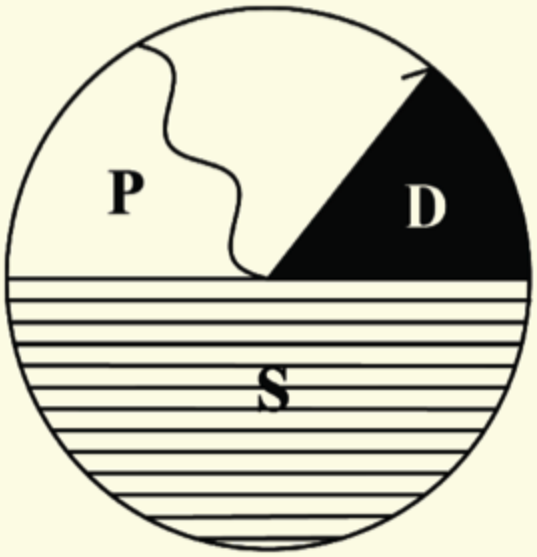
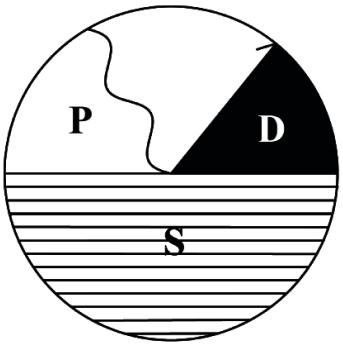
October 26 – 28, 2014

The 72nd Annual Pittsburgh Diffraction Conference



University of Georgia
Athens



The 72nd Annual Pittsburgh Diffraction Conference

Conference Chairman	John Rose
Symposium Organizers	John Rose
	Bi-Cheng Wang
Poster Session Chairman	Bi-Cheng Wang
Local Arrangements Coordinators	John Rose
	Lily Li, Lirong Chen

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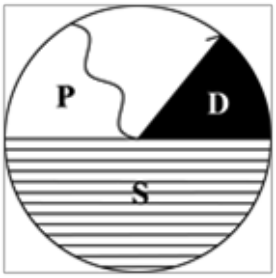


72nd Pittsburgh Diffraction Conference 2014

University of Georgia
Athens, GA
October 26 - 28, 2014

October 26th	**GSAS-II Workshop** (Room F/G)
9:00 am – 10:20 am	**GSAS-II Workshop Session I**
10:20 am – 10:40 am	**Coffee break**
10:40 am – 12:00 pm	**GSAS-II Workshop Session II**
12:00 pm – 1:00 pm	**Lunch (provided)**
1:00 pm – 3:00 pm	**GSAS-II Workshop Session III**
3:00 pm – 3:20 pm	**Coffee break**
3:20 pm – 5:00 pm	**GSAS-II Workshop Session IV**
6:00 pm – 7:00 pm	**Conference Registration**
7:00 pm – 9:00 pm	**Opening reception** (Hill Atrium)

October 27th	**Masters Hall & Vicinity**
8:00 am – 8:45 am	**Late Registration**
8:45 am – 9:00 am	**Opening Remarks – John Rose & B.C. Wang**
Morning session:	**100 years of X-ray Diffraction (Chair John Rose)**
9:00 am – 9:40 am	**Brian W. Matthews**, *University of Oregon* "From Bragg's Hometown to the MRC, Cambridge: Early Experiences in Protein Crystallography"
9:40 am – 10:10 am	**Charles F. Campana**, *Bruker AXS Inc* "The Changing World of Chemical Crystallography - 1964 to 2014"
10:10 am – 10:30 am	**Coffee Break** (poster setup)
10:30 am – 11:00 am	**Davis Blum**, *University of Georgia* "Got Protein? A Historical Perspective"
11:00 am – 11:30 am	**Aina E. Cohen**, *Stanford Synchrotron Radiation Lightsource* "Goniometer-Based Diffraction Studies Of Single Crystals At LCLS"
11:30 am – 12:00 pm	**Bi-Cheng Wang**, *University of Georgia* "Exploring the Use of Wavelength-Dependent Diffraction Data for Future 4D Crystallography"
12:00 pm – 1:30 pm	**Lunch (provided)**
Afternoon session:	**Structure Elucidation, Refinement and Interpretation through Powder Diffraction Crystallography (Chair Charles Lake)**
1:30 pm – 2:00 pm	**Brian H. Toby**, *Advanced Photon Source, Argonne National Laboratory* "Plan B: 98 Years of Powder Diffraction Crystallography"
2:00 pm – 2:30 pm	**Robert B. Von Dreele**, *APS, Argonne National Laboratory* "The Development of GSAS-II"
2:30 pm – 3:00 pm	**Ashfia Huq,** *Oak Ridge National Laboratory* "Neutron Diffraction To Study Energy Storage Materials"
3:00 pm – 3:30 pm	**Coffee Break**
3:30 pm – 4:00 pm	**Angus P. Wilkinson**, *Georgia Institute of Technology* "Stress Induced Phase Transitions in Negative Thermal Expansion Materials"
4:00 pm – 4:30 pm	**Clarina R. Dela Cruz**, *Oak Ridge National Laboratory* "Magnetic Structure Determination from Neutron Powder Diffraction"
4:30 pm – 5:00 pm	**Scott Speakmann**, *PANalytical, Inc*. "Applications and Challenges of In-Situ Diffraction Studies"
5:15 pm – 7:00 pm	**Poster session**
7:00 pm – 9:00 pm	**Banquet** (Magnolia Ballroom)

October 28th	**Masters Hall & Vicinity**
Morning session:	**Crystallographic Education (Chair Josph Ng)**
9:00 am – 9:40 am	**Cora Lind-Kovacs**, *University of Toledo* "Fun with crystals, light and symmetry – IYCr outreach activities"
9:40 am – 10:10 am	**Joseph D. Ng**, *University of Alabama in Huntsville* "Teaching And Motivating High School Students And Teachers About Crystallography Using The International Space Station"
10:10 am – 10:30 am	**Coffee**
10:30 am – 11:00 am	**William L. Duax**, *Hauptman Woodward Medical Research Institute* "Structural Bioinformatics for High School Students"
11:00 am – 11:30 pm	**Claudia J. Rawn**, *University of Tennessee* "Crystallography World of Wonders (CWOW): Workshops for Science Teachers Encouraging Them to Include Crystallography Content in Their Lessons"
11:30 pm – 12:00 pm	**Education Roundtable (Joseph Ng)**
12:00 pm – 12:45 pm	**Lunch (provided) -** Can be taken into the business meeting
12:45 pm – 1:30 pm	**Pittsburgh Diffraction Society Business Meeting**
Afternoon session:	**Advances in Neutron Crystallography (Chair Paul Langan)**
1:30 pm – 2:00 pm	**Irene T. Weber**, *Georgia State University* "Neutron Crystallography and Improved Drug Design for HIV Protease"
2:00 pm – 2:30 pm	**Donald Ronning,** *University of Toledo* "Informing Species-Specific Antibacterial Development; A Combined X-Ray/Neutron Diffraction Study"
2:30 pm – 3:00 pm	**Alison J. Edwards**, *ANSTO* "Single Crystal Neutron Diffraction – A Powerful Tool In The Structural Chemist's Arsenal – Critical Thinking Provides The Key To Valid Application"
3:00 pm – 3:30 pm	**Coffee Break**
3:30 pm – 4:00 pm	**Andrey Kovalevsky**, *Oak Ridge National Laboratory* "Neutron macromolecular crystallography and high-performance computing to study enzyme mechanisms"
4:00 pm – 4:30 pm	**Daniel Unruh**, *Texas Tech University* "Exploration Of Hydrogen Bonding Of Nanoconfined Water: A Comparison Between X-Ray And Neutron Diffraction"
4:30 pm – 5:00 pm	**Mayank Aggarwal**, *Oak Ridge National Laboratory* "Structure Based Drug Design – Targeting Carbonic Anhydrases"
5:00 pm	**Closing**

