

*The 63rd Annual
Pittsburgh Diffraction Conference*

*Argonne National Laboratory
Intense Pulsed Neutron Source - Building 360
Argonne, IL 60439*

November 3-5, 2005

Program and Abstracts

*Symposia to Honor
Prof. L.E. Alexander
Prof. M. Sundaralingam*

*Additional Symposia
Frontiers in Neutron Scattering
Advances in Chemical Biology*

On the occasion of the 63rd Pittsburgh Diffraction Conference, colleagues, collaborators and friends from around the world meet to celebrate the scientific careers of Leroy E. Alexander and of Muttaiya Sundaralingam.

Leroy E. Alexander (1910-2004)

In June, L. E. Alexander passed away in his 94th year. Leroy retired in 1976 from the Mellon Institute of Carnegie-Mellon University in Pittsburgh, Pennsylvania, as Professor of Chemistry and Senior Fellow. To obtain his academic education he had a difficult road to follow. After high school he obtained his teacher's certificate and was teaching in one-room rural schools by the age of eighteen. By alternating teaching and college studies, he was able to earn a bachelor's degree at the State Teacher's College in River Falls, Wisconsin in 1937. During his teaching years, he organized a school band and taught the students how to play all the instruments. He supported himself during graduate school by playing clarinet and saxophone in dance bands, and was awarded a Ph.D. in physical chemistry from the University of Minnesota in 1943. After working at the General Electric Laboratories in Pittsfield, Massachusetts, Leroy was offered a position in the Department of Chemical Physics at the Mellon Institute of Industrial Research in Pittsburgh. He headed up the x-ray diffraction section and became an authority in this field. Together with Harold P. Klug he wrote the classic "X-ray Diffraction Procedures" (Wiley, 1954). This book can still be found in many x-ray diffraction laboratories throughout the world, because it is written in a clear and instructive way. With Gordon S. Smith, he published a number of influential papers on the geometry of single-crystal x-ray diffractometry. His second book "X-ray Diffraction Methods in Polymer Science" (Wiley, 1969), was also a success, and for quite some years was the only book on this subject. He was ACA secretary 1958 to 1960.

In the early sixties Leroy was on sabbatical at the Delft University of Technology in The Netherlands, where he worked with his long time friend the late Peter de Wolff. While at Delft he collected material for his book on diffraction methods in polymer science. Those fifteen months in the Netherlands were a wonderful time for the Alexanders. While he was working on his second book, Leroy started a project to study chain folding in polymers, in particular of polyamides. This subject was a source of controversy and played an important role in the phenomenological description of the deformation of polymers. The study resulted in a series of papers on the structural determination of nylon cyclic oligomers. Together with Roger Pettersen and Earl Baker he worked on the synthesis and the structures of chlorophyll-related compounds.

With his great knowledge of x-ray diffraction and talent for writing well-styled and clearly formulated texts, he was a source of inspiration for all those who had the privilege to work with him. Leroy was a great friend and colleague to many people from different countries and backgrounds. He had a broad range of interests; playing music was one of his greatest pleasures. He was an optimistic and religious man, respected as well as admired by those who knew him. In his work he was strongly supported by his beloved wife Eleanor, who for many years transcribed books into Braille. She died several years ago. Leroy is survived by his daughters Kathryn and Karen and two grandchildren.

Maurits Northolt
(from the ACA Newsletter, Winter 2004)



X-ray crystallographers at the Mellon Institute, 1966

Front, from left: Harold Klug, Leroy Alexander.

Behind, from left: Wayne Orr, Bob Stewart, Sid Pollack, Maurits Northolt, Maureen Sullivan.

Absent: Gordon Smith, Roger Pettersen, Gardner Sumner, Patricia Brown, John Beres.

Note: The biologist Roy Worthington had a separate small-angle X-ray facility.

Leroy Alexander and the Pittsburgh Diffraction Conference

Leroy Alexander joined the staff of the Mellon Institute in Pittsburgh in January 1946. His involvement with the Pittsburgh Diffraction Conference began with the fourth Conference which was held in December, 1946. Thereafter, he was active in the affairs of this annual Conference until his retirement from the Mellon Institute of Carnegie-Mellon University in 1976. Throughout these thirty years he took part in the Conference in two different ways. First he became a regular among the Conference organizers. Second, he joined in the presentation of research that came from a growing X-ray group at the Mellon Institute of whom Harold Klug and Leroy Alexander were the leaders.

Now that the Pittsburgh Diffraction Conference is in its 63rd year, with a history older than that of the ACA, it is important to recognize the work of Leroy Alexander in gathering and preserving records that go back continuously to the first Pittsburgh Diffraction Conference. This took place at the University of Pittsburgh in 1943 (during the siege of Leningrad; now St Petersburg). Leroy made use of his archival material in his account of "*Surhain Sidhu and the Early Pittsburgh Diffraction Conferences*" which appears in abbreviated form in the ACA Newsletter, December 1992 and in full on the website, www.pittdifsoc.org. Leroy includes his own stories of those early years. His article points out that the early Pittsburgh Diffraction Conferences drew an audience of hundreds and were attended by leading figures including Sir Lawrence Bragg, Isadore Fankuchen, Charles Barrett and David Harker.

Bryan Craven and Robert Stewart



Muttaiya Sundaralingam (1931-2004)

thoughts of a former student

From a student's perspective, Professor Muttaiya Sundaralingam, universally known as 'Sunda', was a consummate scientist, both rigorously disciplined and highly creative. Following his Ph. D. work with G. A. Jeffrey at the University of Pittsburgh, and a stage of his career at Case Western Reserve University, he moved to the University of Wisconsin, Madison, in 1970 to direct a laboratory focused on the structures of nucleic acids and their components. He was chemical crystallographer in the classical sense, using high resolution crystal structures to deduce principles about the behavior of molecules from their bond distances, angles, torsions, hydrogen bonding, conformation, and crystal packing. He developed this approach through training with George Jeffrey where the focus was often on carbohydrates. Underlying concepts in this research were the value of atomic resolution, the use of crystals to infer chemical interactions, and the need to understand the subtleties and details of hydrogen bonding.

Sunda subsequently employed crystallography in a systematic, virtually exhaustive manner to the components of nucleic acids, the bases, sugars, nucleosides, and nucleotides, of all kinds, and to polynucleotides. This research was inspired by Linus Pauling's analysis of protein structure, and the principle that through precise definition of the building blocks, one could deduce the structure of the biological macromolecule. Sunda's special gift was to visualize and understand stereochemistry, and so he was not afraid to apply the results of his crystal structures to the complicated nucleotide components of nucleic acids. One of his fundamental contributions was to identify the conformational preferences of furanose sugars, in terms of a newly defined pseudorotation angle. Using this analysis, he was able to unravel the observed conformations of nucleosides and nucleotides, and develop the 'rigid nucleotide hypothesis' based on preferred C2' *endo* and C3' *endo* sugar puckers. His work further defined favored ranges of torsion angles for all of the sugar and phosphate bonds in the polynucleotide, and the preferred torsion angles about the glycosidic bonds of the bases. In concert with stereochemical analysis from crystal structures, Sunda always built models, and he used the models to infer energy landscapes, especially for helical nucleic acids, through rigorous theoretical calculations. In other words, he extended his

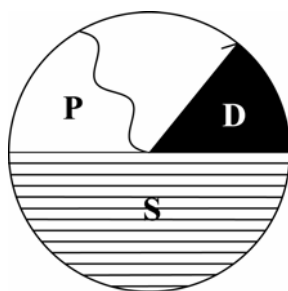
understanding of the repeating units to the macromolecule and its dynamics. Simultaneously, this led him to study crystal structures of transfer RNAs, and RNA and DNA duplexes. It is impossible to imagine a contemporary understanding of nucleic acid structure without Sunda's fundamental insights. He reduced the problem of stereochemical analysis of polynucleotides to simple rules and conformational preferences, much as Ramachandran did for the analysis of protein structure.

The 1999 Pittsburgh Diffraction Conference at Ohio State University was organized to honor Sunda upon his retirement. At that time, a compendium bibliography of Sunda's 330 scientific publications was presented. In his own presentation, entitled 'From Nucleic Acids to Proteins – 40 years of Structural Molecular Biology' he provided an overview of his own career as he focused on the nature of base-base interactions in nucleic acid structures. In his lecture he reviewed many types of base-base hydrogen bonding interactions and their role in RNA tertiary structure and recognition. The lecture was exemplary of Sunda's approach to science: he presented a wide diversity of crystal structures and models, analyzed the complexities seen at high resolution, emphasized the nature of these molecular interactions and hydrogen bonding patterns in folded RNA, and provided a synthesis.

