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Structural Genomics on Membrane Proteins

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Authors from several countries have contributed a total of 18 chapters in the book. The first chapter is contributed by the editor and summarizes the scope of the book. The second chapter by Dr. Bengt Persson explains various methods for membrane protein prediction methods and methods of prediction of membrane spanning regions of proteins. Moreover, evaluation of the methods is also discussed. The third and fourth chapters are contributed by several authors and explain amplified method of expression and purification of the protein. The explanation of choice of *Escherichia coli* host strain and expression condition is excellent and very much useful for the researchers working on the membrane proteins. Aggregation and inclusion body formation of protein is the biggest challenge in the expression of membrane protein. The fifth chapter of the book is mainly focused on various strategies of the refolding of the aggregated membrane protein. Some specific examples where membrane protein is refolded in native form from inclusion bodies are also explained. Because of their low solubility and highly hydrophobic nature, crystallization of membrane proteins is always a challenge. Chapter six of the book explains the possible strategy, including choice of crystallization method and precipitant, for the crystallization of these proteins. Chapter seven is contributed by Bostwick and Hartman and explains the biological functions of the membrane protein with special emphasis on signaling through membrane proteins. All membrane proteins cannot be expressed in *E. coli* due to post-translational modification. Chapters eight to ten explain the expression of these proteins in yeast, Baculovirus, and mammalian cell. Furthermore, the 11th chapter describes the isolation and purification strategies for membrane proteins with few examples. Interestingly, disadvantages of His-tag purification are also discussed. Chapter 12 explains the fluorescence labeling of membrane protein in living cells which has potential application in fast and reliable optimization of expression and purification. Chapters 13 and 14 explain the methods for structure determination by NMR and crystallography. Miniaturization and automation of the crystallization experiments are also discussed. Structure of few

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membrane proteins are also discussed with high quality figures. Chapter 15 is contributed by Andreas Engel and describes the use of atomic force microscopy for structure function studies of membrane protein in their native environment. The editor, K.H. Lundstrom, has contributed the 16th chapter and explains structural genomics networking of membrane proteins. Additionally, the last two chapters of the book describe molecular modeling of membrane proteins using computation tools and ligand binding and associated conformational changes.

Description of each chapter follows with conclusion/future prospects. The book is very useful for researcher working on structural biology, membrane protein, and bioinformatics. The book may be useful as a text book as well as a manual for several procedures.