

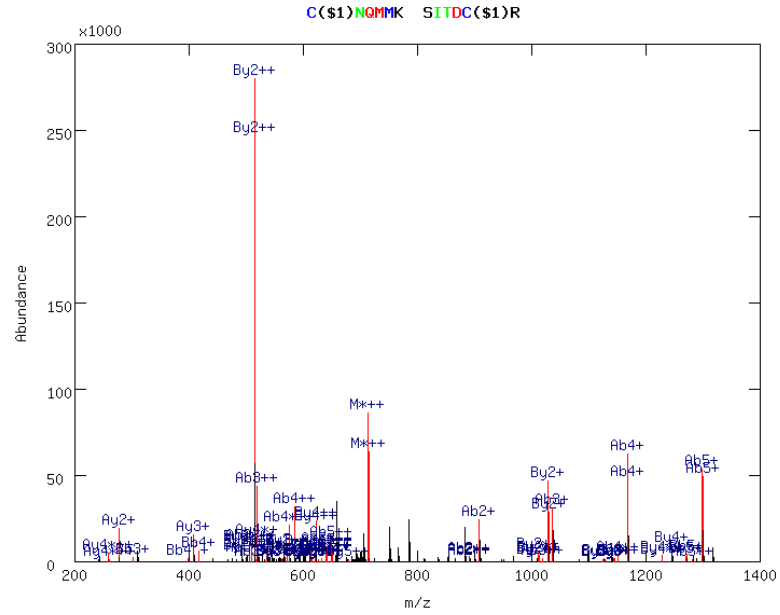
chainA :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	35.52	—	44.52	70.03	—	88.04	S	584.73	585.22	593.74	1168.45	1169.44	1186.47	6
2	92.06	—	101.07	183.11	—	201.12	I	541.22	541.71	550.22	1081.42	1082.41	1099.43	5
3	142.58	—	151.59	284.16	—	302.17	T	484.67	485.17	493.68	968.34	969.32	986.35	4
4	200.10	—	209.10	399.19	—	417.20	D	434.15	434.64	443.15	867.29	868.28	885.30	3
5	497.68	498.17	506.68	994.34	995.33	1012.35	C	376.64	377.13	385.64	752.26	753.25	770.27	2
6	—	—	—	—	—	—	R	79.06	79.55	88.06	157.11	158.09	175.12	1

chainB :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	—	389.65	398.16	—	778.29	795.31	C	—	—	—	—	—	—	4
2	—	446.67	455.18	—	892.33	909.36	N	187.58	188.07	196.58	374.15	375.13	392.16	3
3	—	510.70	519.21	—	1020.39	1037.41	Q	130.56	131.05	139.56	260.11	261.09	278.12	2
4	—	—	—	—	—	—	M	66.53	—	75.53	132.05	—	150.06	1

Scan#	Charge	Score	pp	pp2	Peptide
1293	2	61	17.9	53.3	[26-29]-s-s-[80-85]



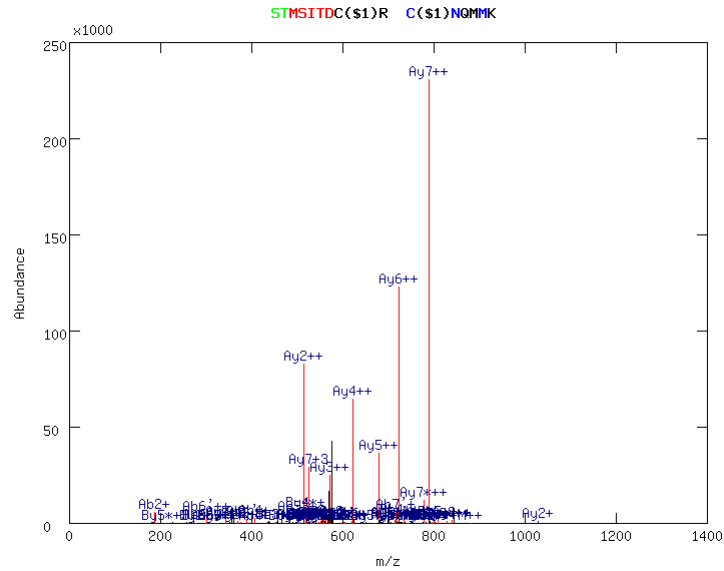
chainA :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	-	389.65	398.16	-	778.29	795.31	C	714.30	714.79	723.30	1427.59	1428.57	1445.60	6
2	-	446.67	455.18	-	892.33	909.36	N	317.15	317.64	326.15	633.29	634.27	651.30	5
3	-	510.70	519.21	-	1020.39	1037.41	Q	260.13	260.62	269.13	519.24	520.23	537.25	4
4	-	576.22	584.73	-	1151.43	1168.45	M	196.10	196.59	205.10	391.18	392.17	409.19	3
5	-	641.74	650.25	-	1282.47	1299.50	M	130.58	131.07	139.58	260.14	261.13	278.15	2
6	-	-	-	-	-	-	K	65.06	65.55	74.06	129.10	130.09	147.11	1

chainB :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	35.52	-	44.52	70.03	-	88.04	S	-	-	-	-	-	-	6
2	92.06	-	101.07	183.11	-	201.12	I	670.78	671.28	679.79	1340.56	1341.54	1358.57	5
3	142.58	-	151.59	284.16	-	302.17	T	614.24	614.73	623.25	1227.47	1228.46	1245.48	4
4	200.10	-	209.10	399.19	-	417.20	D	563.72	564.21	572.72	1126.43	1127.41	1144.44	3
5	627.24	627.74	636.25	1253.48	1254.46	1271.49	C	506.20	506.70	515.21	1011.40	1012.38	1029.41	2
6	-	-	-	-	-	-	R	79.06	79.55	88.06	157.11	158.09	175.12	1

Scan#	Charge	Score	pp	pp2	Peptide
1331	2	57	21.9	38.1	[26-31]-s-s-[80-85]



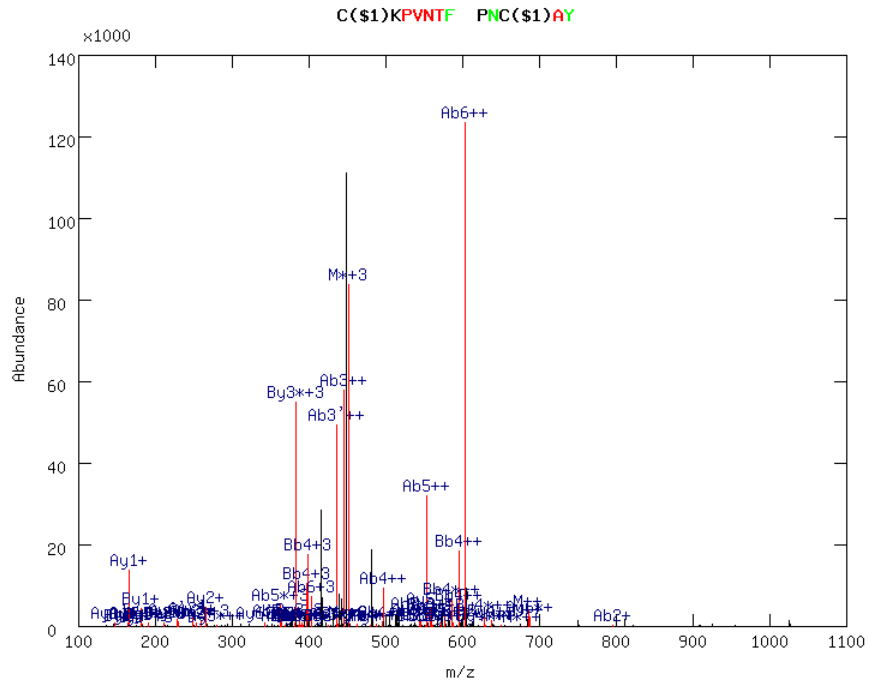
chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	#
1	24.01		30.02	35.52		44.52	70.03		88.04	S	582.91	583.24	588.91	873.86	874.35	882.86	1746.71	1747.69	1764.72		9
2	57.70		63.70	86.04		95.05	171.08		189.09	T	553.90	554.23	559.90	830.34	830.84	839.35	1659.68	1660.66	1677.69		8
3	101.38		107.38	151.56		160.57	302.12		320.13	M	520.22	520.54	526.22	779.82	780.31	788.82	1558.63	1559.61	1576.64		7
4	130.39		136.39	195.08		204.08	389.15		407.16	S	476.54	476.86	482.54	714.30	714.79	723.30	1427.59	1428.57	1445.60		6
5	168.08		174.09	251.62		260.63	502.23		520.24	I	447.52	447.85	453.53	670.78	671.28	679.79	1340.56	1341.54	1358.57		5
6	201.77		207.77	302.14		311.15	603.28		621.29	T	409.83	410.16	415.83	614.24	614.73	623.25	1227.47	1228.46	1245.48		4
7	240.11		246.11	359.66		368.66	718.31		736.32	D	376.15	376.48	382.15	563.72	564.21	572.72	1126.43	1127.41	1144.44		3
8	524.87	525.20	530.88	786.80	787.30	795.81	1572.60	1573.58	1590.61	C	337.81	338.13	343.81	506.20	506.70	515.21	1011.40	1012.38	1029.41		2
9										R	53.04	53.37	59.05	79.06	79.55	88.06	157.11	158.09	175.12		1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	#	
1		366.47	372.15		549.21	557.72		1097.41	1114.43	C												6
2		404.49	410.16		606.23	614.74		1211.45	1228.48	N	211.77	212.09	217.77	317.15	317.64	326.15	633.29	634.27	651.30			5
3		447.17	452.85		670.26	678.77		1339.51	1356.53	Q	173.75	174.08	179.76	260.13	260.62	269.13	519.24	520.23	537.25			4
4		490.85	496.53		735.78	744.29		1470.55	1487.58	M	131.07	131.39	137.07	196.10	196.59	205.10	391.18	392.17	409.19			3
5		534.53	540.21		801.30	809.81		1601.59	1618.62	M	87.39	87.71	93.39	130.58	131.07	139.58	260.14	261.13	278.15			2
6										K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11			1

Scan#	Charge	Score	pp	pp2	Peptide
1756	3	41	11.3	9.9	[26-31]-s-s-[77-85]



