

Supplemental Information

Cross-Linking Evidence for Multiple Interactions of the PsbP and PsbQ Proteins in a Higher Plant Photosystem II Supercomplex

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Table S1: Peptide list for the band P-1 identified by the LC-MS analysis.

Table S2: Peptide list for the band P-2 identified by the LC-MS analysis.

Table S3: Peptide list for the band P-3 identified by the LC-MS analysis.

Table S4: Peptide list for the band P-4 identified by the LC-MS analysis.

Table S5: Peptide list for the band Q-3 identified by the LC-MS analysis.

Table S6: Peptide list for the band Q-4 identified by the LC-MS analysis.

Table S7: The lists of detected product ions derived from peptides that were predicted to be cross-linked between PsbP and PsbR.

Table S8: The lists of detected product ions derived from peptides that were predicted to be cross-linked between PsbP and CP26.

Table S1: Peptide list for the band P-1 identified by the LC-MS analysis

Index	scan#	charge	score	pp	pp2	pp_tag	RT_conf	RT(obs)	RT(pred)	PA	m/z	MW(obs)	MW	delta	miss	peptide+modif	protein
1483	1047	2	88	19.6	13.8	18.2	0.6746	17.13	18.11	178832.06	740.8597	1480.7122	1480.7101	0.0022	0	SPTGEVIFGGETMR	CP43
1488	930	2	71	16.1	12.4	10.7	0.3711	15.46	18.11	12356.65	748.8571	1496.7068	1496.705	0.0019	0	SPTGEVIFGGETMR OxIM(13)	CP43
1446	754	2	51	24.3	10.2	13.6	0.9866	12.3	12.35	1235223.9	713.887	1426.7666	1426.7649	0.0018	0	LGANVGSAQGPTGLGK	CP43
953	389	1	38	10	18.8	5.5	0.3931	7.02	10.39	11763.57	764.3934	764.3934	764.3937	-0.0003	0	AAAAGFEK	CP43
954	422	1	33	10.8	16.9	5.5	0.3931	7.02	10.39	11763.57	764.3945	764.3945	764.3937	0.0007	0	AAAAGFEK	CP43
1573	1238	2	89	16.1	11.1	10.3	0.4356	20.11	23.55	848704.73	910.449	1819.8908	1819.8895	0.0013	1	GIDRDFEPVLSMTPLN OxIM(12)	CP43
1072	1164	2	82	11.6	15.7	9.1	0.6592	18.89	17.87	228372.02	491.2798	981.5523	981.5516	0.0007	0	APWLEPLR	CP43
1163	774	2	26	18.4	6.6	9.9	0.7384	12.62	13.42	494264.82	536.2648	1071.5224	1071.5218	0.0006	0	DIQPWQER	CP43
938	770	1	50	12.2	21	4.6	0.8747	12.65	13.03	94794.62	744.4631	744.4631	744.4614	0.0017	0	LINLSGK	CP43
1289	676	2	23	11.8	7.1	4.9	0.4588	10.98	13.11	9913.74	614.3154	1227.6235	1227.6229	0.0006	1	DIQPWQERR	CP43
59	1666	1	58	7.9	14.2	2.1	0.0966	26.88	8.88	67207.23	460.2545	460.2545	460.2514	0.0031	0	GIDR	CP43
930	1060	1	31	6.2	11.1	2.3	0.4765	17.27	15.5	200745.72	736.3788	736.3788	736.3777	0.0011	0	FWDLR	CP43
1596	1296	3	37	3.9	6.3	5.8	0.5668	20.99	23.19	369505.47	631.3396	1892.0042	1892.0219	-0.0176	1	*APWLEPLRGPNGLDLSR	CP43

