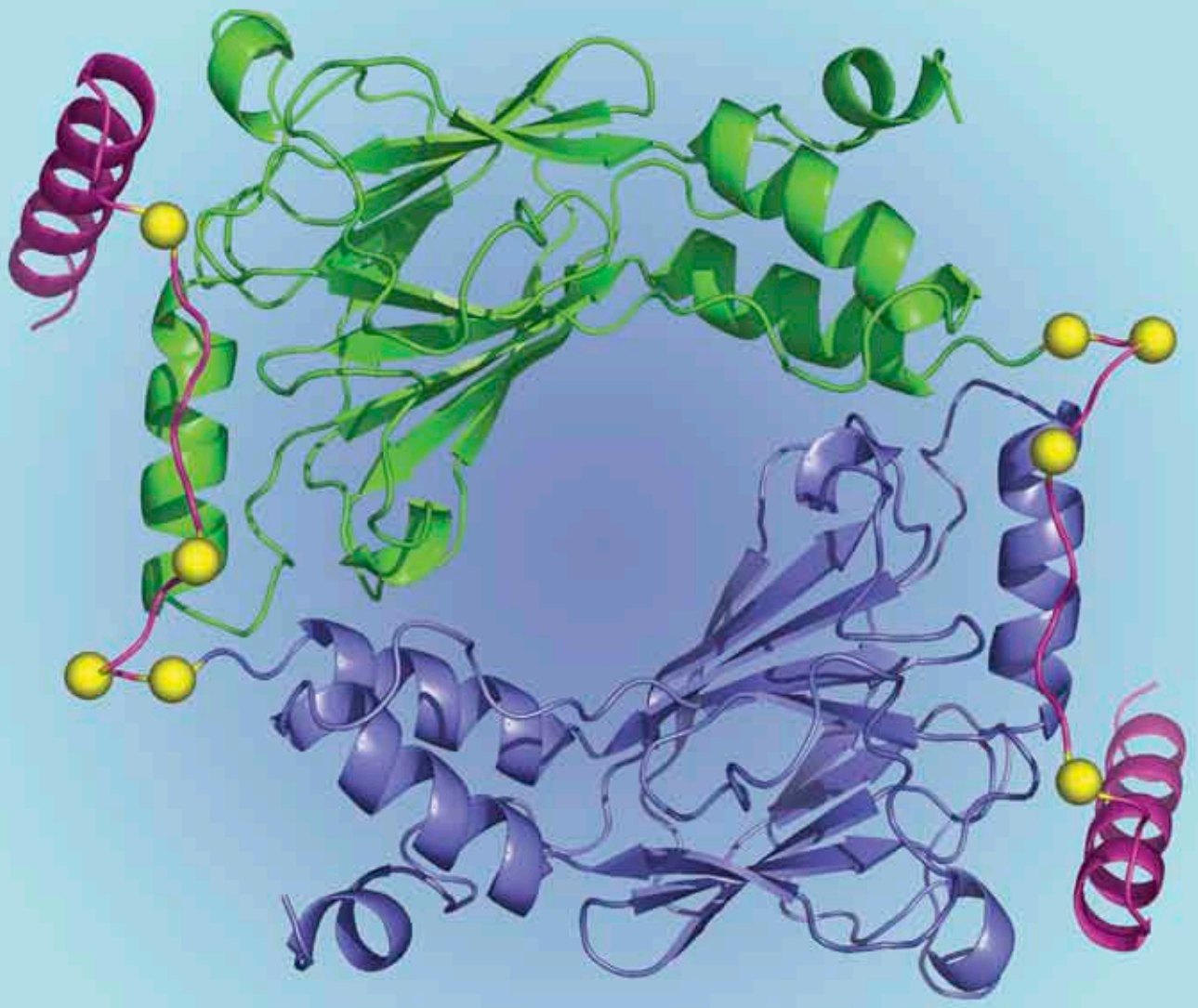
ACA RefleXions

American Crystallographic Association

Number 3
Fall, 2008



The 2008 ACA Meeting in Knoxville, TN

Bruker **AXS**

X8 PROTEUM

The Ultimate Structural Biology System

When you need the best system for Structural Biology, the Bruker X8 PROTEUM offers high-throughput screening AND superb high resolution data in one uncompromising package.

- With our MICROSTAR family of generators, you can rely on the extremely intense micro-focus X-ray beam coupled with the ultra-bright HELIOS optics to handle everything from small crystals to large unit cells
- With over 1000 CCD detectors installed, we know how to optimize the PLATINUM[135] detector for speed, sensitivity, size and dynamic range to give you the best data possible in the home lab
- Our KAPPA goniometer's high precision mechanics allow you to orient the sample along any axis in reciprocal space, while having easy access to mount, cool or anneal your crystals

Get the best data, get the fastest system, get the power to solve your structures – X8 PROTEUM.

www.bruker-axs.com • 1-800-234-XRAY • info@bruker-axs.com

think forward

Crystallography

American Crystallographic Association

ACA RefleXions

ACA HOME PAGE: **www.AmerCrystalAssn.org**

Cover: see page 16.

IRF-5, reported by Bill Royer in the New Structures Session, 2008 ACA Meeting.

Table of Contents

Contributions to ***ACA RefleXions*** may be sent to either of the Editors:

Connie (Chidester) Rajnak
4210 Old Field Trail
Kalamazoo, MI 49008
tel. 269-342-1600
fax 716-898-8695
conniechidester@earthlink.net

Judith L. Flippen-Anderson
3521 Launcelot Way
Annandale, VA 22003
tel. 703-346-2441
fax 716-898-8695
flippen@rcsb.rutgers.edu

Please address matters pertaining to advertisements, membership inquiries, or use of the ACA mailing list to:

Marcia J. Colquhoun, Director of Administrative Services
American Crystallographic Association
P.O. Box 96, Ellicott Station
Buffalo, NY 14203-0906
tel: 716-898-8692; fax: 716-898-8695
marcia@hwi.buffalo.edu

Deadlines for contributions are: February 1 (Spring), May 1 (Summer), August 1 (Fall) and November 1 (Winter)

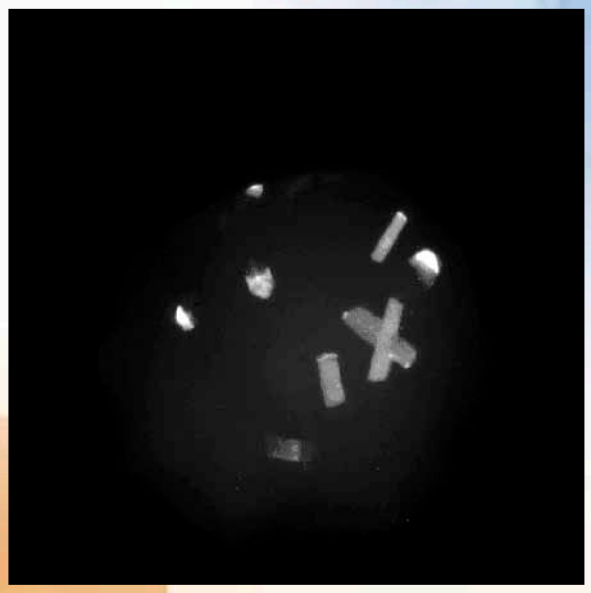
ACA RefleXions (ISSN 1058-9945) Number 3 2008. Published four times per year in the spring, summer, fall and winter for the membership of the American Crystallographic Association, P.O. Box 96, Ellicott Station, Buffalo, NY 14205-0096. Membership in the ACA includes a non-deductible charge of $1.75 from membership dues to be applied to a subscription to the ACA Newsletter. Periodicals postage paid at Buffalo, New York. POST-MASTER: Send address changes to ACA, P.O.Box 96, Ellicott Station, Buffalo, NY, 14205-0096.

See what U'V been missing!

Leading With Innovation

Desktop Minstrel™ UV crystal imaging for protein crystallography

Visible light image



Ultraviolet light image

Screen your crystals quickly, accurately and automatically with both visible and UV light

www.Rigaku.com/automation

Rigaku

Rigaku Americas Corporation phone: (281) 362-2300 e-mail: info@Rigaku.com
Rigaku Europe phone: +[44] 1732 763367

I finished this column just after returning from the very successful XXI IUCr Congress in Osaka, Japan. About 2600 participants attended the meeting, which celebrated the 60th Anniversary of the IUCr. With two Plenary Lectures, 36 Keynote Lectures, and nearly 100 Microsymposia spread over seven parallel sessions in 7 days, there was something for everyone at the meeting. A highlight of the opening ceremony was the presentation of the Ewald Award to our own David Sayre of Stony Brook, NY who was awarded the eighth Ewald Prize for the "unique breadth of his contributions to crystallography, which range from seminal contributions to the solving of the phase problem to the complex physics of imaging generic objects by X-ray diffraction and microscopy, and for never losing touch with the physical reality of the processes involved." Another memorable event was the closing banquet where we were treated to a fantastic evening of Japanese cuisine and music, and where we had the opportunity to visit with friends from around the world. An unexpected but pleasant surprise for the evening came when our IUCr president, Yuji Ohashi, entertained us with the singing of "Sukiyaki".

I also attended the three evening sessions of the IUCr General Assembly. It is at these sessions that the new IUCr President and new members of the IUCr Excecutive Committee are elected, the new members of the various Commissions are confirmed, and the host city for the future IUCr meeting is selected. I can report that Sine Larson, former General Secretary and Treasurer of the IUCr (formerly of Denmark and now France), was elected as the new IUCr President; Peter Colman (Australia) was elected Vice-President, and Montreal, Canada was selected as the host city for the 2014 IUCr Congress. Four new members of the IUCr Executive Committee were also elected. Two of the nine nominees were from the US, but unfortunately neither was elected, leaving the US without a representative on the next IUCr Executive Committee. The ACA, along with the ECA (European Crystallographic Assocication) and the AsCA (Asian Crystallographic Association) are the three Regional Associates of the IUCr. Louis Delbaere of Canada was elected to serve a six-year term and will be our communication link to the next IUCr Executive Committee. The USNCCr proposed several amendments to the by-laws for the Assembly to consider, one of which would have guaranteed a representative of each of the three Regional Associates on the Executive Committee, but all the proposed amendments were voted down. Look for a report from Jim Kaduk and the USNCCr to find out more about these issues.

On the ACA front, you will find more coverage of the Knoxville meeting in this issue of *RefleXions*. As I noted in the summer issue, a personal highlight for me was the opportunity of over 350 members of the ACA to take a field trip to ORNL to tour the new ultra-high-intensity (1.4MW) Spallation Neutron Source. Special thanks again to Al Ekkebus and the folks at ORNL for their hospitality and being such gracious hosts and tour guides.

Another personal highlight was being able to present the 2008 ACA Patterson Award to Bi-Cheng (B.C.) Wang, (see pages 8 and 27). I have known B.C. for many years and it was a great honor to present the award to him with so many of his family members in attendance.

On other fronts, we are busy making plans for our meeting in Toronto next July. Jim Britten, Program Chair, has been working with the SIGs to put the program in place and David Rose is our Local Chair for the meeting. The format for next year's meeting will be slightly different and we hope that will add to the enjoyment of the meeting. The ACA Awards scheduled for presentation next year are the Buerger, Warren and Etter Awards. The Buerger Award will go to Michael James, University of Alberta, and Shih-Lin Chang of National Tsing Hua University in Taiwan will receive the Warren Award; the full citations will be in the next issue of *RefleXions*. The Etter Early Career Award will to Svilen Bobev, University of Deleware, (see page 10). Our upcoming meetings will be in Toronto, July 25-30, 2009; Chicago, July, 2010; New Orleans, May 2011, and Boston, July, 2012.

This is an election year. The Democrats and Republicans have settled on their nominees, and the rehetoric is heating up as we approach the November elections. Connie Rajnak has encouraged several of us to write "advice" to the new President - see the article following this. I remind you that we also have a slate of ACA candidates for our annual elections this fall. My thanks and congratulations go out to Winnie Wong-Ng and Judith Kelly for running for Vice-President, and to Patrick Loll and Carrie Wilmot who are running for Secretary. You can find more information about them and our other candidates in the summer issue of *RefleXions*.

Finally, Grocho Marx once said – "I don't want to belong to any club that will accept me as a member," that is certainly not true for the ACA. I am often reminded how many great members we have in the ACA and how willingly they step up to the plate. Whether it is to serve on an award committee, or program or local committee, it is the dedicated efforts of our members that make the ACA such a superb organization. I want to encourage members to contact me, or any member of Council with ideas for improving the operation of the ACA or our annual meetings.

Marv Hackert

Correction:

The editors regret the error in one of the formulas on the cover of the summer issue. In the 4th expression down the final *H* should be *H - K*, not H_K *i.e.* $F_H = \theta_H \sum_K F_K F_{H-K}$

Editor's note: We do not know whether John McCain or Barack Obama will be elected, but it is a safe bet that either man could benefit from good advice from scientists. With this in mind, I solicited contributions from some of our members. A copy of this article has been forwarded to the science advisors of both men -- to Donald Lamb, Professor of Astronomy and Astrophysics at U. Chicago, the convenor of the Obama Science Committee chaired by Harold Varmus, President of Memorial Sloan-Kettering Cancer Center and formerly Director of NIH; and to Douglas Holtz-Eakin, Senior Policy Advisor for John McCain. Holtz-Eakin was formerly Director of the Greenberg Center for Geoeconomic Studies and Volcker Chair in International Economics at the Council on Foreign Relations, and before that he was the Director of the Congressional Budget Office. I have since thought of many others that I wish I had asked to contribute; perhaps we could run a second column in the winter issue since it will arrive before the inauguration of our next President. So please do respond to either Judy Flippen-Anderson or to me with your sensible and practical advice. We would especially welcome some contributions from younger ACA members. Connie Rajnak

America has always depended on the exchange of skills between her new immigrants and those already here. The Pilgrims' Fathers set this precedent when they learned from the Indians about the use of American plants for food as they taught the Indians about farming implements, building techniques and horses. Later there were waves of immigrants such as the Irish, the Scandinavians, the Jews from Russia, the Chinese railroad workers, the displaced scientists from Hitler's Germany and others, all of whom contributed to the growth of this country and all of whom were grateful for those who had come before them. At this time many scientists from China, India and other countries are clamoring to come to the US or are anxiously struggling to remain here. At the same time our supply of young scientists and engineers is dwindling. It would benefit us and these scientists to welcome them with open arms as had been done in the past. Indeed the current US policy is destroying our technological lead. Not only would a change of visa policy be good for all parties, without a change the US will soon (perhaps in the next 25 years) become a second rate country in terms of its technology and hence its economy as a whole.

Michael Rossmann

Last year, I had a chance to attend a gala performance by a team of thirty young ladies from three high schools in Beijing, China. (They were here on a student exchange program.) These young women were all very talented and captivated the audience with their artistry in dances, songs and instrumental music. Afterwards, we had an opportunity to talk with the students. When asked if they intended to pursue performing arts, we heard the most amazing answers - *they are all going into science and technology.* Mr. President, if the US does not increase scientific support for our students, and fails to encourage our students to study science, we will be in imminent danger of losing the scientific and technological advantage we now claim. Other countries will soon surpass us! Please be aware of the seriousness of this problem, and make sure that the people you appoint are competent to develop sound strategies and take appropriate actions.

Winnie Wong-Ng

Horace Mann felt that the common school was "the greatest invention of man." I would urge the next president to rediscover and re-imagine this magnificent invention, and to make real improvements in our nation's educational system, all the way from preschool to university and beyond. We cannot thrive except through the efforts of a well-educated citizenry.

Patrick Loll

Addressing the challenges facing our country and the world will require a pulling together of the American people in ways probably not seen for 60 years. The next president needs to be a real leader who can focus our attention and galvanize us to work on the daunting issues that confront us - energy, the economy, our environment. Further, he will need to inspire us to work together with faith and trust in our fellow citizens. The best thing he could do to ensure this happens is to appoint people in his administration who are competent, honest, and effective. The sacrifices and changes needed to deal with our big problems will be a lot easier to make if we trust the people leading us and believe in their dedication to working for the common good.

Ron Stenkamp

Mr. President, may I have a quiet word with you? It seems hardly necessary to further belabor the point that science and research is important to national purpose, to our health and well being, security and defense, energy needs, economic growth, agriculture, international competitiveness, and so on. Our government leaders have been told this so many times that they easily recite it back to us, and in fact they generally do whenever they are invited to address our national conferences. They also know equally well that to promote scientific research and continue US dominance in science it is essential that we generously fund scientific research, independent scientists, centers of excellence, and major scientific facilities. This is now a given. I have faith that, being wise and prudent men, either Mr. McCain or Mr. Obama would listen to scientific advisors who have an appreciation for science and the trust of the scientific community.

So, beyond this, what I would advise is that although the quantity of funding for science is important, - how those dollars are appropriated

is even more important. Over the past 20 years at least I have had little argument with how much has been given science. By my standards, (I'm a Scotsman and we may remember that copper wire was invented by two Scotsmen arguing over a penny), US taxpayers have been exceedingly generous with the funding they provided to science, and this regardless of the political party responsible. I have, however, had serious arguments with how those dollars were allocated and spent. Many of the precious resources directed toward science have, frankly, been squandered or misappropriated.

The funds designated for science should not be redirected internally by universities to support non-scientific enterprises (through indirect cost mechanisms); they should not be used to establish job programs for scientists and engineers (see the International Space Station); and they should not be used to buy votes by subsidizing special interests in the private sector (see Congressional earmarks). I would be the last one to suggest additional bureaucracy, more oversight or more layers of regulation. However, I would be among the first to demand greater efficiency, concern, and accountability of public servants at all levels of government with regard to the success and value of the science they watch over. A million dollars well placed and used wisely is worth a billion dollars carelessly allocated and spent. Marshall the resources we already have in play and direct those with the utmost care and economy.

To this end, I implore you to allow more scientists into the higher reaches of government. Attorneys and economists and media experts do not have a monopoly on intelligence, wisdom, or the ability to make clear decisions. Scientists, at least experimentalists, are fairly practical intelligent people who live close to reality. Use them more than has been done in the past. Listen to what they have to say, so long as they can get beyond their own politics.

Finally, I shall emphasize what almost everyone already knows but often represses. It won't hurt to say it again. Science and mathematics education and training in the United States is a shambles. Teachers, in number and training, are inadequate to the task, the curricula is incoherent, funding is haphazard, and innovation is stifled. Were it not for immigrants, we would hardly have enough science students at most high schools and colleges to generate a decent class size. There are very few scientific figures today of national stature and if students today were asked to name a prominent academic scientist, I fear most would reply "Indiana Jones."

Thank you, Mr. President, for so patiently listening to and tolerating my rant.

Alex McPherson

Our country has too many serious challenges for our federal government to delay any longer; we must step up to the plate and address these in real terms. High energy consumption coupled with too much dependence on foreign oil; lack of basic health care even as costs spiral upward; our social security system; our shaky economy; the increasing gap in income between the wealthy few and everyone else; and the need to reassess our foreign, environmental, immigration and education policies. These are not Democratic or Republican issues, but US citizen issues, and many of them will require working with other nations as global partners to find solutions.

Scientists are used to working together to solve problems; they choose the best people for the job and ignore political affiliation. I urge you to utilize this valuable resource and develop ways that our scientists can work with congress and the administration to find viable solutions to these difficult problems. Accordingly, the crux of my advice is to urge an approach that emphasizes cooperation between parties and with other nations and to address these issues in a meaningful way rather than with "band-aid" patches. Scientists are prone to brainstorm: toss lots of ideas on the table, openly discuss the merits of each, and then move forward. In that spirit let me put on the table my personal views on two economic issues that we urgently need to address.

High energy prices: I cringed when I heard politicians during the primary campaign advocating decreasing federal taxes on gasoline as a way of temporarily dealing with the high cost of gasoline. The main problem is that we consume way too much oil. It appears that "we" are only willing to give up our gas-guzzlers when gasoline is over $4/gallon. Our government should have taken steps decades ago to decrease our consumption of non-renewable energy sources, and should have supported the development of alternative, renewable energy sources. We should support higher federal taxes on gasoline and use these tax revenues to support the development of renewable energy sources and to rebuild the infrastructure: highways; bridges; improved mass transportation; help for cities. Workers and businesses who need to drive as part of their job should receive tax breaks to compensate for the higher fuel costs, but we should discourage huge SUVs making frequent runs to the grocery store to pick up a gallon of milk. Wouldn't it be better if our auto industry could focus the talents of its engineers to design and develop fuel-efficient cars? How crazy is it that we have factory workers being laid off due to the cut back in the demand for SUVs while people are signing up on waiting lists for high quality, often foreign, fuel-efficient hybrids?

Social Security: It seems that we have a Social Security system in place that is more like a pyramid scheme than an actuarially sound retirement program. The current program has a genuine retirement component mixed with a social welfare benefit. Retirement plans are well understood in the financial sector; welfare programs are used by governments to address social ills. Why not just separate the two? Have a truly universal retirement plan by collecting social security payments from everyone; have the fund managed the way the Ivy League endowment funds are - these have generated good returns; allow some investment options depending on risk tolerance, and then pay out what each person is entitled to based on the performance of their portfolio. In parallel with this could be a new welfare program to supplement the benefits of low income retirees. Transitioning to such a system would eliminate the dependence of social security on the relative sizes of the future work force vs. retiree group, and make the retirement benefit something that future generations can count on in a way they can understand.

cont'd, next page

We need leaders in Washington that can lead and not simply react to a crisis after the fact. We as individuals, businesses, and agencies need to accept responsibility for our actions and not expect a bail out whenever we make a poor decision or investment. We need to restore America's image in the world community. We need a spirit of cooperation, we need solutions, and we need action. Scientists can and will help – if given the chance to answer the call for involvement.

Marv Hackert

My advice to a US President who wants a world in which it is possible for all people to sustain a decent living standard and quality of life is to be sure to invest in a balanced science portfolio and in science education so that it may play its essential role in enabling this vision. We should put a system in place that enables government to draw upon our science communities to authoritatively provide evidence in their special areas of expertise on issues important for public policy. We need checks and balances that will inhibit decision making based on incomplete or misrepresented data, or simple opinion. As we face a future in which we are challenged by increasingly complex problems that require analysis and understanding at the level of whole systems (e.g. the ecosphere, global markets, the human body), we must have a growing body of foundational knowledge to draw upon. Otherwise technology will not advance fast enough to solve our problems.

Technology has been a powerful force for improving quality of life in our communities, as well as for waging war, since the dawn of human existence. Science, the academic pursuit of understanding our physical universe, has in turn been a powerful driver for technology. The evidence for these assertions was perhaps most apparent in the 20th century when advances in physics, materials science and biology yielded phenomenal breakthroughs in our ability to produce and distribute energy, develop our building and transportation infrastructure, diagnose and treat disease, and to wreak previously unimaginable destruction in anger and in fear. The evident successes of science and technology in the 20th century came at a dizzying pace that has led many to assume that technology can provide security and solve any problem that arises. This assumption is patently not true, especially as we look around the globe and see technology struggling to resolve issues that are political and social in nature. The growing (mis-)assumption that science can be the servant of whatever a society decides are its technology needs has driven public policy toward ever increasing investments in short term applied research and development; skimming the cream from the existing body of scientific knowledge while under investing in the development of new foundational knowledge. This short term view is coupled with increasing focus on fashionable priorities or plain old fashioned pork-barreling. The result is a lack of balance in our science investment portfolios; this has had a negative impact on science education.

Nonetheless science and technology should have essential roles to play in securing our future. We need to develop scientists who enquire for the sake of understanding alone, and who can work alongside those with urgent short term objectives. We need to balance fundamental research with applied research and development so that we may have those future Einstein's. Only then will science drive the truly breakthrough solutions we need.

. *Jill Trewhella*

Mr. President, It's January 2009, and you're working on a $3T budget. The economy is growing at a rate of 1.5%, with an inflation rate of 3.5%, and a predicted deficit of $400B. In spite of the pressure to reduce spending, I urge you to to work with Congress to return funding of worthy programs and to put large federal housing, healthcare, and social service programs on a firm financial footing. Growth in the economy will reduce the deficit, and foster growth in the industrial sectors. Research and education are the fuel for this growth.

President Bush proposed a 5% increase in defense spending while cutting other programs. We do need to modernize our military, but a substantial portion of that 5%, should be directed at R&D. Think of the savings if alternative fuels were used in the military. Think of safe nuclear energy and used (so-called "spent") fuels as energy alternatives.

Funding priorities for education and research need to be realigned. Programs such as *No Child Left Behind*, and *Reading First*, may not be worth funding, but we do need to fund K-12 and higher education to the levels of a decade ago. Federal funding is appropriate because it is an investment in our future; it should not be entirely left to the management of states, counties, and cities, who are suffering from a crippled economy. In addition, program grants for all students like *Even Start* ($10M), grants to states for education technology, technology careers, and incarcerated youth, and funding to keep under-represented students in school, should be re-instated. Funding for college scholarships ($50M) should be reinstated. Retraining programs for older citizens and veterans are necessary; these are proven programs.

Research and health services funding should be restored and increased. Again, this is an investment in our future. President Bush sought to cut more than $400M from the CDC budget, including programs to detect and control infectious diseases ($27M) and chronic disease prevention and health promotion ($28M). Bush further sought to slash $300M from a program that trains 4,700 pediatricians and pediatric specialists at children's teaching hospitals, at a time when pediatric specialties, such as rheumatology and pulmonology, face critical shortages. Cuts in these programs may reduce the budget deficit, but only at the cost of undermining the health of the nation.

Finally, fully fund the US research agencies -NSF, NIH, and the national laboratories. Leave management of these agencies to their directors; micro-management and "populist" funding of special programs is not in the best long term interest of this country. Fund basic research as well as specialized programs. A *Manhattan Project* for alternative energy resources is a good idea. Encourage private sector proposals like the *Windmill Corridor Project* of T. Boone Pickens, the DOE Biomass Projects, and Carbon Geo-sequestration.

Bernie Santarsiero

Bruker AXS

APEX II QUAZAR

The User-friendly High-intensity Microfocus X-ray Source System for Chemical Crystallography

The APEX II QUAZAR features the IμS™ X-ray Source, a 30 W microfocus sealed tube with high brilliance and high-performance focusing Quazar™ multilayer optics, the latest type of Montel mirror. The combination of source and optics exceeds the performance of traditional 5.4 kW rotating anode sources. Unlike rotating anodes, the IμS has no moving parts and does not require water cooling. It has a very long lifetime, does not require maintenance, is extremely stable, easy to replace, and has a low cost of ownership. Available for both Mo and Cu radiation.

Combine the IμS with the best CCD detector available for a high performance system with amazingly low maintenance.

