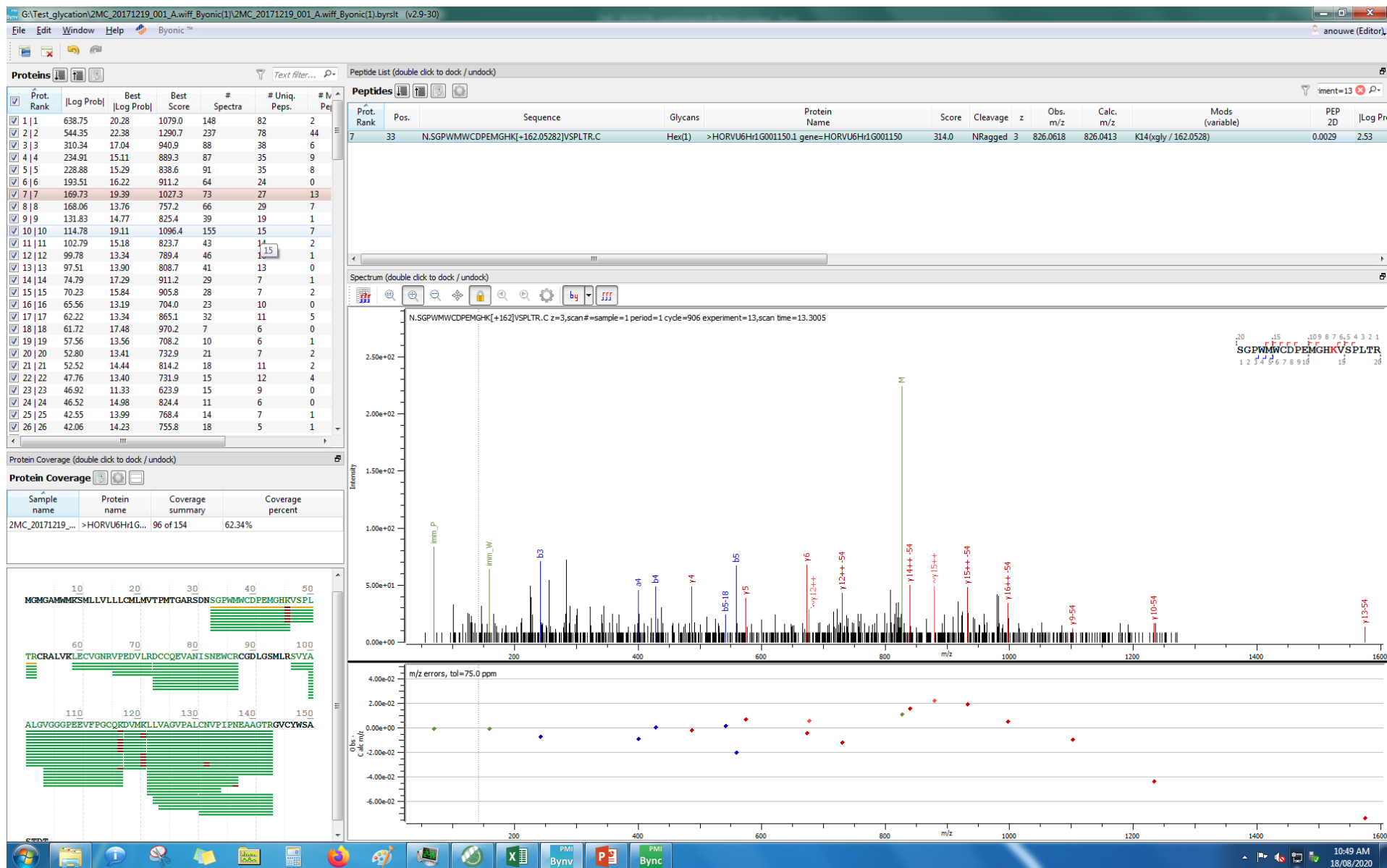
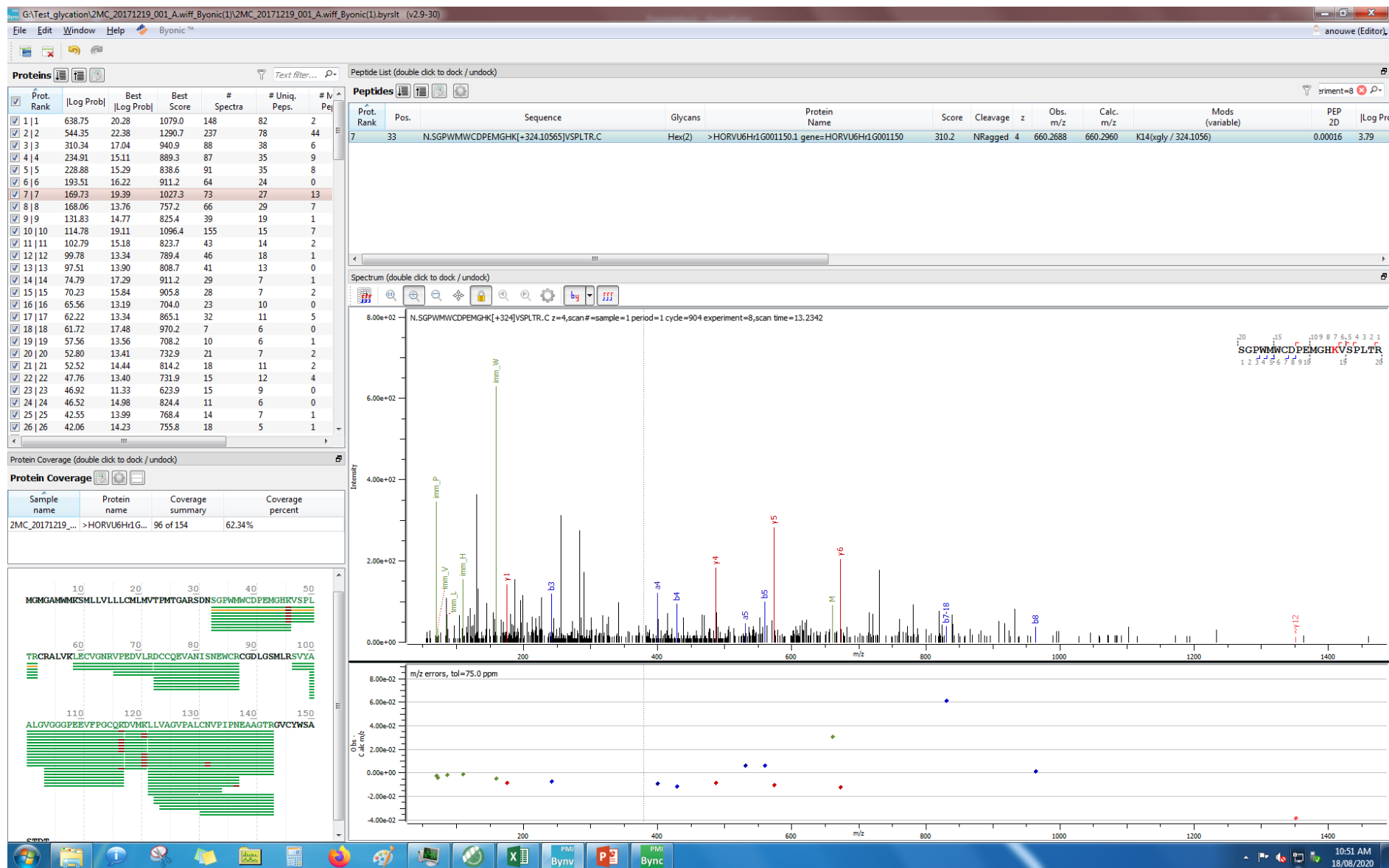


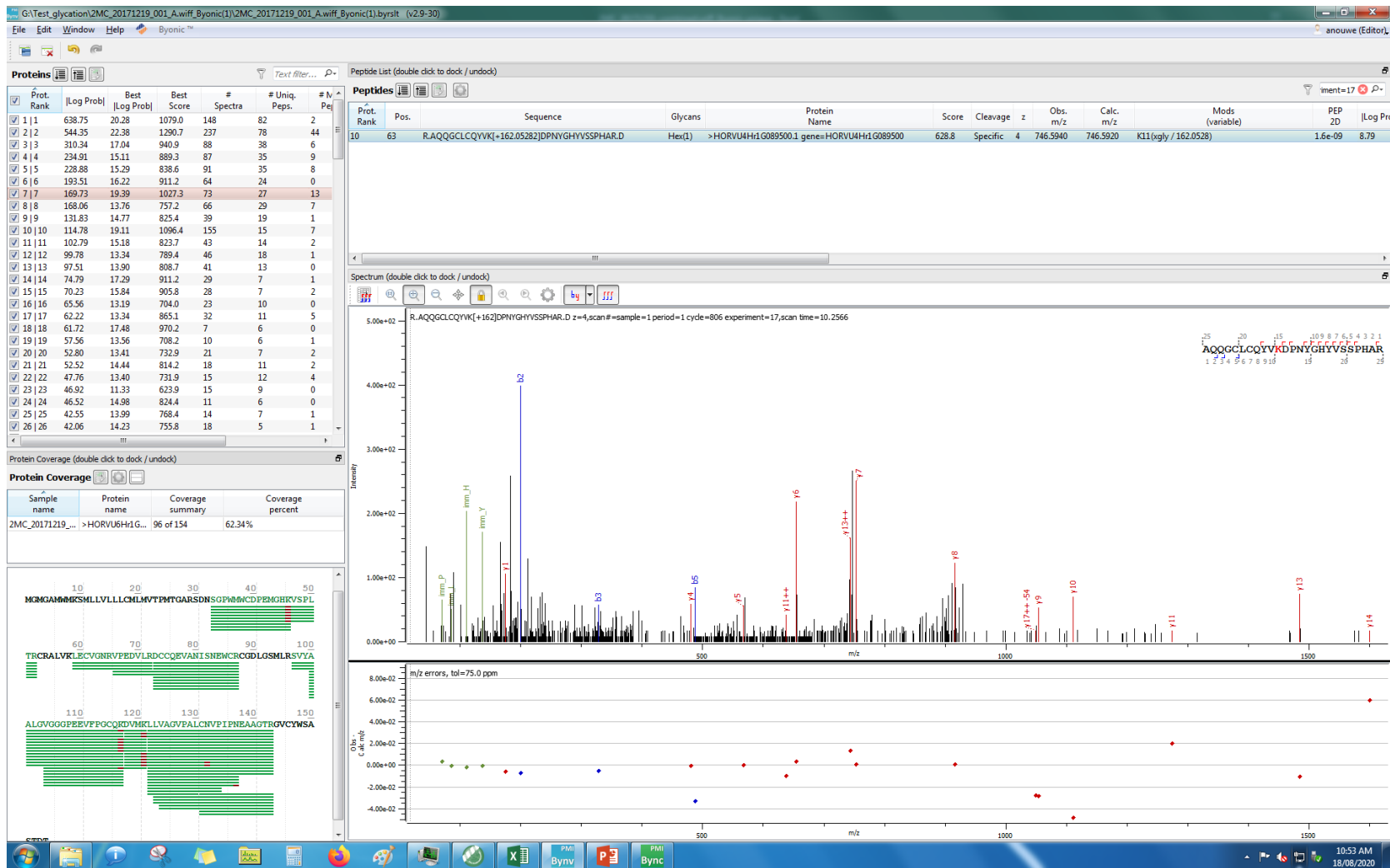
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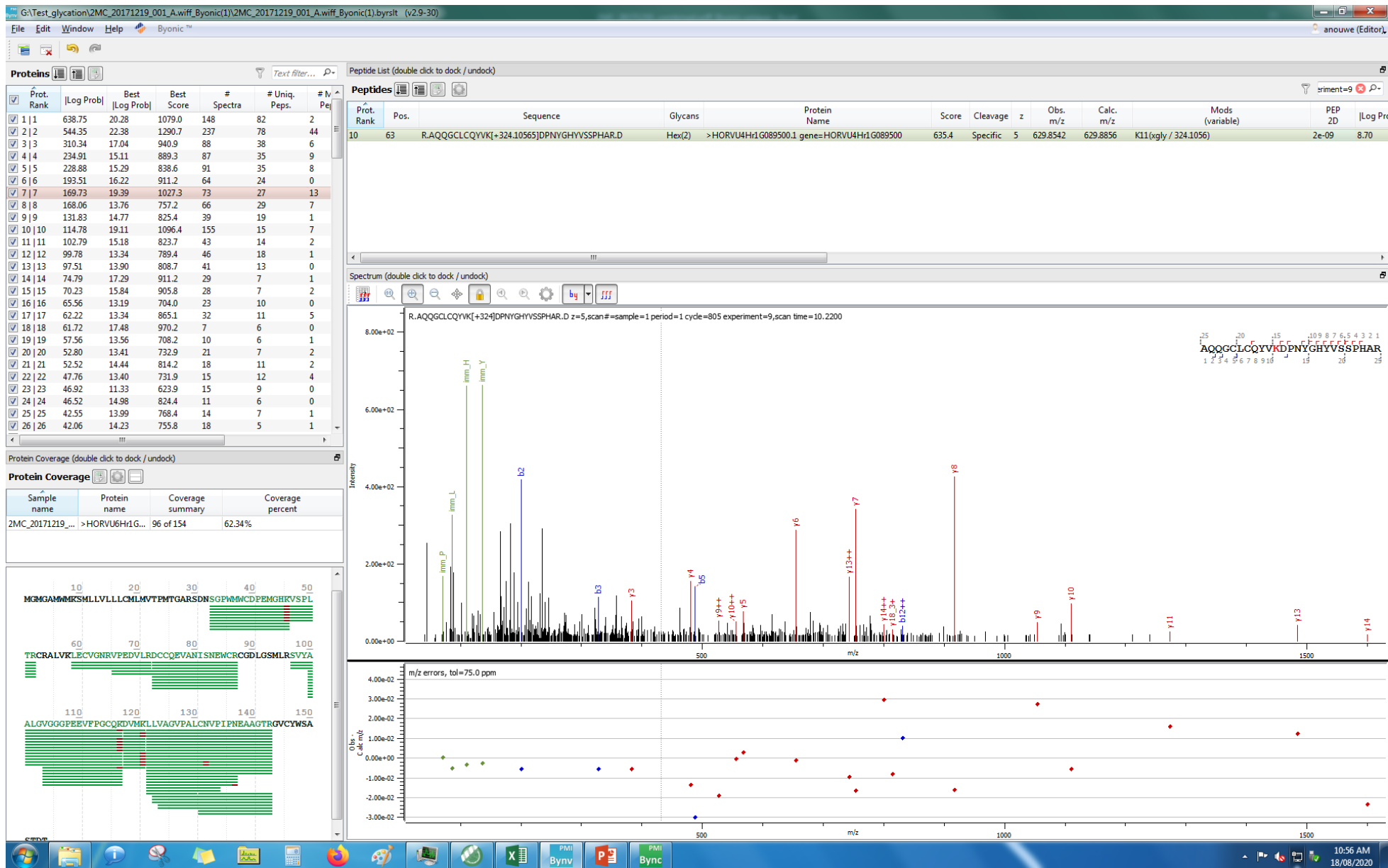


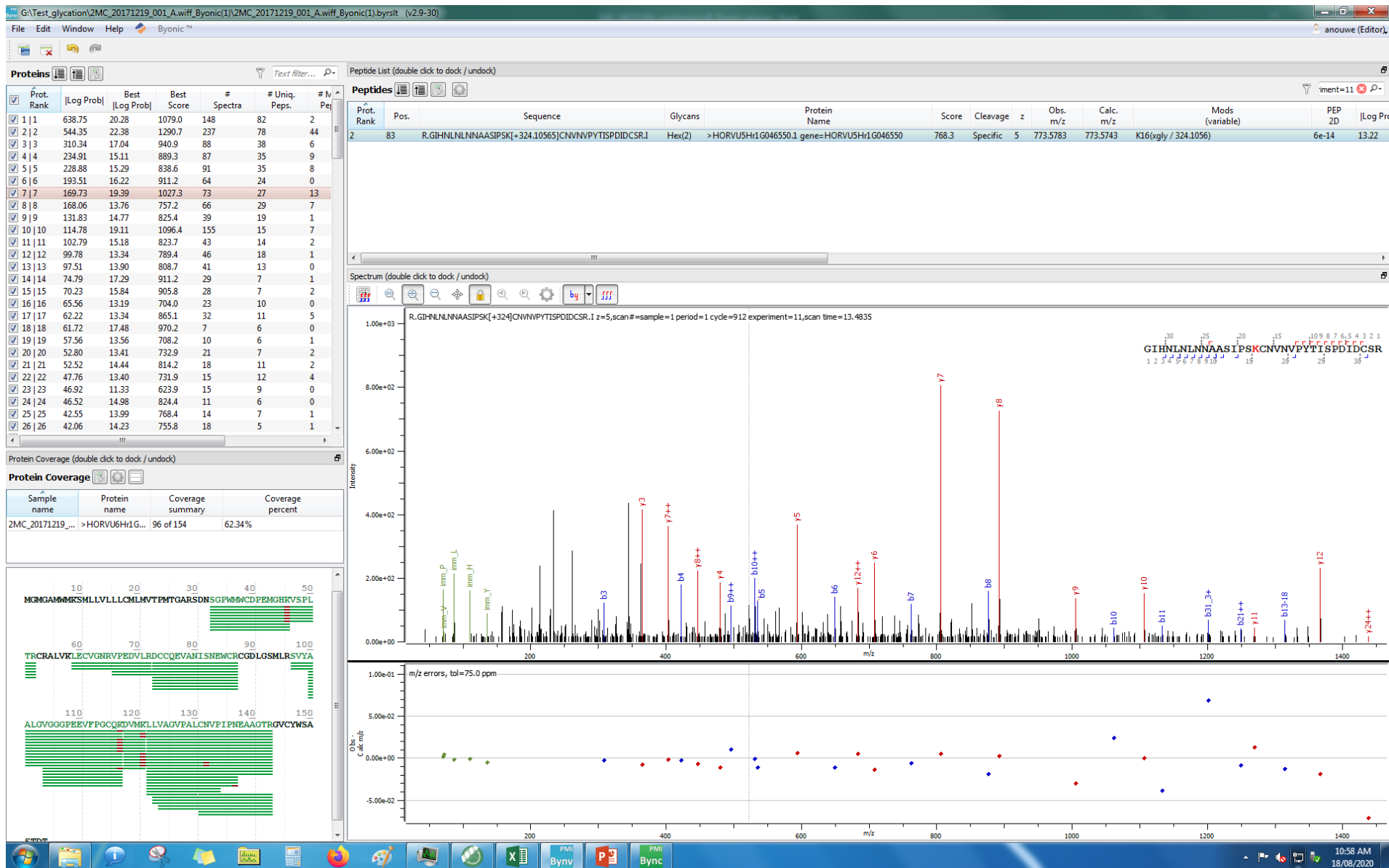


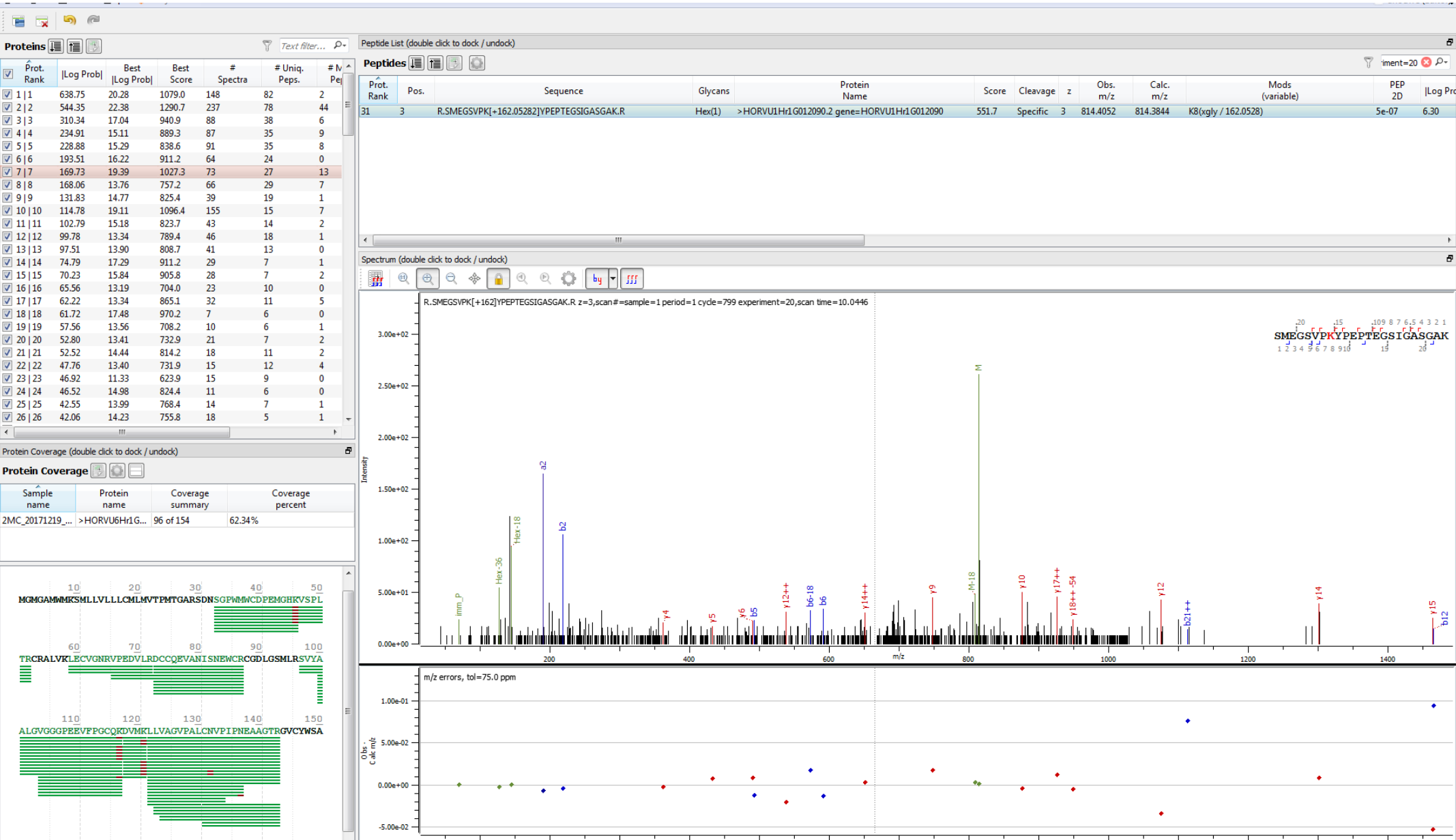


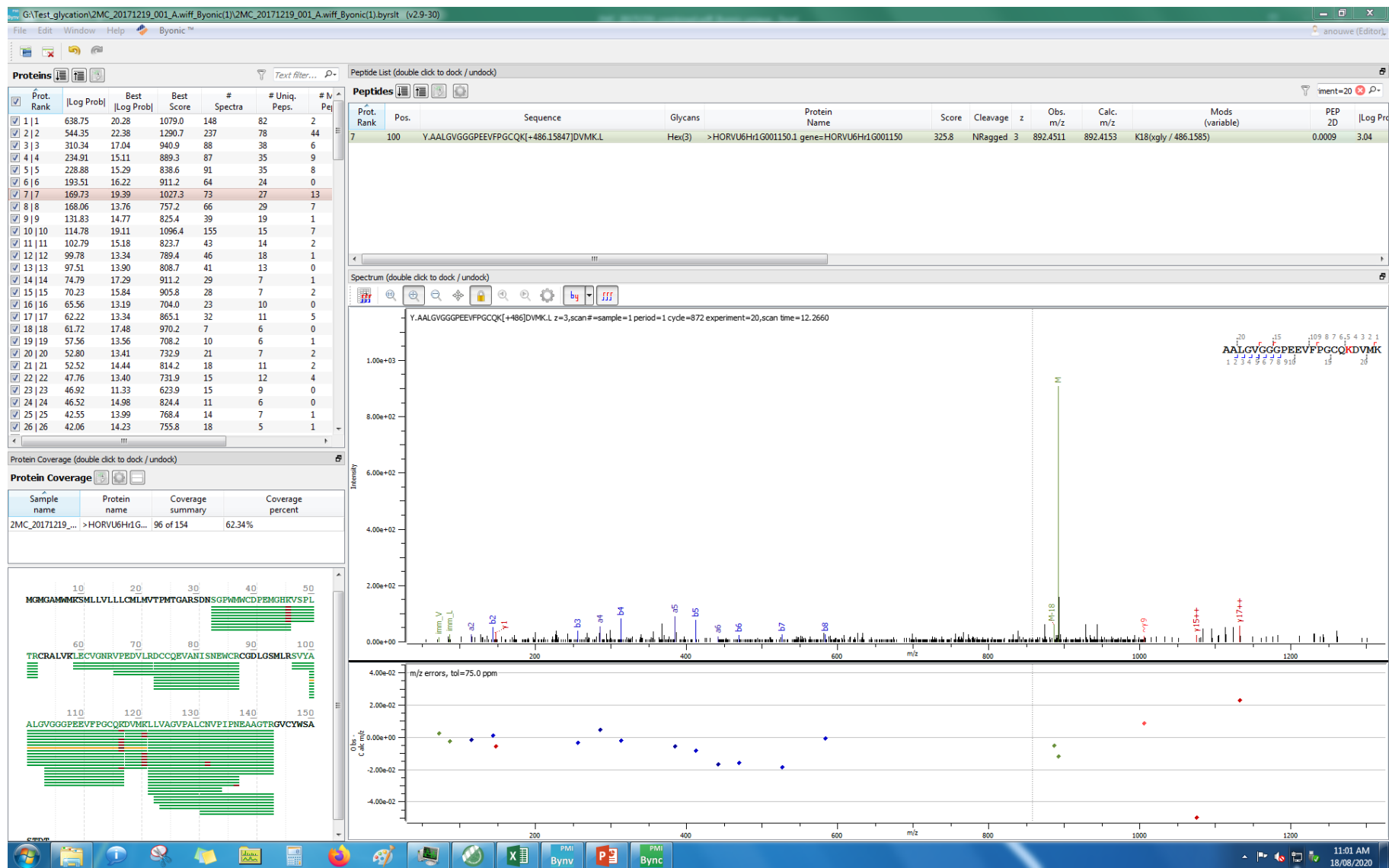


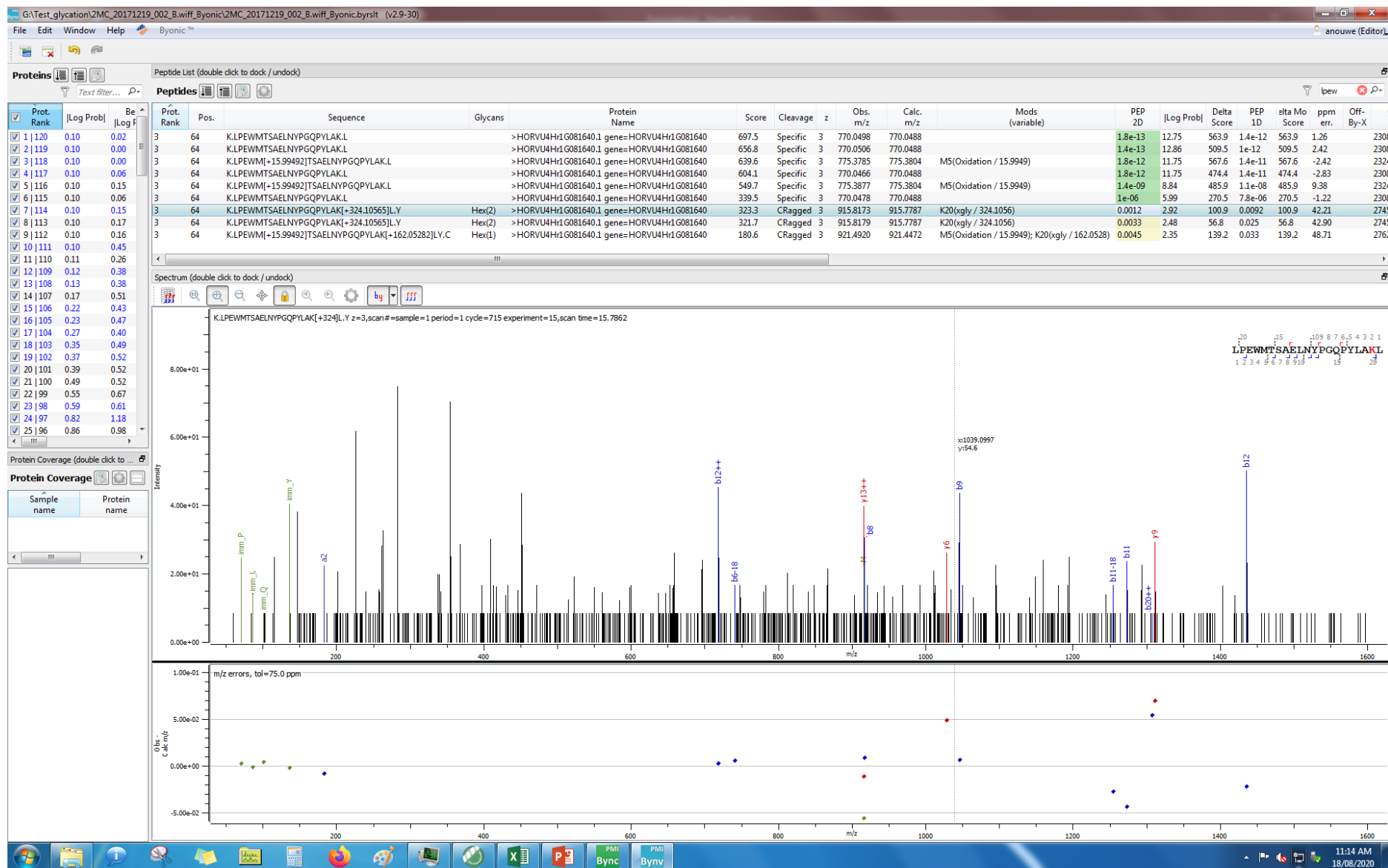


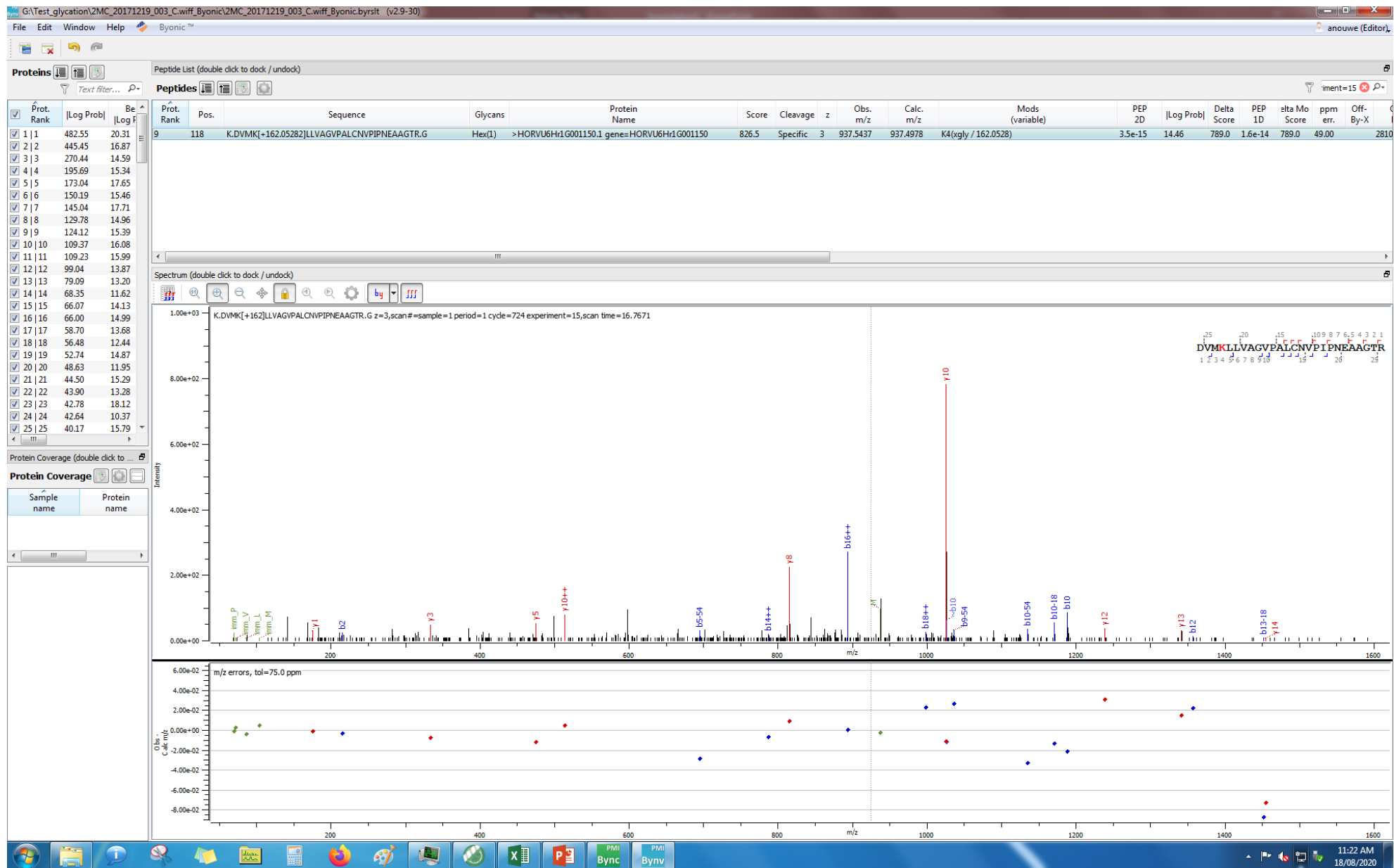


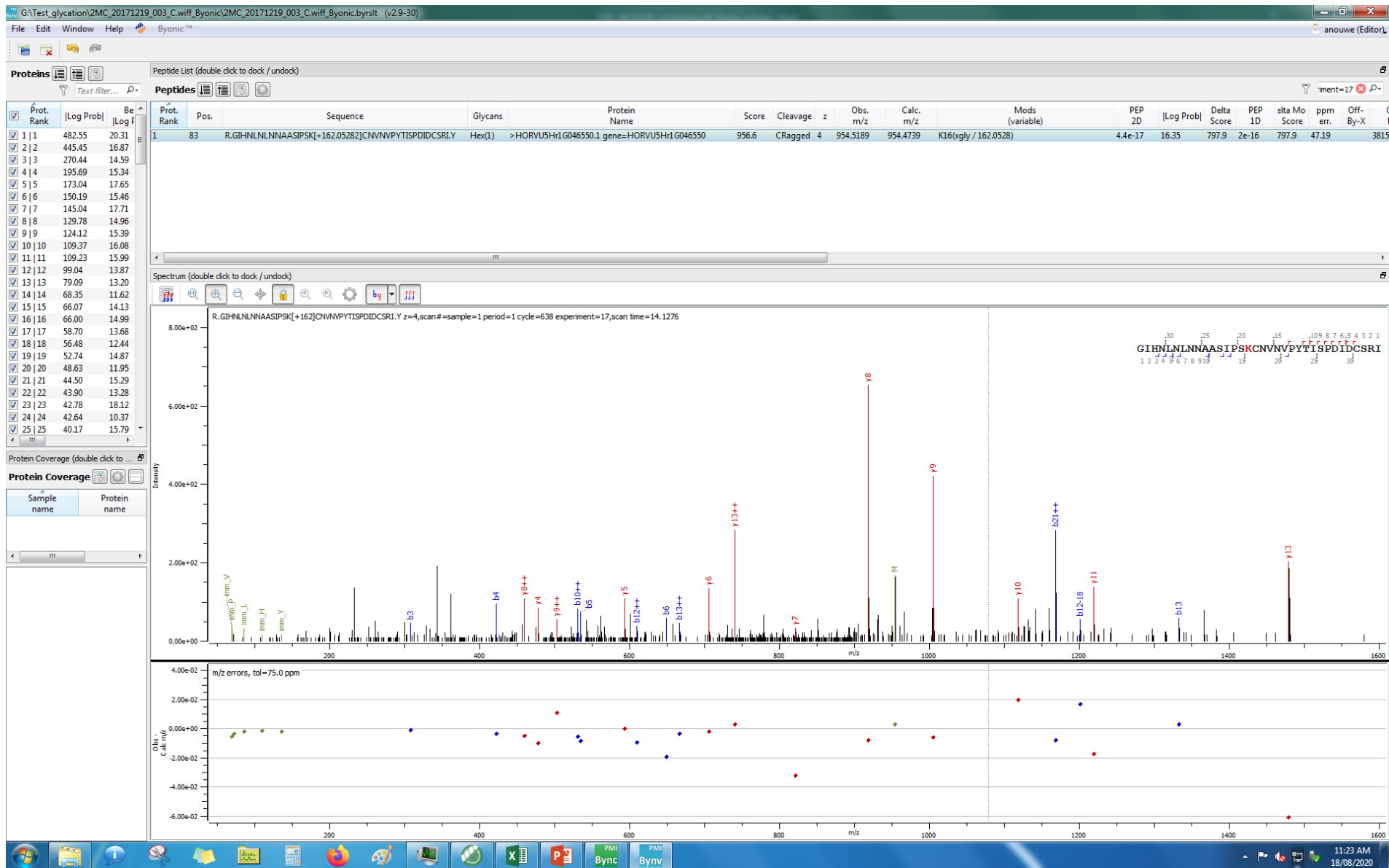














Proteins

Text filter...

Prot. Rank	[Log Prob]	Best [Log Prob]
1 1	364.68	18.44
2 2	258.78	14.80
3 3	249.08	17.19
4 4	223.21	15.26
5 5	217.93	17.98
6 6	151.60	13.45
7 7	115.67	12.47
8 8	72.60	14.13
9 9	58.92	10.79
10 10	53.33	15.21
11 11	49.88	8.57
12 12	48.61	13.55
13 13	45.07	14.99
14 14	44.76	12.86
15 15	43.55	12.44
16 16	42.51	11.08
17 17	39.98	13.19
18 18	38.67	12.39
19 19	38.40	16.20
20 20	38.06	13.28
21 21	36.03	12.43
22 22	33.50	12.03
23 23	32.14	10.48
24 24	31.29	13.44
25 25	27.04	7.19

Protein Coverage (double click to dock / ...)

