Mass spectrometry

# Orbitrap Astral mass spectrometer
## Rethink what is possible
2023 year in review

# Introduction

Powered by the synergy of a high-resolution quadrupole mass filter, the Thermo Scientific™ Orbitrap™ mass analyzer and the novel Thermo Scientific™ Astral™ mass analyzer, this revolutionary new instrument achieves unsurpassed performance and experimental flexibility. The combination of the three mass analyzers enables the rapid acquisition of exceptional quality high resolution accurate mass (HRAM) spectra with high sensitivity and dynamic range. The new performance characteristics of the Thermo Scientific™ Orbitrap™ Astral™ mass spectrometer make it ideally suited for accurate and precise quantitation at an unprecedented depth of coverage and throughput for samples from single cells to body fluids to bulk tissues.
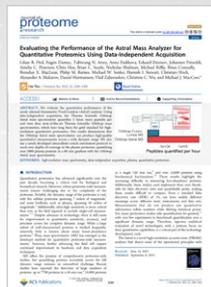
## 56 scientific resources in 7 months

**Table of contents**

# Peer reviewed articles

## Proteomics

### Evaluating the Performance of the Astral Mass Analyzer for Quantitative Proteomics Using Data-Independent Acquisition

Lilian R. Heil, Eugen Damoc, Tabiwang N. Arrey, Anna Pashkova, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Chris Hsu, Brian C. Searle, Nicholas Shulman, Michael Riffle, Brian Connolly, Brendan X. MacLean, Philip M. Remes, Michael W. Senko, Hamish I. Stewart, Christian Hock, Alexander A. Makarov, Daniel Hermanson, Vlad Zabrouskov, Christine C. Wu, and Michael J. MacCoss

*Journal of Proteome Research 2023, 22, 10, 3290–3300*

View article

## Technology
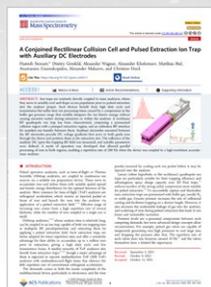
### A Conjoined Rectilinear Collision Cell and Pulsed Extraction Ion Trap with Auxiliary DC Electrodes

Hamish Stewart, Dmitry Grinfeld, Alexander Wagner, Alexander Kholomeev, Matthias Biel, Anastassios Giannakopulos, Alexander Makarov, and Christian Hock

*Journal of the American Society for Mass Spectrometry 2023*

View article

### Multi-reflection Astral Mass Spectrometer with Isochronous Drift in Elongated Ion Mirrors

Dmitry Grinfeld, Hamish Stewart, Wilko Balschun, Michael Skoblin, Christian Hock, Alexander Makarov

*ScienceDirect, Volume 1060, March 2024, 169017*

View article

### Parallelized Acquisition of Orbitrap and Astral Analyzers Enables High-Throughput Quantitative Analysis

Hamish I. Stewart, Dmitry Grinfeld, Anastassios Giannakopulos, Johannes Petzoldt, Toby Shanley, Matthew Garland, Eduard Denisov, Amelia C. Peterson, Eugen Damoc, Martin Zeller, Tabiwang N. Arrey, Anna Pashkova, Santosh Renuse, Amirmansoor Hakimi, Andreas Kühn, Matthias Biel, Arne Kreutzmann, Bernd Hagedorn, Immo Colonius, Adrian Schütz, Arne Stefes, Ankit Dwivedi, Daniel Mourad, Max Hoek, Bastian Reitemeier, Philipp Cochems, Alexander Kholomeev, Robert Ostermann, Gregor Quiring, Maximilian Ochmann, Sascha Möhring, Alexander Wagner, André Petker, Sebastian Kanngiesser, Michael Wiedemeyer, Wilko Balschun, Daniel Hermanson, Vlad Zabrouskov, Alexander A. Makarov, and Christian Hock

