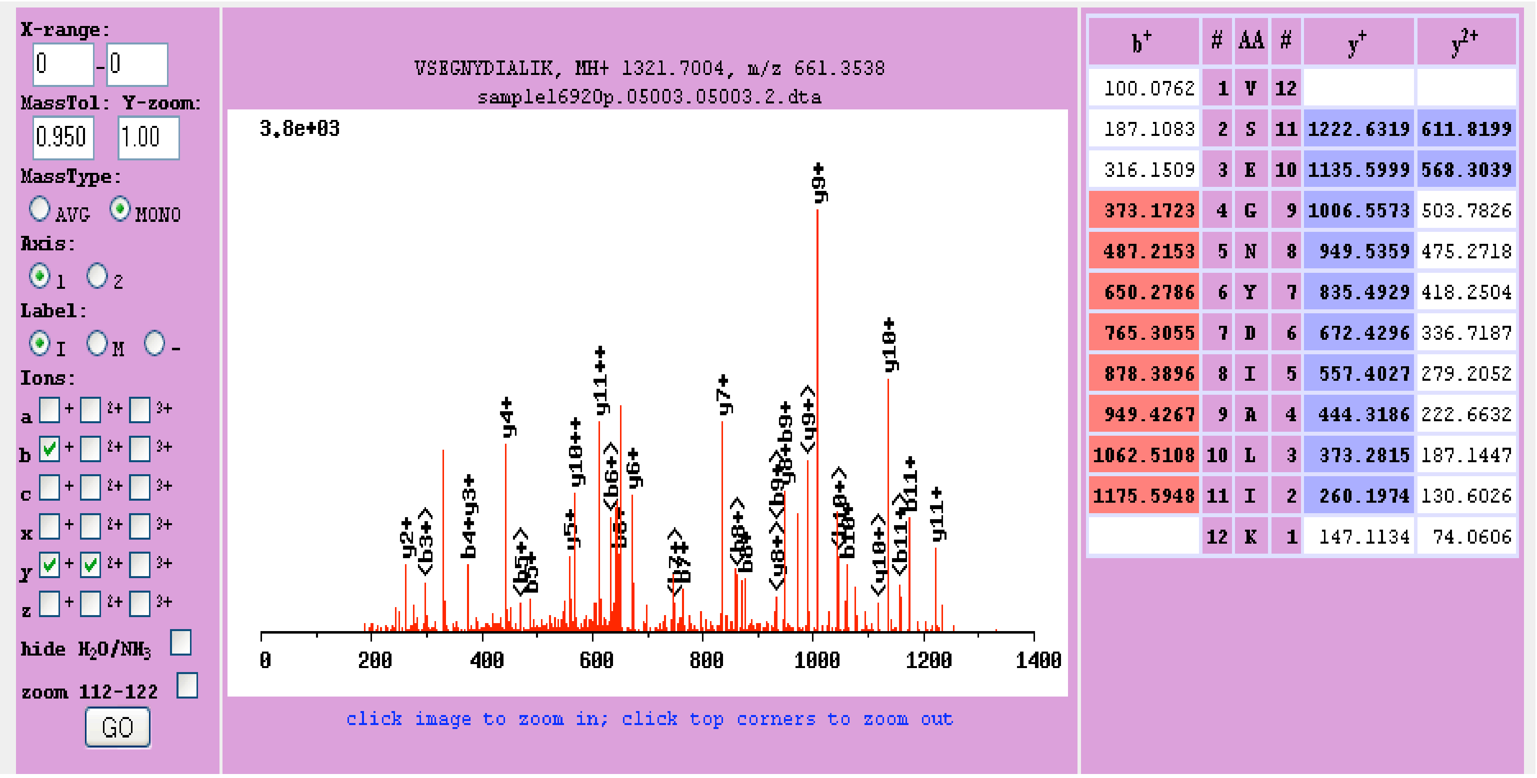
MS/MS data for couple of peptides detected for each proteins Identified in these samples



X-range: 0 - 0

MassTol: 0.950 Y-zoom: 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:
a ☐ + ☐ 2+ ☐ 3+
b ☑ + ☐ 2+ ☐ 3+
c ☐ + ☐ 2+ ☐ 3+
x ☐ + ☐ 2+ ☐ 3+
y ☑ + ☑ 2+ ☐ 3+
z ☐ + ☐ 2+ ☐ 3+