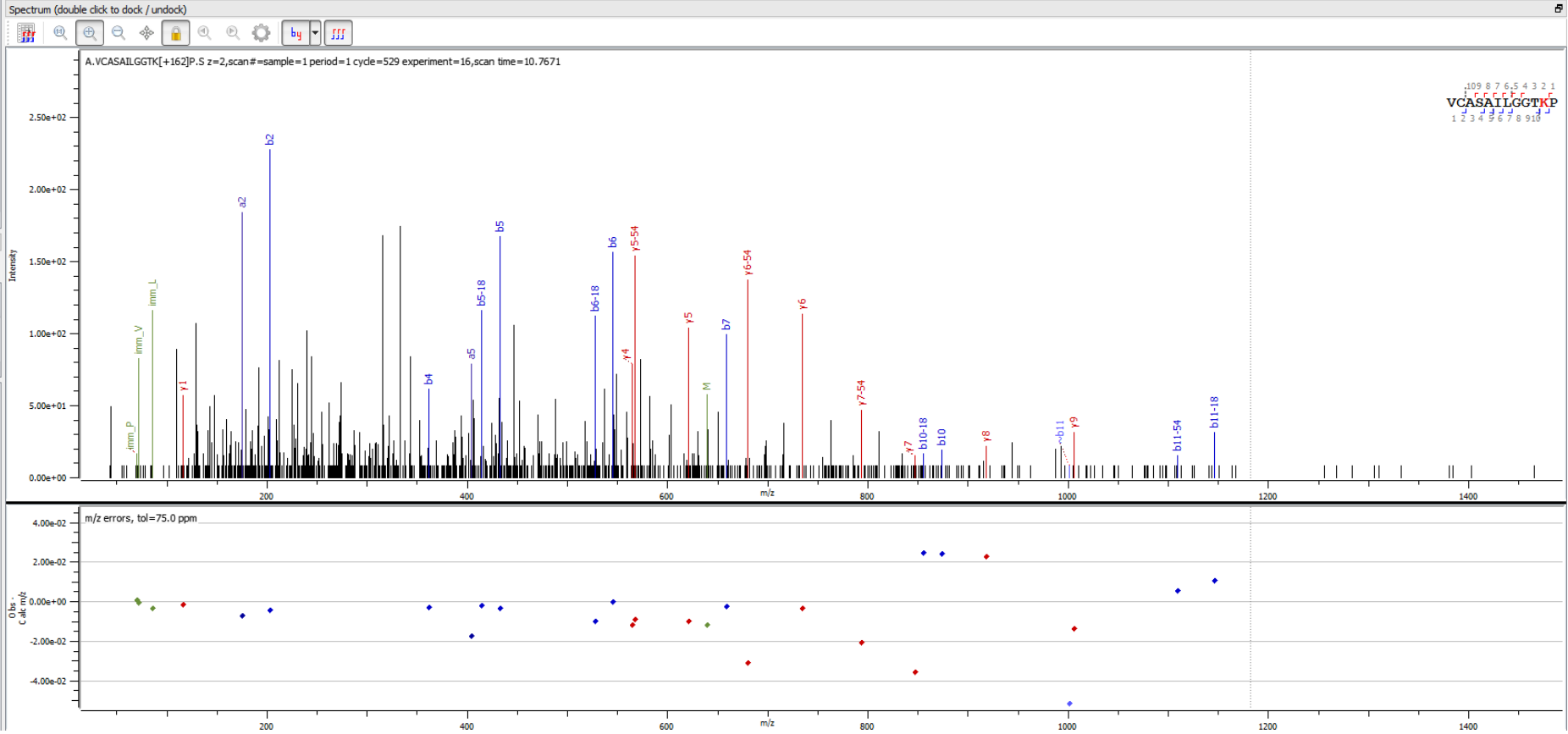
Protein Coverage

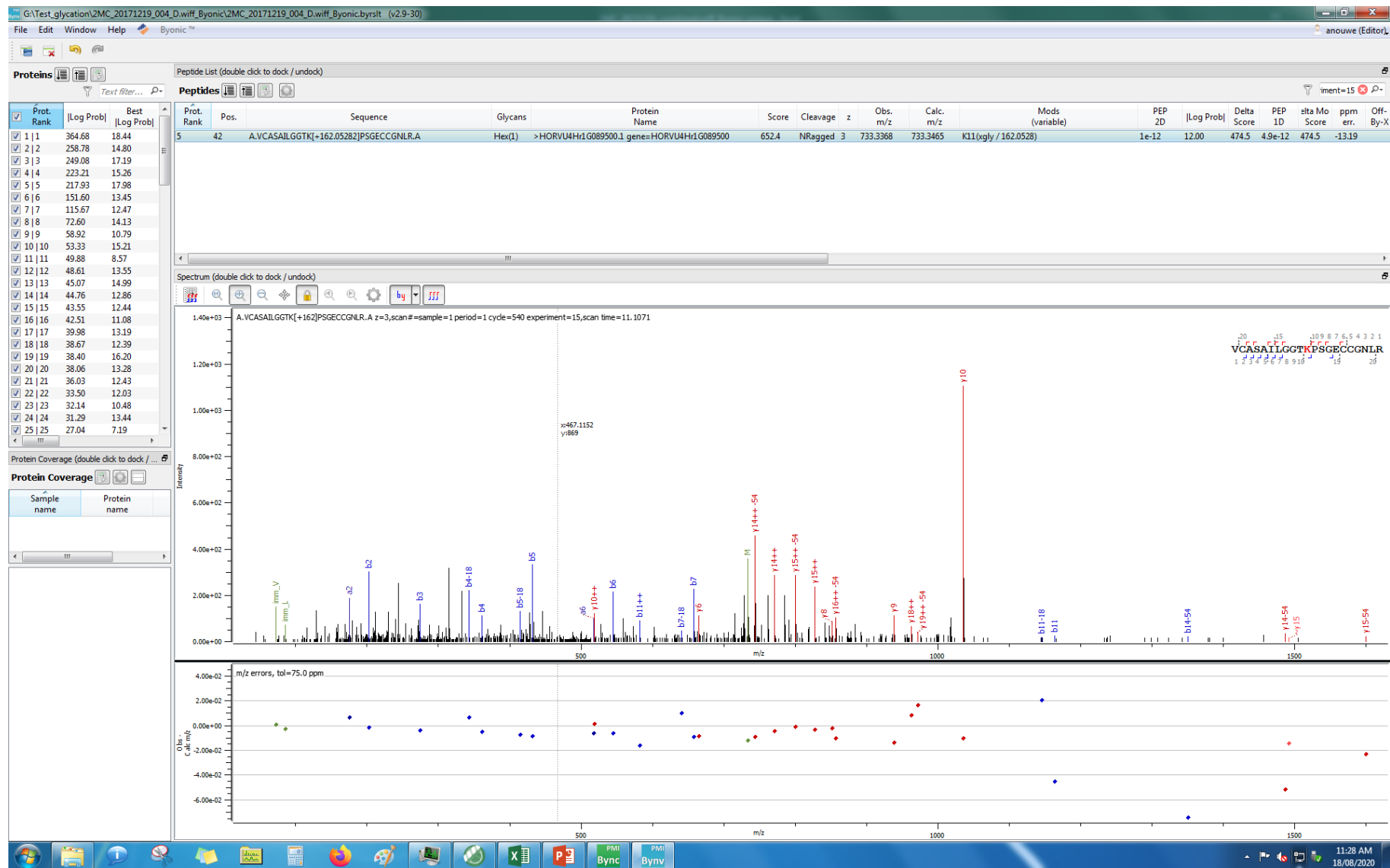
Sample name	Protein name
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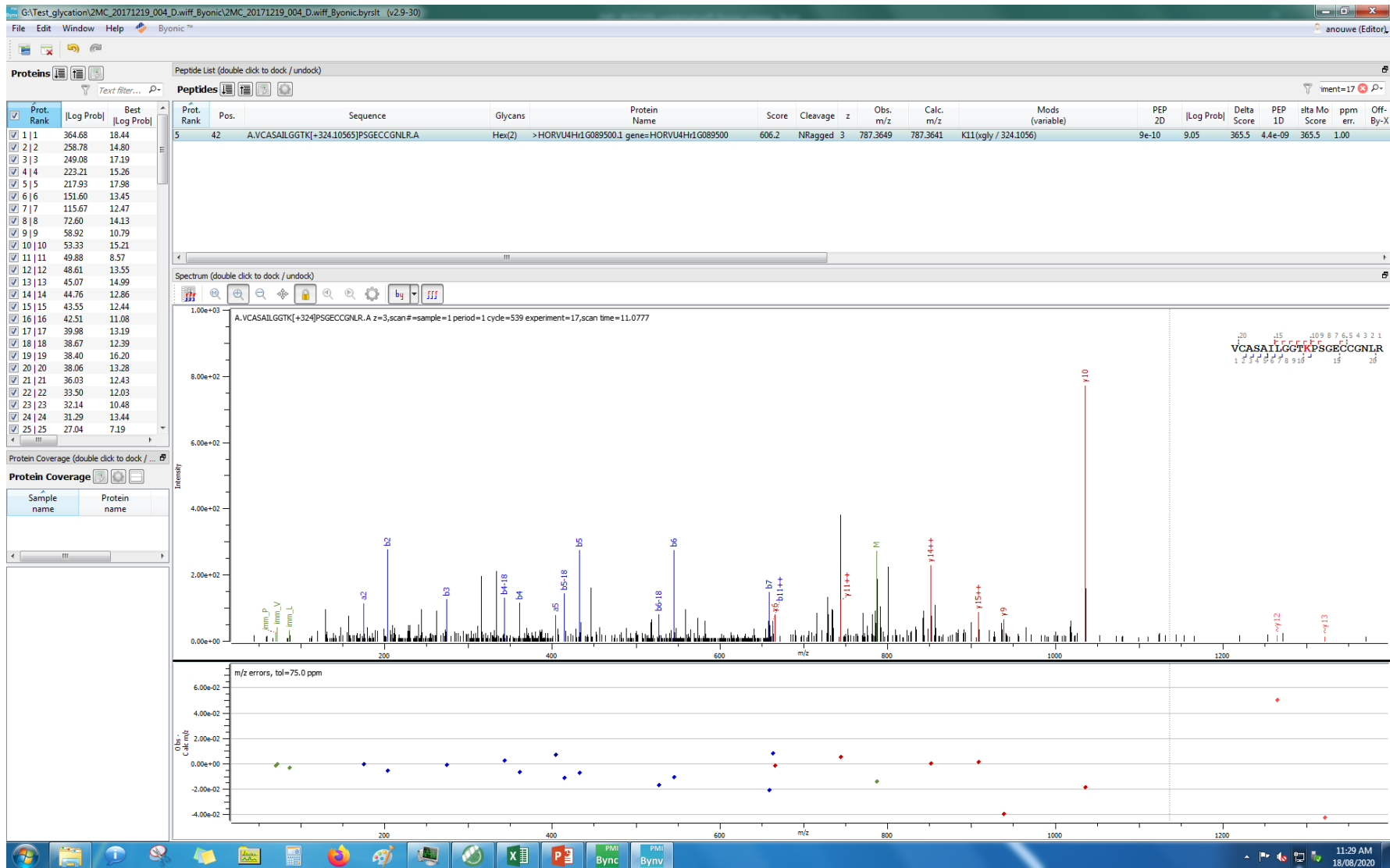
Peptide List (double click to dock / undock)

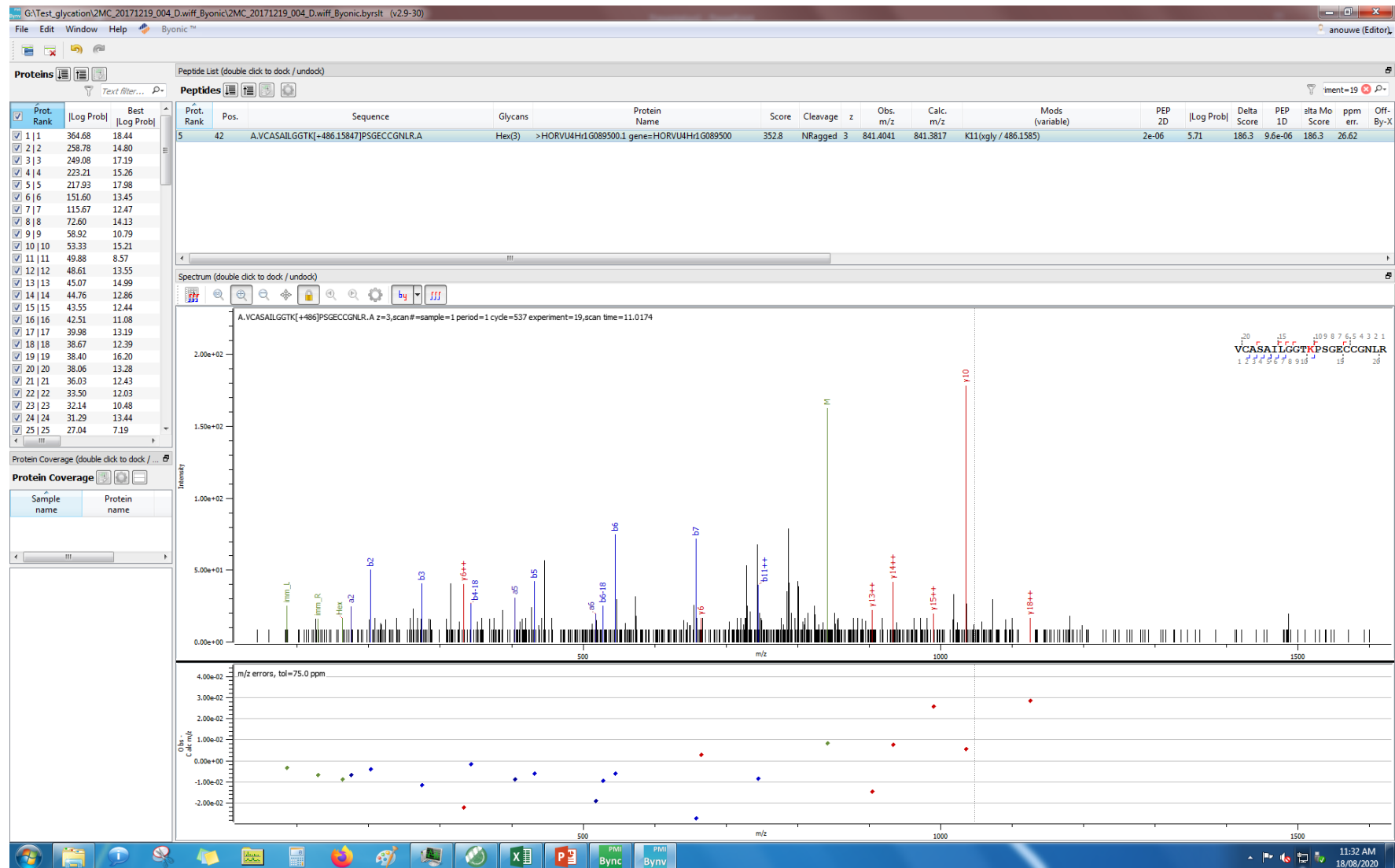
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Prot. Rank	Pos.	Sequence	Glycans	Protein Name	Score	Cleavage	z	Obs. m/z	Calc. m/z	Mods (variable)	PEP 2D	[Log Prob]	Delta Score	PEP 1D	alta Mo Score	ppm err.	Off-By-X
5	42	A.VCASAILGGTK[+162.05282]P.S	Hex(1)	>HORVU4Hr1G089500.1 gene=HORVU4Hr1G089500	506.8	Non	2	639.8030	639.8341	K11(xgly / 162.0528)	1.1e-06	5.95	282.5	5.5e-06	282.5	-48.71	



