Workflow driven informatics for complete

biotherapeutic characterization

- Intact Protein Mass Analysis
- Subunit Mass Analysis
- Peptide Mapping

Thermo
SCIENTIFIC

Taking too much Time
to Analyze your Data?

Simple software workflows guide you along the biocharacterization pathway all centrally managed with the Protein Sequence Manager feature, the integrated library for your sequences.

Struggle to Confidently
Characterize your Intact Proteins?

Novel deconvolution algorithms ensure you determine the correct molecular weight, confidently identify glycoforms and accurately measure drug-antibody ratio (DAR).

Getting Lost
in your Peptide Maps?

Combine in-depth knowledge of post-translational modifications (PTMs), disulfide bonds, and low level impurities with unique data visualization tools to make sure you never lose any data again.

Chances are you think you know your primary sequen**C**e, BioPharma Finder ensures you do.

Complete Protein Characterization...

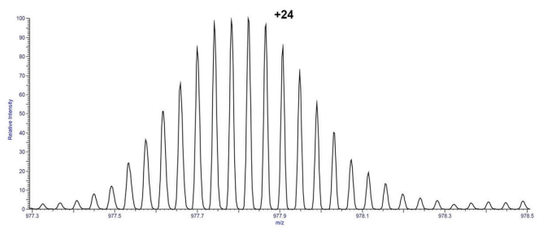
Complete characterization is necessary for the reproducible and safe production of biologics. However this can be complex, from challenging sample preparation to lengthy data-processing routines.

From intact protein mass analysis to peptide mapping, we have created integrated software workflows delivering comprehensive interpretation and visualization allowing you to characterize your biologics with ease.

...trusted by the **Experts**

Orbitrap Power...

Thermo Scientific™ BioPharma Finder™ integrated software allows you to harness the power of the industry leading Thermo Scientific™ Orbitrap™ technology.



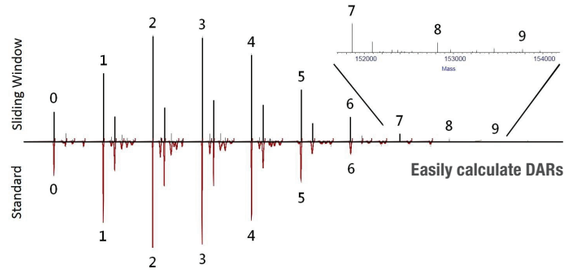
Deconvolve complex spectra

Superior Deconvolution

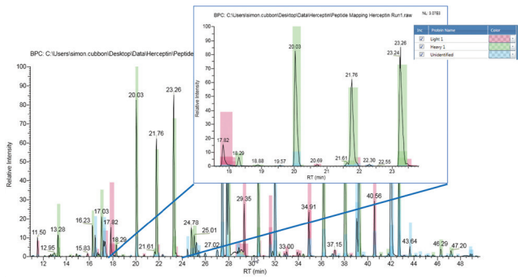
Accurately deconvolute fully or partially resolved data using tested novel Xtract and ReSpect algorithms to provide confident molecular weights of proteins in both acidic and native conditions.

DAR Accuracy. Every time.

Why acquire all of your data and use only a small section to report a DAR? Sliding Window ensures you report the true DAR based upon all your data, not a subset.



Easily calculate DARs



Automatically annotate peptides

PTMs? See everything.

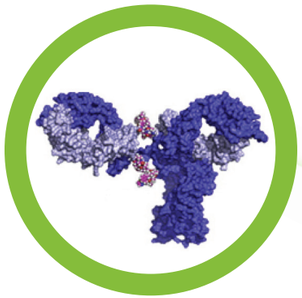
From powerful chromatographic shading, predicted vs. experimental fragmentation spectra to comprehensive sequence variant searching and *de novo* sequencing, you can be confident in your sequence.