hide H_2O/NH_3 ☐

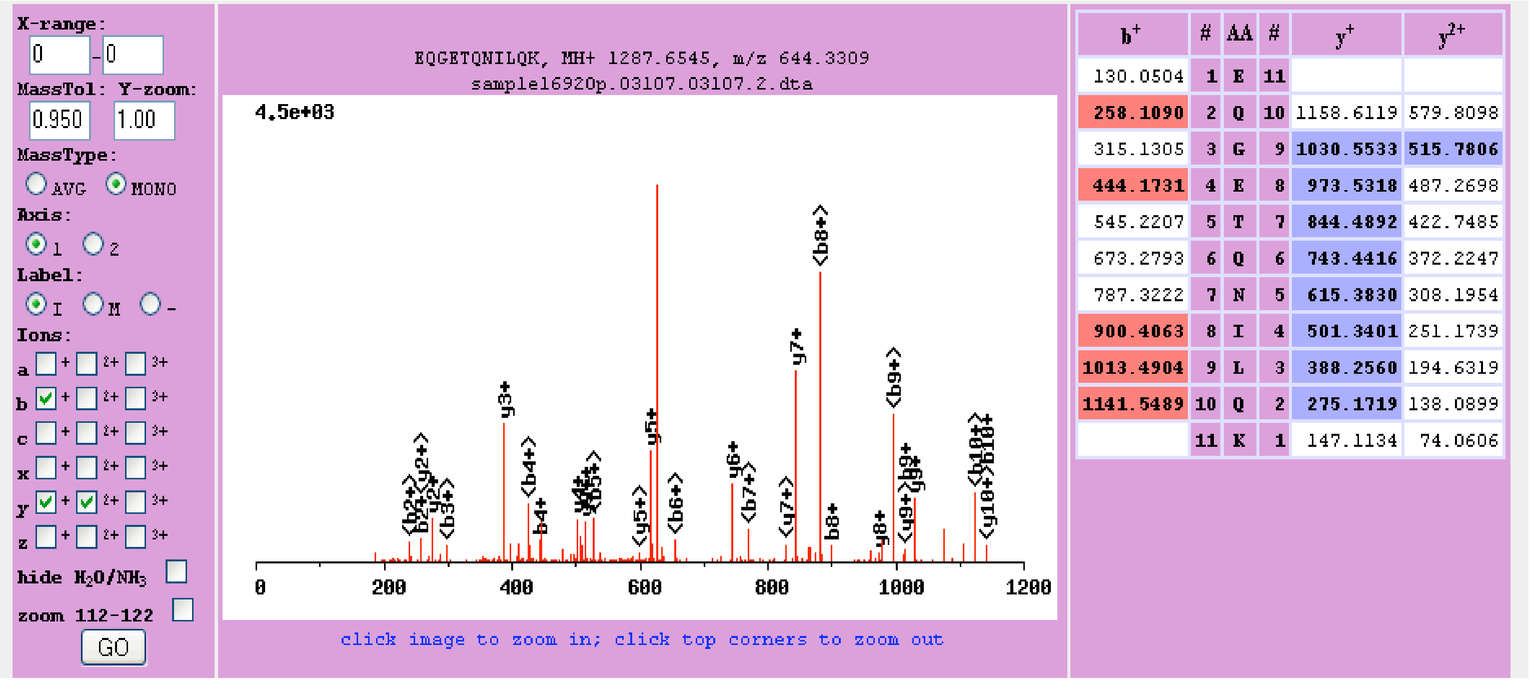
zoom 112-122 ☐

VSEGNYDIALIK, MH+ 1321.7004, m/z 661.3538
sample16920p.05003.05003.2.dta

click image to zoom in; click top corners to zoom out

b^+	#	AA	#	y^+	y^{2+}
100.0762	1	V	12		
187.1083	2	S	11	**1222.6319**	**611.8199**
316.1509	3	E	10	**1135.5999**	**568.3039**
373.1723	4	G	9	**1006.5573**	503.7826
487.2153	5	N	8	**949.5359**	475.2718
650.2786	6	Y	7	**835.4929**	418.2504
765.3055	7	D	6	**672.4296**	336.7187
878.3896	8	I	5	**557.4027**	279.2052
949.4267	9	A	4	**444.3186**	222.6632
1062.5108	10	L	3	**373.2815**	187.1447
1175.5948	11	I	2	**260.1974**	130.6026
	12	K	1	147.1134	74.0606

Protein: Plasma kallikrein precursor, Peptide: VSEGNYDIALIK, MH+ 1321.7004, m/z 661.3538,sample16920p.05003.05003.2.dta



X-range: 0 - 0

MassTol: 0.950 Y-zoom: 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:
a ☐ + ☐ 2+ ☐ 3+
b ☑ + ☐ 2+ ☐ 3+
c ☐ + ☐ 2+ ☐ 3+
x ☐ + ☐ 2+ ☐ 3+
y ☑ + ☑ 2+ ☐ 3+
z ☐ + ☐ 2+ ☐ 3+

