

Supplementary Figure Legends:

Figure S1. Comparison of Standard PAGE with Non-Oxidizing PAGE. In this experiment the Oxy-blot procedure allows identification of proteins which have been artifactually oxidatively modified during electrophoresis. The proteins from PS II membranes were separated by LiDS-PAGE using either non-oxidizing (lanes 1-3) or standard (lane 4) gel systems. After electrophoresis, the proteins were blotted onto a PVDF membrane and either Coomassie blue-stained (lane 1-2) or derivitized with DNP hydrazine, blocked, and probed with an anti-DNP antibody (lanes 3 and 4). After immunolabeling with an anti-rabbit peroxidase conjugate, the DNP-labeled, oxidized proteins were detected using 4-chloro-1-naphthol. Lane 1, standard proteins, lane 2 and 3, non-oxidizing PAGE of PS II membrane proteins; lane 4, standard PAGE of PS II membrane proteins. Apparent molecular masses are shown to the left and identified PS II proteins are shown to the right. Note the high level of oxidative modification of proteins separated using standard PAGE conditions (lane 4 vs. lane 3). The two most prominent bands labeled in lane 3 correspond to LHC II proteins. These chlorophyll-containing proteins exhibit a pseudo-peroxidase activity which can lead to 4-chloro-1-naphthol development even in the absence of oxidative modification.

Figure S2. The Modified Peptide $^{344}\text{SPTGEVIFGGE}^{355}\text{T}+16^{356}\text{M}-32^{357}\text{R}+16$ from Biological Replicate #1. A. Spectra of the CID dissociation of the peptide. B. Table of all predicted masses for the y- and b- ions generated from this peptide sequence. Ions identified in A. are shown in red. The b'^{++} , b'^+ y'^{++} and y'^+ ions are generated by the

neutral loss of water. The control, unmodified peptide from this biological replicate is shown in Fig. 1A in the main body of the paper.

Figure S3. The Unmodified Peptide $^{344}\text{SPTGEVIFGGETM}^{357}\text{R}$ from Biological Replicate #2. A. Spectra of the CID dissociation of the peptide. B. Table of all predicted masses for the y- and b- ions generated from this peptide sequence. Ions identified in A. are shown in red. The b'^{++} , $\text{b}'^+ \text{y}'^{++}$ and y'^+ ions are generated by the neutral loss of water.

Figure S4. The Modified Peptide $^{344}\text{SPTGEVIFGGETM}^{357}\text{R}+16$ from Biological Replicate #2. A. Spectra of the CID dissociation of the peptide. B. Table of all predicted masses for the y- and b- ions generated from this peptide sequence. Ions identified in A. are shown in red. The b'^{++} , $\text{b}'^+ \text{y}'^{++}$ and y'^+ ions are generated by the neutral loss of water. Note the additional mass (in comparison with Fig. S1) from modification of ^{357}R which is evident in all identified y-ions but which is absent in all identified b-ions.

Figure S5. The Modified Peptide $^{344}\text{SPTGEVIFGG}^{354}\text{E}-30^{355}\text{T}^{356}\text{M}+16^{357}\text{R}+14$ from Biological Replicate #2. A. Spectra of the CID dissociation of the peptide. B. Table of all predicted masses for the y- and b- ions generated from this peptide sequence. Ions identified in A. are shown in red. The b'^{++} , $\text{b}'^+ \text{y}'^{++}$ and y'^+ ions are generated by the neutral loss of water.

