

Mass spectrometry

# Rethink what is possible

Orbitrap Astral  
mass spectrometer

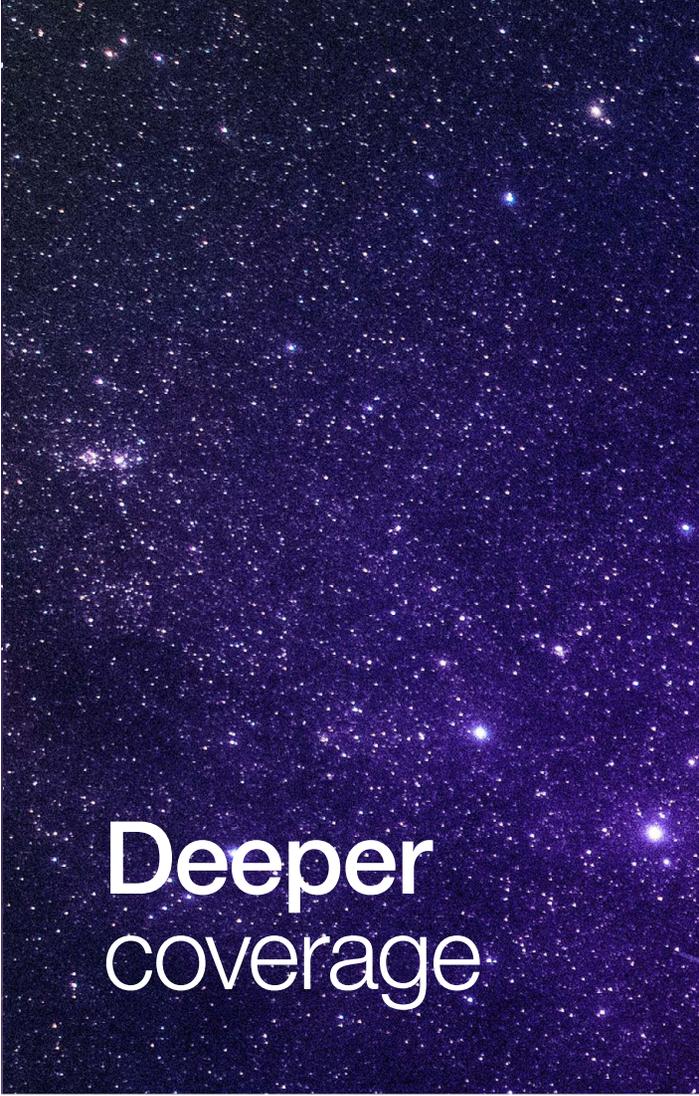


# Rethink what is possible with novel technology

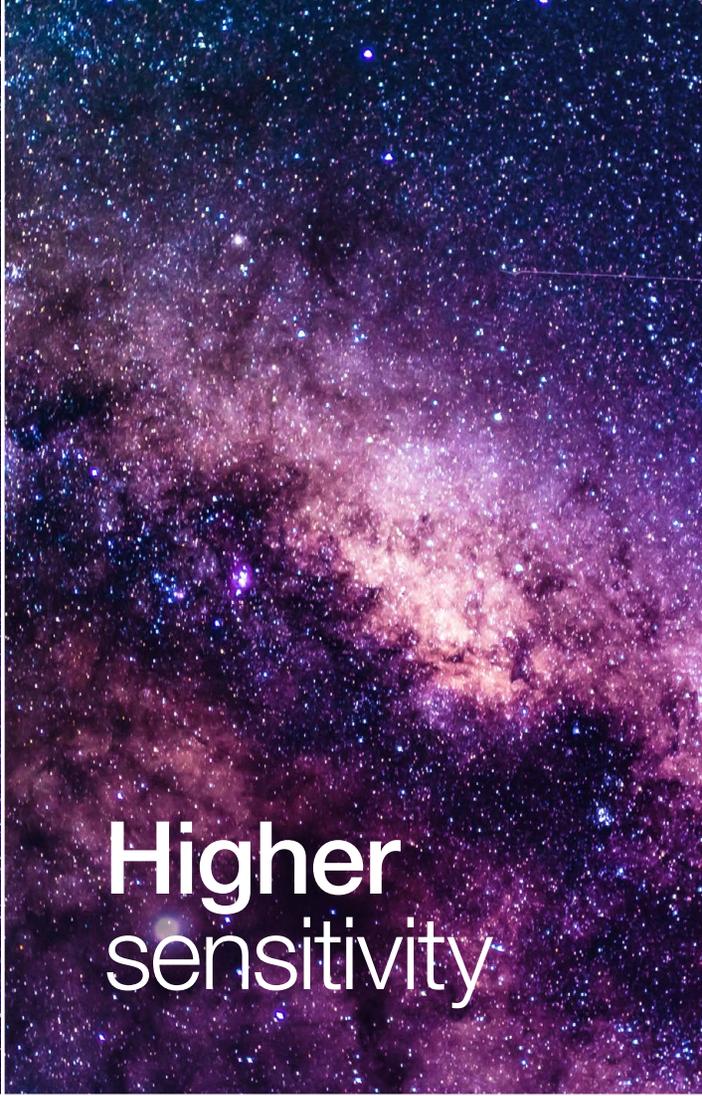
Better understand biology and disease mechanisms with faster throughput, deeper coverage, higher sensitivity, and accurate and precise quantitation using the Thermo Scientific™ Orbitrap™ Astral™ mass spectrometer. The new architecture is the first to combine the novel Thermo Scientific™ Astral™ analyzer with the time-tested Thermo Scientific™ Orbitrap™ mass analyzer, dramatically expanding the scale and scope of your experiments. We've engineered every detail to harmonize these technologies together into a comprehensive mass spectrometer and developed an end-to-end workflow of enabling components to help you rapidly and comprehensively capture the dynamic, temporal, and spatial complexity of biology.



**Faster  
throughput**



**Deeper  
coverage**



**Higher  
sensitivity**



**Accurate & precise quantitation**

# A combination calculated to discover more

- Expand the scope and statistical power of your studies by analyzing over a million protein groups across 180 samples in a single day through the measurement of over 8,000 protein groups in each of the 180 samples
- Attain near whole-proteome coverage at a depth of 12,000 protein groups in one hour
- Achieve higher sensitivity to identify over 5,000 proteins from 250 pg of cell lysate digest at a rate of 80 samples per day
- Discover meaningful biological insights with accurate and precise quantitation over a larger dynamic range with either label-free or multiplexing-based quantitation

## Technology synergy to empower data acquisition

The Orbitrap Astral mass spectrometer contains three mass analyzers: a quadrupole mass analyzer for precursor ion selection, the Orbitrap mass analyzer to acquire high dynamic range HRAM spectra, and the novel Astral mass analyzer to acquire high sensitivity, high dynamic range HRAM spectra at a rate of up to 200 Hz. Together, the analyzers' unique strengths maximize performance and usability in a solution that empowers you to discover more.

## Novel instrument architecture

The front end—ion source to quadrupole—maximizes instrument sensitivity and robustness. The Orbitrap mass analyzer enables the collection of panoramic full scan data at high resolution. The Astral mass analyzer adds fast (up to 200 Hz), sensitive, high dynamic range HRAM capabilities that are fully synchronized with the Orbitrap analyzer acquisition. Due to this synchronization the Orbitrap Astral mass spectrometer excels at many data acquisition strategies including high resolution data-independent acquisition (HR-DIA), and data-dependent acquisition (DDA) for identification and label-free quantitation (LFQ), as well as tandem mass tag (TMT™)-based multiplexed quantification using TMTpro™ 18-plex reagents.

