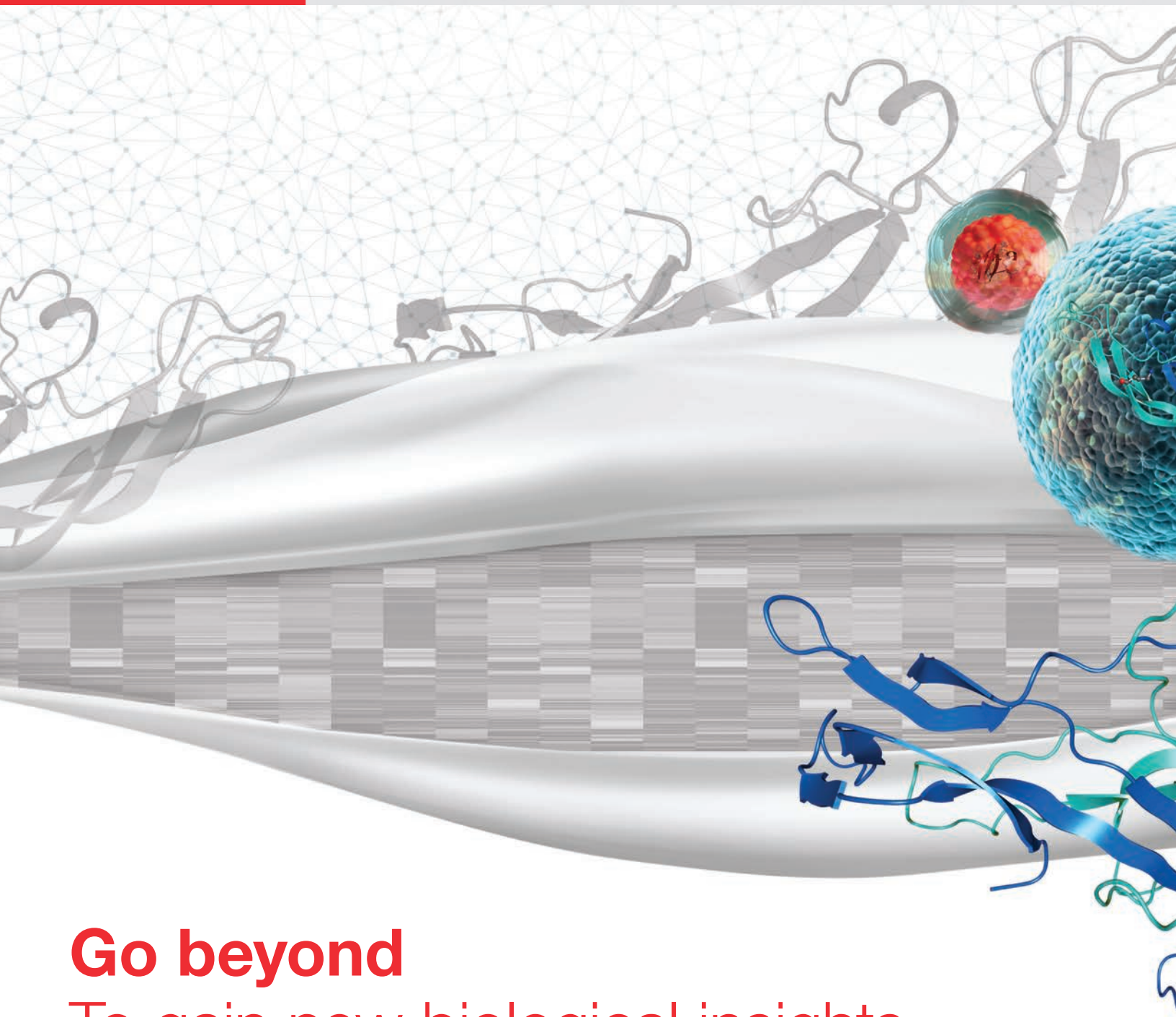


Go beyond

To gain new biological insights

Quantitative proteomics—the new benchmark

ThermoFisher
SCIENTIFIC

Biology is quantitative

Harness the power of quantitative proteomics to gain insights on the dynamic processes that drive the biology of cells, tissues and organisms.

By collaborating with key opinion leaders and the scientific community, Thermo Fisher Scientific is redefining the new benchmark in proteomics—quantifying all identified proteins and delivering high precision and accuracy. And we continue to pursue advancements that deliver confidence and rigor in the results.

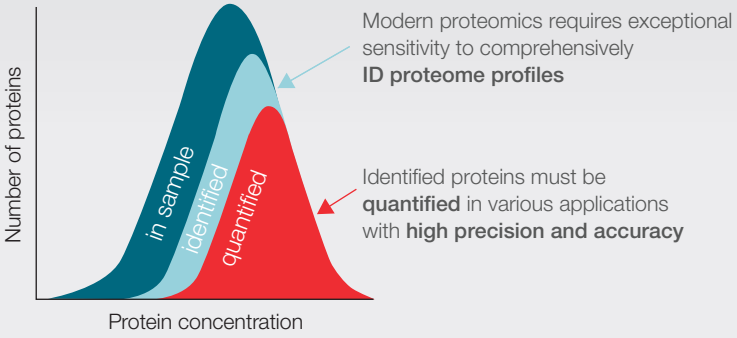
From discovery to development to translational research and validation, we're committed to helping you push the limits of biological innovation.

Qualitative to quantitative proteomics: the new benchmark

For more than 20 years, Thermo Scientific™ mass spectrometers have defined the benchmark in proteomics, cataloging proteins to capture complete profiles of biological systems. While protein identification remains the foundation of all protein research, to truly understand biology, we must move beyond pure identification.

The new benchmark for proteomics requires the precise quantitation of all identified proteins, setting the foundation for bolder hypotheses and deeper understanding. The integration of chromatographic separation methods with a high-resolution detection system (Thermo Scientific™ Orbitrap™ mass spectrometers) on one single platform enables broader, deeper, and faster analysis of complex and diverse proteins—offering a robust system that is more effective than the sum of its parts.

While it began as an almost exclusively qualitative technique, modern proteomics has evolved to span a continuum of qualitative and quantitative approaches.



Paradigm shift in proteomics

Moving quantitative proteomics forward requires an all-in commitment. That's why we, at Thermo Fisher Scientific, have invested in developing fit-for-purpose reagents, software and workflows that live up to the high standards set by our leading instrumentation.

This full suite of complementary tools allows you to explore the functions of individual proteins and protein complexes, determine their places in complex biological systems, and easily translate protein abundance changes. Harness their power to help you turn observations into valuable discoveries.

The core of successful quantitative proteomics: Orbitrap mass spectrometry

Orbitrap mass spectrometers offer leading mass spectrometry (MS) technology for identifying and quantifying complex proteomics samples over a wide dynamic range.

With established sample preparation, chromatographic separation and integrated data analysis tools, Orbitrap mass spectrometers enable researchers to successfully analyze diverse sample matrices with industry-leading sensitivity.

Featured in more than 135,000 peer-reviewed publications, Orbitrap mass analyzer technology has a proven track record as a powerful liquid chromatography-mass spectrometry (LC-MS) platform for proteomics.

Leading-edge quantitative proteomics

Powered by Orbitrap mass spectrometry

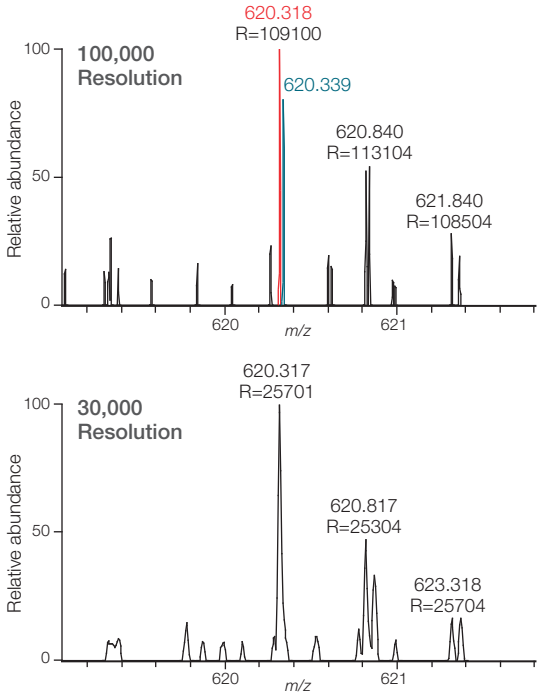
Orbitrap mass spectrometers, renowned for their industry-leading performance, provide high-resolution, accurate-mass (HRAM) measurements and the sensitivity essential for quantitative proteomics. By enhancing your laboratory's high-throughput and quantitative capabilities, this advanced technology broadens comprehension of proteins in biology, biochemistry biomarkers, and precision medicine, thereby facilitating groundbreaking discoveries.

Key attributes of the HRAM Orbitrap mass analyzer enable successful quantitative proteomics

HRAM offers unparalleled precision

With up to 500,000 resolution at 200 *m/z*, Orbitrap mass analyzers enable more confident identification and quantitation. This high specificity allows accurate mass assignments, especially with proteins and peptides of similar mass in complex matrices, as well as in isotope-labeling studies.

High-resolution MS is required to distinguish isobaric co-eluting peptides

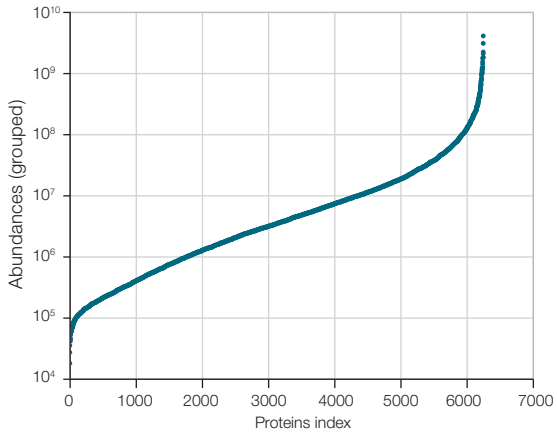


Orbitrap mass analyzer technology offers the simultaneous high-resolution and spectral dynamic range required for label-free quantitation by accurately discriminating between isobaric co-eluting ions and separating analyte signal from noise. In the example above at the 30,000 resolution offered by traditional tools, it is impossible to resolve the co-eluting isobaric peaks at *m/z* 620.317. However, 100,000 resolution reveals two distinct peaks at *m/z* 620.318 and *m/z* 620.339.

