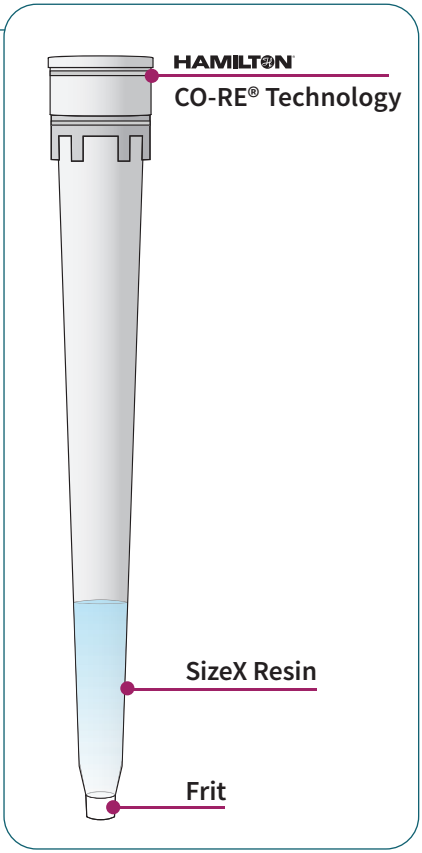
imcsTIPS® + HAMILTON®

Automated Multi-Attribute Method (MAM)

OVERVIEW

Multi-attribute method (MAM) is a mass spectrometry-based technique that enables users to simultaneously monitor and quantify molecular attributes with the potential to impact the efficacy, pharmacokinetics, and safety of biotherapeutic applications. From proof-of-concept and product development to real-time quality control, MAM is intended to consolidate separate assays and streamline laboratory workflows.

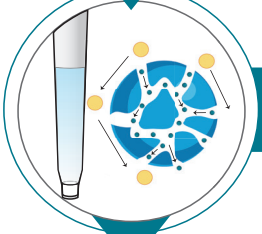
Current sample preparation for MAM relies on a manual buffer exchange step to remove excess denaturant and accelerate subsequent trypsin digestion efficiency. Circumventing the buffer exchange step requires significant sample dilution and prolonged digestion time, which may result in sample preparation artifacts.



SizeX IMCStips® + Hamilton® Microlab® STAR™ = Fully automated, hands-free solution for MAM

Protein Sample

DENATURE
REDUCE
ALKYLATE



Buffer Exchange with SizeX IMCStips

PROTEOLYTIC DIGESTION & QUENCH

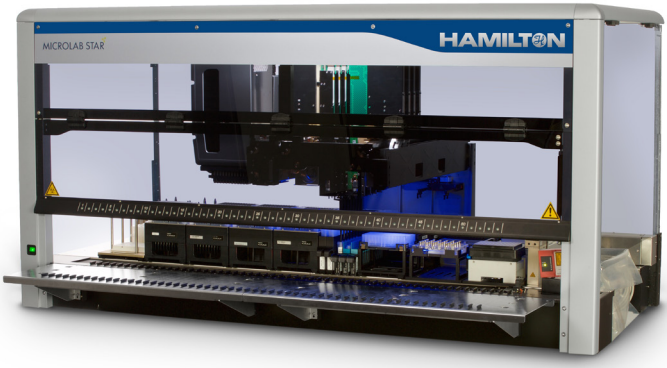
Peptides ready for UHPLC-MS analysis

Efficiency and repeatability in the MAM workflow are further enhanced through the use of novel SizeX IMCStips and a Hamilton Microlab STAR automated liquid handling system during sample preparation. This fully automated, hands-free workflow includes denaturation, reduction, alkylation, buffer exchange using SizeX IMCStips, trypsin digestion, and program termination after acidification to quench proteolytic activity. The resulting peptides are ready for LC-MS analysis.