*Analytical Chemistry 2023, 95, 42, 15656–15664*

View article

# Preprints

## Single-cell proteomics

### Evaluating the Capabilities of the Astral Mass Analyzer for Single-Cell Proteomics

Valdemaras Petrosius, Pedro Aragon-Fernandez, Tabiwang N. Arrey, Nil Üresin, Benjamin Furtwängler, Hamish Stewart, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Christian Hock, Eugen Damoc, Alexander Makarov, Vlad Zabrouskov, Bo T. Porse, and Erwin M. Schoof

*bioRxiv 2023.06.06.543943*

View preprint

### High-Throughput and Scalable Single Cell Proteomics Identifies Over 5000 Proteins Per Cell

Zilu Ye, Pierre Sabatier, Leander Hoeven, Teeradon Phlairaharn, David Hartlmayr, Fabiana Izaguirre, Anjali Seth, Hiren Joshi, Dorte Bekker-Jensen, Nicolai Bache, and Jesper V. Olsen

*bioRxiv 2023.11.27.568953*

View preprint

### One-Tip Enables Comprehensive Proteome Coverage in Minimal Cells and Single Zygotes

Zilu Ye, Pierre Sabatier, Javier Martin-Gonzalez, Akihiro Eguchi, Dorte B. Bekker-Jensen, Nicolai Bache, and Jesper V. Olsen

*bioRxiv 2023.08.10.552756*

View preprint

## Plasma proteomics

### Protein Coronas on Functionalized Nanoparticles Enable Quantitative and Precise Large-Scale Deep Plasma Proteomics

Ting Huang, Jian Wang, Alexey Stukalov, Margaret K. R. Donovan, Shadi Ferdosi, Lucy Williamson, Seth Just, Gabriel Castro, Lee S. Cantrell, Eltaher Elgierari, Ryan W. Benz, Yingxiang Huang, Khatereh Motamedchaboki, Amirmansoor Hakimi, Tabiwang Arrey, Eugen Damoc, Simion Kreimer, Omid C. Farokhzad, Serafim Batzoglou, Asim Siddiqui, Jennifer E. Van Eyk, and Daniel Hornburg

*bioRxiv 2023.08.28.555225*

View preprint

## Whole proteome

### Narrow-Window DIA: Ultra-Fast Quantitative Analysis of Comprehensive Proteomes with High Sequencing Depth

Ulises H Guzman, Ana Martinez Del Val, Zilu Ye, Eugen Damoc, Tabiwang N. Arrey, Anna Pashkova, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Florian Harking, Ole Østergaard, Hamish Stewart, Yue Xuan, Daniel Hermanson, Christian Hock, Alexander Makarov, Vlad Zabrouskov, and Jesper V. Olsen

