Simple Solutions to Complex Workflows
Innovation for Biotherapeutic Peptide Mapping
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.

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.

For more information about the X500B QTOF System, please visit sciex.com/X500
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

1. Define your biotherapeutic sequence and expected disulfide bonds
2. Generate comprehensive reports in multiple output formats, and easily export digital versions to your electronic notebook
3. Analyze common modifications, or proprietary linker and drug conjugates by using the easy add custom modifications feature
4. Save assay information and parameters for characterization and batch processing

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.

Information Dependent Triggering

IDA Top 10-15

High-Resolution MS/MS spectra of Selected Precursors

100% sequence coverage from IDA

Simple, Automated Processing

m/z at RT ± 6 9 2 5 3 27 5 2 10 1 2 10

Low abundance peptide with PTM acquired by SWATH, but missed by IDA

100% sequence coverage from SWATH Acquisition

Gain additional insights into low abundance PTMs

Information Independent Triggering

High-Resolution MS/MS spectra of ALL Precursors

m/z at RT ± 6 9 2 5 3 27 5 2 10 1 2 10

Low abundance peptide with PTM acquired by SWATH, but missed by IDA

Gain additional insights into low abundance PTMs

High-Resolution MS/MS spectra of Selected Precursors
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 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.

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

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

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

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Peptide Deamidation

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 identify 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.

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

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.

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

Fast view confirmation with high-resolution, annotated MS/MS data for both peptides involved in the disulfide bond.
Identify Unknown Sequence Variants:
Minimize the number of false positives by using the unique ProteinPilot software algorithm on a TripleTOF 6600 System

Find the Right Solution For Your Lab

<table>
<thead>
<tr>
<th>TripleTOF® 6600</th>
<th>X500B QTRAP®</th>
<th>X500B QTOF®</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sensitive HRAM at Industry Leading Acquisition Rates</td>
<td>☑</td>
<td>☑</td>
</tr>
<tr>
<td>Enhanced Linear Dynamic Range</td>
<td>☑</td>
<td>☑</td>
</tr>
<tr>
<td>Sequence Variant Identification using ProteinPilot™ Software</td>
<td>☑</td>
<td>☑</td>
</tr>
<tr>
<td>Host Cell Protein Analysis using ProteinPilot Software</td>
<td>☑</td>
<td>☑</td>
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<tr>
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</tbody>
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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.

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.

Find the Right Solution For Your Lab

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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 TDF-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

Separation and detection of glycopolypeptides

Time (min) 100%

Intensity 5e4

Time (min) 100%

Intensity 5e4

Time (min) 100%

Intensity 5e4

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

Calibration for Bivalirudin: y = 0.12073 x - 8.516615 · 10^-4 [r = 0.99725] [weighting: 1 / x^2]

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

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

Data courtesy of Yannis Nicolas Francois

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.
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.

Learn more at sciex.com/customersupport, or locate your local account representative at sciex.com/contactus

For more information on SCIEX biologics characterization solutions, please visit sciex.com/biologics

Answers for Science.
Knowledge for Life.