

Proteins                                                            

File Edit Window Help  Byonic™

Proteins     Text filter... 

Peptide List (double click to dock / undock)

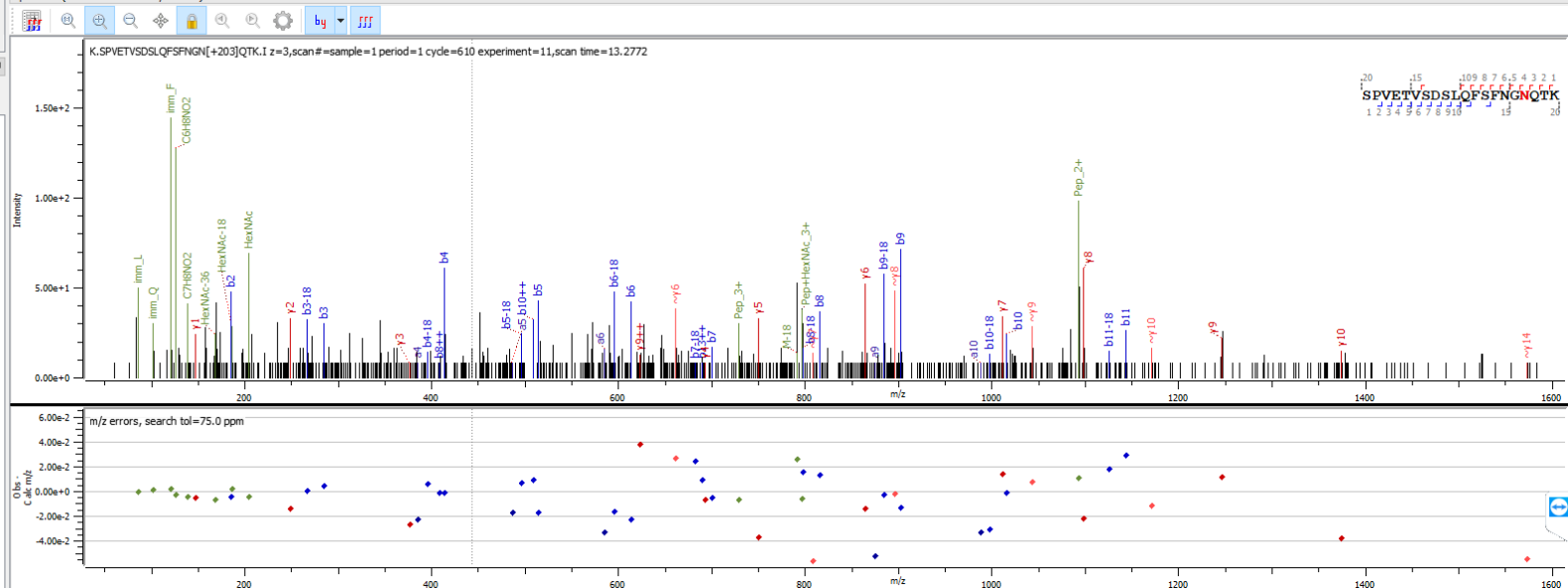
	Prot. Rank	
☒	1	>sp K2C1_HUMAN Common contaminant p
☒	11	>sp TRYP_PLG Common contaminant pro
☒	212	>VD055W PST1 SGID:S000002462, Chr IV fr
☒	313	>sp K1C8_HUMAN Common contaminant p
☒	414	>YGR209C TRX2 SGID:S000003441, Chr VII fr
☒	515	>YBR162C TOS1 SGID:S000000366, Chr I fr
☒	616	>YMR307W GAS1 SGID:S000004924, Chr XIII
☒	717	>YL0154W ZPS1 SGID:S000005514, Chr XV fr
☒	818	>YLN160 WGP1 SGID:S0000005104, Chr XIV
☒	919	>YOL303W GASS5 SGID:S000005390, Chr XV f
☒	1010	>sp K1C8_HUMAN Common contaminant p
☒	1111	>YLR043C TRX1 SGID:S000004093, Chr XII fr
☒	1212	>YBR078W ECM33 SGID:S000000282, Chr IX f
☒	1313	>YLI169C YL169C SGID:S000001431, Chr IX f
☒	1414	>sp K2E2_HUMAN Common contaminant p
☒	1515	>YKR042W UTH1 SGID:S000001750, Chr XI fr
☒	1616	>GR037C ACB1 SGID:S000003269, Chr VII fr
☒	1717	>YKL163W PIR3 SGID:S000001646, Chr XI fr
☒	1818	>YGR282C BGL2 SGID:S000003514, Chr VII fr
☒	1919	

Protein Coverage (double click to dock / undock)

Protein Coverage

Peptides																				ment=11
PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	g Pro	Delta Score	alta Mo	z	Obs. m/z	Calc. m/z	ppm err.	Off-Bs-Y	Obs. MH	Calc. MH	Cleavage	Glycan Pos.
11256967	3	180	K.SPVETVSDSLQFSFGNGI+203.07937...	N17(NGlycan / 203.0794)	605.8	HexNAc(1)	7.3e-12	2.7e-9	11.14	321.5	321.5	3	796.7174	796.7176	7.33	2388.1376	2388.1201		Specific	17

Spectrum (double click to dock / undock)



Proteins Text filter...

Prot. Rank	Protein
1 1	>sp K2C1_HUMAN (Common contaminant p
2 2	>sp TRYF_PIG (Common contaminant protei
3 3	>YDR055W PST1 SGDID:S000002462, Chr IV fr
4 4	>sp K1C10_HUMAN (Common contaminant
5 5	>YGR209C TRX2 SGDID:S000003441, Chr VII fr
6 6	>YBR162C TOS1 SGDID:S000000366, Chr II fro
7 7	>YMR307W GAS1 SGDID:S000004924, Chr XIII
8 8	>YOL154W ZPS1 SGDID:S000005514, Chr XV fi
9 9	>YNL160W YGP1 SGDID:S000005104, Chr XIV
10 10	>YOL030W GAS5 SGDID:S000005390, Chr XV f
11 11	>sp K1C9_HUMAN (Common contaminant p
12 12	>YLR043C TRX1 SGDID:S000004033, Chr XII fr
13 13	>YBR078W ECM33 SGDID:S000000282, Chr II f
14 14	>YIL169C YIL169C SGDID:S000001431, Chr IX f
15 15	>sp K22E_HUMAN (Common contaminant p
16 16	>YKR042W UTH1 SGDID:S000001750, Chr XI fr
17 17	>YGR037C ACB1 SGDID:S000003269, Chr VII fr
18 18	>YKL163W PIR3 SGDID:S000001646, Chr XI fro
19 19	>YGR282C BGL2 SGDID:S000003514, Chr VII fr

Protein Coverage (double click to dock / undock)