October 27th Masters Hall & Vicinity

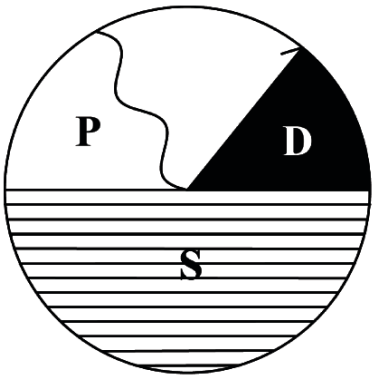
Poster session: **Chair: B. C. Wang**

Number	Presenter
P1	**Cassandra Hanley**, *Indiana University of Pennsylvania* "Using Multiple Wavelength Synchrotron Data to Identify the Cd^{2+} Site in Ag_2CdGeS_4"
P2	**Marta A. Witek**, *Emory University* "Structural Studies Of The *Catenulisporales acidiphilia* 16S rRNA (m^1A1408) Methyltransferase Reveal Unexpected Functional Reorganizations Of A Short Loop Crucial For Enzyme Activity"
P3	**Thomas Hartmann**, *Stoe & Cie GmbH* "Recent results in PDF calculations using a Stoe Stadi P with Ag Ka_1-radiation and a Dectris MYTHEN 1K Detector"
P4	**Joshua T. Greenfield**, *University of California, Davis* "Achieving Superconductivity In Solution-Produced β-FeSe"
P5	**Joseph W. LaMattina,** *University of Georgia* "A Novel Oxygen-Independent Pathway For Heme Degradation"
P6	**David L. Blum**, *University of Georgia* "The Bioexpression and Fermentation Facility: A Driver for Economic Development"
P7	**Leighanne C. Gallington**, *Georgia Institute of Technology* "Pressure-Dependent Phase Transitions And Thermal Expansion Of ZrV_2O_7"
P8	**Eric Hoffer**, *Emory University* "Structural Studies of *Mycobacterium tuberculosis* MazF-mt6: Insights into a Non-Traditional MazF Toxin"
P9	**John Chrzas**, *SER-CAT, University of Georgia* "The SER-CAT virtual beamline: Lessons learned when over 95% of all data is collected remotely"
P10	**Brett A. Duell**, *Indiana University of Pennsylvania* "X-ray Diffraction Investigation of $Na_2(Zn,Co)GeO_4$"
P11	**Marc A. Schureck,** *Emory University* "Mechanism of HigB-Mediated Ribosome-Dependent mRNA Degradation"
P12	**Zhongmin Jin**, *SER-CAT, University of Georgia* "Investigating Data Collection Strategies for the Rayonix MX300HS 10 Hz CCD Detector"
P13	**Charles McLouth Culbertson**, *Indiana University of Pennsylvania* "Synthesis and Characterization of (Zn,Co)Te"

October 27th

Poster session: Chair: B. C. Wang

Number	Presenter
P14	**Jack A. Dunkle**, *Emory University* "The structural basis for recognition and modification of the 30S ribosomal subunit by an antibiotic resistance methyltransferase"
P15	**Michelle K. Deaton,** *University of Georgia* "Investigating A Nairovirus' Ovarian Tumor Domain Protease's Species-Specific Substrate Preference"
P16	**John Rose**, *University of Georgia, SER-CAT* "SER-CAT Scientific Highlights: Award-Winning Projects and Assisting Beamline Technologies"
P17	**Nicholas D. Keul**, University of Georgia "The Role of Intrinsic Disorder in Human UDP-Glucose Dehydrogenase"



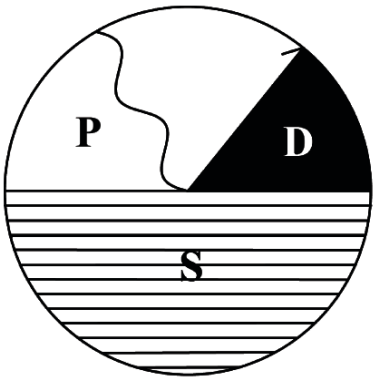
Sidhu Award

This award honors the memory of Professor Surhain Sidhu, who while Professor of Physics and Director of the X-ray Laboratory at the University of Pittsburgh was a founder of the Pittsburgh Diffraction Conference in 1942. Later, Professor Sidhu moved to Argonne National Laboratory, where he pioneered the use of the null matrix technique 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 hydrogen to deuterium is appropriately adjusted.

The award recognizes an outstanding contribution to crystallographic or diffraction research by an investigator whose doctoral degree was conferred within five years before the award date. Previous winners of the award are:

1967 A. I. Bienenstock
1968 R.M. Nicklow
1969 T.O. Baldwin
1970 S.-H. Kim
1971 L.K. Walford
1972 D. E. Sayers
1974 B.C. Larson & N.C. Seeman
1975 P. Argos
1978 K. Hodgson & G. DeTitta
1980 G. Petsko
1985 D.C. Rees
1986 D. Agard & J.M. Newsam
1988 Q. Shen
1989 M. Luo
1990 L. Brammer
1992 R.C. Stevens
1993 M. Pressprich & T. Yeates
1994 A. Vrielink & J. Wang
1995 M. Georgiadis
1996 M.J. Regan
1999 C. Ban & M Wahl
2000 W.R. Wikoff
2001 L. Shapiro
2002 Y. Lee
2003 E. O. Saphire
2004 Y. Xiong
2005 C.-Y. Ruan
2006 P. Chupas
2008 M. Hanson
2010 H. Wu
2013 T. D. Grant

Very regrettably, no nominations were received for the 2014 Sidhu Award.

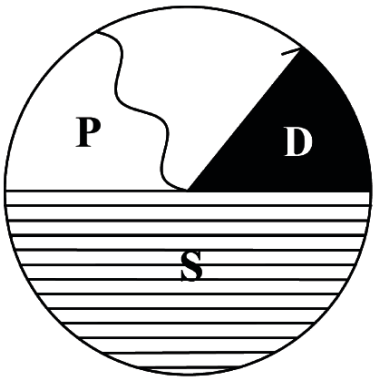


Chung Soo Yoo Award

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 31 August 1983. Dr. Yoo came to the U.S. from Korea in 1965; he obtained his M.S. Degree in Chemistry at Rice University in 1967 and his Ph. D. 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 to honor Dr. Yoo's memory, is given to a graduate student presenting the best poster at the annual Pittsburgh Diffraction Conference.



The PDS Award Funds

Over the years, the Pittsburgh Diffraction Society has created and bestowed awards to scientists and students involved in the many facets of diffraction study of matter. The first of these is the Sidhu Award, which recognizes the work of a young scientist who has made outstanding contributions to diffraction science within five years of earning a Ph.D. The second of these is the Chung SooYoo Award, which is given to the graduate student with the best poster presentation at a Pittsburgh Diffraction Conference. The most recent of these awards is the George A. Jeffrey Award given to meritorious graduate students who desire support to attend the triennial meeting of the International Union of Crystallography.

The three awards were established with generous gifts from family and friends of Sidhu, Chung Soo, and Jeff. Now we are seeking help to secure a more solid financial footing for the three PDS award funds. Please consider making a generous donation to the Pittsburgh Diffraction Society targeting one or more of the award funds.

Checks should be sent to the PDS Treasurer, Dr. Matthias Zeller, Youngstown State University, One University Plaza, Youngstown, Ohio 44555 (mzeller@ysu.edu)

All donations are tax deductible in the USA; check with your tax consultant in foreign countries.

Speaker Abstracts - 100 years of X-ray Diffraction

From Bragg's Hometown to the MRC, Cambridge: Early Experiences in Protein Crystallography

Brian W. Matthews
Institute of Molecular Biology, 1229 University of Oregon, Eugene, OR 97403-1229

I grew up in Adelaide, Australia, and took my Ph.D. at the University of Adelaide where Henry Bragg had been Head of the Physics Department and Lawrence Bragg a student.

My postdoctoral experiences included three years at the MRC Lab, Cambridge, in the group of David Blow, participating in the determination of the structure of alpha-chymotrypsin, one of the earliest known protein structures.

The talk will focus on experiences from that era.

The Changing World of Chemical Crystallography - 1964 to 2014

Charles F. Campana
Bruker AXS Inc., 5465 East Cheryl Parkway, Madison, WI 53711

We will present a historical overview of the many changes that have taken place in the field of chemical crystallography as it has been transformed from a very specialized technique used by diffraction physicists, physical chemists and mineralogists to a mainstream technique used routinely in all fields of chemistry.