Precise sensitivity is crucial for accurate quantitative proteomics

The amounts of different proteins in a given sample can vary by several orders of magnitude, complicating the process of detection and quantitation.

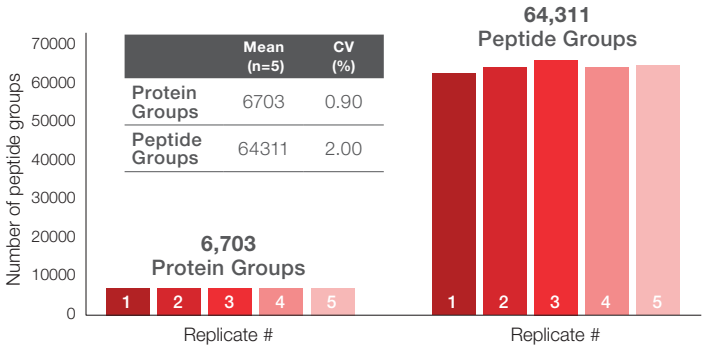
Comprehensive analysis requires tools sensitive enough to accurately record these differences and provide a meaningful view of their biological states. Orbitrap mass analyzer technology enables quantitation down to attamole concentrations, with more than five orders of linear dynamic range and tight coefficients of variation (CV).



This plot shows all proteins detected in a 200 ng HeLa digest using a Thermo Scientific™ Orbitrap Exploris™ 480 mass spectrometer. It plots all detected proteins based on their abundance over five orders of magnitude in dynamic range.

Technical reproducibility adds confidence in results

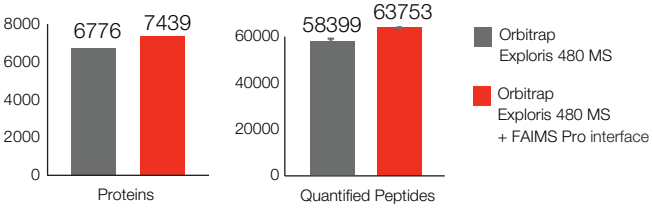
Due to their sensitivity and selectivity, Orbitrap mass spectrometers have become the instruments of choice for proteomics research. Providing accurate and reproducible data from run to run, these reliable tools allow researchers to derive meaningful answers from the large numbers of data sets typically generated in proteomics experiments.

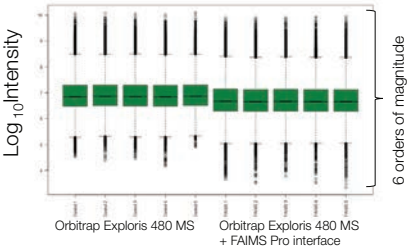


Replicate analysis of 200 ng of HeLa digest on the Orbitrap Exploris 480 MS results in reproducible identifications with CVs of less than 2%.

FAIMS Pro Duo interface offers seamless integration

The growing complexities of quantitative analyses in proteomics demand increasingly sensitive and selective analytical techniques. The Thermo Scientific™ FAIMS Pro Duo interface works seamlessly with next-generation MS technologies to enhance selectivity and enable the identification and quantitation of higher numbers of proteins than ever before. Combining HRAM instrumentation with differential ion mobility methods and orthogonal gas-phase separation techniques can improve proteome profiling as well as label-free and multiplexed protein quantitation. The FAIMS Pro Duo interface reduces the complexity of accumulating and analyzing precursor ions, increasing proteome coverage, decreasing interference and improving quantitative confidence.



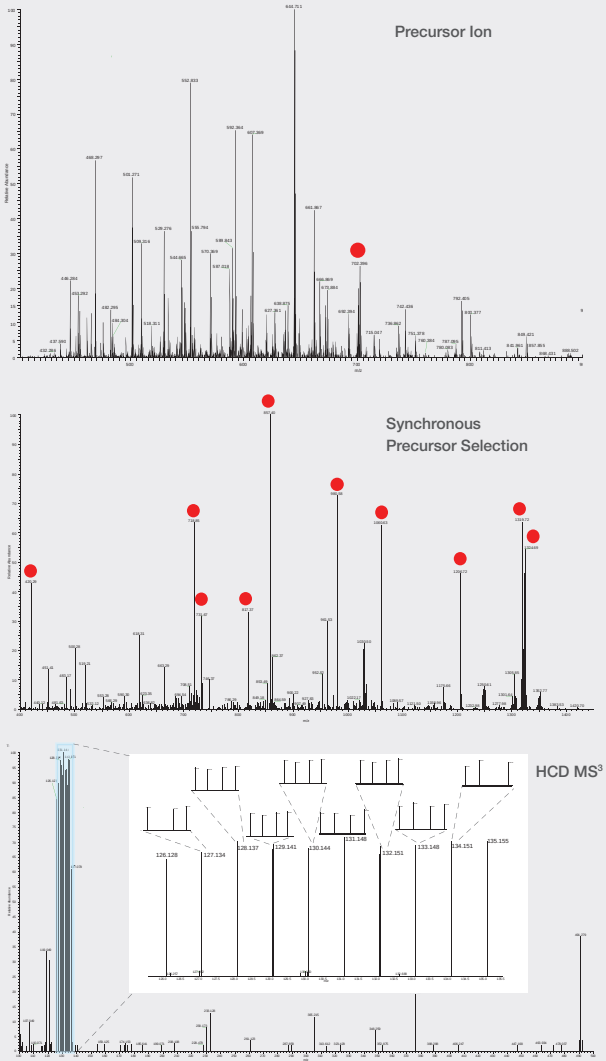


The FAIMS Pro Duo interface increases the quantitation capacity of the Orbitrap Exploris 480 MS across 6 orders of dynamic range quantifying over 7,000 proteins in a 1-hour run with a HeLa digest.

SPS MS³ capabilities allow multiplexed protein quantitation

The Synchronous Precursor Selection (SPS) MS³ multiplexing workflow on Thermo Scientific™ Orbitrap™ Tribrid™ mass spectrometers offers unmatched capability to accurately measure the subtle changes in proteomes for multiplexed proteome analysis.

Compared to MS²-based Tandem Mass Tags™ (TMT) quantitation, SPS MS³ quantitation dramatically increases reporter ion signal intensity and improves ratio accuracy. SPS MS³ provides improved counting statistics that lead to a significant increase in the number of quantified peptides. SPS technology enables the simultaneous isolation of up to 20 MS² fragment ions that undergo higher energy collisional dissociation (HCD) fragmentation along with the MS³ fragments detected in the Orbitrap mass analyzer. This advanced technique further minimizes co-isolated ion interference and ratio compression, compared to MS², providing more accurate results.



SPS MS³ improves experimental throughput and provides the depth and coverage, while eliminating TMT ratio distortions caused by interfering ions.

Multiple targets, unlimited possibilities

Diverse solutions designed to meet your proteomics goals

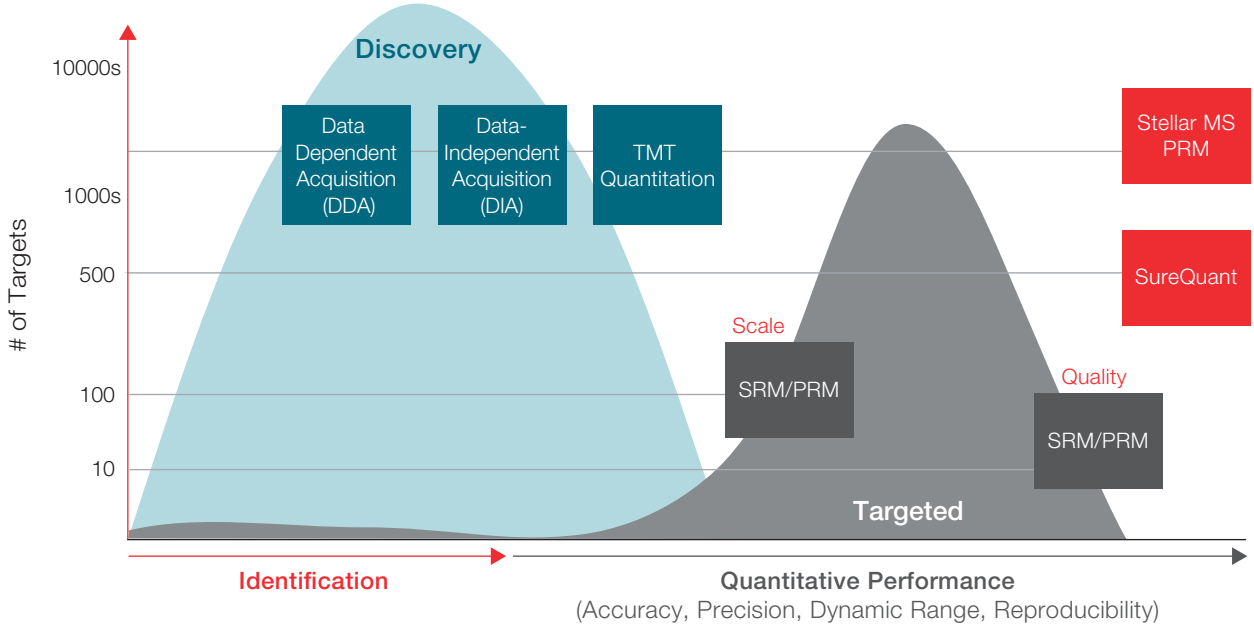
The many advances in MS technologies, software, fit-for-purpose reagents and kits for quantitative proteomics offer a plethora of options for today's researchers. Choosing the workflow best suited to your specific research objectives requires considering the biological goals, sample numbers and costs involved.

Thermo Fisher Scientific's quantitative workflows are designed to quantify all identified proteins with high precision and accuracy, ensuring the confidence and rigor in the results required to enable significant progress in biological research and precision medicine.

