



Biologics Explorer software

**Achieve clarity on
your biotherapeutic**

Wide variety of workflows

Adequately characterizing your biopharmaceutical requires many different LC-MS assays, but you shouldn't need a separate piece of software for each workflow.

Biologics Explorer software supports the most important LC-MS characterization assays right out-of-the-box, based on industry best practices. Even better, the nodal structure is easy to optimize so you can get exactly what you want from your assays.

Currently available workflows include:

- Intact and subunit analysis
- Peptide mapping by EAD or CID
- Disulfide bond analysis, and
- PTM determination, including MAM

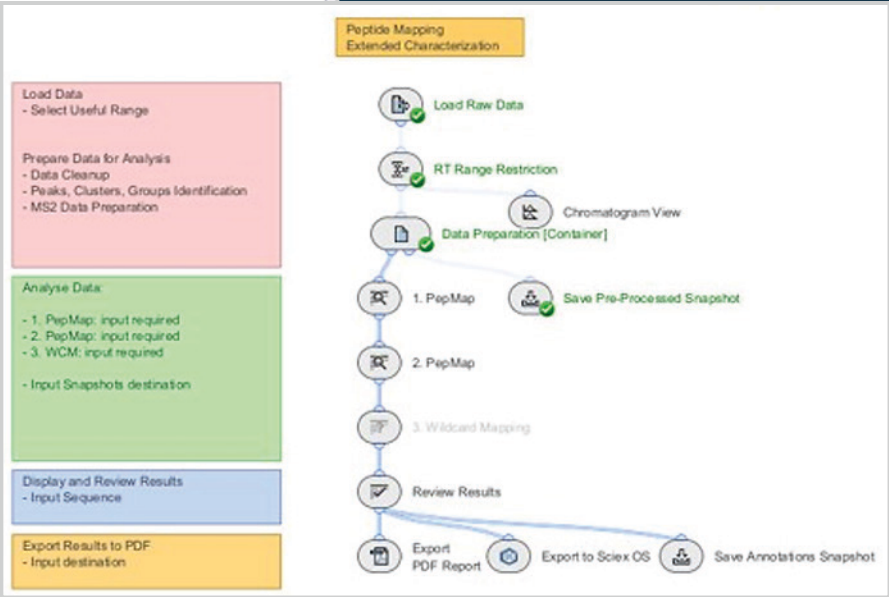
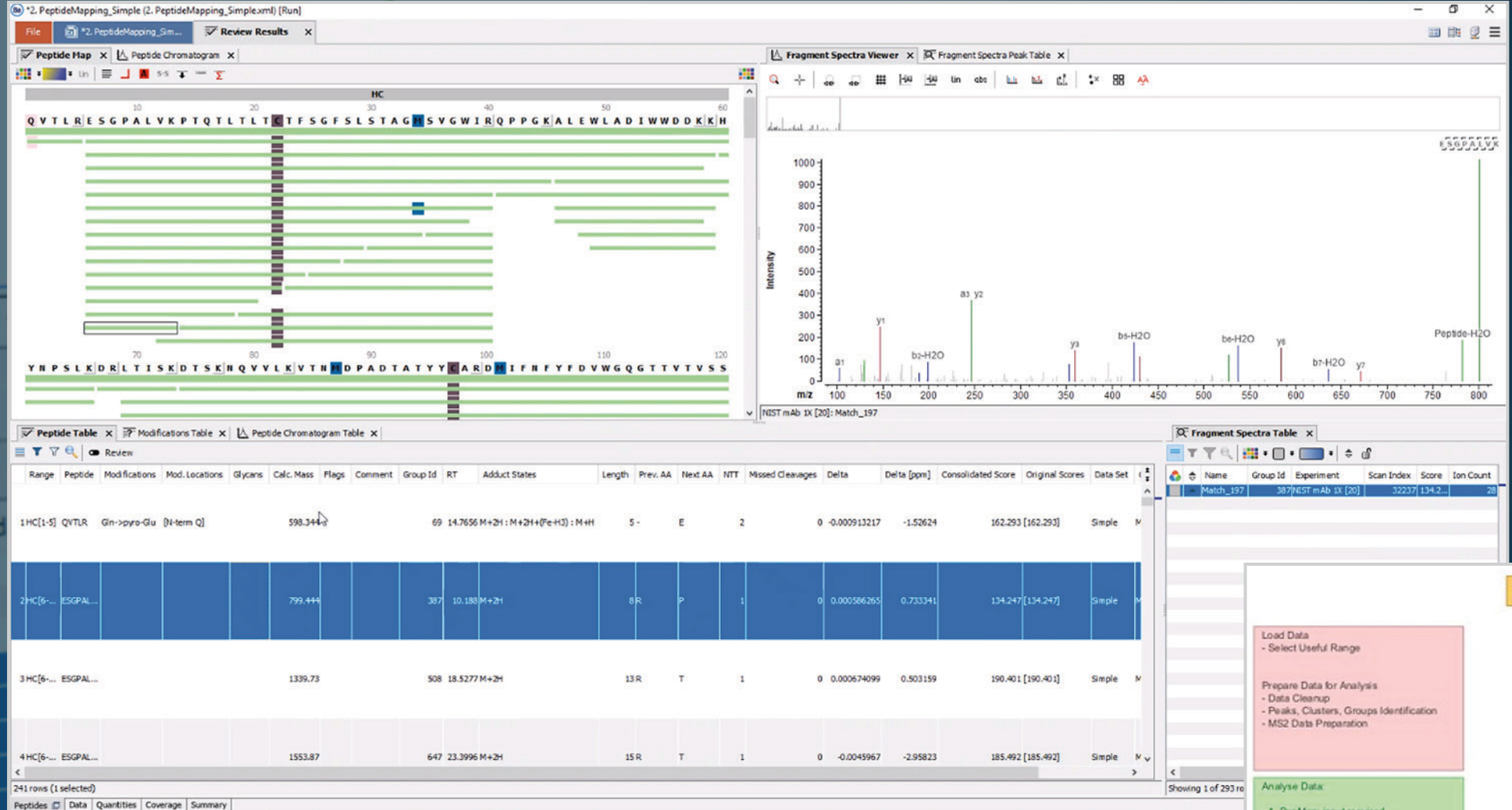


