Preface

Genomics, proteomics, and other types of "omics" approaches have proven most fruitful in both current basic and applied research. There are numerous examples of studies on whole genomes of specific organisms, types of genes/proteins and gene/protein families. In genomics and proteomics strategies, the aims are to study the function of gene activities and to characterize proteins. Structural genomics approaches, again, have the goals set on structure determination of target proteins, which can facilitate rational drug design by speeding up the drug development process and improving the selectivity and efficacy of medicines. In this context, membrane proteins are of great significance as more than 60% of current drugs are based on this group of proteins.

As in many other modern approaches, a thorough knowledge in bioinformatics is a necessity for successful applications in structural genomics. Another cornerstone of any structure determination is the supply of proteins for purification and crystallization attempts. Very few proteins, especially those of therapeutic interest, are available in high quantities in native tissue, and even so, ethical issues prevent proceeding with this approach. The scientific community therefore relies, to a large extent, on recombinant expression technologies. As the requirements for membrane protein expression are more demanding, expression has been evaluated in bacterial, yeast, insect, and animal cells, applying a variety of specifically designed vectors containing various expression-enhancing sequences and tags to facilitate purification. The expression mode dictates the downstream processing requests as recombinant proteins in *Escherichia coli* inclusion bodies need to be subjected to refolding, as those expressed in cell membranes require solubilization procedures. Purification technologies are also of great importance as the presence of detergents makes the procedure more difficult and the target proteins less stable. Furthermore, crystallization of membrane proteins has been more difficult than for their soluble counterparts, clearly indicated by the submission of less than 100 structures in public databases compared with more than 30,000 entries for soluble proteins. However, x-ray crystallography is not the only approach to receive structural information on proteins. Alternative methods include NMR (nuclear magnetic resonance) and EM (electron microscopy) technologies.

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made a significant contribution to the field of recombinant membrane proteins, and his support for many structural genomics programs in Europe has been vital. I dedicate this book to his memory.

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