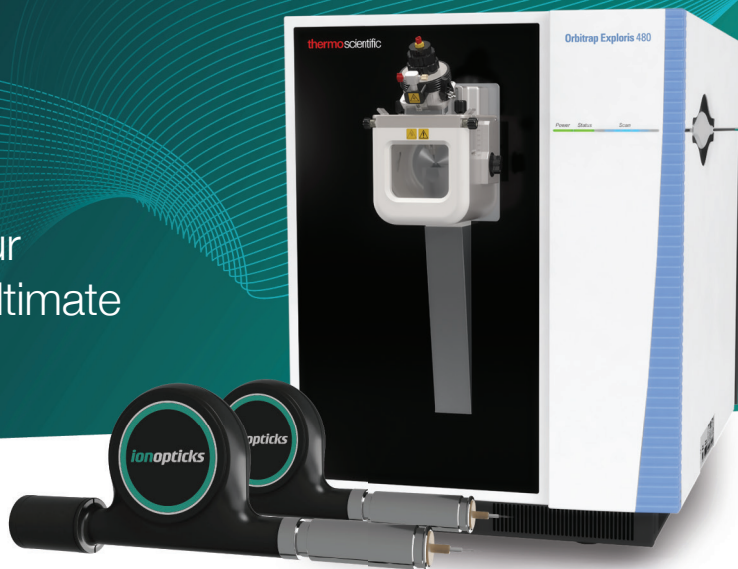


Demonstrate the full potential of your Orbitrap Exploris 480 with Aurora Ultimate UHPLC columns



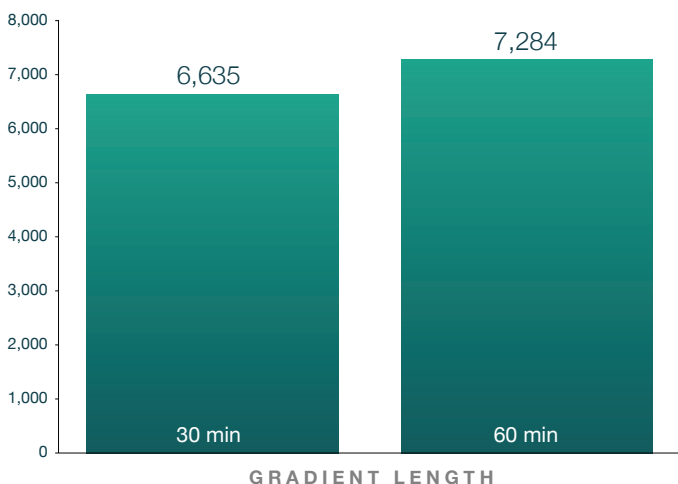
INTRODUCTION

IonOpticks' Aurora Series packed emitter columns represent a significant advancement for scientists desiring deep coverage of proteomics samples. These columns feature our revolutionary nanoZero® fitting, which enables simplified plug-and-play functionality and enhancing overall efficiency in proteomics workflows. When integrated with cutting-edge mass spectrometry platforms, Aurora Series columns exhibit remarkable performance capabilities. In particular, the combination of IonOpticks' Aurora Ultimate 25 cm x 75 µm XT columns with Thermo Fisher Scientific's Orbitrap Exploris 480 mass spectrometer creates a powerful analytical platform. To demonstrate the capabilities of this system, experiments were conducted using 3 replicates across different gradient lengths (30 min and 60 min), allowing for an evaluation of the column's performance under various analytical conditions.

Maximize identifications of peptides and proteins

The Aurora Ultimate 25 cm x 75 µm XT columns demonstrate exceptional performance in discovery proteomics applications. These findings underscore the advantage of using columns with the ability to deliver high-resolution separations, enabling researchers to achieve deeper proteome coverage in their studies.

