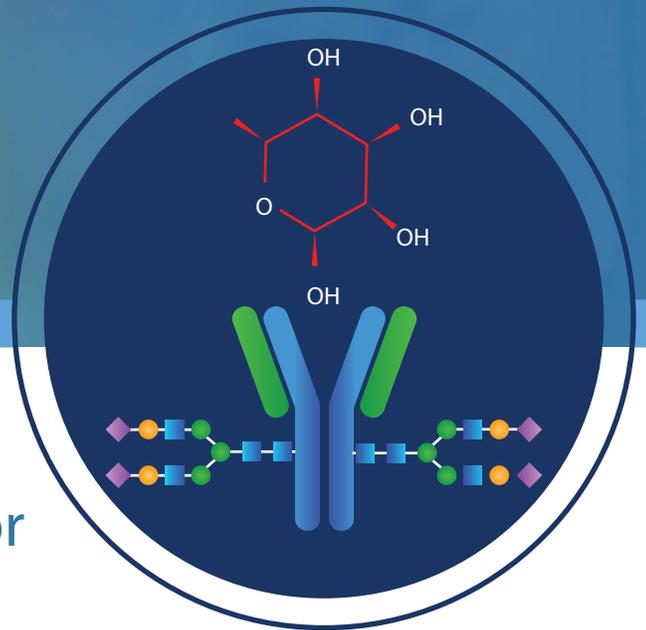


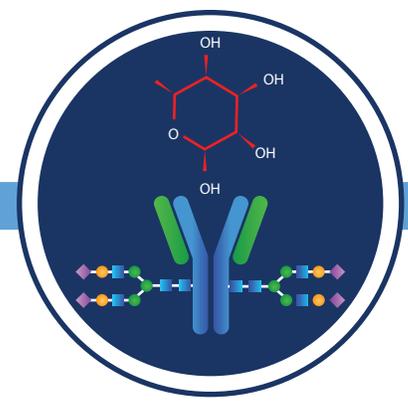
GlycanExplorer



Workflow Driven Informatics for Biotherapeutic Glycan Analysis

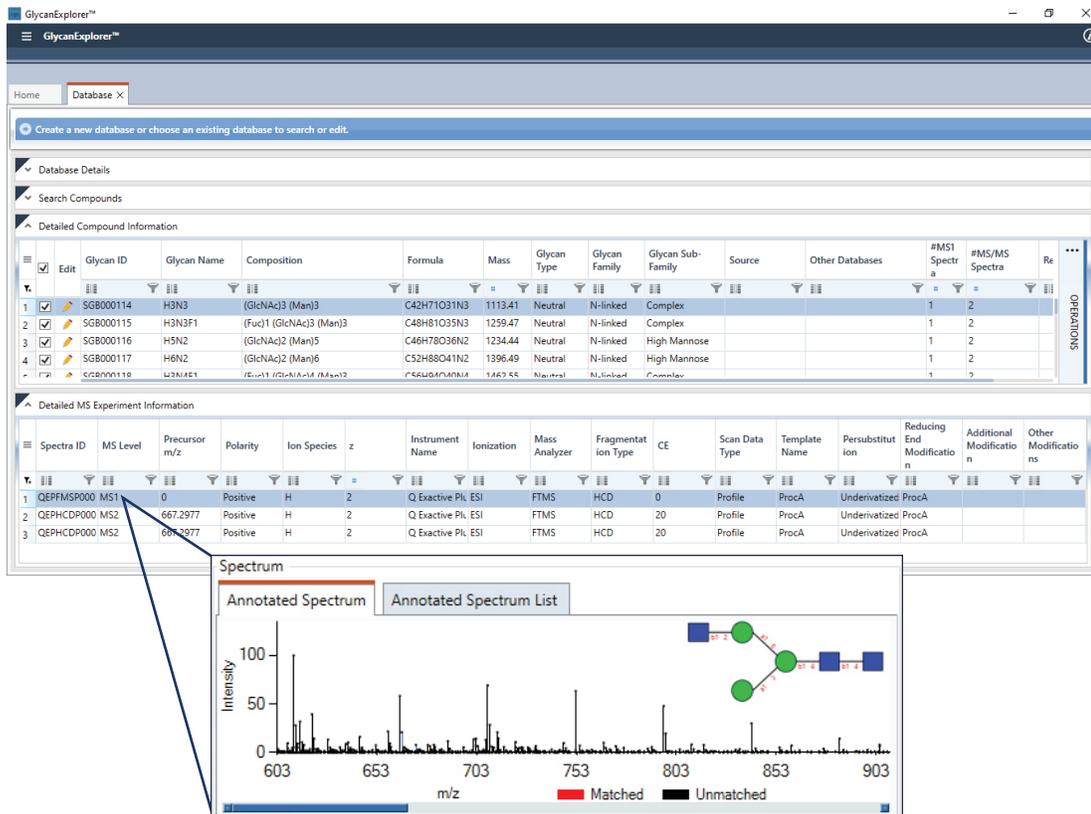
- High-Resolution Accurate-Mass Spectral Library of N-glycans from Therapeutic Glycoproteins
- Glycan Identification using Spectral Pattern Matching
- Glycan Identification using *in-silico* Fragment Matching
- Glycan Mapping