Contact us for more details and a system demonstration!

www.bruker-axs.com • 1-800-234-XRAY • info@bruker-axs.com

think forward

Crystallography

The 2008 Patterson Award to Bi-Cheng Wang

The **A. Lindo Patterson Award** was presented to **Bi-Cheng Wang**, Professor in the Department of Biochemistry and Molecular Biology and Ramsey/Georgia Research Alliance Emminent Scholar in Structural Biology at U. Georgia, for *significant contributions to the methodology of structure determination from single isomorphous replacement or single-wavelength anomalous scattering data and for its impact on structural biology*. B.C. accepted the award at the **Patterson Symposium** organized in his honor at the Knoxville ACA Meeting, where he.gave the keynote address on *Resolution of Phase Ambiguity in Macromolecular Crystallography*. B.C. received his B.Sc. in Chemical Engineering in 1960 from National Cheng Kung University, Taiwan. He then entered the University of Arkansas (Fayetteville) and earned a Ph.D. in Chemistry in 1968 (Wally Cordes, advisor). B.C. and his new bride Johnna moved to Caltech in 1968 where he worked with Dick Marsh. In 1970, B.C. joined the University of Pittsburgh as a research associate and held various positions there and at the VA Medical Center in Pittsburgh. In 1986, he was appointed Professor in the Departments of Crystallography and Biological Sciences at U. Pittsburgh. In 1995, B.C. moved to the University of Georgia (UGA) as a Ramsey Georgia Research Alliance Eminent Scholar in Structural Biology. At UGA, B.C. organized institutions in seven southeastern states with the concept of building a synchrotron beamline at the APS in Chicago. In 1997, the plan became a reality with the start of the construction of the Southeast Regional Collaborative Access Team (SER-CAT) with B.C. as the Director. SER-CAT is now one of the most successful beamlines in the world. In 2000, B.C. became the director of the Southeast Collaboratory for Structural Genomics (SECSG), one of nine PSI-1 NIH centers. Many of the practical advances in the use of sulfur phasing for protein structures were accomplished during this period. In addition, B.C. was heavily involved in the ACA Summer School in Crystallography as co-director at Pittsburgh (1993-1996) and director at UGA (1997-2001). (***See page 27 for a report on the Patterson Session***.)

Top Photo:, ACA President Marvin Hackert (left) and Bi-Cheng Wang. From the left, in back: Marvin Hackert; Tony and Melissa Wang; Bi-Cheng and Johnna Wang; Joyce and Andy Wang; in front: Matthew Wang, Lucas Wang and Brianna Wang. Photos courtesy of Marvin Hackert and Youzhong Guo.

John Rose and Gary Newton

Radu Custelcean Receives 2008 Etter Award

The **Margaret C. Etter Early Career Award** was presented to **Radu Custelcean** by ACA President Marvin Hackert (at right) at the **Etter Award Symposium** during the Knoxville ACA Meeting. Radu is a Research Staff Member in the Chemical Sciences Division at Oak Ridge National Laboratory. The award citation praised him *for his creative research in crystal engineering of novel and functional metal organic framework structures for selective ion binding*. Radu's keynote lecture: *Manipulating Hydrogen Bonds in Crystalline Solids: From Etter's Rules to Anion Recognition* was very well received. ***(See page 5 of the spring 2008 ACA RefleXions for details about Radu's background and accomplishments, and see the report on page 26 on the Etter Award Symposium.)***

2009 Martin J. Buerger Award to Michael James

The 2009 **Buerger Award**, which recognizes *mature scientists who have made contributions of exceptional distinction in areas of interest to the ACA* will be presented to **Michael James**, Professor, University of Alberta, at the 2009 ACA Meeting in Toronto.

2009 Diffraction Physics Award to Shih-Lin Chang

Shih-Lin Chang, Professor, Department of Physics, National Tsing Hua University will receive the **Bertran E. Warren Diffraction Physics Award**, which recognizes *an important recent contribution to the physics of solids or liquids using x-ray, neutron, or electron diffraction techniques* at the 2009 ACA Meeting in Toronto

Special Smposia will be organized in honor of the Buerger and Warren awardees, at which they will deliver the keynote lectures.The full citations, and background information for both awardees will appear in the winter issue of *ACA RefleXions*.

2009 ASBMB Awards

The American Society for Biochemistry and Molecular Biology announced that **David Davies, John Kuriyan, and Douglas Rees** are among the seven recipients of their 2009 awards, which will be presented at the 2009 Experimental Biology Meeting next April. **David Davies**, NIDDK, National Inst. of Health, will present the **Herbert Tabor / *J. Biol. Chem.* Lecture.** Davies studies the structure and mechanism of action of the Toll-like receptors of the innate immune system as well as other proteins such as anti-anthrax lyase.

John Kuriyan, HHMI Investigator and Chancellor's Professor at U. California, Berkeley, will be honored with the **Merck Award** for his exceptional achievements in and contributions to structural biology. Kuriyan is being recognized for his studies of the structure and function of protein kinases and of c-Src, c-Abl, and CaMK11.

Douglas Rees, HHMI Investigator and Roscoe Gilkey Dickinson Professor of Chemistry at Caltech and Adjunct Professor of Physiology at the UCLA School of Medicine, will give the **Fritz Lipmann Lecture**. This award, given every other year, recognizes investigators who have made conceptual advances in biochemistry, bioenergetics and molecular biology. Rees has made pivotal contributions to understanding the structure of integral membrane proteins, membrane transport mechanisms, and metalloenzyme structure and mechanism.

2008 NSSA Prizes

The Neutron Scattering Society of America awarded their 2008 prizes at the May meeting of the ACNS in Santa Fe, NM.

Sow-Hsin Chen, Professor of Nuclear Science and Engineering. MIT, received the 2008 **Clifford G. Shull Prize** *For seminal contributions to understanding the dynamical properties of supercooled and interfacial water using neutron scattering techniques, and for an exceptional record of training young scientists in the use of scattering techniques to solve topical interdisciplinary problems in complex fluids and soft matter.* The Shull Prize in Neutron Science honors Clifford G. Shull, who received the Nobel Prize in 1994 with Bertram N. Brockhouse. Chen received his PhD from McMaster U. under Brockhouse. Chen joined the faculty of MIT in 1968 and was promoted to full professor in 1975. He has received numerous honors and awards; is a fellow of APS, AAAS, and the Japan Society for the Promotion of Science, and is an Academician of the Academia Sinica.

The **NSSA Sustained Research Prize** went to **Frank Bates**, Regents Professor and Head of Chemical Engineering and Materials Science at U. Minnesota *for his pioneering SANS experiments that probe the structure and thermodynamics of polymeric fluids and block copolymers*. Bates' research has involved the use of polymeric materials as test beds for studying a wide variety of critical phenomena encompassing critical scaling, Lifschitz points, and order-disorder transitions. Among his many honors, he won the APS Dillon Prize (1989) and Polymer Prize (1997), and the Materials Research Society's David Turnball Lectureship (2004). He was elected to the National Academy of Engineering and is a fellow of the AAAS. He was President of NSSA from 1996 to 1999.

The **NSSA Science Prize** recognizes major scientific accomplishment or important scientific contribution within the last 5 years to one who has received their doctoral degree within the past 12 years. **Seung-Hun Lee**, U. Virginia, was awarded the 2008 prize *for his innovative and insightful neutron scattering studies of frustrated magnetic systems*. Lee made inportant contributions to understanding the disordered spin liquid state by using inelastic neutron scattering to study the frustrated magnet $ZrCr_2O_4$ where semi-classical (S=3/2) spins form the most frustrating lattice: a network of corner-sharing tetrahedra. Lee and co-workers developed a model that explained their data in terms of a hidden order in the spin-liquid phase. See **www.neutronscattering.org/NSSAPrizes** for more details.

Rich Wins Welch Award

Alexander Rich, the William Thompson Sedgwick Professor of Biophysics at MIT, has won the 2008 Welch Award in Chemistry. The $300,000 award is given annually by Houston's Welch Foundation to foster and encourage basic chemical research. The award will be presented at a banquet in his honor this October. Rich was given the award for his pioneering work on nucleic acids. He was the first to carry out DNA-RNA hybridization, which opened the door to understanding how information can be transferred from DNA to RNA. He also discovered left-handed DNA, which in ensuing years has proven to be extremely important to biological systems and immunology. Rich is currently researching the biological roles of the left-handed form of DNA, called Z-DNA for its zig-zag backbone, and the proteins that bind to it.

2008 ICDD Awards

The International Centre for Diffraction Data 2008 awards were presented at the 57th Annual Denver X-Ray Conference (DXC) in August. The **Birks Award** went to **René Van Grieken**, Professor, U. Antwerp, Antwerp, Belgium. Rene is Editor-in-Chief of *X-Ray Spectrometry*, web-editor of *spectroscopyNOW*, Associate Editor of *Journal of Radioanalytical and Nuclear Chemistry*, and is on the editorial boards of several other journals. **Jeffrey Dann**, Global Tungsten & Powders, Towanda, PA received the **McMurdie Award**, which recognizes distinguished work to improve the Powder Diffraction File; for the past 34 years, Jeff has helped edit the Metals & Alloys portion of the ICDD Powder Diffraction File database.

Photo by Colleen Lewis, G.T.& P.

2009 Etter Early Career Award to Svilen Bobev

Photo by Kathy F. Atkinson, U.Delaware.

Svilen Bobev will be presented with the award and will give the keynote lecture at a symposium organized in his honor at the ACA Annual Meeting in Toronto next July. Svilen is an enormously talented and extraordinarily productive crystallographer and solid state chemist. He joined the Department of Chemistry and Biochemistry at U.Delaware in 2004 as a tenure-track Assistant Professor; he had previously worked at LANL for two years as an independent Director's Award Postdoctoral Fellow. A native of Bulgaria, he received his Ph.D. from Notre Dame in 2002 working with Slavi Sevov. Svilen' s research addresses important issues concerning the relationships between the composition, structure, and electronic structure of complex intermetallic compounds and their properties. He conducts detailed experimental studies on new magnetic materials based on the Rare-Earth elements (RE) and the heavier carbon analogues, Si, Ge and Sn. These metals from the lanthanide family have many scientific and industrial uses as catalysts, phosphors, lasers, hydrogen storage materials, and most importantly - as superior performance magnets for applications in magnetic bearings, switches, and DC motors. The unique magnetic/electronic properties in in RE-Si and RE-Ge systems inspire Svilen in his efforts to understand electron and spin interactions; characterization of the relevant compounds by x-ray diffraction is fundamental to this undertaking.

Since his arrival in Delaware Svilen has quickly built a functioning laboratory and assembled a highly productive research group: one postdoctoral fellow, two graduate students, and a variable but substantial number of undergraduate researchers. Under Svilen's leadership this relatively small group has proven extraordinarily productive. He has published 53(!) papers describing research results from his Delaware lab already, which, together with the 33 papers resulting from his previous work, constitutes a remarkable body of work for someone so early in his career. Svilen's contributions have been recognized by an ACS-PRF grant award, and an NSF Career Award in support of his work.

Klaus Theopold, University of Delaware

2009 Aminoff Prize to Sheldrick and Bricogne

The Royal Swedish Academy of Sciences announced that the **Gregori Aminoff Prize in Crystallography** will be awarded March 31st, 2009 to **Geroge Sheldrick**, and **Gérard Bricogne**, *for their contributions to theoretical development and methodological implementations in crystallography.*

George M. Sheldrick at the Georg-August Universität, Göttingen, Germany *developed the software package SHELX, which early began to dominate structural determinations of smaller molecules. Through continuous development and enhancement SHELX has today become a powerful and easy-to-use tool within all scientific disciplines that uses structural information - from mineralogy to molecular medicine. Because SHELX is free to use it has had a tremendous impact among researchers worldwide.*

Gérard Bricogne, Global Phasing Ltd, UK, *has contributed to the development of crystallographic methods and thus revolutionized the research area for determination of the structure of biological macromolecules. In 1978 he succeeded for the first time in determining virus structures at an atomic scale. He then founded the non-profit company Global Phasing Ltd, which today, free-of-charge, provides researchers with software for crystallographic methods.*

Rigaku Americas Corporation will award summer travel bursaries (to be used for travel to a scientific conference) in the amount of $500 each to five post-doctoral fellows who provide the most compelling explanation as to how they intend to pursue a career in structural biology. Applications must be received by May 4, 2009 (www.rigaku.com/protein/postdoc.html).

New ASBMB President, Greg Petsko

Gregory Petsko, Gyula and Katica Tauber Professor of Biochemistry and Chemistry at Brandeis University took over the presidency of the American Society for Biochemistry and Molecular Biology in July. See the July issue of *ASBMB Today* for their profile article, which characterizes him as combining the qualities of "blunt honesty, valuing a diverse education, recognizing the importance of working with others, and daring to wade into new territory."

New Executive Director of CCDC

The Board of Governors of the Cambridge Crystallographic Data Centre announced that **Colin Groom** has been appointed Executive Director starting October 1st 2008, following the retirement of **Frank Allen**. Groom is currently Head of Computer-Assisted Drug Discovery and Investigative Chemistry at UCB in Cambridge, UK. Colin Groom has a BSc in biotechnology and a PhD in protein crystallography from the University of Leeds, and has held postdoctoral appointments at Leeds and at Massey University, New Zealand. Since then, he has worked in the pharmaceutical industry, joining Pfizer Global Research, Sandwich, UK in 1994, where he established a protein crystallography facility, and then established and headed up molecular informatics units in both Sandwich and in the USA. He joined UCB (Celltech) in November 2002. Groom was Co-Director of the *International School of Crystallography: Molecules to Medicines via Crystallography* in Erice, Italy in 2008. He has been at the forefront of applying structural information to drug design and has a number of publications and patents in this area. He is a Fellow of the Royal Society of Chemistry, a member of the British Crystallographic Association, and has contributed to BBSRC and EPSRC activities as a panel member. He is on the Editorial Boards of *Current Computer-Aided Drug Design* and *Current Drug Discovery Technologies*.

Christopher Cahill will be spending part of the '08-'09 academic year in Wales at the University of Cardiff as a Fulbright Scholar. Chris is currently an Associate Professor of Chemistry at the George Washington University in Washington, DC. His research efforts include small molecule crystallography of f-element materials, and he intends to use this opportunity to do some spectroscopic studies. He'll be working with Simon Pope and Kenneth Harris and also hopes to visit some of his UK crystallography colleagues.

New CEO at Rigaku Americas

Rigaku Americas Corporation of The Woodlands, TX, announced June 30th that **Wes Hardenburg**, its CFO since 2000, has been succeeded **Paul Swepston** as President and CEO. Paul Swepston, who joined Rigaku in 1996, will continue in a strategic capicity as Senior Advisor to the CEO of the parent company Rigaku Corp. in Tokyo. Hardenburg joined Rigaku through the acquisition of Osmic Inc. in 1999.

MicroMax™-007 HF

Leading With Innovation

The most common reaction of a new owner of a Rigaku MicroMax-007 HF generator

Performance comparison

	RU-H3R	MicroMax-007 HF	
Optics	Blue	VariMax™ HF	VariMax VHF
Relative usable flux* through 0.1 mm aperture	1	**20**	**50**
Beam size at crystal position	0.38 mm	0.21 mm	0.10 mm
Generator power	5.4 kW	1.2 kW	
Focal spot	0.3 mm x 0.3 mm	ϕ = 0.07 mm	

* With Cu $K\alpha$ radiation

http://www.rigaku.com/generators/micromax007.html

Your X-ray source
for protein crystallography!

GREEN Solutions

Rigaku

Rigaku Americas Corporation phone: 281-362-2300 e-mail: info@Rigaku.com
Rigaku Europe phone: +[44] 1732 763367

Highlights of Council Meetings

The ACA Council met just prior to the annual ACA meeting in Knoxville, TN to conduct business, and plan for the pending meetings. Key topics that were discussed are summarized here.

Canadian Representative Report: New Council member **Jim Britten** reported that The NRC (National Research Council) of Canada has as the main topic of their next meeting the Montreal bid for the 2014 IUCr Congress, which will be presented at the IUCr Congress in Osaka. (***note: see pages 3 and 16 for reports on elections in Osaka***). He also said that there are plans to have a 2 or 3-day chemical crystallography workshop at McMaster as a satellite to the annual meeting of the Canadian Society for Chemistry in Hamilton in May. Jim reported that arrangements for the 2009 ACA meeting in Toronto are well underway, and there was much discussion about avoiding passport issues for attendees.

Financial Matters: **Rao** presented his report on 2007 taxes and accounts including monthly office bills. The initiative to have an operating endowment that is one year's worth of office expenses was begun in 2007, and we are about 1/3 of the way in building this endowment account. Rao provided a meeting costs analysis, with real costs vs registration fees and attendance figures. He also calculated fixed vs variable costs; fixed costs comprise about 76% of the total meeting budget. The Finance Committee (**S.N. Rao, Bernie Santarsiero, Judith Flippen-Anderson, Marcia Colquhoun and Jen Shepard**) met May 29th, and on behalf of the committee, Rao presented a list of recommendations. The ensuing discussion resulted in several decisions by Council.

From the left, in back: Bernie Santasiero, Alan Pinkerton, Marv Hackert, Bob von-Dreele, Bill Duax. In front: S.N.Rao, Marcia Colquhoun, Iris Torriani, Jim Britten.
Photo courtesy of Marv Hackert.

Council decided the program budget should be set at $32,000 plus $4,000 for the enhancement fund. The Program Chair will decide allocations of both funds. Costs to support the sessions have been escalating, so the Council decided to cap the overall costs for the sessions program. Council will require session organizers to select a minimum of 40% of their speakers from abstracts submitted for the meeting. While we favor inviting outside experts to present state-of-the-art results, we also encourage the selection of ACA members in each session. Speakers in the *Transactions Symposium* will be required to submit a manuscript and/or an annotated presentation, which must be approved by the *Transactions* editor prior to registration reimbursement. The ACA will exploit use of the internet and of prepared presentations (such as PowerPoint) as alternative ways to archive our materials. The financial aspects of workshops were also discussed and it was agreed that in the future workshops should be more uniformly structured, with greater consistency in fees, lunch and coffee breaks, income distribution, etc. and that each should receive the same "perks." The ACA Treasurer will review workshop budgets and expenditures, and the Continuing Education Committee will select and approve workshop topics.

Council also met frequently during the meeting; business matters were discussed at breakfast and lunch meetings where the standing committees and SIG chairs reported on activities for the last year and presented plans for the upcoming year. The ACA business meeting, open to all members, was held after sessions on Wednesday, and was attended by approximately 100 members. The minutes for most meetings are posted on the ACA web site. Finally, a Planning Session for the 2009 ACA meeting was held the day following the meeting with past and future Local and Program Chairs, SIG representatives, and Council in attendance.

Marcia Colquhoun (in Lisa Keefe's absence)

2009 Dues are Due

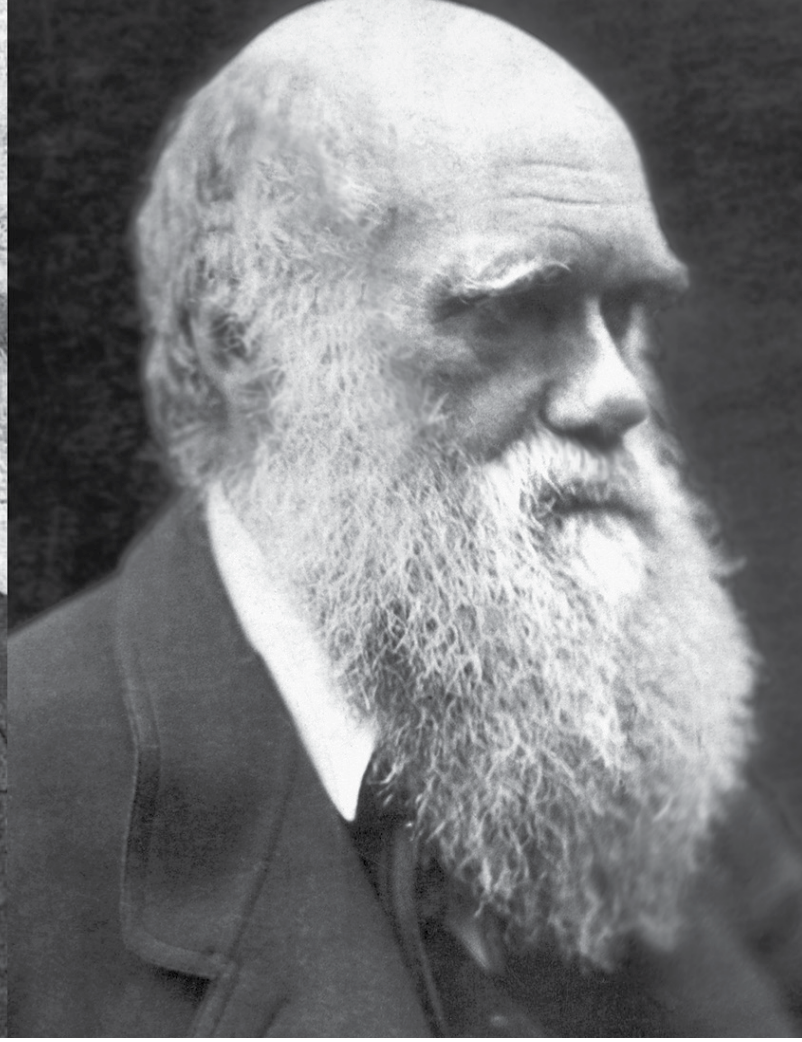
Please renew promptly and remember to support your favorite ACA Award Funds. NOTE: It is now possible to renew online at www.AmerCrystalAssn.org.

Reminder: Please VOTE!

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

Art in Crystallography

We are accepting entries to the **2009 Art in Crystallography Contest** in the form of images emailed to either Editor (**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 consist of a small monetary award and a banquet ticket at the annual meeting. Winning entries will be posted on the web and will be displayed at the ACA Meeting. (Winners are not required to attend the meeting). We will also feature images in *ACA RefleXions* from time to time. Please let us know if you are interested in being a judge.



Are Wyatt instruments the product of intelligent design or evolution? Yes.

There's no debate about it. We *invented* commercial laser light scattering, then built on it to develop a complete family of related instruments, all of which provide unparalleled performance for our customers.

Today, Wyatt's light scattering products are *the* most widely recognized on earth. Thousands of chemical, biotechnology, pharmaceutical, academic and government laboratories around the world rely on them to characterize macromolecules of all kinds. Just some of these examples have been published in *over* 2,500 peer-reviewed articles based on their work using Wyatt instruments. These articles, application notes and other feedback in the scientific environment have helped our 15 PhD scientists and other innovators to refine our instruments more rapidly to meet our customers' needs. And oftentimes, the result is an unprecedented new product.

So, was it intelligent design or evolution? Precisely.

For more information call 805.681.9009 or visit us at **www.wyatt.com**.

Wyatt Technology CORPORATION

DAWN HELEOS. The most advanced commercial light scattering instrument for macromolecular characterization.

Optilab rEX. The refractometer with the greatest combination of sensitivity and range.

ViscoStar. The viscometer with unparalleled signal-to-noise ratios, stable baselines and a 21st-century interface.

Eclipse. The ultimate system for the separation of proteins and nanoparticles in solution.

DynaPro. The world's most popular dynamic light scattering instrument for protein and nanoparticle characterization.

2010 Fankuchen & Trueblood Award Call

Nominations are solicited for the **Fankuchen Memorial Award** and the **Kenneth N. Trueblood Award**. Both awards will be presented at the annual ACA meeting in Chicago in July, 2010. 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, 2009**. 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 Memorial 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: **2007: Frank Herbstein; 2004: Alexander McPherson; 2001: James Stewart; 1998: Elinor Dodson; 1995: Jenny Glusker and Kennth Trueblood; 1992: L. D. Casper; 1989: David Sayre; 1986: Michael Rossmann; 1983: Lyle Jensen; 1980: David Harker; 1977: Dorothy Hodgkin; 1974: André Guinier; 1971: Martin Buerger.**

The **Kenneth N. Trueblood Award** was given for the first time in 2004, to **Richard E. Marsh**; the second award went to **Angelo Gavezotti** in 2007. 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 B_{12} is one example. Ken-Trueblood 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.

2010 E.A.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. Elizabeth Armstrong Wood (1912-2006) was 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*); **Oliver Sacks** (Albert Einstein College of Medicine) and, in 2007, **Lisa Randall**, Theoretical Physics, Harvard.

On the Cover: A New IRF Structure at the 2008 ACA Meeting

Interferon regulatory factors (IRFs) play key roles in host defense mechanisms including innate immunity and tumor suppression. IRF-5 is a potential drug target since human mutations of IRF-5 have been directly associated with the pathogenesis of a number of autoimmune diseases. The cover image is from **William Royer**, Professor of Biochemistry and Molecular Pharmacology at UMass. Medical School. Bill reported on his new IRF-5 crystal structure in the ***New Structures*** session at the Knoxville meeting in June. The interferon regulatory factor (IRF) 5 dimer is shown as a ribbon diagram with one subunit in green and one in blue, except for the C-terminal autoinhibition/dimerization region, which is shown in purple for both subunits. Likely phosphorylation sites are shown as small yellow spheres at their alpha-carbon positions. Comparison of the IRF-5 structure with that of monomeric autoinihibited IRF-3 strongly suggests a common mechanism for activation of the interferon regulatory factors in which phosphorylation triggers a dramatic structural transition of the C-terminal region, resulting in IRF dimerization and exposure of the CBP binding site. These two effects are key steps leading to the transcriptional activation of type I interferons and other target genes. (Chen, et al. (2008) *Nature Structural and Molecular Biology*, in press.)

Editor's note: see the New Structures report on page 31. Bill Royer's work was initiated at UMass by his colleague, Kai Lin, who tragically died of cancer in 2006. See page opposite.

News from Canada

Canadian crystallographers met during the ACA meeting in Knoxville this June; in attendance were: David Rose, Chair; Ian Swainson, Acting Secretary in Pawel Grochulski's absence; John Tse; Wilson Quail; Megan Barker; Louis Delbaere; Gary Enright; Pam Whitfield; Michael Murphy; Michael Jennings; Emil Pai and Rob Thorne.

From left: David Rose, Ian Swainson, Jim Britten.

The position of Secretary is up for election this year, with (so far) Pawel Grochulski and Michael Murphy nomininated. Additional nominations will be solicited. There was much discussion about the 2009 Toronto ACA Meeting and about the bid in Osaka to hold the 2014 IUCr Congress in Montreal. ***See the following note***. The members of the Canadian National Committee of the IUCr are: Louis Delbaere, Chair; Jim Britten, Vice-Chair; Joe Schrag, Secretary; Marie Fraser, Treasurer; S. Cameron; Lachlan Cranswick and Pamela Whitfield.

Jim Britten, Program Chair and David Rose, Local Chair of the Toronto Meeting are collaborating closely. The Local Committee is looking for people to help with fundraising and communication; they are also seeking a workshop coordinator and a webmaster. They are strongly encouraging Canadians to submit abstracts so as to have good Canadian representation on the program. John Tse suggested that the Toronto meeting include a session on minerals (a strength in Canada). David Rose will discuss the minerals session idea with the Synchrotron SIG (the Canadian Division is not a SIG and cannot sponsor sessions). The Materials SIG is another possibility; Pam Whitfield will follow up on this. Various financial support possibilities were discussed including the possibility of support for a session on neutrons. There was also discussion about "getting in the queue" to hold another ACA meeting in Canada – possibly on West coast (Vancouver/Victoria, Calgary/Edmonton) or the East coast (Halifax). Ottawa or Quebec City are also possibilities if Montreal is not successful in its bid for the 2014 IUCr Congress.