Peak Id	Protein Na...	Disulfide B...	Modifications	Glycosylation	Unpaired Cys	Flags	Comment	Calc. Avg. Mass	Avg
672 LC		2*S-S				1		23123.5	
1795 LC-LC		5*S-S				0		46245	
1721 HC		5*S-S	Gln->pyro-Glu + Lys-loss			1		49451.5	
4239 HC-HC-LC-LC		16*S-S	2*Gln->pyro-Glu + 2*Lys-loss	G0F + G0F-GlcNAc		0		147838	
4242 HC-HC-LC-LC		16*S-S	2*Gln->pyro-Glu + 2*Lys-loss	2*G0F		0		148201	
4243 HC-HC-LC-LC		16*S-S	2*Gln->pyro-Glu + 2*Lys-loss	G0F + G1F		0		148525	
4244 HC-HC-LC-LC		16*S-S	2*Gln->pyro-Glu + 2*Lys-loss	G0F + G2F		0		148847	
4244 HC-HC-LC-LC		16*S-S	2*Gln->pyro-Glu + 2*Lys-loss	2*G1F		0		148201	
4245 HC-HC-LC-LC		16*S-S	2*Gln->pyro-Glu + 2*Lys-loss	G1F + G2F		0		148525	
4246 HC-HC-LC-LC		16*S-S	2*Gln->pyro-Glu + 2*Lys-loss	2*G2F		0		148847	

Peptide level analysis

The pre-built peptide mapping workflows enable a quick start for both new and advanced users. State-of-the-art algorithms are highly optimized for processing both CID and EAD data.

Accelerated data analyses through the customizable interface allows for curation of results and comparison of large numbers and types of samples. All of the workflow nodes are highly customizable to particular peptide-level analyses such as peptide mapping, PTM analysis, or even disulfide bond mapping.



Ready to go from install

The Biologics Explorer software interface starts with four sections:

- 1 Workflow preview pane
- 2 Workflow directory
- 3 File menu
- 4 Tools



Leveraging the latest acquisition techniques and built on a heritage of proven performance, Biologics Explorer software delivers highly accurate and informative workflows for fully characterizing protein biotherapeutics.

