MOLECULAR MECHANISMS OF DISEASE

Predoctoral Training Program

Annual Symposium

April 20, 2022

8:00 AM - 5:30 PM Sheldon Art Museum

Program Contacts

Director
Donald Becker
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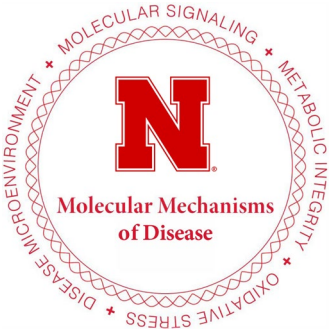

MOLECULAR SIGNALING
METABOLIC INTEGRITY
OXIDATIVE STRESS
DISEASE MICROENVIRONMENT
Molecular Mechanisms
of Disease

Training Program Summary

The goal of the program is to develop outstanding new scientists who work in collaborative multi-disciplinary teams to research disease mechanisms using quantitative approaches that ultimately yield tangible strategies for prevention and therapy. Participants are highly qualified, motivated students with a strong interest in the underlying causes of human disease. The program provides a framework to encourage all students to assemble a broad knowledge base, actively seek research collaborations, produce an outstanding record of original published research, and develop presentation, proposal-writing, and leadership skills that position them for future excellence as independent researchers focused on mechanisms of disease progression.

Administrative Advisors

Ron Yoder
Associate Vice Chancellor, Institute of Agricultural and Natural Resources

Bob Wilhelm
Vice Chancellor for Research and Economic Development

Daniel Duncan
Executive Director of Nebraska Innovation Campus

Debra Hope
Dean of Graduate Studies

Angie Pannier
Maxcy Professor of Agriculture and Natural Resources, Biomedical Engineering

Jennifer Wood
Professor, Animal Science

David Hage
James Hewett University Professor of Chemistry

External Advisors

Leslie Poole
Professor, Biochemistry, Wake Forest School of Medicine

Melanie Simpson
Professor and Head**,** Molecular and Structural Biochemistry, North Carolina State University

If you require special accommodations, please contact Paula Adams at aadams@unl.edu

Molecular Mechanisms of Disease Mentoring Faculty

Jiri Adamec, Biochemistry
Mitochondrial dysfunction biomarkers link to environmental stressors

Matt Andrews, School of Natural Resources
Induction and maintenance of hibernation in mammals

Jennifer Auchtung, Food Science and Tech
Microbiome-targeted therapies

Donald Becker, Biochemistry
Proline metabolism in health and disease, enzyme mechanisms of substrate channeling

David Berkowitz, Chemistry
Chemical biology and synthetic organic chemistry

Nicole Buan, Biochemistry
Contribution of methanogenic bacteria to gut function

James Checco, Chemistry
Neuropeptides and peptide hormones as cell-to-cell signaling molecules

Lindsey Crawford, Biochemistry
Virus manipulation of the human immune system

Andrea Cupp, Animal Science
Role of VEGF in testis morphogenesis

Eric Dodds, Chemistry
Chemical glycobiology

Liangcheng Du, Chemistry
Discovering new anti-infective agents from *Lysobacter*

Catherine Eichhorn, Chemistry
RNA structural dynamics and intermolecular recognition

Rodrigo Franco, Vet and Biomedical Science
Signaling mechanisms and neurotoxicity

Jiantao Guo, Chemistry
Protein tyrosine-O-sulfation, molecular interaction probes

David Hage, Chemistry
Chromatographic automation of immunoassays

Ed Harris, Biochemistry
Liver endothelial scavenger receptor function; systemic clearance of heparin

Tomas Helikar, Biochemistry
Dynamics of molecular and cellular mechanisms, Immune systems

Nicole Iverson, Biol Systems Engineering
Delivery, monitoring and analysis of in vivo nanoparticles as biological sensors

Oleh Khalimonchuk, Biochemistry
Mitochondrial oxidative function and protein homeostasis in health and sickness

Sri Kidambi, Chem & Biomol Engineering
Tissue engineering, stem cells

Forrest Kievit, Biol Systems Engineering
Nanoparticle-based delivery vehicles for brain cancer and brain injury treatments

Jaekwon Lee, Biochemistry
Mechanistic insights in homeostatic copper acquisition and cellular metal detoxification

Yuguo Lei, Chem & Biomol Engineering
Cell biomanufacturing for disease studies and therapeutic applications

Colin Meiklejohn, Biological Sciences
Genetic basis of speciation and regulatory evolution between nuclear and mitochondrial genomes

