STUPKA

UNDERGRADUATE RESEARCH SYMPOSIUM

April 10 & 11, 2015

Presented by the Roy J. Carver Department of Biochemistry, Biophysics and Molecular Biology Undergraduate Club, Iowa State University

Events Schedule

Friday, April 10

9:00 am **Breakfast**
Speaker meet and greet / Atrium

11:00 am **Stupka family**
Visit with Rob's parents / Atrium

noon **Chaput Lunch**
Undergraduates & Graduates Only / 1102 MBB

1:00 pm **Culver Lunch**
Undergraduates & Graduates Only / 1102 MBB

2:00 pm **Poster Session 1**
Atrium

3:00 pm **Poster Session 2**
Atrium

4:10 pm **Welcome**
Kayla Arney, Dean Schmittman, Bob Stupka / 1414 MBB

4:25 pm ALUMNUS SPEAKER: **Tony Cyr**
The Metabolic Regulation of Epigenetic Phenomena Or: Why Everyone Needs to Know the Krebs Cycle

4:40 pm STUDENT SPEAKER: **Ali Tegg**
Mass Spectrometric and anti-viral Investigation of Rhizome Ethanol Extract from Bloodroot (Sanguinaria canadensis L., Papaveraceae)

4:55 pm ALUMNA SPEAKER: **Dayna Peterson**
Using FRET to examine the physical interaction between Rubisco and Rca

5:10 pm **Stupka Scholar Recognition**

5:15-5:40 **Break**

5:45 pm **Alumni Recognition**

5:50 pm KEYNOTE SPEAKER: **John Chaput**
Developing Artificial Genetic Polymers for Synthetic Biology and Molecular Medicine

6:40 pm STUDENT SPEAKER: **Denis Tamiev**
Function of NADH-dependent Nitrite reductase.

6:55 pm ALUMNUS SPEAKER: **Luke Helgeson**
Mechanism of synergistic activation of Arp2/3 complex by cortactin and N-WASP

7:10 pm **Committee Recognition**

7:15 pm **Dinner**
Atrium

8:00 pm **Poster Awards**
Atrium

Saturday, April 11

9:00 am **Breakfast**
Speaker meet and greet / Atrium

9:45 am **Welcome**
Guru Rao, Provost Wickert / 1414 MBB

9:55 am ALUMNUS SPEAKER: **Goran Micevic**
From Moles to Melanoma

10:10 am ALUMNUS SPEAKER: **Zack Young**
Methods for Prokaryotic Expression and Purification of Active Xyloglucan Xylosyltransferases

10:25 am KEYNOTE SPEAKER: **Gloria Culver**
The Global Emergence of Multi-Drug Resistant Bacteria

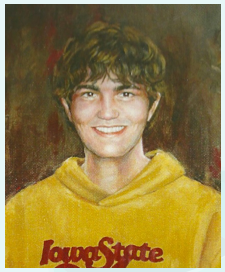
11:15 am ALUMNA SPEAKER: **Jackie Rivas**
B cell Dysregulation in Multiple Sclerosis

11:30 am ALUMNUS SPEAKER: **Matt Mead**
Targets of the Sex Inducer homeodomain proteins link fungal development and virulence in Cryptococcus neoformans

11:45 am **Closing Remarks**

noon **Lunch**
Atrium

Remembering Rob

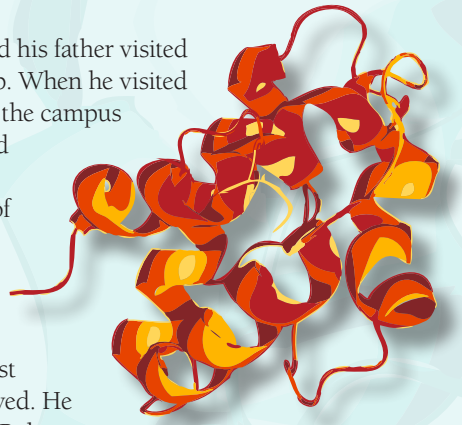


Rob Stupka was an undergraduate student majoring in Biochemistry at Iowa State University. His passion for science and undergraduate research led the effort to establish the BBMB undergraduate research symposium. His unparalleled enthusiasm propelled the planning process forward. Rob was the chair and with fellow students Tony Cyr, Claire Kruesel, Adam Krupicka and Jordan Witmer, they planned the first symposium for spring 2006. Rob saw in the symposium an opportunity for undergraduates to start to truly experience the importance of communication in science and wanted this event to be the first of many, highlighting the efforts of undergraduate researchers.

Rob's life was tragically cut short on November 30, 2005 after a pedestrian vehicle accident in front of the Molecular Biology Building. In tribute to Rob's drive and passion to create this event, the BBMB Undergraduate Symposium appropriately bears his name. The Stupka Undergraduate Symposium is an annual event that has become a source of pride for our department. It continues to be organized by our BBMB undergraduate students and they are inspired by Rob's story. We believe that through your attendance and participation, we continue to honor Rob's memory.

Thank you for being here and enjoy the wonderful research presented by our promising young scientists.