David Rose reported his experience attending the annual meeting of the National Postdoctoral Association in Boston in April, 2008. He thinks the ACA might want to consider the benefits of becoming a Society member. In addition, a small Canadian contingent met at the NPA to discuss forming a Canadian section, preliminarily called CAPS (Canadian Association of Postdoctoral Scholars). The main goals of the NPA are to present ideas on consistent definition and treatment of postdoctoral scholars, areas of interest/training for PDS in areas such as career development and alternative career options, training/workshops on mentorship and other issues, advocacy for science policy, and other issues of interest to Postdoctoral Offices at various Institutions

David Rose, Ian Swainson and Jim Britten

News from the IUCr Congress in Osaka: The XXIII IUCr Congress and General Assembly (2014) will be held in Montreal, Quebec, Canada. In other good news, Canadians have very good representation on the IUCr Commissions. Hanna Dabkowska is chair of Crystal Growth and Characterization of Materials; Lachlan Cranswick will chair Crystallographic Computing, and is on the Crystallographic Teaching commission; Lynne Howell is a member of Biological Macromolecules; Pamela Whitfield will chair Powder Diffraction; Patrick Mercier is on Inorganic and Mineral Structures; Pawel Grochulski is on Synchrotron Radiation; and Farideh Jalilehvand is on the Commission on XAFS. Jim Britten is a member of the International Program Committee for the 2011 Madrid IUCr meeting.

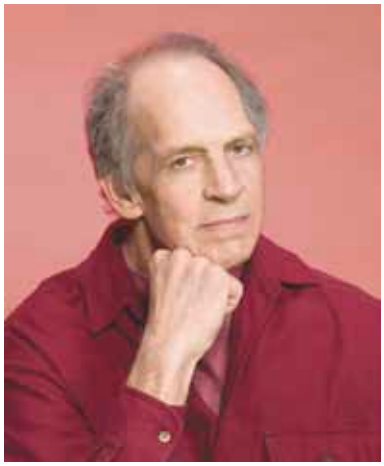
See Marv Hackert's President's Column, page 3, for other news of the IUCr Meeting.

Kai Lin 1965 - 2006

Kai Lin came to the United States from Taiwan to study Biochemistry in 1985. He received his BS in Biochemistry from SUNY Binghamton in 1988 and his PhD in Biochemistry from SUNY Stonybrook in 1993 under the mentorship of Simon Pilkis. His thesis *Structure/function studies of 6-Phosphofructo-2-kinase/fructose-2,6-bisphosphatase* was about a key enzyme in sugar metabolism and therefore important in understanding diabetes. He spent his postdoctoral training under the mentorship of Robert Fletterick at UCSF, and while there he received the prestigious Life Sciences Research Foundation Award from the Burroughs Wellcome Foundation. He became a crystallographer during his postdoctoral years and continued his research in sugar metabolism by investigating the structural basis for allosteric regulation in glycogen phosphorylase. In 1998 he joined the faculty at the University of Massachusetts Medical School, where he rose to the rank of Associate Professor of Biochemistry and Molecular Pharmacology. The underlying theme of his research was to understand the structural, functional and molecular mechanism of phosphorylation, one of the most fundamental chemical signals in biology. When he began his own laboratory, his research interests shifted to understanding how phosphorylation impacts signal transduction in the TGF-β pathway. During his career he had nearly 30 publications, many in top tier journals. His passion for science was exceeded only by his passion for his family, especially his wife and colleague, Suvana, and his young daughter, Shannen.

A close colleague described Kai's major contribution to the TGF-β field as his elucidation of the structural basis for how intracellular signals are transduced by Smads, an important protein complex involved in the progression of cancers. Although the field is highly competitive, Kai was an exceptional structural biologist who fully committed his research career to understanding this system by correlating structure with biological function. In addition to providing an understanding of how Smads function at the structural level, Kai showed that IRF complexes, which are key players in the anti-viral response of cells and in cancer biology, show a remarkable structural similarity to Smads despite a lack of sequence homology. This structural convergence was unexpected and has broad ranging implications for our understanding of the overall mechanisms of signal transduction.

Celia Schiffer, UMass Medical School



Stephen Ernst 1939 - 2008

Stephen Richard Ernst was born in Wichita, Kansas on July 22, 1939 and died in Austin on May 16, 2008 at the age of 68. He earned his BS in chemistry from Carnegie Tech. in 1961, worked as an analytical chemist for four years for the Civil Service, and then earned his PhD in Physical Chemistry from the University of Utah in 1972. Following postdoctoral work in x-ray crystallography at the University of Pittsburgh (1972-76) and Michigan State (1976-78), he joined the protein crystallography teams in the Chemistry Department at The University of Texas at Austin in 1978. He quickly established himself as an expert on both the hardware and software aspects of protein crystallography, serving as Systems Manager for the protein crystallographic computing facility, and Manager for the operation and maintenance of the x-ray facility. Steve was co-author of over two dozen scientific publications, including important contributions in elucidating the structures of amino acid decarboxylases and protein toxins such as ricin.

Marvin Hackert

Contributors to This Issue

Bob Bau, Jeff Bell, Eric Bennett, Jim Britten, Craig Brown, Chris Cahill, Ed Collins, Marcia Colquhoun, Joseph Curtin, Lee Daniels, Zbyszek Dauter, Graciela Díaz de Delgago, Roland Dunbrack, Howard Einspahr, Anna Gardberg, David Giedroc, Richard Gillilan, Marvin Hackert, William Heller, Ken Herwig, Jason Hodges, Peter Horanyi, Bruce Hudson, Bobby Huether, Greg Hura, Tom Koetzle, Susan Krueger, Patrick Loll, Jamie Manson, Alex McPherson, Peter Müeller, Gary Newton, Bruce Noll, Marilyn Olmstead, Allen Orville, Kanagalaghatta Rajashankar, John Rose, David Rose, Michael Rossmann, William Royer, Bernhard Rupp, Tim Rydel, Alec Sandy, Bernie Santarsiero, Celia Schiffer, Tom Smith, Ron Stenkamp, Vukica Strajer, Ian Swainson, Bob Sweet, Jennifer Swift, Klaus Theopold, Pappanan Thiyagarajan, Jill Trewhella, Bob vonDreele, Carrie Wilmot, Mark Wilson, Winnie Wong-Ng, Dinesh Yernool, Andrey Zheludev.

We gratefully acknowledge the continued support of ACA CORPORATE MEMBERS *and welcome new members.*

Area Detector Systems Corp.
www.adsc-xray.com

Art Robbins Instruments
www.artrobbinstruments.com

ATPS Inc.
www.atpsinc.com

Axygen Biosciences
www.axygenbio.com

Bibliothek Technische Hochschule
Hannover, Germany

Biblioteca Universitaria
Oviedo, Spain

Blake Industries, Inc.
blake4xray@worldnet.att.net

Bruker/AXS
www.bruker-axs.com

Cambridge Crystallographic Data Centre
www.ccdc.cam.ac.uk

Charles Supper Company, Inc.
www.charles-supper.com

Cryo Industries of America, Inc.
www.cryoindustries.com

Douglas Instruments Limited
www.douglas.co.uk

Formulatrix
www.formulatrix.com

Hampton Research
www.hamptonresearch.com

Incoatec GmbH
www.incoatec.de

Jena Bioscience GmbH
www.jenabioscience.com

Korima, Inc.
www.korimainc.com

MiTeGen LLC
www.mitegen.com

Molecular Dimensions, Inc.
www.moleculardimensions.com

Oxford Cryosystems
www.oxfordcryosystems.com

Oxford Diffraction Ltd.
www.oxford-diffraction.com

Rayonix/MAR USA
www.mar-usa.com

RCSB-Protein Data Bank
www.rcsb.org/pdb

Rigaku Americas, Inc.
www.Rigaku.com

TTP Labtech
www.ttplabtech.com

Viscotek Corporation
www.viscotek.com

Wyatt Technology
www.wyatt.com

Xenocs **SA**
www.xenocs.com

We are especially grateful to our Corporate Sponsors of the 2008 ACA Meeting

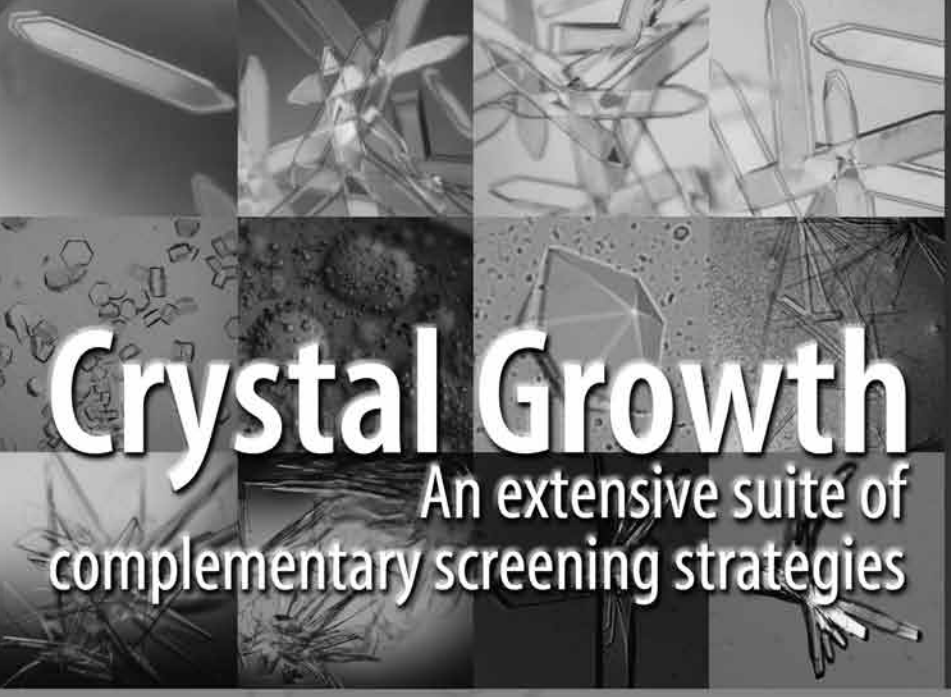
DIAMOND
Bruker AXS
IUCr
Oak Ridge National Lab

RUBY
Area Detector Systems
Hampton Research Corp.
Merck Research Laboratories

SAPPHIRE
Art Robbins Instruments
Bristol-Myers Squibb Pharmaceuticals
Elsevier, Inc.
PartTec, Ltd.
Pulse Ray
Varian, Inc.

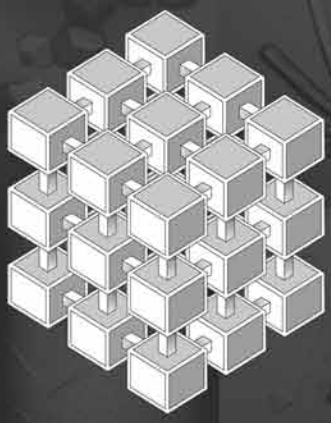
EMERALD
Hoffmann-La Roche, Inc.
Rigaku Americas Corp.
Pfizer Global R&D La Jolla

QUARTZ
Blake Industries
Incoatec GmbH
Oxford Cryosystems
Oxford Diffraction



Crystal Growth

An extensive suite of complementary screening strategies



Molecular Dimensions Limited

Molecular Dimensions Inc.
PO Box 1001
Apopka Florida 32704

UK Tel: +44 (0)1638 782610 Fax: +44 (0)1638 782611
USA Tel: 1877 479 4339 or 407 886 6901 Fax: +1 407 886 4444
Email: enquiries@moleculardimensions.com

MODERN SPARSE MATRIX SCREENS	
JCSG-plus™	Reduced redundancy, increased coverage of both classic and modern conditions.
Morpheus™	**EXCLUSIVE!** **NEW!** A 96 condition screen with original chemistry incorporating 50 low molecular weight ligands associated with almost 34,000 PDB structures.
CLASSICAL SPARSE MATRIX SCREENS	
Structure Screen 1	Explore crystallization space quickly and easily. 50 conditions covering a wide range of pH and precipitants.
Structure Screen 2	Map crystallization space in even more detail. A further 50 complementary conditions.
Mini Screen	Highly efficient protein-based screening. Minimised redundancy and sample-use in this screen of 24 optimised conditions.
3D Structure Screen	**EXCLUSIVE!** Convenient identification of the metastable zone to grow fewer, larger crystals. 24 "nucleation" conditions from the Mini Screen and 24 "backed-off" conditions.
PEG / ION SCREENS	
Clear Strategy Screen™ 1	**EXCLUSIVE!** Have full control of screen solution pH to obtain results that can be easily interpreted. Screen using 6 salts, 4 PEGs, 5 buffers.
Clear Strategy Screen™ 2	**EXCLUSIVE!** A salt screen extension, organic screen and a heavy cation screen provide a flexible complement to CSS 1.
PACT-premier™	Our advanced PEG-ion screen. Systematically test the effect of pH, Anions and, Cations using three different PEGs as the precipitant under pH control.
PROTEIN SOLUBILITY SCREENS	
Stura Footprint	Rapidly screen your protein's solubility curve against a variety of PEGs and salts using the Stura method.
The Solubility Tool Kit™	**EXCLUSIVE!** Determine the crystallization potential of protein salts at net -ve and +ve charge and at the pI with a variety of counter-ions.
NUCLEAR RECEPTOR LIGAND-BINDING DOMAIN SCREENS	
NR-LBD	**EXCLUSIVE!** Data mined from the crystallization of NR-LBDs. 48 unique conditions with various PEGs and carboxylic acids as precipitants from pH 6.0 to 9.0.
NR-LBD extension	**EXCLUSIVE!** A further 48 conditions to extend NR-LBD.
PROTEIN COMPLEX SCREENS	
ProPlex™	96 formulations tailored to the crystallization of protein complexes.
MacroSol™	A Stura footprint style screen for samples of heterogenous solubility such as macromolecular complexes, glycoproteins and proteolysis samples.
MEMBRANE PROTEIN SCREENS	
MemStart™	**EXCLUSIVE!** 48 proven conditions for effective initial screening of membrane proteins. Perfectly complemented by the systematic MemSys screen.
MemSys™	**EXCLUSIVE!** A systematic membrane protein screen to complement Memstart.
MemGold™	**EXCLUSIVE!** The most advanced membrane protein screen available to date.
MemPlus™	**EXCLUSIVE!** A useful addition to MemGold targeting β-barrel type membrane proteins including porins and outer membrane active transporters.
Lipidic-Sponge Phase™ Screen	**EXCLUSIVE!** **NEW!** Ready-to-use screen closely resembling the native lipidic environment. Large aqueous channels able to accommodate membrane proteins with large extra- and/or intra-cellular domains.

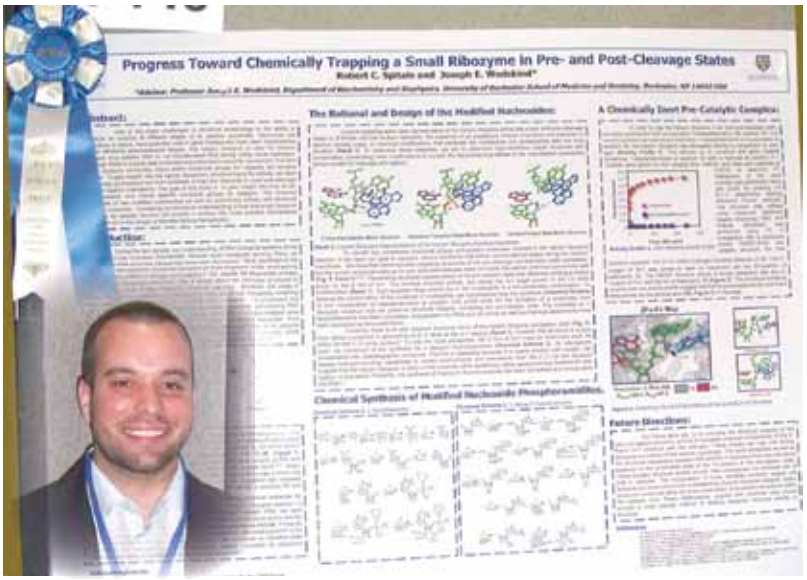
EXCLUSIVE! screens are manufactured under exclusive licenses from academic institutions and are only available from Molecular Dimensions. All other screens have features ***UNIQUE*** to Molecular Dimensions.

See our on-line catalogue for details…

From crystal growth screening to cryo mounting Molecular Dimensions delivers to the demanding standards of BS EN ISO 9001: 2000.

intelligent solutions for protein crystal growth

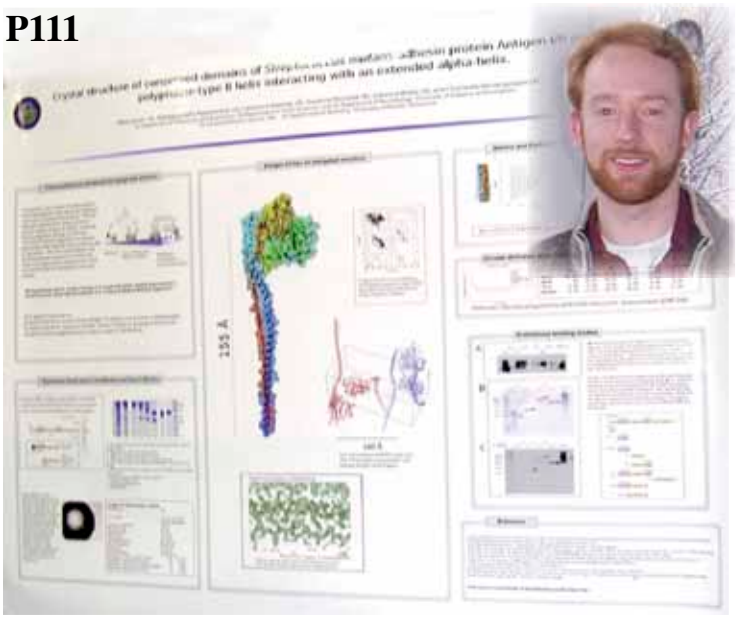
2008 Pauling Poster Awards



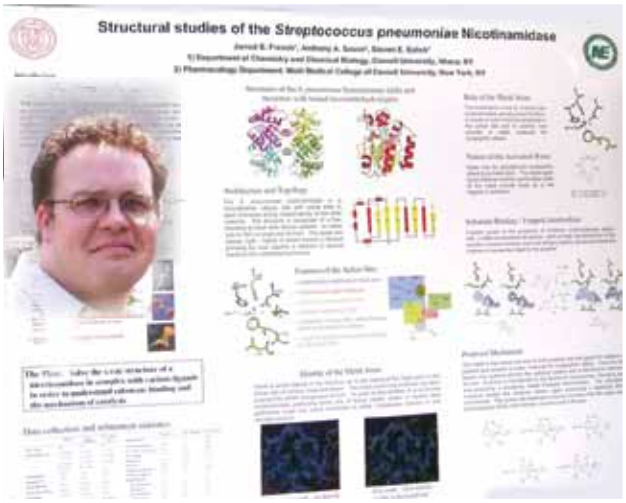
Thirty-two student posters that were eligible for this year's **Pauling/IUCr Prizes** were reviewed by the Pauling Prize Committee: **Thomas Koetzle**, Chair, **Craig Brown, Christina Hoffmann**, and **Allen Oliver**. Each member initially reviewed 8 posters and picked provisional first and second choices from them. The entire committee then judged the eight finalists, interviewing each student at his or her poster. The committee voted and was unanimous in its selection of the top five posters. A second vote was then taken to select the overall winner and was again unanimous.

The finalists were distinguished by the exceptional quality of their science and the attractiveness of their layout, and in their description of their posters and responses to questions from members of the committee. The **IUCr Prize**, which was presented by **Iris Torriani,** went to the overall winner, **Robert Spitale**, U. Rochester, for **P149**: ***Trapping a Pre-Ligation Hairpin Ribozyme Complex by Use of 5'-Deoxy-5'-Fluoro-Guanosine***. Spitale demonstrated exceptional command in his oral presentation. He is studying the binding to the hairpin ribozyme of inhibitors that are designed to help elucidate the mechanism of RNA-catalyzed reversible phosphodiester bond cleavage.

P111



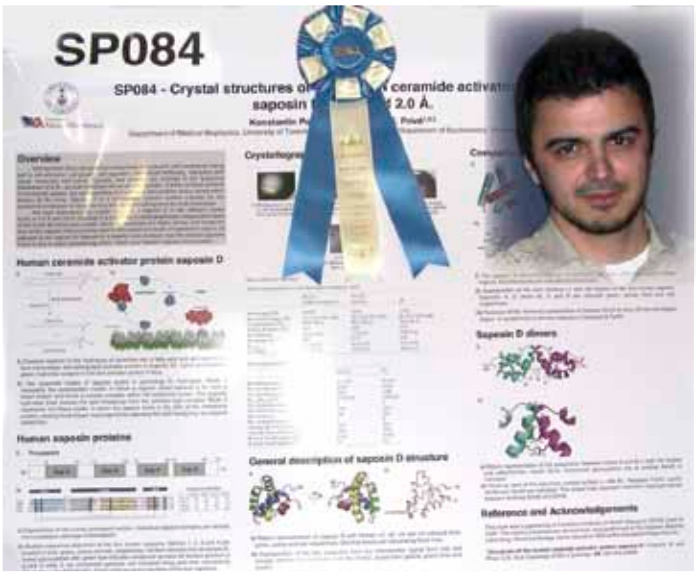
The other winners were: **Matt Larson** U. Alabama, Birmingham for **P111**: ***Crystal Structure of Conserved Domains of Streptococcus mutans Adhesion Protein Antigen I/II Reveals a Polyproline-type II Helix Interacting with an Extended α-helix.*** Larson's striking poster beautifully illustrated his structure of this adhesion protein antigen with its novel extended poly-proline helical domain. In addition to x-ray crystallography, Larson used CD spectra on several domain truncations to probe the relationship between secondary structure in solution and that in the crystal. His results support the hypothesis that the novel extended domain structure in the antigen is important in bacterial tooth adhesion.



Jarrod French Cornell U. for **P141**: ***Crystal Structure of Streptococcus pneumoniae Nicotinamidase with Bound Inhibitor Provided Insight into Mechanism of Catalysis.*** French determined the structure of nicotinamidase from *S. pneumoniae* in the native form and complexed with several inhibitors that he himself synthesized. His results clarify several aspects of the catalytic mechanism, including the role of a +2 metal ion at the active site that appears to activate a water molecule for nucleophilic attack on the nicotinamide substrate. Nicotinamidases are essential for many parasitic microbes, but the enzymes are absent in mammals making them a promising target for a novel class of antibiotic drugs.

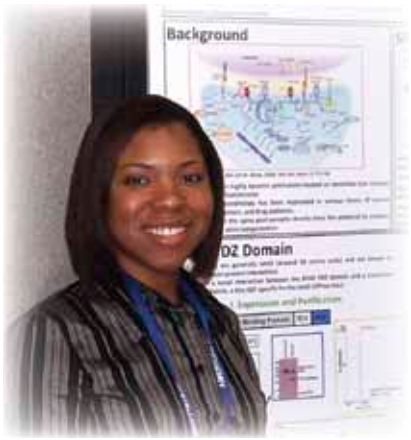
Ilana Goldberg, Georgetown U. for **P207**: ***Characterization of Polymorphic Compounds***. Goldberg, a student in the Swift research group, presented her elegant work in which surface templating techniques were applied in the controlled crystal growth of macromolecules and energetic materials. Her attractive poster highlighted the many techniques she used to characterize the polymorphs obtained in her crystallization studies, including x-ray diffraction and topography, Raman scattering, and Hirschfeld surfaces.

Tobias Beck, Goettingen U. for **P56**: ***A Magic Triangle? Experimental Phasing of Macromolecules with a Triiodo Benzene Derivative***. Tobias presented promising tests of SAD phasing using 5-amino-2,4,6-triiodoisophthalic acid. This molecule was synthesized and then cocrystallized with several test proteins. Trials were performed using the anomalous scattering from the three iodines to successfully phase a number of test data sets.



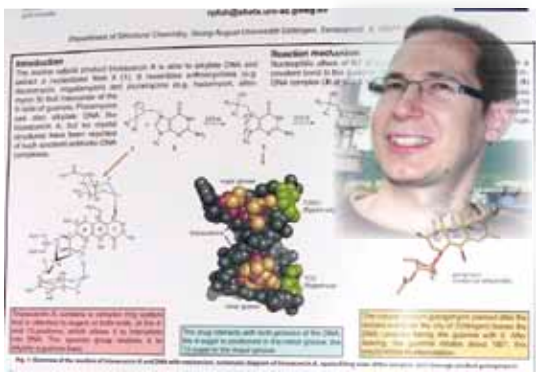
The **Pauling Canadian Poster Prize** for the best student poster from a Canadian Institution went to **Konstantin Popovic** (U of Toronto) for **SP84**: ***Crystal Structures of the Human Ceramide Activator Protein Saposin D at 1.3 and 2.0Å***.