Sunda's life influenced many people, and he had many scientific collaborators. His close colleague of many years, N. Yathindra, has published an excellent and lengthy review of Sunda's life and work in *Acta Cryst.* (vol. D61, pp. 845-849, 2005). As Yathindra points out, 'Sunda attracted a number of bright students and post docs through his charismatic discourse on the unique ability of X-ray diffraction techniques to visualize biological macromolecules'. Personally, I was attracted by exactly such 'charismatic discourse' when as a first year graduate student Sunda enlightened me as to how biochemical molecules could be examined in three dimensions. At that time, in his lab in the 1970s, a number of graduate students were set to work on projects that would influence their careers, especially through a passion for solving structures. Sunda, and other scientists he attracted to his group, in particular S. T. Rao and R. K. McMullan, insisted on and taught crystallographic principles, while the goal was always to solve the next interesting structure. As a mentor, Sunda provided guidance by creating the environment, and generating the energy to ask the interesting questions, but he also left his students to work out the details of the problem on their own. This in turn created an atmosphere that fostered a great deal of interaction and shared learning. Personally, Sunda was a gracious and patient advisor, and fostered the careers of all of his students with care. He and his wife, Indrani, hosted many dinners, picnics and parties, including everyone in his laboratory into his extended family.

This year's special Sunda Symposium at the Pittsburgh Diffraction Conference will include presentations from several of Sunda's students who shared their graduate careers in his laboratory in the period of the 1970s. The aim is to demonstrate that at one time Sunda's lab harbored a special collection of students, who have gone on to do a wide variety of interesting research, all connected in some way to the crystallographic inspiration he provided. This on-going research he inspired, and the careers Sunda mentored, is a testimony to his contribution to crystallography.

Dave Stout



The 63RD Annual Pittsburgh Diffraction Conference

Conference Chair

Thomas Koetzle

Symposia Organizers

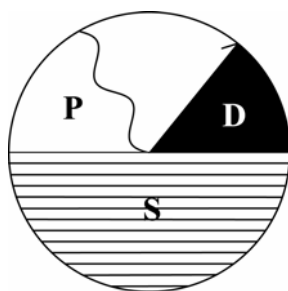
James Kaduk
Craig Ogata
Arthur Schultz
C. David Stout
Robert Von Dreele

Poster Chair

Paula Piccoli

Awards Committee

George DeTitta, Chair
Anthony Kossiakoff
Leonard MacGillivray



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*The Pittsburgh Diffraction Society
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James Kaduk

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Sidhu Award

This award is made in memory of Professor Surhain Sidhu, who was a founding member of the Pittsburgh Diffraction Conference. At the time (1942), he was Professor of Physics and Director of the X-ray Laboratory at the University of Pittsburgh. Later, he moved to Argonne National Laboratory, where he pioneered the use of the null matrix in neutron diffraction. This involves choosing isotopes of an element in the proportion that gives a zero net coherent scattering factor. The procedure has been widely used for studying biological materials in which the isotopic ratio of H to D is appropriately adjusted.

The Sidhu Award is made to a scientist within five years of the PhD who has made an outstanding contribution to crystallography or diffraction. The previous Awardees are listed below:

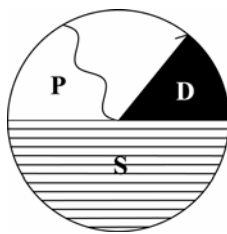
1967	A. I. Bienenstock	1989	M. Luo
1968	R. M. Nicklow	1990	L. Brammer
1969	T. O. Baldwin	1992	R. C. Stevens
1970	S.-H. Kim	1993	M. Pressprich & T. Yeates
1971	L. K. Walford	1994	A. Vrielink & J. Wang
1972	D. E. Sayers	1995	M. Georgiadis
1974	B. C. Larson & N. C. Seeman	1996	M. J. Regan
1975	P. Argos	1999	C. Ban & M. Wahl
1978	K. Hodgson & G. DeTitta	2000	W. R. Wikoff
1980	G. Petsko	2001	L. Shapiro
1985	D. C. Rees	2002	Y. Lee
1986	D. Agard & J. M. Newsam	2003	E. O. Saphire
1988	Q. Shen	2004	Y. Xiong

Chung Soo Yoo Award

Dr. Chung Soo Yoo, Adjunct Associate Professor in the Department of Medicinal Chemistry and Research Associate in the Department of Crystallography of the University of Pittsburgh, was killed in the Korean Airlines Flight 007 disaster of August 31, 1983. Dr. Yoo came to the U.S. from Korea in 1965, obtained his M.S. degree in Chemistry at Rice University in 1967, his PhD in Crystallography at the University of Pittsburgh in 1971, and became a U.S. citizen. He was a member of the Biocrystallography Laboratory of the Veterans Administration Medical Center in Pittsburgh.

Dr. Yoo was one of the most likeable crystallographers among students and colleagues in Pittsburgh, and was always very enthusiastic about the Pittsburgh Diffraction Conference.

The Chung Soo Yoo Award, established by the Pittsburgh Diffraction Society in his honor, is given to a graduate student presenting the best poster in the annual Conference.



The 63RD Annual Pittsburgh Diffraction Conference

*Argonne National Laboratory
Intense Pulsed Neutron Source
Building 360, Room L-119
Argonne, Illinois 60439*

November 3-5, 2005

Conference Chair: Thomas Koetzle

REGISTRATION for the meeting will begin at 12:00 p.m. on Thursday, November 3 in the lobby of building 360. The registration desk will also be open on Friday, November 4 and Saturday November 5.

The 63RD Annual Pittsburgh Diffraction Conference Program Schedule

Thursday, November 3

Conference Room L119

1:40 p.m. *Welcoming Remarks and Announcements*
A. Alan Pinkerton
University of Toledo
President, Pittsburgh Diffraction Society

1:50 p.m. *Welcoming Remarks*
Raymond Teller
Division Director, Intense Pulsed Neutron Source
Argonne National Laboratory

<p>Symposium A X-rays, Crystals, and a Life. Through the Looking Glass of Leroy Alexander Chairs: James Kaduk and Robert Von Dreele</p>

1:55 p.m. *Opening Remarks*
Robert Von Dreele
Argonne National Laboratory

2:00 p.m. **A1.** “Remembering Leroy E. Alexander”
Gordon Smith
Lawrence Livermore National Laboratory (Ret.)

2:30 p.m. **A2.** “Requirements for Accurate Residual Stress Analysis by the
Neutron Diffraction Method”
Camden Hubbard
Oak Ridge National Laboratory

3:00 p.m. *Coffee Break*

3:30 p.m. **A3.** “Quantitative Rietveld Analysis of Powder Diffraction Data”
Pamela Whitfield
National Research Council Canada, Ottawa

- 4:00 p.m. **A4.** “Silver Behenate: Somewhere Between a Molecular Crystal and a Polymer”
 Peter Stephens
 Stony Brook University
- 4:30 p.m. **A5.** “Polymer Fiber Diffraction and Its Quantitative Analysis”
 Christian Burger
 State University of New York at Stony Brook
- 5:00 p.m. **P3.** “High Pressure In Situ Diffraction Study of Gallium Molybdenum Oxide”
 Stacy Gates
 University of Toledo
- 5:30 p.m. *Adjournment*

Thursday, November 3

Building 360, Lobby

POSTER SESSION AND CONFERENCE MIXER
Poster Chair: Paula Piccoli
IPNS, Argonne National Laboratory

7:30 p.m. *Poster Session and Mixer - Cash Bar, Appetizers Will Be Served*

8:30 p.m. *Formal Poster Session and Judging*

Posters should be mounted on Thursday afternoon and left on display throughout the Conference. The formal poster session, including the judging for the Chung Soo Yoo Award, will begin at 8:30 p.m. Thursday evening. The Chung Soo Yoo Award is made to the graduate student who presents the best poster. Candidates must be present to meet with the judges. The Award, consisting of a cash prize of \$200, will be made at the Conference Dinner on Friday evening. All conference attendees are welcome to the mixer.

