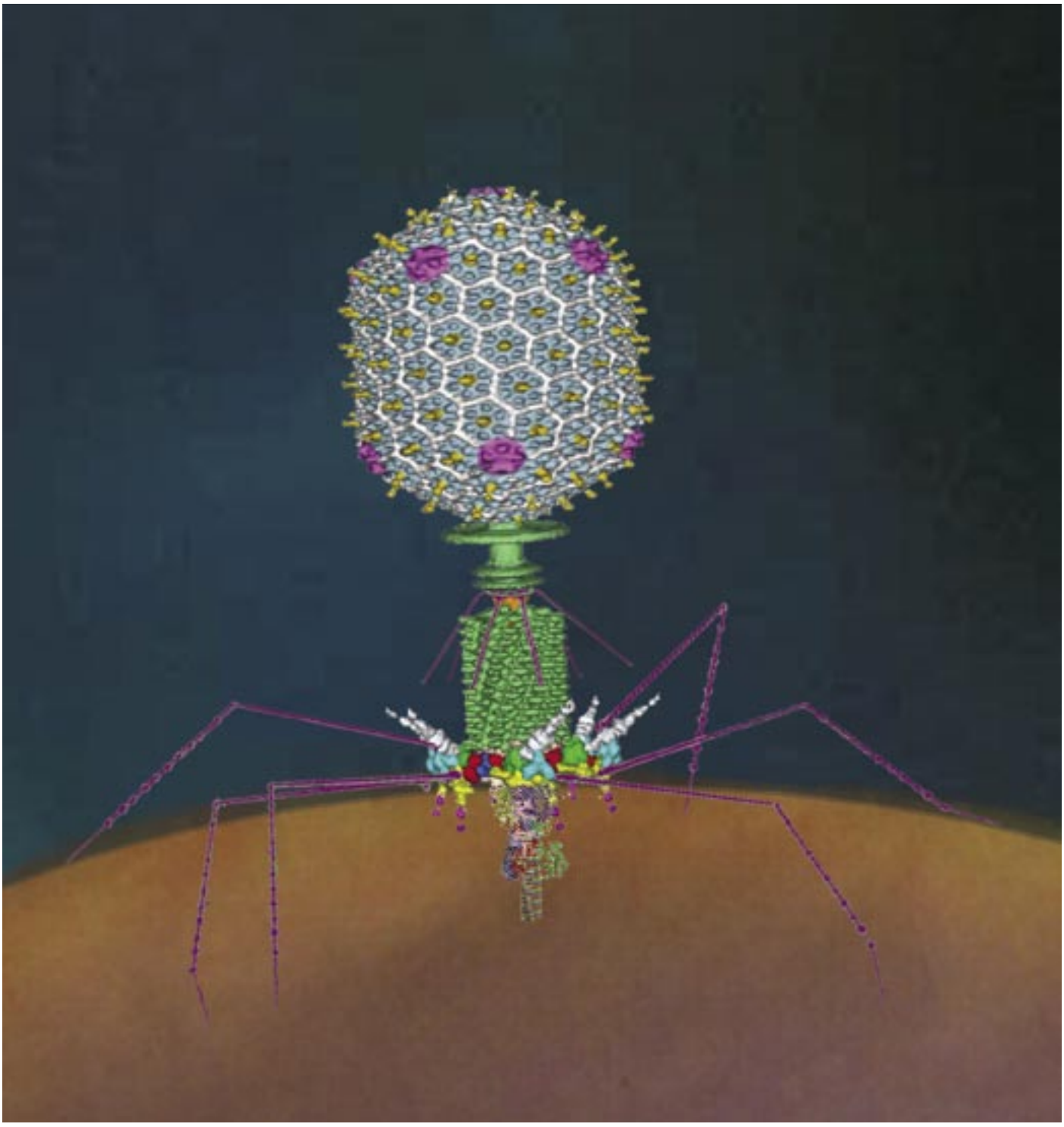
American Crystallographic Association

# NEWSLETTER

Number 3

Fall 2005



## *T4 Bacteriophage*

*from Michael Rossmann's talk at Spring ACA meeting in Orlando*



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# American Crystallographic Association
# NEWSLETTER


**Cover** **The T4 Bacteriophage from Michael Rossmann's talk at the 2005 ACA Meeting.** ***On The Cover*** **article, page 14.**

**ACA HOME PAGE** **http://www.hwi.buffalo.edu/ACA/**

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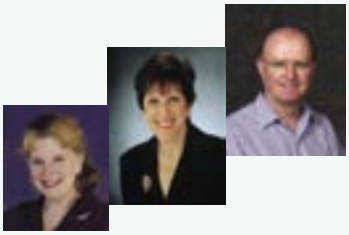




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**Deadlines for contributions are: February 1 (Spring), May 1 (Summer), August 1 (Fall) and November 1 (Winter)**
**Articles by e-mail are especially welcome.**


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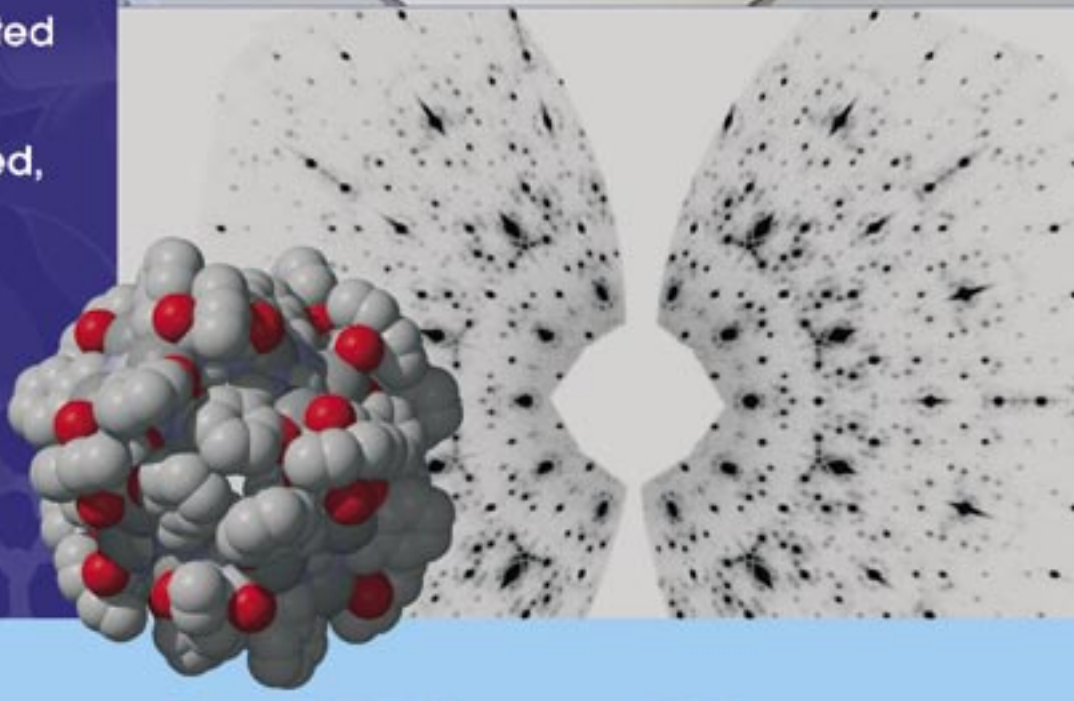

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## President's Column

The devastation from Hurricane Katrina to the the gulf coast area is a great concern to everyone, including members of the ACA. Crystallographers left with non-functional laboratories are encouraged to contact the ACA office in Buffalo to see if alternate temporary research arrangements can be made for themselves and their lab members; principal investigators who are willing to allow such researchers access to their facilities should also contact the ACA office. We hope that this part of the world can return to normal activity as soon as possible. Our sincere condolences go out to people who have lost friends and family in this catastrophe.

The ACA Orlando meeting was a great accomplishment. The scientific program organized by Program Chair, Ed Collins was remarkable in the many different areas of crystallography that were represented – macromolecules, fiber diffraction, materials science, crystal engineering, neutron scattering, powder diffraction, service crystallography, small angle scattering, small molecules and synchrotron radiation. There was something for everyone. Thank you, Ed and the members of the Program Committee - Alicia Beatty, Gregory Beaucage, Henry Bellemy, Stephen Ginell, Chad Haynes, Tom Irving, Jeanette Krause, Allen Oliver, Kevin Paris, Brian Toby, Alexandre Yokochi and Jian-Min Zuo. The site arrangements were also very well organized and we very much appreciated the efforts by the Local Chairs Khalil Abboud and Tomas Selby, and by the Local Committee, Niveen Khashab, James Leonard, Eric Libra and Laurel Reitfort. We are also grateful to our ACA staff Marcia Colquhoun, Patti Coley and Tammy Colley for their help in making the meeting so successful. Highlights of the meeting were the Patterson Award Symposium in honor of Alwyn Jones and the Margaret Etter Early Career Award Session in honor of Jennifer Swift. Thanks to Fran Jurnak for her Past President's address and for engaging the services of a magician who entertained attendees at various tables throughout the banquet evening. We look forward to a successful meeting next year in another beautiful location at the Sheraton Waikiki Beach in Honolulu, Hawaii from July 22-27, 2006. Congratulations to Charles F. Majkrzak from the National Institute of Standards and Technology, the winner of the Bertram Eugene Warren Diffraction Physics Award and to Helen M. Berman of Rutgers University, the winner of the Martin J. Buerger Award. These 2006 awards will be presented at the Hawaii meeting.

Salt Lake City, Utah has been chosen as the 2007 ACA meeting site. Council is considering the possibility of holding the spring ACA meeting at the same site every three years and this would likely be in a warm southern location. The same location every three years would permit reduced rates to be negotiated for that particular site. Another suggestion is to hold joint meetings with other societies. Any ideas/suggestions that you may have for ACA meeting sites would be welcomed by Council – please send them to us. The spring ACA meetings (such as Orlando) occur during the years of the IUCr Congress and General Assembly. I trust that the ACA members in Florence enjoyed the IUCr meeting and I look forward to seeing many of you in Hawaii in 2006.

*Louis Delbaere*

## Guest Editorial by Madeleine Jacobs, *Executive Director and Chief Executive Officer, American Chemical Society*

Some people say that confession is good for the soul. I have a confession to make: When I was Editor-in-Chief of *Chemical & Engineering News* (1995-2003), my favorite articles involved those that featured a crystallographic structure. Perhaps it was because the images were so beautiful and enlivened our pages, or perhaps it was because the field of crystallography was not well developed when I was in graduate school. I always loved how much crystallography revealed about chemical structures. Maybe ACA knew of my secret passion for crystallography when it selected me last summer to receive one of its Public Service Awards. I proudly display my award crystal in my office.

But it is not just C&EN that understands the importance of crystallography. All of the American Chemical Society journals recognize that crystallography is one of the most important methods available for determining molecular structure. And the ACS Publications Division is working to ensure that crystallographic results published in our journals are consistently of the highest standard.

To find out more about what ACS is doing, I turned to my colleague and friend, Richard Eisenberg, who is a chemistry professor at University of Rochester and Editor of *Inorganic Chemistry*. Rich generously provided me with background for ACA members. Rich has spearheaded a pilot project with the Cambridge Crystallographic Data Center (CCDC) and the IUCr to develop procedures for automatic CIF checking and validation. The pilot was run through *Inorganic Chemistry* because it receives a higher percentage of papers having crystallography than any other major ACS journal.

Rich is enthusiastic about the results. "The pilot project was successful in defining in detail the information flow and in identifying and correcting difficulties in the proposed procedures for CIF validation," he says. "The project also helped to identify what must be done in the next web manuscript submission and tracking system to be implemented by ACS."

Rich expects that *Inorganic Chemistry* will be able to implement the new automated procedures with CCDC and IUCr within the next 12-18 months. "The ease and rigor of our CIF checking will be the best available for large-scale chemistry journals, while the ease will be unparalleled for non-crystallographic authors," he says.

Speaking for all ACS journal editors, he adds: "We also appreciate two trends that are serving to increase the role of crystallography in chemical research. The first is the increased facility for obtaining x-ray intensity data through CCD instruments, and the second is the growing focus on supramolecular chemistry and biological systems, both of which deal with systems of greater size and complexity than in the past."

I join Rich and the other ACS journal editors in thanking members of the crystallographic community—many of whom we are pleased to count as ACS members—for their input into this project. We welcome your continued participation as members, authors, and reviewers of papers in ACS journals.

*Madeleine Jacobs*

## *Intelligent Design – A Call to Arms.*

On August 11th, the Kansas Board of Education tentatively approved new state science standards that weaken the role evolution plays in teaching about the origin of life. A final vote is expected in September or October, but the 10 member board is not expected to change it's 6-4 bias. The new science standards would not eliminate the teaching of evolution entirely, nor would they require that religious views, also known as creationism, be taught, but they would encourage teachers to discuss various viewpoints and eliminate core evolution theory as required curriculum. David Shulenberger, provost of U. Kansas told the *Lawrence Journal-World* (August 30, 2005) that he expected this set of deeply flawed science standards to be adopted and that the debate over the place of evolution in the state's science standards was damaging the university's national reputation and its ability to attract top faculty and students.

In 2004 The Ohio State Board of Education approved a "Critical Analysis of Evolution Lesson Plan" which had been vigorously opposed by the NAS, the Ohio Academy of Science and many other science and education organizations. MANY other states have fought back bills that would require disclaimer stickers in textbooks or alter science standards to require that Darwinian evolution be presented as questionable. One prominent example is the Cobb County, GA appeal for which the ACA signed an *amicus curiae* brief (see Council Highlights, page 60, and the Summer, *ACA Newsletter,* p 24 article by Charlie Carter).

It seems we've been fighting this battle for a long time now, but the situation just gets more and more scary. Because it's usually best to know the enemy, I went to the Discovery Institute website. (This is the infamous Seattle think tank that promotes Intelligent Design by funding projects in science and religion. On the home page list of 11 Senior Fellows and 6 Adjunct Fellows, one had an M.D degree, but the academic credentials of the others were in philosophy, theology, business, etc.; no biologists, chemists, or other applied sciences. Among the 14 Senior Fellows and 26 Fellows in their Center for Science and Culture I counted five biologists, one chemical physicist and one mathematician.

Jodi Wilgoren in a front page, Sunday *New York Times* article Aug. 21st, *Politicized Scholars Put Evolution on the Defensive* followed the money, writing that the Discovery Institute receives "financial support from 22 foundations, at least two-thirds of them with explicitly religious missions," …"Although the Discovery Institute also receives funding for work unconnected with antievolutionism from secular foundations such as the Gates Foundation, its antievolution efforts are apparently unwelcome to the Templeton Foundation and the Bullitt Foundation, whose director was quoted as describing Discovery as 'the institutional love child of Ayn Rand and Jerry Falwell.'. ."

Turning to the National Center for Science Education (NCSE), an excellent resource, I found an article published in the May 30th *New Yorker* by H. Allen Orr, a U. Rochester professor, (Biology Dept.) who specializes in evolutionary genetics. To quote and paraphrase from his article: "The (Discovery Institute) center's fellows and advisers - including the emeritus law professor Phillip E. Johnson, the philosopher Stephen C. Meyer, and the biologist Jonathan Wells—have published an astonishing number of articles and books that decry the ostensibly sad state of Darwinism and extoll the virtues of the design alternative. But Johnson, Meyer, and Wells, while highly visible, are mainly strategists and popularizers. The scientific leaders of the design movement are two scholars, one a biochemist and the other a mathematician. To assess intelligent design is to assess their arguments."

Scholar # 1: Michael J. Behe, (professor of biological sciences, Lehigh U.) "who writes technical papers on the structure of DNA, is the most prominent of the small circle of scientists working on intelligent design, and his arguments are by far the best known. Behe's main claim is that cells are complex not just in degree but in kind. Cells contain structures that are 'irreducibly complex.' This means that if you remove any single part from such a structure, the structure no longer functions. In his popular book *Darwin's Black Box,*(1996) Behe maintained that irreducible complexity presents Darwinism with 'unbridgeable chasms.'…Scientists, he argued, must face up to the fact that 'many biochemical systems cannot be built by natural selection working on mutations'.- someone must have designed them."

Scholar # 2: William A. Dembski, (PhDs in mathematics and philosophy; master of divinity in theology; has been a research professor at Baylor) "Dembski publishes at a staggering pace. His books

## Editorial: Intelligent Design - -, con't:

- including *The Design Inference, Intelligent Design, No Free Lunch,* and *The Design Revolution* - are generally well written and packed with provocative ideas. According to Dembski, a complex object must be the result of intelligence if it was the product neither of chance nor of necessity. …. an object was intelligently designed, he says, if it shows 'specified complexity'- complexity that matches an 'independently given pattern.' Dembski's second major claim is that certain mathematical results cast doubt on Darwinism at the most basic conceptual level. In 2002, he focused on so-called No Free Lunch, (NFL) theorems, which were derived in the late nineties by the physicists David H. Wolpert and William G. Macready. These theorems relate to the efficiency of different 'search algorithms.' (Darwin's theory can be thought of as a search algorithm.) "In the end, he argues, the NFL theorems and the displacement problem mean that there's only one plausible source for the design we find in organisms: intelligence." Orr goes on to demolish these arguments elegantly and eloquently; his article *Master Planned* can be found at the NCSE website /**www.ncseweb.org/**.

Also from NCSE, Richard Dawkins and Jerry Coyne, in the Sept. 1, 2005 *Guardian,* take on the "teach both sides" slogan. "As teachers, both of us have found that asking our students to analyze controversies is of enormous value to their education," they comment. "Why, then, would two lifelong educators and passionate advocates of the 'both sides' style of teaching join with essentially all biologists in making an exception of the alleged controversy between creation and evolution? What is wrong with the apparently sweet reasonableness of 'it is only fair to teach both sides'?"… "If ID really were a scientific theory, positive evidence for it, gathered through research, would fill peer-reviewed scientific journals. This doesn't happen. It isn't that editors refuse to publish ID research. There simply isn't any ID research to publish."

Our own past president of ACA, Charlie Carter, passed along this nice quotation in the course of an on-line debate: "that the quality of science is roughly proportional to the quality of the questions it asks. Intelligent Design does not offer questions; it simply offers (rather pompous and doctrinaire) answers."

It is so easy, almost automatic, for scientists to see that the ID arguments are junk science. But from all indications we are not getting this across to the general public. We have to do better.

Sir Harold Kroto, addressing an audience of IUCr Congress attendees in Florence, digressed briefly from his talk about nanotubes and Fullerenes (see page 60) to propose that we scientists have an "image" problem. He noted that when most people think of scientists they naturally think of Albert Einstein, looking like this:

People forget, he said, that at the time he was formulating the theory of relativity he looked more like this:

In fact, PR-wise, according to Kroto, Einstein at that age might well be thought to be better looking than our current promoter of anti-science, Tom Cruise.

Would that we scientists could polish our image enough to be taken seriously, not only with respect to science education, but about global warming, coastal restoration projects in the gulf and other enviornmental issues, dwindling water resources, -- the list goes on.

*Connie Chidester*

***"The events of the weeks since Hurricane Katrina, and the response of the government seem to disprove BOTH Intelligent Design and Evolution."***

***-- Garrison Keillor***

## Letter from Cheryl Klein and Ed Stevens *received Sept. 9th.*

***Editor's note: this was a personal email message rather than a "Letter to the Editor," but it deserves to be shared.***

We stayed in our house during the hurricane and that was OK - there was some damage to the roof - but when the levee broke, our house flooded. We stayed there for two days and then decided we should get out. We borrowed a boat from our neighbor's driveway and used it to gather some supplies from another neighbor's house. Then we (me, Ed, kids, 2 dogs, and 3 cats) took the boat to a bridge and were airlifted out by helicopter. Our time within the FEMA system was the worst. There was little food and water, no bathrooms, and they wouldn't allow us to take our pets on the buses. The SPCA came and we turned our pets over to them and they housed them at the Lamar Dixon facility in Gonzalez while we took a bus to Houston, rented a car and then drove back to Baton Rouge. We looked for housing - very unsuccessfully. Baton Rouge has exploded and can't handle all of the people there - there's not enough housing, food in the grocery stores, or gasoline. On Tuesday morning, we picked up our pets and began driving toward Virginia. We are staying with relatives in Washington DC until Sunday and then will settle for a few months outside of Charlottsville, Virginia where they have a summer home on Lake Montecello - 4 bedrooms, 3 baths and we can stay as long as we need to. We will put the kids in school there. I don't know what will happen after that. You are welcome to put something in the newsletter, if you want to. I have felt very out of touch since the emails have been down.

*Cheryl*
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***"Early life forms" by Nick D. Kim, U. Waikato, New Zealand. See www.nearingzero.net/res.html.***

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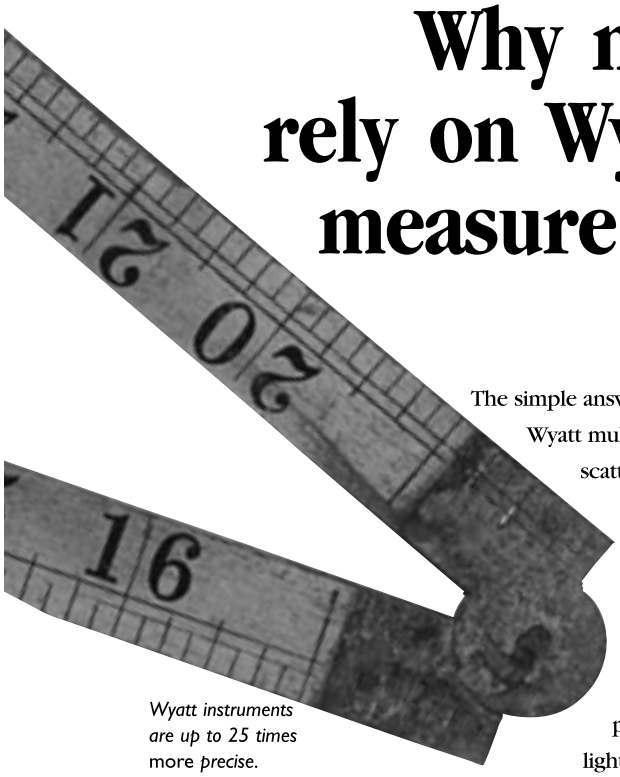


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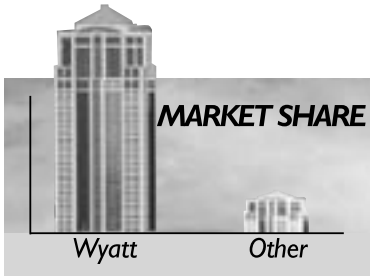


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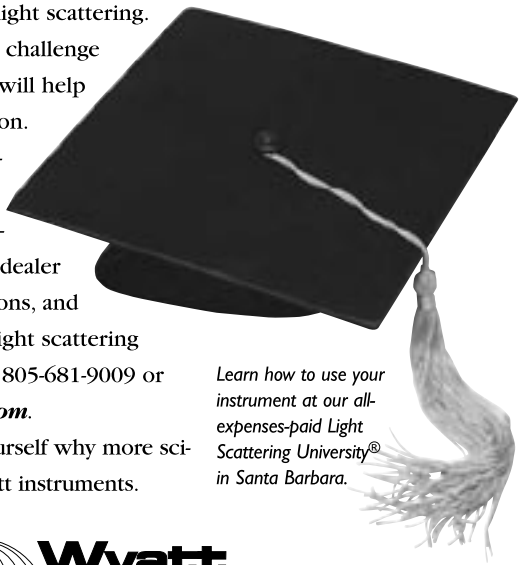

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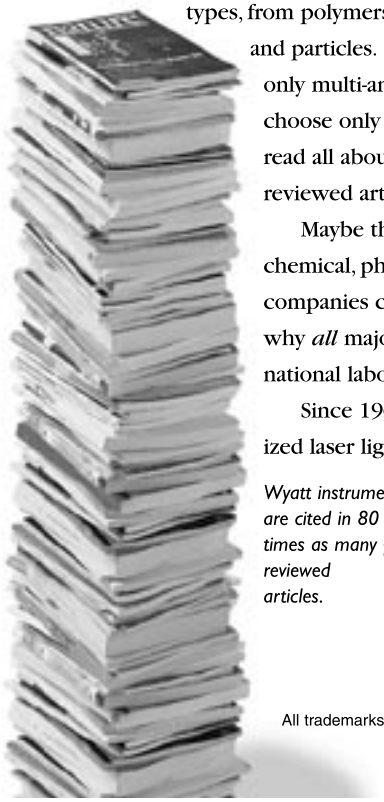

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## *63rd PDC in November*

The 63rd **Pittsburgh Diffraction Conference – PDC '05** – will be held on November 3-5, 2005, at Argonne National Laboratory.

An outstanding scientific program is planned, including sessions on Frontiers in Neutron Scattering and on Advances in Chemical Biology, in addition to symposia to honor the late Professors M. Sundaralingam and Leroy Alexander. Attendees at PDC '05 will have an opportunity to tour Argonne's unique experimental facilities at the Intense Pulsed Neutron Source and at the Advanced Photon Source.

For additional information please see the Pittsburgh Diffraction Society's website at **www.pittdifsoc.org**

*Tom Koetzle*

## *US Team Places 2nd at the IYPT*

For the first time in eighteen years the US Team placed in the finals of the International Young Physicists Tournament (IYPT), tying for 2nd place. The 2005 tournament, held at the Universität Zürich Irchel, involved both theoretical and experimental research and attracted 25 national teams of high school students from 23 countries. Students researched 17 problems and then presented and defended their findings in "Physics Fights" In the final round of competition the US team went against teams from Germany and Belarus by presenting their solution to this problem: *Granular material is flowing out of a vessel through a funnel. Investigate if it is possible to increase the outflow by putting an 'obstacle' above the outlet pipe.*

Phillip Schwartz, a Los Angeles senior and junior Daniel Kerr, Santa Monica, both from Wildwood School in LA, and three 2005 graduates of Rye Country Day School, Westchester, NY: Team Captain Jonathan Bohren, Scarsdale, Robert Kirkham, Larchmont, and Divya Krishnan, Stamford, CT. represented the United States in this contest.

US Physics teachers are encouraged to join the US affiliate of the IYPT, the USAYPT. See **www.usaypt.org**

*Jeanne Fauci, Wildwood School*

## AIP/APS Congressional ScienceFellowships

The American Institute of Physics annually sponsors one scientist to spend a year providing scientific and technical advice to Congress. The American Physical Society also runs its own APS Congressional Science Fellowship program, with the same purpose. Both programs are operated under the auspices of the American Association for the Advancement of Science, which sponsors its own Fellows, as well.

Fellowships are for one year, usually running September through August. The stipend for each Fellow is $50,000 per year, plus allowances toward relocation, in-service travel, and health insurance premiums. Qualifications include a PhD in physics or a closely related field, a strong interest in science and technology policy, and, preferably, some experience in applying scientific knowledge toward the solution of societal problems. The fellowship programs seek candidates with outstanding qualifications. In exceptional cases, the PhD requirement may be waived for applicants with compensating experience.