Angela Pannier, Biol Systems Engineering
Non-viral gene delivery, synthetic extracellular matrices, protein-cell adhesion

Kurt Piepenbrink, Food Science and Tech
Glycoproteins in bacterial pathogenesis

Robert Powers, Chemistry
NMR metabolomics

Amanda Ramer-Tait, Food Science and Tech
Host-microbial interactions in inflammatory bowel disease

Wayne Reikhof, Biological Sciences
Lipid distribution and storage mechanisms

Seung-Hyun Ro, Biochemistry
Sestrins and TORC signaling in metabolism

Jay Storz, Biological Sciences
Functional genetic variation in high-altitude mammals and birds, hypoxia adaptation

Xinghui Sun, Biochemistry
Long non-coding RNA regulation of gene expression in obesity and disease

Molecular Mechanisms of Disease Mentoring Faculty-Continued

Alex Vecchio, Biochemistry
Catalytic asymmetric hydroboration and “green chemistry” synthesis

Bill Velander, Chem & Biomol Engineering
cGMP recombinant factor IX for IV and oral hemophilia B therapy

Rebecca Wachs, Biol Systems Engineering
Tissue engineering and biomaterials-based therapeutics

Mark Wilson, Biochemistry
Redox regulation of DJ-1 function

Jennifer Wood, Animal Science
Steroid hormone sensing and signaling

Dustin Yates, Animal Science
Metabolic fetal programming related to maternal stress

Limei Zhang, Biochemistry
Structural biology, Mycobacterium tuberculosis infectivity

Schedule of Events

WEDNESDAY, April 20, 2022

University of Nebraska Sheldon Art Museum

8:00-9:00 AM POSTER SET UP AND BREAKFAST

9:00-9:15 AM WELCOME AND OPENING REMARKS

Dr. Donald Becker, Program Director

9:15-10:15 AM MORNING PLENARY PRESENTATION (ZOOM)

Co-opting oxylipin signals in fungal disease

Nancy Keller, Ph.D. Professor
Department of Medical Microbiology & Immunology
University of Wisconsin – Madison

10:15-10:55 AM CURRENT TRAINEES

Darcy Cochran
DETERMINING METABOLIC DIFFERENCES FROM THE GUT MICROBIOME OF INDIVIDUALS THAT CONSUME HIGH-ANIMAL OR HIGH-PLANT PROTEIN DIETS

Sydney Caparaso
VALIDATION OF FLUIDICALLY ISOLATED IN VITRO PLATFORM FOR ASSESSING NOCICEPTOR PHENOTYPE

10:55-11:10 PM LIGHTNING TALKS

Phoebe Shi (Poster #1) and Ekta Pandey (Poster #8)

11:10-12:00PM SESSION I POSTER VIEWING (ODD NUMBER POSTERS)

12:00-1:00PM LUNCH (BOX LUNCH PROVIDED)

1:00-2:00 PM AFTERNOON PLENARY PRESENTATION

Regulation of mitochondrial architecture and function: From basics to disease

Oleh Khalimonchuk, Ph.D. Susan J. Rosowski Professor
Department of Biochemistry, University of Nebraska-Lincoln

2:00-2:40 PM AFTERNOON TRAINEE TALKS: SET 1

Noelle Waltenburg
DESIGN OF SYNTHETIC RECEPTOR ACTIVITY MODIFYING PROTEINS AS CHEMICAL PROBES TO STUDY G PROTEIN – COUPLED RECEPTORS

Ivon Acosta
DEVELOPMENT OF CARBON NANOTUBE PLATFORMS FOR EXTRACELLULAR NITRIC OXIDE QUANTIFICATION IN VITRO

2:40-2:55 PM LIGHTNING TALKS

Yafan Yu (Poster #10) and Tyrell Rossman (Poster #9)

2:55-3:40 PM SESSION II POSTER VIEWING (EVEN NUMBER POSTERS)

3:40-4:40 PM AFTERNOON TRAINEE TALKS: SET 2

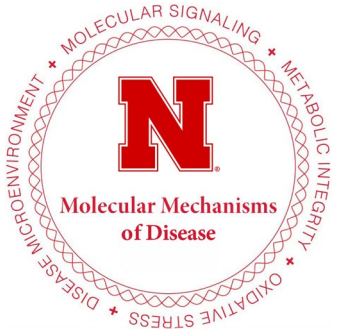
Jacob Jones
DEVELOPMENT OF DJ-1 AFFINTIY MICROCOLUMN UTILIZING PROTEIN ENTRAPMENT

Amanda Maliva
FUNCTIONAL GENOMICS OF PHOSPHATIDYLCHOLINE BIOSYNTHESIS IN *SACCHAROMYCES CEREVISIAE*.

