

ProteinDeconvolution Report

Created: 25/02/2021 10:23:23

Sample Information

Original File Name	C:\Xcalibur\Data\20210225_AA_QF_QBCN.raw
Instrument Method	C:\Xcalibur\methods\Current Orbitrap Methods\Orbi_IntactFlowInjLR_01fast.meth
Vial	BD7
Injection Volume (µL)	1
Sample Weight	0
Sample Volume (µL)	0
ISTD Amount	0
Dil Factor	1

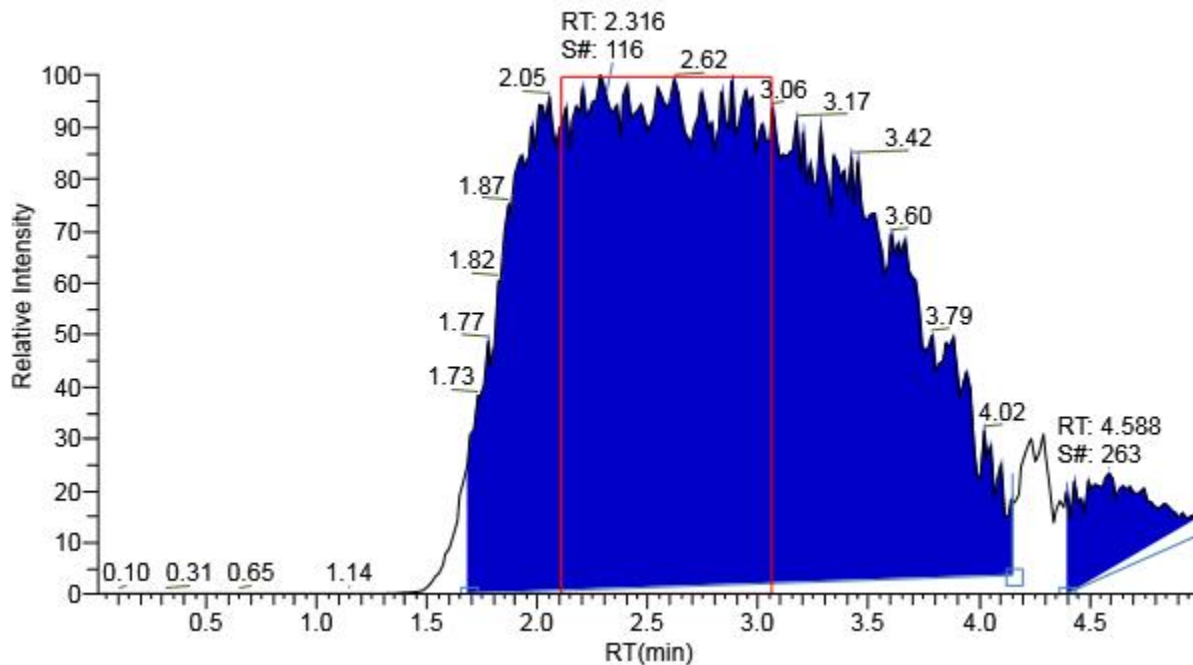
Chromatogram Parameters

Use restricted time.	False
Time Range	0.003 - 4.992 Minutes
Rel. Intensity Threshold (%)	1
Type	Unknown
Sensitivity	High
Chromatogram m/z Range	1000 - 2000
Use Auto Spectral Averaging	False

Source Chromatogram

20210225_AA_QF_QBCN ProteinDeconvolution NL: 4.92E7

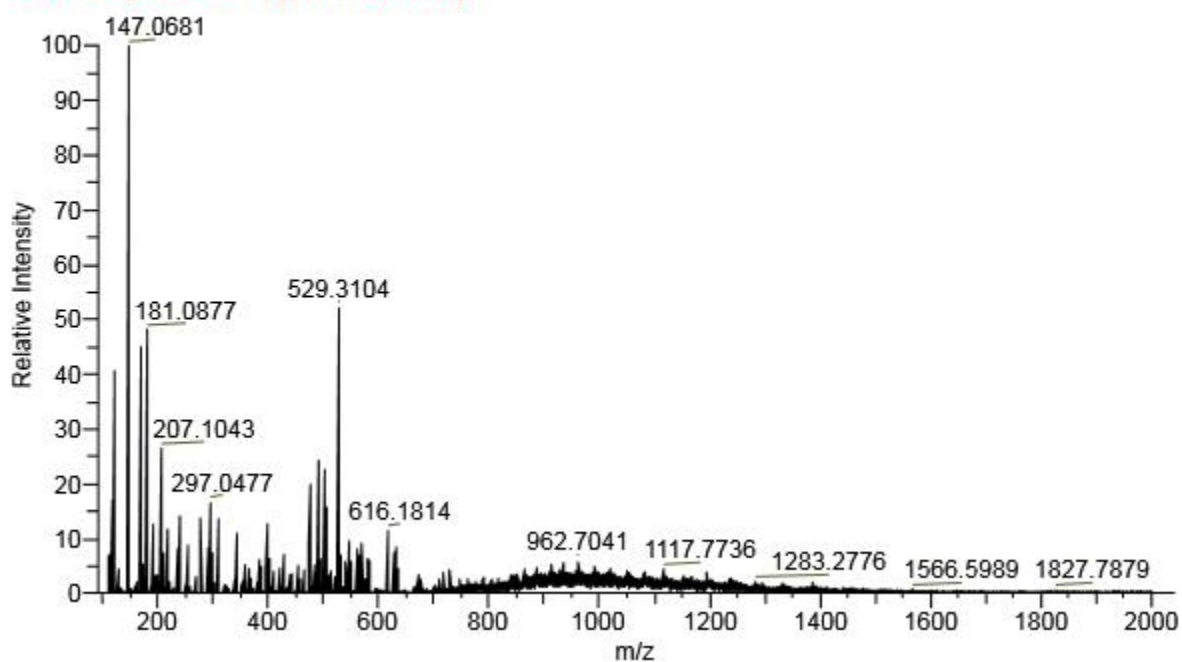
F:

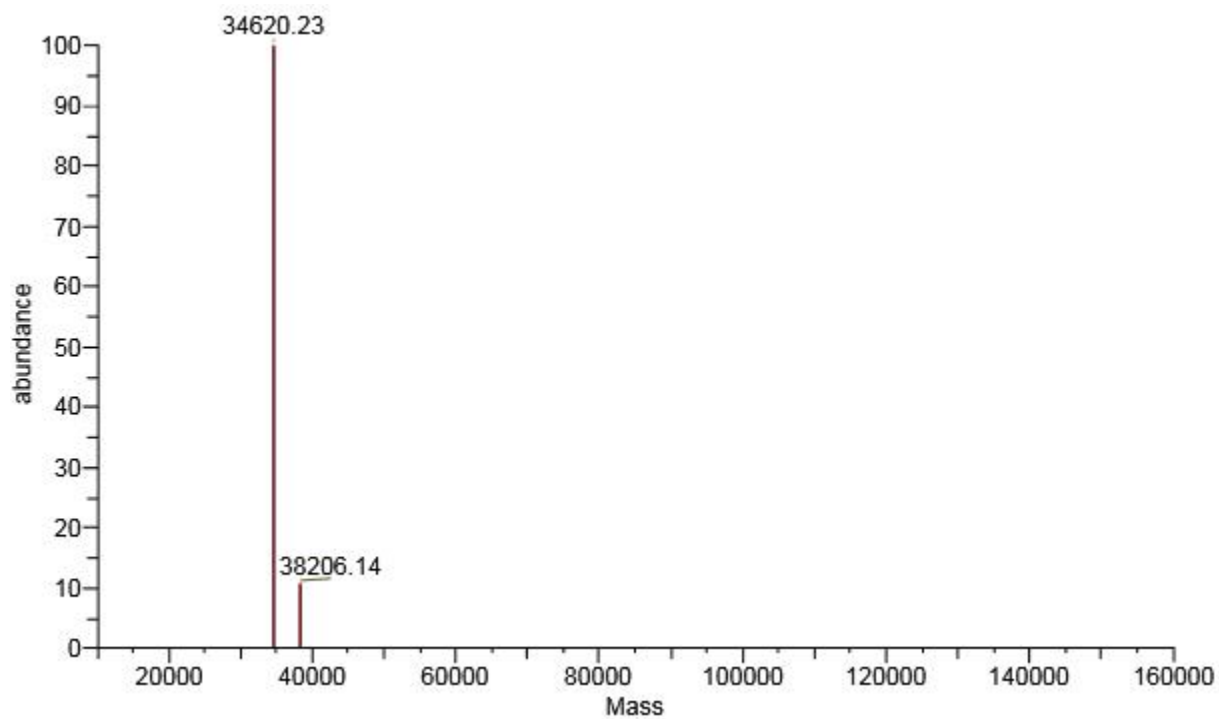


Main Parameters (ReSpect™)	
Negative Charge	False
Minimum Adjacent Charges	6 - 10
Noise Rejection	95% Confidence
Rel. Abundance Threshold (%)	0
Calculate XIC	True
Quality Score Threshold	0
m/z Range	750 - 2000
Output Mass Range	10000 - 160000
Mass Tolerance	20 ppm
Target Mass	15000 Da
Charge State Range	5 - 100
Choice of Peak Model	Intact Protein
Advanced Parameters (ReSpect™)	
Minimum Peak Significance	1
Use Relative Intensities	True
Peak Width	0
Feature Width	0
Degree of Fit	0
Number of Iterations	3
Noise Compensation	True
Charge Carrier	H+ (1.00727663)
Number of Peak Models	1
Resolution at 400 m/z	15000
Left/Right Peak Shape	2:2
Sliding Window Parameters	
Use Sliding Window	False
RT Range	0.003 - 4.992 Minutes
Target Avg Spectrum Width	0.1 Minutes
Target Avg Spectrum Offset (%)	50
Merge Tolerance	30 ppm
Max RT Gap	0.5 Minutes
Min Num of Detected Intervals	3

20210225_AA_QF_QBCN #103-165 RT:2.112-3.064 AV:63

F:FTMS + p NSI Full ms [110.00-2000.00]





ReSpect Masses Table										
Average Mass	Intensity	Number of Charge States	Mass Std Dev	PPM Std Dev	Delta Mass	Relative Abundance	Fractional Abundance	RT Range	Apex RT	Score
34620.23	4743088.00	18	1.14	32.90	0.00	100.0000	90.3578	2.112-3.064	2.542	98.8898
38206.14	506142.34	6	2.21	57.87	3585.91	10.6712	9.6422	2.112-3.064	2.250	34.2110