

Crystallography Times

Rigaku

Protein Crystallography Newsletter
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**Continuing Education Webinar
From Haemoglobin to West Nile Virus**
Presenter: [Prof. M.G. Rossmann](#)
May 13th at 10:30AM EDT
(2:30 GMT)

In this webinar, Prof. Michael Rossmann will provide a personal account of his career in X-ray crystallography, beginning some fifty years ago with Max Perutz and John Kendrew at Cambridge University deciphering the molecular structures of proteins haemoglobin and myoglobin

Software Webinars Available On-demand

Our Spring 2010 webinar program featured well known expert presenters in a mini-series devoted to commonly used data processing packages.



The Rigaku Compact HomeLab is the perfect solution for crystal screening/optimization prior to the synchrotron.

Crystallography in the news



April 16, 2010. The Indian Institute of Science (IISc.) could soon construct a [synchrotron on its new Chitradurga campus](#) - which will be operated through and funded by the Union Department of Science and Technology - according to [M. Vijayan](#), president of the Indian National Science Academy and Homi Bhabha, Professor at IISc.

March 25, 2010. Life scientists have picked up over half of the seventeen Australian Academy of Science Fellowships, including Professor [Michael Parker](#) FAA ARC Federation Fellow and Associate Director, Biota Structural Biology Laboratory, [St Vincent's Institute](#) for protein crystallography of membrane-associated proteins.

March 24, 2010. [Walter and Eliza Hall Institute](#) researchers, led by [Mike Lawrence](#), [Brian Smith](#), John Menting, Geoffrey Kong and [Colin Ward](#) from the institute's Structural Biology division - together with colleagues from the Case Western Reserve University and the University of Chicago - have worked out the complete [structure of the insulin receptor](#).

March 23, 2010. Toyota and the National Science Teachers Association (NSTA) awarded [Hillcrest High School](#) (Dallas, TX) teacher Dr. Ward Coats a \$10,000 Toyota [TAPESTRY grant](#) for excellence and innovation in science education as related to protein crystallization research at the secondary education level.

Screen and optimize crystals before the synchrotron

Rigaku Compact HomeLab is a turnkey, low maintenance system which enables crystal screening through complete protein structure solution in a small-footprint, energy-efficient package. The foundation of this system is the Rigaku MicroMax™-002+, an integrated microfocus sealed tube generator and specialized confocal optic that can be equipped with either a state-of-the-art CCD or Imaging Plate (IP) detector. This is the perfect system for a lab that is in close proximity to a synchrotron and mainly uses the home lab X-ray system in optimizing cryo-protectants and selecting the best crystals for synchrotron data collection. The source is powerful enough though that a structure can often be solved from collected data and the synchrotron is used for obtaining the final high resolution data set.

[Request more information](#) on Compact Homelab.

Lab spotlight:

[Indiana University School of Medicine,
Dept. of Biochemistry and Molecular Biology](#)

The Department of Biochemistry and Molecular Biology at Indiana University School of Medicine is in the midst of a vigorous expansion phase. They have had 9 new faculty members join the department during the past three years and currently have plans to hire 4-6 additional faculty over the next few years. The Department currently has 24 primary faculty members engaged in research and teaching with a focus on understanding the biochemical and molecular basis of fundamentally important life processes.

Eight faculty members comprise the structural biology section of the Department. Chancellor's Professor and Associate Chairman [Thomas D. Hurley](#) serves as the Director of Center for Structural Biology and has - as a major focus of his research - to understand, at the molecular level, the processes involved in the recognition and binding of substrates to enzyme active sites. Associate Professor [Millie M. Georgiadis](#) serves as Graduate Admissions Chairman and has a research focus that includes X-ray crystallographic, biochemical, and thermodynamic studies of protein-nucleic acid interactions



Within the Department of Biochemistry and Molecular Biology at Indiana University School of Medicine, Prof. [Thomas D. Hurley](#)'s area of study involves X-ray crystallography of dehydrogenases, enzyme engineering using site-directed mutagenesis as well as kinetic and thermodynamic analysis of protein ligand interactions.