One entry suffices for application to both programs. Completed files received by the JANUARY 15 DEADLINE will be forwarded to the APS and AIP fellowship selection committees, which will choose, normally by mid-March, several finalists to be invited to Washington for personal interviews in early spring. See **www.aip.org/gov/cf.html.**

## 2006 Art in Crystallography Prize

The *ACA Newsletter* Editors are accepting entries to the **2006 Art in Crystallography** contest in the form of images emailed to either of the us (**conniechidester@earthlink.net** or **flippen@rcsb.rutgers.edu**). Entries should be accompanied by a paragraph explaining the science and the method of producing the image. A photo of the artist would be appreciated but is not required. Prizes will consist of a small monetary award and a banquet ticket and/or waiver of registration fees at the annual meeting. Of course we hope that all the **GLORY** garnered by the winners will be the major incentive. Winning entries will be posted on the web, and there will also be a display of printed images at the annual ACA Meeting. (Winners are not, however, required to attend the meeting). We will also feature images in the *Newsletter* from time to time. Judging will be by a panel appointed by the Editors; please let us know if you are interested in being a judge.

## Apply for ICDD Scholarships Soon!

To encourage promising graduate students to pursue crystallographically oriented research, the International Centre for Diffraction Data has established the **Ludo Frevel Crystallography Scholarship Fund**. Several recipients each year receive an award of $2,250. See: **www.icdd.com/resources/awards/frevel.htm.** Application Deadline: **October 31, 2005.**.

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## NIH's PSI Awards

The Protein Structure Initiative launched it's second (production) phase by announcing $300 million in new awards. With the aim of depositing 5000 protein structures in the PDB, $200 million (over 5 years) will go to four large-scale centers, which are expected to crank out protein structures as rapidly as possible. The remainder will go to six specialized centers that will focus on some of the most challenging proteins, including drug targets. These include small protein complexes; proteins that attach to a cell's outer envelope, or membrane; and many proteins from higher organisms, including humans. "We've already made great technological strides that have enabled us to determine more than 1,100 protein structures during the first half of the PSI, and we expect the large-scale centers to extend this progress," said John Norvell, Ph.D., PSI director. "But the fact remains that some proteins are not amenable to high-throughput approaches." PSI's expansion hit a snag this year when a tight NIH budget forced downscaling from $75 million a year to about $60 million (compared with $68 million for each of the last 2 years of the first phase of the initiative).

**The winners are: Large-Scale Centers:**

**Joint Center for Structural Genomics**, led by Ian Wilson, Scripps.

**Midwest Center for Structural Genomics**, Andrzej Joachimiak, Argonne.

**New York Structural GenomiX Research Consortium**, Stephen Burley.

**Northeast Structural Genomics Consortium**, Gaetano Montelione, Rutgers.

**Specialized Centers:**

**Accelerated Technologies Center for Gene to 3D Structure**, led by Lance Stewart, deCODE Biostructures, WA.

**Center for Eukaryotic Structural Genomics**, John Markley, U.Wisconsin.

**Center for High-Throughput Structural Biology**, George De Titta, HWI.

**Center for Structures of Membrane Proteins**, Robert Stroud, UCSF.

**Integrated Center for Structure and Function Innovation**, led by Thomas Terwilliger, Los Alamos National Laboratory.

**New York Consortium on Membrane Protein Structure**, led by Wayne Hendrickson, New York Structural Biology Center.

## BMS Freedom to Discover Award to Stephen Harrison

**Stephen C. Harrison** has won the 15th annual **Bristol-Myers Squibb Freedom to Discover Award for Distinguished Achievement in Infectious Diseases Research.** He was honored for his pioneering work on virus x-ray crystallography, including determining the first three-dimensional structure of a virus, as well as for his landmark efforts in elucidating virus structures related to HIV. Stephen, an HHMI investigator, is professor of biological chemistry and molecular pharmacology at Harvard, professor of pediatrics, and Director of the Center for Molecular and Cellular Dynamics. He heads the Laboratory of Molecular Medicine at Children's Hospital Boston. He is a member of the National Academy of Sciences, is the author of more than 150 peer-reviewed articles and serves on the editorial boards of *Structure* and *Cell*.

Stephen Harrison began studies in x-ray crystallography while still a graduate student at Harvard, focusing on the tomato bushy stunt virus. By 1978, he had determined a high resolution structure of the virus, the first intact virus structure to be determined, effectively creating the field of structural virology. Stephen and his colleagues then moved to more complex structures of human pathogens, including the human papillomavirus, the dengue virus, the tick-borne encephalitis virus and several components of HIV. He used structural biology to attack the intricacies of HIV-1, solved the structure of CD4, and collaborated in determining the structure of the HIV envelope protein - gp41. Recent work has focused on the fusion machinery that allows viruses to enter and then replicate inside cells, using their genetic information to reprogram normal cellular processes. Among other things, his discoveries have led to a new understanding of how certain viral proteins act as membrane penetration machines to disrupt patches of cell membranes and allow viral cores to invade cells, as well as insights into the mechanisms of virus assembly, virus attachment and virus-receptor interactions.

## Alex Wlodawer elected to Polish Academy of Sciences

Dr. Alexander Wlodawer, who was born in Poland and maintains very active collaborative links with Polish science, was elected a foreign member of the Polish Academy of Sciences (PAN) in recognition of his contribution to the advancement of structural biology, including discoveries fundamental for the development of drugs against AIDS and cancer and for our understanding of enzyme action. PAN has 350 national members and about 200 foreign members. The membership was awarded by PAN President Andrzej Legocki this June, during the opening ceremony of the Inhibitors of Protein Kinases conference held in Warsaw. Since 1999 Alex has been Chief of the Macromolecular Crystallography Laboratory at the National Cancer Institute and is an Adjunct Professor of Biochemistry and Molecular Biology and an Associate Member of the George Washington University Institute of Biomedical Sciences, Washington DC. He serves on the editorial boards of the *Journal of Biological Chemistry, Protein Science,* and *Acta Biochimica Polonica.*

*Mariusz Jaskolski*

## Gérard Bricogne awarded Honorary Doctorate in Uppsala

***Gérard after award presentation; dinner at the Castle in Uppsala: Gérard Bricogne, Sherry Mowbray and Alwyn Jones. Photos courtesy of Gerard Kleywegt.***

In January of this year Gérard Bricogne (Global Phasing Ltd, Cambridge, UK) received an honorary doctorate from Uppsala University in Sweden in recognition of his development of fundamental crystallographic methodologies.

Bricogne has been Directeur de Recherche at LURE (Orsay, France), and, while at LMB Cambridge, held a Howard Hughes International Research Scholarship. He is the recipient of numerous awards, notably the Prix Grammaticakis-Neumann of the French Academy of Sciences, the Dorothy Hodgkin Prize of the BCA, and the ACA Patterson Award. He is a member of the French Academy of Sciences.

Bricogne was born in 1949 in Aix-en-Provence, France. He studied for the Ph.D. degree with David Blow at the MRC Laboratory of Molecular Biology (LMB) in Cambridge, England. There he developed methods that enabled the use of non-crystallographic symmetry for protein and virus structure determination. He implemented real-space averaging in a set of ingenious computer programs and used these in 1978 for the determination of the first two virus structures at atomic resolution (tobacco mosaic virus, TMV, and tomato bushy stunt virus, TBSV) with Aaron Klug and Steven Harrison. This was an astonishing achievement, given the computer power available at the time.

Subsequently, Bricogne held a Research Fellowship in Trinity College (Cambridge) from 1975 to 1981. He was Assistant Professor at Columbia University from 1981 to 1983, then moved to LURE in 1983. In the late 1980s, Bricogne went on to develop the theoretical underpinnings for the application of maximum likelihood methods to macromolecular crystallography. In 1992-93, Bricogne spent a year in the protein crystallography laboratory in Uppsala (as recipient of a Swedish Research Council Tage Erlander Guest Professorship). During this time he began the laborious task of developing the computer programs that would use these new methods. They have now reached maturity and are revolutionizing the way in which macromolecular structures are solved.

After his time in Uppsala, Bricogne returned to Cambridge. He eventually left MRC's LMB and made an unusual move: he founded a not-for-profit company (Global Phasing Ltd.) that is essentially devoted to carrying out his research and development work as if it were in academia. In particular, this Cambridge-based company develops innovative methods and software for the determination and refinement of macromolecular crystal structures. This work is supported by a Consortium of pharmaceutical and drug-discovery companies, and by participation in EU-funded research networks. All of the software is made freely available to academic crystallographers.

Other macromolecular crystallographers who have received an honorary doctorate from Uppsala University include Wayne Hendrickson, Michael Rossmann and Eleanor Dodson.

*Gerard Kleywegt and Alwyn Jones*

## Wood Award Call

The **Elizabeth A. Wood Science Writing Award**, established in 1997, is given to authors of books or articles that bring science to the attention of a wider audience. Nominees need not be crystallographers or scientists and "writing" could include artistic efforts, museum displays, etc. Nominations should include the titles of books and copies of articles or other documentation and should be submitted to the ACA office; selection of the winner will be made by the ACA Council. The award is named to honor Betty Wood, a crystallographer at Bell Labs from 1943 until her retirement in 1967. She was President of the ACA in 1957, and has written interesting accounts of the early history of ACA and its predecessors. The Bylaws of the ACA were drafted by Betty Wood and Lindo Patterson, who chose, contrary to the custom of most other societies at that time, to have two nominees for each office. Betty is a marvelous speaker and gave memorable talks at the Awards Banquet on the occasions of both the 25th and the 50th anniversaries of ACA. In addition to her many research publications and her popular 1964 text "*Crystals and Light,*" she wrote a charming book for lay readers: *"Science From Your Airplane Window."* The recipient of the Wood Award is expected to give a brief talk at the Annual Meeting Awards Banquet. The award consists of travel expenses plus an artwork created especially for the ACA by Vivian Torrence, co-author of *"Chemistry Imagined,"* an art/science/literature collaboration with Chemistry Nobelist and first Wood Award winner **Roald Hoffman.** Other past winners are **Robert Hazen** (Carnegie Institution, Washington, DC); **Robert A. Weinberg** (MIT), **K.C.Cole** (L.A. Times); **Ira Flatow** (NPR host of *Talk of the Nation, Science Friday*); and **Oliver Sacks** (Albert Einstein College of Medicine).

## 'Gemini R' Wins Award

US based *R&D magazine* has awarded Oxford Diffraction an **R&D100** award for the Gemini R dual wavelength x-ray system. The awards are decided by independent judges and go to the top 100 technologically significant products of the year. The defining feature of the Gemini R is that it has two co-mounted x-ray sources.

## Call for Nominations for Fankuchen and Trueblood Awards

Nominations are solicited for the **2007 Fankuchen Memorial Award** and the **2007 Kenneth N. Trueblood Award.** Both awards will be presented at the annual ACA meeting in Salt Lake City in July, 2007. The recipients will give their lectures at the special Fankuchen and Trueblood Award Symposia organized to honor them. Each award is given every three years and each consists of an honorarium plus travel expenses to accept the award. There are no geographic or age restrictions. The Fankuchen Award carries the additional responsibility that the Award Lecture should also be presented at an academic institution of the recipient's choice. Please submit nominations to the ACA office in Buffalo (see page 1 for address) no later than **May 1, 2006.** A nominating letter clearly indicating the accomplishments of the individual is required; an additional supporting letter and a *c.v.* for the nominee may be provided, but are not required.

The **Fankuchen Award** was established in 1971 in memory of Isidor Fankuchen, Professor of Physics at the Polytechnic Institute of Brooklyn from 1942 to 1964. It is given to recognize contributions to crystallographic research by one who is known to be an effective teacher of crystallography. Previous winners were: **2004: Alexander McPherson; 2001: James Stewart; 1998: E. Dodson; 1995: Jenny Glusker and Kennth Trueblood; 1992: L. D. Casper; 1989: David Sayre; 1986: Michael G. Rossmann; 1983: Lyle H. Jensen; 1980: David Harker; 1977: Dorothy Hodgkin; 1974: A. Guinier; 1971: Martin J. Buerger.**

The **Kenneth N. Trueblood Award** was given for the first time in 2004, to **Richard E. Marsh**. It was created to recognize exceptional achievement in computational or chemical crystallography. The award was established in 2001 in memory of Kenneth N. Trueblood, UCLA , who was a major force in the early use of computers and the development of crystallographic computer programs. He applied these programs to the examination of chemical and molecular details of many structures at the frontiers of research. His contribution to the famous work on vitamin B12 is one example. KenTrueblood was a leader in the development of techniques for analysis of anisotropic motion and was also a superb teacher and a lucid author. The award is given every three years and consists of an honorarium plus travel expenses to accept the award. The award selection committees are:

***Fankuchen:*** **Thomas F. Koetzle (Argonne), Chair; Bob Sweet (Brookhaven); Katherine Kantardjieff (Cal State U., Fullerton); Lachlan Cranswick (Chalk River, Canada).**

***Trueblood:*** **Philip Coppens (SUNY Buffalo), Chair; Larry Dahl (Wisconsin); Doug Rees (Caltech); Jim Richardson (Argonne).**

# New Structures at Orlando ACA Meeting

***The T4 Bacteriophage composite image on the cover was derived from a movie created by W. Scott Meador, S. Lee Gooding & James A. Bartek (graduate students at Purdue who have now formed their own computer animation company "Seyet"). The movie, based on work by the authors (see below), was directed by Petr Leiman. The "head" is reprinted (ref. 1) ©2004, National Academy of Sciences, USA.***

The ***New Structures*** session (see p. 24) featured **Michael Rossmann's** presentation: **Structural and Functional Similarities Between the Capsid Proteins of Bacteriophages T4 and HK97: Evolution from a Common Ancestor,** Michael Rossmann, Andrei Fonkine, Petr G. Leiman, Mikhail M. Schneider, Vadim V. Mesyanzhinov, Paul R. Chipman, Shuji Kanamaru, Fumio Arisaka and Victor A. Kostyuchenko.

Many viruses, including most that infect eukaryotic organisms, enter the host by endocytosis. However bacteriophages remain attached to the outer cell surface during infection. When the baseplate of the tail portion of the *Myoviridae* phage T4 attaches to the cell surface it undergoes a conformational change from a hexagonal to a star conformation, initiating contraction of the sheath, which drives the tail tube through the cell envelope. Then the phage DNA stored in the head capsid is passed through the tail tube into the host cytoplasm.

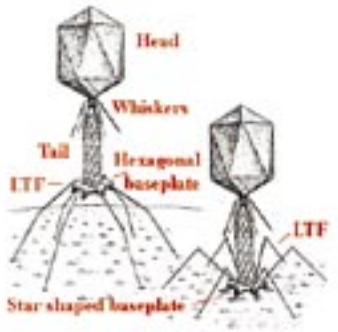



***Figure adapted from a drawing made by Fred Eiserling (UCLA) and published in numerous text books.***

The T4 bacteriophage, which uses *Escherichia coli* as a host, has a double stranded DNA 168kbp genome, (about 300 open reading frames) and about 40 structural proteins, and is too complex to crystallize in one piece. Cryo-EM studies of components and of the whole, and crystal structures of many of the various parts, fitted into the cryo-EM structures, were combined to construct this image.

The three-dimensional structure of the ***T4 head***, a prolate icosahedron with one unique portal vertex to which the phage tail is attached, was determined by cryo-EM[1]. The reconstruction shows hexamers of the major 48.7 Kda capsid protein gene product, gp23*, (which form facets similar to those of the bacteriophage HK97), and, at 11 of the 12 vertices, pentamers of the 46.2 kDa vertex protein gp24*. The 12th vertex, the portal for DNA packaging, tail attachment and DNA exit, is a dodecamer of gp20, often called the "connector."[2]

***Tail*[3]:** The tail tube is composed of a polymer of 138 subunits of gp19. The tail sheath is composed of 138 gp18 subunits, arranged in a helix with a pitch of 41 Å and twist angle of 17°. The hub protein gp29 probably extends through the inside channel of the tail tube, terminating with a gp29 - gp3 interaction that forms a hexameric ring.

***Baseplate assembly*[4,5]:** Crystal structures of six baseplate proteins were fitted into the 12 Å resolution cryo-EM structure (520 Å in diameter by 270 Å high) of the baseplate. In addition to the gp5-gp27 complex, crystal structures of the LTF (long tail fiber) attachment, gp9; the STF (short tail fiber) attachment, gp11; gp8; and STF, gp12 were determined. The outer rim of the baseplate is formed by six STFs (gp12) arranged in a garland such that the C-terminus of one fiber interacts with the N-terminus of a six-fold-related fiber. In the hexagonal conformation, the C-termini of the fibers point to the inside of the baseplate dome and so are protected from interaction with the receptor until the baseplate is brought into proximity with the cell surface when the LTFs make contact with the cell surface.

The conformational switch is triggered by interaction of the STFs with lipopolysaccharides, and the interaction of the LTFs with gp11s.

The 2.9Å crystal structure of the **gp27-gp5 complex**[6] is 190Å long and resembles a flashlight with the gp 27 trimer as the cylindrical "head" and the gp5C trimer the "handle." The gp27 head makes a hollow cylinder about 60 Å long with internal and external diameters 30 and 80Å, and this encompasses the three N-terminal domains of gp5 to which the trimeric gp5C handle is attached.

1) Fokine, A., P. R. Chipman, P. G. Leiman, V. V. Mesyanzhinov, V. B. Rao, M. G. Rossmann. (2004). Molecular architecture of the prolate head of bacteriophage T4. *Proc. Natl. Acad. Sci. U.S.* **101:** 6003-6008.

2) Driedonks, R.A., A. Engel, B. tenHeggeler, R. van Driel, (1981) *J.Mol.Biol.* **152**, 541-662.

3) Rossmann, M. G., V. V. Mesyanzhinov, F. Arisaka, P. G. Leiman. (2004). The bacteriophage T4 DNA injection machine. *Curr. Opin. Struct. Biol.* **14(2):**171-80.

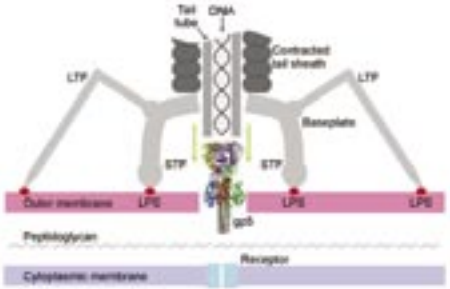
4) Kostyuchenko, V. A., P. G. Leiman, P. R. Chipman, S. Kanamaru, M. J. van Raaij, F. Arisaka, V. V. Mesyanzhinov, M. G. Rossmann. (2003). Three-dimensional structure of bacteriophage T4 baseplate. *Nat.Struct. Biol.* **10(9):** 688-693.

5) Leiman, P. G., M. M. Shneider, V. A. Kostyuchenko, P. R. Chipman, V. V. Mesyanzhinov, M. G. Rossmann. (2003). Structure and location of gene product 8 in the bacteriophage T4 baseplate. *J. Mol.Biol.* **328:** 821-823.

6) Kanamaru, S., P. G. Leiman, V. A. Kostyuchenko, P. R. Chipman, V. V. Mesyanzhinov, F. Arisaka, M. G. Rossmann. (2002). Structure of the cell-puncturing device of bacteriophage T4. *Nature (London).* **415:** 553-557.

Leiman, P. G., S. Kanamaru, V. V. Mesyanzhinov, F. Arisaka, M. G. Rossmann. (2004) Structure and morphogenesis of bacteriophage T4. *Cell. Mol. Life Sci.* **60:** 2356-2370.

Leiman, P. G., P. R. Chipman, V. A. Kostyuchenko, V. V. Mesyanzhinov, M. G. Rossmann. (2004). Structure and transformational transitions of bacteriophage T4 on attachment to a host cell. *Cell.* In press.




***Drawing created by Petr Leiman.***

## Highlights of Spring ACA Council Meeting

*In back. l to r: Bill Duax, Frances Jurnak, Lisa Keefe, Louis Delbaere. Front row: Iris Torriani, S. N. Rao, Marcia Colquhoun, Bob Bau. Inset at left: Doug Ohlendorf.*

The ACA Council met frequently during the annual ACA meeting in Orlando, Florida. Just prior to the start of the annual meeting, there was an all-day council meeting during which ACA business was conducted. On each of the days during the annual meeting, council met with the committees whose activities are so vital to the organization. The standing committees and SIG chairs reported on their activities for the past year and presented their plans for the upcoming year. The newsletter editors reviewed the status and plans for the ACA Newsletter, and the meeting planning committee discussed potential sites for future ACA meetings. On the last day, the session organizers for the 2006 annual meeting met to plan the sessions for the 2006 meeting in Hawaii.

**New Latin American Country Members:** Council passed a motion granting ACA Country memberships to both Argentina and Brazil. A representative from each country member is invited to attend the annual ACA meeting and the associated Council meeting. Council warmly welcomes Argentina and Brazil to the ACA and is optimistic that membership within the ACA will foster scientific interactions between crystallographers in the US and in these two countries. Other countries in Latin America are invited to apply for country membership.

**Science and Intelligent Design (aka Creationism):** Council voted to support and co-sign with other scientific associations a ***Brief Amicus Curiae*** regarding a case pending in Georgia. The case is an appeal by the Cobb County School District Board of Education to sustain its requirement that biology textbooks carry the following disclaimer:

***"This textbook contains material on evolution. Evolution is a theory, not a fact, regarding the origin of living things. This material should be approached with an open mind, studied carefully and critically considered."***

The brief expresses the views of the mainstream scientific community:

***"The scientific community does not qualify evolution as "theory not fact"; scientists do not define evolution using the "origin" language of the disclaimer, and there is no scientific controversy over whether evolution occurs. As explained below, there is no valid scientific or pedagogical reason for the Cobb County disclaimer, which is contrary to the best advice of the scientific community."*** ***(See Editorial, p 5.)***

**The 2006 Meeting in Hawaii:** The 2006 annual ACA meeting is scheduled for July 22 - 27 at the Sheraton Waikiki Beach Hotel in Honolulu, Hawaii. This location presents members of the Pacific Rim societies with the opportunity to attend. The last time that the ACA meeting was held in Hawaii was in 1979. Participation by crystallographers in the Pacific Rim countries was significant and the interactions between crystallographers in the US and in those countries were considerable. The scientific program for this meeting is excellent. Several SIGs have coordinated to organize joint sessions, thereby integrating techniques with multiple scientific disciplines. Two awards will be presented. The Buerger Award will be presented to Helen Berman in recognition for her development of information services, including the Protein Data Bank (PDB), the Nucleic Acids Database, and the Research Collaboratory for Structural Bioinformatics (RCSB). The Warren Award will be presented to Charles Majkrzak for his contributions to the development of neutron reflectivity and its use in interface science.

*Lisa Keefe, ACA secretary*

## Reminder: Please VOTE!

***Please remember to VOTE in ACA Elections! Candidate statements and photos are in the summer ACA Newsletter; The deadline for mailing ballots or electronic voting via the ACA website is November 15th.***

## Free Journals

*Acta Cryst.*: Bound Volumes 1-23 & B24-26, NOT bound Vols A24-A50 & B27-B46. Also, *RevSciInstr.*: BoundVols 27-40 & NOT Bound Vols 41-72.

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## Patterson Award Presented to Alwyn Jones

The 2005 **A. Lindo Patterson Award** was presented to **Alwyn Jones**, Professor of Structural Biology, Department of Molecular Biology, Uppsala University, Sweden , at the Patterson Symposium in his honor during the Orlando ACA meeting. The award recognizes outstanding research in the structure of matter by diffraction methods. Alwyn's citation acknowledged in particular his contributions to the field of macromolecular crystallography which, through his pioneering efforts in the application of computer graphics to the construction of atomic models from electron density maps, revolutionized the methodology of protein structure determination. Alwyn's plenary lecture ***From Inter to 'O'*** was enthusiastically received. See page 22 for the report on the Patterson Symposium.

***Above, ACA President Louis Delbaere presenting the Patterson Award to Alwyn Jones. At right, Alwyn at the banquet with his son and daughter, Daniel and Elanor Mowbray.***

## Margaret C. Etter Student Lecturer Awards

The 2005 winners, were selected from submitted abstracts, independent of oral or poster designation, by the elected officers of the various SIGs, then invited to present their work as lectures. The winners were:

| | |
|---|---|
| Rumana Rashid, FL St. U. | BioMac SIG |
| Soheila Vaezeslami, MI St. U. | General Interest SIG |
| Dugald MacDougall, Notre Dame | Materials Science SIG |
| Elinor Spencer, U. of Durham, UK | Neutron Scattering SIG |
| Yuan Lin, Johns Hopkins U. | Synchrotron Radiation |
| Tamara D. Hamilton, U. of Iowa | Young Scientists SIG |

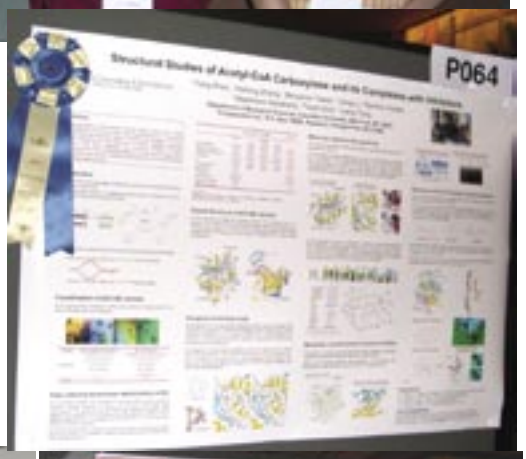
## Etter Early Career Award to Jennifer Swift

In the Etter Award Session at the Orlando meeting, ACA President Louis Delbaere presented the 2005 **Margaret C. Etter Early Career Award** to **Jennifer Swift** (photo at right) to recognize her outstanding achievement and exceptional potential in crystallographic research demonstrated at an early stage of her independent career. Jennifer's award lecture was titled *Growth and Dissolution of Cholesterol Crystals*. See report, page 24.

**Tamara Hamilton**, who received one of the **Margaret C. Etter Student Lecturer** awards, spoke in the same session, on *Metal-Organic Polyhedra Arising from Products of Template Directed Synthesis in the Solid State*.

