

Scale up

your science

ThermoFisher
SCIENTIFIC



Orbitrap Ascend Editions
Tribrid mass spectrometer








thermo scientific

Overcome the challenges in life sciences mass spectrometry

The Orbitrap Ascend Editions Tribrid mass spectrometers offer extraordinary sensitivity and versatility

With improved capabilities for multiplexed quantitative proteomics, post-translational modification (PTM) analysis, native protein characterization and metabolomics, the Thermo Scientific™ Orbitrap™ Ascend Editions Tribrid™ mass spectrometers are among the most powerful, flexible platforms available. The MultiOmics, Structural Biology and BioPharma editions of the Orbitrap Ascend Tribrid mass spectrometer quantify more samples at lower concentrations, achieve greater coverage, analyze the toughest native complexes and characterize the largest biopharmaceuticals on a single platform—all with less instrument setup to optimize ease-of-use.

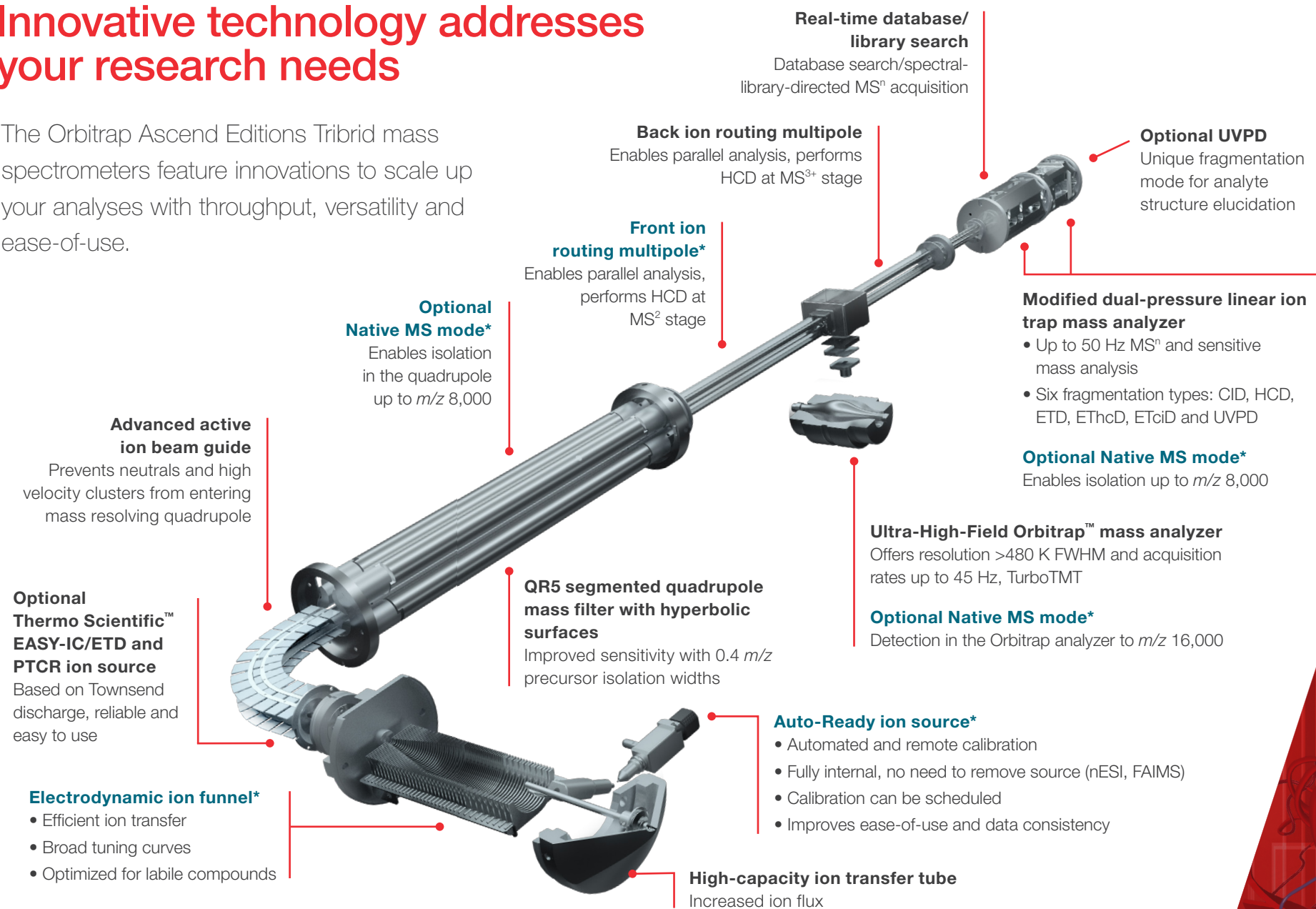
	General proteomics	Complex samples, wide dynamic range, labile PTMs
	Quantitation	Accurate, proteome-wide quantitation with high throughput
	Structural biology	Low-level samples, complex mixtures, high-mass range
	Biopharmaceutical analysis	Protein-drug structure elucidation, impurity ID
	Small molecule analysis	Complex samples, wide dynamic range, labile compounds, isomers