Friday, November 4

Building 360, Room L119

Symposium B
Frontiers in Neutron Scattering
Chairs: Thomas Koetzle and Arthur Schultz

- 8:55 a.m. *Opening Remarks*
 Thomas Koetzle
 Argonne National Laboratory
- 9:00 a.m. **B1.** “Studying the Co-ordination Chemistry of Hydrogen by Neutron Scattering”
 Alberto Albinati
 University of Milan, Italy
- 9:30 a.m. **B2.** “Structural Studies of Very Short Intramolecular Hydrogen Bonds By Neutron Diffraction, Inelastic Neutron Scattering and Ab-Initio Calculations”
 Juergen Eckert
 UC, Santa Barbara and Los Alamos National Laboratory
- 10:00 a.m. *Coffee Break*
- 10:30 a.m. **B3.** “Neutron Investigations of Semi-Conducting Clathrates”
 Mogens Christensen
 University of Aarhus, Denmark
- 11:00 a.m. **B4.** “High-Pressure Applications”
 John Parise
 State University of New York at Stony Brook
- 11:30 a.m. **B5.** “Subatomic Resolution X-ray and Neutron Diffraction Studies of Fully Deuterated Human Aldose Reductase Show Catalytic Proton (Deuterium) Channel”
 Alberto Podjarny
 IGBMC, Illkirch, France
- Lunch Break, 12:00 – 1:25 p.m.*
- 1:25 p.m. *Opening Remarks*
 Arthur Schultz
 Argonne National Laboratory

Friday, November 4

Building 360, Room L119

- 1:30 p.m. **B6.** “pH-Dependent Self-Assembly of A β Congeners into Fibrils and Charged Nanotubes”
Pappannan Thiyagarajan
Argonne National Laboratory
- 2:00 p.m. **B7.** “Grazing Incidence Neutron Diffraction from Lipid Bilayer Membranes”
David Worcester
University of Missouri, Columbia, and National Institute of Standards and Technology
- 2:30 p.m. **P10.** “Preliminary Results of the Recent Charge Density Study of Genistein”
Eric Yearley
University of Toledo
- 3:00 p.m. *Coffee Break*
- 3:30-5:00 p.m. Tours of APS (Advanced Photon Source, Building 401) and IPNS (Intense Pulsed Neutron Source, Building 375) Facilities
- 5:00 p.m. *Adjournment*

CONFERENCE DINNER

Advanced Photon Source, Building 401, 5th Floor Gallery Area

7:00 - 8:00 p.m. *Social Hour - Cash Bar*

8:00 p.m. *Banquet, President's Address and Awards Presentations*

Saturday, November 5

Building 360, Room L119

Symposium C
Symposium to Honor Prof. Muttaiya Sundaralingam
“Sunda’s Children of the 70’s”
Chair: C. David Stout

- 8:55 a.m. *Opening Remarks*
C. David Stout
The Scripps Research Institute
- 9:00 a.m. **C1.** “On the Outside Looking in: A Multiscale Approach to Characterizing Poliovirus Cell Entry”
James Hogle
Harvard Medical School
- 9:30 a.m. **C2.** “Protein Structures as Blurred Snapshots - Extracting Dynamic Information from a Static Experiment”
Ethan Merritt
University of Washington
- 10:00 a.m. *Coffee Break*
- 10:30 a.m. **C3.** “GM/CA Canted Undulator Beamlines for Macromolecular Crystallography”
Janet Smith
University of Michigan
- 11:00 a.m. **C4.** “Regulating G-proteins with Peptides: Mechanistic Insights from Unexpected Sources”
Stephen Sprang
University of Texas Southwestern Medical Center
- 11:30 a.m. **C5.** “Structure and Function of Transhydrogenase”
C. David Stout
Scripps Research Institute
- 12:00 p.m. *PDS General Membership Meeting*

Lunch Break, 12:05 – 1:30 PM

Saturday, November 5

Building 360, Room L119

SIDHU AWARD LECTURE
Chong-Yu Ruan
Michigan State University

1:30 p.m. *Opening Remarks and Sidhu Award*

A. Alan Pinkerton
University of Toledo

1:35 p.m. *Sidhu Award Lecture*

“Ultrafast Electron Crystallography: Atomic Level View of Transient Structures of Molecules, Surfaces, and Nanometer-Scale Materials”
Chong-Yu Ruan
Michigan State University

Symposium D
Advances in Chemical Biology
Chair: Craig Ogata

2:10 p.m. *Opening Remarks*

Craig Ogata
Argonne National Laboratory

2:15 p.m. **D1.** “Structure-Aided Design of a Selective Inhibitor of Factor VIIa”

Charles Eigenbrot
Genentech, Inc.

2:45 p.m. **D2.** “Phosphoryl Transfer in the HAD Enzyme Superfamily”

Karen Allen
Boston University School of Medicine

3:15 p.m. *Coffee Break*

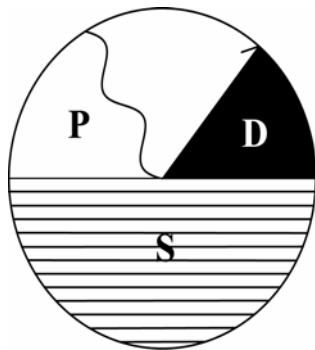
3:45 p.m. **D3.** “Protein Complexes that Mediate Bacterial Chemotaxis”

Brian Crane
Cornell University

4:15 p.m. **D4.** “How Do Macromolecules Respond to Light?”

Keith Moffatt
University of Chicago

4:45 p.m. *Adjournment*



*The 63rd Annual
Pittsburgh Diffraction Conference*

*ABSTRACTS
OF
PRESENTATIONS*

A2. Requirements for Accurate Residual Stress Analysis by the Neutron Diffraction Method

Camden R. Hubbard
Metals & Ceramics Division
Oak Ridge National Laboratory
Oak Ridge, Tennessee 37831-6064 (hubbardcr@ornl.gov)

The use of x-ray diffraction for macro or type I residual stress measurement has been used for over 50 years while the neutron diffraction equivalent has become a common technique just in the last 15 years. Both methods start with a measurement of the diffraction peak profile from which one obtains the d-spacings, typically using profile fitting. At spallation neutron sources the full pattern can be fitted using the Rietveld method to yield the lattice parameters. The X- and N-techniques begin to diverge at this point.

For the x-ray method one frequently assumes that the stress perpendicular to the sample surface is zero. When this condition is observed a strain free d-spacing is not needed, and stress in a particular sample direction can be determined via measurement at various tilts ψ of the incident beam relative to the sample surface. In these cases the well known $\sin^2\psi$ method is used to determine the stress.

Neutrons are far more penetrating than x-rays and as a consequence a volume of several mm^3 is measured. This gage volume is within the sample where the stress can be nonzero in any direction. Thus to obtain strain in the neutron case one must determine quite accurately the stress free d-spacing (d-zero) in order to convert measured d-spacings to strain. Methods for and challenges to the determination of d-zero will be summarized.

Other sources of error have been identified and ways to minimize them have been developed. These include: gage volume being partially outside the sample; wavelength dependent attenuation effects; inadequate number of grains in the gage volume; and intergranular or type II stresses. The role of type II stresses is most interesting as they are orientation and hkl dependent. In the x-ray method they lead to nonlinear $\sin^2\psi$ plots while in the neutron method they make determination of d-zero challenging.

The presentation will introduce the neutron residual stress method and discuss the major sources of aberration and methods adopted to minimize these effects. In favorable cases a strain accuracy of 50 ppm seems possible.

Research sponsored by the Assistant Secretary for Energy Efficiency and Renewable Energy, Office of FreedomCAR and Vehicle Technologies, as part of the High Temperature Materials Laboratory User Program, Oak Ridge National Laboratory, managed by UT-Battelle, LLC, for the U.S. Department of Energy under contract number DE-AC05-00OR22725

A3. Quantitative Rietveld Analysis of Powder Diffraction Data

Pamela Whitfield, Andrea Firth and Lyndon Mitchell*

Institute for Chemical Process and Environmental Technology

**Institute for Research in Construction*

National Research Council Canada, 1200 Montreal Road, Ottawa, ON, K1A 0R6, CANADA

In an industrial environment, X-ray powder diffraction is a valuable tool for the quantitative phase analysis of both routine and unknown samples. Although it is widely used, there are some issues that are often not addressed, which may lead to inaccurate results. Many of these issues involve sample preparation and mounting of the samples in the diffractometer. In time-sensitive industrial Quality Control environments some of these may be neglected and treated as systematic errors, but the same problems also arise in the more sedate academic applications where high absolute accuracy is demanded. Some of the more problematic issues will be highlighted and examples given from a mixtures of industrial interest and the more fundamental world of nanomaterials.

The issue of amorphous content is increasingly important, and the use of a spike in Rietveld analysis will be described together with some of the problems and caveats with the technique. The absolute importance of good sample preparation cannot be emphasized strongly enough, with total quantitative analysis including amorphous content being very sensitive to microabsorption and poor particle statistics. Examples will be given of complex mixtures (unhydrated cements) and the potential use of capillary transmission geometry (hydrated cement phase).