Fig. S1

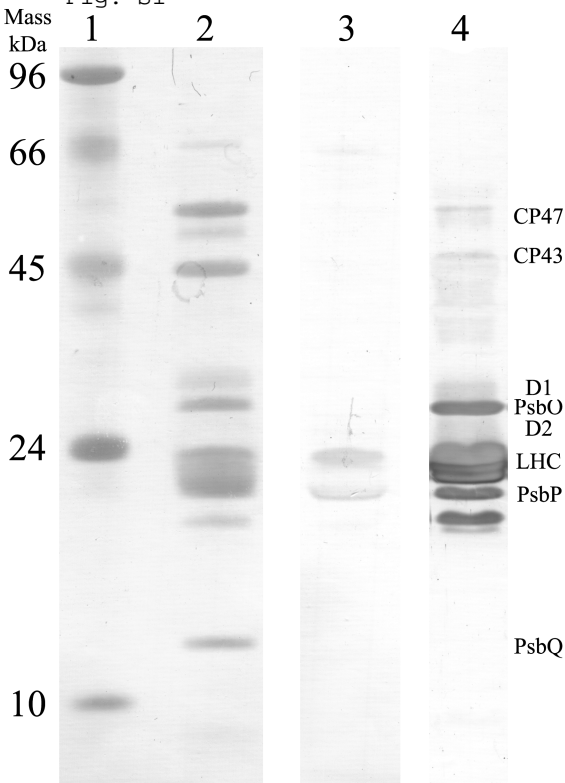