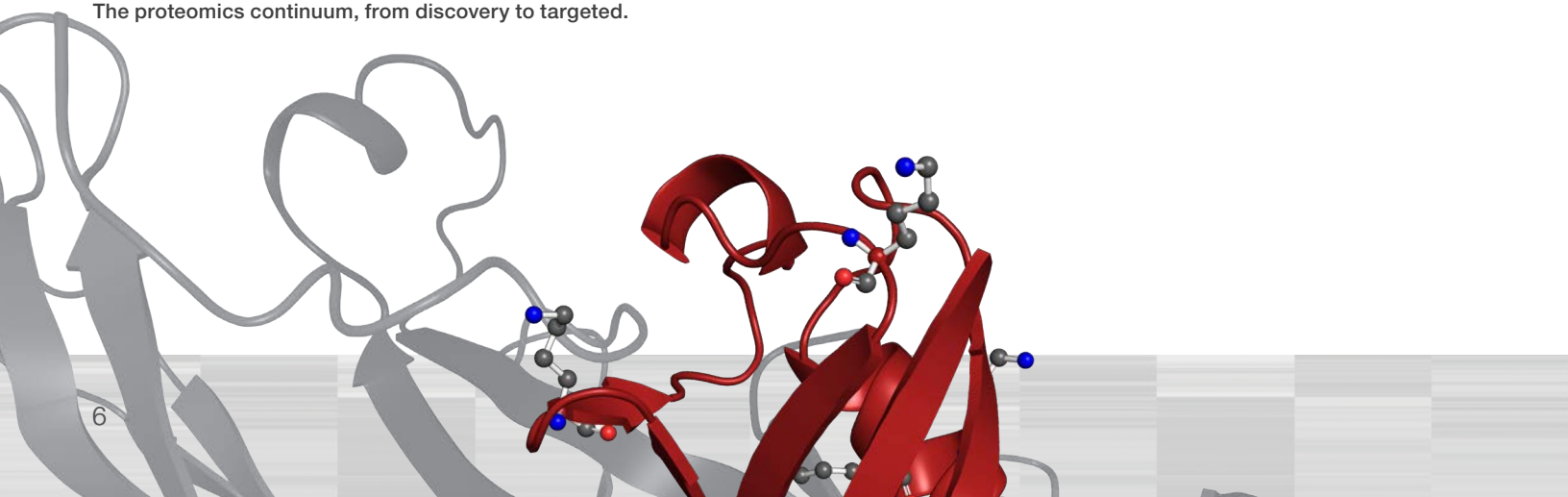
Untargeted versus targeted proteomics

Untargeted proteomics experiments identify as many proteins as possible across a broad dynamic range, while simultaneously measuring the relative abundance changes in these proteins across multiple samples. This process typically occurs during the discovery phase of research. In contrast, targeted proteomics strategies limit the number of proteins monitored while increasing the throughput of hundreds to thousands of samples during the verification and validation phases of research.

Analyzing your specific objectives helps determine whether targeted or untargeted proteomics workflows will be optimal for your work.



The proteomics continuum, from discovery to targeted.



Solutions designed to meet your quantitative proteomics goals

We provide a range of solutions and workflows that are specifically designed to meet your needs.

1 Sample preparation

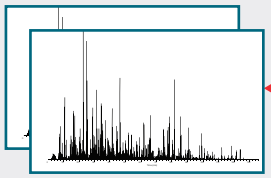
Label-free vs. Label

2 Chromatographic separations

LC: RP (C-18)

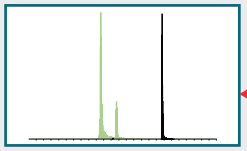
3 Mass spectrometry

Untargeted proteomics
What is the global protein profile of a sample?



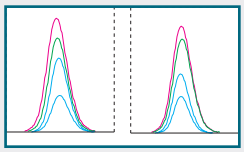
Discovery phase

HRAM detection by Orbitrap mass spectrometry



HRAM detection by Orbitrap mass spectrometry

Targeted proteomics
What are the levels of specific proteins in a sample?



SureQuant method by HRAM Orbitrap MS, PRM on an ion trap mass spectrometer or selected reaction monitoring by triple quadrupole mass spectrometer

4 Data analysis

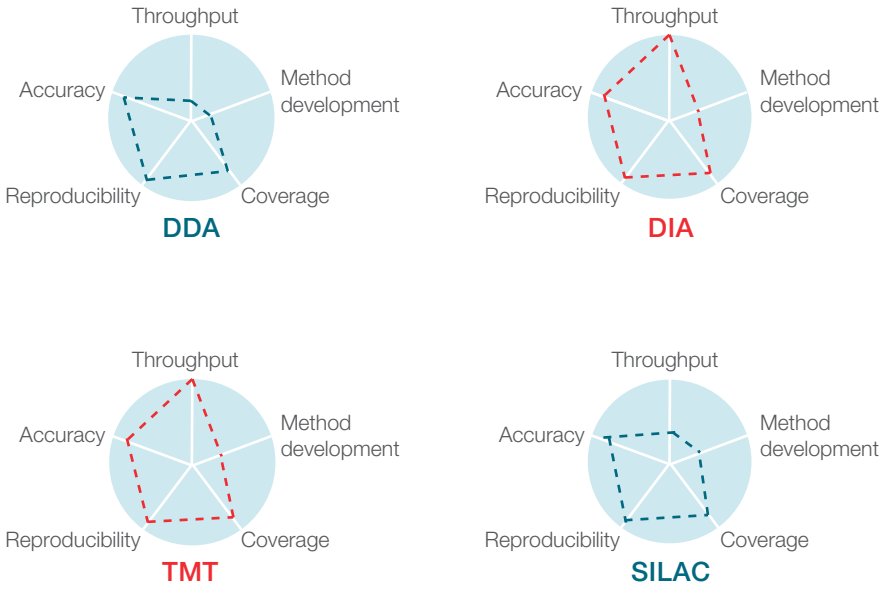
Identification
Quantitation
Statistical analysis
Pathway analysis
Reporting

Statistical analysis
Pathway analysis
Absolute quantitation
Verification
Reporting

Coverage, throughput, method development, reproducibility and precision: how to choose the right approach

Quantitative proteomics relies on a fine balance of proteome coverage, sample throughput, method development, reproducibility and accuracy. Prioritizing these analytical criteria requires tradeoffs, and there is no one-size-fits-all approach.

Versatile Orbitrap MS technology offers researchers the flexibility to choose quantitative workflows that emphasize analytical criteria that are more important to the experiment, based on the biological question and the specific objectives being explored.

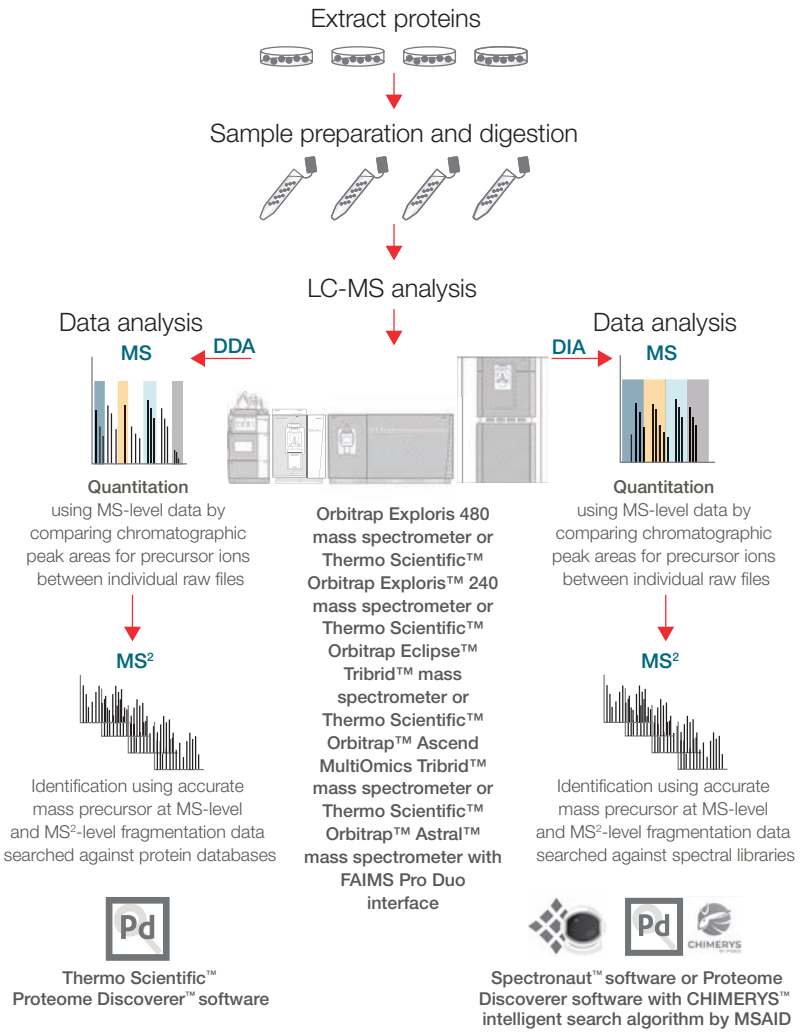


Key factors to consider when selecting the appropriate quantitative proteomics workflow.

Untargeted quantitative proteomics: greater depth of proteome profiling

In discovery-based quantitative analyses, the goal is to identify proteins and measure their relative abundance changes across multiple sample sets, usually on a proteome-wide level. The multiple sample sets could potentially represent different time points in a biological pathway, responses to different stimuli, or different cellular locations.

HRAM Orbitrap MS technology provides the necessary versatility, selectivity, sensitivity and speed for several discovery-based workflows that include both label-free quantitation (LFQ) and stable isotope labeled quantitation approaches.



General overview of the analytical workflow for label-free quantitation.

Label-free quantitation

LFQ is the simplest and most cost-effective way to explore the proteome. This approach offers:

- Deep proteome coverage
- Quantitative accuracy
- Minimal sample preparation
- Relatively large numbers of samples from diverse origins
- Optional FAIMS Pro Duo interface integration to improve depth and quantitative accuracy

LFQ enables the relative quantitation of proteins across multiple samples from any origin. During this process, signals corresponding to unique peptide ions are integrated over the LC time scale, and then different runs are compared and common chromatographic features are aligned.

The high reproducibility offered by HRAM Orbitrap MS and liquid chromatography enable accurate comparisons across samples. The biggest advantage of LFQ compared to other approaches is that it provides an unlimited number of sample comparisons—facilitating new discoveries.

The two types of LFQ approaches differ in how they acquire the identification (MS^2) data. Data-dependent acquisition (DDA) is ideal when analytical robustness and the highest level of data precision are the main priorities, and when working with small to medium sample sizes. In contrast, data-independent acquisition (DIA) is able to rapidly identify and reproducibly quantify all ions within an LC-MS analysis, making this process uniquely suited for large-scale studies.