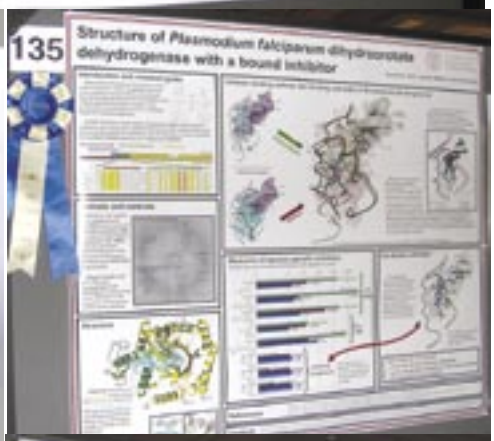
***From left: Arwen Pearson, Etter Award Session Chair, Jennifer Swift, ACA President, Louis Delbaere, and Tamara Hamilton. Photo courtesy of Mark Hollingsworth.***

*L to r: Gautham Desiraju, Chair, Pauling Committee, and Pauling winners Jacob Morris, Darrell Hurt, Jeremiah Wagner and Yang Shen.*




Five outstanding student posters from the US and one from Canada were selected.from a large pool of excellent posters by a diligent and perservering Pauling Prize Committee: Gautham Desiraju, Chair, Xiaodong Cheng, Rob McKenna, Gil Prive and Lee Groat, who presented the Canadian Division prize. Winners were:

**P064 Yang Shen,** Columbia Univ.: ***A Mechanism for the Potent Inhibition of Eukaryotic Acetyl-Coenzyme A Carboxylase by Soraphen A, a Macrocyclic Polyketide Natural Product***;

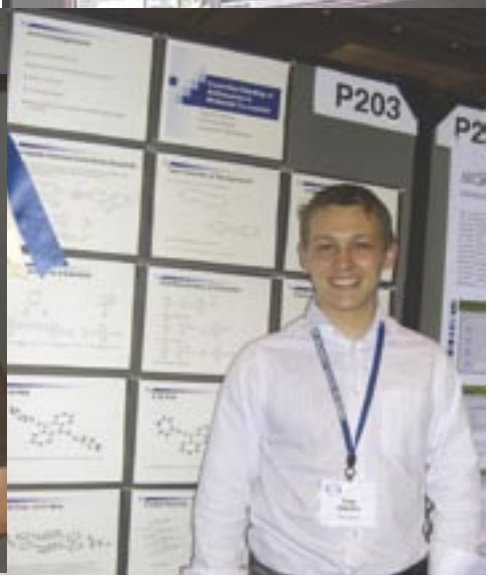



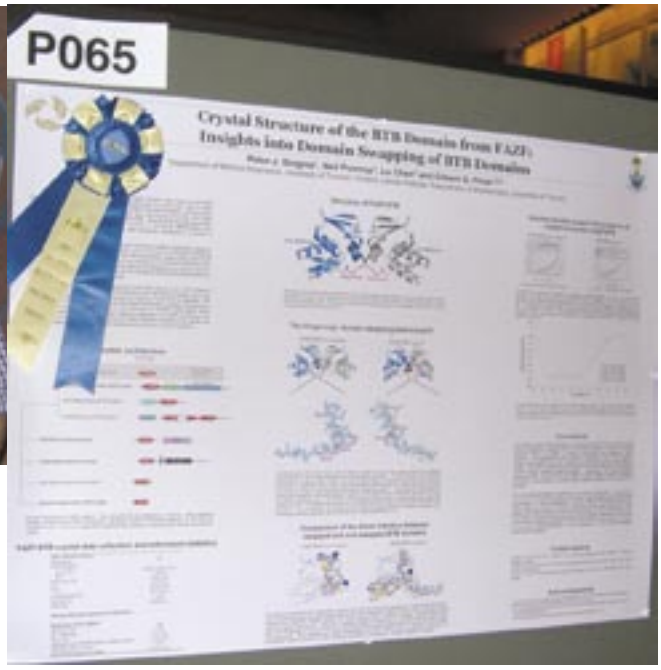

**P135 Darrell Hurt,** Cornell Univ.: ***Structure of Malarial Parasite Plasmodium falciparum dihydroorotate Dehydrogenase: Comparison Provides Clues for Species-specific Drug Design;***

**P172 Jacob Morris,** U. of Notre Dame: ***Self-Assembly of Two and Three Dimensional Networks by Hexameric Sodium Aryloxides***;

**P203 Tony N. Sokolov,** U. of.Iowa: ***Controlled Stacking of Anthracenes in Molecular Co-crystals*** (Tony is shown with his poster, bottom far right);

**P235 Jeremiah Wagner**, U. of Wisconsin: ***Structure of the Chromophore-Binding Domain of a Bacteriophytochrome*** (see Jeremiah with his poster, at immediate right).

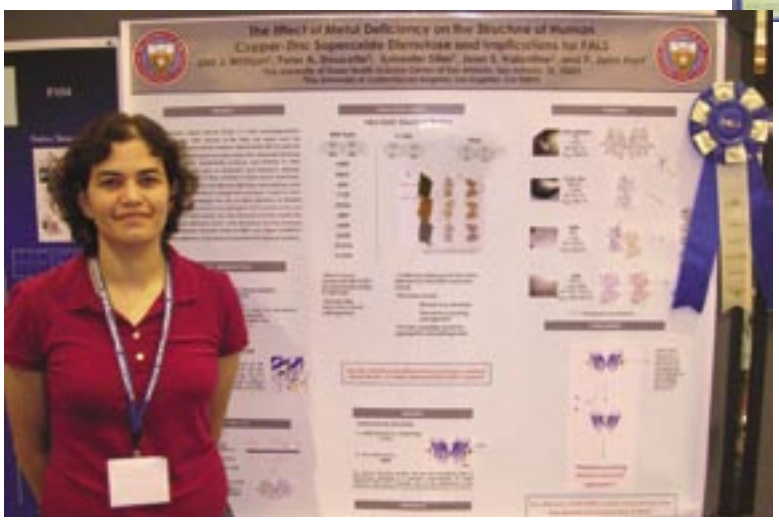





The ***Canadian Division Pauling Poster Prize,*** sponsored by the Canadian National Committee of the IUCr was presented by Lee Groat, at left above, to **Peter J. Stogios,** Univ. of Toronto, for P065: ***Crystal Structures of the BTB Domain - Snapshots of a Versatile Eukaryotic Protein-Protein Interaction Module.*** Lee represented the Canadian Division on the Pauling Selection Committee.

## *JCC Poster Prize*

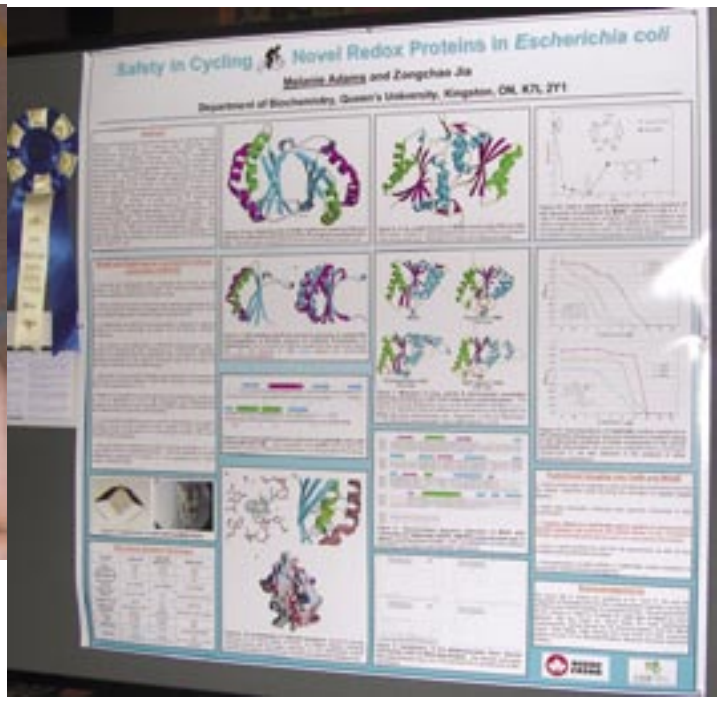
The Journal of Chemical Crystallographic Prize was awarded to **Sean A. Dalrymple**,at right, Univ. of Calgary, for P200: ***Crystal Engineering of Sulfonate-Based Second Sphere Networks.*** The organizers are grateful to the JCC Prize Selection Committee: Jim Kaduk, Chair, Frank Fronczek, and Victor Young.

## *IUCr Poster Prize*

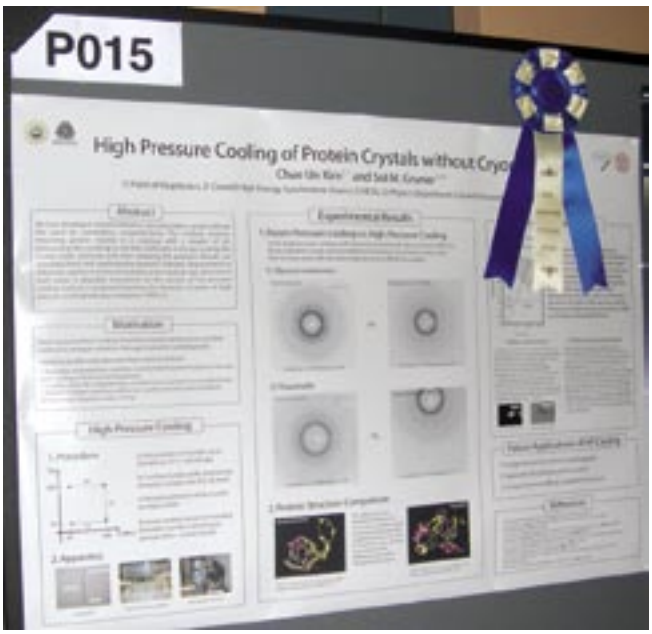
The IUCr Prize went to **Lisa J. Whitson, at left,** UT Health Science Center at San Antonio, for P105: ***The Effect of Metal Deficiency on the Structure of Human Copper-Zinc Superoxide Dismutase and Implications for FALS.***

The efforts of the selection committee: Chris Gilmore, Chair, John Horton, Tom Irving, Alberto Podjarny, and Jimin Wang, are much appreciated.




## RCSB PDB Poster Prize

The Research Collaboratory for Structural Bioinformatics PDB Poster Prize was awarded to **Melanie Adams,** Queen's Univ., for P057: ***Safety in Cycling: Novel Redox Proteins from Escherichia coli.*** Jim Pflugrath, Chair of the PDB Poster Committee, is shown with Melanie, above. Other members of the selection committee were Tim Rydel, Craig Ogata, Michael Sawaya and Marilyn Yoder. The award was *Biochemistry - Vol. I* by Donald and Judith G. Voet and a signed copy of *Introduction to Macromolecular Crystallography* by Alexander McPherson.




## Oxford Cryosystems Poster Prize

The 2005 Oxford Cryosystems Low Temperature Poster Prize was awarded to **Chae Un Kim,** at right, Cornell Univ., for P015: ***High Pressure Cooling of Protein Crystals without Cryoprotectants.*** The efforts of the selection committee: Gloria Borgstahl, Chair, Jeff Deschamps, Travis Gallagher, Annie Heroux, and Jack Tanner, are gratefully acknowledged..

***Special thanks to David Rodgers, U. Kentucky, at right, who was responsible for selecting and organizing all the Poster Prize Selection Committees.***

***Thanks to Local Committee member Eric Libra for the photo at left.***

## 2005 ACA Meeting - Orlando, FL, May 28 - June 2

Highlights of the meeting included the presentations of the **A. L. Patterson Award** to **Alwyn Jones**, and the **Margaret C Etter Early Career Award** to Jennifer Swift and the symposia organized to honor them (see pages 20 -24). Tony Kossiakoff organized the ***Transactions Symposium***, on **New Horizons in Structure-Based Drug Design**. The many poster prizes are reported on pages 17-19. Congratulations to Program Chair Ed Collins and the entire Program Committee for a diverse and stimulating program! Kudos also to Local Chairs Khalil Abboud and Tom Selby. They managed make everything run smoothly, while appearing to be calm and collected the entire time. Of course they had some able assistance from the Locals.

*Local Chairs Khalil Abboud (far left) and Tom Selby; and, at right: Program Chair Ed Collins.*

*Some members of the Local Committee. From left: Eric Libra (UF), James Leonard (UF), (seated behind) Laurel Reitfort (UF), Peter Steele (UCF), Sinem Ozyurt (UCF), and Barbara Mascareno-Shaw (UCF). Maryam Farshid and Niveen Khashab are not in the picture.*

*Editor's note: Except where otherwise noted, the group pictures of session speakers were taken by Local Committee Members Eric Libra, James Leonard, Peter Steele, Sinem Ozyurt, Maryam Farshid and Barbara Mascareno-Shaw.*

*Below, from left: Marcia Colquhoun, Patti Coley, and Tammy Colley at the Awards Banquet.*

*At left: ACA President Louis Delbaere and Carol Delbaere, toasting the Opening of the meeting with those strange potato martinis.*

*Above, ACA President Louis Delbaere performing his "hat tricks: at the Opening Ceremony.*

Whether due to the terrific scientific program or the enticing Disneyland venue, the attendence at the meeting was the highest ever for a spring meeting, 719, plus 200 exhibitors. The YSSIG mixer at the Swan Hotel must have been fun, from the happy looks on faces of people wearing leis. Scenes from the Annual Awards Banquet are on page 26. The winter *ACA Newsletter* will carry reports on the workshops, exhibitors, Travel Award winners, and a photo report on the Mentor-Mentee dinner at the Rainforest Cafe.

***In the foreground at right, Joel Bernstein and Bobby Barnett enjoying the YSSIG mixer.***

***Below, from left: "mystery woman", Robert (Bobbie) Heuther, Tammy Colley, Artem Lyubimov, Tomislav Friscic, Tea Pavkov, and Tony Sokolov. Photos courtesy of the Local Committee.***

# AW.01 Patterson Award Symposium on Macromolecular Model Building and Validation

*From left: Jane Richardson, Tom Terwilliger, Gerard Kleywegt, Alwyn Jones, and Paul Emsley.*

This year, the ACA bestowed its coveted **A. Lindo Patterson Award** on **T. Alwyn Jones**, FRS (Uppsala University), chiefly in recognition of his pioneering work in the development of computer-graphics software for macromolecular model building. Jones obtained his PhD in biophysics from Kings College in the early 1970s, and then moved to Munich, where he began the development of the famous FRODO program (although it was initially called INTER). After moving to Uppsala (Sweden) in 1979, he continued the program's development, but later began work on a successor which he redesigned from scratch. This successor was called "O" for reasons Jones steadfastly refuses to divulge (so we assume they would make him blush). For more than two decades the vast majority of all macromolecular crystal structures were built with these two programs, a fact now recognized by the ACA award, as it had been previously by the Royal Swedish Academy of Sciences through its Aminoff Prize (shared with Axel T. Brunger in 2003). Ever since using Ramachandran plots to select high-quality protein crystal structures for inclusion in O's database in the mid-1980s, Alwyn has also had a keen interest in model validation, and his *Nature* commentary (with Carl-Ivar Brändén; *Nature* **343**, 687-689 (1990)) today stands as a landmark publication in this important area of macromolecular crystallography.

In Alwyn's honor, a special symposium *Macromolecular Model Building and Validation* was organized. ACA President Louis Delbaere presented the Patterson Award to Jones, who reciprocated with his plenary lecture, a very entertaining historical overview of his work in the areas of model building and validation. He recounted how, in the early days of protein crystallography, models were actual physical entities that literally needed to be built by hand. Computer graphics provided a way to simplify, speed up and improve the process of model construction and to expedite the cycling between model building and automatic model refinement. Although there had been earlier attempts, Jones' FRODO program quickly became the accepted software tool for fashioning models out of chicken-wire contour displays of electron-density distributions. In those early days, the use of computer-graphics was an expensive enterprise. Alwyn showed figures demonstrating how his first Vector General display cost the equivalent of 3 Ferraris. Nowadays, a PC with a good graphics card would cost around 100 times less than even a single Ferrari.

Jones described the development of some of the many tools that have been incorporated into (or distributed along with) his model-building software, including database-oriented methods for model construction, model-validation methods (real-space fits, rotamer scores, and peptide-flip analysis), real-space refinement tools (developed as they were needed for the refinement of Satellite Tobacco Necrosis Virus in Uppsala), and non-crystallographic symmetry (NCS) averaging of density (initially as a separate set of programs, but nowadays also available inside O). Among the latest developments he described, the semiautomatic tracing methods were particularly interesting. Besides that, Alwyn announced that O has entered reciprocal space and can now do FFTs, and that eventually the program will be able to do interactive density updating as one rebuilds a residue (through the use of partial structure factors) - a testament to the unheard-of increase in computer power over a period of three decades! Other new developments include a job-management system (to take advantage of multi-processor computers) and tools to interpret difference-density maps (in terms of water or ligand molecules).

The lecture ended with an entertaining question-and-answer session in which serious and less-serious questions were answered (the exception being the inevitable question about the origin of the name "O"). Those of you who missed the plenary lecture by Jones will be pleased to learn that one can read about many of the issues he discussed in his paper in the 2004 CCP4 proceedings (*Acta Cryst.* **D60**, 2115-2125 (2004)). Moreover, although the meaning of the name "O" remains shrouded in mystery, interested readers can actually find out what the "T" in "T. Alwyn" stands for by looking up page 941 of *Acta Cryst.* **D55** (1999).

Besides Alwyn's lecture, there were four shorter contributions to the symposium by people involved in model building or validation. **Paul Emsley** (York University) described and demonstrated the capabilities of his program Coot. His program, a competitor of "O", has quickly gained popularity in the macromolecular crystallography community and Paul's demonstration of some of its powerful features and user interface showed why. With high-quality maps, Coot takes much of the tedium out of building or rebuilding a model, thanks in part to a built-in gradient minimizer that lets one grab a recalcitrant bit of model and drag it toward where it should be, with Coot then settling it into place. Coot is also good at fitting ligands and displaying maps of NCS-related molecules. Certain refinement and validation tasks can be carried out either within Coot, or left to external programs.

**Gerard Kleywegt** (Uppsala University) was (hopefully) the last crystallographer to ever give a talk using overheads (those of you born after 1980 might want to ask an older colleague what these are). He discussed a project that was initiated by Jones, namely the Uppsala Electron-Density Server, EDS: **http://eds.bmc.uu.se/**. The aim of this server is to produce (and make available to anyone) electron-density maps for all crystal structures in the PDB for which experimental data (*viz.* structure-factor intensities or amplitudes) have been deposited. At present, the calculations are successful in ~90% of

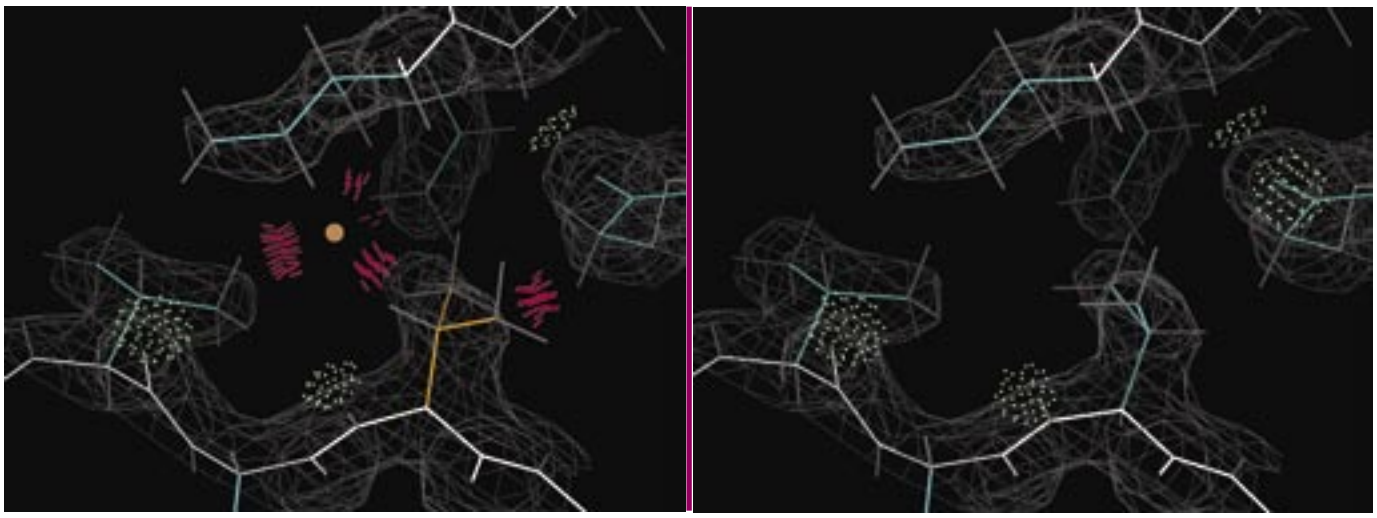
the cases, so that EDS contains maps (and various quality-related statistics) for ~15,000 PDB entries (July, 2005). Since EDS also provides two Java-based viewers, the electron-density maps are available to a wide audience of scientists interested in structural biology. Experience indicates that, besides crystallographers checking their own structures, molecular modellers working in the pharmaceutical industry are some of the heaviest users of the service. Kleywegt also showed figures demonstrating that the structure-factor-deposition behaviour of the community has vastly improved over the past few years. In 1990, only about a fifth of all crystal-structure depositions included the experimental data; in 1995, this was one third, and in 2000 around 57%. In the first few months of the year 2005, the rate had increased to 86% (although there is still significant variation if the numbers are analyzed by journal of publication ...).

While Jones and Emsley discussed traditional, interactive model-building programs, **Tom Terwilliger** (Los Alamos Natl. Laboratory) described his exciting work on automated iterative model building and density modification in the context of the Phenix software project. Terwilliger identified a number of problems in this area that are yet to be solved, including model completion (*e.g.*, ligand-fitting), proper error analysis, automated decision-making, and the incorporation of expert knowledge and experience (*i.e.*, to create an *Electronic Alwyn*). Tom described the Phenix Iterative Build Wizard that cycles between statistical density modification (which can use any prior expectations about the map to improve the phases) and moderate-resolution model building and refinement, similar to the Lamzin-Perrakis approach. According to Terwilliger, such methods work in practice because the model building introduces new information compared to the original density modification, because rebuilding removes correlations of the errors in atomic positions introduced in the refinement steps, and because improvement of the density in one part of the map improves the density everywhere. Nevertheless, a certain amount of bias is introduced, and he advocates use of prior knowledge about one part of a map to improve the density in another part. Such full-omit iterative model building maps yield high quality density from experimental phases and can even be used with (unrefined !) molecular replacement models.

Finally, **Jane Richardson** (Duke University) discussed the application of the validation software developed in the lab of Jane and her husband Dave. They aim to provide tools that can not only diagnose problems (validation), but also methods for fixing them. Their MolProbity web service is available to anyone willing to put their own or their competitors' structures on the line (**http://kinemage.biochem.duke.edu/molprobity/**). It adds all hydrogen atoms to a submitted model, taking H-bonding networks into account, to enable use of the all-atom clash score which reveals physically impossible contacts often indicative of errors in a model. Rotamers and phi, psi angles are evaluated by updated criteria. Side-chain flips of Asn, Gln and His are corrected automatically. Problems that can be fixed interactively include selection of better-fitting rotamers, introduction of small main-chain movements to relieve strain, and selection of "backbone rotamers" for RNA models. In a test comparing representative PDB entries and structures from the South-East Collaboratory for Structural Genomics that used either traditional or MolProbity-based rebuilding, the fixed structures scored 5- to 10-fold better at equivalent resolutions on the criteria tested and adjusted (clash, Ramachandran, and rotamer), with equal or slightly better Rfree values.

In conclusion, the Patterson Award Symposium was an entertaining and highly interactive session (with surprisingly few interruptions by mobile telephones, as these had been announced to be punishable by a compulsory 10 US$ donation to the Kleywegt-Jones Beer Fund) that provided an overview of the history, state-of-the-art, and future directions in two exciting areas of macromolecular crystallography.

*Gerard Kleywegt*



***From Jane Richardson: A local error diagnosed and corrected with the MolProbity tool set. At left, the Val was fit backwards (doubly eclipsed chi1), causing a difference peak fit as a water where there is not room. At right the Val is re-fit and the water deleted, giving better contacts, rotamers, density fit, and Rfree.***

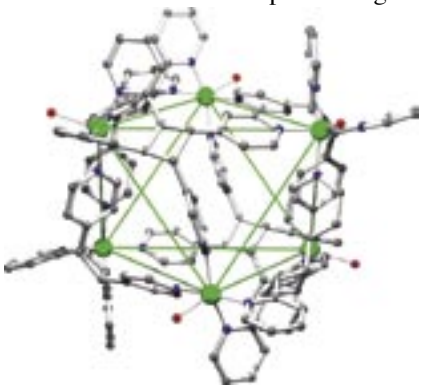
***Editor's note: Images from Alwyn Jone's talk were featured on the cover and on page 25 of the Spring, 2005 ACA Newsletter.***

## AW.02 Etter Early Career Award Session

*From left: Kenneth Henderson, Pius Padayatti, Arwen Pearson, Anna Gardberg, and Shuishu Wang. See page 16 for a photo of Jennifer Swift and Tamara Hamilton.*

This year's session opened with the presentation of the **Margaret C. Etter Early Career Award** to **Jennifer Swift** from Georgetown University (see page 16). Jennifer gave a fascinating talk on her use of atomic force microscopy to study the growth and dissolution dynamics of cholesterol crystals. The uncontrolled deposition of cholesterol is associated with several disease states, including gallstone formation. During her talk she showed movies of real-time crystal growth and dissolution, showing how different additives affected the dynamics of these processes. Using these studies she is able to gain insight into *in vivo* cholesterol deposition and how this could be regulated in the treatment of cardiovascular disease and gallstone formation. ***(Editor's note: Jennifer's crystals were featured in the Spring, 2002 ACA Newsletter; see cover and page 29.)***

The subsequent talks in the session were selected from submitted abstracts with a special focus on young scientist presenters, to reflect the award's emphasis on early career achievement. **Anna Gardberg,** postdoc, U. Tennessee, discussed possible conformations of amyloid Aβ fibrils and showed how modeling Aβ interactions with antibodies specific for its fibril state could help to distinguish between proposed Aβ conformations. The next speaker, **Tamara Hamilton**, graduate student, U. Iowa, received one of the **Margaret C. Etter Student Lecturer Awards** (she was nominated by YSSIG). Tamara presented work on the use of template-directed solid-state synthesis to make novel self assembling polyhedra that could be decorated with a variety of organic substituents. **Pius Padayatti,** postdoc, Case Western Reserve, told us about the use of Raman Crystallography to track the formation of reaction intermediates in the catalytic cycle of β-lactamases, allowing the transenamine intermediate to be trapped for crystallographic studies. He was followed by **Kenneth Henderson,** Assoc. Prof., U. Notre Dame, who discussed the difficulties of using *s*-block metals in network assembly. He then presented work showing that, by careful selection of reaction conditions and the use of pre-assembled *s*-block metal cages, *s*-block metals can be successfully used to create several types of extended network. The final speaker in the session was **Shuishu Wang,** postdoc, UCLA. Shuishu presented the structures of several intermediates in the pantothenate synthetase reaction pathway obtained by soaking in various combinations of substrates and products. He then discussed the implications of these structures for the mechanism of pantothenate synthetase activity.



***From Tamara Hamilton: The metal-organic trigonal antiprism host composed of six copper(II) atoms (green) and six 2,4'-tpcb ligands. The copper atoms have been connected with green lines to show the polyhedral structure. Guests have been omitted.***

If you would like more detail about the presentations in this session, you will be happy to hear that this year's Margaret C. Etter Early Career Award session will be included in the ACA 2005 Meeting *Transactions* which will be available on-line.