Table S2: Peptide list for the band P-2 identified by the LC-MS analysis

Index	scan#	charge	score	pp	pp2	pp_tag	RT_conf	RT(obs)	RT(pred)	PA	m/z	MW(obs)	MW	delta	miss	peptide+modif	protein
1062	741	2	143	21.5	20.3	10.1	0.5185	12.26	12.95	447952.02	485.7641	970.5209	970.5204	0.0005	0	DPDQAALLK	CP26
1063	743	1	33	15.1	9.8	7.3	0.5193	12.26	12.95	109155.25	970.5219	970.5219	970.5204	0.0015	0	DPDQAALLK	CP26
1427	1191	2	33	9.8	6.2	9.1	0.518	19.62	18.89	70567.57	709.8929	1418.7785	1418.7791	-0.0006	0	LHPGGPFDPLGLAK	CP26
1428	1193	3	54	10.4	11.2	15.3	0.5396	19.58	18.89	229904.81	473.5984	1418.7807	1418.7791	0.0016	0	LHPGGPFDPLGLAK	CP26
1472	1181	2	89	19.9	16.1	11.8	0.4813	19.44	18.64	193796.92	741.8465	1482.6857	1482.6834	0.0023	0	FGANCGPEAVWFK	CP26
1313	997	2	54	16.7	11.5	11.2	0.3144	16.46	17.62	1391716	624.3302	1247.6531	1247.6531	0	0	YQAFELIHAR	CP26
1577	1265	2	37	10.9	8	15.8	0.0138	20.75	25.98	118436.63	925.9523	1850.8973	1850.8928	0.0045	0	WAMLGAAGCVIPEAFNK Oxim(3)	CP26
723	269	1	67	12.4	16.2	3.7	0.6648	4.91	4.4	20464.54	616.4026	616.4026	616.4028	-0.0002	1	VKEIK	CP26
724	300	1	64	13	16.5	3.7	0.6648	4.91	4.4	20464.54	616.4036	616.4036	616.4028	0.0008	1	VKEIK	CP26
986	329	1	59	13.7	14.7	4.2	0.8887	5.46	5.62	53169.74	834.4376	834.4376	834.4356	0.002	1	KPEDFAK	CP26
1524	1313	2	40	14.1	7.9	7.1	0.0088	21.52	27.84	39241.89	848.9509	1696.8945	1696.8905	0.004	0	TGALLLDGNTLNLYFGK	CP26
723	269	1	40	9.6	13.1	3.7	0.4877	4.91	4.06	20464.54	616.4026	616.4026	616.4028	-0.0002	1	IEKVK	N/A
1669	1271	3	30	10.7	3.8	6.3	0.0115	20.82	26.42	105744.81	790.7662	2370.284	2370.2816	0.0024	1	LHPGGPFDPLGLAKDPDQAALLK	CP26

Table S3: Peptide list for the band P-3 identified by the LC-MS analysis

Index	scan#	charge	score	pp	pp2	pp_tag	RT_conf	RT(obs)	RT(pred)	PA	m/z	MW(obs)	MW	delta	miss	peptide+modif	protein
1185	320	2	59	20.8	10.5	8.7	0	4.89	0	122623.51	531.2708	1061.5343	1061.5334	0.0009	1	LRDGVDSGR	PsbR
1186	289	2	47	10.9	10.5	3.6	0	4.8	0	275617.58	531.2718	1061.5363	1061.5334	0.0029	1	LRDGVDSGR	PsbR
1187	297	1	19	18.3	5.8	5.2	0	5	0	5088.55	1061.5372	1061.5372	1061.5334	0.0038	1	LRDGVDSGR	PsbR
1095	842	2	74	17.7	11.3	7.3	0	13.92	0	29584.61	478.2484	955.4895	955.4884	0.0012	0	GVYQFVDK	PsbR
1096	844	1	34	11.4	16.8	4.8	0	13.85	0	8046.28	955.4903	955.4903	955.4884	0.0019	0	GVYQFVDK	PsbR
1470	731	3	32	12.2	5.4	16.1	0	12.17	0	20967.73	476.9469	1428.8261	1428.8243	0.0018	2	IKVDKPLGIGGMK Oxim(13)	PsbR
1302	616	2	39	18.5	6.2	8.2	0	9.86	0	357613.82	594.327	1187.6468	1187.6453	0.0015	1	VDKPLGIGGMK Oxim(11)	PsbR
1405	247	2	41	10.8	8.9	6.2	0	4.02	0	5405	652.3341	1303.6609	1303.6601	0.0009	2	DGVDSSGRKPTGK	PsbR

