The SER-CAT SPECTRUM

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Director's Message

Bi-Cheng Wang

Welcome to the summer 2010 issue of *The SER-CAT Spectrum*. We bring to you in this issue the relevant news on SER-CAT's recent advances, developments and activities.

On January 19-20, 2010, SER-CAT participated in the APS' Crosscut Review for macromolecular crystallography at the APS. I am pleased to say that all of the 8 MX CATs at the APS are doing well. The crosscut review provided an opportunity for reviewers and participants at the meeting to learn about the unique features and/or major niches of each of the MX CATs.

For SER-CAT, I reported that the mail-in services, remote operations with optional 12-hour access, 16-hour on-site staff assistance (8 am to 12 am), Bylaws and Executive Board Member group, Annual Research Symposium, Outstanding Science and Young Investigator Awards, and annual ACA booth display are among some of our most unique features and niches. SER-CAT's objective for providing "Light when YOU need it" was also highlighted as a major focus in the report.

This year's SER-CAT Symposium was hosted by Dr. Leighton Coates and held at the Oak Ridge National Laboratory on March 19, 2010. Again, it was a successful SER-CAT event. You may read more about the Symposium on pages 2 and 3 of this newsletter. Thanks to Leighton for a job well done! The 2011 meeting will be hosted by Dr. Robert Rose at North Carolina State University. Details will be announced on SER-CAT's website soon.

At its 2008 Board Meeting held in Charleston, South Carolina, SER-CAT announced that it would carry out systematic upgrades to keep SER-CAT a top notch facility. Since then, several special instrumentation proposals were submitted to the NIH and NSF for funding consideration. In the Phase I upgrade, our aim was to provide a micro X-ray beam source on 22ID as small as 10 µm. We are very grateful that the NIH funded Dr. John Rose's proposal for the MD2 Microdiffractometer in 2009. The installation of the unit is still in progress and going well. We plan to test the micro X-ray source in August, or during the first part of the fall run this year.

I am very pleased to inform you that the NIH/NCRR has officially funded our second upgrade proposal entitled, "Phase II SER-CAT optimization: acquisition of a next generation area detector" beginning July 1, 2010. The proposal was submitted in May 2009 under PAR-09-118: Recovery Act Limited Competition: High-End Instrumentation Grant Program. This award will provide substantial support to SER-CAT for the purchase of a fast detector and will enable us to do more effective data collection on weakly diffracting micro crystals. SER-CAT has also committed a significant match as institutional support. Again, my sincere thanks to NIH/NCRR and many of you who contributed in making this award possible.

You may be interested in reading the NSF Career Award programs (pages 5-6) in which three SER-CAT PIs, Raquel Lieberman, Carla Mattos and Robert Rose are engaged. Also, SER-CAT team members - John Rose, John Chrzas, and Albert Fu - are organizing a workshop and a scientific session at the 2010 ACA meeting. Thanks for their community outreach efforts.

As part of our efforts to provide enhanced support to our users for remote access during the evenings and weekends, we have added an additional person to our operational team. Please join us in welcoming Dr. Palani Kandavelu (please see page 7), who began working with SER-CAT on July 1, 2010.

Again, SER-CAT will have a display booth at the ACA meeting July 24-27, 2010. Please stop by to chat about SER-CAT's recent facility upgrades and let us know your suggestions, concerns, or praises. I wish you a wonderful summer and look forward to seeing you in Chicago.

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ORNL Hosts Seventh Annual SER-CAT Meeting

Gary Newton

The 7th Annual SER-CAT Symposium was hosted by the Oak Ridge National Laboratory (ORNL) in Oak Ridge, TN and was held at the ORNL Spallation Neutron Source (SNS), Building 8600, Room C-156. **Dr. Leighton Coates** (Lead Instrument Scientist: MaNDi, SNS, ORNL) was the primary organizer and coordinator for this symposium. SER-CAT is very grateful for his time and effort for this meeting. Similar to previous meetings, the overall theme was "Interesting structures, methods and advances in SER-CAT facilities" and it attracted over 50 participants (see group photograph) mostly from the southeastern US. This symposium showcases the diverse and often outstanding science emanating from the use of the SER-CAT facility and this year's meeting was no exception.

