Electronic Supplementary Material (ESI) for Food & Function.

Electronic supplementary information (ESI)

Milk-derived bioactive peptides protect against oxidative stress in a Caco-2 cell model

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[c] Institute of Neuroscience, CNR, Padova, Italy.

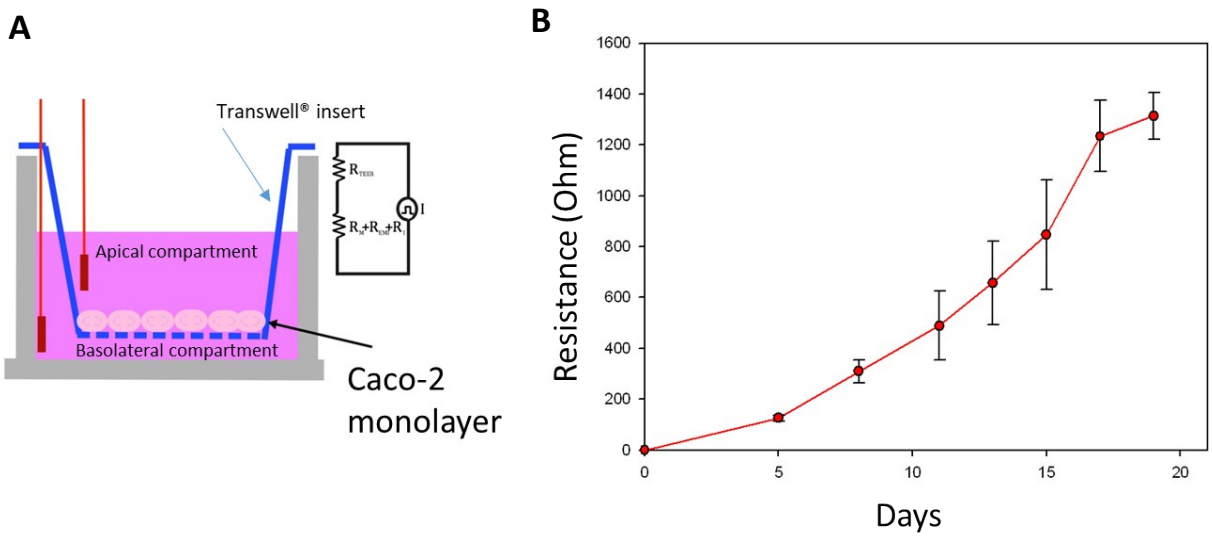


Fig. 1. TEER measurament during Caco-2 cells differentiation. Cells were seeded onto a Transwell® insert (A) and the integrity of the monolayer was assessed evaluating TEER values, using Millicell® ERS-2 volt-ohmmeter (Millipore) (B).

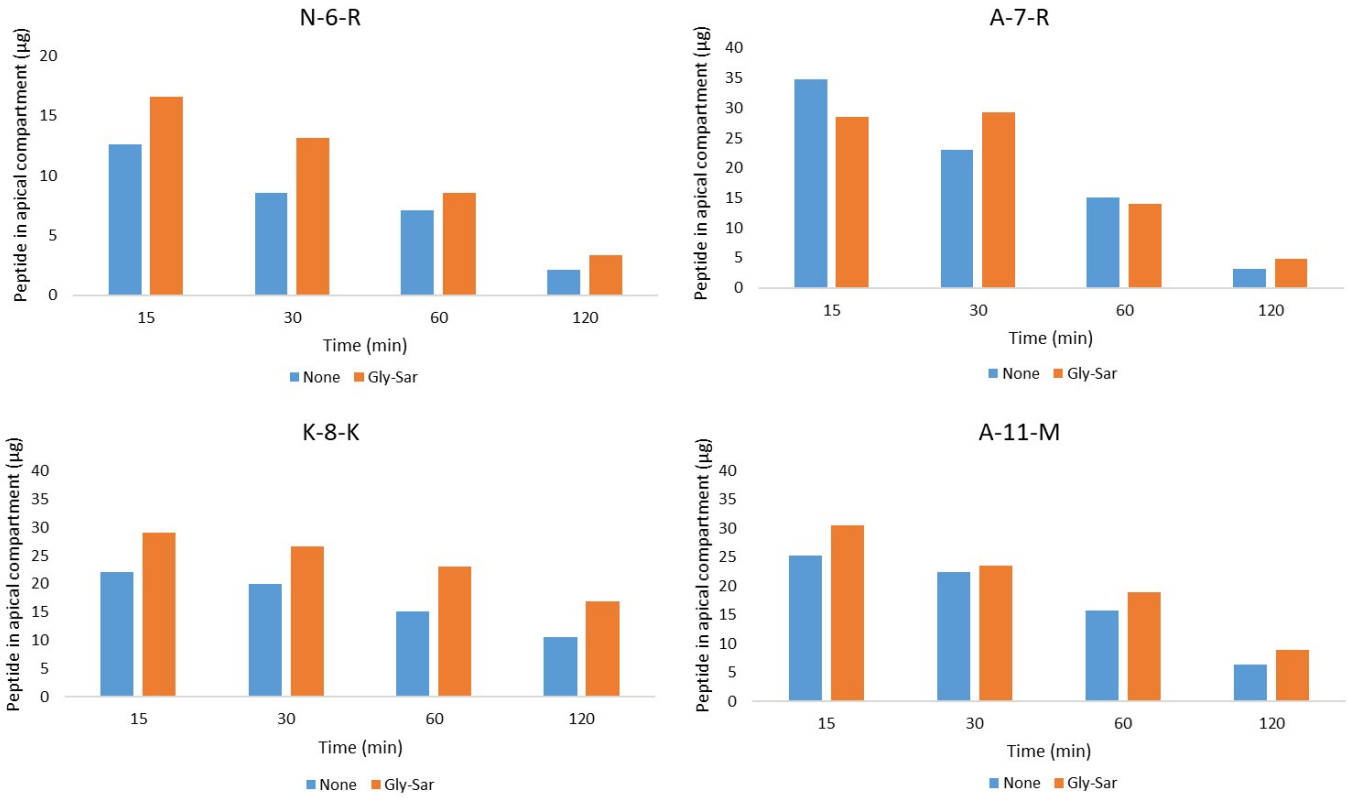
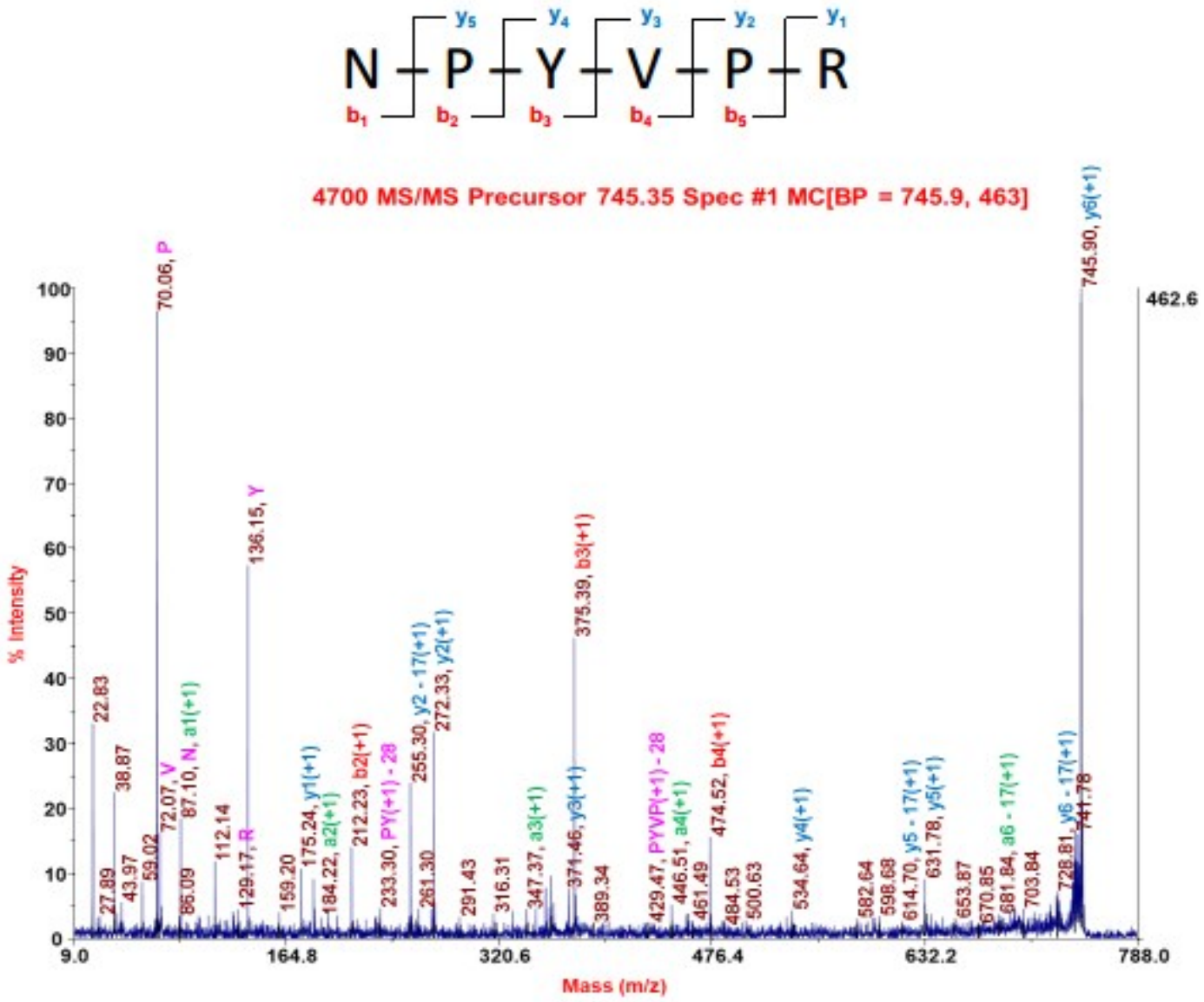


