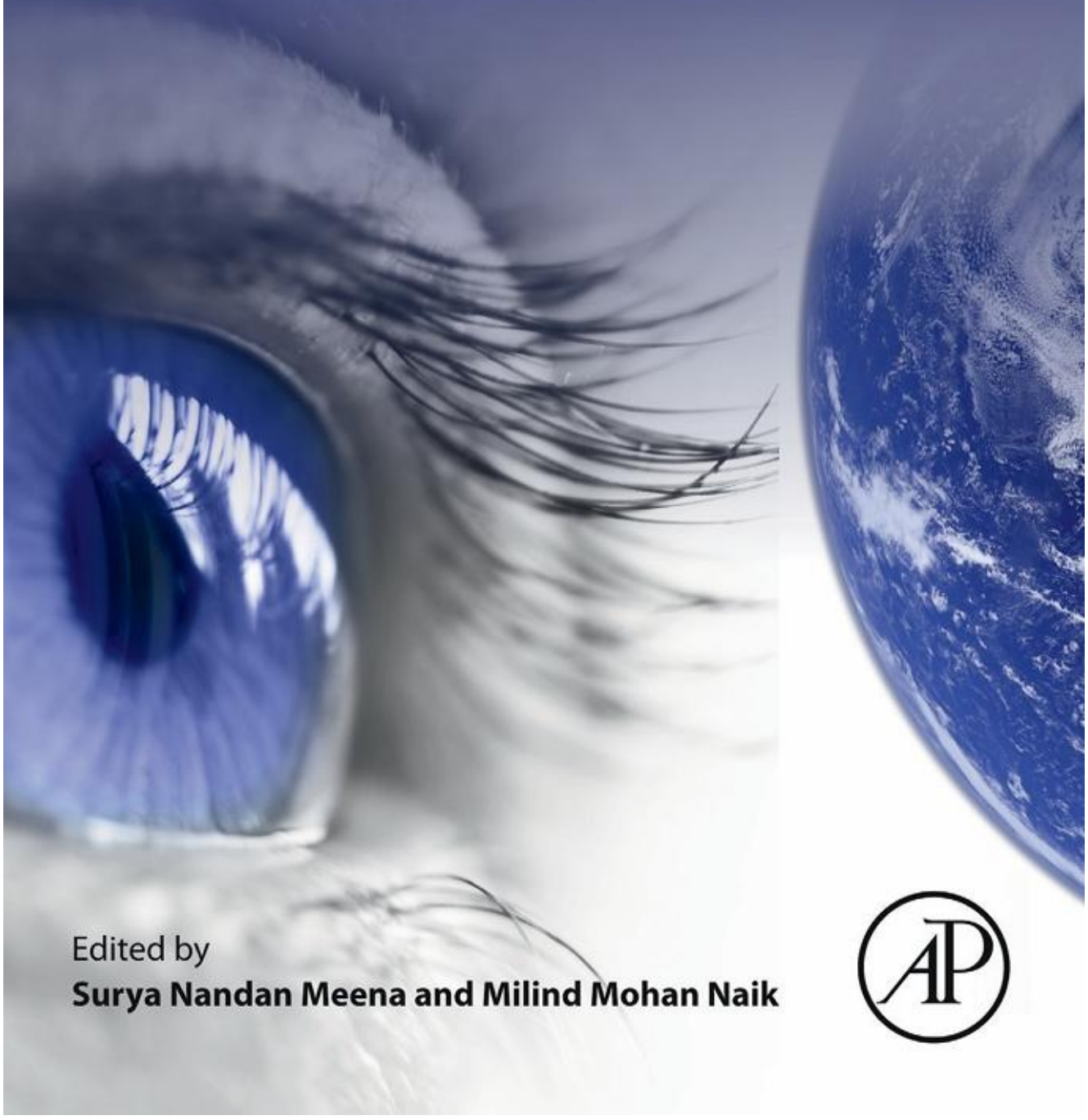
Advances in Biological Science Research

A Practical Approach



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ACADEMIC PRESS
An imprint of Elsevier

Academic Press is an imprint of Elsevier
125 London Wall, London EC2Y 5AS, United Kingdom
525 B Street, Suite 1650, San Diego, CA 92101, United States
50 Hampshire Street, 5th Floor, Cambridge, MA 02139, United States
The Boulevard, Langford Lane, Kidlington, Oxford OX5 1GB, United Kingdom

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Library of Congress Cataloging-in-Publication Data
A catalog record for this book is available from the Library of Congress

British Library Cataloguing-in-Publication Data
A catalogue record for this book is available from the British Library

ISBN: 978-0-12-817497-5

Publisher: Andre G. Wolff
Acquisition Editor: Linda Versteeg-buschman
Editorial Project Manager: Sandra Harron
Production Project Manager: Poulouse Joseph
Cover Designer: Vicky Pearson Esser

Typeset by TNQ Technologies

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Chapter 5

Structural analysis of proteins using X-ray diffraction technique

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5.1 Introduction

Proteins are large complex biomolecules that form an essential component of diet. They are indispensable for normal functioning of biological systems in all forms of life and play a central role in determining nutritional value of food. Besides their nutritional role, proteins also form a structural basis of various functional properties of foods. The functional roles of proteins result from physicochemical properties such as solubility, viscosity, water binding, gelation, cohesion/adhesion, elasticity, emulsification, and foaming. The structure of proteins determines their shape, size, amino acid sequence, hydrophobicity, hydrophilicity, charge, and ability to change in a given environment [1]. The structures of proteins are classified as: (1) primary, which refers to linear sequence of amino acid polypeptide chain, (2) secondary, in which highly regular local substructures like α-helix and β-sheet are formed due to hydrogen-bonding interactions between main chain polypeptide groups, (3) tertiary, which refers to three-dimensional (3D) form of a single protein, and (4) quaternary, are those that contain complex 3D multisubunits. Proteins form the important component of structure, function, and regulation of cells, tissues, and organs in the body. In order to understand the working of biosystems, detailed knowledge of 3D structures of proteins becomes inevitable; the folding of protein and biofunction cannot be evaluated from protein sequence alone. Also, the 3D structure is important in the study of diseases as well as development of medicines for treatment. Structure-based drug design approaches have helped in engineering new molecules with potential pharmaceutical applications [2]. Above all, the heterogeneous nature and post translational modifications are responsible for cellular localization and functional partners. The structures of

Advances in Biological Science Research. https://doi.org/10.1016/B978-0-12-817497-5.00005-7