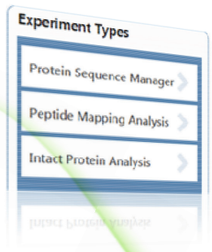
...with **BioPharma** Finder

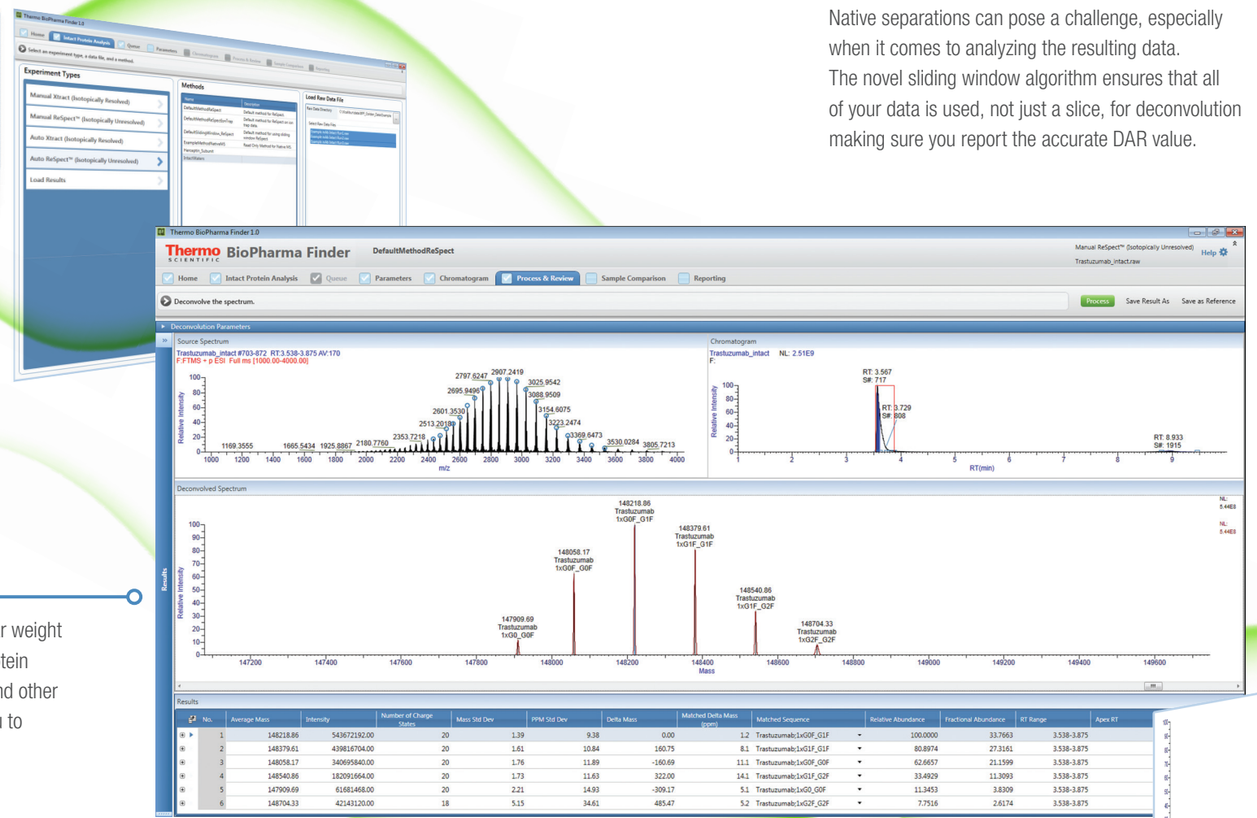
> Historically it took weeks to evaluate data, ruling out many false positives. BioPharma Finder is a **unique solution** that has **efficient workflows** meaning that you don't need to spend hours fine tuning parameters to get the **right answer the first time.** For comparative quantitative modification analyses, we have gone from **two weeks** of analysis down to **one day** for multi-batch samples.
>
> *Guilong Charles Cheng, Alexion Pharmaceutical Inc.*

Intact Protein & Subunit Mass Analysis

The development of monoclonal antibodies (mAbs) and ADCs is challenging. There is now an easier path to take for the analysis of critical quality attributes in these challenging biologics – BioPharma Finder Software.



