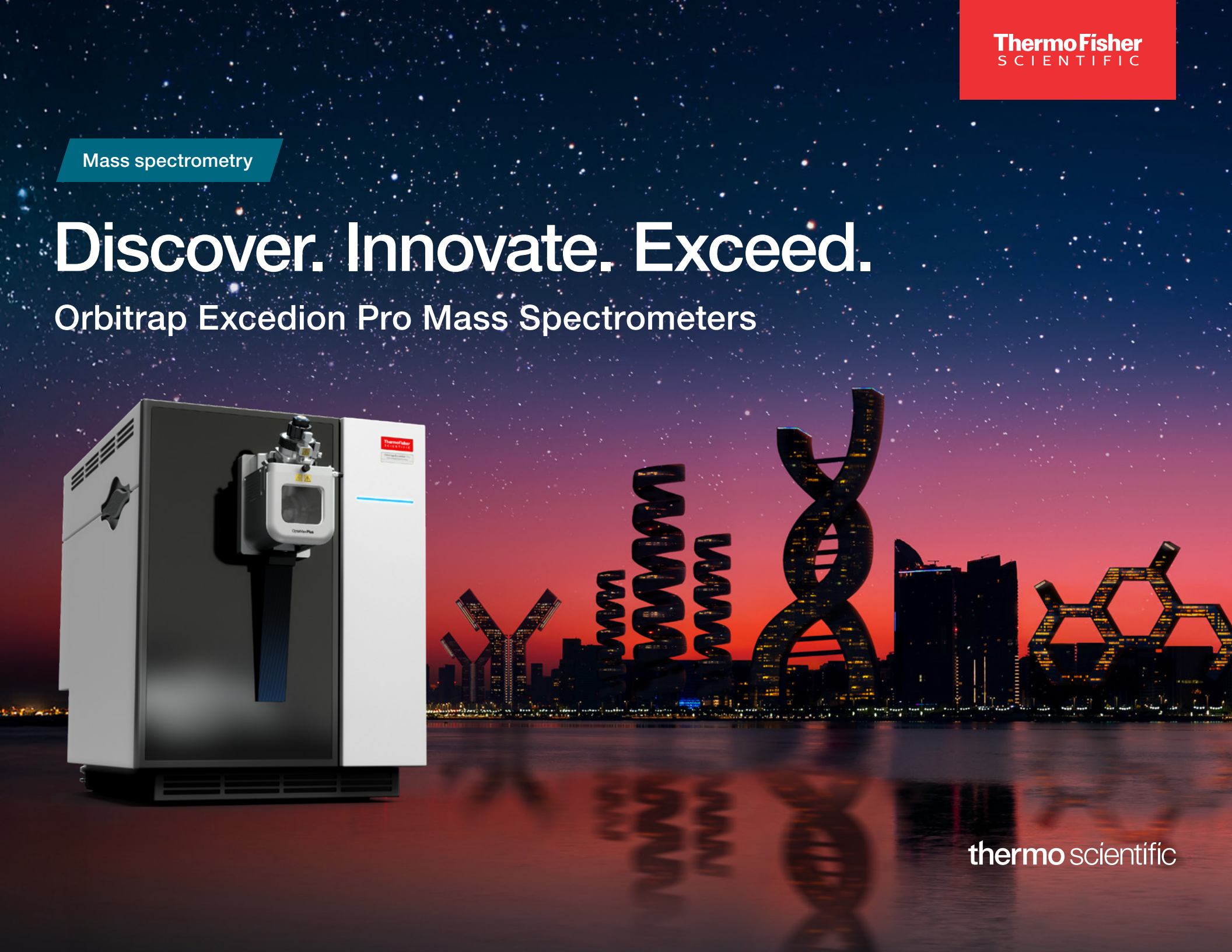
Thermo Fisher SCIENTIFIC

Mass spectrometry

Discover. Innovate. Exceed.

Orbitrap Excedion Pro Mass Spectrometers



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Discover. Innovate. Exceed.

Welcome to the next generation of mass spectrometry with Thermo Scientific™ Orbitrap™ Excedion™ Pro hybrid mass spectrometers (MS). Building on our outstanding legacy quadrupole-Orbitrap mass spectrometry technology, Orbitrap Excedion Pro mass spectrometers deliver enhanced sensitivity, dynamic range, fast and sensitive (optional field upgradable) electron-based fragmentation, and unique capabilities transforming everyday analysis into exceptional results. **Designed for biopharma, metabolomics, proteomics and structural biology applications**, these advanced benchtop hybrid mass spectrometers set a new standard in analytical performance, empowering you to make groundbreaking discoveries.

Orbitrap Excedion Pro **BioPharma** MS shown with **OptaMax Plus** ion source

Orbitrap Excedion Pro MS shown with **OptiSpray** technology

For complete technical details on each model instrument, download the product specifications sheet.

The Thermo Scientific™ OptaMax™ Plus ion source comes standard with every Orbitrap Excedion Pro MS configuration. The optional Thermo Scientific™ OptiSpray™ technology dramatically simplifies acquisition of high-quality, reproducible LC-MS data for your most challenging biological samples. Compatible with Thermo Scientific™ Orbitrap™ MS and the Thermo Scientific™ Vanquish™ Neo UHPLC systems, it combines automated spray optimization with cartridge-based nano and capillary columns to deliver high-sensitivity, quantitative accuracy and precision, and maximum robustness.

