

LC- and CE-MS ANALYSIS IN BIOTECHNOLOGY : A STATUS REPORT

In this presentation, we will first speak on the career of Wolfgang Goetzinger who was a post doc in my lab in the 1990s. It is very fitting to have this memorial symposium in his memory. We will then turn to discuss peptide and protein analysis in biotechnology using liquid phase separations (LC and CE) coupled to mass spectrometry. The increasing power of MS in terms of sensitivity, scan speed, and mass range has opened up new opportunities for separations. In terms of increased sensitivity, new approaches to host cell analysis are allowing identification of individual impurities down to the low ppm level. Advances in CE microfluidics and small particle LC columns coupled to MS are having an impact as MS speed increases. In terms of the high mass range, improved analysis of intact proteins and large fragments are occurring, leading to a more complete characterization of biopharmaceuticals. To fully utilize the advances in MS will require further improvements in separations. We will suggest several areas of further development, stressing the need to focus on the integration of the full workflow, and not the component parts in isolation.

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Barry L. Karger is the Emeritus James L. Waters Chair in Analytical Chemistry and Distinguished Professor. He was the Founding Director of the Barnett Institute of Chemical and Biological Analysis at Northeastern University. He has been an active researcher with 375 publications and 50 patents in the field of bioanalytical chemistry, with particular emphasis in liquid chromatography, capillary electrophoresis and mass spectrometry. Dr. Karger has received many honors including three American Chemical Society awards, the prestigious Bergman Medal from the Swedish Chemical Society, the Herovsky Gold Medal from the Czech Academy of Sciences, and the Beckman Medal for major contributions to electrophoretic separations. He has been a major contributor to the development of HPLC, and his technology in capillary electrophoresis played a significant role in the Human Genome Project. More recently he was involved in the development of new technologies for proteomics, especially trace level LC/MS analysis of proteins in biological matrices, and comprehensive characterization of complex protein structures. He has actively collaborated with a number of companies in the biotechnology industry, especially in the characterization of biopharmaceuticals and the biology of production cell lines.