

STUPKA

**UNDERGRADUATE
RESEARCH
SYMPOSIUM**



April 7, 2016

Presented by the
Undergraduate Club
of the Roy J. Carver
**Department of Biochemistry,
Biophysics & Molecular Biology**

IOWA STATE UNIVERSITY
OF SCIENCE AND TECHNOLOGY

EVENTS SCHEDULE

THURSDAY

- 9:00 am Breakfast**
Keynote and Alumni speaker meet and greet
Atrium
- 11:00 am Stupka Family Welcome**
Atrium
- 12:10 pm Weibel Lunch**
Undergraduates & Graduates Only
1102 MBB
- 1:10 pm Kuriyan Lunch**
Undergraduates & Graduates Only
1102 MBB
- 2:10 pm Poster Session 1**
Atrium
- 3:10 pm Poster Session 2**
Atrium
- 4:10 pm Welcome and Introductions**
Dr. Kristen Johansen
Provost Jonathan Wickert
1414 MBB
- 4:20 pm Natalie Whitis – STUDENT SPEAKER**
Control of CRISPR Activity by a Cascade Switch
- 4:35 pm Dr. Douglas Weibel – KEYNOTE SPEAKER**
Mechanical genomics
- 5:15 pm Adrienne Smith – STUDENT SPEAKER**
Expression and Characterization of Xyloglucan Xylosyltransferases
- 5:30 pm Break and Refreshments**
- 5:50 pm Sam Schulte – STUDENT SPEAKER**
Controlling Product Stereochemistry in Class II Diterpene Cyclases
- 6:05 pm Mariah Lawler – ALUMNA SPEAKER**
Defining miRNA in motor neurons in ALS
- 6:30 pm Dr. John Kuriyan – KEYNOTE SPEAKER**
Protein kinases as highly adaptable molecular switches
- 7:10 pm Poster Awards**
1414 MBB
- 7:15 pm Dinner**
Atrium

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save the date for the 12th annual
Stupka Symposium
Thursday, April 6, 2017

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

REMEMBERING ROB



Rob Stupka was an undergraduate student majoring in Biochemistry at Iowa State University. His passion for science and research led the effort to establish the BBMB 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. Their vision for this symposium was for it to be a medium for scientific research interactions between undergraduates and professionals. Rob, also, wanted this to be a place where undergraduate researchers could be recognized for their achievements in science.

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 bears his name. BBMB undergraduates, who are inspired by Rob's story, continue to organize this event. We believe that through your attendance and participation, we continue to honor Rob's memory.

The 2016 Stupka Undergraduate Research Symposium would like to thank you for being here. We hope you enjoy the wonderful research presented by our promising young scientists.

LIPID TRANSFER PROTEIN

Rob and his father visited several universities in early 2002. In June of that year, they visited Iowa State University. The beauty of the campus and the friendliness of the staff convinced them that this was Rob's new home. Rob initially entered ISU in the Fall of 2002 as a chemical engineering student. During his first semester, he took BBMB 101: Introduction to Biochemistry as an elective. Rob was so captivated by the biochemical discoveries explained in class, that he became a biochemistry student at the end of his first semester. He worked on making cDNA libraries from floral nectaries. This molecule is the nectary Lipid Transfer Protein (LTP2). The cDNA that encodes this protein was made by Rob. It was subsequently cloned and characterized. It is currently being expressed in bacterial cells with the goal of determining its antimicrobial activity.





- Front:** Amanda Gorniak, Lisa Warnock, Flora Yen, Joseph Washington, Victoria Ridout, Samuel Tufts, Morgan Barrett
- Middle:** Kia Barry, Alissa Mathisen, Lauran Chambers, Alex Donelson, Natalie Whitis, Tyler Gilbreath
- Back:** Brittany Bolerjack, Drew Tonsager, David Rosenthal, Adrienne Smith, Ben Brown, Jeff Carley
- Not Pictured:** Julia Nguyen, Bailey Mooney, Maddison Wild, Sarah Brinkman

