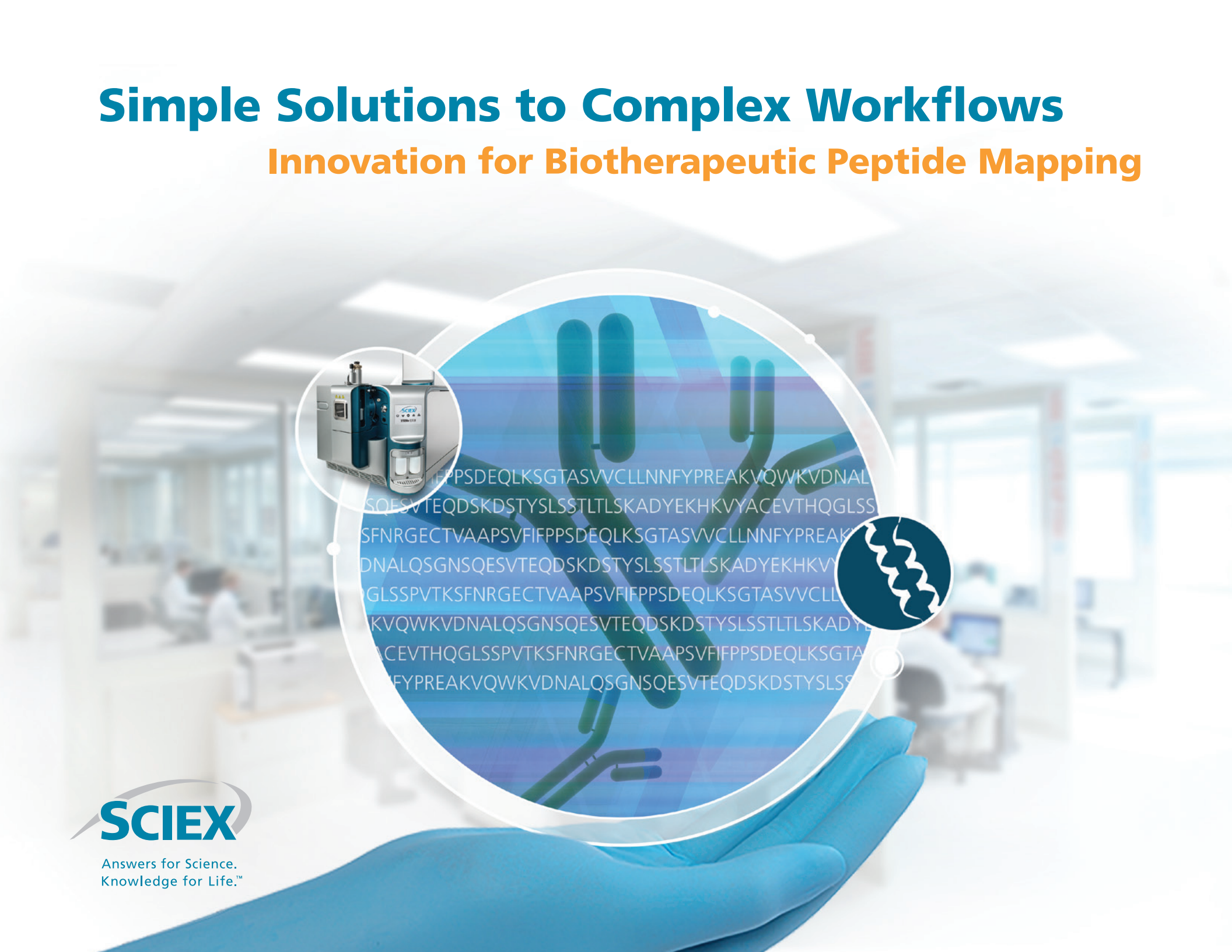
Simple Solutions to Complex Workflows

Innovation for Biotherapeutic Peptide Mapping



SCIEX

Answers for Science.
Knowledge for Life.™

Simplify Biotherapeutic Peptide Mapping for Better Information, Faster

Accelerate your peptide mapping workflows with SCIEX QTOF platforms, separation systems and software. The compact and user-friendly X500B QTOF system speeds your standard mapping workflow, and powerful BioPharmaView™ software automates data processing to get you answers faster.