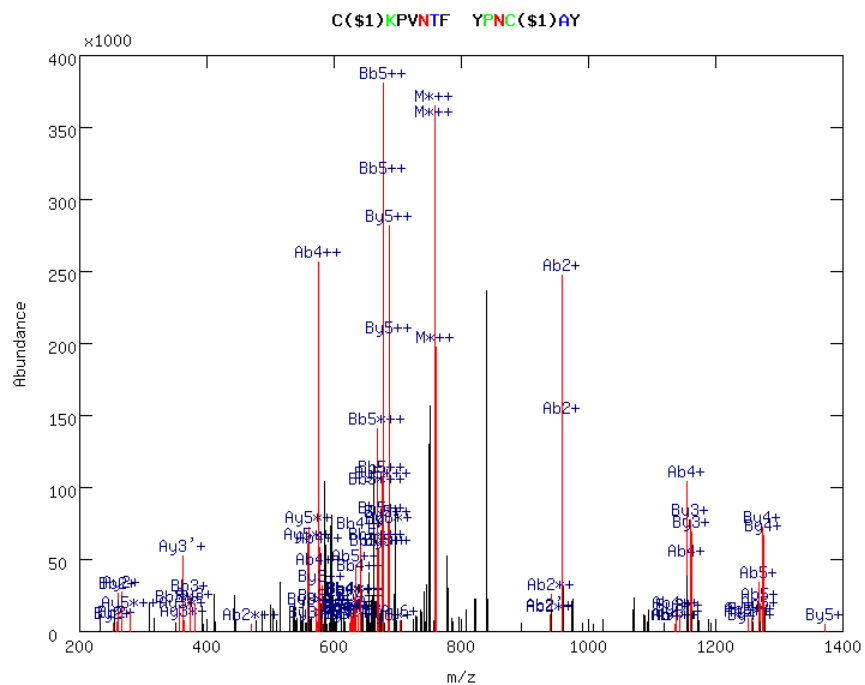
chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#	
1	217.41	217.74	223.41	325.61	326.10	334.61	650.21	651.19	668.22	C	452.20	452.53	458.21	677.80	678.29	686.81	1354.59	1355.58	1372.60	7
2	260.11	260.43	266.11	389.65	390.15	398.66	778.30	779.29	796.31	K	229.80	230.13	235.80	344.20	344.69	353.20	687.38	688.37	705.39	6
3	292.46	292.78	298.46	438.18	438.67	447.19	875.35	876.34	893.36	P	187.10	187.43	193.10	280.15	280.64	289.15	559.29	560.27	577.30	5
4	325.48	325.81	331.48	487.72	488.21	496.72	974.42	975.41	992.43	V	154.75	155.08	160.75	231.62	232.11	240.63	462.24	463.22	480.25	4
5	363.49	363.82	369.50	544.74	545.23	553.74	1088.47	1089.45	1106.48	N	121.73	122.06	127.73	182.09	182.58	191.09	363.17	364.15	381.18	3
6	397.18	397.50	403.18	595.26	595.75	604.27	1189.51	1190.50	1207.52	T	83.71	—	89.72	125.07	—	134.07	249.12	—	267.13	2
7	—	—	—	—	—	—	—	—	—	F	50.03	—	56.03	74.54	—	83.55	148.08	—	166.09	1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#	
1	—	—	33.36	—	—	49.53	—	—	98.06	P	—	—	—	—	—	—	—	—	5	
2	—	65.70	71.37	—	98.04	106.56	—	195.08	212.10	N	419.85	420.18	425.86	629.27	629.77	638.28	1257.54	1258.52	1275.55	4
3	—	368.49	374.17	—	552.24	560.75	—	1103.47	1120.49	C	381.84	382.17	387.84	572.25	572.74	581.26	1143.50	1144.48	1161.51	3
4	—	392.17	397.85	—	587.76	596.27	—	1174.50	1191.53	A	79.04	—	85.04	118.06	—	127.06	235.11	—	253.12	2
5	—	—	—	—	—	—	—	—	—	Y	55.36	—	61.37	82.54	—	91.54	164.07	—	182.08	1

Scan#	Charge	Score	pp	pp2	Peptide
1729	3	42	11.1	7.9	[40-46]-s-s-[93-97]



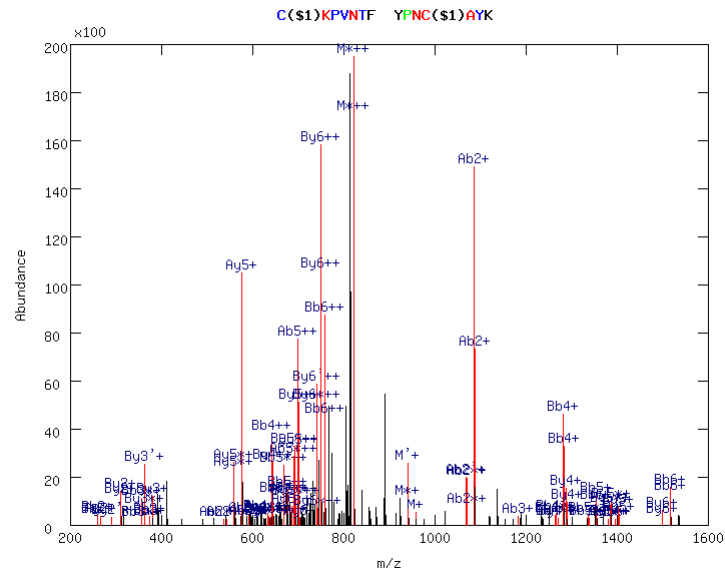
chainA :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺	y ⁺	#
1	407.14	407.63	416.14	813.27	814.25	831.28	C	759.33	759.82	768.34	1517.66	1518.64	1535.67	7
2	471.19	471.68	480.19	941.36	942.35	959.38	K	344.20	344.69	353.20	687.38	688.37	705.39	6
3	519.71	520.20	528.72	1038.42	1039.40	1056.43	P	280.15	280.64	289.15	559.29	560.27	577.30	5
4	569.25	569.74	578.25	1137.49	1138.47	1155.50	V	231.62	232.11	240.63	462.24	463.22	480.25	4
5	626.27	626.76	635.27	1251.53	1252.51	1269.54	N	182.09	182.58	191.09	363.17	364.15	381.18	3
6	676.79	677.28	685.80	1352.58	1353.56	1370.59	T	125.07	—	134.07	249.12	—	267.13	2
7	—	—	—	—	—	—	F	74.54	—	83.55	148.08	—	166.09	1

chainB :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺	y ⁺	#
1	—	—	82.54	—	—	164.07	Y	—	—	—	—	—	—	6
2	—	—	131.07	—	—	261.12	P	677.80	678.29	686.81	1354.59	1355.58	1372.60	5
3	—	179.57	188.09	—	358.14	375.17	N	629.27	629.77	638.28	1257.54	1258.52	1275.55	4
4	—	633.77	642.28	—	1266.53	1283.56	C	572.25	572.74	581.26	1143.50	1144.48	1161.51	3
5	—	669.29	677.80	—	1337.57	1354.59	A	118.06	—	127.06	235.11	—	253.12	2
6	—	—	—	—	—	—	Y	82.54	—	91.54	164.07	—	182.08	1

Scan#	Charge	Score	pp	pp2	Peptide
1915	2	130	18.9	44.3	[40-46]-s-s-[92-97]



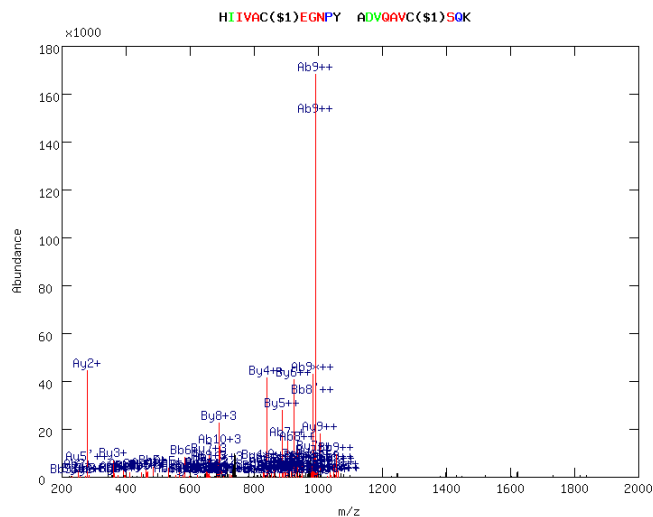
chainA :

#	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	471.19	471.68	480.19	941.36	942.35	959.38	C	823.38	823.87	832.38	1645.75	1646.73	1663.76	7
2	535.23	535.73	544.24	1069.46	1070.44	1087.47	K	344.20	344.69	353.20	687.38	688.37	705.39	6
3	583.76	584.25	592.77	1166.51	1167.50	1184.52	P	280.15	280.64	289.15	559.29	560.27	577.30	5
4	633.29	633.79	642.30	1265.58	1266.57	1283.59	V	231.62	232.11	240.63	462.24	463.22	480.25	4
5	690.32	690.81	699.32	1379.62	1380.61	1397.63	N	182.09	182.58	191.09	363.17	364.15	381.18	3
6	740.84	741.33	749.85	1480.67	1481.66	1498.68	T	125.07	—	134.07	249.12	—	267.13	2
7	—	—	—	—	—	—	F	74.54	—	83.55	148.08	—	166.09	1

chainB :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	—	—	82.54	—	—	164.07	Y	—	—	—	—	—	—	7
2	—	—	131.07	—	—	261.12	P	741.85	742.34	750.85	1482.69	1483.67	1500.70	6
3	—	179.57	188.09	—	358.14	375.17	N	693.32	693.81	702.33	1385.63	1386.62	1403.65	5
4	—	633.77	642.28	—	1266.53	1283.56	C	636.30	636.79	645.31	1271.59	1272.58	1289.60	4
5	—	669.29	677.80	—	1337.57	1354.59	A	182.11	182.60	191.11	363.20	364.19	381.21	3
6	—	750.82	759.33	—	1500.63	1517.66	Y	146.59	147.08	155.59	292.17	293.15	310.18	2
7	—	—	—	—	—	—	K	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1709	2	95	16.6	26.2	[40-46]-s-s-[92-98]



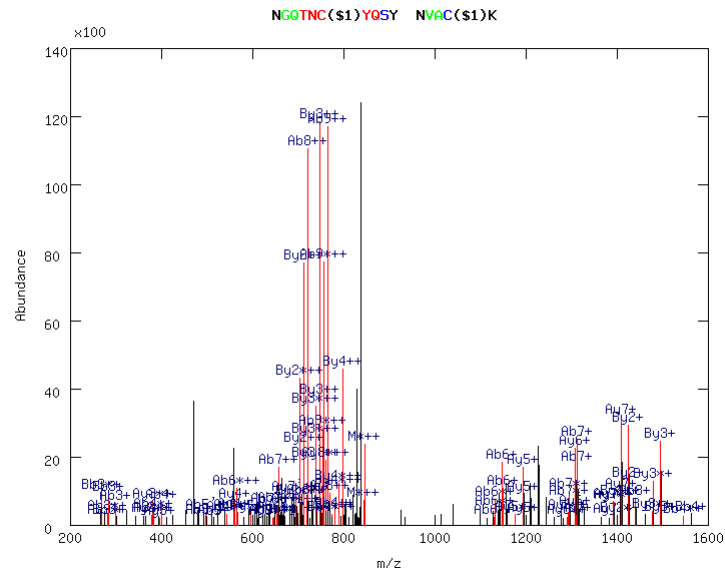
chainA :

#	b*3	b*3	b*3	b**	b**	b**	b*	b*	b*	seq	y*3	y*3	y*3	y**	y**	y**	y*	y*	y*	#
1	-	-	46.69	-	-	69.54	-	-	138.07	H	748.36	748.69	754.36	1122.03	1122.53	1131.04	2243.06	2244.04	2261.07	11
2	-	-	84.39	-	-	126.08	-	-	251.15	I	702.67	703.00	708.68	1053.50	1054.00	1062.51	2106.00	2106.98	2124.01	10
3	-	-	122.08	-	-	182.62	-	-	364.23	I	664.98	665.31	670.98	996.96	997.45	1005.97	1992.92	1993.90	2010.93	9
4	-	-	155.11	-	-	232.16	-	-	463.30	V	627.28	627.61	633.29	940.42	940.91	949.43	1879.83	1880.82	1897.84	8
5	-	-	178.79	-	-	267.67	-	-	534.34	A	594.26	594.59	600.26	890.89	891.38	899.89	1780.76	1781.75	1798.77	7
6	555.61	555.94	561.62	832.92	833.41	841.92	1664.83	1665.81	1682.84	C	570.58	570.91	576.58	855.37	855.86	864.37	1709.73	1710.71	1727.74	6
7	598.63	598.96	604.63	897.44	897.93	906.44	1793.87	1794.85	1811.88	E	187.75	188.08	193.75	281.12	281.61	290.12	561.23	562.21	579.24	5
8	617.63	617.96	623.64	925.95	926.44	934.95	1850.89	1851.87	1868.90	G	144.73	145.06	150.74	216.60	217.09	225.60	432.19	433.17	450.20	4
9	655.65	655.98	661.65	982.97	983.46	991.98	1964.93	1965.92	1982.94	N	125.73	126.06	131.73	188.09	188.58	197.09	375.17	376.15	393.18	3
10	688.00	688.33	694.00	1031.50	1031.99	1040.50	2061.99	2062.97	2080.00	P	87.71	-	93.72	131.07	-	140.07	261.12	-	279.13	2
11	-	-	-	-	-	-	-	-	-	Y	55.36	-	61.37	82.54	-	91.54	164.07	-	182.08	1

chainB :