Our approach will be to look a ten-year periods and to compare the current state-of-the-art of chemical crystallography for each period in terms of:

- Data Collection Methods
- Equipment
- Computers
- Software Packages
- Size of Structures
- Time per Structure
- Total Structures Published
- New Areas of Research

Got Protein? A Historical Perspective

David L. Blum
Bioexpression and Fermentation Facility, University of Georgia, Athens, GA 30602

Protein expression and purification is a critical need for X-ray crystallography experiments. Historically, starting material for many projects has consisted of animal organs and fluids. With the advent of recombinant DNA technology, starting material is more and more readily available through heterologous expression. The challenge today is to maximize yields from expression and purification in order to decrease costs and timelines for production of material for crystallization. This presentation will focus on a historical view of protein expression and purification moving through evolving technologies to current trends in this field.

Goniometer-Based Diffraction Studies Of Single Crystals At LCLS

A.E. Cohen representing the entire SSRL SMB and LCLS XPP team
Stanford Synchrotron Radiation Lightsource, SLAC National Accelerator Laboratory
Menlo Park, CA 94025

Femtosecond crystallography (FX) is an emerging method that expands the structural information accessible from very small or very radiation sensitive macromolecular crystals. Utilizing extremely bright, short-time-scale X-ray pulses produced by X-ray free electron lasers (XFELs), this method exploits a 'diffraction before destruction' phenomenon where a still diffraction image is produced by a single X-ray pulse before significant radiation induced electronic and atomic rearrangements occur within the crystal. FX confronts a major challenge impeding progress in structural enzymology by providing a means to determine catalytically accurate structures of acutely radiation sensitive metalloenzymes which may be significantly photo-reduced during a single X-ray exposure at the synchrotron, even at very small doses.

A diffractometer-based experimental setup for FX experimentation was developed and installed at LCLS XPP. This instrumentation provided an efficient flexible framework to carry out FX experiments using automated strategies tailored to handle a variety of sample requirements, crystal sizes and experimental goals. These developments coupled with recent improvements in data processing algorithms make it now possible to derive high resolution crystal structures using only 100 to 1000 still diffraction images. In the case of the needle shaped hydrogenase crystals, only 5 crystals and about a half an hour of LCLS beam time were used to obtain 125 still diffraction patterns used to produce a high quality 1.6 Å resolution electron density map. The exposure of over 930 myoglobin crystals using only 32 grids demonstrates the utility of high-density sample containers, such as grids to optimize throughput and sample consumption. Diffraction quality screening results from acutely radiation sensitive crystals of large multi-protein complexes will be described that illustrate the utility of this setup to extend the resolution that can be obtained from very radiation sensitive samples.

Exploring the Use of Wavelength-Dependent Diffraction Data for Future 4D Crystallography

Bi-Cheng Wang, Palani Kandavelu, Lirong Chen, John Rose, Dayong Zhou, Hua Zhang, Zheng-Qing Fu, Unmesh Chinte, James Fait & John Chrzas
SER-CAT and the Department of Biochemistry and Molecular Biology, University of Georgia, Athens, GA

Crystallography can provide detailed 3-D coordinate information about atoms in molecules using diffraction data collected at a single wavelength. However, new and important information may be obtained from a series of diffraction experiments whose wavelengths span over an extended wavelength region either in small increments, such as crossing the absorption-edge of a metal or from experiments using large wavelength increments with data collected away from the absorption-edge of the light atoms in the sample or crystal. By interpreting the complete set of data composed of the multiple data sets from these experiments new information about the properties of the target atoms can be mapped onto their 3D location in the crystal. This new information essentially provides another dimension to the diffraction experiment by adding information about the electronic identity of the atom. We call this process 4D Crystallography.

SER-CAT initiated a pilot project in 2012 that aimed at expanding the use of longer wavelength X-rays and wavelength-dependent diffraction for native atom phasing of macromolecules and other opportunities, which are the focus of the current study.

Specifically, the project is focused on developing a robust and user-friendly experimental platform for data collection over an extended (1.5 to 2Å) wavelength range that is available at SER-CAT, and a computational system for extracting this new 4D information from the data. In addition, the project also aims to discover additional requirements that are needed for 4D crystallography to become generally applicable in the future. In the area of protein crystallography, our studies are presently focused on the unambiguous identification of the nature of metals, including their oxidation states, in metalloenzymes. Our approach may also be useful for studying special atoms in small molecule crystals. Both the initial results and theoretical background of our approach will be presented.

Work supported in part by SER-CAT, the University of Georgia, the Georgia Research Alliance, and the Advanced Photon Source.

Speaker Abstracts - Structure Elucidation, Refinement and Interpretation through Powder Diffraction Crystallography

Plan B: 98 Years of Powder Diffraction Crystallography

Brian H. Toby
Advanced Photon Source, Argonne National Laboratory, Argonne Illinois 60439 (USA).

In this centennial of crystallography, it may come as a surprise to many that powder diffraction is nearly as old as single-crystal diffraction. Powder diffraction was developed independently in Germany and the US and published by P. Debye and P. Scherrer in 1916 and A.W. Hull in 1917, with both groups interested (and successful) in solving crystal structures from powder samples. Over nearly a century there have been many advances in instrumentation: Parrish's Bragg-Brentano powder diffractometer (1947); reactor-based *neutron* powder diffractometers (1950's and 60's); spallation neutron and synchrotron instruments (1980's through present); area detection (2000's), but the most importance advance is arguably the development of Rietveld analysis software (1969) which allowed direct fitting of structures to powder diffraction data. Likewise, advances in structure solution through direct methods, charge flipping and Monte Carlo techniques have allowed powder diffraction to become a commonly-used, though by no means routine, tool in the crystallographic toolkit. Single crystal diffraction is still the preferred technique, when it is possible, but for many studies it is not.

The Development of GSAS-II

Robert B. Von Dreele
Advanced Photon Source, Argonne National Laboratory, Lemont, Il, USA 60439

The General Structure Analysis System (GSAS) was originally developed more than 25 years ago to analyze multipattern single crystal and powder diffraction data sets produced at the Los Alamos spallation neutron source (LANSCE) and was written in Fortran for VAX computers. The complexity of the control file ("experiment file") required the development of an interactive editor (EXPEDT) that by means of multilayered menus allowed the user to enter values and set controls without being concerned about the details of how the records of that file were constructed. Expansion of GSAS quickly followed to include the analysis of x-ray data as well as extending the models to include e.g. complex molecular constraints and restraints, texture analysis, complex microstrain models and ultimately fitting of macromolecular structures from powder data as well as moving it to more common computer operating systems (MS Windows, linux & Mac OSX). Meanwhile, a more modern graphical user interface (EXPGUI) was developed that allowed user interaction via a mouse as well as adding more functionality. Consequently, it now enjoys widespread use (>6000 citations to date).

However, GSAS is no longer a viable platform for future development in crystal structure analysis. Thus, we have made a new start, GSAS-II, written using the Python language loaded with graphics, GUI and mathematical packages (matplotlib, pyOpenGL, wx, numpy and scipy). However, the structure and operation of Python has required new approaches to many of the algorithms used in crystal structure analysis. A very small number of old GSAS Fortran routines are imbedded within GSAS-II where computational speed was required. This talk will cover the developments for crystallographic data analysis that are now part of GSAS-II. Of particular significance are facilities for sequential analysis of data collected under changing experimental conditions and subsequent parametric analysis.

Neutron Diffraction To Study Energy Storage Materials

Ashfia Huq
Chemical and Engineering Materials Division, Spallation Neutron Source, Oak Ridge National Laboratory, Oak Ridge, TN, United States. E-mail: huqa@ornl.gov

Sustainability is where society overlaps with the environment and the economy. With concerns over the future availability of fossil fuels and climate change Scientist and Engineers from all disciplines are focusing their research on materials for a sustainable future. Examples of areas where crystallographers are taking up the charge include Li-ion batteries for electric cars, materials for oxygen sensors and solid oxide fuel cells, thermoelectric materials, materials for solar energy. This is also reflected in the user research that is carried out at the POWGEN diffractometer, the general purpose neutron powder diffraction instrument at the Spallation Neutron Source. I will show some examples of how structural information obtained from energy storage materials can help us understand their functional properties primarily concentrating on Li-ion batteries.

