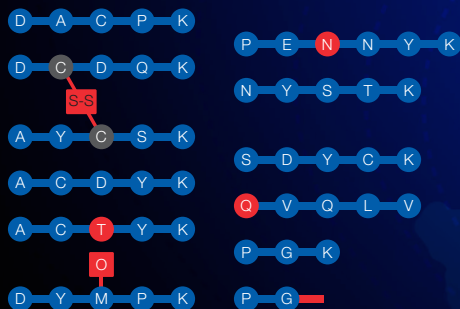


HR Multi-Attribute Method for Biopharma Analysis

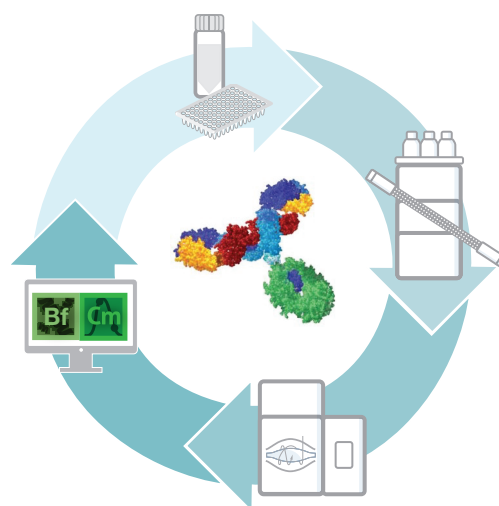
Resolution Matters
from Research to Routine



Reasons to invest in HR MAM workflow

- Comprehensive high resolution accurate mass LC/MS Workflow
- Confident peptide identification and accurate quantitation of potential critical quality attributes
- Reliable new peak detection
- Verified protocol with dedicated standards and reagents
- Global expert support network
- Compliant-ready software to ensure data integrity

An end-to-end analytical workflow verified and fully supported by the world leader in serving science



Resolution Matters
from Research to Routine

Thermo Scientific HR Multi-Attribute Method

An end-to-end analytical solution, verified and supported by a single vendor

Standard

The Thermo Scientific™ Pierce™ BSA Protein Digest Standard is a stable lyophilized peptide mixture standard, ideal to verify the suitability of the LC/MS system for HR MAM with defined acceptance criteria.



Separation

The Thermo Scientific™ Vanquish™ Horizon UHPLC System offers exceptional robustness, high gradient precision, low dispersion, improved reproducibility and peak efficiency for the high resolution separation needed for targeted peptide quantitation utilized by the HR MAM workflow.

The Thermo Scientific™ Accucore™ Vanquish™ C18+ UHPLC Column coupled with the Vanquish Horizon UHPLC system takes advantage of the extended pressure capabilities and utilizes the system to its full potential. 1.5 μm solid core particles deliver exceptionally sharp peaks, maximal peak capacities and remarkably low retention time variations delivering reproducible LC-MS analysis for reliable batch-to batch analysis in a routine QC environment.



Mass Detection

Thermo Scientific™ Q Exactive™ Plus Hybrid Quadrupole-Orbitrap™ Mass Spectrometer provides the high resolution and accurate mass detection for essential specificity ensuring confident identification of all peptides and post translational modifications (PTMs) with a narrow mass window (± 3 ppm). This leads to high sequence coverage and in-depth characterization, from confident peptide identification to accurate peak extraction and quantitation of PTMs and monitoring of critical quality attributes. It is linear across 5 orders of magnitude, proving ideal for the analysis of complex and varied peptide mixtures and detection of very low abundant modifications.



Data Analysis

For Discovery analytics the BioPharma Finder software harnesses the power of the industry leading Orbitrap technology.

Novel MS2 prediction algorithm utilized by BioPharma Finder software increases the confidence in peptide sequence assignments, identification of the site and type of expected and unknown PTMs, detection of low-level impurities and sequence variants.

Thermo Scientific™ Chromeleon™ Chromatography Data System delivers superior control of UHPLC and high resolution MS instruments with CFR 21 Part 11 compliant-ready data acquisition, automation, and data processing as well as reporting for compliant GxP biopharmaceutical manufacturing and QA/QC environments. Unique new peak detection functionality enables detection of 'impurities' while avoiding false positives during lot release testing.

Run your routine LC-MS peptide mapping analyses in a network deployable enterprise environment from method creation to final reporting.



Global expert support network

We provide all the support you need to achieve your goals with the HR MAM workflow: service excellence, system verification at installation and specialized customer training. Expert technical and application support with a dedicated Global HR MAM workflow specialist network to safeguard your journey into confidence.



Find out more at thermofisher.com/MAM