#### K-State **Biochemistry**





# BMB est. 1968 Active Site News

Fall 2014

The Active Site



#### Jenny Barriga: 69th Goldwater Scholar

Last year, I was honored as the 69<sup>th</sup> recipient of the Barry M. Goldwater Scholarship at KSU. The Goldwater

scholarship was established to provide financial support to promising students interested in research careers in science, mathematics, or engineering. While attending KSU, I performed cancer related research in the laboratory of Dr. Stefan Bossmann. I graduated from KSU with a BS in both Biochemistry and Chemistry. I now work at National Institutes of Health performing molecular biology research as a part of the National Cancer Institute.

When I first transferred to KSU, I did not think that I would have the opportunity to work for a full year at a national laboratory or get my PhD at one of the top ranked schools in my field. Contrastingly, I was surprised when I was nominated to represent KSU as a Goldwater applicant. I found the application process to be very helpful. I learned how to make myself stand out as an applicant and was surprised to see what I had accomplished in three years as an undergraduate taking class with graduate students. The classes were extremely helpful in making me a competitive applicant for the Goldwater scholarship. Most importantly, I learned how to communicate complex biochemical research to an audience from various backgrounds.

After receiving the scholarship, I became more confident in myself and decided to apply to graduate programs at Harvard, UC Berkeley, and Stanford. While interviewing at these schools, I felt confident in my research and was more concerned with figuring out which school suits me best.

#### **Nicole Green:** NSF GK-12 Program Recipient

This year I was honored as the recipient of the NSF GK-12 program at KSU. The NSF GK-12 program helps to



improve communication, teaching, and leadership skills for graduate students in science, technology, engineering, and mathematics (STEM). As the NSF GK-12 recipient, I will be working with local teachers and students in K-12 schools to enrich STEM content and instruction for their science programs.

My research is on the molecular level in the fruit fly Drosophila melanogaster. This is often hard to explain to people, but I am excited about bringing my research into the classroom and giving the high school students in USD 475 a chance to experience science as a researcher. My partner teacher and I are busy designing modules for the upcoming 2014-2015 AP Biology classroom to extend the required content and engage students in the new scientific practices outlined by the Next Generation Science Standards (NGSS). I hope that the laboratory experiences the students undergo will prepare them for entry into the university environment and potentially unveil an interest in research early in their scientific careers. I will also introduce many of these students to the field of biochemistry for the first time. This will challenge me to be intentional with communication, so that students will understand what we do as biochemists and why that is important to science. I am confident that my participation in the GK-12 program this year will make me a more organized and efficient communicator with strong leadership and teaching skills.



## Working Together to Advance Science

Jianhan Chen, AssociateProfessor of Biochemistry and Molecular Biophysics, is part of international research team that received a four-year grant jointly sponsored by the US National Science Foundation (NSF) and UK Engineering and Physical Sciences Research Council (EPSRC). The total budget of the project is \$1.1 million from NSF and £1.25 million from EPSRC. The main objective of this project is to develop advanced tools for analysis of structural data in chemical biology and soft condensed matter. The tools will be made available to researchers worldwide through a web proxy (www.ccpsas.org).

The major infrastructural investment by the US and UK in high brilliance multiuser X-ray synchrotrons and neutron sources during the last two decades has been immensely

successful in allowing external (university and

commercial) users to exploit these facilities for data collection on ever more challenging and important systems. This project will develop computational tools that help to realize the full benefit of the instrumental investment for novel engineering and material science applications, by integrating the plethora of X-ray and neutron data with user-friendly, high-throughput, molecular modeling of the data. The collaboration is motivated by the recognized importance of structural modelling at the large multiuser synchrotron and neutron facilities in both the US and the UK.

Research in the Chen lab mainly involves theoretical and computational study of biomolecular structure, dynamics and



Distributions of possible conformations of the human HIV-1 Gag protein, generated based on molecular modeling and small-angle neutron scattering (Datta et al J. Mol. Biol. 2011)

function, with particular emphasis on modeling

weakly stable proteins and understanding their roles in important biological processes such as regulation of transcription and translation, signal transduction and disease -related protein misfolding. Research in the lab has been supported by NSF, National Institutes of Health (NIH), as well as the Johnson Center for Basic Cancer Research at Kansas State University.

Key collaborators of this project include Paul Bulter from University of Tennessee at Knoxville and National Institute of Standard and Technology (NIST), Emre Brooks from University of Texas Health Science Center San Antonio, Joseph Curtis from NIST Center for Neutron Research, Stephen J Perkins from University College London (UK), Karen Edler from University of Bath (UK), David Scott from Nottingham University (UK) and David Barlow from Kings College London (UK).



### Progress in Dystonia Research

A neurological disorder called dystonia affects close to half million people in North America. The symptoms of dystonia manifest as painful and uncontrollable body movements and abnormal and twisted postures. There are many forms of dystonia, but there is no cure. In fact, the physiological reasons for dystonic symptoms and the underlying biological processes are completely unknown. Dr. Michal Zolkiewski's group at BMB has been interested in dystonia for over a decade. Recently, a paper published in the Journal of Biological Chemistry (http://1.usa.gov/1kxpWuI) reported the results of a collaborative project of the Dr. Zolkiewski's group with scientists from the University of Pittsburgh led by Dr. Jeffrey Brodsky. The joint research project was funded



with a grant from the Dystonia Medical Research Foundation. Dr. Zolkiewski has previously received several DMRF grants and has been serving as a member of the DMRF Medical and Scientific Advisory Council.

One of the most severe forms of dystonia called early-onset torsion dystonia (EOTD) is linked to a mutation in the gene encoding a protein torsinA. The amino-acid sequence of torsinA bears similarities to that of ClpB, a bacterial molecular chaperone investigated by Dr. Zolkiewski's group since 1999. Similarities to molecular chaperones provided some hints about the function of torsinA in humans. However, the biological role of torsinA and its functional link with dystonia remain elusive. It is known that torsinA is located in the endoplasmic reticulum (ER), part of the secretory pathway of eukaryotic cells. From the amino acid sequence, it can be predicted that torsinA binds ATP, which suggests an energy-dependent function, but how and why torsinA might use the energy is unknown.

In addition to Drs. Zolkiewski and Brodsky, researchers involved in the recent study included Dr. Lucia Zacchi from the University of Pittsburgh and Hui-Chuan (Arleen) Wu, a doctoral student at BMB. In order to study the function of torsinA in the cellular context, several yeast strains were engineered to produce human torsinA. Experiments revealed that another ER molecular chaperone called BiP helps process torsinA and maintain its stability. Additionally, researchers found that BiP also promotes the degradation of torsinA if the protein is defective. BiP is the first known cellular factor that affects the fate of torsinA. Unlike torsinA, whose function is not understood, BiP is a well-studied chaperone, which plays essential role in maintaining the quality of proteins in the secretory pathway. Until a clear picture of the torsinA function emerges, dystonia research may focus on BiP as a potential therapeutic target, as modulating the BiP activity in human cells would indirectly affect torsinA.



Predicted structure of human torsinA. The site of the dystonia-linked mutation is shown in purple.



Kansas State University Department of Biochemistry & Molecular Biophysics 141 Chalmers Manhattan, Ks 66506-3702 312





KSU Biochemistry & Molecular Biophysics On the Web: www.k-state.edu/bmb "Like" us on Facebook "KSU Biochemistry & Molecular Biophysics" Or "Follow us on Twitter @KStateBMB K-State Alumni foundation: www.k-state.com & E-Collegian Newspaper: www.spub.ksu.edu