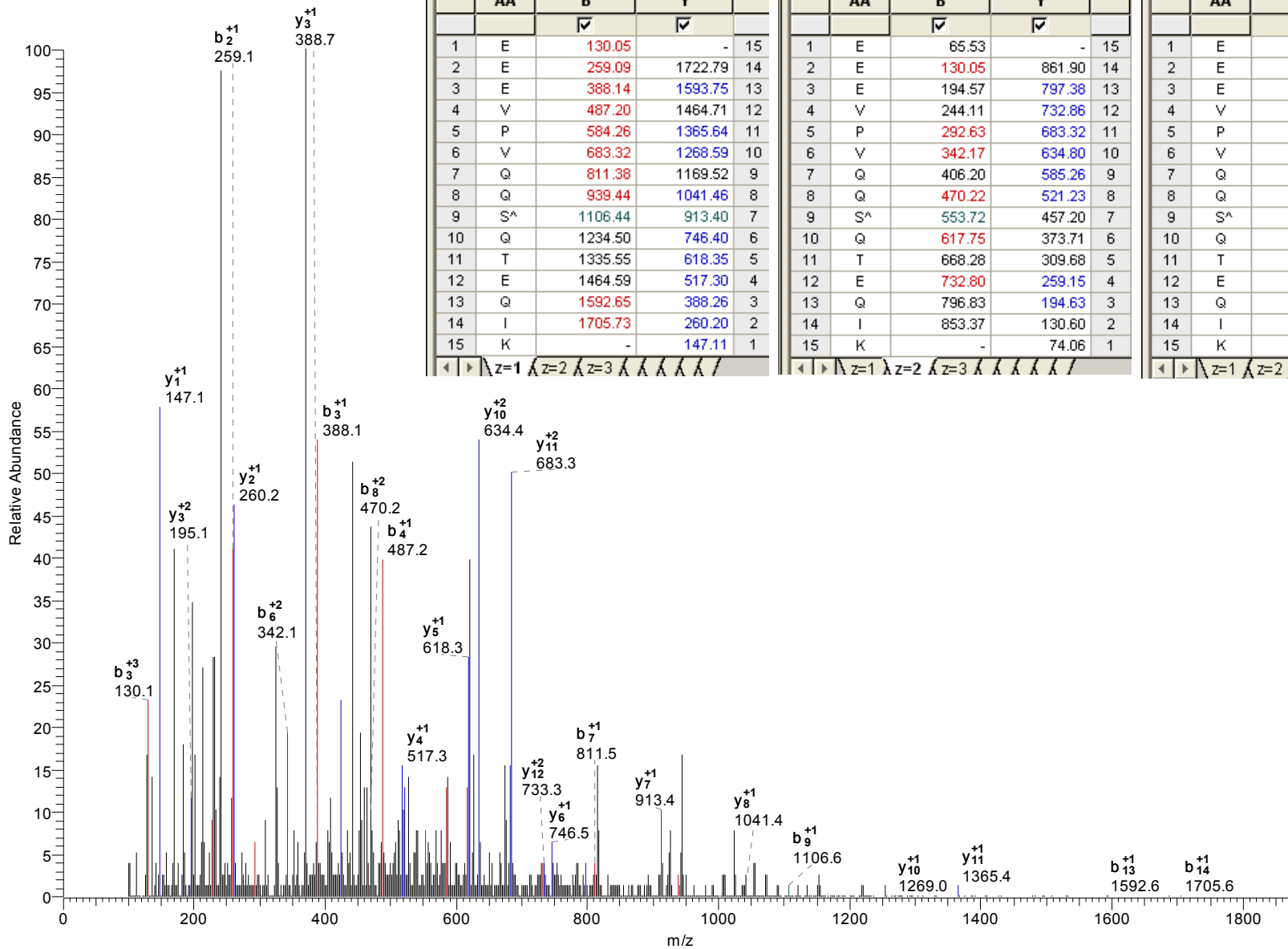
Testis-specific actin-related protein 3

#1673-1673 NL: 7.20E1



Sp3111 Sperm protein SSP3111

#1588-1588 NL: 7.90E1



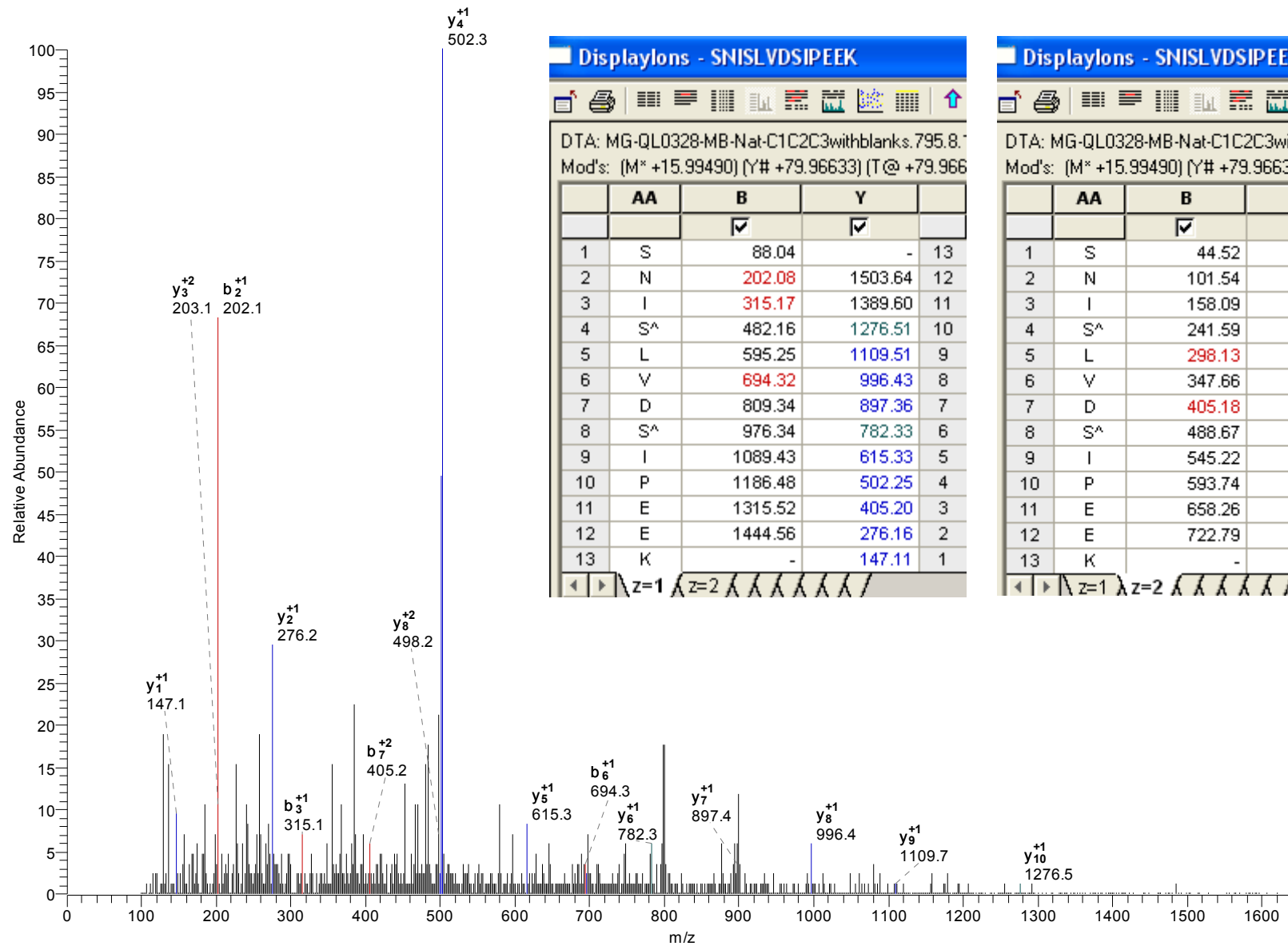
Displaylons - EEEVPVQQSQTEQIK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.617.9.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
		☒	☒	
1	E	130.05	-	15
2	E	259.09	1722.79	14
3	E	388.14	1593.75	13
4	V	487.20	1464.71	12
5	P	584.26	1365.64	11
6	V	683.32	1268.59	10
7	Q	811.38	1169.52	9
8	Q	939.44	1041.46	8
9	S^	1106.44	913.40	7
10	Q	1234.50	746.40	6
11	T	1335.55	618.35	5
12	E	1464.59	517.30	4
13	Q	1592.65	388.26	3
14	I	1705.73	260.20	2
15	K	-	147.11	1