When to choose LFQ DDA

- Small and medium sample sets
- Unlabeled samples
- Preliminary quantitation studies
- Unlimited instrument time

When to choose LFQ DIA

- Relatively large sample sets
- Unlabeled samples
- Preliminary quantitation studies
- Unlimited instrument time
- Ideal for short LC gradients
- Unbiased sampling
- No missing values

Stable Isotope Labeling with Amino Acids in Cell Culture (SILAC)

Measuring differential changes in proteomes with more quantitative accuracy

SILAC offers numerous advantages:

- Deep proteome coverage
- Less variability between samples
- Multiplexing for increased throughput and sensitivity
- Compatibility with any fragmentation method

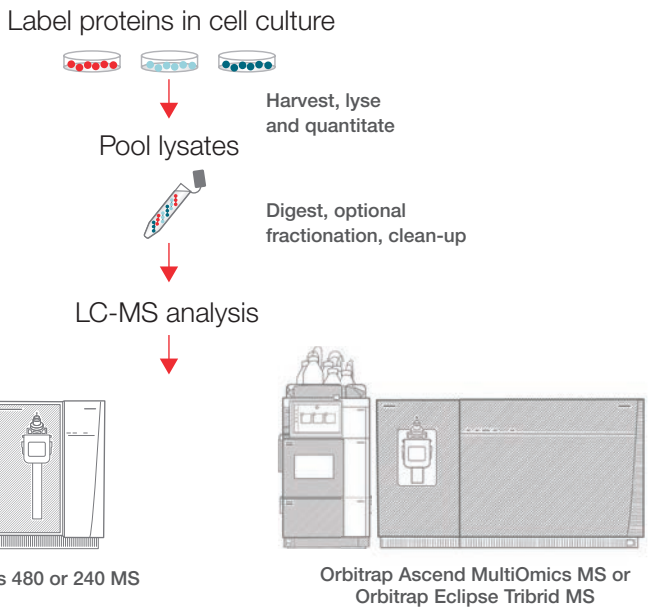
When to choose SILAC

- Relatively small sample set (n ≤ 3)
- The priority is to minimize variability across samples

SILAC is a powerful method for identifying and quantifying relative differential changes in complex protein samples. The SILAC method involves *in vivo* metabolic incorporation of "heavy" ^{13}C- or ^{15}N-labeled amino acids into proteins, followed by HRAM Orbitrap MS analysis. This process offers accelerated and comprehensive identification, characterization, and quantitation of proteins.

Thermo Scientific™ SILAC Protein Quantitation Kits contain all reagents necessary for successful isotope metabolic protein labeling. This complete package enables accurate quantitation of protein expression levels from differentially treated cell populations.

Thermo Scientific™ SILAC Protein Quantitation Kits



General overview of the analytical workflow for SILAC quantitation.

Multiplexed quantitation with Tandem Mass Tag Reagents

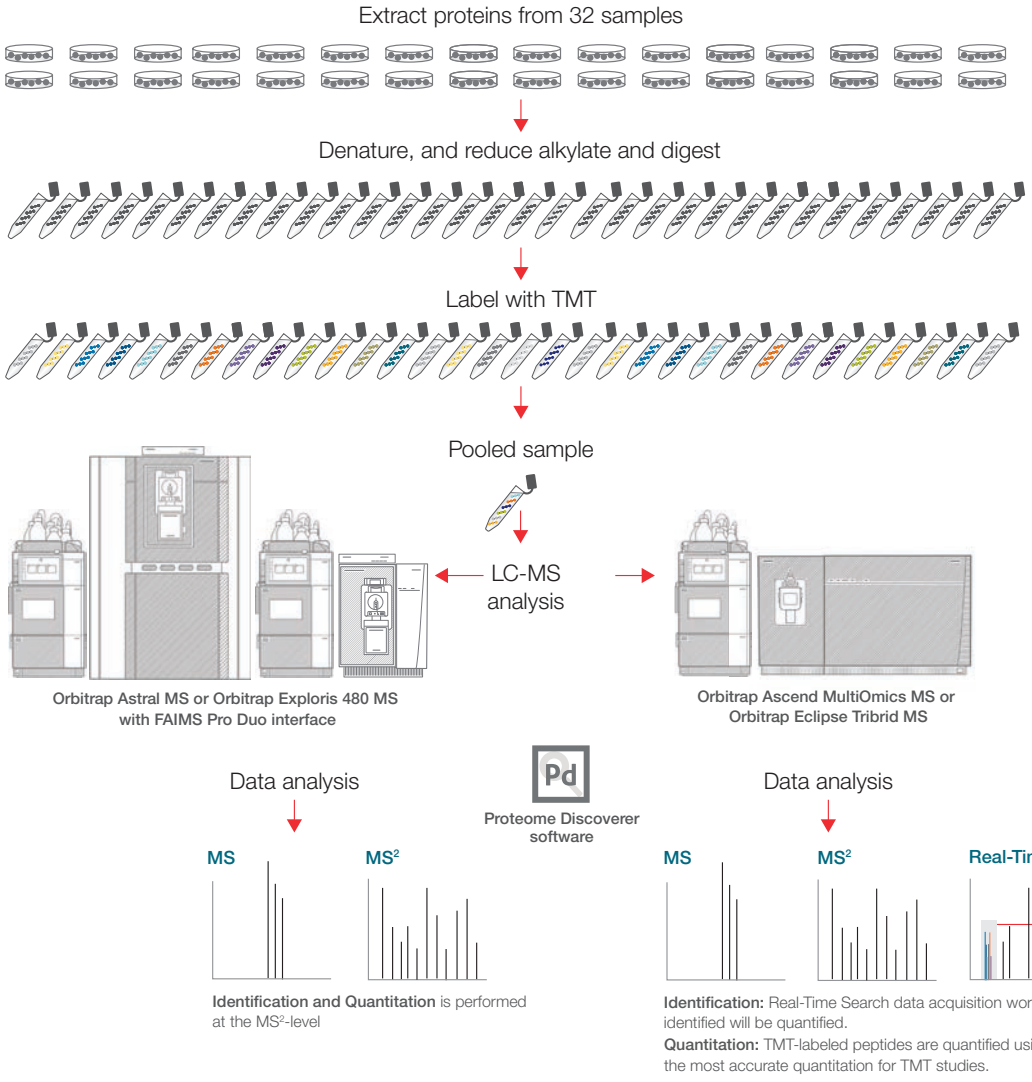
Multiplying the power of proteomics to explore any objective

Advantages of TMT include:

- Deepest proteome coverage of any available method
- Less variability between samples
- Highest quantitative accuracy with optional FAIMS Pro Duo interface
- Up to 32-plex for maximum throughput and sensitivity in a single LC-MS run
- Suitable for diverse samples and applications
- Thermo Scientific™ Real-Time Search data acquisition workflow adds throughput and confidence

Isobaric tagging strategies using Thermo Scientific™ Tandem Mass Tags are powerful tools for simultaneous identification and quantitation of proteins in multiple sample sets. The multiplexed quantification workflows enable the analysis of up to 32 samples in a single LC-MS experiment. Leveraging intelligent acquisition schemes built into the HRAM Orbitrap mass spectrometers allows the quantification of proteins with the highest possible confidence, accuracy and precision.

Thermo Fisher Scientific offers a wide selection of TMT kits that contain all of the reagents needed to pursue your experimental objectives, whether you're comparing two samples in a small profiling study or 32 samples in complex analyses with multiple conditions (e.g., time courses, dose responses, replicates and multiple-sample comparisons).



General overview of the analytical workflow for TMT quantitation.

Thermo Scientific™ TMTpro 32-plex Label Reagent

When to choose TMT

- Relatively large sample set
- Instrument time is limited
- A quick turnaround time is required

Targeted quantitative proteomics: a new paradigm in protein quantitation

The goal of targeted quantitative analyses is to investigate selected protein targets from discovery or hypothesis-driven studies to understand biological pathways or the verification and selection of biomarkers across large numbers of samples from multiple biological sources and conditions.

Targeted analyses require a fast, robust and cost-effective platform, and both the HRAM Orbitrap mass spectrometers and Thermo Scientific™ TSQ™ triple quadrupole mass spectrometers are ideally suited for the role.

SureQuant IS targeted protein quantitation workflow

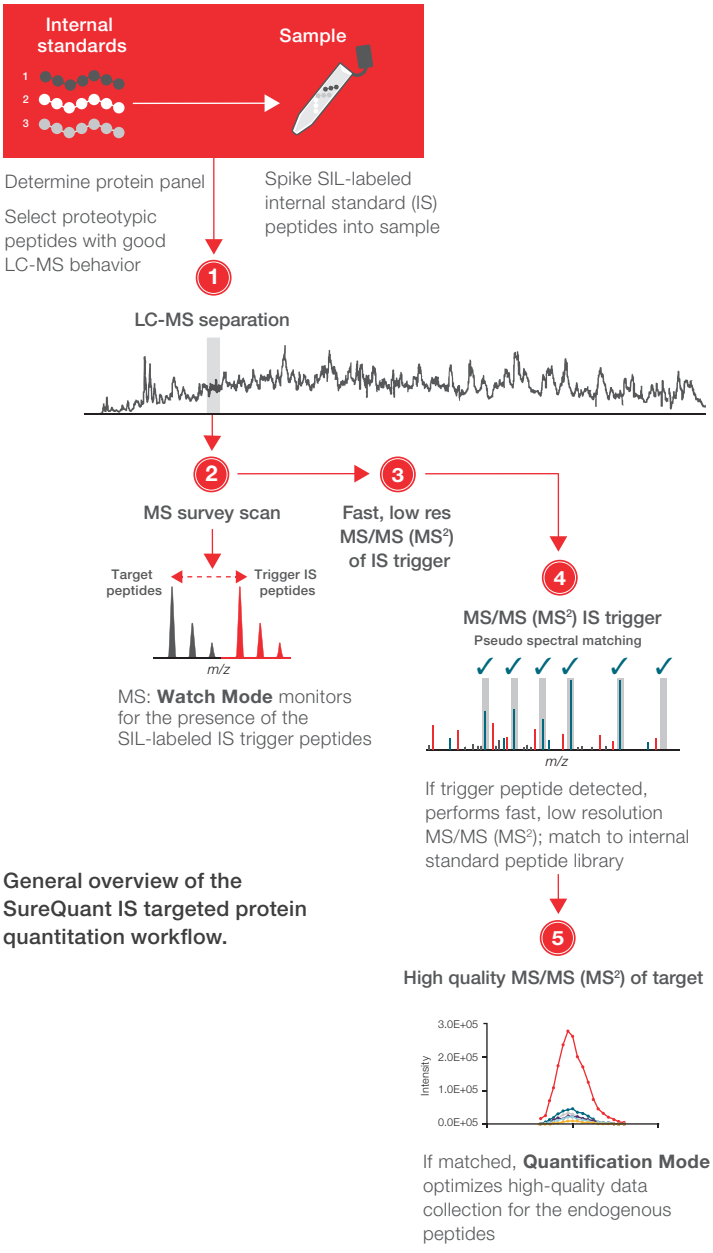
Quantifying more targets in complex matrices with confidence and precision