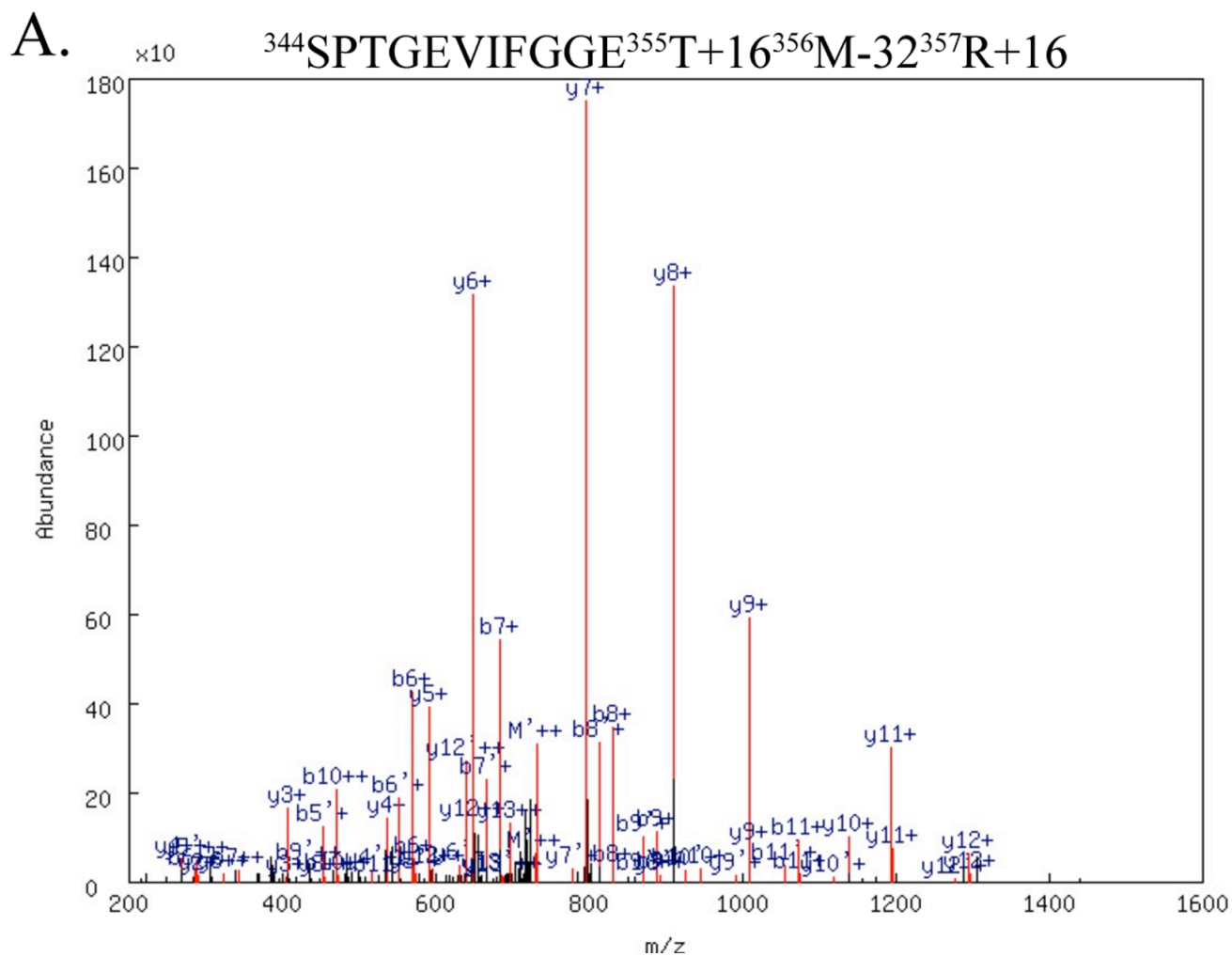
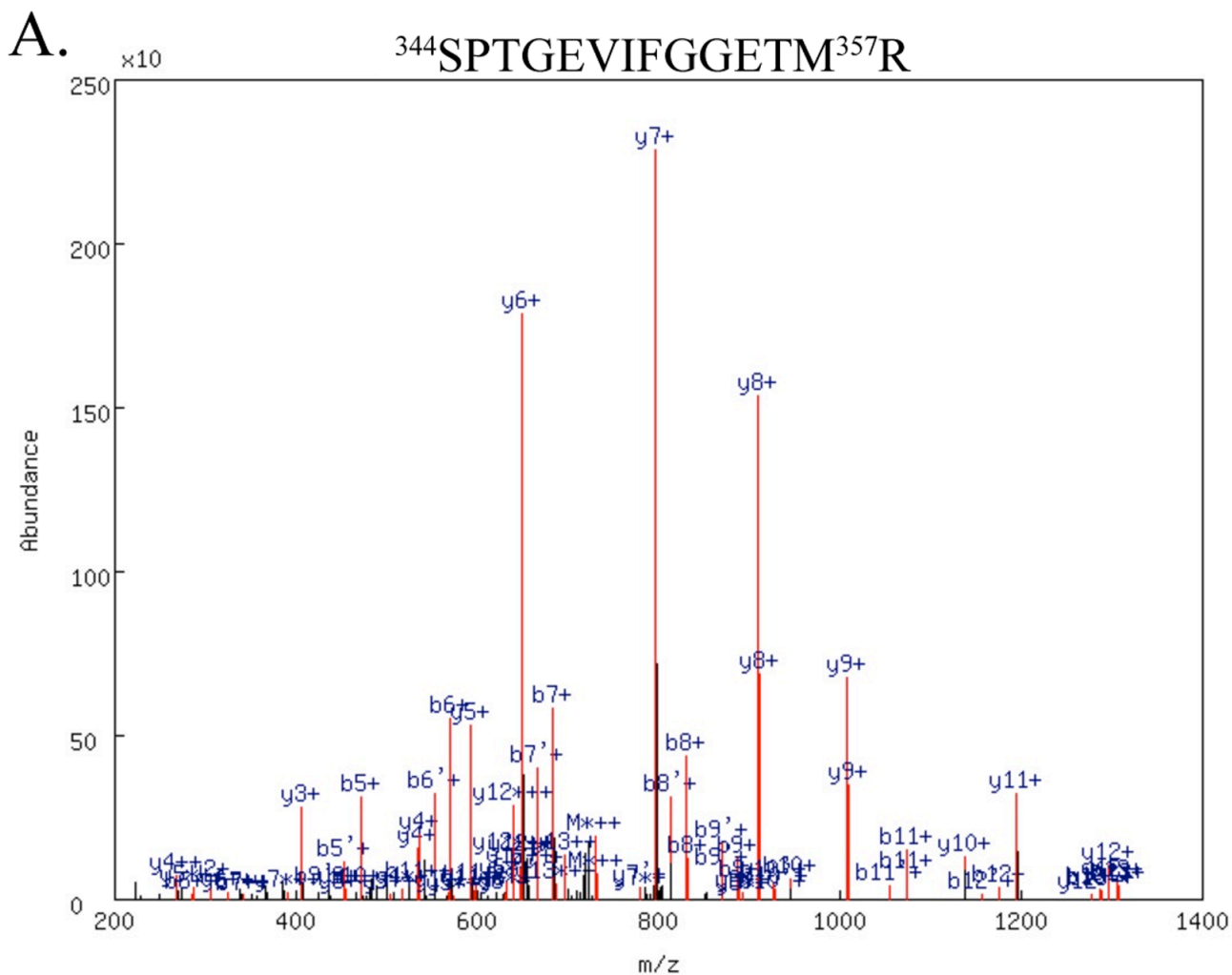