After welcoming remarks by Dr. Coates, Session 1 (SER-CAT Science), chaired by Dr. Coates, began with a keynote talk by **Dr. Brian Davison** (Chief Scientist for Systems Biology and Biotechnology, ORNL) who spoke about "Biomass to Biofuels: Overcoming Biomass Recalcitrance". He explained that the three components of biomass – cellulose microfibrils, hemicellulose and lignin – present a challenge in understanding how to convert these components to a monomeric form. There is a need for detailed structural analysis of the biomass structures themselves, the plant formation mechanisms, enzymes for deconstruction and the impact of pretreatment. The next talk was presented by **Prof. Carla Mattos** (NC State University, Raleigh, NC) titled "Allosteric Modulation of Ras Positions Glutamine 61 for a Direct Role in Catalysis". The mechanism through which Q61 contributes to catalysis has been somewhat elusive. It is now essential to know the position of hydrogen atoms in the catalytic residues and water molecules in the active site. Work is underway to produce crystals of Ras-GppNHp for determination of the neutron crystal structure to fine tune H positions in the hydrolysis site. The next talk by **Mr. Ronny Hughes** (University of Alabama, Huntsville) was titled "The Mechanism of IPPase Catalyzed Phosphoryl Transfer". It was stated that many aspects of the IPPase catalytic process remain unclear or have been difficult to validate due to the lack of information about hydrogen positions in the active site. Large volume crystals (>6 mm3) of the enzyme suitable for neutron structural studies have been obtained in an effort to determine the precise location of hydrogen atoms within the active site.

Session 2 (SER-CAT Awards and APS Status), chaired by **Prof. John Rose** (UGA), began with a presentation of a honorary plaque to this year's SER-CAT winner of the Outstanding Science Award, **Dr. Xinhua Ji** (Center for Cancer Research, National Cancer Institute, Frederick, MD). His talk was titled "Structure of ERA in Complex with the 3′ End of 16S rRNA: Implications for Ribosomal Biogenesis". Dr. Ji explained how he and his co-workers have been able to explain an important step in the biogenesis of ribosomes and to establish a role for protein ERA in the process. The overall results, together with the structure of ERA in complex with GNP, have established a functional cycle of the protein, suggesting that ERA serves as a chaperone for the maturation of 16S rRNA and a checkpoint for the assembly of the 30S ribosome subunit. Potential future developments made possible by this work are novel antibiotics and use in tumor suppression. (Please find the article written with Dr. Ji in this issue on page 4.) This presentation was followed with a talk by **Dr. John Quintana** (Advanced Photon Source [APS], Argonne National Laboratory) titled "APS Update: Funding, Operations and Future Plans". Dr. Quintana gave an update on the anticipated future developments at APS.

Following an on-site boxed lunch, a tour of the Spallation Neutron Source (SNS) was conducted by Dr. Coates and colleagues. The tour included an up-close look at the TOPAZ single crystal neutron diffraction system and goniometer sphere, a view of the Macromolecular Neutron Diffraction (MaNDi) site and the Small Angle Neutron Diffraction (SANS) instrumentation facility.

