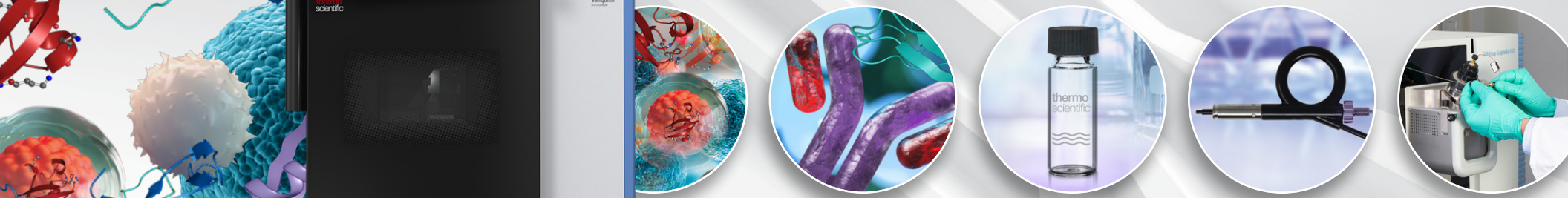
ebook

Vanquish Neo UHPLC System

Boost your proteomics sensitivity and throughput



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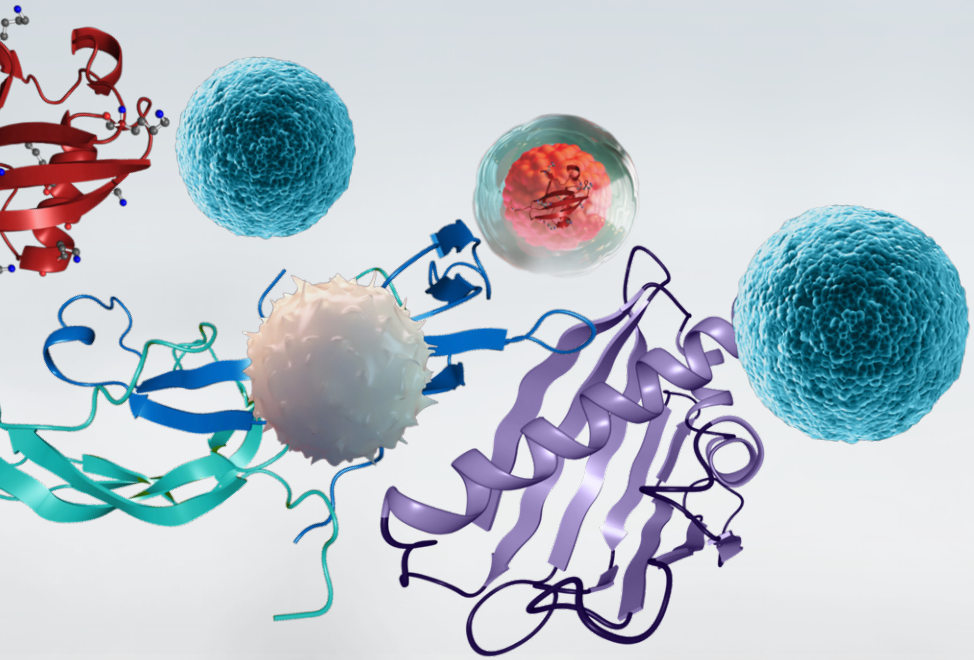
The Thermo Scientific™ Vanquish™ Neo UHPLC system has become a workhorse for a wide range of cutting-edge proteomics research. Below are a number of peer-reviewed articles that highlight how researchers are using the power of the Vanquish Neo UHPLC system to enhance their understanding of the proteome. Publications are split into two groups—**Section 1** reviews the use of nano/capillary flow for sensitive, in-depth characterization of the proteome, particularly beneficial when the amount of sample is limited; **Section 2** explores the use of micro-flow LC for rapid proteome profiling, popular for large-scale studies and clinical diagnostic assays.



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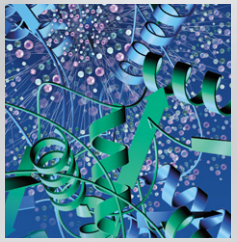

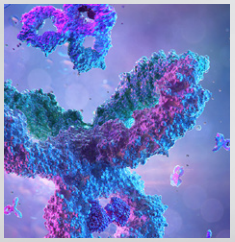

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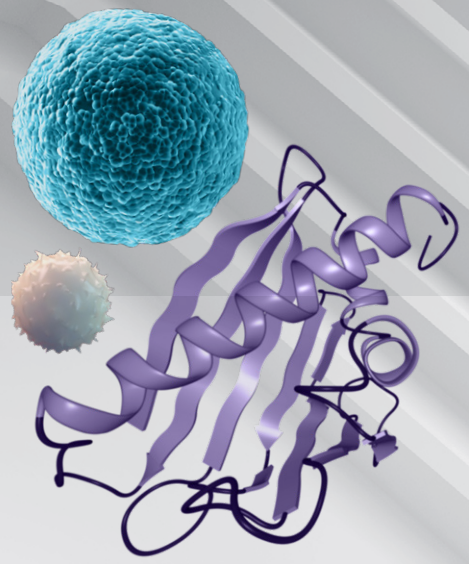
Introduction: The proteome and proteomics

Approaches to proteomics

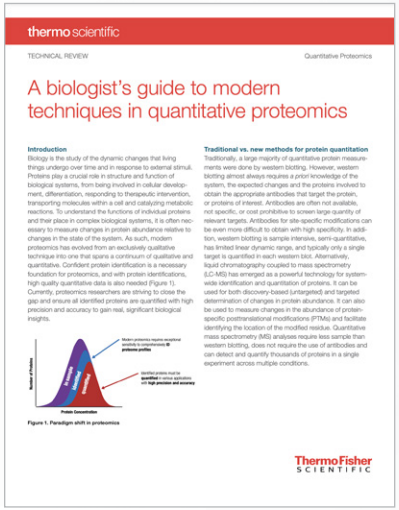


The proteome is the complete set of proteins expressed by a genome, cell, tissue, or organism at a particular time. The complexity derives from several key factors including: the large number of distinct proteins, the number of potential proteoforms for a given protein, and the broad dynamic range of physiologically relevant protein concentrations. Additionally, the proteome is in a constant state of flux and can change markedly over time. In proteomics, such changes are used to correlate specific proteins with their functions and healthy or disease states. In turn, this knowledge is leveraged for diagnosing diseases and developing new drug targets.