Lipid Transfer Protein



In the spring and summer of 2002, Rob and his father visited a series of universities to find a college for Rob. When he visited Iowa State on a warm June day, the beauty of the campus and the friendliness of the ISU staff convinced them both that they had found a new home for Rob. Rob initially entered ISU in the Fall of 2002 as a chemical engineering student, but during his first semester he took BBMB 101 as an elective. Discovering the beauty of biochemistry in that class, Rob changed his major to Biochemistry at the end of his first semester. In the BBMB Department, Rob thrived. He began conducting undergraduate research in Robert Thornburg's laboratory during his second semester.
As an undergraduate Rob worked on making cDNA libraries from floral nectaries. The molecule above is the nectary Lipid Transfer Protein (LTP2). The cDNA that encodes this protein was made by Rob. It was subsequently cloned and characterized and is currently being expressed in bacterial cells with the goal of determining its antimicrobial activity.

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SAVE THE DATE FOR THE 11TH ANNUAL

STUPKA

Thursday, April 7, 2016

email: stupkaugrs@iastate.edu
website: stupka.las.iastate.edu

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graduate presenter

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JUDGES

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Amy Andreotti
Ted Huiatt
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Olga Zabotina
Basil Nikolau

undergraduate presenter
graduate presenter
alumni presenter
faculty/staff presenter

Alumnus Speaker

Tony Cyr

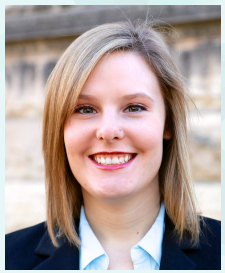
As a 2006 graduate of the BBMB undergraduate program at Iowa State, Tony Cyr was involved in the planning of the first Stupka Undergraduate Research Symposium as a tribute to his friend and lab partner, Rob Stupka. He went on to pursue his MD/Ph.D. degree at the University of Iowa, working in the labs of Frederick Domann, Ph.D., and Ronald Weigel, MD Ph.D. from 2006-2014. During his research training, he successfully obtained an NRSA F30 award for individual predoctoral research funding, and was involved in the publication of over 13 peer-reviewed publications. He has presented nationally at the annual meetings of the Society of Surgical Oncology, and the Society for Free Radical Biology and Medicine – where he received a Young Investigator Award. He is presently continuing his training as a resident in general surgery at the University of Pittsburgh Medical Center. He plans on using his basic science training to pursue a career in academics as a surgeon scientist.

The Metabolic Regulation of Epigenetic Phenomena Or: Why Everyone Needs to Know the Krebs Cycle

Epigenetic phenomena encompass a broad spectrum of post-translational modifications to nuclear proteins as well as chemical modifications of the DNA bases themselves. Increasingly, researchers are identifying linkages between central metabolic pathways and the epigenetic regulation of gene expression through intermediates such as succinate and 2-oxoglutarate. Fluctuations in these intermediates caused by both physiologic and pathologic stimuli leads to demonstrable changes in epigenetic marks in the nucleus, which in turn can alter gene expression. This process may play an important role in the development of cancer, among other human diseases. In this presentation, a brief overview of epigenetic regulation, the enzymes responsible, and their linkages with central metabolism will be introduced. The presentation will close with a series of examples relevant to human disease, including the role of succinate dehydrogenase and isocitrate dehydrogenase as relatively novel tumor suppressors.

Student Speaker

Alexandra Tegg



Alexandra is from Caledonia, Michigan and currently a third year Biochemistry student pursuing a Bachelor's degree at Iowa State University. Upon graduation, her career aspirations involve medical research and development in the pharmaceutical industry. Alexandra is a research assistant at W.M. Keck Metabolomics Research Laboratory under Dr. Ann Perera and Dr. Zhihong Song.

ABSTRACT

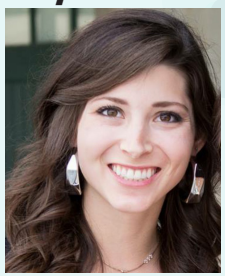
Mass Spectrometric and anti-viral Investigation of Rhizome Ethanol Extract from Bloodroot (Sanguinaria canadensis L., Papaveraceae)

The bloodroot plant *(Sanguinaria Canadensis L.)* is a monotypic genus of the family Papaveracea. Bloodroots, and plants with similar compounds, have been suggested for anti-viral activity. Extracts from the bloodroot plant and the rhizome itself have been used medicinally by the Native Americans; bloodroot extract is predominantly composed of benzophenanthridine alkaloids. However, which of these alkaloid(s) is/are acting as the anti-viral agent is not yet known. Metabolite profiling has not yet been used to discover bioactivity of the bloodroot extract. Bloodroot samples from different locations around Iowa were collected in early spring of 2014 to conduct a metabolite profile. We have developed a novel LC-MS method to profile metabolites in bloodroot extracts using electro spray ionization (ESI). We were able to confidently identify about a dozen alkaloids using MS/MS capabilities. Quantification parameters were optimized with multiple reactions monitoring (MRM) to accurately quantitate the amount of alkaloids present in each extract. The metabolite profiling was addressed in two steps. First, we profiled to pinpoint the most active metabolite/s for anti-viral assays, and secondly we profiled across different tissue types in the same plant to discover the alkaloid distribution pattern. The results from the metabolic profile will be used to investigate the anti-viral activity of the individual alkaloids. Interestingly, the alkaloid distribution pattern varied among the different tissues within the same plant. Of the different tissues, we found the rhizome to contain the most abundant amount of alkaloids. To our knowledge this is the first metabolite profiling done on the bloodroot plant.

