ionopticks

PRODUCT OVERVIEW

Aurora® Rapid™ 8x75

8 cm x 75 µm

Maximal throughput for single-cell and low input samples.

Aurora® Rapid™ 8×75 columns deliver high-throughput analysis of single cells and small sample loads, providing extreme sensitivity in shorter gradients. With further improved spray stability and increased robustness in Generation 4 Aurora® Rapid™ 8x75, achieve exceptional depth of coverage and high throughput without compromising data quality.

Product Benefits

- High throughput
- Nanoflow
- Sensitivity
- Analyse more cells in less time

Ideal for:
High-throughput single cell proteomics

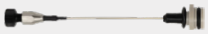
50-100
SPD

10-30 min
Gradients

Specifications

Column format	Analytical column
Column type	Reversed-phase
For use with	UHPLC
Length	8 cm
Inner Diameter	75 µm
Pore size	120 Å
Pressure	>1700 bar
Temp. limits	60°C
Particle size	1.7 µm
pH stability	1–8
Stationary phase	C18
Suggested flow rate	100-1000 nL/min

Compatibility



	Aurora® CSI	Aurora® XT
CaptiveSpray	✓	
CaptiveSpray 2	✓	
CaptiveSpray Ultra	✓	
EASY-Spray		✓
Nanospray Flex		✓
Newomics UniESI		✓
Newomics DuoESI		✓
OptiFlow Turbo V		
OptiFlow Pro		

HEATSYNC™

Introducing the HeatSync™ range - the perfect companion to make the world's best chromatography even better. Includes the new HeatSync™ Controller and HeatSync™ Column Heater.

4 GENERATION
Generation 4
Aurora Series®

Ion Opticks Pty Ltd
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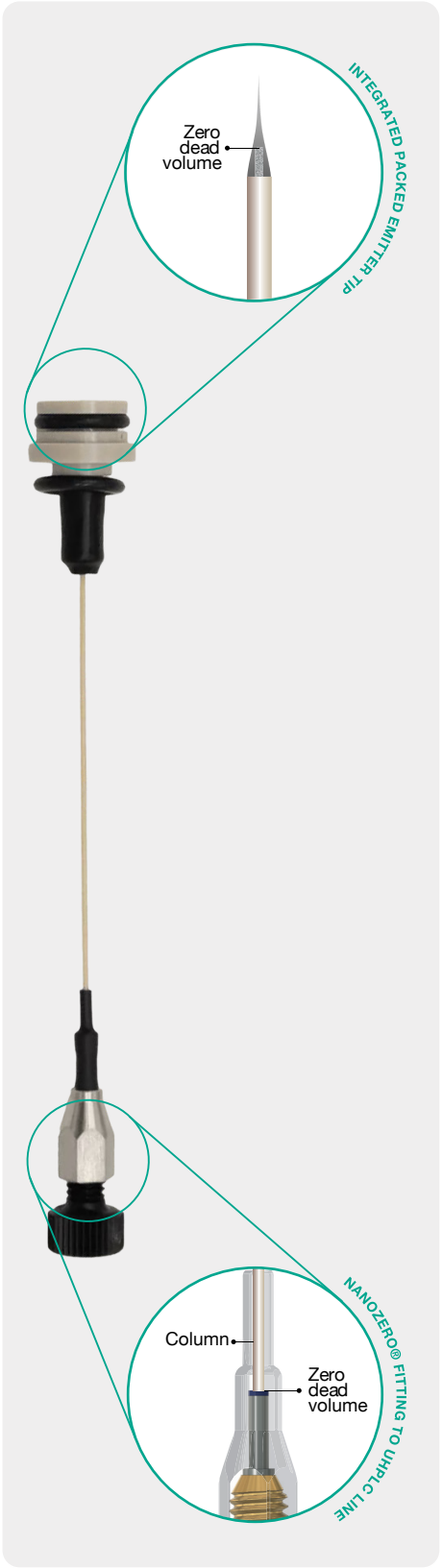