#	b*3	b*3	b*3	b**	b**	b**	b*	b*	b*	seq	y*3	y*3	y*3	y**	y**	y**	y*	y*	y*	#
1	-	-	24.69	-	-	36.53	-	-	72.04	A	-	-	-	-	-	-	-	-	-	10
2	57.03	-	63.03	85.03	-	94.04	169.06	-	187.07	D	724.68	725.01	730.68	1086.51	1087.01	1095.52	2172.02	2173.01	2190.03	9
3	90.05	-	96.05	134.57	-	143.57	268.13	-	286.14	V	686.34	686.66	692.34	1029.00	1029.49	1038.01	2056.99	2057.98	2075.01	8
4	132.73	133.06	138.74	198.60	199.09	207.60	396.19	397.17	414.20	Q	653.31	653.64	659.32	979.47	979.96	988.47	1957.93	1958.91	1975.94	7
5	156.41	156.74	162.42	234.12	234.61	243.12	467.23	468.21	485.24	A	610.63	610.96	616.63	915.44	915.93	924.44	1829.87	1830.85	1847.88	6
6	189.44	189.76	195.44	283.65	284.14	292.66	566.29	567.28	584.30	V	586.95	587.28	592.95	879.92	880.41	888.92	1758.83	1759.81	1776.84	5
7	627.96	628.29	633.96	941.44	941.93	950.44	1881.86	1882.85	1899.87	C	553.93	554.25	559.93	830.39	830.88	839.39	1659.76	1660.75	1677.77	4
8	656.97	657.30	662.97	984.95	985.44	993.96	1968.89	1969.88	1986.91	S	115.40	115.73	121.41	172.60	173.09	181.61	344.19	345.18	362.20	3
9	699.66	699.98	705.66	1048.98	1049.47	1057.99	2096.95	2097.94	2114.96	Q	86.39	86.72	92.40	129.08	129.58	138.09	257.16	258.15	275.17	2
10	-	-	-	-	-	-	-	-	-	K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1593	3	75	11.0	29.8	[52-61]-s-s-[105-115]



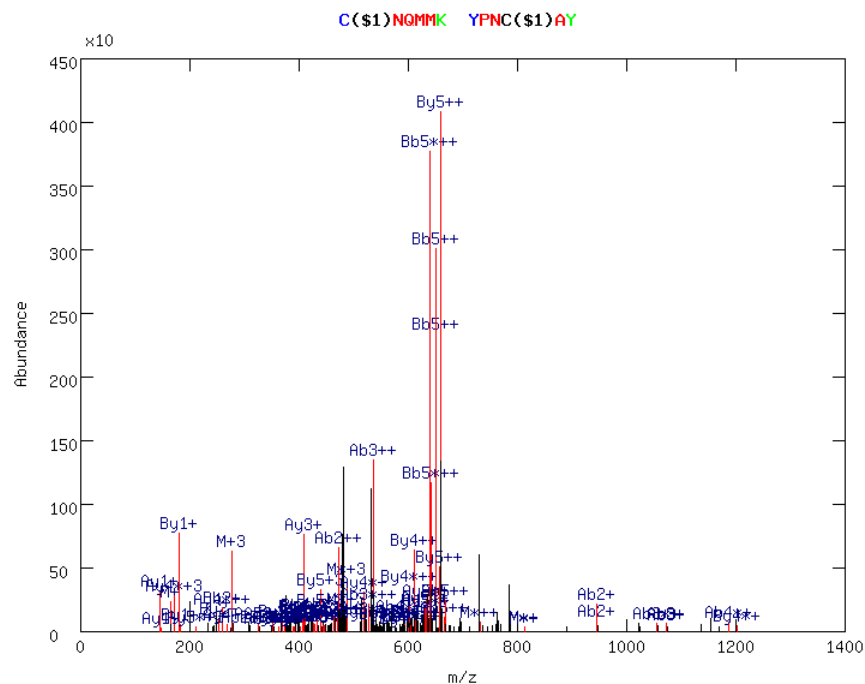
chainA :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	—	49.52	58.03	—	98.02	115.05	N	845.85	846.34	854.86	1690.70	1691.68	1708.71	10
2	—	78.03	86.54	—	155.05	172.07	G	788.83	789.32	797.84	1576.65	1577.64	1594.66	9
3	—	142.06	150.57	—	283.10	300.13	Q	760.32	760.81	769.32	1519.63	1520.61	1537.64	8
4	192.09	192.58	201.09	383.17	384.15	401.18	T	696.29	696.78	705.30	1391.57	1392.56	1409.58	7
5	249.11	249.60	258.11	497.21	498.19	515.22	N	645.77	646.26	654.77	1290.52	1291.51	1308.54	6
6	566.24	566.73	575.24	1131.47	1132.45	1149.48	C	588.74	589.24	597.75	1176.48	1177.47	1194.49	5
7	647.77	648.26	656.77	1294.53	1295.51	1312.54	Y	271.62	272.11	280.62	542.23	543.21	560.24	4
8	711.80	712.29	720.80	1422.59	1423.57	1440.60	Q	190.08	190.58	199.09	379.16	380.15	397.17	3
9	755.31	755.81	764.32	1509.62	1510.61	1527.63	S	126.06	—	135.06	251.10	—	269.11	2
10	—	—	—	—	—	—	Y	82.54	—	91.54	164.07	—	182.08	1

chainB :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	—	49.52	58.03	—	98.02	115.05	N	—	—	—	—	—	—	5
2	—	99.05	107.56	—	197.09	214.12	V	788.83	789.32	797.84	1576.65	1577.64	1594.66	4
3	—	134.57	143.08	—	268.13	285.16	A	739.30	739.79	748.30	1477.58	1478.57	1495.59	3
4	—	773.29	781.80	—	1545.57	1562.60	C	703.78	704.27	712.78	1406.55	1407.53	1424.56	2
5	—	—	—	—	—	—	K	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1405	2	79	19.3	22.2	[62-66]-s-s-[67-76]



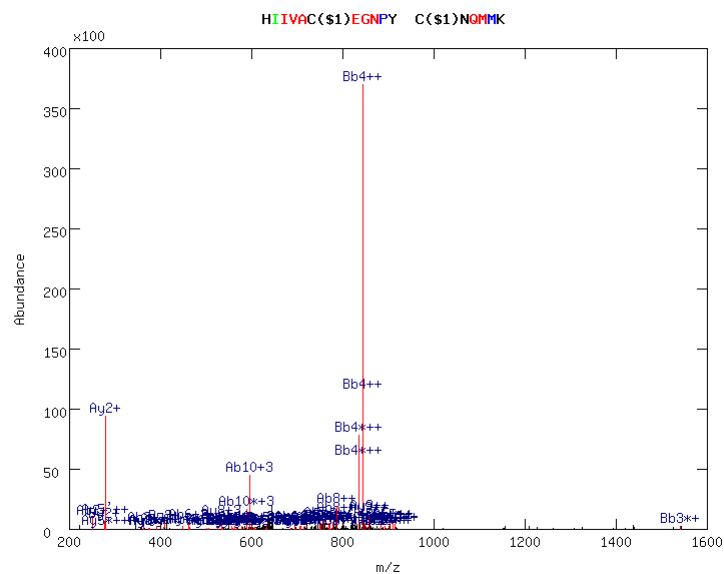
chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	—	272.09	277.77	—	407.63	416.14	—	814.25	831.28	C	488.52	488.85	494.53	732.28	732.77	741.29	1463.56	1464.54	1481.57	6
2	—	310.10	315.78	—	464.65	473.17	—	928.30	945.32	N	211.77	212.09	217.77	317.15	317.64	326.15	633.29	634.27	651.30	5
3	—	352.79	358.47	—	528.68	537.19	—	1056.36	1073.38	Q	173.75	174.08	179.76	260.13	260.62	269.13	519.24	520.23	537.25	4
4	—	396.47	402.15	—	594.20	602.72	—	1187.40	1204.42	M	131.07	131.39	137.07	196.10	196.59	205.10	391.18	392.17	409.19	3
5	—	440.15	445.83	—	659.72	668.24	—	1318.44	1335.46	M	87.39	87.71	93.39	130.58	131.07	139.58	260.14	261.13	278.15	2
6	—	—	—	—	—	—	—	—	—	K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	—	—	55.36	—	—	82.54	—	—	164.07	Y	—	—	—	—	—	—	—	—	—	6
2	—	—	87.71	—	—	131.07	—	—	261.12	P	434.17	434.50	440.17	650.75	651.24	659.76	1300.49	1301.48	1318.51	5
3	—	120.05	125.73	—	179.57	188.09	—	358.14	375.17	N	401.82	402.15	407.82	602.22	602.72	611.23	1203.44	1204.43	1221.45	4
4	—	404.82	410.49	—	606.72	615.23	—	1212.43	1229.46	C	363.80	364.13	369.81	545.20	545.70	554.21	1089.40	1090.38	1107.41	3
5	—	428.49	434.17	—	642.24	650.75	—	1283.47	1300.49	A	79.04	—	85.04	118.06	—	127.06	235.11	—	253.12	2
6	—	—	—	—	—	—	—	—	—	Y	55.36	—	61.37	82.54	—	91.54	164.07	—	182.08	1

Scan#	Charge	Score	pp	pp2	Peptide
1751	3	58	13.5	17.5	[26-31]-s-s-[92-97]



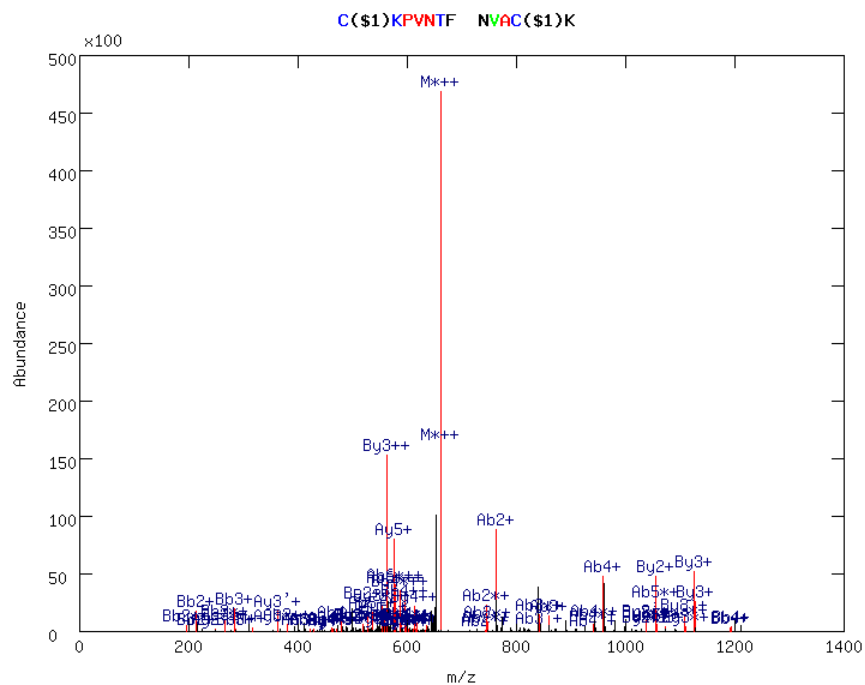
chainA :