Daisy Beltran
A SHARED ANCHOR ON PRIMARY SIGMA FACTOR SIG_A BY THE WHIB-LIKE PROTEINS

4:40-5:00 PM AWARD PRESENTATIONS

5:00-5:30 PM POSTER TAKE DOWN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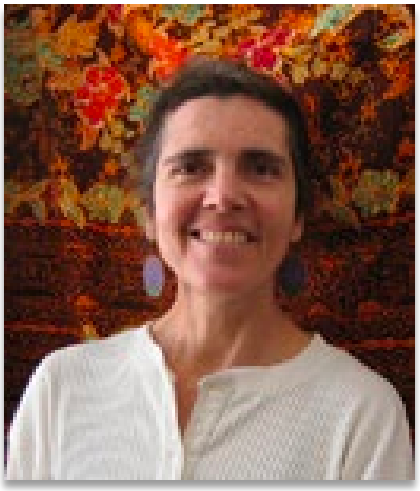
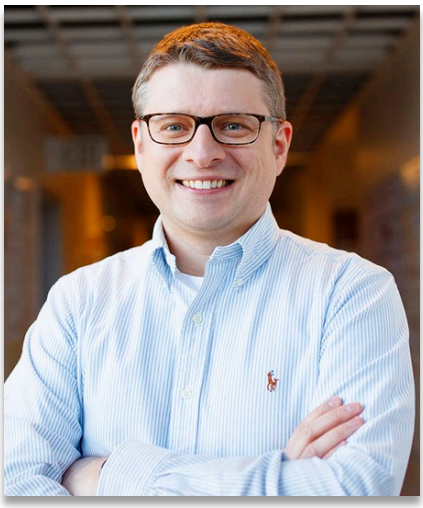
PLENARY SPEAKER PROFILES



Dr. Nancy Keller's research focus lies in genetically dissecting those aspects fungi have that render them potent pathogens and superb natural product (also called secondary metabolite) machines. Her lab (i) elucidates molecules involved in the virulence of plant, animal and human pathogenic fungi and (ii) methods to express and characterize novel bioactive fungal secondary metabolites for drug development. Pathogenic fungi she works with include *Aspergillus flavus* which contaminates seed crops worldwide with the carcinogen aflatoxin, *Penicillium expansum* that contaminates apple with the mycotoxin patulin, *Pseudogymnoascus destructans*, the causal agent of White Nose Syndrome of bats and the human pathogen *A. Fumigatus* causing invasive aspergillosis, a disease with a mortality rate ranging from 50 to 90%.



Dr. Oleh Khalimonchuk is a Susan J. Rosowski Professor in the Biochemistry Department, University of Nebraska in Lincoln, Nebraska. He is also serving as a current director of the Nebraska Redox Biology Center. He is a member of Fred & Pamela Buffett Cancer Center at the University of Nebraska Medical Center in Omaha, Nebraska, and of the University of Utah Center for Iron & Heme Disorders. Dr. Khalimonchuk's research uses yeast, roundworm, and mammalian cell culture models and is focused on fundamental understanding of processes behind vital mitochondrial functions and their contribution to complex diseases in humans. His current research interests include the mechanisms of mitochondrial heme transport and the neuroprotective roles of mitochondrial quality control factors. His work led to seminal discoveries in the field of mitochondrial biology and received several prestigious awards including Ruth E. Branham Award and Rosowski Professorship from the University of Nebraska, and a MIRA Award for Established Investigators from NIH.

MMoD Trainee Abstracts

Morning Session

DETERMINING METABOLIC DIFFERENCES FROM THE GUT MICROBIOME OF INDIVIDUALS THAT CONSUME HIGH-ANIMAL OR HIGH-PLANT PROTEIN DIETS

Darcy Cochran[1], Marissa Behnouek[2], Robert Powers [1], and Devin Rose[2]

[1]Department of Chemistry, University of Nebraska-Lincoln

[2]Department of Food Science and Technology, University of Nebraska-Lincoln

The number of commercial protein isolates is increasing as the demand for a high-protein, low-carbohydrate diet also increases. Common sources of protein isolates are pea, soy, beef, and egg. The gut microbiome consists of trillions of microbes that inhabit the human gastrointestinal tract. Also known as gut flora, these microbe populations are strongly affected by the diet of their host. If the gut flora is disrupted, the dysbiosis can cause a myriad of common diseases. As the gut bacteria metabolize various sources of protein, the produced metabolites can affect overall individual health. The research discussed in this talk will cover the development of a robust analytical NMR method that can help researchers understand the effect that protein isolates have on the gut microbiome in multiple carbohydrate conditions. Six types of protein isolates were fed to microbiome samples from individuals with either high-plant or high-animal protein diet. Samples underwent fermentation in either high or low carbohydrate fermentation broth and samples were taken at 0, 8, and 24 hours. Samples were analyzed via 1D 1H NMR for 8 targeted metabolites.