The extreme peak broadening of many nanoparticles can make the possibility of multi-phase/polymorph behaviour very difficult to exclude. Rietveld analysis does present the possibility of deconvoluting severely overlapped patterns to quantify mixtures of closely related phases, e.g. cubic and hexagonal semiconductor quantum dots. The poor packing behaviour of nanomaterials can make surface roughness effects more pronounced than usual, and the inclusion of surface roughness corrections can greatly improve the results of refinements.

A4. Silver Behenate: Somewhere Between a Molecular Crystal and a Polymer

Peter Stephens
Department of Physics and Astronomy
Stony Brook University
Stony Brook, NY 11794-3800

Silver alkane carboxylates are very simple from the molecular standpoint, but have so far eluded true crystal structure solution. Some simplified models have been published as though they were structures.

A5. Polymer Fiber Diffraction and Its Quantitative Analysis

C. Burger, H. Zhou, X. Chen, J.K. Keum, B.S. Hsiao, B. Chu

Department of Chemistry

State University of New York at Stony Brook, Stony Brook, NY 11794-3400

Polymeric materials, both synthetic and natural, do not usually form large single crystals suitable for single crystal diffraction.

Due to imperfections and small crystallite sizes, only a small number of relatively broad diffraction peaks can normally be observed. Thus, the information contained in isotropic polymer powder diffraction is limited. The intermediate situation of a preferentially ordered polymer system, especially one with cylindrical rotational symmetry (fiber symmetry), is of special interest, both because synthetic and natural polymers often appear in the form of polymer fibers, and because a modern-day 2D detector is able to cover almost the complete information contained in reciprocal space in a single detector frame, thereby enabling time-resolved measurements of oriented samples for a sufficiently bright x-ray source. An analysis of fiber diffraction patterns will not only reveal information about the structure but also about the preferred orientation which can be related to the mechanical properties of the fiber. The quantitative treatment of preferred orientation effects in fiber diffraction patterns, together with applications to examples of polyethylene, polypropylene, polyethyleneterephthalate, carbon nanofibers and their composites in polymer matrices, cellulose and collagen will be presented.

B1. Studying the Co-ordination Chemistry of Hydrogen by Neutron Scattering

Alberto Albinati

Department of Structural Chemistry, University of Milan, Milan, Italy

E-mail: alberto.albinati@unimi.it.

Transition metal hydrido-complexes are intermediates of paramount importance in many catalytic reactions, such as hydrogenations, and much work has been carried out, in recent years, to obtain a detailed understanding of the role of the hydrogen-ligand in determining the reactivity of these complexes. A rich variety of co-ordination modes has been found by neutron diffraction: from simple terminal hydrides to bridging species and the co-ordination of intact dihydrogen molecules (i.e.: non-classical hydrides).

In the latter case single crystal neutron diffraction has unambiguously established the co-ordination geometry of the “M-(η^2 -H₂)” moiety. The H-H separation covers a wide range of distances, $\sim 0.8 \text{ \AA} - 1.4 \text{ \AA}$, (corresponding to various stages of the H-H activation) describing the oxidative-addition reaction-path for the dihydrogen molecule.

However, it is worth noting that a more satisfactory understanding of the reactivity in hydrido-complexes can be achieved by combining the results from neutron diffraction with those on the H-ligand dynamics that can be obtained from neutron incoherent inelastic scattering (INS spectroscopy).

In this presentation, I will discuss some results on the chemistry of transition metal hydrides obtained by combining results from neutron elastic and inelastic scattering and DFT calculations.

B2. Structural Studies of Very Short Intramolecular Hydrogen Bonds by Neutron Diffraction, Inelastic Neutron Scattering and Ab-Initio Calculations

Juergen Eckert

Materials Research Laboratory, University of California, Santa Barbara, CA 93106, USA; and
LANSCE-12, Los Alamos National Laboratory, Los Alamos, NM 87545, USA

The structure and dynamics of very short ($d(\text{OO}) < 2.50 \text{ \AA}$) have in recent years attracted new interest because of the proposal that the formation of such bonds facilitates some catalytic reactions in enzymes in addition to the very fundamental nature of hydrogen bonds in this limit. The richest single source of information on protonic structure and dynamics of hydrogen bonded molecular assemblies may well be the vibrational spectra, provided that two conditions can be met, namely: (i) acquisition of precise experimental, band characterizing parameters (frequency, intensity, band shape) and (ii) theories which connect the experimental data with the physical determinants of bonding as reflected in the potential energy surface and electron topology. The latter also require accurate knowledge of all relevant structural parameters, which are best determined by single crystal neutron diffraction methods. Much of this information is, however, rather difficult to extract for most of the very short intramolecular hydrogen bonds because of extremely anharmonic potential energy surface. Although the X-H stretching mode is the signature of infrared spectra that is most useful for detecting and characterizing the type of H-bonding, a precise determination of band parameters may be hampered by the presence of a multitude of bands not or only indirectly relevant to the H-bond dynamics. Even the very identification may become questionable in adverse cases, and this applies to inelastic neutron scattering spectra (INS) as well. In order to fill the gap in our knowledge of the protonic modes and dynamics in short intramolecular H-bonds we have carried out extensive inelastic neutron scattering and IR spectroscopic studies, along with single crystal diffraction and periodic DFT computational studies on a large number of compounds containing such bonds. We will describe our findings on the hydrogen bond structure and dynamics in tetraacetylene, picolinic acid N-oxide and some enolized β -diketones.

This work is the result of extensive collaborations with Dusan Hadzi, Jernej Stare, Luke Daemen, Monika Hartl, Sax Mason, Paula Briggs-Piccoli, Tom Koetzle and Art Schultz. It has benefited from the use of facilities at the Lujan Center of the Los Alamos Neutron Science Center, and the Intense Pulsed Neutron Source at Argonne National Laboratory, both National User facilities funded as such by the Office of Basic Energy Sciences, U S Department of Energy.

B3. Neutron Investigations of Semi-Conducting Clathrates

Mogens Christensen
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Cage structures allow exciting possibilities of encapsulating guest atoms which provides a mechanism for tuning properties such as magnetism, thermal conductivity, resistivity, etc. The clathrates are a family of cage structures containing guest atoms and the most remarkable feature of the clathrates are their extremely low thermal conductivity, which is comparable to that of amorphous glasses. Europium containing clathrates are known to form with the type I (β - $\text{Eu}_8\text{Ga}_{16}\text{Ge}_{30}$) and type VIII (α - $\text{Eu}_8\text{Ga}_{16}\text{Ge}_{30}$) crystal structures, which both are ferromagnetic. The clathrate like compound $\text{Eu}_4\text{Ga}_8\text{Ge}_{16}$ on the other hand shows an anti-ferromagnetic magnetic behaviour. The difference can be explained within the RKKY magnetic exchange model. The europium atoms appear to be disordered in both cases giving a low thermal conductivity. To elucidate the nature of the low thermal conductivity; barium containing clathrates have been investigated.

B4. Neutron Scattering Studies at High Pressures: Recent Developments

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New high-pressure cells, neutron focusing techniques, and detector commissioning provide new opportunities for high-pressure (P) neutron science at both reactor and spallation sources. Possible applications of single-crystal Laue diffraction technique with a large image-plate detector, to high-pressure studies, were examined at Vivaldi at the ILL. For even quite complex materials (say 30 independent atoms + soft constraints) powder techniques work very well. For higher pressures and for more complex substances, single crystals contained in moissanite (SiC) anvil cells with reasonably large accessibility to reciprocal space, are shown to offer impressive gains in data collection rate as compared to the monochromatic technique. Moreover, the projected forms of the reflections from the sample and anvils facilitate alignment, and the wide wavelength band of the Laue technique allows recovery of reflections masked by the cell pillars, simply by rotation of the cell. When coupled with new focusing K-B focusing optics impressive gains are realized and preliminary data clearly show order of magnitude, or better, gains in S/N compared to unfocused beams.

For powder studies at $P > 5$ GPa, angle dispersive techniques have been largely abandoned in favor of work at spallation sources. Recent studies suggest use of c-BN anvils provided impressive self-collimation of monochromatic beams. Studies of magnetic transitions in hematite (α -Fe₂O₃) and CoO will be used to illustrate this point.