The Orbitrap Ascend Editions Tribrid mass spectrometer equipped with the Thermo Scientific™ FAIMS Pro™ Interface and the Thermo Scientific™ Vanquish™ Neo UHPLC system.

Innovative technology addresses your research needs

The Orbitrap Ascend Editions Tribrid mass spectrometers feature innovations to scale up your analyses with throughput, versatility and ease-of-use.



OPTIONS IC | ETD | PTCR | Native MS* | UVPD | FAIMS Pro Duo interface

*New on this platform

Native

Identify native membrane proteins using PTCR and top-down techniques

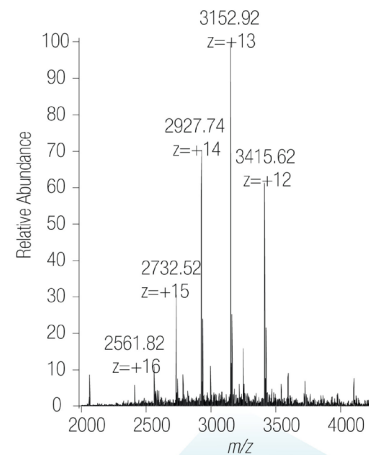
With the Thermo Scientific™ Orbitrap™ Ascend Structural Biology Tribrid™ mass spectrometer, it's now possible to realize the potential of native proteomics, particularly for difficult-to-analyze membrane proteins. Using native protein sample preparation techniques, complexes can be directly injected into the mass spectrometer and the proteins elucidated using their precursor and fragmentation patterns. At the intact protein level, Proton Transfer Charge Reduction (PTCR) simplifies the spectra produced from complex samples. For top-down analysis, very difficult-to-break proteins can be fragmented using multiple fragmentation options, generating enough sequence coverage for high-confidence identification of proteins within complex samples.