(A) UNIQUE PROTEIN GROUPS



(B) UNIQUE PEPTIDES

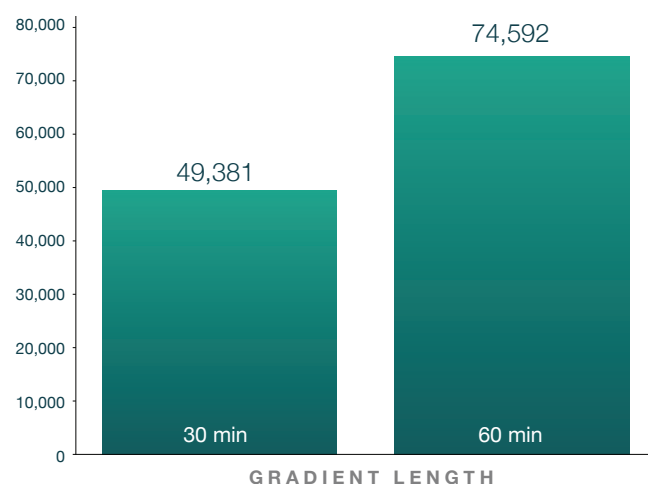


Figure 1: (A) Average protein group identifications across different gradients. (B) Average unique peptide identifications across different gradients. A HeLa tryptic digest (200 ng) was separated on an Aurora Ultimate 25 cm x 75 µm XT column. 3 replicates were run per condition. Samples were run on Thermo Fisher Scientific's Vanquish Neo LC and Orbitrap Exploris 480 mass spectrometer with FAIMS Pro Duo. FAIMS CVs of -45V for 30 min gradient and -45/-65V for 60 min gradient were used. Data analysis was performed using Spectronaut 18 (Biognosys AG).

More than
49k
unique peptides
using a 30 min gradient

More than
74k
unique peptides
using a 60 min gradient

3.3secs
Full-width half-max
using a 30 min gradient

6.3secs
Full-width half-max
using a 60 min gradient



FEATURED PRODUCT

Aurora Ultimate 25x75 XT packed emitter column for EASY-Spray and Nanospray Flex
(25 cm x 75µm ID, 1.7µm C18) Part No. AUR3-25075C18A-XT

Narrow peak widths

The Aurora Ultimate 25 cm x 75 µm XT columns demonstrate exceptional chromatographic performance, with narrow peak widths across different gradient lengths. The 30 minute gradient demonstrates particularly sharp peaks with average FWHM values around 3.3 sec, with the 60 minute gradient demonstrating FWHM values around 6.3 sec.

Figure 2: Average full width at half maximum (FWHM) for all identified peptides from HeLa Tryptic Digest injections (200 ng) on an Aurora Ultimate 25 cm x 75 µm XT column. 3 replicates were run per condition. Each point represents the average FWHM for an individual replicate. Samples were run on Thermo Fisher Scientific's Vanquish Neo LC and Orbitrap Exploris 480 mass spectrometer with FAIMS Pro Duo. FAIMS CVs of -45V for 30 min gradient and -45/-65V for 60 min gradient were used. Data analysis was performed using Spectronaut 18 (Biognosys AG).

FIG 2 AVERAGE FULL-WIDTH HALF-MAX

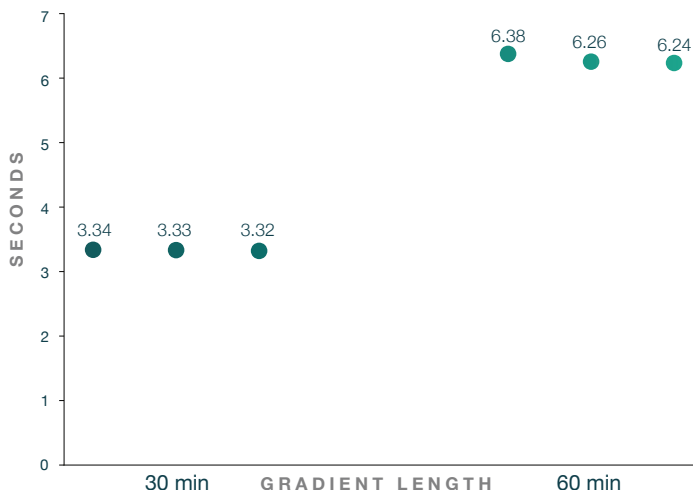
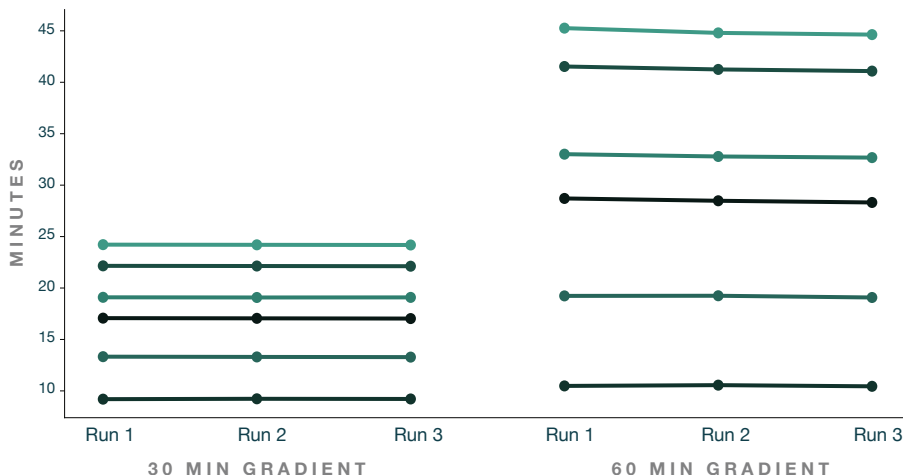