Biopharma	Versatile tools for characterization of different molecular domains
Structural biology	Novel workflows for higher order structure characterization
Metabolomics	Advanced instrument for sensitive analysis
Proteomics	New capabilities for targeted and discovery proteomics

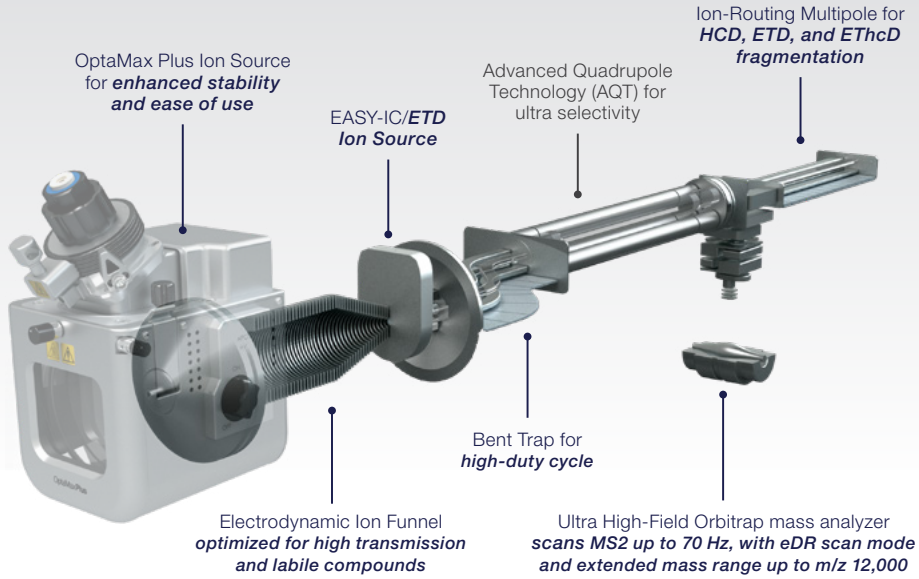
Innovate with Enhanced Orbitrap Technology

Introducing Orbitrap Excedion Pro mass spectrometers: an advancement that elevates the acclaimed Orbitrap technology to enhanced levels of performance. With fast and sensitive alternative fragmentation techniques, enhanced ion optics, higher scan rates, and superior data quality, they deliver outstanding results.

The unique design of Orbitrap Excedion Pro mass spectrometers provides improved sensitivity, an extended dynamic range, a broader mass range, and exceptional mass accuracy that builds upon the capabilities of the legacy Thermo Scientific™ Orbitrap Exploris™ 480 mass spectrometer. These features work together to ensure the accurate identification and quantification of analytes, making Orbitrap Excedion Pro mass spectrometers the definitive choice for cutting-edge mass spectrometry in their class.

Schematic of Orbitrap Excedion Pro Mass Spectrometers

New features highlighted in ***bold***



Orbitrap Excedion Pro Workflow

End-to-end solutions for seamless operation

Thermo Scientific™ Vanquish™ Neo UHPLC system
Versatile, high performance for nano, capillary, and micro-flow LC-MS

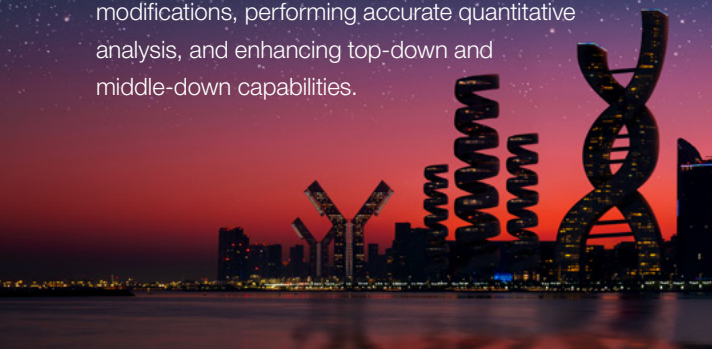
Thermo Scientific™ OptiSpray technology
Reliably achieve maximum low-flow ESI performance

Orbitrap Excedion Pro mass spectrometer
Next-generation hybrid MS with fast and sensitive alternative fragmentation for increased sequence coverage

Thermo Scientific™ Ardia™ platform
Central data storage, automated data processing, and tools to manage instruments, data, and users

Elevate
Your Biopharma Characterization

The Orbitrap Excedion Pro **BioPharma** mass spectrometer is a high-resolution, accurate mass solution tailored for the biopharmaceutical industry. It enables confident characterization of intact proteins under native and denatured conditions with mass detection up to *m/z* 12,000 and high-sequence coverage using Higher-energy Collisional Dissociation (HCD), optional Electron Transfer Dissociation (ETD), and optional combination of HCD and ETD fragmentation—Electron-Transfer Higher-energy Collisional Dissociation (EThcD)—at all analysis levels. The instrument excels in elucidating post-translational modifications (PTM) and identifying structural isomers, while its high dynamic range scan mode supports the detection of low abundant species with exceptional sensitivity. With a resolving power of up to 480,000 (FWHM) at *m/z* 200, the Orbitrap Excedion Pro **BioPharma** mass spectrometer provides deep insights into monoclonal antibodies at the subunit and enables comprehensive characterization by detecting and quantifying impurities and modifications, performing accurate quantitative analysis, and enhancing top-down and middle-down capabilities.