Table S4: Peptide list for the band P-4 identified by the LC-MS analysis

Index	scan#	charge	score	pp	pp2	pp_tag	RT_conf	RT(obs)	RT(pred)	PA	m/z	MW(obs)	MW	delta	miss	peptide+modif	protein
1515	1189	2	139	24.5	18.3	12.4	0.6734	19.34	20.51	68839.77	743.3467	1485.6862	1485.6856	0.0006	0	FDSLEQLDEFSR	PsbE
1239	1329	2	89	11.5	15.8	14.4	0.6603	21.36	20.16	123110.61	561.8125	1122.6177	1122.6154	0.0024	0	SFADIITSIR	PsbE
1088	1065	2	65	14.2	9	9.8	0.4571	17.18	14.9	1082437.6	477.7901	954.573	954.5731	-0.0001	0	QGIPLITGR	PsbE
1089	1063	1	36	14.9	7.6	7.1	0.4502	17.23	14.9	96215.35	954.5731	954.5731	954.5731	0	0	QGIPLITGR	PsbE
1265	640	2	81	14.6	15.2	7.6	0.9887	10.4	10.44	15465.55	571.7604	1142.5136	1142.5113	0.0023	0	PNEYFTESR	PsbE

Table S5: Peptide list for the band Q-3 identified by the LC-MS analysis

Index	scan#	charge	score	pp	pp2	pp_tag	RT_conf	RT(obs)	RT(pred)	PA	m/z	MW(obs)	MW	delta	miss	peptide+modif	protein
1303	840	3	111	15.4	14.6	16.8	0.1984	13.69	16.98	4109.76	499.5737	1496.7065	1496.705	0.0015	0	SPTGEVIFGGETMR OxiM(13)	CP43
1304	839	2	69	16	12.2	16.8	0.1851	13.44	16.98	244874	748.857	1496.7067	1496.705	0.0017	0	SPTGEVIFGGETMR OxiM(13)	CP43
1241	1179	2	58	23.4	9.4	13.2	0.3279	19.52	22.51	9807.78	689.8323	1378.6573	1378.6559	0.0014	0	DFEPVLSMTPLN OxiM(8)	CP43
1273	707	2	41	20.5	9.4	10.7	0.2975	11.6	9.71	7199.87	713.8873	1426.7673	1426.7649	0.0024	0	LGANVGSAQGPTGLGK	CP43
905	651	2	59	17.1	11.7	9.8	0.6596	10.27	10.8	57769.27	464.7458	928.4844	928.4847	-0.0003	0	GPNGLDLSR	CP43
948	1015	2	123	11.6	16.3	9.1	0.9875	16.7	16.68	12589.58	491.2798	981.5524	981.5516	0.0007	0	APWLEPLR	CP43
769	696	1	54	14	20.6	4.6	0.6741	11.07	10.57	11538.93	744.4622	744.4622	744.4614	0.0007	0	LINLSGK	CP43
1030	727	2	30	15.3	7.1	8.6	0.6833	11.54	11.06	102991.38	536.2645	1071.5217	1071.5218	-0.0001	0	DIQPWQER	CP43
791	371	1	44	7.9	17.6	4	0.5087	6.1	7.24	294.33	764.3952	764.3952	764.3937	0.0015	0	AAAAGFEK	CP43
1383	1117	2	80	9.7	10.3	6.2	0.2034	18.21	23.85	147761.65	910.4489	1819.8906	1819.8895	0.0011	1	GIDRDFEPVLSMTPLN OxiM(12)	CP43
1589	1144	3	41	9.6	6.7	7.9	0.2113	18.68	24.25	171536.04	1107.5476	3320.6283	3320.6216	0.0067	0	SAEYMTHAPLGSLNSVGGVATEINAVNYVSPR OxiM(5)	CP43