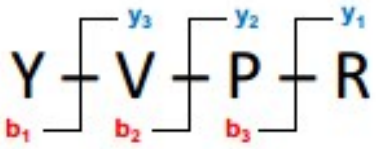
Fig. 2. Caco-2 epithelium crossing capacity of peptides (0.1 mg/mL) in presence of 10 mM Gly-Sar.

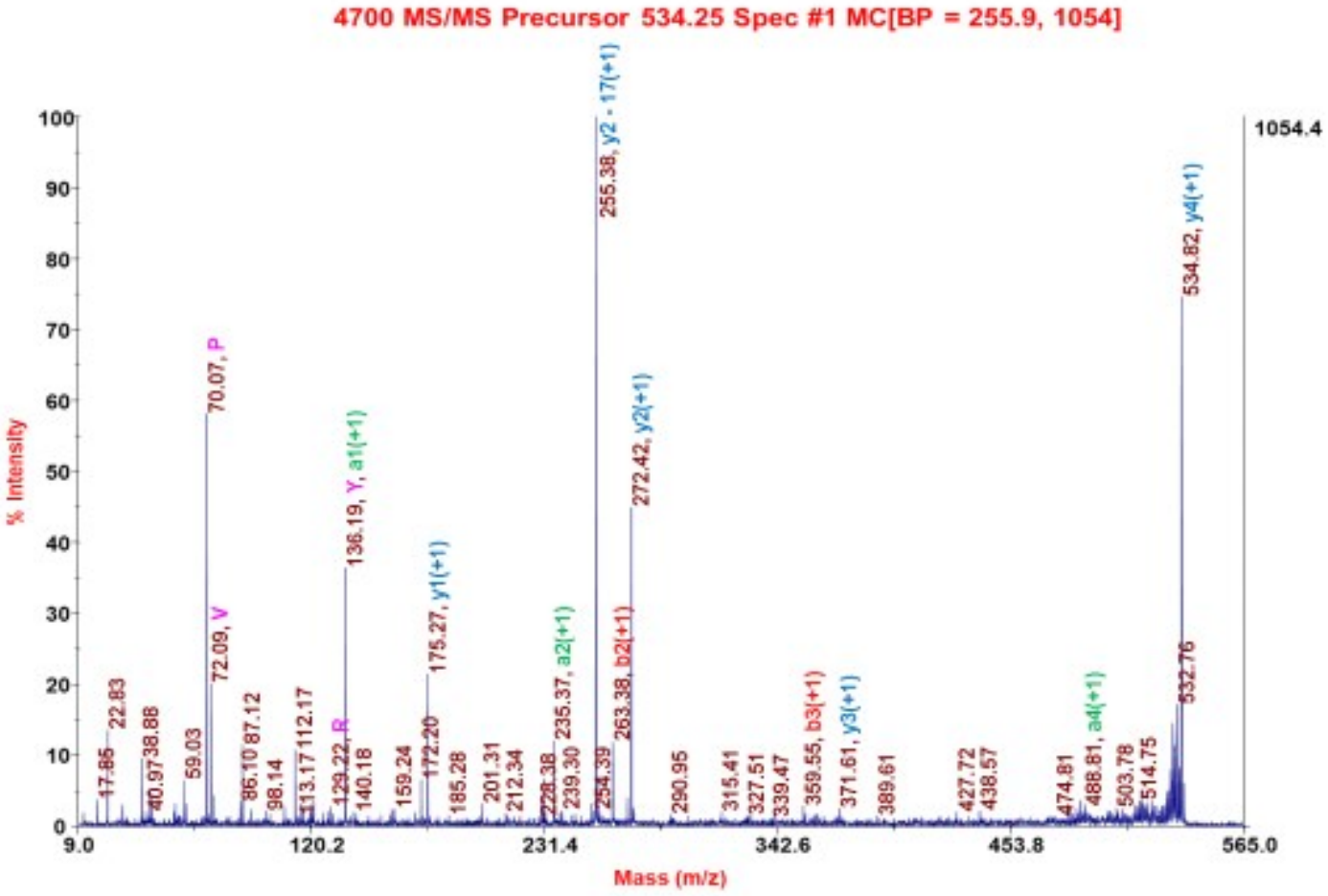
N-6-R



#1	b+	Seq.	y+	#2
1	115.11116	N	745.85580	6
2	212.22784	P	631.75196	5
3	375.40380	Y	534.63528	4
4	474.53636	V	371.45932	3
5	571.65304	P	272.32676	2
6	727.84052	R	175.21008	1