*Arwen Pearson*

## 1.01: New Structures Session

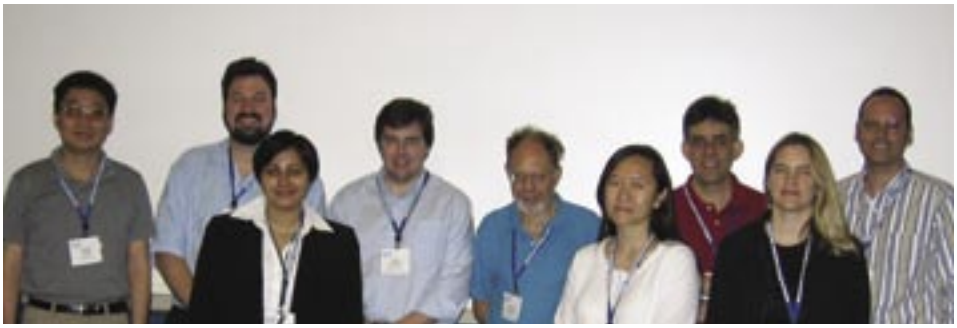
**Michael Rossmann** opened with a brilliant and inspiring lecture on the bacteriophage T4 structure. The crystal structures and cryo-electron microscopy images revealed key insights into this efficient infection machine. For example, the insertion domain of head capsid protein gp24 provides stability to the head shell and this role appears to be similar to the chain-mail stabilization observed for the related phage HK97. These results suggest an ancestral relationship between the two phages. The tail assembly of bacteriophage T4 consists of a base plate connected to a sheathed tube that is essential for the initial stages of infection. Crystal structures of several base plate proteins were determined and these structures were docked into 3-dimensional cryo-electron microscopy reconstructions to reveal a detailed picture of the supramolecular architecture of the tail. Michael ended his lecture with an astounding movie showing the dynamics of infection by bacteriophage T4. He noted that the movie was not a simulation since real structural data were used. (See *On the Cover*, page 14.)

**Allen Sickmier** from the Burley lab had the unfortunate task of following Michael Rossmann, but he successfully delivered the goods in his lecture on redox-sensing repressor (REX). Allen described the 2.9-Å structure of *Thermus aquaticus* REX (T-REX) complexed with NADH. The structure consists of a winged helix DNA binding domain and, quite appropriately, a Rossmann fold domain. The structure is inconsistent with DNA-binding because the two winged helix domains of the dimer are too close together to support association with DNA. Thus, the winged helix domains must separate in order to bind DNA, implying a dynamic mechanism of DNA recognition.

**Young Jun Im** from Jim Hurley's lab presented the first structure of oxysterol binding protein (Osh4). The apo protein plus complexes with four different sterol ligands were described. The ligand is buried in the beta-barrel substructure

## New Structures , con't

and this mode of binding is similar to that found in lipid transfer proteins. Conserved basic residues appear to be functionally important. Interestingly, the N-terminal lid, which is highly ordered in the liganded structures, is disordered in the apo structure. Moreover, ligand binding induces a 15 Å movement of the 340s helix. Thus, ligand recognition by Osh4 appears to be an extreme case of induced fit binding.



*From left: Liang Tong John Horton, Akanksha Nepal, Allen Sickmier, Michael Rossmann, Vivien Yee, Alfonzo Mondragon, Cathy Drennan, Jack Tanner.*

**Alfonso Mondragon** led us into the RNA world with his superb lecture on RNaseP, a catalytic RNA/protein molecule that processes the 5' end of tRNA. RNaseP consists of 300 RNA nucleotides and a 12 kDa protein, and this RNA/protein complex is highly conserved across all kingdoms of life. Alfonso's work has focused on the RNA part of the complex because it contains the active site (C-domain) and the specificity domain (S-domain). Structures of the S-domains of type A and type B RNasePs were presented. Despite having identical functions, the two S-domains have significantly different folds. This result suggests that RNA displays the kind of structural diversity that is typically associated with proteins. In addition to discussion of the structures, Alfonso revealed some interesting details of the structure determination process. For example, the type A structure was determined using SAD data from $Ba^{2+}$ ions, which was achieved by substituting $BaCl_2$ for the commonly used $MgCl_2$. Interestingly, data were collected at the Br edge, at which f'' for $Ba^{2+}$ is approximately equal to 4 electrons. Alfonso ended his lecture by describing a preliminary 4 Å resolution structure of a full length RNaseP RNA molecule, which is the first of its kind. The keys to structure determination included homology screening, attention to the effects of temperature and pH on folding, and microseeding using a crystallization robot.

**Cathy Drennan** described her structure of free lysine 5,6-aminomutase, which revealed a lysine in the Rossmann-like domain covalently bound to its pyridoxal-5'-phosphate cofactor in the putative active site of the adjacent TIM-barrel domain. Since the second cofactor, adenosylcobalamin, was found 25 Å away from the active site, she speculated that the free enzyme is locked in a resting state, and that substrate binding followed by transaldimination of the lysine linkage allows rearrangement of the domains to an active conformation such that the two cofactors and substrate are in close proximity.

**John Horton** from Xiaodong Cheng's group described a series of DNA adenine methyltransferase crystal structures which revealed a variety of enzyme:DNA interactions. Previously published structures revealed non-specific loose binding while more recent structures showed specific tight binding modes. The assembly of structures provided snapshots of the enzyme as it diffuses along DNA searching for its recognition site.

**Akanksha Nagpal** from Allen Orville's group described structures of the FAD-dependent nitroalkane oxidase in several enzyme states: reduced, oxidized, and bound to the weak inhibitor spermine. Structural comparison reveals subunit rotation upon oxidation and suggests a basis for substrate recognition and reaction mechanism.

**Liang Tong** ended the session with a very entertaining bait-and-switch, presenting his structure of CPSF100, a protein involved in pre-mRNA 3'-end processing, instead of the advertised carboxylases. Preparation of 130 constructs of four human and yeast proteins led to only one construct which yielded soluble protein that was then crystallized for structure determination. Crystals could be grown only with an old tube of commercial screening solution, because cleavage by a protease from the contaminating pencillium proved to be crucial for crystallization. The resulting structure of yeast CPSF100 allowed modeling of the putative endonuclease CPSF73 which in turn guided biochemical work, providing the first experimental evidence that CPSF73 has endonuclease activity.

*From Liang Tong: Crystal structure of CPSF-100*

Finally, we would like to thank the following companies for their generous support of the New Structures Session: **Hampton Research; Nextal Biotechnologies; Rigaku/MSC, Inc.**

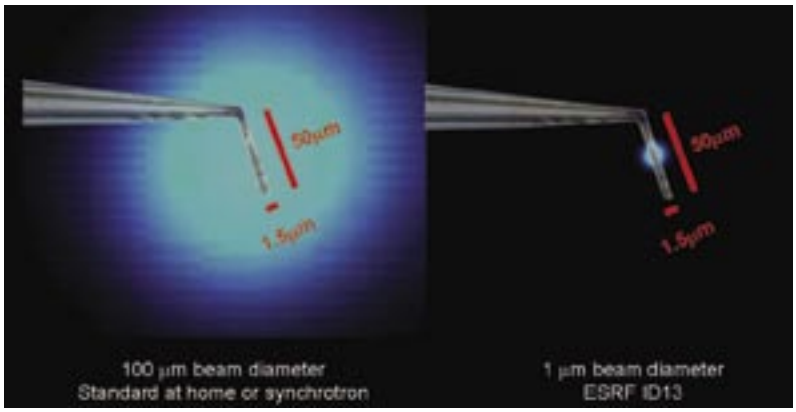
*Jack Tanner and Vivien Yee*

*In the center: Narasinga and Shobha Rao; clockwise from top left: George DeTitta, Suzanne Fortier and Chris Gilmore; Andrey Kovalevsky and Angelique Lagoutte; Jenny Glusker, Amy Katz, Gerry Bunick and Charlie Carter; Bob Bau and Margaret Churchill; Alex McPherson, Paula Fitzgerald and Judy Flippen-Anderson.*

## 1.02 Difficult Structures

The speakers presented interesting and successful approaches to a variety of tricky problems in macromolecular crystallography. **Mike Sawaya** (UCLA) solved the structure of the seven-residue peptide that causes yeast prion protein Sup35 to form fibrils. The microfocus beamline at the ESRF (ID-13) was essential to collecting useful diffraction data from the 2 x 2 x 50 mm crystals *(see figure below)*. The structure reveals how the sequence of the peptide reinforces the cross-beta fibril structure.

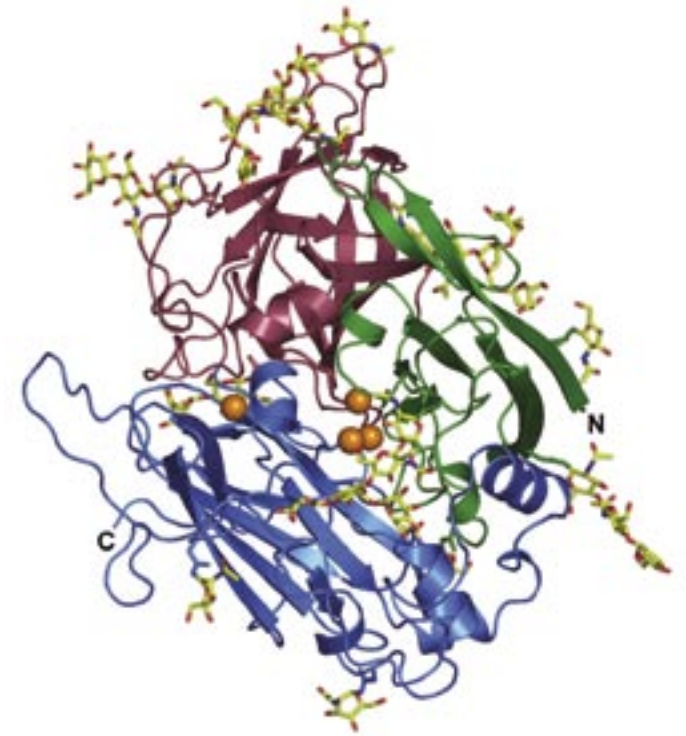
***From left: Janet Smith, Susan Heffron, Mike Sawaya, Alex Taylor, John Hart, Dan Anderson, Hong Li, Jimin Wang.***




***Comparison of beam sizes relative to a crystal of the fibril-forming peptide from yeast prion Sup35. The crystal is mounted on the end of a glass fiber, frozen in a cold nitrogen gas stream, and viewed along the x-ray beam on ESRF beamline ID-13. The beam is viewed on a fluorescent detector mounted downstream of the crystal.***

**Jiming Wang** (Yale) developed techniques for handling the systematic smearing of diffraction patterns caused by lattice translocations. Realignment to a single lattice allowed the data to be processed and structures of f29 DNA polymerase and HslV-HslU to be solved. **Hong Li** (Florida State) investigated a series of RNA constructs to optimize crystallization of a splicing endonuclease protein with its RNA substrate. **Dan Anderson** (UCLA) phased 9-Å data from crystals of the eukaryotic major vault protein (MVP) with an envelope from electron cryomicroscopy and 48-fold averaging about a single axis. The map suggests discreet folded domains within the 96 MVP subunits that form the vault shell. **Alex Taylor** solved a tricky merohedral twinning problem and partially deglycosylated a heavily glycosylated multicopper oxidase. The resulting structure was of suitable quality for detailed analysis of the multiple copper sites in the enzyme (see figure at left). **Susan Heffron** (UC-Irvine) painstakingly processed a dataset from elongation factor Tu (EF-Tu) to integrate the predominant lattice from a split crystal and at the same time correct a beam position error. The resulting data allowed determination of the binding status of a potential inhibitor compound.

*Janet Smith and John Hart*




***From Alex Taylor: Fet3p is a multicopper-containing glycoprotein in yeast that catalyzes the oxidation of Fe(II) to Fe(III) prior to its import into the cell by a coupled iron permease. Fet3p represents a molecular paradigm for the link between copper and iron metabolism in eukaryotes (i.e. it is an ortholog to ceruloplasmin, a multicopper oxidase in humans). The ribbon diagram highlights its three cupredoxin-like domains and shows its copper cofactors and carbohydrates in orange and yellow, respectively.***

## 1.04:Ultra-High Resolution Structures

Crystallographic methods have experienced a series of methodological developments ranging from crystallization and data collection to better refinement algorithms, leading to an increase in the number of structures of biological macromolecules solved at sub-atomic resolutions. The purpose of this session was to review these developments, notably the specificities of data collection and multipolar refinement, and to show that the resulting structures can significatively improve our level of knowledge of biological macromolecules in operation.

The session was opened by **Stephan Ginell,** who reviewed the special experimental requirements for collecting data at ultra-high resolution. In particular, maximizing the intensities of the weak reflections at the resolution limit needs a minimization of radiation damage. He also showed also that the data collection at 15º K using a helium cryostat lowered the B-factors and better defined the multiple conformations. **Ruslan Sanishvili** then compared data collections of different structures at ultra-high resolution (crambin, aldose reductase and anti-freeze protein). He explained in detail the geometrical limitations for high resolution data collection and how they can be overcome. Taken together, both talks gave a clear picture of high resolution data collection at synchrotrons.

**Artem Lyubimov** then presented results on cholesterol oxidase, complexed with a non-covalently bound flavin adenine dinucleotide (FAD) prosthetic group, known to be reversibly deactivated at pH > 7.5. To understand the effect of pH on the enzyme activity, six different structures were solved in the pH range 4.5-9.0. As diffraction data extended to 0.82 Å resolution, hydrogen atoms were clearly seen. A change of the protonation state of catalytically active residues is observed when the pH increases, possibly linked to the change in activity.

**Claude Lecomte** described his progress in multipolar modelling studies. Due to the latest improvements, the program MOPRO is able to apply this modelling if the resolution is better than 1.0 Å. For doing this, a data base of multipolar parameters has been compiled, and the parameters are transposed from the data base to the macromolecule being analyzed. For cases with the best resolution, these parameters can be refined. The resulting multipolar parameters can then be used to calculate electrostatic fields and interaction energies.

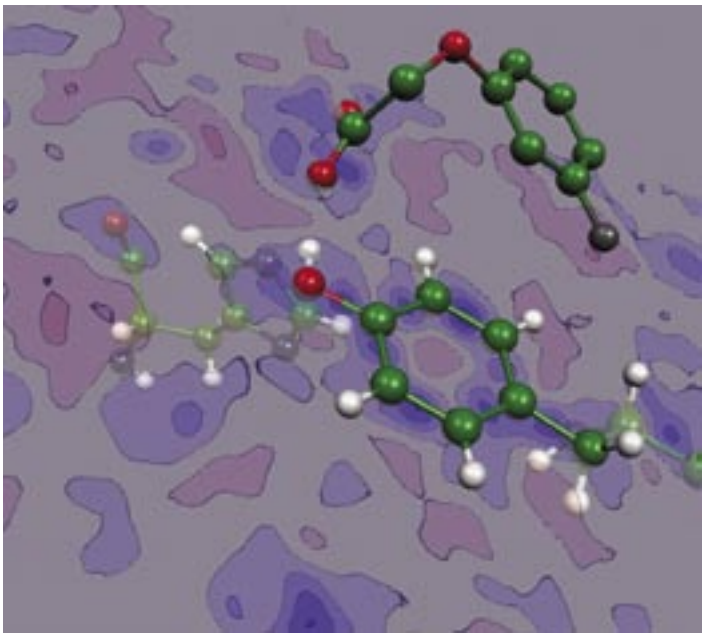
**Andre Mitschler** reviewed the most recent results on his ultra-high resolution studies of aldose reductase. He described the sharing of a proton between the inhibitor Fidarestat and the enzyme, which is crucial for the *in-vivo* potency of this inhibitor (currently undergoing Phase III clinical trials). He also described the analysis of the binding selectivity of this inhibitor against aldehyde reductase using a mutant Leu 300 Pro, which showed two distinct factors contributing to the selectivity, one hydrogen bond and one conformation change. Finally, he showed a case in which two charged inhibitors, IDD 594 and Tolrestat, bind simultaneously to the same crystal, giving information about competitive ligand binding inside a crystal. In all these cases, the high resolution (~0.9 Å) of the studies was essential for identifying hydrogen atoms and multiple conformations.

Structural studies of complexes of HIV1-protease with the potent inhibitor TMC114 were then described by **Andrey Kovalevsky.** These studies included the wild type enzyme as well five high level resistant mutants (V82A,I84V,L90M, D30N and M46L). The results are compared with those seen in complexes with clinical inhibitors. The structures give the molecular basis for the resistance, and therefore can be used to develop new drugs against the resistant mutants. The atomic resolution (1.1-1.5 Å) of these studies was essential to accurately determine the inhibitor-protein contacts.

**Yuan Lin** (an **Etter Student Lecturer Awardee**) described the structure of a small anti-microbial polyamide (SMAT) in complex with a DNA decamer at 0.95 Å resolution. The structure was solved from MAD data using the anomalous scattering from a Br atom, and the resulting map was of very high quality. Unexpectedly, the polyamide binds as a dimer. The high resolution allowed visualization of the fine details of local disorder, hydration, hydrogen bonds and polyamide stacking. The tight packing of sulphur and fluorine atoms within the DNA minor groove explains the improved affinity of DNA for SMATs, compared with other related polyamides.

In summary, the session material was useful both to show the general user how to go about collecting high resolution data and to highlight unexpected results of biological interest that can be obtained from these high resolution structures.

*Alberto Podjarny*



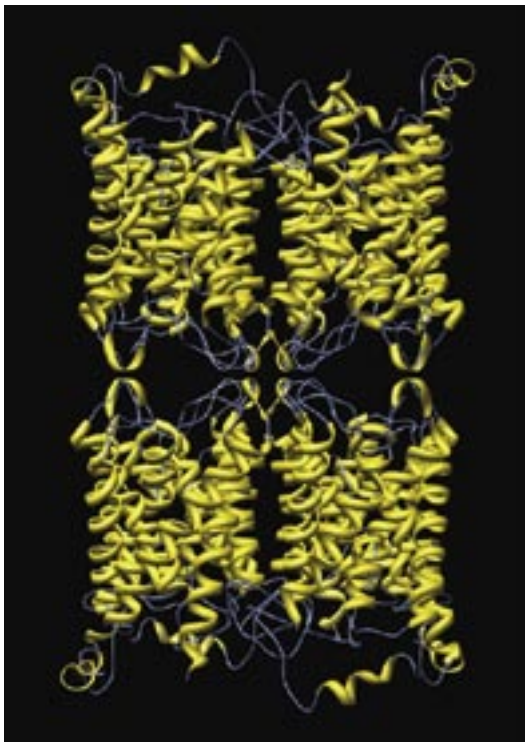
***From Christian Jelsch and Claude Lecomte: Seeing Covalent Bonds in Enzymes: Residual Electron Density of Human Aldose Reductase at 0.65 Å resolution using MoPro. Jelsch, C., Guillot, B., Lagoutte, A. & Lecomte, C., (2004). J. Appl. Cryst. 38, 38-54.***

## 1.05: Biomolecules and Membrane Proteins

This session focused on the technical and practical aspects of membrane protein crystallography. **Michael Wiener** gave an information packed, very useful overview on how to make the transition from crystallizing soluble proteins to crystallizing membrane-bound proteins, sharing hard won know-how from his own lab. **Ina Urbatsch** described her highly positive experiences using yeast as an over-expression host to purify P-glycoprotein, a large integral membrane protein that spans the lipid bilayer multiple times.

By carefully optimizing detergents for purification and then again for crystallization **Ling Qin** obtained well diffracting crystals of cytochrome *c* oxidase. Head groups of detergent molecules and a histidine affinity-tag chelated $Cd^{2+}$ ion form crystal contacts. Lipids that co-purified with the protein are found in the crystal structure as well and may be important to obtaining well-ordered crystals.

Regarding his work on aquaporin 0 crystals **Tamir Gonen** reported how lipids played a crucial role in forming crystal contacts and that obtaining good crystals involved screening different lipids to aid crystal growth. The structure (determined by electron crystallography to 1.9 Å) reveals no direct protein:protein interactions. Remarkably, what holds the molecules in place is a single layer of lipids, see figure at right.



***From Tamir Gonen: the structure of AQP0 junctions was determined by electron crystallography. Two AQP0 tetramers interact with each other via the extracellular domains to form a junction between two opposing membranes.***

In the case of the vasopressin receptor **Chuck Sanders** described how painstaking optimization of the growth conditions used to overexpress the protein in *E. coli* finally gave folded protein that yielded beautifully resolved *TROSY* NMR spectra. **Ken Lundstrom** reported on major European initiatives to apply structural genomics to the area of membrane protein crystallography (**MePNet** and **E-MeP**). Targets include many exciting proteins, including G protein-coupled receptors (GPCRs) and other proteins of clinical interest.

Finally, not satisfied with just a single membrane protein structure **Raj Pokkuluri** solved the structures of many mutant forms of the bacterial photosynthetic reaction center, probing the proton transfer mechanism in exquisite detail.

In short this was a fascinating session which we hope will inspire work on new membrane protein structures.

*Gabby Rudenko and Michael Wiener*

***Marilyn Olmstead and Frank Fronczek.***

## Index of Advertisers

## 3.01 Advances in Neutron Fiber Diffraction

*From left: Rengaswami Chandrasekaran, Kohji Tashiro, Paul Langan, Tom Irving, Gerald Stubbs, Ingrid Parot, Trevor Forsyth and Masahisa Wada. Photo courtesy of Paul Langan.*

Neutron diffraction has provided some key insights into the structure and properties of biological, industrial and chemical fibers over recent years. Although x-ray diffraction remains the primary method for determining fiber structures, neutron diffraction is an important supplementary technique with some distinct advantages for providing certain types of information. An important goal of this half-day session, jointly organized by the Neutron Scattering and the Fiber Diffraction SIGs, was to illustrate to the U.S. polymer and fiber communities the unique type of information that can be obtained using neutrons. International leaders in the field were invited to present current research. A supporting goal was to present a review of current and planned facilities that will be made available to U.S. scientists who wish to initiate neutron fiber diffraction studies. A program of seven speakers, including two from Europe and two from Japan was made possible through generous sponsorship from Fibnet, the North American research coordination network for biological fiber diffraction, and the Spallation Neutron Source at Oak Ridge National Laboratory (ORNL). The session was chaired by Tom Irving, Trevor Forsyth and Paul Langan.

The session opened with **Trevor Forsyth**, from the Institut Laue Langevin (ILL) in Grenoble, describing instrument D19 at the high flux reactor run by the ILL, the instrument on which high-angle neutron fiber diffraction was first developed back in the 1980's. A highlight of this talk was recent work on poly(p-phenylene terephthalamide) (PPTA), better known to some as Kevlar®. Although the conformation of the chains and their assembly into hydrogen-bonded sheets is well established from x-ray studies, the stacking interactions of these sheets and their relative displacements are still in question. Trevor, along with his colleagues Kenn Gardner and Tony English from Dupont, took the ingenious step of selectively deuterating the terephthaloyl residues in order to greatly increase their neutron scattering density with respect to the phenylene residues (hydrogen and deuterium have very different neutron scattering powers). The neutron studies show conclusively that the terephthalyol residues are positioned at the same height as the terephthalyol residues in adjacent sheets, clarifying a long-standing question.

**Masahisa Wada** from the University of Tokyo described studies of cellulose, the most abundant renewable material on earth. Cellulose is biosynthesized by polymerization of glucosyl residues at the cell membrane by an ordered synthase complex, followed by assembly of the extended parallel chains into nanometer thick crystalline microfibrils. The microfibrils consist of a mixture of two crystal forms Iαβ and Iβ. A number of industrial applications involve processing raw cellulosic material so that its crystal structure is transformed. Masahisa presented the structure of one of those transformed types of cellulose, cellulose IIII, the latest result from a series of combined x-ray and neutron fiber diffraction studies that have provided detailed crystal structures and hydrogen bonding arrangements for most of the cellulose polymorphs.

Although x-rays can be used to visualize the carbon and oxygen atoms that form the skeleton of cellulose chains, the smaller more mobile atoms of hydrogen are harder to see. The reason for this is that x-rays interact with the atomic electron field and with only one electron hydrogen is nearly invisible. Neutrons are highly sensitive to hydrogen atoms and in particular to their isotope deuterium. Neutron diffraction is therefore a powerful method of locating hydrogen atoms.

Industrial polymers were the subject of a talk by **Kohji Tashiro** from the Toyota technology institute, Tempaku, in which the use of the neutron diffractometer BIX-3 for extracting hydrogen atom positions from polyethylene, isotactic polypropylene and poly(vinyl alcohol) amongst others was described. BIX-3, located at the nuclear reactor run by the Japanese Atomic Energy Research Institute, was the first diffractometer to be equipped with a large two-dimensional neutron image plate detector. Deuteration was used in these studies to enhance the visibility of the hydrogen atom positions and also to reduce the large scattering background from hydrogen. By comparing structure refinements based on data from a variety of experimental techniques including x-ray, neutron and electron diffraction Kohji Tashiro clearly demonstrated the advantages of locating hydrogen atoms using neutrons in combination with deuteration.

ACA Travel Award winner **Ingrid Parrot** from the ILL described the latest results from fiber diffraction studies of DNA hydration on D19. Water is of critical importance in maintaining the double helical structure of DNA. Changing hydration can cause the double helix to adopt a variety of different conformations, a fact elegantly illustrated by SAX/WAXD studies of the transition between the A and B forms of DNA carried out at the ESRF in Grenoble. Whereas mobile weakly scattering molecules such

## *Advances in Neutron Fiber Diffraction, con't:*

as water are difficult to see with x-rays, they are more easily located using neutrons in combination with H2O/$D_2O$ isotopic replacement. Neutron fiber diffraction has provided information about ordered water around many of the DNA conformations, one of which, the D form, is of particular interest because it is only observed for synthetic DNA with alternating base-pair sequences. Ingrid presented new neutron data collected from DNA in the D form in which the scattering power of every second base residue had been increased through specific deuteration. These studies will benefit greatly from a new array of detectors due to be installed on D19 by the end of 2006 that will improve data collection efficiency by up to a factor of 50.

A possible future instrument for fiber diffraction is the Macromolecular Neutron DIffraction (MANDI) beam line being built for the next generation Spallation Neutron Source (SNS) that will come on line next year at ORNL. Although this beam line is designed for rapid data collection from protein crystals, it has a high intensity capability that also makes it ideal for fibers. Paul Langan from Bioscience division of Los Alamos National Laboratory described how MANDI will not only be competitive with existing beam-lines for routine fiber diffraction work, but how it will also offer some new and unique capabilities. At most spallation neutron sources the use of time-of-flight techniques in combination with large electronic detectors allows wavelength-resolved Laue patterns to be collected. It will be possible on MANDI to collect fiber diffraction patterns over a range of different wavelengths and their corresponding length-scales simultaneously in a unique SANS/WAND fashion, making it ideal for studying such things as polymer processing and nanocomposite materials.

