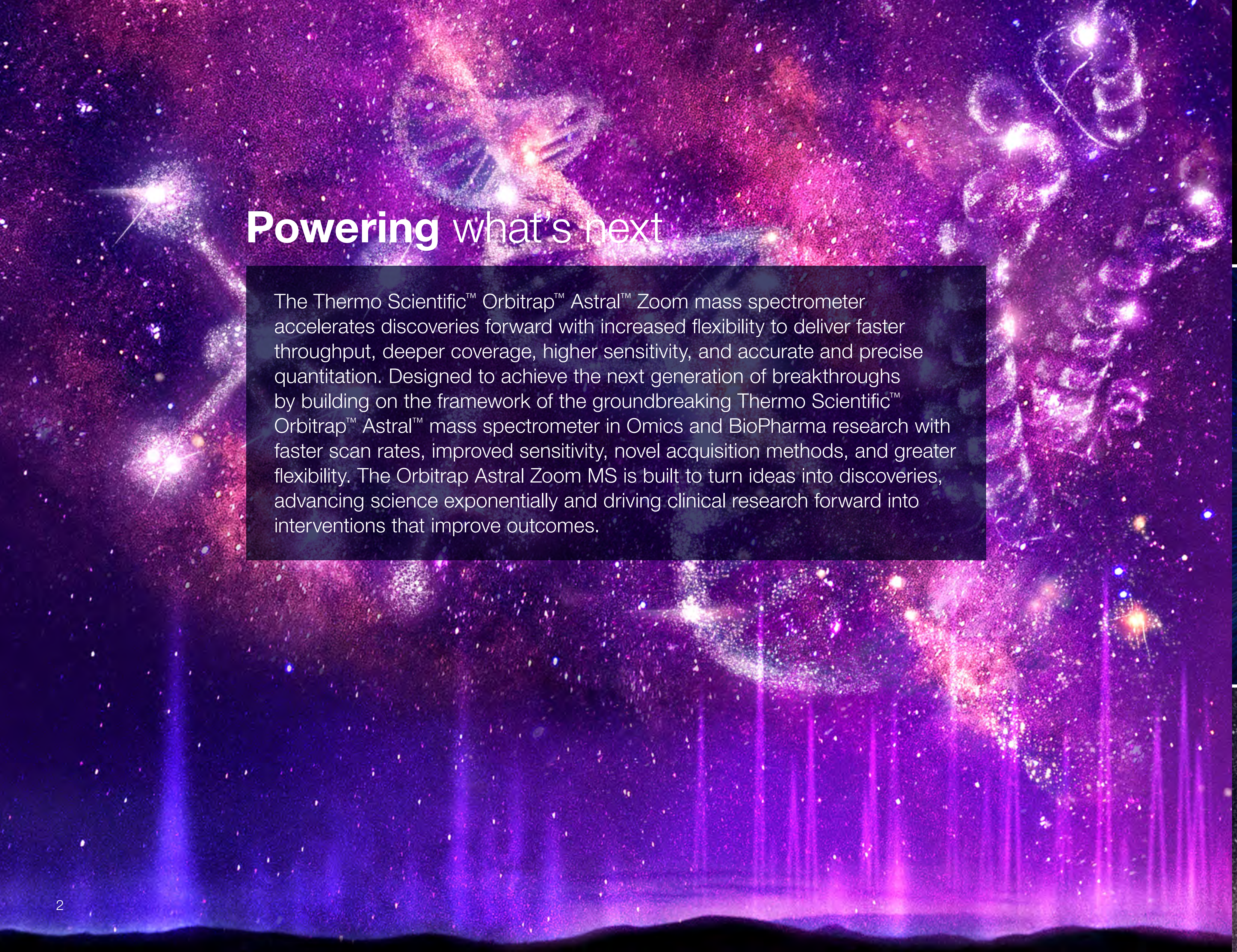
Mass spectrometry

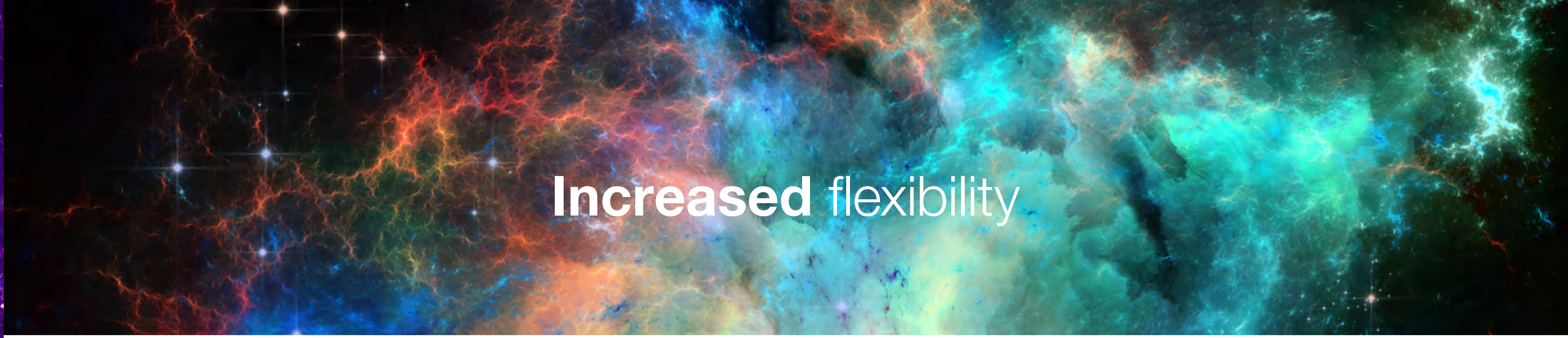
Realize a universe of possibilities

Orbitrap Astral Zoom Mass Spectrometer

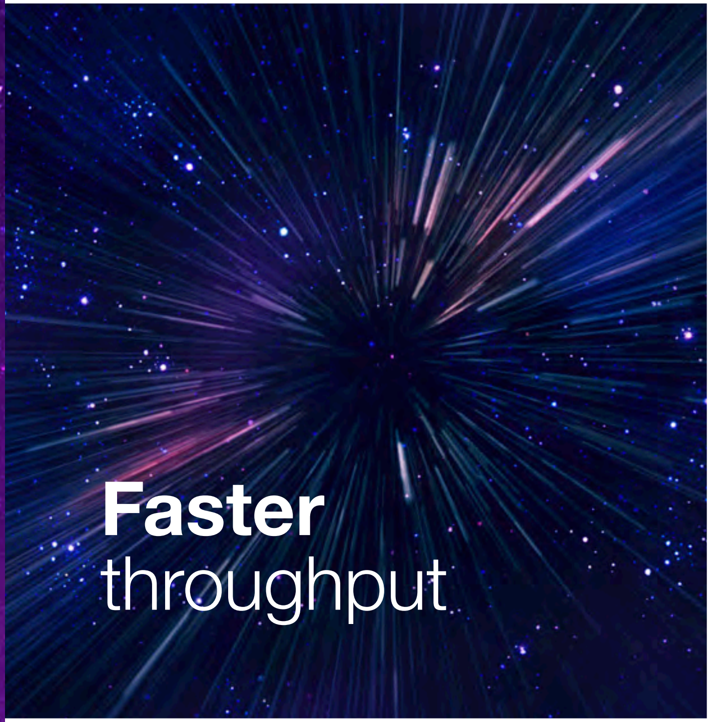


Powering what's next

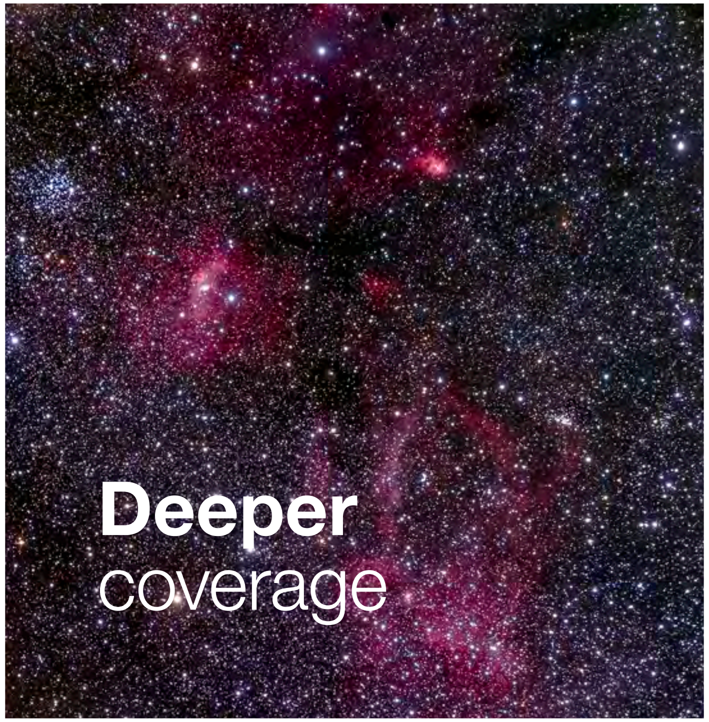
The Thermo Scientific™ Orbitrap™ Astral™ Zoom mass spectrometer accelerates discoveries forward with increased flexibility to deliver faster throughput, deeper coverage, higher sensitivity, and accurate and precise quantitation. Designed to achieve the next generation of breakthroughs by building on the framework of the groundbreaking Thermo Scientific™ Orbitrap™ Astral™ mass spectrometer in Omics and BioPharma research with faster scan rates, improved sensitivity, novel acquisition methods, and greater flexibility. The Orbitrap Astral Zoom MS is built to turn ideas into discoveries, advancing science exponentially and driving clinical research forward into interventions that improve outcomes.