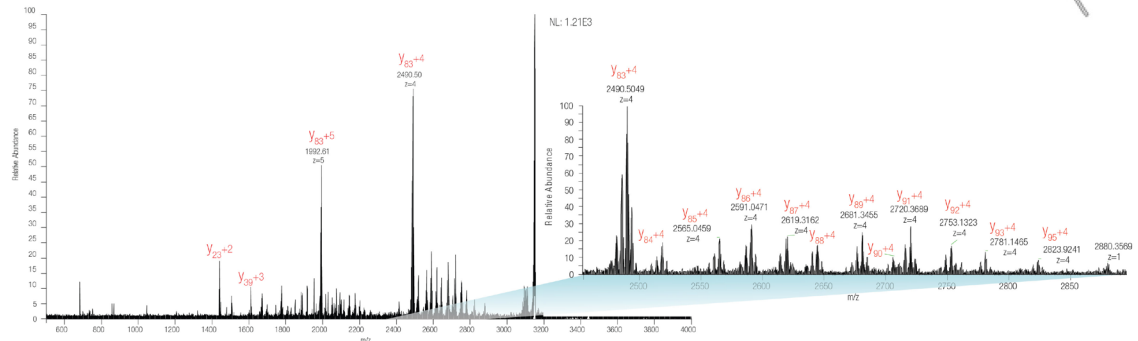
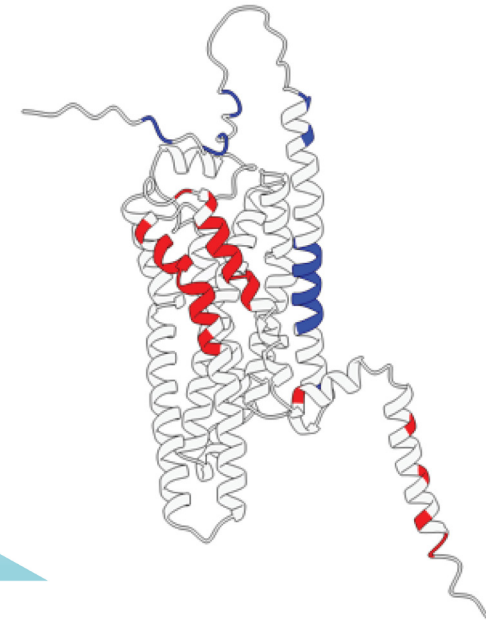
“I’m delighted that we now have an Orbitrap Ascend Structural Biology edition, because this Tribrid mass spectrometer has transformed our ability to study complicated systems.”

Professor Dame Carol Robinson DBE FRS FMedSci FRSC
Director of the Kavli Institute for Nanoscience Discovery
University of Oxford

Fragments mapped onto structure of β 1AR



5 m/z width quadrupole isolation of precursor m/z 3152.92 and HCD CE95



Data courtesy of Corinne Lutomski, Jack Bennett and Tarick El-Baba, Professor Dame Carol Robinson's lab, University of Oxford, and Idir Liko, OMass Therapeutics.