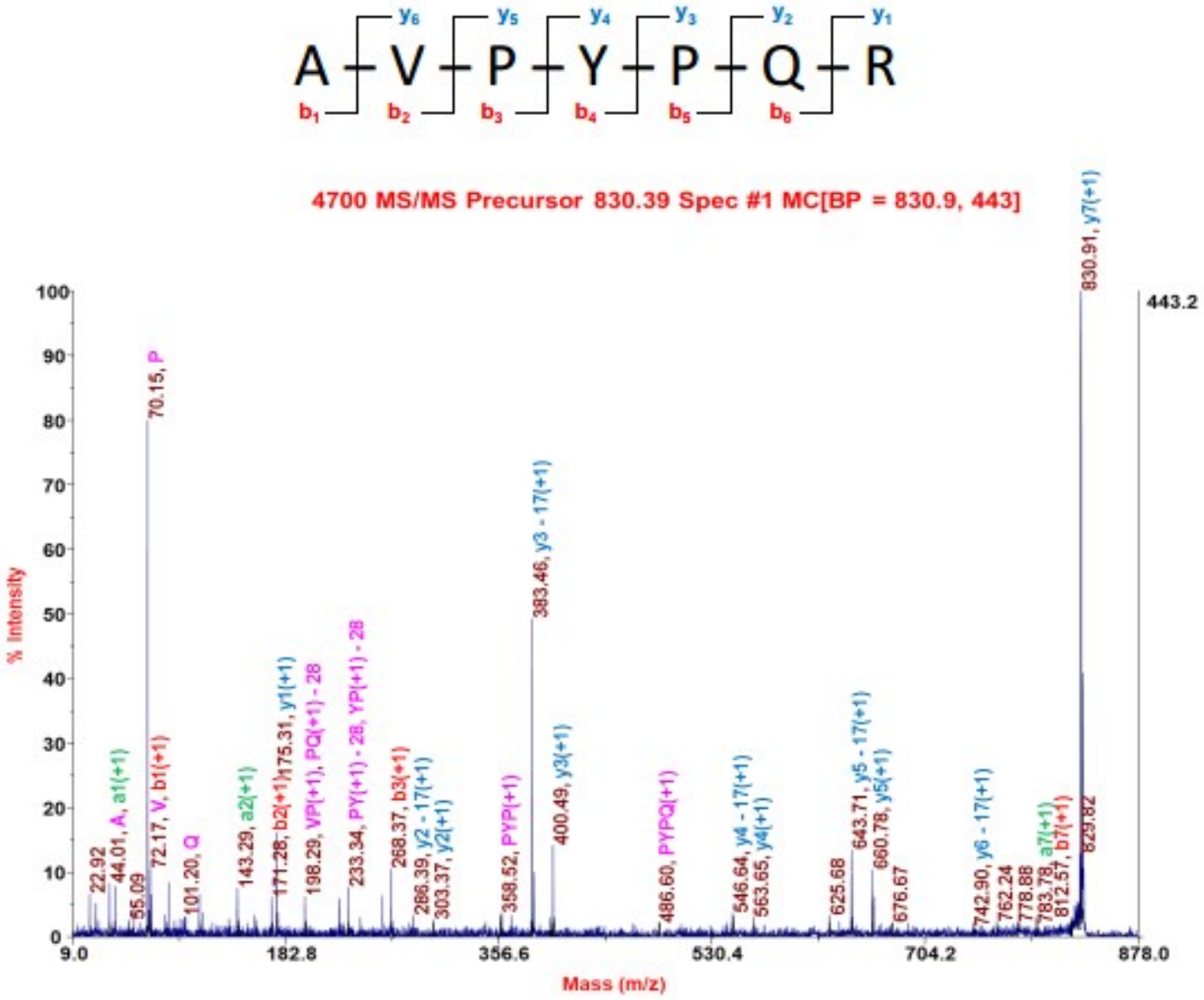
Y-4-R





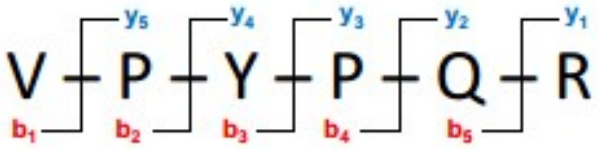
#1	b+	Seq.	y+	#2
1	164.18328	Y	534.63528	4
2	263.31584	V	371.45932	3
3	360.43252	P	272.32676	2
4	516.62000	R	175.21008	1

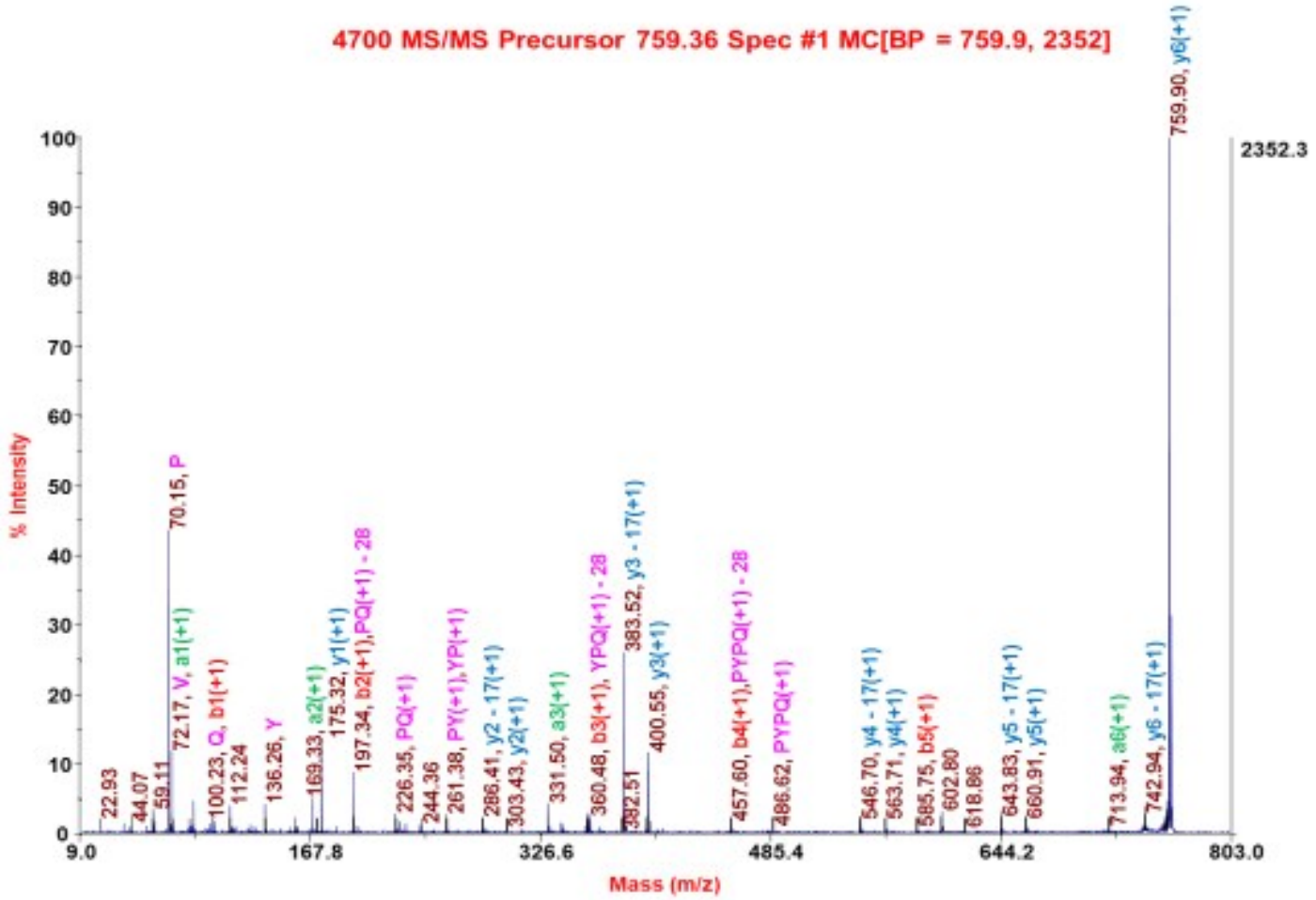
A-7-R



#1	b+	Seq.	y+	#2
1	72.08612	A	830.96148	7
2	171.21868	V	759.88268	6
3	268.33536	P	660.75012	5
4	431.51132	Y	563.63344	4
5	528.62800	P	400.45748	3
6	656.75872	Q	303.34080	2
7	812.94620	R	175.21008	1