Table S6: Peptide list for the bandQ-4 identified by the LC-MS analysis

Index	scan#	charge	score	pp	pp2	pp_tag	RT_conf	RT(obs)	RT(pred)	PA	m/z	MW(obs)	MW	delta	miss	peptide+modif	protein
1158	796	2	195	19	22.8	10.1	0.487	12.63	14.34	168644.39	485.7641	970.5209	970.5204	0.0005	0	DPDQAALLK	CP26
1159	801	1	31	14	8.9	4.8	0.4734	12.57	14.34	1816.49	970.521	970.521	970.5204	0.0006	0	DPDQAALLK	CP26
1160	832	2	12	19	5.8	10.1	0.5102	12.73	14.34	56588.05	485.765	970.5228	970.5204	0.0024	0	DPDQAALLK	CP26
1436	1177	3	66	12.8	11.5	18.5	0.4636	19.25	17.57	33085.85	473.5978	1418.779	1418.7791	-0.0001	0	LHPGGPFDPGLAK	CP26
1437	1215	3	20	7.1	7.6	7.2	0.5941	18.76	17.57	1397492.6	473.5983	1418.7804	1418.7791	0.0014	0	LHPGGPFDPGLAK	CP26
1438	1179	2	30	7.5	5.6	1.7	0.5372	18.96	17.57	29727.6	709.894	1418.7807	1418.7791	0.0016	0	LHPGGPFDPGLAK	CP26
1511	1318	2	124	23.1	18	11.5	0.6393	21.15	22.43	1155430.1	848.9495	1696.8916	1696.8905	0.0012	0	TGALLLDGNTLNLYFGK	CP26
1472	1186	2	102	18.5	17.3	10.7	0.4823	19.03	17.43	53228.27	741.8461	1482.6849	1482.6834	0.0014	0	FGANCGPEAVWFK	CP26
1289	889	2	75	24.2	12.1	8.1	0.8993	14.1	14.39	91890.21	576.2838	1151.5604	1151.5579	0.0025	0	ITNGLDFEDK	CP26
1544	1366	2	43	9.7	10.1	11.1	0.8118	22.02	21.42	36545.05	917.9539	1834.9004	1834.8979	0.0026	0	WAMLGAAGCVIPEAFNK	CP26
1358	1013	2	46	11.2	10.8	10	0.7755	16.25	16.88	8775.65	624.3327	1247.6581	1247.6531	0.005	0	YQAFELIHAR	CP26

Table S7: The lists of detected product ions derived from peptides that were predicted to be cross-linked between PsbP and PsbR.

Index scan# charge score pp pp2 ppTag m/z MW(obs) MW delta miss Unique sequence + modifications
 1998 372 +4 49 24.0 9.6 4.7 505.7815 2020.1043 2020.0934 0.0109 0 ✓ RD(\$1)GVDSSGRKPTGKGVY K(\$1)L

chainA :