There are two major approaches to proteomics:

- In **top-down** proteomics, the proteins in the sample are first separated before being characterized intact.
- In **bottom-up** proteomics, sometimes called shotgun proteomics or peptide-based proteomics, all the proteins in a sample are first digested into a complex mixture of peptides. These peptides are then analyzed to identify which proteins were present in the sample.

While top-down proteomics is often used to generate an in-depth understanding of a single or small number of proteins, bottom-up proteomics is more widely used and focuses on capturing a snapshot of the entire proteome in each sample. The most prominent analytical technique for bottom-up proteomics is liquid chromatography-mass spectrometry (LC-MS). LC-MS can be utilized for both targeted and untargeted proteomics. The goal of targeted analysis is to quantify a set of previously identified proteins, while untargeted analysis (often referred to as discovery) seeks to both identify and quantify as many unique proteins in a sample as possible. More in-depth explanation can be found in *A biologist's guide to modern techniques in quantitative proteomics*.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TECHNICAL REVIEW

Quantitative Proteomics

A biologist's guide to modern techniques in quantitative proteomics

Introduction

Biology is the study of the dynamic changes that living things undergo over time and in response to external stimuli. Proteins play a crucial role in structure and function of biological systems, from being involved in cellular development, differentiation, responding to therapeutic intervention, transporting molecules within a cell and catalyzing metabolic reactions. To understand the functions of individual proteins and their place in complex biological systems, it is often necessary to measure changes in protein abundance relative to changes in the state of the system. As such, modern proteomics has evolved from an exclusively qualitative technique into one that spans a continuum of qualitative and quantitative. Confident protein identification is a necessary foundation for proteomics, and with protein identifications, high quality quantitative data is also needed (Figure 1). Currently, proteomics researchers are striving to close the gap and ensure all identified proteins are quantified with high precision and accuracy to gain real, significant biological insights.

Traditional vs. new methods for protein quantitation

Traditionally, a large majority of quantitative protein measurements were done by western blotting. However, western blotting almost always requires *a priori* knowledge of the system, the expected changes and the proteins involved to obtain the appropriate antibodies that target the protein, or proteins of interest. Antibodies are often not available, not specific, or cost prohibitive to screen large quantity of relevant targets. Antibodies for site-specific modifications can be even more difficult to obtain with high specificity. In addition, western blotting is sample intensive, semi-quantitative, has limited linear dynamic range, and typically only a single target is quantified in each western blot. Alternatively, liquid chromatography coupled to mass spectrometry (LC-MS) has emerged as a powerful technology for system-wide identification and quantitation of proteins. It can be used for both discovery-based (untargeted) and targeted determination of changes in protein abundance. It can also be used to measure changes in the abundance of protein-specific posttranslational modifications (PTMs) and facilitate identifying the location of the modified residue. Quantitative mass spectrometry (MS) analyses require less sample than western blotting, does not require the use of antibodies and can detect and quantify thousands of proteins in a single experiment across multiple conditions.

Figure 1. Paradigm shift in proteomics

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View technical review

The impact of flow rate

Because sensitivity is paramount to understanding low-level protein expression and inversely correlated with the flow rate in LC-MS, here LC is performed at much lower flow rates than standard analytical HPLC.[1] This falls into three general flow rate regimes—nano [<1 µL/min], capillary [1–5 µL/min], and micro-flow [5–100 µL/min], (Figure 1).

While there is significant overlap between use cases for each flow regime, they most often fall into the following three categories:

- **Nano-flow LC-MS**: deep quantitative and sample-limited proteome profiling
- **Capillary-flow LC-MS**: balancing high throughput and high sensitivity
- **Micro-flow LC-MS**: robust profiling of thousands of samples, such as clinical proteomics

The ideal flow rate for a given study depends on a number of factors such as the sample volume, total number of samples, target proteome depth, and required throughput. There are also trade-offs to consider with respect to robustness. While offering the highest sensitivity, small I.D. nano-flow LC columns (e.g., 75 µm) are also the most prone to clogging. For limited samples such as single cells in which there is less than 1 ng of total protein, investigators routinely use nano and even ultra-low nano-flow LC (≤100 nL/min). Micro-flow LC, on the other hand, provides the highest robustness and throughput at a sacrifice to sensitivity. The third flow regime, capillary-flow, represents a balance between sensitivity, throughput, and robustness. When choosing a column and flow rate, it is important to consider the sample type and overall goal of the study.

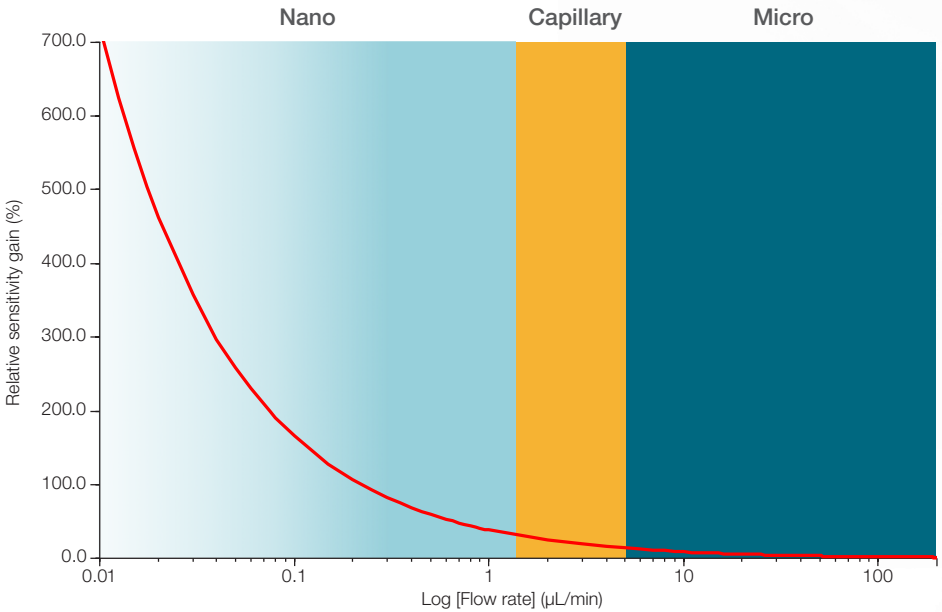


Figure 1. Comparison of relative LC-MS sensitivity at varying flow rates. Red trace is sensitivity gain relative to a 2.1 mm I.D. column operated at 450 µL/min.

