Crystallography Times

Rigaku

Protein Crystallography Newsletter

Volume 1, No.1, February 2009

In this issue:

Continuing education webinar

Macromolecular cryo-crystallography: some opinions about best practices

Presenter: Dr. Jim W. Pflugrath
March 24, 2009
12:00 PM EDT (16:00 GMT)

New very high flux motorized VariMax VHF optic

Crystallography in the news

February 13, 2009. Diamond team unveil the structure of a biological protein from the vaccinia virus at the American Association for the Advancement of Science meeting in Chicago—an important step in developing new therapies to treat viruses.

February 10, 2009. Long-sought protein structure may help reveal how the "Gene Switch" works. The biochemical puzzle surrounding the switch is the mechanism by which the protein binds cAMP at one end, then attaches to and activates a gene (DNA) at the other end.

January 21, 2009. New Jersey-based biotechnology start-up company Nexomics Biosciences is to apply cutting edge platform technologies based on large scale protein production, Nuclear Magnetic Resonance (NMR), and X-ray crystallography in drug discovery efforts.

The ultimate homelab optic for small crystals?

High-throughput crystallization methodologies often result in smaller crystals. In addition, new research is increasingly focused on proteins that form crystals with longer unit cell lengths. VariMax™ optics were designed with the performance and flexibility to meet both of these twin challenges by providing either exceptional spatial resolution or very high flux depending on the sample and experimental design.

The new Rigaku **VariMax VHF** represents the pinnacle of current X-ray optics engineering for today's smaller protein crystals. It delivers a 100 µm (FWHM) beam in which the divergence can be easily adjusted in software to optimize performance for any unit cell length.

Optimization of the X-ray beam is accomplished using a motorized, patented adjustable slit assembly that sets the beam divergence. The VariMax VHF optic is capable of delivering very high flux when working with systems requiring moderate resolving power and high speed data collection. When greater peak separation is needed, it is readily available with a lower beam divergence and some attenuation of flux.

Protein crystallography webinar series

The new Rigaku Life Sciences Webinar Series begins in March with a course on cryo-crystallography. These free instructional lectures are designed to provide continuing education in protein crystallography methods. Each webinar in the series will tackle a new topic ranging from optimization of crystallization conditions to SAD phasing.

The West Coast Protein Crystallography Workshop

APRIL 5-8, 2009

American Crystallographic Association

Toronto 2009

JULY 25-30, 2009

Click here for a comprehensive list of upcoming crystallography meetings and conferences

SURVEY QUESTION

Do you plan to use "FedEx" data collection services at a synchrotron over the next 6 months?

●	Yes
○	No
○	Maybe

Submit

Cryo-mounting tools of the trade

Selected recent crystallographic papers

X-ray structure of native scorpion toxin BmBKTx1 by racemic protein crystallography using direct methods. K. Mandal, B.L. Pentelute, V. Tereshko, A.A. Kossiakoff and S.B. Kent. J Am Chem Soc. 131(4), 1362-3 (2009).

X-ray imaging: Caught in a spin. Keith A. Nugent. Nature Physics, 5, 17-18 (2009). An algorithm that enables a protein's molecular structure to be determined from the faintest of diffraction patterns could increase the potential of next-generation X-ray sources.

Molecular Mechanisms of HipA-Mediated Multidrug Tolerance and Its Neutralization by HipB. Maria A. Schumacher, Kevin M. Piro, Weijun Xu, Sonja Hansen, Kim Lewis and Richard G. Brennan. Science, 323, 396-401 (2009).

FAQ: How to cryo-protect and mount crystals

Diffraction data collection at cryogenic temperatures, from flash-cooled protein crystals, has become a routine part of protein crystallography. In both the home laboratory environment, and at the synchrotron, the benefits of low-temperature data collection are such that room temperature work is now a rarity. An understanding of best practices that have been refined over the years is essential for acquiring high quality data sets so as to refine maximum resolution structures.

These best practices have been distilled into a easy-to-follow pamphlet as part of Rigaku's Techniques in Cryocrystallography Series. The document, Cryoprotecting & Mounting Crystals, covers all aspects of the procedure—from the application of cryo-protectant, to crystal and loop wafting, and then dewar to goniometer transfer. Please share this document with colleagues and students.

To subscribe to this newsletter or cancel your subscription, e-mail the webmaster.

Rigaku Americas
e-mail: info@Rigaku.com
Tel: (281) 362-2300

Rigaku Europe
e-mail: info@Rigaku.com
Tel: +[44] 1732 763 367

Rigaku Corporation
e-mail: rinttyo@rigaku.co.jp
Tel: +[81] 3-3479-0618

Rigaku China
e-mail: info@rigaku.com.cn
Tel: +[86] 010-82800840