Displaylons - EEEVPVQQSQTEQIK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.617.9.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
		☒	☒	
1	E	65.53	-	15
2	E	130.05	861.90	14
3	E	194.57	797.38	13
4	V	244.11	732.86	12
5	P	292.63	683.32	11
6	V	342.17	634.80	10
7	Q	406.20	585.26	9
8	Q	470.22	521.23	8
9	S^	553.72	457.20	7
10	Q	617.75	373.71	6
11	T	668.28	309.68	5
12	E	732.80	259.15	4
13	Q	796.83	194.63	3
14	I	853.37	130.60	2
15	K	-	74.06	1

Displaylons - EEEVPVQQSQTEQIK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.617.9.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
		☒	☒	
1	E	44.02	-	15
2	E	87.04	574.94	14
3	E	130.05	531.92	13
4	V	163.07	488.91	12
5	P	195.42	455.89	11
6	V	228.45	423.53	10
7	Q	271.13	390.51	9
8	Q	313.82	347.83	8
9	S^	369.48	305.14	7
10	Q	412.17	249.47	6
11	T	445.85	206.79	5
12	E	488.87	173.10	4
13	Q	531.55	130.09	3
14	I	569.25	87.40	2
15	K	-	49.71	1

105 kDa protein

#1692-1692 NL: 8.60E1



Displaylons - SNISLVDSIPEEK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.795.8.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	S	88.04	-	13
2	N	202.08	1503.64	12
3	I	315.17	1389.60	11
4	S^	482.16	1276.51	10
5	L	595.25	1109.51	9
6	V	694.32	996.43	8
7	D	809.34	897.36	7
8	S^	976.34	782.33	6
9	I	1089.43	615.33	5
10	P	1186.48	502.25	4
11	E	1315.52	405.20	3
12	E	1444.56	276.16	2
13	K	-	147.11	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13

Displaylons - SNISLVDSIPEEK

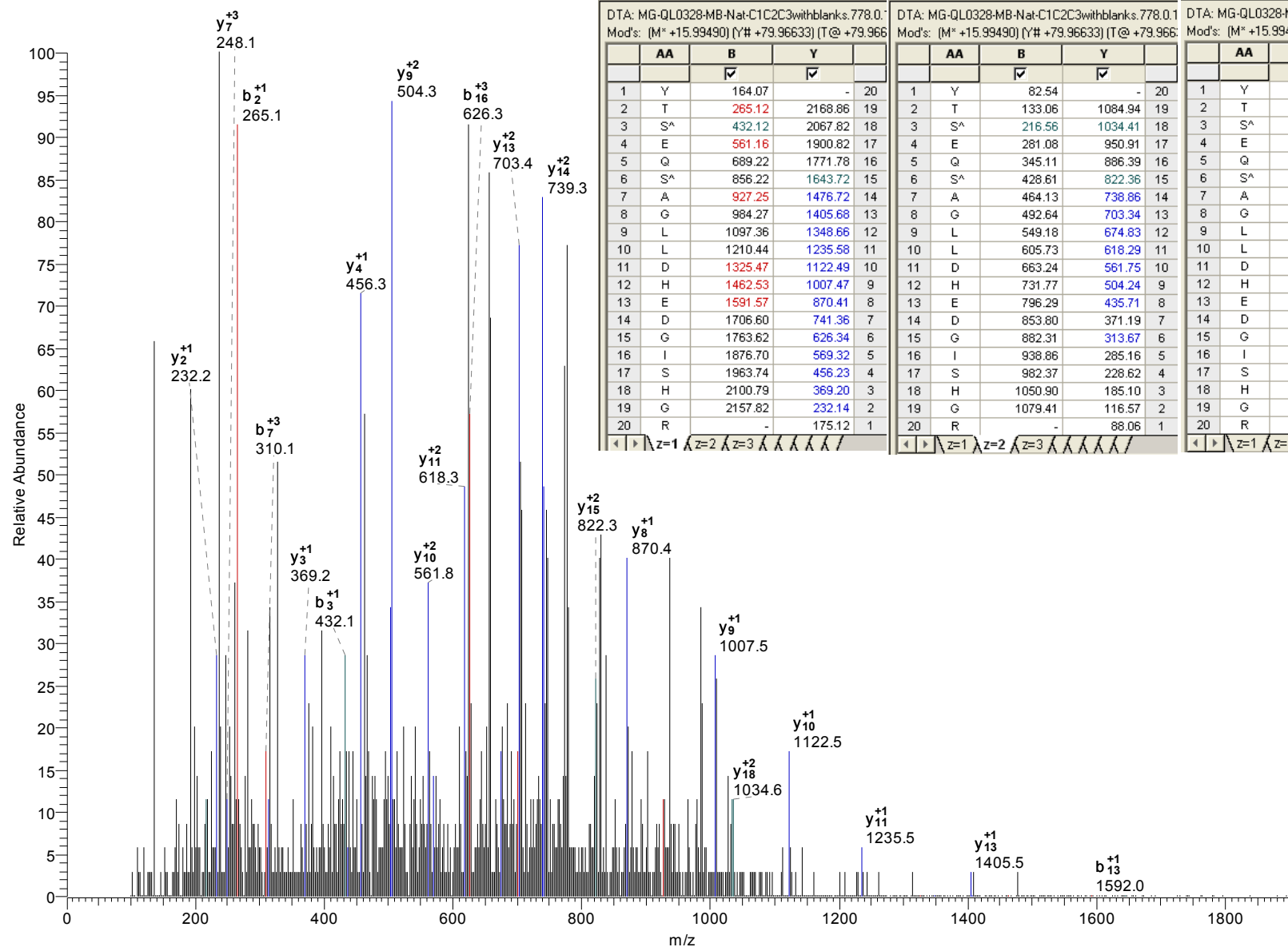
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.795.8.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	S	44.52	-	13
2	N	101.54	752.32	12
3	I	158.09	695.30	11
4	S^	241.59	638.76	10
5	L	298.13	555.26	9
6	V	347.66	498.72	8
7	D	405.18	449.18	7
8	S^	488.67	391.67	6
9	I	545.22	308.17	5
10	P	593.74	251.63	4
11	E	658.26	203.10	3
12	E	722.79	138.58	2
13	K	-	74.06	1