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B5. Subatomic Resolution X-ray and Neutron Diffraction Studies of Fully Deuterated Human Aldose Reductase Show Catalytic Proton (Deuterium) Channel

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Human Aldose Reductase (AR), an enzyme in the polyol pathway belonging to the aldoketoreductase family, is implied in diabetic complications. Its ternary complexes (AR-coenzyme NADPH-selected inhibitor) provide a good model to study the inhibition and enzymatic mechanisms. Indeed, X-ray electron density maps solved at very high resolution of AR complexes with different inhibitors (IDD-594, 0.66 Å; IDD-552; IDD-393; Fidarestat, 0.90 Å) show within the active site crucial protonation states. To confirm them, we have started neutron diffraction experiments. First trials based on H₂O/D₂O exchange, using crystals of 0.1 mm³, showed neutron diffraction up to only ~4.5 Å. New crystallisation trials, with fully deuterated protein (EMBL/ILL, Grenoble) complexed with the inhibitor IDD-594, succeeded. X-Ray tests of these crystals at the SBC-APS achieved a resolution of 0.8 Å at 15K (refined mosaicity 0.2°) and the structure was refined using SHELX. Neutron Laue diffraction measured on LADI (ILL/EMBL, Grenoble) achieved a resolution of 2.2 Å at room temperature, despite a small crystal volume of only 0.15 mm³. Larger crystal growth is under way.

After refinement with CNS, the resulting neutron density maps showed clearly the deuterium atoms in the active site region. In particular, the polarization of Tyr48 by Lys77, important for the catalytic reaction, is confirmed by a proton (deuterium) channel between these two residues.

B6. pH-Dependent Self-assembly of A β Congeners into Fibrils and Charged Nanotubes

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The primary component in the amyloid plaques in the brains of Alzheimer's patients is a peptide (A β) consisting of 39-43 amino acid residues. Due to its unique amphiphilic character, the peptide self-assembles in aqueous media into well-organized fibrillar structures. Understanding the detailed mechanism of the self-assembly of A β in solution and the structure of these resulting assemblies will be useful for the development of methods for altering or preventing the process of fibrillogenesis. By using solid-state NMR, CD, EM, AFM, biochemical assays and SANS/SAXS, a detailed atomic scale structure of the fibrils formed by A β_{10-35} has been developed. The pH-dependent self-assembly of smaller variants of the A β peptide (A β_{16-22}) and their mutants form charged nanotubular structures with a wide range of radii. These simpler peptides shed new light on the relationship between the length and the protonation sites of the peptide and the extent of lamination of the β -sheets. These unique supramolecular self-assemblies formed by the variants of A β peptide may have important applications in nanotechnology.

Work benefited from the use of IPNS and APS funded by the DOE, BES under contract W-31-109-ENG-38 to the U. Chicago and funding from W Packard Foundation (99-8327) to DGL and PT and DOE ER15377.

B7. Grazing Incidence Neutron Diffraction from Lipid Bilayer Membranes

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Highly oriented multilayer membranes of phospholipids and cholesterol give lamellar Bragg diffraction of neutrons to about 5Å resolution. There is also in-plane scattering. Renewed interest in neutron diffraction studies of these membranes has occurred for at least two purposes: 1) obtaining detailed experimental data on structure and dynamics for comparison with molecular dynamics simulations. 2) studying in-plane miscibility transitions and “raft” formation processes with nano-scale measurement capability. Examples using neutron diffraction with specific deuterium labeling for these two purposes are presented. Measurements were made primarily at reactor sources but the use of a pulsed source is demonstrated with data from the SAND instrument at IPNS.

C1. On the Outside Looking in: A Multiscale Approach to Characterizing Poliovirus Cell Entry

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Viruses that have an external membrane envelop gain entry to host cells via a conceptually simple mechanism that results in the fusion of the viral membrane with a host cell membrane. In contrast viruses lacking an external envelope must provide a mechanism for either the viral particle or at least the viral genome to cross the cell membrane, a process that remains poorly understood for all nonenveloped viruses. We have focused on poliovirus as a simple model system for probing the cell entry mechanisms of nonenveloped viruses, combining biochemical and structural characterization of cell entry intermediates both in isolation and more recently in the context of artificial membranes and cells. The structural characterizations span a wide range of scale, and our approach has been to combine the high resolution x-ray crystallographic structure of the virus itself with cryoEM structures of cell entry intermediates *in vitro* at moderate resolution ($\sim 10\text{\AA}$), cryo EM structures cell entry intermediates in the context of artificial membranes at low to moderate resolution, cryo electron tomographic reconstructions of entry intermediates in the context of the whole cell, and live cell single particle optical microscopic characterization of the cell entry process. In this presentation, I will review the progress of these studies, present our current working models derived from available structures, and preview methods that we hope will lead to a detailed understanding of the cell entry process at the molecular level.

C2. Protein Structures As Blurred Snapshots – Extracting Dynamic Information From A Static Experiment

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Single crystal structures are usually thought of as providing only static information, i.e. a snapshot of a protein at rest. But in fact the distribution of thermal parameters in a well-refined structure can be strongly indicative of dynamic motions and allowed flexibility. This distribution of B_{iso} or U^{ij} terms can be modelled as arising from TLS (Translation/Libration/Screw) rigid-body vibrational motion. A single-group TLS model can be used to approximate the vibration of an entire protein molecule within the crystal lattice. More complex TLS models are broadly applicable to describe inter-domain and other internal vibrational modes of proteins. We are developing a web-based analysis tool, **TLSMD THAT** generates optimal multi-segment TLS models. These may be used to analyze the presence and physical significance of TLS motion in existing structures, to guide additional crystallographic refinement, or to generate target models of protein flexibility for use in computational protein-protein or protein-ligand docking. The interactive graphics program **TLSVIEW** [2] allows visualization of these and other models for rigid-body motion in proteins, using animation and a variety of static representations. Both tools are applicable to protein structures at any resolution.

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C3. GM/CA Canted Undulator Beamlines for Macromolecular Crystallography

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The GM/CA Collaborative Access Team (CAT) has been established to build and operate a national user facility for macromolecular crystallography at Sector 23 of the Advanced Photon Source (APS). The scientific and technical goals of the CAT address problems at the cutting edge of structural biology research, as well as targeted programs of the sponsoring institutes in structural genomics and structure-based drug design. The three-beamline facility includes two insertion-device (ID) beamlines based on the APS dual-canted-undulator geometry and one bending-magnet beamline. The independently tunable ID beamlines are being commissioned, and a user program has begun on one beamline; the bending-magnet beamline will be installed in 2006. The beamlines are rapidly tunable (MAD capable), encompassing an energy range from 3.5 keV to 35 keV (wavelength 3.5 Å to 0.35 Å). The CAT emphasizes streamlined, efficient throughput for a variety of sample types, sizes and qualities, including weakly diffracting samples as small as 10 μm, and unit cells as large as 2000 Å. Several novel features implemented to achieve these goals include “bimorph” mirrors, feedback stabilization of beam position and intensity, air-bearing goniometry, miniature piezo translation stages, and high-resolution on-axis sample viewing. The control system has been designed to provide capabilities for fast automation. Fast scans have been implemented for all beamline components at the hardware level based on novel motion controllers utilizing fiber links. The user interface is a lightweight version of SSRL’s Blulce that has been converted into a client of the EPICS distributed control environment. A capability for automated sample handling is under development.

GM/CA-CAT was established and is funded by the National Institute of General Medical Sciences (GM) and the National Cancer Institute (CA) within the National Institutes of Health.

C4. Regulating G-proteins with Peptides: Mechanistic Insights from Unexpected Sources

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Members of the G protein superfamily are GTP hydrolases that regulate diverse biological processes by associating with effector proteins in the GTP-bound state. G proteins have low catalytic rate constants for GTP hydrolysis, and even lower rate constants for GDP (product) dissociation, and consequently, GTP binding. The activity of G proteins is controlled by Guanine nucleotide Exchange Factors (GEFs) that catalyze GDP release and GTP binding, and Guanine nucleotide Dissociation Inhibitors (GDIs) that inhibit nucleotide release. GEFs and GDIs, respectively, stimulate and prevent G protein activation. GTPase Activating Proteins (GAPs) increase the rate at which G proteins hydrolyze GTP, and thus promote dissociation of G proteins from their effectors. GEFs, GDIs and GAPs are typically proteins. However, certain peptides can exhibit the activities expressed by these proteins, although with far less potency. Here, we describe crystal structures that show how GEF, GDI or GAP activity can be achieved by specific peptides when bound to heterotrimeric G protein alpha subunits. A peptide fragment derived from the Galpha(13) effector p115RhoGEF is an effective GAP that forms electrostatic interactions with the switch regions of Galpha(13), and appears to stimulate GTP hydrolysis in part by orienting the enzyme moieties that promote nucleophilic attack upon GTP by water. Two research groups, working independently, used library screening methods to discover peptides with similar sequences that act either as GDIs or GEFs towards Galpha(i1). The difference in function of these peptides can be traced largely to the identity of a signal residue in the peptide sequence. Crystallographic studies show that GDI and GEF peptides induce different conformations within the nucleotide binding site that either promote or prevent nucleotide release. This surprising result provides insight into the mechanism of G protein-coupled receptors, which serve as GEFs for Galpha proteins in eukaryotes.