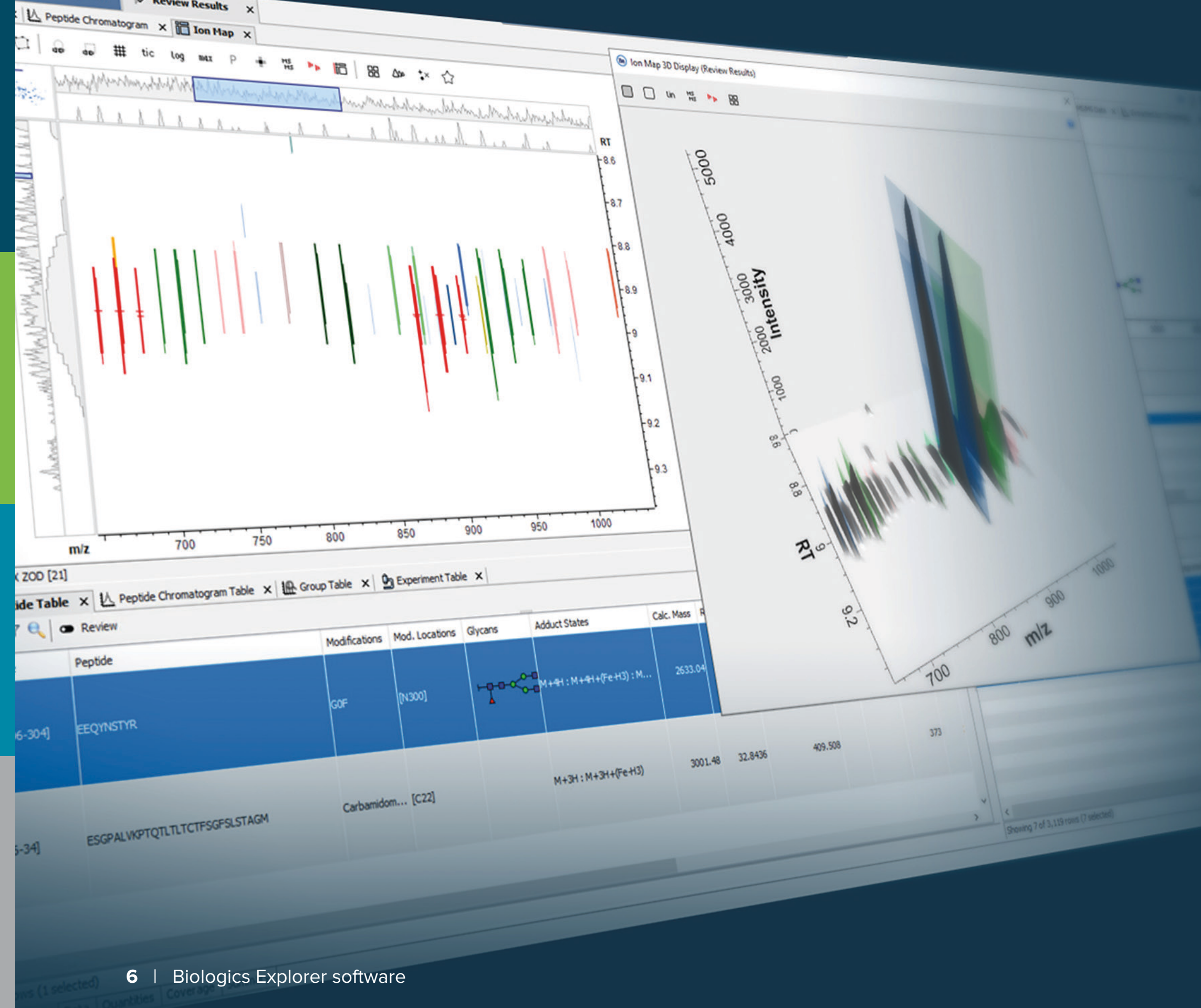
Reach decisions on the most important critical quality attributes for biopharmaceuticals faster and more confidently.

Pre-built workflow templates for a variety of characterization workflows are fast and easy to use for consistent, automated data processing and method optimization.

Visualizations provide insight

Next generation biotherapeutics are becoming more complex with more potential post translational modifications and protein forms. Characterization by mass spectrometry also produces a vast amount of information. This can make it very difficult to quickly interpret what is going on with your protein therapeutic.