Stress Induced Phase Transitions in Negative Thermal Expansion Materials

Angus P. Wilkinson, Cody R. Morelock, & Leighanne C. Gallington
School of Chemistry and Biochemistry, Georgia Institute of Technology, Atlanta, GA 30332

Many features that are often associated with negative thermal expansion (NTE), such as low density, a flexible framework, and the existence of phonons that soften on compression (leading to negative mode Gruneisen parameters), also lead to rich and complex behavior when stressed. The occurrence of crystal to crystal and/or crystal to glass phase transitions at modest pressures is common. Stresses capable of inducing these transitions can often be realized in composites, due to thermal expansion mismatch. This presentation will focus on our recent investigations of how pressure effects both the properties of ReO_3-type NTE materials, such as ScF_3, and the order disorder phase transitions seen in ZrW_2O_8 and HfW_2O_8. The apparatus developed to study these materials in the pressure range 0 – 400 MPa and 25 – 250 ºC, using diffraction, will be described along with the principle results of the investigations.

Magnetic Structure Determination from Neutron Powder Diffraction

Clarina R. Dela Cruz
Quantum Condensed Matter Division, Oak Ridge National Laboratory, Oak Ridge, TN USA

An important field of experimental Condensed Matter Physics focuses on studying correlated electron systems including frustrated magnetism, unconventional superconductors, iron-based superconductors and multifunctional systems such as multiferroic compounds. The use of various bulk measurement techniques to characterize the physical properties in these systems is an essential first step in revealing the novel electronic and magnetic ground states. Further studies using powerful microscopic probes such as neutron scattering methods are crucial in advancing the central theme in understanding correlated electron systems, which is to make the correlation between structure, magnetism and physical properties. As is common across correlated electron systems, highly degenerate ground states abound which are readily disturbed by chemical dopants and perturbing fields such as an applied magnetic field or pressure. Thus, studying these systems, using neutron scattering techniques in particular, in various extreme conditions reveals new emergent ground states with tunable magnetic, electronic or ferroelectric order parameters. In this talk I will present selected work done at the ORNL neutron scattering diffractometers on magnetism studies in correlated electron systems.

Applications and Challenges of In-Situ Diffraction Studies

Scott Speakmann
PANalytical Inc., Westborough MA 01581

A tremendous amount of information can be learned when samples are studied within in-situ environments, whether the conditions be non-ambient temperatures, pressures, humidity, or atmosphere. Modern instrumentation, from powerful beamline sources to fast laboratory detectors, have increased the speed and sensitivity with which X-ray diffraction data can be collected under non-ambient conditions. However, data collected in-situ often come with inherent limitations. This presentation will use several examples to illustrate the information that can be learned from in-situ diffraction experiments, and the care that must be taken to understand the limitations. Examples will include crystallographic phase transformations, phase diagram mapping, quantification of thermophysical properties such as thermal expansion coefficients, time-resolved studies of chemical reactions, and time-resolved studies of microstructural evolution.

Speaker Abstracts - Crystallographic Education

Fun with crystals, light and symmetry – IYCr outreach activities

Cora Lind-Kovacs[1] & *Martha M. Teeter*[2]
[1]Department of Chemistry & Biochemistry, The University of Toledo, Toledo, OH 43606, USA and [2]Department of Internal Medicine, UC Davis, Medical Center, 4150 V Street, Suite 3100, Sacramento, CA 95817, USA

The importance of crystallography was recognized by Nobel Prizes to Max von Laue in 1914, and Sir William Henry and William Lawrence Bragg in 1915. At the centennial of these events, insights gained from crystallographic experiments have revolutionized virtually all science and engineering disciplines, and benefited society through advanced materials, drugs, an amazing understanding of the human body and many more aspects. Yet few non-experts have much of an idea of what crystallography is, or why its study and use will remain important in the future. The fact that crystallography forms the basis for knowing the atomic level structure of solids is unknown or forgotten by many, even by other scientists and engineers who use such knowledge of atomic level structure and the resulting properties of materials in their own research. During this International Year of Crystallography 2014, the ACA is reaching out to proudly claim the accomplishments of our science, and to introduce all age and education levels to fun and exciting crystallographic topics. In the long run, we hope to leave a legacy that will result in lasting recognition and appreciation of our field. This will be crucial to ensure both continued funding for crystallography related research, and for attracting and training the next generation(s) of crystallographers into the field. This presentation will give an overview of many major IYCr projects that ACA members are involved in.

Teaching And Motivating High School Students And Teachers About Crystallography Using The International Space Station

Joseph D. Ng
Department of Biological Sciences, University of Alabama in Huntsville

The International Space Station has been used as a platform for crystallography education for high school students and teachers. The goal is to teach high-school students and teachers about the nature of biological macromolecules and, in particular, what proteins are and why they are important. The program focuses on what a protein crystal is and why it is important to crystallize proteins. Why do we want to grow crystals of proteins at all, and in particular, why do we want to grow them in space? The classroom and space experience was used to provide teachers with the opportunity to display and illustrate a broad a range of new and significant ideas in the areas of biology, physics and chemistry. The program consisted of four principal demonstrations of laboratory and research techniques used in structural biological studies within different stations. The students were divided into small groups and spent about 1–2 h (depending on the station) with a real investigator demonstrating (1) protein purification and characterization; (2) vapor diffusion and batch crystallization; (3) fundamentals of X-ray diffraction; and (4) three-dimensional visualization of a protein molecule using computer graphics. Since the emphasis of the workshop was focused on protein crystallization, most of the hands-on experience was setting up protein crystallization experiments. Preparation of crystallization samples is technically very simple; requiring limited manual skills and very limited training. The process is so simple that high school students could likely assist in the crystallization of protein samples, and in that way, they could directly participate in flight experiments aboard the ISS. Students could be enlisted to prepare protein crystallization samples for this program, under strict supervision and guidance by professionally trained and experienced personnel, and these samples can be frozen in liquid nitrogen and carried into space. The samples would be returned to the classrooms, after being on the ISS for two to four weeks, and returned to the students who prepared them for examination and data processing. The experiments would, therefore, provide a student flight experience, but at the same time also be part of an important, ongoing scientific investigation in crystallography.

Structural Bioinformatics for High School Students

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Over 200 students from 25 schools in the area have been trained in structural bioinformatics at the Hauptman Woodward. The goals of the program are to have students experience the challenges of research and the joy of discovery. The summer program consists of a three-week bioinformatics workshop. The students study the evolution of the genetic code and the amino acid composition and three-dimensional fold of protein families present in every living thing. They are creating evolutionary trees of all species and identifying the last universal common ancestor of their protein families. They use web based programs (ScanProsite and PYMOL) to analyze gene and amino acid sequences in SwissProt/TrEMBL and protein structures in the PDB and master a suite of programs developed at HWI to improve sequence alignment and trace evolution. The students work in teams led by student veterans of the program and make presentations weekly. They learn teamwork, organizational and speaking skills while performing meaningful research. They have learned to communicate the essence of their work to a broad audience from grade school students and laymen to professional scientists, an ability that will help them in whatever career they choose. The program helps students to recognize and achieve their potential. The goal is to give students an enriching and life-altering experience that in the long term will provide a satisfying and sustainable career path. The program is promoted through presentations at area high schools, to civic groups, word of mouth, science fairs, etc. Past students have competed as finalists in statewide and national science competitions. The program has gender and ethnic balance. The program receives modest support from local sources in Buffalo.

Crystallography World of Wonders (CWOW): Workshops for Science Teachers Encouraging them to Include Crystallography Content in Their Lessons

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Three CWOW workshops have been offered, jointly supported and sponsored by the American Crystallographic Association (ACA), the U.S. National Committee for Crystallography and a National Science Foundation supplement, in conjunction with the ACA Annual meetings in Chicago (2010), Boston (2012), and Albuquerque (2014). An abbreviated (1 h) CWOW workshop was also presented at the National Science Teachers Association (NSTA) National Conference in Boston (April 2014). The workshops are designed to get teachers thinking about crystal structures of a variety of materials and about characterization at the atomic level. The general schedule of the full workshops starts with an introduction to ceramics, metals, and polymers, continues with close packed planes and the three dimensional stacking of these planes, and then introduces the concept of filling of interstitial sites between the planes (the 1h workshops stop here). Crystal structures of a face centered cubic material and sodium chloride are built from Lego® bricks to illustrate these concepts further. To complement these structural units, characterization of structures using x-ray diffraction is then highlighted. After the diffraction basics are introduced, examples of characterizing everyday materials and biological materials using x-ray diffraction are presented. The teachers are introduced to local crystallographers, databases, and remote facilities. A CWOW workshop kit has been developed, which includes a materials matching game with spheres of a variety of metals (Al, stainless steel, brass), ceramics (Al_2O_3, WC), and polymeric materials (acrylic, polypropylene, polytetraflouroethylene, nylon 6/6), close packed planes to compare Face Centered Cubic (FCC) and Hexagonal Close Packed (HCP) stacking, Lego® bricks to build FCC and rocksalt structures, and optical gratings and a laser to visualize diffraction using light waves.

