Supporting Information

Proteomic Analysis of *Plasmodium* Merosomes: The Link Between Liver and Blood Stages in Malaria

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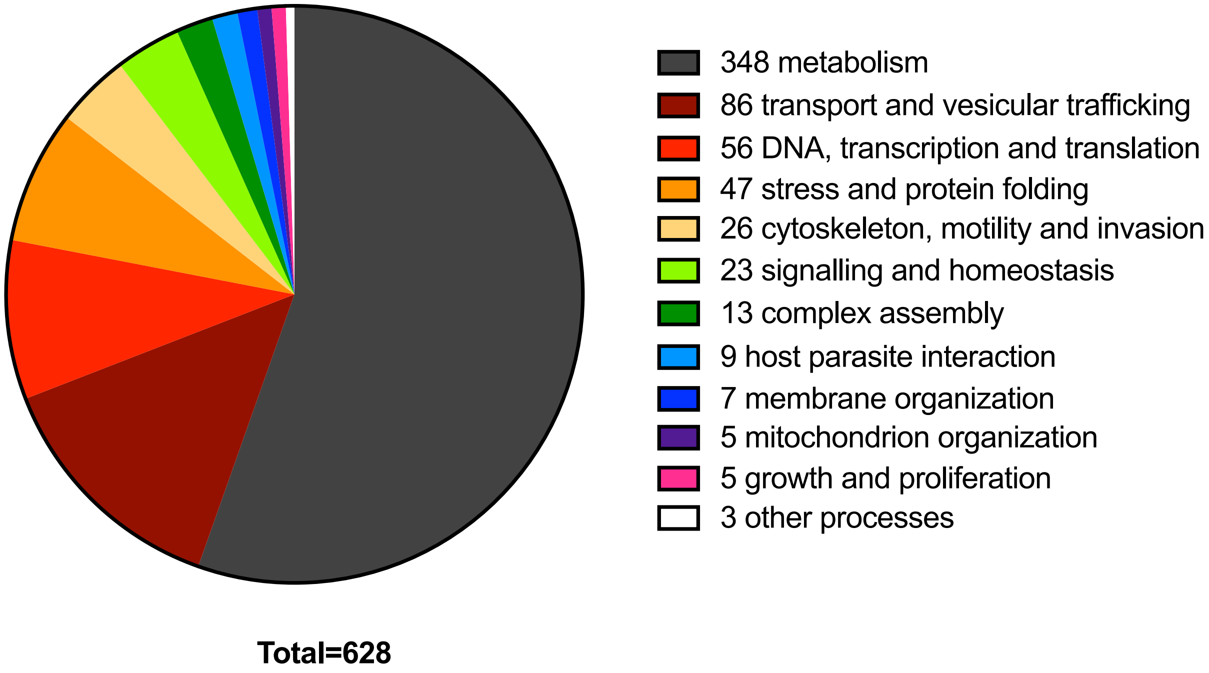
Manipal Academy of Higher Education (MAHE), Manipal 576104, Karnataka, India
Satish Mishra: Division of Parasitology, CSIR-Central Drug Research Institute, Lucknow 226031 India

Supplementary Figures Table of Contents

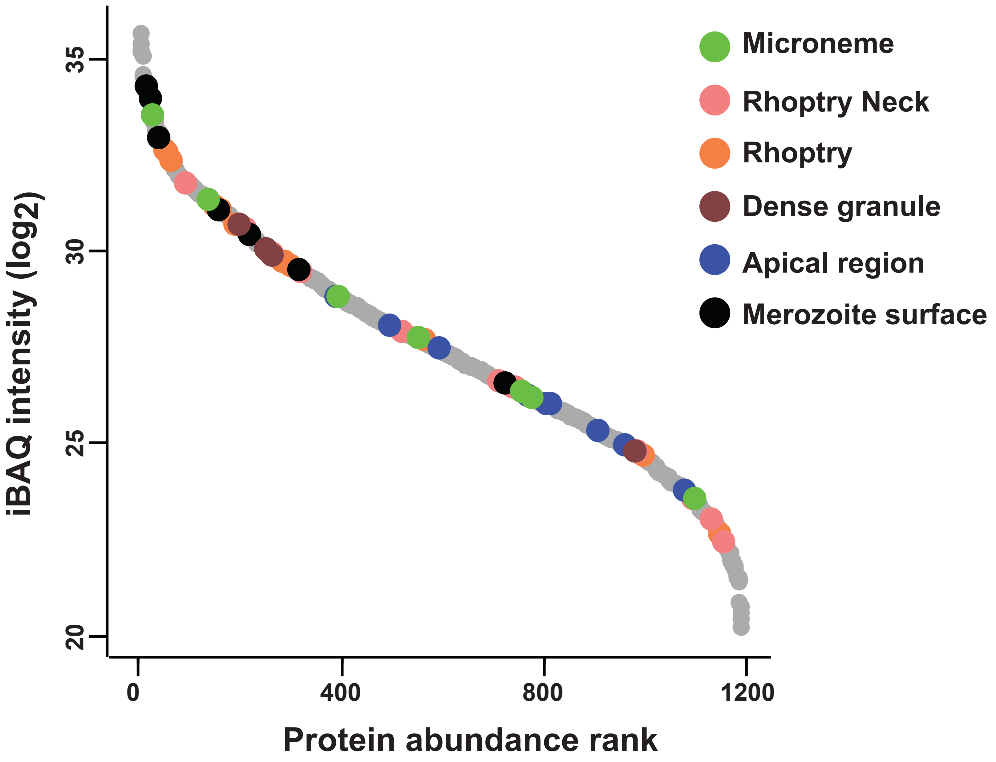
Supplementary Figures

Supplementary Figure 1



Supplementary Figure 1. GO Biological Process terms for proteins in the core merosome proteome. GO Biological Process terms were inferred from *P. falciparum* orthologs due to the relative paucity of annotations for *P. berghei*. Raw data for this graphic can be found in Supplementary Table 3. For this figure, GO terms were manually combined into groups of interest.

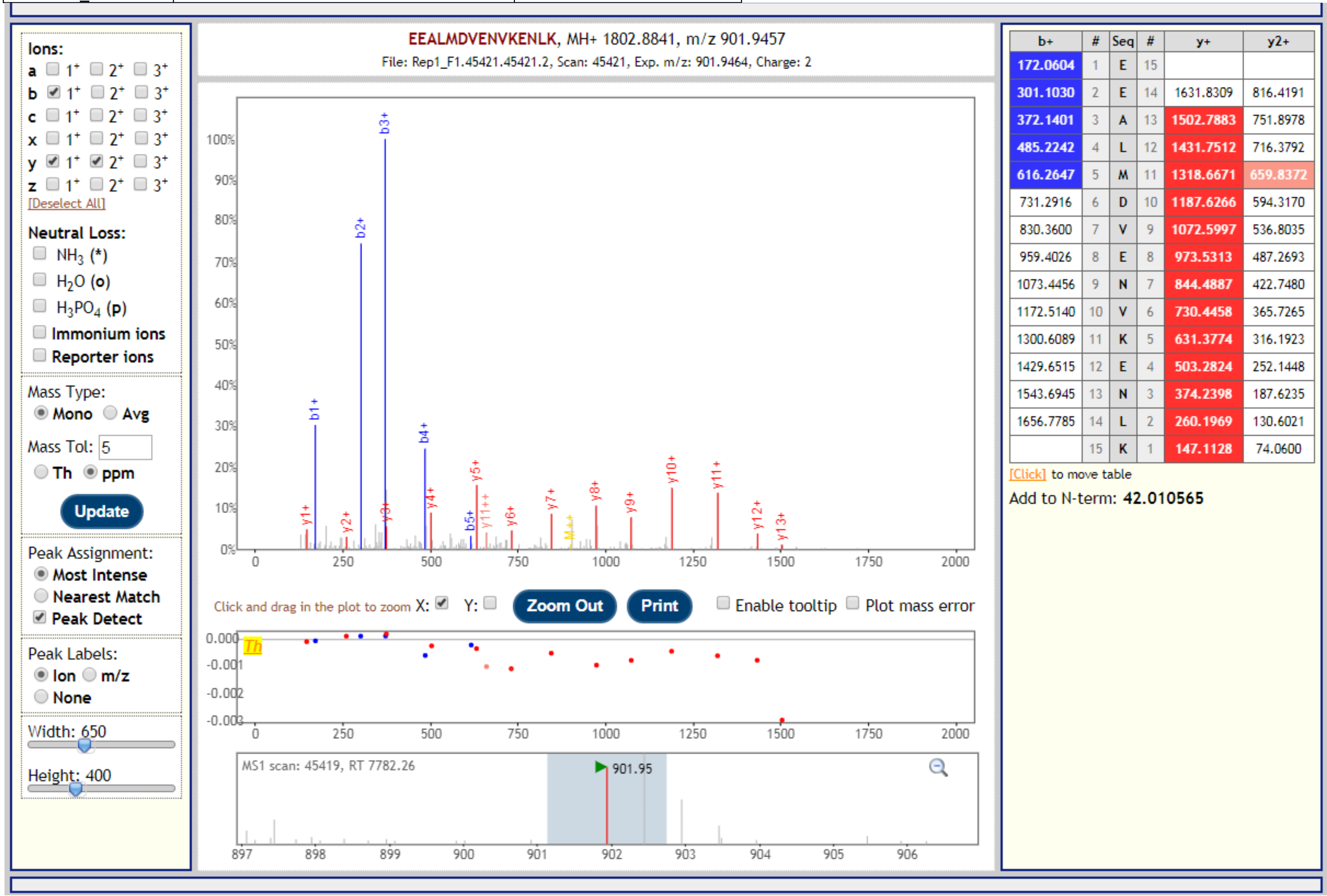
Supplementary Figure 2.



Supplementary Figure 2. Scatterplot of iBAQ intensities for proteins in the core merosome proteome, with apical and merozoite surface proteins highlighted. Proteins in the core *P. berghei* merosome proteome are ranked based on their summed iBAQ intensities. The abundance was spanned over five orders of magnitude. The apical organelle and merozoite surface proteins are color-coded. Categories and rank abundances as described in Table 1.

Supplementary Figure 3. Annotated representative MS/MS spectra identifying putatively cleaved and acetylated PEXEL motifs.

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0208900	StAR-related lipid transfer protein, putative	RIL.EEALMDVENVKENLK



EEALMDVENVKENLK, MH+ 1802.8841, m/z 901.9457

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b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5

○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

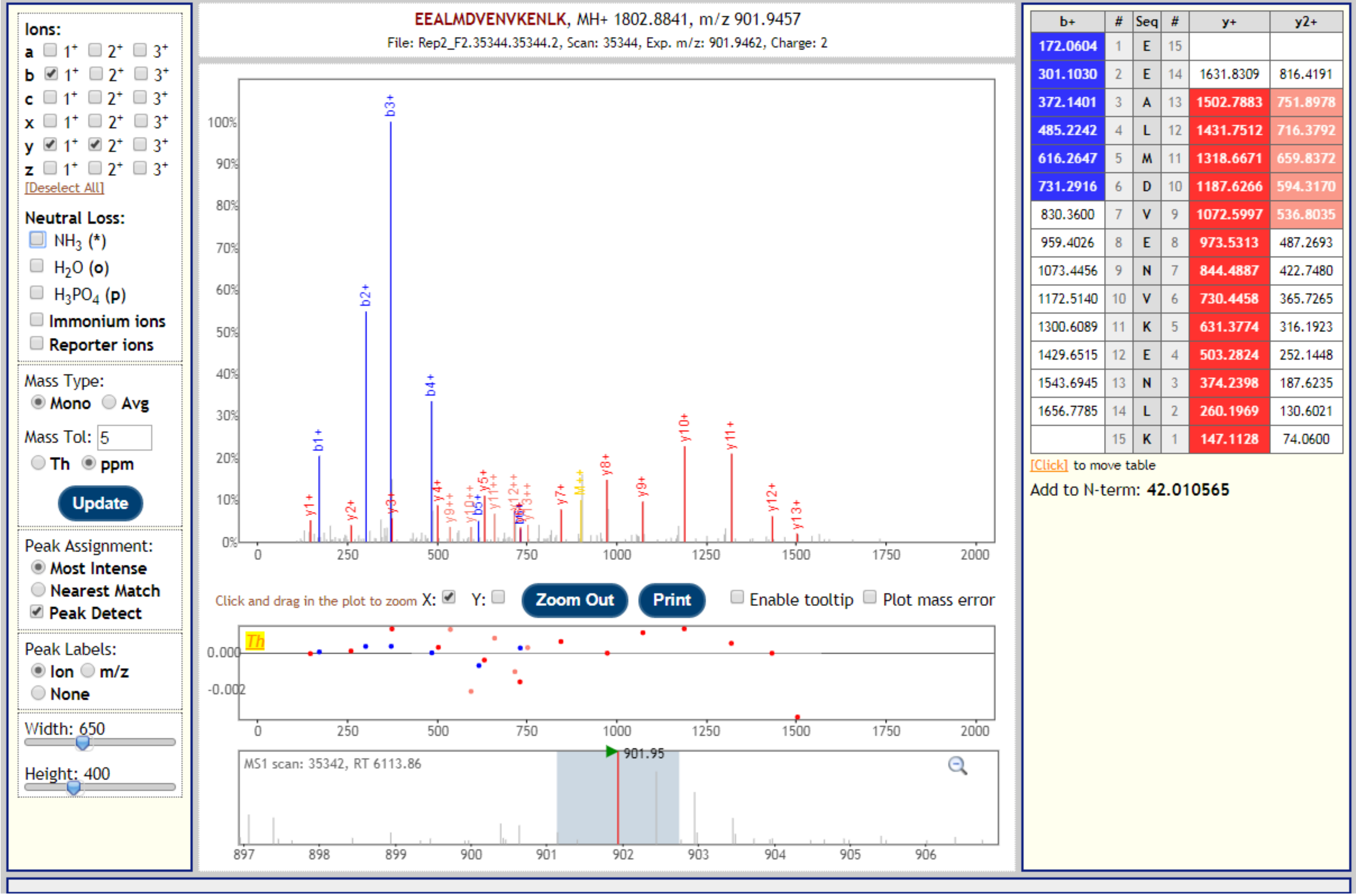
Height: 400

b+	#	Seq	#	y+	y2+
172.0604	1	E	15		
301.1030	2	E	14	1631.8309	816.4191
372.1401	3	A	13	1502.7883	751.8978
485.2242	4	L	12	1431.7512	716.3792
616.2647	5	M	11	1318.6671	659.8372
731.2916	6	D	10	1187.6266	594.3170
830.3600	7	V	9	1072.5997	536.8035
959.4026	8	E	8	973.5313	487.2693
1073.4456	9	N	7	844.4887	422.7480
1172.5140	10	V	6	730.4458	365.7265
1300.6089	11	K	5	631.3774	316.1923
1429.6515	12	E	4	503.2824	252.1448
1543.6945	13	N	3	374.2398	187.6235
1656.7785	14	L	2	260.1969	130.6021
	15	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0208900	StAR-related lipid transfer protein, putative	RIL.EEALMDVENVKENLK



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b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg
Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

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Height: 400

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☐ Enable tooltip ☐ Plot mass error

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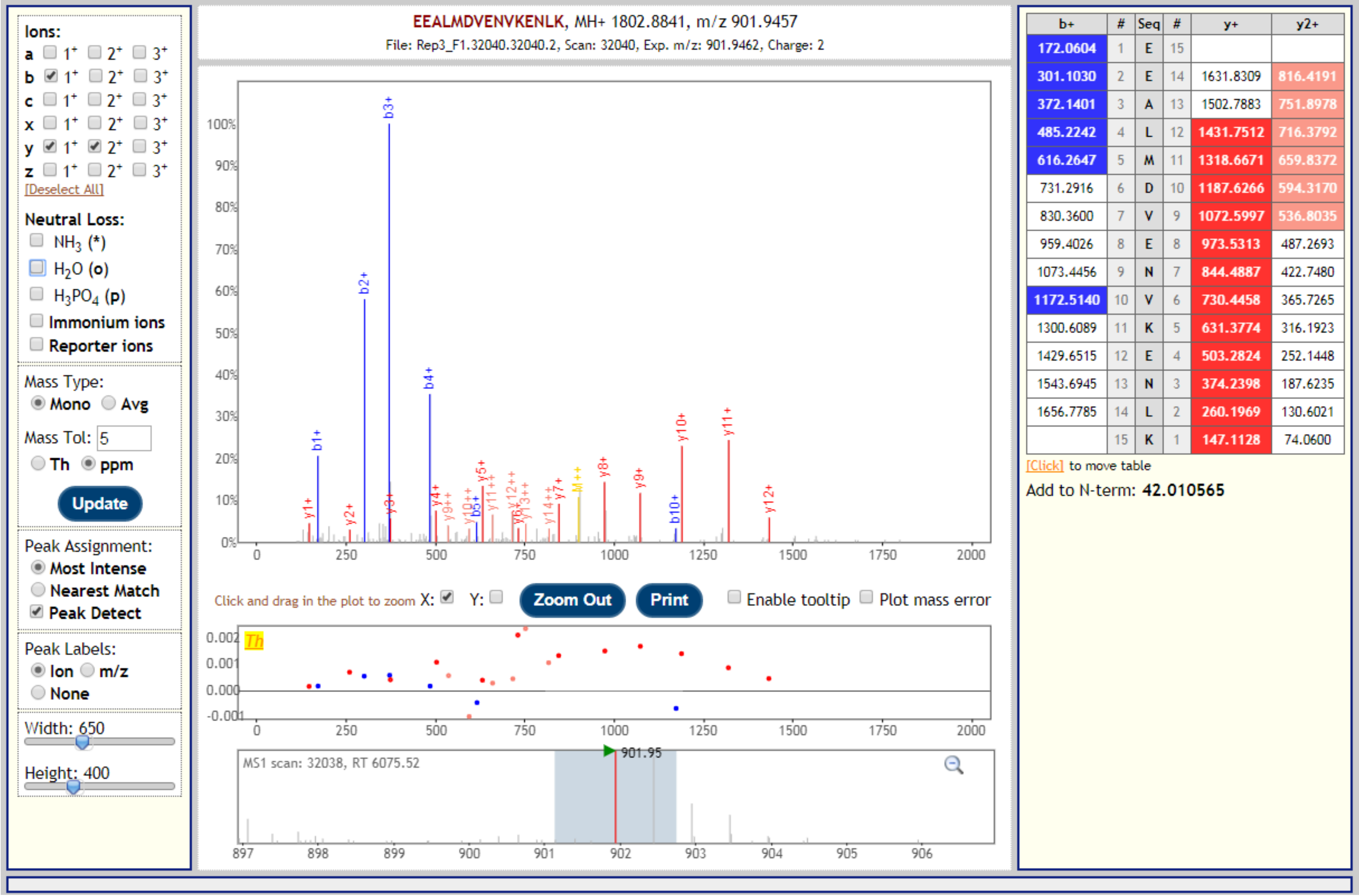
b+	#	Seq	#	y+	y2+
172.0604	1	E	15		
301.1030	2	E	14	1631.8309	816.4191
372.1401	3	A	13	1502.7883	751.8978
485.2242	4	L	12	1431.7512	716.3792
616.2647	5	M	11	1318.6671	659.8372
731.2916	6	D	10	1187.6266	594.3170
830.3600	7	V	9	1072.5997	536.8035
959.4026	8	E	8	973.5313	487.2693
1073.4456	9	N	7	844.4887	422.7480
1172.5140	10	V	6	730.4458	365.7265
1300.6089	11	K	5	631.3774	316.1923
1429.6515	12	E	4	503.2824	252.1448
1543.6945	13	N	3	374.2398	187.6235
1656.7785	14	L	2	260.1969	130.6021
	15	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0208900	StAR-related lipid transfer protein, putative	RIL.EEALMDVENVKENLK



EEALMDVENVKENLK, MH+ 1802.8841, m/z 901.9457

File: Rep3_F1.32040.32040.2, Scan: 32040, Exp. m/z: 901.9462, Charge: 2

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- b ☑ 1+ ☐ 2+ ☐ 3+
- c ☐ 1+ ☐ 2+ ☐ 3+
- x ☐ 1+ ☐ 2+ ☐ 3+
- y ☑ 1+ ☑ 2+ ☐ 3+
- z ☐ 1+ ☐ 2+ ☐ 3+

[Deselect All]

Neutral Loss:
- ☐ NH_3 (*)
- ☐ H_2O (o)
- ☐ H_3PO_4 (p)
- ☐ Immonium ions
- ☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5 ○ Th ● ppm

Peak Assignment: ● Most Intense ○ Nearest Match ☑ Peak Detect

Peak Labels: ● Ion ○ m/z ○ None

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Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip ☐ Plot mass error

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172.0604	1	E	15		
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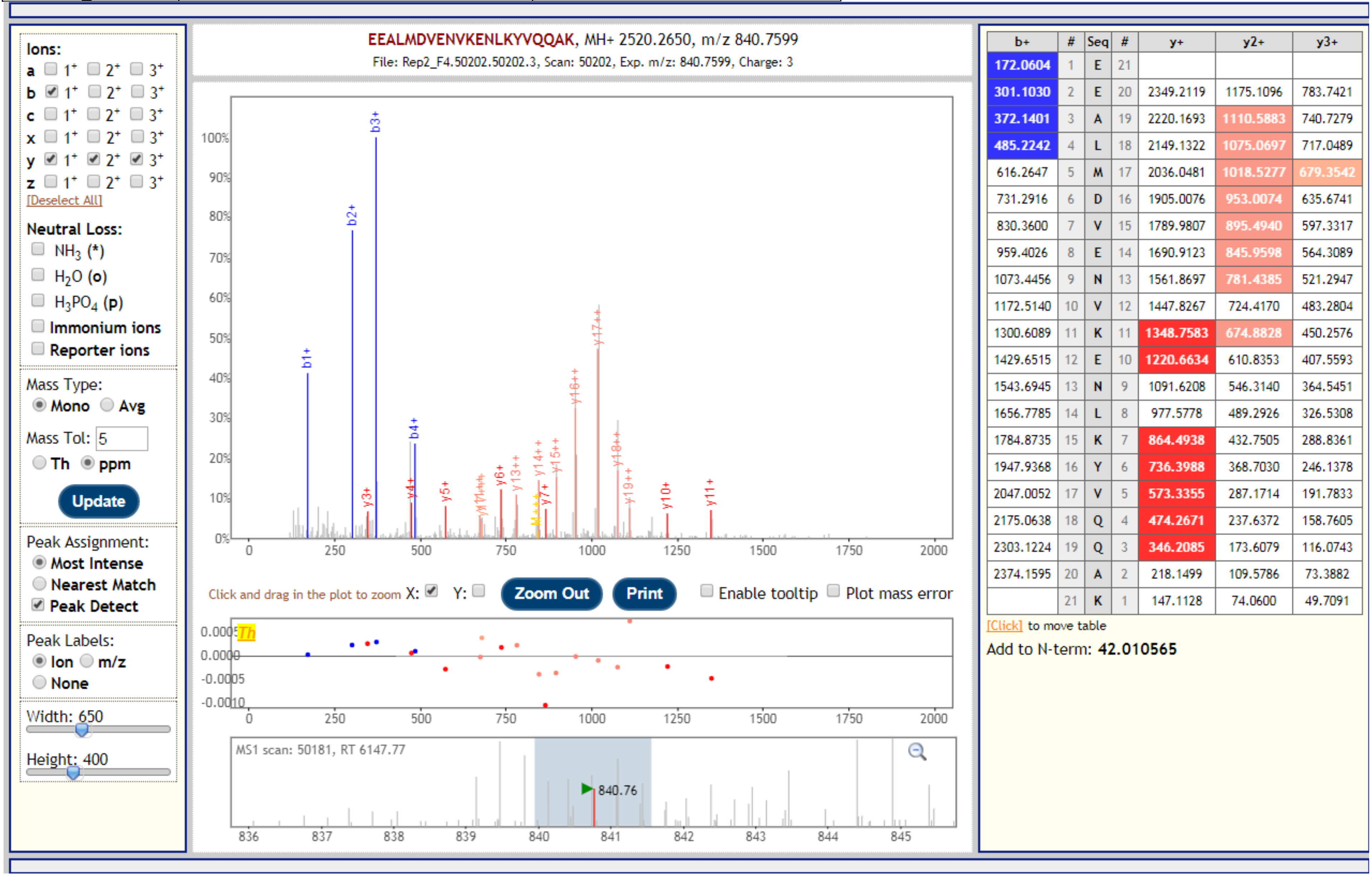
372.1401	3	A	13	1502.7883	751.8978
485.2242	4	L	12	1431.7512	716.3792
616.2647	5	M	11	1318.6671	659.8372
731.2916	6	D	10	1187.6266	594.3170
830.3600	7	V	9	1072.5997	536.8035
959.4026	8	E	8	973.5313	487.2693
1073.4456	9	N	7	844.4887	422.7480
1172.5140	10	V	6	730.4458	365.7265
1300.6089	11	K	5	631.3774	316.1923
1429.6515	12	E	4	503.2824	252.1448
1543.6945	13	N	3	374.2398	187.6235
1656.7785	14	L	2	260.1969	130.6021
	15	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0208900	StAR-related lipid transfer protein, putative	RIL.EEALMDVENVKENLKYVQQAK



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b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
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EEALMDVENVKENLKYVQQAK, MH+ 2520.2650, m/z 840.7599

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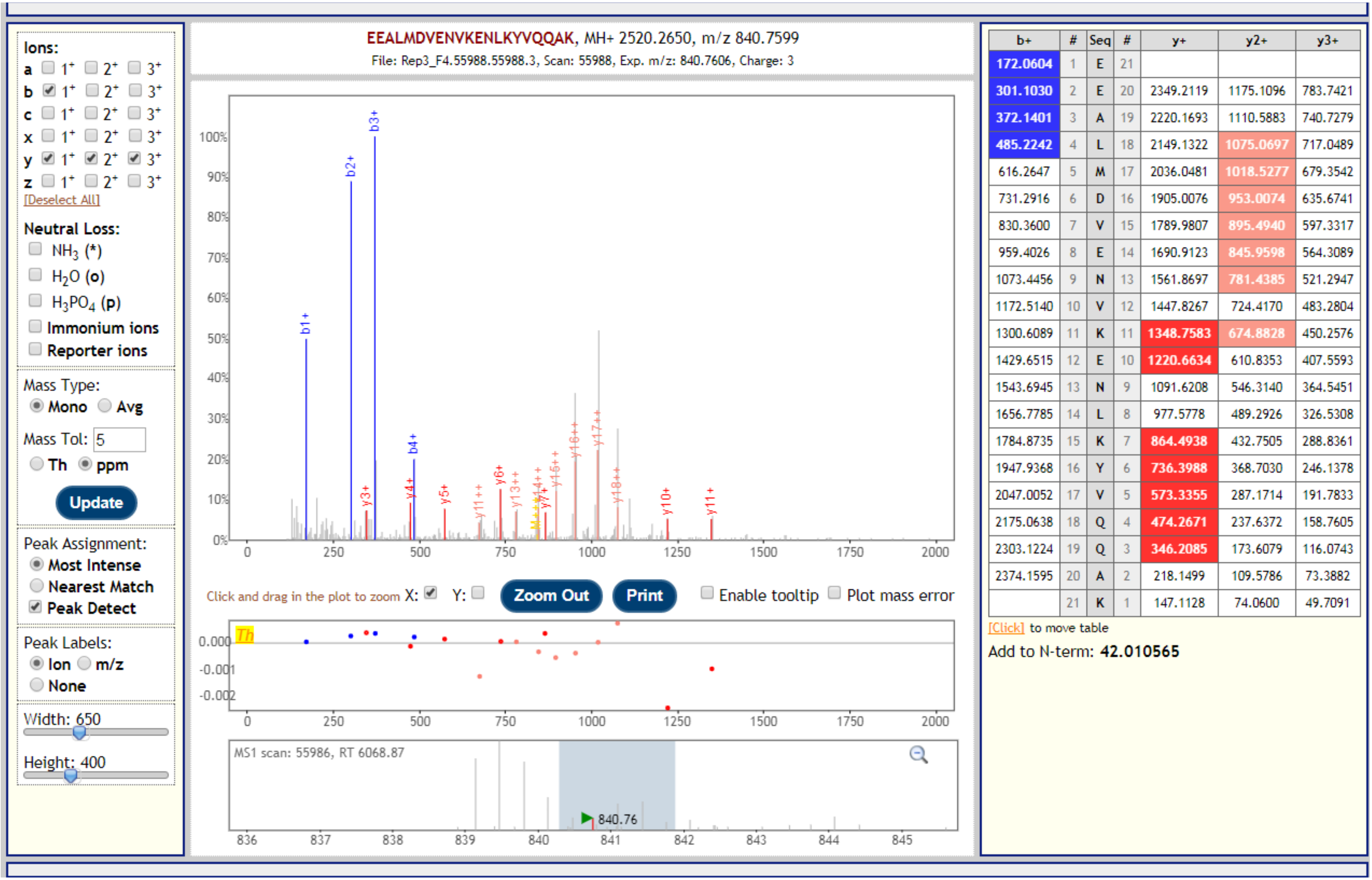
485.2242	4	L	18	2149.1322	1075.0697	717.0489
616.2647	5	M	17	2036.0481	1018.5277	679.3542
731.2916	6	D	16	1905.0076	953.0074	635.6741
830.3600	7	V	15	1789.9807	895.4940	597.3317
959.4026	8	E	14	1690.9123	845.9598	564.3089
1073.4456	9	N	13	1561.8697	781.4385	521.2947
1172.5140	10	V	12	1447.8267	724.4170	483.2804
1300.6089	11	K	11	1348.7583	674.8828	450.2576
1429.6515	12	E	10	1220.6634	610.8353	407.5593
1543.6945	13	N	9	1091.6208	546.3140	364.5451
1656.7785	14	L	8	977.5778	489.2926	326.5308
1784.8735	15	K	7	864.4938	432.7505	288.8361
1947.9368	16	Y	6	736.3988	368.7030	246.1378
2047.0052	17	V	5	573.3355	287.1714	191.7833
2175.0638	18	Q	4	474.2671	237.6372	158.7605
2303.1224	19	Q	3	346.2085	173.6079	116.0743
2374.1595	20	A	2	218.1499	109.5786	73.3882
	21	K	1	147.1128	74.0600	49.7091

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0208900	StAR-related lipid transfer protein, putative	RIL.EEALMDVENVKENLKYVQQAK



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x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

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Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