Let us help automate your MAM workflow:

- Achieve consistent recoveries after buffer exchange across a range of proteins
- Eliminate time-consuming, repetitive manual pipetting
- Streamline protein attribute characterization
- Reduce the risk of variability and human error

We Make Automating Your Sample Preparation as Easy as *Just Click Go*



You need fast, accurate results, so we designed IMCStips to make their adoption as easy as possible. In addition to on-site technical support, IMCStips come with software scripts designed for Hamilton liquid handling platforms. Through collaborations with our R&D team, we create fully developed user guidelines to help you navigate each phase of the implementation process, ensuring seamless integration of the technology into your laboratory's customized workflows.

SizeX$_{100}$

Tip Size	Sample Volume	Tip Quantity	Catalog Number
1 mL	100 µL	8	04T-H6R76-0-220-8
1 mL	100 µL	96	04T-H6R76-0-220-96

SizeX$_{150}$

Tip Size	Sample Volume	Tip Quantity	Catalog Number
1 mL	150 µL	8	04T-H6R76-0-350-8
1 mL	150 µL	96	04T-H6R76-0-350-96

Results below were obtained using SizeX IMCStips on a Hamilton Microlab STAR.

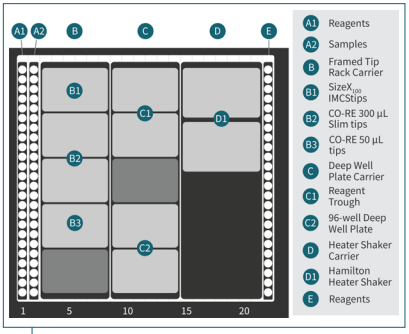


Figure 1. Example of a deck layout for automated MAM on Hamilton Microlab STAR using SizeX IMCStips.

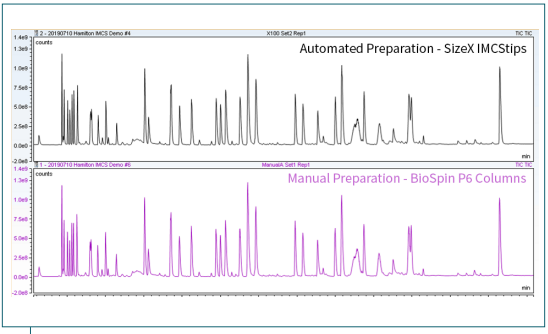


Figure 2. Total ion chromatograms comparing automated (SizeX IMCStips) and manual (Bio-Spin P6) preparation are identical.

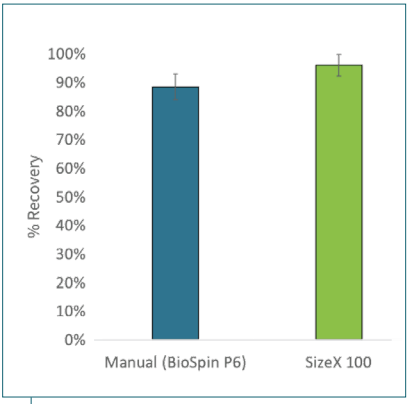


Figure 3. Antibody recovery from manual and automated MAM using Bio-Spin P6 columns and SizeX IMCStips, respectively (n=4).

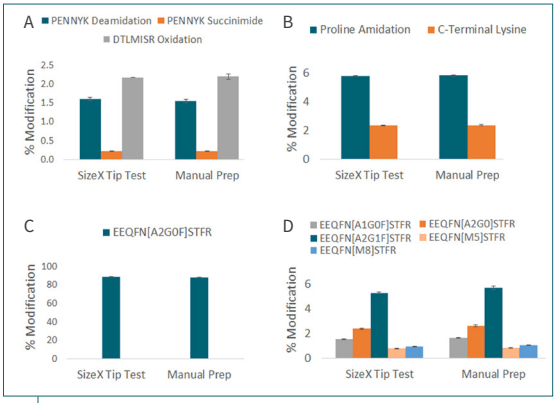


Figure 4. Comparison of percent modifications for manually prepared and automated samples. (A) Deamidation, succinimide, methionine oxidation, (B) proline amidation, C-terminal lysine truncations, and (C,D) Fc glycosylation patterns are shown (n=4).

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