2016 Committee Leadership

Symposium Chairs: Amanda Gorniak, Flora Yen

Speaker Chair: Adrienne Smith, Tyler Gilbreath

Publicity Chair: Morgan Barrett

Funding Chair: Victoria Ridout

Operations Chair: Lauran Chambers

Food Chair: Natalie Whitis

Secretary: Jeff Carley

Treasurer: Ben Brown

Web Master: Drew Tonsager

Poster Coordinator: Kia Barry

Volunteer Coordinator: Julia Nguyen

Registration Coordinator: Drew Tonsager

TShirt Coordinator/ Risk Management: David Rosenthal

Advisers: Desi Gunning, Gustavo MacIntosh

POSTER SESSION 1 (2:10-3:00)

1	Ana Mia Corujo	"NSC 145366" is a novel C-terminal Hsp90 binder
2	Stephanie Morriss	Loss of function of RNS2, a housekeeping RNase T2 enzyme, causes alterations in cellular homeostasis and growth in Arabidopsis
3	Hannah Yang	Functional Characterization of Acetyl-CoA Synthetase in Arabidopsis Thaliana
4	Saheli Sengupta	Digitor, an essential protein with homology to mammalian ATMIN is involved in brain development and oxidative stress pathways in Drosophila
5	Jena Gilbertson	Imaging Non-uniform Spatial Distribution of Energy Dense Metabolites for Efficient Capture and Chemical Storage of Solar Energy by Plants
6	Martha Ibore	Characterization of the Molecular Basis of Resistance to Soybean Aphids (<i>Aphis glycines</i> Matsumura)
7	Victoria Ridout	Exploring potential effects of oxidative stress on genes linked to RNA-selective autophagy in Arabidopsis Thaliana
8	Nikita Chopra	Identifying a compensatory mutation in Btk kinases capable of stabilizing its active conformation in the presence of an inactivating XLA mutation
9	Tyler Gilbreath	Toward mapping the phosphorylation-induced conformational changes underlying nNOS activation
10	Sujan Devkota	Role of PH domain in ITK regulation
11	Matthew Cook	Site-directed mutagenesis on XXT2 reveals critical cysteine residues for in-vitro catalytic activity
12	Neha Amatya	NMR Backbone Assignment of kinase domain of Bruton Tyrosine Kinase
13	Lauran Chambers	Modification of Binary Vectors for Plant Transformation by Swapping Selectable Markers
14	Meirong Jia	Investigating (di)terpene synthase mechanisms in vascular plants
15	Benjamin Wherry	Characterization of Arabidopsis DEAD/DEVH-box helicases with a putative role in rRNA degradation

POSTER SESSION 2 (3:10-4:00)

16	Selina Shiqing K. Teh, Nick Mulderink, and Hongdi Song	Development of Metal Sensor using RNA Aptamers
17	Michael Schelling	Investigating the role of Zea mays Glossy 2 family in extracellular epicuticular lipid biosynthesis using Arabidopsis thaliana expression system
18	Jeff Carley and Morgan Barrett	Mapping Calmodulin-Induced Conformational Changes During Activation of Neuronal Nitric Oxide Synthase by H/D Exchange Mass Spectrometry
19	Paul Parisot	Characterizing Fatty Acid Biosynthesis Regulator Genes by Evaluating Yeast Double Knockouts and their Effect on Lipid Metabolism
20	Kia Barry	Investigation of the Role of Isoflavones in Soybean Response to Soybean Aphids
21	Muneaki Watanabe	Halide, Adduct and Substrate Stabilization of b-Ketoacyl-(Acyl-Carrier-Protein) Synthase III
22	Andrew Tonsager	Investigation of expression between the Arabidopsis QQS and a potential interacting partner in Saccharomyces cerevisiae
23	Alex Donelson	Understanding ionic dependencies of aptamer-ligand interactions for better sensor design
24	Kyle Mcalpine	Mutational analysis of Pyruvate phosphate dikinase (PPDK) function in maize endosperm and leaf
25	Ellie Clark and Jennifer Demiter	Sleep quality and gender: Men and women's sleep quality relates differently to physical symptoms but not emotional effects
26	Karthik Murugan	Cataloging the effects of chemical modifications in crRNA on CRISPR-Cas9 activity
27	Jennifer Gribble	Fat content and nutrient usage controlled by chromatin organization: Drosophila histone modifier JIL-1 H3S10 kinase loss-of-function mutants predict obesity
28	Ben Brown	Biochemical characterization of new P450s in rice diterpenoid metabolism
29	Chaoyou Xue	Two different Cascade binding modes related to PAMs

