



Applying lessons from sequencing the first human genomes to top-down proteomics

Neil L. Kelleher, PhD

Kelleher Research Group, Northwestern University, Illinois, USA

With advances in protein research, the demand for analytical tools within the field of proteomics is steadily increasing. In recent years, CE-MS has gained increasing interest in the scientific and industrial community. This is due to its many advantages and the fundamentals of its separation principle for intact protein analysis. Top-down mass spectrometry (TDMS), as an emerging proteomics approach, provides an in-depth characterization of posttranslational modifications and proteoforms. In addition, native separation can also be achieved using CE, enabling the characterization of proteins and related interactions in their biologically functional states. Therefore, native CE in combination with TDMS represents a promising concept to face and overcome current and future challenges associated with protein analysis. Denaturing-mode TDMS will also be described for proteoform sequencing, which has a poetic link to scale-up phase of the Human Genome Project in the late 1990's that will be described in the course of this brief seminar.