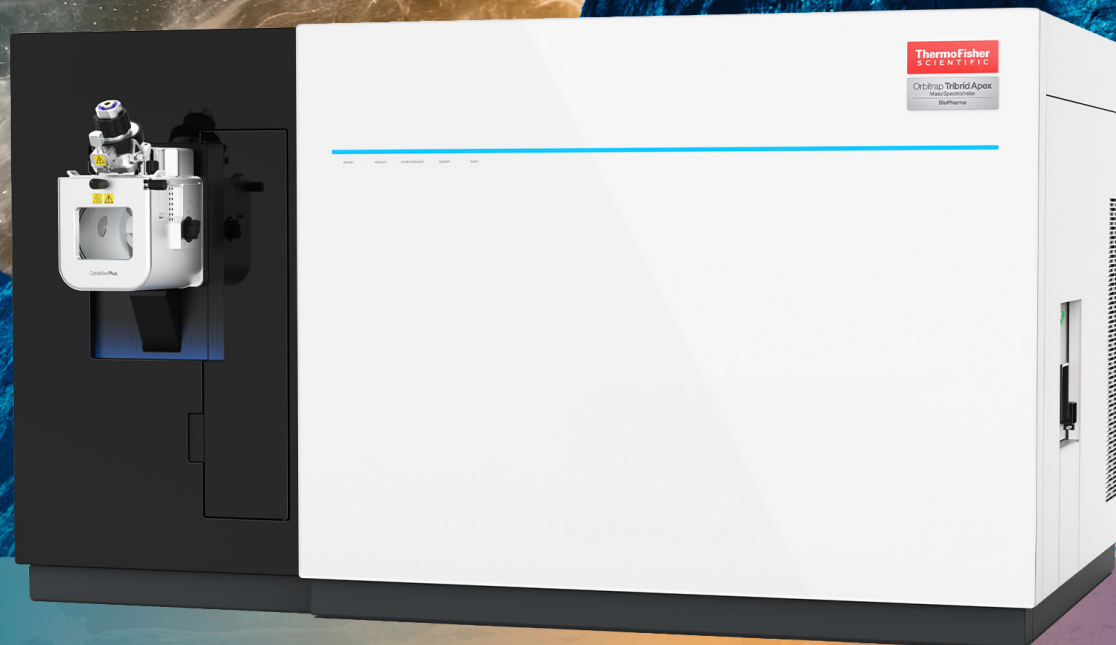


Mass spectrometry

Rise to the molecular challenges of tomorrow

Thermo Scientific™ Orbitrap™ Tribrid™ Apex Mass Spectrometers



thermo scientific

Rise to the molecular challenges of tomorrow

With four new Tribrid editions, purpose-built for small molecule, multiomics, structural biology, and biopharma applications

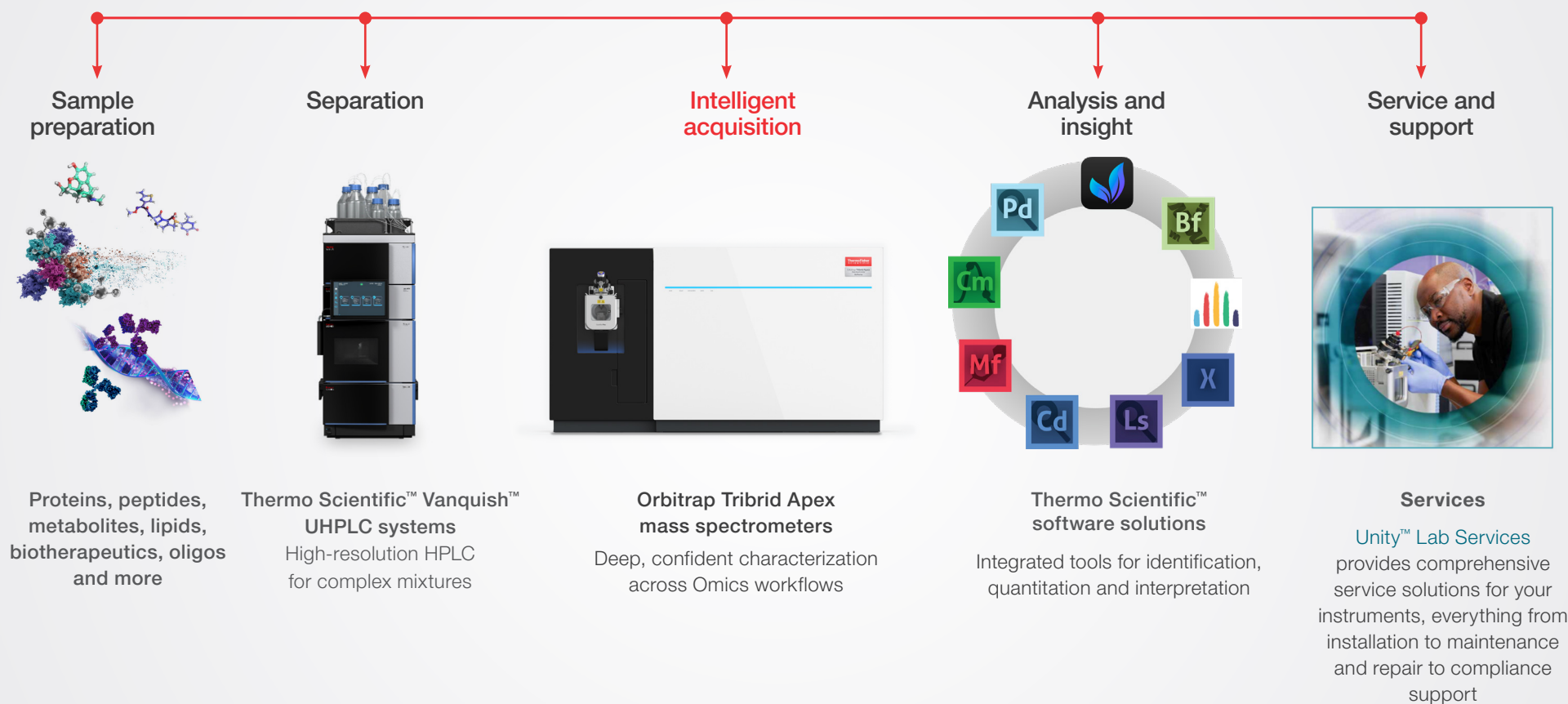
Introducing the Thermo Scientific™ Orbitrap™ Tribrid™ Apex Mass Spectrometer, a powerful new platform engineered for greater speed, sensitivity, fragmentation flexibility, and performance across today's most demanding analyses. With advanced ion parallelization, infrared-enabled fragmentation, and flexible MSⁿ workflows, it is available in four application-focused editions for small molecule, multiomics, structural biology, and biopharma workflows, helping researchers solve complex challenges today and seize tomorrow's opportunities.