■ undergraduate presenter
 ■ graduate presenter
 ■ Linder scholar
 ■ Stupka scholar

Natalie R. Whitis

STUPKA SCHOLAR 2016

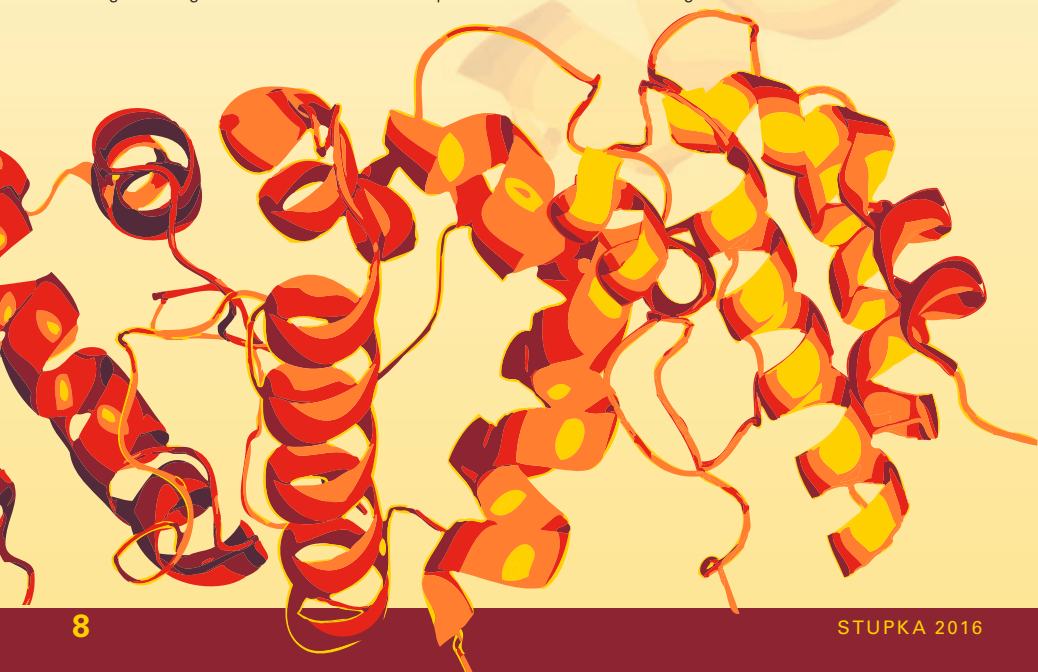


Natalie Whitis is a senior at Iowa State and is majoring in Biophysics. She is the Breakfast Club Chair for the BBMB Club as well as Food Chair for the Stupka Symposium. After she graduates from Iowa State she plans to attend graduate school and work towards a PhD. Then, she plans to work in academic research. Since the fall of 2014, she has been an undergraduate research assistant with the Sashital Lab studying the mechanism of the CRISPR-Cas immune system in *E. coli*.

ABSTRACT

Control of CRISPR priming and interference activities by a Cascade-activated switch

CRISPR-Cas (Clustered Regularly Interspaced Short Palindromic Repeats – CRISPR-associated proteins) is an adaptive immune system in bacteria that scans DNA within the cell and integrates pieces of viral DNA into the bacterial genome (acquisition) in order to recognize and destroy the virus the next time it infects the cell (interference). The immune system differentiates the viral genome from its own CRISPR loci by recognizing PAM (protospacer-adjacent motif) sequences that are present in viral targets but not in the host genomic locus. Mutations in the PAM trigger a more efficient method of integrating new spacers (priming), which requires both the acquisition and the interference machinery. Based on structural analysis of the target-binding interference complex Cascade, we identified several amino acid residues that may have a role in PAM recognition and tested the effects of alanine mutations at these positions on Cascade function. Surprisingly, we identified several mutants with measurable defects in interference but no effects on priming. Our *in vitro* DNA-binding assays have revealed that these Cascade mutants cause modest defects in target binding, but completely block target cleavage by the interference endonuclease Cas3, consistent with the observed loss of interference *in vivo*. Together, these results suggest that Cascade may bind DNA in two alternate conformations that switches activity from interference to priming and that the PAM-recognition region of Cascade controls this putative conformational change.



