Biocat Spring Symposium – Friday, May 8, 2026

Big Ten Theater, Iowa Memorial Union (348 IMU)

	Time	Speaker	Title	Advisor	Program/Department
1	8:00-8:20	Joseph Correa	Formulating Epinephrine-loaded Dissolving Microneedles for Acute Anaphylaxis	Nicole Brogden	Pharmaceutics
2	8:20-8:40	Sarah Jordan	The Molecular Dance of Translesion Synthesis	Todd Washington	Biochemistry
3	8:40-9:00	Elizabeth Walker	Developing Next-Generation PHA Bioplastics: Expanding the *Cupriavidus necator* Synthetic Biology Toolkit Through Strain Diversification, Promoter Engineering, and CRISPR-Cas9 Recombineering	Hyeongmin Seo	Chem. and Biochem. Engineering
4	9:00-9:20	Sarah Torrence	Investigating the Role of mTORC1 in the Development of Dilated Cardiomyopathy in Conditional PHB1 Knockdown Model	Ethan Anderson	Drug Discovery and Exp. Therapeutics
Break: 9:20-9:40					
5	9:40-10:00	Zoe Kramin	Predicting Anaerobic Co-digestion Process Health with Novel Stability Indicators	Craig Just	Civil and Environmental Engineering
6	10:00-10:20	Sophie Granger	Dynamic Mechanisms of Allosteric Regulation in Glutamate Racemase: Implications for Drug Design	Ashley & Maria Spies	Molecular Medicine
7	10:20-10:40	Sourdip Sinha	The ATAC Histone Acetyltransferase Complex Drives Oncogenic Phenotypes in Sarcomas	Munir Tanas	Pathology
Break: 10:40-11:00					
8	11:00-11:20	Atonu Chakrabortty	Mapping the Transition of ABC Transporter Responses from Initial Drug Tolerance to Stable Chemoresistance in Ovarian Cancer	Jared McLendon	Drug Discovery and Exp. Therapeutics
9	11:20-11:40	Emily Jansen	Long-read Metagenomic Characterization of a Novel 1,4-Dioxane Degrading Mixed Culture	Tim Mattes	Civil and Environmental Engineering
10	11:40-12:00	Luke Handlos	Structural Dynamics of DNA Damage Tolerance: Rad6-Rad18 Complex Assembly and TLS Polymerase Translocation	Todd Washington	Biochemistry
11	12:00-12:20	Sam Yu	Epigenetic Approaches to Targeting PI3K and Hippo Pathways in Sarcomas	Munir Tanas	Pathology

Light refreshments will be provided.

Formulating Epinephrine-loaded Dissolving Microneedles for Acute Anaphylaxis

Joseph Correa and Nicole Brogden, Department of Pharmaceutical Sciences and Experimental Therapeutics

Anaphylaxis is a potentially life-threatening allergic response with symptom onset in just minutes. Epinephrine autoinjectors are typical first-line treatments for acute anaphylaxis that reach peak serum concentrations within 10 minutes. However, challenges with these systems can lower patient compliance and require multiple doses before further medical help can arrive. To overcome issues with pain, needle phobia, improper technique, and rapid drug clearance, we are developing easily applied dissolving microneedle arrays with biphasic transdermal delivery of epinephrine. When subjected to axial compression to simulate insertion into the skin, the arrays withstood up to nearly 20 N of force, demonstrating robust mechanical strength. In vitro tests revealed rapid epinephrine release from gels within 5 minutes, sustaining for up to 30 minutes. This approach shows potential in providing a fast initial response comparable to currently available products and continued delivery to avoid the need for additional doses while awaiting advanced medical care.

The Molecular Dance of Translesion Synthesis

Sarah Jordan, and Todd Washington, Biochemistry and Molecular Biology

DNA damage is a cause of genome instability, which is a hallmark of cancer and aging. Cells have evolved DNA damage bypass mechanisms to reduce genome instability. One of these mechanisms is translesion synthesis (TLS), which is signaled through the monoubiquitylation of PCNA by Rad6-Rad18. Once initiated, TLS utilizes non-classical polymerases, such as polymerase eta (η), to bypass DNA damage. While the activities of these polymerases and their interacting partners are understood, how they coordinate to undergo TLS is unknown.