hide H_2O/NH_3 ☐

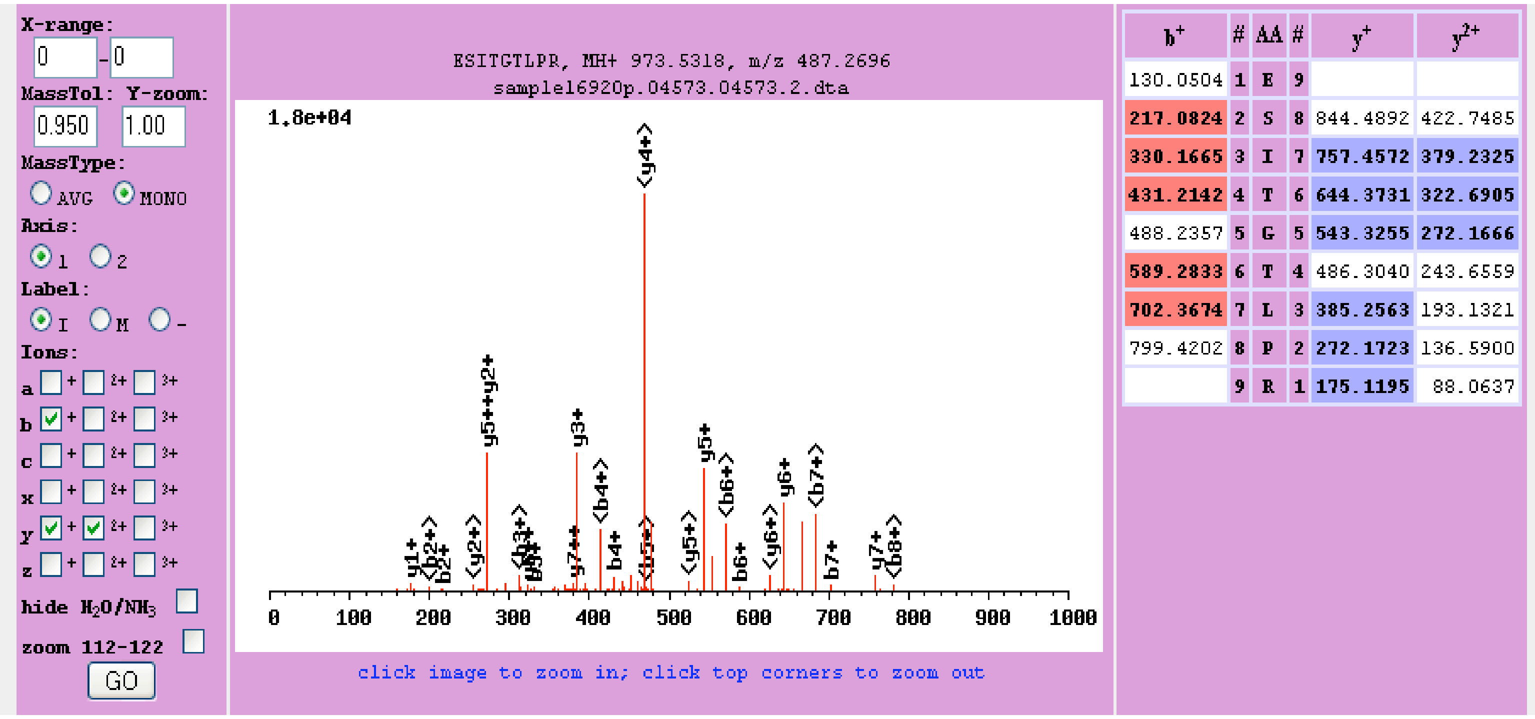
zoom 112-122 ☐

EQGETQNILQK, MH+ 1287.6545, m/z 644.3309
sample16920p.03107.03107.2.dta

click image to zoom in; click top corners to zoom out

b^+	#	AA	#	y^+	y^{2+}
130.0504	1	E	11		
258.1090	2	Q	10	1158.6119	579.8098
315.1305	3	G	9	**1030.5533**	**515.7806**
444.1731	4	E	8	**973.5318**	487.2698
545.2207	5	T	7	**844.4892**	422.7485
673.2793	6	Q	6	**743.4416**	372.2247
787.3222	7	N	5	**615.3830**	308.1954
900.4063	8	I	4	**501.3401**	251.1739
1013.4904	9	L	3	**388.2560**	194.6319
1141.5489	10	Q	2	**275.1719**	138.0899
	11	K	1	147.1134	74.0606

Protein: Plasma kallikrein precursor, Peptide: EQGETQNILQK, MH+ 1287.6545, m/z 644.3309, sample16920p.03107.03107.2.dta



X-range: 0 - 0

MassTol: 0.950 Y-zoom: 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:
a ☐ + ☐ 2+ ☐ 3+
b ☑ + ☐ 2+ ☐ 3+
c ☐ + ☐ 2+ ☐ 3+
x ☐ + ☐ 2+ ☐ 3+
y ☑ + ☑ 2+ ☐ 3+
z ☐ + ☐ 2+ ☐ 3+

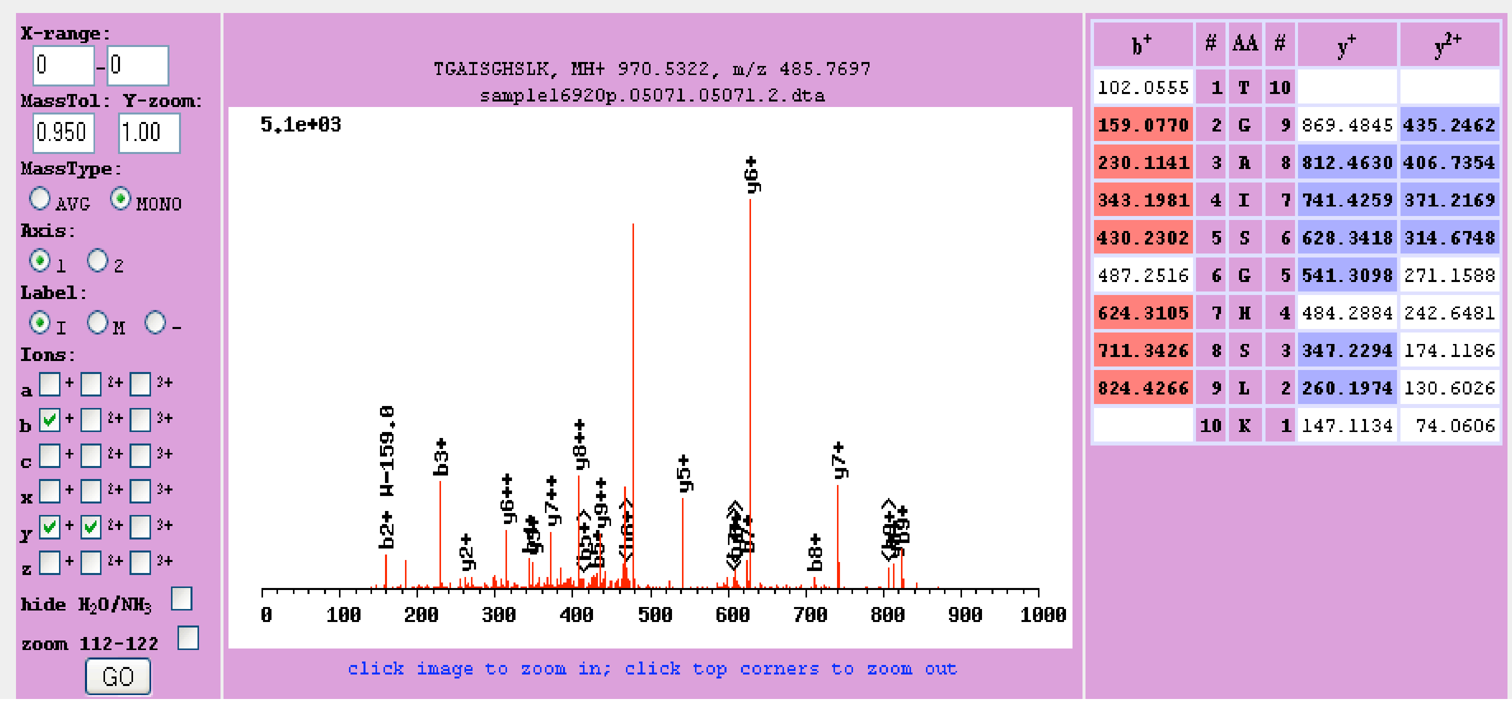
hide H_2O/NH_3 ☐

zoom 112-122 ☐

ESITGTLPR, MH+ 973.5318, m/z 487.2696
sample16920p.04573.04573.2.dta

b^+	#	AA	#	y^+	y^{2+}
130.0504	1	E	9		
217.0824	2	S	8	844.4892	422.7485
330.1665	3	I	7	757.4572	379.2325
431.2142	4	T	6	644.3731	322.6905
488.2357	5	G	5	543.3255	272.1666
589.2833	6	T	4	486.3040	243.6559
702.3674	7	L	3	385.2563	193.1321
799.4202	8	P	2	272.1723	136.5900
	9	R	1	175.1195	88.0637

Protein: Plasma kallikrein precursor, Peptide: ESITGTLPR, MH+ 973.5318,
m/z 487.2696,sample16920p.04573.04573.2.dta