More than 3200 proteins identified from inputs as low as 125 pg

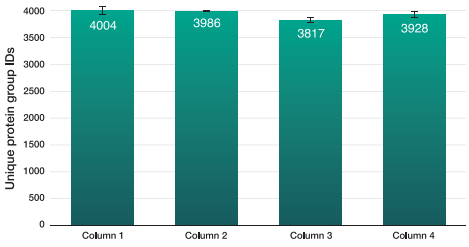


Figure 1: Unique protein group identifications across different columns. A HeLa tryptic digest (250 pg) was separated on an Aurora Rapid 8 cm × 75 µm column using an 80 SPD method on a Vanquish Neo system coupled to a Bruker timsTOF Ultra 2 mass spectrometer. Three runs were performed per column. Raw data were analyzed in Spectronaut version 19.8 with the "Match between runs" feature disabled

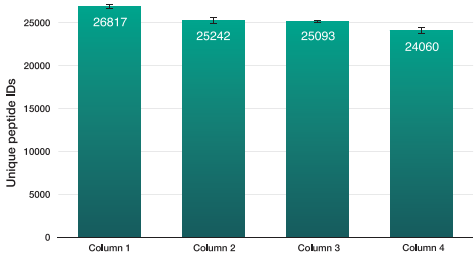
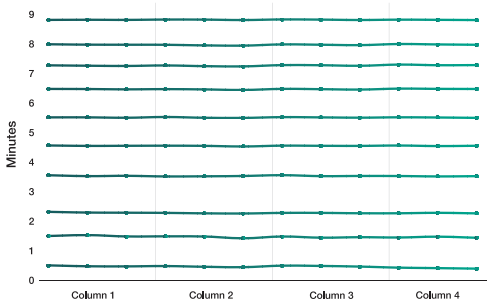


Figure 2: Unique peptide identifications across different columns. A HeLa tryptic digest (250 pg) was separated on an Aurora Rapid 8 cm × 75 µm column using an 80 SPD method on a Vanquish Neo system coupled to a Bruker timsTOF Ultra 2 mass spectrometer. Three runs were performed per column. Raw data were analyzed in Spectronaut version 19.8 with the "Match between runs" feature disabled.

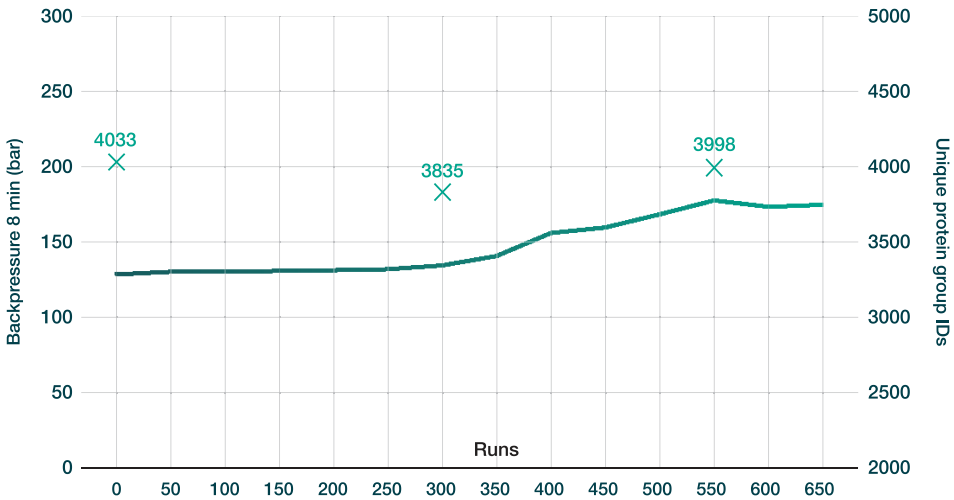
Incredibly stable retention times

Figure 3: Stable peptide retention times across different columns. Ten peptides were selected and their retention times assessed across all columns from 3 HeLa tryptic digest injections (250 pg) on Aurora Rapid 8 cm × 75 µm columns, using an 80 SPD method. Samples were run on a Vanquish Neo and Bruker timsTOF Ultra 2 mass spectrometer. Raw data were analyzed in Spectronaut version 19.8 with the "Match between runs" feature disabled.



Column backpressure stability and protein group IDs over extended use

Figure 4: Backpressure stability and protein group IDs over extended column use from HeLa tryptic digest QC injections (250 pg) on Aurora Rapid 8 cm × 75 µm columns, using a 60 SPD method. Samples were run on a Vanquish Neo and Bruker timsTOF Ultra 2 mass spectrometer. Raw data were analyzed in Spectronaut version 19.8 with the "Match between runs" feature disabled.



Further literature at:
ionopticks.com
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