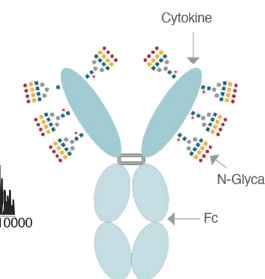
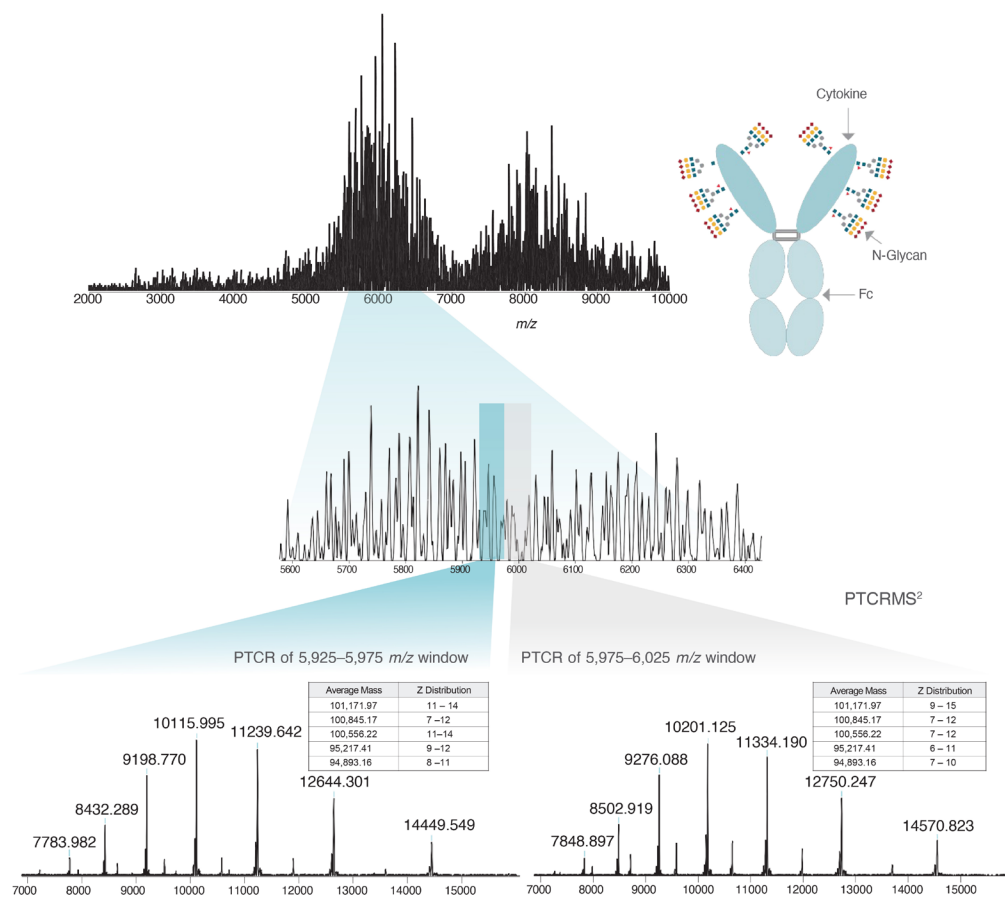
Comprehensively analyze therapeutic proteins with Native MS and PTCR

Biopharma

Protein therapeutics often generate undecipherable spectra due to their high levels of intrinsic heterogeneity. By using the Thermo Scientific™ Orbitrap™ Ascend BioPharma Tribrid™ mass spectrometer's recommended Native MS and PTCR options, interpretable spectra can be generated from heterogeneous protein samples. The Native MS option extends the quadrupole isolation range to m/z 2,000–8,000, which can be used in combination with narrow data-independent acquisition (DIA) windows to simplify the ion population in each scan. The Native MS option also extends Orbitrap analyzer detection to m/z 16,000. These capabilities enable unambiguous identification of previously indiscernible or low-abundance proteoforms. PTCR generates perfluoroperhydrophenanthrene (PFPP) ions for subsequent gas-phase, ion-ion reactions that produce lower charge state distributions to enhance protein characterization.

The flexibility of the Orbitrap Ascend BioPharma Tribrid mass spectrometer enables scientists to carry out unique experiments that combine the recommended Native MS option with PTCR, as well as other dissociation techniques, making it a powerful instrument for comprehensive characterization of therapeutic proteins in their native state.

MS spectrum of native desialylated cytokine-Fc



“The m/z 16,000 range and large ion transmission capabilities of the Orbitrap Ascend Tribrid mass spectrometer enable full use of PTCR charge reduction for complete characterization of even the most complicated molecules.”

Wendy Sandoval
Distinguished Scientist

Data courtesy of Wendy Sandoval.

Quantify more low-level proteins with increased confidence and sample throughput using multiplexed quantitative proteomics

Scale up proteomics productivity

Increasing quantitative coverage of low-abundance proteins is essential to detect biologically important molecules, understand biological systems and substantiate dataset claims. Improving experimental throughput is also desirable because it can proportionally reduce experimental costs. Compared to label-free quantitation (LFQ) methods, multiplexing is a powerful way to increase sample throughput.

With the Thermo Scientific™ Orbitrap™ Ascend MultiOmics Tribrid™ mass spectrometer's fast scanning power and Thermo Scientific™ Tandem Mass Tag (TMT™) multiplexing reagents, you obtain the high protein coverage you expect while analyzing about 30% fewer fractions and substantially increasing experimental productivity.