V-6-R





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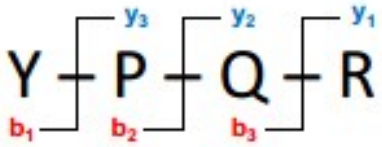
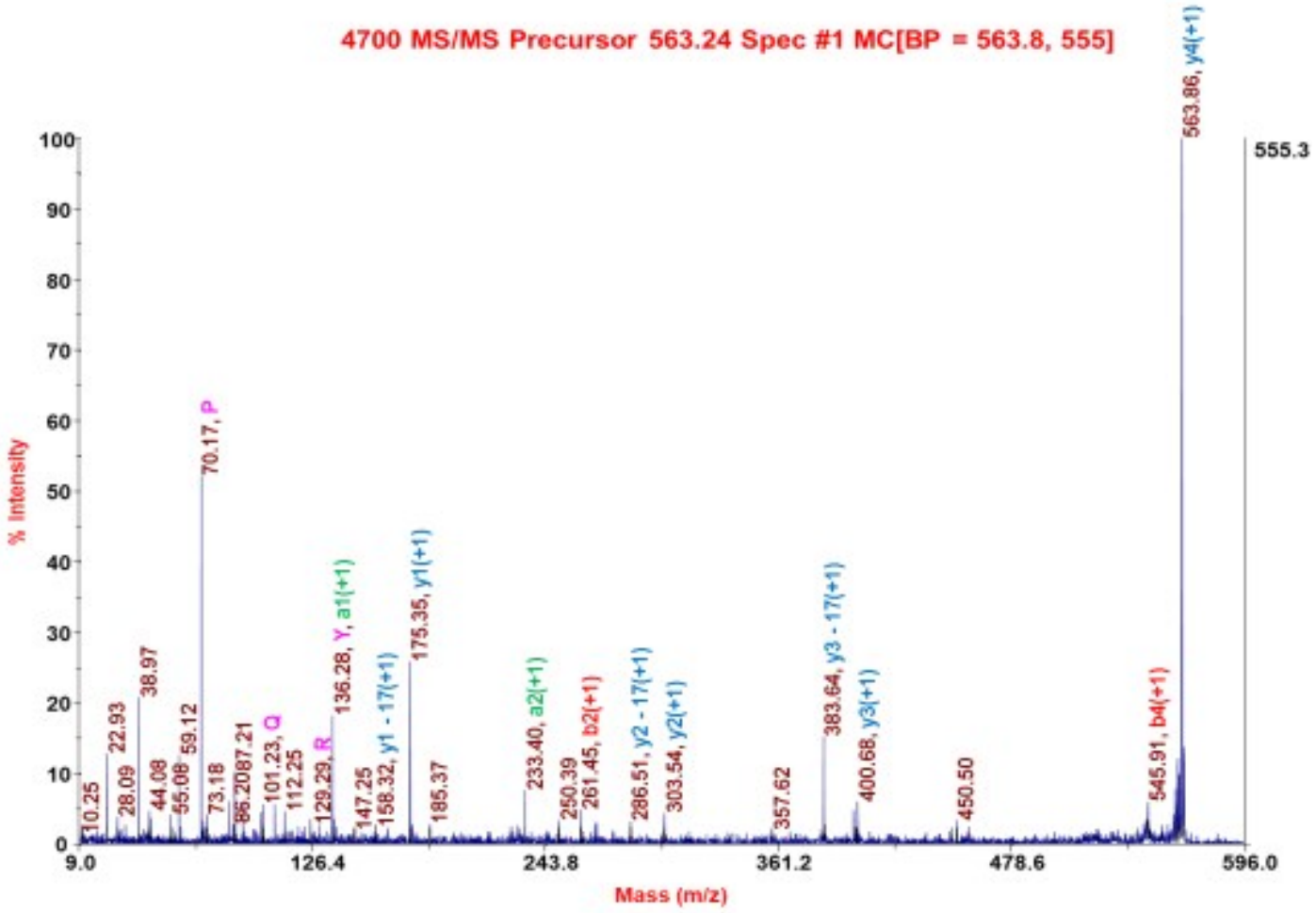
1	100.13988	V	759.88268	6
2	197.25656	P	660.75012	5
3	360.43252	Y	563.63344	4
4	457.54920	P	400.45748	3
5	585.67992	Q	303.34080	2
6	741.86740	R	175.21008	1

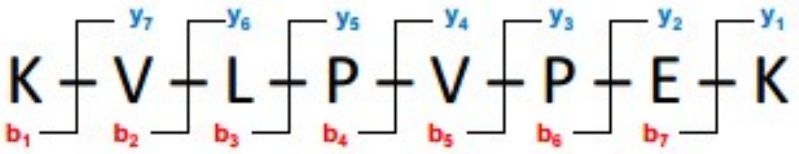
Y-4-R

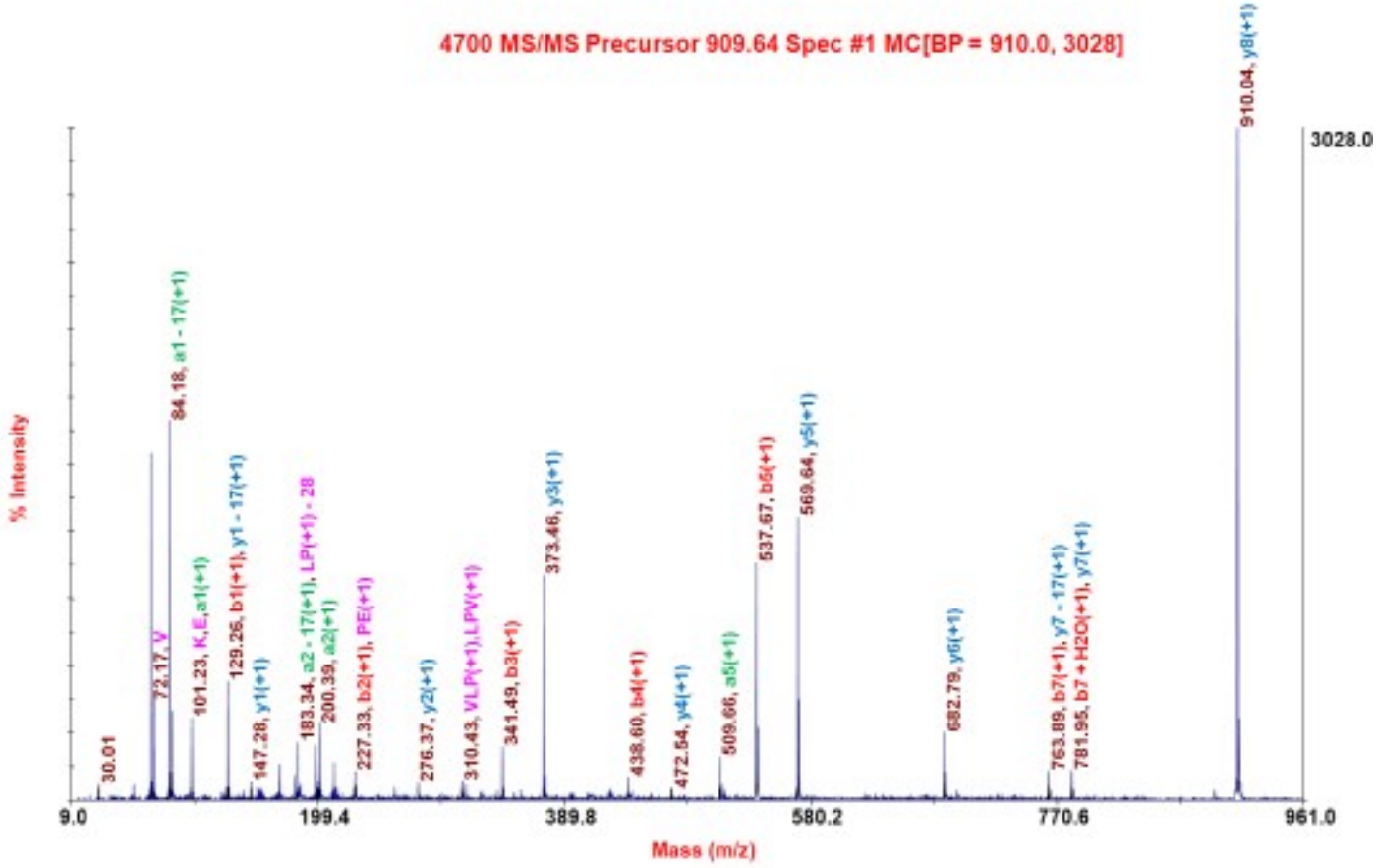




#1	b⁺	Seq.	y⁺	#2
1	164.18328	Y	563.63344	4
2	261.29996	P	400.45748	3
3	389.43068	Q	303.34080	2
4	545.61816	R	175.21008	1