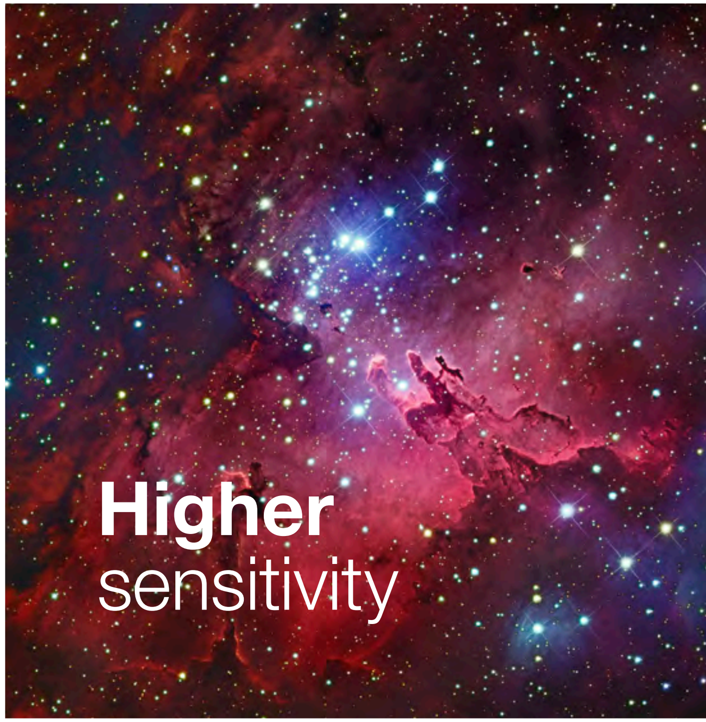
Increased flexibility



Faster throughput



Deeper coverage



Higher sensitivity

Accurate and precise quantitation

Synchronized synergy

The Orbitrap Astral Zoom MS contains three mass analyzers: a quadrupole mass analyzer for ion isolation, a Thermo Scientific™ Orbitrap™ analyzer to acquire high dynamic range, high resolution accurate mass (HRAM) spectra, and a Thermo Scientific™ Astral™ analyzer to acquire high sensitivity, high dynamic range HRAM spectra at rates up to 270 Hz. The Orbitrap and Astral analyzers are operated in parallel, enabling the simultaneous acquisition of high-quality HRAM data in each analyzer. Due to this synchronized data acquisition, the Orbitrap Astral Zoom MS excels at multiple experiment types including narrow-window data-independent acquisition (nDIA), data-dependent acquisition (DDA), simultaneous quantitation and discovery (SQUAD), Hybrid DIA, and parallel reaction monitoring (PRM).

Upgraded instrument architecture

The Orbitrap Astral Zoom MS delivers new hardware and software features designed to achieve the next generation of breakthroughs.

- The fast ion filter and bent trap combine to enable the pre-accumulation of ions, increasing duty cycle and ion utilization
- The high-speed quadrupole, improved ion routing multipole, and faster ion processor combined with the pre-accumulation empower an increased scan speed of up to 270 Hz
- The enhanced dynamic range (eDR) mode provides panoramic full scan data with the Orbitrap analyzer
- The Astral analyzer features a relay prism for a multi-lap asymmetric track ion path, enabling measurements with a resolution of at least 100,000 at *m/z* 138 that resolve the quadruplet of Thermo Scientific™ TMTpro™ reporter ions, empowering workflows with multiplexing of up to 35 samples in a single injection
- The Astral analyzer high dynamic range detector has been upgraded with a low-input mode to improve sensitivity by increasing the probability of single ion detection by 10%
- Increased duty cycle to enable higher performance at even higher throughput of 300 samples in a single day
- Increased depth of coverage to measure over 10,000 proteins groups and 200,000 unique peptides from a single shot
- Increased quantitative dynamic range with support for both label-free quantitation (LFQ) and multiplexing with TMTpro label reagents
- Improved ion routing multipole hardware enables faster stepped collision energy experiments at rates in excess of 200 Hz
- Added flexibility to enhance performance and enable more applications

Low-input mode
Increased detector sensitivity

Faster stepped collision energy
Fragmentation of precursors with up to 3 energies at speeds over 150 Hz

Relay prism
Extended asymmetric track for higher resolution to increase throughput by multiplexing up to 35 samples with TMTpro label reagents

High-speed quadrupole
Faster settling time to increase scan rate

Faster ion processor
Increased ion transfer speed, enabling operation at 270 Hz

Bent trap
AGC controlled pre-accumulation to increase duty cycle and remove neutrals

Ultra-high-field Orbitrap analyzer with enhanced dynamic range (eDR) mode
Multiplexed injection to increase dynamic range

Fast ion filter
Pre-filtering of ions

Upgraded Astral analyzer

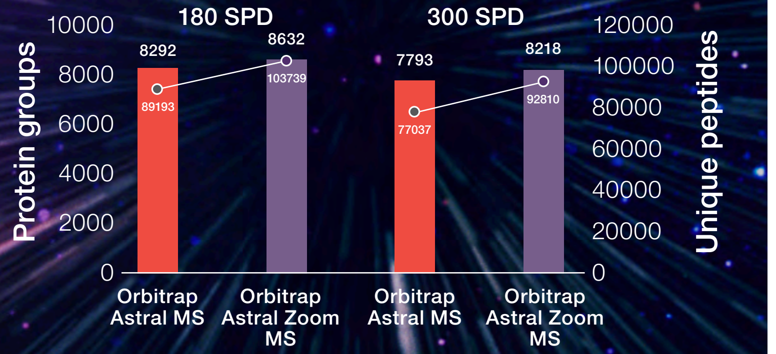
Improved architecture to enable improved performance

- Increased scan rates of up to 270 Hz
- Increased resolution with TMT HR mode to support multiplexing up to 35 samples with TMTpro label reagents
- Increased sensitivity with low-input mode to increase single ion detection
- Enhanced spectral processing to improve data quality and peak resolution
- Available Biopharma option to enable top-down and middle-down Astral analyzer MS^2 experiments along with an extended Orbitrap analyzer mass range of 40-8,000 and improved pressure regulation

Faster throughput

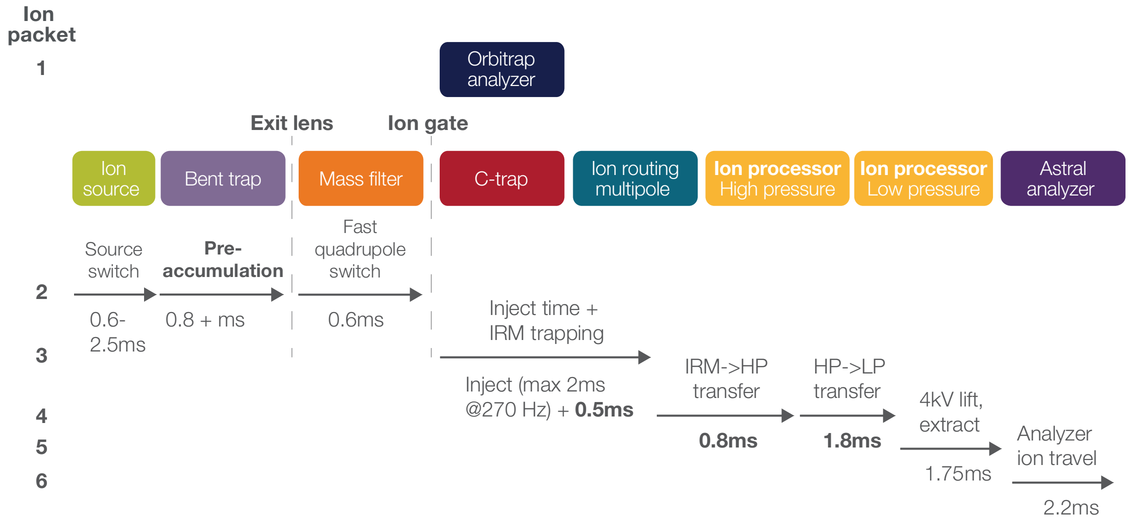
Throughput remains a significant requirement for large cohort studies that seek to analyze thousands of samples. Now the Orbitrap Astral Zoom mass spectrometer unlocks the next level of throughput with the ability to analyze 300 samples per day (SPD), meaning the analysis time is just 4.8 minutes from sample injection to sample injection. Now experiments can be performed at a pace to advance past the throughput bottleneck.

Analyze 300 samples in a single day at a depth of over 8,000 proteins per sample

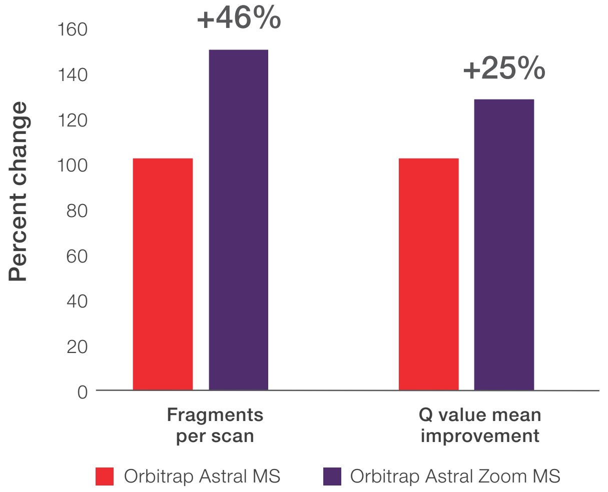


The Orbitrap Astral Zoom mass spectrometer identifies over 8,200 protein groups from 200 ng of Thermo Scientific™ Pierce™ HeLa digest standard using a 4.8-minute long method (injection-to-injection) on a Thermo Scientific™ Vanquish™ Neo UHPLC system (operated in a trap and elute mode) and a Thermo Scientific™ EASY-Spray™ PepMap™ 15 cm × 150 µm HPLC column. The Orbitrap Astral Zoom mass spectrometer was operated with 240,000 FWHM full MS in the Orbitrap analyzer and nDIA using quadrupole isolation window widths of 2 Th with the Astral analyzer for MS^2. Data was processed with the CHIMERYS™ intelligent search algorithm using Thermo Scientific™ Proteome Discoverer™ 3.3 software and filtered to <1% FDR.

