Preface

This book introduces the basic biology of proteins and the advancing science called proteomics which looks into the protein properties from a global perspective. Proteomics aims to study all the proteins of human and other living systems and their properties to provide an integrated view of cellular processes. Proteomics study involves the application of high-throughput technologies that are rapidly evolving and new platforms are coming forward regularly with versatile novel applications and are valuable tools for biomedical and pharmaceutical applications. This book will be beneficial for undergraduate and postgraduate students having a basic knowledge of biology and will provide them with a detailed understanding of proteins, proteomics technology, and its applications.

The concept and content of this book arose from the National Programme on Technology Enhanced Learning (NPTEL) online course on "Introduction to Proteomics" conducted by Prof. Sanjeeva Srivastava and initiated by the Indian Institute of Technology Bombay. The NPTEL has offered open online courses (https://onlinecourses.nptel.ac.in/noc20_bt20/preview) since 2014 along with certificates from the IITs/IISc for those that complete the courses successfully. This course is an extensive 8-week program with around 2000 participants every year including graduate students, researchers, as well as faculty. In addition, the YouTube channel for NPTEL is the most subscribed educational channel, with 1 billion views and 31+ lakh subscribers. The enormous enthusiasm from the participants led to this book material which is easily accessible to all the students and researchers that are beginners in this field.

This book is divided into five modules providing a detailed understanding of the basics of proteins and proteomics, gel-based proteomics techniques, basics of mass spectrometry and quantitative proteomics, interactomics: basics and applications, and advancements in proteomics. Module I includes two chapters describing the basics of amino acids, the backbone of the protein molecule, and also covers the proteomics evolution that emerged from protein chemistry solely due to technological advancements.

Modules II and III cover in detail the two major aspects of proteomics, gel-based proteomics, and mass spectrometry-based proteomics. The gel-based module presents different techniques like SDS-PAGE, 2-DE, 2D-DIGE, and so on. These techniques have had a major contribution to the transition from protein chemistry to proteomics. Mass spectrometry, on the other hand, is an advanced analytical technique for accurate mass measurement. These chapters also discuss the basics of mass spectrometry, sample preparation, liquid chromatography, hybrid mass spectrometers, and quantitative proteomics techniques such as iTRAQ, SILAC, and TMT using mass spectrometry. The course also provides basic knowledge about sample preparation, mass spectrometry workflow, different chromatography technologies, and quantitative proteomics.

Module IV focuses on interactomes, providing a better understanding of genomes and proteomes, which govern the network of interactions in a cell. This module also discusses various technology platforms such as protein microarrays, label-free biosensors, and surface plasmon resonance. Module V highlights the application and challenges of various high-throughput integrated proteomics technologies capable of fast and accurate screening of thousands of biomolecules that are found to be very effective for studying disease pathobiology and identification of next-generation biomarkers and potential drug/vaccine targets, and therefore considered valuable tools for multidisciplinary research.

This book thus aims to provide readers with the basic knowledge of proteins, proteomics, and translation of proteomics knowledge for clinical application. We hope the knowledge gained from the reading of the text will intrigue young minds to explore future opportunities in the constantly evolving field of proteomics.