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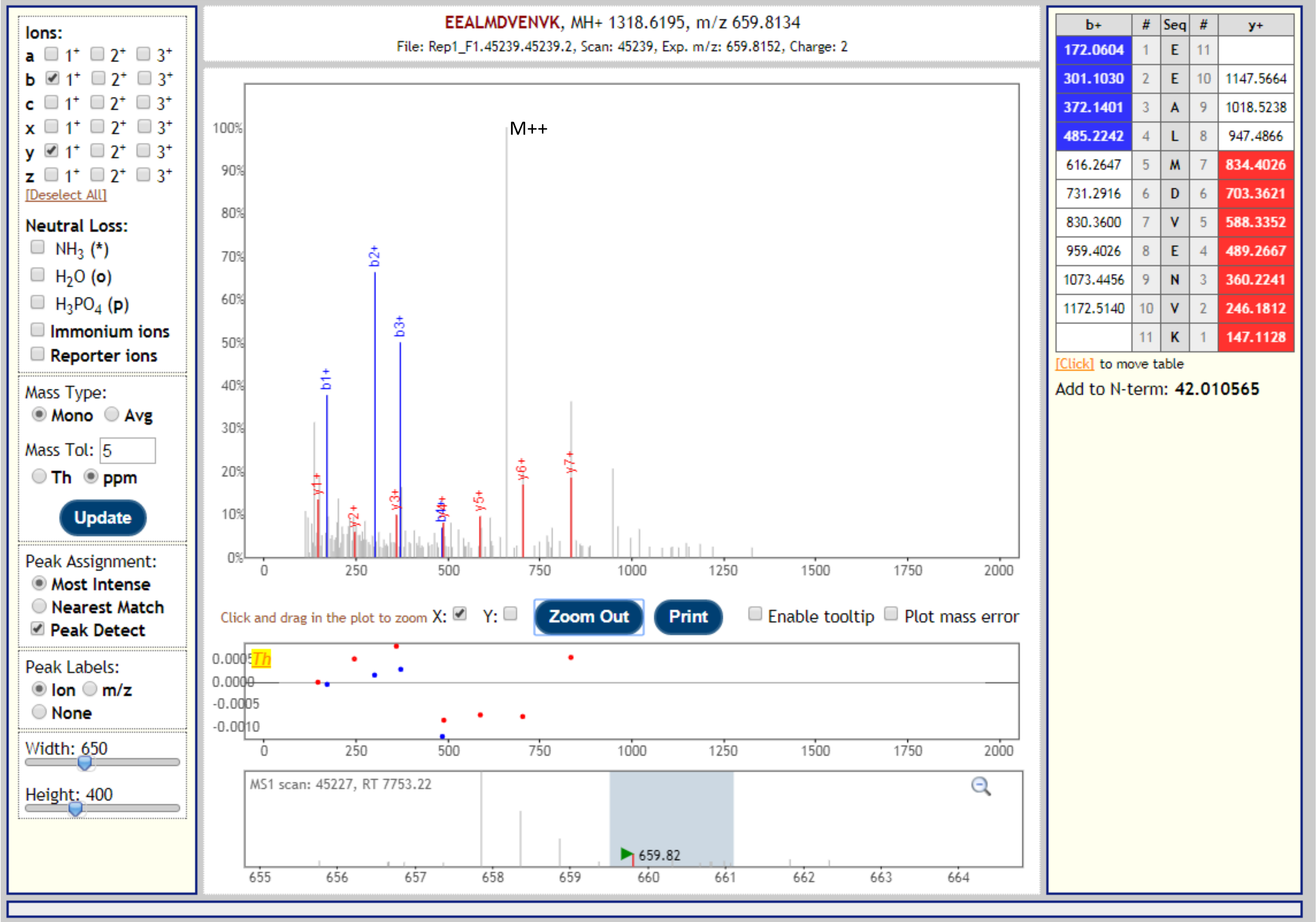
372.1401	3	A	19	2220.1693	1110.5883	740.7279
485.2242	4	L	18	2149.1322	1075.0697	717.0489
616.2647	5	M	17	2036.0481	1018.5277	679.3542
731.2916	6	D	16	1905.0076	953.0074	635.6741
830.3600	7	V	15	1789.9807	895.4940	597.3317
959.4026	8	E	14	1690.9123	845.9598	564.3089
1073.4456	9	N	13	1561.8697	781.4385	521.2947
1172.5140	10	V	12	1447.8267	724.4170	483.2804
1300.6089	11	K	11	1348.7583	674.8828	450.2576
1429.6515	12	E	10	1220.6634	610.8353	407.5593
1543.6945	13	N	9	1091.6208	546.3140	364.5451
1656.7785	14	L	8	977.5778	489.2926	326.5308
1784.8735	15	K	7	864.4938	432.7505	288.8361
1947.9368	16	Y	6	736.3988	368.7030	246.1378
2047.0052	17	V	5	573.3355	287.1714	191.7833
2175.0638	18	Q	4	474.2671	237.6372	158.7605
2303.1224	19	Q	3	346.2085	173.6079	116.0743
2374.1595	20	A	2	218.1499	109.5786	73.3882
	21	K	1	147.1128	74.0600	49.7091

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0208900	StAR-related lipid transfer protein, putative	RIL.EEALMDVENVK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

EEALMDVENVK, MH+ 1318.6195, m/z 659.8134

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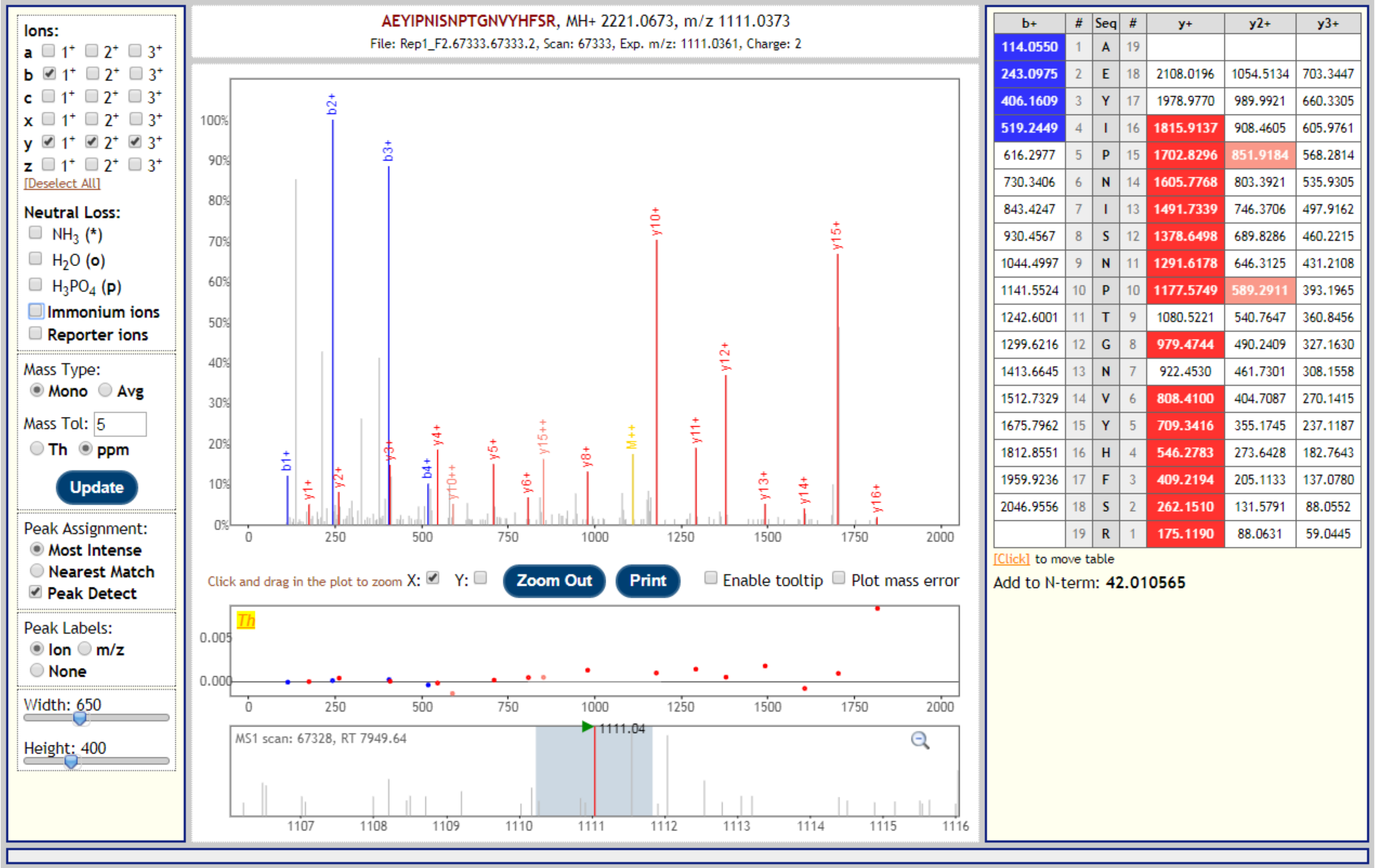
485.2242	4	L	8	947.4866
616.2647	5	M	7	834.4026
731.2916	6	D	6	703.3621
830.3600	7	V	5	588.3352
959.4026	8	E	4	489.2667
1073.4456	9	N	3	360.2241
1172.5140	10	V	2	246.1812
	11	K	1	147.1128

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1400700	Plasmodium exported protein, unknown function	RHL.AEYIPNISNPTGNVYHFSR



Ions:
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b ☑ 1^+ ☐ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☑ 2^+ ☑ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

AEYIPNISNPTGNVYHFSR, MH+ 2221.0673, m/z 1111.0373
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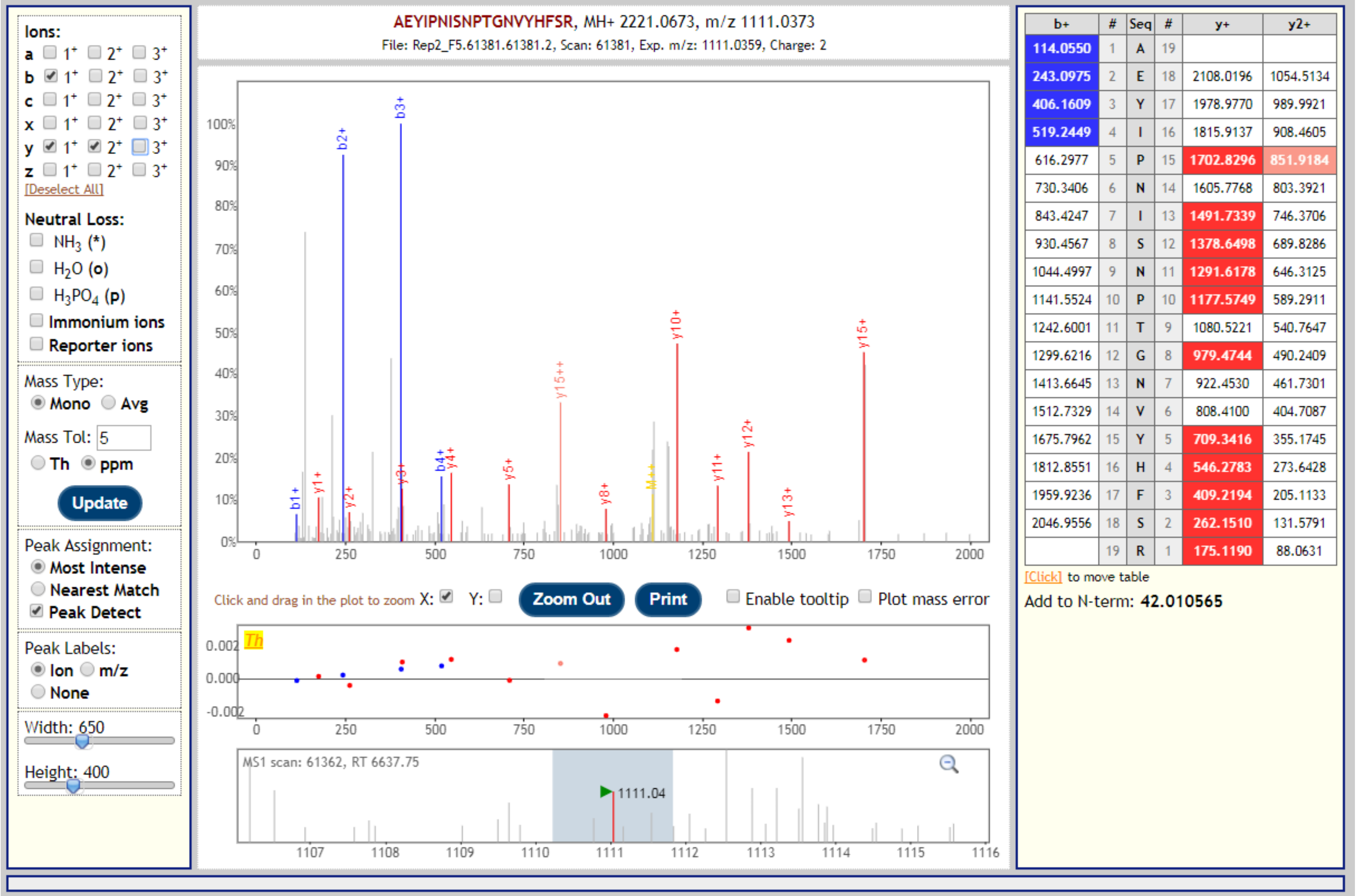
b+	#	Seq	#	y+	y2+	y3+
114.0550	1	A	19			
243.0975	2	E	18	2108.0196	1054.5134	703.3447
406.1609	3	Y	17	1978.9770	989.9921	660.3305
519.2449	4	I	16	1815.9137	908.4605	605.9761
616.2977	5	P	15	1702.8296	851.9184	568.2814
730.3406	6	N	14	1605.7768	803.3921	535.9305
843.4247	7	I	13	1491.7339	746.3706	497.9162
930.4567	8	S	12	1378.6498	689.8286	460.2215
1044.4997	9	N	11	1291.6178	646.3125	431.2108
1141.5524	10	P	10	1177.5749	589.2911	393.1965
1242.6001	11	T	9	1080.5221	540.7647	360.8456
1299.6216	12	G	8	979.4744	490.2409	327.1630
1413.6645	13	N	7	922.4530	461.7301	308.1558
1512.7329	14	V	6	808.4100	404.7087	270.1415
1675.7962	15	Y	5	709.3416	355.1745	237.1187
1812.8551	16	H	4	546.2783	273.6428	182.7643
1959.9236	17	F	3	409.2194	205.1133	137.0780
2046.9556	18	S	2	262.1510	131.5791	88.0552
	19	R	1	175.1190	88.0631	59.0445

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1400700	Plasmodium exported protein, unknown function	RHL.AEYIPNISNPTGNVYHFSR



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg
Mass Tol: 5
○ Th ● ppm
Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650
Height: 400

AEYIPNISNPTGNVYHFSR, MH+ 2221.0673, m/z 1111.0373
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Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

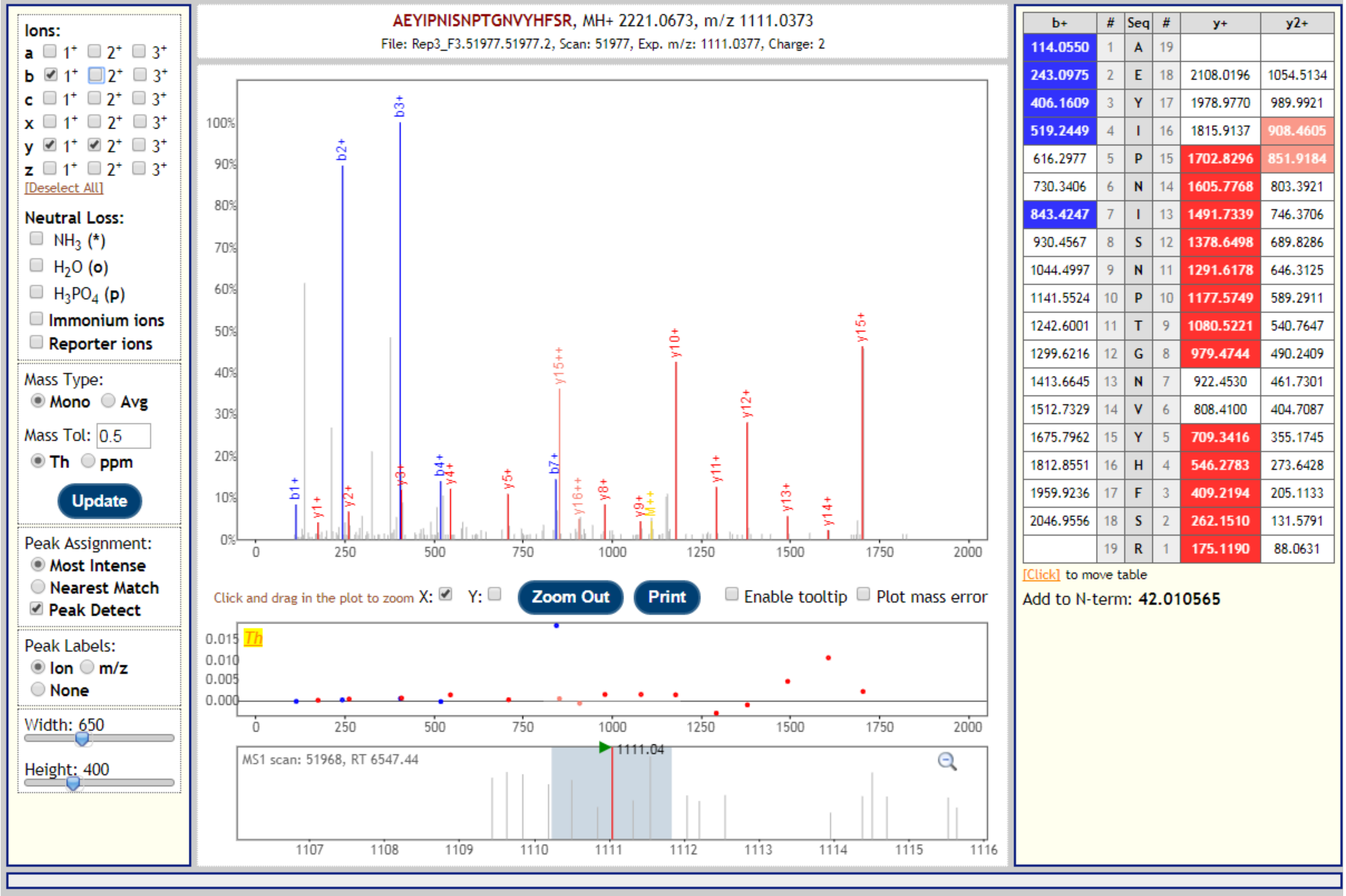
MS1 scan: 61362, RT 6637.75

b+	#	Seq	#	y+	y2+
114.0550	1	A	19		
243.0975	2	E	18	2108.0196	1054.5134
406.1609	3	Y	17	1978.9770	989.9921
519.2449	4	I	16	1815.9137	908.4605
616.2977	5	P	15	**1702.8296**	**851.9184**
730.3406	6	N	14	1605.7768	803.3921
843.4247	7	I	13	**1491.7339**	746.3706
930.4567	8	S	12	**1378.6498**	689.8286
1044.4997	9	N	11	**1291.6178**	646.3125
1141.5524	10	P	10	**1177.5749**	589.2911
1242.6001	11	T	9	1080.5221	540.7647
1299.6216	12	G	8	**979.4744**	490.2409
1413.6645	13	N	7	922.4530	461.7301
1512.7329	14	V	6	808.4100	404.7087
1675.7962	15	Y	5	**709.3416**	355.1745
1812.8551	16	H	4	**546.2783**	273.6428
1959.9236	17	F	3	**409.2194**	205.1133
2046.9556	18	S	2	**262.1510**	131.5791
	19	R	1	**175.1190**	88.0631

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1400700	Plasmodium exported protein, unknown function	RHL.AEYIPNISNPTGNVYHFSR



AEYIPNISNPTGNVYHFSR, MH+ 2221.0673, m/z 1111.0373

File: Rep3_F3.51977.51977.2, Scan: 51977, Exp. m/z: 1111.0377, Charge: 2

Ions:
a ☐ 1^+ ☐ 2^+ ☐ 3^+
b ☑ 1^+ ☐ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☑ 2^+ ☐ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 0.5

● Th ○ ppm

Update

Peak Assignment: ● Most Intense ○ Nearest Match

☑ Peak Detect

Peak Labels: ● Ion ○ m/z ○ None

Width: 650

Height: 400

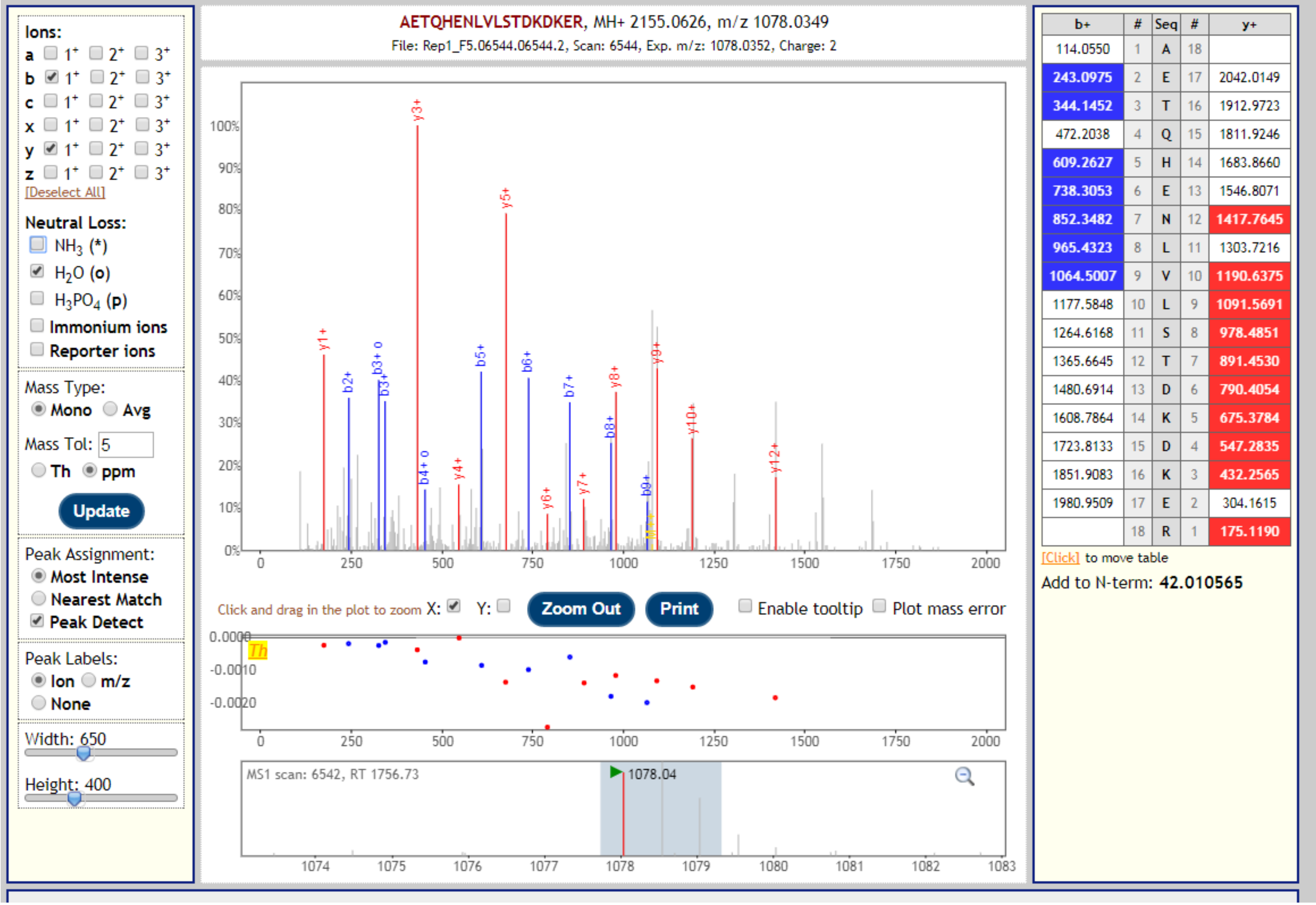
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

b+	#	Seq	#	y+	y2+
114.0550	1	A	19		
243.0975	2	E	18	2108.0196	1054.5134
406.1609	3	Y	17	1978.9770	989.9921
519.2449	4	I	16	1815.9137	908.4605
616.2977	5	P	15	1702.8296	851.9184
730.3406	6	N	14	1605.7768	803.3921
843.4247	7	I	13	1491.7339	746.3706
930.4567	8	S	12	1378.6498	689.8286
1044.4997	9	N	11	1291.6178	646.3125
1141.5524	10	P	10	1177.5749	589.2911
1242.6001	11	T	9	1080.5221	540.7647
1299.6216	12	G	8	979.4744	490.2409
1413.6645	13	N	7	922.4530	461.7301
1512.7329	14	V	6	808.4100	404.7087
1675.7962	15	Y	5	709.3416	355.1745
1812.8551	16	H	4	546.2783	273.6428
1959.9236	17	F	3	409.2194	205.1133
2046.9556	18	S	2	262.1510	131.5791
	19	R	1	175.1190	88.0631

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RIL.AETQHENLVLSTDKDKER



AETQHENLVLSTDKDKER, MH+ 2155.0626, m/z 1078.0349

File: Rep1_F5.06544.06544.2, Scan: 6544, Exp. m/z: 1078.0352, Charge: 2

Ions:
a ☐ 1^+ ☐ 2^+ ☐ 3^+
b ☑ 1^+ ☐ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☐ 2^+ ☐ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5

○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

MS1 scan: 6542, RT 1756.73

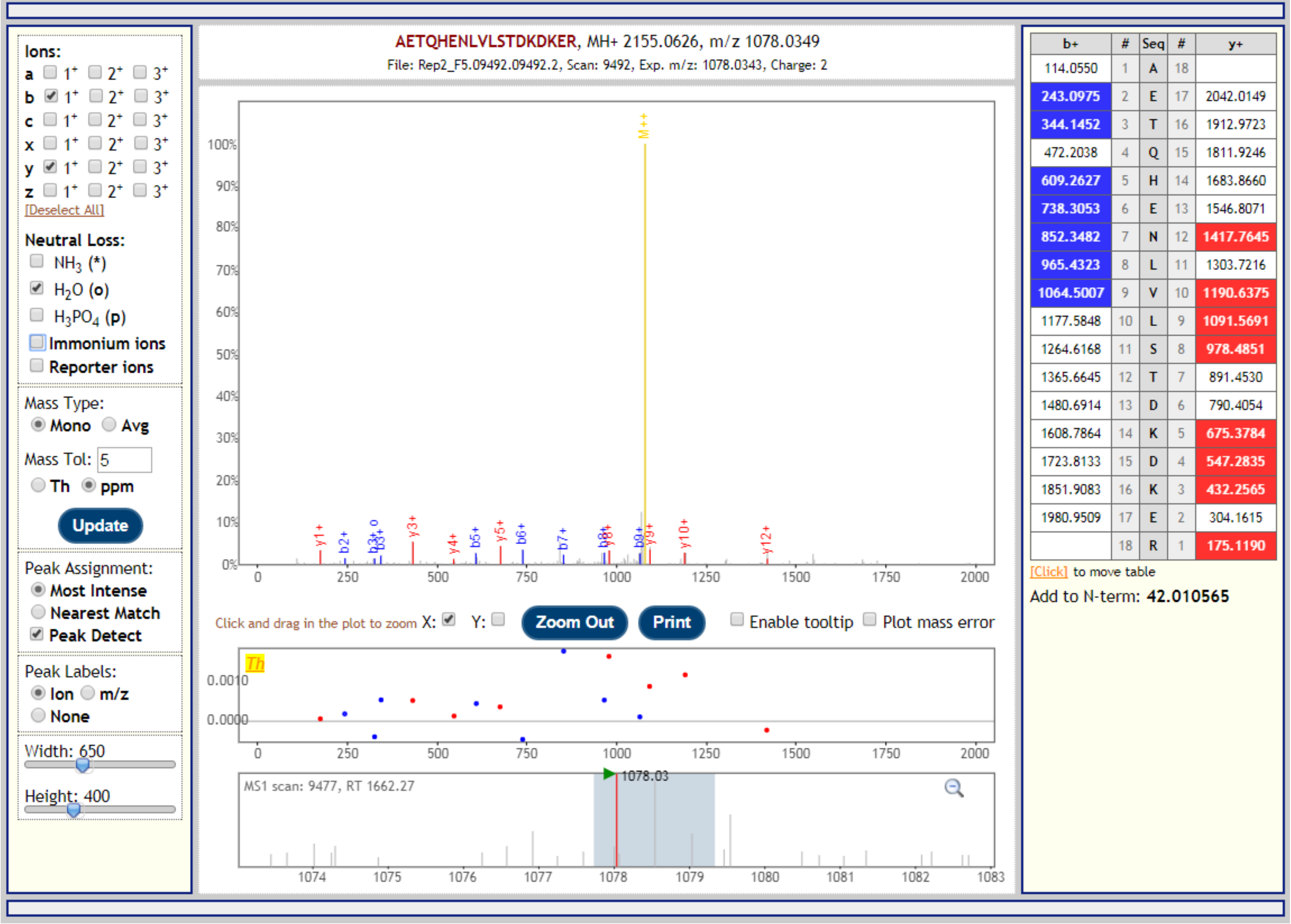
1078.04

b+	#	Seq	#	y+
114.0550	1	A	18	
243.0975	2	E	17	2042.0149
344.1452	3	T	16	1912.9723
472.2038	4	Q	15	1811.9246
609.2627	5	H	14	1683.8660
738.3053	6	E	13	1546.8071
852.3482	7	N	12	1417.7645
965.4323	8	L	11	1303.7216
1064.5007	9	V	10	1190.6375
1177.5848	10	L	9	1091.5691
1264.6168	11	S	8	978.4851
1365.6645	12	T	7	891.4530
1480.6914	13	D	6	790.4054
1608.7864	14	K	5	675.3784
1723.8133	15	D	4	547.2835
1851.9083	16	K	3	432.2565
1980.9509	17	E	2	304.1615
	18	R	1	175.1190