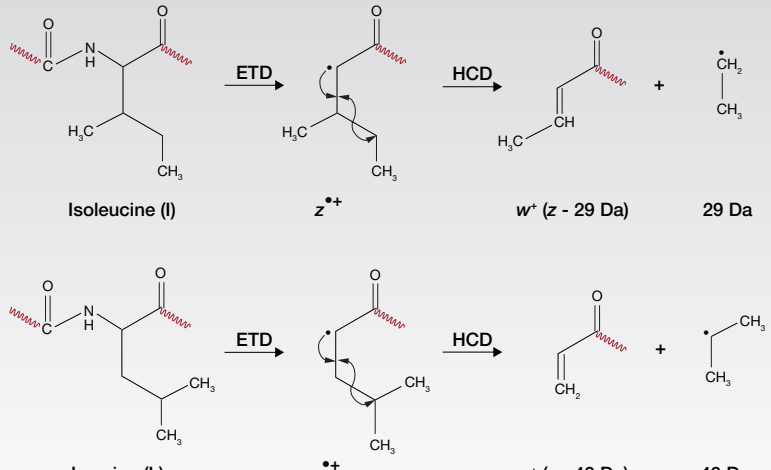


Figure 1a: Formation of signature with ion fragments by EThcD distinguishes isomeric amino acids, such as isoleucine (I) from leucine (L) in peptides.

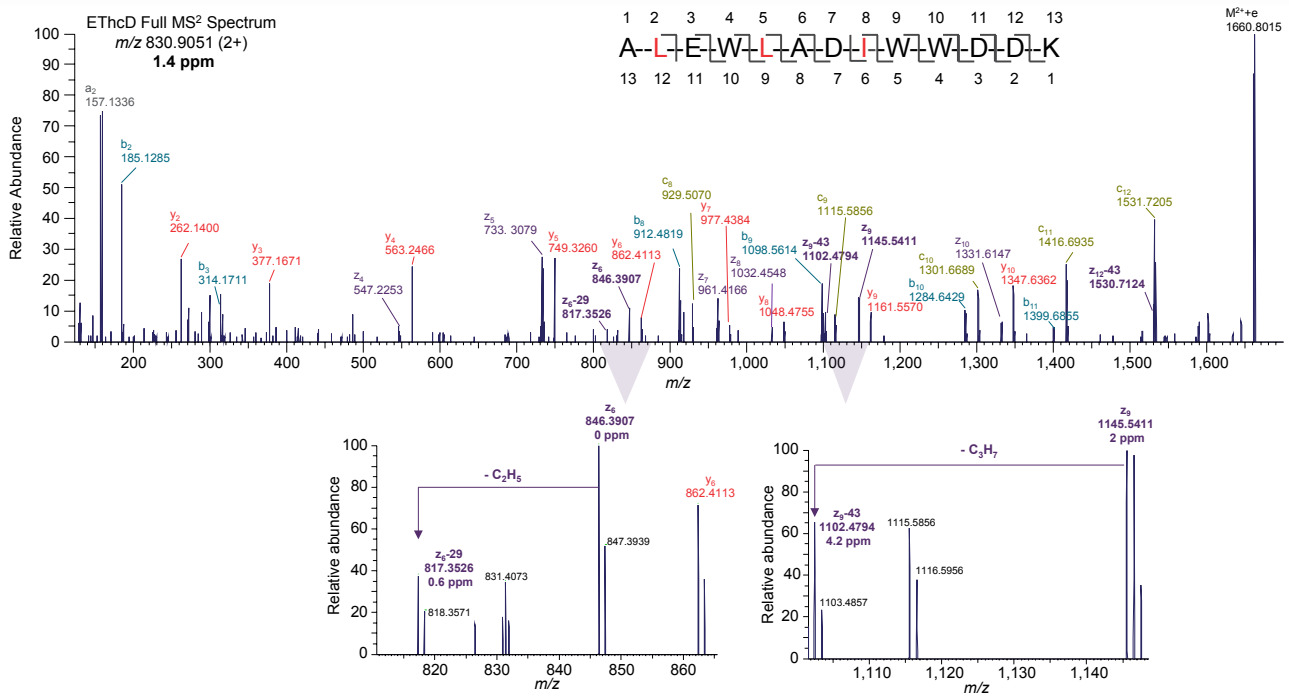


Figure 1b: In UHPLC-HRAM-MS-ddMS² analysis of NISTmAb tryptic digest peptide mapping experiment, EThcD unambiguously identified the two leucine residues (loss of 43 Da from z_9 and z_{12} fragments) and one isoleucine residue (loss of 29 Da from z_6 fragments) in this 13-amino acids doubly charged peptide with complete sequence coverage. Example zoom-in insets show the high mass accuracy (<5 ppm) achieved for the signature fragments.

