High Performance PepSep UHPLC nanoFlow Columns

Quality Materials

PepSep columns are created with industry leading materials and connections to accommodate all your chromatographic separation needs. Our column portfolio offers a range of columns covering most Proteomic applications. Columns are available with or without fittings for easy and reliable connections to the HPLC system and the emitter.

For safe and easy connections to the high-pressure end of the column, a 10-32 thread female union connects to most LC systems. The UHP connection is tested for use up to 1000 bar. At the low pressure end we have a nanoConnect fitting that ensures a zero dead volume connection.

All columns are packed in polyimide coated fused silica and the entrance/exit points are finely polished and individually inspected.

A short frit (250-350 µm) is precisely positioned to minimize post-column eluent mixing.

High Performance

PepSep C18 nanoFlow columns pair well with most UHPLCs and are ideal for the separation of peptides using polar aqueous mobile phases. The PepSep column portfolio is an indispensable tool for the classical separation approach in proteomics and enables the analysis of samples with high sensitivity. Our shorter columns, 5 cm, 10 cm, and 15 cm, enable faster separations, yielding incredible ID-based results up to three times faster than columns used in standard proteomics workflows. Our longer TWENTY-FIVE cm columns were designed for high sensitivity analysis >50 ng (TWENTY-FIVE) and <50 ng targeting single cell applications (TWENTY-FIVE UHS).

Robustness

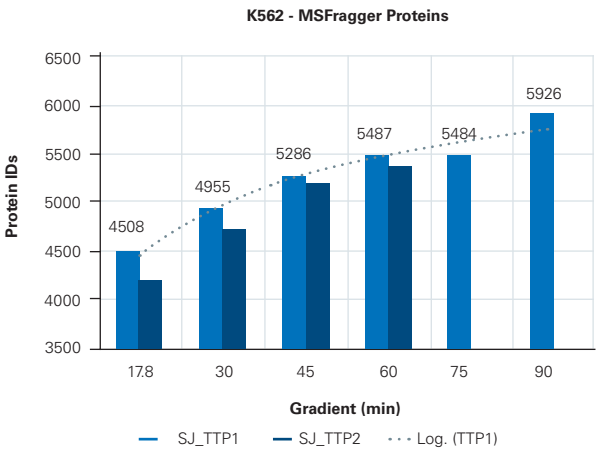
When coupled to the Bruker timsTOF Pro Series, PepSep columns demonstrated unparalleled results in a fraction of the time with unmatched sensitivity. When tested in core labs, using standardized sample prep, PepSep columns on average lasted over 1000 injections.

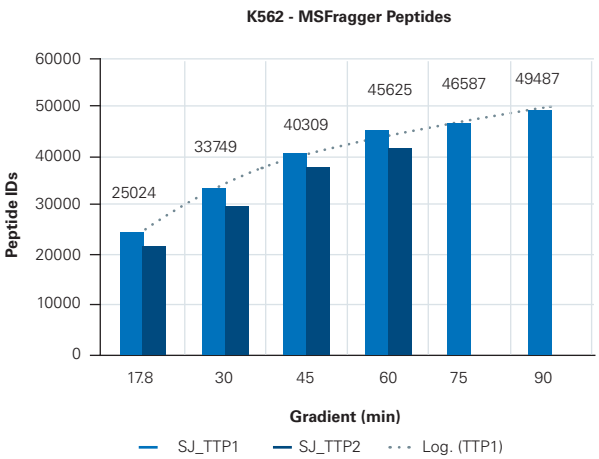
» "I'm happy to use PepSep columns in my laboratory. They are better than what I can make myself, and my short gradient results are impressive. These are by far the best columns I've used to date."

Brett Phinney, Genome Center Proteomics Core Director, University of California, Davis, CA, USA

High-throughput For All Your Proteomics Workflows

High-throughput proteomics applications require columns that generate high protein/peptide IDs, demonstrate chromatographic reproducibility, and can last hundreds to thousands of samples. In preliminary testing, PepSep columns lasted twice as long as standard C18 separation columns. In an in-house study using the 50 samples per day method, the PepSep TEN averaged more than 4200 protein groups and 21,000 peptides.