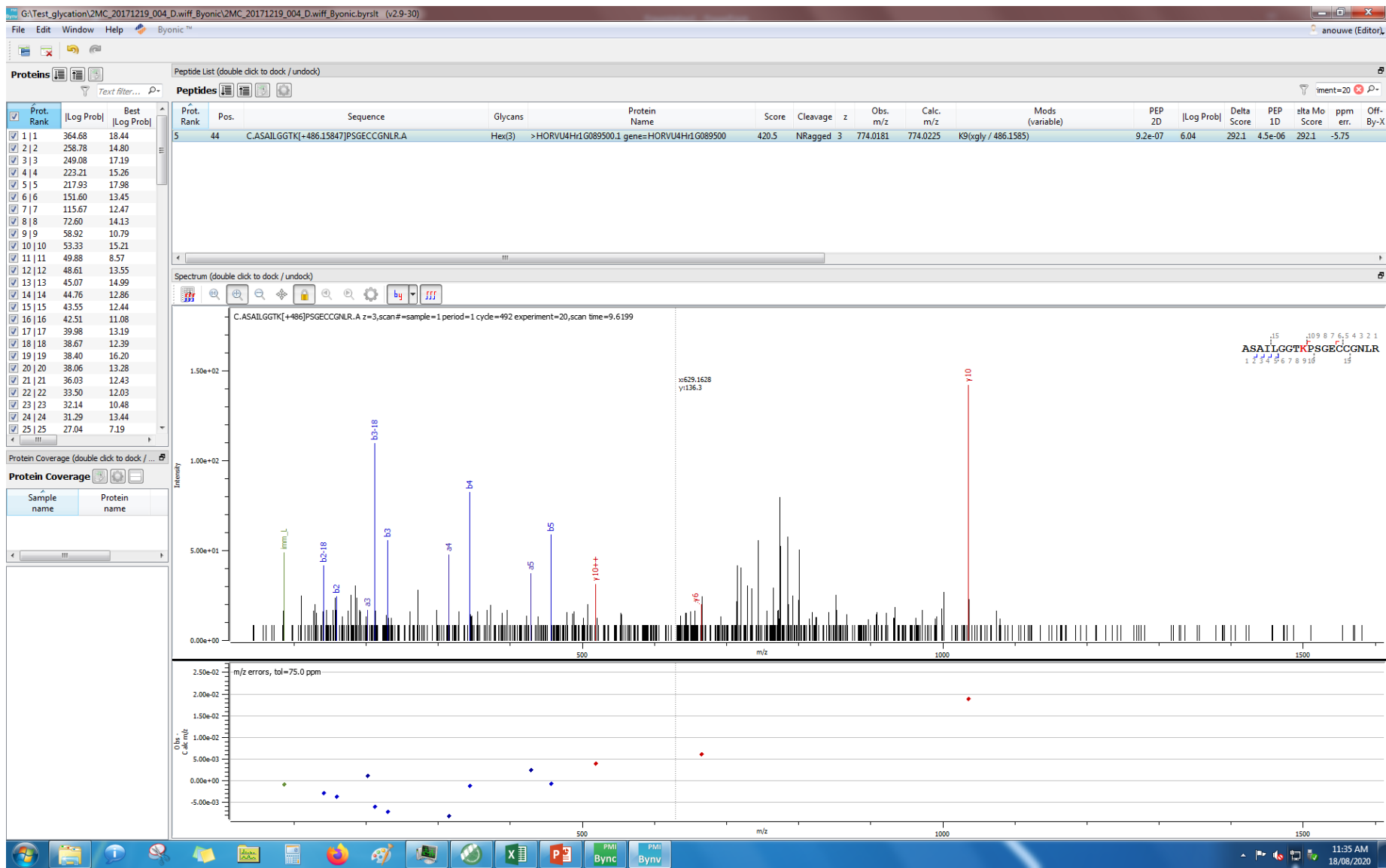


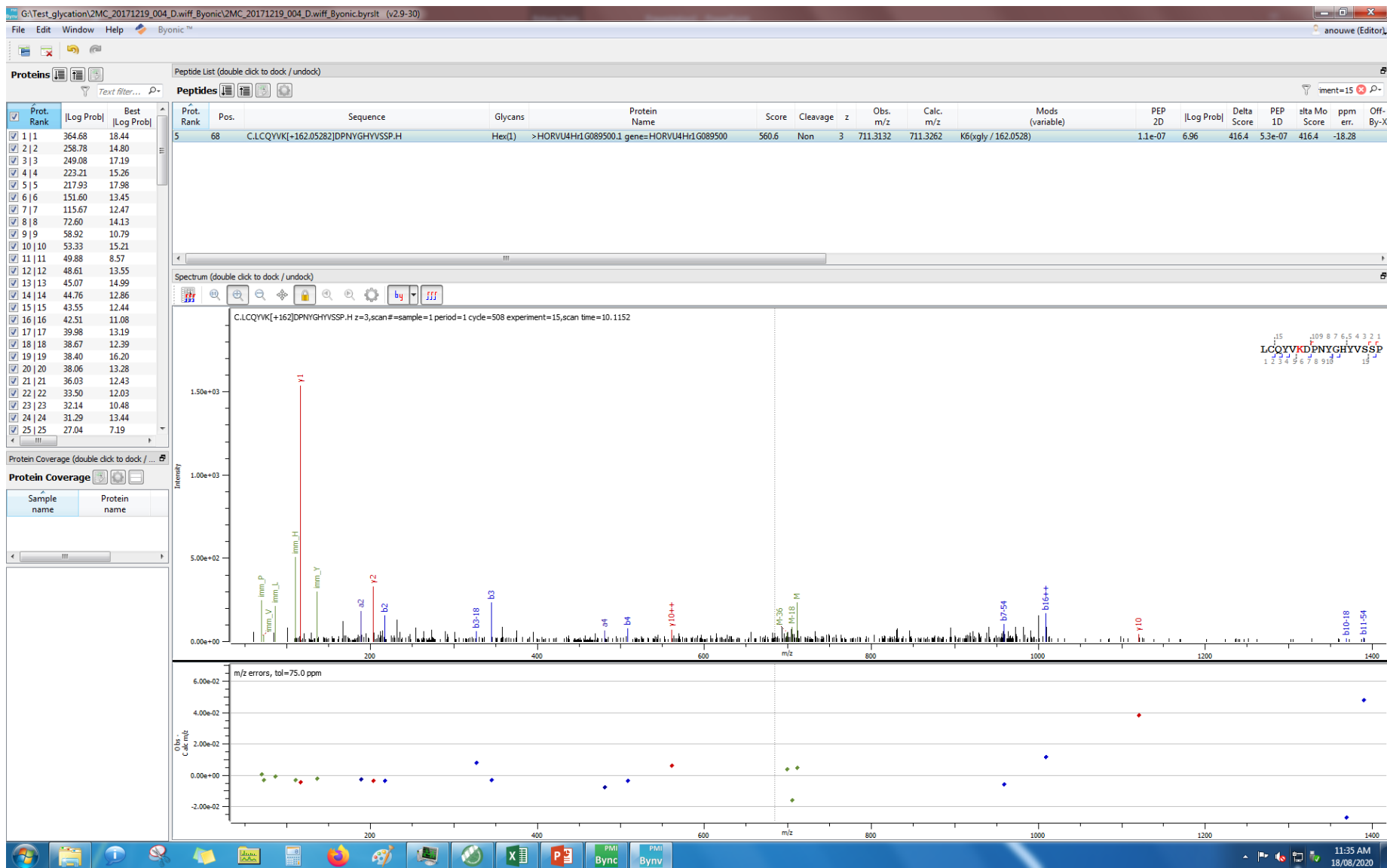


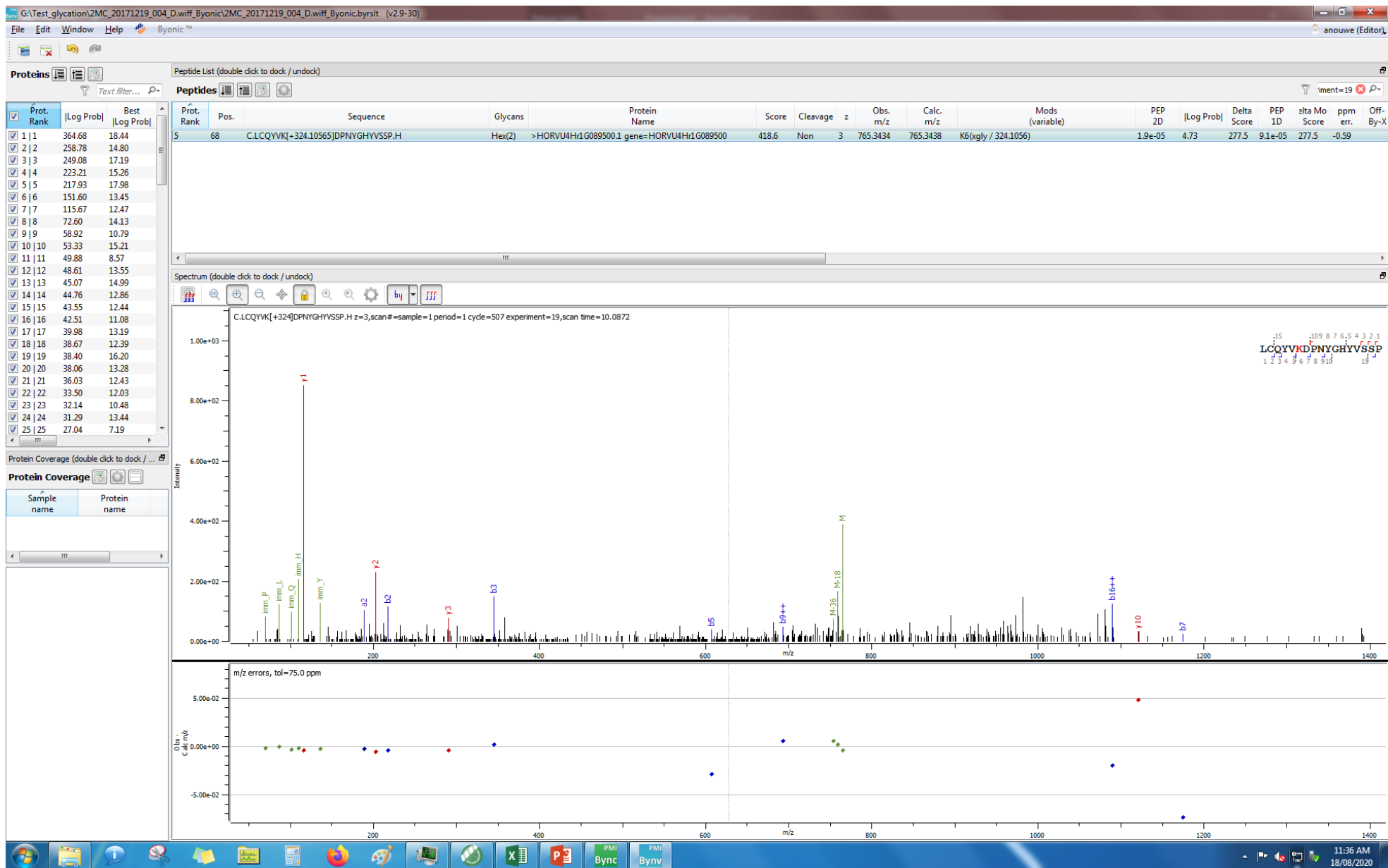


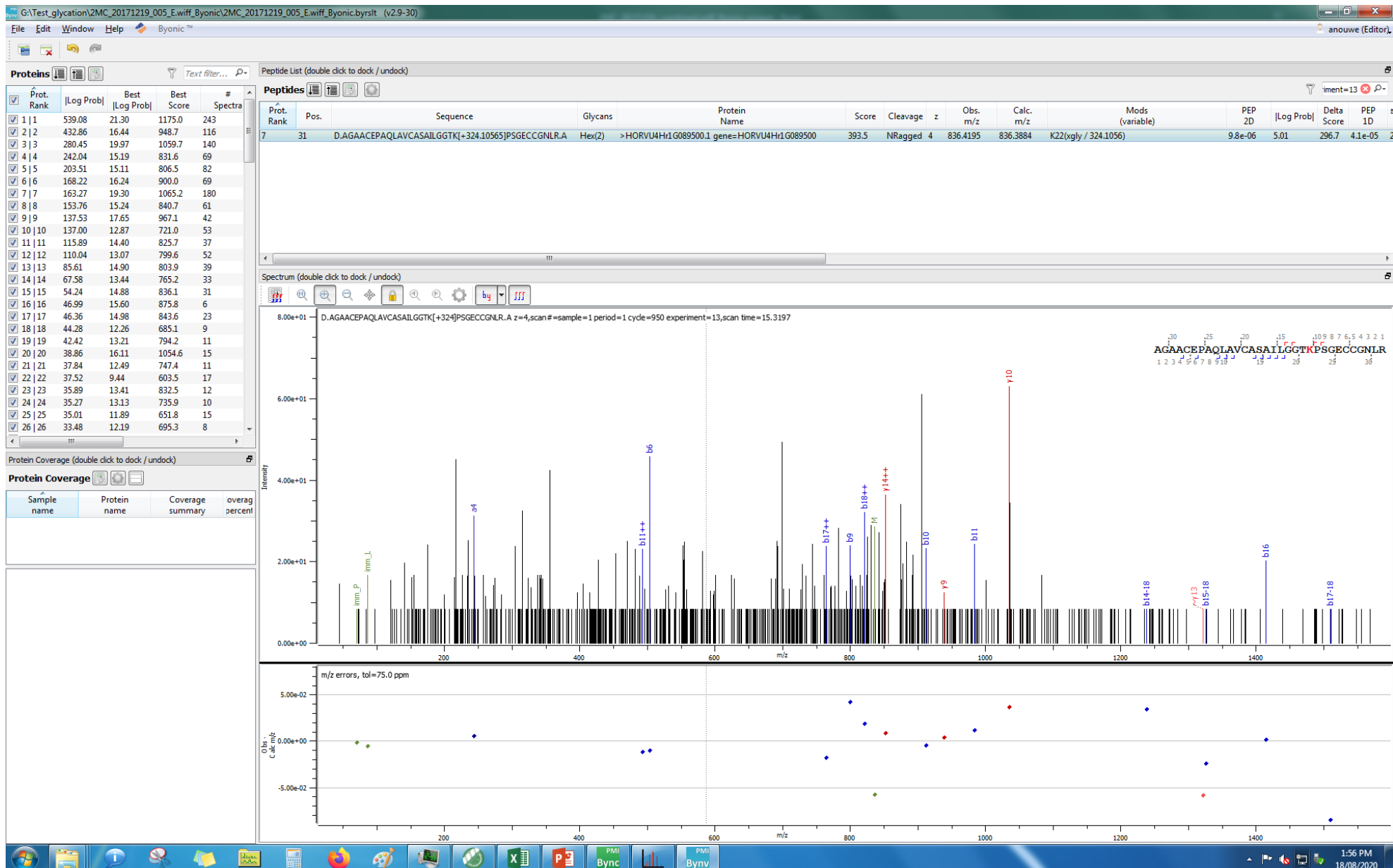




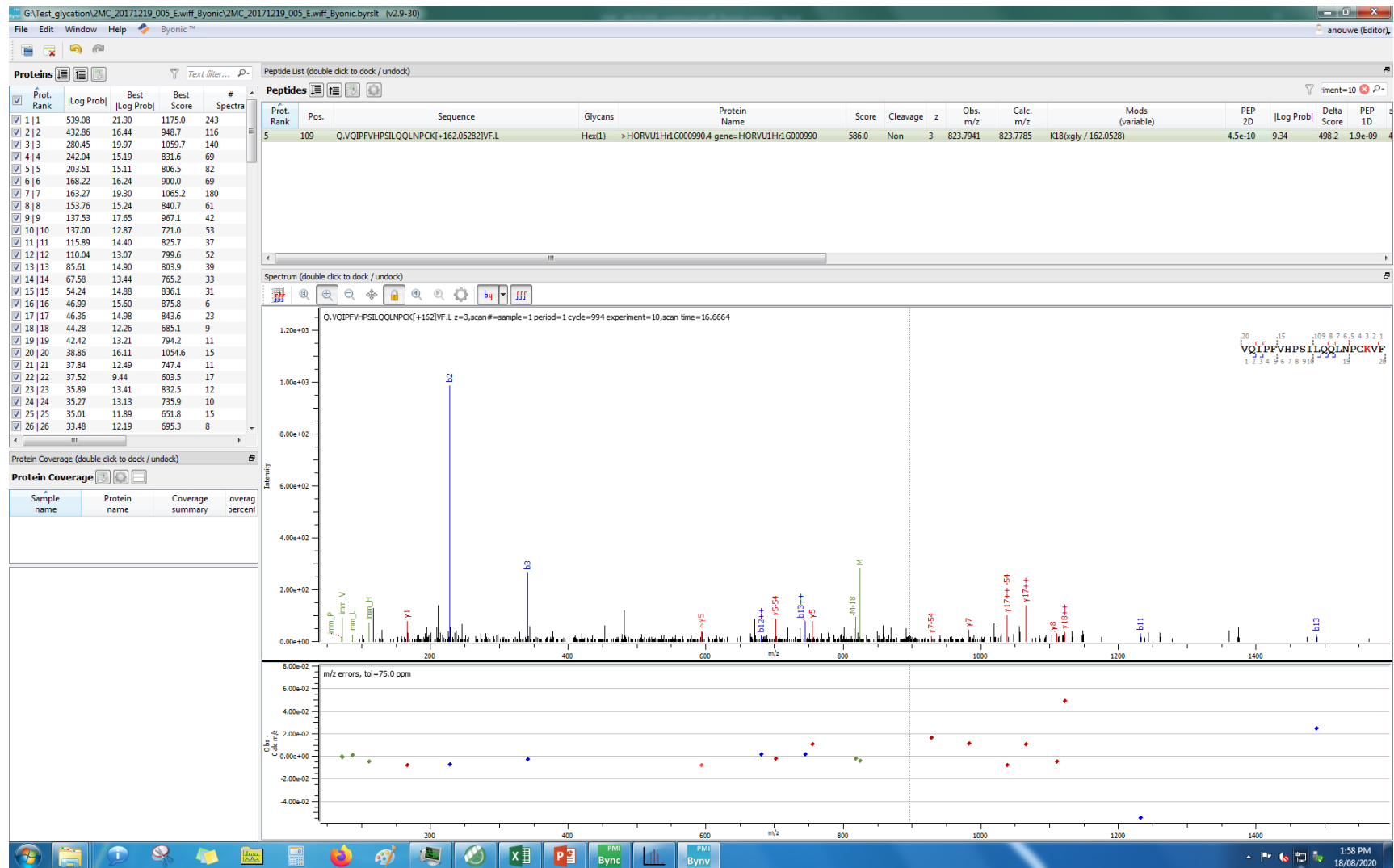


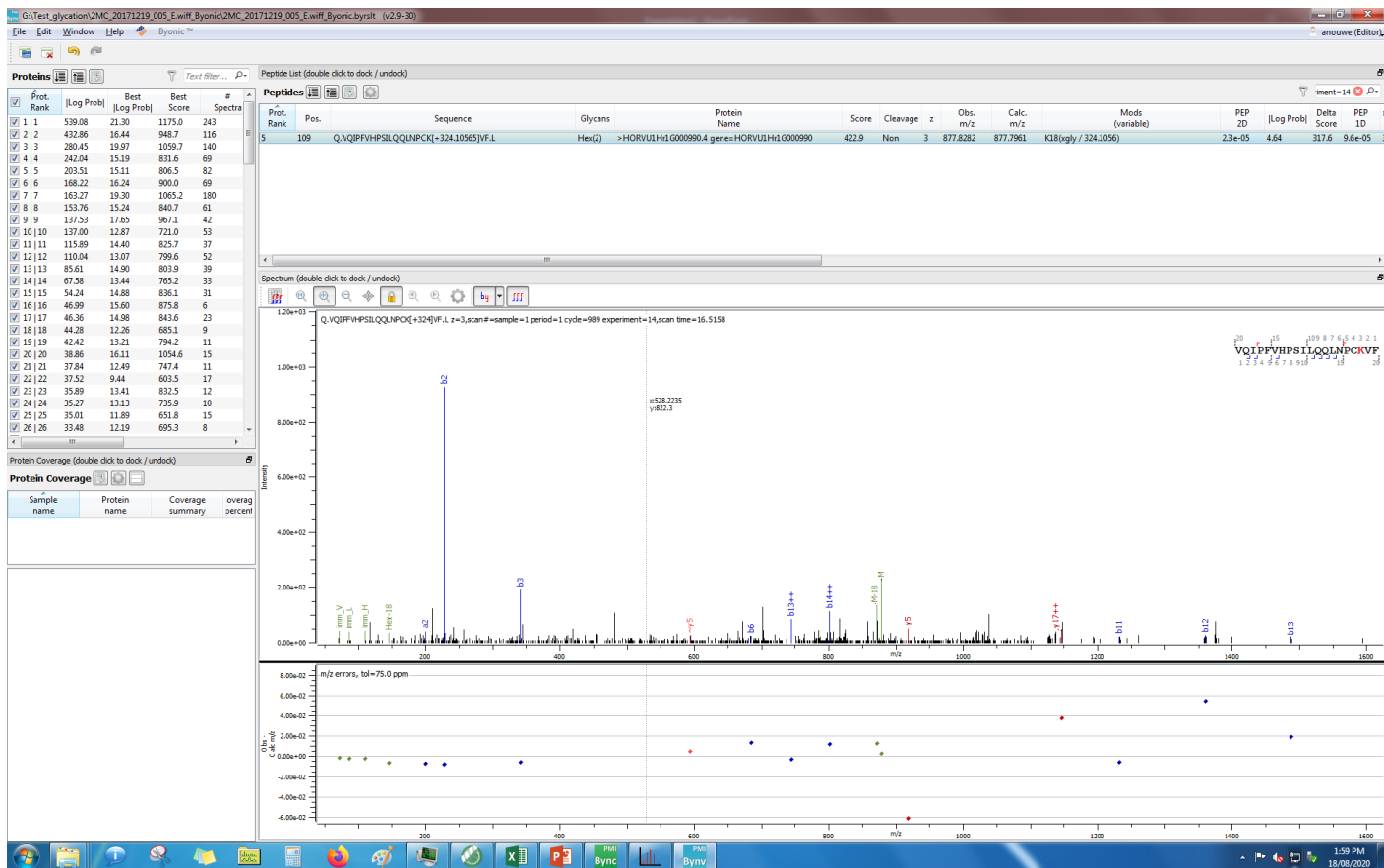


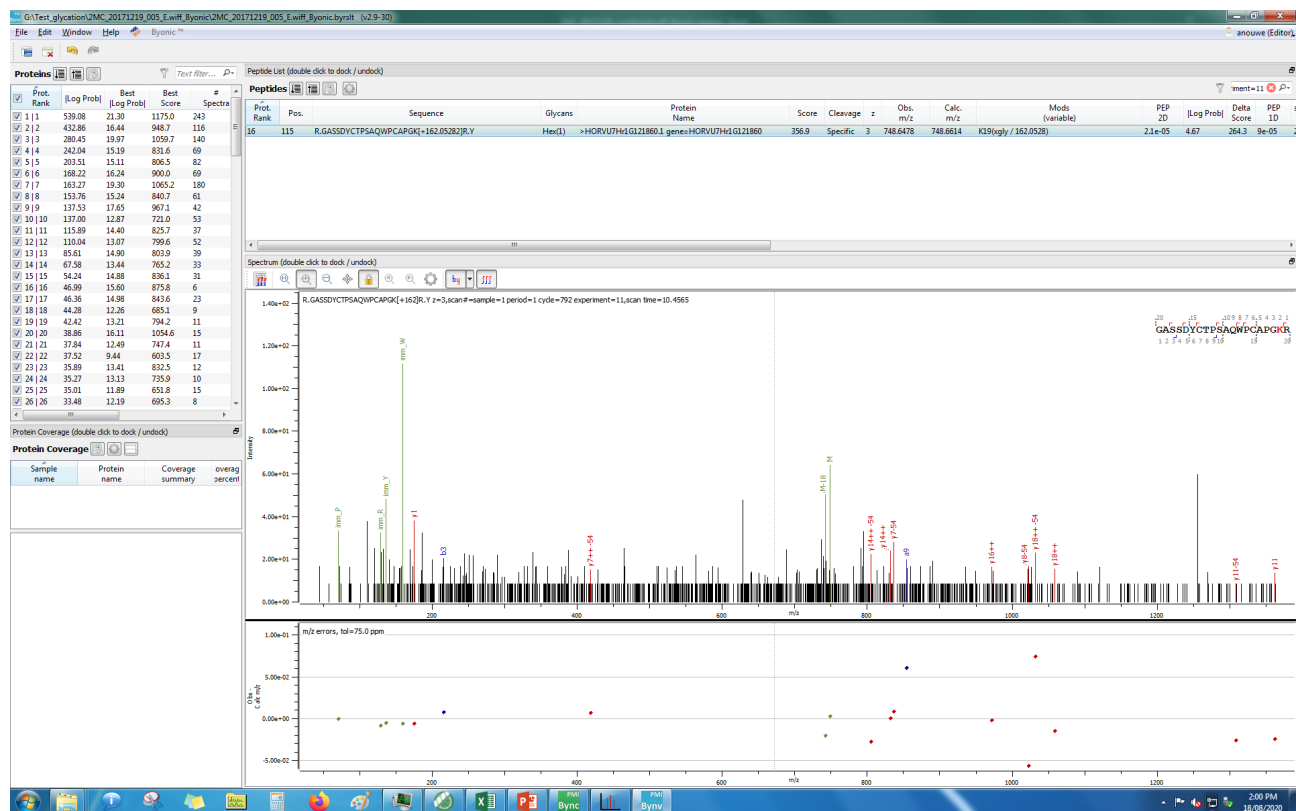


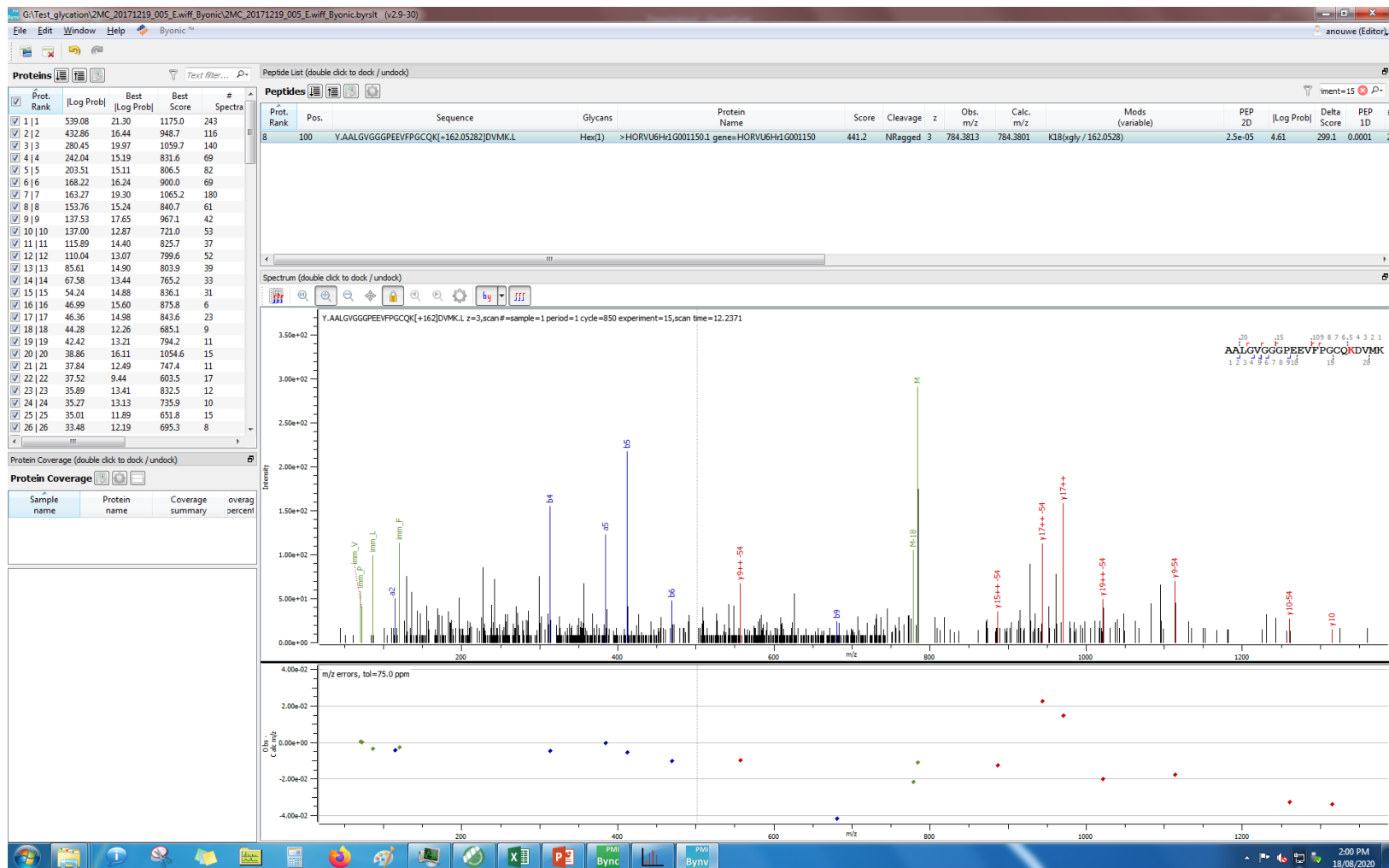


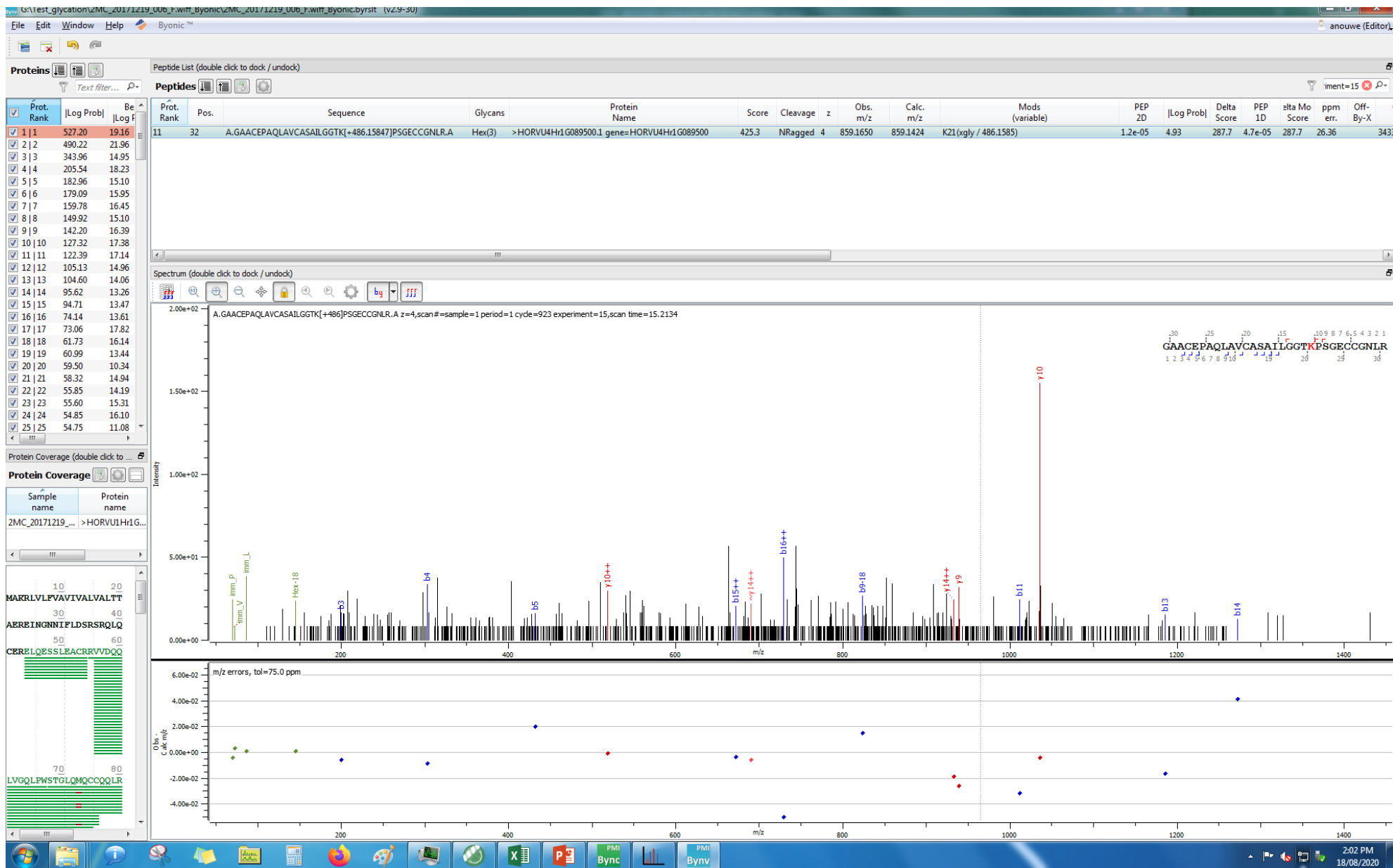


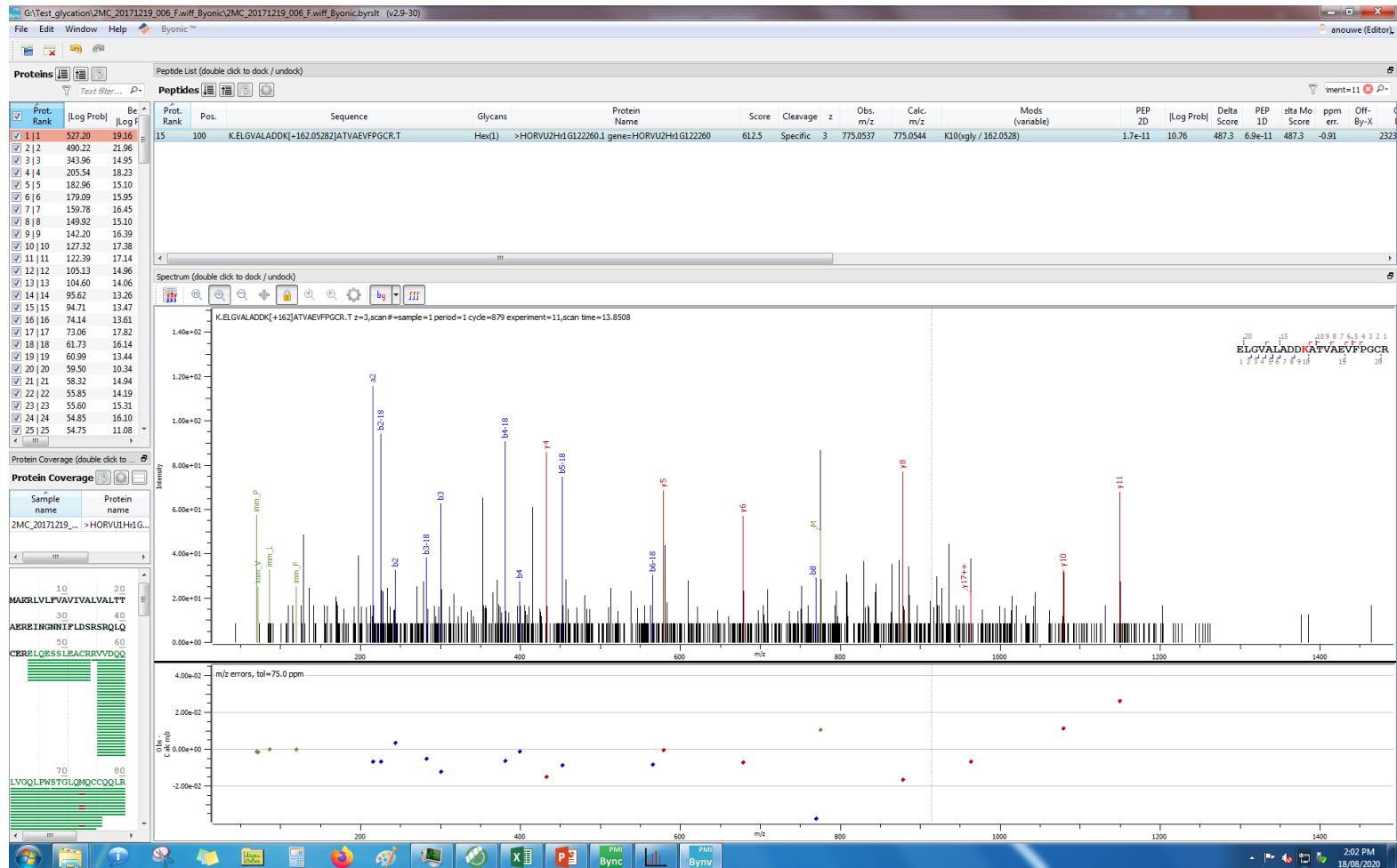


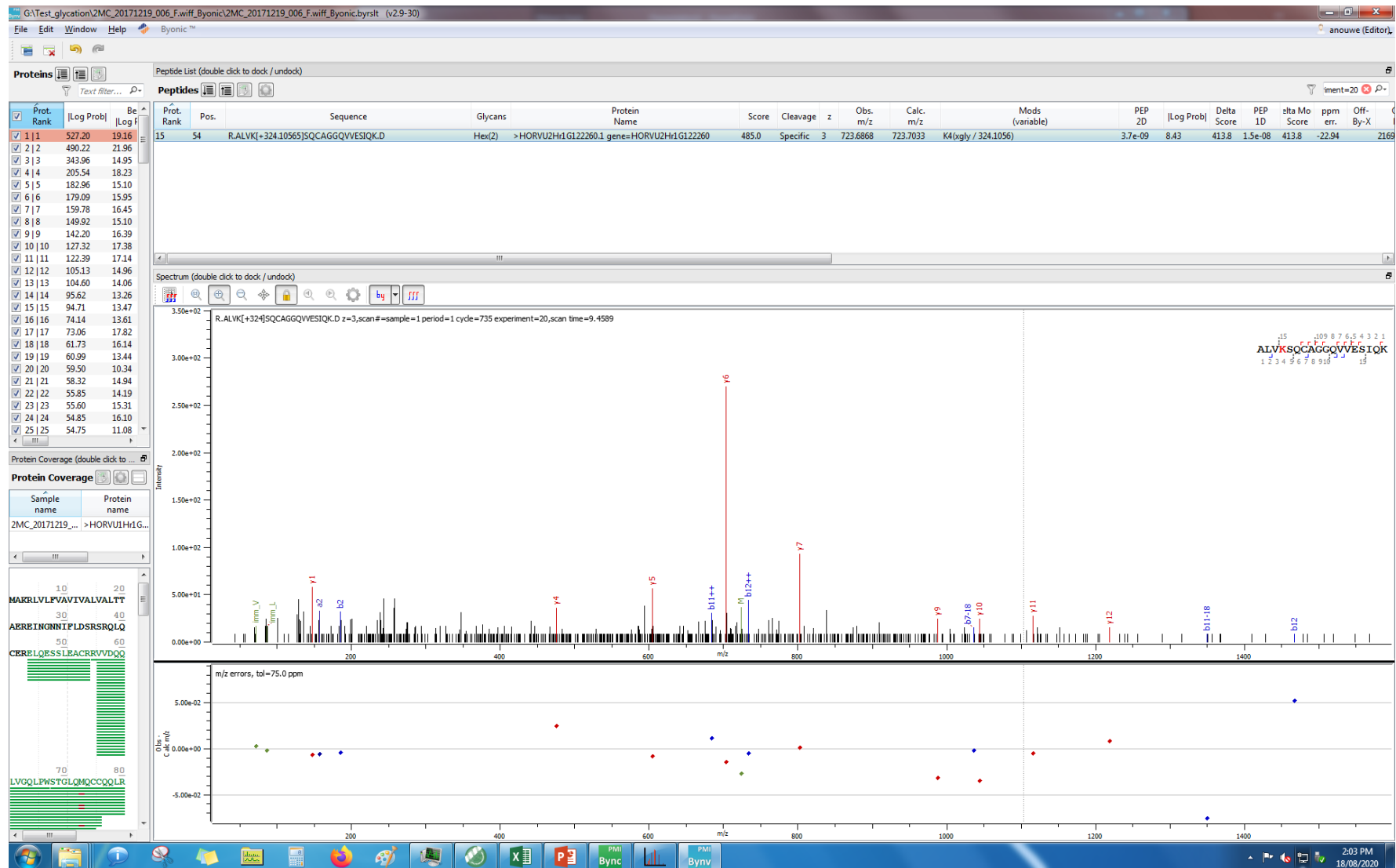




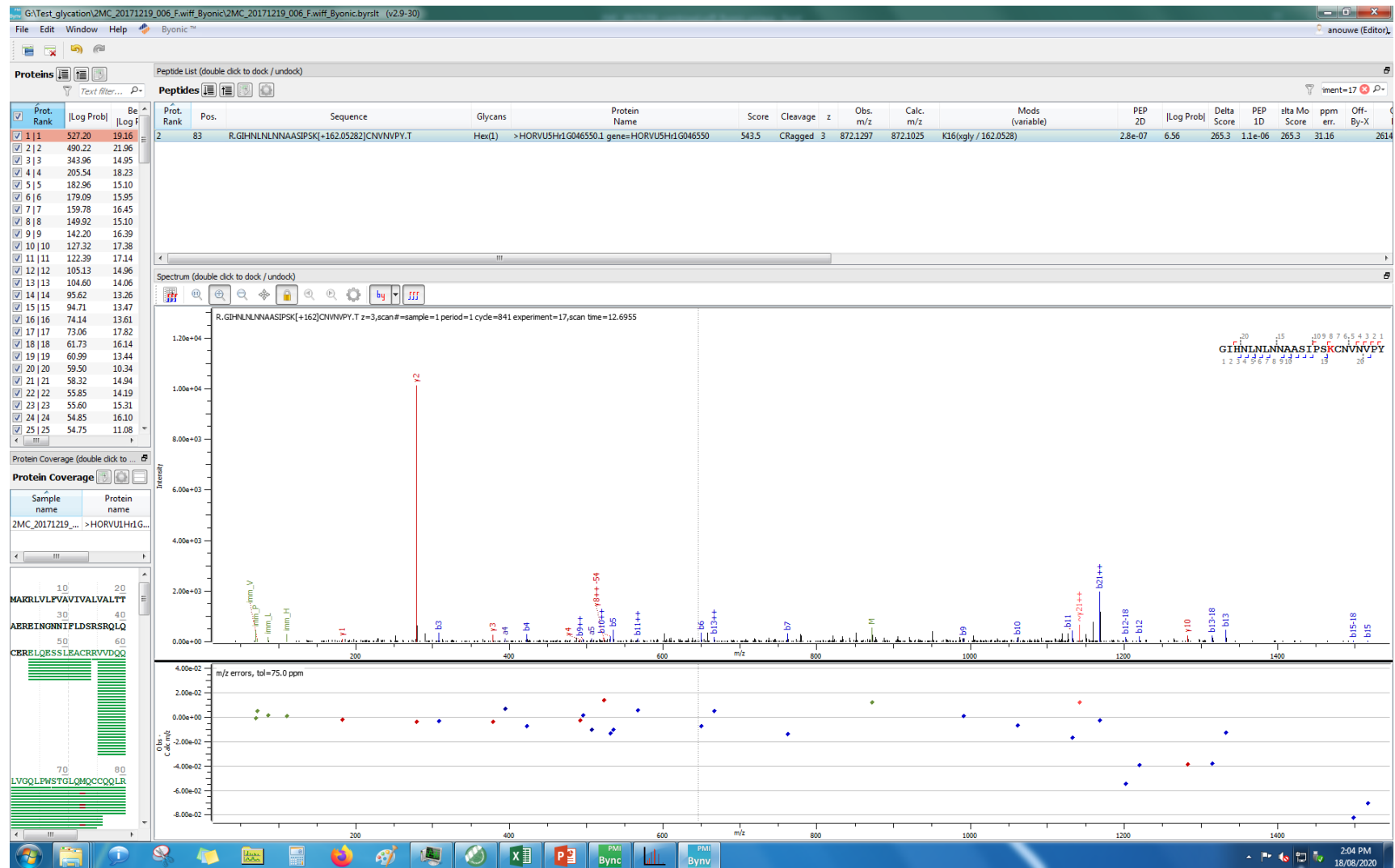


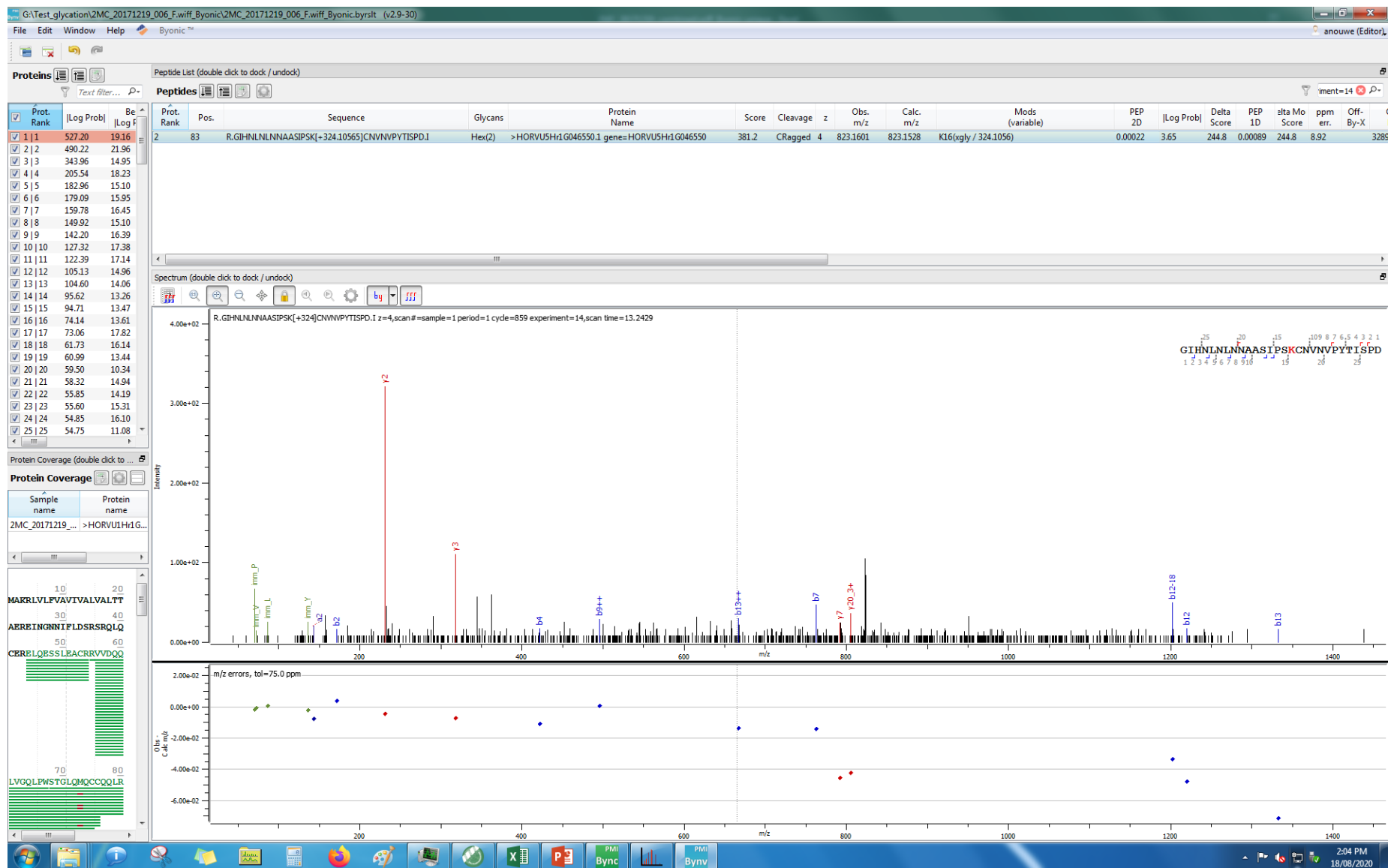


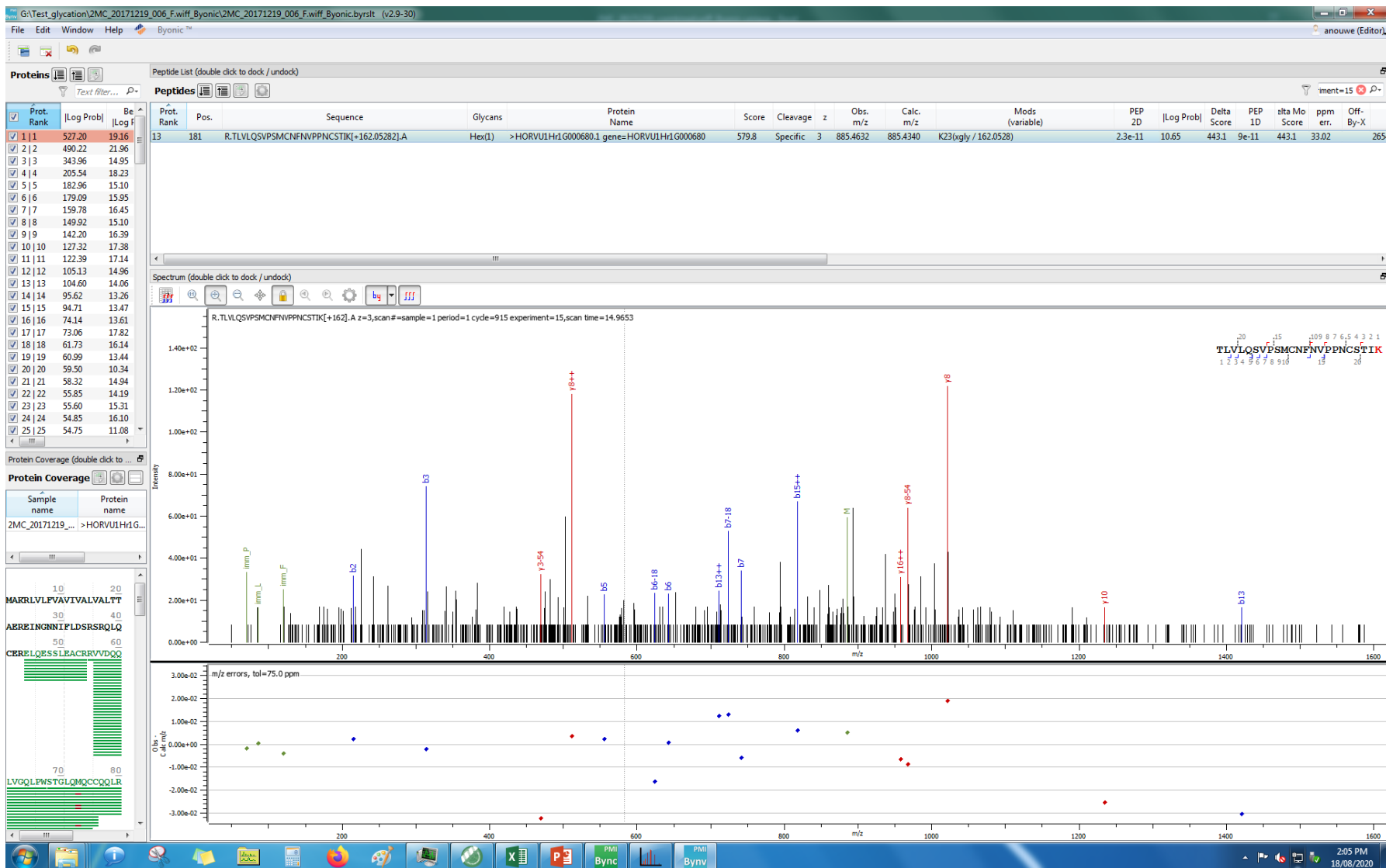








