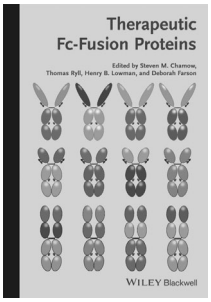
Building Blocks of Life

Therapeutic Fc-Fusion Proteins

Edited by *Steven M. Chamow, Thomas Ryll, Henry B. Lowman, Deborah Farson*

Wiley Blackwell, Weinheim 2014. 400 pp., hardcover, €126.00.—ISBN 978-3-527-33317-2



In 2015, we will commemorate the centenary of the death of the Nobel Prize winner Paul Ehrlich. He developed the side-chain theory to explain how antibodies react with other substances. Ehrlich also pioneered the development of chemotherapy. In this field, he envisioned the magic bullet—drugs that go straight to their intended targets. After a century of work in medicinal chemistry, achievements in both of Ehrlich's fields have been realized with the clinical use of monoclonal antibodies. Antibodies have exceptional targeting and pharmacokinetic properties, and monoclonal antibody technology has allowed the development of highly selective therapeutic agents.

However, there is still room for improvement, and antibody variants such as bispecific antibodies and antibody–drug conjugates expand the possibilities for antibodies in therapeutic applications. Among those improved antibody variants, we find Fc-fusion proteins and peptides, the topic of the book edited by Chamow, Ryll, Lowman and Farson, all pioneers in this field. Functional domains of proteins and therapeutic peptides often exhibit poor pharmacokinetic properties that prevent their clinical development. Fusion of these therapeutic amino acid chains to the fraction of antibodies that stabilize the structure and that impart a longer half-life in circulation is a strategy to construct stable chimeric molecules that can be developed as drugs.

This book is divided in two parts. In the first part, the authors provide a detailed description of the production, purification, formulation, and characterization of therapeutic Fc-fusion proteins and peptides. Each section covers all possibilities and variables to be considered in the production of an Fc-fusion protein, and the authors illustrate the theory with case studies, capturing the reader's attention. The second part of the book is devoted to case studies. Seven molecules that have reached the market are covered in this part: alefacept, a chimeric protein that contains a domain of the lymphocyte function-associated antigen 3; etanercept, a soluble tumor necrosis factor receptor fusion protein; abatacept and belatacept, two fusion proteins that contain the extracellular domain of cytotoxic T lymphocyte-associated antigen 4; aflibercept, a soluble receptor decoy that binds to several molecules of the family of vascular endothelial growth factor (VEGF); and two Fc-fusion proteins with coagulation factors. The authors describe the biology of the molecule fused to the Fc fragment and provide a basic description of the diseases that can be treated with the chimeric molecules. Then, a detailed description of the preclinical and clinical trials is provided.

Therefore, this book provides the reader with a strong theoretical background supported by the profound professional experience of the authors. For instance, Robert T. Peters and Judy R. Berlfein describe the development of the fusions to coagulation factors as an exciting professional adventure in Chapter 13. In addition, the book contains several tables and illustrations that could be very useful for the professional working in antibodies or Fc-fusions.

In conclusion, this is an excellent book that combines the theory and practice of the Fc-fusion protein and peptides. It is a valuable book for those readers working in the development of biologics but also for the general readers interested in how the most advanced and sophisticated drugs are developed.

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Next-Generation Sequencing: Current Technologies and Applications

Edited by *Jianping Xu*

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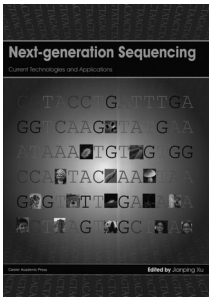

Little over 40 years ago, the first nucleotide sequence was published by Gilbert and Maxam. They developed a sequencing method and were able to identify 24 bases of lactose operon. At the end of the 1970s, it took about a week to read 100 bases in a row. Frederick Sanger adapted the Maxam and Gilbert sequencing method in 1975, making it possible to read up to a 1000 bases per week. This was a major breakthrough, and it allowed Sanger to publish the whole genome of bacteriophage ϕX174, which consisted of 170 000 base pairs.