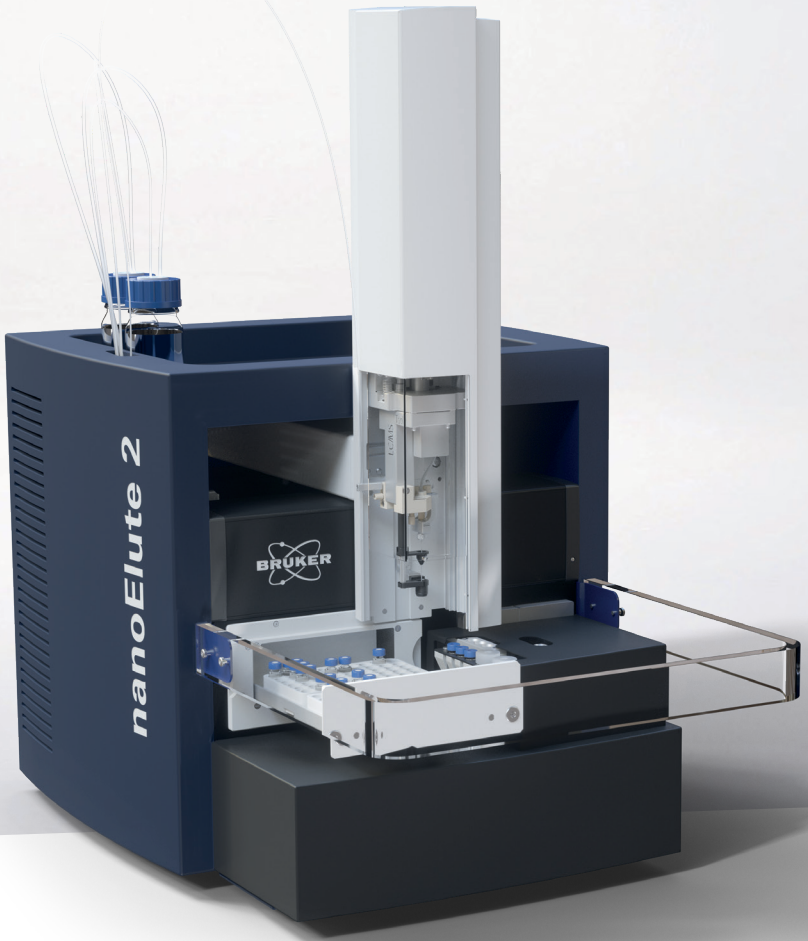


LIQUID CHROMATOGRAPHY SYSTEMS

nanoElute 2

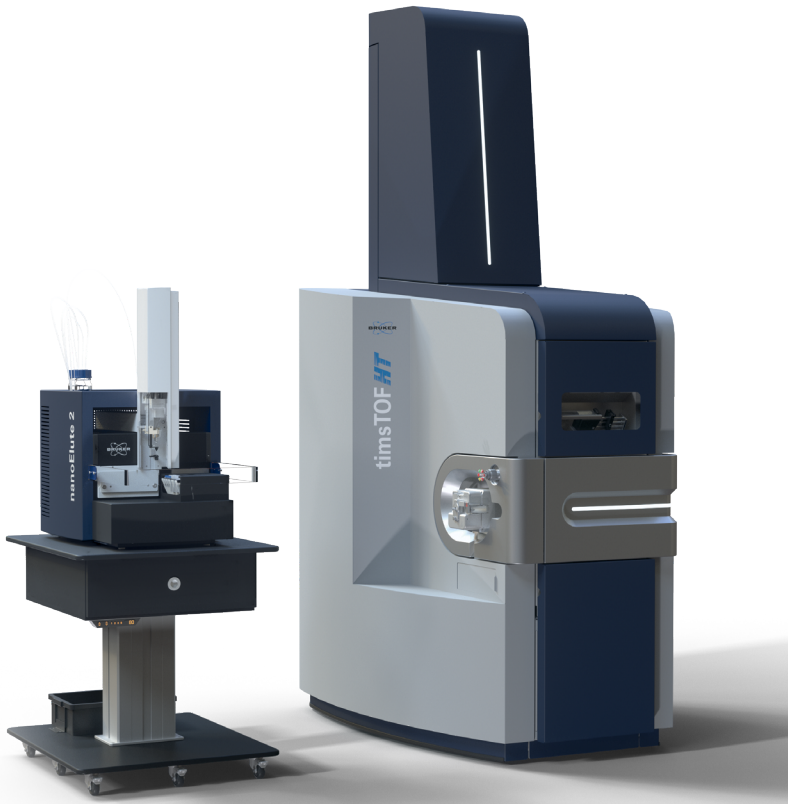
Ready for the Next Generation of 4D-Proteomics™