VALIDATION OF FLUIDICALLY ISOLATED IN VITRO PLATFORM FOR ASSESSING NOCICEPTOR PHENOTYPE

Sydney Caparaso[1], Adan Redwine[1], and Rebecca Wachs[1]

[1]Department of Biological Systems Engineering, University of Nebraska-Lincoln

Peripheral chronic pain is the leading cause of disease and disability worldwide; however, there is a lack of clinically effective permanent solutions. Animal models and molecular probing are the current methods for identifying novel pain therapeutics. However, complications with clinical translation highlight a need for novel screening models. Phenotypic screening platforms rely on modeling and assessing high-level cellular function and are promising tools for chronic pain and other pathologies with complex mechanisms. A key feature of peripheral chronic pain patients is innervation of painful nerves, termed nociceptors, into inflamed joints where continuous exposure to inflammatory mediators increases excitability and enhances pain. Nociceptors extend from dorsal root ganglion (DRG) cell bodies, which are located outside the spinal cord. Nociceptor phenotype is characterized by level of excitability, where painful nociceptors display lowered thresholds for ion channel firing. Measuring nociceptor excitability in response to a therapeutic would provide relevant information about the transduction of signals and treatment efficacy. This research aims to 1) develop a physiologically relevant in vitro DRG culture model 2) use fluorescent calcium imaging as a phenotypic screening platform to assess nociceptor excitability. We engineered a device that

maintains key anatomical features of in vivo DRGs including isolation between distal nociceptors and ganglion cell bodies, presence of native non-neuronal support cells, and a three-dimensional environment of relevant stiffness. We developed a platform to screen nociceptor phenotype through measuring fluorescent changes in response to capsaicin, a nociceptive agonist. Additional experiments are underway to validate that theoretical model predictions of fluidic isolation are maintained over time and to validate calcium imaging with DRGs embedded in our devices. Future work includes using our platform as a tool to study nociceptor excitability relevant to peripheral chronic pain states by mimicking the degenerative inflammatory environment in the outer compartments of the device. The goal of this research is to use this platform to probe changes in excitability of various disease microenvironments with the goal of screening therapeutics to improve clinical translation.

MMoD Trainee Abstracts

Afternoon Session #1

DESIGN OF SYNTHETIC RECEPTOR ACTIVITY MODIFYING PROTEINS AS CHEMICAL PROBES TO STUDY G PROTEIN – COUPLED RECEPTORS

Noelle Waltenburg[1], James W. Checco[1], and Robert Powers[1]

[1]Department of Chemistry, University of Nebraska-Lincoln

Receptor-activity modifying proteins (RAMPs) are small transmembrane proteins associated with eleven known class B G protein-coupled receptors (GPCRs) that modulate the activation of signaling pathways within the cell.[1] These RAMPs aid in receptor trafficking, ligand recognition, and changes in the GPCR signaling pathways. There are three known RAMPs linked with ligand binding and receptor activation: RAMP1, associated with calcitonin gene related peptide; RAMP2 associated with adrenomedullin; and RAMP3 associated with adrenomedullin.[2] These proteins are composed of three domains: a three-helix extracellular domain (ECD), transmembrane domain (TM), and an inner membrane domain (IM). Previous literature has shown that when cells are co-transfected with calcitonin-like receptor (CLR) and truncated regions of RAMP ECD, a 4000-fold activity decrease was observed when compared to endogenous RAMP+CLR.[3] With *cell-based* studies showing limited activity of RAMP ECD, we hypothesize new *in vitro* studies could be completed to determine the bifunctionality of the association of RAMP to class B GPCRs. To assess if CLR modulation occurs when co-expressed with the three-helix RAMP ECD, cyclic AMP production would be monitored upon ligand binding. In addition, analogues of both RAMP1 and RAMP2 three-helix ECD composed of truncated regions of their endogenous ECDs would be evaluated to further test for activity and ligand specificity. Future synthetic designs include a lipid tail to the N- or C- terminus of these truncated proteins to fixate to the exterior cell membrane. The optimized method for these synthetic RAMPS can be used to evaluate additional unidentified GPCRs.