Session 3 (Interesting Methods), chaired by **Prof. Joe Ng** (UAH), began with a talk by **Dr. William Heller** (ORNL) titled "An Introduction to Small-Angle Neutron Scattering for Structural Biology". Small-angle neutron scattering (SANS) shares fundamental concepts with small-angle X-ray scattering (SAXS) but the properties of the neutron opens additional avenues for understanding the structure of biological macromolecular systems. His presentation was an introduction to SANS that included basic theory, practical experimental considerations, data analysis and modeling and an overview of the facilities available in the Center for Structural Molecular Biology (CSMB) at Oak Ridge National Laboratory. Next, **Prof. B.C. Wang** (UGA) discussed a novel approach to data collection titled "The MDS Strategy: Collecting Multiple Data Sets with Short Exposures Can Produce Better Data than Traditional Long Exposures Within a Fixed X-ray Dose". Dr. Wang explained both the theoretical and practical aspects of a novel data collection strategy; the Multi Data Set or MDS approach. The MDS approach differs from traditional data collection in that for the same fixed X-ray dose, N data sets are collected using a fraction (1/N) of the exposure time used in traditional data collection. It can be shown mathematically that a significant improvement in the overall σ_I for the data set can be achieved using MDS. This effect has also been shown with actual data measurements. The following talk by **Dr. Christina Hoffmann** (ORNL) was titled "Single Crystal Neutron Diffraction at ORNL". Dr. Hoffman described various neutron diffraction facilities at ORNL. At the Spallation Neutron Source (SNS), a high-pressure diffractometer "SNAP" and a general purpose single crystal diffractometer "TOPAZ" are in the user program. A macromolecular diffractometer "MaNDi" is scheduled for commissioning in 2012 and an elastic diffuse scattering spectrometer "Corelli" is scheduled for commissioning in 2013. At the High Flux Isotope

Reactor (HFIR), a four-axis monochromatic single crystal diffractometer is currently in the user program and a Quasi-Laue SCD "Imagine" is scheduled for commissioning in 2011. The last talk of the session, presented by **Dr. Christopher Stanley** (ORNL), was titled "Utilizing Small-Angle Neutron Scattering to Investigate the Polyglutamine Aggregation in Huntington's Disease". Dr. Stanley's research uses time-resolved small-angle neutron scattering (SANS) to probe the aggregates of huntingtin exon 1 protein fragments with varying polyGln lengths. The time-resolved snapshots yield quantitative information on the size and shape of precursors and the internal structure of the resulting fibrils. This research is providing new insights into the pathway of polyGln aggregation and should later assist in determining the role that precursors play in neuronal toxicity.

Session 4 (SER-CAT: The Way Forward), chaired by **Prof. B. C. Wang,** featured talks by SER-CAT experienced beamline personnel: **Dr. John Chrzas** and **Dr. Albert Fu.** Dr. Chrzas' talk was titled "Update on SER-CAT Upgrades and Others". He reported that there has been a large increase in the SER-CAT "Virtual Home Synchrotron" program during 2009. SER-CAT has worked with users to help improve their beam time efficiency, especially in view of new 12 hour shift allocations. Recent software upgrades and future hardware/software upgrades in support of mini-beam operations on 22ID were described. Next, Dr. Fu spoke about "Single-Line-Command Driven UI's for Data Processing at SER-CAT". He explained the new single-line-command driven user interfaces for data processing at SER-CAT. As part of SER-CAT efforts to monitor the data quality on-the-fly at SERCAT, command-line interfaces have been developed for DENZO/SCALEPACK, D*TREK, XDS and X-GEN. These non-graphic user interfaces provide a quick way to automatically process, diagnose and characterize a data set.

At 5PM, a Poster Session was held in the lobby outside the meeting room. Later, just before dinner, Dr. Dean Myles (ORNL Director of the Center for Molecular Biology) presented an interesting, exciting and informative overview of future plans and developments at ORNL.

SER-CAT thanks the Oak Ridge National Laboratory for their sponsorship and support of this symposium and Dr. Leighton Coates and his Organization Committee for another outstanding meeting! SER-CAT also thanks all the speakers and attendants for their strong participation and support.

Participants at the ORNL 7th Annual SER-CAT Symposium

Structure/Functional Cycle of ERA, a GTPase Dependent Ribosome Biogenesis Factor

Dr. Xinhua Ji,
National Cancer Institute, NIH

Editor's Note: We are pleased to include this article written by the 2010 SER-CAT Outstanding Science Award Winner further explaining his important contributions to the understanding of complex ribosomal pathways.