Photo cropped from one taken by Peter Müeller

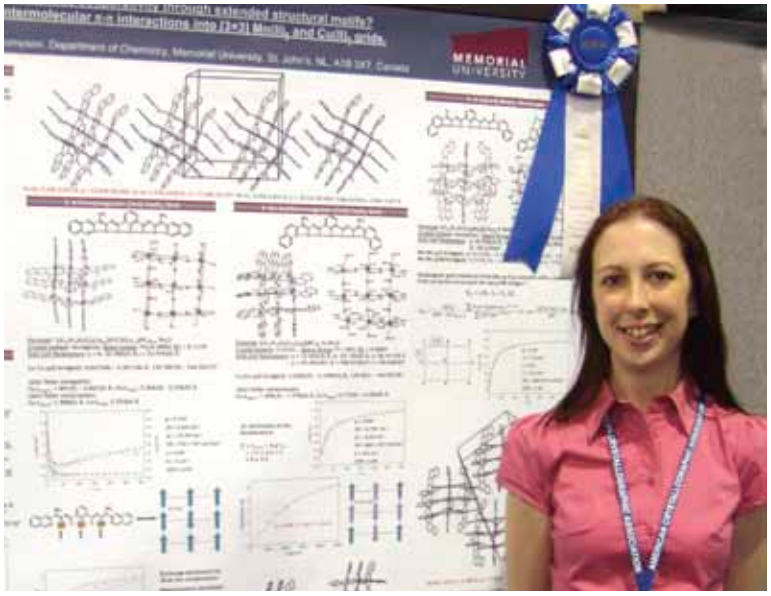


Breann Brown, Brown U. for SP199: ***Molecular Basis for Actin Reorganization by the Neuronal Protein SPAR.***

Pauling Prize Honorable mentions



Roland Pfoh, Goettingen U. for SP97: ***Crystal Structure of Trioxacarcin A Covalently Bound to DNA.***



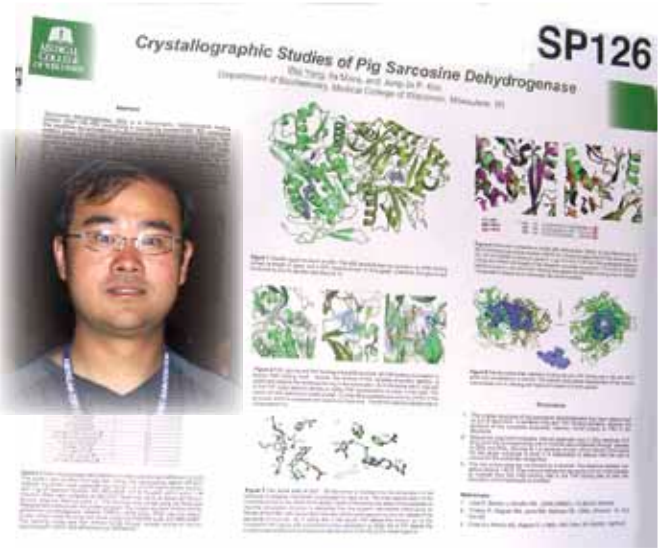
2008 JCC Poster Prize

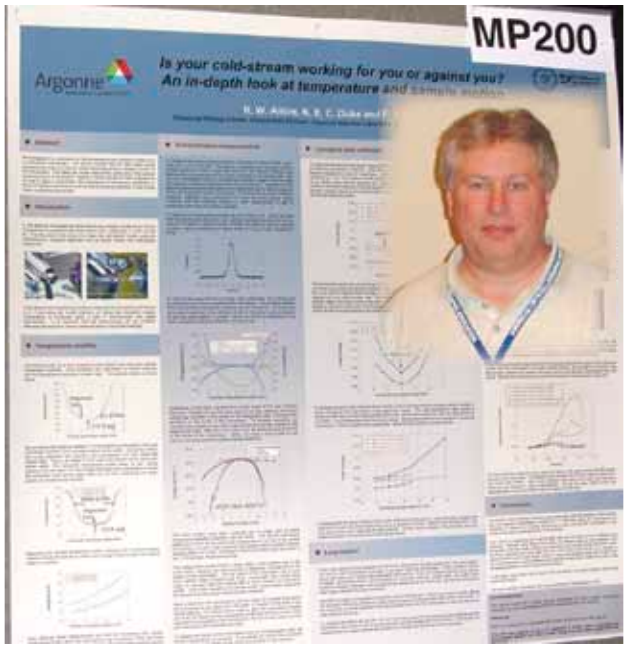
The **Journal of Crystallography Poster Prize** is awarded to the best student poster presented at the ACA Annual Meeting in the areas of chemical crystallography or small molecule structure determination or analysis. The 2008 JCC Prize Committee: **Robert Bau**, Chair, **Victor Young**, and **Xiao-Ping Wang** selected **P182**: ***Long Range Magnetic Cooperativity Through Extended Structural Motifs*** by **Louise Dawe** (Memorial University, St. John's Newfoundland, Canada).

Photo courtesy of Victor Young.

2008 RCSB Protein Data Bank Prize

The **Research Collaboratory for Structural Bioinformatics Protein Data Bank Prize** is awarded to the best student poster presented at the ACA Annual meeting in the area of macromolecular crystallography. This year the RCSB Prize Committee, **Robert Rose**, Chair, **Antonella Longo, Gloria Borgstahl, Rob McKenna**, and **Joseph Wedekind** selected **P126** by **Wei Yong** (Medical College of Wisconsin) ***X-ray Crystallographic Studies of Pig Sarcosine Dehydrogenase***.





2008 Oxford Cryosystems Poster Prize

The **Oxford Cryosystems Low Temperature Prize** is awarded to the poster that best describes work in low temperature crystallography. The judges wish to remind future presenters that, while routine use of cryogenic technology continues to make many landmark crystallographic studies possible, it is the intent of this award to encourage work specifically aimed at low temperature phenomena and techniques. More than half of the posters entered in this competition failed to even cite the temperature at which they were working and so did not qualify for consideration. Presenters also need to be reminded that literature citations and acknowledgments are essential.

The 2008 prize committee, consisting of **Richard Gillilan** (chair), **Henry Bellamy, Elspeth Garman, Joel Harp**, and **B. Leif Hanson**, selected poster **MP200**, ***Is your cold-stream working for you or against you? An in-depth look at temperature and sample motion*** by **Randy Alkire**, **Norma Duke**, and **Frank Rotella** (ANL), as the winner of this year's award. This systematic study revealed that the impact of minor cold-stream alignment variations and sample loop flexibility on data quality can be surprisingly large. The judges felt that this study should motivate widespread rethinking of standard practice at both synchrotrons and home sources.

You've helped us with our research...

...now let us return the favor

With over 20 years experience in developing low temperature devices for X-ray crystallography, we've learnt a lot about our customers.

Keeping in close contact with the crystallographic community has allowed us to listen to your requirements and ideas, adapt our systems to suit and now enables us to offer a broad range of systems to cater for a variety of needs.

For instance, we have developed a wider range of temperatures with our Cryostream Plus and created the Cryostream Compact for optimal alignment with capillary powder samples in smaller enclosures. For those who prefer to use gaseous rather than liquid nitrogen, we have also introduced the Cobra non-liquid Cryostream.

In addition, our excellent reputation for technical support further explains why we are the preferred provider of variable temperature devices to the global crystallographic community.

For further information visit our website at www.oxcryo.com

OxfordCryosystems

Alan Pinkerton giving his Past-President's Address at the Annual Awards Banquet.

The *a capella* *TALKING* Reciprocal Space Blues

Strolling around in reciprocal space
Where ev'ry reflection knows its place
To the law of Bragg we must adhere
To take our place in the Ewald sphere
Lattice points
Symmetry related
Intensity weighted

0 0 2 says to 0 0 3
You're so weak, you're hard to see
Says 0 0 3 to 0 0 2
I think that you've just found a screw
Axis that is
2 sub one
Rotate and move

So a screw operation does the trick
But if I'm weakly here think harmonic
Or Renninger, if you will
Yes, reciprocal space is such a pill
To the uninitiated
But ACA members
See order
Ah! Long range

So point up for a, out for b*
Left for c 'cos you see*
The right hand rules, so get it right
Or chiral left will be chiral right
That's d to l
Or R to S
Thank you Louis,
Or we wouldn't care less

So a photon here and a photon there
Do the Ewald construction 'till we're all there
Then Fourier transform and surprise, surprise
A molecule before your eyes
Bond lengths
Angles
Chemistry heaven

Alan Pinkerton

Photos from the BrukerAXS and Rayonix boat cruises. Clockwise from the top: Alan Pinkerton, Jeannette Krause and Jim Kaduk; Joe Miller and Abe Clearfield (PM); Ima Dix and Elspeth Garman (PM); Marvin Hackert, Bretna Hackert and Anna Gardberg (JP); David Rae and Allen Oliver; and Eva Blanpied and Sue Byram.
Photos courtesy of Peter Müeller (PM), and Jim Pflugrath (JP).

Photo courtesy of Peter Müeller.

2008 ACA Meeting - Knoxville, TN, May 31st-June 5th

The ***Transactions* Symposium on Complementary Methods for Structure / Function Studies of Biomolecules** (see page 29); the **Patterson Award Symposium**, in honor of **Bi-Cheng Wang** (page 27) and the **Etter Early Career Award Symposium** in honor of **Radu Custelcean** (page 26) were meeting highlights. The tour of the new Spallation Neutron Source sponsored by the Oak Ridge National Laboratory was a huge success; an excellent buffet dinner at ORNL was an unexpected bonus. Dinner cruises down the scenic Tennessee River were sponsored by Bruker AXS and by Rayonix on different evenings (see opposite), and the Mentor-Mentee dinner at Calhoun's on the river was very enjoyable. ACA President **Marvin Hackert**, left, presided over the Awards Banquet, and after the awards, Past President **Alan Pinkerton** entertained us with an original semi-musical (but *very* rhythmic) performance appropriate to bluegrass country (opposite page).

The winter issue of *RefleXions* will carry photos from the Mentor-Mentee dinner and the Rigaku-sponsored Fun Run, as well as the reports about the workshops preceding the meeting and from the Travel Award winners.

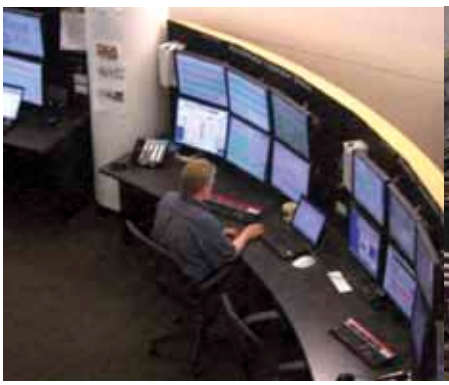
Program Chair **Paul Butler**, left, and Local Chairs **Dean Myles**, and **Jason Hodges** looking relaxed at the President's Reception on the first day of the meeting.

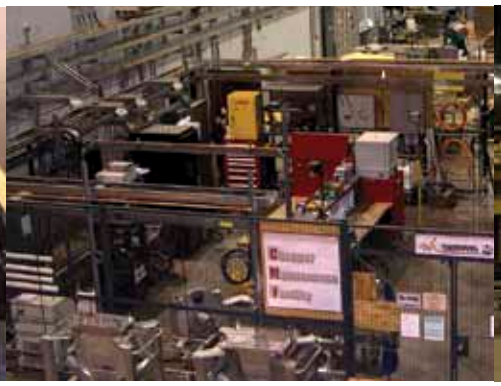
Below, From the ACA office in Buffalo, Administrative Director **Marcia Colquhoun**, **Patti Coley** and **Jennifer Shepard** at the Awards Banquet.

Below, **Paul Butle**r at the Awards Banquet presenting the first ***Transportation Award*** to **Marcia Colquhoun**, in memory of all the logistical problems they overcame.

Photos courtesy of Peter Müeller

Below, scenes from the tour of the Spallation Neutron Source. At left: looking down on their NASA-like command center where the experiments are monitored. Center: big science requires BIG rooms, one of which houses the *Chopper Maintenance Facility*. In the photo on the right below Bob Bau, center, is explaining some of the intricacies of neutron science to colleagues.

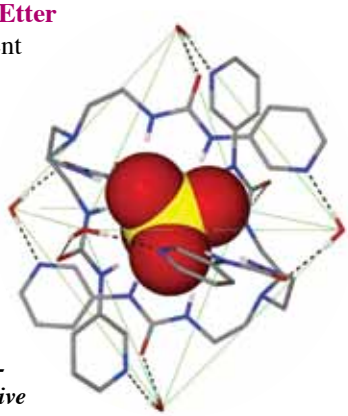




L to r: Jose Antonio Cuesta-Setjo, Christina Capacci, Tamam Baiz, Anna Gardberg, Christine Beavers, Aruna Shankaranarayanan, Radu Custelcean, Megan Barker.

AW.01 Etter Early Career Award

After the presentation of the **Margaret C. Etter Early Career Award** by ACA President Marvin Hackert (*see page 8*), the recipient, **Radu Custelcean**, gave an engaging talk about using *Etter's Rules* to design materials to sequester sulfate selectively.



From Radu Custelcean: Hydrogen-bonded capsule that selectively binds sulfate by 12 complementary hydrogen bonds from the 6 urea groups that internally functionalize the capsule. Selective crystallization of this capsule provides an effective method for the separation of sulfate from highly competitive aqueous anionic mixtures. Custelcean, R., Remy, P., Bonnesen, P. V., Jiang, D.-E., Moyer, B. A., Angew. Chem. Int. Ed. 2008, 47, 1866.

Polymorphism is a topic that all crystallographers face, and the next talk by **Christina Capacci** gathered an attentive audience of both small-molecule and macromolecular crystallographers. Capacci did not disappoint; she provided a solid conceptual background to the issue and presented her work on controlling polymorphism with templated growth and nucleation. **Tamam Baiz** and **Christine Beavers** presented their work on negative thermal expansion materials and M3N fullerenes, respectively, generating interesting Q&A.

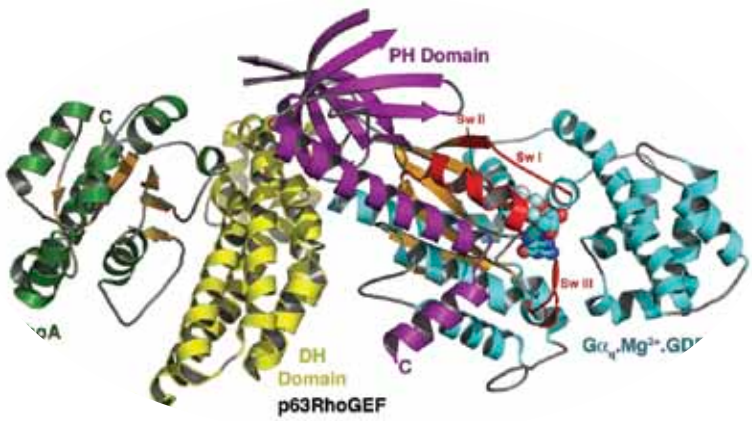
Other talks were more focused on topics of interest to macromolecular crystallographers, beginning with **Aruna Shankaranarayanan**, who received the YS-SIG's **Etter Student Lecturer Award** for her work with Gq coupled receptors.

René Jørgensen described his work characterizing cholix toxin, demonstrating the molecular features responsible for infection by diphtheria, cholera, and whooping cough.

Three techniques shared by the speakers were highlighted. **Jose Cuesta-Seijo** described the use of MPD as a refolding agent for inclusion bodies, as well as his technique of "aging" protein crystals at 4°C for 4 days to enhance diffraction. **Megan Barke**r took microseeding to its logical conclusion by microseeding from one condition of an initial crystallization screen into all of the empty conditions, thus obtaining crystals more suitable for diffraction experiments.

Anna Gardberg

Anna Gardberg (left) presenting the Student Lecturer Award to Aruna Shankaranarayanan.



From Aruna Shankaranarayanan: Crystal Structure of Gaq-p63RhoGEF-RhoA Complex: Ga_q interacts with both DH and PH domains of p63RhoGEF that in turn activates RhoA. Ga_q is shown in cyan with orange colored ß strands. The switch regions of Ga_q are colored red. The DH and PH domain of p63RhoGEF is shown in yellow and purple, respectively. RhoA is shown in green with sand-colored ß strands. GDP.Mg^{2+} $AlF4^-$ is shown as spheres. N and C refers to amino and carboxyl termini of the protein. Science 2007, 318, 1923 - 1927.

AW.02: Advances in Macromolecular Phasing; Impact on Molecular Biology

The symposium opened with the award presentation to **Bi-Cheng Wang** by ACA President Marvin Hackert (*see p. 8*). In his keynote address *Resolution of Phase Ambiguity in Macromolecular Crystallography: 25 Years Later*. B.C. explained the problems of macromolecular phasing in the 1970-80s. The standard procedure for phasing macromolecular structures employed Perutz's multiple isomorphous replacement method (MIR) which required at least two heavy atom derivatives and the native data, used in combination, to resolve the phase ambiguity. At that time, BC was faced with the problem of having only one useful derivative out of over 100 attempts. Thus began an analysis of the single isomorphous replacement (SIR) phase ambiguity problem that eventually led to a successful protein structure analysis. A prime factor in resolving the single-derivative phase ambiguity was the invention of a simple algorithm applied to electron density maps, which distinguished protein electron density from solvent regions, thus defining the molecular envelope. This procedure made *solvent flattening* a routine and easily used process that *could locate and enhance the protein image, i. e. whatever is not solvent must be protein*. Using the enhanced protein image, improved phases are calculated which could then be processed through additional cycles of refinement in an iterative procedure. A similar phase ambiguity exists for single wavelength anomalous scattering phasing procedures (SAS) and can be treated in a similar manner. The entire SIR and SAS procedure was coded into an easy-to-use computer program and generally distributed to all who requested a copy during the mid-1980s.

From left: Wim Hol, Quan Hao, Wayne Hendrickson, John Rose, Emil Pai, Bi-Cheng Wang, Zbigniew Dauter and David Langs. ***Photo courtesy of Gary Newton.***

With regard to developments since 1990, B.C. talked about an idea he calls *Direct Crystallography* which makes use of anomalous scatterers that are naturally occuring in proteins, such as metals like iron or zinc or perhaps small substrates with built-in heavy atoms. One particularly interesting element is sulfur, present in nearly all proteins, with a small but measurable anomalous scattering component. If the anomalous differences from sulfur scattering can be measured accurately enough, then many native proteins can be solved without the need of a derivative, and from one data set. This idea galvanized efforts to measure data more accurately. The use of longer wavelength radiation at home lab sources and at synchrotrons for which the sulfur anomalous signal is substantially increased was one result. A new method under development at SER-CAT and UGA: *Signal Based Data Collection* utilizes real-time data monitoring and feedback of the anomalous signal strength during data collection, combining automation, robotics and multiple crystals. The program will sense when the current crystal has decayed to the point that the anomalous signal is unacceptable; cause a fresh crystal to be mounted automatically; and resume the data collection.

Wayne Hendrickson, HHMI Investigator, Columbia, and recipient of the first Patterson Award in 1981, spoke on the *Evolution of Phase Evaluation from MAD and SAD Measurements*. He recalled the use of anomalous dispersion measurements from sulfur only in the solution of the protein crambin, the first successful sulfur anomalous dispersion (SAD) structure. Later, the structure of lamprey hemoglobin was successfully solved with the use of the multiple wavelength anomalous dispersion (MAD) from iron, (1988). Soon after, the incorporation of selenium, with it's large anomalous signal, resulted in a highly successful MAD procedure. By 2000, the majority of *de novo* structures were solved using MAD procedures. In 2007, however, more structures were solved by SAD than MAD, probably because of improved data measurements and the need for only one data set. Wayne concluded by mentioning two new approaches: the incorporation of generically methionine-enriched Fab phasing vectors, and the use of very large metal clusters with "colossal" anomalous signals.

Zbigniew Dauter, APS, Argonne, talked about the *Wang Limit*. This term became widely used in the late 1980s and was applied to data sets in which only sulfur atoms provided the maximum anomalous signal. An error-free data set was calculated based on the anomalous scattering from two sulfur atoms (Bence-Jones protein Rhe, 114 amino acid residues). This simulation, by B. C. Wang, provided an example that suggested a macromolecular structure could be successfully phased even when the average anomalous scattering signal was as low as 0.6% of the average structure factor values. From B.C.'s 1985 paper: *"…we see that the best strategy for a macromolecular structure determination in the future is not to aim for more isomorphous derivatives but to concentrate on one 'good' derivative and to improve the quality of its SIR and SAS data, because, as long as one can accurately measure the data, a macromolecular structure can be determined from SIR or SAS data even when the occupancy of the heavy atom or the size of the anomalous scatterer is relatively small*. Zbigniew pointed out that a majority of novel structures today are solved by a Se-SAS approach, concluding that there is no such thing as the *Wang Limit;* everything depends on the diffraction data accuracy.

cont'd, next page

Emil Pai, U.Toronto, talked about direct sulfur SAS phasing, emphasizing the use of longer wavelength radiation, especially CrKα (2.29Å), where the anomalous signal from sulfur is twice that for CuKα. He also presented some practical tips on selecting crystals suitable for sulfur phasing (no split spots, no ice rings, no high mosaicity) and on data collection (high redundancy, increased signal/noise ratio). He noted that solving the Patterson function in lower space groups might help by displaying symmetry relationships. In his feasibility study of structures that failed to solve by a Se-Met approach, he has to date solved solved 10 of 23 structures using the native sulfur anomalous signal alone. His message: *the higher the I/σ(I), the better the chances for a structure solution – there is no substitute for signal!*

David Langs, Hauptman-Woodward Inst., recalled numerous Pittsburgh Diffraction Conferences and one particular Direct Methods Workshop in Buffalo in 1984. B.C. presented his new solvent flattening procedure, supported by calculations on the VAX 11/780 computer in Buffalo. His work certainly inspired the development of the real space component for phase refinement used in HWI's Shake and Bake minimal function program. B.C. also indirectly influenced the Buffalo group to refocus their efforts from "large" small molecules to the determination of macromolecular heavy atom substructures. David went on to describe a new SnB-based phasing method that can identify large subgroups of phases having a lower mean phase error than the rest, an idea that came to him while preparing his talk for this symposium. For the first time individual phases can be directly determined outside the trial-and-error construct of refining phases to fit the probabilistic constraints of the three phase invariant relationships.

Quan Hao, Cornell, followed with a talk jointly prepared by Quan and **Hai-fu Fan** and colleagues, Inst. Physics, Beijing, China. A central feature of the phasing process is the OASIS program, developed in Fan's group. This program implements a direct method for solving the phase ambiguity, originally proposed in 1965. More recently, OASIS has been improved by the inclusion of a dual-space iterative procedure including solvent flattening, model building and structure refinement and is included in the CCP4 program package. Quan listed numerous examples of successful phasings on a variety of proteins with various combinations of OASIS, SOLVE/RESOLVE, ARP/wARP and DM. One particularly impressive example was a protein TTHA1634 with 1206 residues, a resolution of 2.1Å, 22 sulfur atoms per ASU and a Bijvoet ratio of 0.55% that was solved by OASIS and DM. Another impressive example was a model completion procedure using OASIS starting from a partial (20%) model produced by molecular replacement.

Wim Hol, U. Washington, presented an intriguing talk: *Molecular Machines, Tropical Diseases and the Power of Llamas*. As is well known in the macromolecular crystallographic community, Wim has spent many years studying the structural biochemistry of global diseases. Wim focused on two components of the Type II Secretion System (T2SS), a sophisticated "machine" that secretes nasty toxins like cholera toxin and homologs. The first example was the structure determination of protein peri-D from enterotoxigenic *E. coli*. Initial attempts to solve the structure produced crystals which diffracted to no more than 6-7Å. This difficulty led to the use of llama antibodies in search of an answer to the problem. Unlike normal antibodies, camelid (llamas and camels, etc.) antibodies have a single-domain 15 kDa antigen binding fragment resembling a 2.4 nm x 4 nm prolate ellipsoid, here termed a *nanobody*. Briefly, the process involved, in close collaboration with the group of Jan Steyaert in Brussels: injection of llamas with the protein of interest; waiting for the immune system to work; extracting lymphocytes from the blood and nanobody DNA from the lymphocytes; expressing nanobodies in *E. coli*; and binding the antibody to the protein (in this example, a SeMet derivative). This effort was successful in producing a structure of the nanobody-peri-D complex. Another example, the EpsI-EpsJ heterodimer complex from *Vibrio vulnificus*, required species variation, truncations and SER mutations to produce crystals which diffracted to 2.1Å. The llama antibody route again proved successful in this case: crystals of the IJ-nanobody complex appeared within days. The "IJ" pseudopilin heterodimer has a remarkable shape: a "hand" waiting for partner(s). Wim's final slide showed the many structures of T2SS proteins which have been solved in his group by SIR or SAS procedures.

John Rose, UGA, reviewed early *de novo* structure determinations using Wang's ISAS technique. Bovine neurophysin (isolated from the posterior pituitary gland) complexed with an iodinated Phe-Tyr dipeptide was successfully solved with iodine-SAS in 1987, and the next year the structure of ferrochelatase, which converts protoporphyrin to heme, was solved by iron-SAS.The iodine and iron atoms furnished a strong anomalous signal using a CuKα home source. A quest for a synchrotron beamline with stable x-radiation generation at longer wavelengths -so that the sulfur anomalous signal would be enhanced.- was successful in 1999 when the structure of protein obelin was solved using sulfur SAD with data measured at 1.74Å at IMCA-CAT at APS. In conclusion John showed 26 structures in the current PDB solved by sulfur SAD.

Gary Newton and John Rose

AV and registration desk crew (they also took most of the photos of speakers): In back, from left: Max Trent, Jonathan Page, Nicholas Sanjines, Will Zhou; in front: Brenda Dougan, Julia Abbott, Michelle Minton.

TR.01: The ACA Transactions Symposium*, *Complementary Methods for Structure/Function Studies of Biomolecules included twelve talks in four complementary subject areas: Redox Chemistry and Associated Single Crystal Spectroscopies, Neutron Methods, Small-Angle Scattering and Dynamics and Function Studies using NMR and Crystallography.

Above, from left, in back: Douglas Tobias, Leighton Coates, Dominique Bourgeois, James Holton; in front: Britt Hedman, Susan Krueger, Carrie Wilmot.

From left, in back: Joseph Wedekind, Carrie Wilmot, Shuji Akiyama, James Stivers; in front: Kylie Walters, Susan Krueger, Jill Trewhella, Son Lam.

Redox Chemistry and Associated Single Crystal Spectroscopies: **Dominique Bourgeois**, European Synchrotron Radiation Source, detailed the impressive set-up that the ID23 beamline has to measure single crystal UV/visible, Raman or fluorescence spectra both on-line during x-ray diffraction experiments and off-line. As single crystal UV/visible spectroscopy is more established, he focused on Raman and fluorescence. Raman spectroscopy on crystals has great advantages compared to solution. The high concentration of protein and conformational restrictions created in crystals leads to stronger signals and narrower bands respectively. Disulfide breakage can be followed at ~510 cm^{-1}, crystal structures can be validated against solution structures, bound ligands can be identified by difference Raman and enzymatic reactions in the crystal can be monitored. Research on superoxide reductase illustrated how Raman can be used to advantage. Fluorescence can be used to follow the dynamics of binding through lifetime studies, determining the redox state of NAD(P)H, and also in locating small crystals within loops for centering in the x-ray beam.

Britt Hedman, SLAC, detailed work on single crystal x-ray absorption spectroscopy (XAS). The position of the edge can define redox state, whilst pre-edge features can give information about the ligand field, and the extended x-ray absorption fine structure (EXAFS) enabled ligand models to be validated. She focused her talk on using XAS to detect photoreduction in cytochrome c peroxidase and putidaredoxin (Pdx). In the case of Pdx, her group was able to demonstrate that photoreduction was temperature dependent.

James Holton, LBNL, gave an overview of his work on loss of Se-Met due to radiation damage through monitoring the x-ray absorption near-edge structure (XANES). His conclusion was that a high proportion of MAD experiments failed due to Se-Met damage; a sobering thought considering the extensive use of Se-Met as a phasing tool. He suggested first collecting a complete dataset using short exposures (< 5 MGy), followed by a longer exposures dataset (< 30 MGy). He found there was no dark progression, and that ascorbic acid, nitrate or acidic conditions could protect Se-Met, but the extent of protection was very protein / crystal form dependent.

Neutron Methods: **Douglas Tobias**, UC - Irvine, began the neutron methods talks with an overview of the dynamics of both soluble and membrane proteins. He described how both experimental neutron spectroscopy methods and molecular dynamics (MD) simulations can work together to explain not only the motions of the proteins but also of their surrounding environment. He presented data on a soluble protein, maltose binding protein. In order to study the hydration water and protein dynamics separately, both deuterated protein hydrated in H_2O and hydrogenated protein hydrated in D_2O were measured. A similar study was performed on a membrane protein, bacteriorhodopsin, and its hydration water. It was found that the dynamical transition in the hydration water of maltose binding protein is tightly coupled to the same transition in the protein, with both occurring at the same temperature. However, the transitions occurred at different temperatures in the case of bacteriorhodopsin and its hydration water. Corresponding MD simulations revealed that the hydration water transitions are due to the onset of translational diffusion. These studies helped to clarify how the lipid dynamics are coupled to the water and protein motions.

