

Agilent MassHunter BioConfirm Software

ENHANCED PROTEIN AND PEPTIDE CHARACTERIZATION

The Measure of Confidence



Agilent Technologies

ENVISION HIGHER CONFIDENCE IN YOUR PROTEIN/PEPTIDE CHARACTERIZATION

Agilent's sophisticated MassHunter BioConfirm Software brings you greater confidence in your protein/peptide analysis. Together with Agilent's high performance liquid chromatography/mass spectrometry (LC/MS) systems, it provides an intelligent solution for rapid confirmation of synthetic peptides and characterization of proteins and peptides. Now you can elevate your discovery by confirming your data with confidence and ease.

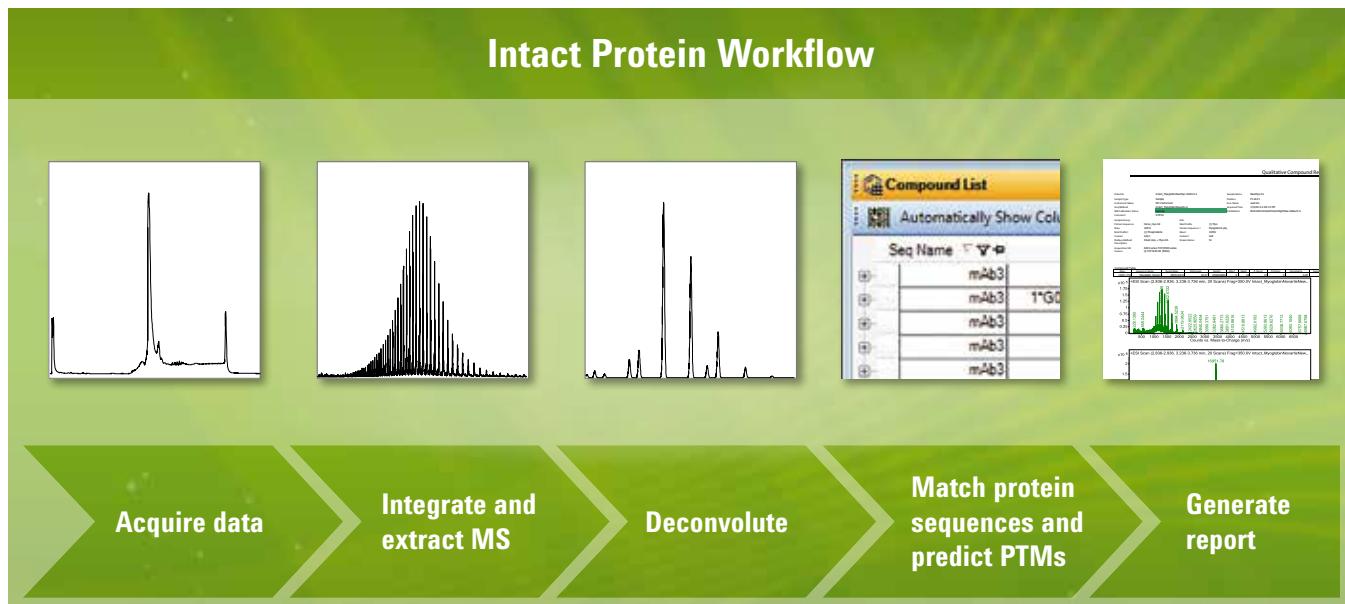


BioConfirm Software Delivers:

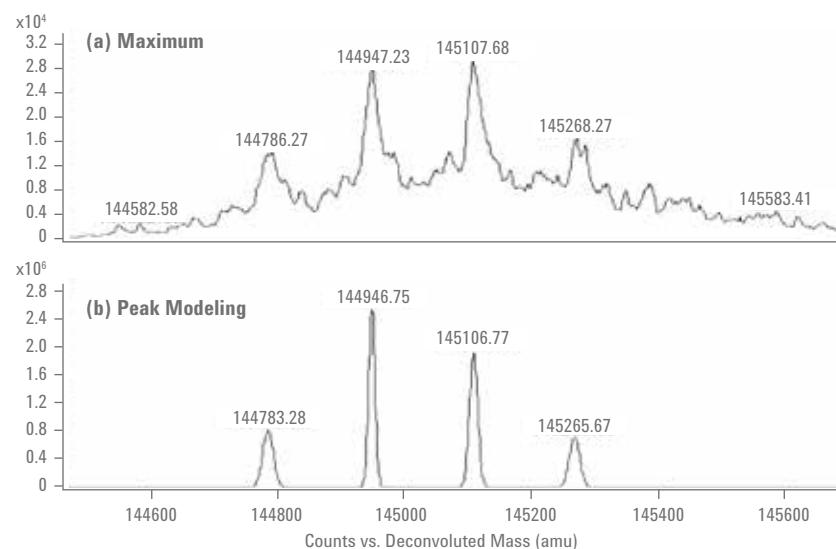
- Precise and rapid protein confirmation
- Easier batch-to-batch analysis
- Comprehensive peptide mapping

ENVISION PRECISE PROTEIN CONFIRMATION

BioConfirm provides both classical maximum entropy deconvolution and enhanced peak modeling (pMod) to determine the molecular weight of intact proteins.



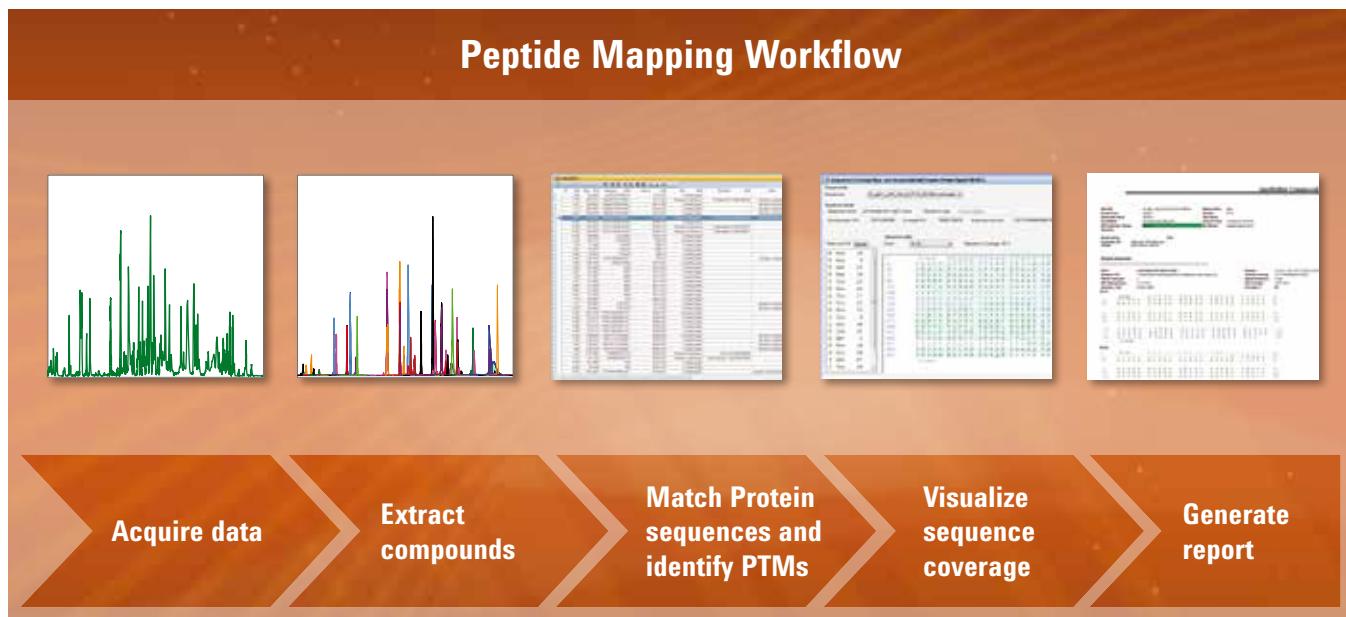
Maximum entropy deconvolution provides rapid mass resolution, especially for simple protein mixtures. For complex protein mixtures, the enhanced pMod algorithm removes artifacts from the spectrum and helps to resolve overlapping peaks—even severely overlapping peaks—providing cleaner spectra and more precise mass measurement. This enables fast confirmation of intact protein sequences and modifications.



