# Fast, Efficient, and Simplified MetID

**Routine Biotransform Solution** 



High Productivity Drug Metabolism and Biologics Catabolism

Answers for Science.

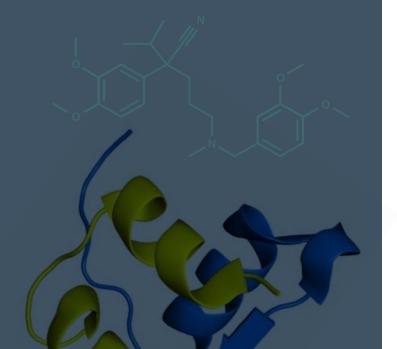
Knowledge for Life.™

# **MetID Analyses**

In therapeutic development the clock is ticking, and samples are coming into your lab fast and furiously. You have to identify soft spots and the top metabolites quickly, so chemists and biologists can optimize the effectiveness of the therapeutic candidate.

The Routine Biotransform Solution from SCIEX offers a simple and streamlined platform for high-throughput MetID analyses for both small and large molecule therapeutics. The compact, easy-to-use instrumentation and powerful automated data processing software helps you achieve the productivity and throughput you need to keep your projects moving.

Explore the Routine Biotransform Solution and learn how to accelerate your MetID studies.





#### Streamlined Hardware for **Efficient Metabolite ID**

The **X500 QTOF** high-resolution, accurate mass system is an easy-to-use, robust platform for streamlining your high-throughput metabolic stability and MetID studies.

#### **Robustness with Ultra-Low Downtime**

The **ExionLC<sup>™</sup> AD** delivers high accuracy, reliability and repeatability across thousands of injections, with maximum uptime.



#### **Simplified Set-Up for Accelerated Results**

Save time and energy with the intuitive and user friendly **SCIEX OS** user interface. Simplified set-up makes creating and running methods easy, even for non-mass spec experts.

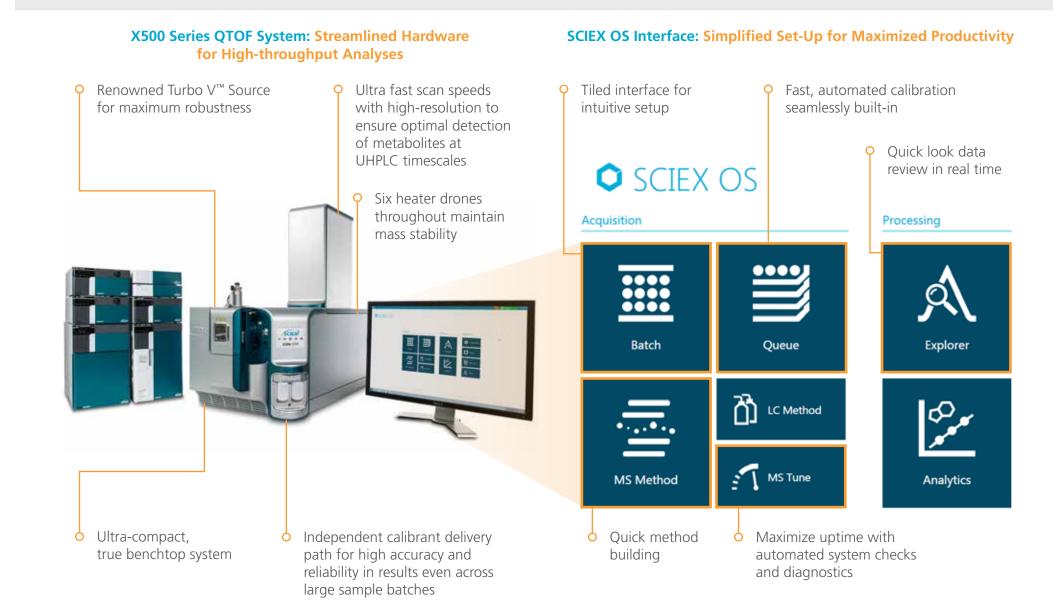


#### Small Molecule Metabolism and Biologics Catabolism **Analysis in the Same Package**

MetabolitePilot Software 2.0 offers small molecule drug metabolite profiling and structure determination as well as the industry leading solution for peptide and biologic catabolism analysis. All from the same platform and software you know and trust.