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RIL.AETQHENLVLSTDKDKER



AETQHENLVLSTDKDKER, MH+ 2155.0626, m/z 1078.0349

File: Rep2_F5.09492.09492.2, Scan: 9492, Exp. m/z: 1078.0343, Charge: 2

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

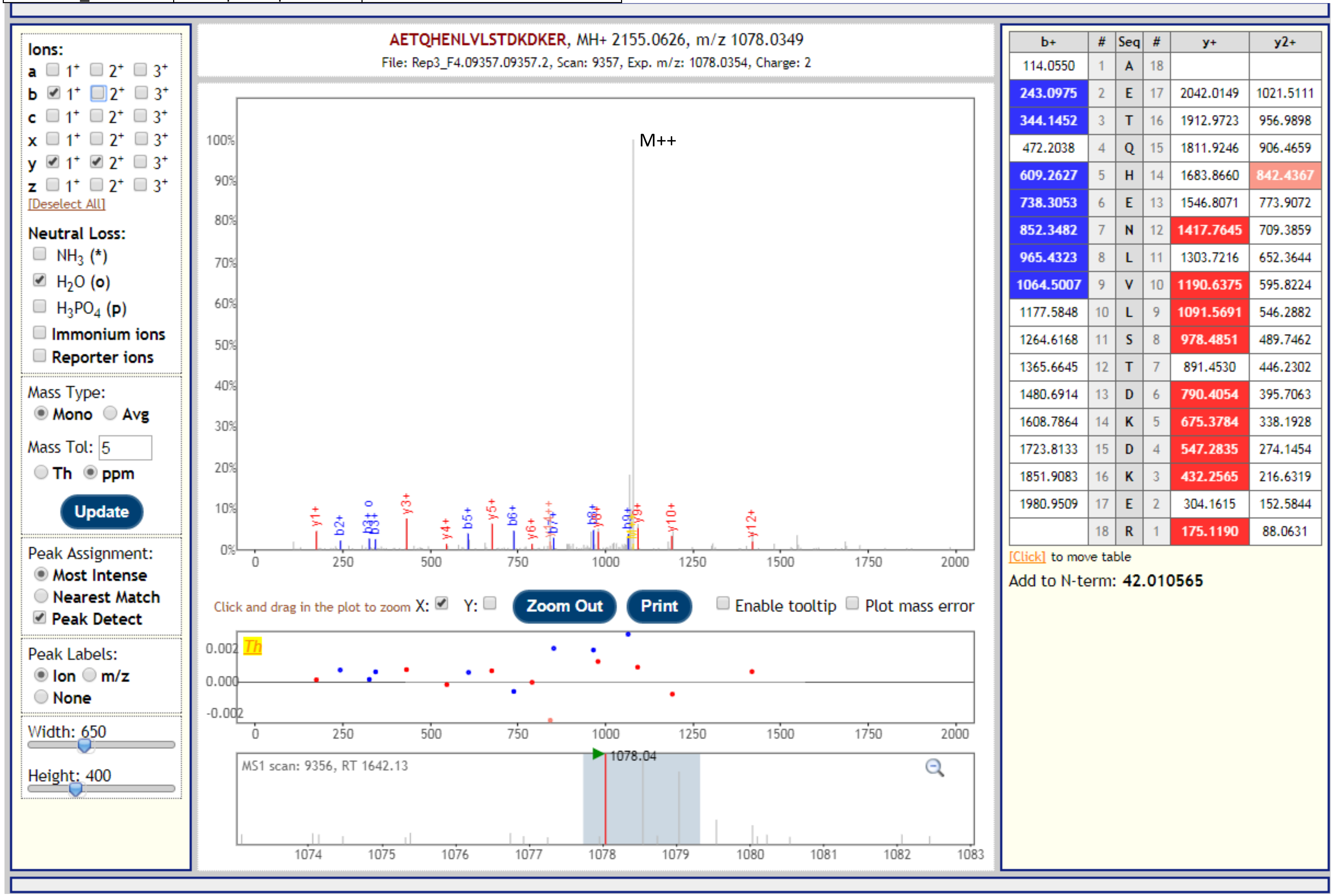
MS1 scan: 9477, RT 1662.27

b+	#	Seq	#	y+
114.0550	1	A	18	
243.0975	2	E	17	2042.0149
344.1452	3	T	16	1912.9723
472.2038	4	Q	15	1811.9246
609.2627	5	H	14	1683.8660
738.3053	6	E	13	1546.8071
852.3482	7	N	12	1417.7645
965.4323	8	L	11	1303.7216
1064.5007	9	V	10	1190.6375
1177.5848	10	L	9	1091.5691
1264.6168	11	S	8	978.4851
1365.6645	12	T	7	891.4530
1480.6914	13	D	6	790.4054
1608.7864	14	K	5	675.3784
1723.8133	15	D	4	547.2835
1851.9083	16	K	3	432.2565
1980.9509	17	E	2	304.1615
	18	R	1	175.1190

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RIL.AETQHENLVLSTDKDKER



AETQHENLVLSTDKDKER, MH+ 2155.0626, m/z 1078.0349

File: Rep3_F4.09357.09357.2, Scan: 9357, Exp. m/z: 1078.0354, Charge: 2

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5

○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

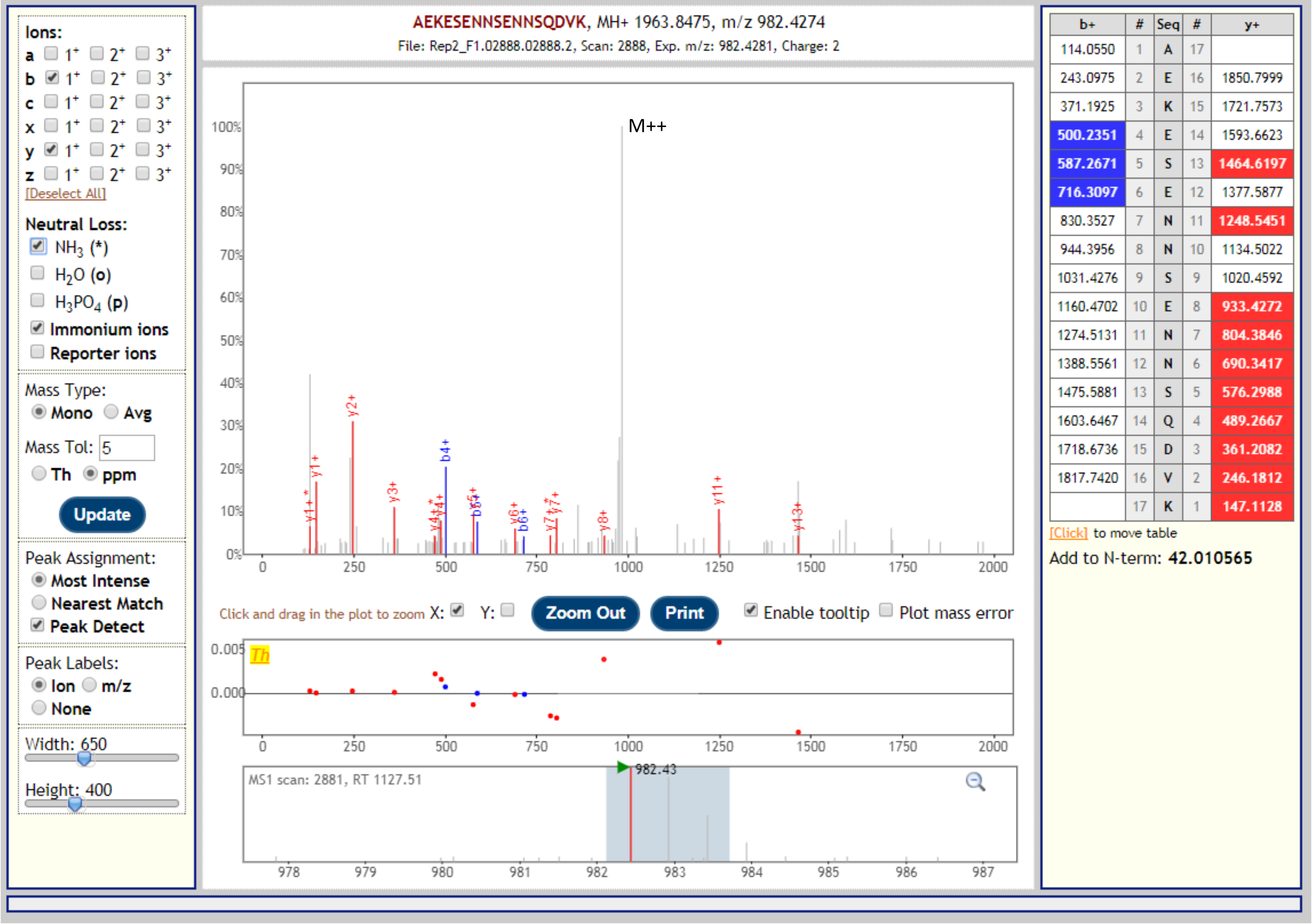
MS1 scan: 9356, RT 1642.13

b+	#	Seq	#	y+	y2+
114.0550	1	A	18		
243.0975	2	E	17	2042.0149	1021.5111
344.1452	3	T	16	1912.9723	956.9898
472.2038	4	Q	15	1811.9246	906.4659
609.2627	5	H	14	1683.8660	842.4367
738.3053	6	E	13	1546.8071	773.9072
852.3482	7	N	12	1417.7645	709.3859
965.4323	8	L	11	1303.7216	652.3644
1064.5007	9	V	10	1190.6375	595.8224
1177.5848	10	L	9	1091.5691	546.2882
1264.6168	11	S	8	978.4851	489.7462
1365.6645	12	T	7	891.4530	446.2302
1480.6914	13	D	6	790.4054	395.7063
1608.7864	14	K	5	675.3784	338.1928
1723.8133	15	D	4	547.2835	274.1454
1851.9083	16	K	3	432.2565	216.6319
1980.9509	17	E	2	304.1615	152.5844
	18	R	1	175.1190	88.0631

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSQDVK



AEKESENNSENNSQDVK, MH+ 1963.8475, m/z 982.4274

File: Rep2_F1.02888.02888.2, Scan: 2888, Exp. m/z: 982.4281, Charge: 2

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☑ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☑ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5 ○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels: ● Ion ○ m/z ○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐

☑ Enable tooltip ☐ Plot mass error

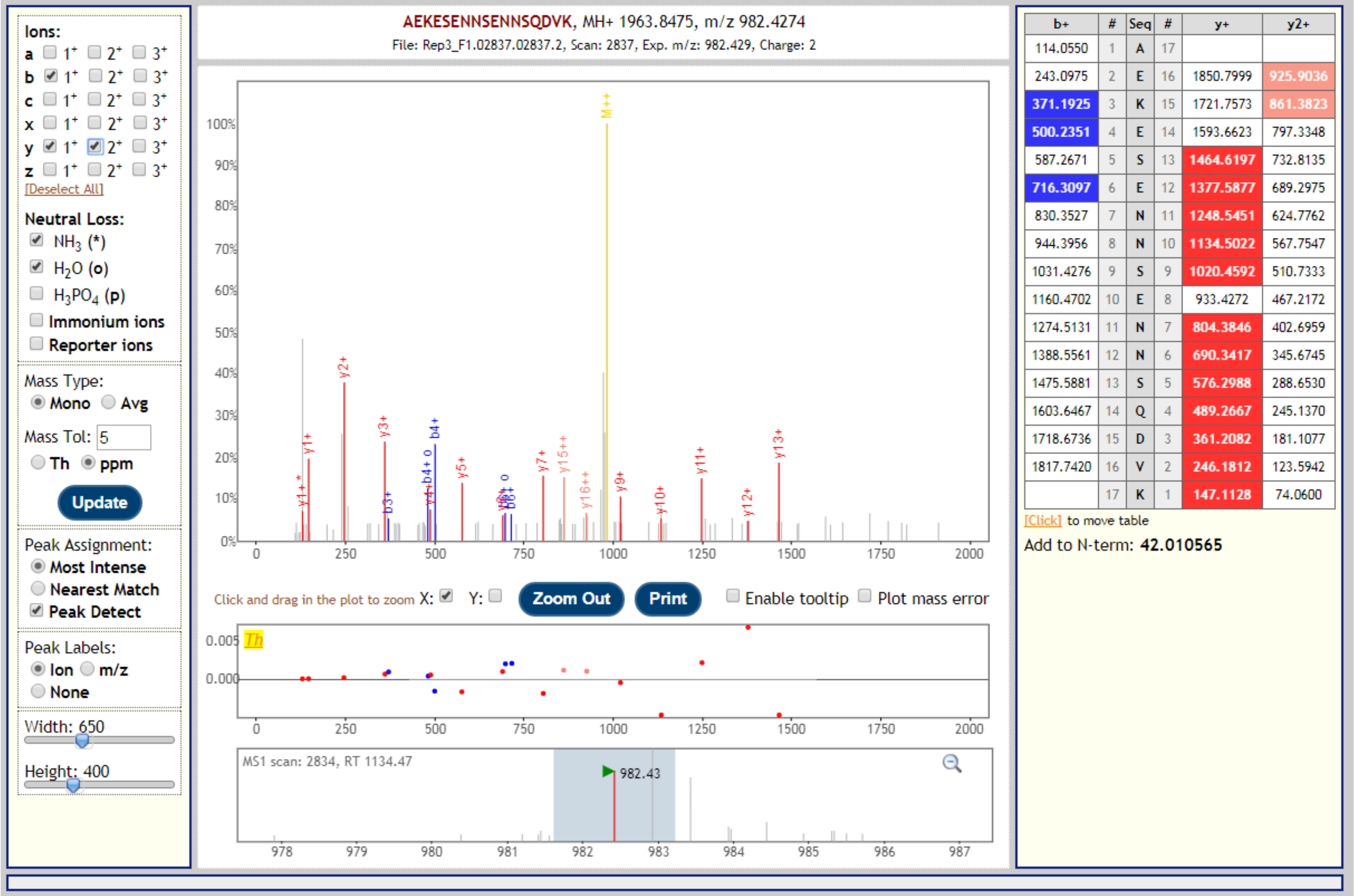
MS1 scan: 2881, RT 1127.51

b+	#	Seq	#	y+
114.0550	1	A	17	
243.0975	2	E	16	1850.7999
371.1925	3	K	15	1721.7573
500.2351	4	E	14	1593.6623
587.2671	5	S	13	**1464.6197**
716.3097	6	E	12	1377.5877
830.3527	7	N	11	**1248.5451**
944.3956	8	N	10	1134.5022
1031.4276	9	S	9	1020.4592
1160.4702	10	E	8	**933.4272**
1274.5131	11	N	7	**804.3846**
1388.5561	12	N	6	**690.3417**
1475.5881	13	S	5	**576.2988**
1603.6467	14	Q	4	**489.2667**
1718.6736	15	D	3	**361.2082**
1817.7420	16	V	2	**246.1812**
	17	K	1	**147.1128**

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSQDVK



AEKESENNSENNSQDVK, MH+ 1963.8475, m/z 982.4274

File: Rep3_F1.02837.02837.2, Scan: 2837, Exp. m/z: 982.429, Charge: 2

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

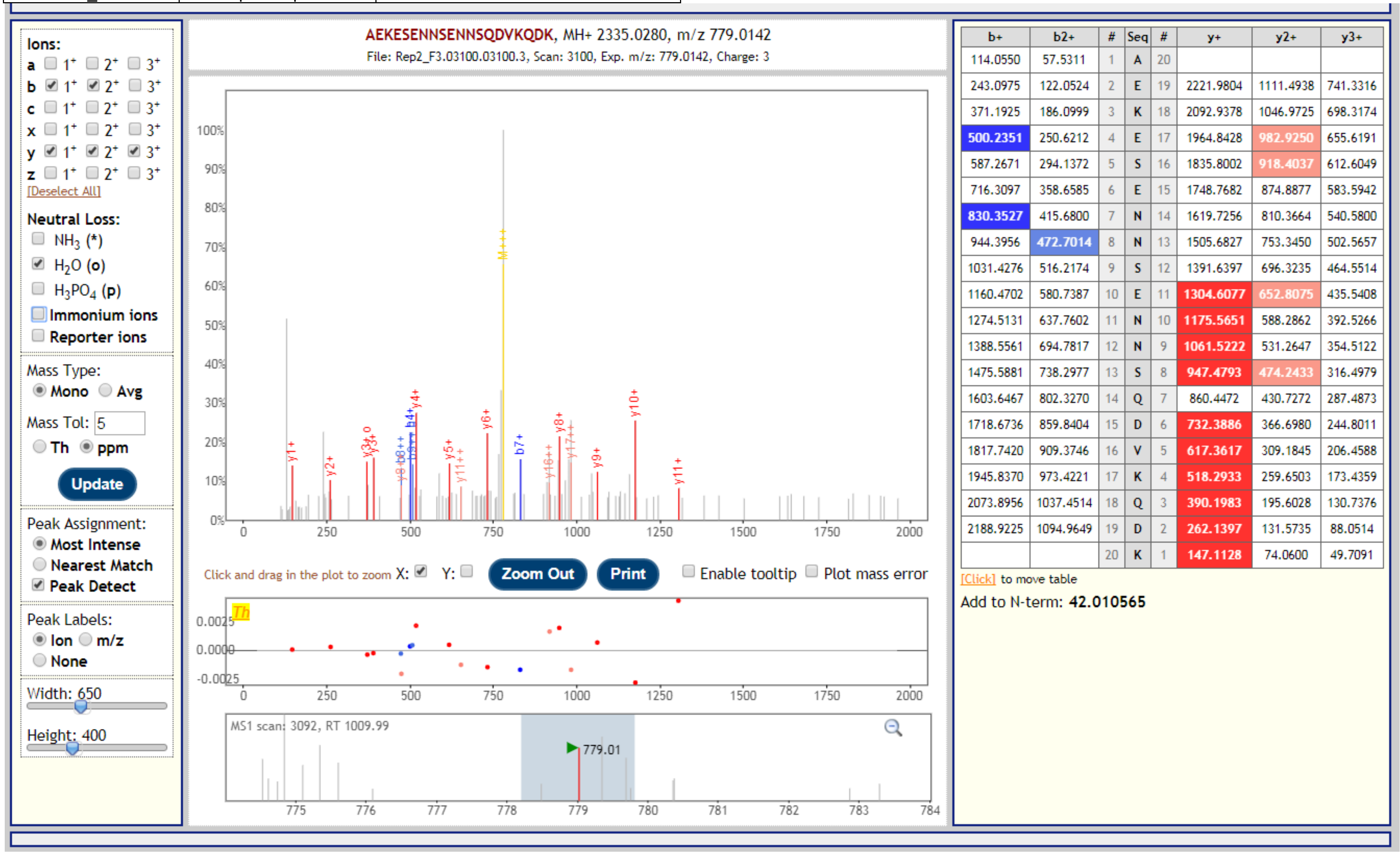
MS1 scan: 2834, RT 1134.47

b+	#	Seq	#	y+	y2+
114.0550	1	A	17		
243.0975	2	E	16	1850.7999	925.9036
371.1925	3	K	15	1721.7573	861.3823
500.2351	4	E	14	1593.6623	797.3348
587.2671	5	S	13	1464.6197	732.8135
716.3097	6	E	12	1377.5877	689.2975
830.3527	7	N	11	1248.5451	624.7762
944.3956	8	N	10	1134.5022	567.7547
1031.4276	9	S	9	1020.4592	510.7333
1160.4702	10	E	8	933.4272	467.2172
1274.5131	11	N	7	804.3846	402.6959
1388.5561	12	N	6	690.3417	345.6745
1475.5881	13	S	5	576.2988	288.6530
1603.6467	14	Q	4	489.2667	245.1370
1718.6736	15	D	3	361.2082	181.1077
1817.7420	16	V	2	246.1812	123.5942
	17	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSQDVKQDK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

AEKESENNSENNSQDVKQDK, MH+ 2335.0280, m/z 779.0142

File: Rep2_F3.03100.03100.3, Scan: 3100, Exp. m/z: 779.0142, Charge: 3

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

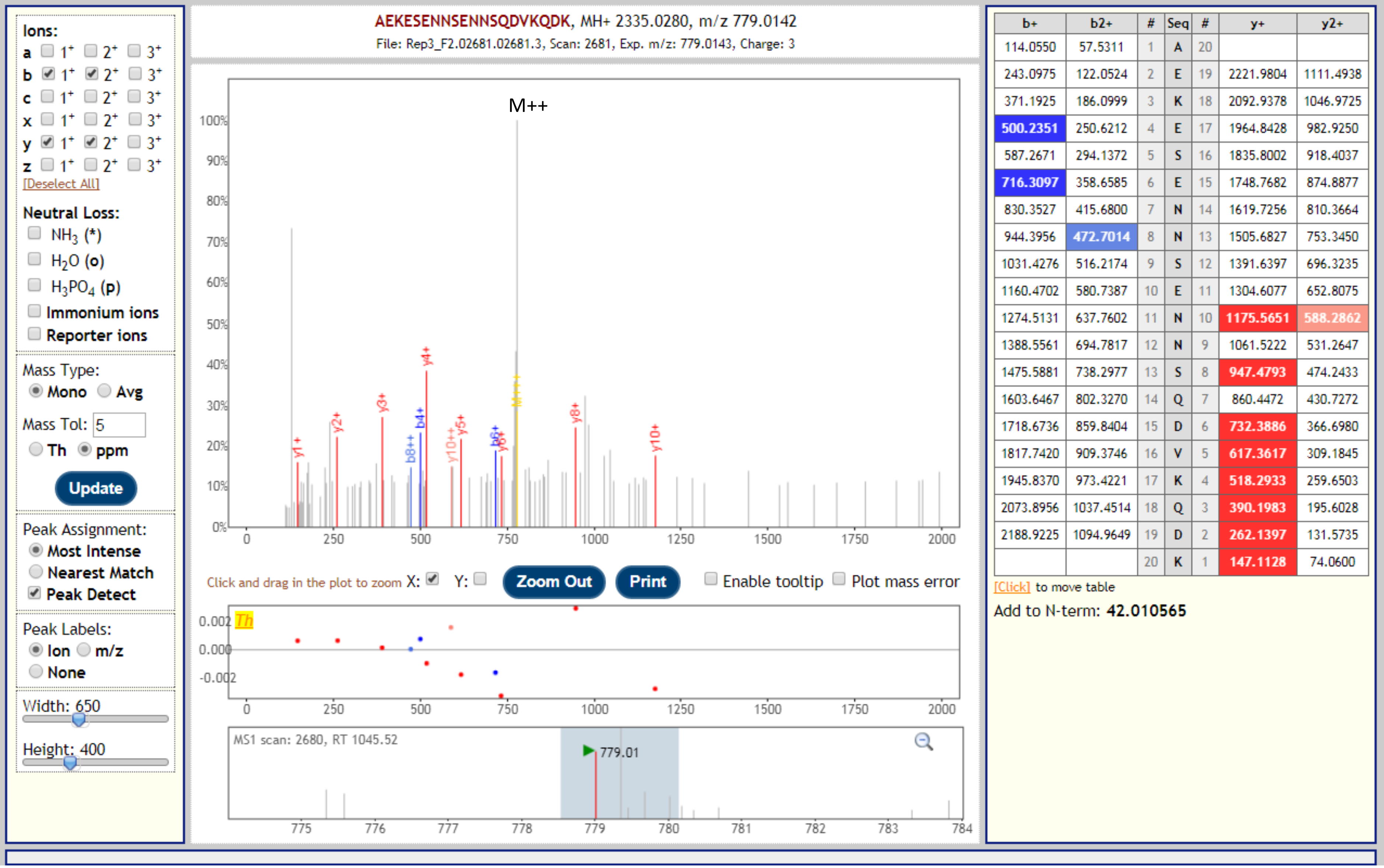
MS1 scan: 3092, RT 1009.99

b+	b2+	#	Seq	#	y+	y2+	y3+
114.0550	57.5311	1	A	20			
243.0975	122.0524	2	E	19	2221.9804	1111.4938	741.3316
371.1925	186.0999	3	K	18	2092.9378	1046.9725	698.3174
500.2351	250.6212	4	E	17	1964.8428	982.9250	655.6191
587.2671	294.1372	5	S	16	1835.8002	918.4037	612.6049
716.3097	358.6585	6	E	15	1748.7682	874.8877	583.5942
830.3527	415.6800	7	N	14	1619.7256	810.3664	540.5800
944.3956	472.7014	8	N	13	1505.6827	753.3450	502.5657
1031.4276	516.2174	9	S	12	1391.6397	696.3235	464.5514
1160.4702	580.7387	10	E	11	1304.6077	652.8075	435.5408
1274.5131	637.7602	11	N	10	1175.5651	588.2862	392.5266
1388.5561	694.7817	12	N	9	1061.5222	531.2647	354.5122
1475.5881	738.2977	13	S	8	947.4793	474.2433	316.4979
1603.6467	802.3270	14	Q	7	860.4472	430.7272	287.4873
1718.6736	859.8404	15	D	6	732.3886	366.6980	244.8011
1817.7420	909.3746	16	V	5	617.3617	309.1845	206.4588
1945.8370	973.4221	17	K	4	518.2933	259.6503	173.4359
2073.8956	1037.4514	18	Q	3	390.1983	195.6028	130.7376
2188.9225	1094.9649	19	D	2	262.1397	131.5735	88.0514
		20	K	1	147.1128	74.0600	49.7091

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSQDVKQDK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5

○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

AEKESENNSENNSQDVKQDK, MH+ 2335.0280, m/z 779.0142

File: Rep3_F2.02681.02681.3, Scan: 2681, Exp. m/z: 779.0143, Charge: 3

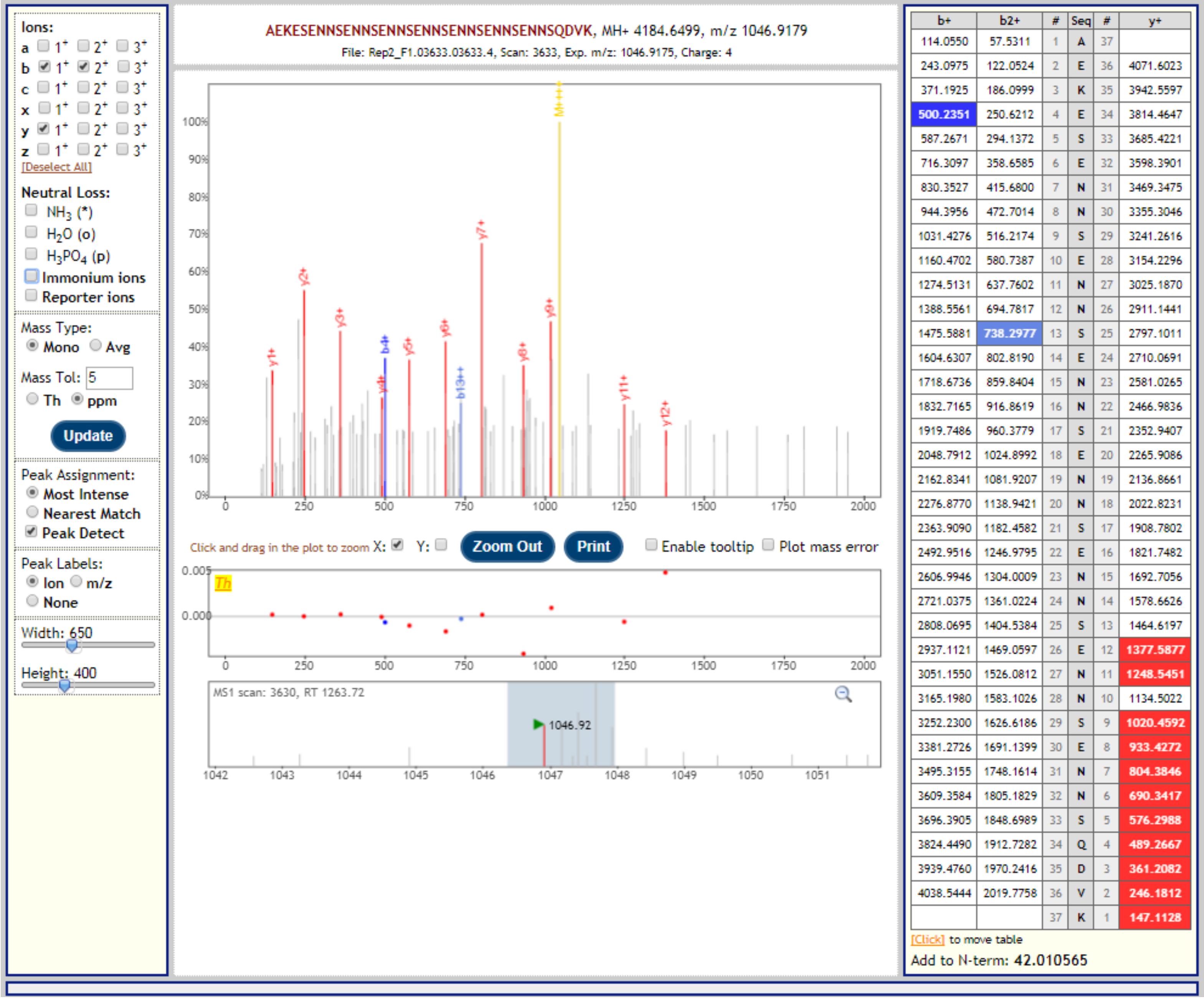
Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

b+	b2+	#	Seq	#	y+	y2+
114.0550	57.5311	1	A	20		
243.0975	122.0524	2	E	19	2221.9804	1111.4938
371.1925	186.0999	3	K	18	2092.9378	1046.9725
500.2351	250.6212	4	E	17	1964.8428	982.9250
587.2671	294.1372	5	S	16	1835.8002	918.4037
716.3097	358.6585	6	E	15	1748.7682	874.8877
830.3527	415.6800	7	N	14	1619.7256	810.3664
944.3956	472.7014	8	N	13	1505.6827	753.3450
1031.4276	516.2174	9	S	12	1391.6397	696.3235
1160.4702	580.7387	10	E	11	1304.6077	652.8075
1274.5131	637.7602	11	N	10	1175.5651	588.2862
1388.5561	694.7817	12	N	9	1061.5222	531.2647
1475.5881	738.2977	13	S	8	947.4793	474.2433
1603.6467	802.3270	14	Q	7	860.4472	430.7272
1718.6736	859.8404	15	D	6	732.3886	366.6980
1817.7420	909.3746	16	V	5	617.3617	309.1845
1945.8370	973.4221	17	K	4	518.2933	259.6503
2073.8956	1037.4514	18	Q	3	390.1983	195.6028
2188.9225	1094.9649	19	D	2	262.1397	131.5735
		20	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSENNSENNSENNSENNSENNSQDVK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5 ○ Th ● ppm

