

# Preface

## Chapter 1

Methods combined with separation techniques such as HPLC or electrophoresis for detection, identification, and quantification of proteins in complex biological matrices are essentially requisite to understand biochemical events in living cells, tissues, and organs. Especially, in searching for the difference in proteins, the specifically expressed proteins in various circumstances, such as between diseased and normal state, aging, exposed and unexposed by drugs, and so forth, a reproducible quantitative method to distinguish between minute changes in amounts of proteins is required. This book focuses on describing the advantages and disadvantages of each of such methods in terms of accuracy, sensitivity, and especially reproducibility. Its other key feature is the description of the effective application of these methods, which result in many discoveries regarding the role of the proteins expressed in living cells.

In the last decade, more than a thousand papers were published on the proteome analysis acquired by the application of these methods in various areas of life sciences. For junior researchers, the first major interest should be the selection of the method when they start their proteome analysis in valuable biological specimens. However, there are few textbooks or monographs showing the evaluation of each method. That is why this book is published.

**Kazuhiro Imai**

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