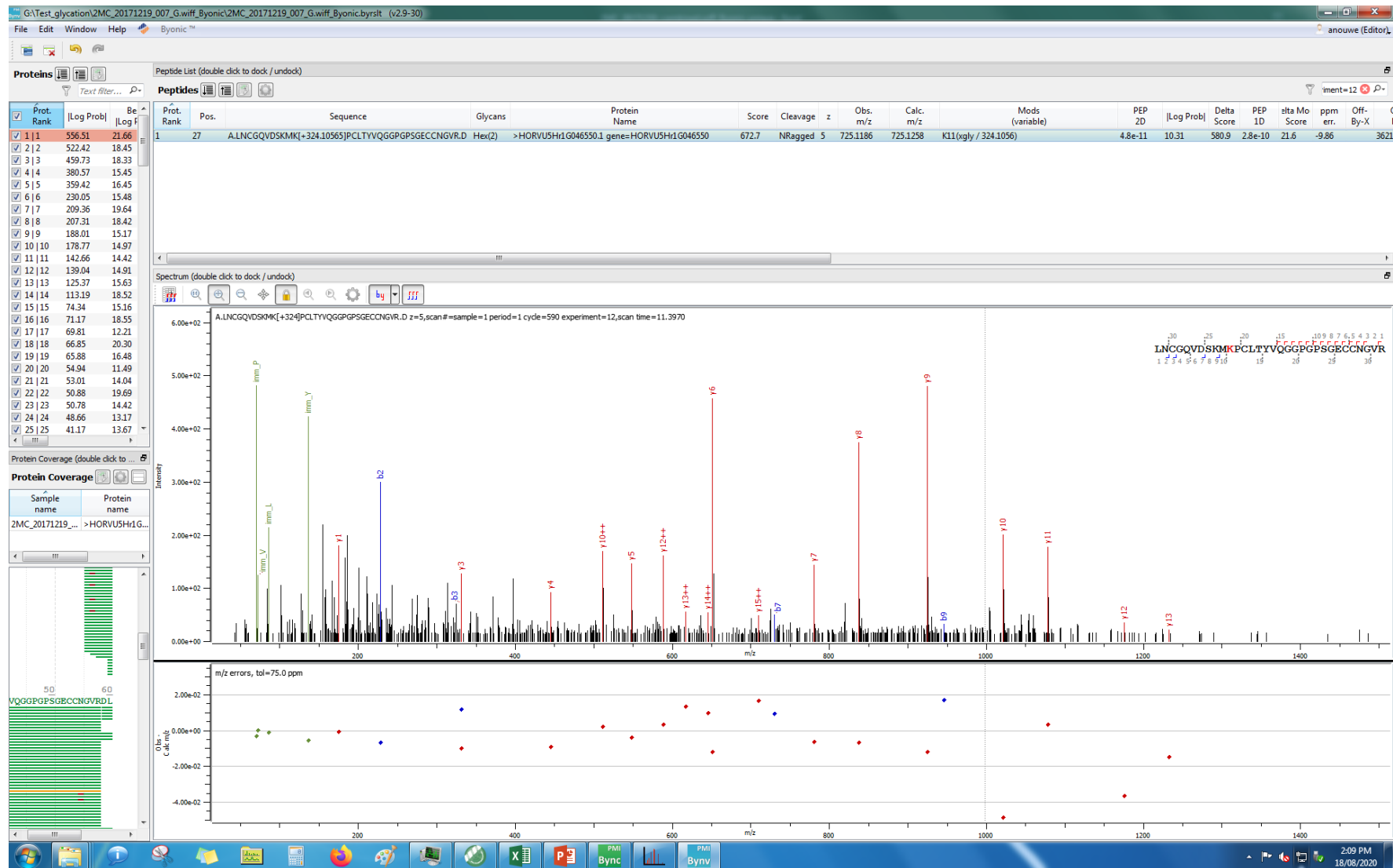


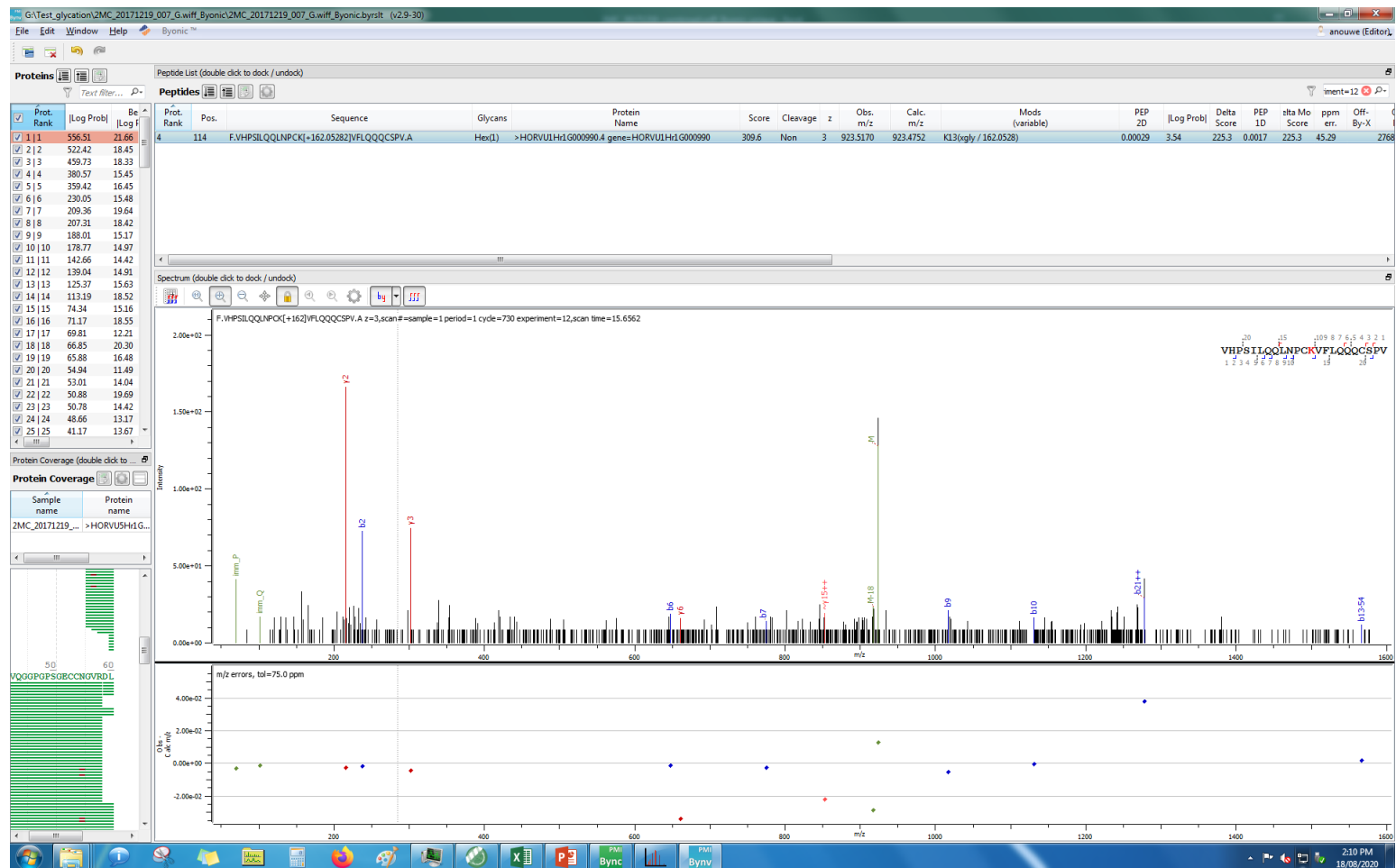


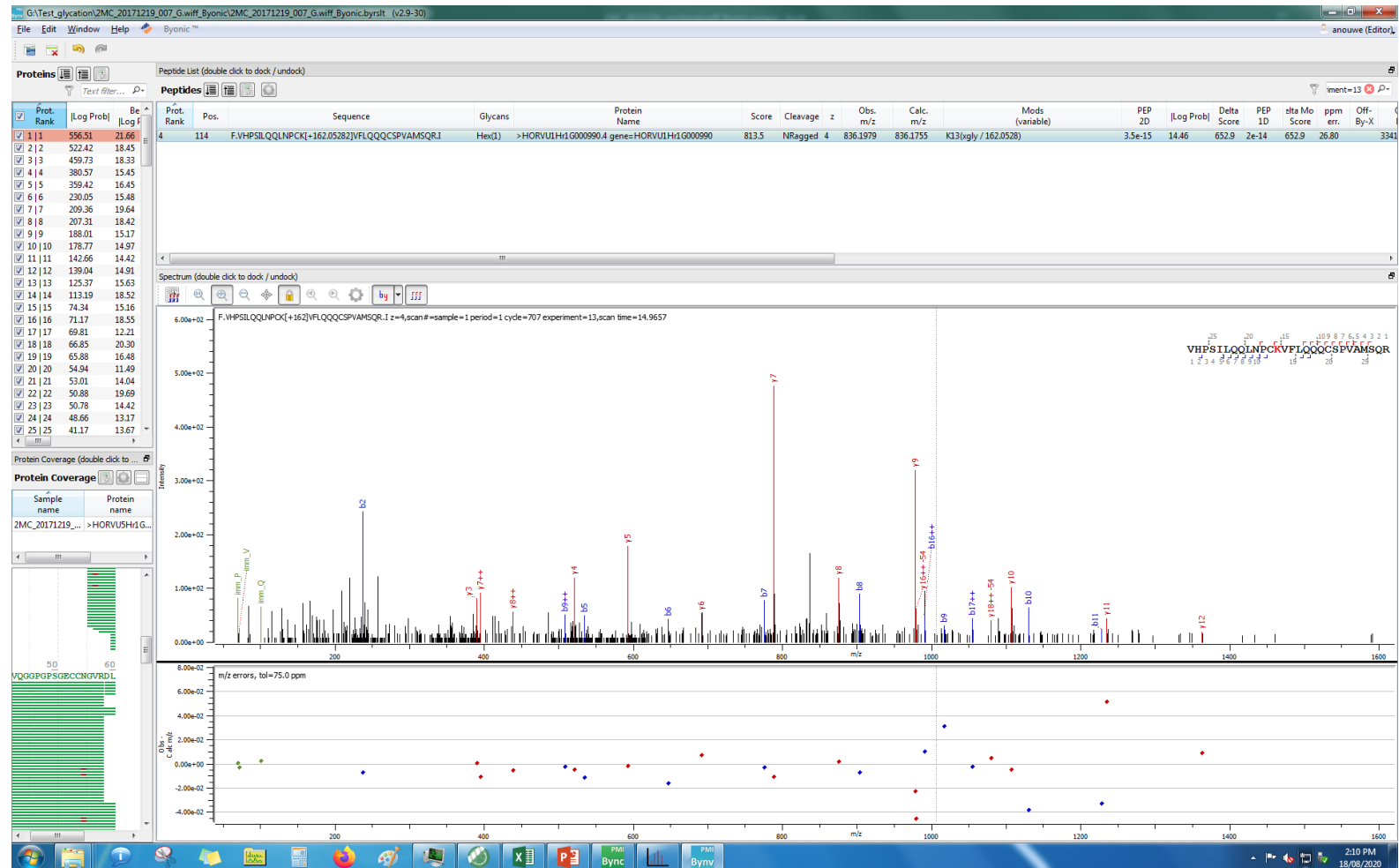


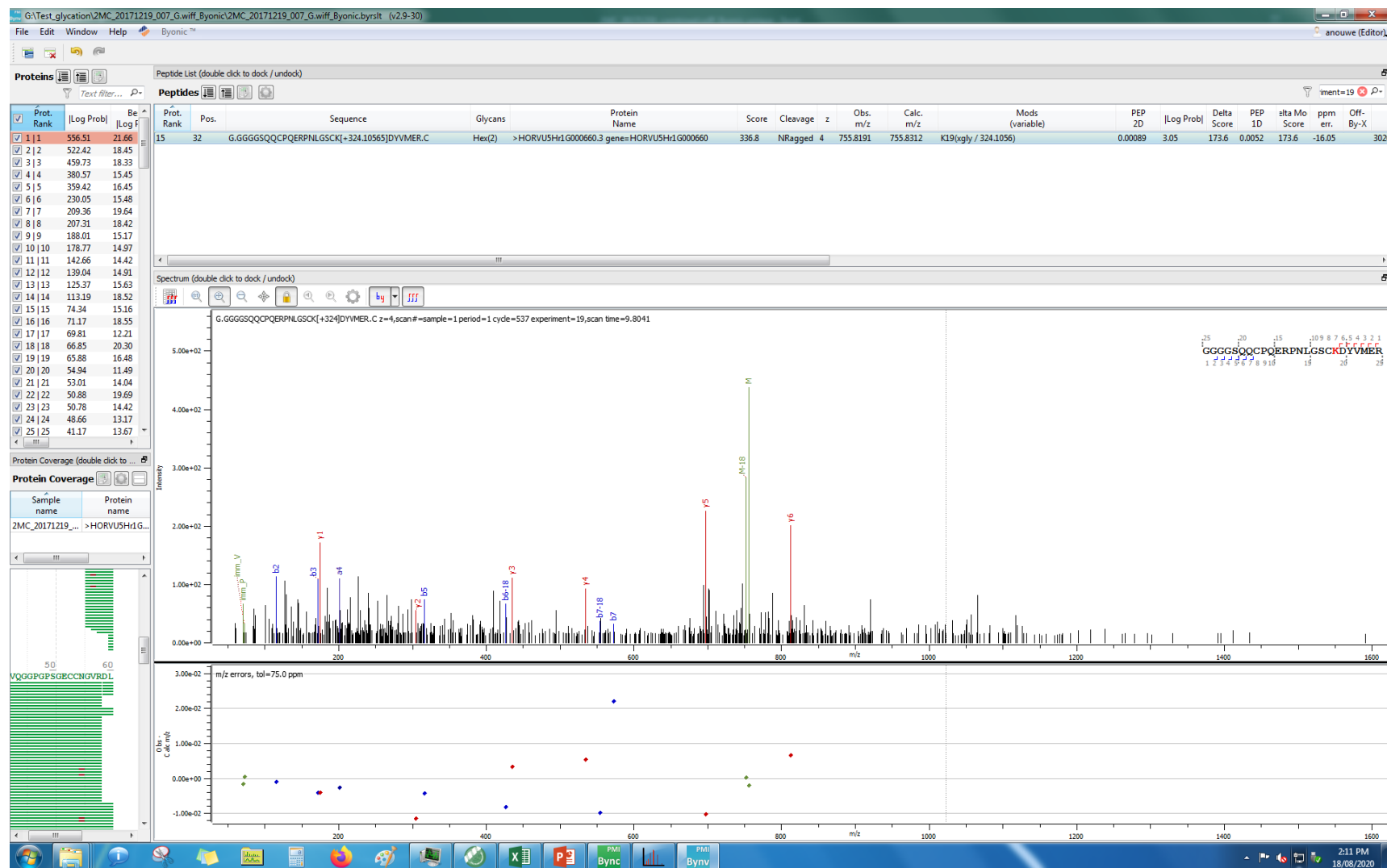




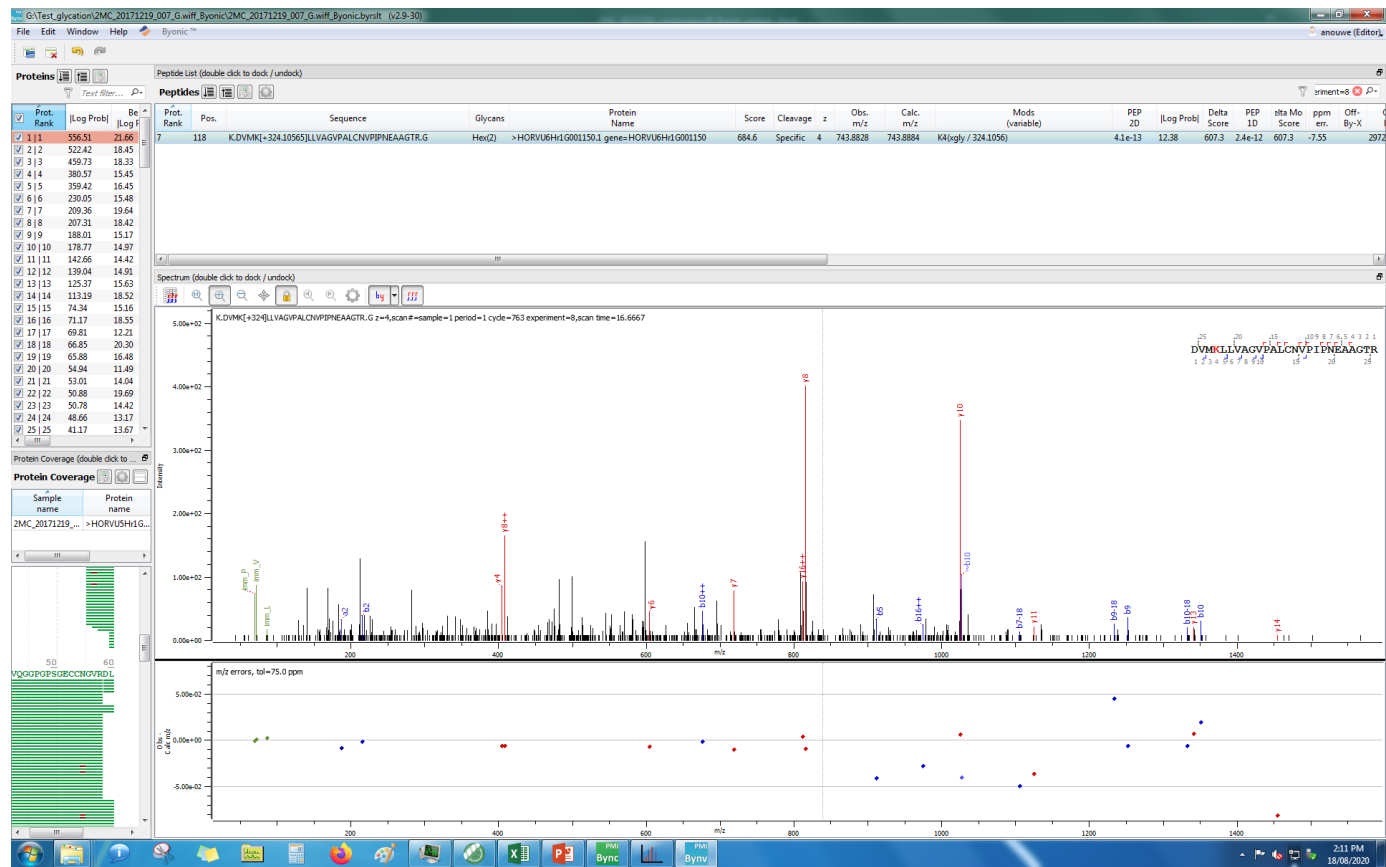










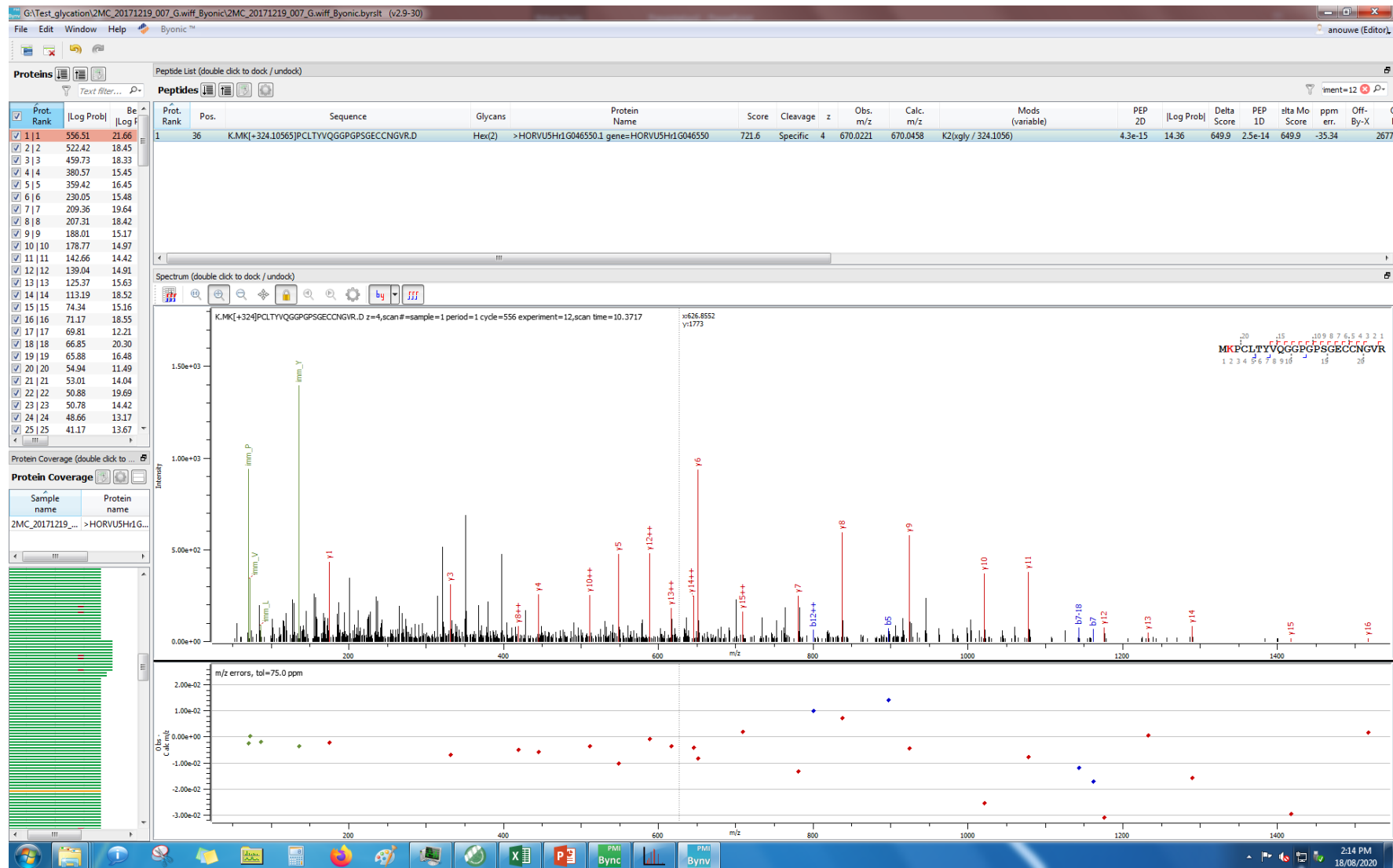


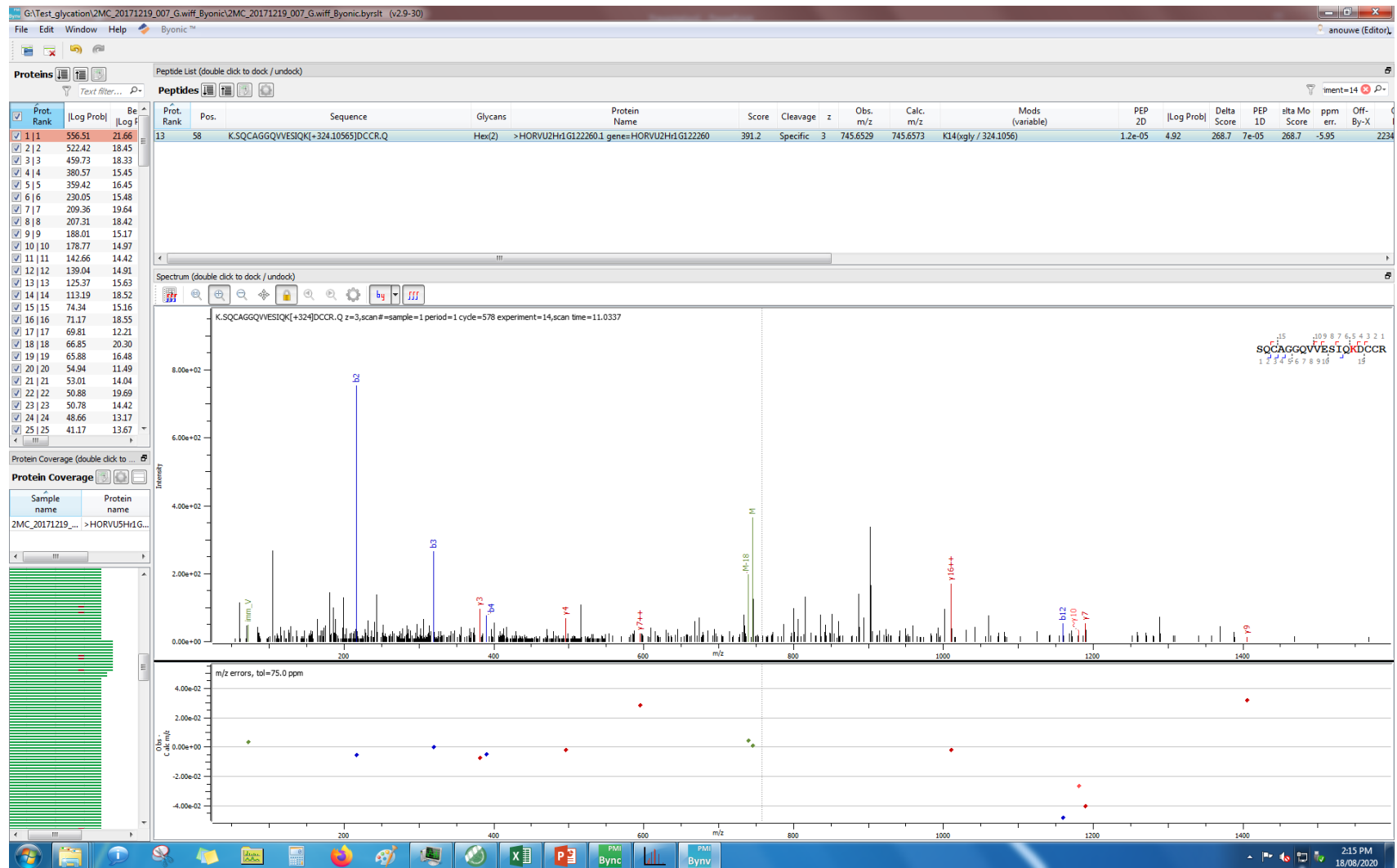


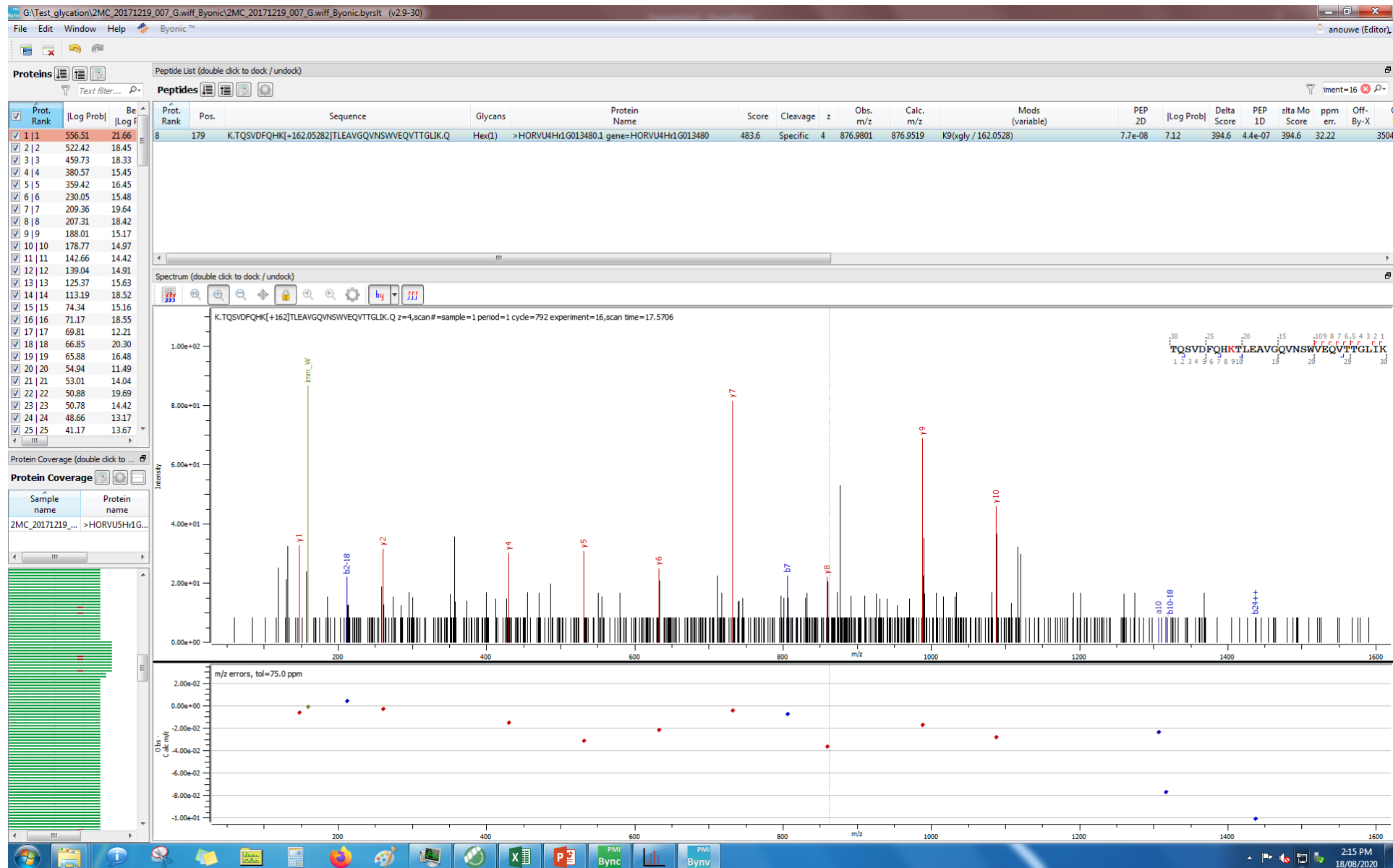


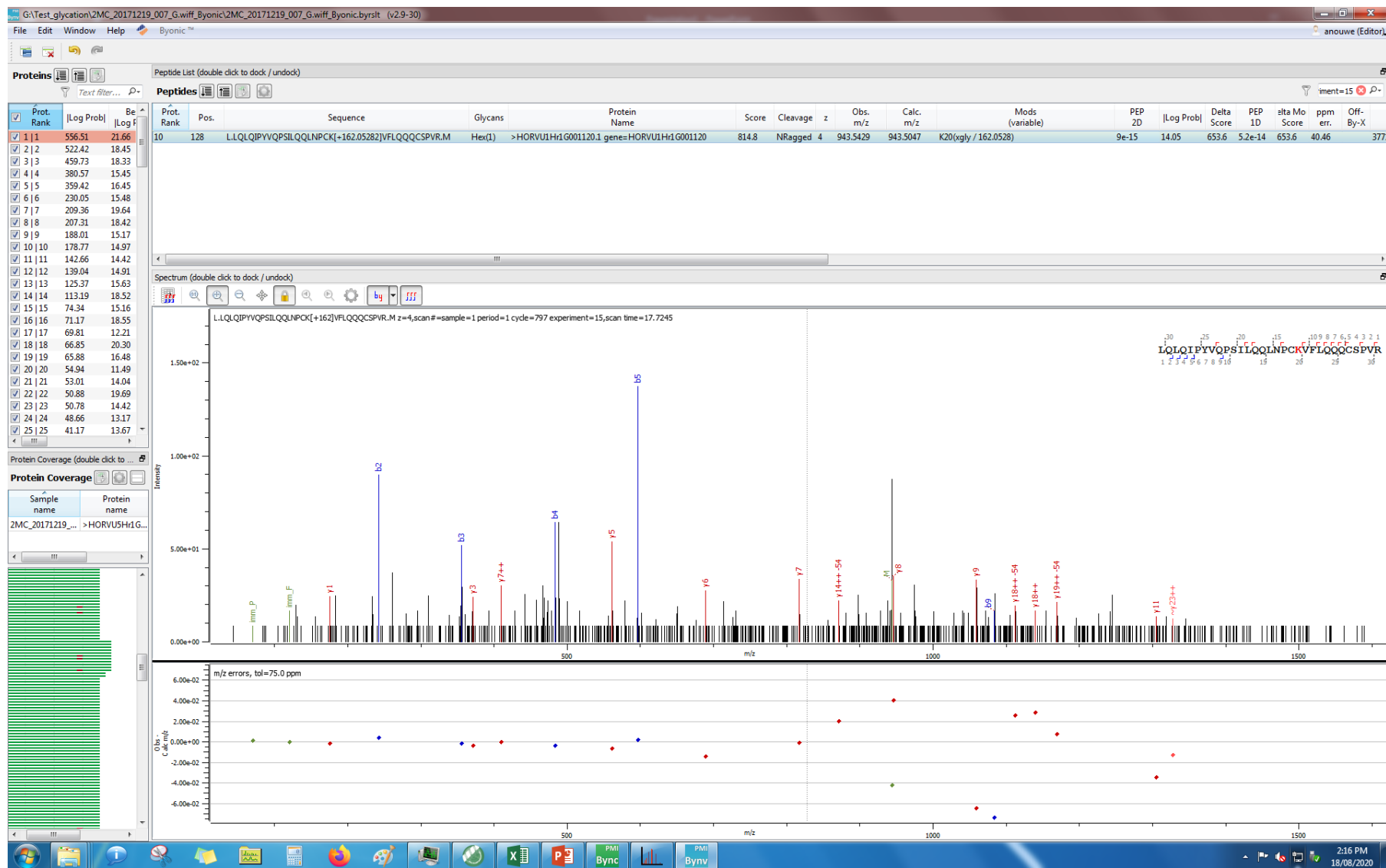


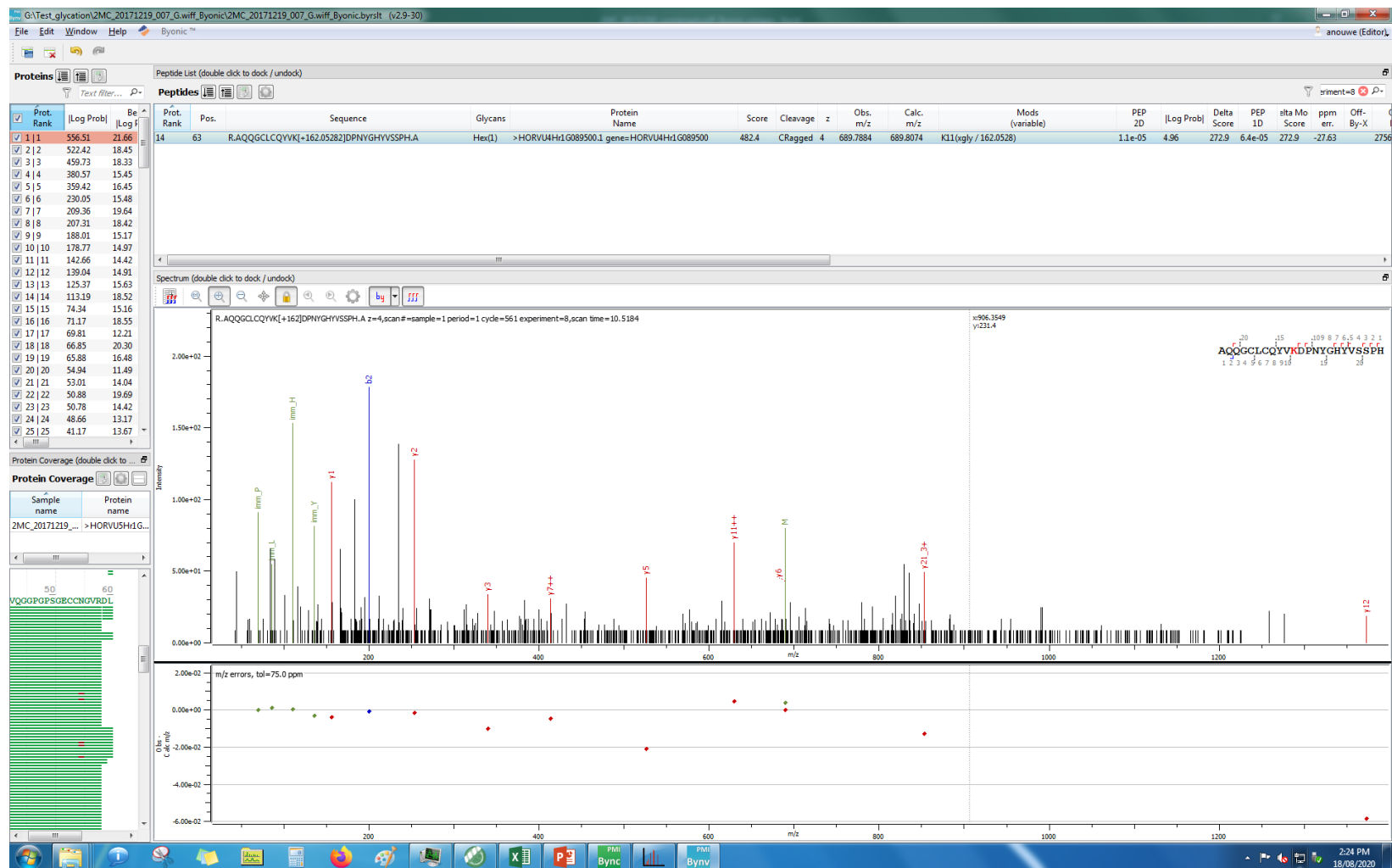


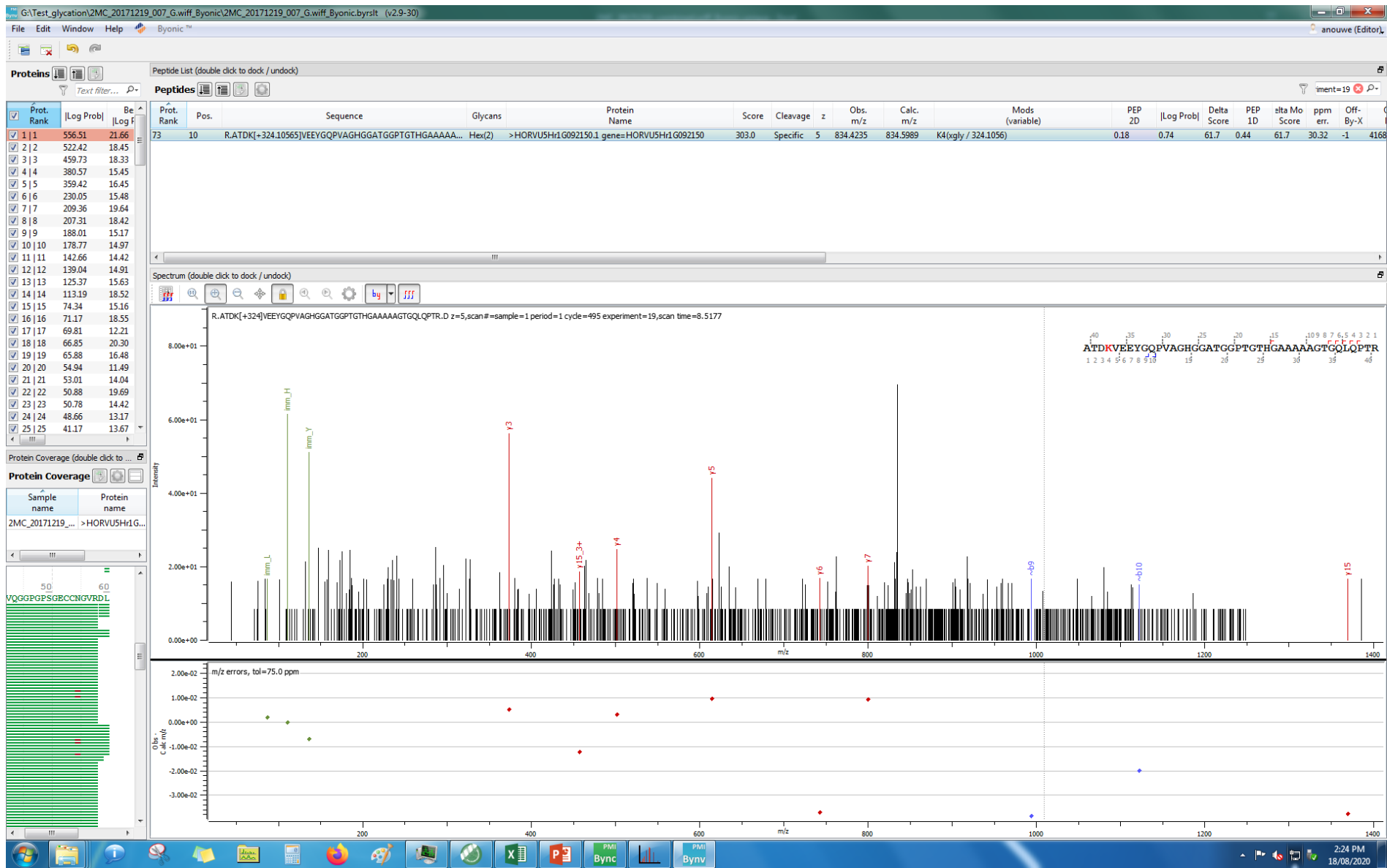


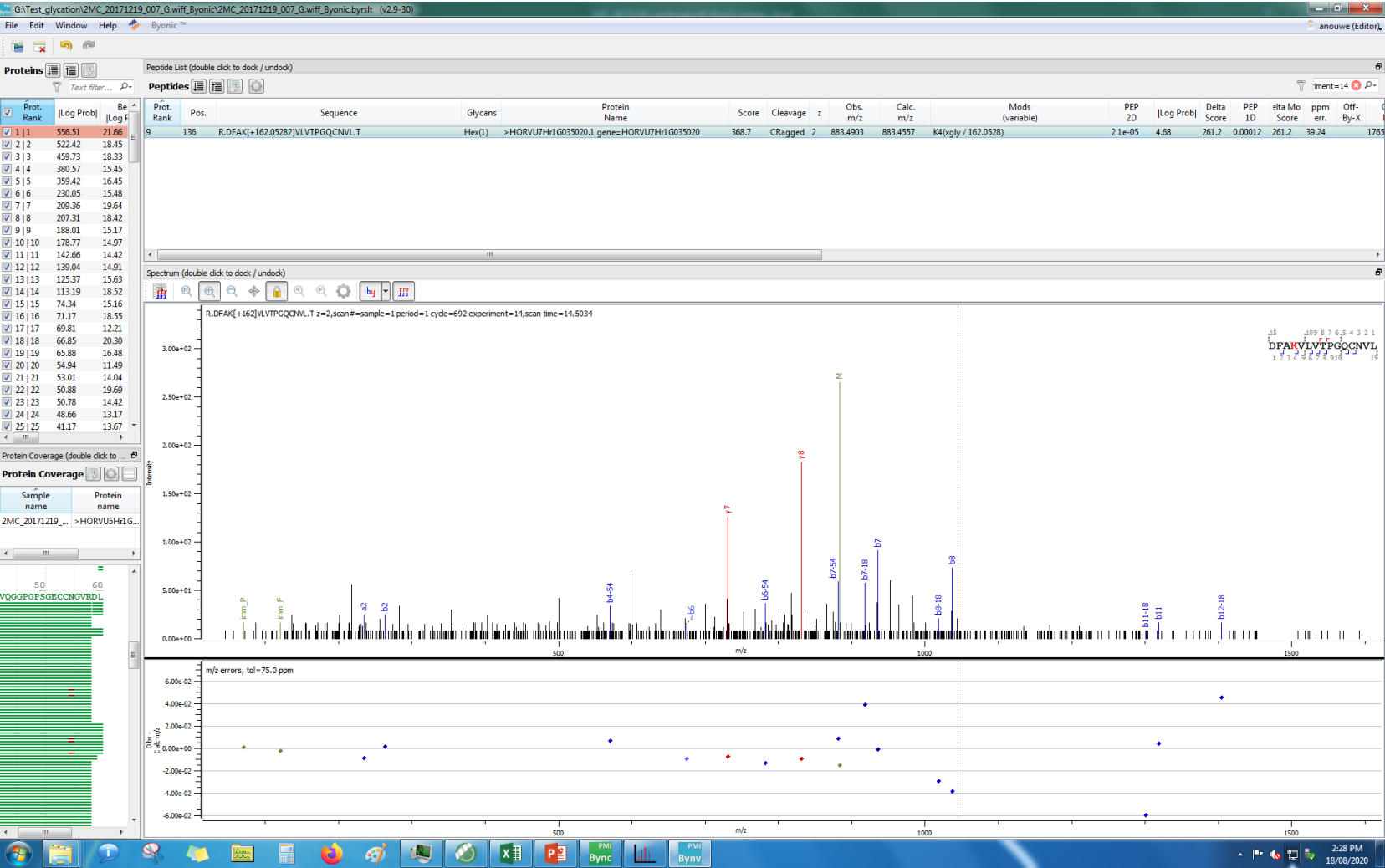






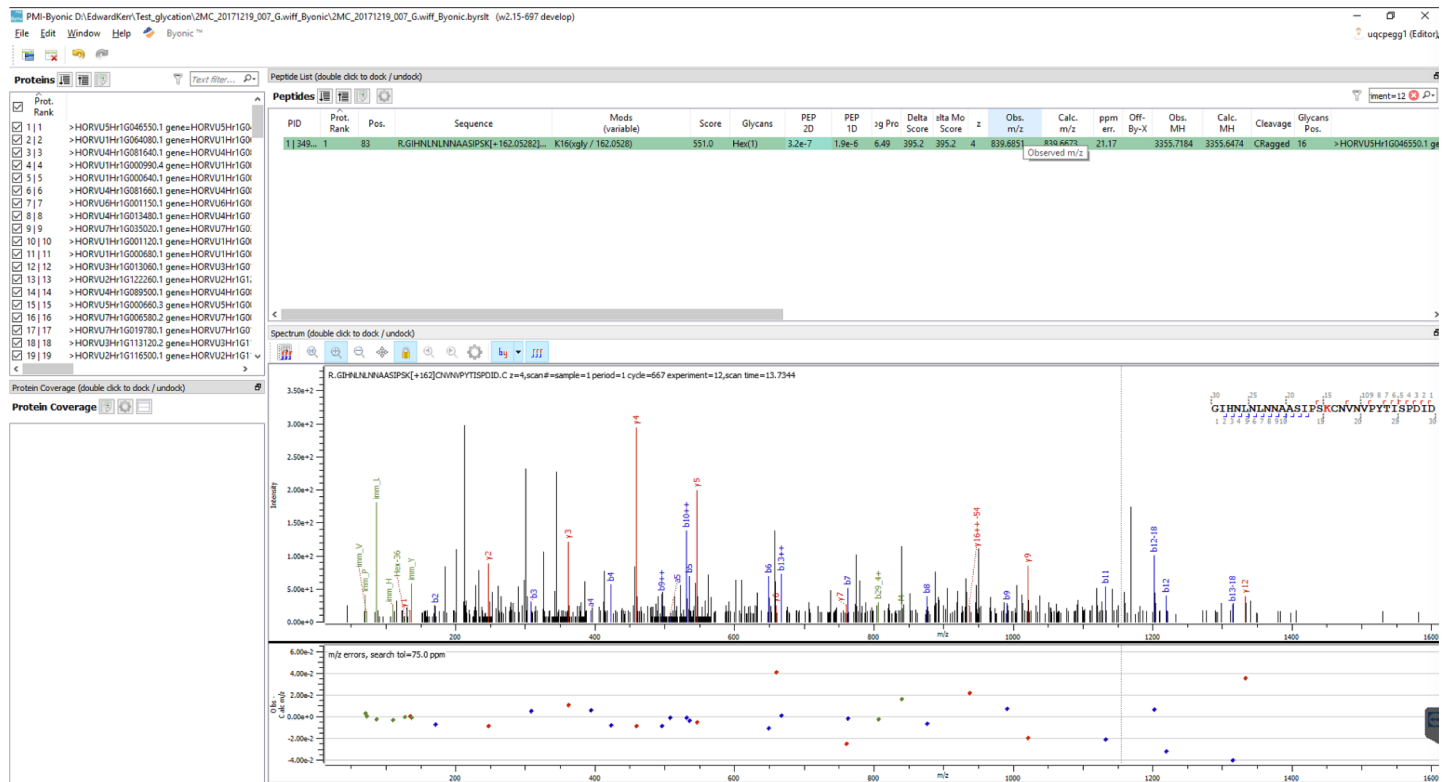












Proteins Text filter...

