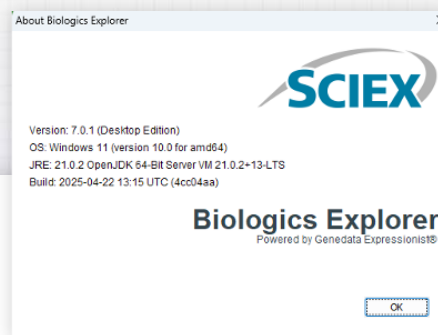
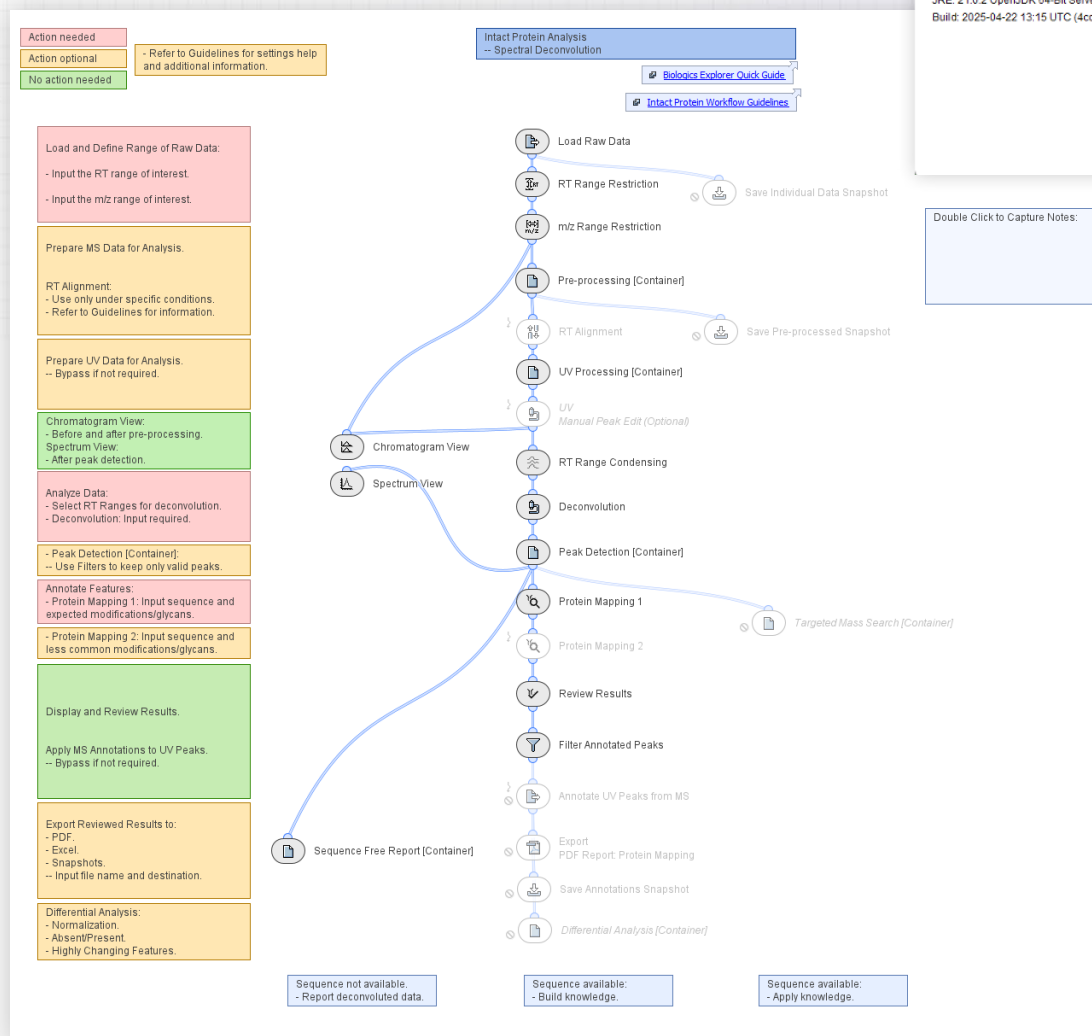