*bioRxiv 2023.06.02.543374*

View preprint

## Phosphoproteomics

### One-Hour Phosphoproteome Analysis with the Orbitrap Astral Mass Spectrometer

Noah M. Lancaster, Pavel Sinitcyn, Patrick Forny, Trenton M. Peters-Clarke, Caroline Fecher, Andrew J. Smith, Evgenia Shishkova, Tabiwang N. Arrey, Anna Pashkova, Margaret Lea Robinson, Nicholas Arp, Jing Fan, Juli Hansen, Andrea Galmozzi, Lia R. Serrano, Michael S. Westphall, Hamish Stewart, Christian Hock, Eugen Damoc, David J. Pagliarini, Vlad Zabrouskov and Joshua J. Coon
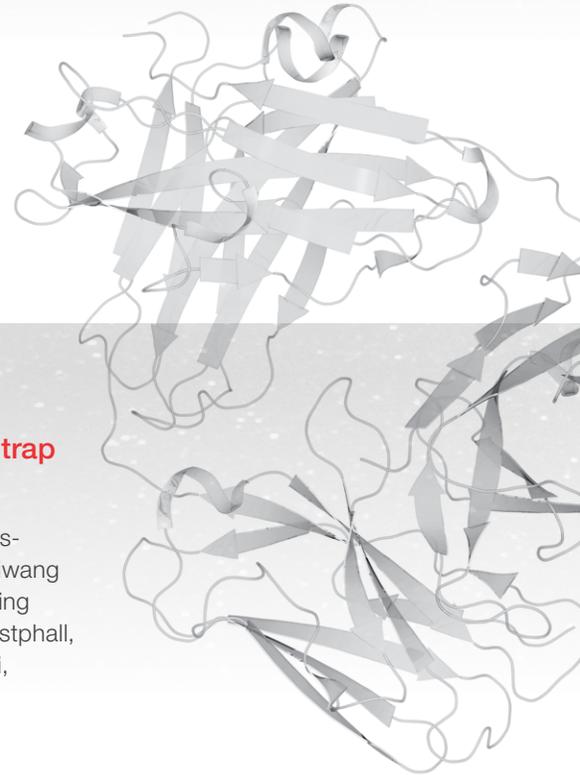
*bioRxiv 2023.11.21.568149*

View preprint

### Systematic Optimization of Automated Phosphopeptide Enrichment for High-Sensitivity Phosphoproteomics

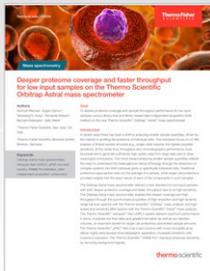Patricia Bortel, Ilaria Piga, Claire Koenig, Christopher Gerner, Ana Martinez del Val, and Jesper V. Olsen
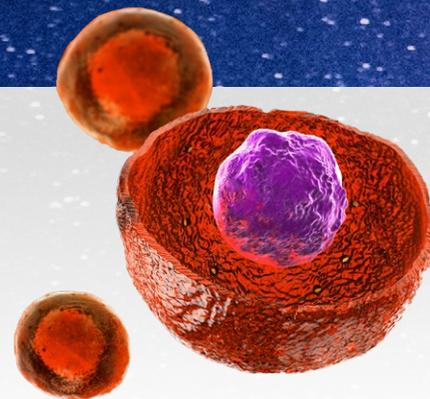
*bioRxiv 2023.11.23.568418*

View preprint

# Technical note

## Single-cell proteomics

### Deeper Proteome Coverage and Faster Throughput for Low Input Samples on the Thermo Scientific Orbitrap Astral Mass Spectrometer

Santosh Renuse, Eugen Damoc, Tabiwang N. Arrey, Fernanda Salvato, Bernard Delanghe, and Sally Webb

View note

# Application note

## Plasma proteomics

### New Standards for Plasma Proteomics—Balancing Throughput for Large Sample Cohorts and Depth of Analysis for Biomarker Discovery

Amirmansoor Hakimi, Eugen Damoc, Tabiwang N. Arrey, Philip L. Loziuk, David Horn, Amarjeet Flora, and Sally Webb

View note

# White papers

## Proteomics and metabolomics

### Rethink What is Possible with the Orbitrap Astral Mass Spectrometer

Vlad Zabrouskov, Eugen Damoc, Tabiwang N. Arrey, Anna Pashkova, Martin Zeller, Christian Hock, Hamish Stewart, and Daniel Hermanson

View paper

### Simultaneous Quantitation and Discovery (SQUAD) Analysis: Combining Targeted and Untargeted Metabolomics on Orbitrap-Based Mass Spectrometers

