

This book presents a survey of recent developments in protein biochemistry. As new analytical methods and techniques become available to the protein chemist for isolating, purifying, analyzing, and characterizing novel proteins, new insights into basic and applied biochemistry are made possible. Top researchers in the field of protein biochemistry describe modern methods to address the challenges of protein purification by three-phase partitioning, and their folding and degradation by the functions of chaperones, or the folding of membrane proteins in detergents, or of the control of glycoprotein folding in the endoplasmic reticulum. Methods are described to follow dynamic changes in conformation and folding processes, or the protein import into the intermembrane space. Direct on membrane identification of gel-resolved proteins by Maldi mass spectrometry allows proteome analysis after D-DIGE and discovery of biomarkers in pathophysiological conditions (Chronic Obstructive Pulmonary Disease, Duchenne Muscular Dystrophy). Mass spectrometry determines protein complexes after chemical cross-linking and small molecule binding sites by Capture Compound MS. Correlated single-crystal spectroscopy and synchrotron X-ray crystallography are described as well as wide-angle X-ray solution scattering (WAXS) of proteins to generate information about structure, flexibility and dynamics. The significance of peptide purity for fibril formation is addressed as well as the use of target oriented peptide arrays in palliative approaches in mucoviscidose. The chemical modification in living cells has become possible and also probing of protein dynamics in vivo. The design and application of protein epitope mimetics just as the structural resolving of the misfolding of various mutant proteins in serpinopathies (α_1 -antitrypsin) enlarge our tools in resolving pathophysiological imbalances.



www.degruyter.com
ISBN 978-3-11-025233-0