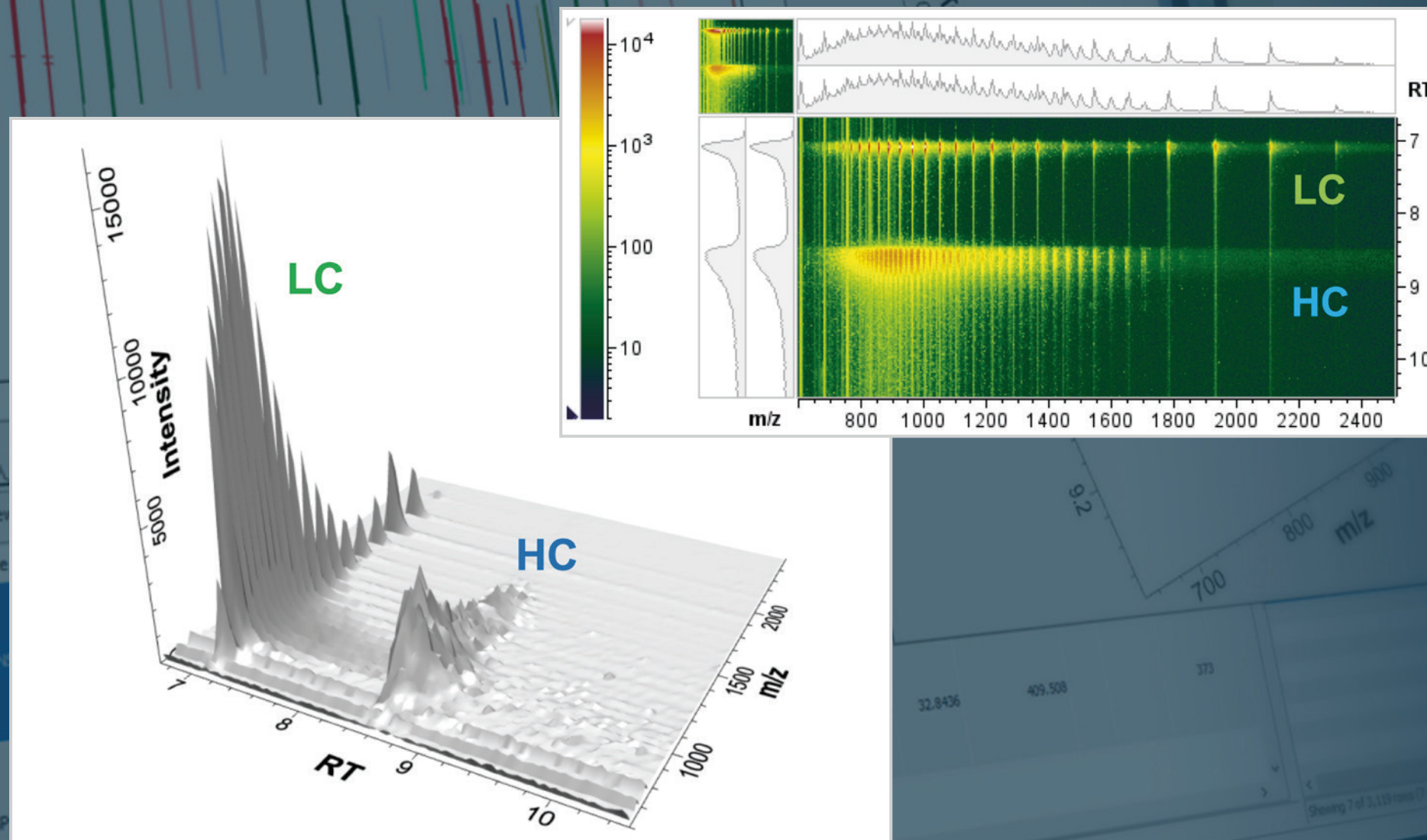
With the use of intuitive visualizations, Biologics Explorer software gets you from sample to insight – fast! Even in raw data, you have the ability to immediately see patterns and features so you can avoid missing anything important.



Visualizations of intact data

The results shown here are an intact analysis of reduced NIST mAb antibody. The ion map provides a highly informative snapshot of the MS ion series for the reduced heavy and light chains. Ions in the sample that are not related to the heavy chain and light chain can be clearly observed.

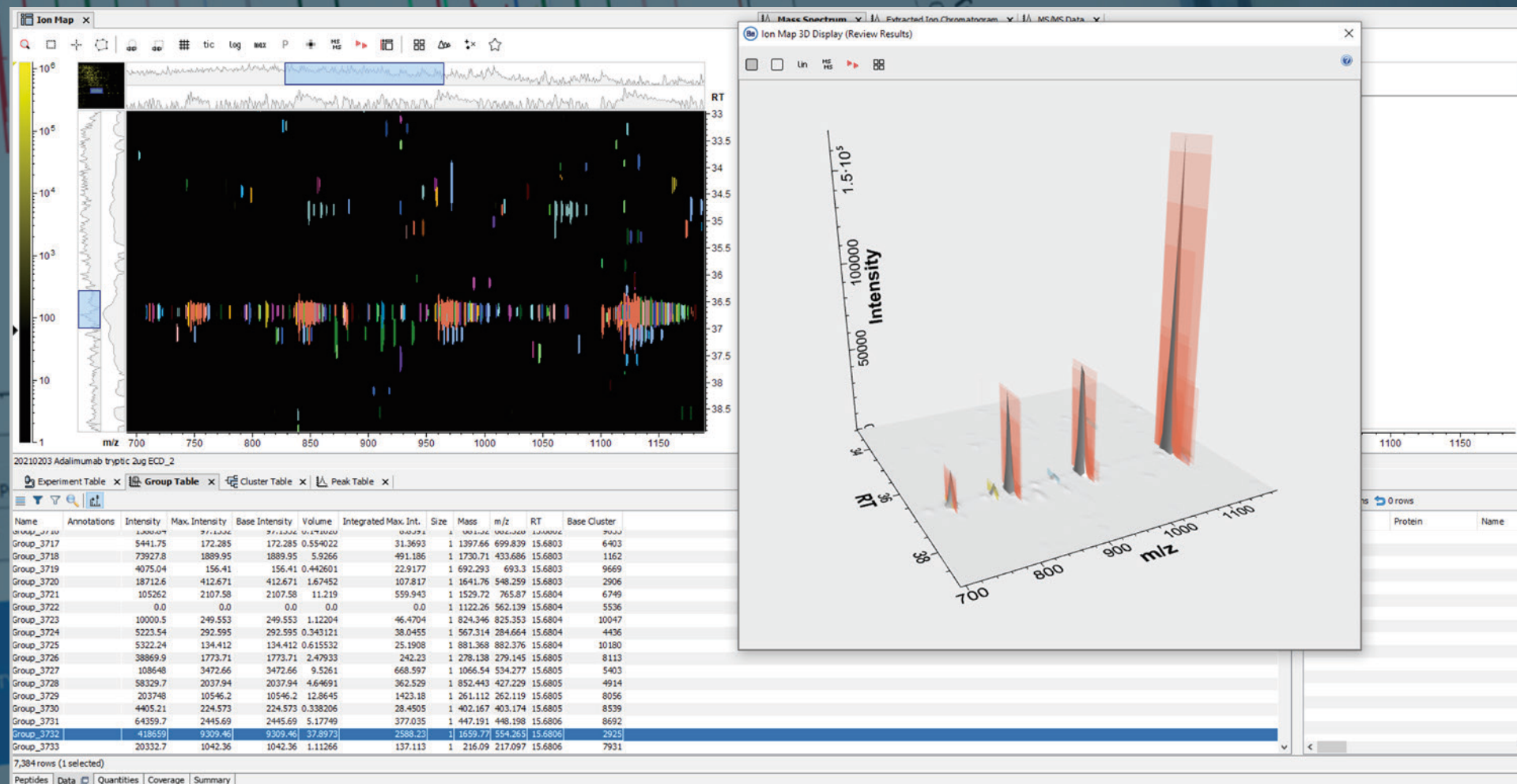
Likewise, the same data are represented as a 3D display. Similar conclusions about contaminating ions can be observed even quicker from this view. The display can be rotated in any direction and zoomed in or out to focus on areas of interest.