z=1 z=2 z=3 z=4 z=5 z=6 z=7 z=8 z=9 z=10 z=11 z=12 z=13

Hypothetical protein

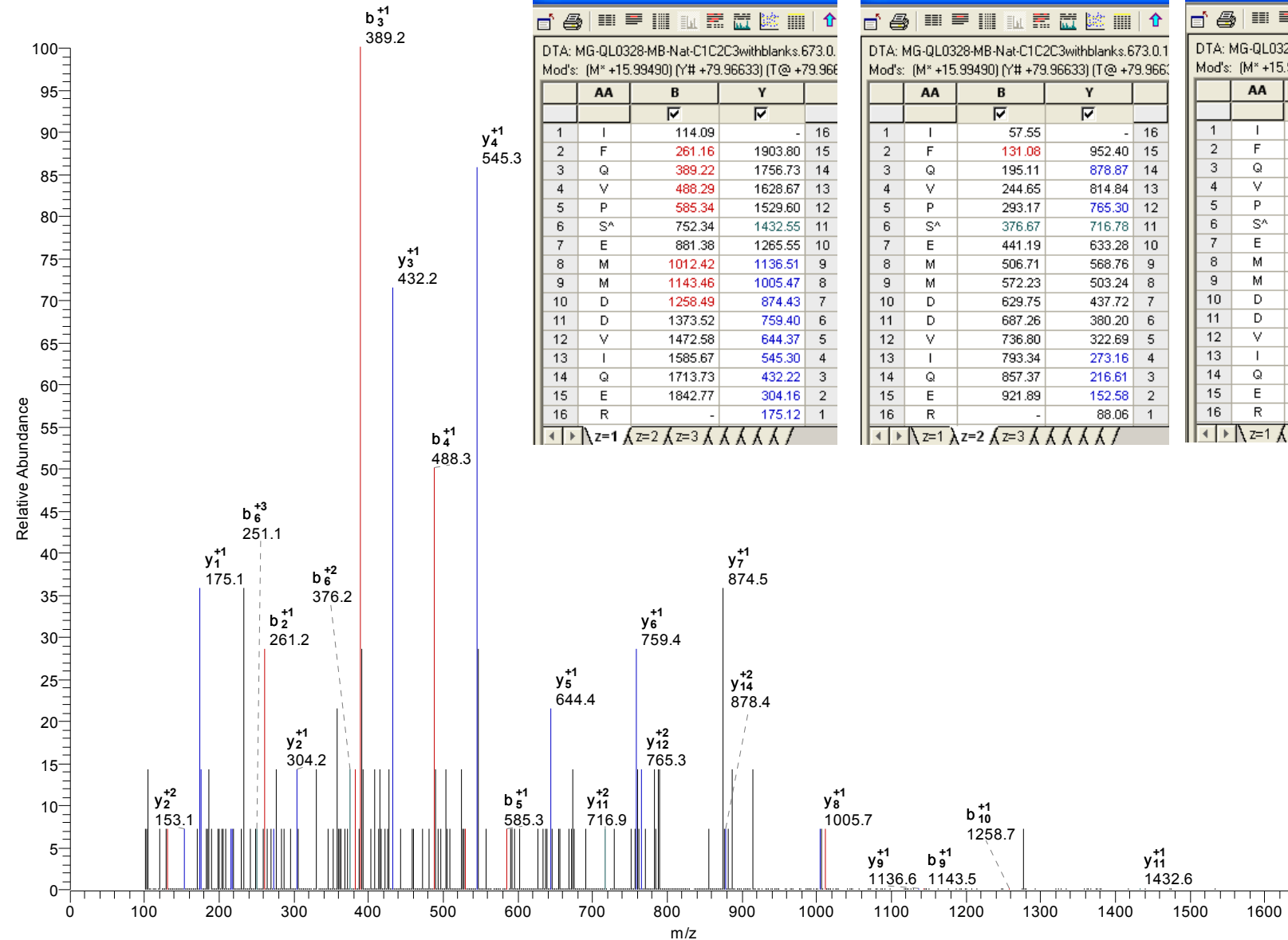
#1635-1635 NL: 3.60E1



Displaylons - YTSEQSAGLLDHEDGISHGR					Displaylons - YTSEQSAGLLDHEDGISHGR					Displaylons - YTSEQSAGLLDHEDGISHGR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.778.0.1					DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.778.0.1					DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.778.0.1				
Mod's: (M ⁺ +15.99490) (Y# +79.96633) (T@ +79.966)					Mod's: (M ⁺ +15.99490) (Y# +79.96633) (T@ +79.966)					Mod's: (M ⁺ +15.99490) (Y# +79.96633) (T@ +79.966)				
	AA	B	Y			AA	B	Y			AA	B	Y	
1	Y	164.07	-	20	1	Y	82.54	-	20	1	Y	55.36	-	20
2	T	265.12	2168.86	19	2	T	133.06	1084.94	19	2	T	89.04	723.63	19
3	S [^]	432.12	2067.82	18	3	S [^]	216.56	1034.41	18	3	S [^]	144.71	689.94	18
4	E	561.16	1900.82	17	4	E	281.08	950.91	17	4	E	187.72	634.28	17
5	Q	689.22	1771.78	16	5	Q	345.11	886.39	16	5	Q	230.41	591.26	16
6	S [^]	856.22	1643.72	15	6	S [^]	428.61	822.36	15	6	S [^]	286.08	548.58	15
7	A	927.25	1476.72	14	7	A	464.13	738.86	14	7	A	309.76	492.91	14
8	G	984.27	1405.68	13	8	G	492.64	703.34	13	8	G	328.76	469.23	13
9	L	1097.36	1348.66	12	9	L	549.18	674.83	12	9	L	366.46	450.22	12
10	L	1210.44	1235.58	11	10	L	605.73	618.29	11	10	L	404.15	412.53	11
11	D	1325.47	1122.49	10	11	D	663.24	561.75	10	11	D	442.49	374.84	10
12	H	1462.53	1007.47	9	12	H	731.77	504.24	9	12	H	488.18	336.49	9
13	E	1591.57	870.41	8	13	E	796.29	435.71	8	13	E	531.20	290.81	8
14	D	1706.60	741.36	7	14	D	853.80	371.19	7	14	D	569.54	247.79	7
15	G	1763.62	626.34	6	15	G	882.31	313.67	6	15	G	588.54	209.45	6
16	I	1876.70	569.32	5	16	I	938.86	285.16	5	16	I	626.24	190.44	5
17	S	1963.74	456.23	4	17	S	982.37	228.62	4	17	S	655.25	152.75	4
18	H	2100.79	369.20	3	18	H	1050.90	185.10	3	18	H	700.94	123.74	3
19	G	2157.82	232.14	2	19	G	1079.41	116.57	2	19	G	719.94	78.05	2
20	R	-	175.12	1	20	R	-	88.06	1	20	R	-	59.04	1

