BIOGNOSYS GROUP

PepSep Mass Spectrometry Life Science Consumables

High-quality Peptide Separation with PepSep Advanced

- **Comprehensive Coverage**
  Sharp peak shapes increase peptide and protein identifications.
- **Accurate Quantification**
  Symmetrical peaks enable reliable area quantification.
- **Robust Performance**
  Stable backpressure ensures consistent, dependable operation.
- **Confident Identifications**
  Reproducible retention times for consistent separations.

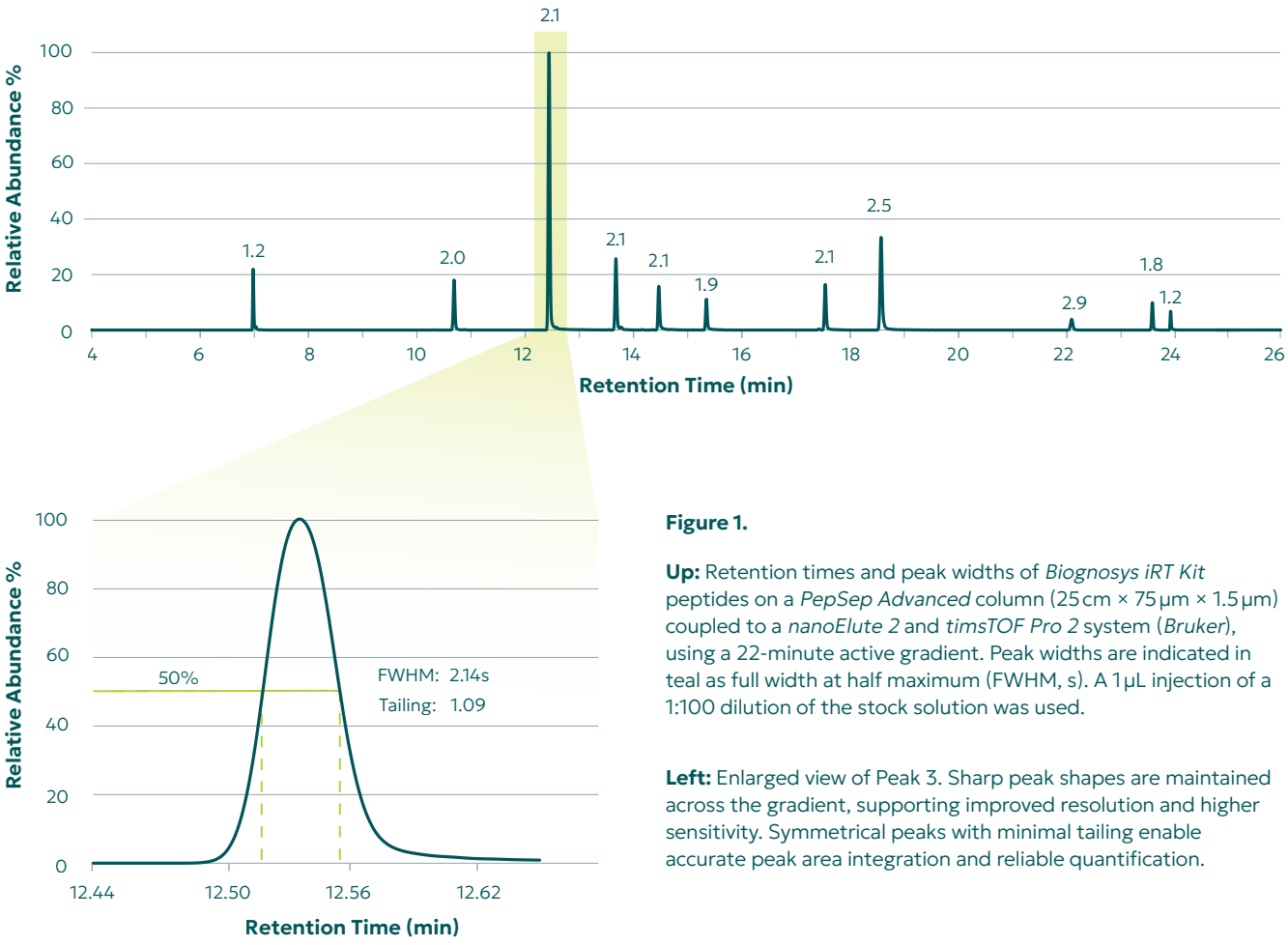


Figure 1.