Peak Assignment: ● Most Intense ○ Nearest Match ☑ Peak Detect

Peak Labels: ● Ion ○ m/z ○ None

Width: 650

Height: 400

AEKESENNSENNSENNSENNSENNSENNSENNSQDVK, MH+ 4184.6499, m/z 1046.9179

File: Rep2_F1.03633.03633.4, Scan: 3633, Exp. m/z: 1046.9175, Charge: 4

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip ☐ Plot mass error

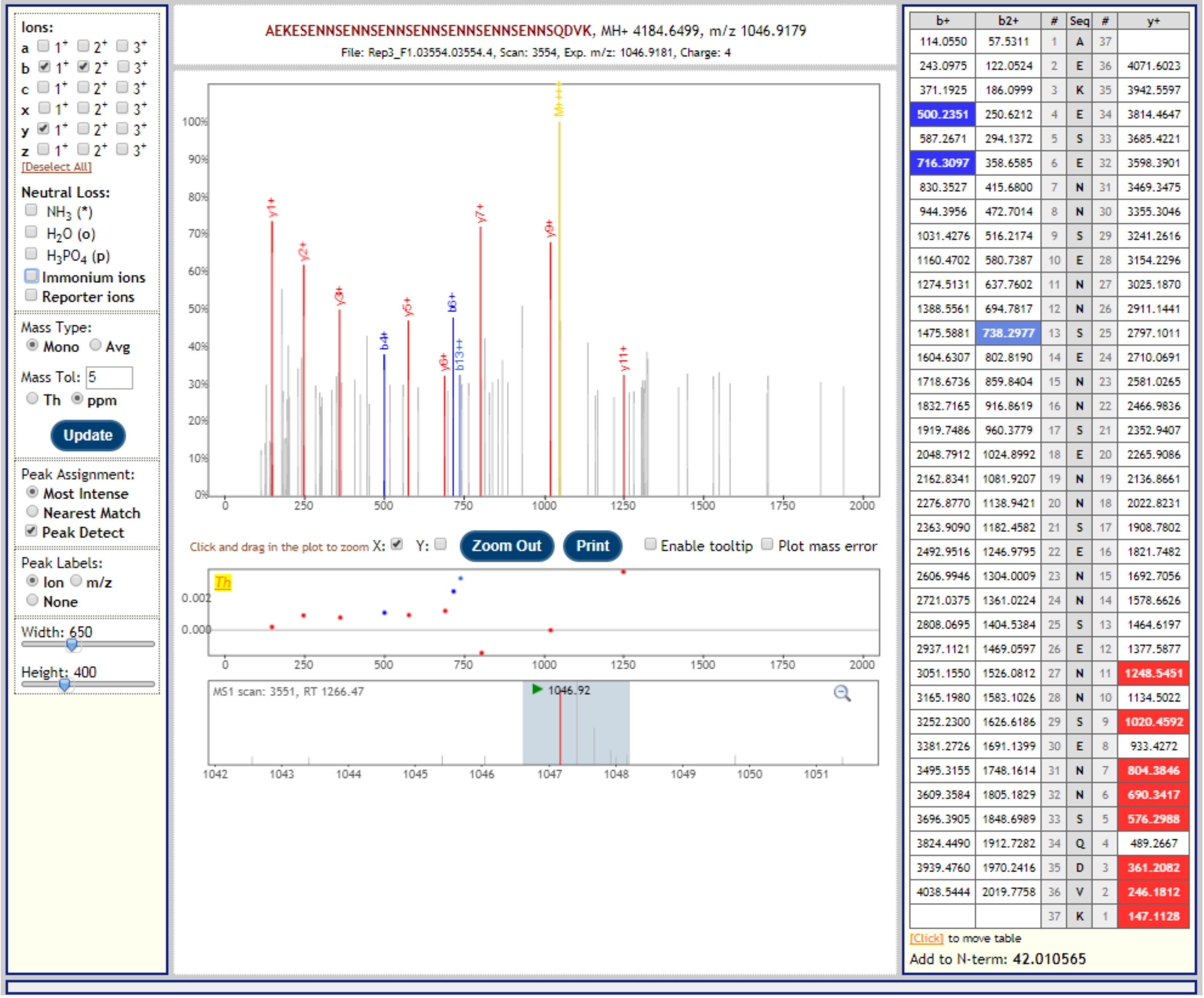
MS1 scan: 3630, RT 1263.72

b+	b2+	#	Seq	#	y+
114.0550	57.5311	1	A	37	
243.0975	122.0524	2	E	36	4071.6023
371.1925	186.0999	3	K	35	3942.5597
500.2351	250.6212	4	E	34	3814.4647
587.2671	294.1372	5	S	33	3685.4221
716.3097	358.6585	6	E	32	3598.3901
830.3527	415.6800	7	N	31	3469.3475
944.3956	472.7014	8	N	30	3355.3046
1031.4276	516.2174	9	S	29	3241.2616
1160.4702	580.7387	10	E	28	3154.2296
1274.5131	637.7602	11	N	27	3025.1870
1388.5561	694.7817	12	N	26	2911.1441
1475.5881	738.2977	13	S	25	2797.1011
1604.6307	802.8190	14	E	24	2710.0691
1718.6736	859.8404	15	N	23	2581.0265
1832.7165	916.8619	16	N	22	2466.9836
1919.7486	960.3779	17	S	21	2352.9407
2048.7912	1024.8992	18	E	20	2265.9086
2162.8341	1081.9207	19	N	19	2136.8661
2276.8770	1138.9421	20	N	18	2022.8231
2363.9090	1182.4582	21	S	17	1908.7802
2492.9516	1246.9795	22	E	16	1821.7482
2606.9946	1304.0009	23	N	15	1692.7056
2721.0375	1361.0224	24	N	14	1578.6626
2808.0695	1404.5384	25	S	13	1464.6197
2937.1121	1469.0597	26	E	12	1377.5877
3051.1550	1526.0812	27	N	11	1248.5451
3165.1980	1583.1026	28	N	10	1134.5022
3252.2300	1626.6186	29	S	9	1020.4592
3381.2726	1691.1399	30	E	8	933.4272
3495.3155	1748.1614	31	N	7	804.3846
3609.3584	1805.1829	32	N	6	690.3417
3696.3905	1848.6989	33	S	5	576.2988
3824.4490	1912.7282	34	Q	4	489.2667
3939.4760	1970.2416	35	D	3	361.2082
4038.5444	2019.7758	36	V	2	246.1812
		37	K	1	147.1128

[Click] to move table

Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSENNSENNSENNSENNSENNSQDVK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

AEKESENNSENNSENNSENNSENNSENNSENNSQDVK, MH+ 4184.6499, m/z 1046.9179

File: Rep3_F1.03554.03554.4, Scan: 3554, Exp. m/z: 1046.9181, Charge: 4

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

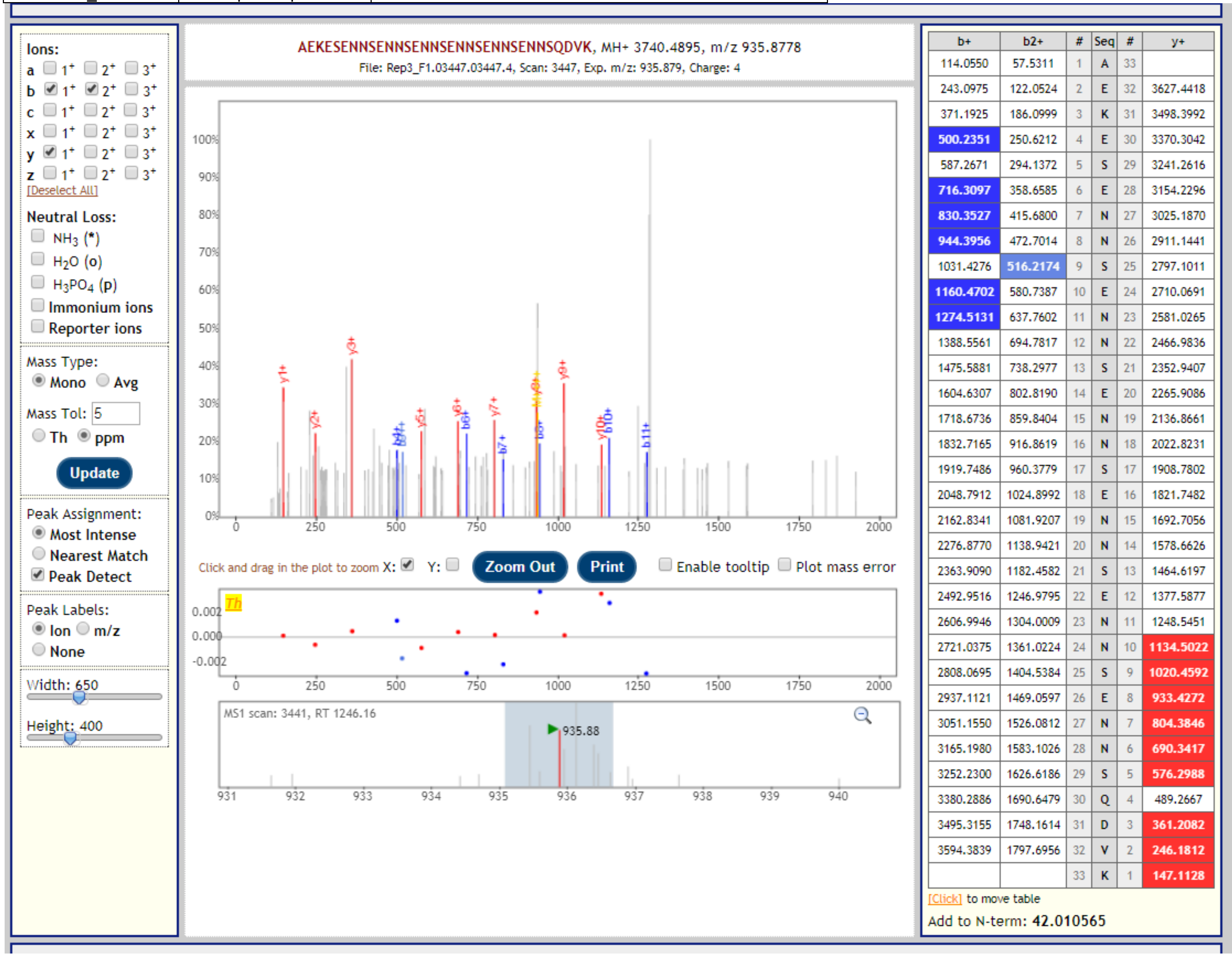
MS1 scan: 3551, RT 1266.47

b+	b2+	#	Seq	#	y+
114.0550	57.5311	1	A	37	
243.0975	122.0524	2	E	36	4071.6023
371.1925	186.0999	3	K	35	3942.5597
500.2351	250.6212	4	E	34	3814.4647
587.2671	294.1372	5	S	33	3685.4221
716.3097	358.6585	6	E	32	3598.3901
830.3527	415.6800	7	N	31	3469.3475
944.3956	472.7014	8	N	30	3355.3046
1031.4276	516.2174	9	S	29	3241.2616
1160.4702	580.7387	10	E	28	3154.2296
1274.5131	637.7602	11	N	27	3025.1870
1388.5561	694.7817	12	N	26	2911.1441
1475.5881	738.2977	13	S	25	2797.1011
1604.6307	802.8190	14	E	24	2710.0691
1718.6736	859.8404	15	N	23	2581.0265
1832.7165	916.8619	16	N	22	2466.9836
1919.7486	960.3779	17	S	21	2352.9407
2048.7912	1024.8992	18	E	20	2265.9086
2162.8341	1081.9207	19	N	19	2136.8661
2276.8770	1138.9421	20	N	18	2022.8231
2363.9090	1182.4582	21	S	17	1908.7802
2492.9516	1246.9795	22	E	16	1821.7482
2606.9946	1304.0009	23	N	15	1692.7056
2721.0375	1361.0224	24	N	14	1578.6626
2808.0695	1404.5384	25	S	13	1464.6197
2937.1121	1469.0597	26	E	12	1377.5877
3051.1550	1526.0812	27	N	11	1248.5451
3165.1980	1583.1026	28	N	10	1134.5022
3252.2300	1626.6186	29	S	9	1020.4592
3381.2726	1691.1399	30	E	8	933.4272
3495.3155	1748.1614	31	N	7	804.3846
3609.3584	1805.1829	32	N	6	690.3417
3696.3905	1848.6989	33	S	5	576.2988
3824.4490	1912.7282	34	Q	4	489.2667
3939.4760	1970.2416	35	D	3	361.2082
4038.5444	2019.7758	36	V	2	246.1812
		37	K	1	147.1128

[Click] to move table

Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSENNSENNSENNSENNSQDVK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg
Mass Tol: 5 ○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650
Height: 400

AEKESENNSENNSENNSENNSENNSENNSQDVK, MH+ 3740.4895, m/z 935.8778
File: Rep3_F1.03447.03447.4, Scan: 3447, Exp. m/z: 935.879, Charge: 4

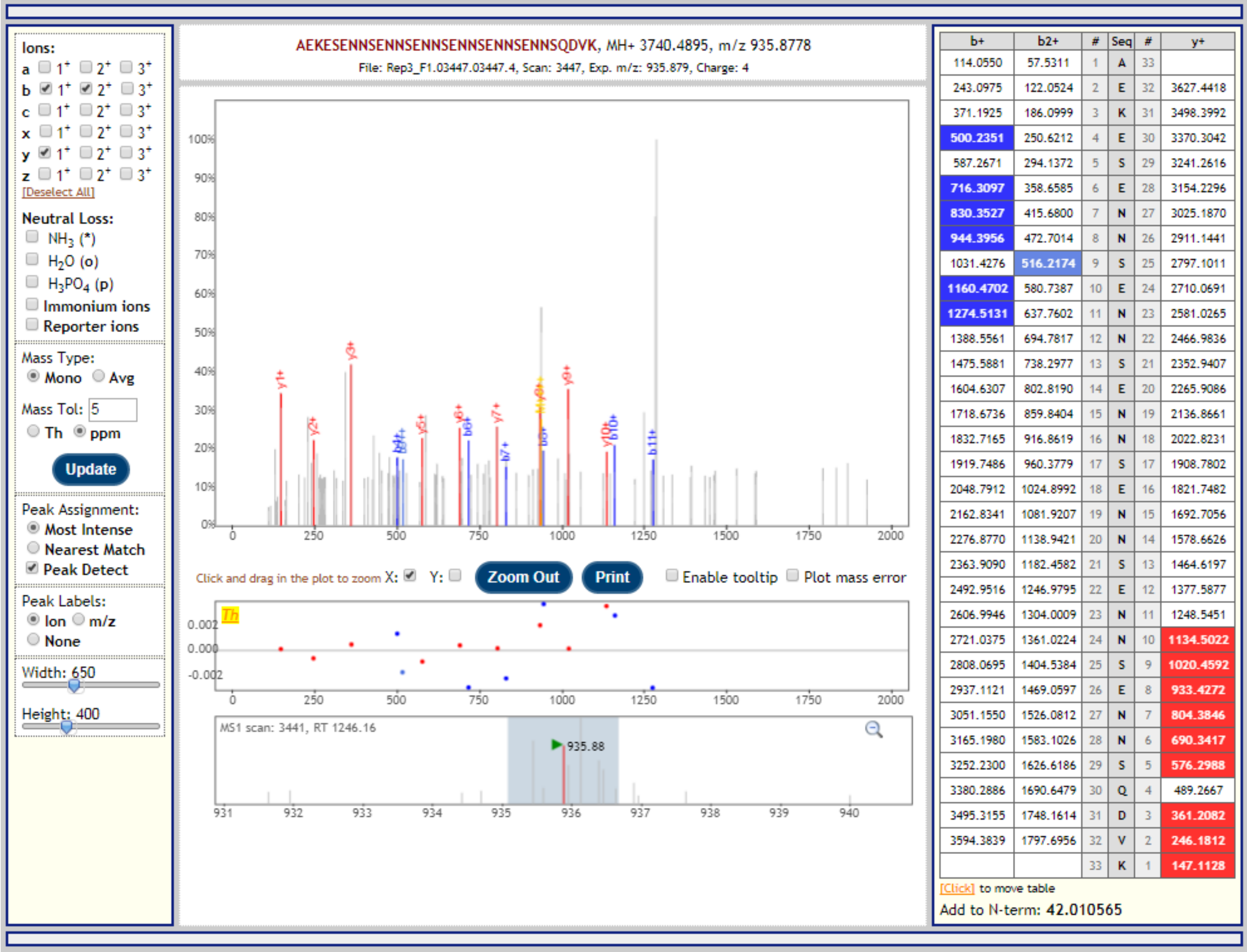
Click and drag in the plot to zoom X: ☑ Y: ☐ Enable tooltip ☐ Plot mass error

MS1 scan: 3441, RT 1246.16

b+	b2+	#	Seq	#	y+
114.0550	57.5311	1	A	33	
243.0975	122.0524	2	E	32	3627.4418
371.1925	186.0999	3	K	31	3498.3992
500.2351	250.6212	4	E	30	3370.3042
587.2671	294.1372	5	S	29	3241.2616
716.3097	358.6585	6	E	28	3154.2296
830.3527	415.6800	7	N	27	3025.1870
944.3956	472.7014	8	N	26	2911.1441
1031.4276	516.2174	9	S	25	2797.1011
1160.4702	580.7387	10	E	24	2710.0691
1274.5131	637.7602	11	N	23	2581.0265
1388.5561	694.7817	12	N	22	2466.9836
1475.5881	738.2977	13	S	21	2352.9407
1604.6307	802.8190	14	E	20	2265.9086
1718.6736	859.8404	15	N	19	2136.8661
1832.7165	916.8619	16	N	18	2022.8231
1919.7486	960.3779	17	S	17	1908.7802
2048.7912	1024.8992	18	E	16	1821.7482
2162.8341	1081.9207	19	N	15	1692.7056
2276.8770	1138.9421	20	N	14	1578.6626
2363.9090	1182.4582	21	S	13	1464.6197
2492.9516	1246.9795	22	E	12	1377.5877
2606.9946	1304.0009	23	N	11	1248.5451
2721.0375	1361.0224	24	N	10	1134.5022
2808.0695	1404.5384	25	S	9	1020.4592
2937.1121	1469.0597	26	E	8	933.4272
3051.1550	1526.0812	27	N	7	804.3846
3165.1980	1583.1026	28	N	6	690.3417
3252.2300	1626.6186	29	S	5	576.2988
3380.2886	1690.6479	30	Q	4	489.2667
3495.3155	1748.1614	31	D	3	361.2082
3594.3839	1797.6956	32	V	2	246.1812
		33	K	1	147.1128

[Click] to move table
Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSENNSENNSENNSENNSQDVK



AEKESENNSENNSENNSENNSENNSENNSQDVK, MH+ 3740.4895, m/z 935.8778

File: Rep3_F1.03447.03447.4, Scan: 3447, Exp. m/z: 935.879, Charge: 4

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5 ○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip ☐ Plot mass error

MS1 scan: 3441, RT 1246.16

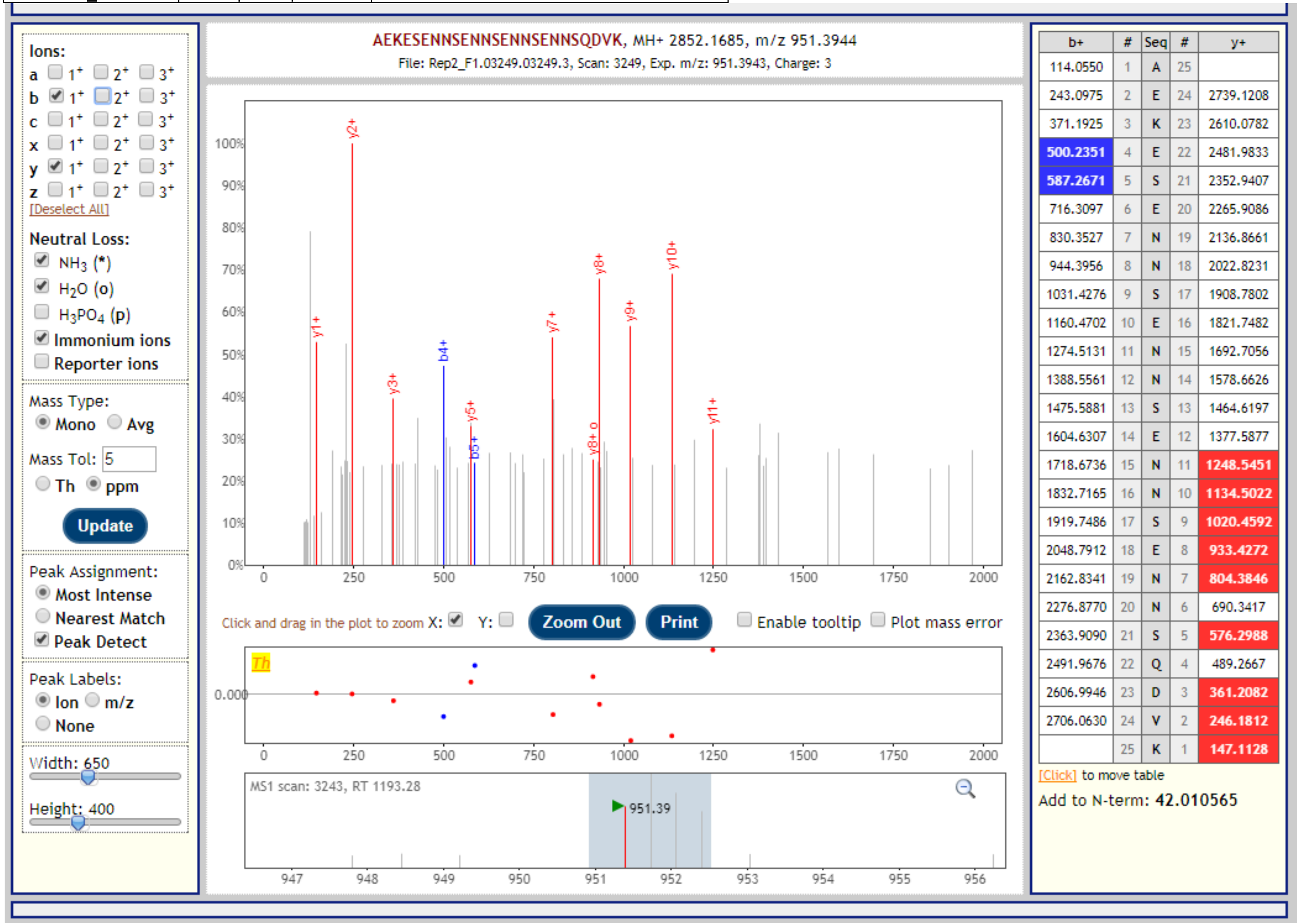
935.88

b+	b2+	#	Seq	#	y+
114.0550	57.5311	1	A	33	
243.0975	122.0524	2	E	32	3627.4418
371.1925	186.0999	3	K	31	3498.3992
500.2351	250.6212	4	E	30	3370.3042
587.2671	294.1372	5	S	29	3241.2616
716.3097	358.6585	6	E	28	3154.2296
830.3527	415.6800	7	N	27	3025.1870
944.3956	472.7014	8	N	26	2911.1441
1031.4276	516.2174	9	S	25	2797.1011
1160.4702	580.7387	10	E	24	2710.0691
1274.5131	637.7602	11	N	23	2581.0265
1388.5561	694.7817	12	N	22	2466.9836
1475.5881	738.2977	13	S	21	2352.9407
1604.6307	802.8190	14	E	20	2265.9086
1718.6736	859.8404	15	N	19	2136.8661
1832.7165	916.8619	16	N	18	2022.8231
1919.7486	960.3779	17	S	17	1908.7802
2048.7912	1024.8992	18	E	16	1821.7482
2162.8341	1081.9207	19	N	15	1692.7056
2276.8770	1138.9421	20	N	14	1578.6626
2363.9090	1182.4582	21	S	13	1464.6197
2492.9516	1246.9795	22	E	12	1377.5877
2606.9946	1304.0009	23	N	11	1248.5451
2721.0375	1361.0224	24	N	10	1134.5022
2808.0695	1404.5384	25	S	9	1020.4592
2937.1121	1469.0597	26	E	8	933.4272
3051.1550	1526.0812	27	N	7	804.3846
3165.1980	1583.1026	28	N	6	690.3417
3252.2300	1626.6186	29	S	5	576.2988
3380.2886	1690.6479	30	Q	4	489.2667
3495.3155	1748.1614	31	D	3	361.2082
3594.3839	1797.6956	32	V	2	246.1812
		33	K	1	147.1128

[Click] to move table

Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSENNSENNSQDVK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☑ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg
Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650
Height: 400

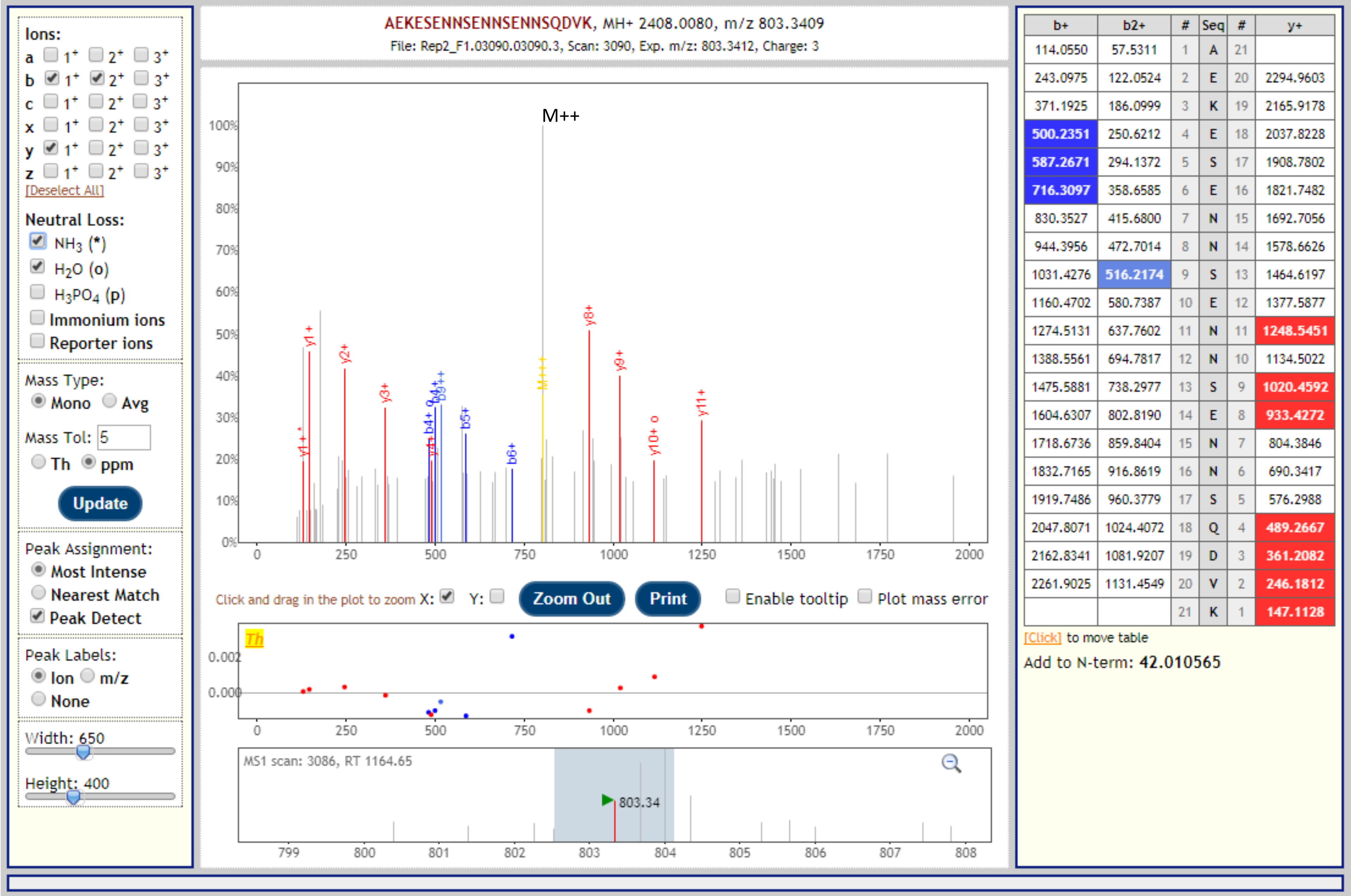
AEKESENNSENNSENNSENNSQDVK, MH+ 2852.1685, m/z 951.3944
File: Rep2_F1.03249.03249.3, Scan: 3249, Exp. m/z: 951.3943, Charge: 3

Click and drag in the plot to zoom X: ☑ Y: ☐
☐ Enable tooltip ☐ Plot mass error

b+	#	Seq	#	y+
114.0550	1	A	25	
243.0975	2	E	24	2739.1208
371.1925	3	K	23	2610.0782
500.2351	4	E	22	2481.9833
587.2671	5	S	21	2352.9407
716.3097	6	E	20	2265.9086
830.3527	7	N	19	2136.8661
944.3956	8	N	18	2022.8231
1031.4276	9	S	17	1908.7802
1160.4702	10	E	16	1821.7482
1274.5131	11	N	15	1692.7056
1388.5561	12	N	14	1578.6626
1475.5881	13	S	13	1464.6197
1604.6307	14	E	12	1377.5877
1718.6736	15	N	11	1248.5451
1832.7165	16	N	10	1134.5022
1919.7486	17	S	9	1020.4592
2048.7912	18	E	8	933.4272
2162.8341	19	N	7	804.3846
2276.8770	20	N	6	690.3417
2363.9090	21	S	5	576.2988
2491.9676	22	Q	4	489.2667
2606.9946	23	D	3	361.2082
2706.0630	24	V	2	246.1812
	25	K	1	147.1128

[Click] to move table
Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1003000	liver specific protein 2	RLI.AEKESENNSENNSENNSQDVK



AEKESENNSENNSENNSQDVK, MH+ 2408.0080, m/z 803.3409

File: Rep2_F1.03090.03090.3, Scan: 3090, Exp. m/z: 803.3412, Charge: 3

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5 ○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels: ● Ion ○ m/z ○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip ☐ Plot mass error