Speaker Abstracts - Advances in Neutron Crystallography

Neutron Crystallography and Improved Drug Design for HIV Protease

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HIV-1 protease (PR) is an important target for antiviral inhibitors to treat the pandemic disease of HIV/AIDS. Drug resistance is a critical medical challenge necessitating development of better drugs. We employ neutron crystallography in conjunction with atomic resolution X-ray crystallography to analyze the hydrogen atoms and their interactions in hydrogenated and perdeuterated HIV PR-inhibitor complexes. We compare the H/D atoms visible in the room temperature neutron structure at 2.0 Å resolution with those observed in 1.03 Å resolution X-ray structures from cryo-cooled crystals. We assess the contributions of H atoms and H bonding to the inhibitor binding in our joint X-ray/neutron structure of PR in complex with clinical drug amprenavir (APV) [1]. Analysis based on the determined positions of D atoms shows that some PR-drug interactions are significantly distorted from the accepted values for H-bonds. This neutron structure suggests that H-bonding of APV to PR contributes less to its nanomolar affinity than was inferred from X-ray structures [2], which will be valuable guidance in the design of inhibitors with improved interactions suitable for treatment of resistant virus. Hence, neutron crystallography has potential applications in rational drug design.

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Informing Species-Specific Antibacterial Development; A Combined X-Ray/Neutron Diffraction Study

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5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase (MTAN) is a bacterial nucleosidase essential in *Helicobacter pylori*, which is the causative agent of stomach ulcers and is strongly correlated with gastric cancer. This essentiality is due to the role it plays in hydrolyzing the *N*-ribosidic bond of a menaquinone precursor called 6-amino-6-deoxyfutalosine. To structurally characterize the polar interactions between MTAN and its substrates and products, two co-crystal structures have been solved. In one structure, an inactive mutant of the *Helicobacter pylori* MTAN was complexed with the substrate *S*-adenosylhomocysteine (SAH). The neutron and X-ray data used for refinement extend to 2.5 and 2.0 Å, respectively. At the current stage of co-refinement of this structure, the overall R_{factor} and R_{free} values are 27 and 29 %, respectively. The second co-crystal structure represents the MTAN/product complex resulting from hydrolysis of SAH. The neutron and X-ray data used for refinement extend to 2.5 and 1.8 Å, respectively. The overall R_{factor} and R_{free} values are 2e and 25 %, respectively. The information from these structures has given new insight concerning the enzyme mechanism. This talk describes and discusses these structures as well as the application of this new information toward drug discovery.

Single Crystal Neutron Diffraction – A Powerful Tool In The Structural Chemist's Arsenal – Critical Thinking Provides The Key To Valid Application

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The utility of neutron diffraction in the elucidation of hydrogen atom positions is a dominant theme in discussions of the application of this technique to chemistry. At modest resolution and with relatively few observations (compared to the enormous high resolution data sets potentially accessible with modern X-ray methods), enumeration and location of hydrides in the presence of much heavier atoms is straightforward if neutron diffraction can be used. Neutrons are also applicable to differentiating atoms of similar atomic number where, in many instances, the neutron scattering factors of near neighbour elements are strongly differentiated.

As a chemist, the critical review of data from all sources, including neutron diffraction is fundamental to reaching self-consistent conclusions regarding the structure and constitution of any compound presented for analysis. The significant barriers to accessing neutron diffraction – especially the process of applying for beam-time (and even funding) to complete a project can lead to a situation where researchers are heavily "pre-invested" in their proposed model. This can make it difficult to play "devil's advocate" and consider alternative models, which must be tested against both the data and sound chemical reasoning.

The notion of "The Crystal Structure" as some kind of "gold standard" which "trumps" or renders superfluous, application of the full suite of analyses to any compound significantly diminishes chemistry. Neutron diffraction is a powerful method and the integration of insights gained from it require open-minded assessment of all available data, not just that from diffraction.

Neutron macromolecular crystallography and high-performance computing to study enzyme mechanisms

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Enzymes continue to expand their role in industry as a "green" option for the synthesis of value-added products. They are targeted for the design of drugs in pharmaceutical applications and also for protein engineering in industry to improve their efficiency, stability, and specificity. In-depth understanding of mechanisms of enzymatic reactions may provide essential information for more effective drug design and enzyme engineering. We are employing a joint X-ray/neutron (XN) protein crystallographic technique in combination with high-performance computing, including QM and QM/MM calculations, and MD simulations, to investigate the mechanisms of enzymes that are important to renewable energy and chemical synthesis. D-xylose isomerase (XI) is an enzyme which can be used to increase the production of biofuels from lignocellulosic biomass and also to synthesize rare sugars for pharmaceutical industry. XI catalyzes the reversible multi-stage sugar inter-conversion reaction facilitated by the presence of two divalent metal cations in its active site. It primarily catalyzes the isomerization of the aldo-sugar D-xylose to the keto-isomer D-xylulose, but can also epimerize L-arabinose into L-ribose, albeit much less efficiently. The reaction involves moving hydrogen atoms between the protein residues, sugar and water molecules, and can only be understood if hydrogen atoms are visualized at each reaction stage. We have obtained a number of joint XN structures of XI complexes representing snapshots along the reaction path with D-glucose, D-xylose and L-arabinose. The suggested reaction mechanism has been verified by QM calculations using the novel $O(N)$ methodology. We are using this structural and mechanistic information to re-design XI to be more efficient on D-xylose and L-arabinose for biofuels and biomedical applications by employing QM/MM, MD, and Rosetta methodologies.

Exploration Of Hydrogen Bonding Of Nanoconfined Water: A Comparison Between X-Ray And Neutron Diffraction

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As important as water is to our everyday survival, how water influences and interacts with molecular species, as well as solid state materials, is still being explored. During our studies of molecular uranyl species in aqueous systems, a fortuitous experiment resulted in the formation of a uranyl based nanotubular material (UMON) (Unruh, 2013). While the structure itself was an interesting study in potential mechanisms for constructing nanotubular solid state materials, the interstitial water molecules within the tubes were the real interest. Materials containing nanoconfined water are nothing new, studies of water in carbon nanotubes, metal-organic frameworks (MOFs), and biological systems are well documented. The interesting aspect of this material was the hexagonal arrangement of water molecules within the nanotube without apparent interactions between the water molecules and the tube. Classically, the uranyl ion $(O=U=O)^{2+}$ is thought to have little to no interaction with the hydrogen atoms of water molecules. However, our initial X-ray studies demonstrated the potential for weak hydrogen bonding interactions with the oxygen atoms of the uranyl ions. To help explore this interesting material, crystals of UMON were analyzed at SNS on the TOPAZ beam line and those results will be the focus of this talk.

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Structure Based Drug Design – Targeting Carbonic Anhydrases

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Carbonic anhydrases (CAs) are ubiquitous enzymes found in all kingdoms of life, and catalyze the interconversion of CO2 to HCO3- with a subsequent proton transfer (PT) step that completes the catalytic cycle. Proton and bicarbonate production is related to everything from respiration, photosynthesis, cerebral spinal fluid production, ureagenesis, to blood pH control. Besides CA's many important physiological functions, it is also a prominent clinical target. The clinically used drug, acetazolamide (AZM, sold as Diamox® by Merck), is a sulfonamide-based drug that binds with nanomolar affinity to human α-CA II. It is used to treat a spectrum of diseases such as altitude sickness and epilepsy, but was initially developed for the treatment of glaucoma. However, due to an off-target binding of the currently available CA inhibitors (CAIs) to other HCA isoforms causes undesirable side effects. Hence there is a need for CAIs that bind with similar/higher affinity without causing side effects. A major thrust in this area is to design isoform-specific inhibitors, which requires extensive knowledge about hydrogen bonding patterns within the active site of an enzyme.