Up: Retention times and peak widths of *Biognosys iRT Kit* peptides on a *PepSep Advanced* column (25 cm × 75 µm × 1.5 µm) coupled to a *nanoElute 2* and *timsTOF Pro 2* system (*Bruker*), using a 22-minute active gradient. Peak widths are indicated in teal as full width at half maximum (FWHM, s). A 1 µL injection of a 1:100 dilution of the stock solution was used.

Left: Enlarged view of Peak 3. Sharp peak shapes are maintained across the gradient, supporting improved resolution and higher sensitivity. Symmetrical peaks with minimal tailing enable accurate peak area integration and reliable quantification.

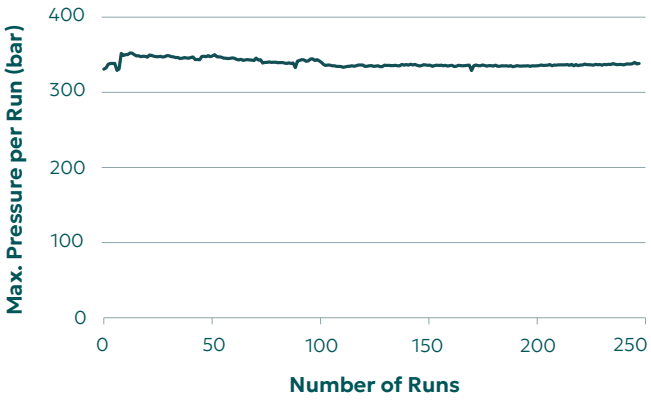
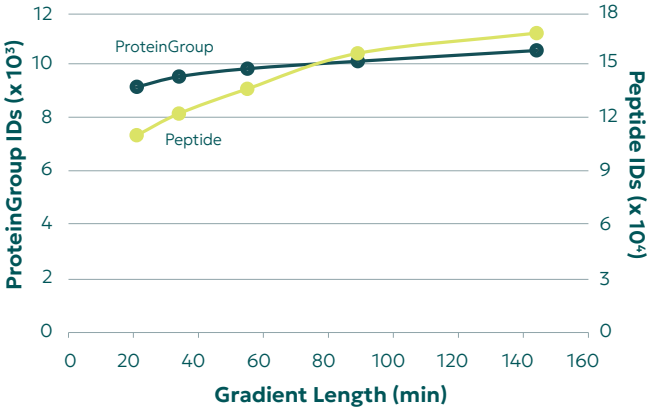


Figure 2. Maximum backpressure recorded across 240 sequential injections of different sample types, with 800 ng peptides injected per run, using a single *PepSep Advanced* 25 cm × 75 µm × 1.5 µm column.

Operating pressure remains highly consistent over extended use, indicating robust packing quality, minimal drift, and dependable long-run performance for demanding proteomics workflows.

Figure 3. Protein group and peptide identifications from triplicate analyses of 800 ng HEK293 tryptic digest acquired on the same *PepSep Advanced* column described in Fig. 1 across five gradient lengths.

Strong protein group and peptide identifications are maintained across all evaluated gradient lengths, enabling flexible method selection for high-throughput proteome-wide screening, and in-depth peptide-level profiling.



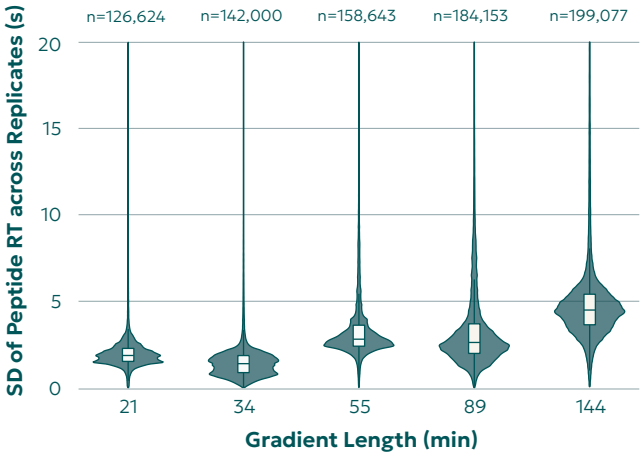


Figure 4. Standard deviation of peptide retention time across triplicate runs for each gradient length from the same experiment shown in Fig. 2; n indicates the number of modified sequences.

Retention time variation remains tightly controlled across all evaluated gradient lengths, demonstrating consistent chromatographic performance. This allows precise retention time prediction and precise iRT regression, ideal for high-throughput targeted proteomics, robust spectral-library alignment in DIA and reliable match-between-runs in DDA.

Shared note: All data were acquired on a *proteoElut-timsTOF HT* system using a range of gradient lengths. *diaPASEF* methods were optimized for each gradient. Data were processed in *Spectronaut 20* using *directDIA*.

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