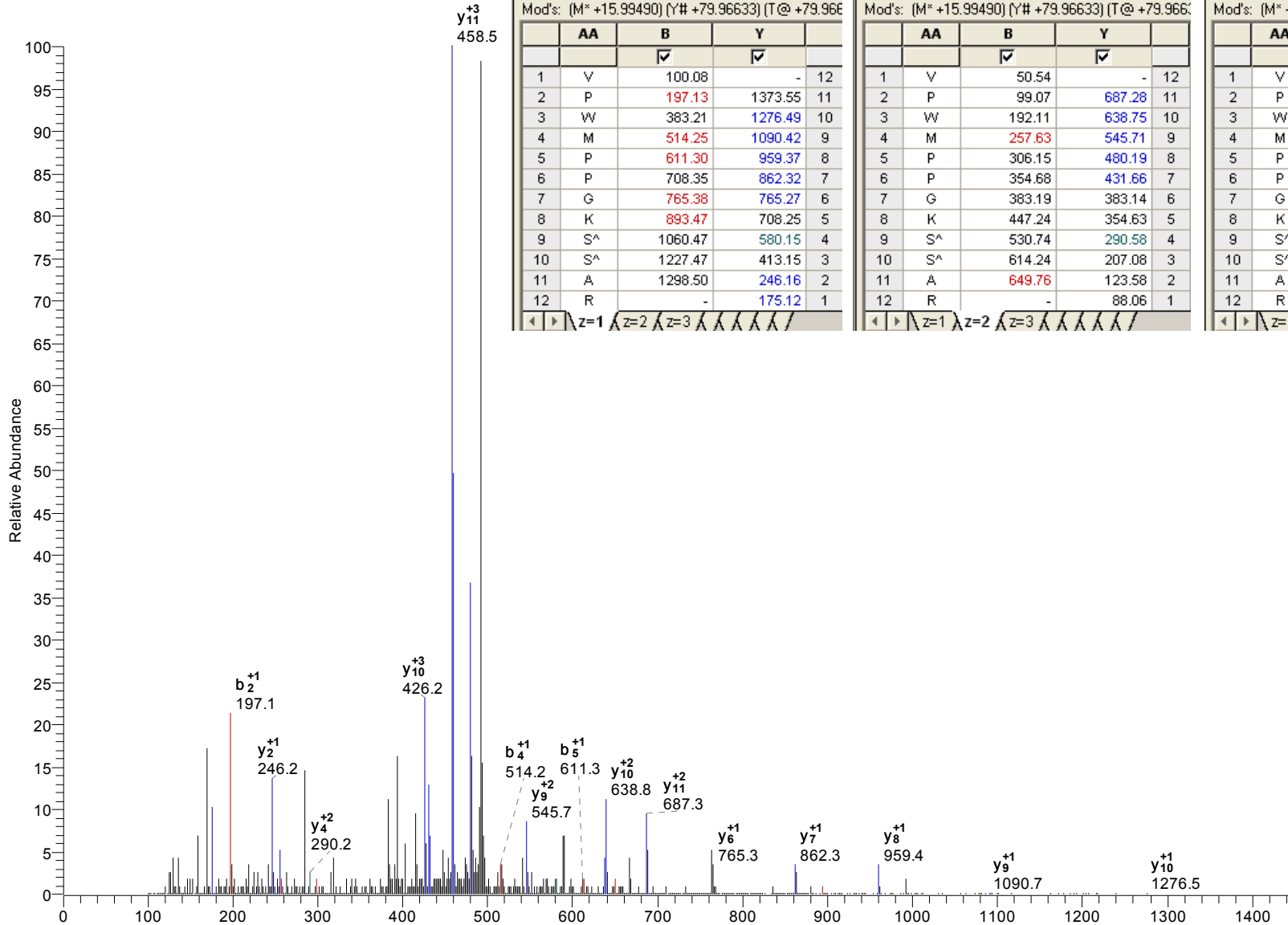
Spas1 Spermatogenesis-associated protein 19, mitochondrial precursor

#1883-1883 NL: 1.50E1



Odf2 Cenexin 2

#1657-1657 NL: 1.18E2



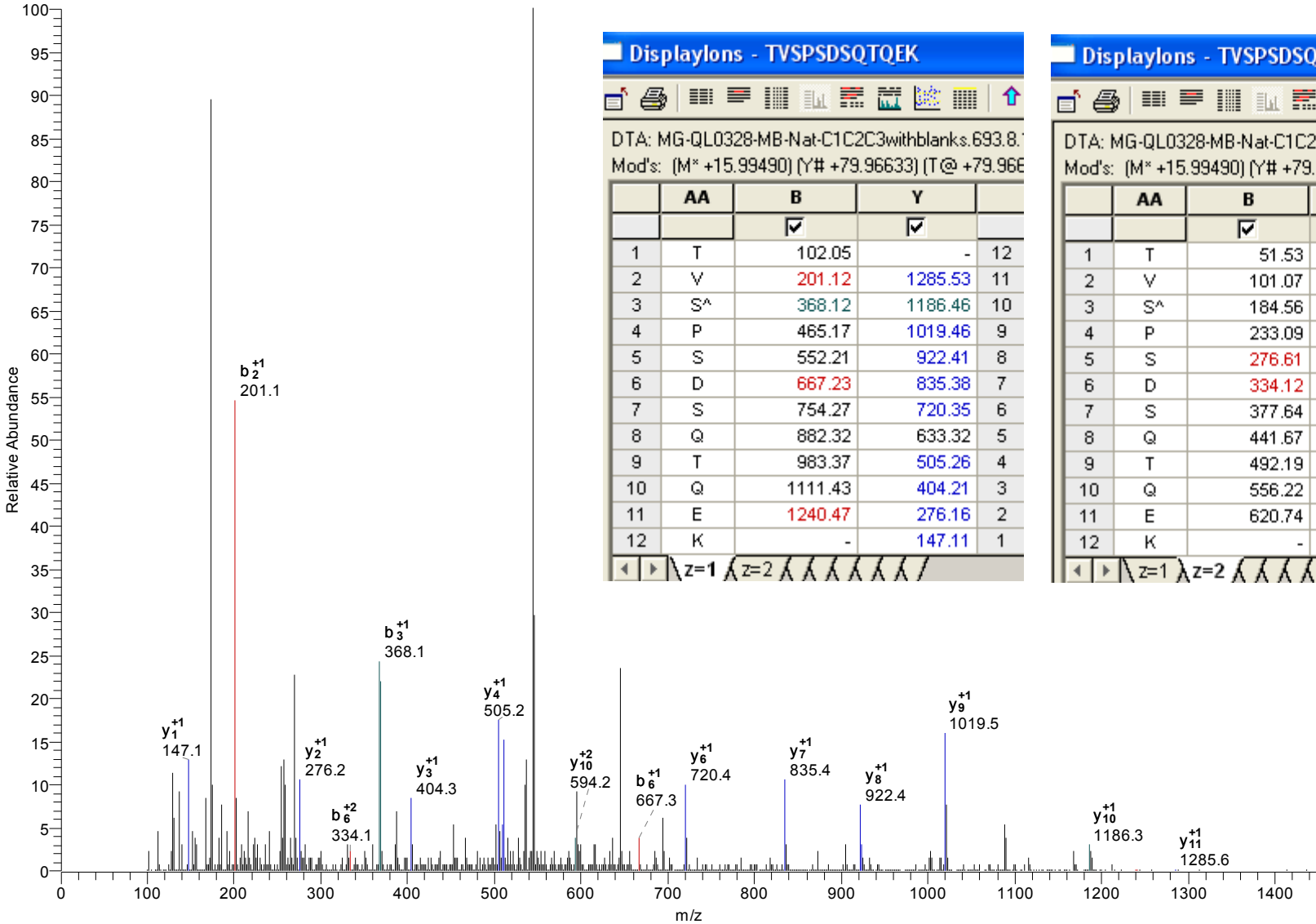
Displaylons - VPWMPPGKSSAR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.491.5.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	V	100.08	-	12
2	P	197.13	1373.55	11
3	W	383.21	1276.49	10
4	M	514.25	1090.42	9
5	P	611.30	959.37	8
6	P	708.35	862.32	7
7	G	765.38	765.27	6
8	K	893.47	708.25	5
9	S^	1060.47	580.15	4
10	S^	1227.47	413.15	3
11	A	1298.50	246.16	2
12	R	-	175.12	1

