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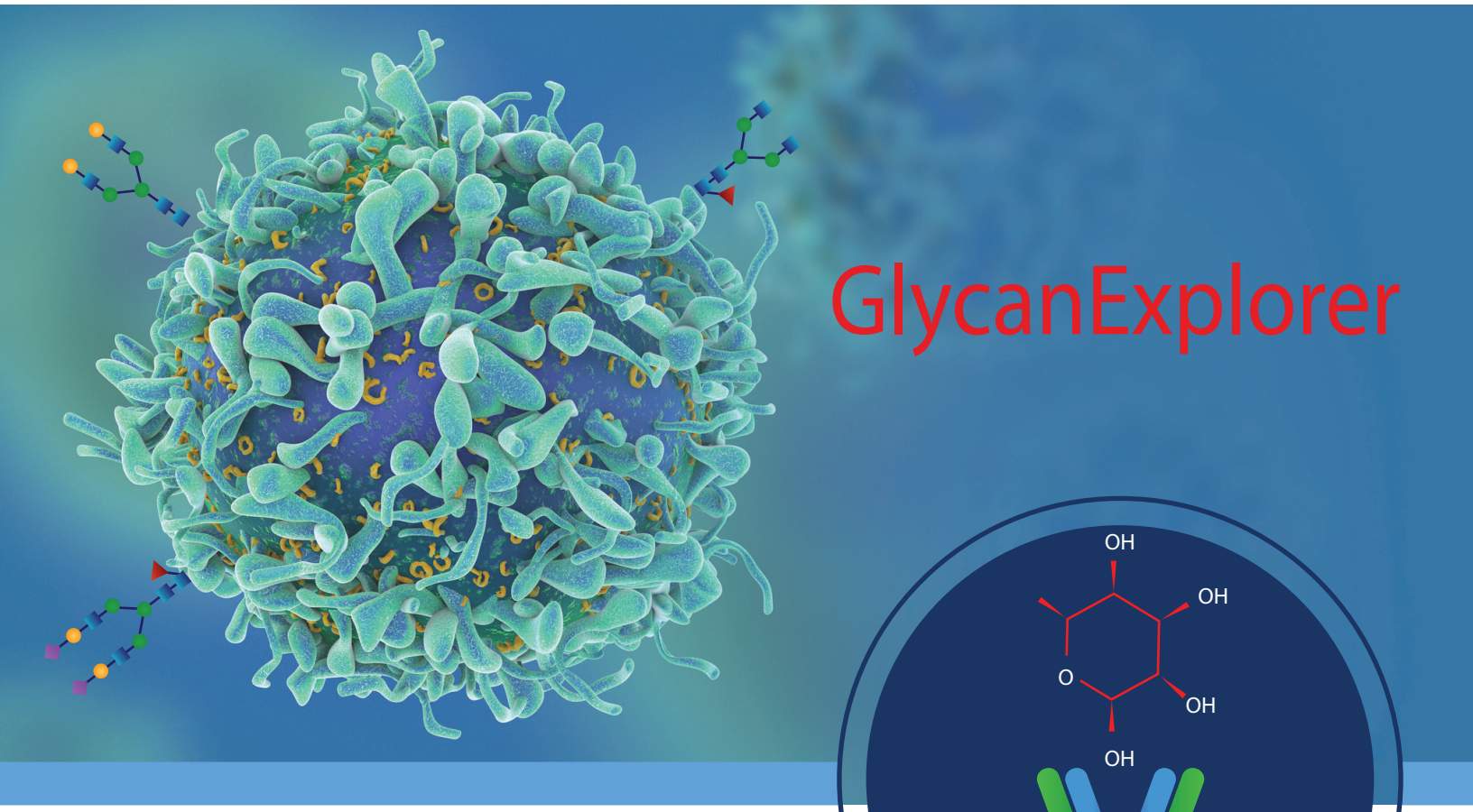

GlycanExplorer

Workflow Driven Informatics for Biotherapeutic Glycan Analysis

- **High-Resolution Accurate-Mass Spectral Library of *N*-glycans from Therapeutic Glycoproteins**
- **Glycan Identification using Spectral Pattern Matching**
- **Glycan Identification using *in-silico* Fragment Matching**
- **Glycan Mapping**