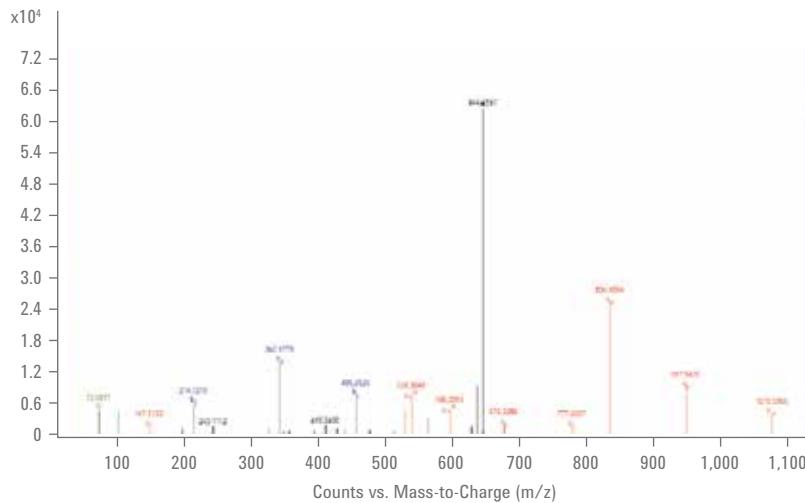
Deconvoluted spectra. (a) Maximum entropy deconvoluted spectrum. (b) Peak modeling deconvoluted spectrum.

ENVISION POWERFUL PEPTIDE MAPPING CAPABILITIES

BioConfirm provides enhanced processing of MS/MS data for streamlined mapping and data interpretation.



BioConfirm identifies peptides and PTMs based on peptide masses and product ions (b, y, and immonium ions) in the MS/MS spectra. This allows for faster and more streamlined processing of MS/MS data for peptide mapping.



Peptide MS/MS spectrum product ion assignment.

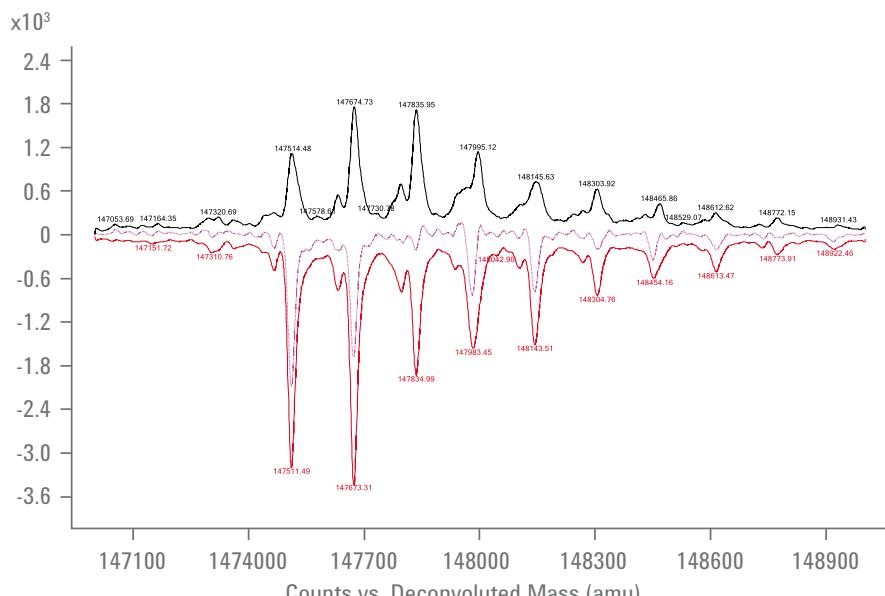
ENVISION EASY BATCH-TO-BATCH COMPARISON

BioConfirm provides easy visual comparison among samples, allowing for fast batch-to-batch analysis on both protein and peptide levels.