Douglas B. Weibel

UNIVERSITY OF WISCONSIN



Douglas B. Weibel is an Associate Professor of Biochemistry, Chemistry, and Biomedical Engineering at the University of Wisconsin-Madison. He received his B.S. degree in chemistry in 1996 from the University of Utah (with Prof. C. Dale Poulter). From 1996-1997 he was a Fulbright Fellow at Tohoku University, Japan and studied organometallic chemistry (with Prof. Yoshinori Yamamoto). He received his Ph.D. in chemistry from Cornell University in 2002 (with Prof. Jerrold Meinwald). During his graduate studies he was an intern at Orchid Biosciences Inc. (now LabCorp) and a visiting scientist at the Max Planck Institute for Chemical Ecology, Jena, Germany (with Prof. Wilhelm Boland). From 2002-2006 he was a postdoctoral fellow with Prof.

George M. Whitesides at Harvard University and in 2005 he was a student in the Physiology Course ('Modern Cell Biology using Microscopic, Biochemical, and Computational Approaches') at the Marine Biological Laboratory at Woods Hole (Course Directors, Prof. Ron Vale and Prof. Tim Mitchison). Since joining the faculty at UW-Madison 2006, he has received a number of research and teaching accolades, including: the Class of 1955 Distinguished Teaching Award (2014), the Early Career Life Science Award from the American Society for Cell Biology (2013), the NIH Director's New Innovator Award (2011), a DuPont Professorship (2010-2013), an Alfred P. Sloan Fellowship (2009), the DARPA Young Faculty Award (2009), and a Search Scholar Award (2008). He was a visiting professor of physics at the University of Washington, Seattle and a principal scientist at Amazon.com, Inc. from 2014-2015. He has consulted for a range of public and privately held companies (including Google[X], Cubist Pharmaceuticals [now Merck] and Amazon.com, Inc.) in the areas of biotechnology, bioengineering, chemistry, applied biology, materials science, and manufacturing and has participated in a range of government advisory positions in the areas of biodefense, infectious diseases, and biomedicine. He is a co-founder of two start-up companies: Agri Diagnostics Inc. develops products that improve agricultural yields; Avilas Health Inc. develops quantitative, at-home fertility tests. His research interests span the fields of chemistry, biochemistry, biophysics, materials science and engineering, and microbiology.

ABSTRACT

Mechanical genomics

Bacteria and other microorganisms have to solve an important physical problem for their survival: how do they mechanically resist the large pressure drop across their cell wall (~105 Pa) that arises due to mismatch in concentrations of dissolved solutes inside and outside of the cell?

We still know very little about bacterial mechanics, and yet one of the most clinically used family of drugs discovered to-date (the beta-lactam antibiotics), alter cell wall mechanics, create defects, and cause cell lysis. Understanding how bacteria control their mechanical properties will define new targets for developing clinical antibiotics and lay the foundation for studying mechanobiology in the most tractable model organism available.

In this talk I describe two approaches we have developed to identify the biochemical regulators of mechanical properties in bacteria: 1) CLAMP (cell length analysis of mechanical properties) is a medium-throughput technique to measure the effective Young's modulus of growing bacterial cells; and 2) GRABS (general regulators affecting bacterial stiffness) is a high-throughput technique that assigns stiffness scores to every gene in a bacterial genome.

Using this suite of tools, I describe the surprising regulators of stiffness in bacteria and how these techniques are enabling us to lay the foundation for understanding mechanobiology in microbes (from components of the human microbiome, to bacterial pathogens, to infectious eukaryotic microbes).

Adrienne Smith

STUPKA SCHOLAR 2015 & 2016



Adrienne is a senior 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 Zobotina, Ph.D. Adrienne also serves the Biochemistry, Biophysics, and Molecular Biology Club as the Liberal Arts and Sciences Representative and is the chair for the Speaker Committee for the Stupka Symposium. In addition, she tutors Organic Chemistry for the Hixson-Lied Academic Success Center. She plans to continue undergraduate research at Iowa State in the hopes of attending a graduate program in molecular biology.