Upgraded instrument architecture to enable additional parallelization and scan rates up to 270 Hz



Faster throughput with higher data quality



Platform	Fragments per ID
Orbitrap Astral MS	6.5
Orbitrap Astral Zoom MS	7.3

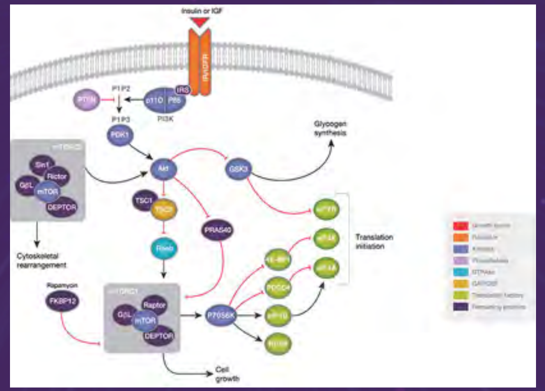
- The increased scan rate of up to 270 Hz with the Orbitrap Astral Zoom mass spectrometer empowers the acquisition of 35% more MS^2 spectra per second when compared to the Orbitrap Astral mass spectrometer, increasing the number of data points per peak for improved quantitative accuracy and precision even with the shortest gradients.
- Through improved ion utilization with pre-accumulation in the bent trap, even with these increased scan rates the Orbitrap Astral Zoom mass spectrometer generates high quality data with a 46% increase in the number of fragments per MS^2 scan, a 25% improvement in mean Q Value, and an increased number of fragments per identification. More confidently analyze the most challenging samples at higher throughputs with higher data quality by identifying more fragment ions.

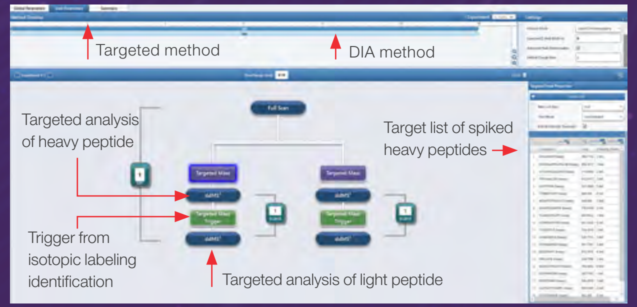
Translational research **at scale**

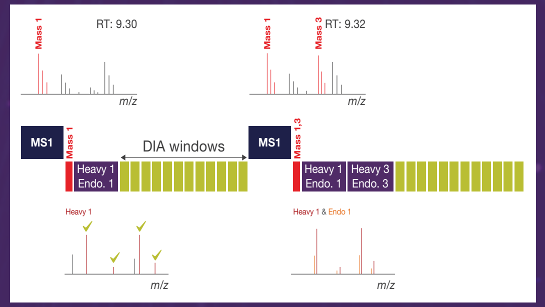
The Orbitrap Astral Zoom mass spectrometer delivers significant performance improvements to further enable large-scale studies. Researchers can analyze thousands of samples with a single instrument in just months with the increased sample throughput. Importantly, this increase in throughput is accompanied by robust and reproducible data generation that delivers high quantitative accuracy and precision, ensuring consistent performance and improved statistical power to provide confident results. The Orbitrap Astral Zoom mass spectrometer enables the measurement of both known and unknown biomarkers through deep and unbiased sample analysis, including the measurement of post-translational modifications. The implementation of Hybrid DIA experiments combine targeted quantitation and untargeted discovery into a single injection, increasing data completeness and sensitivity for biomarkers of interest while maintaining deep unbiased proteome coverage.

ⓘ Hybrid DIA

Hybrid DIA enables the acquisition of untargeted DIA and targeted quantitative data in a single injection with intelligent triggers to maximize instrument utilization. This enables the optimization of methods that can bridge the gap between discovery and targeted workflows, reducing missing values and ensuring robust quantitative measurements of biomarkers of interest while simultaneously collecting unbiased data. Utilize pre-built Thermo Scientific™ SureQuant™ kits covering biomarkers of interest such as the AKT Pathway or customize.







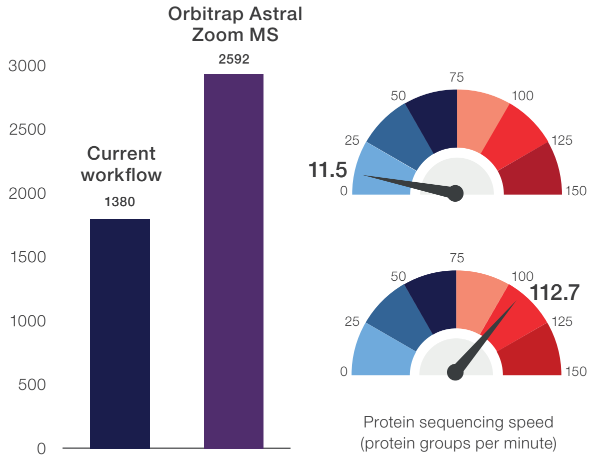
Yu-Ju Chen, Ph.D.

Distinguished research fellow at the Institute of Chemistry, Academica Sinica, Taiwan

> “With the super-fast scanning speed of the Orbitrap Astral Zoom mass spectrometer we are able to shorten the analysis time for 6,000 patient research samples from 1,000 days to 100 days.”

Comparison of total number of protein groups and protein sequencing speed (proteins identified per minute) from depleted plasma patient research samples by the Orbitrap Astral Zoom MS and current MS. The Orbitrap Astral Zoom MS identifies more total protein groups at nearly 10x the number of protein groups per minute, highlighting the efficiency, scalability, and increase in plasma proteome depth of coverage needed for clinical cohorts. Data courtesy of Yu-Ju Chen, Academica Sinica.

Proteins identified



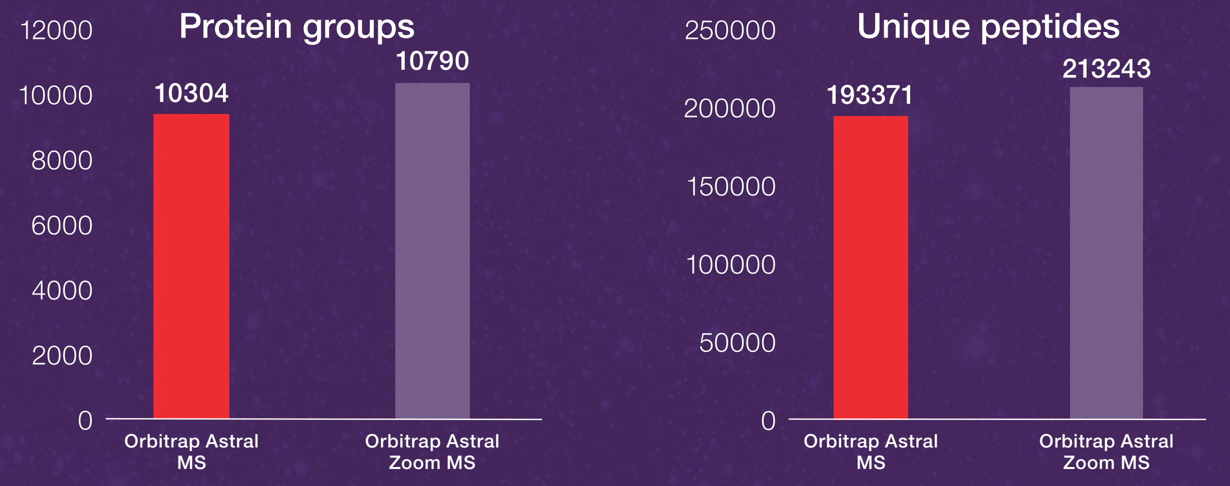
Deeper coverage

The Orbitrap Astral Zoom MS features increased scan rates of up to 270 Hz and pre-accumulation to boost sensitivity and depth of coverage, uncovering more proteins and peptides. The added depth provides more comprehensive protein sequence coverage and expanded pathway annotation to unlock additional biological insight.

Jesper Olson, Ph.D.

Deputy Center Director, Professor, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen

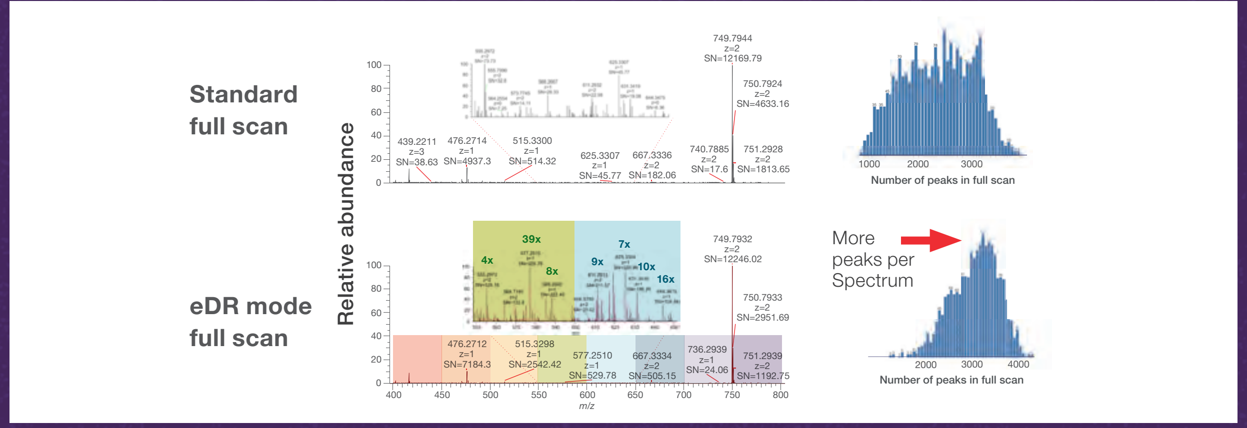
> "The Orbitrap Astral MS has been a huge step forward in performance for us, but the data we have generated with the Orbitrap Astral Zoom MS is even more exciting – we can now routinely do 300 human proteomes per day. This allows us to do very systematic, systems biology type studies, where we get sufficient coverage of close to eight thousand proteins and more than 100,000 peptides across all the samples."



Orbitrap Astral MS and Orbitrap Astral Zoom MS analysis of 500 ng Pierce HeLa digest with a throughput of 30 SPD. The Orbitrap Astral Zoom MS increases the depth of protein and peptide coverage compared to Orbitrap Astral MS. This additional depth enables further insights into biological processes, for example Zinc finger domain proteins are significantly enriched and have been shown to regulate key cellular functions using chemoproteomics approaches.[1]

ⓘ Enhanced Dynamic Range (eDR) mode

Uncover more analytes with eDR mode panoramic full scan spectra. Detect more compounds from Orbitrap analyzer full scans using eDR mode and pair with data-dependent acquisition (DDA) methods to increase the number of precursors available for MS^2 fragmentation by the Astral analyzer.