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

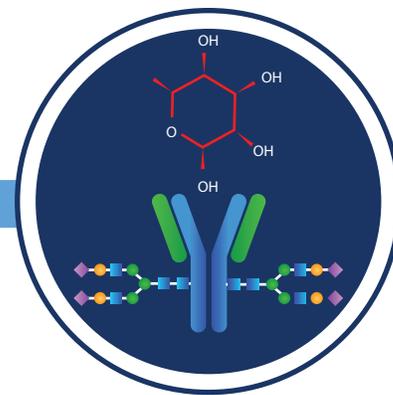
2. Store multiple spectra of a glycan belonging to different ion species acquired using different instrumental and experimental conditions

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, Golilumab, Nivolumab, and NIST mAb
 - Others: Apotransferrin, Orosomuroid, Ovalbumin, RNaseB etc.

GlycanExplorer

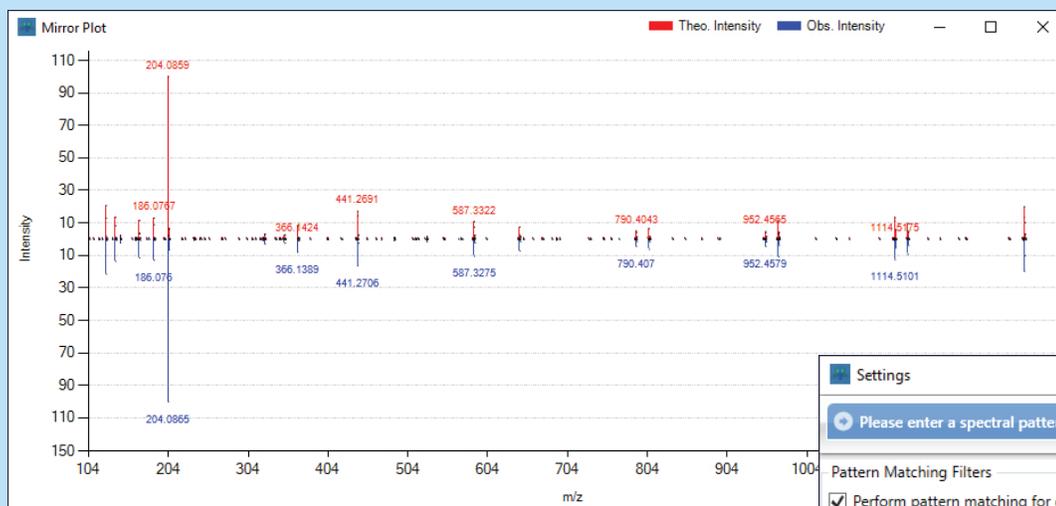


An efficient fragment m/z calibration facility allows you to create a High-Resolution Glycan Mass Spectral Library

Annotated Spectrum		Annotated Spectrum List				
	Structure	Fragment Name	Observed m/z	Intensity	Relative Intensity	Theoretical m/z
1	<input checked="" type="checkbox"/>	B ₄ /Y ₂	204.087055	21765.880	100	204.086654
2	<input type="checkbox"/>	C ₄ /Z ₂	204.087055	21765.880	100	204.086654
			204.087055	21765.880	100	204.086654

Spectral Pattern Matching

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



Additional filters help you report the accurate glycan structures.

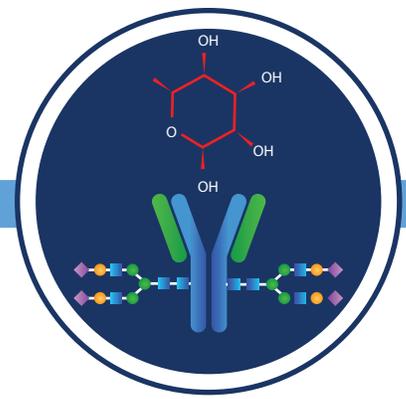
Settings

Please enter a spectral pattern matching RI tolerance. Valid range [0-100]%.