K-8-K





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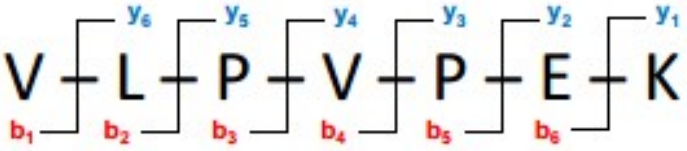
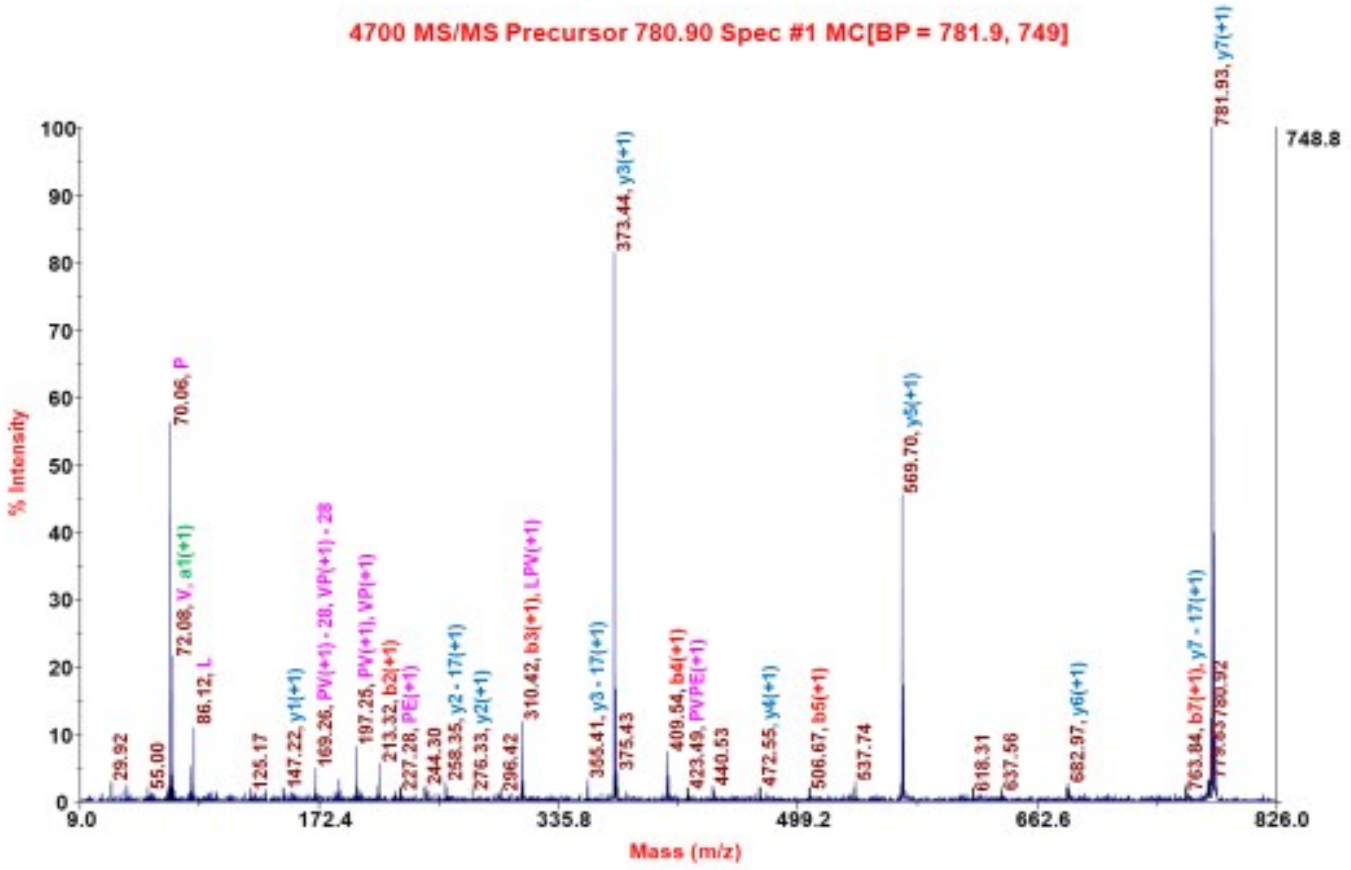
1	129.18140	K	910.14416	8
2	228.31396	V	781.97008	7
3	341.47340	L	682.83752	6
4	438.59008	P	569.67808	5
5	537.72264	V	472.56140	4
6	634.83932	P	373.42884	3
7	763.95480	E	276.31216	2
8	892.12888	K	147.19668	1

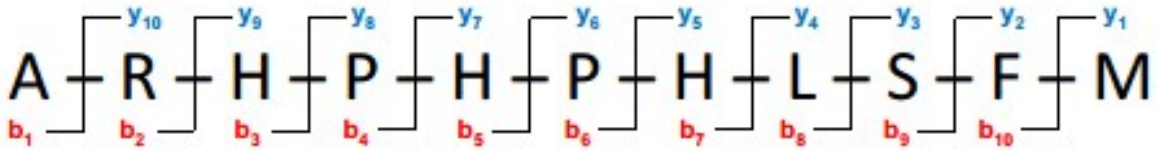
V-7-K

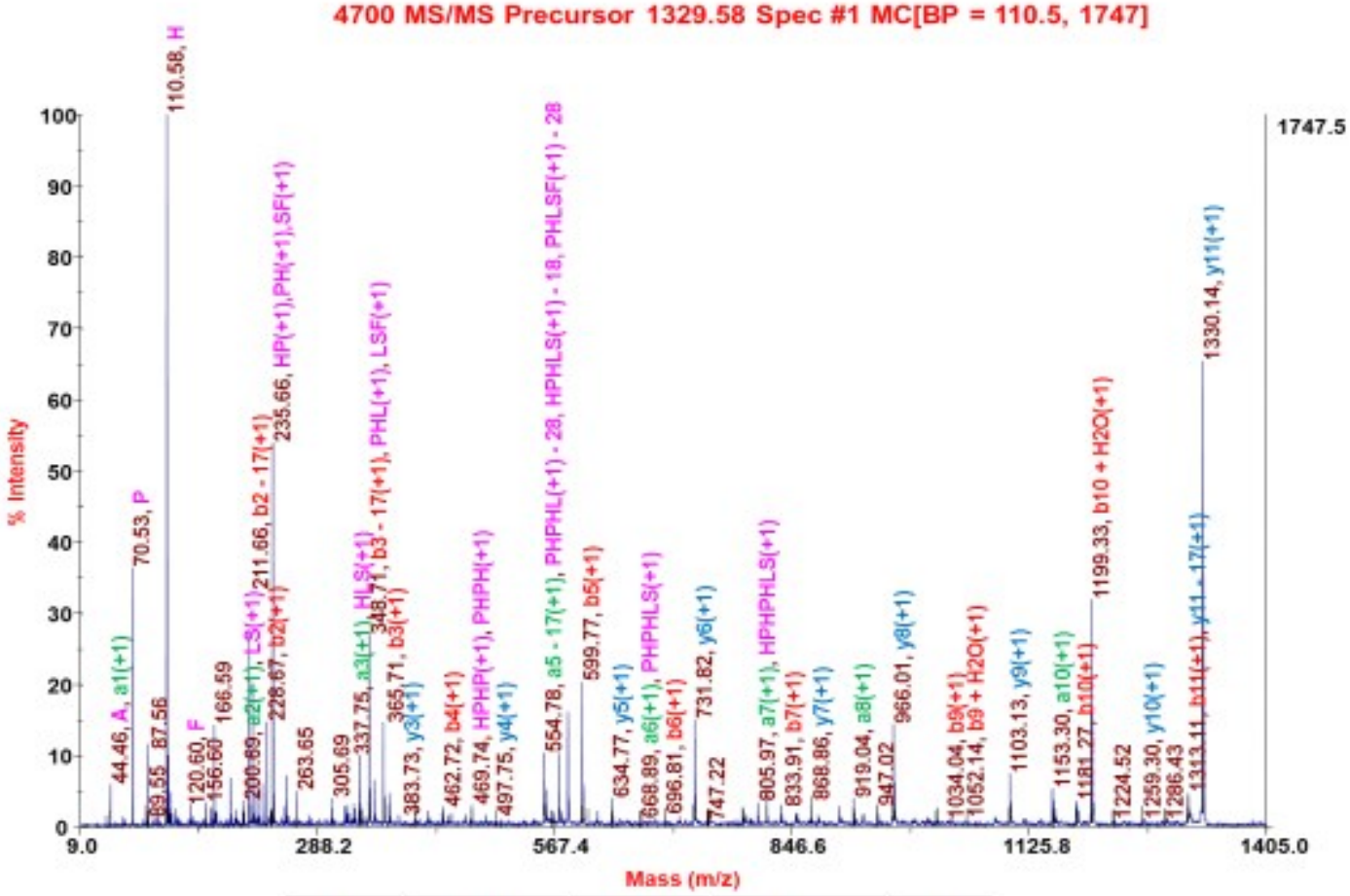




#1	b⁺	Seq.	y⁺	#2
1	100.13988	V	781.97008	7
2	213.29932	L	682.83752	6
3	310.41600	P	569.67808	5
4	409.54856	V	472.56140	4
5	506.66524	P	373.42884	3
6	635.78072	E	276.31216	2
7	763.95480	K	147.19668	1