I thank the SER-CAT Science Award Committee for the honor of receiving the 2010 SER-CAT Outstanding Science Award. This award is based on the advancement of our ERA research, for which I am grateful to my colleagues for their creative work. ERA is required for the processing of 16S ribosomal RNA (rRNA) and the assembly of 30S ribosomal subunit. It contains an N-terminal GTPase domain followed by a KH domain (Chen *et al*., 1999). The protein binds to 16S rRNA and 30S ribosomal subunit, interacting with the 1531AUCACCUCC1539 sequence near the 3′ end of 16S rRNA (Tu et al., 2009). The AUCA sequence is highly conserved among bacteria, archaea, and eukaryotes, whereas the CCUCC is conserved in non-eukaryotes only.

Four crystal structures of ERA are available, including ligand-free ERA (apo-ERA, PDB entry 1EGA), ERA in complex with a non-hydrolysable GTP analog, GDPNP, (ERA-GNP, PDB entry 1WF3), ERA in complex with both GDPNP and the 1531AUCACCUCCUUA1542 sequence at the 3' end of 16S rRNA (ERA-GNP-RNA, PDB entry 3IEV), and ERA in complex with GDP (ERA-GDP, PDB entry 3IEU). The four structures reveal two distinct conformations of ERA. ERA-GNP-RNA and ERA-GNP exhibit conformation 1, indicating that the binding of RNA does not elicit significant conformational changes in the protein. ERA-GDP and apo-ERA display conformation 2, indicating that the release of GDP also does not cause significant changes in ERA. Unlike RNA binding or GDP release, GTP binding or hydrolysis triggers the transition of ERA between the two conformations. In conformation 2, the RNA-binding surface of ERA is blocked by its C-terminal helix (a9), whereas in conformation 1, a9 is distant from the RNA-binding site. Therefore, the relocation of a9 regulates the RNA-binding activity of ERA, suggesting that GTP binding is a prerequisite for RNA recognition by ERA. The intrinsic GTP-hydrolyzing activity of ERA is low. RNA recognition, however, stimulates the GTPase activity of ERA. Furthermore, the recognition of AUCA is required for the stimulation, and the recognition of both AUCA and CCUCC is necessary for optimally stimulated activity. Upon GTP hydrolysis, ERA changes its conformation from 1 to 2. The dramatic conformational change of the protein may be sufficient to facilitate the departure of the ERA-GDP complex from the 30S ribosomal subunit. These data have significantly advanced our understanding of the functional cycle of ERA, in which the protein serves as a chaperone for the processing and maturation of 16S rRNA and a checkpoint for the assembly of 30S ribosomal subunit.

RNase III cleaves the primary rRNA transcript and produces precursor 16S rRNA (pre-16S rRNA) that features a 26-basepair stem. To convert a pre-16S into a mature 16S rRNA, 115 nucleotides are removed from the 5′ end by RNases E and G, and 33 nucleotides are removed from the 3′ end by an unknown RNase. ERA facilitates these activities. In the absence of ERA, the 5' end processing of pre-16S becomes inefficient. Without ERA, however, the 3' end processing is impossible. The 1531AUCACCUCC1539 sequence is only 3 nucleotides away from the cleavage site of the unknown RNase. ERA binding to this sequence may protect it from accidental damage during processing. Furthermore, ERA binding likely changes the conformation of rRNA, which may assist/allow the unknown RNase to function and may also facilitate the activity of other factors such as KsgA (Lu & Inouye, 1998). Very recently, it was demonstrated that ERA caused several late-binding ribosomal proteins to bind rRNA faster when it is included in a 30S reconstitution (Bunner et al.). Therefore, we believe that ERA functions as a chaperone for the processing and maturation of 16S rRNA.

For most mRNAs, selection of the correct start codon and translational reading frame is dependent on base pairing between the Shine-Dalgarno (SD) sequence (GGAGG) upstream from the initiator codon in the mRNA and the anti-SD sequence (CCUCC) near the 3' end of 16S rRNA. The binding of the AUCACCUCC sequence by ERA prevents base pairing between the anti-SD and SD sequences, thereby preventing mRNA recruitment to the pre-30S particle. Ribosomal protein S1 is known to directly affect the SD/anti-SD interaction. The S1-binding site on the 30S, however, significantly overlaps with that of ERA. Therefore, the binding of 16S rRNA by ERA also occludes the binding of S1. Taken together, the initiation of mRNA translation by the 30S ribosomal subunit appears to be possible only after ERA is released, suggesting that ERA functions as a checkpoint for ribosome assembly and final activation of mature 30S ribosomal subunit.

