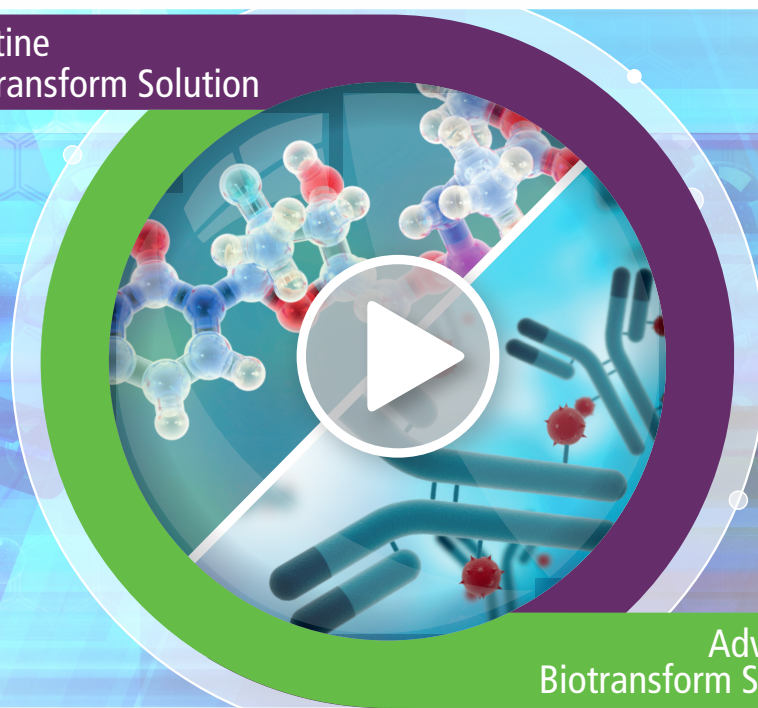


Metabolism and Biotransformation Application eBook

High Productivity and Total Confidence with High-Resolution
Accurate Mass Spectrometry



Routine
Biotransform Solution



Advanced
Biotransform Solution





Routine Biotransform Solution

Fast and Efficient MetID

Quickly and efficiently run metabolic stability, MetID, and soft spot analyses for both small and large molecules in a high-throughput manner with the easy-to-use X500R QTOF system and intuitive, point-and-click SCIEX OS user interface.

The streamlined LC-MS system seamlessly integrates with MetabolitePilot™ Software 2.0 to help you achieve the productivity and throughput you need to keep your projects moving.

Visit our Application Page to Learn More ►

Click Below to Access Technical Notes:

Rapid Peptide Catabolite ID

Rapid Soft Spot Analysis

Solution Guide



Fast, Efficient
MetID with HRMS

Webinar



Confident and Powerful MetID for
All Your Therapeutic Molecules



Advanced Biotransform Solution

Comprehensive Detection, Total Confidence

Achieve ultimate confidence in your metabolism and catabolism studies with the maximal sensitivity and dynamic range for low-level metabolite ID, along with single injection comprehensive coverage with the high-resolution TripleTOF® 6600 System and SWATH® Acquisition.

Data independent SWATH Acquisition collects high-resolution MS/MS data of all detectable metabolites and catabolites, allowing you to dig deeper in a single injection. Future proof your metabolism studies by keeping a SWATH digital archive of your sample, allowing for sample re-interrogation without re-analysis.

Visit our Application Page to Learn More ►

Click Below to Access Technical Notes:

Streamlining Discovery Metabolite ID with SWATH® Acquisition

Therapeutic Peptide Catabolite Identification

Metabolite ID of Payload Species of Antibody Drug Conjugates with Noncleavable Linkers

Sensitive Microflow Analysis of Peptide Catabolism

Solution Guide



Comprehensive Metabolism Analysis with HRMS

Webinar



Comprehensive MetID with SWATH® Acquisition



MetabolitePilot™ Software

Advanced metabolite identification and quantitation for small molecule metabolism and biotherapeutic catabolism

Try the software for free ▶

Industry leading software for both small molecule metabolite identification and for large molecule catabolite investigation:

- Confident, automated identification
- Advanced processing for biotherapeutic catabolism
- Same software for both small molecule and large molecule metabolism studies
- Sophisticated processing logic specific for peptides, proteins, and antibody drug conjugates (ADCs)
- Compatible with both X500 and TripleTOF high-resolution QTOF platforms

Webinar

SWATH® Acquisition and SCIEX TripleTOF®: Powerful Hardware for the Challenge of Drug Metabolism

- Data independent SWATH Acquisition enables the detection and identification of low metabolites and catabolites, by always collecting MS/MS
- What makes SWATH key for MetID? Speed plus resolution coupled to sensitivity

MetabolitePilot Software
Capabilities for Metabolism and
Biotransformation

Visit the Software Page to Learn More ▶

Learn more in the software bulletin

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

Drug Discovery and Development

MetabolitePilot™ Software 2.0

Advanced Metabolite Identification and Quantitation for Small Molecule Metabolism and Biotherapeutic Catabolism

MetabolitePilot Software offers an integrated and easy to use workspace for high throughput processing and interrogation of your advanced drug metabolism and biologics catabolism data. Powerful data processing algorithms accelerate metabolite and catabolite identifications, enables effective time-point and cross species comparisons, and simplifies reporting so you can drive your drug development program more efficiently.