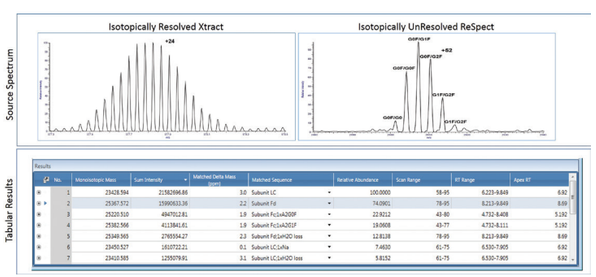




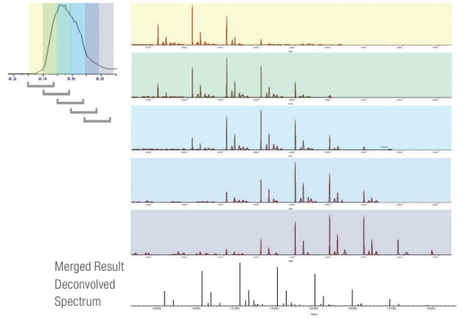
Simple, intuitive user interface

Whether resolved or unresolved, your proteins are in safe hands with **superior deconvolution** algorithms (Xtract & ReSpect) to determine accurate information on various protein properties, such as intact molecular mass, glycosylation forms, amino acid sequence, posttranslational modifications, disulfide linkages as well as higher order structural information.

The software **provides confident deconvolved** molecular weight of proteins in both denaturing and native conditions and protein sequence matching **identifies N-linked glycoylations** and other common modifications via intact mass analysis, helping you to understand your biologics hetergeneity.

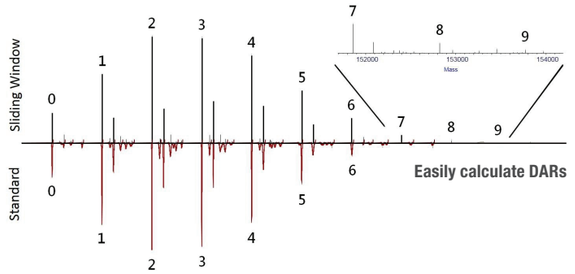


Deconvoluted high resolution Orbitrap MS spectra provides **low-ppm** mass accuracy molecular weights and relative quantitation of glycoform heterogeneity.



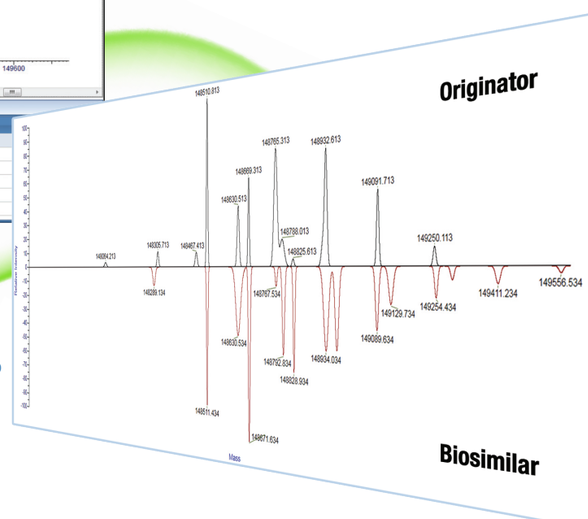
Sliding window is a novel algorithm for the interpretation of LC/MS data of intact proteins. Moving averaged spectrum across the chromatogram generates deconvoluted spectra, resulting in a single deconvoluted spectrum of all protein components. This is supported for both high resolution (Xtract) and low resolution (ReSpect) data.