One platform. Four editions. Limitless possibilities.



Complete workflow. One partner.

From sample to insight, Thermo Fisher Scientific solutions integrate seamlessly to accelerate discovery and deliver confident answers.



More than an instrument. A complete solution

End-to-end workflows
Integrated solutions designed to work seamlessly together from sample to insight.

Integrated hardware and software
Engineered to deliver performance you can trust.

Scalable across applications
Flexible solutions that grow with your research and your goals.

Global service and support
Expert service and training to keep your workflows running at its best.

Built for what you're solving

Each edition is purpose built to address unique scientific challenges, extending the core versatility and performance with enhanced capabilities designed for your research needs.



Small Molecule edition

Turn unknowns into answers faster

Quickly identify and characterize unknown compounds in complex samples

- Confidently identify low-level unknowns
- Gain deeper structural insight
- Quantify more compounds across samples



Structural Biology edition

From complexes to detailed structure insights

Understand protein structure, interactions, and dynamics at every level

- Study low-abundance complexes
- Preserve native membrane protein structure
- Analyze structure and interactions in one platform



MultiOmics edition

More IDs. Better quantitation.

Drive deeper, more accurate insights across proteomics and multiomics studies

- Enhance characterization of the proteome including peptides, PTMs, and proteoforms
- Improve quantitation accuracy for TMT
- Quantify low-level targets smartly



BioPharma edition

Confident characterization of biotherapeutics

Simplify analysis of complex biologics for development and QC in one instrument

- Characterize from intact to peptide levels
- Increase sequence coverage confidence
- Understand molecular heterogeneity

Small molecule: Characterization



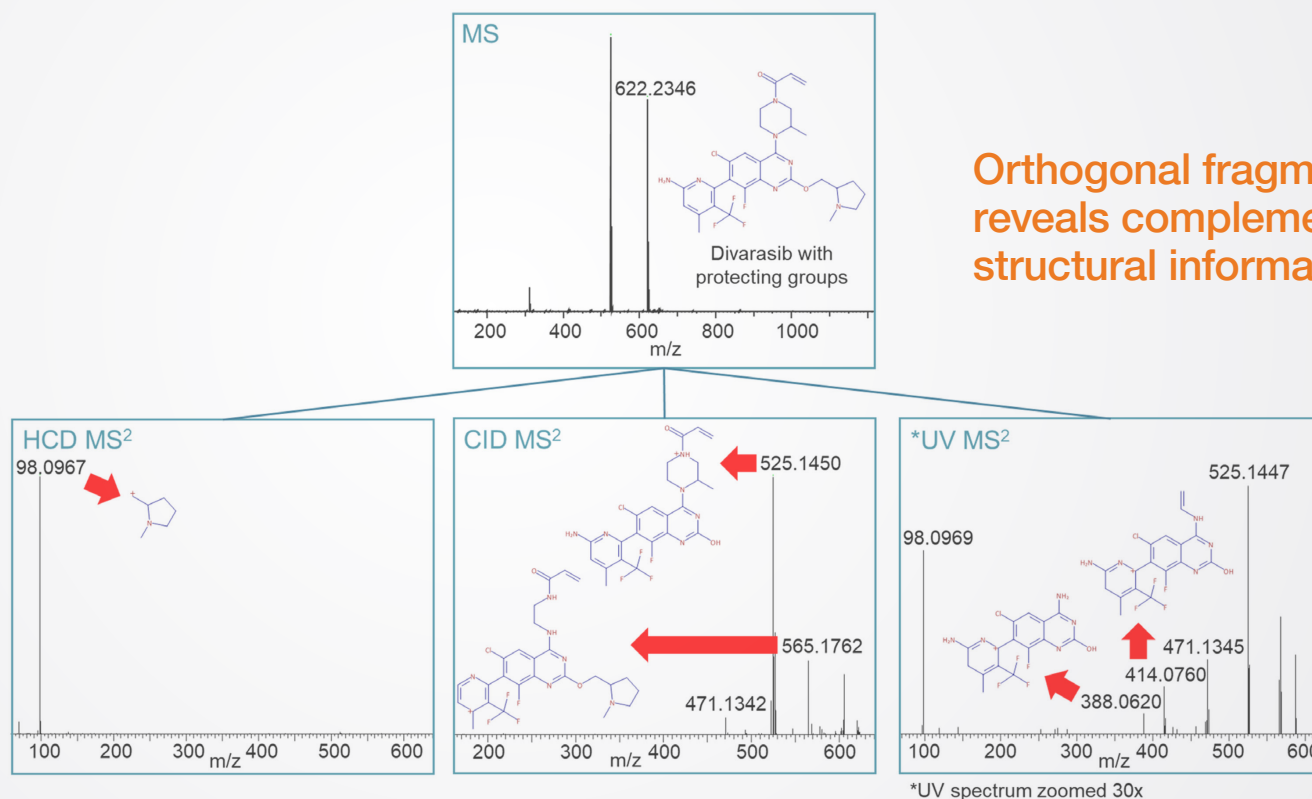
"Fungal biofilms promote chronic infections and antifungal resistance to severely limit treatment options against disease. With the new [Orbitrap Tribrid Apex Small Molecule] mass spectrometer, instrument-driven multi-stage and alternative fragmentation schemes are uncovering a hidden world of small molecules that transform natural products into precision antifungal and antibiofilm therapeutics."