These data suggest a common mechanism for a highly conserved ERA function in all forms of life by recognizing the AUCA sequence with a "twist" for non-eukaryotic ERA proteins by also recognizing the CCUCC. ERA is present in nearly every bacterial species and is essential for growth and division, which is unique among all other known protein functions of bacteria. Inhibition of bacterial ERA function will likely stop the synthesis of bacterial ribosome. Hence, ERA is a potential target for the development of novel antibiotics to fight the worldwide crisis of antibiotic resistance. The eukaryotic homologs of ERA (EARL1) is an attractive candidate for a tumor suppressor (Britton et al., 2000). It is located in the small subunit of mito-

chondrial ribosome and interacts with the 12S rRNA, playing important roles in mitochondrial ribosome assembly and cell viability (Uchiumi *et al.*). Currently, structural and functional studies of human and mouse ERAL1 proteins are undertaken in my laboratory

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Dr. Ji (right) receives the 2010 SER-CAT Outstanding Science Award from Prof. B.-C. Wang

NSF Career Awardees at SER-CAT by Gary Newton

We have realized that several SER-CAT users are also NSF Career Award winners. We focus on three of these users in this issue: **Raquel Lieberman** at Georgia Tech, **Carla Mattos** and **Robert Rose**, both at North Carolina State. These NSF awards also have a strong component for training and involvement of high school teachers and students. This aspect will be mentioned in the writeups. Here are their stories...

Raquel Lieberman, Georgia Tech

In an impressive chemical feat, intramembrane cleaving proteases (I-CLips) perform hydrolysis chemistry within the confines of the membrane to initiate cell signaling. Unlike soluble proteases, which evolved separately and utilize bulk solvent for peptide bond cleavage, I-CLips catalyze hydrolysis within a hydrophobic membrane environment. I-CLips are found throughout biology, but their transmembrane substrates are largely unknown. On the molecular level, how substrates are presented within the lipidic milieu, how chemistry occurs, and what protein interactions regulate this critical cell process are a biochemical mystery.

Prof. Lieberman's CAREER award involves female and minority graduate, undergraduate, and high school students in X-ray crystallographic, biophysical, and biochemical research activities at Georgia Tech that will lead to a detailed molecular understanding of the structure and function of an aspartyl I-CLip, as well as develop new methods for membrane protein structure determination. The group has already expressed and purified SPPs from a variety of organisms in the presence of detergents, and characterization is well underway.

Beyond the intellectual merit of this proposal in advancing our understanding of the hydrolysis chemistry performed by intramembrane proteases, Dr. Lieberman will parlay her expertise in protein structure and function to engage students at an Atlanta public high school as part of her broader mentoring and educational mission. In collaboration with the biology teacher and undergraduate Biochemistry majors at Georgia Tech, Dr. Lieberman will (a) host the teacher and her students to conduct research in the Georgia Tech lab and (b) develop real-world-motivated and discovery-based modules to investigate amino acid and protein structure, intra- and intermolecular forces, sequence homology, and structural similarity. These modules also feature a science art component. After their implementation in high school, the modules will be adapted for a week-long middle school science camp. In the long term, through these integrated education, training, and research activities, we hope to have the broader impact of better preparing students, particularly women and underrepresented minorities, for scientific and engineering careers. In doing so, she hopes to aid in the diversification of the future science and engineering workforce.

Continued on Page 6...

Continued from Page 5...