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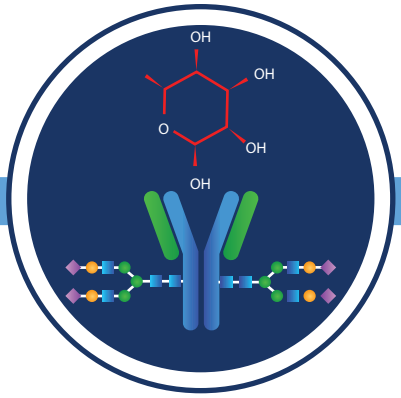
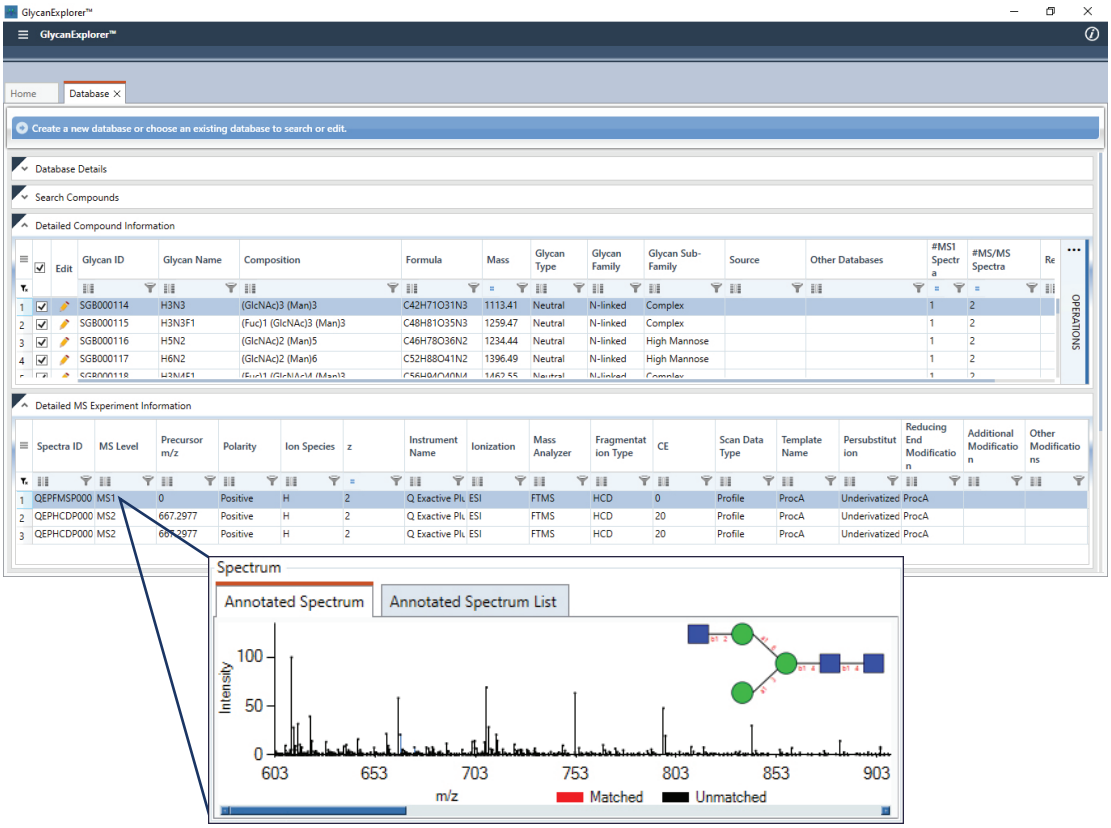
GlycanExplorer



High-Resolution Accurate-Mass Spectral library

The built-in reference mass spectral library contains mass spectra (MS1 and MS2) of glycans from various therapeutic glycoproteins.



Database Statistics

- *14 glycoproteins*
- *10000+ MS/MS Spectra*
- *200+ MS1 Spectra*

Scalable Database

1. Store glycan structures along with retention times, and other experimental and chromatographic details as LC-MS templates

2. Store multiple spectra of a glycan belonging to different ion species acquired using different instrumental and experimental conditions

3. Create multiple custom database or LC-MS templates

The Glycoproteins

- Built-in spectral libraries for glycoproteins labeled with various fluorescent tags such as 2-AB, RapiFluor-MS, Procainamide

- Glycoproteins included:
  - mAb variants: Cetuximab, Ipilimumab, Infliximab, Pertuzumab, Gololimab, Nivolumab, and NIST mAb
  - Others: Apotransferrin, Orosomucoid, Ovalbumin, RNaseB etc.