ZenoTOF 8600 system Intact data share

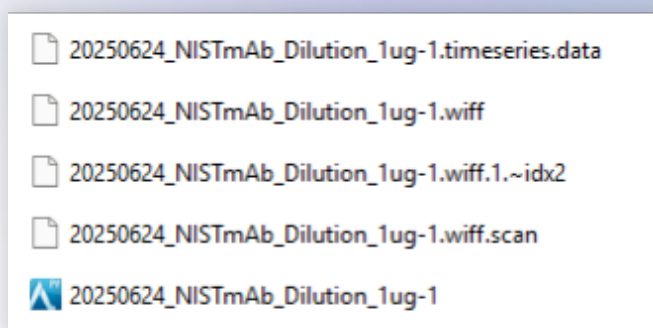
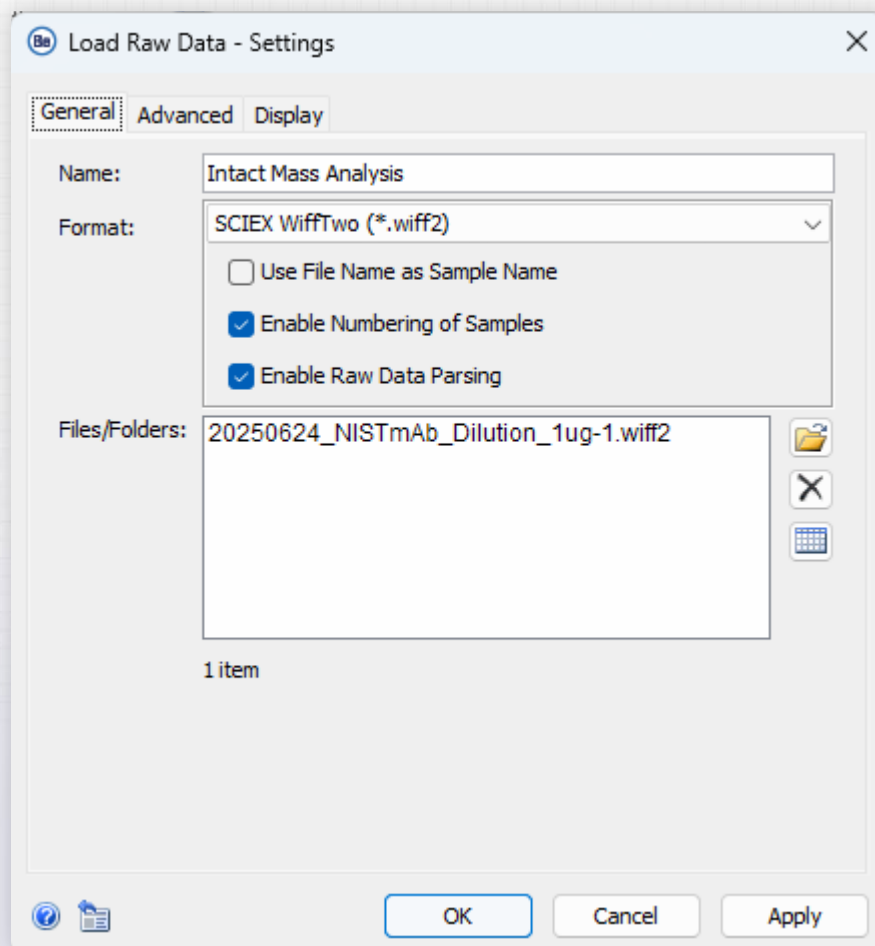
Biologics Explorer – intact spectral deconvolution template



Native MS Analysis

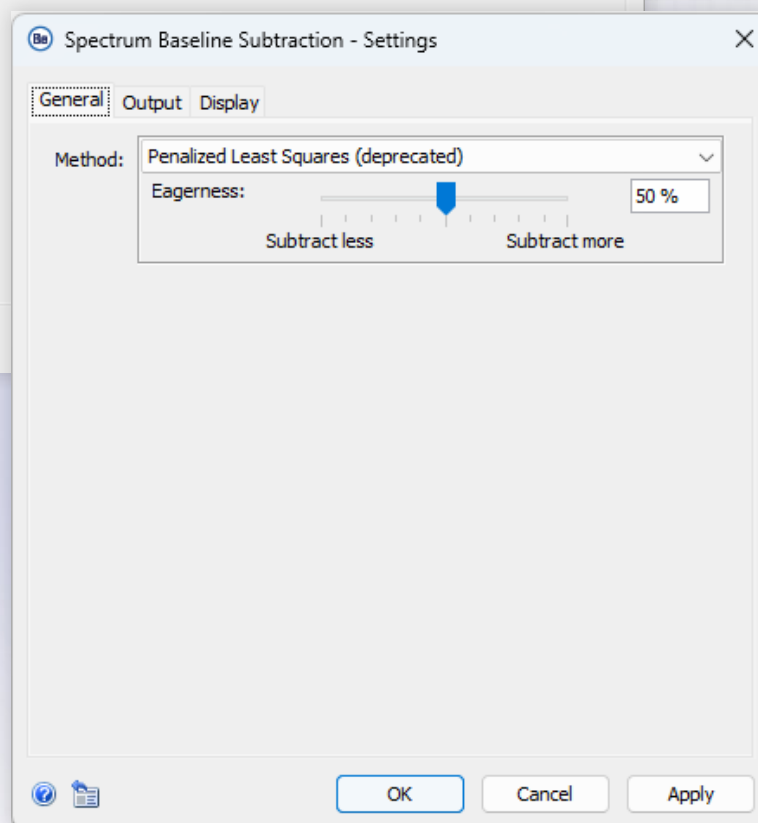
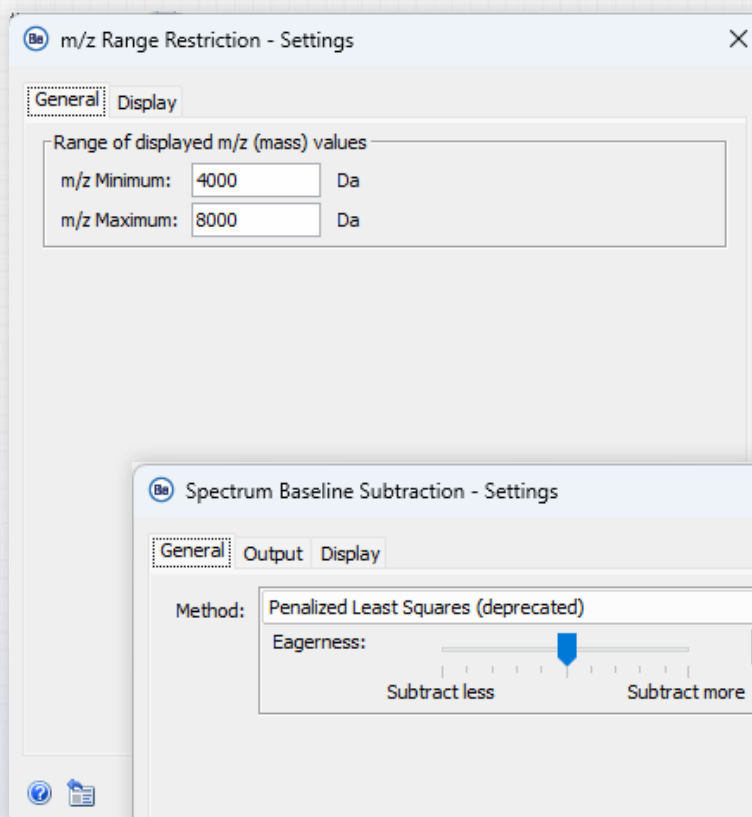
Data file

