Electronic Supplementary Material (ESI) for Analyst.

Electronic Supplementary Information

Nanospray HX-MS configuration for structural interrogation of large protein systems

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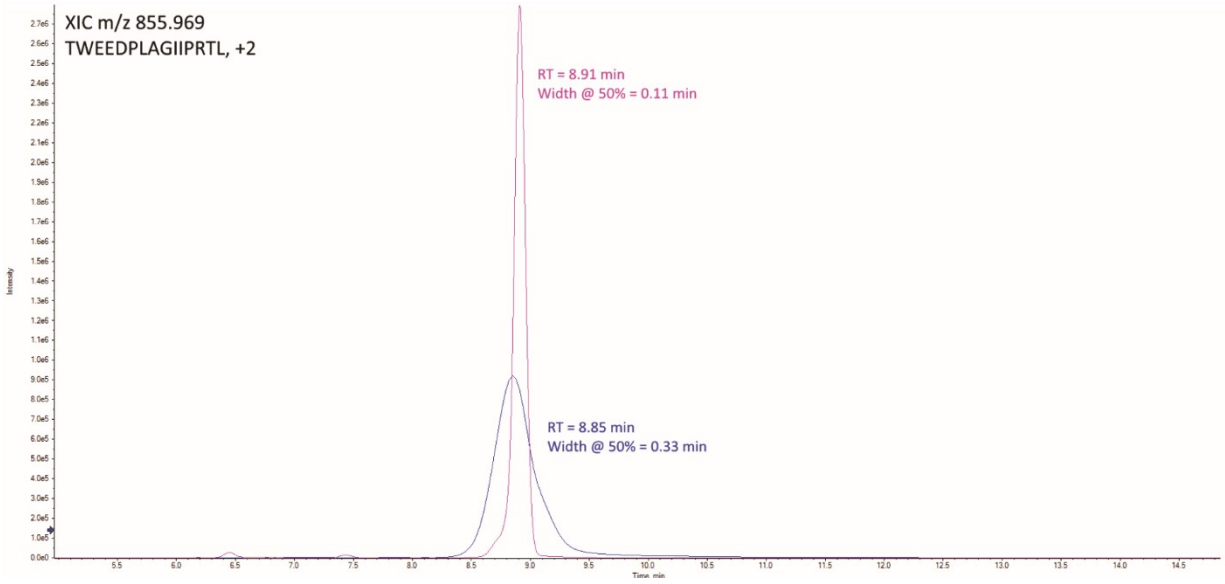

Figure S1. Extracted ion chromatograms for m/z 855.969 (Eg5, TWEEDPLAGIIPRTL, +2) collected in the micro flow regime with a conventionally-cooled column (blue) and the in-source cooler (pink). Identical amounts injected (10 pmol).

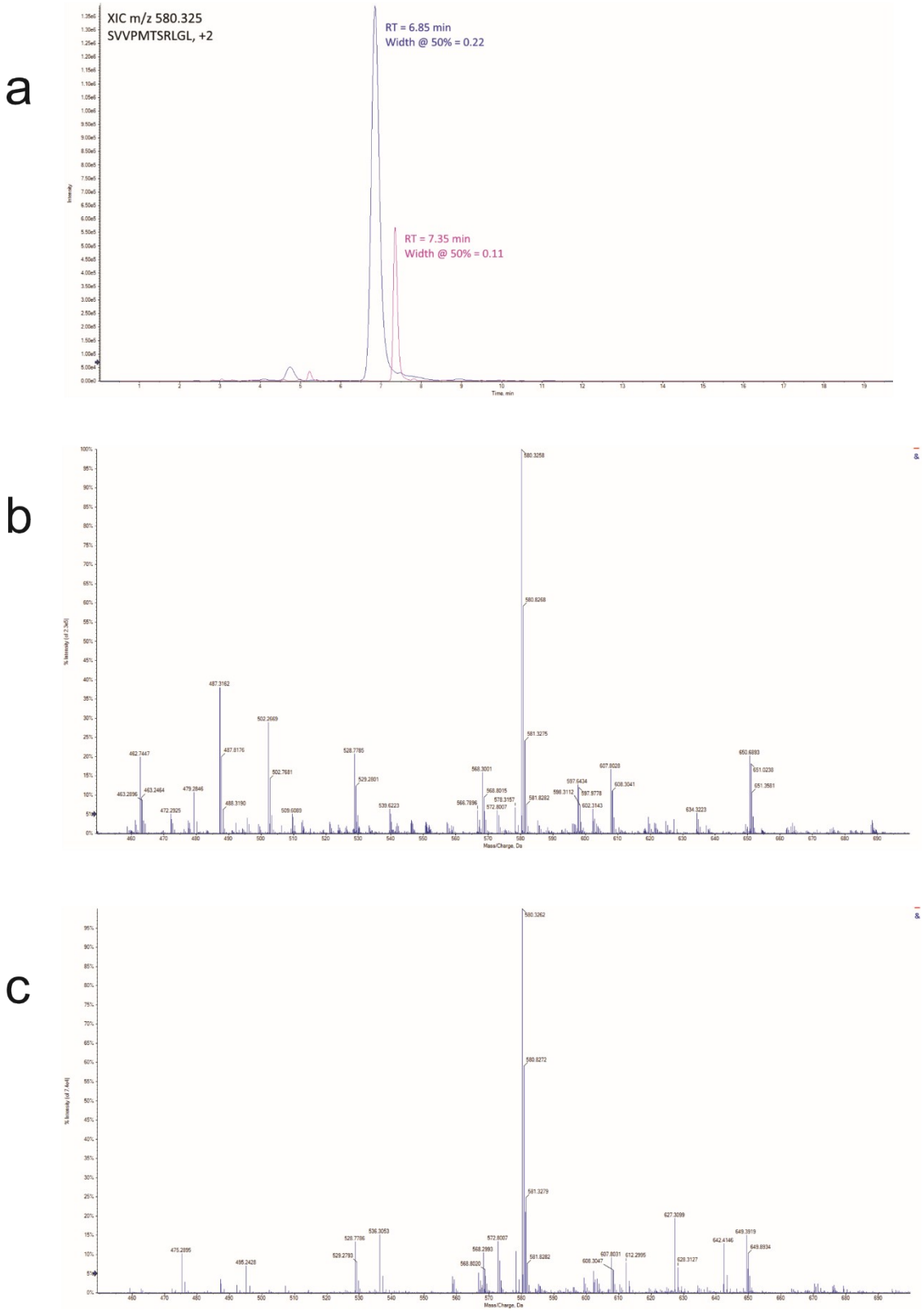

Figure S2. (a) Extracted ion chromatograms for m/z 580.325 (DNA-PKcs, SVVPMTSRLGL, +2) collected with the conventional microflow system (blue) and the in-source nanoHX-MS configuration (pink). Injected amounts were 10-fold lower for the nanoHX-MS system (0.5 pmol vs 5 pmol). (b) Corresponding MS spectrum extracted from a 0.22 window centered on 6.85min for the sample collected with the conventional microflow system. (c) Corresponding MS spectra extracted from a 0.11 window centered around 7.35min for sample collected with the in-source

nanoHX-MS configuration. MS intensities are shown relative to the most intense peak in the spectrum. For (b) and (c), spectra represent integrations over the natural peak width of a representative LC feature, and show a reduction in spectral complexity for the nano source when attempting to get the “best” data for a given feature.

[see separate file]

Figure S3. Sequence coverage map for DNA-PKcs for deuterated proteolytic peptides analyzed with the in-source nanoHX-MS system.