### **Streamlined Instrumentation and Software for Rapid Results**

Choose between the new X500R or X500B QTOF Systems that were designed to be compact, robust, and easy-to-use even for non-mass spec experts. X500 QTOF systems run on SCIEX OS, a revolutionary new control and acquisition interface that makes setup and data acquisition a breeze. The unique, tiled interface in SCIEX OS will help you get your metabolism and catabolism studies up and running guickly, so you can get results faster.



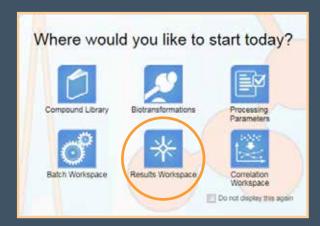
### Intelligent and Flexible Data Acquisition to Get Answers Fast

Despite its uncomplicated exterior, SCIEX OS packs powerful sample data acquisition within its interface. For efficiency and effectiveness, you can choose standard Information Dependent Acquisition (IDA), which picks the top intensity MS peaks for MS/MS acquisition. Alternatively, take your assay to the next level with SCIEX proprietary Real-Time Multiple Mass Defect Filtering (RT-MMDF) acquisition, which intelligently picks the most likely drug related MS peaks for MS/MS analysis, based on information about the parent molecule, so only relevant information is collected. You can even pursue a Data Independent Acquisition Strategy (DIA) with SWATH® Acquisition, which enables unbiased MS/MS acquisition of all detectable precursors, and allows you to retrospectively mine the data, even on high-throughput MetID analyses.

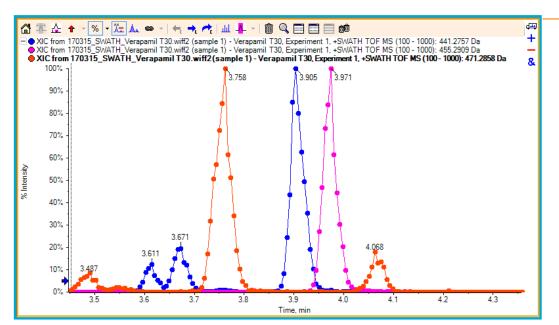


#### **Powerful, Automated Data Processing**

New MetabolitePilot™ Software 2.0 automates assignment of MS/MS data to metabolites, with advanced identification, interpretation, visualization and correlation for a wide variety of molecule types. The processing power and flexibility in MetabolitePilot Software means you have a single go-to software for all your MetID assays.



The user-friendly software interface puts processing, interpretation, visualization, and reporting all in one place

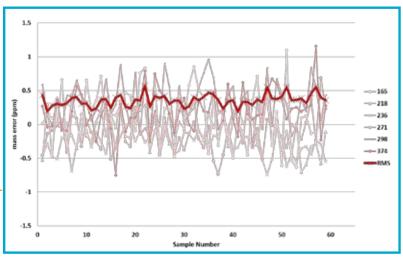


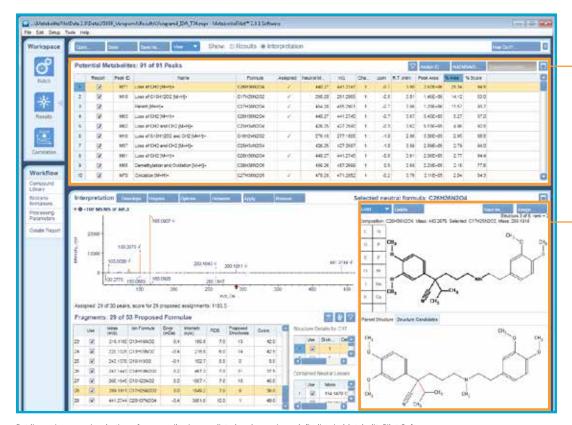
Rat liver microsome incubation of verapamil, showing major oxidized (red), methylated (blue) metabolites, along with parent (pink).

