Member Education - Biochemistry

Thursday Oct. 16, 2025 125 Lakeshore Room – University Center		
1:25 - 1:30	Welcome – Caroline Szczepanski	
1:30 to 2:00	**Neil White** CENTRAL MICHIGAN UNIVERSITY	Uncovering Elemental Ion Biology with Riboswitches
2:00 to 2:30	**Issac Angera** NOTRE DAME	b-Arch Peptide Macrocycles as Structural and Functional Mimics of Pathological tau
2:30 to 3:00	**Tami Sivy** SVSU SAGINAW VALLEY STATE UNIVERSITY	Using Molecular Methods in an Undergraduate Laboratory to Measure Microbial Contamination in Freshwater
3:00 - 3:10	Break	
3:15 to 3:55	**Panel**	Discussion: The Path to a Career *Speakers: Alyssa Fielitz (Dow), Neil White (CMU), Isaac Angera (ND), Tami Sivy (SVSU)*

Uncovering Elemental Ion Biology with Riboswitches

Neil A. White
Assistant Professor Chemistry and Biochemistry
Central Michigan University

Riboswitches are structured noncoding RNA devices (aptamers) that selectively bind a diverse set of ligands, such as metabolites or elemental ions, and regulate gene expression. They are typically found in the 5' UTRs of bacterial genes. We have recently validated the nhaA-I, nhaA-II and DUF1646 motif RNAs as riboswitch classes that selectively bind Na+ or Li+. The Na+ riboswitch is only the second device, in all domains of

life, known to bind Na+ and regulate gene expression. The Li+ riboswitch represents the first biological aptamer for Li+. Thus, RNA plays a major role in elemental ion biology which is just starting to be appreciated.

The broad distribution of natural-occurring Li+ riboswitches makes clear that Li+ must be more often encountered than previously thought. As such, Li+ biology is understudied and underappreciated. We hypothesize that microorganisms are affected by Li+ differently, regarding toxicity and metabolism, and we will outline the research plan to elucidate those mechanisms. We expect these studies will make significant discoveries in the fundamental biology of Li+ in bacteria and have important implications for human mental health.

b-Arch peptide macrocycles as structural and functional mimics of pathological tau

Isaac J. Angera
Department of Chemistry and Biochemistry
University of Notre Dame

Tauopathies are a class of neurodegenerative disorders that include Alzheimer's disease, corticobasal degeneration, chronic traumatic encephalopathy, and many others. A predominant feature of these diseases is tau protein deposits in the brain. Tau is intrinsically disordered and involved in microtubule dynamics but can transition into pathological amyloid structure. Misfolded tau can template or "seed" the aggregation of naïve tau, leading to the prion-like transcellular spread of tau filaments. Tau protomers within filaments exhibit cross-β amyloid structure, but distinct conformations often correlate with specific diseases. An understanding of how tau misfolded conformation impacts seeding activity remains elusive. Identification of the minimal epitopes required for transcellular propagation represents a key step toward more relevant models of disease progression. Here, we present a diversity-oriented peptide macrocyclization approach toward seed-competent miniature tau, or "mini-tau", proteomimetics derived from 4R tauopathic folds. Mini-tau macrocycles exhibit several amyloid characteristics including thioflavin T binding, formation of filamentous species observed by transmission electron microscopy, and canonical β-sheet rich circular dichroic spectra. Mini-tau macrocycles induce endogenous tau inclusions in engineered biosensor cells and primary hippocampal neurons. Structural elucidation of potent seed competent mini-tau filaments by cryo-electron microscopy reveals close conformational mimicry of pathological tau misfolds. These studies aid in delineating the structural epitopes necessary for prion-like tau seeding and pave the way for the development of tauopathy specific antibodies.

Using Molecular Methods in an Undergraduate Laboratory to Measure Microbial Contamination in Freshwater

Tami Sivy
Professor of Chemistry
Saginaw Valley State University

The Saginaw Bay/River is on the USEPA's Area of Concern (AOC) list because of several Beneficial Use Impairments (BUI), one of which is beach closings. In a longstanding collaboration with the USEPA, the Michigan Department of Environment, Great Lakes, and Energy (EGLE), and local health departments, our lab has been working on better and more timely methods to determine beach closings for Saginaw Bay beaches. The historic method required an18-24 hour culture incubation, thereby delaying closing decisions. With the advent of nucleic acid analysis in past decades, we have implemented a quantitative Polymerase Chain Reaction (qPCR) method that measure the levels of a fecal indicator organism (*E. coli*) via DNA content and provides results within hours of sampling. In recent years, we have utilized digital droplet PCR (ddPCR) to undertake Microbial Source Tracking (MST), that targets DNA sequences from host microbes in a sensitive and specific manner. Using MST has allowed for steps to be taken to remediate fecal inputs to area beaches, with the hope of decreasing or eliminating beach closings. An overview of the evolution of the work of our lab, the methods, and the collaborative network that has grown from these efforts will be presented, along with some results of our studies.