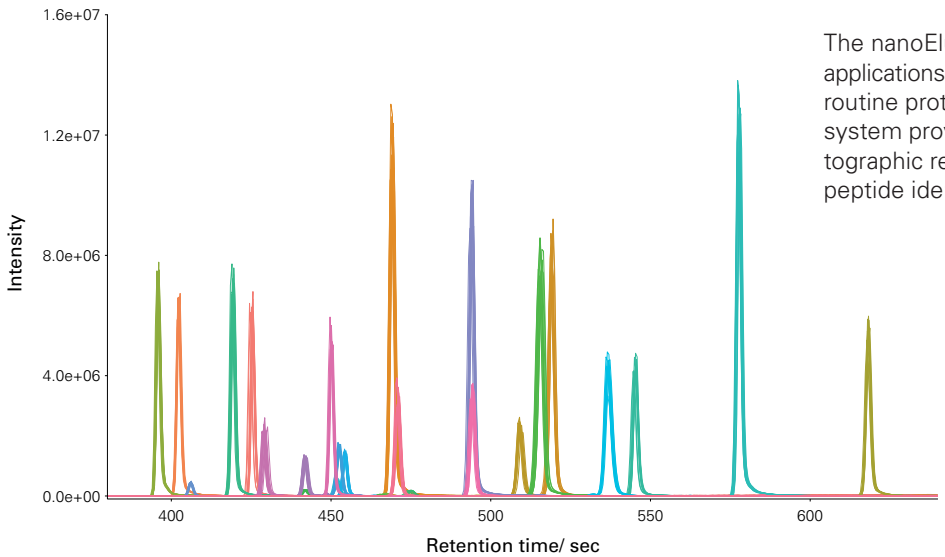
Innovation with Integrity

nanoElute 2

Built on the core principles of its predecessor, the nanoElute® 2 has been refined for unrivalled robustness, ultimate chromatographic performance, and ease-of-use.

- Unprecedented pump reproducibility and robustness
- Ultra-sharp peaks for the best proteomics performance
- Flexible user-controlled features and injection modes
- User friendly interface for early-adopters
- Assisted troubleshooting procedures for expert users
- Automatable sample preparation workflows
- Reach extreme LC-MS sensitivity for "label-free single-cell level" workflows