1. Double click on "Load Raw Data"
2. Click on  to select the .wiff2 data file from your output



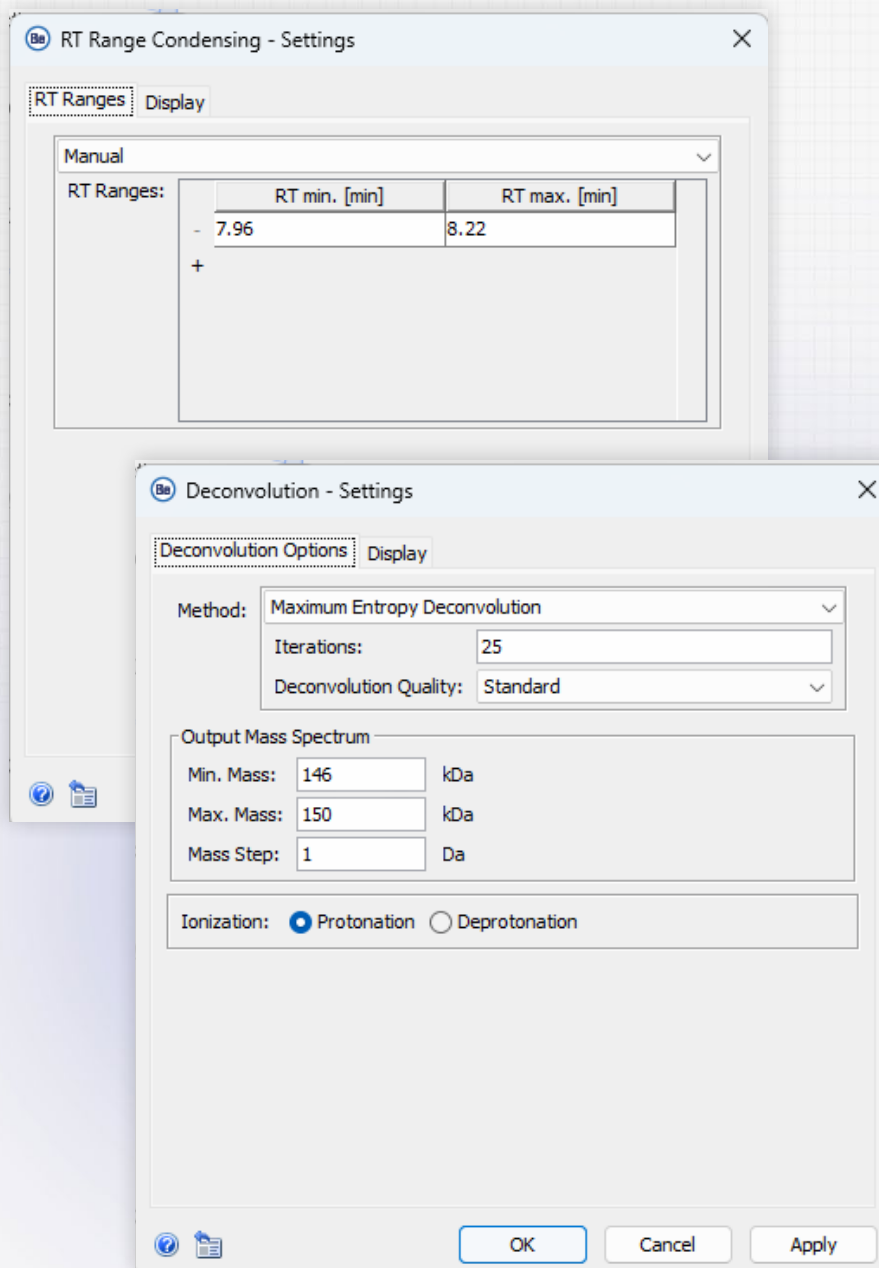
Pre-processing parameters

1. Select the appropriate pre-processing parameters
 - a) Define the m/z range of interest
 - b) Define the spectrum baseline subtraction as 50%