#	b ⁺⁺³	b ^{*+3}	b ⁺³	b ⁺⁺	b ^{*+}	b ⁺	b ⁺⁺	b ^{*+}	b ⁺	seq	y ⁺⁺³	y ^{*+3}	y ⁺³	y ⁺⁺	y ^{*+}	y ⁺	y ⁺⁺	y ^{*+}	y ⁺	#
1	---	---	46.69	---	---	69.54	---	---	138.07	H	650.29	650.62	656.29	974.93	975.42	983.94	1948.85	1949.84	1966.86	11
2	---	---	84.39	---	---	126.08	---	---	251.15	I	604.60	604.93	610.61	906.40	906.89	915.41	1811.80	1812.78	1829.81	10
3	---	---	122.08	---	---	182.62	---	---	364.23	I	566.91	567.24	572.91	849.86	850.35	858.86	1698.71	1699.70	1716.72	9
4	---	---	155.11	---	---	232.16	---	---	463.30	V	529.21	529.54	535.22	793.32	793.81	802.32	1585.63	1586.61	1603.64	8
5	---	---	178.79	---	---	267.67	---	---	534.34	A	496.19	496.52	502.19	743.78	744.28	752.79	1486.56	1487.54	1504.57	7
6	457.55	457.87	463.55	685.81	686.31	694.82	1370.62	1371.60	1388.63	C	472.51	472.84	478.52	708.26	708.76	717.27	1415.52	1416.51	1433.53	6
7	500.56	500.89	506.56	750.34	750.83	759.34	1499.66	1500.65	1517.67	E	187.75	188.08	193.75	281.12	281.61	290.12	561.23	562.21	579.24	5
8	519.57	519.89	525.57	778.85	779.34	787.85	1556.68	1557.67	1574.70	G	144.73	145.06	150.74	216.60	217.09	225.60	432.19	433.17	450.20	4
9	557.58	557.91	563.58	835.87	836.36	844.87	1670.73	1671.71	1688.74	N	125.73	126.06	131.73	188.09	188.58	197.09	375.17	376.15	393.18	3
10	589.93	590.26	595.94	884.39	884.89	893.40	1767.78	1768.76	1785.79	P	87.71	---	93.72	131.07	---	140.07	261.12	---	279.13	2
11	---	---	---	---	---	---	---	---	---	Y	55.36	---	61.37	82.54	---	91.54	164.07	---	182.08	1

chainB :

#	b ⁺⁺³	b ^{*+3}	b ⁺³	b ⁺⁺	b ^{*+}	b ⁺	b ⁺⁺	b ^{*+}	b ⁺	seq	y ⁺⁺³	y ^{*+3}	y ⁺³	y ⁺⁺	y ^{*+}	y ⁺	y ⁺⁺	y ^{*+}	y ⁺	#
1	---	433.86	439.53	---	650.28	658.79	---	1299.55	1316.58	C	---	---	---	---	---	---	---	---	---	6
2	---	471.87	477.55	---	707.30	715.81	---	1413.59	1430.62	N	211.77	212.09	217.77	317.15	317.64	326.15	633.29	634.27	651.30	5
3	---	514.56	520.23	---	771.33	779.84	---	1541.65	1558.68	Q	173.75	174.08	179.76	260.13	260.62	269.13	519.24	520.23	537.25	4
4	---	558.24	563.91	---	836.85	845.36	---	1672.69	1689.72	M	131.07	131.39	137.07	196.10	196.59	205.10	391.18	392.17	409.19	3
5	---	601.92	607.59	---	902.37	910.88	---	1803.73	1820.76	M	87.39	87.71	93.39	130.58	131.07	139.58	260.14	261.13	278.15	2
6	---	---	---	---	---	---	---	---	---	K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
2000	3	34	6.3	14.2	[26-31]-s-s-[105-115]



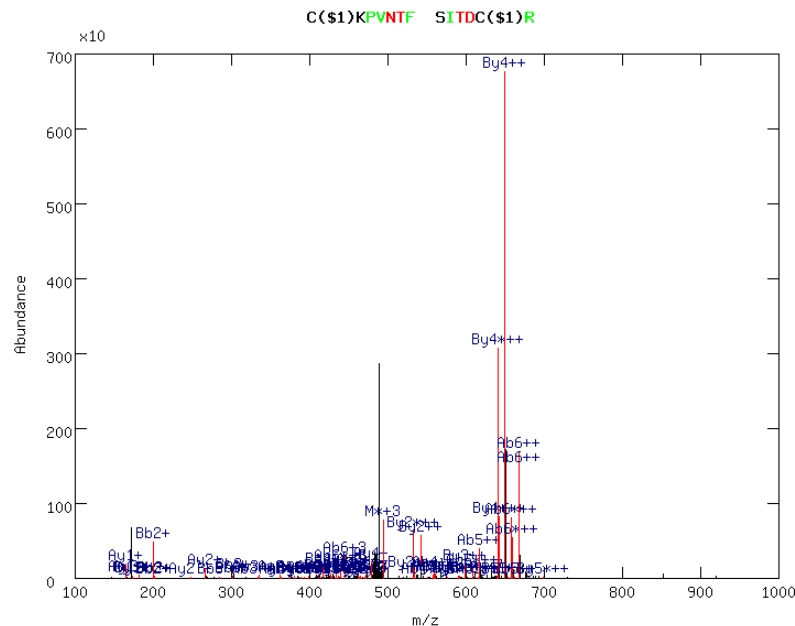
chainA :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	309.13	309.62	318.14	617.25	618.24	635.26	C	661.32	661.82	670.33	1321.64	1322.62	1339.65	7
2	373.18	373.67	382.18	745.35	746.33	763.36	K	344.20	344.69	353.20	687.38	688.37	705.39	6
3	421.70	422.20	430.71	842.40	843.39	860.41	P	280.15	280.64	289.15	559.29	560.27	577.30	5
4	471.24	471.73	480.24	941.47	942.45	959.48	V	231.62	232.11	240.63	462.24	463.22	480.25	4
5	528.26	528.75	537.27	1055.51	1056.50	1073.52	N	182.09	182.58	191.09	363.17	364.15	381.18	3
6	578.78	579.28	587.79	1156.56	1157.54	1174.57	T	125.07	—	134.07	249.12	—	267.13	2
7	—	—	—	—	—	—	F	74.54	—	83.55	148.08	—	166.09	1

chainB :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	—	49.52	58.03	—	98.02	115.05	N	—	—	—	—	—	—	5
2	—	99.05	107.56	—	197.09	214.12	V	604.30	604.79	613.31	1207.60	1208.58	1225.61	4
3	—	134.57	143.08	—	268.13	285.16	A	554.77	555.26	563.77	1108.53	1109.51	1126.54	3
4	—	588.76	597.28	—	1176.52	1193.54	C	519.25	519.74	528.25	1037.49	1038.48	1055.50	2
5	—	—	—	—	—	—	K	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1270	2	45	18.5	41.2	[40-46]-s-s-[62-66]



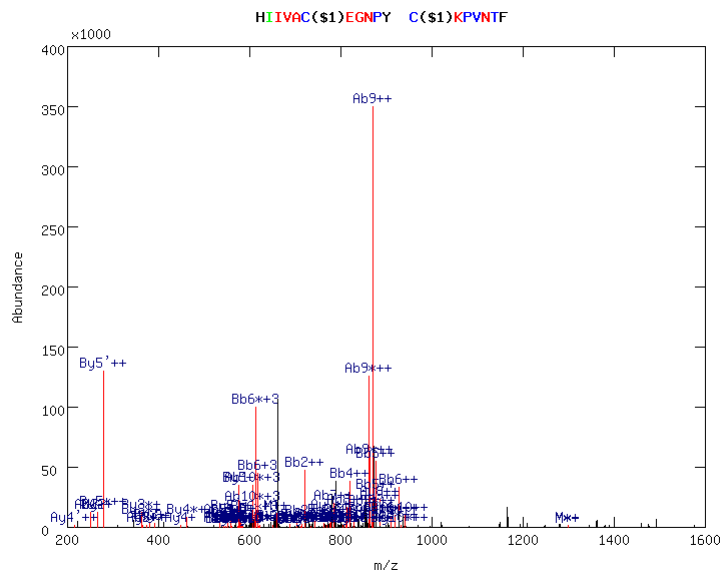
chainA :

#	b ⁺⁺³	b ⁺⁺⁺	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺⁺	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	259.77	260.10	265.78	389.16	389.65	398.16	777.30	778.29	795.31	C	494.57	494.90	500.57	741.35	741.84	750.35	1481.69	1482.67	1499.70	7
2	302.47	302.80	308.47	453.20	453.69	462.21	905.40	906.38	923.41	K	229.80	230.13	235.80	344.20	344.69	353.20	687.38	688.37	705.39	6
3	334.82	335.15	340.83	501.73	502.22	510.73	1002.45	1003.43	1020.46	P	187.10	187.43	193.10	280.15	280.64	289.15	559.29	560.27	577.30	5
4	367.84	368.17	373.85	551.26	551.76	560.27	1101.52	1102.50	1119.53	V	154.75	155.08	160.75	231.62	232.11	240.63	462.24	463.22	480.25	4
5	405.86	406.19	411.86	608.28	608.78	617.29	1215.56	1216.55	1233.57	N	121.73	122.06	127.73	182.09	182.58	191.09	363.17	364.15	381.18	3
6	439.54	439.87	445.55	658.81	659.30	667.81	1316.61	1317.59	1334.62	T	83.71	—	89.72	125.07	—	134.07	249.12	—	267.13	2
7	—	—	—	—	—	—	—	—	—	F	50.03	—	56.03	74.54	—	83.55	148.08	—	166.09	1

chainB :

#	b ⁺⁺³	b ⁺⁺⁺	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺⁺	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	24.01	—	30.02	35.52	—	44.52	70.03	—	88.04	S	—	—	—	—	—	—	—	—	—	6
2	61.71	—	67.71	92.06	—	101.07	183.11	—	201.12	I	465.56	465.89	471.56	697.83	698.32	706.84	1394.66	1395.64	1412.67	5
3	95.39	—	101.40	142.58	—	151.59	284.16	—	302.17	T	427.86	428.19	433.87	641.29	641.78	650.30	1281.57	1282.56	1299.58	4
4	133.73	—	139.74	200.10	—	209.10	399.19	—	417.20	D	394.18	394.51	400.18	590.77	591.26	599.77	1180.52	1181.51	1198.53	3
5	436.53	436.86	442.53	654.29	654.78	663.30	1307.58	1308.56	1325.59	C	355.84	356.17	361.84	533.25	533.74	542.26	1065.50	1066.48	1083.51	2
6	—	—	—	—	—	—	—	—	—	R	53.04	53.37	59.05	79.06	79.55	88.06	157.11	158.09	175.12	1

Scan#	Charge	Score	pp	pp2	Peptide
1742	3	35	11.7	9.2	[40-46]-s-s-[80-85]



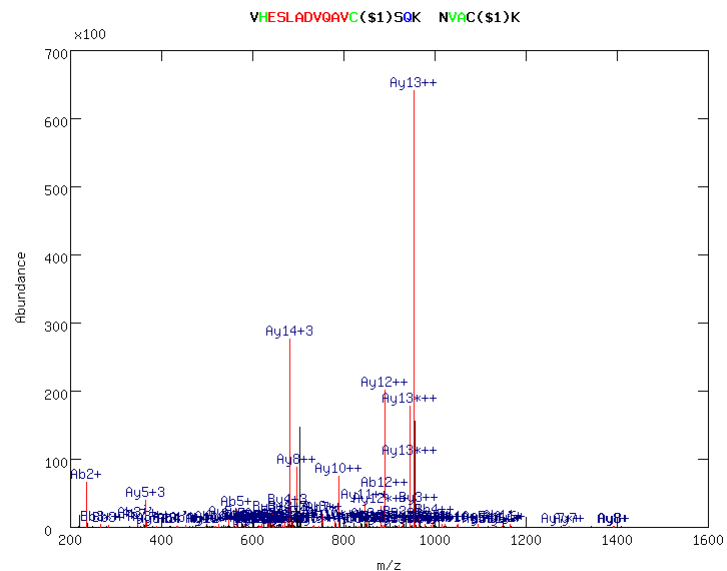
chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1			46.69			69.54			138.07	H	668.32	668.65	674.33	1001.98	1002.47	1010.99	2002.95	2003.94	2020.96	11
2			84.39			126.08			251.15	I	622.64	622.96	628.64	933.45	933.94	942.46	1865.89	1866.88	1883.90	10
3			122.08			182.62			364.23	I	584.94	585.27	590.95	876.91	877.40	885.91	1752.81	1753.79	1770.82	9
4			155.11			232.16			463.30	V	547.25	547.57	553.25	820.37	820.86	829.37	1639.72	1640.71	1657.74	8
5			178.79			267.67			534.34	A	514.22	514.55	520.23	770.83	771.32	779.84	1540.66	1541.64	1558.67	7
6	475.58	475.91	481.58	712.86	713.36	721.87	1424.72	1425.70	1442.73	C	490.54	490.87	496.55	735.31	735.81	744.32	1469.62	1470.60	1487.63	6
7	518.59	518.92	524.60	777.38	777.88	786.39	1553.76	1554.74	1571.77	E	187.75	188.08	193.75	281.12	281.61	290.12	561.23	562.21	579.24	5
8	537.60	537.93	543.60	805.90	806.39	814.90	1610.78	1611.77	1628.79	G	144.73	145.06	150.74	216.60	217.09	225.60	432.19	433.17	450.20	4
9	575.61	575.94	581.62	862.92	863.41	871.92	1724.83	1725.81	1742.84	N	125.73	126.06	131.73	188.09	188.58	197.09	375.17	376.15	393.18	3
10	607.96	608.29	613.97	911.44	911.93	920.45	1821.88	1822.86	1839.89	P	87.71		93.72	131.07		140.07	261.12		279.13	2
11										Y	55.36		61.37	82.54		91.54	164.07		182.08	1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	433.53	433.86	439.53	649.79	650.28	658.79	1298.57	1299.55	1316.58	C										7
2	476.23	476.55	482.23	713.83	714.33	722.84	1426.66	1427.65	1444.67	K	229.80	230.13	235.80	344.20	344.69	353.20	687.38	688.37	705.39	6
3	508.58	508.90	514.58	762.36	762.85	771.37	1523.71	1524.70	1541.72	P	187.10	187.43	193.10	280.15	280.64	289.15	559.29	560.27	577.30	5
4	541.60	541.93	547.60	811.90	812.39	820.90	1622.78	1623.77	1640.79	V	154.75	155.08	160.75	231.62	232.11	240.63	462.24	463.22	480.25	4
5	579.61	579.94	585.62	868.92	869.41	877.92	1736.83	1737.81	1754.84	N	121.73	122.06	127.73	182.09	182.58	191.09	363.17	364.15	381.18	3
6	613.30	613.62	619.30	919.44	919.93	928.45	1837.87	1838.86	1855.88	T	83.71		89.72	125.07		134.07	249.12		267.13	2
7										F	50.03		56.03	74.54		83.55	148.08		166.09	1