DEVELOPMENT OF CARBON NANOTUBE PLATFORMS FOR EXTRACELLULAR NITRIC OXIDE QUANTIFICATION IN VITRO

Ivon Acosta Ramirez[1], Carley Conover[1], Becca Francis[1], and Nicole Iverson[1]

[1]Department of Biological Systems Engineering, University of Nebraska-Lincoln

Nitric oxide (NO) is a ubiquitous messenger molecule that acts in both physiological and pathological signaling pathways depending on its local concentration and the duration of the expression. Carcinogenesis is largely dictated by the cellular chemical microenvironment. Molecular events underlying tumor progression are unclear, specifically for NO. There is a debatable correlation between high NO levels and its role in promoting or inhibiting cancer. The contradictory effect is related to the difficulty of detecting NO, a reactive molecule with a half-life shorter than one millisecond in blood. Current NO sensing methods for biological systems present limitations such as indirect NO detection (either upstream or downstream components), photobleaching, a lack of spatial detection (providing information for the entire solution or only one specific point), and/or a lack of biocompatibility. The lack of accuracy in the methods represents a relevant degree of uncertainty about the real NO effect on cancer progression. However, the ability of a single walled carbon nanotube (SWNT) platform, previously developed in the Iverson lab, to detect NO in a temporal and spatial manner will provide unique extracellular information about NO in cancer. The platform is synthesized through multiple non-sterile steps, making the platform unsuitable for cell culture. This research aims to create a sterile platform development process and characterize its functionality for in vitro applications in terms of biocompatibility and fluorescence emission. Each step of the platform building process was adapted and developed in sterile environments, requiring the development of specially made instruments and techniques. The platform was assessed under cytotoxicity, proliferation, and morphology parameters, and compared with plain glass slides and cell culture treated plates. Fluorescence data were collected on a custom-built hyperspectral microscope located within the Iverson Laboratory. The research was initially performed with a triple-negative breast cancer line (MDA MB 231), after post-optimization other breast cell lines will be used, during which the NO expression of various cell types will be quantified and compared. Extending NO knowledge in breast cancer progression will be the baseline for optimizing the prevention, detection, and future treatments.

MMoD Trainee Abstracts

Afternoon Session Set 2

DEVELOPMENT OF A DJ-1 AFFINITY MICROCOLUMN UTILIZING PROTEIN ENTRAPMENT

Jacob Jones[1], David S. Hage[1], Mark Wilson[2]

[1]Department of Chemistry, University of Nebraska-Lincoln

[2]Department of Biochemistry, University of Nebraska-Lincoln

Parkinson's disease (PD) is a debilitating neurodegenerative disease characterized by motor dysfunction, driven by dopaminergic neuronal cell death in the *substantia nigra*. Treatment for PD is limited to improving the function of surviving neurons. DJ-1 is a protein involved in responding to oxidative stress and has been closely linked with PD. DJ-1 is believed to protect neurons through a variety of functions, including gene regulation, protein chaperoning, and enzymatic activity. DJ-1 is of great interest as a target for therapeutics against PD and for broader investigations into PD. The ability to rapidly and accurately evaluate binding by small molecules to DJ-1 would greatly aid in the development of therapeutics and in more broadly probing DJ-1's role in PD. High performance affinity chromatography (HPAC) is being developed as a means to examine such interactions. Non-covalent protein entrapment is being used as an immobilization technique in this method to place DJ-1 and model proteins within HPAC columns for this work. This research seeks to 1.) develop DJ-1 affinity microcolumns utilizing protein entrapment, and 2.) utilize these microcolumns to examine a group of small molecule candidates for binding to DJ-1. We have recently developed a procedure for entrapping proteins within HPLC grade silica using mildly oxidized glycogen as a capping agent, which can be used to construct a DJ-1 affinity microcolumn. This column will then be used to evaluate a group of small molecule candidates that have been designed using artificial intelligence. Binders will be identified and their binding parameters determined. Future work will focus on screening larger groups of drug candidates, as well as endogenous small molecule ligands. This work is expected to lead to the development of an approach that can rapidly screen possible binding agents for DJ-1 for the development of new PD therapeutics.

FUNCTIONAL GENOMICS OF PHOSPHATIDYLCHOLINE BIOSYNTHESIS IN *SACCHAROMYCES CEREVISIAE*.