Rad6-Rad18 interacts with DNA polymerase η, which forms one of two complexes thought to be required for TLS. This talk will focus on the structural and mechanistic basis of the first complex, composed of Rad6-Rad18 and DNA Polymerase η.

Sequential Microbial Upcycling of Polycotton Blends: Transforming Recalcitrant Textile Waste into High-Value Polyhydroxybutyrate

Elizabeth Walker and Hyeongmin Seo, Department of Chemical and Biochemical Engineering,

Global textile waste represents a critical environmental challenge, driven by the prevalence of complex synthetic and natural fiber blends contributing to the plastic waste crisis. These heterogenous materials are inherently resistant to conventional mechanical and chemical recycling due to their mixed composition, high crystallinity, and synthetic dyes that can act as enzymatic inhibitors.

This study proposes a sequential bioprocessing platform for the concurrent depolymerization and upcycling of polycotton blends. By utilizing an engineered thermophilic bacterium (*Clostridium thermocellum*) to depolymerize both fiber fractions, the cellulose fraction is selectively metabolized leaving the free polyester monomer fraction for further processing. Subsequently, the resulting monomers are used as a feedstock for an engineered mesophilic bacterium (*Cupriavidus necator*) for the synthesis of polyhydroxybutyrate (PHB). This approach establishes a closed-loop upcycling process for converting recalcitrant textile waste into a high-value, biodegradable alternative to petroleum-based plastics.

Investigating the Role of mTORC1 in the Development of Dilated Cardiomyopathy in Conditional PHB1 Knockdown Model

S. Torrence[1], R. Huo[1], K. Berns[1], R. Crawford[1], B. Chen[2], Q. Shi[2], B. Darbro[3], A. Alowaisi[1], J. Mahoney[1], L.-S. Song[2,4,5], Ethan J. Anderson[1,4,5]

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Prohibitins 1 and 2 (PHB1/2) are ubiquitously expressed lipid raft proteins that form a multimeric ring supercomplex in cellular membranes where they regulate numerous processes including cellular metabolism and signaling. The role of the PHBs in maintaining homeostasis and metabolism in the heart is not well understood. To address this question, we created a cardiomyocyte-specific PHB1 knockdown (cPHB1^{ko}) mouse model. Cardiac ejection fraction (EF) in the cPHB1^{ko} mice progressively declined and by 12 weeks post-tamoxifen, mice had developed severe dilated cardiomyopathy. Additionally, there was substantial up-regulation of mammalian target of rapamycin complex 1 (mTORC1) activity in cPHB1^{ko} mice. Treatment with mTORC1 inhibitor rapamycin at 2 mg/kg every other day mitigated hypertrophy and delayed the decline in EF in female, but not male cPHB1^{ko} mice. These findings demonstrate that the PHB complex plays a critical role in maintaining cardiomyocyte function and metabolism, and that this role may be sex-specific.

Predicting Anaerobic Co-digestion Process Health with Novel Stability Indicators

Zoe Kramin and Craig Just, Department of Civil and Environmental Engineering

Anaerobic co-digestion is a strategy for organic waste management resulting in renewable energy generation, yet maximized efficiency is limited by instability and insufficient process control. Conventional monitoring relies on intermittent digestate sampling, leaving operators without real-time insight into changing conditions. This work demonstrates that diffuse reflectance spectroscopy, paired with partial least squares regression, can rapidly predict key physicochemical parameters in full-scale anaerobic co-digestion systems. Downsampling analysis shows that robust models can be developed with relatively few training samples, reducing implementation costs for utilities. Additionally, preliminary data indicate that shifts in *Methanosarcina barkeri* and *Methanothrix soehngenii* gene copy numbers may serve as early-warning indicators of digester stability. Together, these advances integrate molecular and spectroscopic approaches to enable informed diagnostics and support more resilient anaerobic co-digestion operations.