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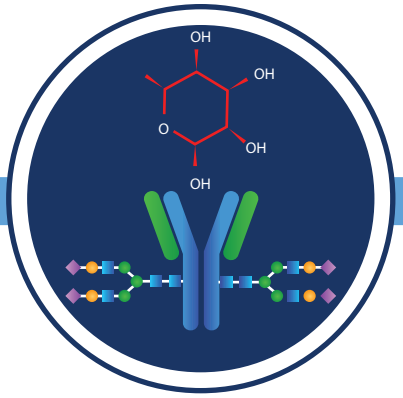
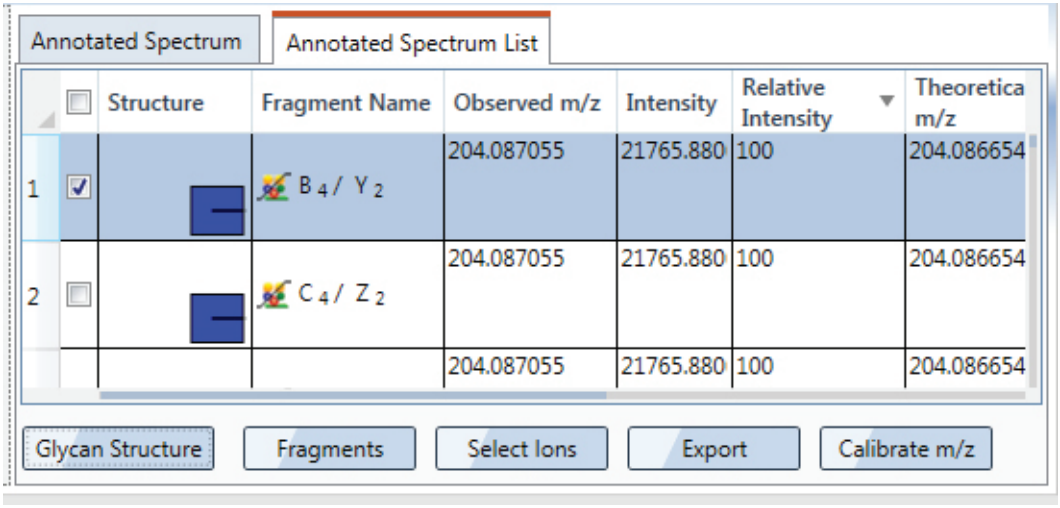
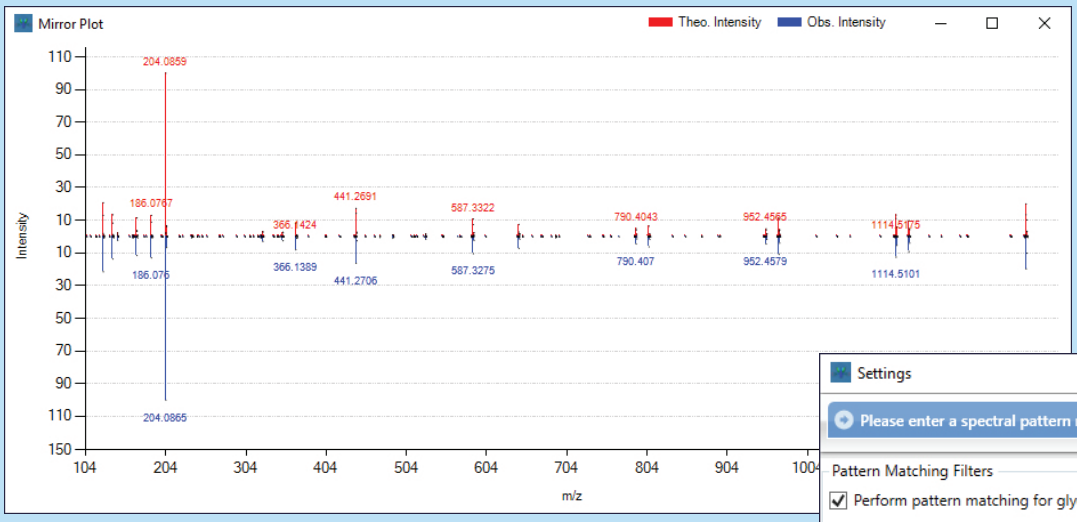