Deconvolution parameters

1. Define the deconvolution parameters
 - a) Select the RT range to be used
 - b) Define the deconvolution settings



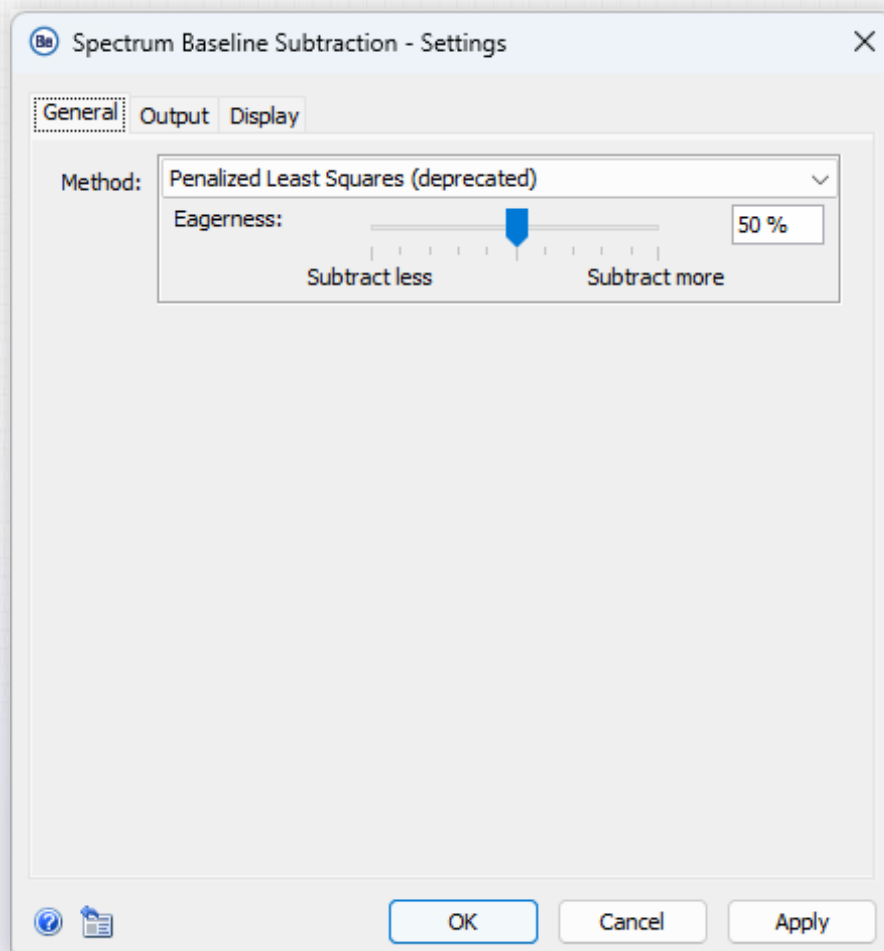
The image shows two overlapping software dialog boxes. The top dialog is titled "RT Range Condensing - Settings" and has a "Display" tab. It shows a "Manual" selection and a table of RT Ranges with one entry: RT min. [min] is 7.96 and RT max. [min] is 8.22. The bottom dialog is titled "Deconvolution - Settings" and has a "Display" tab. It shows the following settings:

- Method: Maximum Entropy Deconvolution
- Iterations: 25
- Deconvolution Quality: Standard
- Output Mass Spectrum:
 - Min. Mass: 146 kDa
 - Max. Mass: 150 kDa
 - Mass Step: 1 Da
- Ionization: Protonation Deprotonation

Both dialogs have "OK", "Cancel", and "Apply" buttons at the bottom.

