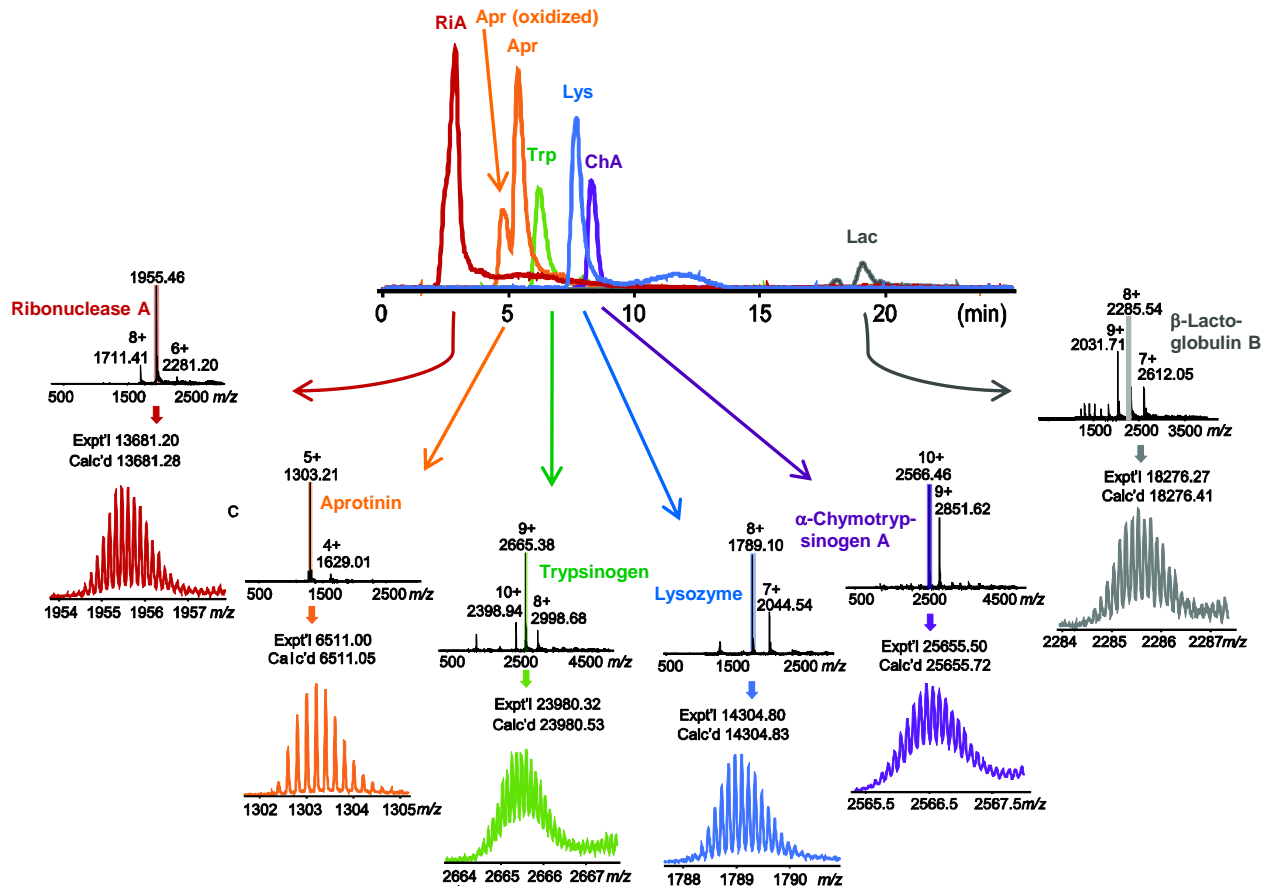


***** **NEW! HIC-MS for Top-Down Proteomics** *****

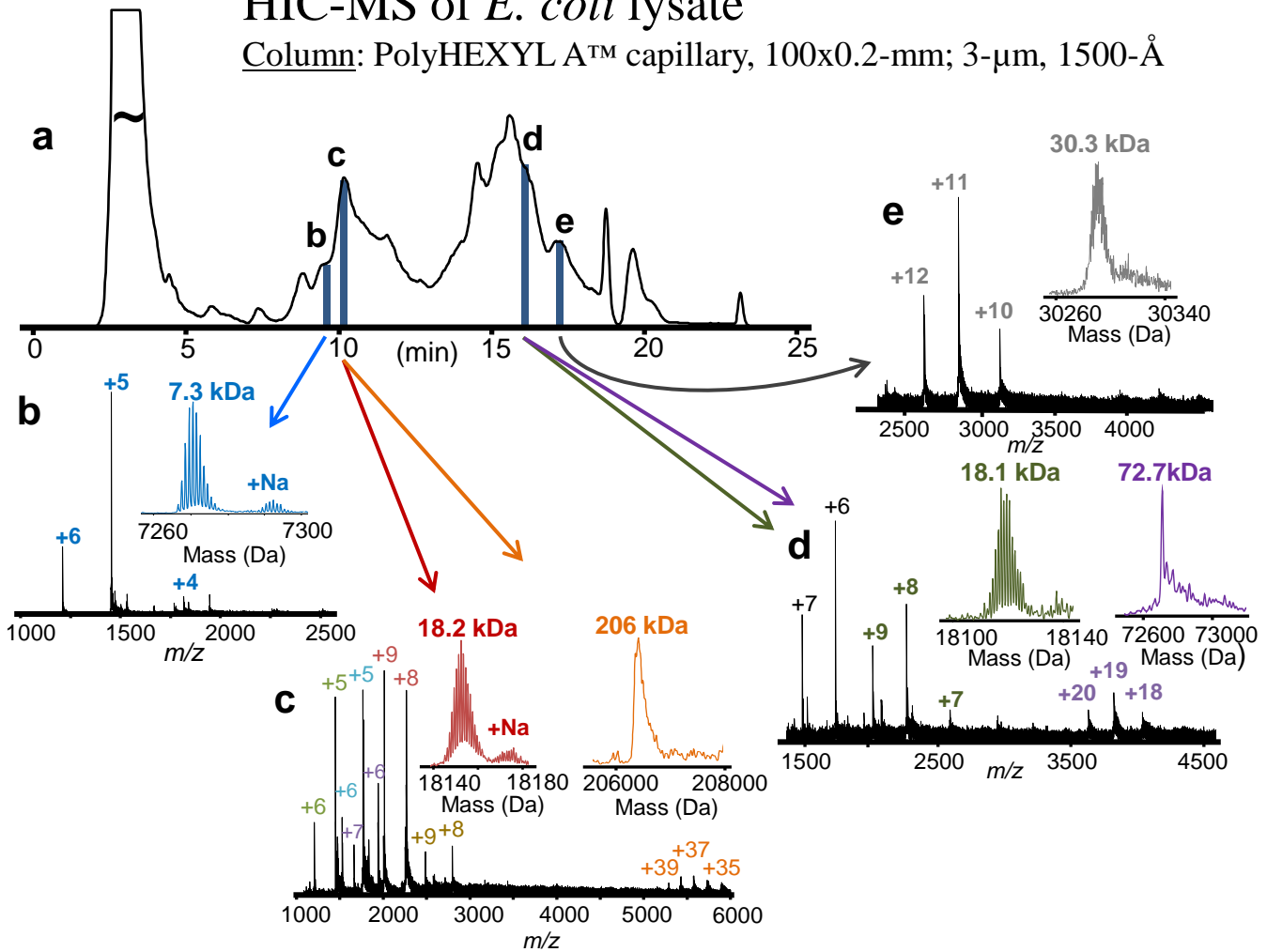
Our **new series of materials** for HIC (**Hydrophobic Interaction Chromatography**) permit the retention of proteins using concentrations of ammonium acetate that are compatible with direct analysis via mass spectrometry. Proteins can be separated and eluted with their native structures intact. This is useful for top-down proteomics and permits the analysis of some proteins that are not compatible with the conditions of reversed-phase chromatography. The example below shows base peak chromatograms of some protein standards, their mass spectral charge state patterns, and isotopic resolution in the deconvoluted mass spectra. Note the separation of aprotinin from an oxidized variant.



Column: PolyHEPTYL A™ capillary, 100x0.2 mm; 3-μm, 1500-Å
Mobile Phase: A) 1 M ammonium acetate; B) 20 mM ammonium acetate with 50% ACN
Gradient: 15' linear, 0-100% B, then 5' at 100% B Flow: 2.4 μl/min