Prot. Rank	
1 1	> HORVU5H1G046550.1 gene=HORVU5H1G046550.1
2 2	> HORVU1H1G064080.1 gene=HORVU1H1G064080.1
3 3	> HORVU4H1G081640.1 gene=HORVU4H1G081640.1
4 4	> HORVU1H1G000990.4 gene=HORVU1H1G000990.4
5 5	> HORVU1H1G000640.1 gene=HORVU1H1G000640.1
6 6	> HORVU4H1G081660.1 gene=HORVU4H1G081660.1
7 7	> HORVU9H1G001150.1 gene=HORVU9H1G001150.1
8 8	> HORVU4H1G013480.1 gene=HORVU4H1G013480.1
9 9	> HORVU7H1G035020.1 gene=HORVU7H1G035020.1
10 10	> HORVU1H1G001120.1 gene=HORVU1H1G001120.1
11 11	> HORVU1H1G000680.1 gene=HORVU1H1G000680.1
12 12	> HORVU3H1G013060.1 gene=HORVU3H1G013060.1
13 13	> HORVU2H1G122260.1 gene=HORVU2H1G122260.1
14 14	> HORVU4H1G089550.1 gene=HORVU4H1G089550.1
15 15	> HORVU5H1G000660.3 gene=HORVU5H1G000660.3
16 16	> HORVU7H1G006580.2 gene=HORVU7H1G006580.2
17 17	> HORVU7H1G019780.1 gene=HORVU7H1G019780.1
18 18	> HORVU3H1G113120.2 gene=HORVU3H1G113120.2
19 19	> HORVU2H1G116500.1 gene=HORVU2H1G116500.1

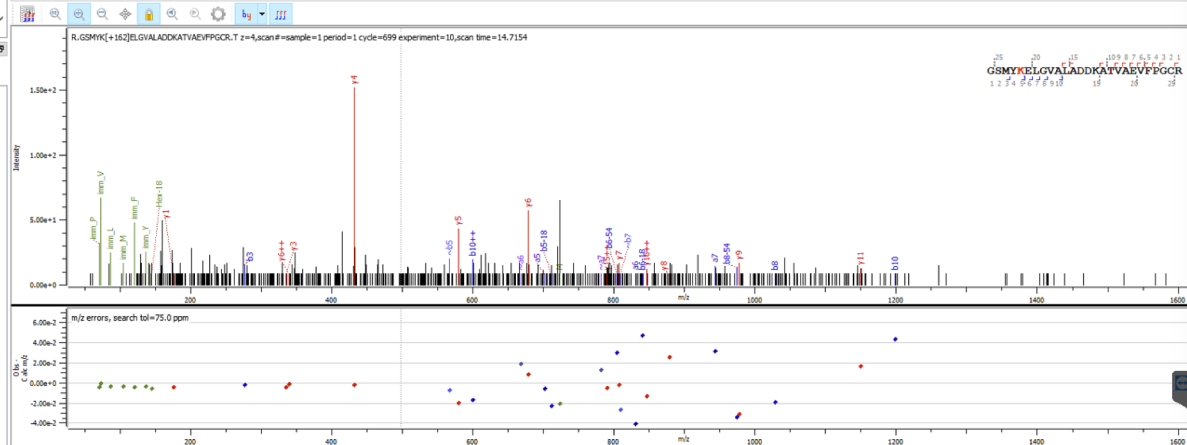
Protein Coverage (double click to dock / undock)

Protein Coverage

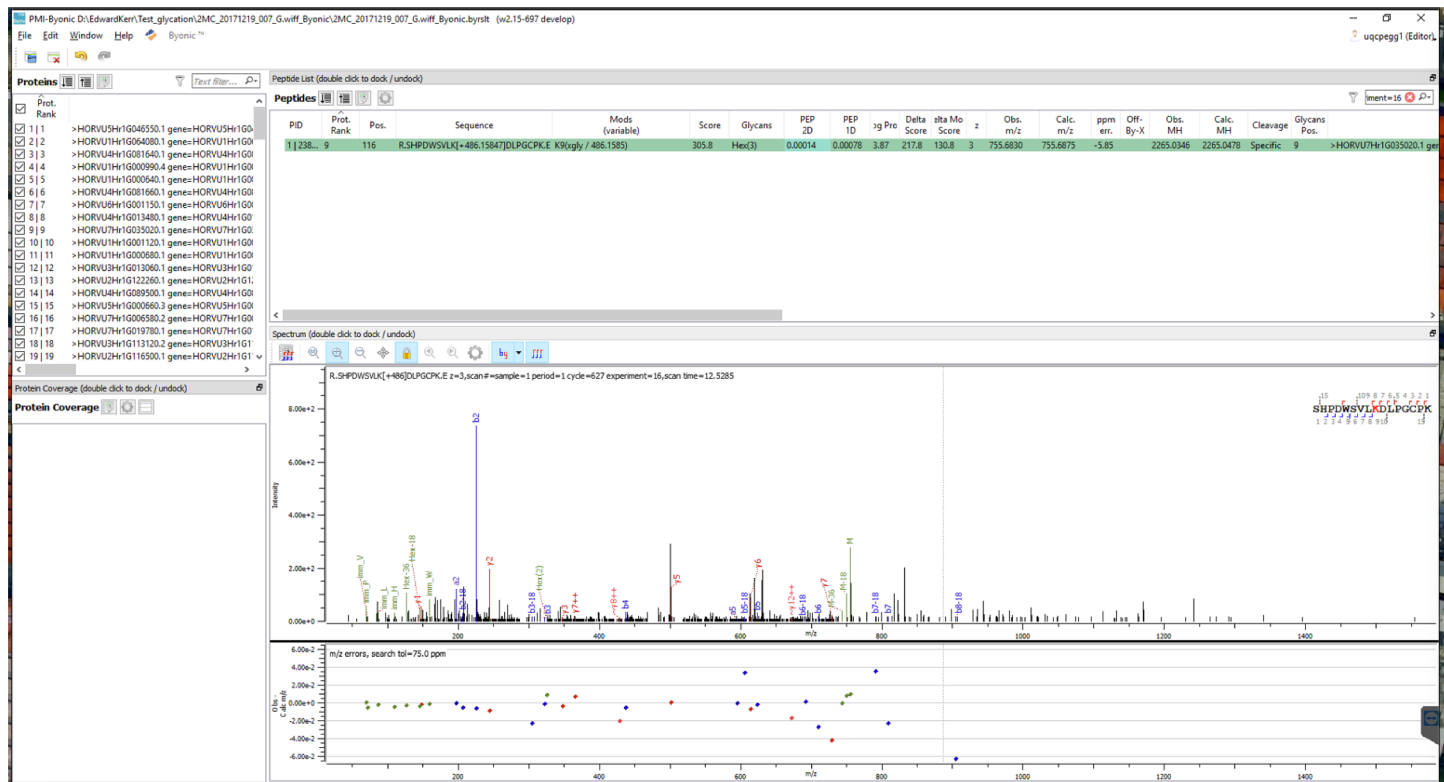
Peptide List (double click to dock / undock)

PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	g Pro	Delta Score	alt Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glycans	
1 315...	13	95	R.GSMYK[+162.05282]ELGVALADDKA...K50gylg / 162.0528		344.7	Hex(1)	0.00011	0.00064	3.96	259.8	49.4	4	723.1153	723.1057	13.40		2889.4395	2889.4008	Specific	5	> HORVU2H1G122260.1 ge

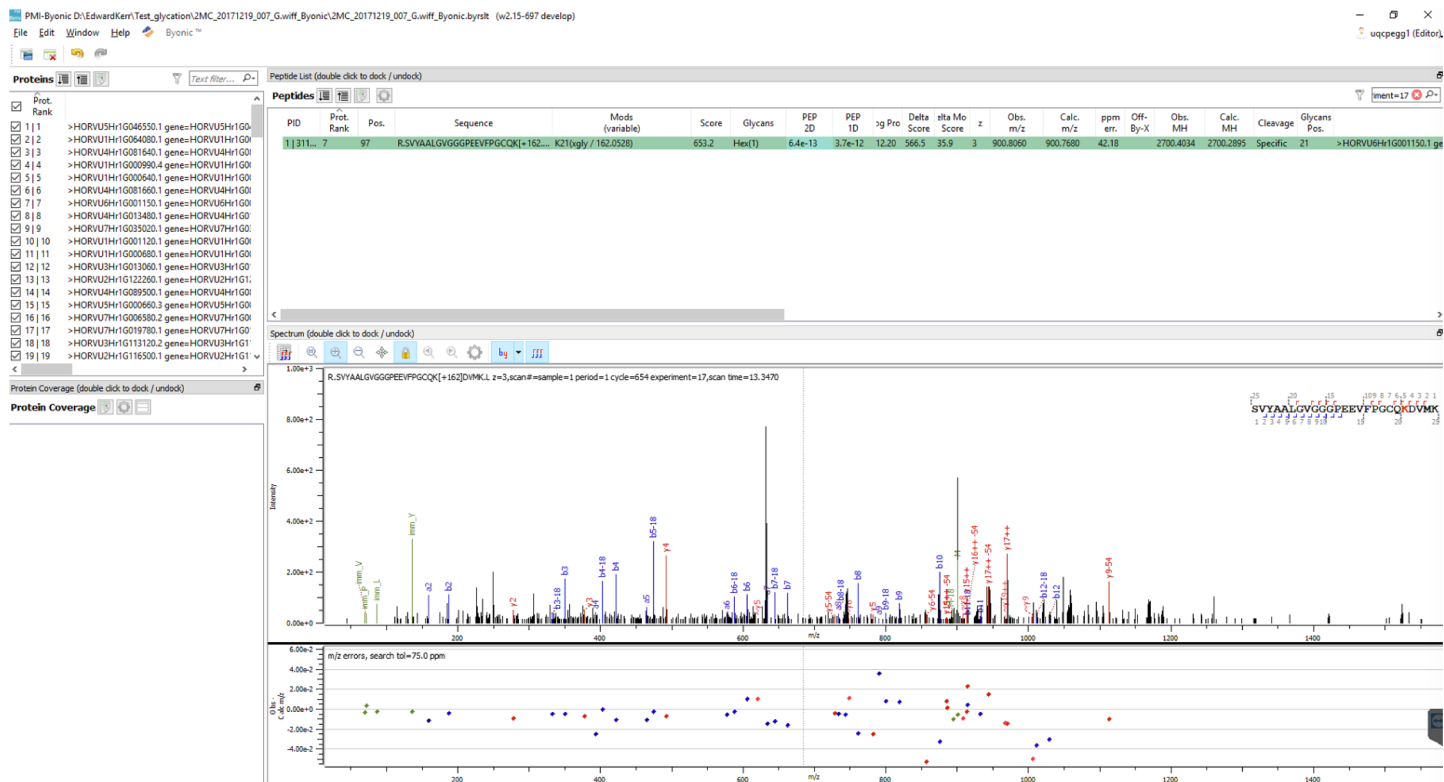
Spectrum (double click to dock / undock)