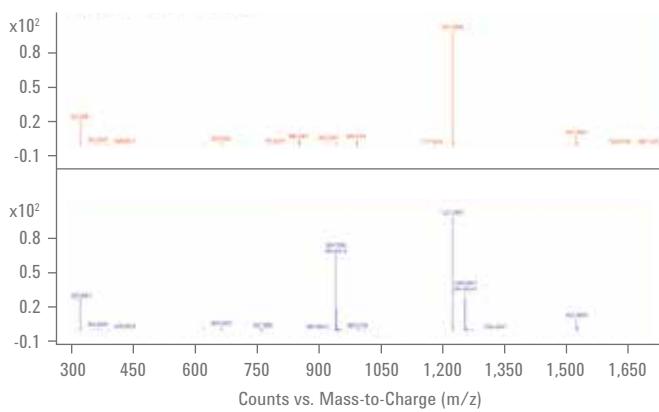
Mirror Plot functionality enables rapid and reliable comparison of two samples, such as two batches of an engineered protein or biosimilars—an essential part of biopharmaceutical analysis. Samples in the Mirror Plot can be switched quickly without reprocessing the data.

Monitor Biosimilars and Batch-to-batch Variation by Quickly Comparing Samples and Reference

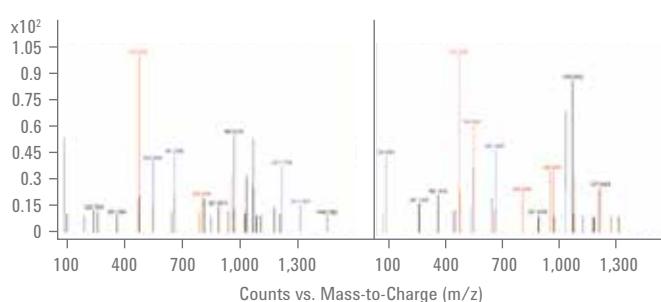
The comparative analysis module facilitates the identification and visualization of the differences between two batches of data for easy inspection. Samples can be compared to a reference using chromatograms, MS, and MS/MS spectra.



Mirror Plot of two engineered proteins.



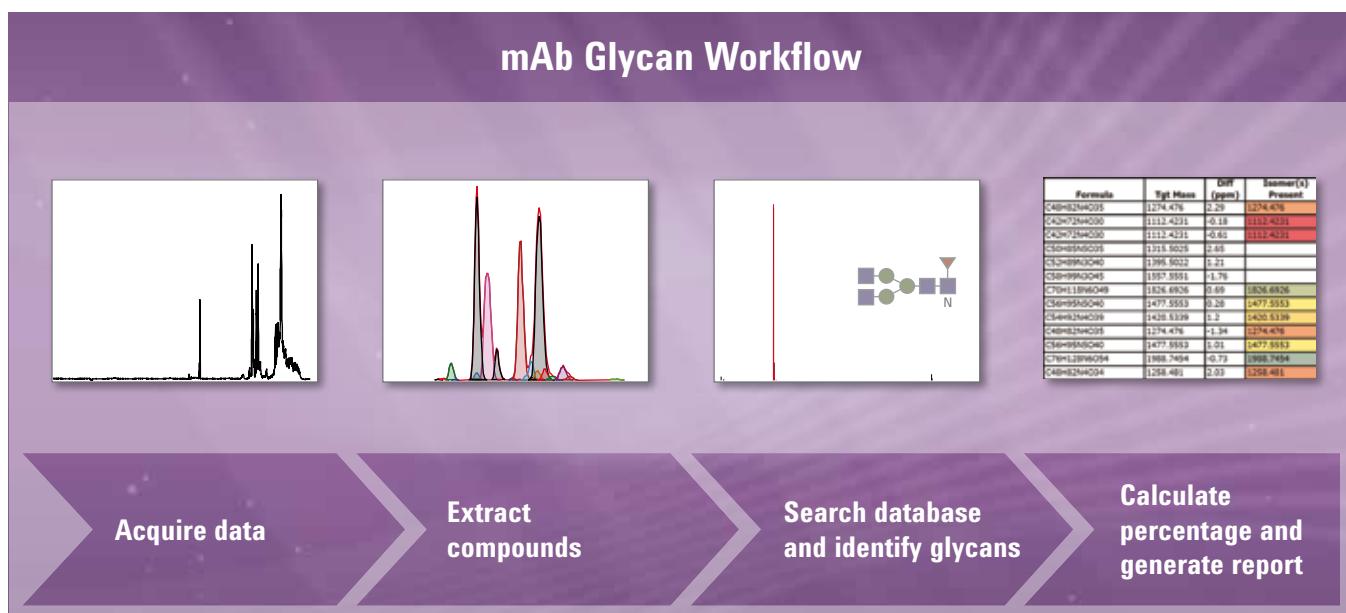
MS Spectrum comparison results.