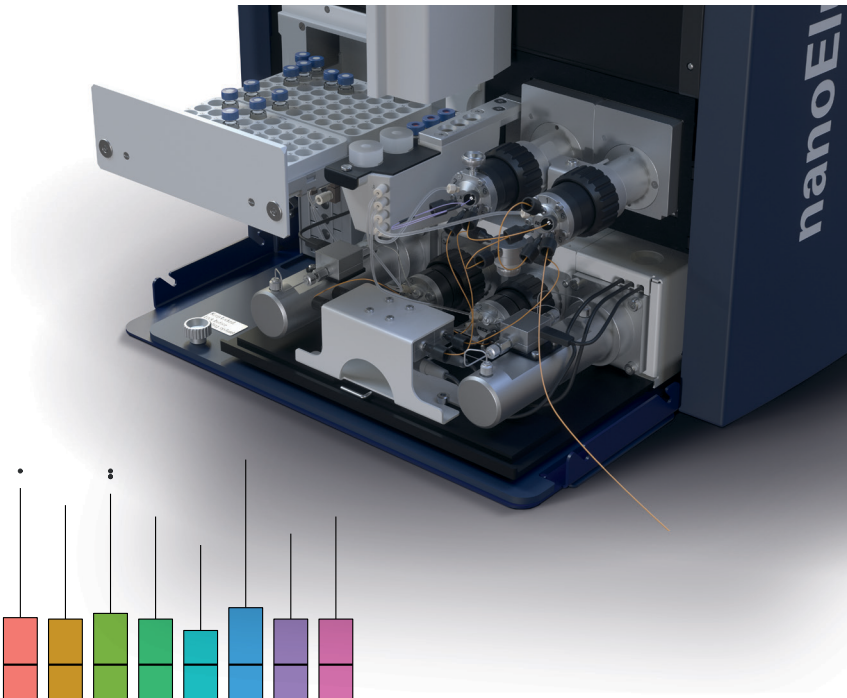
The nanoElute 2 covers a broad range of applications from single-cell to high-throughput routine proteomics. This next generation system provides you with the highest chromatographic resolution resulting in exceptional peptide identification and quantification.

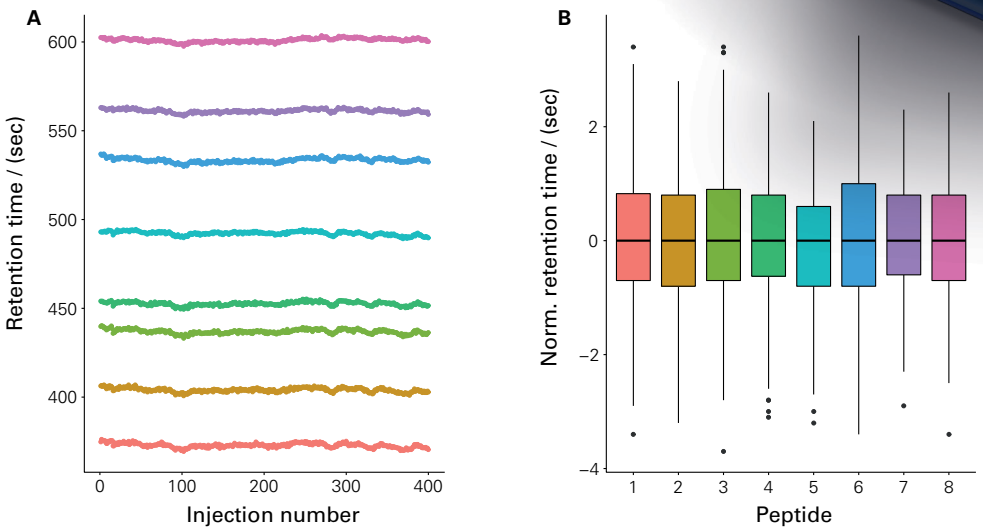
Robust chromatography
Overlaid extracted ion chromatograms (27 peptides) of 10 consecutive injections.
20 fmol BSA tryptic digest (Bruker Daltonics 8217498) have been injected onto a PepSep TWENTY-FIVE column (Part No. 1893476, 150 µm ID, 1.5 µm particle size) and separated by a 10 min gradient.

Unprecedented reproducibility and robustness

Unprecedented reproducibility and robustness achieved with:

- New, hardened switching valves, for extended lifetime
- Improved pump design
- Finger-tight, torque-limiting capillaries, for leak-free, zero dead volume connections, without risk of overtightening or damaging capillaries.