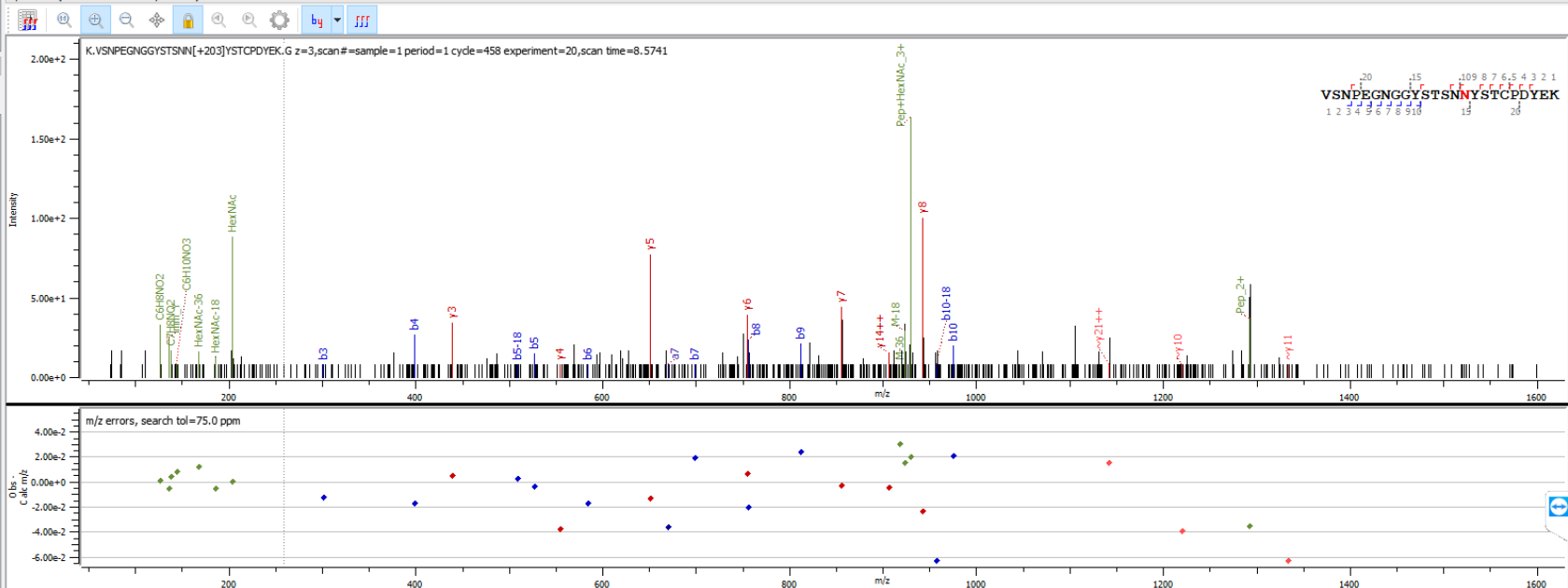
Protein Coverage

Peptide List (double click to dock / undock)

Peptides iment=20

PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	sg Pro	Delta Score	alta Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glycan Pos.
1 283534	10	330	K.VSNPEGNGGYSTSN[+203.07937]...	N15(NGlycan / 203.0794)	456.3	HexNAc(1)	3.3e-8	1.2e-5	7.49	313.1	313.1	3	929.4246	929.3838	43.84		2786.2591	2786.1370	Specific	15

Spectrum (double click to dock / undock)



Proteins

Text filter...

Prot. Rank	
1 1	>sp K2C1_HUMAN (Common contaminant p
2 2	>sp TRYP_PIG (Common contaminant protei
3 3	>YDR055W PST1 SGDID:S000002462, Chr IV fr
4 4	>sp K1C10_HUMAN (Common contaminant
5 5	>YGR209C TRX2 SGDID:S000003441, Chr VII fr
6 6	>YBR162C TOS1 SGDID:S000000366, Chr II fro
7 7	>YMR307W GAS1 SGDID:S000004924, Chr XIII
8 8	>YOL154W ZPS1 SGDID:S000005514, Chr XV f
9 9	>YNL160W YGP1 SGDID:S000005104, Chr XIV
10 10	>YOL030W GAS5 SGDID:S000005390, Chr XV f
11 11	>sp K1C9_HUMAN (Common contaminant p
12 12	>YLR043C TRX1 SGDID:S000004033, Chr XII fr
13 13	>YBR078W ECM33 SGDID:S000000282, Chr II f
14 14	>YIL169C YIL169C SGDID:S000001431, Chr IX f
15 15	>sp K22E_HUMAN (Common contaminant p
16 16	>YKR042W UTH1 SGDID:S000001750, Chr XI fr
17 17	>YGR037C ACB1 SGDID:S000003269, Chr VII fr
18 18	>YKL163W PIR3 SGDID:S000001646, Chr XI fro
19 19	>YGR282C BGL2 SGDID:S000003514, Chr VII fr

Protein Coverage (double click to dock / undock)

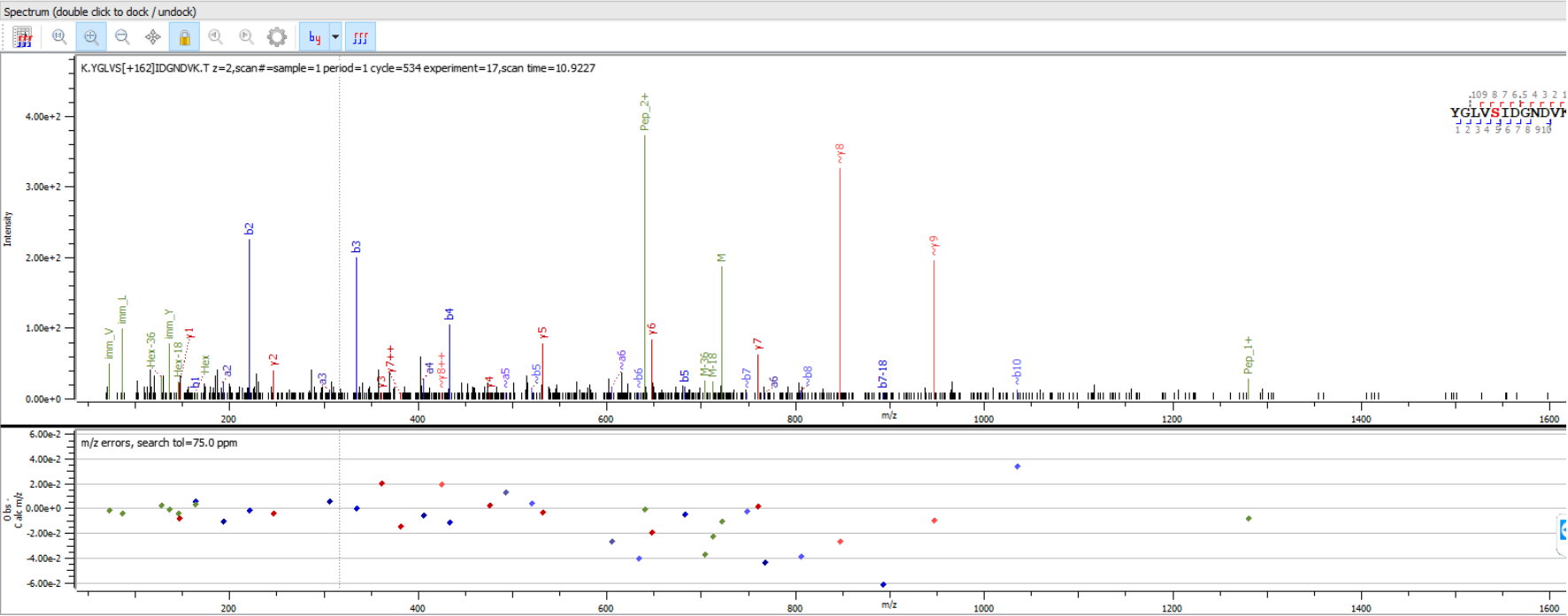
Protein Coverage

Peptides

Peptide List (double click to dock / undock)