Visualizations of peptide-level data

The results at left are the MS spectrum of a peptide-level analysis of a tryptically digested monoclonal antibody. The ion map shows different colors, with each color representing a different component. The ion map can be easily customized with many different color schemes to suit your needs.

The 3D display shows a zoomed-in region of the ion map. The coloring by component can extend to the 3D display as well. In this example, a component and its isotope series are clearly indicated with red highlighting. Other ions are highlighted with different colors making it immediately obvious which ions are related and how. The filters for coloring, clustering and visualization can all be easily set and modified.



Built for EAD

Electron activated dissociation (EAD) in the ZenoTOF 7600 system breaks new ground in depth of coverage for peptide mapping and PTM analysis of biopharmaceuticals. EAD produces incredibly rich MS/MS spectra.

Biologics Explorer software is critical for transforming those rich spectra into incredibly informative results. The data processing engine is optimized to extract the maximum amount of information from every CID and EAD spectrum.



Transparency from start to report

The biologics characterization in some applications can leave you wondering exactly how the result was reached. The data can go in, and an answer can come out, without any clarity around how it happened.

Biologics Explorer software is all about transparency. The workflow-based setup allows you to see all the steps of what is happening with your data. You can also customize the workflow for your specific needs.

Biologics Explorer is also transparent in reporting. You can not only save results, but also the entire workflow, just in case you ever need to reprocess results – and from the PDF!

3. PeptideMapping_Extended (Personal)

.....1020304050607080
DIQMTQSPSS	LSASVGDRTV	ITCRASQGIR	NYLAWYQOKP	GKAPKLLIYA	ASTLQSGVPS	RFSGSGSGTD	PTLTISSLQP
DIQMTQSPSS	LSASVGDRTV	ITCRASQGIR	NYLAWYQOKP	GKAPKLLIYA	ASTLQSGVPS	RFSGSGSGTD	PTLTISSLQP
DIQMTQSPSS	LSASVGDRTV	ITCRASQGIR	NYLAWYQOKP	GKAPKLLIYA	ASTLQSGVPS	RFSGSGSGTD	PTLTISSLQP
DIQMTQSPSS	LSASVGDRTV	ITCRASQGIR	NYLAWYQOKP	GKAPKLLIYA	ASTLQSGVPS	RFSGSGSGTD	PTLTISSLQP
DIQMTQSPSS	LSASVGDRTV	ITCRASQGIR	NYLAWYQOKP	GKAPKLLIYA	ASTLQSGVPS	RFSGSGSGTD	PTLTISSLQP

3. PeptideMapping_Extended (Personal)

3. PeptideMapping_Extended

Peptide Mapping
Extended Characterization

- Load Data
 - Select Useful Range
- Prepare Data for Analysis
 - Data Cleanup
 - Peaks, Clusters, Groups Identification
 - MS2 Data Preparation
- Analyse Data:
 - 1. PepMap: input required
 - 2. PepMap: input required
 - 3. WCM: input required
 - Input Snapshots destination
- Display and Review Results
 - Input Sequence
- Export Results to PDF
 - Input destination