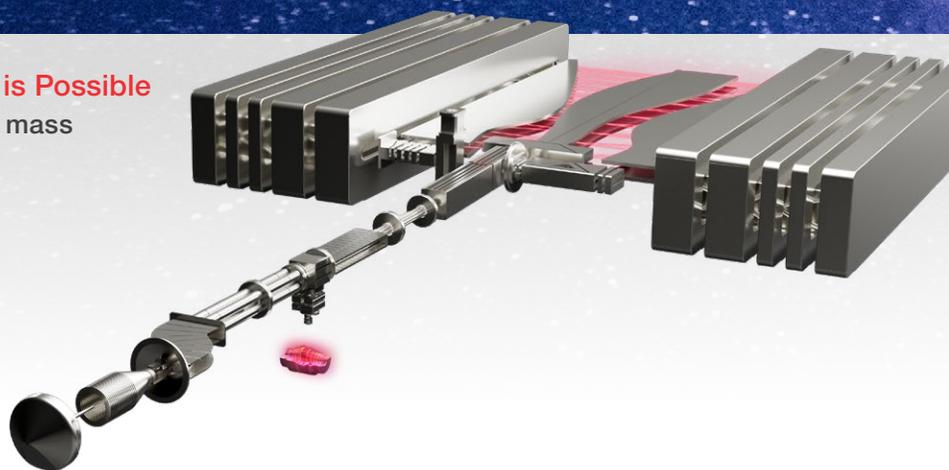Bashar Amer, Julian Saba, Rahul R. Deshpande, and Susan S. Bird

View paper

# Brochure

### Rethink What is Possible
Orbitrap Astral mass spectrometer

View brochure

# Specification sheet

### Rethink What is Possible
Orbitrap Astral mass spectrometer

View sheet

# Published raw data

### Evaluating the Performance of the Astral Mass Analyzer for Quantitative Proteomics Using Data-Independent Acquisition

Lilian R. Heil, Eugen Damoc, Tabiwang N. Arrey, Anna Pashkova, Eduard Denisov, Johannes Petzoldt, Amelia C. Peterson, Chris Hsu, Brian C. Searle, Nicholas Shulman, Michael Riffle, Brian Connolly, Brendan X. MacLean, Philip M. Remes, Michael W. Senko, Hamish I. Stewart, Christian Hock, Alexander A. Makarov, Daniel Hermanson, Vlad Zabrouskov, Christine C. Wu, and Michael J. MacCoss

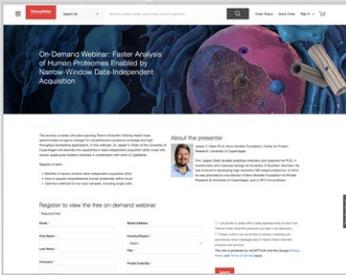*Journal of Proteome Research 2023, 22, 10, 3290-3300*

View article

Raw data

### One-Tip Enables Comprehensive Proteome Coverage in Minimal Cells and Single Zygotes

Zilu Ye, Pierre Sabatier, Javier Martin-Gonzalez, Akihiro Eguchi, Dorte B. Bekker-Jensen, Nicolai Bache, and Jesper V. Olsen
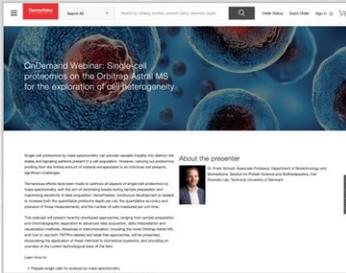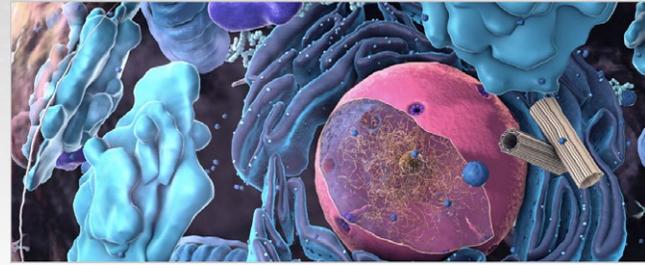
*bioRxiv 2023.08.10.55275*

