Charge heterogeneity analysis of monoclonal antibodies is a crucial area of research. Similar to polar pesticides, LC-MS methods have short-comings in terms of separation selectivity and sensitivity. Capillary electrophoresis (CE)-based separation coupled with mass spectrometry is a powerful tool for analyzing such molecules. Deconvoluted masses were consistent with expected mass shifts, within the error of the mass detection, from a prior characterization by CE.[1]

Results illustrate the potential of CE-MS for analyzing complex mixtures. For such we have evaluated a varied collection of real-world analytes, primarily biomolecules, to verify the method’s ability to analyze complex samples. Metabolites can also be resolved and identified in negative ESI mode by a CE-based separation. Larger oligosaccharides, when labeled with an anionic dye like aminopyrene-trisulfonic acid (APTS), enable released glycans analysis from proteins of therapeutic and clinical nature. Moving higher in the mass range, peptides, translational modifications, and binding partners can be separated to identify charge variants that contribute to stability and efficacy. Collectively these examples demonstrate the power of CESI-MS for analyzing complex mixtures in a high-throughput manner.

Impact Protein Analysis. Change heterogeneity analysis of monoclonal antibodies is a crucial area of research. Capillary electrophoresis (CE)-based separation coupled with mass spectrometry is a powerful tool for analyzing such molecules. Deconvoluted masses were consistent with expected mass shifts, within the error of the mass detection, from a prior characterization by CE.[1]

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