Jennifer Geddes-McAlister,
Canada Research Chair/
Associate Professor
University of Guelph

Turn unknowns into structural answers

Comprehensive structural insight in a single injection: Unknown compounds are difficult to characterize because no single fragmentation method tells the full story. The Thermo Scientific™ Orbitrap™ Tribrid™ Apex Small Molecule Mass Spectrometer solves this by combining orthogonal fragmentation pathways in a single experiment to reveal complementary structural information.

- Reveal complementary structural information by mixing and matching up to four orthogonal fragmentation techniques
- Elucidate complex unknown structures with faster and more sensitive MSⁿ
- Reduce method development time with intelligent data acquisition



Orthogonal fragmentation
reveals complementary
structural information

HCD, CID, and UVPD provide complementary information about different structural elements of the compounds, increasing confidence in structural annotation

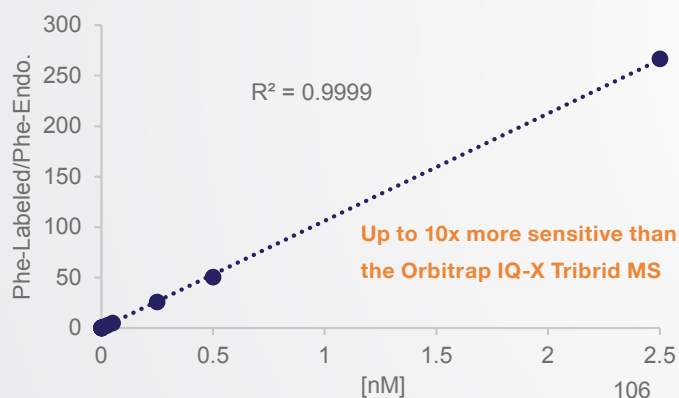
One injection. Multiple fragmentation pathways. Complete structural clarity.

From unknowns to confident quantitation

Measure what matters across complex samples and wide dynamic ranges: The Orbitrap Tribrid Apex Small Molecule mass spectrometer delivers the sensitivity, dynamic range, and intelligent acquisition needed to move from discovery to confident quantitation, capturing this information for both known targets and unexpected compounds in a single LC-MS analysis.

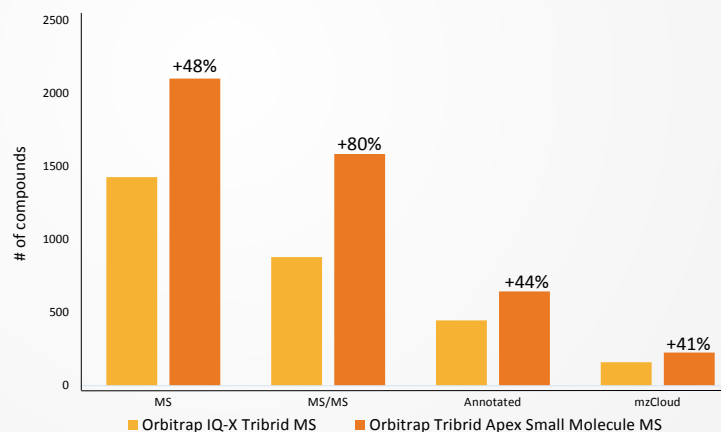
- Quantify known targets and identify unexpected compounds in a single LC-MS run using Simultaneous Quantitation and Discovery (SQUAD) analysis
- More comprehensive sample analysis with 40% faster polarity switching in a single injection
- Measure from trace levels to high abundance with accurate quantitation across 7 orders

Confident quantitation from trace to high abundance



Phenylalanine quantitation demonstrated an LLOQ of 0.5 femtomole and linear dynamic range across 7 orders of magnitude in SQUAD analysis

Do discovery and quantitation in a single run



SQUAD analysis of NIST SRM 1950 plasma spiked with stable isotope-labeled amino acids.

Wide dynamic range targeted quantitation with expanded compound discovery coverage in a single run

Small molecule: Quantitation

Confident quantitation without compromise

The Orbitrap Tribrid Apex Small Molecule mass spectrometer enables confident quantitation across complex matrices and wide concentration ranges without sacrificing sensitivity, dynamic range, or throughput. With parallelized acquisition using multiple mass analyzers achieve simultaneous targeted and untargeted analysis in a single injection using SQUAD, it delivers trace-level detection, precise quantitation, and broader compound coverage in a streamlined workflow that reduces reanalysis and accelerates insight.

Structural biology: Native MS



"I am very excited about the Orbitrap Tribrid Apex Structural Biology MS. Its single-ion detection capability and multistage MSⁿ fragmentation significantly expand the detection and structural characterization of low-abundance protein complexes. It is a powerful discovery tool for discerning how critical membrane-associated signaling complexes drive cell biology of human health and disease."

Kallol Gutpa, Ph.D.
Associate Professor
Yale University

Resolve native structures while preserving complex formations

Characterize intact protein complexes with integrated native, top-down, and MSⁿ workflows:

Native mass spectrometry (native MS) enables direct analysis of protein complexes in their native state, preserving structure and interactions. The Thermo Scientific™ Orbitrap™ Tribrid™ Apex Structural Biology Mass Spectrometer combines native MS with advanced fragmentation and Direct Mass Technology mode to deliver detailed structural insight without requiring dedicated instrument.

Analyze native protein complexes:

Observe intact protein complexes as they exist in biology, with various subunits combined in their native state.