View article

Raw data

# Webinars



## Faster Analysis of Human Proteomes Enabled by Narrow-Window Data-Independent Acquisition
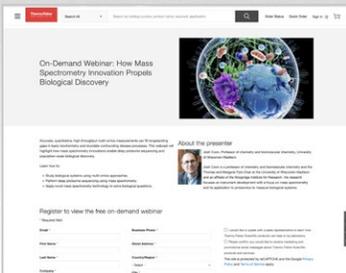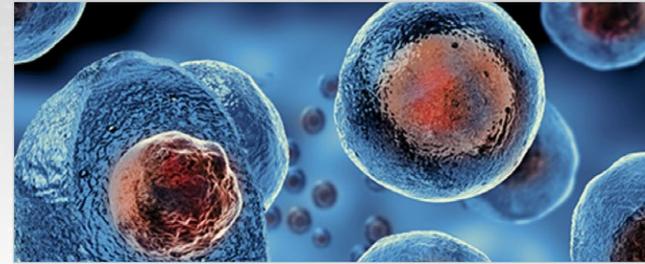
Jesper Olsen

*University of Copenhagen*

View webinar



## Single-Cell Proteomics for the Exploration of Cell Heterogeneity

Erwin Schoof

*Technical University of Denmark*
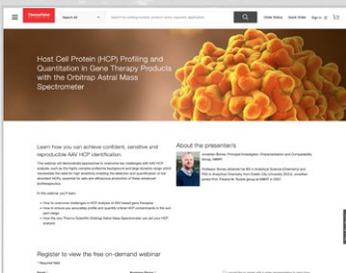
View webinar



## How Mass Spectrometry Innovation Propels Biological Discovery
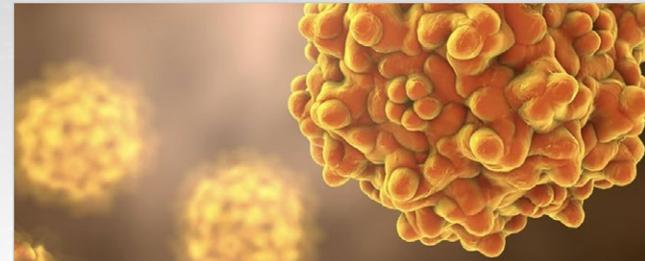
Joshua Coon

*University of Wisconsin Madison*

View webinar



## Host Cell Protein (HCP) Profiling and Quantitation in Gene Therapy Products with the Orbitrap Astral Mass Spectrometer

Jonathan Bones

*NIBRT*

View webinar

# Posters

## Proteomics

### DIA

Single-Shot LC-MS Workflow for Comprehensive Proteome Identification on an Orbitrap Astral Mass Spectrometer

View poster

Accurate and Precise Label-Free Quantification with Comprehensive Proteome Coverage Using a Novel HRAM Platform

View poster

Fast Multi-Shot Acquisition of Comprehensive Proteomes by DIA Using Narrow Isolation Windows on a Novel High-Resolution Accurate Mass LC/MS Platform

View poster

A Novel Ion Processor Device for High Throughput Analysis in a High Resolution Mass Analyzer

View poster

A Benchmarking Workflow for High Throughput DIA Label Free Quantification Using a Novel High Resolution Accurate Mass Platform

View poster

Unveiling the Performance of a Novel High Resolution Accurate Mass Platform for Proteomics Applications

View poster

High Throughput Proteomics on a Novel High Resolution Accurate Mass (HRAM) Platform

View poster

Unlocking the Potential of large Cohort Proteomics Studies with a Novel High Resolution Accurate Mass Platform

View poster

### Peptide ID

Unveiling the Performance of a Novel High Resolution Accurate Mass Platform for Proteomics Applications

View poster

### Single-cell proteomics

Enhancing Single-Cell Proteome Coverage with a Novel High-Resolution Accurate Mass Platform

View poster

Evaluation of a Novel High-Resolution Accurate Mass Platform for its Application on Acute Myeloid Leukemia Heterogeneity at Single Cell Resolution

View poster

### TMT

A Novel Ion Processor Device for High Throughput Analysis in a High Resolution Mass Analyzer