Robust mass accuracy for routine metabolite analysis as shown by ppm mass error over 60 injections on a single system calibration

Accurate metabolite ID at UHPLC timescales with ultra-fast acquisition capabilities without sacrificing resolution.

TOF-MS Resolution >37,000 TOF- MS/MS Resolution >36,000





Get identification and assignment with predicted metabolite peak finding using multiple peak finding algorithms based on TOF-MS, mass defect and isotope pattern as well from TOF-MS/MS characteristic product ions and neutral losses

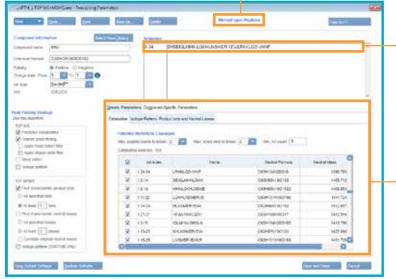
Speed your time to answers with automated structure assignment correlated with high-resolution MS/MS data

Rat liver microsome incubation of verapamil using predicted and generic peak finding in MetabolitePilot Software

### Say Goodbye to Manua Catabolism Processing

MetabolitePilot™ Software 2.0 not only handles small molecule MetID, it now includes powerful processing for biotherapeutic catabolite analysis, all in the same interface. That means you can expect fast, and accurate peptide catabolism and biotransformation identifications, which allow you to find liabilities and soft spots in the molecule.

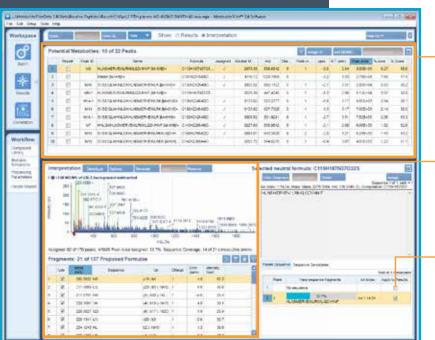
 Processing logic specific for large molecule catabolism including peptides, proteins, mAbs and ADCs



Simplified input of 1-letter amino acid codes. Supports non-natural amino acids, cross-linking and side chain modifications

Automated prediction of catabolites and hydrolytic cleavages for use in targeted searching

Example processing parameters for analysis of parathyroid hormone (PTH) peptide metabolism



Quickly view the top catabolites with automated sequence assignments. Advanced peak finding strategies are based on TOF-MS and high-resolution MS/MS data

MS/MS interpretation view where the proposed metabolite sequence is annotated using a-, y- and b- ions

Assigned catabolites with associated score

Example results interpretation workspace for analysis of PTH peptide metabolism

#### **Choose the Solution for Your Needs**

Biotransformation studies are a necessary part of therapeutic development, for both small and large molecule drugs. Whether you're working against the clock to locate soft spots and identify metabolites upstream, or you need total confidence that you're identifying every detectable metabolite or peptide catabolite downstream, SCIEX offers an integrated solution to meet your requirements.



When it's time for a comprehensive understanding of drug metabolites or biotherapeutic catabolites, you have to be 100% confident that you've identified everything in the sample. When identifying low level or toxic metabolites is paramount, the SCIEX Advanced Biotransform Solution has you covered:

- Maximum sensitivity and Dynamic Range for Low Level Metabolite ID with the TripleTOF® 6600 System
- Single Injection Comprehensive Coverage for Ultimate Confidence with SWATH® Acquisition

# 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 about SCIEX Metabolism Solutions, Visit sciex.com/biotransform

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