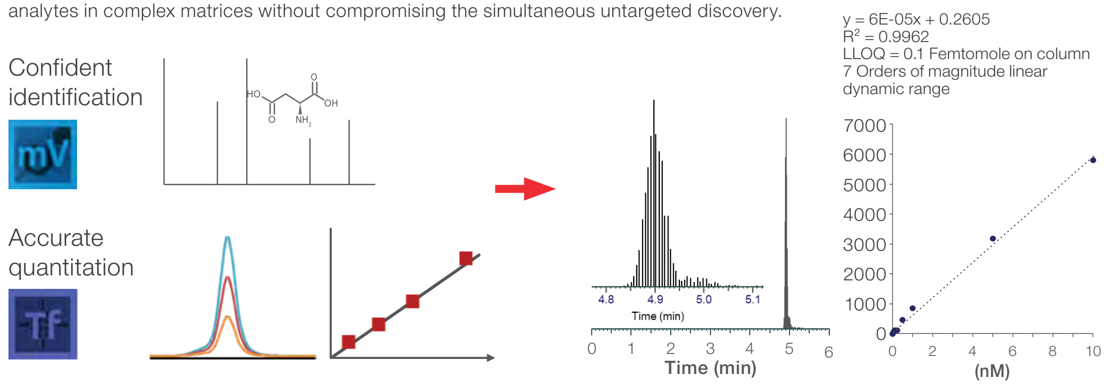


A new paradigm for small molecule analysis

Simultaneous Quantitation and Discovery (SQUAD) analysis seamlessly combines discovery and targeted workflows into a single experiment, optimizing the information generated from each injection. The Orbitrap Astral Zoom mass spectrometer synchronizes the acquisition of untargeted full scan Orbitrap analyzer and data-dependent MS^2 Astral analyzer scans along with targeted MS^2 Astral analyzer scans in a single injection.

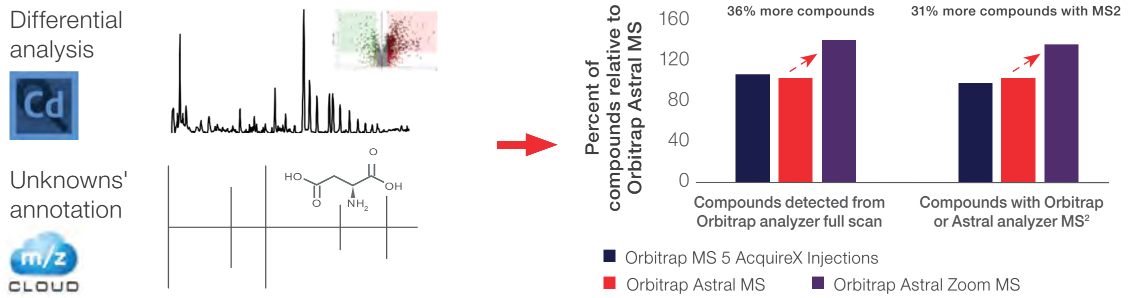
Targeted analysis

Targeted analysis of phenylalanine using a SQUAD workflow using NIST SRM 1950 plasma enables a lower limit of quantitation of 0.1 femtomole on column, illustrating the exceptional sensitivity of the Orbitrap Astral Zoom mass spectrometer to quantify analytes in complex matrices without compromising the simultaneous untargeted discovery.



Untargeted analysis

Untargeted SQUAD workflow analysis of NIST SRM 1950 plasma reveals more compounds detected from full scan data and more compounds with MS^2 fragmentation data using the Orbitrap Astral Zoom mass spectrometer, extending the depth of compound detection and improving compound annotation capabilities.



Jonathan Martin, Ph.D.

Professor, Stockholm University, Scientific Director of the National Facility for Exposomics, SciLifeLab.

> "In exposomics we need dynamic instruments that can support combined targeted and untargeted data acquisition while simultaneously pushing the boundaries of sensitivity, resolution and MS2 coverage. The Orbitrap Astral Zoom mass spectrometer looks like it was designed with chemical exposomics in mind and should significantly boost research efforts to discover low abundance toxic substances in complex samples such as human blood, drinking water and air."

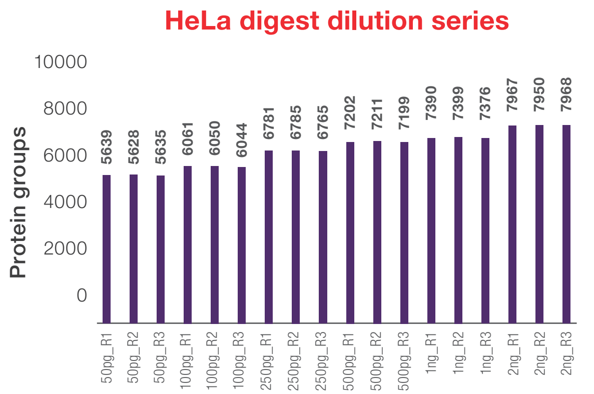
Higher sensitivity

The Orbitrap Astral Zoom MS provides higher sensitivity, faster throughput, and increased reproducibility with the Astral analyzer enhancements of low-input mode and TMT HR mode. Low-input mode extends the performance for sparse samples, including the identification of over 6,500 proteins from 250 pg HeLa digest or over 5,800 proteins on average from HEK293F single cells using LFQ DIA acquisition. With high resolution Orbitrap analyzer full scan acquisition and increased Astral analyzer MS^2 resolution, either MS^1 or MS^2 based multiplexing strategies can be leveraged to substantially increase throughput to thousands of single-cells per day.

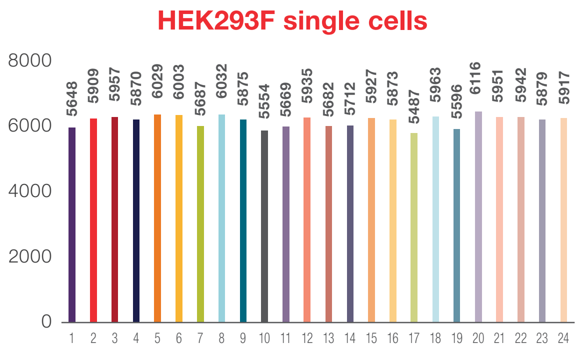
Erwin Schoof, Ph.D.

Associate Professor, Department of Biotechnology and Biomedicine, Section for Protein Science and Biotherapeutics, Cell Diversity Lab, Technical University of Denmark

> "The Orbitrap Astral Zoom MS improves the performance for single-cell proteomics by increasing the depth of coverage for DIA experiments but also by enabling very high throughput experiments through multiplexing with TMTpro to analyze over 2,000 single cells per day."



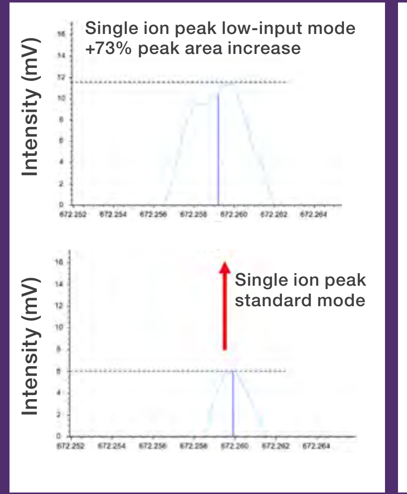
Orbitrap Astral Zoom mass spectrometer performance for a dilution series from 2 ng to 50 pg of HeLa digest run at 50 SPD. Excellent reproducibility with median protein CV values of 6% and data completeness is observed with over 6,500 proteins identified from 250 pg of HeLa digest. Samples were run on a Vanquish Neo UHPLC (in direct injection mode) using a 50 SPD method including a Thermo Scientific™ FAIMS Pro Duo interface and data analysis was performed using Spectronaut™ 19 software using a directDIA™ workflow.



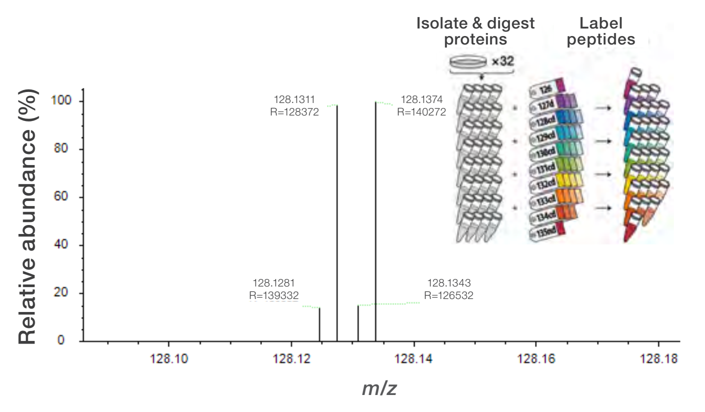
Analysis of HEK293F single cells using LFQ DIA with the Orbitrap Astral Zoom mass spectrometer enables identification of an average of 5,800 proteins across 24 single cells using a 50 samples per day method. Isolated and digested HEK293F single cells were run on a Vanquish Neo UHPLC system (in direct injection mode) using a 50 SPD method including a FAIMS Pro Duo interface and data analysis was performed using Spectronaut 19 software using a directDIA workflow.

Technology spotlight

Higher sensitivity and resolution for high throughput single-cell multiomics



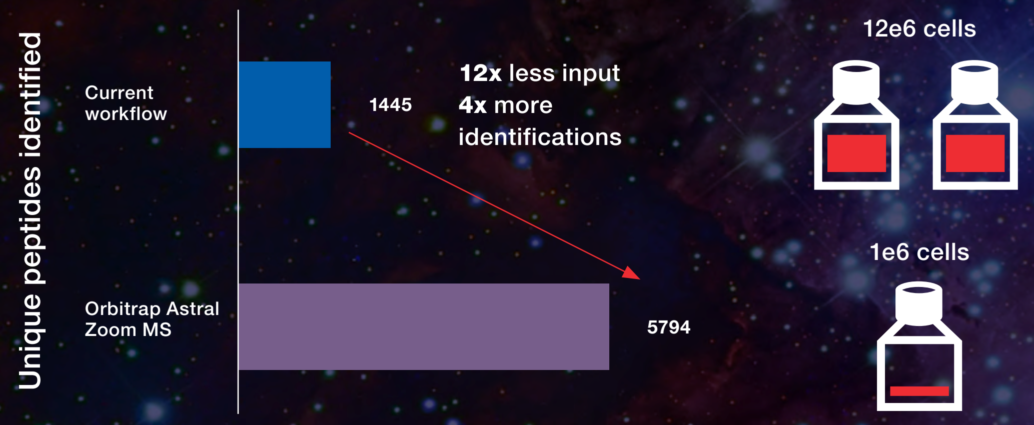
Confidently analyze samples with ultimate sensitivity using low-input mode to increase the signal generated by the Astral analyzer HDR detector, increasing the detection probability for single ions by 10%.