Access the power of SPS mass spectrometry methods with Real-Time Search

The Synchronous Precursor Selection (SPS) MS³ methods with Real-Time Search for TMT experiments provide unprecedented quantitative accuracy while maximizing the number of peptide identifications. The SPS MS³ acquisition improves the quantitative ratio accuracy of TMT reporter ions, thereby increasing the number of peptides correctly quantified. The Real-Time Search adds speed and further improves quantification accuracy because the MS³ scans are only triggered when a peptide-spectrum match (PSM) occurs from the preceding MS² scan.

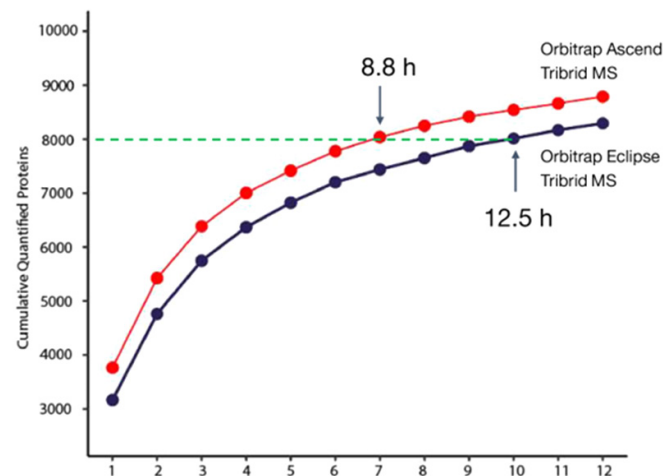


“We need to continue reducing the LC-MS acquisition time even further with a better depth of analysis of smaller numbers of fractionated biological samples. Orbitrap Ascend Tribrid mass spectrometer enables this solution.”

Steven P. Gygi, PhD
Professor of Cell Biology
Harvard Medical School

Identify more proteins per fraction and save time

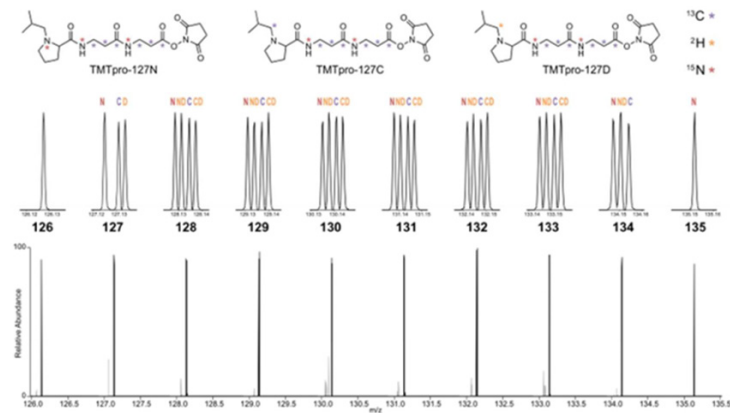
Twelve high-pH fractions of 1 µg of HYPER standard analyzed using a 65-min SPS MS³ Real-Time Search method on Thermo Scientific™ Orbitrap Eclipse™ and Orbitrap Ascend Tribrid mass spectrometers. The data were processed using Harvard pipeline. Similar results are obtained with Thermo Scientific™ Proteome Discoverer™ software.



Sample courtesy of Professor Steven Gygi, Harvard Medical School.

Multiplex analysis of more samples with next-generation TMT reagents

Analysis of 1:1 HeLa using TMTpro 32-plex reagents with the Orbitrap Ascend MultiOmics Tribrid mass spectrometer at 90,000 resolution.



Sample courtesy of Steven Shuken, Qing Yu and Professor Steven Gygi, Harvard Medical School.