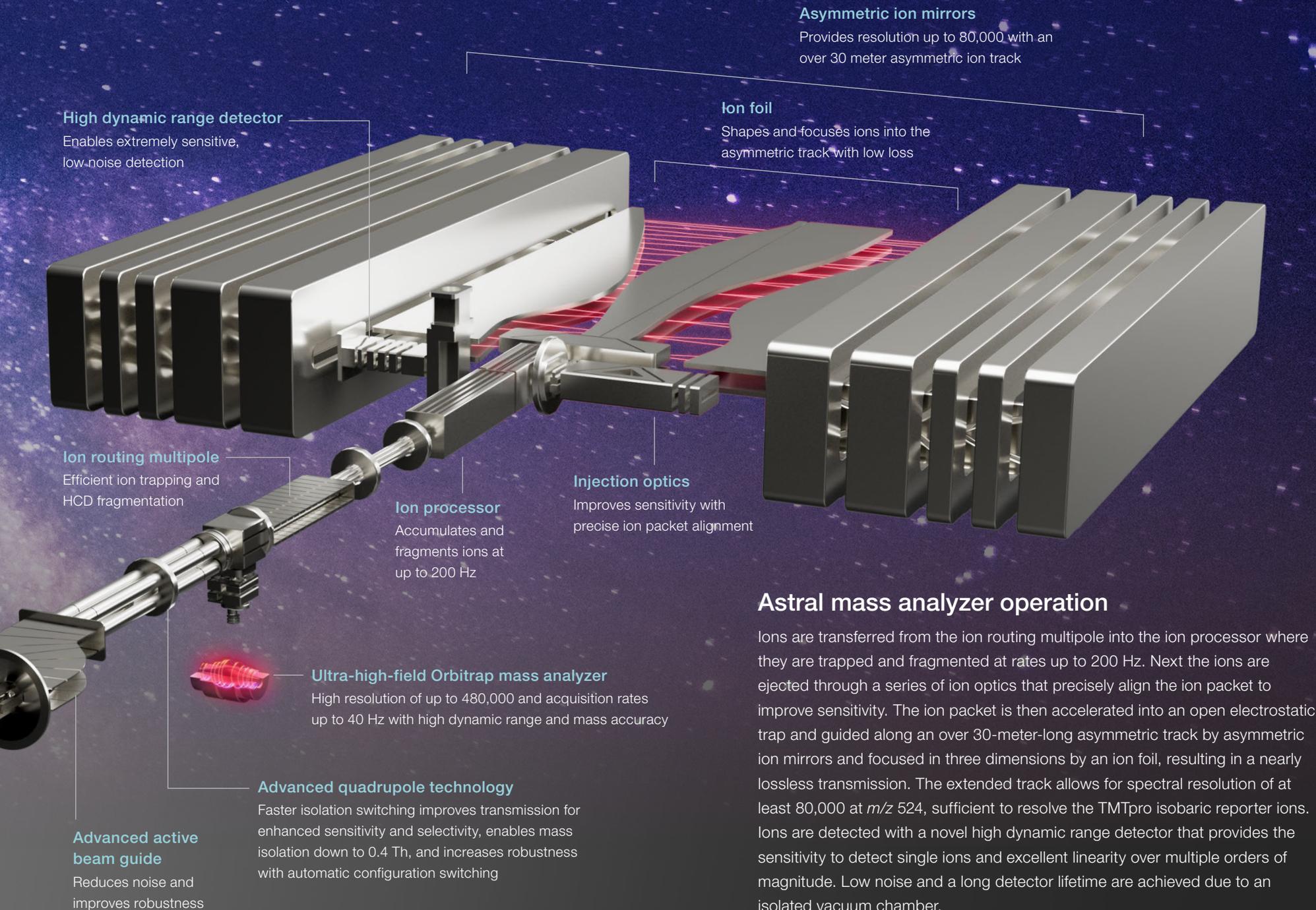
### Thermo Scientific™ EASY-IC™ internal calibration source

Improves mass accuracy

### Brightest ion source

Increases sensitivity





## Astral mass analyzer operation

Ions are transferred from the ion routing multipole into the ion processor where they are trapped and fragmented at rates up to 200 Hz. Next the ions are ejected through a series of ion optics that precisely align the ion packet to improve sensitivity. The ion packet is then accelerated into an open electrostatic trap and guided along an over 30-meter-long asymmetric track by asymmetric ion mirrors and focused in three dimensions by an ion foil, resulting in a nearly lossless transmission. The extended track allows for spectral resolution of at least 80,000 at  $m/z$  524, sufficient to resolve the TMTpro isobaric reporter ions. Ions are detected with a novel high dynamic range detector that provides the sensitivity to detect single ions and excellent linearity over multiple orders of magnitude. Low noise and a long detector lifetime are achieved due to an isolated vacuum chamber.

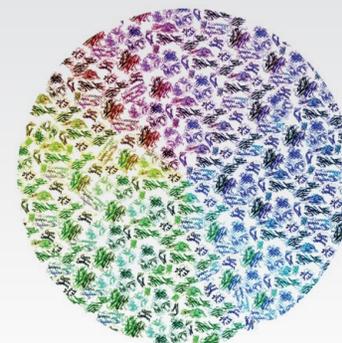
# Faster throughput

Although mass spectrometry has driven remarkable advances, it has historically struggled to provide the requisite throughput to tackle large cohort studies. The Orbitrap Astral mass spectrometer unlocks a new level of faster throughput with the ability to analyze 180 samples in a single day, that's 8 minutes from sample injection to sample injection, with exceptional performance. Now it's possible to analyze four samples in the time it used to take to measure one, breaking through the bottleneck to empower large-scale studies.

## Quadrupled throughput expands experimental scope

The Orbitrap Astral mass spectrometer enables identification of over 8,000 protein groups from a Human cell line digest in eight minutes, injection to injection. In just one hour, analyze over 60,000 protein group data points across 7.5 samples. Scale this impressive speed to a 24-hour day and expect to measure over 1.4 million protein groups across 180 samples. With just one Orbitrap Astral mass spectrometer tens of thousands of samples can be analyzed in a year, dramatically increasing the scale of experiments and improving statistical power.

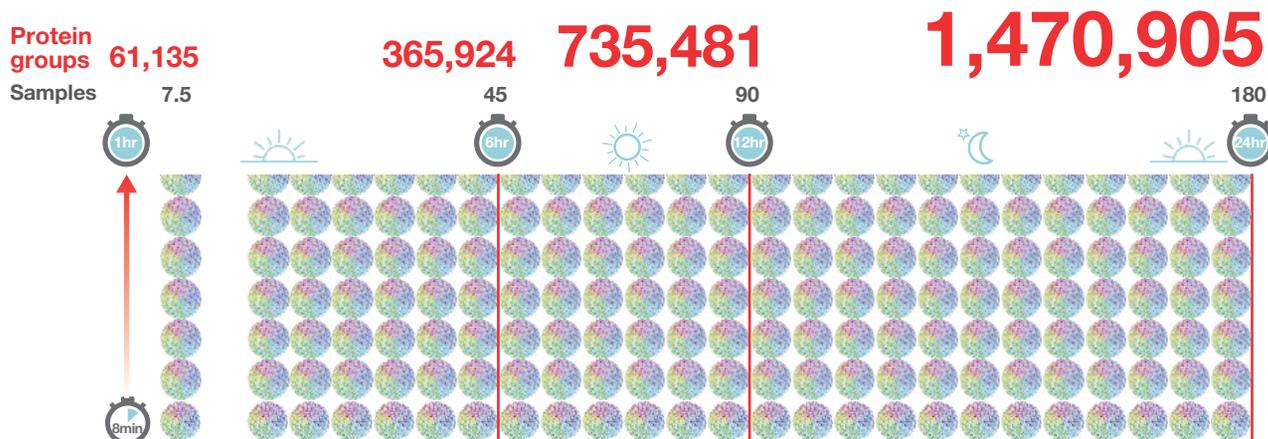
## Analyze one sample in only 8 minutes



**8,135**  
protein groups

1 sample 

## In one day, analyze over 1.4 million protein groups from 180 samples



Orbitrap Astral mass spectrometer analysis of 200 ng HeLa identifies over 8,000 protein groups in an 8-minute run. Under continuous operation for 24 hours, the system measures about 1.4 million protein groups across 180 HeLa samples. Thermo Scientific™ Pierce™ HeLa digest standard (200 ng) was analyzed using an 8 minute long method (injection-to-injection) on a Thermo Scientific™ Vanquish™ Neo UHPLC (operated in a trap and elute mode) and a Thermo Scientific™ EASY-Spray™ PepMap™ 15 cm x 150 μm column. The Orbitrap Astral mass spectrometer was operated with 240,000 FWHM full MS in the Orbitrap analyzer and DIA *m/z* scan range of 380–980 using quadrupole isolation window widths of 2 Th with the Astral analyzer for MS<sup>2</sup>. Data was processed with the CHIMERY™ intelligent search algorithm using Thermo Scientific™ Proteome Discoverer™ 3.1 software and filtered to <1% FDR.