Native separations can pose a challenge, especially when it comes to analyzing the resulting data. The novel sliding window algorithm ensures that all of your data is used, not just a slice, for deconvolution making sure you report the accurate DAR value.



> The BioPharma Finder software export feature has the potential to significantly reduce the time it takes to prepare figures for FDA filings.
>
> *Richard Rogers, Just Biotherapeutics*

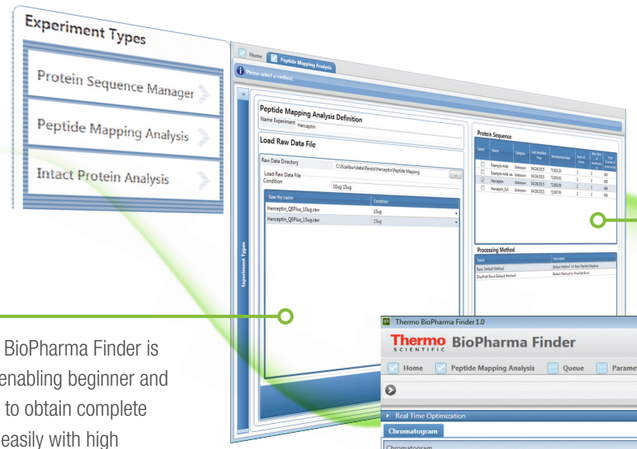
Are they really the same? When it comes to biosimilars you can't afford to miss a thing. Demonstrate equivalence or identify differences through unique comparison and visualization tools.



Easy, yet powerful mirror plotting

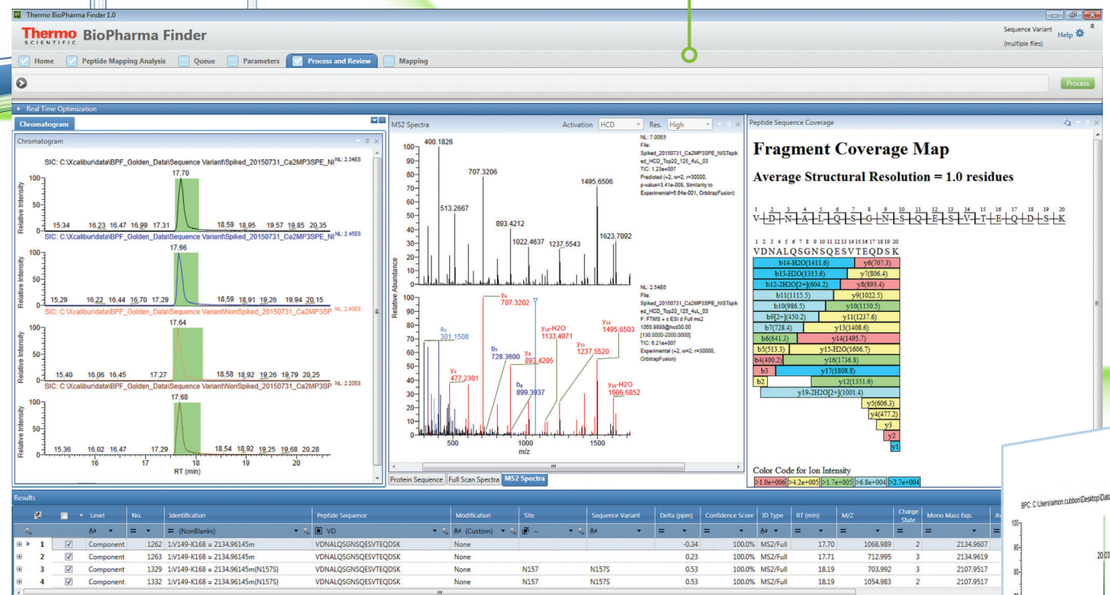
Peptide Mapping

Small changes in peptide sequence can result in changes to higher order protein structures, compromising biotherapeutic safety and efficacy. Complete peptide map coverage guarantees you see the whole picture.

