

STUPKA

UNDERGRADUATE
RESEARCH
SYMPOSIUM



April 6, 2017

Presented by the
Undergraduates
of the Roy J. Carver
Department of Biochemistry,
Biophysics & Molecular Biology

IOWA STATE UNIVERSITY
OF SCIENCE AND TECHNOLOGY

EVENTS SCHEDULE

THURSDAY

- 8:30 am Breakfast** – Open to all – Hosted by BBMB Breakfast Club
Keynote and Alumni speaker meet and greet
Atrium
- 11:00 am Alumni Reception and Lunch**
Atrium
- 12:10 pm Culver Lunch**
Undergraduates & Graduates Only
1102 MBB
- 1:10 pm Espinosa 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 Opening Remarks**
Dr. Guru Rao, Vice President for Research
1414 MBB
- 4:20 pm Cody Lemke** – STUDENT SPEAKER
Predicting Function of Class II Diterpene Cyclases in Bacterial Species
Using a Sequence Similarity Network
- 4:35 pm Dr. Gloria Culver** – KEYNOTE SPEAKER
Checks and Balances – How to Make a Ribosome
- 5:15 pm Lauran Chambers** – STUDENT SPEAKER
Arabidopsis Plants Expressing a Fungal Pectin Methylesterase Have
Reduced Degree of Polysaccharide Methylation and Exhibit a Dwarfed
Phenotype and Resistance to Stresses
- 5:30 pm Break and Refreshments**
- 5:50 pm Morgan Barrett & Jeff Carley** – STUDENT SPEAKERS
Mapping calmodulin-induced conformational changes during activation of
neuronal nitric oxide synthase by H/D exchange mass spectrometry
- 6:05 pm Samson Condon** – ALUMNI SPEAKER
Coevolutionary analysis and structural prediction of the bacterial divisome
proteins FtsB and FtsL
- 6:30 pm Dr. Joaquín M. Espinosa** – KEYNOTE SPEAKER
Mechanisms of gene expression control in the p53 network
- 7:10 pm Poster Awards**
1414 MBB
- 7:15 pm Dinner**
Atrium

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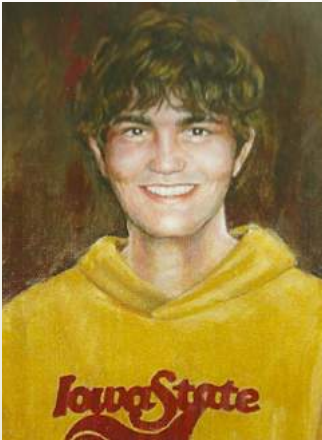
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SAVE THE DATE FOR THE 13TH ANNUAL
Stupka Symposium
Thursday, April 5, 2018

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

REMEMBERING ROB



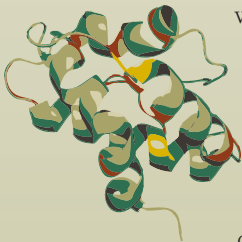
Rob Stupka was an undergraduate student majoring in Biochemistry at Iowa State University. His passion for science and research led the effort to establish the BBMB research symposium. His unparalleled enthusiasm propelled the planning process forward. Rob was the chair and with fellow students Tony 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 2017 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.

2017 STUPKA COMMITTEE



- Front row:** (from left) Sarah Zelle, Tiffany Farrell, Bailey Mooney, Lauran Chambers, Jacqueline Ehrlich, Julia Nguyen, Kennedy Goodell, Kayla Uthe
- Second row:** Grace Kline, Jillian Streit, Lisa Warnock, Joseph Washington, Alex Donelson, Matt Cook
- Third row:** Christian Johnson, Claire Vogl, Morgan Barrett, Natalie Whitis, Tyler Gilbreath, Laura Kurr
- Back row:** Adrienne Smith, Jeff Carley, David Rosenthal, Drew Tonsager, Spydel Nardy
- Not Pictured:** Alyssa Lantz, Emily Knuth, Brittany Bolerjack, Mustafa Mirza, Samuel Tufts, Dirk Winkelman, Isaac Stine, Mark Heggen, DeVaughn Jones, Courtney Smith, Rachel Garlock, Olivia Gray, Emily Juhl

