



Configuration of membrane-bound proteins by x-ray reflectivity

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Abstract

In this presentation we review our recent work using x-ray reflectivity to determine the configuration of membrane-bound proteins. The reflectivity data is analyzed in terms of the known crystallographic structure of proteins and a slab model representing the lipid layer to yield an electron density profile of the lipid/protein system. Our recent modified analysis methodology for the lipid/protein system is concisely described in this report. In addition, some results of the configuration of the membrane-bound proteins cPLA₂α-C2, p40^{phox}-PX, and PKCα-C2 are highlighted.

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Article outline:

I. INTRODUCTION II. EXPERIMENTAL METHODS A. X-ray reflectivity III. DATA ANALYSIS A. Electron density profile of a protein in a box at an arbitrary orientation B. Electron density profile of the whole system C. Reflectivity fitting procedure IV. RESULTS V. CONCLUSION