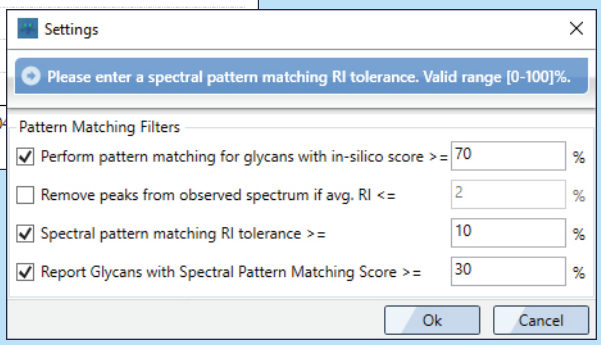
An efficient fragment m/z calibration facility allows you to create a High-Resolution Glycan Mass Spectral Library



Spectral Pattern Matching

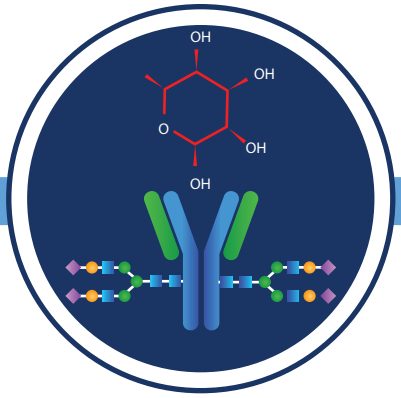
Accurate Identification of glycans using robust and reliable spectral pattern matching algorithm.





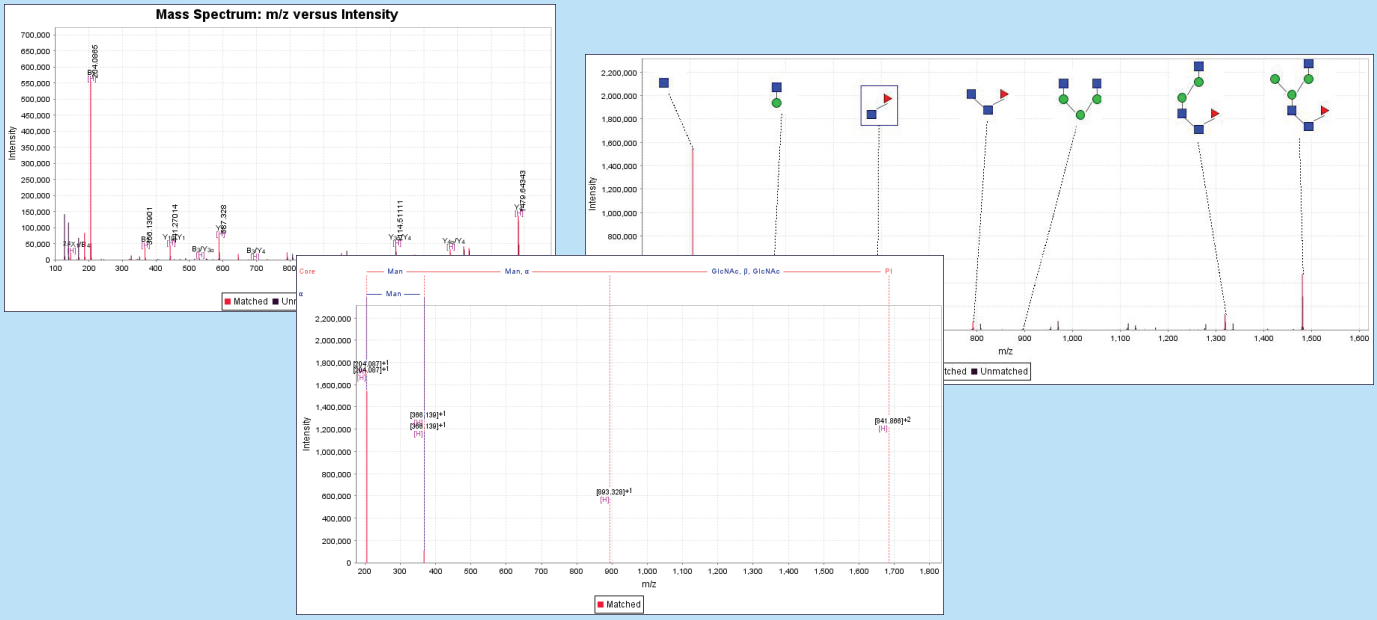
Additional filters help you report the accurate glycan structures.