Carla Mattos, North Carolina State

My NSF PACASE project, funded from 2003-2008 and subsequently renewed, was designed to advance our understanding of protein binding sites while directly engaging students in the scientific research process. The project aims to probe binding surfaces on proteins using the Multiple Solvent Crystal Structures (MSCS) method which involves detailed analysis of organic solvent clusters, plasticity and the role of conserved water in protein structure and binding sites (Denchene et al., 2009). For this, the crystal structure of a protein is solved in about 10 organic solvent environments. To get at general properties of binding sites, such as plasticity, anchor points for ligand binding and hydration patterns, we work with some of the very well known classic proteins: serine proteases, RNAse A, Hen Egg-white Lysozyme and others. The 10 resulting crystal structures for a given protein are superimposed to reveal characteristic patterns of bound organic solvents for analysis. Each year of the PECASE a group of about 10 students were recruited from my classes to participate in structure refinement for the "protein of the year". Each student was given a diffraction data set and a starting model for refinement and worked with close supervision from members of our research team. Graduate students, postdocs and I work individually with the undergraduates in a coordinated fashion. The project brought together various groups that are often separated in the traditional academic setting to accomplish common goals in a situation that (1) decreases the gap between teaching and research, (2) exposes students to topics discussed in traditional classrooms in the context of the pressing questions guiding cutting edge research, (3) motivates graduate students and postdocs to be excellent teachers because the results provided by the undergraduates feed into their research and publications.

All of the data sets for this project have been collected at SER-CAT. Two of nearly 30 undergraduate students involved have travelled to Chicago for data collection. Many have gone on to graduate school at places such as the University of Pennsylvania, University of California-San Diego, University of Minnesota –Twin Cities, Boston University, Wake Forest University, UNC-Chapel Hill, NC State University and most lately MIT. In addition to having full MSCS data sets for the classic proteins we now have MSCS data sets for Ras and Bacteriophate P22 Tail Spike Protein to decipher sites of protein-protein interactions that were previously unknown and that add to our understanding of the function of those proteins. We are also developing software to automate some of the features of MSCS analysis.

Dechene, M., *Wink, G., *Smith, M., Swartz, P. and Mattos, C., Multiple Solvent Crystal Structures of Ribonuclease A: "An Assessment of the Method, Proteins: Structure, Function and Bioinformatics", 76, 861-881 (2009).

*Undergraduate Students

Robert Rose, North Carolina State

The NSF Career award was designed to support new, untenured investigators and to encourage the integration of research and education. The grant is a 5-year grant. The research side of the grant is judged with all other research grants. In addition the grant requires a major educational initiative.

I received my Career Award in 2007. My grant is entitled: "Structural studies of basic-helix-loop-helix and homeodomain interactions that elicit cell-specific gene expression". For the research portion of my grant, my lab is characterizing interactions between transcription factors that regulate the insulin promoter. We are using the insulin promoter as a model system for understanding cell-specific transcription.

A major goal of the NSF is to develop science education, and to promote interest in science among American students. In all of their grants they expect a discussion of "broader impacts", which means not just scientifically but educationally and reaching out to minorities. During the time that I received the award, the emphasis for the educational initiative of the Career Award was to reach out to different constituencies that you would not normally interact with. In my case, I developed a project to teach molecular biology skills to high school teachers. The goal is to encourage teachers to do more experiments in their classrooms by developing their lab skills and confidence. We also hope to encourage "inquiry" in the classroom, which is an important buzz word in the science education field. In their Education Standards, the NSF emphasizes the need to foster inquiry in science education.

The class also provides a format for developing ties between the Biochemistry Department and the Department of Math, Science & Technology Education. There are currently few ties between the science and education departments at NCSU. Science teachers have to take science credits, but not necessarily lab credits so they may not develop lab skills. The course provides a forum for student teachers to gain lab experience.

The Career Award prompted me to develop an educational initiative that I would not have developed otherwise. The educational initiative requires a significant time commitment, which does take me away from research. On the other hand interacting with high school teachers has been rewarding and a valuable experience. The teachers are very enthusiastic about learning techniques. They all love science. Working with teachers made me realize how few resources teachers have, much less than at universities. A little help from universities goes a long way for them. Ties between universities and our schools are very beneficial for encouraging teachers, and students.

MD2 Installation and Other Upgrades

by John Chrzas

During the recent SER-CAT executive board meeting, an installation and commissioning plan for the Bruker /Maatel micro diffractometer (MD2) was discussed. The result of this discussion was that the MD2 would be installed/commissioned during the last 2 weeks of the 2010 Summer run and the first week of the 2010 Fall run. The project is on track and we expect to have the MD2 installed on schedule. The Sergui modifications to integrate the MD2 into the 22ID control environment are complete and some of them will be discussed below.