Rigaku Hardware Training Classes

Rigaku has scheduled our next training session, at our Texas facility, tailored towards the needs of macromolecular crystallographers and their staff. Course format will be a series of short lectures on theory followed by hands-on activities with detectors and X-ray generators. Safety will be emphasized.

SURVEY QUESTION

What is your favorite structure solution/refinement package?

☐ CCP4

☐ Phenix

☐ Other (please specify)

Click to take survey
or cut-and-paste
<http://www.surveymonkey.com/s/2MMGXMM>
into your browser.

involved in replication, nuclear export, and temporal gene expression. Assistant Professor [Quyen Hoang's group](#) works on the structural biology of neurodegenerative disease and structure-based drug design. The research in Assistant Professor [Yuichiro Takagi's](#) laboratory focuses on biochemical and structural analysis of the multi-protein complexes that control gene regulation in eukaryotes. Associate Professor [Qi-Zhuang Ye's](#) research currently focuses on studying structure and function of methionine aminopeptidases (MetAPs).

Interests of Prof. [William F. Bosron](#) include the structure and mechanism of alcohol dehydrogenases and carboxylesterases, regulation of ethanol, as well as retinoid and drug ester metabolism. Molecular design of small molecules and proteins to modulate cellular processes in cancer is the focus of Assistant Professor [Samy Meroueh](#). Finally, Chairman of the Department, Professor [Zhong-Yin Zhang](#) is active in researching the signaling mediated by tyrosine dephosphorylation and targeting protein tyrosine phosphatases for the treatment of cancer, diabetes/obesity, autoimmune disorders, and infectious diseases.

Useful links for crystallography

[Structural Biology Grid](#) (SBGrid) at Harvard Medical School is a computing collaboration of more than 130 X-ray crystallography, NMR and electron microscopy laboratories. Participating laboratories include groups at Harvard Medical School, Harvard University and Yale Medical School and many other institutions in the United States and internationally.

Selected recent crystallographic papers

pH-dependent structural changes in haemoglobin component V from the midge larva *Prosillocerus akamusi* (Orthocladiinae, Diptera). T. Kuwada, T. Hasegawa, T. Takagi, I. Sato, and F. Shishikura. *Acta Cryst. D.* 2010; **66** (Pt 3): 258-67.

Bridging the solution divide: comprehensive structural analyses of dynamic RNA, DNA, and protein assemblies by small-angle X-ray scattering. R.P. Rambo and J.A. Tainer. *Current Opinion in Structural Biology* 2010, **20**: 128-137.

Diffraction data analysis in the presence of radiation damage. D. Borek, M. Cymborowski, M. Machius, W. Minor and Z. Otwinowski. *Acta Cryst. D.* 2010; **66**, 426-436.

A Gating Charge Transfer Center in Voltage Sensors. X. Tao, A. Lee, W. Limapichat, D.A. Dougherty and R. MacKinnon. *Science* **2** April 2010; **328** (5974), 67-73.

