

Crystallography Times

Rigaku

Protein Crystallography Newsletter
Volume 1, No. 8, September 2009

Crystallography in the news



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Continuing Education Webinar

High-Throughput Structural Biology at the JCSG

Presenter: Dr. Ian Wilson
October 28th at 12:00 PM EDT
(16:00 GMT)



September 2, 2009. New York University chemists, lead by Prof. Nadrian Seeman, have created [three-dimensional DNA structures](#), by using single-stranded sticky ends that link double helices in DNA triangles that point in different directions, a breakthrough bridging the molecular world to the world where we live.

September 2, 2009. [Boron-based compounds](#) trick a biomedical protein. University of Oregon team, lead by Prof. Shih-Yuan Liu, used X-ray crystallography to demonstrate that specially synthesized boron compounds are readily accepted in biologically active enzymes.

September 3, 2009. Vanderbilt chemists, led by Prof. Billy Hudson, have identified a unique chemical bond that holds together type IV collagen dimer molecules. The [sulfilimine \(N=S\) bond](#) has never been observed in biological molecules before, but is responsible for the strength of these collagen networks in all animals from sea sponges to humans.

September 13, 2009. Brookhaven National Laboratory biologist Dr. Dax Fu reports a high-resolution X-ray crystallography view of [zinc transport protein](#) that reveals shape-shifting atomic interactions suggesting a mechanism and possible drug targets.

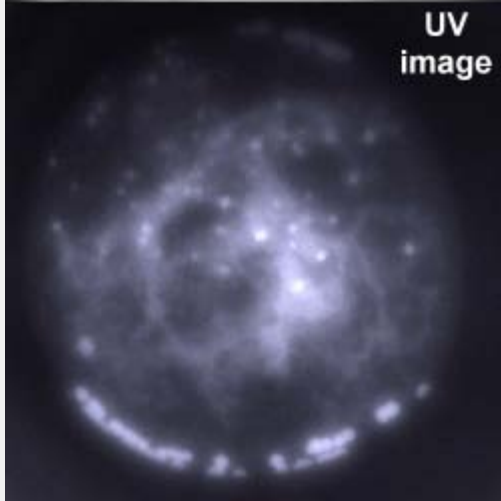
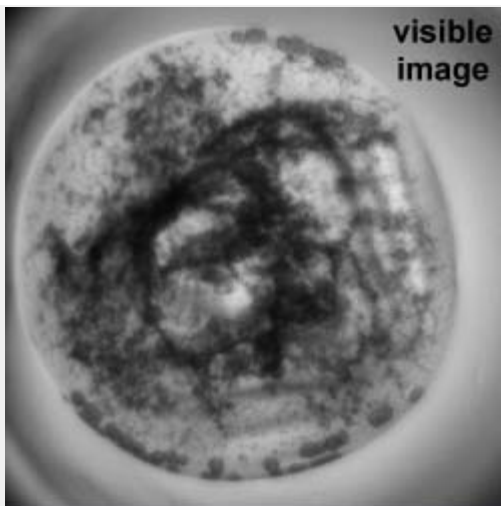
September 21, 2009. Rice University biochemists are developing a system of "[evolutionary forecasting](#)" to better understand the mechanisms of antibiotic resistance with the goal of showing which sets of genes a pathogen will modify to become drug-resistant.

New high-throughput crystal imaging system

New from Rigaku, the Minstrel™ HT UV imaging system is the world's first high-throughput UV imaging and protein crystal monitoring system. Built upon the platform of Rigaku's state-of-the-art imaging and analysis system, the Minstrel HT UV employs both visible and UV fluorescence microscopy to successfully detect crystals where visible imaging alone falls short and to monitor crystal growth by distinguishing protein crystals from non-protein crystals, such as salt. Employing a 5.1 megapixel CCD, with a single optical train for superior optical quality, this new automated system offers the highest available optical resolution for combined visible and UV spectrum imaging systems. The instrument features polarization and both monochromatic & color imaging in visible spectrum. With multi-slice capability, and combined image capability, the Minstrel HT UV ensures that all features within a drop can be clearly observed.

In the Minstrel HT UV, an ultraviolet microscope is mated with a *patent pending* ultraviolet light emitting diode (LED) illumination source (bright and dark field), called Clean Light Technology™, providing minimal UV exposure and adding no additional heat to the well. Clean Light Technology eliminates photo damage and has no impact on resulting X-ray diffraction data quality. The wavelength of the LED is matched to the absorption peak of tryptophan, which is one of the fluorescing amino acids found in almost all protein crystals. This allows for definitive detection of protein crystals within opaque or heavily precipitated drops and eliminates time spent screening or optimizing around salt crystals, thereby increasing your productivity and the reliability of the experimental results.

Request a copy of the [Minstrel HT UV](#) brochure.



How many crystals have you missed? Protein crystals in heavy precipitate imaged (visible top and UV bottom) with the new Rigaku Minstrel HT UV system.



CCP4 Study Weekend (6th - 8th January 2010)
"From Crystal to Structure with CCP4"

Lab Spotlight: What is P-CUBE?