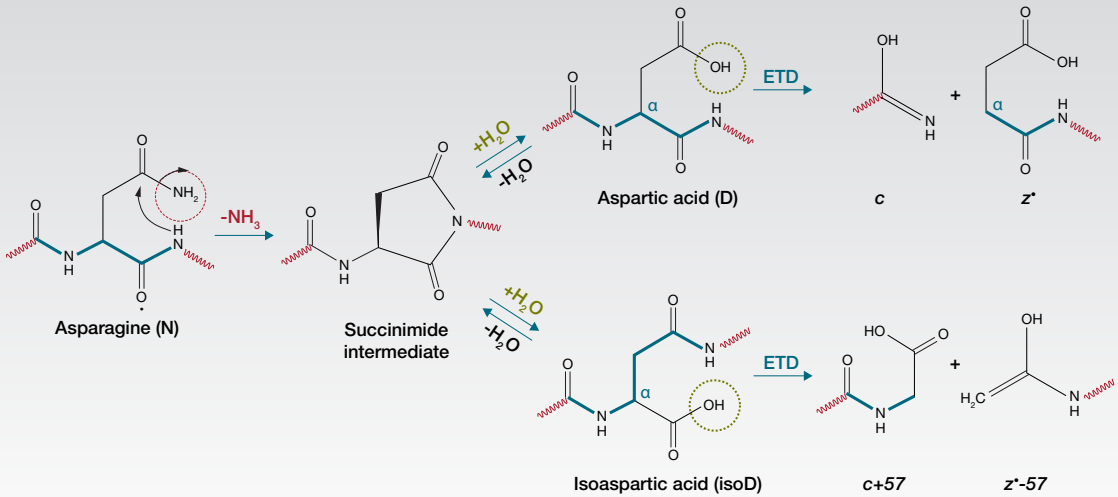


Figure 2a: Formation of isoaspartic acid (isoD) occurs via the deamidation of asparagine (N) or the isomerization of aspartic acid (D). ETD generates signature fragments (c+57 and z-57) indicative for isoaspartic acid but not present from aspartic acid.

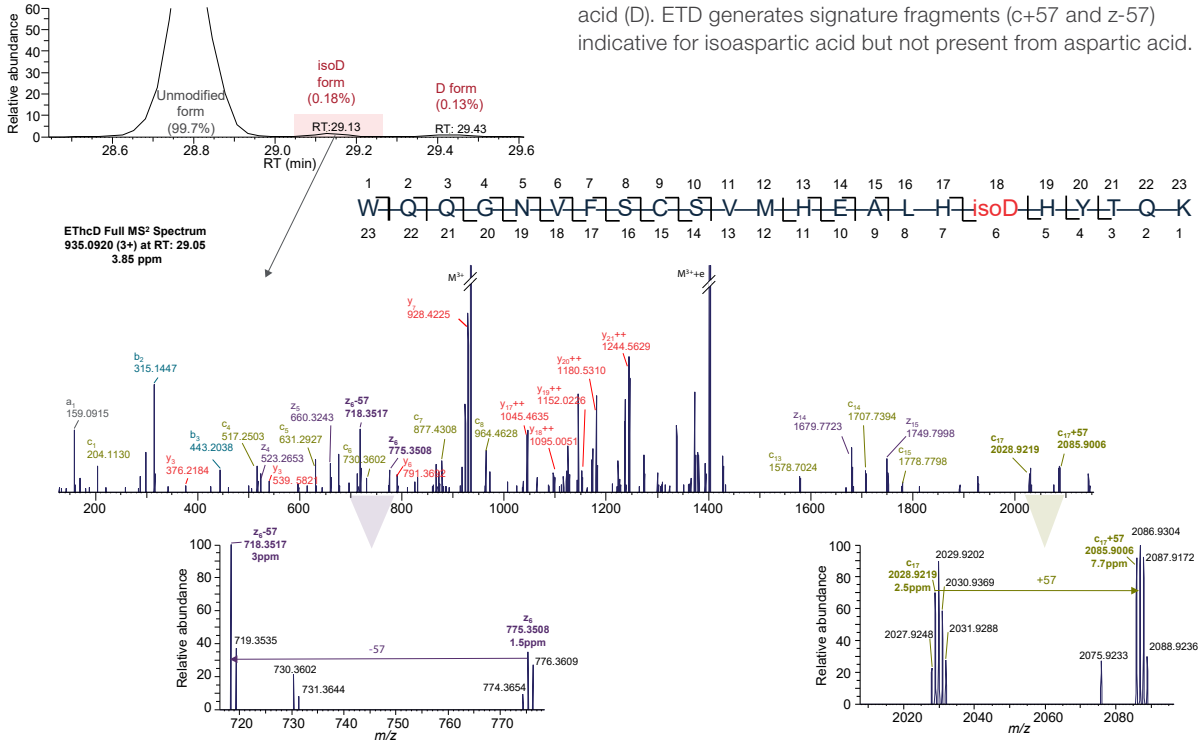


Figure 2b: In a UHPLC-HRAM-MS-ddMS^2 analysis of NISTmAb tryptic digest peptide mapping experiment, EThcD achieved high sequence coverage and unambiguously identified isoaspartic acid in a 23-amino acid triply charged deamidated peptide present at a low abundance level (0.18%) with high confidence. The zoom-in insets show the high mass accuracy (<8 ppm) achieved for both signature fragments (z_6-57 and c_{17}+57).

"The Orbitrap Exploris 480 MS has been indispensable for biotherapeutic characterization, running continuously in our lab and producing high-quality data. The Orbitrap Excedion Pro BioPharma MS enhances this platform through the addition of electron transfer dissociation (EASY-ETD) and an extended mass range. Initial data shows that high spectral acquisition rate of EASY-ETD results in deeper protein sequence coverage, improved PTM characterization, detection of large aggregate impurities, and richer fragmentation patterns for confident disulfide linkage assignments. These improvements provide immediate value to our biotechnology work and will serve as our next generation platform."