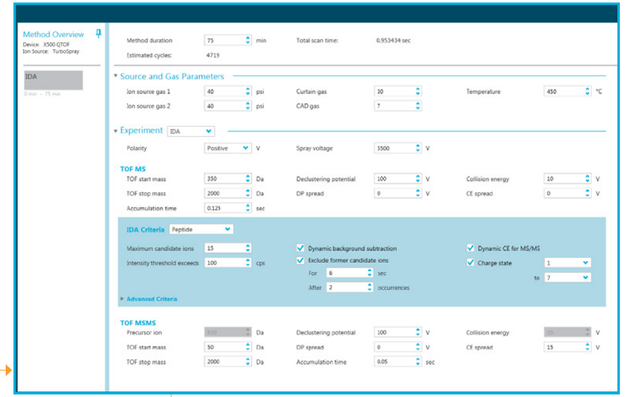
Streamlined analyses help you make better decisions about your biologic development and speed your time to market.

Peptide Mapping for Every Mass Spec User

Comprehensive peptide mapping of biologics is not a simple task. Usually, a mass spec expert needs to develop protocols and analyze the data to ensure the biotherapeutic is being produced as expected. The easy, point-and-click interface of SCIEX OS, exclusively on X500 series QTOF systems, makes setup of your peptide mapping workflow rapid and simple. In fact, even novice mass spec users should have no trouble getting up and running quickly.

No-Worry Sample Queue:

X500B calibration seamlessly integrates into your sample queue for rock-solid, accurate performance



Easy-to-Learn User Interface:

Simply build and optimize high-performance peptide mapping methods with SCIEX OS

Fast Peptide Mapping MS Method Setup

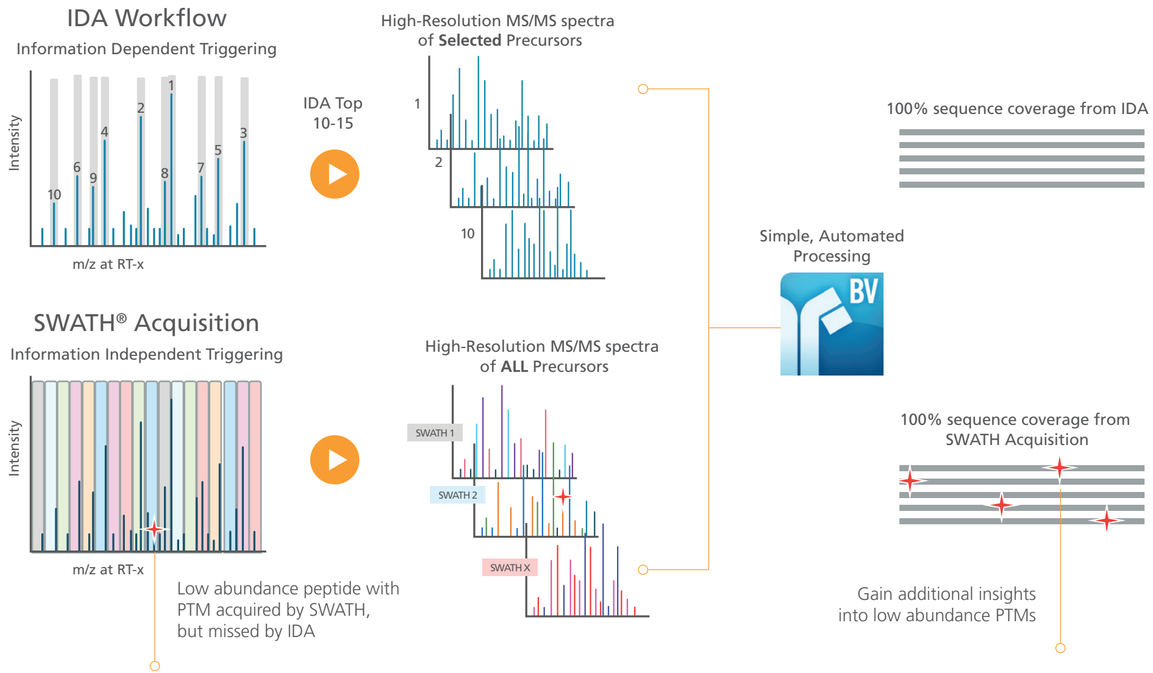
It's easier than ever with point-and-click parameter definition and intuitive layout, even for novice users

For more information about the X500B QTOF System, please visit sciex.com/X500B

Low Abundance Peptides and PTMs Can't Hide from SWATH® Acquisition

In addition to traditional information dependent acquisition (IDA) methods, the X500B QTOF supports proprietary SWATH® Acquisition for peptide mapping, which provides comprehensive data collection and eliminates the need for IDA criteria set-up and traditional method development.

