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Electron Crystallography of Soluble and Membrane Proteins: Methods and Protocols (Methods in Molecular Biology)

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The basic principle of electron crystallography is to calculate a 3D density map by combining the amplitudes obtained from electron diffraction patterns with the experimental phases calculated from images of two-dimensional crystals of membrane or soluble proteins. This technology is very well developed and has produced a number of atomic models of membrane proteins in a lipid environment. Focused on comprehensive experimental protocols, *Electron Crystallography of Soluble and Membrane Proteins: Methods and Protocols* covers the entire range of techniques used in electron crystallography, including protein sample preparation, 2D crystallization, and screening in negative stain over electron cryo-microscopy (cryo-EM) and data processing, as well as modeling of conformational changes. Additional chapters provide perspective on past, present, and future challenges as well as complementary methods. Written for the popular *Methods in Molecular Biology*™ series, the work contains the kind of detailed descriptions and implementation advice necessary to ensure successful results.

Comprehensive and cutting-edge, *Electron Crystallography of Soluble and Membrane Proteins: Methods and Protocols* serves laboratories new to the methods as well as state-of-the-art facilities pursuing this exciting area of protein science.

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