Fig. S2

**B.**

#	b ^{'++}	b ⁺⁺	b ⁺	b	seq	y ^{'++}	y ⁺⁺	y ⁺	y	#
1	35.52	44.52	70.03	88.04	S	731.85	740.86	1462.70	1480.71	M
2	84.04	93.05	167.08	185.09	P	688.34	697.34	1375.67	1393.68	13
3	134.57	143.57	268.13	286.14	T	639.81	648.82	1278.61	1296.63	12
4	163.08	172.08	325.15	343.16	G	589.29	598.29	1177.57	1195.58	11
5	227.60	236.61	454.19	472.20	E	560.78	569.78	1120.55	1138.56	10
6	277.13	286.14	553.26	571.27	V	496.26	505.26	991.50	1009.51	9
7	333.68	342.68	666.35	684.36	I	446.72	455.73	892.43	910.45	8
8	407.21	416.22	813.41	831.42	F	390.18	399.18	779.35	797.36	7
9	435.72	444.73	870.44	888.45	G	316.64	325.65	632.28	650.29	6
10	464.23	473.24	927.46	945.47	G	288.13	297.14	575.26	593.27	5
11	528.75	537.76	1056.50	1074.51	E	259.62	268.63	518.24	536.25	4
12	587.27	596.28	1173.54	1191.55	T	195.10	204.11	389.20	407.21	3
13	636.80	645.81	1272.59	1290.60	M	136.58	145.59	272.15	290.16	2
					R	87.06	96.06	173.10	191.11	1

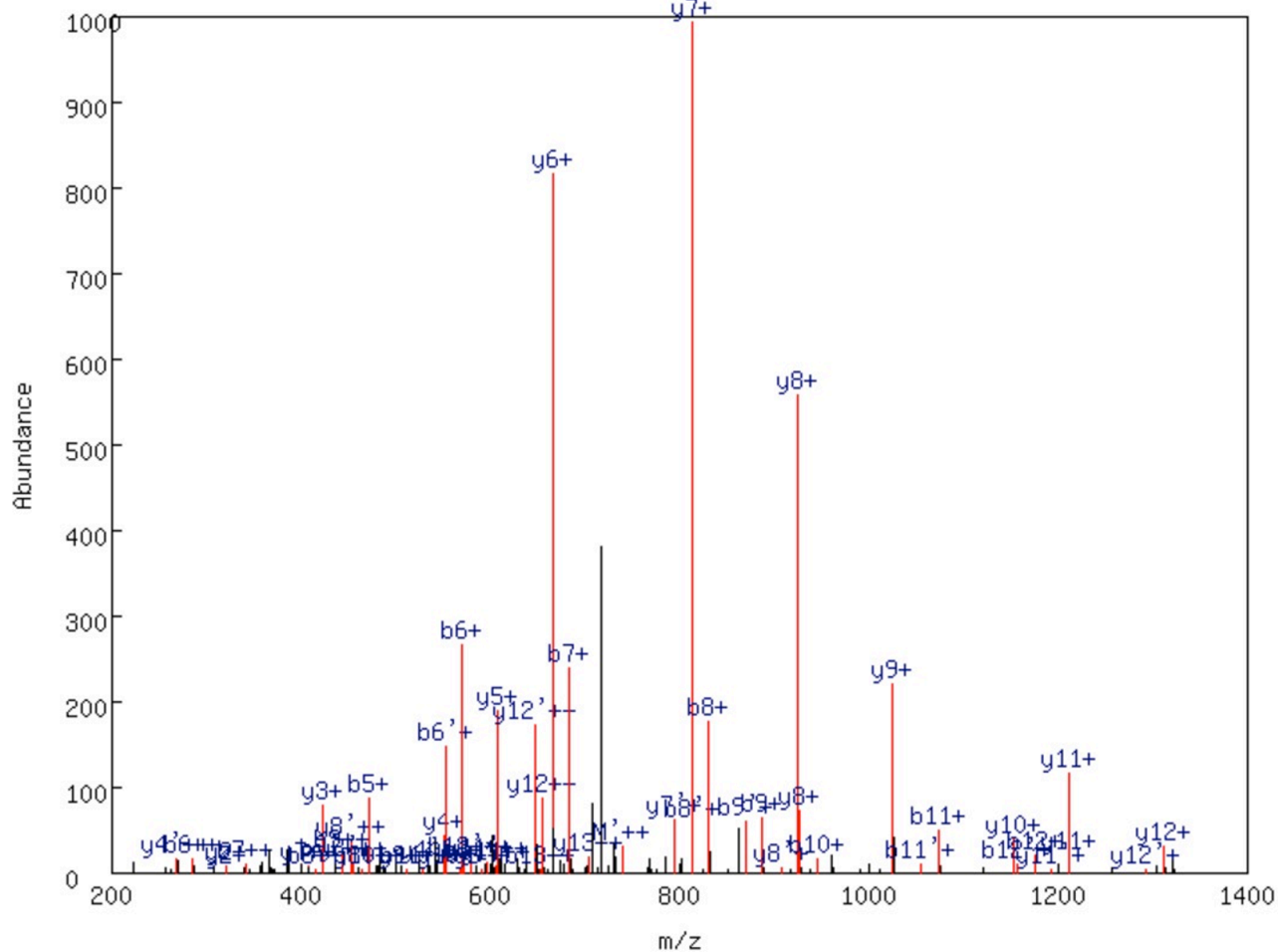


B.