ABSTRACT

Expression and Characterization of Xyloglucan Xylosyltransferases

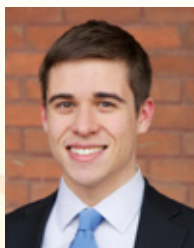
Xyloglucan (XyG) is the main hemicellulosic component of the primary cell wall in eudicots and nongraminaceous monocots. Three xyloglucan xylosyltransferases, including XXT2, are known to encode XyG xylosyltransferases, key enzymes in the process of XyG biosynthesis. A computational model of XXT2 was used to identify amino acids, F204, K207, D228, S229, D230, H378, putatively localized in the active site of XXT2 and mutagenesis study was performed to confirm predictions. All created mutants were expressed in *E. coli* SoluBL21 in pET20b plasmids containing an N-terminal GB1 fusion tag. To increase yield and purity for future biophysical experiments, such as isothermal titration calorimetry and circular dichroism, the mutated genes were amplified from the pET20b plasmids, ligated into pGen2 plasmids and transfected into HEK293 cells. Results of the enzyme assay demonstrated that K207, D228, D230, and H378 are critical for enzyme activity due to their proposed coordination of the divalent cation. Reduced activity seen for the mutation made at F204 suggests that while this site is important for enzyme activity, it is not as crucial as the other sites tested. In addition, cysteine residues were selected for mutagenesis to investigate their effect on disulfide bond formation shown to be involved in hetero- and homo- dimer formations. Expression and analysis of these mutants is currently in process.

Truncations of XXT2 from both the N- and C-ends were used to examine the contributions of these termini to protein solubility and activity. In N-terminal truncations longer than 31 residues, both protein expression and activity of XXT2 were negatively affected, indicating a possible effect on protein folding. Increasing sizes of truncations from the C-terminus showed an increase in protein expression but a decrease in its catalytic activity. We conclude that the C-terminus is not involved in protein folding but rather substrate binding. This truncation identified a series of six positively charged residues between 24 and 44 amino acids from the C-terminus that may play a role in substrate binding. Mutagenesis of these residues revealed that four of the mutants have reduced catalytic activity.

We conclude that the N-terminal of XXT2 is involved in protein folding while the C-terminal is involved in substrate binding. Furthermore, active site residues K207, D228, D230 and H378 are proved to be critical for enzymatic activity of XXT2.

Sam Schulte

LINDER SCHOLAR 2015



Sam is a senior at Iowa State and is pursuing a Biochemistry degree and a Computer Science minor. Sam is involved in research in the laboratory of Dr. Reuben J. Peters, where he studies the catalysis of class II diterpene cyclases. Previously, he has worked as a Borlaug-Ruan Intern at the International Maize and Wheat Improvement Center in Mexico, as a USDA Wallace-Carver Fellow, and as a Discovery Research Intern at Kemin Industries. When outside the Molecular Biology Building, Sam is the Principal Euphonium in the Iowa State University Wind Ensemble and has been in Student Government for three years. After graduating, Sam intends to earn a Ph.D. in Biochemistry.

ABSTRACT

Controlling Product Stereochemistry in Class II Diterpene Cyclases

Class II diterpene cyclases (DTCs) catalyze the committed step in production of the large class of labdane-related diterpenoid natural products, many of which function as important primary and secondary metabolites in plants. Mechanistic studies of DTCs, which bicyclize geranylgeranyl diphosphate (20-C), have revealed the importance of a variable set of two amino acids comprising a catalytic base dyad. Here, the catalytic base dyads of the closely related DTCs DsCPS (Danshen copalyl diphosphate synthase) and MvPPS (*Marrubium vulgare* peregriinol diphosphate synthase) were probed to further elucidate the evolution and mechanisms of these enzymes. Such studies were completed using site-directed mutagenesis, with the mutated DTCs expressed in an *Escherichia coli* metabolic engineering system. DsCPS ordinarily produces copalyl diphosphate (CPP), which adopts the chair-chair conformation. However, upon mutating the catalytic base dyad residues (along with one other neighboring residue) to the amino acids of the catalytic base dyad in MvPPS, the DsCPS mutant produces terpenedieryl diphosphate (TPP). Intriguingly, TPP adopts the chair-boat conformation, corresponding to the stereochemistry of the MvPPS product. Thus, simply introducing the catalytic base dyad of one DTC into another is sufficient to change product stereochemistry in this instance, illustrating the critical role of these two amino acids. This research provides insight into how specific mutations in closely related DTCs have created the capacity to produce such a wide array of labdane-related diterpenoids.