X-range: 0 - 0

MassTol: 0.950 Y-zoom: 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:
a ☐ + ☐ 2+ ☐ 3+
b ☑ + ☐ 2+ ☐ 3+
c ☐ + ☐ 2+ ☐ 3+
x ☐ + ☐ 2+ ☐ 3+
y ☑ + ☑ 2+ ☐ 3+
z ☐ + ☐ 2+ ☐ 3+

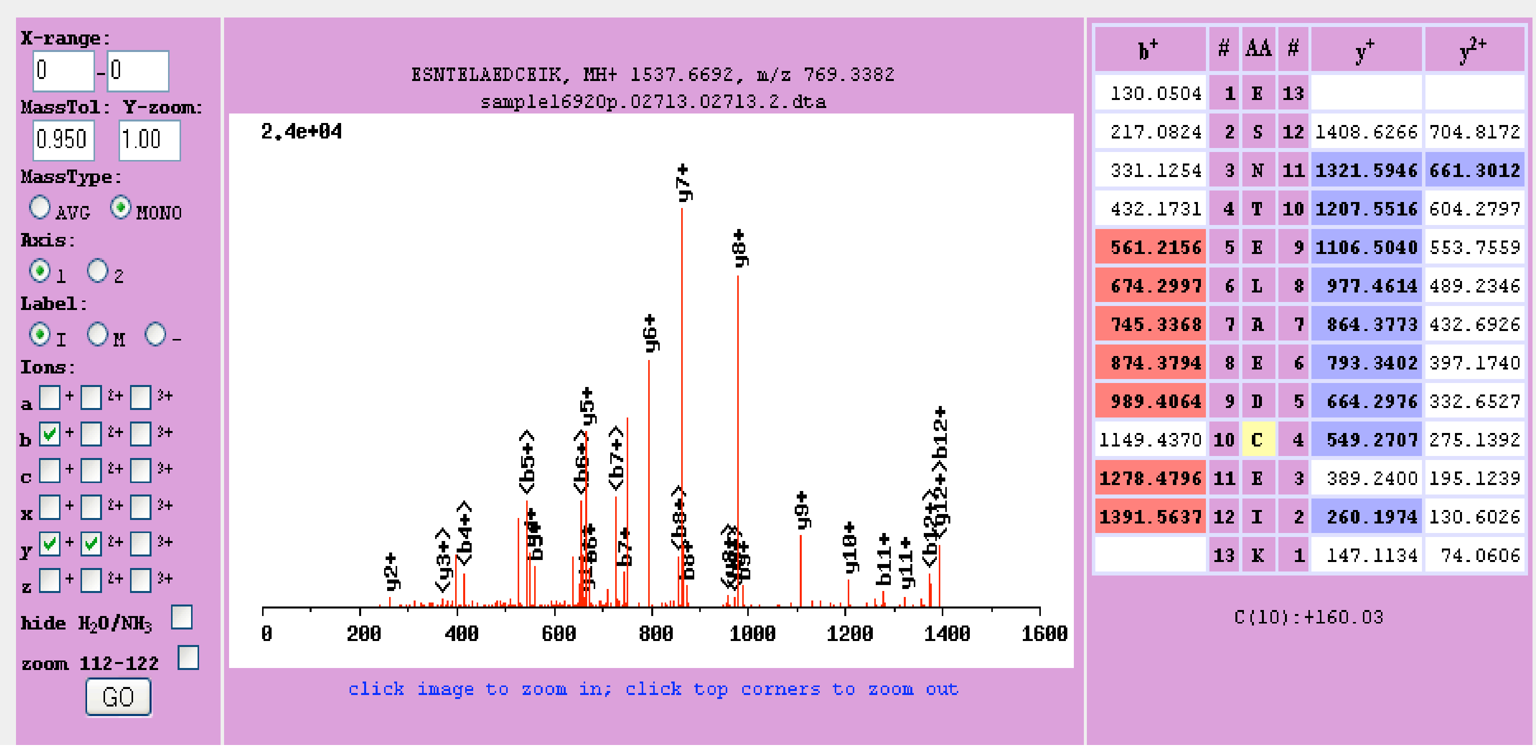
hide H_2O/NH_3 ☐

zoom 112-122 ☐

TGAISGHSLK, MH+ 970.5322, m/z 485.7697
sample16920p.05071.05071.2.dta

b^+	#	AA	#	y^+	y^{2+}
102.0555	1	T	10		
159.0770	2	G	9	869.4845	435.2462
230.1141	3	A	8	812.4630	406.7354
343.1981	4	I	7	741.4259	371.2169
430.2302	5	S	6	628.3418	314.6748
487.2516	6	G	5	541.3098	271.1588
624.3105	7	H	4	484.2884	242.6481
711.3426	8	S	3	347.2294	174.1186
824.4266	9	L	2	260.1974	130.6026
	10	K	1	147.1134	74.0606

Protein: Plasma kallikrein precursor, Peptide:TGAISGHSLK, MH+ 970.5322,
m/z 485.7697,sample16920p.05071.05071.2.dta



X-range: 0 - 0

MassTol: 0.950 Y-zoom: 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:

a ☐ + ☐ 2+ ☐ 3+

b ☑ + ☐ 2+ ☐ 3+

c ☐ + ☐ 2+ ☐ 3+

x ☐ + ☐ 2+ ☐ 3+

y ☑ + ☑ 2+ ☐ 3+

z ☐ + ☐ 2+ ☐ 3+

hide H_2O/NH_3 ☐

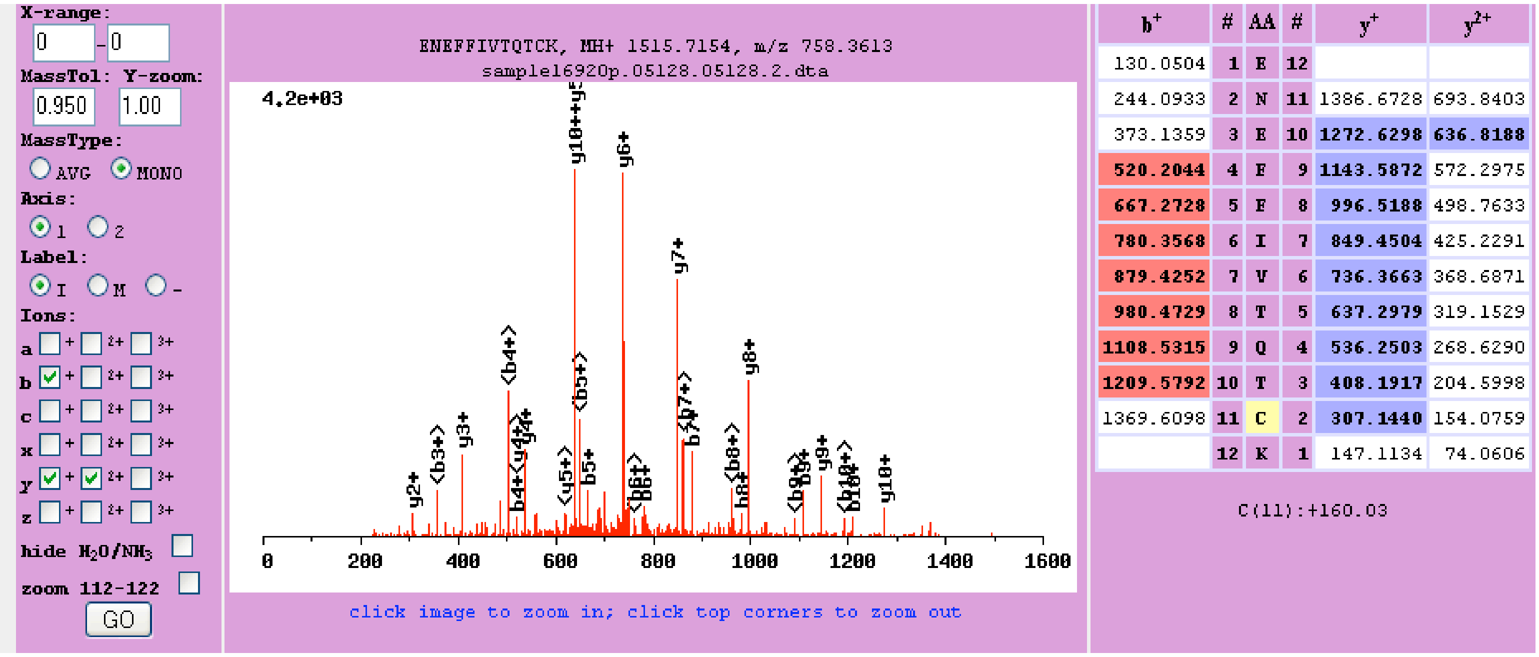
zoom 112-122 ☐

GO

b^{+}	#	AA	#	y^{+}	y^{2+}
130.0504	1	E	13		
217.0824	2	S	12	1408.6266	704.8172
331.1254	3	N	11	**1321.5946**	**661.3012**
432.1731	4	T	10	**1207.5516**	604.2797
561.2156	5	E	9	**1106.5040**	553.7559
674.2997	6	L	8	**977.4614**	489.2346
745.3368	7	A	7	**864.3773**	432.6926
874.3794	8	E	6	**793.3402**	397.1740
989.4064	9	D	5	**664.2976**	332.6527
1149.4370	10	C	4	**549.2707**	275.1392
1278.4796	11	E	3	389.2400	195.1239
1391.5637	12	I	2	**260.1974**	130.6026
	13	K	1	147.1134	74.0606

C(10):+160.03

Protein: HMW kininogen-I variant, Peptide: ESNTELAEDCEIK, MH+ 1537.6692, m/z 769.3382, sample16920p.02713.02713.2.dta



X-range: 0 - 0

MassTol: 0.950 Y-zoom: 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:

a ☐ + ☐ 2+ ☐ 3+

b ☑ + ☐ 2+ ☐ 3+

c ☐ + ☐ 2+ ☐ 3+

x ☐ + ☐ 2+ ☐ 3+

y ☑ + ☑ 2+ ☐ 3+

z ☐ + ☐ 2+ ☐ 3+

hide H_2O/NH_3 ☐

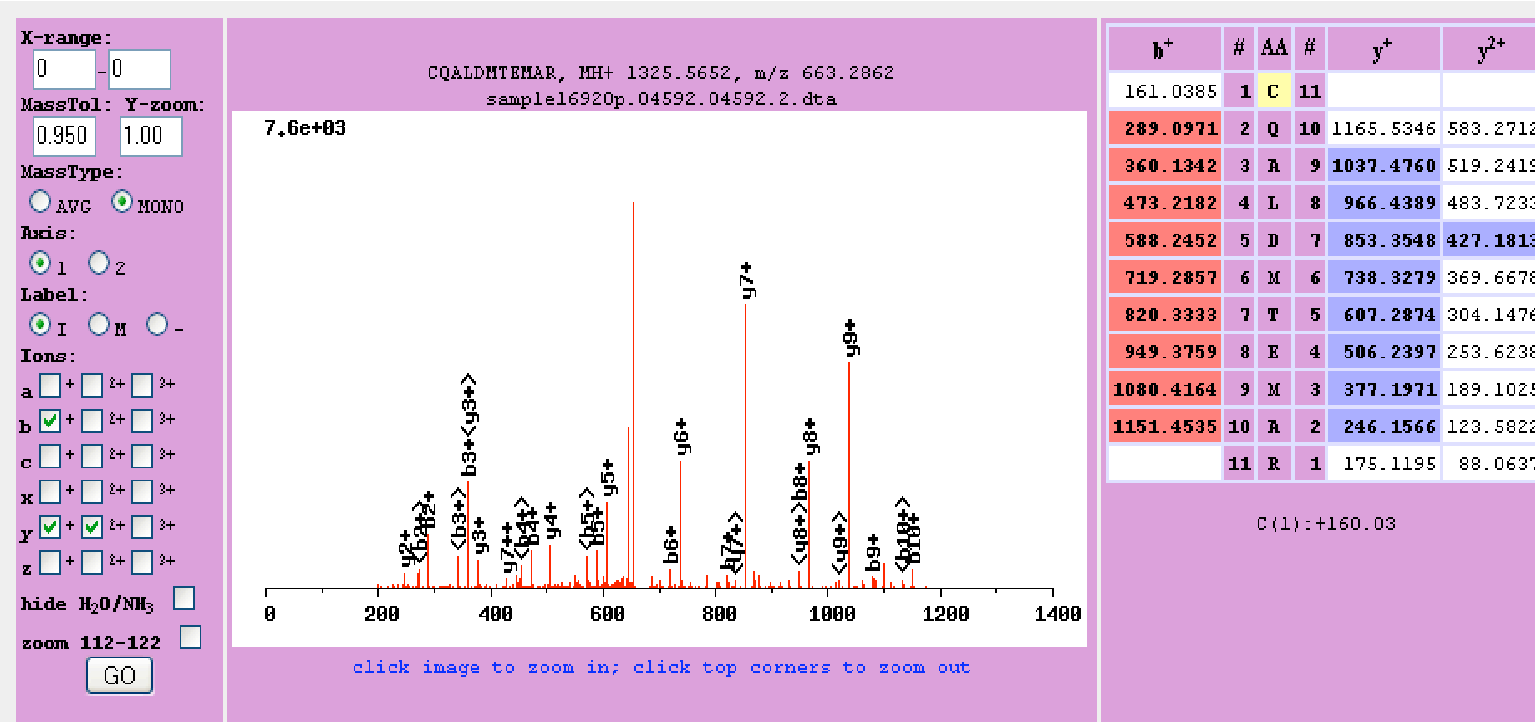
zoom 112-122 ☐

GO

b^{+}	#	AA	#	y^{+}	y^{2+}
130.0504	1	E	12		
244.0933	2	N	11	1386.6728	693.8403
373.1359	3	E	10	**1272.6298**	**636.8188**
520.2044	4	F	9	**1143.5872**	572.2975
667.2728	5	F	8	**996.5188**	498.7633
780.3568	6	I	7	**849.4504**	425.2291
879.4252	7	V	6	**736.3663**	368.6871
980.4729	8	T	5	**637.2979**	319.1529
1108.5315	9	Q	4	**536.2503**	268.6290
1209.5792	10	T	3	**408.1917**	204.5998
1369.6098	11	C	2	**307.1440**	154.0759
	12	K	1	147.1134	74.0606

C(11):+160.03

Protein: HMW kininogen-I variant, Peptide: ENEFFIVTQTCK, MH+ 1515.7154, m/z 758.3613,sample16920p.05128.05128.2.dta



X-range: 0 - 0

MassTol: 0.950 Y-zoom: 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:

a ☐ + ☐ 2+ ☐ 3+

b ☑ + ☐ 2+ ☐ 3+

c ☐ + ☐ 2+ ☐ 3+

x ☐ + ☐ 2+ ☐ 3+

y ☑ + ☑ 2+ ☐ 3+

z ☐ + ☐ 2+ ☐ 3+

hide H_2O/NH_3 ☐

zoom 112-122 ☐

GO

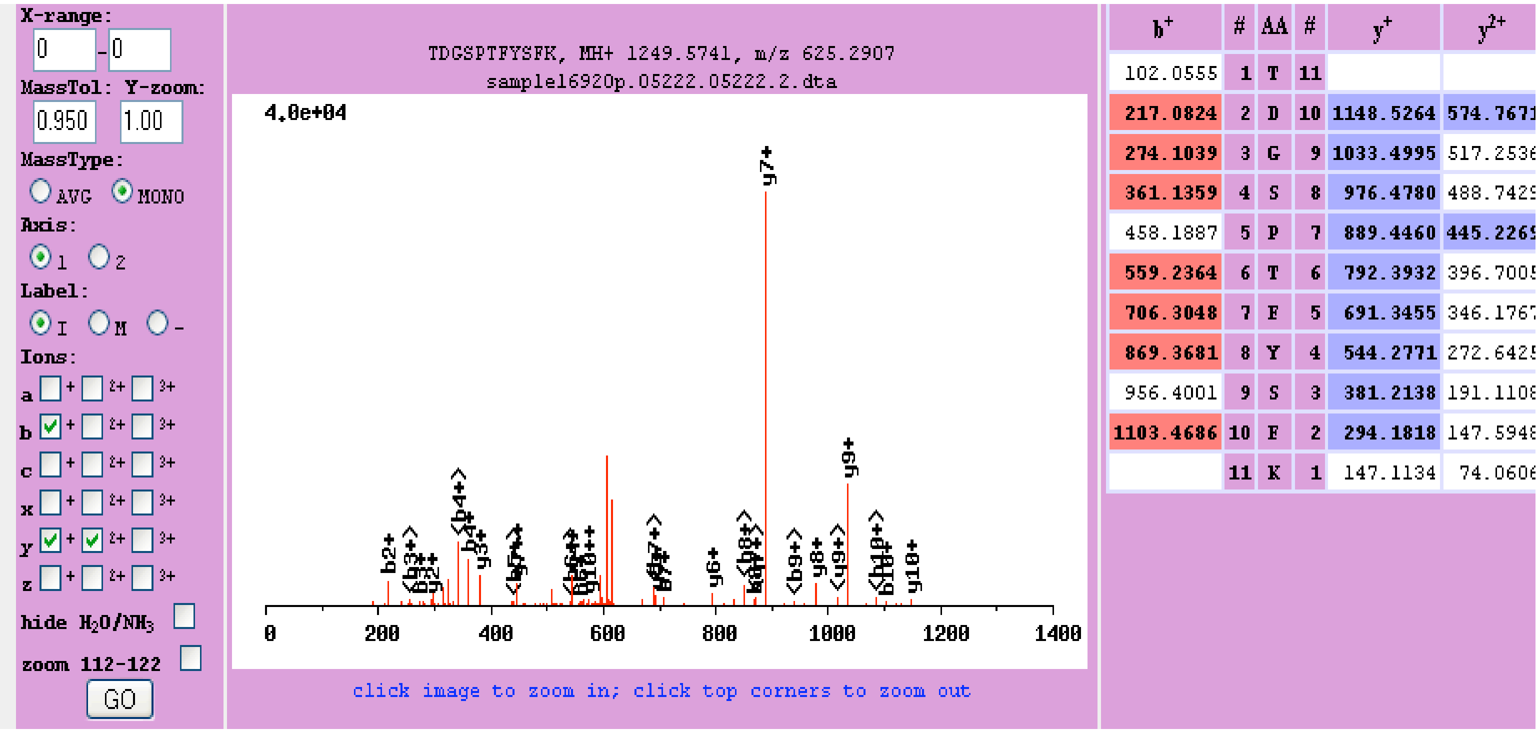
CQALDMTEMAR, MH+ 1325.5652, m/z 663.2862
sample16920p.04592.04592.2.dta

click image to zoom in; click top corners to zoom out

b^+	#	AA	#	y^+	y^{2+}
161.0385	1	C	11		
289.0971	2	Q	10	1165.5346	583.271
360.1342	3	A	9	**1037.4760**	519.241
473.2182	4	L	8	**966.4389**	483.723
588.2452	5	D	7	**853.3548**	**427.181**
719.2857	6	M	6	**738.3279**	369.667
820.3333	7	T	5	**607.2874**	304.147
949.3759	8	E	4	**506.2397**	253.623
1080.4164	9	M	3	**377.1971**	189.102
1151.4535	10	A	2	**246.1566**	123.582
	11	R	1	175.1195	88.063