1. Resolve heterogeneity in the sample:

Observe intact protein complexes as they exist in biology, with various subunits combined in their native state. Acquire native MS with Direct Mass

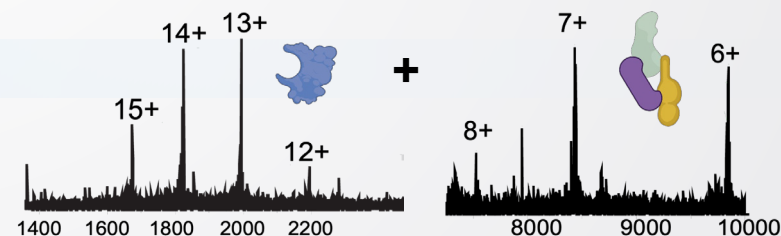
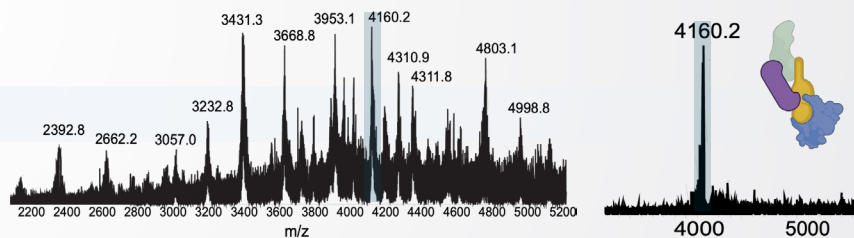
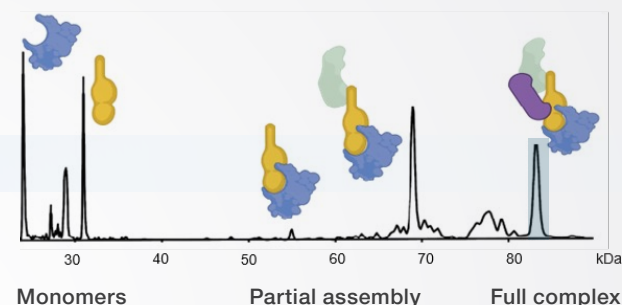
Technology mode to distinguish overlapping masses from coexisting protein complexes and reveal finer structural detail.

2. Isolate the target complex for MS/MS:

Use Direct Mass Technology mode to resolve overlapping signals and select the correct precursor, while IR-assisted desolvation boosts signal intensity 10x and gentle ETD fragmentation helps preserve native structure.

3. Fragment and identify the complex:

Fragment the isolated precursor using MSⁿ workflows to reveal monomers, ligands, interactions, and detailed structural information.



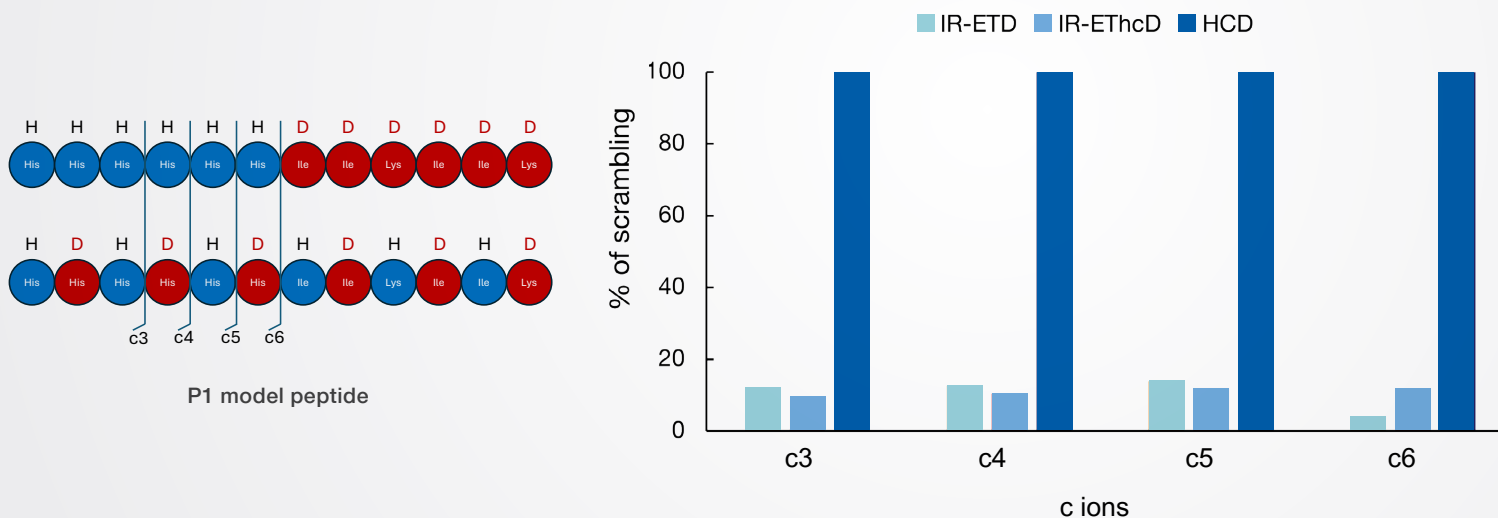
From intact complexes to detailed structural insights in a single platform

Reveal single residue-level structural dynamics with HDX-MS

Preserve deuterium labeling for confident localization of structural change: Single-residue hydrogen-deuterium exchange mass spectrometry (HDX-MS) helps map protein structure, dynamics, and interactions at amino acid-level resolution. The Orbitrap Tribrid Apex Structural Biology mass spectrometer uses IR-assisted ETD and EThcD to reduce deuterium scrambling while improving fragmentation, enabling more confident localization of exchange and deeper structural insight.

- Map protein dynamics at single-residue resolution
- Protect labeling integrity with low-scrambling fragmentation
- Unlock confident structural insight with enhanced fragmentation

IR-assisted ETD and EThcD minimizes scrambling while improving fragmentation



Scrambling evaluation using P1 model peptide. IR-assisted ETD and EThcD reduce scrambling compared with HCD, helping preserve deuterium labeling for more confident residue-level HDX-MS analysis.