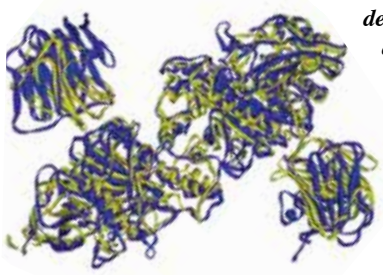
Leighton Coates, ORNL, presented the results of studies that have been conducted on protein crystallography instruments at both Los Alamos National Lab and the Institut Laue Langevin. He also described the new Macromolecular Neutron Diffractometer (MaNDI) that is being constructed at the Spallation Neutron Source at ORNL and is scheduled to begin operations in around 2012. This advanced instrument will allow for greatly reduced crystal sizes and data collection times, thus opening up the field

cont'd next page

of macromolecular neutron crystallography to many more protein systems.

David Worcester, U. Missouri, Columbia and NIST, described studies of biomembranes using neutron diffraction from multilayers that were conducted on the Advanced Neutron Diffractometer/Reflectometer (AND/R) at the NIST Center for Neutron Research. Deuterium labeling was used in order to label specific amino acids in membrane associated peptides or specific sites in the lipid molecules, taking advantage of the fact that neutrons can distinguish between hydrogen and deuterium to provide additional information on the positions of the labeled components. In addition to describing traditional membrane multilayer studies, measurements from one-dimensionally oriented multilayered microcrystals were presented. Such samples provide data to nearly atomic resolution. Finally, methods of sample preparation were described that allowed measurements on the sample using neutrons as well as other complementary techniques such as x-rays, FTIR and oriented circular dichroism spectroscopy.

Small-Angle Scattering: Jill Trewhella, U. Sydney, Australia, spoke about combining small-angle scattering (SAS) and neutron contrast variation with high resolution structures to study protein complexes in solution. She stressed that SAS provides low-resolution information that can complement high-resolution techniques such as crystallography and NMR. With the advent of new developments in sources, instrumentation and computer algorithms that perform 3-D structure modeling, the SAS technique is becoming more popular for the study of complex biological systems that are not amenable to higher resolution studies. However, many model structures can fit a single SAS profile. The use of neutron contrast variation to aid in the determination of the structure of complexes involved in bio-molecular signaling and regulation was emphasized, along with the importance of obtaining good data under all solvent conditions and use of analysis methods to examine the quality of the data. Finally, it was shown that structure modeling software, in combination with neutron contrast variation data and information obtained from complementary techniques all must be used together to gain knowledge into the nature of the protein interactions in a complex.



from Jill Trewhella: The post-synaptic neuronal receptor neuroligin and its complex with the pre-synaptic ligand neurexin. The two traces compare the crystal structure (yellow) with that determined by a combination of SAS with contrast variation and homology modeling (blue), demonstrating that the solution scattering data positioned the neurexin ligands accurately with respect to the neuroligen receptors. They differ only in their orientation, likely due to the relatively weak binding interaction with a very small interaction surface (560 Å²). The neuroligins are of high interest due to their identification with autism-linked mutations.

Shuji Akiyama, Japan Science and Technology Agency, described real-time small-angle x-ray scattering (SAXS) studies of the dynamic oscillatory processes of the three cyanobacterial circadian clock proteins, KaiA, KaiB and KaiC. The process is initiated when the three proteins are incubated with ATP. The scattering pattern from the protein mixture changed in a oscillatory manner over a 24-hour period. Using real-time SAXS, snapshots of the oscillatory cycle were taken at regular intervals so that the scattering from the Kai complexes could be monitored as they assembled and disassembled. Structure models of the clock protein complexes during the assembly/disassembly cycle were presented and discussed.

Joseph Wedekind, U. Rochester, described the use of SAXS along with the known x-ray crystal structure of a related protein to determine the solution structure of HIV defense factor APOBEC3G (hA3G) protein. hA3G acts on HIV DNA by deaminating dC to dU which prevents infection. hA3G is active only in the absence of the HIV protein, Vif, which degrades hA3G. In order to better understand the hA3G interaction with Vif, hA3G was studied in solution by SAXS. The crystal structure of a distant family member, A2, was used as a starting point for structure modeling. A2 has been used as a model for hA3G in the past. However, this experiment illustrates the first time that the hA3G SAXS data were directly compared to model SAXS data from the A2 crystal structure. Initial results showed that A2 is not a good model structure for either dimeric or monomeric hA3G in solution. The broader issue of using SAXS to assess the use of crystal structures of related proteins as modeling templates was discussed.

Dynamics and Function Studies using NMR and Crystallography. Speakers in this section were all NMR experts who had teamed up with crystallographers to understand the functional dynamics of different systems. **Jim Stivers**, Johns Hopkins Medical School, described trapping and understanding an unstable intermediate of DNA glycosylase. Chemical "tampering" enabled the intermediate to be stabilized for crystallography and NMR. By tracking the solvent exchange in real time, they were able to demonstrate that the enzyme only accelerates the exchange of T/U bases, not G/C. The enzyme can distinguish between T and U without fully binding, and releases T, but goes on to bind U. This speeds up the process and involves less interaction energy. The rates were too fast for a random encounter, suggesting the enzyme was initially scanning the DNA duplex through the use of non-specific interactions.

Kylie Walters, U.Minnesota, detailed the finding of a new ubiquitin receptor in the proteosome, Rpn13. His group has mapped out the structure and dynamics of complexes between ubiquitin and Rpn13 using the crystal structures of the individual components to speed up the assignment of individual resonances within the NMR data. Attempts to obtain crystals of the complexes have been unsuccessful, and the dynamical relationship between the proteins as determined by NMR explained why.

Son Lam, NIDDKD, described how NMR had been used to understand the interactions of HIV envelope glycoproteins with an N-teminal peptide derived from cellular co-receptor CCR5, thus gaining a structural window into HIV-1 entry into cells. CCR5 contains a critical sulfotyrosine that enables interaction with gp120 on the surface of HIV.

Carrie Wilmot & Susan Krueger

1.01: New Structures

L to r: Mark Wilson, Jeffrey Kieft, Steve Ealick, Bill Royer, David Giedroc, Young-In Chi, Jack Tanner.

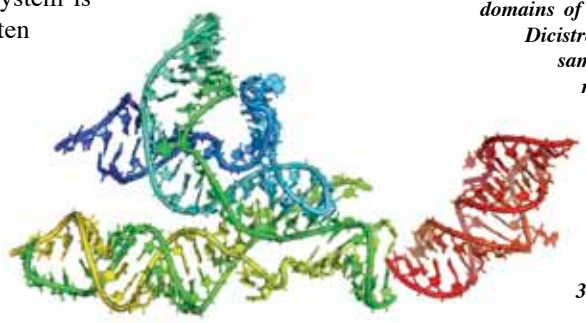
This year both new protein and new nucleic acid structures were presented, but there was a unifying theme because all the speakers emphasized the common methodological challenges of crystal growth, data collection, and model optimization that unite (and frequently frustrate) macromolecular crystallographers. **Steve Ealick**, Cornell, presented his new, pre-publication structure of 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate synthase (HMP-P synthase). HMP-P synthase is a new member of the radical S-adenosyl methionine (SAM) class of enzymes, which has attracted recent attention due to the unusual chemistry that these enzymes can perform. HMP-P synthase is no exception, and Steve's talk made clear that a careful comparison of this new structure with some of the previously determined radical SAM enzymes shows a broad similarity in fold but significant differences in loop and active site architecture. In addition, the structure of HMP-P synthase is a further contribution toward the nearly complete structural elucidation of the enzymes of thiamine anabolism and catabolism.

Young-In Chi, U. Kentucky, presented a new and unpublished twist on an old story, yet another chapter in the evolution of the hammerhead ribozyme as a model catalytic RNA. Chi took advantage of a slowly cleaving variant of a full length construct of the satellite tobacco ringspot virus sTRSV hammerhead RNA in which the general base of the enzyme G12 was substituted by A12. This permitted him to solve the crystallographic structures of what he proposed were active pre-catalytic (enzyme-substrate complex) and post-catalytic (enzyme-product complex) intermediates. The structure of the enzyme-product complex was particularly interesting, as it allowed Chi and coworkers to observe long-range tertiary structural RNA and RNA-Mg^{2+}interactions that may well be relevant for understanding catalysis as well as the nuclease-ligase internal equilibrium linked to rolling circle replication by these and related RNAs. **Bill Royer**, UMass Medical School, presented his recent pre-publication work on the crystal structures of Interferon Regulatory Factors (IRFs), which are critical for proper immune function. The new dimeric structure of IRF-5 demonstrates how physiologically important phosphorylation of these proteins is coupled to changes in oligomerization that regulate protein binding. The clear structural connection between phosphorylation and changes in oligomerization in this system is especially satisfying because quite often the structural basis for regulation of protein function by phosphorylation is unclear. Bill also made note of the untimely passing of his valued collaborator Professor Kai Lin, who had contributed greatly to this work.

Note: See p. 17 , Kai Lin Memorial. Also, Bill's structure is featured on the cover and on p. 16.

Arati Ramesh, a postdoctoral scientist in Wade Winkler's group, UT-SW, presented the 2.6 Å structure of the *B. subtilis* Mg^{2+}-sensing RNA riboswitch. Although the molecular architectures of protein-based intracellular metal sensors have been known for some time, this is first description of an RNA-based metal sensor. This structure is remarkable for its complex core of six Mg^{2+} ions and 4 K^{+} ions, which collectively provide an atomic-level view of how RNA uses inner-sphere coordination bonds to Mg^{2+} to drive a conformational change that leads to termination of transcription of the high affinity magnesium uptake system in response to excess Mg^{2+}. **Jack Tanner** U.Missouri, described the structure of bifunctional *E. coli* proline metabolic protein PutA. PutA contains a proline dehydrogenase domain that is connected by a channel to a second domain containing the pyrroline-5-carboxylate dehydrogenase active site. The structure determination process was challenging for the Tanner group due to unusual crystal pathology that was not standard merohedral twinning, as well as various refinement problems. Evaluation of several crystal forms finally yielded a problem-free monoclinic crystal. Analysis of the PutA structure revealed a long channel that connects the two active sites of PutA and suggests a mechanism by which a facile non-enzymatic chemical step is accomplished in the channel environment. Jack emphasized that a key lesson learned from this structure determination is that crystallographers should be willing to disregard a mediocre bird in the hand for the two that may be lurking in the bush. **Jeff Kieft**, U. Colorado Med. School, presented two crystal structures that together provide the first comprehensive picture of the structure and function of an internal ribosome entry site (IRES) RNA, this one from the model *Dicistroviridae* intergenic region (IGR). Of particular interest was the new structure of the pseudoknot domain which mimics precisely the transfer RNA anticodon-messenger RNA codon interaction. The work is ground-breaking because it provides novel insight into how an IRES manipulates the ribosome to initiate translation by translocating without peptide bond formation.

Mark Wilson and David Giedroc



From Jeffrey Kieft: Crystal structures of both independently folded domains of the intergenic region IRES RNA found in Dicistroviruses. The two structures are placed in the same relative orientation that they adopt on the ribosome. This RNA is able to bind to the ribosome and drive translation initiation without the use of any protein initiation factors, and hence is an all RNA-based translation initiation apparatus. Costantino, D.A., Pfingsten, J.S., Rambo, R.P., & Kieft. J.S. (2008), Nat. Struct. Mol. Biol. 15, 57-64; Pfingsten, J.S., Costantino, D.A & Kieft, J.S. (2006), Science, 314, 1450-1454.

1.02 Engage Your Brain Automation is not the ultimate solution for all problems encountered during the process of macromolecular structure determination. Fortunately (or unfortunately depending on the point of view), some crystallographic problems still require intervention and engagement of the human brain. **Zbyszek Dauter**, NCI; Argonne, began with, appropriately, *Data collection - not enough to press the button*. Several examples of complications that may be encountered during diffraction data collection were demonstrated, along with the reasons why automation cannot deal with such cases successfully. **Charlie Carter**, U. North Carolina, introduced the principles of maximum likelihood and Bayesian statistics; he described the application of these methods in macromolecular phasing and refinement and clearly explained why these methods are superior to their classical counterparts. **Dominika Borek**, UT, Dallas, discussed experimental errors. She demonstrated how various random or systematic errors with complex characteristics contribute to the overall uncertainties of experimentally measured intensities and how one can deal with these in practice using a hierarchical, iterative algorithm.

Gerard Bricogne, Global Phasing, Cambridge, UK, spoke on *Phasing in spite of complications, and sometimes thanks to the complications*. He described how x-ray polarization anisotropy of anomalous scattering, which used to be treated as a nuisance, can be used to enhance the power of anomalous phasing signal. This novel approach based on representation of anomalous scattering components f' and/or f" as tensors, can boost the SAD phasing signal to a level comparable with that of MAD. **Champion Deivanayagam**, UA, Birmingham, presented a structural biology project that got complicated by polymorphism involving pseudo-symmetry. He described how monoclinic crystals of Adhesion Protein Antigen I/II with close to an orthorhombic lattice metric (~ 90°) were transformed to the triclinic form upon soaking in a ligand solution. **Kanagalaghatta Rajashankar,** NE-CAT, APS, talked about non-merohedral twinning. He described crystals that produced two partially overlapping diffraction patterns resulting from two twin domains. Several analogous examples of non-merohedral twinning from PDB deposited structures were also presented.

In back: Raj Rajashankar and Dominika Borek; in front, l to r: Charlie Carter, Gerard Bricogne, Champion Deivanayagam, and Zbyszek Dauter.

Kanagalaghatta Rajashankar & Zbyszek Dauter

1.03 Difficult Structures **Min Lu**, Brookhaven, presented his structure of the zinc transporter, YiiP. The difficulty he had with these membrane protein crystals was that they were extremely unstable and MAD phasing experiments failed. The structure was solved by MIR methods and fortunately the crystals modified by mercurial agents diffracted to much higher resolution. **Jue Chen**, Purdue, had very different problems when determining the structure of the maltose transporter complex. Crystals of this membrane transporter in complex with the maltose binding protein were extremely unstable; they formed within hours but lost their ability to diffract within two days.In this case non-hydrolyzable ATP analogs and ATP-vanadate complexes did not yield high quality crystals, so Jue and coworkers mutated the Walker motif of the ATPase such that it could bind ATP but not hydrolyze it, and then managed to trap the complex in a state where the maltose binding protein was in an open conformation and the maltose was bound within the membrane spanning domain. **Jeff Speir**, Scripps, presented work on Providence virus, unusual because they had only one crystal and could collect only 1/3 of the data. There was enough non-crystallographic symmetry to to determine the structure using averaging and phase extension. **Jie-oh Lee**, KAIST, Rep. of Korea, presented work showing that the structure of human toll-like receptors could be determined by creating fusions of these leucine-rich-repeats (LRR) with soluble LRRs from hagfish. At least half of the hybrids formed crystals of this protein that, alone, could not be crystallized. **Alexey Amunts**, Tel Aviv U., presented work on plant photosystem I, the crystals of which had an extremely high content of non-protein material (~1/3 total mass). His difficulties were solved by controlling the dehydration of poorly diffracting crystals by increasing the concentration of PEG. **Changrui Li**, Cornell, had to resort to tricks in his work on the structure of Smk riboswitch. The crystals were extremely small (~10×10×200 μ) and decayed within 5 frames. In the end a finely focused beam (<10 μ) was used to shoot along the length of the crystals. Only half of the structure was visible from the SAD phasing experiments and the other half was phased using molecular replacement and gradual bootstrapping. **Gebhard Schertler**, MRC, Cambridge, presented work on a β1 adrenergic receptor. As with Changrui Li's work, the crystals were extremely small and unstable in the beam and required a finely focused beam. About half of the insect cell-expressed protein was soluble but not active; the active fraction was purified using affinity chromatography with its cognate ligand. The final break came from a series of 6 mutations that increased the thermal stability of the protein by ~20°C.

Dinesh Yernool and Tom Smith

Back: Changrui Lu, Tom Smith, Gebhard Schertler, Jeff Speir; front: Jie-Oh Lee, Jue Chen, Dinesh Yernool, Min Lu.

1.04 Structural Enzymology

This session, organized and chaired by **Allen Orville** and **Carrie Wilmot**, was intended to feature talks that described crystal structures of reactive intermediates, and/or which used techniques that provided strong correlation(s) to the proposed reaction mechanism. Consequently, the speakers described methods and structures of macromolecular catalysts that were poised, trapped or stalled along the reaction coordinate, rather than ground-state structures of resting systems that are more typical of macromolecular crystal structures. Four of the talks were selected from the submitted abstracts.

L to r, in front: Christopher Jurgenson, Nathalie Colloc'h, Allen Orville, C. Nicklaus Streussy; in back: Shelagh Ferguson-Miller, Carrie Wilmot, Michael Murphy, Tom Ellenberger, Ilme Schlichting.

Ilme Schlichting, Max Planck Inst., Germany talked about *Insights into Blue-light Photoreceptors - How to BLUF.* This family of proteins take their name from their function; sensor of Blue Light Using FAD. The various family members control diverse cellular processes including gene expression, nucleotide metabolism and cell motility in direct response to blue light stimulus and interaction with appropriate "output" domains or proteins. She described structures of dark-adapted and light-activated BLUF domains, correlated them with single crystal optical absorption spectroscopy, and compared them to those of analogous BLUF domains from other species. Her results supported a model for how light stimulus induces a conformational change within the BLUF domain that propagates across the BLUF domain-"output" protein interface. The putative mechanism thus translates the absorption of photons into biologically useful signal(s) that are exploited in various ways to enhance survival by the organism.

C. Nicklaus Steussy, Purdue, clearly described a complex enzyme from *Pseudomonas mevalonii* that catalyzes the four-electron reduction of HMG-CoA to free CoA and mevalonate. Steussy and co-workers have collected more than 70 structures of mechanistically relevant ligand complexes that probe most of the steps in the reaction cycle. A few of these were especially relevant to this discussion. For example, some of the complexes revealed different conformations of the pantothenic backbone in the HMG-CoA ligand. One conformation appeared to ideally position the substrate for hydride transfer from NADH. They also observed that in some ligand complexes the previously disordered "flap domain" was ordered. He suggested that this is the mechanism by which the two-electron reduced substrate intermediate is retained, while the NAD^+ is exchanged for a second molecule of NADH.

Shelagh Ferguson-Miller, Michigan State U. described crystal structures of oxidized, reduced and re-oxidized forms of the cytochrome c oxidase from *R. sphaeroides*, typically to about 2 Å resolution. Her comparisons of the structures from reduced and oxidized enzymes indicate that the heme a3 shifts and rotates relative to the oxidized state. She postulated that this may serve to open the top of the K channel and thus impact the proton pumping function of the enzyme. Their laboratory deployed a somewhat unorthodox purification and crystallization strategy that resulted in the observation of several new steroid and lipid binding sites. Moreover, the occupancy of these sites was also linked to the redox state of the enzyme. Her comparisons of these structures with analogous bovine cytochrome c oxidase structures highlighted some significant similarities and differences between the distantly related enzymes. She suggested that the redox state-induced conformational changes around the active site and also the conserved steroid binding site could regulate proton uptake in the K path.

The talk by **Christopher Jurgenson**, Cornell, described perhaps the most complex, multistep reaction mechanism in the session. The enzyme catabolizes NAD to form an adenylated thiazole carboxylate (ADT) product, which is then used for thiamin biosynthesis. The previously reported Thi4 structure was the first protein structure with a glutathione reductase type II domain that binds NAD instead of FAD. The structure was also used to create a number of mutants that did not co-purify with tightly bound ADT and therefore provided an opportunity to determine structures with a variety of additional, mechanistically relevant ligands. Remarkably, the sulfur transfer step in the mechanism was shown to come from an internal cysteine residue by ESI-MS and electron density maps. However, this raised the interesting question as to how the enzyme catalyzes more than one complete reaction.

Tom Ellenberger, Washington U. Med. School, gave a fascinating talk describing strategies to trap structures of site-specific DNA recombination intermediates in the bacteriophage lambda integrase protein. The enzyme reaction strategy involved strand cleavage by Tyr sidechains to form a stable enzyme Tyr-DNA intermediate. The structures of the integrase bound to synaptic and Holliday junctions supported his proposed mechanism for the allosteric control of the recombination reaction through arm DNA binding interactions. Several common mechanistic strategies were apparent in his proposal for formation of covalently closed DNA hairpin structures that are catalyzed by the hairpin telomere resolvase, TelK. His structures supported the proposal that the hairpinning reaction is made effectively irreversible by protein-induced distortions of the DNA substrate that prevents re-ligation of the cleaved DNA substrate.

cont'd, next page

Nathalie Colloc'h, CI-NAPS, Université de Caen, talked about insights into the mechanism of the cofactor-less urate oxidase that her structures provided This enzyme catalyzes the O2-dependent hydroxylation of uric acid to yield 5-hydroxyisourate, which is then transformed in a second reaction to yield S-allantoin. Some of her results were derived from urate oxidase crystals in complex with a competitive inhibitor and then exposed to1.0, 2.5 or 4.0 MPa of O2 pressure. The crystal structures clearly showed a dioxygen molecule bound adjacent to the inhibitor, and in an orientation consistent with reactivity in a natural enzyme-substrate-O2 complex. Her results indicated that the dioxygen site is largely comprised of polar residues that may assist in the O-O bond cleavage and hydroxylation step of the reaction. Another set of ligand complexes revealed a solvent molecule that appeared to mimic the role(s) of solvent in the hydration and decarboxlation steps of the second reaction catalyzed by the enzyme.

Michael Murphy, U. British Columbia, focused on enzymes cloned from the pathogenic organism, *Staph. aureus*, in which they likely evolved to reductively degrade hemin in the blood of infected hosts. The structures of these two paralogous enzymes are clearly distinct from members of the other well-known heme oxygenase family. He presented structures of enzyme containing an inactive Co^{3+} protoporphyrin IX, and from several active site mutant enzymes containing Fe^{3+} protoporphyrin IX. All the structures indicated that the metal was five coordinate, and that the porphyrin ring forms extensive steric interactions in the binding cleft enzyme residues. An interesting feature was that the porphyrin rings are more highly distorted from planarity than typically observed in most other hemeproteins. Murphy postulated that these distortions were an important feature of the reaction and likely enhanced the susceptibility of the β and δ-meso carbons to O2 attack during the reaction cycle.

Allen Orville, Brookhaven, described the new single crystal spectroscopy facility that he recently deployed at beamline X26-C of the NSLS, and announced that the dedicated facility is now available to the general community. He also presented recent results from choline oxidase from *Arthrobacter globiformis* that revealed a distorted flavin isoalloxazine ring that was consistent with a C4a-OOH or C4a-OH intermediate. The spectroscopic analysis he presented indicated that the adduct formed rapidly *in-situ* in an x-ray dependent process. He hypothesized that the choline oxidase active site structure promoted and stabilized the C4a-adduct, and that the photoreduction and cryogenic conditions failed to establish the correct proton inventory required to complete the reduction of oxygen to hydrogen peroxide.

Allen Orville and Carrie Wilmot

1.05: Computational Crystallography Nuts and Bolts was a survey of best practice of software used for crystallographic structure determination. **Jim Pflugrath**, Rigaku USA, started by talking about ways to get the best diffraction from your crystal and continued with a discussion of new features in d*TREK® that allow for diverse spot shapes across the face of the detector and generic mechanisms for identifying collisions in various detector/goniometer combinations. **George Sheldrick**, Göttingen U., spoke on the best way to determine experimental phases using MAD, SIR or SAS and also mentioned that free lunches seem not so free if you must attend BIOMAC SIG meetings. **Tom Tewilliger**, LANL, finished the first part of the morning by summarizing the speed and ease of structural determination of relatively easy problems using automated systems such as PHENIX. **Paul Emsley**, Oxford, described the best features of COOT, including the ability to script and interface with a great variety of validation tools such as MolProbity. **David Richardson**, Duke, described the best way to get to easy validation: be sure that you are using good model building practices including detection of clashing side chains that would not be seen in the absence of hydrogens in the structure. **Hongliang Xu**, Hauptman-Woodward Institute, presented a comparison of phasing methods using the four combinations of three wavelength MAD data sets and gave good evidence to advocate using combinations of sets of wavelengths to arrive at the best solution. To conclude, **Dale Tronrud** described the origins of least squares refinement (and libraries containing "ideal" values) and showed that interesting information about deviations from ideality was being lost because of the lack of ability to deviate from ideality even at moderate resolution. Although not implemented in a refinement program yet, he showed how weighting functions for various stereochemical restraints depend on the resolution of the data. All slides from the talks are available on the ACA website, **www.AmerCrystAssn.com.**

Ed Collins and Peter Horanyi

L to r, in back: Jim Pflugrath, Peter Horanyi, Hongliang Zu, Dale Tronrud; in front: George Sheldrick, David Richardson, Tom Terwilliger, Ed Collins, and Paul Emsley.

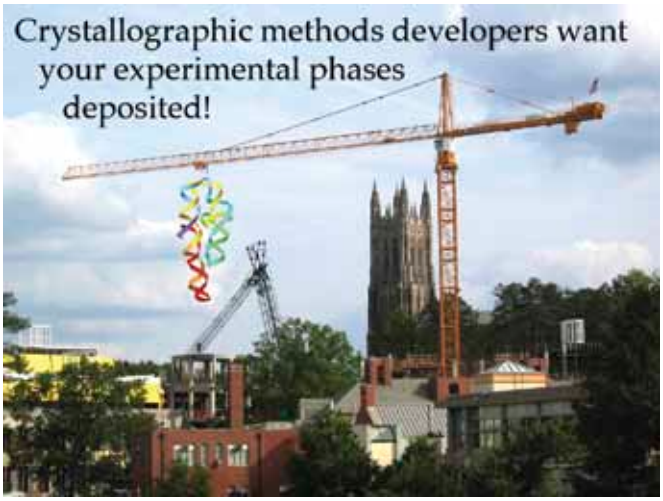
Photo courtesy of Peter Müeller.

1.07 How Structures Are Used By Others

Roland Dunbrack and **Eric Bennett** brought together several speakers from the areas of structural bioinformatics, molecular biophysics, and structure prediction to discuss how crystallographic structures deposited into the Protein Data Bank are used by researchers to develop and test hypotheses on what determines protein structures, how to predict them, and how they evolve.

Front row, left to right: Donald Hamelberg, Roland Dunbrack, Jane Richardson; in back: Eric Bennett, Nick Grishin, Jeff Gray.

Jane Richardson, Duke, gave many examples of important structural features that should be included in statistical studies of protein side chains and backbone conformations even though they might be far from the active site. They might be found to be involved in allosteric regulation, for example. She pointed out many ways that structures might be used - as models of individual proteins that can be fit into low-resolution cryoEM density, as future test beds for improvements in refinement methods and as objects of study by students and teachers. Crystallographers can make their data more useful if they anticipate these other uses.



Words to the wise -- an image from Jane Richardson's talk.