The impact of separation efficiency

Irrespective of the flow rate, chromatographic efficiency (defined in gradient chromatography as “peak capacity”) is crucial to generating quality proteomics data.[2] Efficient separations have two fundamental advantages that enable deeper coverage and superior quantitation. First, narrower peaks result in higher signal intensity (Figure 2). As the peak width is decreased, the number of ions entering the mass spectrometer per unit time increases. This results in higher sensitivity and, ultimately, the ability to identify and quantify lower-level peptides/proteins.

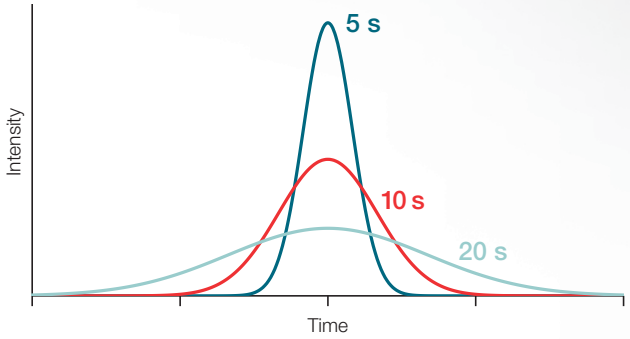


Figure 2. The effect of peak width on detector signal intensity.

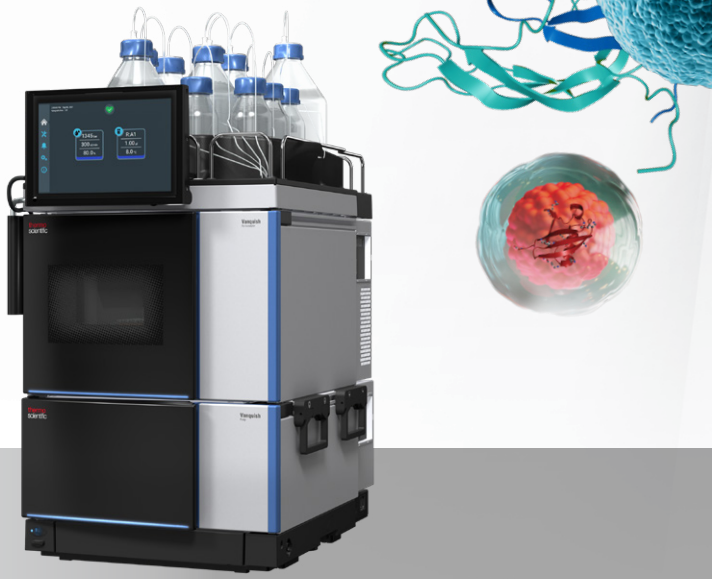
The second key advantage of a high-efficiency separation is that it limits co-elution. Less co-elution of peptides (and matrix interferants) decreases the number of unique precursor ions entering the mass spectrometer at a given time, which decreases the burden on mass spectrometer scan speed. In data-dependent acquisition, the mass spectrometer is able to isolate and fragment more unique precursors for deeper coverage. In data-independent acquisition, fewer co-eluting ions reduces spectral complexity (i.e., chimeric spectra), providing higher-confidence identifications.

Low-flow UHPLC optimization

Achieving efficient LC separations requires optimized conditions including the column, mobile phases, flow rate, temperature, fluidics, gradient program, and injection volume, among others. In addition, generating meaningful biological insight often requires analysis of large sample cohorts, placing additional emphasis on throughput and robustness. The Thermo Scientific Vanquish Neo UHPLC system offers industry-leading performance across the full flow range (0.001–100 µL/min) while maintaining the reliability of a workhorse instrument up to 1,500 bar.[3-4] In addition, the Vanquish Neo UHPLC system supports a range of workflows including direct inject and trap-and-elute without hardware modifications.

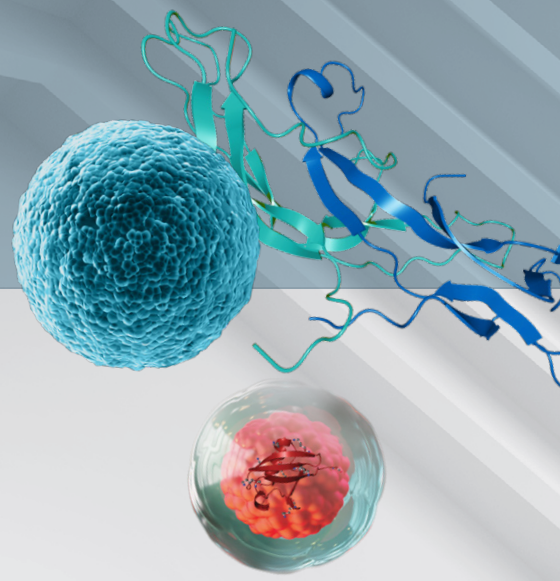
1. Wilm, M. and Mann, M. Analytical properties of the nanoelectrospray ionization source. Anal. Chem. 1996, 68, 1, 1-8.
2. Lenčo, J. et al. Reversed-Phase Liquid Chromatography of Peptides for Bottom-Up Proteomics: A Tutorial. J. Proteome Res. 2022, 21, 12, 2846-2892.
3. Fast, Sensitive, And Reproducible Nano- And Capillary-Flow LCMS Methods For High–Throughput Proteome Profiling Using The Vanquish Neo UHPLC System Hyphenated With The Orbitrap Exploris 480 MS.
4. Ultra-Robust Micro-Flow LC-MS/MS For Targeted High-Throughput Peptide Quantification Using The Vanquish Neo UHPLC System.

