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This volume describes novel and emerging analytical technologies for analysis of proteins with the emphasis on technologies aimed to address characterization "knowledge gaps" and/or improve our ability to measure specified attributes with improved selectivity, sensitivity, resolution, and throughput.

Higher order structure of proteins is a recognized important attribute of mAbs, with potential implications on stability, safety, and biological function of these large molecules. This book, the last in a series of three volumes, touches on topics ranging from X-ray crystallography, NMR, hydrogen-deuterium exchange mass spectrometry, covalent labeling techniques, and ion mobility mass spectrometry.

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