Structural biology: HDX-MS

Single-residue HDX-MS for higher-resolution structural insight

Map structural changes at the residue level with fragmentation approaches designed to preserve deuterium labeling. With high sensitivity, gentle ion handling, and IR-assisted fragmentation, the Orbitrap Tribrid Apex Structural Biology mass spectrometer minimizes scrambling while improving fragmentation efficiency for confident, high-resolution HDX-MS analysis.

Preserve labeling. Improve fragmentation. Enable single residue-level insight.

MultiOmics: Peptide quantitation



“The Orbitrap Tribrid Apex MultiOmics MS continues to set the standard for TMT-multiplexed quantitative proteomics, making large and complex studies more reliable. It delivers the most accurate and reproducible quantification with improved sensitivity and precision enabled by an IR laser, enhanced acquisition cycles, and SPS-MS³ technology without sacrificing depth of coverage.”

Steven Gygi, Ph.D.

Professor
Harvard Medical School

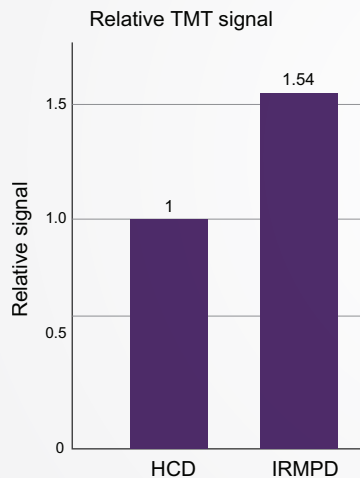
From deep discovery proteomics to advanced targeted quantitation

Reach your peak quantitative proteomics productivity: Quantitative proteomics requires both broad discovery and confident validation across complex sample sets. The Thermo Scientific™ Orbitrap™ Tribrid™ Apex MultiOmics Mass Spectrometer delivers workflow flexibility for label-free discovery quantitation, including DDA, DIA, and hybrid DIA, as well as Thermo Scientific™ Tandem Mass Tag™ (TMT) workflows, while supporting targeted validation through parallel reaction monitoring (PRM) and a new smart targeted TMT workflow. With improved ion parallelization and IR-assisted fragmentation, the Orbitrap Tribrid Apex MultiOmics MS enhances TMT performance by increasing reporter ion signal, peptide quantitation, and target coverage for more confident multiplexed analysis.

- Uncover new biology with deep, unbiased label-free discovery quantitation workflows
- Compare more samples with high-precision using multiplexed TMT quantitation
- Validate key targets with sensitive, accurate smart targeted quantitation workflows

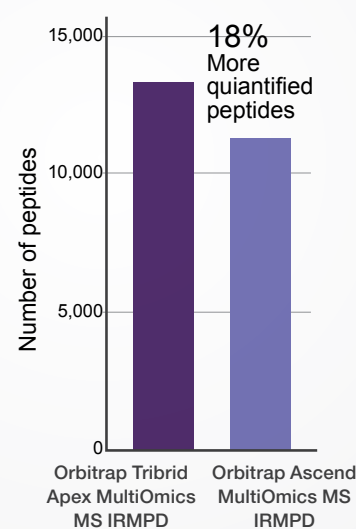
Discovery proteomics

Improved TMT quantitation sensitivity



Comparison of the signal-to-noise ratio of the TMT reporter ions from SPS MS³ method using HCD or IRMPD as fragmentation.

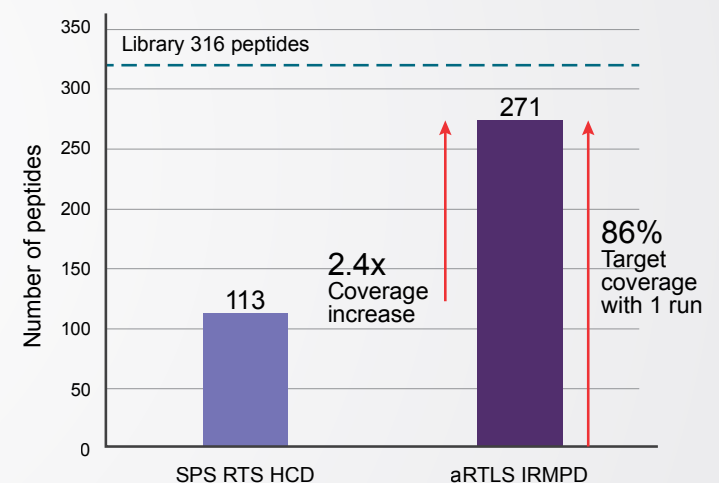
More quantified peptides



Number of quantified peptides on a discovery experiment on human cell lines labeled with Thermo Scientific™ TMTpro™ 18-plex with SPS MS³ method.

Targeted validation

Deep targeted coverage



Peptides of interest identified in a discovery experiment are used to build a target list using Thermo Scientific™ Proteome Discoverer™ Software. During acquisition, the adaptive RTLS tool enables selective fragmentation of target peptides and real-time library searching to trigger confident SPS MS³ quantitation.