Dr. Andrew Mahan
Associate Director and
Mass Spec Group Leader,
Johnson & Johnson
Innovative Medicine

Innovate Higher-order Structure Characterization of Biomolecules

Hydrogen-Deuterium Exchange Mass Spectrometry (HDX-MS) has become an essential analytical tool in the biopharmaceutical industry, providing critical insights into protein dynamics, conformational changes, and molecular interactions. HDX-MS plays a pivotal role in epitope mapping, enabling precise identification of antigen-antibody binding sites. While traditional HDX-MS offers valuable insights at the peptide level, achieving residue-level resolution has remained a significant challenge due to the limitations of conventional fragmentation techniques. The fast and sensitive (optional) ETD in the Orbitrap Excedion Pro BioPharma mass spectrometer enables researchers to localize deuterium exchange at individual amino acid residues. This allows for a more precise characterization of protein conformational changes, drug-binding sites, and allosteric effects, pushing the boundaries of HDX-MS applications in biopharma research.

- **Fast scan speed** for Data Independent Acquisition (DIA)-HDX workflows increases protein coverage
- **Higher sensitivity** allows analysis of low sample amounts at cap-flow gradients
- **Impressive results** in a 6 min gradient at 4 µL/min flow rate with only 300 ng injection for Rituximab

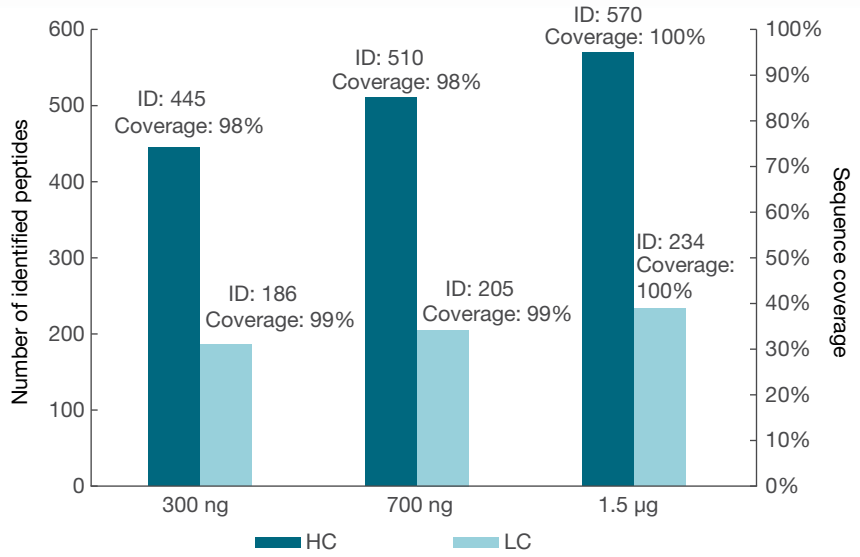


Figure 3: Peptide identification and sequence coverage of Rituximab heavy chain (HC) and light chain (LC) across different on-column injection amounts (300 ng, 700 ng, and 1.5 µg) using a 6-minute gradient. The bar graph represents the number of identified peptides for HC (dark blue) and LC (light blue).

Identification of binding pocket on KRAS G12C upon Adagrasib binding using DIA-HDX

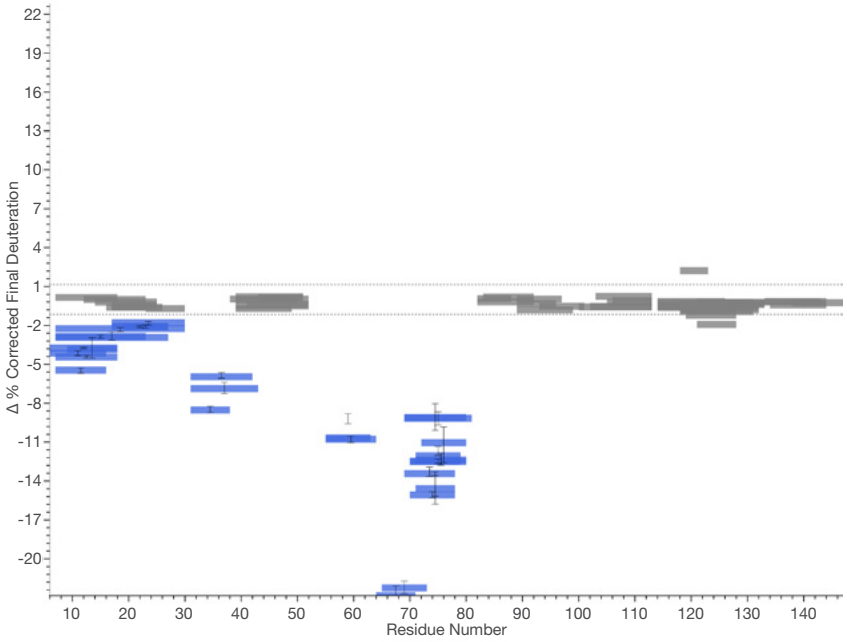


Figure 4a: Woods plot. The x-axis denotes the residue number, while the y-axis shows the percentage change in deuteration. The blue bars with error bars indicate experimental data points at 20 second labeling time, representing regions with significant deuteration changes. Dashed lines indicate a threshold for significant changes in deuteration.