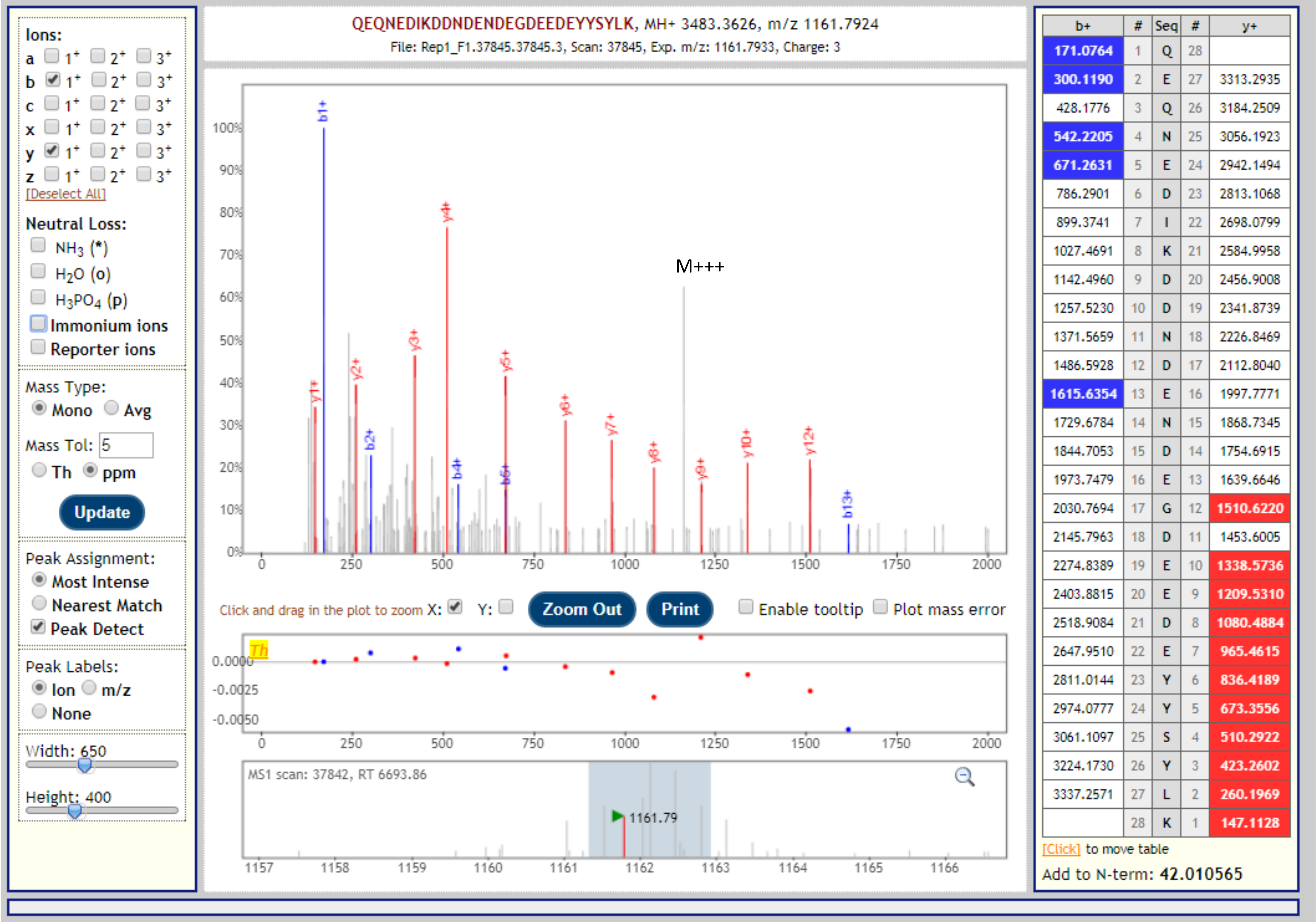
MS1 scan: 3086, RT 1164.65

b+	b2+	#	Seq	#	y+
114.0550	57.5311	1	A	21	
243.0975	122.0524	2	E	20	2294.9603
371.1925	186.0999	3	K	19	2165.9178
500.2351	250.6212	4	E	18	2037.8228
587.2671	294.1372	5	S	17	1908.7802
716.3097	358.6585	6	E	16	1821.7482
830.3527	415.6800	7	N	15	1692.7056
944.3956	472.7014	8	N	14	1578.6626
1031.4276	516.2174	9	S	13	1464.6197
1160.4702	580.7387	10	E	12	1377.5877
1274.5131	637.7602	11	N	11	1248.5451
1388.5561	694.7817	12	N	10	1134.5022
1475.5881	738.2977	13	S	9	1020.4592
1604.6307	802.8190	14	E	8	933.4272
1718.6736	859.8404	15	N	7	804.3846
1832.7165	916.8619	16	N	6	690.3417
1919.7486	960.3779	17	S	5	576.2988
2047.8071	1024.4072	18	Q	4	489.2667
2162.8341	1081.9207	19	D	3	361.2082
2261.9025	1131.4549	20	V	2	246.1812
		21	K	1	147.1128

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1328000	serine/threonine protein phosphatase UIS2	RVL.QEQNEDIKDDNDENDEGDEEDEYYSYLK


QEQNEDIKDDNDENDEGDEEDEYYSYLK, MH+ 3483.3626, m/z 1161.7924

File: Rep1_F1.37845.37845.3, Scan: 37845, Exp. m/z: 1161.7933, Charge: 3

Ions:
a ☐ 1^+ ☐ 2^+ ☐ 3^+
b ☑ 1^+ ☐ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☐ 2^+ ☐ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5 ○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels: ● Ion ○ m/z ○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

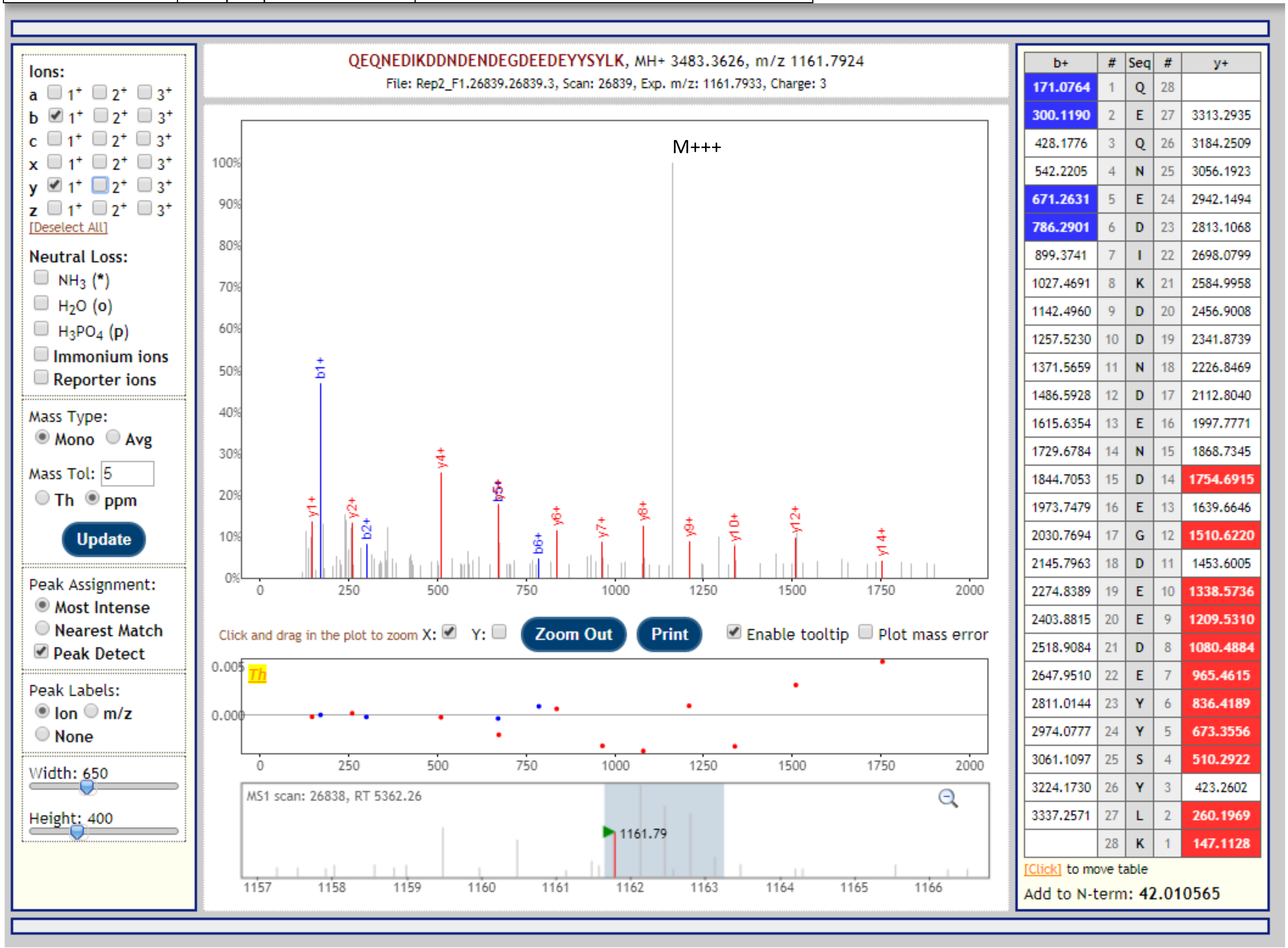
MS1 scan: 37842, RT 6693.86

b+	#	Seq	#	y+
171.0764	1	Q	28	
300.1190	2	E	27	3313.2935
428.1776	3	Q	26	3184.2509
542.2205	4	N	25	3056.1923
671.2631	5	E	24	2942.1494
786.2901	6	D	23	2813.1068
899.3741	7	I	22	2698.0799
1027.4691	8	K	21	2584.9958
1142.4960	9	D	20	2456.9008
1257.5230	10	D	19	2341.8739
1371.5659	11	N	18	2226.8469
1486.5928	12	D	17	2112.8040
1615.6354	13	E	16	1997.7771
1729.6784	14	N	15	1868.7345
1844.7053	15	D	14	1754.6915
1973.7479	16	E	13	1639.6646
2030.7694	17	G	12	1510.6220
2145.7963	18	D	11	1453.6005
2274.8389	19	E	10	1338.5736
2403.8815	20	E	9	1209.5310
2518.9084	21	D	8	1080.4884
2647.9510	22	E	7	965.4615
2811.0144	23	Y	6	836.4189
2974.0777	24	Y	5	673.3556
3061.1097	25	S	4	510.2922
3224.1730	26	Y	3	423.2602
3337.2571	27	L	2	260.1969
	28	K	1	147.1128

[Click] to move table

Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1328000	serine/threonine protein phosphatase UIS2	RVL.QEQNEDIKDDNDENDEGDEEDEYYSYLK



QEQNEDIKDDNDENDEGDEEDEYYSYLK, MH+ 3483.3626, m/z 1161.7924

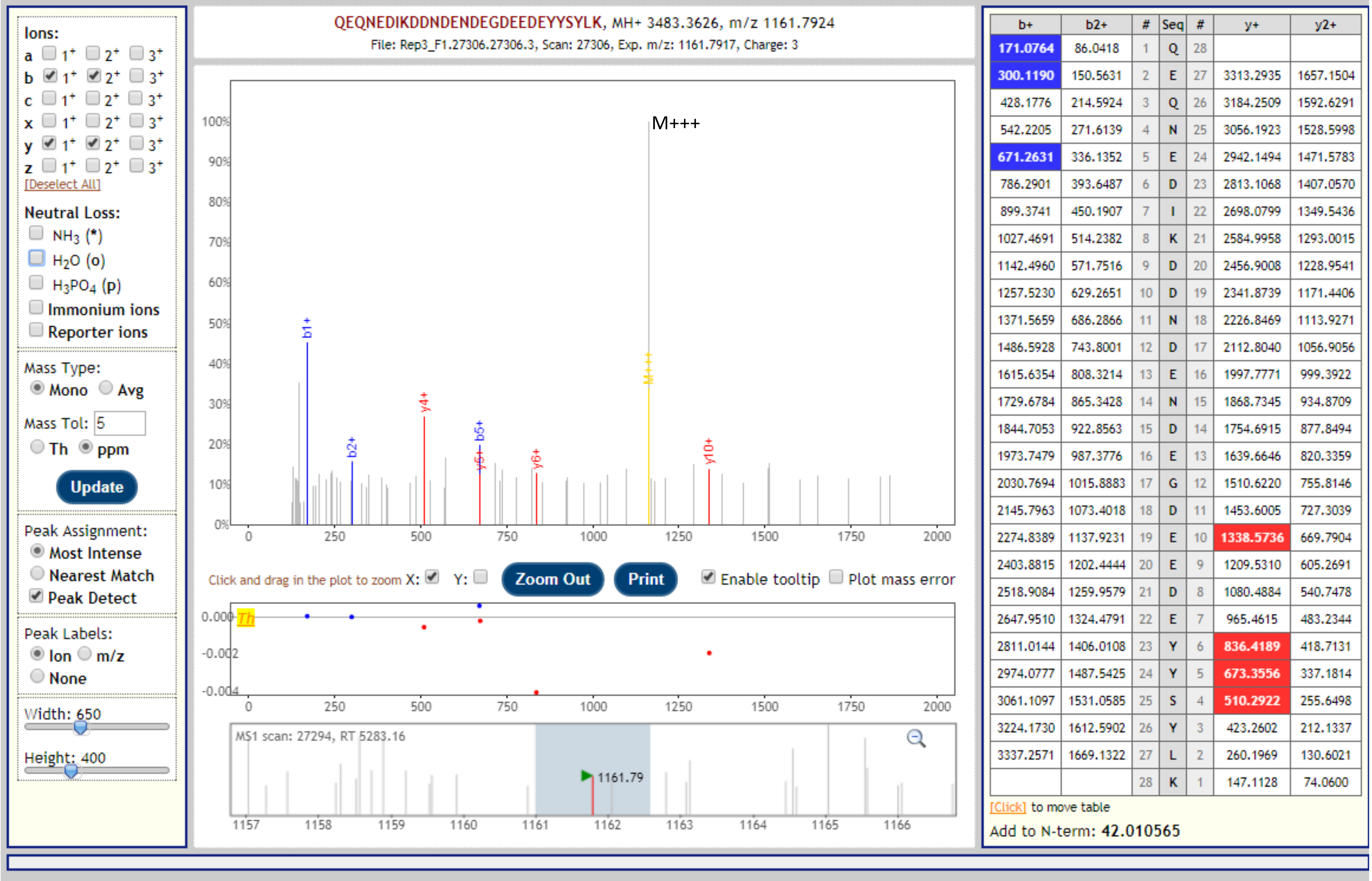
File: Rep2_F1.26839.26839.3, Scan: 26839, Exp. m/z: 1161.7933, Charge: 3

b+	#	Seq	#	y+
171.0764	1	Q	28	
300.1190	2	E	27	3313.2935
428.1776	3	Q	26	3184.2509
542.2205	4	N	25	3056.1923
671.2631	5	E	24	2942.1494
786.2901	6	D	23	2813.1068
899.3741	7	I	22	2698.0799
1027.4691	8	K	21	2584.9958
1142.4960	9	D	20	2456.9008
1257.5230	10	D	19	2341.8739
1371.5659	11	N	18	2226.8469
1486.5928	12	D	17	2112.8040
1615.6354	13	E	16	1997.7771
1729.6784	14	N	15	1868.7345
1844.7053	15	D	14	**1754.6915**
1973.7479	16	E	13	1639.6646
2030.7694	17	G	12	**1510.6220**
2145.7963	18	D	11	1453.6005
2274.8389	19	E	10	**1338.5736**
2403.8815	20	E	9	**1209.5310**
2518.9084	21	D	8	**1080.4884**
2647.9510	22	E	7	**965.4615**
2811.0144	23	Y	6	**836.4189**
2974.0777	24	Y	5	**673.3556**
3061.1097	25	S	4	**510.2922**
3224.1730	26	Y	3	423.2602
3337.2571	27	L	2	**260.1969**
	28	K	1	**147.1128**

[Click] to move table

Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1328000	serine/threonine protein phosphatase UIS2	RVL.QEQNEDIKDDNDENDEGDEEDEYYSYLK



QEQNEDIKDDNDENDEGDEEDEYYSYLK, MH+ 3483.3626, m/z 1161.7924

File: Rep3_F1.27306.27306.3, Scan: 27306, Exp. m/z: 1161.7917, Charge: 3

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5

○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐

☑ Enable tooltip ☐ Plot mass error

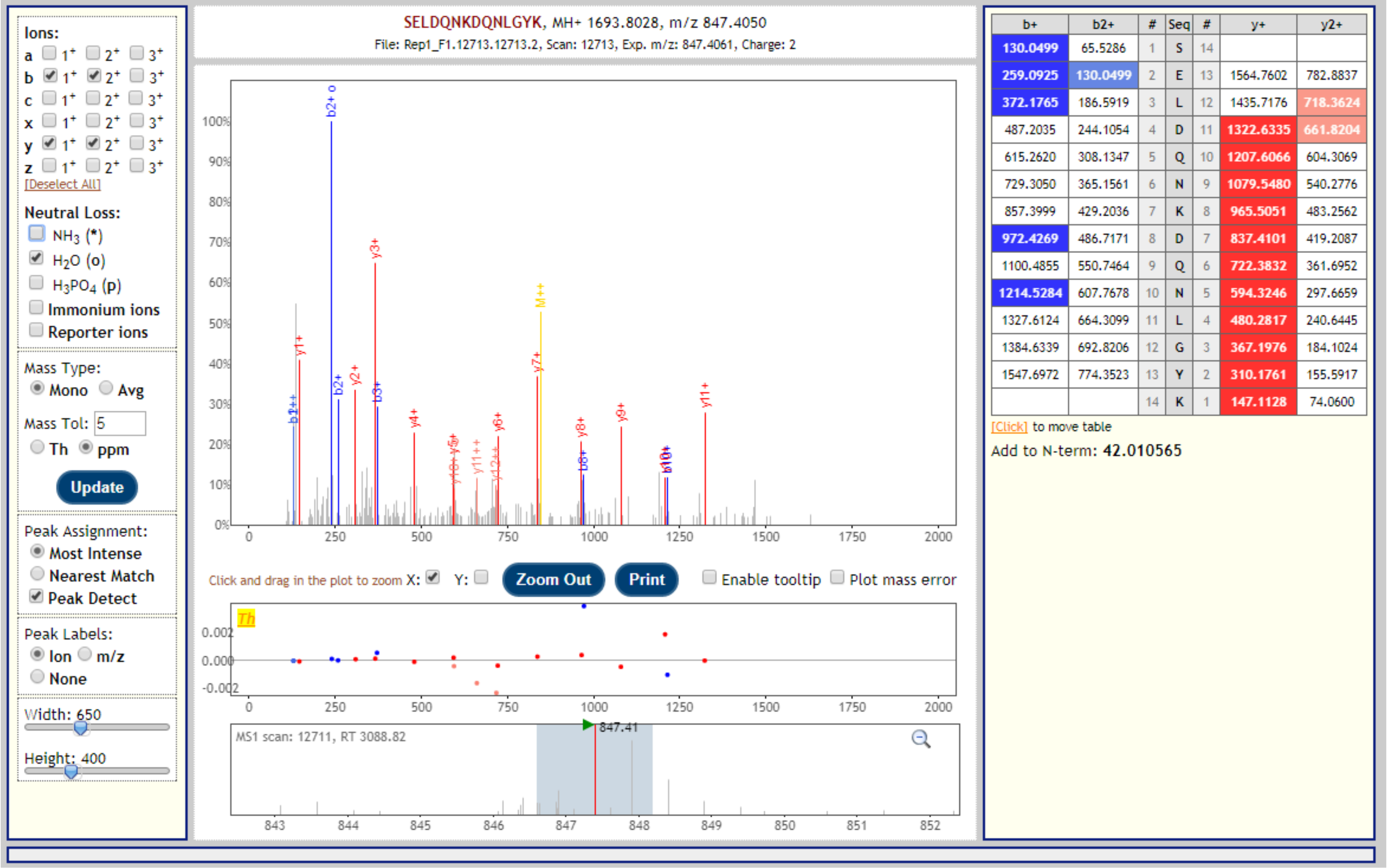
MS1 scan: 27294, RT 5283.16

b+	b2+	#	Seq	#	y+	y2+
171.0764	86.0418	1	Q	28		
300.1190	150.5631	2	E	27	3313.2935	1657.1504
428.1776	214.5924	3	Q	26	3184.2509	1592.6291
542.2205	271.6139	4	N	25	3056.1923	1528.5998
671.2631	336.1352	5	E	24	2942.1494	1471.5783
786.2901	393.6487	6	D	23	2813.1068	1407.0570
899.3741	450.1907	7	I	22	2698.0799	1349.5436
1027.4691	514.2382	8	K	21	2584.9958	1293.0015
1142.4960	571.7516	9	D	20	2456.9008	1228.9541
1257.5230	629.2651	10	D	19	2341.8739	1171.4406
1371.5659	686.2866	11	N	18	2226.8469	1113.9271
1486.5928	743.8001	12	D	17	2112.8040	1056.9056
1615.6354	808.3214	13	E	16	1997.7771	999.3922
1729.6784	865.3428	14	N	15	1868.7345	934.8709
1844.7053	922.8563	15	D	14	1754.6915	877.8494
1973.7479	987.3776	16	E	13	1639.6646	820.3359
2030.7694	1015.8883	17	G	12	1510.6220	755.8146
2145.7963	1073.4018	18	D	11	1453.6005	727.3039
2274.8389	1137.9231	19	E	10	1338.5736	669.7904
2403.8815	1202.4444	20	E	9	1209.5310	605.2691
2518.9084	1259.9579	21	D	8	1080.4884	540.7478
2647.9510	1324.4791	22	E	7	965.4615	483.2344
2811.0144	1406.0108	23	Y	6	836.4189	418.7131
2974.0777	1487.5425	24	Y	5	673.3556	337.1814
3061.1097	1531.0585	25	S	4	510.2922	255.6498
3224.1730	1612.5902	26	Y	3	423.2602	212.1337
3337.2571	1669.1322	27	L	2	260.1969	130.6021
		28	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

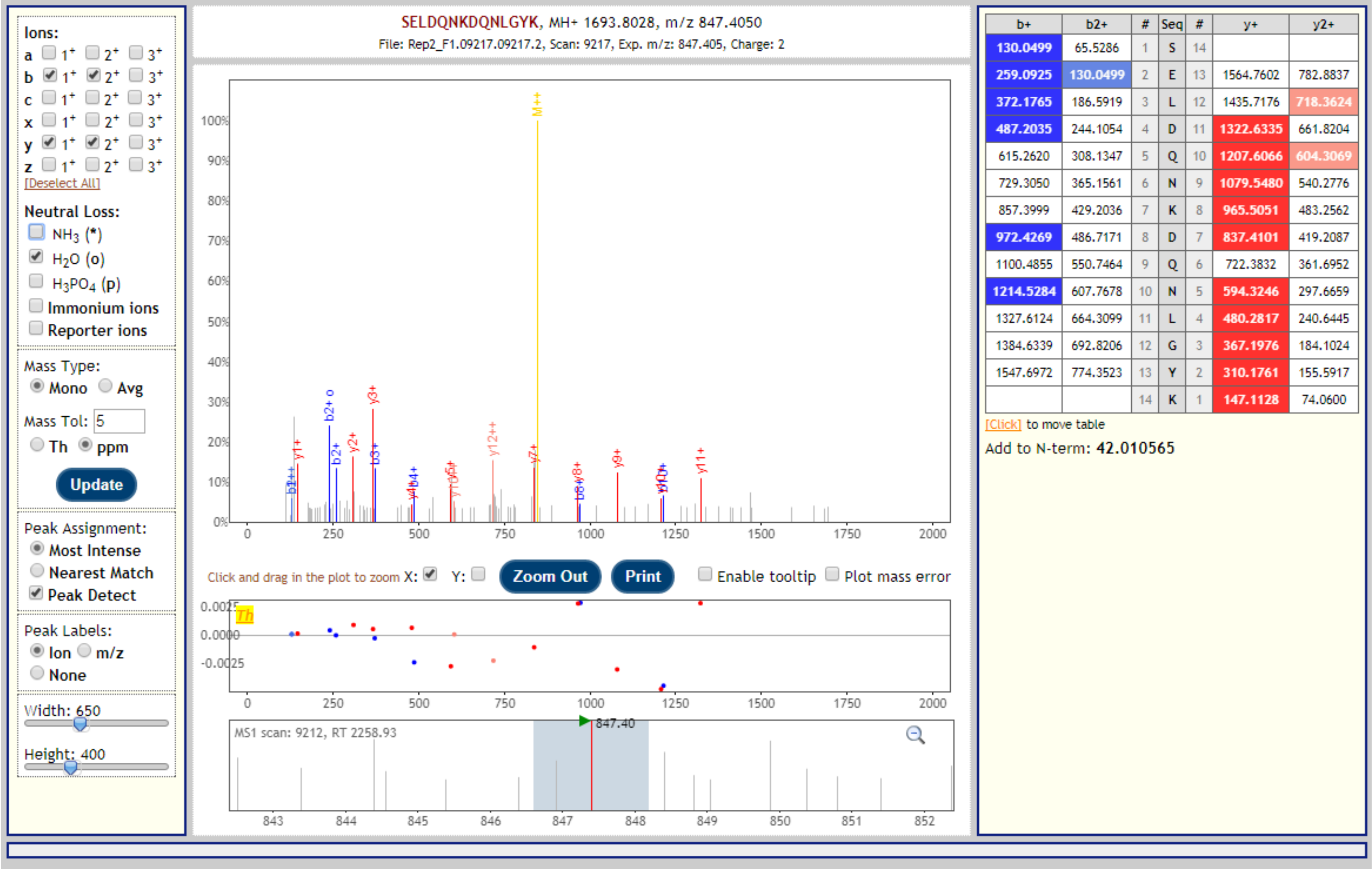
Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1365500	exported protein IBIS1	RIL.SELDQNKDQNLGYK



b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	S	14		
259.0925	130.0499	2	E	13	1564.7602	782.8837
372.1765	186.5919	3	L	12	1435.7176	718.3624
487.2035	244.1054	4	D	11	1322.6335	661.8204
615.2620	308.1347	5	Q	10	1207.6066	604.3069
729.3050	365.1561	6	N	9	1079.5480	540.2776
857.3999	429.2036	7	K	8	965.5051	483.2562
972.4269	486.7171	8	D	7	837.4101	419.2087
1100.4855	550.7464	9	Q	6	722.3832	361.6952
1214.5284	607.7678	10	N	5	594.3246	297.6659
1327.6124	664.3099	11	L	4	480.2817	240.6445
1384.6339	692.8206	12	G	3	367.1976	184.1024
1547.6972	774.3523	13	Y	2	310.1761	155.5917
		14	K	1	147.1128	74.0600

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1365500	exported protein IBIS1	RIL.SELDQNKDQNLGYK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg
Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650
Height: 400

SELDQNKDQNLGYK, MH+ 1693.8028, m/z 847.4050
File: Rep2_F1.09217.09217.2, Scan: 9217, Exp. m/z: 847.405, Charge: 2

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip ☐ Plot mass error

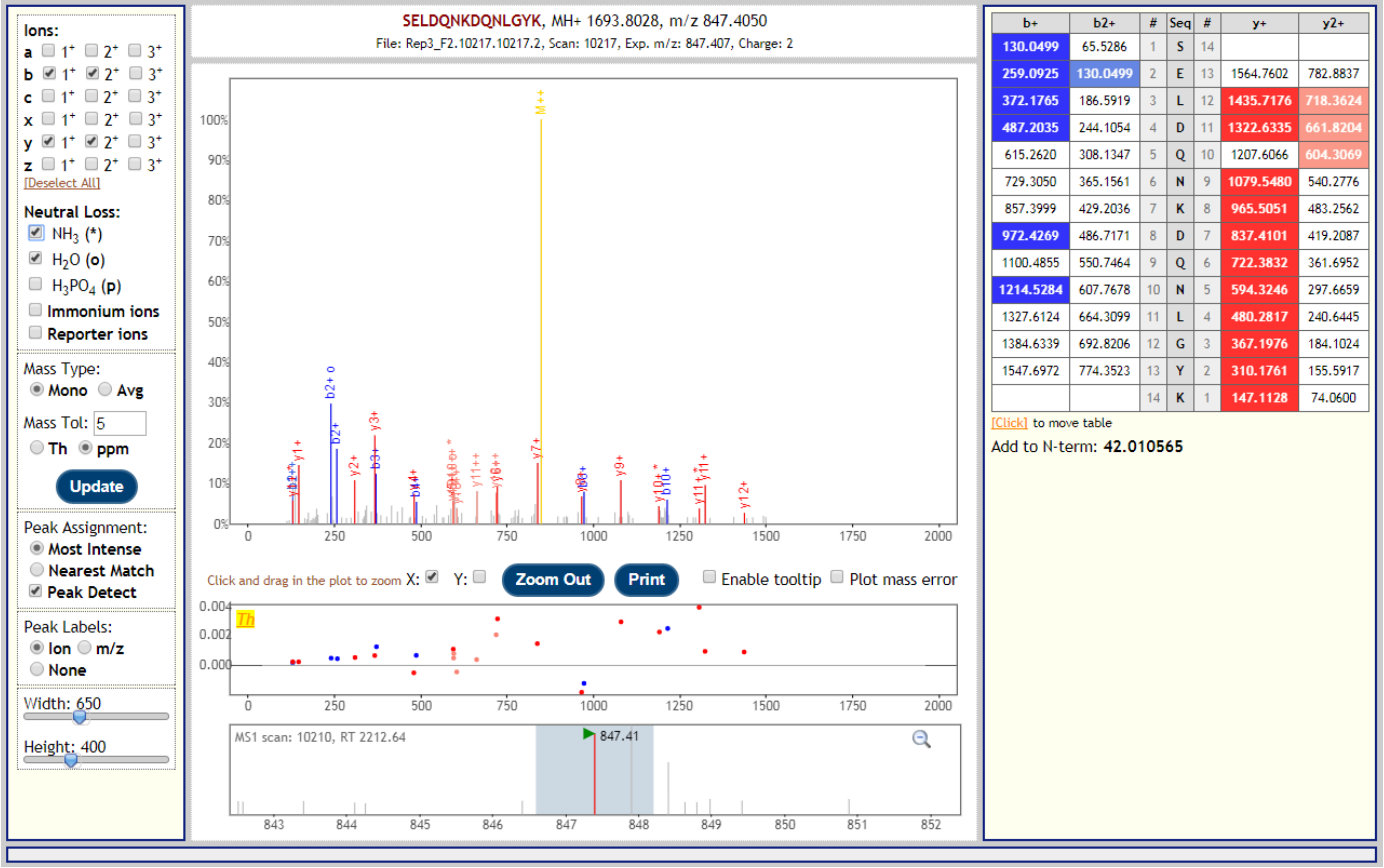
MS1 scan: 9212, RT 2258.93

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	S	14		
259.0925	130.0499	2	E	13	1564.7602	782.8837
372.1765	186.5919	3	L	12	1435.7176	718.3624
487.2035	244.1054	4	D	11	1322.6335	661.8204
615.2620	308.1347	5	Q	10	1207.6066	604.3069
729.3050	365.1561	6	N	9	1079.5480	540.2776
857.3999	429.2036	7	K	8	965.5051	483.2562
972.4269	486.7171	8	D	7	837.4101	419.2087
1100.4855	550.7464	9	Q	6	722.3832	361.6952
1214.5284	607.7678	10	N	5	594.3246	297.6659
1327.6124	664.3099	11	L	4	480.2817	240.6445
1384.6339	692.8206	12	G	3	367.1976	184.1024
1547.6972	774.3523	13	Y	2	310.1761	155.5917
		14	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1365500	exported protein IBIS1	RIL.SELDQNKDQNLGYK