MS/MS Spectrum comparison results.

ENVISION RAPID AND ACCURATE mAb GLYCAN ANALYSIS

BioConfirm provides an easy and effective workflow for the analysis of mAb glycans.

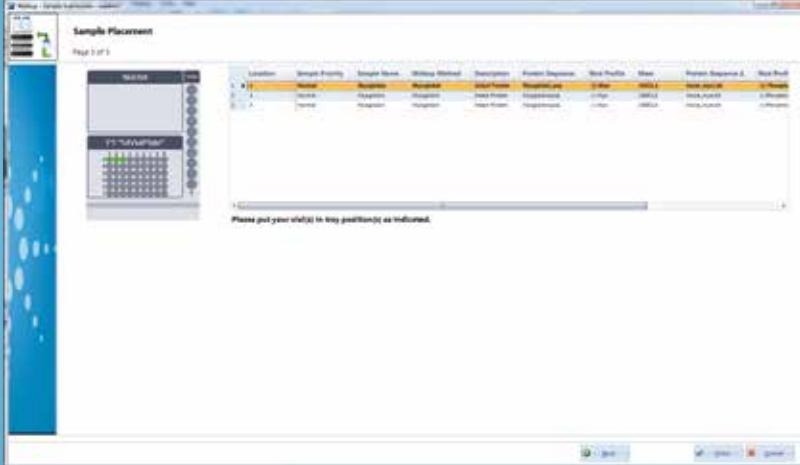


BioConfirm enables users to accurately identify and visualize glycan structures in their mAb samples using Agilent's Glycan Personal Compound Database (PCD) and extensive predefined glycan modifications. Using Agilent's mAb-Glyco Chip, customers have a comprehensive workflow for glycan analysis including hardware, software, and consumables—a complete workflow that includes on-chip deglycosylation of the mAb as well as enrichment, chromatographic separation, and detection of the cleaved glycans. All activities, including data processing using BioConfirm, can be completed in less than 15 minutes.

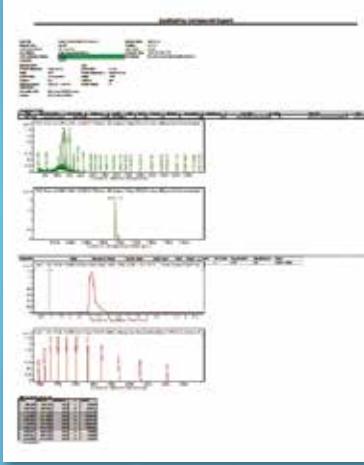
ENVISION WALK UP ANALYSIS FOR NON-EXPERT MS USERS

BioConfirm—part of Agilent's MassHunter Walkup solution.

Sample Submission in Three Easy Steps



The screenshot shows the 'Sample Placement' window of the BioConfirm software. It displays a grid for sample placement and a table with columns: Location, Sample Priority, Sample Name, Workflow Method, Description, Protein Sequence, Score, Protein Response 1, and Protein Response 2. A message at the bottom says, 'Please put your vial(s) in any position(s) as indicated.'



The chromatogram displays four stacked mass spectra. The top spectrum is labeled 'Reference' and shows a broad peak. The bottom spectrum shows a sharp, narrow peak. The middle spectra are partially visible.

1 Login

2 Enter sample information

3 Place vial in ALS

Reports delivered to email inbox

MassHunter Walkup provides a simple-to-use interface that provides novice users the ability to analyze protein and peptide samples in three easy steps with minimal training. Users do not need to concern themselves with complex mass spec conditions; instead, they can run their samples with standard acquisition and data processing methods. Results are directly delivered to their email Inbox.

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