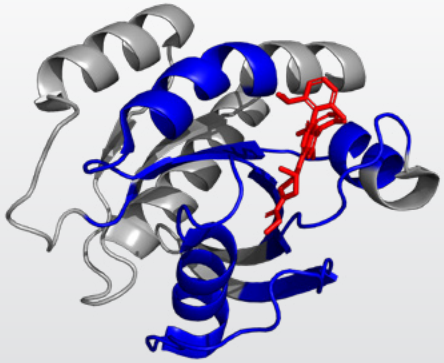


Figure 4b: Structural representation of KRAS G12C in complex with Adagrasib. KRAS G12C binds with Adagrasib drug. The protein backbone is depicted in gray, with the G12C mutation region and key structural changes highlighted in blue.

"The Orbitrap Exploris 480 MS has been essential for our high-throughput HDX-MS workflows, consistently delivering reproducible and reliable peptide-level deuterium uptake data. The Orbitrap Excedion Pro mass spectrometer further enhances this capability with exceptional sensitivity, optimized low-flow setup, and advanced data-independent acquisition strategies. Our initial evaluation demonstrated high-quality peptide-level resolution and improved detection of low-abundance peptides, enabling more comprehensive and precise characterization of protein-ligand and protein-protein interactions. These advancements make the Orbitrap Excedion Pro MS an invaluable platform for next-generation HDX-MS studies."

Dr. Malvina Papanastasiou
Group Leader, Research Scientist, Broad Institute of MIT and Harvard

Discover More in Metabolomics and Lipidomics Research

The Orbitrap Excedion Pro mass spectrometer is an essential tool for metabolomics research, providing numerous advantages that enhance the analytical capabilities for comprehensive metabolite profiling and targeted metabolite analysis:

- **Increased sensitivity**
- **Enhanced Dynamic Range (eDR)**
- **Increased annotation of unknowns**

Unintentional fragmentation is an aspect of mass spectrometry-based small molecule research that impacts both discovery and targeted applications. With the Orbitrap Excedion Pro mass spectrometer, the new electrodynamic funnel design minimizes unwanted fragmentation, preserving the integrity of fragile metabolites and ensuring increased precursor signal-to-noise. By utilizing the eDR scan capability, metabolomics researchers can now detect and quantify a wide range of metabolites with high sensitivity and specificity, including those present in low concentrations. This technology boosts the signal-to-noise ratio of the low abundant compounds in complex mixtures without compromising the detection of high abundant species and results in an additional order of magnitude depth of sample coverage. Additionally, this increased depth results in both a greater number of annotated compounds in an untargeted method as well as greater confidence in all annotated compounds.

Improved dynamic range of detected compounds with eDR

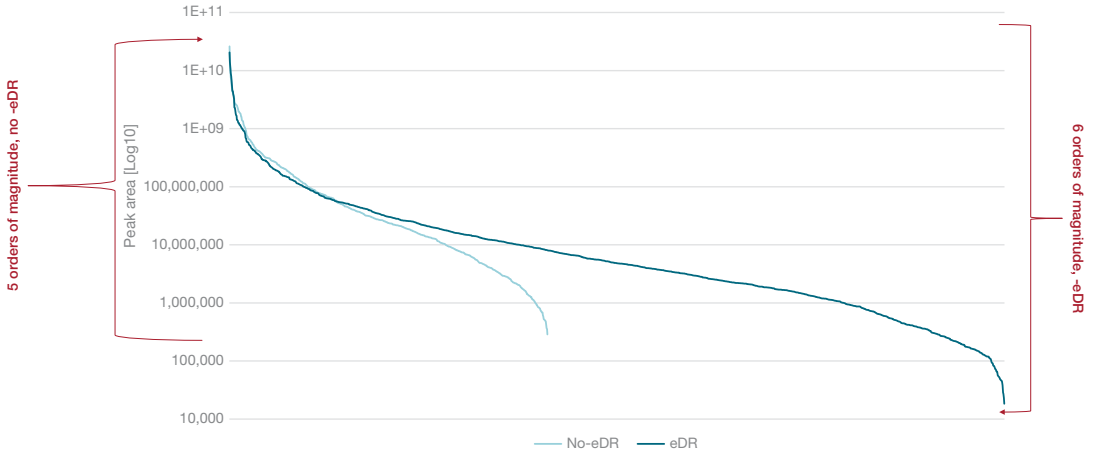


Figure 5: When plotting a regression of peak area versus total number of compounds detected in SRM 1950, eDR achieves an additional order of magnitude of depth for plasma metabolite identification indicating that the greater than 2X gain in compounds are on the low end of the dynamic range without compromising the high-end measurements.