With SWATH Acquisition, high-resolution MS/MS are acquired for all precursor ions, providing truly comprehensive and unbiased data collection. The unbiased approach enables acquisition of high-resolution, accurate mass MS/MS spectra of all low abundance peptides and post translational modifications (PTMs) that could be missed by information dependent peptide map workflows. Furthermore, a standard, generic SWATH method can be used for almost every biotherapeutic peptide mapping analysis, further simplifying your workflow setup and helping you get answers faster.



Four Easy Steps from Data to Answers

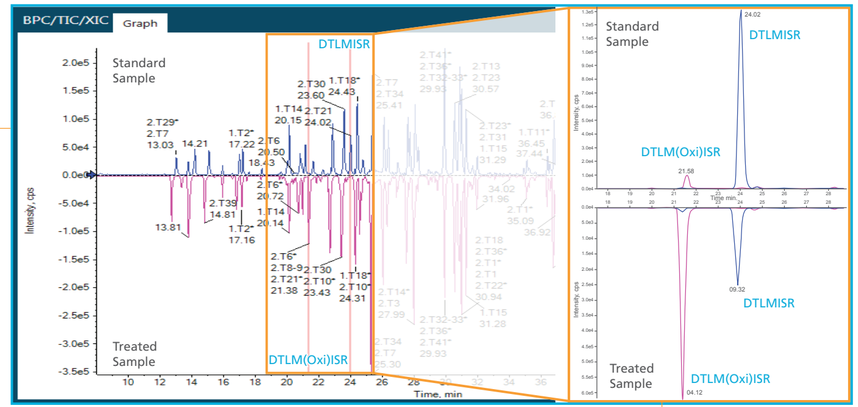
Data acquisition by an IDA or SWATH Acquisition method is only the first part of the story. To get faster answers to your peptide mapping questions, you need powerful data processing. BioPharmaView™ Software, connected to the X500B system and SCIEX OS, is a rapid and intuitive package for the analysis of your peptide mapping data.

Peptide mapping using SWATH Acquisition showing 100% sequence coverage of rituximab biotherapeutic on the X500B system.

See It All, Fast

Comprehensive SWATH Acquisition with high-resolution MS/MS data at lightning speeds means you won't miss low level peptides and PTMs. You'll quickly and easily identify changes in modification state using advanced visualization and automated PTM ratio calculations in BioPharmaView Software.

Identify changes in modification state for important peptides using the clear visualization and reporting functions in BioPharmaView Software



Focus in on the altered levels of peptide oxidation between samples in the Explorer view

Peptide Results | Matched | Unmatched

	Filename	Sequence	Modifications	Modification Percent	Charge	Observed Mono m/z	Theoretical Mono m/z	Error (PPM)	XIC Area
1	SWATH.wiff2	DTLMISR	Oxidation@4(256)	4.2% ±3.1 (Oxidation@4(256) : None@4(256))	1	851.4316	851.4291	2.8	9.81e3
2	SWATH.wiff2	DTLMISR		95.8% ±3.0 (None@4(256) : None@4(256))	1	835.4347	835.4342	0.6	8.12e5
3	SWATH.wiff2	DTLMISR	Oxidation@4(256)	4.2% ±3.1 (Oxidation@4(256) : None@4(256))	2	426.2184	426.2182	0.5	1.43e5
4	SWATH.wiff2	DTLMISR		95.8% ±3.0 (None@4(256) : None@4(256))	2	418.2206	418.2207	-0.3	1.87e6
5	treated_SWATH.wiff2	DTLMISR	Oxidation@4(256)	70.8% ±3.0 (Oxidation@4(256) : None@4(256))	1	851.4308	851.4291	2.0	1.61e5
6	treated_SWATH.wiff2	DTLMISR		29.2% ±0.7 (None@4(256) : None@4(256))	1	835.4360	835.4342	2.1	6.43e4
7	treated_SWATH.wiff2	DTLMISR	Oxidation@4(256)	70.8% ±3.0 (Oxidation@4(256) : None@4(256))	2	426.2182	426.2182	-0.1	8.81e5
8	treated_SWATH.wiff2	DTLMISR		29.2% ±0.7 (None@4(256) : None@4(256))	2	418.2206	418.2207	-0.3	3.77e5