Alumna Speaker

Dayna Peterson

STUPKA SCHOLAR 2010



Now a fourth year Biochemistry Ph.D. candidate at Arizona State University, Dayna Peterson was the 2010 Stupka Scholar and graduated from Iowa State in May 2011. During her time in Ames, Dayna worked in Dr. Gaya Amarasinghe's lab, served on the 2009-2011 Stupka Symposium Planning Committees, served as the BBMB Undergraduate Club President, a member of Alpha Gamma Delta sorority, and an active volunteer in the community. Dayna currently lives in Tempe, AZ and is in her fourth year of the Biochemistry Ph.D. program at Arizona State University studying the physical interaction between Rubisco and Rubisco Activase.

ABSTRACT

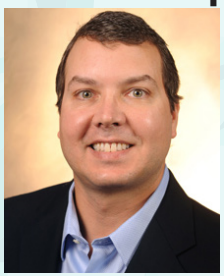
Using FRET to examine the physical interaction between Rubisco and Rca

Ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco) is the most abundant enzyme on Earth and represents the primary entry point of CO_2 into the biosphere. Rubisco's extremely slow carboxylation rate of ribulose-1,5-bisphosphate and its propensity toward inhibition make it a notoriously inefficient enzyme, however, Rubisco activase (Rca) is essential in maintaining Rubsico activity by catalyzing the rapid release of trapped inhibitors to reactivate Rubisco for CO_2 fixation. Rca uses ATP hydrolysis as the driving force behind a conformational motion that restores activity to inhibited Rubisco active sites. Adding to the complexity of this system is the high size polydispersity of Rca in solution, as well as the species dependent variations in reactivation: in some cases, Rca reactivates Rubisco from a different species more effectively than Rubisco from its own species. A bound complex of Rubisco-Rca has not yet been isolated, but the interaction has been proposed to be weak and transient. Information about the physical interaction of Rca and Rubsico will assist in deconstructing the Rubisco reactivation mechanism and may lead to a more efficient enzyme and therefore, increase the efficiency of carbon fixation in plants. Based on our fluorescence correlation spectroscopy (FCS) assembly studies of Rca showing a primarily hexameric species in solution at 30μM, a fluorescence based,steady state Rubisco-Rca binding assay is being developed to study their interaction. Chlamydomonas reinhardtii Rubisco mutants have been designed and isolated to target site specific labeling of introduced cysteine residues. Both Rca and Rubisco have been successfully labeled with specific fluorophores and utilized in a Förster resonance energy transfer (FRET) based binding assay to monitor their proximity and calculate equilibrium binding constants. As of yet, an indisputable FRET response has not been seen, but many parameters, such as using different combinations of species (i.e. cotton Rubisco+cotton Rca or Chlamy Rubisco+spinach Rca) and varying nucleotide concentrations, are still being altered. These FRET assays, along with FCS, reactivation and kinetic assays, and crystallographic studies, will provide critical information about how Rca interacts and reactivates Rubisco. Through the work in the Wachter lab, we hope to gain a full understanding of the mechanism of Rubisco remodeling from a structural and mechanistic point of view.

Keynote Speaker

John C. Chaput

ARIZONA STATE UNIVERSITY



Professor Chaput received a Bachelor of Science in Chemistry from Creighton University in 1994 and a Ph.D. in Chemistry from the University of California, Riverside in 2000. For his Ph.D. thesis, he studied the molecular recognition properties of unnatural nucleic acid polymers. Under the guidance of Professor Chris Switzer, he designed and characterized the first five-stranded DNA helix that self-assembles around a metal-nucleated iso-guanine repeat motif. From 2000-2004, he was an HHMI Post-Doctoral Fellow in Prof. Jack Szostak's lab at Harvard Medical School. While at Harvard, he studied the de novo evolution of functional proteins by mRNA display and developed early methods for synthesizing artificial genetic polymers.

In 2005, he joined the faculty at Arizona State University as an Assistant Professor in the Department of Chemistry and Biochemistry, and a Research Investigator in the Biodesign Institute. Students in his laboratory study a range of topics from fundamental questions about origins of life to the development of xenobiotic cells for synthetic biology.

Dr. Chaput is currently a Professor of Chemistry and Biochemistry, and a member of the Virginia G. Piper Center for Personalized Diagnostics in the Biodesign Institute at ASU.