Key Challenges in Advanced Drug Metabolism

- Missing low level and toxic metabolites/catabolites
- Repeat analysis to understand complete metabolite profile and structure due to missing, or poor quality, MS/MS spectra
- Complicated processing to understand metabolite profile across multiple time points and species
- Complex data processing for biotherapeutic catabolism analysis (peptides, proteins, ADCs)
- Manual interpretation of biotherapeutic catabolite structures and profile

NEW Capabilities in MetabolitePilot Software 2.0

Automated and Powerful Catabolism Data Processing for Therapeutic Peptides

- Catabolism analysis for therapeutic peptides, including non-linear, cross-linked and cyclic structures
- Support of non-natural amino acids and modifications
- Targeted searching of predicted hydrolytic cleavages
- Calculation and assignment of a-, b-, y- and internal fragments for linear and non-linear peptides

Advanced Catabolism Data Processing for Antibody Drug Conjugates

- Dedicated biologic protein processing templates to simplify analysis of cytotoxic drugs, linker, antibody, and antibody drug conjugation chemistry

Process SWATH® Acquisition Data for Small Molecules and Large Molecule Biotherapeutics

- Ensure important metabolite or catabolite information is not missed by acquiring high-resolution MS/MS data on all sample components in a single run using SWATH Acquisition
- Improved identification of drug-related material based on characteristic fragment ions, neutral losses, and fragment isotope patterns
- Multiple filters for processing SWATH MS/MS spectra. The filters allow you flexibility to interpret your MS/MS data regardless of the number of points across the peak.

Prediction and targeted searching of catabolite structures for payload cleavages and biotransformations on drug linkers

- Targeted searching of predicted hydrolytic cleavages along antibody backbone, including ADC conjugation sites and specified amino acid modifications
- MS/MS annotations for ADCs with combined assignment of small molecule fragments and peptide fragments
- Interactive interpretation tool for MS/MS annotation and assignment

SCIEX Biotransform Solutions

Learn how to transform your metabolism studies with SCIEX High-Resolution Accurate Mass Spectrometry Systems and Software.

Achieve the productivity and throughput you need to keep your projects moving, and achieve complete confidence that you're not missing any low level or parent-like metabolite in your sample.



Routine MetID and Soft Spot Analysis

Quickly identify soft spots and the top metabolites to maximize therapeutic candidate effectiveness



| | |
|-----------------------|---|
| Mass Spec | X500R or X500B QTOF System |
| User Interface | SCIEX OS |
| HPLC | ExionLC™ AD |
| Processing & Analysis | MetabolitePilot™ Software 2.0 |
| Optimized Workflows | Fast and high-throughput small molecule and large molecule metabolic stability and soft spot analysis. Analysis of top 5-10 metabolites |



Comprehensive Metabolism and Catabolism

Gain a comprehensive understanding of your drug metabolites or biotherapeutic catabolites, with the confidence that low level components are not missed



| | |
|-----------------------------|---|
| Mass Spec | TripleTOF® 6600 System |
| User Interface | AnalystTF |
| HPLC | ExionLC AD |
| Processing & Analysis | MetabolitePilot Software 2.0 |
| Variable Swath® Acquisition | Comprehensive unbiased data independent acquisition to store high-resolution MS/MS data for all detectable metabolites? catabolites in a single injection |
| Optimized Workflows | Comprehensive small molecule metabolism, peptide? protien catabolism, ADC analysis. Low level metabolite detection and analysis |



Your Success is Our Success

We take it personally

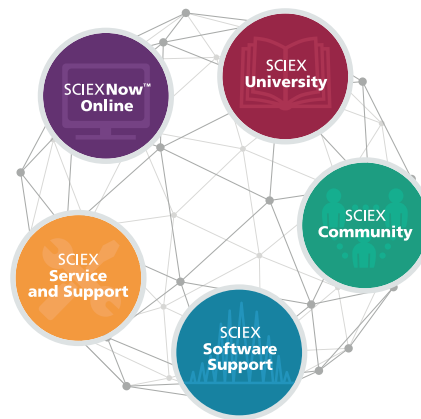
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