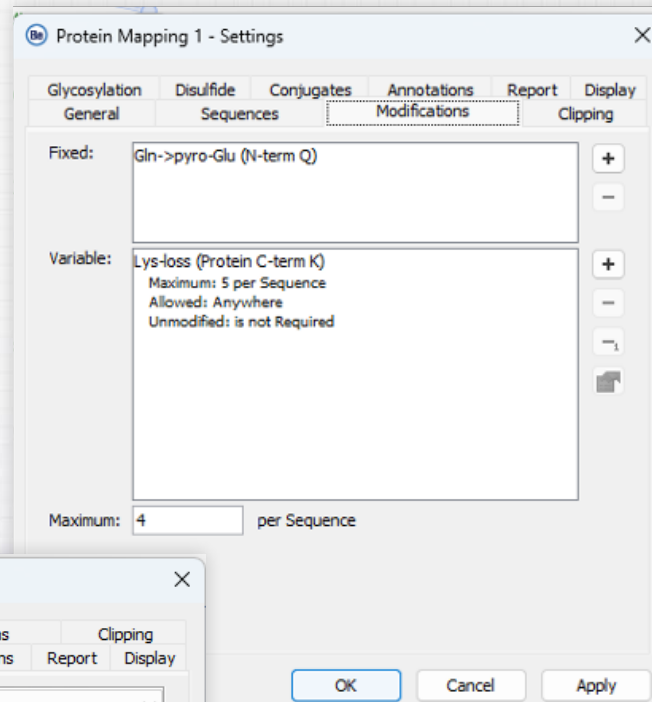
Peak detection parameters

1. Define the spectrum baseline subtraction



Protein mapping parameters

1. Define the protein mapping parameters
 - a) Modifications
 - b) Glycosylation
 - c) Disulfide



Protein Mapping 1 - Settings

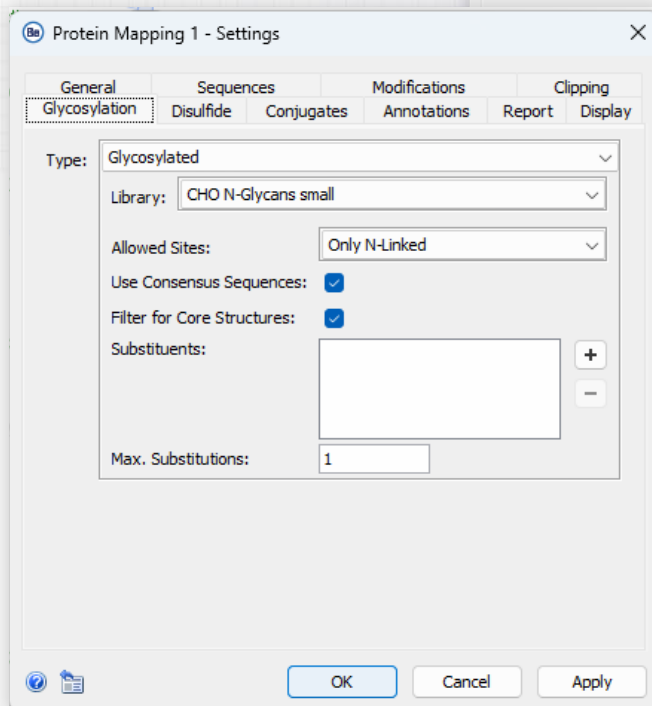
Glycosylation Disulfide Conjugates Annotations Report Display
 General Sequences **Modifications** Clipping

Fixed: Gln->pyro-Glu (N-term Q) +
 -

Variable: Lys-loss (Protein C-term K) +
 Maximum: 5 per Sequence
 Allowed: Anywhere
 Unmodified: is not Required
 -
 -

Maximum: 4 per Sequence

OK Cancel Apply



Protein Mapping 1 - Settings

General **Glycosylation** Sequences Modifications Clipping
 Disulfide Conjugates Annotations Report Display

Type: Glycosylated

Library: CHO N-Glycans small

Allowed Sites: Only N-Linked

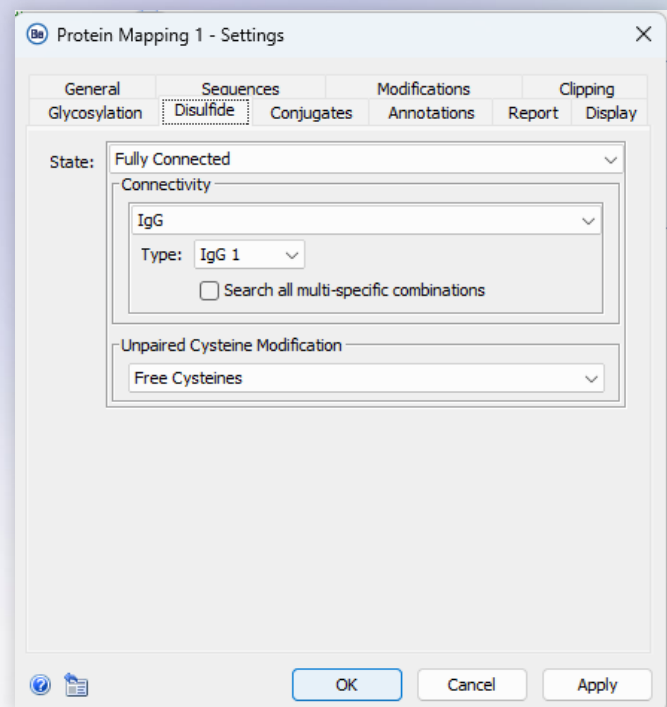
Use Consensus Sequences:

Filter for Core Structures:

Substituents: +
 -

Max. Substitutions: 1

OK Cancel Apply



Protein Mapping 1 - Settings

General Sequences Modifications Clipping
 Glycosylation **Disulfide** Conjugates Annotations Report Display