iment=17

PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	og Pro	Delta Score	elta Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glyc Pc
1 105051	7	303	K.YGLV[S(+162.05282)]IDGNDVK.T	S5(OGlycan / 162.0528)	504.6	Hex(1)	5.7e-9	2.1e-6	8.24	249.0	249.0	2	721.3447	721.3565	-16.25		1441.6822	1441.7057	Specific	5



Proteins (double click to dock / undock)

Prot. Rank	Protein
1	>sp K2C1_HUMAN (Common contaminant p
2	>sp TRYF_PIG (Common contaminant protei
3	>YDR055W PST1 SGDID:S000002462, Chr IV fr
4	>sp K1C10_HUMAN (Common contaminant
5	>YGR209C TRX2 SGDID:S000003441, Chr VII fr
6	>YBR162C TOS1 SGDID:S000000366, Chr II fro
7	>YMR307W GAS1 SGDID:S000004924, Chr XIII
8	>YOL154W ZPS1 SGDID:S000005514, Chr XV fr
9	>YNL160W YGP1 SGDID:S000005104, Chr XIV
10	>YOL030W GAS5 SGDID:S000005390, Chr XV f
11	>sp K1C9_HUMAN (Common contaminant p
12	>YLR043C TRX1 SGDID:S000004033, Chr XII fr
13	>YBR078W ECM33 SGDID:S000000282, Chr II f
14	>YIL169C YIL169C SGDID:S000001431, Chr IX f
15	>sp K22E_HUMAN (Common contaminant p
16	>YKR042W UTH1 SGDID:S000001750, Chr XI fr
17	>YGR037C ACB1 SGDID:S000003269, Chr VII fr
18	>YKL163W PIR3 SGDID:S000001646, Chr XI fro
19	>YGR282C BGL2 SGDID:S000003514, Chr VII fr

Protein Coverage (double click to dock / undock)

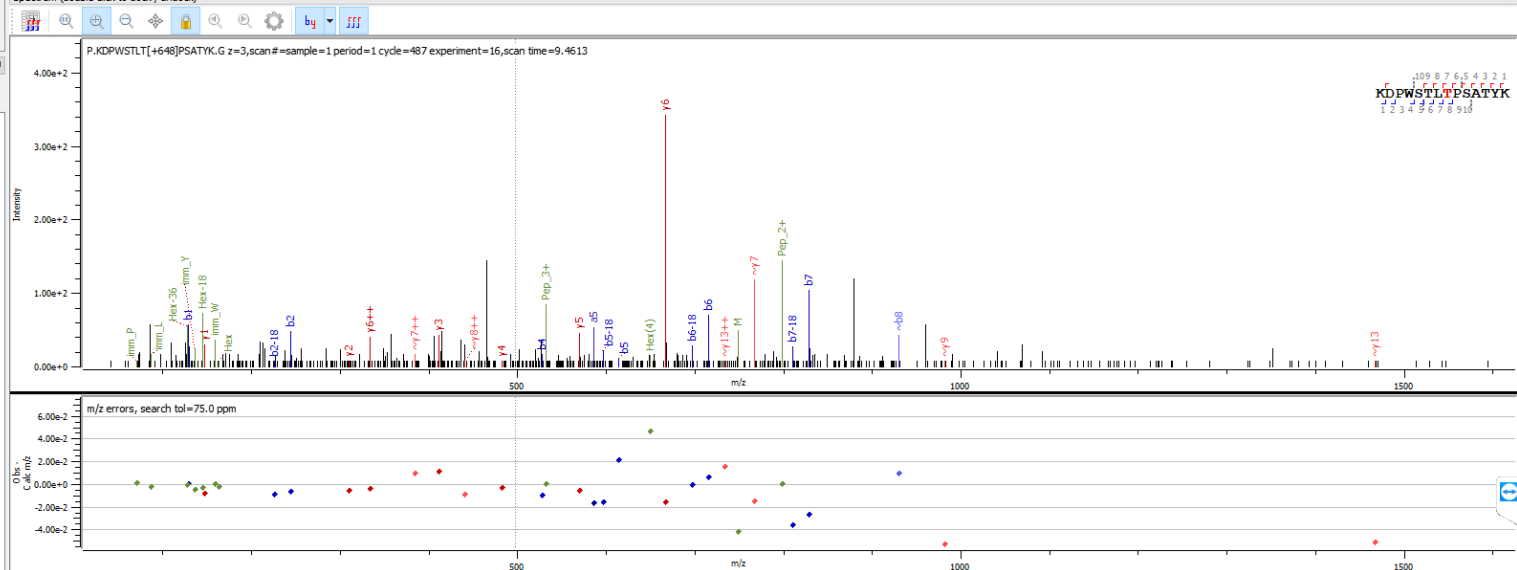
Protein Coverage

Peptide List (double click to dock / undock)

Peptides

PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	log Pro	Delta Score	Delta Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glycan Pos.
1 244722	18	23	P.KDPWSTLT[+648.21129]PSATYK.G	T8(OGlycan / 648.2113)	474.1	Hex(4)	1.1e-9	4.3e-7	8.95	268.9	0.0	3	748.3393	748.3457	-8.48		2243.0034	2243.0224	NRagged	8

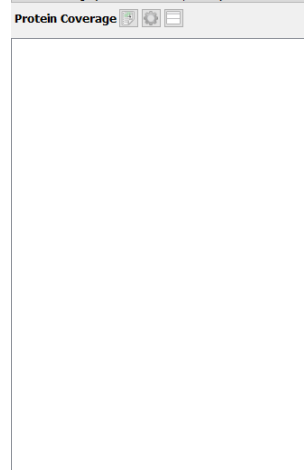
Spectrum (double click to dock / undock)