Dynamic Mechanisms of Allosteric Regulation in *H. Pylori* Glutamate Racemase: Implications for Drug Design

Sophie L. Granger, Department of Pharmaceutical Sciences and Experimental Therapeutics
Lilly A. Duff, Department of Pharmaceutical Sciences and Experimental Therapeutics
Jonah Pascal Propp, Department of Pharmaceutical Sciences and Experimental Therapeutics
Maria Spies, Department of Biochemistry and Molecular Biology
and M. Ashley Spies, Department of Pharmaceutical Sciences and Experimental Therapeutics

Cryptic allosteric pockets in flexible enzymes remain difficult to mechanistically understand and exploit in effective drug design. In developing selective antibiotics against *Helicobacter pylori* while sparing the healthy gut microbiome, we investigated HpMurI, a cofactor-independent glutamate racemase essential for peptidoglycan biosynthesis whose catalysis depends on conformational flexibility. Previous studies have identified selective allosteric inhibitors targeting multiple pockets, including both the monomer–monomer interface and a distal cryptic allosteric site. To establish the first biophysical signatures of these mechanisms, we combined correlated optical tweezers and fluorescence microscopy (CTFM) with mass photometry (MP). CTFM showed that native substrate binding strongly stabilizes HpMurI dimers, while allosteric inhibitor binding collapses rupture forces toward the apo-like regime. MP further revealed altered monomer–dimer equilibria upon inhibitor binding, indicating that allosteric inhibition reshapes the HpMurI conformational ensemble in solution. Together, these findings establish a direct biophysical link between small-molecule binding and HpMurI conformational flexibility.

The ATAC Histone Acetyltransferase Complex Drives Oncogenic Phenotypes in Sarcomas

Souradip Sinha[1,2,3], Krishnendu Ghosh[1], Gillian DeWane[1], Ali Khan[1,3,4], Samuel Yu[1,3,4], Yuliia Drebot[1], Keith Garcia[1,4], Nicholas Scalora[1,2], Munir Tanas[1,2,3,4]

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Sarcomas are genetically diverse cancers originating from mesenchymal tissues, and most lack effective targeted therapies. In epithelioid hemangioendothelioma (EHE), TAZ-CAMTA1 and YAP-TFE3 fusion proteins recruit the ATAC histone acetyltransferase (HAT) complex to remodel chromatin and drive oncogenic transformation.

YEATS2 and ZZZ3, key scaffolds of the ATAC complex, are overexpressed across sarcomas. We therefore investigated ATAC complex function in both EHE and fusion-negative sarcomas. siRNA-mediated knockdown of YEATS2 or ZZZ3 reduced histone H3K9 acetylation in multiple sarcoma cell lines. In SKLMS-1 and HT1080 cells, shRNA-mediated knockdown of YEATS2 or ZZZ3 decreased H3K9 acetylation, 2D proliferation, and anchorage-independent growth.

Proximity labeling and proteomics identified E2F3 as a transcription factor that interacts with the ATAC complex, suggesting a mechanism for ATAC recruitment in fusion-negative sarcomas.

Ongoing studies are evaluating pharmacological inhibition of the ATAC complex in vitro and investigating how distinct domains of YEATS2 and ZZZ3 regulate ATAC complex localization and catalytic activity.

Mapping the Transition of ABC Transporter Responses from Initial Drug Tolerance to Stable Chemoresistance in Ovarian Cancer

Atonu Chakrabortty, Kaleb A Feia, Melissa Fath, Jill Kolesar, Jared M McLendon

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Time-dependent regulation of the ABC transporter network reveals distinct cisplatin- and paclitaxel-specific resistance mechanisms in ovarian carcinoma. We tested whether chemoresistance arises from coordinated remodeling of multiple ABC transporters rather than dependence on ABCB1 alone. Ovarian cancer cell lines (OVCAR3, OVCAR8, OV-90, TOV-21G) were profiled for drug sensitivity using 72-hour IC_{50} measurements and for transporter expression via qRT-PCR following 48-hour drug exposure and in chronically resistant derivatives. Paclitaxel induced coordinated upregulation, including ABCB1 (approximately 4–7-fold), ABCG2 (approximately 2–5-fold), and TAP1 (approximately 3–5-fold). In contrast, cisplatin triggered a distinct response, with strong ABCB1 induction (approximately 8–12-fold) and moderate changes in ABCA family members, particularly in OV-90 cells. These transcriptional shifts persisted in resistant populations. Complementary RNA-seq analyses from The Cancer Genome Atlas and GEO datasets revealed widespread ABC transporter dysregulation in chemoresistant tumors, supporting resistance as a dynamic, drug-specific network adaptation.