2017 Committee Leadership

Symposium Chairs: Morgan Barrett, Jeff Carley

Treasurer: Bailey Mooney

Secretary: Drew Tonsager

Sub-committee Coordinators

Speaker: Tyler Gilbreath, Samuel Tufts

Publicity: David Rosenthal

Sponsorship: Alex Donelson

Fundraising: Julia Nguyen

Operations: Lauran Chambers

Food: Natalie Whitis

Website and Registration: Brittany Bolerjack

Poster: Matt Cook

Volunteer: Adrienne Smith, Lisa Warnock

T-Shirt: Alyssa Lantz

Advisers: Desi Gunning, Gustavo MacIntosh

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

1	Febriana Pangestu	Functional characterization of acetyl-CoA synthetases in <i>Arabidopsis thaliana</i>
2	Kacie Struve	Searching for XLA compensatory mutations in Bruton's tyrosine kinase
3	Jared Haupt	Assessment of specific N-terminal-region interactions on <i>Plasmodium falciparum</i> apicoplast polymerase fidelity
4	James Klimavicz	Monoterpenoid esters as biorational mosquito repellents
5	Michael Schelling	In vitro characterization of GLOSSY2 protein
6	Hanna Wokpetah Graciela Gautier	Illuminating Ca ²⁺ -induced scaffolding and kinase regulation mechanisms of Pyk2
7	Yang Sheng	Activation of the WAVE Regulatory Complex (WRC) by Rac1 and Arf1 GTPases
8	Nicholas Thoma	Metabolite profiling of nectar to reveal the taxonomic classification of <i>Brassica</i>
9	Adam Willerth	Diversity of fatty acids in different species
10	Kristen McKibben	N-terminal inserts of Tau and their interactions with Tubulin
11	Jeremy Schuster	Twins sectors caused by alternative transpositions in maize
12	Hannah Loghry	Validation of candidate fatty acid biosynthesis (FAB-R) genes in <i>Saccharomyces cerevisiae</i>
13	Jena Gilbertson	Direct profiling and imaging of plant metabolites in intact tissues by using mass spectrometry imaging
14	Christopher Fritz	Applying the spinach and broccoli light-up aptamers to lead detection
15	Jennifer Demiter	Role of stress in an individual's ability to track their sleep
16	Alan Culbertson	Heterologous expression of three xyloglucan xylosyltransferases provides insights to the function of N- and C-terminus and mode of substrate binding
17	Katherine Johnson	The production and isolation of heterodimeric Rad50 protein
18	Ben Brown	Phylogenetically-directed mutagenesis of a subset of the P450 CYP76M subfamily


 Undergraduate


 Graduate

 Staff

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

19	 Drew Tonsager	Investigating the <i>Arabidopsis thaliana</i> QQS gene and its impact on carbon partitioning in <i>Saccharomyces cerevisiae</i>
20	 Chaoyou Xue	Real-time observation of target searching by the CRISPR surveillance complex cascade
21	 Matt Cook	Optimization of the UDP-xylose biosynthetic pathway
22	 Bailey Mooney	Investigating retinal development using a gain-of-function strategy
23	 Samuel Tufts	A pair of residues that interactively affect diterpene synthase product outcome
24	 Neha Amatya	Develop tools and screen for small molecules that allosterically bind and inhibit BTK
25	 Margeaux Nall	3D modeling of a regulatory RNA structure from the oncogenic Epstein-Barr virus
26	 Courtney Smith	CRISPR/Cas9 genome editing in the zebrafish <i>Danio rerio</i> as a tool to examine ALS-associated gene function in motor neurons
27	 Kenna Goodlaxson	Identification and characterization of the <i>Zea mays</i> fatty acid elongase catalytic components
28	 Sharif Anisuzzaman	Investigations of the interactions of fluorinated super-ligands with the Broccoli and Spinach2 aptamers
29	 Liza Alexander	Evaluating intracellular and extracellular lipid metabolic networks at the level of individual cells
30	 Daniel Kramer	Membrane proteins use diverse mechanisms to interact with the WAVE regulatory complex
31	 Hayun Lee	A Cas1-Cas4 complex efficiently integrates long protospacers during CRISPR adaptation
32	 Sydney Boyle	Evaluating the effect of external application of phytohormone combinations (jasmonic acid and ethylene) on performance of soybean aphids
33	 Ai Chen	Optimization of a crystallographic protocol for screening inhibitors of the DNA polymerase from the apicoplast of <i>Plasmodium falciparum</i>
34	 Tyler Gilbreath	Toward mapping phosphorylation-induced conformational changes in nitric oxide synthase
35	 Martha Ibore	Characterization of the molecular basis of resistance to soybean aphids using RNA sequencing
36	 Surya-Tej Akavaram	Stabilization of CvfA by binding of the metK2 substrate in <i>Streptococcus pyogenes</i>