GlycanExplorer



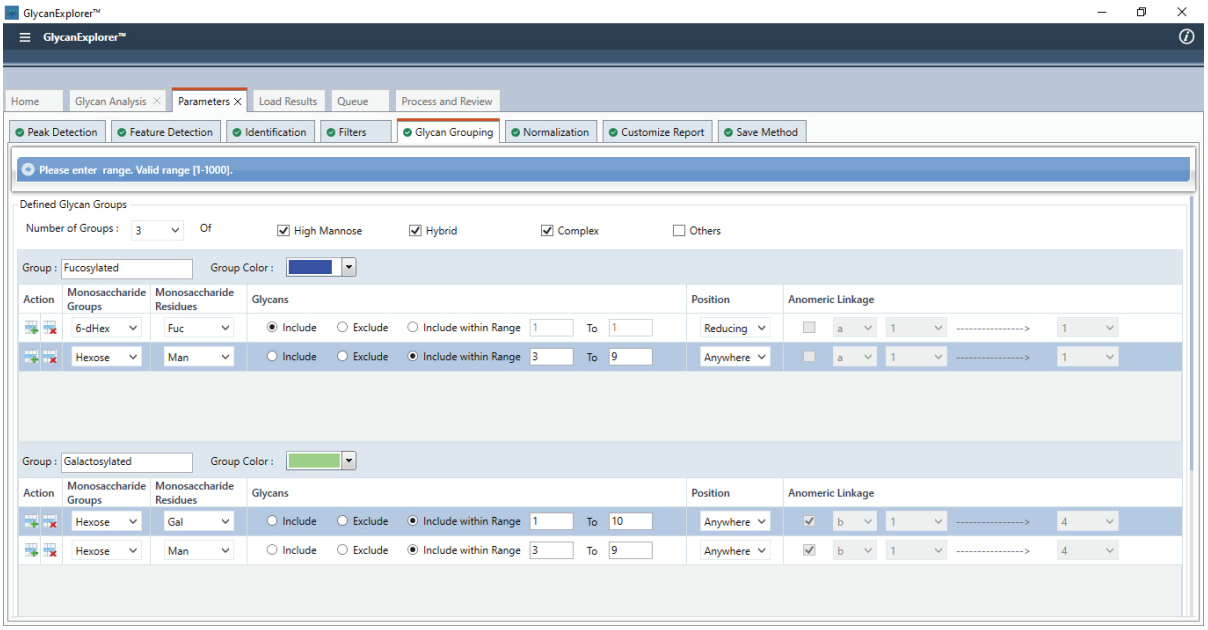
in-silico Fragment Matching

Identify glycans by matching the experimental fragment ions with *in-silico* fragment ions.



Glycan Grouping

Classify the identified glycans in groups such as Fucosylated, Galactosylated, or Sialylated.