Accurately and completely identify modified peptides from the SWATH Acquisition data

Speed analysis time and comparisons between samples with automated calculation of modification levels from multiple charge states of peptides

Identify Glycopeptides with Confidence

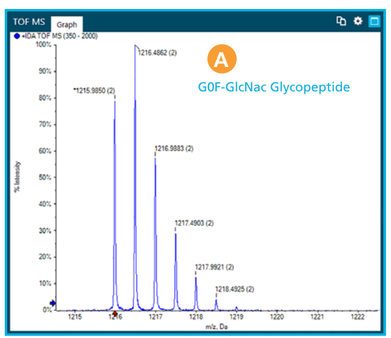
By monitoring glycan species at the peptide level, you can reduce some of the difficulty often associated with glycan release and labeling. BioPharmaView Software presents clear glycopeptide information in table format, links directly to the MS data, and shows high-resolution MS/MS for structural confirmation for reversed phase and HILIC separations.

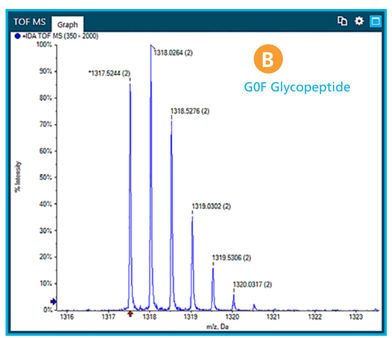
Peptide Results | Matched | Unmatched

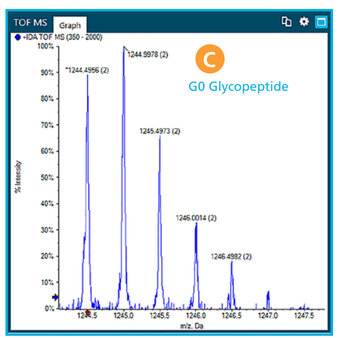
	Sequence	Modifications	Modification Percent	Charge	Observed Mono m/z	Theoretical Mono m/z	Error (PPM)	XIC Area
1	EEQYNSTYR	G0F-GlcNAc@5(301)	42.3% ±4.6 (G0F-GlcNAc@5(301) : G0@5(301))	2	1215.9850	1215.9869	-1.5	4.13e5
2	EEQYNSTYR	G2F@5(301)	1.7% ±0.2 (G2F@5(301) : G0@5(301))	3	986.7199	986.7220	-2.1	7.00e3
3	EEQYNSTYR	G0F@5(301)	39.0% ±9.7 (G0F@5(301) : G0@5(301))	2	1317.5244	1317.5266	-1.6	2.94e5
4	EEQYNSTYR	G0F@5(301)	39.0% ±9.7 (G0F@5(301) : G0@5(301))	3	878.6853	878.6868	-1.7	2.02e5
5	EEQYNSTYR	G1F@5(301)	11.7% ±6.4 (G1F@5(301) : G0@5(301))	2	1398.5518	1398.5530	-0.8	5.25e4
6	EEQYNSTYR	G1F@5(301)	11.7% ±6.4 (G1F@5(301) : G0@5(301))	3	932.7033	932.7044	-1.3	7.60e4
7	EEQYNSTYR	G0@5(301)	5.4% ±0.6 (G0@5(301) : G0@5(301))	2	1244.4956	1244.4976	-1.6	5.25e4
8	EEQYNSTYR	G0@5(301)	5.4% ±0.6 (G0@5(301) : G0@5(301))	3	829.9975	830.0008	-4.0	2.28e4

A
B
C

Confidently identify glycopeptides using high-resolution accurate mass TOF-MS data. High-resolution MS/MS data can be used for structural confirmation