Untargeted discovery with eDR to unlock deeper insights

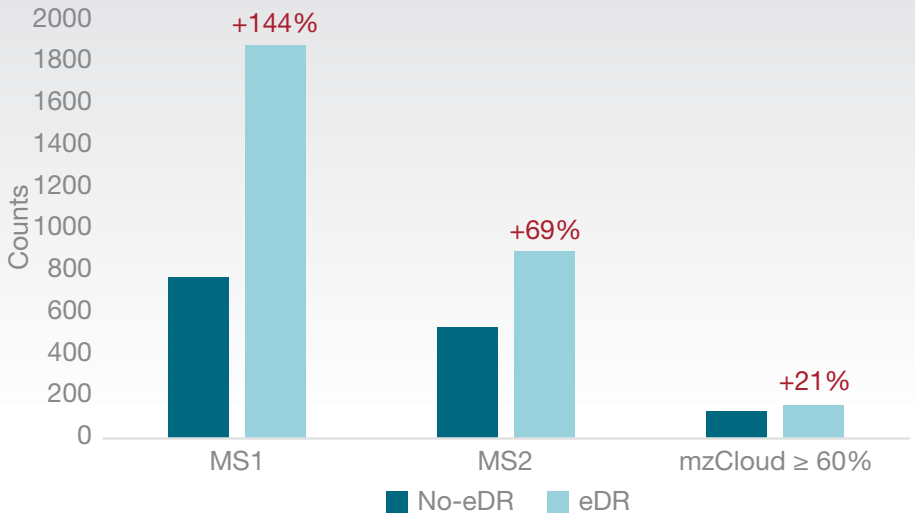


Figure 6: NIST SRM 1950 plasma metabolite extracts were separated using reversed phase and interrogated with iterative data dependent MS2 analysis using the Thermo Scientific™ AcquireX™ intelligent data acquisition deep-scan workflow. The AcquireX workflow was further used to generate comprehensive fragmentation coverage of unique sample-relevant compounds by automated exclusion of non-biological and redundant features through iterative data-dependent injections of a sample. The full scan MS1 used to generate the precursor inclusion list for the data dependent workflow was done using either the eDR workflow or Orbitrap full scan without eDR. Results were then processed using Thermo Scientific™ Compound Discover™ 3.4 software. The bar graph shows that over 2X the number of compounds were detected with MS1. Here, a compound refers to a unique *m/z* and RT pair, after background subtraction, with isotopes, adducts and in-source fragments coalesced into a single entry. After several injections with AcquireX over 21% more compounds were annotated using Thermo Scientific™ mzCloud™ mass spectral fragmentation library.

"Mass spectrometers with extended dynamic range offer a significant advantage by enabling the simultaneous analysis of both trace-level and highly-abundant analytes without signal saturation or the loss of low-intensity peaks. This perspective will benefit the analysis of biological, environmental, and industrial samples with a broad range of analyte concentrations. By improving isotopic and adduct distribution analysis and enhancing detection limits, such advanced mass spectrometers can significantly improve quantitative accuracy, making them indispensable for high-precision analytical applications."

Dr. Oliver Fiehn
Director, West Coast Metabolomics Center, UC Davis Genome Center

Exceed in Proteomics Research

The Orbitrap Excedion Pro mass spectrometer transforms everyday proteomics into exceptional results.

- **Accurate quantification with extended dynamic range**
- **Hybrid-DIA supported by adaptive RT routine**
- **Deep proteome coverage**
- **PTMs analysis with ETD fragmentation**
- **Immunopeptidomics with EThcD fragmentation**

Achieve higher intra-scan dynamic range—up to five orders of magnitude—with the Orbitrap Excedion Pro mass spectrometer, leading to improved detection and quantitation of low-abundance proteins and PTMs in MS full scan.

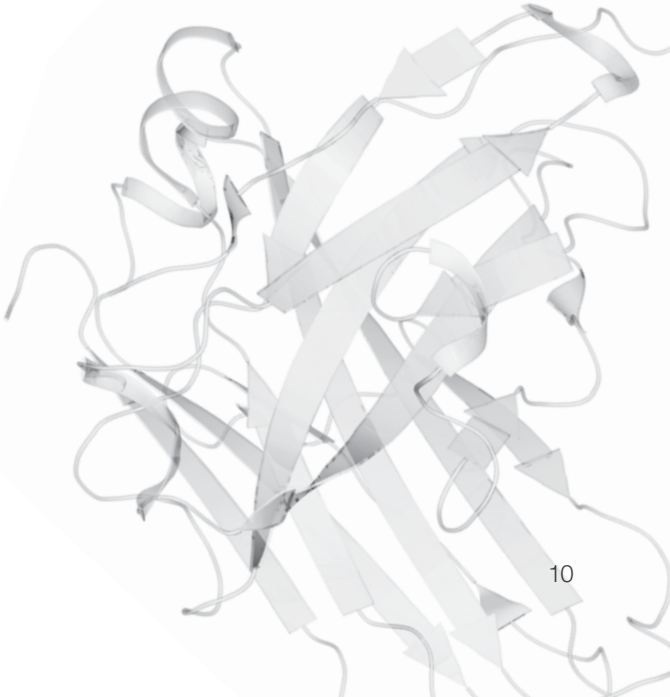
Support up to Thermo Scientific™ TMTpro™ 32plex deuterated label reagents for comprehensive and efficient analysis, significantly increasing throughput with advanced multiplexing capabilities.

Employ high-resolution MS1 scans and hybrid-DIA supported by adaptive RT routine workflows for precise and accurate quantification of proteins and peptides, ensuring accurate quantification.

Benefit from fast and sensitive alternative fragmentation with ETD & EThcD to address difficult samples like immunopeptides, glycopeptides, or post-translationally modified peptides. Ion pre-accumulation and innovative detection technologies ensure high sensitivity for both targeted and discovery proteomics workflows, providing improved sensitivity in your research Hybrid-DIA experiment.

Immunopeptidomics with EThcD – Maximize sequence coverage for comprehensive and confident identification.