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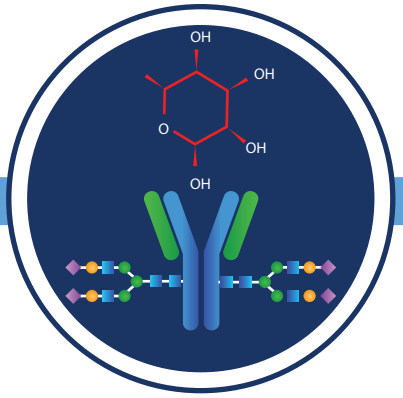
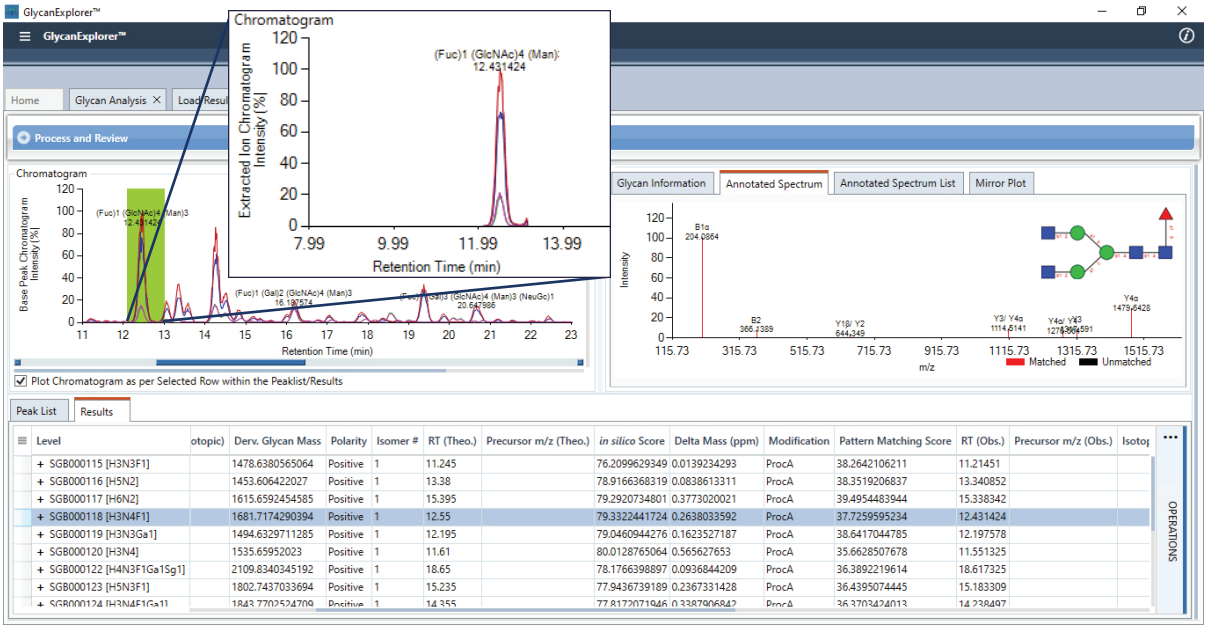
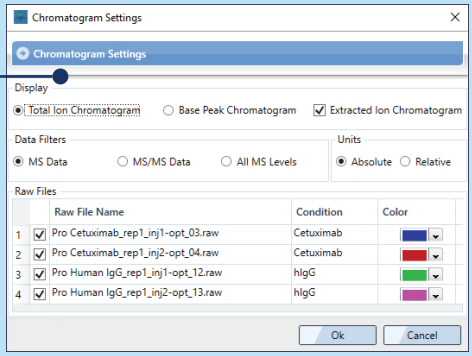


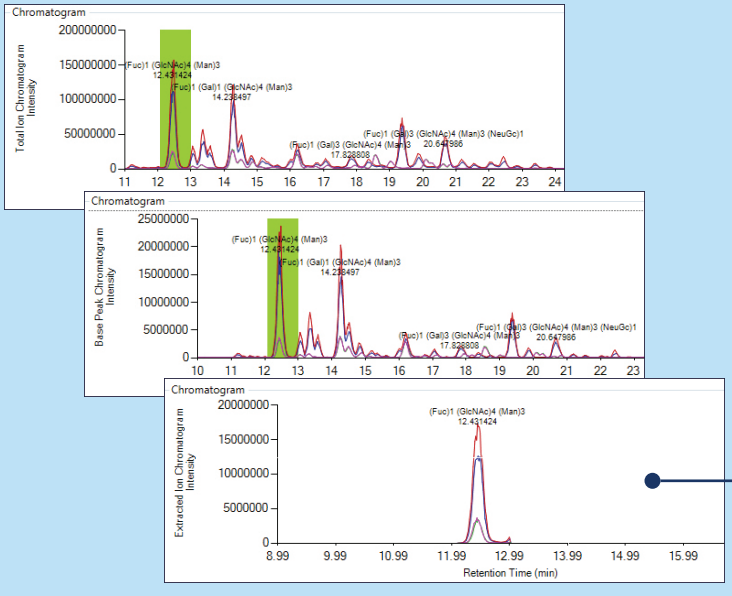
Visualize Your Data

A single workbench view of glycan IDs, associated chromatograms, and Spectra helps you easily review the result of your analysis.