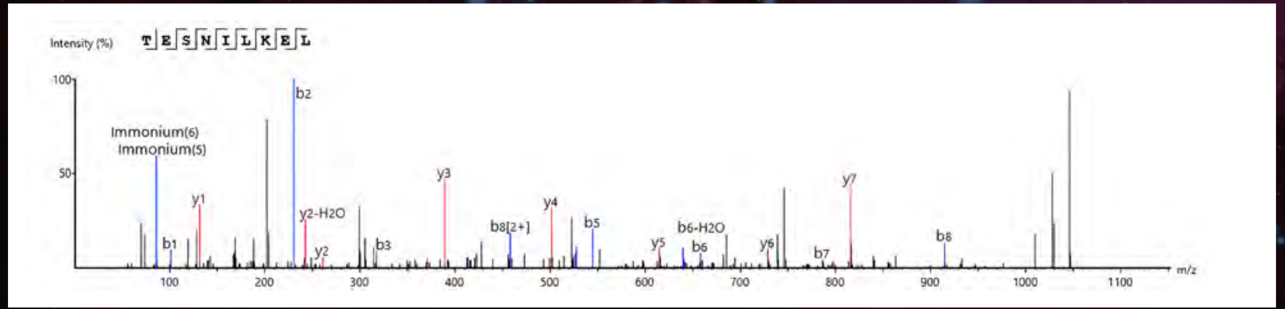
Addition of the relay prism to the Astral analyzer enables an extended asymmetric track length and resolution of 100,000 at *m/z* 138. This increased resolution of TMT HR mode provides support for higher multiplexing with TMTpro labeling reagents, enabling high throughput single-cell proteomics experiments that measure thousands single-cells per day.

Immunopeptidomics spotlight

The Orbitrap Astral Zoom mass spectrometer enables the confident and comprehensive analysis of immunopeptides for sample inputs across the dynamic range from bulk cellular extracts to low input biopsy samples. The parallelized acquisition of high-resolution accurate mass full MS precursor data with the Orbitrap analyzer and fast and sensitive full spectrum MS^2 data for peptide sequencing using the Astral analyzer delivers confident results for both DDA and DIA based immunopeptidomics workflows.



Analysis of immunopeptides prepared from THP1 cells comparing performance of current workflow and Orbitrap Astral Zoom MS. With a 12x lower input of just 1 million cells the Orbitrap Astral Zoom MS identifies over 5200 unique peptides, an increase of 1.8x. Orbitrap Astral Zoom mass spectrometer data was acquired using a Vanquish Neo UHPLC system along with a FAIMS Pro Duo interface. Data courtesy of Greg Potts, AbbVie.



The Orbitrap Astral Zoom mass spectrometer collects full spectrum MS^2 data with high resolution and accurate mass measurements starting at *m/z* 40 in the Astral analyzer, providing comprehensive fragmentation coverage of immunopeptides to increase identification confidence. For example, the experimental spectrum for TESNILKEL provides full ion series coverage to identify this immunopeptide, which is a predicted binder to multiple HLA alleles.

Greg Potts, Ph.D.

Principal Research Scientist, AbbVie

> "The Orbitrap Astral Zoom mass spectrometer improves throughput, identification depth, and sensitivity to comprehensively profile immunopeptidomics samples, facilitating analyses from 10-100 times fewer cells per experiment. This advancement not only enables the investigation of more biologically relevant precious samples, but also allows for testing more experimental conditions per study to open up new opportunities for profiling drug-induced perturbations to the immunopeptidome.

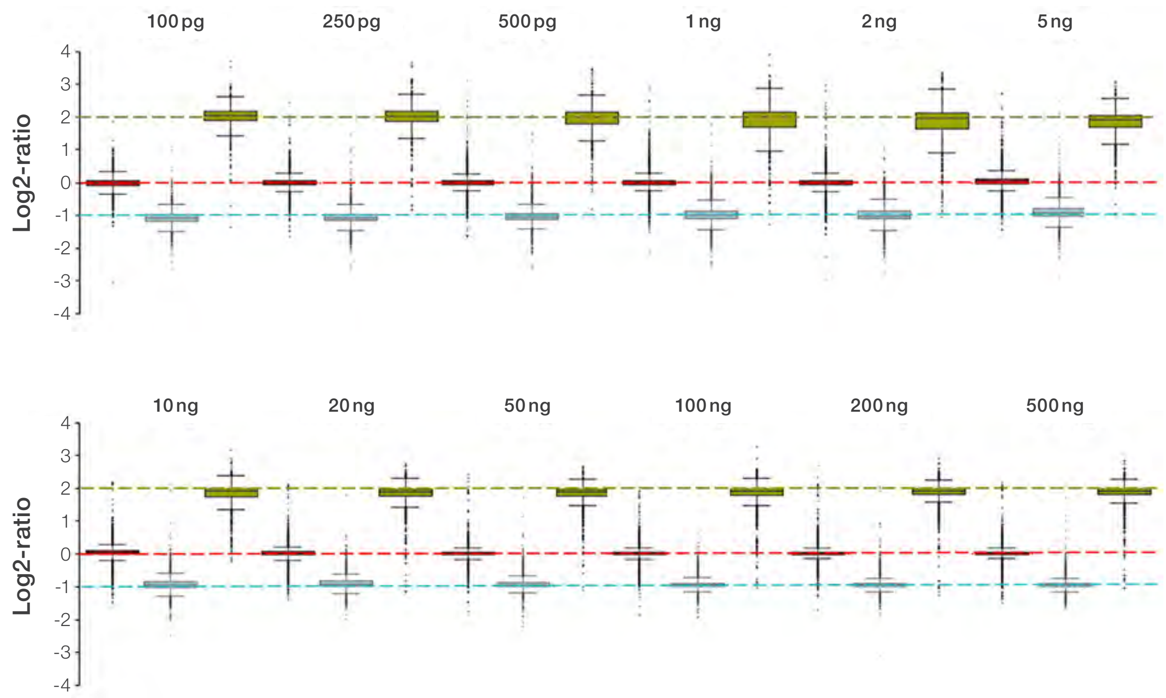
Accurate and precise quantitation

Mike MacCoss, Ph.D.

Professor, Department of Genome Sciences, University of Washington

> "We see a significant increase of up to 50% more ions measured with the Orbitrap Astral Zoom mass spectrometer due to the faster scan rate and pre-accumulation. This improves the quantitative accuracy and precision for complex plasma proteomics samples, particularly for low abundance proteins and large fold changes."

Accurate and precise quantitation is essential to determine statistical significance for changes in biological samples. The Orbitrap Astral Zoom mass spectrometer provides accurate and precise quantitation using label-free quantitation with high-resolution-data-independent acquisition (LFQ HR-DIA) for sample inputs from picograms to nanograms, enabling high quantitative performance across the entire dynamic range of samples.



Analysis of quantitative accuracy and precision across a large dynamic range of input loads using three proteome mixtures of *E. coli*, Yeast, and Human. Mix A comprised 65:15:20 Human:Yeast:E. coli and Mix B comprised 65:30:5 Human:Yeast:E. coli, with total sum protein digest amount mixed between 100 pg and 500 ng. Across all loads accurate and precise ratios are measured for each of the three species proteomes, demonstrating excellent quantitative performance across a wide dynamic range of input loads. Data was acquired using a Vanquish Neo UHPLC system (operated with direct injection mode) at a throughput of 50 samples per day with the Orbitrap Astral Zoom mass spectrometer.

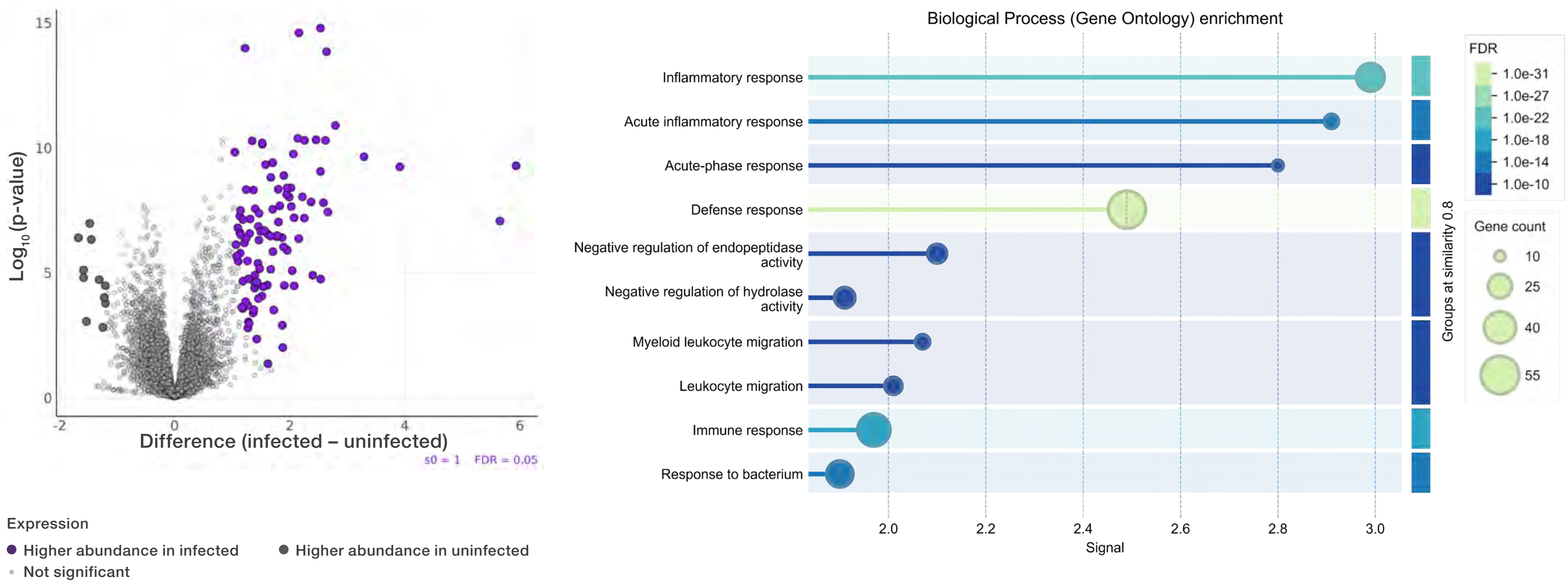
Jennifer Geddes-McAlister, Ph.D.