Amanda Maliva [1], Wayne Riekhof[1]

[1]School of Biological Sciences, University of Nebraska-Lincoln

Phosphatidylcholine (PtdCho) is the most abundant phospholipid in most eukaryotic membranes, and the cell must regulate its synthesis in order to maintain membrane integrity and biophysical properties. The genes encoding enzymes of PtdCho biosynthesis are largely known, and a great deal is understood about their regulation (Carman & Han, 2009) however a complete and precise

description of molecular mechanisms of the regulation of PtdCho and other lipid biosynthesis pathways remain incomplete. The acyltransferase pathway is responsible for converting lysophosphatidylcholine (LPC) into PtdCho within the cell. Following the transport of LPC into the cell via the P-type ATPase complex LEM3 & DNF2, the ER-localized enzyme ale1 must acylate it to form an active PtdCho molecule. In order to identify potential transporters and regulators that interact in the trafficking of LPC from the plasma membrane to the location of ALE1, we will perform a genetic screen on the Saccharomyces cerevisiae knockout mutant collection using extracellular LPC and the PtdEtn methyltransferase inhibitor 2- hydroxyethylhydrazine (2-HEH; (Jun-Ichi & Satoshl, 1983). 2-HEH functions by selectively targeting the methylation pathway through the inhibition of both methylation enzymes, PEM1 and PEM2. Our objective is to identify any mutants that are unable to grow in the presence of HEH and at a concentration of LPC that normally overcomes cell susceptibility to 2-HEH. Through the inhibition of the methylation pathway via 2-HEH and the lack of choline addition into the media, which would supplement the Kennedy pathway, the cells are entirely dependent on the acyltransferase pathway as the sole mean for PtdCho biosynthesis. This research will further the knowledge surrounding genetic involvement in PtdCho biosynthesis, and has potential applications in the creation of antifungal drug targets and treatment of pathogenic fungi.

A SHARED ANCHOR ON PRIMARY SIGMA FACTOR SIGA BY THE WHIB-LIKE PROTEINS

Daisy Guiza Beltran[1], Magdaléna Horová[1], Huey-Xian Wong[1], Li-Mei Zhang[1,2]

[1]Department of Biochemistry and Redox Biology, University of Nebraska-Lincoln

[2]Nebraska Center of Integrated Biomolecular Communication, University of Nebraska-Lincoln

WhiB-like (Wbl) proteins are a unique group of iron-sulfur cluster ([4Fe4S])-containing transcription factors exclusive to actinobacteria. They play crucial roles in the virulence, survival, and propagation of Mycobacterium tuberculosis (Mtb), the causative agent of tuberculosis. Seven Wbl proteins (WhiB1-WhiB7) are found in Mtb with diverse regulatory roles. All Mtb Wbl proteins except for WhiB5 have been shown to interact with the conserved region 4 of the primary sigma factor ($SigAr_4$) in RNA polymerase holoenzyme. Our recent structural and biochemical analyses indicate that two Wbl proteins, WhiB1 and WhiB7, bind to the same site on $SigAr_4$ unexpectedly through tight hydrophobic interactions involving several conserved aromatic residues of the Wbl proteins and His516 of $SigAr_4$. Substitution of these aromatic residues in either WhiB1 or WhiB7 at the molecular interface abolishes their binding to $SigAr_4$. Here, we hypothesize that all Mtb Wbl proteins share a similar molecular interface when in complex with $SigAr_4$, based on the primary sequence analysis and structural modeling. Using the site-directed mutagenesis and the in vitro protein-protein interaction assays, we confirm that all Mtb Wbl proteins, including WhiB5, bind to the same site on SigA centered on His516, and the conserved aromatic residues within the Fe-S cluster binding pocket are required for SigA binding. The results from this study will offer insights into how the Wbl proteins are utilized in Mtb to orchestra gene expression in response to environmental cues in the host.

Poster Presentation

1. The Gut Microbiota Modulates the Severity of Experimental Autoimmune Myocarditis.

Xu Shi[1], Paul Velander[1], Robert Schmaltz[1], Jeff Price[1], Amanda Ramer-Tait[1]

[1]University of Nebraska-Lincoln, Lincoln, NE.

2. Dietary Fiber from Sorghum Protects Mice Harboring Human Gut Microbiotas Against Colitis.

A.F. Juritsch1, S. Al-Hamedi2, M.A. Cade3, Q. Yang1, K. Beede1, R. Schmaltz1, J. Price1, D. Rose1, S. Sattler4, A. Benson1,5, A.E. Ramer-Tait1,5.