Scan#	Charge	Score	pp	pp2	Peptide
2113	3	44	6.3	10.7	[40-46]-s-s-[105-115]



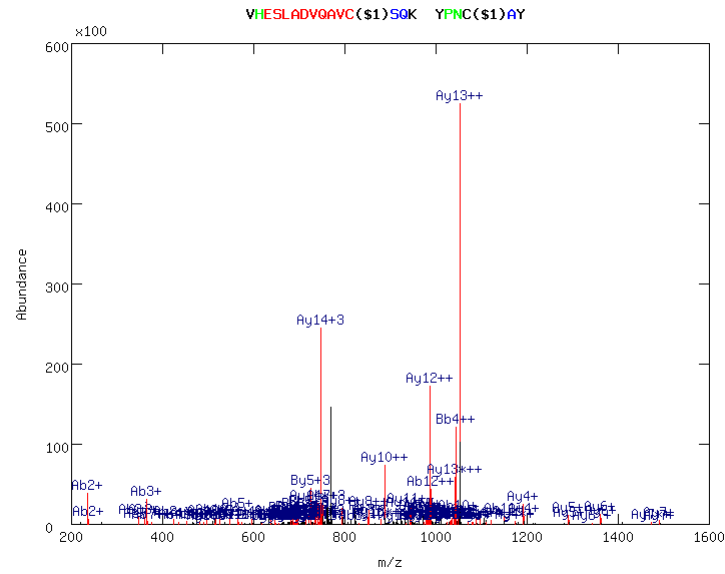
chainA :

#	b ⁺⁺³	b ⁺⁺²	b ⁺⁺¹	b ⁺⁺⁰	b ⁺⁺⁻¹	b ⁺⁺⁻²	b ⁺⁺⁻³	b ⁺⁺⁻⁴	b ⁺⁺⁻⁵	seq	y ⁺⁺³	y ⁺⁺²	y ⁺⁺¹	y ⁺⁺⁰	y ⁺⁺⁻¹	y ⁺⁺⁻²	y ⁺⁺⁻³	y ⁺⁺⁻⁴	y ⁺⁺⁻⁵	#
1			34.03			50.54			100.08	V	709.68	710.01	715.69	1064.02	1064.51	1073.03	2127.03	2128.02	2145.04	15
2			79.72			119.07			237.14	H	676.66	676.99	682.66	1014.49	1014.98	1023.49	2027.96	2028.95	2045.97	14
3	116.73		122.73	174.59		183.59	348.17		366.18	E	630.97	631.30	636.98	945.96	946.45	954.96	1890.91	1891.89	1908.92	13
4	145.74		151.74	218.10		227.11	435.20		453.21	S	587.96	588.29	593.96	881.44	881.93	890.44	1761.86	1762.85	1779.87	12
5	183.43		189.44	274.65		283.65	548.28		566.29	L	558.95	559.28	564.95	837.92	838.41	846.92	1674.83	1675.81	1692.84	11
6	207.11		213.12	310.16		319.17	619.32		637.33	A	521.25	521.58	527.26	781.38	781.87	790.38	1561.75	1562.73	1579.76	10
7	245.45		251.46	367.68		376.68	734.35		752.36	D	497.58	497.90	503.58	745.86	746.35	754.86	1490.71	1491.69	1508.72	9
8	278.48		284.48	417.21		426.22	833.42		851.43	V	459.23	459.56	465.24	688.35	688.84	697.35	1375.68	1376.67	1393.69	8
9	321.16	321.49	327.17	481.24	481.73	490.25	961.47	962.46	979.48	Q	426.21	426.54	432.21	638.81	639.30	647.82	1276.61	1277.60	1294.62	7
10	344.84	345.17	350.85	516.76	517.25	525.76	1032.51	1033.50	1050.52	A	383.52	383.85	389.53	574.78	575.27	583.79	1148.56	1149.54	1166.57	6
11	377.87	378.19	383.87	566.29	566.79	575.30	1131.58	1132.56	1149.59	V	359.84	360.17	365.85	539.26	539.76	548.27	1077.52	1078.50	1095.53	5
12	589.28	589.61	595.29	883.42	883.91	892.43	1765.84	1766.82	1783.85	C	326.82	327.15	332.83	489.73	490.22	498.73	978.45	979.43	996.46	4
13	618.29	618.62	624.30	926.94	927.43	935.94	1852.87	1853.85	1870.88	S	115.40	115.73	121.41	172.60	173.09	181.61	344.19	345.18	362.20	3
14	660.98	661.31	666.98	990.97	991.46	999.97	1980.93	1981.91	1998.94	Q	86.39	86.72	92.40	129.08	129.58	138.09	257.16	258.15	275.17	2
15										K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

chainB :

#	b ⁺⁺³	b ⁺⁺²	b ⁺⁺¹	b ⁺⁺⁰	b ⁺⁺⁻¹	b ⁺⁺⁻²	b ⁺⁺⁻³	b ⁺⁺⁻⁴	b ⁺⁺⁻⁵	seq	y ⁺⁺³	y ⁺⁺²	y ⁺⁺¹	y ⁺⁺⁰	y ⁺⁺⁻¹	y ⁺⁺⁻²	y ⁺⁺⁻³	y ⁺⁺⁻⁴	y ⁺⁺⁻⁵	#
1		33.35	39.02		49.52	58.03		98.02	115.05	N										5
2		66.37	72.04		99.05	107.56		197.09	214.12	V	671.67	672.00	677.67	1007.00	1007.49	1016.00	2012.99	2013.97	2031.00	4
3		90.05	95.72		134.57	143.08		268.13	285.16	A	638.65	638.97	644.65	957.46	957.96	966.47	1913.92	1914.91	1931.93	3
4		661.31	666.98		991.46	999.97		1981.91	1998.94	C	614.97	615.29	620.97	921.95	922.44	930.95	1842.88	1843.87	1860.89	2
5										K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1864	3	38	5.2	8.2	[47-61]-s-s-[62-66]



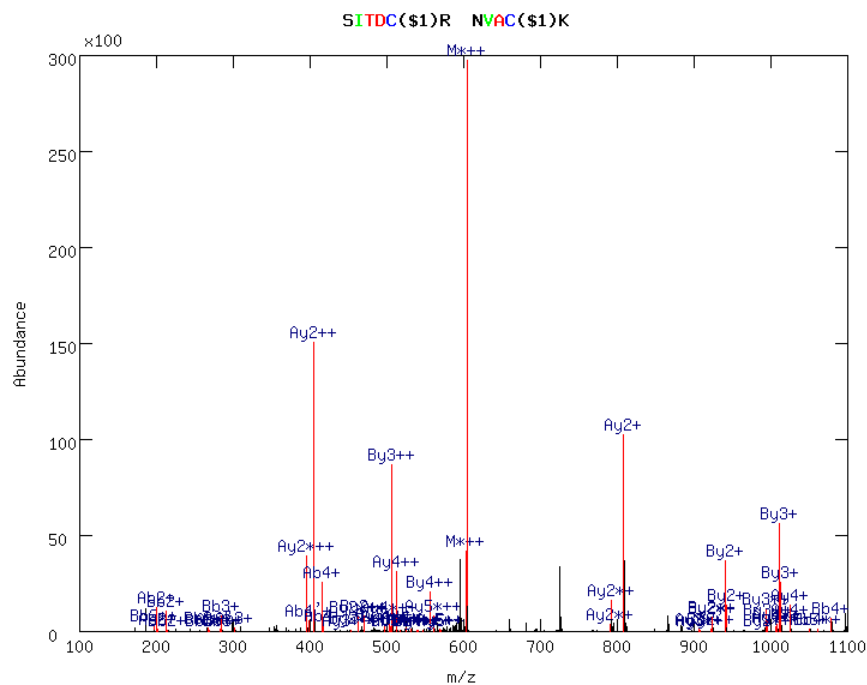
chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	seq	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	#
1	-	-	34.03	-	-	50.54	-	-	100.08	V	775.02	775.35	781.02	1162.03	1162.52	1171.03	2323.05	2324.03	2341.06	15
2	-	-	79.72	-	-	119.07	-	-	237.14	H	742.00	742.33	748.00	1112.49	1112.99	1121.50	2223.98	2224.96	2241.99	14
3	116.73	-	122.73	174.59	-	183.59	348.17	-	366.18	E	696.31	696.64	702.32	1043.96	1044.46	1052.97	2086.92	2087.91	2104.93	13
4	145.74	-	151.74	218.10	-	227.11	435.20	-	453.21	S	653.30	653.63	659.30	979.44	979.94	988.45	1957.88	1958.86	1975.89	12
5	183.43	-	189.44	274.65	-	283.65	548.28	-	566.29	L	624.29	624.62	630.29	935.93	936.42	944.93	1870.85	1871.83	1888.86	11
6	207.11	-	213.12	310.16	-	319.17	619.32	-	637.33	A	586.59	586.92	592.60	879.39	879.88	888.39	1757.76	1758.75	1775.77	10
7	245.45	-	251.46	367.68	-	376.68	734.35	-	752.36	D	562.91	563.24	568.92	843.87	844.36	852.87	1686.73	1687.71	1704.74	9
8	278.48	-	284.48	417.21	-	426.22	833.42	-	851.43	V	524.57	524.90	530.57	786.35	786.85	795.36	1571.70	1572.68	1589.71	8
9	321.16	321.49	327.17	481.24	481.73	490.25	961.47	962.46	979.48	Q	491.55	491.88	497.55	736.82	737.31	745.82	1472.63	1473.61	1490.64	7
10	344.84	345.17	350.85	516.76	517.25	525.76	1032.51	1033.50	1050.52	A	448.86	449.19	454.87	672.79	673.28	681.80	1344.57	1345.56	1362.58	6
11	377.87	378.19	383.87	566.29	566.79	575.30	1131.58	1132.56	1149.59	V	425.18	425.51	431.19	637.27	637.76	646.28	1273.53	1274.52	1291.55	5
12	654.62	654.95	660.63	981.43	981.92	990.44	1961.85	1962.84	1979.86	C	392.16	392.49	398.16	587.74	588.23	596.74	1174.47	1175.45	1192.48	4
13	683.63	683.96	689.64	1024.95	1025.44	1033.95	2048.88	2049.87	2066.90	S	115.40	115.73	121.41	172.60	173.09	181.61	344.19	345.18	362.20	3
14	726.32	726.65	732.32	1088.98	1089.47	1097.98	2176.94	2177.93	2194.95	Q	86.39	86.72	92.40	129.08	129.58	138.09	257.16	258.15	275.17	2
15	-	-	-	-	-	-	-	-	-	K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	b ⁺⁺³	seq	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	y ⁺⁺³	#
1	-	-	55.36	-	-	82.54	-	-	164.07	Y	-	-	-	-	-	-	-	-	-	6
2	-	-	87.71	-	-	131.07	-	-	261.12	P	720.67	721.00	726.67	1080.50	1080.99	1089.50	2159.99	2160.97	2178.00	5
3	-	120.05	125.73	-	179.57	188.09	-	358.14	375.17	N	688.32	688.64	694.32	1031.97	1032.46	1040.98	2062.93	2063.92	2080.94	4
4	-	691.31	696.99	-	1036.46	1044.98	-	2071.92	2088.95	C	650.30	650.63	656.31	974.95	975.44	983.95	1948.89	1949.87	1966.90	3
5	-	714.99	720.67	-	1071.98	1080.50	-	2142.96	2159.99	A	79.04	-	85.04	118.06	-	127.06	235.11	-	253.12	2
6	-	-	-	-	-	-	-	-	-	Y	55.36	-	61.37	82.54	-	91.54	164.07	-	182.08	1