ABSTRACT

Developing Artificial Genetic Polymers for Synthetic Biology and Molecular Medicine

Synthetic biology holds great promise as a scientific discipline with practical applications in material science, human health, and the environment. However, the potential for dual-use applications has raised new concerns about the safety of using DNA as an engineering tool for synthetic biology. One possible solution to this problem is to develop a firewall that impedes the exchange of genetic information between synthetic biology and natural biology. This could be done, for example, by creating orthogonal life forms that carry genetic information in the form of synthetic genetic polymers (termed 'xeno nucleic acids' or XNA) that store genetic information in the canonical bases of adenine (A), thymine (T), cytosine (C), and guanine (G), but use a backbone structure that contains a sugar other than ribose or deoxyribose. Such systems would render genetic messages invisible to nature, because the enzymes that make and degrade DNA do not recognize XNA. While the appearance of orthogonal life forms may be years away, progress towards this long-term goal has given rise to engineered polymerases that can copy genetic information back and forth between DNA and certain XNA polymers. These systems have immediate practical applications in molecular medicine where a critical need exists for nuclease resistant affinity reagents (aptamers) and catalysts that can function in complex biological environments. In this talk, I will provide a model for how orthogonal life forms could be developed, and describe recent advances in the replication of XNA polymers.

Student Speaker

Denis Tamiev

STUPKA SCHOLAR 2014

Denis is a third year Biochemistry student at Iowa State University, who is planning to attend a medical school after completing his undergraduate degree. During his undergraduate career, he has been a member of the Stupka committee and has helped to organize the symposium during the past two years. Outside of academics, Denis volunteers at the Boone County Hospital, and serves as member of the Service and Justice team through Saint Thomas Aquinas. Denis also conducts research under the supervision of Dr. Mark Hargrove on the nitrogen metabolism and anaerobic respiration of *E. Coli*.

ABSTRACT

Function of NADH-dependent Nitrite reductase.

E coli uses NADH-dependent (Nir) and Formate-dependent (Nrf) Nitrite reductases in order to survive during anaerobic conditions. Previously it was proposed that the physiological function of Nir is to detoxify the buildup of Nitrite that is formed during anaerobic respiration on Nitrate. In the course of this study, it was determined that Nir does not play a role in detoxification of nitrite, but rather aids in assimilation during nitrate respiration. The results of this study are based on the analysis of cell cultures grown under anaerobic conditions with the use of 1D n15-NMR, N15-HMSQC NMR and UV-vis techniques.

Assimilation and dissimilation of Nitrite to ammonium are two distinct pathways of respiration of *E coli*. A series of experiments with the Nrf mutant and a wild type strains of E coli showed that the respiratory dissimilation of Nitrite to ammonium is possible only in the presence of Nrf. The presence of Nir does not aid in dissimilation, and the possible reasons for that phenomenon are mentioned in the discussion. However, it was determined that the Nir plays a crucial role in assimilation of Nitrite to ammonium, because the Nir mutant is incapable of growing on Nitrate as a sole nitrogen source. These results were further tested by the N15-HMSQC NMR, where it was shown that labelled nitrogen is incorporated in the organic matter in the case of the WT cells, but it is not in the case of the mutant. The detoxification of Nitrite suggests that ammonium should build up in the medium as a byproduct of this reaction. In the course of this study no detectable amount of ammonium were found in the medium regardless of the growth conditions. These results show that the physiological purpose of Nir is to assimilate nitrite derived from nitrate respiration. Contrary to the previous studies, no evidence of detoxification of Nitrite was found.

Alumnus Speaker

Luke Helgeson

STUPKA SCHOLAR 2008

For two years at Iowa State University, Luke performed research in the biochemistry and structural biology lab of Dr. Gaya Amarasinghe. In the Amarasinghe lab, he was tasked with crystallizing a functionally inactive mutant of a double-stranded RNA binding protein from the deadly Ebola virus. Dr. Gaya Amarasinghe's mentoring significantly fostered Luke's love for protein science and was instrumental in convincing him to pursue graduate school. Luke graduated from Iowa State University in 2009 with a Bachelor of Science and then headed west to start his graduate work at the University of Oregon in the Institute of Molecular Biology. Luke joined the lab of Dr. Brad Nolen and began his research on the regulation of branched actin network formation. Luke is now a Postdoctoral fellow at Oregon Health Sciences University in Portland, OR.

ABSTRACT

Mechanism of synergistic activation of Arp2/3 complex by cortactin and N-WASP

Nucleation promoting factors (NPFs) initiate branched actin network assembly by activating Arp2/3 complex, a branched actin filament nucleator. Cellular actin networks contain multiple NPFs, but how they coordinately regulate Arp2/3 complex is unclear. Cortactin is an NPF that activates Arp2/3 complex weakly on its own, but with WASP/N-WASP, another class of NPFs, potently activates. We dissect the mechanism of synergy and propose a model in which cortactin displaces N-WASP from nascent branches as a prerequisite for nucleation. Single-molecule imaging revealed that unlike WASP/N-WASP, cortactin remains bound to junctions during nucleation, and specifically targets junctions with a 160-fold increased on rate over filament sides. N-WASP must be dimerized for potent synergy, and targeted mutations indicate release of dimeric N-WASP from nascent branches limits nucleation. Mathematical modeling shows cortactin-mediated displacement but not N-WASP recycling or filament recruitment models can explain synergy. Our results provide a molecular basis for coordinate Arp2/3 complex regulation.