Pattern Matching Filters

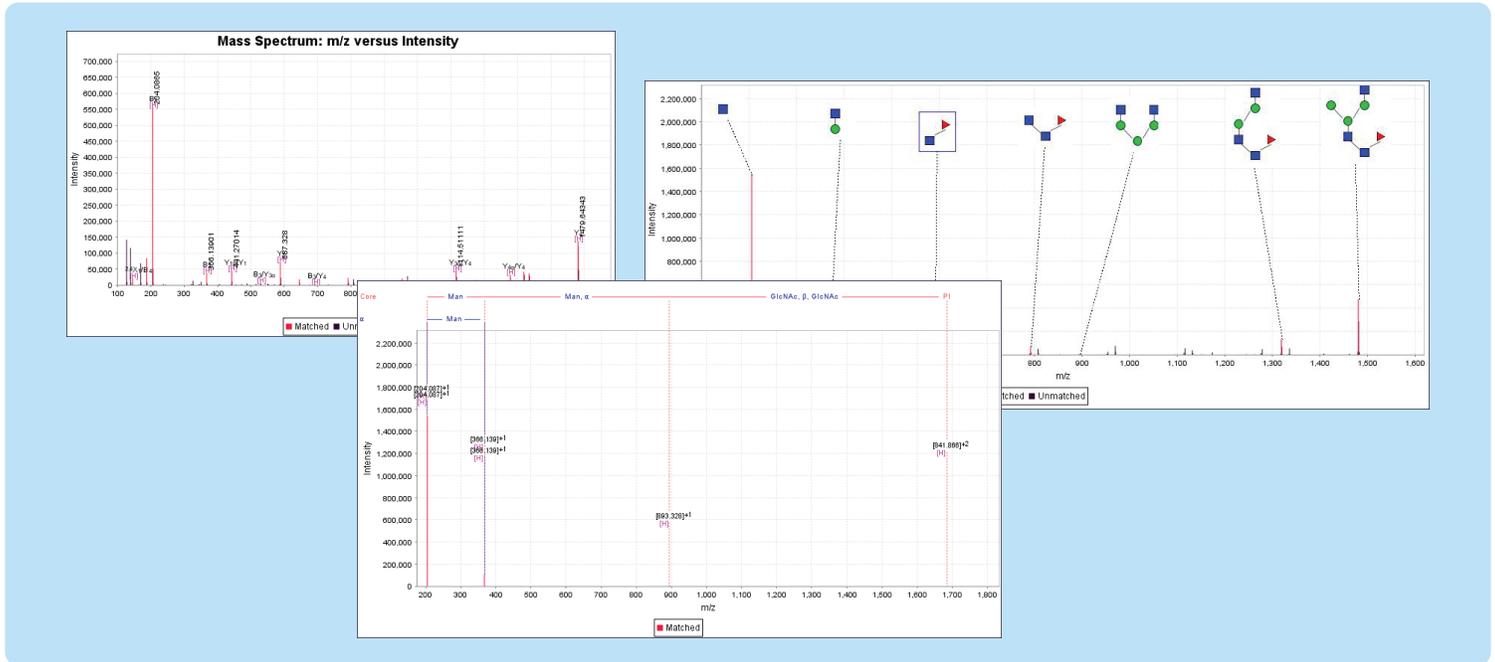
- Perform pattern matching for glycans with in-silico score >= %
- Remove peaks from observed spectrum if avg. RI <= %
- Spectral pattern matching RI tolerance >= %
- Report Glycans with Spectral Pattern Matching Score >= %

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.

GlycanExplorer™

Home Glycan Analysis Parameters Load Results Queue Process and Review

Peak Detection Feature Detection Identification Filters Glycan Grouping Normalization Customize Report Save Method

Please enter range. Valid range [1-1000].

Defined Glycan Groups

Number of Groups: 3 Of High Mannose Hybrid Complex Others

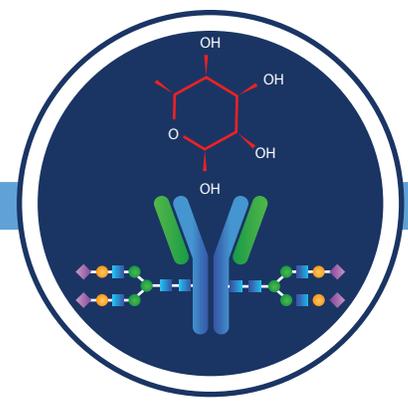
Group: Fucosylated Group Color: ■

Action	Monosaccharide Groups	Monosaccharide Residues	Glycans	Position	Anomeric Linkage
	6-dHex	Fuc	<input type="radio"/> Include <input type="radio"/> Exclude <input type="radio"/> Include within Range 1 To 1	Reducing	<input type="checkbox"/> a 1 -----> 1
	Hexose	Man	<input type="radio"/> Include <input type="radio"/> Exclude <input checked="" type="radio"/> Include within Range 3 To 9	Anywhere	<input type="checkbox"/> a 1 -----> 1

