Genome-level and transcriptome-level information cannot accurately reflect proteome-level information because post-transcriptional regulations modulate gene expression, because protein post-translational modifications (PTMs) influence protein function, and because most proteins in the cell function as protein complexes. Characterization of the proteome is imperative to understand the roles played by proteoforms and protein complexes in development and diseases. We believe top-down proteomics is a powerful strategy for delineating proteoforms and even protein complexes in the cell in discovery mode and at a global scale. Novel analytical tools with high peak capacity and high sensitivity are vital for boosting the proteome coverage from top-down proteomics because of the high complexity of the proteome. In my talk, I will introduce our recent progress in developing novel capillary electrophoresis (CE)-mass spectrometry (MS)-based analytical methods for large-scale and highly sensitive top-down proteomics.