

Structure Determination Methods Program

Written by Administrator

Tuesday, 01 March 2011 22:00 - Last Updated Thursday, 26 July 2012 14:29



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One of the main aims of the Structure Determination Methods Program is the development of novel experimental techniques and data analysis methods for extracting structural information from 2-dimensional crystals, especially relating to the determination of the structure of integral membrane proteins (IMPs).

The Program includes the fabrication of 2-D arrays by novel methods. It also includes the exploitation of grazing incidence X-ray diffraction (GIXD) methods to obtain high sensitivity structural information for thin samples. A powerful aid to the development of these techniques is simulation software being developed in order to help better understand the likely nature of diffraction data on such systems, including the influence of structural disorder. Methods of data analysis proposed for implementation include Bayesian and MaxEnt methods that seek to incorporate both data and a priori information.

Initial system being studied is Purple Membrane, a naturally occurring 2-d crystal. This is a classical membrane protein system that has been much studied by high resolution cryo-electron-microscopy and so valuable comparisons can be made about the efficacy of both electron and X-ray methods.

A long-term aim of the Program is to develop novel instruments and techniques for the structure determination of integral membrane proteins, which might be implemented at the Australian Synchrotron.