A.F. Juritsch[1], S. Al-Hamedi[2], M.A. Cade[3], Q. Yang[1], K. Beede[1], R. Schmaltz[1], J. Price[1], D. Rose[1], S. Sattler[4], A. Benson[1,5], A.E. Ramer-Tait[1,5].
[1] Department of Food Science and Technology, University of Nebraska-Lincoln; [2] Department of Biochemistry, University of Nebraska-Lincoln; [3] Department of Biological Sciences, University of Nebraska-Lincoln; [4] Wheat, Sorghum and Forage Research Unit, United States Department of Agriculture – Agriculture Research Service (USDA-ARS), Lincoln, Nebraska; [5] Nebraska Food for Health Center, Lincoln, Nebraska

3) Proteomics & Metabolomics Facility: Nebraska Center for Biotechnology.

Sophie Alvarez[1], Mike Naldrett[1], Anne Fischer[1], Lori Loucks[1.]

[1]University of Nebraska-Lincoln, Lincoln, NE.

4) Assessment of Commensal E. coli Outer Membrane Vesicles for Application in a Bacterial-Derived Oral Gene Delivery System.

Kari Heck [1], Amanda E. Ramer-Tait [2], Angela K. Pannier [1]

[1]Department of Biological Systems Engineering – University of Nebraska-Lincoln, Lincoln, NE.
[2]Department of Food Science and Technology – University of Nebraska-Lincoln, Lincoln, NE.

5) Optimization of a mouse model to investigate the effects of Bifidobacterium infantis on the severity of peanut allergy.

rgan Cade[1], Tasneem Ali[1], Anthony Juritsch[2], Kristin Beede[2], Robert Schmaltz[2], Bethany Henrick[3], Amanda Ramer-Tait[2]

[1]School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE.
[2]Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, NE. [3]Evolve Biosystems, Davis, CA.

6) Identification, Biosynthetic Mechanism and Biological Function of Lysochelin in Lysobacter.

Amanda Miller[1], Yongbiao Zheng[1], Shanren Li[1], Richard Bell[1], Eric Dodds[1], and Liangcheng Du[1]
[1]Department of Chemistry, University of Nebraska-Lincoln, Lincoln, NE.

7) Characterization of a pyrroline-5-carboxylate reductase 1 (PYCR1) variant found in cancer.

Oseeyi Daudu[1], Lu Zhang[1], and Donald Becker[1]

[1]Department of Biochemistry, Redox Biology Center, University of Nebraska-Lincoln, NE.

8) Understanding the Stabilin receptor mediated endosomal escape mechanism of PS-ASOs.

Ekta Pandey[1], Edward Harris[1]

[1]University of Nebraska-Lincoln, Lincoln, NE.

9) Exploration of cysteine modifications in Δ1-pyrroline-5-carboxylate reductase 2 (PYCR2).

Tyrell Rossman[1], Sagar Patel[1], Donald Becker[1]

[1]University of Nebraska-Lincoln, Lincoln, NE.

10) The structure basis for natural competence in Acinetbacter

Yafan Yu[1], Kurt Piepenbrink[1,2]

[1]Department of Biochemistry, University of Nebraska-Lincoln, Lincoln, NE.
[2]Department of Food Science, University of Nebraska-Lincoln, Lincoln, NE.

11) LACTB deletion alters mitochondrial metabolism and expression of the MICOS complex proteins.

Gunjan Purohit[1], Oleh Kahlimonchuk[1,2]

[1]Department of Biochemistry, University of Nebraska-Lincoln, Lincoln, NE.
[2]Nebraska Redox Biology Center, University of Nebraska-Lincoln, Lincoln, NE.

12) Functional characterization of mitochondrial proteins Imo32 and Ykro70w in yeast Saccharomyces cerevisiae.

Ganapathi Kandasamy[1], Iryna Bohovych[1], and Oleh Khalimonchuk[1]

[1]Department of Biochemistry, University of Nebraska-Lincoln, Lincoln, NE.

13) A new long noncoding RNA regulates stress response in endothelial cells

Matthew Moran[1], Jiyao Zhu[1], Xiao Cheng[1], and Xinghui Sun[1,2]

[1]Department of Biochemistry, University of Nebraska-Lincoln, Lincoln, NE.
[2]Nebraska Center for the Prevention of Obesity Diseases through Dietary Molecules, University of Nebraska-Lincoln, Lincoln, NE

14) Genetic interactome of a yeast mitochondrial K+ homeostasis factor Mdm38/LETM1

Iryna Bohovych[1], Oleh Khalimonchuk[1,2,3]

[1]Department of Biochemistry, University of Nebraska-Lincoln, NE
[2]Nebraska Redox Biology Center, University of Nebraska-Lincoln, Lincoln, NE.
[3]Fred & Pamela Buffett Cancer Center, University of Nebraska Medical Center, Omaha, NE.

