Crystallography Times

Protein Crystallography Newsletter Volume 1, No. 6, July 2009

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Continuing Education Webinar Caveat Emptor: What is the Right X-ray Source for You? Presenter: Joseph D. Ferrara, Ph.D. August 26th at 11:00 AM EDT (15:00 GMT)



New CrystalMationTM Intelli-PlateTM 96-3 well crystallization plate that is optically clear, UVtransmissible, with low birefringence properties.

Reference Tables Resolution vs. Crystal-to-Detector Distance

Crystallography in the news



Rigaku

July 23, 2009. Rice University researchers have used X-ray crystallography to solve the structure of the shell of the hepatitis E virus.

July 17, 2009. Prof. Wladek Minor, and his research team at the University of Virginia Health System within the Midwest Center for Structural Genomics (MCSG), celebrate the deposit of their thousandth protein structure into the Protein Data Bank (PDB).

July 14, 2009. Prof. Andrzej Joachimiak and a team of researchers at the U.S. Department of Energy's (DOE) Argonne National Laboratory, in collaboration with scientists at the University of Chicago, have determined the structure of a protein crucial to the virulence of anthrax bacteria.

June 11, 2009. The Faculty of Health Sciences at the University of Copenhagen has opened the doors of its <u>new research center</u>, The Novo Nordisk Foundation Center for Protein Research headed by director Michael Sundström.

Low birefringence crystallization plate

Rigaku has just introduced the NEW CrystalMation[™] Intelli-Plate[™] 96-3 well low-profile crystallization plate designed for sitting drop vapor diffusion crystallization experiments. The CrystalMation Intelli-Plate is constructed from optically clear, UV-transmissible, chemically resistant plastic with superior lowbirefringence. The low-profile construction allows for higher density in plate storage and imaging systems, maximizing your investment and valuable space. Designed to be a substantial improvement in existing low-profile plates, the new CrystalMation Intelli-Plate 96-3 allows for superior sealing due to thicker well design and a flat sealing surface. It has been built to the SBS (Society for Biomolecular Screening) standard dimensions with 8 vertical reservoirs versus 12 horizontal reservoirs and is compatible with automated instrumentation including the CrystalMation line of instruments from Rigaku.

Request a copy of the Intelli-Plate 96-3 product document.

What is the right X-ray source for you?

Rigaku Life Sciences Webinar Series continues on August 26th. In the previous webinar in this series, we reviewed some of the maintenance procedures associated with rotating anode X-ray generators. Now we will explore the properties of X-ray sources, that is, the combination of X-ray generator and X-ray optic. The discussion will cover properties such as focal spot size, divergence, spectral purity, beam size and shape and how they affect data quality. Upon completion you will have a better understanding of what type of source best suits your needs.

Click here to register.

Useful links for crystallography

Protein Science - virtual issues are now available.

UCLA Merohedral Twinning Server - twinning continues to plague

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crystallographers. Luckily there are a number of useful websites that offer assistance when encountering this problem. Todd Yeates and Barry Fam maintain the UCLA Merohedral Twinning Server as a service to the community. You can submit a data set and test whether you have a perfect merohedral twin or a partial merohedral twin.

Selected recent crystallographic papers

Robust, high-throughput solution structural analyses by small angle X-ray scattering (SAXS). G. Hura, A. Menon, M. Hammel, R. Rambo, F. Poole, S. Tsutakawa, F. Jenney, S. Classen, K. Frankel, R. Hopkins, S. Yang, J. Scott, B. Dillard, M. Adams and J. Tainer. *Nature Methods* Published online: 20 July (2009).

Mapping the structure and conformational movements of proteins with transition metal ion FRET. J. Taraska, M. Puljung, N. Olivier, G. Flynn and W. Zagotta. *Nature Methods* **6**, 532-537 (2009).

The Human SepSecS-tRNA^{Sec} Complex Reveals the Mechanism of Selenocysteine Formation. S. Palioura, R. Sherrer, T. Steitz, D. Söll and M. Simonovic. *Science* **325**, No. 5938, 321-325 (2009).

G-protein-coupled receptor structures were not built in a day. T. Blois and J. Bowie. *Protein Science* **18**, No. 7, 1335-1342 (2009).

Book review:

Remarkable Creatures: Epic Adventures in the Search for the Origin of Species

by Sean B. Carroll

I first heard about this book in an interview with the author on Science Friday. I was intrigued and ordered myself a copy the same day. The book is an elucidation of our understanding of evolution. This book describes the three categories of scientists involved in this process: naturalists, paleontologists and molecular biologists. The naturalists include Alexander von Humboldt, Charles Darwin, Alfred Russel Wallace and Henry Walter Bates. These scientists risked life and limb in pursuit of answers.

The paleontologists included Eugene Dubois, Roy Chapman Andrews, Neil Shubin and the Leakeys. Dubois is the discoverer of Java Man. Andrews began his career mopping floors at the American Museum of Natural History and became director many years later. Several character traits given to Indiana Jones came from Andrews, including the six-shooter and the fear of snakes. Shubin discovered the Tiktaalik, a sea-to-land transitional species, in 2004. The Leakeys, of course, are responsible for much our knowledge of early hominids and how they used tools.

The last section covers the modern scientists who have helped us understand evolution including, Linus Pauling, who really needs no further introduction, and Allan Wilson. Wilson first studied the genetics of chimpanzees and humans, and Remarkable Creatures: Epic Adventures in the Search for the Origin of Species by Sean B. Carroll. provided the idea of a mitochondrial Eve. A great tribute to Charles Darwin, the book celebrates the 200th anniversary of his birth and 150th anniversary of the publication of The Origin of Species.

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