Increase phosphopeptide and glycopeptide IDs and site localization

PTMs

Scale up PTM identification and localization

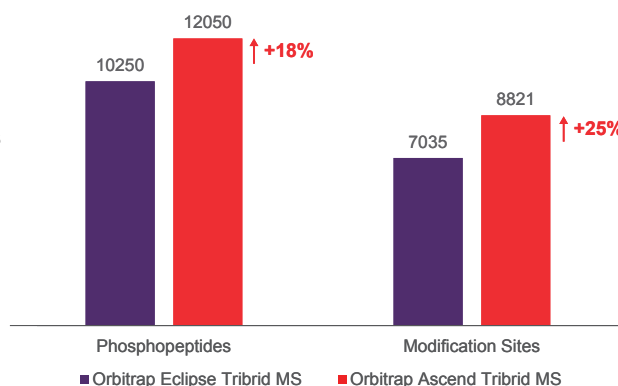
The Orbitrap Ascend MultiOmics Tribrid mass spectrometer increases confidence in results obtained from analysis of labile PTMs thanks to the availability of alternative fragmentation techniques such as electron transfer dissociation (ETD). ETD is better suited for labile PTMs such as glycopeptide because of their non-ergodic type of dissociation. ETD produces extensive fragmentation of the peptide backbone, enabling sequencing of the peptide while preserving glycans on the peptide backbone. This allows for unambiguous assignment of the glycosylation sites. ETD can be used in parallel with high-energy collisional dissociation (HCD) fragmentation, which provides information about glycan composition for thorough characterization of the glycopeptide structure. The availability of electron transfer/higher energy collision dissociation (EThcD) fragmentation can further increase identification and characterization confidence of labile PTMs. The electrodynamic ion funnel improves the capture and transmission of labile PTMs. The front ion routing multipole increases the speed of complex data acquisition—such as that encountered during O-linked glycopeptides EThcD analysis—increasing the number of MS² scans by almost 50%.



“Heterogeneity of protein glycosylation creates different analytical demands. Flexibility is key, making the Orbitrap Ascend MultiOmics Tribrid mass spectrometer particularly valuable for glycopeptide analysis. Its architecture allows manipulation of multiple ion populations simultaneously. This lets us accumulate more ions without slowing acquisition of MS/MS scans, or even speeds it up depending on the method design. This translates to more, and higher quality, MS/MS spectra that ultimately improve our glycopeptide characterization.”

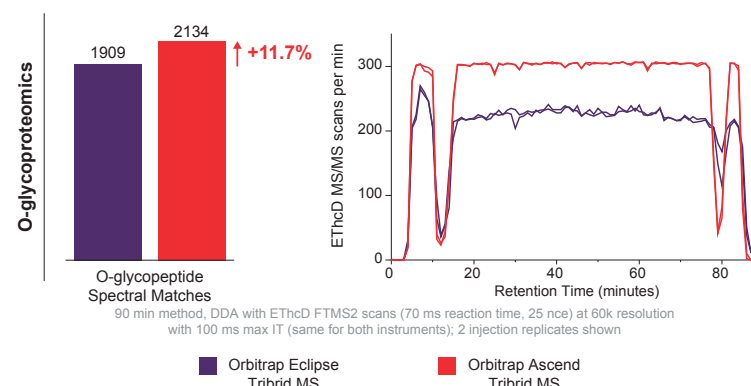
Nick Riley, PhD
Assistant Professor of Chemistry
University of Washington

Improve phosphopeptide and glycopeptide analysis



Phosphopeptide analysis of 0.5 µg sample load in a 90-min gradient on an ES903 column using the Orbitrap Eclipse or Orbitrap Ascend MultiOmics Tribrid mass spectrometer at 15,000 resolution at m/z 200 and 27 ms maximum injection time.

Data courtesy of Yuchen He, Professor Joshua Coon's lab, University of Wisconsin–Madison.