After recently publishing a neutron structure of CA II complexed with AZM, we have again prepared large crystals of CA II in complex with another drug: methazolamide. The overall goal is to formulate rules for designing novel, isoform specific inhibitors against CA. We intend to achieve this by developing a database of protonation states of classic sulfa-drugs of CA and use that information to map out structure activity relationships.

Neutron diffraction is a very strong technique that can be exploited to directly observe these hydrogen bonding differences and hydration states of the inhibitor/residues. This study add to the knowledge base of the role of H atoms in drug interactions, but it could give clues for future drug development efforts of non-sulfonamide based CA inhibitors for the treatment of glaucoma, epilepsy, and altitude sickness.

Poster Presentations

P1

Using Multiple Wavelength Synchrotron Data to Identify the Cd^{2+} Site in Ag_2CdGeS_4

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The compound Ag_2CdGeS_4 is of interest due to its second harmonic generation properties. The crystal structure of this compound was ambiguous due to similarities between the Ag^+ and Cd^{2+} ions. This study will use resonant diffraction to distinguish the crystallographic sites occupied by these ions.

Atomic scattering factors for atoms in X-ray diffraction are dependent on the number of electrons present at each atomic site. Thus, X-ray crystallographic methods encounter difficulty distinguishing between isoelectronic heavy atoms. In the study of Ag_2CdGeS_4, the Cd^{2+} and Ag^+ sites were indistinguishable with 46 electrons each. Metal-sulfide bond distances were not definitively different to differentiate between the ions. To solve this dilemma, the X-ray wavelength was tuned to the Ag^+ and Cd^{2+} absorption edges. At these wavelengths, anomalous dispersion effects can reveal the actual site which the Cd^{2+} ions occupy.

For Mo radiation (0.71073 Å) the anomalous dispersion coefficients for Ag^+ are $\Delta f'$=-0.892, $\Delta f''$ =1.104 and for Cd^{2+} are $\Delta f'$=-0.802, $\Delta f''$=1.206. These coefficients are too similar to distinguish with conventional X-ray analysis. Using a synchrotron source, the wavelengths can be tuned. For example, at a wavelength of 0.464217 Å (the absorption edge for Cd^{2+}), the anomalous dispersion coefficients show significant differences, with $\Delta f'$=-2.190, $\Delta f''$=3.338 for Ag^+ and $\Delta f'$=-8.419, $\Delta f''$=0.557 for Cd^{2+}. From these differences, coupled with the fact that the Ag^+ and Cd^{2+} ions account for the majority of the scattering, the precise location of the Cd^{2+} ions in the crystal structure can be determined. The data for this work was collected at the Advanced Photon Source, Argonne National Laboratory. Analysis of the resonant diffraction data allowed the identification of the Ag^+ and Cd^{2+} sites in the crystal structure.

P2

Structural Studies Of The *Catenulisporales acidiphilia* 16S rRNA (m^1A1408) Methyltransferase Reveal Unexpected Functional Reorganizations Of A Short Loop Crucial For Enzyme Activity

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Methylation of the bacterial small ribosomal subunit (16S) rRNA on the N1 position of A1408 confers exceptionally high-level resistance to a broad spectrum of aminoglycoside antibiotics. To expand our understanding of these important enzymes, we solved the crystal structure of the *C. acidiphilia* 16S rRNA (m^1A1408) methyltransferase ("*Cac*Kam") at 1.7 Å resolution. The *Cac*Kam structure closely resembles other m^1A1408 methyltransferases within its conserved S-adenosyl-L-methionine (SAM) binding core but exhibits unique differences in a region ("β6/7 linker") critical for enzyme-30S recognition. Several residues are dramatically repositioned in this novel conformation, which is stabilized by cation-π stacking interactions involving the universally conserved and functionally critical W203 residue. To test the hypothesis that SAM binding reorganizes the β6/7 linker (and thus W203) into a conformation competent for 30S binding, wild-type and mutant *Cac*Kam structures were determined in complex with SAM. One mutant *Cac*Kam structure with SAM revealed increased flexibility but not complete 'closure' of the β6/7 linker. Critical residues for SAM binding and 16S rRNA interaction were identified by protein mutagenesis, bacterial growth assays with antibiotic, and *in vitro* methylation and binding assays. These studies revealed that W203 and W113, previously known only for their role in sequestering A1408 in the enzyme active site, may also directly influence enzyme turnover, potentially in a manner requiring the flexible nature of the β6/7 linker. Whether this mechanism of enzyme regulation is unique to *Cac*Kam or common to all m^1A1408 methyltransferases is currently under investigation.

P3

Recent results in PDF calculations using a Stoe Stadi P with Ag Ka_1-radiation and a Dectris MYTHEN 1K Detector

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An impressive comparison of $G(r)$ calculated with PDFgetX2 [1] from data of Naphthalene in a 1mm capillary taken at room temperature with a STOE STADI P powder diffractometer in transmission mode equipped with a Ag-tube, a Ge(111)-monochromator for pure Ag-Ka_1-radiation (0.5594 Å) as well as the Dectris MYTHEN 1K with 1mm chip size and from synchrotron data, beamline X17A, NSLS Brookhaven with a wavelength of 0.1839 Å, yields amazingly similar peak widths for both experiment sites.

To observe the temperature dependence of this resolution, the same laboratory setup with an additional Oxford Cryosystems Cobra and smallest sample amounts of LaB_6 as a crystalline standard as well as Naphthalene as a well-known organic phase has been chosen to get low temperature data for the PDF calculation experiments.

A STOE furnace instead of the cryostat has been chosen to get high temperature G(r)-data from Ammonium Nitrate to compare the signal width as a function of T.

The support of DECTRIS Ltd., Baden, Switzerland and of Lothar Fink, Institute for Inorganic and Analytical Chemistry, Goethe University, Frankfurt, Germany, is kindly acknowledged.

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P4

Achieving Superconductivity In Solution-Produced *β*-FeSe

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A new low-temperature solvothermal synthesis of superconducting *β*-FeSe has been developed using elemental iron and selenium as starting materials. We have shown that syntheses performed in aerobic conditions resulted in the formation of non-superconducting antiferromagnetic *β*-FeSe, while syntheses performed in ultra-dry and oxygen-free conditions produced superconducting *β*-FeSe. Detailed characterization of both types of samples with magnetometry, resistivity, Mössbauer spectroscopy, synchrotron X-ray and neutron powder diffraction, and pair-distribution function analysis uncovers factors that trigger the loss of superconductivity in *β*-FeSe. Vacancies in the iron sublattice and the incorporation of disordered oxygen- and hydrogen-containing species are typical for non-superconducting antiferromagnetic samples, while a pristine structure is required to preserve superconductivity. Exposure to ambient atmosphere resulted in the conversion of superconducting samples to antiferromagnetic ones. This synthetic method creates new possibilities for soft chemistry approaches to the synthesis and modification of iron-based superconductor.

P5

A Novel Oxygen-Independent Pathway For Heme Degradation

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Iron acquisition is a significant barrier pathogenic bacteria must overcome during colonization of its host. For mammals, heme is the most abundant source of iron and can be exploited through the uptake and degradation of the iron-containing tetrapyrrole. Heme oxygenases are the canonical enzymes that perform this degradation activity through the activation of molecular oxygen, however, not all enzymes result in the production of biliverdin. Despite the ability to use heme as an iron source, no canonical heme oxygenases have been identified in the Gram-negative enteric pathogens *Escherichia coli O157:H7*, *Shigella dysenteriae*, and *Vibrio cholerae*. Here, we describe the function of the ChuW and ChuY from *E. coli O157:H7*, of which are associated with the heme uptake machinery and expressed during iron duress. Notably, unlike the traditional heme oxygenase, this system functions under strictly anaerobic conditions. Specifically, we demonstrate the role of ChuW as a radical SAM methyltransferase, which coordinates a $[4Fe\text{-}4S]^{2+/+}$ cluster, and, can use low potential electrons to generate 5'-deoxyadenosine and S-adenosylhomocysteine, to, subsequently, produce a methylated porphyrin-like molecule, product W. Product W can be reduced by ChuY, using either NADPH or NADH, however, the structure of these products have yet to be determined. Finally, we have solved the native ChuY structure to 2.0Å resolution by molecular replacement. Structural overlays suggest homology to biliverdin reductase and other NAD(P)H dehydrogenases/reductases, with conserved residues in the NADPH binding site. Taken together, these data suggest an oxygen-independent pathway for heme/iron utilization.