View poster

# Posters <span>(continued)</span>

## Structural biology
### XL-MS

High-Throughput XL-MS Analysis on a
New High-Resolution Accurate Mass Platform

View poster

## Metabolomics
### SQUAD

Simultaneous Quantitation and Discovery (SQUAD)
Metabolomics: An Intelligent Combination pf
Targeted and Untargeted Workflows Using the
Novel Orbitrap Astral Mass Spectrometer

View poster

### Untargeted Metabolomics

Advantages of a Novel High Resolution Accurate
Mass Analyzer for Metabolite Identification in
Untargeted Metabolomics Studies

View poster

## Technology

Characterization of a Detection System with High
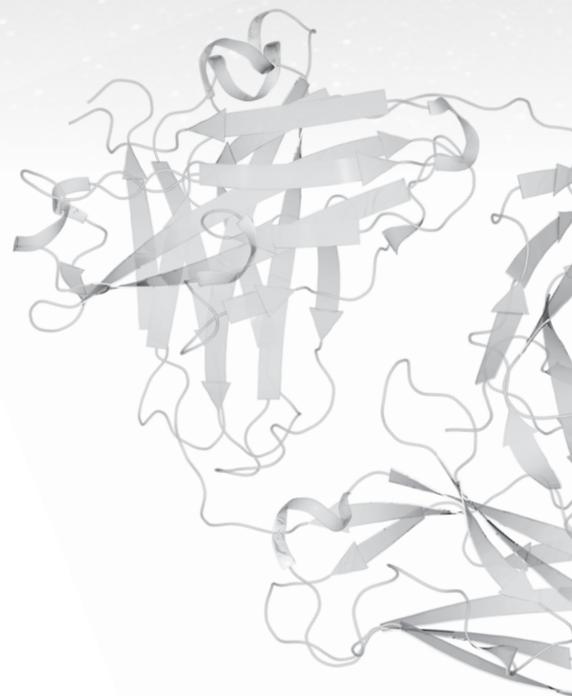Sensitivity and Dynamic Range for a Novel HRAM
Mass Spectrometers

View poster

A Novel Ion Processor Device for High Throughput
Analysis in a High Resolution Mass Analyzer

View poster

Theory and Performance of a Novel High
Resolution Mass Analyzer

View poster

# Presentations

## Proteomics
### DIA

**Rapid Single Shot Proteomics Using Narrow Window DIA on a Novel High Resolution Accurate Mass (HRAM) Platform**

View presentation

**Rapid Analysis of Protein-Protein Interactions Using a Novel High-Resolution Accurate Mass Platforms**

View presentation

**Pushing the Boundaries Of Quantitative Proteomics with Data Independent Acquisition Using a Novel High-Resolution Accurate Mass Analyzer**

View presentation

**New High-Resolution Accurate Mass (HRAM) platform Enables Rapid And Deep Mouse And Human Phosphoproteomics**

View presentation

**One-Minute Proteome Analysis Using a Novel High-Resolution Accurate Mass Platform**

View presentation

**Mag-Net Combined with the Orbitrap Astral MS Enables Measurements for >4,500 Proteins in Plasma**

View presentation

### Phosphoproteomics

**New High-Resolution Accurate Mass (HRAM) Platform Enables Rapid and Deep Mouse and Human Phosphoproteomics**

View presentation

### Single-cell proteomics

**Sensitive and Robust High Throughput Workflow for Qualitative and Quantitative Single-Cell/Single Cell Like Analysis**

View presentation

### TMT

**Evaluation of the Relative Quantitative Performance Using Tandem Mass Tags on a New High Resolution Accurate Mass Platform**

View presentation

**High Throughput Multiplexed Chemoproteomics in 96 Well Plates on a High Resolution Accurate Mass Platform with a New Mass Analyzer**