P-CUBE is an EU-funded project, coordinated and managed by Prof. Markus G. Grütter and Dr. Jutta Tatzel respectively, that offers free access to infrastructures for the European science community in structural biology.

The first project within the Seventh Framework Program that brings together research, networking and service activities, **P-CUBE** offers exciting cutting edge technologies in contemporary structural biology and provides access to: high-throughput cloning and expression technologies in prokaryotic and eukaryotic cells, high-throughput crystallization facilities, the DARPIn-selection methodology, ESPRIT technology, and advanced light microscopy. Service and access to these infrastructures are free of charge for scientists all across Europe from now until March 2013.

Useful links for crystallography

COPS (Classification Of Protein Structures) web server is a next-generation web application that provides fast and intuitive access to the entire set of currently available protein structures. COPS organizes structural domains by quantified structural similarities which can be visualized immediately with Jmol. Additionally, structural biologists can employ iCOPS to classify their own structures.

Selected recent crystallographic papers

Three-Dimensional Structural View of the Central Metabolic Network of *Thermotoga maritima*. Y. Zhang, I. Thiele, D. Weekes, Z. Li, L. Jaroszewski, K. Ginalski, A. Deacon, J. Wooley, S.A. Lesley, I.A. Wilson, B. Palsson, A. Osterman, and A. Godzik. *Science* Vol. 325, **5947**, 1544-1549 (2009).

Optics: Ultrafast X-ray photography. Margaret M. Murnane and Jianwei Miao. *Nature* **460**, 1088-1090 (2009).

Structure of a tetrameric MscL in an expanded intermediate state. Z. Liu, C.S. Gandhi and D.C. Rees. *Nature* **461**, 120-124 (2009).

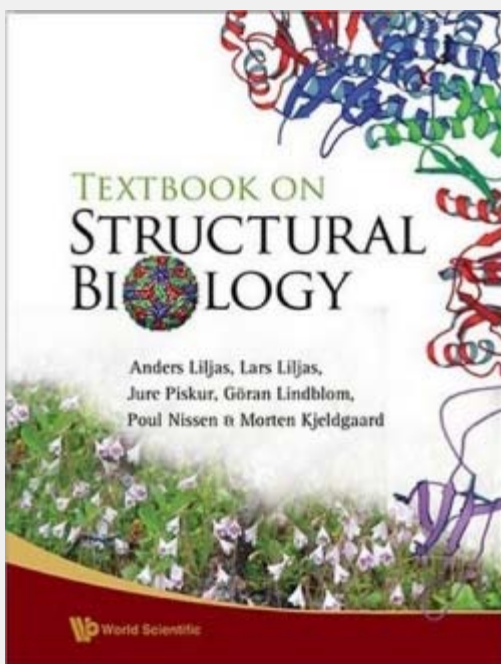
Engineering of recombinant crystallization chaperones. Shohei Koide. *Current Opinion in Structural Biology* Vol. 19, **4**, 449-457 (2009).

Survey Question

What functional title(s) best describe you (check all that apply)?

- Biochemist
- Cell biologist
- Macromolecular crystallographer
- Molecular biologist
- Structural biologist
- Other (please specify)

Click on image or [here](#) to take the one question survey.



Textbook of Structural Biology
by Anders Liljas, et al.

Book review:

Textbook of Structural Biology

by A. Liljas, L. Liljas, J. Piskur, G.n Lindblom, P. Nissen and M. Kjeldgaard

As promised, this review is of a book directly relevant to structural biology ? just check out the title. I started this book not knowing what level of prior experience the reader needed. After reading the first few chapters, I concluded that the reader had better have an organic chemistry, biology and crystallography course under their belts, since advanced concepts are introduced without description. I read the book and I realized that this text provides a well thought out and reasonably current survey of structural biology.

The first four chapters introduce structural biology, protein and DNA structure, as well as lipids and membrane structure. The remaining twelve chapters describe, in great detail, the current state of the art in structural biology, including: enzymes, DNA replication and recombination, transcription, protein synthesis and translation, protein folding and degradation, membrane proteins, signal transduction, cell motility and transport, cell-cell interactions, the immune system, viruses and the evolution of macromolecules. The last chapter on macromolecule evolution is particularly interesting in that this year is the 150th anniversary of the publication of On the Origin of Species. Each chapter is elucidated with structures from the recent literature as well as historical examples where appropriate. Each protein is provided with its PDB code so it very easy to study a given structure in depth. However, this is also my one complaint, as the reader is forced to go to the PDB to find references for the structures.

There are six appendices on diverse topics such as energetics, fold comparison, prediction of conformation, assignment of function, protein modification and a current list of Nobel laureates. The main text is 484 pages with well written prose. I enjoyed reading this book and recommend it for an advanced level class in structural biology or as a current reference text.

I have preordered my copy of Biomolecular Crystallography: Principles, Practice, and Application to Structural Biology by Bernhard Rupp, so look for a review of that book here in October or November. Finally, I am pleased to report that Sean B. Carroll, an author reviewed here in the past, now has a monthly column in the New York Times titled "[Remarkable Creatures](#)"

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