Proteins

Prot. Rank	Protein
1	>sp K2C1_HUMAN (Common contaminant p
2	>sp TRYF_PIG (Common contaminant protei
3	>YDR055W PST1 SGDID:S000002462, Chr IV fr
4	>sp K1C10_HUMAN (Common contaminant
5	>YGR209C TRX2 SGDID:S000003441, Chr VII fr
6	>YBR162C TOS1 SGDID:S000000366, Chr II fro
7	>YMR307W GAS1 SGDID:S000004924, Chr XIII
8	>YOL154W ZPS1 SGDID:S000005514, Chr XV fr
9	>YNL160W YGP1 SGDID:S000005104, Chr XIV
10	>YOL030W GAS5 SGDID:S000005390, Chr XV f
11	>sp K1C9_HUMAN (Common contaminant p
12	>YLR043C TRX1 SGDID:S000004033, Chr XII fr
13	>YBR078W ECM33 SGDID:S000000282, Chr II f
14	>YIL169C YIL169C SGDID:S000001431, Chr IX f
15	>sp K22E_HUMAN (Common contaminant p
16	>YKR042W UTH1 SGDID:S000001750, Chr XI fr
17	>YGR037C ACB1 SGDID:S000003269, Chr VII fr
18	>YKL163W PIR3 SGDID:S000001646, Chr XI fro
19	>YGR282C BGL2 SGDID:S000003514, Chr VII fr

Protein Coverage

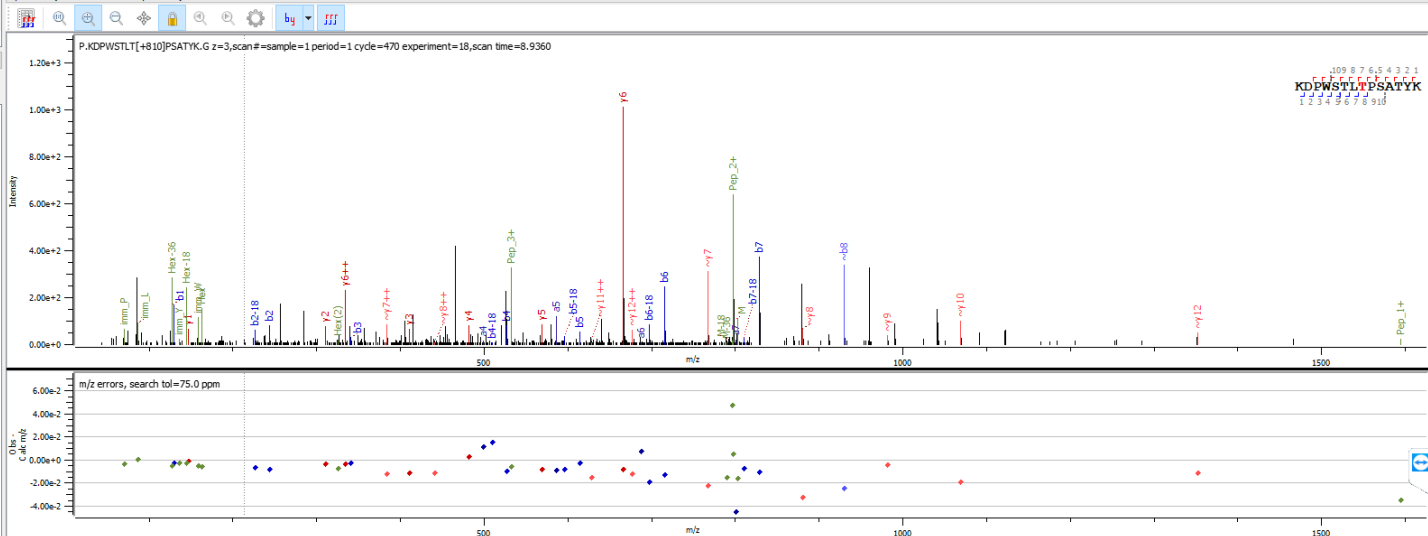


Peptide List (double click to dock / undock)

PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	pg Pro	Delta Score	delta Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glycan Pos.
1	243204	18	23	P.KDPWSTLT[+810.26412]PSATYK.G	T8(OGlycan / 810.2641)	553.8	Hex(5)	1.1e-10	4.2e-8	9.96	347.1	0.0	3	802.3733	802.3633	12.51	2405.1053	2405.0752	NRagged	8

PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	pg Pro	Delta Score	delta Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glycan Pos.
1	243204	18	23	P.KDPWSTLT[+810.26412]PSATYK.G	T8(OGlycan / 810.2641)	553.8	Hex(5)	1.1e-10	4.2e-8	9.96	347.1	0.0	3	802.3733	802.3633	12.51	2405.1053	2405.0752	NRagged	8

Spectrum (double click to dock / undock)



Prot. Rank	Protein
1	>sp K2C1_HUMAN Common contaminant p
2	>sp TRVP_PIG Common contaminant protei
3	>YDR055W PST1 SGDID:S000002462, Chr IV fr
4	>sp K1C10_HUMAN Common contaminant
5	>YGR209C TRX2 SGDID:S000003441, Chr VII fr
6	>YBR162C TOS1 SGDID:S000000366, Chr II fro
7	>YMR307W GAS1 SGDID:S000004924, Chr XIII
8	>YOL154W ZPS1 SGDID:S000005514, Chr XV fr
9	>YNL160W YGP1 SGDID:S000005104, Chr XV
10	>YOL030W GAS5 SGDID:S000005390, Chr XV f
11	>sp K1C3_HUMAN Common contaminant p
12	>YLR043C TRX1 SGDID:S000004033, Chr XII fr
13	>YBR078W ECM33 SGDID:S000002382, Chr II f
14	>YIL169C VIL169C SGDID:S000001431, Chr IX f
15	>sp K2E_HUMAN Common contaminant p
16	>YKR042W UTH1 SGDID:S000001750, Chr XI fr
17	>YGR037C ACB1 SGDID:S000003269, Chr VII fr
18	>YKL163W PIR3 SGDID:S000001646, Chr XI fro
19	>YGR282C BGL2 SGDID:S000003514, Chr VII fr