Displaylons - VPWMPPGKSSAR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.491.5.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	V	50.54	-	12
2	P	99.07	687.28	11
3	W	192.11	638.75	10
4	M	257.63	545.71	9
5	P	306.15	480.19	8
6	P	354.68	431.66	7
7	G	383.19	383.14	6
8	K	447.24	354.63	5
9	S^	530.74	290.58	4
10	S^	614.24	207.08	3
11	A	649.76	123.58	2
12	R	-	88.06	1

Displaylons - VPWMPPGKSSAR				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.491.5.1				
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
1	V	34.03	-	12
2	P	66.38	458.52	11
3	W	128.41	426.17	10
4	M	172.09	364.14	9
5	P	204.44	320.46	8
6	P	236.79	288.11	7
7	G	255.80	255.76	6
8	K	298.49	236.75	5
9	S^	354.16	194.06	4
10	S^	409.83	138.39	3
11	A	433.51	82.72	2
12	R	-	59.04	1

Hypothetical protein LOC501180

#1501-1501 NL: 1.33E2

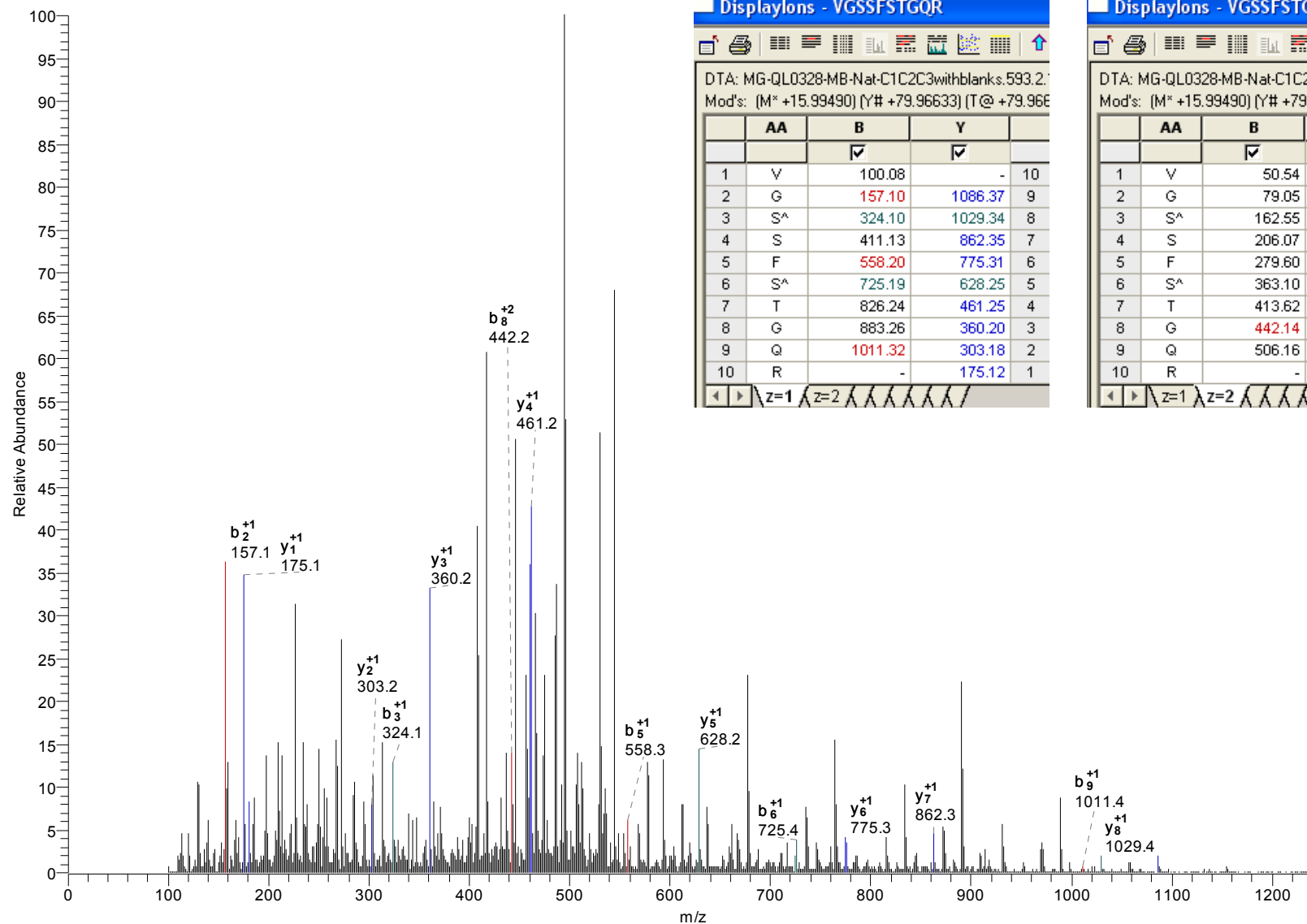


Displaylons - TVSPSDSQTQEK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.693.8.1				
Mod's: [M* +15.99490] (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
		☒	☒	
1	T	102.05	-	12
2	V	201.12	1285.53	11
3	S^	368.12	1186.46	10
4	P	465.17	1019.46	9
5	S	552.21	922.41	8
6	D	667.23	835.38	7
7	S	754.27	720.35	6
8	Q	882.32	633.32	5
9	T	983.37	505.26	4
10	Q	1111.43	404.21	3
11	E	1240.47	276.16	2
12	K	-	147.11	1

Displaylons - TVSPSDSQTQEK				
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.693.8.1				
Mod's: [M* +15.99490] (Y# +79.96633) (T@ +79.96633)				
	AA	B	Y	
		☒	☒	
1	T	51.53	-	12
2	V	101.07	643.27	11
3	S^	184.56	593.73	10
4	P	233.09	510.24	9
5	S	276.61	461.71	8
6	D	334.12	418.19	7
7	S	377.64	360.68	6
8	Q	441.67	317.16	5
9	T	492.19	253.13	4
10	Q	556.22	202.61	3
11	E	620.74	138.58	2
12	K	-	74.06	1