Stable retention times across hundreds of injections

(A) Extraction of 8 peptides (400 consecutive injections). 20 fmol BSA tryptic digest (8217498) have been injected onto a PepSep FIFTEEN column (Part No. 1895814 , 75 µm ID, 1.9 µm particle size) and separated by a 10 min gradient.

(B) Boxplot for median-normalized retention times show an average retention time deviation for each of the 8 peptides of < 2 sec.

Frank Menke, Ph.D.

Head of Proteomics at The Sainsbury Laboratory and honorary lecturer at the University of East Anglia, UK

"The simple-to-use nanoElute 2 LC system coupled to a timsTOF Pro has significantly enhanced our protein IDs in comparison to our other platforms. Coupled to superb Aurora column separation, it looks to be a step change in chromatographically resolving isobaric phosphopeptides, enabling even more unambiguous phosphosite annotations."

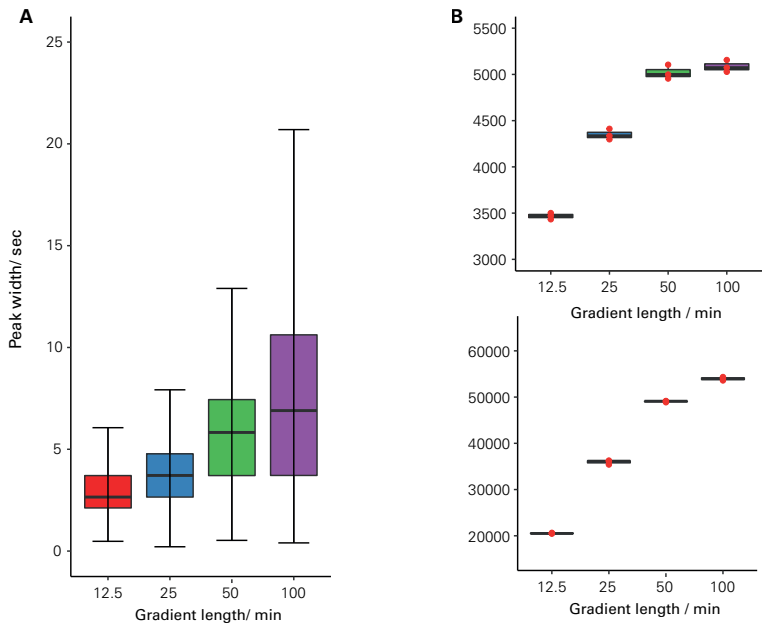
Ultra-sharp peaks and best proteomics performance

The nanoElute 2 provides precise and reproducible gradient separation for different gradient lengths, resulting in narrow peak widths and excellent peak capacity.

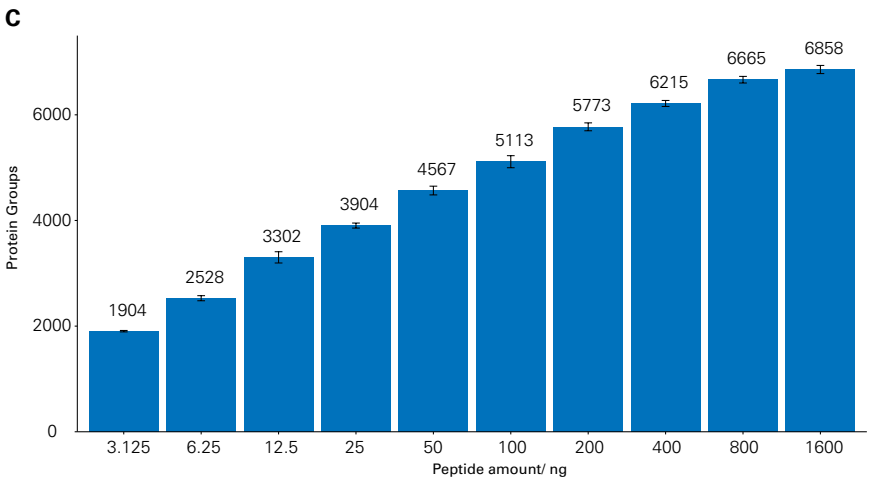
In combination with the timsTOF HT reliable performance was achieved for all injected quantities. (see Figure C)

This within a 41 min runtime method for 1600 ng K562 tryptic digest by data dependent acquisition parallel accumulation serial fragmentation PASEF (DDA).