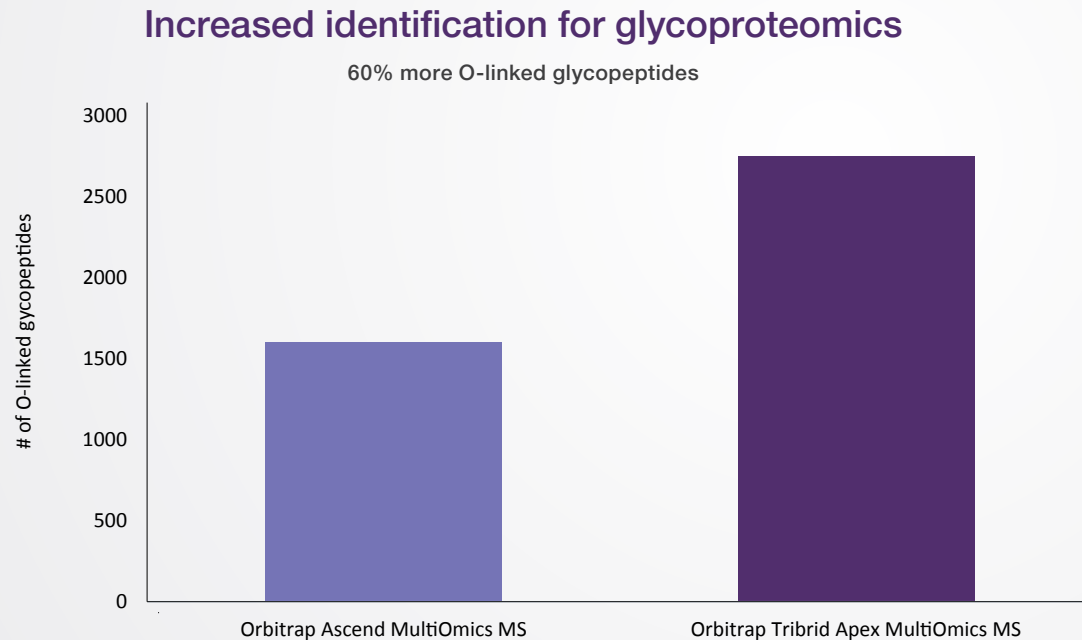
One platform. End-to-end quantitative proteomics solutions

Go beyond quantitation to PTM-level insight

Identify and characterize complex post-translational modifications (PTMs) with improved fragmentation

and instrument parallelization: Glycosylation is one of the most common and structurally complex PTMs, shaping protein function, interactions, stability, and disease biology. The Orbitrap Tribrid Apex MultiOmics mass spectrometer helps researchers move beyond protein quantitation to deeper characterization of complex PTMs such as glycosylation. Improved ion parallelization and IR-assisted EThcD increase fragmentation efficiency, sequence coverage, identification and confidence in glycopeptide analysis, especially for O-linked glycopeptides. This enables researchers to connect specific molecular modifications to meaningful biological insight.

- High-throughput glycoproteomics enabling glycan composition, peptide sequence and site localization in single analysis
- Intelligent mass spectrometer acquisition approaches to simplify data analysis throughput
- Add additional biological context beyond glycopeptide analysis with flexible MSⁿ workflows for released glycans and intact glycoprotein analysis



IR-assisted EThcD on the Orbitrap Tribrid Apex MultiOmics MS nearly doubles O-linked glycopeptide identifications.

Expanded glycopeptide coverage for more confident PTM insight

MultiOmics: Peptide characterization



"Electron transfer dissociation continues to be highly advantageous for characterizing numerous post-translational modifications, especially glycosylation that is the focus of my research group. The improvement made to ETD technology on Orbitrap Tribrid Apex MS, including significant speed increases for more high-quality spectra and new modalities for supplemental activation to improve the information available in each spectrum, directly translate to better characterization of the glycoproteome for both routine and bespoke experiments."

Nicholas Riley, Ph.D.
Assistant Professor
University of Washington

BioPharma: ADCs



“The Orbitrap Tribrid Apex BioPharma MS addresses the challenge of analyzing complex biotherapeutics such as ADCs and multispecific antibodies by combining top-down, middle-down, and peptide mapping at LC timescales, with expanded versatility from IR-ETHcD, PTCR, high resolution, and extended mass range in one instrument.”

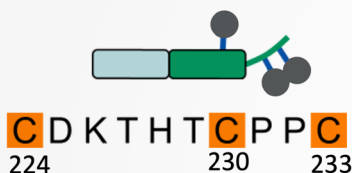
Luca Fornelli, Ph.D.
Associate Professor
University of Oklahoma

Characterize heterogeneous ADCs with deeper structural insight

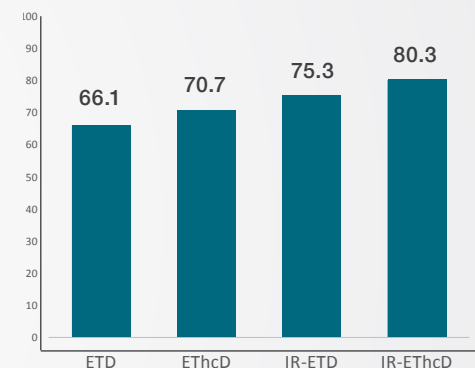
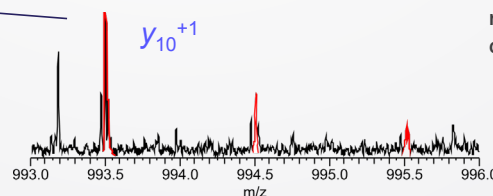
Resolve complex biotherapeutic heterogeneity with greater confidence: Antibody-drug conjugates (ADCs) are highly heterogeneous biotherapeutics that require precise structural characterization. The Thermo Scientific™ Orbitrap™ Tribrid™ Apex BioPharma Mass Spectrometer combines IR-assisted ETD with proton transfer charge reduction (PTCR) MS³ to improve fragmentation, expand complex ions across a wider m/z range, and clarify heterogeneous spectra, enabling deeper sequence coverage and more confident ADC characterization within an LC-MS timeframe.