C(1):+160.03

Protein: HMW kininogen-I variant, Peptide: CQALDMTEMAR, MH+ 1325.5652,
m/z 663.2862,sample16920p.04592.04592.2.dta



X-range: 0 - 0

MassTol: 0.950 Y-zoom: 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:

a ☐ + ☐ 2+ ☐ 3+

b ☑ + ☐ 2+ ☐ 3+

c ☐ + ☐ 2+ ☐ 3+

x ☐ + ☐ 2+ ☐ 3+

y ☑ + ☑ 2+ ☐ 3+

z ☐ + ☐ 2+ ☐ 3+

hide H_2O/NH_3 ☐

zoom 112-122 ☐

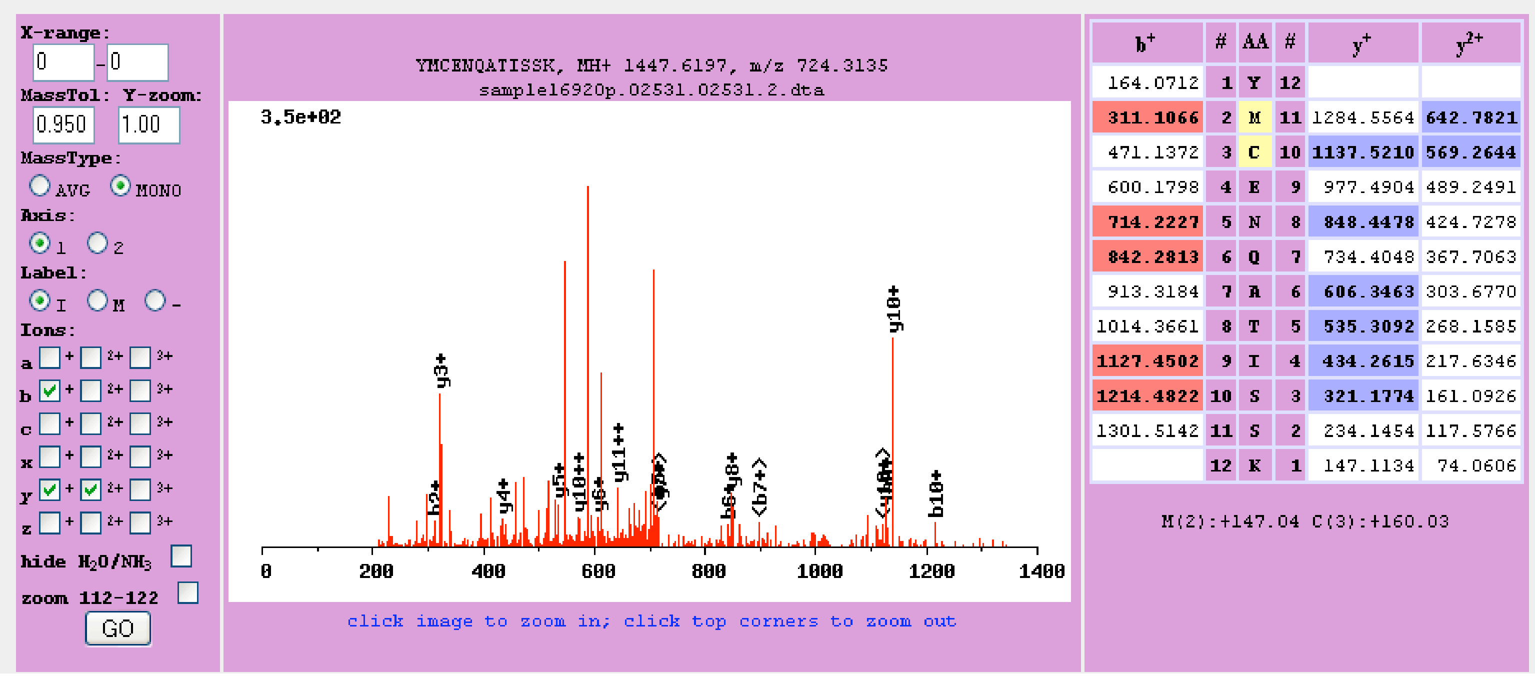
GO

TDGSPTFYSFK, MH+ 1249.5741, m/z 625.2907
sample16920p.05222.05222.2.dta

click image to zoom in; click top corners to zoom out

b^+	#	AA	#	y^+	y^{2+}
102.0555	1	T	11		
217.0824	2	D	10	**1148.5264**	**574.767**
274.1039	3	G	9	**1033.4995**	517.253
361.1359	4	S	8	**976.4780**	488.742
458.1887	5	P	7	**889.4460**	**445.226**
559.2364	6	T	6	**792.3932**	396.700
706.3048	7	F	5	**691.3455**	346.176
869.3681	8	Y	4	**544.2771**	272.642
956.4001	9	S	3	**381.2138**	191.110
1103.4686	10	F	2	**294.1818**	147.594
	11	K	1	147.1134	74.060

Protein: HMW kininogen-I variant, Peptide: TDGSPTFYSFK, MH+ 1249.5741,
m/z 625.2907,sample16920p.05222.05222.2.dta