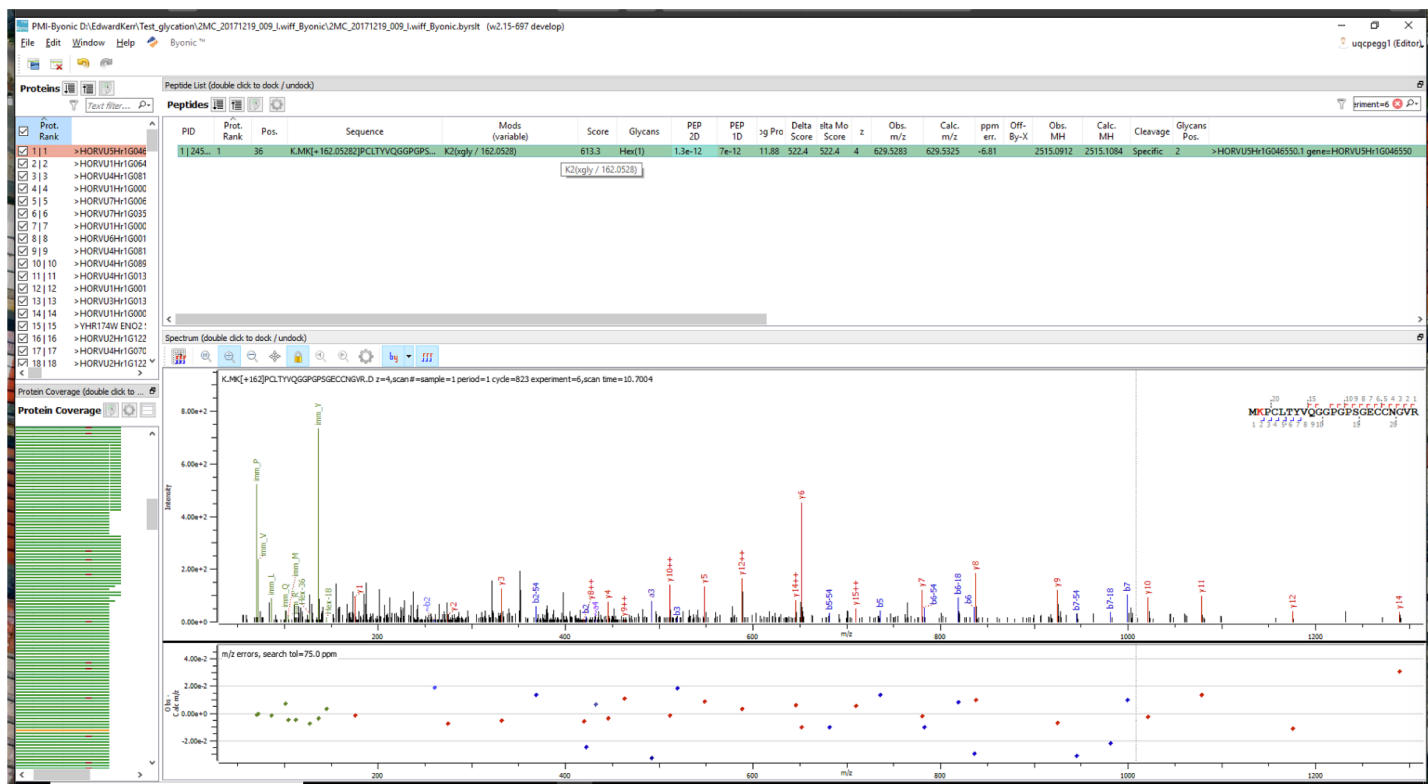


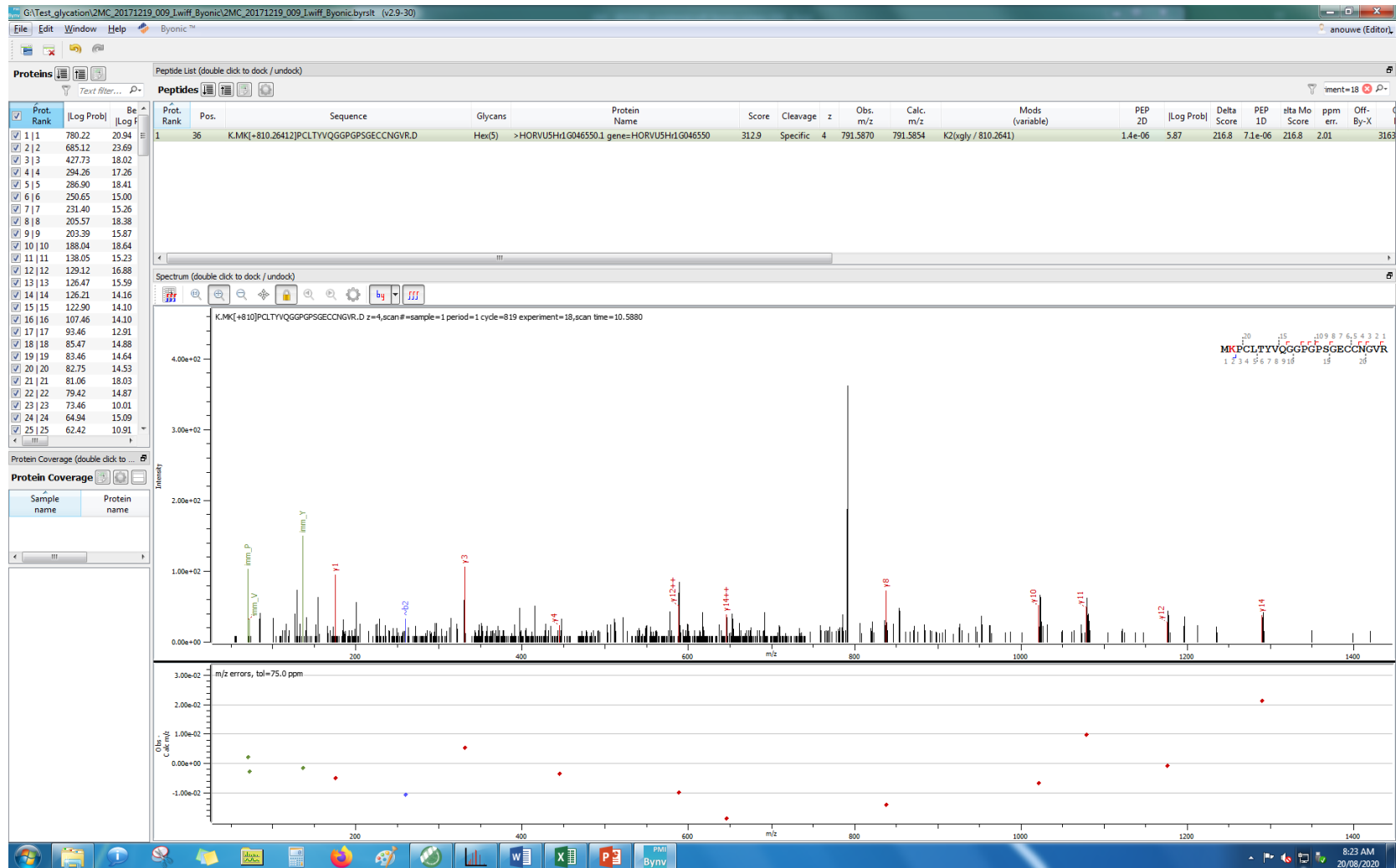


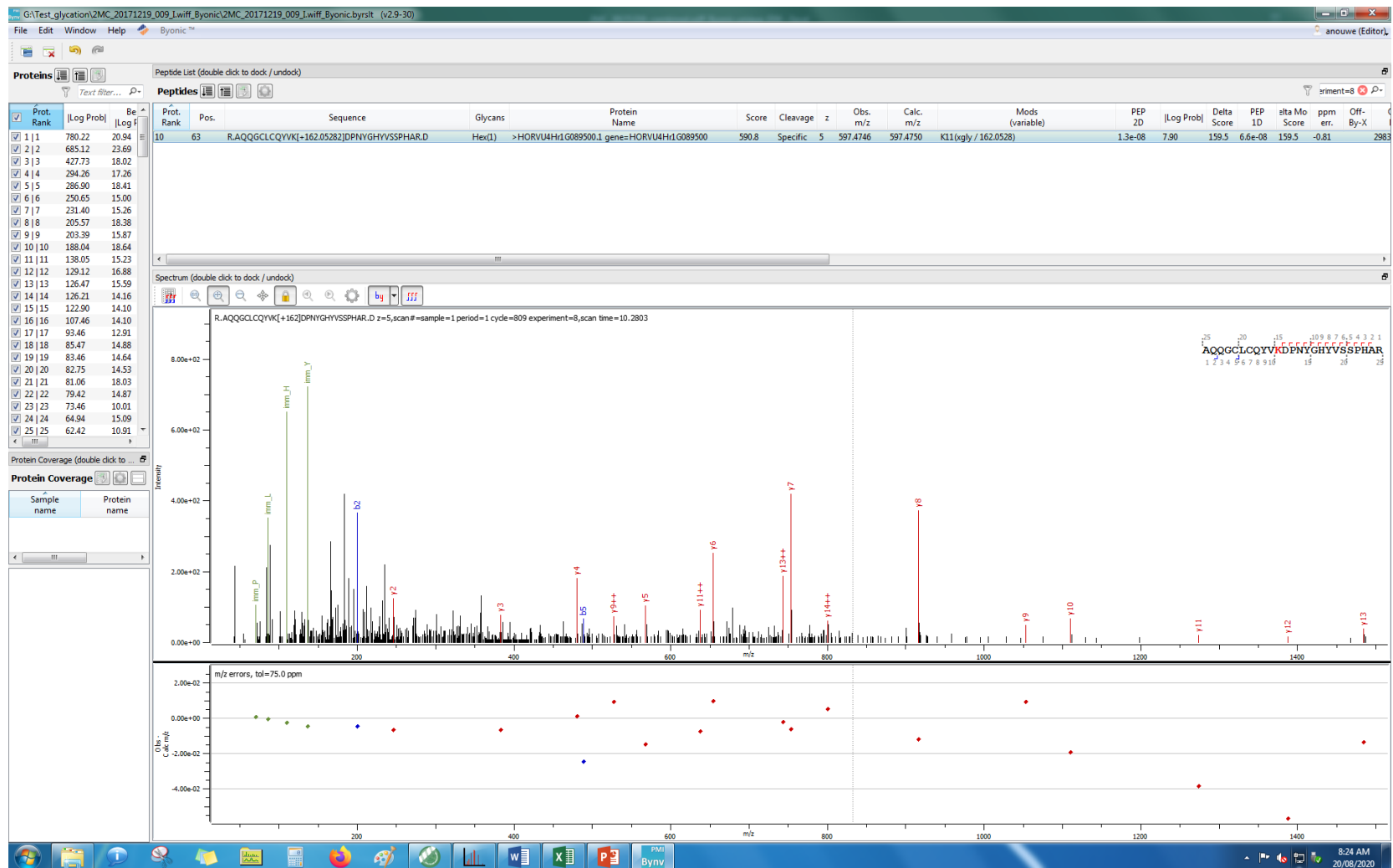




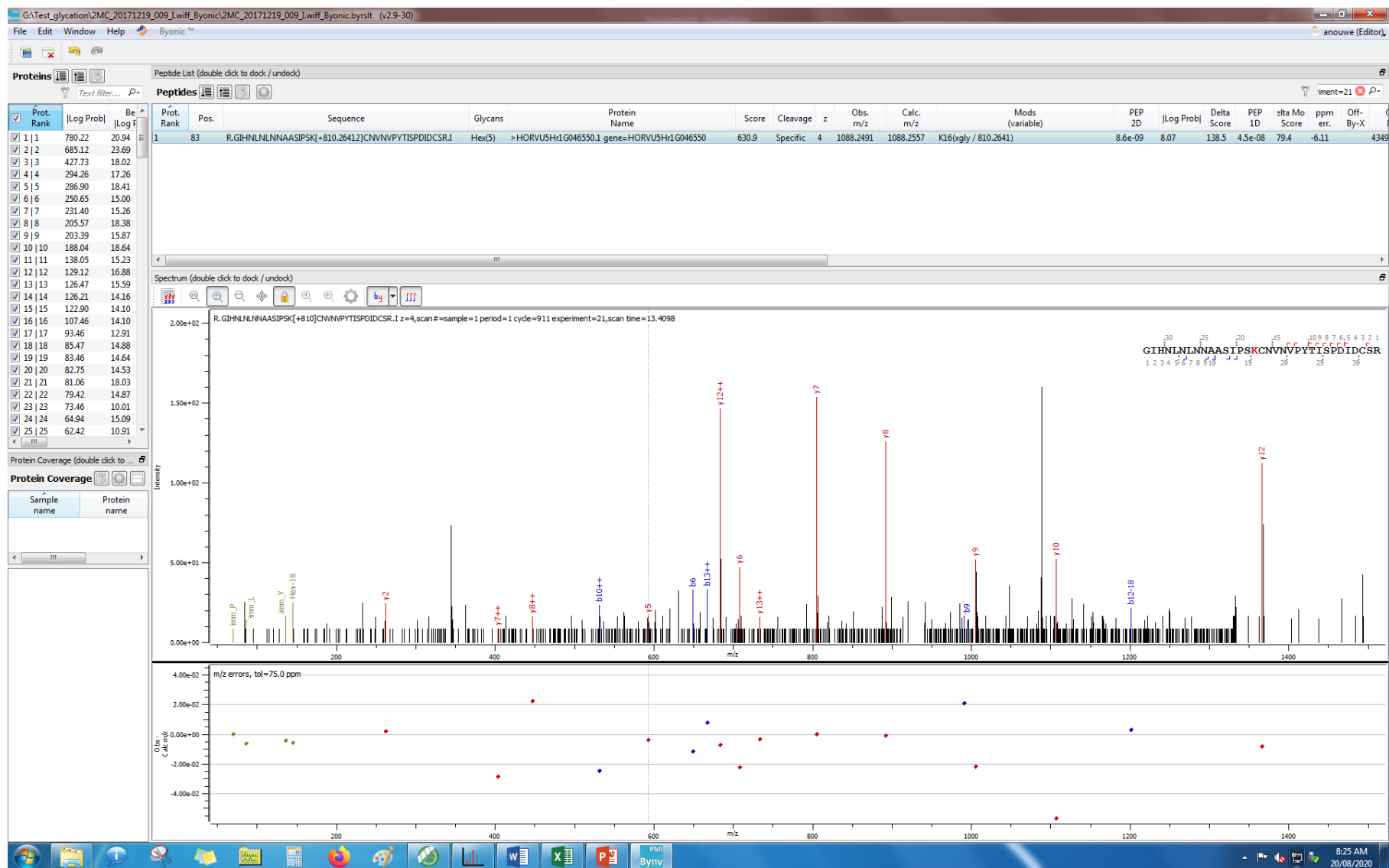


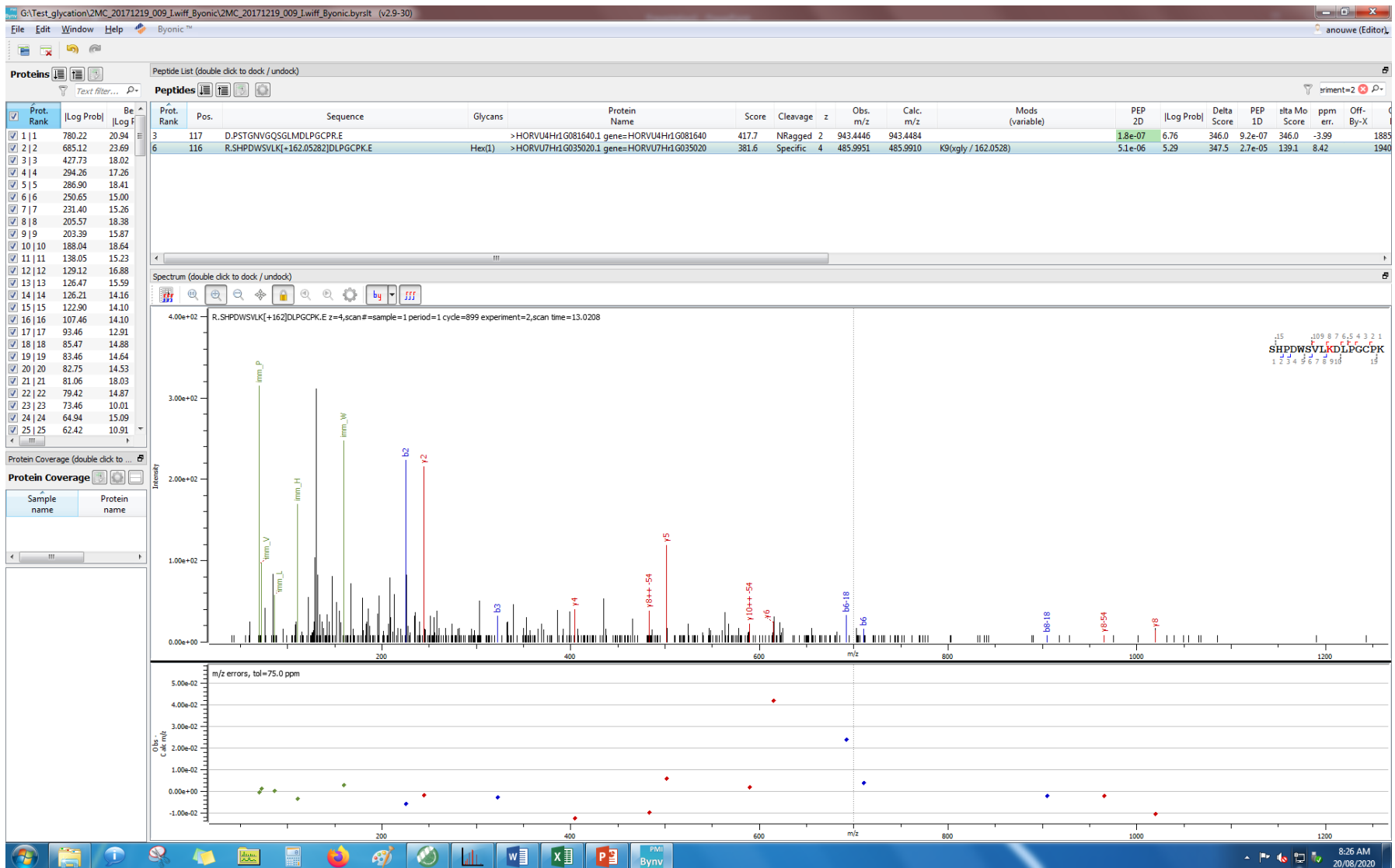


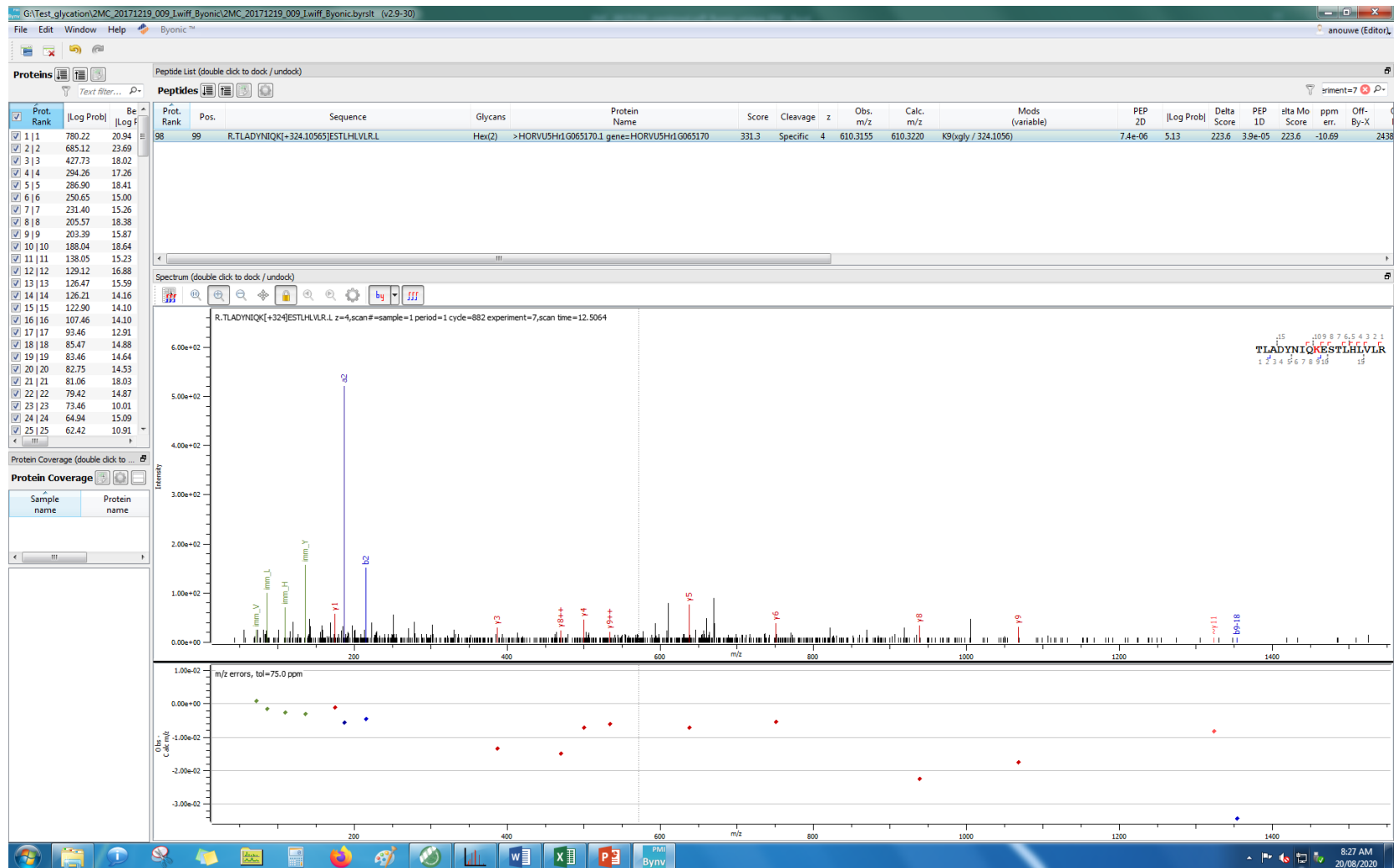




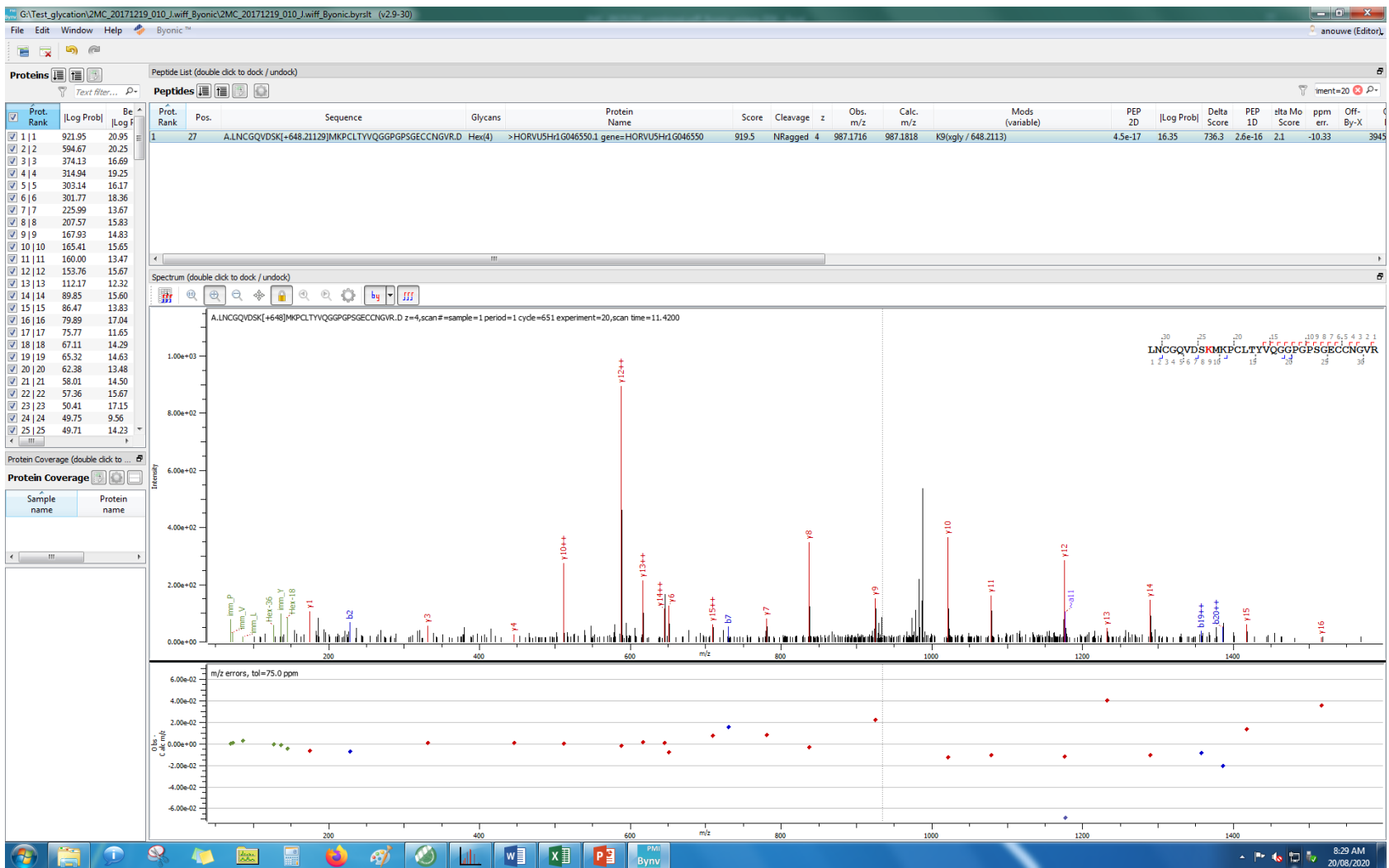


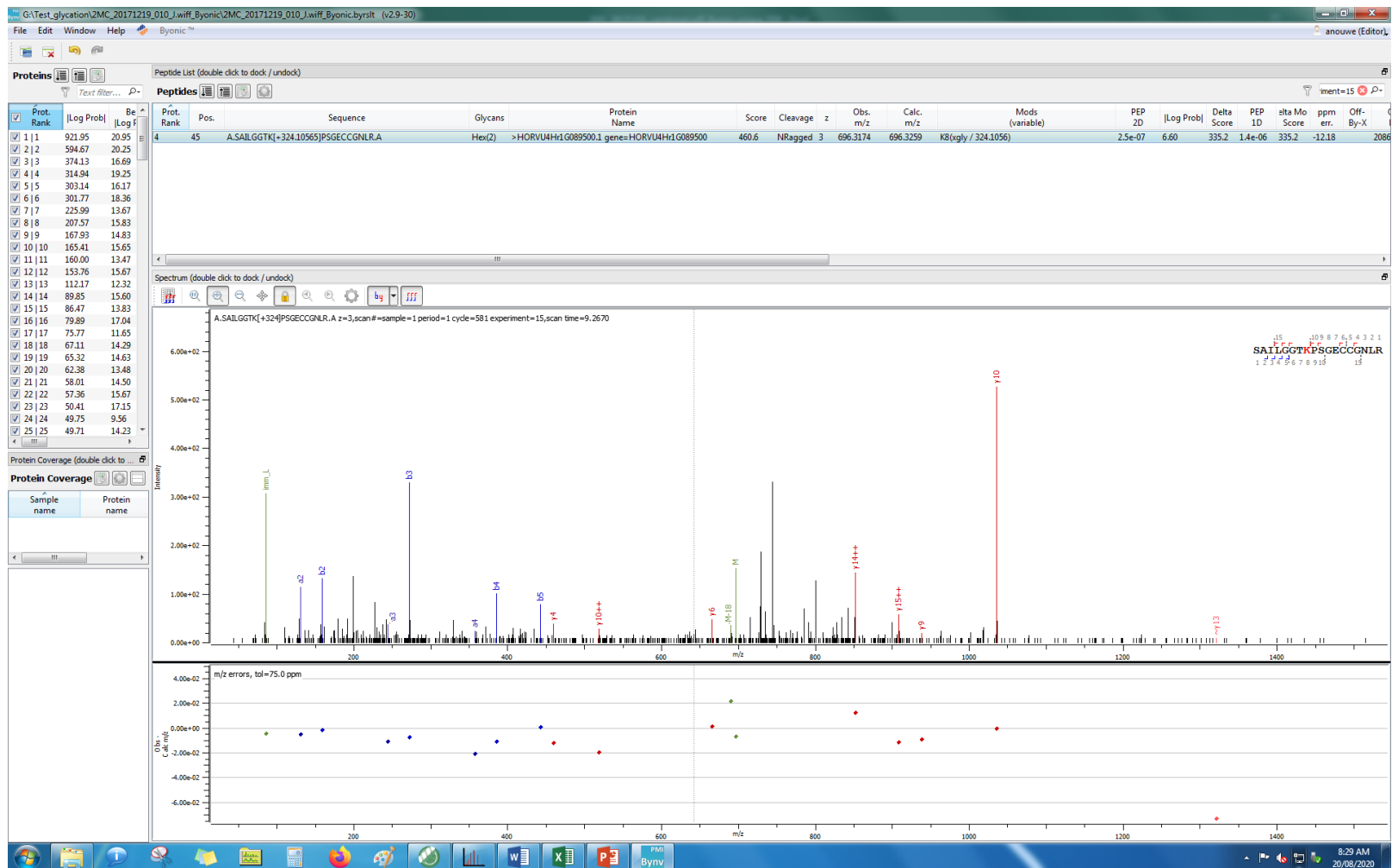


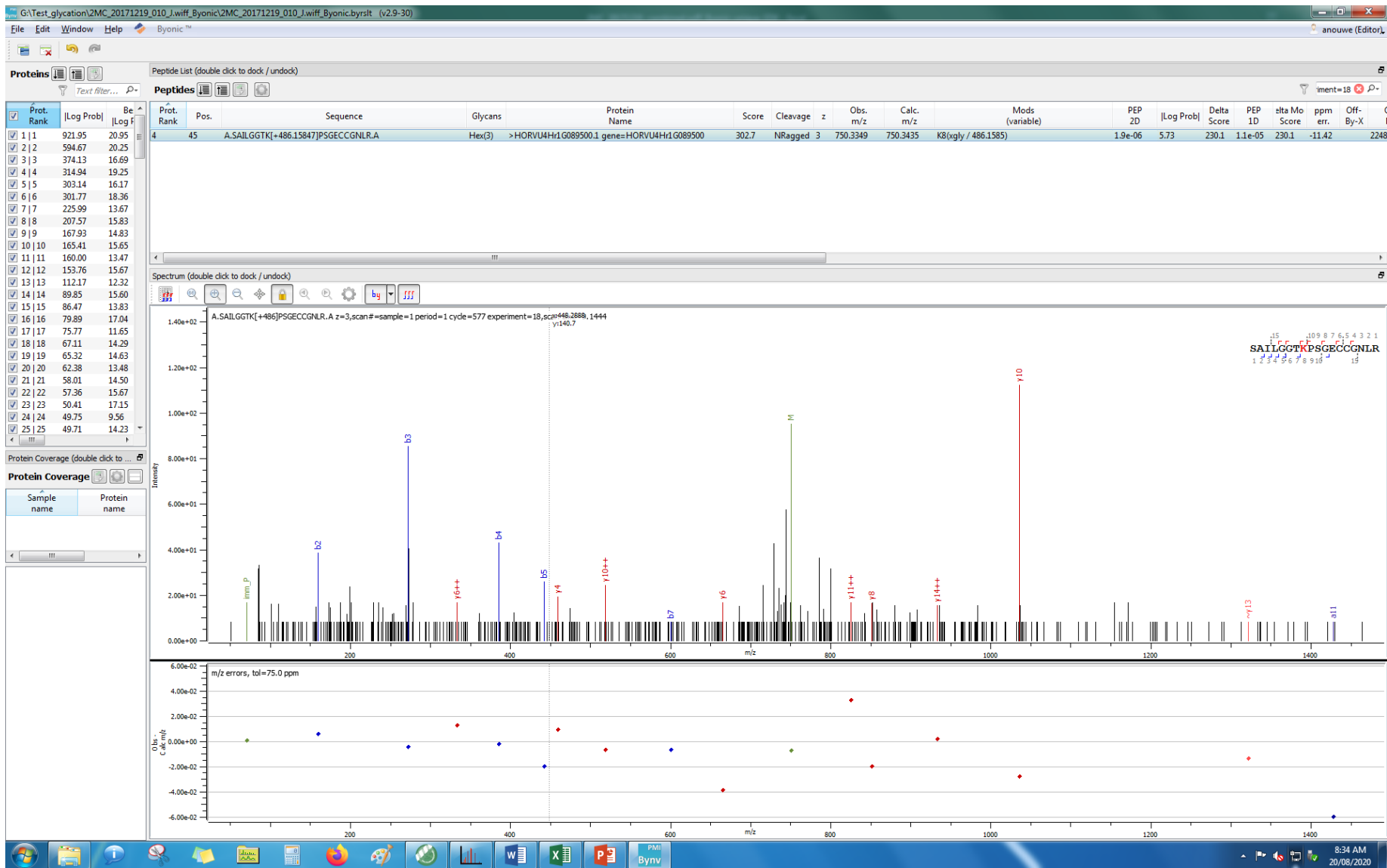




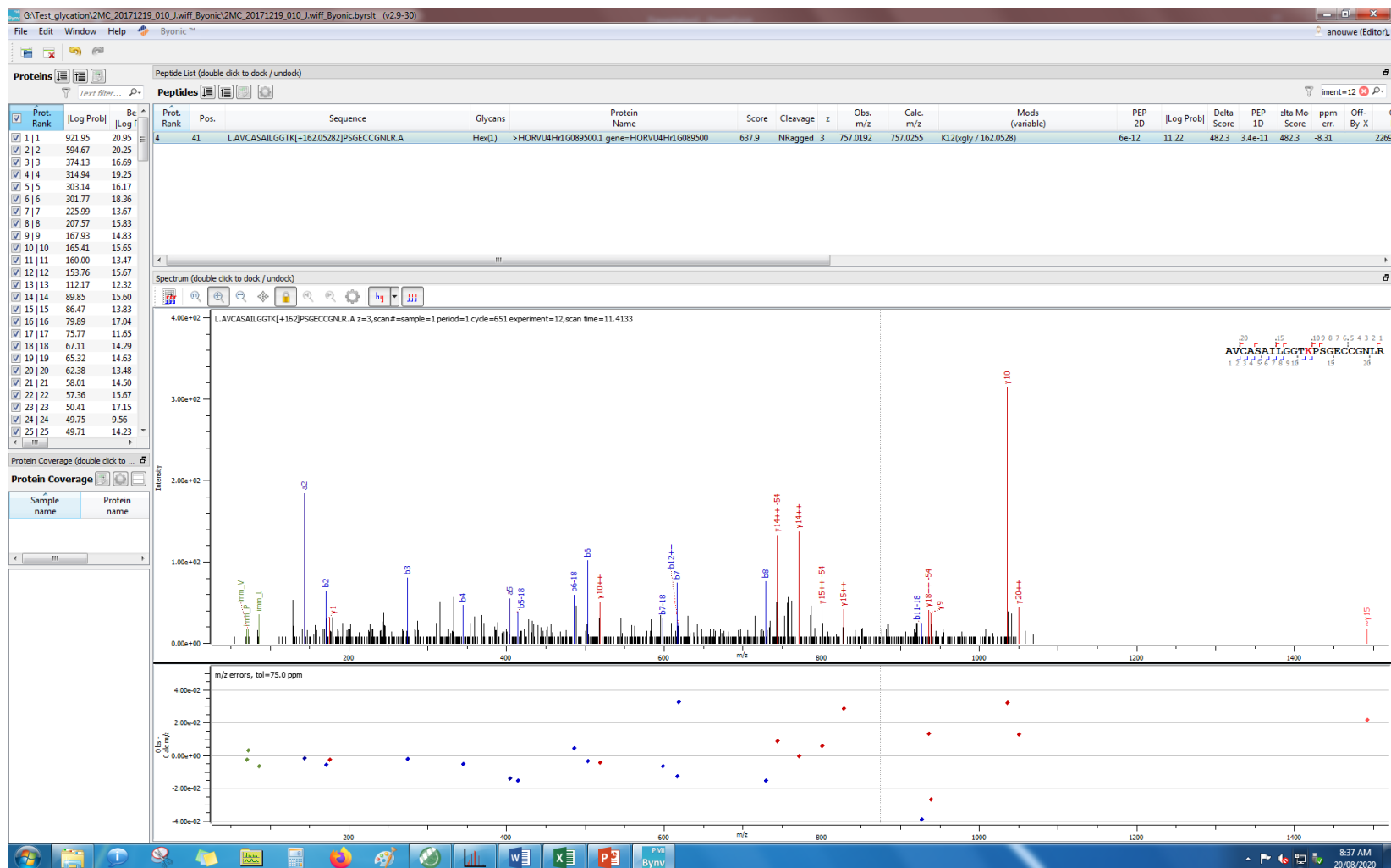


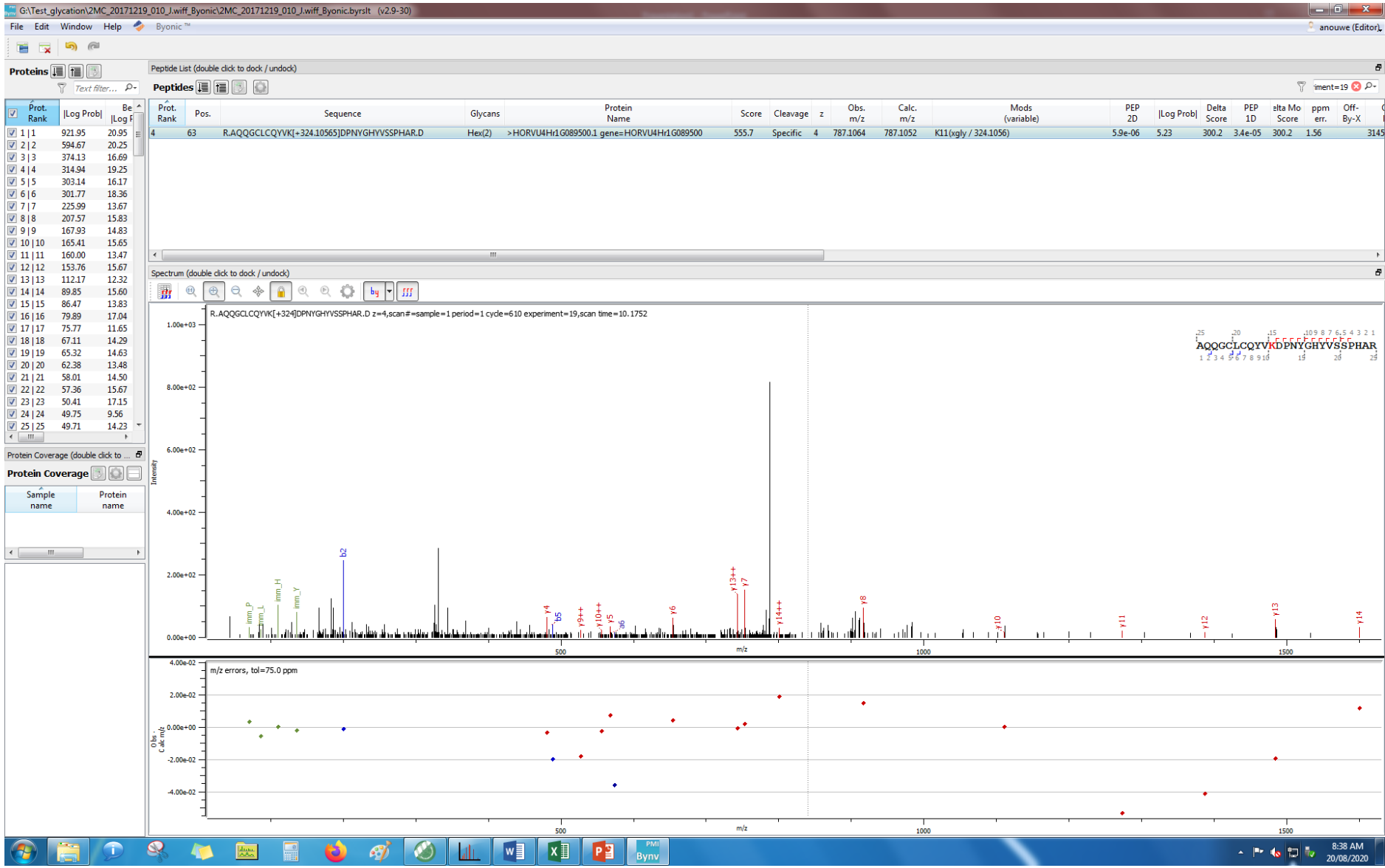


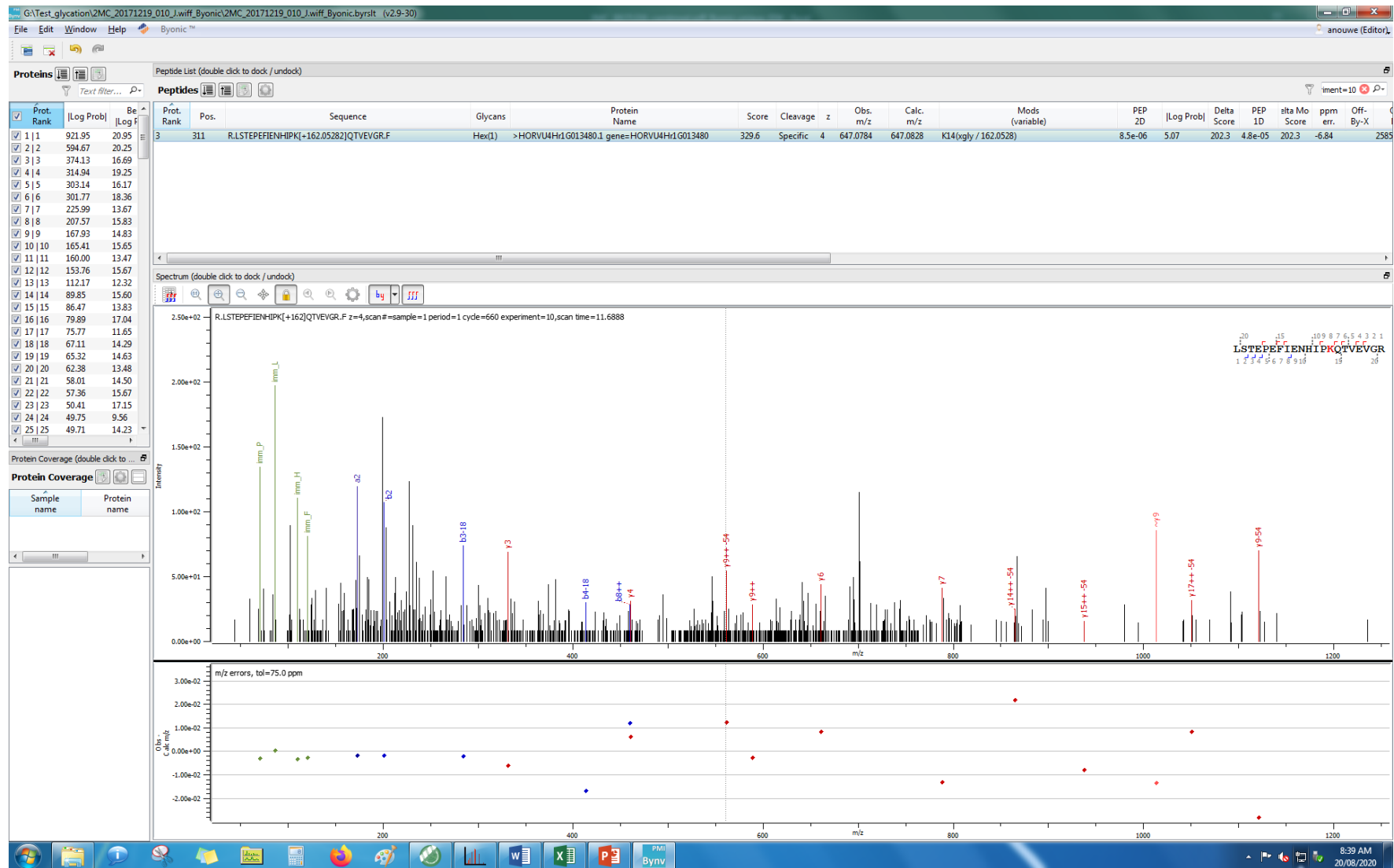


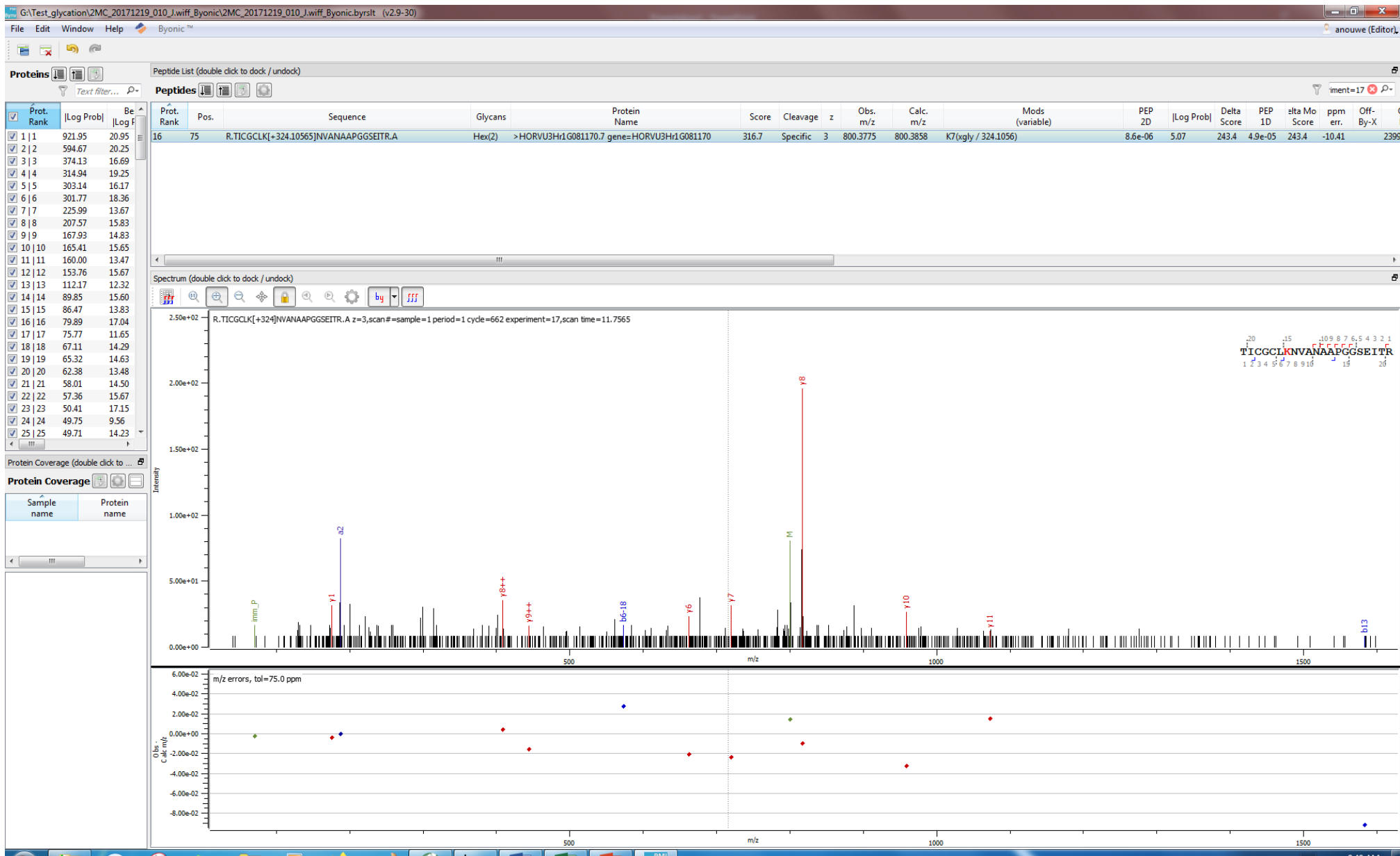


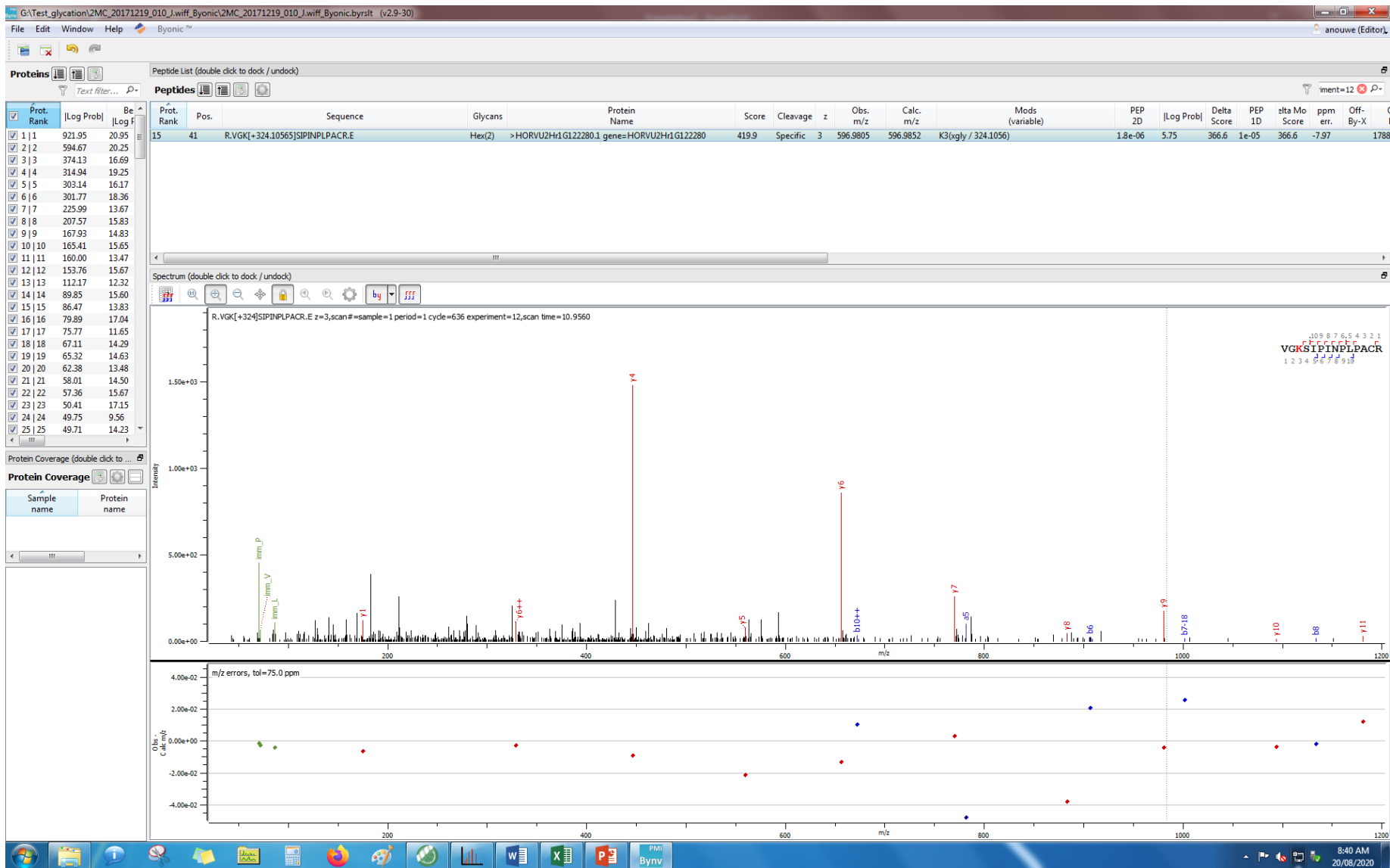


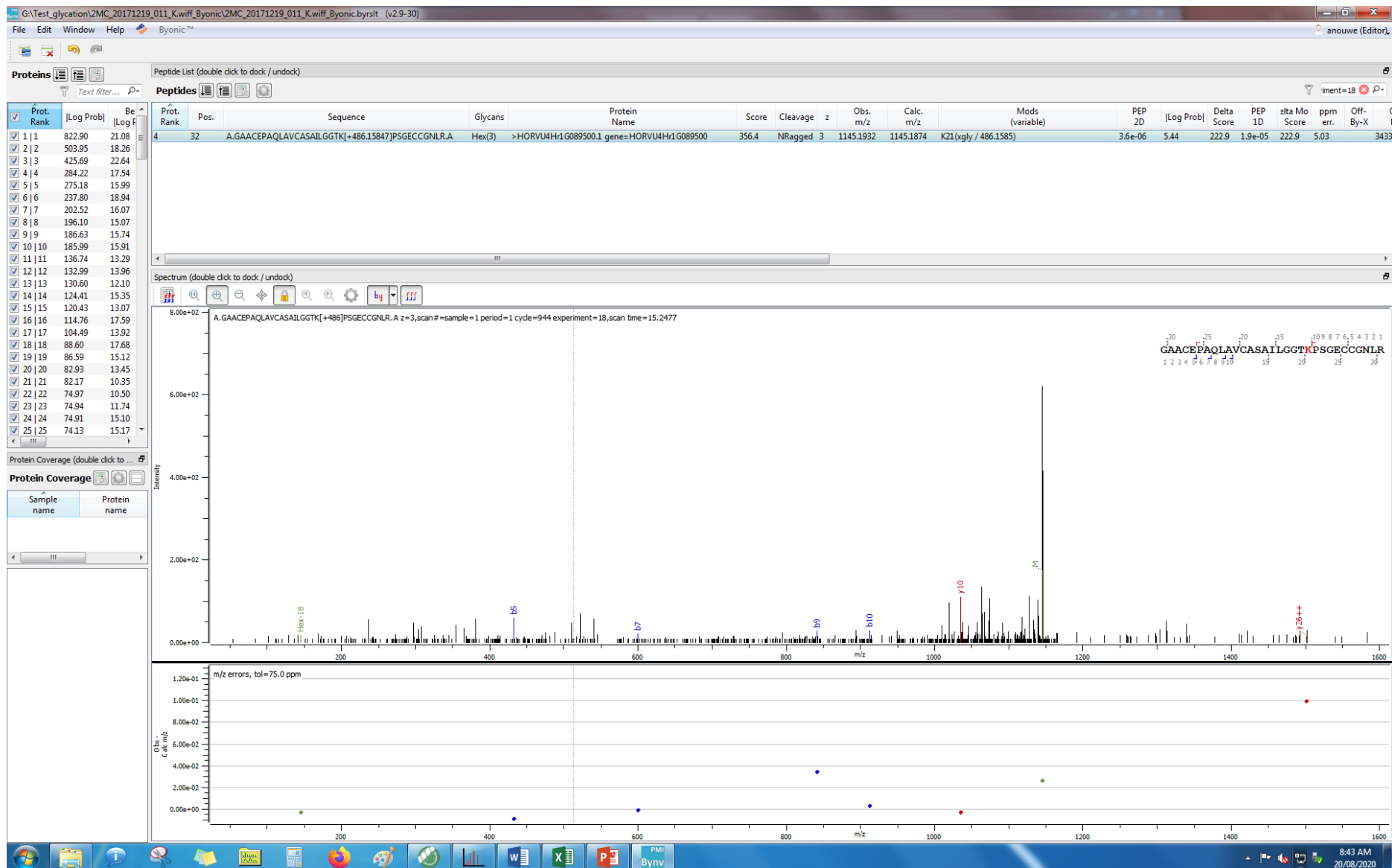


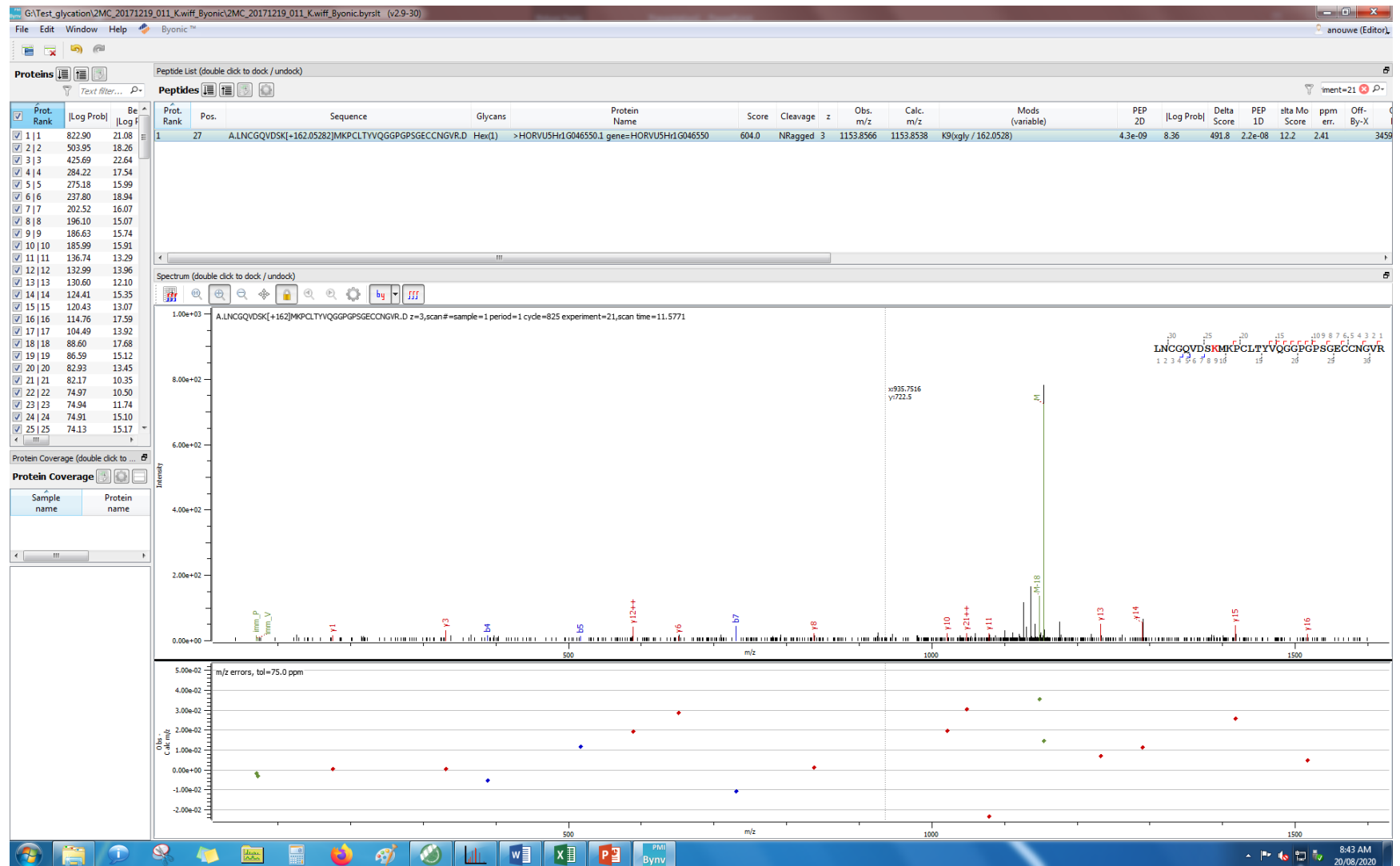




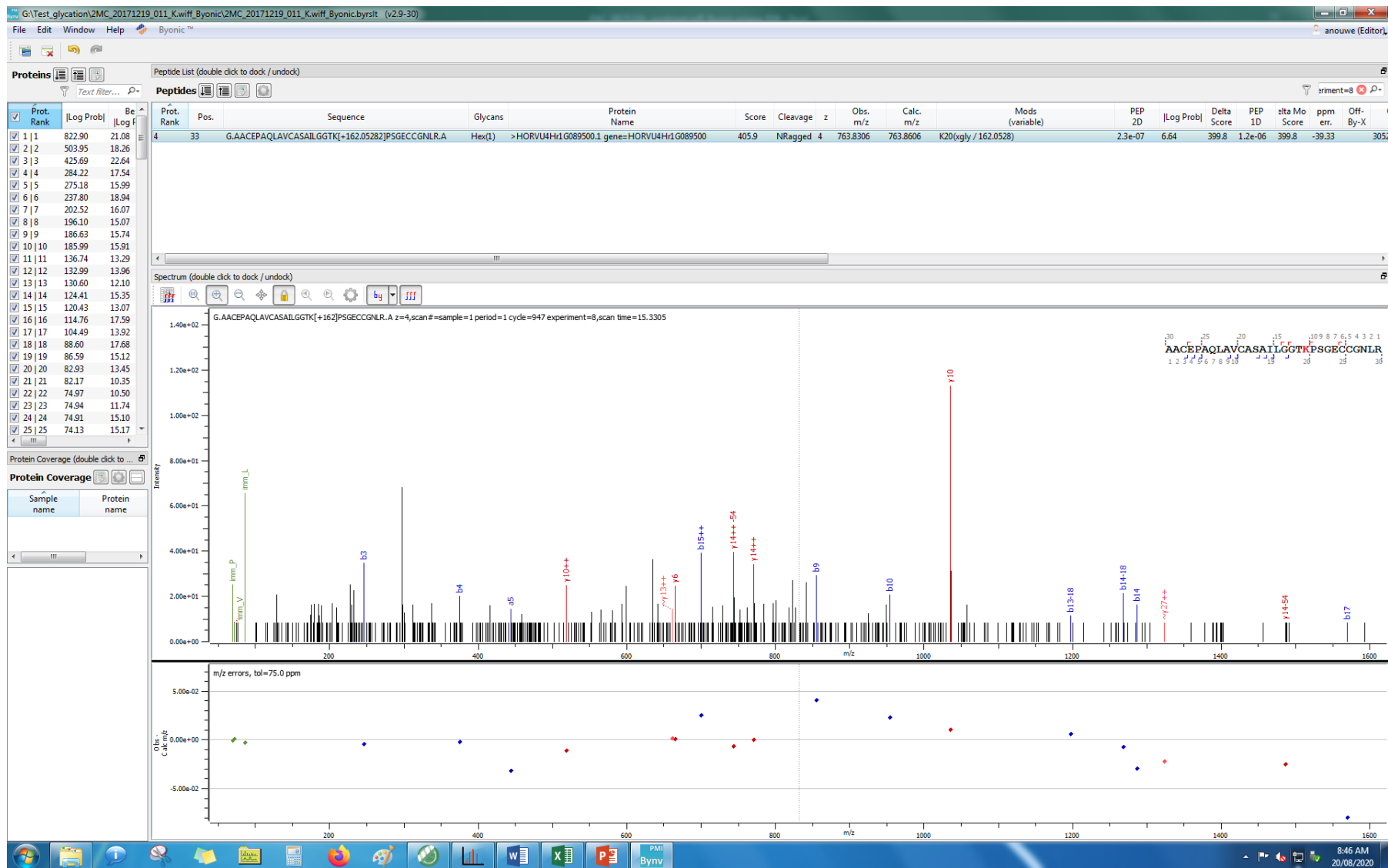




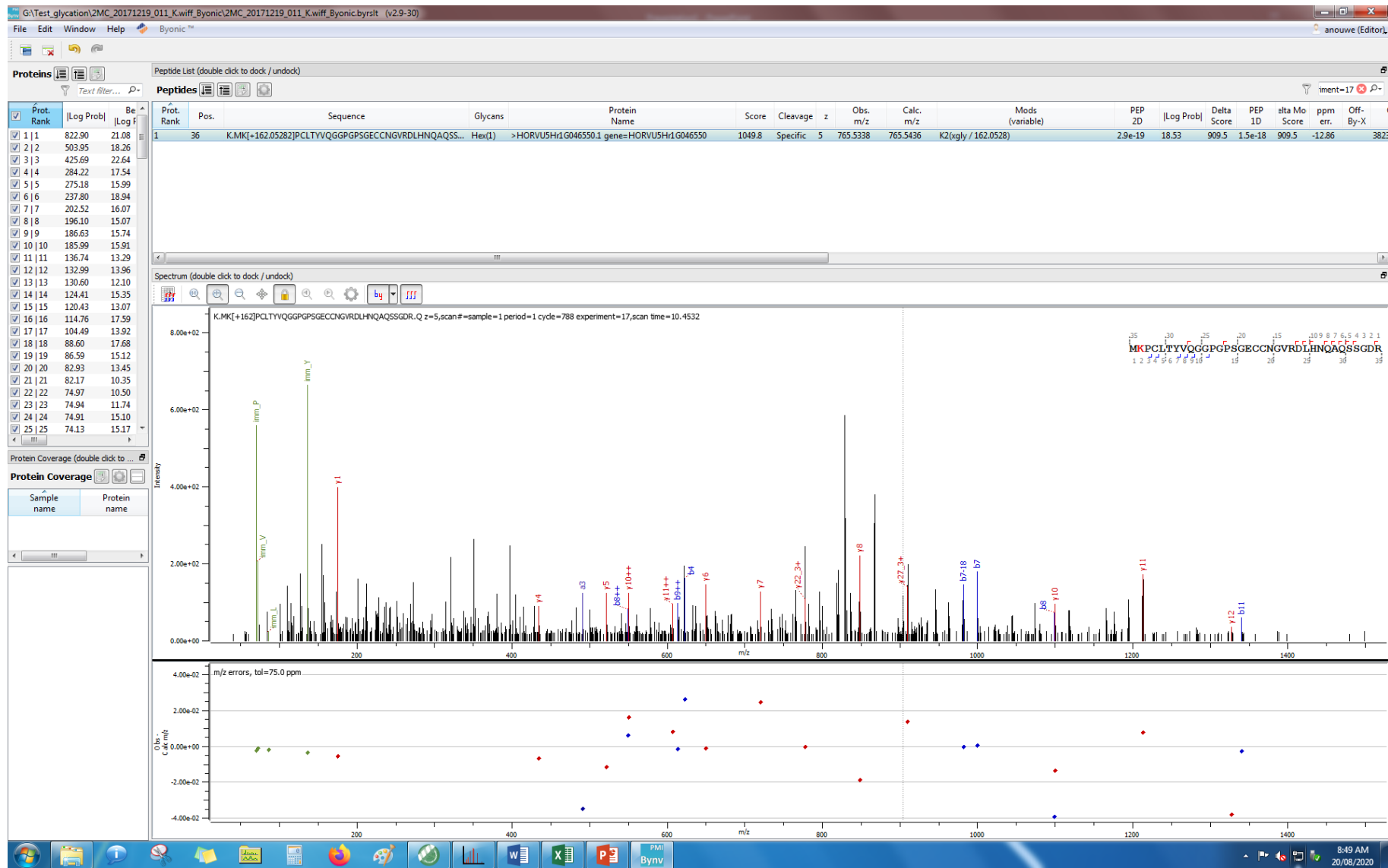


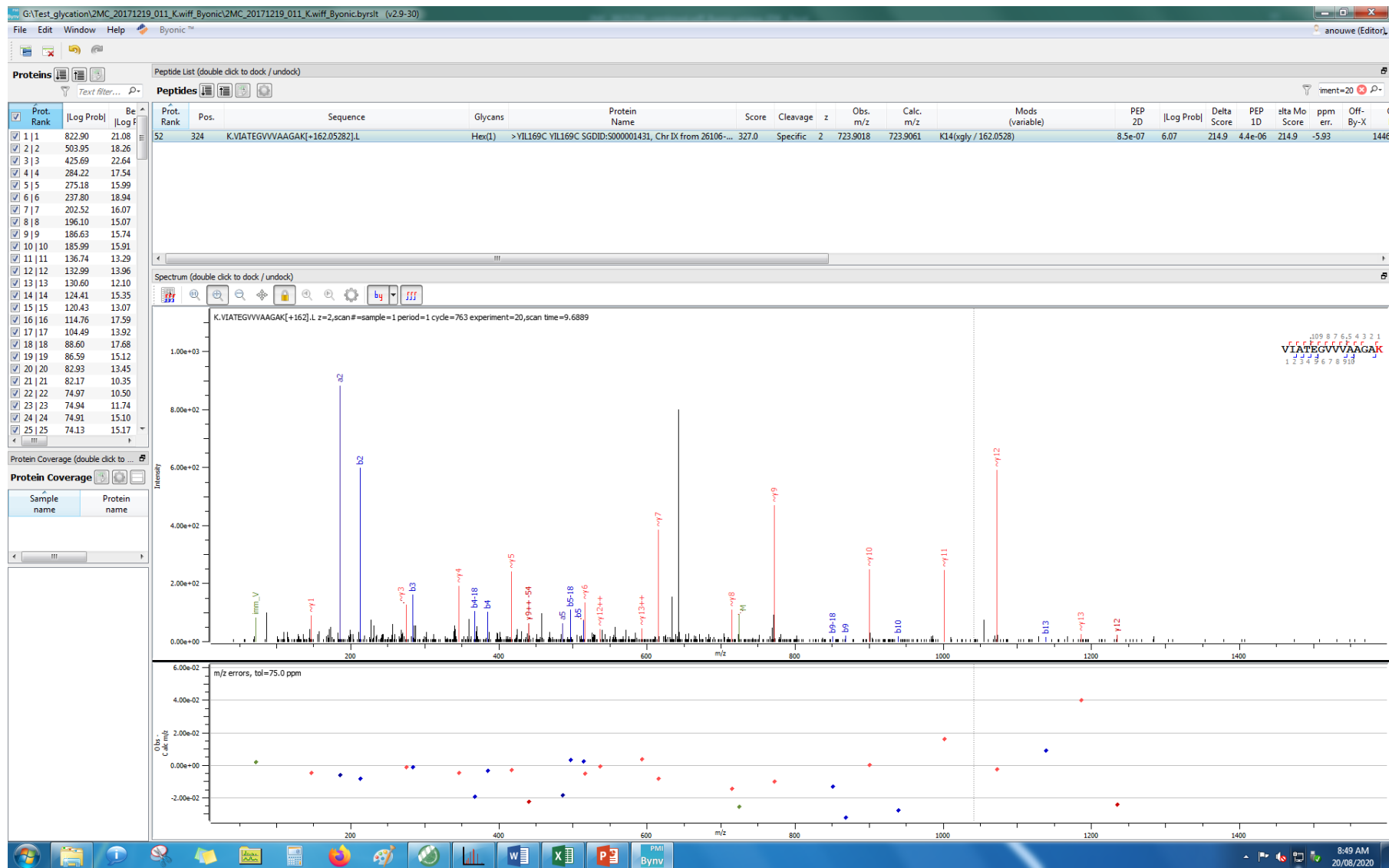


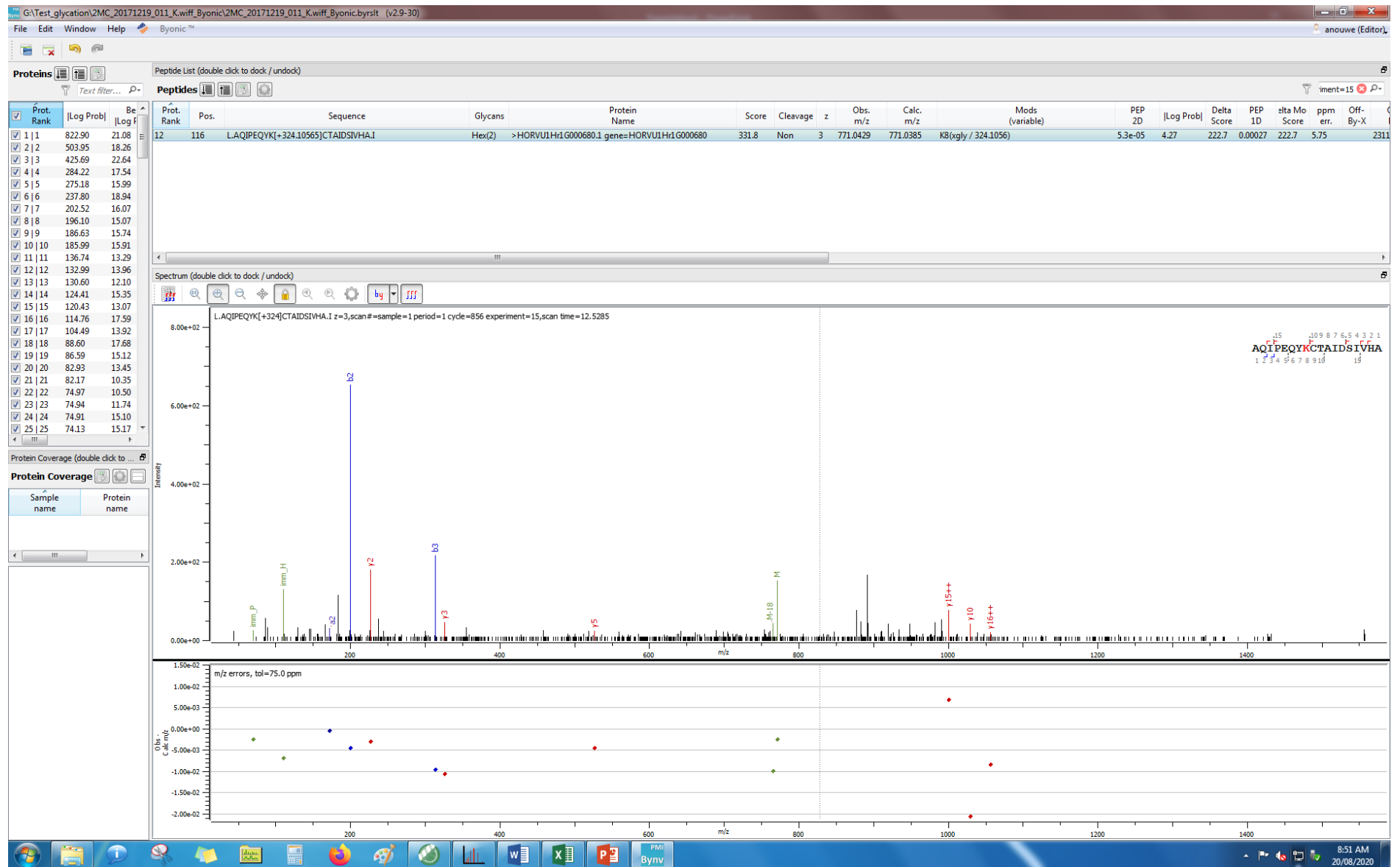


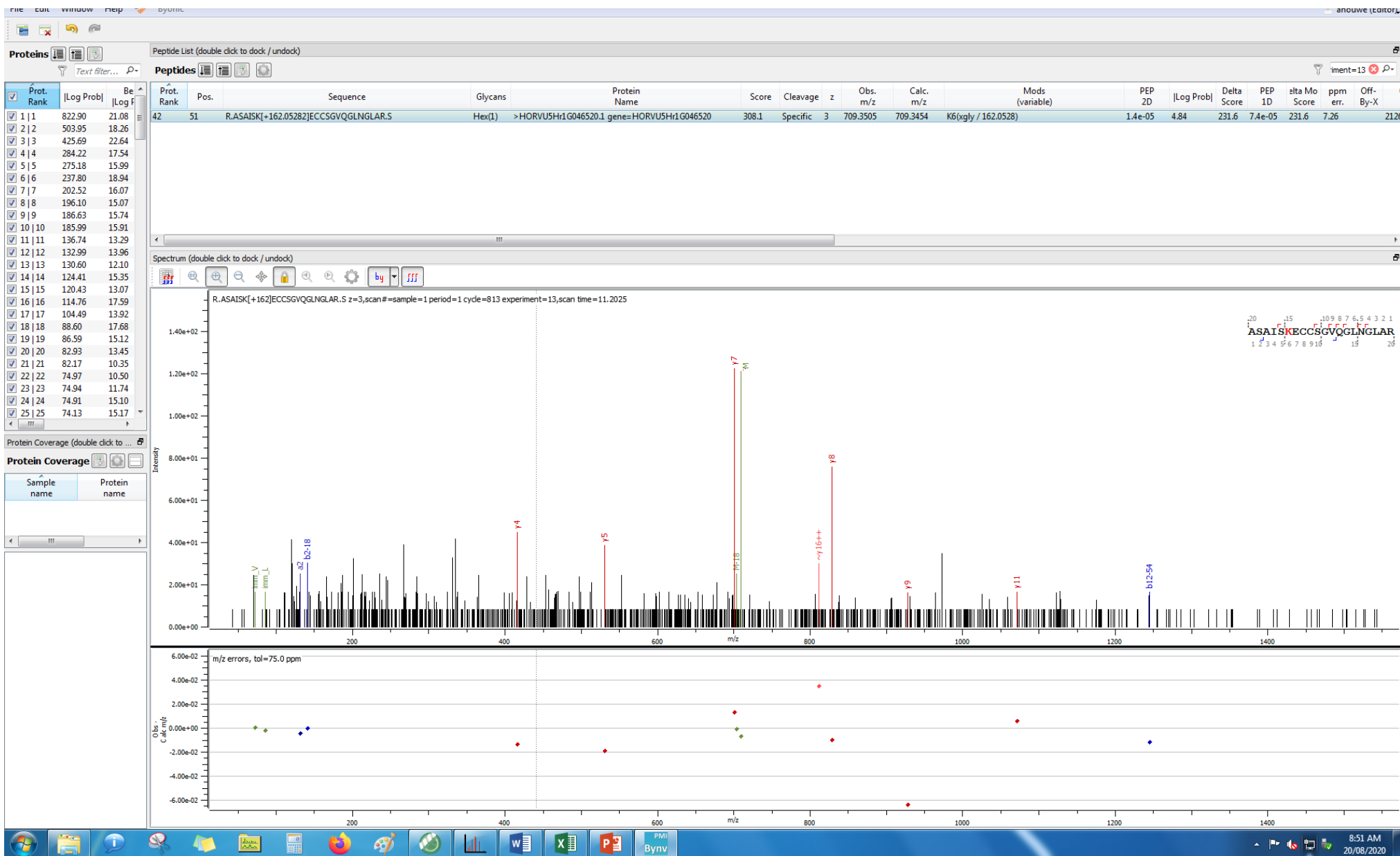


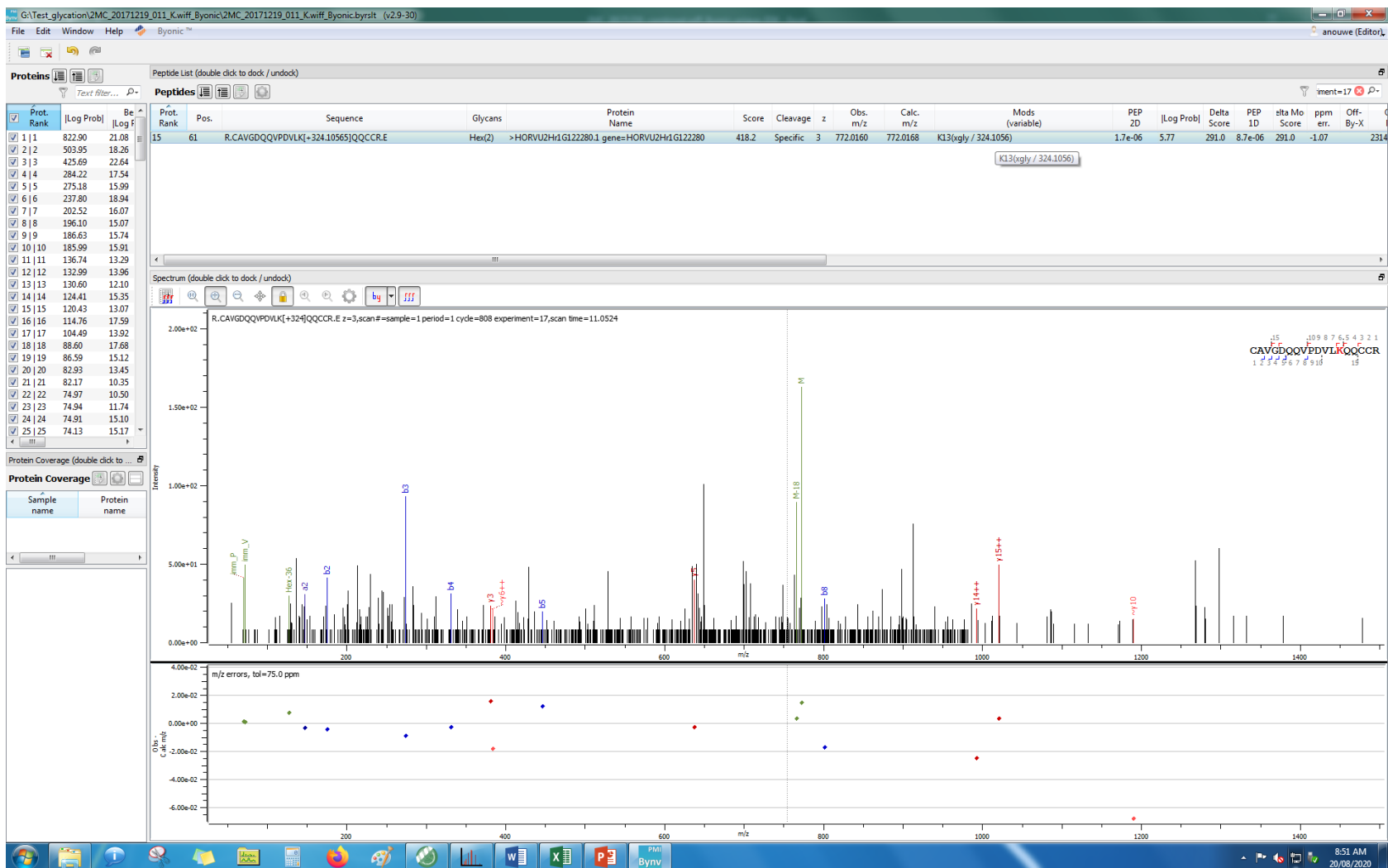




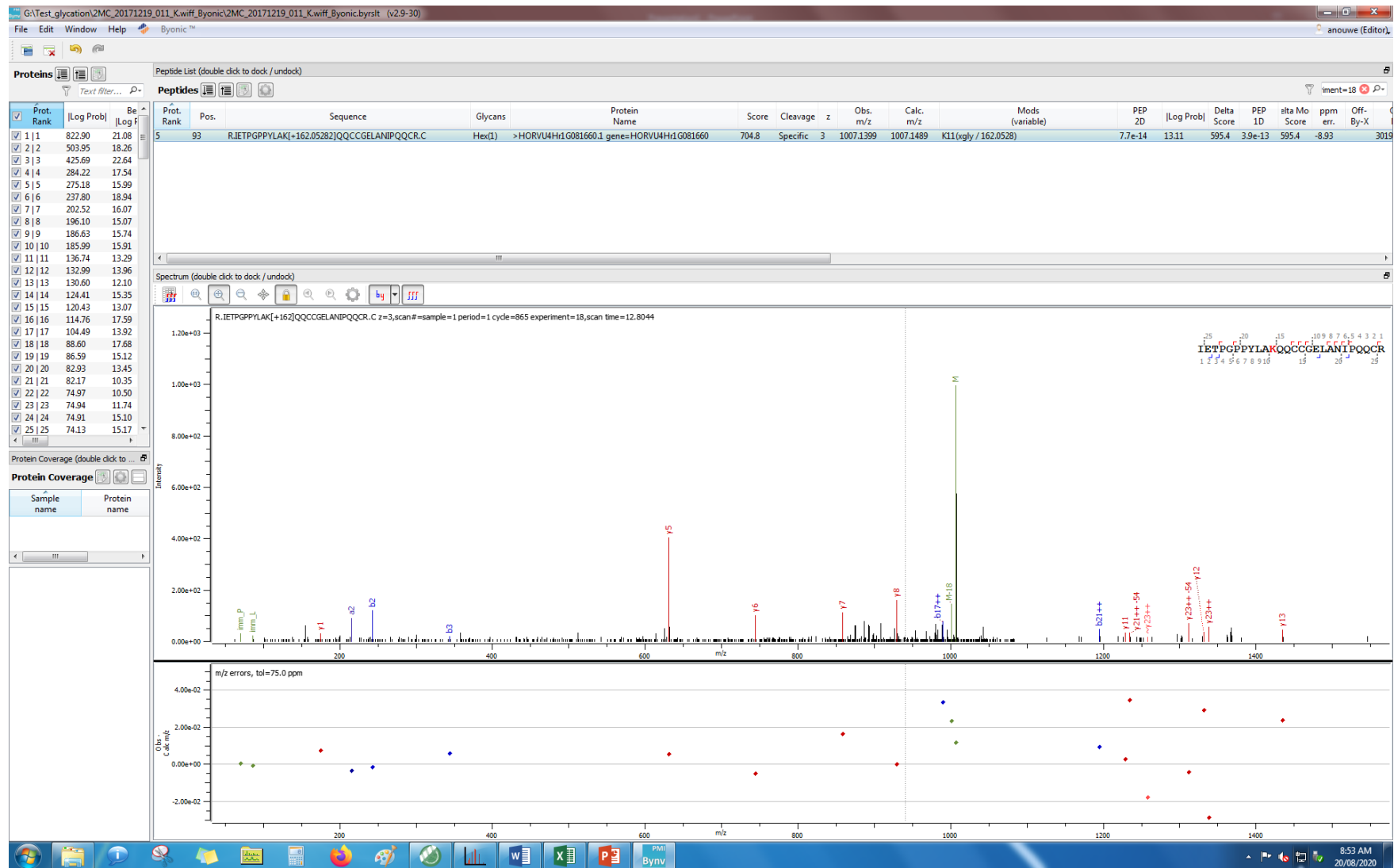


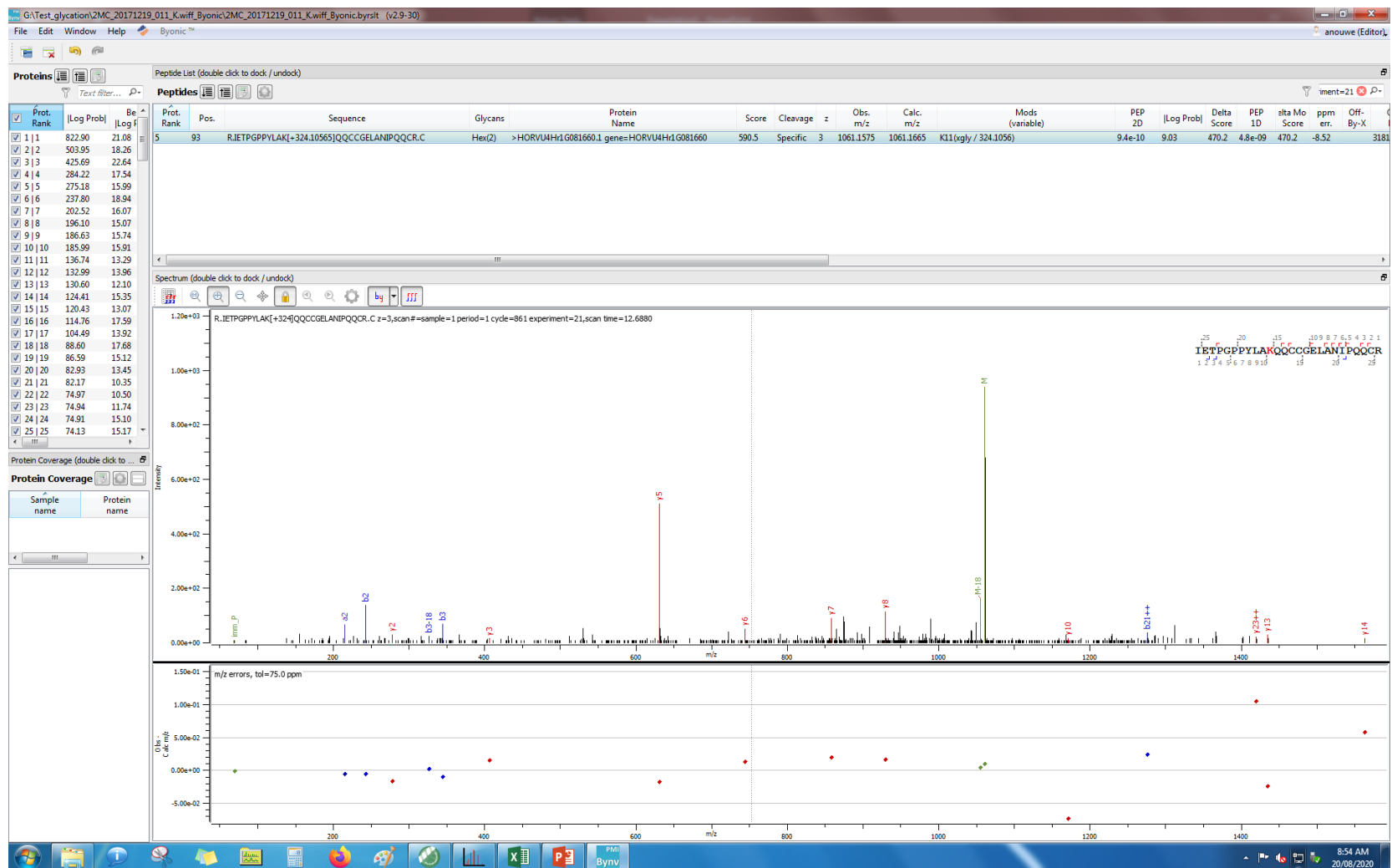


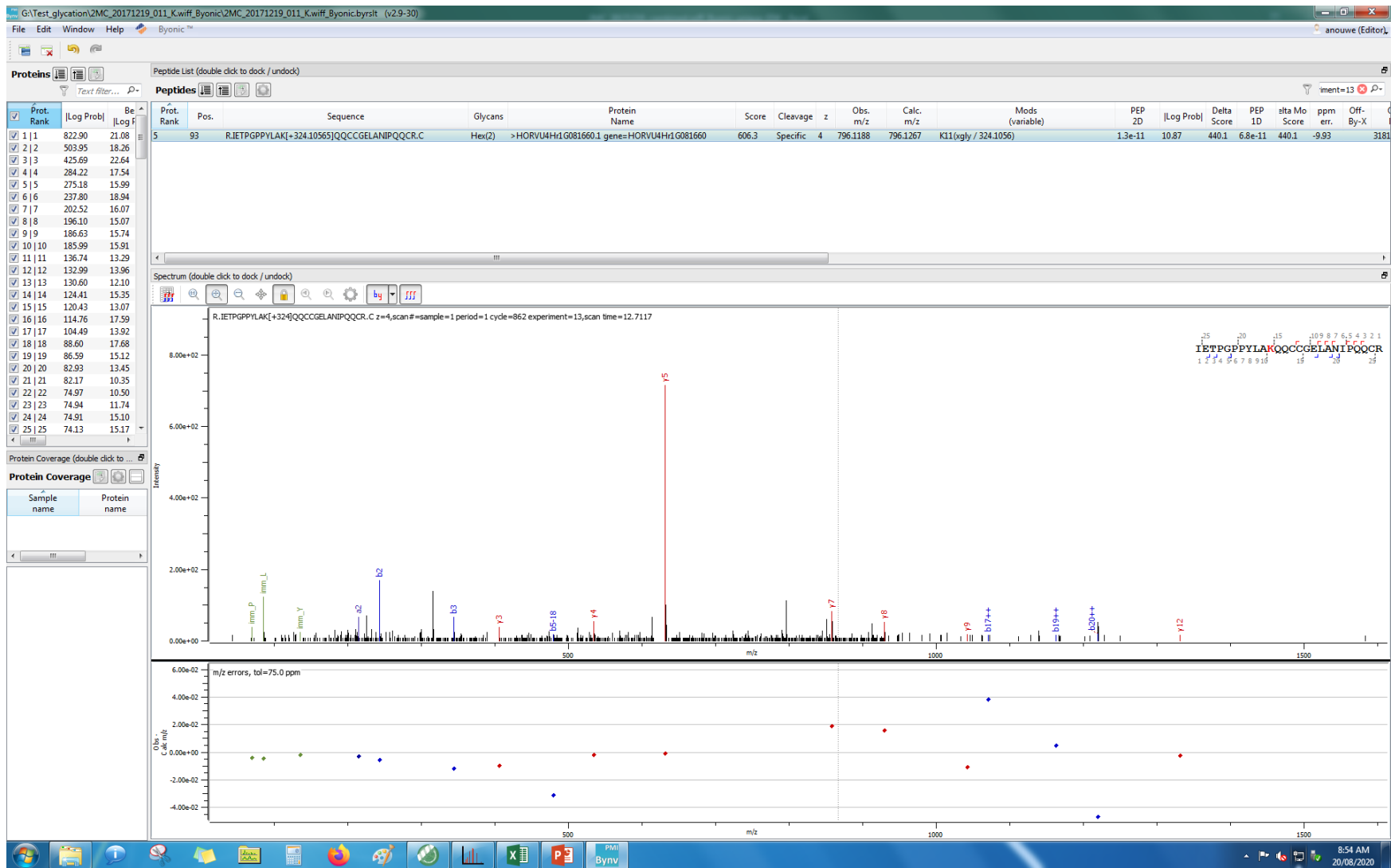


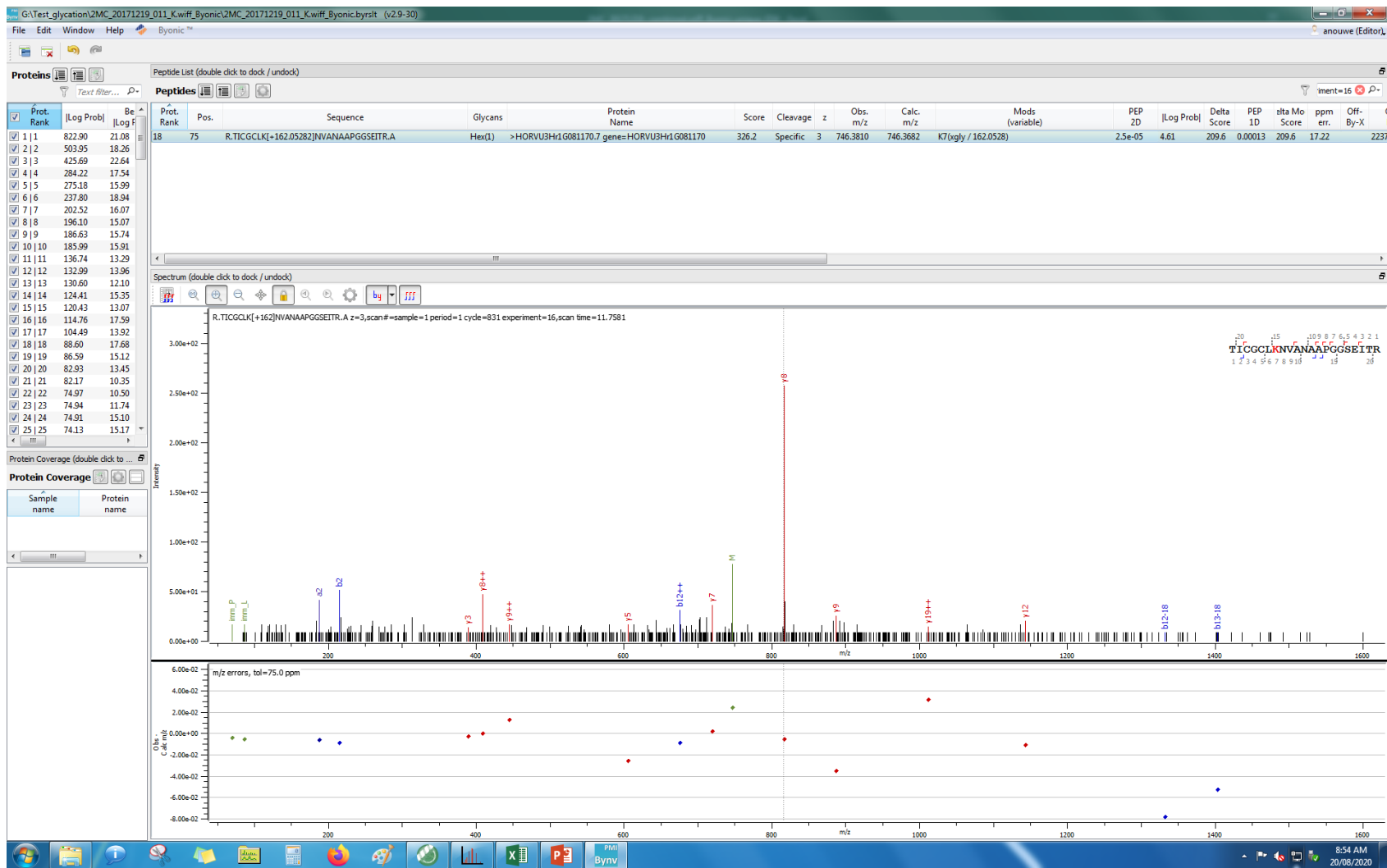


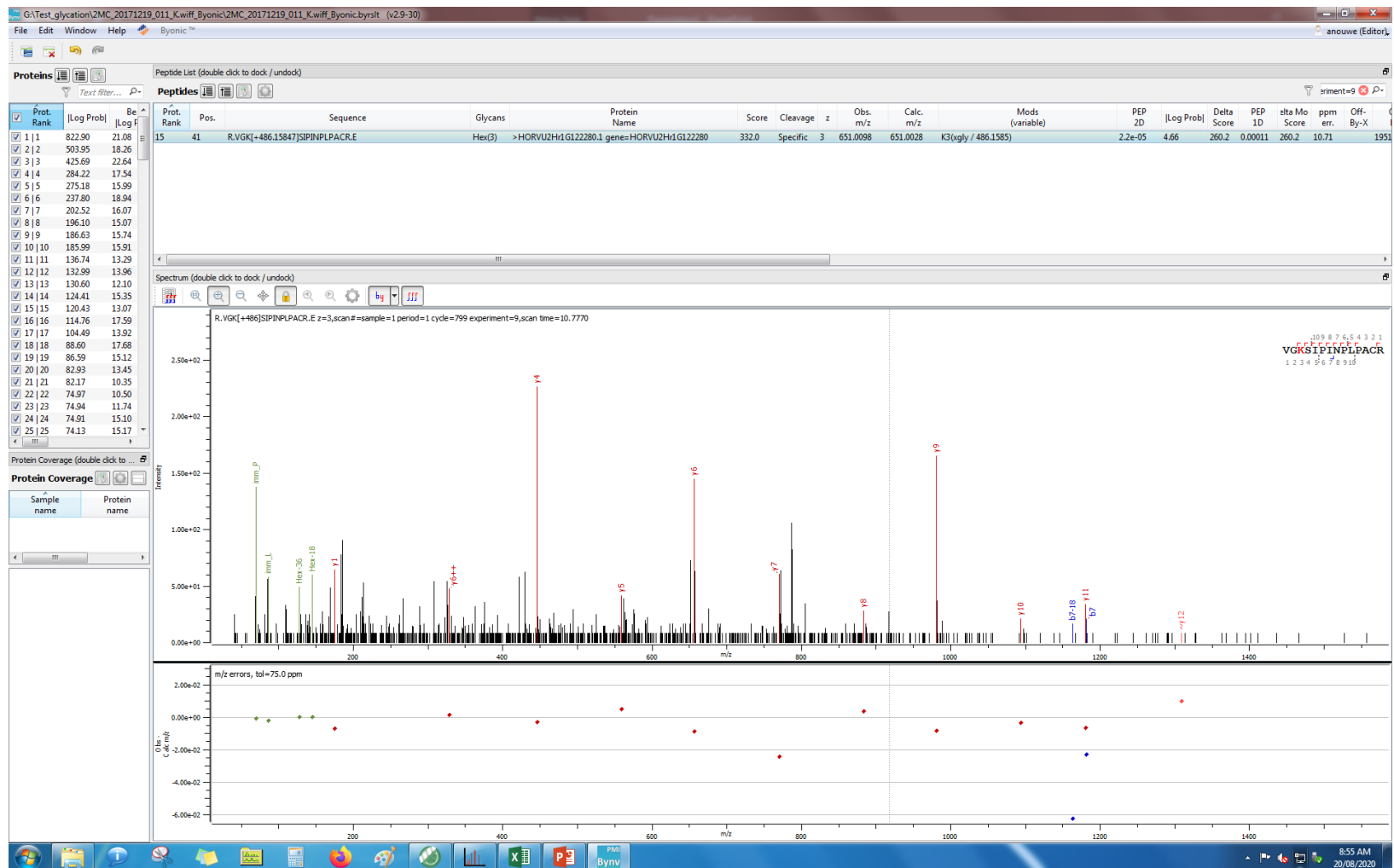


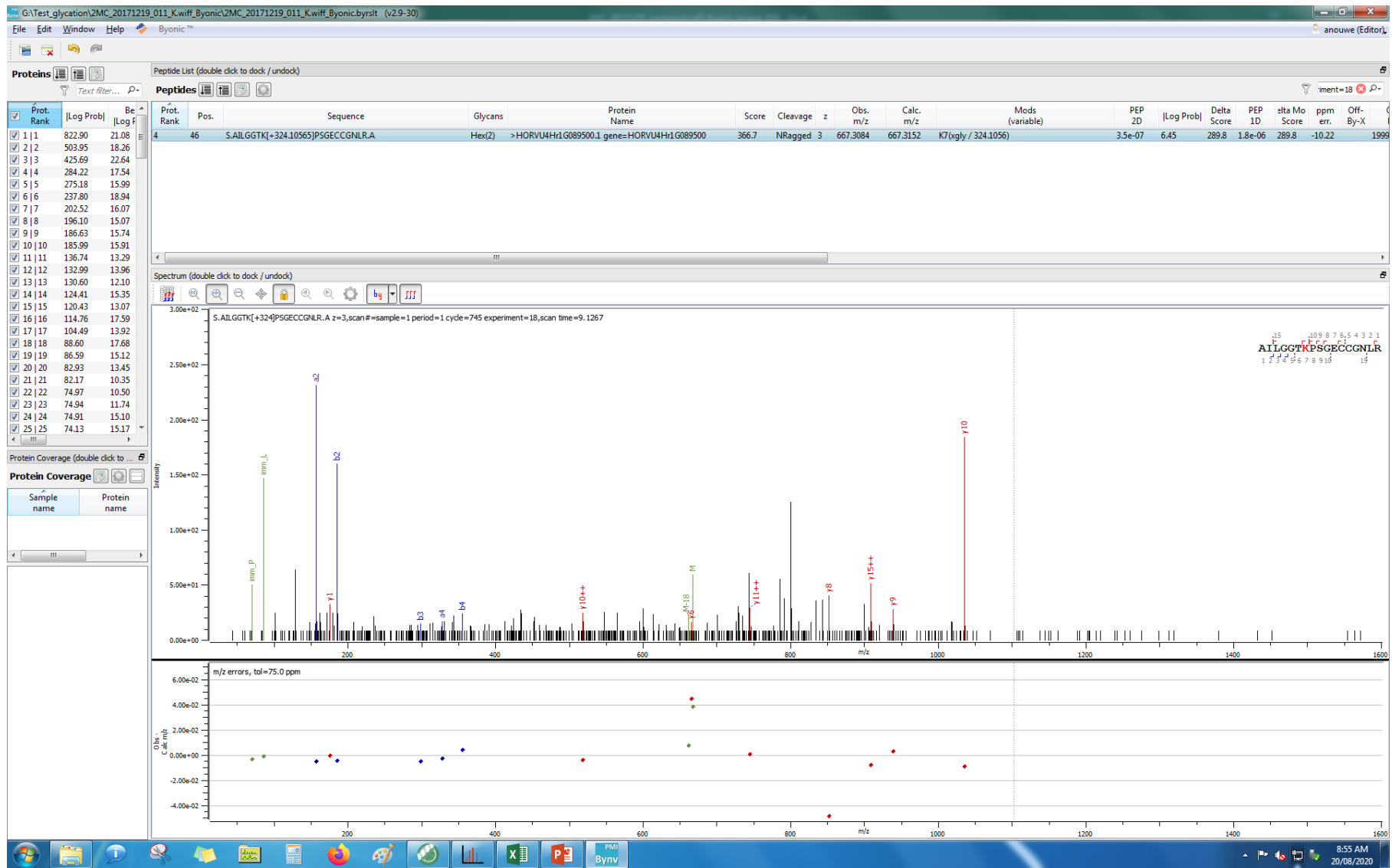














Proteome Discoverer 2.5.0.107

File Edit Window Help

Proteins

Peptide List (double click to dock / undock)

Peptides