FIG 3 RETENTION TIME FOR SELECTED PEPTIDES



Stable retention times ensure confidence in results

The Aurora Ultimate 25 cm x 75 µm XT columns demonstrate exceptional retention time stability across multiple runs for both 30 minute and 60 minute gradients. This reproducibility is critical in proteomics, ensuring reliable peptide identification across different experimental conditions.

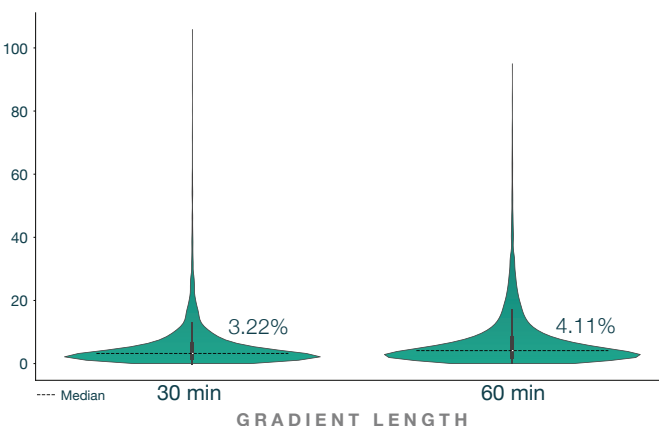
Figure 3: Stable peptide retention times across all runs. 6 peptides were selected and their retention time assessed across all runs from HeLa Tryptic Digest injections (200 ng) on an Aurora Ultimate 25 cm x 75 µm XT column. Samples were run on Thermo Fisher Scientific's Vanquish Neo LC and Orbitrap Exploris 480 mass spectrometer with FAIMS Pro Duo. FAIMS CVs of -45V for 30 min gradient and -45/-65V for 60 min gradient were used. Data analysis was performed using DIA-NN software (Version 1.9).

Low CVs

Analysis of protein intensity reproducibility, visualized through coefficient of variation (CV), demonstrates the exceptional consistency of the Aurora Ultimate columns across different gradient lengths. Both 30 minute and 60 minute gradients exhibit low median CV values (3.22% and 4.11% respectively). Ultimate 25 cm x 75 µm XT columns demonstrate remarkable consistency and reliability across different experimental conditions, offering researchers a robust platform for generating accurate and reproducible proteomics data.

Figure 4: Low CVs across different gradients. Violin plot of the Coefficient of Variation for all protein intensities identified across all replicates from HeLa Tryptic Digest injections (200 ng) on an Aurora Ultimate 25 cm x 75 µm XT column. 3 replicates were run per condition. Samples were run on Thermo Fisher Scientific's Vanquish Neo LC and Orbitrap Exploris 480 mass spectrometer with FAIMS Pro Duo. FAIMS CVs of -45V for 30 min gradient and -45/-65V for 60 min gradient were used. Data analysis was performed using Spectronaut 18 (Biognosys AG).

FIG 4 COEFFICIENT OF VARIATION (CV %)



CONCLUSION

The combination of the IonOpticks' Aurora Series columns and Thermo Fisher Scientific's Vanquish Neo LC and Orbitrap Exploris 480 mass spectrometer enabled maximum protein and peptide identifications. This powerful integration significantly enhances analytical capabilities, providing researchers with a robust and precise platform for conducting cutting-edge proteomics studies and unlocking deeper insights into complex samples.