- Characterize heterogeneous ADCs with deeper sequence coverage
- Improve fragmentation of complex biotherapeutics with IR-assisted ETD
- Clarify highly charged spectra using PTCR MS³ for confident interpretation

Detailed structural characterization of ADCs



N E V Q L V E S G G G L V Q P G I G S L R L S C V A S I 25
26 G F T L N N Y D M H W V R Q G I G K G L E W V S K I 50
51 I G T A G D R Y Y A G S V K G R F T I S R L E N A K I 75
76 D S L Y L Q M N S L R V G D A A V Y Y C A R I G A G I 100
101 R W A P L G A F D I I W G Q G T M V T V S L A S L T K I 125
126 G P S V F P L L A P S I S K I S T S G G T A A L G C L V 150
151 K D Y F P E P V T V S W N S I G A L L T S G V H T F P 175
176 A V L L Q S S G L Y S L S S V V T V P S S S L L G T Q 200
201 T Y I C N V N H K P S N T K V D K K V E P K S C D 225
226 K T H T C P P C P A P E L L G C



IR-ETHcD with PTCR increases sequence coverage generating a more complete set of backbone fragments for improved structural characterization.

IR-ETHcD MS² with PTCR MS³ reduces spectral congestion and improves signal-to-noise ratio, revealing diagnostic ions for confident drug-conjugation site assignment.

Deeper sequence coverage enables confident site-specific ADC characterization

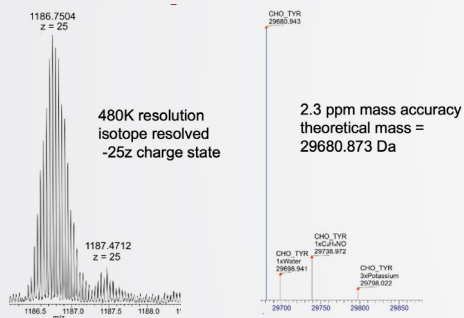
Characterize oligonucleotides from intact, top-down, or bottom-up methodologies

Gain comprehensive structural insight from intact mass to full sequence coverage within a single

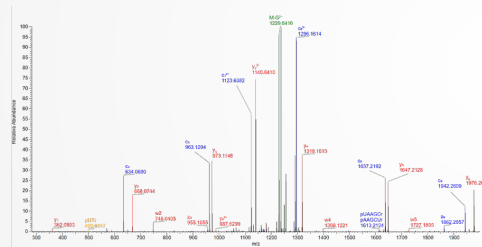
LC-MS workflow: Comprehensive oligonucleotide characterization requires approaches that resolve impurities, generate rich fragment ions, and confirm sequence coverage. The Orbitrap Tribrid Apex Biopharma MS brings intact, top-down, and bottom-up analysis together on a single platform.

- Reveal impurities and intact mass information in complex oligonucleotide samples
- Confirm sequence information with rich top-down fragmentation
- Increase sequence coverage with complementary bottom-up LC-MS analysis

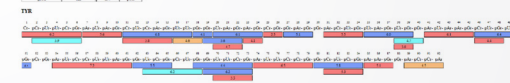
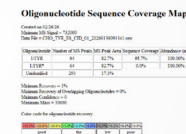
Intact mass analysis $\longrightarrow$ Top-down analysis $\longrightarrow$ Bottom-up sequence mapping



Intact mass analysis of CHO Tyr-tRNA results in ID of multiple impurities and sub-3 ppm error.



Top-down analysis produces rich fragment ions for confident sequencing.



tRNA sequence mapping by LC-MS produces nearly 100% coverage and high abundant fragment peaks.

Complete oligonucleotide characterization, from intact mass to full sequence coverage

Biopharma: tRNA

Rise to the molecular challenges of oligonucleotide-based therapeutics

Transfer RNA (tRNA) is essential to protein translation and emerging RNA therapeutics. Its structural complexity and dense modifications make it difficult to characterize. With advanced fragmentation and high-resolution MS, the Orbitrap Tribrid Apex BioPharma MS enables confident sequence confirmation, modification mapping, and intact mass analysis in one platform.

BioPharma: Antibody sequencing



“Direct Mass Technology mode on the Orbitrap Tribrid Apex mass spectrometers opens an exciting frontier to obtain deep sequence coverage for proteoform targets with unparalleled sensitivity. This technology is highly versatile, and it is the best proteoform sequencer I’ve seen in my 25 years in translational research.”

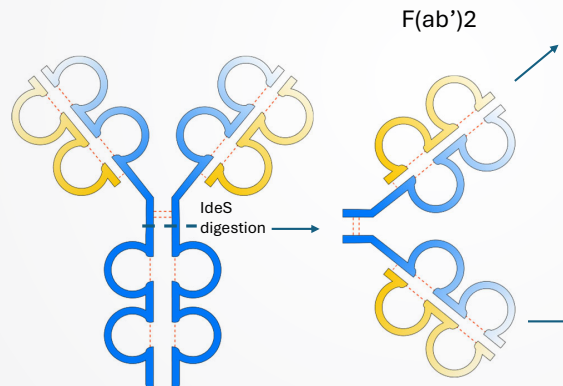
Prof. Neil Kelleher, Ph.D
Director, Northwestern
Proteomics Center of
Excellence,
Northwestern University

Confident antibody sequencing

Characterize the variable region of mAbs. Direct Mass Technology mode assists in increasing sequence coverage by directly gaining mass domain information from complex top-/middle-down spectra. This translates to more sequence coverage especially in the middle of the protein’s sequence where it can often be difficult for traditional ensemble-based methods to deconvolute.

- Increase antibody sequence coverage across light and Fd chains
- Resolve complex subunit spectra with Direct Mass Technology mode
- Enable confident characterization of variable regions in mAbs

IdeS cleavage of intact IgG (mAb)



IdeS digestion products after reduction

Light chain - Lc

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N D I Q M L T Q S L P S T L S A S V G D R V L T I T C S L A 25
26 S S R V G Y M H W Y Q Q K P G K L A P K L L I Y D T 50
51 S K L A S G V P S R F S G S G S G T E F T L T I S 75
76 S L Q P D D F A T Y Y C F Q G S G Y P F T F G G G 100
101 T K V E L I K R T V A A P S V F I F P P S D E Q L K 125
126 S G T A S V V C L L N N F Y P R E A K V Q W K V D 150
151 N A L Q S G N S Q E S V T E Q D S K D S T Y S L S 175
176 S T L T L S K A D Y E K H K V Y A C E V T H Q G L 200
201 S S P V T K S F N R G E C C
    