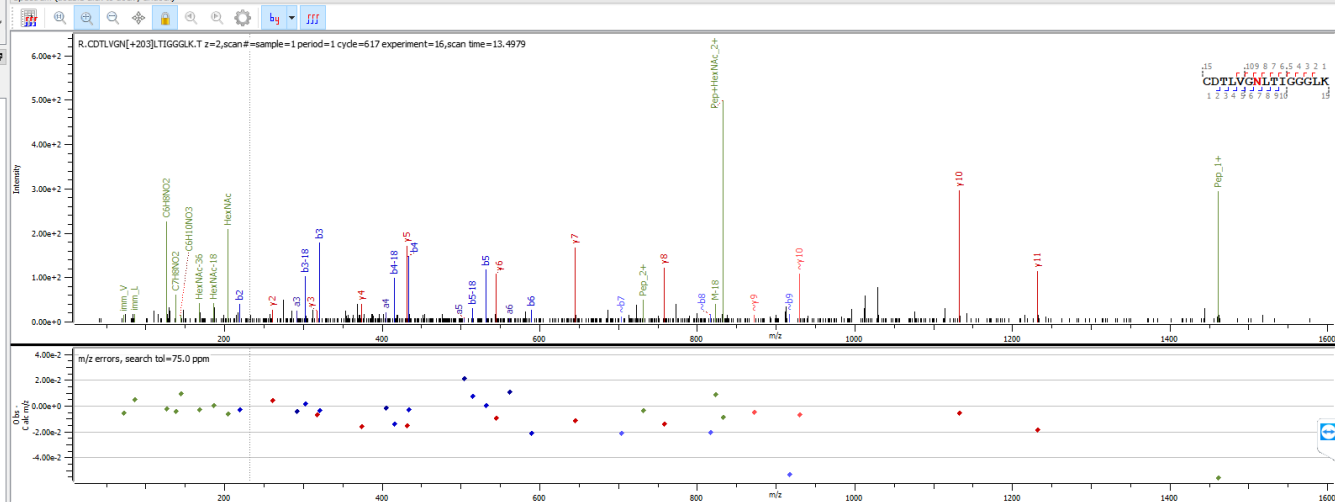
Protein Coverage (double click to dock / undock)

Protein Coverage

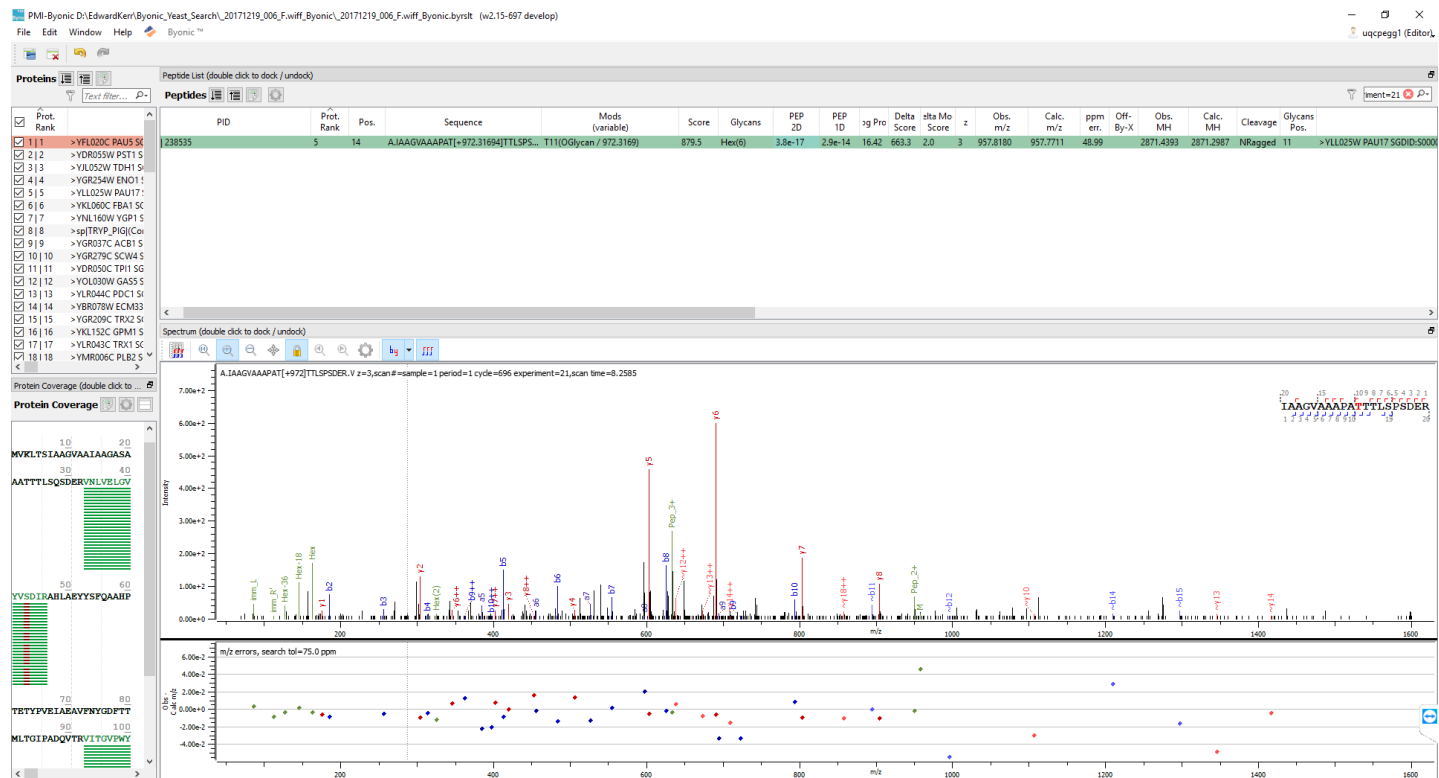
Peptide List (double click to dock / undock)

PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP ZD	PEP TD	sg Pro	Delta Score	alta Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glycan Pos.
1	211005	3	51	R.CDTLVGN[+203.07937]LTIGGGLK.T	N7(N)Glycan / 203.0794	611.7	HexNAc(1)	5.8e-13	2.2e-10	12.23	445.4	445.4	2	832.4493	832.4322	20.54	1663.8913	1663.8571	Specific	7

Spectrum (double click to dock / undock)



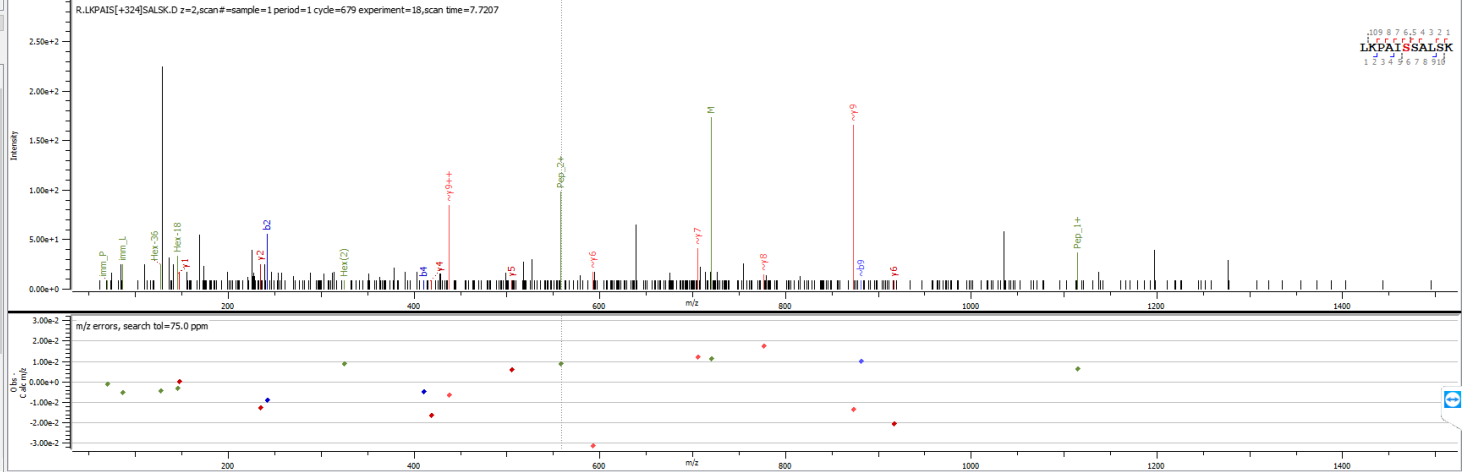
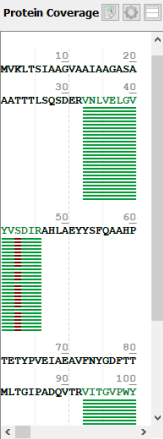