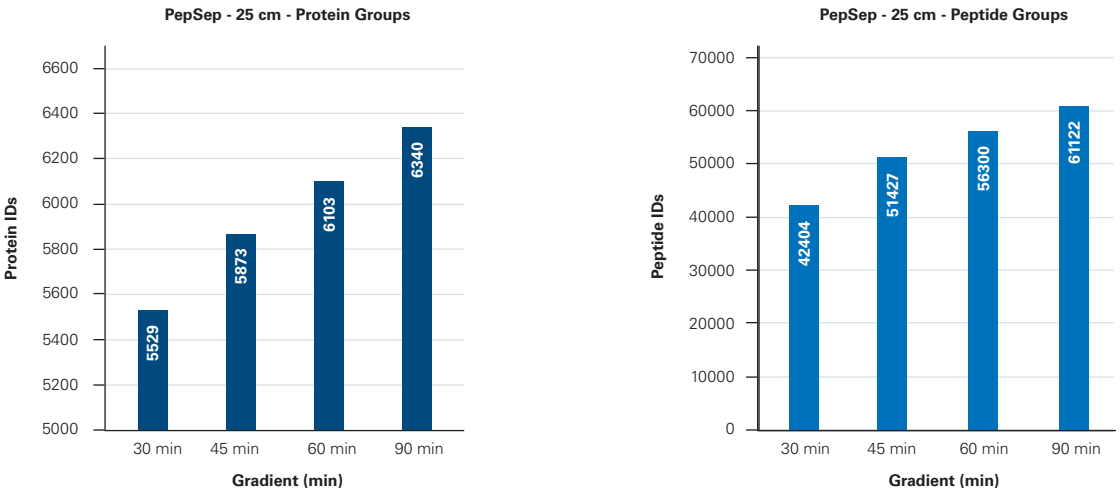




Results of 200 ng K562 run on the Bruker TEN using the nanoElute UHPLC coupled to the timsTOF Pro. The default DDA short gradient MS method was used. Data was analyzed using MSFragger

High Sensitivity IDs Leading to Excellent Performance

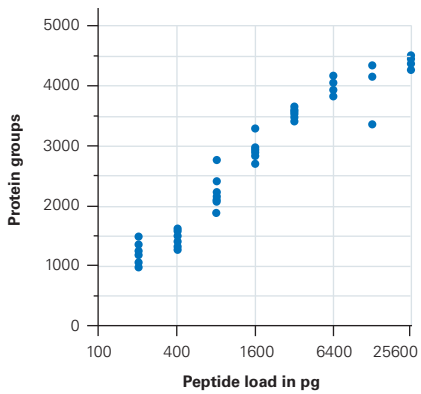
As mass spectrometers evolve to become more technologically advanced and sensitive, so have C18 columns. The High Sensitivity PepSep TWENTY-FIVE was fashioned to provide unmatched performance due to its stationary phase packed with twice the material compared to standard C18 columns creating more peptide active binding sites. When tested on several timsTOF Pro instruments in North America, the PepSep TWENTY-FIVE demonstrated more than 5500 protein groups, 42,000 peptides in a 30 min gradient.



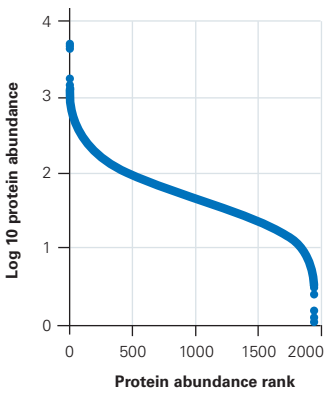
Results of 200 ng K562 run on the PepSep TWENTY-FIVE column w/5mm Thermo Pepmap trap using the nanoElute UHPLC coupled to the timsTOF Pro. The default DDA short gradient MS method was used. Data was analyzed using MSFragger.