Single 5 µm, 20 µm and 50 µm beam shaping apertures were purchased together with a triple aperture system consisting of 10 µm, 20 µm and 50 µm pinholes. The triple aperture system will be installed during normal operations – we will have to verify the usefulness of the single 5 µm aperture before we allow its use. The MD2 will allow for automated selection of any of the 3 pinholes in the triple aperture. The SERGUI hutch page has been modified such that the "slits" section has been renamed to "Beam Shaping" and a pull down menu of the 3 choices will allow for automated pinhole selection.

The most drastic SERGUI modifications were on the Sample Page. The input from a number of users was accumulated and their comments were the motivating force behind most of the following changes. The left hand section of this page now has two primary functions: **Sample Alignment** and **Robot**.

Sample Alignment: The "Select Active Camera/Zoom" section allows the user to easily change cameras as well as zoom value. Sergui has been modified to allow for 1, 2, 4, and 8 times optical zooms of the MD2 camera. The optical zooms have been calibrated using an optical grating with 50 mm divisions. The x1 zoom has a 2 mm horizontal field of view while the x8 has a 250 µm horizontal field of view. The light for each zoom value is automatically adjusted for optimal contrast. The current camera digital zooms have been setup to provide 1, 2, 3, and 4 times zoom.

The **2-point alignment button** has been moved to this section. This capability allows the user to align the sample using 2 different phi positions. The 2-Point alignment uses the fact that z (horizontal) is always uniquely defined with any camera orientation. Therefore, 2 different phi values provide enough information to solve the parametric equations for x and y (which are always the vertical).

The process requires the user to follow the following procedure: (1) Activate the 2-point alignment process by clicking on the 2-point alignment button;. (2) Designate the observed crystal center by clicking (left mouse) on it. This will record the crystal center (x, y, and z) and initiate phi rotation to the second centering point.; and (3) After phi has completed its rotation designate the observed crystal center by clicking on it. The two points will be used to automatically center the crystal.

Robot: The Sample size pull down option now sets the diameter of the circle cursor on the camera display. The option is purely cosmetic and can be used to help sample alignment.

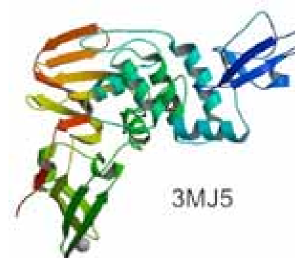
Camera Display: The camera display has had a number of modifications to help with sample alignment, all of which are consistent with camera and zoom: (1) The red crosshair now has 50 µm tic marks, (2) The "Sample Size" selected in the Robot section of this page is shown as a green circle cursor, and (3) The pinhole size is shown as a circle cursor as well as displayed in the upper right hand corner of the image.

These modifications were developed for the MD2 installation, but most have been implemented into the current version of SERGUI on both 22ID and 22BM. The only capability not implemented is the automated pinhole selection, since the 22BM hardware does not support this capability.

Welcome Palani Kandavelu to SER-CAT User Support

SER-CAT extends a warm welcome to Dr. Palani Kandavelu who joined the SER-CAT User Support team on July 1st. Palani comes to SER-CAT from Brookhaven National Laboratory where he has had three years of experience working with Dr. S. Swaminathan in protein crystallography. His Ph.D. was awarded in 2006 by the Centre of Advanced Study in Crystallography and Biophysics, University of Madras, Chennai, India where he worked with Prof. M. N. Ponnuswamy. Palani has also determined and deposited 31 protein structures to the PDB.

Recent SER-CAT Structure



A. K. Ghosh et al., J. Med Chem. (2010) **53,** 4968
Severe Acute Respiratory Syndrome
Protease Inhibitors

The SER-CAT Spectrum

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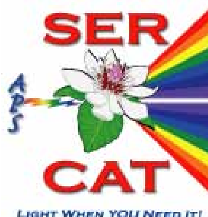

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