Prot. Rank	Pos.	Sequence	Glycans	Protein Name	Score	Cleavage	z	Obs. m/z	Calc. m/z	Mods (variable)	PEP 2D	[Log Prob]	Delta Score	PEP 1D	slts Mo Score	ppm err.	Off-By-X
1	83	R.GIHNLNLNNAASIPSK[+162.05282]CNVNVPTTSPDIDCSR.I	Hex(1)	>HORVU5Hr1G046550.1 gene=HORVU5Hr1G046550	781.0	Specific	3	1234.5804	1234.6014	K16(xgly / 162.0528)	3.1e-13	12.51	430.9	1.3e-12	430.9	-17.08	3701

Spectrum (double click to dock / undock)

R.GIHNLNLNNAASIPSK[+162]CNVNVPTTSPDIDCSR.I z=3,scan#==sample=1 period=1 cycle=877 experiment=21,scan time=13.4648

Intensity

m/z

Protein Coverage (double click to dock / undock)

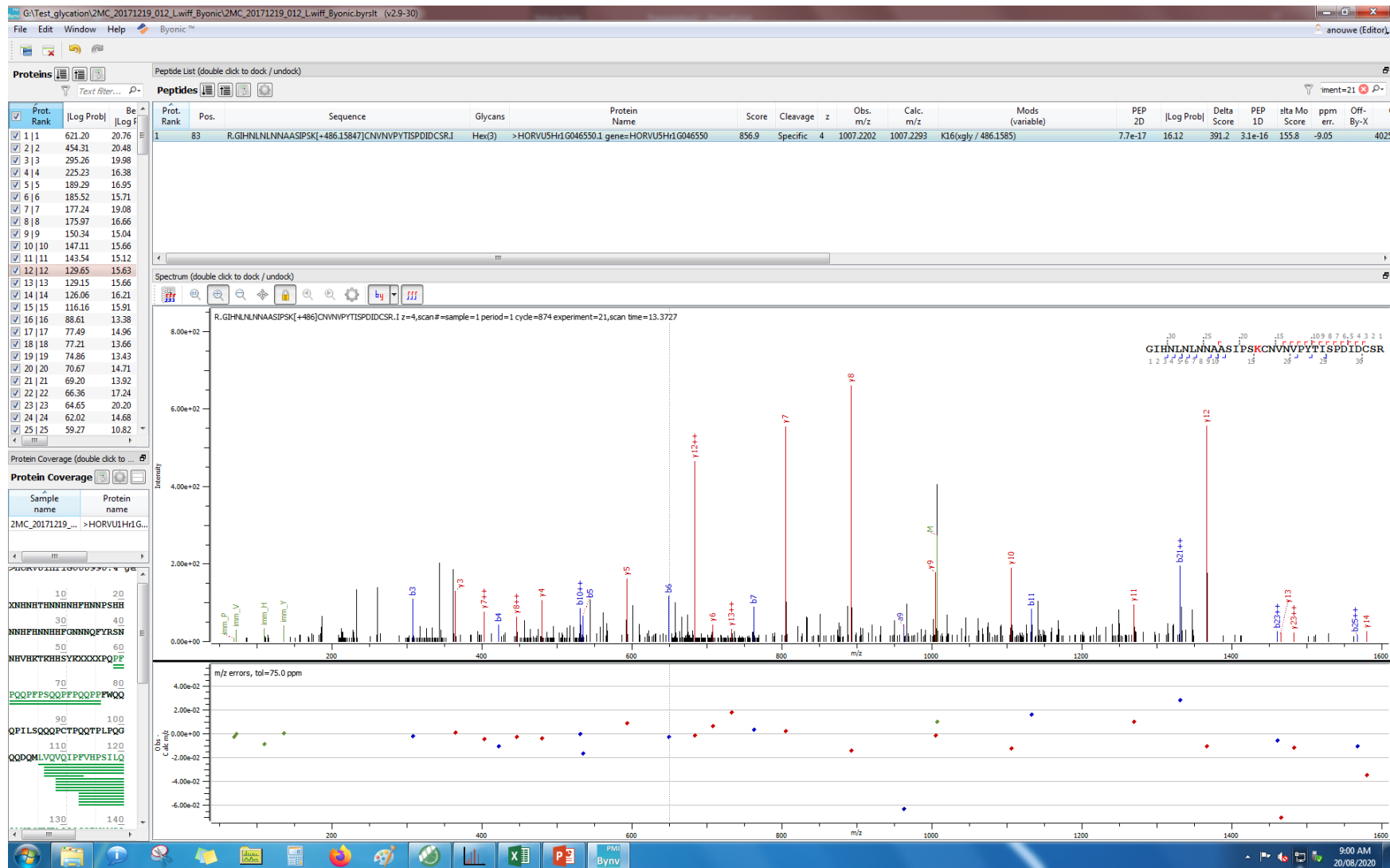
Protein Coverage

Sample name	Protein name
2MC_20171219...	>HORVU1Hr1G...

m/z errors, tol=75.0 ppm

Obs - Calc m/z

m/z



Proteins

Prot. Rank	[Log Prob]	Best [Log Prob]	Best Score
1 1	870.46	22.45	1288.0
2 2	736.81	21.67	1239.4
3 3	368.19	15.57	929.7
4 4	359.78	18.25	997.5
5 5	278.78	19.13	1056.4
6 6	247.00	14.63	826.1
7 7	216.57	16.57	883.7
8 8	212.18	19.54	1049.5
9 9	204.17	17.34	946.3
10 10	196.88	16.57	877.5
11 11	188.48	16.34	938.9
12 12	155.03	15.91	909.8
13 13	131.06	13.57	741.3
14 14	127.08	15.89	864.9
15 15	123.13	15.40	814.7
16 16	113.70	14.05	796.4
17 17	103.13	16.62	894.7
18 18	102.96	14.71	812.2
19 19	100.59	18.33	1043.1
20 20	97.44	12.62	681.0
21 21	95.23	13.62	723.7
22 22	88.14	13.63	741.0
23 23	85.28	14.98	809.4
24 24	82.71	15.68	804.4
25 25	77.10	14.63	792.8
26 26	72.22	14.68	753.0

Protein Coverage (double click to dock / undock)