Proteins Peptide List (double click to dock / undock)

Prot. Rank	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	3g Pro	Delta Score	Delta Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glycans Pos.
1	1	28	102	R.LKPAIS[+324.10565]SALSK.D	S6(OGlycan / 324.1056)	315.3	Hex(2)	0.02	0.033	1.70	99.8	99.8	2	719.8912	719.8980	-9.41	1438.7751	1438.7887	Specific	6

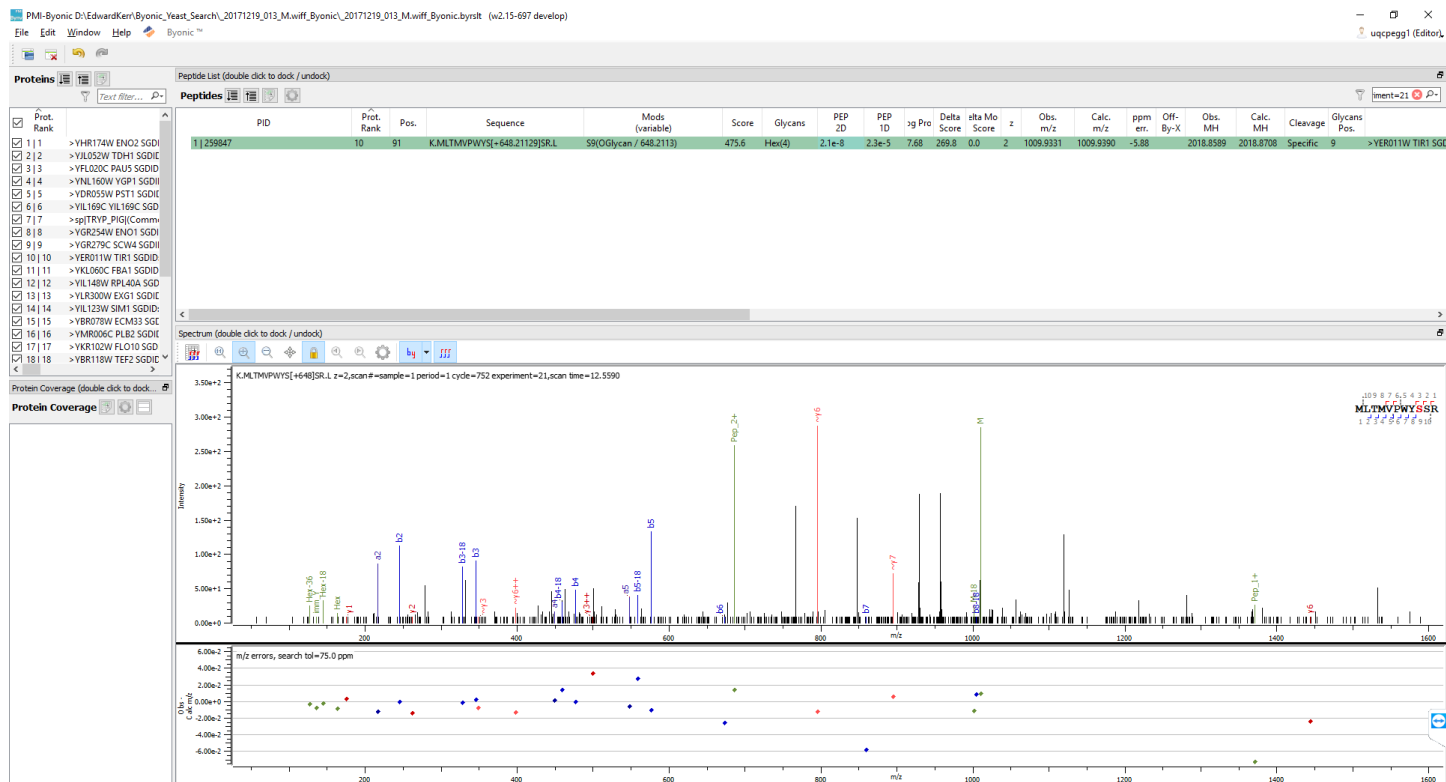
Protein Coverage (double click to ...)













The screenshot displays the Proteomic Data Analysis (PDA) software interface, which is used for analyzing proteomic data. The interface is divided into several panels:

- Top Panel:** Contains a menu bar (File, Edit, Window, Help) and a toolbar with icons for file operations and analysis.
- Protein List:** A table listing identified proteins. The first column shows checkboxes, the second shows protein names and accession numbers (e.g., >YNR041W PAU15 SGDID:5000001480, Chr IX from 48), and the third shows protein ranks.
- Peptide List:** A table listing identified peptides. The first column shows checkboxes, the second shows peptide names and accession numbers (e.g., K.DGYIT[+324E]IAN-), the third shows peptide ranks, and the fourth shows peptide sequences.
- Protein Coverage:** A bar chart showing the coverage of each protein. The x-axis represents the protein name and the y-axis represents the coverage percentage.
- Spectrum:** A mass spectrum plot showing relative intensity versus m/z. The x-axis ranges from 0 to 1500 m/z, and the y-axis ranges from 0.00e+0 to 8.00e+2. The spectrum shows several peaks, with the most prominent one at m/z 116.
- m/z errors:** A scatter plot showing the m/z errors for the identified peptides. The x-axis represents m/z, and the y-axis represents the m/z error (m/z error, search tol=75.0 ppm).