## A paradigm shift for clinical research

Clinical cohorts can contain thousands of samples, but it's been extremely challenging to analyze such a massive number, even using state-of-the-art MS technology. With the Orbitrap Astral mass spectrometer you can make large-scale studies feasible. Expand your experimental scope to tens of thousands of samples per year and multiply the statistical power of your results to inform better clinical interventions. The throughput provided by the Orbitrap Astral mass spectrometer is due to the combination of high resolution and fast ion selection in the quadrupole with synchronized parallel acquisition of

high dynamic range HRAM full MS spectra with the Orbitrap analyzer and high speed HRAM MS<sup>2</sup> spectra with the Astral analyzer.

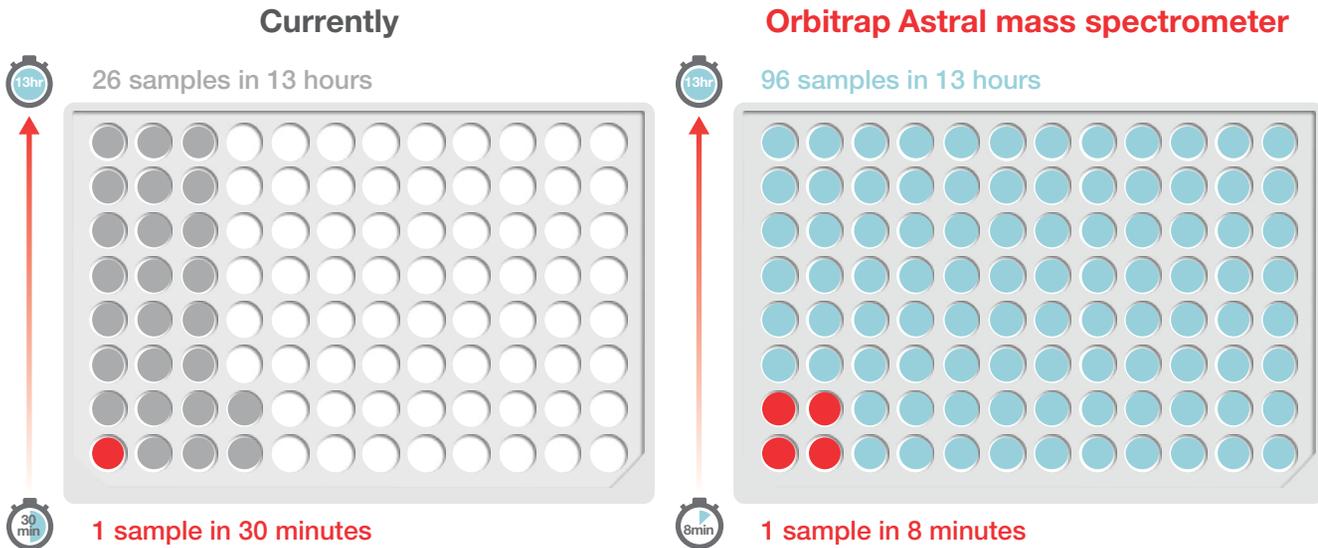
This synergistic pairing unlocks incredible benefits. In just over half a second, the Orbitrap Astral mass spectrometer collects both: a full scan at 240,000 resolution with the Orbitrap analyzer and 100 MS<sup>2</sup> scans in the Astral mass analyzer in a carefully coordinated scan management process that maximizes instrument utilization.



Jennifer Van Eyk, Ph.D.,  
Director, Basic Science Research,  
Barbra Streisand Women's Heart  
Center Director, Advanced Clinical  
Biosystem Institute Center, Cedars-  
Sinai Hospital

“The Orbitrap Astral mass spectrometer quickly and reproducibly delivers deeper and broader coverage of the plasma proteome with the accuracy and precision required to produce predictive information on the best treatment course for each of our patients in the clinic. That is precision medicine in action.”

## The Orbitrap Astral mass spectrometer delivers **4x** the throughput



With the Orbitrap Astral mass spectrometer one can analyze four times the samples in the same amount of time. Measure an entire 96-well plate of samples in just 13 hours to reach a new scale of large cohort analysis.



# Deeper coverage

The Orbitrap Astral mass spectrometer is the first technology to offer near-whole proteome coverage. Traditional MS-based proteomics coverage of a Human cell lysate is limited to about 12,000 protein groups. While the depth of 12,000 protein groups is on par with what can be identified using other technologies like mRNA sequencing, achieving this coverage has been a painstaking process that involved offline fractionation, multiple injections, and more than 24 hours of MS acquisition time.<sup>1</sup>

## Record setting single-shot coverage

The Orbitrap Astral mass spectrometer delivers incredibly deep coverage from single-shot proteomics experiments. Expect to identify over 9,000 proteins in 15 minutes or 12,000 proteins in 60 minutes. Until now,

proteome coverage like this was simply unheard of. This performance and flexibility allows you to balance throughput and depth based on your experimental needs.

## Incredible flexibility to deliver high coverage at high throughput or unprecedented depth in 1 hour



Orbitrap Astral mass spectrometer analysis of a single shot of Human cell lysate. In 14.4, 24, or 60 minute injection-to-injection times, corresponding to 100 samples per day, 60 samples per day, and 24 samples per day, respectively, the Orbitrap Astral mass spectrometer can identify over 9,000, 10,000, or 12,000 protein groups, respectively. HeLa digest (200 ng for 100 SPD and 60 SPD; 2 µg for 24 SPD) was analyzed using various gradient lengths using a Vanquish Neo UHPLC and an EASY-Spray PepMap 15 cm × 150 µm column (for 100 and 60 SPD) or a Thermo Scientific™ µPAC™ Neo 110 cm column (for 24 SPD). The Orbitrap Astral mass spectrometer was operated with 240,000 FWHM full MS in the Orbitrap Analyzer, and DIA *m/z* scan range of 380-980, isolation window width of 2 Th for MS<sup>2</sup> in the Astral analyzer. Data was processed with CHIMERY5 using Proteome Discoverer 3.1 software and filtered to <1% FDR.

## Experience a new paradigm of whole proteome sequencing

While the entire human genome has been sequenced, the complete proteome has eluded comprehensive coverage. Using multi-shot approaches with fractionated samples enables even deeper proteome coverage.