Analysis of semi-complex mixtures of recombinant/purified glycoproteins in a 90-min gradient with Orbitrap Ascend MultiOmics Tribrid mass spectrometer using DDA, EThcD FTMS² scans (70 msec reaction time 25 nce, 60,000 resolution at m/z 200 and 100 ms maximum injection time).

Data courtesy of Professor Nick Riley, University of Washington.

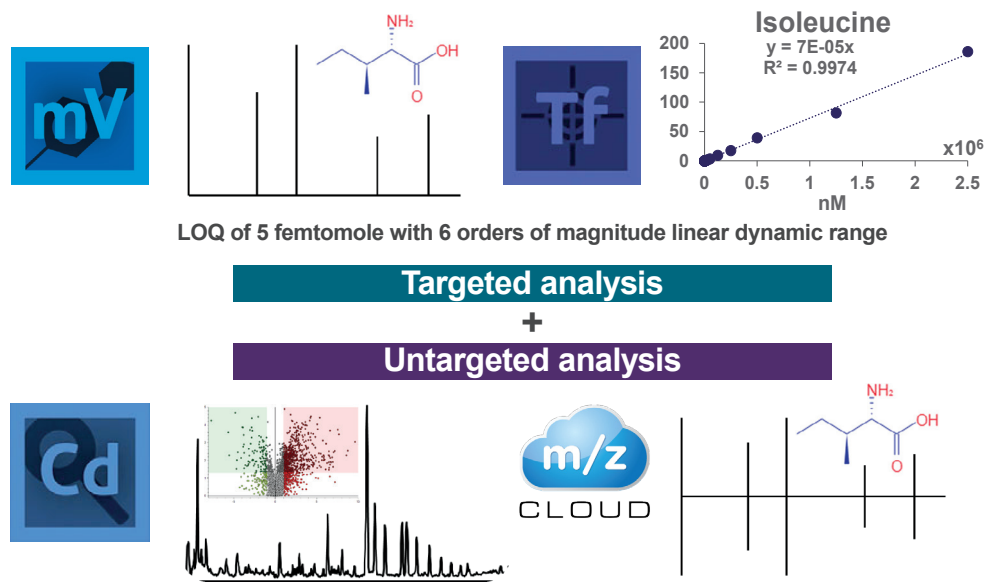
Scale up metabolomics productivity

To increase productivity and accelerate time-to-insight, metabolomics researchers are looking to perform untargeted discovery profiling and targeted quantitation in a single analysis on one MS platform. This is also essential when dealing with limited sample amounts. SQUAD analysis combines the strengths of both methods. It quantifies a predefined set of metabolites, like targeted analysis, but also confidently annotates unknown metabolites like untargeted analysis. Thus, it enhances the understanding of molecular relationships within biological systems. The increased parallelization provided by the dual ion routing multipoles allows the Orbitrap Ascend MultiOmics Tribrid mass spectrometer to acquire more scans for both discovery and targeted quantitation when using the SQUAD workflow. The approach enables metabolomics researchers to save instrument time and samples without compromising the quality of their results. Compared to the previous Orbitrap Tribrid architecture, the new system measures 55% and 25% more MS and MS² ions, respectively.



“The idea of combining true targeted MS/MS while screening for nontargeted compounds is fascinating. It not only extends the sensitivity and scope for metabolomics and exosome research, but it also opens the door for better clinical studies. The Orbitrap Ascend MultiOmics Tribrid mass spectrometer release is very timely and just what we need today.”

Oliver Fiehn, PhD
 Director West Coast Metabolomics Center
 UC Davis



Analysis of isoleucine using the SQUAD workflow on the Orbitrap Ascend MultiOmics Tribrid mass spectrometer. The single-injection workflow combines untargeted data analysis and interpretation using Thermo Scientific™ Compound Discoverer™ software with the mzCloud™ advanced mass spectral database for feature extraction, differential analysis and annotation. Targeted quantification uses Thermo Scientific™ TraceFinder™ software. The mzVault™ application can be used for offline searching of mzCloud MS²-level spectral data in either Compound Discoverer or TraceFinder software. Compared to similarly run sample and experiment on the Thermo Scientific™ Orbitrap™ IQ-X Tribrid™ mass spectrometer.

