

Preface

During protein folding, the linear information encoded in the amino acid sequence of a polypeptide chain is transformed into a defined three-dimensional structure. Although it was established decades ago that protein folding is a spontaneous reaction, a complete understanding of this fundamental process is still lacking. Since its humble beginnings in the fields of biophysical chemistry and biochemistry, the analysis of protein folding and stability has spread into a wide range of disciplines including physics, cell biology, medicine and biotechnology. The recent discovery of the sophisticated cellular machinery of molecular chaperones and folding catalysts which assists protein structure formation *in vivo* and the analysis of protein folding diseases have added additional twists to the study of protein folding. Consequently, the field has undergone a significant transformation over the last decade.

The increasing interest in protein folding considerably improved our knowledge of the physical principles underlying protein stability and folding and stimulated the development of powerful new techniques for their analysis both *in vitro* and *in vivo*. Aspects that had been studied previously in splendid isolation such as basic principles and protein folding diseases are now growing together, experimentally and conceptually.

Over the past years, a number of excellent books on protein folding were published, starting with the famous 'red bible of protein folding' (Jaenicke, 1980). The *Protein Folding Handbook* takes a different approach as it combines in-depth reviews with detailed experimental protocols. Thus, a comprehensive, multi-faceted view of the entire field of protein folding from basic physical principles to molecular chaperones, protein folding diseases and the biotechnology of protein folding – is presented. The *Protein Folding Handbook* intends to provide those who become interested in a specific aspect of protein folding with both the scientific background and the experimental approaches. Ideally, the protocols of the methods sections will allow and stimulate even the novice to boldly enter new experimental territory.

We are grateful to the authors who embarked with us on this endeavour. It was a pleasure to see how, chapter by chapter, the current state of the art in this field emerged and the common themes became apparent.

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Reference

Jaenicke, R. (1980) Protein Folding. Elsevier, Amsterdam, New York