Ultra-high Sensitivity for Single Cell Proteomics

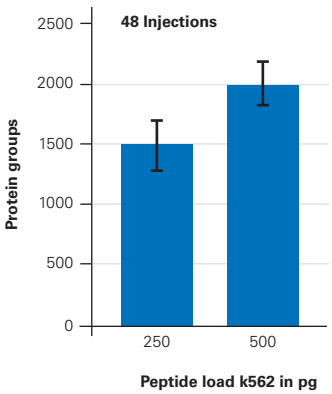
Combining low flow liquid chromatography on the Evosep One UHPLC, running the Whisper method attached to the timsTOF SCP using dia-PASEF®, over 2000 proteins were identified from 500 pg of cell digest and 1500 proteins identified from 250 pg, demonstrating the sensitivity needed for single cell proteomics. The proteins identified from 250 pg covered an abundance range of about 4 orders of magnitude, enabling quantitative proteome analysis at single cell level.



Identified proteins from a dilution series of HeLa digest ranging from 250 pg to 25 ng of peptide load using the Evosep Whisper method.



Protein distribution according to abundance rank shows a dynamic range of about 4 orders of magnitude.



Number of identified proteins from 250 and 500 pg of k562 cell digest over 48 consecutive runs.

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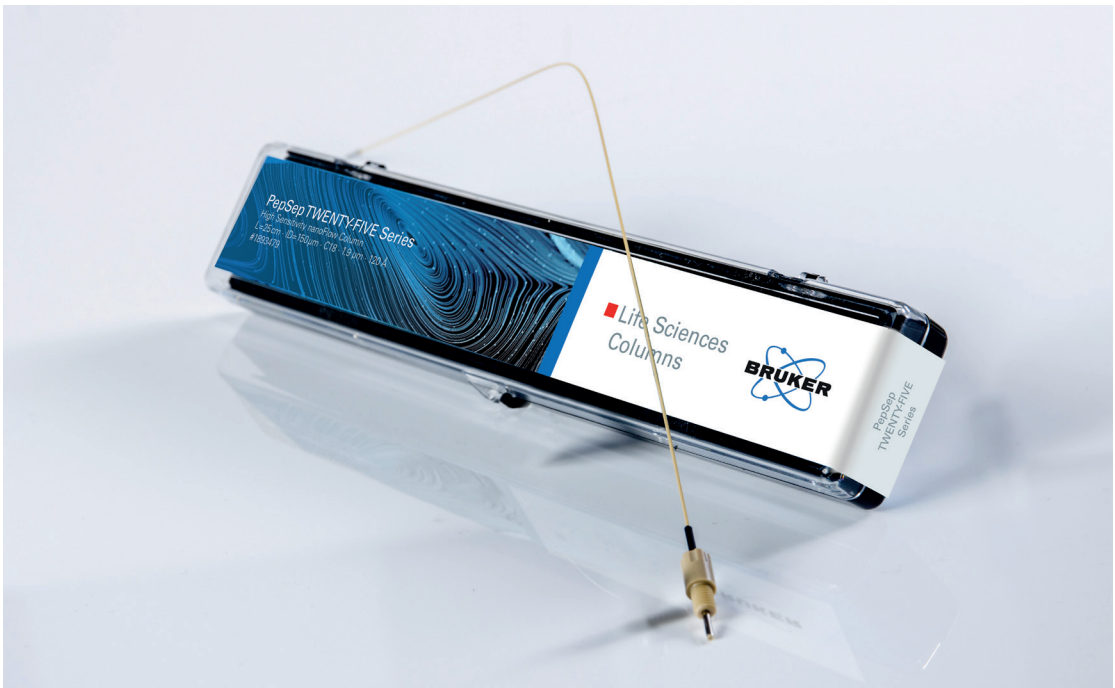
Order Information

Bruker PN#	Name	Application	Connection(s)
1895619	PepSep FOUR C18 4 cm x 150 µm x 1.9 µm	High Throughput	UHP/nanoConnect
1893472	PepSep TEN C18 10 cm x 75 µm, 1.9 µm	High Throughput	UHP/nanoConnect
1893473	PepSep FIFTEEN C18 15 cm x 75 µm, 1.9 µm	High Throughput	UHP/nanoConnect
1893476	PepSep TWENTY-FIVE C18 25 cm x 150 µm x 1,5 µm	High Sensitivity	UHP/nanoConnect
1893484	PepSep TWENTY-FIVE UHS C18 25 cm x 75 µm x 1,5 µm	Ultra-high Sensitivity Single Cell Immunopeptidomics	UHP/nanoConnect



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