

# Preface

Proteins are biologically important molecules coded on DNA of the genes of living organisms. They play the essential roles for biological functions through their three-dimensional structures. Thus the studies of the structures, which have been undertaken over almost whole range of 20th century by many scientists, are still the central problem of the structural biology. In effect experimental as well as theoretical studies of protein structure and its folding have revealed before us a lot of beautiful and skillful aspects of proteins or Nature herself.

The authors intend to present the folding mechanism of a nascent protein synthesized according to the information of DNA into the complex three-dimensional structure. They also propose an *ab initio* method of prediction of protein structure on the basis of folding mechanism, because they think that these kinds of research provide a fundamental contribution to the structural biology. Now that the human genome project has successfully revealed the whole sequence of the human DNA, and also the DNA sequences of some of other organisms such as *escherichia coli* become available, proteins are the next target of research. The main interest is, besides the experimental determination of three dimensional structures by X-rays, electron microscope or NMR etc, to develop the techniques of rapid determination of protein structures from their sequences, by comparative methods such as homology recognition and fold recognition method, or by theoretical *ab initio* methods.

This book is a revised edition of the review article of the same title appeared in International Journal of Modern Physics B in 1999. In particular a new section on ferredoxin is added, and several rewritings are carried out.

In writing this book the authors tried to begin with rather elementary description to meet the possible requirements from students of physics, chemistry or biology, but assumed the least knowledge of statistical mechanics. The authors hope that this small book could afford to the readers some aspects of wonderful biological world through the window of proteins, and further contribute to open one doorway to the new era of biophysics in 21st century.

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Nobuhiko Saitô  
Yukio Kobayashi