 Linder scholar

 Stupka scholar

 Alumni

Cody Lemke



Cody Lemke is a senior at Iowa State University concurrently pursuing a Bachelor's degree and a Master's degree in Biochemistry with a minor in Microbiology. Cody conducts research on Class II diterpene cyclases in the laboratory of Dr. Reuben Peters. He was admitted to Iowa State University as a transfer student from the College of Lake County and is also currently serving as the Vice President of the Gymnastics Club.

ABSTRACT

Predicting Function of Class II Diterpene Cyclases in Bacterial Species Using a Sequence Similarity Network

Diterpenoids are natural products commonly derived from plants as well as bacteria and fungi. Many of these secondary metabolites have been shown to possess anti-inflammatory, antimicrobial, insecticidal, and even antitumor properties making them of great interest in the pharmaceutical and agricultural industries. However, due to their complex structure, metabolic engineering is typically a necessary means of producing these compounds. For this reason, it is important to understand the function and mechanisms of the enzymes that often perform the committed step in diterpenoid biosynthesis, class II diterpene cyclases (DTCs). To better understand the breadth and diversity of bacterial DTCs, a protein sequence similarity network (SSN) was constructed from a previously characterized DTC involved in the synthesis of the plant hormone, gibberellin. This network established a representation of homology between putative DTCs in bacteria that could potentially be used to predict function of uncharacterized genes. Interestingly, this method also demonstrated that some bacterial DTCs have similarity to plant and fungal DTCs, suggesting a possible evolutionary relationship. To assess the SSN results, we cloned and expressed several putative bacterial DTCs in our metabolic engineering system, and in doing so have confirmed their functionality as DTCs. These newly characterized enzymes exhibit a wide range of functionality, and active site analysis suggests that only a few key amino acids may be involved in determining product outcome. Thus, our results demonstrate the efficacy of SSNs for identifying potential DTCs, along with providing insight into the mechanisms underlying the biochemical diversity exhibited by bacterial DTCs.



Dr. Gloria Culver

UNIVERSITY OF ROCHESTER



Gloria Culver, Ph.D. is a graduate of Ithaca College with a BA in Biology (minor: Art History). She earned her Ph.D. at the 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 Department of Biology, the Department of Biochemistry & Biophysics and as a member of the Center for RNA Biology. Dr. Culver served as Chair for the Department

of Biology for four years, and since the Spring of 2015 has been serving as Dean of the School of Arts and Sciences since Spring 2015. 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 served on the NIH Molecular Genetics A Study Section and acted as its Chair from Fall of 2014. Currently, Dr. Culver is a Director of the RNA Society.

Dr. Culver's research centers on the assembly of ribosomal machinery essential for growth of all cells. By focusing on bacterial ribosomes, she has contributed to understanding how infections might be controlled through selective inhibition of specific control points of ribosomal assembly. Her research has been continuously funded by the NIH for more than 16 years, and her lab's work has also received funding from the American Cancer Society and the NSF.

ABSTRACT

Checks and Balances – How to Make a Ribosome

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. The 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.

Lauran Chambers

LINDER SCHOLAR 2016
STUPKA SCHOLAR 2017



Lauran is currently a senior at Iowa State pursuing a major in Biochemistry and a minor in Nutrition. She is an undergraduate research assistant in Dr. Olga Zabolina's laboratory, is the president of the Biochemistry, Biophysics, and Molecular Biology Club, and Operations Chair of the Stupka Symposium Planning Committee. Outside of school, Lauran is a volunteer at LifeServe Blood Center of Des Moines. After graduation, she plans on attending medical school.