SELDQNKDQNLGYK, MH+ 1693.8028, m/z 847.4050

File: Rep3_F2.10217.10217.2, Scan: 10217, Exp. m/z: 847.407, Charge: 2

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

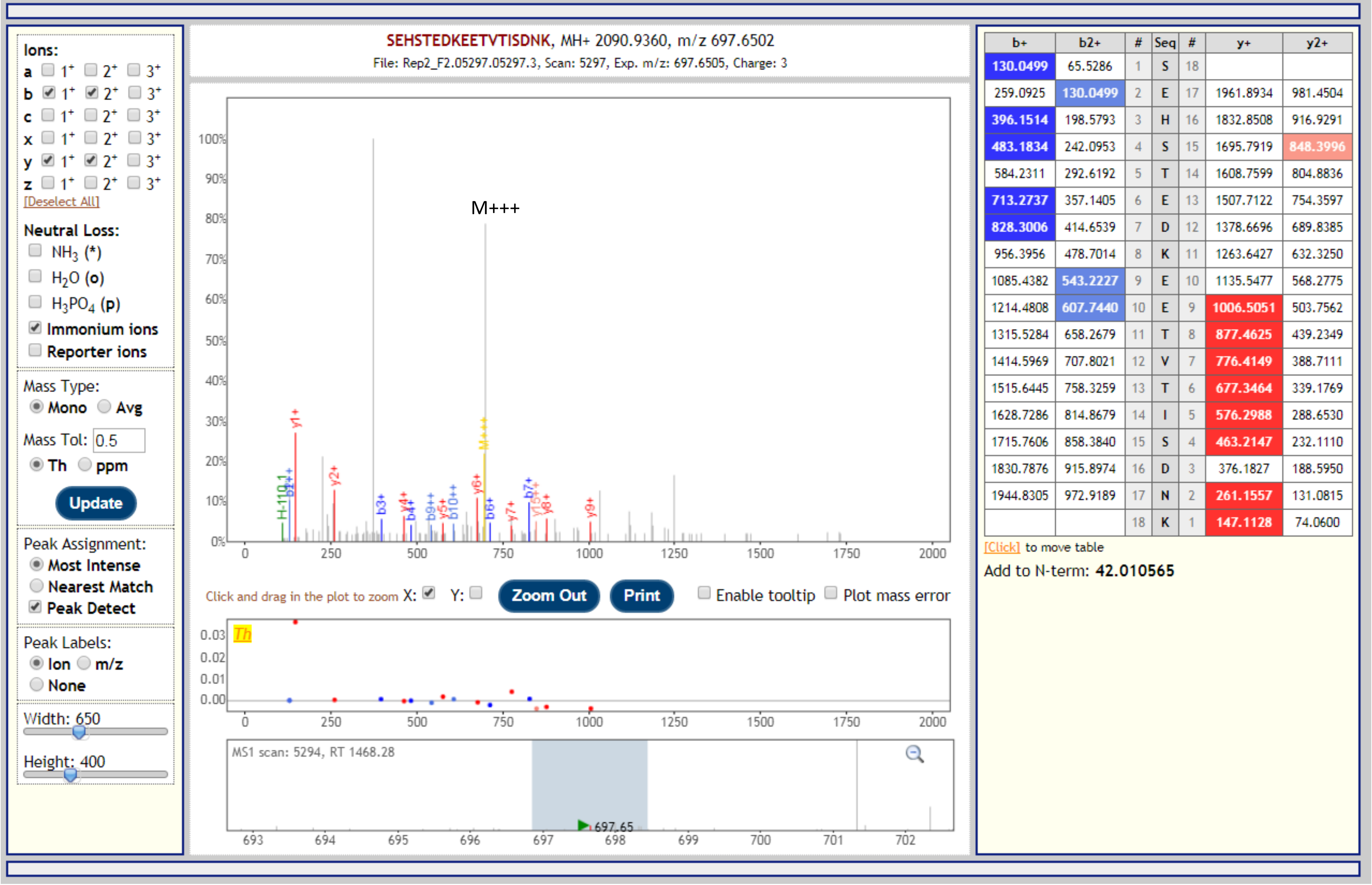
MS1 scan: 10210, RT 2212.64

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	S	14		
259.0925	130.0499	2	E	13	1564.7602	782.8837
372.1765	186.5919	3	L	12	1435.7176	718.3624
487.2035	244.1054	4	D	11	1322.6335	661.8204
615.2620	308.1347	5	Q	10	1207.6066	604.3069
729.3050	365.1561	6	N	9	1079.5480	540.2776
857.3999	429.2036	7	K	8	965.5051	483.2562
972.4269	486.7171	8	D	7	837.4101	419.2087
1100.4855	550.7464	9	Q	6	722.3832	361.6952
1214.5284	607.7678	10	N	5	594.3246	297.6659
1327.6124	664.3099	11	L	4	480.2817	240.6445
1384.6339	692.8206	12	G	3	367.1976	184.1024
1547.6972	774.3523	13	Y	2	310.1761	155.5917
		14	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1465000	fam-c protein	RSL.SEHSTEDKEETVTISDNK



SEHSTEDKEETVTISDNK, MH+ 2090.9360, m/z 697.6502

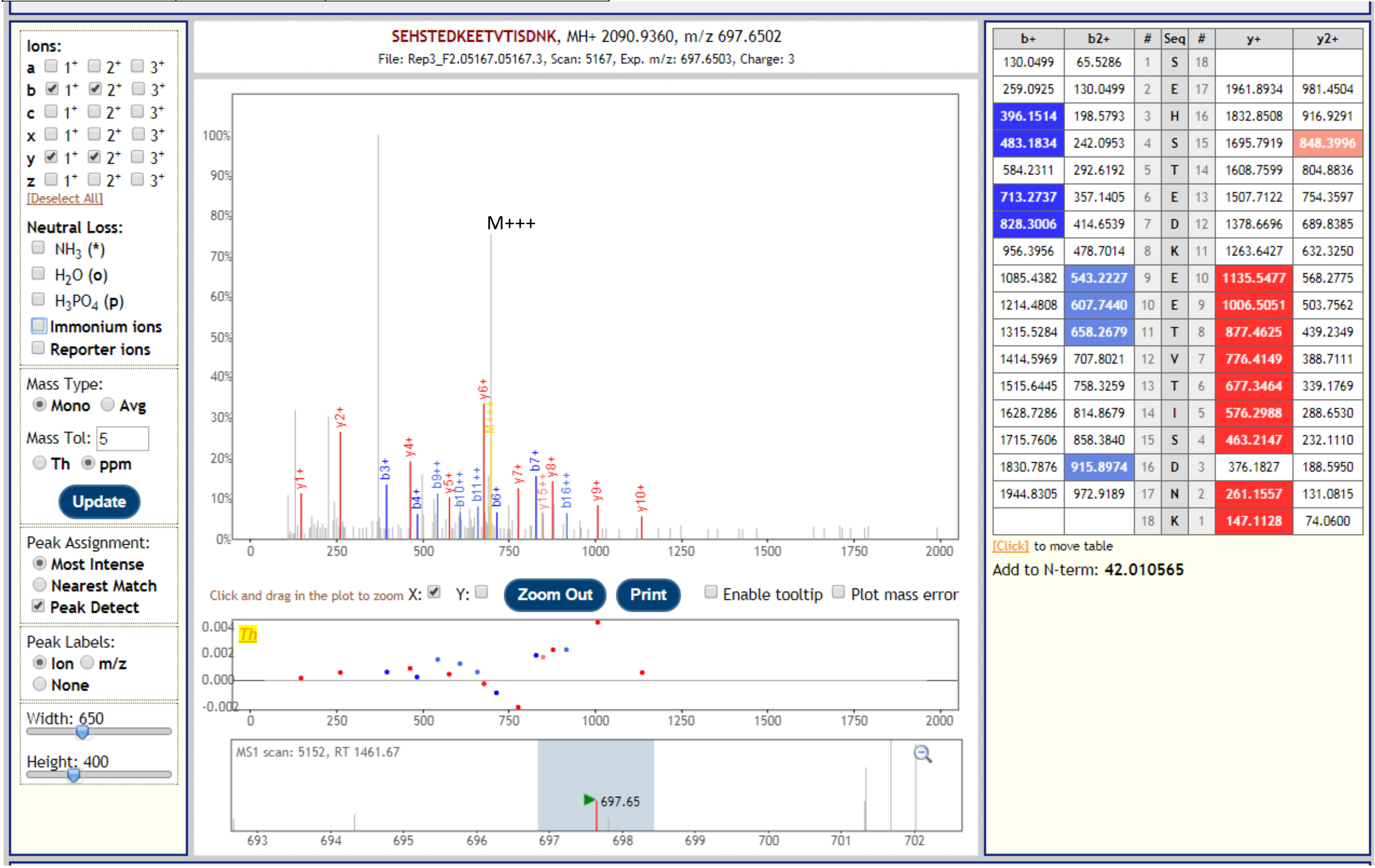
File: Rep2_F2.05297.05297.3, Scan: 5297, Exp. m/z: 697.6505, Charge: 3

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	S	18		
259.0925	130.0499	2	E	17	1961.8934	981.4504
396.1514	198.5793	3	H	16	1832.8508	916.9291
483.1834	242.0953	4	S	15	1695.7919	848.3996
584.2311	292.6192	5	T	14	1608.7599	804.8836
713.2737	357.1405	6	E	13	1507.7122	754.3597
828.3006	414.6539	7	D	12	1378.6696	689.8385
956.3956	478.7014	8	K	11	1263.6427	632.3250
1085.4382	543.2227	9	E	10	1135.5477	568.2775
1214.4808	607.7440	10	E	9	1006.5051	503.7562
1315.5284	658.2679	11	T	8	877.4625	439.2349
1414.5969	707.8021	12	V	7	776.4149	388.7111
1515.6445	758.3259	13	T	6	677.3464	339.1769
1628.7286	814.8679	14	I	5	576.2988	288.6530
1715.7606	858.3840	15	S	4	463.2147	232.1110
1830.7876	915.8974	16	D	3	376.1827	188.5950
1944.8305	972.9189	17	N	2	261.1557	131.0815
		18	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1465000	fam-c protein	RSL.SEHSTEDKEETVTISDNK



SEHSTEDKEETVTISDNK, MH+ 2090.9360, m/z 697.6502

File: Rep3_F2.05167.05167.3, Scan: 5167, Exp. m/z: 697.6503, Charge: 3

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5

○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels: ● Ion ○ m/z ○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

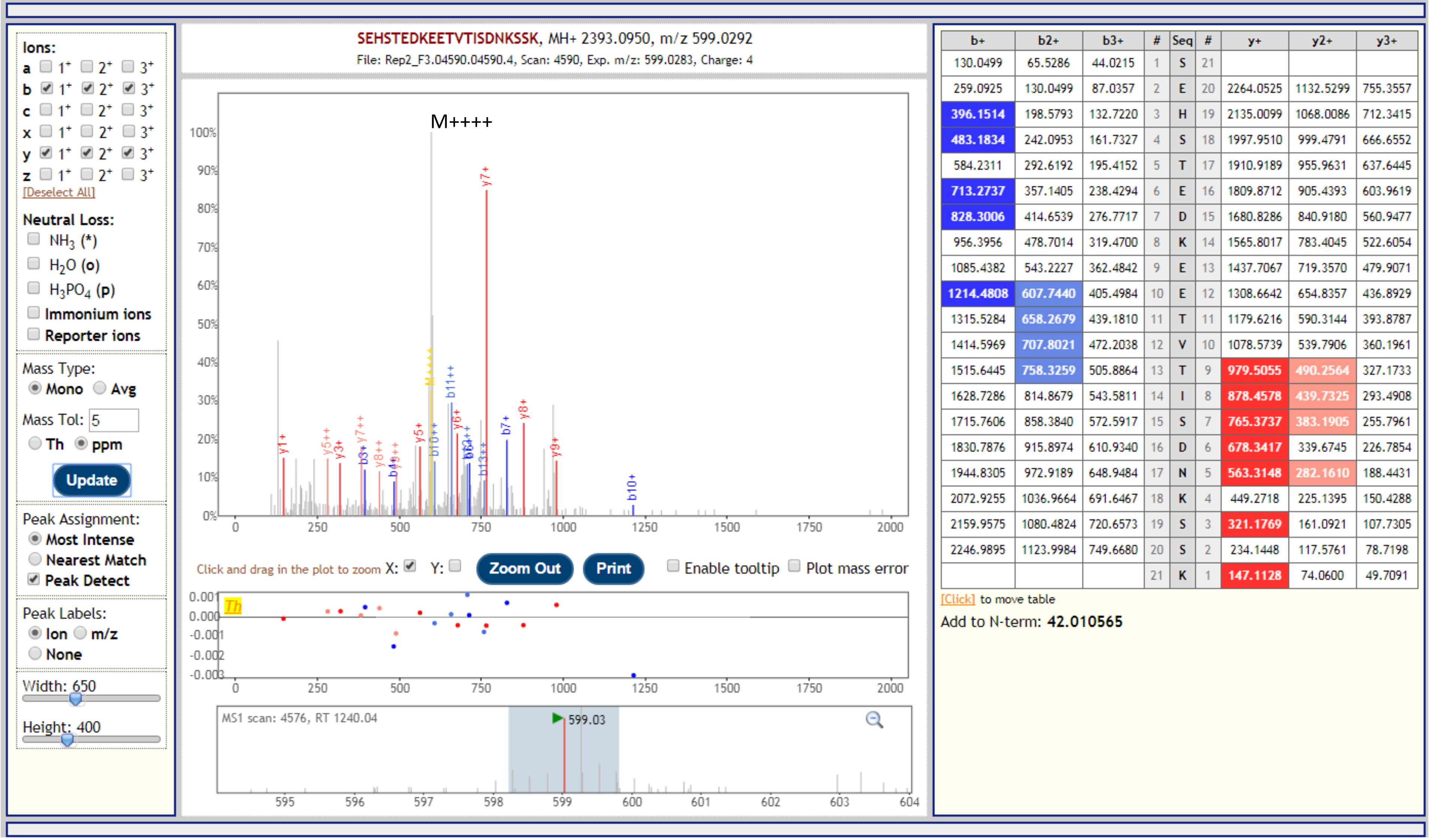
MS1 scan: 5152, RT 1461.67

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	S	18		
259.0925	130.0499	2	E	17	1961.8934	981.4504
396.1514	198.5793	3	H	16	1832.8508	916.9291
483.1834	242.0953	4	S	15	1695.7919	**848.3996**
584.2311	292.6192	5	T	14	1608.7599	804.8836
713.2737	357.1405	6	E	13	1507.7122	754.3597
828.3006	414.6539	7	D	12	1378.6696	689.8385
956.3956	478.7014	8	K	11	1263.6427	632.3250
1085.4382	**543.2227**	9	E	10	**1135.5477**	568.2775
1214.4808	**607.7440**	10	E	9	**1006.5051**	503.7562
1315.5284	**658.2679**	11	T	8	**877.4625**	439.2349
1414.5969	707.8021	12	V	7	**776.4149**	388.7111
1515.6445	758.3259	13	T	6	**677.3464**	339.1769
1628.7286	814.8679	14	I	5	**576.2988**	288.6530
1715.7606	858.3840	15	S	4	**463.2147**	232.1110
1830.7876	**915.8974**	16	D	3	376.1827	188.5950
1944.8305	972.9189	17	N	2	**261.1557**	131.0815
		18	K	1	**147.1128**	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1465000	fam-c protein	RSL.SEHSTEDKEETVTISDNKSSK



Ions:
a ☐ 1^+ ☐ 2^+ ☐ 3^+
b ☑ 1^+ ☑ 2^+ ☑ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☑ 2^+ ☑ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

SEHSTEDKEETVTISDNKSSK, MH+ 2393.0950, m/z 599.0292
File: Rep2_F3.04590.04590.4, Scan: 4590, Exp. m/z: 599.0283, Charge: 4

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

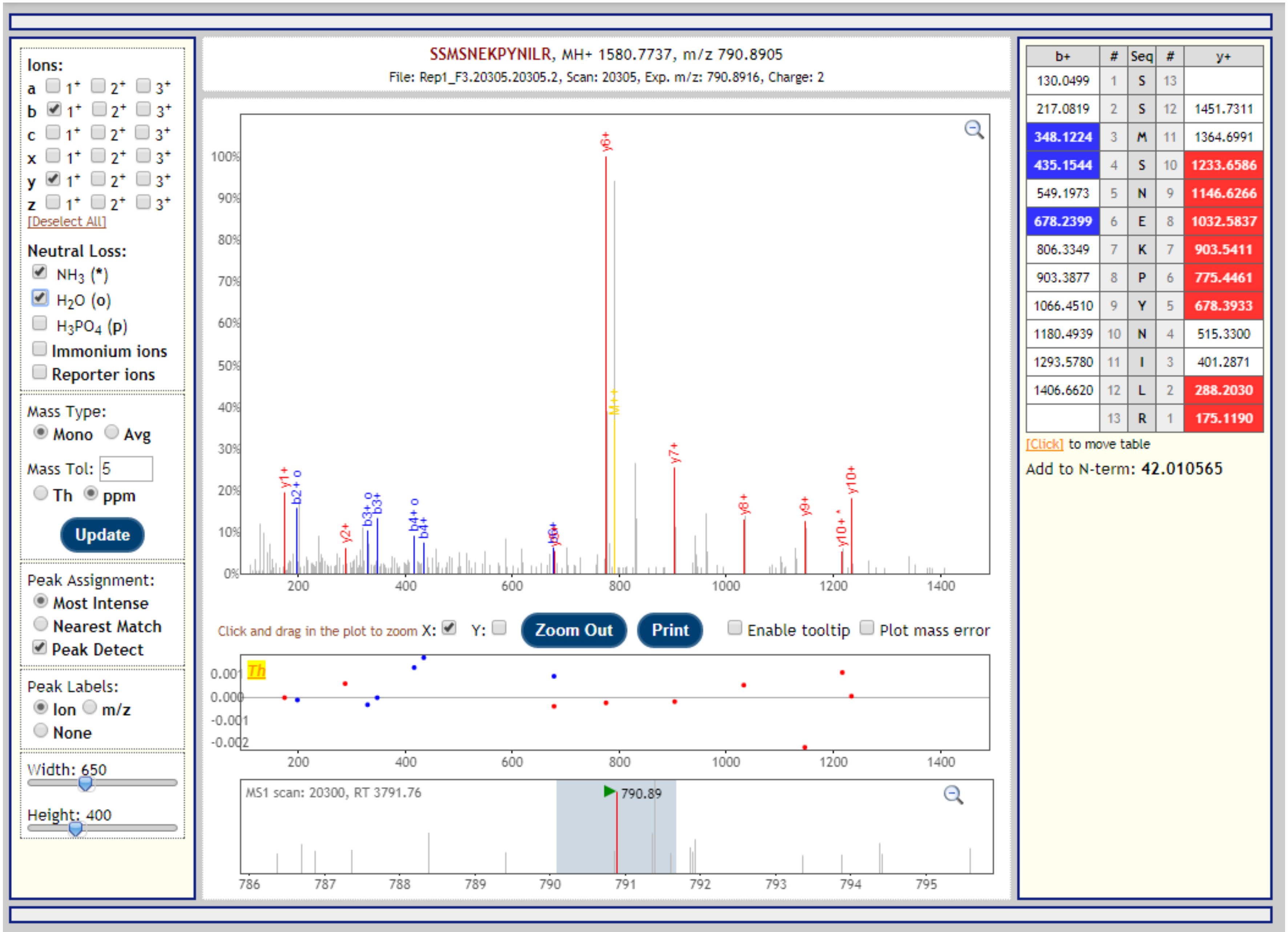
MS1 scan: 4576, RT 1240.04

b+	b2+	b3+	#	Seq	#	y+	y2+	y3+
130.0499	65.5286	44.0215	1	S	21			
259.0925	130.0499	87.0357	2	E	20	2264.0525	1132.5299	755.3557
396.1514	198.5793	132.7220	3	H	19	2135.0099	1068.0086	712.3415
483.1834	242.0953	161.7327	4	S	18	1997.9510	999.4791	666.6552
584.2311	292.6192	195.4152	5	T	17	1910.9189	955.9631	637.6445
713.2737	357.1405	238.4294	6	E	16	1809.8712	905.4393	603.9619
828.3006	414.6539	276.7717	7	D	15	1680.8286	840.9180	560.9477
956.3956	478.7014	319.4700	8	K	14	1565.8017	783.4045	522.6054
1085.4382	543.2227	362.4842	9	E	13	1437.7067	719.3570	479.9071
1214.4808	607.7440	405.4984	10	E	12	1308.6642	654.8357	436.8929
1315.5284	658.2679	439.1810	11	T	11	1179.6216	590.3144	393.8787
1414.5969	707.8021	472.2038	12	V	10	1078.5739	539.7906	360.1961
1515.6445	758.3259	505.8864	13	T	9	979.5055	490.2564	327.1733
1628.7286	814.8679	543.5811	14	I	8	878.4578	439.7325	293.4908
1715.7606	858.3840	572.5917	15	S	7	765.3737	383.1905	255.7961
1830.7876	915.8974	610.9340	16	D	6	678.3417	339.6745	226.7854
1944.8305	972.9189	648.9484	17	N	5	563.3148	282.1610	188.4431
2072.9255	1036.9664	691.6467	18	K	4	449.2718	225.1395	150.4288
2159.9575	1080.4824	720.6573	19	S	3	321.1769	161.0921	107.7305
2246.9895	1123.9984	749.6680	20	S	2	234.1448	117.5761	78.7198
			21	K	1	147.1128	74.0600	49.7091

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0700700	Plasmodium exported protein, unknown function	RIL.SSMSNEKPYNILR



SSMSNEKPYNILR, MH+ 1580.7737, m/z 790.8905

File: Rep1_F3.20305.20305.2, Scan: 20305, Exp. m/z: 790.8916, Charge: 2

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

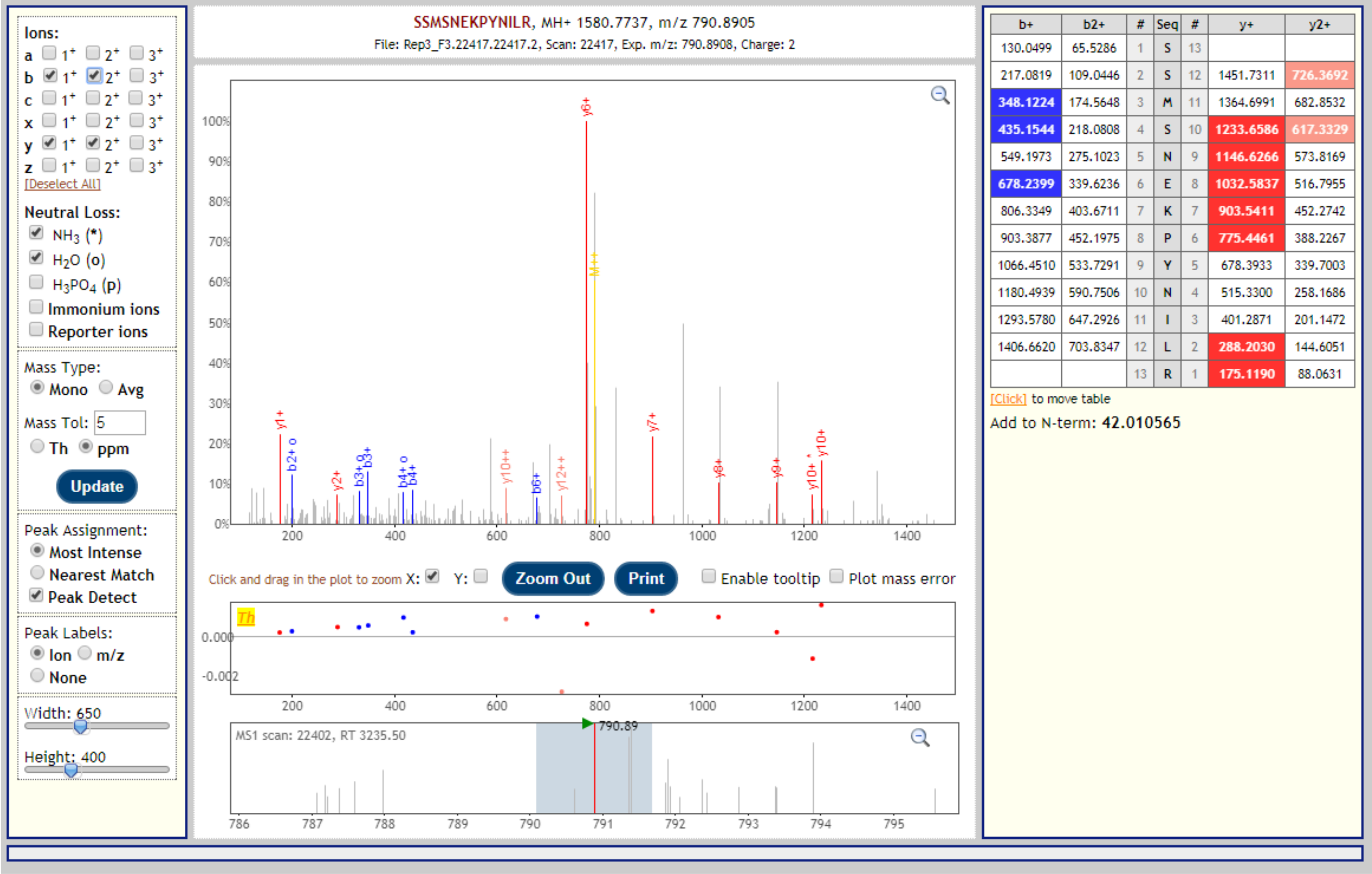
MS1 scan: 20300, RT 3791.76

b+	#	Seq	#	y+
130.0499	1	S	13	
217.0819	2	S	12	1451.7311
348.1224	3	M	11	1364.6991
435.1544	4	S	10	1233.6586
549.1973	5	N	9	1146.6266
678.2399	6	E	8	1032.5837
806.3349	7	K	7	903.5411
903.3877	8	P	6	775.4461
1066.4510	9	Y	5	678.3933
1180.4939	10	N	4	515.3300
1293.5780	11	I	3	401.2871
1406.6620	12	L	2	288.2030
	13	R	1	175.1190

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0700700	Plasmodium exported protein, unknown function	RIL.SSMSNEKPYNILR



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg
Mass Tol: 5 ○ Th ● ppm
Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650
Height: 400

SSMSNEKPYNILR, MH+ 1580.7737, m/z 790.8905
File: Rep3_F3.22417.22417.2, Scan: 22417, Exp. m/z: 790.8908, Charge: 2

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

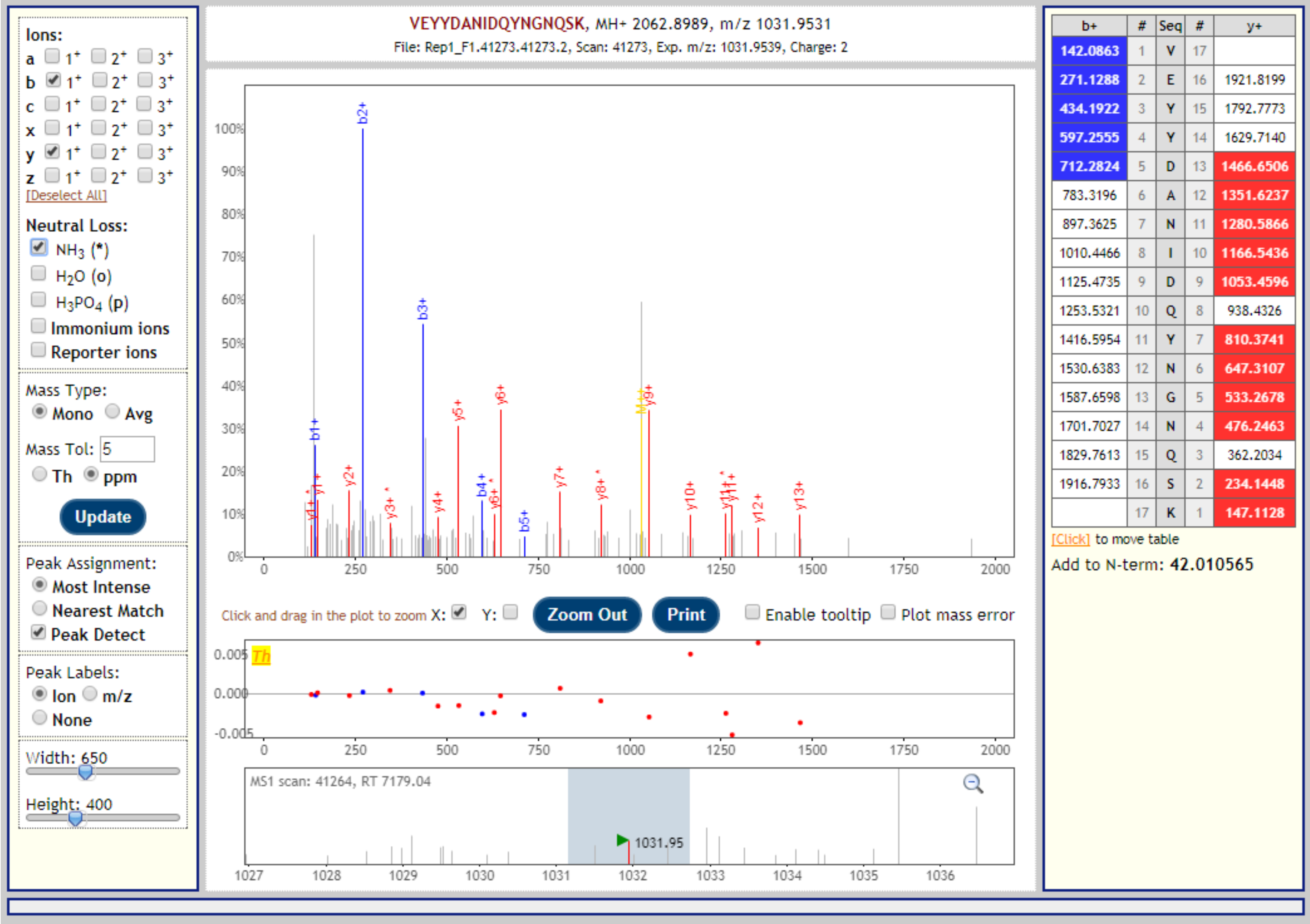
MS1 scan: 22402, RT 3235.50

b+	b2+	#	Seq	#	y+	y2+
130.0499	65.5286	1	S	13		
217.0819	109.0446	2	S	12	1451.7311	726.3692
348.1224	174.5648	3	M	11	1364.6991	682.8532
435.1544	218.0808	4	S	10	1233.6586	617.3329
549.1973	275.1023	5	N	9	1146.6266	573.8169
678.2399	339.6236	6	E	8	1032.5837	516.7955
806.3349	403.6711	7	K	7	903.5411	452.2742
903.3877	452.1975	8	P	6	775.4461	388.2267
1066.4510	533.7291	9	Y	5	678.3933	339.7003
1180.4939	590.7506	10	N	4	515.3300	258.1686
1293.5780	647.2926	11	I	3	401.2871	201.1472
1406.6620	703.8347	12	L	2	288.2030	144.6051
		13	R	1	175.1190	88.0631

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0100600	schizont membrane associated cytoadherence protein	RFL.VEYYDANIDQYNGNQSK



VEYYDANIDQYNGNQSK, MH+ 2062.8989, m/z 1031.9531

File: Rep1_F1.41273.41273.2, Scan: 41273, Exp. m/z: 1031.9539, Charge: 2

Ions:
a ☐ 1^+ ☐ 2^+ ☐ 3^+
b ☑ 1^+ ☐ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☐ 2^+ ☐ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5