A dedicated Chromatogram Settings window help you plot the chromatograms as you want





Plot three different types of chromatograms: Total Ion Chromatogram (TIC), Base Peak Chromatogram (BPC), and Extracted Ion Chromatogram (XIC)

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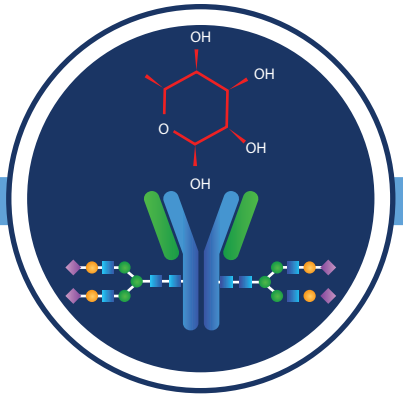
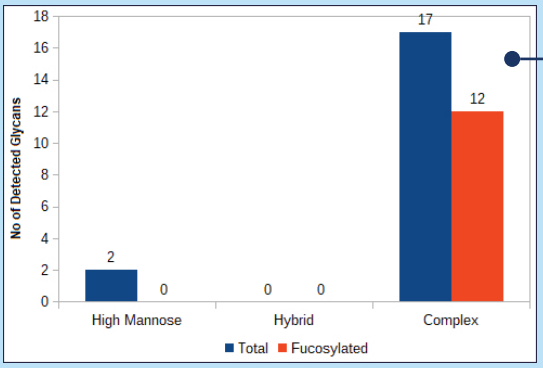
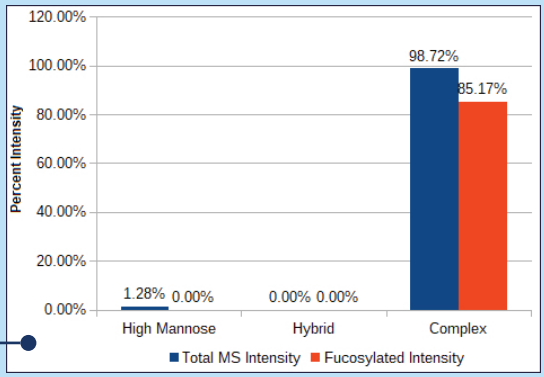


Glycan Mapping

Interactive charts and plots tell you more about your data, help you reach a meaningful biological conclusion.

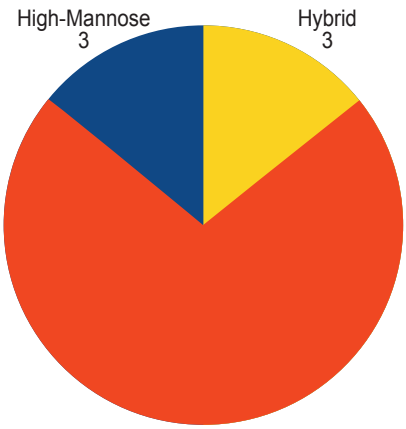


A bar chart depicting the breakdown of the *N*-glycans of Human IgG: High Mannose (n = 2), Complex (n=17; fucosylated =12), and Hybrid (n =0)

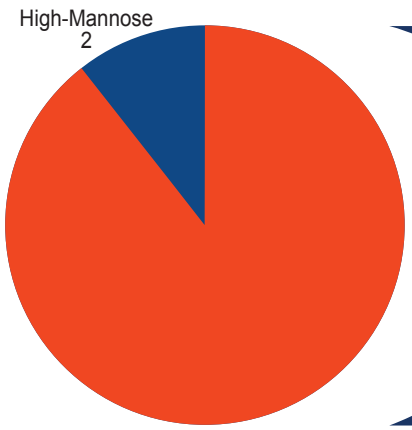


A bar chart depicting the breakdown of the relative abundance of hIgG *N*-glycans sub families: Complex (98.72%), High Mannose (1.28%)

N-glycans of Cetuximab



N-glycans of Human IgG



Pie charts depicting the comparative breakdown of *N*-glycans of Cetuximab (n =21) and Human IgG (n = 19)

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