See product specifications



Publications

Boost sensitivity with nano/capillary flow LC-MS



Section 1 | High-sensitivity nano/capillary-flow LC-MS

Deep Single-Shot NanoLC-MS Proteome Profiling with a 1,500 Bar UHPLC System, Long Fully Porous Columns, and HRAM MS

Zheng, R.; Stejskal, K.; Pynn, C.; Mechtler, K.; Boychenko. A.; Journal of Proteome Research, 2022, 21, 2545–2551

Content summary	
Application	Bottom-up proteomics
Sample type	HeLa digest
Instrumentation	Vanquish Neo UHPLC system and Thermo Scientific™ Orbitrap Exploris™ mass spectrometer
Acquisition mode	DDA
Column	Thermo Scientific™ EASY-Spray™ PepMap™ Neo UHPLC column or Thermo Scientific™ Double nanoViper™ PepMap™ Neo column, 75 µm × 750 mm or 75 µm × 500 mm
Flow rate	200–500 nL/min
Throughput	12 samples/day

Conventional proteome analyses are usually based on nanoLC-MS methods. The use of long columns and shallow gradients give the high peak capacity needed to resolve the multitude of proteins found in biological samples. Unfortunately, conventional low-flow LC technology limits the use of long columns at practical sample throughputs. The authors used the Vanquish Neo UHPLC combined with high-resolution accurate-mass mass spectrometry to improve bottom-up proteomics analysis with nano LC-MS methods. The versatility of the Vanquish Neo system, and its ability to use longer columns, optimized flow rates, and increased gradient lengths, enabled deep proteome profiling and precise quantification of >7,000 proteins in a single-shot analysis. It is now possible to conduct high throughput large-scale discovery studies for probing in-depth protein-level alterations and to identify proteins and peptides that would otherwise remain undiscovered by other methods.

Related resources from Thermo Scientific

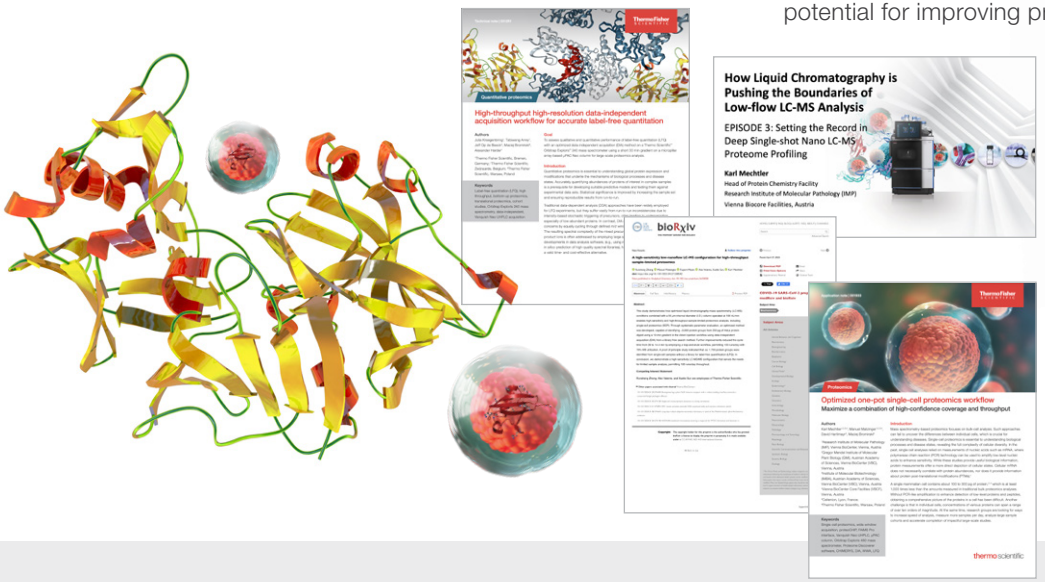
- Vanquish Neo UHPLC system sets new performance standards for single-shot nanoLCMS bottom-up proteomics
- Robust long-term Vanquish Neo UHPLC system operation enabling high-performance high-pressure nanoLC separations

Deep Proteome Profiling with Reduced Carryover Using Superficially Porous Microfabricated nanoLC Columns

Stejskal, K.; Op de Beeck, J.; Matzinger, M.; Dürnberger, G.; Boychenko, A.; Jacobs, P.; Mechtler, K.;
Analytical Chemistry, 2022, 94, 46, 15930–15938

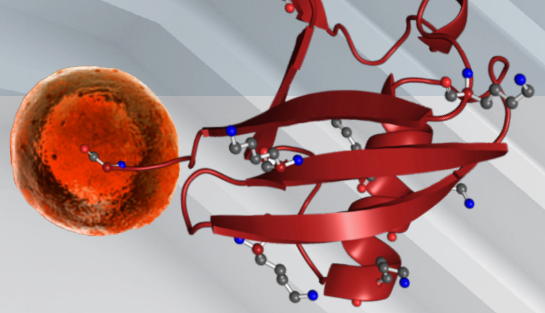
Content summary	
Application	Bottom-up proteomics
Sample type	HeLa digest
Instrumentation	Vanquish Neo UHPLC system and Orbitrap Exploris mass spectrometer
Acquisition mode	DDA
Column	Thermo Scientific µPAC Neo HPLC column, 50 cm
Flow rate	200 nL/min
Throughput	7–56 samples/day

Rapid progress in the field of LC-MS based proteomics is often attributed to major advances in MS technology. However, it also depends upon the capability of the nano LC system and the performance of the analytical column. In this article, the authors evaluated a prototype column—the 2 µPAC nano LC column—which uses C18-functionalized superficially porous micropillars as a stationary phase and compared it to the performance of traditional fully porous silica stationary phases. Sample carryover was minimized as the autosampler of the Vanquish Neo UHPLC system executed a rigorous system washing cycle using a high volume of organic solvent to clean the entire injection fluidics path, including the inside and outside of the injection needle. Delay time was minimized as the wash cycle that occurred after each injection was conducted in parallel to the peptide separation step. The authors found a marked increase in the number of protein groups (30%) and unique peptides (60%) identified for short gradients (10 min) and limited sample amounts (10–100 ng of cell lysate digest). For long gradients (180 min), 8,174 protein groups were identified (2,000 ng of the sample load). Overall, the article highlights the potential for improving proteome coverage using micropillar array column technology.