○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

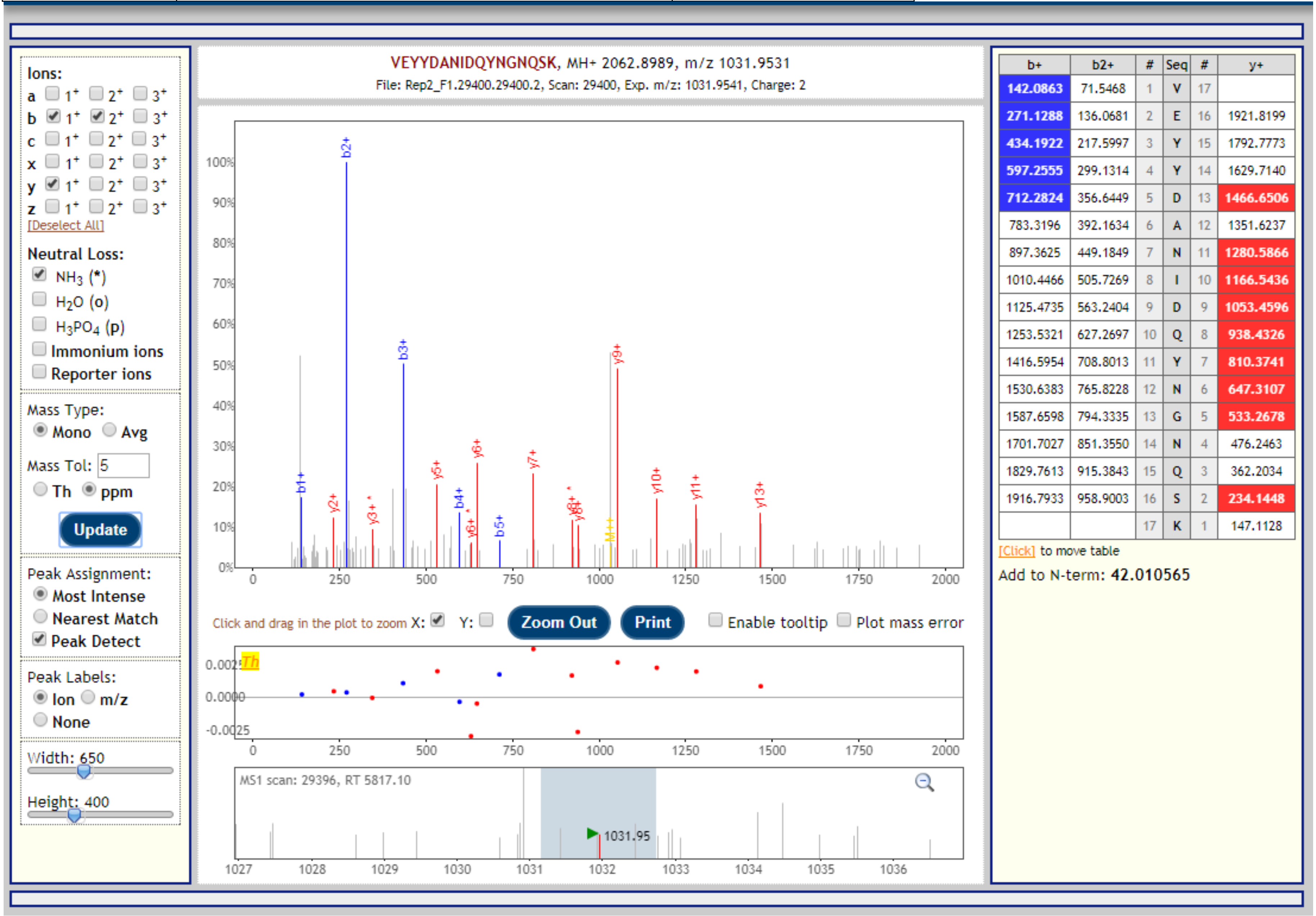
MS1 scan: 41264, RT 7179.04

b+	#	Seq	#	y+
142.0863	1	V	17	
271.1288	2	E	16	1921.8199
434.1922	3	Y	15	1792.7773
597.2555	4	Y	14	1629.7140
712.2824	5	D	13	1466.6506
783.3196	6	A	12	1351.6237
897.3625	7	N	11	1280.5866
1010.4466	8	I	10	1166.5436
1125.4735	9	D	9	1053.4596
1253.5321	10	Q	8	938.4326
1416.5954	11	Y	7	810.3741
1530.6383	12	N	6	647.3107
1587.6598	13	G	5	533.2678
1701.7027	14	N	4	476.2463
1829.7613	15	Q	3	362.2034
1916.7933	16	S	2	234.1448
	17	K	1	147.1128

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0100600	schizont membrane associated cytoadherence protein	RFL.VEYYDANIDQYNGNQSK



VEYYDANIDQYNGNQSK, MH+ 2062.8989, m/z 1031.9531

File: Rep2_F1.29400.29400.2, Scan: 29400, Exp. m/z: 1031.9541, Charge: 2

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

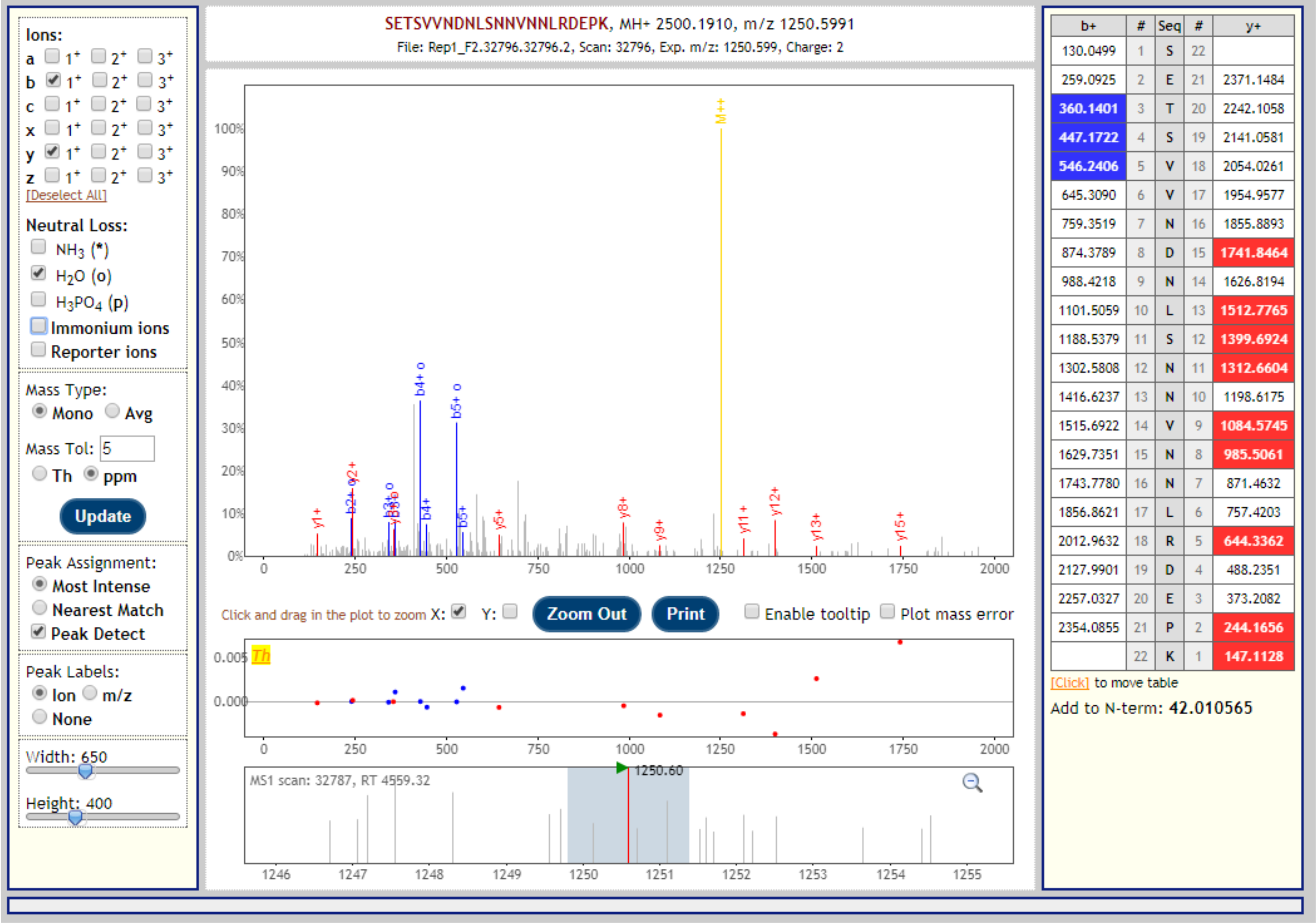
MS1 scan: 29396, RT 5817.10

b+	b2+	#	Seq	#	y+
142.0863	71.5468	1	V	17	
271.1288	136.0681	2	E	16	1921.8199
434.1922	217.5997	3	Y	15	1792.7773
597.2555	299.1314	4	Y	14	1629.7140
712.2824	356.6449	5	D	13	1466.6506
783.3196	392.1634	6	A	12	1351.6237
897.3625	449.1849	7	N	11	1280.5866
1010.4466	505.7269	8	I	10	1166.5436
1125.4735	563.2404	9	D	9	1053.4596
1253.5321	627.2697	10	Q	8	938.4326
1416.5954	708.8013	11	Y	7	810.3741
1530.6383	765.8228	12	N	6	647.3107
1587.6598	794.3335	13	G	5	533.2678
1701.7027	851.3550	14	N	4	476.2463
1829.7613	915.3843	15	Q	3	362.2034
1916.7933	958.9003	16	S	2	234.1448
		17	K	1	147.1128

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1145400	Plasmodium exported protein (PHIST), unknown function	RNL.SETSVVNDNLSNNVNNLRDEPK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☐ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

SETSVVNDNLSNNVNNLRDEPK, MH+ 2500.1910, m/z 1250.5991

File: Rep1_F2.32796.32796.2, Scan: 32796, Exp. m/z: 1250.599, Charge: 2

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

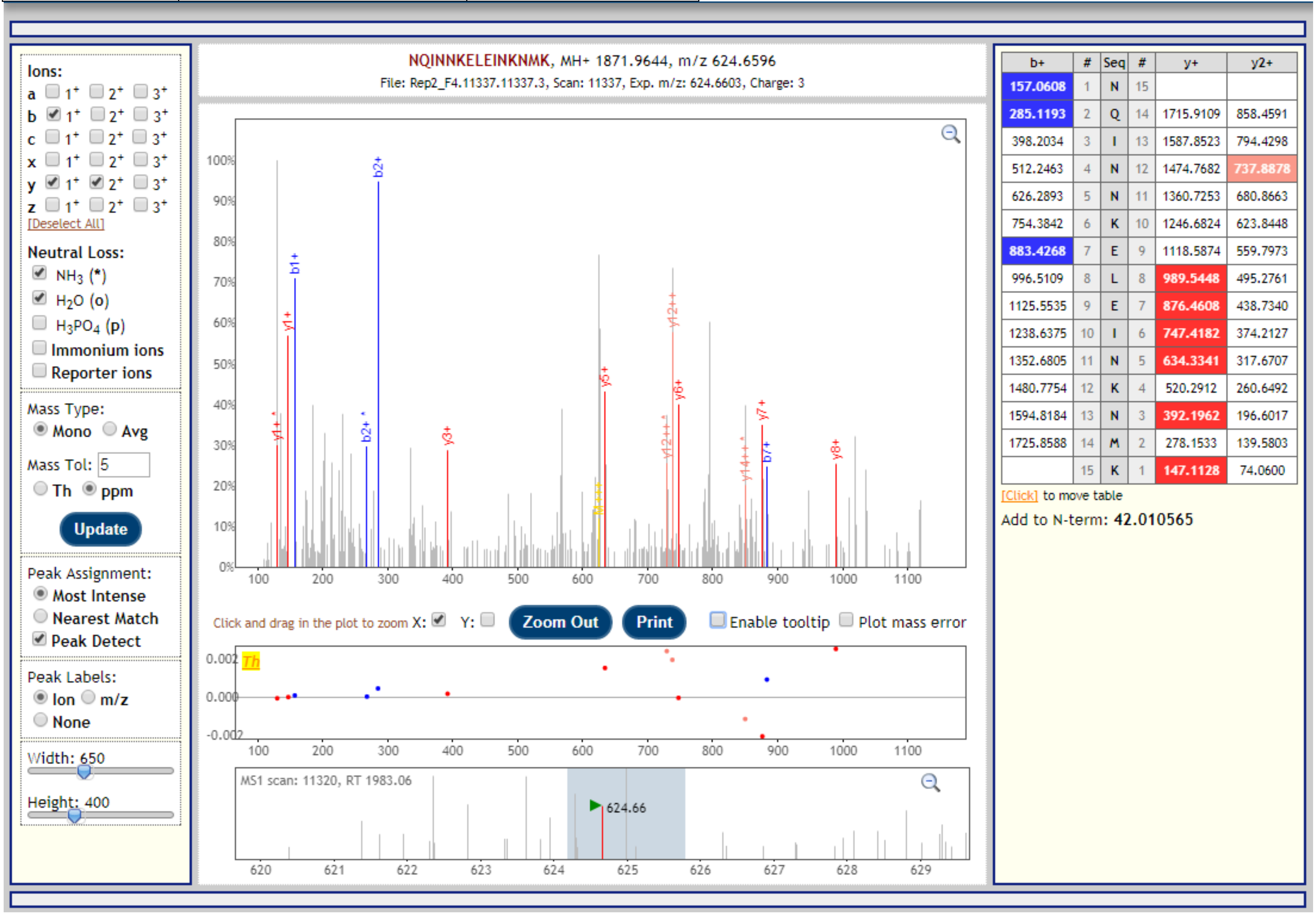
MS1 scan: 32787, RT 4559.32

b+	#	Seq	#	y+
130.0499	1	S	22	
259.0925	2	E	21	2371.1484
360.1401	3	T	20	2242.1058
447.1722	4	S	19	2141.0581
546.2406	5	V	18	2054.0261
645.3090	6	V	17	1954.9577
759.3519	7	N	16	1855.8893
874.3789	8	D	15	1741.8464
988.4218	9	N	14	1626.8194
1101.5059	10	L	13	1512.7765
1188.5379	11	S	12	1399.6924
1302.5808	12	N	11	1312.6604
1416.6237	13	N	10	1198.6175
1515.6922	14	V	9	1084.5745
1629.7351	15	N	8	985.5061
1743.7780	16	N	7	871.4632
1856.8621	17	L	6	757.4203
2012.9632	18	R	5	644.3362
2127.9901	19	D	4	488.2351
2257.0327	20	E	3	373.2082
2354.0855	21	P	2	244.1656
	22	K	1	147.1128

[Click] to move table

Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1106800	subtilisin-like protease 3, putative	RIL.NQINNKELEINKNMK



Ions:
a ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
b ☑ 1⁺ ☐ 2⁺ ☐ 3⁺
c ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
x ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
y ☑ 1⁺ ☑ 2⁺ ☐ 3⁺
z ☐ 1⁺ ☐ 2⁺ ☐ 3⁺
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

NQINNKELEINKNMK, MH+ 1871.9644, m/z 624.6596
File: Rep2_F4.11337.11337.3, Scan: 11337, Exp. m/z: 624.6603, Charge: 3

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip ☐ Plot mass error

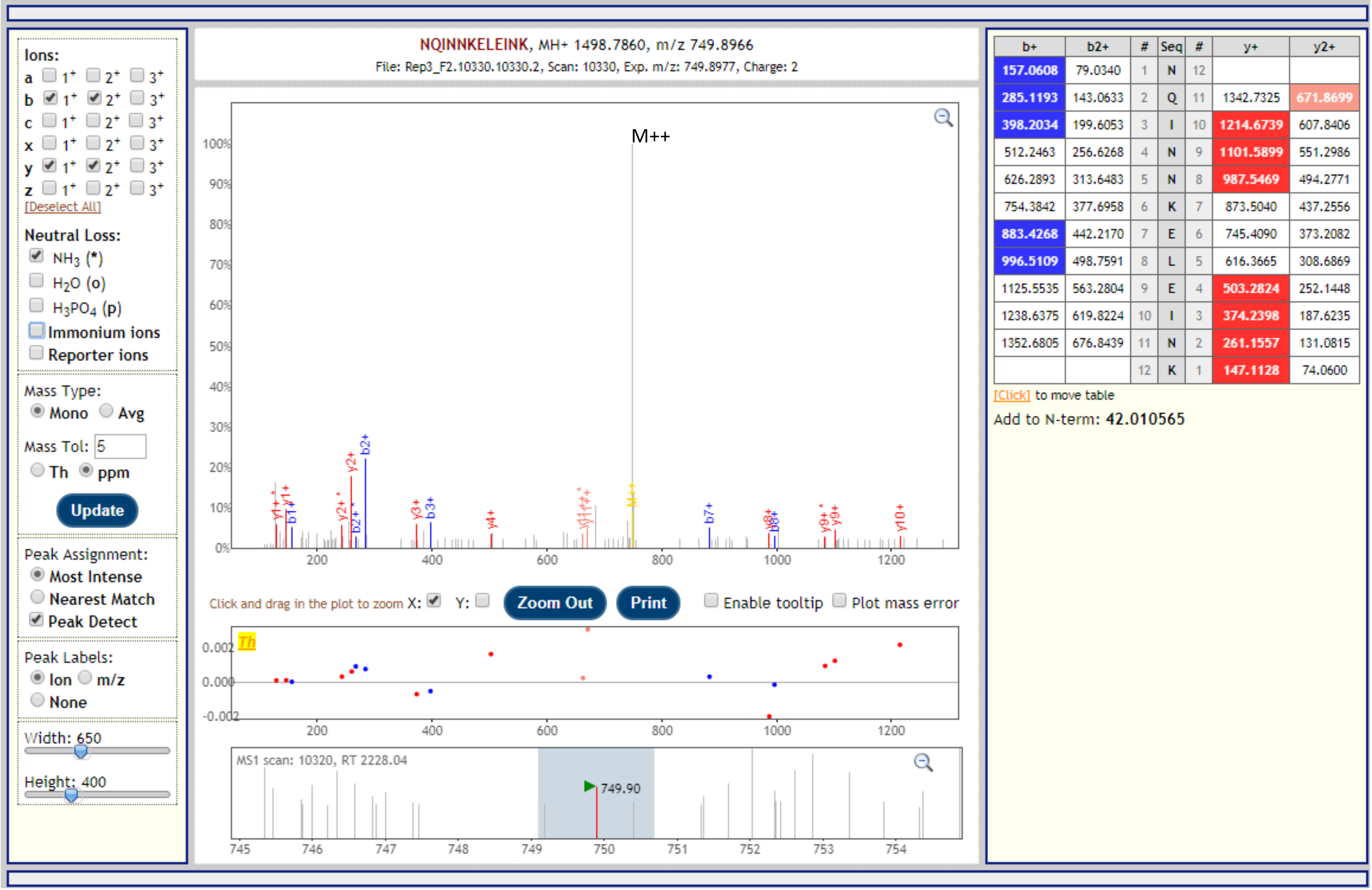
MS1 scan: 11320, RT 1983.06

b+	#	Seq	#	y+	y2+
157.0608	1	N	15		
285.1193	2	Q	14	1715.9109	858.4591
398.2034	3	I	13	1587.8523	794.4298
512.2463	4	N	12	1474.7682	737.8878
626.2893	5	N	11	1360.7253	680.8663
754.3842	6	K	10	1246.6824	623.8448
883.4268	7	E	9	1118.5874	559.7973
996.5109	8	L	8	989.5448	495.2761
1125.5535	9	E	7	876.4608	438.7340
1238.6375	10	I	6	747.4182	374.2127
1352.6805	11	N	5	634.3341	317.6707
1480.7754	12	K	4	520.2912	260.6492
1594.8184	13	N	3	392.1962	196.6017
1725.8588	14	M	2	278.1533	139.5803
	15	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Protein	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1106800	SUB3	subtilisin-like protease 3, putative	RIL.NQINNKELEINK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☑ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☑ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

NQINNKELEINK, MH+ 1498.7860, m/z 749.8966

File: Rep3_F2.10330.10330.2, Scan: 10330, Exp. m/z: 749.8977, Charge: 2

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

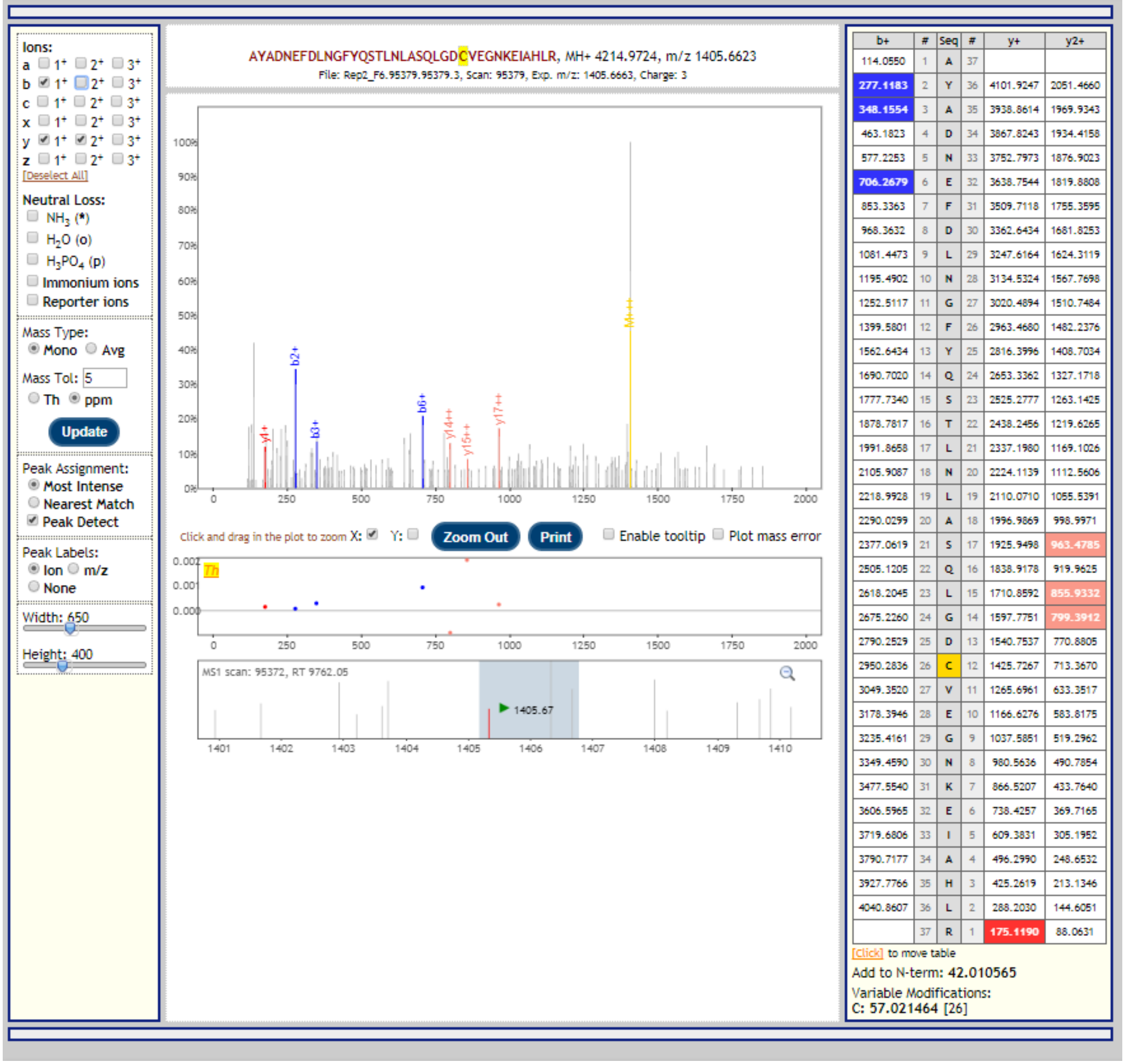
MS1 scan: 10320, RT 2228.04

b+	b2+	#	Seq	#	y+	y2+
157.0608	79.0340	1	N	12		
285.1193	143.0633	2	Q	11	1342.7325	671.8699
398.2034	199.6053	3	I	10	1214.6739	607.8406
512.2463	256.6268	4	N	9	1101.5899	551.2986
626.2893	313.6483	5	N	8	987.5469	494.2771
754.3842	377.6958	6	K	7	873.5040	437.2556
883.4268	442.2170	7	E	6	745.4090	373.2082
996.5109	498.7591	8	L	5	616.3665	308.6869
1125.5535	563.2804	9	E	4	503.2824	252.1448
1238.6375	619.8224	10	I	3	374.2398	187.6235
1352.6805	676.8439	11	N	2	261.1557	131.0815
		12	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1200041, PBANKA_1246961, PBANKA_1300041, PBANKA_0007801	fam-b protein	RIL.AYADNEFDLNGFYQSTLNLASQLGDCVEGNKEIAHLR



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg
Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650
Height: 400

AYADNEFDLNGFYQSTLNLASQLGDCVEGNKEIAHLR, MH+ 4214.9724, m/z 1405.6623
File: Rep2_F6.95379.95379.3, Scan: 95379, Exp. m/z: 1405.6663, Charge: 3

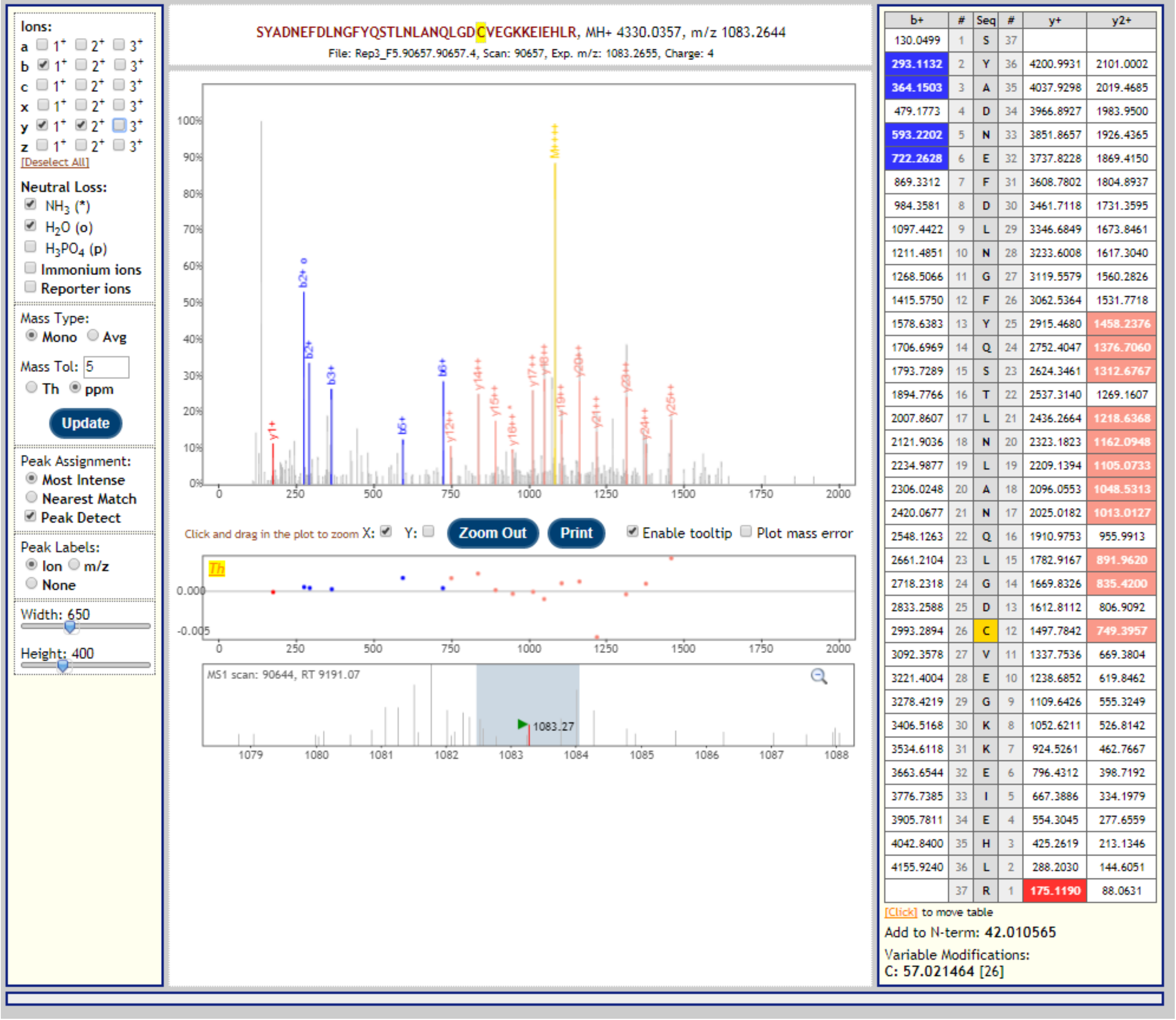
Click and drag in the plot to zoom X: ☑ Y: ☐
☐ Enable tooltip ☐ Plot mass error

MS1 scan: 95372, RT 9762.05

b+	#	Seq	#	y+	y2+
114.0550	1	A	37		
277.1183	2	Y	36	4101.9247	2051.4660
348.1554	3	A	35	3938.8614	1969.9343
463.1823	4	D	34	3867.8243	1934.4158
577.2253	5	N	33	3752.7973	1876.9023
706.2679	6	E	32	3638.7544	1819.8808
853.3363	7	F	31	3509.7118	1755.3595
968.3632	8	D	30	3362.6434	1681.8253
1081.4473	9	L	29	3247.6164	1624.3119
1195.4902	10	N	28	3134.5324	1567.7698
1252.5117	11	G	27	3020.4894	1510.7484
1399.5801	12	F	26	2963.4680	1482.2376
1562.6434	13	Y	25	2816.3996	1408.7034
1690.7020	14	Q	24	2653.3362	1327.1718
1777.7340	15	S	23	2525.2777	1263.1425
1878.7817	16	T	22	2438.2456	1219.6265
1991.8658	17	L	21	2337.1980	1169.1026
2105.9087	18	N	20	2224.1139	1112.5606
2218.9928	19	L	19	2110.0710	1055.5391
2290.0299	20	A	18	1996.9869	998.9971
2377.0619	21	S	17	1925.9498	963.4785
2505.1205	22	Q	16	1838.9178	919.9625
2618.2045	23	L	15	1710.8592	855.9332
2675.2260	24	G	14	1597.7751	799.3912
2790.2529	25	D	13	1540.7537	770.8805
2950.2836	26	C	12	1425.7267	713.3670
3049.3520	27	V	11	1265.6961	633.3517
3178.3946	28	E	10	1166.6276	583.8175
3235.4161	29	G	9	1037.5851	519.2962
3349.4590	30	N	8	980.5636	490.7854
3477.5540	31	K	7	866.5207	433.7640
3606.5965	32	E	6	738.4257	369.7165
3719.6806	33	I	5	609.3831	305.1952
3790.7177	34	A	4	496.2990	248.6532
3927.7766	35	H	3	425.2619	213.1346
4040.8607	36	L	2	288.2030	144.6051
	37	R	1	175.1190	88.0631