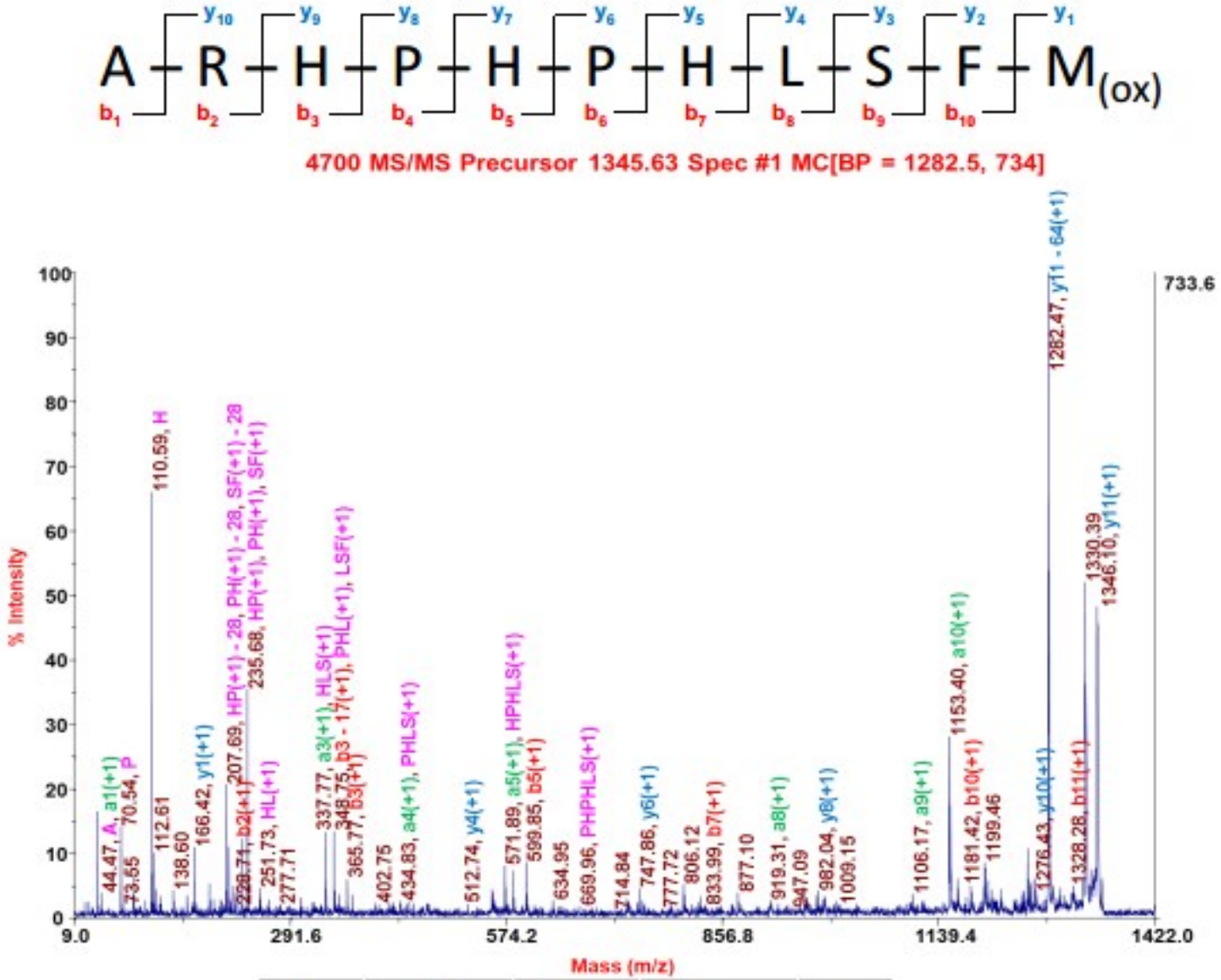
A-11-M





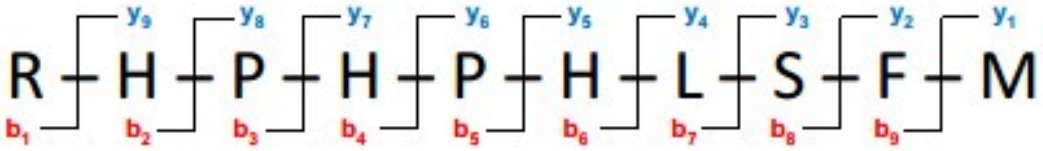
#1	b⁺	Seq.	y⁺	#2
1	72.08612	A	1330.55224	11
2	228.27360	R	1259.47344	10
3	365.41468	H	1103.28596	9
4	462.53136	P	966.14488	8
5	599.67244	H	869.02820	7
6	696.78912	P	731.88712	6
7	833.93020	H	634.77044	5
8	947.08964	L	497.62936	4
9	1034.16784	S	384.46992	3
10	1181.34440	F	297.39172	2
11	1312.53696	M	150.21516	1

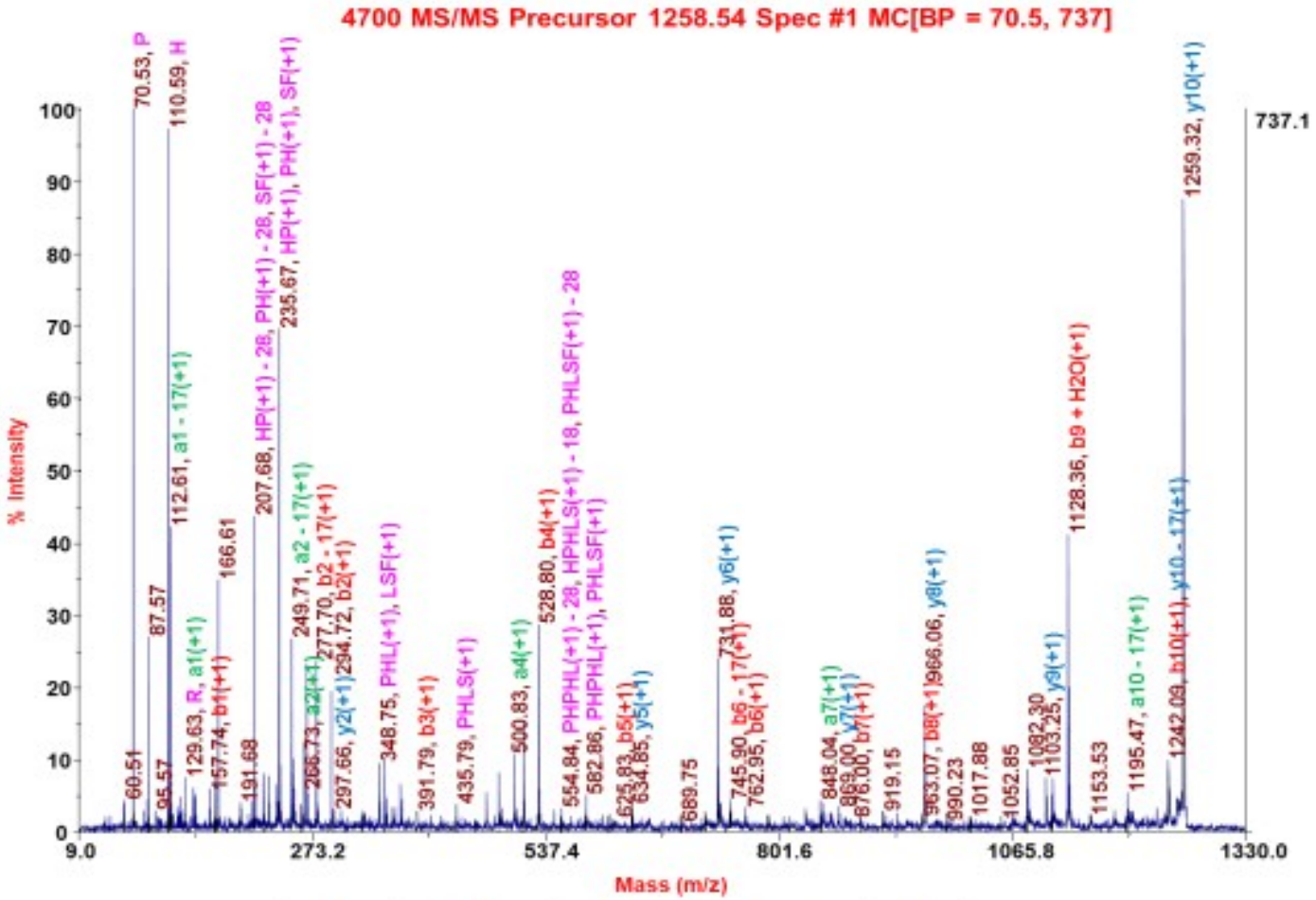
A-11-M(ox)