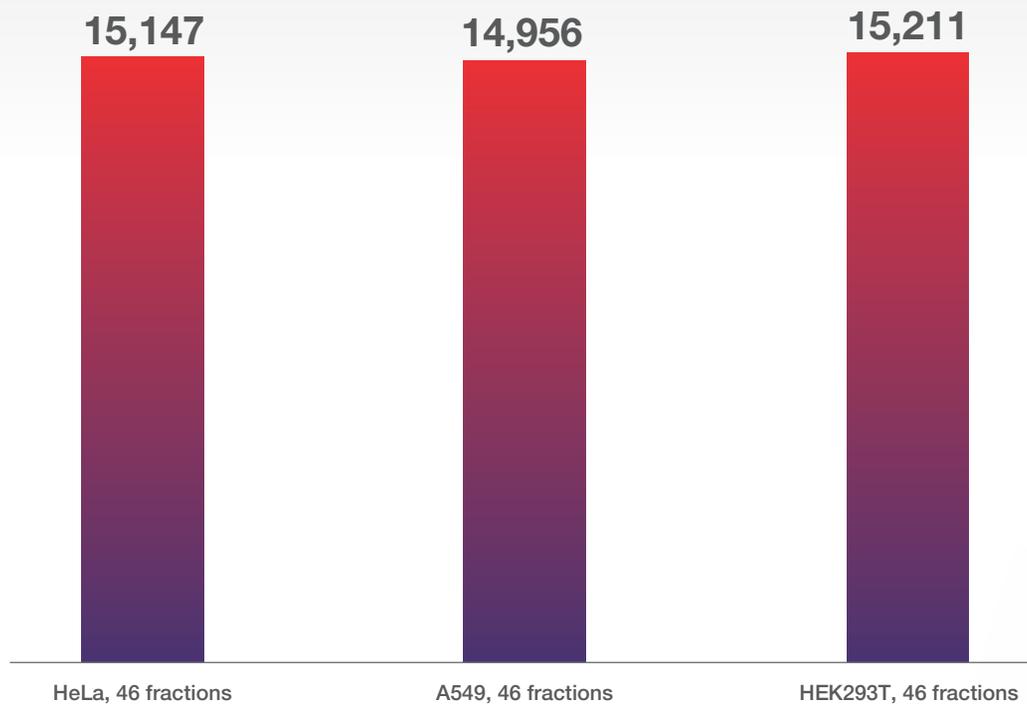
With the Orbitrap Astral mass spectrometer, it's possible to identify over 15,000 protein groups from a fractionated sample in just hours. That's up to eight nearly complete proteomes per day, unlocking a new era of whole proteome sequencing.



Jesper Olsen, Ph.D.,  
Deputy Center Director,  
Professor, Novo Nordisk Foundation  
Center for Protein Research,  
University of Copenhagen

“The Orbitrap Astral mass spectrometer enables routine acquisition of essentially complete Human proteomes with a throughput of up to eight proteomes per day—ten times higher than current state-of-the-art.”

### Near whole-proteome depth of coverage in 4.5 hours



Orbitrap Astral mass spectrometer analysis of fractionated samples from three different cell lines enabled measurement of more than 15,000 protein groups. 46 high-pH fractions were collected then separately analyzed using 5.5 minute gradients. A Vanquish Neo UHPLC and an EASY-Spray PepMap 15 cm x 150 µm column were used with a 200 ng fraction injection. The Orbitrap Astral mass spectrometer was operated with 240,000 FWHM full MS in the Orbitrap analyzer and DIA *m/z* scan range of 380–980, isolation window width of 2 Th for MS<sup>2</sup> in the Astral analyzer. Data was processed with CHIMERYS using Proteome Discoverer 3.1 software and filtered to <1% FDR. Data courtesy of Jesper Olsen, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen.



# Higher sensitivity

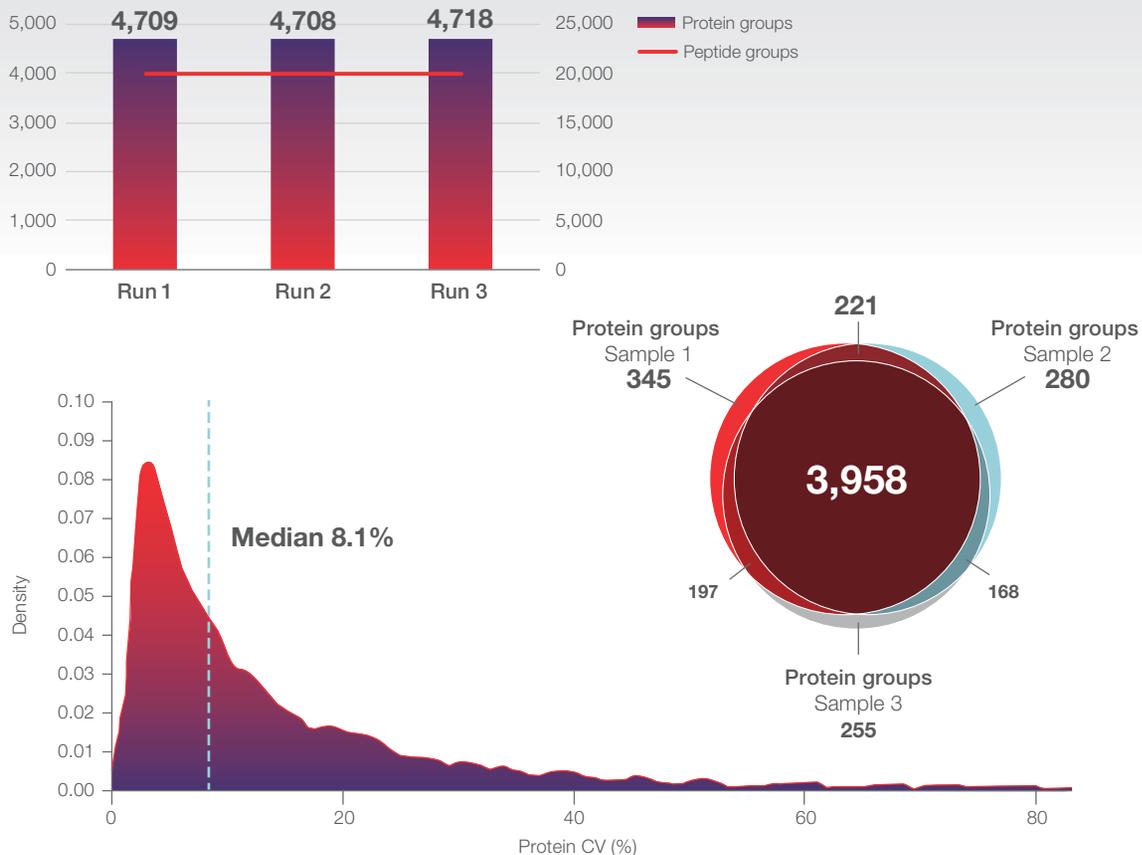
Improved sensitivity is required to deliver further proteomic insights in low input samples such as single cells, and for low-abundance proteins in bulk samples. Sensitivity is essential because many functionally critical proteins, for example transcription factors, are present at low abundance. Not only is high sensitivity required for identifying these biologically significant proteins, but it is also essential to quantify their changes precisely and accurately to better understand the biological processes that they regulate. The Orbitrap Astral mass spectrometer offers high sensitivity due to the high transmission and sensitivity of the Astral mass analyzer, allowing deep sample coverage with high quality data measurements that were previously impossible to achieve. Even at low sample loads, identification of proteins are exceptionally reproducible, ensuring high confidence in results.

## Data completeness at high speed and low input

Low input samples can lead to missing values and inconsistent results. The high sensitivity at high speed of the Orbitrap Astral mass spectrometer

empowers a deeper coverage of low input samples with high quality quantitation.

## Consistent results from low input samples run at high throughput



The Orbitrap Astral mass spectrometer enables excellent reproducibility and data completeness for low-input sample analysis as illustrated by performance on 1 ng cell lysate samples. Across 3 replicate runs over 4,700 proteins and 20,000 peptide groups were identified in each run. 3,958 of the protein groups were shared in every injection and 4,544 were shared in at least two of the samples. The median CV of identified protein groups across the 3 injections was 8.1%. Samples were run on a Vanquish Neo UHPLC (in direct injection mode) and separated with a Thermo Scientific™  $\mu$ PAC™ Neo Low Load column with a 10-minute active gradient and 18 minute injection-to-injection cycle. Data analysis was performed using Spectronaut™ 17 software using a DirectDIA workflow.