#	b ¹⁺	b ²⁺	b ³⁺	b ⁴⁺	b ⁵⁺	b ⁶⁺	b ⁷⁺	b ⁸⁺	b ⁹⁺	b ¹⁰⁺	b ¹¹⁺	b ¹²⁺	seq	y ¹⁺	y ²⁺	y ³⁺	y ⁴⁺	y ⁵⁺	y ⁶⁺	y ⁷⁺	y ⁸⁺	y ⁹⁺	y ¹⁰⁺	y ¹¹⁺	y ¹²⁺	#
1		35.78	40.03		47.37	53.04		70.54	79.06		140.08	157.11	R	501.28	501.52	505.78	668.03	668.36	674.04	1001.55	1002.04	1010.55	2002.08	2003.07	2020.09	M
2	124.58	124.83	129.08	165.77	166.1	171.78	248.16	248.65	257.16	495.3	496.29	513.31	D	462.25	462.5	466.75	616	616.33	622	923.49	923.99	932.5	1845.98	1846.97	1863.99	16
3	138.84	139.08	143.34	184.78	185.11	190.78	276.67	277.16	285.67	552.33	553.31	570.34	G	373.2	373.45	377.7	497.26	497.59	503.27	745.39	745.88	754.4	1489.78	1490.76	1507.79	15
4	163.6	163.85	168.11	217.8	218.13	223.81	326.2	326.69	335.21	651.39	652.38	669.4	V	358.94	359.19	363.45	478.26	478.58	484.26	716.88	717.37	725.89	1432.75	1433.74	1450.76	14
5	192.36	192.61	196.86	256.15	256.47	262.15	383.71	384.21	392.72	766.42	767.4	784.43	D	334.18	334.42	338.68	445.23	445.56	451.24	667.35	667.84	676.35	1333.69	1334.67	1351.7	13
6	214.12	214.36	218.62	285.16	285.48	291.16	427.23	427.72	436.24	853.45	854.44	871.46	S	305.42	305.67	309.92	406.89	407.22	412.89	609.83	610.33	618.84	1218.66	1219.64	1236.67	12
7	235.88	236.12	240.38	314.17	314.49	320.17	470.75	471.24	479.75	940.48	941.47	958.5	S	283.66	283.91	288.16	377.88	378.21	383.88	586.32	586.81	575.32	1131.63	1132.61	1149.64	11
8	250.13	250.38	254.63	333.17	333.5	339.18	499.26	499.75	508.26	997.51	998.49	1015.52	G	261.9	262.15	266.41	348.87	349.2	354.87	522.8	523.29	531.81	1044.59	1045.58	1062.61	10
9	289.16	289.4	293.66	385.21	385.54	391.21	577.31	577.8	586.31	1153.61	1154.59	1171.62	R	247.65	247.89	252.15	329.86	330.19	335.87	494.29	494.78	503.3	987.57	988.56	1005.58	9
10	321.18	321.43	325.68	427.91	428.23	433.91	641.35	641.85	650.36	1281.7	1282.69	1299.71	K	208.62	208.87	213.13	277.83	278.16	283.83	416.24	416.73	425.25	831.47	832.46	849.48	8
11	345.44	345.69	349.95	480.26	480.58	466.26	689.88	690.37	698.89	1378.75	1379.74	1396.77	P	176.6	176.85	181.1	235.13	235.46	241.13	352.19	352.68	361.2	703.38	704.36	721.39	7
12	370.71	370.95	375.21	493.94	494.27	499.94	740.4	740.9	749.41	1479.8	1480.79	1497.81	T	152.34	152.58	156.84	202.78	203.11	208.78	303.67	304.16	312.67	606.32	607.31	624.34	6
13	384.96	385.21	389.46	512.95	513.27	518.95	768.92	769.41	777.92	1536.82	1537.81	1554.83	G	127.07	127.32	131.58	169.1	169.43	175.1	253.14	253.63	262.15	505.28	506.26	523.29	5
14	416.99	417.23	421.49	555.64	555.97	561.65	832.96	833.46	841.97	1664.92	1665.9	1682.93	K	112.82	113.07	117.32	150.09	150.42	156.09	224.63	225.12	233.64	448.26	449.24	466.27	4
15	431.24	431.49	435.74	574.65	574.98	580.66	861.47	861.97	870.48	1721.94	1722.92	1739.95	G	80.8		85.3	107.39		113.4	160.58		169.59	320.16		338.17	3
16	456.01	456.25	460.51	607.67	608	613.68	911.01	911.5	920.01	1821.01	1821.99	1839.02	V	66.54		71.04	88.38		94.39	132.07		141.08	263.14		281.15	2
													Y	41.77		46.28	55.36		61.37	82.54		91.54	164.07		182.08	1

chainB :

#	b ¹⁺	b ²⁺	b ³⁺	b ⁴⁺	b ⁵⁺	b ⁶⁺	b ⁷⁺	b ⁸⁺	b ⁹⁺	b ¹⁰⁺	b ¹¹⁺	b ¹²⁺	seq	y ¹⁺	y ²⁺	y ³⁺	y ⁴⁺	y ⁵⁺	y ⁶⁺	y ⁷⁺	y ⁸⁺	y ⁹⁺	y ¹⁰⁺	y ¹¹⁺	y ¹²⁺	#
1	468.5	468.75	473.01	624.33	624.66	630.34	936	936.49	945	1870.99	1871.97	1889	K													
													L	29.28		33.78	38.7		44.71	57.55		66.55	114.09		132.1	1