ABSTRACT

Arabidopsis Plants Expressing a Fungal Pectin Methylesterase Have Reduced Degree of Polysaccharide Methylation and Exhibit a Dwarfed Phenotype and Resistance to Stresses

Pectin is a major component of the plant cell wall and is involved in functions including growth of the plant cell, organ development, and defense against pathogens. Our lab has developed a suite of transgenic *Arabidopsis thaliana* plants expressing microbial-derived cell wall-degrading enzymes to study Cell Wall Integrity (CWI) responses. Plants expressing one such enzyme, *A. nidulans* Pectin Methylesterase (AnPME), exhibit dwarfism beginning with emergence of the first true leaves and affecting all specialized organs and structures throughout their lifetime. These plants also possess reduced sensitivity to salt stress; while roots of AnPME plants are much smaller than wild-type roots under unstressed conditions, root growth was not inhibited by 100 mM NaCl treatment. Preliminary results have also shown that AnPME plants are less susceptible to infection by the cyst-forming nematode *H. schachtii*. Ongoing research aims to quantify the degree of cell wall de-methylesterification to correlate with degree of dwarfism, and further confirm resistance of roots to nematode penetration. These results illustrate the importance of pectin methylesterification status in plant fitness and development, as well as response to both biotic and abiotic stresses, most likely through CWI response.



Morgan Barrett



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

STUPKA SCHOLAR 2016

Jeff Carley



Jeff is a senior, studying Biochemistry and Spanish. He has worked as an undergraduate research assistant in Dr. Eric Underbakke's lab since the spring of 2014. Within the department, Jeff has been involved as a Peer Mentor for the Learning Community, former President of the BBMB Club, and Co-Chair of the Stupka Symposium Planning Committee. He also serves as the Vice President of Iowa State's Student Admissions Representatives (STARS), organizing campus tours for prospective students. Next fall, Jeff will begin medical school, aspiring to a career in academic medicine that integrates clinical practice with research.

LINDER SCHOLAR 2015 & 2016

ABSTRACT

Mapping calmodulin-induced conformational changes during activation of neuronal nitric oxide synthase by H/D exchange mass spectrometry

Nitric oxide (NO) is a short-lived, freely diffusible gas that serves as an omnidirectional neurotransmitter. As such, it must be controlled through regulation of localization and activation. Homodimeric neuronal nitric oxide synthase (nNOS) is composed of a reductase and oxidase subdomain, connected by a mobile FMN subdomain. The reductase domain delivers reducing equivalents from NADPH through FAD and FMN to the heme-containing active site of the oxidase domain, where NO is generated from arginine. This process is tightly regulated by Ca^{2+} via the intermediary Ca^{2+} -sensor, calmodulin (CaM). We performed hydrogen/deuterium exchange mass spectrometry (HDX-MS) to investigate the activation mechanisms of NO synthesis by comparing inactive nNOS with Ca^{2+} -CaM-activated nNOS.

HDX-MS revealed major effects in all three nNOS subdomains. Changes in the reductase domain were most pronounced in a regulatory beta-finger, a structural element unique to the CaM-regulated isoforms of NOS. Interestingly, the CaM-perturbed regions encompass two serine residues that are subject to phosphorylation, a modification reported to tune nNOS activity. Changes in the mobile FMN subdomain were more distributed, largely localized to the distal surface opposite the FMN cofactor. This surface includes an auto-inhibitory insert involved in docking the FMN subdomain to the reductase domain. Near the oxidase domain, the CaM-binding linker exhibited profound decreases in exchange rate, indicating burial and helix formation. Activated nNOS also exhibited exchange rate changes in the oxidase domain that suggest a delivery mechanism for reducing equivalents into the active site. Taken together, the HDX-MS results define several important nNOS conformational changes and inter-domain dynamics responsible for Ca^{2+} /CaM-gated activation of NO production.