Workflow steps:

- Load Raw Data
- RT Range Restriction
- Data Preparation (Container)
1. PepMap
2. PepMap
3. Wildcard Mapping
- Review Results
- Export PDF Report

Table: Confirmed position

Overall	Adalimumab
20210203	Adalimumab
20210203	Adalimumab
20210203	Adalimumab
20210203	Adalimumab
20210203	Adalimumab

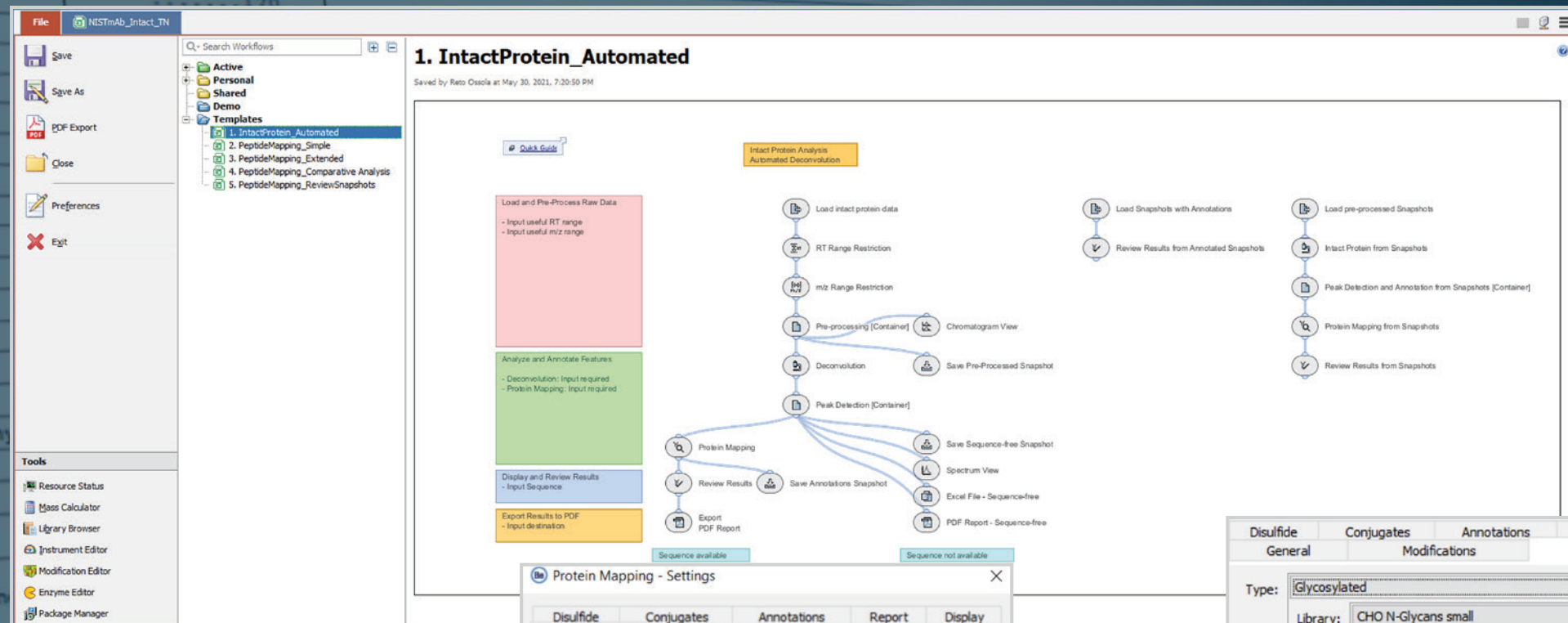
Table: Confirmed position

.....10203040
IQVRLGGEHNI	DVLEGNBQFI	NAAKIITHPN	FNGNTL
LGEHNI	DVLEGNBQFI	NAAKIITHPN	FNGNTL
LGEHNI	DVLEGNBQFI	NAAKIITHPN	FNGNTL
LGEHNI	DVLEGNBQFI	NAAKIITHPN	FNGNTL
LGEHNI	DVLEGNBQFI	NAAKIITHPN	FNGNTL

Transparency in processing

Biologics Explorer gives you unprecedented visibility to the algorithms in the pre-built methods. You have the ability to view or modify nearly all of the settings for each node in a workflow.

Your processing method is no longer a “black box”.