Advantages of Thermo Scientific™ SureQuant™ IS targeted protein quantitation workflow include:

- High sensitivity
- Quantitative specificity
- High accuracy and precision
- Ability to identify and quantify several hundred targets
- Thermo Scientific™ SureQuant™ Targeted Assay Kits include all the standards and reagents required for monitoring and quantitation
- Kit-specific and custom method templates to fit any experimental objectives
- Built in verification is generated with full MS/MS spectra for the targeted peptide

The SureQuant IS targeted protein quantitation workflow leverages labeled internal standard peptides to guide the acquisition of MS/MS spectra for endogenous peptides in real time. This leading-edge method enables the monitoring and quantitation of target peptides and identification with MS/MS spectra with easy setup and high confidence results.

The high selectivity of HRAM Orbitrap mass spectrometers has enabled a new paradigm for targeted proteomics. Its extremely sensitive approach is able to quantify hundreds of protein targets in complex matrices with high quantitative accuracy, precision and specificity—opening the door for new discoveries.



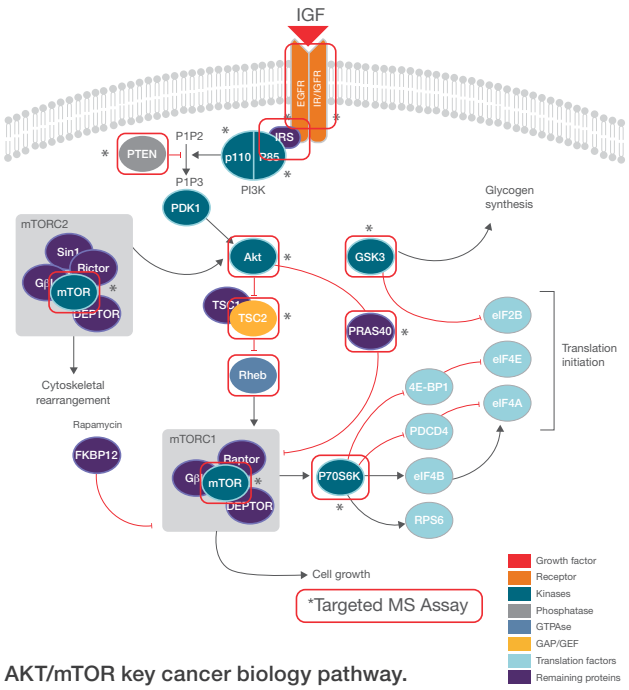
General overview of the SureQuant IS targeted protein quantitation workflow.

When to choose a SureQuant IS targeted workflow

- Targeting proteins as panels in complex pathways of matrix
- Hundreds of protein targets
- Limited instrument time

Sensitive, accurate, precise and more complete targeted protein analysis

Compared to traditional methods, the SureQuant method increases resolution and ion fill time without compromising cycle time, resulting in higher sensitivity and more reliable detection of peptide targets. The SureQuant method can also monitor large panels of proteins, such as in plasma with the PQ500 human plasma kit (Biognosys AG, Schlieren, Switzerland). Its outstanding dynamic range and quantitative precision make it possible to increase throughput without any loss in reproducibility.



AKT/mTOR key cancer biology pathway.

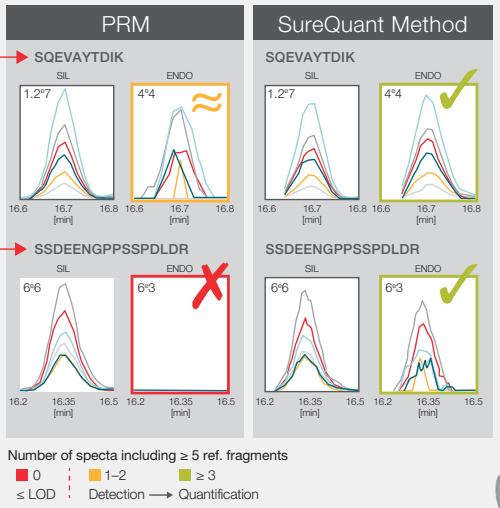
The new gold standard: Intelligence-driven acquisition for the highest quantitative performance

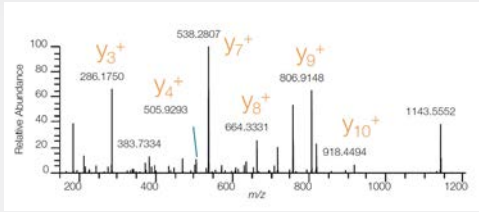
By leveraging SureQuant Targeted Assay Kits, the SureQuant method provides an easy-to-use assay that delivers the quantitation of more targets without compromising sensitivity. An intelligence-driven acquisition scheme, the SureQuant method uses internal standards to guide and dynamically manage the quantitation of peptide targets, while maintaining the highest accuracy and precision.

Compared to parallel reaction monitoring (PRM) methods, the SureQuant method increases resolution by a factor of four and fill time by a factor of six, without compromising cycle time. The result is higher sensitivity and more reliable detection of targets, as shown here for peptides from the protein targets GSK3α and AKTS1 from the AKT/mTOR pathway—a key cancer biology pathway.

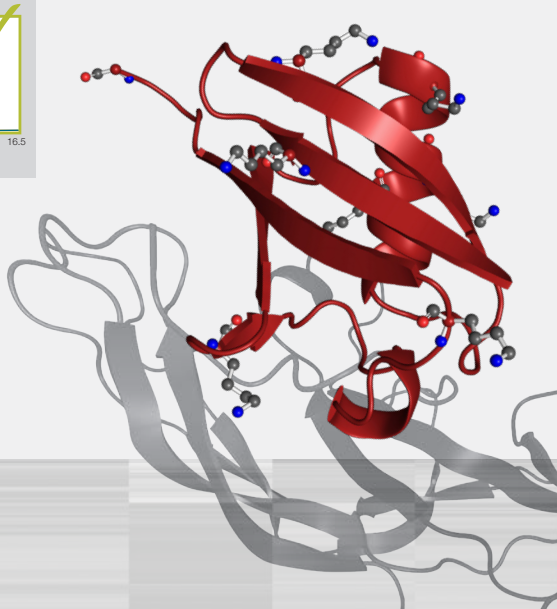
Peptide	PRM Method	SureQuant Method
AENGPGPGVLVLR	1	15
AQEALDFYGEVR	10	11
DGFYPAPDFR	0	1
ETSFNQAYGR	2	6
FEISETSVNR	0	9
GALAEAAR	5	13
GNNLQDTLR	0	6
GQPEGPLPSSSPR	0	8
GYTISDSAPSR	0	5
IDIHSC[Carbamidomethyl]NHEAEK	1	12
IYNLC[Carbamidomethyl]AER	0	15
LC[Carbamidomethyl]DSGELVAIK	5	15
LFDAPEAPLPSR	11	11
LLEYTPTAR	0	15
LPFYNQDHER	0	17
LVPPFKPQVTSETDTR	0	0
NDGTFIGYK	0	13
NNIDDVVR	0	4
SDGSFIGYK	0	13
SNPTDIYPSK	0	9
SQEVAYTDIK	1	9
SSDEENGPPSSPDLDR	0	8
SVSAPQQIINPIR	0	0
TFHVDTPEER	0	0
TGIAAEEVSLPR	0	0
TLDQSPELR	2	10
TPPEAIALC[Carbamidomethyl]SR	1	20
TTINNEYNYR	0	7
VTTVVATLGQGPER	6	15
YSFQTHDR	0	10
# of endogenous peptides detected	11/30	26/30

From cancer pathway to reliable assay.





Built-in verification is generated with MS/MS spectrum for the targeted peptide GALAEAAR.



Selected reaction monitoring targeted workflow

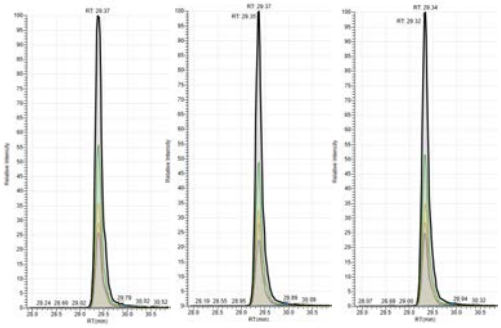
When your experimental objectives require the highest possible sensitivity

Advantages of the selected reaction monitoring workflow include:

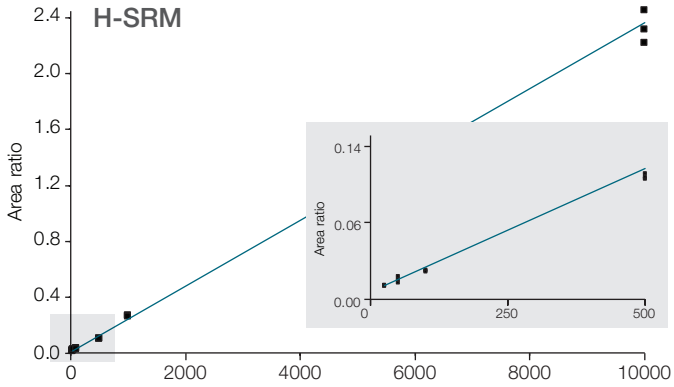
- Highly sensitive
- Highly robust
- Cost-effective, dedicated system for quantitation
- Able to accurately and precisely quantify large numbers of samples while targeting several hundreds of analytes
- Superior quadrupole specificity with H-SRM
- Combines with FAIMS Pro Duo interface to enhance selectivity and sensitivity to peptides

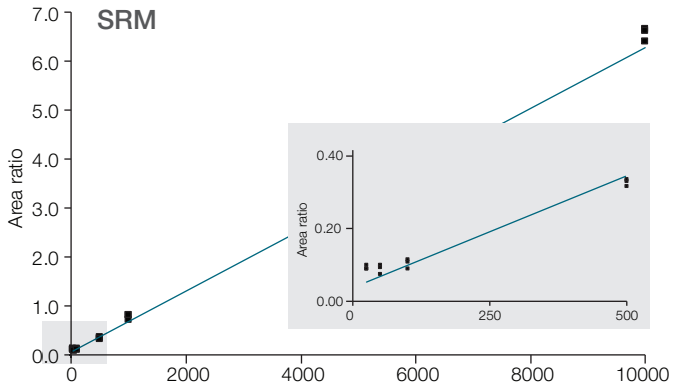
Selected reaction monitoring (SRM) quantitation is extremely sensitive, reliable and proficient at analyzing large numbers of well-characterized analytes and samples. Peptides unique to the protein of interest are selected for targeted quantitation using a triple quadrupole mass spectrometer. SRM can be used to perform absolute quantitation of targeted proteins by incorporating the appropriate stable isotope-labeled peptides as internal standards. Absolute quantitation can provide precise determination of protein expression and post-translational modification levels, and allows comparison between samples and studies.