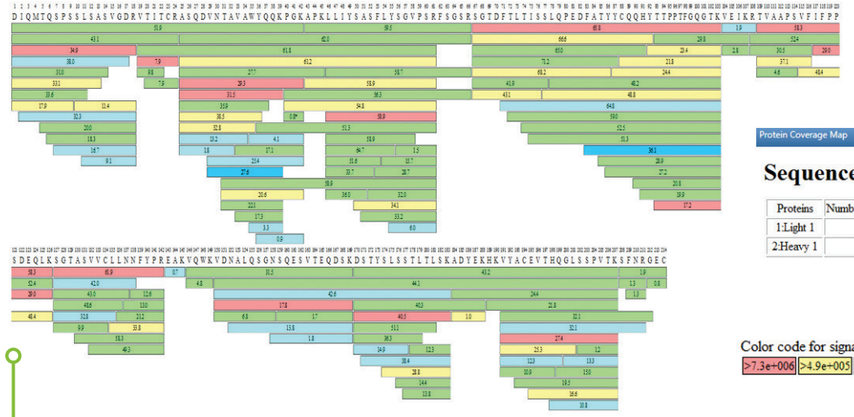


Batch processing capabilities together with an interactive wizard for editing process methods allows easy and efficient data analysis with maximum throughput.

Thermo Scientific BioPharma Finder is workflow-driven, enabling beginner and expert users alike to obtain complete peptide coverage easily with high confidence.

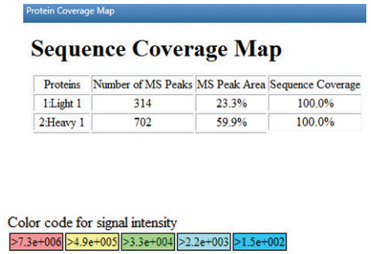


Full MS, MS² experimental vs. predicted spectra and fragment coverage maps for each identification help to ***increase confidence in your peptide sequence.*** *Compare extracted ion chromatograms for batch evaluation, with relative quantitation information for each sample.*



Informative peptide fragment map coverage.

Informative and interactive sequence coverage map, colored by peptide intensity.



Multiple interactive plot display options so you can see what you want, when you need it.

The ability to perform Sequence Variant Searching, disulfide link analysis and de novo sequencing with quantitation of post-translational modifications assures you wont miss anything.

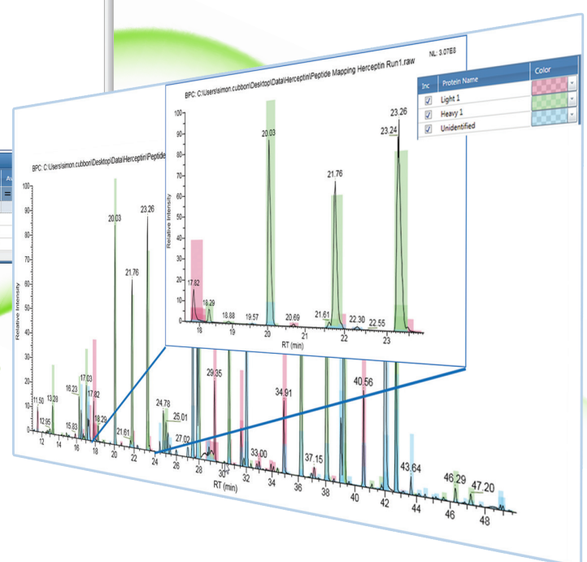
> Being able to sort for sequence variants gives me the confidence that I'm not overlooking any.
>
> *Shannon Williams, Coherus Biosciences*