Scan#	Charge	Score	pp	pp2	Peptide
2118	3	45	13.7	19.3	[47-61]-s-s-[92-97]



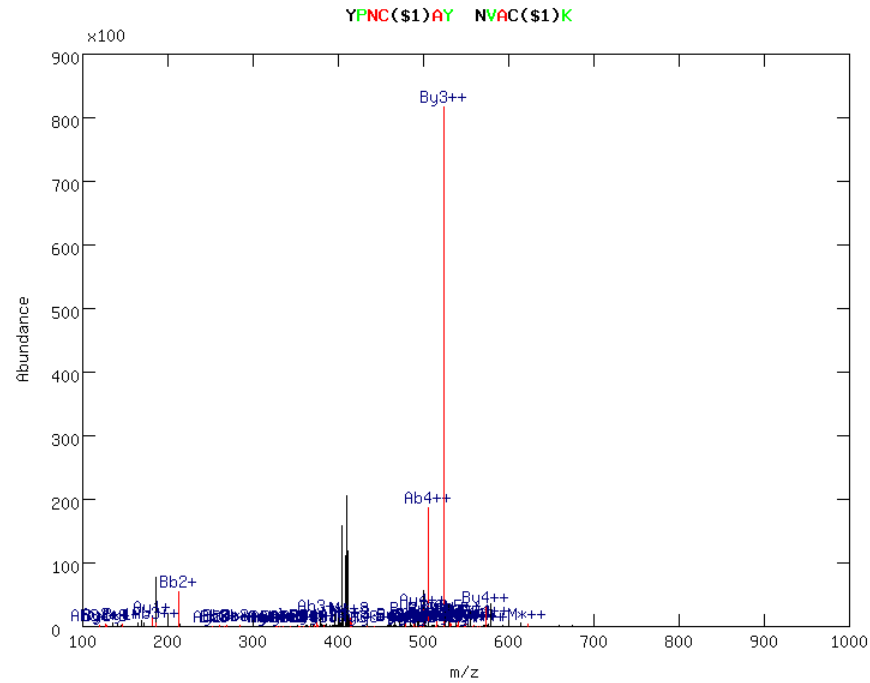
chainA :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	35.52	—	44.52	70.03	—	88.04	S	604.28	604.77	613.29	1207.56	1208.54	1225.57	6
2	92.06	—	101.07	183.11	—	201.12	I	560.77	561.26	569.77	1120.52	1121.51	1138.53	5
3	142.58	—	151.59	284.16	—	302.17	T	504.22	504.72	513.23	1007.44	1008.42	1025.45	4
4	200.10	—	209.10	399.19	—	417.20	D	453.70	454.19	462.71	906.39	907.38	924.40	3
5	517.23	517.72	526.23	1033.44	1034.43	1051.46	C	396.19	396.68	405.19	791.37	792.35	809.38	2
6	—	—	—	—	—	—	R	79.06	79.55	88.06	157.11	158.09	175.12	1

chainB :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	—	49.52	58.03	—	98.02	115.05	N	—	—	—	—	—	—	5
2	—	99.05	107.56	—	197.09	214.12	V	547.26	547.75	556.27	1093.51	1094.50	1111.52	4
3	—	134.57	143.08	—	268.13	285.16	A	497.73	498.22	506.73	994.45	995.43	1012.46	3
4	—	531.72	540.23	—	1062.43	1079.46	C	462.21	462.70	471.21	923.41	924.39	941.42	2
5	—	—	—	—	—	—	K	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1218	2	51	16.7	37.9	[62-66]-s-s-[80-85]



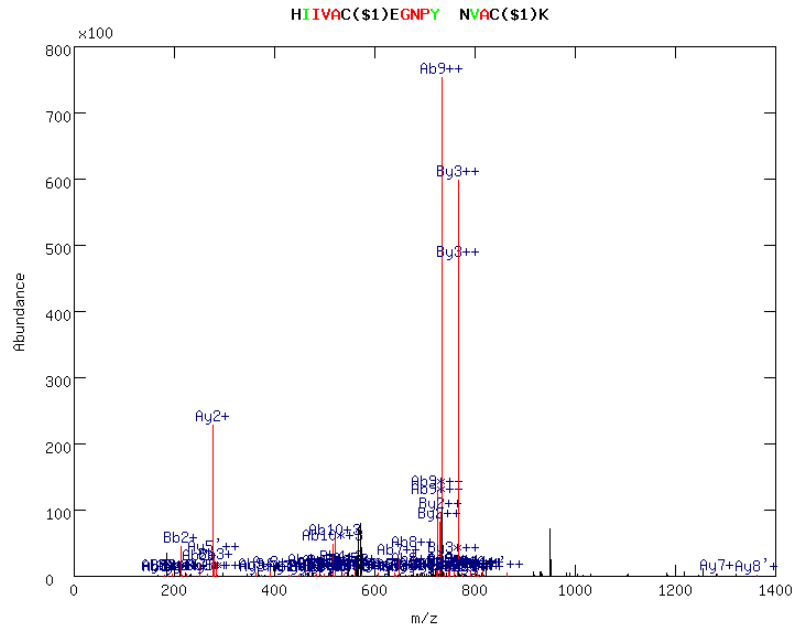
chainA :

#	b ⁺⁺³	b ⁺³	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	—	—	55.36	—	—	82.54	—	—	164.07	Y	415.18	415.51	421.18	622.27	622.76	631.27	1243.52	1244.51	1261.53	6
2	—	—	87.71	—	—	131.07	—	—	261.12	P	360.83	361.15	366.83	540.73	541.23	549.74	1080.46	1081.44	1098.47	5
3	—	120.05	125.73	—	179.57	188.09	—	358.14	375.17	N	328.47	328.80	334.48	492.21	492.70	501.21	983.41	984.39	1001.42	4
4	—	331.47	337.15	—	496.70	505.22	—	992.40	1009.42	C	290.46	290.79	296.46	435.19	435.68	444.19	869.36	870.35	887.38	3
5	—	355.15	360.83	—	532.22	540.73	—	1063.43	1080.46	A	79.04	—	85.04	118.06	—	127.06	235.11	—	253.12	2
6	—	—	—	—	—	—	—	—	—	Y	55.36	—	61.37	82.54	—	91.54	164.07	—	182.08	1

chainB :

#	b ⁺⁺³	b ⁺³	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	—	33.35	39.02	—	49.52	58.03	—	98.02	115.05	N	—	—	—	—	—	—	—	—	—	5
2	—	66.37	72.04	—	99.05	107.56	—	197.09	214.12	V	377.17	377.49	383.17	565.24	565.74	574.25	1129.48	1130.47	1147.49	4
3	—	90.05	95.72	—	134.57	143.08	—	268.13	285.16	A	344.14	344.47	350.15	515.71	516.20	524.72	1030.41	1031.40	1048.42	3
4	—	366.81	372.48	—	549.71	558.22	—	1098.40	1115.43	C	320.46	320.79	326.47	480.19	480.68	489.20	959.38	960.36	977.39	2
5	—	—	—	—	—	—	—	—	—	K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1667	3	11	13.7	2.6	[62-66]-s-s-[92-97]



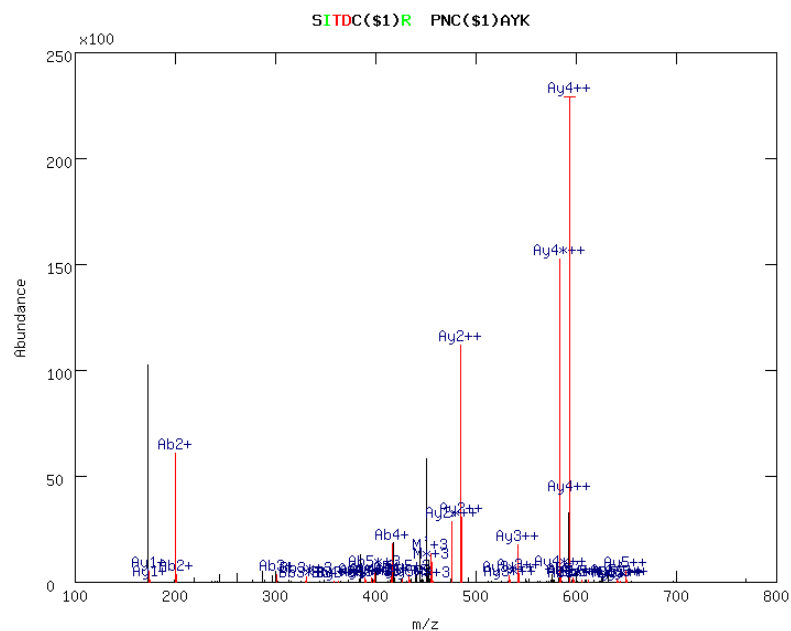
chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1			46.69			69.54			138.07	H	576.95	577.27	582.95	864.91	865.41	873.92	1728.82	1729.80	1746.83	11
2			84.39			126.08			251.15	I	531.26	531.59	537.26	796.38	796.88	805.39	1591.76	1592.75	1609.77	10
3			122.08			182.62			364.23	I	493.56	493.89	499.57	739.84	740.33	748.85	1478.68	1479.66	1496.69	9
4			155.11			232.16			463.30	V	455.87	456.20	461.87	683.30	683.79	692.31	1365.59	1366.58	1383.60	8
5			178.79			267.67			534.34	A	422.85	423.17	428.85	633.77	634.26	642.77	1266.52	1267.51	1284.54	7
6	384.20	384.53	390.20	575.80	576.29	584.80	1150.59	1151.57	1168.60	C	399.17	399.50	405.17	598.25	598.74	607.25	1195.49	1196.47	1213.50	6
7	427.21	427.54	433.22	640.32	640.81	649.32	1279.63	1280.61	1297.64	E	187.75	188.08	193.75	281.12	281.61	290.12	561.23	562.21	579.24	5
8	446.22	446.55	452.23	668.83	669.32	677.83	1336.65	1337.63	1354.66	G	144.73	145.06	150.74	216.60	217.09	225.60	432.19	433.17	450.20	4
9	484.24	484.56	490.24	725.85	726.34	734.86	1450.69	1451.68	1468.70	N	125.73	126.06	131.73	188.09	188.58	197.09	375.17	376.15	393.18	3
10	516.59	516.92	522.59	774.38	774.87	783.38	1547.75	1548.73	1565.76	P	87.71		93.72	131.07		140.07	261.12		279.13	2
11										Y	55.36		61.37	82.54		91.54	164.07		182.08	1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1		33.35	39.02		49.52	58.03		98.02	115.05	N										5
2		66.37	72.04		99.05	107.56		197.09	214.12	V	538.93	539.26	544.93	807.89	808.38	816.90	1614.78	1615.76	1632.79	4
3		90.05	95.72		134.57	143.08		268.13	285.16	A	505.91	506.24	511.91	758.36	758.85	767.36	1515.71	1516.69	1533.72	3
4		528.57	534.25		792.35	800.87		1583.70	1600.73	C	482.23	482.56	488.23	722.84	723.33	731.85	1444.67	1445.66	1462.68	2
5										K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1910	3	53	11	17.1	[62-66]-s-s-[105-115]