Alumnus Speaker

Goran Micevic

Goran Micevic graduated summa cum laude from the honors program at Iowa State University in 2010, with a B.S. degree in Biochemistry. At ISU, Goran was an undergraduate researcher in the lab of Dr. Kristen and Jorgen Johansen in the Department of Biochemistry, Biophysics and Molecular Biology (BBMB). He was a Mayo Clinic Summer Research Fellow in 2009, and interned as a visiting scientist at the German Cancer Research Center in Heidelberg in the summer of 2008. While at ISU, Goran was awarded a Goldwater Scholarship and a Phi Kappa Phi graduate fellowship. Upon graduation from ISU, he enrolled in the combined MD/Ph.D. program at Yale University School of Medicine and is currently a doctoral candidate in the Department of Experimental Pathology. Goran is interested in tumor biology and currently studies mechanisms of melanoma formation and progression using genetically engineered mouse models of melanoma in the lab of Marcus Bosenberg, MD, Ph.D. at Yale. In 2014, Goran received The 2014 Research Scholar Award from the Joanna M. Nicolay Melanoma Foundation and was recently awarded a grant to target melanoma by the American Skin Association.

ABSTRACT

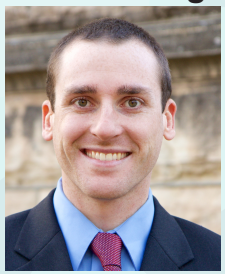
From Moles to Melanoma

Despite recent progress in targeted therapies and immunotherapies, melanoma remains one of the deadliest human cancers and the vast majority of patients with advanced melanoma will die of their disease. It is estimated that 76,100 new cases and 9,710 deaths will occur in the United States in 2014. With no effective cure available for most patients, increasing incidence and poor 5-year survival, there is a pressing need to better understand the molecular changes that drive melanoma development and growth. A significant proportion of melanomas develop from previously growth-arrested BrafV600E (mutant) melanocytic nevi, suggesting this process is reversible. An in vivo model of BrafV600E-induced senescence with defined kinetics including reproducible progression to melanoma has not been previously described. We have developed such a model using Cdkn2a and/or Lkb1 inactivation in the context of BrafV600E mutation and investigated the relationship between pathways mediating transient proliferation, oncogene induced senescence/growth arrest and progression to melanoma. This model is consistent with observations from human tissue and helps to explain the variable phenotypes observed in benign melanocytic neoplasms which can lead to melanoma.

Alumnus Speaker

Zack Young

STUPKA SCHOLAR 2014



Zack recently graduated with a degree in Biochemistry from Iowa State University. He conducted research on the expression and purification of recombinant xyloglucan xylosyltransferases (XXTs) in *E. coli* and their interactions related to xyloglucan biosynthesis under Dr. Olga Zabotina. This research will help with the understanding of the polysaccharide biosynthesis and also assist in plant cell wall modifications to improve biomass properties for industrial applications. In addition to research and academics, he was involved in the BBMB department as the vice president of the BBMB Club and is Committee Co-Chair for the 2015 Stupka Symposium.

ABSTRACT

Methods for Prokaryotic Expression and Purification of Active Xyloglucan Xylosyltransferases

The biosynthesis of plant cell wall polysaccharides has been recently extensively studied for the production of the raw materials for food, fuel, and fiber. The polysaccharide xyloglucan, the most abundant hemicellulose in dicotyledonous plants, plays an important role in the structure of the primary cell wall. In Arabidopsis thaliana, xyloglucan biosynthesis involves at least seven different glycosyl transferases localized in Golgi. Currently, xyloglucan xylosyltransferases have only been expressed in eukaryotic systems, yet we sought to develop a protocol using *E. coli* to reduce cost with an easily sustainable system which does not glycosylate proteins and can produce acceptable quantities of soluble protein. Using xyloglucan xylosyltransferase 2 (XXT2), a type II transmembrane glycosyltransferase involved in xylosylation of glucan backbone in xyloglucan, we experimented with various strains of *E. coli*, expression vectors, expression methods, fusion tags, protease cleavage sites, truncation positions, and purification techniques to effectively produce recombinant proteins which are active in vitro. In addition, we also have mutated several amino acids predicted to be critical for the activity of XXT2. As a result of this work, we obtained the best expression of XXT2 (2mg/L) with GFP and 6xHis tags using pET20b in SoluBL21 cells. The XXT2 expressed in E.coli cells showed enzymatic activity confirmed by analyzing the product of the assay on HPLC and MALDI-TOF. Site-directed mutagenesis studies revealed that H378 is critical for enzyme activity. Further improvements in XXT2 purification will allow us to perform the structural characterization of the protein and protein-protein interaction studies. This work has demonstrated that the XXT protein can be effectively expressed in prokaryotic cells to produce recombinant proteins, and that activity of XXTs does not depend on glycosylation.