[illegible]











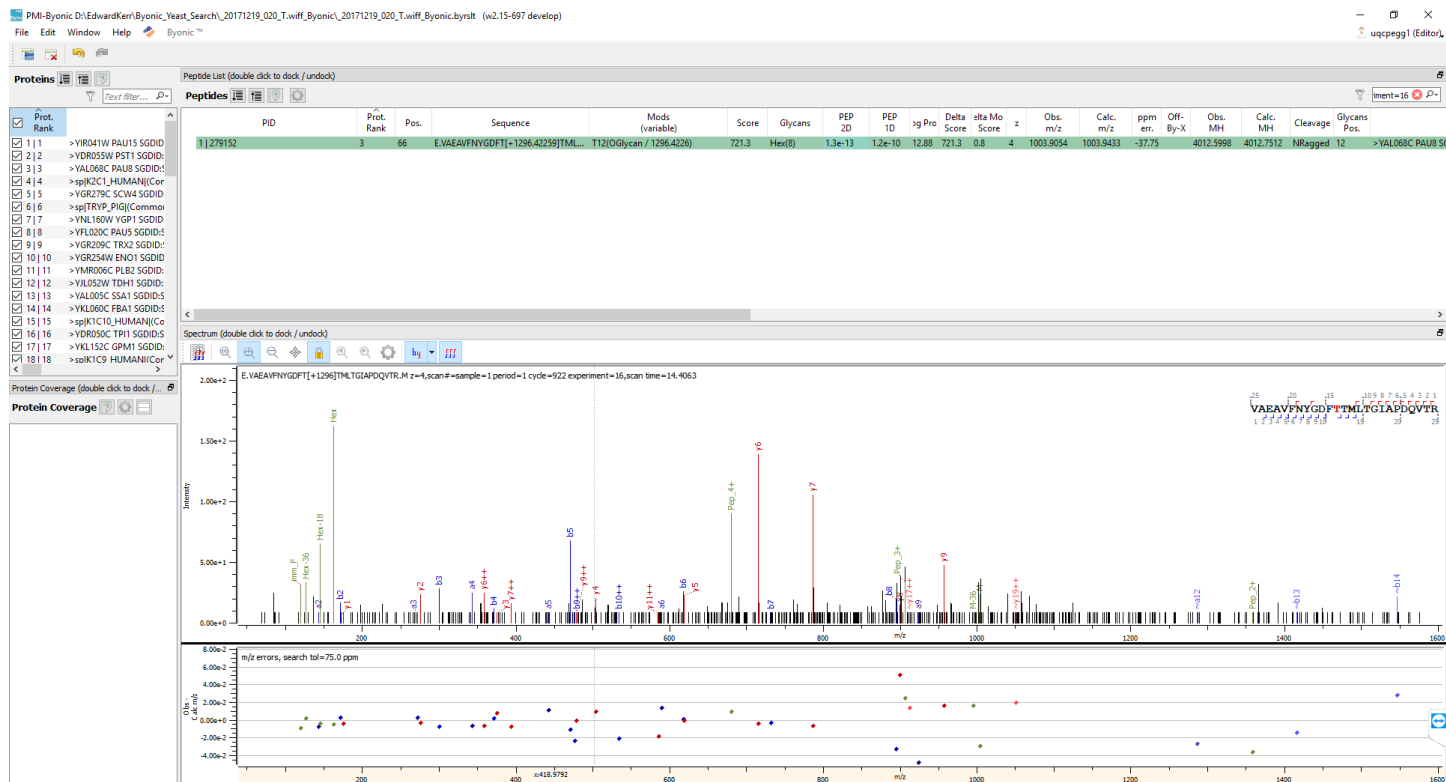


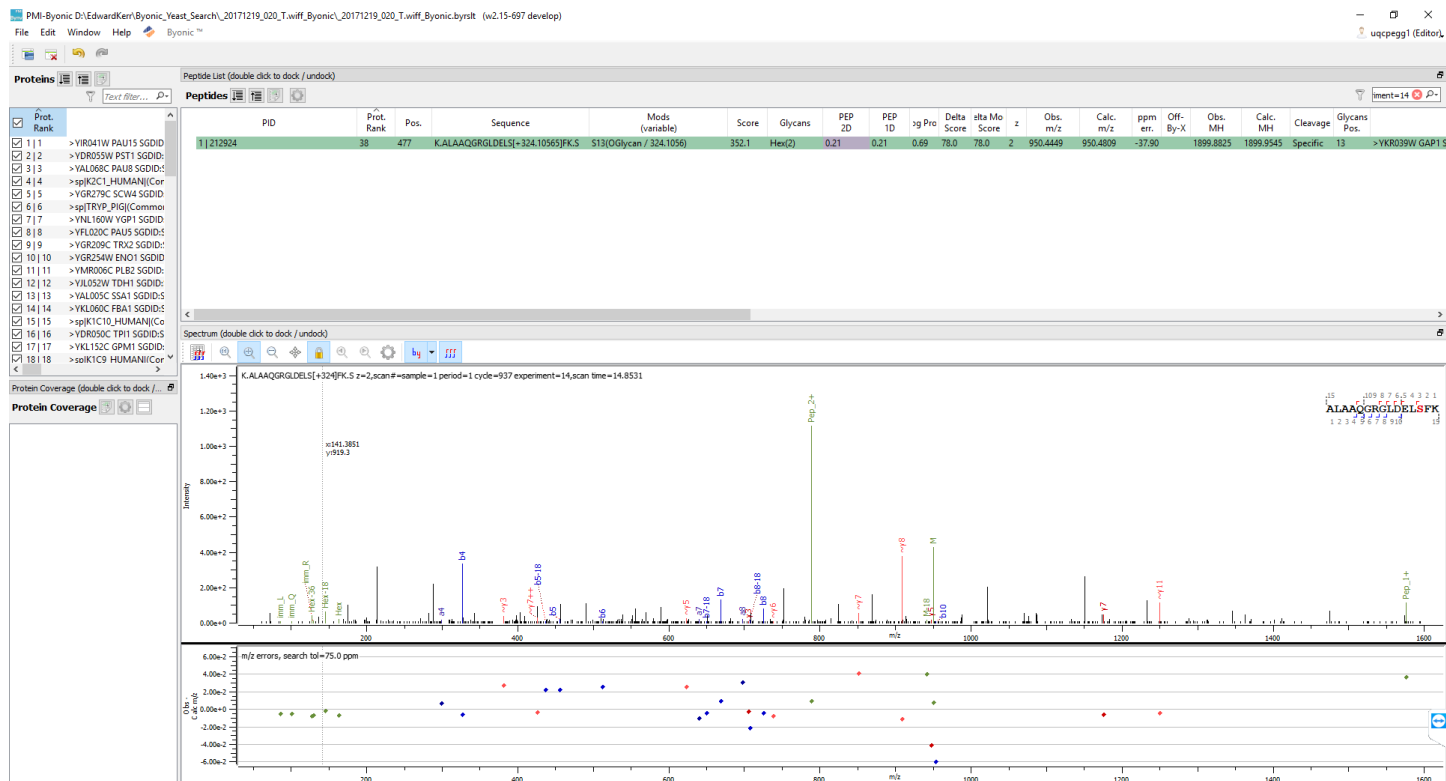




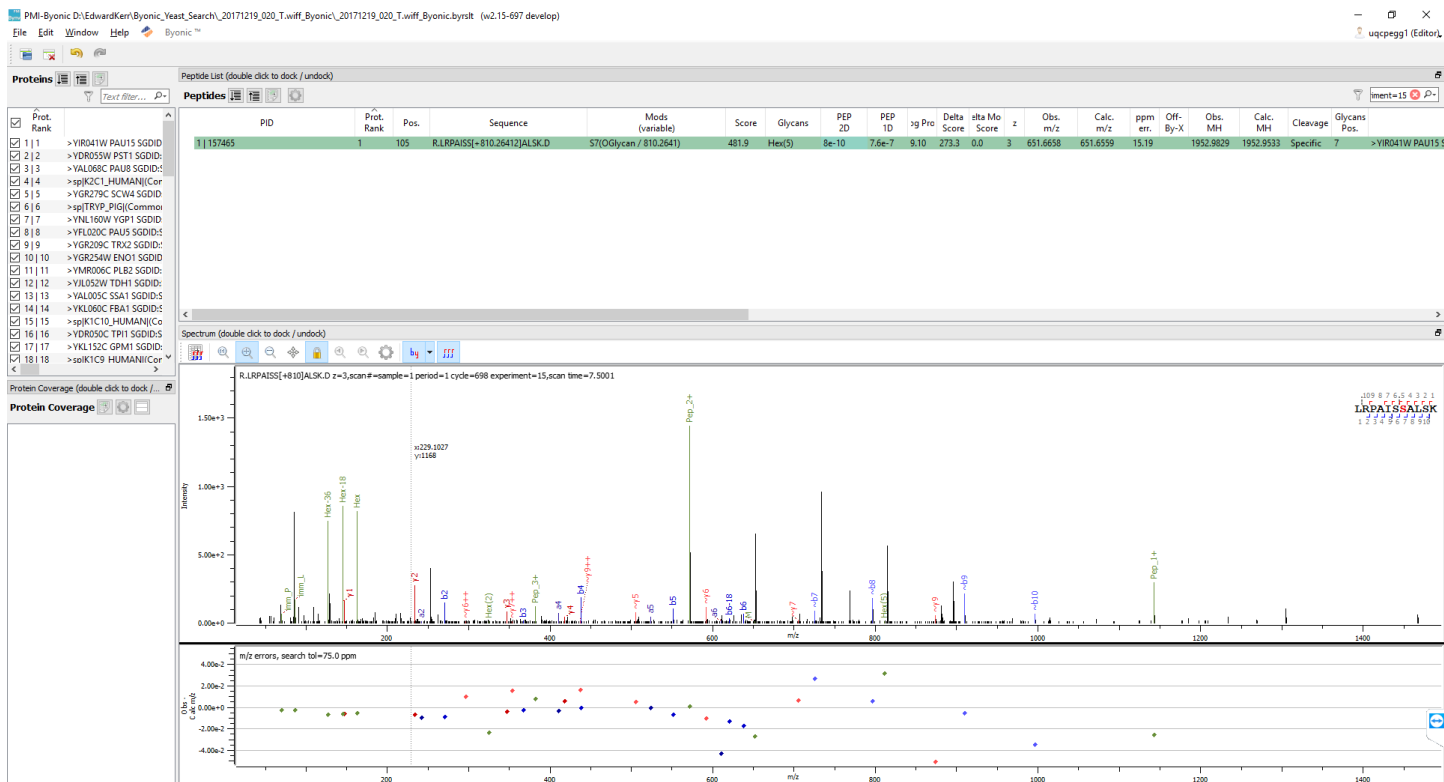








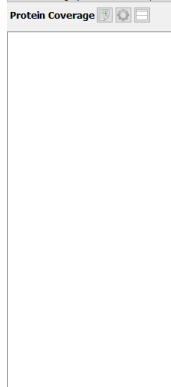




Proteins

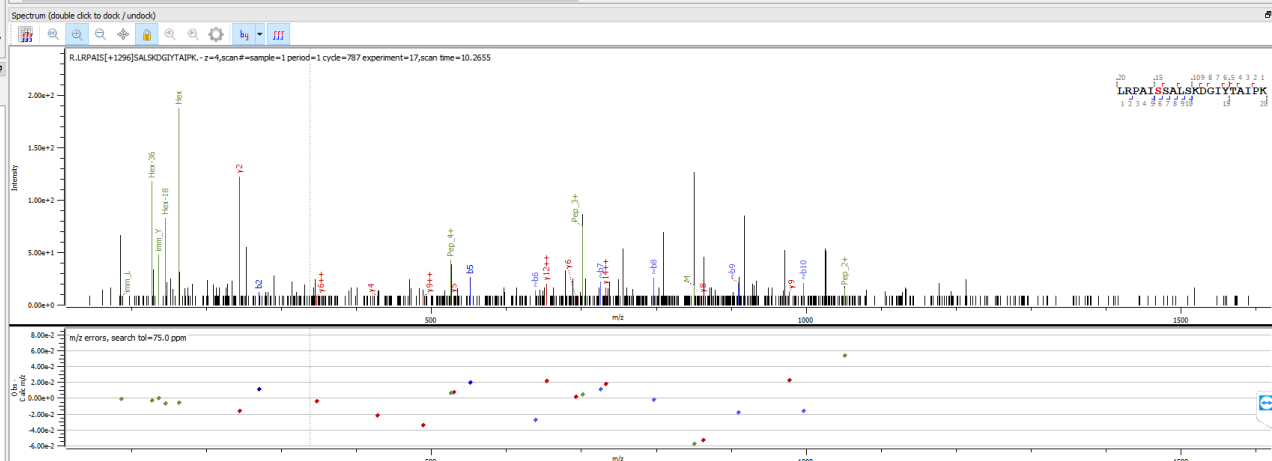
Prot. Rank	Protein
1	>YIR041W PAU15 SGDI
2	>YDR055W PST1 SGDI
3	>YAL068C PAU8 SGDI
4	>sp K2C1_HUMAN Cor
5	>YGR279C SCW4 SGDI
6	>sp TRYP_PIG Commo
7	>YNL160W VGP1 SGDI
8	>YKL202C PAU5 SGDI
9	>YGR209C TRX2 SGDI
10	>YGR254W ENO1 SGDI
11	>YMR006C PLB2 SGDI
12	>YIL052W TDH1 SGDI
13	>YAL055C SSA1 SGDI
14	>YKL060C FBA1 SGDI
15	>sp K1C10_HUMAN Co
16	>YDR050C TP11 SGDI
17	>YKL152C GPM1 SGDI
18	>so K1C9_HUMAN Co

Protein Coverage



Peptide List

PID	Prot. Rank	Pos.	Sequence	Mods (variable)	Score	Glycans	PEP 2D	PEP 1D	sg Pro	Delta Score	Delta Mo Score	z	Obs. m/z	Calc. m/z	ppm err.	Off-By-X	Obs. MH	Calc. MH	Cleavage	Glycans Pos.
1	1	105	R.LRPAIS(+1296.42259)SALSKDGIYTA...	56(Oglycan / 1296.4226)	524.3	Hex(1)	4.7e-10	4.4e-7	9.33	307.8	2.0	4	850.1303	850.1615	-36.66		3397.4995	3397.6241	Specific	6



7:59 AM
4/10/2020

[illegible]