Recognize Deamidation Instantly

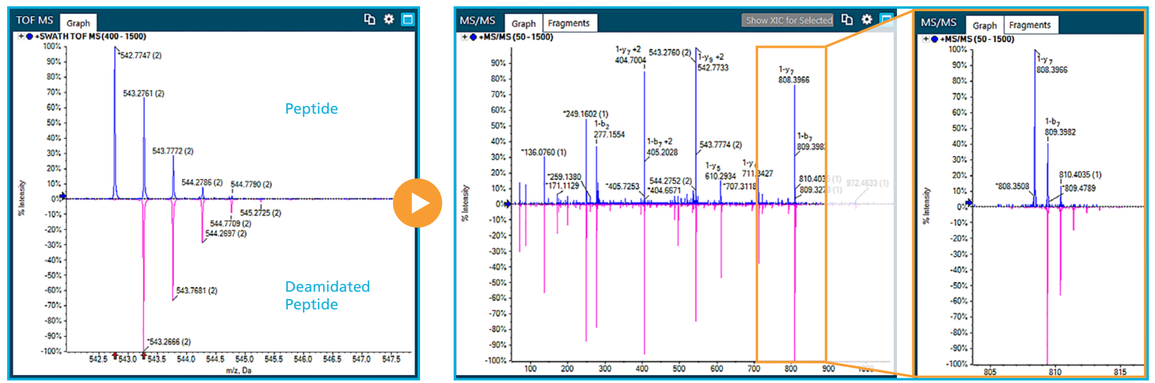
Deamidation is a common and important PTM which is often monitored at the peptide level to detect and localize susceptible sites in the biologic. You can easily identity and localize even low level peptide modifications using SWATH Acquisition along with BioPharmaView Software, which provides automated ratio calculations.

High-resolution MS and MS/MS makes identification and confirmation of peptide deamidation sites straightforward

Peptide Results | Matched | Unmatched

	Sequence	Modifications	Modification Percent	Charge	Observed Mono m/z	Theoretical Mono m/z	Error (PPM)	XIC Area
1	IYPTNGYTR		10.6% (None@5(55) : None@5(55))	2	542.7747	542.7747	0.0	2.80e5
2	IYPTNGYTR	Deamidated@5(55)	89.4% (Deamidated@5(55) : None@5(55))	2	543.2666	543.2667	-0.3	2.35e6

Reveal deamidated peptides and obtain relative quantitation levels in a simple format with the peptide results table in BioPharmaView Software



Trastuzumab sample analyzed using using SWATH acquisition on the X500B QTOF System. IYPTNGYTR peptide was identified in unmodified as well as in deamidated state, with confirmation available at both the MS1 peptide level as MS/MS fragment ion level.

Automatically Map Disulfide Bonds

Disulfide bond localization and confirmation is now even simpler, because BioPharmaView Software intuitively presents high-resolution, annotated MS/MS spectra, including multiple charge state identification.

Let the software quickly and accurately map disulfide bond locations to simplify your data analysis

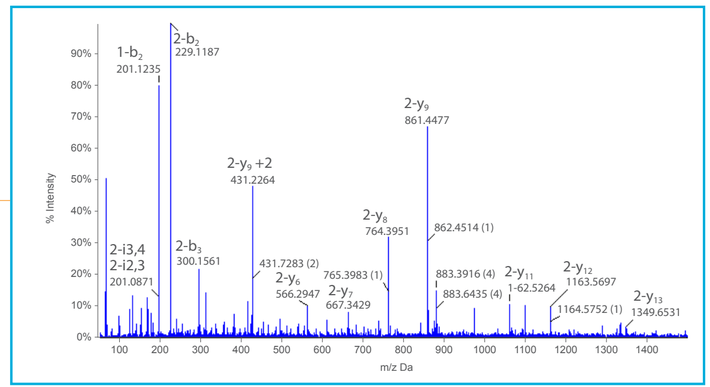
Peptide Results | Matched | Unmatched | Filte

	Sequence	Disulfide Bonds	Theoretical Mono m/z	Observed Mono m/z	Error (PPM)	Char...	XIC Area	Peptide
13	VTMTCR VEAEDAATYYCQQWTSNPPTFGGGTK	(1,4)T2@5(23)=(1,4)T5@11(87)	882.8931	882.8929	-0.2	4	7.0457e5	T2 T5
14	VTMTCR VEAEDAATYYCQQWTSNPPTFGGGTK	(1,4)T2@5(23)=(1,4)T5@11(87)	1176.8550	1176.8570	1.7	3	1.1517e5	T2 T5

Gain confidence from multiple charge state identification of the disulfide bond location

VTMTCR
|
VEAEDAATYYCQQWTSNPPTFGGGTK

Fast view confirmation with high-resolution, annotated MS/MS data for both peptides involved in the disulfide bond



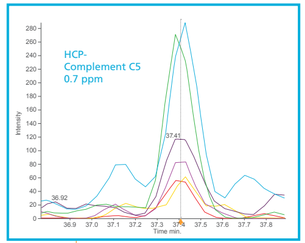
Unreduced, trypsin digested therapeutic mAb analysis using SWATH acquisition on the X500B QTOF System.