Group: Galactosylated Group Color: ■

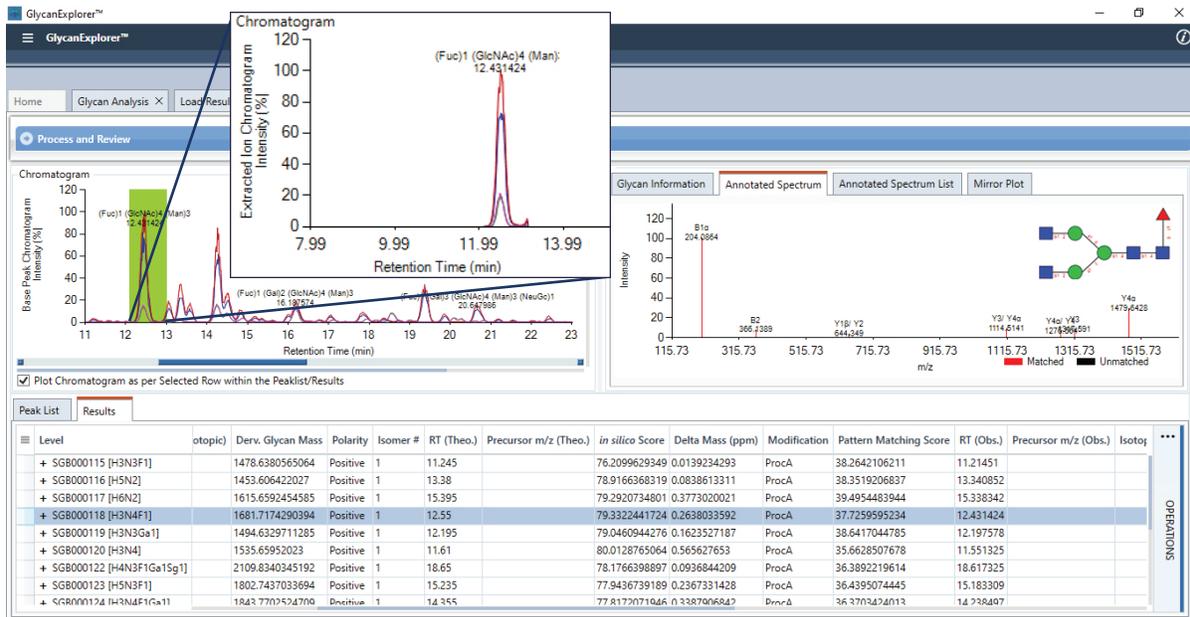
Action	Monosaccharide Groups	Monosaccharide Residues	Glycans	Position	Anomeric Linkage
	Hexose	Gal	<input type="radio"/> Include <input type="radio"/> Exclude <input checked="" type="radio"/> Include within Range 1 To 10	Anywhere	<input checked="" type="checkbox"/> b 1 -----> 4
	Hexose	Man	<input type="radio"/> Include <input type="radio"/> Exclude <input checked="" type="radio"/> Include within Range 3 To 9	Anywhere	<input checked="" type="checkbox"/> b 1 -----> 4

GlycanExplorer

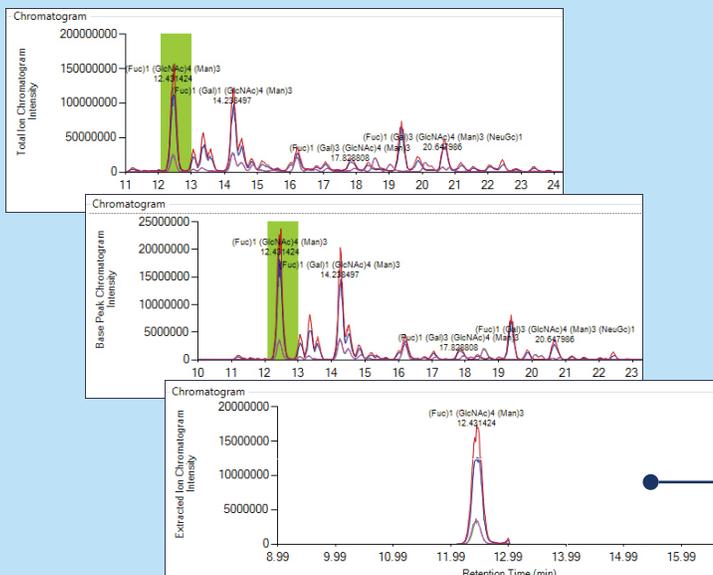
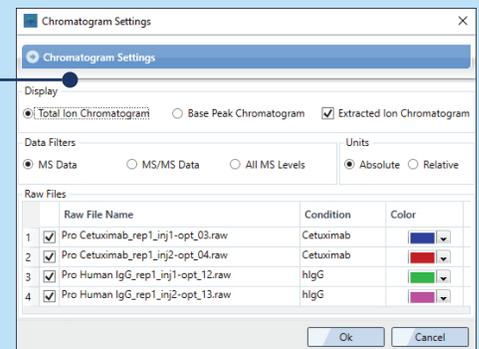