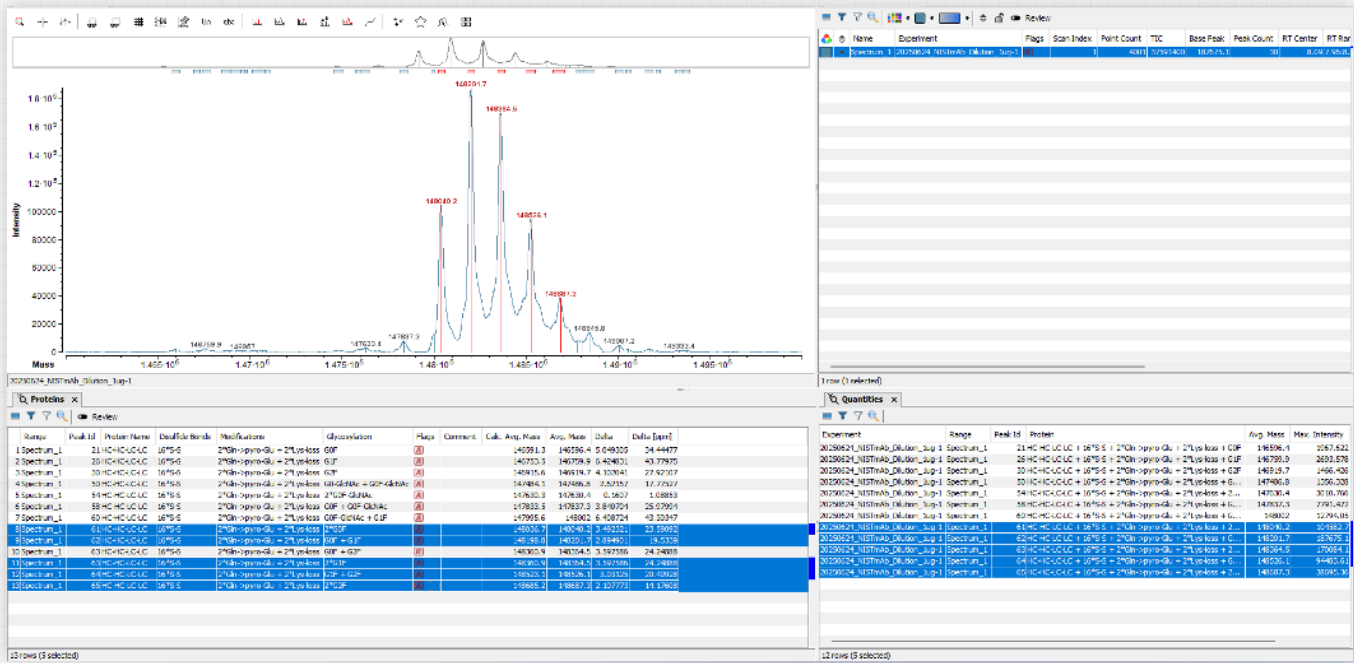
State: Fully Connected

Connectivity
 IgG
 Type: IgG 1
 Search all multi-specific combinations

Unpaired Cysteine Modification
 Free Cysteines


OK Cancel Apply

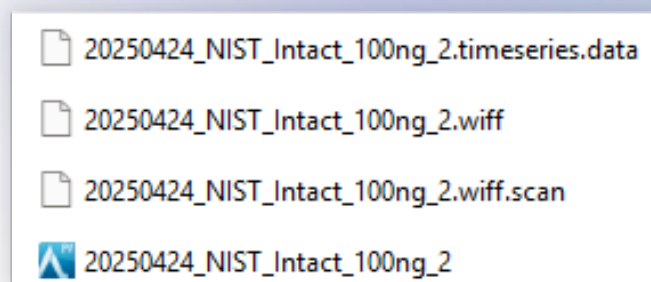
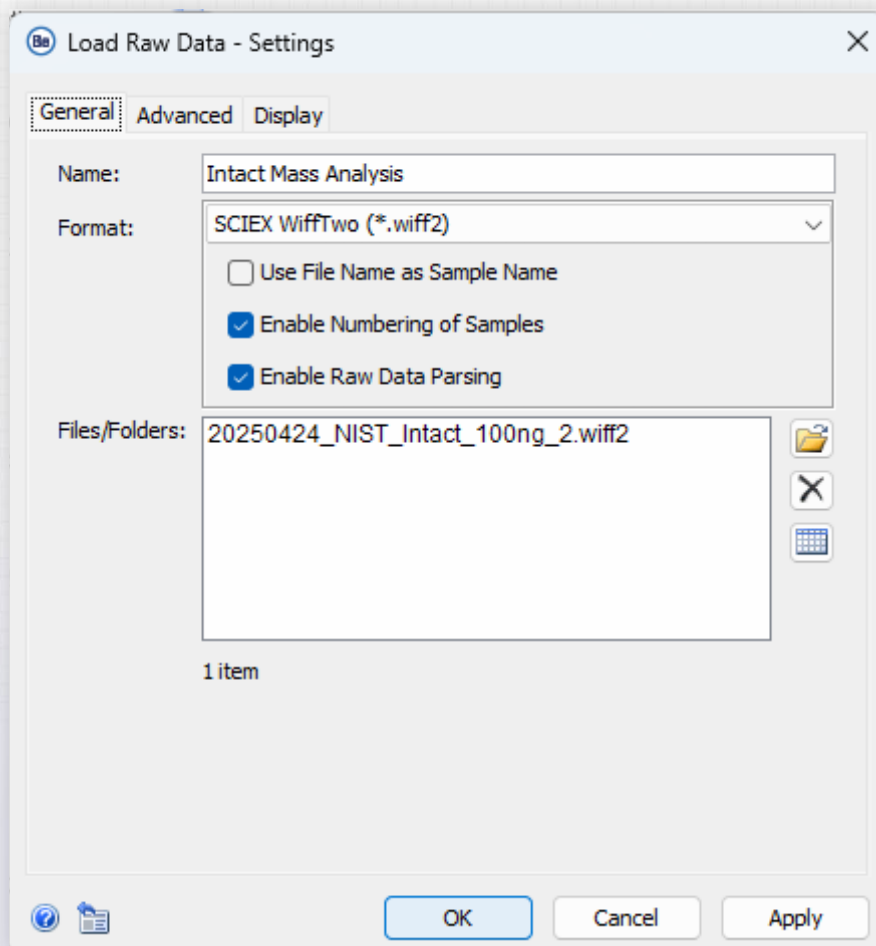
Expected annotation results