#	b^{'++}	b⁺⁺	b⁺	b⁺	seq	y^{'++}	y⁺⁺	y⁺	y⁺	#
1	35.52	44.52	70.03	88.04	S	731.85	740.86	1462.70	1480.71	M
2	84.04	93.05	167.08	185.09	P	688.34	697.34	1375.67	1393.68	13
3	134.57	143.57	268.13	286.14	T	639.81	648.82	1278.61	1296.63	12
4	163.08	172.08	325.15	343.16	G	589.29	598.29	1177.57	1195.58	11
5	227.60	236.61	454.19	472.20	E	560.78	569.78	1120.55	1138.56	10
6	277.13	286.14	553.26	571.27	V	496.26	505.26	991.50	1009.51	9
7	333.68	342.68	666.35	684.36	I	446.72	455.73	892.43	910.45	8
8	407.21	416.22	813.41	831.42	F	390.18	399.18	779.35	797.36	7
9	435.72	444.73	870.44	888.45	G	316.64	325.65	632.28	650.29	6
10	464.23	473.24	927.46	945.47	G	288.13	297.14	575.26	593.27	5
11	528.75	537.76	1056.50	1074.51	E	259.62	268.63	518.24	536.25	4
12	579.28	588.28	1157.55	1175.56	T	195.10	204.11	389.20	407.21	3
13	644.80	653.80	1288.59	1306.60	M	144.58	153.58	288.15	306.16	2
	--	--	--	--	R	79.06	88.06	157.11	175.12	1

Fig. S4

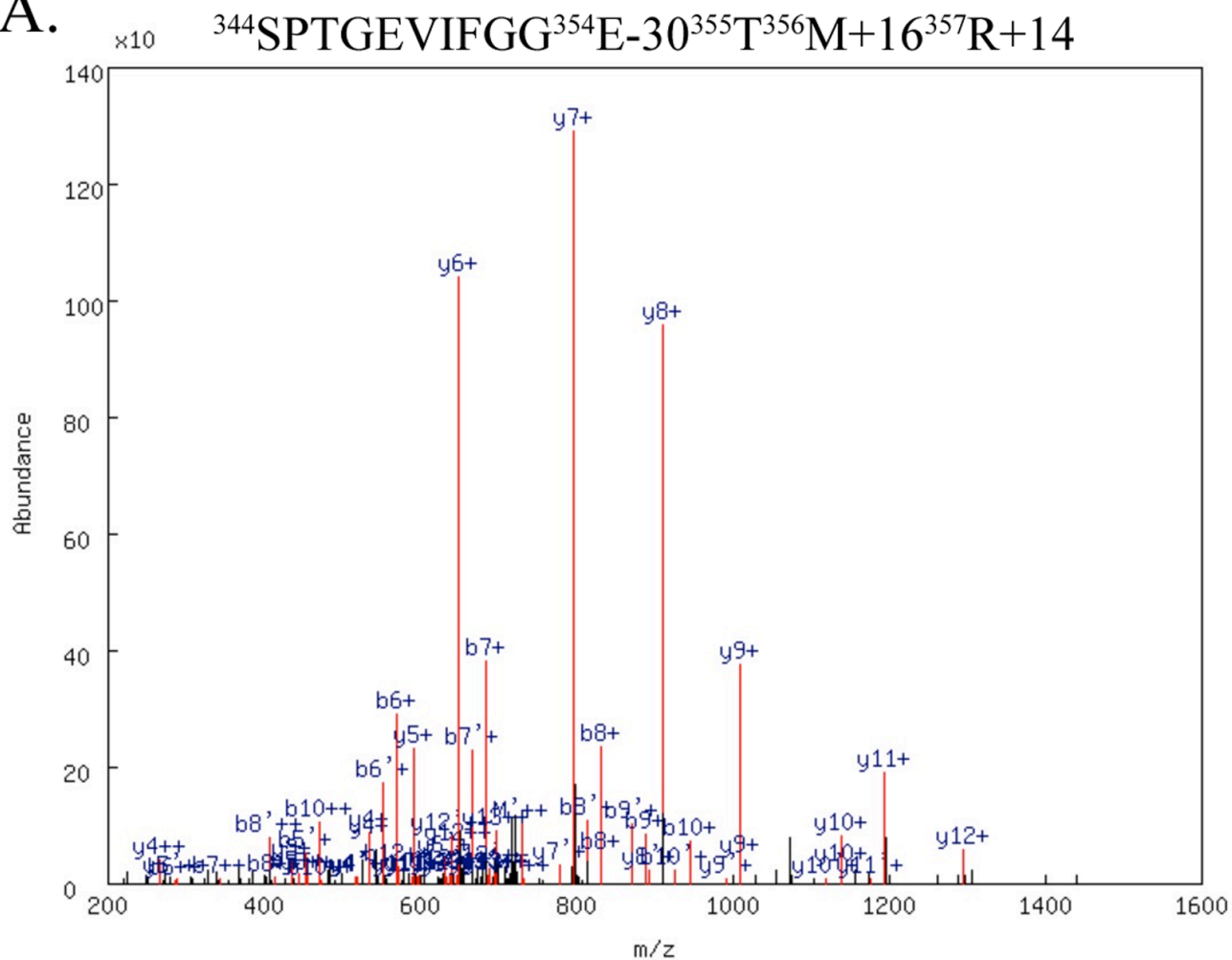
A.