## Identify more proteins from single cells

Due to its exceptional sensitivity and data completeness, the Orbitrap Astral mass spectrometer enables reproducible identification of over 5,000 proteins from 250 pg of cell lysate—nearly double the number of identifications of current instruments while simultaneously doubling the throughput to 80 single cells per day. Using one high-sensitivity instrument that takes rapid

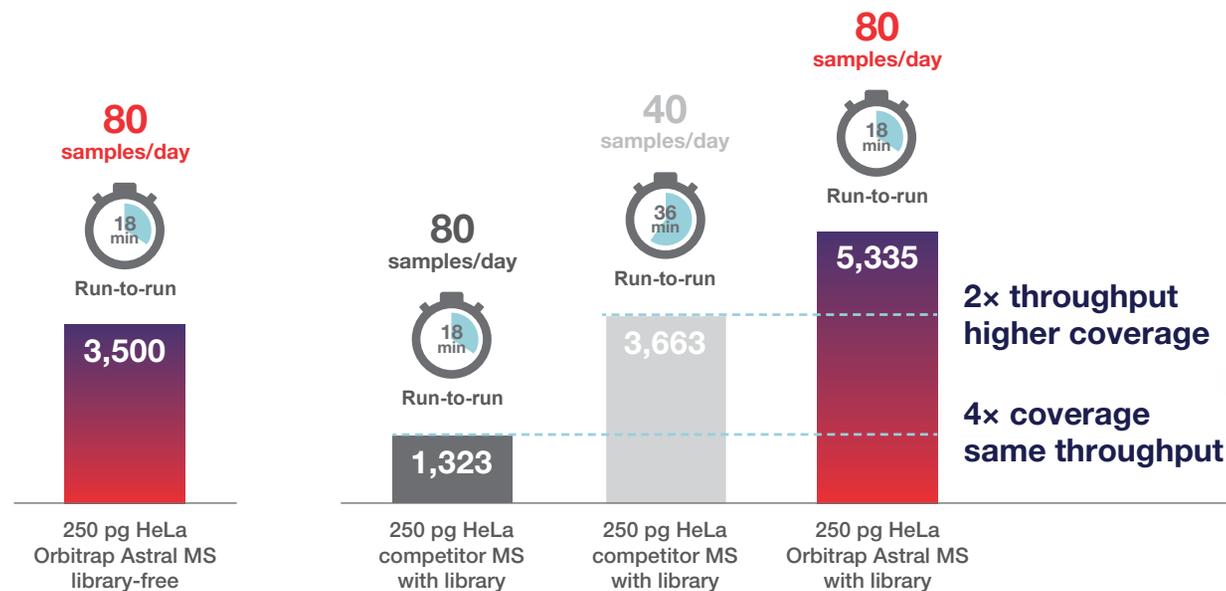
measurements maximizes productivity and minimizes complexity. Also, with the ability to multiplex the analysis of single cells with pooling and the use of tandem mass tags (TMT), throughput can be extended even further with accurate and precise quantitative measurements to improve the classification of single cells.



Erwin Schoof, Ph.D.,  
Associate Professor, Department  
of Biotechnology and Biomedicine,  
Section for Protein Science and  
Biotherapeutics, Cell Diversity Lab,  
Technical University of Denmark

“With the Orbitrap Astral mass spectrometer we were able to double the throughput for single cells, while also increasing the number of proteins per cell by 50%. This means we start picking up key cellular decision making proteins like transcription factors, epigenetic regulators and kinases to better understand the biological heterogeneity of single cells.”

## Deeper coverage from single cells at faster throughput with DIA



Comparison of Orbitrap Astral mass spectrometer DirectDIA and spectral library search performance for single cell equivalents using Spectronaut 17 software. The Orbitrap Astral mass spectrometer identifies 4x more proteins at the same throughput or nearly 1.5x more proteins with double the throughput compared to competitor mass spectrometers when using a spectral library. With library-free directDIA approaches nearly as many proteins can be identified with double the throughput as competitor MS instruments that use spectral libraries for data processing.



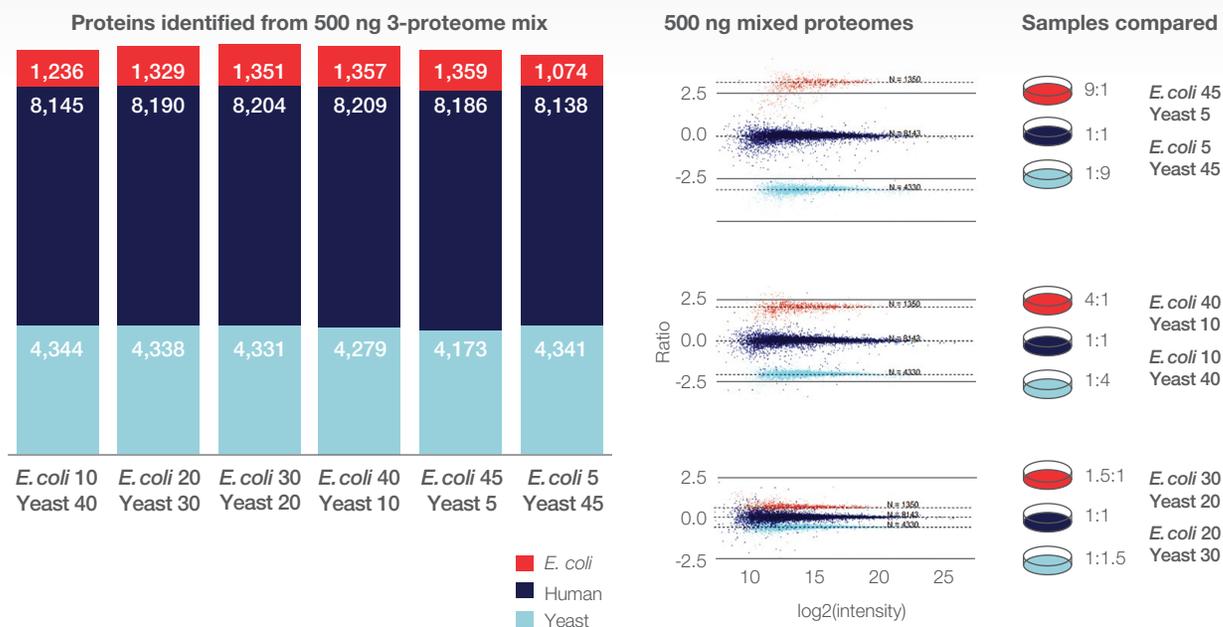
# Accurate & precise quantitation

The Orbitrap Astral mass spectrometer delivers accurate and reproducible quantitation of thousands of proteins from difficult samples like plasma, even when using short gradients, unlocking new possibilities for population based proteomic studies. The novel design of the Orbitrap Astral mass spectrometer excels at data independent acquisition (DIA) for LFQ, it also sets a new standard for TMT analysis to probe deeper into the proteome in record time. Using TMT workflows, expect to quantify 10,000 proteins from 18 samples in just 6 hours, a much deeper quantitative proteome coverage versus the current state-of-the-art.