Mariah Lawler**WASHINGTON UNIVERSITY, ST. LOUIS**

Mariah's adventure at ISU began as a biology major. But – when everyone else in her introductory biology class was excited for the section on “mammals” – Mariah had the lurking feeling she was in the wrong place. After a BBMB student suggested meeting with Desi Gunning, Mariah knew she had finally found home. During her time at ISU, Mariah worked in the laboratory of Dr. Ravi Singh at the Vet Med School. Under the guidance of Dr. Natalia Singh, Mariah characterized a long-distance intronic interaction that contributed to pre-mRNA alternative splicing of Survival Motor Neuron 2, which is associated with Spinal Muscular Atrophy. Mariah became fascinated

by the regulatory roles of RNA, particularly as they pertain to human disease.

Mariah is currently a fourth-year graduate student in the laboratory of Timothy Miller at Washington University in St. Louis. Her doctoral work focuses on the contributions of small regulatory RNAs, microRNAs, to the selective vulnerability of motor neurons to Amyotrophic Lateral Sclerosis (aka the “Ice Bucket Challenge” disease). She is the recipient of both a pre-doctoral fellowship from the NIH and from Sigma-Aldrich. Mariah has thoroughly enjoyed her time in St. Louis, which seems like big city living in comparison with her beloved Ames. Finally, to address the question on everyone's minds (or at least her mother's), Mariah does not yet know when she will graduate. TBD!

ABSTRACT**Cell type miRNA profiling reveals candidate biomarker of motor neuron disease**

Amyotrophic Lateral Sclerosis (ALS) is a progressive neurodegenerative disorder marked by the loss of motor neurons (MNs) in the brain and spinal cord, leading to fatally debilitating muscle atrophy. For diseases in which a single cell type is predominantly affected by disease pathology, characterizing the distinct expression profile of that cell type may serve to elucidate underlying disease mechanisms and identify novel targets of therapeutic or diagnostic utility. microRNAs (miRNAs) are short, non-coding RNAs that can shape the expression profile of a cell and, consequently, often exhibit cell type enriched expression. Because they are actively released from cells and detectable in clinically accessible fluids, such as cerebrospinal fluid (CSF), miRNAs have been increasingly used for diagnostic purposes. Utilizing Cre-dependent miRNA tagging and affinity purification in mice, we defined the *in vivo* miRNA expression of all neurons as well as MNs, astrocytes and microglia, leading to the specific identification of MN-enriched miRNAs. Characterizing the levels of the MN-enriched miRNAs in CSF harvested from models of MN disease led to the development of a novel biomarker (miR-218) that tracked with disease progression and was responsive to an ALS therapy in rodent models. Thus, we have employed cellular expression profiling tools to assess the distinct miRNA expression of our cell type of interest, which enabled a hypothesis-driven approach for development of a novel, drug-responsive biomarker of MN disease.

John Kuriyan

UNIVERSITY OF CALIFORNIA, BERKELEY



Dr. Kuriyan earned his PhD in 1986 from the Massachusetts Institute of Technology. He was a post-doctoral fellow with Professors Martin Karplus (Harvard) and Gregory A. Petsko (MIT). From 1987 to 2001 he was on the faculty of The Rockefeller University, New York, where he was promoted to full Professor in 1993. He is a Professor of Molecular and Cell Biology and also of Chemistry at the University of California, Berkeley, a position he has held since 2001. Dr. Kuriyan is also an investigator of the Howard Hughes Medical Institute, having been appointed in 1990.

Dr. Kuriyan's research concerns the atomic-level structure and mechanism of the enzymes and molecular switches that carry out cellular signal transduction. His laboratory uses x-ray crystallography to determine the three-dimensional structures of proteins involved in signaling, as well as biochemical, biophysical, and cell biological analyses to elucidate mechanisms. Breakthroughs from the lab have included determining the auto-inhibited structures of several tyrosine kinases, including Src family kinases and elucidating the mechanism of allosteric activation of the kinase domains of the EGF receptor. His laboratory has provided a fundamental understanding of the structure and regulation of several other signaling proteins, including STATs, the Ras activator SOS, and calcium/calmodulin-dependent protein kinase-II. Their structural insights have helped understand how the misregulation of these enzymes is often coupled to cancer and immune diseases and has implications for the development of kinase-targeted drugs to treat these diseases. His lab has also made fundamental contributions to understanding the structural basis for high-speed DNA replication.