Mass of detected product ions are shown in red. Precursor ion charges, score values by MassMatrix (score, pp, pp2, and pptag), m/z of precursor ions, observed molecular weight of the peptides, theoretical molecular weight of the peptide, delta = MW(obs) - MW, and peptide sequence are also shown. Pair of residues that have the same label (\$1 or \$2) are predicted to be cross-linked.

Table S8: The lists of detected product ions derived from peptides that were predicted to be cross-linked between PsbP and CP26

Index scan# charge score pp pp₂ pp_{tag} m/z MW(obs) MW delta miss Unique sequence + modifications
 1459 1088 +3 36 8.4 10.0 7.5 1121.8658 3363.5830 3363.6103 -0.0273 2 ✓ E(\$1)SSTPVVDGKQYY_FKGAK(\$1)K(\$2)F_GANCGPE(\$2)AVW + CaAK(17)

chainA :

#	b ⁺⁸	b ⁺⁹	b ⁺⁸	b ⁺⁹	b ⁺¹⁰	b ⁺¹¹	b ⁺¹²	b ⁺¹³	b ⁺¹⁴	seq	y ⁺⁸	y ⁺⁹	y ⁺⁸	y ⁺⁹	y ⁺¹⁰	y ⁺¹¹	y ⁺¹²	y ⁺¹³	y ⁺¹⁴	#
1	668.32	668.65	674.33	1002	1002.5	1011	2003	2003.9	2021	E	1115.9	1116.2	1121.9	1673.3	1673.8	1682.3	3345.6	3346.6	3363.6	M
2	697.34	697.66	703.34	1045.5	1046	1054.5	2090	2091	2108	S	442.55	442.88	448.55	663.32	663.81	672.33	1325.6	1326.6	1343.7	12
3	726.35	726.67	732.35	1089	1089.5	1098	2177	2178	2195	S	413.54	413.87	419.54	619.81	620.3	628.81	1238.6	1239.6	1256.6	11
4	760.03	760.36	766.03	1139.5	1140	1148.5	2278.1	2279.1	2296.1	T	384.53	384.86	390.53	576.29	576.78	585.3	1151.6	1152.6	1169.6	10
5	792.38	792.71	798.38	1188.1	1188.6	1197.1	2375.1	2376.1	2393.1	P	350.85	351.17	356.85	525.77	526.26	534.77	1050.5	1051.5	1068.5	9
6	825.4	825.73	831.41	1237.6	1238.1	1246.6	2474.2	2475.2	2492.2	V	318.5	318.82	324.5	477.24	477.73	486.25	953.47	954.46	971.48	8
7	858.43	858.75	864.43	1287.1	1287.6	1296.1	2573.3	2574.2	2591.3	V	285.47	285.8	291.48	427.71	428.2	436.71	854.4	855.39	872.41	7
8	896.77	897.1	902.77	1344.7	1345.1	1353.7	2688.3	2689.3	2706.3	D	252.45	252.78	258.45	378.17	378.66	387.18	755.34	756.32	773.35	6
9	915.77	916.1	921.78	1373.2	1373.7	1382.2	2745.3	2746.3	2763.3	G	214.11	214.44	220.11	320.66	321.15	329.66	640.31	641.29	658.32	5
10	958.47	958.8	964.48	1437.2	1437.7	1446.2	2873.4	2874.4	2891.4	K	195.1	195.43	201.1	292.15	292.64	301.15	583.29	584.27	601.3	4
11	1001.2	1001.5	1007.2	1501.2	1501.7	1510.2	3001.5	3002.5	3019.5	Q	152.4	152.73	158.41	228.1	228.59	237.11	455.19	456.18	473.2	3
12	1055.5	1055.8	1061.5	1582.8	1583.3	1591.8	3164.5	3165.5	3182.5	Y	109.72		115.72	164.07		173.08	327.13		345.14	2
										Y	55.36		61.37	82.54		91.54	164.07		182.08	1

chainB :