The Orbitrap Astral mass spectrometer significantly extends the dynamic range of quantitation due to the high speed and sensitivity of the Astral analyzer. Across multiple mixing ratios of Human, *E. coli*, and Yeast samples accurate and precise ratios can be obtained while identifying nearly 14,000 proteins, including nearly the entire Yeast proteome. In this ground truth experiment the median CV for proteins across the three

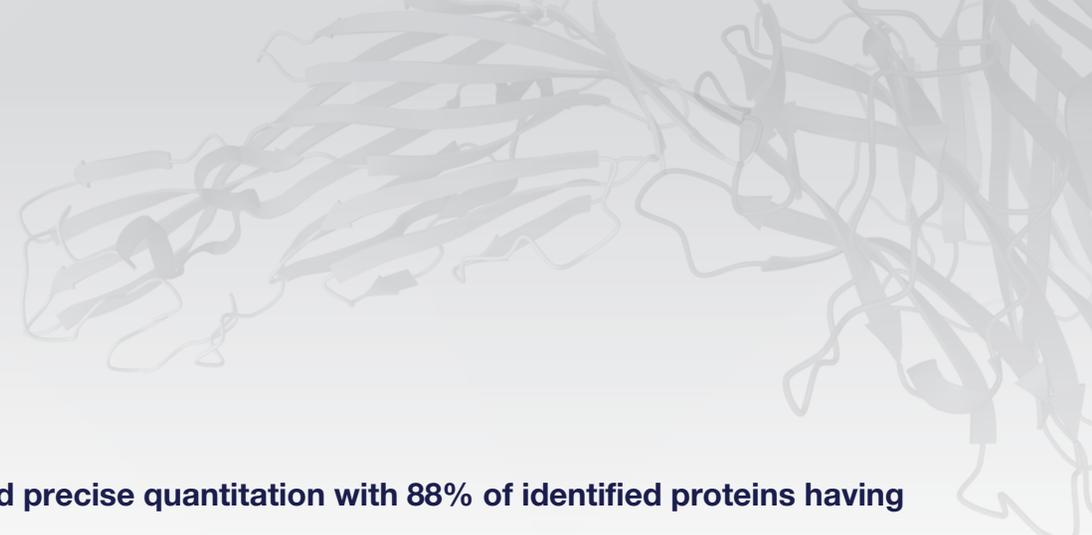
proteomes is 4.7%, demonstrating the excellent reproducibility of data collection. The quantitative accuracy and precision of the Orbitrap Astral mass spectrometer is sufficient to differentiate small biological changes down to 1.5-fold in complex mixtures for both high and low abundance proteins, allowing for the discovery of more significant differences between samples.

## Accurate and precise quantitation of three-proteome mixtures

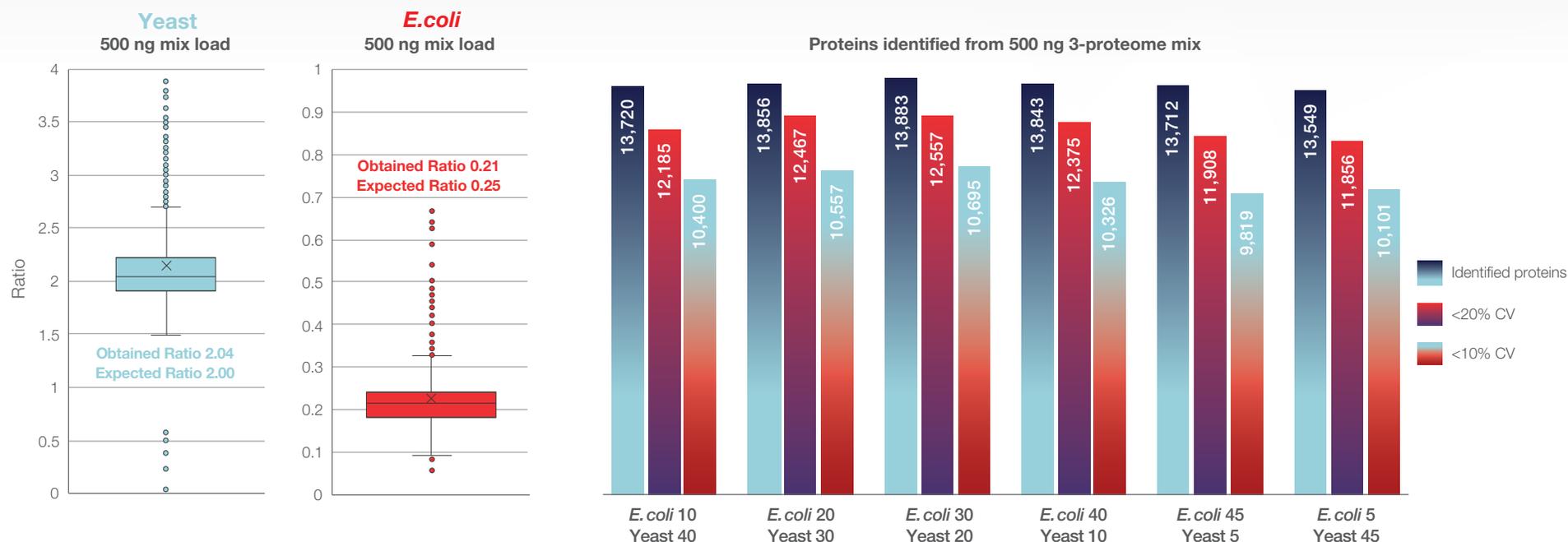


The Orbitrap Astral mass spectrometer provides accurate and precise quantitation as determined by LFQ HR-DIA data using three-proteome mixtures with known amounts of Yeast, *E. coli*, and Human proteomes. Across the various mixing ratios deep coverage of each of the three proteomes is obtained even when including just 5% of *E. coli* or Yeast mix in the sample. Comparing the ratios of different sample mixtures to their expected ratios demonstrates the ability to accurately and precisely measure the expected ratios of 9, 4, and even 1.5 across a high dynamic range of protein intensities.

Data courtesy of Jesper Olsen, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen.



**The Orbitrap Astral mass spectrometer enables accurate and precise quantitation with 88% of identified proteins having CV <20% and 75% having CV <10%.**



Quantitative accuracy and precision are shown through the measurement of the correct ratios of proteins across multiple mixing amounts, for example comparing two samples with an expected ratio of 2 for Yeast provides an observed ratio of 2.04 and comparing two samples with an expected ratio of 0.25 for *E. coli* provides an observed ratio of 0.21. With the three proteome mixtures at a 500 ng total protein load, the Orbitrap Astral mass spectrometer collects incredibly precise data with nearly 90% of proteins having a CV less than 20% and over 75% of proteins having a CV less than 10%. This quantitative accuracy and precision is sufficient to differentiate small biological changes in complex mixtures for both high and low abundance proteins. Data courtesy of Jesper Olsen, Novo Nordisk Foundation Center for Protein Research, University of Copenhagen.



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

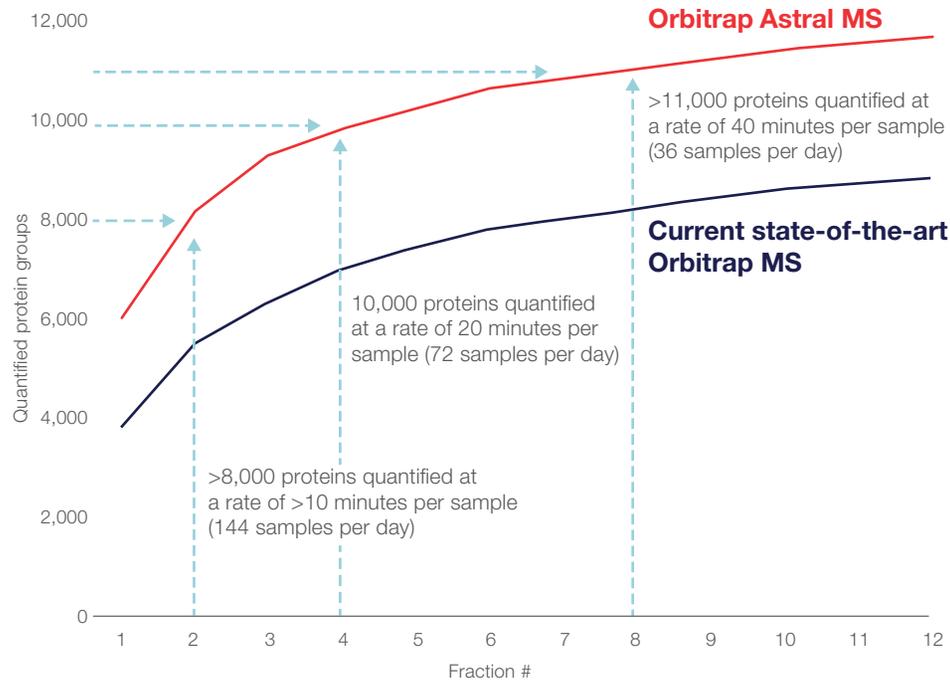
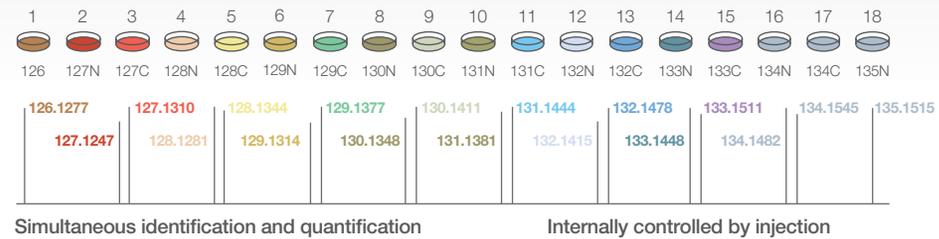
“The Orbitrap Astral mass spectrometer comes with extraordinary gains in both sensitivity and scan speed, filling it with proteomic possibilities. Our very first full-proteome datasets using TMT were already remarkably deeper (>11,000 proteins) and were acquired in only two-thirds the normal analysis time.”