Keynote Speaker

Gloria Culver

UNIVERSITY OF ROCHESTER

Gloria Culver, Ph.D. is a graduate of Ithaca College with a BA in Biology and a minor in Art History. She earned her Ph.D. at University of Rochester in Biochemistry before going to the University of California, Santa Cruz for a post-doctoral appointment with Professor Harry Noller. Dr. Culver came to Iowa State University as an Assistant Professor in Biochemistry, Biophysics and Molecular Biology. After more than 6 years at ISU, Dr. Culver returned to the University of Rochester as an Associate Professor in the Departments of Biology, of Biochemistry and Biophysics and as a member of the Center for RNA Biology. Dr. Culver has served as Chair of the Department of Biology and is currently Interim Dean of the School of Arts and Sciences for the 2014-15 academic year. In this role, she handles matters relating to eighteen departments and twelve programs covering the areas of arts and humanities, social sciences, and natural and physical sciences. She also currently serves on the NIH Molecular Genetics A Study Section and acts as its Chair from Fall of 2014. Dr. Culver's research centers on the assembly of ribosomal machinery essential for growth of all cells. By focusing on bacterial ribosome, she has contributed to understanding how infections might be controlled through selective inhibition of specific control points of ribosomal assembly. Her research has received funding from NIH, the American Cancer Society, and NSF.

ABSTRACT

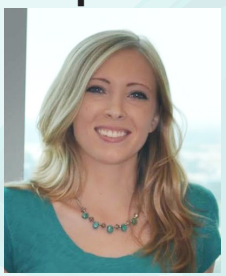
The Global Emergence of Multi-Drug Resistant Bacteria

The global emergence of multi-drug resistant bacteria threatens human health and the realized benefits of a post-antibiotic society. One major problem in development of new antibiotics is identification of novel targets. Recent work suggests that studying the process of ribosome biogenesis/production in bacteria will allow findings that are important for understanding cell physiology, at a fundamental level, and identification of novel targets for antibiotic development. The essential and universally conserved process of translation is catalyzed by ribosomes, and thus production/biogenesis of ribosomes is an essential process in all cells. Ribosomes are intricate ribonucleoprotein particles (RNPs), whose biogenesis involves transcription, folding, processing, and modification of ribosomal RNA (rRNA), as well as binding of ribosomal proteins (r-proteins) and factors. Understanding of the dynamic assembly and function of these RNPs will impact thinking about basic scientific processes and drug discovery. Work in bacteria, such as *E. coli*, can reveal fundamental and evolutionarily important ribosome biogenesis events. Thus, identification of such events/factors would be readily transferable to studies of ribosome biogenesis across kingdoms. Alternatively, and perhaps more importantly for human health, are the emerging data that altered ribosome biogenesis directly influences virulence and drug resistance in several pathogenic bacteria. Some of our recent work on ribosome biogenesis will be highlighted during this discussion.

Alumna Speaker

Jacqueline Souleyrette Rivas

STUPKA SCHOLAR 2011



Jacqueline R. Rivas grew up in the nearby town of Nevada, Iowa and worked on her B.S. in biochemistry at ISU from 2008 to 2012. For three of those four years she worked in the laboratory of Dr. Amy Andreotti, studying structural interactions of proteins in T cell signaling. It was here that Dr. Andreotti gave her opportunities to begin a career in science and where her interest in immunology was peaked. In the fall of 2012 she started her Ph.D. in immunology at UT Southwestern Medical Center. She was intrigued by autoimmunity and the idea of translational research, which lead her to the laboratory of Dr. Nancy Monson. Now she researches B cell involvement in Multiple Sclerosis. Most of her work has focused on the potential contribution of antibodies to disease. One day she hopes to study molecular immunology as a professor.

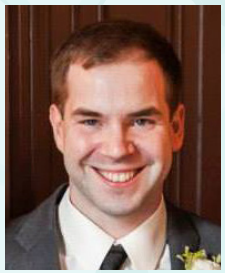
ABSTRACT

B cell Dysregulation in Multiple Sclerosis

Multiple Sclerosis (MS) is an immune mediated demyelinating disorder of the central nervous system (CNS) that results in a loss of neurological function. It is the most common neurodegenerative disease to affect adults under the age of 40. B and T cells are the major culprits of MS, and effective therapeutics deplete these cells or prevent their entry into the CNS. T cells can attack neuronal axons and the myelin that shields them leading to neuronal death. B cells arm T cells in the attack against the CNS and a critical tolerance checkpoint for eliminating autoreactive B cells is defective in MS patients. Currently it is not known how B cells escape this checkpoint to become instigators of neuro-inflammation, nor are all the ways that B cells contribute to MS known. In our laboratory we have found that naïve and memory B cells exhibit increased levels of the pro-inflammatory cytokine IL-6 compared to B cells from healthy donors that might be linked to dysregulation of the NF-B pathway. Activity of NF-B is important for shaping the adaptive immune response to pathogens, and increased activity could affect the survival and development of B cells. Additionally, we have assessed the antibody genetics of B cells in the cerebrospinal fluid of patients and found a mutation pattern that predicts whether those experiencing their first symptoms will continue on the disease track for MS. We are investigating the potential of the antibody itself to contribute to damage of the CNS, and have found that these antibodies are capable of binding neurons and astrocytes in the brain. Investigating B cells in MS patients will not only develop our understanding of the pathogenesis of this disease, but could unveil better targets for therapies that prevent relapse without the dangers of nonspecific inhibition of the immune system.