C5. Structure and Function of Transhydrogenase

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Transhydrogenase is essential enzyme of the respiratory system in mitochondria and bacteria that couples hydride transfer between NAD(H) and NADP(H), bound to extramembranous domains, to proton translocation through a membrane-intercalated domain. The mechanism for coupling binding energy and conformational change with proton translocation is unknown. Experiments in progress are directed at the site of proton uptake and release in the NADP(H) binding domain, the mechanism of hydride transfer between NAD(H) and NADP(H) binding domains, identification of helices and residues defining the proton conducting channel, and the structure of the intact enzyme.

Results from crystal structures of soluble domains, individually and in complex, combined with NMR, mutagenesis, kinetic and electron microscopy experiments will be presented, in addition to progress toward crystallization of the detergent solubilized enzyme.

D1. Structure-Aided Design of a Selective Inhibitor of Factor VIIa

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The serine protease factor VIIa (FVIIa) in complex with its cellular cofactor tissue factor (TF) initiates blood coagulation. The TF•FVIIa complex is also implicated in thrombosis-related disorders and constitutes an attractive target for therapeutic intervention in cardiovascular disease. We have generated an active site inhibitor G17905 which is potent ($K_i = 0.35 \pm 0.11$ nM) and selective (no appreciable inhibition of 12 of 14 tested trypsin-like proteases). Crystal structures of G17905 and related inhibitors complexed with a short form of FVIIa have guided this effort, and have been used to rationalize the effect of the addition of an *ortho*-hydroxy group to the inhibitor's aminobenzamidine moiety. Additionally, these structures reveal that G17905 binds to a novel, non-standard conformation of the FVIIa oxyanion hole wherein the Lys192–Gly193 peptide bond is “flipped”.

D2. Phosphoryl Transfer in the HAD Enzyme Superfamily

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The haloalkanoate dehalogenase superfamily (HADSf) is a ubiquitous family of enzymes, the vast majority of which are phosphotransferases that have evolved to perform a multitude of different biochemical functions essential to cell growth and adaptation. Each phosphotransferase contains a highly conserved core domain that catalyzes phosphoryl transfer mediated by an Asp nucleophile. Our overall goal is to determine the mechanisms of catalysis and substrate recognition in selected HADSf members. The X-ray crystal structure of β -phosphoglucosyltransferase with substrate to 1.2Å resolution reveals a stabilized pentacovalent phosphorane, formed in the phosphoryl transfer from the C(1)O of glucose 1,6-(bis)phosphate to the nucleophilic Asp carboxylate, consistent with an associative mechanism for phosphoryl transfer by this enzyme. In each catalytic cycle, the β - glucose 1,6-(bis)phosphate must become reoriented in the active site so that the C(1)phosphoryl group is aligned for transfer to the Asp nucleophile en route to glucose 6-phosphate. Does the β - glucose 1,6-(bis)phosphate "flip" within the confines of the active site or does it dissociate into solution then rebind? Preliminary kinetic studies show the rapid exchange of radiolabel from [¹⁴C] β -glucose 1-phosphate to the solvent pool of β - glucose 1,6-(bis)phosphate during a single catalytic cycle indicate that the intermediate dissociates, and then rebinds in the opposite orientation to form glucose 6-phosphate. We provide a model wherein the synchronization of such binding events and conformational changes with acid/base catalysis allows adaptation of the HADSf catalytic scaffold from phosphohydrolase to phosphomutase.

D3. Protein Complexes that Mediate Bacterial Chemotaxis

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In bacterial chemotaxis, assembly of transmembrane receptors, the CheA histidine kinase, and the adaptor-protein CheW regulates motility in response to changes in the chemical environment. The structure of a receptor cytoplasmic domain defines negative charge centers that coordinate metal ions, undergo deamidation, and provide sites for reversible methylation. In crystals, the receptors stack in layers mediated by contacts involving the modification sites. Crystallography and novel pulsed-ESR spectroscopic experiments reveal the structure and dynamics of dimeric CheA:CheW, in which two facing CheWs form a canyon wide enough to clamp one receptor. CheA regulatory domains symmetrically interact in crystals via conserved residues; propagation of CheA self-contacts aligns the CheW receptor clamps. Rows of receptors can extend from the clamps and link layers of CheA:CheW complexes. This assembly explains CheA/W-dependent clustering of receptors, how teams of receptors function in signaling, and provides a molecular model to test *in vivo*.

D4. How Do Macromolecules Respond to Light?

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The primary photochemical events in the chromophores of biological photoreceptors take a variety of forms: isomerization, formation or rupture of covalent bonds, and electron transfer. These events occur within the “solvent” provided by the protein framework that surrounds the chromophore, and the path that they take and the rate coefficients are often greatly influenced by that framework. Ultimately they lead to tertiary structural changes within the protein that generate a structural signal, conveyed across the sensor domain in which the chromophore is embedded to an effector domain, whose biological activity is thereby modulated. We explore these processes by time-resolved X-ray crystallography of photoreceptors, and monitor directly the structural changes that follow absorption of a photon with 100 ps – ns time resolution and a crystallographic resolution ~1.5 to 2.0Å. All experiments are conducted in pump-probe mode and exploit the high brilliance and the pulsed time structure of the X-rays emitted by synchrotron sources such as the APS. Illustrations will include bacterial and plant photoreceptors.

P1. High Resolution Data Collection in the Home Lab

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Data collection on protein crystals to very high resolution ($> 1.3\text{\AA}$) typically requires a trip to the synchrotron. Due to advances in optics and the introduction of micro-focus rotating anode generators, there has been a remarkable increase in brightness and flux density available in home laboratory systems. When combined with ultra-sensitive detectors, these systems provide an alternative means of extending the diffraction limit of samples. In some cases, X-ray data extending out to atomic resolution is obtainable. Methods of data collection as well as example data sets will be presented.

P2. Winners and Losers – Automatic Crystal Ranking of Diffraction Images

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With the advent of automation, the frequency of crystal screening has increased. As a result, many home labs and beamlines have developed robotic systems for high-throughput evaluation of crystal samples. Most of these systems still depend on human intervention to judge the quality of crystal samples. Ideally, an automated system should provide methods to identify desirable samples. We have implemented a method in d*TREK® to evaluate the quality of diffraction images and assign a rank per sample. This ranking software evaluates images in terms of several rules and calculates an award or penalty for each rule. The awards and penalties are then summed and updated on a per sample basis. Samples can then be ranked according to these values, and data collected in descending rank order. In general, these rules include the number of reflections per resolution shell, the $\langle I/s(I) \rangle$ of reflections per shell, the spot sharpness, the presence of sharp or diffuse rings, sample mosaicity, refinement statistics, and the number of accepted reflections from refinement. We discuss the utility of these rules, their usefulness in the evaluation of diffraction images, and those rules which seem most important for ranking of crystals.

P3. High Pressure *In Situ* Diffraction Study of Gallium Molybdenum Oxide

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Recently, interest in NTE materials has increased because of their effects when incorporated into composites. Since many metals, ceramics, and polymers tend to have large expansion coefficients, using them in applications could be problematic when interfaced with materials of mismatched α -values. Scientists discovered that incorporation of NTE materials into composites could reduce thermal expansion; however, there is concern about their stability under pressure. Preparation and use of composites will expose incorporated NTE materials to stress/pressure. Literature shows that earlier attempts to prepare composites with NTE materials have failed due to irreversible transformations of the NTE material to a high-pressure phase that no longer displayed NTE.¹ Therefore, there is a need to investigate the stability of NTE materials under pressure before they can be used in composites.

Some of the NTE materials in the $A_2M_3O_{12}$ family are known to undergo phase transitions as a function of temperature, while others show phase transitions that are induced by pressure. Presently, literature reports phase transition behavior for some $A_2M_3O_{12}$ compounds. We have synthesized a previously unknown member of this family, $Ga_2Mo_3O_{12}$. $Ga_2Mo_3O_{12}$ cannot be prepared by traditional solid-state methods. Thus, our research uses a non-hydrolytic sol-gel process to form this crystalline compound.

