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Book Review

Sheldon J. Park, Jennifer R. Cochran (Eds.), Protein Engineering and Design, CRC Press 416 pp., $119,95, ISBN: 978-1-4200-7658-5

Proteins are at the molecular core of essentially all biological functions. Consequently, a host of methods and strategies have been developed over the years that enable the synthesis of natural, as well as the design of novel proteins. The common goal of such efforts is to explore protein structure and function, as well as to create new molecules for biotechnological and medical applications.

This book gives a concise yet comprehensive account of existing protein design and engineering methods, as well as major fields of application of such synthetic proteins. What sets this book apart from similar reviews is the fact that it covers not only the multitude of concepts and methods for the *in vitro* generation of natural and non-natural proteins, including the selection of novel proteins from vast combinatorial libraries, but also the *in silico* design of novel proteins predicted to have desired structures and/or functions. This illustrates the evolving synergism between these two conceptually different approaches, which is increasingly appreciated by protein researchers.

In the first part of the book, experimental methods are reviewed, including various display systems (phage, cell, cell-free) for protein engineering, library construction, the use of nonantibody scaffolds for the design of synthetic binding proteins, as well as the incorporation of noncanonical amino acids into proteins. Two chapters are dedicated to the use of engineered proteins as pharmaceuticals, such as monoclonal antibodies, enzymes, cytokines, hormones, and as biomaterials for medical implants, tissue engineering and drug delivery, respectively.

The second part of the book focuses on strategies and algorithms used in computational protein design to predict protein modifications that would result in a modulation of protein structure, interactions and function, or to design entirely new proteins. This section is opened by an introduction into general terms of bioinformatic protein sequence and structure analysis. The following chapters provide an account of existing strategies in computational protein design, including knowledge-based approaches (modular design, designed libraries, design of novel folds) and heuristic algorithms (Monte Carlo, genetic algorithms, dead-end elimination).

One point of criticism I have to make pertains to the rather prosaic visual, i.e. black-and-white, presentation of the chapters. Considering the not exactly low price of the book, at least some of the figures could and should have been in color, which would have made the protein structure figures in particular clearer than the presentation in shades of gray. A touch of color would also have enhanced the visual attractiveness of the entire book. Furthermore, since each of the 18 chapters has been written by different authors, it is understandable that the style and quality of writing is diverse, which makes continuous reading somewhat difficult. Then again, this book is meant to be a reference, and as that, I consider it a valuable and essential addition to the shelves of life sciences libraries in academia and industry.

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