P6

The Bioexpression and Fermentation Facility: A Driver for Economic Development

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The Bioexpression and Fermentation Facility (BFF) was established in 1967 and is one of the largest fermentation pilot plants in the Southeast offering a variety of services from recombinant protein production to monoclonal antibodies. The BFF consists of the Fermentation Research Facility, Protein Purification Laboratory, Cell Culture Facility and Monoclonal Antibody Facility. These four divisions enable the BFF to provide clients with a comprehensive array of services covering a wide range of biomanufacturing areas. The BFF has the capability to provide expertise and training in the biotech industry from biofuels and other environmentally-friendly products to biomedical technology.
The BFF is located at the University of Georgia, in Athens, GA, occupying approximately 9500 square feet of lab space. The BFF has 22 bioreactors ranging from 1 L to 800 L, with centrifugation and tangential flow filtration available for all reactor sizes in addition to cell homogenization and other downstream processing capabilities. In addition, the BFF has 10 HPLCs capable of flow rates from 1 mL/min to 800 mL/min, and processing at temperatures from 4 ˚C to 80 ˚C. There are 13 staff members with 4 PhD scientists.

In 2012, the BFF completed over 120 discrete projects for more than 45 clients.

In addition to providing services to several in-state biotech companies and academic researchers the BFF has served hundreds of clients including organizations in 37 states and six countries. The facility has a solid International reputation for providing fermentation and protein purification services. In addition, significant equipment upgrades have been funded by income from service work and government grants over the past decade to ensure we can continue to- grow even more in the future.

In addition to services, BFF also is involved in training of students through the Master's in Biomanufacturing and Bioprocessing as well as other undergraduate and graduate students on campus. The training opportunities and services offered at BFF will continue to be an economic driver in Georgia and the Southeast.

P7

Pressure-Dependent Phase Transitions And Thermal Expansion Of ZrV_2O_7

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Unlike ZrW_2O_8, which exhibits negative thermal expansion over a broad temperature range, the ambient temperature phase (α) of ZrV_2O_7 exhibits positive thermal expansion. Heating ZrV_2O_7 initially results in formation of an incommensurate phase with even more positive thermal expansion, then a high temperature phase (β) that exhibits negative thermal expansion (NTE).[1] The thermal expansion behavior of NTE materials has been shown to be sensitive to pressure in some instances. A previous study of ZrW_2O_8 showed that induction of disorder via compression of the orientationally ordered phase led to enhanced NTE.[2] *In situ* variable temperature/variable pressure powder x-ray diffraction experiments were conducted in a recently designed sample environment to determine the effects of compression on the thermal expansion of ZrV_2O_7.[3] The phase transition temperature was observed to be strongly pressure-dependent. Increasing the sample pressure from 52 MPa to 103 MPa shifted the α->incommensurate transition from 373K to 402K and the incommensurate->β transition from 417K to 453K. At 310 MPa, even the transition to the incommensurate phase was not observed below 513K. The thermal expansion of the α phase also exhibits a strong pressure dependence: its CTE drops about 9ppm/K (~35%) when the pressure is increased from 52 MPa to 310 MPa.

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P8

Structural Studies of *Mycobacterium tuberculosis* MazF-mt6: Insights into a Non-Traditional MazF Toxin

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Toxin-Antitoxin (TA) systems are ubiquitously used by prokaryotes for survival by metabolically regulating essential processes during stress conditions. *Mycobacterium tuberculosis (Mtb)* has a total of 88 putative TA systems, the largest TA gene family expansion currently known in bacteria. Nine of those 88 putative TA systems belong to the well-studied MazEF family. In the *E. coli* MazEF TA system, a protein antitoxin MazE regulates the ribonuclease MazF, which cleaves single-stranded mRNA. However, *Mtb* MazF-mt6 was recently determined to cleave the 23S rRNA of the 50S ribosomal subunit at a consensus sequence of 5'-UUCCU-3'.[1] It is unclear how *Mtb* MazF-mt6 specifically recognizes a very structured rRNA region given the predicted similarity with *E. coli* MazEF. Here, we report the purification, crystallization and preliminary X-ray crystal structure of *Mtb* MazF-mt6. These studies provide a platform to biochemically test MazF-m6 residues for functions in catalysis and RNA recognition. Given that toxin proteins of TA systems are proposed novel antimicrobial targets, understanding the molecule mechanism of RNA target recognition is critical in effectively designing potential inhibitors.

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P9

The SER-CAT virtual beamline: Lessons learned when over 95% of all data is collected remotely

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For the past 15 years, SER-CAT has been striving to provide its members with access to a "virtual beamline" which could be integrated into their daily workflow much like the X-ray lab down the hall. Working with Oceaneering Space Systems a conceptual design for automated data collection robot (ASTRO) was developed in 2000. In 2003, using funds from the Georgia Research Alliance, automation of the SER-CAT beamlines began with the installation of a highly modified Berkeley/ALS automounter (6 pucks) on beamline 22BM followed by a higher capacity system (15 pucks) installed on 22ID.

SER-CAT automation also includes seamless integration with the SERGUI beamline control system, SER-CAT/UGA production of the tools (pucks, etc.) users need to ship crystals to the beamline and automated crystal screening and data reduction systems. Today over 95% of SER-CAT members routinely collect data remotely. Efficient and reliable automation has also allowed SER-CAT to offer two 12-hour data collection shifts per day with extended 16-hour/day on-site user support. An overview of SER-CAT beamline automation including robotics, beamline/experiment control, and automated data processing and structure determination will be described.

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P10

X-ray Diffraction Investigation of $Na_2(Zn,Co)GeO_4$

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Previous studies of the dilute magnetic semiconductor (DMS), $Na_2(Zn_x,Co_{1-x})SiO_4$, showed band gaps of 1.7 eV and Néel transition temperatures of 5.70 K. The crystal structures were refined with synchrotron data collected at the APS in monoclinic space group, P 1 1 *n*. Neutron diffraction data collected at SNS showed a solid solution formation with Co^{2+} ions randomly doped into the Zn^{2+} sites.

This study will examine the effect of substituting germanium (IV) ions into the tetravalent silicon sites. Once a pure phase of the $Na_2(Zn_x,Co_{1-x})GeO_4$ analog is synthesized, magnetic transition temperatures will be studied. Four samples with different levels of Co^{2+} doping were prepared using standard ceramic methods. Phase purity was determined using data collected with a Rigaku Miniflex II powder diffractometer (Cu Kα radiation, 30 kV, 15 mA). High levels of Co^{2+} led to significant fluorescence from the Co^{2+} ions, which were mitigated by using a monochromator.

The 1% Co^{2+} sample led to a phase pure solid. Higher levels of Co^{2+} contained a Co_3O_4 impurity phase that could not be removed. The crystal structure of $Na_2(Zn_{0.99},Co_{0.01})GeO_4$ was refined using GSAS/EXPGUI. Rietveld analysis converged to $\chi^2 = 5.007$ and an R^2 value of 4.05 % with unit cell parameters of a = 7.18302(6) Å, b = 5.57789(4) Å, c = 5.33194(4) Å, γ = 90.067(2)º. The crystal structure is adamantine-like with all atoms tetrahedrally coordinated with significant distortions among the sodium tetrahedra. The Na-O bonds were roughly 2.1-2.4 Å with O-Na-O bond angles ranging from 101-128°. This is attributed to the larger Na^+ tetrahedral being more polarizable.