Alumnus Speaker

Matt Mead



Matt is a graduate student in the Integrated Program in Biochemistry at the University of Wisconsin-Madison. He works under the direction of Dr. Christina Hull determining the molecular mechanisms governing development in a fungal pathogen. Specifically, Matt studies the transcriptional network that regulates sexual reproduction in Cryptococcus neoformans, a major cause of death for those with compromised immune systems, especially individuals with HIV/AIDS. Matt graduated with a Bachelor of Science degree in Biochemistry from Iowa State University in 2009 where he worked with Dr. Reuben Peters studying diterpene biosynthesis in plants. While at ISU Matt participated in a variety of groups and clubs, including the BBMB undergraduate club and the Stupka Undergraduate Symposium Organizing Committee, serving as the chair of the latter for the 2009 symposium.

ABSTRACT

Targets of the Sex Inducer homeodomain proteins link fungal development and virulence in Cryptococcus neoformans

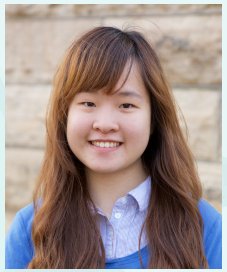
Cryptococcus neoformans is a global human fungal pathogen that kills more than 600,000 individuals annually. The organism is acquired via inhalation, and spores are likely infectious particles. C. neoformans spores are the products of a sexual development process that is controlled by two heterodimeric homeodomain transcription factors, Sex Inducer 1 (Sxi1) and Sex Inducer 2a (Sxi2a). To better understand the mechanisms used by fungi to control development, we took a multi-pronged approach to determine the direct targets of Sxi2a-Sxi1. We used whole genome expression analyses paired with binding site identification methods that included in silico predictions and in vitro protein-binding arrays. This unbiased approach identified Sxi-regulated genes that contained a site bound directly by the Sxi proteins that is required for full regulation in vivo. Among the targets of the Sxi2a-Sxi1 complex were many genes known to be involved in sexual reproduction, as well as several well-studied virulence genes. Our findings suggest that genes involved in sexual development are also important in mammalian disease, and the Sxi proteins connect these seemingly disparate processes via a shared response to starvation that includes metal ion transport, -oxidation, and flux through the TCA cycle. This work advances our understanding of how homeodomain transcription factors control complex developmental events, including infectious particle production, and support a role for fungal sex in the evolution of virulence.

2015 Stupka Scholars

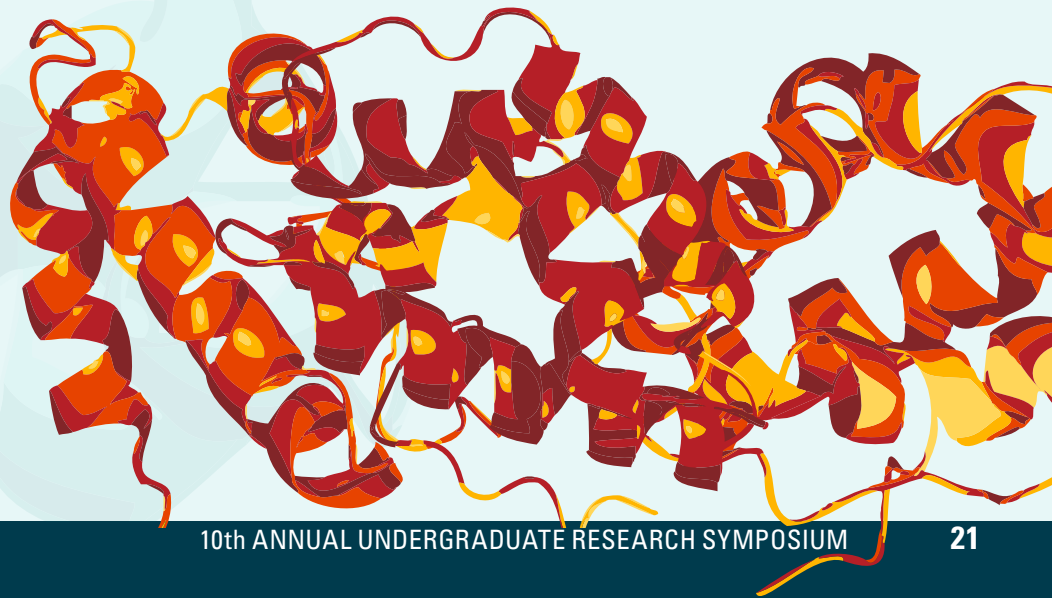
Adrienne Smith

Adrienne is a sophomore pursuing a degree in Biochemistry with a minor in Microbiology. Her research studies the amino acids involved in substrate binding and enzymatic catalysis of the Arabidopsis protein Xyloglucan Xylosyltransferase under Olga Zabotina, Ph.D. Adrienne has also served the BBMB Undergraduate Club as the Liberal Arts and Sciences Council Representative and as a part of the Speakers Committee for the Stupka Symposium. She plans to continue undergraduate research at Iowa State in the hopes of attending a graduate program in molecular biosciences.