 $^{344}\text{SPTGEVIFGG}^{357}\text{ETM}^{16}\text{R}$ 

B.

#	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺	#
1	35.52	44.52	70.03	88.04	S	739.85	748.86	1478.69	1496.70	M
2	84.04	93.05	167.08	185.09	P	696.33	705.34	1391.66	1409.67	13
3	134.57	143.57	268.13	286.14	T	647.81	656.81	1294.61	1312.62	12
4	163.08	172.08	325.15	343.16	G	597.28	606.29	1193.56	1211.57	11
5	227.60	236.61	454.19	472.20	E	568.77	577.78	1136.54	1154.55	10
6	277.13	286.14	553.26	571.27	V	504.25	513.26	1007.50	1025.51	9
7	333.68	342.68	666.35	684.36	I	454.72	463.72	908.43	926.44	8
8	407.21	416.22	813.41	831.42	F	398.18	407.18	795.35	813.36	7
9	435.72	444.73	870.44	888.45	G	324.64	333.65	648.28	666.29	6
10	464.23	473.24	927.46	945.47	G	296.13	305.14	591.26	609.27	5
11	528.75	537.76	1056.50	1074.51	E	267.62	276.63	534.23	552.24	4
12	579.28	588.28	1157.55	1175.56	T	203.10	212.10	405.19	423.20	3
13	644.80	653.80	1288.59	1306.60	M	152.58	161.58	304.14	322.15	2
	---	---	---	---	R	87.06	96.06	173.10	191.11	1

A.



B.

#	b ^{'++}	b ⁺⁺	b ⁺	b ⁺	seq	y ^{'++}	y ⁺⁺	y ⁺	y ⁺	#
1	35.52	44.52	70.03	88.04	S	731.84	740.84	1462.66	1480.67	M
2	84.04	93.05	167.08	185.09	P	688.32	697.32	1375.63	1393.64	13
3	134.57	143.57	268.13	286.14	T	639.79	648.80	1278.58	1296.59	12
4	163.08	172.08	325.15	343.16	G	589.27	598.27	1177.53	1195.54	11
5	227.60	236.61	454.19	472.20	E	560.76	569.76	1120.51	1138.52	10
6	277.13	286.14	553.26	571.27	V	496.24	505.24	991.47	1009.48	9
7	333.68	342.68	666.35	684.36	I	446.70	455.71	892.40	910.41	8
8	407.21	416.22	813.41	831.42	F	390.16	399.17	779.31	797.32	7
9	435.72	444.73	870.44	888.45	G	316.63	325.63	632.25	650.26	6
10	464.23	473.24	927.46	945.47	G	288.12	297.12	575.22	593.23	5
11	513.75	522.75	1026.49	1044.50	E	259.61	268.61	518.20	536.21	4
12	564.27	573.28	1127.54	1145.55	T	210.09	219.09	419.17	437.18	3
13	637.79	646.80	1274.57	1292.58	M	159.57	168.57	318.12	336.13	2
	--	--	--	--	R	86.05	95.05	171.09	189.10	1