**Gerald Stubbs** from Vanderbilt University is one of the directors of Fibnet, a network established to coordinate biological fiber diffraction activities in the USA. Meetings, workshops and retreats sponsored by Fibnet include sessions of the ACA organized by the Fiber Diffraction Special Interest Group. Gerald Stubbs took the opportunity of his talk on the goals of Fibnet to break the exciting news that the next FiberNet retreat will take place August 6-9, 2006, at Fall Creek Falls State Park in Tennessee. More details on this meeting and other FiberNet activities will be available on the FiberNet website (**www.fiberdiffraction.org**).

**Rengaswami Chandrasekaran** from Purdue University, or Chandra as he is known to many of us, then closed with an outline of neutron fiber diffraction studies that have been scheduled for the Protein Crystallography Station at Los Alamos Neutron Science Center later this year. Since biopolymer structures are stabilized by intra- and intermolecular hydrogen bonds, the precise position of hydrogen atoms are very important in understanding fine structural details. One of the first polymers that Chandra will study, along with his colleague Srinivas Janaswamy, is Iota-carrageenan, a gel forming polysaccharide extracted from red algae used in the food and pharmaceutical industries. Chandra gave an overview of results from his laboratory on carrageenans, including some recent data collected on the BioCAT facility at the Advanced Photon Source at Argonne National Laboratory and directed by Tom Irving.

*Paul Langan*

## *4.01 Experimental*

The Experimental session was lively, well attended and informative. **Mirta Mir Caraballo**, USP, San Carlos, Brazil, opened with a detailed introduction to the structure of homometallic Fe Ludwigite, describing many of the features responsible for Ludwigite's interesting, unusual properties. Mirta's contribution to extending the current knowledge on the subject involved the study of single Ludwigite crystals by x-ray diffraction over a temperature range 15 K to 144 K.

***From left: Miriam Rossi, Charles Simmond, Arwen Pearson, Randy Alkire, Jeff Lovelace, Cory Momany, Chad Haynes***

**Charles Simmons,** U. Hawaii, Hilo, spoke on his research of six coordinated $Cu^{2+}$ complexes with distorted octahedral geometry, a result of the Jahn-Teller effect. Charles utilized both EPR and x-ray diffraction methods to study temperature dependent bond length perturbations. Using the Tutton salts as a model system, Charles demonstrated a convergence between the long and intermediate Cu-O as a function of increasing temperature. The g-values from the EPR spectrum of the compound displayed similar phenomena. These data were used to model the effect of crystal lattice interactions on Jahn-Teller distortion. Charles was not at all bashful about concluding his presentation with a wonderful advertisement for ACA 2006, in paradise!

**Miriam Rossi**, Vassar College presented her research on anti-convulsing therapeutics. Working with synthetic chemists, Miriam helped design novel drugs based on structures of known anti-seizure molecules. She described the crystal structure of several of these molecules, many of which had been incorrectly assigned by spectroscopic analysis. Miriam also presented some structure-activity data. Despite some deviations between the proposed, designed structures and actual, crystallographic structures, some drugs displayed promising activities. ***continued, page 34***

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## 4.01 Experimental, con't

**Jeff J. Lovelace**, Eppley Institute, U. Nebraska, presented his research on the relationship between cryo-cooling and protein crystal mosaicity. Cryo-cooling is widely accepted as a possible contributor to enhanced mosaicity, and in trying to understand this, Jeff and co-workers designed an experiment utilizing super fine ϕ slicing and digital topography. Their ambitious experiment was well executed, but some concerns were raised regarding the use of epoxy. Nonetheless, Jeff's talk was lively and marked the high point for attendance.

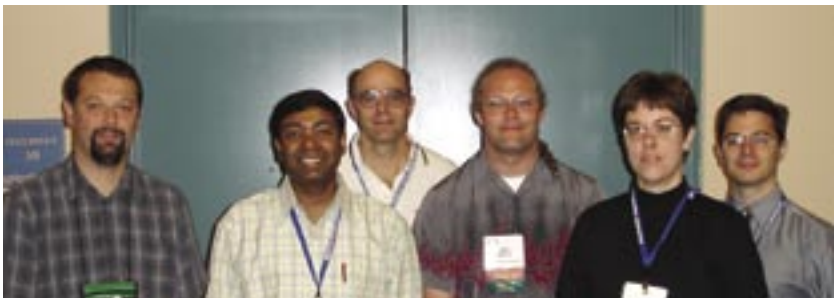
**Arwen Pearson**, U. Minnesota, always a class act, spoke on her work on the enzyme methylamine dehydrogenase (MADH) which contains a unique quinone-like cofactor derived from the modification of tryptophan residues. Arwen described the structure of the enzyme and the electron transfer pathway. In the process of identifying catalytic reaction intermediates for crystallographic analysis, it became apparent that these structures within the crystal lattice were highly sensitive to photoreduction during data collection.To overcome this hurdle, Arwen used an in-line single crystal visible microspectrometer on BioCars 14BM-C to monitor the redox state of the MADH-amicyanin complex. Using the spectroscopic data, composite data sets could be collected for each intermediate prior to radiation effects.

**Randy Alkire**, Argonne, is very interested in understanding causes and consequences of sample movement at synchrotron beamlines, SBC 19BM in particular. Randy showed that cryo-loop movement during data collection could be a large source of experimental error, using low mosaic lysozyme crystals as a probe for cryo-loop motion. Randy offered some technical advice, suggesting that the length of the nylon loop should be kept short and the exposure time should be increased.

Finally, **Cory Momany**, U. Georgia, described his work on the development of a novel microscope for protein crystal detection, one which can theoretically identify crystals within a live cell. Despite some legal restrictions, Cory managed to describe the instrument and present preliminary proof-of-concept data. Eventually Cory plans to utilize the microscope to probe living cells and to screen proteins that display a tendency to self associate *in vivo*.

*Chad A. Haynes*

## 4.03: Interesting Structures, Computational Techniques



***From left: Nenad Judas, Asim Bera, James Fettinger, Allen Oliver, Carla Slebodnick, Scott Mough.***

***Allen Oliver presenting the Etter Student Lecturer Award to Soheila Vaezeslami.***

In keeping with the broad interests of General Interest Group a broad range of topics from small molecule studies to computing techniques to macromolecular structures were represented. The excellent presentation by **Etter Student Lecturer Awardee Soheila Vaezeslami** on her research into protein mimics of rhodopsin, an essential protein in the visual process, was definitely a highlight.

The symposium was divided into themed portions and attracted a steady audience throughout. To begin the small molecule segment, **Nenad Judas** presented the structures of three copper compounds complexed by various aminoacidato ligands in order to predict structural networks built upon intra and intermolecular bonding interactions. **James Fettinger** demonstrated how to deal with twinned data, with particular emphasis on a cyclic, step-wise analysis. **Carla Slebodnick** then detailed her challenges with highly symmetric structures and the analysis and refinement of the disorder inherent in such compounds. **Scott Mough** discussed the stepwise synthesis and characterization of several cryptophanes with a view to enhancing the desirable characteristics of these cage-like compounds for potential application as storage materials, nanoreaction vessels or sensors. **Asim Bera** reported on the structure of a thiamine diphosphate enzyme that was found to contain an unusual, previously unseen molecule at the active site. This unusual molecule was assigned as a disordered bicarbonate anion, explaining some of the observed reactivity of the enzyme.

Computing techniques were the next theme. **John Bollinger** (Reciprocal Net project) and **Joerg Kaercher** (Relational Database for Report Generation) presented two complementary talks on crystallographic database software. Both dealt with information gathered throughout a crystallographic study with the intent of using it for publication, archiving and visualization purposes. The Reciprocal Net project is a distributed molecular structure database which can be used as a laboratory information management system, while the Relational Database approach is geared towards collecting data throughout the various stages of the crystallographic experiment and emphasizes procedure tracking and report generation. Both John and Joerg concluded that there is a general need to enhance data dissemination to external users or auditors and that their respective programs address this need. **Cikui Liang** then described the difficulties and successes encountered in developing crystal structure prediction software, particularly with reference to drug design. The challenges are many-fold, from

## 4.03 Interesting Structures, Computing, con't

*From left: Jeannette Krause, Sohelia Vaezeslami, John Bollinger, Carrie Wilmot, Joerg Kaercher, Cikui Liang, Kam Zhang.*

molecular "shape" (functional group torsions) to packing of the molecules, but it is clear that progress is being made. In contrast, **Kam Zhang** discussed the emerging synthetic technique of scaffold-based drug design and how crystallography is integral to the design and decision-making processes in this method. The closing presentation by **Carrie Wilmot** dealt with the inhibition of copper amine oxidases, enzymes that are important in the conversion of amines to aldehydes, and that have been linked with processes such as growth, development and cell signaling.

The associated General Interest poster session encompassed equally varied topics. To list a few, there were posters on methods used for hydrogen atom location in structures; H-bonding patterns adopted by waters of crystallization; computational techniques for applying more accurate absorption corrections; and the use of crystalline polymorphs as a technique for enantioselectivity in drug design. The highlight of the poster session was Frank Fronczek's contribution ***Crystallography in Fiction*** in which he cited the use of crystallography and crystal science in popular fiction. See pages 51-52.

*Allen Oliver and Jeannette Krause*

## *5.01: High Throughput Crystallization & Visualization: Focus on Hardware & Methodology*

This well attended session was sponsored by the newly formed Industrial SIG. At the 2005 meeting, the Industrial SIG also successfully petitioned the ACA council for recognition as an accredited SIG.

*From left: Chunmin Li, Charles Kissinger, Kevin Parris, Jose Martin Cilroy, John Rose, Joseph Luft.*

**Joseph Luft** described the approach and results for primary screening at the Structural Biology laboratory of The Hauptman Woodward Medical Research Institute (SUNY Buffalo, NY). In the past five years, their laboratory has screened over 4600 samples using a total of over 7 million crystallization experiments. For scientists using their facility for crystallization, they request 400 microliters of protein at 10 mg/mL. Typically for each sample, 1536 conditions are examined using 400 nanoliter drops and upwards of 200 samples are examined each month. The set of 1536 conditions were chosen to generate a greater coverage of crystallization space. With such a large primary screen, their intention is to generate multiple leads in hopes of generating crystals with different properties. With such a huge turnover of material each month, Joseph indicated it is easy to become an automaton during the process, which is not necessarily a good thing! In their experience it is critical to document and continuously analyze everything. For example, they found one protein required a freeze/thaw cycle before it would crystallize. Only their meticulous note taking allowed them correlate the way this protein was shipped over various months to crystallization success. Joseph's advice to us all was "THINK as you work."

**Joel Bard** presented the strategy employed at Wyeth Research to automate their protein crystallography lab. Wyeth has robots for the preparation of solutions, setup of hanging drops, automated imaging and a custom laboratory information management system known as RoCKS, a version of which is now sold by Formulatrix, Inc. The Genomic Solutions hanging drop robots were chosen since the hanging drops most closely mimicked the experiments previously done in the lab and hanging drops are easier to image. For each of the automation steps at Wyeth, Joel described the current state of the equipment, their strengths and weaknesses. For the Packard Multiprobe liquid handling robot, its versatility in both source and target geometries was described. The drawbacks were mostly related to the tips used for reagent transfer. For contamination control, Wyeth decided that level-sensing disposable tips were preferable to the washing of static tips. This decision is the source of most of the drawbacks to this system: the limited number of disposable tips available at once (192) and the high cost of supplies ($0.05 per tip). Additionally, the foil seals used on deep well blocks easily confuse the capacitance based liquid level sensing feature. Various settings that affected the quality of the hanging drop robot were airgap volume, prepressurization, predispense volume, syringe speed, and valve open times. The importance of each of these factors was detailed and need critical need for precise determination of the correct values emphasized. Planned preventative measures such as daily purging of lines, weekly sonication of tips and the replacement schedule for syringes and valves were also discussed.

***con't, page 37***

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## 5.01 High Throughput Crystallization & Visualization, con't:

**Jack Silberman** described an ultra-high capacity crystal storage and imaging system developed at Structural GenomiX in collaboration with RoboDesign. Each unit can hold up to 10,000 trays and was designed to allow storage, tracking and imaging of many different types of trays with a flexible imaging schedule. Careful attention was paid to minimizing vibration and temperature and humidity variations in these very large systems. The machinery is self-monitoring, and can be operated and maintained by non-experts. The successful development of the system was attributed to comprehensive and rigorous performance specifications and extensive interaction with the vendor during the development process.

**John Rose** described his experience in developing a high-throughput crystallization facility for the Southeast Collaboratory for Structural Genomics. The facility was designed to meet a projected need for screening eight new proteins per day (to meet a goal of 100 structures per year). Commercial robotics systems (Tecan Genesis, Cartesian Honeybee, Douglas ORYX) were employed with a mix of commercial (Wizard, Hampton) and proprietary screens using both sitting drop and micro-batch-under-oil methods along with an in-house diffraction screening facility. The capabilities of the facility now exceed the original design goals, allowing screening of up to twelve new proteins per day, along with optimization of five proteins, and diffraction characterization of up to twelve proteins per day. John also described techniques used successfully when initial protein samples failed to yield well-diffracting crystals, including additional purification steps such as a "heat cut" at 70°C and carrying out reductive methylation of lysine residues. These steps resulted in crystals for six out of a sample of fifty proteins that had initially failed in crystallization attempts. The use of a microfluidic crystallization system for initial screening gave similar results to that of conventional sitting drops. John also provided a very useful "report card" for six commercial robotic systems, with user ratings of their throughput, reliability, software and support. Most of the systems performed well overall, with the control software being a weak point common to several of the systems.

The final two talks of the session described two different approaches to developing comprehensive databases of crystallization conditions designed to assist the crystallographer in making the best use of already published information when attempting to crystallize a new protein. **Chunmin Li** described the "Biological Crystallization Resource", a project at the University of British Columbia in which crystallization information was drawn primarily from Protein Data Bank entries along with information communicated directly from structural genomics consortia and from mining the literature. Over 15,000 entries have been compiled. In an example of the successful use of the database, they extracted crystallization conditions for fifty glycosyltransferases and used this information to narrow the set of screening conditions for a new member of the glycosyltransferase family. Their results suggested that biasing the crystallization experiment with information about related proteins (rather than using a random set of conditions) resulted in more efficient screening. **Jose Martin Ciloy** described a new software product, Crystal T. B., from the Japanese company, Maruwa Food Industry, Ltd. Their database is a compilation of crystallization conditions gleaned from the literature, and was also developed with the goal of allowing a knowledge-based approach to crystallization of proteins. Over 7,000 entries had been compiled so far. Examples of applying prior information about crystallization conditions for related proteins to narrow the screening conditions were given, including successful crystallization of dipeptidyl peptidase IV using information about crystallization of other oligopeptidases.

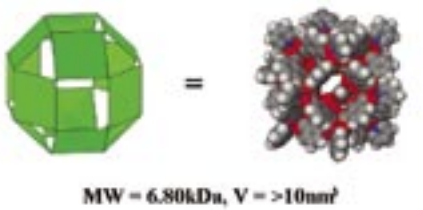
*Kevin Parris and Chuck Kissinger*

***Dusan Turk and Bob Sweet.***

## 6.01: Microporous Metal-Organic Framework Solids

*From left: Wenbin Lin, Susumu Kitagawa, Mohamed Eddaoudi, Mike Zaworotko, Radu Custelcean, Dugald MacDougall, George Shimizu.*

This well-attended half-day session highlighted recent advances in the area of metal-organic frameworks through eight presentations that focused on the design, synthesis, and characterization of some of these promising crystalline organic-inorganic hybrid materials. **Mike Zaworotko**, U. South Florida, one of the pioneers in this field, opened the session with an overview on the design of metal-organic frameworks based on a rigorous topological analysis. He showed how a combination of 3- and 4-connected nodes could be used for the assembly of ternary nets containing three different polygons or polyhedra, a modular strategy that is leading the way towards the design of novel coordination polymers with unprecedented topologies. A similar geometrical analysis led to the discovery of discrete coordination polyhedra (see picture) that were used as nanoscale building blocks for extended frameworks through decoration with sulfonate functional groups.




**Susumu Kitagawa**, Kyoto University, Japan, followed with a presentation on his recent work on flexible pillared layered coordination polymers that adjust their pores reversibly to the included guest molecules in a way reminiscent of enzymes. He demonstrated through careful structural analysis by single-crystal and powder x-ray diffraction, aided by quantum mechanical calculations, that various gas molecules like oxygen or acetylene can be aligned inside the pores of these materials, a discovery that has important implications for gas storage and separations.

**Wenbin Lin**, U. North Carolina, Chapel Hill, then presented his recent results on the design of chiral porous metal-organic frameworks functionalized with transition metal centers for asymmetric catalysis. He convincingly showed how one could use the power of organic synthesis to build chiral organic ligands that can be incorporated into coordination polymers displaying enantioselective properties comparable or even superior to the analogous systems in solution.

The role played by constant curvature structures in small amphiphilic molecules and coordination polymers was examined by **Qiyu Zheng** from Cornell University. He showed that, similar to amphiphilic systems, whose architectures are controlled by the ratio of the volumes of their hydrophobic and hydrophilic domains, the packing of small molecules in crystals could be rationalized and predicted based on the same principles.

**Leonard MacGillivray,** U. Iowa, described an innovative method for building metal-organic frameworks using organic linkers obtained by solid-state synthesis aided by linear templates that align functionalized olefins for [2+2] photodimerization. He further showed some very recent results on using Ag-Ag interactions to serve the same purpose, a strategy that also resulted in the formation of a one-dimensional coordination polymer in the solid state via a single-crystal-to-single-crystal process.

In an interesting talk, **George Shimizu,** U. Calgary, described his recent work on the design and synthesis of coordination frameworks using weakly coordinating organosulfonate anions that may nevertheless yield structurally robust, porous materials. Some of these materials showed unusual flexibility or thermal stability, as well as gas inclusion abilities.

**Mohamed Eddaoudi**, U. South Florida, taught us about the design of metal-organic frameworks with zeolite-net-like topologies. Of noteworthy importance was the finding that as in the synthesis of inorganic zeolites, organic molecules of various sizes and shapes can be used as templates to control the size and porosity of these materials. Another interesting result was the utilization of metal heterochelating ligands for the assembly of both discrete polyhedra or extended frameworks with Kagomé topologies.

The session concluded with a student presentation by **Dugald MacDougall**, U. Notre Dame, who demonstrated in an ingenious way the use of lithium organyloxides as secondary building blocks for the controlled synthesis of coordination polymers of various dimensionalities.

*Radu Custelcean*

***Katherine Kantardjieff, in the hallway of the Swan.***

***The photographer must remain anomymous- the credit was unfortunately lost.***

## 7.01: Neutrons 101: Getting Started with Neutron Diffraction

The goal of this session was to introduce neutron scattering to scientists who are not active users of the techniques and to bring them in contact with each of the five North American neutron centers. While the session attracted many members of the contemporary neutron community, the session organizer was gratified to see many unfamiliar faces.

The session was scheduled to start with an introductory lecture by John Copley, NIST Center for Neutron Research. John asked to be replaced by a substitute, as his former teammates of the rowing team at St. Johns College (Oxford) had arranged on short notice a reunion to celebrate the 30-year anniversary of their brilliant 4-bump series of victories. This reunion, alas, was in conflict with the ACA meeting. After attempting to find another speaker, the session chair **(Brian Toby)** pinch-hit (to use an inappropriate metaphor) for John and delivered a lecture that outlined how neutrons interact with atoms and then illustrated with modern scientific examples, how neutron absorption and neutron scattering can be used for chemistry and physics studies. The focus of these examples was to highlight techniques that are less commonly reported at ACA meetings, such as activation analysis, magnetic scattering and neutron spectroscopies, as opposed to crystallography, which was the focus of the remainder of the session, and reflectometry and small-angle scattering -- which are frequently presented at ACA meetings. The talk concluded with a shameless pitch for US citizens to apply for the well-paid NRC postdoc fellowships at the NCNR. John Copley did provide many copies of his booklet, "*The Fundamentals of Neutron Powder Diffraction,*" which were popular with session attendees as souvenirs. Additional copies are available from the NCNR.

**Alberto Podjarny,** showed a nearly full-room audience how single-crystal neutron diffraction is being used at present at the LADI instrument at the Institut Laue-Langevin. The Human Aldose Reductase enzyme was chosen for study due to the implications of this system in diabetes mellitus complications. The enzyme was prepared fully deuterated(!) using a special fermentation facility, also in Grenoble, to produce fully deuterated proteins. On the scale of specimens typically used for neutron work, an extremely small single crystal (0.15 $mm^3$) was used for data collection, although data collection consumed a total of several weeks. Combining x-ray data and this neutron data, it was possible to locate unequivocally individual proton sites, which helped to provide additional information on the catalytic pathway employed in the enzyme.

The post-coffee-break set of three talks highlighted materials chemistry studies using neutron diffraction techniques. **Thomas Proffen**, LANSCE neutron center, Los Alamos, explained how the "real space" technique of pair distribution function (PDF) analysis provides information on local structure that is not available from traditional crystallographic techniques, which analyze Bragg scattering. He described the NPDF instrument at LANSCE and showed the importance of using high-resolution data for PDF study of crystalline materials. He then provided several topical examples.

***From left: Alberto Podjarny, Brian Toby, Tom Proffen, Paula Piccoli, and Ian Swainson.***

**Ian Swainson**, Chalk River, Canada then gave examples of phase transitions in which amines are involved. In order-disorder transitions, orientational ordering of amines is strongly coupled to and mediated by strain. Where these transitions are discontinuous, which is very common, powder diffraction is the only means of studying the associated structural changes since single crystals break apart during the phase transformation. In such cases neutron diffraction may be the only source of orientational information for ammonium ions. Such data can help differentiate between models for mechanisms of phase transitions. Understanding the details of hydrogen bonding is needed to test theory and shed light on mechanisms of solid-state reactions. Ian presented structural studies of an interesting family of perovskite materials, where amines occupy the A-site of the structure. For this work, a combination of synchrotron and neutron measurements were used both to index the patterns and to obtain final structure solutions. The solutions revealed that the counterions are concatenated into a 3-dimensional framework. While perovskite octrahedra are usually thought of as rigid bodies, this work showed that in fact the amines deform less than the octahedra.

**Paula Piccoli,** IPNS neutron center, Argonne, presented some information about the suite of instruments available at IPNS, then focused on the SCD single crystal instrument at that center. She described research results on a series of molybdenum "scorpionates" (polypryazolylborates) that were studied using neutron single-crystal diffraction studies. The pyrazole rings were substituted with groups of varying steric or electronic properties in order to systematically study their effect on the bonding geometry of the three-center B-H-Mo agostic bond. Based on her single crystal very precise characterizations of bonding geometries, a general trend of shorter Mo-H distance with greater electron-withdrawing substituents on the scorpionate ligand was identified.

*Brian H. Toby*

## 8.01: Inorganic Materials in Biological Systems

*From left: Michael Fleet, Rory Wilson, Theodora Leventouri, Nearchos Papanearchou, Lazaro Calderin.*

The session focused on the structure of apatite based biomaterials. Type B carbonated hydroxyapatite (HAp), chemical formula $Ca_5[(CO_3)_x(PO_4)_{3-x}]OH$, with multiple substitutions and deficiencies at all ionic sites attracts a great deal of research interest since it is the closest compound to the mineral phase of bone, dentin and enamel.

It is well known that crystal structure properties of HAp are critical in determining the bioactivity of the material and that many of the biological functions of bone, enamel, and dentin are controlled by the composition and crystal structure of the mineral phase. However, there are still controversies related to the decades-old problem of the exact location of the carbonate substitution in the phosphate tetrahedron, and the amount of hydroxyl ions in bone, enamel, and dentin mineral crystallites.

**Michael Fleet**, U. Western Ontario, Canada, presented crystal structures of type A and A-B carbonate apatites (CAps) from x-ray measurements of single crystals. **Rory Wilson**, Queen Mary U. of London, UK, compared Rietveld refinements of neutron diffraction data by introducing several models for the carbonate substitution. **Nearchos Papanearchou**, Ph.D. student, Florida Atlantic U., discussed a model from Rietveld analysis of neutron diffraction patterns of natural and synthetic CAps. **Lazaro Calderin**, Ph.D. student, Queen's U., Canada, presented electronic, crystallographic and dynamical properties of apatite and silicon doped HAp from theoretical and experimental work.

**Theodora Leventouri**, Florida Atlantic U. discussed a Rietveld quantitative phase analysis of ferrimagnetic bioglass ceramics from x-ray data. Interesting discussions, interactions and plans for a next meeting on the question of the carbonate substitution followed the end of the session.

*Theodora Leventouri*

## 8.02: In-situ Powder Diffraction: New Sample Environments Performing New Science

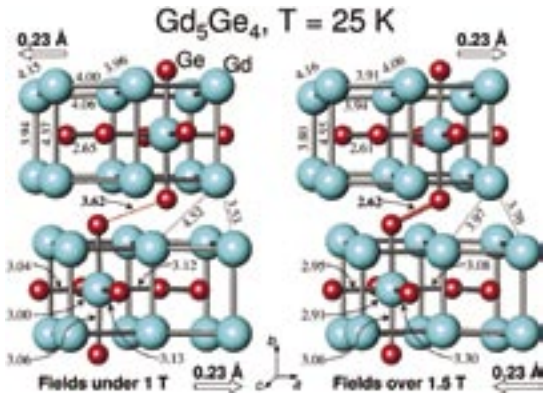
The speakers in this session used a wide range of non-ambient techniques, including sub-Kelvin low temperature neutron diffraction of complex magnetic phase transitions (**Dominic Ryan**, McGill U., Canada); *in-situ* high temperature powder x-ray diffraction of photovoltaic thin films (**Andrew Payzant**, Oak Ridge National Laboratory); variable humidity XRD studies of pharmaceuticals (**Chris Frampton**, Pharmorphix Ltd., Cambridge, UK); careful locatton of hydrogen positions at pressure via *in-situ* neutron diffraction of hydrogen storage materials (**Robert Delaplane**, Studsvik reactor, Sweden); and *in-situ* neutron diffraction of solid oxide fuel cell materials under varying oxygen partial pressures (**James Richardson**, Argonne).

*From left: James Richardson, Lachlan Cranswick, Andrew Payzant, Robert Delaplane, Vitalij Pecharsky, Dominic Ryan, Chris Frampton.*

By general agreement, the highlight of the session was the presentation by **Vitalij Pecharsky**, Ames Laboratory, Iowa State U., on the use of *in-situ* powder diffraction involving magnetic fields (0 to 4 T) under variable temperature (2.5K to 315K). These conditions facilitated studies of the magnetic field induced phase transitions of Silicon-Germanium-lanthanide compounds. The concise and careful use of animations to show the subtleties of the science were an asset in explaining the science, not a distraction; and a superb tour-de-force in non-ambient diffraction was presented to the audience.

Overall, the variety the presentations showed some of the crystallographic possibilities that modern non-ambient diffraction techniques can explore.