The sample was characterized using thermal analysis (TG-DTA), scanning electron microscopy (SEM), and powder X-ray diffraction (PXRD). To investigate the chemical and physical properties of our material, we performed variable temperature X-ray diffraction to identify potential phase transition temperatures. To address the material's behavior under pressure, an *in situ* diffraction study was carried out. Since laboratory diffractometers do not provide enough power to produce high quality data from diffraction inside a pressure cell, we used synchrotron radiation. *In situ* experiments can be used to determine any irreversible, or reversible structural changes of the material studied. We performed high-pressure diffraction at CHESS (beamline B-2) in a hydrothermal diamond anvil cell (HDAC). This cell can reach pressures up to 10 GPa. The pressure was determined using a combination of Raman spectroscopy and the fluorescence of ruby chips included in the DAC. Data was collected with a Mar345 2D detector; and a short wavelength was used (~ 0.5 Å) to minimize absorption. We found that $Ga_2Mo_3O_{12}$ undergoes three pressure-induced phase transitions, and amorphization above approximately 8.5 GPa.

Reference:

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P4. In Situ Powder Neutron Diffraction Measurements Of Model Ammoxidation Catalyst Systems

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In situ powder neutron diffraction measurements on the General Purpose Powder Diffractometer (GPPD) at the Intense Pulsed Neutron Source (IPNS) that mimic catalytic reactions for the conversion of propylene and ammonia to acrylonitrile (feed: C₃H₆/NH₃/O₂/N₂=1/1.2/2/8) at 430-450C have been carried out with two model catalyst systems: ferric molybdate (Fe₂Mo₃O₁₂) and a ferric molybdate/bismuth molybdate (Bi₂MoO₆) mixture. The purpose of these experiments is to understand the formation of phases present in an equilibrated catalyst under industrially relevant conditions. Results from the Fe₂Mo₃O₁₂ reduction experiment show two step process: initial reduction Fe⁺³ to Fe⁺² (Fe₂Mo₃O₁₂ → b-FeMoO₄ and MoO₃) followed by reduction of Mo⁺⁶ to Mo⁺⁴ (Fe₂Mo₃O₈, Fe₃O₄ and MoO₂ are formed). Results from the Fe₂Mo₃O₁₂ /Bi₂MoO₆ mixture experiment parallel results from the ferric molybdate experiment with the excess MoO₃ reacting with Bi₂MoO₆ to form more molybdenum rich phases. Three results that were not expected for the 2nd in-situ experiment are 1) the apparent inclusion of iron in a bismuth molybdate phase (Bi_{2+x}Fe_xMo_{3-x}O₁₂), 2) the significant dependence of the rate of reduction upon flow rates and 3) the gradual loss of crystallinity of the catalyst with time on stream.

P5. Structural and Magnetic Transitions in YbBaCo4O7+x

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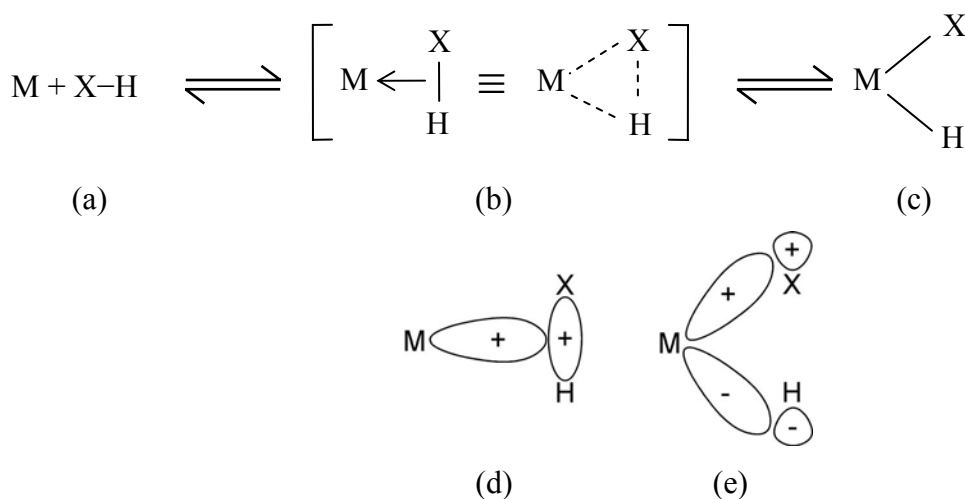
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The study of transition metal oxide physics has been dominated by octahedral coordination of the transition metal, such as in perovskite manganites and cobaltites. A less common coordination is the tetrahedron, whose weaker crystal field favors high-spin complexes across the periodic table. Here we discuss the crystal and magnetic structure of one such tetrahedral cobalt oxide, YbBaCo4O7, a member of the recently discovered RBaCo4O7 family (R-114). These R-114 compounds formally contain Co²⁺/Co³⁺ in a 3:1 ratio are structurally comprised of Kagome sheets of CoO4 tetrahedra joined in the third dimension by a triangular layer of CoO4 tetrahedra. The potential for magnetic frustration in the Kagome lattice motivated us to explore the magnetic and crystallographic behavior of this system with temperature. We show from joint neutron and synchrotron x-ray powder diffraction that Yb-114 undergoes a first order structural transition at 175 K that buckles the Kagome planes and allows a long-range antiferromagnetic order to set in at T~60 K. We argue that this transition is not due to charge order of Co²⁺/Co³⁺ ions, but rather to an attempt by Ba²⁺ to increase its bond-valence from XXX to 1.538. We also show magnetization data indicating a field-induced suppression of this antiferromagnetic state and discuss the possibility of inhibiting the structural phase transition by adding interstitial O.

P6. Single-Crystal Neutron Diffraction on Sigma Complexes: Recent Results from IPNS

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Sigma complexes of transition metals are coordination compounds in which two electrons in an X–H σ -bond form a dative bond with a transition metal as illustrated in Scheme 1. This bond can be further stabilized by π -backbonding from the metal to the X–H π^* antibonding orbital. Sigma complexes are of special interest because they are ubiquitous intermediates in metal-catalyzed reactions including hydrogenations, activation and functionalization of hydrocarbons, and hydroborations. Here we will report on some recent results obtained using the SCD instrument at IPNS, which has been upgraded with two new position-sensitive Anger detectors to achieve increased data collection efficiency. In the future, we hope to be able to dramatically extend these studies at the SNS using the Topaz single-crystal diffractometer instrument that is under development there and is scheduled to be completed in 2009.



SCHEME 1. (a-c) Oxidative addition reaction pathway (a \rightarrow c) of an X–H group to a transition metal coordination complex. (d) Donation of two electrons in the X–H σ bond to an empty metal d orbital of appropriate symmetry. (e) π -Backbonding from the occupied metal d orbital to the X–H σ^* antibonding orbital.

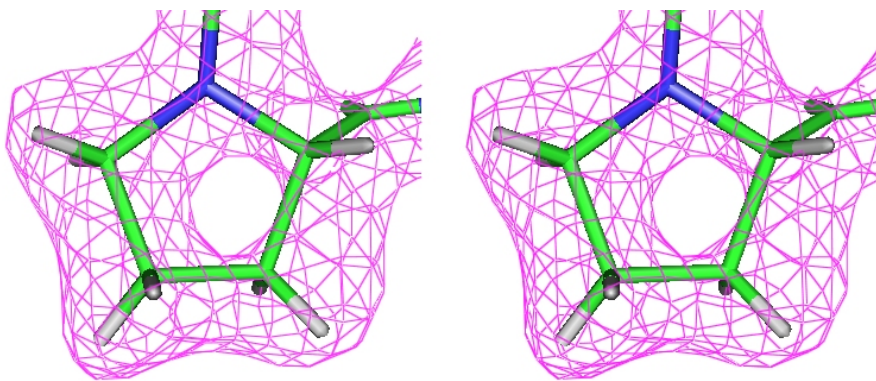
Acknowledgement. This work was supported by the U. S. Department of Energy, Office of Basic Energy Sciences, under Contract W-31-109-ENG-38.