Reliable performance of 50 ng K562 digest injections at different gradient length
(A) Corresponding boxplots with FWHM for eluting peaks indicate consistent and narrow peak widths and just a moderate increase for longer gradients. **(B)** Boxplot for protein group and precursor identifications dependent on gradient length (DDA-PASEF - timsTOF Pro 2, and PaSER realtime search engine with TIMScore).

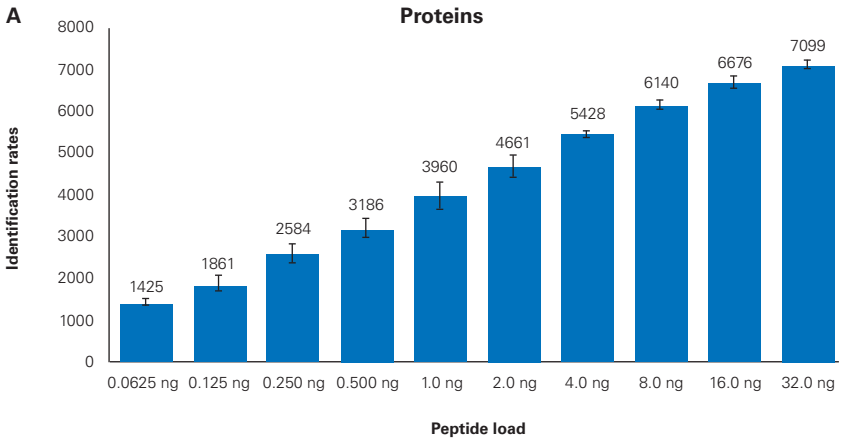


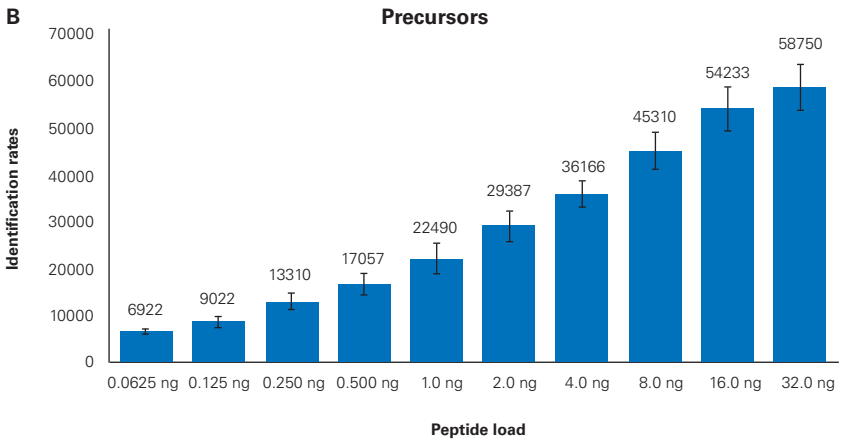
Reliable performance for high peptide amount
More than 6800 protein groups identified using the PaSER realtime search engine with TIMScore™ for dda-PASEF of K562 tryptic digest with a PepSep Twenty-five series column (150 µm ID, 1.5 µm particle size) within a 41 min runtime on the timsTOF HT.



Optimized platform for challenging OMICS analysis

The timsTOF SCP in combination with the nanoElute 2 UHPLC system achieves unprecedented sensitivity. About 4000 protein groups and over 22,000 precursors were identified from 1 ng of HeLa using a 80 min runtime method (i.e. gradient length of 66 min) and a data-independent acquisition parallel accumulation serial fragmentation (dia-PASEF).