Hspb9_predicted similar to Heat-shock protein beta-9

#1555-1555 NL: 2.66E2



Displaylons - VGSSFSTGQR

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.593.2.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	V	100.08	-	10
2	G	157.10	1086.37	9
3	S^	324.10	1029.34	8
4	S	411.13	862.35	7
5	F	558.20	775.31	6
6	S^	725.19	628.25	5
7	T	826.24	461.25	4
8	G	883.26	360.20	3
9	Q	1011.32	303.18	2
10	R	-	175.12	1

z=1 z=2

Displaylons - VGSSFSTGQR

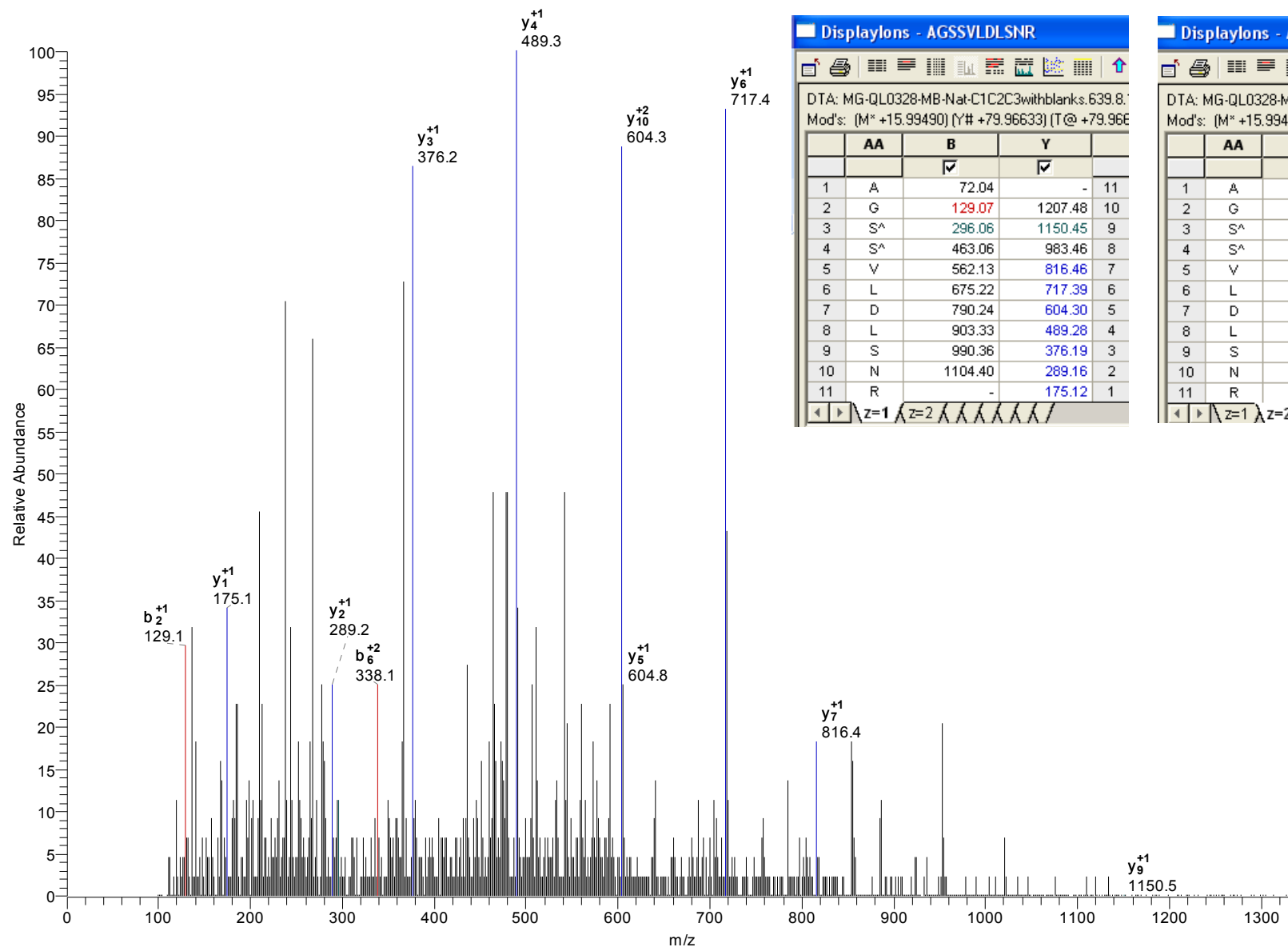
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.593.2.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	V	50.54	-	10
2	G	79.05	543.69	9
3	S^	162.55	515.18	8
4	S	206.07	431.68	7
5	F	279.60	388.16	6
6	S^	363.10	314.63	5
7	T	413.62	231.13	4
8	G	442.14	180.60	3
9	Q	506.16	152.09	2
10	R	-	88.06	1

z=1 z=2

LOC500060 Similar to testes development-related NYD-SP18

#1664-1664 NL: 4.50E1



Displaylons - AGSSVLDLSNR

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.639.8.
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	A	72.04	-	11
2	G	129.07	1207.48	10
3	S^	296.06	1150.45	9
4	S^	463.06	983.46	8
5	V	562.13	816.46	7
6	L	675.22	717.39	6
7	D	790.24	604.30	5
8	L	903.33	489.28	4
9	S	990.36	376.19	3
10	N	1104.40	289.16	2
11	R	-	175.12	1

z=1 z=2

Displaylons - AGSSVLDLSNR

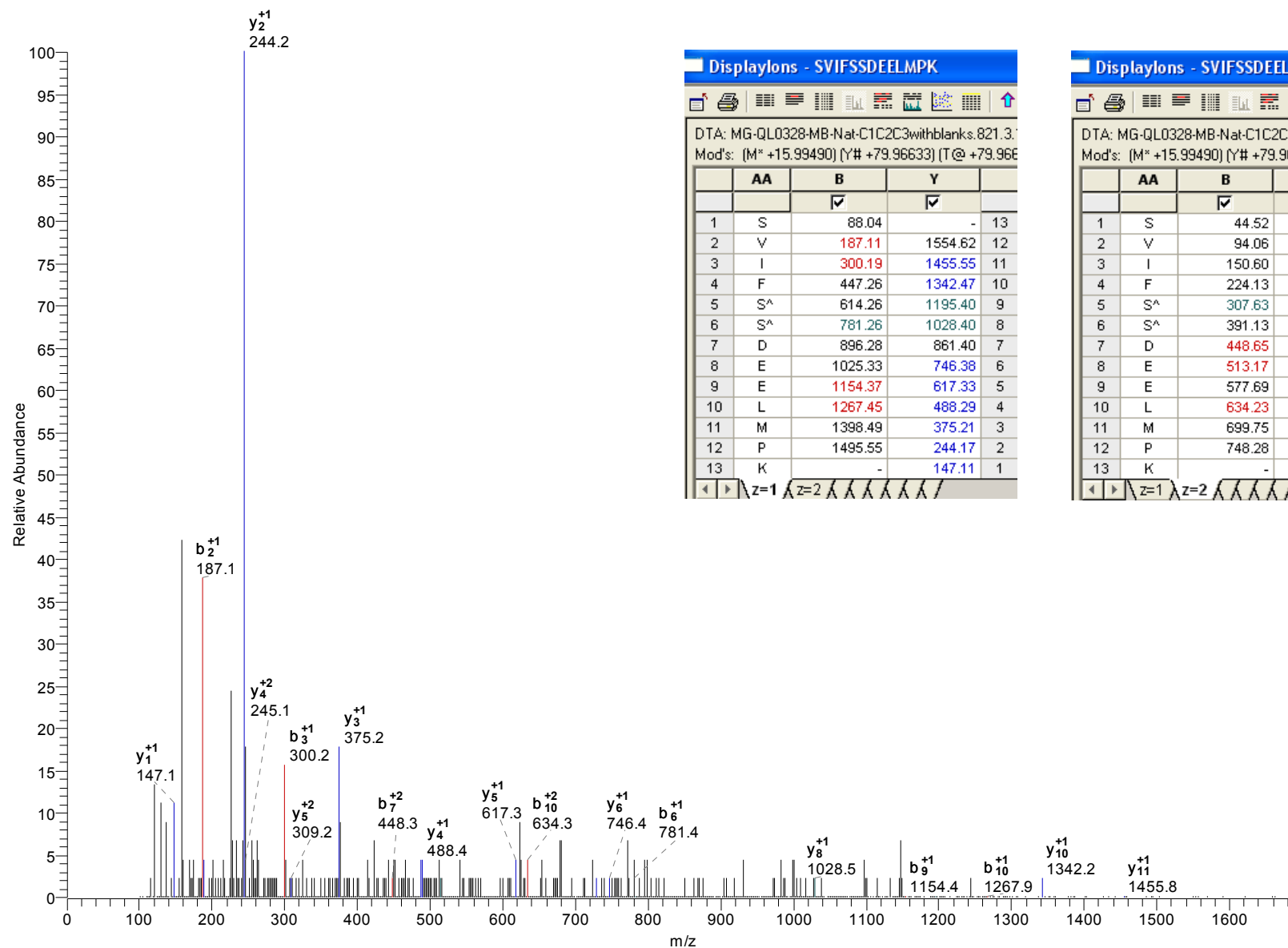
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.639.8.
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	A	36.53	-	11
2	G	65.04	604.24	10
3	S^	148.54	575.73	9
4	S^	232.03	492.23	8
5	V	281.57	408.73	7
6	L	338.11	359.20	6
7	D	395.62	302.66	5
8	L	452.17	245.14	4
9	S	495.68	188.60	3
10	N	552.70	145.08	2
11	R	-	88.06	1