The Thermo Scientific™ TSQ Altis™ Plus triple quadrupole mass spectrometer is the only triple quadrupole MS capable of performing high-resolution SRM (H-SRM). Using 0.2 Dalton resolution for precursor ion selection, the TSQ Altis Plus MS dramatically reduces chemical interference while maintaining high transmission efficiency. With short dwell times and ultrafast SRM speed (up to 600 SRMs/sec), the TSQ Altis Plus MS allows researchers to analyze more peptides per sample, accelerating the pace of discovery.



Triplicate analysis of peptides in human plasma tryptic digest.

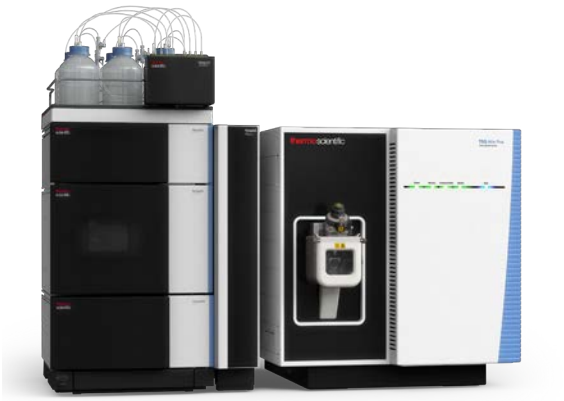




The two figures demonstrate the superior sensitivity of TSQ Altis MS for GPSVFPLAPSSK when operating in H-SRM mode (0.2 Da FWHM).

When to choose SRM

- Well-characterized targets
- Large number of samples
- Priority is superior sensitivity, precision and accuracy
- Cost-effectiveness is important



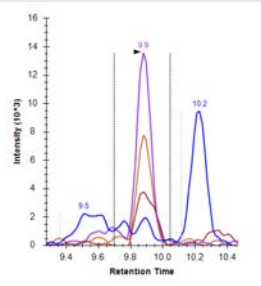
Thermo Scientific™ Vanquish™ Horizon UHPLC system with the TSQ Altis Plus triple quadrupole mass spectrometer.

Enhanced targeted peptide quantification with FAIMS Pro interface

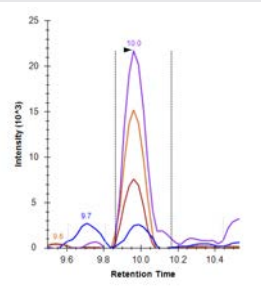
Combining the TSQ Altis MS with the FAIMS Pro interface improves the signal-to-noise ratio, and therefore sensitivity, in assays compromised by chemical background. The example below highlights tryptic peptides from *E. coli* at 5e4 CFU/mL in urine, analyzed with and without the FAIMS Pro interface.

ILEVPVGR

Standard Setup

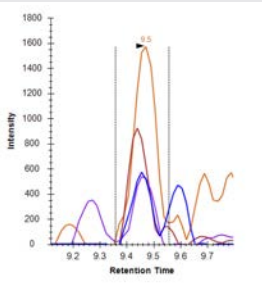


FAIMS Pro interface

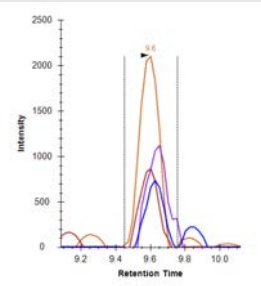


AYGSTNPINVVR

Standard Setup



FAIMS Pro interface

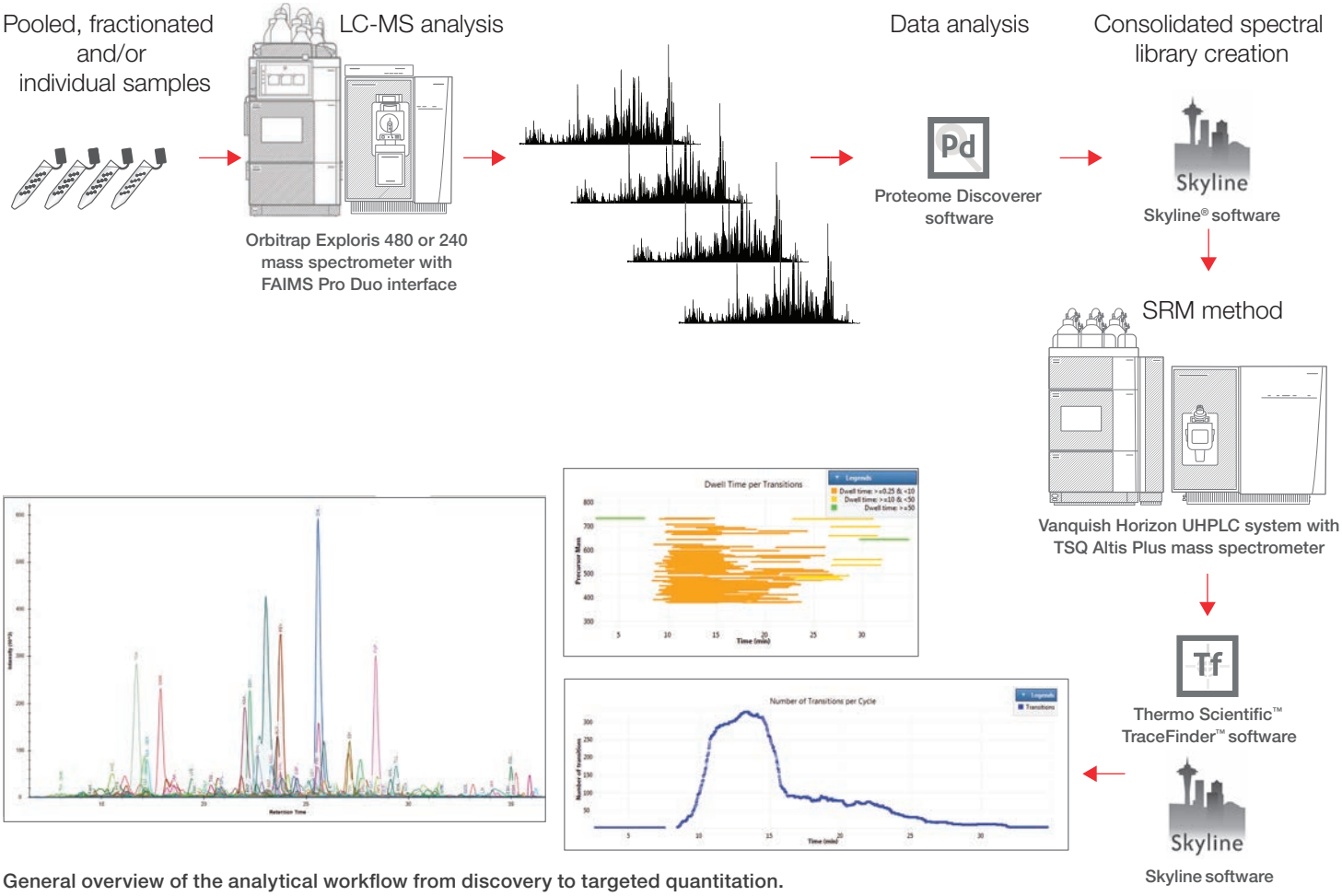


Tryptic peptides from *E. coli* at 5e4 CFU/mL in urine, analyzed with and without the FAIMS Pro interface.

Accelerating the transition from discovery to validation: SRM targeted quantitation

The big challenge of proteomics is the validation of protein biomarkers across a large biological sample set. Thermo Fisher Scientific offers leading technology that enables researchers to quickly progress from discovery to validation.

The superior reliability, speed and sensitivity of the TSQ Altis Plus MS, combined with Orbitrap mass analyzer technology and market-leading software tools, ensure a fast and cost-effective development of high-throughput assays.



General overview of the analytical workflow from discovery to targeted quantitation.