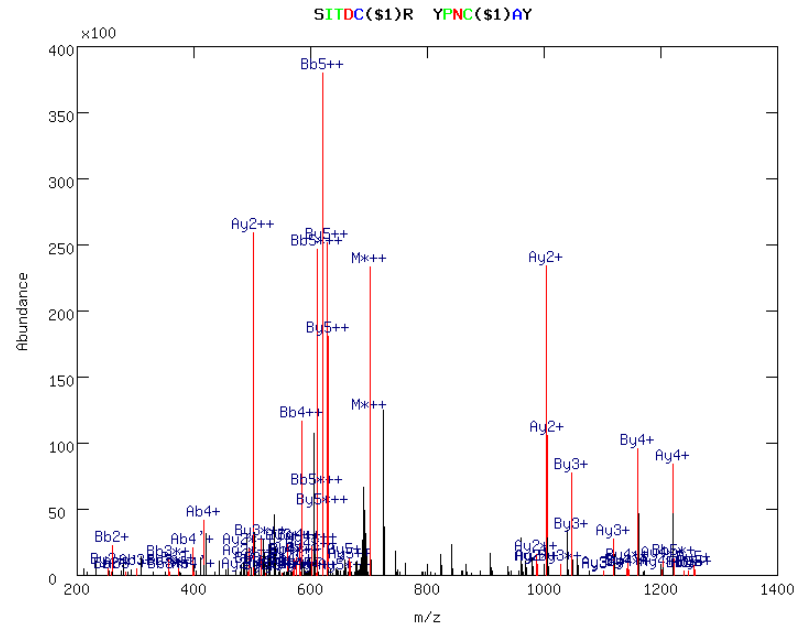
chainA :

#	b ⁺⁺³	b ⁺⁺⁺³	b ⁺³	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺⁺³	y ⁺³	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#	
1	24.01	—	30.02	35.52	—	44.52	70.03	—	88.04	S	456.87	457.20	462.88	684.81	685.30	693.81	1368.60	1369.59	1386.61	6
2	61.71	—	67.71	92.06	—	101.07	183.11	—	201.12	I	427.86	428.19	433.87	641.29	641.78	650.30	1281.57	1282.56	1299.58	5
3	95.39	—	101.40	142.58	—	151.59	284.16	—	302.17	T	390.17	390.50	396.17	584.75	585.24	593.75	1168.49	1169.47	1186.50	4
4	133.73	—	139.74	200.10	—	209.10	399.19	—	417.20	D	356.49	356.81	362.49	534.22	534.72	543.23	1067.44	1068.42	1085.45	3
5	398.84	399.16	404.84	597.75	598.24	606.76	1194.49	1195.48	1212.50	C	318.14	318.47	324.15	476.71	477.20	485.72	952.41	953.40	970.42	2
6	—	—	—	—	—	—	—	—	—	R	53.04	53.37	59.05	79.06	79.55	88.06	157.11	158.09	175.12	1

chainB :

#	b ⁺⁺³	b ⁺⁺⁺³	b ⁺³	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺⁺³	y ⁺³	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#	
1	—	—	33.36	—	—	49.53	—	—	98.06	P	—	—	—	—	—	—	—	—	6	
2	—	65.70	71.37	—	98.04	106.56	—	195.08	212.10	N	424.52	424.85	430.53	636.28	636.77	645.28	1271.55	1272.54	1289.56	5
3	—	330.47	336.14	—	495.19	503.71	—	989.38	1006.41	C	386.51	386.84	392.51	579.26	579.75	588.26	1157.51	1158.49	1175.52	4
4	—	354.14	359.82	—	530.71	539.23	—	1060.42	1077.45	A	121.74	122.07	127.74	182.11	182.60	191.11	363.20	364.19	381.21	3
5	—	408.50	414.17	—	612.25	620.76	—	1223.48	1240.51	Y	98.06	98.39	104.06	146.59	147.08	155.59	292.17	293.15	310.18	2
6	—	—	—	—	—	—	—	—	—	K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
1669	3	24	9	6.8	[80-85]-s-s-[93-98]



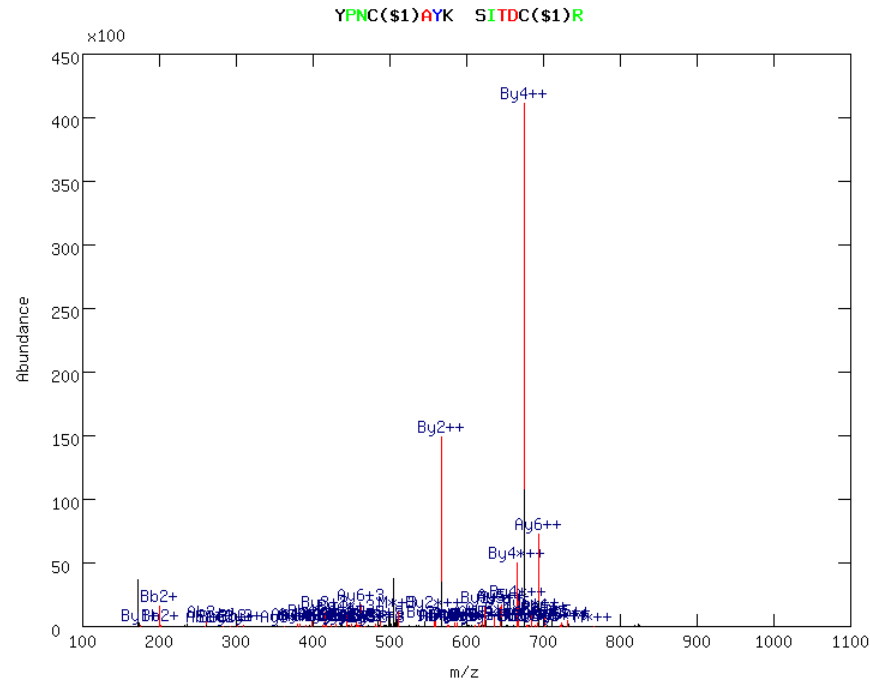
chainA :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	35.52	—	44.52	70.03	—	88.04	S	702.29	702.78	711.30	1403.57	1404.56	1421.58	6
2	92.06	—	101.07	183.11	—	201.12	I	658.77	659.27	667.78	1316.54	1317.52	1334.55	5
3	142.58	—	151.59	284.16	—	302.17	T	602.23	602.72	611.24	1203.46	1204.44	1221.47	4
4	200.10	—	209.10	399.19	—	417.20	D	551.71	552.20	560.71	1102.41	1103.39	1120.42	3
5	615.23	615.73	624.24	1229.46	1230.44	1247.47	C	494.19	494.69	503.20	987.38	988.37	1005.39	2
6	—	—	—	—	—	—	R	79.06	79.55	88.06	157.11	158.09	175.12	1

chainB :

#	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	—	—	82.54	—	—	164.07	Y	—	—	—	—	—	—	6
2	—	—	131.07	—	—	261.12	P	620.76	621.25	629.76	1240.51	1241.49	1258.52	5
3	—	179.57	188.09	—	358.14	375.17	N	572.23	572.72	581.24	1143.46	1144.44	1161.47	4
4	—	576.73	585.24	—	1152.45	1169.47	C	515.21	515.70	524.22	1029.41	1030.40	1047.42	3
5	—	612.25	620.76	—	1223.48	1240.51	A	118.06	—	127.06	235.11	—	253.12	2
6	—	—	—	—	—	—	Y	82.54	—	91.54	164.07	—	182.08	1

Scan#	Charge	Score	pp	pp2	Peptide
1900	2	80	15.9	41.9	[80-85]-s-s-[92-97]



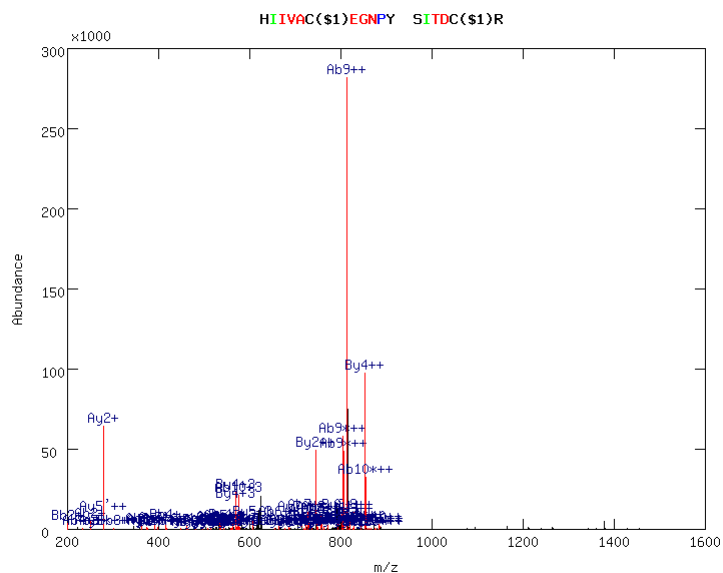
chainA :

#	b ⁺⁺³	b ⁺⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	-	-	55.36	-	-	82.54	-	-	164.07	Y	511.23	511.56	517.23	766.34	766.83	775.34	1531.67	1532.65	1549.68	7
2	-	-	87.71	-	-	131.07	-	-	261.12	P	456.87	457.20	462.88	684.81	685.30	693.81	1368.60	1369.59	1386.61	6
3	-	120.05	125.73	-	179.57	188.09	-	358.14	375.17	N	424.52	424.85	430.53	636.28	636.77	645.28	1271.55	1272.54	1289.56	5
4	-	384.82	390.50	-	576.73	585.24	-	1152.45	1169.47	C	386.51	386.84	392.51	579.26	579.75	588.26	1157.51	1158.49	1175.52	4
5	-	408.50	414.17	-	612.25	620.76	-	1223.48	1240.51	A	121.74	122.07	127.74	182.11	182.60	191.11	363.20	364.19	381.21	3
6	-	462.85	468.53	-	693.78	702.29	-	1386.55	1403.57	Y	98.06	98.39	104.06	146.59	147.08	155.59	292.17	293.15	310.18	2
7	-	-	-	-	-	-	-	-	-	K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

chainB :

#	b ⁺⁺³	b ⁺⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺	y ⁺⁺	y ⁺	#
1	24.01	-	30.02	35.52	-	44.52	70.03	-	88.04	S	-	-	-	-	-	-	-	-	-	6
2	61.71	-	67.71	92.06	-	101.07	183.11	-	201.12	I	482.22	482.54	488.22	722.82	723.31	731.83	1444.64	1445.62	1462.65	5
3	95.39	-	101.40	142.58	-	151.59	284.16	-	302.17	T	444.52	444.85	450.53	666.28	666.77	675.28	1331.55	1332.54	1349.56	4
4	133.73	-	139.74	200.10	-	209.10	399.19	-	417.20	D	410.84	411.17	416.84	615.76	616.25	624.76	1230.50	1231.49	1248.51	3
5	453.19	453.52	459.19	679.28	679.77	688.29	1357.56	1358.54	1375.57	C	372.50	372.83	378.50	558.24	558.73	567.25	1115.48	1116.46	1133.49	2
6	-	-	-	-	-	-	-	-	-	R	53.04	53.37	59.05	79.06	79.55	88.06	157.11	158.09	175.12	1

Scan#	Charge	Score	pp	pp2	Peptide
1692	3	29	16.4	8	[80-85]-s-s-[92-98]