z=1 z=2

LOC501147 Similar to RIKEN cDNA 1700052H20

#1819-1819 NL: 4.60E1



Displaylons - SVIFSSDEELMPK

DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.821.3.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	S	88.04	-	13
2	V	187.11	1554.62	12
3	I	300.19	1455.55	11
4	F	447.26	1342.47	10
5	S^	614.26	1195.40	9
6	S^	781.26	1028.40	8
7	D	896.28	861.40	7
8	E	1025.33	746.38	6
9	E	1154.37	617.33	5
10	L	1267.45	488.29	4
11	M	1398.49	375.21	3
12	P	1495.55	244.17	2
13	K	-	147.11	1

z=1 z=2

Displaylons - SVIFSSDEELMPK

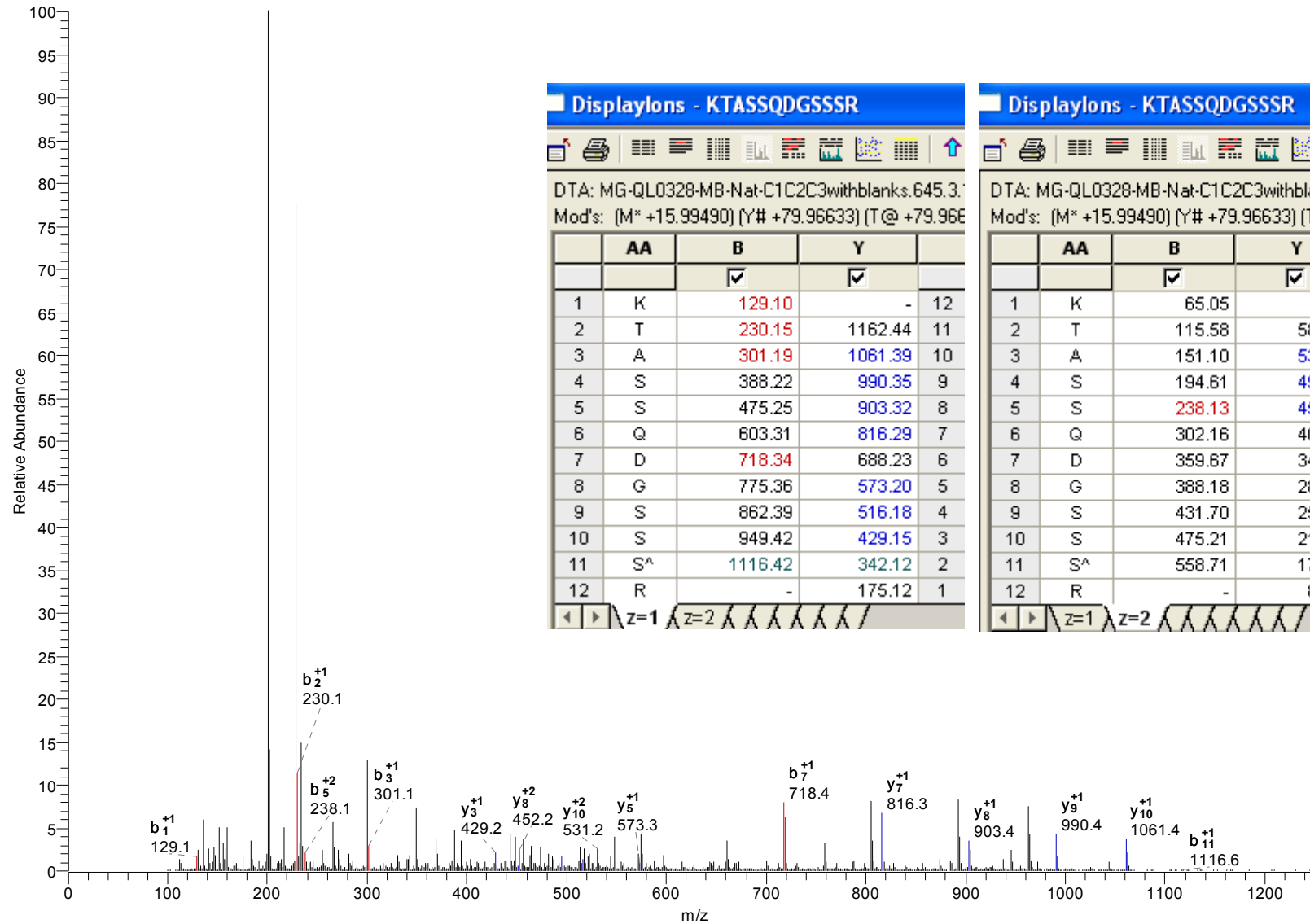
DTA: MG-QL0328-MB-Nat-C1C2C3withblanks.821.3.1
Mod's: (M* +15.99490) (Y# +79.96633) (T@ +79.96633)

	AA	B	Y	
1	S	44.52	-	13
2	V	94.06	777.81	12
3	I	150.60	728.28	11
4	F	224.13	671.74	10
5	S^	307.63	598.20	9
6	S^	391.13	514.70	8
7	D	448.65	431.20	7
8	E	513.17	373.69	6
9	E	577.69	309.17	5
10	L	634.23	244.65	4
11	M	699.75	188.11	3
12	P	748.28	122.59	2
13	K	-	74.06	1