Canada Research Chair, Associate Professor, University of Guelph

> "The increased dynamic range of the Orbitrap Astral Zoom MS provides us with improved depth of coverage for low abundant fungal peptides during an infection. These peptides provide new biological insights into mechanisms driving fungal virulence and antifungal resistance."

Increased quantitative dynamic range to uncover novel biological insights

Studying high dynamic range samples, such as plasma or tissues, requires instrumentation that can measure both high and low abundance proteins with high quantitative accuracy and precision. The faster acquisition rate of up to 270 Hz and improved sensitivity from pre-accumulation endow the Orbitrap Astral Zoom mass spectrometer with a larger quantitative dynamic range, enabling the study of very low abundance proteins and peptides in complex matrices.

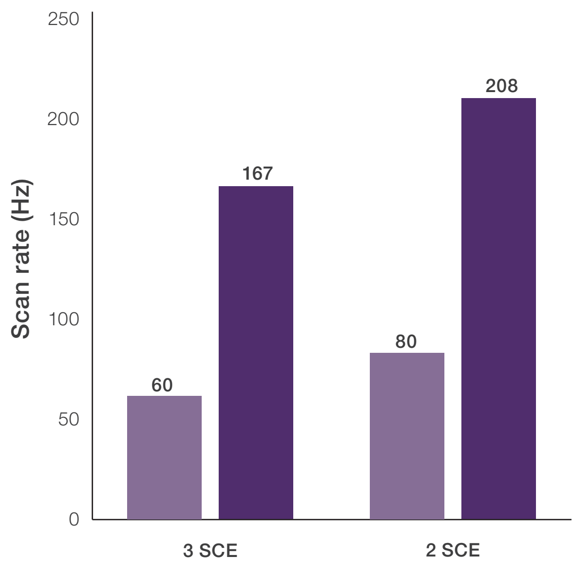


The analysis of mouse spleen samples from *Cryptococcus neoformans* infected and uninfected animals using the Orbitrap Astral Zoom mass spectrometer reveals significantly changing proteins with specific Gene Ontology enrichments for host immune responses. Data was acquired by loading 500 ng of sample input using a Vanquish Neo UHPLC system with separation on a Thermo Scientific™ EASY-Spray™ PepMap™ Neo 75 µm x 500 mm UHPLC column using a 54-minute gradient (24 SPD) and acquiring HR-nDIA data with the Orbitrap Astral Zoom mass spectrometer. Data courtesy of Jennifer Geddes-McAlister, University of Guelph.

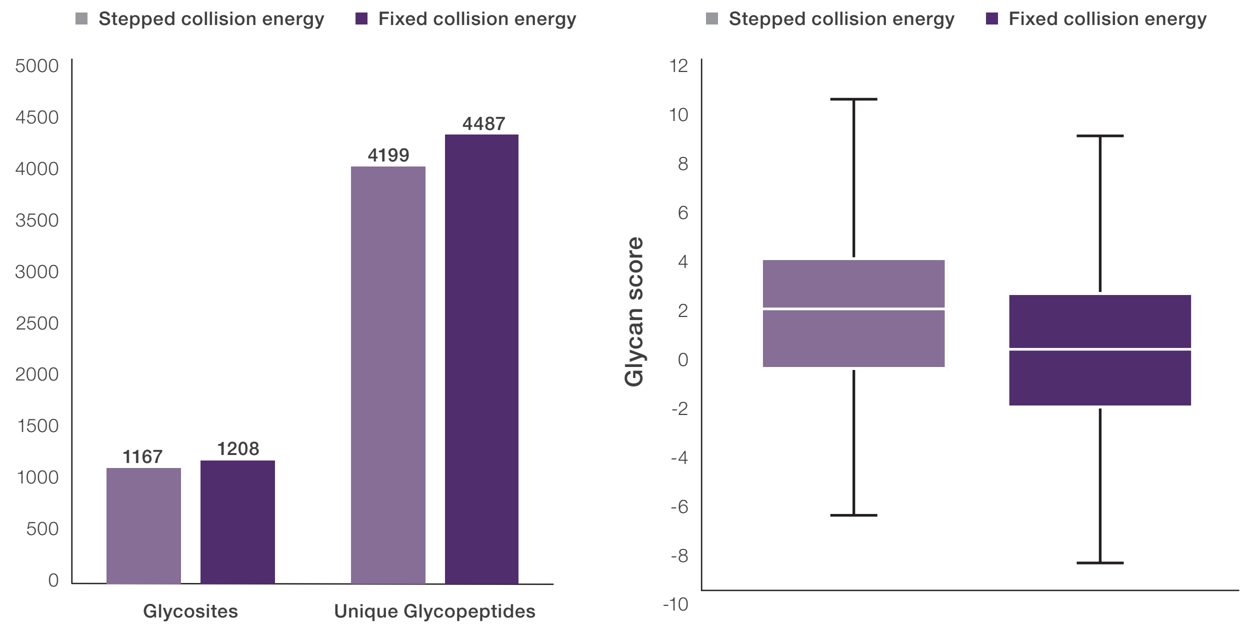
Increased flexibility

With additional capabilities including faster stepped collision energy and the BioPharma option, the Orbitrap Astral Zoom mass spectrometer facilitates higher performance for a larger set of applications.

Stepped collision energy scan rate as a function of injection time



The upgraded ion routing multipole on the Orbitrap Astral Zoom mass spectrometer provides faster stepped collision energy capabilities with scan rates of 208 Hz and 167 Hz for 2 and 3 stepped collision energy experiments, respectively. Stepped collision energy experiments can provide richer fragmentation spectra on the Orbitrap Astral Zoom mass spectrometer at more than double the speed relative to the Orbitrap Astral mass spectrometer.



Analysis of mouse brain enriched for N-glycopeptides using SAX-ERLIC with either stepped normalized collision energies of 25 and 35 or a fixed normalized collision energy of 35 using the Orbitrap Astral Zoom mass spectrometer operated in DDA mode. While stepped and fixed collision energy methods identify a similar number of glycosites and unique glycopeptides, the stepped collision energy method provides a higher median glycan score of 1.76 compared to the fixed energy median glycan score of 0.23, providing increased identification confidence. Data courtesy of Joshua Coon, University of Wisconsin – Madison.

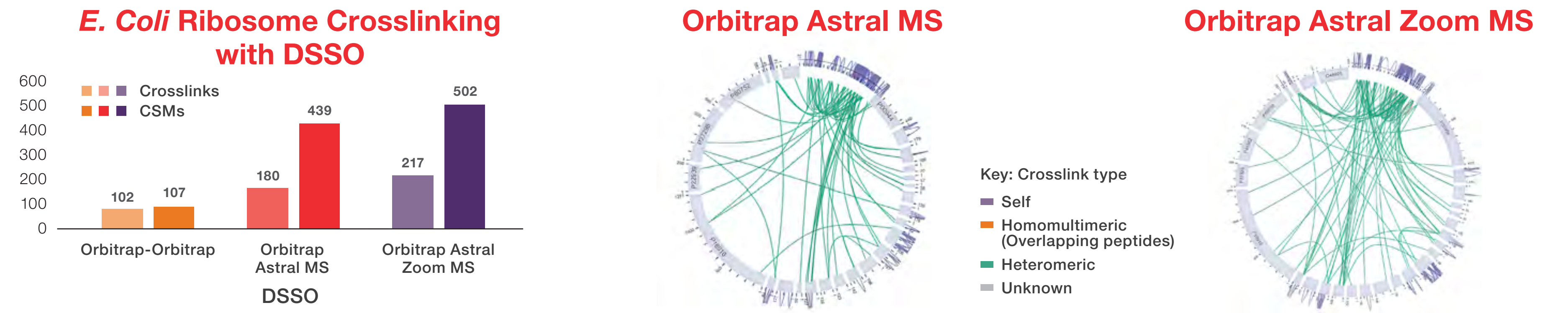
Joshua Coon, Ph.D.

Professor, Biomolecular Chemistry, University of Wisconsin – Madison

> "We have been very impressed with the Orbitrap Astral Zoom MS, especially for its increased depth and confidence for analyzing critical PTMs like glycosylation. In such applications the sensitivity, scan rate, and stepped collision energy makes a big difference."

Increased structural biology insights

The higher sensitivity of the Orbitrap Astral Zoom mass spectrometer paired with faster stepped collision energy enhances the detection of MS-cleavable crosslinks, unlocking new insights into structural biology.

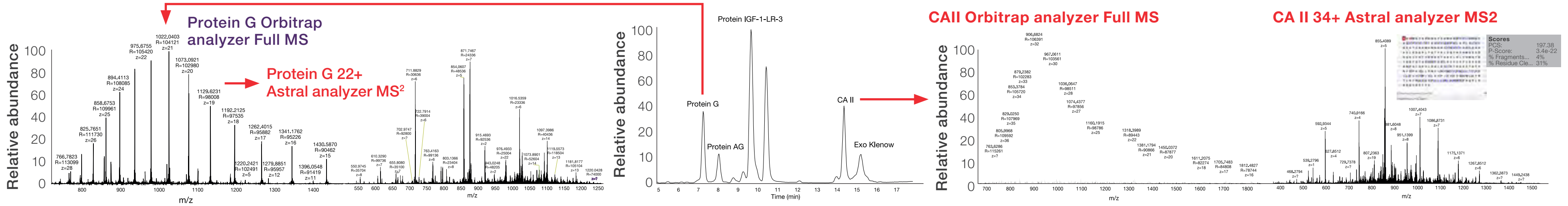


The analysis of DSSO-crosslinked *E. coli* ribosome proteins using faster stepped collision energy with the Orbitrap Astral Zoom mass spectrometer results in the doubling of crosslink identifications and a quadrupling of crosslink spectrum matches (CSMs) compared to Orbitrap-Orbitrap acquisition along with a 20% increase in crosslink identifications and 14% increase in CSMs when compared to the Orbitrap Astral MS. DSSO-crosslinked samples were separated using a 60-minute gradient on a Vanquish Neo UHPLC system and an EASY-Spray PepMap 25 cm × 75 µm HPLC column. Data was processed with the XlinkX node (open_XL algorithm, XlinkX score > or = to 30) in Proteome Discoverer 3.2 software and with FDR set to 1% at CSM and crosslink levels.