	Protein	Residue #	Modification	Category	Normalized Time Shift	Predicted Time Shift	Confidence	Recovery	% Abundance Sample	% Abundance Reference
1	Light Chain	48	Y48+125.8970	Unknown Modification	27.1%	N/A	100.0%	38.2%	0.0543%	0.0536%
2	Light Chain	157	N157(N157S)	Sequence Variant	1.3%	2.1%	100.0%	21.1%	0.6265%	0.0002%
3	Light Chain	166	D166+Isomerization	Modification	-3.0%	-1.0%	100.0%	13.2%	0.1201%	0.1285%
4	Heavy Chain	162	N162+Deamidation	Modification	1.1%	N/A	100.0%	7.8%	11.5107%	9.8140%
5	Heavy Chain	255	M255+Oxidation	Modification	-4.8%	-10.0%	100.0%	7.7%	81.0324%	75.4649%
6	Heavy Chain	318	N318+NH3 loss	Modification	5.8%	8.0%	100.0%	25.4%	2.1513%	2.1317%
7	Heavy Chain	384	W384+Double Oxidation	Modification	-8.2%	-8.0%	100.0%	14.9%	0.3724%	0.3042%

Interactive Modification Summary
Identify and localize glycoforms, deamidations, oxidations, other sequence variants and PTMs.

Comprehensive results table providing amino acid sequence confirmation with mass tolerance, modification, identification, retention time and confidence information. Real-time filtering to optimize your data, all exportable.

Powerful visualization tools such as **chromatographic shading** afford increased efficiency in data mining and interpretation.



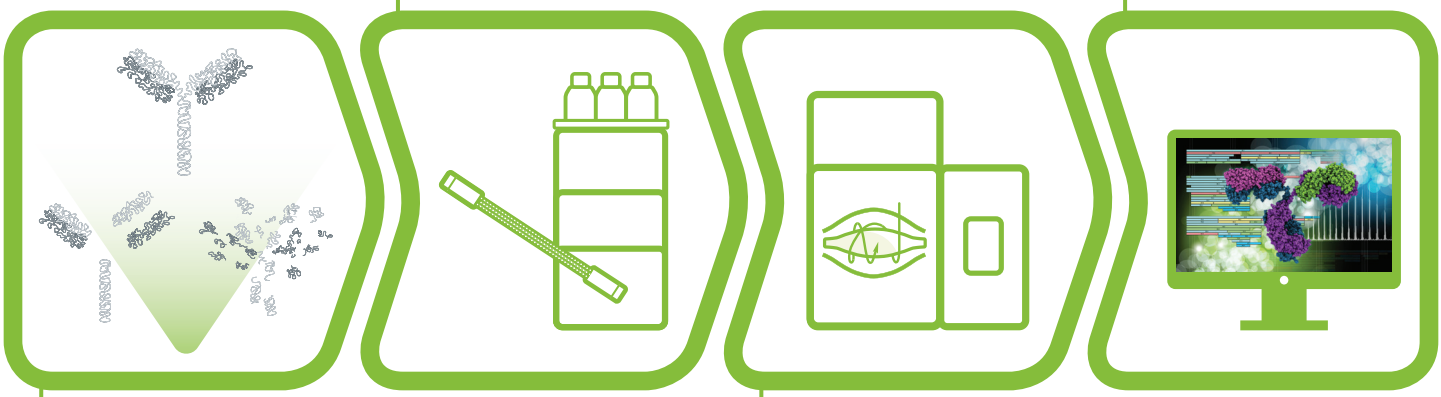
Annotated peptide map

Robust Separations

Purpose-built biocompatible systems yield precise retention times from sample to sample and increase confidence in peak assignments.

Thermo Scientific BioPharma Finder

From novel deconvolution algorithms generating comprehensive results to easy to understand data visualization tools, BioPharma Finder helps you to take the right path. Every time.



Rapid User-friendly Sample Preparation

Whether you are analyzing intact proteins or peptides, we have sample preparation and chromatographic columns that allow you to get the most out of your samples.

High Resolution Accurate Mass MS

Obtain excellent resolution, mass accuracy and dynamic range for the most challenging samples from the gold-standard in mass spectrometry.

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