

ProteinDeconvolution Report

Created: 23/02/2021 11:38:11

Sample Information

Original File Name	C:\Xcalibur\Data\20210223_AA_QF_Q0.raw
Instrument Method	C:\Xcalibur\methods\Current Orbitrap Methods\Orbi_IntactFlowInjLR_01fast.meth
Vial	GE3
Injection Volume (µL)	1
Sample Weight	0
Sample Volume (µL)	0
ISTD Amount	0
Dil Factor	1

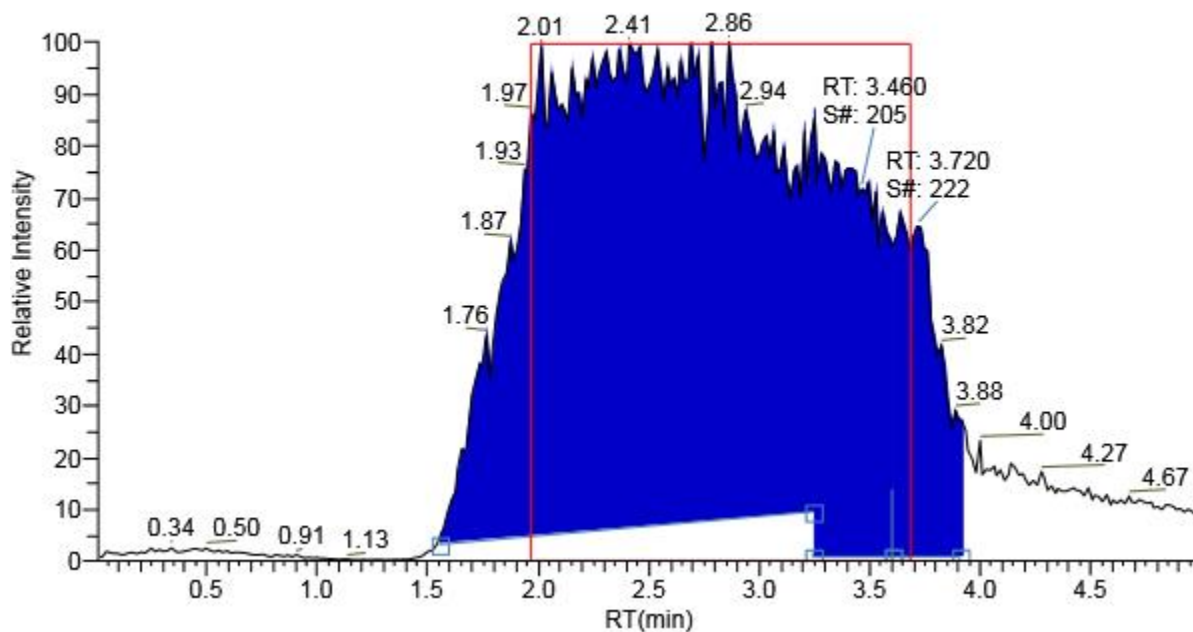
Chromatogram Parameters

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

20210223_AA_QF_Q0 ProteinDeconvolution NL: 3.03E7

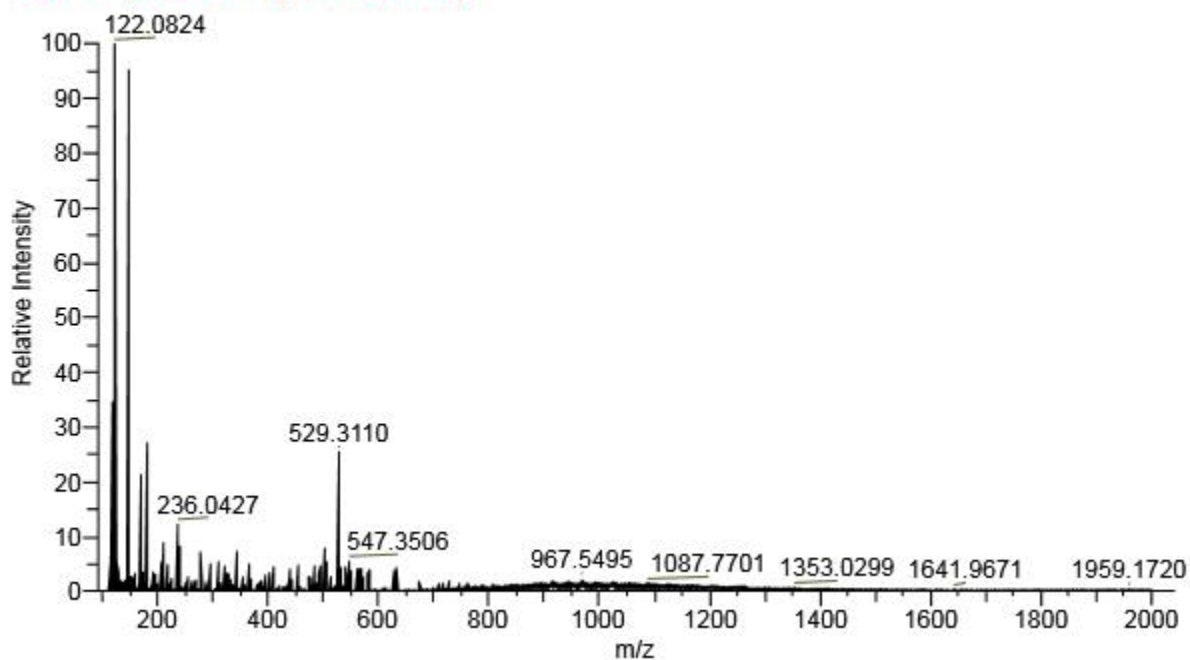
F:

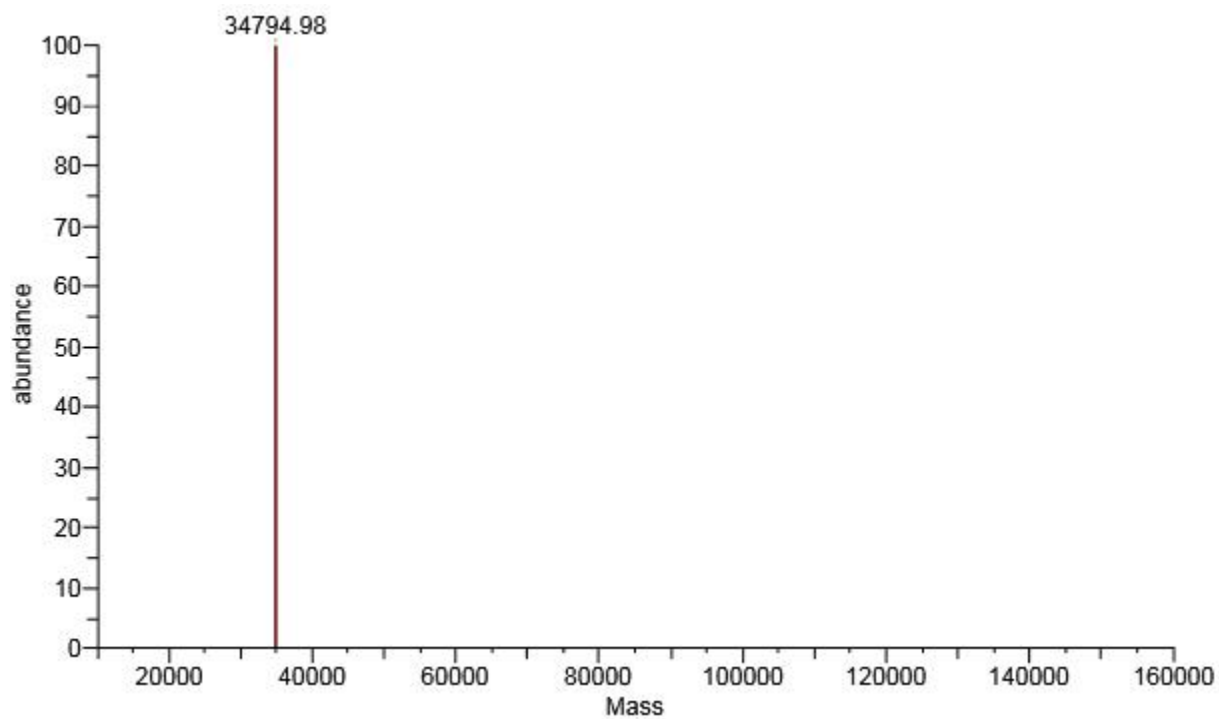


Main Parameters (ReSpect™)	
Negative Charge	False
Minimum Adjacent Charges	6 - 10
Noise Rejection	95% Confidence
Rel. Abundance Threshold (%)	0
Calculate XIC	True
Quality Score Threshold	0
m/z Range	750 - 2000
Output Mass Range	10000 - 160000
Mass Tolerance	20 ppm
Target Mass	15000 Da
Charge State Range	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

20210223_AA_QF_Q0 #108-219 RT:1.966-3.681 AV:112

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
34794.98	598352.25	7	0.94	27.01	0.00	100.0000	100.0000	1.966-3.681	2.567	44.7431