Experience more high-quality results with less hassle using automated, remote and schedulable system checks and calibrations

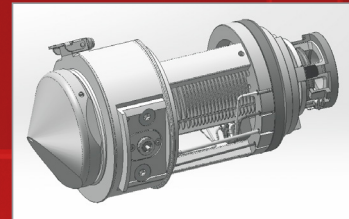
Scale up convenience and ease-of-use

The Auto-Ready ion source is a fully integrated, standard, easy-to-use feature that increases laboratory productivity with automated, remote and schedulable system checks and internal calibrations. Because there is no need to remove the source (HESI, nESI or high-field asymmetric waveform ion mobility spectrometry [FAIMS]), there are no experimental setup interruptions required to perform internal calibrations. The user can automate the calibration to start at a scheduled time—for example, every week—when there are no experiments planned to run on the instrument. The calibration can run completely remotely, regardless of the nature of the last experiment. Because the calibration can be scheduled to occur regularly and automatically without interrupting vital work, users can expect to maintain mass spectrometer performance, improve data consistency and achieve more accurate and precise quantitation.

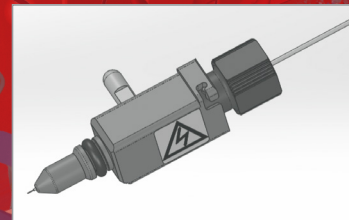


Auto-Ready ion source

Separate ion transfer tube



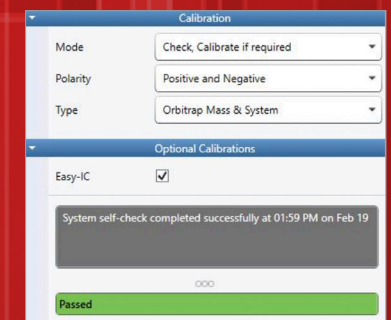
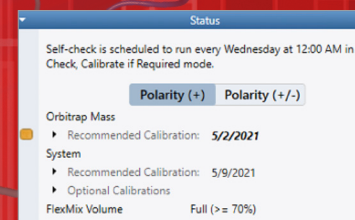
Dedicated emitter



Robust delivery system



Automated weekly calibrations



Resources and support



Services Central—All your service information at your fingertips

Spend less time searching for support and more time focusing on your important work. This online platform has what you need to easily manage your instruments and equipment.

Learn more at thermofisher.com/servicescentral



Protect your investments with expert lab 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 help ensure performance throughout your laboratory.

Learn more at unitylabservices.com



Technical and online support

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.

Learn more at thermofisher.com/technicalresources

More resources

Thermo Scientific™ Ardia™ Platform
thermofisher.com/ArdiaProteomics

Thermo Scientific™ BioPharma Finder™ software
thermofisher.com/biopharmafinder

Thermo Scientific Compound Discoverer software
thermofisher.com/CompoundDiscoverer

mzCloud mass spectral library
thermofisher.com/mzCloud

Thermo Scientific Proteome Discoverer software
thermofisher.com/ProteomeDiscoverer

 Learn more at thermofisher.com/OrbitrapAscend

General Laboratory Equipment – Not For Diagnostic Procedures. © 2024 Thermo Fisher Scientific Inc. All rights reserved. TMT and TMTpro are trademarks of Proteome Sciences plc. All other trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified. This information is presented as an example of the capabilities of Thermo Fisher Scientific products. It is not intended to encourage use of these products in any manner that might infringe the intellectual property rights of others. Specifications, terms and pricing are subject to change. Not all products are available in all countries. Please consult your local sales representative for details. **24-085-1057 | BR001028-EN 0524C**