Roland Dunbrack, Fox Chase Cancer Center, discussed several projects in structural bioinformatics, the statistical study of proteins and protein complexes of known structure which is used both as a means to understand protein biophysics and to provide "knowledge-based" potential energy functions for protein structure prediction. As the size of the database has increased, it is now much easier to obtain data on even relatively rare structural features and to provide statistical treatments of certain features based on the values of other features. For instance, Dunbrack showed Ramachandran maps for residues in loops that depend not only on the residue type but also the residue type of the neighbors to the right and left; that a new backbone-dependent rotamer library now provides continuous density estimates for some dihedral angles (such as χ_2 of Asp and Asn) as a function of the backbone dihedral angles ϕ and ψ; and that observation of interfaces in homodimeric proteins across many different crystal forms can be used to identify the most likely biological interactions.

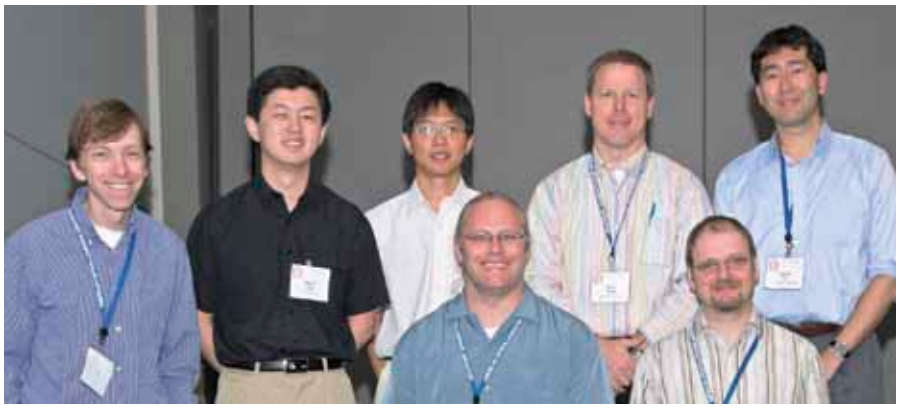
Nick Grishin, UT Southwestern, studies large structural changes among homologous proteins, and gave a number of beautiful examples of evolution- related proteins with major changes in basic fold topology. He showed that some such changes can be caused by single or multiple amino acid changes, insertions, deletions, and rearrangements of sequence; for example structures of the proteins SasA and KaiB, which interact with the protein KaiC to regulate the molecular clock in cyanobacteria. KaiB has an internal β-sheet strand that is missing in SasA; replaced by a long α helix, while one of SasA's edge strands is replaced by a helix in KaiB. Although selective advantages of this change are not clear, it is likely that oligomerization of KaiB is involved. Through point mutations and some insertions, KaiB evolved a conformationally promiscuous sequence in its C-terminal half that folded in a way different from the standard conformation present in SasA.

Donald Hamelberg, Andrew McCammon lab, UCSD, described accelerated molecular dynamics as applied to problems outside the time scale of traditional MD approaches. By applying a reversible scaling function to the potential energy surface, high-energy barriers to conformational change are reduced, allowing much more rapid sampling of conformational space. A simulation which might be difficult to run at microsecond time scales with older approaches can effectively be run to millisecond or greater lengths. Hamelberg demonstrated the method on enzyme catalysis of *cis*/*trans* peptide bond isomerization, a process which was difficult to model with older methods because of the large energy barrier involved. **Jeffrey Gray**, Johns Hopkins, covered recent advances in the area of protein-protein docking. Although older methods of protein docking often treated proteins as rigid objects, newer approaches such as the RosettaDock program under continuing development in his lab allow an induced fit approach. One challenge is that induced fit docking can tend to bias the algorithm towards selecting larger surface areas, and in validation studies, the least accurate results generally involve interactions with small surface areas. However, the methods are increasingly robust for interactions involving moderate to large surface areas. Gray showed useful applications of the method in predicting assembly of domain insertion proteins, such as methionine aminopeptidase, where one domain is inserted into the middle of another.

Roland Dunbrack and Eric Bennett

3.01 General Interest I

The first of two General Interest sessions opened with a computational discussion by **Werner Kaminsky**, who introduced several software packages to view and analyze crystal structures. The software was developed to ease students into understanding crystallography. **Joseph Ng** followed with a very lively talk on how it is possible for a small group to tackle the large scale problem of structural genomics. By incorporating strategies the large conglomerates use, a small group can effectively construct a "mini-pipeline" and survey open reading frames for cloning, expression, crystallization and stucture determination. **Jia Sheng** discussed how the replacement of oxygen with selenium in proteins has been utilized to enhance the signal from the crystal during diffraction. In addition the protein is less distorted from its original shape compared to other doping techniques.



L to r; in back: Joel Bard, Jin-Yi Zhu, Jiansheng Jiang, Kris Tesh, Joseph Ng; in front: Allen Oliver and Werner Kaminsky. Photo courtesy of Peter Müeller.

Jun-Yi Shen talked about the use of sulfur phasing from macromolecular structures in conjunction with the use of soft x-rays. More technical aspects were discussed in **Kris Tesh**'s talk on the development of new optics and how these optics can help crystallographers obtain better data while maintaining an otherwise current configuration. The final talk by **Joel Bard** discussed the use of automation and computer aided methods for drug development and how these challenges are being addressed by the pharmaceuticals industry.

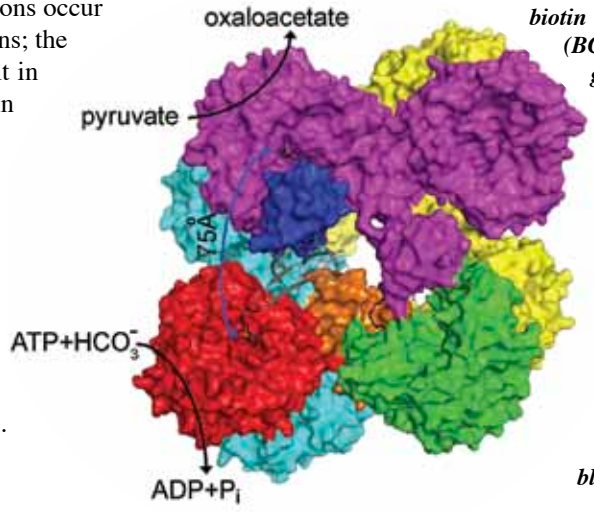
Allen Oliver

New Macromolecular Structure Posters

There were numerous exciting posters presenting new macromolecular structures at the Knoxville meeting; the following is a brief description of three posters that were particularly interesting to this reporter.

A poster from **Jim Thompson**'s laboratory **SP028** presented crystallographic and biochemical data showing intriguing changes in the dimeric arrangement of immunoglobulin light chains that possess a tendency to assemble into amyloids. Light chain amyloidosis results when secreted immunoglobulin light chains aggregate into fibrils, which can be fatal due to organ failure. The poster reported analysis of an amyloidosis protein (AL-09) and the wild-type light chain protein of the same germline subtype. The AL-09 protein, from a patient with cardiac light chain amyloidosis, has seven changes relative to wild-type germline, three of which are non-conservative. All three of the non-conservative mutations occur in the dimeric interface between the two light chains; the crystal structures reveal that these mutations result in a profound change in the subunit orientations within the dimer, in which one subunit is rotated by about 90° relative to the wild-type protein. The AL-09 protein exhibits decreased thermal stability and more rapid amyloid formation than the germline protein. Mutation of one key residue back to the germline sequence (H87Y) fully recovers germline stability, delays amyloid formation and restores the germline dimer interface. These results strongly suggest that formation of a stable germline-type dimer could be protective against amyloid formation. (***See Baden et al., 2008, JBC 283, 15853-15860.***)

Song Xiang and **Liang Tong** presented new structures of Human and *S. aureus* Pyruvate carboxylase in poster **SP045**. Pyruvate carboxylase is a complex biotin-dependent enzyme that catalyzes the production of oxaloacetate. Because of its role in gluconeogenesis and other important metabolic processes, pyruvate carboxylase is a potential drug target in type 2 diabetes. New mechanistic insight into the function of this enzyme was elucidated by this structure, providing the first structural information on the biotin moiety (which was disordered in a previously reported structure) whose binding domains attain alternate conformations in the human and *S. aureus* structures. The three structures now available may represent functionally distinct conformational states of this enzyme. (***See Xiang & Tong, 2008, NSMB 15, 295-302***).



From Song Xiang: crystal Structure of S. aureus Pyruvate Carboxylase (PC). The domains in monomer 1 are color coded with biotin carboxylase (BC) domain in red, carboxyltransferase (CT) domain in green, PC tetramerization domain in gold and biotin carboxyl carrier potein (BCCP) domain in blue and gray. Monomers 2, 3 and 4 are colored in magenta, cyan and yellow. The biotin groups are shown as sticks in black. The conformational change of the BCCP domain during the reaction is represented by the blue arrow. Reactions catalyzed by the BC and CT domains are represented by the black arrows.

Three-dimensional models of cyanobacterial circadian clock proteins KaiA/KaiC and KaiB/KaiC complexes were presented in **MP085** by **Rekha Pattanayek** (Egli laboratory) based on a combination of x-ray crystallography, electron microscopy, biochemical and mutagenic experiments. These results provide important structural details of the interactions between the clock proteins that underlie the circadian clock of the cyanobacterium *Synechococcus elongatus*. The interactions between KaiB and Kai C suggest a mechanism by which KaiB antagonizes the effect of KaiA to enhance phosphorylation of KaiC (see **Pattanayek *et al.*, 2008, *EMBO J* 27,1767-1778**). The work presented in this poster complemented the *Transactions* Symposium talk by Shuji Akiyama (TR.01.08) on the application of SAXS to these complexes, even though differences in conclusions were evident. A full understanding of the interactions that govern these clock proteins will require a range of complementary structural techniques.

Bill Royer

6.01: Structure and Dynamics of Hydrogen Bonded Systems

From left: George Reiter, Gerard Harbison, Srini Iyengar, Jagat Lamsal, Matt Hudson, David Allan, Paula Piccoli, Tom Koetzle.

Matt Hudson, Syracuse U., who won the **Etter Student Lecturer Award** for the Neutron Scattering SIG, spoke on his research combining neutron diffraction and inelastic scattering measurements with DFT calculations to elucidate the structure and understand the vibrational spectrum of lithium hydrazinium sulfate, an interesting protonic conductor.

Tom Koetzle gave an overview of the history and results of neutron diffraction studies of H-bonded systems, including the pioneering studies of water and KDP at Oak Ridge and Harwell, subjects that are still of interest, especially since the rise of pulsed sources. Recent progress at SNS, with TOPAZ and MaNDi coming on line, will result in a reduction in the need for mm size crystals. Some particularly interesting structures including tetraacetylethane, TAE, and andrographolide (MP173) were discussed, both have interesting intramolecular H-bonds. **David Allan** discussed the importance of combined synchrotron x-ray and neutron diffraction data of both single crystal and powder samples in studies of structure determination at elevated pressure. Emphasis was placed on the differences in interactions in molecular crystals and their differential response to pressure. Recent studies of sulfuric, phosphoric, and nitric acid and their hydrates were discussed. **Gerard Harbison** discussed his recent studies of strongly H-bonded systems using solid state NMR. Dipolar couplings provide very precise root mean cubed distances of H to $^{14}N/^{15}N$ and ^{17}O. The unusual chemical shift and the temperature dependence of the quadrupolar splitting of ^{2}H (which provides a measure of the electric field gradient) are unusual in short H-bonds. These features of solid state NMR spectra can be understood and often quantitatively computed with modern quantum chemical methods. It is important to include interactions of neighboring molecules within or between unit cells. Good examples including cases of isotopic polymorphism and the preferential partitioning of H/D within the Zundel cation of $(H_5O_2)_2SO_4$ were discussed.

George Reiter gave an interesting summary of his pioneering work employing deep inelastic neutron scattering measurements to study the dynamics of H-bonds; the work was done at ISIS. Reiter showed how these measurements are sensitive to coherent motions of the protons and thus can provide direct confirmation of tunneling in those H-bonds governed by a symmetric double-well potential. **Srini Iyengar** discussed the development in his group of a novel quantum wavepacket *ab initio* molecular dynamics method that includes critical nuclear quantum effects. This approach successfully models the response of H-bonded protons in systems that display a large degree of anharmonicity. Iyengar showed how it can account for the shift in mean position of the proton with temperature that has been observed frequently in neutron diffraction studies, e.g. in the TAE structure discussed earlier in the session by Koetzle. **Paula Piccoli** closed the session by discussing interesting results obtained on the structure of a tris(diisopropylamino)cyclopropenium salt. In this study Piccoli and her co-workers at IPNS used single-crystal neutron diffraction to characterize the structure of a discrete dichloride hexahydrate cube. The detailed structure, which may suggest a model for the solvated halide ion, shows that the H-atom positions along the O···O edges of the cube are half occupied similar to the situation in Pauling's original (1935) disordered model for ice-Ih.

Bruce Hudson and Tom Koetzle

Photo of the Sun Sphere, courtesy of Peter Müeller.

4.01 Crystallographic Challenges in Industry

L to r. In back: Tim Rydel, Scott Misture, Jim Kaduk, John Spurlino, Jeff Bell; in front: Robert Dinnebier, Melissa Harris, Ravi Kurumbail, Doug Dorset, Charles Campana.

James Kaduk, INEOS Techologies, described the structure of synthetic hydrotungstite, an investigation that developed as an offshoot of a study on a tungsten-based catalyst. The powder diffraction pattern was similar to, but more complex than, previous work on hydrotungstite had demonstrated. Reasoning from the analogous molybdenum structure, the synthetic hydrotungstite proved to be composed of a supercell of the originally-described hydrotungstite structure. Quantum mechanics was an aid in elucidating the hydrogen bonding in this layered structure.

Doug Dorset, ExxonMobil, described his use of electron crystallography to study microcrystalline materials in greater detail than can be done with powder techniques, including individual microcrystals and their arrangement. Using a tilt series in the electron microscope, a large section of reciprocal space can be observed, allowing determination of structures of new zeolite catalysts, polyolefins and waxes. Paracrystalline order in cokes resulting from the processing of asphaltene-containing crudes aids studies of the early stages of graphitization. **Scott Misture**, Alfred U., described challenges in studies of material behavior at high temperatures (HT) in fuel cells. The performance of $LaSrCoO_3$ cathodes degrades at HT, resulting in chemical inter-conversions and regeneration of the original catalytic material; the material changes from the active nanopowder to a coarser microcrystalline structure. Seal failure on fuel cells was also explored by HT diffraction. The inorganic glass seal was shown to be a multiphasic system in which each of the phases was vulnerable to previously unsuspected phase changes at high temperature. Some of the phases discovered had not previously been described and had no published structures. **Robert Dinnebier**, Max-Planck Inst., studied cracking of sorel cement floors. Sorel cement is formed from the mixture of MgO with an aqueous solution of magnesium chloride. It has many superior properties to Portland cement except for its sensitivity to water. The ternary phase diagram of the MgO-MgCl2-H_2O system revealed 20 compounds, only 2 of which were known; powder diffraction was used to determine the others. Cracking was associated with floor samples that contain greater than 10% of the chloratinite phase, while the most stable floors contain less than 1% of this phase. Careful formulation of the cement during construction and control of the humidity of the floor environment can produce floors with superior composition that are stable for many decades.

Charles Campana, Bruker AXS, provided a personal account of his long career in a pivotal position that requires facilitation of information transfer in two directions: training in equipment use, proficiency in demonstrating techniques and creative problem solving when out-facing; and when in-facing, to explain the needs of crystallographers to equipment engineers and programmers. **Ravi Kurumbail**, Pfizer, described the challenges of discovering inhibitors for the MAPKAP Kinase-2 (MK-2), a target whose inhibition could provide relief to patients with rheumatoid arthritis. Six crystal forms of MK-2 were known, none of which diffracted beyond 3 Å. After a major effort to obtain improved crystals, exploring more than 300,000 crystallization conditions and ~100 different protein truncation constructs, the best crystals still had a diffraction limit near 3Å. Nevertheless, several crystal structures at 3 Å provided enough information to design inhibitors with selectivity for MK-2. **Melissa Harris**, Pfizer, described her research on the N-methyl-D-aspartate (NMDA) receptor NR1. After the protein expression, purification and crystallization challenges, her initial work with 14 constructs led to adequate expression in a baculovirus expression system. The His-tagged material was deglycosylated and treated with proteases before final purification, yielding 20mg of receptor from 45L of culture. Microcrystalline aggregates (spherulites) were first observed and provided material for successful crystallization using micro-seeding. With a redesigned construct. a random sequence of residues that were an artifact of the cloning method were removed, and that improved the His-tag at the N-terminus; 30mg of receptor were obtained from 20L of culture. The improved solubility properties of this material led to crystals that routinely diffract in the 2.1-2.4 Å resolution range.

John Spurlino, Johnson & Johnson, described how his group uses fragment-based drug discovery with crystallography as the primary screening method. They screen fragments containing 6 -15 non-hydrogen atoms and, for example, ~1000 compounds in groups of 5. Compounds are grouped by shape rather than trying to provide distinct electron density profiles. No particular effort is made to prove the identity of the bound species; rather, the characteristics of the site and the mixture have proven to be adequate starting information. In one project, 6 fragment binding observations resulted in a lead compound, and in a second project, a high 25% hit rate led to the identification of two distinct binding pockets, one of which was previously unsuspected.

A provocative panel discussion about the challenges and rewards of industrial crystallography followed.

Jeff Bell and Timothy Rydel

9.02 Macromolecular Dynamics

From left: Bob Leheny, Kathleen Wood, Hirsh Nanda, Alec Sandy, Maikel Rheinstadter, and Jeremy Smith.

Our session focused on the application of complementary experimental probes and simulations to understand the dynamical properties of macromolecules. **Maikel Rheinstadter,** U. Missouri-Columbia, provided an excellent introduction by discussing both the importance and complexity of quantitatively studying dynamics in biological systems. Important because molecular dynamics plays a key role in the biological function of membranes; complex because of the extent of the time and length scales that must be studied to understand membrane functionality. He presented data from membranes, obtained by a variety of neutron techniques, and demonstrated how this comprehensive data provides insight into physiological function. **Bob Leheny**, Johns Hopkins U. presented x-ray photon correlation spectroscopy (XPCS) measurements of gold nanoparticles in a homopolymer matrix. Because the nanoparticle suspension was very dilute, his measurements could probe the dynamical nature of the matrix. Above the polymer glass transition, simple diffusive motion is observed while below the transition the observed dynamics are considerably more complex and depend on aging effects and intermittent stress relaxation in the polymer. **Dobrin Bossev**, Indiana U., presented investigations into the collective dynamics of long cylindrical micelles formed by cationic surfactants. Organic and inorganic counter ions were used to produce branched, linear and entangled micellular morphologies. Neutron spin echo (NSE) measurements were used to determine the persistent length and bending moduli of these systems. **Jeremy Smith**, U. Tennessee and ORNL, presented a comprehensive talk on protein dynamics combining x-ray crystallography, neutron scattering and molecular simulations. An investigation into low temperature methyl group dynamics showed such activation to be a result of protein packing defects. Smith also compared simulations of crystalline protein lattices with x-ray data. Atomistic simulations were able to reproduce many experimental parameters and provide additional insight into inter-protein interactions in lattices. **Kathleen Wood**, U. Groningen, addressed the coupling between dynamics of proteins and their environment. For water soluble proteins the onset of hydration dynamics directly coincides with the proteins biological activity. By taking advantage of neutron spectroscopy and isotopic labeling, Wood showed that for the purple membrane system containing the trans-membrane protein bacteriorhodopsin, dynamic activation of the lipids occurred at temperatures 50°K higher than water. Her work presents a new paradigm where activation of membrane proteins is potentially dictated by dynamic transitions of the lipid chains, decoupled from the water activation. **Hirsh Nanda**, NIST presented neutron scattering and molecular simulation data on the diffusive motions of saturated and unsaturated lipids, both important in biological membranes. First order phase transitions in saturated lipids are absent in unsaturated species. Atomistic simulations showed a decoupling between water exposed head groups and lipid chain motion. Coarse grain models properly represent average lipid motion but fail to get accurate relative relaxation rates.

Poster **MP156** presented by **Aravinda Raghavan**, ORNL, and **MP159** by **David Bohnsack**, Argonne, complemented the oral session. Both posters described the application of XPCS to study the dynamics of nanoparticles in polymer matrices. MP156 discussed novel changes in the bulk mechanical properties of a polymer system when heavily doped with nanoparticles and the accompanying microscopic stresses and long range interactions as probed by XPCS. MP159 described the effect of confinement on the mobility of nanoparticles within novel block-copolymer hompolymer sub-phases.

Joseph Curtis and Alec Sandy

At the opening reception, top, from left: Gurkan Yardimci, Ozgun Erdogan, Yen Pham, Violetta Weinreb; below, from left: Bob Bau, Bob vonDreele, and B.C. Wang.

L. to r., in back: Marilyn Olmstead, Gary Nichol, Karah Knope; in front: Bruce Noll, Gary Enright, Liangming Hu, Patrick Carroll, Allen Oliver.

Photo courtesy of Peter Müeller.

10.01 Cool Structures The Cool Structures symposium attracted a sizeable audience on the final day of the meeting. **Gary Nichol** introduced neutron diffraction studies for beginners with an overview of the technique and some surprising results from cyanuric acid complexes of group I metals. Metal-organic frameworks and hybrids were discussed by **Liangming Hu**. He observed several new structural motifs in the copper complexes of 4, 4' imidazoyl biphenyls, one of which was dubbed "Bamboo Tubes" for its resemblance in packing to the segment stalks of bamboo shoots. **Karah Knope** continued the metal-organic framework theme, with her presentation on the relatively unexplored field of lanthanide-organic frameworks. A variety of UO_2 building blocks were demonstrated to give controllable packing patterns.

The lanthanides were also featured in **Patrick Carroll**'s talk especially their utility in asymmetric synthesis. The complexes were studied using the JMOL software package, allowing researchers to better understand where active sites and sites of attack may appear within the complex.

Macromolecular Neutron Diffraction Posters

The poster by Zoe Fisher and coworkers in the Langan and Schoenborn group, **MP113**, described not only existing per-deuteration facilities, but also preliminary results from three proteins, DFPase (diisopropyl fluorophosphatase), PYP (photoactive yellow protein), and HbA (human hemoglobin). The latter was further elaborated in poster **SP179**, by Andrey Kovalevsky and collaborators in which all four heme groups in the deoxy form of human hemoglobin were described at 1.8 Å resolution..**TP-022** by Andre Mitschler and coworkers, describes results froma tiny (0.12 mm^3) perdeuterated crystal of Type III AntiFreeze Protein isolated from the Arctic fish *Macrozoarces Americanus*. Data werecollected up to a resolution of 2.0 Å at the new LADI-3 diffractometer at theInstitut Laue-Langevin. Finally, an important poster by **Flora Meilleur** *et al*, **MP-125**, describesd plans to construct a new diffractometer (tentatively called IMAGINE)to be used at the upgraded HFIR (High Flux Isotope Reactor) at Oak Ridge.When completed, IMAGINE (which is based on the LADI-3 design of ILL) will be the second macromolecular instrument at Oak Ridge; the first one, MaNDi (Macromolecular Neutron Diffractometer) will be using the brand-new high-intensity Spallation Neutron Source, while IMAGINE will use neutrons from their HFIR.

Bob Bau

Adamantane guest complexes within a cyclodextrin core were the topic of **Gary Enright**'s presentation. The difficulties and challenges faced in determining the structure of these essentially isolated and spherical molecules were discussed. **Marilyn Olmstead** continued the host-guest studies with a talk on the development of new host molecules to trap and co-crystallize with fullerene molecules. The hosts were developed taking into account the curvature of a fullerene. The final presentation, by **Bruce Noll**, was on the packing of thirane, a known gelatinase inhibitor that has been implicated in anti-cancer activity. Thiirane is shown to crystallize with six independent molecules in the asymmetric unit.

From Gary Enright: The ß-cyclodextrin / adamantane inclusion compound transforms over several years from an orthorhombic form (left) with four host and four guest molecules in the au to a triclinic form with six host and seven guest molecules in the au. The equivalent molecules are color coded. Water molecules located at interstitial sites between columns are not shown.

Allen Oliver

Macromolecular Neutron Diffraction Posters, con't: The poster by **Richard Ibberson**, *et al*, ISIS: *Design and Performance of the New Supermirror Guide on HRPD at ISIS*, **TP034**, presents impressive performance gains for this newly refurbished high resolution neutron powder dffractometer. They show intensity gains of 10-100× the old instrument which allows data collection of a much higher Q range with even better powder resolution than before. **TP083**, by **David Langs**, *et al*, HWI, gives new techniques for solving macromolecular structures from neutron data that can be obtained now from the new PCS instument at Los Alamos and soon from the eagerly awaited MANDi instrument at SNS.

Bob vonDreele

L to r, in back: Olivier Gourdon, Michael Ruf, Branton Campbell, Michal Dusek; in front: Jeff Lovelace, Lee Daniels, Ian Swainson, Peter Zavalij. Photo courtesy of Peter Müeller.

13.01 Incommensurate & Modulated Structures

By design, this session provided tutorial and educational material in the first half, followed by research-oriented material in the latter half. The highlight of the session was **Michal Dusek**'s nice description of the recently updated Jana2006 program. The latest version provides both solution and refinement of structures having up to three modulation vectors. Data from single crystals and powders are handled, measured with either or both x-rays and neutrons. The new menu-driven interface promises to be useful for an ever-widening audience. Systems that allow the collection, indexing and integration of single-crystal modulated data were introduced and demonstrated by **Lee Daniels** of Rigaku and **Michael Ruf** of Bruker. Both presenters provided useful explanations of the techniques involved and straightforward examples.

Branton Campbell, BYU piqued our interest with very nice demonstrations of his ISODISPLACE software for the visualization and demonstration of superspace-group symmetries. ISODISPLACE is available at **http://stokes.byu.edu/isodisplace.html**.

Jeff Lovelace, Eppley Inst., provided a protein crystallographer's example of modulation to the mostly non-macromolecular audience, and he included a quick description of the cow-in-a-blender method of gathering starting materials. Jeff's interesting example included pH-dependent modulation. **Ian Swainson**, Chalk River Labs, demonstrated predicting and modeling modes that lead to modulation in Perovskite-like materials. Analysis of tilt and buckling modes reveals the limited sets possible.

Peter Zavalij, U. Maryland, discussed disorder and the temperature-dependence of modulation in ammonium trivanadates, and included details of the integration and refinement techniques used. Finally, **Olivier Gourdon**, ORNL, broadened the discussion to include x-ray and neutron data in the study of long-range periodicity, emphasizing the role of displacement parameter analysis. The session generated so much interest in modulated structures that a call was made to host a workshop at ACA 2009. Details to follow!

Lee Daniels

L to r: Arthur Schultz, Ross Angel, Marilyn Olmstead, Shao-Liang Zheng, Ilia Guzel, Graciela Díaz de Delgado, Alexander Briceño, Bruce Foxman.

Photo courtesy of Bruce Noll.