Reliable for low sample amount and single-cell applications
Identification of **(A)** 1400 to 7100 protein groups and **(B)** 7000 to 59,000 precursors from 62.5 pg to 32 ng HeLa tryptic digest within 45 min run time on a IonOpticks Aurora column (75 µm ID x 25 cm) (dia-PASEF - timsTOF SCP, and PaSER™ realtime search engine with TIMScore™).

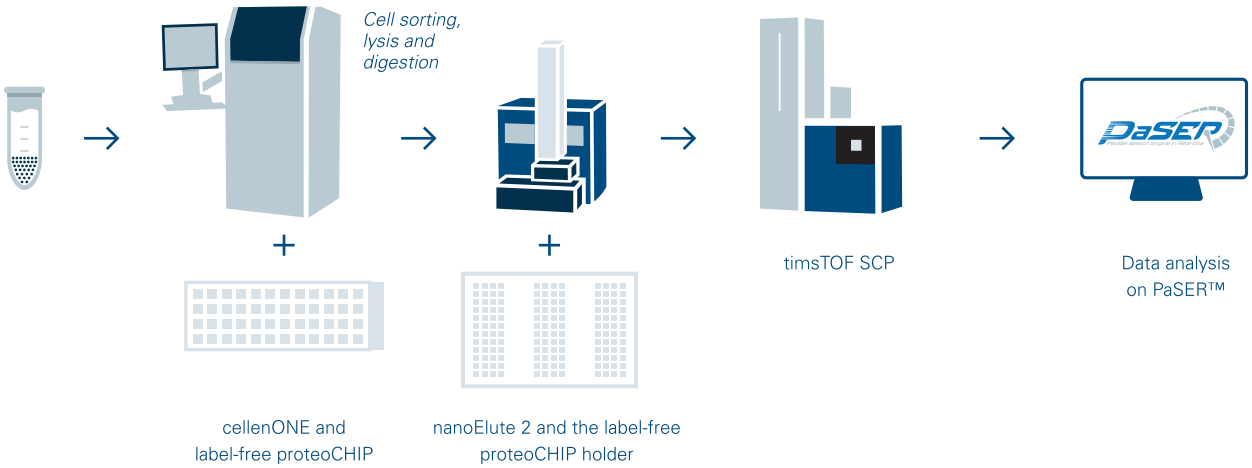
Prof. Dr. Stefan Tenzer

Institute for Immunology, University Medical Center of the Johannes-Gutenberg University, Mainz, Germany

"The combination of the nanoElute 2 with a timsTOF SCP enables the reproducible identification of >1300 proteins from only 62.5 pg of HeLa digest, making this an optimal platform for our most challenging proteomics and immunopeptidomics projects."

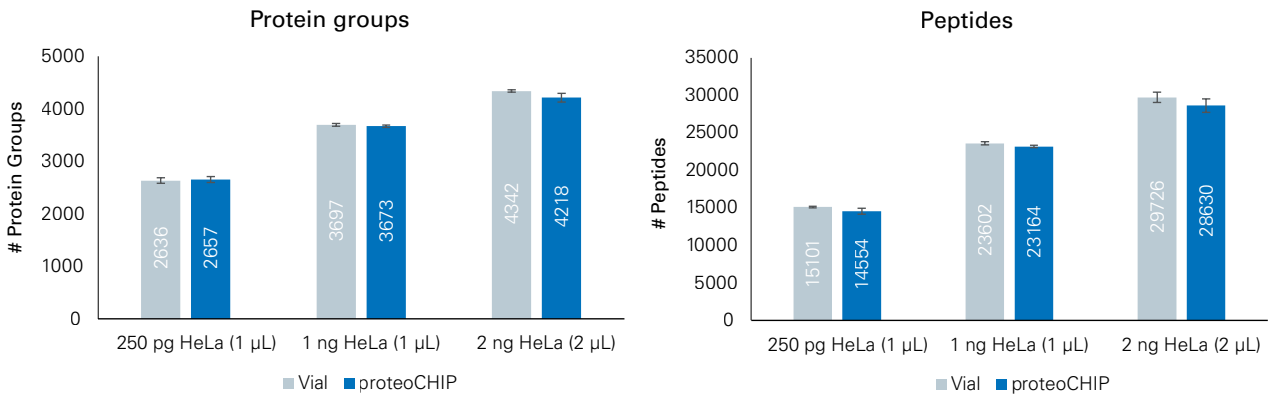
Extreme sensitivity for label-free single-cell level workflows