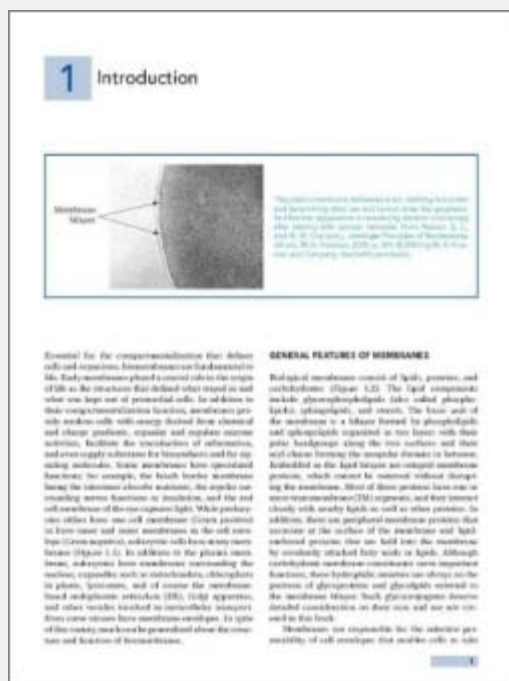
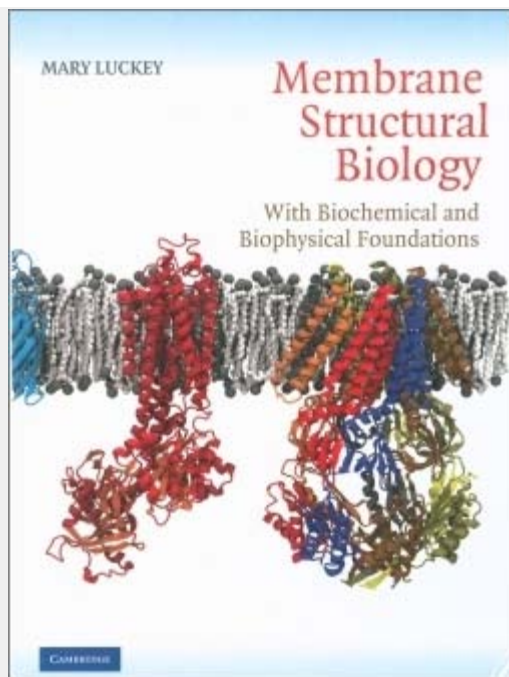
The minimum crystal size needed for a complete diffraction data set. J.M. Holton and K.A. Frankel. *Acta Cryst. D.* 2010; **66**, 393-408.

Book review: *Membrane Structural Biology*

by **Mary Luckey**

Believe it or not, the recommendation for [Membrane Structural Biology with Biochemical and Biophysical Foundations](#) came from Amazon as the result of purchasing Rupp's Biomolecular Crystallography. Being adventurous, I ordered a copy and found it well written and enlightening. In particular, the extensive use of "highlight boxes" provides useful background information in more detail without cluttering the main text. Not being a membrane structural biologist by formal training, I found this textbook to be both quite informative and accessible.

Chapter 1: Introduction. This provides an excellent review of our current understanding of membranes as well as a historical context for the next chapters.



Chapter 2: The Diversity of Membrane Lipids. Here is given a description of the most common lipids and their properties as a prelude to understanding the thermodynamics of lipid bilayers.

Chapter 3: The Tools for Studying Membrane Components: Detergents and Model Systems. This chapter describes the detergents used for extracting and crystallizing membrane proteins as well some of the analytical tools used for determining the states of the proteins.

Chapter 4: Proteins in or at the Bilayer. This chapter describes proteins that sit on the surface of the membrane, with examples of toxins, colicins and peptides. The latter part of the chapter gives the basics of transmembrane proteins, essentially an introduction to the next chapter.

Chapter 5: Bundles and Barrels. I think this is the meat of the book. Here is given a detailed view of both bundles of alpha-helices and barrels of beta-sheets, with numerous examples from the recent literature. An excellent description of photosynthesis is provided as a description of various transporters.

Chapter 6: Functions and Families. This chapter introduces the concept of families and superfamilies - as applied to membrane proteins. It also provides a view into the bioinformatics of membrane proteins ... and readers are introduced to current tools for analysis of sequence, structure and function.

Chapter 7: Protein Folding and Biogenesis. Translation, translocation, folding, insertion and diseases of misfolding are covered in this chapter.

Chapter 8: Diffraction and Simulation. A brief description of liquid crystallography of the bilayer is provided. A detailed explanation of modeling of the bilayer is given next along with several examples of X-ray structures with lipids associated to the protein.

Chapter 9: Membrane Enzymes and Transducers and Chapter 10: Transporters and Channels. These chapters survey the current known space of the title classes in detail.

Chapter 11: Membrane Protein Assemblies. The penultimate chapter provides detailed information about the structure and mechanism of the F_1F_0 -ATPase, complexes of the respiratory chain, the translocon, and complexes responsible for vitamin B12 and drug transport.

Chapter 12: Themes and Future Directions. This chapter is a final review of the book and a look forward. I am surprised that SAXS as a method for looking at proteins, specifically complexes, was not mentioned in the book, as I think this is an up and coming technique for the field.

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