15) Matrin-3 deficiency aggravates hepatic steatosis and acute phase response

Xiao Cheng[1], Vijaya Bhaskar Baki[1], Matthew Moran[1], and Xinghui Sun[1]

[1]Department of Biochemistry, University of Nebraska-Lincoln, Lincoln, NE.

16) Exploring Interactions between Primary Hepatocytes and Non-Parenchymal Cells on Physiological and Pathological Liver Stiffness

Vaishaali Natarajan[1], Youra Moeun[1], and Srivatsan Kidambi[1,2]

[1]Department of Chemical and Biomolecular Engineering, University of Nebraska-Lincoln, Lincoln, NE.
[2]Fred & Pamela Buffett Cancer Center, University of Nebraska Medical Center, Omaha, NE.

17) Substrate stiffness regulates microglial phenotype and function

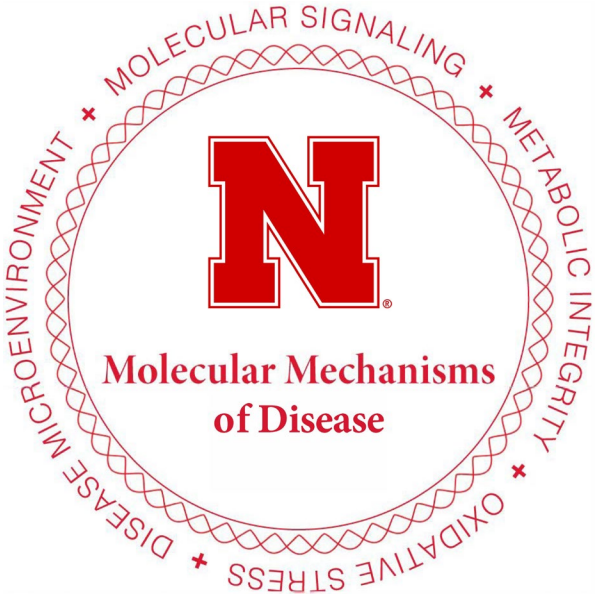
Timothy Hackett[1], Srivatsan Kidambi[2]

[1]Department of Biochemistry, University of Nebraska - Lincoln, Lincoln, NE
[2]Department of Chemical and Biomolecular Engineering, University of Nebraska-Lincoln, Lincoln, NE.

18) Recognition of extracellular DNA by type IV pili promotes biofilm formation by Clostridioides difficile

Leslie A. Ronish[1], Ben Sidner[2], Yafan Yu[1,2], Kurt H. Piepenbrink[1,2,3]

[1]Department of Biochemistry, University of Nebraska-Lincoln, Lincoln, NE.
[2]Department of Food Science and Technology, University of Nebraska-Lincoln, Lincoln, NE.
[3]Department of Chemistry, University of Nebraska-Lincoln, Lincoln, NE.



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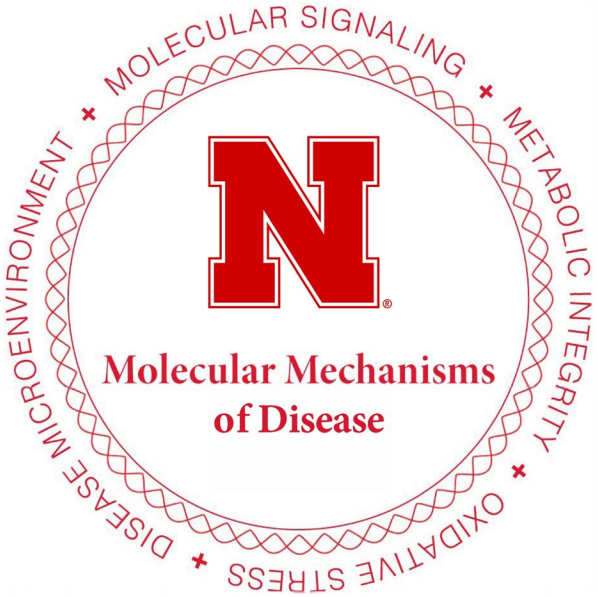
Participating Departments

Animal Science, Biochemistry, Biological Systems Engineering, Chemical and Biomolecular Engineering, Chemistry, Food Science and Technology, and the School of Biological Sciences



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