Samson Condon

STUPKA SCHOLAR 2012



Samson Condon is a Ph.D. candidate in the Department of Biochemistry at the University of Wisconsin-Madison. He graduated from Cedar Falls High School in 2009 and began attending Iowa State University in the Department of Biochemistry, Biophysics, and Molecular Biology that fall. Samson joined the Nikolau Group as an undergraduate researcher in 2010 under the mentorship of Dr. Marna Yandeau-Nelson. There, he analyzed the cuticular wax composition of maize silks using gas chromatography-mass spectroscopy and developed new protocols to increase sample throughput. He spent the summer of 2010 at SUNY-Albany as an REU intern and the spring of

2012 at the Nihon University School of International Relations in Mishima, Japan through the ISEP study-abroad program. He graduated *summa cum laude* with Honors from Iowa State University in 2013 with a B.S. in Biochemistry. For his involvement in academics, research, and the BBMB Undergraduate Club, he was named a Goldwater Scholar and a Robert Stupka III Scholar.

Samson joined the laboratory of Professor Alessandro Senes at the University of Wisconsin-Madison in 2013. His research there focuses on using computational tools and biophysical experiments to understand how membrane proteins fold and interact. Specifically, he is interested in modeling the quaternary interactions of proteins within the bacterial divisome and measuring the thermodynamics of transmembrane helix association for a common structural motif. He is currently a predoctoral fellow in the Computation and Informatics in Biology and Medicine (CIBM) Training Program.

ABSTRACT

Coevolutionary analysis and structural prediction of the bacterial divisome proteins FtsB and FtsL

One of the most fundamental processes in the bacterial life cycle is division. This process is mediated by the divisome, a multi-protein complex whose core subunits are conserved across bacterial phyla. Though many protein-protein interactions between divisomal subunits are known, there is very little information on how these interactions are mediated. Additionally, most divisome proteins have essential transmembrane domains that resist biochemical characterization. By taking advantage of computational protein structure prediction and the vast evolutionary sequence record for divisomal proteins, it may be possible to determine how divisome proteins associate and carry out cell division. For example, the intermediate divisomal proteins FtsB and FtsL exhibit a large number of strongly coevolving positions that span their transmembrane and periplasmic domains. With this information, the FtsB-FtsL subcomplex was modeled as a four-helix bundle that is consistent with the coevolutionary data as well as mutagenesis experiments, single-molecule studies of FtsB-FtsL stoichiometry, and molecular dynamics simulations. The coevolving positions in FtsL were consistent with a continuous helix spanning the transmembrane and coiled coil domains, but in FtsB the transmembrane interface was shifted relative to the coiled-coil interface. This shift is mediated by a conserved glycine-rich juxtamembrane region of FtsB which may allow conformational flexibility. Other proteins within the bacterial divisome also have strong coevolutionary signals, which will be useful for modeling their interactions and identifying important interfaces where bacterial cell division might be disrupted.

Dr. Joaquín M. Espinosa

UNIVERSITY OF COLORADO



Dr. Espinosa is the Associate Director for Science at the Linda Crnic Institute for Down Syndrome. He is also a Professor in the Department of Pharmacology at the University of Colorado Denver School of Medicine, the co-Leader of the Molecular Oncology program at the University of Colorado Cancer Center, and the founding Director of the Functional Genomics Facility at the University of Colorado.

Dr. Espinosa received his B.S. in Biology from the Universidad Nacional de Mar del Plata, Argentina, in 1994, and a PhD in Biology from the Universidad de Buenos Aires, Argentina, in 1999. Supported by a fellowship from the PEW Charitable Trusts, Dr. Espinosa completed his post-doctoral at the Salk Institute for Biological Studies in La Jolla, California. In 2004, supported by a fellowship from the Leukemia and Lymphoma Society, he began his independent appointment at the University of Colorado Boulder, in the Department of Molecular, Cellular and Developmental Biology. In 2009, he was appointed to the Howard Hughes Medical Institute as an Early Career Scientist, an appointment that he held until his move from Boulder to the Anschutz Medical Campus in 2015.

Dr. Espinosa directs a diverse research program both at the Department of Pharmacology and the Linda Crnic Institute, with an emphasis on understanding how gene networks control cell behavior and organismal function. The programs' two main focus areas are cancer biology and Down syndrome.