Protein Mapping - Settings

Disulfide Conjugates Annotations Report Display
General Modifications Glycosylation

Sequence(s): From Text
Sequences: >HC
QVTLRESGPALWKPTQLTLCTFSGFSLSTAGM
>LC
DIQMTQSPSTLSASVGRVITTCASASSRVGYMH

Mass Tolerance: 20 ppm
 Use Monoisotopic Mass if Available

Consolidate Matches

Delta Mass Tolerance: 1.0 Da
 Ignore Annotated Features

Disulfide Conjugates Annotations Report Display
General Modifications Glycosylation

Type: Glycosylated
Library: CHO N-Glycans small
Allowed Sites: Only N-Linked
Use Consensus Sequences:
Filter for Core Structures:
Substituents:
Max. Substitutions: 1

Disulfide Conjugates Annotations Report Display
General Modifications Glycosylation

Fixed: Gln->pyro-Glu (N-term Q)
Lys-loss (Protein C-term K)

Variable:

General Modifications Annotations Report Display
Disulfide Conjugates Glycosylation

State: Fully Connected
Connectivity: Unspecified
 Search all combinations
Additional chains: 2

Unpaired Cysteine Modification: CysteinyI (C)

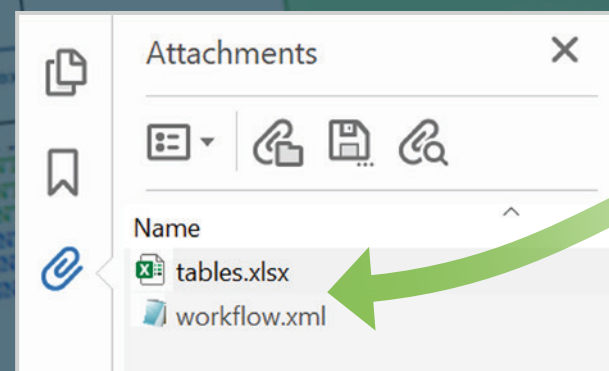
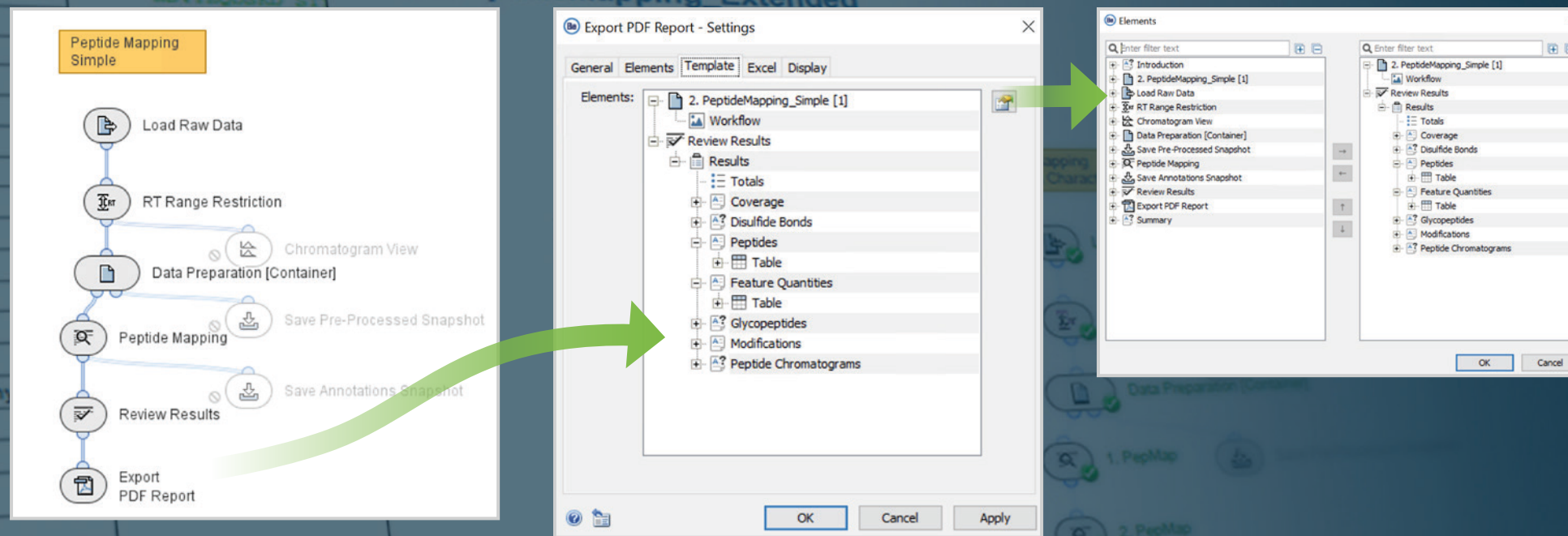
Transparency in reporting

Biologics Explorer gives you the ability to report nearly every possible raw or processed data point within a workflow. There are many different elements, i.e., tables, spectra, and figures, that can be easily incorporated into reports. Filters and report templates make it fast and effective to get to the report definition that is most impactful.

The PDF reports have additional embedded information such as Excel spreadsheets and complete workflows.

Never worry about having to save a workflow backup.

You can save it in the report!



Additional Excel summary spreadsheets can be embedded and accessed from within the PDF.