View presentation

**Multiplexed Proteomics with Next Generation Instrumentation**

View presentation

**The Next Era of Multiplexed Proteomics**

View poster

## Metabolomics
### SQUAD

**Simultaneous Quantitation and Discovery (SQUAD) Metabolomics: an Intelligent Combination of Targeted and Untargeted Workflows**

View presentation

**Metabolomics SQUAD Goals: Orbitrap Workflows to Empower Your Research**
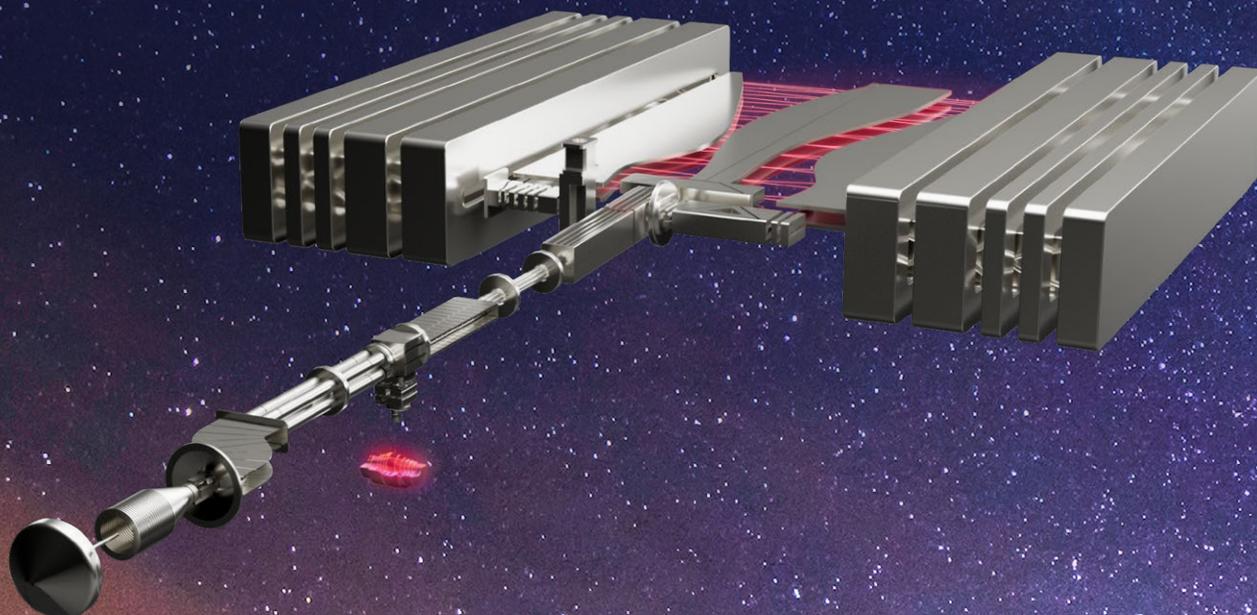
View presentation

## Technology

**Pushing Frontiers Of High-Throughput High-Resolution Analysis: Orbitrap Technology Unites with a New Star**

View presentation

# Rethink what is possible
## with novel technology

## Next generation end-to-end workflows, sample to knowledge solutions

**Thermo Scientific™ AccelerOme™ automated sample preparation platform**

Easy to use, reproducible sample preparation

**Thermo Scientific™ Vanquish™ Neo UHPLC system**

Flexible, high performance from nano- to capillary flow rates

**Thermo Scientific™ µPAC™ Neo HPLC columns**

Excellent performance and reproducibility with a long lifetime

**Thermo Scientific™ FAIMS Pro Duo interface**

Reduces matrix inferences, increases workflow robustness

**Thermo Scientific™ Orbitrap™ Astral™ mass spectrometer**

Redefines MS-based proteomics analyses

**Thermo Scientific™ Proteome Discoverer™ software powered by Thermo Scientific™ Ardia™ Platform**

Central data storage, automated data processing, tools for instrument, data and user management

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