In his role as the Associate Director for Science, Dr. Espinosa works in collaboration with all the scientists in the Institute, both in the intramural and extramural programs, to identify research priority areas, promote collaborations within and outside the Institute, facilitate interactions with the clinical care operations at the Sie Center for Down Syndrome, facilitate adoption of new technologies, and advance the research mission of the Institute in the national and international arenas.

ABSTRACT

Mechanisms of gene expression control in the p53 network

p53 is the most commonly inactivated tumor suppressor gene in human cancer. The p53 gene network is composed of functionally distinct gene modules mediating diverse cellular responses to stress including cell cycle arrest, senescence, apoptosis and autophagy. The molecular mechanisms defining how cells adopt a specific response upon p53 activation are poorly understood, which hampers the development of therapies harnessing the apoptotic potential of p53 for selective elimination of cancer cells. Why do some cell types survive whereas others die upon p53 activation?

Several projects in our lab investigate how pleiotropy is generated within the p53 transcriptional program and how the network can be manipulated to produce specific cellular responses upon p53 activation. We performed mechanistic studies using global measurements of nascent RNA synthesis (GRO-seq), steady state RNA levels (RNA-seq, both total and polysome-bound), and p53 occupancy (ChIP-seq) to investigate how the p53 transcriptional program is qualified at the transcriptional, post-transcriptional and translational levels. We performed these investigations in cell types undergoing diverse p53 responses. In parallel, we performed genome-wide shRNA and CRISPR screens to identify signaling pathways that control the cellular response to p53 activation.

These studies revealed multiple mechanisms by which the p53 signaling cascade is qualified in a cell type-specific manner, from enhancer priming to translational control at the ribosome. For example, these efforts revealed how p53 works in coordination with cell type-specific transcription factors to drive distinct changes in the transcriptome. Finally, we have employed this knowledge to improve the therapeutic efficacy of p53-based targeted therapies currently being tested in clinical trials for the treatment of various cancers.



Lauran Chambers

Lauran is currently a senior at Iowa State University pursuing a major in Biochemistry and a minor in Nutrition. She is an undergraduate research assistant in Dr. Olga Zabolina's laboratory, is the president of the Biochemistry, Biophysics, and Molecular Biology Club, and Operations Chair of the Stupka Symposium Planning Committee. Outside of school, Lauran is a volunteer at LifeServe Blood Center of Des Moines. After graduation, she plans on attending medical school.



Alex Donelson

Alex is a junior at Iowa State University pursuing a B.S. in Biochemistry and minors in Genetics, Philosophy, and Astronomy. He is a research assistant in Dr. Marit Nilsen-Hamilton's lab, where he studies the dynamics of small RNA and DNA molecules (aptamers) and their use in biosensors. Alex is also an active member in both the BBMB Undergraduate Club and the Stupka Committee; he serves as the secretary and LAS representative for the Club and as the Treasurer for the Committee. Outside of school, he is an amateur astronomer and a professional Trekkie.



Drew Tonsager

Drew is a 4th year Iowa State University student pursuing Bachelor's and Master's degrees in Biochemistry as well as a minor in Mathematics. He currently works with the Campbell/Nikolau lab group, where he investigates the Arabidopsis Qua-Quinine-Starch gene and its impact on carbon-nitrogen partitioning in yeast. Aside from his research, Drew is involved in the Biochemistry department on campus as a volunteer in the Stupka Symposium Planning Committee. Additionally, Drew is in his third year as a peer mentor for the BBMB Learning Community. After graduating from Iowa State, Drew plans to continue his education and pursue a doctorate in Biochemistry.