Related resources from Thermo Scientific

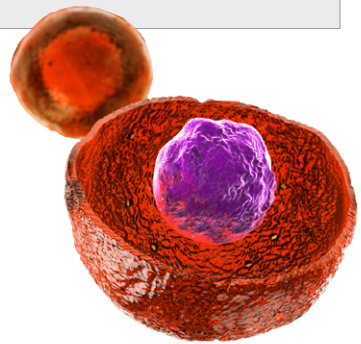
- High-throughput high-resolution data-independent acquisition workflow for accurate label-free quantitation
- Podcast: Prof. Karl Mechtler - Setting the record in deep single-shot nanoLC-MS proteome profiling
- High-sensitivity low-nano flow LC-MS methods for high-throughput sample-limited proteomics
- Optimized one-pot single-cell proteomics workflow



A High-Sensitivity Low-Nanoflow LC-MS Configuration for High-Throughput Sample-Limited Proteomics

Zheng, R.; Matzinger, M.; Mayer, R.; Valenta, A.; Sun, X.; Mechtler, K.;
Analytical Chemistry, 2023, 95, 51, 18673–18678

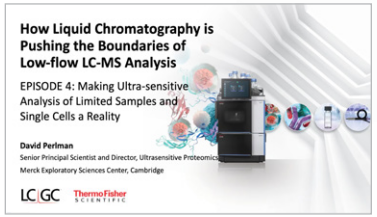
Content summary	
Application	Bottom-up Proteomics
Sample type	HeLa digest; Single cell - HeLa and K562 cells
Instrumentation	Vanquish Neo UHPLC system and Orbitrap Exploris mass spectrometer
Acquisition mode	DDA, WWA, and DIA
Column	Thermo Scientific™ Acclaim™ PepMap™ 100 C18 HPLC column, 50 µm × 150 mm
Flow rate	100 nL/min
Throughput	100 samples/day

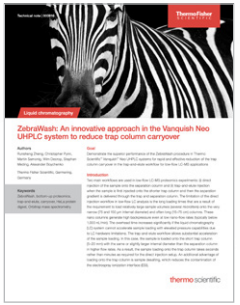


One major challenge for proteomic researchers is maintaining high-sensitivity measurements without sacrificing sample throughput. The authors addressed this by using a Vanquish Neo UHPLC system to develop several high-throughput, high-sensitivity methods for label-free, sample-limited proteomics. The LC fluidics were optimized for direct injection low nano-flow LC to maximize sensitivity. The gradient length was selected to balance throughput with depth of proteome coverage. As many as 3,000 protein groups were identified in 250 pg of HeLa protein digest using a 20 min cycle time. Further improvements in throughput were obtained using a trap-and-elute workflow, which decreased total cycle time to 10 min. When applying this method to the library-free analysis of individual HeLa cells, they identified ca. 1,700 protein groups.

Related resources from Thermo Scientific

- David Perlman - Making ultra-sensitive analysis of limited samples and single cells a reality
- ZebraWash: An innovative approach in the Vanquish Neo UHPLC system to reduce trap column carryover
- Deeper proteome coverage and faster throughput for low inpute samples on the Thermo Scientific Orbitrap Astral mass spectrometer





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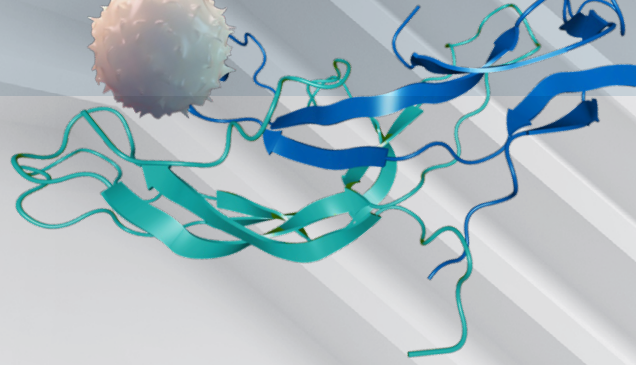


Robust, Reproducible and Quantitative Analysis of Thousands of Proteomes by Micro-Flow LC–MS/MS

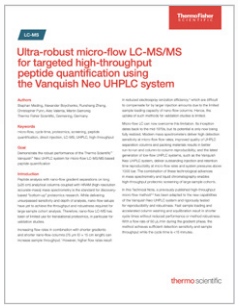
Bian, Y.; Zheng, R.; Bayer, F. P.; Wong, C.; Chang, Y-C.; Meng, C.; Zolg, D. P.; Reinecke, M.; Zecha, J.; Wiechmann, S.; Heinzlmeir, S.; Scherr, J.; Hemmer, B.; Baynham, M.; Gingras, A-C.; Boychenko, O.; Kuster, B.; Nature Communications, 2020, 11, 157

Content summary	
Application	Bottom-up Proteomics sub-proteome, multiplexed proteome, phospho proteome
Sample type	HeLA digest and human placenta protein digest
Instrumentation	Thermo Scientific™ UltiMate 3000 RSLCnano UHPLC system, Vanquish Neo UHPLC system, and Thermo Scientific™ Q Exactive™ HF-X Hybrid Quadrupole-Orbitrap™ mass spectrometer
Acquisition mode	DDA
Column	Acclaim PepMap 100 C18 HPLC column, 1 mm × 150 mm
Flow rate	50 µL/min
Throughput	96 samples/day