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Total: 77% sequence coverage

Fd region

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N Q V T L R E S G P A L V K P T Q T L T L T C T F S 25
26 G F S L S T A G M S V G W I R Q P P G K A L E W L 50
51 A D I W W D D K K H Y N P S L K D R L L T I S K D T 75
76 S K N Q V V L K V T N M D P A D T A T Y Y C A R D 100
101 M I F N F Y F D V W G Q G T T V T V S S A S T K G 125
126 P S V F P L L A P S S K S T S G G T A A L G C L V K 150
151 D Y F P E P V T V S W N S G A L T S G V H T F P A 175
176 V L Q S S G L Y S L S S V V T V P S S L L G T Q T 200
201 Y I C N V N H K P S N T K V D K R V E P K S C D K 225
226 T H T C P P C P A P E L L G C
    
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Total: 73% sequence coverage

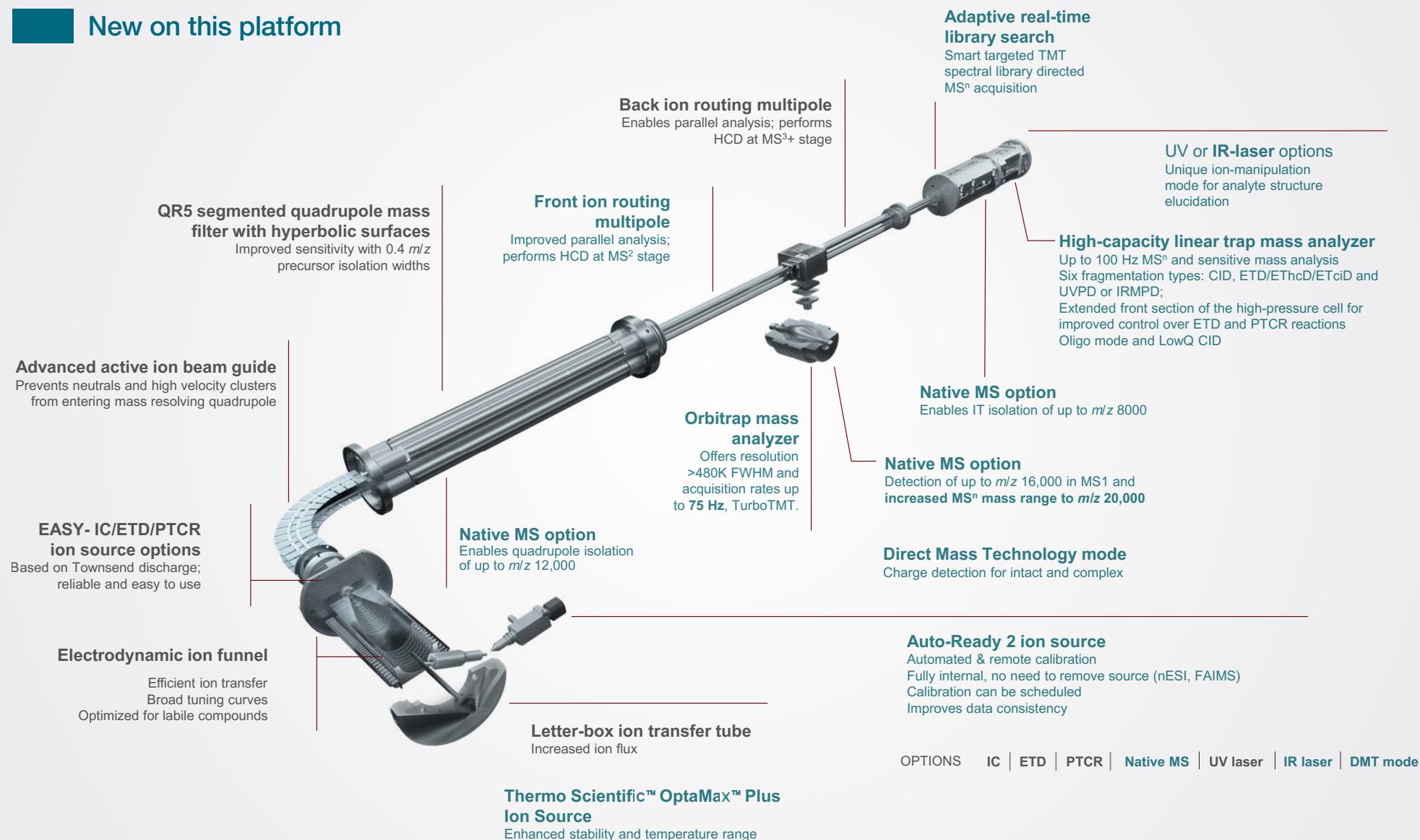
■ CDR1
■ CDR2
■ CDR3

IdeS digestion followed by reduction generates Fd and light chain fragments from intact IgG, enabling high-confidence mass spectrometry sequencing of antibody variable regions using Direct Mass Technology mode.

Deeper subunit coverage. More confident antibody characterization

Orbitrap Tribrid Apex MS innovations

New on this platform





Technical and online support:

Peak performance for your instruments Helping you keep your instruments running at peak performance is our goal. Whether you're looking for an instrument manual or spare parts, want to submit a repair request, or check on the status of your warranty or service contract, we have every support option you're looking for.

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Protecting your investments:

Unparalleled laboratory services Unity™ Lab Services provides a single source for integrated lab service, support, and supply management. Our customized service offerings and world-class service experts have the flexibility and experience to address your laboratory's needs. We provide a complete portfolio of services and support solutions designed to help you improve productivity, reduce total cost of ownership, and ensure performance throughout your laboratory.

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thermofisher.com/mzcloud

Thermo Scientific™ Proteome Discoverer™ Software

thermofisher.com/proteomediscoverer

Thermo Scientific™ Compound Discoverer™ Software

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