PAST STUPKA SCHOLARS

Claire Kruesel 2006

Lecturer for the English Department at Iowa State University

Mara Determan Alexeev 2007

M.D. University of Iowa Now a pediatrician with the Hawaii Permanente Medical Group

Luke Helgeson 2008

Ph.D. Biochemistry now a postdoctoral fellow at the University of Washington

Mina Farahbakhsh 2009

Completed M.D. 2016 and now in the Ph.D. program at the University of Kansas

Dayna Peterson-Forbrook 2010

Graduate Research Assistant at Arizona State University and will complete Ph.D. in 2017

Jacqueline Souleyrette Rivas 2011

Ph.D. in Immunology 2017 from University of Texas Southwestern Medical Center and will begin working as Commercialization Manager for the Office of Technology Commercialization, University of Kentucky

Craig Brown 2011

M.D. from University of Iowa 2016 and now a resident in surgery at University of Michigan

Johanna Jass Bailey 2011

Master of Public Health, University of Missouri, 2015 and is now a Site Manager at Elemental Enzymes in Columbia, MO

Mollie Tiernan Schubert 2011

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

Samson Condon 2012

Ph.D. candidate at University Wisconsin-Madison

Alana Jackson 2012

M.D. in rural medicine from University Minnesota, Duluth, 2016 and will begin residency this spring

Kristen McKibben 2013

Ph.D. candidate at the University of Pennsylvania

Kinsey Cornick 2013

Third year osteopathic medicine student at Des Moines University

Jennifer Kaczynski Meyer 2013

Scribe in the Dermatology Department at Unity and Mercy Hospital, MN

Denis Tamiev 2014

First year graduate student at Iowa State University

Zack Young 2014

Research assistant at Oklahoma Medical Research Foundation

Flora Yen 2015

First year student at the University of Iowa School of Dentistry

Adrienne Smith 2015, 2016

Completed her B.S. in Biochemistry, fall 2016 graduated *summa cum laude*

Morgan Barrett 2016

Will complete her B.S. in Biochemistry and Genetics, spring 2017 and pursue a graduate education in Forensic Science

Natalie Whitis 2016

Will complete her B.S. in Biophysics and attend graduate school in the fall

IN MEMORY OF ADRIENNE SMITH



On February 27, 2017, we lost a very special member of our BBMB family, Adrienne Leah Smith. In 2011, she was diagnosed with Hodgkin's lymphoma. She never let cancer limit or define her; most never knew of her battle.

In the fall of 2013, Adrienne joined BBMB as a freshman and immediately got involved with the undergraduate club, Stupka Planning Committee, and of course, research! She worked with Dr. Olga Zabolina and was preparing for graduate training. Adrienne loved research, and in 2015 and 2016 she was recognized as a Stupka Scholar, BBMB's most

prestigious undergraduate award. In 2016, she was a featured student speaker for the Stupka Undergraduate Research Symposium. Her presentation, "Expression and characterization of xyloglucan xylosyltransferases," was outstanding.

Last spring, Adrienne presented her research poster at the American Society for Biochemistry and Molecular Biology national meeting. She received the "Best Thematic Poster Award" competing against graduate students, postdocs and principle investigators. A truly impressive accomplishment for an undergraduate student!

In the fall of 2016, Adrienne earned her B.S. in Biochemistry and graduated *summa cum laude*. She was a remarkable and brilliant young woman and will be greatly missed. In her honor and with her blessing, the 2017 Stupka Planning Committee dedicated a new feature for this year's event, the Adrienne Smith Alumni Dinner. Stupka alumni are growing in number, and this event will celebrate their return to campus and give today's students an opportunity to visit with our impressive alums. This is a perfect tribute to Adrienne, as she loved Stupka and serving on the planning committee. Adrienne will forever be with us and continue to inspire us all.

Thank you!

Your generous support makes the
Stupka Undergraduate Research Symposium possible.

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In grateful appreciation for your generous and continued support.

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Baoyu Chen • Alan DiSpirito • Jack Girton • Mark Hargrove • Richard Honzatko
Robert Jernigan • Jorgen Johansen • Kristen Johansen • Gustavo MacIntosh
Walter Moss • Alan Myers • Scott Nelson • Basil Nikolau • Marit Nilsen-Hamilton
Reuben Peters • Guru Rao • Julien Roche • Dipali Sashital • Yeon-Kyun Shin
Michael Shogren-Knaak • Robert Thornburg • Eric Underbakke • Olga Zabolina

POSTER JUDGES

Scott Nelson (head judge) • Linda Ambrosio • Alan DiSpirito • Mark Hargrove
Richard Honzatko • Raji Joseph • Alan Myers • Marit Nilsen-Hamilton
Julien Roche • Dipali Sashital • Robert Thornburg • Eric Underbakke