P7. Neutron Diffraction Structure of Fully Deuterated Aldose Reductase: A Necessary Complement to X-ray Ultra-High Resolution Structures

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Full deuteration of human Aldose Reductase (MW=36kDa) significantly improved the neutron diffraction signal/noise ratio, compared to that obtained with Hydrogen/Deuterium partially exchanged samples. Consequently, a good quality data set (2.2 Å resolution at room temperature) was collected on the LADI diffractometer at the neutron source ILL-France, with a crystal volume (0.15 mm³) – radically smaller than usual for neutron diffraction studies. Experimental requirements for the high quality neutron data set are highlighted in the poster, as well as a comparison between the X-Ray electron density maps from the hydrogenated protein and the neutron scattering density from the deuterated protein. Deuterium atoms are clearly visible in neutron scattering density maps at 2.2 Å resolution (see below Proline 13, 2Fo-Fc map, 1.5 rms contour). Deuterium atoms important for catalysis are also reported in the poster.



P8. A High Resolution Macromolecular Neutron Diffractometer (MaNDi) at the SNS

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The construction of the Spallation Neutron Source (SNS) at Oak Ridge National Laboratory provides a unique opportunity for the development of a powerful, high resolution neutron diffractometer for structural biology. SNS will produce more than an order of magnitude higher intensity than existing pulsed spallation neutron facilities. A fully optimized diffractometer for neutron macromolecular crystallography (NMC) that also benefits from improved cryogenic moderators, state-of-the-art neutron guides, and high sensitivity, high resolution detectors should provide additional factors for increased data rates and improved resolution.

This poster presents the design criteria, calculations and simulations for a high-resolution Macromolecular Neutron Diffractometer (MaNDi) for the Spallation Neutron Source (SNS). MaNDi is optimized to achieve 1.5 Å resolution from crystals of 0.1 to 1 mm³ with lattice repeats in the range of 150 Å. We determined that locating MaNDi on a decoupled hydrogen moderator beamline with a curved guide will provide data of higher resolution and higher signal-to-noise than a coupled hydrogen moderator at the SNS. In addition, for an instrument with an initial flight path of 24 m at the 60 Hz source and a wavelength bandwidth of $\Delta\lambda \sim 2.7$ Å, bandwidth selection disk choppers can shift the wavelength range higher or lower for different experiments. With a wavelength range of 1.5–4.2 Å and $d_{\min} = 2.0$ Å, simulations predict experiment duration times of 1 to 7 days (Fig. 1) which is expected to revolutionize neutron macromolecular crystallography (NMC) for applications in the fields of structural biology, enzymology and computational chemistry.

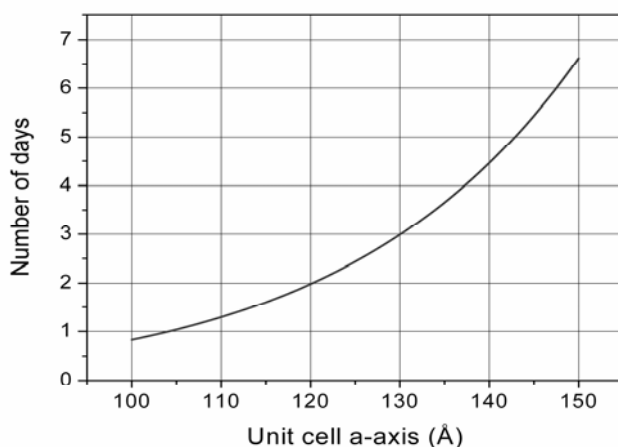


Figure 1. Data collection time vs. cubic unit cell size for a 0.125 mm³ deuterated crystal to 2 Å resolution.

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P9. Crystal Structure of PrgX, PrgX/cCF10 and PrgX/iCF10: The Role of Tetramerization of PrgX in Controlling the Pheromone Induction of pCF10 Transfer

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PrgX, a key player in controlling conjugation induced by the peptide pheromone cCF10 in *Enterococcus faecalis*, is a 33 kDa cytoplasmic protein encoded by pCF10. iCF10 is a plasmid-encoded peptide analogue of cCF10 that functions to prevent pCF10-containing donor cells from self-induction by endogenous cCF10. PrgX is the cytoplasmic receptor for the cCF10 peptide pheromone and has been shown to bind to two DNA sequences in the intergenic region of pCF10 between *prgX* and *prgQ* (the *prgQ* operon encodes the conjugative transfer functions of pCF10). The binding of PrgX to the two operators is involved in both the repression of transcription from the *prgQ* promoter P_Q and positive regulation of its own expression through the formation of a PrgX/DNA loop complex. The crystal structures show that PrgX can be divided into three functional domains: an N-terminal domain containing a helix-turn-helix motif responsible for DNA binding, a central dimerization domain (also for pheromone binding) and a C-terminal regulatory domain. The invariant existences of tetrameric form of PrgX molecules in different uncomplexed crystal structures suggest that PrgX functions in the tetrameric form *in vivo*. Upon cCF10 binding, the C-terminal domain of PrgX rotates about 120° covering the cCF10 molecule and the spatial arrangement of the PrgX tetramer is changed. In both PrgX and PrgX/cCF10 structures, amino acids 304-317 are invisible. In the crystal structure of the PrgX/iCF10 complex, iCF10 binds to PrgX in the pheromone-binding pocket the same way as cCF10 does. However, the PrgX molecule in the PrgX/iCF10 complex keeps the same conformation as the uncomplexed PrgX. Furthermore, amino acids 304-317 can be seen interacting with iCF10, stabilizing the "native conformation" of PrgX, and thus stabilizing the PrgX tetramers. Overall, PrgX functions in the tetrameric form *in vivo* and the binding of the pheromone to PrgX destabilizes the PrgX tetramers and thus induces the expression of *prgQ* operon. iCF10 competitively inhibits cCF10 induced transcription by directly binding to PrgX and stabilizing the PrgX tetramers, which is essential to the formation of the PrgX/DNA loop complex.

P10. Preliminary Results of the Recent Charge Density Study of Genistein

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Abstract

In an effort to determine a relationship between the biological function and the electronic properties of steroidal and nonsteroidal estrogens, a charge density study has been pursued on the nonsteroidal phytoestrogen, genistein. Crystals of genistein were crystallized from methanol by slow evaporation (Breton *et al.*, 1975) and X-ray diffraction data then obtained using a Rigaku R-Axis Rapid high-power rotating anode diffractometer with a curved image plate detector at 20.0(1)K. In order to obtain a high amount of redundancy, five runs were collected at 300 sec. with 4⁰ images. Adjacent images that overlapped by 2⁰ were collected to ensure correct scaling between the images for a total of 89 images per run. The data collection lasted less than two days.

This data collection technique gave a completeness of 88.0% (data up to 0.7Å⁻¹) to a maximum resolution of 1.32Å⁻¹ with a redundancy of 12.9 for all data. The data was indexed with the program HKL2000 (Otwinowski & Minor, 1997) and the predicted positions of the reflections were then used for data integration with the program VIIPP (Zhurov *et al.*, 2005; Zhurova *et al.*, 1999). The program SORTAV (Blessing, 1987) was then implemented to scale each run and average equivalent measurements. The use of the program SORTAV (Blessing, 1987) gave R_{int} = 0.0262 for all data and the scales between the runs were very close to unity as they did not differ more than 1%.

A preliminary refinement was then completed on genistein with the Hansen-Coppens multipole model (Hansen & Coppens, 1978) using the program XD (Koritsanszky *et al.*, 1995). A preliminary R(F²) value of 0.0311 has been obtained. Residual and experimental deformation maps along with a preliminary topological analysis of genistein will be reported.

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S1. Ultrafast Electron Crystallography: Atomic Level View of Transient Structures of Molecules, Surfaces, and Nanometer-Scale Materials

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Abstract

The static structure of macromolecular assemblies can be mapped out with atomic scale resolution using electron diffraction and microscopy of crystals. For transient non-equilibrium structures, which are critical to the understanding of mechanisms and functions, both spatial and temporal resolutions are required -- the shortest scales of length (0.1 to 1nm) and time (fs to ps) represent the quantum limit, the non-statistical regime of rates. I will outline the recent development of ultrafast electron crystallography, which can be employed in a grazing incidence diffraction mode in an ultrahigh vacuum environment to reach atomic scale detection with Submonolayer sensitivity. In these first experiments, we use crystalline silicon substrate as a template for making chemically modified layers or supramolecular assemblies; their local structures and periodic orders in the long range reflect their affinities to the substrates. With controls of laser fluences, energies, and surface characters, we observed different strongly driven (either from charges or from thermal strains) restructuring of the surfaces and adspecies with sub-angstrom displacement of atoms following the ultrashort laser impulse in the far-from-equilibrium regime at short time and at near-equilibrium at long times. The sensitivity achieved here, with the six orders of magnitude larger cross section than X-ray diffraction, and with the new capabilities of combined spatial (~ 0.01 Å) and temporal (300-600 fs) resolutions, promise diverse applications using this UEC tabletop methodology.