[Click] to move table
Add to N-term: **42.010565**
Variable Modifications:
C: 57.021464 [26]

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0500741, PBANKA_1000071, PBANKA_1146781	fam-b protein	RIL.SYADNEFDLNGFYQSTLNLANQLGDCVEGKKEIEHLR



SYADNEFDLNGFYQSTLNLANQLGDCVEGKKEIEHLR, MH+ 4330.0357, m/z 1083.2644

File: Rep3_F5.90657.90657.4, Scan: 90657, Exp. m/z: 1083.2655, Charge: 4

Ions:

a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+

[Deselect All]

Neutral Loss:

☑ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐

☑ Enable tooltip ☐ Plot mass error

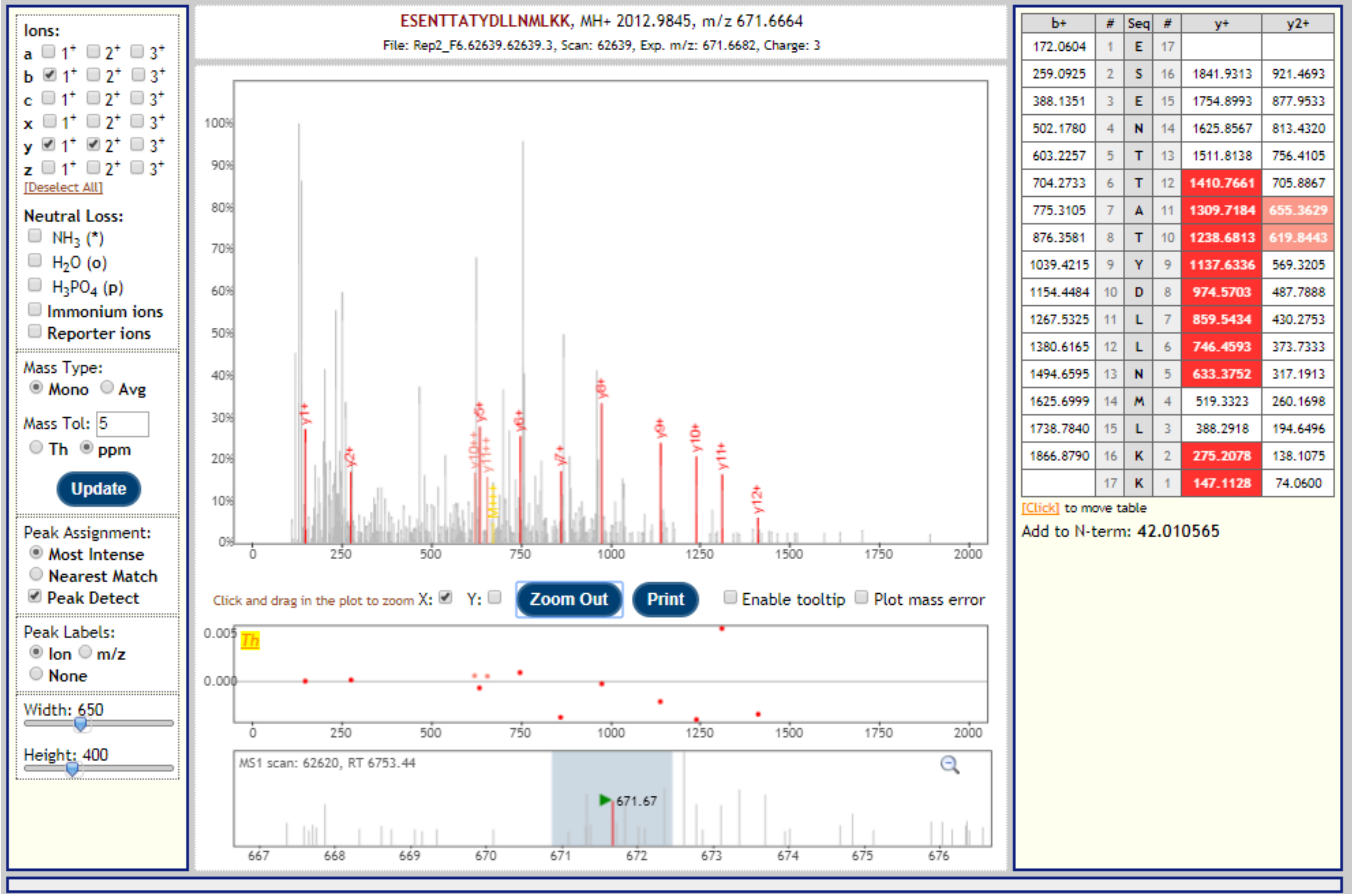
b+	#	Seq	#	y+	y2+
130.0499	1	S	37		
293.1132	2	Y	36	4200.9931	2101.0002
364.1503	3	A	35	4037.9298	2019.4685
479.1773	4	D	34	3966.8927	1983.9500
593.2202	5	N	33	3851.8657	1926.4365
722.2628	6	E	32	3737.8228	1869.4150
869.3312	7	F	31	3608.7802	1804.8937
984.3581	8	D	30	3461.7118	1731.3595
1097.4422	9	L	29	3346.6849	1673.8461
1211.4851	10	N	28	3233.6008	1617.3040
1268.5066	11	G	27	3119.5579	1560.2826
1415.5750	12	F	26	3062.5364	1531.7718
1578.6383	13	Y	25	2915.4680	1458.2376
1706.6969	14	Q	24	2752.4047	1376.7060
1793.7289	15	S	23	2624.3461	1312.6767
1894.7766	16	T	22	2537.3140	1269.1607
2007.8607	17	L	21	2436.2664	1218.6368
2121.9036	18	N	20	2323.1823	1162.0948
2234.9877	19	L	19	2209.1394	1105.0733
2306.0248	20	A	18	2096.0553	1048.5313
2420.0677	21	N	17	2025.0182	1013.0127
2548.1263	22	Q	16	1910.9753	955.9913
2661.2104	23	L	15	1782.9167	891.9620
2718.2318	24	G	14	1669.8326	835.4200
2833.2588	25	D	13	1612.8112	806.9092
2993.2894	26	C	12	1497.7842	749.3957
3092.3578	27	V	11	1337.7536	669.3804
3221.4004	28	E	10	1238.6852	619.8462
3278.4219	29	G	9	1109.6426	555.3249
3406.5168	30	K	8	1052.6211	526.8142
3534.6118	31	K	7	924.5261	462.7667
3663.6544	32	E	6	796.4312	398.7192
3776.7385	33	I	5	667.3886	334.1979
3905.7811	34	E	4	554.3045	277.6559
4042.8400	35	H	3	425.2619	213.1346
4155.9240	36	L	2	288.2030	144.6051
	37	R	1	175.1190	88.0631

[Click] to move table

Add to N-term: **42.010565**

Variable Modifications:
C: **57.021464** [26]

Gene	Protein	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1342800	NMNAT	nicotinamide/nicotinic acid mononucleotide adenylyltransferase, putative	KDL.ESENTTATYDLLNMLKK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

ESENTTATYDLLNMLKK, MH+ 2012.9845, m/z 671.6664

File: Rep2_F6.62639.62639.3, Scan: 62639, Exp. m/z: 671.6682, Charge: 3

Click and drag in the plot to zoom X: ☑ Y: ☐

☐ Enable tooltip ☐ Plot mass error

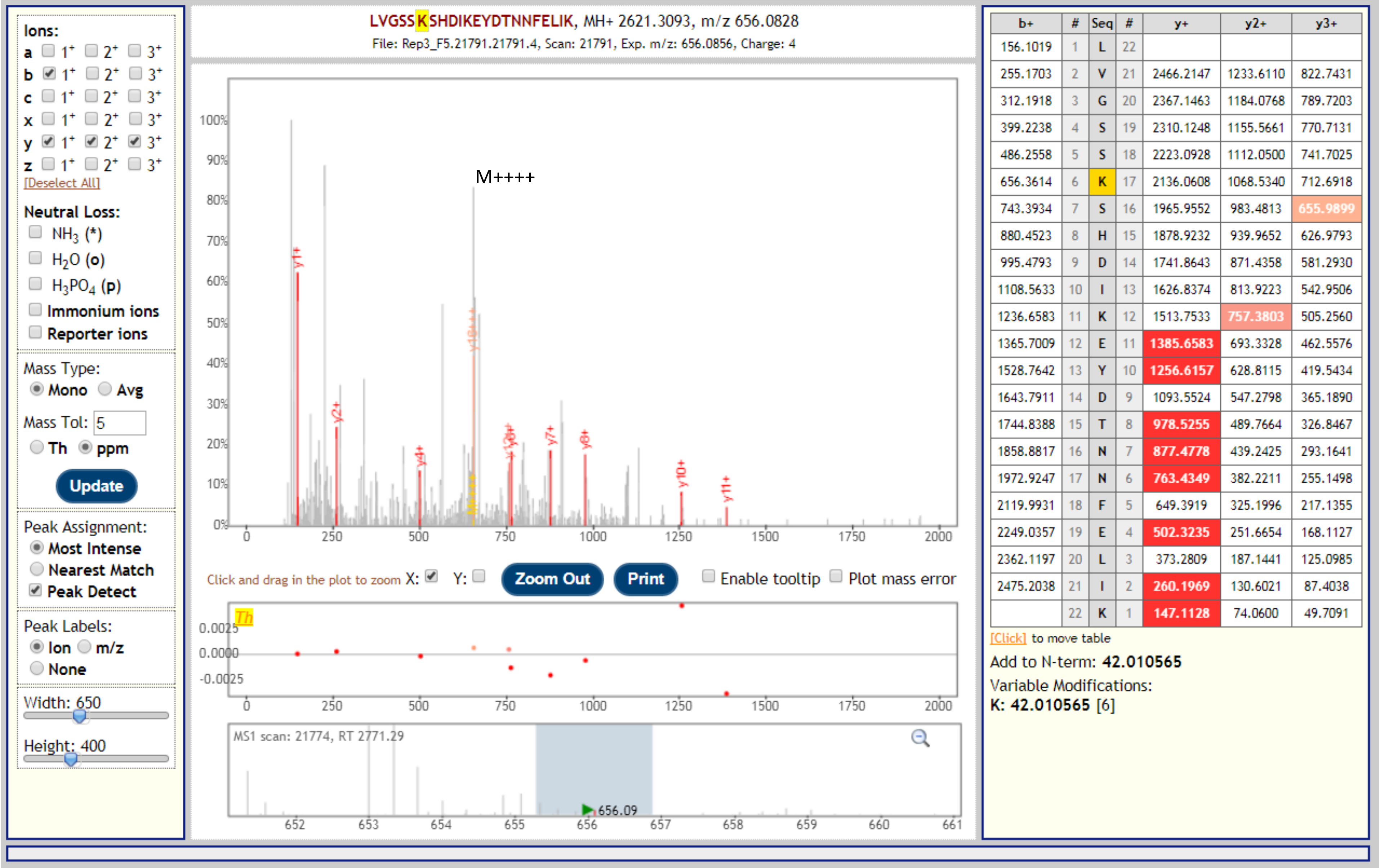
MS1 scan: 62620, RT 6753.44

b+	#	Seq	#	y+	y2+
172.0604	1	E	17		
259.0925	2	S	16	1841.9313	921.4693
388.1351	3	E	15	1754.8993	877.9533
502.1780	4	N	14	1625.8567	813.4320
603.2257	5	T	13	1511.8138	756.4105
704.2733	6	T	12	1410.7661	705.8867
775.3105	7	A	11	1309.7184	655.3629
876.3581	8	T	10	1238.6813	619.8443
1039.4215	9	Y	9	1137.6336	569.3205
1154.4484	10	D	8	974.5703	487.7888
1267.5325	11	L	7	859.5434	430.2753
1380.6165	12	L	6	746.4593	373.7333
1494.6595	13	N	5	633.3752	317.1913
1625.6999	14	M	4	519.3323	260.1698
1738.7840	15	L	3	388.2918	194.6496
1866.8790	16	K	2	275.2078	138.1075
	17	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: 42.010565

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_1437200	conserved Plasmodium protein, unknown function	RIL.VGSSKSHDIKEYDTNNFELIK



LVGSSKSHDIKEYDTNNFELIK, MH+ 2621.3093, m/z 656.0828

File: Rep3_F5.21791.21791.4, Scan: 21791, Exp. m/z: 656.0856, Charge: 4

Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☑ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip ☐ Plot mass error

MS1 scan: 21774, RT 2771.29

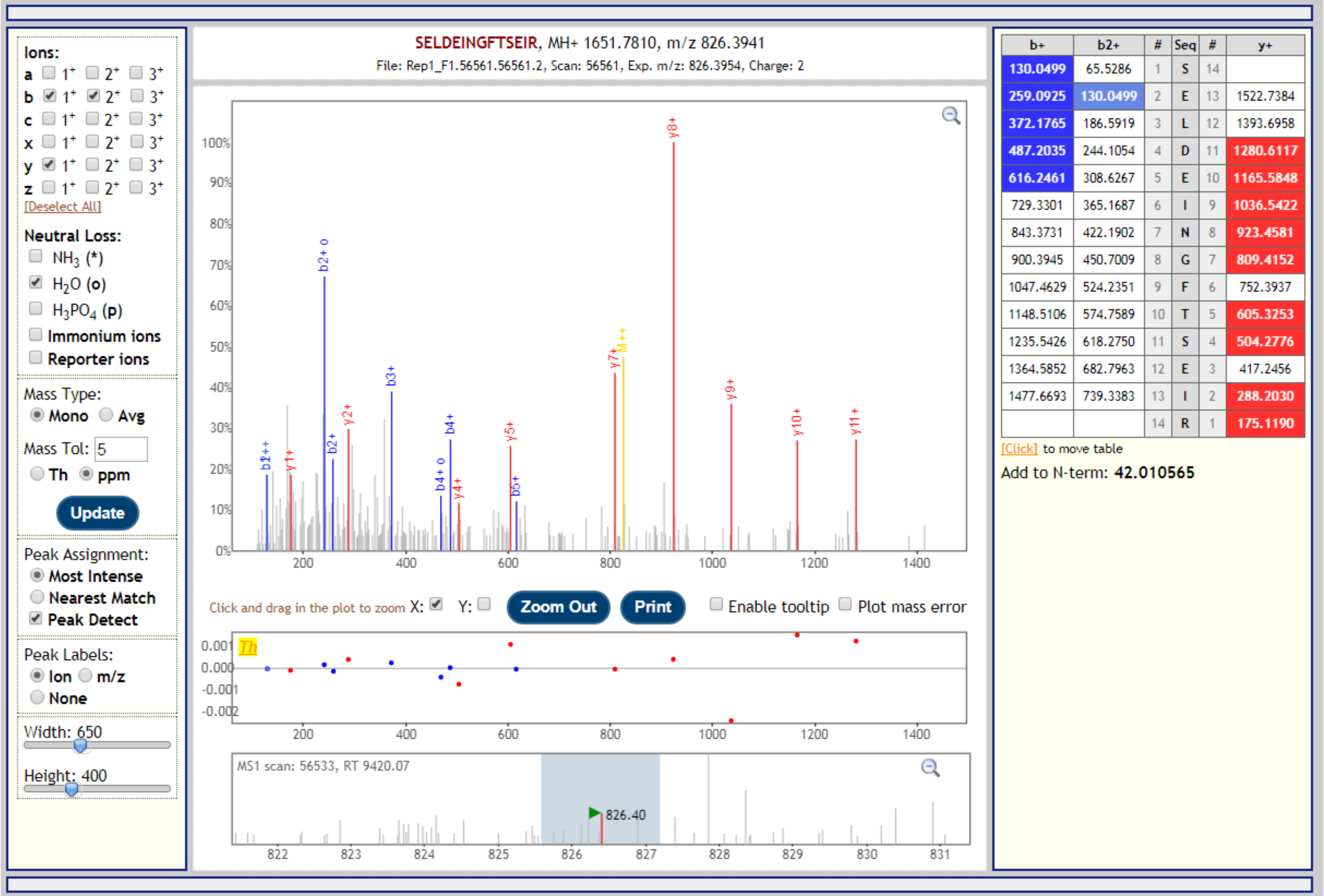
b+	#	Seq	#	y+	y2+	y3+
156.1019	1	L	22			
255.1703	2	V	21	2466.2147	1233.6110	822.7431
312.1918	3	G	20	2367.1463	1184.0768	789.7203
399.2238	4	S	19	2310.1248	1155.5661	770.7131
486.2558	5	S	18	2223.0928	1112.0500	741.7025
656.3614	6	K	17	2136.0608	1068.5340	712.6918
743.3934	7	S	16	1965.9552	983.4813	655.9899
880.4523	8	H	15	1878.9232	939.9652	626.9793
995.4793	9	D	14	1741.8643	871.4358	581.2930
1108.5633	10	I	13	1626.8374	813.9223	542.9506
1236.6583	11	K	12	1513.7533	757.3803	505.2560
1365.7009	12	E	11	1385.6583	693.3328	462.5576
1528.7642	13	Y	10	1256.6157	628.8115	419.5434
1643.7911	14	D	9	1093.5524	547.2798	365.1890
1744.8388	15	T	8	978.5255	489.7664	326.8467
1858.8817	16	N	7	877.4778	439.2425	293.1641
1972.9247	17	N	6	763.4349	382.2211	255.1498
2119.9931	18	F	5	649.3919	325.1996	217.1355
2249.0357	19	E	4	502.3235	251.6654	168.1127
2362.1197	20	L	3	373.2809	187.1441	125.0985
2475.2038	21	I	2	260.1969	130.6021	87.4038
	22	K	1	147.1128	74.0600	49.7091

[Click] to move table

Add to N-term: **42.010565**

Variable Modifications:
K: 42.010565 [6]

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0316200	Plasmodium exported protein, unknown function	RIL.SELDEINGFTSEIR



SELDEINGFTSEIR, MH+ 1651.7810, m/z 826.3941

File: Rep1_F1.56561.56561.2, Scan: 56561, Exp. m/z: 826.3954, Charge: 2

Ions:
a ☐ 1^+ ☐ 2^+ ☐ 3^+
b ☑ 1^+ ☑ 2^+ ☐ 3^+
c ☐ 1^+ ☐ 2^+ ☐ 3^+
x ☐ 1^+ ☐ 2^+ ☐ 3^+
y ☑ 1^+ ☐ 2^+ ☐ 3^+
z ☐ 1^+ ☐ 2^+ ☐ 3^+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg

Mass Tol: 5

○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

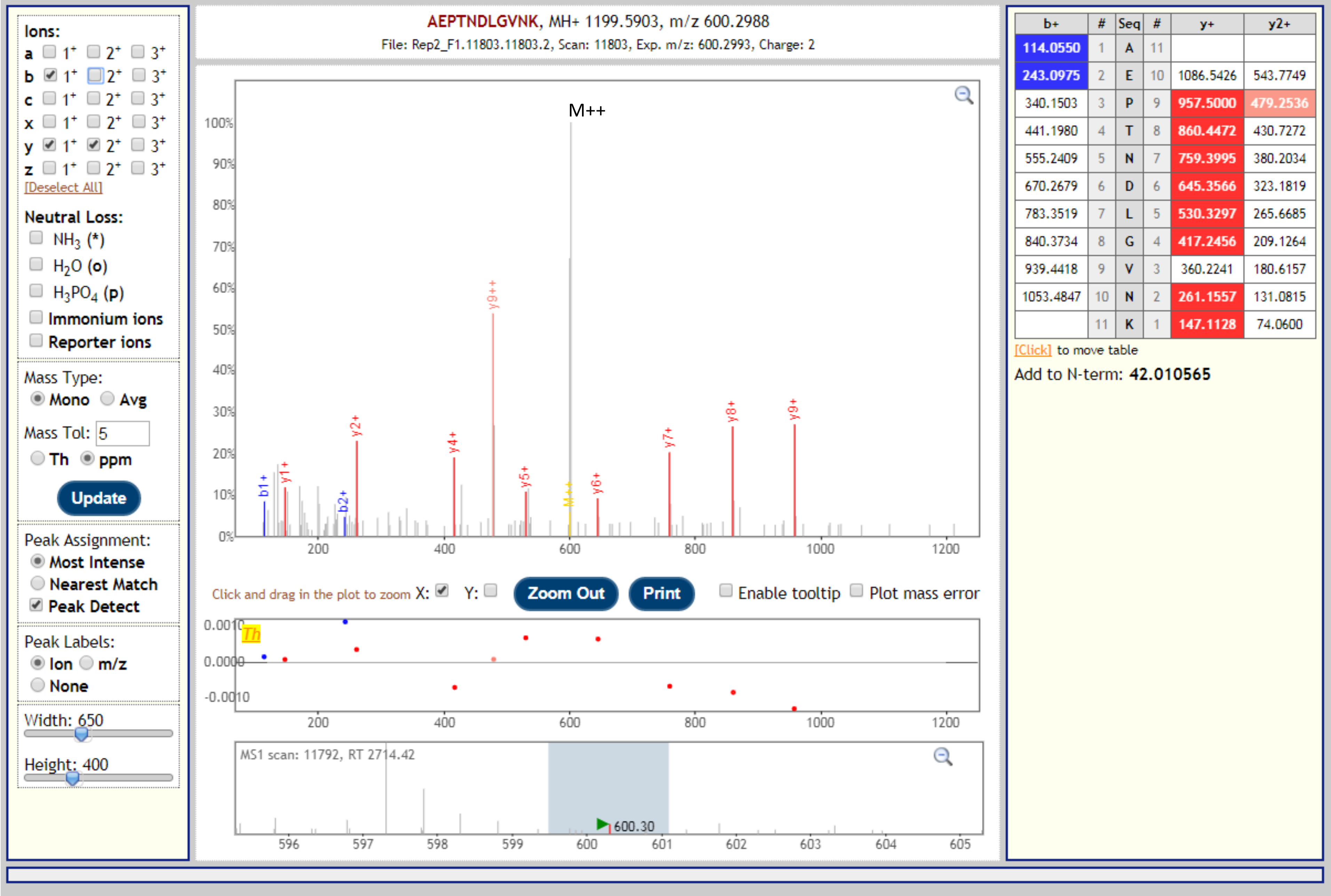
MS1 scan: 56533, RT 9420.07

b+	b2+	#	Seq	#	y+
130.0499	65.5286	1	S	14	
259.0925	130.0499	2	E	13	1522.7384
372.1765	186.5919	3	L	12	1393.6958
487.2035	244.1054	4	D	11	1280.6117
616.2461	308.6267	5	E	10	1165.5848
729.3301	365.1687	6	I	9	1036.5422
843.3731	422.1902	7	N	8	923.4581
900.3945	450.7009	8	G	7	809.4152
1047.4629	524.2351	9	F	6	752.3937
1148.5106	574.7589	10	T	5	605.3253
1235.5426	618.2750	11	S	4	504.2776
1364.5852	682.7963	12	E	3	417.2456
1477.6693	739.3383	13	I	2	288.2030
		14	R	1	175.1190

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0100700	Plasmodium exported protein, unknown function	RLL.AEPTNDLGVNK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☐ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type:
● Mono ○ Avg

Mass Tol: 5
○ Th ● ppm

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650

Height: 400

AEPTNDLGVNK, MH+ 1199.5903, m/z 600.2988
File: Rep2_F1.11803.11803.2, Scan: 11803, Exp. m/z: 600.2993, Charge: 2

Click and drag in the plot to zoom X: ☑ Y: ☐ ☐ Enable tooltip ☐ Plot mass error

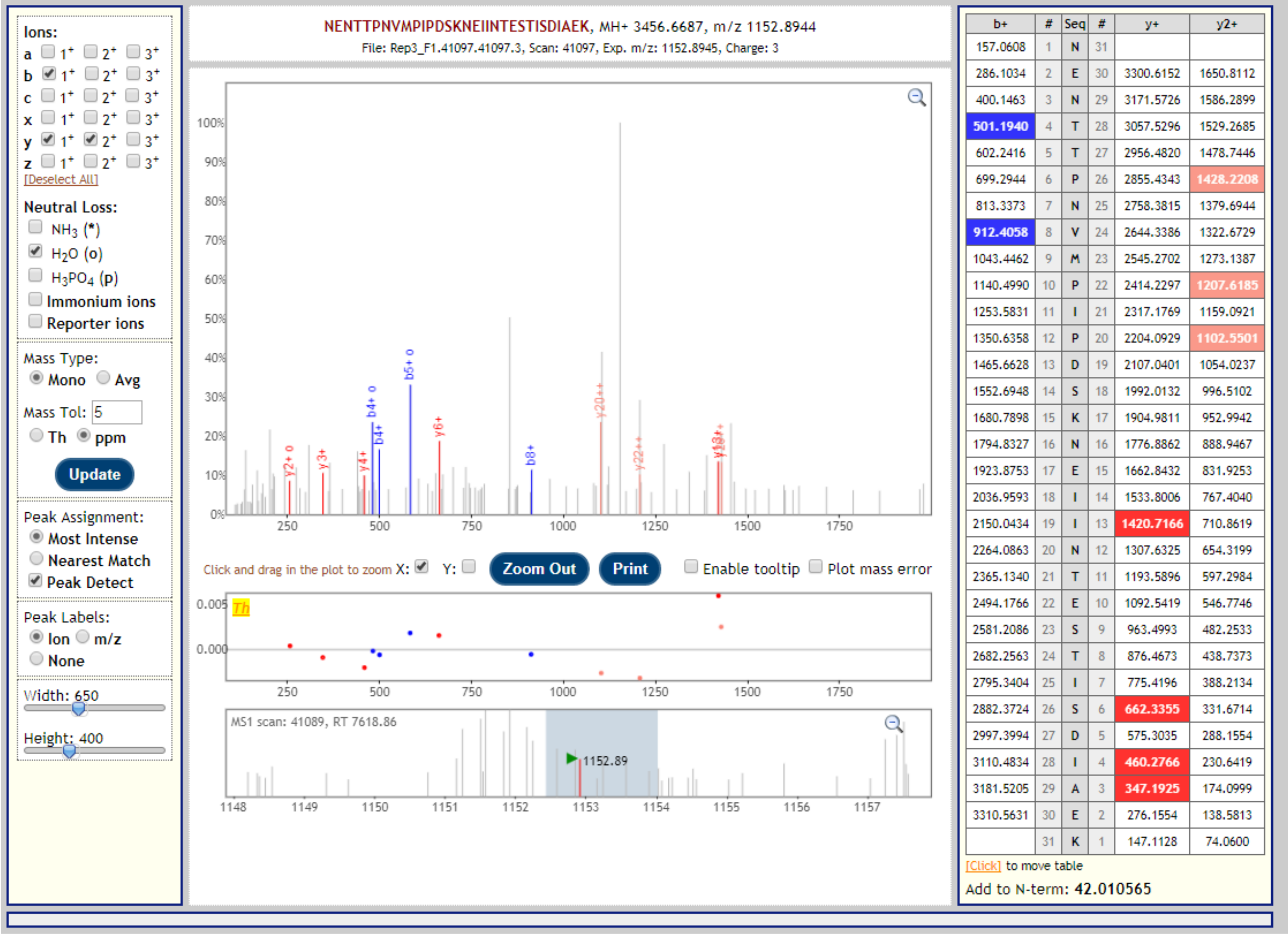
MS1 scan: 11792, RT 2714.42

b+	#	Seq	#	y+	y2+
114.0550	1	A	11		
243.0975	2	E	10	1086.5426	543.7749
340.1503	3	P	9	957.5000	479.2536
441.1980	4	T	8	860.4472	430.7272
555.2409	5	N	7	759.3995	380.2034
670.2679	6	D	6	645.3566	323.1819
783.3519	7	L	5	530.3297	265.6685
840.3734	8	G	4	417.2456	209.1264
939.4418	9	V	3	360.2241	180.6157
1053.4847	10	N	2	261.1557	131.0815
	11	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**

Gene	Description	Peptide with cleaved & acetylated PEXEL
PBANKA_0715300	conserved Plasmodium protein, unknown function	RSL.NENTTPNVMPIPDSKNEIINTESTISDIAEK



Ions:
a ☐ 1+ ☐ 2+ ☐ 3+
b ☑ 1+ ☐ 2+ ☐ 3+
c ☐ 1+ ☐ 2+ ☐ 3+
x ☐ 1+ ☐ 2+ ☐ 3+
y ☑ 1+ ☑ 2+ ☐ 3+
z ☐ 1+ ☐ 2+ ☐ 3+
[Deselect All]

Neutral Loss:
☐ NH_3 (*)
☑ H_2O (o)
☐ H_3PO_4 (p)
☐ Immonium ions
☐ Reporter ions

Mass Type: ● Mono ○ Avg
Mass Tol: 5
○ Th ● ppm

Update

Peak Assignment:
● Most Intense
○ Nearest Match
☑ Peak Detect

Peak Labels:
● Ion ○ m/z
○ None

Width: 650
Height: 400

NENTTPNVMPIPDSKNEIINTESTISDIAEK, MH+ 3456.6687, m/z 1152.8944
File: Rep3_F1.41097.41097.3, Scan: 41097, Exp. m/z: 1152.8945, Charge: 3

Click and drag in the plot to zoom X: ☑ Y: ☐ Zoom Out Print ☐ Enable tooltip ☐ Plot mass error

b+	#	Seq	#	y+	y2+
157.0608	1	N	31		
286.1034	2	E	30	3300.6152	1650.8112
400.1463	3	N	29	3171.5726	1586.2899
501.1940	4	T	28	3057.5296	1529.2685
602.2416	5	T	27	2956.4820	1478.7446
699.2944	6	P	26	2855.4343	1428.2208
813.3373	7	N	25	2758.3815	1379.6944
912.4058	8	V	24	2644.3386	1322.6729
1043.4462	9	M	23	2545.2702	1273.1387
1140.4990	10	P	22	2414.2297	1207.6185
1253.5831	11	I	21	2317.1769	1159.0921
1350.6358	12	P	20	2204.0929	1102.5501
1465.6628	13	D	19	2107.0401	1054.0237
1552.6948	14	S	18	1992.0132	996.5102
1680.7898	15	K	17	1904.9811	952.9942
1794.8327	16	N	16	1776.8862	888.9467
1923.8753	17	E	15	1662.8432	831.9253
2036.9593	18	I	14	1533.8006	767.4040
2150.0434	19	I	13	1420.7166	710.8619
2264.0863	20	N	12	1307.6325	654.3199
2365.1340	21	T	11	1193.5896	597.2984
2494.1766	22	E	10	1092.5419	546.7746
2581.2086	23	S	9	963.4993	482.2533
2682.2563	24	T	8	876.4673	438.7373
2795.3404	25	I	7	775.4196	388.2134
2882.3724	26	S	6	662.3355	331.6714
2997.3994	27	D	5	575.3035	288.1554
3110.4834	28	I	4	460.2766	230.6419
3181.5205	29	A	3	347.1925	174.0999
3310.5631	30	E	2	276.1554	138.5813
	31	K	1	147.1128	74.0600

[Click] to move table

Add to N-term: **42.010565**