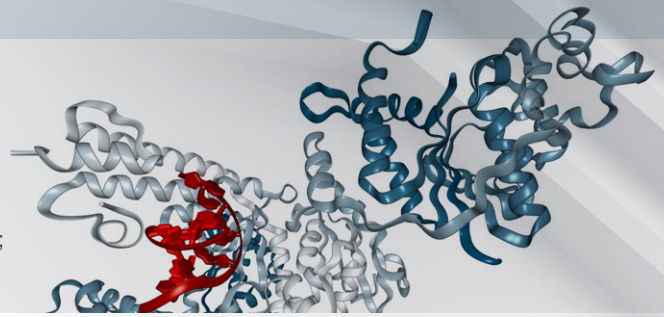
Nano-flow liquid chromatography tandem mass spectrometry is the most common analytical approach used in proteome research due to its excellent sensitivity, but this typically comes at the expense of robustness. The authors show that micro-flow LC-MS/MS using a Vanquish Neo UHPLC system and 1 mm I.D. columns can be a viable alternative to traditional nano-flow approaches. Using Tandem Mass Tags (TMT) they were able to identify >9,000 proteins in 16 h and >30,000 phosphopeptides in 12 h at 20 min/sample. They demonstrated the utility of their approach for improved robustness by analyzing >7,500 samples without apparent loss of performance, suggesting the method's viability for a broad range of clinical applications.

Related resources from Thermo Scientific

- Ultra-robust micro-flow LC-MS/MS for targeted high-throughput peptide quantification using the Vanquish Neo UHPLC system


Ultra-robust micro-flow LC-MS/MS for targeted high-throughput peptide quantification using the Vanquish Neo UHPLC system

Robust Microflow LC-MS/MS for Proteome Analysis: 38,000 Runs and Counting



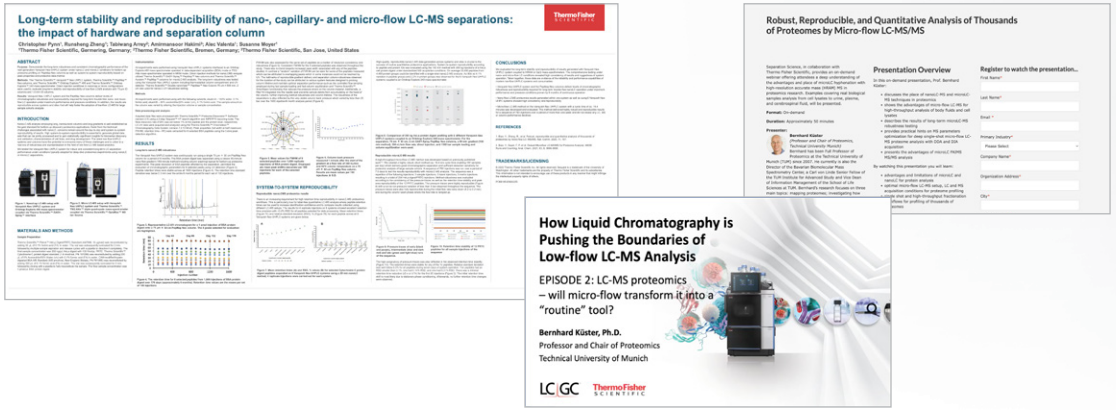
Bian, Y.; Bayer, F. P.; Chang, Y-C.; Meng, C.; Hoefer, S.; Deng, N.; Zheng, R.; Boychenko, O.; Kuster, B.;
Analytical Chemistry, 2021, 93, 8, 3686–3690

Content summary	
Application	Bottom-up Proteomics
Sample type	TMT and label-free cell lines, tissues, and human body fluids
Instrumentation	Vanquish Neo UHPLC system, and Thermo Scientific™ Orbitrap Fusion™ Lumos™ Tribrid™ mass spectrometer
Acquisition mode	DDA
Column	Acclaim PepMap 100 C18 HPLC column, 1 mm × 150 mm
Flow rate	50 µL/min
Throughput	24 samples/day

The authors developed a micro-flow LC-MS/MS-based method for the analysis of the proteome in a variety of samples including cell lines, tissues and human body fluids. They reported that their method was extremely robust based on the analysis of ~38,000 samples over a period of two years. They were able to analyze over 14,000 samples on a single column without suffering losses in performance. Due to the high degree of reliability, the authors concluded that their approach is preferable to those that use traditional nanoLC-MS/MS methods and is ideal for high-throughput clinical studies where the amount of sample available is not limited.

Related resources from Thermo Scientific

- Long-term stability and reproducibility of nano-, capillary-, and micro-flow LC-MS separations: the impact of hardware and separation column
- Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LC-MS
- Prof. B. Kuster - LC-MS proteomics- will micro-flow transform it into a “routine” tool?



Unified Workflow for the Rapid and In-Depth Characterization of Bacterial Proteomes

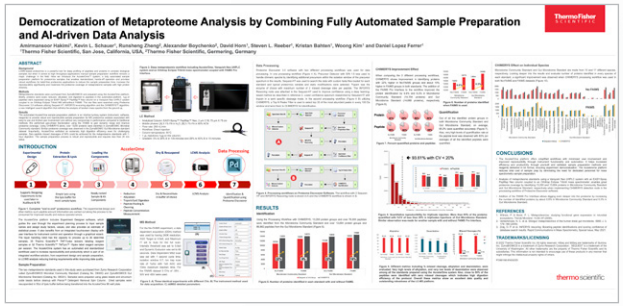
Abele, M.; Doll, E.; Bayer, F. P.; Meng, C.; Lomp, N.; Neuhaus, K.; Scherer, S.; Kuster, B.; Ludwig, C.;
Molecular and Cellular Proteomics, 2023, 22, 100612