Flora Yen



Flora Yen is a third year honors student in Biochemistry. She studies structure and assembly of scaffolded signaling complexes in Dr. Eric Underbakke's lab. She is currently researching the activation mechanism of Sirtuin1. In addition to research, she has been involved in the BBMB department throughout her time at Iowa State University. She currently serves as the publicity co-chair of the Stupka Symposium Committee, the president of the undergraduate BBMB club, and a peer mentor for the freshman learning community. Outside of biochemistry, Flora volunteers at the ISU food pantry (SHoP) and events hosted by WiSE. She hopes to pursue a career in dentistry.



Past Scholars

Claire Kruesel 2006
Master of Fine Arts in Creative Writing and Environment student at Iowa State University graduating in May 2015

Mara Determan 2007
Resident Physician in Pediatrics at Kaiser Permanente Medical Center in Oakland, CA

Luke Helgson 2008
Biography on page 15

Mina Farahbakhsh 2009
5th year M.D./Ph.D. candidate at Kansas University Medical Center graduating in 2018

Dayna Peterson 2010
Biography on page 12

Jackie Rivas 2011
Biography on page 19

Craig Brown 2011
M.D. Candidate at Pritzker School of Medicine at University of Chicago graduating in 2016

Johanna Jass Bailey 2011
Laboratory Manager at Elemental Enzymes in Columbia, MO and Master of Public Health Graduate student at University of Missouri graduating in Decemeber 2015

Mollie Tiernan 2011
Research Assistant II in the Molecular Genetics research group at Integrated DNA Technologies in Coralville, IA

Samson Condon 2012
2nd year Ph.D. student in the University of Wisconsin Madison Department of BIochemistry

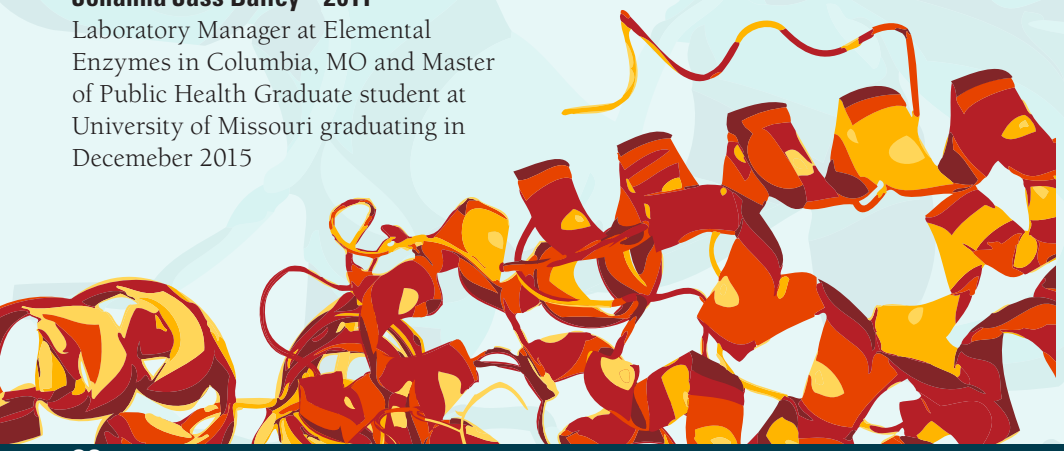
Alana Jackson 2012
Pursuing her M.D. at the University of Minnesota Medical School Duluth

Kristen McKibben 2013
1st year Biophysics Ph.D. student at the University of Pennsylvania graduating in 2020.

Kinsey Cornick 2013
1st year student at Des Moines University in the College of Osteopathic Medicine

Jennifer Kaczynski 2013
Working as an ER scribe at Unity and Mercy Hospital, MN

Zack Young 2014
Biography on page 17



2015 Stupka Committee

1st Row (L to R): Kia Barry, Elizabeth Clark, Derek Loneman, Flora Yen, Morgan Barrett, Mandy Gorniak, Natalie Whitis
2nd Row (L to R): Kayla Arney, Laura Hansen, Sarah Brinkman, Brendan Bartels, Lauran Chambers, Zack Young, Benjamin Brown, Adrienne Smith, Alissa Mathisen
3rd Row (L to R): Drew Tonsager, David Rosenthal, Denis Tamiev
Not pictured: Jeff Carley, Cathryn Ciarfella, Sean Siberski

2015 Committee Leadership

Symposium Co-Chairs: Kayla Arney, Zack Young
Speaker: Mandy Gorniak, Adrienne Smith
Publicity: Brendan Bartels, Flora Yen
Funding: Benjamin Brown, Jeff Carley, Lauran Chambers, Drew Tonsager
Operations: Lauran Chambers, Denis Tamiev
Food: Morgan Barrett, Sarah Brinkman
Poster: Alissa Mathisen
Volunteers: Cathryn Ciarfella
Registration: Laura Hansen
T-Shirt: Derek Loneman, David Rosenthal
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