13.02 Solid State Transformations and Reactions

Ilia Guzei set the theme for the session with a detailed and thorough study of a dual phase transformation involving dichloro-*bis*(η5-tert-butylcyclopentadienyl)titanium(IV). Although there are two phase transformations, one at 147°K and another at 293°K, only the first one shows up as a small blip in a DSC study. Furthermore, there are clear crystallographic indications for the transformations, but the structural changes are so slight as to be non-discernable. The use of a Si-diode temperature measuring device, designed in collaboration with Håkon Hope, that is inserted in the cold stream at the crystal position generated considerable interest. **Bruce Foxman**'s classification scheme for the various kinds of phase transformations and reactions added focus. His notation is: **Tn**, multiple phase topotactic reactions and solid-state polymerization; **T1**, one phase topotactic reactions; **SP**, single phase polycrystalline transformation; **SA**, single phase crystal-to-amorphous transformation; and **SCSCRs**, single crystal to single crystal reactions. Foxman also offered historical enlightenment in his inimitable way. **Dejan-Kresimir Bucar** presented elegant templates and new strategies for steering pairs of molecules into position for 2+2 addition reactions. He also showed how some of the product cyclobutane pyridyl molecules could be used as linkers for frameworks with unusual angular directionality. **Ross**

cont'd, next page

Angel offered further classifcation of structural phase transformations through the use of the order parameter Q and showed how it relates to changes in unit cell dimensions and diffracted intensities. **Art Schultz** gave an overview of how Tutton's salts have fascinated solid-state scientists for more than 200 years. Even today, our ability to understand thoroughly such effects as switching of the direction of Jahn-Teller disorder when D is substituted for H. **Shao-Liang Zheng** expanded on the 2+2 addition story with evidence that in some cases (when T=90° rather than 280°K) isomerization in addition to dimerization occurs. His "photodifference maps" show that when cavities of sufficient size exist, the addition product forms preferentially because at higher temperature greater molecular motion can occur. The reduction of molecular vibrations at low temperature makes isomerization competitive with addition and allows for a small fraction of the molecules to isomerize from E to Z.

Marilyn Olmstead and Graciela Díaz de Delgado

13.04: Diffraction Studies of Correlated Electron Systems

L to r: Andrew Christianson, Michel Kenzelmann, Andrey Zheludev, Peter Gehring, Jamie Fernandez-Baka, Igor Zaliznyak.

This session focused on the electronic phenomena; with crystallography used as an important tool for characterizing exciting new correlated electron systems.

Ferroelectricity has re-emerged as one on the hottest topics in condensed matter physics. **Michel Kenzelmann**, Paul Schereer Inst., dealt with a new breed of materials that combine ferroelectricity with ferromagnetism, the so-called multiferroics. In such compounds magnetic properties can be controlled by applying an electric field and vice versa. Obviously, they have an enormous potential for practical applications, but the microscopic mechanisms of the multiferroic effect are still debated. Kenzelmann demonstrated that competing ground states are essential, and that ferroelectricity is induced by magnetic order only if the magnetic structure creates a polar axis. A particular and somewhat mysterious multiferroic compound $LuFe_2O_4$ was described by **Andrew Christianson**, ORNL. **Peter Gehring**, NIST, focused on the so-called relaxor ferroelectrics that exhibit the largest reported piezoelectric coefficients and strain. The results of both diffraction and inelastic neutron experiments presented in this talk reveal a strong coupling between TA phonons and diffuse scattering due to short-range polar order. This conclusively relates the exceptional piezoelectricity to the quenched disorder endemic to relaxors.

Karen Mulfort was selected by the Small Angle Scattering SIG for an **Etter Student Lecturer Award.** She presented her talk *Solution Phase X-Ray Scattering: Structural Characterization of Supramolecular Porphyrin Assemblies* in session ***13.08: Catalysis Studies using SAXS and High Energy Scattering with PDF.***

Short-range charge and spin ordering in layered perovskite cobaltates, the less known relatives of the cuprate high-temperature superconductors, were topics addressed by **Igor Zalyznyak**, Brookhaven. As demonstrated by quasielastic neutron scattering studies, the superlattice ordering in Co-based materials is, in fact, driven by a number of competing mechanisms, such as CDW instabilities, spin exchange, Jahn-Teller instabilities and electrostatic interactions. Of particular interest is the fact that in most cases the emerging superlattices are short-range ordered.

Jaime Fernandez-Baka, ORNL, spoke on another popular topic, namely ***colossally magnetoresistive* manganites**. The focus was primarily on the highly anisotropic smectic liquid-crystal-like textures with ferromagnetic quasi-long-range one-dimensional order in half-doped perovskite PCSMO compounds. This is a dramatic example of strong coupling between spin and lattice degrees of freedom.

These diverse topics were unified by one central theme. The interplay between competing interactions in complex correlated electron systems culminates in long- or short-range superstructures involving spin, charge or orbital degrees of freedom. Crystallographic studies aimed at mapping out these superstructures are crucial to understanding the magnetic, electrostatic and transport properties of these novel materials.

Andrey Zheludev

13.05: Modern Teaching Tools for 21st Century Science

From left: Bernhard Rupp, Katherine Kantardjieff, and Brian Toby. Photo courtesy of Katherine Kantardjieff.

In his talk about educating virtual APS users, **Brain Toby**, APS, Argonne, pointed out that the increasing use of mail-in samples and remote data collection at synchrotron sources does not exempt users from proper training in sample preparation and analysis of their diffraction data. The education needed to analyze powder diffraction data which was formerly obtained from the resident expert beam scientist now must be gleaned from sources such as audio-visual web based lectures or interactive training tutorials. The APS powder diffraction online material includes access to all the necessary tools and analysis software as well as webcast lectures.

Katherine Kantardjieff, Keck Center, Cal State-Fullerton, pointed out that while non-curricular resources such as web tools and tutorials are a step in the right direction, they often remain fragmented and are insufficient to support the migration of academic crystallography from a research specialty to a technique employed by a wide community of users. With modern remote access tools for diffractometers and the available cyberinfrastructure for webcasting and web-conferencing, one can effectively provide practical, hands-on experience by broadening access to instrumentation, data handling, and data analysis. A large and diverse user community can acquire the knowledge necessary to use crystallographic results as well as to critically review published structures. Kantardjieff recently received the 2008 Campus Technology Innovators Award for her implementation of web conferencing, blended learning, and remote instrument access at CSU Fullerton.

Bernhard Rupp, q.e.d.Life Sci. Discoveries, author of the venerable web tutorial *Crystallography 101* (**www.ruppweb.org**), observed that many of the recent problems affecting published high-profile structures may not be only a result of poor formal crystallographic training. A close inspection of several questionable structures revealed general disregard for the process of scientific inquiry, which is of even more concern because it leads to improbable structures and misinterpretations. We should try to teach crystallography in a larger framework, consistently emphasizing the role of evidence, likelihood, and probability. Then, even if the details of crystallographic theory are forgotten, the fundamentals of proper inquiry and inference will remain and will be useful.

Bernhard Rupp

13.06: Molecular Magnets

Joel Miller, U. Utah, opened with a talk describing new materials for the new millennium. He described his work to characterize the crystal structures of cyano-based magnets by synchrotron powder x-ray diffraction. **Andrey Zheludev**, ORNL, summarized his work on magnetized chains and ladders. **Louise Dawe**, Memorial U., CA, gave a talk on $n \times n$ (n up to nine) molecular grids and described their complex magnetic behaviors in terms of zero-field splittings and exchange coupling of paramagnetic centers. Dawe also won the ***JCC Poster Prize*** **(see p.20)**. **Paul Lahti**, U. Mass.-Amerherst, described the structural and magnetic properties of a novel class of organic magnets comprised of benzimidazole-based nitronyl nitroxides. **John Schlueter**, Argonne, and **Jan Musfeldt**, U. Tennessee, presented complimentary talks on copper pyrazine coordination polymers, specifically x-ray structural, magnetic and infrared properties of a class of materials that contain strong F···H-O or F···H···F hydrogen bonds. The talks clearly demonstrated the importance of crystallography in establishing structure-property relationships in molecular magnets.

L to r: Andrey Zheludev, Joel Miller, Jamie Manson, Janice Musfeldt, Louise Dawe, John Schlueter, Arsen Gukasov, Paul Lahti. Photo courtesy of Victor Young.

Jamie Manson

13.07 Professional Directions

This session was a panel discussion with five scientists participating who represented different scientific careers: **David Rose**, U.Toronto, **Jane Richardson**, Duke U., **Jeanette Krause**, U.Cincinnati, **William Duax**, Hauptman-Woodward Inst., and **Charles Campana**, Bruker AXS. The session was well received and well-attended.

The panel delivered many years' worth of lessons for those attending as they addressed questions a young scientist would ask while progressing through different stages of his career, *i.e.* graduate student, postdoc, etc. In addition the panel provided good insights about the various experiences one might expect from different career paths. If you missed this panel discussion, do not fret; we plan on a similar session in Toronto '09.

Bobby Huether

L to r: Bobby Huether, Jane Richardson, Jennifer Krause, Charles Campana, Bill Duax, David Rose.

13.09 Emerging Opportunities for X-ray and Neutron Scattering: New Sources and New Techniques

As many as 70 were in the audience to learn about construction, and plans for upgrades, of new x-ray and neutron sources. **Keith Hodgson**, Stanford U. and SSRL, reported on the Linac Coherent Light Source (LCLS, **www-ssrl.slac.stanford.edu/lcls/**, which should begin operation in about a year. A 130m-long undulator will produce repetitive pulses at 120Hz. The electron beam emittance is 0.03nmrad. Each 100fs-long pulse will carry 4×10^{12} x-ray photons. A diffraction pattern might be obtained from a single protein molecule, leading to potential new modes of structure solution.

From left: in back, Edgar Weckert, Bob Sweet, Mateusz Pita, Richard Ibberson; middle: Liz Duke, Keith Hodgson, Jennifer Doebbler, Ken Herwig; in front, Dennis Mills, John Hill, John Spence, Ed Mitchell.

Edgar Weckert reported from the German synchrotron source DESY, in Hamburg: **www.desy.de/**. The original Petra ring will begin operating as the Petra III light source in 2009, functioning at 6GeV with a 1 nmrad horizontal emittance. Their new 300m-long experimental hall will contain 14 undulator stations, nine for diffraction studies. FLASH is a VUV free-electron laser which produces 10-25 fs pulses at 700Hz. Peak brilliance: 2×10^{29}; spectral width: <1%. Beginning in 2009, they hope to create a x-ray free-electron laser (XFEL) that would produce 30k pulses per second, with 10^{12} Xph/pulse. **John Hill** described the progress and prospects for NSLS-II, a third-generation synchrotron for Brookhaven National Laboratory, **www.bnl.gov/nsls2/**. The ring will operate at 3GeV, 500mA, with a horizontal emittance of 0.6nmrad. There will be over 60 individual sources. The ultimate goals are 1nm spatial resolution or 0.1meV energy resolution, with experimental stations to exploit these characteristics. Stations are planned for additional diffraction and imaging studies, including life science.

John Spence, Arizona State U., described work on methods to exploit the energy-recovery linac source planned for Cornell, **www.lepp.cornell.edu/Research/AP/ER/**. It would have properties approaching those of a free-electron laser, and provide capabilities beyond those of a storage ring. The plan is to pass streaming particles by the ultra-bright x-ray beam. They simulated the single-molecule experiment envisaged for the Stanford LCLS, then experimented with micro crystals, demonstrating a powder pattern from half-micron crystallites of Photosystem 1 protein. They also reconstructed the projection image of 50nm gold balls in submicron water droplets. **Dennis Mills**, Argonne and APS, described their planning for an upgrade to the APS. How does one improve a world-leading source? Eight systems are proposed to employ the existing ring, producing brightness increases from about two to a few hundred, **www.aps.anl.gov/Renewal/APS2020UpgradePlan/index.html.** In every case the cost and technical risk roughly matches the increase in brightness. Workshops will engage the user community to create a full plan.

Edward Mitchell described upgrades planned for the ESRF, Grenoble, France, **www.esrf.eu/AboutUs/Upgrade/purple-book/**. They emphasize five scientific themes: nanoscience and nanotechnology; structural and functional biology and soft matter; pump-and-probe experiments and time-resolved science; science at extreme conditions; and x-ray imaging.

13.09 Emerging Opportunities, cont'd

The upgrade will include reconstruction of about one half of the existing 31 sectors to improve nanofocussing, permit more undulators and a brigher lattice, build several >100m beamlines, and make more space. **Elizabeth Duke** described opportunities for diffraction at the Diamond synchrotron source near Oxford, UK., **www.diamond.ac.uk**. Diamond is a 3GeV machine producing x-rays of energy between 100eV and 20keV, which began operation in 2007 with eight beamlines. Six are for hard x-ray diffraction, and include three for macromolecular crystallography (MX), one for materials and magnetism, one for the study of materials at extreme conditions, and one for non-crystalline diffraction. One of the three MX beamlines has Category 3 biocontainment. One nearing completion will produce a 5μm beam.

Kenneth Herwig, Deputy Director of the Neutron Scattering Science Division at Oak Ridge National Laboratory (ORNL), introduced the two neutron-scattering facilities at ORNL, the new Spallation Neutron Source (SNS) and the upgraded High Flux Isotope Reactor: **neutrons.ornl.gov/**. The SNS is the highest power pulsed spallation source in the world, while the HFIR has an unsurpassed cold source for producing long wavelength neutrons. The SNS has three scientific instruments with seven more coming by the end of 2008. The HFIR has two SANS instruments; six more stations will be completed by the end of the year. The facilities are rapidly enhancing their capabilities for SANS and both powder and single-crystal diffraction. **Brian Maranville**, staff scientist at the NIST Center for Neutron Research, presented the status of the NCNR second cold source/guide hall project: **www.ncnr.nist.gov/**. New instruments include novel neutron reflectometers that use multiple, polychromatic neutron beams for specular studies (CANDoR), and methods to enable off-specular measurements of in-plane magnetic and chemical order.

Richard Ibberson reported on the recently upgraded High Resolution Powder Diffractometer (HRPD) at the ISIS pulsed neutron facility at the Rutherford Appleton Laboratory near Oxford, UK: **www.isis.rl.ac.uk/**. ISIS just began operation of a second station for three disciplines: soft matter, bio-sciences, and advanced materials. Richard described the evolving instruments at the new target station and developments on the crystallography instruments installed on the first station. A high-performance neutron guide produces a dramatic gain in performance.

Mateusz Pitak, SUNY, Buffalo, presented time-resolved diffraction studies of metallo-organic complexes collected at the NW14 beamline at the Photon Factory's Advanced Ring at Tsukuba, Japan. **Jennifer Doebbler**, ANL, described an intriguing study that explored the applicability and limitations of macromolecular powder diffraction.

Bob Sweet and Ken Herwig

From left: Venkat Thalladi, Lian Yu, Jerome Delhomelle, Bart Kahr, Kraig Wheeler, Nair Rodriguez-Hornedo, Matthew Peterson, Graciela Díaz de Delgado, Ray Davis, Chris Cahill, Carol Brock, Ryan Sours, Lara Estroff, Clare Yannette, Jennifer Swift.

Photo courtesy of Peter Müeller.

13.10 Supramolecular Chemistry

Three half-day sessions, co-sponsored by the small molecule and material science SIGs, addressed the topic *Organic Crystals from Assembly to Function*.

In the session emphasizing assembly aspects of crystals – *i.e.* nucleation and growth, **Bart Kahr**, U. Washington, presented an inspired update to last year's ACA talk on the history of induced optical activity. In reproducing some experiments on doped single crystals of sodium chlorate first performed by Eligio Perucca, Bart was able to describe complex optical behavior in understandable terms. Through his friendship and collaboration with Davide Viterbo he was able to paint a more accurate picture of the character of Perucca than that which emerged the previous year. Ryan Sours, Towson State University, reported on his ongoing chromatography studies which cleverly seek to elucidate the residence time of impurities on mineral surfaces that can affect their growth rates. **Venkat Thalladi**, Worcester Polytechnic Inst., described the virtues of controlling nucleation and growth on templates through either attractive or repulsive interactions as well as new microwave methods for achieving polymorph control.

Lian Yu, U. Wisconsin-Madison, and **Jerome Delhommelle**, U. South Carolina (soon to be U. North Dakota) spoke on the experimental (Lian) and computational (Jerome) aspects of polymorph cross-nucleation. By examining the cross-nucleation kinetics of various polymorphs, Lian was able to conclude that only some polymorphs exhibit diffusionless growth modes, notably the ones with more isotropic unit cell parameters. Jerome's Monte Carlo calculations necessarily focused on simpler colloidal systems and aluminum, but similarly demonstrated that less stable phases do appear to nucleate on the surfaces of more stable phases.

cont'd, next page

13.10: Supramolecular Chemistry, cont'd:

Clare Yannette, Georgetown U., on the left, was selected by the small molecule SIG to receive a **Margaret C. Etter Student Lecturer Award** which was presented by Chair Jennifer Swift. Yanette described her *in situ* AFM and dynamic light scattering studies on monosodium urate monohydrate, the gout crystals.

Continuing this theme and extending it to include important thermodynamic aspects of cocrystals and other multicomponent assemblies, **Nair Rodriguez-Hornedo**, U Michigan, described some alternative strategies to prepare cocrystals such as tweaking the solution composition. **Ray Davis**, U Texas, provided an update on the interesting isomerism observed in dimers of phenylpropiolyl chloride (first isolated in 1949 by Elga Wasserman). **Carol Brock**, U Kentucky, likewise pursued a nagging crystallographic puzzle. She described her work on 1:1 cocrystals of TPPO:1,2-cyclohexanediol which her group first began studying 17 years ago. Their diffraction patterns were curiously sensitive to the growth solvent. Both Ray and Carol's studies are good examples of the rewards of persistence. **Matt Peterson**, Transform Pharmaceuticals, did calorimetric studies on isostructural cocrystals. He emphasized the importance of considering enthalpic factors in solution in order to fully understand cocrystal formation.

Kraig Wheeler, Eastern Illinois U., told of his latest adventures in quasiracemates, concluding with some remarkable crystal habits observed for ammonium bitartrate/bimalate.

From Kraig Wheeler: unusual crystals of ammonium (+)-bitartrate (center crystal) and ammonium (+)-bitartrate/ammonium (-)-bimalate (outer laths) formed from heteroepitaxial growth. See Rediscovering Pasteur's Quasiracemates, Ang. Chem., Int. Ed. Engl. 2008, 47, 78-81, Wheeler, K.A., Grove, R.C., Davis, R.E., Kassel, W.S..

Lara Estroff, Cornell, emulated biogenic $CaCO_3$ by growing crystals in certain hydrogel media. Her methods provide a means not only to elucidate fundamental biomineralization pathways, but also to create synthetic materials with enhanced mechanical properties.

In the final session new materials and the functional aspects of structure-property relationships were emphasized. **Chris Cahill**, George Washington U, reminded us that the often overlooked f-elements at the bottom of (some) periodic tables can definitely make for interesting crystal chemistry experiments. Continuing with the organometallic theme, **Graciela Díaz de Delgado**, U. de Los Andes, Venezuela, presented her work on metal citraconates prepared using hydrothermal methods and described the sometimes surprising phases that can result under these conditions.

Jamie Manson, Eastern Washington U, brought the session squarely into the territory of functional materials with his detailed description of the magnetic properties exhibited by a set of layered copper pyrazine complexes. **Mike Ward**, NYU, spoke about the predictable solid state assembly of guanidinium organosulfonates and the many practical applications of theses robust hydrogen bonded framework materials. **Nenad Judas**, U. Zagreb, described his ongoing work on a class of metal(II)-β-diketonate coordination polymers. **Elinor Spencer**, VA Tech, gave a terrific talk on her recent discovery of a seemingly irreversible phase transformation that is observed under high pressure conditions but which is not obtainable by conventional growth methods. **Nick Deifel**, George Washington U, wrapped up the supramolecular chemistry session with a description of the preparation and characterization of uranium phosphate materials.

There were a number of beautiful high quality posters that were related to the topics in these sessions. Among them, **SP205**, by **Marta Dabros**, Worcester Polytechnic Inst., won the **CrystEngComm** poster award for *Multicomponent Organic and Pharmaceutical Solid Solutions*, and **SP207** by **Ilana Goldberg**, was awarded a **Pauling Prize** (*see p. 19*).

Jennifer Swift

Jennifer Swift, at right, presenting the CrystEngComm poster award to Marta Dabros. Both photos are courtesy of Jennifer Swift.

Index of Advertisers

L to r: Gregory Beaucage, Michal Hammel, Thomas Weiss, Greg Hura, Jennifer Hinerman, Efstraitios Mylonas, Dilano Saldin, Robert Briber, William Heller.

13.11 Biological Applications of SAXS and SANS

This session, co-sponsored by the small-angle and synchrotron SIGs, showcased topics in biological small-angle scattering, including protein folding studies by small-angle x-ray scattering, SAXS, and small-angle neutron scattering, SANS as well as modeling and analysis methods and experimental facilities.

Robert Briber, U. Maryland, used SAXS to investigate structural collapse and folding of the Azoarcus ribozyme in response to Mg^{2+}. Steady state studies indicate that the ribozyme initially collapses into an intermediate state before transitioning into the native fold. Stopped-flow SAXS was performed at the BioCAT beamline at the APS at Argonne. The results show a two-state folding process with time constants of 2-4 msec and 0.5-50 sec. **Efstratios Mylonas**, EMBL-Hamburg, presented SAXS studies of natively unfolded proteins and subsequent analyses. Natively unfolded proteins and dynamic structures have been shown to be important to biological function. A modeling approach was presented to characterize the structural ensemble present in solution that can also incorporate data from other sources such as FRET, electron microscopy and NMR to provide additional modeling constraints. **Thomas Weiss,** SSRL/SLAC, presented a talk about Beamline 4-2, the small-angle scattering/diffraction instrument at the Stanford Synchrotron Radiation Laboratory. Recent improvements to the beamline were presented, along with sample environments for single crystal and fiber diffraction, grazing incidence SAXS, lipid diffraction and time resolved studies using a stopped-flow apparatus. The instrument specific Blu-ICE/DCS data acquisition software was also discussed. **Gregory Beaucage**, U. Cincinnati, presented an improved model to describe SAXS data from unfolded and disordered proteins, which has applications to protein folding and denaturing, as well as to natively unfolded proteins. The model developed provides a means of quantifying the degree of disorder in the unfolded state. The model was applied to three example systems from the literature.

Michal Hammel, Lawrence Berkeley Natl. Lab., presented a modeling method for SAXS data that explores conformational space with molecular dynamics simulations. The approach is ideally suited for multidomain proteins and complexes that contain flexible linker regions. The application of computational docking to model SAXS data of biological complexes in solution was also described. Examples presented included the cohesin-dockerin complex and the Ku/DNA system, a complex integral to repair of damaged DNA.

Dilano Saldin, UW-Milwaukee, described an improved approach for shape restoration from SAXS data using spherical harmonics. The work is driven by the development of the x-ray free electron laser, which is expected to enable the collection of SAXS data from a single protein. The combination of successive images from the protein collected at different angles relative to the incident beam, providing single molecule diffraction data, is expected to enable reconstruction of molecular envelopes.

Jennifer Hinerman, U.Toledo, presented the results of investigations of the Bacteriophage T4 replication complex using SAXS, SANS and crystallography. Two proteins, the gp59 helical assembly protein and the gp32 single-strand DNA binding protein, and their complexes with DNA were studied using the ChemMatCARS facility at the APS at Argonne and the BioSANS instrument of the Center for Structural Molecular Biology at the High Flux Isotope Reactor at ORNL.

Additionally, several posters were presented including a description of a high-throughput approach for studying proteins by SAXS by **Greg Hura** and coworkers, **MP013**. The natively unfolded protein FEZ1 was probed by SAXS by **Julio Silva** and coworkers, **TP012**. **William Heller** and coworkers, **TP024**, described SAXS studies of detergent-associated membrane proteins. Time-resolved SAXS studies of the AAA+ ATPase were presented by **Tracy Nixon** and coworkers, **TP092**. **Antoello Longo** and coworkers, **TP096**, studied complexes of proteins from the insulin promoter with DNA with small-angle scattering and crystallography. SAXS was used to characterize the solution structure of the APOBEC3G and APOBEC-1 complementation factor by **Jason Salter** and coworkers, **MP146**.

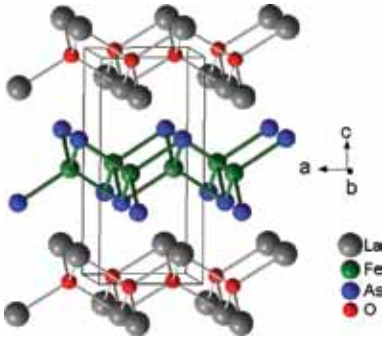
William Heller and Greg Hura

Photo of the Knoxville Sun Sphere, courtesy of Peter Müeller.

L to r: Xiaoping Wang, Winnie Wong-Ng, Jason Hodges, Craig Brown, Jae-Hyuk Her, Michael McGuire, Hui Wu.

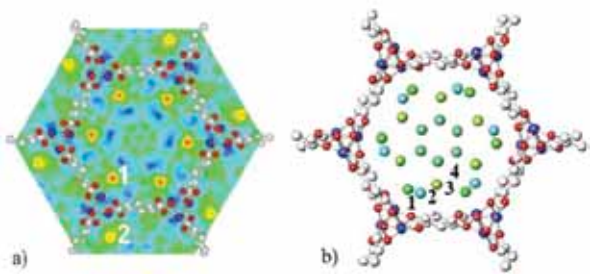
13.13 Materials for Energy Applications

Michael McGuire, ORNL, began by introducing the basic concepts of thermoelectricity, thermoelectric devices and the highly sought material properties conducive to high ZT efficiency thermoelectric modules. After reviewing signature traits in the crystal structures of good known thermoelectric materials,



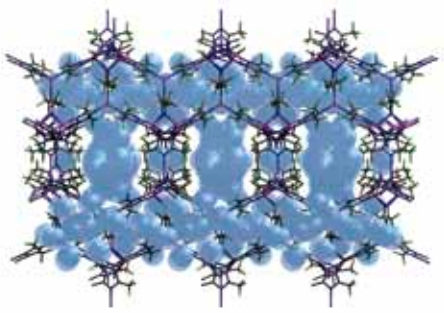
From Michael McGuire: the crystal structure of LaFeAsO. When doped with fluorine this material becomes superconducting below 28ºK. Above this temperature promising thermoelectric properties are observed.

Michael moved on to his own observations of relatively high ZT values at LT in the fluorine-doped LaFeAsO class of high-temperature superconductors. Their "dopability" and compositional variability makes the lanthanide iron oxide-pnictides and their relatives potential advanced thermoelectric materials. In light of recent interest in coordination polymer frameworks as physisorbents, **Craig Brown**, NIST, presented both neutron diffraction and inelastic neutron scattering of archetypal systems as they relate to average structures and described the local rotational potential where the quantum mechanical rotor, hydrogen, sits. In a variety of materials that are hydrogen adsorbents, exposed metal centers aid in increasing the enthalpy of adsorption for hydrogen by allowing for a direct interaction between the hydrogen and the metal. Craig also showed crystallographic evidence for monolayer hydrogen packing densities greater than bulk solid hydrogen at 4ºK in MOF-74. Continuing the theme of physisorption-based hydrogen storage materials,



From Craig Brown: a) Fourier Difference of adsorbed deuterium in MOF-74 and b) resulting Rietveld refinements of locations.