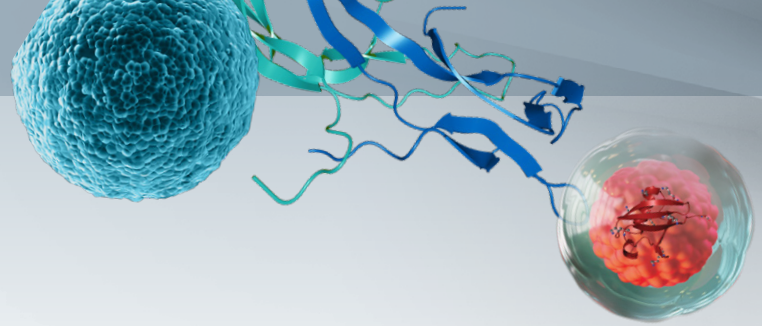
Content summary	
Application	Bottom-up Proteomics
Sample type	Bacteria digest
Instrumentation	Vanquish Neo UHPLC system and Orbitrap Exploris mass spectrometer
Acquisition mode	DDA or DIA
Column	Acclaim PepMap 100 C18 HPLC column, 1 × 150 mm
Flow rate	50 µL/min
Throughput	48 samples/day

Quantitative bacterial proteomics is challenging due to the great diversity of bacteria and an excessive variance in their proteome. The authors addressed this problem by investigating and optimizing different sample preparation approaches, as well as MS data acquisition and data analysis strategies. Peptides were separated using a microflow-Vanquish Neo UHPLC system DIA MS/MS method with a 30-min linear gradient. They concluded that their approach “represents a safe, rapid, cost-effective, in-depth, and highly reproducible sample preparation workflow that opens up the potential for large-scale bacterial proteomic studies”.

Related resources from Thermo Scientific

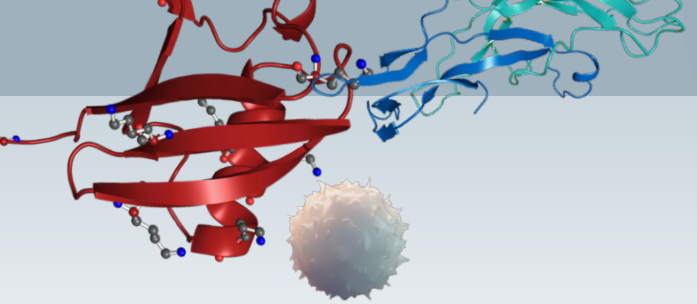
- Democratization of metaproteome analysis by combining fully automated sample preparation and AI-driven data analysis





Section 3 | Vanquish Neo publications

- A high-sensitivity low-nanoflow LC-MS configuration for high-throughput sample-limited proteomics
- ALK signalling primes the DNA damage response sensitizing ALK-driven neuroblastoma to therapeutic ATR inhibition
- An essential endoplasmic reticulum-resident N-acetyltransferase ortholog in *Plasmodium falciparum*
- Borrelia PeptideAtlas: A proteome resource of common *Borrelia burgdorferi* isolates for Lyme research
- Brain-specific glycosylation enzyme GnT-IX maintains levels of protein tyrosine phosphatase receptor PTPRZ, thereby mediating glioma growth
- Bromodomain protein BRD8 regulates cell cycle progression in colorectal cancer cells through a TIP60-independent regulation of the pre-RC complex
- Cannflavins isolated from *Cannabis sativa* impede *Caenorhabditis elegans* response to noxious heat
- Chapter Fourteen - Identification of MPK4 kinase interactome using TurboID proximity labeling proteomics in *Arabidopsis thaliana*
- Chapter Thirteen - Proteomics and phosphoproteomics of C_3 to CAM transition in the common ice plant
- Characterization of choroid plexus in the preterm rabbit pup following subcutaneous administration of recombinant human IGF-1/IGFBP-3
- Comparison of the proteomes and phosphoproteomes of *S. cerevisiae* cells harvested with different strategies
- Comprehensive characterization of protein turnover by comparative SILAC labeling analysis in 3T3-L1
- Cooperation between bHLH transcription factors and histones for DNA access
- CRISPRi-mediated Silencing of *Burkholderia* O-Linked glycosylation systems enables the depletion of glycosylation yet results in modest proteome impacts
- Deep paleoproteotyping and microtomography revealed no heart defect nor traces of embalming in the cardiac relics of blessed Pauline Jaricot
- Differentiation of isobaric cross-linked peptides prepared via maleimide chemistry by MALDI-MS and MS/MS
- Discovery and characterization of a chemical probe targeting the zinc-finger ubiquitin-binding domain of HDAC6
- Dynamic metabolome profiling uncovers potential TOR signaling genes
- Effect of plant produced Anti-hIL-6 receptor antibody blockade on pSTAT3 expression in human peripheral blood mononuclear cells
- Effects of tartary buckwheat protein on gut microbiome and plasma metabolite in rats with high-fat diet
- Evaluating the capabilities of the Astral mass analyzer for single-cell proteomics
- Evaluating the performance of the Astral mass analyzer for quantitative proteomics using data independent acquisition
- Evaluation of the Orbitrap Ascend tribrid mass spectrometer for shotgun proteomics