The Orbitrap Astral mass spectrometer also improves the throughput and depth of coverage with isobaric labeling reagents such as TMT. Since the Astral mass analyzer combines high speed and sensitivity with high resolution and accurate mass measurements, it can resolve TMTpro 18plex isobaric reporter ions for multiplexed quantitation. The Astral analyzer transmits and detects ions over a wide  $m/z$  range, meaning a

single spectrum can be used to measure both the TMT reporter ions and peptide fragment ions simultaneously. The combination of high resolution and high dynamic range full MS scans acquired with the Orbitrap analyzer with synchronized fast and sensitive data-dependent HRAM MS<sup>2</sup> scans acquired by the Astral analyzer dramatically increases the depth of coverage and throughput for TMT analysis.

### Multiplexing 18 samples for high throughput and deep quantitative coverage



In this experiment the Orbitrap Astral mass spectrometer quantified over 8,000 proteins using TMTpro 18-plex tags with only 2 fractions analyzed using 90-minute gradients, equivalent to a throughput of 144 samples per day. With 4 fractions over 10,000 proteins are quantified at a throughput of 72 samples per day, and with 8 fractions over 11,000 proteins are quantified at a rate of 36 samples per day. The enhanced depth and throughput of the Orbitrap Astral mass spectrometer combined with TMT multiplexing facilitates deep quantitative proteome coverage at speed. Data courtesy of Steven Gygi, Harvard Medical School.

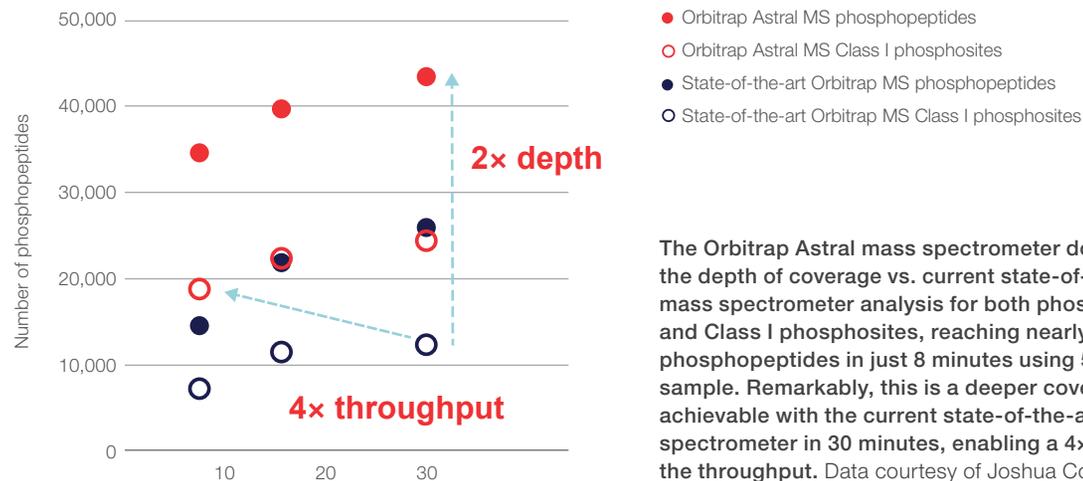
# Go beyond the genomic blueprint

While the genome provides the blueprint for biology, it is the proteome that actualizes the blueprint. Splice variants, protein isoforms, and post-translational modifications generate a wide range of protein molecular species (proteoforms) that are the functional units of cell biology. For example, protein phosphorylation is a critical driver of cellular signaling through the modification of protein structure and function.

The Orbitrap Astral mass spectrometer empowers rapid profiling of nearly twice the number of phosphopeptides with precise localization of the phosphorylated residue, while using low input amounts. With a 50 ng of enriched phosphopeptide sample the Orbitrap Astral mass

spectrometer identifies nearly as many Class I phosphosites as current state-of-the-art Orbitrap mass spectrometers identify phosphopeptides in a 30-minute run. In addition, the Orbitrap Astral mass spectrometer provides deeper coverage with just an 8-minute gradient.

## Double the depth and quadruple the throughput for phosphoproteomics



The Orbitrap Astral mass spectrometer doubles the depth of coverage vs. current state-of-the-art Orbitrap mass spectrometer analysis for both phosphopeptides and Class I phosphosites, reaching nearly 20,000 Class I phosphopeptides in just 8 minutes using 50 ng of enriched sample. Remarkably, this is a deeper coverage than achievable with the current state-of-the-art Orbitrap mass spectrometer in 30 minutes, enabling a 4x improvement in the throughput. Data courtesy of Joshua Coon, University of Wisconsin–Madison.



Joshua Coon, Ph.D., Professor,  
Biomolecular Chemistry,  
University of Wisconsin–Madison

“The Orbitrap Astral mass spectrometer enables sensitive, rapid, and ultra-deep phosphoproteomics.”