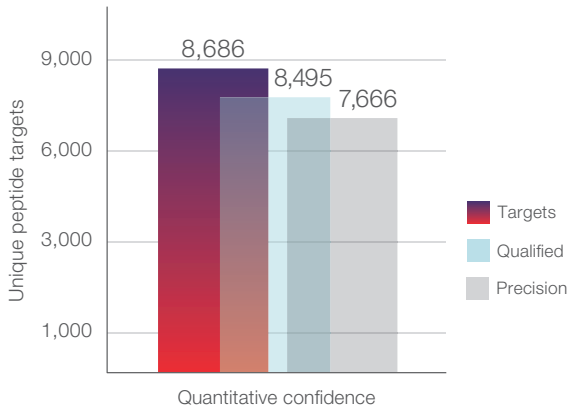
Discovery to validation at unprecedented scale

A new standard for targeted quantitation with PRM on Stellar mass spectrometer

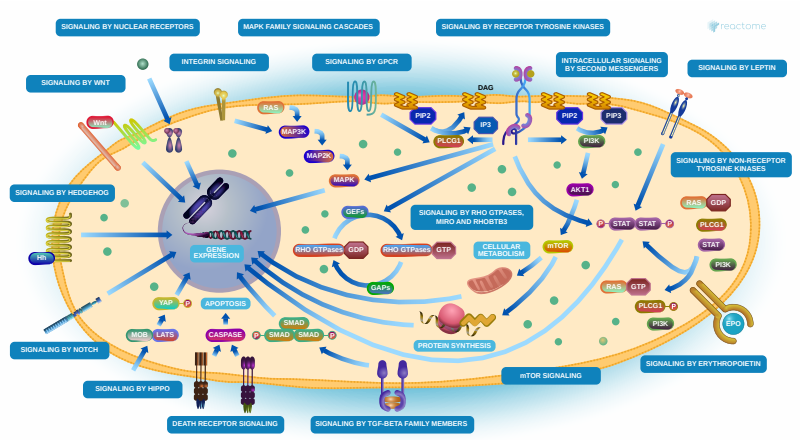
Advantages of PRM on Thermo Scientific™ protein quantitation workflow include:

- High sensitivity
- High quantitative specificity, accuracy and precision
- High throughput. biased systems biology analysis by confidently quantifying nearly 10,000 peptides/hour
- Overcomes challenging background matrices by using fast and sensitive full-scan Synchronous Precursor Selection (SPS) MS3 acquisition
- Accelerate targeted method creation and implementation via PRM Conductor

The Stellar mass spectrometer offers higher acquisition rates, enabling the analysis of more peptide targets than existing selected reaction monitoring or parallel reaction monitoring instruments.



The total number of targeted peptides reproducibly measured across technical replicates (red) as compared to the number of targeted peptides measured with CV values ≤50% (light blue), and the number of targeted peptides measured with CV values ≤20%.



This is achieved through faster acquisition rates and real-time chromatogram alignment, which adjusts for retention time drift and allows for narrow time-scheduled acquisition windows. Combining a quadrupole mass filter, collision cell, and linear ion trap architecture, the Stellar MS achieves acquisition rates of 70-100 Hz, targeting 5000 to 10000 peptides per hour.

The Stellar MS was employed for the discovery and targeted quantitative analysis of digested extracellular vesicles (EV) extracted from a donor pool with neurodegenerative decline. For the creation of the targeted library, 500 ng of the EV digest was loaded onto a column and analyzed using LC-DIA MS with 100 sequential 2 Th-wide DIA scan events. Four replicate injections were conducted over a precursor m/z range of 400–1,200 Da. The resulting DIA data were processed using Proteome Discoverer software, and the search results were uploaded into Skyline for filtering and targeted-MS2 (tMS2) method creation via the Thermo Scientific™ PRM Conductor tool. This process filtered the 11,092 identified peptides down to a final set of 8,686 based on user-defined LC and MS criteria. Replicates were analyzed to assess the reproducibility of the tMS2 method.

Samples courtesy of Prof. Michael J. MacCoss, University of Washington.

When to choose a Stellar MS PRM workflow

- Targeting proteins as panels in complex pathways of matrix
- Characterization of multiple signaling pathways
- Thousands of protein targets
- Overcoming challenging backgrounds
- Low-input samples

Streamlined data analysis solutions

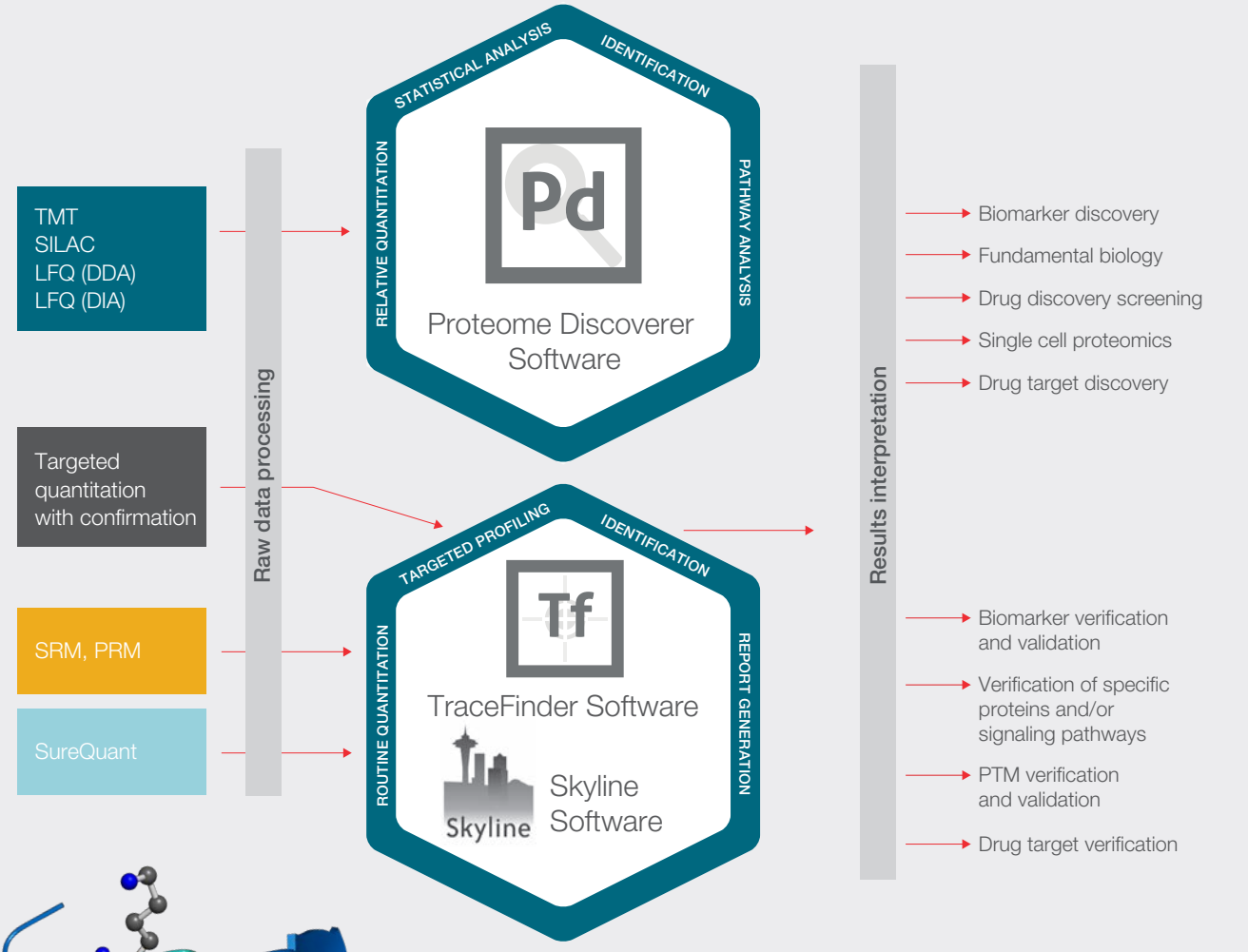
Delivering the total package of validated tools

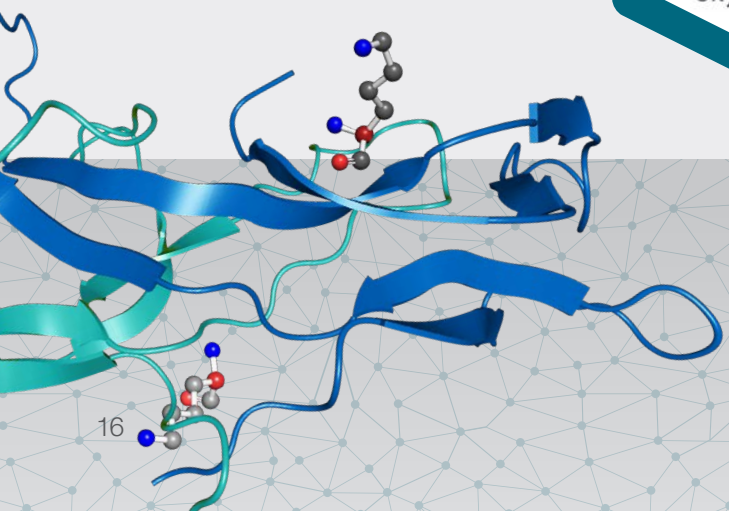
To live up to the high standards set by our leading instrumentation, Thermo Fisher Scientific has invested heavily in developing new qualitative and quantitative software. This innovative technology upholds the same values of quality, usability and performance that have earned us the trust of labs worldwide.

Our premier suite of integrated applications is designed to take you quickly from data acquisition to interactive analysis and interpretation of results. Customize your workflow with flexible architecture to match your objectives and number of samples.

Tailor your approach to prioritize the most important analytical criteria. Depend on the highest possible degree of precision, accuracy and rigor.

Together, Thermo Fisher Scientific tools are the total package your lab needs to explore bolder hypotheses, perform increasingly complex analyses and lead the way to high-impact discoveries.





User-friendly software experience

Proteome Discoverer software

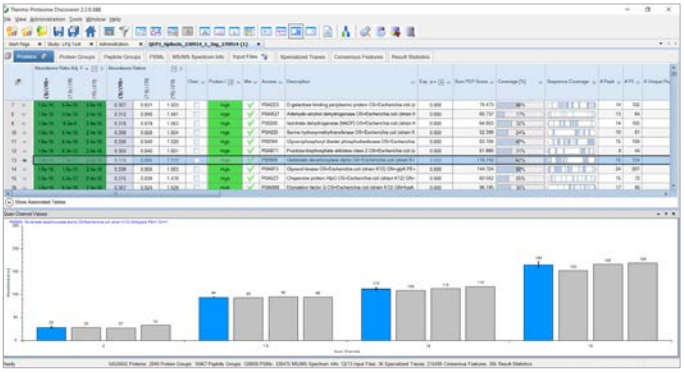
Proteome Discoverer software is a client-server application that uses workflows to process and report mass spectrometry data, and its versatility allows labs to push their discoveries further, faster. Proteome Discoverer software handles a wide range of qualitative and quantitative proteomics workflows to enable either relative or absolute quantitation. It supports multiple database search algorithms and multiple dissociation techniques for more comprehensive analyses. Additionally, it supports third-party nodes to handle data processing. This unlimited flexibility makes it easy to customize a workflow to your proteomics goals.