#1	b⁺	Seq.	y⁺	#2
1	72.08612	A	1346.54224	11
2	228.27360	R	1275.46344	10
3	365.41468	H	1119.27596	9
4	462.53136	P	982.13488	8
5	599.67244	H	885.01820	7
6	696.78912	P	747.87712	6
7	833.93020	H	650.76044	5
8	947.08964	L	513.61936	4
9	1034.16784	S	400.45992	3
10	1181.34440	F	313.38172	2
11	1328.52696	M(ox)	166.20516	1

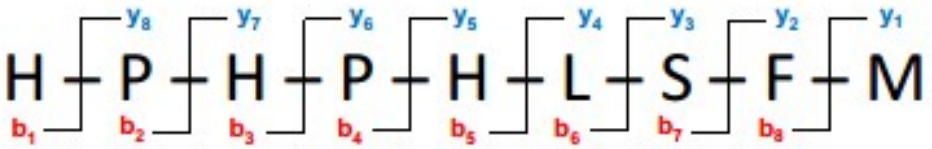
R-10-M

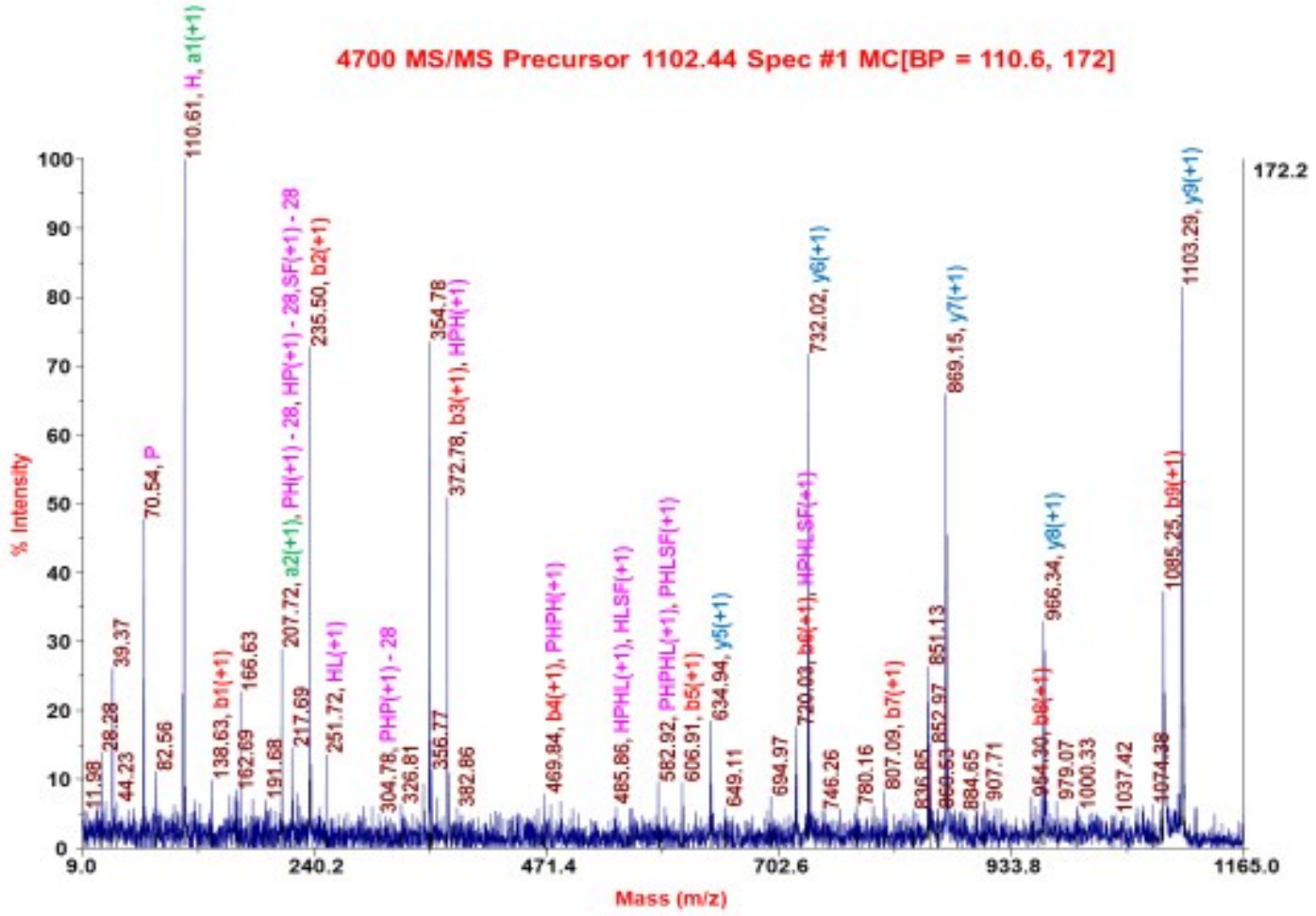




#1	b+	Seq.	y+	#2
1	157.19480	R	1259.47344	10
2	294.33588	H	1103.28596	9
3	391.45256	P	966.14488	8
4	528.59364	H	869.02820	7
5	625.71032	P	731.88712	6
6	762.85140	H	634.77044	5
7	876.01084	L	497.62936	4
8	963.08904	S	384.46992	3
9	1110.26560	F	297.39172	2
10	1241.45816	M	150.21516	1