Dr. Kuriyan's achievements in science have been recognized by numerous honors, including:

- Foreign Member of The Royal Society, London. Elected April 2015.
- Doctor of Humane Letters, honoris causa, Juniata College, Huntington, PA. May 2014.

ABSTRACT

Protein kinases as highly adaptable molecular switches

Protein kinases are signaling switches that phosphorylate proteins and thereby control decisions in the cell. The targets of protein kinases regulate most cell functions, and they are especially important in sending messages across the cell membrane. Ultimately, kinases can prompt cells to divide, move, and even die. Our studies on the structural mechanisms of kinases encoded by oncogenes have shown us how the structure of the catalytic core is flipped between off and on states by very different kinds of accessory elements. Understanding how to toggle these switches has helped us understand how drugs that block the catalytic activity of kinases work, and how they might be improved. I will discuss our current studies, which include analysis of the mechanism by which a cell-surface receptor, known as the epidermal growth factor (EGF) receptor, communicates across the cell membrane, how these two receptors form an active signaling complex, and how a calcium/calmodulin-dependent protein kinase II responds to activating signals.

2016 STUPKA SCHOLARS



Morgan Barrett

Morgan is a senior majoring in Biochemistry and Genetics. Throughout her time at Iowa State, she has been actively involved in the Stupka Symposium Planning Committee, where she is currently Publicity Chair, and the BBMB Undergraduate Club, where she is currently Vice President. She has been an undergraduate research assistant in Dr. Eric Underbakke's lab since spring 2014. After graduating from Iowa State, Morgan plans on pursuing further education in forensic science with the ultimate goal of working as a DNA analyst/criminalist.



Adrienne Smith

Bio on page 10



Natalie Whitis

Bio on page 8

PAST STUPKA SCHOLARS

Claire Kruesel 2006

Lecturer for the English Department at Iowa State University

Mara Alexeev 2007

Public health Masters student at University of California, Berkeley

Luke Helgeson 2008

Postdoctoral researcher in the laboratory of Dr. Trisha Davis at University of Washington studying the regulation of kinetochore microtubule attachments

Mina Farahbakhsh 2009

6th year M.D./Ph.D. candidate at University of Kansas Medical Center graduating in 2019

Dayna Peterson 2010

5th year Biochemistry Ph.D. candidate at Arizona State University

Jackie Rivas 2011

Ph.D. candidate in immunology at UT Southwestern Medical Center

Craig Brown 2011

M.D. candidate at Pritzker School of Medicine at University of Chicago, graduating in 2016, will begin general surgery residency after graduation

Johanna Jass Bailey 2011

Laboratory and Site Manager at Elemental Enzymes in Columbia, MO, Master of Public Health, University of Missouri, 2015.

Mollie Schubert 2011

Research Scientist II in the Molecular Genetics research group at Integrated DNA Technologies in Coralville, IA

Samson Condon 2012

3rd 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

2nd year Ph.D. student at University of Pennsylvania studying physical and organic chemistry

Kinsey Cornick 2013

2nd year osteopathic medical student at Des Moines University

Jennifer Kaczynski 2013

Working as a dermatology scribe at Unity and Mercy Hospital, MN

Denis Tamiev 2014

Senior at Iowa State University, graduating in May 2016 with a degree in Biochemistry and a minor Economics

Zack Young 2014

Research assistant at Oklahoma Medical Research Foundation

Flora Yen 2015

Senior in Biochemistry at Iowa State University, graduating in 2016 to pursue further education at University of Iowa studying Dentistry

Adrienne Smith 2015, 2016

Senior in Biochemistry at Iowa State University

Thank you!

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Dipali Sashital • Yeon-Kyun Shin • Michael Shogren-Knaak
Robert Thornburg • Eric Underbakke • Edward Yu • Olga Zabolina

POSTER JUDGES

Scott Nelson (head judge) • Linda Ambrose • Adam Barb
Bayou Chen • Mark Hargrove • Richard Honzatko • Dipa Sashital
Robert Thornburg • Eric Underbakke • Olga Zabolina

Thank you for attending!