Fan Liu, Ph.D.

Professor, Leibniz-Forschungsinstitut für Molekulare Pharmakologie (FMP) Charité – Universitätsmedizin Berlin

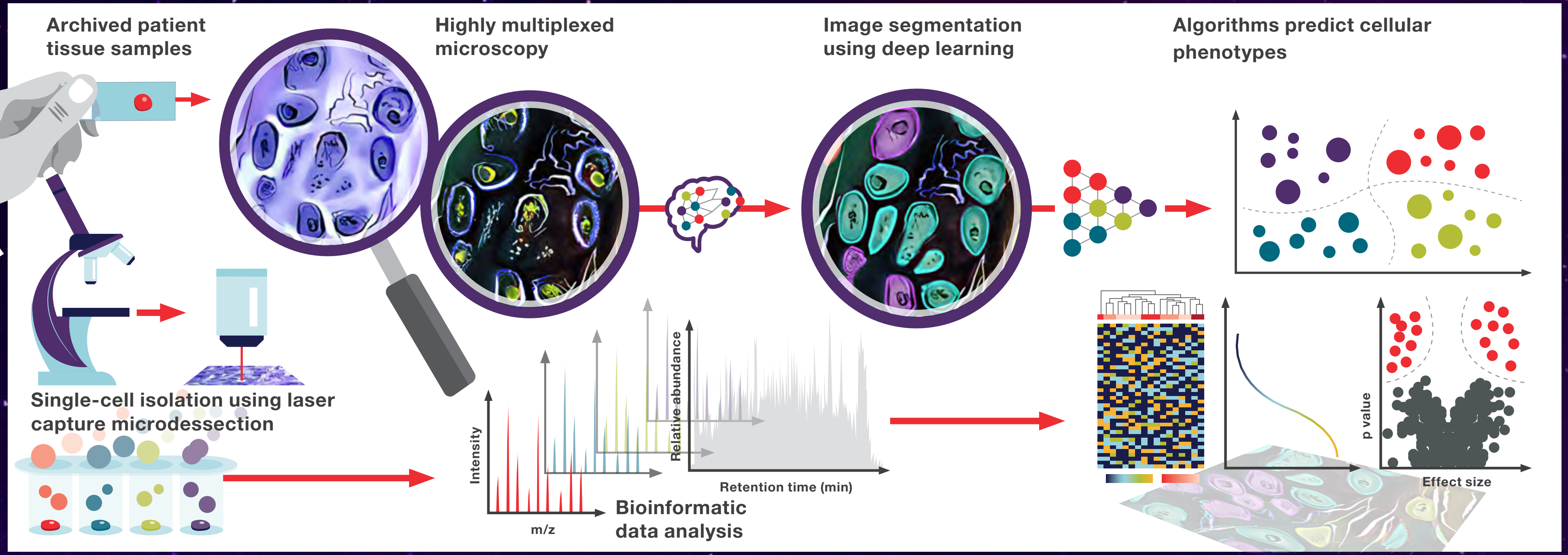
> "The Orbitrap Astral Zoom mass spectrometer greatly benefits crosslink identification by its highly sensitive and ultra fast Astral analyzer and its narrow window DIA capability. This instrument significantly boosts detection of protein interactions from highly complex and low abundant samples."



The Orbitrap Astral Zoom mass spectrometer BioPharma option extends the mass range of the Orbitrap analyzer from 40-8,000 *m/z*, provides improved pressure regulation, and enables top-down and middle-down experiments with Astral analyzer MS^2 scans with averaging of up to 100 µscans. The parallelization of intact precursor mass measurement in the Orbitrap analyzer and fast and sensitive MS^2 fragmentation in the Astral analyzer provides rapid and high-quality top-down and middle-down data acquisition.

Spatial omics

Spatial omics is an emerging field that focuses on the distribution of proteins and metabolites within cells and tissues. Since different cellular compartments and spatial distributions can have dramatic impacts on function and interactions, critical insights into cellular processes and cell-cell communication can be discerned through spatial omics techniques. By mapping the localization of proteins and metabolites, a more complete understanding of cellular organization, signaling networks, and the molecular basis of diseases can be achieved to identify potential biomarkers or develop targeted therapies.



Matthias Mann, Ph.D.

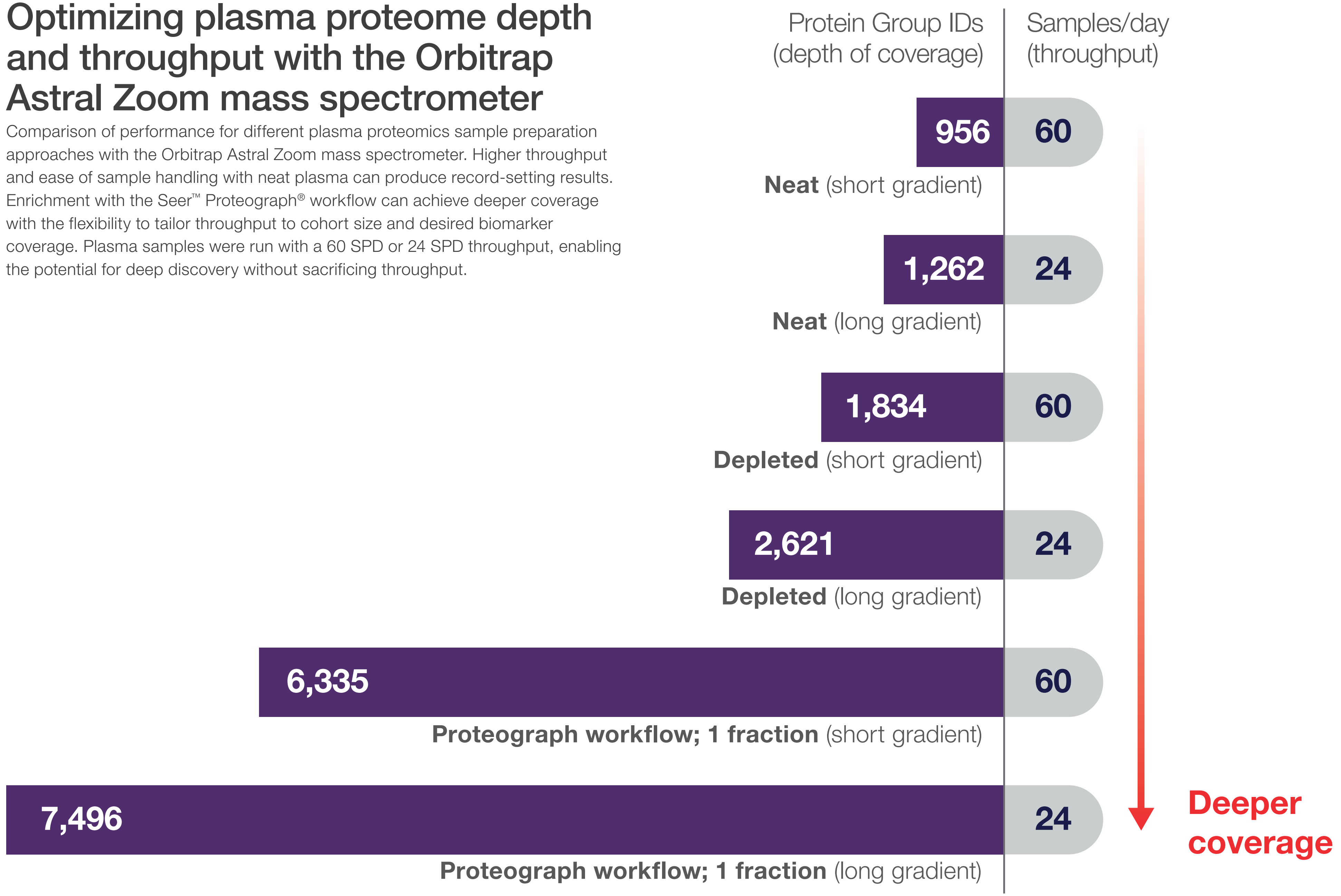
Professor, Proteomics and Signal Transduction, Max Planck Institute of Biochemistry and Director, Novo Nordisk Foundation Center for Protein Research

> “Deep Visual Proteomics enables single-cell resolved analysis of tissue architecture and molecular pathology. In our recent work (Nordmann et al. Nature, 2024 and Rosenberger et al., Nature, 2025), we combined high sensitivity tip-based liquid chromatography methods with the Orbitrap Astral mass spectrometer to achieve unprecedented depth and precision in spatial proteomics. This was key to shed light and even curing one of two very serious diseases.[2,3]”