RPLC-MS Intact

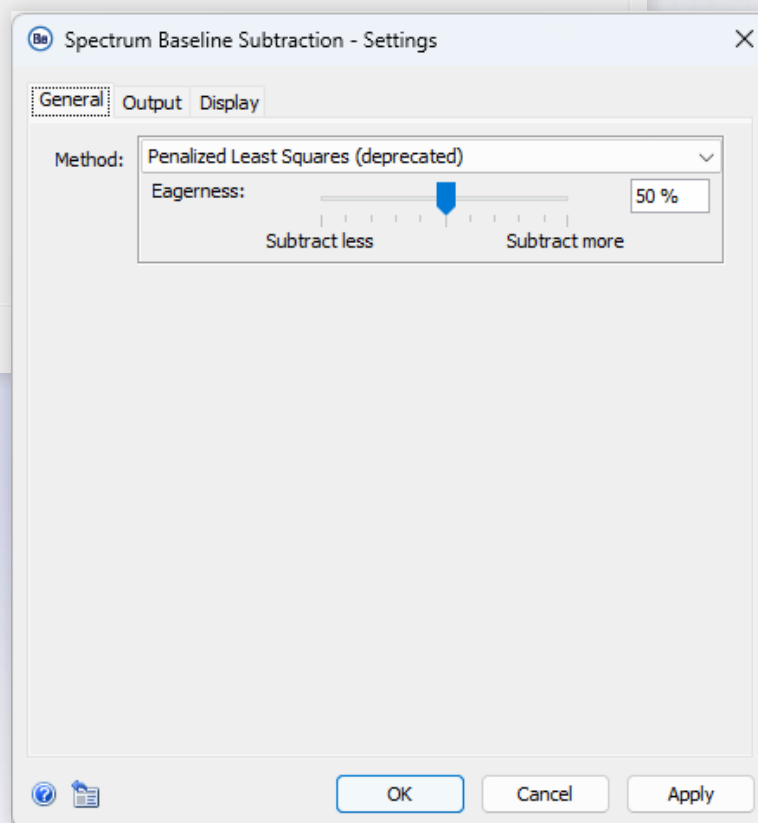
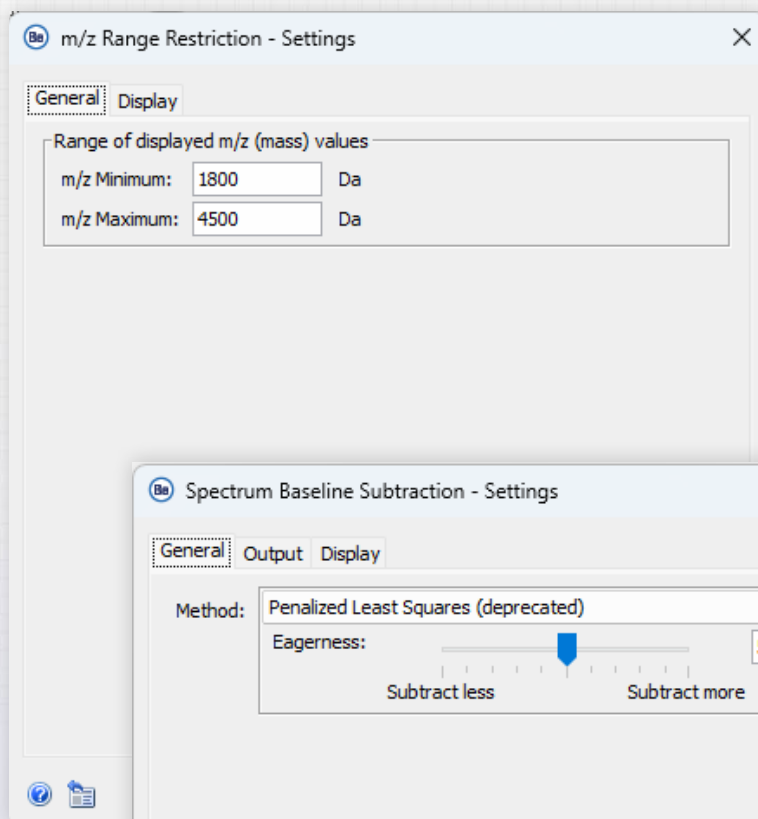
Data file