*Lachlan Cranswick*




***From Vitalij Pecharsky. Fragments of the antiferromagnetic low field Gd 5 Ge 4 (left) and ferromagnetic high field Gd 5 Ge 4 crystal structures (right) viewed along the Z axes with selected distances labeled in A. The intralayer distances vary by a maximum of 5%, while the interlayer distances change by as much as 27.6% during the magnetic field-induced polymorphic transformation. The thick white arrows on the left and on the right indicate the directions and the magnitudes of the shifts of the layers during the low-field to high-field and high-field to low-field transitions, respectively. V.K. Pecharsky, A.P. Holm, K.A.Gschneidner, Jr., R. Rink, Phys. Rev. Lett. 91, 197204 (2003).***

## 8.03: Crystalline Hydrogen Storage Materials

Hydrogen storage materials will be one of the hot topic research areas for several years to come, as the U.S. attempts to move into the hydrogen powered motor vehicles. The ambitious goals and requirements spelled out by the Department of Energy were described in the overview by **John Petrovic** (DOE and LANL). Five of the six remaining talks focused on alanates, which offer some good opportunities. Optimizing their properties will probably be a stepping-stone towards the DOE goals. The mechanisms for how the Ti-doping in sodium alanate improves the kinetics of decomposition and reformation are still unsettled. Various aspects of this problem were addressed theoretically (**Vidvuds Ozolins**, UCLA) and experimentally (**Craig Jensen**, U. Hawaii; **Eric Majzoub**, SNL; **Scott Speakman**, ORNL; **Jacques Huot**, U. Quebec). The final talk, *Location of hydrogen absorption sites in crystalline materials using single-crystal neutron diffraction*, was given by **Elinor Spencer** (Durham U.), who was the recipient of a **Margaret C. Etter Student Lecturer Awar**

*Bryan Chakoumakos*

***From left: Bryan Chakoumakos, Eric Majzoub, Jacques Huot, Scott Speakman, John Petrovic, Elinor Spencer, Craig Jensen.***

***Session Chair Bryan Chakoumakos presenting an Etter Student Lecturer Award to Elinor Spencer.***

## 9.01: Data Collection Strategies

*Roland Boese, Peter Müller, Zbigniew Dauter, Jim Pflugrath, Maksymilian Chruszcz, Michael Ruf, Lee Daniels. The photo, courtesy of Peter, was taken by Claire Gallou.*

The session about data collection strategies, organized by Tom Emge, Lee Daniels and Peter Müller, was the first of its kind in this millennium – at least at an ACA meeting. In front of a large audience, six experienced crystallographers gave presentations on various aspects of data collection strategies.

**Peter Müller**, one of the session-chairs, opened. He stressed the benefits of high Multiplicity of Observations (MoO) and pointed out that the combination of phi- with omega-scans can significantly improve absorption corrections with semi-empirical methods. Giving three real-life examples, Müller showed how much better a final model can be when it is based on optimal data.

**Zbigniew Dauter** is one of the grand masters of data collection, and some people distinguish between ordinary data and Dauter Data, the latter being the best data you can get from a given crystal. Dauter shared some of his experiences with the collection of high-quality protein data. Among other things, he explained that the benefits of high MoO can be obliterated by radiation damage and crystal decay when the crystal remains in the beam too long. Several years ago another superb experimentalist, **Roland Boese**, introduced a method to grow crystals of gaseous substances directly on the diffractometer. Now that this method is technically mature, Boese has been expanding its use to mixtures of gases and liquids, such as acetylene in acetone. When he grows crystals from such mixtures, frequently crystals of several different molecular complexes are obtained at the same time. Boese calls his technique for analyzing diffraction patterns from such a mixtures oligo diffractometry.

Turning from more practical aspects to software designed to calculate an individual data collection strategy for each crystal, **Jim Pflugrath**, (Rigaku/MSC, Inc.) and **Michael Ruf** (Bruker AXS Inc.) introduced their companies' respective products. The Rigaku program d*TREK was described as a customizable, device-independent toolkit designed to help optimize the diffraction data collection experiment with 2D detectors including choice of crystal, exposure time, rotation width per image, axes to scan, total degrees to scan, integration, and treatment of systematic, random, and erratic errors. The Bruker program COSMO, written by Jörg Kärcher, can be customized to work with any given diffractometer setup and takes general criteria into account such as the availability of time, the desired redundancy, or collision restrictions on the goniometer and low temperature device. The program was described as a tool to design an individual and efficient data collection strategy for every single crystal in order to acquire better data than a generic standard strategy would generally yield. Finally, **Max Chruszcz** described the integration of data collection, data reduction, and structure solution into one software package, which should also be able to simulate the whole experiment ahead of time in order to optimize the individual steps. This simulation takes into account blind regions, including regions generated by moving parts, as well as the shape and curvature of the detector.

*Peter Müller*

## 10.01: In situ Small Angle Scattering

*From left: Randall Winans, Jan Hessler, Gregory Beaucage, Barbara Wyslouzil, Thomas Weiss, P. Thiyagarajan.*

Eight presentations covered some of the areas of current interest for *in situ* studies using small angle scattering of x-rays, neutrons and light. The session had a dual focus on recent studies of aerosols and nanoparticles as well as studies of biological systems. **Beaucage**. (U. Cincinnati) began the session with an overview of aerosol studies being conducted using x-ray scattering at APS and ESRF. **Chris Sorensen** (Kansas State U.) gave an interesting talk on the use of light scattering to study gelation in carbon aerosols. **Jan Hessler** (Argonne) spoke on x-ray scattering from carbon soot aerosols, and **Barbara Wyslouzil** (Ohio State U.) spoke on water aerosols as studied with neutron scattering. This was the first coordinated presentation of scattering studies of aerosols. Bridging the aerosol and biological segments **Randy Winans** (Argonne) spoke on *in situ* studies of catalysts. The second

half of the session focused on *in situ* studies of biological systems in keeping with the theme of several other sessions plus the workshop on colloid to nanoscale biology. **H. Grigoriew** from Poland spoke on the application of Svergun's methods to monosaccharide gels. **Thomas Weiss** (ESRF) spoke on *in situ* studies of unilamellar vesicles and **P. Thiyagarajan** (Argonne's IPNS) spoke about studies of protein chaperones and their effect on the dynamics of protein folding using x-ray scattering. The session was well attended and gave a sampling of *in situ* studies using small angle scattering.

*Greg Beaucage*

## 10.02: Reflectivity/Scattering from Membranes and Membrane Components

**Tonya Kuhl** (UC-Davis) spoke about x-ray and neutron scattering from model membrane systems including lipid monolayers at the air-water interface and lipid bilayers on solid supports. She explained how one uses neutron or x-ray reflectometry techniques to obtain scattering length density profiles perpendicular to the plane of the lipid layer and the grazing incidence (x-ray) diffraction (GID) technique to obtain information on local ordered structures below the critical angle. She then showed an example of x-ray reflectometry of a lipid bilayer in contact with an aqueous solution using high energy x-rays (20 keV). At this energy, the transmission of the photons through the sample is 40%. Thus, one can obtain reflectivities out to much higher angles than is normally possible with neutron reflectometry. Tonya finished with a discussion of GID from ordered domains. Once this method is perfected, it will be possible to probe leaflet separation in lipid bilayers.

***From left: Susan Krueger, Ursula Perez-Salas, Vadim Cherezov, Kent Blasie, Stephen White, Tonya Kuhl, Jeremy Pencer.***

**Ursula Perez-Salas** (UC-Irvine), discussed the phase-sensitive neutron reflectometry (NR) technique. She explained that phase-sensitive NR makes it possible to obtain scattering length density (SLD) profiles by directly inverting the reflectometry data without the need for fitting. In order to accomplish this, one must essentially solve the phase problem by making two measurements on the same sample. This can be accomplished by measuring the sample on two different substrates, or by measuring the sample on a single substrate containing a buried magnetic layer using polarized neutrons. In each case, one obtains the real part of the reflection amplitude rather than the reflectivity, which is the square of the reflection amplitude. Thus, the SLD profile can be obtained directly from the data. Ursula also explained how the complex part of the reflection amplitude can be used as a diagnostic for film homogeneity and described experiments characterizing the structure of a polymeric biomimetic membrane and the orientation of peptides bound at surfaces with different chemical properties.

**Vadim Cherezov** (Ohio State), substituting for Martin Caffrey, focused on the crystallization of membrane proteins in lipidic mesophases. He pointed out that, despite the fact that this *in meso* method is about 8 years old, only 36 out of a total of 300 membrane protein structures have been solved

***From Vadim Cherezov: Cartoon representation of the events proposed to take place during the crystallization of an integral membrane protein from the lipidic cubic mesophase. The process begins with the protein reconstituted into the highly curved bilayers of the bicontinuous cubic phase (bottom left hand corner of the figure). Added precipitants shift the equilibrium away from stability in the cubic membrane. This leads to phase separation wherein protein molecules diffuse from the continuous bilayered reservoir of the cubic phase by way of a sheet-like or lamellar portal (left upper midsection of figure) to lock into the lattice of the advancing crystal face (right upper midsection of figure). Salt (positive and negative signs) facilitates crystallization by charge screening. Cocrystallization of the protein and its native lipid is shown in this illustration. As much as possible, the dimensions of the lipid (light brown oval with tail), detergent (pink oval with tail), native membrane lipid (purple oval with tails), protein (blue; outer membrane Vitamin B12 transporter, BtuB; PDB code 1NQE), bilayer and aqueous channels (purple) have been drawn to scale. The lipid bilayer is approximately 40 Å thick. This was a cover image for Structure 12, 12 ( 2004) and is reprinted with permission from Elsevier.***

## 10.02: Reflectivity/Scattering from Membranes, con't

from crystals produced in this manner. While some of the crystals have produced high resolution structures (1.3Å), others have diffracted poorly. Vadim stressed the need for an understanding of the crystallization process *in meso*, including the interactions between the protein and the lipids and/or detergents. The structures of the various lipidic mesophases currently being used can be examined by SAXS or SANS. He discussed crystallization of proteins from the cubic phase formed with a detergent and from lipid bilayer phases that have the advantage of being less viscous. However, since there are so many possible combinations of protein and lipid mixtures, Vadim pointed out that a high throughput method for screening conditions for crystallization is necessary. They have built a robotic device for just this purpose so that only the mesophases that produce the best crystals can be examined in detail by scattering methods.

**Jeremy Pencer** (Chalk River) described the use of SANS to characterize lateral inhomogeneities in mixtures of lipids and cholesterol. He used a mixture of chain-deuterated DPPC, DOPC and cholesterol in equal quantities. In order to be sure the domain sizes were not too large for SANS measurements, he restricted the overall vesicle size by extrusion methods. The sample was measured over a wide range of temperatures so that the difference between a homogeneous and inhomogeneous distribution of lipids became apparent. To model the SANS data, he constructed model spherical shells with different sized domains and then calculated their corresponding SANS intensities. He found that nanoscale-sized domains can be measured with SANS. Furthermore, Jeremy showed that the scattered intensities differed in a predictable manner when the vesicles contained a small number of large domains rather than a large number of smaller, nanosized domains.

**Stephen White** (UC-Irvine) focused on high resolution structures of membrane proteins using multilayer x-ray and neutron diffraction techniques combined with molecular dynamics (MD) simulations. Specifically, he discussed the energetics of melittin folding as ascertained from diffraction data and MD simulations. He stressed the importance of dynamic 3-dimensional protein models that are constrained by the lamellar diffraction data. He explained that x-ray and neutron diffraction data can be combined to obtain more diffraction orders and specific deuteration or bromination can be used to enhance the double bonds, thus providing 20 parameters for the refinement of the structure. Finally, Steve discussed the importance of absolute scaling of the data for obtaining correct lipid density profiles. In cases where the bilayer is perturbed by the protein, MD simulations on bilayers containing the protein are necessary to obtain the structure of the perturbed bilayer.

**Kent Blasie** (U. Penn.) also spoke about membrane protein structure-function relationships studies using a combination of x-ray scattering, neutron scattering, and MD simulation techniques. He explained the utility of using amphiphilic 4-helix bundle peptides that have been designed to incorporate both biological and non-biological cofactors. These artificial proteins are engineered with functionality such as electron transfer, light-induced energy transfer and heme binding to gain insight into the structural changes of membrane proteins with similar functions. Kent showed that x-ray reflectivity and GID from Langmuir monolayers of the artificial peptides at air-water interfaces can provide the necessary structural information. The reflectivity data can provide SLD profiles perpendicular to the plane of the monolayer while GID provides information in the plane of the monolayer. With heme binding proteins, GID would be used to show the in-plane heme positions. Finally, Kent explained that the peptide monolayers can be oriented at the water surface and deposited onto solid supports in order to perform phase-sensitive NR.

*Susan Krueger*

## 10.04: Biology on the Colloid to Nanoscale

All speakers emphasized the importance of small-angle scattering techniques in the investigation of non-crystalline nanoscale biological complexes. Topics included solution structure of functional complexes; folding, interactions and crystallization; counterion distribution; membrane - protein interactions; and membrane fusion. In addition several speakers discussed recent advances in combined techniques such as stopped-flow and continuous flow mixing, pressure jump, and contrast variation.

***From left: Tobin Sosnick, Rhiju Das, Elena Kondrashkina, Cristiano Oliveira, Theyencheri Narayana, B. Tracy Nixon, P. Thiyagarajan, Huey Huang.***

**Tobin Sosnick** (U. Chicago) discussed the synchrotron SAXS studies of chain collapse and hydrogen bond formation in protein folding. These studies demonstrated that early collapse is not an obligatory step in the folding process; rather secondary structures are formed commensurately with the surface burial of hydrophobic chains. **Annette Tardieu** (U. Paris) presented synchrotron SAXS studies of crystallization from solution upon the addition of PEG. The results revealed the optimum conditions for PEG-induced crystallization and excluded liquid-liquid separation as a transient intermediate stage. In an illuminating talk, **Rhiju Das** (Stanford) presented an anomalous SAXS study of counterion distribution around RNA and how this ion atmosphere influences the folding process. In model systems, the ion atmosphere screens the coulomb interactions between double helices but not sufficient to produce a net attraction. Furthermore, simple theory of linear polyelectrolytes satisfactorily describes the shape, composition and energetics of the counterions in RNA. **Huey Huang** (Rice)

## 10.04: Biology on Colloid-Nanoscale, con't.

discussed how the mode of action of antimicrobial- and fusion-peptides and the structures induced by these peptides in lipid membranes can be studied by small angle scattering and diffraction at grazing incidence. By contrast matching with partial deuteration, the inplane structure of peptide-induced membrane pores could be established. In addition, he pointed out the need for a better high resolution grazing incidence neutron diffraction instrument for the investigation of lipid-protein complexes. **B.Tracy Nixon** (Penn State) presented solution scattering studies of molecular motor AAA+ ATPase. The conformational changes associated with binding and regulatory action of AAA+ ATPase provide insights about signal transduction and motor function. This example vividly demonstrated the complimentarity of SAXS/WAXS techniques for providing *ab initio* solution structure of macromolecular assemblies.

Overall the session was well attended and the discussions were lively. In addition, many topics involved strong cross-fertilization with the related field of soft matter.

*Theyencheri Narayanan & Pappannau Thiyagarajan*

***Douglas (Darth) Ho, Session 11.01.***

## 11.01: Advances & Insights in SM Crystallization & Handling

***Back, l to r: Xiaoping Wang, Vic Young, Ken Poeppelmeier, Colin Seaton, and Vic Rosso. Front: Bart Kahr, Marilyn Olmstead, "Darth Douglas", Bob Bau, Andy Parkin, and John DiMarco. (Photo courtesy of Douglas Ho.).***

This half-day session on crystal growth and handling was sponsored by the Small Molecule SIG, in partnership with Wyeth Pharmaceuticals and Wyeth Research. Special thanks go to Magid Abou-Gharbia, Guy Carter, Oliver McConnell and Christina Kraml, Wyeth, for their interest and support. The idea for the session came from conversations with Nancy Tsou, Merck, and Wes Cosand, BMS, and the SMSIG charged Co-chairs Doug Ho (Princeton) and Xiaoping Wang (Texas A&M) with organizing it, not knowing that ACA Vice President Bob Bau had said to a then young graduate student nearly 30 years ago, "Let your imagination run wild!"

We were all at at Disney World, and suffice it to say that in keeping with a family theme park setting, and the release of Episode III in mid-May, a last minute decision was made to invest the session with a Star Wars theme. Special thanks to two Destination ImagiNation (**www.maom.org/**) veterans, Amy and Laura Vogelaar (Blacksburg Middle School); Amy for the initial testing of the Jedi outfit, and Laura for the loan of her computer cable that allowed us to pipe Star Wars music directly into the lecture room's PA system.

Expect the unexpected! **Bart Kahr** (U. Washington), who had lectured on genetic takeover and the Cairns-Smith hypothesis in Chicago, returned to the podium in Orlando to tell us about Dyeing Crystals (well, in part). It seems that in the course of discussing dyed crystals with his then 5 year old son, he happened upon the Norman Brosterman book *Inventing Kindergarten*, and was fascinated to learn that kindergarten was in fact invented by a crystallographer, Friederich Froebel! To the delight of the audience, Bart proceeded to deliver a mind-bending tour through mid-nineteenth century kindergartens and the impact of Froebel's crystallography, on art and architecture as well as children, before returning to the growth of dyed crystals at the end of his lecture. **Marilyn Olmstead** (UC Davis) is best known for her contributions to porphyrin and fullerene chemistry, but complied with the organizers' request to talk about growing crystals in sub- and supercritical $CO_2$. In collaboration with Philip Jessop, Queen's U, Marilyn developed a comprehensive short course on the subject matter, complete with phase and volumetric expansion diagrams, miscibility and immiscibility data, pictures of the specialized equipment, and a digital movie of a $CO_2$-induced solvent expansion. For those of us without prior experience in using $CO_2$ to crystallize compounds (probably 99% of the audience), the material presented was an absolute treat.

**Ken Poeppelmeier** (Northwestern) delivered a very "how-to" lecture on crystal growth by solvatothermal methods. His slides were beautiful examples of the hydrothermal growth of crystals in Teflon® pouches at modest temperatures in an autoclave. Yes, Virginia, high-temperature supercon chemists aren't the only people that know how to cook. Ken treated us to a full course meal of ionic and solid-state materials that had a direct bearing to batteries, electronic, and medical implantation technologies. **Andy Parkin** and **Chick Wilson** (U. Glasgow) treated us to an update on experiences with electrocrystallizations and *in situ* electrocrystallography, presenting the rationale behind two electrochemical cell designs and the problems encountered using them. Arguments were also made for which diffractometer geometry and detector would best facilitate such studies. **Vic Young** (U. Minnesota) is noted for his superb lectures on twinning, but we asked him to cover laboratory techniques and methods used to handle difficult samples. His immediate response was dubious, but

## 11.01 Small Molecule Crystallization, con't.

like Marilyn, he rose admirably to the challenge. Vic's slides were like flipping through the pages of a wonderfully illustrated manual on laboratory practices. The tricks he presented for manipulating and handling air-, moisture- and temperature-sensitive crystals, mechanically fragile crystals, and other problematic samples were a must-see for both young and old crystallographers.

**Vic Rosso** and **John DiMarco** (BMS) gave back-to-back talks that provided insights into the world of crystal growth and handling and, ultimately, small molecule high throughput crystallography in a pharmaceutical setting. Increased productivity and cost savings were achieved through automation, sample minimization and preliminary screening techniques to identify suitable candidates for larger scale single-crystal growth. Stage filters for powder diffraction analyses were reported to boost productivity by up to 3 orders of magnitude. Combinatorial and multiwell techniques were exploited, and Raman microscopy employed. **John DiMarco** (BMS) (also **Mike Galella, in P191**) illustrated the benefits of HTC when faced with a mine field of polymorphic forms for a single drug candidate. Of course, nature does as nature will, and invariably a number of those forms required special handling techniques due to phase transitions, solvent loss and/or problems in crystal shape, size and morphology during larger scale workups.

**Bob Bau** (USC), a guiding light in neutron diffraction, was a totally unexpected addition to the program. However, since neutron sized crystals are usually at least 100x larger than x-ray sized crystals, crystal growth has always been a problem. The big news is that crystal size will soon not be an issue! Key points from Bob's talk: (1) Crystals 0.5 mm x 0.5 mm x 0.5 mm in size and maybe even smaller, *i.e., x-ray sized crystals*, will be suitable for neutron diffraction experiments on the SNS/Topaz diffractometer in 2009, (2) $OsH_3Cl(PPh_3)^3$ contains the most significantly "stretched" dihydrogen ligand to date, and (3) a $Y_4H_8(C_5Me_4SiMe_3)^4$ compound that contained a 4-coordinate (!) hydrogen has been characterized by neutron diffraction at the VIVALDI site. Kudos to everyone involved with these significant developments. **Colin Seaton** (U. Bradford) was our go-to-guy to provide alternative methods that one might try in the event of such a worst case scenario when sizable single crystals simply will not grow. Colin described the structure determination of a sulfathiazole:glucose complex which had failed to solve by powder diffraction and direct space methods. Solid state NMR, and single crystal diffraction on a tiny crystal at a synchrotron eventually revealed that the sulfathiazole:glucose co-crystal had undergone a reaction during the experiment. Oops - expect the unexpected!

*"Darth" (Douglas) Ho and Xiaoping Wang*

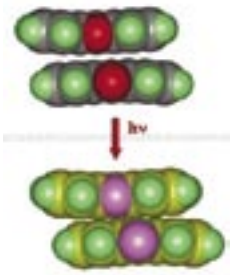
## 11.04 Chemical Crystallography at Synchrotrons

While powder diffraction and macromolecular crystallography are widely practiced at synchrotron facilities, there seems to be much less small molecule single-crystal work going on; this session, organized by the ACA Data, Standards, and Computing Committee, was meant for expert practitioners to discuss their experiences and problems, and to promote wider use of synchrotrons in this area of research.

***From left: Peter Stephens, Philip Coppens, Sue Peiris, Fred Hollander, Yongjae Lee, Jeff Deschamps.***

**Yongjae Lee** spoke about single crystal and powder experiments on over-hydrated states of framework compounds under pressure. Some of these materials actually increase their unit cell volume at high pressure because water is driven into the framework, where it can influence the chemical properties of the zeolite and its interactions with guest molecules. Related by technique, but of entirely different motivation, **Sue Peiris** described single crystal experiments at high pressure to study the important problem of pressure-induced phase transitions in explosives. **Jae-Hyuk Her** discussed the importance of high resolution powder diffraction to obtain correct solutions of perovskite-related materials containing small molecules in the A-site. Contrary to the usual picture of rigid rotations of octahedral framework atoms, the $PbCl_6$ units in methylammonium lead chloride are extremely distorted.

**Phillip Coppens** gave a very exciting talk on recent time-resolved crystallography measurements on photo-excited molecules that his group has been doing at the APS. They use a pulsed laser and a fast x-ray chopper for time resolution of tens of microseconds in pump-probe experiments with an integrating (CCD) detector. Achieving submicrosecond time resolution, ultimately limited by the ~100 ps time structure of the synchrotron source, would require special bunch structures and more advanced excitation laser systems. He described results on three materials, and the audience was struck by the fact that the field has advanced to the point that a majority of his talk was devoted to scientific results rather than experimental techniques. In the phosphorescent state (53 μsec lifetime) of a Cu(I) pyrazolate trimer, the formation of an intermolecular Cu-Cu bond is clearly seen, and experiments exclude the shortening of intramolecular Cu-Cu contacts. He also discussed salts of the $Pt(II)_2$ tetrapyrophosphate ion, in which a photo-excited electron is transferred to a methylviologen cation, which largely quenches the




***From Philip Coppens: the contraction of a xanthone dimer on excitation; Shao-Liang Zhang, Milan Gembicky, Tim Graber, Yu-Sheng Chen, Paulina Dominiak, Ivan Vorontsov, Marc Messerschmidt & Philip Coppens.***

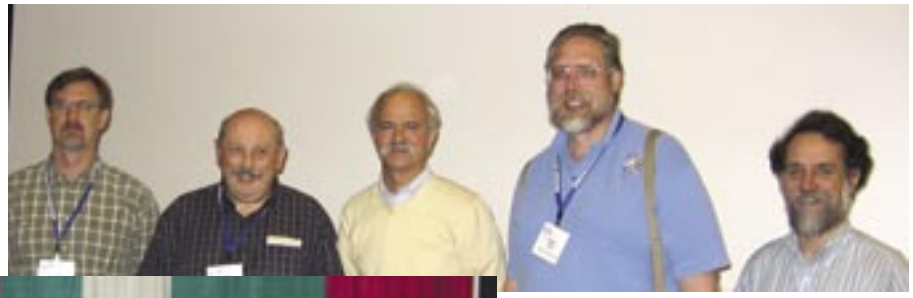
***Philip Coppens and friend. (Photo courtesy of Peter Stephens).***

phosphorescence. The largest structural change yet observed on photo-excitation is an 0.86Å shortening between rhodium atoms in a dimer complex, where it is just barely possible to see the motion of light atoms bonded to the metals.

In a last-minute change of schedule, **Fred Hollander** spoke on *A head-to-head comparison of synchrotron and laboratory-based crystal structures*. Fred presented the results from several compounds for which both laboratory data and synchrotron data were available. In comparing the results Fred and his co-authors searched for an unbiased way of evaluating the data - they defined the resolution of a dataset as the point at which I/<I> = 1.0. Based on maximum resolution, R(int), and sigma(I) the synchrotron did not always produce the best dataset, although in every case the synchrotron data collection was faster by a factor of 40 to 50. Of course only samples for which both synchrotron and laboratory data could be collected were included in this comparison, and Fred emphasized that however interesting, his results were not a controlled comparison of the two families of sources. There are certainly some crystals too small for data collection on a laboratory source, even if you are willing to spend the extra time required. If nothing else the talk got the audience thinking about what constitutes a good dataset and how different datasets can be compared.

*Jeffrey Deschamps & Peter Stephens*

## *12.01: Shifting Landscape at Macromolecular Crystallography Beamlines*



***From left: Chuck Kissenger, Wladek Minor, Bob Sweet, James Fait, Andy Howard.***

***From left: Ward Smith, Peter Kuhn, Howard Robinson, Graham Winter, Ana Gonzales, James Holton.***

Macromolecular diffraction data collection at synchrotron beamlines is being transformed by the introduction of new technologies. Some of these transforming technologies were detailed in a full day session held on Sunday entitled "Integration of Structure Solution with Data Collection and Beamline Operation", sponsored by the Synchrotron Radiation SIG. Speakers in this session presented approaches to integration of beamline automation, data collection, data reduction, phasing and model building and experiment design to significantly enhance and accelerate the process of structure determination. The tone for the day was set by **Graham Winter** who presented the efforts of the European DNA Project to incorporate expert system software to aid the user in making data-collection decisions during a synchrotron visit. The goal of the DNA Project is to produce software that will allow fully automated collection and processing of diffraction data, including rapid crystal screening. This will be achieved by providing software to bridge existing data processing and beamline control software. A database to track experiments is also a component of the system. DNA programs will make decisions about data collection based on information provided by the data processing software and some basic parameters relating to the project that will be supplied by the user. Version 1 of the package in being tested at Daresbury, NSLS, ESRF and DESY. **Peter Kuhn** discussed a data-centric environment with mechanisms for tracking experimental procedures within the context of a high throughput protein structure initiative at the Joint Center for Structural Genomics. He presented a wide variety of technology initiatives, including the use of micro-fluidics for crystallization, a novel micro-calorimeter and the development of a compact light source at Lyncean Technologies, Inc. **James Holton** described the ideal GUI in part by pointing out the shortcomings of some existing interfaces. He presented an analysis of the true productivity of a beamline which turns out to be alarmingly low, and discussed some reasons for this, including radiation damage and several additional factors which together might be described as poor experiment design. **Ana Gonzales** wrapped up a very well-attended morning session with a summary of recent developments at SSRL towards automation and remote presence with new the newly released Web-Ice browser-based interface.