Recreate a workflow from the PDF. Dragging and dropping the XML file from the PDF automatically recreates the workflow from which the results were produced.

Powered by Genedata Expressionist®

Biologics Explorer software is built upon an industry-leading platform for biopharmaceutical mass spectrometry.

Biologics Explorer leverages the expert knowledge and proven capabilities of Genedata Expressionist.

This also gives a natural and seamless transition to Genedata Expressionist, if you need customized workflow solutions or an enterprise implementation.





ZenoTOF 7600 system

This mass spectrometer gives richer, more comprehensive data with new innovations that have never been seen in an accurate mass system. EAD fragmentation and the Zeno trap pave the way for precise and accurate MS and MS/MS data.



X500B QTOF system

This high resolution Quadrupole Time-of-Flight (QTOF) system combines robust and reliable instrumentation with powerful and intuitive software to get you to characterization answers faster and easier, in a true benchtop platform.



TripleTOF 6600+ system

This high-performance accurate mass solution offers a combination of qualitative and quantitative analysis and advanced workflow capabilities. Optimized for large-scale quantitative mass spectrometry, the TripleTOF 6600+ system offers sensitive and robust performance.

SCIEX Now support network

The destination for all your support needs



Biologics Explorer software

Achieve better insights on biotransformation and impurities

Learn more about what Biologics Explorer Software can do for you!

Data integrity

Increase your confidence with compliance services to help you safeguard your data, confirm data integrity and ensure system modifications can be traced.

Onboarding

We register you to SCIEX Now Online, enroll you in your Learning Hub learning path and send you a welcome email.

Lab enhancement services

SCIEX lab enhancement services apply a holistic approach to your lab to increase productivity and reduce system downtime.

Self-help resources

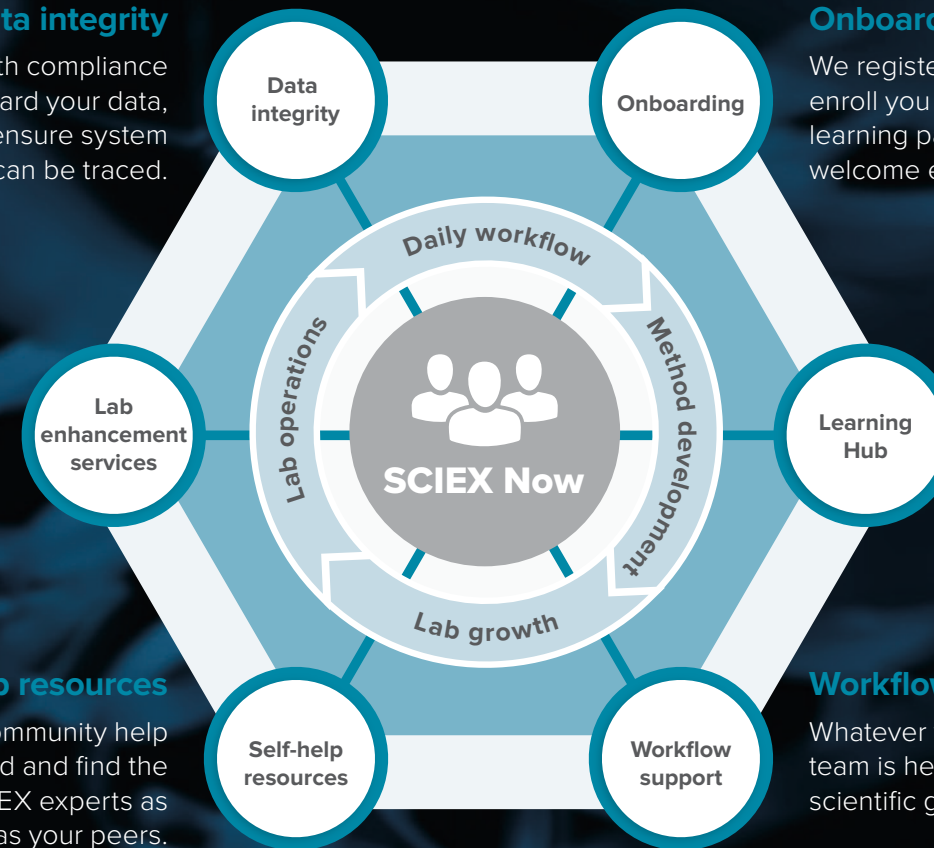
Our knowledge base and community help you move your science forward and find the answers you need from SCIEX experts as well as your peers.

Learning Hub

Best-in-class content and personalized learning paths—delivered using the latest memory science techniques.

Workflow support

Whatever your challenge, the SCIEX support team is here to help you achieve your scientific goals quickly and efficiently.



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Headquarters
500 Old Connecticut Path
Framingham, MA 01701 USA
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[sciex.com](https://www.sciex.com)

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