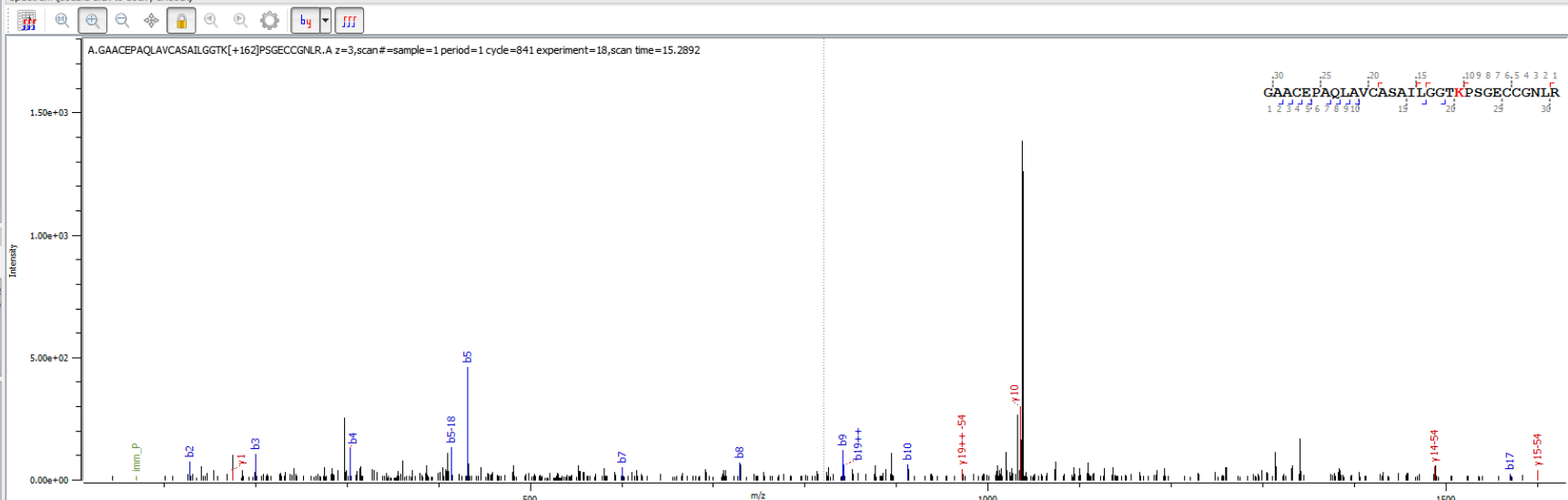
Protein Coverage

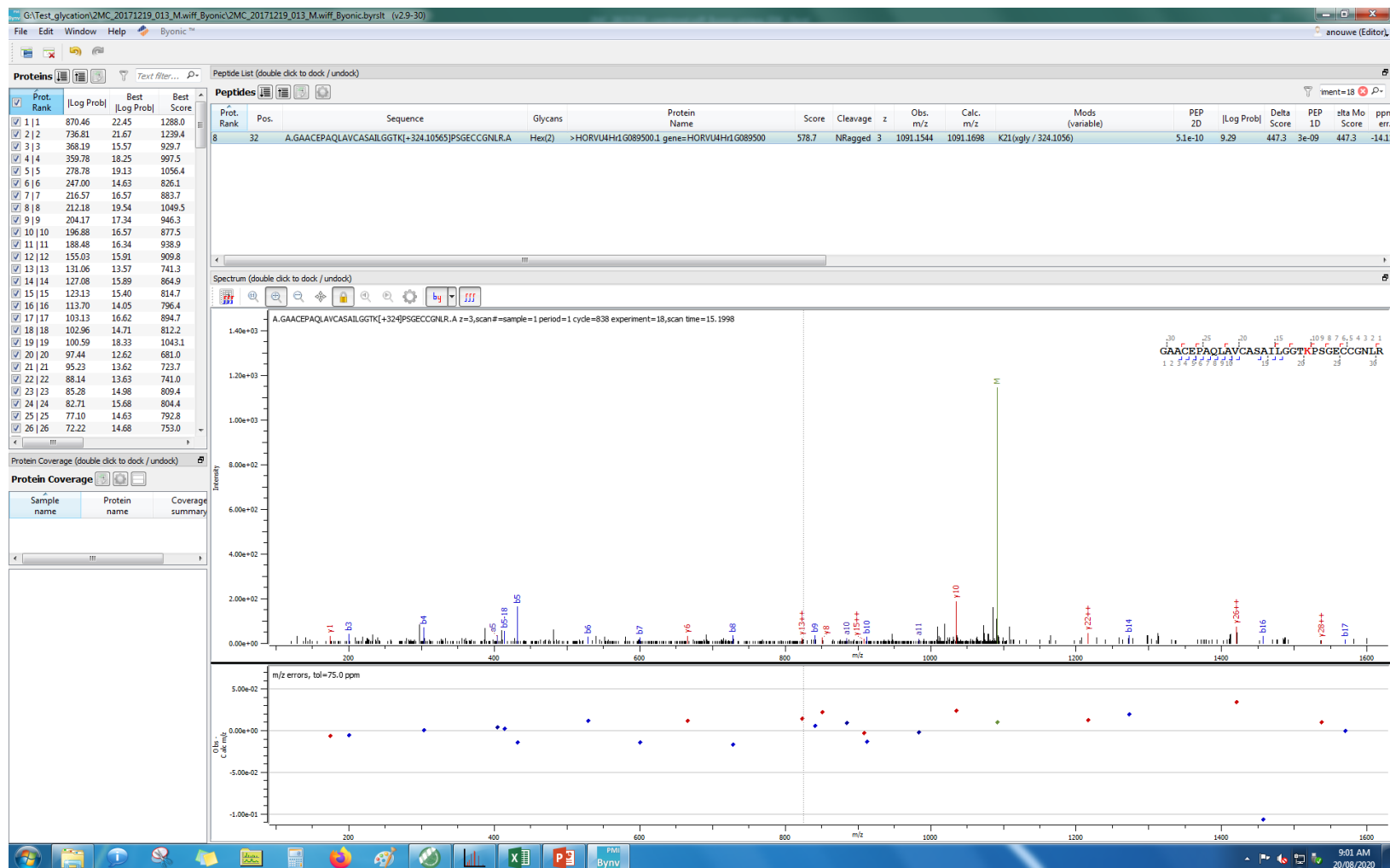
Sample name	Protein name	Coverage summary
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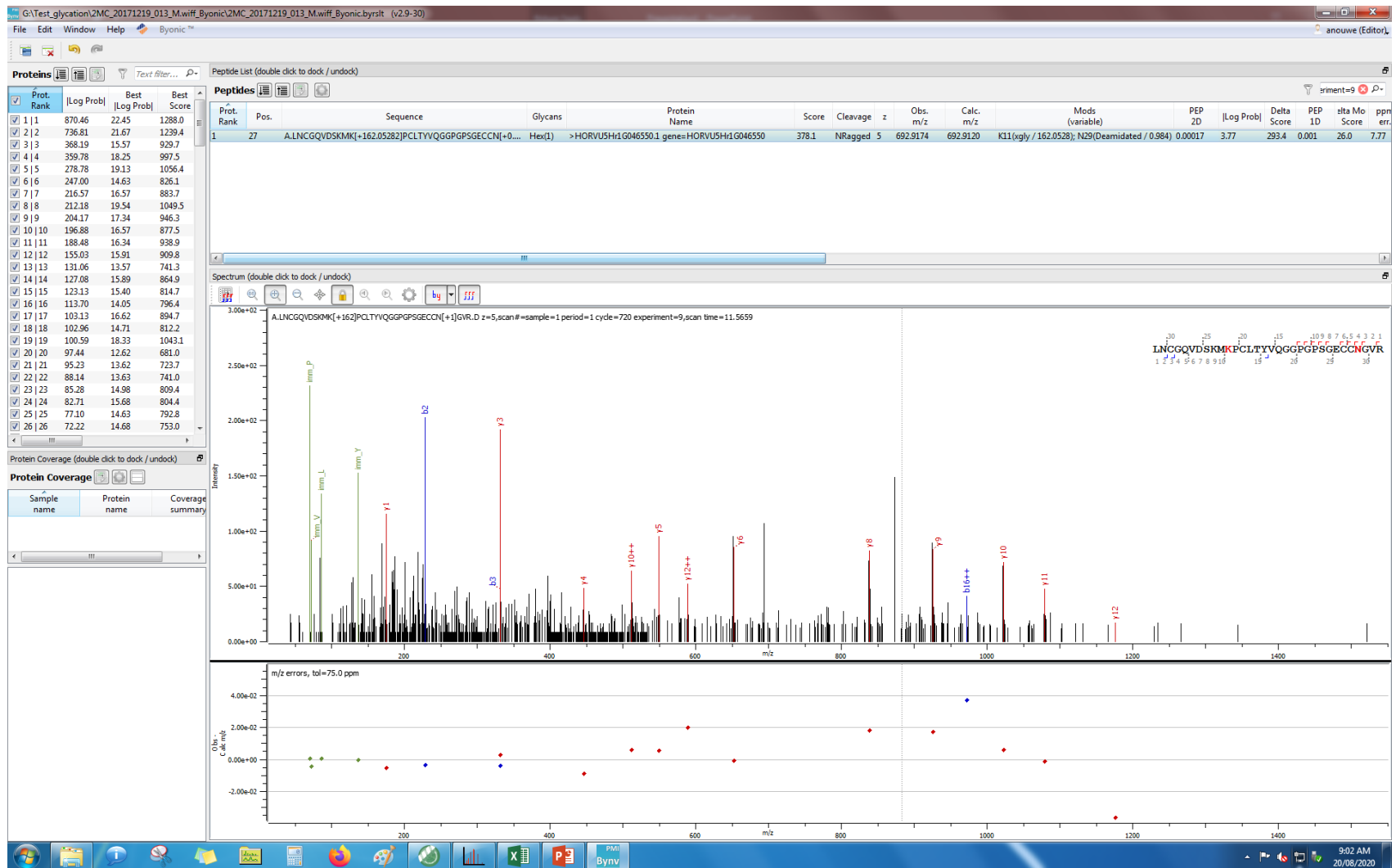
Peptide List (double click to dock / undock)

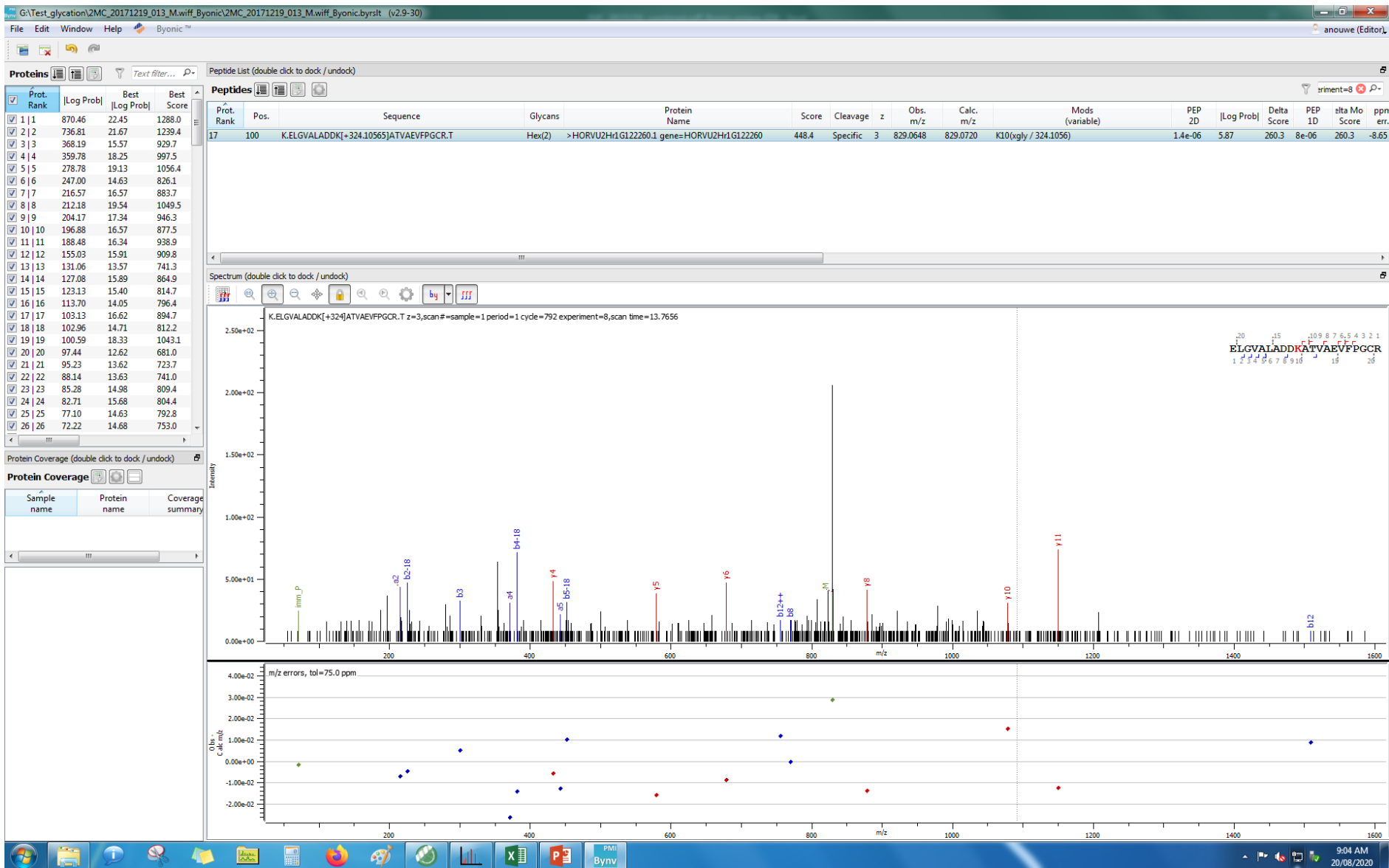
Prot. Rank	Pos.	Sequence	Glycans	Protein Name	Score	Cleavage	z	Obs. m/z	Calc. m/z	Mods (variable)	PEP 2D	[Log Prob]	Delta Score	PEP 1D	sta Mo Score	ppm err.
8	32	A.GAAACEPAQLAVCASAILGGTK[+162]PSGECCGNLR.A	Hex(1)	>HORVU4Hr1G089500.1 gene=HORVU4Hr1G089500	737.3	NRagged	3	1037.1422	1037.1522	K21(xgly / 162.0528)	2.7e-14	13.57	511.4	1.6e-13	511.4	-9.63

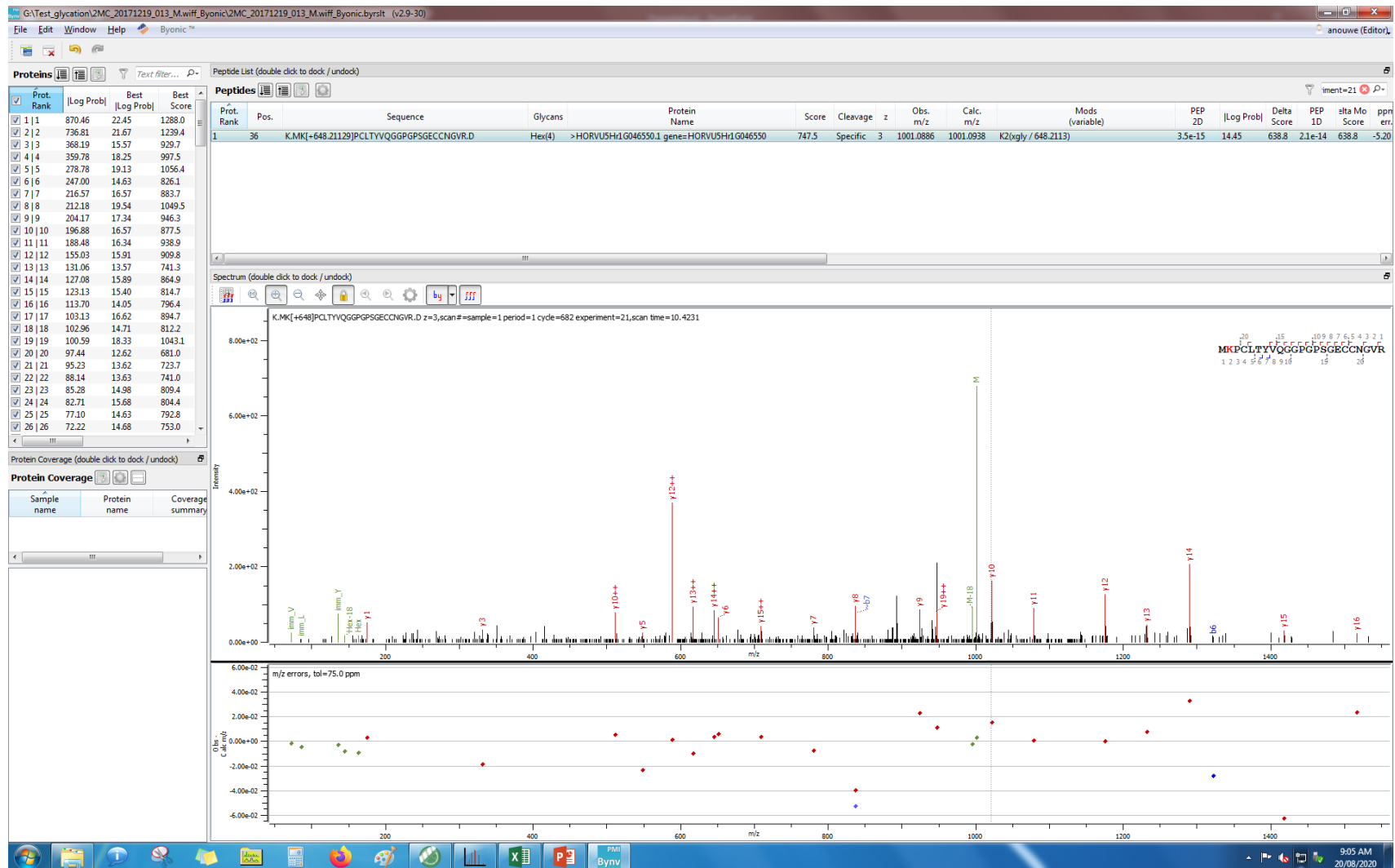
Spectrum (double click to dock / undock)



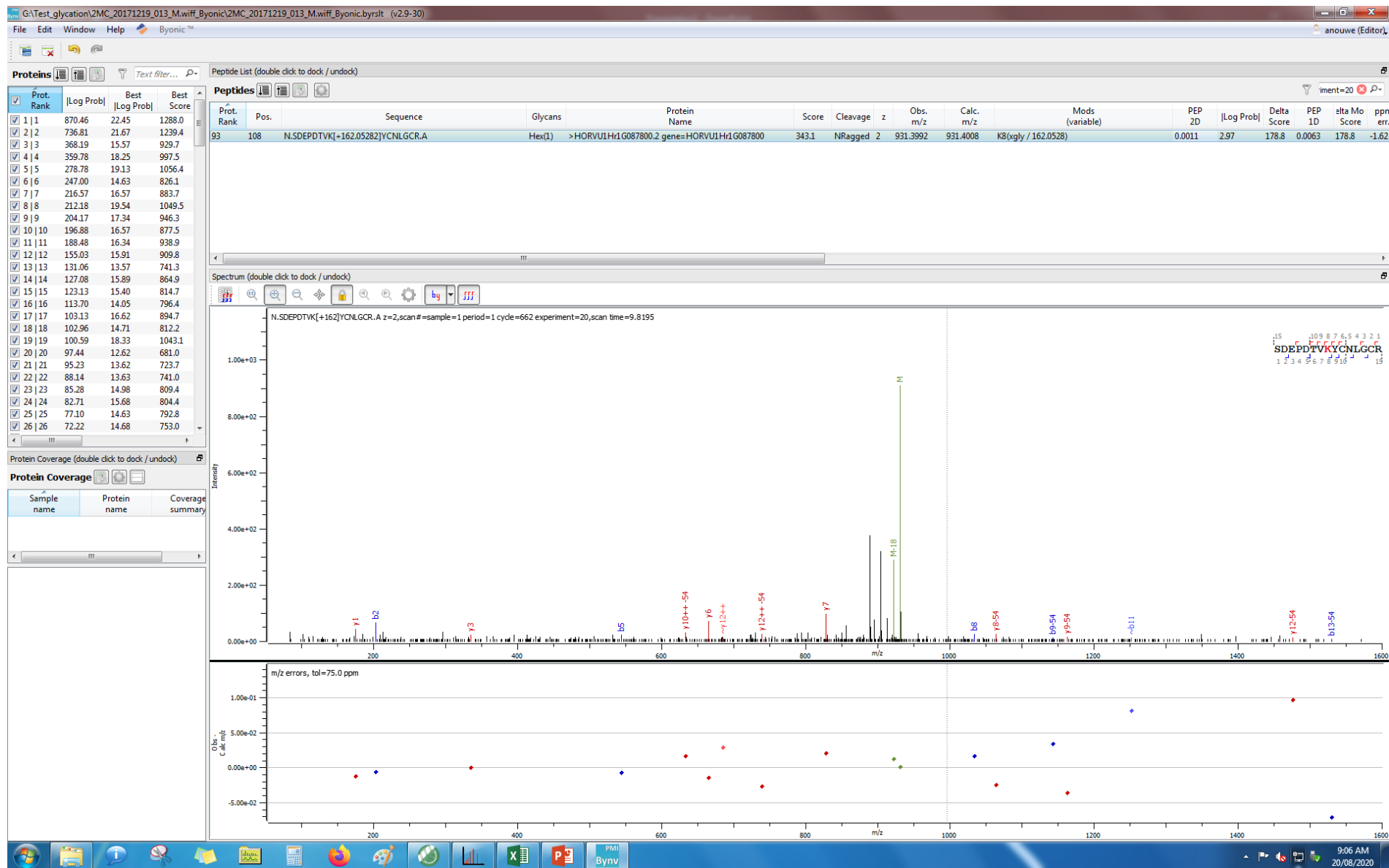


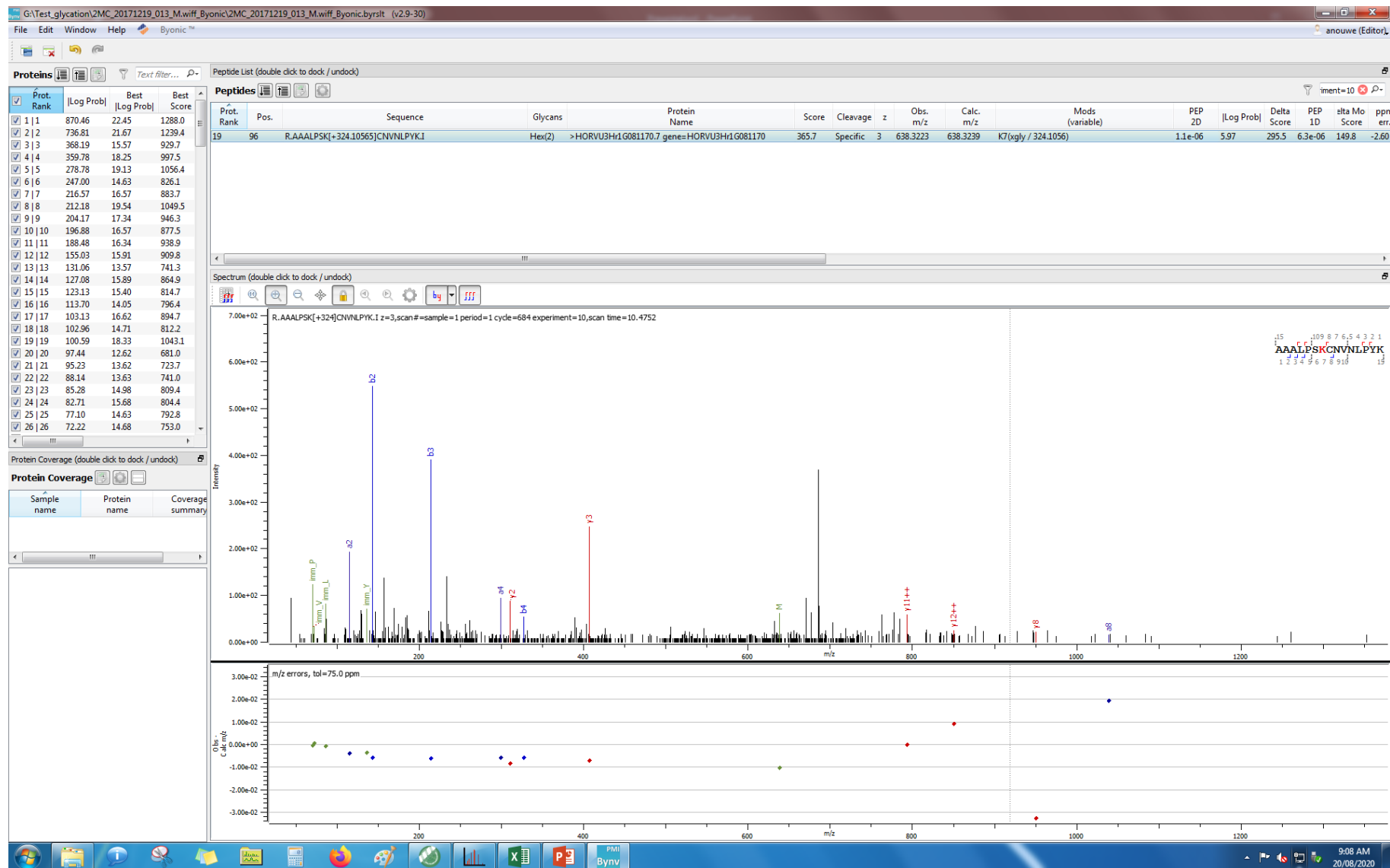












Proteins Text filter...

Prot. Rank	[Log Prob]	Best [Log Prob]	Best Score
1 1	870.46	22.45	1288.0
2 2	736.81	21.67	1239.4
3 3	368.19	15.57	929.7
4 4	359.78	18.25	997.5
5 5	278.78	19.13	1056.4
6 6	247.00	14.63	826.1
7 7	216.57	16.57	883.7
8 8	212.18	19.54	1049.5
9 9	204.17	17.34	946.3
10 10	196.88	16.57	877.5
11 11	188.48	16.34	938.9
12 12	155.03	15.91	909.8
13 13	131.06	13.57	741.3
14 14	127.08	15.89	864.9
15 15	123.13	15.40	814.7
16 16	113.70	14.05	796.4
17 17	103.13	16.62	894.7
18 18	102.96	14.71	812.2
19 19	100.59	18.33	1043.1
20 20	97.44	12.62	681.0
21 21	95.23	13.62	723.7
22 22	88.14	13.63	741.0
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Protein Coverage (double click to dock / undock)

Protein Coverage

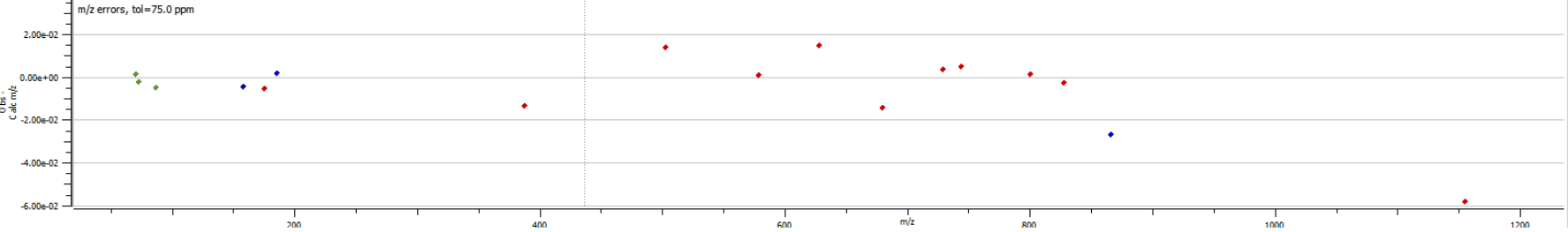
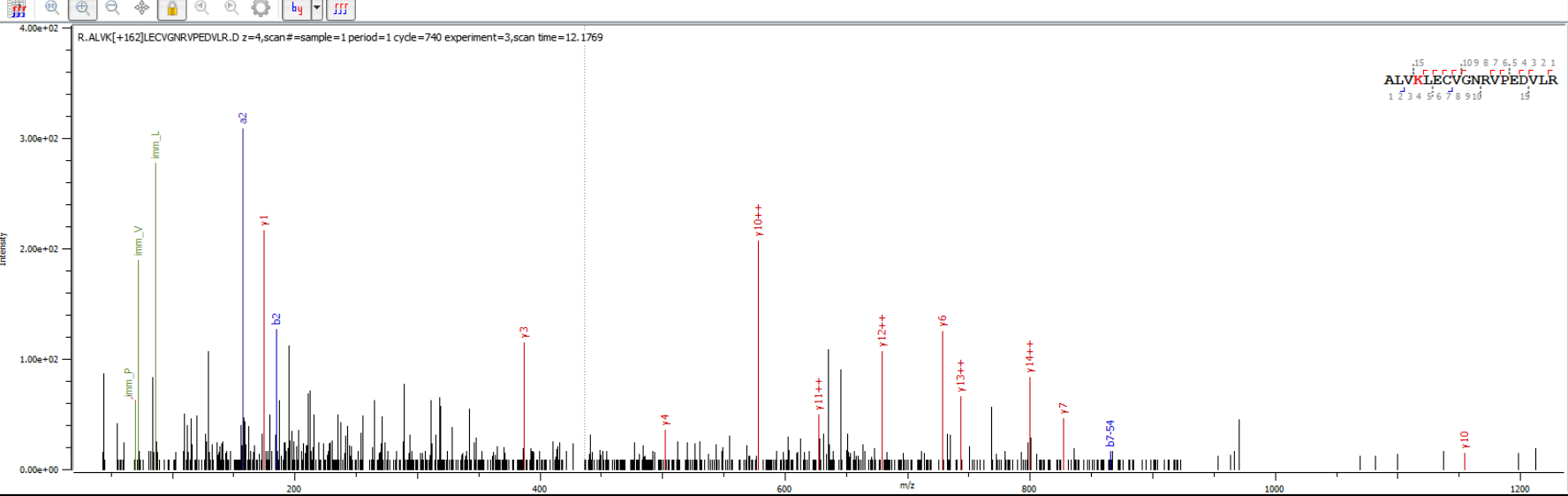
Sample name	Protein name	Coverage summary

Peptide List (double click to dock / undock)

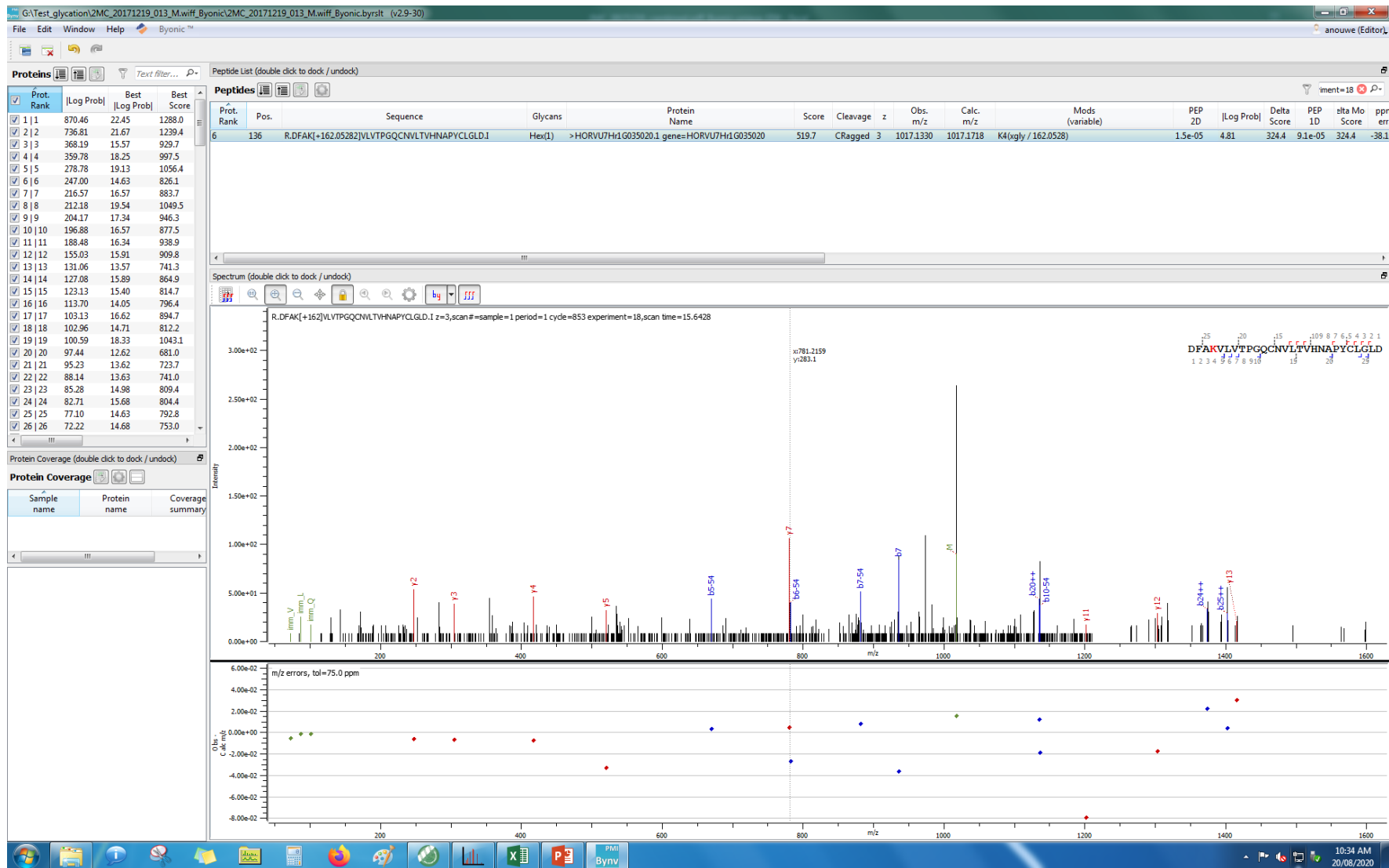
Peptides

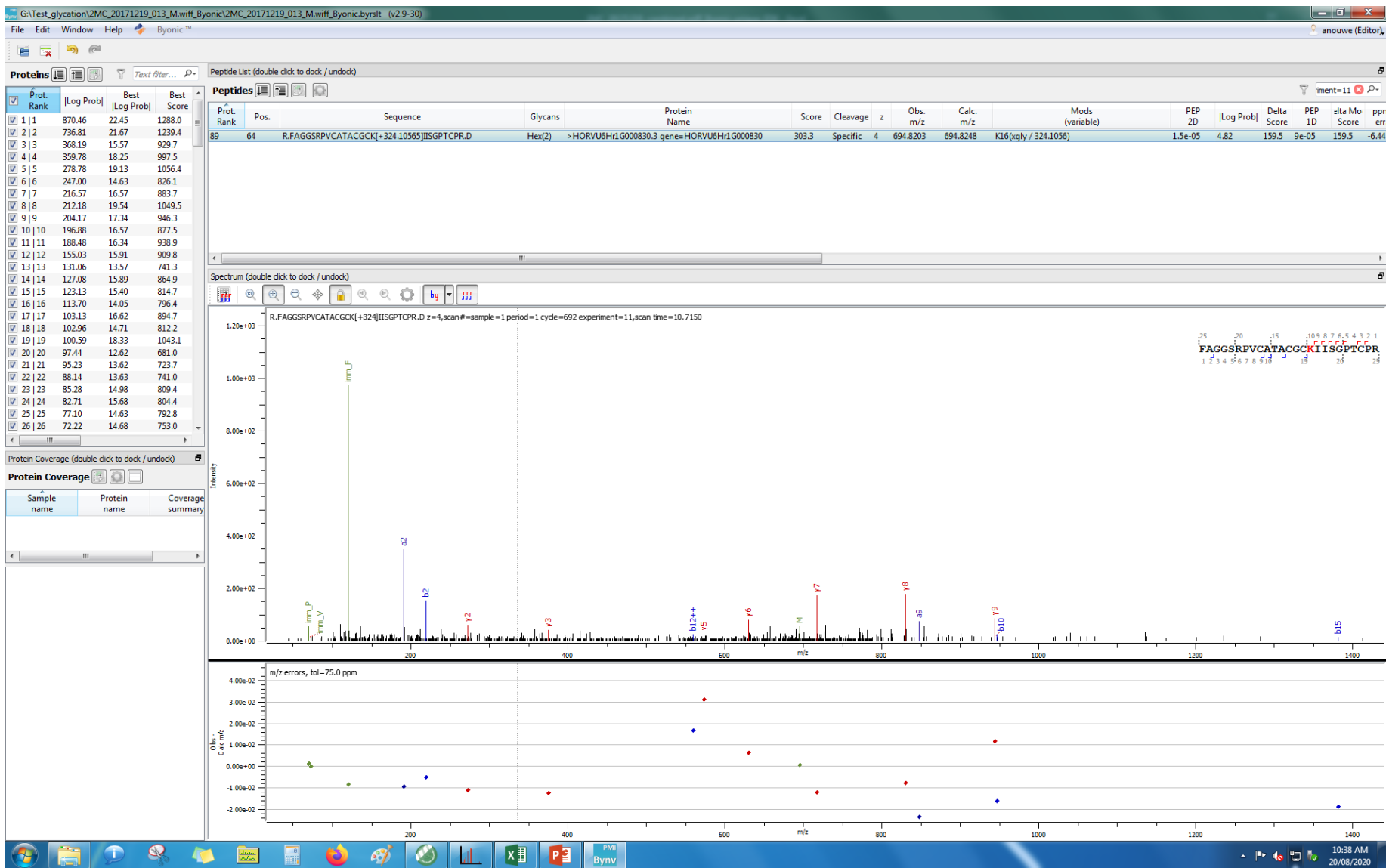
Prot. Rank	Pos.	Sequence	Glycans	Protein Name	Score	Cleavage	z	Obs. m/z	Calc. m/z	Mods (variable)	PEP 2D	[Log Prob]	Delta Score	PEP 1D	elta Mo Score	ppm err.
11	55	R.ALVK[+162.05282]LECVGNRPEDVLR.D	Hex(1)	> HORVU6Hr1G001150.1 gene=HORVU6Hr1G001150	358.4	Specific	4	543.7992	543.7978	K4(xgly / 162.0528)	8.7e-06	5.06	290.3	5.2e-05	290.3	2.69

Spectrum (double click to dock / undock)

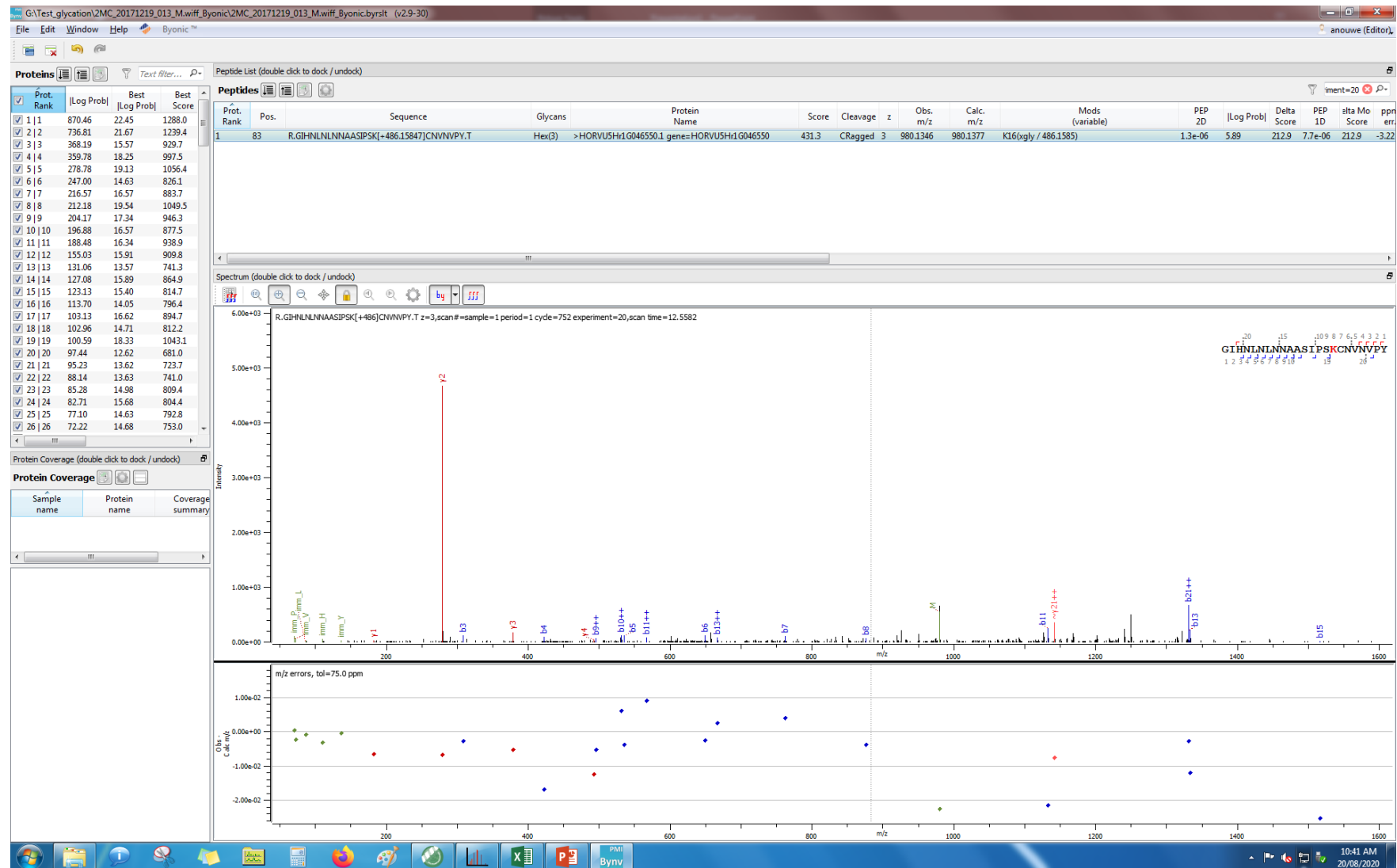












Proteins Text filter...

Peptide List (double click to dock / undock)

Prot. Rank	[Log Prob]	Best [Log Prob]	Best Score
1 1	870.46	22.45	1288.0
2 2	736.81	21.67	1239.4
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4 4	359.78	18.25	997.5
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Peptides

Prot. Rank	Pos.	Sequence	Glycans	Protein Name	Score	Cleavage	z	Obs. m/z	Calc. m/z	Mods (variable)	PEP 2D	[Log Prob]	Delta Score	PEP 1D	Delta Mo Score	ppm err.
1	83	R.GIHNLNLNNAASIPSK[+648.21129]CNVNVVPY.T	Hex(4)	>HORVU5Hr1G046550.1 gene=HORVU5Hr1G046550	381.1	Cragged	3	1034.1435	1034.1553	K16(xgly / 648.2113)	3e-05	4.53	156.9	0.00017	156.9	-11.4

Spectrum (double click to dock / undock)