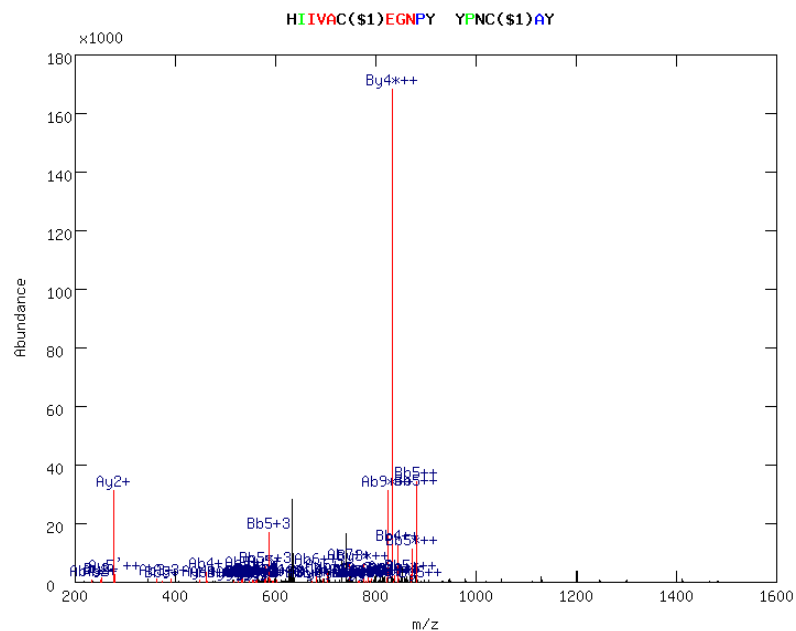
chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1			46.69			69.54			138.07	H	630.29	630.62	636.30	944.94	945.43	953.94	1888.87	1889.85	1906.88	11
2			84.39			126.08			251.15	I	584.61	584.94	590.61	876.41	876.90	885.41	1751.81	1752.79	1769.82	10
3			122.08			182.62			364.23	I	546.91	547.24	552.92	819.87	820.36	828.87	1638.73	1639.71	1656.74	9
4			155.11			232.16			463.30	V	509.22	509.55	515.22	763.32	763.82	772.33	1525.64	1526.63	1543.65	8
5			178.79			267.67			534.34	A	476.20	476.52	482.20	713.79	714.28	722.80	1426.57	1427.56	1444.58	7
6	437.55	437.88	443.55	655.82	656.31	664.83	1310.63	1311.62	1328.65	C	452.52	452.85	458.52	678.27	678.76	687.28	1355.54	1356.52	1373.55	6
7	480.56	480.89	486.57	720.34	720.83	729.35	1439.68	1440.66	1457.69	E	187.75	188.08	193.75	281.12	281.61	290.12	561.23	562.21	579.24	5
8	499.57	499.90	505.58	748.85	749.35	757.86	1496.70	1497.68	1514.71	G	144.73	145.06	150.74	216.60	217.09	225.60	432.19	433.17	450.20	4
9	537.59	537.91	543.59	805.87	806.37	814.88	1610.74	1611.73	1628.75	N	125.73	126.06	131.73	188.09	188.58	197.09	375.17	376.15	393.18	3
10	569.94	570.26	575.94	854.40	854.89	863.41	1707.79	1708.78	1725.81	P	87.71		93.72	131.07		140.07	261.12		279.13	2
11										Y	55.36		61.37	82.54		91.54	164.07		182.08	1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	24.01		30.02	35.52		44.52	70.03		88.04	S										6
2	61.71		67.71	92.06		101.07	183.11		201.12	I	601.28	601.61	607.29	901.42	901.91	910.43	1801.84	1802.82	1819.85	5
3	95.39		101.40	142.58		151.59	284.16		302.17	T	563.59	563.92	569.59	844.88	845.37	853.89	1688.75	1689.74	1706.76	4
4	133.73		139.74	200.10		209.10	399.19		417.20	D	529.91	530.23	535.91	794.36	794.85	803.36	1587.70	1588.69	1605.72	3
5	572.26	572.59	578.26	857.88	858.37	866.89	1714.76	1715.74	1732.77	C	491.56	491.89	497.57	736.84	737.33	745.85	1472.68	1473.66	1490.69	2
6										R	53.04	53.37	59.05	79.06	79.55	88.06	157.11	158.09	175.12	1

Scan#	Charge	Score	pp	pp2	Peptide
2060	3	42	11.4	16	[80-85]-s-s-[105-115]



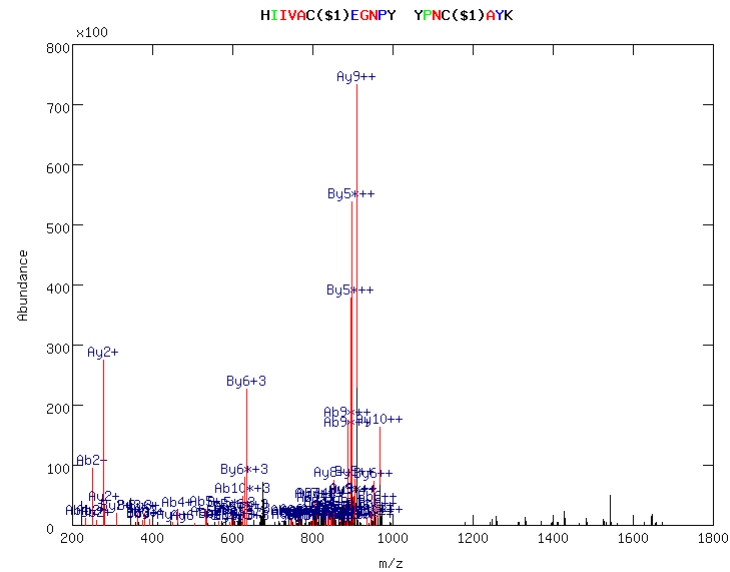
chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	-	-	46.69	-	-	69.54	-	-	138.07	H	642.28	642.61	648.29	962.92	963.41	971.93	1924.84	1925.82	1942.85	11
2	-	-	84.39	-	-	126.08	-	-	251.15	I	596.60	596.93	602.60	894.39	894.88	903.40	1787.78	1788.76	1805.79	10
3	-	-	122.08	-	-	182.62	-	-	364.23	I	558.90	559.23	564.91	837.85	838.34	846.86	1674.69	1675.68	1692.70	9
4	-	-	155.11	-	-	232.16	-	-	463.30	V	521.21	521.54	527.21	781.31	781.80	790.31	1561.61	1562.59	1579.62	8
5	-	-	178.79	-	-	267.67	-	-	534.34	A	488.19	488.51	494.19	731.77	732.27	740.78	1462.54	1463.52	1480.55	7
6	449.54	449.87	455.54	673.81	674.30	682.81	1346.60	1347.59	1364.61	C	464.51	464.83	470.51	696.26	696.75	705.26	1391.50	1392.49	1409.51	6
7	492.55	492.88	498.56	738.33	738.82	747.33	1475.65	1476.63	1493.66	E	187.75	188.08	193.75	281.12	281.61	290.12	561.23	562.21	579.24	5
8	511.56	511.89	517.56	766.84	767.33	775.84	1532.67	1533.65	1550.68	G	144.73	145.06	150.74	216.60	217.09	225.60	432.19	433.17	450.20	4
9	549.58	549.90	555.58	823.86	824.35	832.86	1646.71	1647.69	1664.72	N	125.73	126.06	131.73	188.09	188.58	197.09	375.17	376.15	393.18	3
10	581.93	582.25	587.93	872.39	872.88	881.39	1743.76	1744.75	1761.77	P	87.71	-	93.72	131.07	-	140.07	261.12	-	279.13	2
11	-	-	-	-	-	-	-	-	-	Y	55.36	-	61.37	82.54	-	91.54	164.07	-	182.08	1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺⁺	b ⁺⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺⁺	y ⁺⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1	-	-	55.36	-	-	82.54	-	-	164.07	Y	-	-	-	-	-	-	-	-	-	6
2	-	-	87.71	-	-	131.07	-	-	261.12	P	587.93	588.26	593.93	881.39	881.88	890.40	1761.77	1762.76	1779.78	5
3	-	120.05	125.73	-	179.57	188.09	-	358.14	375.17	N	555.58	555.91	561.58	832.86	833.36	841.87	1664.72	1665.70	1682.73	4
4	-	558.57	564.25	-	837.36	845.87	-	1673.71	1690.74	C	517.56	517.89	523.57	775.84	776.33	784.85	1550.68	1551.66	1568.69	3
5	-	582.25	587.93	-	872.88	881.39	-	1744.75	1761.77	A	79.04	-	85.04	118.06	-	127.06	235.11	-	253.12	2
6	-	-	-	-	-	-	-	-	-	Y	55.36	-	61.37	82.54	-	91.54	164.07	-	182.08	1

Scan#	Charge	Score	pp	pp2	Peptide
2159	3	22	2.9	6.7	[92-97]-s-s-[105-115]



chainA :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1			46.69			69.54			138.07	H	684.98	685.31	690.99	1026.97	1027.46	1035.97	2052.93	2053.92	2070.94	11
2			84.39			126.08			251.15	I	639.30	639.62	645.30	958.44	958.93	967.45	1915.87	1916.86	1933.88	10
3			122.08			182.62			364.23	I	601.60	601.93	607.60	901.90	902.39	910.90	1802.79	1803.77	1820.80	9
4			155.11			232.16			463.30	V	563.91	564.23	569.91	845.36	845.85	854.36	1689.70	1690.69	1707.71	8
5			178.79			267.67			534.34	A	530.88	531.21	536.89	795.82	796.31	804.83	1590.64	1591.62	1608.65	7
6	492.24	492.57	498.24	737.85	738.34	746.86	1474.70	1475.68	1492.71	C	507.20	507.53	513.21	760.30	760.80	769.31	1519.60	1520.58	1537.61	6
7	535.25	535.58	541.26	802.37	802.87	811.38	1603.74	1604.72	1621.75	E	187.75	188.08	193.75	281.12	281.61	290.12	561.23	562.21	579.24	5
8	554.26	554.59	560.26	830.88	831.38	839.89	1660.76	1661.75	1678.77	G	144.73	145.06	150.74	216.60	217.09	225.60	432.19	433.17	450.20	4
9	592.27	592.60	598.28	887.91	888.40	896.91	1774.80	1775.79	1792.82	N	125.73	126.06	131.73	188.09	188.58	197.09	375.17	376.15	393.18	3
10	624.62	624.95	630.63	936.43	936.92	945.44	1871.86	1872.84	1889.87	P	87.71		93.72	131.07		140.07	261.12		279.13	2
11										Y	55.36		61.37	82.54		91.54	164.07		182.08	1

chainB :

#	b ⁺⁺³	b ⁺⁺³	b ⁺³	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺⁺	b ⁺	seq	y ⁺⁺³	y ⁺⁺³	y ⁺³	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺⁺	y ⁺	#
1			55.36			82.54			164.07	Y										7
2			87.71			131.07			261.12	P	630.63	630.96	636.63	945.44	945.93	954.44	1889.87	1890.85	1907.88	6
3		120.05	125.73		179.57	188.09		358.14	375.17	N	598.28	598.60	604.28	896.91	897.40	905.92	1792.82	1793.80	1810.83	5
4		558.57	564.25		837.36	845.87		1673.71	1690.74	C	560.26	560.59	566.27	839.89	840.38	848.90	1678.77	1679.76	1696.78	4
5		582.25	587.93		872.88	881.39		1744.75	1761.77	A	121.74	122.07	127.74	182.11	182.60	191.11	363.20	364.19	381.21	3
6		636.61	642.28		954.41	962.92		1907.81	1924.84	Y	98.06	98.39	104.06	146.59	147.08	155.59	292.17	293.15	310.18	2
7										K	43.71	44.03	49.71	65.06	65.55	74.06	129.10	130.09	147.11	1

Scan#	Charge	Score	pp	pp2	Peptide
2050	3	50	3.5	12.9	[92-98]-s-s-[105-115]