1. Double click on "Load Raw Data"
2. Click on  to select the .wiff2 data file from your output



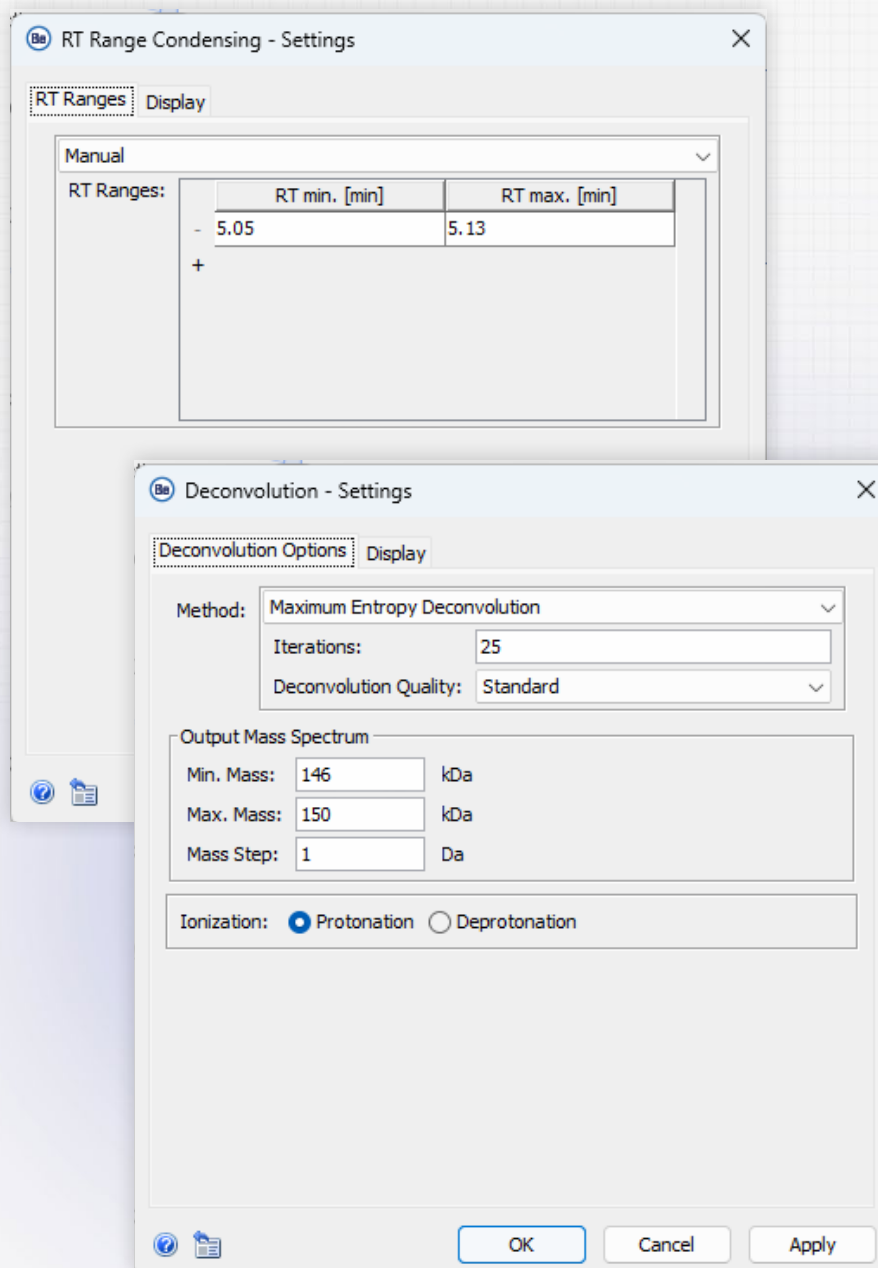
Pre-processing

1. Select the appropriate pre-processing parameters
 - a) Define the m/z range of interest
 - b) Define the spectrum baseline subtraction as 50%



Deconvolution parameters

1. Define the deconvolution parameters
 - a) Select the RT range to be used
 - b) Define the deconvolution settings



The image shows two overlapping software dialog boxes. The top dialog is titled "RT Range Condensing - Settings" and has a "Display" tab. It shows a "Manual" selection and a table for "RT Ranges:" with one row containing "5.05" and "5.13". The bottom dialog is titled "Deconvolution - Settings" and has a "Display" tab. It contains several input fields and options for deconvolution parameters.

RT Range Condensing - Settings

RT Ranges: Display

Manual

	RT min. [min]	RT max. [min]
-	5.05	5.13
+		

Deconvolution - Settings

Deconvolution Options: Display

Method: Maximum Entropy Deconvolution

Iterations: 25

Deconvolution Quality: Standard

Output Mass Spectrum

Min. Mass: 146 kDa

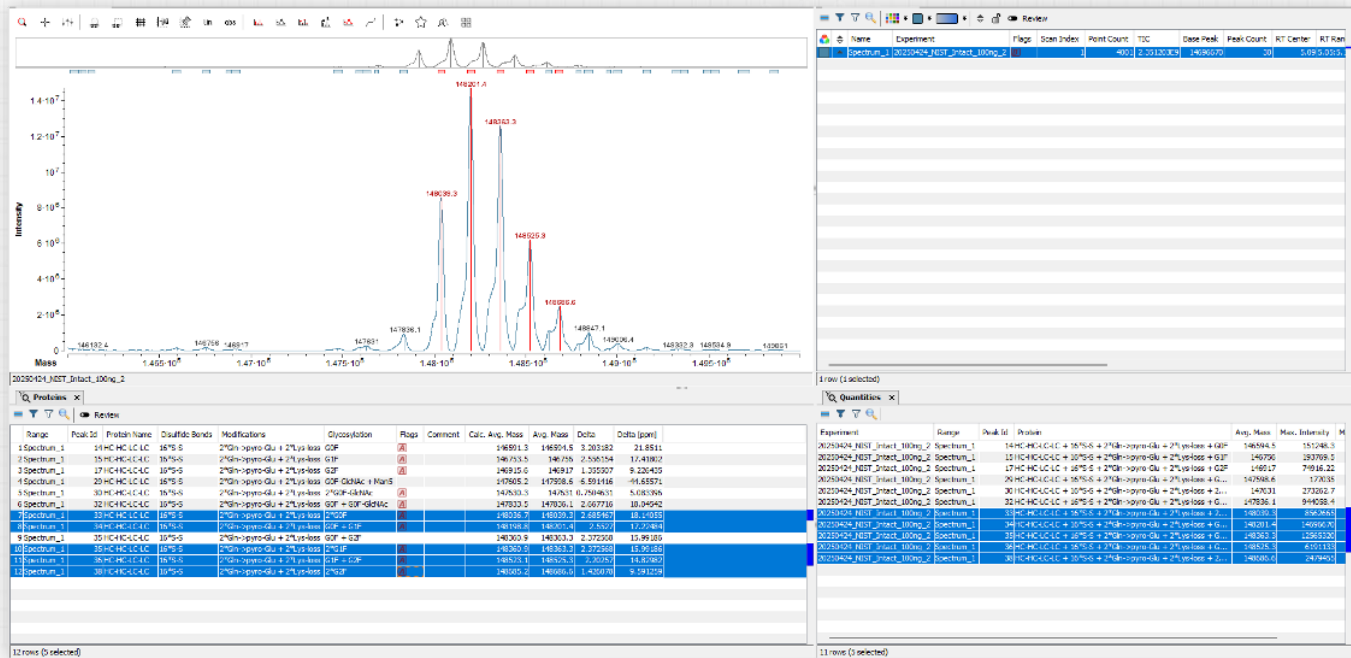
Max. Mass: 150 kDa

Mass Step: 1 Da

Ionization: Protonation Deprotonation

Buttons: OK, Cancel, Apply

Expected annotation results



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