Analyzing the composition of Human Leukocyte Antigen (HLA) class I bound immunopeptidomes using mass spectrometry is crucial for developing new therapies for cancer, autoimmune diseases, and infectious diseases. A major challenge in immunopeptidomics is that only a small portion of MS2 spectra provide enough information for clear sequence identification. To overcome this, EThcD can be employed to produce dual-fragment ion series covering *b*- and *y*-type ions as well as *c*- and *z*-type ions, resulting in more spectrally dense and informative MS2 spectra.



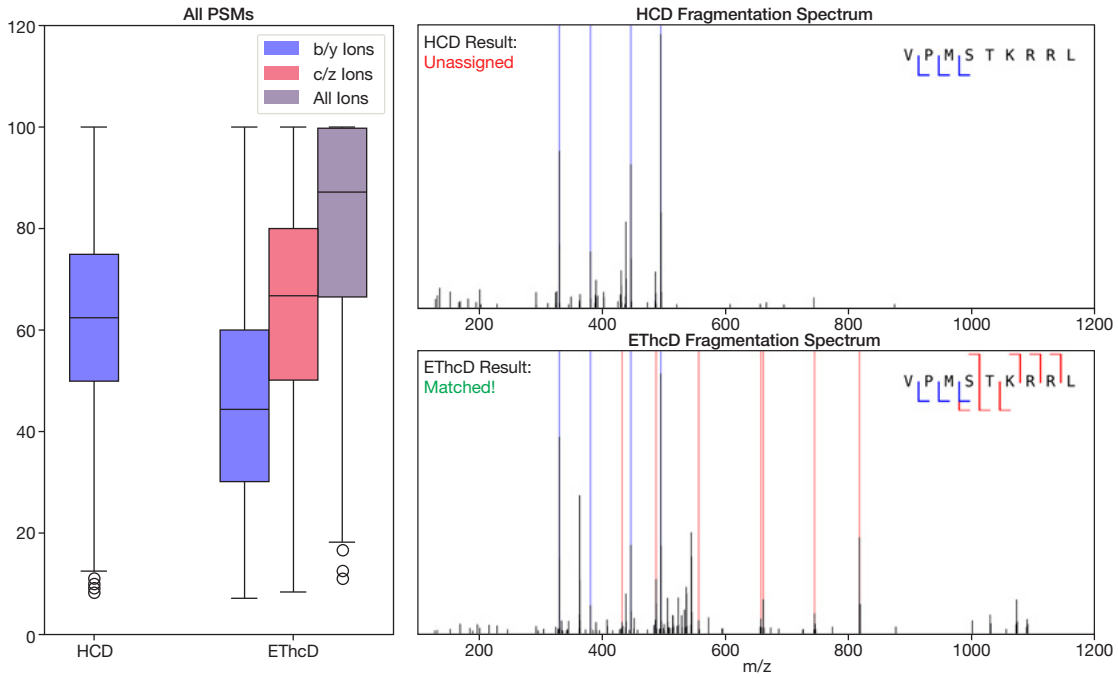


Figure 7: Sequence coverage of all PSMs (left panel) from GR cell analysis using either HCD fragmentation or EthcD fragmentation. The increased sequence coverage afforded by EThcD due to the presence of complimentary b/y and c/z ion series allows for improved identification as shown by the example spectra on the right. HCD fragmentation (right panel, top spectrum) shows limited sequence coverage and the data processing software is unable to assign the spectrum. EthcD fragmentation (right panel, bottom spectrum) shows a full sequence ladder of fragment ions. These ions provide full sequence coverage, allowing for confident spectral assignment. Moreover, these contiguous fragments and the resulting high sequence coverage they afford are vital for de novo sequencing. Annotated fragments were assigned by matching theoretical fragments with 10 ppm mass accuracy and confirmation of fragment charge state. Sequence coverage was calculated using these annotated fragments. Sample: Immunopeptides from GR cell and JY cells, courtesy of Prof. Dr. Albert Heck.

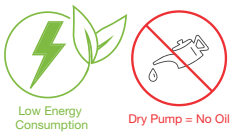
> “EThcD fragmentation on the Orbitrap Excedion Pro mass spectrometer boosts peptide sequence coverage, minimizing detrimental sequence gaps, even for peptides with unfavorable physicochemical properties, allowing less error-prone immunopeptidomics, glycoproteomics, and de novo sequencing.”

Dr. Albert Heck
Professor of Pharmaceutical Sciences, Biomolecular Mass Spectrometry and Proteomics, Utrecht University, the Netherlands

Improve
Sustainability with Less Maintenance

To reduce carbon footprint and overall maintenance, Orbitrap Excedion Pro mass spectrometers come standard with a single rough dry pump instead of two oil pumps.

- 30% less energy consumption
- Reduced noise and heat production
- No maintenance for five years



Learn more at **thermofisher.com/orbitrapexcedionpro**

Experience
the Advantages of Thermo Fisher Scientific Service

Choosing Orbitrap Excedion Pro mass spectrometers means more than just acquiring advanced technology; it means partnering with Thermo Fisher Scientific, a leader in scientific innovation and support. **Our Unity™ Lab Services** delivers world-class service solutions to support your instruments. Our comprehensive service portfolio includes instrument service plans, on-demand services (compliance services, maintenance, and installation), and education support.

Services Central allows you to easily request, manage and view services via a centralized online platform. You can also check service plan or warranty coverage, access manuals, and more.

Learn more at **unitylabservices.com**

For more information or to schedule a demonstration, contact us today. Discover what the Orbitrap Excedion Pro mass spectrometer can do for you!