Use the nanoElute 2 and the timsTOF SCP for end-to-end single cell label-free proteomics workflows. The nanoElute 2 injects directly from the label-free proteoCHIP holder used in the cellenONE cell sorter. In this workflow up to 144 single cells can directly be tranferred from the cellenONE to the nanoElute 2 autosampler, after sorting and preparation, without pipetting steps, for ultra-sensitive proteomics analysis using the timsTOF SCP and TIMS-DIA-NN.



Fully automated label-free single cell proteomics workflow using the cellenONE with the lable-free proteoCHIP and with holder support in the nanoElute 2 for ultra-sensitive single cell analysis on the timsTOF SCP and data analysis on the PaSER™ using TIMS-DIA-NN.

Assessment of sample pick-up of 250 pg and 1 ng in 1 µL total volume, and 2 ng in 2 µL total volume of peptides from a HeLa cell lysate digest directly injected from wells of the label-free proteoCHIP showed excellent reproducibility in protein group and peptide identification rates. Injections from the label-free proteoCHIP and from an autosampler vial demonstrated comparable results on protein group and peptide identification rates at different peptide concentrations and volumes.



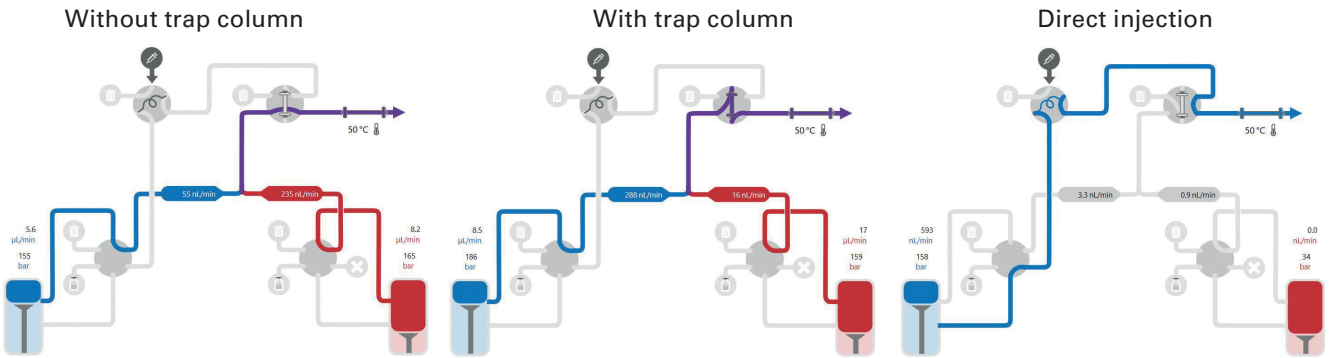
Repetitive injections of different peptide concentration (250 pg, 1 ng or 2 ng) of a HeLa cell lysate digest either injected from an autosampler vial (grey) or from the proteoCHIP (blue) (25 min total run time) with indicated volumes pipetted into each well show excellent reproducibility on protein group (A) and peptide (B) level.