P11

Mechanism of HigB-Mediated Ribosome-Dependent mRNA Degradation

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Bacterial toxin-antitoxin complexes regulate cell growth according to their metabolic needs and environmental conditions and they play roles in biofilm formation, bacterial pathogenesis and survival during stress conditions. My goal is to elucidate the molecular mechanism of the ribosome-dependent RNase family of toxins. Host inhibition of growth B (HigB) is a toxin family member and was first identified in *Proteus vulgaris*[1]. HigB cleaves ribosome-bound A-site mRNA and in contrast to most toxins, HigB recognizes mRNA in a codon-independent manner[2]. Using microbial, structural and biochemical techniques, we are beginning to unravel the mechanism by which HigB recognizes a large number of A-site codons. Our X-ray crystal structures of HigB in complex with the *Thermus thermophilus* 70S ribosome and an uncleaved A-site codon reveal that HigB dramatically reorients mRNA to promote catalysis. Further we show that HigB has loose specificity for the first two A-site nucleotides while it requires an adenosine in the third or "wobble" A-site position for rapid mRNA cleavage. This sequence specificity is in stark contrast to how tRNAs and release factors recognize A-site codons. Taken together, our results indicate that the HigB toxin acts as a novel translation factor and that the traditional lack of specificity of the third A-site nucleotide is not inherent to the ribosome but rather a product of the interaction between the translation factor, mRNA and ribosome.

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P12

Investigating Data Collection Strategies for the Rayonix MX300HS 10 Hz CCD Detector

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Earlier this year SER-CAT took delivery of a Rayonix MX300HS high-speed area detector. The detector is a CCD based device (4X4 taper/chip array) with a 1-2 millisecond readout (78 micron pixels) providing 10Hz data collection capabilities. The detector was installed on beamline 22BM for integration with beamline controls and commissioning in late January. The detector is the first of its kind and its short readout time will allow us to collect data in both the traditional shuttered mode using 1 sec exposures or in shutter-less mode using 0.1 second exposures. Importantly, shutter-less mode will significantly enhance system precision and the quality of the resulting data since it eliminates errors associated with shutter jitter, shutter synchronization and goniometer backlash during data collection. Shutter-less data collection also offers the ability to efficiently collect fine slice data, which will further improve the signal to noise in the data. We will present the results from systematic tests of the detector in terms of frame width (rotation angle per frame), rotation speed, exposure time, dynamic range etc.

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P13

Synthesis and Characterization of (Zn,Co)Te

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There has been much interest in the last decade towards finding compounds that exhibit high magnetic transition temperatures. With the increasing price of Helium it is of great interest to find compounds, which have magnetic transition temperatures above the boiling of liquid nitrogen (~77 K). Dilute magnetic semiconducting materials based upon ZnTe are suspected to have magnetic transition temperatures above 77 K. This research is focused with the synthesis, purification, and characterization of these materials.

These compounds were synthesized via standard ceramic methods, where stoichiometric amounts of reagents were mixed in an Argon environment and subsequently sealed into a evacuated fused silica tube. The reaction vessels were then heated to 700^{o} C for 28 hours. The resulting products were characterized by powder X-ray diffraction with data collected with a Rigaku Miniflex II Powder Diffractometer. Reitveld refinement of this data was accomplished with GSAS/EXPGUI.

Thus far, three (Zn, Co)Te compounds have been synthesized with varying levels of cobalt-ion dopant. All (Zn, Co)Te compounds crystallized with the cubic space group F-43m. All atoms are located at special positions with -43m symmetry imposing tetrahedral environments upon the atoms. Reitveld Refinement converged with $X^2 = 9.447$ and $R_{(F2)} = 7.14\%$.

To date several impurity phases have been identified, including ZnO and excess Te. Reitveld refinement of diffraction data revealed impurity levels as high as 10% ZnO and 5% Te by mass. Methods to increase the purity of these compounds are currently under investigation. Once the pure compounds are synthesized magnetic properties will be investigated.

P14

The structural basis for recognition and modification of the 30S ribosomal subunit by an antibiotic resistance methyltransferase

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Ribosomal RNA contains modifications at specific nucleotides in all organisms, some of which control resistance to antibiotics. However, the mechanisms are not well understood controlling how modification enzymes recognize their specific target nucleotide and position it within the active site. We report the crystal structure of the pathogen-derived aminoglycoside-resistance rRNA methyltransferase NpmA bound to the 30S ribosomal subunit in a pre-catalytic state. The structure reveals that NpmA recognizes conserved rRNA tertiary structure rather than RNA sequence. Additionally, the structure shows NpmA flips the target nucleotide from its position within the helical base stack to position it within the active site. The structure, together with biochemical data, provides a detailed understanding of the enzyme's mechanism. This data provides a general framework for investigating the mechanisms of other rRNA modification enzymes.

P15

Investigating A Nairovirus' Ovarian Tumor Domain Protease's Species-Specific Substrate Preference

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Nairoviruses are negative-sense single stranded RNA viruses, which infect both animals and humans. Disease outcomes in humans can range from mild symptoms, such as headache, as is the case with the Erve virus, to hemorrhaging and death with Crimean Congo Hemorrhagic Fever (CCHF) virus. Within the L-segment of narioviruses' genome is an ovarian tumor domain protease (vOTUs), which has been identified as a potential virulence factor. Investigations into these vOTUs have revealed differing specificities toward different host's interferon stimulated gene product 15 (ISG15). The vOTU from CCHF has been shown to be highly specific to human ISG15, while the vOTU from the Erve virus can recognize both mouse and human ISG15. In order to further understand this behavior, a complex of the Erve vOTU with the C-terminal domain of mouse ISG15 was elucidated to 2.5 Å. This has provided insight for probing specific residues of these vOTUs to identify key regions for this observed specificity.

P16

SER-CAT Scientific Highlights: Award-Winning Projects and Assisting Beamline Technologies

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The Southeast Regional Collaborative Access Team (SER-CAT) was founded in 1997 to provide access to the newly constructed high brilliance X-ray source, the Advanced Photon Source (APS) located at Argonne National Laboratory outside of Chicago, IL. In October 2003, the first of SER-CAT's two X-ray beamlines was commissioned and began to serve the SER-CAT membership. Over the years, SER-CAT has grown into a consortium of 25 institutions (academic, private, government and industry) representing over 150 research groups scattered throughout the country.

To serve this diverse user base, SER-CAT beamlines emphasize operational efficiency, automation, remote user participation and outstanding support. SER-CAT's motto and goal is to provide its members "Light when **You** need it" via the concept of the *"virtual beamline"* and today over 95% of user data is collected remotely.

Employing the latest technologies in crystal mounting automation, beam conditioning, goniometry, detector design and remote operation SER-CAT has matured into one of the world's finest facilities for single crystal diffraction studies of macromolecules. SER-CAT's technology and infrastructure is augmented by a dedicated and highly experienced user support staff that continually strives to make SER-CAT the best place in the world to collect X-ray diffraction data. For example, as of March 2014, SER-CAT data produced over 1,200 peer reviewed publications and 2,283 PDB entries.

The research that SER-CAT data supports is, in many cases, highly significant. The poster will present a few representative examples of the scientific impact from our user's work, which was based on SER-CAT data. In addition, assisting beamline technologies that made the data collection possible will also be discussed.

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P17

The Role of Intrinsic Disorder in Human UDP-Glucose Dehydrogenase

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Human UDP-α-D-glucose-6-dehydrogenase (hUGDH) catalyzes the NAD^+-dependent oxidation of UDP-α-D-glucose (UDG) to UDP-α-D-glucuronic acid. Our previous studies show that hUGDH undergoes hysteresis whereby the enzyme transitions slowly from an inactive state (E*) to an active state (E). Here we show that the C-terminus is important to hUGDH hysteresis. The C-terminus is comprised of 30 residues that are predicted to be intrinsically disordered in solution (ID-tail). We are the first group to crystallize the structure of hUGDH with the ID-tail. As expected, the ID-tail is not visible in the crystal structure. NMR analysis confirms the ID-tail is also disordered in solution. Using small angle X-ray scattering, we show that the removal of the ID-tail alters the conformational ensemble of hUGDH in solution. Regions of potential interaction (hotspots) on the surface of hUGDH were identified based on co-evolutionary analysis. A point mutation in the hotspot region alters the hysteretic lag similar to truncation of the ID-tail. We have identified a specific interaction between hUGDH and the ID-tail using NMR.

The Pittsburgh Diffraction Society (PDS) is a not-for-profit organization which promotes fundamental and applied diffraction and crystallographic research and the exchange of ideas and information concerning such research. The PDS was founded by Professor Surain S. Sidhu who organized the first Pittsburgh Diffraction Conference in 1943. The goal of the conference is to bring together researchers in all areas of fundamental and applied diffraction and crystallographic research to present current topics.