Detection: maXis™ Plus Q-TOF mass spectrometer (Bruker Daltonics)

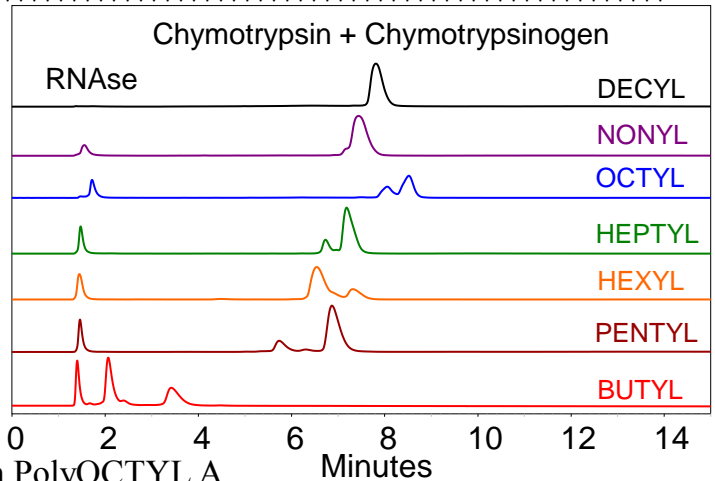
HIC-MS of *E. coli* lysate

Column: PolyHEXYL A™ capillary, 100x0.2-mm; 3-μm, 1500-Å



Comparison of different HIC materials

Conventional HIC materials like PolyBUTYL A are not hydrophobic enough to retain many proteins well with Am-OAc buffers. Our PolyPENTYL A and more hydrophobic new materials do retain them. However, sensitive proteins (here, RNase) may denature on PolyOCTYL A



and more hydrophobic materials before they can elute. The new method is probably going to be implemented using PolyPENTYL A, PolyHEXYL A, and PolyHEPTYL A. A particularly hydrophobic protein, such as an **antibody-drug conjugate** (ADC), might best be run using PolyPENTYL A or even PolyBUTYL A.

PolyBUTYL A, PolyPENTYL A, PolyHEXYL A, PolyHEPTYL A, PolyOCTYL A, PolyNONYL A, and PolyDECYL A are trademarks of PolyLC Inc.

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