**Bob Sweet** presented new methods, hardware, and software implemented in the Protein Crystallography Research Resource at NSLS at Brookhaven National Laboratory. He described in

## 12.01: Structure Solution, Data Collection, Beamlines, con't.

detail a mail-in (so-called FedEx) mode of the data collection, wherein investigators send frozen specimens for data collection and optionally structure solution performed by PXRR staff. **James Fait**, speaking for John Chrzas, presented the South East Regional Collaborative Access Team's implementation of a reliable remote access capability to provide its membership with a virtual synchrotron in their home labs. **Chuck Kissinger** presented a fascinating talk describing an automatic system for determination of protein-ligand structures. This high throughput system, developed by SGX for their beamline at APS, integrates automated data collection and data reduction processes with automated co-crystal structure determination software into a single system. The endpoint of the procedure, prior to any human intervention, is a refined model including an optimized conformer of a density-fitted ligand, together with electron density maps, density images of the active site and structure validation diagnostics. The last speaker was **Wladek Minor** who presented an approach that integrates data collection, data reduction, phasing and model building to significantly accelerate the process of structure determination and, on average, minimize the number of data sets and synchrotron time required for a structure solution. Typically, this HKL-2000 based system results in an interpretable electron density map, a partially built structure and in some cases, a completely refined model. Current development of this system is oriented towards very fast structure solution which will provide feedback during the diffraction experiment. Indeed, the system is fast enough to permit solving two SAD structures during the presentation.

All together, an exciting look at the future of synchroton macromolecular crystallography.

*Howard Robinson, Ward Smith, Andy Howard, & Wladek Minor*

## *13.01: Topics of Interest to the Young Scientist*

After some opening remarks by 2005 YS-SIG Chair, **Chad Haynes**, Caltech, **Catherine Drennan**, MIT, got the session off to a great start by sharing her view on the precarious world of academic hiring. She detailed key events that had influenced her career. In her advice to academic job seekers, she not only emphasized the importance of publications and letters of recommendation but also the importance of evaluating how well the applicant feels he or she fits the potential position. Next, **Len Banaszak**, U. Minnesota, took us through a romp of crystallographic history, reminding us of where we have been.He showed how simple changes in technology, *e.g*. micropipettes changed the way crystals are grown and also showed incredible images of early scaled wire models built by hand for the first protein structures. The world of crystallography has definitely become simpler for the young scientist but hopefully not at the cost of understanding the details.

***From left: David Goetz, Steve Ealick, Len Banaszak, Catherine Drennan, Chandra Patel, Chad Haynes.***

**Steven Ealick**, Cornell, filled us in on the do's and don'ts of academic publishing. Most important in getting published, according to Steve, is to make the commitment to write and to set a timeline. Few can argue with that simple bit of advice. He also recommends resisting the urge to speculate in the paper. In the off-chance that the paper is sent back for corrections or rejected, he suggests reading the reviewers comments, then putting them away and reading them again a few days later. Don't reply to reviewers in the heat of the moment! **Mari Rains**, currently in the HR department of U. Central Florida, had hiring advice for all future managers in the audience. This was an informative seminar supplying information that the average young scientist will rarely think about (at least not until there is a problem) such as key employment laws. Her talk also included the idea of finding an employee who not only has the right credentials but is also a good fit. Finally, we had a fellow young scientist, **David Goetz**, UCSF, give a seminar guiding students through the resources available when applying for fellowships. The talk included a myriad of web based resources and David's own experience in the process. He also put together an information packet for attendees that helped summarize the information and directed them to useful websites.

We are grateful to Nextal Biotechnologies for sponsoring the highly attended Young Scientist Mixer and for their continued monetary support to the YS-SIG. Thanks to all the mentors who joined us at the mentor/mentee dinner; we hope to see even more next year! Also, a special thanks to Arwen Pearson, U Minnesota, who continues to play an important role in the YS-SIG.

*Chandra Patel*

***Bill Duax, Jenny Glusker and Michael Rossmann.***

## 13.02 Research Presentations

Session 13.02 showcased ACA Young Scientists, and served as a fitting bookend to a fantastic meeting. **Melanie Adams**, Queen's U., Canada, opened the afternoon session by presenting her graduate thesis work. Melanie spoke on her crystallographic and biochemical work on the enzymes YgiN and MdaB, proteins of yet unknown function. Melanie described the respective enzyme folds of each enzyme, pointing out structural similarities to a monooxygenase and the well characterized enzyme DT-diaphorase. Her biochemical evidence implicated both enzymes in a novel quinone redox cycle in E. coli. Melanie won the RCSB PDB Prize for her poster P57. See page 19.

**Francisco G. Hernandez-Gozman,** Accelrys, presented his study on the use of homology modeling as a mechanism to enhance the phasing power of an initial search object during molecular replacement. Francisco described the procedure of automated homology model construction within the program MODELER prior to automated molecular replacement and rebuilding.

**Ping Liu**, Georgia State, presented the crystal structure of a covalent reaction intermediate in the carboxyesterase Est30. Ping's structure, refined to 1.6 Å, revealed a tetrahedral ligand bound to residue Ser94, a member of the catalytic core of the enzyme. The covalently bound intermediate represents the first catalytic step in the reaction mechanism and will aid in deciphering the overall mechanism.

**Lisa Whitson**, U. Texas Health Science Center, concluded the session. She presented one of the most interesting talks of the meeting, describing the relationship between FALS, a fatal neurodegenerative disease, and mutations within the enzyme copper-zinc superoxide dismutase (SOD1). Aggregation of SOD1 is largely believed to contribute to neuron dysfunction and disease. Lisa described structures of several pathogenic SOD1 mutants which exhibit amyloid-like packing arrangements. She also investigated the role of metal deficiency on amyloidosis, showing how metal loss, in particular zinc, is a primary step towards SOD1 filamentous packing. Lisa's poster P105, won the IUCr Poster Prize, see page 18.

*Chad A. Haynes*

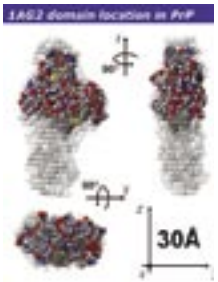
## Macromolecular Posters, Structure and Function

The 250 poster contributions to the Orlando meeting covered the full spectrum of interests found in the ACA. There were many interesting and exciting macromolecular poster contributions, including a number that used other biophysical techniques to complement the x-ray studies.

For example, **P002** by **Jie Qin** and colleagues (U. South Carolina & U.Georgia) used isothermal titration calorimetry to augment their structural studies of the metalloenzyme enolase. Different dissociation constants for the four fluoride ions per dimer and the asymmetry of their complex indicate negative cooperativity between the subunits. In **P051**, kinetic studies of D- and L-tyrosine as substrates for tyrosyl-tRNA synthetase prompted structural studies by **Eric First** and coworkers (LSU Health Sciences Center & UNC Chapel Hill). They found the orientations of L- and D-tyr differ by 180,° leading to overall similar binding of the side chain, amino group, and one carboxylate oxygen on each enantiomer.

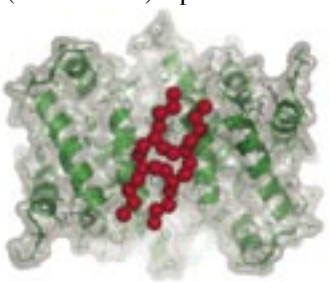
Actin filament nucleation by the formin homology 2 domain was the focus of **P047** by **Mischa Machius** and colleagues (UT Southwestern Medical Center). The structure of the FH2 domain in complex with actin monomers, along with kinetic and thermodynamic data, suggests a ratchet model for addition of actin molecules. In **P050**, **Bog Stec** et al. (UT El Paso) combined their crystallographic information with data from NMR, SAXS, and fluorescence anisotropy to propose an interesting model for the toxicity of thionins. They speculate that portions of the affected membrane are rigidified, allowing nearby regions to liquefy, which facilitates the removal by the toxin of fatty acid from the membrane.

Another study related to membranes was that of **Young Jun Im** and colleagues (Gwangju Institute, Korea) on the proteolytic domain of the Lon protease from *Methanococcus jannaschii*, **P249**. Comparison of the Mj-Lon to that from *E. coli* suggests that Lon proteases can be classified into two groups based on active site configurations and sequence data. **Iris Torriani** and her coworkers (Institute de Física, Brazil) used elegant SAXS and NMR studies to examine free prion protein (PrP) and PrP with DNA bound in **P190**. Their work reveals the nature of the complex formed, which should aid in understanding how the nucleic-acid mediated prion structural conversion takes place.




***From Iris Torriani: Location of the 1AG2.PDB domain in the low resolution model for $rPrP^{23-231}$. Colored spheres: 1AG2.PDB atomic structure. Semitransparent spheres: $rPrP^{\Delta 32-121}$ SAXS model.***

**Desigan Kumaran** and **Subramanyam Swaminathan** (Brookhaven) reported in **P043** on the structure of phosphatidylglycerophosphatase (PGPase), an enzyme involved in lipid metabolism. Two inter-linked linear water molecule chains serve as "proton wires" at the tetrameric interface as PGPase acts as the exit port for protons from the membrane. **Kunchithapadam Swaminathan** and colleagues, (National U.Singapore) studied AtFKBP13, an FKBP-type chloroplast immunophilin (**P151**). The presence of disulfides, which are not found in animal or yeast FKBPs, suggests redox regulation in chloroplasts where the sulfhydryl form is the active enzyme form.



***From Desigan Kumaran: Structural representation of the two long inter-linked (25Å) linear water chains, putative 'proton wires', observed in the crystal structure of PGPase tetramer. These proton wires are sandwiched between the two dimers, forming a tetramer. Cross sectional view of the tetramer with embedded water molecules is shown here. Surface and secondary elements are shown in gray and green, respectively. Water molecules are shown as red spheres.***

*Judy Kelly*


*Candid photos from the Poster Sessions: clockwise from top left: Lynne Howell and Zongchao Jia; Erick First, Judith Kelly and Bog Stec; Santino Russo and Agnieszka Szyk; Adviye Tolun and Tim Rydel; Graciela Diaz de Delgado and Peter Müller; and Herb Axelrod and Glen Spraggon. Richard Bott and Gerry Bunick are in the center photo.*

## Selected Posters:

Flash from the Disney's Swan Ballroom: Keep doors closed! The fantastical air from Mickey's magic, The Tower of Terror, and Epcot Center nearby is reaching the posters! Disney cannot be held liable if creative speculation and far-reaching interpretations begin to appear in the Discussion Sections! Or if poster graphics switch to primary colors and start to become animated cartoons! The surroundings were entertaining, even distracting, but most of the posters remained crisply factual.

Outstanding among the colorfully- presented new structures were a novel Thymidylate Synthase, ThyX, in poster **P071** by **Parthasarathi Sampathkumar** et al., and a Pentapeptide Repeat Beta-helix in **P029** by **Matthew Vetting** et al. In the methods development category, noteable contributions included **P106** by **Constance Jeffery** et al., which described a systematic study of membrane protein expression, and **P015** by **Chae Kim** and Sol Gruner, which took the Oxford Prize (see p. 19) for its novel solution (and hardware demonstration) for cryoprotection. Work-in-progress posters included many impressive virus projects such as **P019** by **Michael Lane** et al (U.FL), which described work toward the structure of a liver-specific adenovirus capsid.

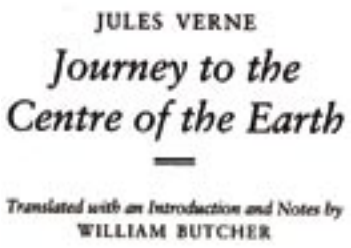
Fantasy and imagination were explicitly welcomed on at least one poster: **Frank Fronczek**'s **P152**: *Crystallography in Fiction*. This unique assembly neatly covered, with thoughtful commentary, the most famous instances of crystals in literature, such as Kurt Vonnegut's fateful "Ice Nine" in *Cat's Cradle*.

*Travis Gallagher*

## *P152: Crystallography in Fiction* by Frank R. Fronczek, Louisiana State U., Baton Rouge, LA

**Introduction:** Crystallography and crystallographers are rarely mentioned in works of fiction, but some examples exist, mostly in the genre of science fiction. The earliest I have found is a brief mention in Jules Verne's *A Journey to the Centre of the Earth* (1864). A rare occurrence of a crystallographer as the protagonist in a novel is found in C. P. Snow's *The Search* (1934). Several good examples come from the 1950s and '60s: Kurt Vonnegut Jr.'s *Cat's Cradle* (1963), his short story *A Deer in the Works* (1955), Michael Crichton's *The Andromeda Strain* (1969), and mention of crystallography books in Anthony Burgess's *A Clockwork Orange* (1962). In the descriptions of each, excerpts are given in **RED**, while my remarks are in **BLUE**

*Editor's note: two excerpts from Frank's poster follow. See the winter ACA Newsletter for more. Frank's disclaimer and appeal: "I am by no means an authority on this topic, but am interested in learning of other instances of crystallography or crystallographers in fictional works. If you are aware of any not discussed here, please give title, author, and a brief description below, or contact me by email (ffronz@lsu.edu).*"




**The earliest mention which I have found of crystallography in fiction is in Verne's 1864 classic. The narrator, Axel, describes the difficulty of some geological pronunciations:**

**"But when one is in the presence of rhombohedral crystallisations, retinasphalt resins, gehlenites, fangasites, lead molybdates, manganese tungstates, or zircon titanites, the most agile tongue is allowed to get tied in knots."**

**A little later, this appears:**

**"In 1853 there had appeared in Leipzig a *Treatise upon Transcendental Crystallography* by Professor O. Lidenbrock, printed in large-folio pages with plates — but without covering its costs."**

**He doesn't explain what "Transcendental Crystallography" is. Note that in some translations into English, these passages do not appear. Verne also describes quartz crystals in a lava flow, similar to Mark Twain's description of crystals seen by Tom Sawyer and Becky while lost in a cave.**


**Snow's *The Search* was originally published in 1934, and is a bit unusual in that it is not science fiction. The main character is a promising young British crystallographer, and the book gives glimpses into how crystallography was done 70 years ago. In the first excerpt, he explains his attraction to the science. This will sound familiar to you all:**

**… For by this time, a few months before my degree, I had nearly decided to do my research on crystallography. I had narrowed it down to that or nuclear physics, and on the whole crystallography was attracting me the more. Crystals, their shapes and colour and growth, had fascinated me since I first saw needles of cinnamic acid glinting at the bottom of a test-tube while the light shone through them and was reflected glitteringly at each line-sharp edge. At the University I seized hold of Bragg's work; it fed my interest to learn how in every crystal there is one regular simple pattern of atoms, which repeats itself indefinitely until we get the crystal we can see and touch; there was something beautifully satisfying about this crystal architecture, and often I longed to trace the atomic patterns for myself. Walking home on the nights when I left Sheriff and Hunt too late to catch the tube, I devised atoms in patterns of my own: tried to find connections between the arrangements of atoms inside the crystals, and the shape of the crystals themselves: saw extensions of this new method - into the older, more conservative sciences of chemistry and metallurgy.**

**As a beginner, he chooses a project, and foresees protein crystallography:**

**To begin with, I was going to start on a safe problem. It was not exciting, but almost certain to give me some results. So I decided to work immediately on the structure of some of the manganates; the arrangement of the atoms seemed to me almost certain to fall into one of the simpler symmetries**

**P152: Crystallography in Fiction, con't**

**and yet, for some reason, they were still unknown. If I could bring this off, it would give me a little reputation.**

**I weighed it up as dispassionately as I could. I wanted to get at a big problem soon. I had my schemes for tackling one of the simpler families of organic compounds, where no one had dared to guess at the structure. I could foresee the method of analysis, with sidelines of analogy and dissimilarity, which later I actually employed: I was ambitious enough to look further ahead, to, the proteins and others of the vital substances, whose chemical formulae were uncertain—I was sure that with courage and luck crystallography could carry me even there.**

**In trying to guess the structure of an organic molecule, he does a little "molecular modeling":**

**According to my guess, the structure was very different from anything one would have imagined; but that must be true, since the obvious structure didn't fit any of my facts. Soon I was designing structures with little knobs of plasticine for atoms and steel wires to hold them together; I made up the old ones, for comparison's sake, and then I built my new one, which looked very odd, very different from any structure I had ever seen. Yet I was excited—"I think it works," I said, "I think it works."**

**Darkroom work was tedious, but the results were satisfying:**

**And so for weeks I was alone in the laboratory, taking photographs, gazing under the red lamp at films which still dripped water, carrying them into the light and studying them until I knew every grey speck on them, from the points which were testing my structures down to flaws and scratches on the surface. Then, when my eyes tired, I put down my lens and turned to the sheets of figures that contained the results, the details of the structure and the predictions I was able to make. Often I would say—if this structure is right, then this crystal here will have its oxygen atom 1.2 a.u. from the nearest carbon; and the crystal will break along this axis, and not along that; and it will be harder than the last crystal I measured, but not so hard as the one before, and so on. For days my predictions were not only vaguely right, but right as closely as I could measure.**

**I still possess those lists of figures, and I have stopped writing to look over them again. It is ten years and more since I first saw them and yet as I read:**

| Predicted | Observed |
|---|---|
| 1.435 | 1.44 |
| 2.603 | 2.603 |

**and so on for long columns, I am warmed with something of that first glow.**

**He describes the joys of publishing:**

**My first piece of work did all that I wanted of it. I wrote it up in three weeks, and after a long and stately process of submission to referees it appeared months later in the Proceedings of the Royal Society. The title stood out on the glossy paper, and I didn't want to read any further: "The Structure of Crystals of the Manganates," by A. R. Miles, Physics Laboratory, King's College, London (communicated by N. E. Austin, F.R.S.). I remember, too, the fondness with which I handled the green-covered offprints and the inscriptions I wrote on them as I gave them to my friends.**

**In the end, largely because of departmental politics, he becomes disillusioned with science, but certainly had fun for awhile.**

## *Selected Neutron Posters:*

The power of neutron protein crystallography for visualizing functionally important hydrogen atoms and water molecules in proteins was elegantly illustrated in **P177** by **Amy Katz** et al. They described the latest results from on-going studies of the enzyme D-xylose isomerase. A series of neutron diffraction data sets is being collected on the PCS at Los Alamos from crystals of D-xylose isomerase with various bound metal cations and substrates in order to elucidate the details of its mechanism; the inter-conversion of glucose to fructose and of xylose to xylulose. Although D-xylose isomerase has been studied to 0.94Å resolution with synchrotron x-rays, not all of the hydrogen atoms of interest can be visualized in the resultant electron density maps. The neutron scattering density maps, calculated to 1.8Å, reveal the protonation states of residues that might play a role in catalytic mechanism. In particular there is evidence that the fifty-fourth amino acid residue, a histidine, acts as an acid in ring opening, an important insight.

Two posters described currently available beam-lines for neutron protein crystallography: the quasi-Laue neutron diffractometer, LADI, at the high flux reactor run by the Institut Laue Langevin, ILL, in Grenoble, **P073: Flora Meilleur**, and **P213** by **Paul Langan** and coworkers at the Protein Crystallography Station, PCS, at the spallation source run by Los Alamos Neutron Science Center, LANSCE. Innovations that increase data collection efficiency are allowing studies of millimeter and sub-millimeter sized protein crystals; LADI, positioned on the end of a cold guide, uses a broad wavelength band in combination with a large neutron image plate detector to collect quasi-Laue diffraction patterns, whereas the PCS uses time-of-flight techniques in combination with a large electronic position sensitive detector to collect wavelength-resolved Laue diffraction patterns. Enhancements scheduled for next year, include relocation of LADI on a higher flux guide, focusing optics and a new image plate detector that will provide gains of x2-4, x1-4 and x3, respectively, on LADI-III.

Perdeuteration, replacing all hydrogen atoms by deuterium atoms, can greatly increase the neutron scattering power of protein crystals and is essential for the efficient use of neutron protein crystallography beam-lines. Laboratories for perdeuteration were described that support the user programs on LADI, as well as other neutron experiments in biology, the ILL-EMBL Deuteration Laboratory in Grenoble, **P232**: **Flora Meilleur** et al, and the PCS, the Biological Deuteration Laboratory in Los Alamos, **P115**: **Benno Schoenborn** et al. Both laboratories are central user facilities that provide expertise, facilities and resources and also an economy of scale for deuteration. The laboratory in Grenoble is jointly supported by

the ILL, the EMBL, the European Union and the EPSRC (UK); the laboratory in Los Alamos is funded by the Office of Biological and Environmental Research of the US Department of energy.

Both LADI and the PCS are oversubscribed with user projects and although proposed upgrades will greatly increase user throughput there is clearly a need for more neutron protein crystallography beam-lines, particularly in the US where the PCS is the only resource of its kind. Poster **P180**, **Arthur Schultz** et al described the design parameters for a Macromoleculer neutron diffraction station, MaNDi, that has been proposed for the next generation spallation neutron source being built at Oak Ridge National Laboratory. If funded, MaNDi, will use time-of-flight techniques in combination with an array of modular detectors that completely surround the sample to collect wavelength-resolved Laue data up to 10-100 times more efficiently than current facilities.

**Bryan Chakoumakos** and coworkers, **P176**, described upgrades to diffractometers at the High Flux Isotope Reactor run by Brookhaven National Laboratory, the diffractometers being the 4-circle single crystal diffractometer on HB3A, the powder diffractometer on HB2A and WAND on HB2C. All instruments will benefit from new monochromators, and the powder diffractometer on HB2A will also have additional detectors, increasing the scattering angle range and allowing more rapid data collection. WAND, which can be used for both single crystal (flat cone geometry) or powder diffraction, the result of a collaboration with the Japanese Atomic Energy Research Institute will now have a flux of over 107ncm-2s-1 because of the larger size of tube HB2C and its more efficient Ge monochromator. The HB2A powder diffractometer also has a high intensity mode (by removing the collimation) for PDF studies. The single crystal diffractomer, WAND is scheduled to be commissioned this fall; the powderdiffractometer next spring.

*Paul Langan*

## *Conference on New Frontiers in Neutron Macromolecular Crystallography*

The conference was held at Oak Ridge National Laboratory, Oak Ridge, TN, July 12-13, 2005. The meeting focused on the role of hydrogen atoms in biological structure and function and highlighted problems where neutron diffraction studies that provide such information will become essentially routine at the proposed Macromolecular Neutron Diffractometer (MaNDi) facility at the Spallation Neutron Source (SNS),in Oak Ridge.

Neutron Macromolecular Crystallography (NMC) can provide accurate hydrogen atom positions, protonation states and hydration states, as well as information on hydrogen/deuterium exchange in macromolecular crystal structures, even at a moderate 2 Å resolution. In contrast, to observe hydrogen atoms via ultra-high resolution x-ray crystallography requires diffraction data beyond 1.0 Å. This limit accounts for less than 1% of all protein systems being studied by x-ray diffraction.

The advent of the SNS, with more than an order of magnitude increase in neutron flux, combined with advances in neutron optics and detectors, structural genomics, and protein deuteration, promises to revolutionize NMC. In order to realize this potential, a dedicated, best-in-class high-resolution time-of-flight single crystal macromolecular neutron diffractometer (MaNDi) has been proposed for the SNS. An optimized instrument design has been developed that will enable data collection rates over 50 times faster than at existing facilities. Furthermore, it will enable studies of crystals with lattice constants substantially larger than currently possible. The MaNDi Instrument Development Team secured beam line 11B at the SNS in October, 2004. It is expected that the unprecedented speed and resolution limits achievable with MaNDi will greatly advance the fields of structural biology, enzymology, and computational chemistry. The project is

*con't, page 55*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## New Frontiers in Neutron Macromolecular Crystallography, con't

now at an advanced stage. It is necessary to secure funding for the engineering design and construction of the diffractometer and the associated infrastructure at SNS. This will be possible only with the strong support of the broader structural biology community.

An outstanding scientific program attracted about 100 macromolecular x-ray crystallographers and structural biologists from research institutions across the US, Europe and Japan. Invited talks by **Jenny Glusker, Herbert Hauptman, Wayne Hendrickson, Andrzej Joachimiak, Anthony Kossiakoff, Brian Matthews, Alberto Podjarny, Dagmar Ringe, Gerald Stubbs** and **B.C. Wang** plus posters on current research in high resolution neutron diffraction in structural biology as well as potential scientific problems for NMC were presented. In addition, the status of the SNS, MaNDi and of NMC programs worldwide were given by **Thom Mason, P. Thiyagarajan** and **Dean Myles**.

***Herbert Hauptman talked on how neutrons break the low resolution barrier to direct methods.***

A highlight of the conference was the tour of the SNS experimental hall containing the target and the instruments in various stages of construction.

The conference was highly successful in meeting its planned objectives: 1) To increase interest and awareness of the important new capabilities of neutron diffraction in structural biology; 2) To engage and involve the community in defining challenge areas and problems that can be addressed by high resolution neutron macromolecular crystallography and 3) To showcase the novel and interesting macromolecular systems that will be amenable to neutron diffraction studies upon completion of MaNDi.

In the final panel-led discussion, highly enthusiastic remarks and unanimous support were expressed both by the audience and all the scientists. With such endorsement and with the active participation and support of the wider structural biology community, the US now has an opportunity to obtain a world-leading new facility for NMC. Further details of the conference can be found at **www.sns.gov/MaNDi2005**.