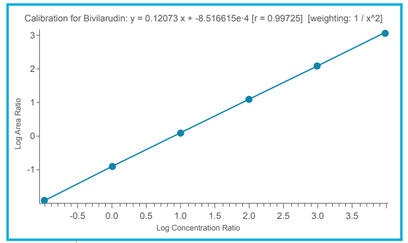
Take Your Analysis to the Next Level with TripleTOF® 6600 systems

When you have more advanced and complex questions about your biotherapeutic, the TripleTOF 6600 System can help you get the answers you need.

Increased sensitivity and dynamic range help you see deeper into your peptide maps. You can also use orthogonal separation technologies for extra clarity to make better decisions, with confidence.

Find the Right Solution For Your Lab	TripleTOF® 6600	X500B QTOF
Sensitive HRAM at Industry Leading Acquisition Rates	• •	•
Enhanced Linear Dynamic Range	• •	•
Sequence Variant Identification using ProteinPilot™ Software	•	
Host Cell Protein Analysis using ProteinPilot Software	•	
User-friendly SCIEX OS Interface for Simplified Setup and Use		•





Maximum Sensitivity:

Detect host cell proteins at low ppm levels on the TripleTOF 6600 System

Broad Quantitation Range:

Up to 5 orders of linear dynamic range for large molecules in TOF-MS and MS/MS

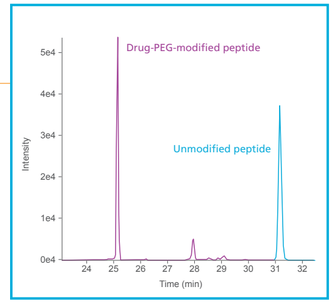
Identify Unknown Sequence Variants:

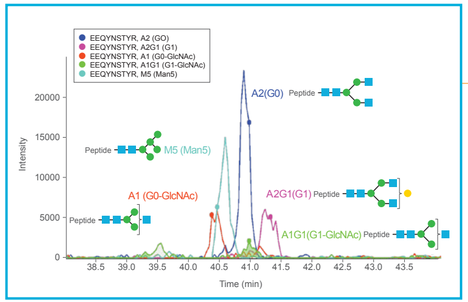
Minimize the number of false positives by using the unique ProteinPilot software algorithm on a TripleTOF 6600 System

Expand the coverage of your TripleTOF System with CESI-MS

Enhance your peptide mapping with the high-efficiency separation of capillary electrophoresis on the CESI 8000 Plus High Performance Separation-ESI Module, coupled to the TripleTOF 6600 system. High resolution separations enable a more thorough characterization of your digested biologic product—especially short peptides, long hydrophobic peptides, drug-linked peptides, glycopeptides, and deamidated peptides—which can be challenging for conventional HPLC. Additionally, CESI-MS requires only limited sample volumes, making it a powerful option for ADCs and mAbs in early discovery.

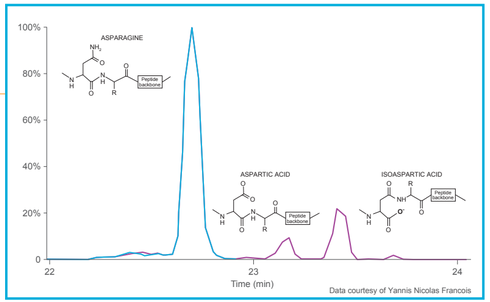
CESI-MS offers efficient separation and relative quantitation of drug-linked peptides





Separation and detection of glycopeptides

Achieve high resolution of isobaric deamidated and iso-aspartyl containing peptides



Gain a clearer picture of your biologic faster, with 100% sequence coverage from a single digest and single injection

Your Success is Our Success

We take it personally

As a SCIEX customer you have access to a world-class customer support organization. Wherever you are, we're there with you as a trusted partner to answer questions, provide solutions, and maximize lab productivity.

Our customer support organization has access to the latest product updates, software revisions, methods and repair procedures to make sure that you stay on top of your game.

When you have questions, we have answers.

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Headquarters
500 Old Connecticut Path
Framingham, MA 01701 USA
Phone 508-383-7700
sciex.com

International Sales
For our office locations please call the division headquarters or refer to our website at
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