#	b ⁺⁸	b ⁺⁹	b ⁺⁸	b ⁺⁹	b ⁺¹⁰	b ⁺¹¹	b ⁺¹²	b ⁺¹³	b ⁺¹⁴	seq	y ⁺⁸	y ⁺⁹	y ⁺⁸	y ⁺⁹	y ⁺¹⁰	y ⁺¹¹	y ⁺¹²	y ⁺¹³	y ⁺¹⁴	#
1			50.03			74.54			148.08	F										
2			107.06			160.09			319.18	K	1066.9	1067.2	1072.9	1599.8	1600.3	1608.8	3198.5	3199.5	3216.5	6
3			126.07			188.6			376.2	G	1009.8	1010.1	1015.8	1514.2	1514.7	1523.2	3027.4	3028.4	3045.4	5
4			149.75			224.12			447.24	A	990.81	991.14	996.81	1485.7	1486.2	1494.7	2970.4	2971.4	2988.4	4
5	671	671.33	677.01	1006	1006.5	1015	2011	2012	2029	K	967.13	967.46	973.13	1450.2	1450.7	1459.2	2899.4	2900.4	2917.4	3
6	1060.9	1061.2	1066.9	1590.8	1591.3	1599.8	3180.5	3181.5	3198.5	K	439.87	440.2	445.88	659.31	659.8	668.31	1317.6	1318.6	1335.6	2
										F	50.03		56.03	74.54		83.55	148.08		166.09	1

chainC :

#	b ⁺⁸	b ⁺⁹	b ⁺⁸	b ⁺⁹	b ⁺¹⁰	b ⁺¹¹	b ⁺¹²	b ⁺¹³	b ⁺¹⁴	seq	y ⁺⁸	y ⁺⁹	y ⁺⁸	y ⁺⁹	y ⁺¹⁰	y ⁺¹¹	y ⁺¹²	y ⁺¹³	y ⁺¹⁴	#
1			20.01			29.52			58.03	G										
2			43.69			65.04			129.07	A	1096.9	1097.2	1102.9	1644.8	1645.3	1653.8	3288.6	3289.6	3306.6	9
3		76.03	81.71		113.54	122.06		226.08	243.11	N	1073.2	1073.5	1079.2	1609.3	1609.8	1618.3	3217.5	3218.5	3235.6	8
4		129.38	135.05		193.56	202.07		386.11	403.14	C	1035.2	1035.5	1041.2	1552.3	1552.7	1561.3	3103.5	3104.5	3121.5	7
5		148.38	154.06		222.07	230.58		443.13	460.16	G	981.83	982.16	987.83	1472.2	1472.7	1481.2	2943.5	2944.5	2961.5	6
6		180.73	186.41		270.6	279.11		540.19	557.21	P	962.82	963.15	968.82	1443.7	1444.2	1452.7	2886.5	2887.4	2904.5	5
7	991.14	991.47	997.14	1486.2	1486.7	1495.2	2971.4	2972.4	2989.4	E	930.47	930.8	936.47	1395.2	1395.7	1404.2	2789.4	2790.4	2807.4	4
8	1014.8	1015.2	1020.8	1521.7	1522.2	1530.7	3042.4	3043.4	3060.5	A	119.74		125.74	179.1		188.1	357.19		375.2	3
9	1047.8	1048.2	1053.8	1571.3	1571.8	1580.3	3141.5	3142.5	3159.5	V	96.06		102.06	143.58		152.59	286.16		304.17	2
										W	63.03		69.04	94.05		103.05	187.09		205.1	1

Mass of detected product ions are shown in red. Precursor ion charges, score values by MassMatrix (score, pp, pp₂, and pp_{tag}), m/z of precursor ions, observed molecular weight of the peptides, theoretical molecular weight of the peptide, delta = MW(obs) - MW, and peptide sequence are also shown. Pair of residues that have the same label (\$1 or \$2) are predicted to be cross-linked.