Section 3 | Vanquish Neo publications *continued*

- Experimental characterization of de novo proteins and their unevolved random-sequence counterparts
- Getting ready for large-scale proteomics in crop plants
- Glucose intolerance in aging is mediated by the Gpcpd1-GPC metabolic axis
- High resolution mass spectrometry-driven metabolite profiling of baricitinib to report its unknown metabolites and step-by-step reaction mechanism of metabolism
- High-throughput screening and proteomic characterization of compounds targeting myeloid-derived suppressor cells
- Identification of 7,000–9,000 proteins from cell lines and tissues by single-shot microflow LC–MS/MS
- Identification of membrane proteins regulated by ADAM15 by SUSPECS proteomics
- IDH3γ functions as a redox switch regulating mitochondrial energy metabolism and contractility in the heart
- Inflammation causes insulin resistance via interferon regulatory factor 3 (IRF3)-mediated reduction in FAHFA levels
- Initial high throughput proteomic analysis reveals alterations in $CD19^{+}$ B lymphocyte profile in acute COVID-19 patients
- Insights into peculiar fungal LPMO family members holding a short C-terminal sequence reminiscent of phosphate binding motifs
- Integrated metagenomics and metabolomics analysis reveals changes in the microbiome and metabolites in the rhizosphere soil of *Fritillaria unibracteata* sequence reminiscent of phosphate binding motifs
- Intrinsic sexual dimorphism in the placenta determines the differential response to benzene exposure
- Itaconate stabilizes CPT1a to enhance lipid utilization during inflammation
- Mass spectrometry detection of monkeypox virus: Comprehensive coverage for ranking the most responsive peptide markers
- Mast cell-derived BH4 is a critical mediator of postoperative pain
- Microglial REV-ERBα regulates inflammation and lipid droplet formation to drive tauopathy in male mice
- Mitigation of peanut allergenic reactivity by combined processing: Pressured heating and enzymatic hydrolysis
- Molecular asymmetry of a photosynthetic supercomplex from green sulfur bacteria
- Molecular dissection and testing of PRSS37 function through LC–MS/MS and the generation of a PRSS37 humanized mouse model
- Multi-tissue proteomics identifies a link between satellite DNA organization and transgenerational transposon repression in Drosophila
- Narrow-window DIA: Ultra-fast quantitative analysis of comprehensive proteomes with high sequencing depth
- Nisin S, a Novel Nisin Variant Produced by *Ligilactobacillus salivarius* P1CEA3
- Nodule-specific Cu^{+}-chaperone NCC1 is required for symbiotic nitrogen fixation in *Medicago truncatula* root nodules
- Optimization of a high-throughput shotgun immunoproteomics pipeline for antigen identification

Section 3 | Recent Vanquish Neo publications *continued*

- Optimization of instrument parameters for efficient phosphopeptide identification and localization by data-dependent analysis using Orbitrap tribrid mass spectrometers
- Organ-oriented proteogenomics functional atlas of three aquatic invertebrate sentinel species | Scientific Data (nature.com)
- Orphan quality control shapes network dynamics and gene expression
- Parallelized acquisition of Orbitrap and Astral analyzers enables high-throughput quantitative analysis
- Phosphorylation-linked complex profiling identifies assemblies required for Hippo signal integration
- Pptc7 maintains mitochondrial protein content by suppressing receptor-mediated mitophagy
- Production and characterization of an AAV1-VP3-only capsid: An analytical benchmark standard
- Profiling of the *Helicobacter pylori* redox switch HP1021 regulon using a multi-omics approach
- Protein interaction network revealed by quantitative proteomic analysis elucidates TFIIB role in multiple aspects of the transcription cycle
- Proteomic profiling of regenerated urinary bladder tissue with stem cell seeded scaffold composites in a non-human primate bladder augmentation model
- Quartet protein reference materials and datasets for multi-platform assessment of label-free proteomics
- Reversed-phase liquid chromatography of peptides for bottom-up proteomics: A tutorial
- Robust and easy-to-use one pot workflow for label free single cell proteomics
- Robust, precise, and deep proteome profiling using a small mass range and narrow window data-independent-acquisition scheme
- Role of Oatp2b1 in drug absorption and drug-drug interactions
- Sensitive, high-throughput HLA-I and HLA-II immunopeptidomics using parallel accumulation-serial fragmentation mass spectrometry
- The catalytic-independent function of LSD1 modulates the epigenetic landscape of mouse embryonic stem cells
- The mature N termini of *Plasmodium* effector proteins confer specificity of export
- Thermal proteome profiling for drug target identification and probing of protein states
- Unified workflow for the rapid and in-depth characterization of bacterial proteomes
- Wide Window Acquisition and AI-based data analysis to reach deep proteome coverage for a wide sample range, including single cell proteomic inputs

Section 4 | Additional resources

Thermo literature

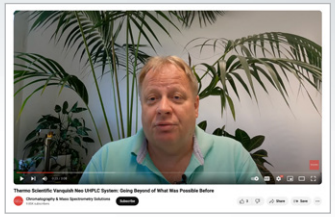
- Brochure: Vanquish Neo UHPLC System—Beyond brilliant
- Specification sheet: Vanquish Neo UHPLC System—The new standard in nano-, capillary-, and micro-flow LC
- Technical note: Multi-draw: Enabling large volume injections for lyophilization-free LC-MS proteomics workflows on the Vanquish Neo UHPLC system
- Technical note: Quantitative targeted nano- and capillary-flow LC-MS peptide analysis using the Vanquish Neo UHPLC System coupled to a triple quadrupole mass spectrometer
- Technical note: Vanquish Neo UHPLC system-to-system reproducibility ensures consistent and reliable results in nanoLC-MS proteomics

Videos/testimonials

- Customer video: Karl Mechtler, Institute of Molecular Biotechnology - Vienna Biocenter
- Customer video: Bernhard Kuster, Technical University Munich
- Customer video: David H. Perlman, Merck
- Customer video: Jonathan Bones, National Institute for Bioprocessing Research and Training (NIBRT)
- Vanquish Neo product video

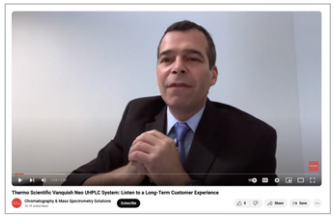
Product tour

- Take a virtual 3D product tour

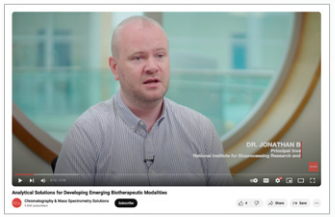


View testimonial video

View testimonial video

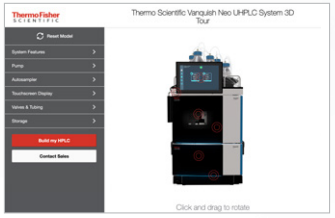


View testimonial video



View testimonial video

View Vanquish Neo video



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