For Research Use Only. Not for Use In Diagnostic Procedures.

Drug Discovery and Development

SCIEX

BioPharmaView™ Software 2.0

Innovation for Biotherapeutic Characterization and Comparability

Maturation of the biotherapeutics market is pressuring organizations to speed development, and become more efficient in the production and monitoring of their biologics products. Simplifying the processing of biotherapeutic data for characterization and comparability can dramatically improve productivity. BioPharmaView software accelerates characterization and comparability studies and simplifies reporting, so you can make better decisions, faster.

Key Challenges in Biologics Characterization

- Accurate deconvolution of intact protein and subunit data is necessary to achieve confident molecular weight determination of biotherapeutics, and to assess drug to antibody ratio of antibody drug conjugates (ADCs)
- Comprehensive peptide mapping data can require complex and time consuming data processing to determine sequence coverage, post-translation modifications (PTMs) and PTM ratios, as well as localization of disulfide bonds
- Multiple batches of samples need to be analyzed to establish comparability and to highlight any specific differences
- Detailed calculations of unmodified to modified peptides need to be performed to assess differences in PTM levels across samples

NEW Capabilities in BioPharmaView 2.0 Software

Automated drug to antibody ratio (DAR) calculations for antibody drug conjugates (ADCs)

- No more manual calculation of DAR
- Quickly visualize drug load on ADCs

Significantly faster peptide mapping data processing speed

- Enhanced data processing algorithms speed data analysis from hours to minutes

Process SWATH® Acquisition data

- Simplify LC-MS method development by using a generic SWATH Acquisition method on TripleTOF® 5600+ and 6600 systems

- Ensure important peptide and PTM information is not missed by acquiring high-resolution MS/MS data on all sample components in a single run

Automated PTM ratio calculations

- Save time and energy when comparing modified peptide levels
- Obtain modified peptide ratios for all your important PTMs, such as oxidation and deamidation

Incorporation of UV data viewing

- Simplify data comparisons to other analytical techniques utilizing UV acquisition
- Easily compare UV trace data to MS data traces
- Enhance method portability to later stage analyses

BioPharmaView Software Features and Benefits

Simplified processing setup

- Getting started is easy with intuitive main window
- Define the biotherapeutic sequence and choose from common post-translation modifications of interest
- Easily add custom modifications like proprietary linkers and drug conjugates
- Processes LC-MS as well as CESI-MS acquired data

Rapid and accurate protein deconvolution of intact protein or subunit data

- Protein deconvolution in seconds

- Protein form matching and automated ratio calculations for PTMs, including glycosylation
- Ability to save and use batch processing parameters
- Multi-pane view allows you to see processed and raw data from multiple samples side by side
- Enhanced visualization tools, such as mirror plots and overlays

Simplified Peptide mapping analysis

- Comprehensive list of identified peptides and modifications
- Visualize peptide mapping sequence coverage
- Direct visualization of raw MS level data and annotated high-resolution MS/MS data
- Ability to easily filter peptide list based on multiple criteria, such as mass accuracy, for simplified viewing
- Assess data quality and processing parameters with enhanced MS/MS scoring

Automated disulfide bond localization

- Quickly and accurately map disulfide bond locations
- Bond localization confirmation using high-resolution, annotated MS/MS data for both peptides involved in the disulfide bond

Comprehensive Reporting

- Reports available in multiple output formats
- Show products that passed or failed your customized flagging criteria
- Easily transfer processed data exports to electronic notebook applications

BioPharmaView 2.0 Software Compatibility Matrix

Operating System	Windows 7 64-bit, SP1
Supported Mass Spectrometers	X500B QTOF System TripleTOF® 5600 system TripleTOF 5600+ system TripleTOF 6600 system ***Note:** Compatible with CESI 8000 Plus High-Performance Separation-ESI Module up-front of TripleTOF 5600+ or 6600 systems
Compatible Analyst TF® Software	SCIEX OS 1.2 software Analyst® TF 1.5.1 software Analyst TF 1.6 software Analyst TF 1.7 software Analyst TF 1.7.1 software
Free Trial Download Link	http://sciex.com/licensing

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
sciex.com/offices