*Andrew Mesecar, Dean Myles, Arthur Schultz and P. Thiyagarajan, organizers*

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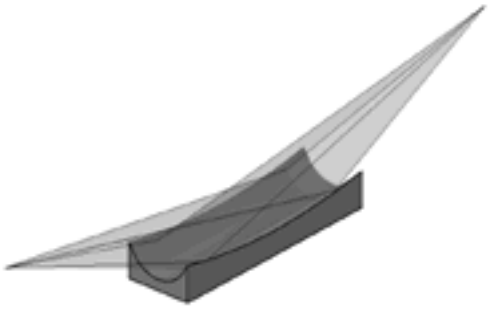

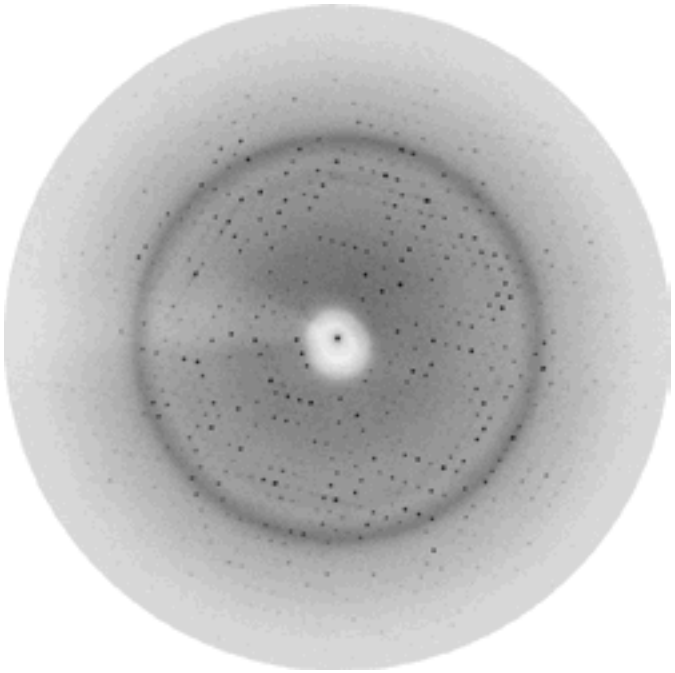

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**Data Courtesy of Dr. Andrew GW Leslie**
**MRC Laboratory of Molecular Biology, Cambridge.**

*The crystal belongs to space group C222 with cell dimensions a=72.1Å, b=97.4Å, c=191.0Å. Images were collected with an oscillation angle of 0.4°.*
*The crystal was a thin plate with approximate dimensions 200x75x50 µm³.*
*The generator was a Rigaku RuH3R running at 50kV, 100mA (300 µm focus) and the data were collected on a Mar345 image plate detector.*

| | classical confocal multilayer system | Xenocs *FOX2D CU 25_25P* |
|---|---|---|
| Exposure time per frame | 4 min | 4 min |
| $R_{merge}$ (22.7.-2.43A) | 8.8% | 6.4% |
| $R_{merge}$ (2.57-2.43A) | 44.1% | 26.2% |
| <I>/<sigI> (22.7.-2.43A) | 12.1 | 15 |
| <I>/<sigI> (2.57-2.43A) | 2.5 | 4.1 |
| Mean multiplicity | 3.3 | 3.3 |

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# Evolving Methods for Macromolecular Crystallography: 37th Course at Erice

The 37th course of the International School of Crystallography on Evolving Methods for Macromolecular Crystallography gathered about 150 participants, lecturers and students, in Erice, Sicily, 12 - 22 May 2005. It started with the traditional get together with marsala wine on the first day and ended with the dinner at the San Francisco Institute (the old monastery). The time in between, apart from a few more social events, was filled by lectures and tutorials delivered by experts selected by the School directors, **Randy Read** and **Joel Sussman**. There was also plenty of time and opportunity each day for the students to talk to the specialists. This was fostered by the superb atmosphere, relaxed, but devoted to science. In addition Erice, which is located on top of a mountain, proved to be a place where scientists could have a real chance to walk with their heads in the clouds.

The scientific program covered all aspects of macromolecular crystallography, theoretical and practical. Presentations ranged from preparation of biological materials, through various experimental and computational techniques for crystal structure elucidation, to the implications of structural results for biology and medicine. The fine lecture by **David Sayre** proved an appropriate finale to the scientific program. David, 50 years after pioneering Direct Methods, is now actively developing single particle diffraction imaging, a fascinating new way of investigating large biological structures, including whole bacterial cells.

The students presented more than 60 posters in two sessions and each presenter had 90 seconds to verbally summarize the work. **George Sheldrick** presented a diploma for the best poster to **Hans-Petter Hersleth** from Oslo, Norway for his work on intermediates in the myoglobin-peroxide reaction. The well deserved prize for the most "dynamic" (active in discussions) student went to **Stephen Graham** from Sydney, Australia.

The School owes a great deal of it's enormous success to both Italian organizers, **Paola Spadon** and **Lodovico Riva di Sanseverino** and to their young helpers from several labs in Italy, all wearing orange scarves in the group photo above. Their altruistic efforts made all events, scientific and social, as smooth as the surfaces of medieval stones in the narrow streets of Erice.

*Zbigniew Dauter*

## XX Congress and General Assembly of the IUCr, Florence, Italy, 23-31 August, 2005

The Scientific Chair, Carlo Mealli, the Local Organizing Chair, Paola Paoli and their committee members deserve thanks and applause from all the participants in this highly successful Congress. The scientific presentations were exciting, with much of the research either hot off the press or in press. The sessions were very well attended, especially considering the lure of the surroundings, surely one of the world's most fascinating cities, and that the ambient temperatures were several degrees below "normal" and very pleasant. The local arrangements were flawless: imagine pulling off delicious, varied, no-hassle ***free*** lunches for probably 2000 people every day! The Congress banquet. held outdoors in the beautiful Boboli Gardens, served a lovely dinner to 1490 people - no small accomplishment. This was an exceptionally big meeting: there were 3000 registrants; 36 keynote speakers; 98 microsymposia, most with 5 speakers, so nearly 500 oral presentations; and 1480 posters.

***Top, at left: IUCr President William L. Duax at the Opening Ceremony, and, below, presenting the Ewald Prize to Philip Coppens.***

The prestigious **Ewald Prize** was awarded to **Philip Coppens,** Distinguished Professor, SUNY, Buffalo. *for his contributions to developing the fields of electron density determination and the crystallography of molecular excited states, and for his contributions to the education and inspiration of young crystallographers as an enthusiastic teacher by participating in and organizing many courses and workshops*. Philip delivered his Ewald lecture at the opening ceremony. Using photo-excitation at pulsed x-ray sources, Philip and his coworkers conduct time-resolved experiments on very short-lived species,thereby studying chemical changes in real time. Philip talked about some of their results at the 2005 ACA Meeting; see pages 46-47 for more details.


Among the poster prizes at the closing ceremony, the **ACA Poster Prize** was presented to Magdelena Korczynska of Canada, for her poster *Structural Studies of an Antibiotic Resistance Factor.*

***At the Opening Ceremony the announcement was made that at the Congress Banquet the First IUCr Prize for Exceptional Service would be given to Lodovico Riva Di Sanseverino, Istituto di Mineralogia e Petrografia, Universitd di Bologna. Carlo Mealli and Paola Pauli are just visible in the picture.***

At the General Assembly of Delegates to the Congress, **Yuji Ohashi** of Japan was elected to the Presidency of the IUCr Executive Committee; Sven Lidin, Sweden, will be the new General Secretary and Treasurer, replacing Sine Larsen, Denmark; and **Iris Torriani**, Brazil, will replace Leonid Aslanov, Russia, as Vice President. Past President Henk Schenk, The Netherlands, is retiring from the Committee, as are Maria Carrondo, Portugal, and Ze Zhang, China. Bill Duax is of course now Past President. Chris Gilmore, UK, Peter Colman, Australia, and Gautham Desiraju, Italy, were elected to six year terms on the Exectuve Committee, and Claude LeComte, France, was elected to a three-year term. The next IUCr Congress will be held in Japan in 2008; Spain was provisionally selected in an election by the delegates to be the 2011 site.

***Photo at left: Yuji Ohashi and Bill Duax. Near left photo (courtesy of Philip Coppens): Gautham Desiraju and Yuji Ohashi.***

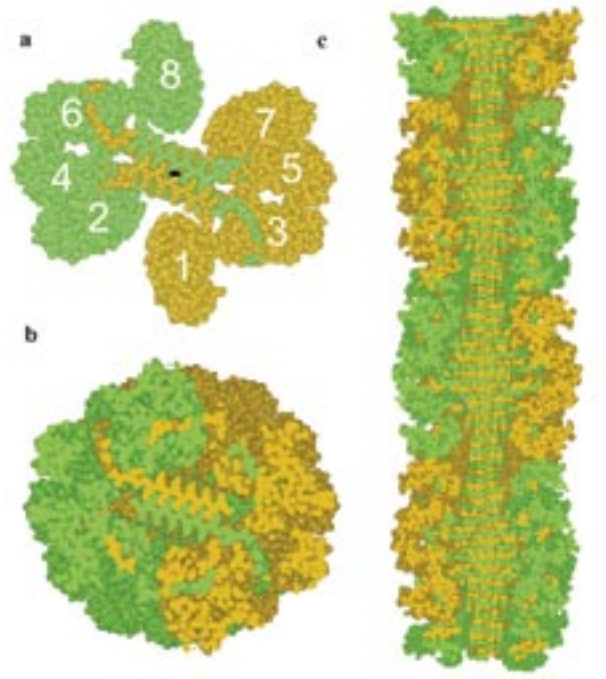
*At left: the USNCCr delegation to the General Assembly. L to r: Jim Kaduk, Brian Toby, Katherine Kantardjieff, Judith Flippen-Anderson, and Jon Clardy.*

*At right, Yuji Ohashi being congratulated by the Spanish delegate, Enrique Gutierrez-Puebla.*

The coming issues of the *IUCr Newsletter* will feature more extensive reports from Microsymposia and Keynote Chairs, but some comments on personal favorite presentations follow.

**David Eisenberg** (HHMI Inst.,UCLA) gave a fascinating keynote lecture on the recent structural studies that he and coworkers in his group have done on amyloid and amyloid-like fibrils. He first described the structure of the cross-ß spine of amyloid-like fibrils. They determined, to 1.8 Å resolution, the structure of a seven-residue peptide segment from Sup35 (GNNQQNY) that forms microcrystals. Double ß-sheets are formed, with each sheet having parallel segments stacked in register. There are no hydrogen bonds between sheets, but the Glu and Asn residues form tight 2-fold contacts - the tightest interface that could be found in the PDB. The side-chains protruding from the two sheets form a dry, tightly self-complementing steric zipper that bonds the sheets.

Using insights from this work, the group designed amyloid-like fibrils of ribonuclease A that had 3-dimensional domain-swapped and native-like structure, and moreover, were enzymatically active. They engineered a hinge region to include 10 Glu residues (Q10) flanked by Gly at each end, a known amyloidogenic sequence, thereby setting the modified Rnase up for fibril formation based on "runaway domain swapping." Using the known structure of native Rnase A, x-ray studies of their modified RnaseA, and electron microscopy, they were able to build a model that clearly suggests a mechanism for amyloid formation that is applicable to proteins involved in amyloid diseases.




***From Michael Sawaya, modified from figure in: Shilpa Sambashivan, Yanshun Liu1, Michael R. Sawaya, Mari Gingery and David Eisenberg, Nature 437, 266-269, (8 September 2005): Domain-swapped zipper-spine model for the Rnase A protofibril. a, The model is a 'runaway' domain swap between the Rnase A monomers, with swaps occurring within one half protofibril but not between half protofibrils. Monomers 1-4 compose half the protofibrillar unit and are colored to emphasize domain swapping. The C-terminal ß -strand of monomer 1 swaps into monomer 2; monomer 2 swaps into monomer 3; and monomer 3 swaps into 4, rising along the axis of the fibril. Q10 segments from these monomers form one antiparallel ß-sheet in the spine. Monomers 5-8 form the other ß -sheet, related to monomers 1-4 by a 21 axis along the fibril. Eight Rnase A monomers comprise the asymmetric unit of the fibril. A similar model can be built from domain-swapped dimers; the currently available data do not favor one of these models over the other. b, The protofibril cross-section reveals the steric zipper, the interdigitation of Gln side chains in the spine of the fibril, modeled on the structure of GNNQQNY, (Nelson, R. et al. Nature 435, 773-777 (2005). c, A cut-away view perpendicular to the fibril axis reveals the stacking of hydrogen-bonded Q10 ß-strands (4.88 Å apart) in the spine. The spine is largely shielded from solvent by the tight packing of globular domains around the periphery. The fibril model ranges from 100 to 140 Å in diameter, which agrees with the diameter of the fibrils obtained from electron microscopy images.***

Even to the naïve observer, it is evident that finding ways to mine the database of macromolecular structures so as to identify relationships that make sense with respect to function is an important challenge. **Adam Godzik** (The Burnham Inst., CA), speaking in the microsymposium **Improving Structures Using Bioinformatics**, described the program FATCAT, Yuzhen Ye & Adam Godzik, *Nucleic Acids Research* **32**, 582-585 (2004) and a new program POSA, Yuzen Ye & Adam Godzik, *Bioinformatics*, **21**,10,2362-2369 (2005) **http://fatcat.burnham.org/POSA**. They seek to describe structural divergence and flexibility among the structures compared. POSA identifies and classifies regions that are conserved only in a subset of input structures and allows internal rearrangements in protein structures. Using pivot points and angles of rotation to characterize structural variation in comparisons of structures within the same fold group, they found similarities in the ways the structures change in response to mutations and inhibitor/substrate binding.

In his keynote lecture *Structural and Functional Studies of Large Macromolecular Assemblies*.**Nenad Ban** ( ETH-Hönggerberg, Switzerland) described some work as yet unpublished, on the structure of fungal fatty acid synthase. Nenad and co-workers in his group are using crystallography, electron microscopy,

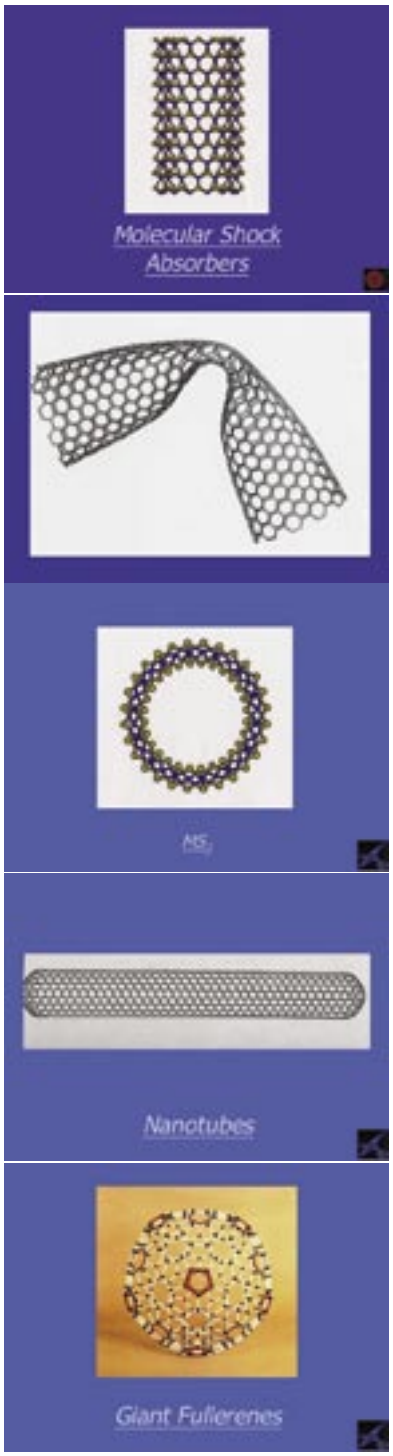
and biochemical experiments to elucidate the structure of fFAS complexes, which are paradigms for eukaryotic mega-synthases. He described their studies with twinned crystals ($P2_1$; cell dimensions ~ 215 x 415 x 222; they used the Lieven Buts program, Untangle). Their fFAS structure explains the presence of ACP synthase within the FAS complex.

In the microsymposium on **Protein Interactions With Other Biological Macromolecules**, **Chris Hill** (U.Utah) talked about *Activating the Molecule of Mass Destruction*. He described proteasomes as proteases that function to degrade a wide variety of proteins in the cytosol and nucleus of eukaryotes. They are cylindrical structures comprised of 4 stacked rings, with the two outer rings each containing 7 different α subunits and the central rings each containing 7 different β subunits. Their proteolytic sites are sequestered in the central chamber of their hollow structure, and substrates enter by passing through an axial pore in the center of the α rings, a process facilitated by an activator. Chris and his colleagues determined high resolution structures of the 11S activator PA26 in complex with 20S proteasome and their structures revealed previously obscure details. C-terminus residues which are important to proteasome binding were ordered and the mode of binding was clear. The structures also confirmed that interactions between Try 8, Asp 9, Pro 17 and Tyr 26 residues (which are conserved in all subunits from *archaea* to yeast to human) are important to the stabilization of the open conformation. Chris showed a beautiful moving slide showing the circular donut-shaped complex with the "gate" opening.

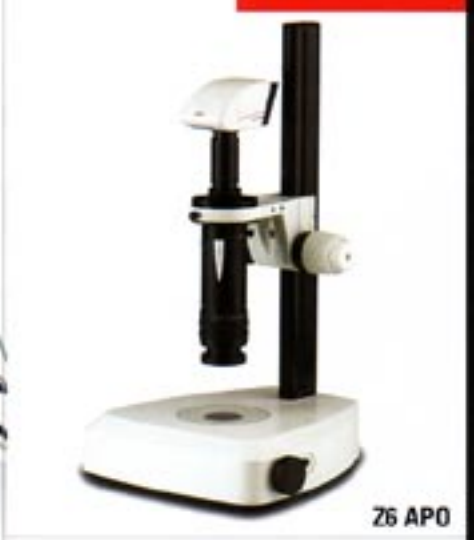
***From Andreas Förster and Chris Hill: The 1.9 Å structure of a 1.1 MDa proteasome-activator complex viewed along a molecular 2-fold axis. The 7-fold axis is vertical. Individual PA26 activator and proteasome α and β subunits are highlighted. A. Förster, E.I. Masters, F.G. Whitby, H. Robinson and C.P. Hill, Molecular Cell 18, 589-599 (2005).***

Even for one without any background whatsoever in inorganic chemistry, it was fun to listen to **Bob Bau** (USC). His lecture in **Applications of Synchrotron and Neutron Facilities in Structural Chemistry**: *Location of a 4-coordinate H Atom via Neutron Diffraction*, described the attainment of his personal "Holy Grail." From their exploration of high-connectvity hydride ligands in interstitial cavities of molecular cluster complexes, Bob and his colleagues had previously reported numerous instances of 6-coordinate and 5-coordinate hydrogen, but a 4-coordinate hydrogen had long eluded them. This first instance of a 4-coordinate hydrogen was found in the center of the tetrahedral complex $Y_4H_8(C_5Me_4SiMe_3)_4(THF)$ in a neutron study at VIVALDI. This work is in press, but see Tardif et al., *Organometallics*, **22**, 1171, (2003) for the preliminary x-ray study.

The figures forming the border at right are courtesy of Nobelist **Sir Harold Kroto** (Florida State U.), who delivered an entertaining and provocative keynote lecture on the mechanisms of fullerene and nanotube formation. His recent research has focused on metal-catalyzed nanostructure formation. (See his personal website at **http://www.kroto.info/** and also **http://www.sussex.ac.uk/chemistry/profile1523.html.**




***Opposite page, clockwise from top: (free) lunch at the Congress; Paola Spadon, Joel Bernstein and Suzanne Fortier; the view from the Mar party in the hills above Florence; in the courtyard after lunch, l to r: Daniel Riley, Simon Billinge, Dimitry Arguriou, and in back of them, Carroll Johnson; Cele Abad-Zapetero and Andy Howard; the portal to the Mar party villa; poster session. Note all the red congress bags (kindly supplied by Bruker). They made it so easy to follow other crystallographers in navigating the city.***



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**Abstract Deadline: March 1, 2006**

**Advance Registration Deadline: June 1, 2006**

**Advance Hotel Registration Deadline: June 13, 2006**

Aloha! As we learned from Karl Seff and Charlie Simmons, our 2006 Local Chairs, aloha has many meanings. For the ACA in Hawaii next year, it surely will mean a warm welcome. On-line abstract submission instructions, on-line registration, and a preliminary meeting program are posted on the ACA website at: **www.hwi.buffalo.edu/ACA/**

The 2006 ACA meeting will begin with workshops on Saturday, July 22. Symposia and sessions will begin on Sunday morning, July 23. Consult the Call for Papers, which will be on the website mid-November, for detailed information on workshops and sessions.

*Karl, below, and Charlie, at right, promoting ACA 2006 during ACA 2005 in Orlando.*

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**judith.kelly@uconn.edu**

*Judy Kelly at the Awards Banquet in Orlando.*

**2006 LOCAL CHAIRS:**

**Charlie Simmons**
**(808) 974-7317**
**simmonsc@hawaii.edu**

**Karl Seff**
**(808) 956-7665**
**seff@hawaii.edu**

## Symposia:

***Transactions* Symposium: Neutron Diffraction (featuring its uses in studying biological macromolecules as well as small molecules and recent developments in neutron techniques), organized by Tom Koetzle, Paul Langan, and Alberto Podjarny.**

**Buerger Award Symposium to honor Helen Berman, 2006 Awardee.**

**Warren Award Symposium to honor Charles Majkrzak, 2006 Awardee.**

## Workshops:

**Advanced CCP4, organized by the Continuing Education Committee.**

**Grazing Incidence Methods for Nanoscience and Biotechnology, organized by the Small Angle Scattering SIG, Chairs: R. Winans and Jin Wang.**

**Methods in Neutron Protein Crystallography, organized by Neutron Diffraction SIG, Chairs: Paul Adams and Paul Langan.**

## Sampling of Scientific Sessions:

**Whole-Molecule Disorder, PDF Analysis of Industrially Relevant Materials, Detectors, Solving Difficult Organics and Organometallics, Macromolecular Assemblies, Non-Ambient Crystallography, Structural Genomics, Natural Products and Drugs, Polymer Science and Technology, Cell Surface Proteins/Host-Pathogen Interactions, Computational Methods, Crystal Engineering, Time Resolved Crystallography, Membrane Proteins, Pair Distribution Function Analysis and Small Angle Scattering, Radiation Damage.**

*Photos are courtesy of the Polynesian Cultural Center.*

## Meeting Calendar

### OCTOBER 2005

14-16 **First Annual UK-Southeast USA Symposium on Structural Genomics and Proteomics of Membrane- and Metallo-proteins** at the Georgia Center for Continuing Education, Athens, Georgia, Program Chair, B. C. Wang. **http://www.bmb.uga.edu/uk-seusa/**

### NOVEMBER 2005

3-5 **63rd Pittsburgh Diffraction Conference -PDC '05**, Argonne National Laboratory, **www.pittdifsoc.org.**

6 –10 **Sociedad Venezolana de Cristalografía** (SVCr) is planning a full day session at the next congress of **Sociedad Venezolana de Química** (SVQ), Mérida, Venezuela. An advanced course on Powder Diffraction will be conducted as a satellite activity of the Congress. For more information, please contact: Graciela Díaz de Delgado: **diaz@ula.ve** (SVQ-SVCr meeting) or Miguel Delgado: **migueld@ula.ve** (PD course).

19 **Canadian Light Source 8th Annual Users' Meeting** at the University of Saskatchewan, Canada.

### JANUARY 2006

26-27 **Advances in Protein Crystallography, Conference & Exhibition,** South San Francisco, CA **www.ProtCrystConf.com.**

### JUNE 2006

9-18 **Structural Biology of Large Molecular Assemblies**; 38th crystallographic course at the Ettore Majorana Centre, Erice, Italy. **www.crystalerice.org/futuremeet.htm**

### JULY 2006

22-27 **ACA Annual Meeting, ACA 2006, Sheraton Wakiki, Honolulu, Hawaii.**

### AUGUST 2006

4-6: **Satellite Conference of ECM-23, Mathematical and Theoretical Crystallography,** Katholieke Universiteit Leuven, Belgium**, http://www.lcm3b.uhp-nancy.fr/mathcryst/leuven2006.htm**

### JUNE 2007

7-17 **Engineering of Crystalline Materials Properties: State-of-the-Art in Modeling, Design, and Applications**, the 39th crystallographic course at the Ettore Majorana Centre, Erice, Italy.

### JULY 2007

**ACA Annual Meeting, ACA 2007,** Salt Lake City, Utah. Local Chair, Christopher Hill.

## Contributors to this issue:

**Khalil Abboud, Bryan Chakoumakos, Vadim Cherezov, Ed Collins, Marcia Colquhoun, Philip Coppens, Lachlan Cranswick, Radu Custelcean, Zbigniew Dauter, Louis Delbaere, Jeffrey Deschamps, Howard Einspahr, David Eisenberg, Maryam Farshid, Jeanne Fauci, Andreas Förster, Frank Fronczek, Tom Furnas, Travis Gallagher, Tamir Gonen, Tamara Hamilton, John Hart, Chad Haynes, Chris Hill, Douglas Ho, Mark Hollingsworth, Andy Howard, Madeleine Jacobs, Mariusz Jaskolski, Christian Jelsch, Alwyn Jones, Lisa Keefe, Judy Kelly, Chuck Kissinger, Cheryl Klein, Gerard Kleywegt, Tom Koetzle, Jeannette Krause, Harold Kroto, Susan Krueger, Desigan Kumaran, Paul Langan, Claude Lecomte, James Leonard, Theodora Leventouri, Eric Libra, Barbara Macareno-Shaw, Andrew Mesecar, Wladek Minor, Peter Müller, Dean Myles, Theyencheri Narayanan, Pappannau Thiyagarajan, Allen Oliver, Sinem Ozyurt, Kevin Parris, Chandra Patel, Arwen Pearson, Vitalij Pecharsky, Alberto Podjarny, Jane Richardson, Howard Robinson, Michael Rossmann, Gabby Rudenko, Michael Sawaya, Arthur Schultz, Karl Seff, Tom Selby, Charlie Simmons, Janet Smith, Ward Smith, Peter Steele, Peter Stephens, Jack Tanner, Alex Taylor, Brian Toby, Liang Tong, Iris Torriani, Michael Wiener, Vivien Yee.**

**Special thanks to Local Committee members Eric Libra, James Leonard, Peter Steele, Sinem Ozyurt, Maryam Farshid and Barbara Mascareno-Shaw for the group photographs of session speakers.**

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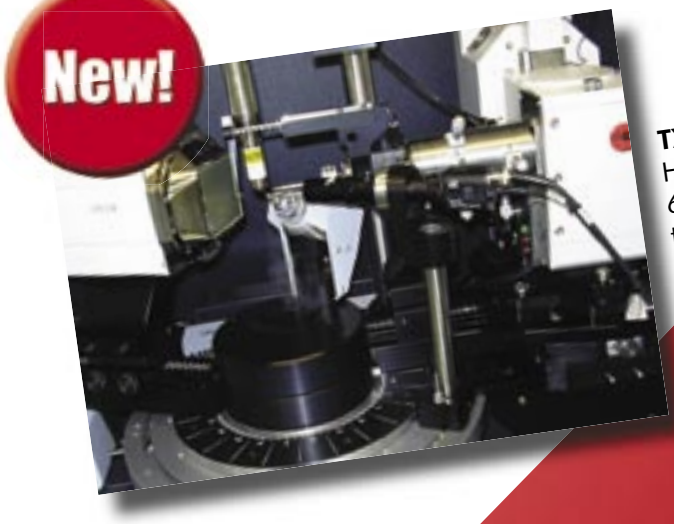


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