Visualize Your Data

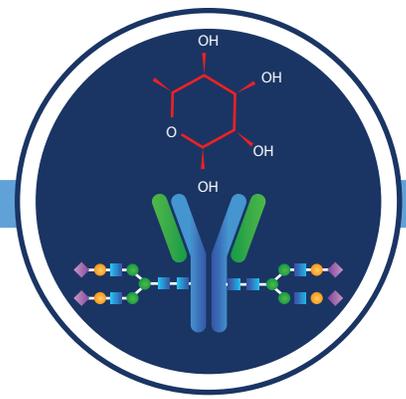
A single workbench view of glycan IDs, associated chromatograms, and Spectra helps you easily review the result of your analysis.



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

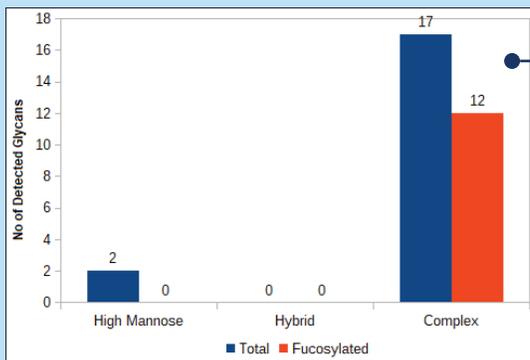


Plot three different types of chromatograms: Total Ion Chromatogram (TIC), Base Peak Chromatogram (BPC), and Extracted Ion Chromatogram (XIC)



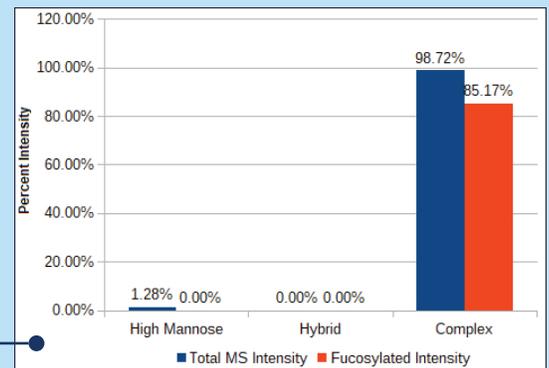
Glycan Mapping

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

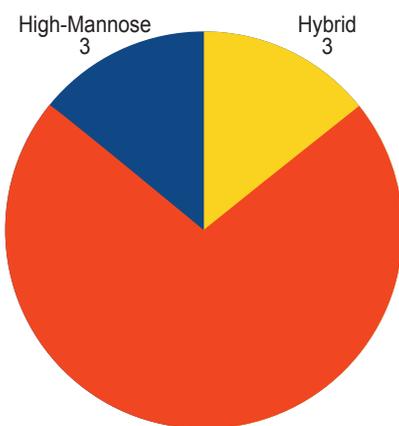


A bar chart depicting the breakdown of the N-glycans of Human IgG: High Mannose (n = 2), Complex (n=17; fucosylated =12), and Hybrid (n =0)

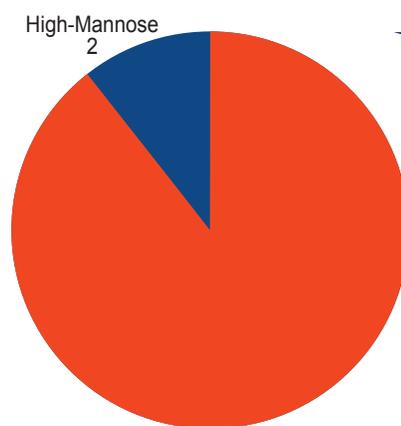
A bar chart depicting the breakdown of the relative abundance of hlgG N-glycans sub families: Complex (98.72%), High Mannose (1.28%)



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)