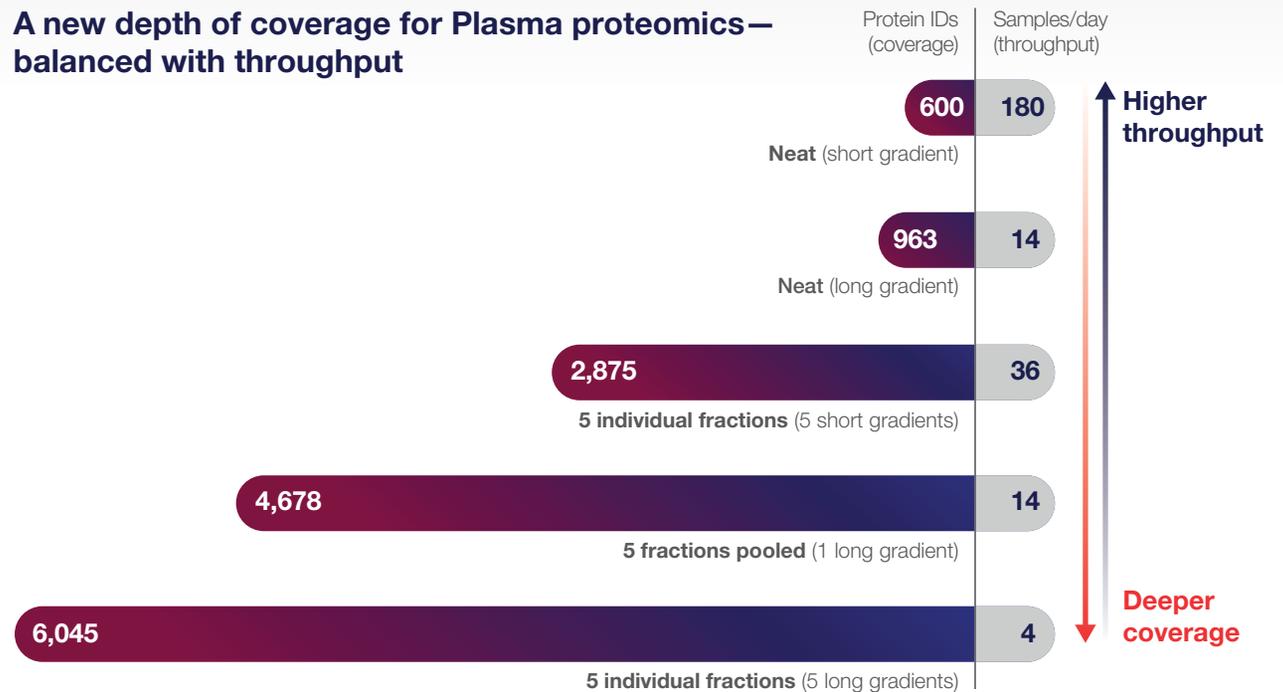
# Science at scale

With the ability to achieve higher throughput and generate the highest quality data from plasma samples, the applications of the Orbitrap Astral mass spectrometer extend from early-stage discovery through to translational research and beyond. While plasma is the most common type of sample analyzed in clinical studies, the ability to screen large patient cohorts has been restricted by the detection, quantitation, and throughput limits of MS analysis. In particular, the prevalence of albumin and other high abundance proteins in plasma makes it difficult to obtain high coverage at high throughput.

The Orbitrap Astral mass spectrometer offers new possibilities for translational proteomics with reproducible quantitation of thousands of proteins from plasma using relatively short gradients. This is due to the improved selectivity of narrow 2 Th DIA isolation windows that reduce interference from high abundance proteins,

higher MS<sup>2</sup> sensitivity, and an exceptional dynamic range. Neat, depleted, and enriched plasma samples can now be analyzed with a faster throughput of 180 samples per day and at a depth of over 6,000 proteins with accurate and precise quantitation of novel biomarkers for better clinical insights.

## A new depth of coverage for Plasma proteomics—balanced with throughput



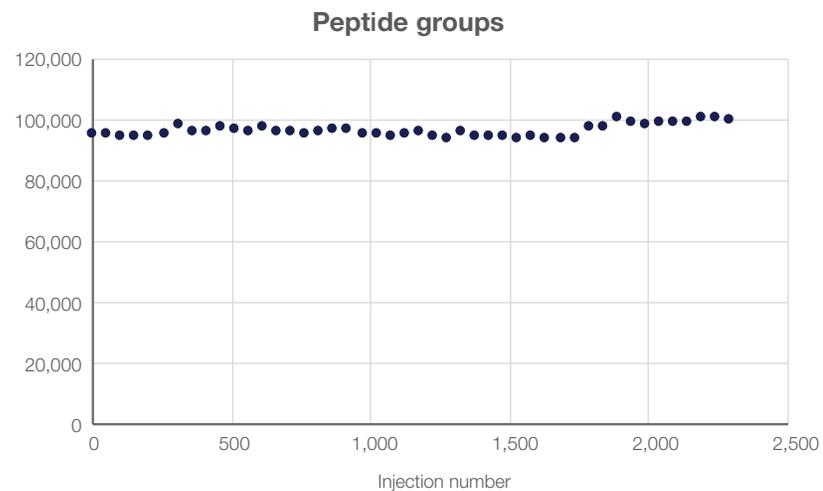
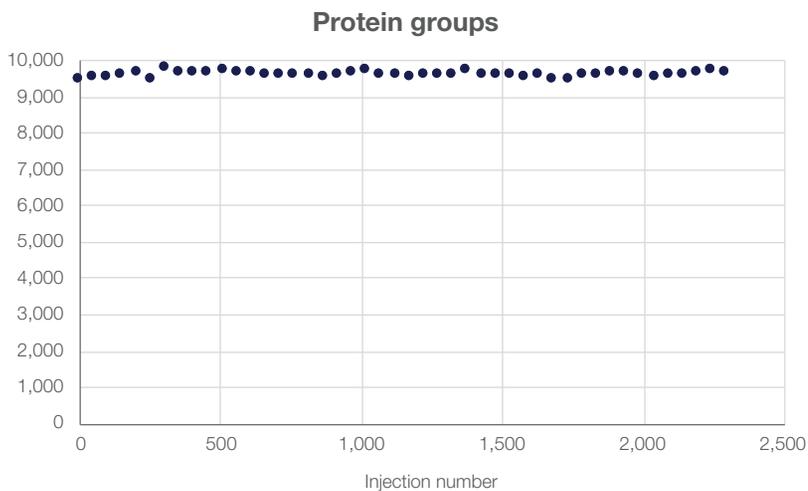
Comparison of performance for different plasma proteomics approaches with the Orbitrap Astral mass spectrometer. Higher throughput and ease of sample handling with neat plasma can produce record-setting results. Enrichment with Seer™ nanoparticle preparations can achieve deeper coverage with the flexibility to tailor throughput to cohort size and desired biomarker coverage. Plasma samples were run with an 8-minute injection-to-injection cycle using trap-and-elute for short gradient runs or a 60-minute active gradient using direct injection for long gradients. Data was processed with CHIMERY5 using Proteome Discoverer 3.1 software and filtered to <1% FDR.

# Robust to keep pace with your science

The Orbitrap Astral mass spectrometer is designed for robust performance that helps you see more in your proteomics samples faster. The instrument enables the analysis of thousands of samples in a sequence without loss in performance. Because the Orbitrap Astral mass spectrometer is extremely sensitive, five to ten times lower amount—just 100–200 ng—is sufficient to achieve outstanding performance while reducing the amount of matrix entering the instrument. In addition, the use of the Thermo Scientific™ FAIMS Pro Duo interface increases robustness by an additional factor of three through pre-filtering undesirable matrix in samples using ion mobility to further increase instrument uptime.



## Robust and reproducible performance across thousands of injections



200 ng neat plasma was run continuously using a 100 samples per day method on the Orbitrap Astral mass spectrometer and on every 50th injection 200 ng HeLa was used to determine system robustness and reproducibility. Across over 2,200 continuous injections the HeLa standard demonstrates consistent performance with an average of 9,625 protein groups and 96,459 peptide groups identified with standard deviations of 71 and 1,972, respectively. Data was processed with CHIMERYS using Proteome Discoverer 3.1 software and filtered to <1% FDR.

# Next-generation proteomics workflows

The Orbitrap Astral mass spectrometer is more than an instrument that provides extraordinary results. It's part of our next-generation end-to-end Thermo Scientific<sup>™</sup> Velocity<sup>™</sup> workflow for LFQ HR-DIA, which brings together best-in-class components covering everything from sample preparation, liquid chromatography and ion mobility to data acquisition and interpretation. The Velocity workflow enables seamless operation to go from sample to insight. Pre-built method templates that are already optimized for specific applications help you start generating high quality results immediately.

**End-to-end workflows for seamless operation, sample to insight**



**Thermo Scientific<sup>™</sup> AccelerOme<sup>™</sup>  
automated sample  
preparation platform**

Easy to use, reproducible sample preparation



**Thermo Scientific<sup>™</sup> Vanquish<sup>™</sup> 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 interferences,  
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



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### 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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#### Thermo Scientific FAIMS Pro Duo Interface

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#### Thermo Scientific Proteome Discoverer software by Ardia

[thermofisher.com/ProteomeDiscoverer](https://thermofisher.com/ProteomeDiscoverer)

1. Bekker-Jensen et al, An Optimized Shotgun Strategy for the Rapid Generation of Comprehensive Human Proteomes, Cell Syst. 2017 Jun 28; 4(6): 587–599.e4., <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5493283/>

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