X-range: 0 - 0

MassTol: 0.950 **Y-zoom:** 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:

a ☐ + ☐ 2+ ☐ 3+
b ☑ + ☐ 2+ ☐ 3+
c ☐ + ☐ 2+ ☐ 3+
x ☐ + ☐ 2+ ☐ 3+
y ☑ + ☑ 2+ ☐ 3+
z ☐ + ☐ 2+ ☐ 3+

hide H_2O/NH_3 ☐

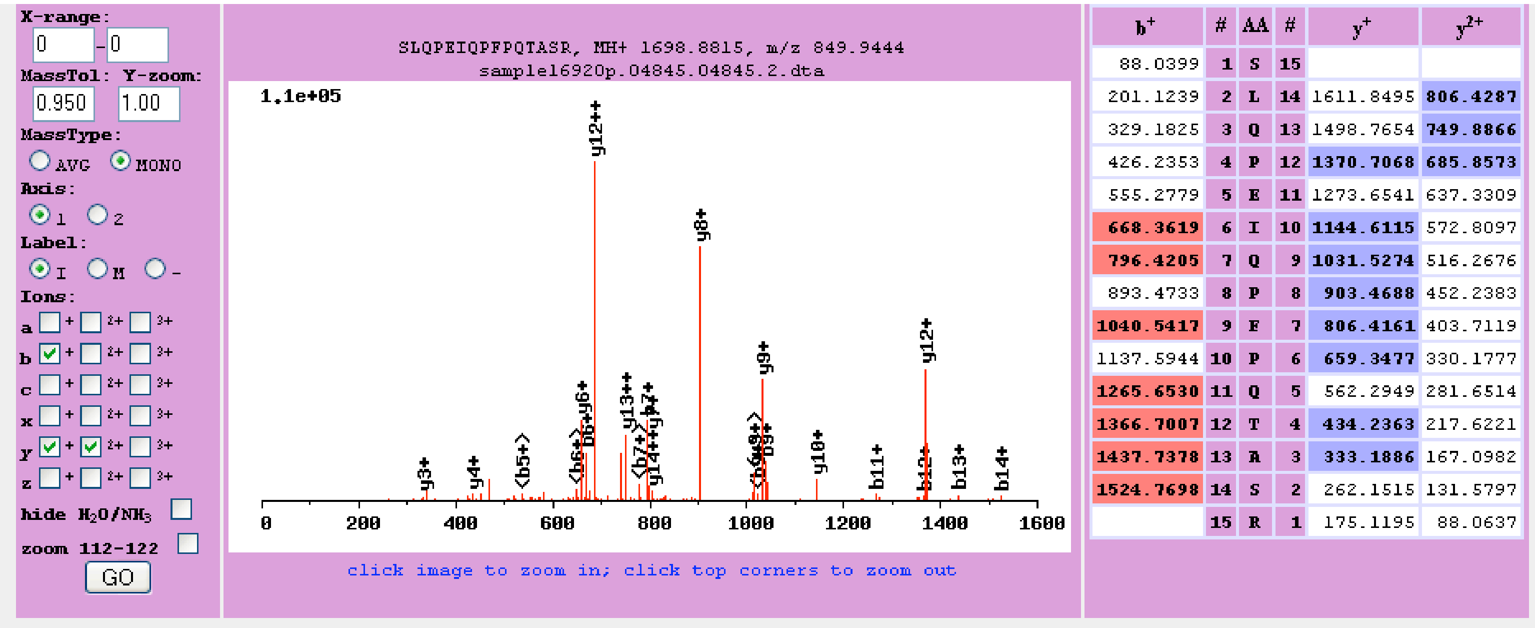
zoom 112-122 ☐

YMCENQATISSK, MH+ 1447.6197, m/z 724.3135
sample16920p.02531.02531.2.dta

b^+	#	AA	#	y^+	y^{2+}
164.0712	1	Y	12		
311.1066	2	M	11	1284.5564	**642.7821**
471.1372	3	C	10	**1137.5210**	**569.2644**
600.1798	4	E	9	977.4904	489.2491
714.2227	5	N	8	**848.4478**	424.7278
842.2813	6	Q	7	734.4048	367.7063
913.3184	7	A	6	**606.3463**	303.6770
1014.3661	8	T	5	**535.3092**	268.1585
1127.4502	9	I	4	**434.2615**	217.6346
1214.4822	10	S	3	**321.1774**	161.0926
1301.5142	11	S	2	234.1454	117.5766
	12	K	1	147.1134	74.0606

M(2):+147.04 C(3):+160.03

Protein: Serum albumin precursor,, Peptide: YMCENQATISSK,
MH+ 1447.6197, m/z 724.3135,sample16920p.02531.02531.2.dta



X-range: 0 - 0

MassTol: 0.950 **Y-zoom:** 1.00

MassType: ○ AVG ● MONO

Axis: ● 1 ○ 2

Label: ● I ○ M ○ -

Ions:

a ☐ + ☐ 2+ ☐ 3+
b ☑ + ☐ 2+ ☐ 3+
c ☐ + ☐ 2+ ☐ 3+
x ☐ + ☐ 2+ ☐ 3+
y ☑ + ☑ 2+ ☐ 3+
z ☐ + ☐ 2+ ☐ 3+

hide H_2O/NH_3 ☐

zoom 112-122 ☐

SLQPEIQPFPQTASR, MH+ 1698.8815, m/z 849.9444
sample16920p.04845.04845.2.dta

b^+	#	AA	#	y^+	y^{2+}
88.0399	1	S	15		
201.1239	2	L	14	1611.8495	**806.4287**
329.1825	3	Q	13	1498.7654	**749.8866**
426.2353	4	P	12	**1370.7068**	**685.8573**
555.2779	5	E	11	1273.6541	637.3309
668.3619	6	I	10	**1144.6115**	572.8097
796.4205	7	Q	9	**1031.5274**	516.2676
893.4733	8	P	8	**903.4688**	452.2383
1040.5417	9	F	7	**806.4161**	403.7119
1137.5944	10	P	6	**659.3477**	330.1777
1265.6530	11	Q	5	562.2949	281.6514
1366.7007	12	T	4	**434.2363**	217.6221
1437.7378	13	A	3	**333.1886**	167.0982
1524.7698	14	S	2	262.1515	131.5797
	15	R	1	175.1195	88.0637

Protein: Histidine-rich glycoprotein HRG,, Peptide: SLQPEIQPFPQTASR,
MH+ 1698.8815, m/z 849.9444,sample16920p.04845.04845.2.dta