Illuminating the plasma proteome

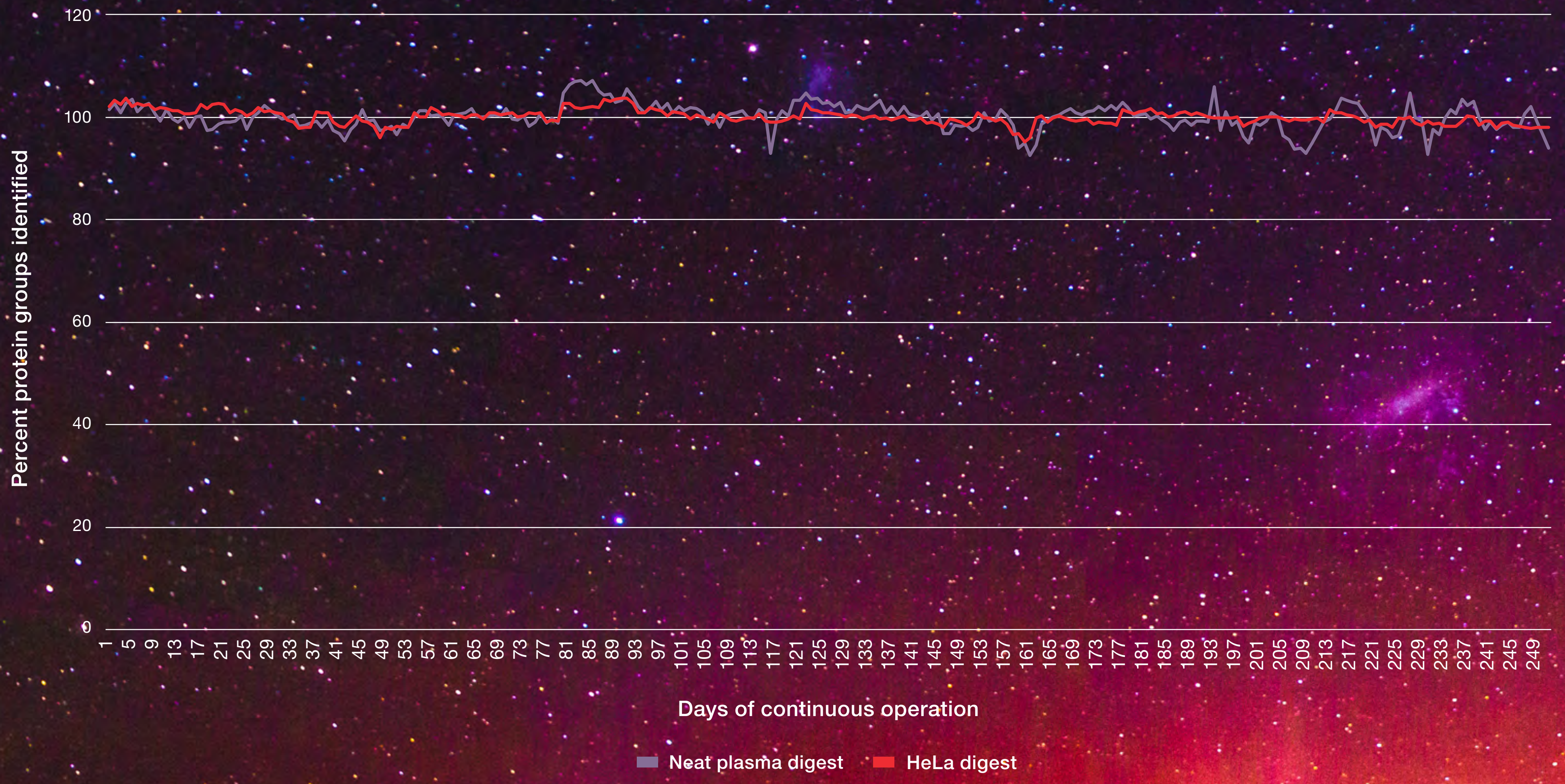
Optimizing plasma proteome depth and throughput with the Orbitrap Astral Zoom mass spectrometer

Comparison of performance for different plasma proteomics sample preparation approaches with the Orbitrap Astral Zoom mass spectrometer. Higher throughput and ease of sample handling with neat plasma can produce record-setting results. Enrichment with the Seer™ Proteograph® workflow can achieve deeper coverage with the flexibility to tailor throughput to cohort size and desired biomarker coverage. Plasma samples were run with a 60 SPD or 24 SPD throughput, enabling the potential for deep discovery without sacrificing throughput.

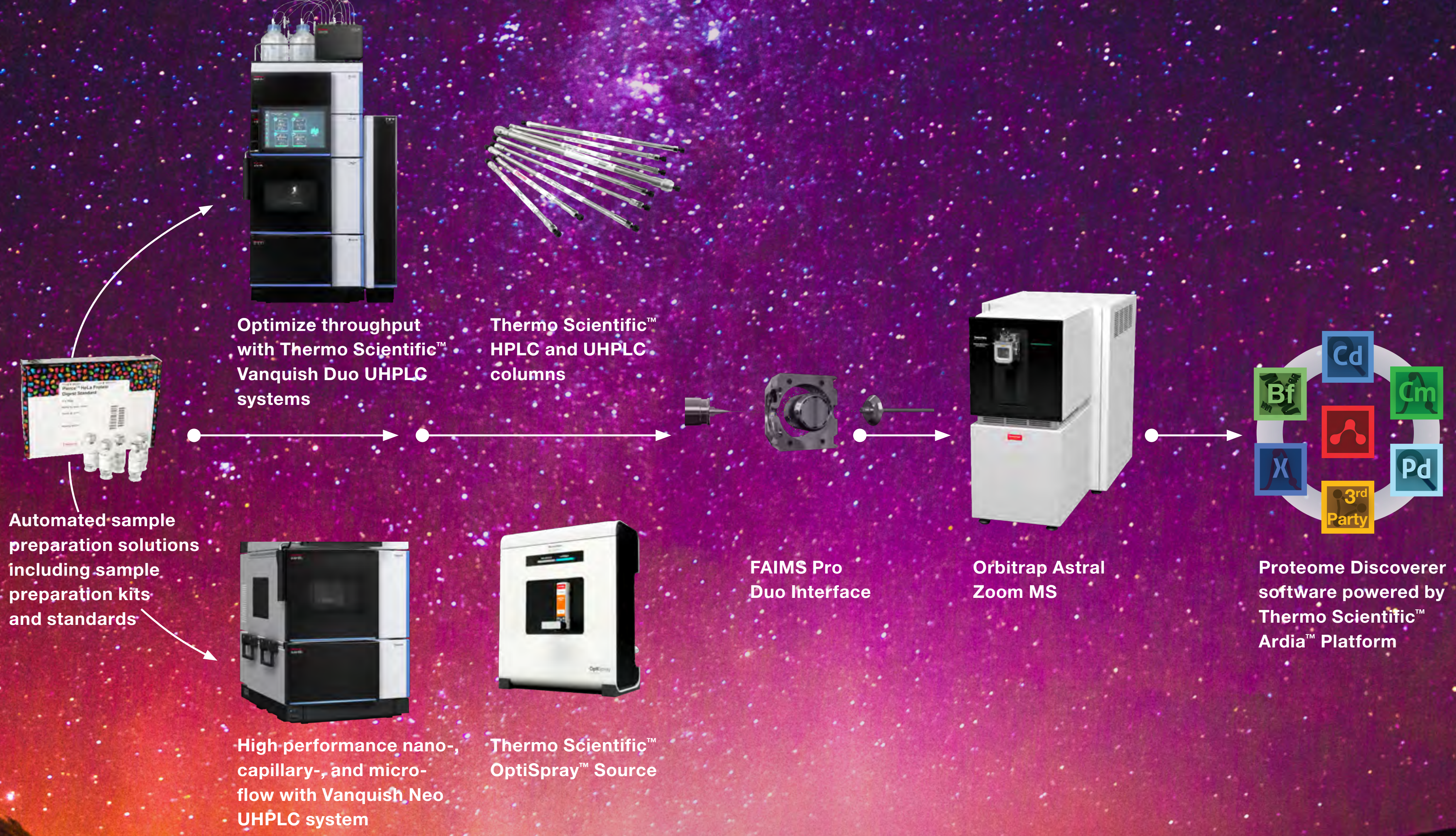


Exceptional end-to-end workflow robustness

Over 250 days of continuous operation with 90 daily neat plasma digest injections and 6 daily HeLa quality control runs to monitor performance – 2.55 mg total protein input and 24,000 injections.



End-to-end workflows to support small molecule, BioPharma, and proteomics applications including **expert service and support**



Automated sample preparation solutions including sample preparation kits and standards

Optimize throughput with Thermo Scientific™ Vanquish Duo UHPLC systems

High-performance nano-, capillary-, and micro-flow with Vanquish Neo UHPLC system

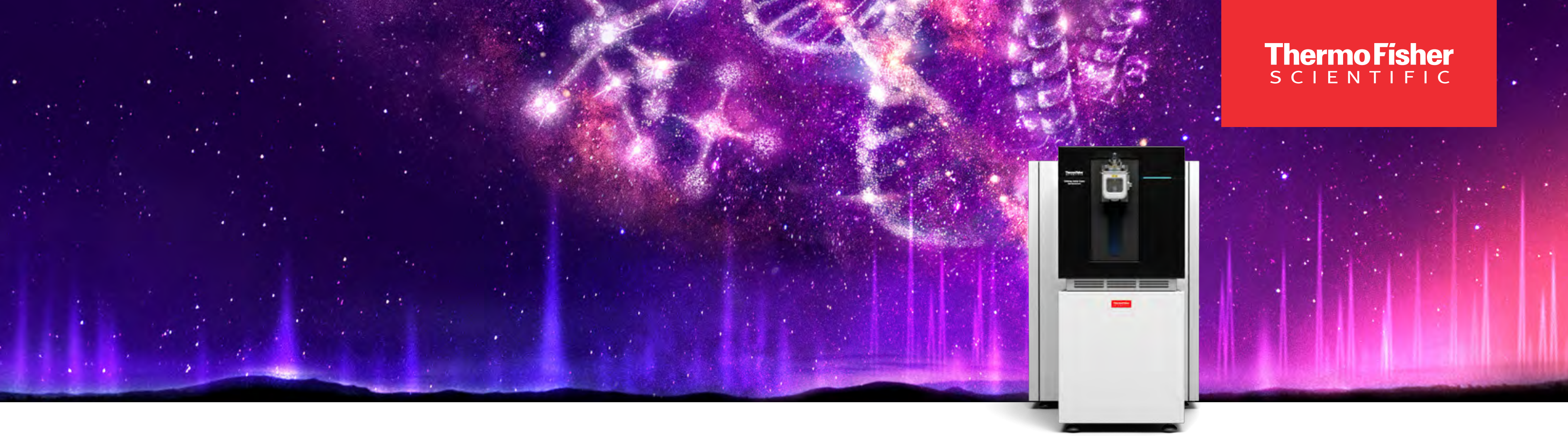
Thermo Scientific™ HPLC and UHPLC columns

Thermo Scientific™ OptiSpray™ Source

FAIMS Pro Duo Interface

Orbitrap Astral Zoom MS

Proteome Discoverer software powered by Thermo Scientific™ Ardia™ Platform



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2. Nordmann, et al. (2024) Nature 635, 1001-1009. https://doi.org/10.1038/s41586-024-08061-0. 3. Rosenberger, et al. (2025) Nature https://doi.org/10.1038/s41586-025-08885-4.

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