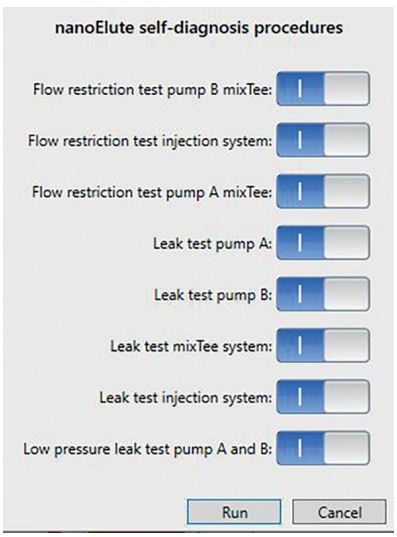
User-friendly and trouble-free chromatography

With its unique valve design the nanoElute 2 enables software-controlled flow paths for dynamic inclusion of the trap column and backflushing the sample for sharper peaks. It retains the top desirable functionalities of its predecessor ensuring:

- Dynamic on-the-fly method configuration
- Efficient, predefined column washing and re-equilibration
- Fully integrated and intelligent software-control
- Built-in quality control and leak management
- Seamless switch between trap-and-elute, direct load and direct infusion experiments

These features reduce the need to compromise between high performance, flexibility and robustness, therefore giving you full confidence in your results!





Fully automated self-testing and diagnosis is embedded into a user-friendly interface for early adopters, as well as assisted troubleshooting procedures for experts.

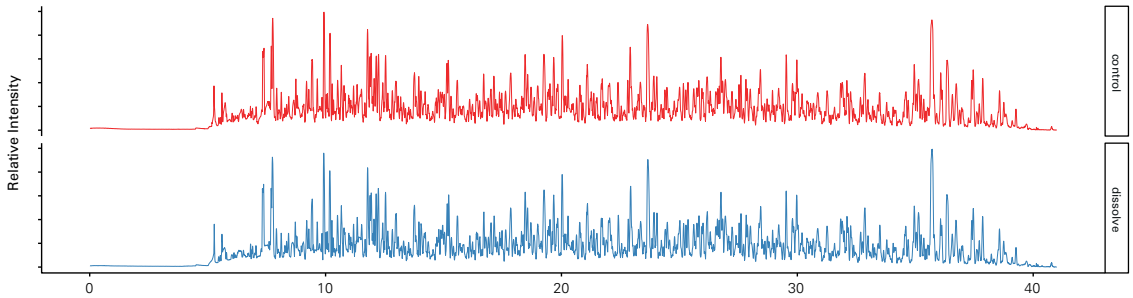
New procedures allow for step-by-step evaluation of flow-paths to readily locate potential issues for easy troubleshooting and maintenance.

Sample preparation procedures provide flexibility for user-defined performance evaluation, autosampler washing, and solvent exchange procedures.

Automatable sample preparation workflows

Automatable sample preparation procedures alleviate the need for manual intervention can be configured based on user-defined input settings. The following liquid handling functionalities provide the means to dissolve and mix samples just prior to LC-MS analysis:

- Add from vial
- Dissolve
- Derivatize



Consistent sample preparation prior to injection

Base peak chromatogram of 100 ng K562 tryptic digest injected onto a PepSep Twenty-five series column (150 µm ID, 1.5 µm particle size). Peptides were resuspended in 0.001 % DDM by the autosampler (dissolve) just prior to Injection (52589 +/- 1020 precursors identified). Peptides dissolved in 0.001 % DDM in advance served as control (51475 +/- 699 precursors identified).

Henrik Johansson, Ph.D.,

Senior Scientist in Cancer Proteomics, Department Oncology-Pathology, Karolinska Institute, Solna, Sweden

"The nanoElute 2 autosampler is providing key benefits for our clinical research proteomics pipeline. It enables us to monitor the LC performance and now perfectly supports 96 or 384 well plates coming from our robotic platform. The tryptic peptides are directly dissolved in the plate prior to injection, avoiding manual intervention and thus streamlining our workflows."

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