Long-read Metagenomic Characterization of a Novel 1,4-Dioxane Degrading Mixed Culture

Emily Jansen and Tim Mattes, Department of Civil and Environmental Engineering

1,4-Dioxane is a persistent groundwater contaminant requiring cost-effective remediation. While *Rhodococcus ruber* 219 effectively degrades dioxane, its thiamine auxotrophy limits field application. We developed a syntrophic mixed culture combining *R. ruber* 219 with VB1-producing bacteria to achieve self-sustained biodegradation. I utilized Oxford Nanopore long-read metagenomic sequencing to characterize this consortium. Binning yielded high-quality metagenome-assembled genomes (MAGs) for *Rhodococcus*, *Cupriavidus*, *Microbacterium*, and *Rhizobium*. Functional annotation revealed that *R. ruber* 219 possesses two distinct monooxygenase operons (*thmABCD* and *prmABCD*), potentially enhancing degradation capacity. Crucially, metagenomic analysis uncovered a vital cooperative relationship: *Cupriavidus* has a key thiamine biosynthesis gene (*thiC*) that is absent in *R. ruber*. This metabolic syntrophy has enabled the culture to degrade 500 ppm dioxane to <0.05 ppb without VB1 supplementation. This work highlights a promising engineered consortium for 1,4-dioxane biodegradation and shows how long-read sequencing can shed light on the complex interdependencies of bioremediation as a whole.

Structural Dynamics of DNA Damage Tolerance: Rad6-Rad18 Complex Assembly and TLS Polymerase Translocation

Luke Handlos and Todd Washington, Department of Biochemistry and Molecular Biology

Translesion synthesis (TLS) is a DNA damage tolerance pathway that utilizes TLS polymerases recruited to Rad6-Rad18-dependent monoubiquitylated PCNA to synthesize through DNA lesions. There are unresolved questions in this pathway. My research addresses two of these questions. First, how does Rad6-Rad18 ubiquitin ligase complex assemble in solution? To address this, small angle X-ray scattering (SAXS) and Brownian dynamics (BD) simulations were performed to define its structure and conformational flexibility. Second, what conformational changes do TLS polymerases undergo during DNA translocation, a process poorly understood in most polymerases? To investigate this, steered molecular dynamics simulations that drive Pol η-DNA complexes from pre- to post-translocation states were performed, generating translocation-related conformational change predictions. I have currently identified several possible residues that may be crucial to DNA translocation, which I plan to assess further with umbrella sampling and site-directed mutagenesis. Overall, my research advances our mechanistic understanding of TLS initiation and DNA translocation.

Epigenetic Approaches to Targeting PI3K and Hippo Pathways in Sarcomas.

Samuel Yu and Munir Tanas, Department of Pathology, Cancer Biology Graduate Program

Sarcomas are a heterogeneous group of cancers that arise in soft tissues and bone, with few effective targeted therapies. One frequently dysregulated pathway in sarcomas is PI3K signaling, due to PTEN loss in 30–60% of patient samples. PI3K activation promotes tumor growth via the Akt–mTORC1 axis and parallel PI3K–TAZ/YAP–TEAD axis. TAZ/YAP are transcriptional co-activators that drive oncogenic gene expression and are regulated by the Hippo pathway, consisting of the MST1/2, MAP4K, and LATS1/2 kinases. In sarcomas, loss of Hippo kinases occurs in 30–50% of samples, leading to aberrant TAZ/YAP activation. Epigenetic silencing of MST1/2 and MAP4Ks via histone deacetylation account for a subset of these cases. Preliminary data show HDAC inhibition with romidepsin restores MST1 and MAP4K4 expression while reducing TAZ/YAP transcriptional activity. These findings provide a rationale for further investigation into dual-pathway inhibition as a therapeutic strategy, including mechanistic studies and *in vivo* validation.