z=1 z=2

Cldn23 Claudin 23

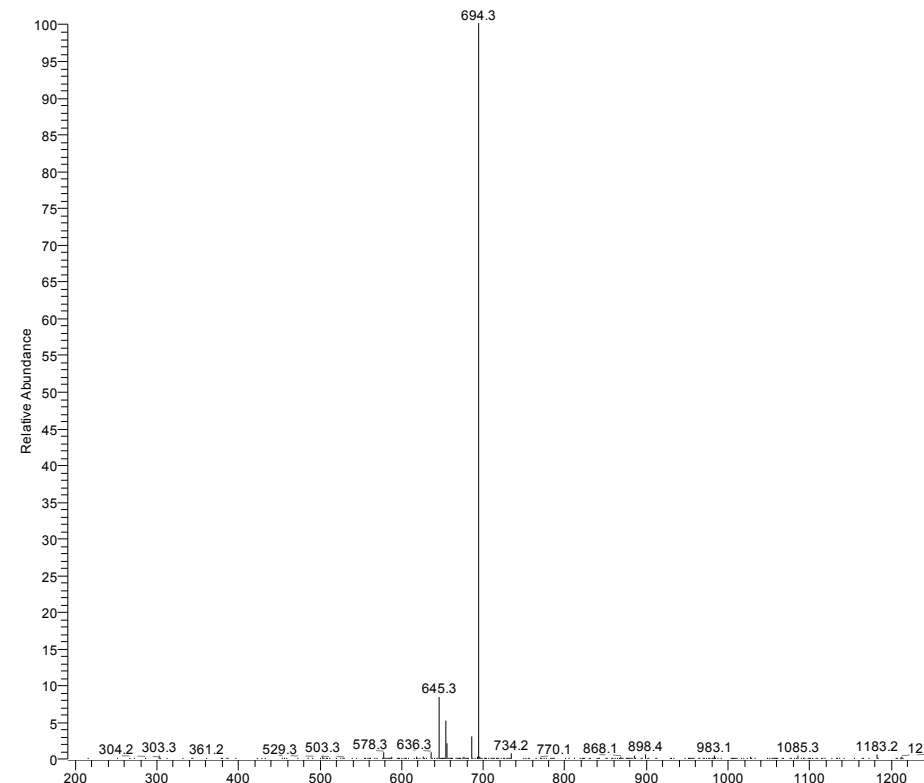
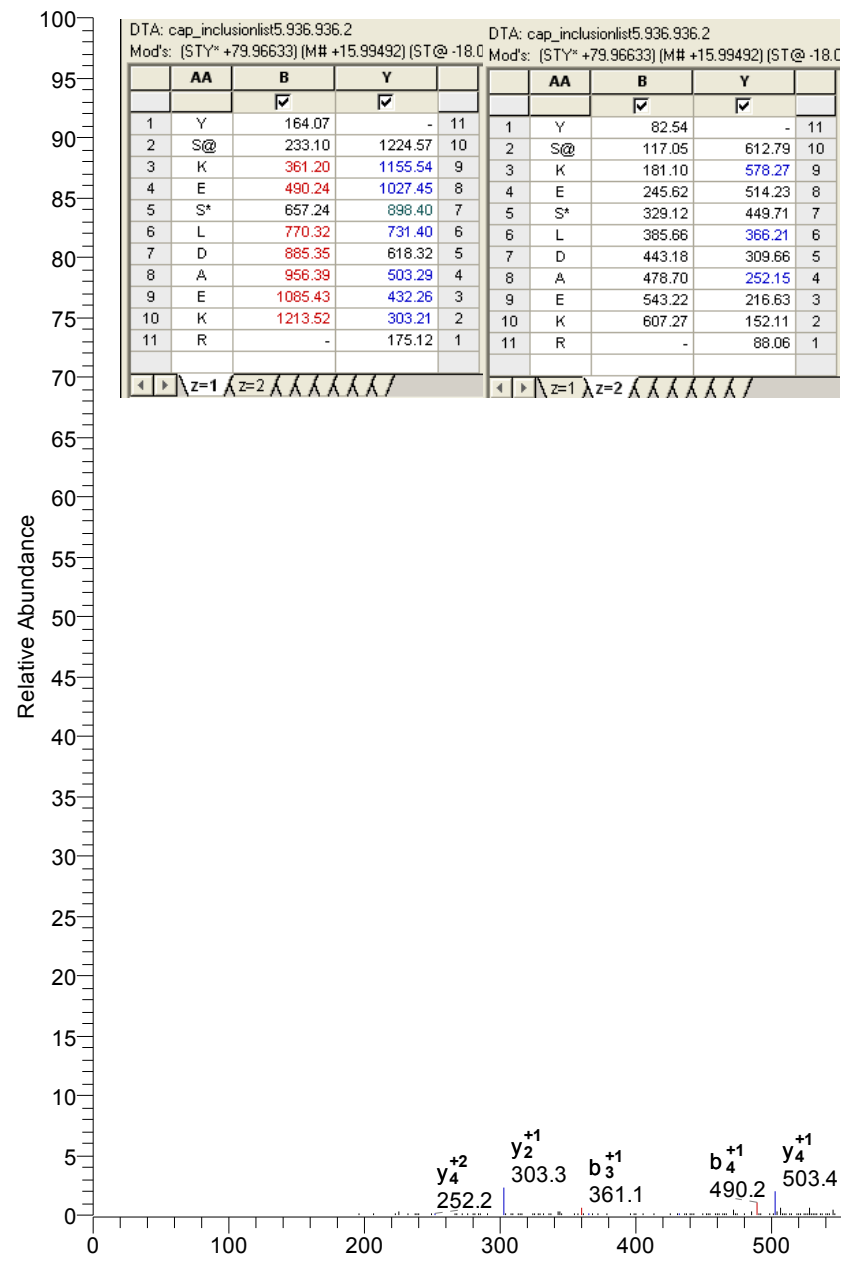
#1512-1512 NL: 5.20E2



Rdh14 Retinol Dehydrogenase 14

#936-936 RT:25.86-25.86 NL: 6.79E4

cap_inclusionlist5 #935 RT: 25.837 NL: 1.49E5
F: ITMS + c NSI d E Full ms2 743.36@cid35.00 [190.00-1500.00]



Sccpdh Probable saccharopine dehydrogenase

#1676-1676 RT:34.43-34.43 NL: 2.03E6

non3 #1675 RT: 34.425 NL: 2.03E6
F: ITMS + c NSI d Full ms2 502.45@cid26.00 [125.00-1015.00]

DTA: non3.1676.1676.3				
Mod's: (STY* +79.96633) (M# +15.99492) (ST@ -18.0)				
	AA	B	Y	
1	S*	168.01	-	14
2	V	267.07	1337.82	13
3	S	354.11	1238.75	12
4	N	468.15	1151.71	11
5	L	581.23	1037.67	10
6	K	709.33	924.59	9
7	P	806.38	796.49	8
8	V	905.45	699.44	7
9	P	1002.50	600.37	6
10	V	1101.57	503.32	5
11	I	1214.65	404.25	4
12	G	1271.68	291.17	3
13	S	1358.71	234.14	2
14	K	-	147.11	1

DTA: non3.1676.1676.3				
Mod's: (STY* +79.96633) (M# +15.99492) (ST@ -18.0)				
	AA	B	Y	
1	S*	84.51	-	14
2	V	134.04	669.41	13
3	S	177.56	619.88	12
4	N	234.58	576.36	11
5	L	291.12	519.34	10
6	K	355.17	462.80	9
7	P	403.69	398.75	8
8	V	453.23	350.22	7
9	P	501.75	300.69	6
10	V	551.29	252.16	5
11	I	607.83	202.63	4
12	G	636.34	146.09	3
13	S	679.86	117.58	2
14	K	-	74.06	1

DTA: non3.1676.1676.3				
Mod's: (STY* +79.96633) (M# +15.99492) (ST@ -18.0)				
	AA	B	Y	
1	S*	56.67	-	14
2	V	89.70	446.61	13
3	S	118.71	413.59	12
4	N	156.72	384.58	11
5	L	194.42	346.56	10
6	K	237.11	308.87	9
7	P	269.47	266.17	8
8	V	302.49	233.82	7
9	P	334.84	200.80	6
10	V	367.86	168.44	5
11	I	405.56	135.42	4
12	G	424.56	97.73	3
13	S	453.57	78.72	2
14	K	-	49.71	1