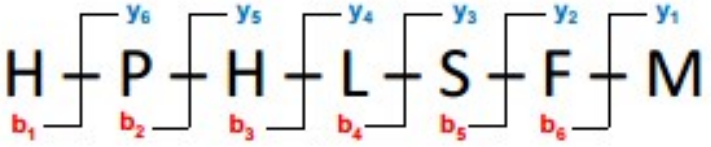
H-9-M

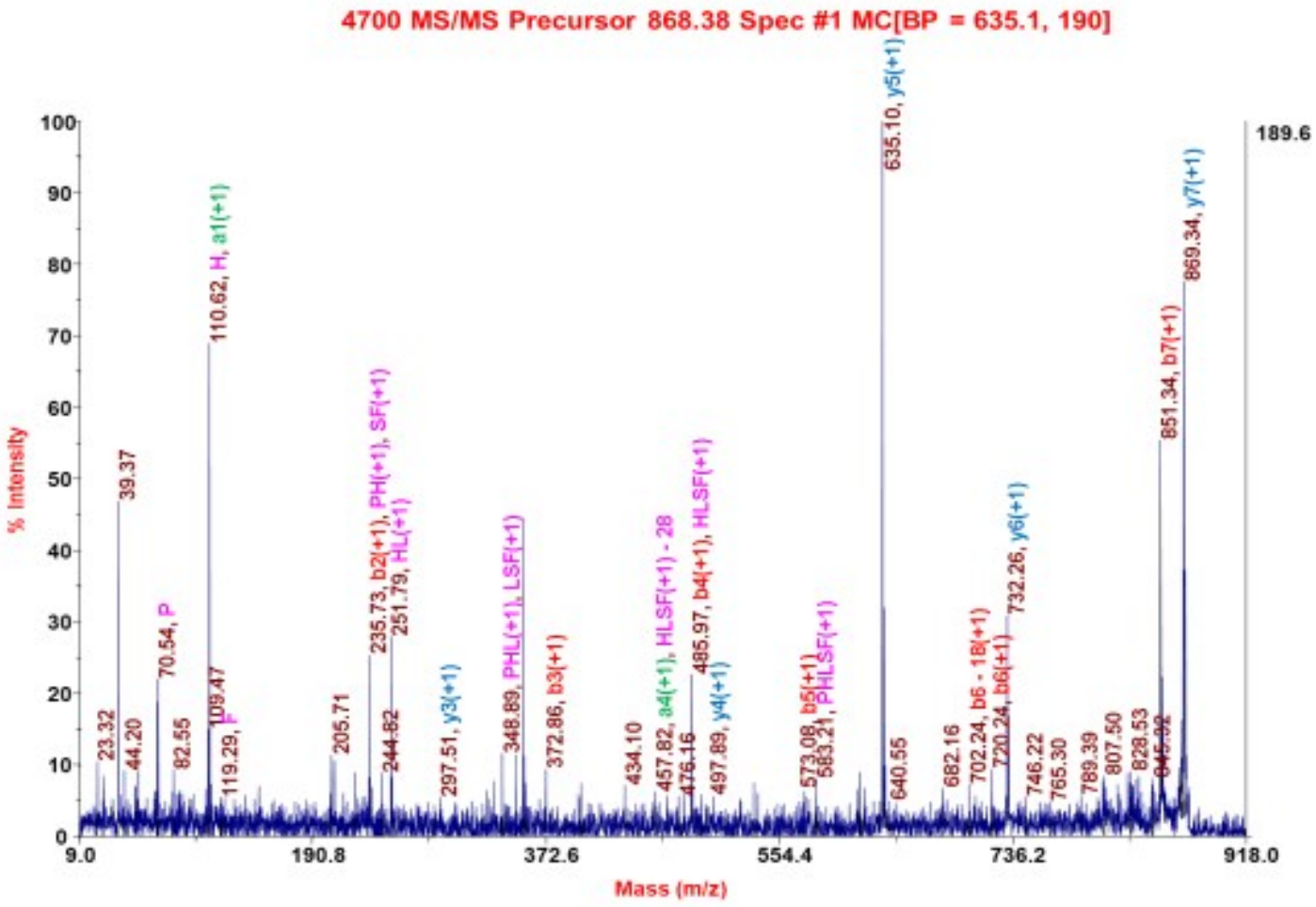




#1	b+	Seq.	y+	#2
1	138.24840	H	1103.28596	9
2	235.26508	P	966.14488	8
3	372.40616	H	869.02820	7
4	469.52284	P	731.88712	6
5	606.66392	H	634.77044	5
6	719.82336	L	497.62936	4
7	806.90156	S	384.46992	3
8	954.07812	F	297.39172	2
9	1085.27068	M	150.21516	1

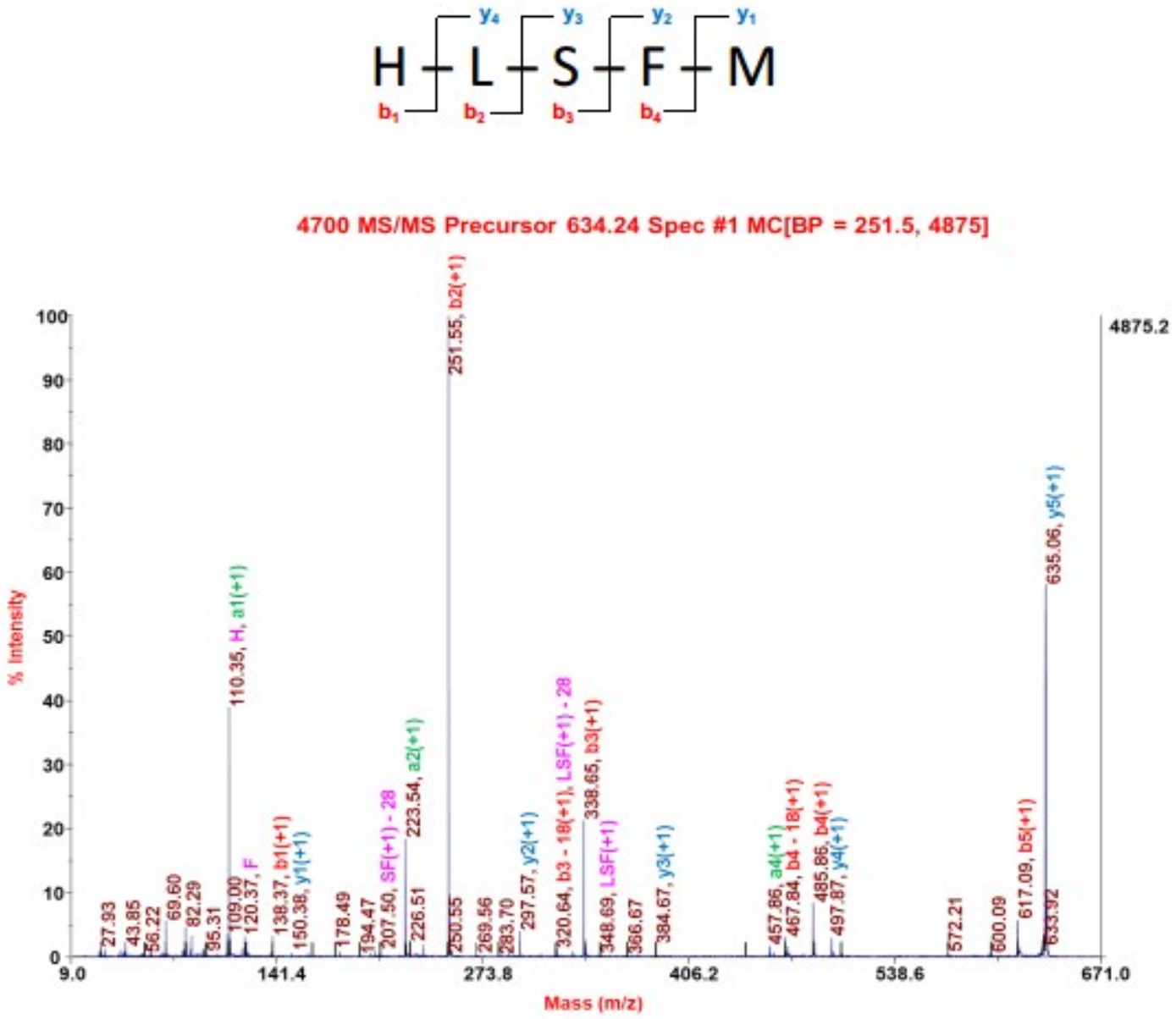
H-7-M





#1	b+	Seq.	y+	#2
1	138.14840	H	869.02820	7
2	235.26508	P	731.88712	6
3	372.40616	H	634.77044	5
4	485.56560	L	497.62936	4
5	572.64380	S	384.46992	3
6	719.82036	F	297.39172	2
7	851.01292	M	150.21516	1

H-5-M



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1	138.14840	H	634.77044	5
2	251.30784	L	497.62936	4
3	338.38604	S	384.46992	3
4	485.56260	F	297.39172	2
5	616.75516	M	150.21516	1

Fig. 3. MS/MS sequencing of peptides identified in basolateral MS analysis. The expected mass of each a,b,y ions and internal fragments were calculated and identified by Data Explorer (AB Sciex). In each table are highlighted in red or blue the identified b or y ions; in black the ions not detected.