

PREFACE

The preceding decade brought spectacular developments in human genome sequencing. *Proteomics* (from “protein complement of the genome”) is aimed at the analysis of the entire protein content of a cell, tissue, or organism, not a simple identification of cell components. Proteomics was established in 1985 as a set of methodologies to resolve protein sequences on a large scale. Present challenges include proteins function(s) and interactions of protein network(s).

This rapidly expanding strategy integrates several disciplines, including fast and ultrasensitive methods for protein separation, bioinformatics, materials engineering, crystallography, and spectroscopy. The wide range of uses emphasizes the fact that proteomics is not just mass spectrometry, as is sometimes thought, but a link between genes and proteins and their functions, and a disease. The long-term goal is to find markers of various diseases in the hope to design new, more effective, personalized therapies. The rationale behind the concept is that pathogenic mechanisms cause changes in protein content, and the discovery of such differences between healthy and disease states may lead to a better understanding of the molecular mechanisms that occur in the cells. Thus, the main beneficiaries would be the life sciences, the pharmaceutical industry, and most of all, us — *Homo sapiens*.

This monograph is dedicated primarily to undergraduates and graduates (chemistry, biochemistry, pharmacy, medicine) but also to those interested in this continuously developing strategy. Some chapters are more detailed, as they describe new, important directions. There are also descriptions of several laboratory practices that can be used in any student's laboratory to improve practical skills in this methodology.

We do hope that this book will be a first step toward understanding the background and trends in modern proteomics. We would be grateful for feedback, and all comments will be welcome: kraj@chemia.uj.edu.pl; silber@chemia.uj.edu.pl.

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