Jae-Hyuk Her, U.Maryland and NIST, has investigated MOF aluminum terephthalate. After a recent publication showed a large hysteresis in the isothermal hydrogen adsorption, he undertook a LT x-ray powder diffraction study of the bare material. The results showed an unexpected structural phase transition from an open-pore to closed-pore structure with an extremely large hysteresis between ≈ 100ºK and ≈ 300ºK. This is very unusual, as observations of similar structural transitions have been reported only in the cases of solvation where there is significant solvent-framework interaction. Neutron powder diffraction studies of this material loaded with D_2 gas showed that this open – closed pore structural transition could be suppressed, and Rietveld analysis revealed two sites for the D_2 molecules within the pores. Moving on to zeolitic imidazolate frameworks **Hui Wu**, U.Maryland, presented a neutron powder diffraction study of the methane sorption sites in $Zn_6(N_2C_4H_5)_{12}$, (ZIF8). This differs from $Zn_4O_{13}(C_8H_4)_3$ (MOF-5), where methane adsorption is primarily associated with the zinc oxide cluster; in ZIF8, methane was observed binding to the organic linkers. **Winnie Wong-Ng**, NIST, presented her latest results on a combinatorial survey of ternary series (Ca-Sr-Co-O) of thermoelectrics, related to the layered cobaltites of $Ca_3Co_2O_6$ and $Ca_3Co_4O_9$, that exhibit both large Seebeck coefficients and low resistivities. Winnie continued, describing the standardization and metrology efforts at NIST and in particular the future production of a Seebeck coefficient standard reference material. **Xiaoping Wang**, U.North Texas, presented a series of single crystal studies on a perfluorinated MOF with



From Xiaoping Wang: The crystal structure of FMOF-1 under nitrogen at 100°K. The crystal structure of FMOF-1 in a vacuum-sealed capillary tube is published in: Yang, C., Wang, X., Omary, M. A., J. Am. Chem. Soc. 2007, 129, 15454.

silver–triazolate clusters (FMOF-1). The simultaneous *in-situ* nitrogen adsorption measurements were performed under extremely slow changes in temperature to preserve the single crystal. A mechanism for gas adsorption and subsequent trapping was illustrated with the aid of the single crystal refinements where the pendent methyl groups of the triazole rotate into the pore openings and provide a kinetic barrier to gas desorption at higher temperatures.

Jason Hodges & Craig Brown

L to r: Ruslan Sanishvili, Robert Fischetti, Gwyndaf Evans, Gebhard Schertler, Claudio Nicolini, Richard Gillilan, Eugenia Pechkova, Sterling Cornaby, Jan Abrahams.

13.14: Microcrystallography

In his introduction, **Richard Gillilan**, MacCHESS presented some preliminary statistics on crystal size to illustrate the magnitude of the problems faced by structural biologists today, as well as an overview of the current state of microcrystallography at synchrotron sources worldwide. There are now 11 synchrotron beamlines capable of microcrystallography; an additional 6 are expected in the near future.

Eugenia Pechkova, Nanoworld Inst., U. Genova, Italy talked about Grazing-Incidence Small-Angle X-ray Scattering (GISAXS), a popular technique for examining nanoscale structure in thin films. Pechkova introduced an experimental setup which enables GISAXS to be applied to hanging drop protein crystallization experiments. An x-ray microbeam passes through a sample cell, glancing off the cover slip surface supporting the inverted drop. Nanostructure formation on the glass surface is revealed in the 2D scattering patterns. Protein crystal formation can be facilitated by creating a nanotemplate on the glass composed of protein monolayers deposited as Langmuir-Blodgett (LB) films. **Claudio Nicolini** of Nanoworld Inst. and also Fondazione Elba, discussed nanotemplate-induced growth by presenting a detailed comparison between standard hanging drop and LB-modified hanging drop crystallizations using submicron GISAXS. Time evolution of intensities in the region around the Yoneda peak support the notion that seed formation and crystal growth are rapid at the LB-modified surface compared to standard conditions. The data were collected on ID13 at ESRF. **Jan Abrahams**, Leiden U., The Netherlands, talked about high resolution electron diffraction of nanocrystals. Because electrons interact with matter more strongly than photons, electron diffraction patterns can be collected from much smaller crystals than presently possible with x-rays. The amount of information obtained for a given amount of radiation damage is also larger. Abrahams obtained high-resolution diffraction patterns (2.0 Å and better) from protein crystals as small as 200 nm in diameter using electron microscopy techniques. Because it is difficult to rotate samples under these conditions, it was necessary to tilt the electron beam using special optical elements; the limited tilt range made it necessary to use multiple crystals. Processing electron diffraction data poses some special challenges, particularly in indexing the patterns. Abrahams used this technique to examine protein crystal nucleation on human hairs.

Sterling Cornaby, Cornell, has constructed a unique "transmission mirror" system using a 300 nm thick silicon nitride film that allows him to precisely control the energy bandwidth of the x-ray beam. At a bandwidth of approximately 30% and energy 12 keV, a single snapshot captures the equivalent of 3-8° of crystal rotation with very high flux. *By focusing down to a 16 µm ×10 µm beam using capillary optics, Cornaby was able to deliver 1.9×10^{11} photons/sec to microcrystal samples on a bending magnet line (CHESS D1).* A complete lysozyme structure was obtained from 3 microcrystals with a total of only 14 images using the Daresbury Laue processing suite. Laue microdiffraction using capillary optics is a promising new technique that could dramatically expand the abilities of even weak beamlines to handle the smallest crystals. **Sterling Cornaby**, at left below, was presented with the Synchrotron SIG's **Etter Student Lecturer Award** by Richard Gillilan.

Gwyndaf Evans, Diamond Light Source, UK, unveiled I24, a dedicated microfocus beamline at the Diamond Light Source that came online this summer. For very small diameter beams, motion in the source and optical components becomes an important issue for stability at the focal spot. Evans outlined I24's unique design solution to this problem. In addition to beamline optics design, other endstation developments were discussed, including an impressive demonstration of optical tweezers for manipulating microcrystals. **Gebhard Schertler**, Cambridge, collected diffraction data on xylanase II using a 1 µm diameter x-ray beam with flux density of 3×10^{10} photons/sec/µm^2 at ESRF's ID13. Even with a sample volume of only 20 µm^3, good high-resolution data were obtained. The absence of radiation damage suggests that small samples may indeed suffer less damage due to escape of photoelectrons. This finding is consistent with recent Monte Carlo calculations. Schertler also described using special carbon film sample supports to hold crystals without excess liquid. **Robert Fischetti**, APS, reported obtaining the first 1 µm beam at GM/CA-CAT using a long focal

cont'd, next page

13.14 Microcrystallograpy, cont'd

length Fresnel Zone Plate in combination with KB mirrors. Data from horizontally and vertically scanned 1 mm spots on a single crystal support the idea that damaging photoelectrons are preferentially ejected according to beam polarization and thus crystals subjected to small beams may experience reduced radiation damage in certain directions. Fischetti also described recent station innovations including an aperture scatter guard assembly that can be switched automatically to provide different sized beams. Automated sample scanning is also being implemented that should prove useful for locating the best diffracting spots on larger crystals. Microcrystallography techniques have appeared in several other sessions. Two of the speakers in the Difficult Structures session presented structures that required using microbeam techniques, Changrui Lu and Gebhard Schertler. Microbeam optics and methodology are also finding their way to lab sources as evidenced by Jörg Wiesmann's talk in General Interest II, and Daniel Frankel's poster TP194. The organizers thank the ACA and PulseRay for the additional support that made this session possible.

Richard Gillilan and Ruslan Sanishvili

13.16 Time Resolved Scattering

Although scheduled late on the last day, the attendance at this joint session between BioMac and SAS SIGs, pleasantly surprised organizers **Vukica Srajer** and **Pappanan Thiyagarajan**. **Dominique Bourgeois**, CNRS/ESRF, presented sub-ns time-resolved Laue diffraction studies on a triple mutant of myoglobin conducted at ESRF. The studies explored the migration of the photo-dissociated CO ligand through the network of protein cavities as well as the very early phases of heme and protein relaxation following ligand release. A bi-phasic heme relaxation was observed, with a fast, ps phase and a slower phase, extending into the ns time domain. In his talk **Marius Schmidt**, U.Wisconsin-Milwaukee, discussed the latest time-resolved Laue diffraction experiments conducted at the newly upgraded 14-ID beamline for time-resolved protein crystallography at APS. These experiments aim at unambiguous determination of the chemical kinetics mechanism of the photoactive yellow protein (PYP) photocycle by utilizing singular value decomposition analysis of time-resolved crystallographic data as a function of temperature. He also presented his recent work with photoactive proteins that could be used as stable photo-optical switches. A detailed description of how such molecular photo-switches work will be obtained by time-resolved methods. Hyotcherl Ihee (KAIST) presented a very nice overview of the mechanism of the PYP photocycle, pointing at some presently unresolved inconsistencies in results obtained from various spectroscopic and diffraction measurements. He then discussed the latest results from state-of-the-art time-resolved Laue diffraction experiments at the ID09 beamline at ESRF, which elucidated the earliest intermediates in the PYP photocycle, from 100ps into the ns time domain. Fascinating applications of time-resolved small angle x-ray scattering in a time domain of sub ms to seconds were presented on three different biological systems.

Satoshi Takahashi, Osaka U. presented an elegant talk on the mechanism of protein folding probed by TR-SAXS and a continuous flow mixer with sub ms mixing time developed at Spring8. His data revealed that proteins with 100 residues or less follow a common folding mechanism termed "collapse and search", in which the collapse occurs within several hundreds of microseconds followed by the formation of the native structure in the time domain from milliseconds to seconds. A scaling law involving the radius of gyration and the number of residues was seen for the collapsed states of proteins. They are interested in developing new faster mixers to access faster time scales of protein folding and investigate larger proteins. **Roland Winter**, Technical U., Dortmund, highlighted the use of pressure as a thermodynamic variable in their pioneering pressure dependent time resolved scattering studies of protein folding, phase transition in lipids and lipid protein complexes at the beam lines at the APS and ESRF. He showed evidence for the differences between the unfolded states attained by pressure jump and other means and the slower rates of folding from the pressure unfolded states and potential reasons for that. **Hiro Tsuruta**, SSRL/SLAC presented his long term research on the allosteric mechanism involved in the function of ATCase mediated by the hydrolysis of various nucleoside phosphates. Although earlier studies were carried out at high protein concentration in ethylene glycol solutions and at low temperature to slow down the kinetics, the higher flux with the current synchrotron sources enables them to follow the faster kinetics in their recent studies.

Pappanan Thiyagarajan and Vukica Srajer

Accompanying Members; clockwise, from the far left: Joan Schwalbe, Nancy Fratini, Haruko Hamlin, Annas Rae, Ruth Clearfield, Bretna Hackert, Carol Johnson and Sharon Davis.

Across the top: Peter Horanyi, Ryan Jackson, and Matthew Cheever (JP); Christine Beaver, Marilyn Olmstead, Peter Müeller, and Joerg Kaercher (BN). Next row: Bob Finnegan; Victor Young and Richard Staples (PM); Shiva Bhowmik. Next row down: Bill Duax and Judy Flippen (JP); Rekha Pattanayek and Jim Pflugrath (JP); Jason Hodges and Mahadevan Lakshminarasimhan (JP). Across bottom: Gerard Bricogne and Charlie Carter (JF), and, at the banquet, the "Tulinsky connection" group: Kahlil Abboud, Ruth Clearfield, Shelegh Ferguson-Miller, Bobby Barnett, Ann Wolff, Sharon Davis and Ray Davis.

Photos courtesy of Bruce Noll (BN); Peter Müeller (PM); Jim Pfflugrath (JP); andd Judy Flippen-Anderson (JF).

From Molecules to Medicines: Integrating Crystallography in Drug Discovery

Centro Ettore Majorana, Erice (Sicily) Italy, 29th May - 8th June

This crystallography school, the 40th consecutive Erice course, a remarkable anniversary, certainly deserved the **RUBY** status it was accorded. The drug discovery focus is a recurring theme begun in 1983 and this year's scientific program, the collaboration of Directors Colin Groom of UCB UK, and Joel Sussman,Weizmann Inst., featured several presenters who were regulars from the earliest meetings, notably **Tom Blundell**, U. Cambridge and Astex Therapeutics, and now Director of the Erice International School of Crystallography, **Peter Goodford**, U. Oxford, formerly of Wellcome and creator of GRID, **Trevor Petcher**, U. Bern, formerly of Novartis. The program offered a rich diet of recent structural and bio-informatics results from academia: **Bill Weis**'s (Stanford) β-andrenergic receptor and **Gabriele Cruciani**'s (Perugia) probing of the impact of structure on metabolic studies are only two examples. Drug-design applications from industry included **Giovanna Scapin**'s (Merck) studies of dipeptidyl peptidase-4 inhibition and **Sandra Cowan-Jacob**'s (Novartis) work on countering Gleevec resistance, (again to name only two). Piquing widespread interest was the introduction of some nifty new tools for communication of structure by **Eran Hodis** and **Joel Sussman**, including Proteopedia, see **http://www.proteopedia.org/**).

In the final analysis, though, the Erice meeting is a school and the emphasis was firmly on students. They made up the majority of the 165 scientific participants and came from countries all across the globe including Turkey, Croatia, Latvia, Lithuania, Brazil, Nigeria, South Africa, India, Malaysia, Australia, New Zealand and Vietnam. After lectures in the morning, the program most days shifted to workshops in the afternoon. These offered demonstration sessions by experts on crystallization, database resources like CCDC, EBI and PDB, CCP4 and computational and bio-informatics tools like CCP4, DOCK and GRID. Among the several innovations targeting young scientists were the special priorities awarded to younger questioners in discussion periods after lectures and the spirited oral poster sessions where presenters had two minutes to preview and promote their posters. Supervisors and mentors take note: this is a powerful and intense experience for young scientists, one they benefit from greatly in terms of new knowledge, new techniques, new friendships, new self-confidence and new spirit. It was a wonderful thing to witness.

There were many opportunities for attendees to interact outside formal settings. Most meals were informal collections around tables at local restaurants and covered by the registration fees. Many evening meals after workshops were social events: pizza and pasta parties, the **RUBY** dinner and dance. In addition there were two excursions to archeological and historical sites of Phoenician, Elymian (they were said to be refugees who fled the victors after the fall of Troy) and Greek heritage.

None of this could have happened without the careful preparation and precise execution of the schedule by the local organizers, **Paola Spadon**, Università di Padova, and **Lodovico Riva di Sanseverino**, Università di Bologna. The computational and communications resources were the work of **John Irwin** (UCSF), a permanent member

From left: Marcelo Guerin (Colorado State) is discussing his poster with Peter Rose (Supercomputing Center, UCSD) and Jordi Quintana (Barcelona Science Park).

Prizewinners and Organizers. from left: Taiana de Oliveira, Alice Clark, Joel Sussman, Paola Spadon, Colin Groom and Lodovico Riva di Sanseverino (Ida Rosnes not present).

of the team. As in the past, an enthusiastic cadre of young scientists, immediately recognizable by the orange scarves they flourished, provided all manner of assistance to the organizers.Arrivals, departures, lectures, workshops, parties, excursions, everything worked, everything was on time. It's safe to say that none will forget their time in Erice this year. That is especially true of the young scientists.

Prizewinners. Annually, now, the organizers assign the **Vaciago Award** to the young scientist judged most energetic questioner in discussion after lectures. The **2008 Vaciago Award** winner was the Brazilian **Taiana de Oliveira**, PhD student at the U. Tromso, Norway. In addition, the IUCr presented two poster prizes, a copy of *International Tables, Volume F*, signed by Editors **Michael Rossmann** and **Eddy Arnold**, both of whom presented this year, and a copy of *International Tables, Volume A*. They went to **Alice Clark** from Massey U., New Zealand, for her poster on Filamin A and **Ida Rosnes** from the National University Hospital, Oslo, Norway for her poster on Endonuclease V.

At the end of the **RUBY** dance, **" RUBY "** necklaces and crystals, as well as local souvenir tiles, were awarded to several participants for exceptional displays of elegance, ability, spirit and luck.

Ruby Ball, Vivian Cody (HWMRI) receives award from Paola and Lodovico.

Statistics.Two weeks after the close of the school this year, a better than 75% response to an anonymous web-based questionnaire gave a record average score of 91.41 to the question "Score the meeting 0 to 100, 100 maximum."

Howard Einspahr

All photos courtesy of Howard Einspahr

Future Meetings

The 66th Pittsburgh Diffraction Conference

Oct. 30th - Nov. 1st, 2008, Holiday Inn University Ctr., Pittsburgh. The goal is to bring together researchers in all areas of fundamental and applied diffraction and crystallographic research to present current topics. The 2008 program includes diffraction phasing, structure refinement and validation, synchrotron data collection, environmental science, materials science, chemistry and combined methods for structural biology research including NMR, Cryo-EM, EXAFS, and Raman spectroscopy. The preceding workshop *Crystallography Made Easy through Automation* on Oct. 29th. at the U. Pittsburgh Structural Biology Dept. will introduce the basics of crystallographic techniques (protein crystallization, x-ray diffraction data collection, and data analysis), describe the structural information that crystallography can provide, and then demonstrate how the whole process may be simplified by taking advantage of the automated facilities available at Stanford Synchrotron Radiation Laboratory and the Hauptman Woodward Medical Research Institute. The workshop is open to 24 participants and advanced registration is required. For more information and to register, please visit the workshop website: **www-conf.slac.stanford.edu/crystallography**

Conference social events include a reception on October 30th and a banquet on October 31st. Student poster abstracts will be considered for oral presentations and are eligible for the **Chung Soo Yoo** Award. A highlight of the conference will be the **Sidhu Award** presentation, in memory of **Surhain Sidhu**, which honors significant contributions to the science of crystallography and/or diffraction by an outstanding scientist who is within six years of having earned the Ph.D. or its equivalent. For additional information see: **www.pittdifsoc.org/PDC_2008/** or contact any of the PDC Session Organizers: **Julian Adams, Paul Adams, James Conway, Steve Geib, Ana Gonzalez, Mark Macbeth, Apurva Mehta, Edward Snell, and Andy Vandenmark.**.

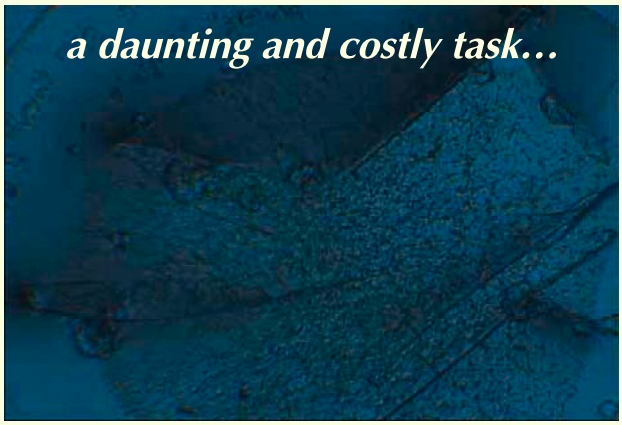
Sagamore XVI

IUCr sponsored, Santa Fe, New Mexico, Aug 2-7, 2009;
Thomas Proffen, organizer.

Past Sagamore conferences have addressed broad-ranging issues concerning electron charge, spin and momentum densities in a wide class of materials, as well as highlighting the most exciting recent developments. The next Sagamore conference will adhere to this tradition and will be held at the Inn at Loretto Spa and Resort **www.innatloretto.com** in Santa Fe, New Mexico. The conference is hosted by the Lujan Neutron Scattering Center: **www.lansce.lanl.gov/lujan** at Los Alamos National Laboratory **www.lanl.gov.**.

from the Loretto Inn website.

Suddenly…



Visible

UV

Korima's Exclusive Technology

Revolutionizing Protein Crystal Recognition

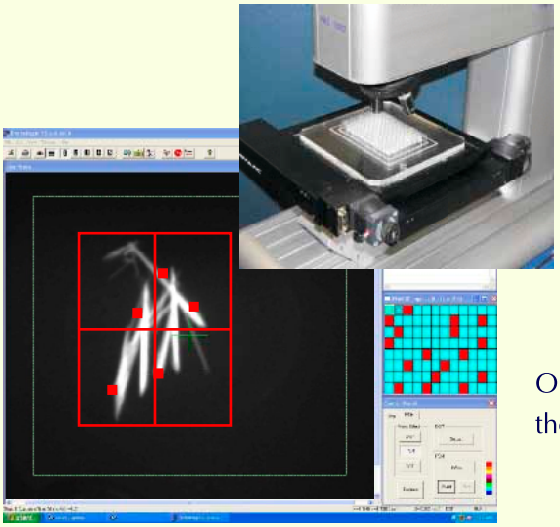
in X-Ray Crystallography

With Korima's exclusive PRS-1000 protein review station, you'll streamline perhaps the most daunting, error-prone challenge for even the most experienced x-ray crystallographers—distinguishing protein crystals from salts and other residue.

Quick to set up and easy to operate, the PRS-1000's split fluorescent beam exploits tryptophan fluorescence. As a result, target proteins—and only target proteins—stand out dramatically from non-fluorescing crystals, salt, and other materials. You will recognize target proteins—all of them, instantly!—in every solution.

Korima's PRS-1000 is the key to accelerating, fine-tuning, and optimizing protein crystal screenings. By eliminating guesswork, you'll save hours upon hours of tedious effort, achieve the highest possible accuracy, and slash costs.

The PRS-1000. With a growing list of laboratory installations—including the UCLA, UCSF, UC Berkeley, University of Oregon, University of Chicago, and the National Institute of Health—you'll be glad you looked into it!



High-Throughput Option

Electronically Pinpoints Target Crystals—in Seconds!

With the PRS-1000 HT option, 96-well plates traverse a motorized stage beneath the microscope's objective—all in less than five minutes. At the same time, Korima's proprietary software analyzes each image.

On-screen displays spotlight any target proteins present in the sample in real-time, and flag all protein-positive wells.

119 E. Star of India Lane • Carson, CA 90746 • (310) 532-2222
www.korimainc.com • email: info@korimainc.com

KORIMA

ACA 2009 July 25 - 30

Toronto Sheraton City Centre Hotel, Toronto, CA

Abstract Deadline: March 31, 2009

Student and Young Scientist Travel Grant Applications: March 31, 2009

Advance Registration Deadline: May 31, 2009

Advance Hotel Registration for Conference Rates: June 24, 2009

Register online and see Call for Papers at www.AmerCrystAssn.org

Meeting website: www.cins.ca/aca2009/

The photos are of the new Michael Lee-Chin Crystal building of the Royal Ontario Museum, in downtown Toronto.

PROGRAM CHAIR
James F Britten
Dept of Chem ABB-417
McMaster University
Hamilton, ON, L8S 4M1 Canada
905 525 9140 ext 23481
Fax: 905 522 2509
britten@mcmaster.ca

LOCAL CHAIR
David Rose
Dept of Medical Biophysics
University of Toronto
Toronto ON M5G 1L7 Canada
416 581 7537
Fax: 416 581 7562
drose@uhnres.utoronto.ca

Workshops, Saturday, July 25th

See www.cins.ca/aca2009/
or link from ACA website: www.AmerCrystAssn.org

Award Symposia

Martin J. Buerger Award in honor of Michael James

Warren Award in Diffraction Physics in honor of Shih-Lin Chang

Margaret C Etter Early Career Award to honor Svilen Bobev

Transactions Symposium

on Phase Transitions, Monday, July 27th
organized by Ross Angel and sponsored by the Powder, Materials, Service, Small Molecule, and General Interest SIGs

NOVEMBER 2008

9-14 **EMBO World Lecture Course - Recent Developments in Macromolecular Crystallography.** Pune, India. *cwp.embo.org/wpc08-02/index.html*.

16-20 **SARX2008: XI Latin American Seminar of Analysis by X-Ray Techniques.** Cabo Frio, Rio De Janeiro, Brazil. *www.lin.ufrj.br/sarx2008/*.

APRIL 2009

5-8 **The 19th West Coast Protein Crystallography Workshop**. Asilomar, CA The schedule will be dominated by oral presentation by students and postdocs, *wcpcw.org*.

MARCH 2009

9-12 **17th Annual Meeting of the German Crystallographic Society**, Hannover, Germany. **www.conventus.de/dgk2009.** Josef-Christian Buhl, Conference Chair. Contact Mareike Schandor, tel. 0049 3641 35 33 27 01, **mareike.schandor@conventus.de.**

18-22 **ASBMB'09 Meeting**, New Orleans, LA. **www.asbmb.org/Page.aspx?id=146.** Note: **Eliz Getzoff**, **Tina Iverson**, and **Ya Ha**, will be presenting in the *Structure & Enzymology of Membrane Proteins* symposium. **Ada Yonath** will speak in the *Ribosome Structure & Function* session, and **Chris Hill**, will speak in the *Proteasome Structure and Function* session.

MAY - JUNE 2009

30-3 **Small Molecule Workshop at the 92nd Canadian Chemistry Conference.** Hamilton, ON, Canada.

JUNE 2009

4-14 **High Pressure Crystallography: From Novel Experimental Approaches to Applications to Cutting Edge:** Erice, Italy. **www.crystalerice.org/2009.htm.**

JULY 2009

9-14 **XXV European Crystallographic Meeting.** Istanbul, Turkey. **ecm25.ecanews.org/**

25-30 **ACA Annual Meeting - Toronto, Ontario - Canada** *Program Chair: Jim Britten, McMaster University, britten@mcmaster.ca.*

JULY 2010

24-29 **ACA Meeting - Chicago, IL**.

rayonix mx series

Seamless multi-element CCD X-ray detectors

mx225 **9 CCDs; 3k × 3k readout in 1 sec.**

mx300/mx325 **16 CCDs; 4k × 4k readout in 1 sec.**

- Low noise
- Lowest achievable dark current

Options:

- Ultrastable background for SAXS/WAXS
- Custom taper ratios
- Custom phosphor options

HE **High Efficiency models available**
High electro-optical gain design

The single CCD design **sx165** also offers the frame shift option to facilitate consecutive exposures only miliseconds apart in time.

rayonix

High-performance X-ray technology

www.rayonix.com

1880 Oak Avenue
Evanston, IL 60201 USA
info@rayonix.com

Tel: +1 (847) 869-1548
Fax: +1 (847) 869-1587
Toll Free in USA: (877) 627-XRAY

oxford diffraction
Now a part of Varian, Inc.

NEW

driving X-ray innovation

The Best Data from the Fastest CCD System

Gemini A Ultra

Equipped with the brand new Atlas CCD the Gemini A Ultra is:

- Up to 3.5x faster than its competitors
- 70% more sensitive
- And has the strongest Mo and Cu X-ray sources of any dual wavelength diffractometer

Available for demo now!

sales@oxford-diffraction.com **www.oxford-diffraction.com**

Europe Tel: +44 (0)1235 443630 Fax: +44 (0)1235 443631
North America Tel: +1 540 443 9272 Fax: +1 540 443 3672
Asia Tel: +852 2571 9188 Fax: +852 2571 9855

THE QUEEN'S AWARDS FOR ENTERPRISE: INTERNATIONAL TRADE 2006