Versatile, powerful quantitation

Whether you plan to conduct relative or absolute quantitation, Proteome Discoverer software offers options:

- Isobaric mass tagging (TMT, iTRAQ)
- Isotope labeling (SILAC)
- Heavy-peptide techniques
- Protein and peptide identification
- PTM analysis
- LFQ (DDA, DIA, WWA)

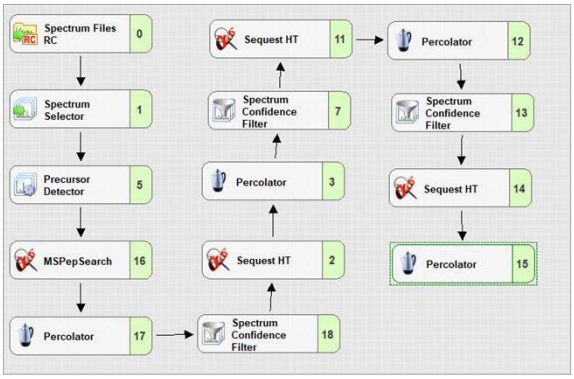
With reliable statistics, the innovative system makes it easy to validate quantification results visually. It also enables the processing of large data sets.

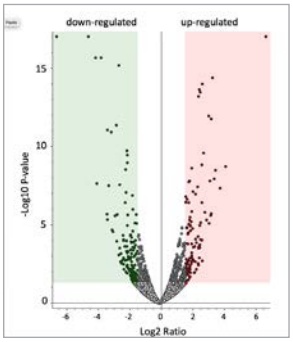


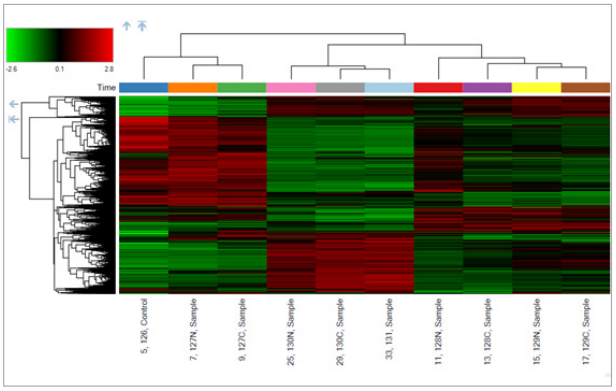
Easily customized workflows

Ready-made optimized workflows allow you to hit the ground running, while the flexible node-based workflow editor lets you create custom workflows for processing complex data sets with optimal search parameters and multiple dissociation techniques (CID, HCD, ETD and EThcD).

Integrate database search results from multiple search engines such as SEQUEST HT, Mascot, MS Amanda and Byonic to identify more proteins. Enhance confidence in peptide identification and quantification with INFERYS Rescoring, and enable deeper exploration of your DIA, DDA, or WWA data using the CHIMERYS 2.0 intelligent search algorithm.







Find and visualize real differences

Proteome Discoverer software makes it easy to visualize results in a meaningful way to quickly find real statistical differences—the differences that matter—between sample sets.

Customizable data visualization allows you to review only the data you choose, and configurable layouts let you quickly change between views. The software also retrieves GO and protein family annotations to illuminate the biological context of the identified proteins and allow a deeper understanding of the results.

Unlock the future of proteomics

Bring your laboratory into a new era of connectivity with the Ardia Platform

Benefits of Thermo Scientific™ Ardia Platform:

- Centralized data management with automated transfer of data and results to an expanding array of software tools
- Data security
- Instrument management

Over the years, the throughput, sensitivity, and sophistication of mass spectrometers have significantly advanced, yielding results with increasingly rich biological information for proteomics datasets. As we gather more meaningful data, new challenges arise in data management, security, throughput, and collaboration. The Ardia Platform consolidates scientific data and results into a centralized location, allowing users to interface with data intuitively, automate processing, and seamlessly share results with colleagues and collaborators. Engineered to adapt to your evolving requirements, the Ardia Platform seamlessly integrates with an expanding array of software tools and applications, facilitating direct data access and automated data transfer. This enables you to leverage a unified platform, effectively eliminating data silos. The platform automates the transfer of data and results from Thermo Scientific software, such as Xcalibur and Proteome Discoverer software, as well as from third-party applications through the Ardia Data Sync functionality. This creates an open ecosystem that enhances your collaboration, discovery, and research clarity and effectiveness.

Through streamlined proteomics analysis, data is collected and automatically uploaded to the Ardia Platform. It is then processed using Proteome Discoverer software, and the results are automatically returned to the platform for secure storage.

Reagents for quantitative proteomics

Trusted tools and reagents to prepare samples for mass spectrometry

Thermo Scientific™ Pierce™ TMT11plex Yeast Digest Standard

A ready-to-use lyophilized yeast peptide mixture of four congenic strains labeled with TMT11plex reagents to monitor LC-MS² system performance for TMT quantitation and MS optimization and validation.

TMTpro 32-plex Label Reagent Set

The next generation of tandem mass tags, designed to increase the level of sample multiplexing up to 32 without compromising on protein identification and quantitation. After MS² fragmentation, each TMTpro tag generates a unique reporter mass used for the relative quantitation of protein expression levels. These TMTpro 32-plex label reagents are ideal for analyses of multiple protein samples, such as inhibitor dose-response experiments, time-course experiments, thermal shift assays or biological replicates.

SureQuant Targeted Assay Kits

The kits enable multiplex immunoprecipitation to mass spectrometry (mIP-MS) for the simultaneous enrichment and quantitation of multiple total and phosphorylated proteins (13 in total, including 11 phosphorylated states) in the AKT/mTOR signaling pathway. Each multiplex panel contains two modules:

1. IP and MS sample prep module to immunoenrich AKT/mTOR pathway proteins and perform in-solution MS sample preparation.

2. Absolute or relative quantitation module, which includes a system suitability standard and AQUA Ultimate Heavy and/or Light Peptide mixtures.

Thermo Scientific™ HeavyPeptide™ AQUA Custom Peptide Synthesis Service

Provides isotopically labeled, AQUA-grade peptides for the relative and absolute quantitation of proteins at very low concentrations in complex mixtures. All HeavyPeptide sequences come with MS analysis and analytical HPLC data. A wide range of labels, modifications, scales and purities allows you to choose the optimal tool for your experimental objectives.

Thermo Scientific™ SILAC Protein Quantitation Kits with DMEM, DMEM:F12 or RPMI 1640

Contains all reagents necessary for successful isotope metabolic protein labeling, enabling the quantitation of protein expression levels from differentially treated cell populations. SILAC is a simple and accurate method for quantifying differential changes in the proteome, and this comprehensive kit allows efficient, precise analysis.

Thermo Scientific™ EasyPep™ Mini MS Sample Prep Kit

Provides pre-formulated reagents and a robust method for preparing high-quality samples for MS analysis in less than three hours. The kit is optimized to process protein samples from 10 to 100 µg with a high yield of MS-ready peptides, improving reproducibility while saving hands-on and processing time. The resulting high-quality peptides are also compatible with TMT labeling and other downstream applications.

Thermo Scientific™ EasyPep™ Magnetic MS Sample Preparation Kits and Proteomics Magnetic Clean-up Beads

EasyPep Magnetic MS Sample Preparation Kits and Proteomics Magnetic Clean-up Beads contain MS-compatible magnetic beads specifically designed to tolerate harsh MS sample prep conditions to improve sample quality and reproducibility for both manual and automated sample preparation methods.

A comprehensive portfolio

Our complete Thermo Scientific quantitative proteomics lineup

A validated global suite of resources

Thermo Fisher Scientific is a partner in the life sciences, providing innovative quantitative solutions to address the challenges of biological research. We enable customizable end-to-end workflows with fit-for-purpose reagent kits, column chemistries, separation systems, mass spectrometry and integrated software. For targeted routine analyses, the Stellar MS and TSQ Altis Plus triple quadrupole mass spectrometer completes the lineup with leading HRAM Orbitrap mass spectrometers.

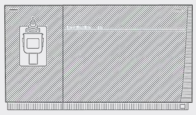
Column and reagents lineup

- Thermo Scientific™ EASY-Spray™ LC columns
- Thermo Scientific™ µPAC™ Neo HPLC columns
- SILAC Metabolic Labeling systems
- SureQuant Targeted Mass Spec Assay Kits
- TMTpro 32-plex Label Reagents

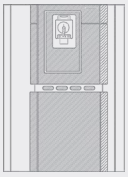
Software lineup

- Proteome Discoverer software
- TraceFinder software
- Ardia Platform

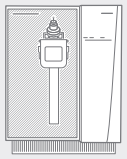
Instrument lineup



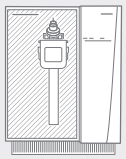
Orbitrap Ascend MultiOmics mass spectrometer



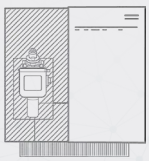
Orbitrap Astral mass spectrometer



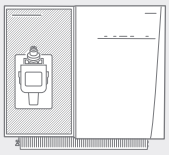
Orbitrap Exploris 480 mass spectrometer



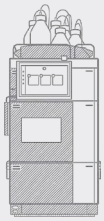
Orbitrap Exploris 240 mass spectrometer



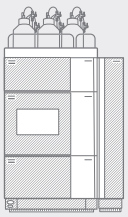
Stellar MS



TSQ Altis Plus triple quadrupole mass spectrometer

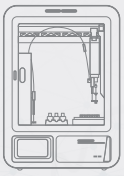


Thermo Scientific™ Vanquish™ Neo UHPLC system

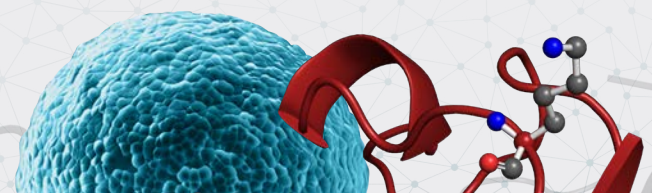


Vanquish Horizon UHPLC system

FAIMS Pro Duo interface



Thermo Scientific™ AccelerOme™ automated sample preparation platform



thermo scientific

Ardia Platform

Discover our interconnected and collaborative software environment, designed to unify an ever-expanding collection of software tools and applications. This platform centralizes scientific data and results, enhances instrument utilization, and speeds up data analysis

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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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